SUPPLEMENTARY TABLES

Phosphatases modified by LH signaling in ovarian follicles: testing their role in regulating the NPR2 guanylyl cyclase

Jeremy R. Egbert, Ivan Silbern, Tracy F. Uliasz, Katie M. Lowther, Siu-Pok Yee, Henning Urlaub, and Laurinda A. Jaffe

Table S1. Antibodies used for western blotting.

Table S2. Statistically significant LH-induced changes in phosphopeptide intensity of proteins in rat ovarian follicles that have been reported to form complexes with PPP family phosphatase catalytic subunits, other than those listed in Table 1.

Table S1. Antibodies used for western blotting

Target	Supplier	Host species	Catalog #	Dilution	RRID
HA epitope tag (6E2)	Cell Signaling Technology	mouse	2367	1:1000	AB_10691311
Phospho-S507 PPP1R12A (P-MYPT1)[a]	Cell Signaling Technology	rabbit	3040	1:1000	AB_2168424
Phospho-S668 PPP1R12A (P-MYPT1)	Cell Signaling Technology	rabbit	3048	1:1000	AB_2168418
Phospho-S472 PPP1R12A (P-MYPT1)	Invitrogen	rabbit	PA5-114608	1:1000	AB_2899244
Phospho-T696 PPP1R12A (P-MYPT1)	Cell Signaling Technology	rabbit	5163	1:1000	AB_10691830
Phospho-T853 PPP1R12A (P-MYPT1)	Cell Signaling Technology	rabbit	4563	1:1000	AB_1031185
Total PPP2R5D	Abcam	rabbit	ab188323	1:10000	--
Phospho-S133 CREB	EMD Millipore	mouse	05-667	1:500	AB_309889
Total CREB	Cell Signaling Technology	rabbit	9197	1:1000	AB_331277
Goat-anti-mouse IgG (H+L), HRP conjugate	Advansta	goat	R-05071-500	1:20000	--
IRDye® 800CW Goat anti-Rabbit IgG Secondary Antibody	LI-COR	goat	925-32211	1:15000	AB_10956166
IRDye® 680RD Goat anti-Rabbit IgG Secondary Antibody	LI-COR	goat	926-68071	1:15000	AB_621842
IRDye® 800CW Goat anti-Mouse IgG Secondary Antibody	LI-COR	goat	926-32210	1:15000	AB_10718209

[a]The antigen used to make this antibody is 100% identical to the mouse PPP1R12A sequence, and 85% identical to the mouse PPP1R12B sequence. Therefore, this antibody would also recognize Phospho-S502 of PPP1R12B.

Table S2. Statistically significant LH-induced changes in phosphopeptide intensity of proteins in rat ovarian follicles that have been reported to form complexes with PPP family phosphatase catalytic subunits, other than those listed in Table 1. Previously published lists of validated PPP family-interacting proteins (19, 20) were used to query the phosphopeptide database for significant differences in response to LH. Multiplicity refers to either singly phosphorylated (1) or doubly phosphorylated (2) peptides. Significant increases in phosphopeptide intensity following LH treatment are above the dashed line; significant decreases in phosphopeptide intensity with LH treatment are below the dashed line.

Gene name	UniProt accession	Amino acid	Site #	Multiplicity	Phosphopeptide intensity (log_2 mean ± SEM)		Fold change
					Control	350 nM LH	
HDAC6*	A0A0G2QC41	S	59	1	14.56 ± 0.61	18.64 ± 1.07	18.0
STRN3*	E9PT82	S	239	2	15.24 ± 0.08	19.02 ± 0.18	14.6
STRN3*	E9PT82	S	255	2	15.24 ± 0.08	19.02 ± 0.18	14.6
PLCL1	F1LP62	S	19	2	17.04 ± 0.13	20.14 ± 0.06	9.1
EIF2AK2	M0RDJ3	S	212	1	18.95 ± 0.18	21.94 ± 0.26	8.5
FARP1*	F1LYQ8	S	513	2	13.80 ± 0.21	16.70 ± 0.18	7.9
FARP1*	F1LYQ8	S	517	2	13.80 ± 0.21	16.70 ± 0.18	7.9
MAP1B*	P15205	S	561	1	22.90 ± 0.12	25.52 ± 0.31	6.5
ZFYVE16	D4ADF6	S	903	2	17.57 ± 0.24	20.17 ± 0.09	6.5
ZFYVE16	D4ADF6	S	907	2	17.57 ± 0.24	20.17 ± 0.09	6.5
PHACTR4*	M0R7T1	S	159	2	18.97 ± 0.16	21.52 ± 0.12	6.2
APC*	G3V8Q9	S	2793	1	18.43 ± 0.11	20.87 ± 0.19	5.8
MKI67	D4A0Y6	S	124	1	17.98 ± 0.02	20.41 ± 0.24	5.7
PHACTR4*	M0R7T1	S	162	2	19.29 ± 0.20	21.68 ± 0.13	5.5
AKAP1	D4A9M6	S	425	1	17.01 ± 0.06	29.39 ± 0.11	5.5
APC*	G3V8Q9	S	2817	2	15.38 ± 0.33	17.67 ± 0.21	5.2
APC*	G3V8Q9	S	2829	2	15.67 ± 0.27	17.77 ± 0.18	4.6
APC*	G3V8Q9	T	2819	2	14.37 ± 0.25	16.23 ± 0.10	3.8
PLCL1	F1LP62	T	15	2	19.78 ± 0.11	21.58 ± 0.07	3.7
SH2D4A	Q6AYC8	S	51	1	18.21 ± 0.21	20.01 ± 0.39	3.7
PCIF1	D4A417	T	135	3	14.49 ± 0.25	16.29 ± 0.14	3.7
SLC9A1	P26431	S	707	2	19.21 ± 0.14	20.98 ± 0.09	3.6
AKAP11	A0A0G2JZI9	S	21	1	17.30 ± 0.37	19.05 ± 0.37	3.6
PLCL1	F1LP62	S	491	1	11.53 ± 0.35	13.23 ± 0.24	3.4
PCIF1	D4A417	T	150	2	18.36 ± 0.37	20.05 ± 0.09	3.4
PCIF1	D4A417	T	135	2	16.05 ± 0.44	17.73 ± 0.28	3.4
PCIF1	D4A417	S	140	3	16.06 ± 0.23	17.66 ± 0.16	3.2
PLCL1	F1LP62	S	17	2	19.58 ± 0.13	21.12 ± 0.07	3.1
SLC9A1	P26431	S	697	2	20.56 ± 0.11	22.09 ± 0.14	3.1
SLC9A1	P26431	S	776	2	16.38 ± 0.10	17.86 ± 0.17	3.0
MAP1B*	P15205	S	985	2	23.10 ± 0.09	24.56 ± 0.16	2.9

MAP1B*	P15205	S	988	2	23.10 ± 0.09	24.56 ± 0.16	2.9
MAP1B*	P15205	S	1454	2	17.42 ± 0.41	18.86 ± 0.14	2.9
MAP1B*	P15205	S	1465	2	17.42 ± 0.41	18.86 ± 0.14	2.9
MAP1B*	P15205	T	1262	3	19.12 ± 0.26	20.51 ± 0.06	2.8
SLC9A1	P26431	S	606	2	17.61 ± 0.02	19.00 ± 0.15	2.8
MKI67	D4A0Y6	S	336	1	19.80 ± 0.08	21.09 ± 0.22	2.6
SLC9A1	P26431	S	790	2	19.02 ± 0.07	20.22 ± 0.12	2.4
SET*	Q63945	S	28	2	18.89 ± 0.06	20.09 ± 0.11	2.4
SET*	Q63945	S	30	2	18.89 ± 0.06	20.09 ± 0.11	2.4
MAP1B*	P15205	S	1471	1	17.76 ± 0.11	18.90 ± 0.32	2.3
CASP9	Q9JHK1	S	348	2	14.65 ± 0.09	15.70 ± 0.26	2.2
CASP9	Q9JHK1	S	350	2	14.65 ± 0.09	15.70 ± 0.26	2.2
AKAP1	D4A9M6	S	101	1	18.57 ± 0.07	19.60 ± 0.31	2.2
HDAC6*	A0A0G2QC41	S	43	1	22.25 ± 0.11	19.52 ± 0.37	-6.2
HDAC6*	A0A0G2QC41	S	859	1	21.50 ± 0.12	19.27 ± 0.61	-4.4
MAP1B*	P15205	T	527	1	21.25 ± 0.23	19.10 ± 0.73	-4.2
AKAP1	D4A9M6	S	103	1	19.38 ± 0.19	17.48 ± 0.51	-3.5
PHACTR2*	A0A0G2K8Q4	T	22	1	20.29 ± 0.23	18.48 ± 0.73	-3.3
FARP1*	F1LYQ8	S	427	2	20.51 ± 0.31	18.85 ± 0.13	-3.0
FARP1*	F1LYQ8	S	435	2	20.51 ± 0.31	18.85 ± 0.13	-3.0
PHACTR2*	A0A0G2K8Q4	S	154	1	18.30 ± 0.08	16.65 ± 0.40	-3.0
MAP1B*	P15205	S	541	1	24.80 ± 0.03	23.33 ± 0.40	-2.6
APC*	G3V8Q9	S	2556	2	17.80 ± 0.18	16.35 ± 0.19	-2.6
MAP1B*	P15205	T	1959	1	17.86 ± 0.12	16.45 ± 0.35	-2.5
SLC9A1	P26431	S	790	1	22.26 ± 0.11	20.91 ± 0.47	-2.4
APC*	G3V8Q9	S	2556	2	19.43 ± 0.08	18.22 ± 0.36	-2.2

* Proteins known to regulate the cytoskeleton and/or cell motility according to the National Center for Biotechnology Information (NCBI) gene summaries.

SUPPLEMENTARY FIGURES

Phosphatases modified by LH signaling in ovarian follicles: testing their role in regulating the NPR2 guanylyl cyclase

Jeremy R. Egbert, Ivan Silbern, Tracy F. Uliasz, Katie M. Lowther, Siu-Pok Yee, Henning Urlaub, and Laurinda A. Jaffe

Figure S1. Generation of *Ppp1r12a*-S507A mice.

Figure S2. Generation of *Ppp2r5d*-S53A/S81A/S82A/S566A mice.

Figure S3. PPP1R12A mRNA is ~5 times more abundant than PPP1R12B mRNA in mouse ovarian follicles.

Figure S4. Rp-8-CPT-cAMPS effectively inhibits LH-induced PKA activation in mouse preovulatory follicles.

Supplementary Data File 1. Full table of phosphorylation changes in rat follicles ± LH (Excel)

Supplementary Data File 2. Full table of quantified protein intensities in rat follicles ± LH (Excel)

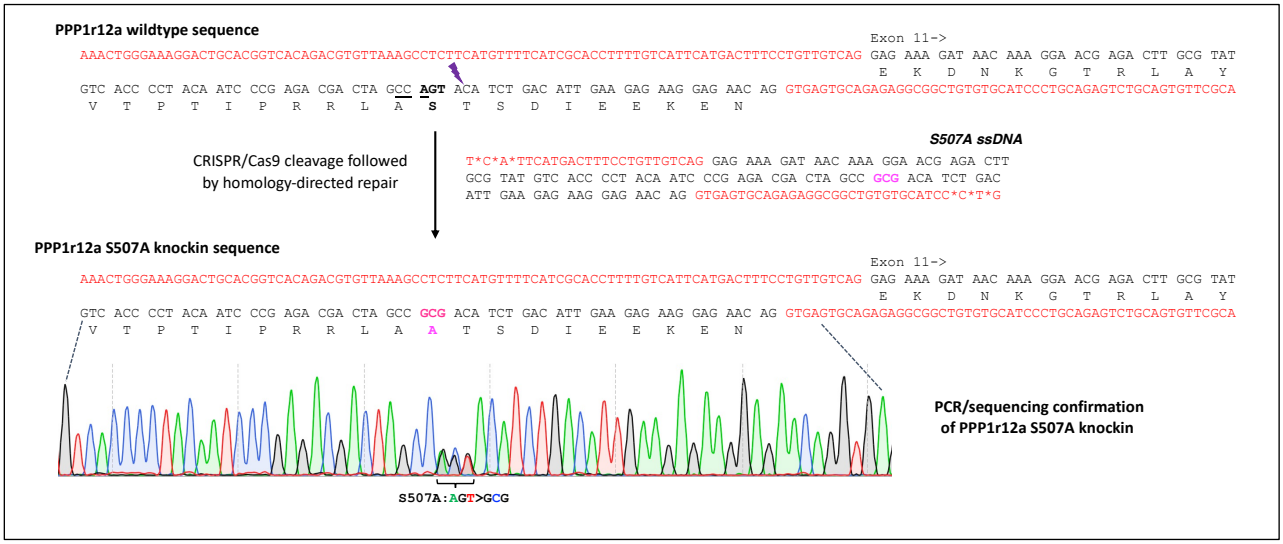
Supplementary Data File 3. Full list of plots visualizing phosphorylation changes in rat follicles (PDF)

Supplementary Data File 4. Gene Ontology—Biological Process enrichment analysis of rat follicle proteins that are significantly differentially phosphorylated in response to LH (Excel)

Supplementary Data File 5. Gene Ontology—Cellular Compartment enrichment analysis of rat follicle proteins that are significantly differentially phosphorylated in response to LH (Excel)

Supplementary Data File 6. Gene Ontology—Molecular Function enrichment analysis of rat follicle proteins that are significantly differentially phosphorylated in response to LH (Excel)

Figure S1. Generation of *Ppp1r12a*-S507A mice. To introduce the S507A mutation into *Ppp1r12a* (indicated in bold pink type), we employed CRISPOR (http://crispor.tefor.net) and identified a CRISPR cleavage site (5'- CTC TTC AAT GTC AGA TGT AC) adjacent to S507 in exon 11 of *Ppp1r12a*. The PAM sequence is underlined. CRISPR/Cas9 ribonucleoprotein together with single-strand DNA donor were electroporated into one-cell embryos from C57BL/6J mice that had been previously modified to insert an HA tag on the N-terminus of *Npr2* (21). The embryos were then transferred into foster females for subsequent development. PCR genotyping was performed to screen for potential founders using the primer pair PS507AF and P1r12a I12R, which amplifies a fragment of 135 bp specific to the S507A knockin mutation. Founders were further confirmed by PCR using primer pair P1r12a I11F and P1r12a I12R to amplify a fragment of 258 bp containing the S507A mutation followed by sequencing of the PCR product. Founders were then bred with C57BL/6J mice (with HA-tagged *Npr2*) to establish the *Ppp1r12a*-S507A mouse line.

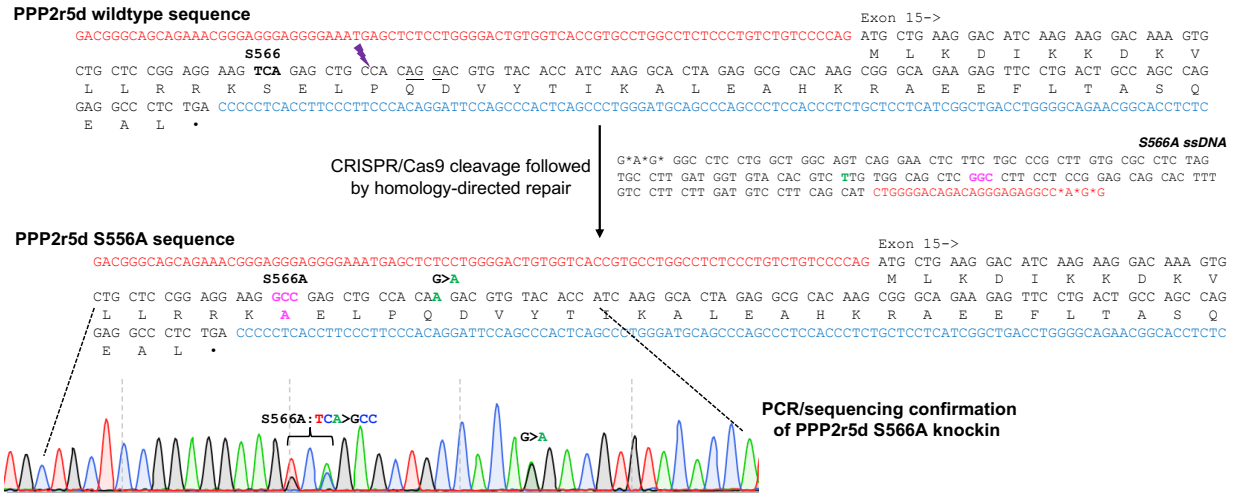


DNA sequences for generation and genotyping of PPP1R12A-S507A mice.
(* represents phosphorothioate linkages to prevent degradation from exonuclease)

Type of sequence	Sequence
sgRNA	5'- CTCTTCAATGTCAGATGTAC
S507A ssDNA donor (sense)	5'- T*C*A*TTCATGACTTTCCTGTTGTCAG GAG AAA GAT AAC AAA GGA ACG AGA CTT GCG TAT GTC ACC CCT ACA ATC CCG AGA CGA CTA GCC **GCG** ACA TCT GAC ATT GAA GAG AAG GAG AAC AG GTGAGTGCAGAGAGGCGGCTGTGTGCATCC*C*T*G
PS507AF (Fwd genotyping primer)	5'- CAATCCCGAGACGACTAGCCGCG
P1r12a I12R (Rev genotyping)	5'- GCTCGCATCAGTCCTCACATC
P1r12a I11F (PCR/sequencing)	5'- GACTGCACGGTCACAGACGTG
P1r12a I12R (PCR/sequencing)	5'- GCTCGCATCAGTCCTCACATC

Figure S2. Generation of *Ppp2r5d*-S53A/S81A/S82A/S566A mice, nicknamed *Ppp2r5d*-4A. These mice were generated in a two-step process. *Ppp2r5d*-S566A mice were generated first, then bred to homozygosity to provide embryos for generation of the final *Ppp2r5d*-4A mice. (**A**) We identified a CRISPR site cleavage site (5'- GAG GAA GTC AGA GCT GCC AC) close to S566 in exon 15 using CRISPOR (http://crispor.tefor.net). The PAM site is underlined. A G>A silent mutation in Q560 was included in the S566A ssDNA donor to eliminate the PAM in order to prevent re-cleavage of the S566A knockin allele. S566A ssDNA and CRISPR/Cas9 ribonucleoprotein were electroporated into one-cell embryos from C57BL/6J mice that had been previously modified to insert an HA tag on the N-terminus of *Npr2* (21). The embryos were then transferred into a foster mother for subsequent development. Founder pups were identified by PCR genotyping using the primer pair PS566AF and PppE15R1, to amplify a 157 bp fragment specific to the S566A knockin. Their genotypes were confirmed by PCR using primer pair Ppp I14F1 and Ppp E15R1 to amplify a fragment of 255 bp containing the S566A knockin mutation followed by sequencing of the PCR product. (**B**) Two CRISPR sites adjacent to S53 (sgRNA1) and S81/S82 (sgRNA2) were identified. CRISPR/Cas9 ribonucleoproteins and 3A ssDNA were electroporated into homozygous *Ppp2r5d*-S566A one-cell embryos. Founders containing the S53A/S81A/S82A knockin mutations were identified using the primer pair S53.E3F1 and S81.82E3R1 to specifically amplify a fragment of 120 bp, and their identities were further confirmed by PCR using primer pair P2r5d.SeqF and P2r5d.SeqR to amplify a fragment of 383 bp containing the S53A/S81A/S82A mutations followed by sequencing of the PCR product. Founders were bred with C57BL/6J mice (with HA-tagged *Npr2*) to establish the *Ppp2r5d*-4A mouse line.

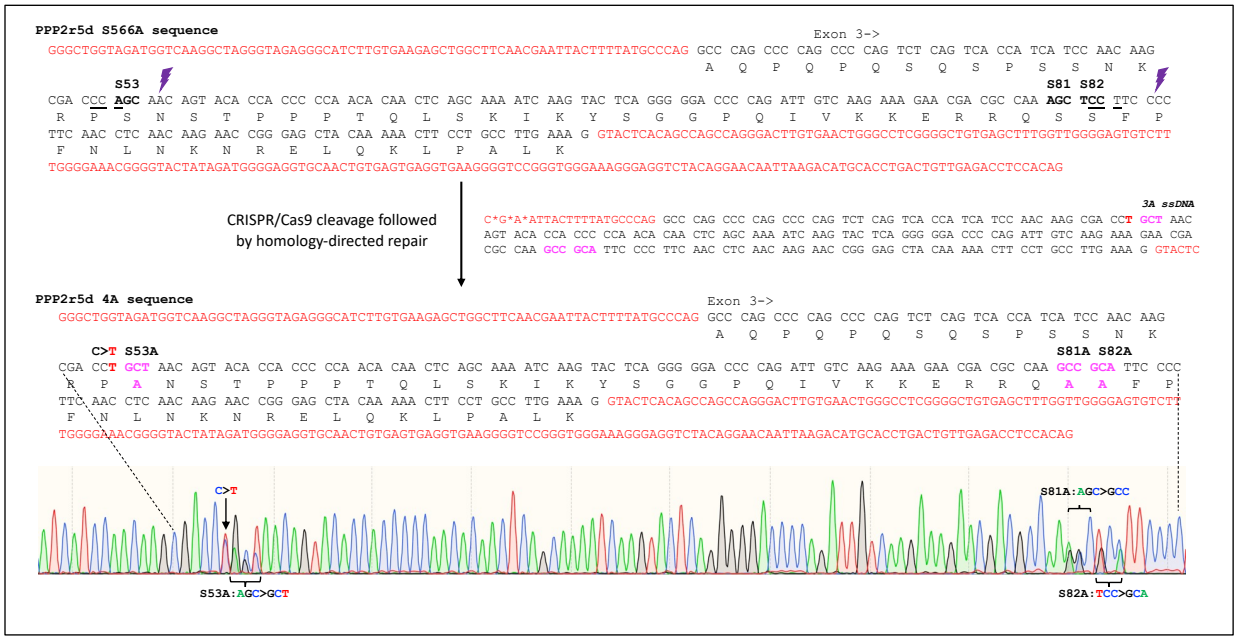
A



DNA sequences for generation and genotyping of PPP2R5D-S566A mice.
(* represents phosphorothioate linkages to prevent degradation from exonuclease)

Type of sequence	Sequence
sgRNA	5'- GAGGAAGTCAGAGCTGCCAC
S566A ssDNA donor (antisense)	5'- G*A*G*GGCCTCCTGGCTGGCAGTCAGGAACTCTTCTGC CCGCTTGTGCGCCTCTAGTGCCTTGATGGTGTACACGTC TTGTGGCAGCTC**GGC**CTTCCTCCGGAGCAGCACTTTGT CCTTCTTGATGTCCTTCAGCATCTGGGGACAGACAGGGA GAGGCC*A*G*G
PppS566AF (Forward genotyping primer)	5'- AAGTGCTGCTCCGGAGGAAGGCC
PppE15R1 (Reverse genotyping primer)	5'- GGGCTGAGTGGGCTGGAATCC
Ppp I14F1 (PCR/sequencing)	5' - ACGGGAGGGAGGGGAAATGAGC
Ppp E15R1 (PCR/sequencing)	5' - GGGCTGAGTGGGCTGGAATCC

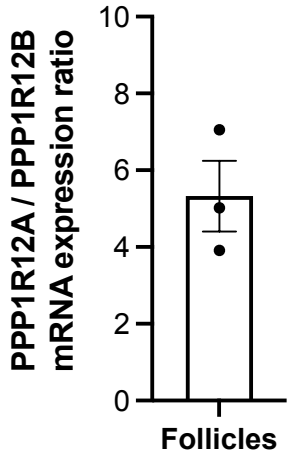
B



DNA sequences for generation and genotyping of PPP2R5D-4A mice.
(* represents phosphorothioate linkages to prevent degradation from exonuclease)

Type of sequence	Sequence
sgRNA1	5'- TGGGGGTGGTGTACTGTTGC
sgRNA2	5'- CTTGTTGAGGTTGAAGGGGA
3A ssDNA donor (sense)	5'- C*G*A*ATTACTTTTATGCCCAGGCCCAGCCCCAGCCCCAGTC TCAGTCACCATCATCCAACAAGCGACC**TGCT**AACAGTACACC ACCCCCAACACAACTCAGCAAAATCAAGTACTCAGGGGGAC CCCAGATTGTCAAGAAAGAACGACGCCAA**GCCGCA**TTCCCC TTCAACCTCAACAAGAACCGGGAGCTACAA AAACTTCCTGCCTTGAAAGGTACTC
S53.E3F1 (Forward genotyping primer)	5'- CATCCAACAAGCGACCTGCT
S81.82E3R1 (Reverse genotyping primer)	5'- GAGGTTGAAGGGGAATGCGGC
P2r5d.SeqR (PCR/sequencing)	5' - GAGGGCTGGTAGATGGTCAAG
P2r5d.SeqR (PCR/sequencing)	5' - CTCACAGTTGCACCTCCCCAT

Figure S3. PPP1R12A mRNA is ~5 times more abundant than PPP1R12B mRNA in mouse ovarian follicles. The bars show the mean ± SEM for analysis of 3 independent preparations of RNA.



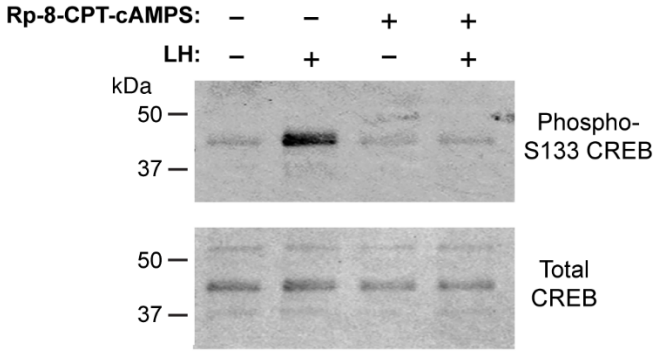
Methods: RNA from mouse preovulatory follicles was extracted with Trizol and treated with DNAse. ddPCR was performed using a Bio-Rad QX-200 Droplet Digital system and primers as listed below. We thank Andrew Collins and Angela Ross (Bio-Rad) for performing the ddPCR assay.

Primer sequences used for ddPCR to compare amounts of PPP1R12A and PPP2R12B mRNA.

Gene name	Forward	Reverse	Amplicon
Ppp1r12a	5'-CTCTATGCCTCAAGTCAGCTC	5'-GCTGTGACTTATCTTCCCCTTC	139 bp
Ppp1r12b	5'-AGAAGCTTGAAGATCCTGGTG	5'-TGGGTTTGTCTGGTTGAGTTG	150 bp

Figure S4. Rp-8-CPT-cAMPS effectively inhibits LH-induced PKA activation in mouse preovulatory follicles. (**A**) Follicles were treated with or without Rp-8-CPT-cAMPS (10 mM, 4 hr) then stimulated with 10 nM LH (30 min). Follicle proteins were separated on a standard SDS-PAGE gel (no Phostag) and western blots were probed with an antibody recognizing phosphorylated serine 133 of the PKA substrate CREB, and with an antibody against total CREB. Signals were detected with fluorescent secondary antibodies to ensure linearity (see methods). (**B**) Summary of ratios of signal intensities for pS133 CREB/total CREB, for 2 blots like those shown in A. Each symbol represents a set of samples that were treated as indicated and then analyzed together on the same blot. Bars show mean ± SEM. Values were normalized to the control with no Rp-8-CPT-cAMPS and no LH.

A



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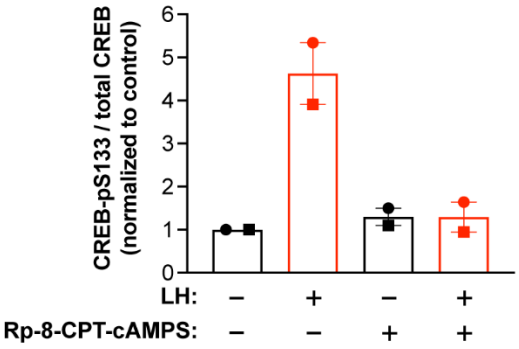

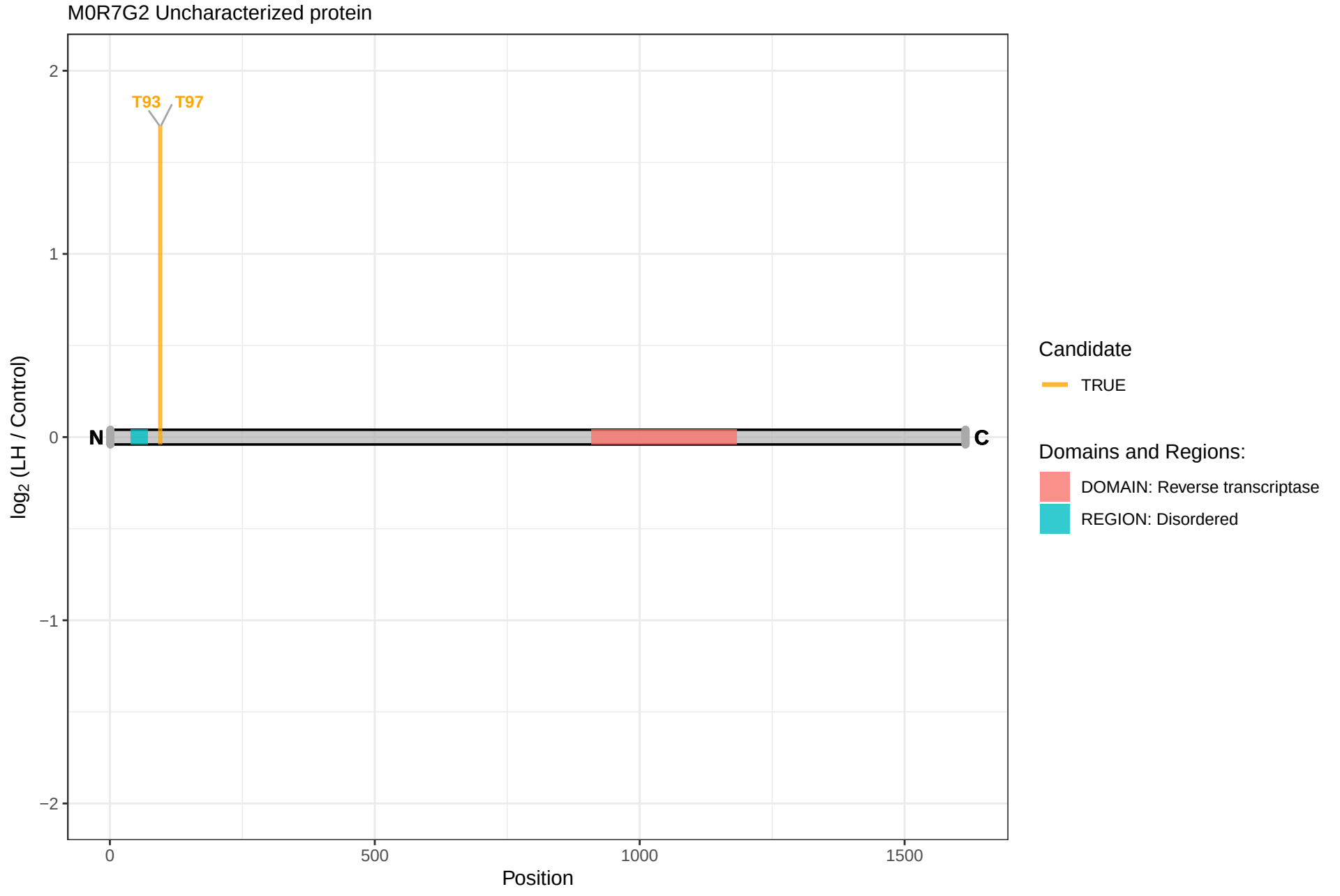
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T93
T97
N
C
2
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0
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−2
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1000
1500
Position
Candidate
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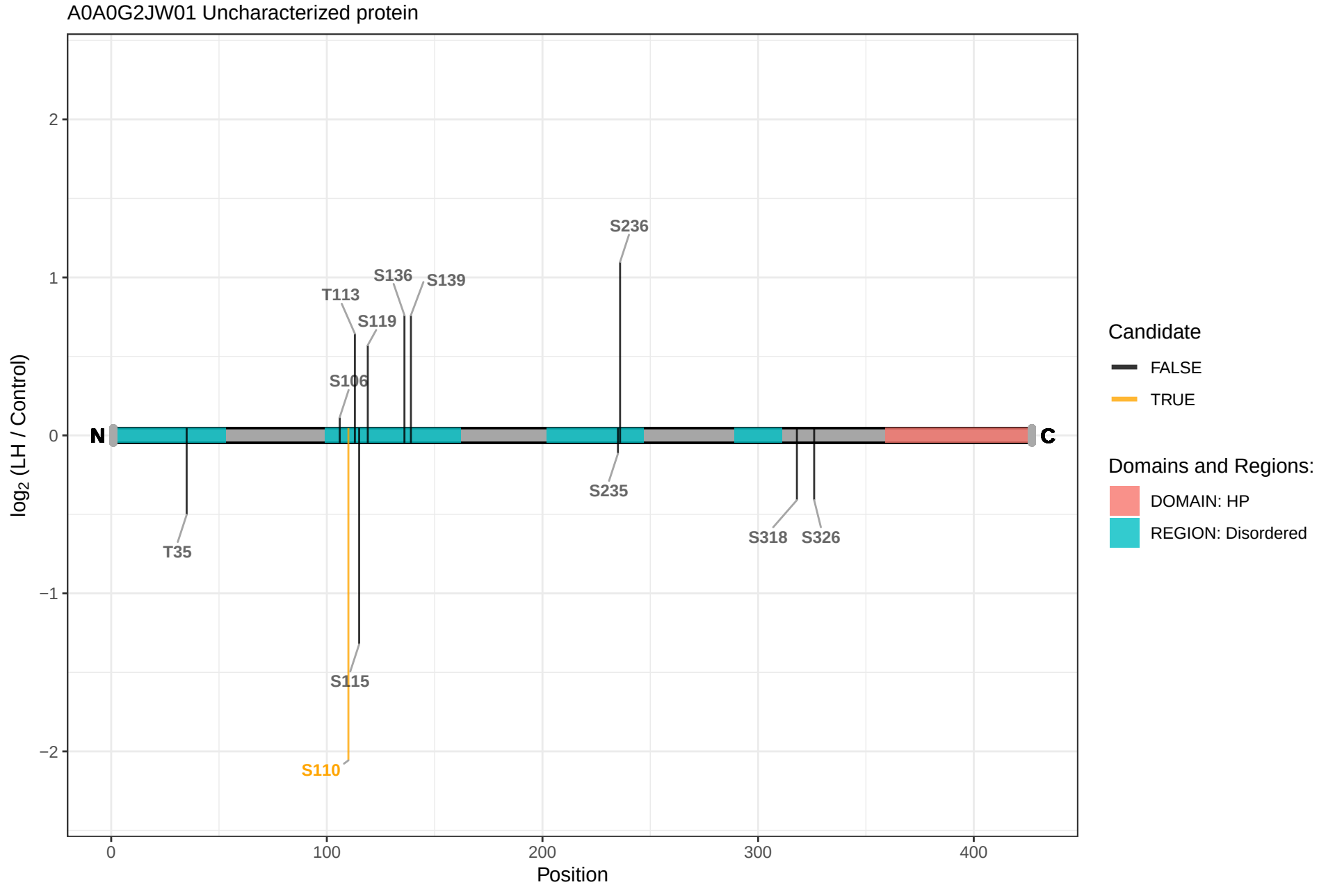
REGION: Disordered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log2 (LH / Control)
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C
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T113
S119
S136
S139
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S235
S318
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Candidate
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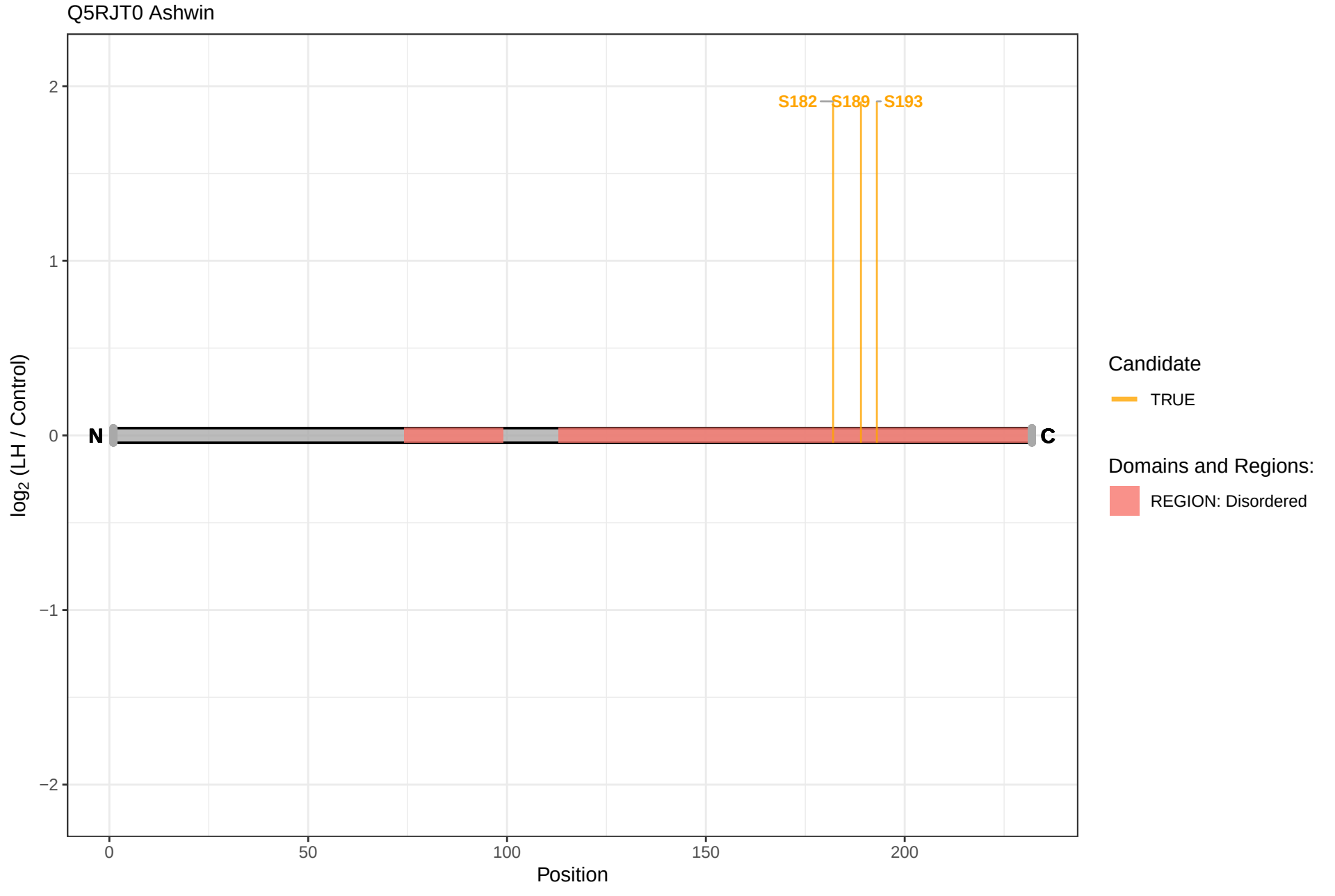
Q5RJT0 Ashwin
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S189
S193
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Position
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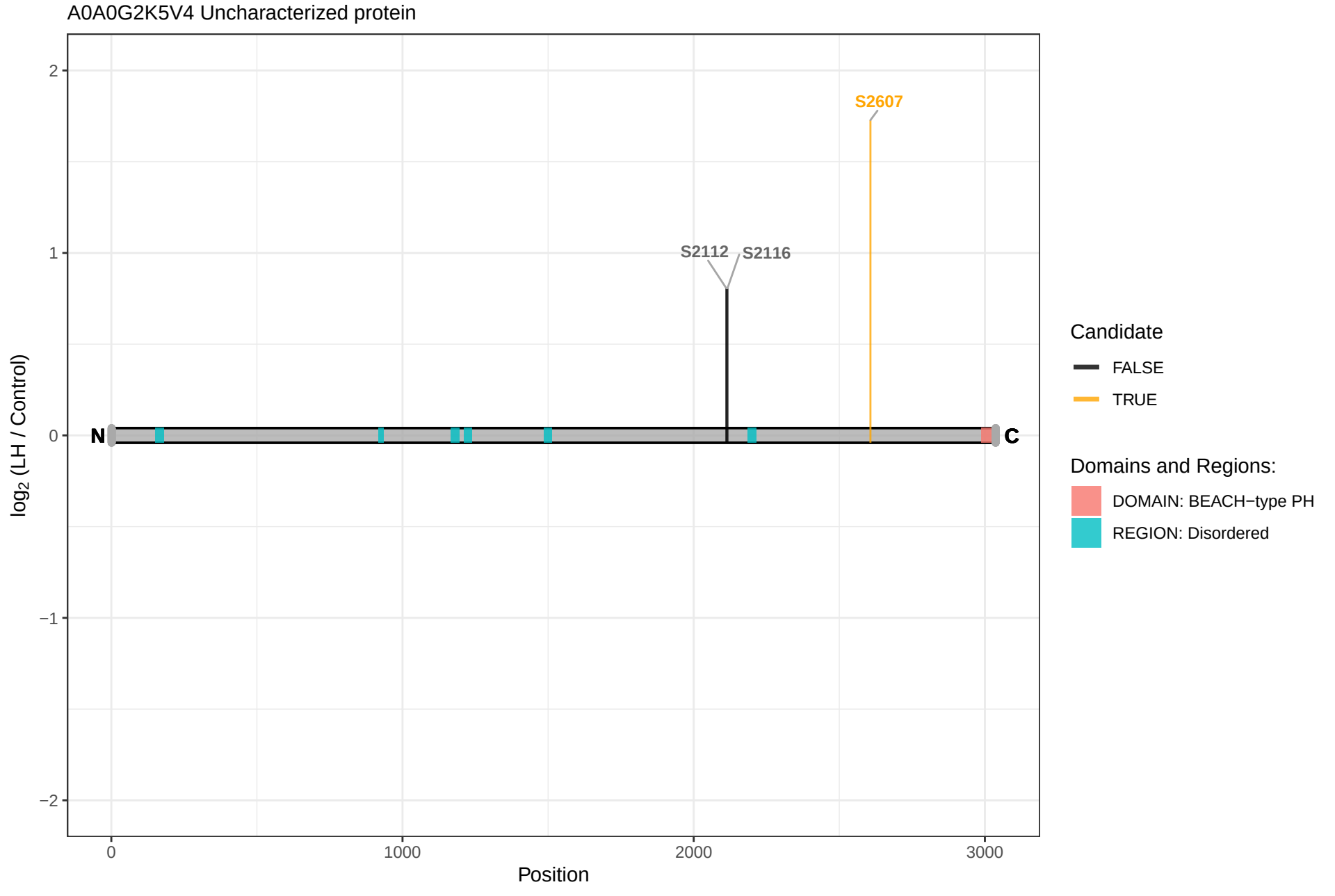
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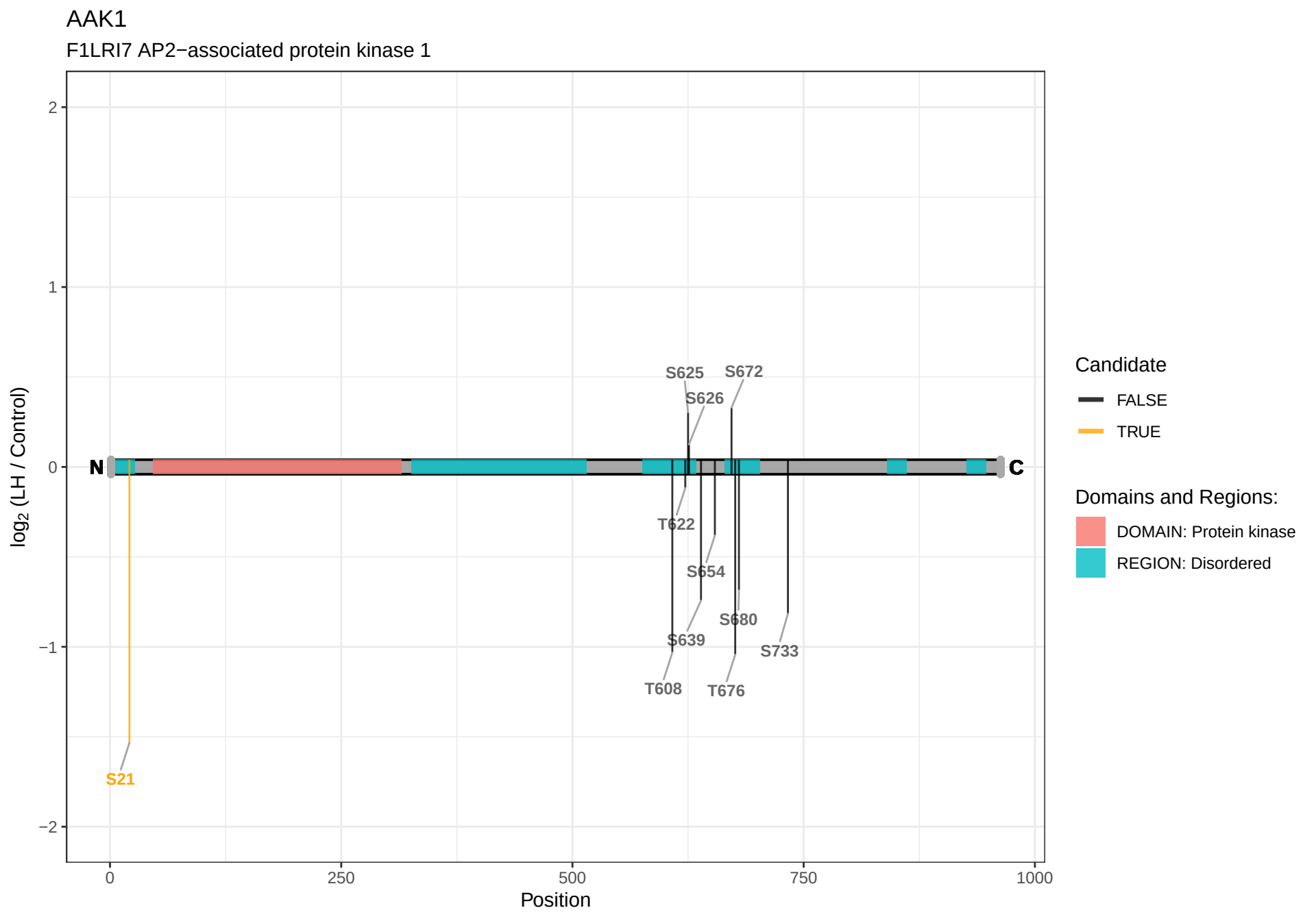
REGION: Disordered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F1LRI7 AP2−associated protein kinase 1
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S626
T622
S654
S680
S639
S733
T608
T676
S21
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250
500
750
1000
Position
Candidate
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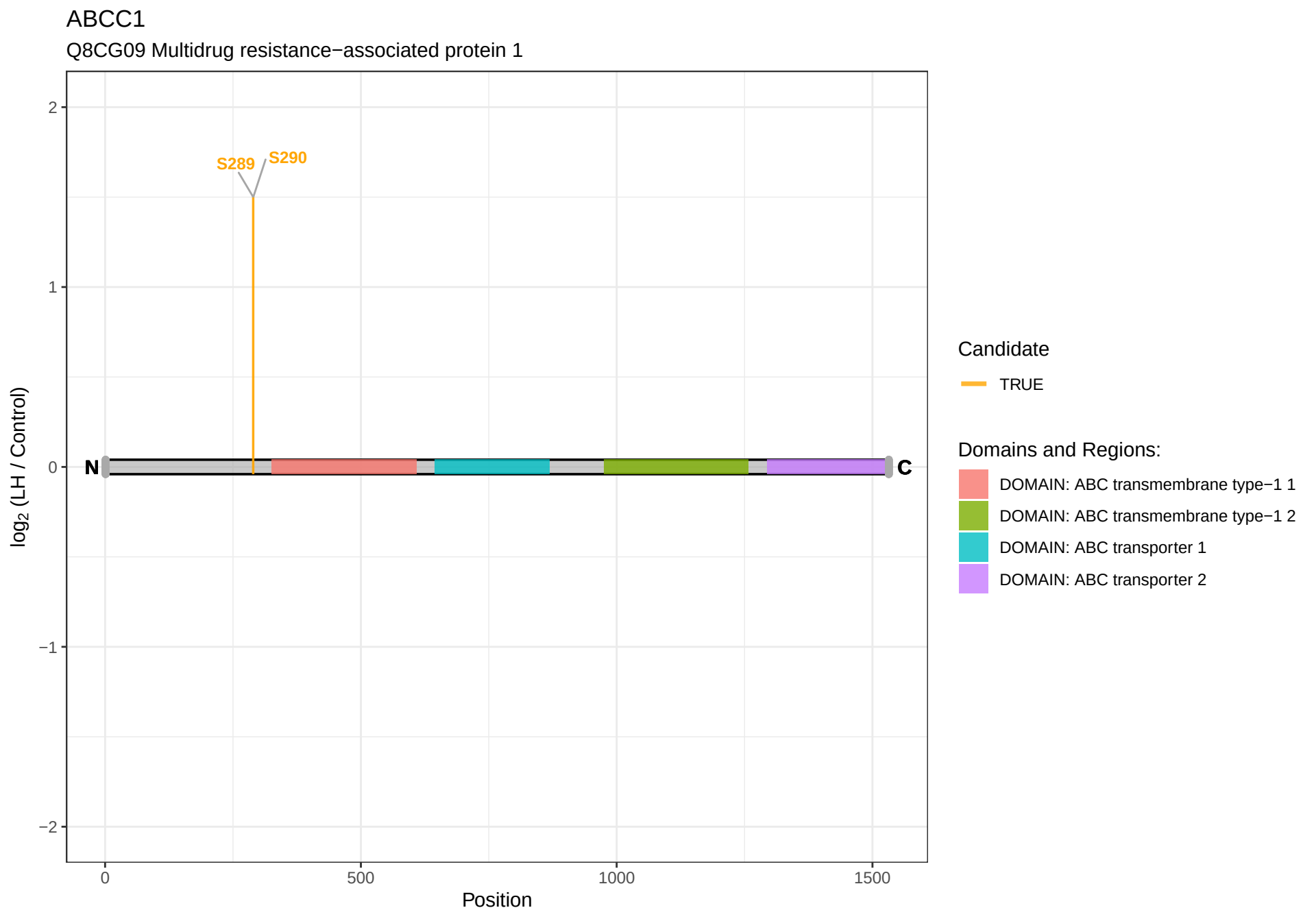
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered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Q8CG09 Multidrug resistance−associated protein 1
S289
S290
N
C
log2 (LH / Control)
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−1
−2
0
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1000
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Candidate
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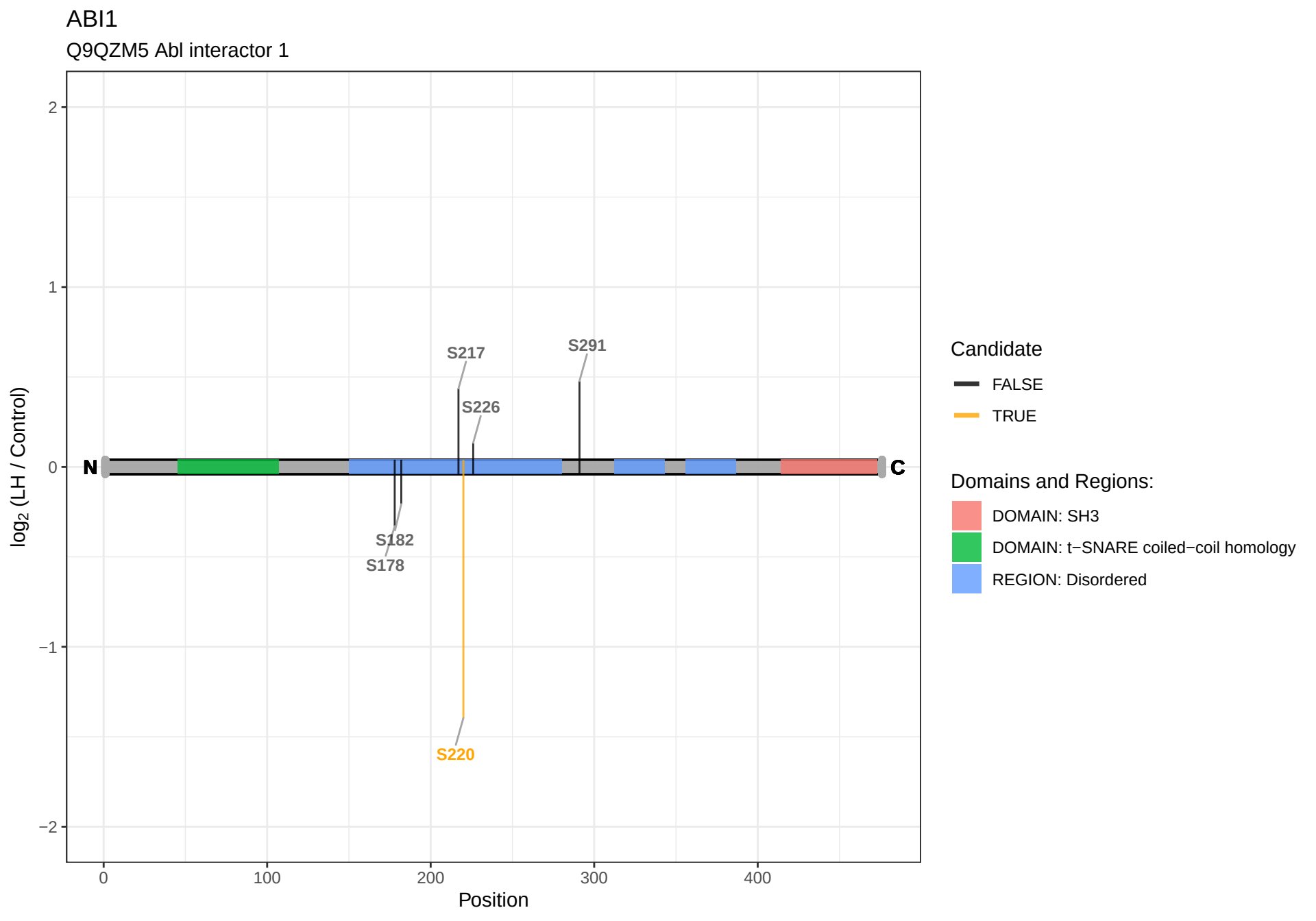
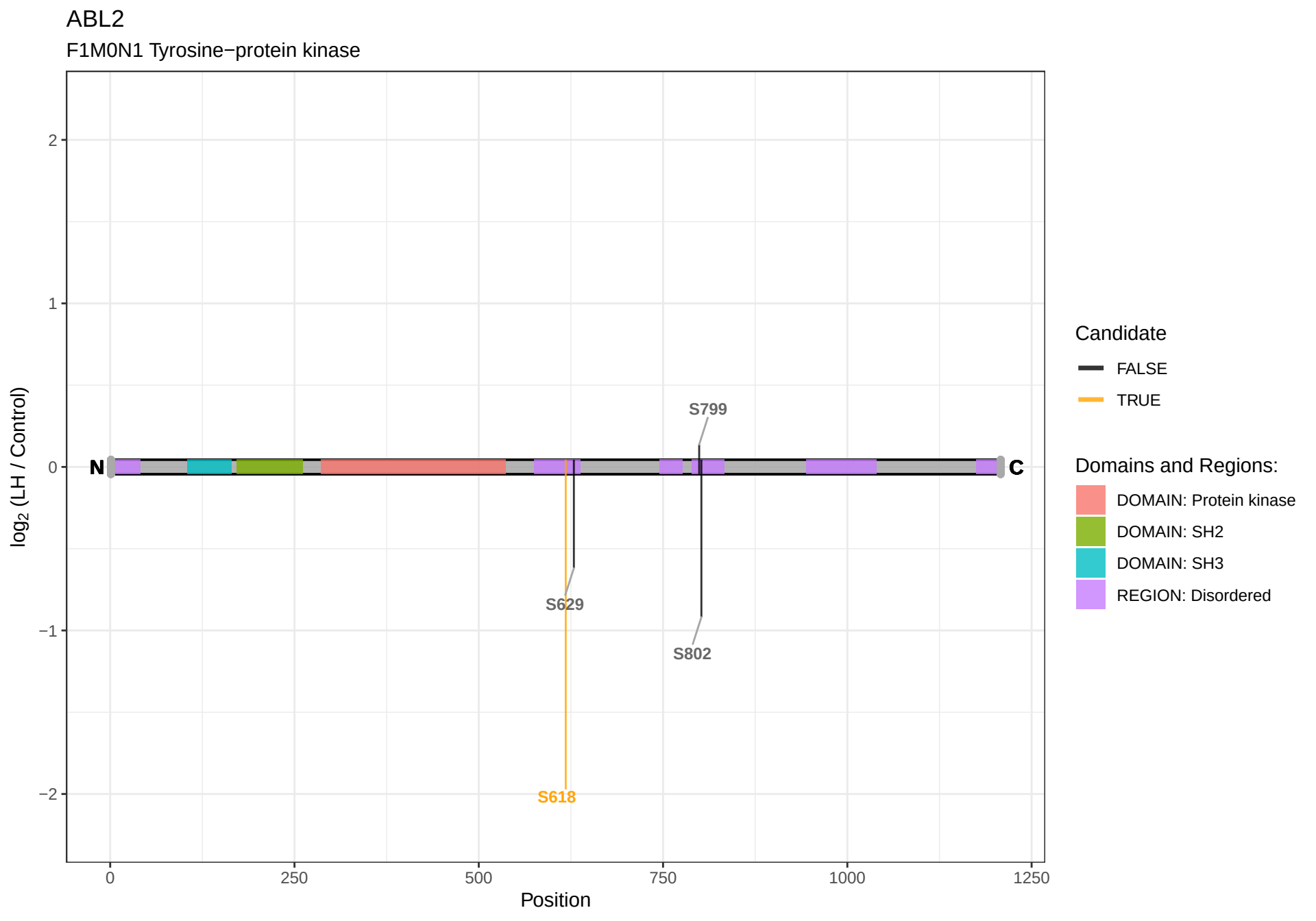
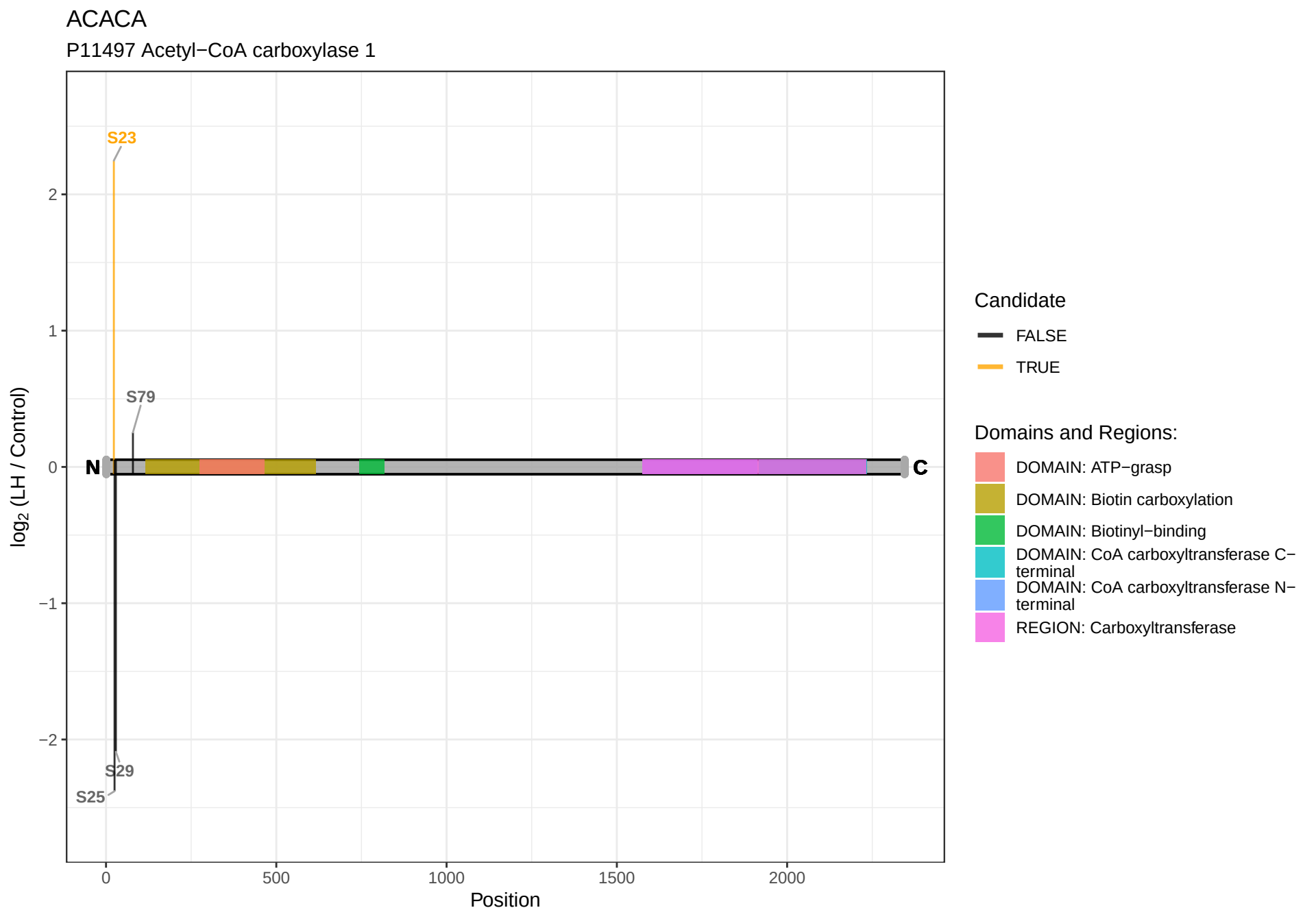
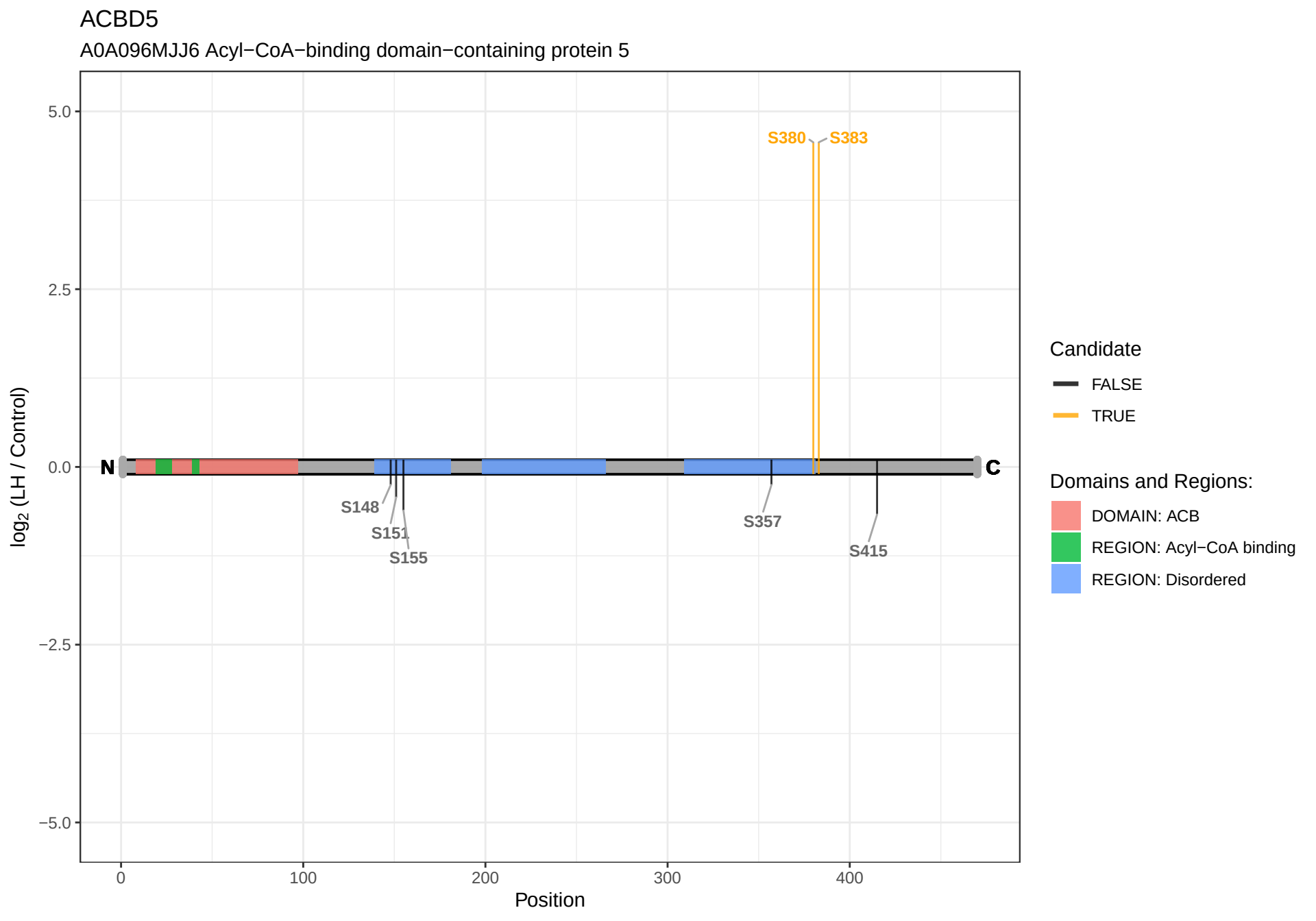
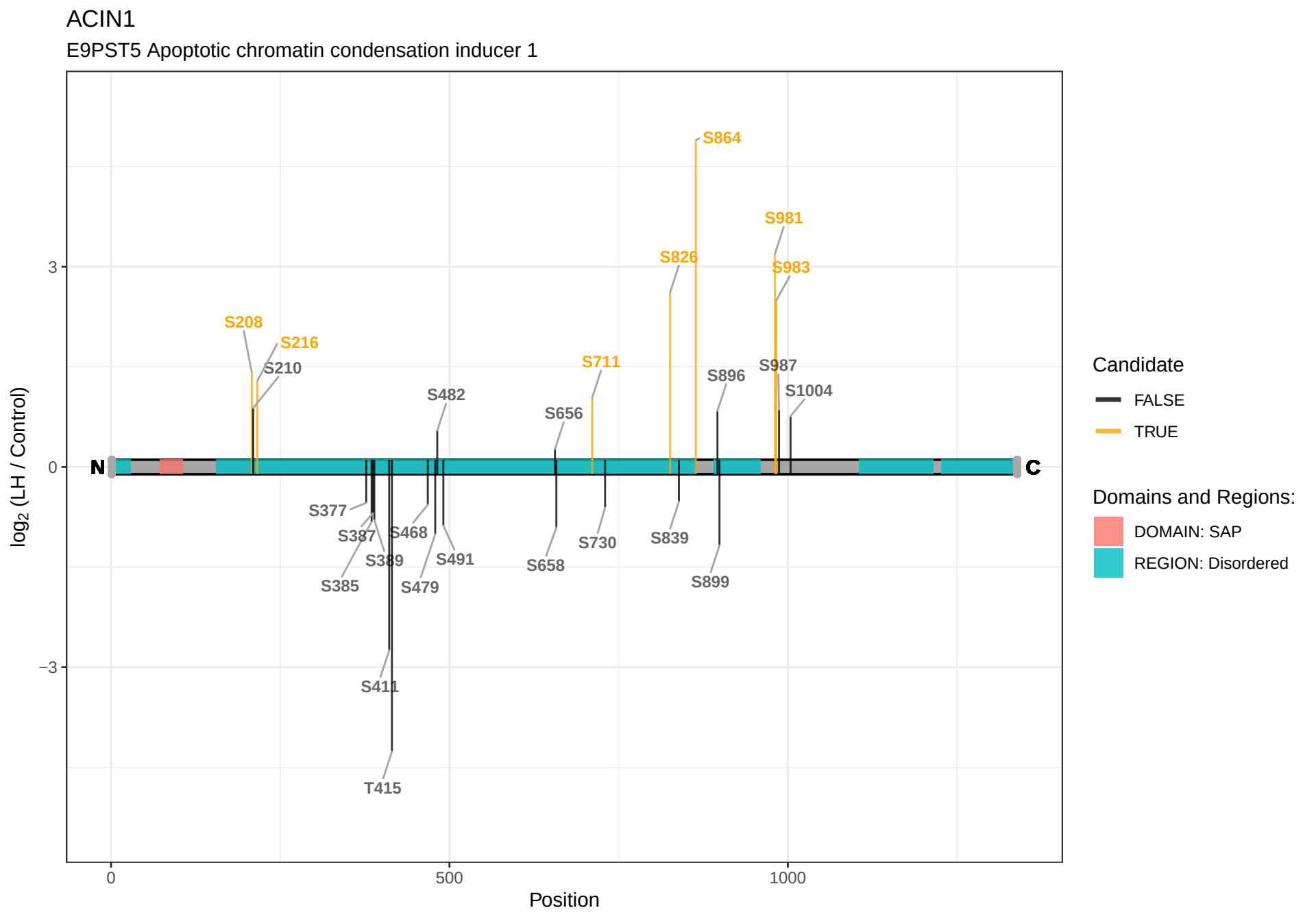
DOMAIN: ABC transmembrane type−1 2
DOMAIN: ABC transporter 1
DOMAIN: ABC transporter 2

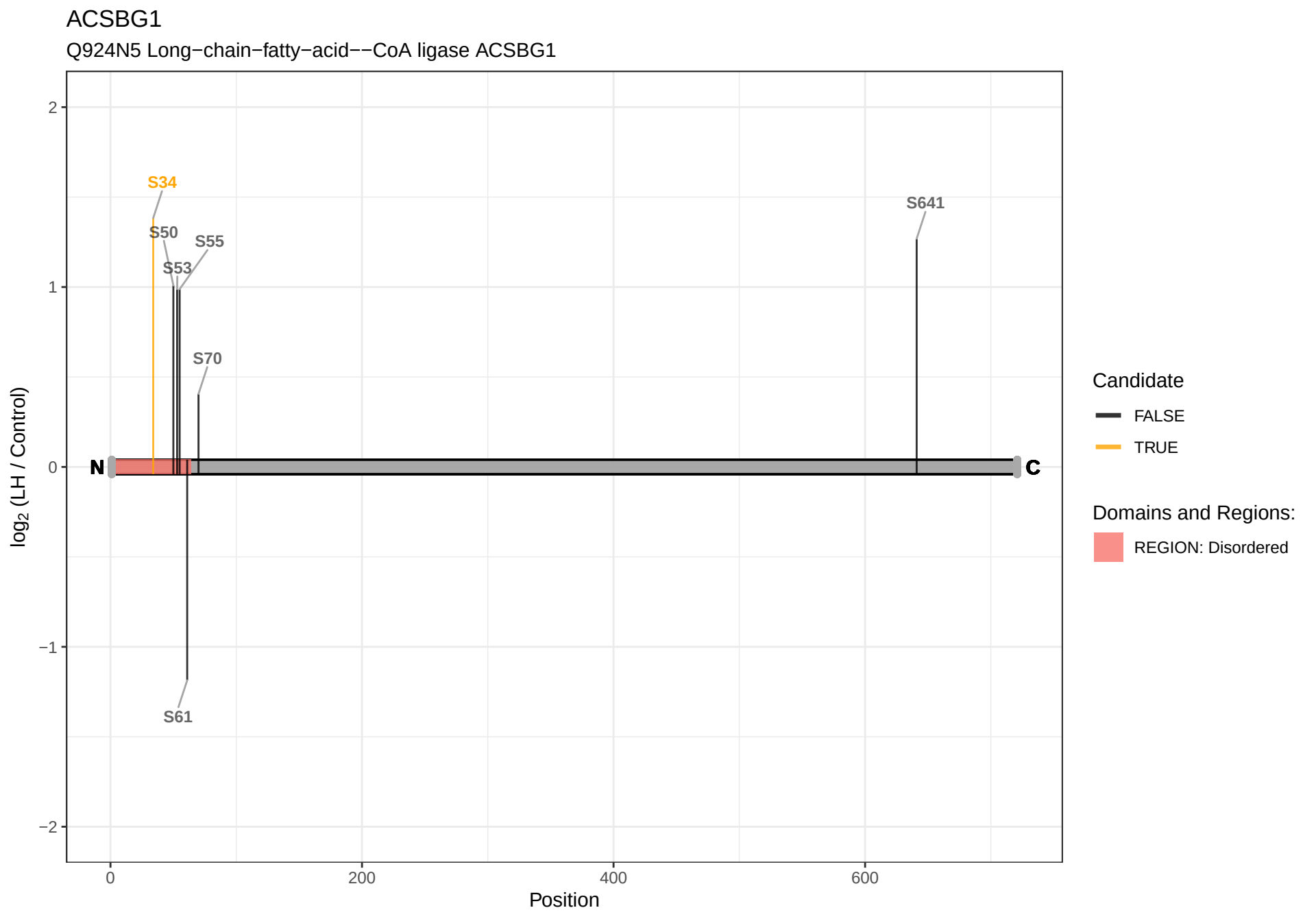

ABI1
Q9QZM5 Abl interactor 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S217
S291
S226
S182
S178
S220
0
100
200
300
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SH3
DOMAIN: t−SNARE coiled−coil homology
REGION: Disordered

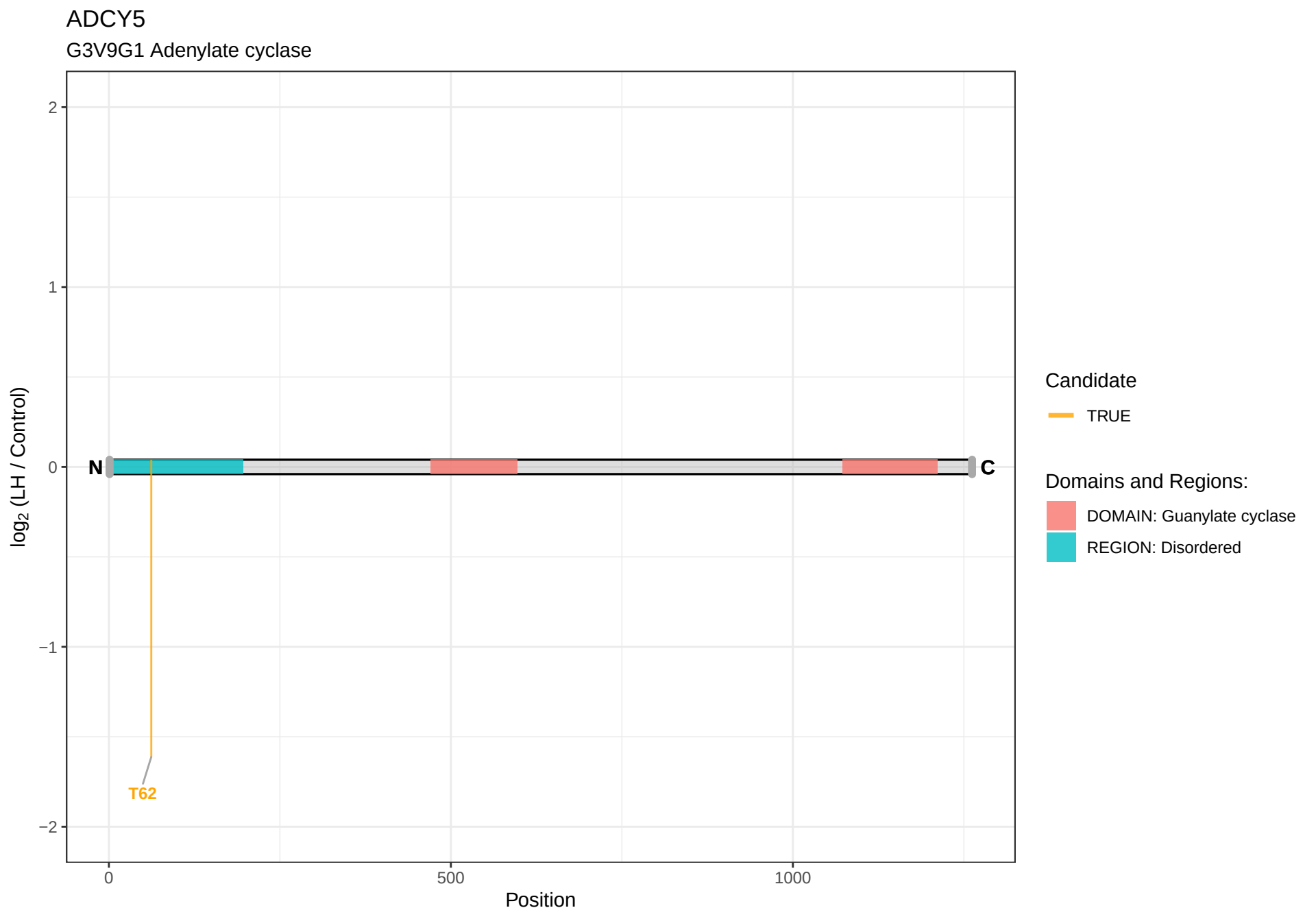

ABL2
F1M0N1 Tyrosine−protein kinase
log2 (LH / Control)
2
1
0
−1
−2
N
C
S799
S629
S802
S618
0
250
500
750
1000
1250
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
DOMAIN: SH2
DOMAIN: SH3
REGION: Disordered

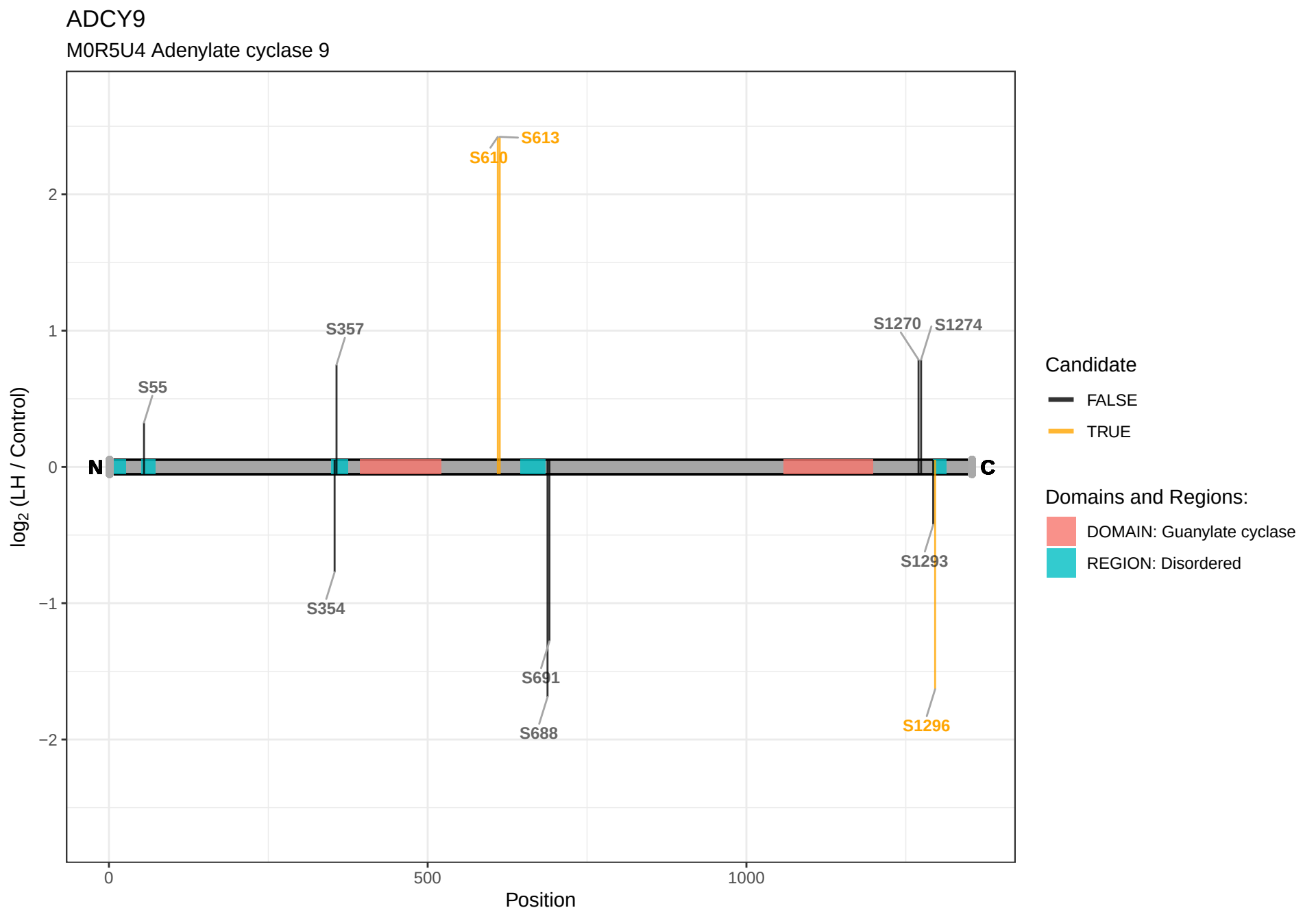

ACACA
P11497 Acetyl−CoA carboxylase 1
S23
S79
S29
S25
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
1500
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ATP−grasp
DOMAIN: Biotin carboxylation
DOMAIN: Biotinyl−binding
DOMAIN: CoA carboxyltransferase C−terminal
DOMAIN: CoA carboxyltransferase N−terminal
REGION: Carboxyltransferase

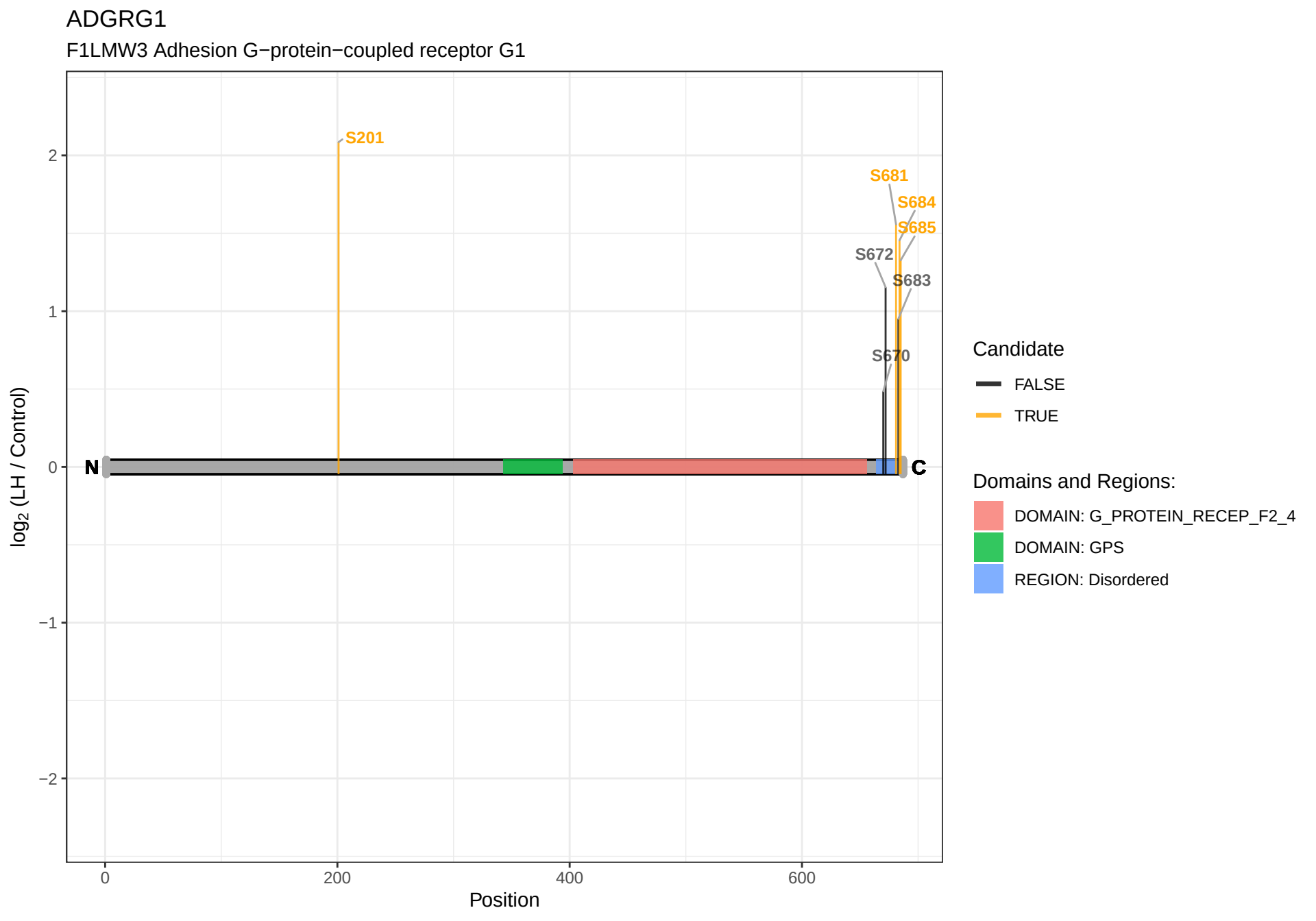

ACBD5
A0A096MJJ6 Acyl−CoA−binding domain−containing protein 5
5.0
2.5
0.0
−2.5
−5.0
log2 (LH / Control)
0
100
200
300
400
Position
N
C
S380
S383
S148
S151
S155
S357
S415
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ACB
REGION: Acyl−CoA binding
REGION: Disordered

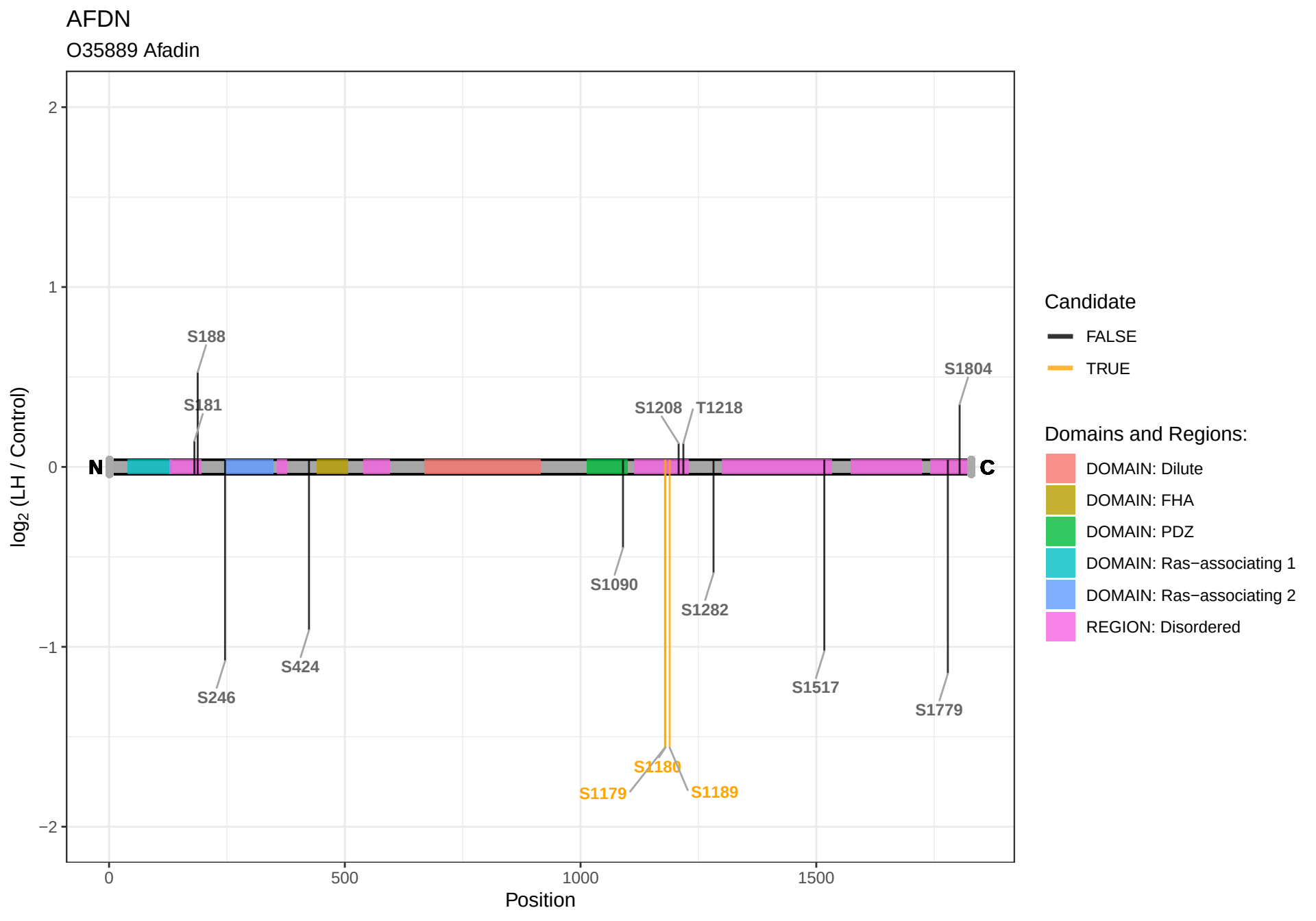

ACIN1
E9PST5 Apoptotic chromatin condensation inducer 1
log2 (LH / Control)
3
0
−3
N
C
S864
S981
S826
S983
S208
S216
S210
S711
S987
S896
S1004
S482
S656
S377
S387
S468
S730
S839
S389
S491
S658
S385
S479
S899
S411
T415
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SAP
REGION: Disordered

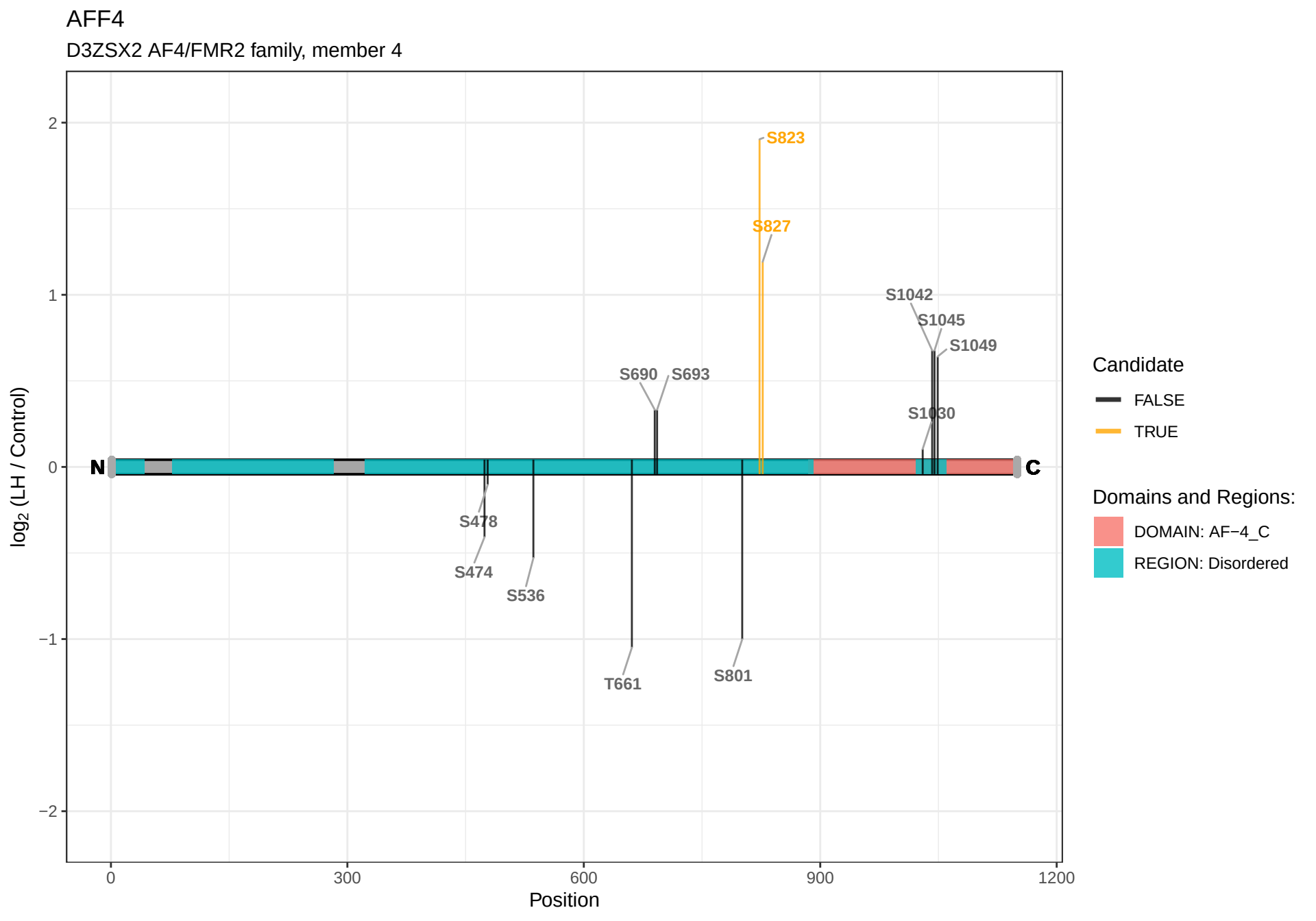

ACSBG1
Q924N5 Long−chain−fatty−acid−−CoA ligase ACSBG1
S34
S50
S55
S53
S70
S61
S641
N
C
2
1
0
−1
−2
0
200
400
600
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

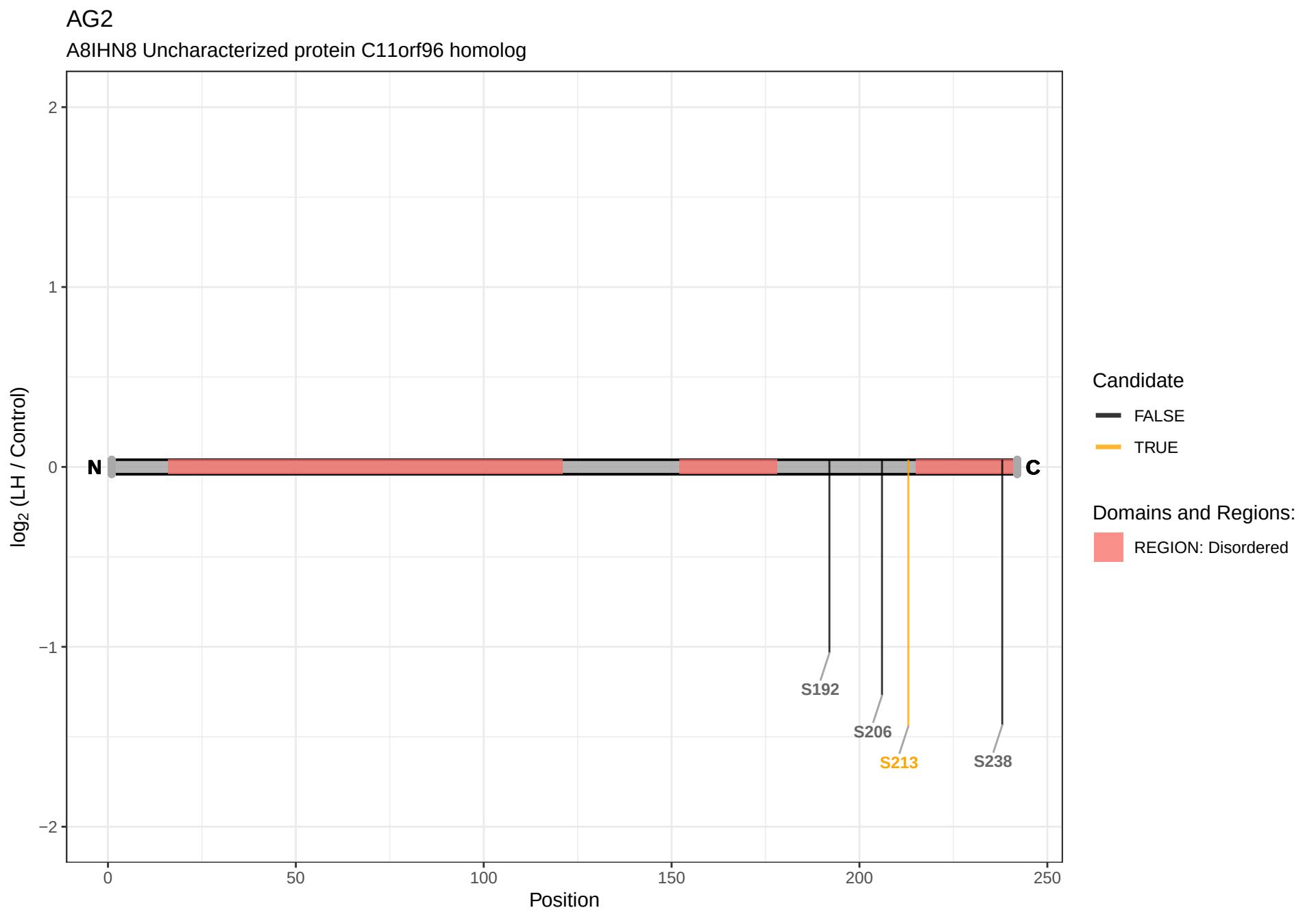

ADCY5
G3V9G1 Adenylate cyclase
2
1
0
−1
−2
log2 (LH / Control)
N
C
T62
0
500
1000
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Guanylate cyclase
REGION: Disordered

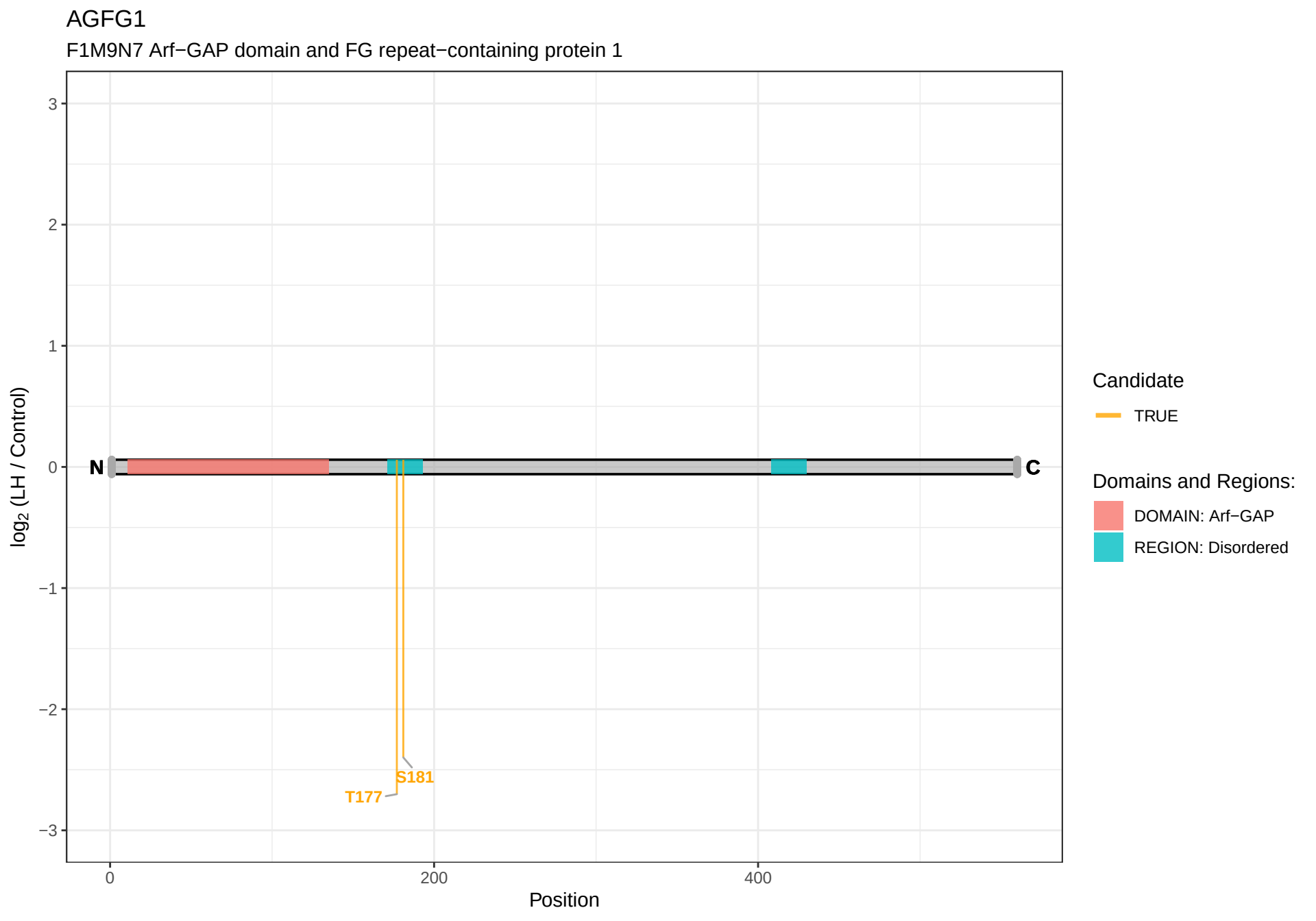

ADCY9
M0R5U4 Adenylate cyclase 9
S613
S610
S357
S55
S1270
S1274
S1293
S354
S691
S688
S1296
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Guanylate cyclase
REGION: Disordered

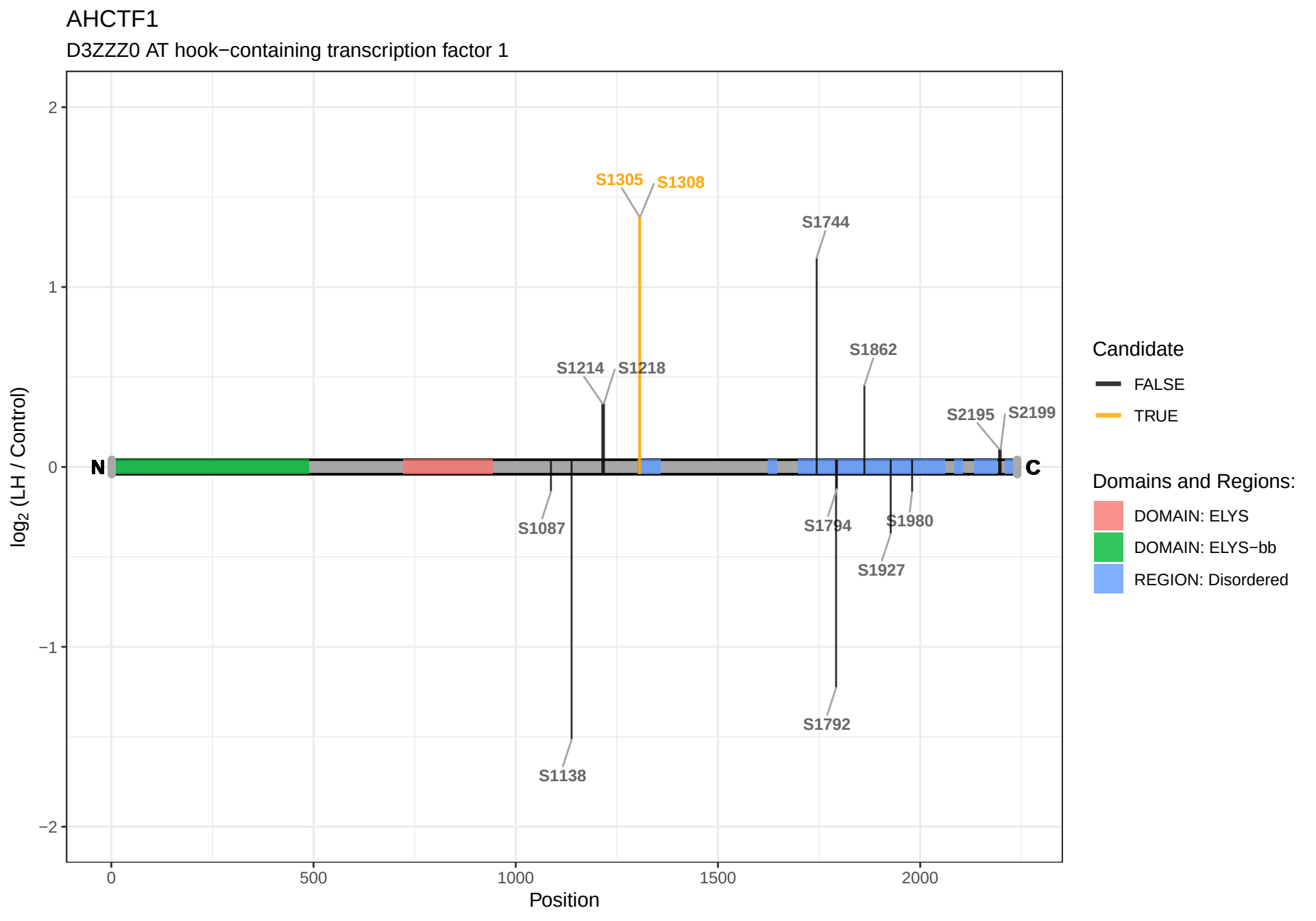

ADGRG1
F1LMW3 Adhesion G−protein−coupled receptor G1
S201
S681
S684
S685
S672
S683
S670
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: G_PROTEIN_RECEP_F2_4
DOMAIN: GPS
REGION: Disordered

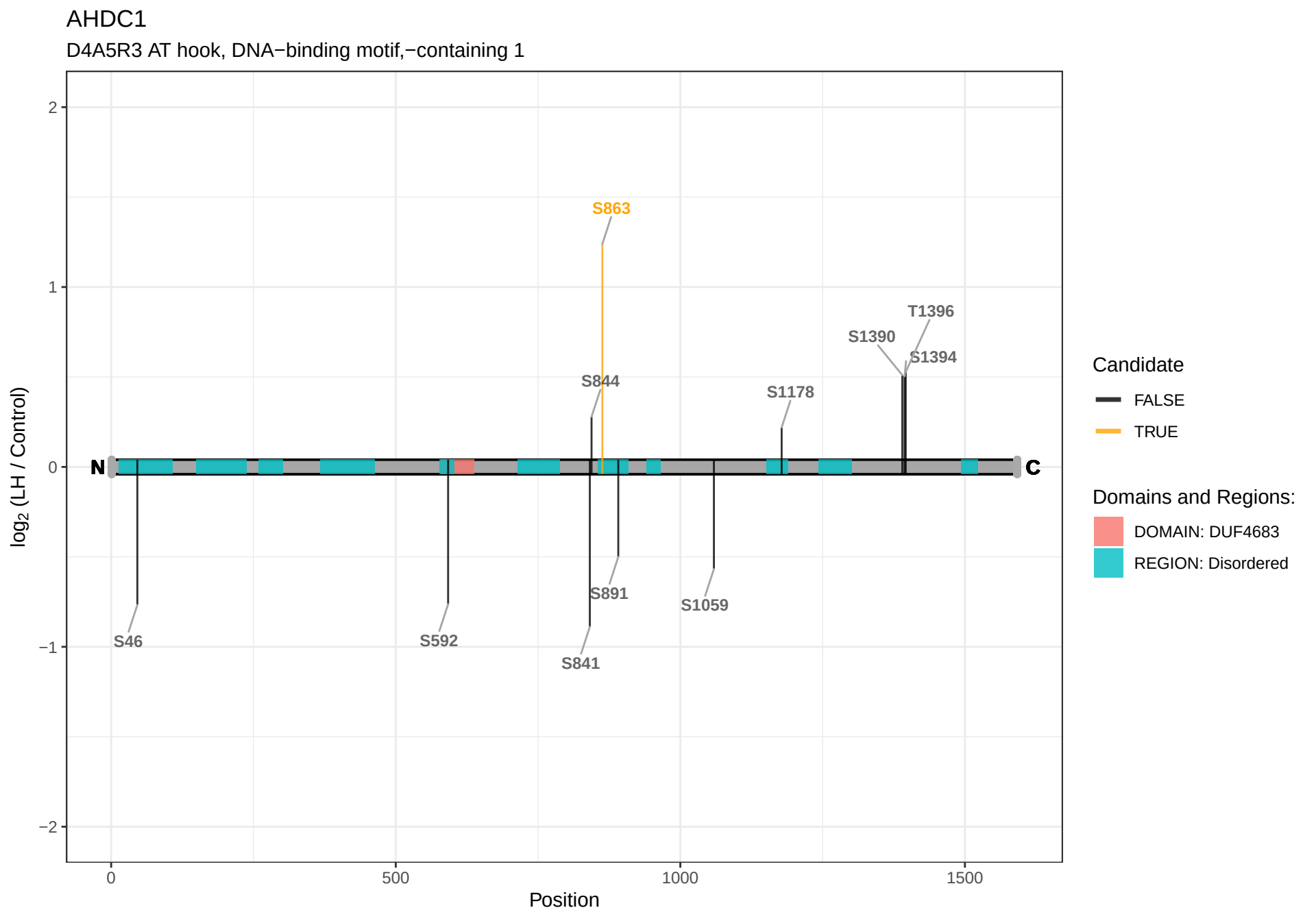

AFDN
O35889 Afadin
log2 (LH / Control)
Position
N
C
S188
S181
S246
S424
S1090
S1208
T1218
S1282
S1804
S1517
S1779
S1179
S1180
S1189
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Dilute
DOMAIN: FHA
DOMAIN: PDZ
DOMAIN: Ras−associating 1
DOMAIN: Ras−associating 2
REGION: Disordered

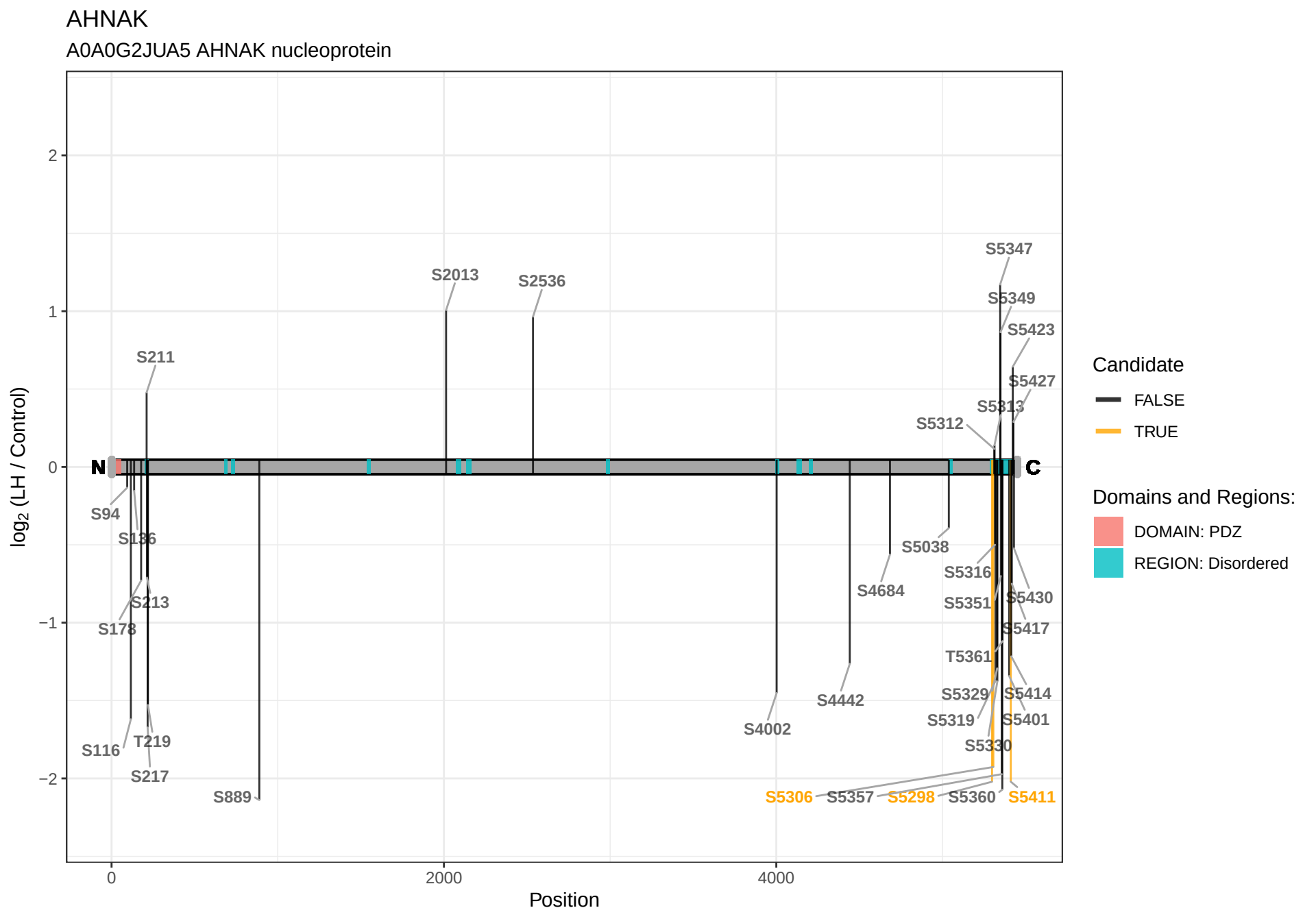

AFF4
D3ZSX2 AF4/FMR2 family, member 4
log2 (LH / Control)
2
1
0
−1
−2
0
300
600
900
1200
Position
N
C
S823
S827
S1042
S1045
S1049
S690
S693
S1030
S478
S474
S536
T661
S801
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AF−4_C
REGION: Disordered

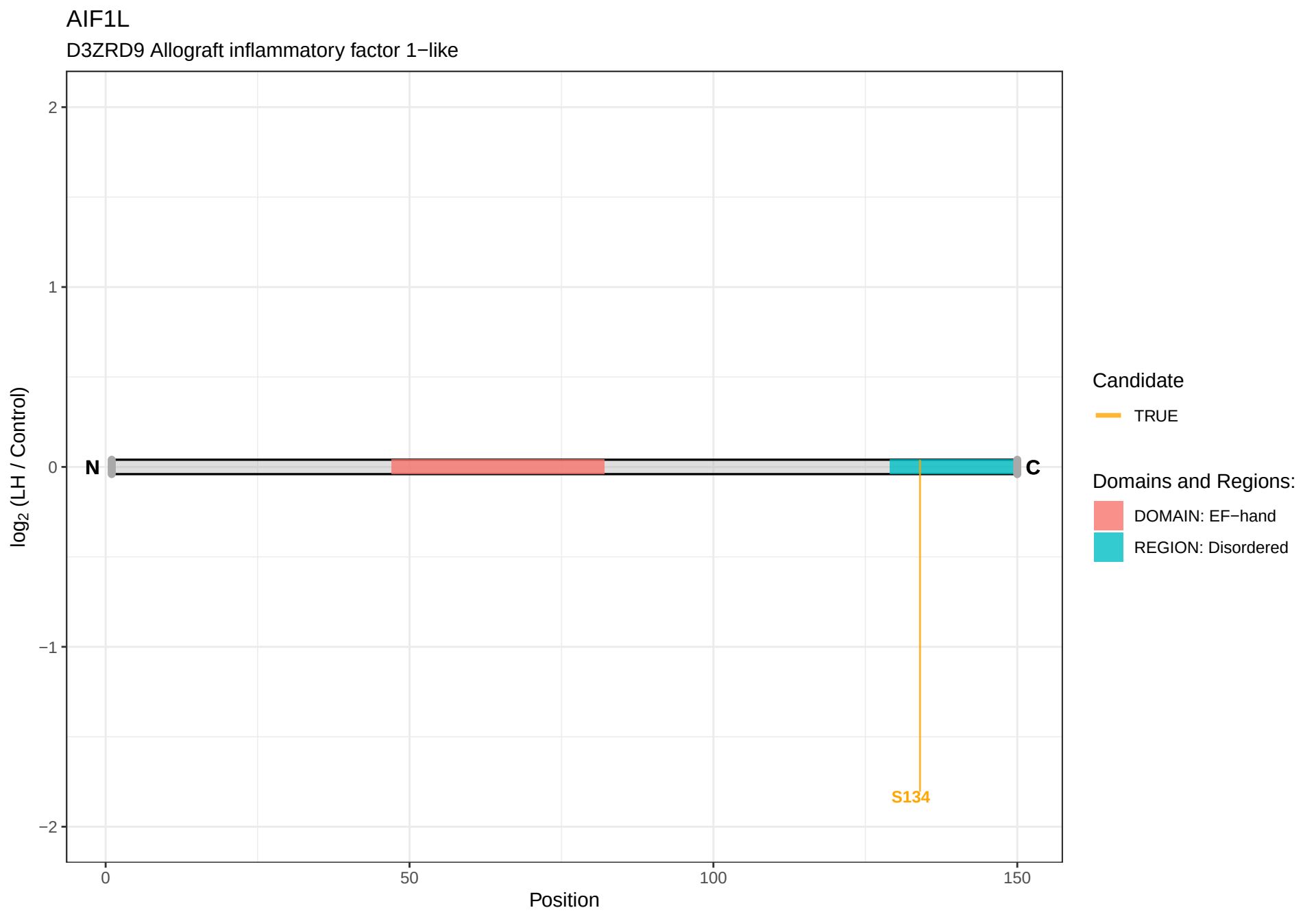

AG2
A8IHN8 Uncharacterized protein C11orf96 homolog
log2 (LH / Control)
2
1
0
−1
−2
N
C
S192
S206
S213
S238
0
50
100
150
200
250
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

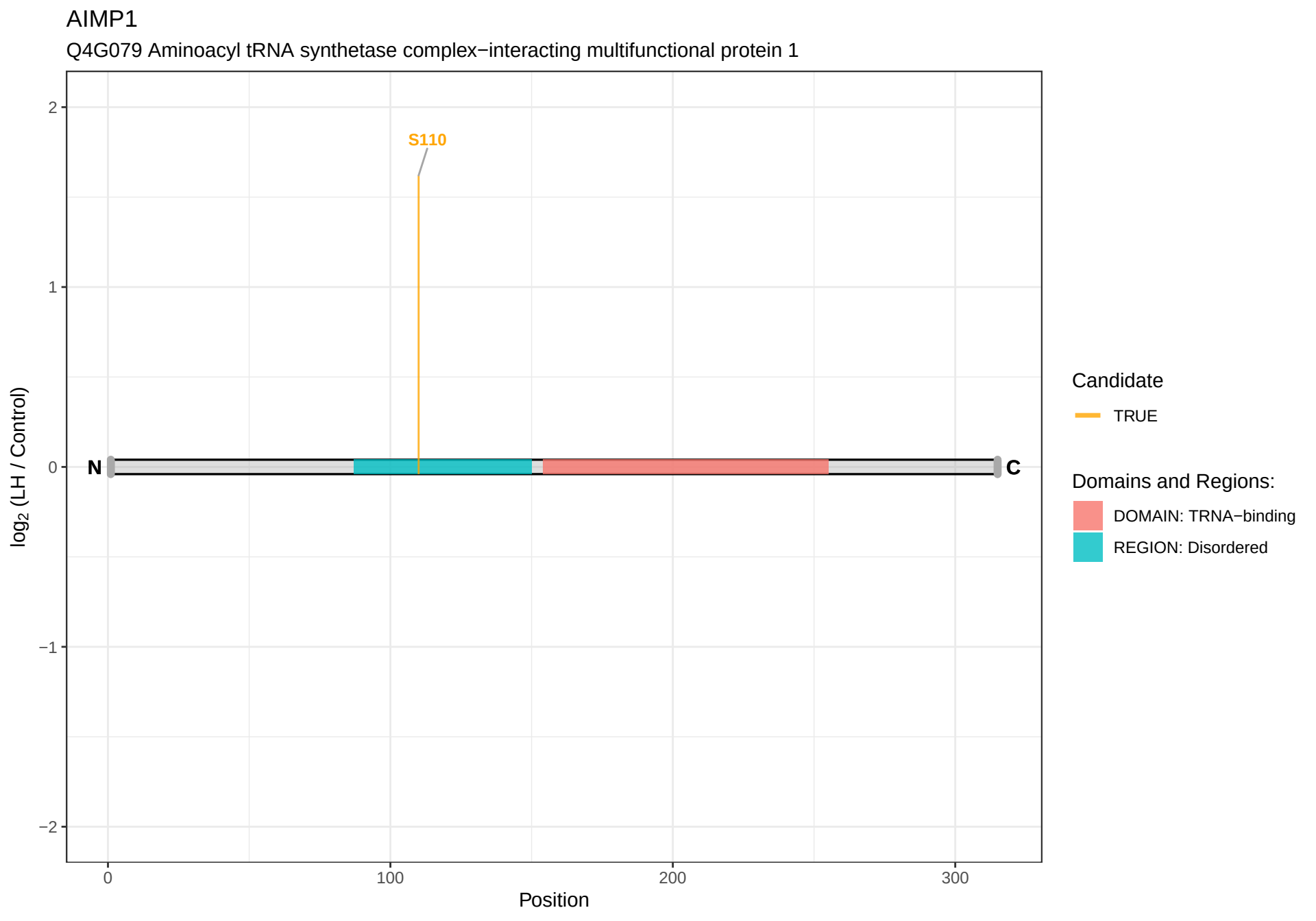

AGFG1
F1M9N7 Arf−GAP domain and FG repeat−containing protein 1
log2 (LH / Control)
3
2
1
0
−1
−2
−3
N
C
T177
S181
0
200
400
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Arf−GAP
REGION: Disordered

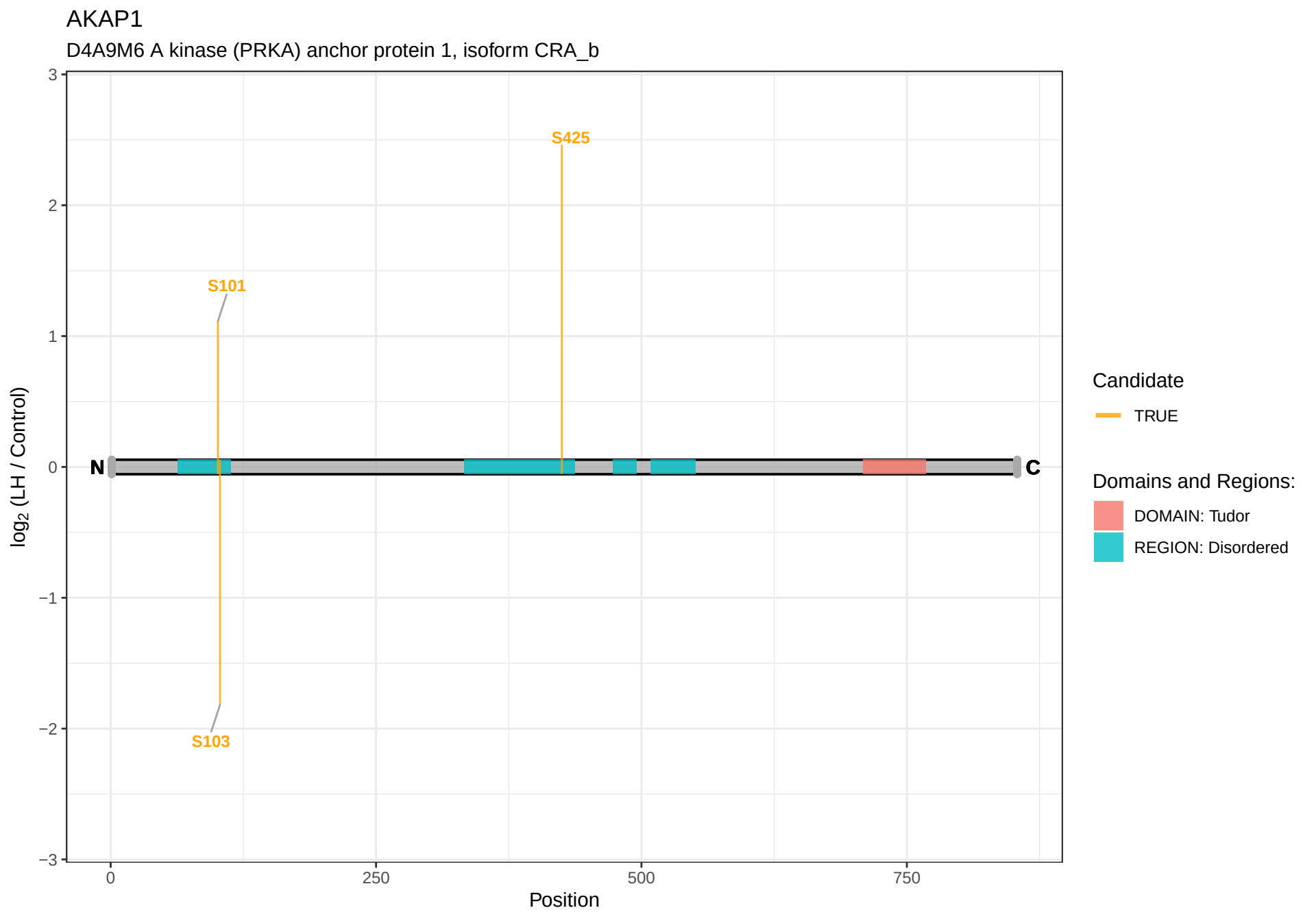

AHCTF1
D3ZZZ0 AT hook−containing transcription factor 1
log2 (LH / Control)
Position
2
1
0
−1
−2
0
500
1000
1500
2000
N
C
S1305
S1308
S1744
S1862
S1214
S1218
S2195
S2199
S1087
S1794
S1980
S1927
S1792
S1138
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ELYS
DOMAIN: ELYS−bb
REGION: Disordered

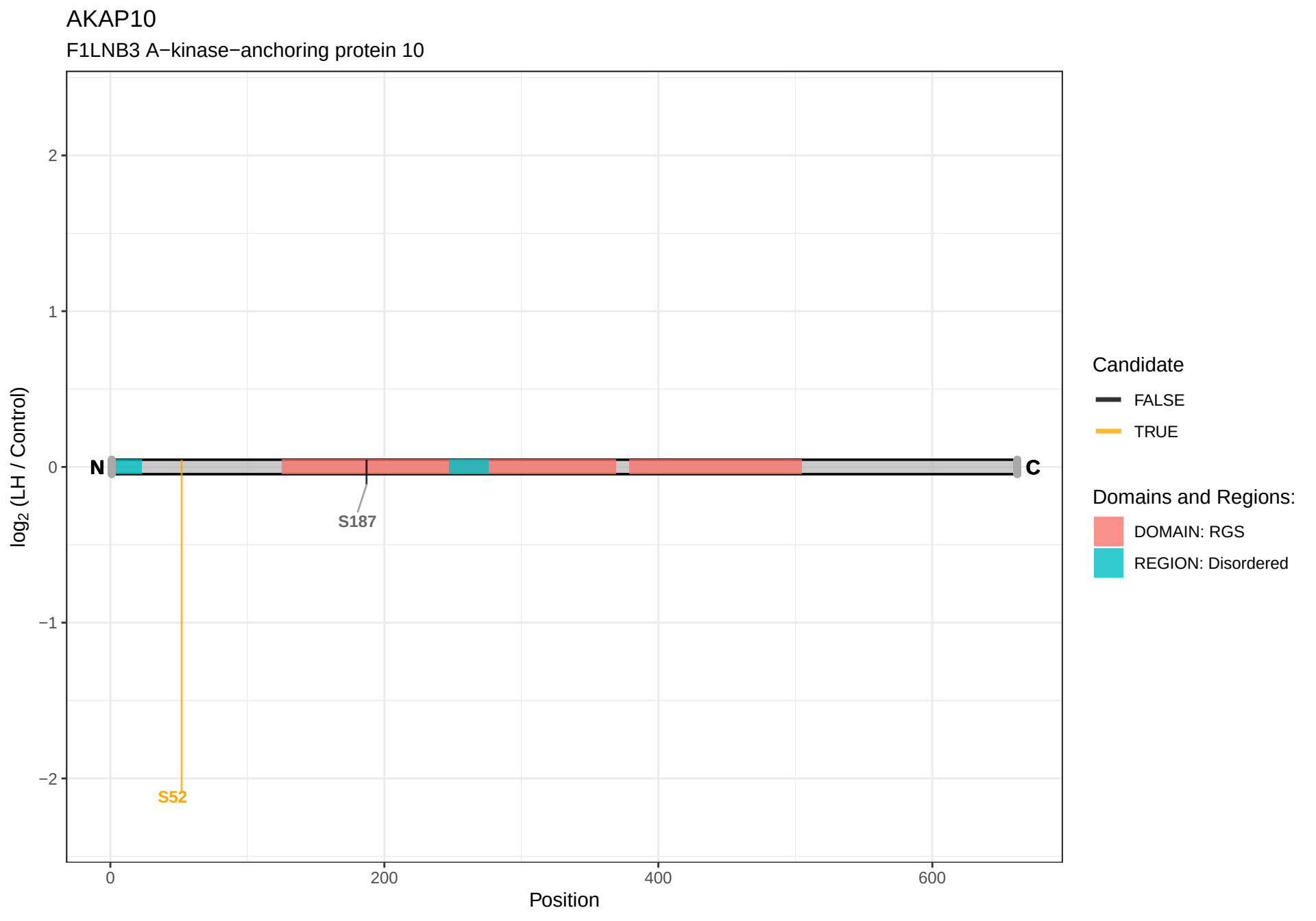

AHDC1
D4A5R3 AT hook, DNA−binding motif,−containing 1
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
Position
N
C
S863
T1396
S1390
S1394
S844
S1178
S891
S1059
S46
S592
S841
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DUF4683
REGION: Disordered

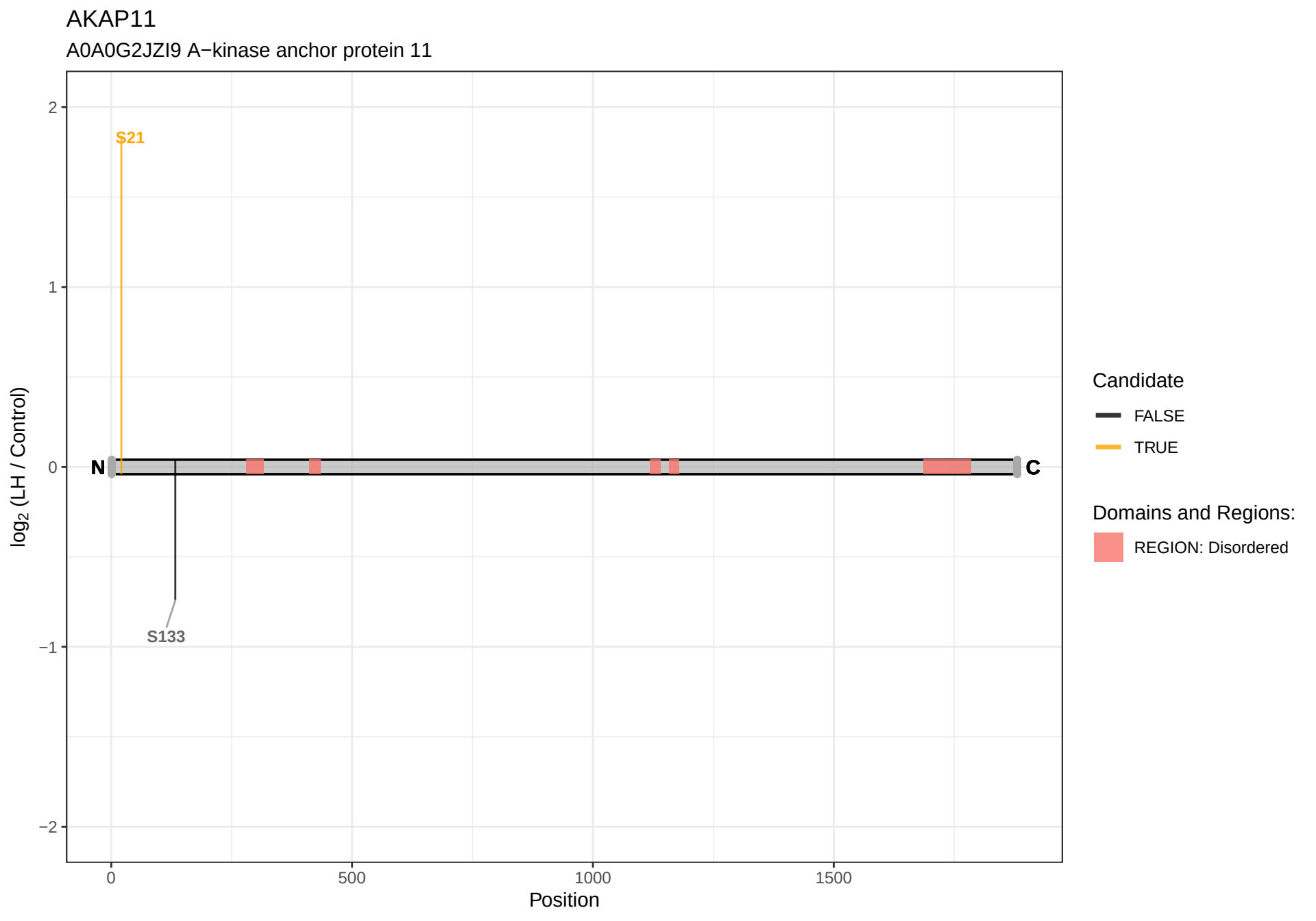

AHNAK
A0A0G2JUA5 AHNAK nucleoprotein
log2 (LH / Control)
Position
N
C
S211
S2013
S2536
S5347
S5349
S5423
S5427
S5313
S5312
S94
S136
S213
S178
S116
T219
S217
S889
S4002
S4442
S4684
S5038
S5316
S5351
S5430
S5417
T5361
S5329
S5414
S5319
S5401
S5330
S5306
S5357
S5298
S5360
S5411
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PDZ
REGION: Disordered

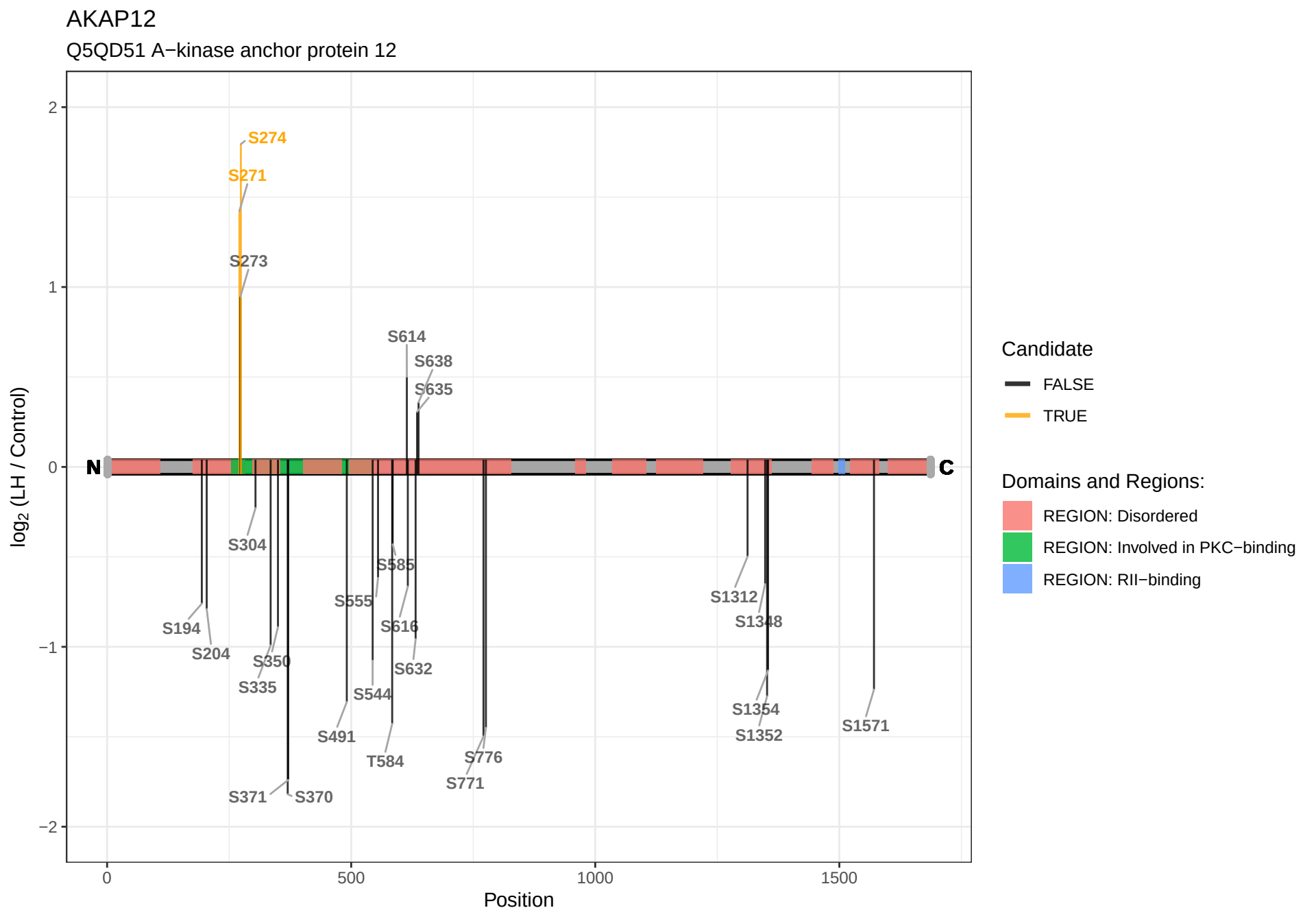

AIF1L
D3ZRD9 Allograft inflammatory factor 1−like
2
1
0
−1
−2
log2 (LH / Control)
N
C
S134
0
50
100
150
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: EF−hand
REGION: Disordered

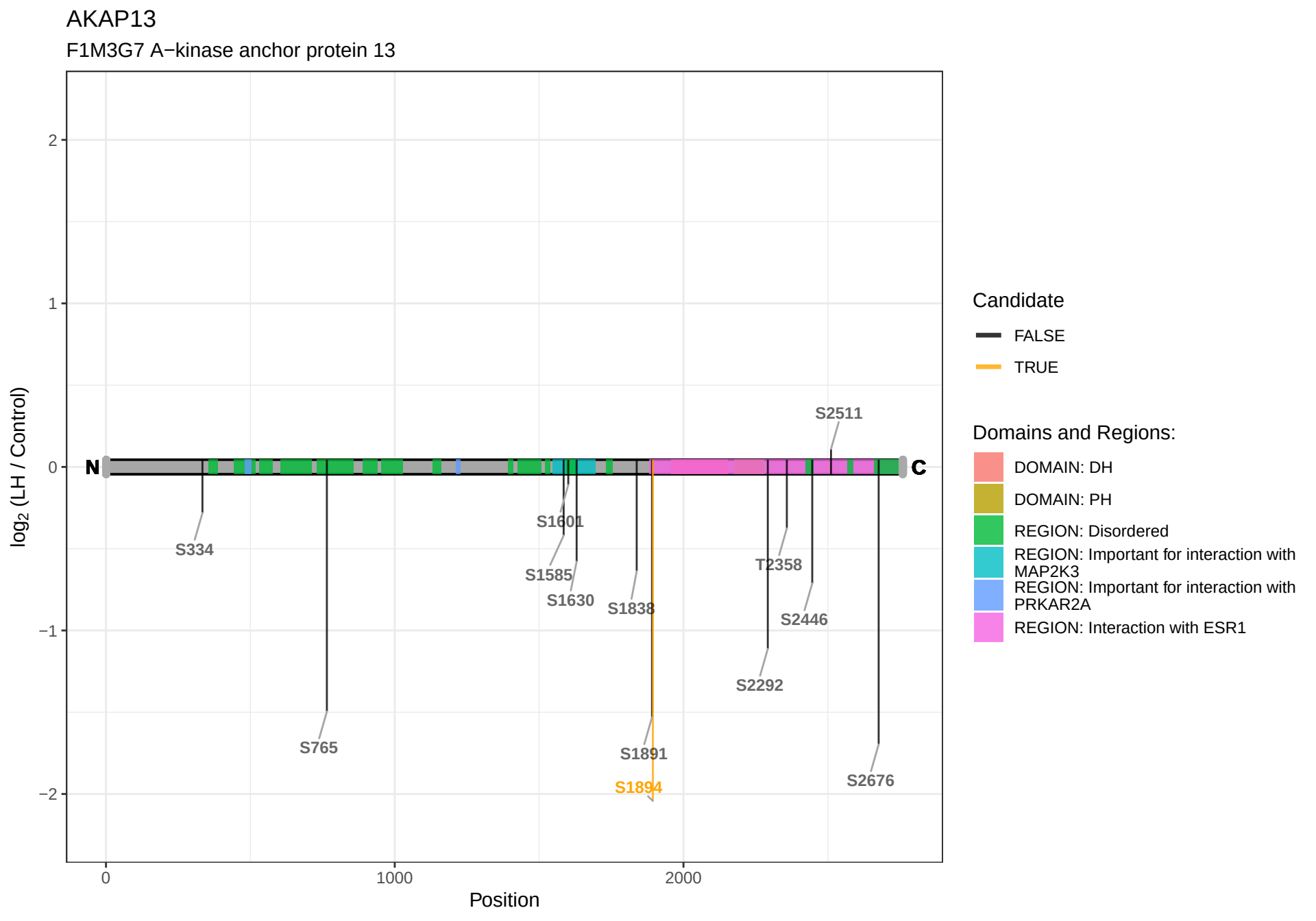

AIMP1
Q4G079 Aminoacyl tRNA synthetase complex−interacting multifunctional protein 1
S110
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
100
200
300
Candidate
TRUE
Domains and Regions:
DOMAIN: TRNA−binding
REGION: Disordered

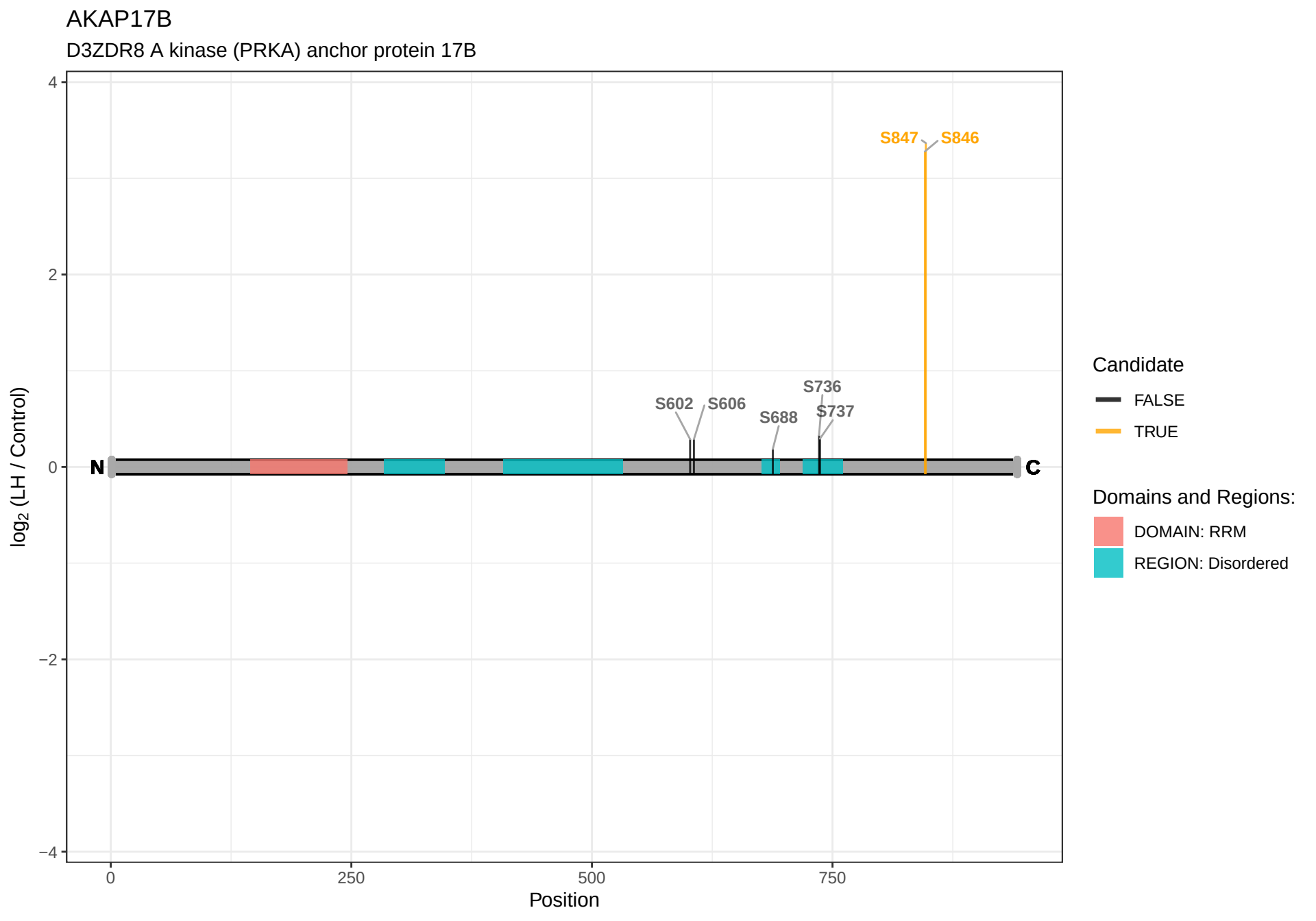

AKAP1
D4A9M6 A kinase (PRKA) anchor protein 1, isoform CRA_b
S425
S101
S103
N
C
log2 (LH / Control)
Position
3
2
1
0
−1
−2
−3
0
250
500
750
Candidate
TRUE
Domains and Regions:
DOMAIN: Tudor
REGION: Disordered

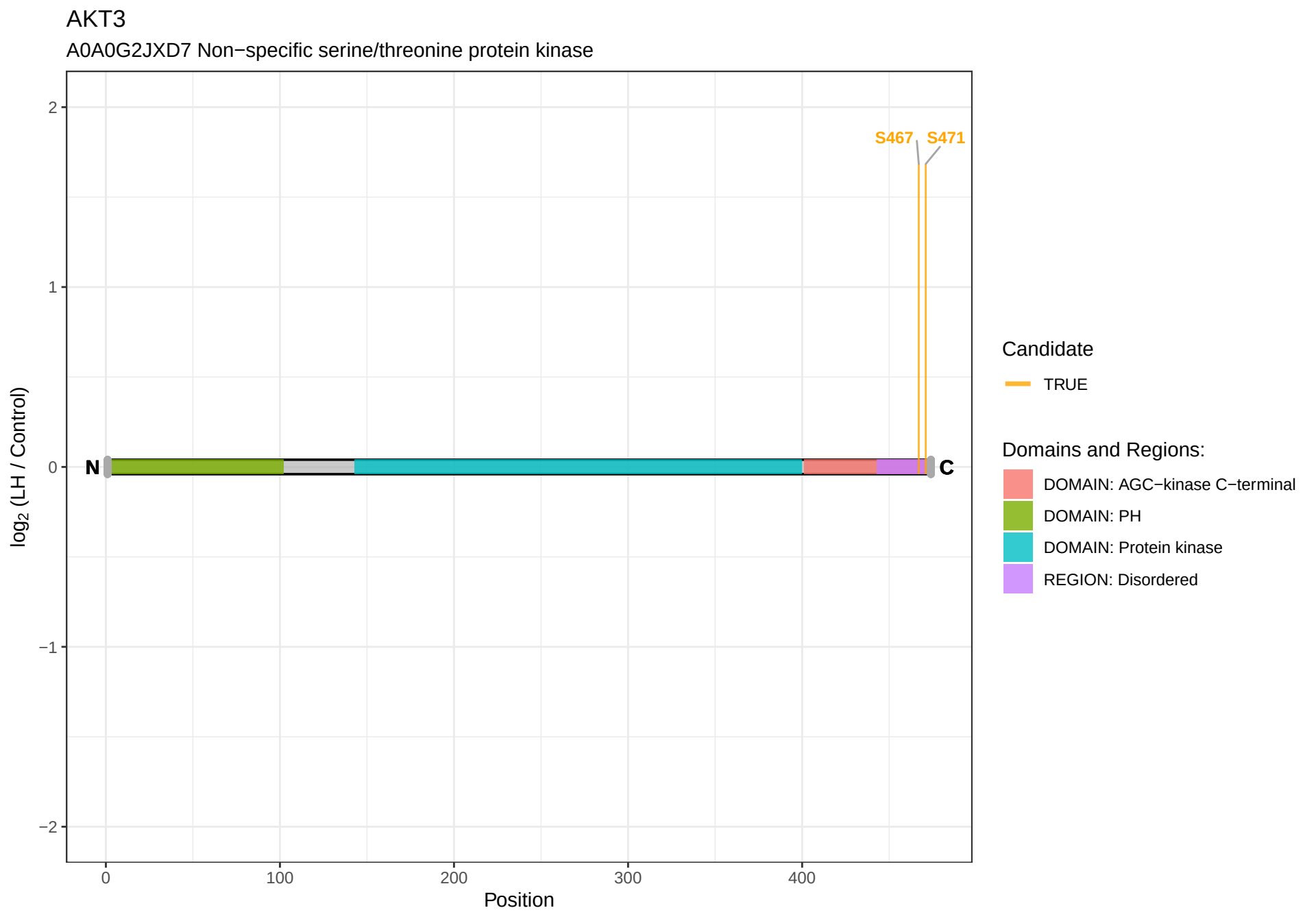

AKAP10
F1LNB3 A−kinase−anchoring protein 10
log2 (LH / Control)
2
1
0
−1
−2
N
C
S187
S52
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RGS
REGION: Disordered

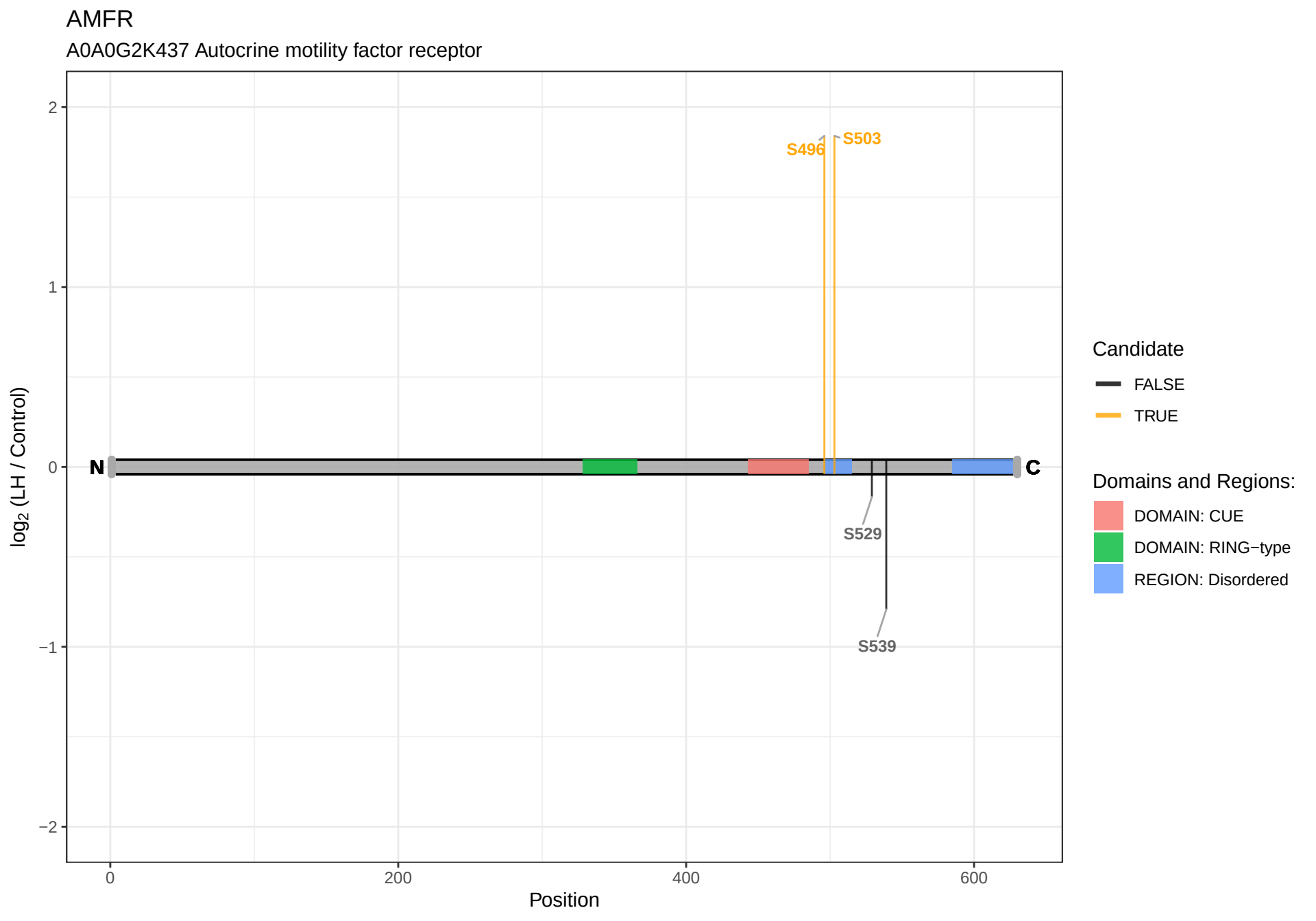

AKAP11
A0A0G2JZI9 A−kinase anchor protein 11
S21
S133
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

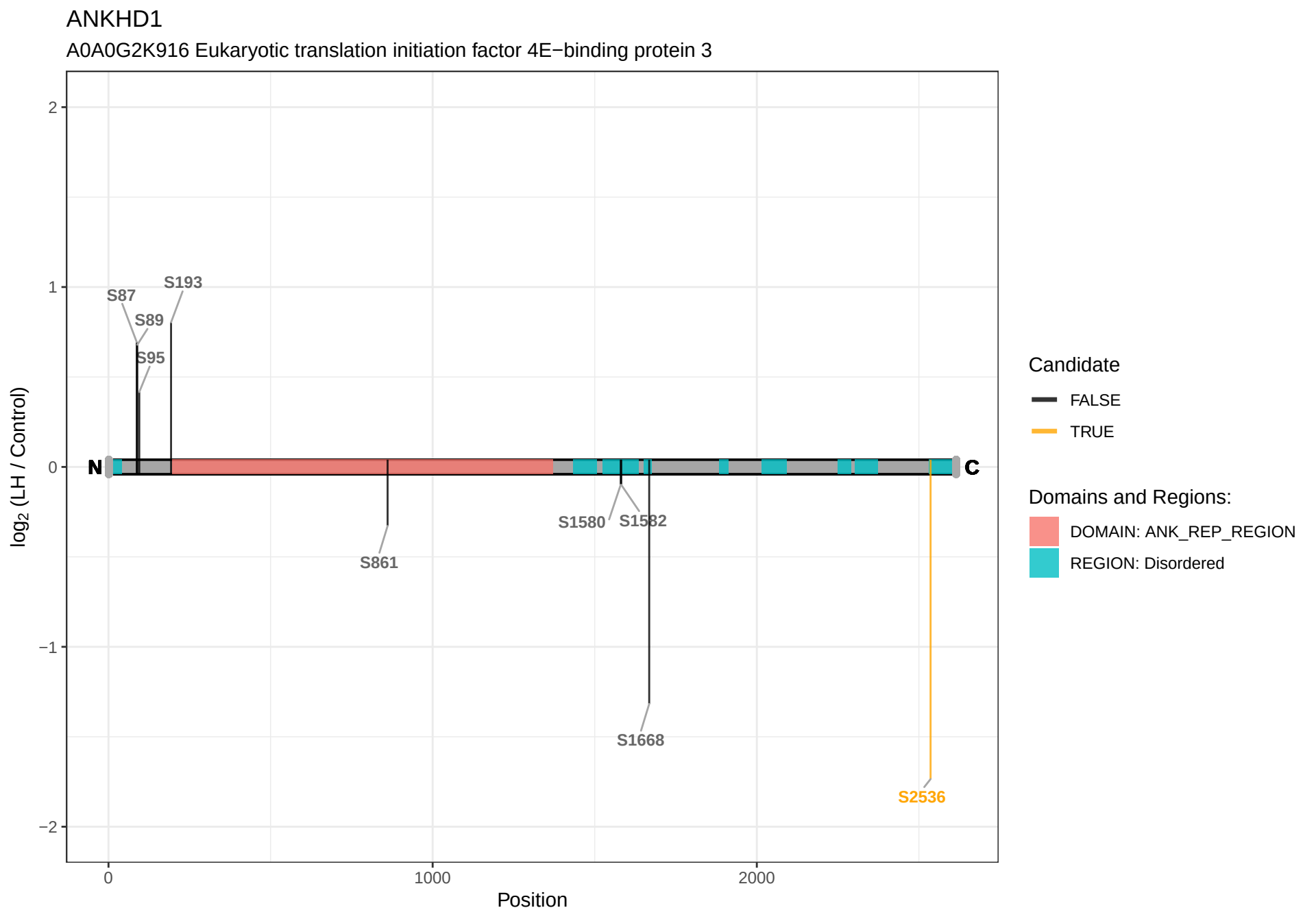

AKAP12
Q5QD51 A−kinase anchor protein 12
log2 (LH / Control)
Position
N
C
S274
S271
S273
S614
S638
S635
S304
S585
S555
S616
S194
S204
S350
S632
S335
S544
S491
T584
S776
S771
S371
S370
S1312
S1348
S1354
S1352
S1571
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Involved in PKC−binding
REGION: RII−binding

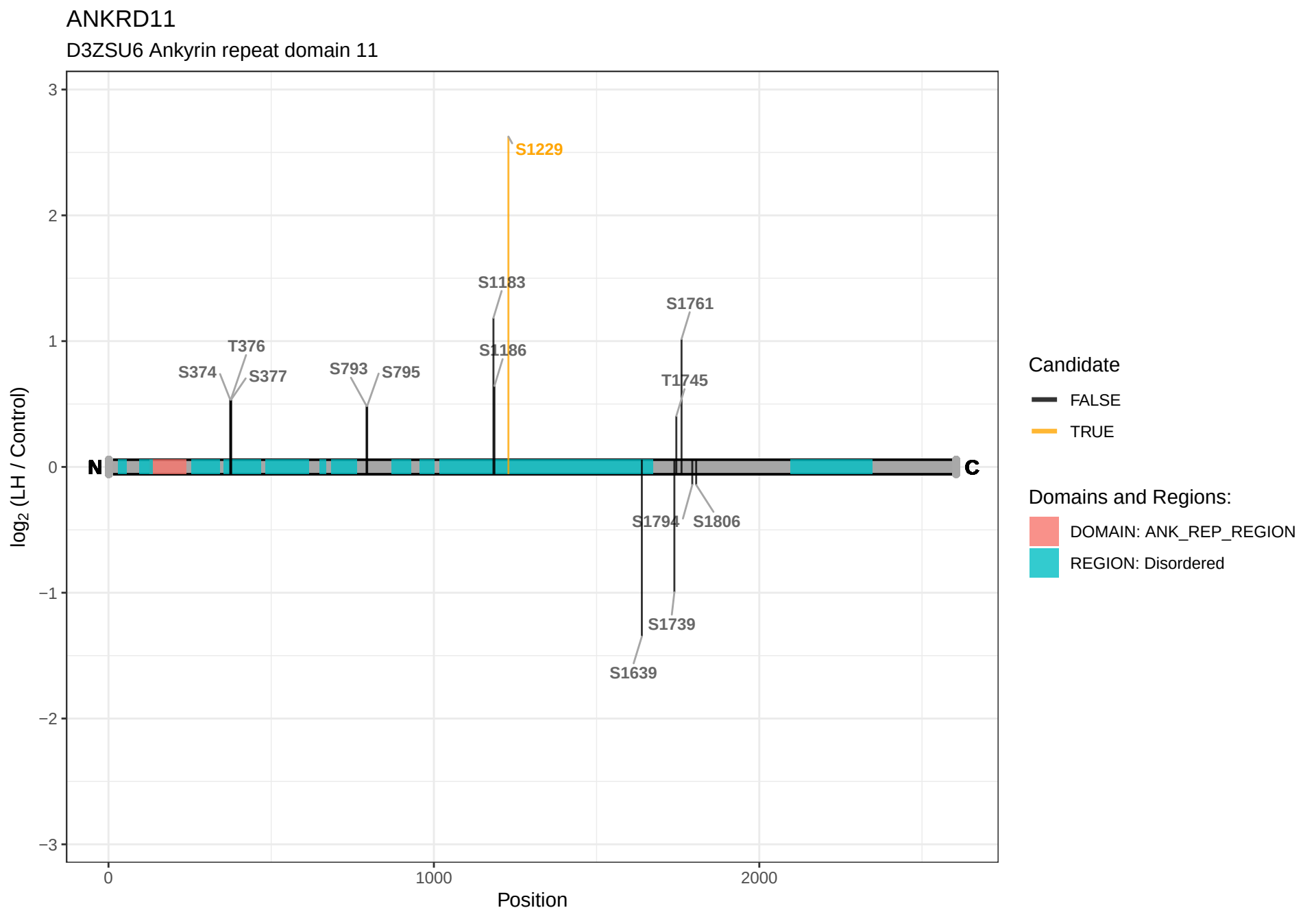

AKAP13
F1M3G7 A−kinase anchor protein 13
log2 (LH / Control)
2
1
0
−1
−2
N
C
S334
S765
S1601
S1585
S1630
S1838
S1891
S1894
S2292
T2358
S2446
S2511
S2676
0
1000
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DH
DOMAIN: PH
REGION: Disordered
REGION: Important for interaction with MAP2K3
REGION: Important for interaction with PRKAR2A
REGION: Interaction with ESR1

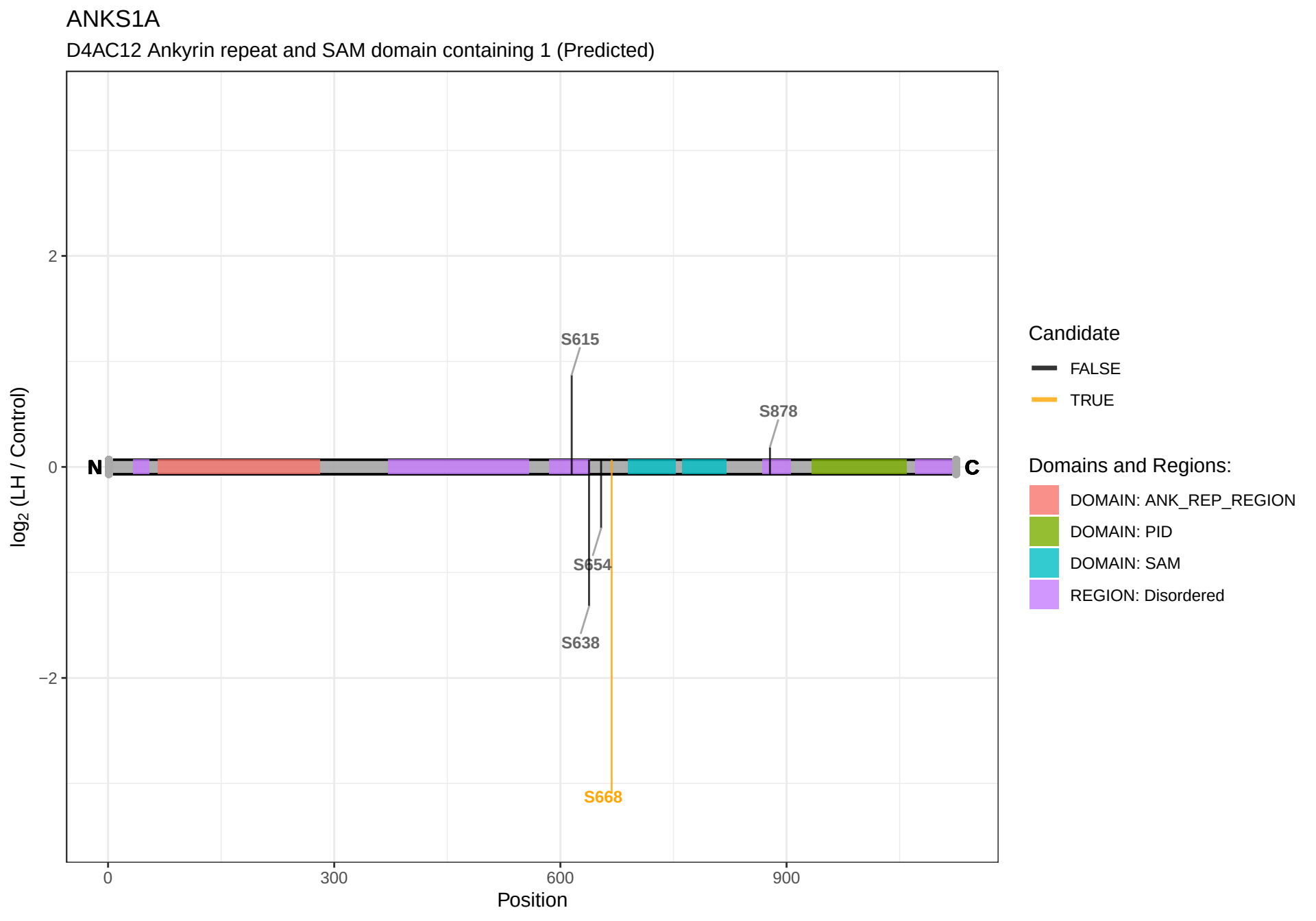

AKAP17B
D3ZDR8 A kinase (PRKA) anchor protein 17B
log2 (LH / Control)
4
2
0
−2
−4
0
250
500
750
Position
N
C
S847
S846
S602
S606
S736
S737
S688
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RRM
REGION: Disordered

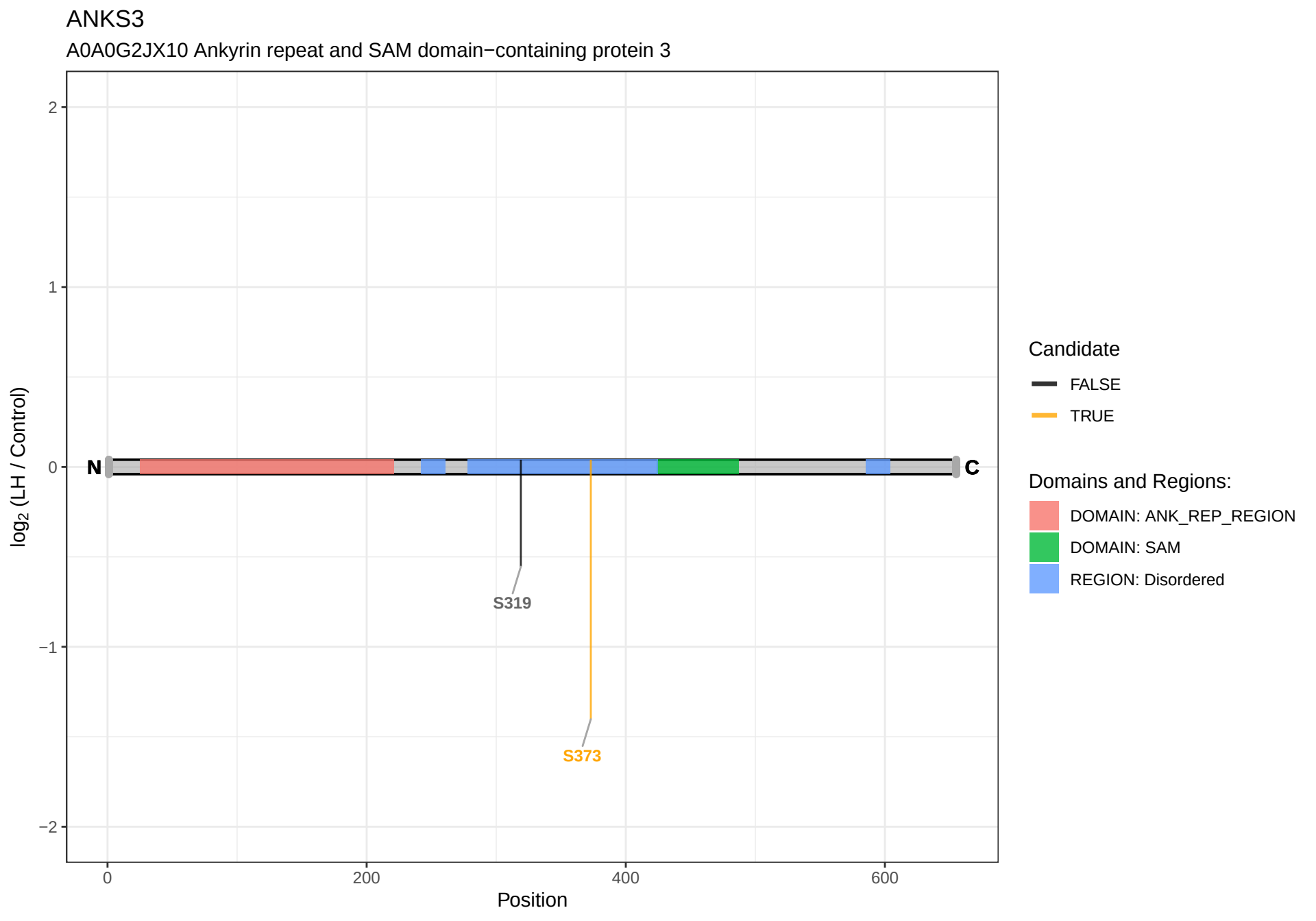

AKT3
A0A0G2JXD7 Non−specific serine/threonine protein kinase
S467
S471
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
100
200
300
400
Candidate
TRUE
Domains and Regions:
DOMAIN: AGC−kinase C−terminal
DOMAIN: PH
DOMAIN: Protein kinase
REGION: Disordered

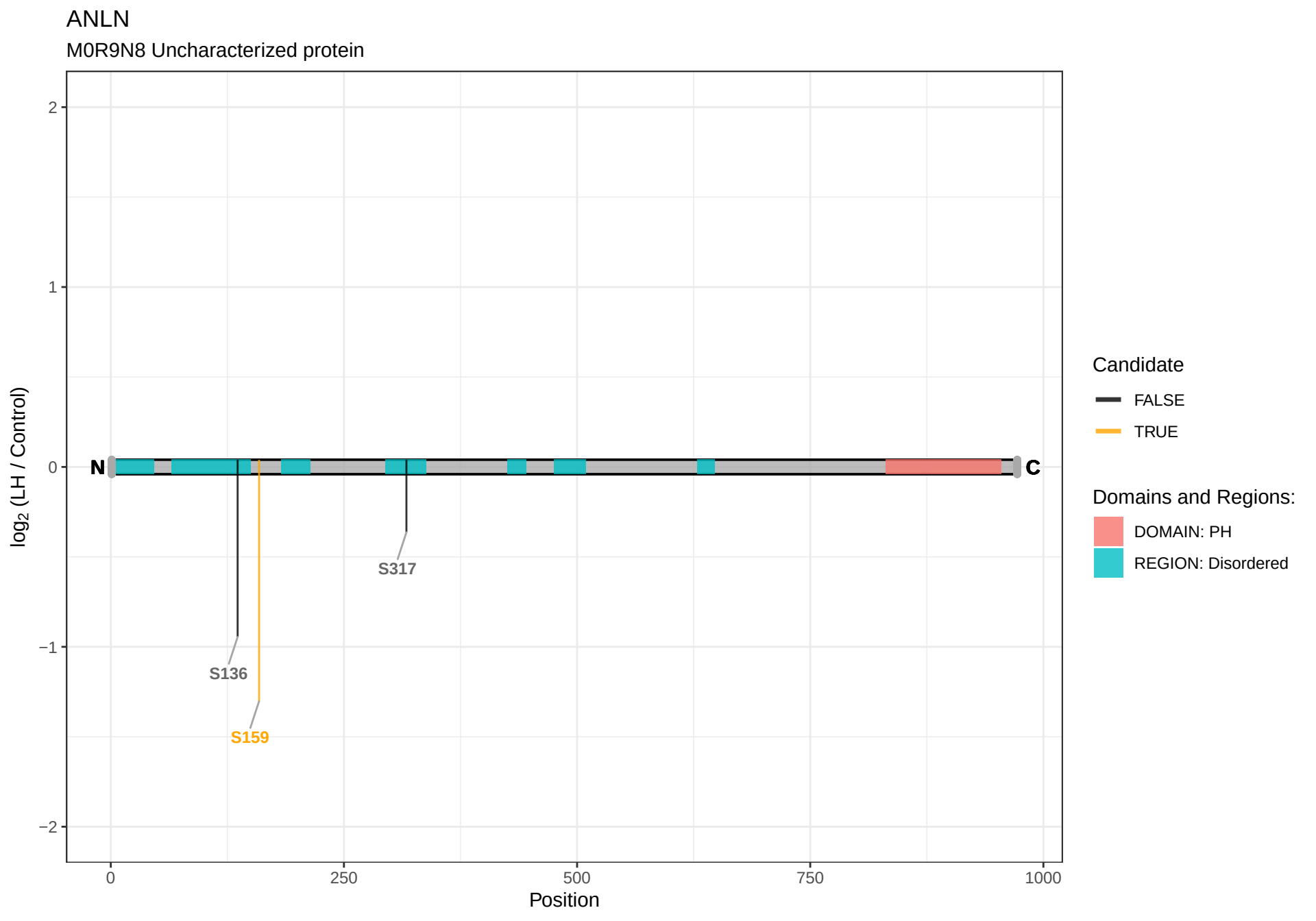

AMFR
A0A0G2K437 Autocrine motility factor receptor
log2 (LH / Control)
2
1
0
−1
−2
N
C
S496
S503
S529
S539
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CUE
DOMAIN: RING−type
REGION: Disordered

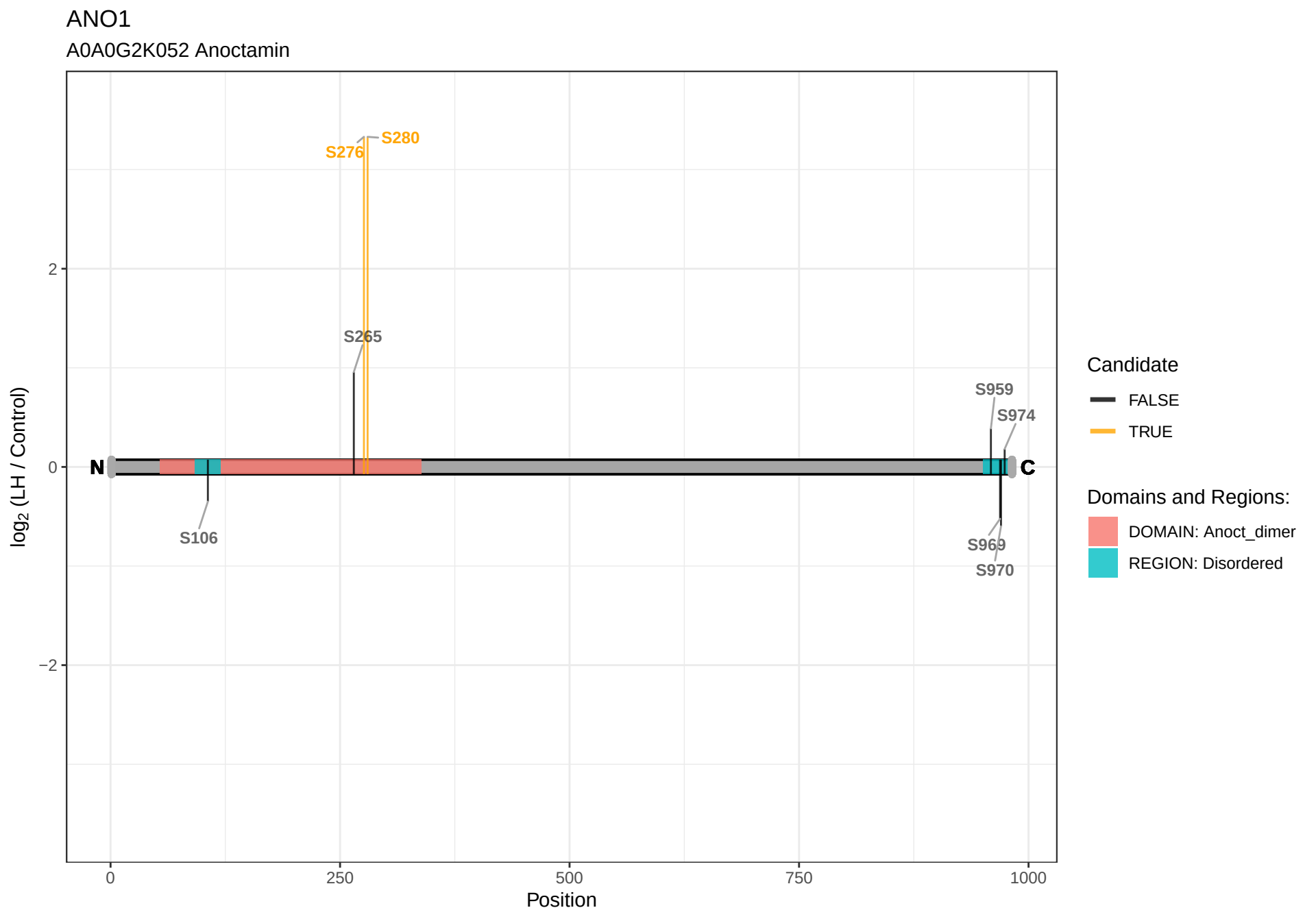

ANKHD1
A0A0G2K916 Eukaryotic translation initiation factor 4E−binding protein 3
log2 (LH / Control)
2
1
0
−1
−2
0
1000
2000
Position
N
C
S87
S89
S95
S193
S861
S1580
S1582
S1668
S2536
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ANK_REP_REGION
REGION: Disordered

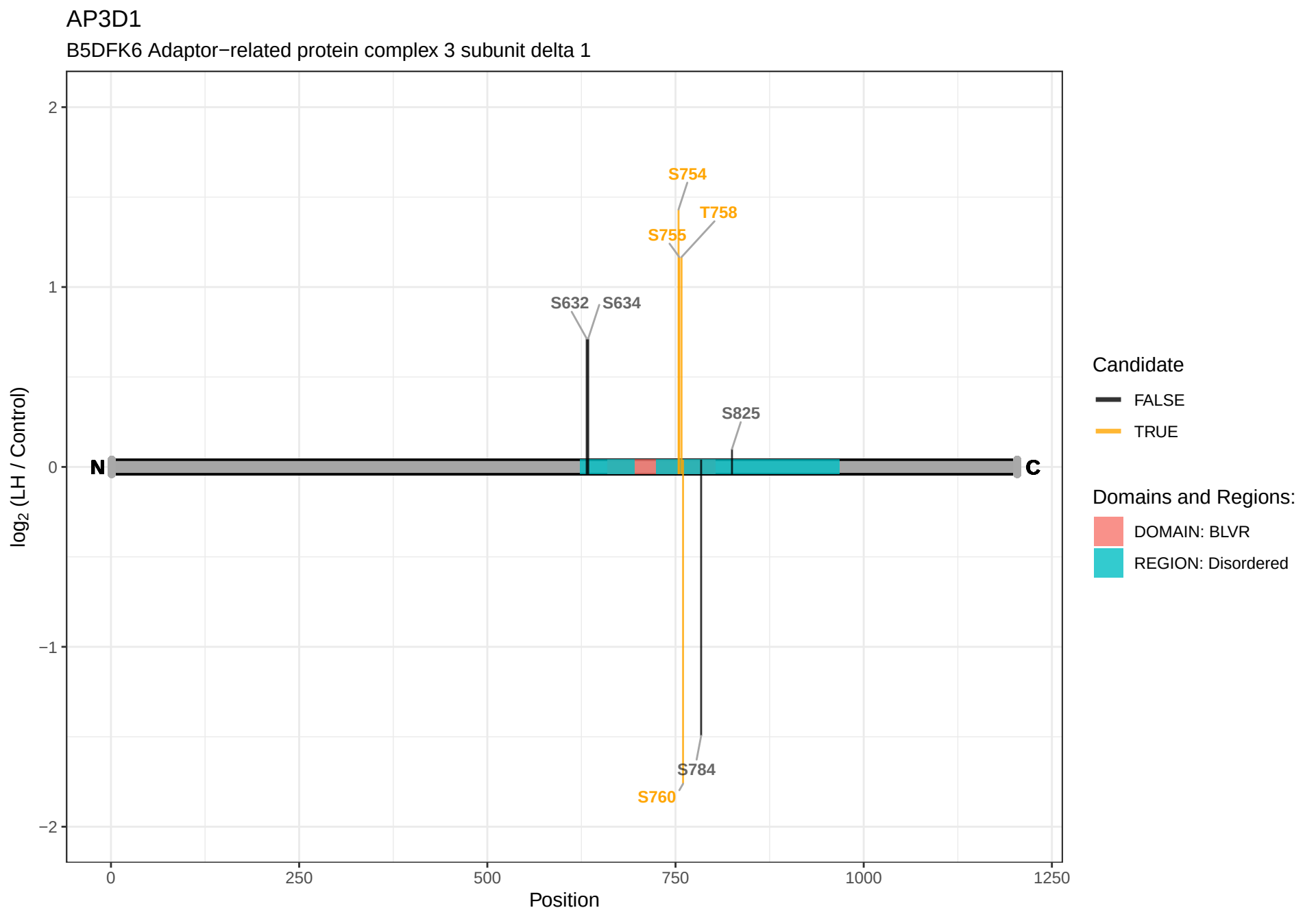

ANKRD11
D3ZSU6 Ankyrin repeat domain 11
log2 (LH / Control)
Position
N
C
S1229
S1183
S1761
T376
S374
S377
S793
S795
S1186
T1745
S1794
S1806
S1739
S1639
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ANK_REP_REGION
REGION: Disordered

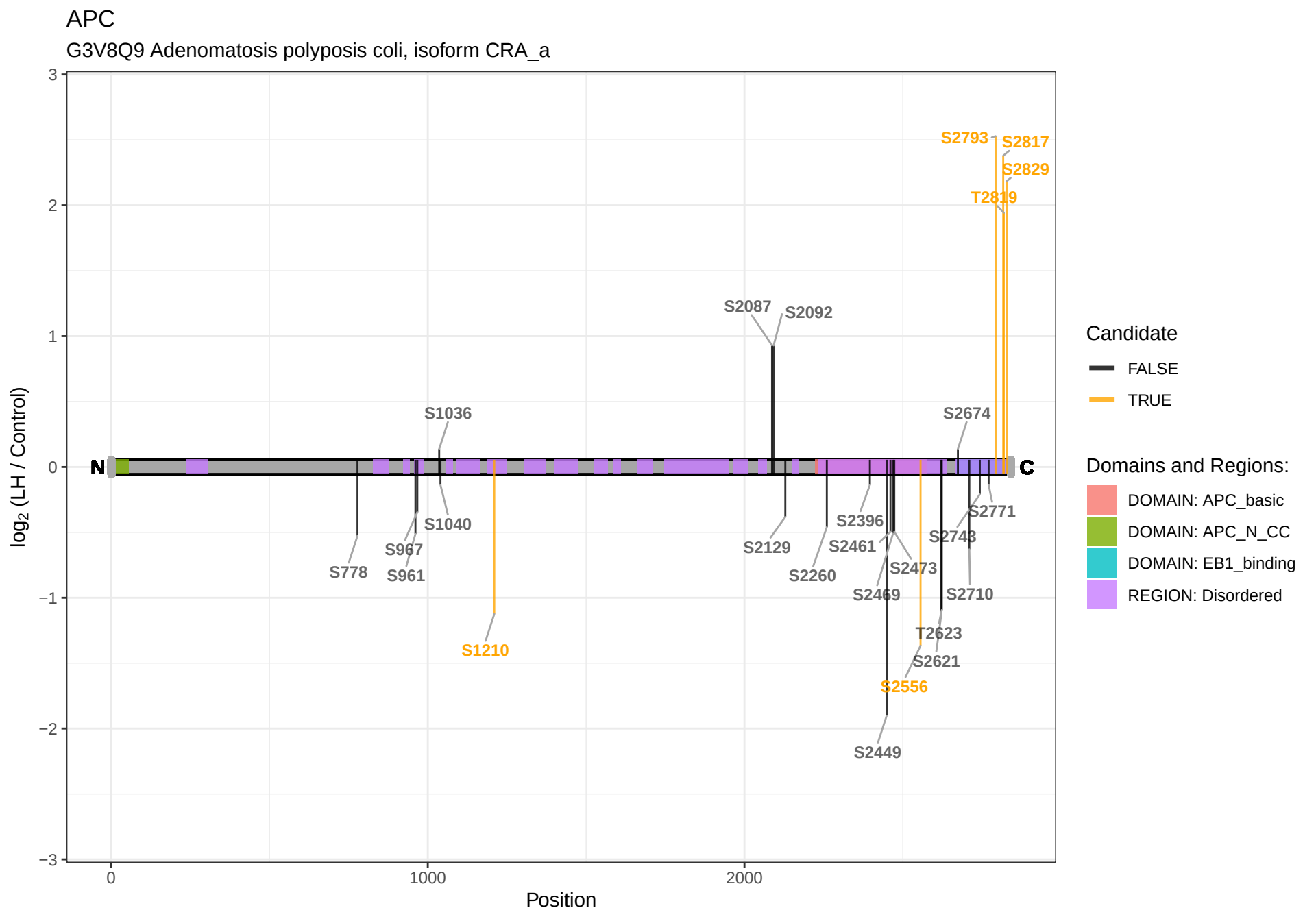

ANKS1A
D4AC12 Ankyrin repeat and SAM domain containing 1 (Predicted)
log2 (LH / Control)
2
0
−2
N
C
S615
S878
S654
S638
S668
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ANK_REP_REGION
DOMAIN: PID
DOMAIN: SAM
REGION: Disordered

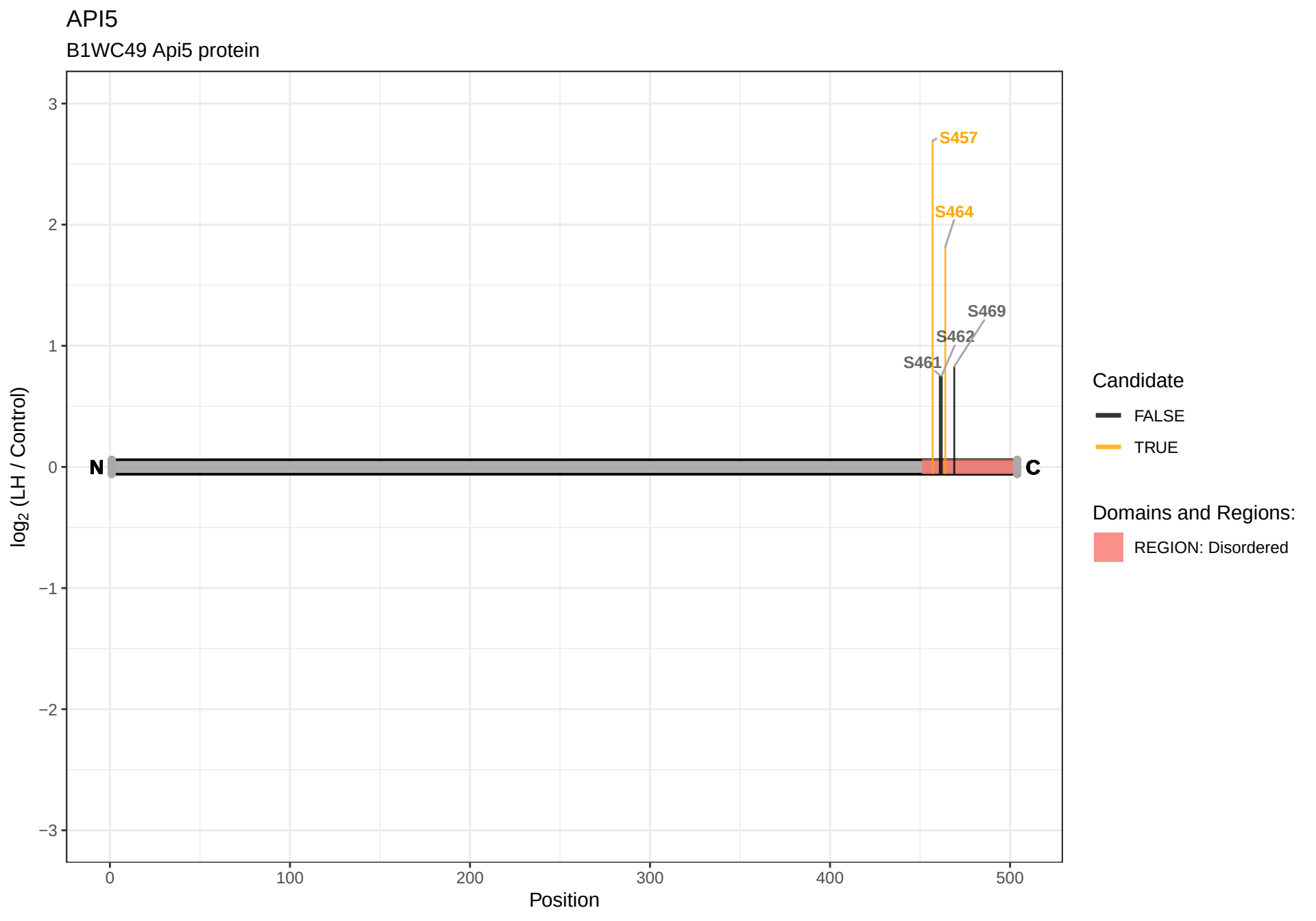

ANKS3
A0A0G2JX10 Ankyrin repeat and SAM domain−containing protein 3
log2 (LH / Control)
2
1
0
−1
−2
N
C
S319
S373
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ANK_REP_REGION
DOMAIN: SAM
REGION: Disordered

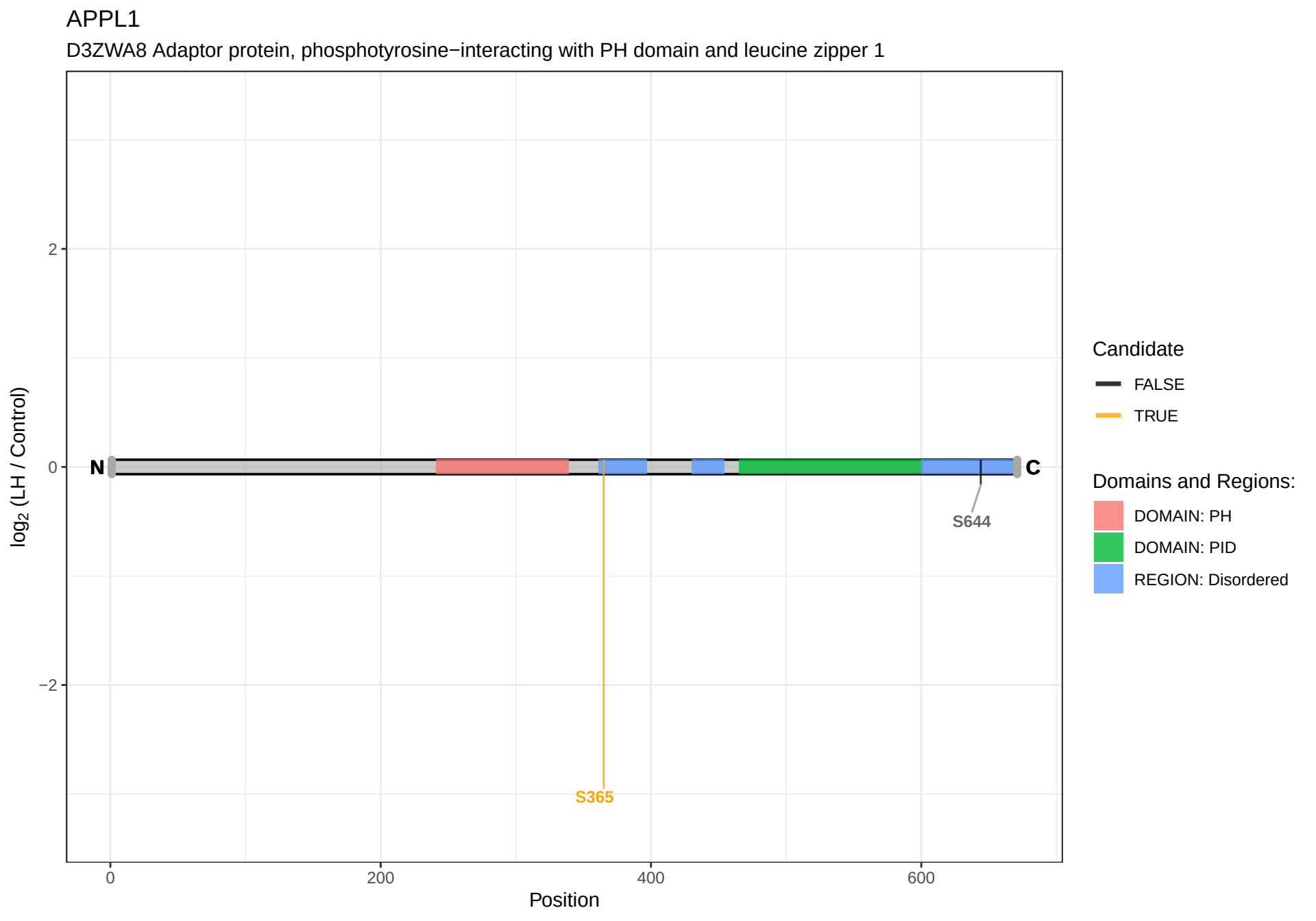

ANLN
M0R9N8 Uncharacterized protein
2
1
0
−1
−2
log2 (LH / Control)
N
C
S317
S136
S159
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PH
REGION: Disordered

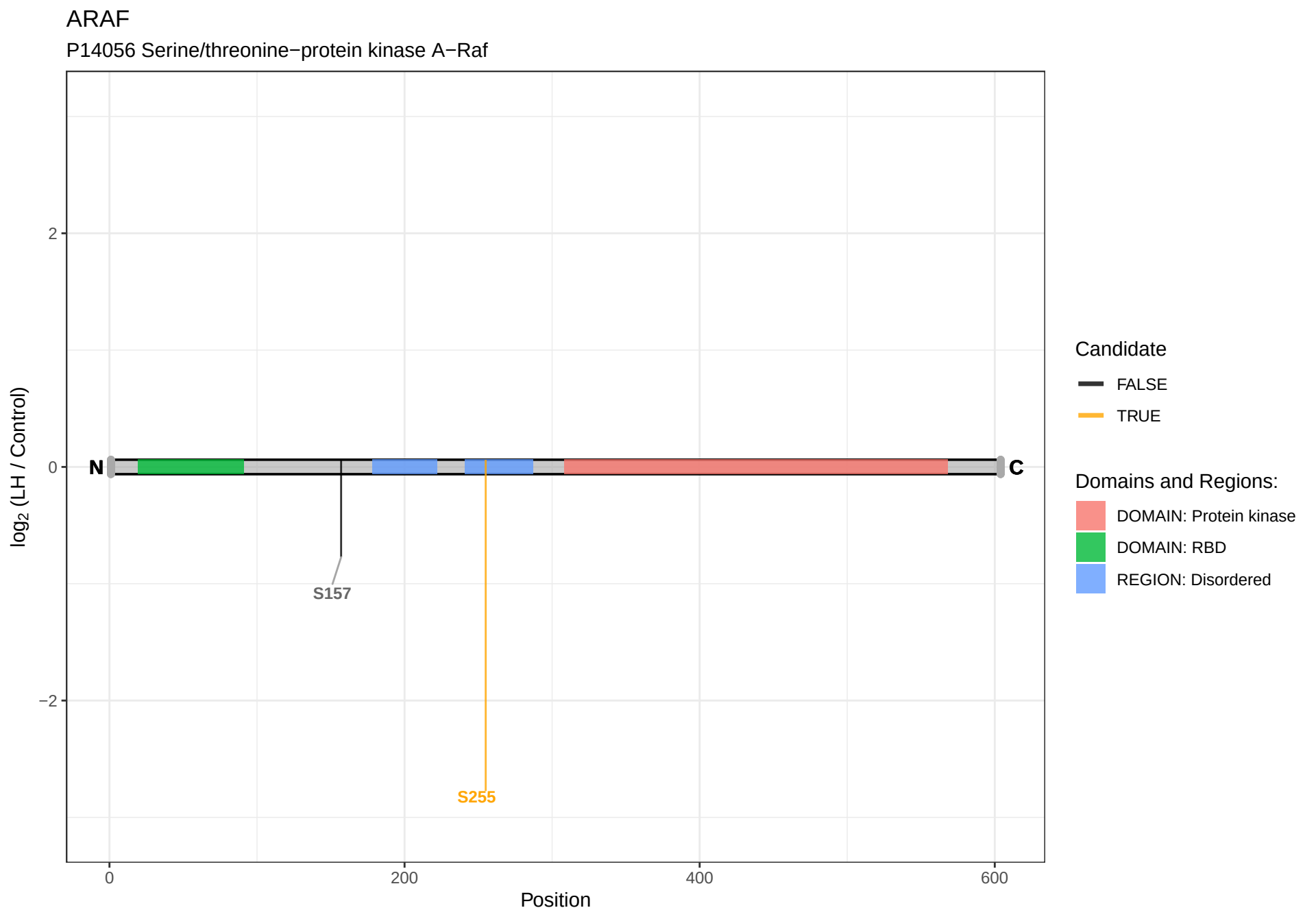

ANO1
A0A0G2K052 Anoctamin
S276
S280
S265
S106
S959
S974
S969
S970
N
C
2
0
−2
log2 (LH / Control)
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Anoct_dimer
REGION: Disordered

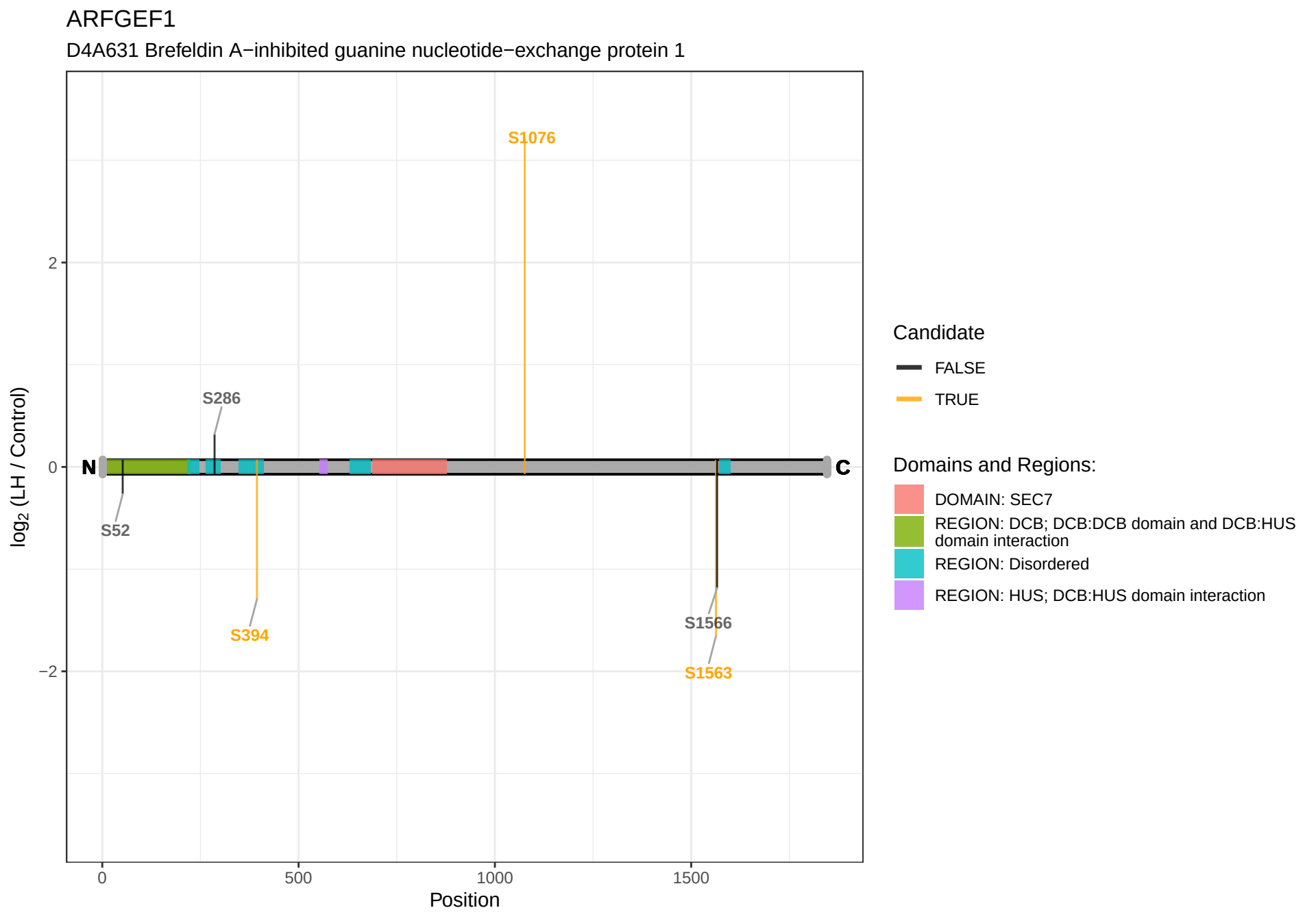

AP3D1
B5DFK6 Adaptor−related protein complex 3 subunit delta 1
log2 (LH / Control)
2
1
0
−1
−2
0
250
500
750
1000
1250
Position
N
C
S754
T758
S755
S632
S634
S825
S784
S760
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: BLVR
REGION: Disordered

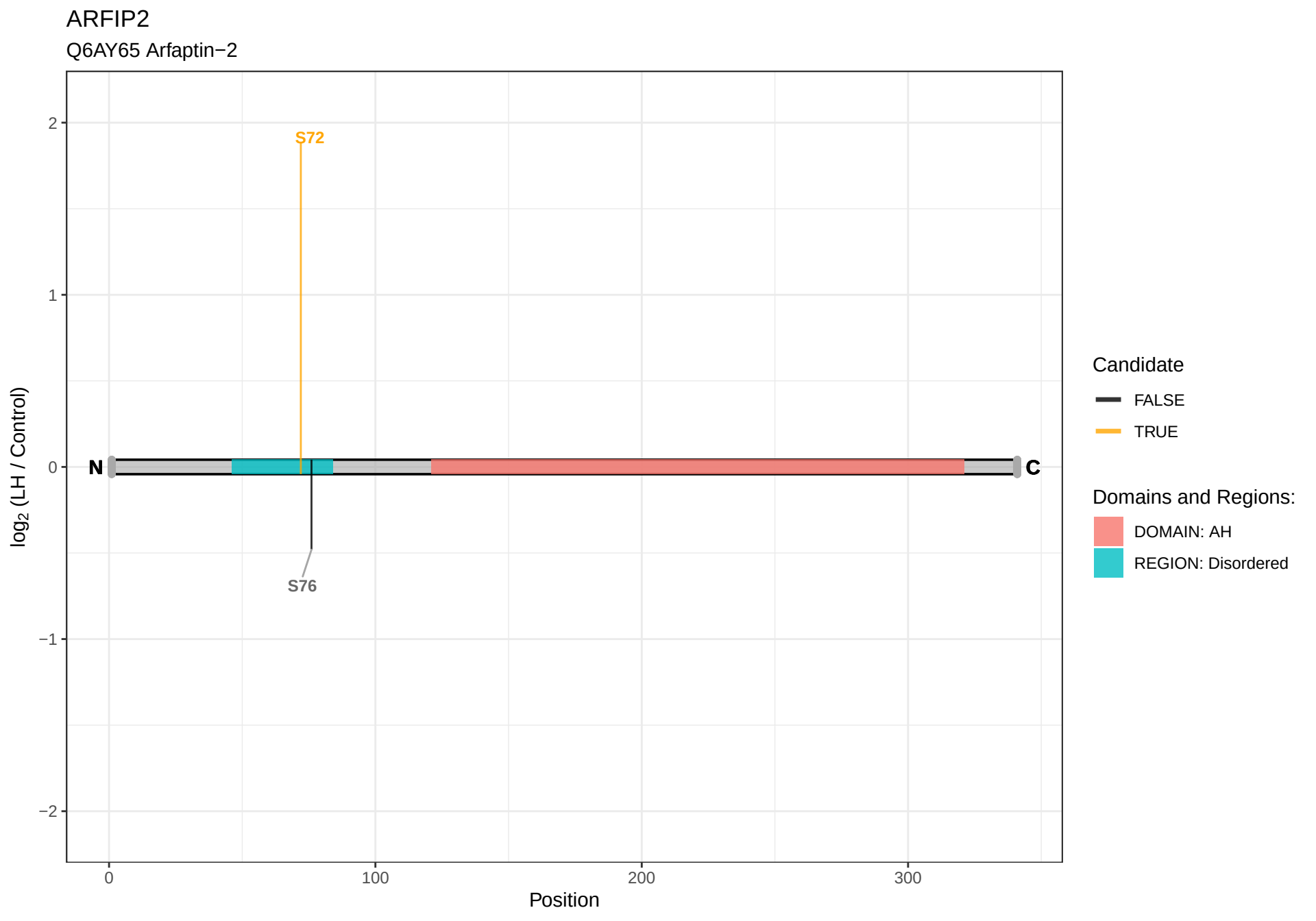

APC
G3V8Q9 Adenomatosis polyposis coli, isoform CRA_a
log2 (LH / Control)
Position
N
C
S2793
S2817
S2829
T2819
S2087
S2092
S1036
S2674
S1040
S967
S961
S778
S1210
S2129
S2396
S2461
S2260
S2473
S2469
S2771
S2743
S2710
T2623
S2621
S2556
S2449
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: APC_basic
DOMAIN: APC_N_CC
DOMAIN: EB1_binding
REGION: Disordered

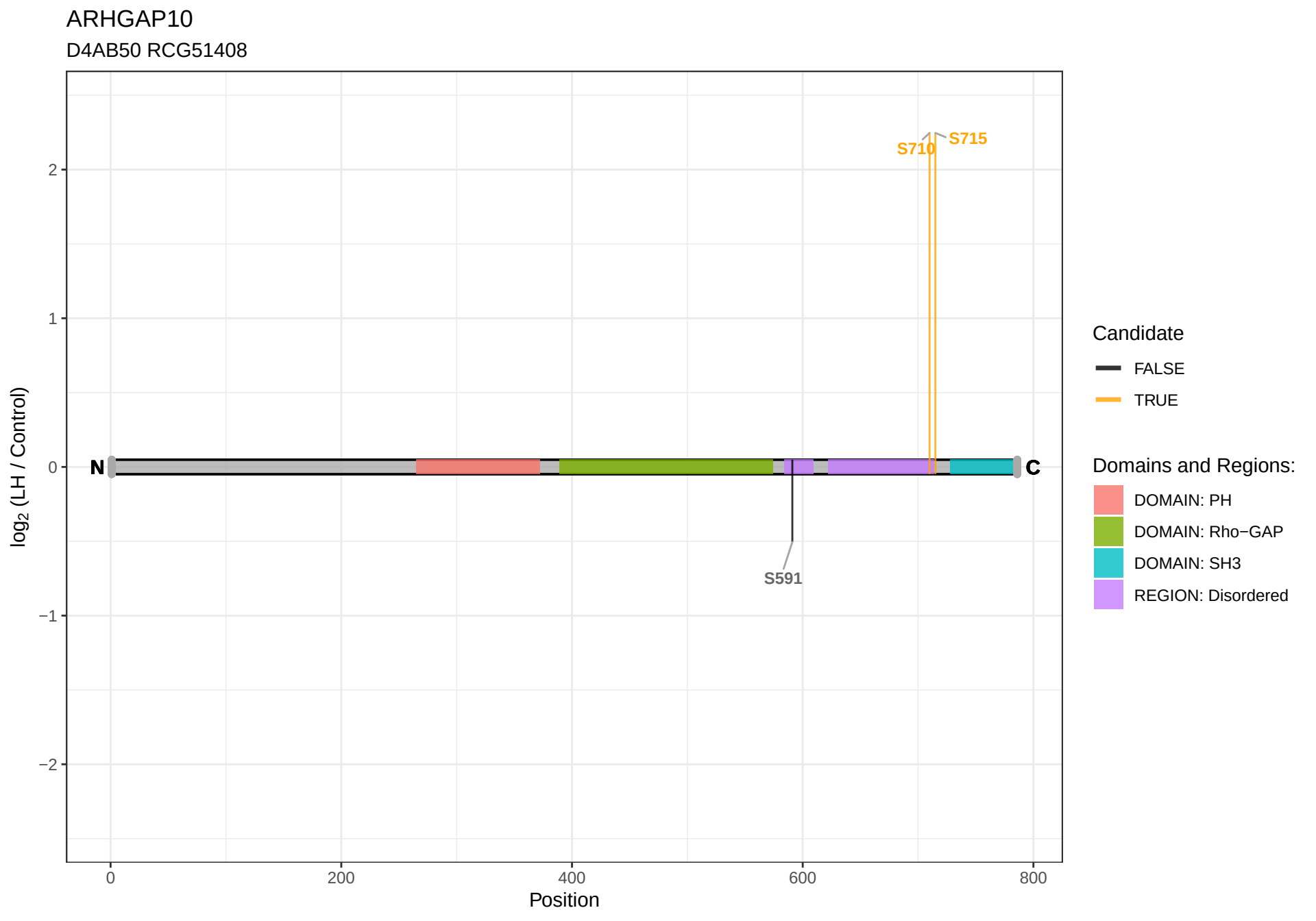

API5
B1WC49 Api5 protein
S457
S464
S469
S462
S461
N
C
log2 (LH / Control)
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

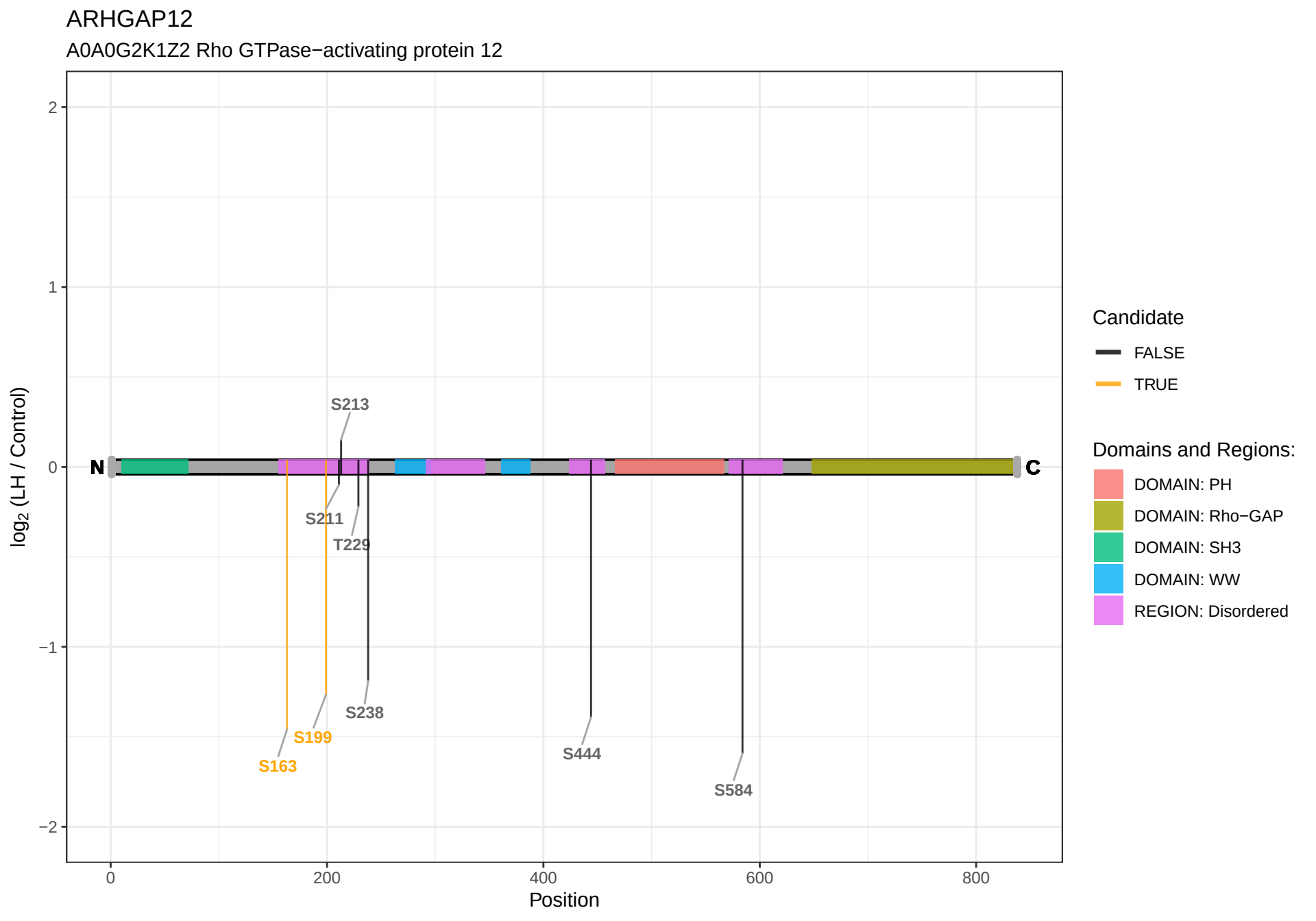

APPL1
D3ZWA8 Adaptor protein, phosphotyrosine−interacting with PH domain and leucine zipper 1
log2 (LH / Control)
2
0
−2
N
C
S644
S365
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PH
DOMAIN: PID
REGION: Disordered

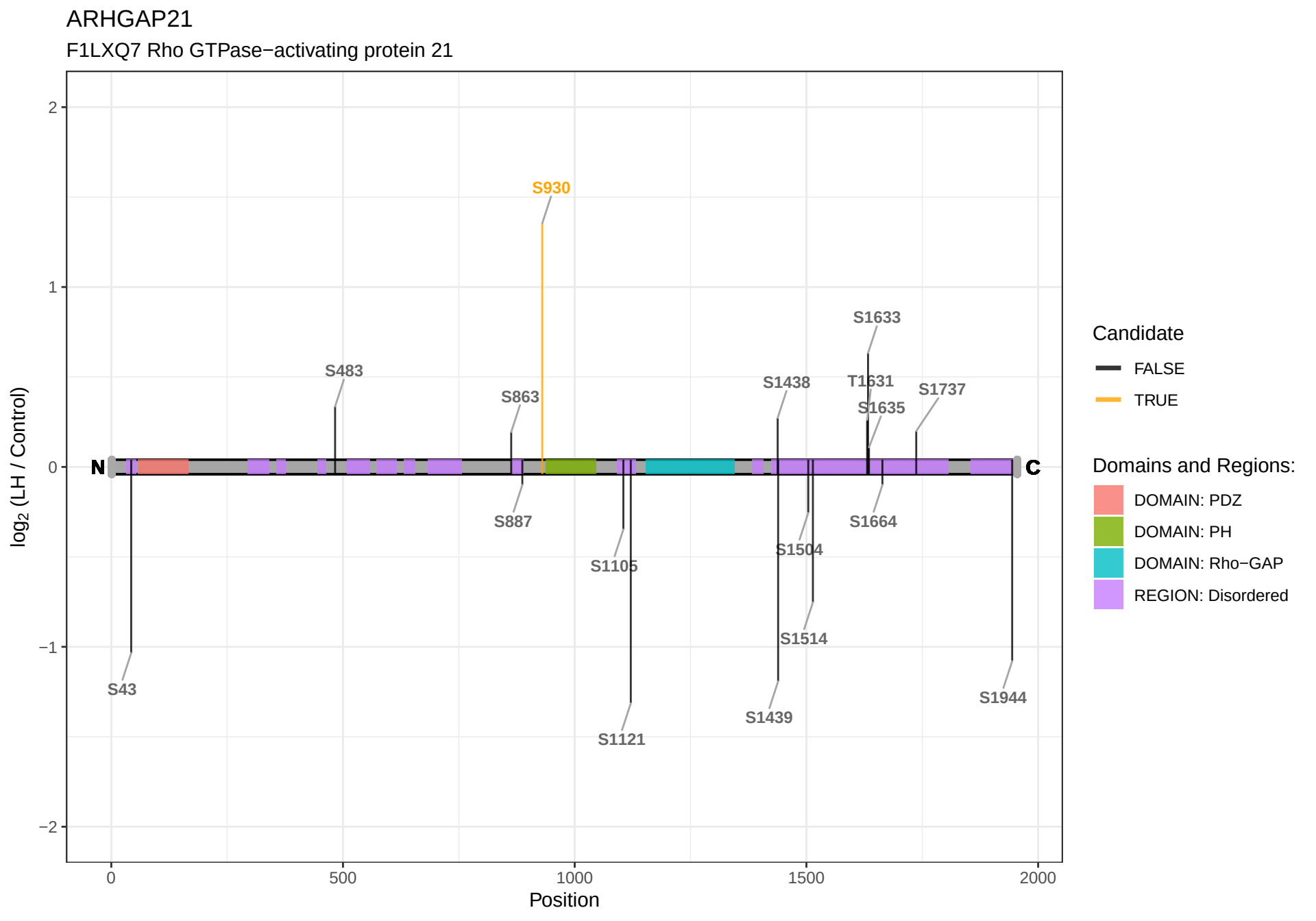

ARAF
P14056 Serine/threonine−protein kinase A−Raf
log2 (LH / Control)
2
0
−2
N
C
S157
S255
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
DOMAIN: RBD
REGION: Disordered

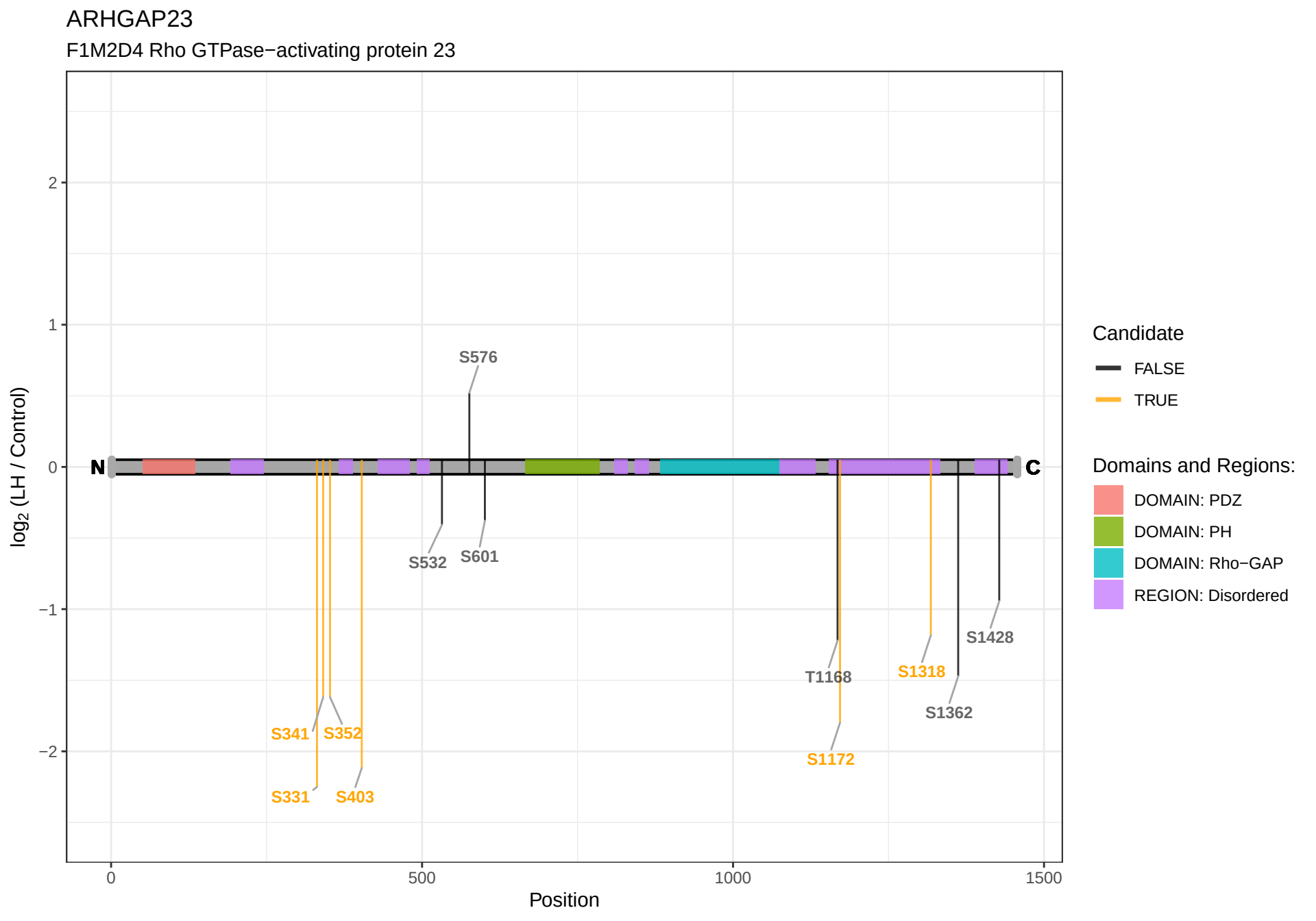

ARFGEF1
D4A631 Brefeldin A−inhibited guanine nucleotide−exchange protein 1
S1076
S286
N
C
S52
S394
S1566
S1563
2
0
−2
log2 (LH / Control)
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SEC7
REGION: DCB; DCB:DCB domain and DCB:HUS domain interaction
REGION: Disordered
REGION: HUS; DCB:HUS domain interaction

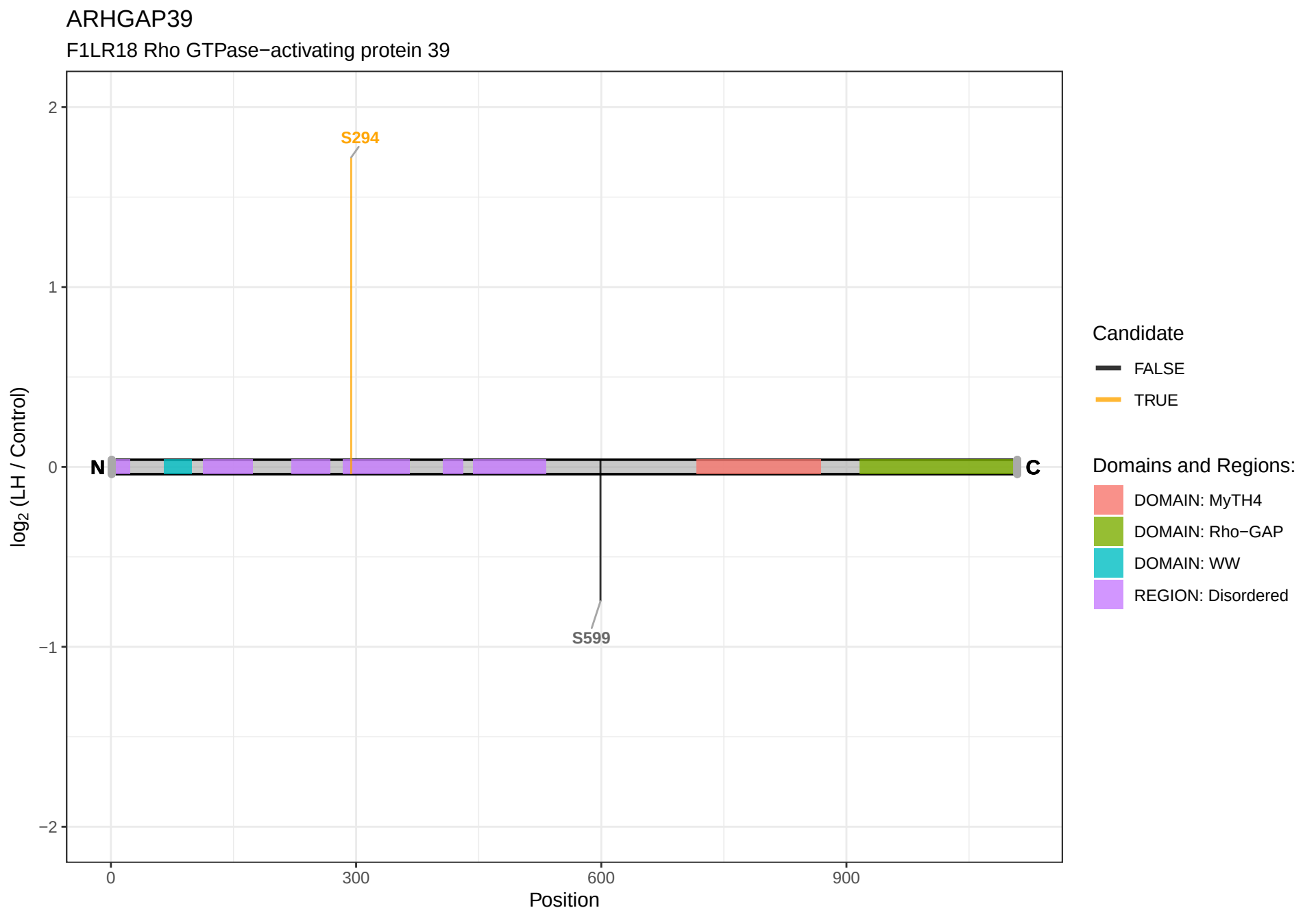

ARFIP2
Q6AY65 Arfaptin−2
S72
S76
N
C
2
1
0
−1
−2
0
100
200
300
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AH
REGION: Disordered

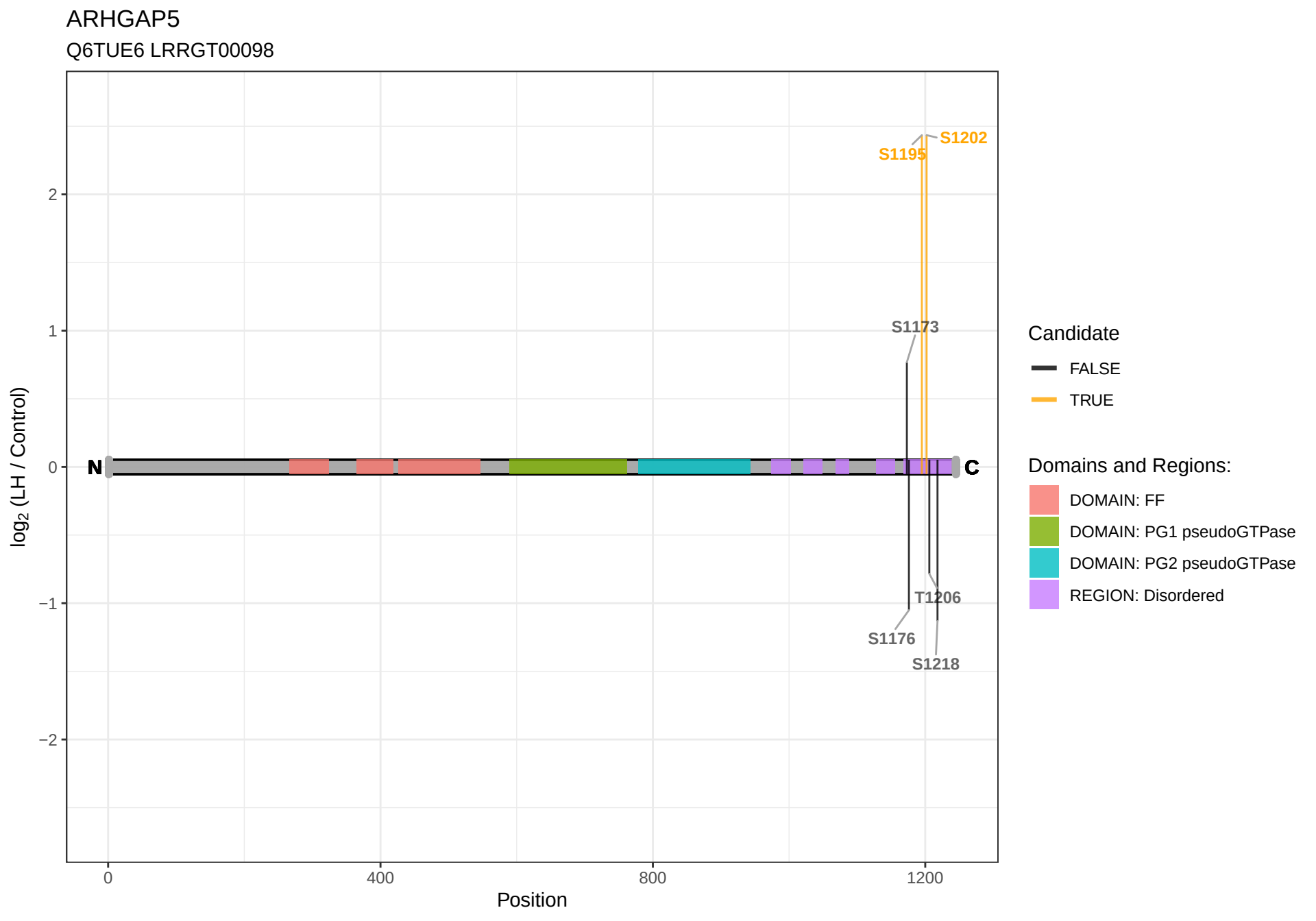

ARHGAP10
D4AB50 RCG51408
S710
S715
S591
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PH
DOMAIN: Rho−GAP
DOMAIN: SH3
REGION: Disordered

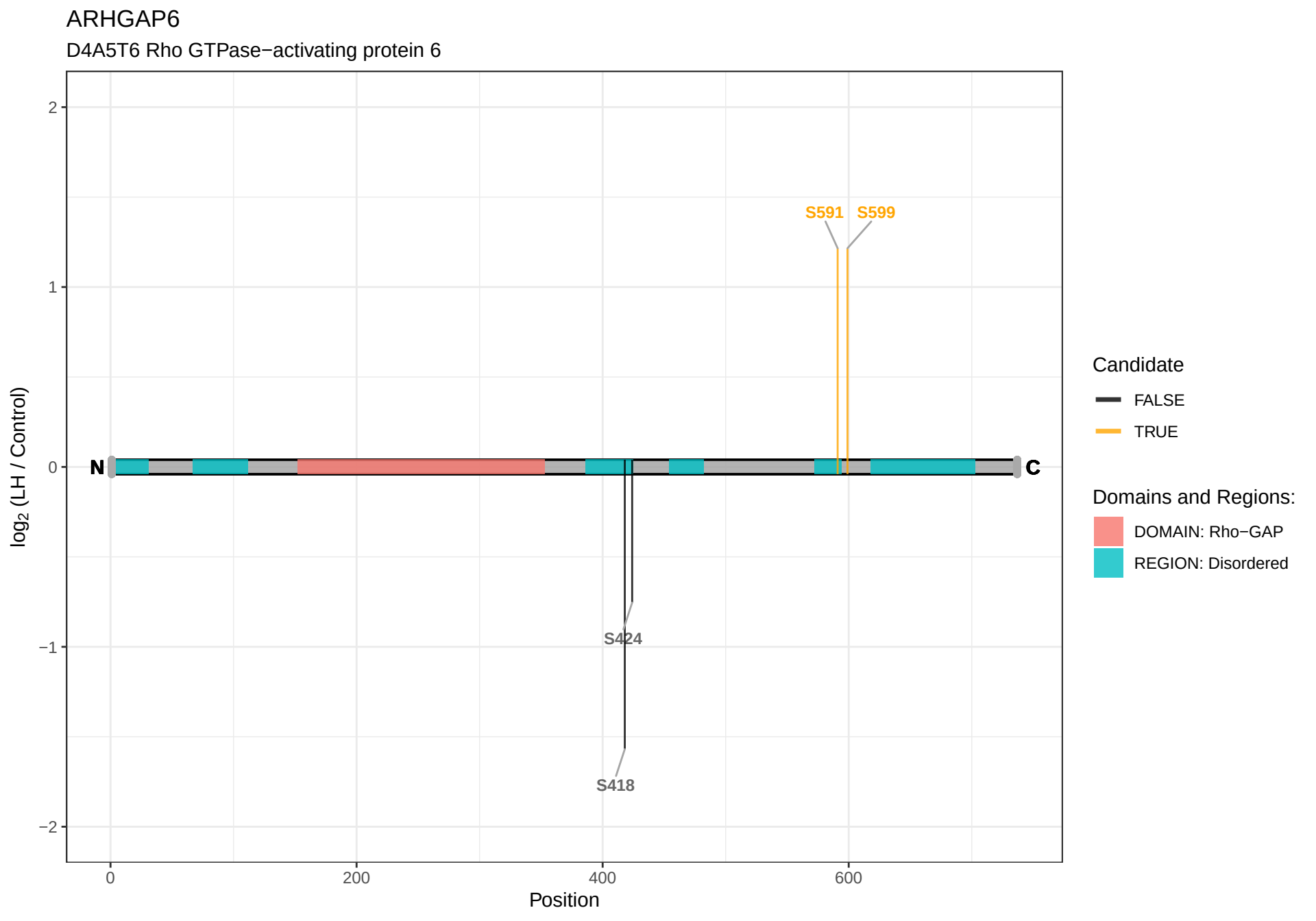

ARHGAP12
A0A0G2K1Z2 Rho GTPase−activating protein 12
log2 (LH / Control)
2
1
0
−1
−2
N
C
S213
S211
T229
S238
S199
S163
S444
S584
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PH
DOMAIN: Rho−GAP
DOMAIN: SH3
DOMAIN: WW
REGION: Disordered

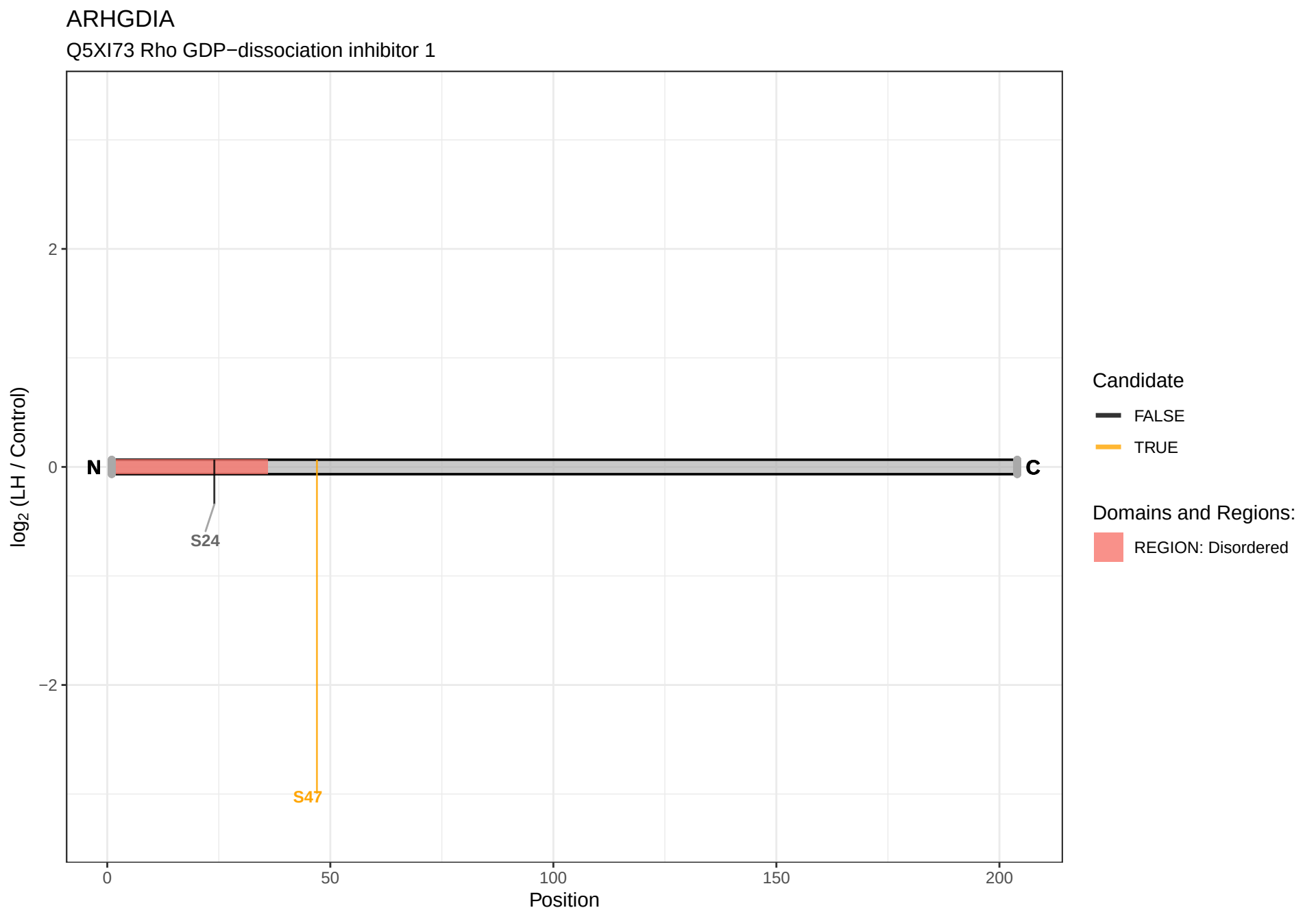

ARHGAP21
F1LXQ7 Rho GTPase−activating protein 21
log2 (LH / Control)
Position
N
C
S930
S483
S863
S1633
S1438
T1631
S1737
S1635
S887
S1664
S1105
S1504
S1514
S43
S1439
S1944
S1121
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PDZ
DOMAIN: PH
DOMAIN: Rho−GAP
REGION: Disordered

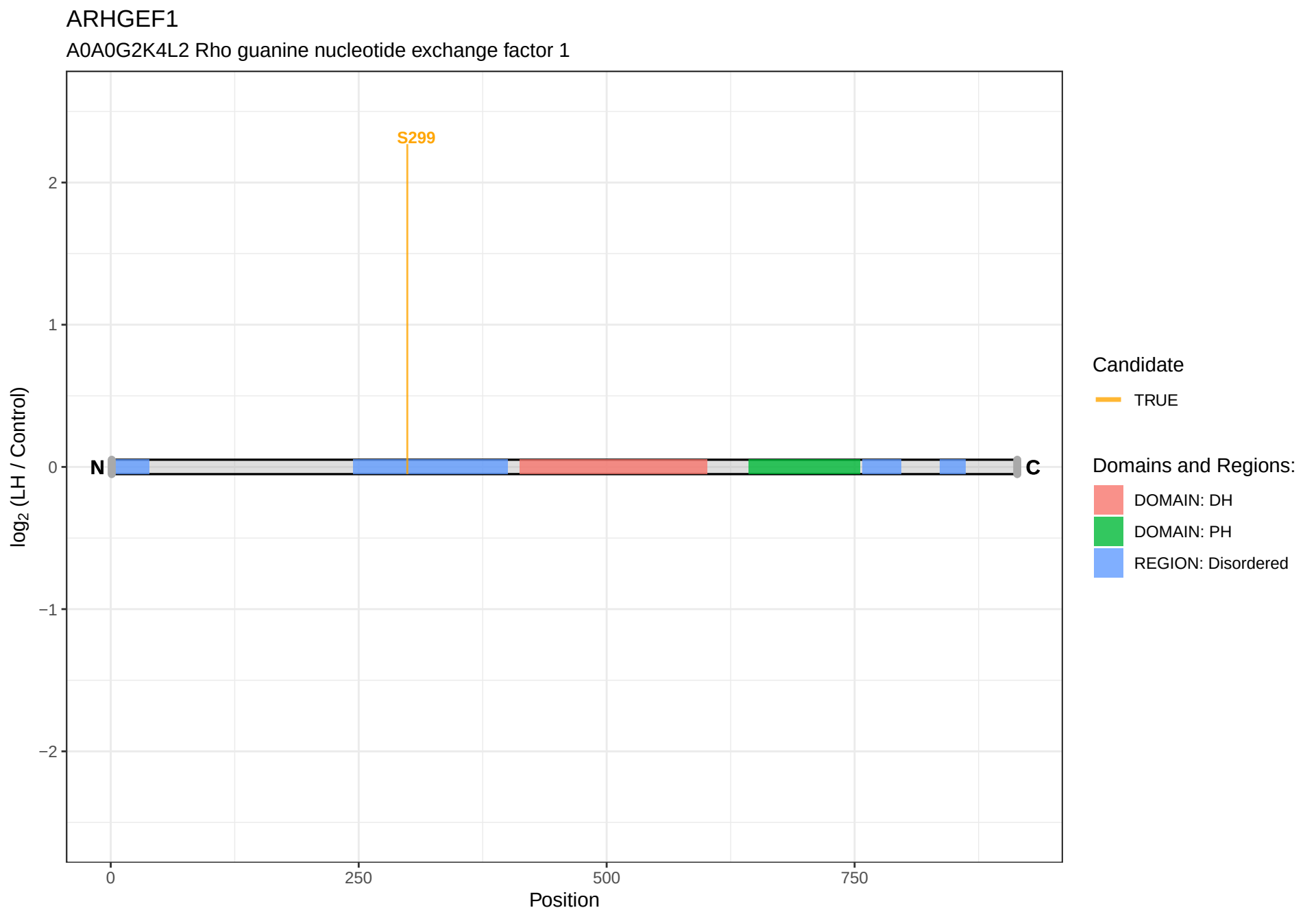

ARHGAP23
F1M2D4 Rho GTPase−activating protein 23
log2 (LH / Control)
2
1
0
−1
−2
N
C
S576
S532
S601
S341
S352
S331
S403
T1168
S1172
S1318
S1362
S1428
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PDZ
DOMAIN: PH
DOMAIN: Rho−GAP
REGION: Disordered

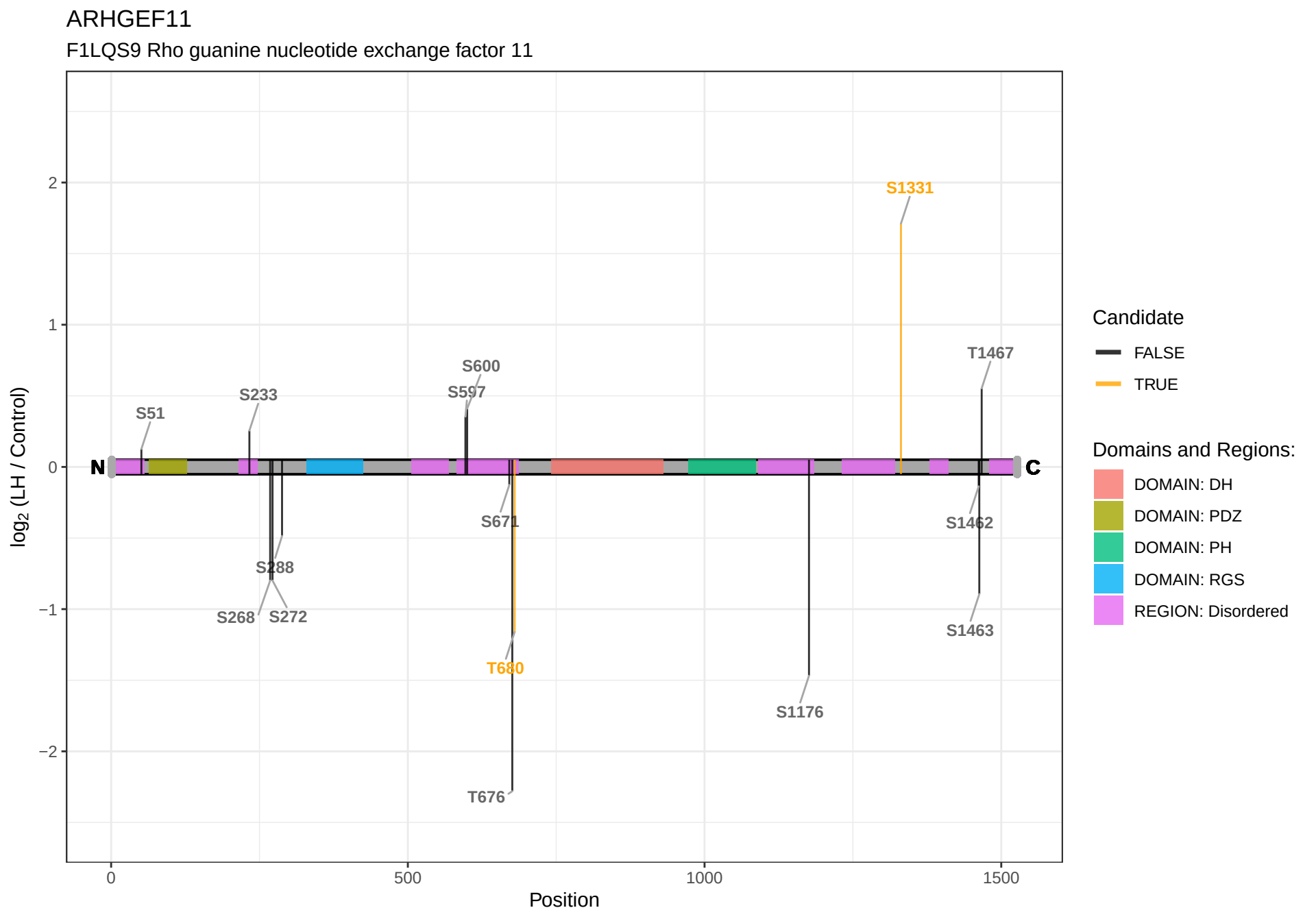

ARHGAP39
F1LR18 Rho GTPase−activating protein 39
S294
S599
N
C
log2 (LH / Control)
Position
0
300
600
900
2
1
0
−1
−2
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: MyTH4
DOMAIN: Rho−GAP
DOMAIN: WW
REGION: Disordered

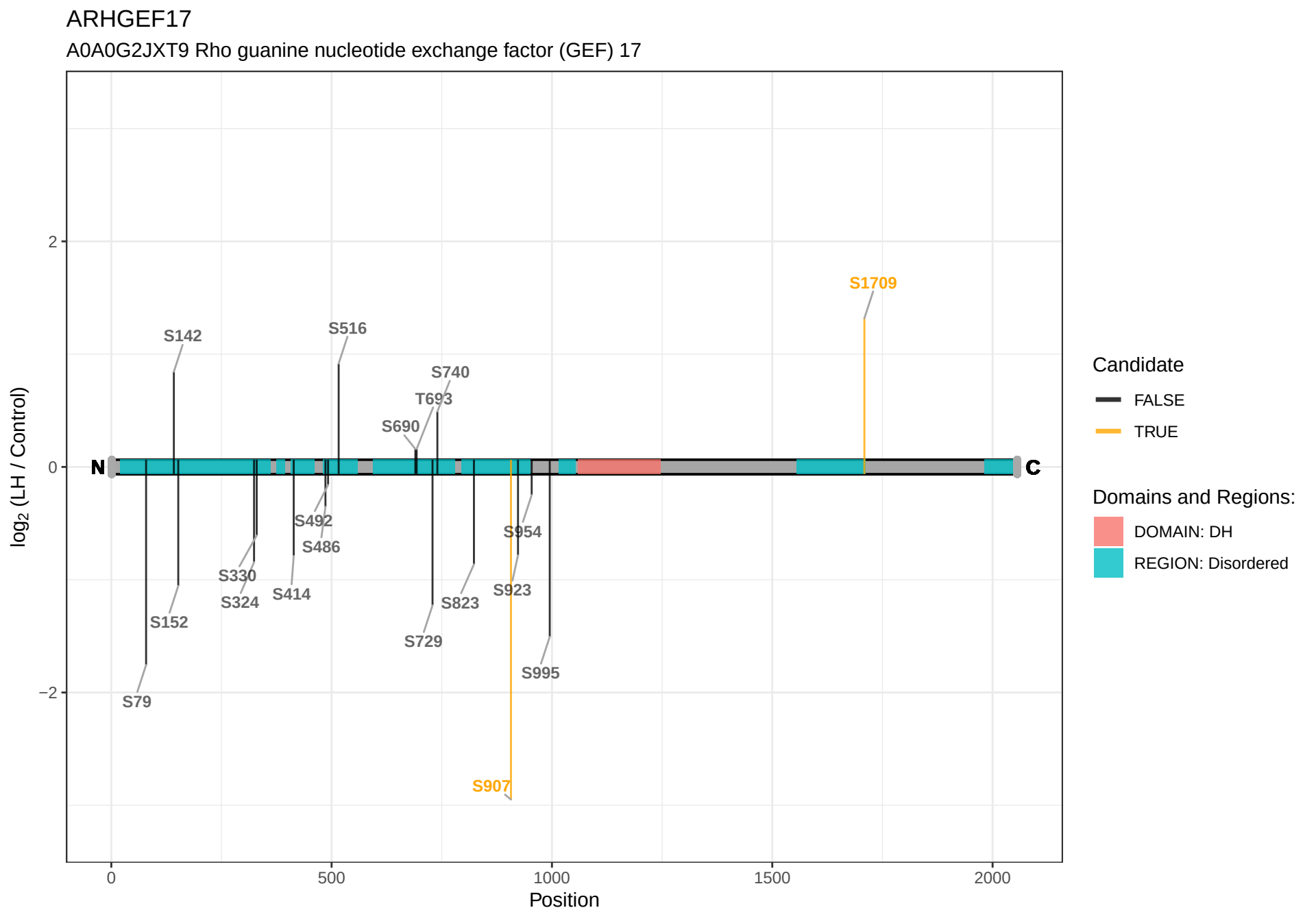

ARHGAP5
Q6TUE6 LRRGT00098
S1202
S1195
S1173
T1206
S1176
S1218
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
400
800
1200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: FF
DOMAIN: PG1 pseudoGTPase
DOMAIN: PG2 pseudoGTPase
REGION: Disordered

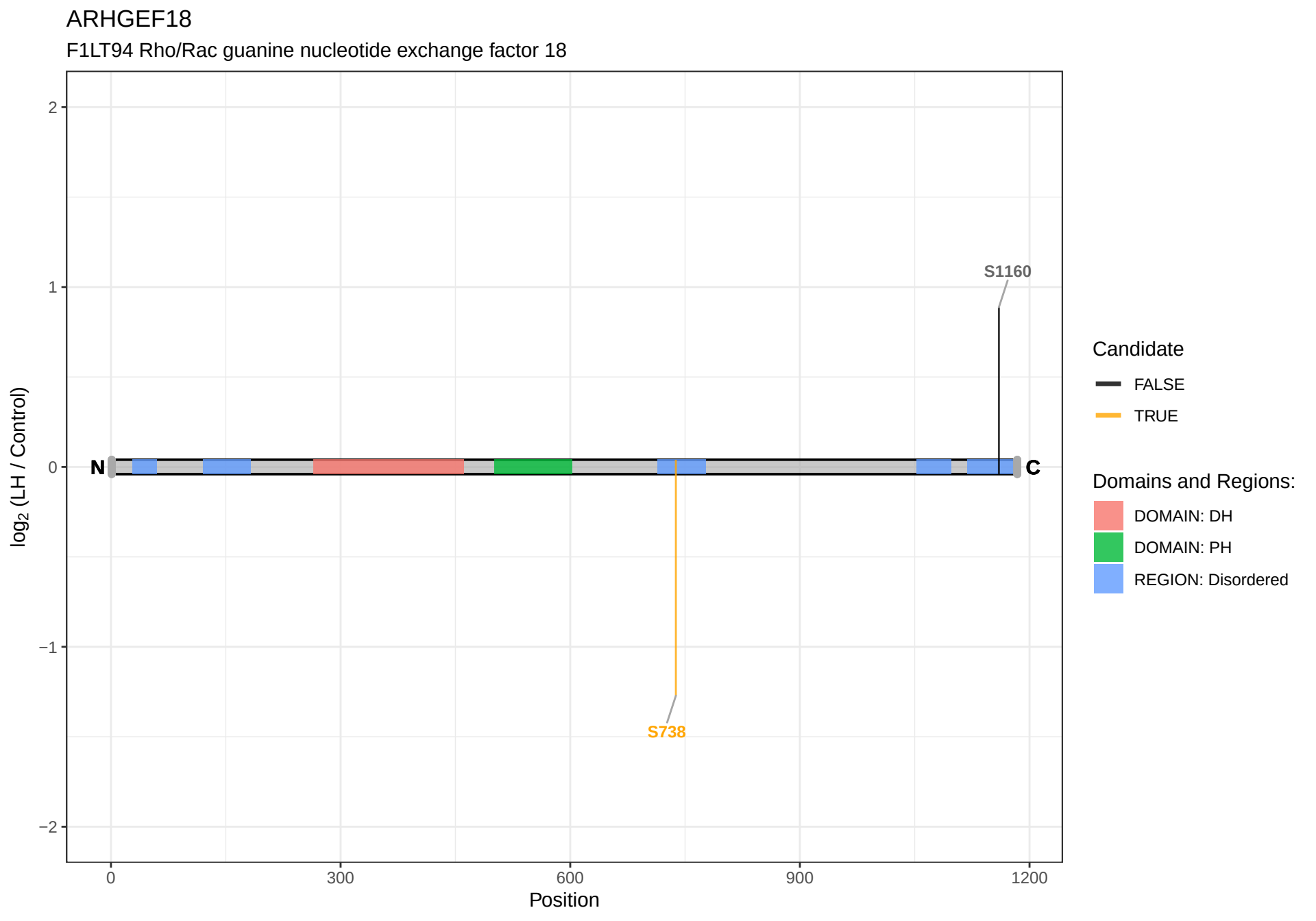

ARHGAP6
D4A5T6 Rho GTPase−activating protein 6
log2 (LH / Control)
2
1
0
−1
−2
N
C
S591
S599
S424
S418
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Rho−GAP
REGION: Disordered

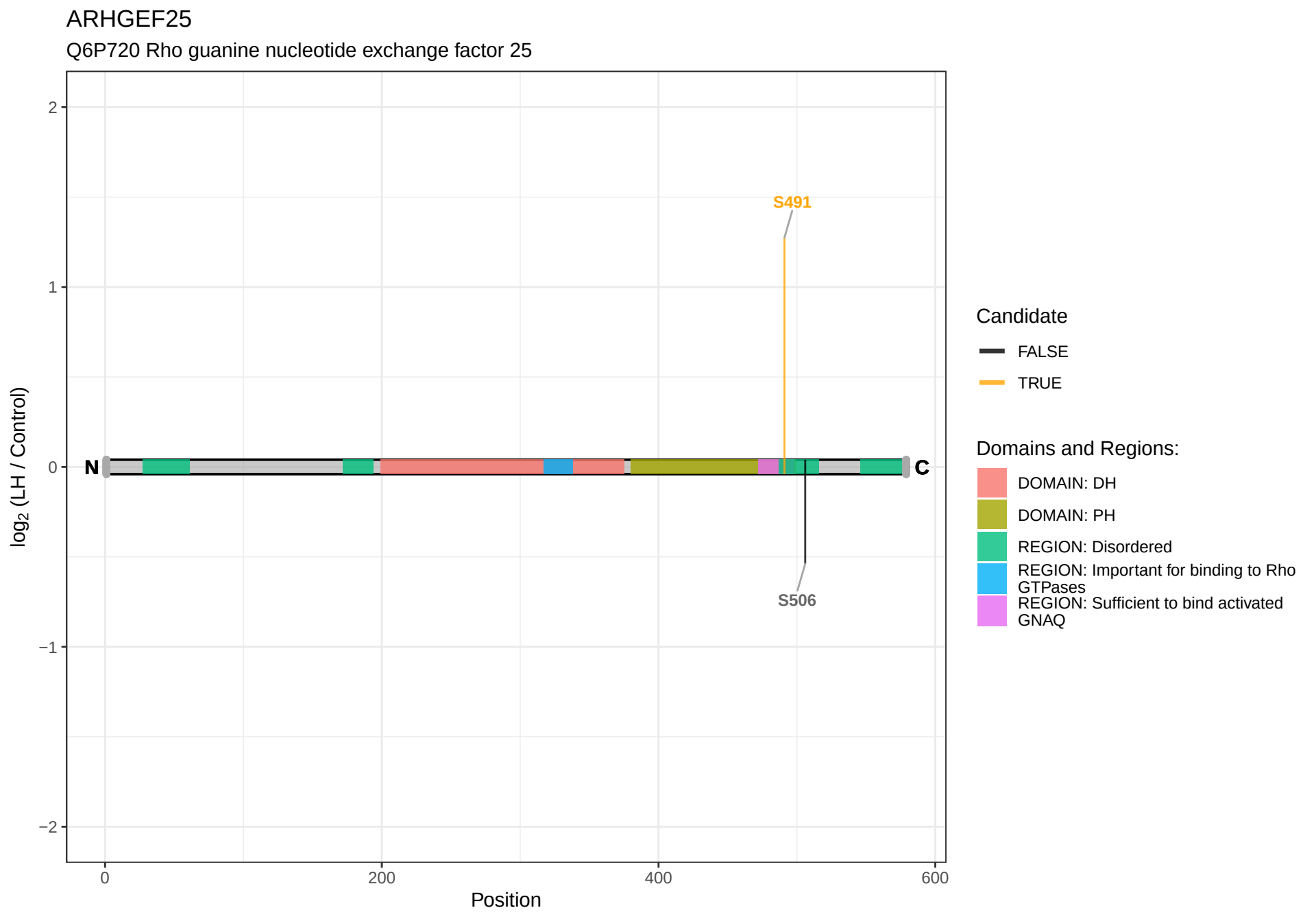

ARHGDIA
Q5XI73 Rho GDP−dissociation inhibitor 1
log2 (LH / Control)
2
0
−2
N
C
S24
S47
0
50
100
150
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

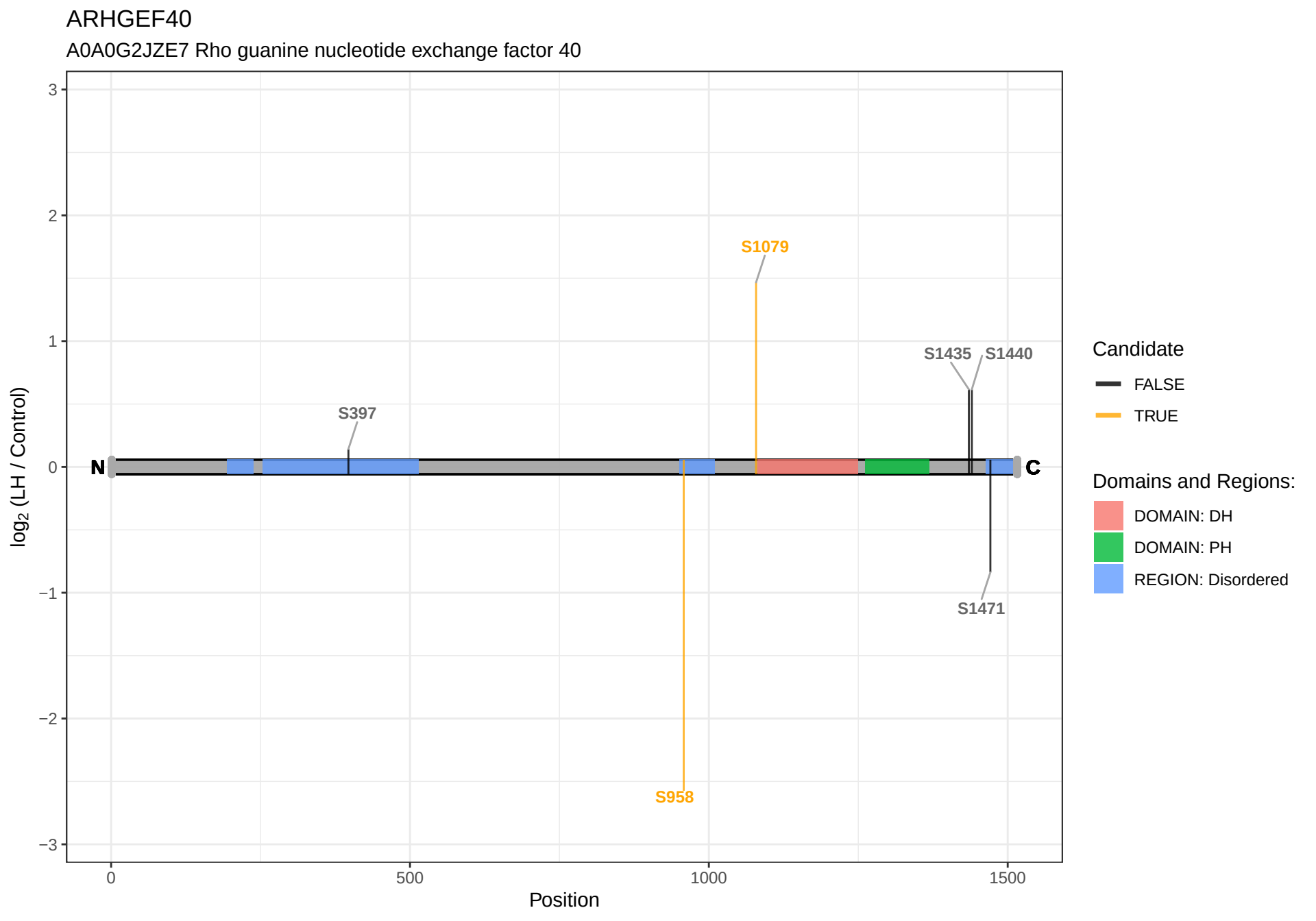

ARHGEF1
A0A0G2K4L2 Rho guanine nucleotide exchange factor 1
S299
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
250
500
750
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: DH
DOMAIN: PH
REGION: Disordered

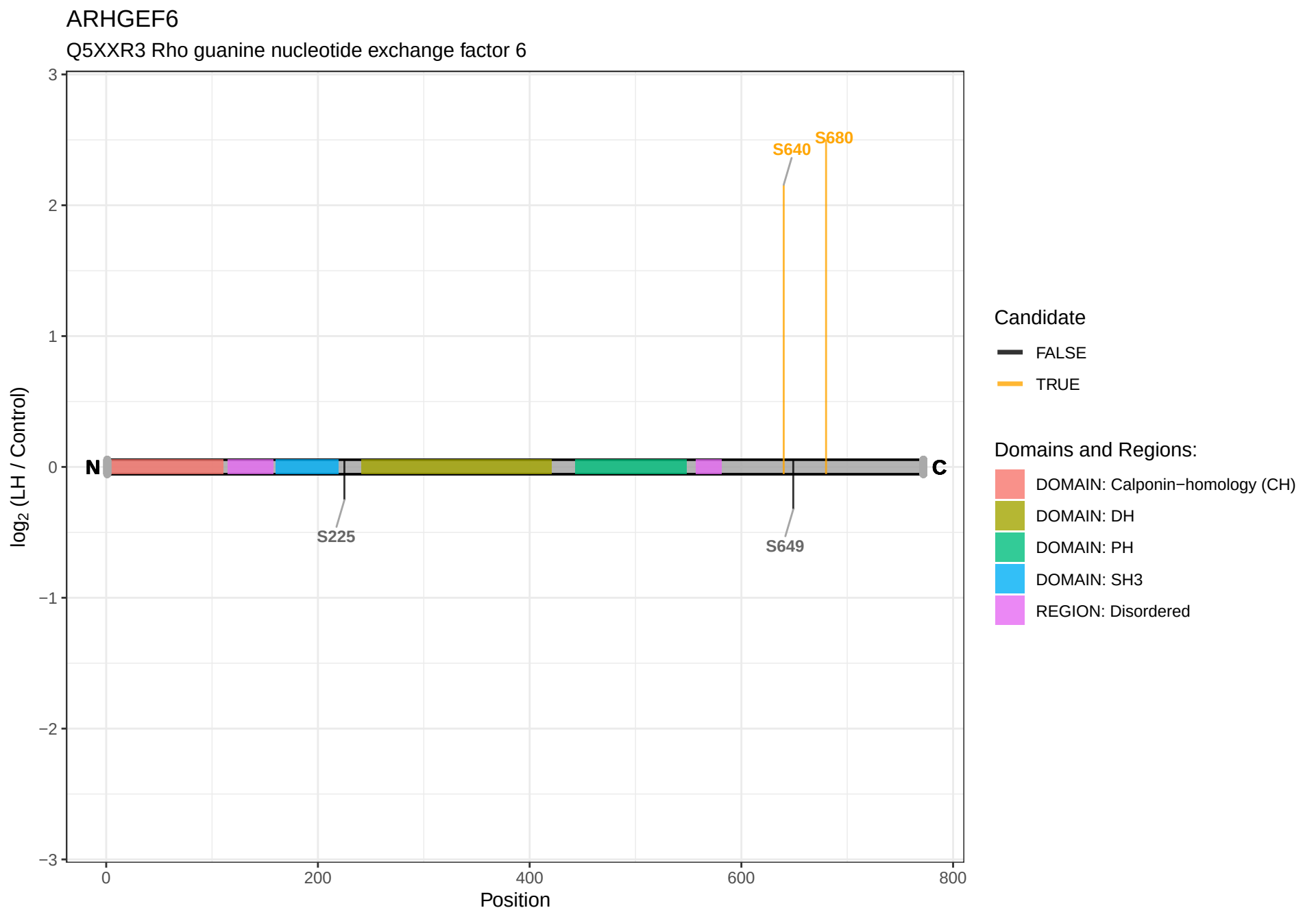

ARHGEF11
F1LQS9 Rho guanine nucleotide exchange factor 11
log2 (LH / Control)
2
1
0
−1
−2
N
C
S51
S233
S600
S597
S1331
T1467
S671
S288
S268
S272
T680
S1176
S1462
S1463
T676
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DH
DOMAIN: PDZ
DOMAIN: PH
DOMAIN: RGS
REGION: Disordered

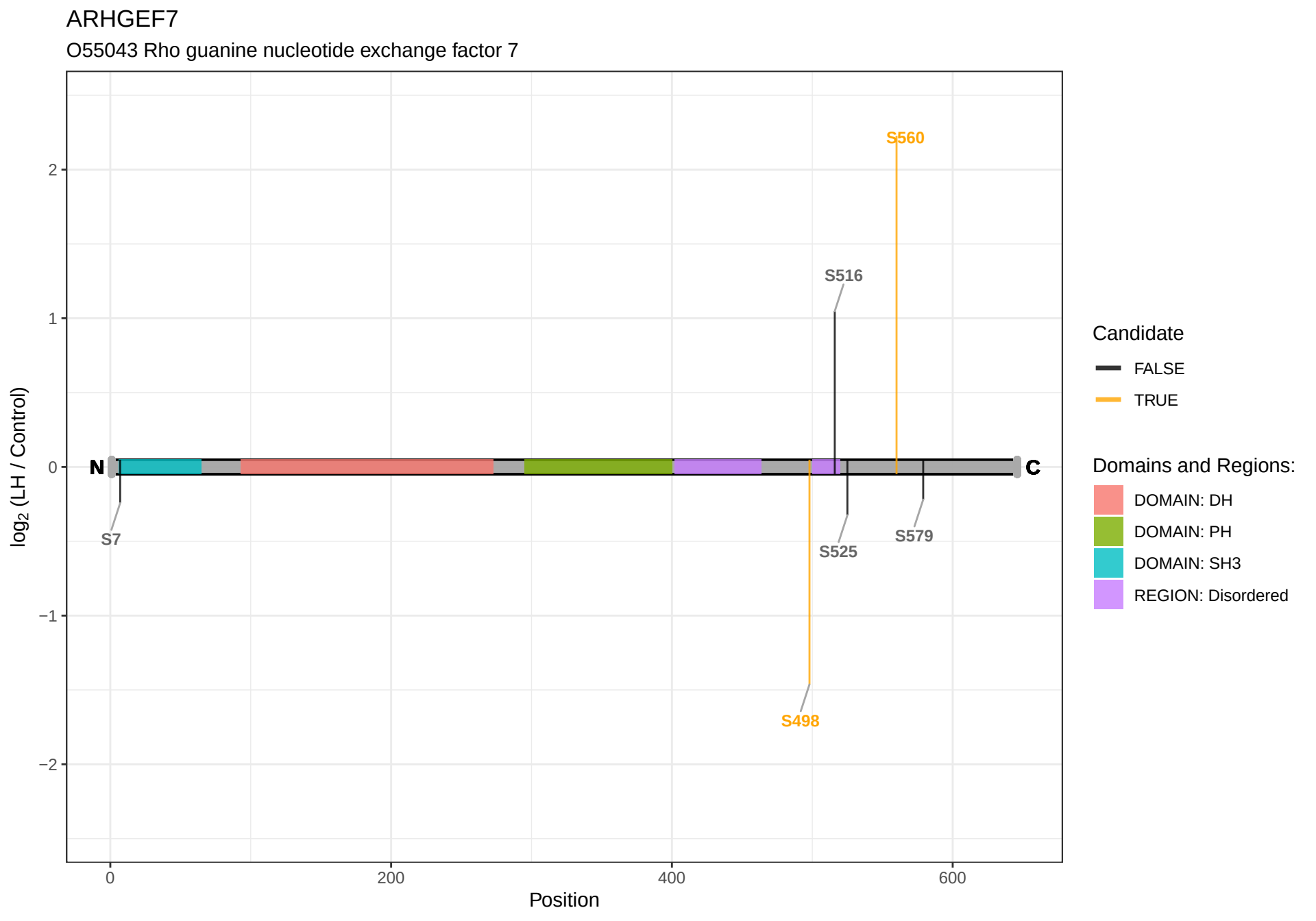

ARHGEF17
A0A0G2JXT9 Rho guanine nucleotide exchange factor (GEF) 17
log2 (LH / Control)
2
0
−2
N
C
S142
S516
S740
T693
S690
S1709
S492
S486
S330
S324
S414
S954
S923
S823
S152
S729
S995
S79
S907
0
500
1000
1500
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DH
REGION: Disordered

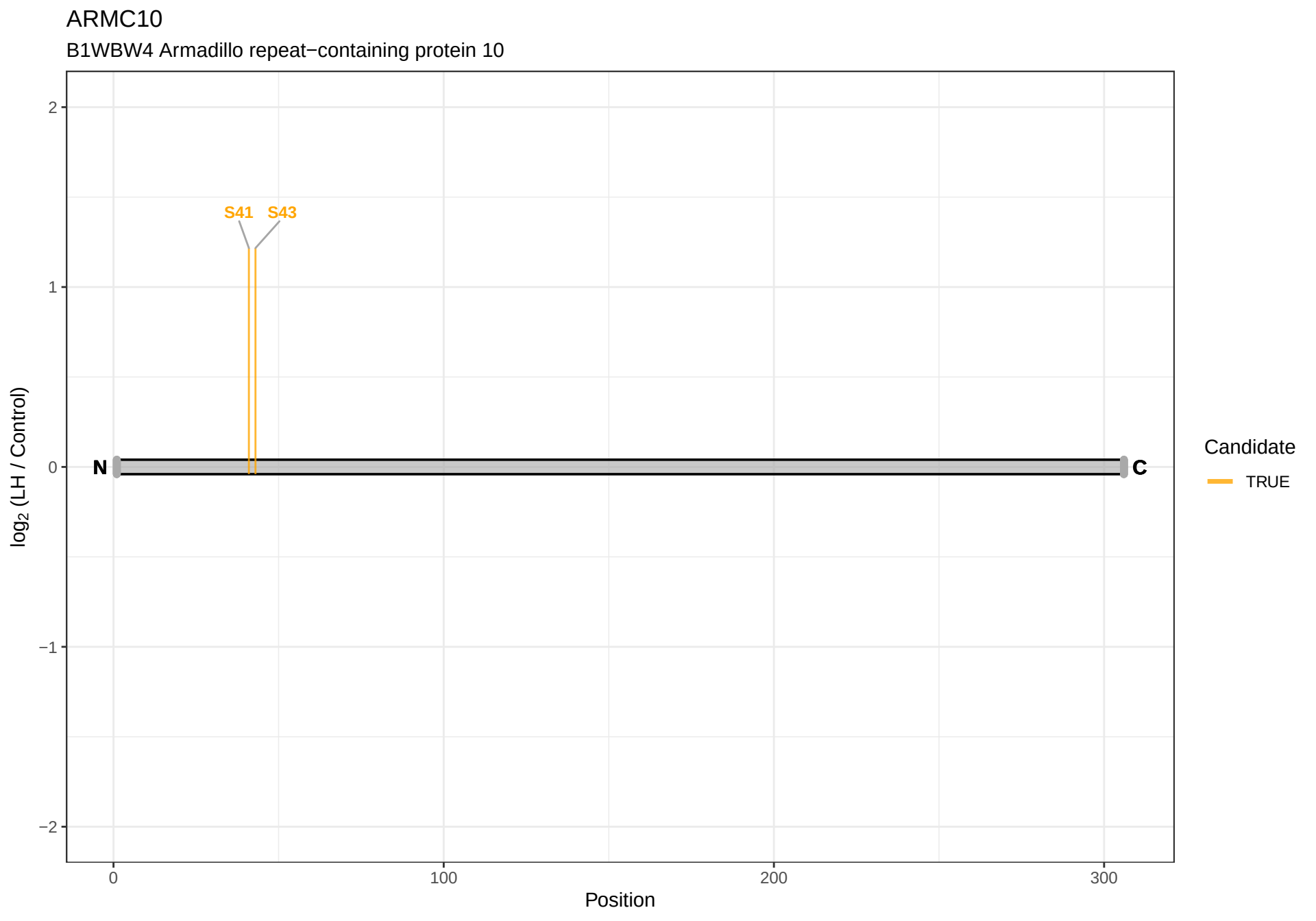

ARHGEF18
F1LT94 Rho/Rac guanine nucleotide exchange factor 18
log2 (LH / Control)
2
1
0
−1
−2
N
C
S1160
S738
0
300
600
900
1200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DH
DOMAIN: PH
REGION: Disordered

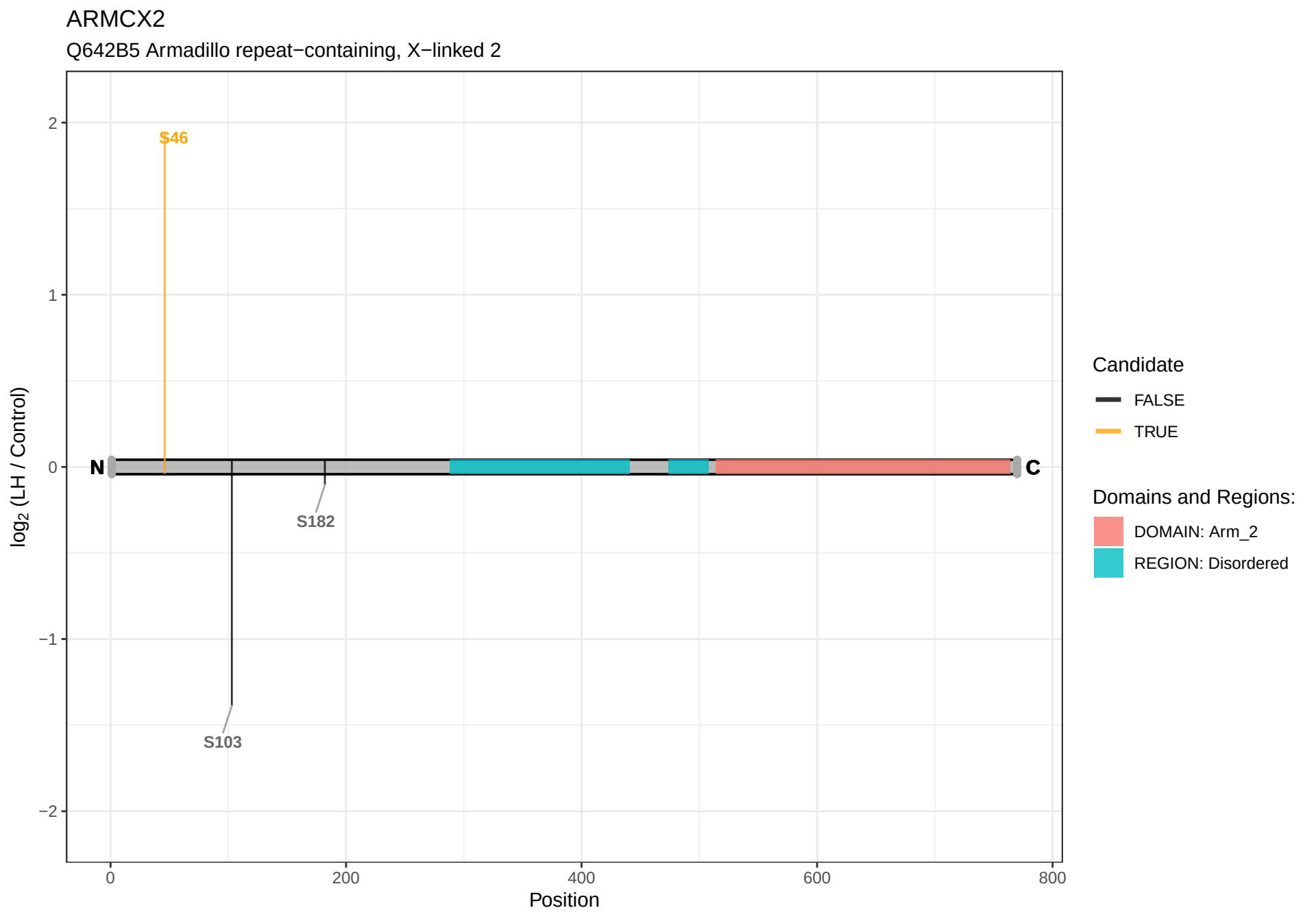

ARHGEF25
Q6P720 Rho guanine nucleotide exchange factor 25
log2 (LH / Control)
2
1
0
−1
−2
N
C
S491
S506
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DH
DOMAIN: PH
REGION: Disordered
REGION: Important for binding to Rho GTPases
REGION: Sufficient to bind activated GNAQ

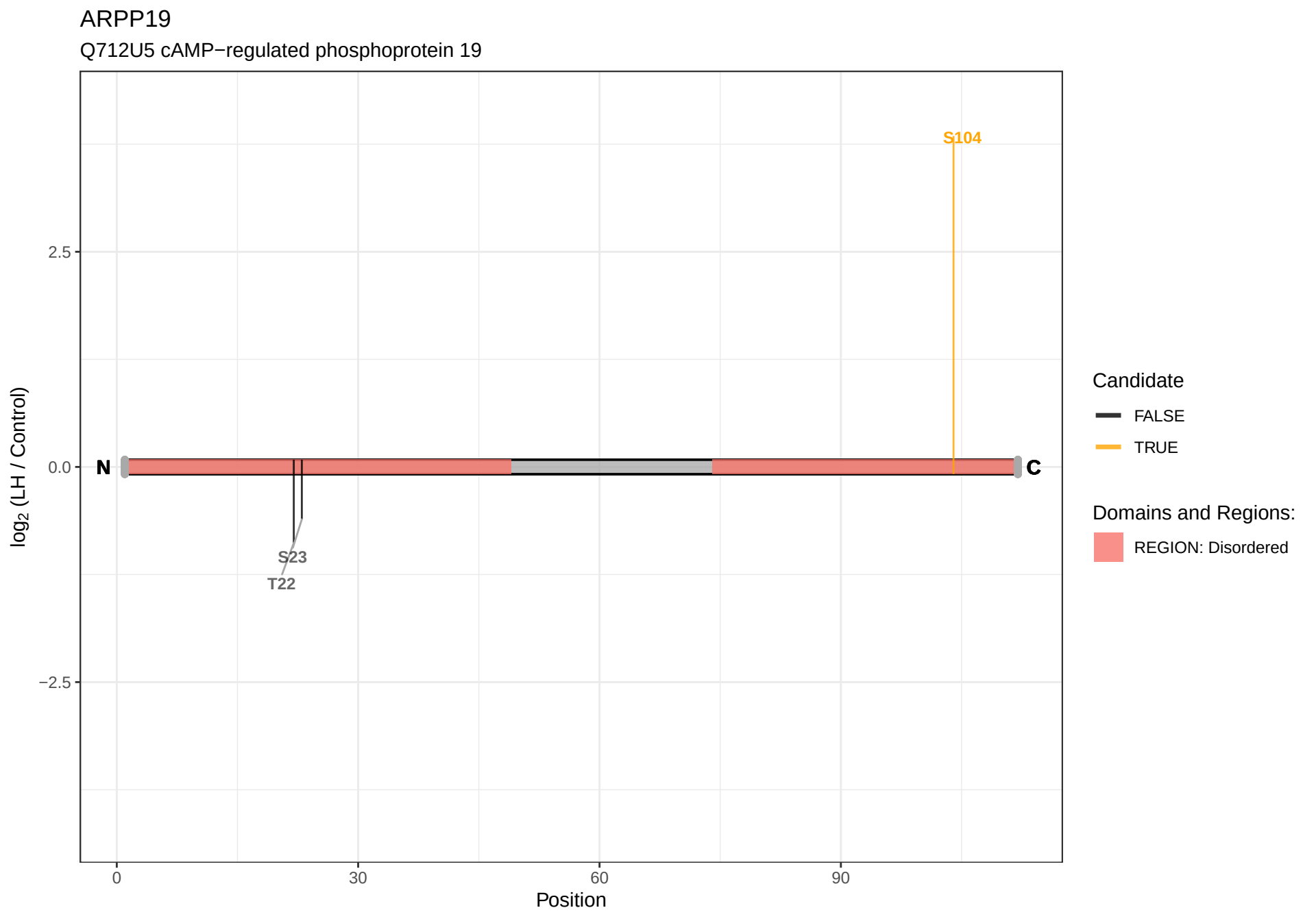

ARHGEF40
A0A0G2JZE7 Rho guanine nucleotide exchange factor 40
log2 (LH / Control)
Position
N
C
S397
S1079
S1435
S1440
S1471
S958
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DH
DOMAIN: PH
REGION: Disordered

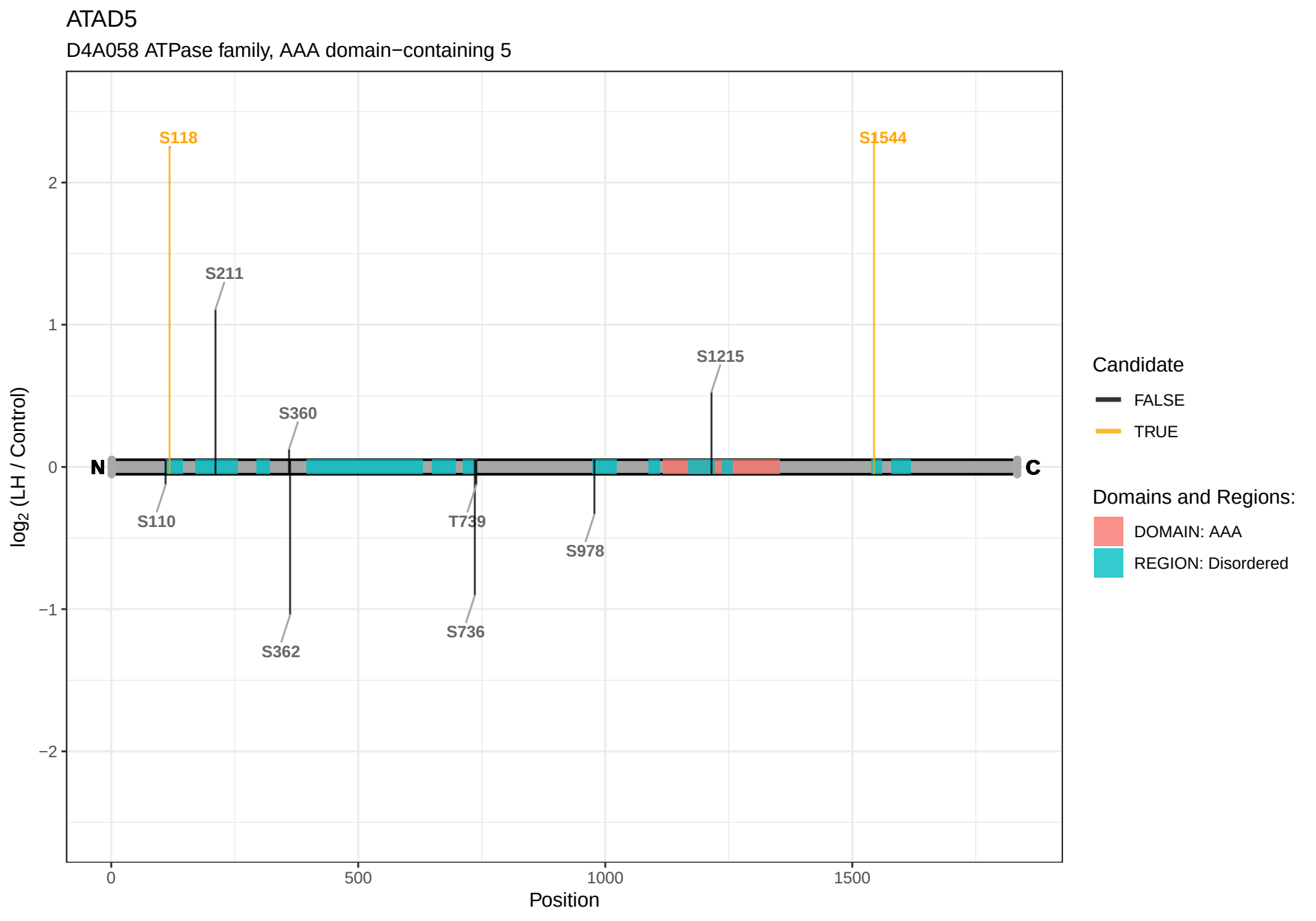

ARHGEF6
Q5XXR3 Rho guanine nucleotide exchange factor 6
log2 (LH / Control)
Position
N
C
S225
S640
S649
S680
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Calponin−homology (CH)
DOMAIN: DH
DOMAIN: PH
DOMAIN: SH3
REGION: Disordered

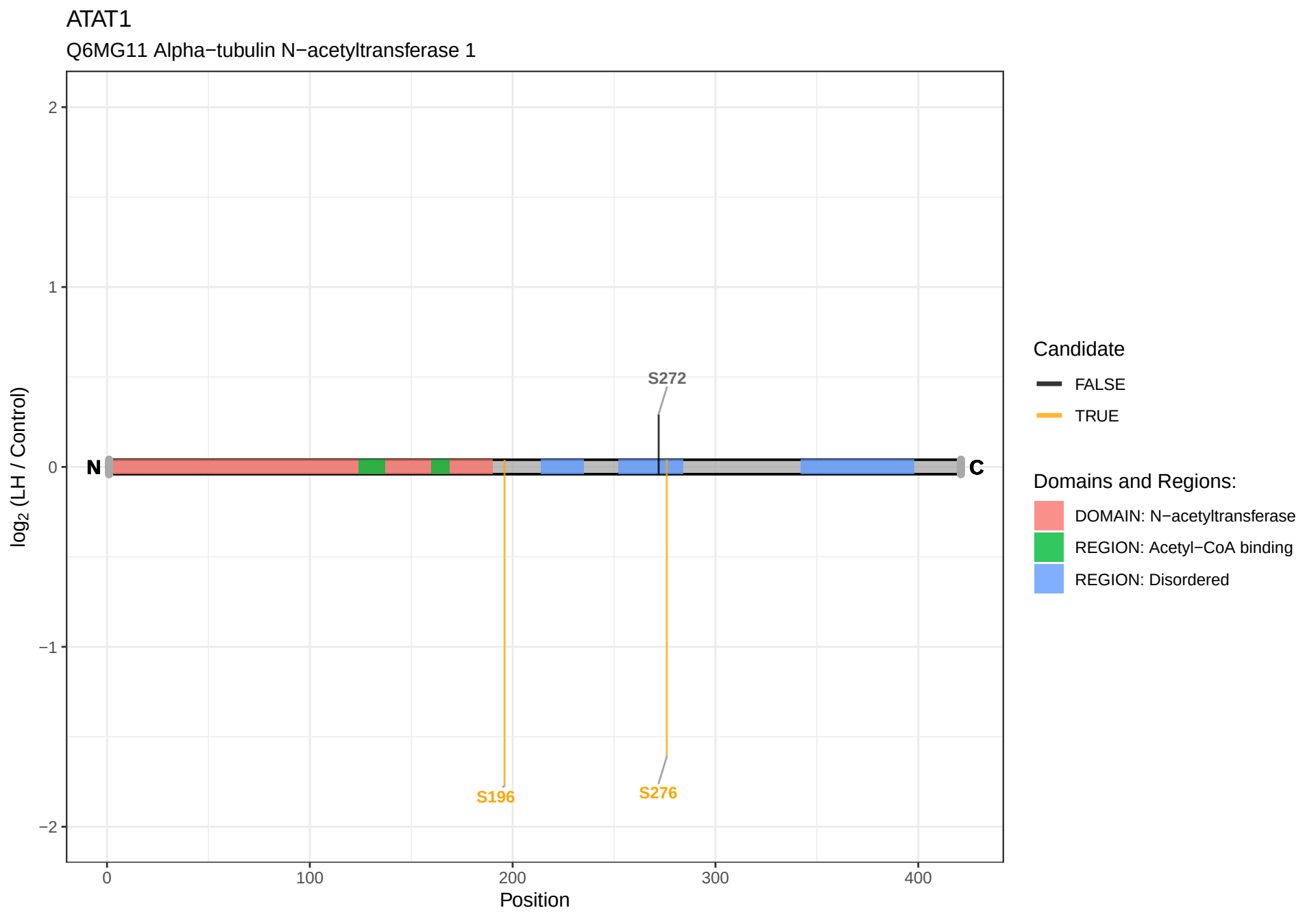

ARHGEF7
O55043 Rho guanine nucleotide exchange factor 7
log2 (LH / Control)
2
1
0
−1
−2
N
C
S7
S516
S560
S525
S579
S498
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DH
DOMAIN: PH
DOMAIN: SH3
REGION: Disordered

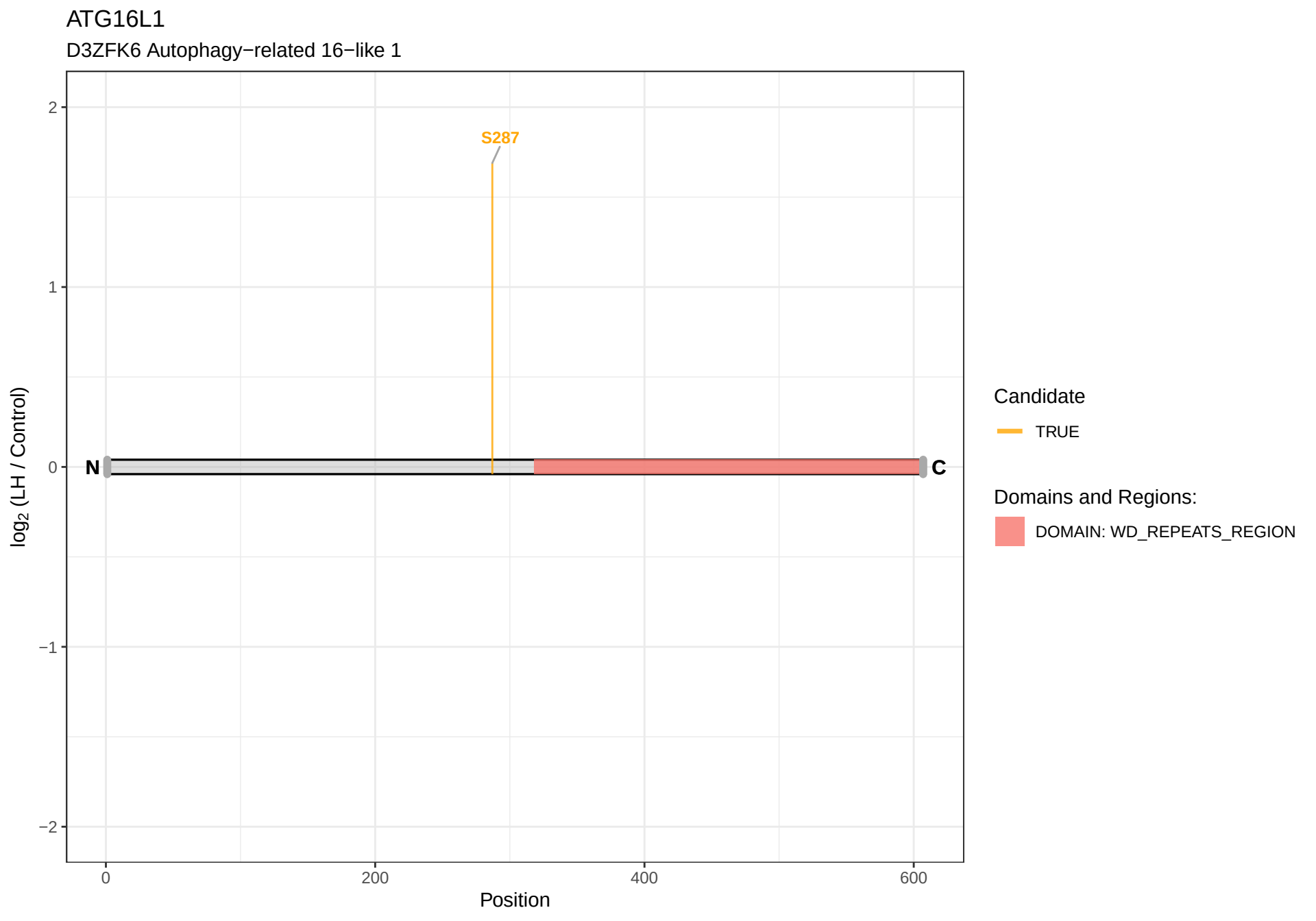

ARMC10
B1WBW4 Armadillo repeat−containing protein 10
S41
S43
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
Position
Candidate
TRUE

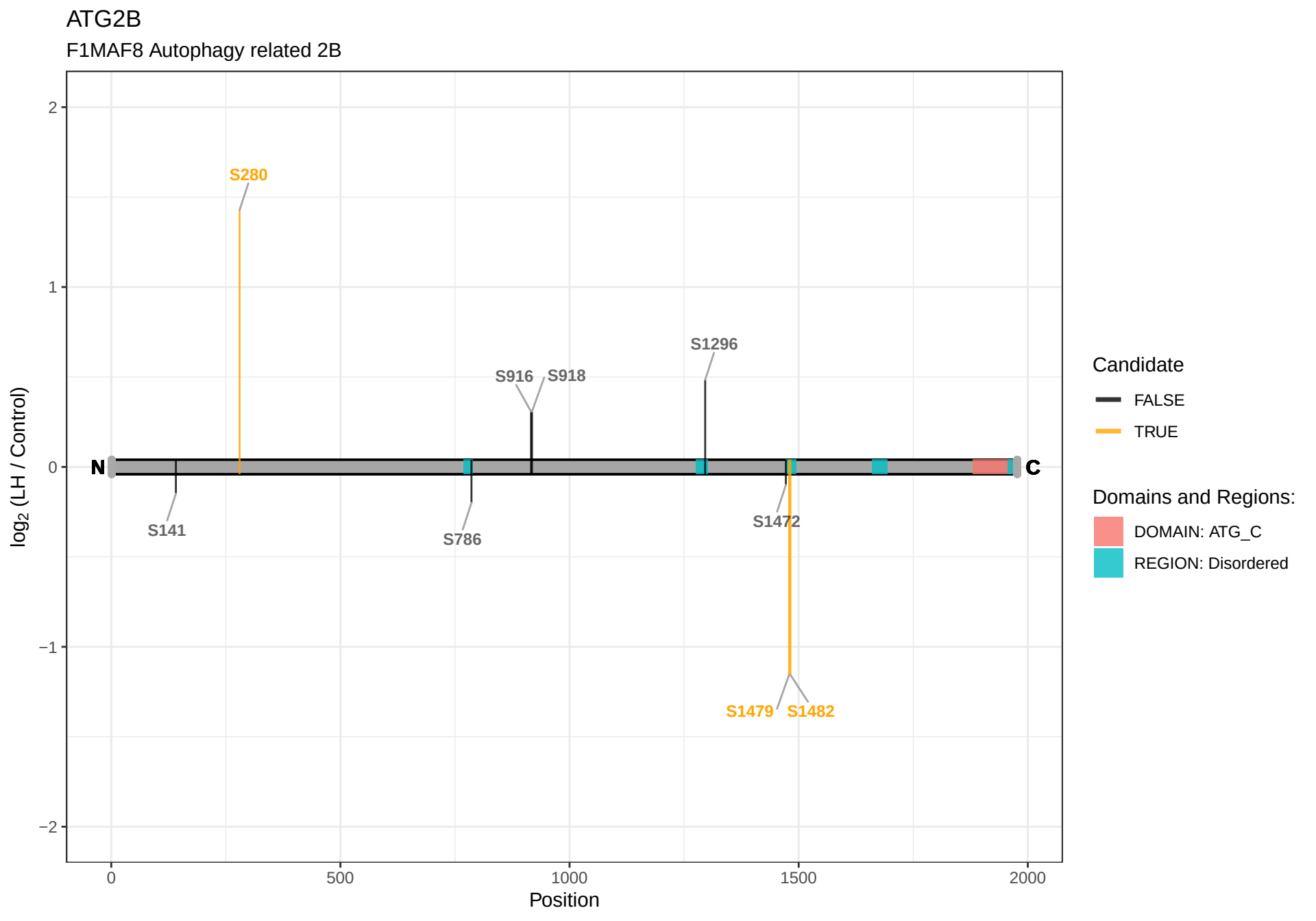

ARMCX2
Q642B5 Armadillo repeat−containing, X−linked 2
S46
S182
S103
N
C
2
1
0
−1
−2
0
200
400
600
800
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Arm_2
REGION: Disordered

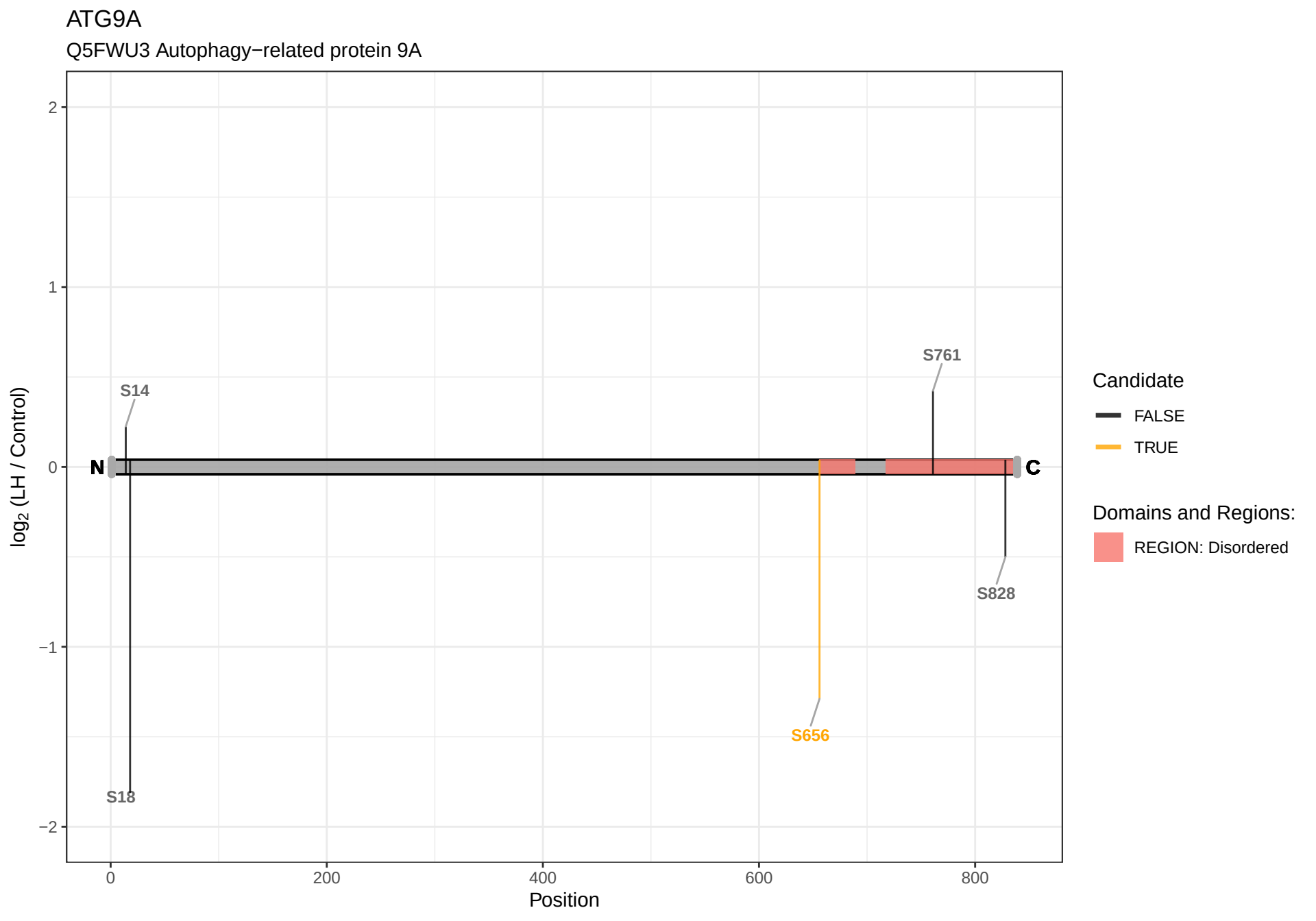

ARPP19
Q712U5 cAMP−regulated phosphoprotein 19
S104
2.5
0.0
−2.5
N
C
S23
T22
log2 (LH / Control)
0
30
60
90
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

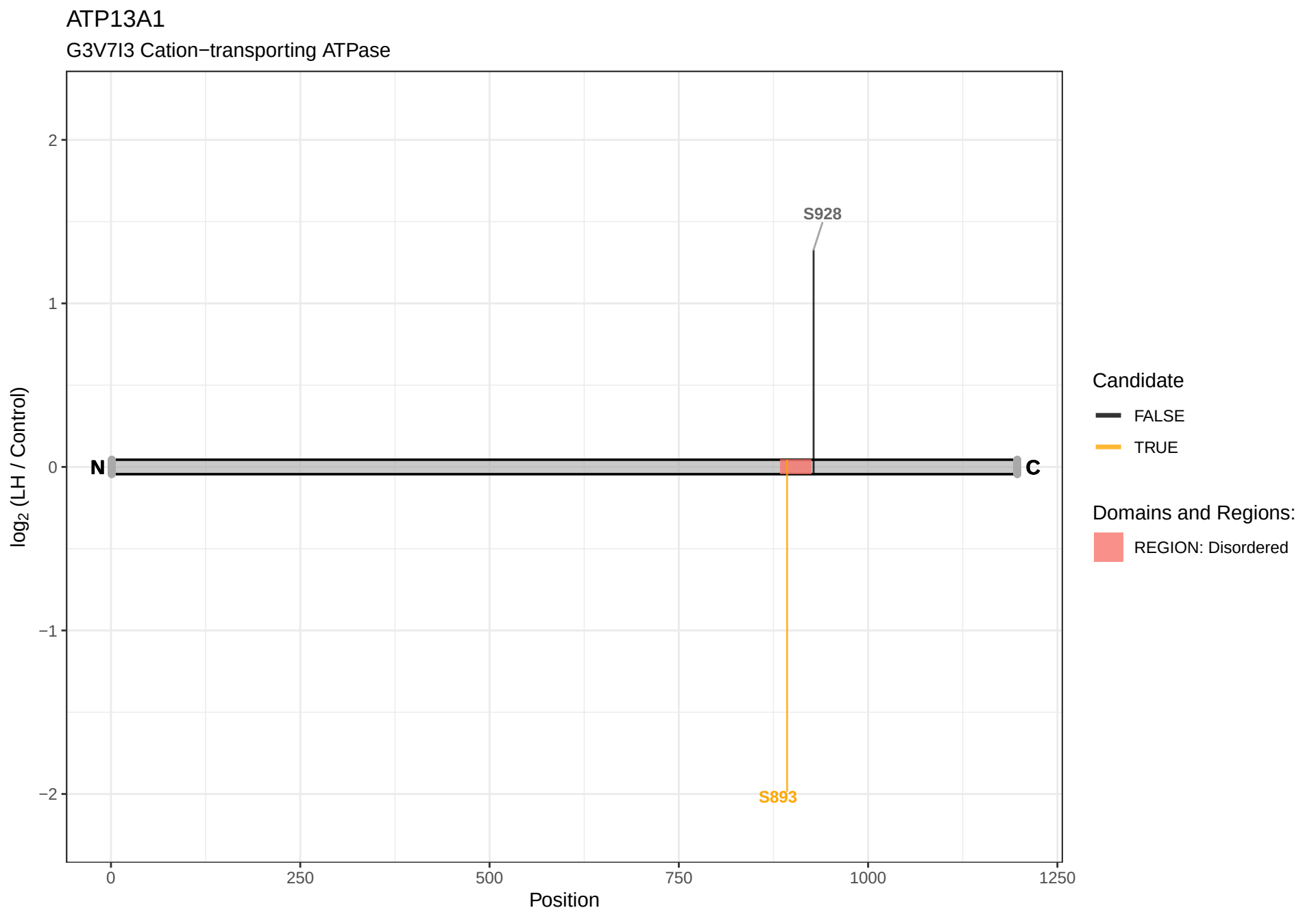

ATAD5
D4A058 ATPase family, AAA domain−containing 5
S118
S1544
S211
S1215
S360
N
C
S110
T739
S978
S362
S736
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AAA
REGION: Disordered

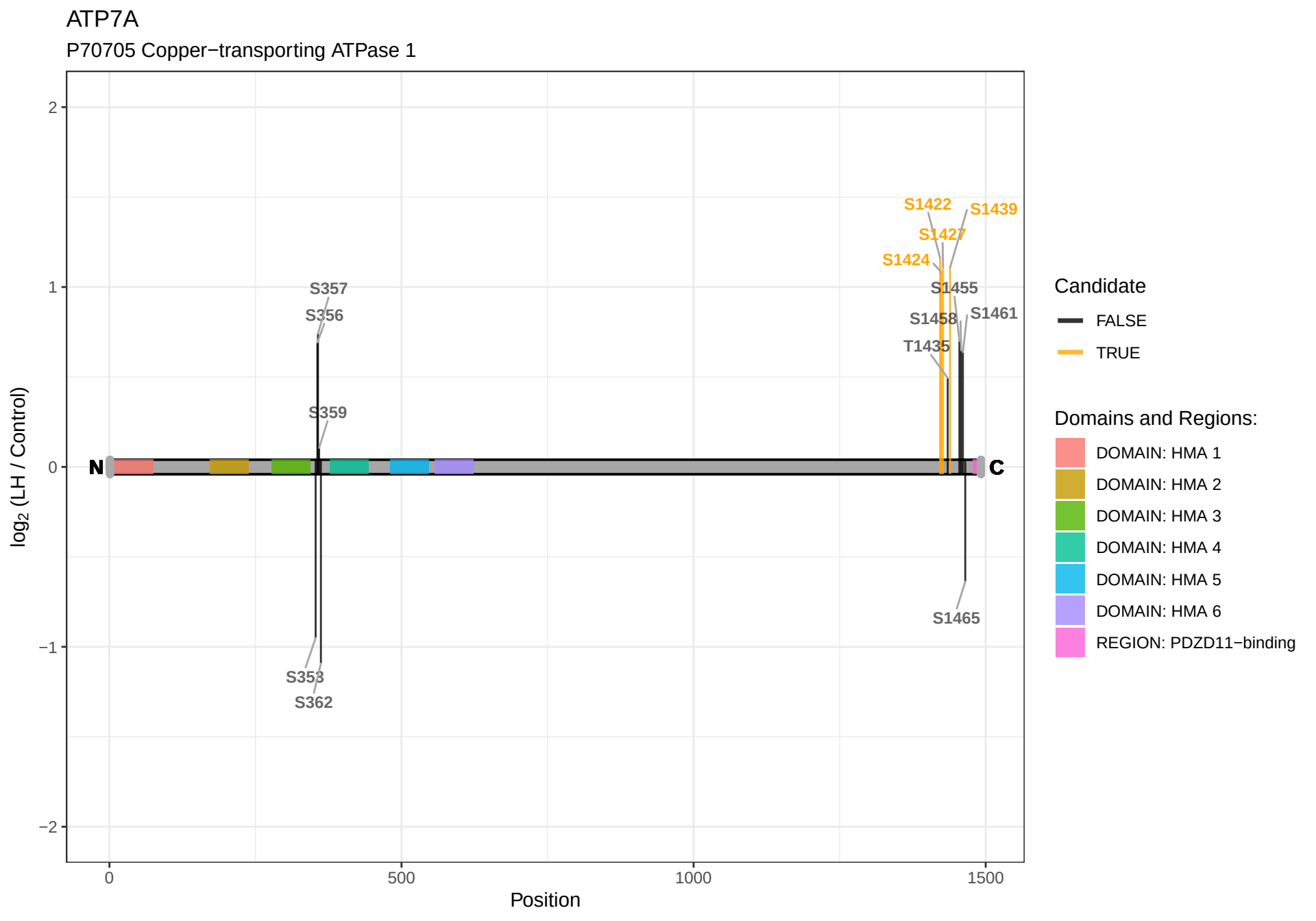

ATAT1
Q6MG11 Alpha−tubulin N−acetyltransferase 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S272
S196
S276
0
100
200
300
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: N−acetyltransferase
REGION: Acetyl−CoA binding
REGION: Disordered

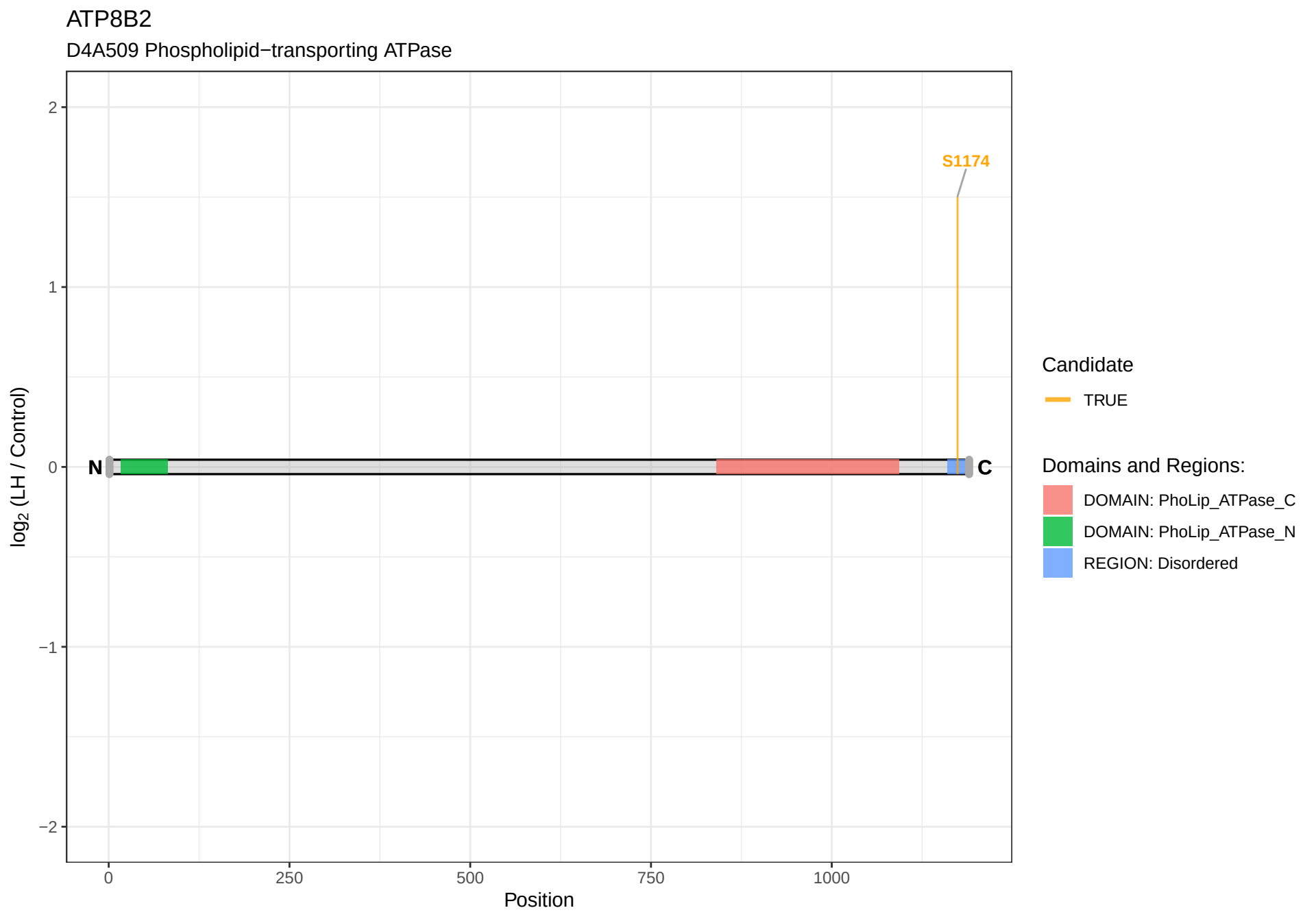

ATG16L1
D3ZFK6 Autophagy−related 16−like 1
S287
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: WD_REPEATS_REGION

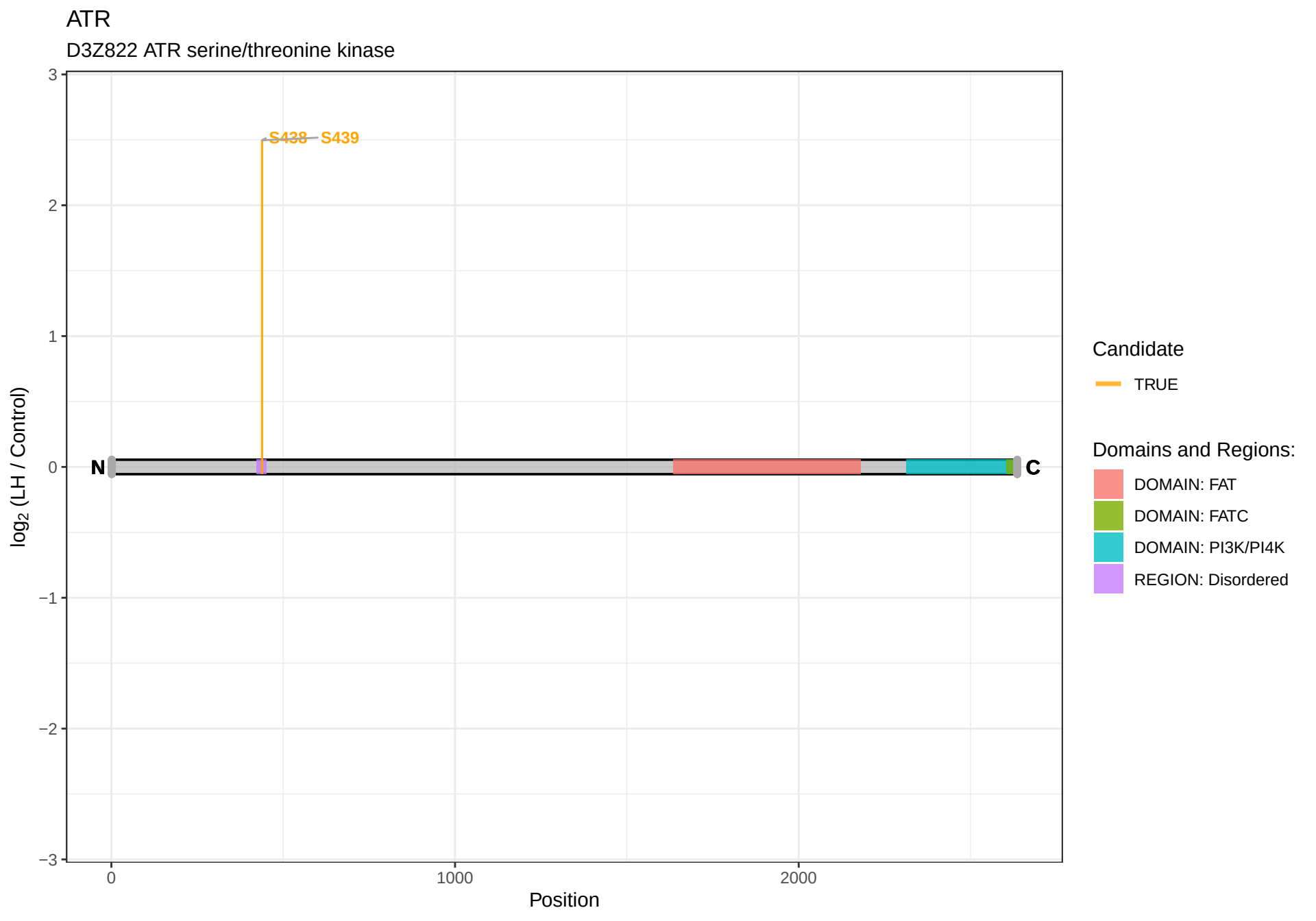

ATG2B
F1MAF8 Autophagy related 2B
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
2000
Position
N
C
S280
S141
S786
S916
S918
S1296
S1472
S1479
S1482
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ATG_C
REGION: Disordered

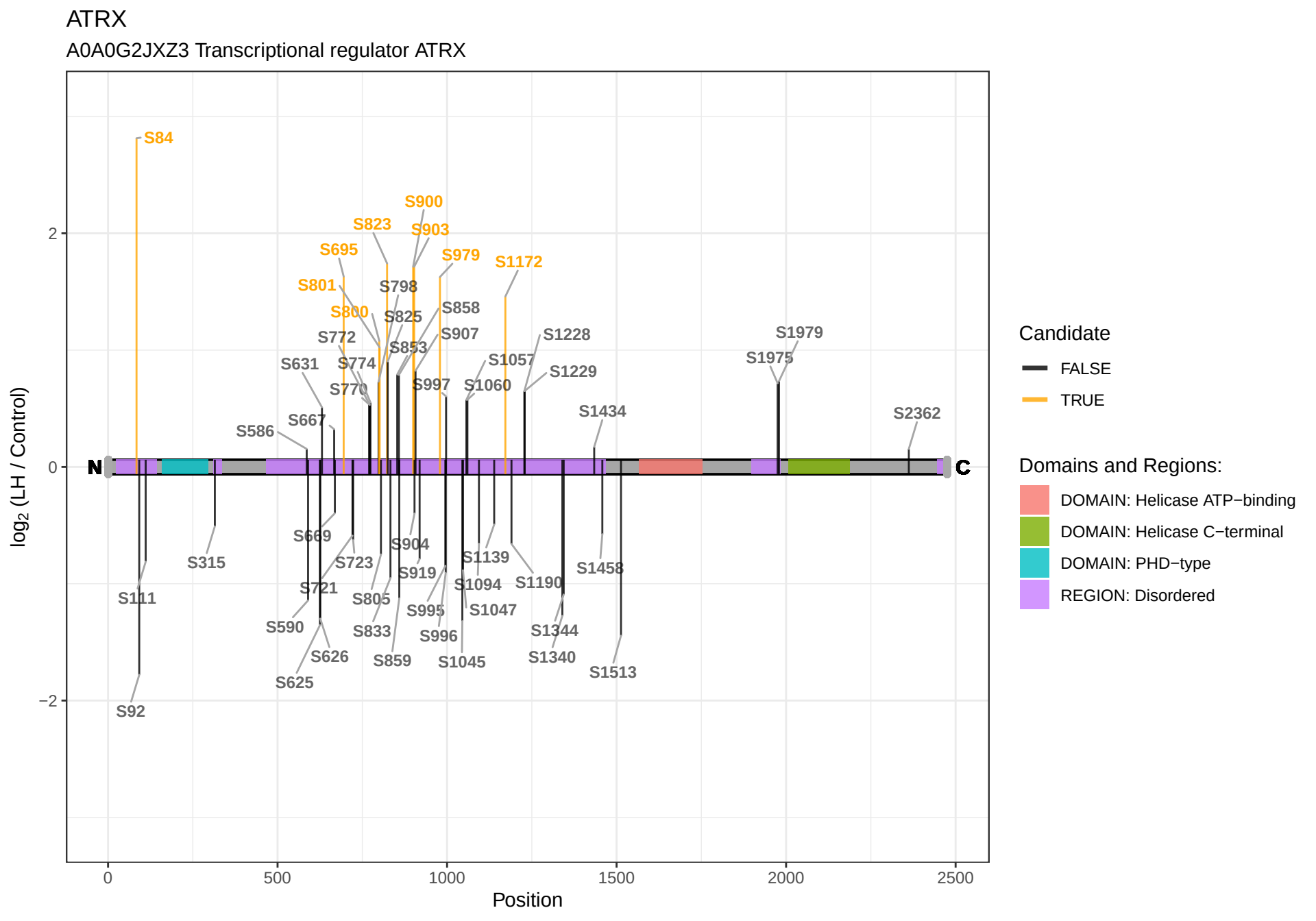

ATG9A
Q5FWU3 Autophagy−related protein 9A
log2 (LH / Control)
2
1
0
−1
−2
N
C
S14
S18
S656
S761
S828
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

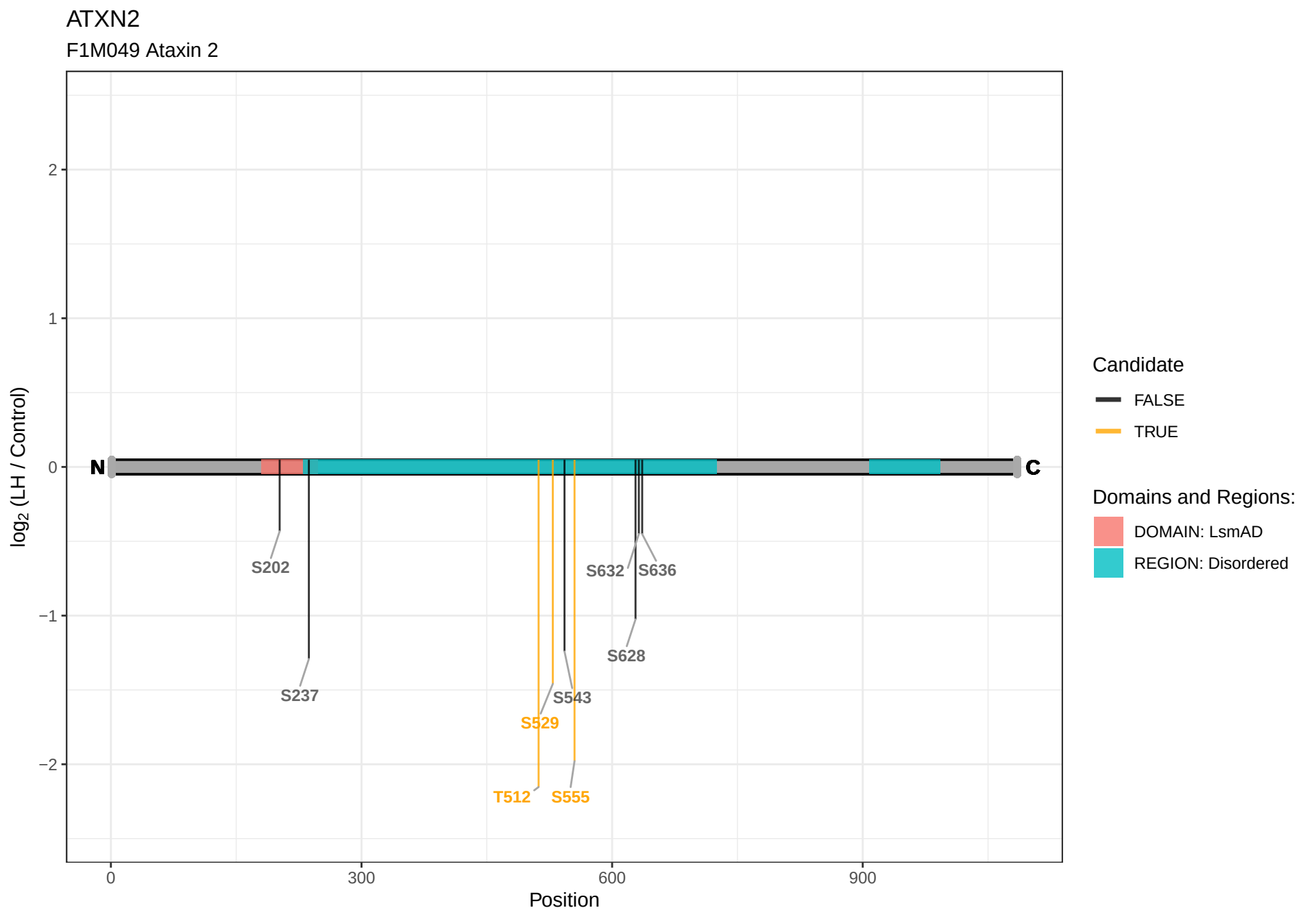

ATP13A1
G3V7I3 Cation−transporting ATPase
log2 (LH / Control)
2
1
0
−1
−2
N
C
S928
S893
0
250
500
750
1000
1250
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

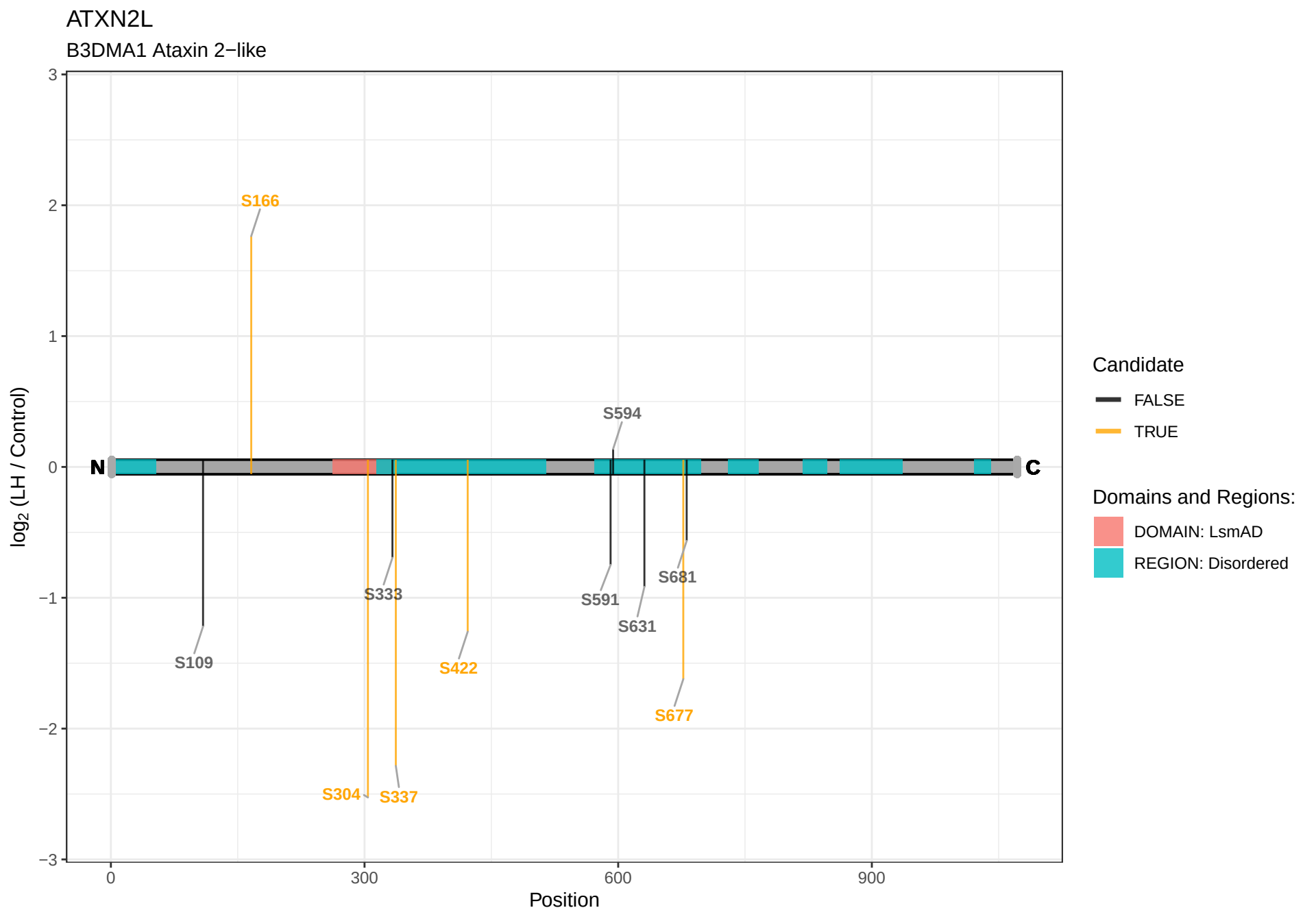

ATP7A
P70705 Copper−transporting ATPase 1
log2 (LH / Control)
Position
2
1
0
−1
−2
0
500
1000
1500
N
C
S357
S356
S359
S353
S362
S1422
S1439
S1427
S1424
S1455
S1458
S1461
T1435
S1465
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: HMA 1
DOMAIN: HMA 2
DOMAIN: HMA 3
DOMAIN: HMA 4
DOMAIN: HMA 5
DOMAIN: HMA 6
REGION: PDZD11−binding

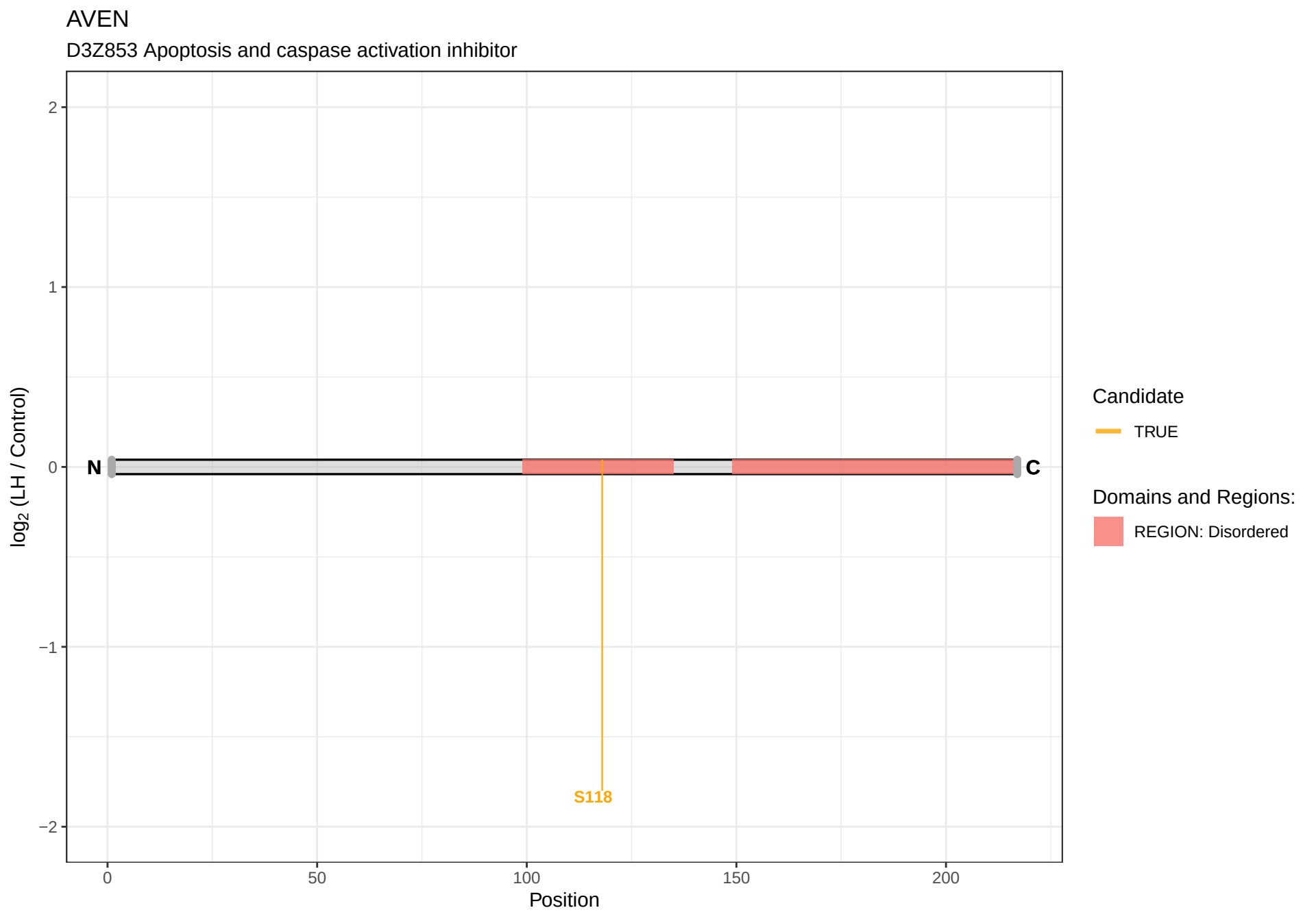

ATP8B2
D4A509 Phospholipid−transporting ATPase
S1174
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
250
500
750
1000
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: PhoLip_ATPase_C
DOMAIN: PhoLip_ATPase_N
REGION: Disordered

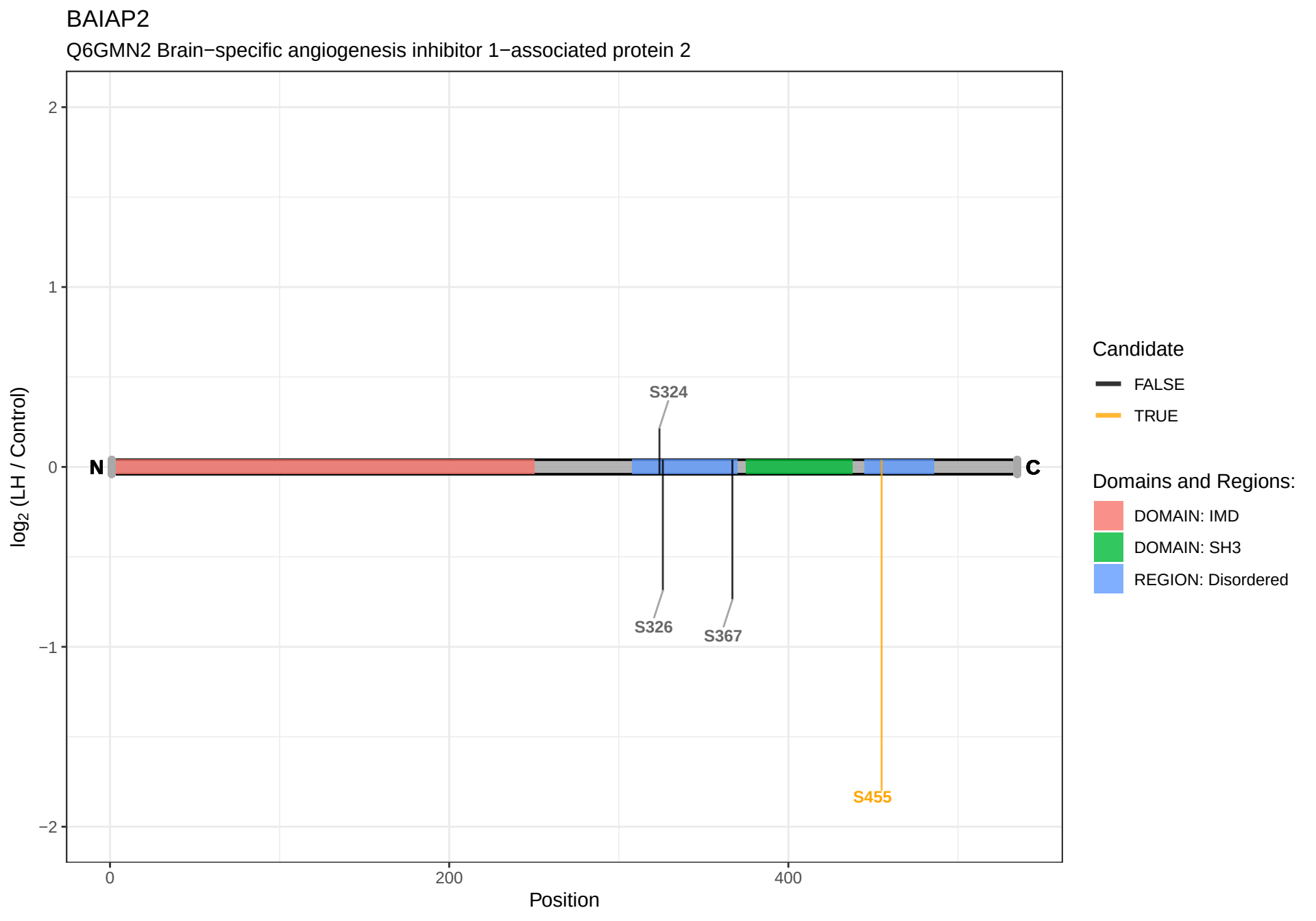

ATR
D3Z822 ATR serine/threonine kinase
S438
S439
N
C
log2 (LH / Control)
Position
3
2
1
0
−1
−2
−3
0
1000
2000
Candidate
TRUE
Domains and Regions:
DOMAIN: FAT
DOMAIN: FATC
DOMAIN: PI3K/PI4K
REGION: Disordered

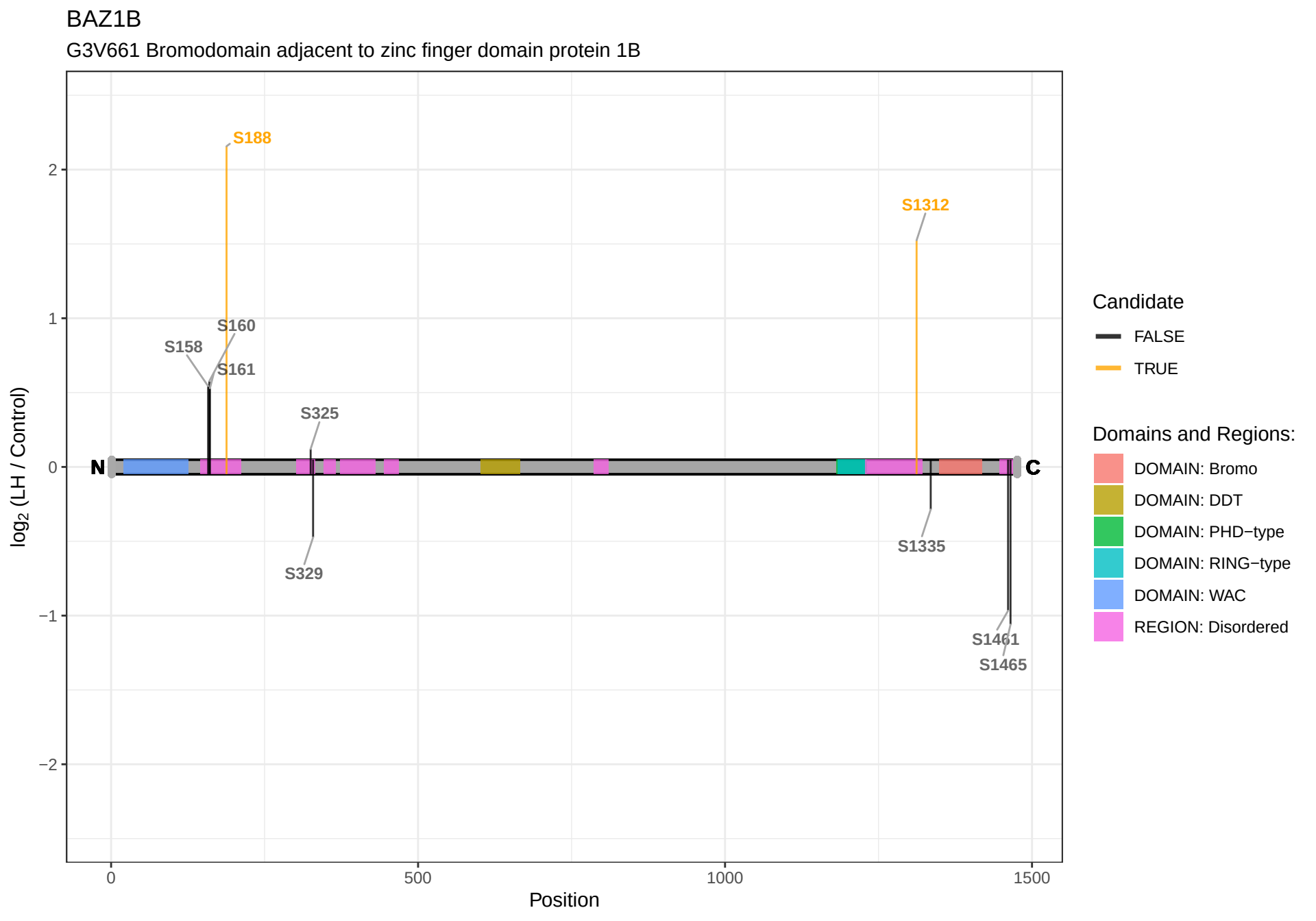

ATRX
A0A0G2JXZ3 Transcriptional regulator ATRX
log2 (LH / Control)
Position
N
C
S84
S900
S823
S903
S695
S979
S1172
S801
S798
S858
S800
S825
S772
S907
S1228
S1979
S853
S631
S774
S1057
S1975
S1229
S770
S997
S1060
S1434
S2362
S586
S667
S669
S904
S315
S723
S1139
S919
S1458
S721
S1094
S1190
S111
S805
S995
S1047
S590
S833
S1344
S996
S626
S859
S1045
S1340
S625
S1513
S92
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Helicase ATP−binding
DOMAIN: Helicase C−terminal
DOMAIN: PHD−type
REGION: Disordered

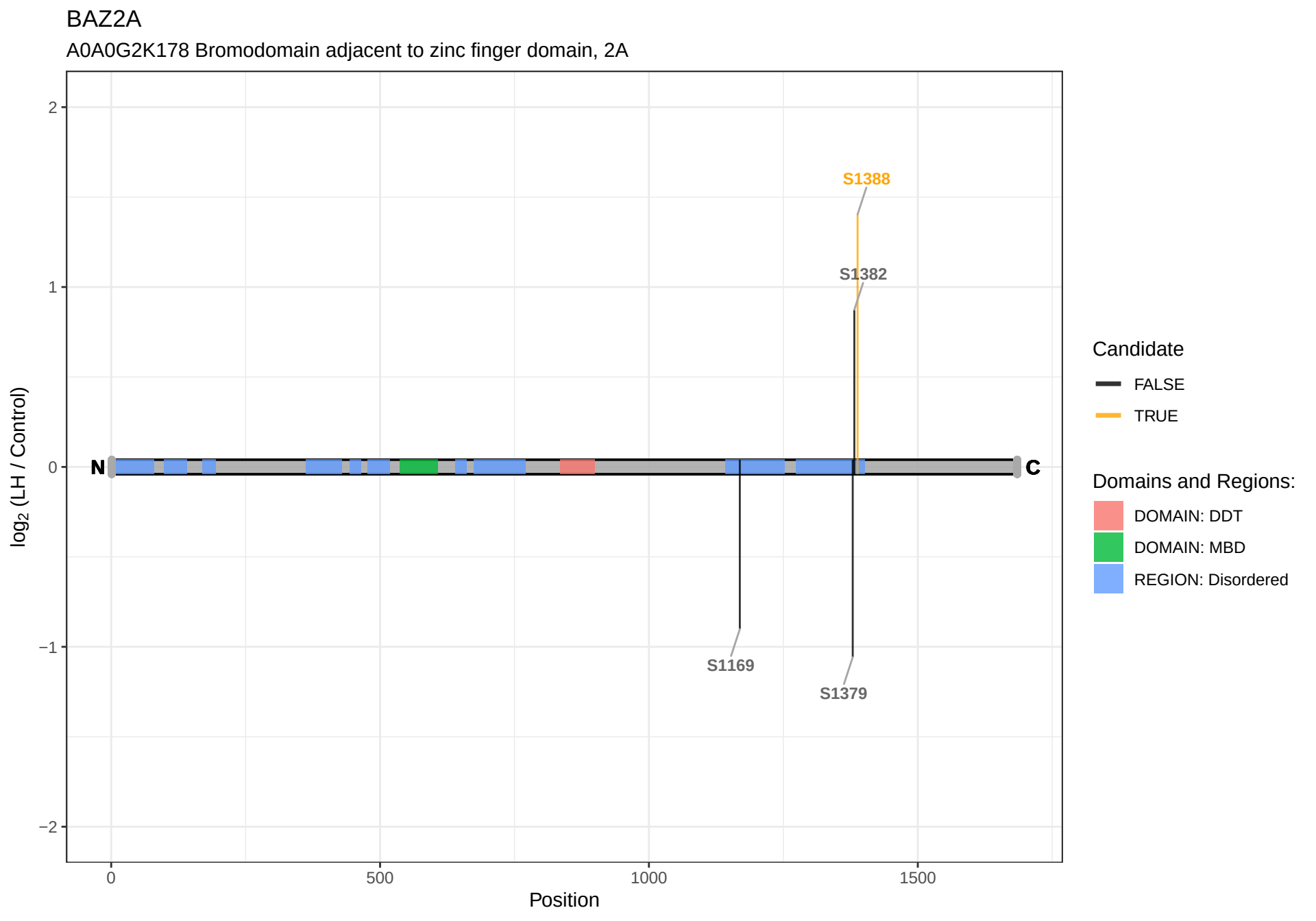

ATXN2
F1M049 Ataxin 2
log2 (LH / Control)
2
1
0
−1
−2
N
C
S202
S237
S632
S636
S628
S543
S529
T512
S555
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: LsmAD
REGION: Disordered

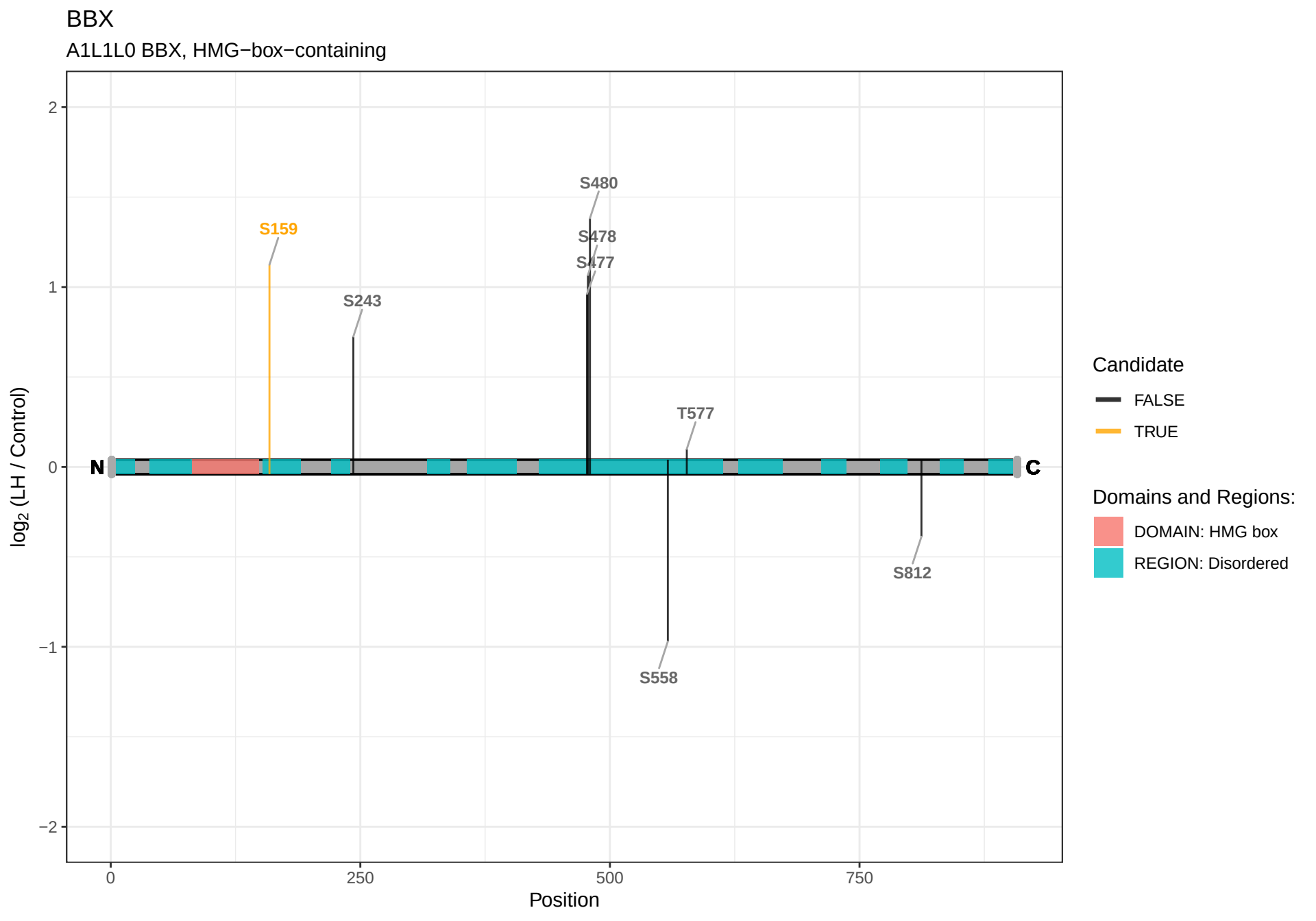

ATXN2L
B3DMA1 Ataxin 2−like
log2 (LH / Control)
Position
N
C
S166
S109
S333
S304
S337
S422
S594
S591
S631
S681
S677
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: LsmAD
REGION: Disordered

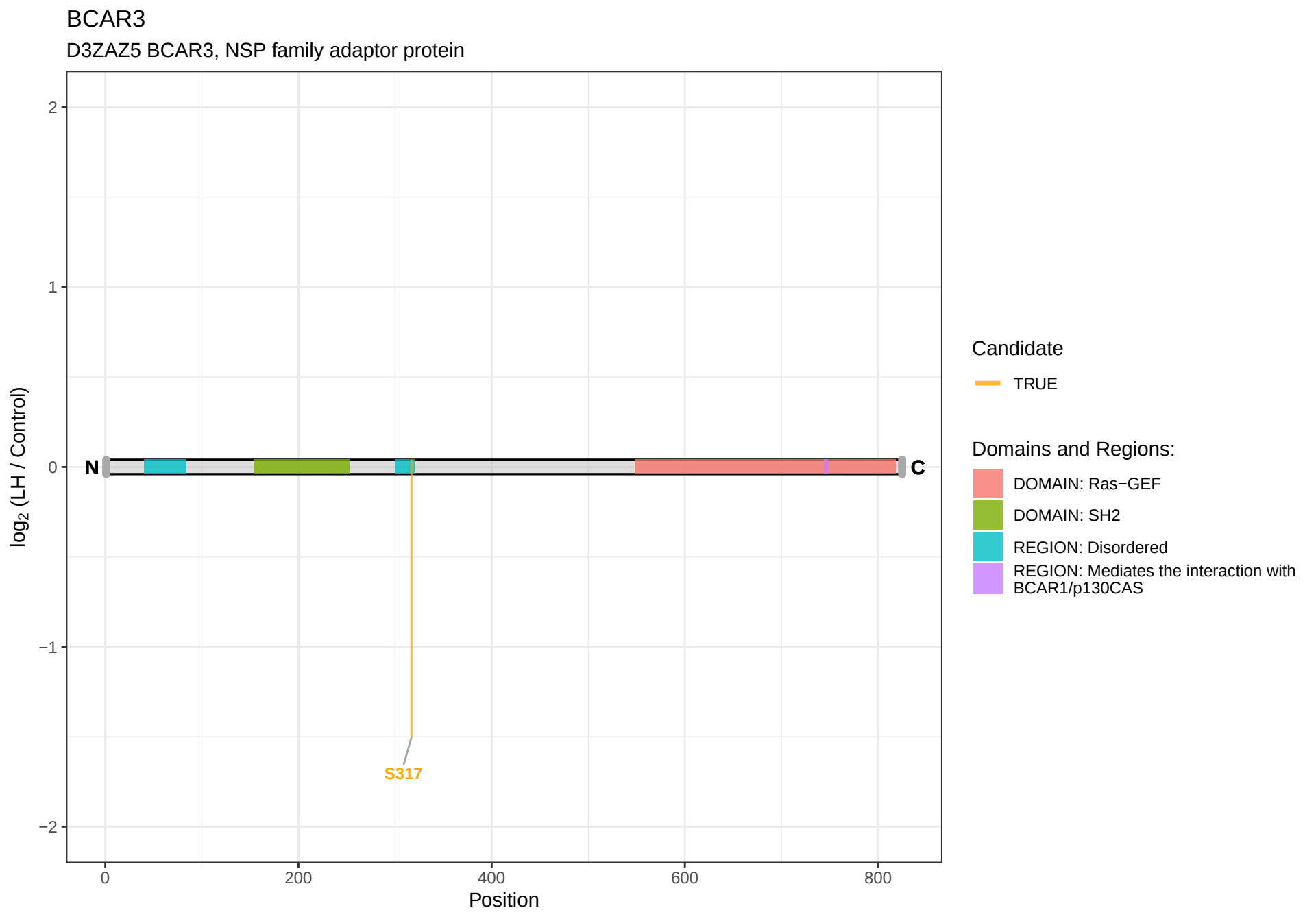

AVEN
D3Z853 Apoptosis and caspase activation inhibitor
log2 (LH / Control)
2
1
0
−1
−2
N
C
S118
0
50
100
150
200
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

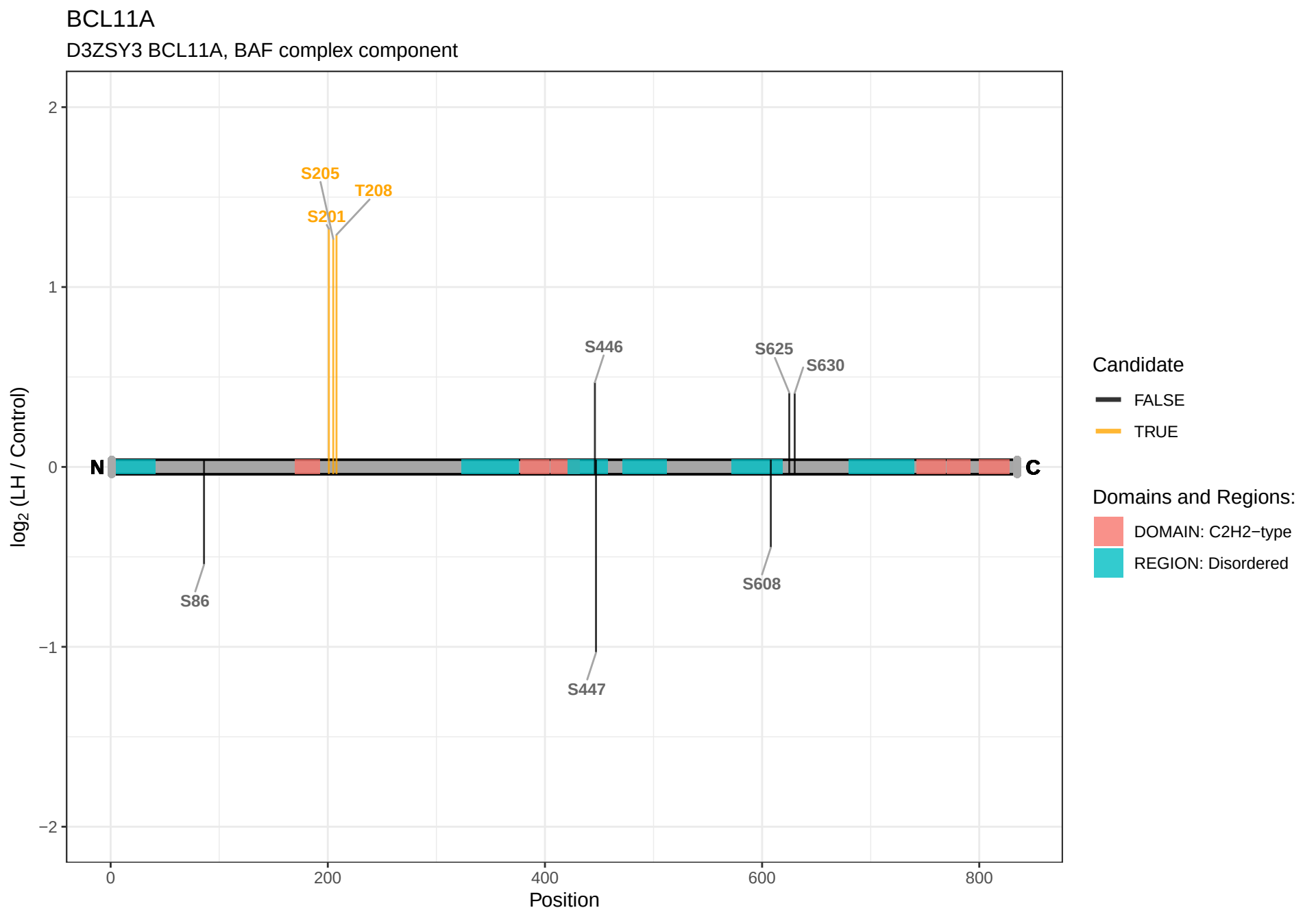

BAIAP2
Q6GMN2 Brain−specific angiogenesis inhibitor 1−associated protein 2
log2 (LH / Control)
2
1
0
−1
−2
N
C
S324
S326
S367
S455
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: IMD
DOMAIN: SH3
REGION: Disordered

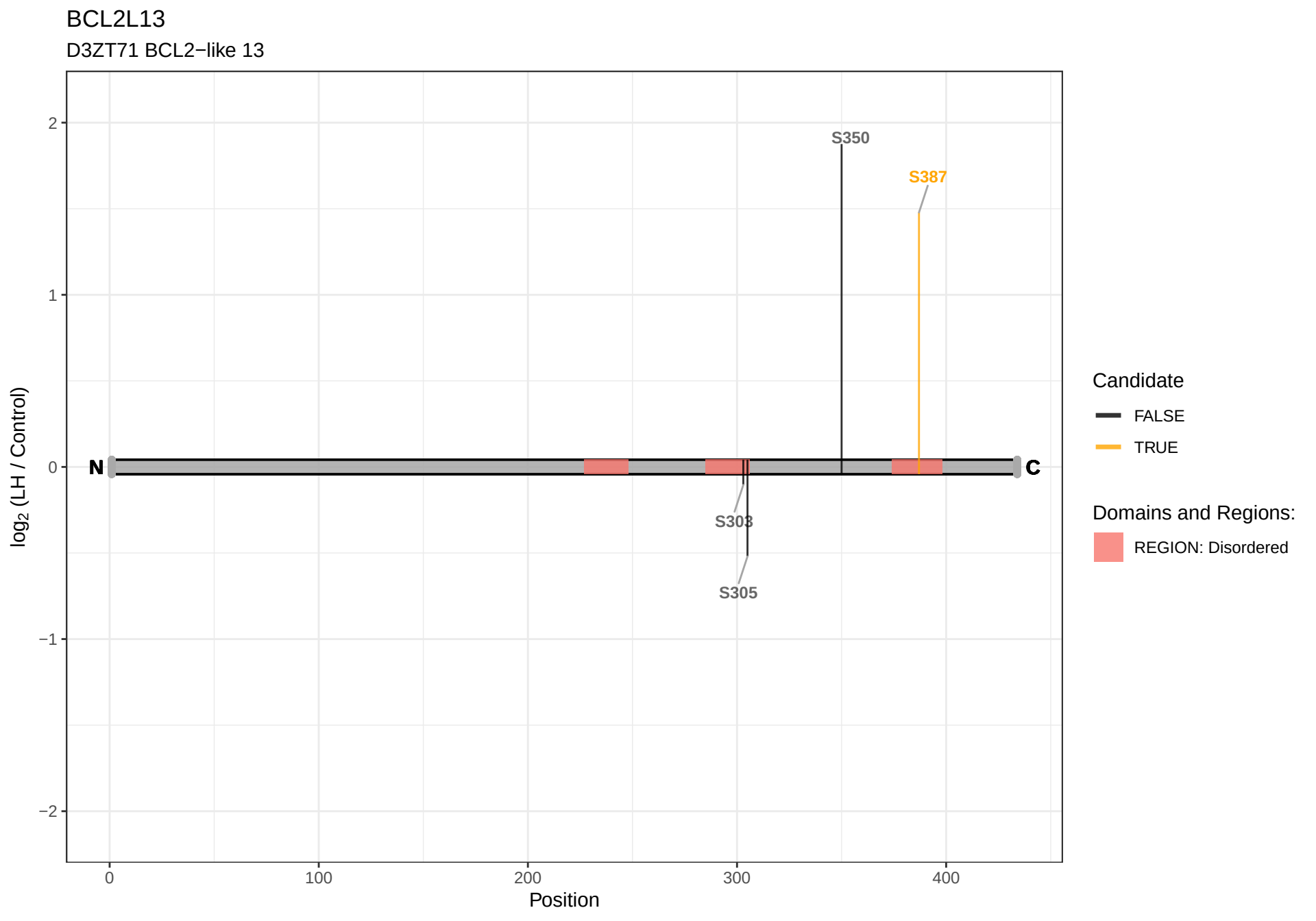

BAZ1B
G3V661 Bromodomain adjacent to zinc finger domain protein 1B
S188
S1312
S160
S158
S161
S325
N
C
S1335
S329
S1461
S1465
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Bromo
DOMAIN: DDT
DOMAIN: PHD−type
DOMAIN: RING−type
DOMAIN: WAC
REGION: Disordered

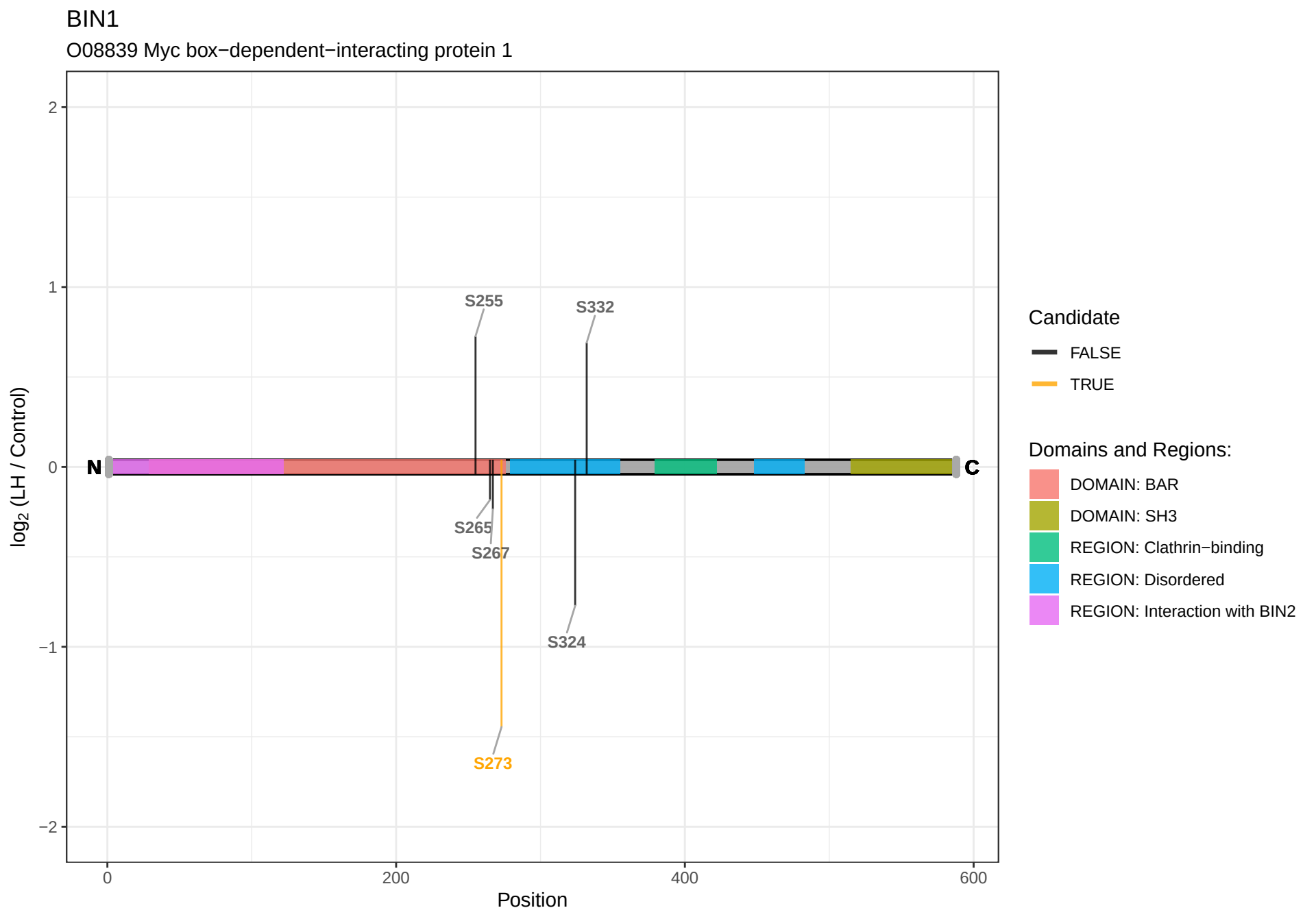

BAZ2A
A0A0G2K178 Bromodomain adjacent to zinc finger domain, 2A
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
Position
N
C
S1388
S1382
S1169
S1379
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DDT
DOMAIN: MBD
REGION: Disordered

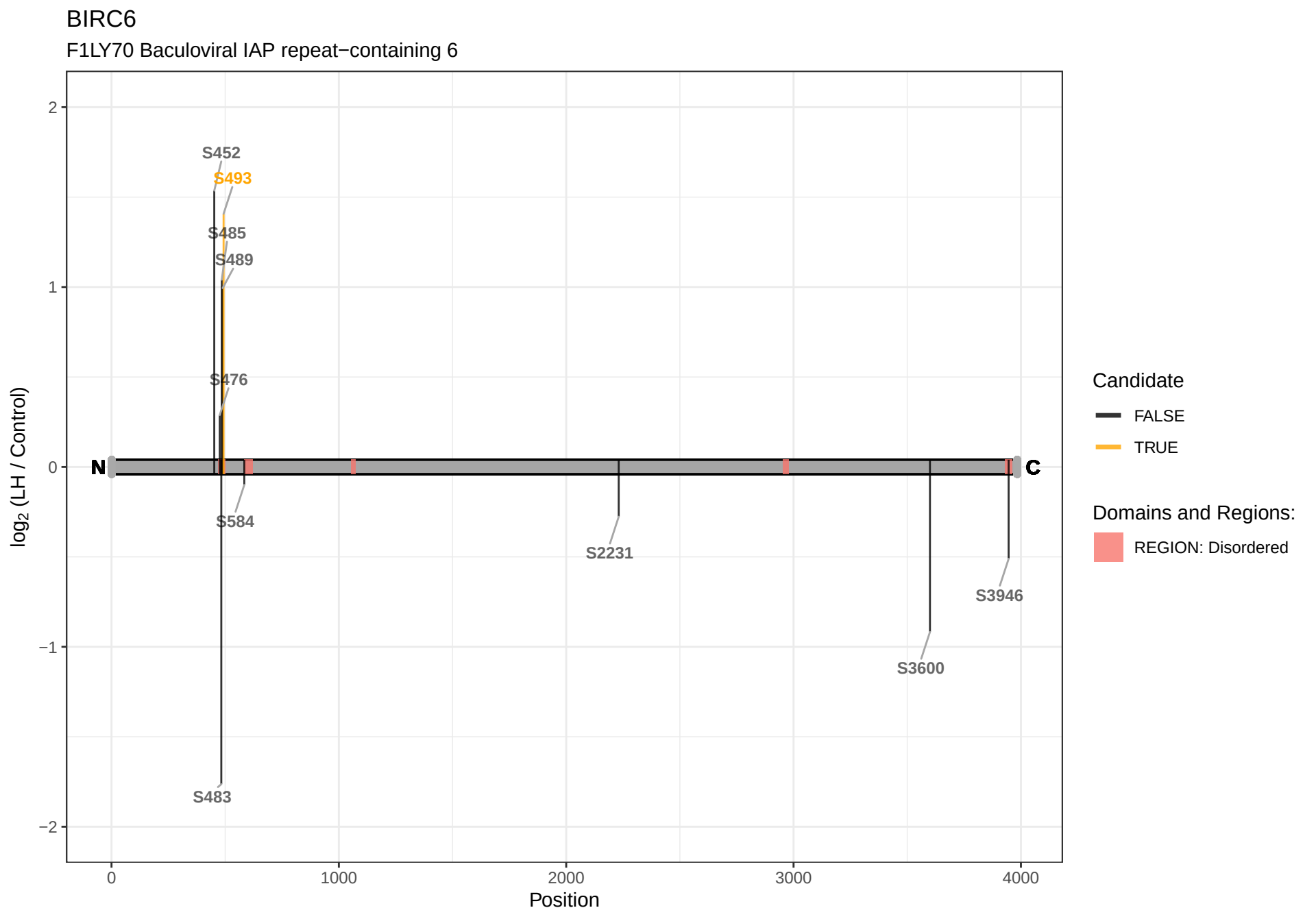

BBX
A1L1L0 BBX, HMG−box−containing
log2 (LH / Control)
2
1
0
−1
−2
0
250
500
750
Position
N
C
S159
S480
S478
S477
S243
T577
S812
S558
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: HMG box
REGION: Disordered

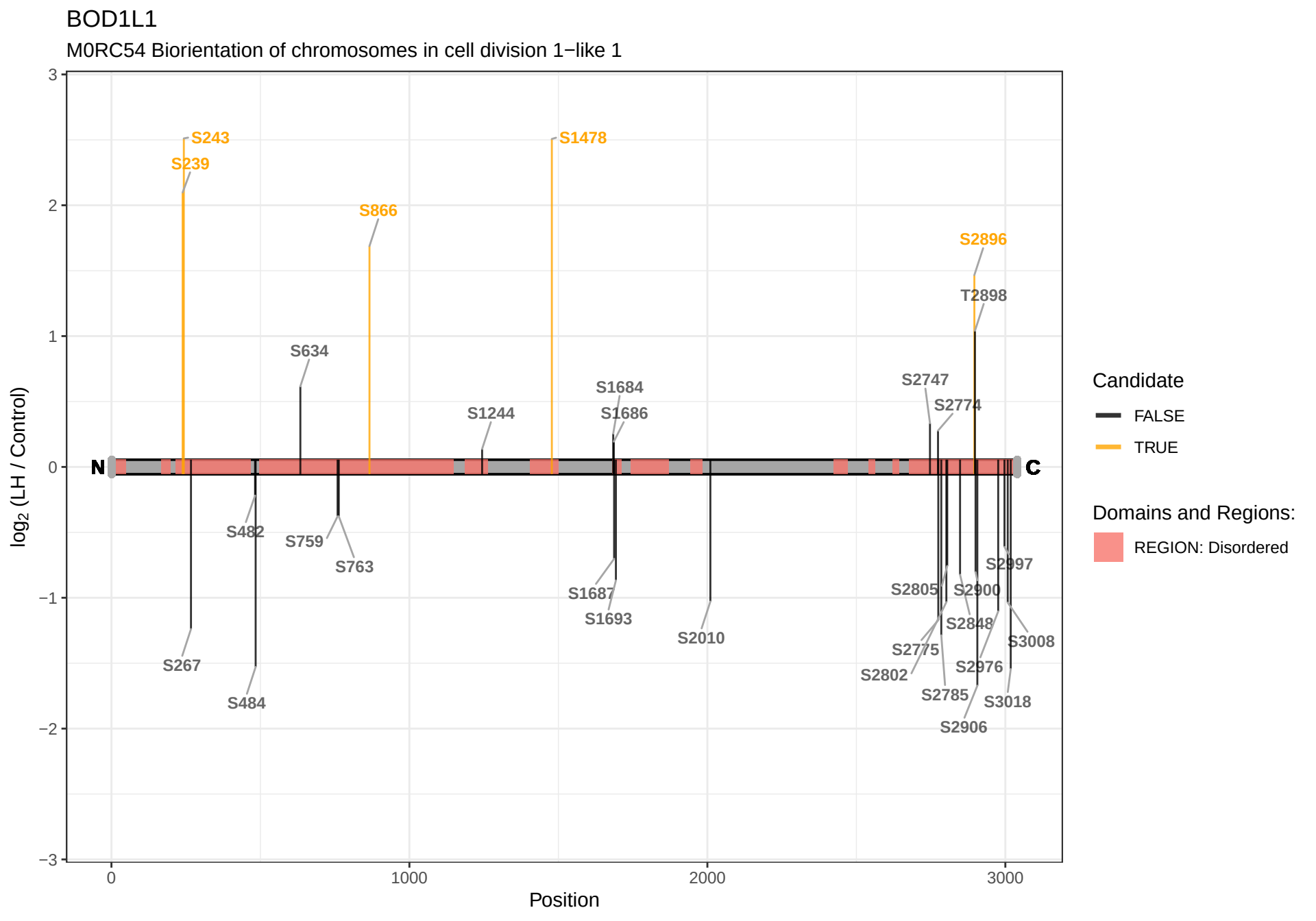

BCAR3
D3ZAZ5 BCAR3, NSP family adaptor protein
log2 (LH / Control)
2
1
0
−1
−2
N
C
S317
0
200
400
600
800
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Ras−GEF
DOMAIN: SH2
REGION: Disordered
REGION: Mediates the interaction with BCAR1/p130CAS

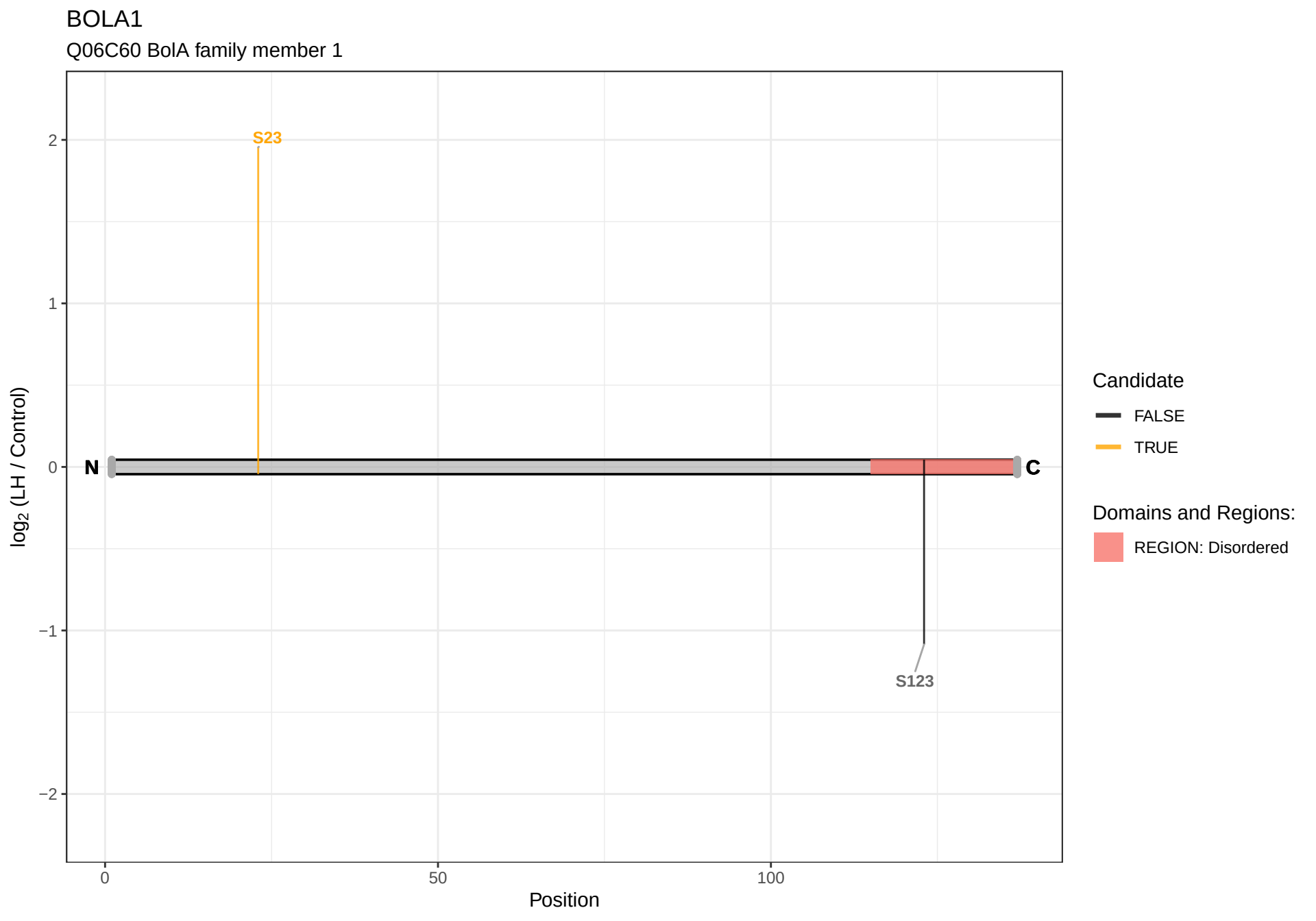

BCL11A
D3ZSY3 BCL11A, BAF complex component
log2 (LH / Control)
2
1
0
−1
−2
S205
T208
S201
S446
S625
S630
S86
S608
S447
N
C
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2H2−type
REGION: Disordered

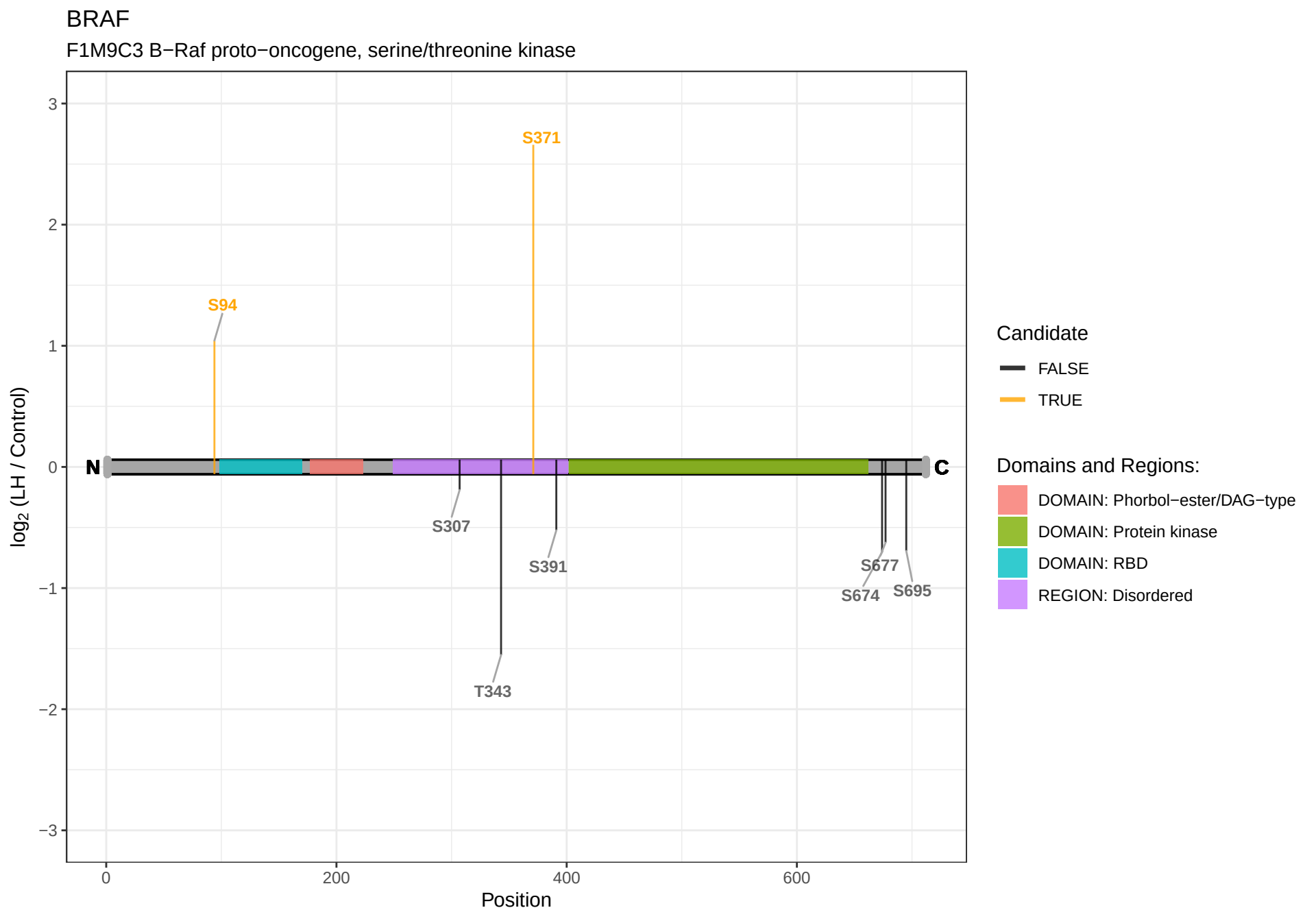

BCL2L13
D3ZT71 BCL2−like 13
log2 (LH / Control)
2
1
0
−1
−2
N
C
S350
S387
S303
S305
0
100
200
300
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

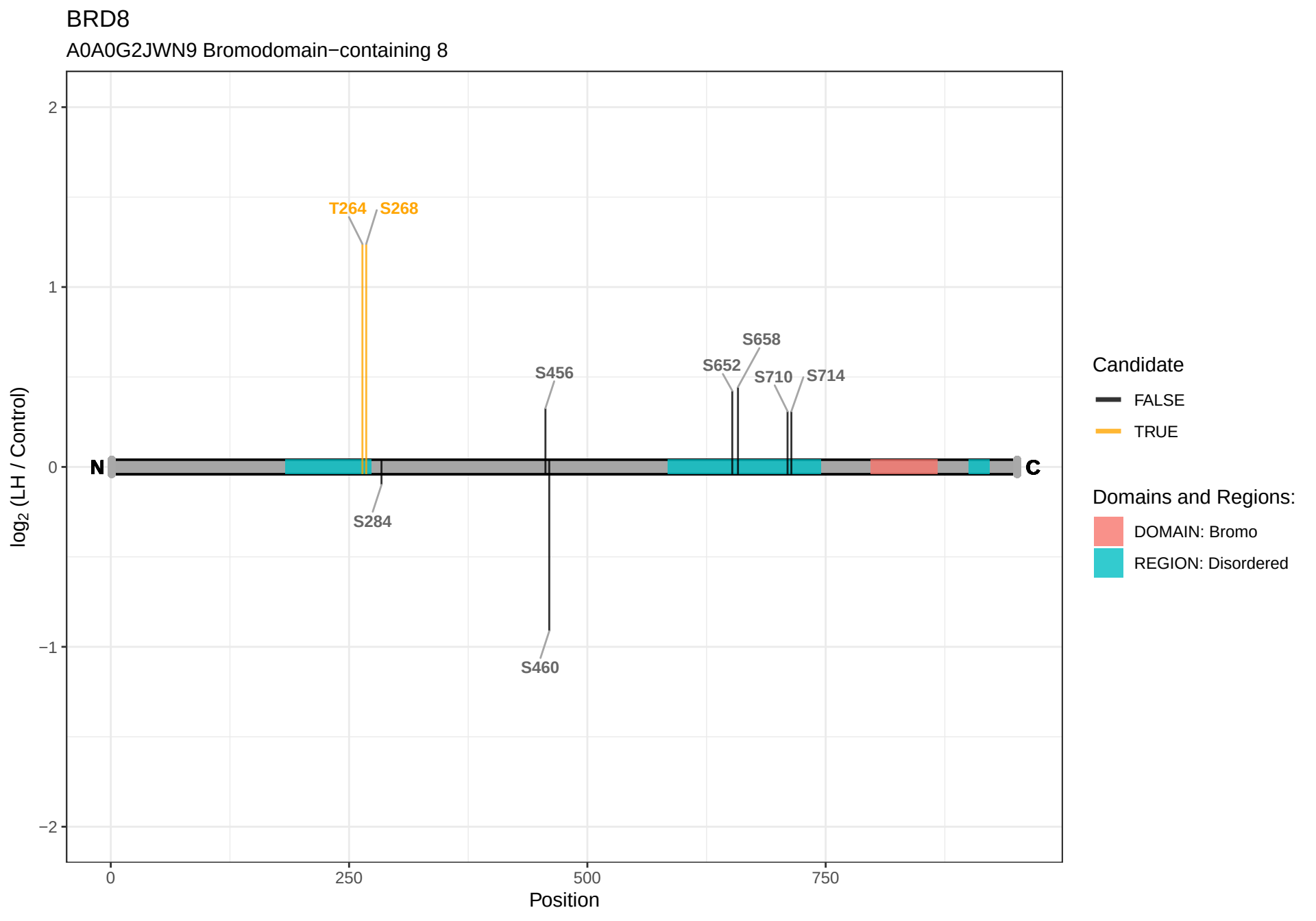

BIN1
O08839 Myc box−dependent−interacting protein 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S255
S332
S265
S267
S324
S273
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: BAR
DOMAIN: SH3
REGION: Clathrin−binding
REGION: Disordered
REGION: Interaction with BIN2

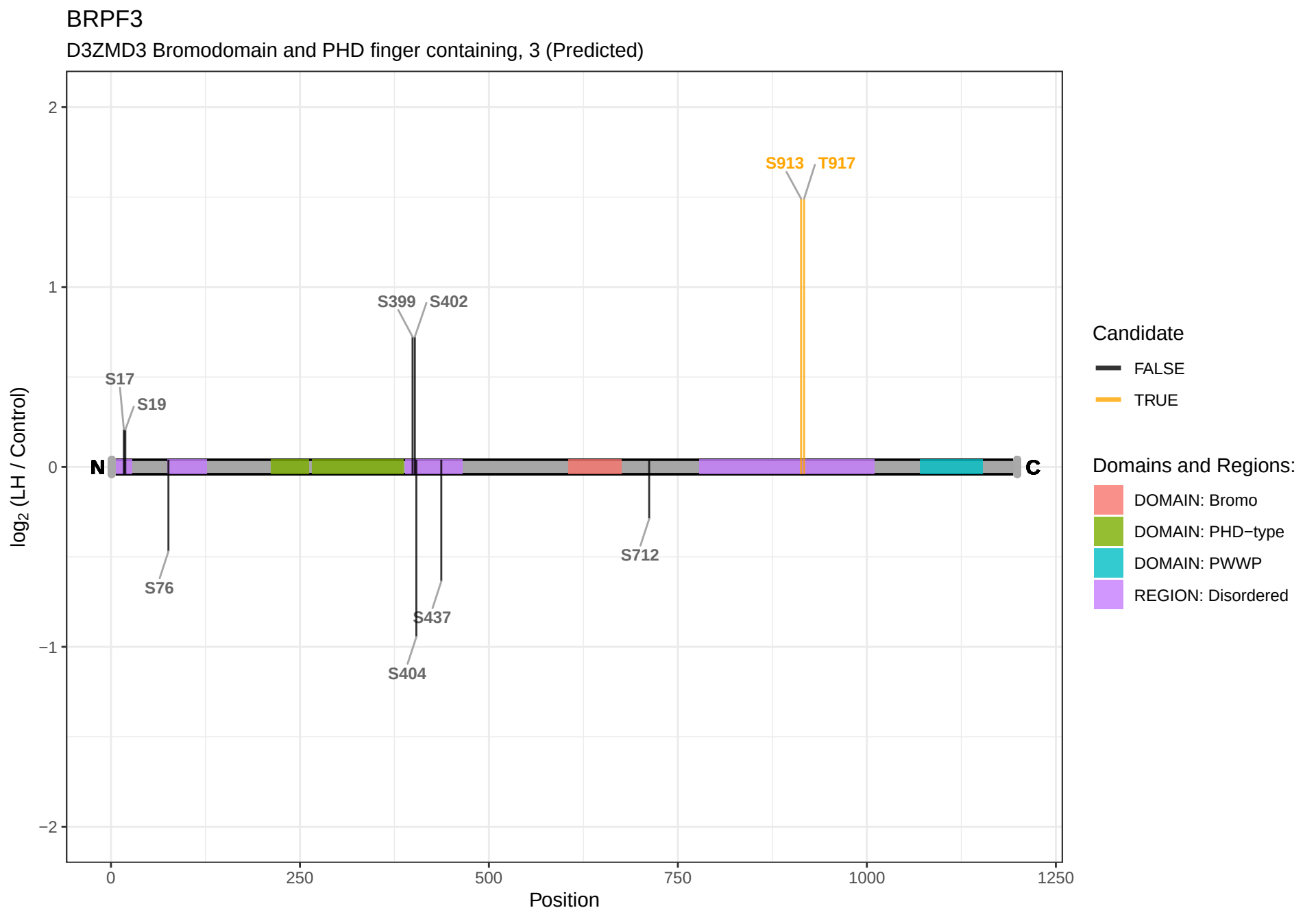

BIRC6
F1LY70 Baculoviral IAP repeat−containing 6
log2 (LH / Control)
Position
N
C
S452
S493
S485
S489
S476
S584
S483
S2231
S3600
S3946
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

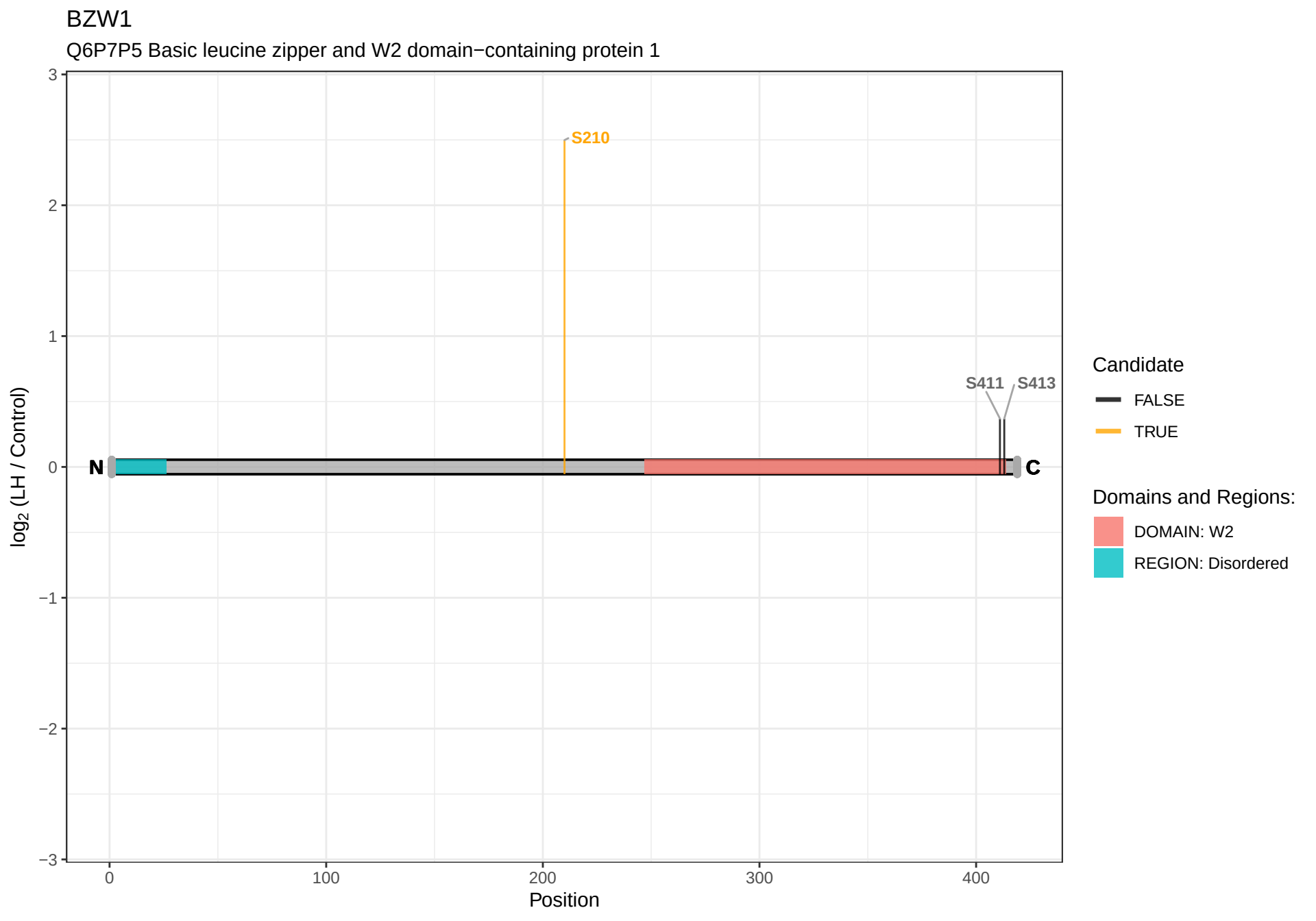

BOD1L1
M0RC54 Biorientation of chromosomes in cell division 1−like 1
log2 (LH / Control)
Position
N
C
S243
S239
S866
S1478
S2896
T2898
S634
S1684
S1686
S1244
S2747
S2774
S482
S759
S763
S1687
S1693
S2010
S2997
S2805
S2900
S2848
S3008
S2775
S2802
S2976
S2785
S3018
S2906
S267
S484
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

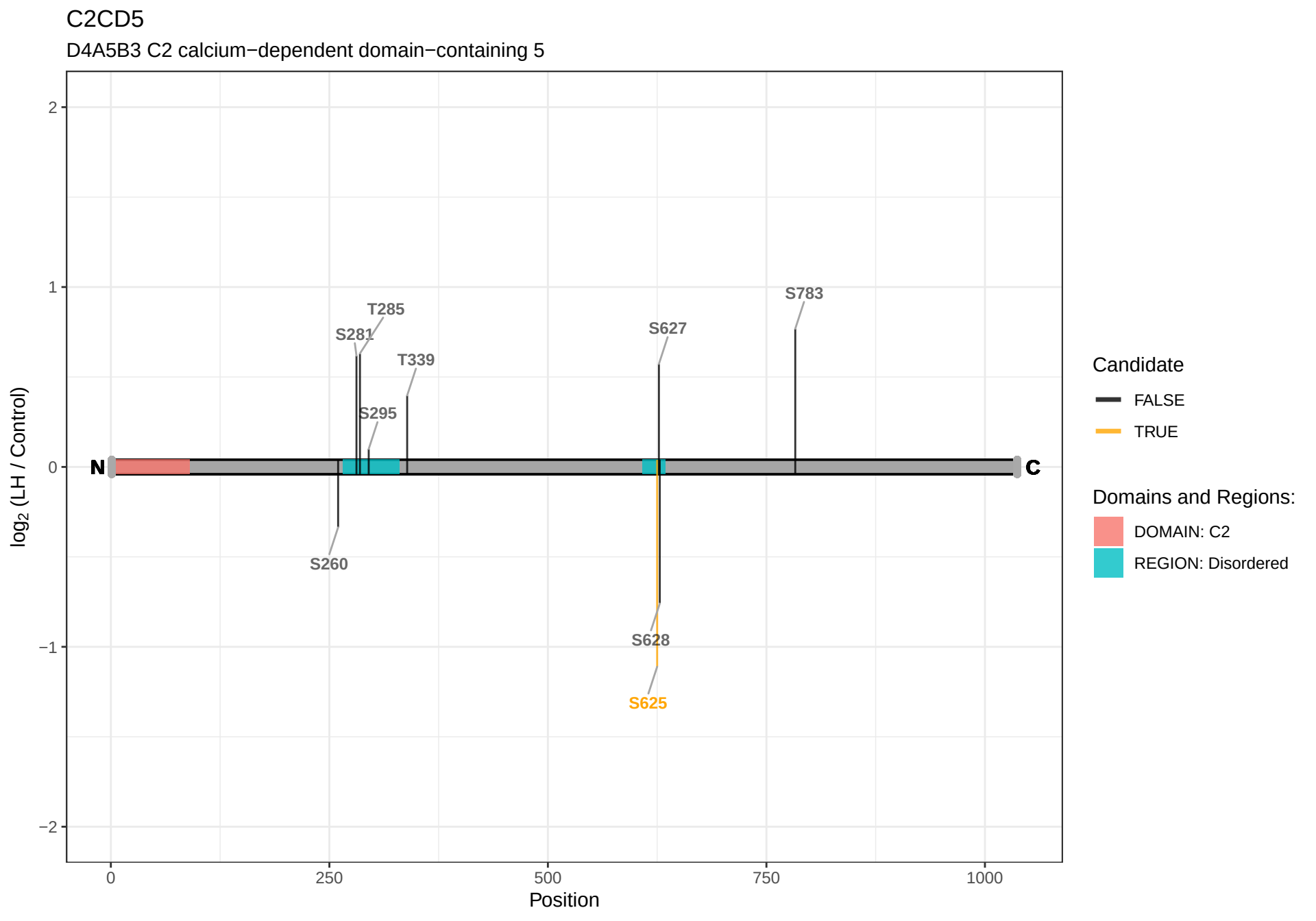

BOLA1
Q06C60 BolA family member 1
S23
S123
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
50
100
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

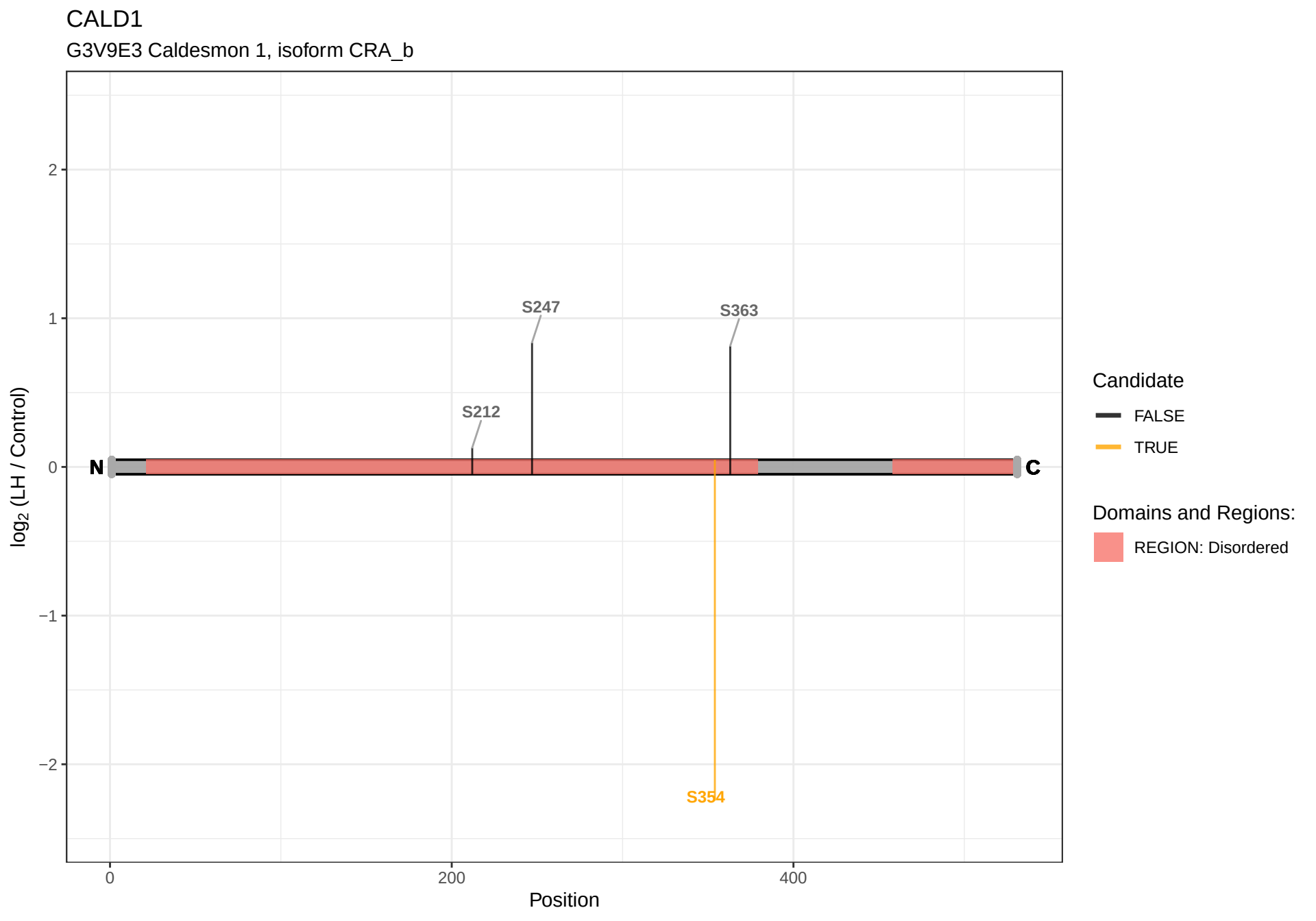

BRAF
F1M9C3 B−Raf proto−oncogene, serine/threonine kinase
log2 (LH / Control)
3
2
1
0
−1
−2
−3
0
200
400
600
Position
N
C
S94
S371
S307
S391
T343
S677
S674
S695
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Phorbol−ester/DAG−type
DOMAIN: Protein kinase
DOMAIN: RBD
REGION: Disordered

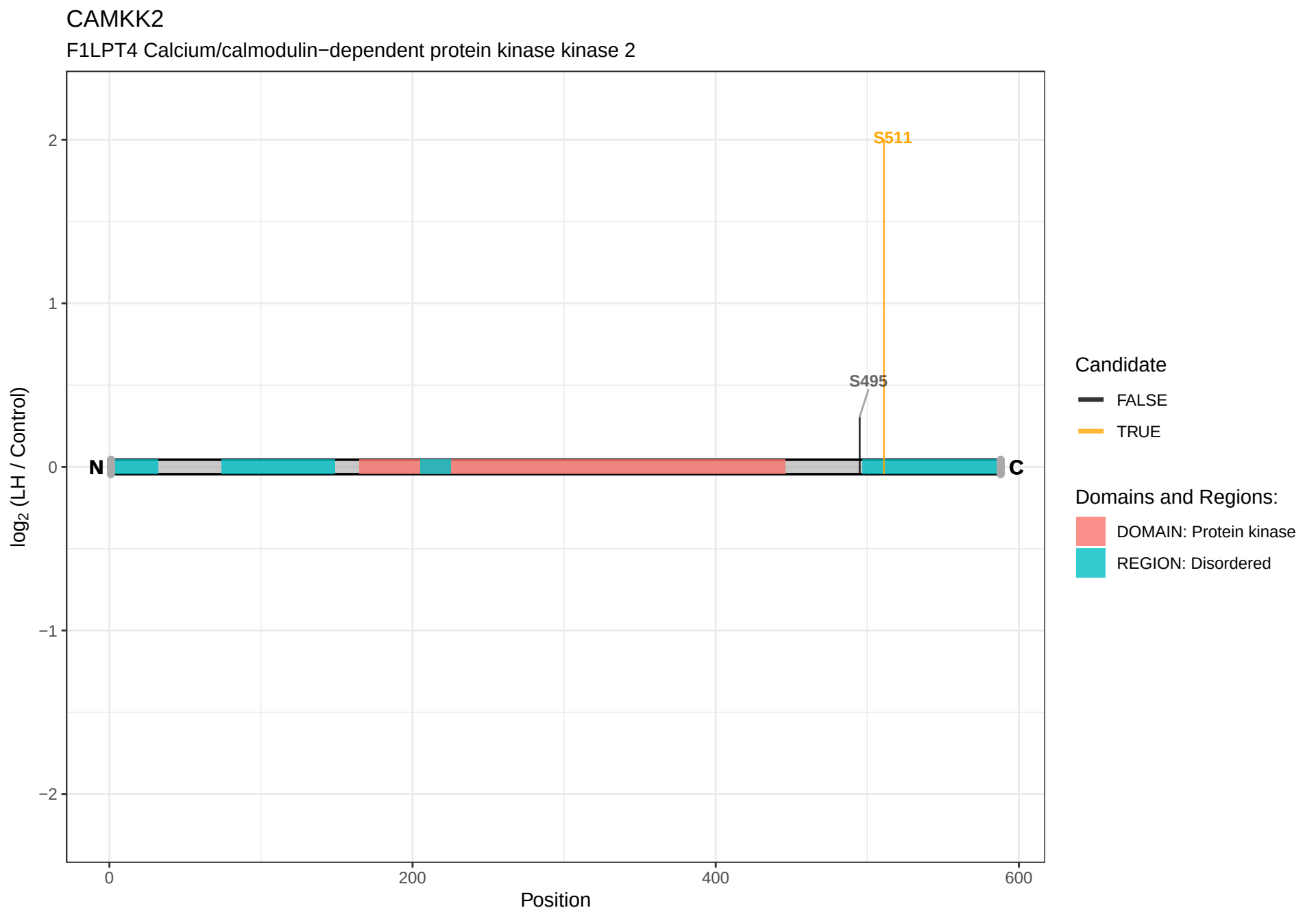

BRD8
A0A0G2JWN9 Bromodomain−containing 8
log2 (LH / Control)
2
1
0
−1
−2
0
250
500
750
Position
N
C
T264
S268
S284
S456
S460
S652
S658
S710
S714
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Bromo
REGION: Disordered

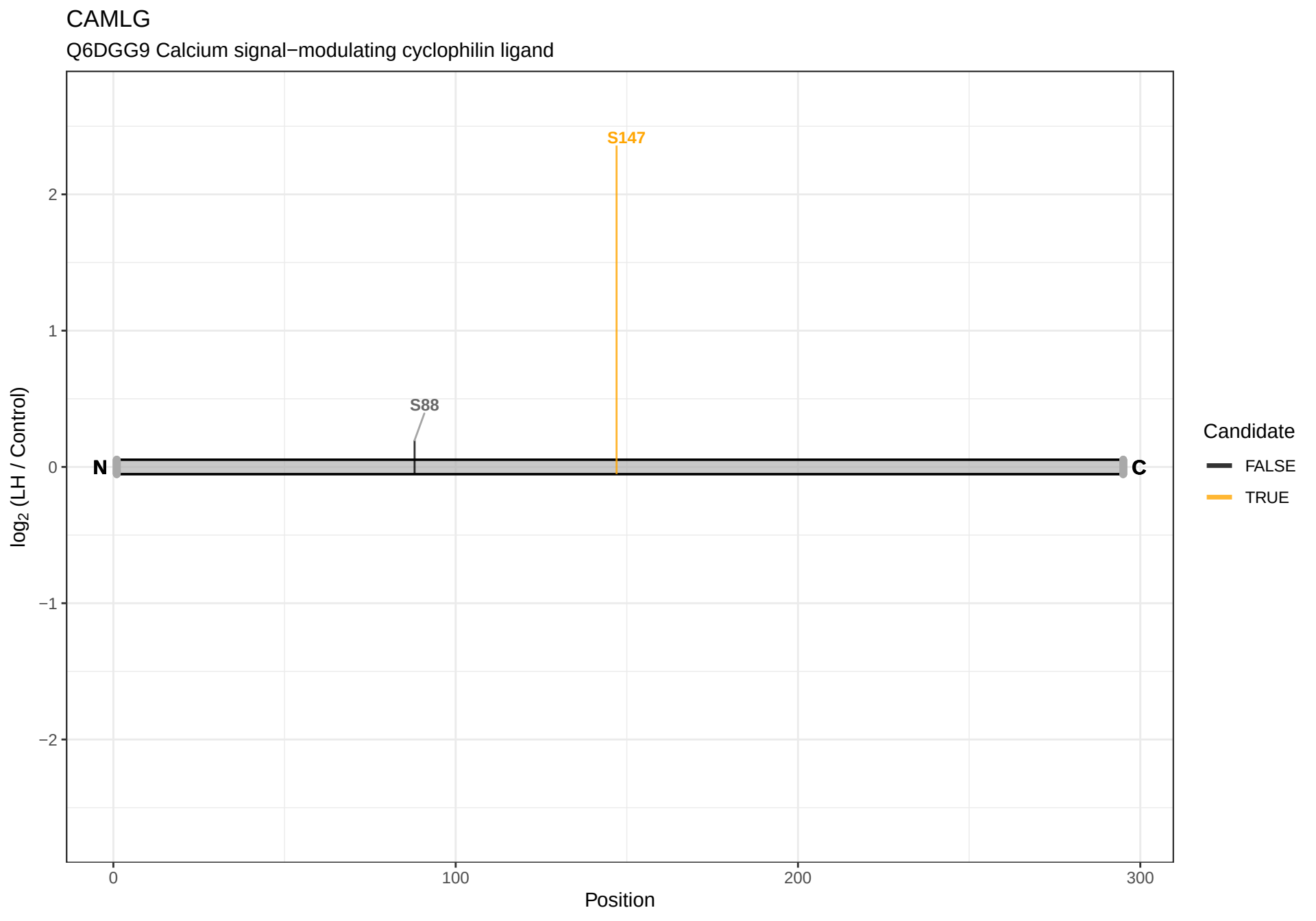

BRPF3
D3ZMD3 Bromodomain and PHD finger containing, 3 (Predicted)
log2 (LH / Control)
Position
2
1
0
−1
−2
0
250
500
750
1000
1250
N
C
S913
T917
S399
S402
S17
S19
S76
S437
S404
S712
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Bromo
DOMAIN: PHD−type
DOMAIN: PWWP
REGION: Disordered

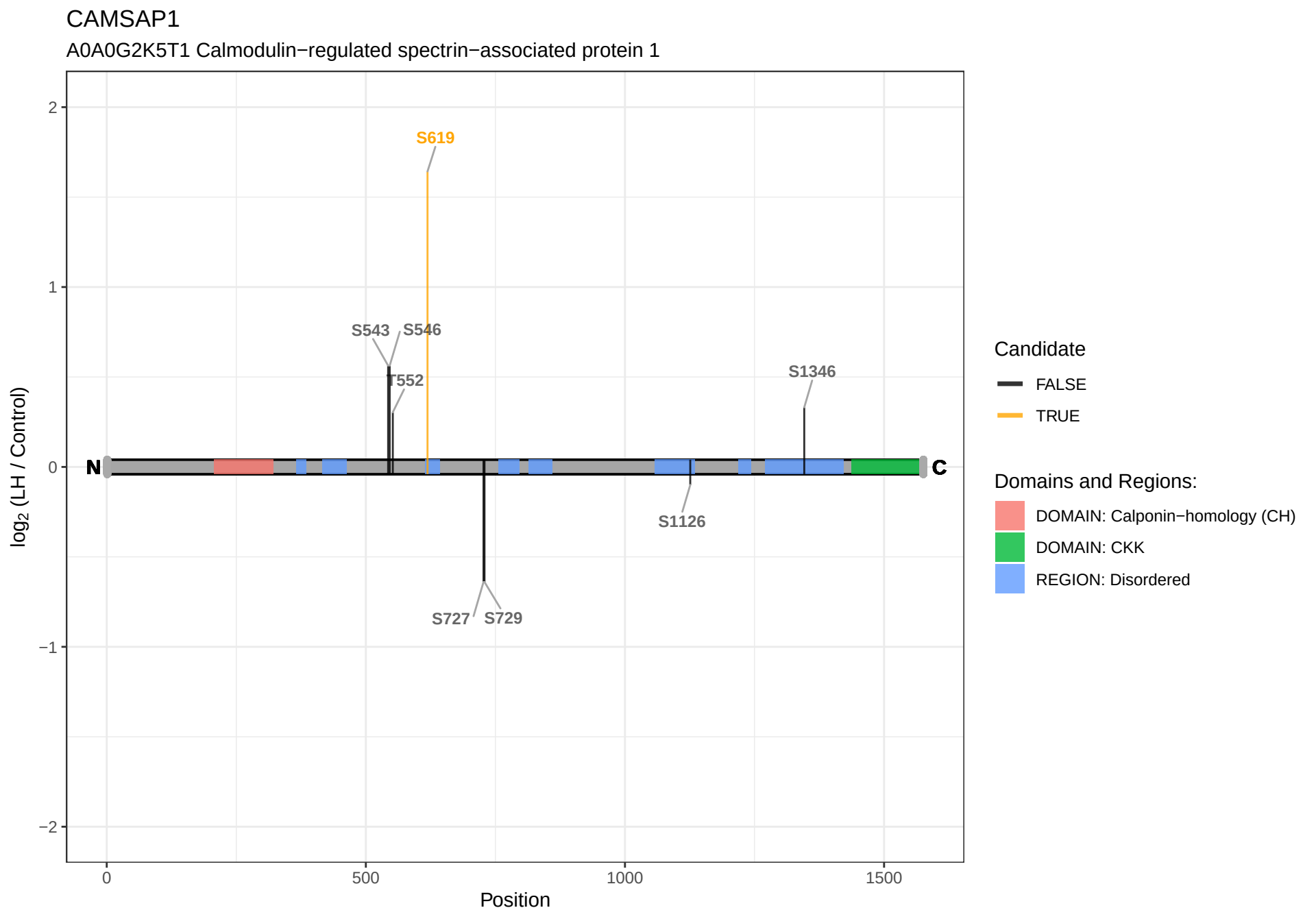

BZW1
Q6P7P5 Basic leucine zipper and W2 domain−containing protein 1
log2 (LH / Control)
3
2
1
0
−1
−2
−3
S210
S411
S413
N
C
0
100
200
300
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: W2
REGION: Disordered

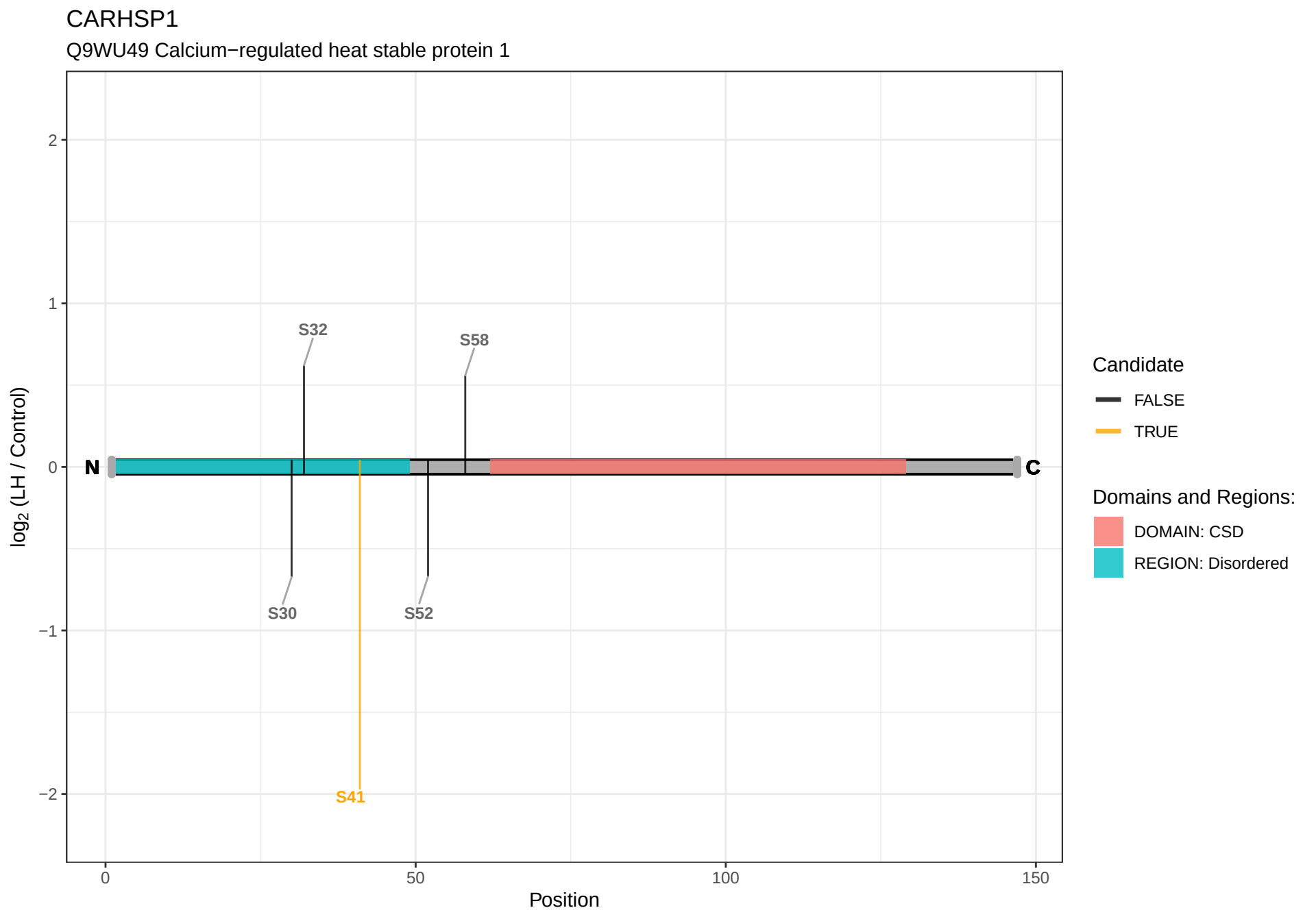

C2CD5
D4A5B3 C2 calcium−dependent domain−containing 5
log2 (LH / Control)
2
1
0
−1
−2
0
250
500
750
1000
Position
N
C
T285
S281
T339
S295
S260
S627
S783
S628
S625
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2
REGION: Disordered

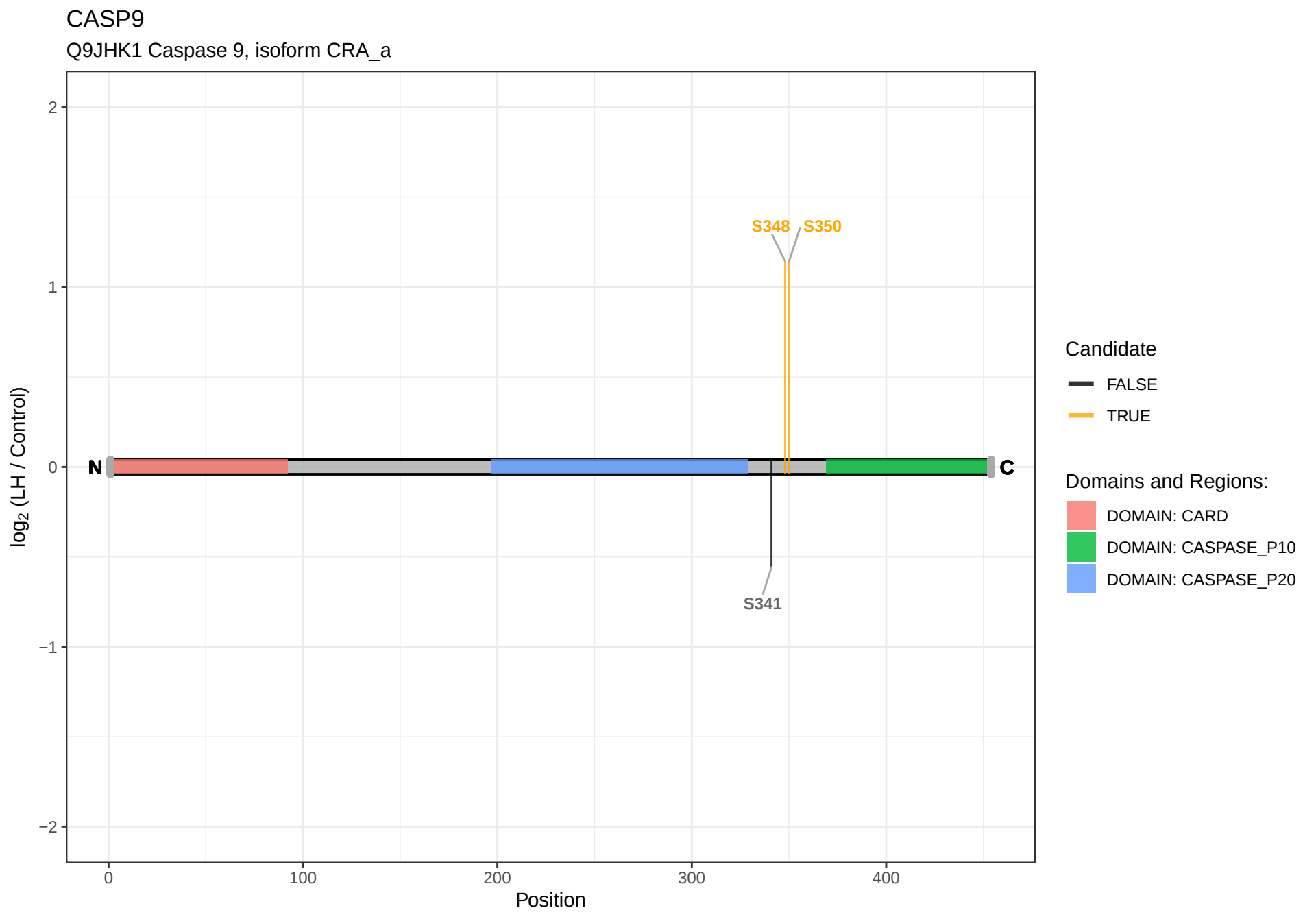

CALD1
G3V9E3 Caldesmon 1, isoform CRA_b
log2 (LH / Control)
2
1
0
−1
−2
S247
S363
S212
S354
N
C
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

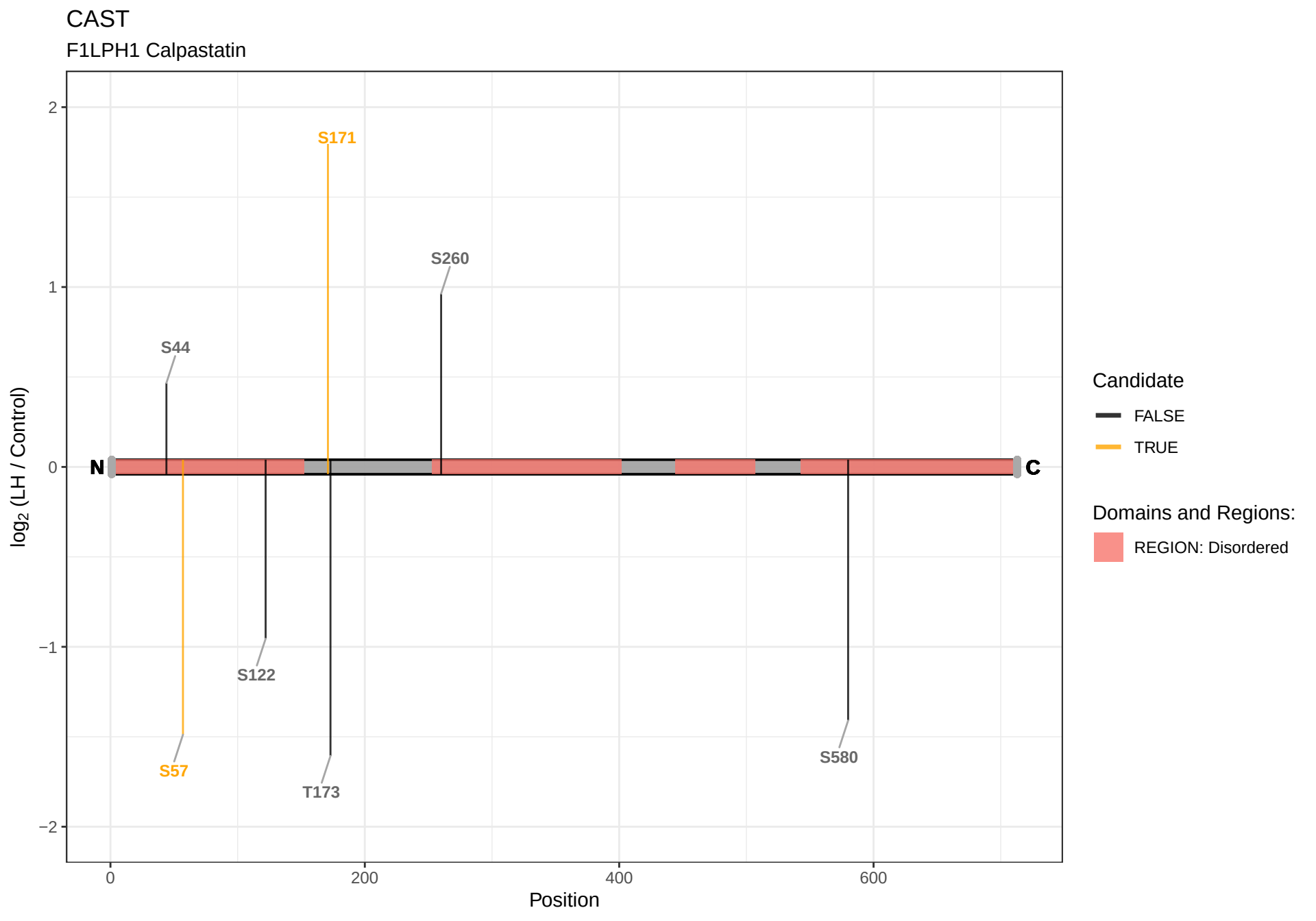

CAMKK2
F1LPT4 Calcium/calmodulin−dependent protein kinase kinase 2
S511
S495
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered

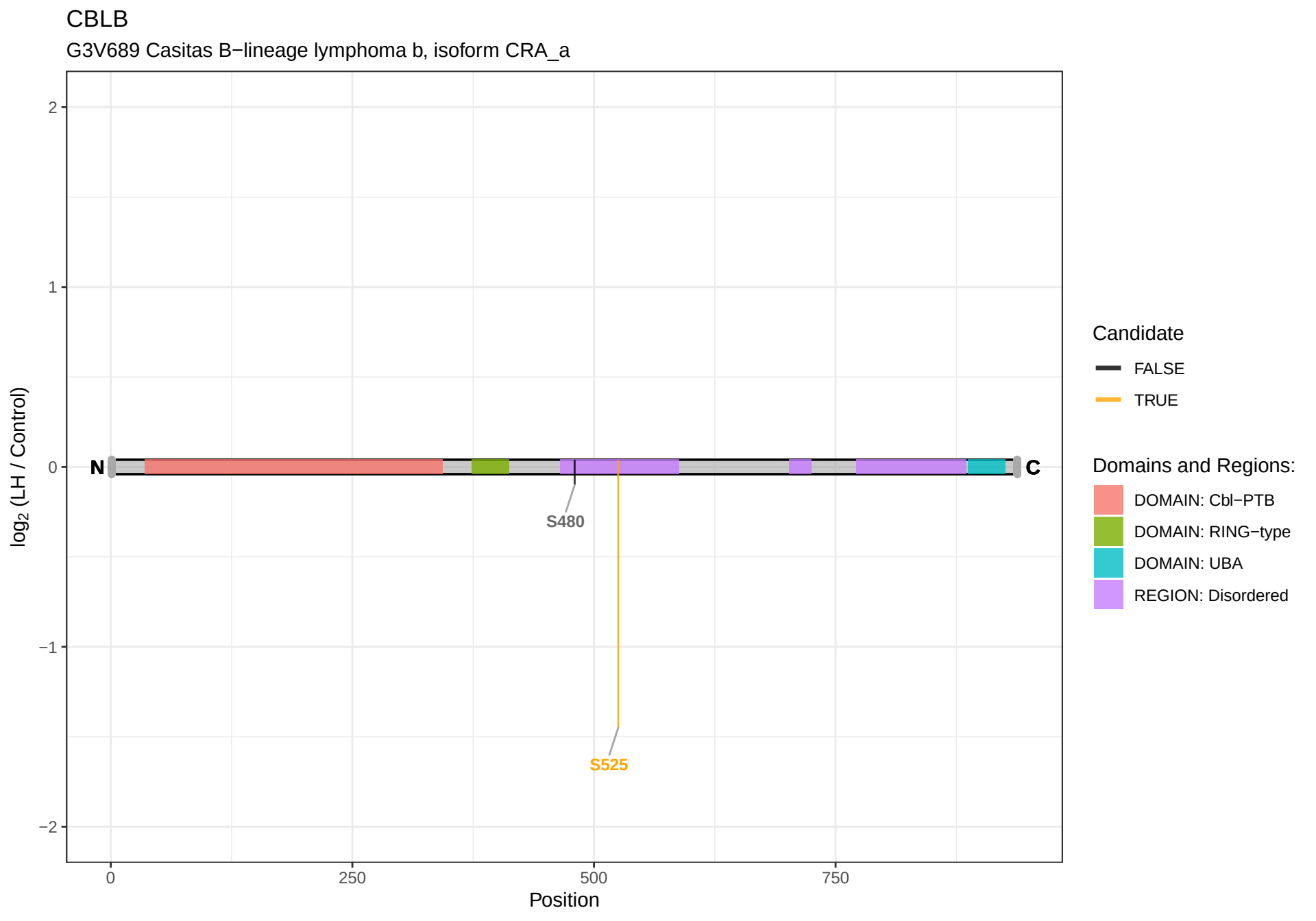

CAMLG
Q6DGG9 Calcium signal−modulating cyclophilin ligand
S147
S88
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
Position
Candidate
FALSE
TRUE

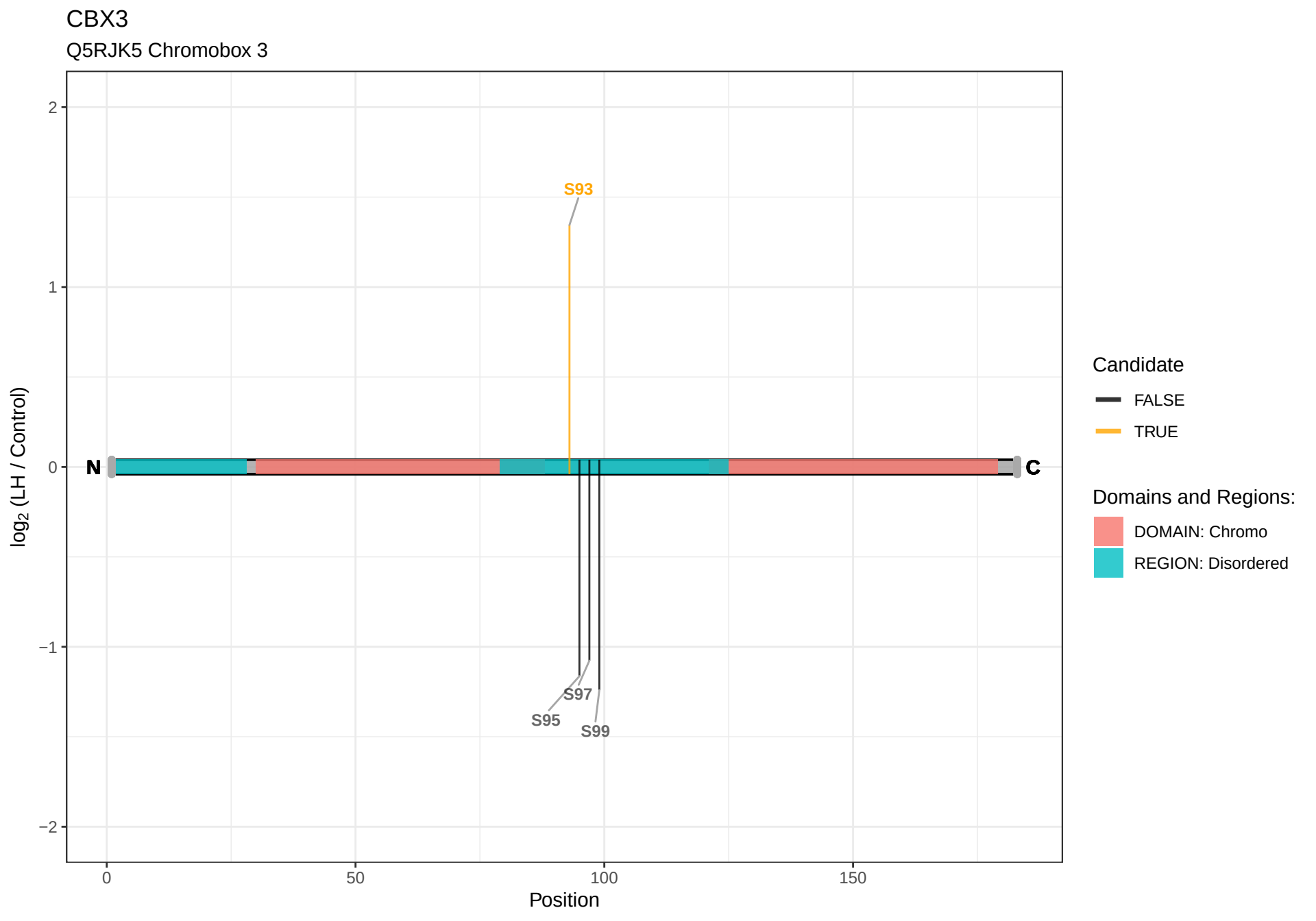

CAMSAP1
A0A0G2K5T1 Calmodulin−regulated spectrin−associated protein 1
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
Position
N
C
S619
S543
S546
T552
S1346
S1126
S727
S729
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Calponin−homology (CH)
DOMAIN: CKK
REGION: Disordered

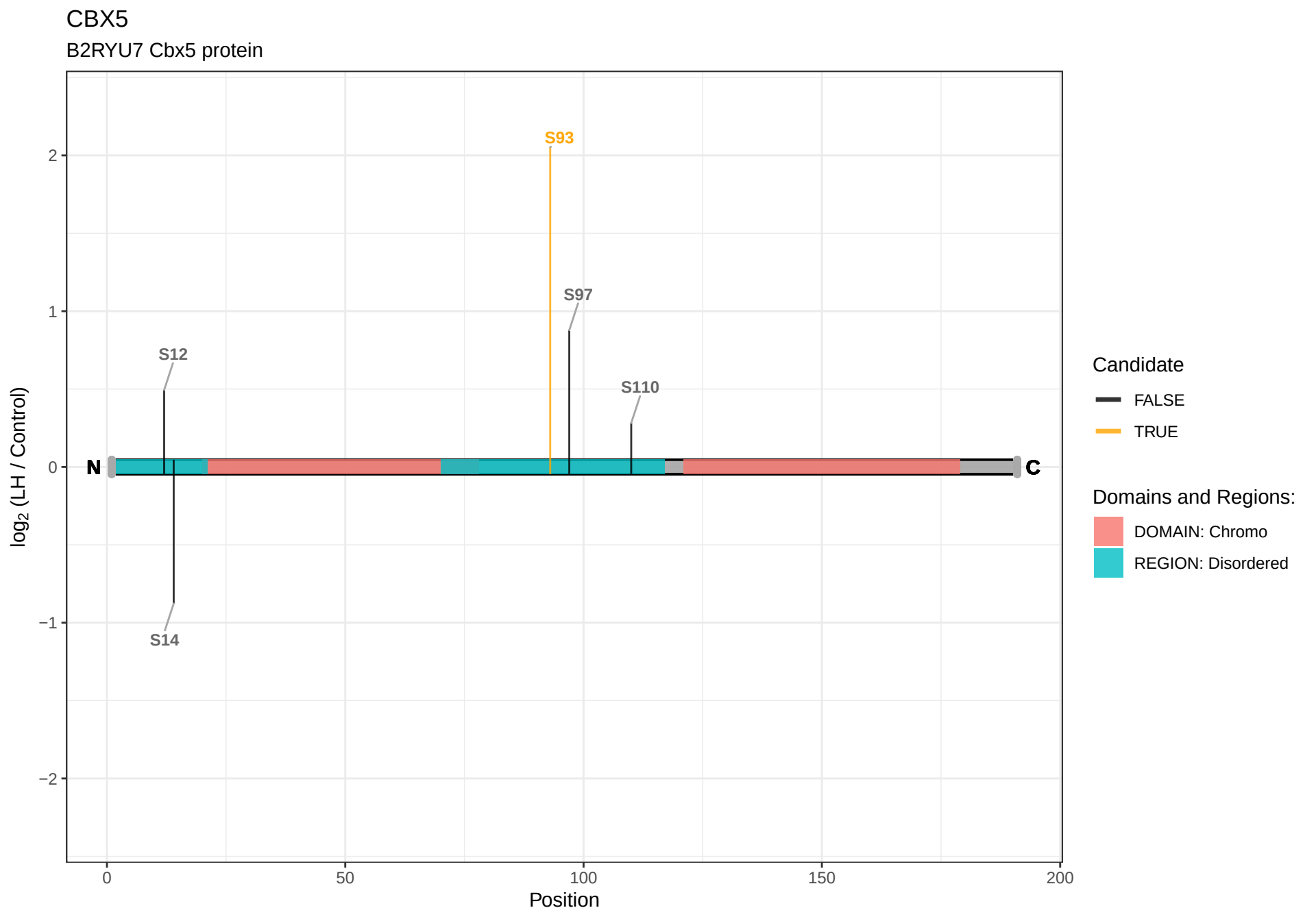

CARHSP1
Q9WU49 Calcium−regulated heat stable protein 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S32
S58
S30
S52
S41
0
50
100
150
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CSD
REGION: Disordered

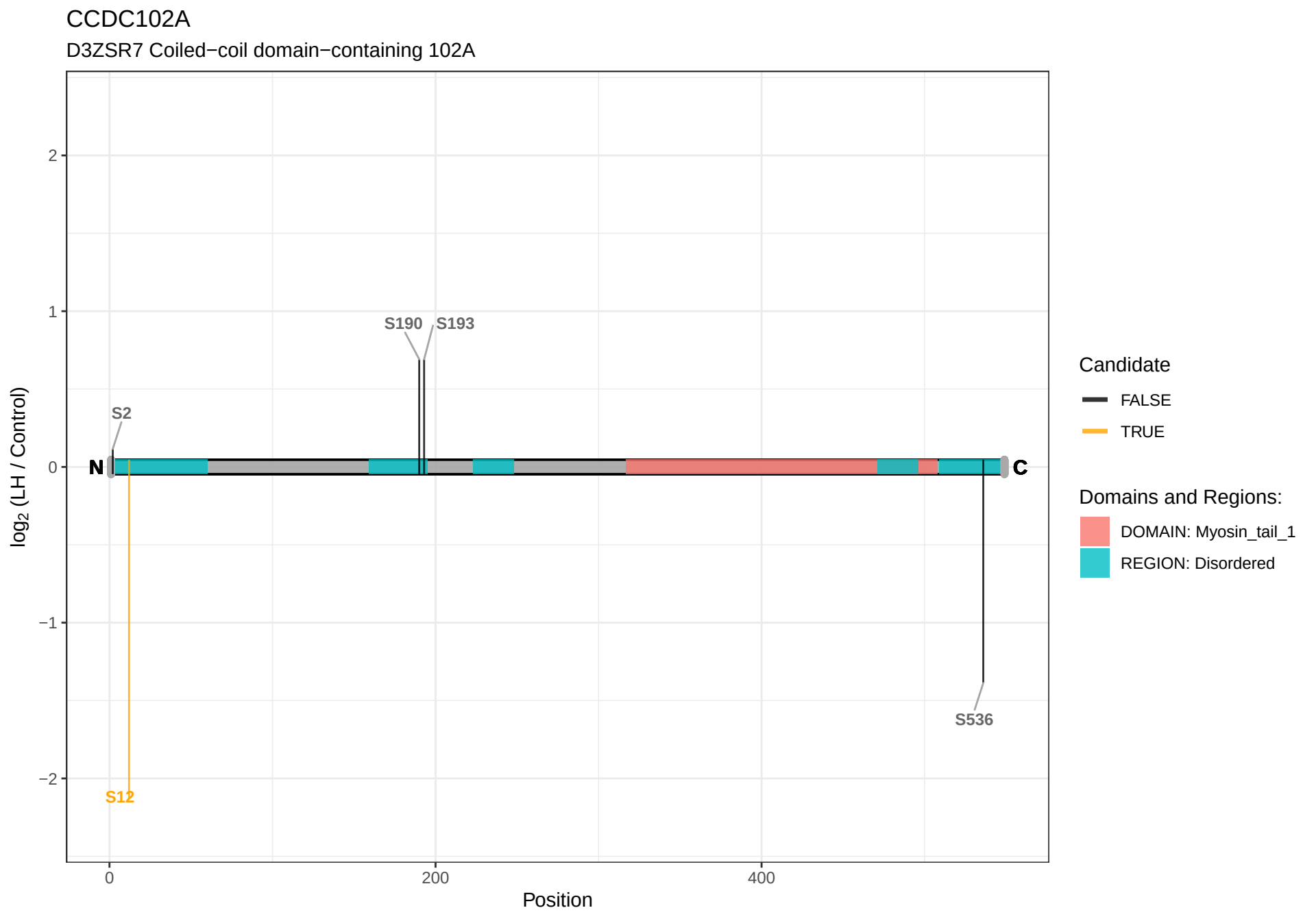

CASP9
Q9JHK1 Caspase 9, isoform CRA_a
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
400
Position
N
C
S348
S350
S341
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CARD
DOMAIN: CASPASE_P10
DOMAIN: CASPASE_P20

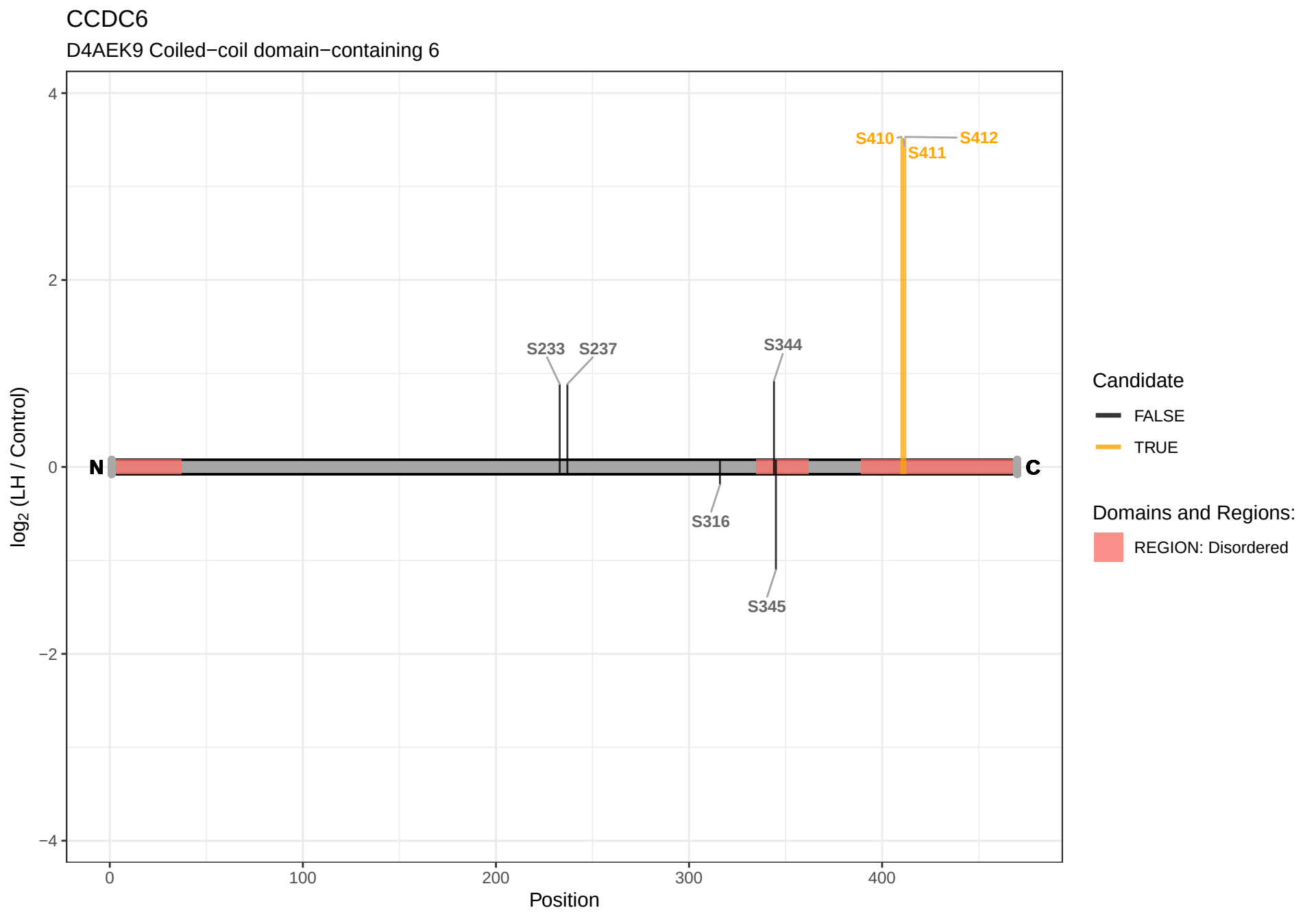

CAST
F1LPH1 Calpastatin
S171
S260
S44
N
C
S57
S122
T173
S580
2
1
0
−1
−2
0
200
400
600
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

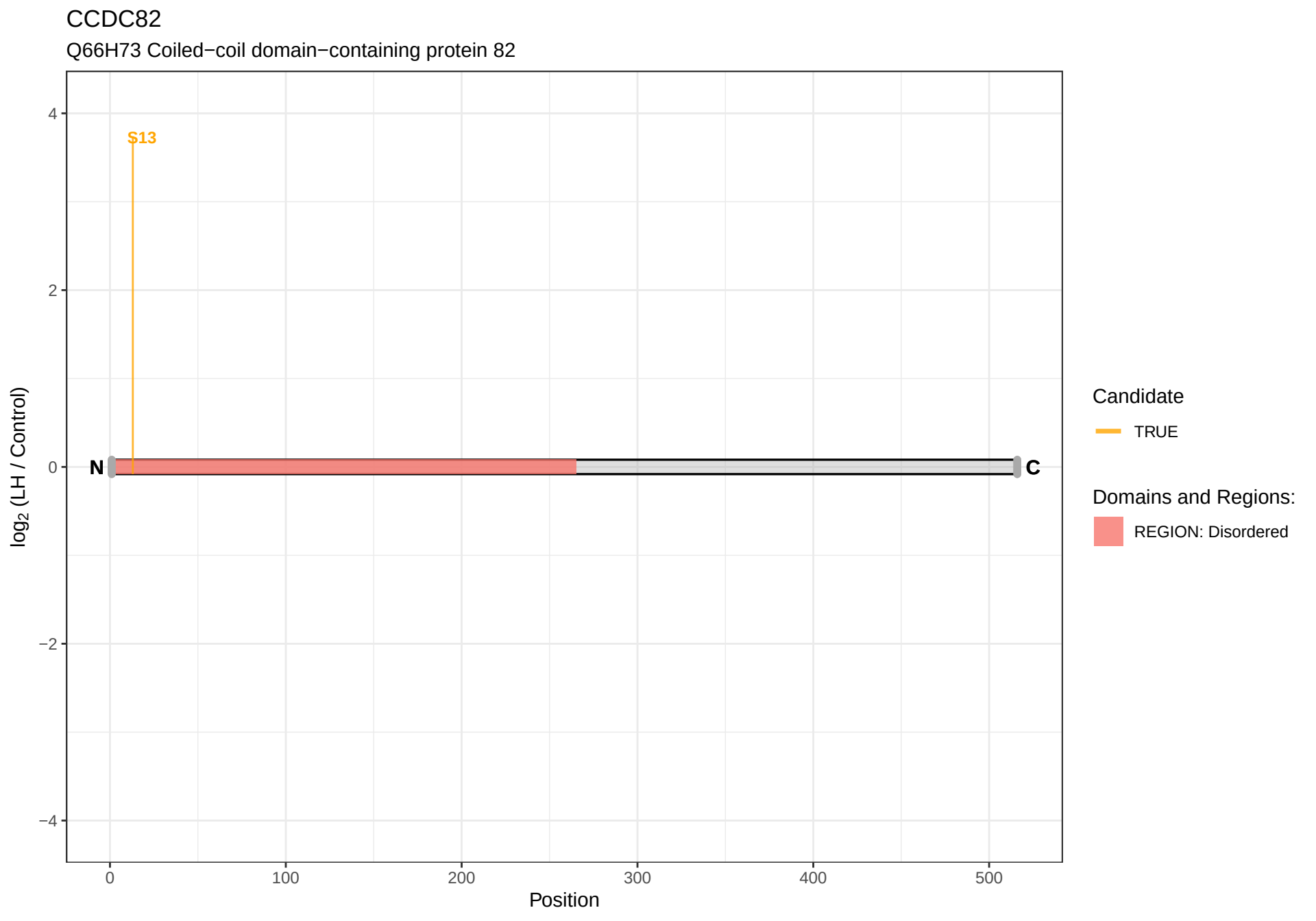

CBLB
G3V689 Casitas B−lineage lymphoma b, isoform CRA_a
log2 (LH / Control)
2
1
0
−1
−2
N
C
S480
S525
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Cbl−PTB
DOMAIN: RING−type
DOMAIN: UBA
REGION: Disordered

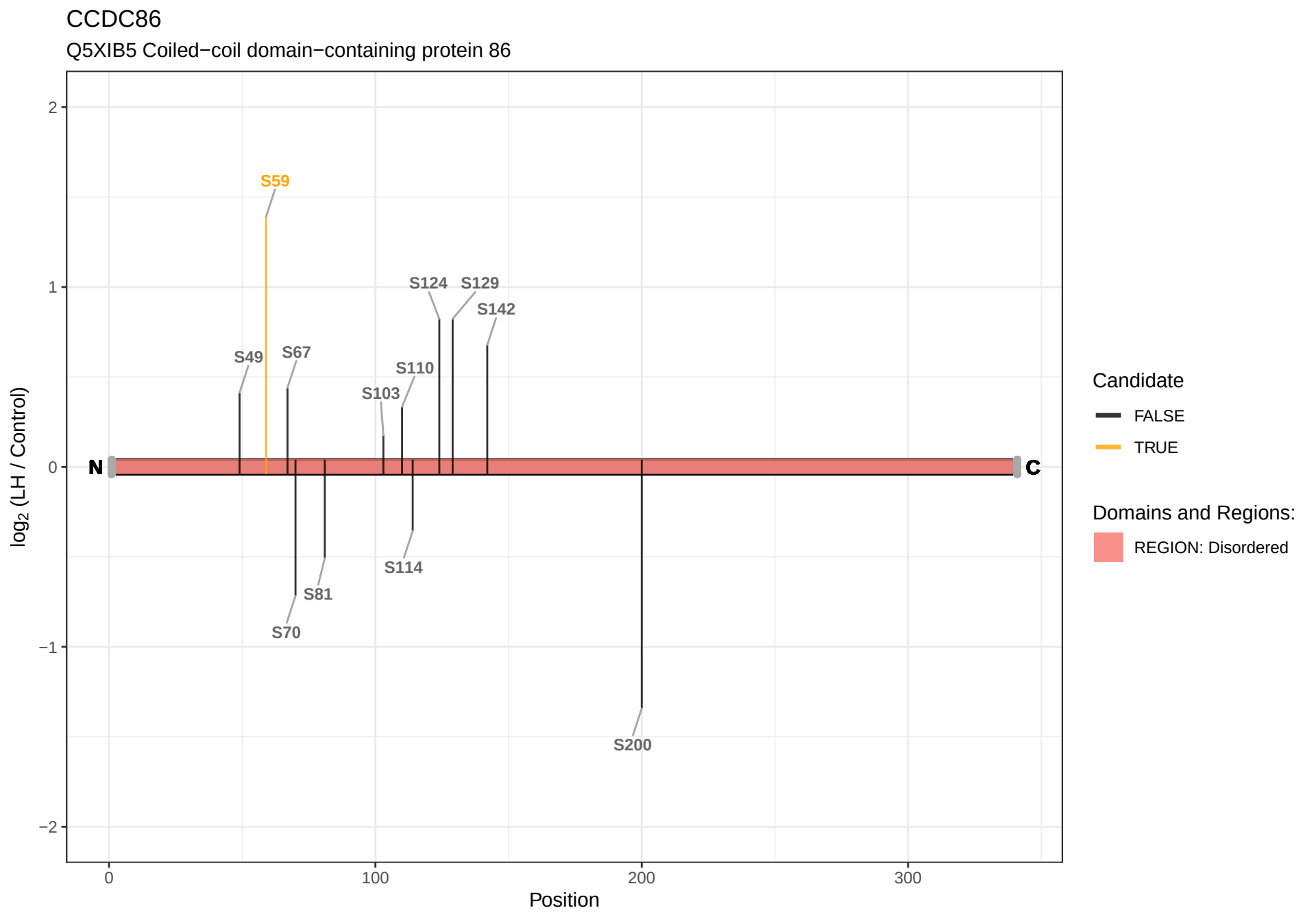

CBX3
Q5RJK5 Chromobox 3
2
1
0
−1
−2
log2 (LH / Control)
S93
N
C
S97
S95
S99
0
50
100
150
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Chromo
REGION: Disordered

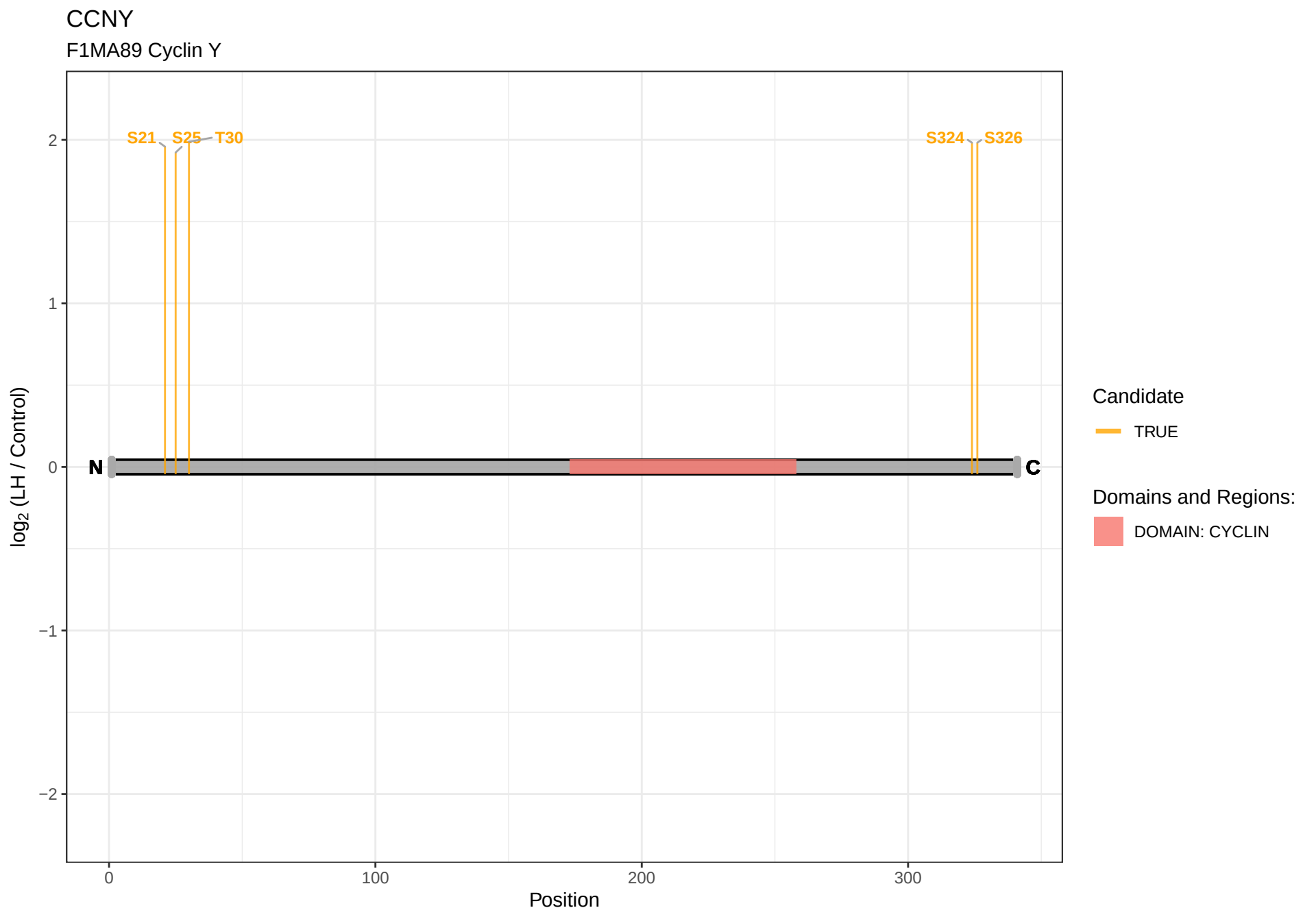

CBX5
B2RYU7 Cbx5 protein
S93
S97
S12
S110
S14
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
50
100
150
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Chromo
REGION: Disordered

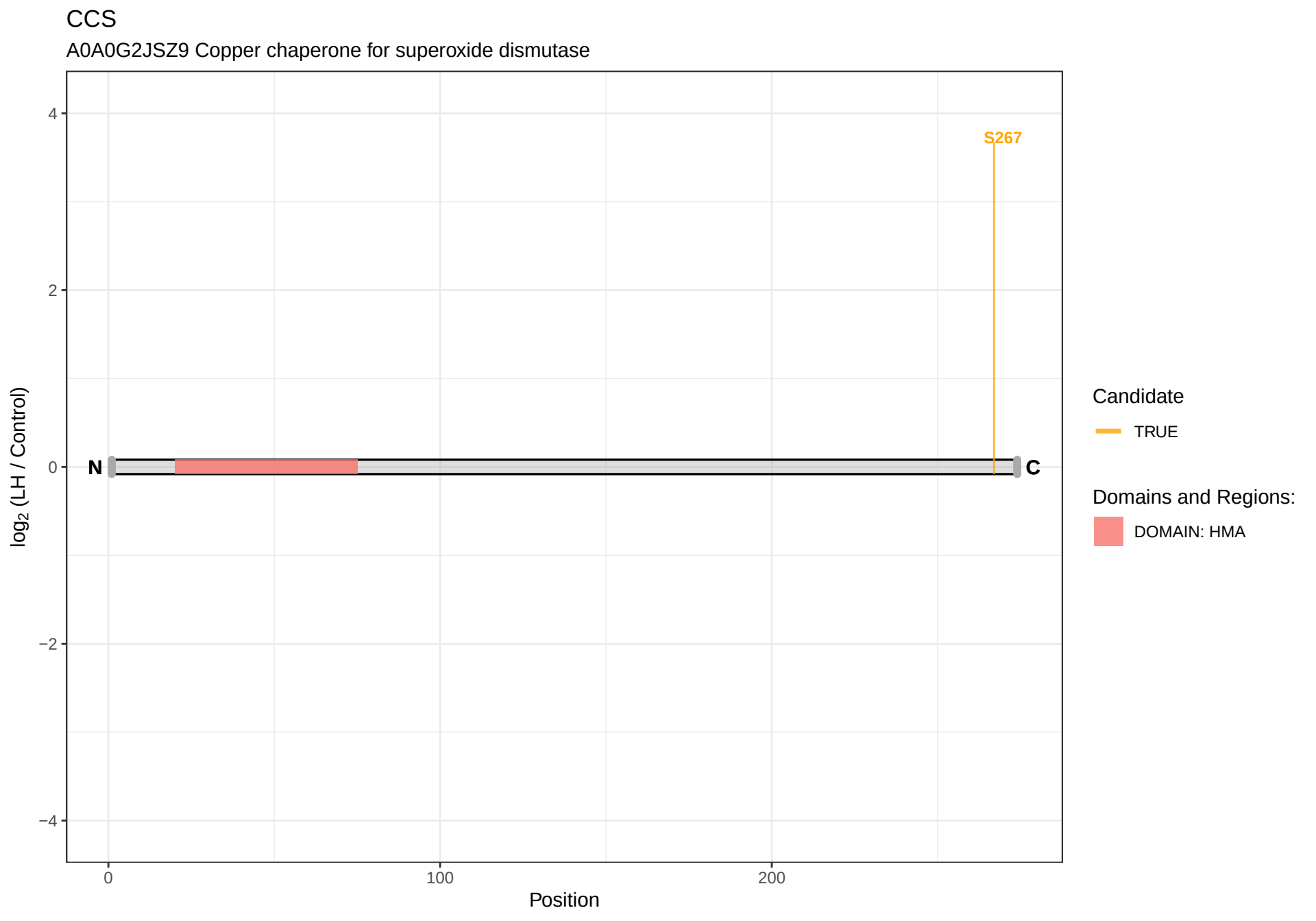

CCDC102A
D3ZSR7 Coiled−coil domain−containing 102A
log2 (LH / Control)
2
1
0
−1
−2
S190
S193
S2
N
C
S12
S536
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Myosin_tail_1
REGION: Disordered

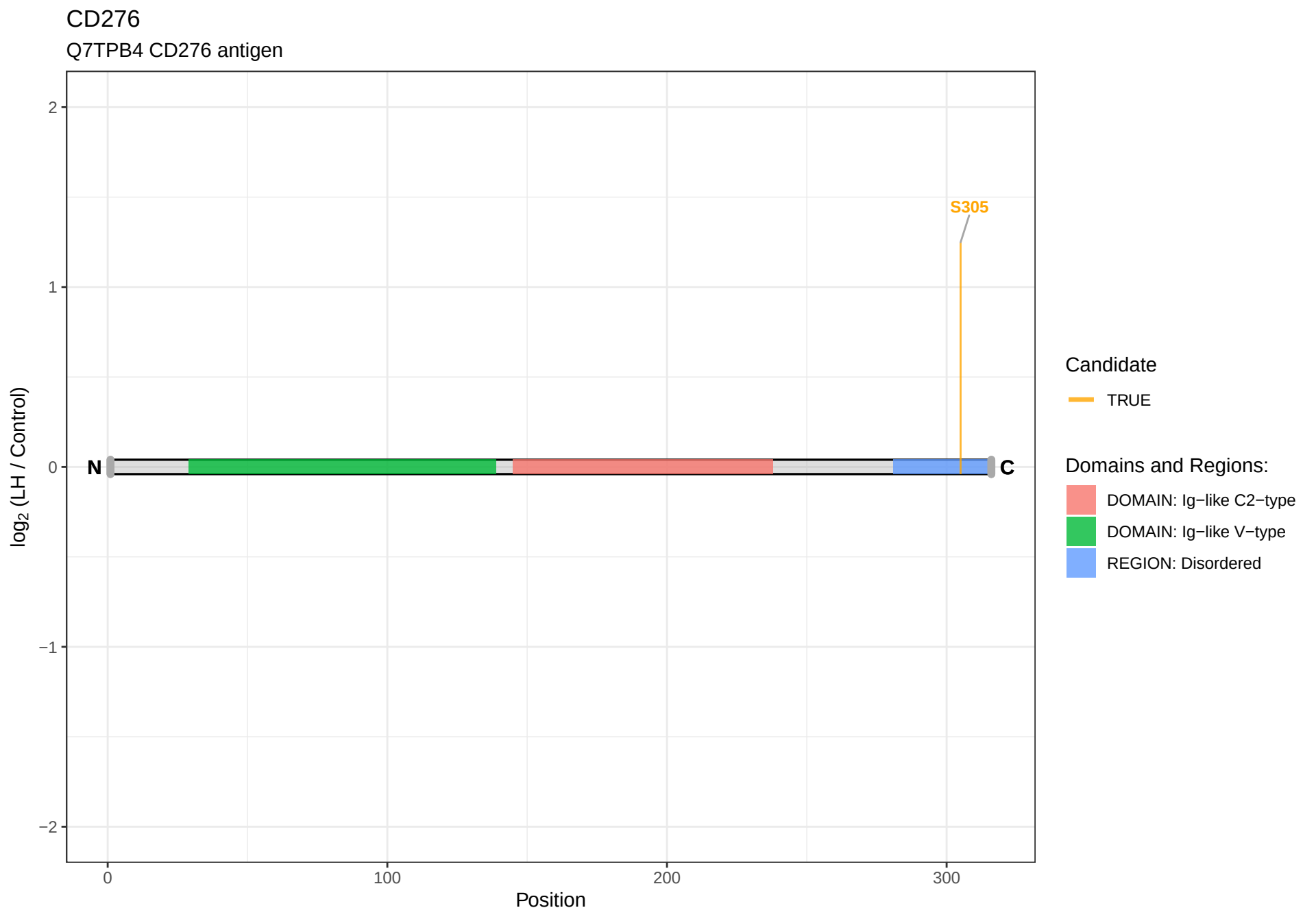

CCDC6
D4AEK9 Coiled−coil domain−containing 6
log2 (LH / Control)
4
2
0
−2
−4
0
100
200
300
400
Position
N
C
S410
S411
S412
S233
S237
S344
S316
S345
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

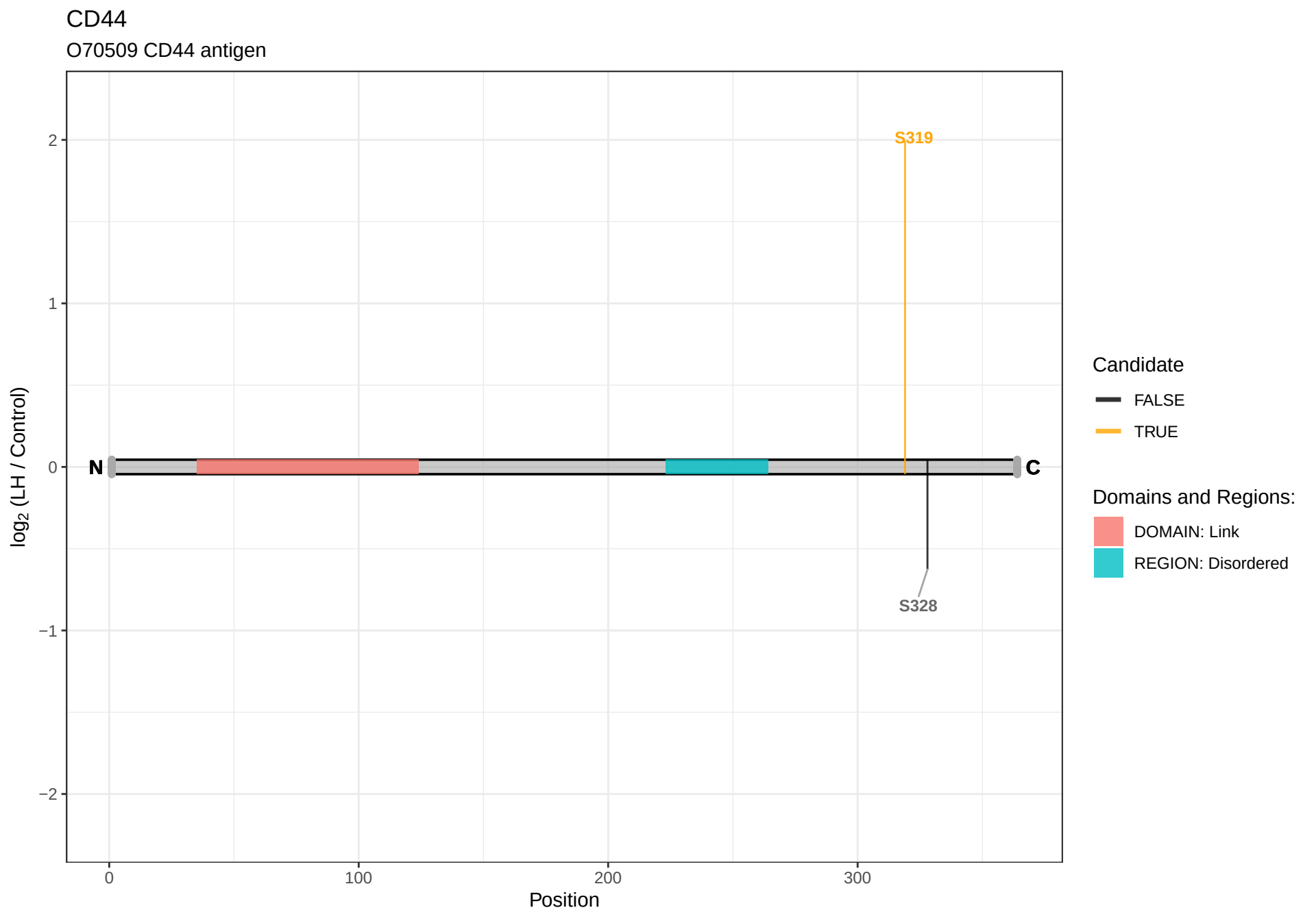

CCDC82
Q66H73 Coiled−coil domain−containing protein 82
S13
N
C
log2 (LH / Control)
4
2
0
−2
−4
0
100
200
300
400
500
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

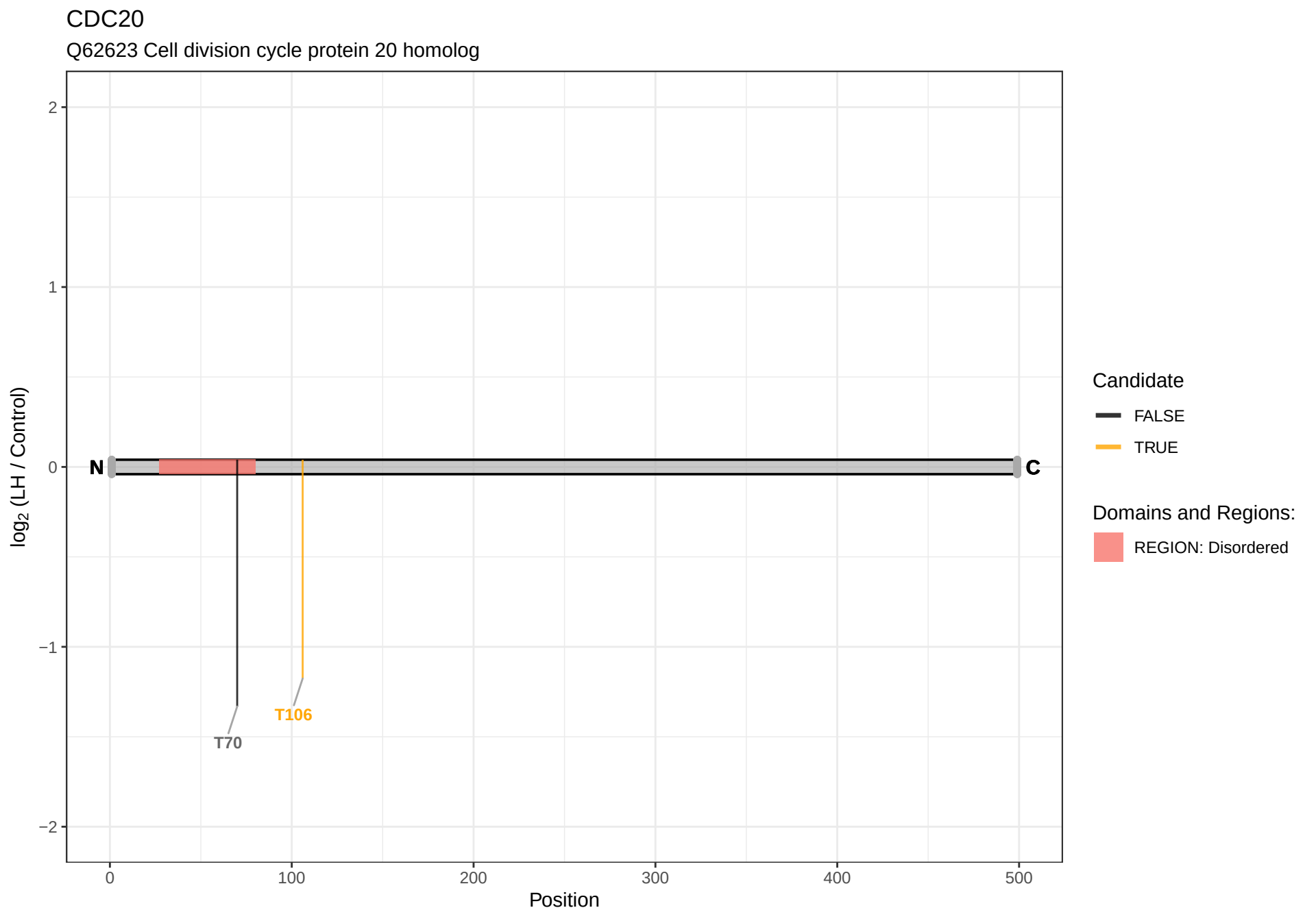

CCDC86
Q5XIB5 Coiled−coil domain−containing protein 86
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
Position
N
C
S59
S124
S129
S142
S49
S67
S110
S103
S114
S81
S70
S200
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

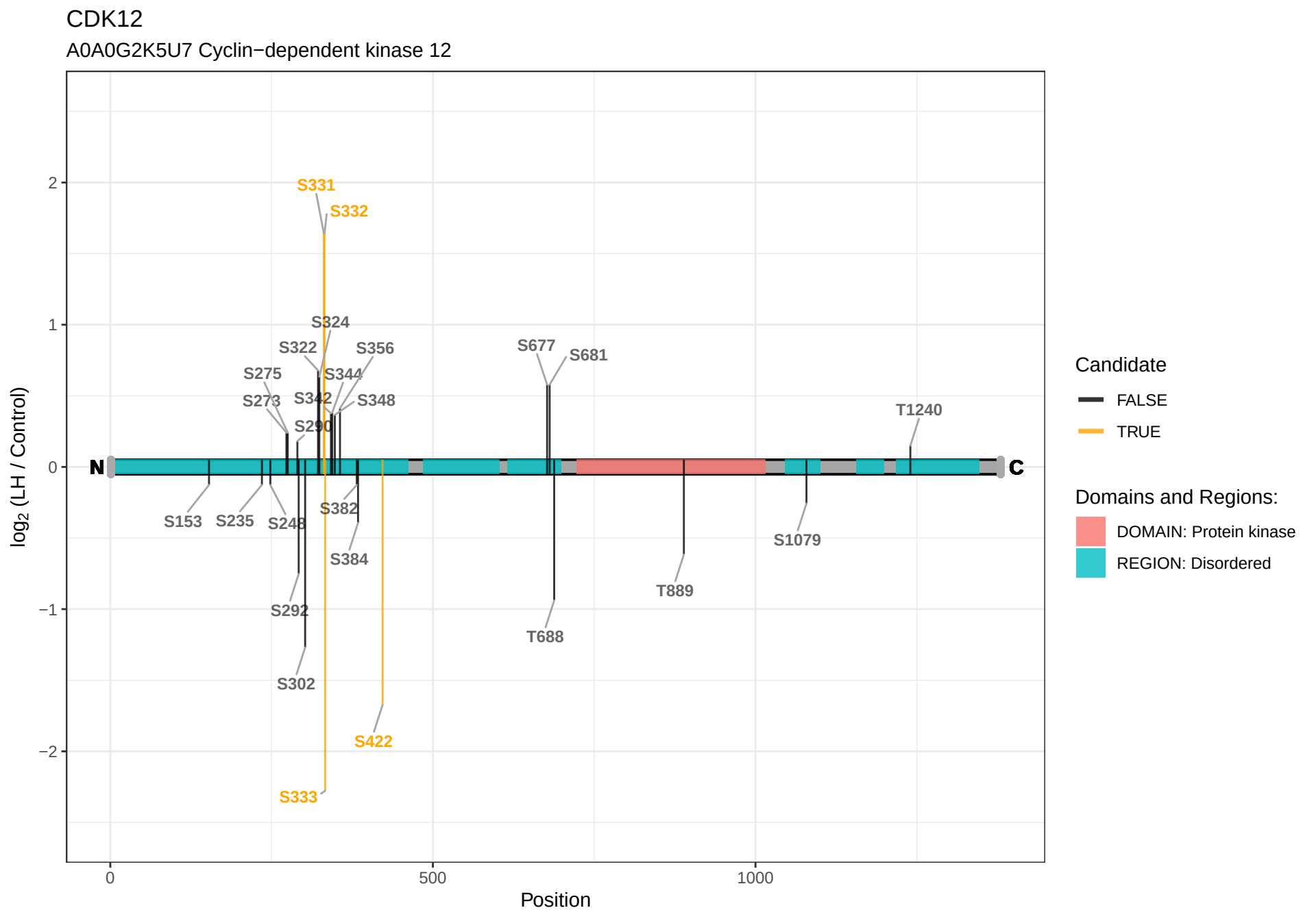

CCNY
F1MA89 Cyclin Y
S21
S25
T30
S324
S326
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: CYCLIN

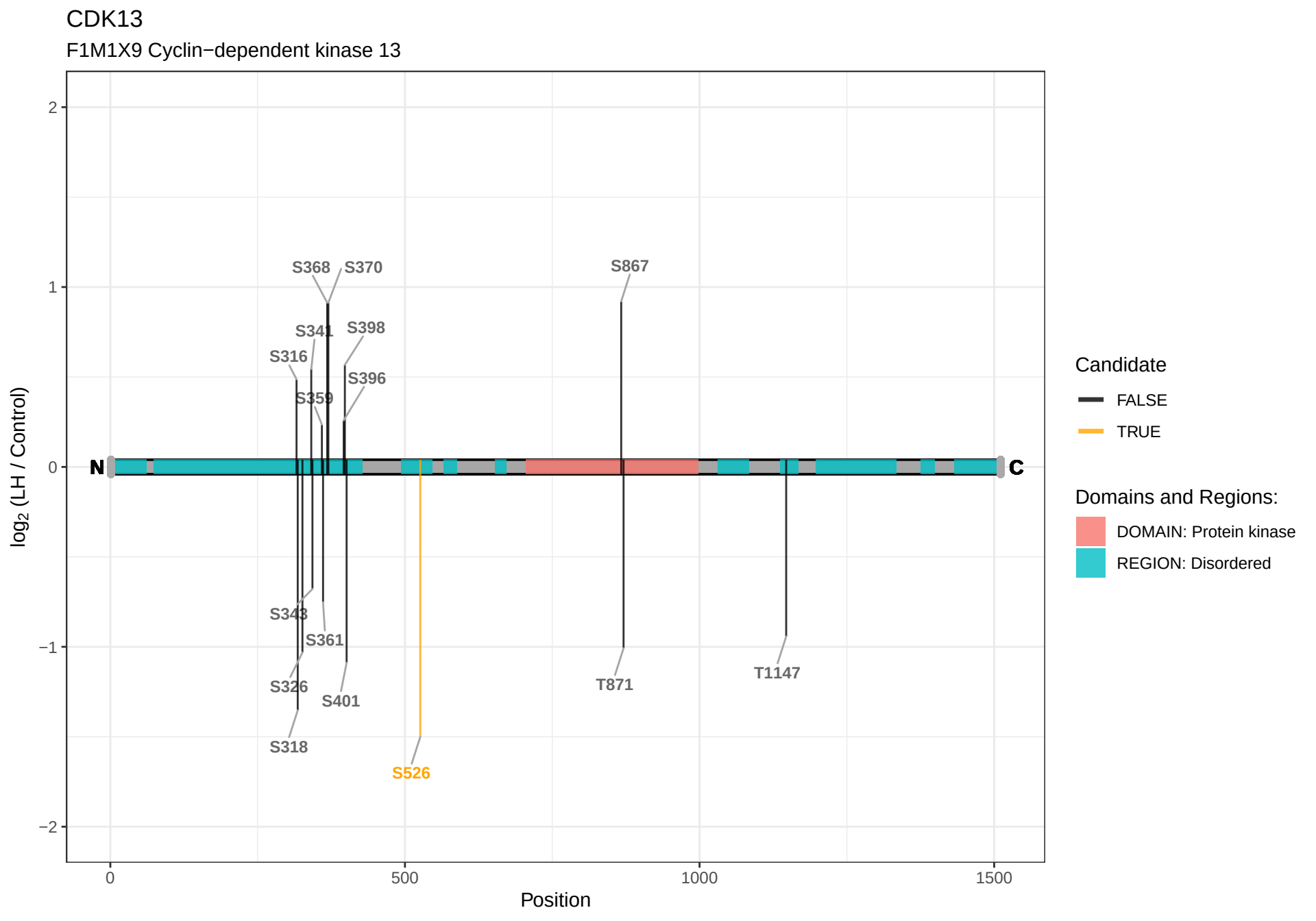

CCS
A0A0G2JSZ9 Copper chaperone for superoxide dismutase
S267
N
C
log2 (LH / Control)
Position
4
2
0
−2
−4
0
100
200
Candidate
TRUE
Domains and Regions:
DOMAIN: HMA

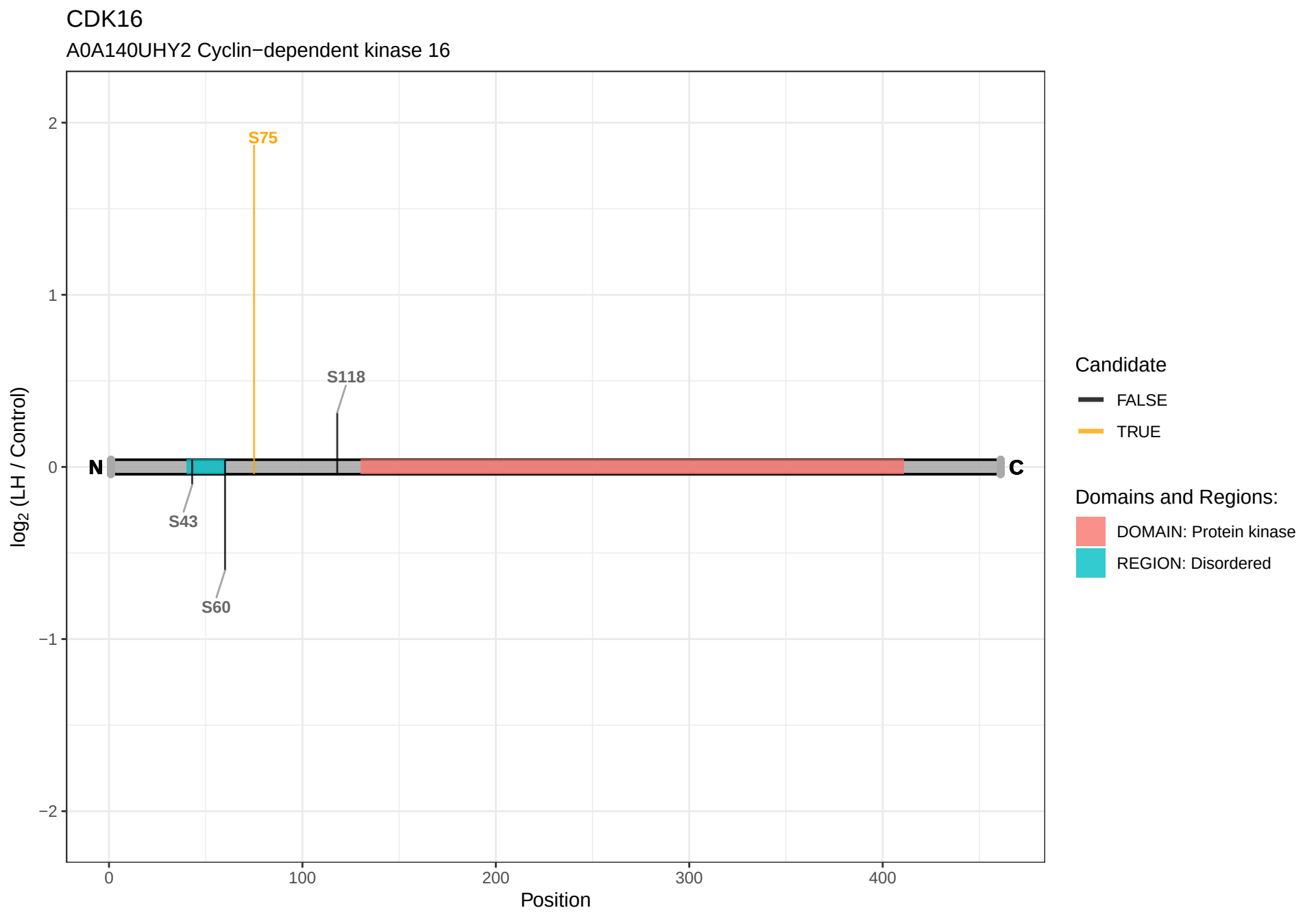

CD276
Q7TPB4 CD276 antigen
log2 (LH / Control)
2
1
0
−1
−2
N
C
S305
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Ig−like C2−type
DOMAIN: Ig−like V−type
REGION: Disordered

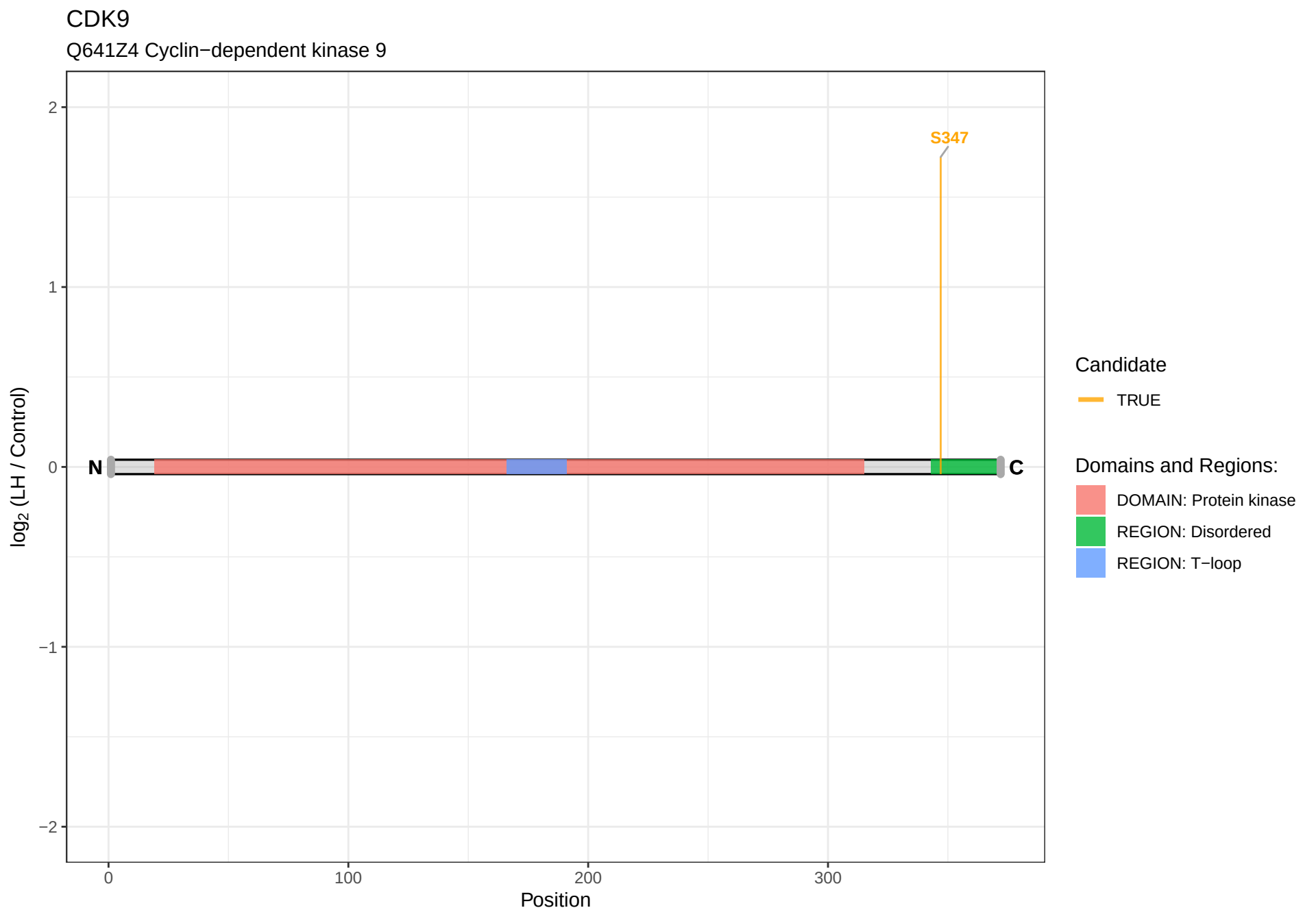

CD44
O70509 CD44 antigen
S319
S328
N
C
2
1
0
−1
−2
0
100
200
300
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Link
REGION: Disordered

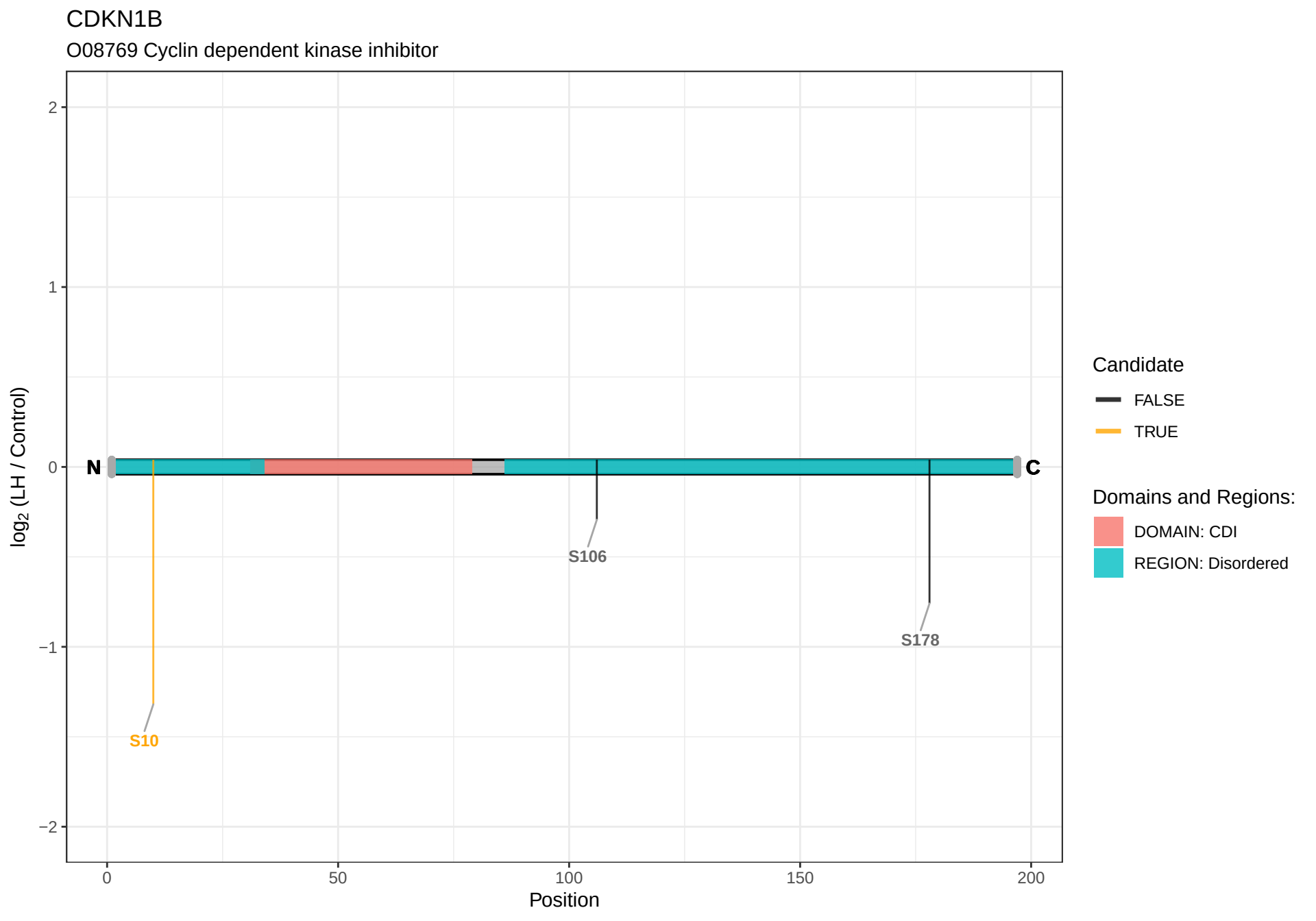

CDC20
Q62623 Cell division cycle protein 20 homolog
log2 (LH / Control)
2
1
0
−1
−2
N
C
T70
T106
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

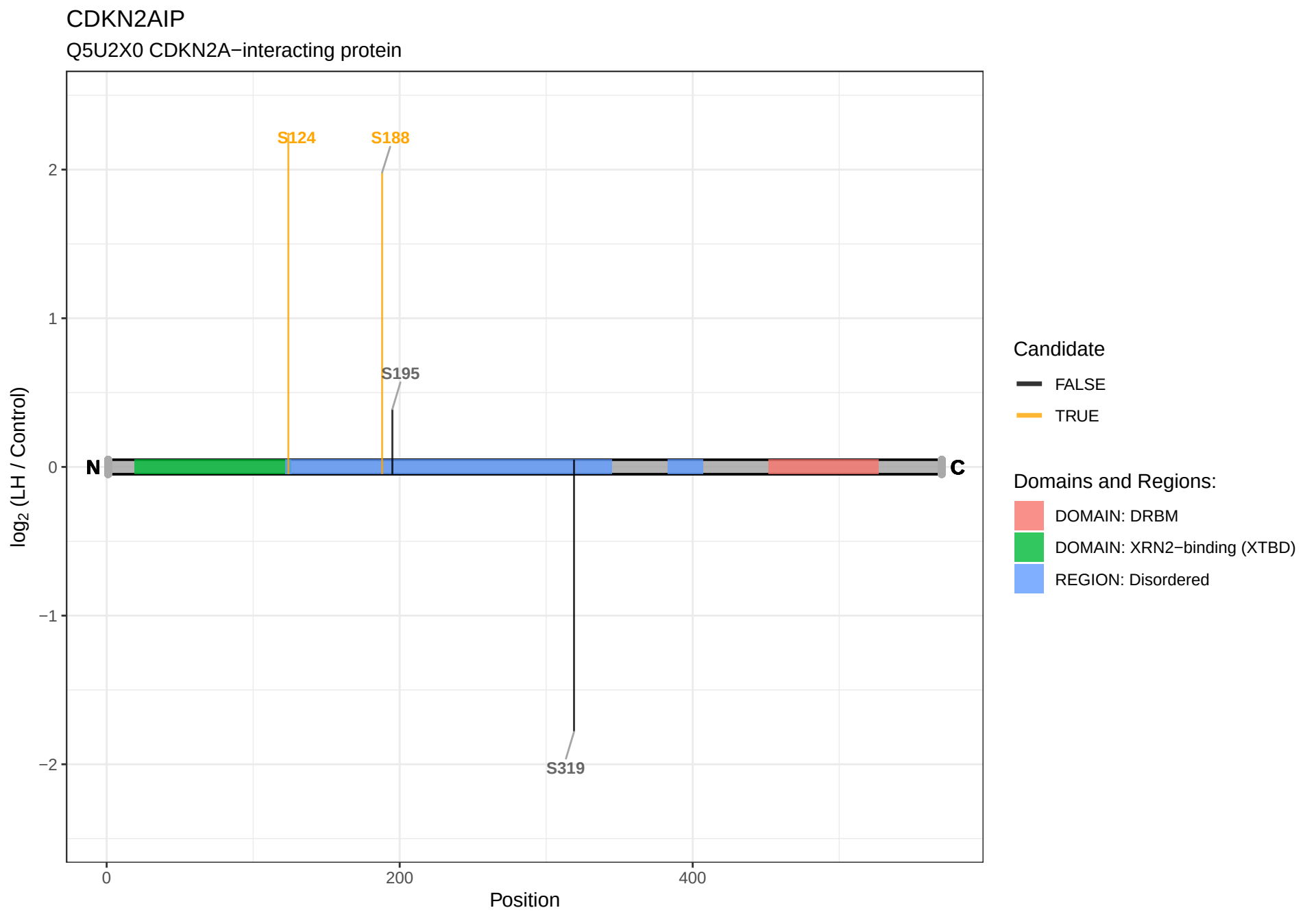

CDK12
A0A0G2K5U7 Cyclin−dependent kinase 12
log2 (LH / Control)
Position
2
1
0
−1
−2
0
500
1000
N
C
S331
S332
S324
S322
S356
S677
S681
S275
S344
S273
S342
S348
S290
T1240
S153
S235
S248
S382
S384
S1079
S292
T889
T688
S302
S422
S333
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered

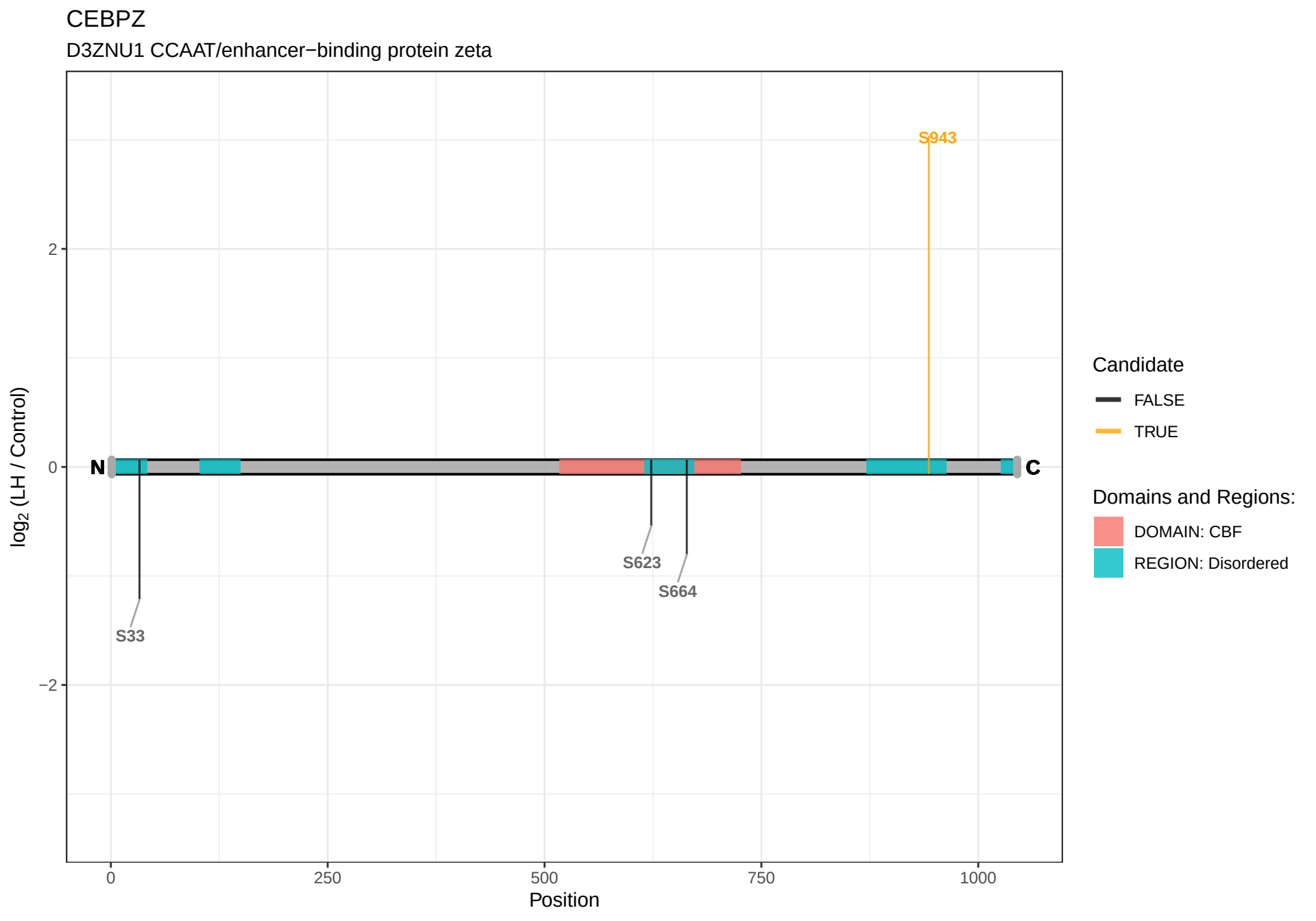

CDK13
F1M1X9 Cyclin−dependent kinase 13
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
Position
N
C
S368
S370
S867
S341
S398
S316
S396
S359
S343
S361
S326
S401
S318
S526
T871
T1147
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered

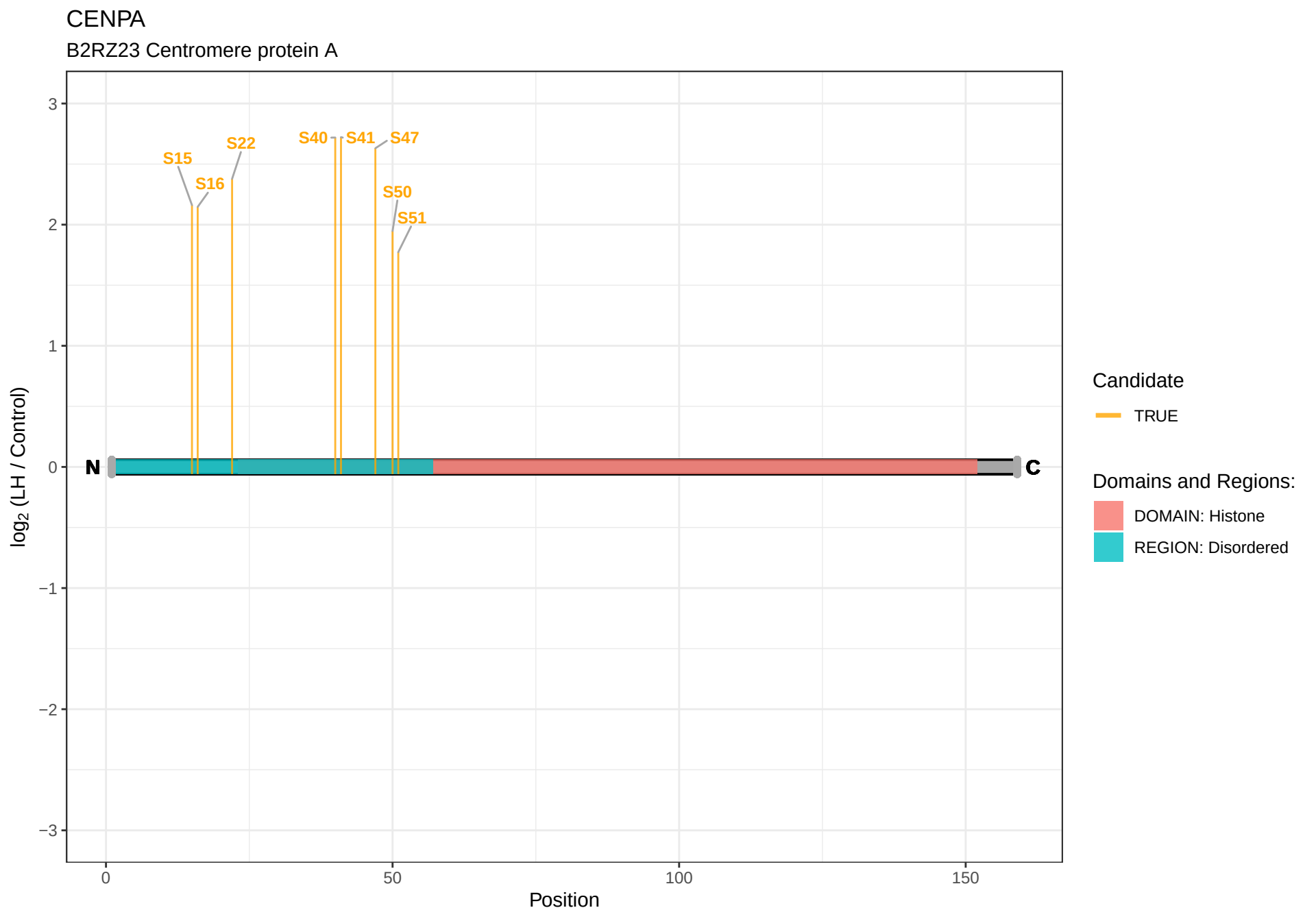

CDK16
A0A140UHY2 Cyclin−dependent kinase 16
S75
S118
S43
S60
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered

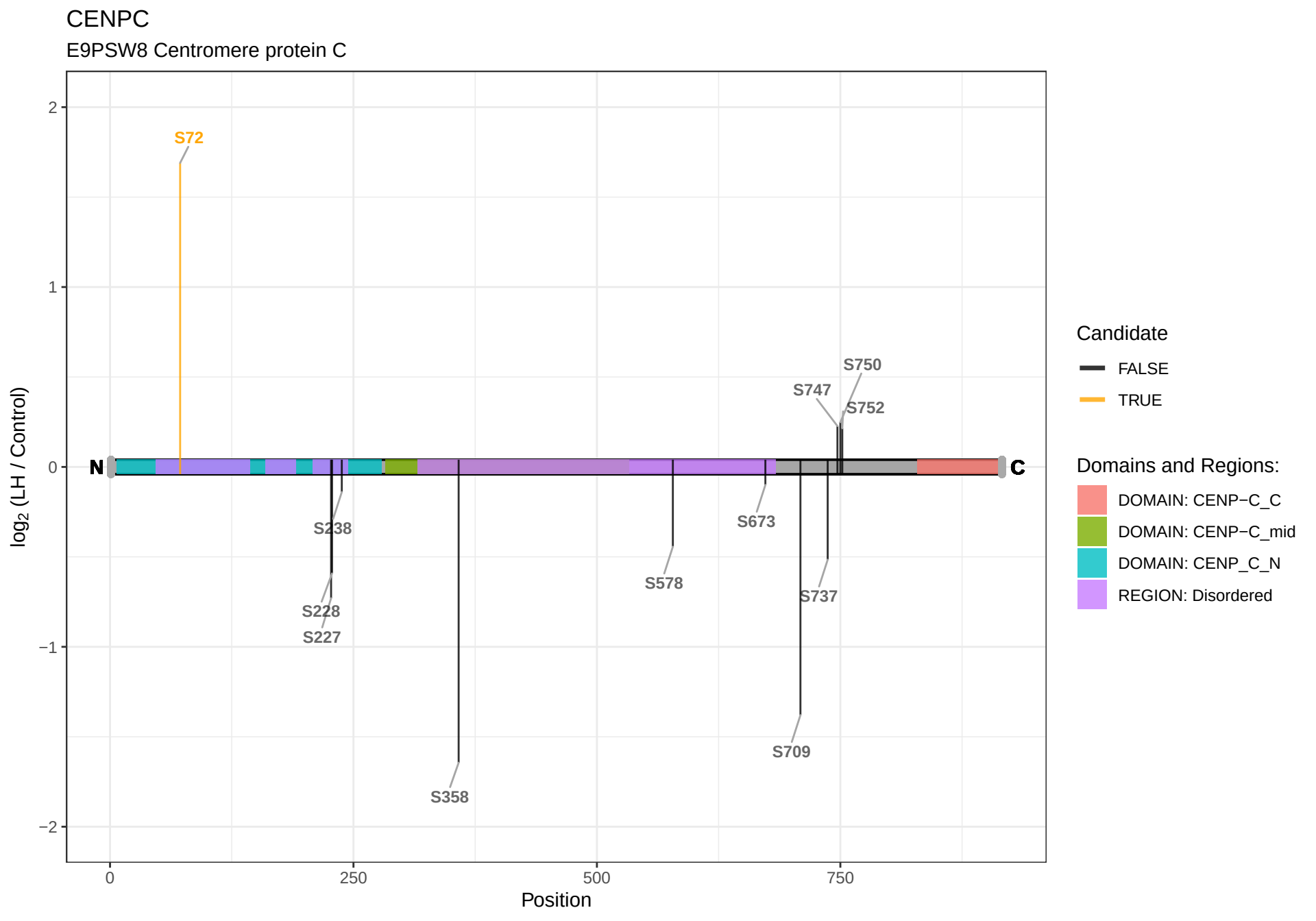

CDK9
Q641Z4 Cyclin−dependent kinase 9
S347
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered
REGION: T−loop

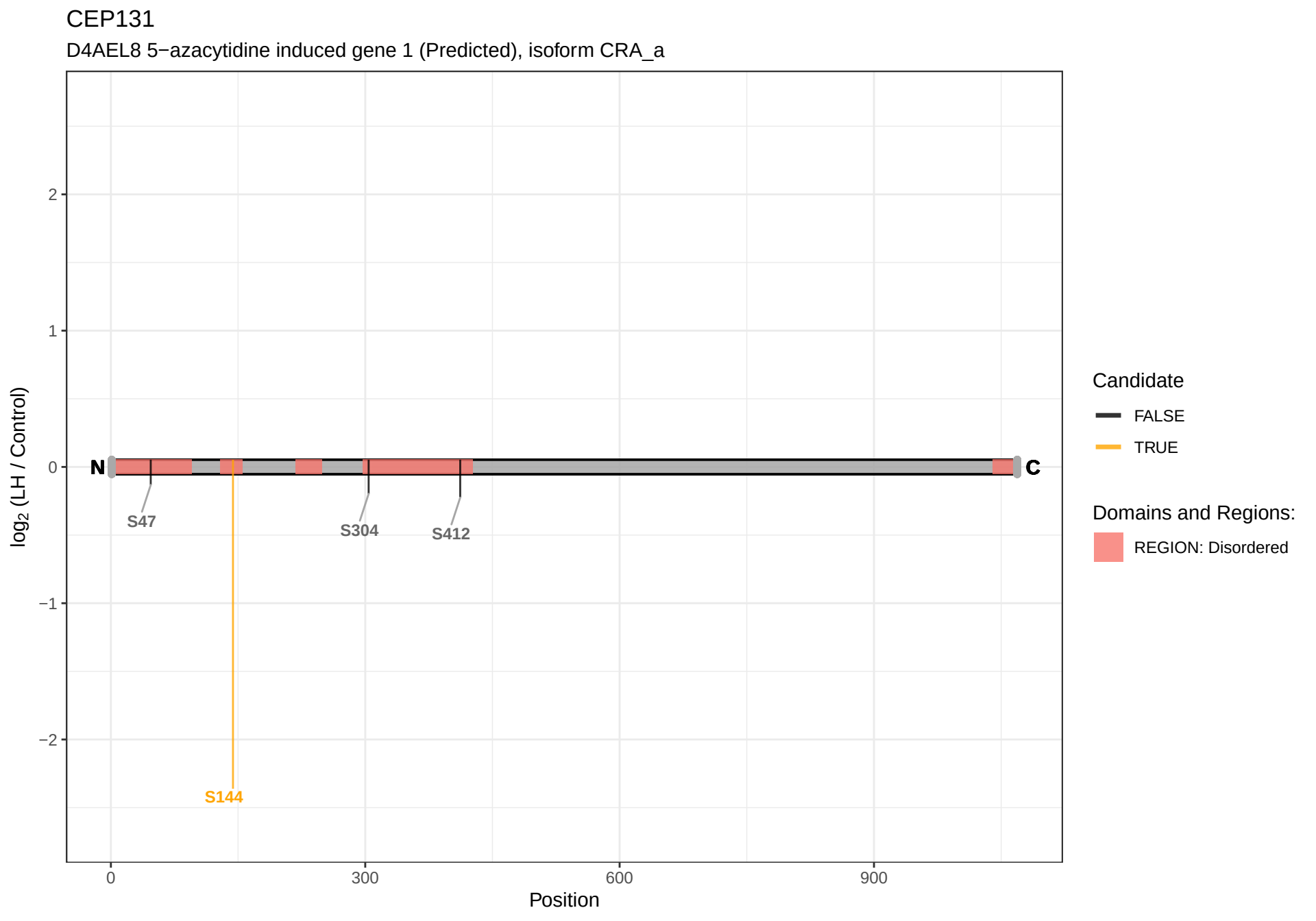

CDKN1B
O08769 Cyclin dependent kinase inhibitor
log2 (LH / Control)
2
1
0
−1
−2
N
C
S10
S106
S178
0
50
100
150
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CDI
REGION: Disordered

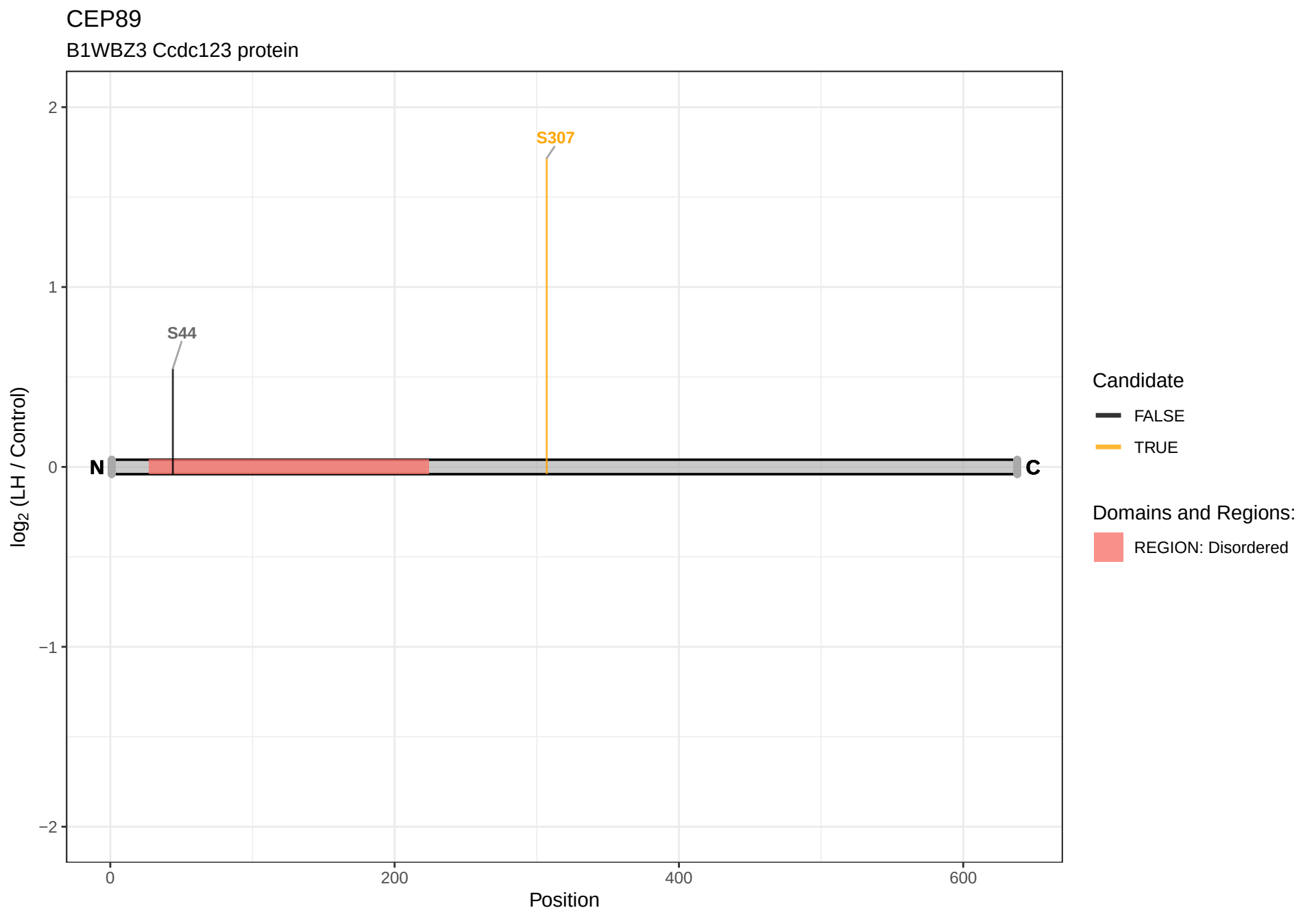

CDKN2AIP
Q5U2X0 CDKN2A−interacting protein
S124
S188
S195
S319
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DRBM
DOMAIN: XRN2−binding (XTBD)
REGION: Disordered

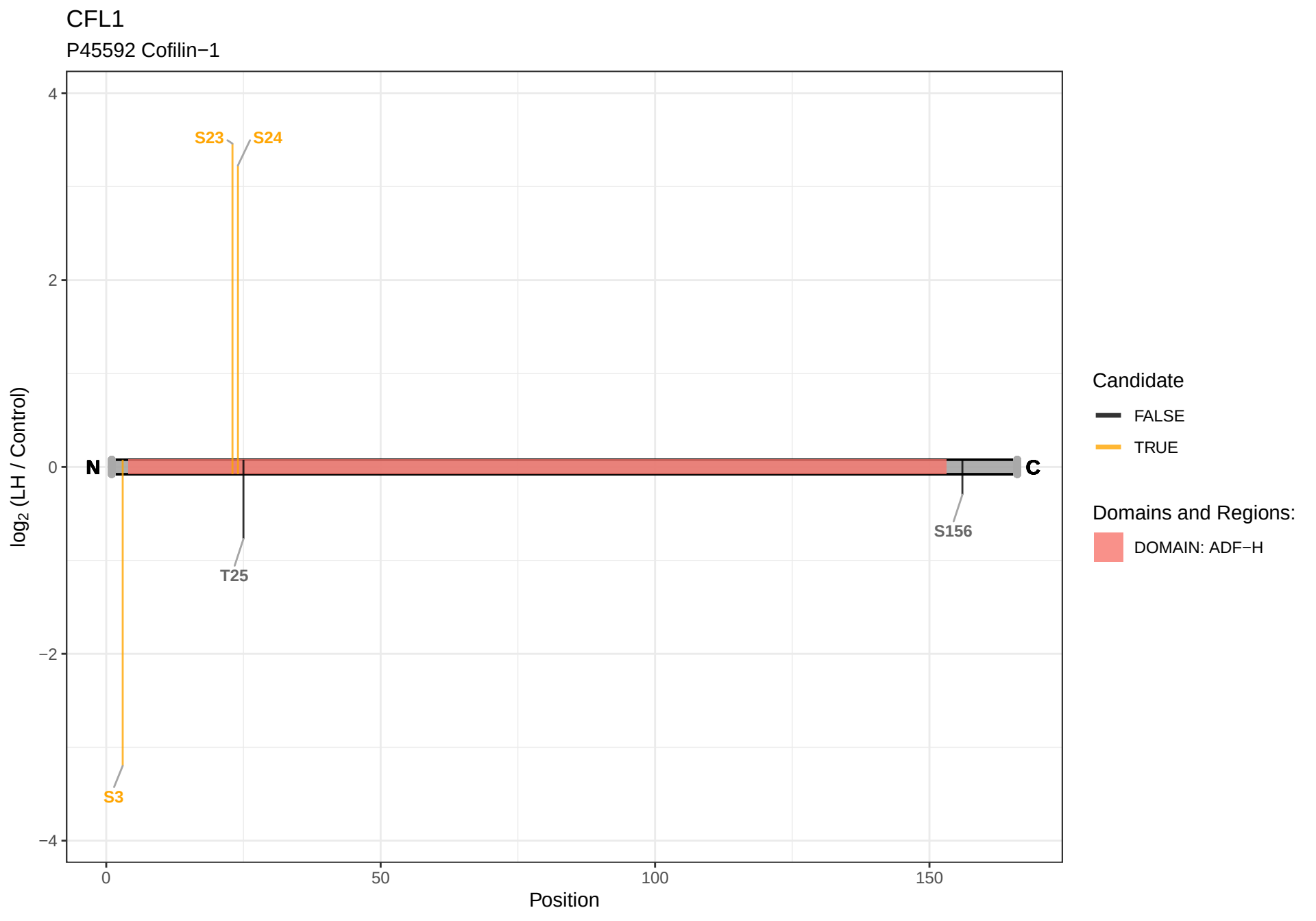

CEBPZ
D3ZNU1 CCAAT/enhancer−binding protein zeta
log2 (LH / Control)
2
0
−2
N
C
S943
S623
S664
S33
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CBF
REGION: Disordered

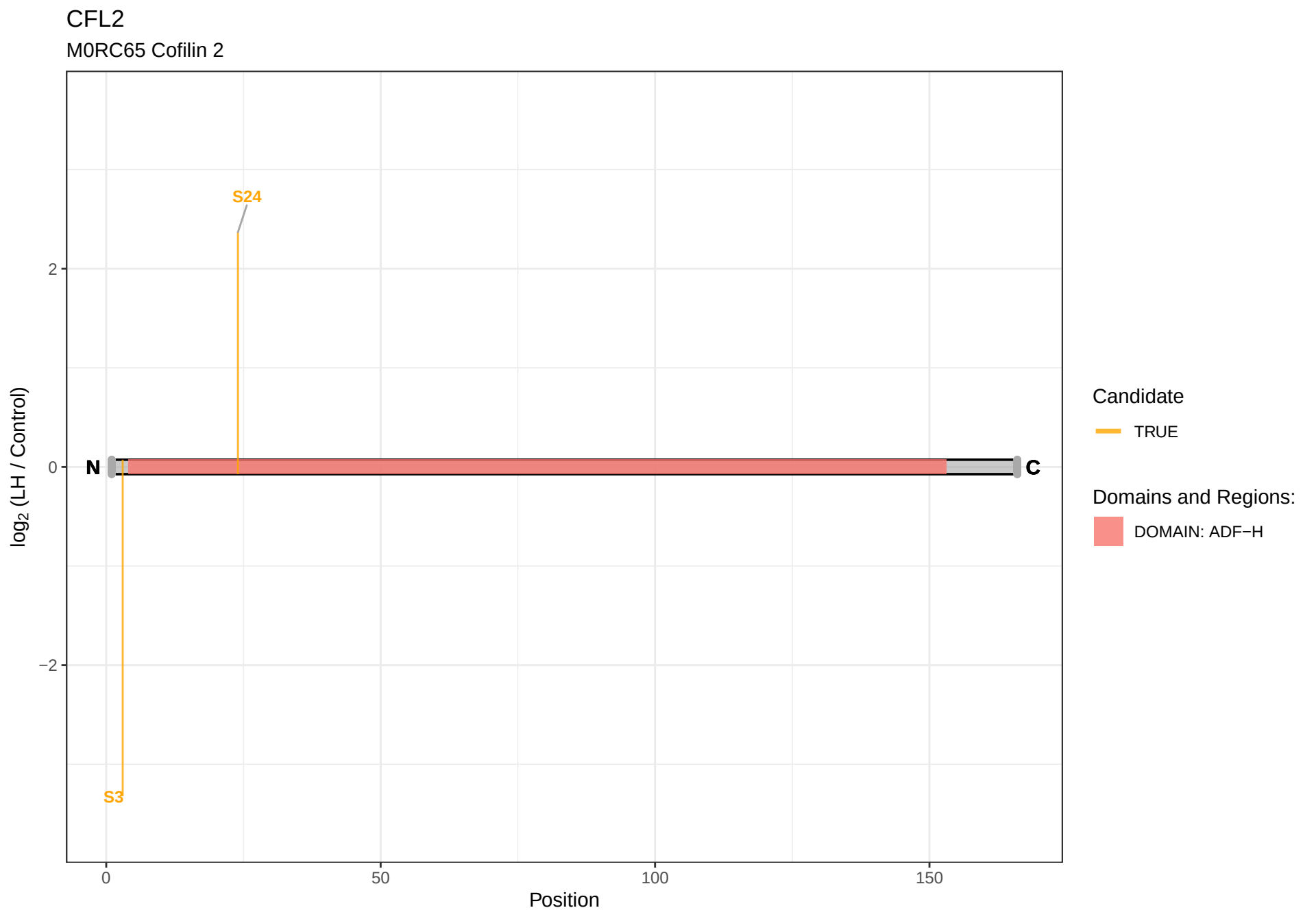

CENPA
B2RZ23 Centromere protein A
S15
S16
S22
S40
S41
S47
S50
S51
N
C
log2 (LH / Control)
Position
0
50
100
150
3
2
1
0
−1
−2
−3
Candidate
TRUE
Domains and Regions:
DOMAIN: Histone
REGION: Disordered

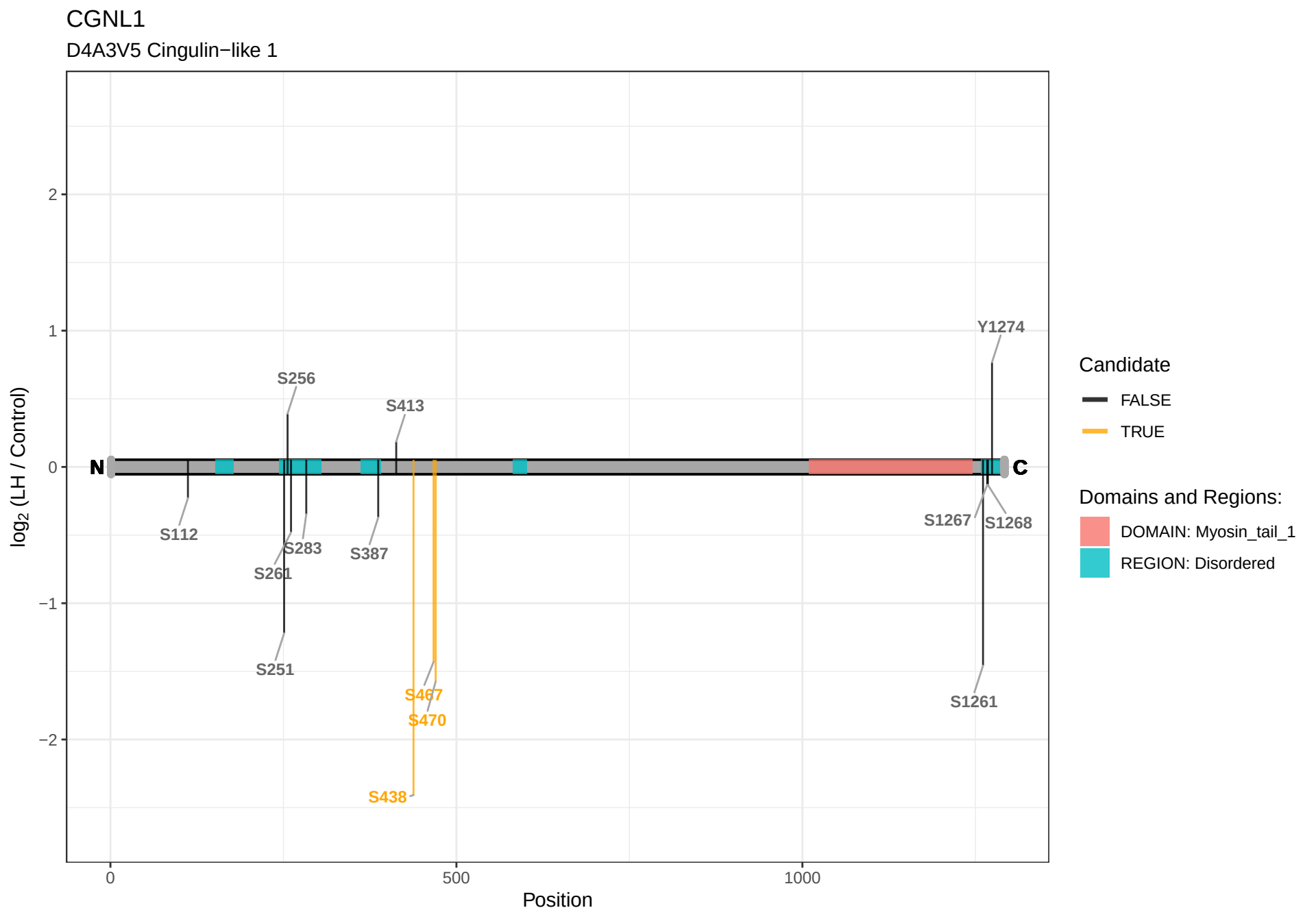

CENPC
E9PSW8 Centromere protein C
log2 (LH / Control)
Position
N
C
S72
S238
S228
S227
S358
S578
S673
S747
S750
S752
S737
S709
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CENP−C_C
DOMAIN: CENP−C_mid
DOMAIN: CENP_C_N
REGION: Disordered

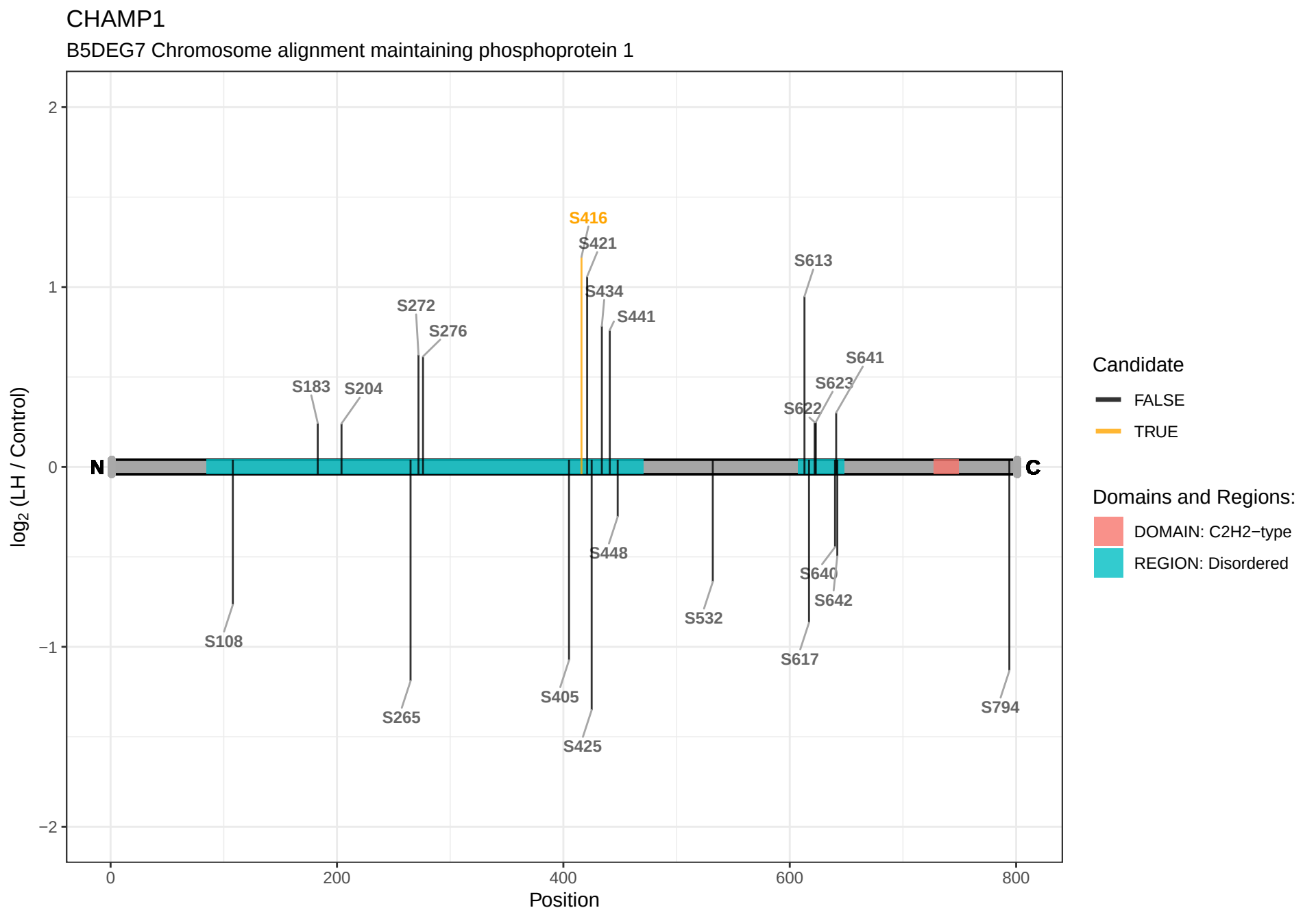

CEP131
D4AEL8 5−azacytidine induced gene 1 (Predicted), isoform CRA_a
log2 (LH / Control)
2
1
0
−1
−2
N
C
S47
S144
S304
S412
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

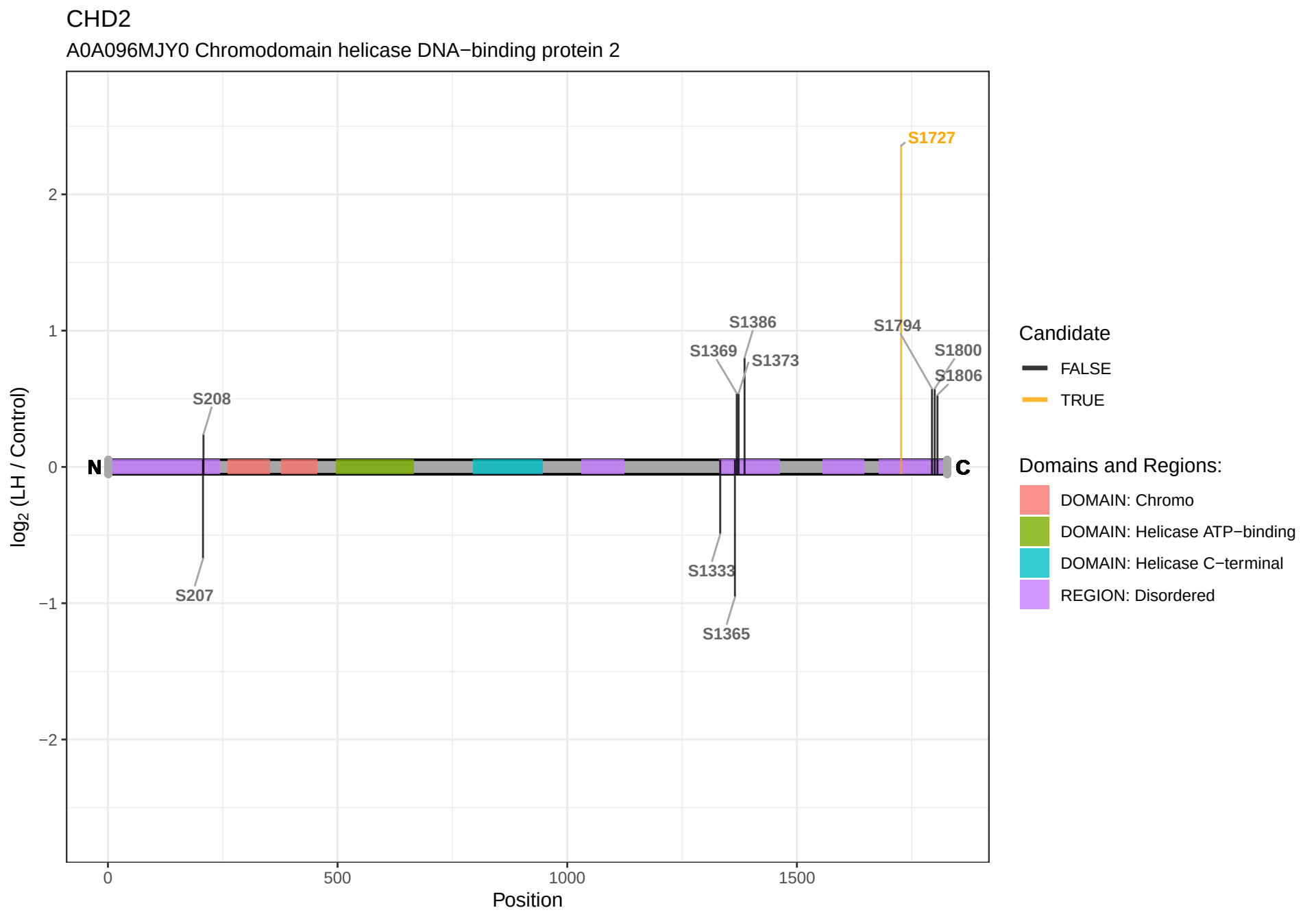

CEP89
B1WBZ3 Ccdc123 protein
S307
S44
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

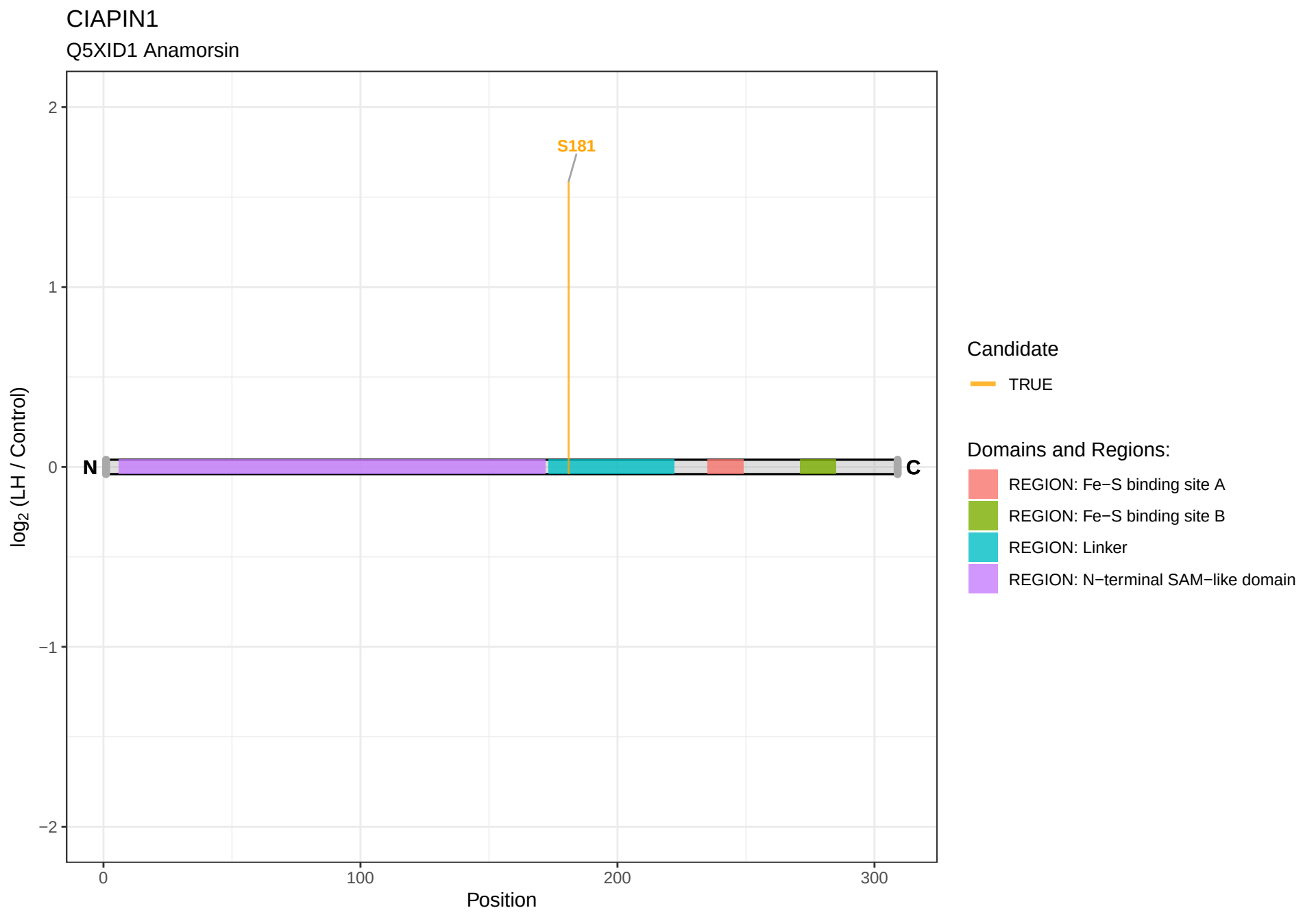

CFL1
P45592 Cofilin−1
4
2
0
−2
−4
log2 (LH / Control)
S23
S24
N
C
T25
S156
S3
0
50
100
150
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ADF−H

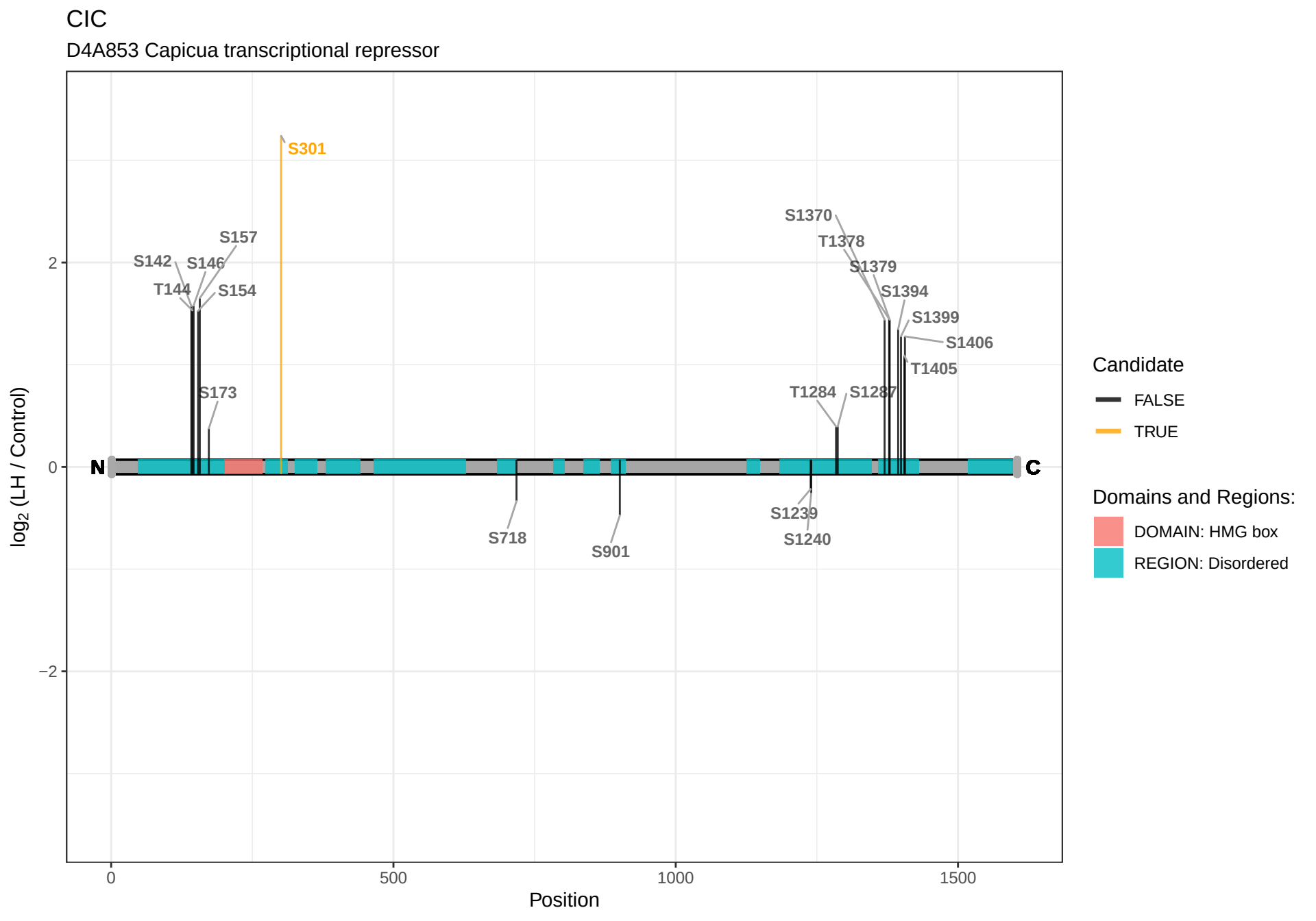

CFL2
M0RC65 Cofilin 2
S24
S3
N
C
2
0
−2
log2 (LH / Control)
0
50
100
150
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: ADF−H

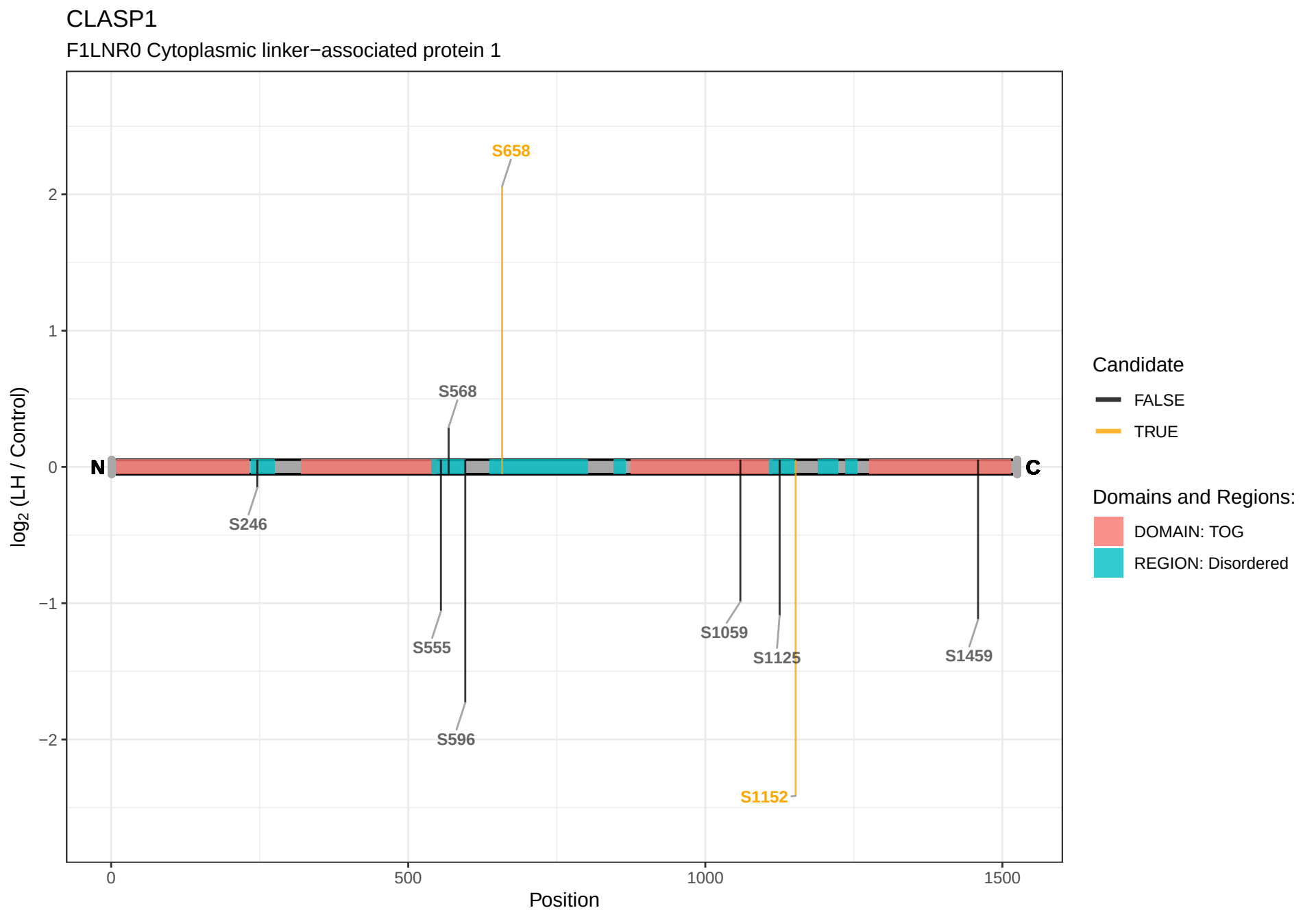

CGNL1
D4A3V5 Cingulin−like 1
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
Position
N
C
S112
S256
S261
S283
S387
S413
S251
S467
S470
S438
Y1274
S1267
S1268
S1261
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Myosin_tail_1
REGION: Disordered

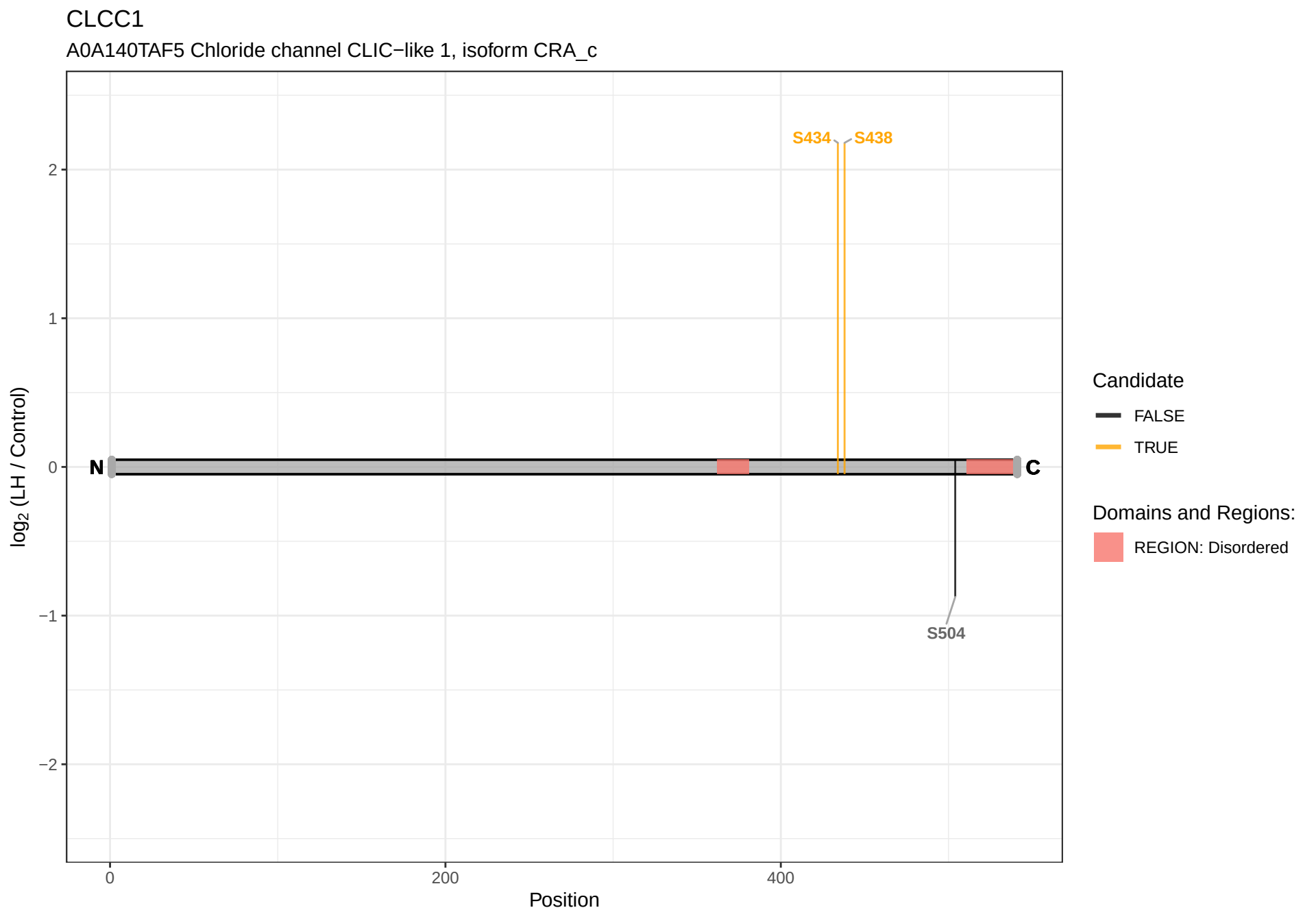

CHAMP1
B5DEG7 Chromosome alignment maintaining phosphoprotein 1
log2 (LH / Control)
Position
N
C
S416
S421
S434
S441
S272
S276
S183
S204
S613
S641
S623
S622
S448
S640
S642
S532
S108
S617
S405
S265
S425
S794
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2H2−type
REGION: Disordered

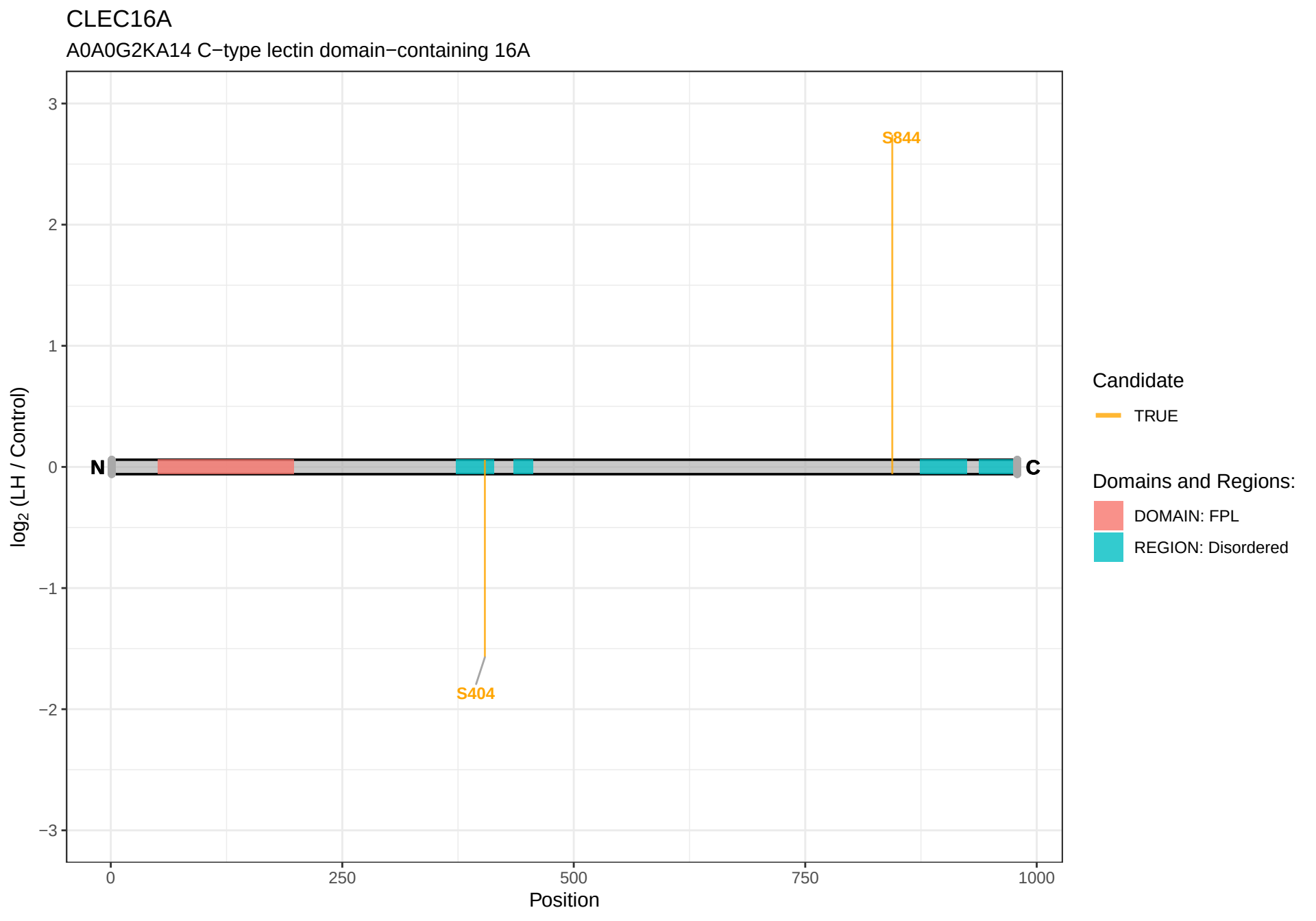

CHD2
A0A096MJY0 Chromodomain helicase DNA−binding protein 2
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
Position
N
C
S1727
S1386
S1794
S1369
S1373
S1800
S1806
S208
S207
S1333
S1365
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Chromo
DOMAIN: Helicase ATP−binding
DOMAIN: Helicase C−terminal
REGION: Disordered

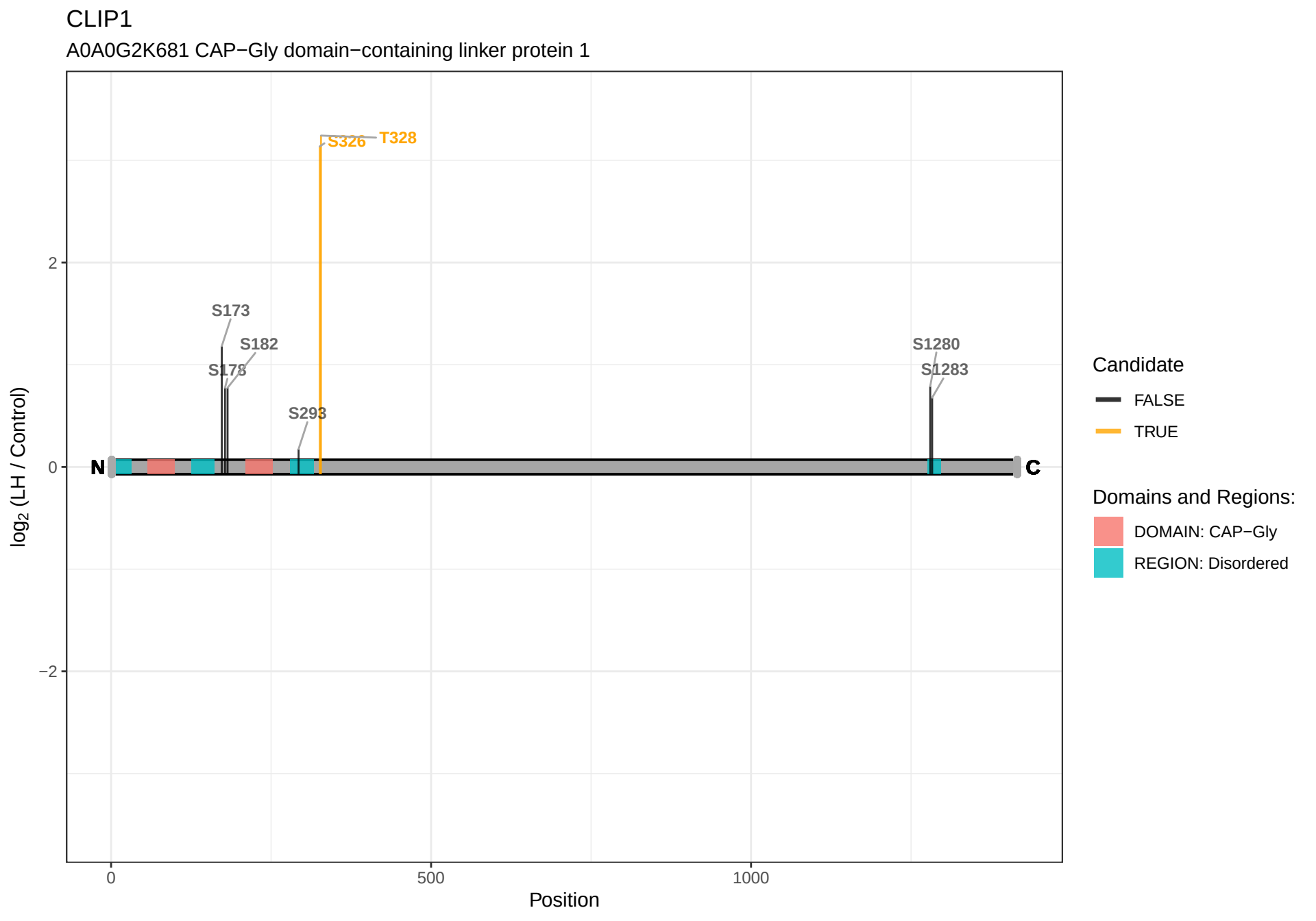

CIAPIN1
Q5XID1 Anamorsin
S181
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
100
200
300
Candidate
TRUE
Domains and Regions:
REGION: Fe−S binding site A
REGION: Fe−S binding site B
REGION: Linker
REGION: N−terminal SAM−like domain

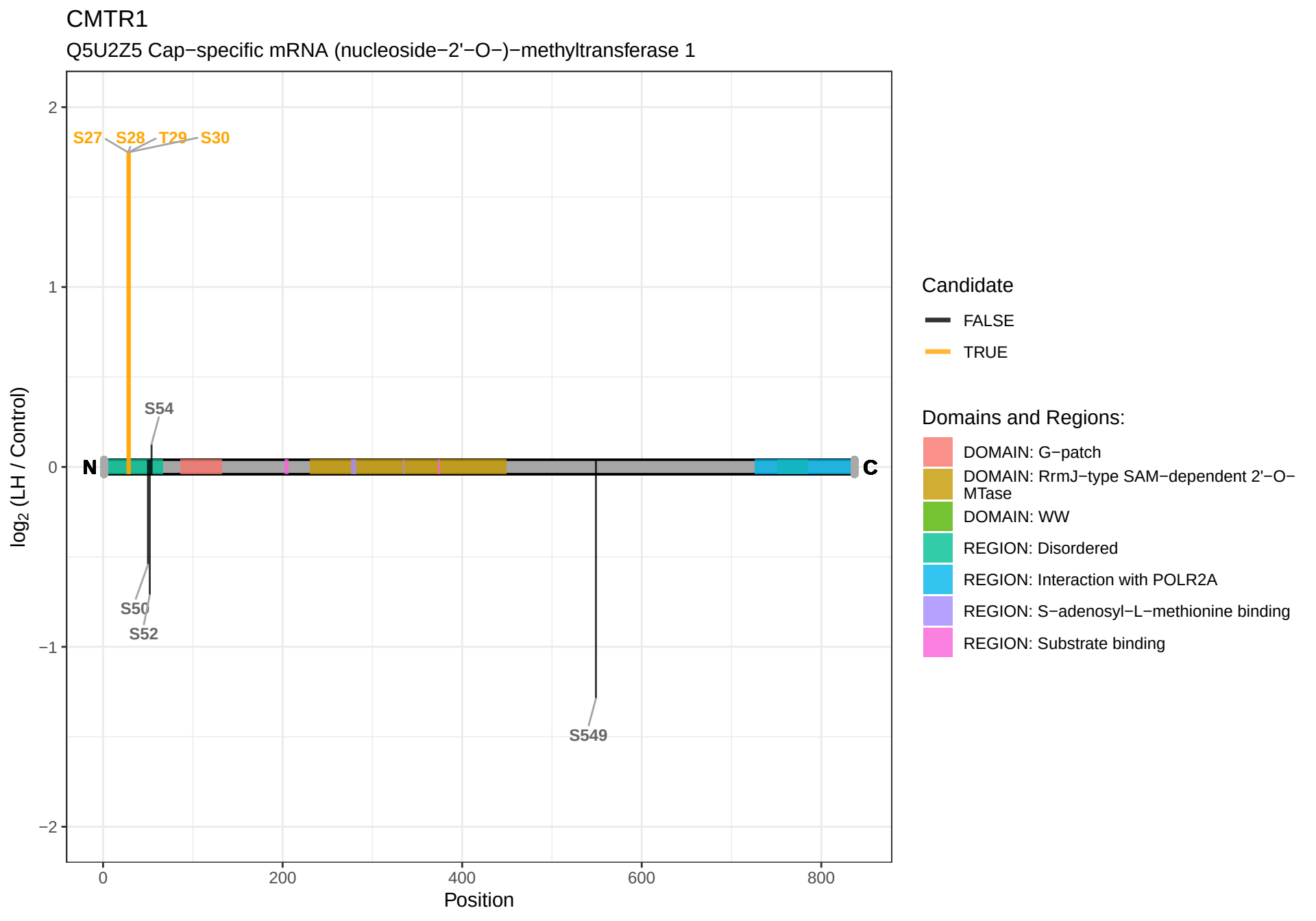

CIC
D4A853 Capicua transcriptional repressor
S301
S157
S142
S146
T144
S154
S173
S1370
T1378
S1379
S1394
S1399
S1406
T1405
T1284
S1287
S718
S901
S1239
S1240
N
C
2
0
−2
log2 (LH / Control)
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: HMG box
REGION: Disordered

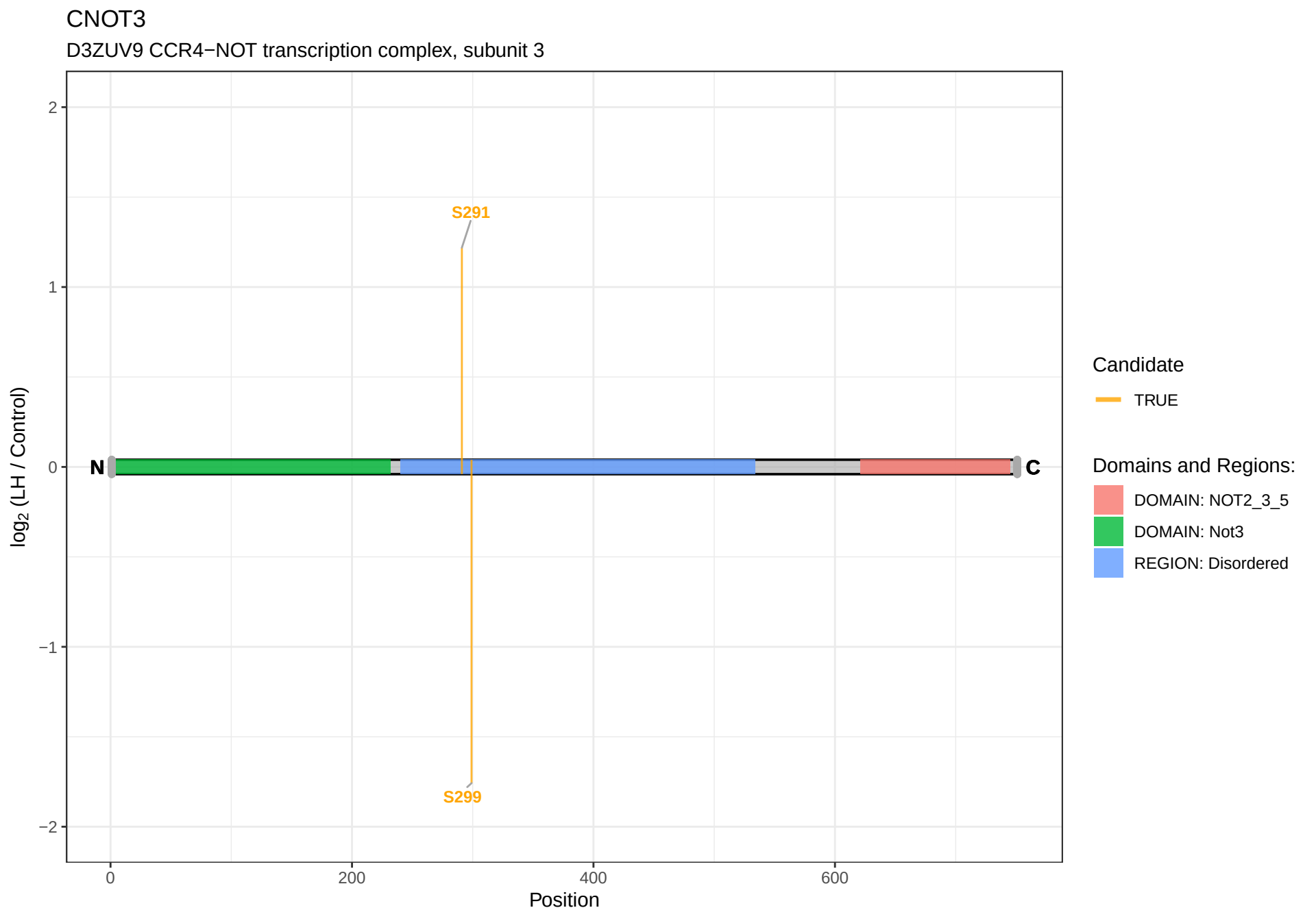

CLASP1
F1LNR0 Cytoplasmic linker−associated protein 1
S658
S568
N
C
S246
S555
S596
S1059
S1125
S1152
S1459
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: TOG
REGION: Disordered

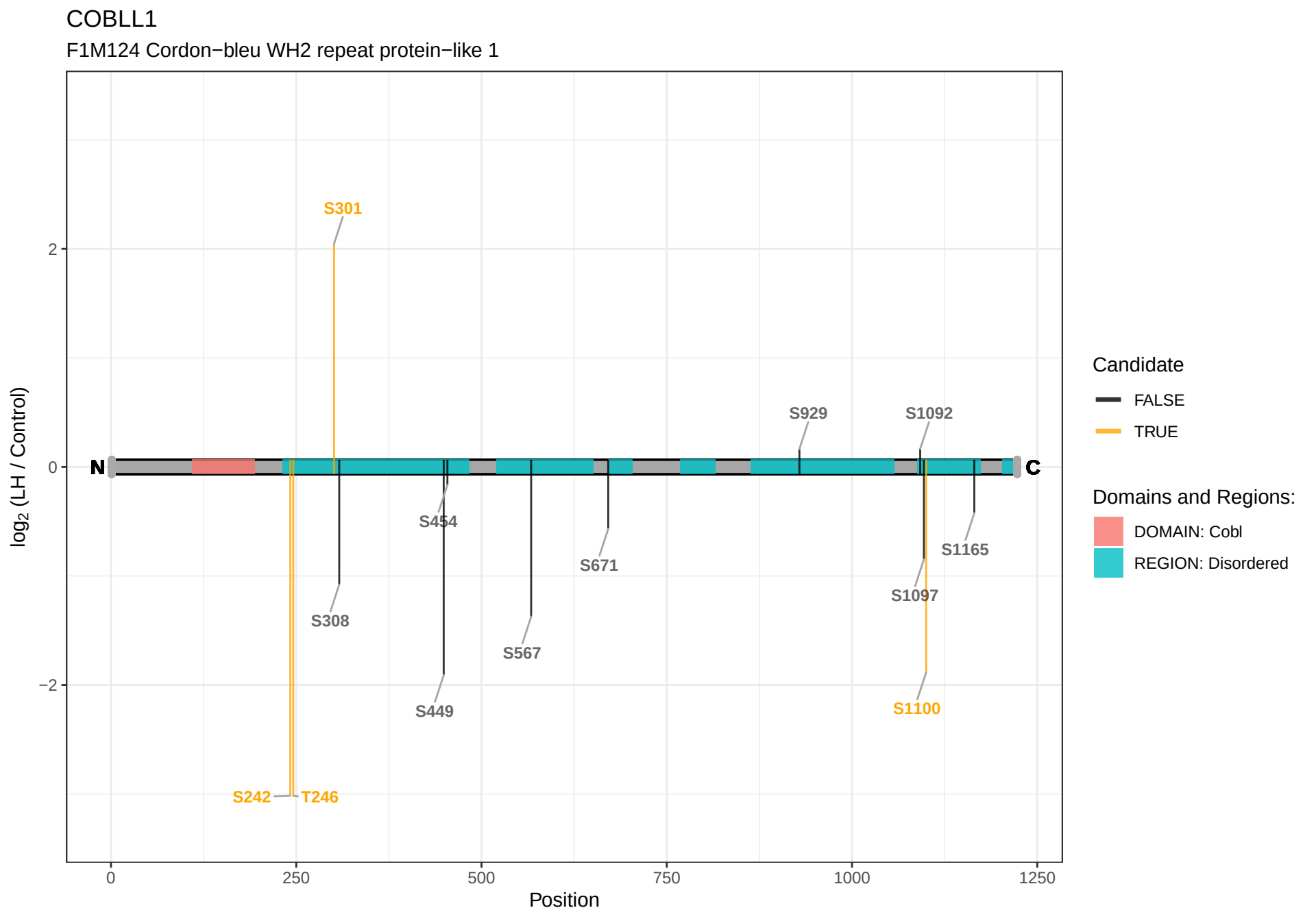

CLCC1
A0A140TAF5 Chloride channel CLIC−like 1, isoform CRA_c
S434
S438
S504
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

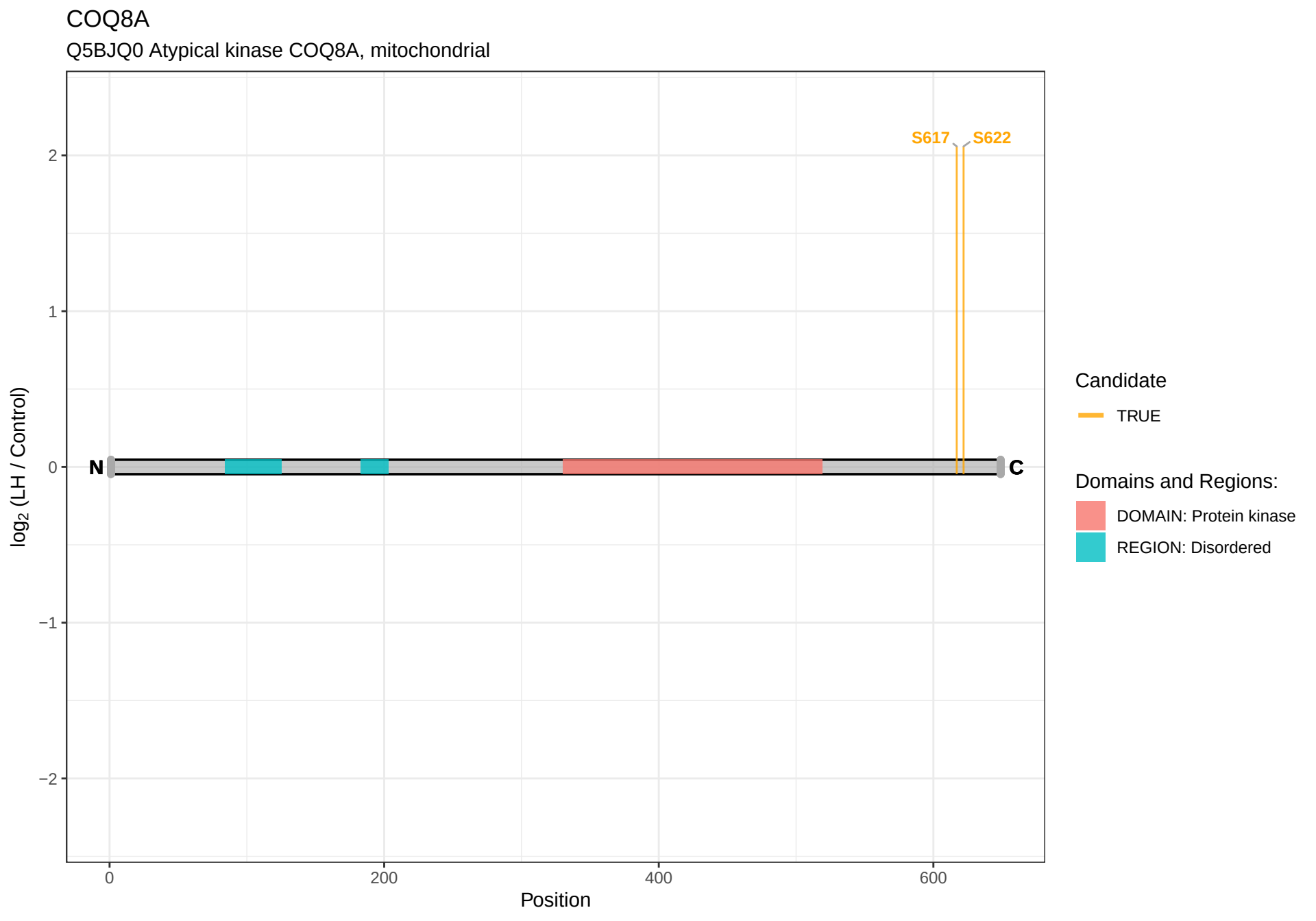

CLEC16A
A0A0G2KA14 C−type lectin domain−containing 16A
log2 (LH / Control)
3
2
1
0
−1
−2
−3
S844
S404
N
C
0
250
500
750
1000
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: FPL
REGION: Disordered

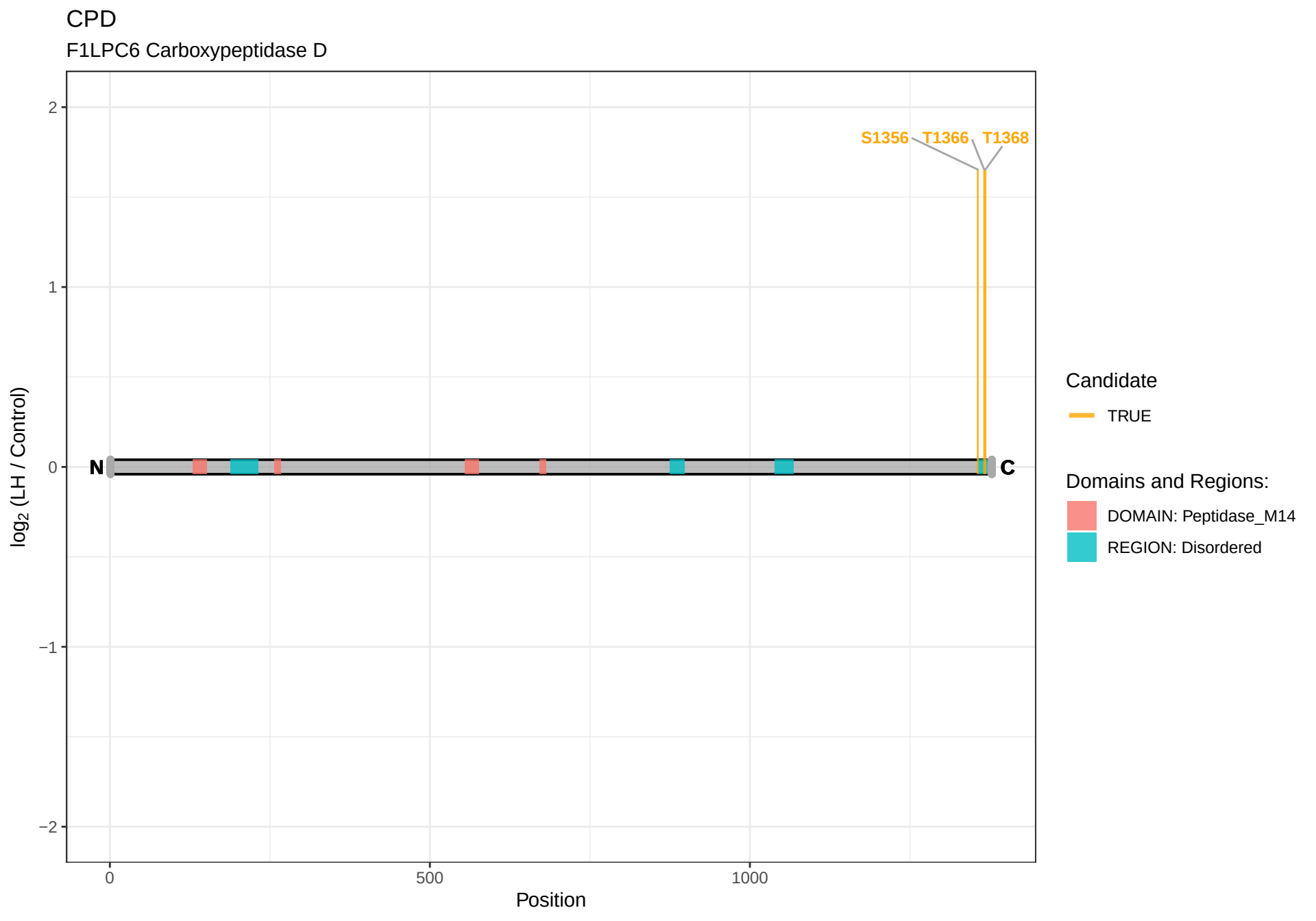

CLIP1
A0A0G2K681 CAP−Gly domain−containing linker protein 1
S326
T328
S173
S182
S178
S293
S1280
S1283
N
C
2
0
−2
log2 (LH / Control)
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CAP−Gly
REGION: Disordered

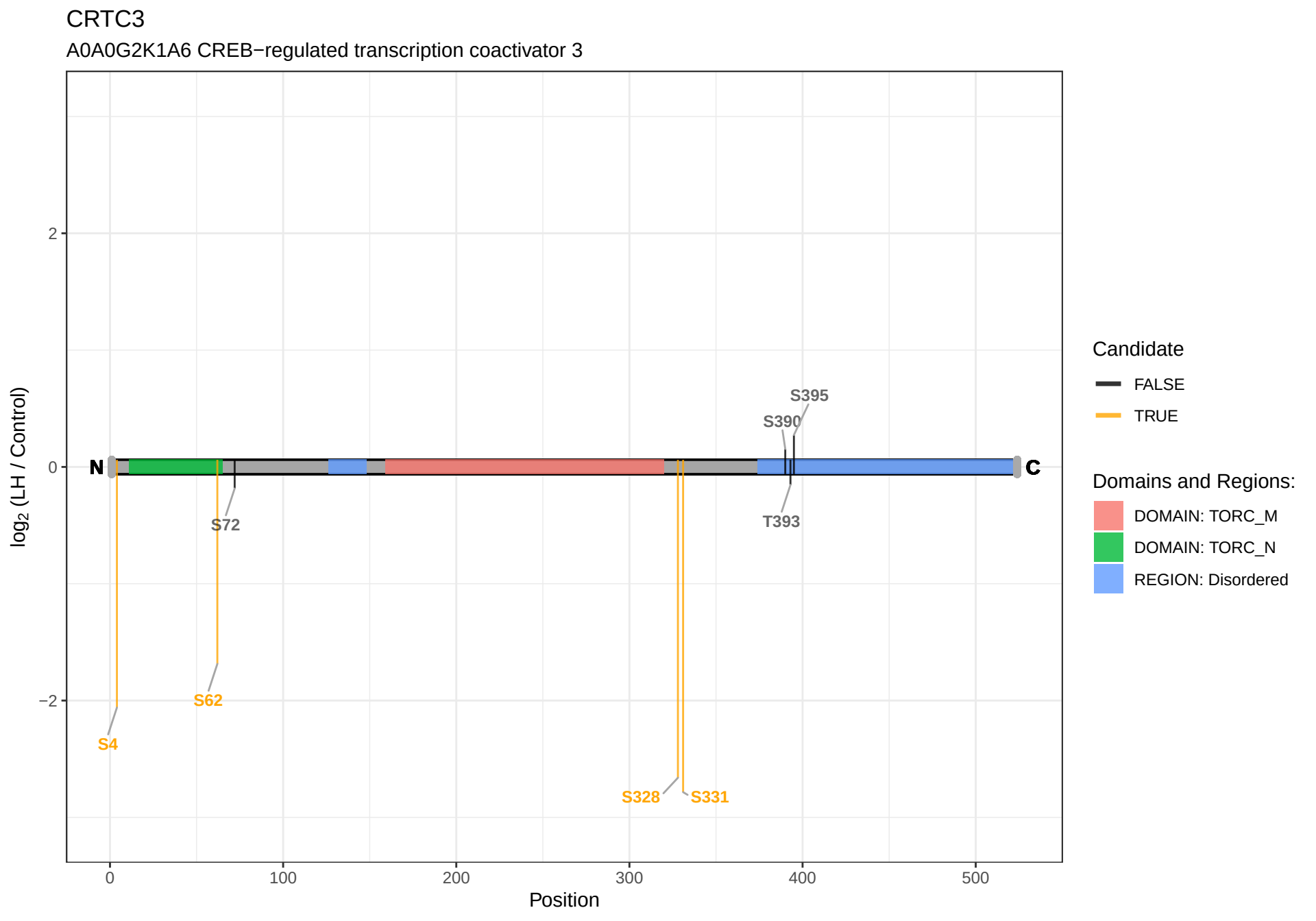

CMTR1
Q5U2Z5 Cap−specific mRNA (nucleoside−2'−O−)−methyltransferase 1
S27
S28
T29
S30
S54
S50
S52
S549
N
C
2
1
0
−1
−2
0
200
400
600
800
log2 (LH / Control)
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: G−patch
DOMAIN: RrmJ−type SAM−dependent 2'−O−MTase
DOMAIN: WW
REGION: Disordered
REGION: Interaction with POLR2A
REGION: S−adenosyl−L−methionine binding
REGION: Substrate binding

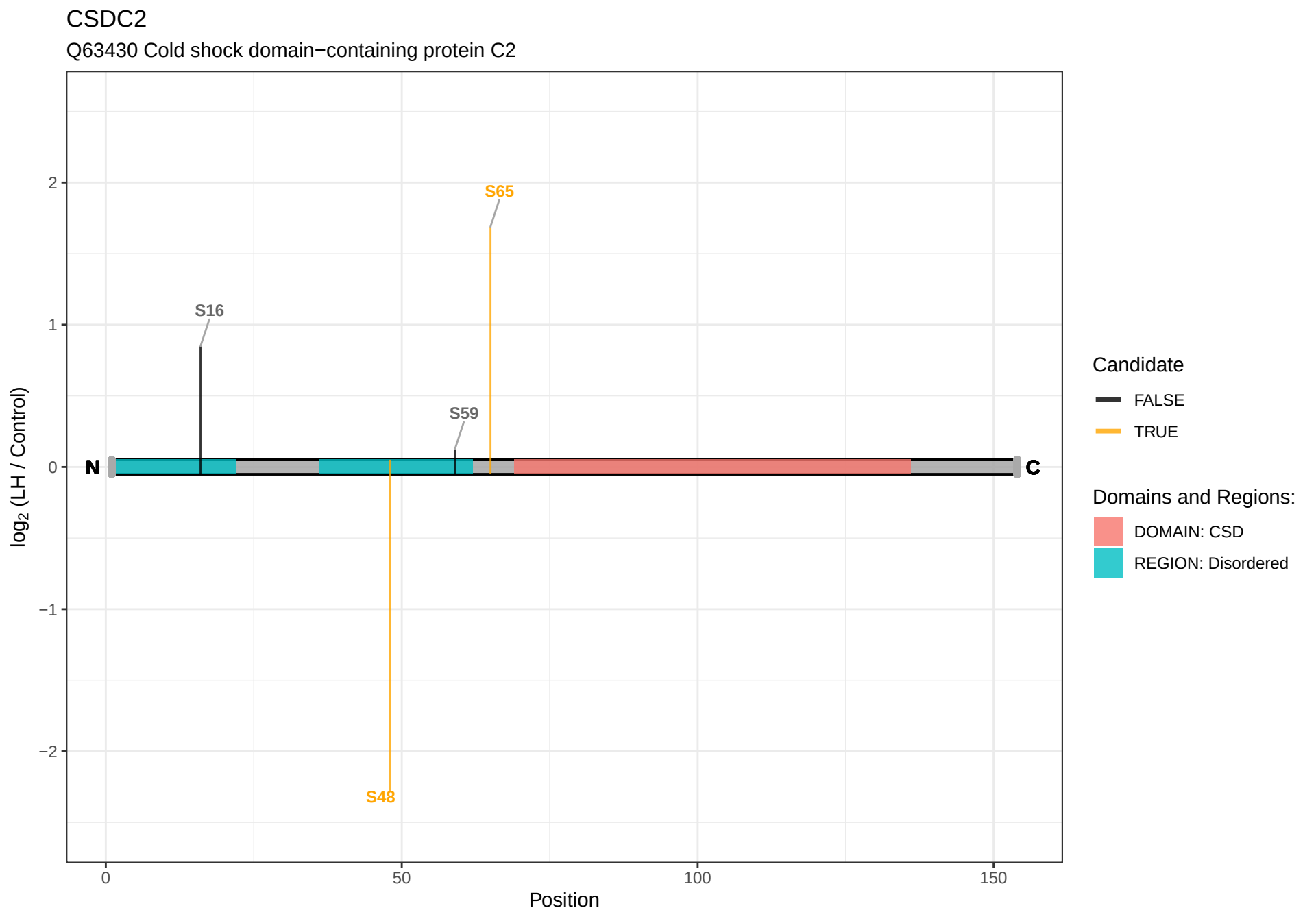

CNOT3
D3ZUV9 CCR4−NOT transcription complex, subunit 3
2
1
0
−1
−2
log2 (LH / Control)
S291
S299
N
C
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: NOT2_3_5
DOMAIN: Not3
REGION: Disordered

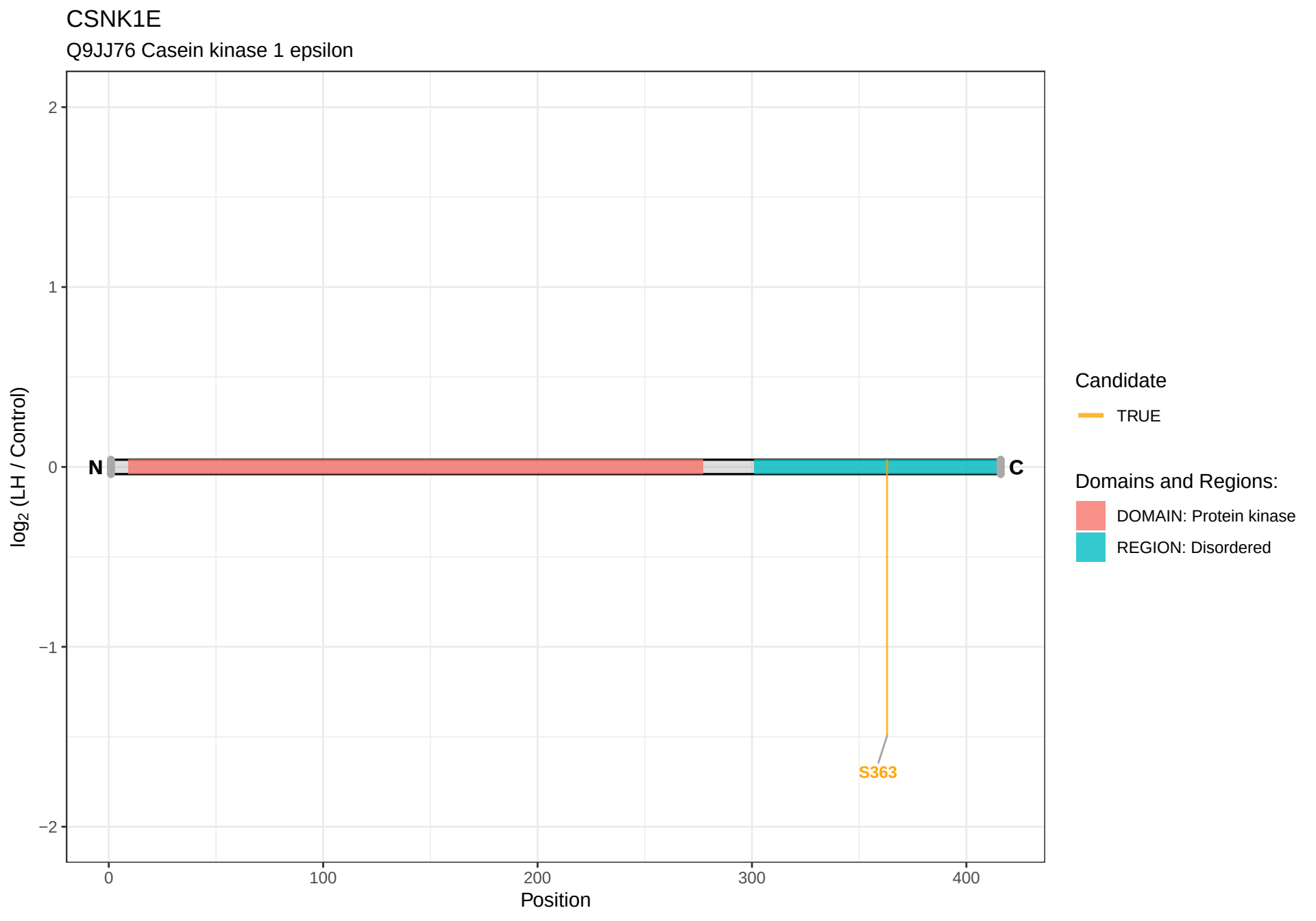

COBLL1
F1M124 Cordon−bleu WH2 repeat protein−like 1
log2 (LH / Control)
2
0
−2
N
C
S301
S308
S454
S449
S567
S671
S929
S1092
S1097
S1165
S1100
S242
T246
0
250
500
750
1000
1250
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Cobl
REGION: Disordered

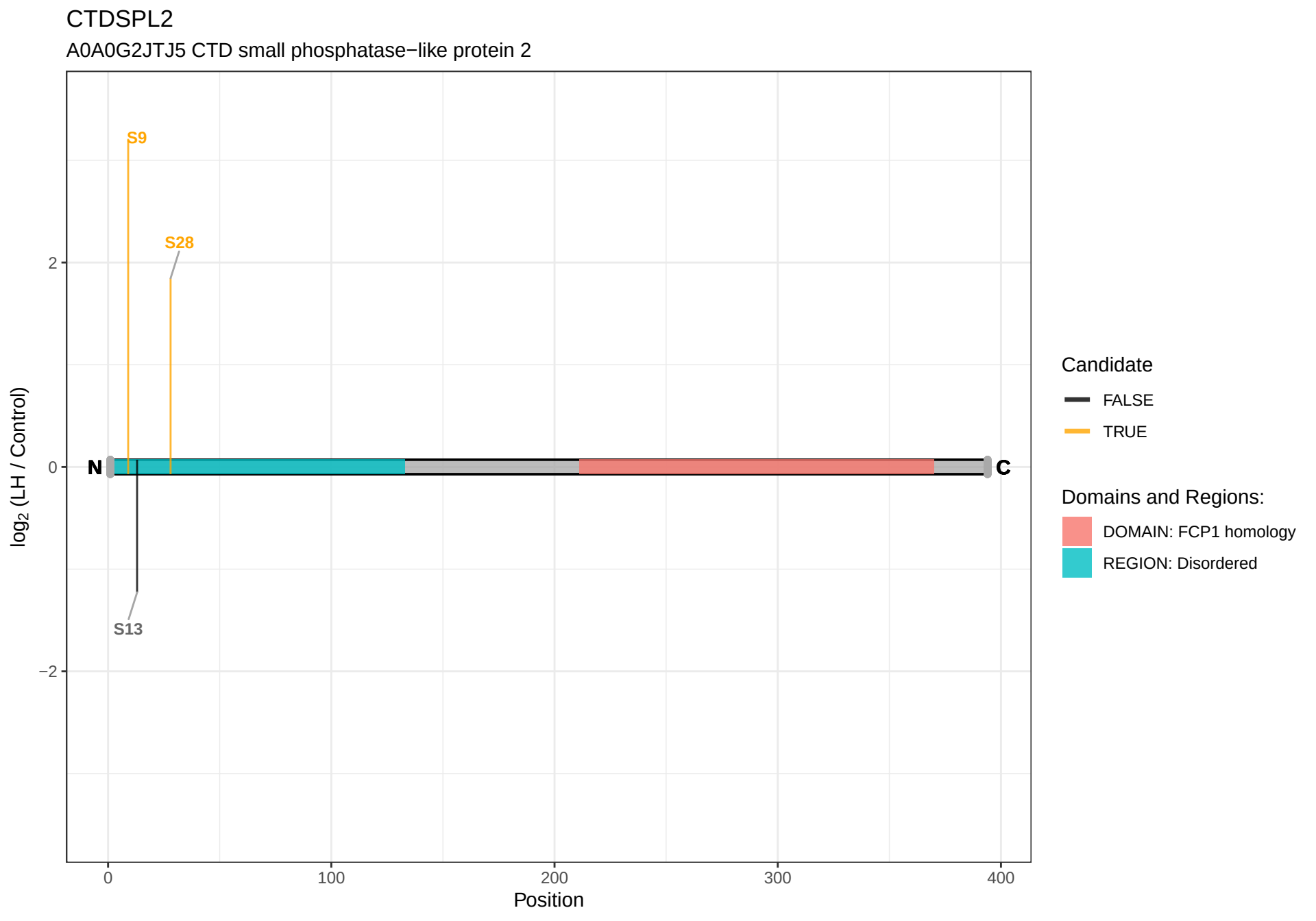

COQ8A
Q5BJQ0 Atypical kinase COQ8A, mitochondrial
S617
S622
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered

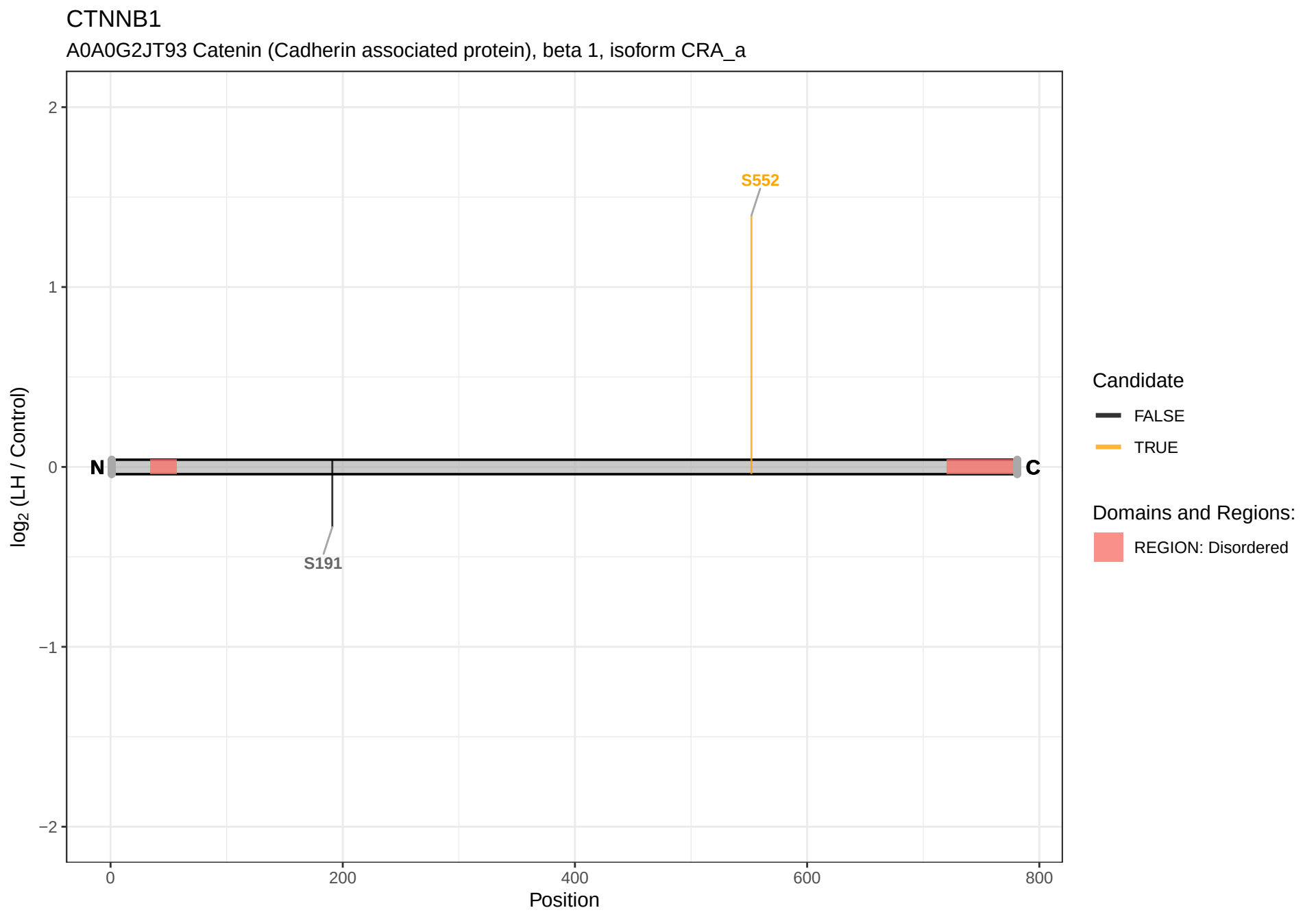

CPD
F1LPC6 Carboxypeptidase D
S1356
T1366
T1368
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Peptidase_M14
REGION: Disordered

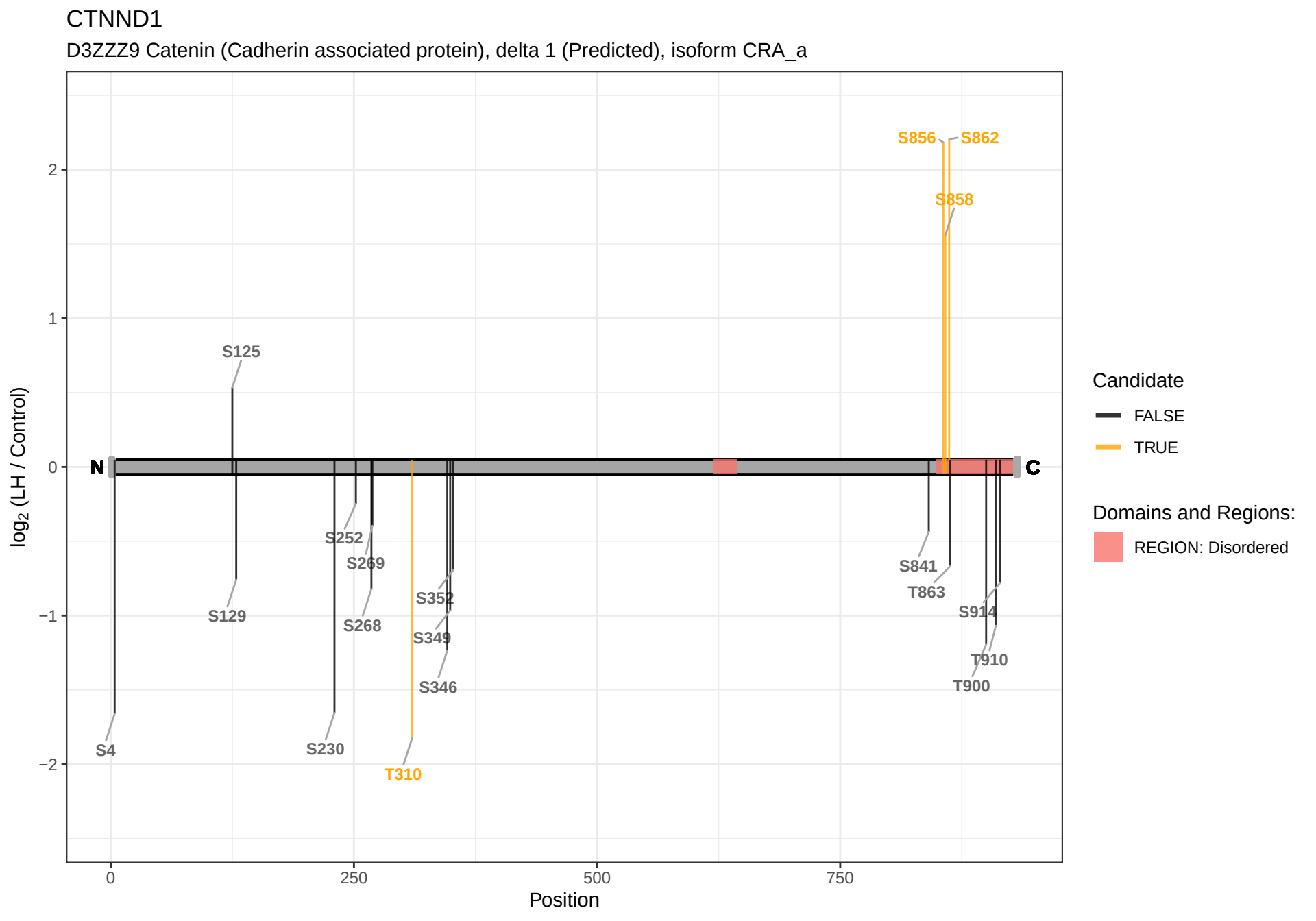

CRTC3
A0A0G2K1A6 CREB−regulated transcription coactivator 3
log2 (LH / Control)
2
0
−2
N
C
S4
S62
S72
S328
S331
S390
S395
T393
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: TORC_M
DOMAIN: TORC_N
REGION: Disordered

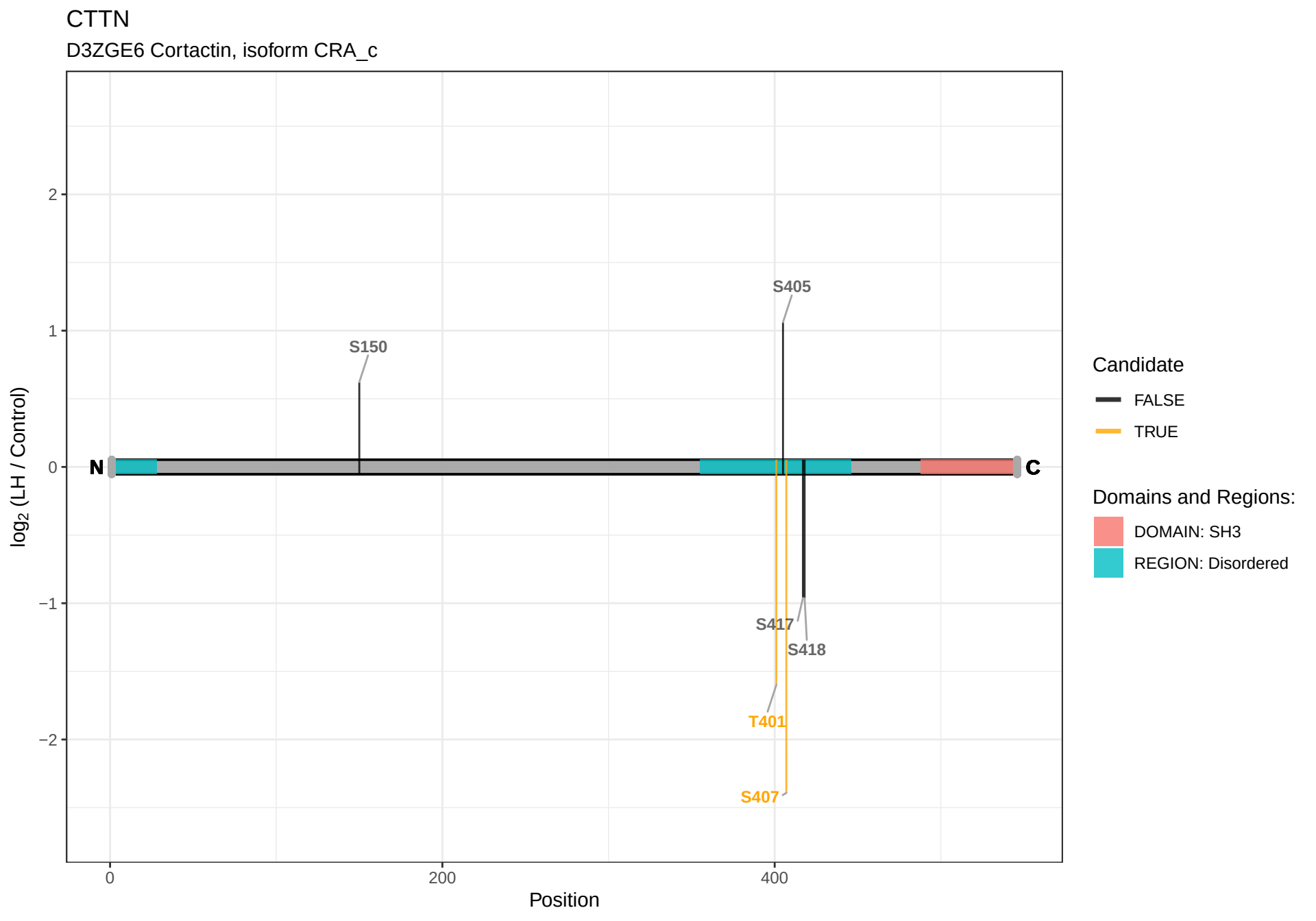

CSDC2
Q63430 Cold shock domain−containing protein C2
S65
S16
S59
S48
N
C
2
1
0
−1
−2
0
50
100
150
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CSD
REGION: Disordered

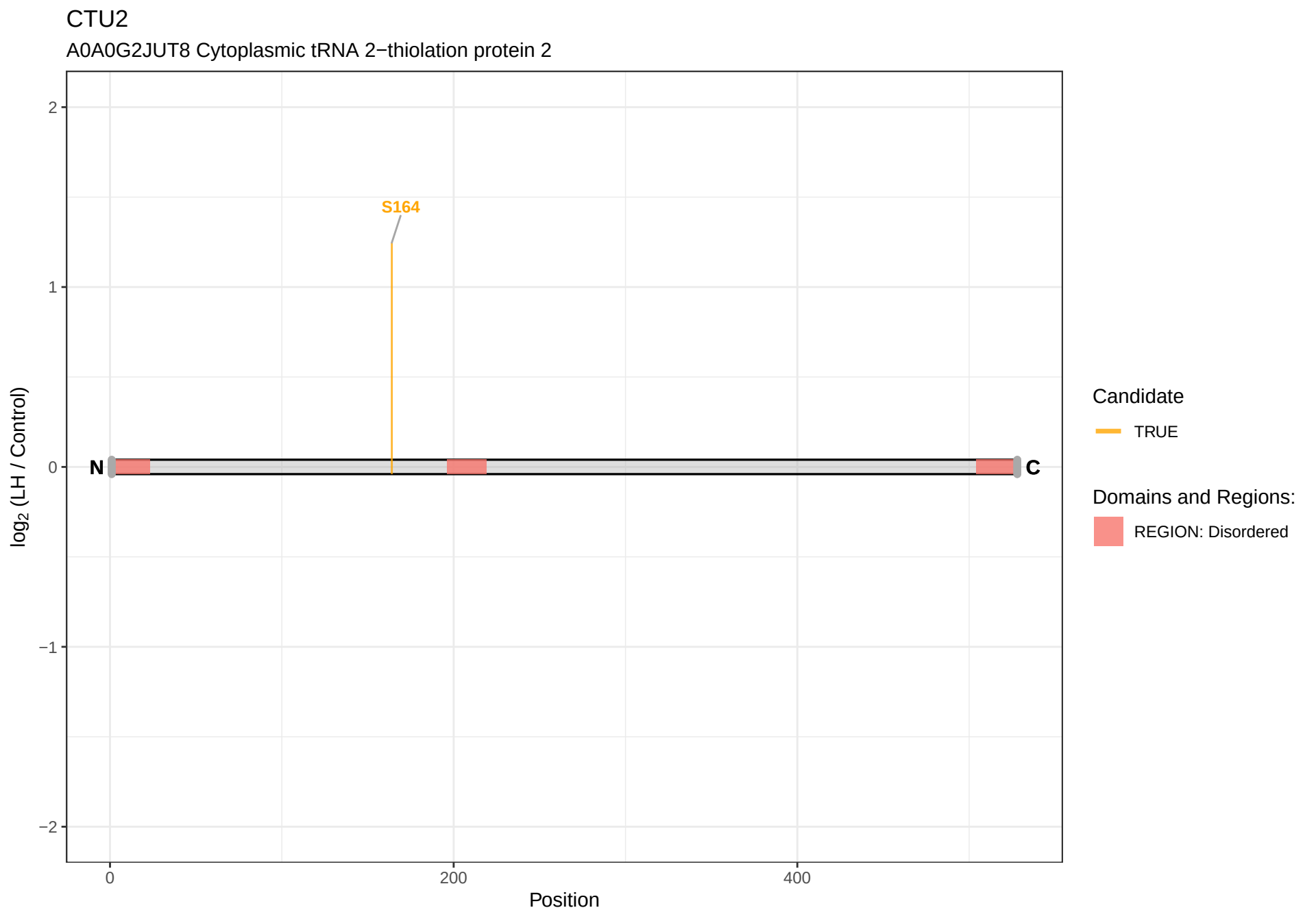

CSNK1E
Q9JJ76 Casein kinase 1 epsilon
log2 (LH / Control)
2
1
0
−1
−2
N
C
S363
0
100
200
300
400
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered

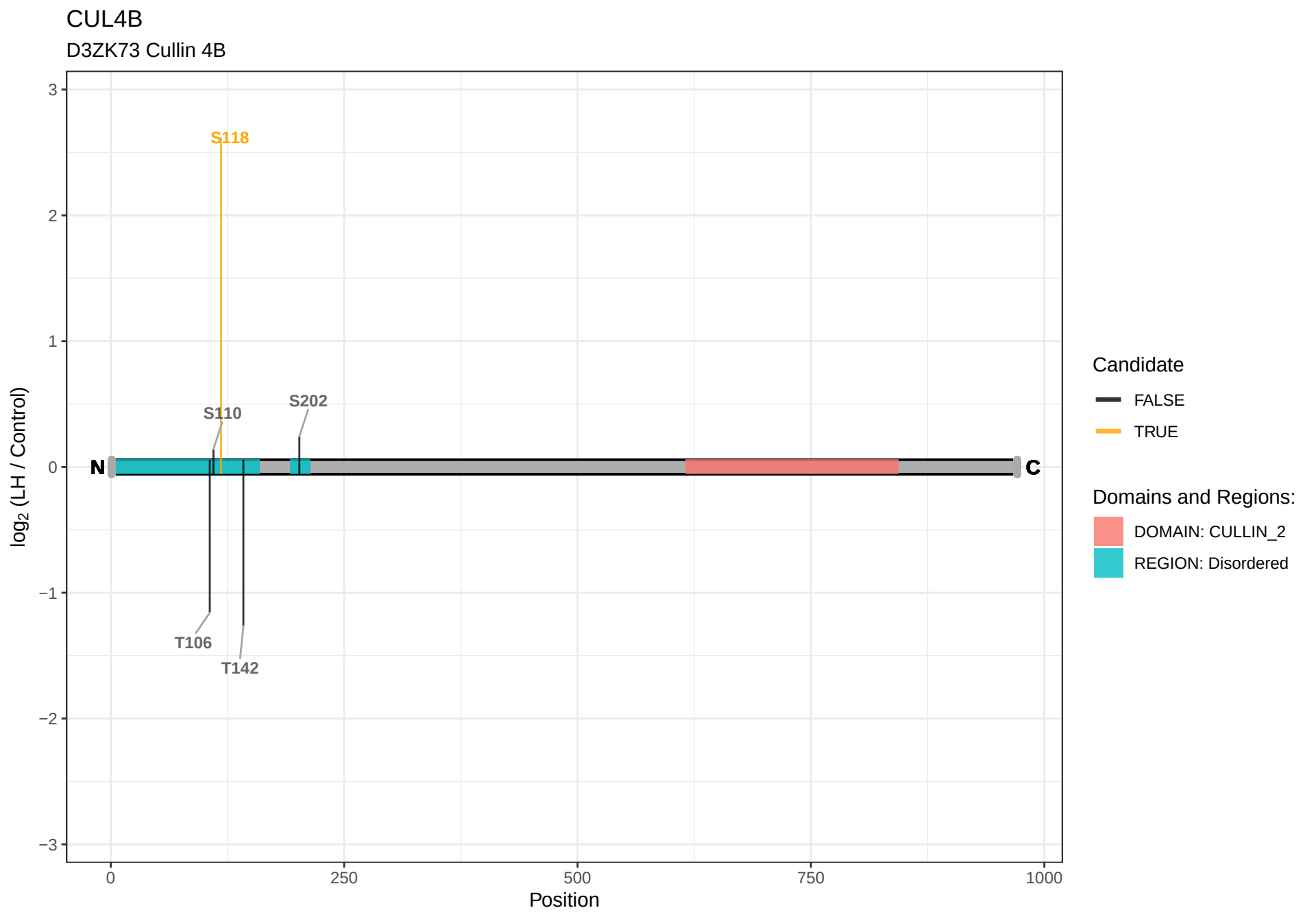

CTDSPL2
A0A0G2JTJ5 CTD small phosphatase−like protein 2
S9
S28
S13
N
C
2
0
−2
log2 (LH / Control)
0
100
200
300
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: FCP1 homology
REGION: Disordered

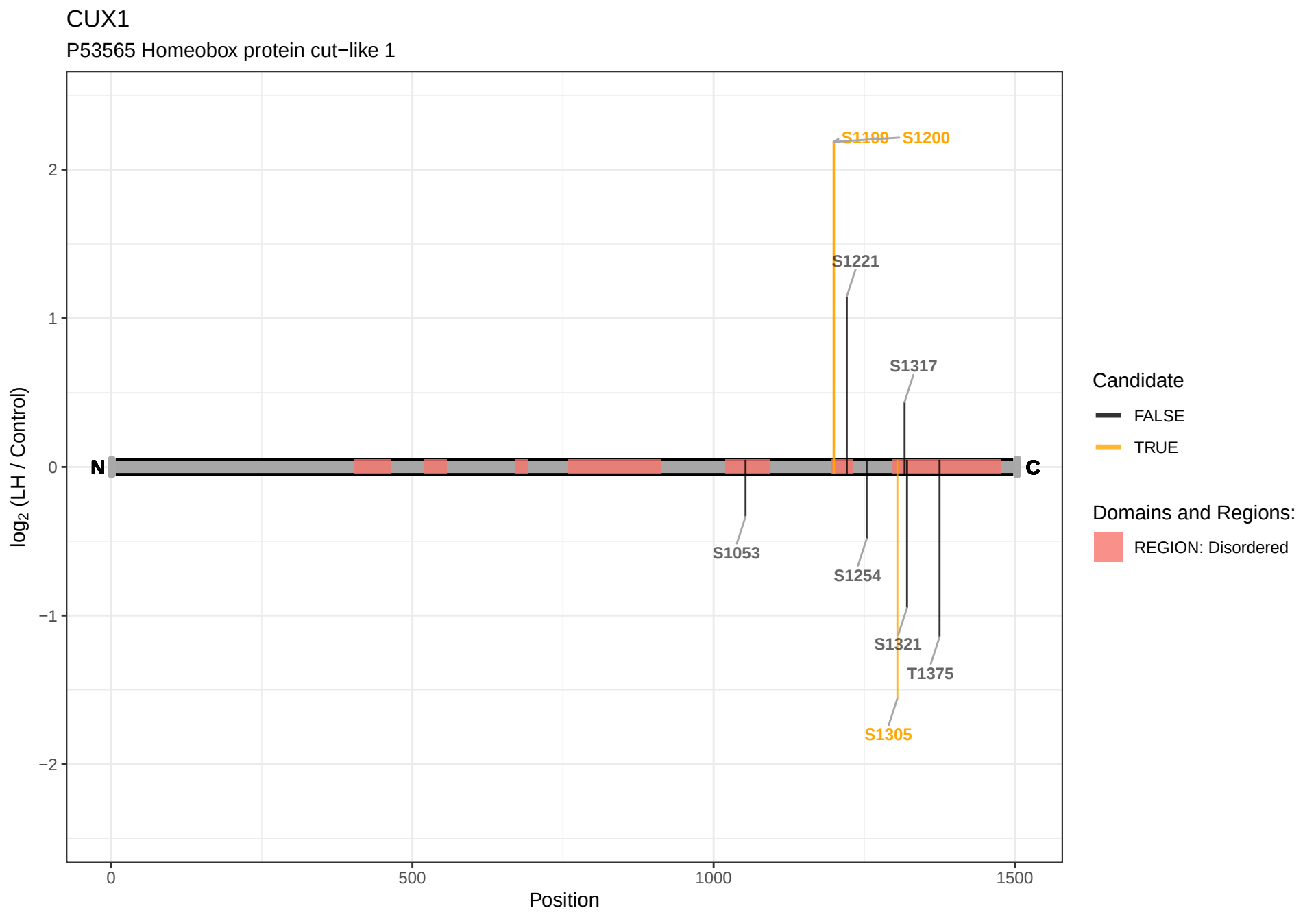

CTNNB1
A0A0G2JT93 Catenin (Cadherin associated protein), beta 1, isoform CRA_a
log2 (LH / Control)
2
1
0
−1
−2
N
C
S552
S191
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

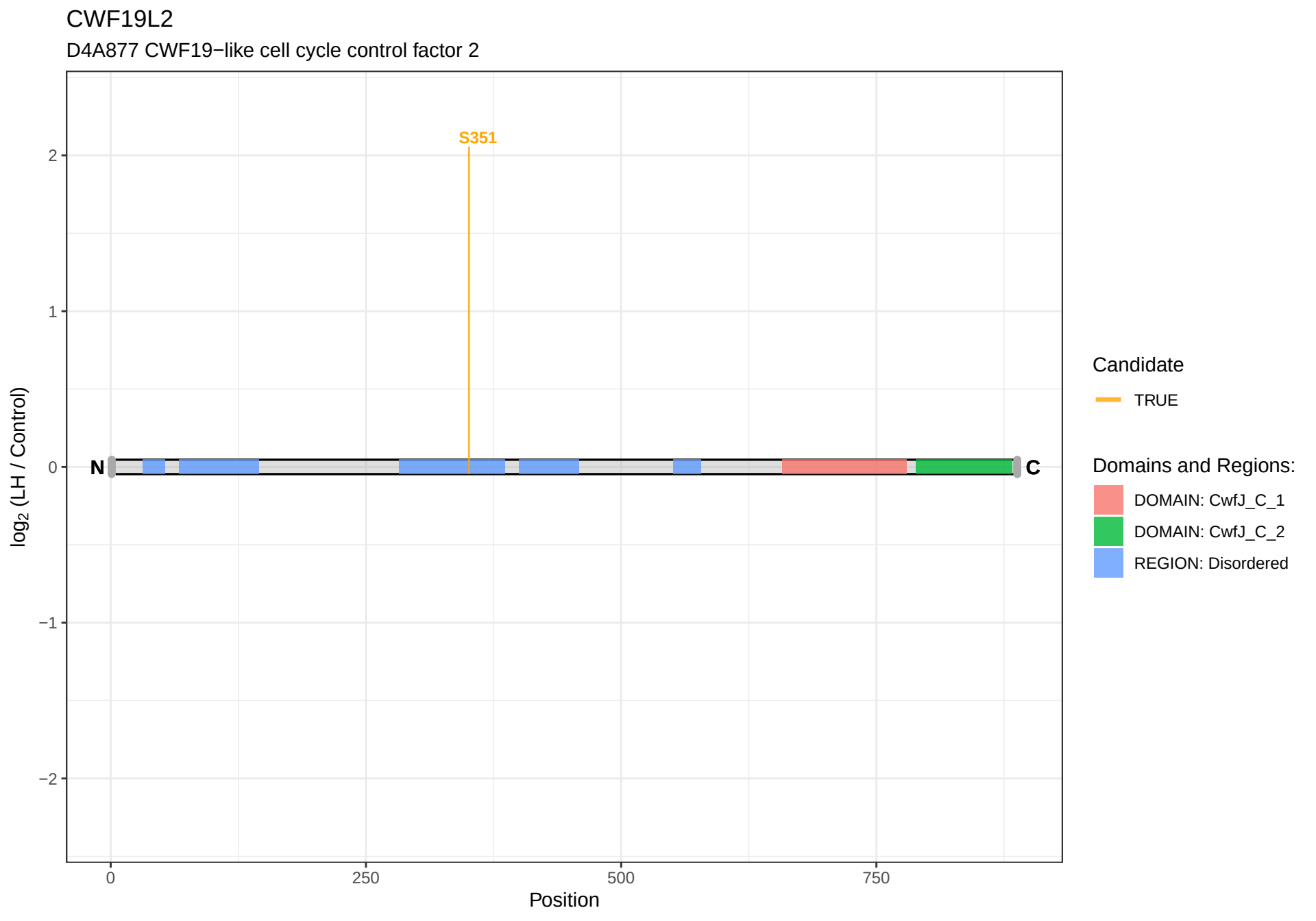

CTNND1
D3ZZZ9 Catenin (Cadherin associated protein), delta 1 (Predicted), isoform CRA_a
log2 (LH / Control)
2
1
0
−1
−2
N
C
S856
S862
S858
S125
S252
S269
S129
S352
S268
S349
S346
S841
T863
S914
T910
T900
S4
S230
T310
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

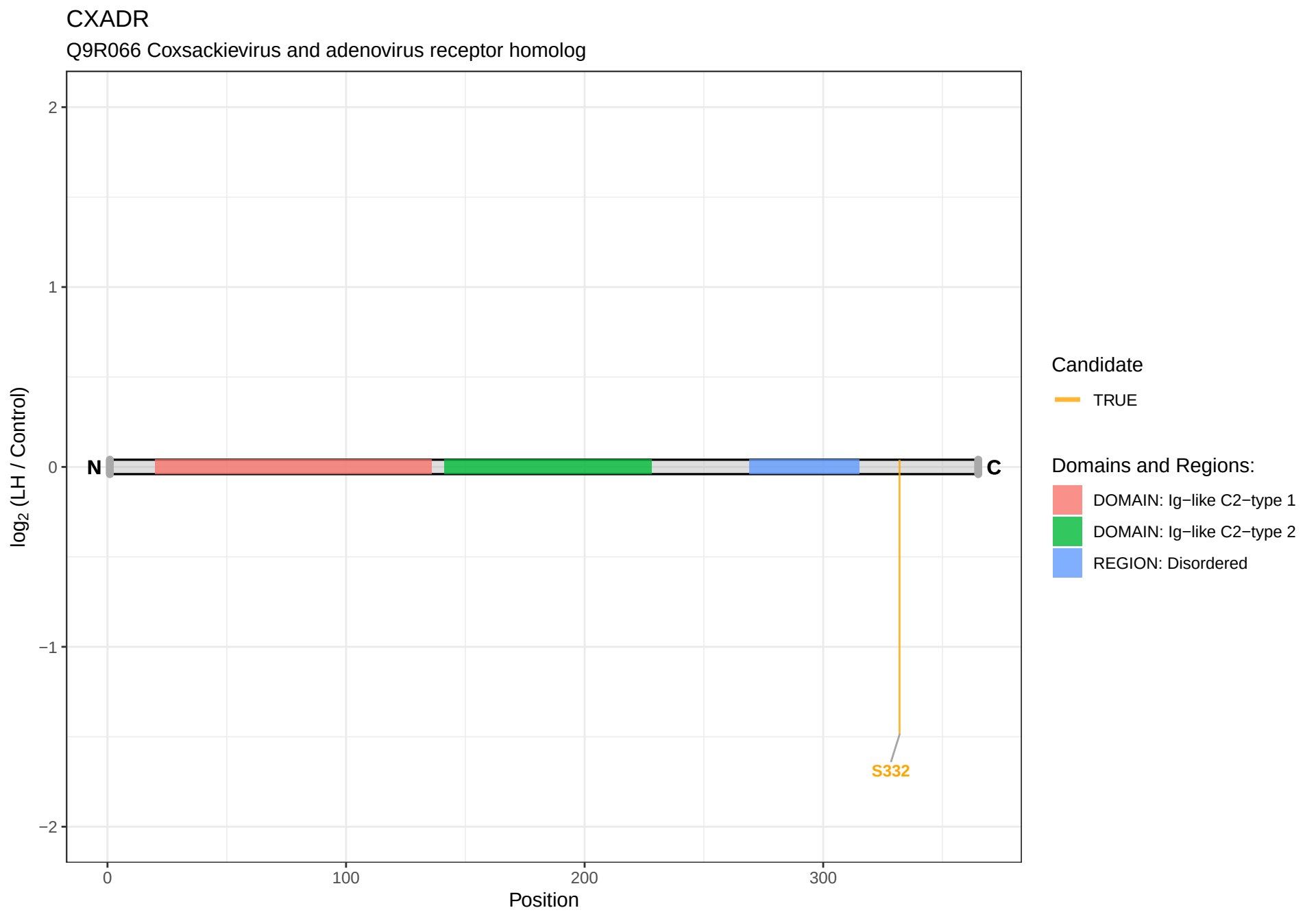

CTTN
D3ZGE6 Cortactin, isoform CRA_c
log2 (LH / Control)
2
1
0
−1
−2
N
C
S150
S405
S417
S418
T401
S407
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SH3
REGION: Disordered

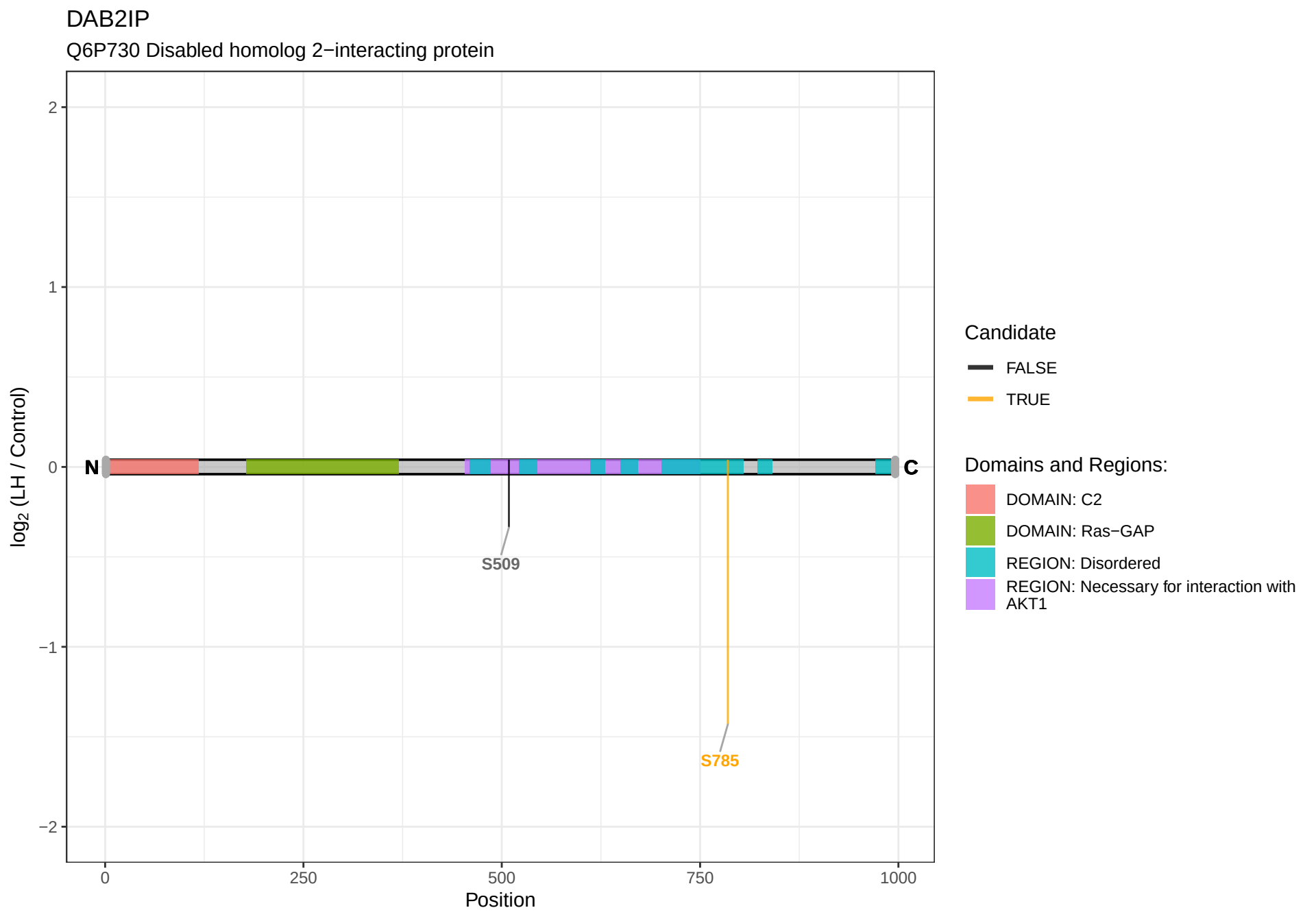

CTU2
A0A0G2JUT8 Cytoplasmic tRNA 2−thiolation protein 2
S164
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

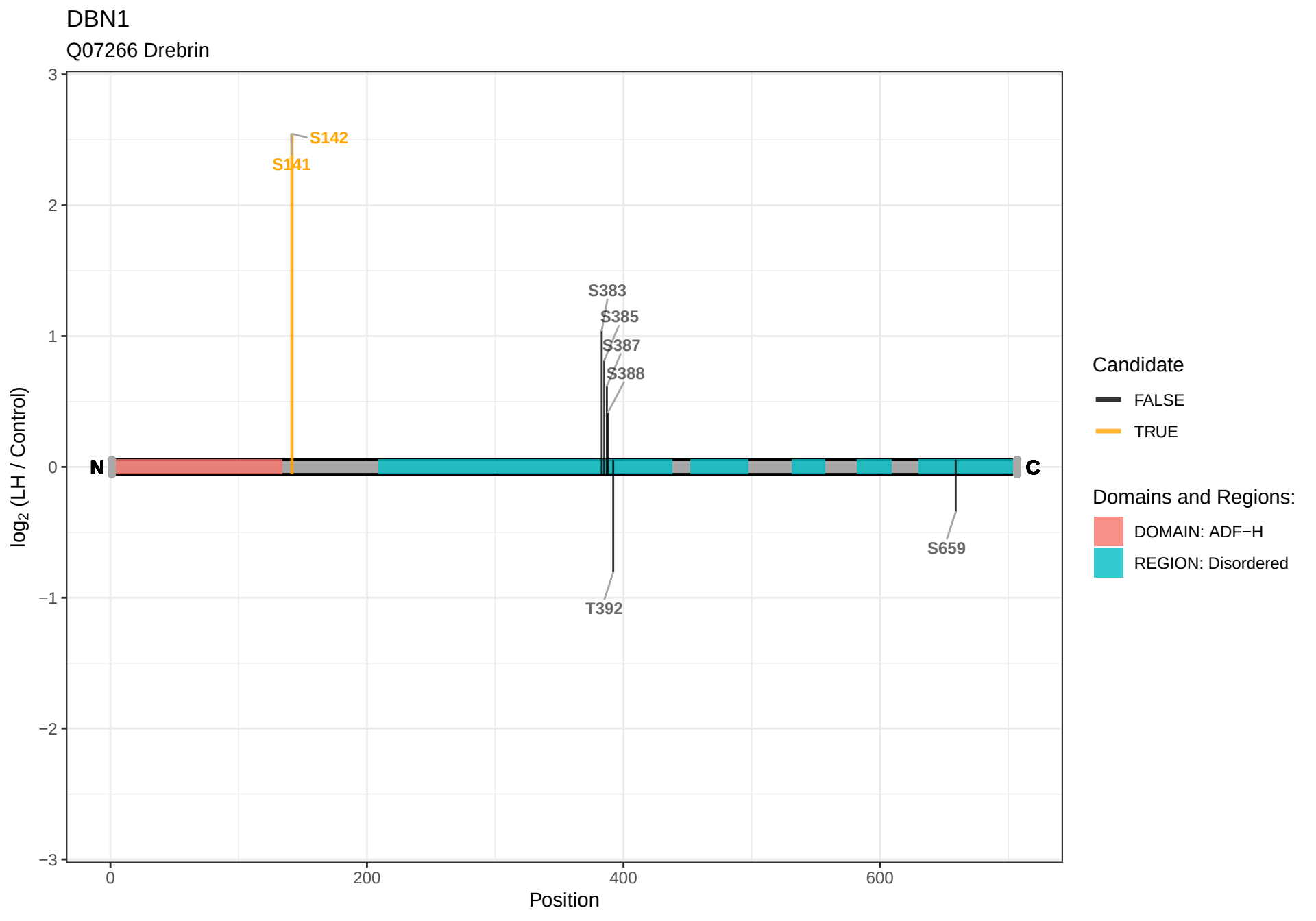

CUL4B
D3ZK73 Cullin 4B
S118
S110
S202
T106
T142
N
C
log2 (LH / Control)
Position
0
250
500
750
1000
3
2
1
0
−1
−2
−3
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CULLIN_2
REGION: Disordered

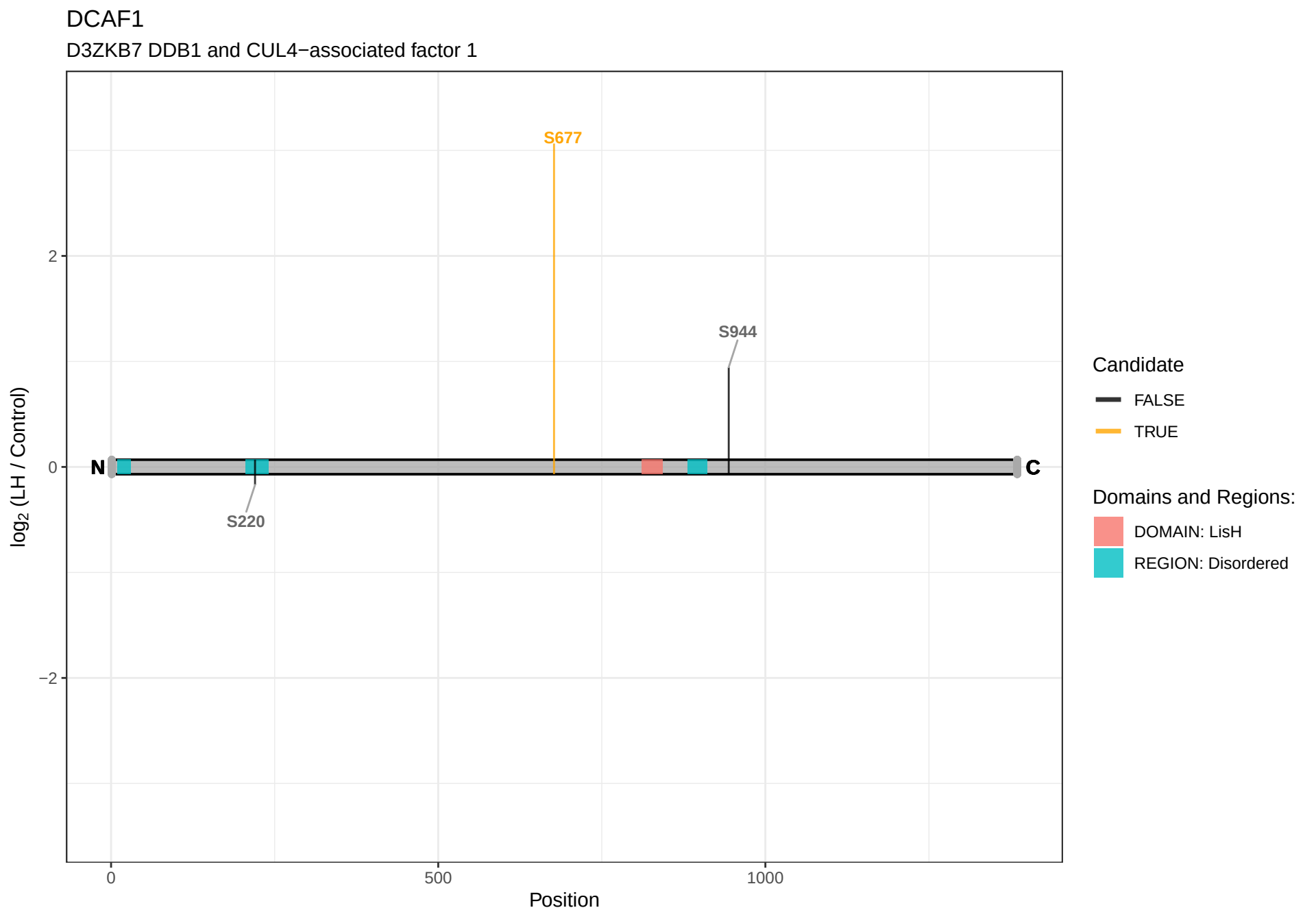

CUX1
P53565 Homeobox protein cut−like 1
S1199
S1200
S1221
S1317
S1053
S1254
S1321
T1375
S1305
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

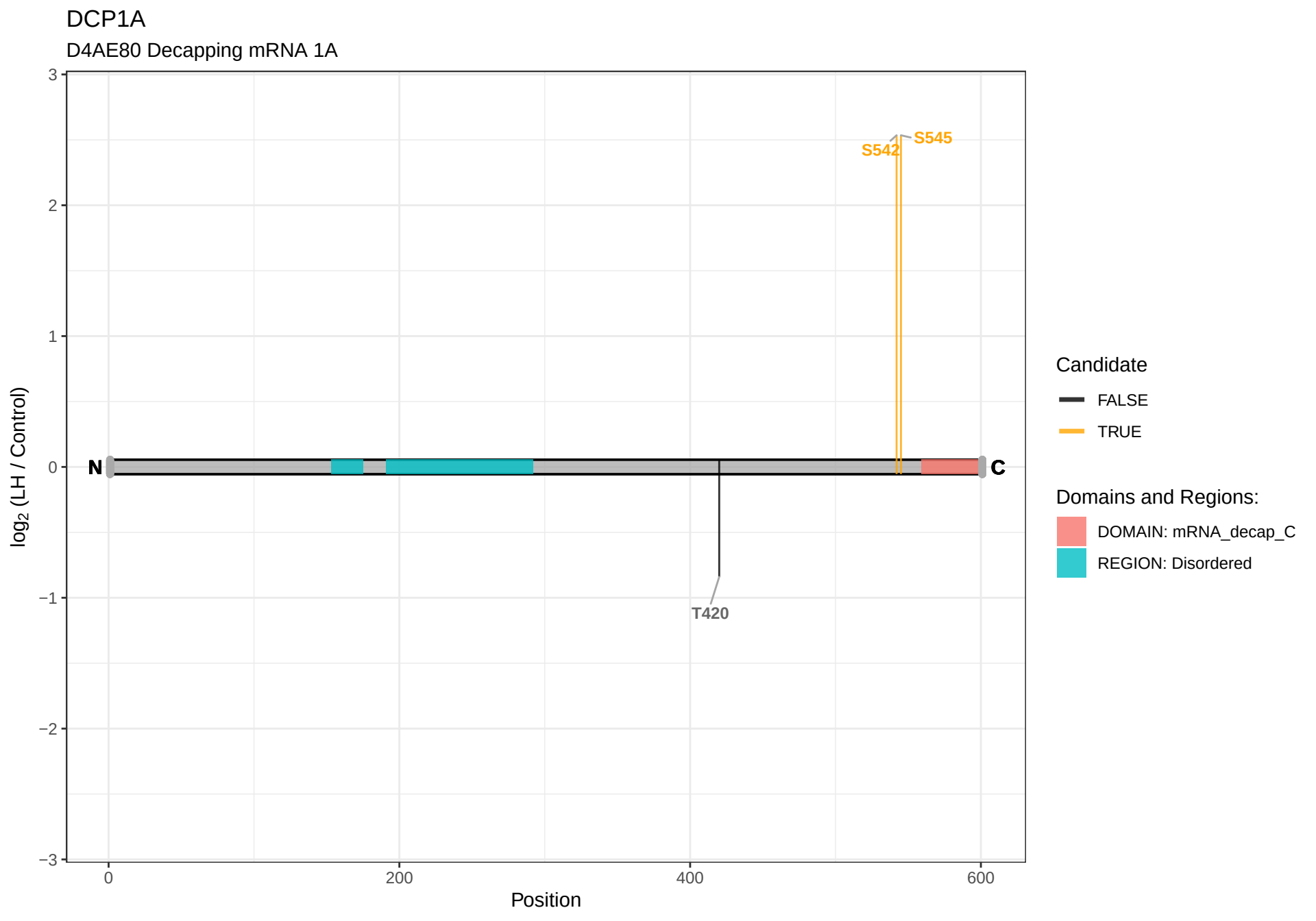

CWF19L2
D4A877 CWF19−like cell cycle control factor 2
S351
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
250
500
750
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: CwfJ_C_1
DOMAIN: CwfJ_C_2
REGION: Disordered

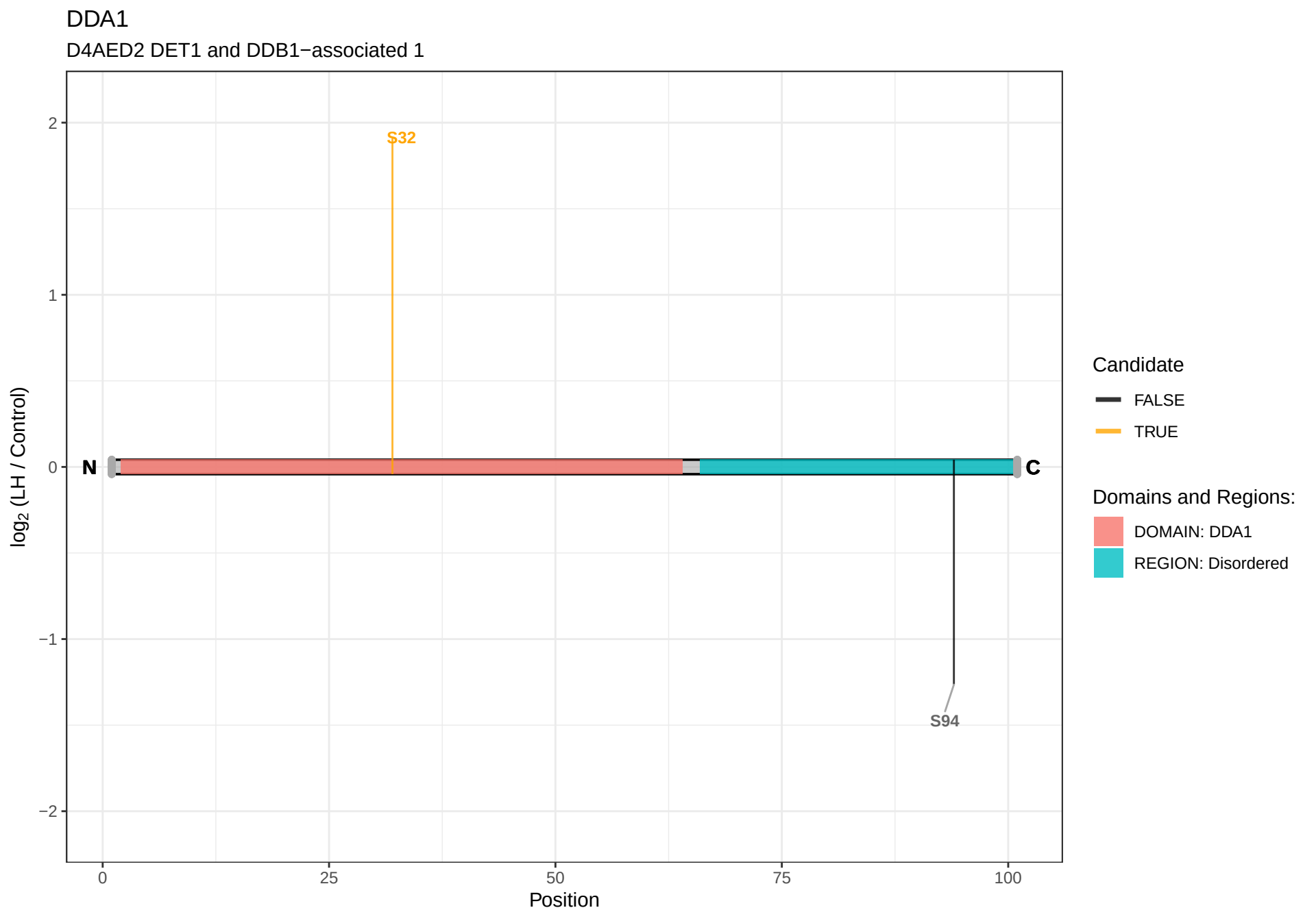

CXADR
Q9R066 Coxsackievirus and adenovirus receptor homolog
log2 (LH / Control)
2
1
0
−1
−2
N
C
S332
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Ig−like C2−type 1
DOMAIN: Ig−like C2−type 2
REGION: Disordered

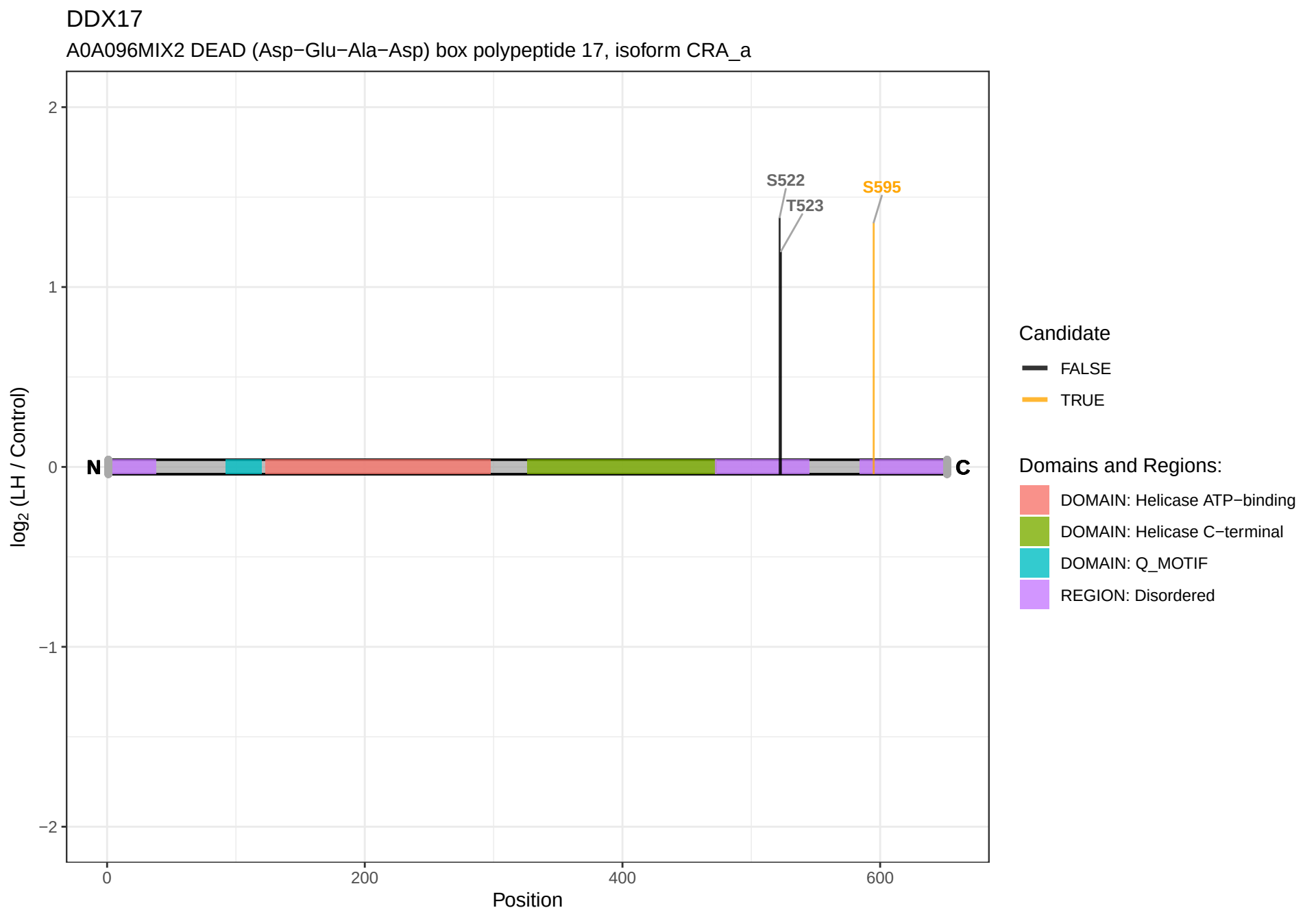

DAB2IP
Q6P730 Disabled homolog 2−interacting protein
log2 (LH / Control)
2
1
0
−1
−2
N
C
S509
S785
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2
DOMAIN: Ras−GAP
REGION: Disordered
REGION: Necessary for interaction with AKT1

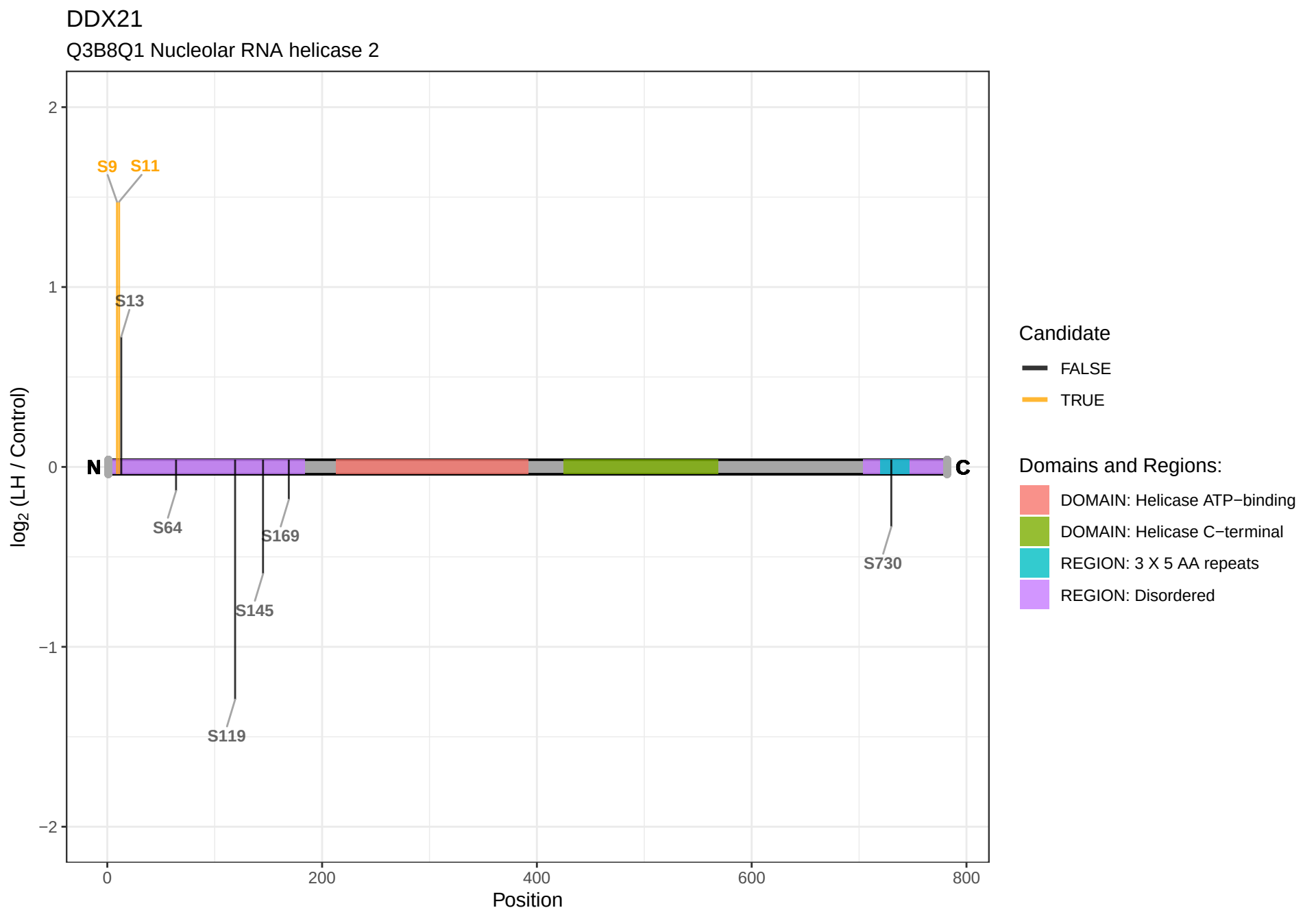

DBN1
Q07266 Drebrin
S142
S141
S383
S385
S387
S388
S659
T392
N
C
3
2
1
0
−1
−2
−3
0
200
400
600
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ADF−H
REGION: Disordered

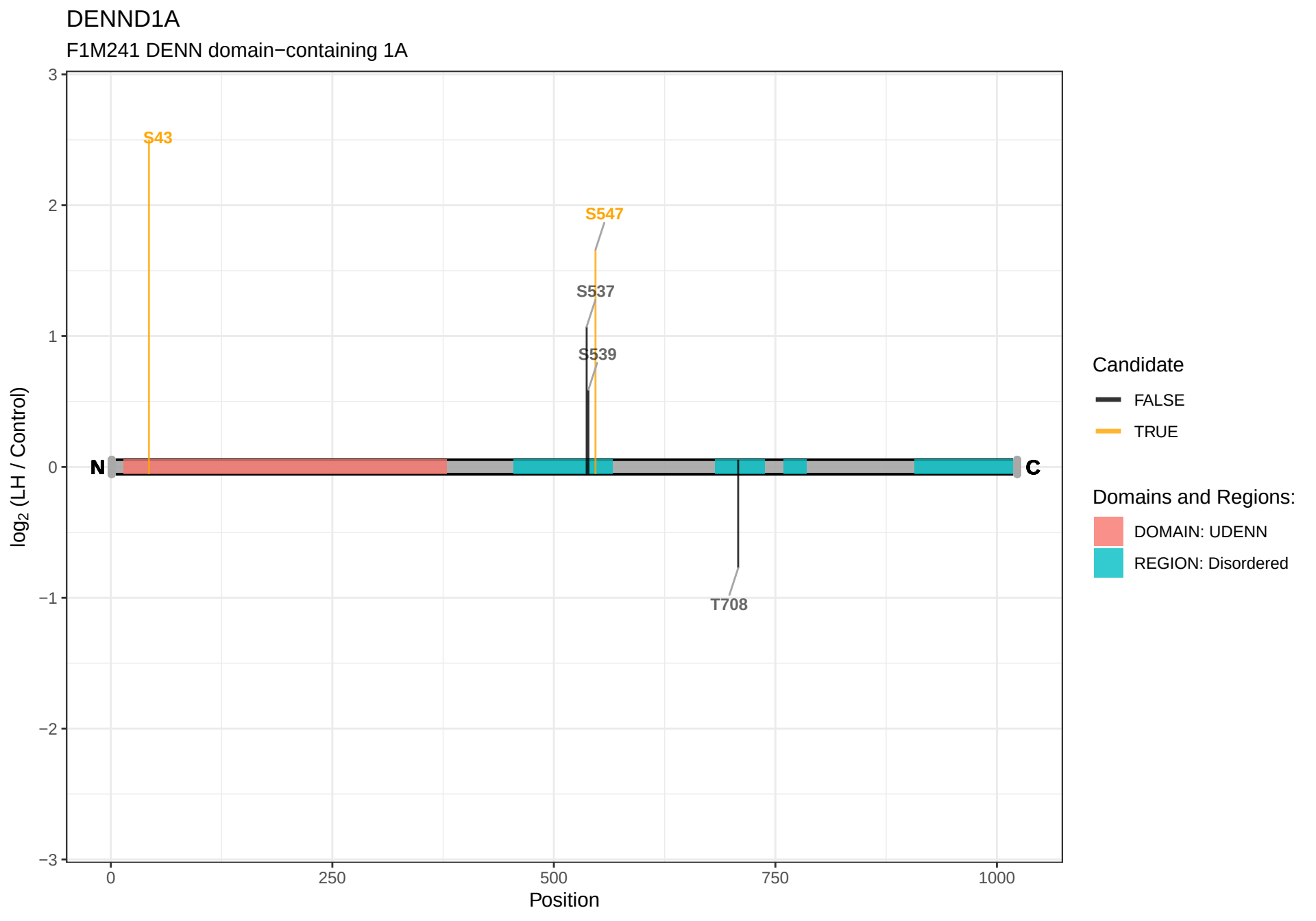

DCAF1
D3ZKB7 DDB1 and CUL4−associated factor 1
S677
S944
S220
N
C
2
0
−2
log2 (LH / Control)
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: LisH
REGION: Disordered

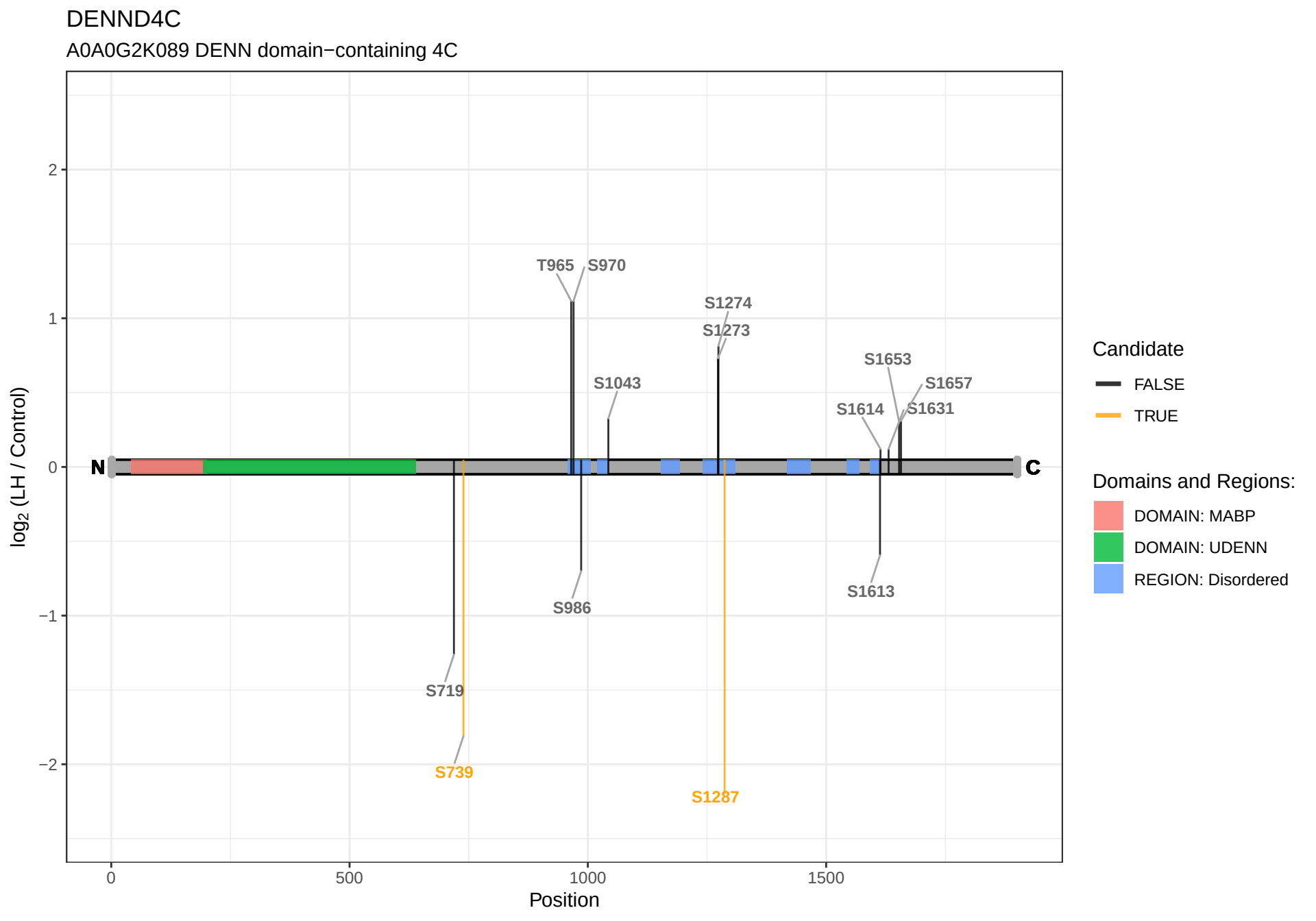

DCP1A
D4AE80 Decapping mRNA 1A
log2 (LH / Control)
3
2
1
0
−1
−2
−3
0
200
400
600
Position
N
C
S542
S545
T420
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: mRNA_decap_C
REGION: Disordered

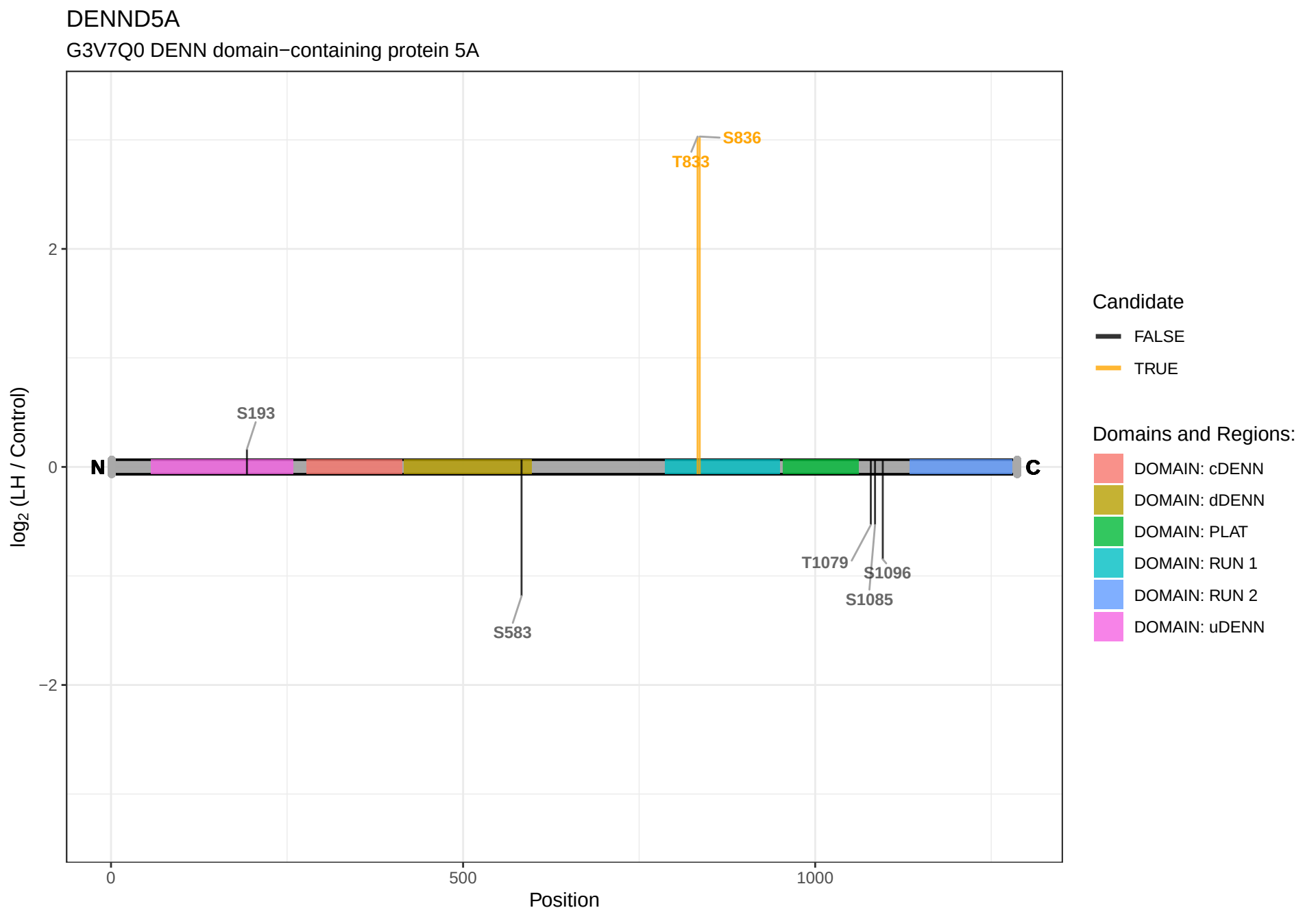

DDA1
D4AED2 DET1 and DDB1−associated 1
S32
S94
N
C
log2 (LH / Control)
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DDA1
REGION: Disordered

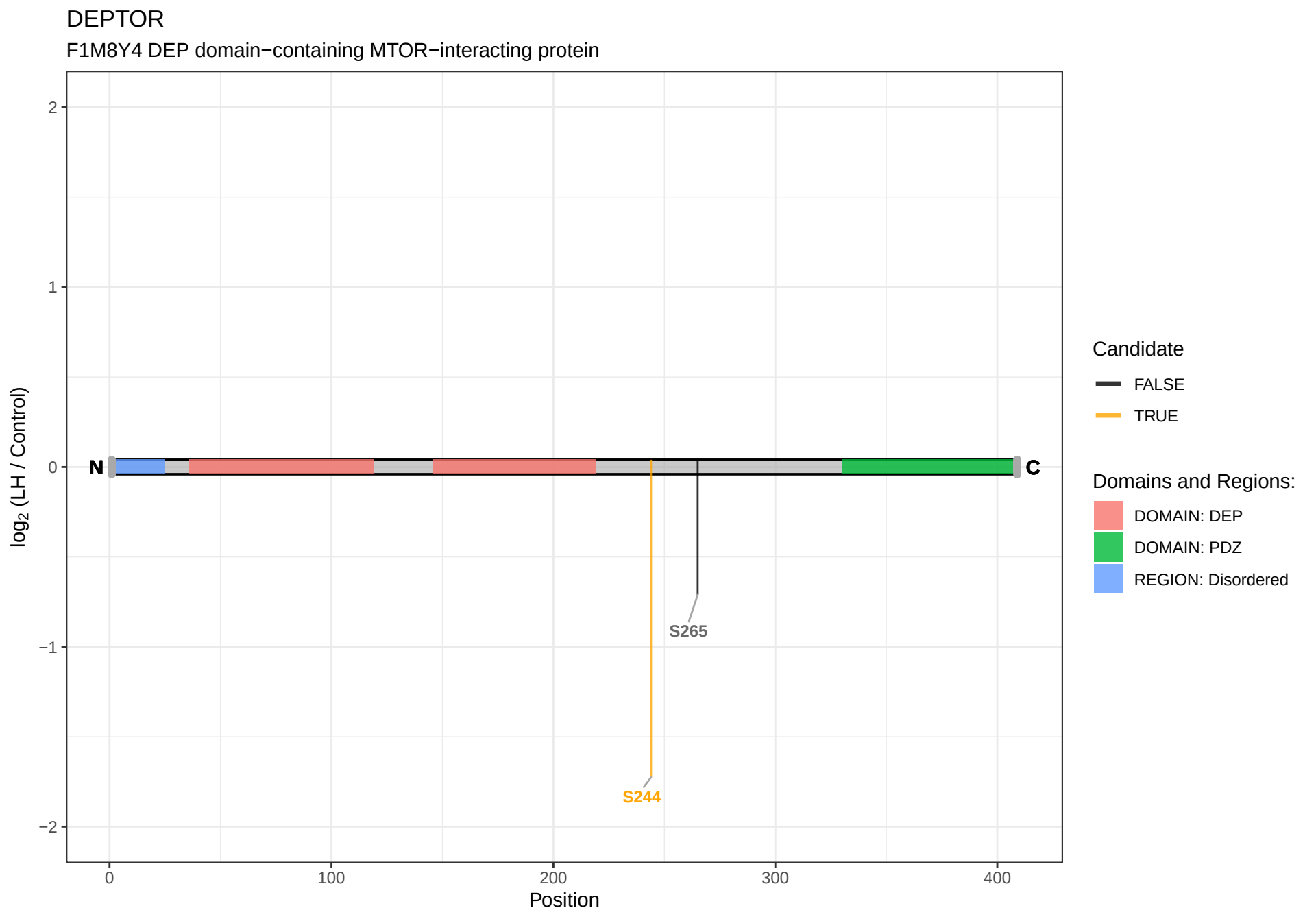

DDX17
A0A096MIX2 DEAD (Asp−Glu−Ala−Asp) box polypeptide 17, isoform CRA_a
S522
T523
S595
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
200
400
600
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Helicase ATP−binding
DOMAIN: Helicase C−terminal
DOMAIN: Q_MOTIF
REGION: Disordered

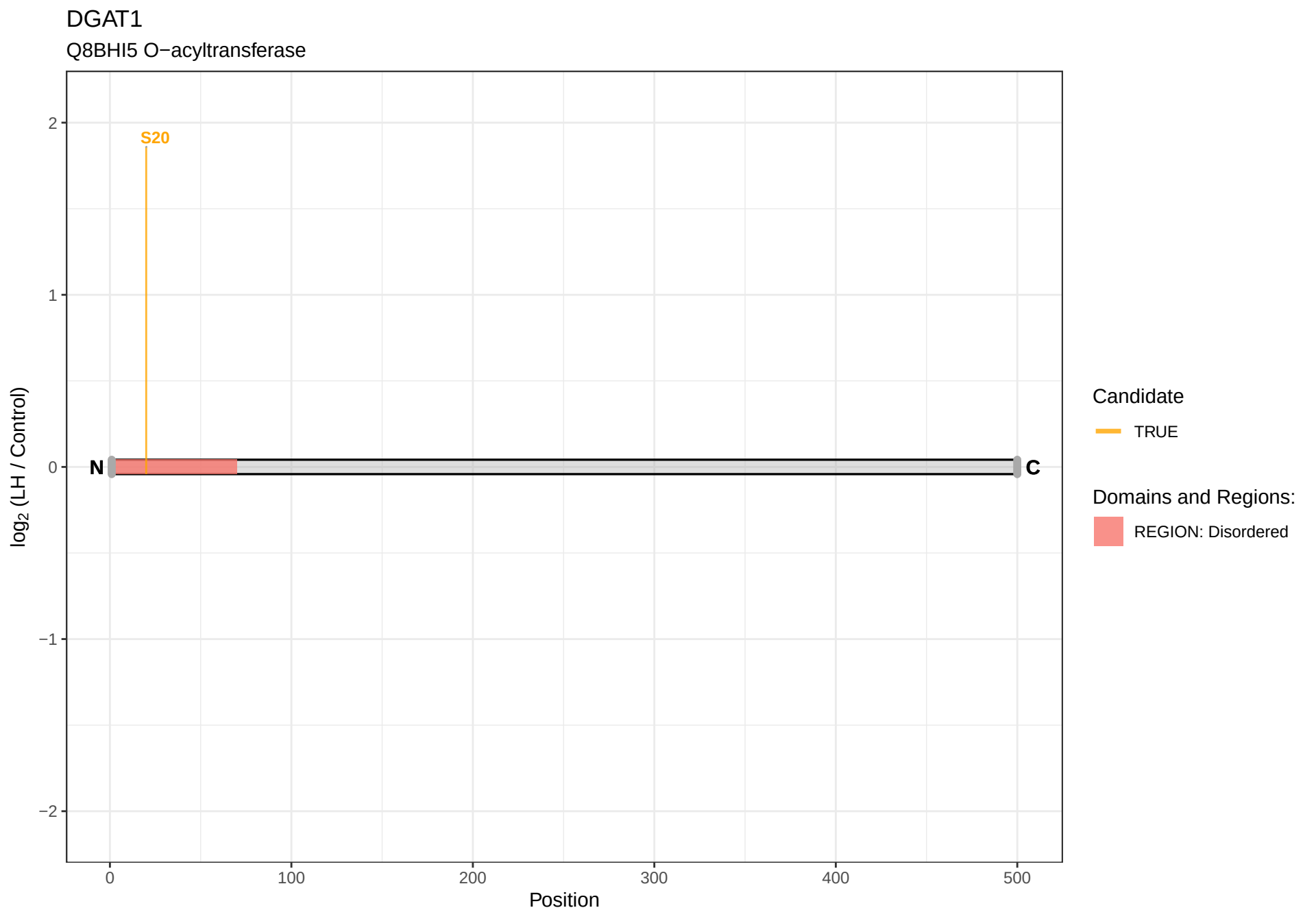

DDX21
Q3B8Q1 Nucleolar RNA helicase 2
log2 (LH / Control)
2
1
0
−1
−2
S9
S11
S13
S64
S119
S145
S169
S730
N
C
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Helicase ATP−binding
DOMAIN: Helicase C−terminal
REGION: 3 X 5 AA repeats
REGION: Disordered

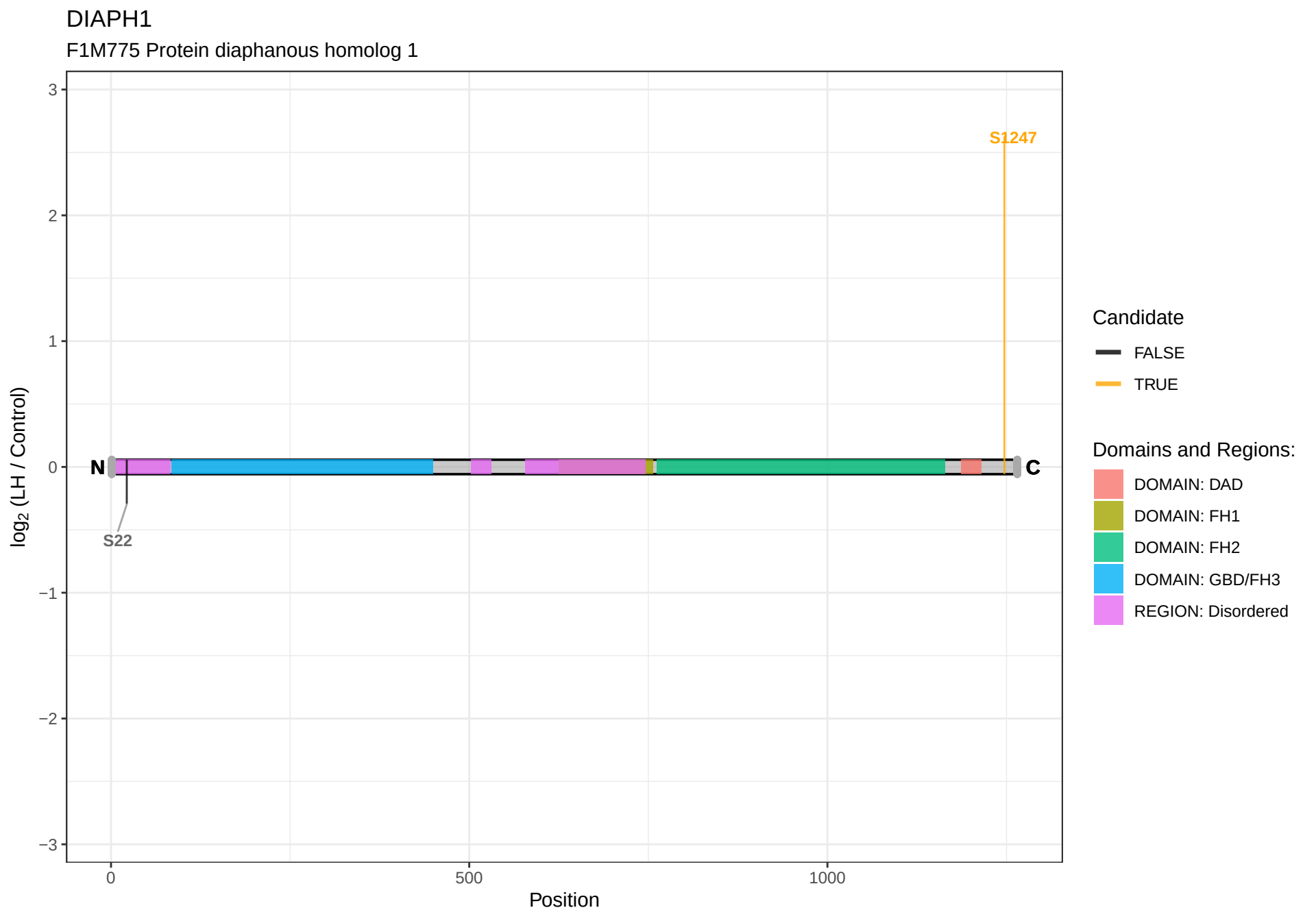

DENND1A
F1M241 DENN domain−containing 1A
S43
S547
S537
S539
T708
N
C
log2 (LH / Control)
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: UDENN
REGION: Disordered

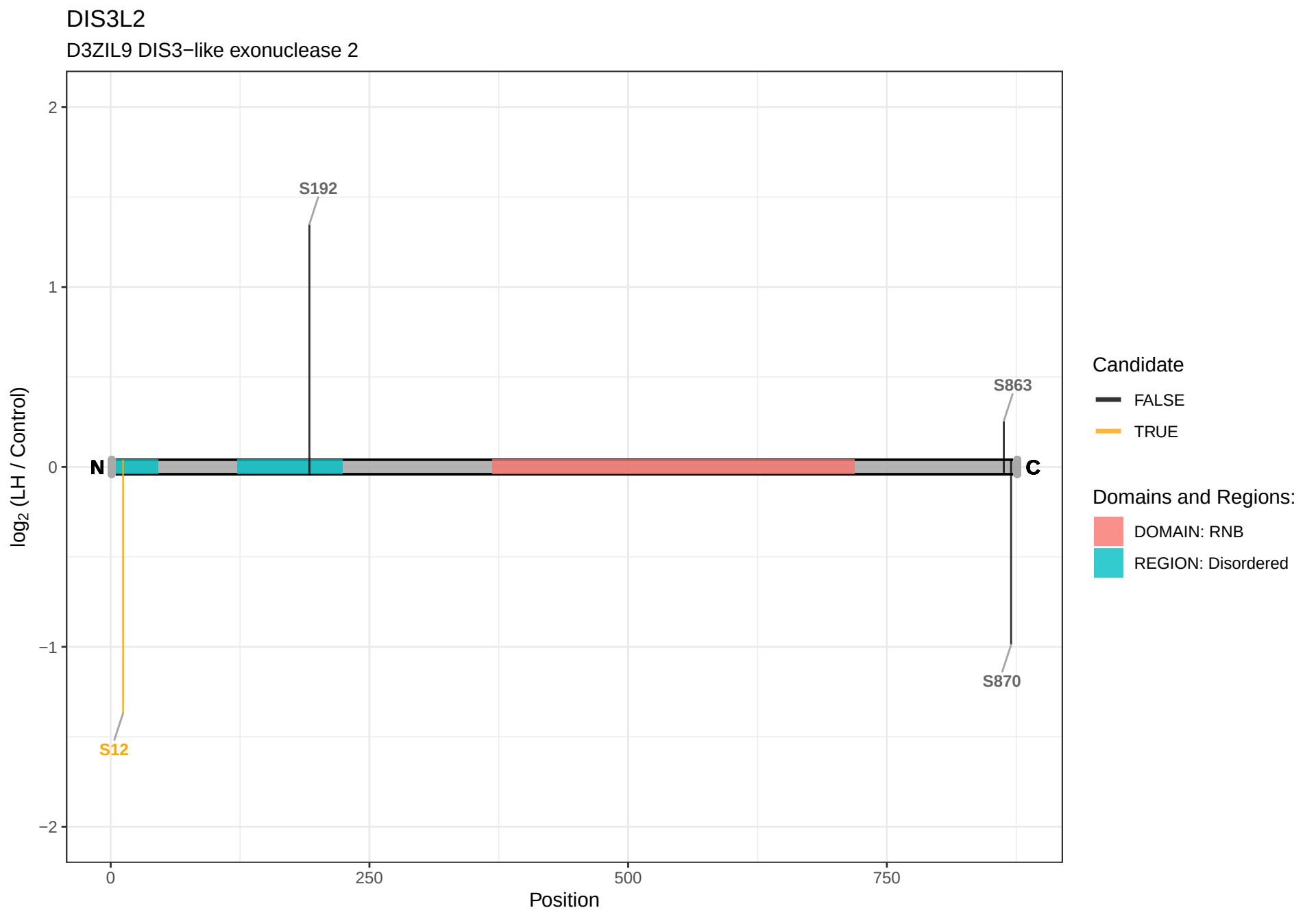

DENND4C
A0A0G2K089 DENN domain−containing 4C
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
Position
N
C
T965
S970
S1274
S1273
S1043
S1653
S1657
S1614
S1631
S986
S1613
S719
S739
S1287
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: MABP
DOMAIN: UDENN
REGION: Disordered

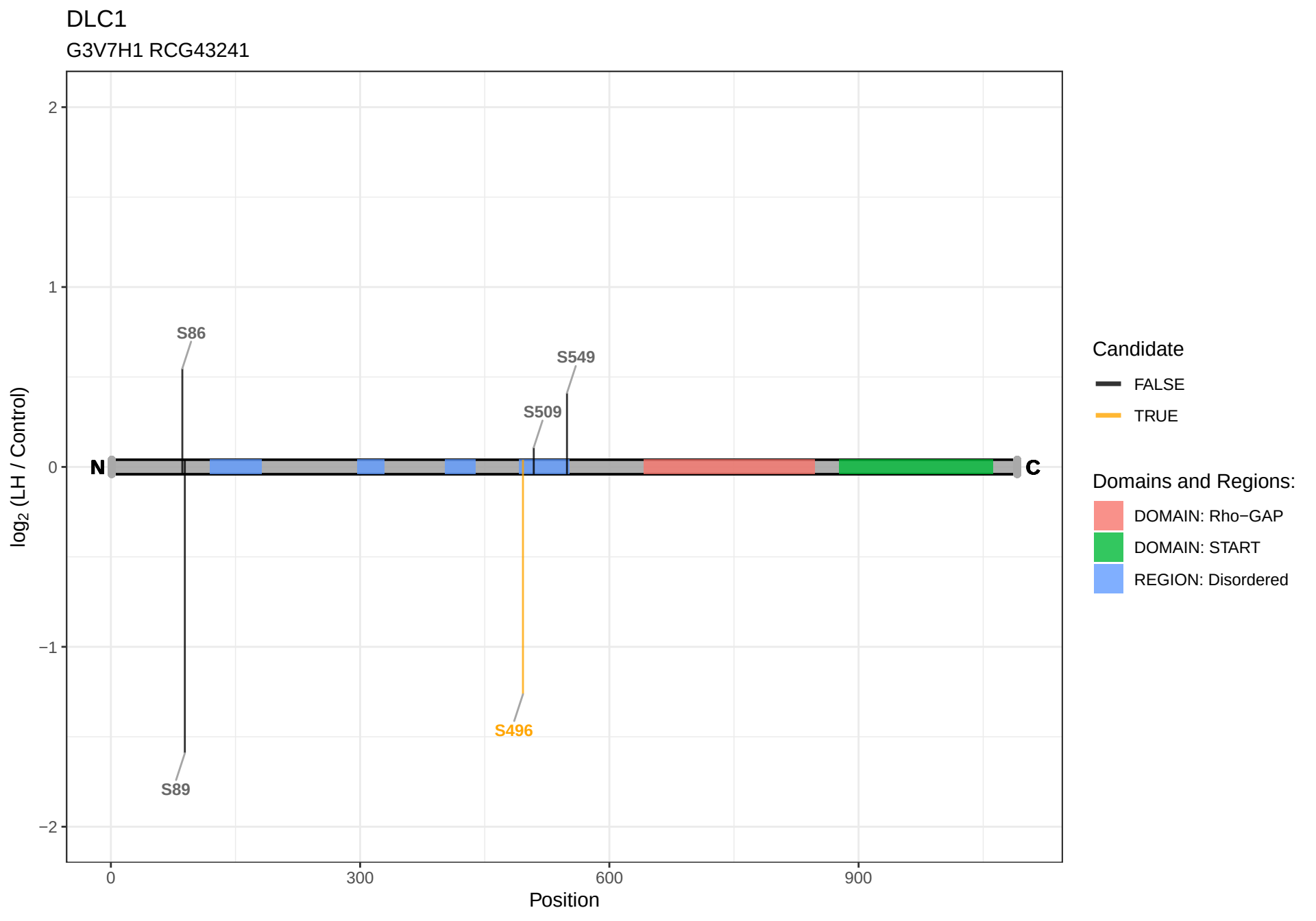

DENND5A
G3V7Q0 DENN domain−containing protein 5A
S836
T833
S193
N
C
S583
T1079
S1096
S1085
2
0
−2
log2 (LH / Control)
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: cDENN
DOMAIN: dDENN
DOMAIN: PLAT
DOMAIN: RUN 1
DOMAIN: RUN 2
DOMAIN: uDENN

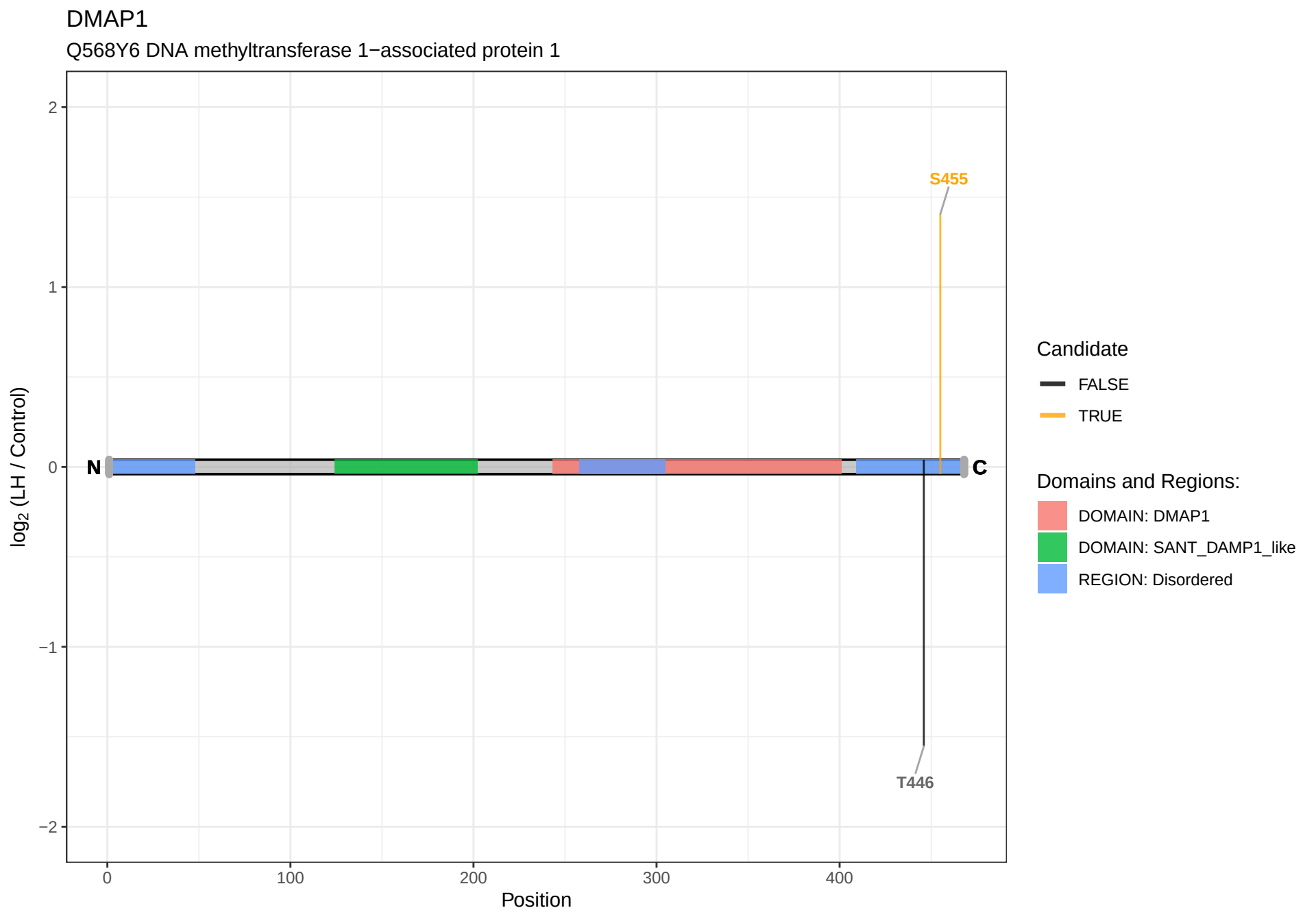

DEPTOR
F1M8Y4 DEP domain−containing MTOR−interacting protein
log2 (LH / Control)
2
1
0
−1
−2
N
C
S265
S244
0
100
200
300
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DEP
DOMAIN: PDZ
REGION: Disordered

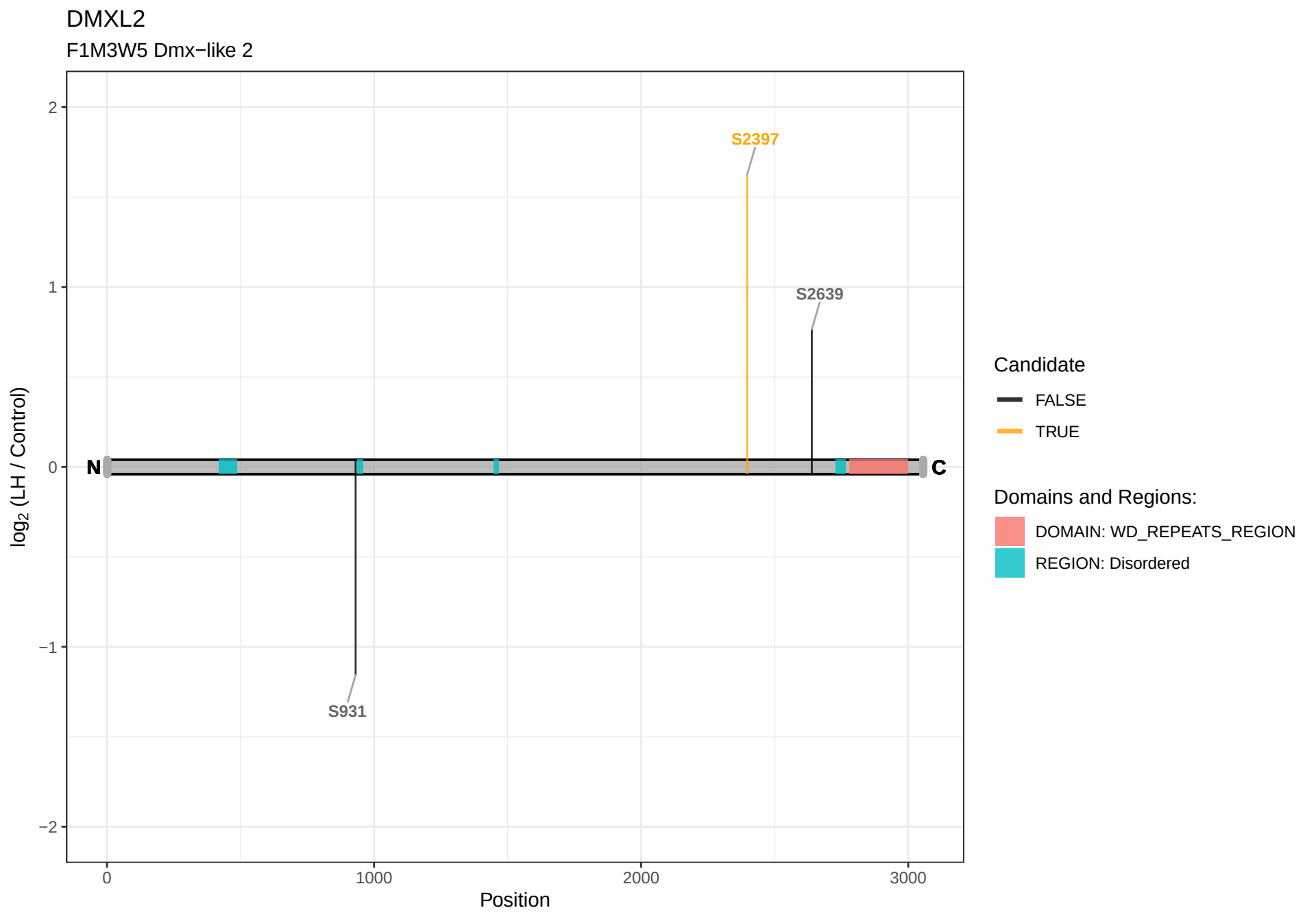

DGAT1
Q8BHI5 O−acyltransferase
S20
N
C
2
1
0
−1
−2
0
100
200
300
400
500
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
REGION: Disordered

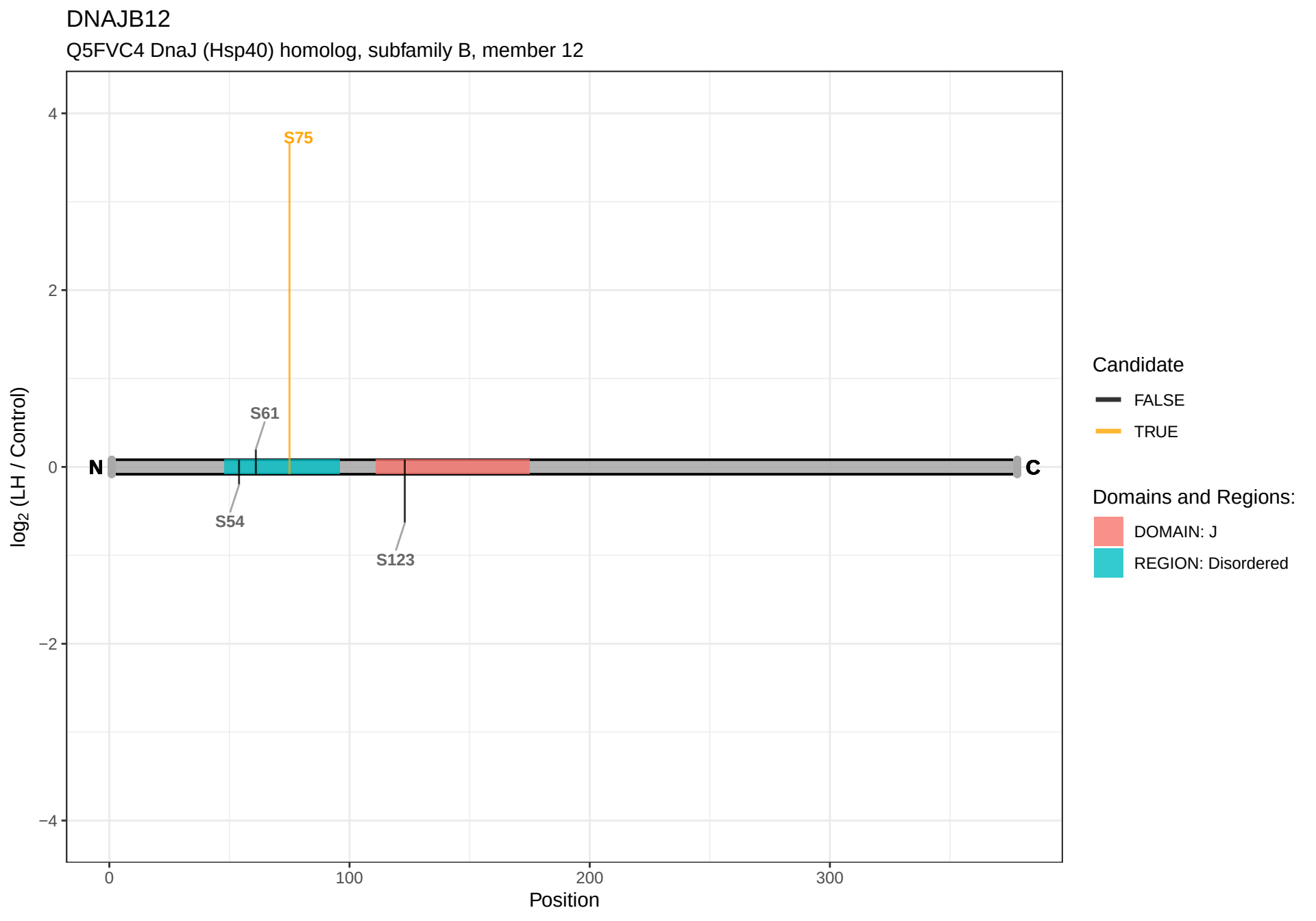

DIAPH1
F1M775 Protein diaphanous homolog 1
log2 (LH / Control)
3
2
1
0
−1
−2
−3
0
500
1000
Position
N
C
S1247
S22
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DAD
DOMAIN: FH1
DOMAIN: FH2
DOMAIN: GBD/FH3
REGION: Disordered

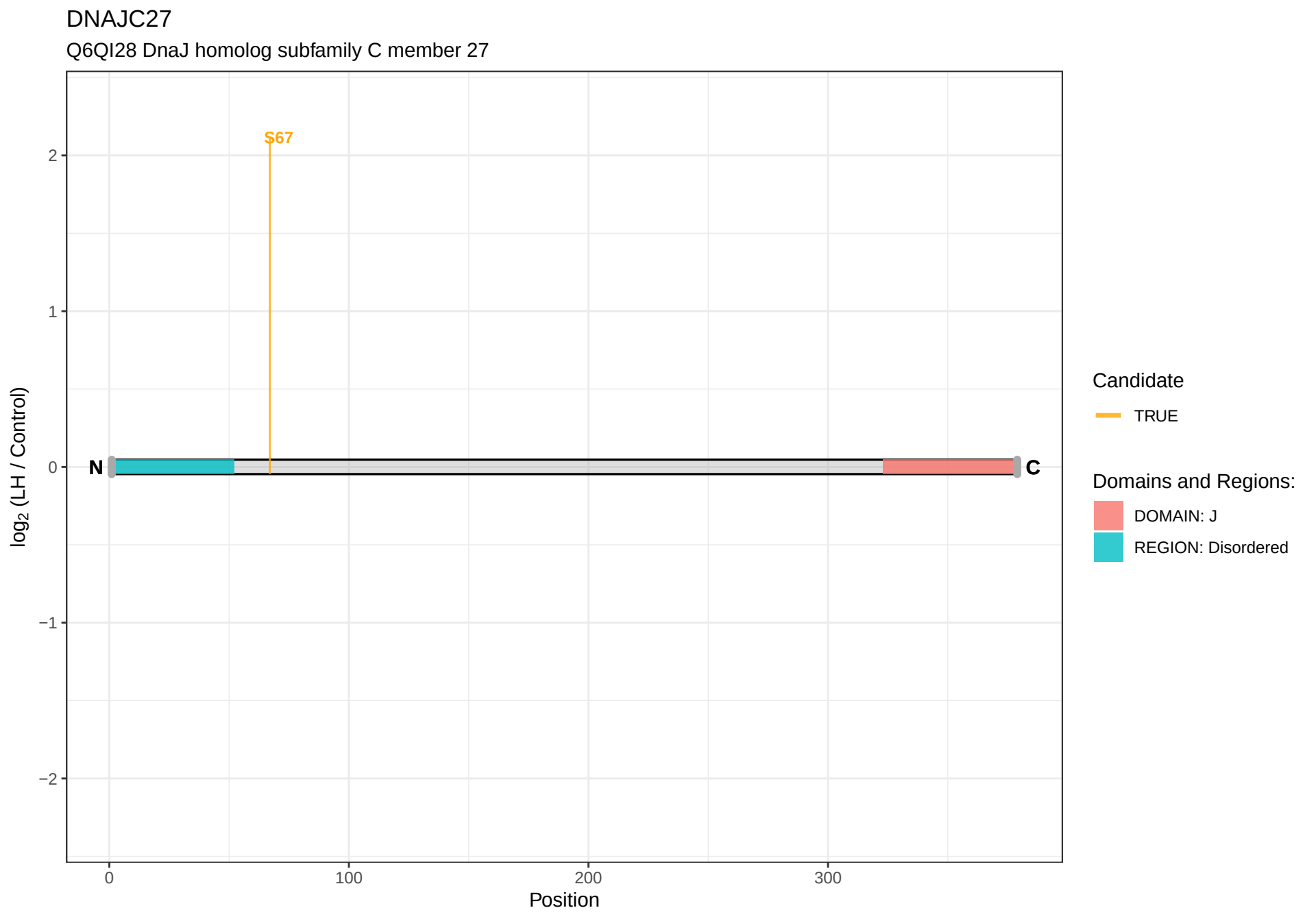

DIS3L2
D3ZIL9 DIS3−like exonuclease 2
log2 (LH / Control)
2
1
0
−1
−2
S192
S863
S870
S12
N
C
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RNB
REGION: Disordered

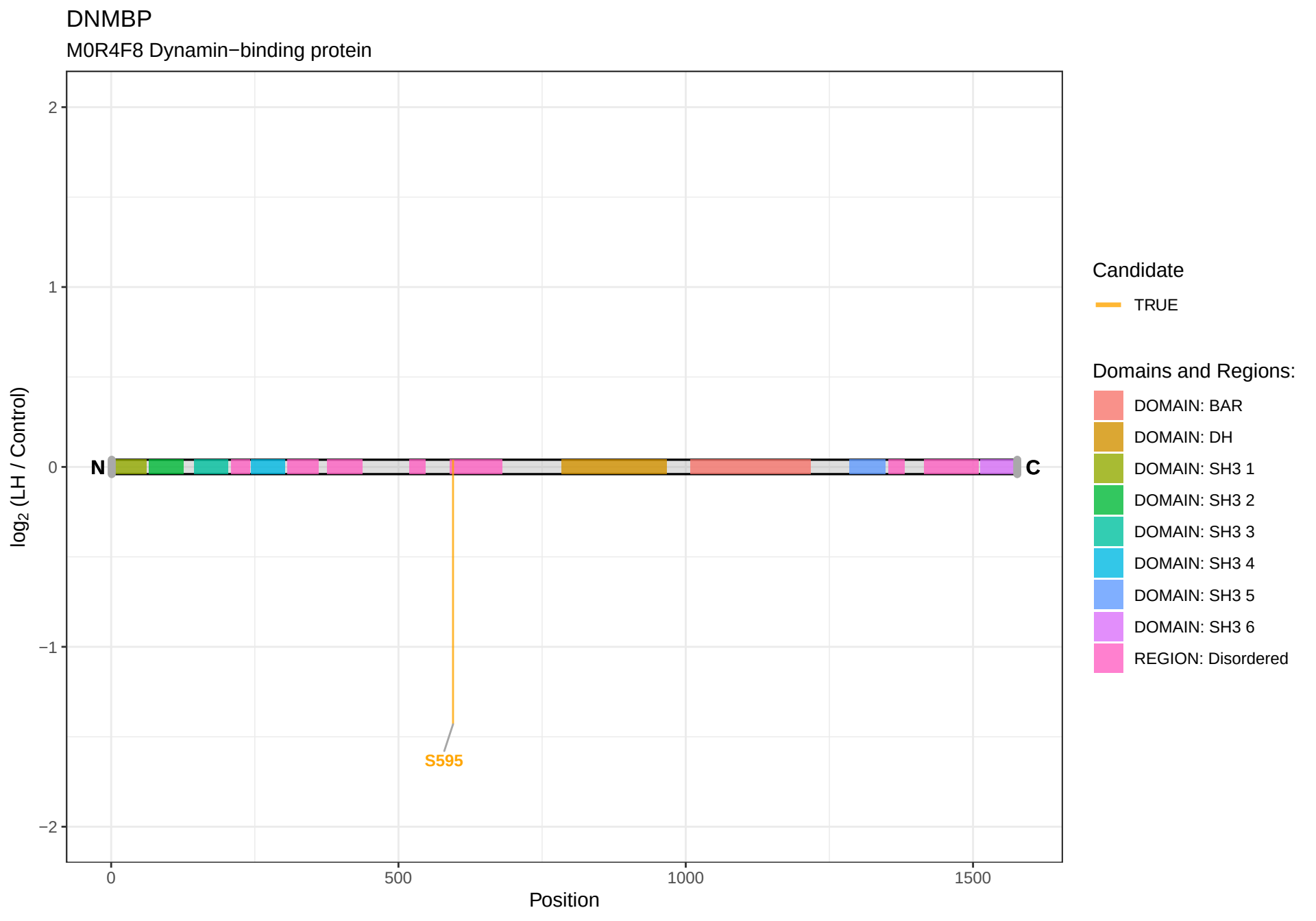

DLC1
G3V7H1 RCG43241
2
1
0
−1
−2
log2 (LH / Control)
S86
S549
S509
S496
S89
N
C
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Rho−GAP
DOMAIN: START
REGION: Disordered

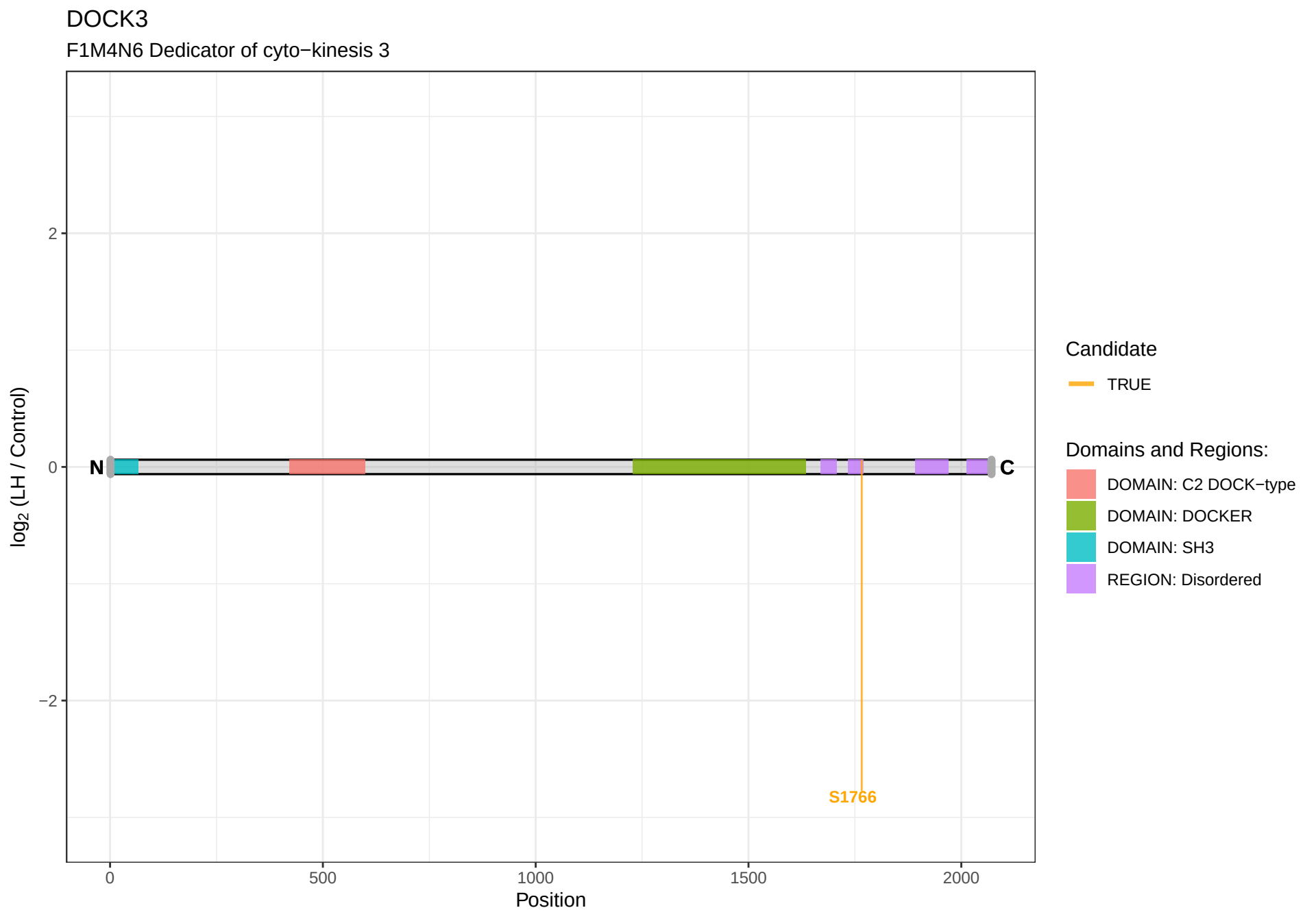

DMAP1
Q568Y6 DNA methyltransferase 1−associated protein 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S455
T446
0
100
200
300
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DMAP1
DOMAIN: SANT_DAMP1_like
REGION: Disordered

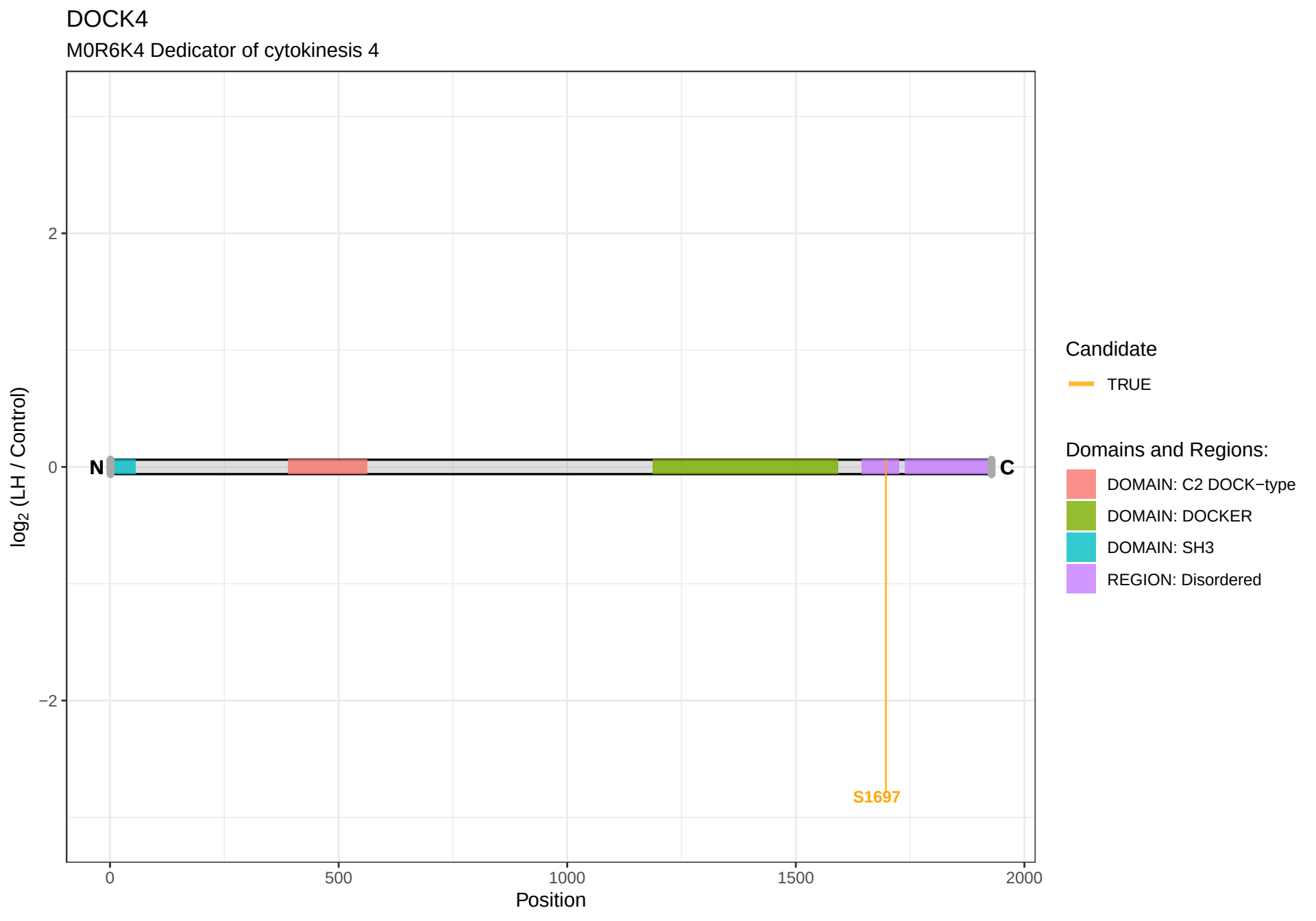

DMXL2
F1M3W5 Dmx−like 2
S2397
S2639
S931
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
1000
2000
3000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WD_REPEATS_REGION
REGION: Disordered

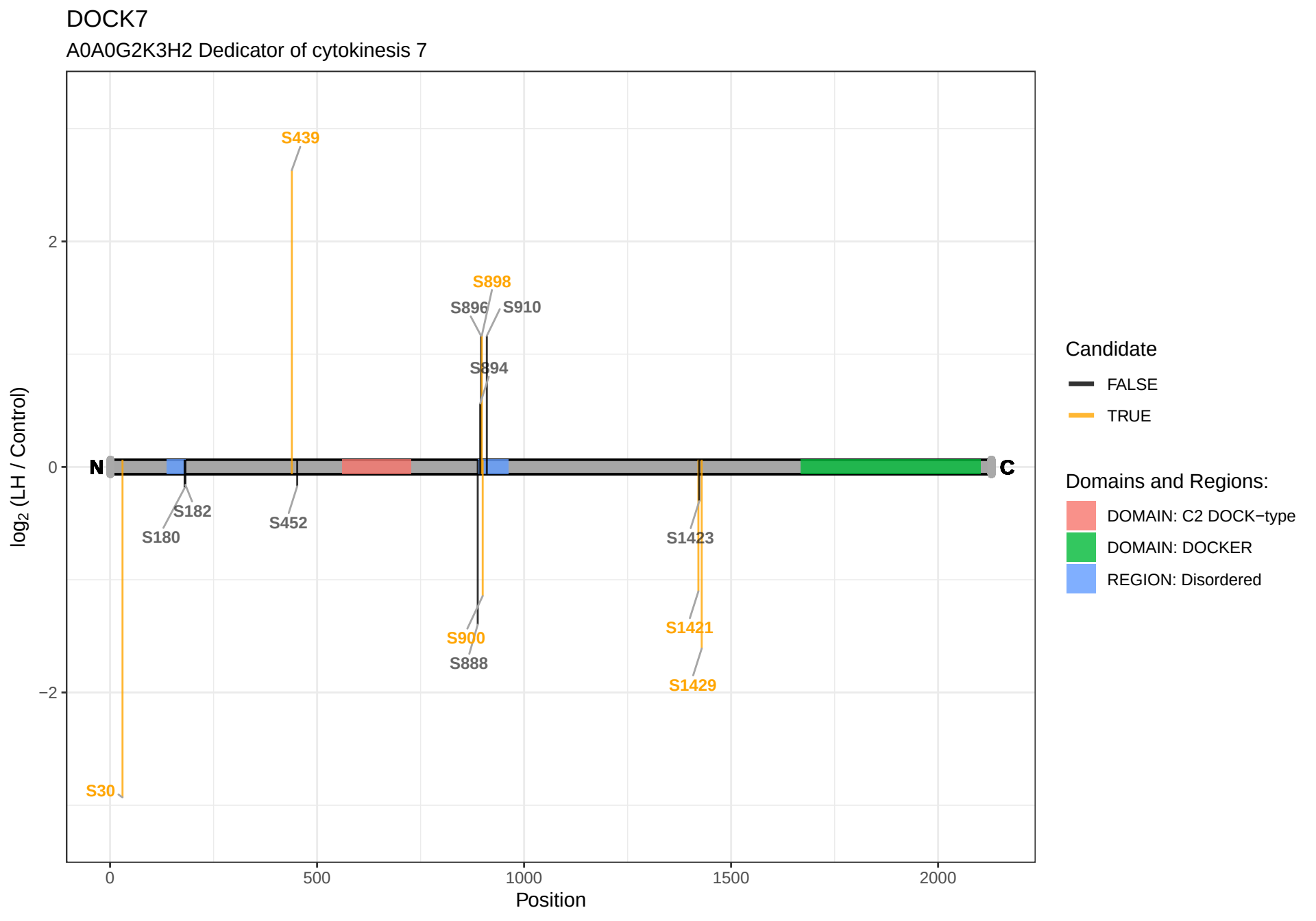

DNAJB12
Q5FVC4 DnaJ (Hsp40) homolog, subfamily B, member 12
S75
S61
S54
S123
N
C
4
2
0
−2
−4
log2 (LH / Control)
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: J
REGION: Disordered

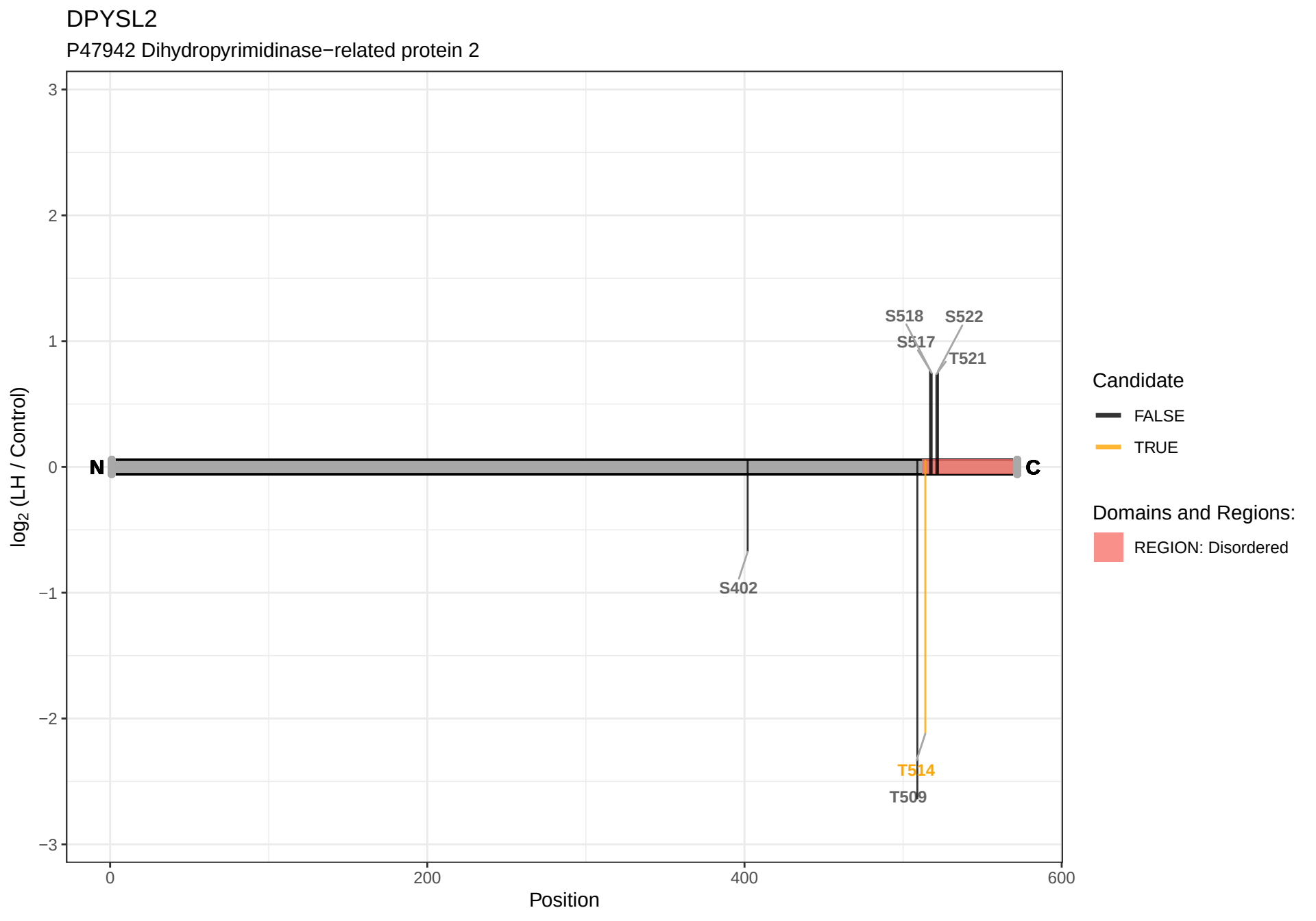

DNAJC27
Q6QI28 DnaJ homolog subfamily C member 27
S67
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: J
REGION: Disordered

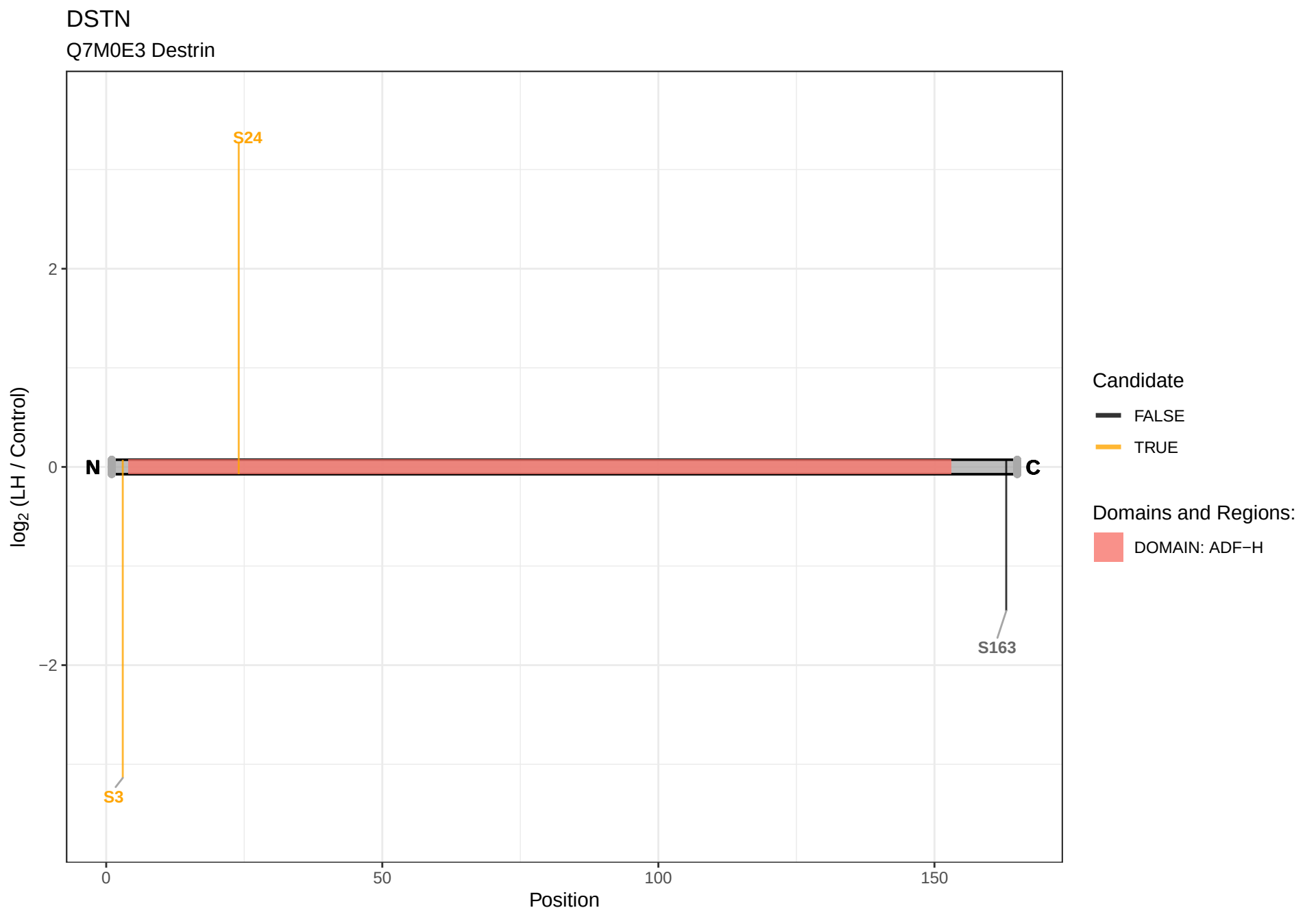

DNMBP
M0R4F8 Dynamin−binding protein
log2 (LH / Control)
2
1
0
−1
−2
N
C
S595
0
500
1000
1500
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: BAR
DOMAIN: DH
DOMAIN: SH3 1
DOMAIN: SH3 2
DOMAIN: SH3 3
DOMAIN: SH3 4
DOMAIN: SH3 5
DOMAIN: SH3 6
REGION: Disordered

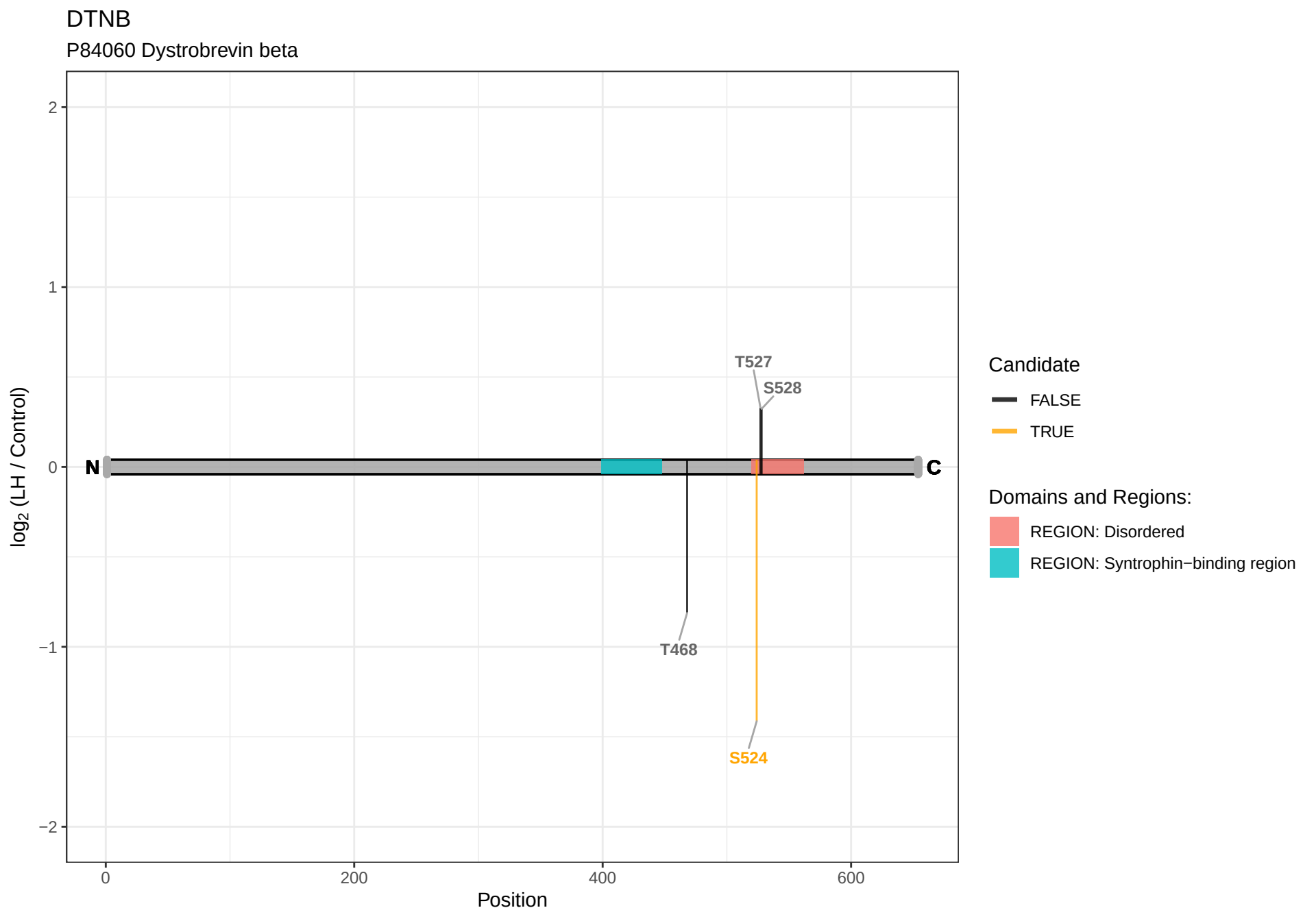

DOCK3
F1M4N6 Dedicator of cyto−kinesis 3
log2 (LH / Control)
2
0
−2
N
C
S1766
0
500
1000
1500
2000
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: C2 DOCK−type
DOMAIN: DOCKER
DOMAIN: SH3
REGION: Disordered

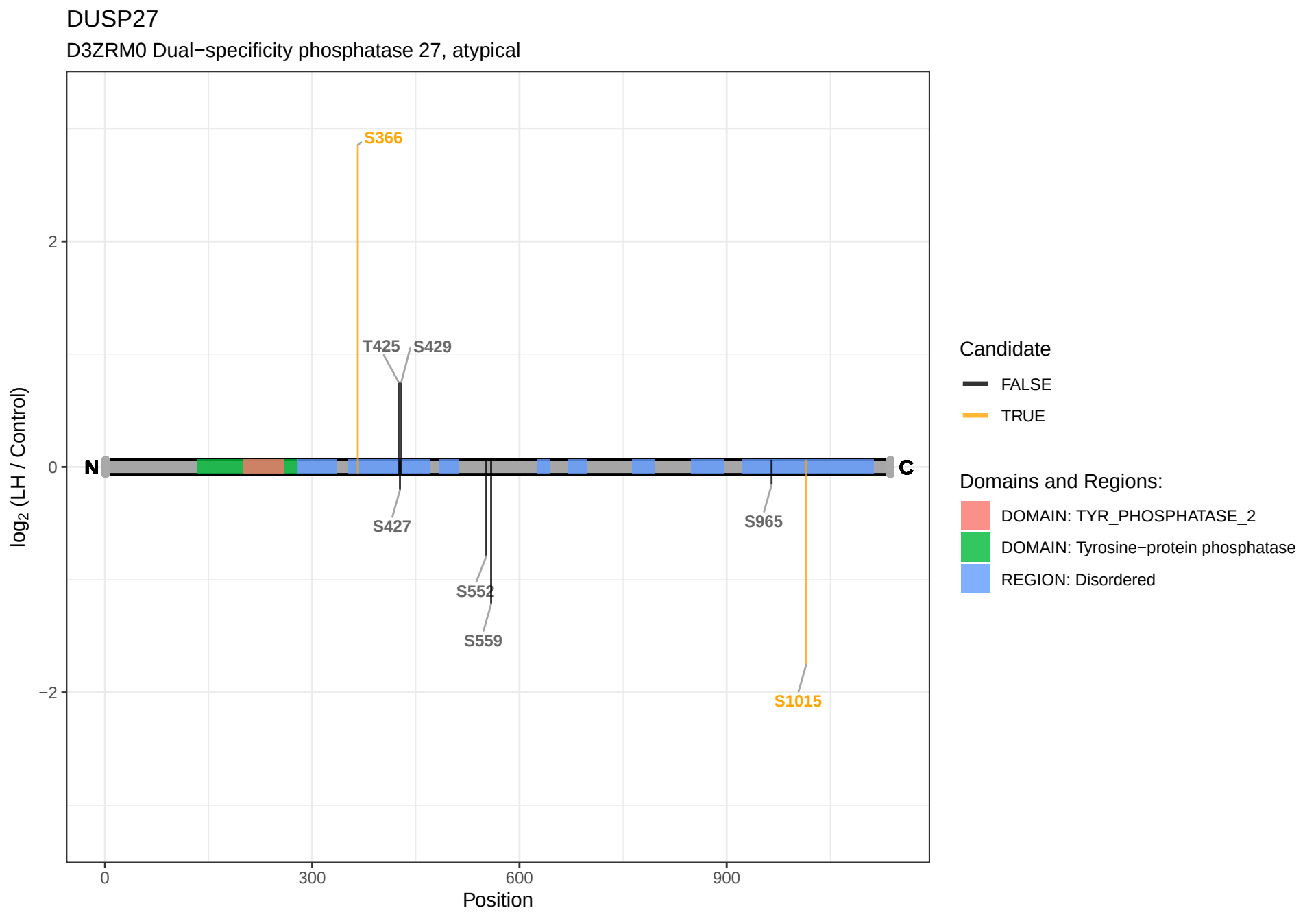

DOCK4
M0R6K4 Dedicator of cytokinesis 4
log2 (LH / Control)
2
0
−2
N
C
S1697
0
500
1000
1500
2000
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: C2 DOCK−type
DOMAIN: DOCKER
DOMAIN: SH3
REGION: Disordered

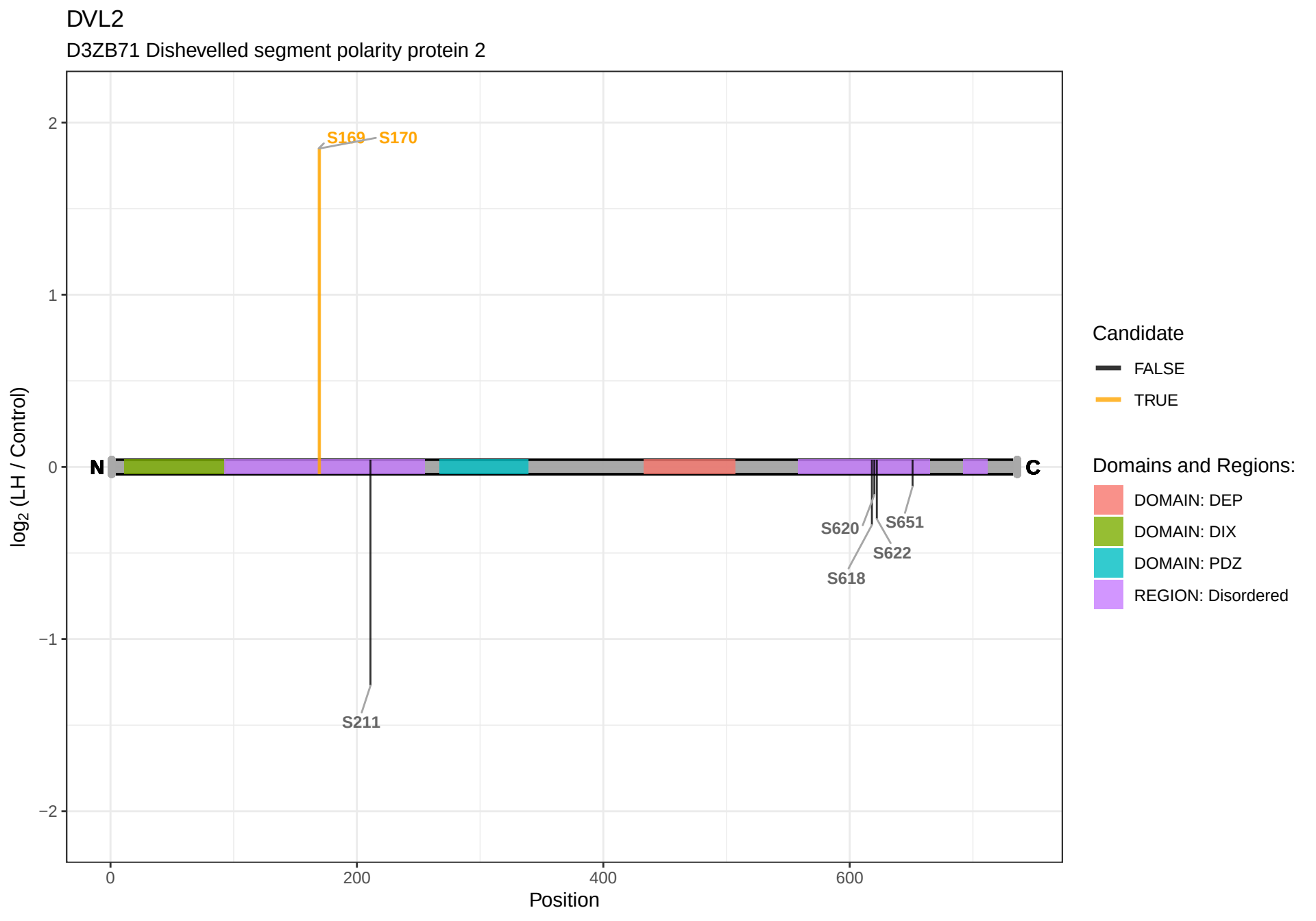

DOCK7
A0A0G2K3H2 Dedicator of cytokinesis 7
S439
S898
S896
S910
S894
S182
S180
S452
S1423
S900
S888
S1421
S1429
S30
N
C
2
0
−2
0
500
1000
1500
2000
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2 DOCK−type
DOMAIN: DOCKER
REGION: Disordered

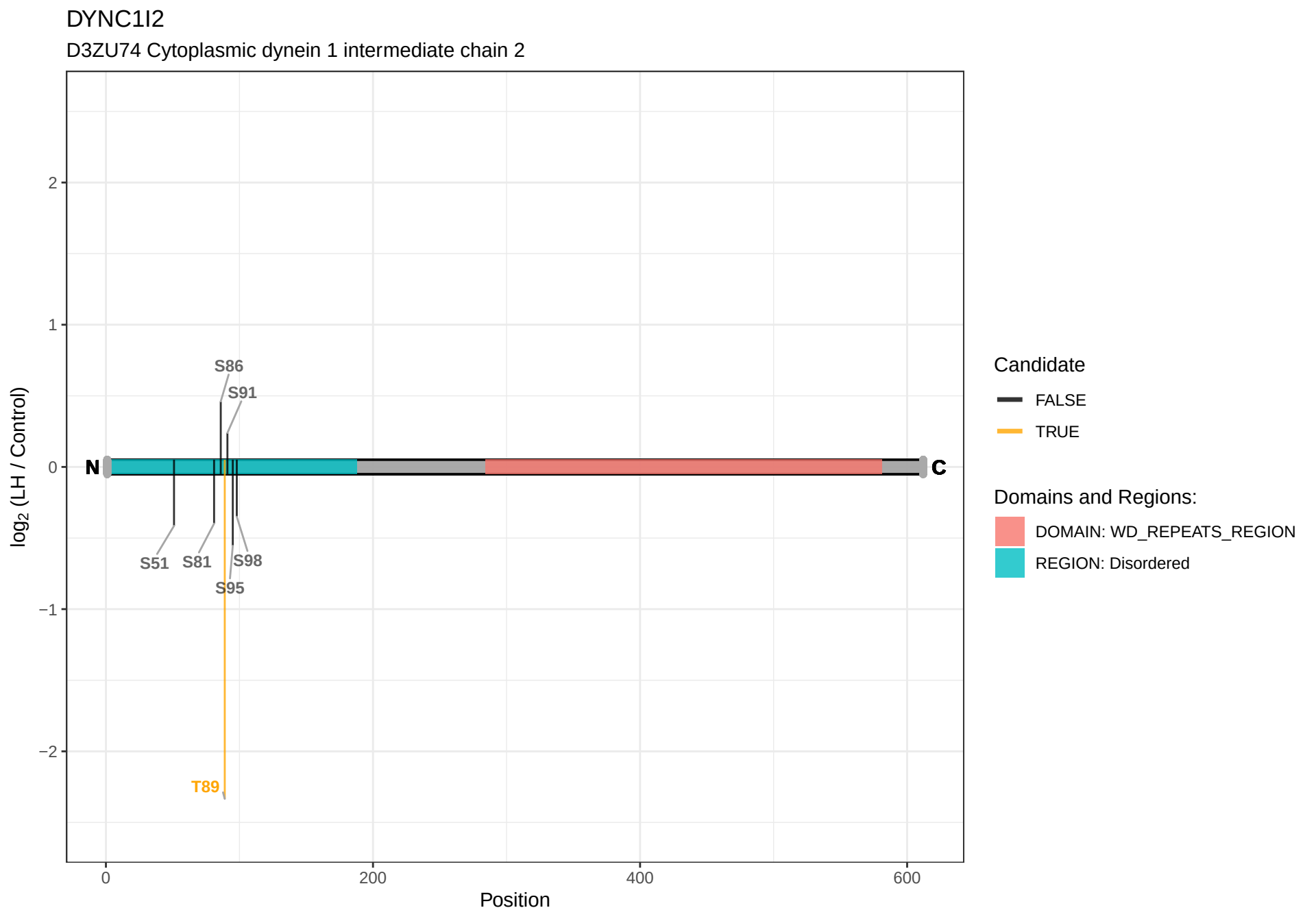

DPYSL2
P47942 Dihydropyrimidinase−related protein 2
log2 (LH / Control)
3
2
1
0
−1
−2
−3
0
200
400
600
Position
N
C
S518
S522
S517
T521
S402
T514
T509
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

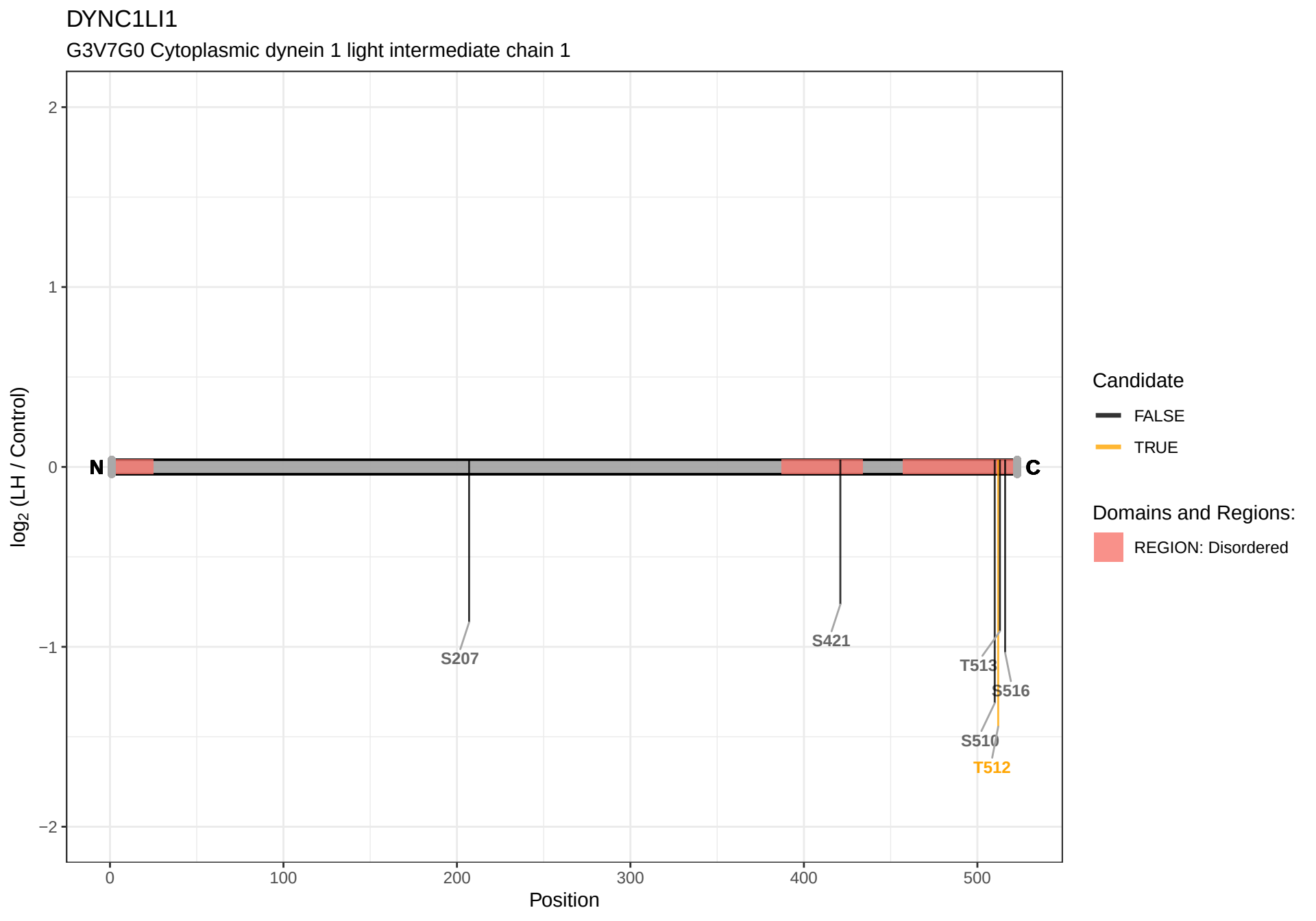

DSTN
Q7M0E3 Destrin
S24
S3
S163
N
C
2
0
−2
log2 (LH / Control)
0
50
100
150
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ADF−H

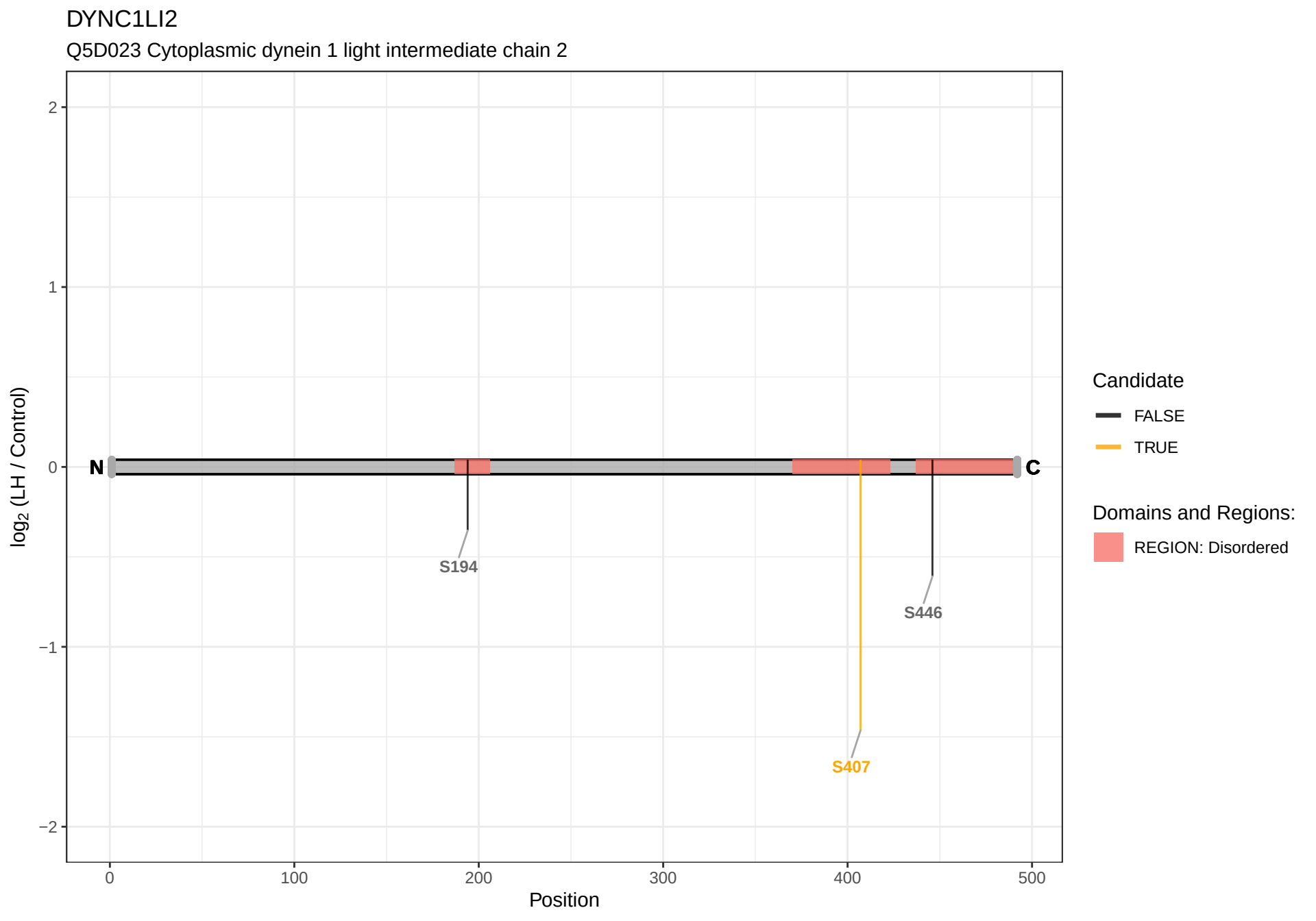

DTNB
P84060 Dystrobrevin beta
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
N
C
T527
S528
T468
S524
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Syntrophin−binding region

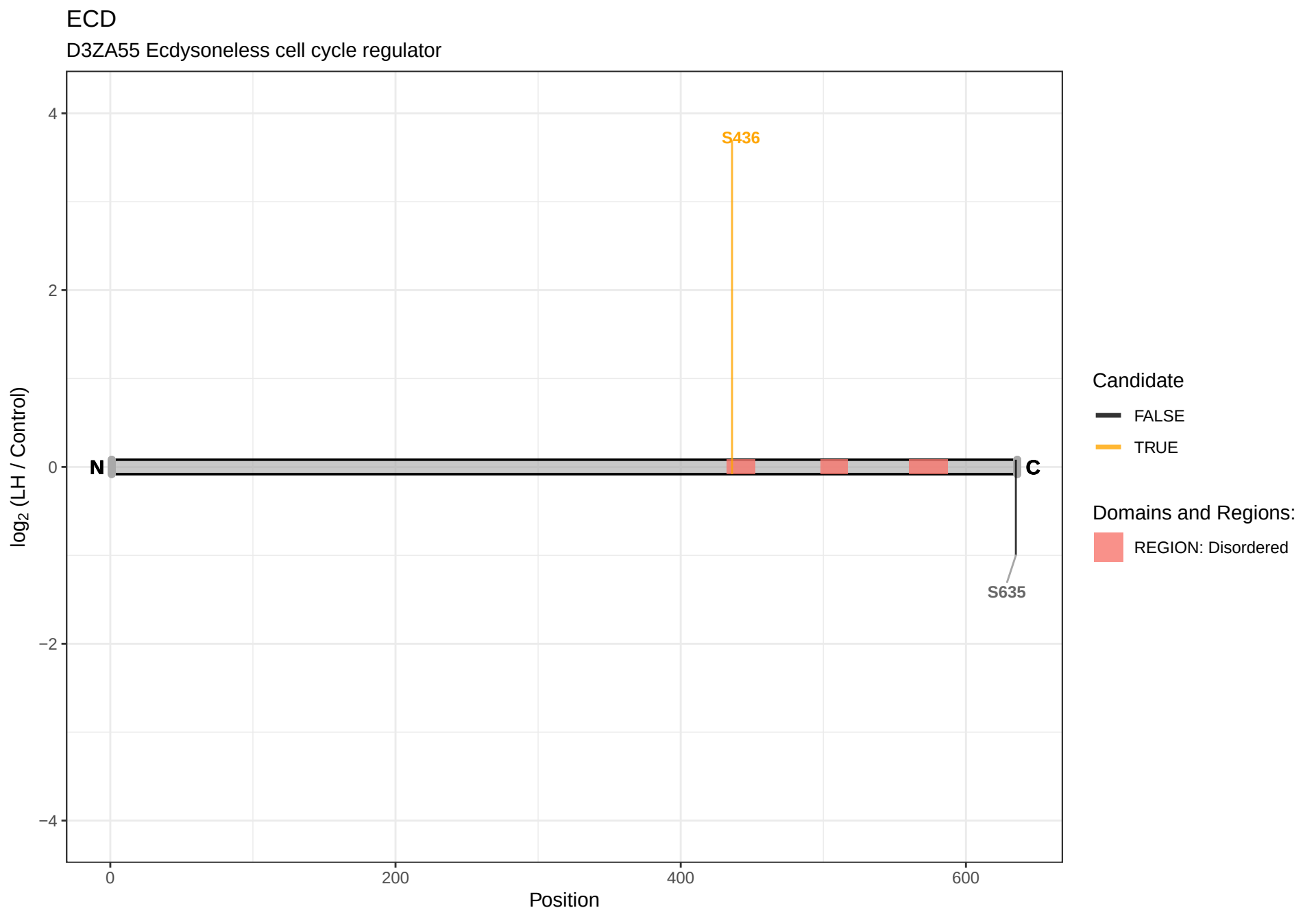

DUSP27
D3ZRM0 Dual−specificity phosphatase 27, atypical
S366
T425
S429
S427
S552
S559
S965
S1015
N
C
2
0
−2
log2 (LH / Control)
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: TYR_PHOSPHATASE_2
DOMAIN: Tyrosine−protein phosphatase
REGION: Disordered

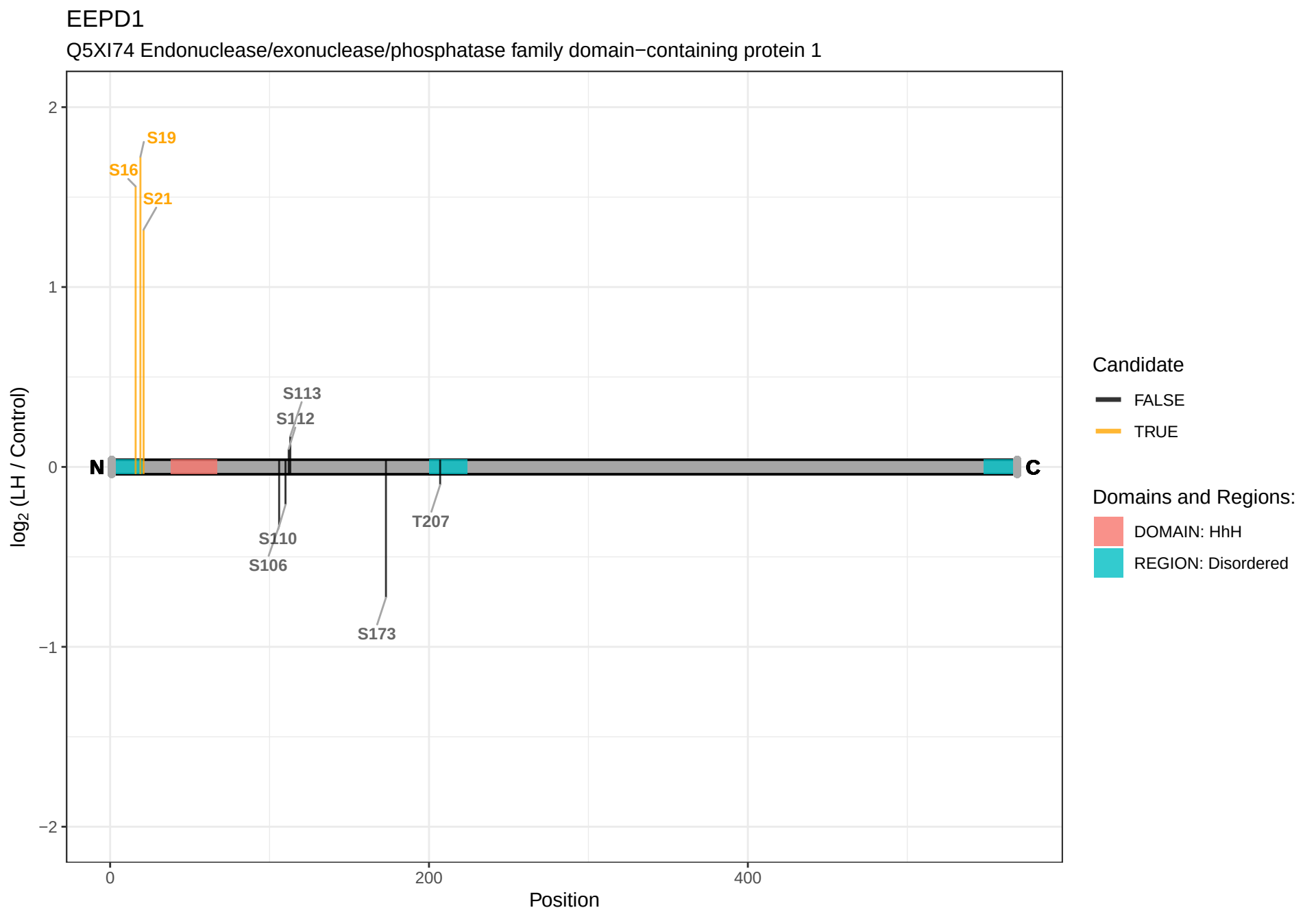

DVL2
D3ZB71 Dishevelled segment polarity protein 2
S169
S170
S211
S620
S622
S618
S651
N
C
log2 (LH / Control)
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DEP
DOMAIN: DIX
DOMAIN: PDZ
REGION: Disordered

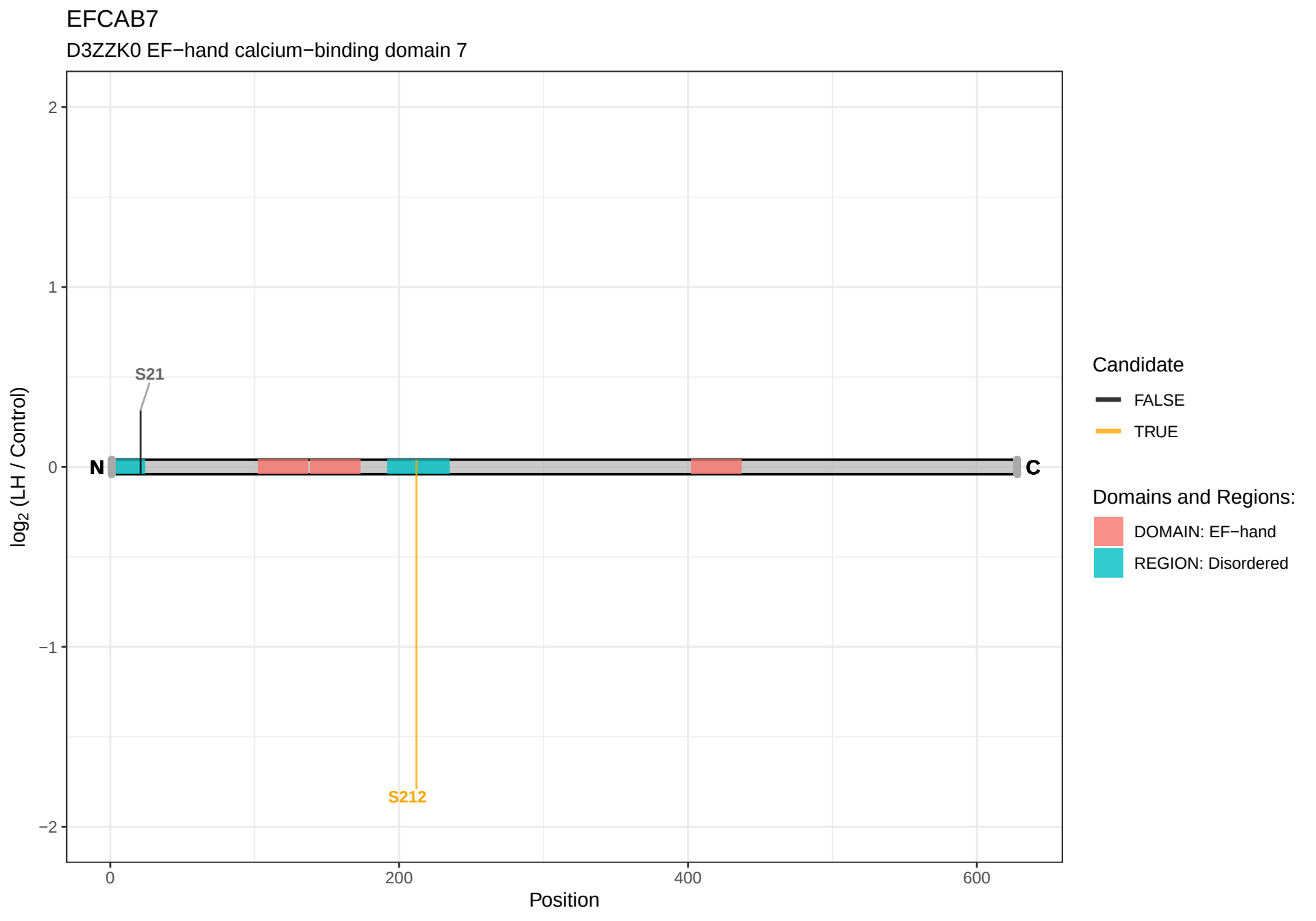

DYNC1I2
D3ZU74 Cytoplasmic dynein 1 intermediate chain 2
log2 (LH / Control)
2
1
0
−1
−2
N
C
S86
S91
S51
S81
S98
S95
T89
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WD_REPEATS_REGION
REGION: Disordered

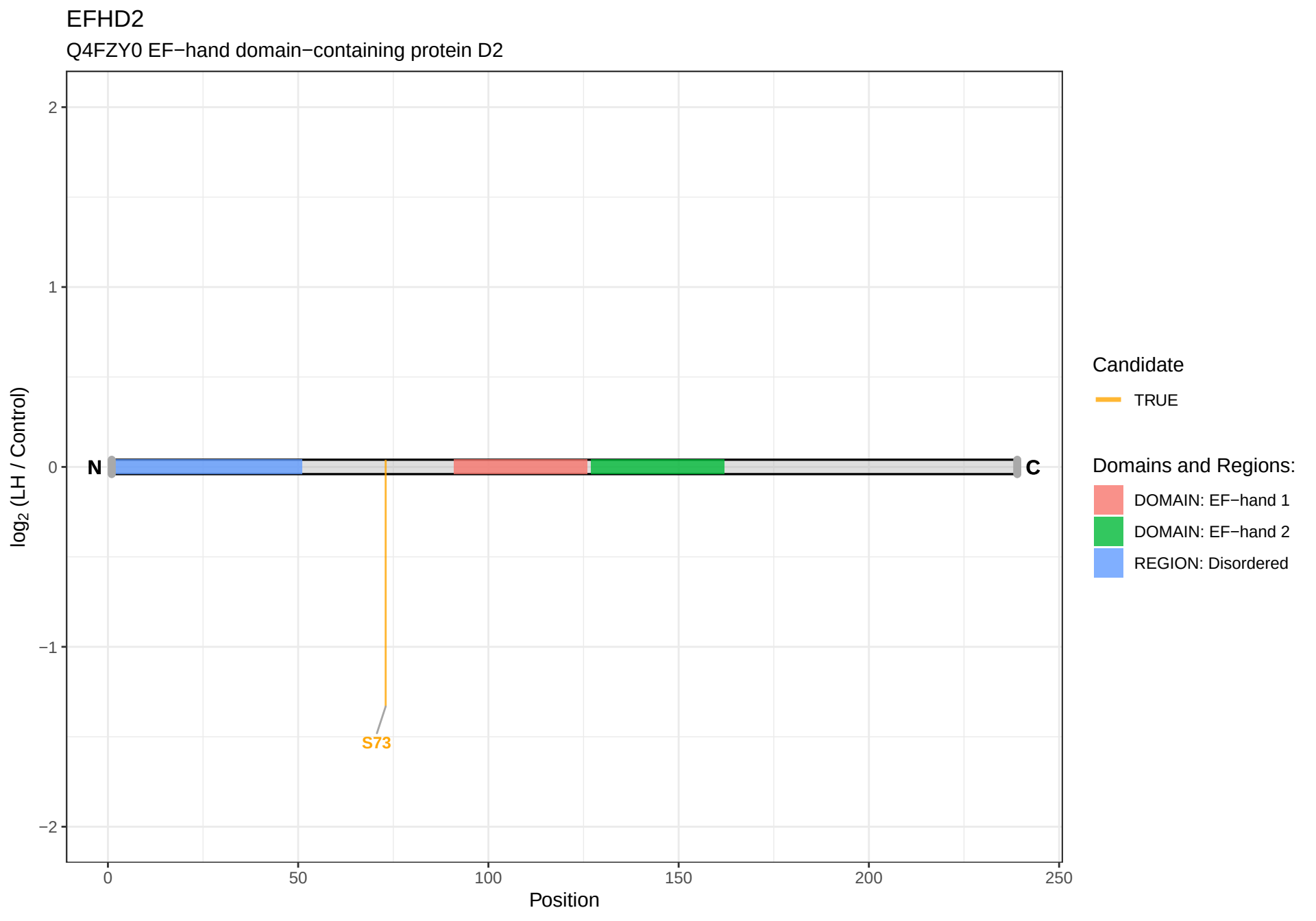

DYNC1LI1
G3V7G0 Cytoplasmic dynein 1 light intermediate chain 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S207
S421
T513
S516
S510
T512
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

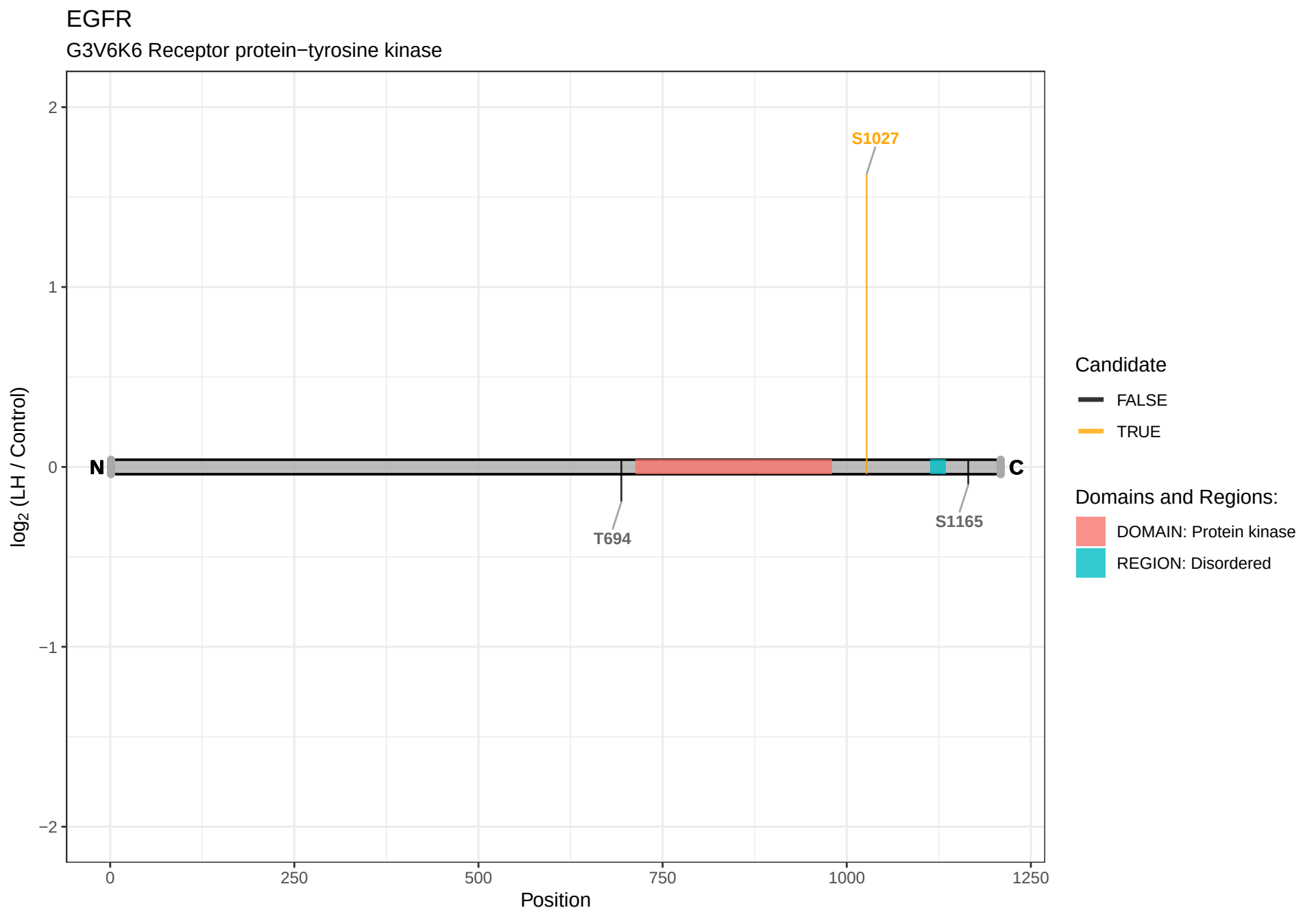

DYNC1LI2
Q5D023 Cytoplasmic dynein 1 light intermediate chain 2
log2 (LH / Control)
2
1
0
−1
−2
N
C
S194
S446
S407
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

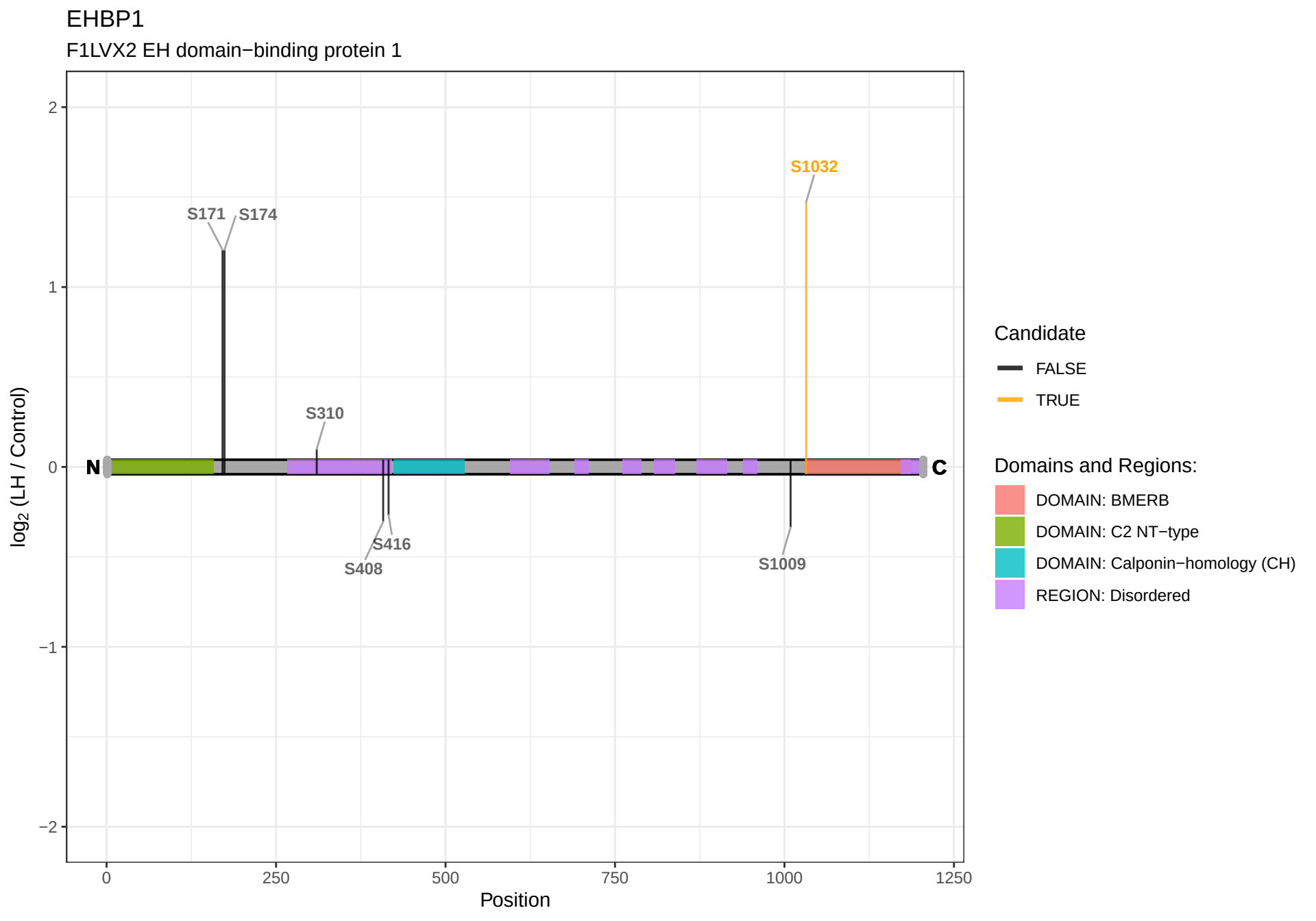

ECD
D3ZA55 Ecdysoneless cell cycle regulator
S436
S635
N
C
4
2
0
−2
−4
0
200
400
600
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

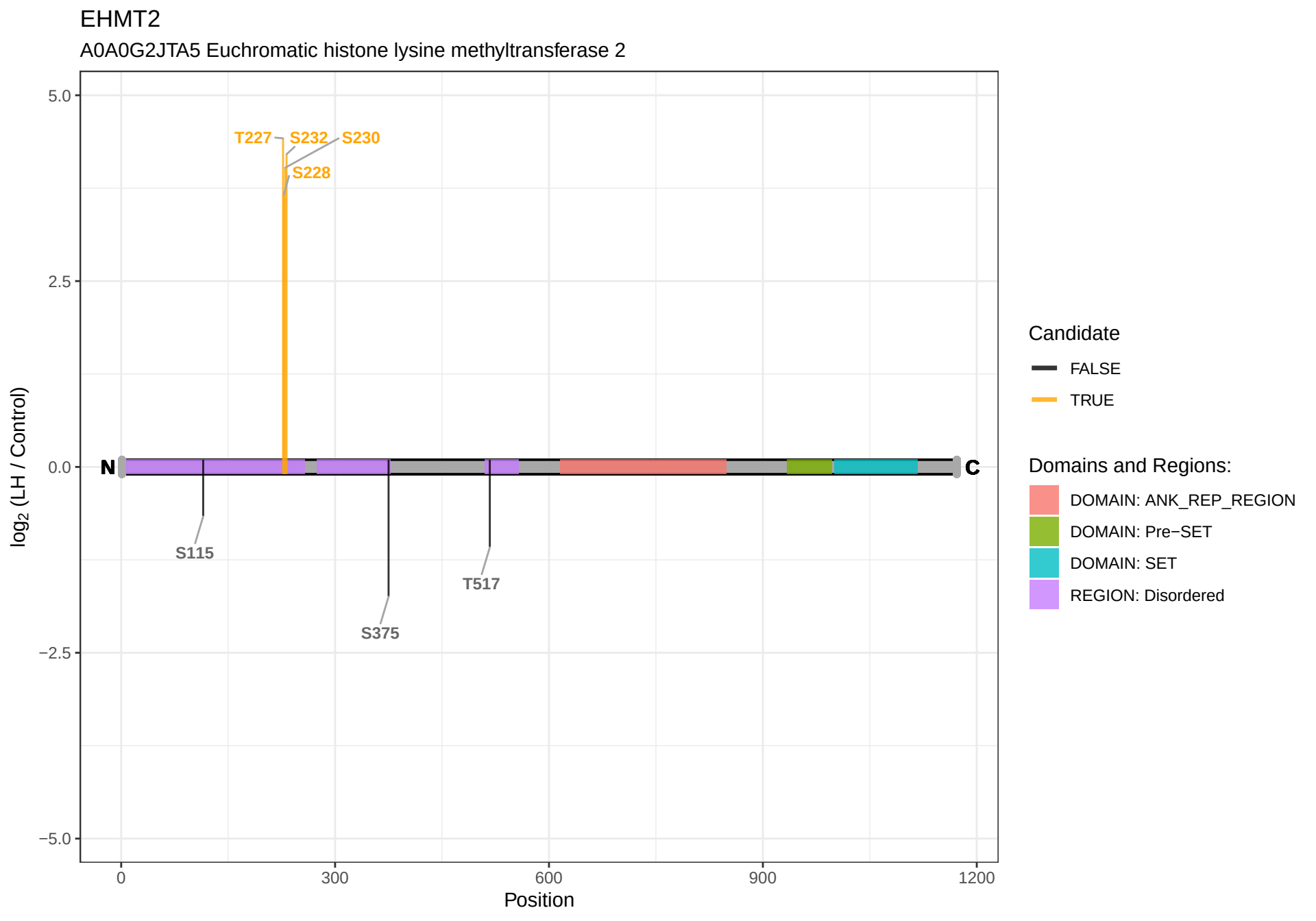

EEPD1
Q5XI74 Endonuclease/exonuclease/phosphatase family domain−containing protein 1
log2 (LH / Control)
2
1
0
−1
−2
S19
S16
S21
S113
S112
N
C
S110
S106
T207
S173
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: HhH
REGION: Disordered

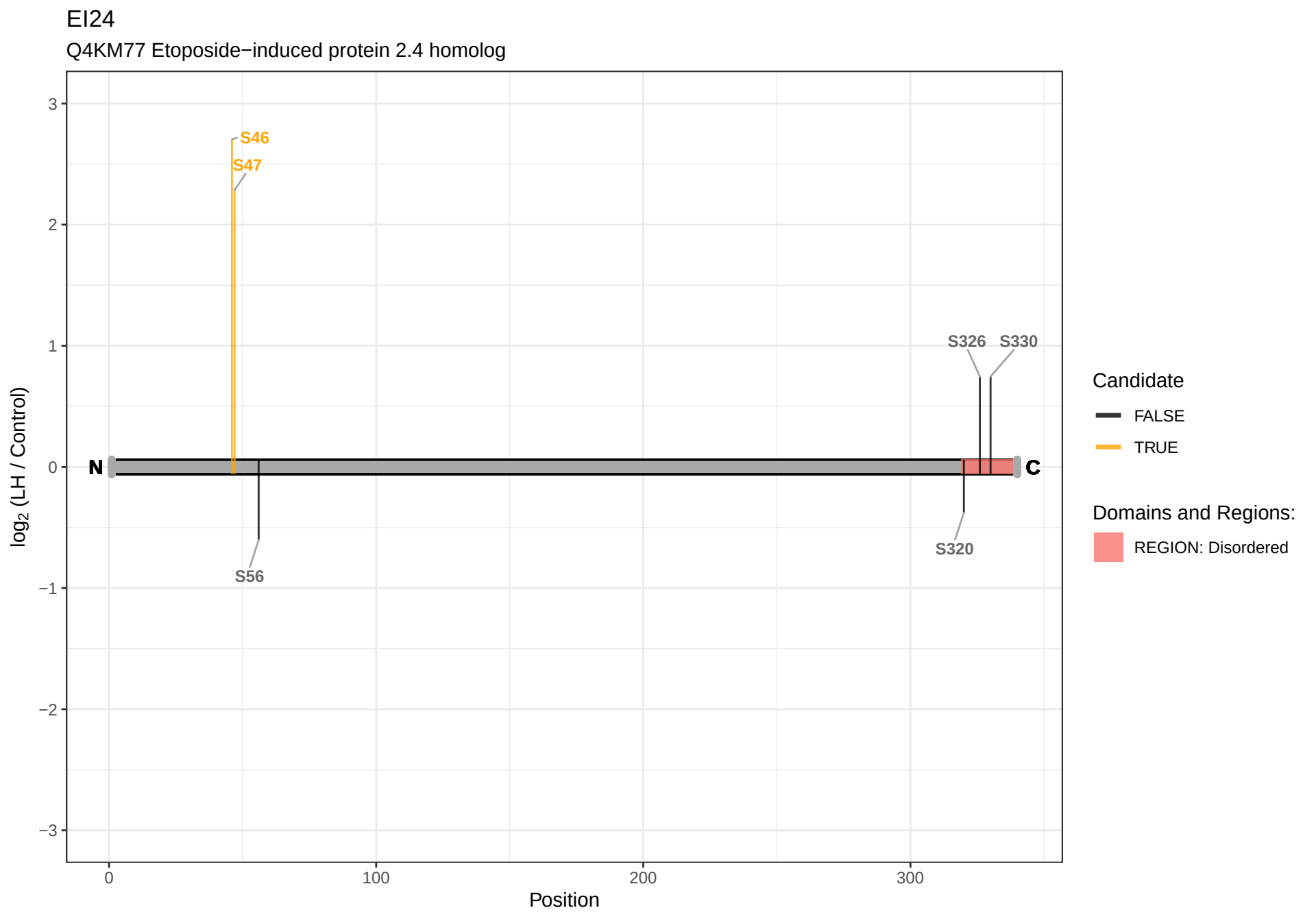

EFCAB7
D3ZZK0 EF−hand calcium−binding domain 7
log2 (LH / Control)
2
1
0
−1
−2
S21
S212
N
C
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: EF−hand
REGION: Disordered

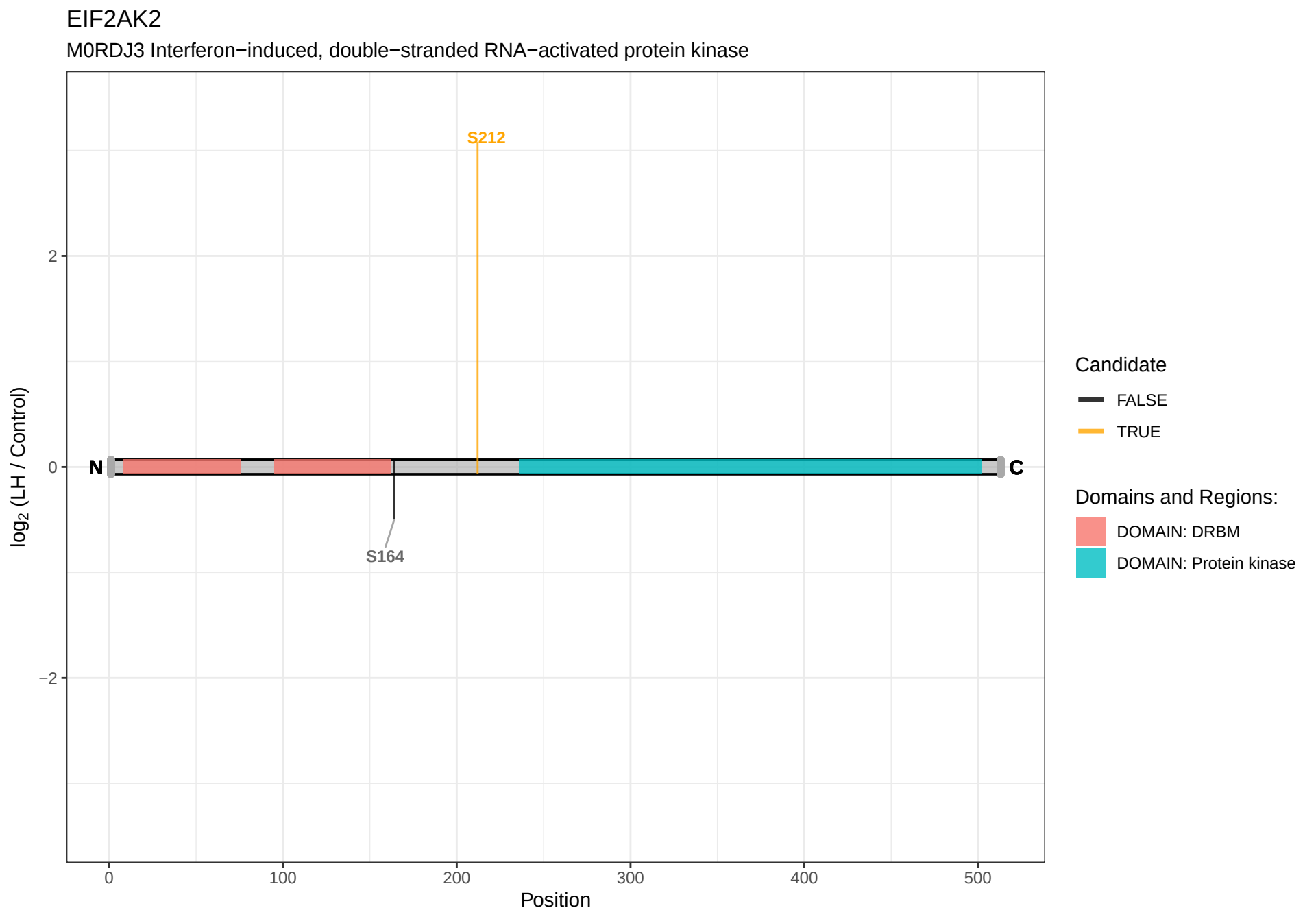

EFHD2
Q4FZY0 EF−hand domain−containing protein D2
log2 (LH / Control)
2
1
0
−1
−2
N
C
S73
0
50
100
150
200
250
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: EF−hand 1
DOMAIN: EF−hand 2
REGION: Disordered

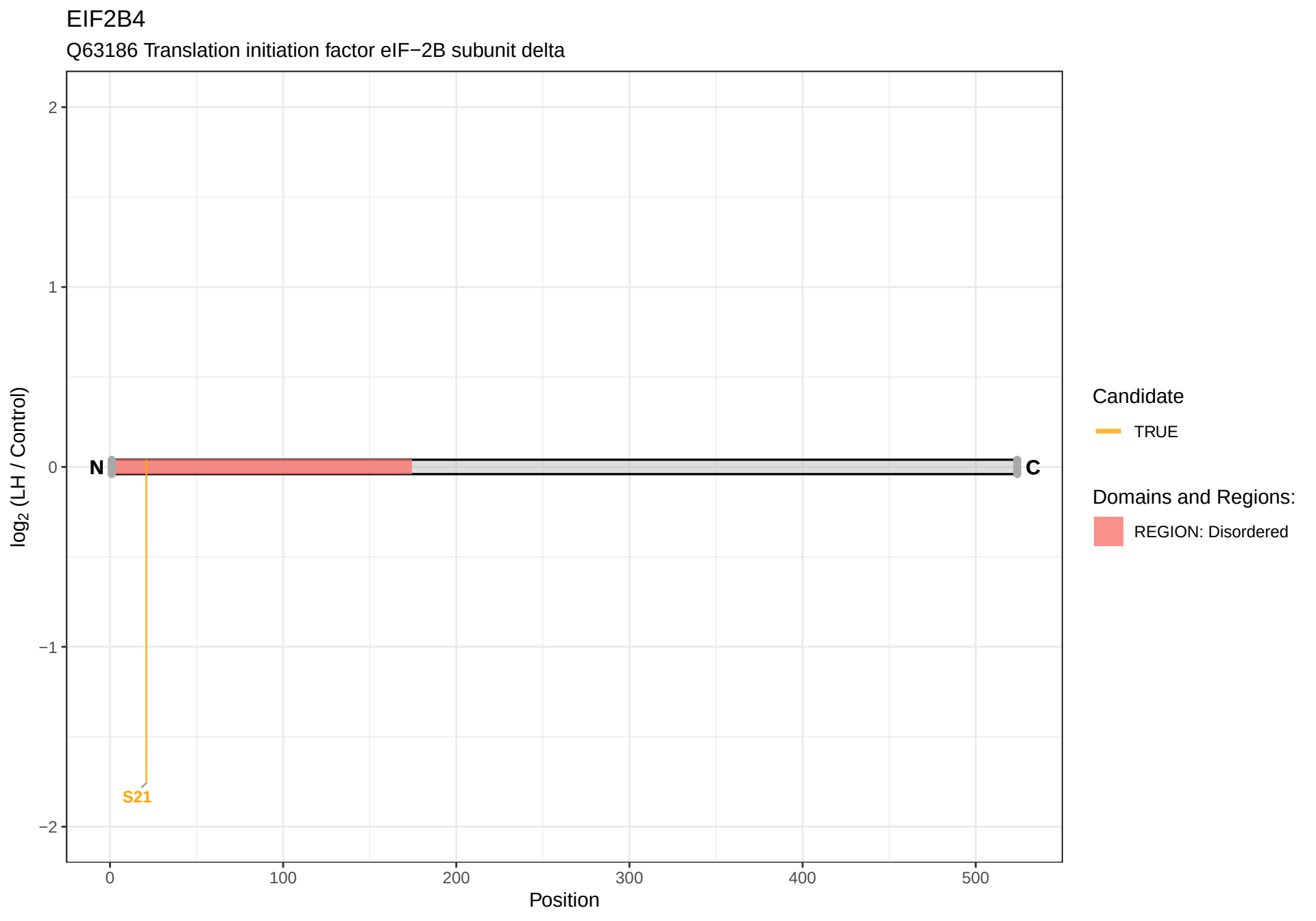

EGFR
G3V6K6 Receptor protein−tyrosine kinase
log2 (LH / Control)
2
1
0
−1
−2
S1027
N
C
T694
S1165
0
250
500
750
1000
1250
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered

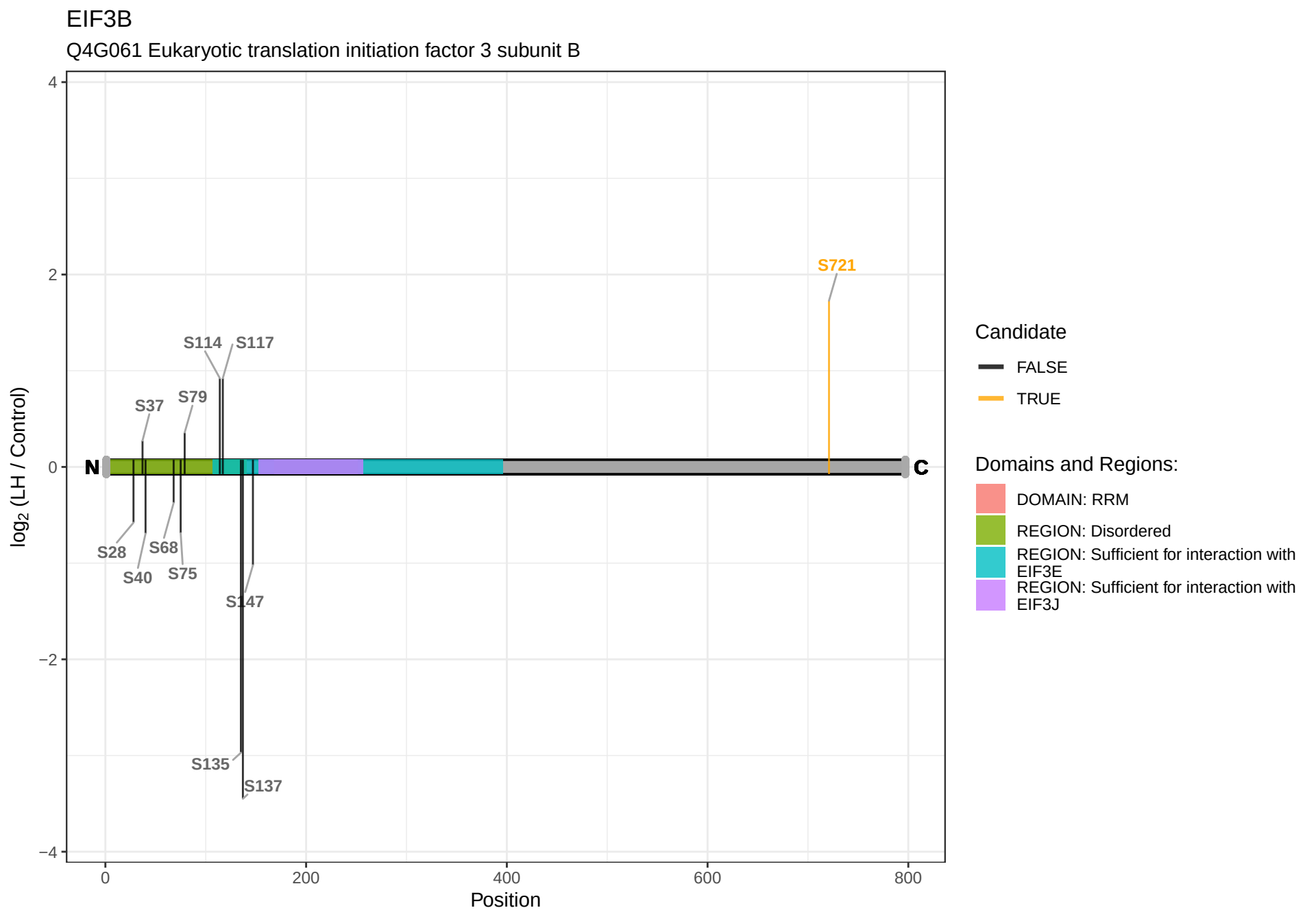

EHBP1
F1LVX2 EH domain−binding protein 1
log2 (LH / Control)
2
1
0
−1
−2
0
250
500
750
1000
1250
Position
N
C
S171
S174
S310
S408
S416
S1009
S1032
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: BMERB
DOMAIN: C2 NT−type
DOMAIN: Calponin−homology (CH)
REGION: Disordered

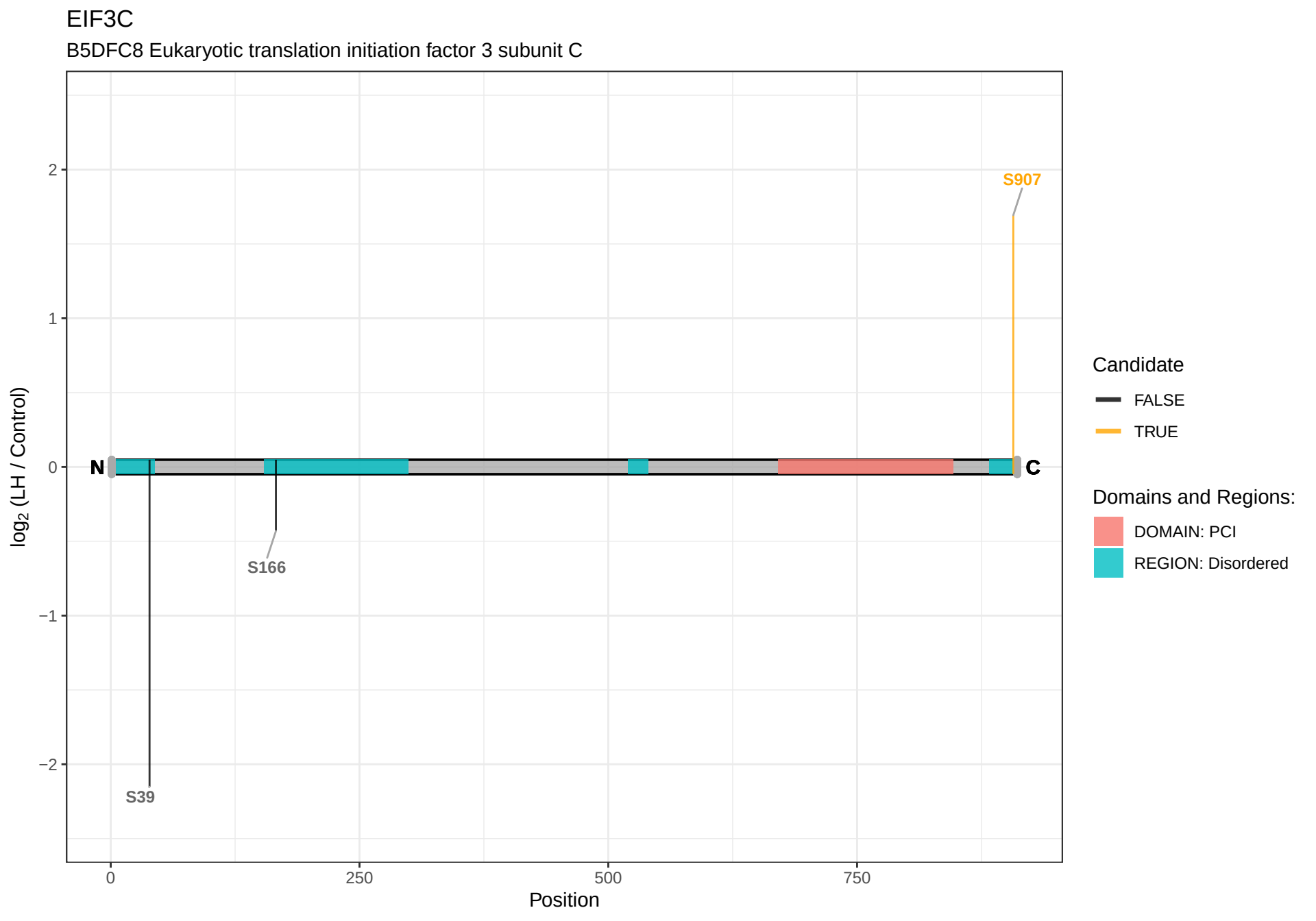

EHMT2
A0A0G2JTA5 Euchromatic histone lysine methyltransferase 2
5.0
2.5
0.0
−2.5
−5.0
log2 (LH / Control)
T227
S232
S230
S228
N
C
S115
S375
T517
0
300
600
900
1200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ANK_REP_REGION
DOMAIN: Pre−SET
DOMAIN: SET
REGION: Disordered

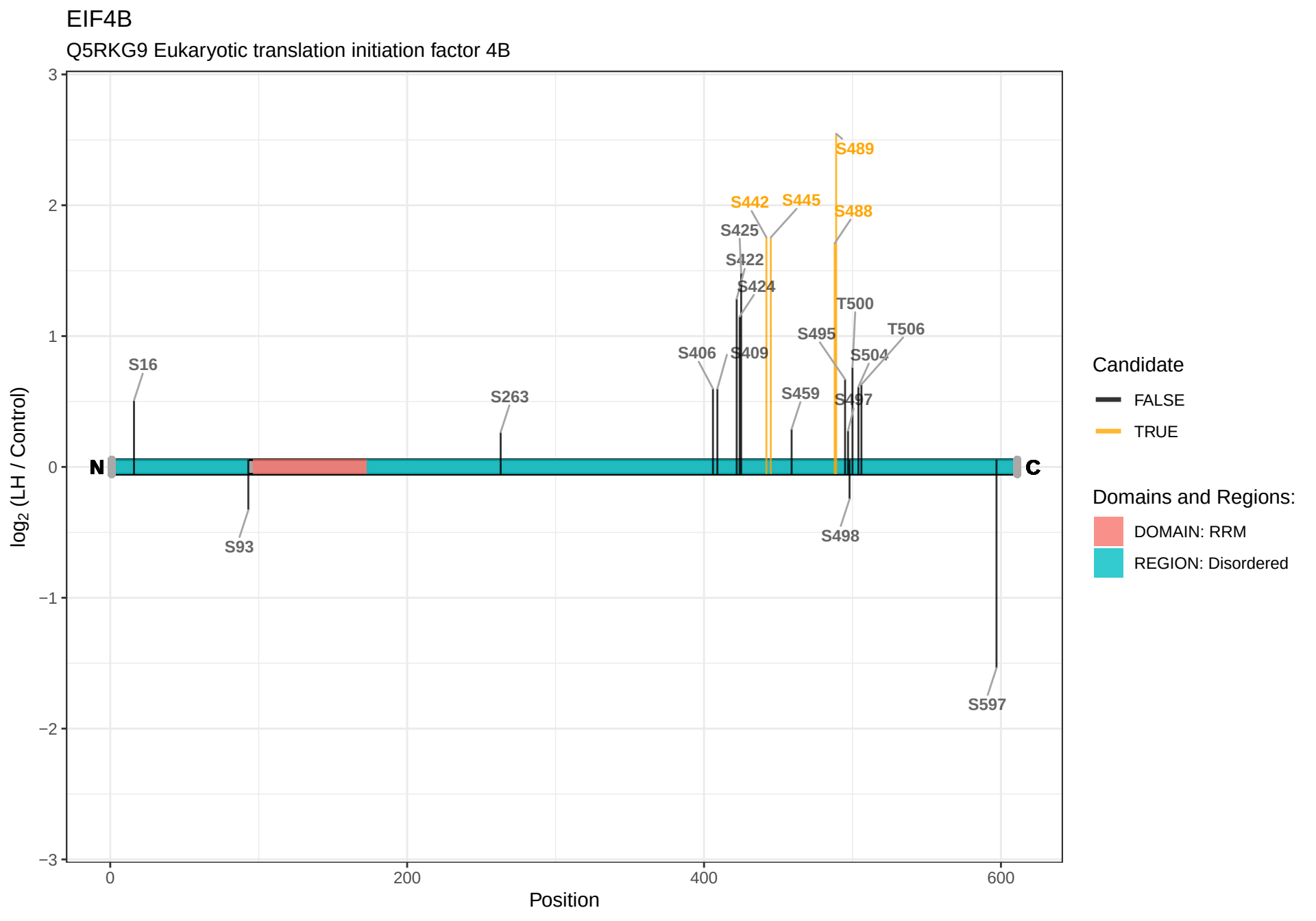

EI24
Q4KM77 Etoposide−induced protein 2.4 homolog
log2 (LH / Control)
3
2
1
0
−1
−2
−3
S46
S47
S56
S326
S330
S320
N
C
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

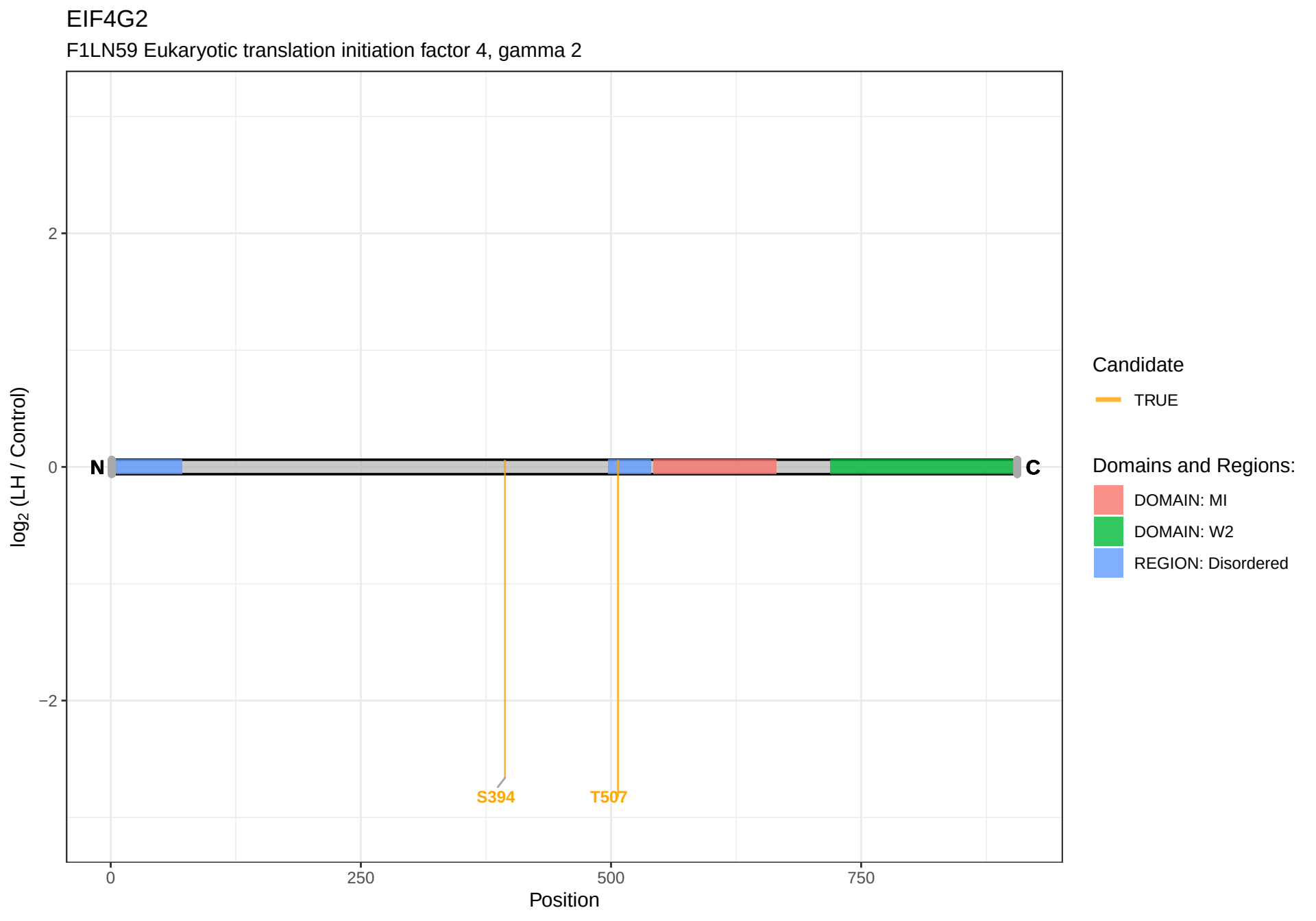

EIF2AK2
M0RDJ3 Interferon−induced, double−stranded RNA−activated protein kinase
S212
S164
N
C
2
0
−2
log2 (LH / Control)
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DRBM
DOMAIN: Protein kinase

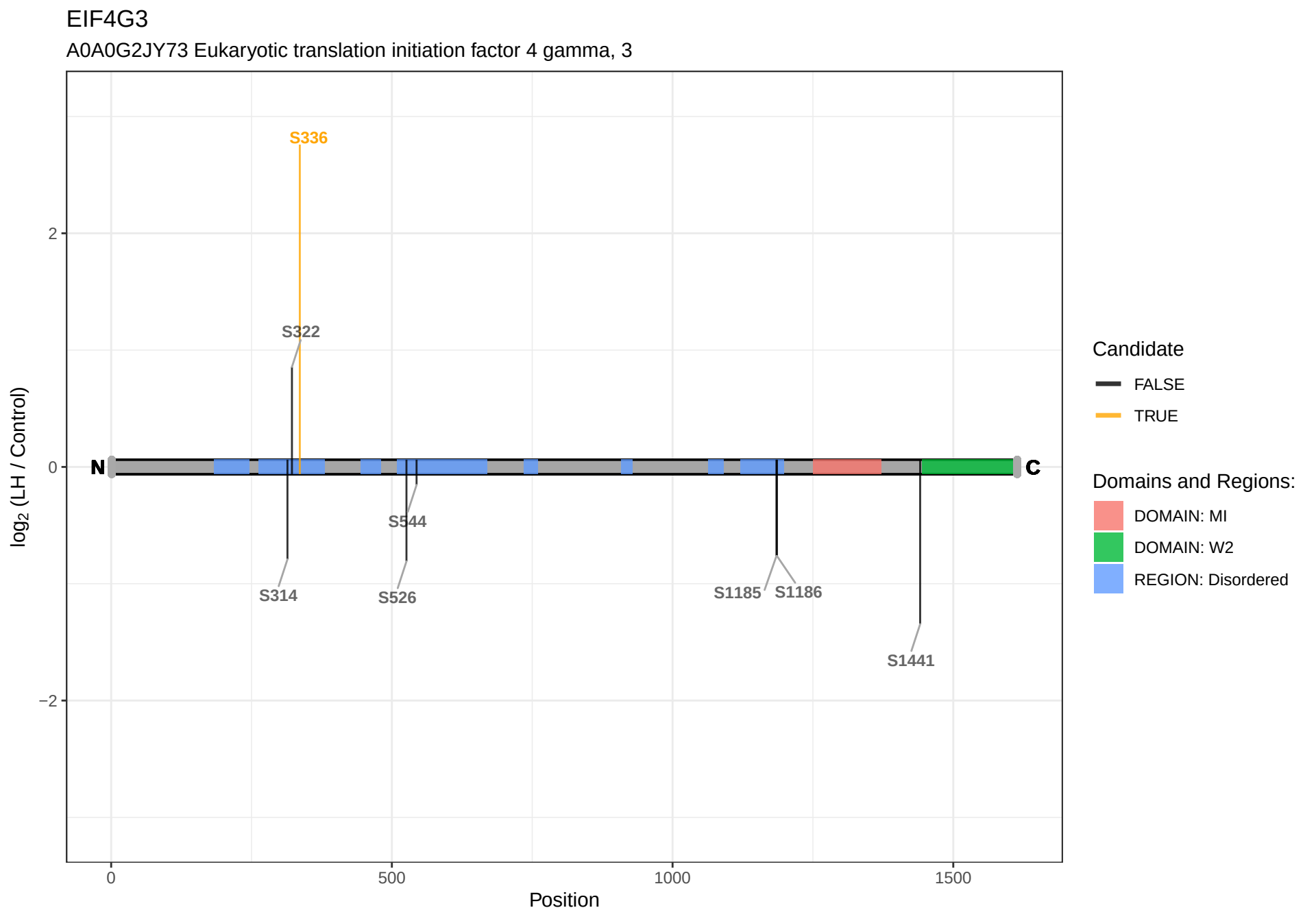

EIF2B4
Q63186 Translation initiation factor eIF−2B subunit delta
log2 (LH / Control)
2
1
0
−1
−2
N
C
S21
0
100
200
300
400
500
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

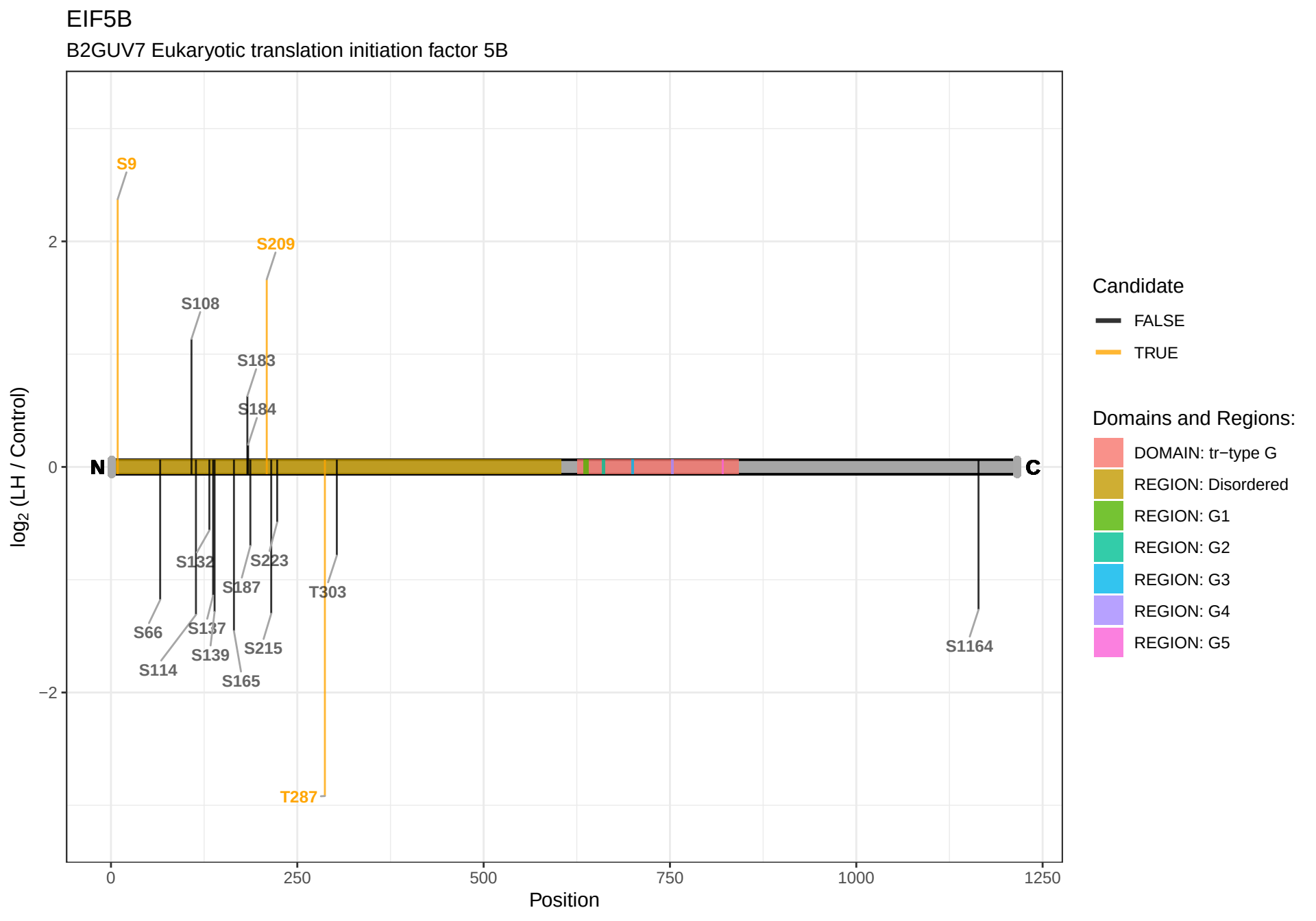

EIF3B
Q4G061 Eukaryotic translation initiation factor 3 subunit B
log2 (LH / Control)
Position
N
C
S721
S114
S117
S37
S79
S28
S68
S40
S75
S147
S135
S137
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RRM
REGION: Disordered
REGION: Sufficient for interaction with EIF3E
REGION: Sufficient for interaction with EIF3J

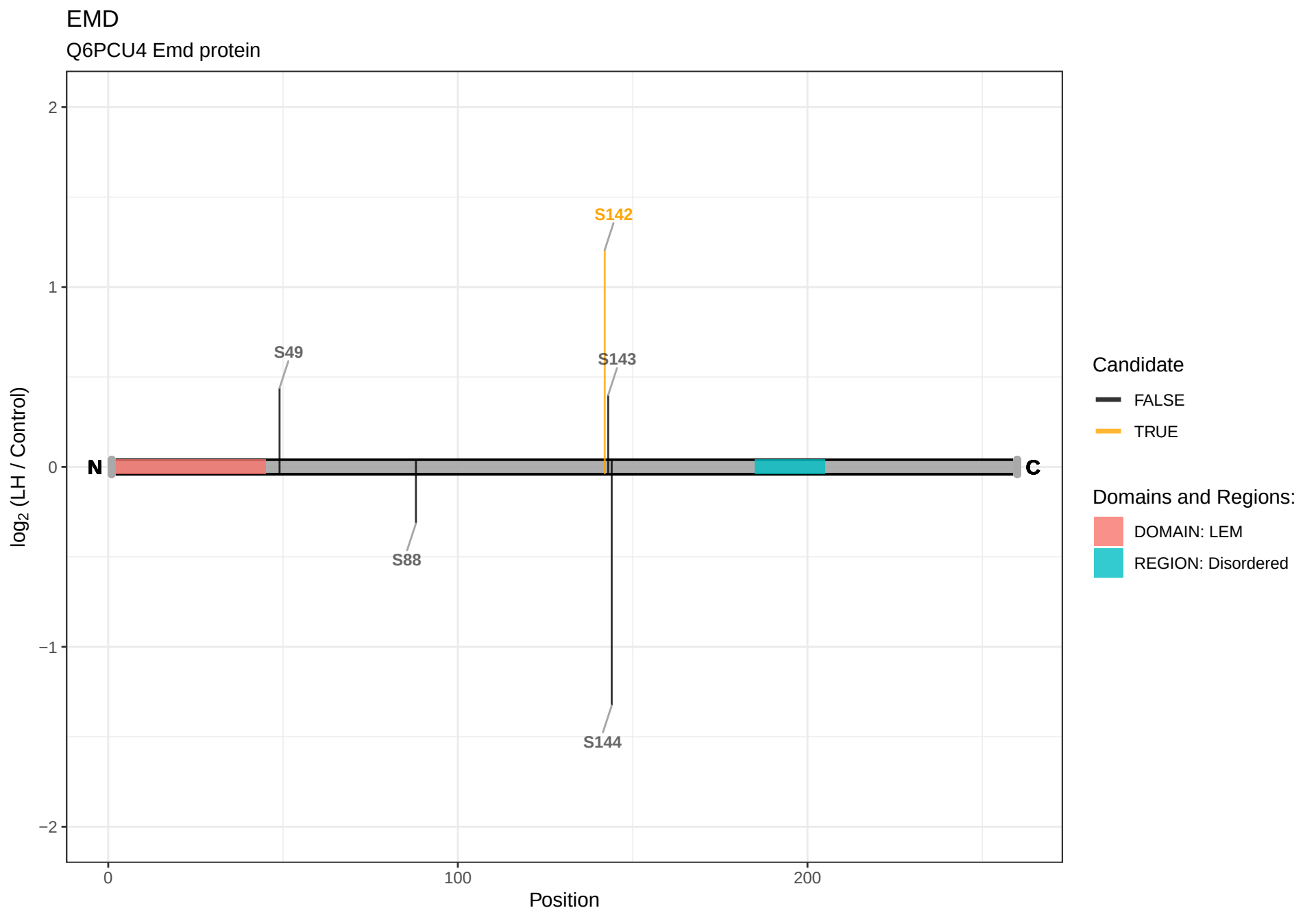

EIF3C
B5DFC8 Eukaryotic translation initiation factor 3 subunit C
log2 (LH / Control)
2
1
0
−1
−2
N
C
S907
S166
S39
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PCI
REGION: Disordered

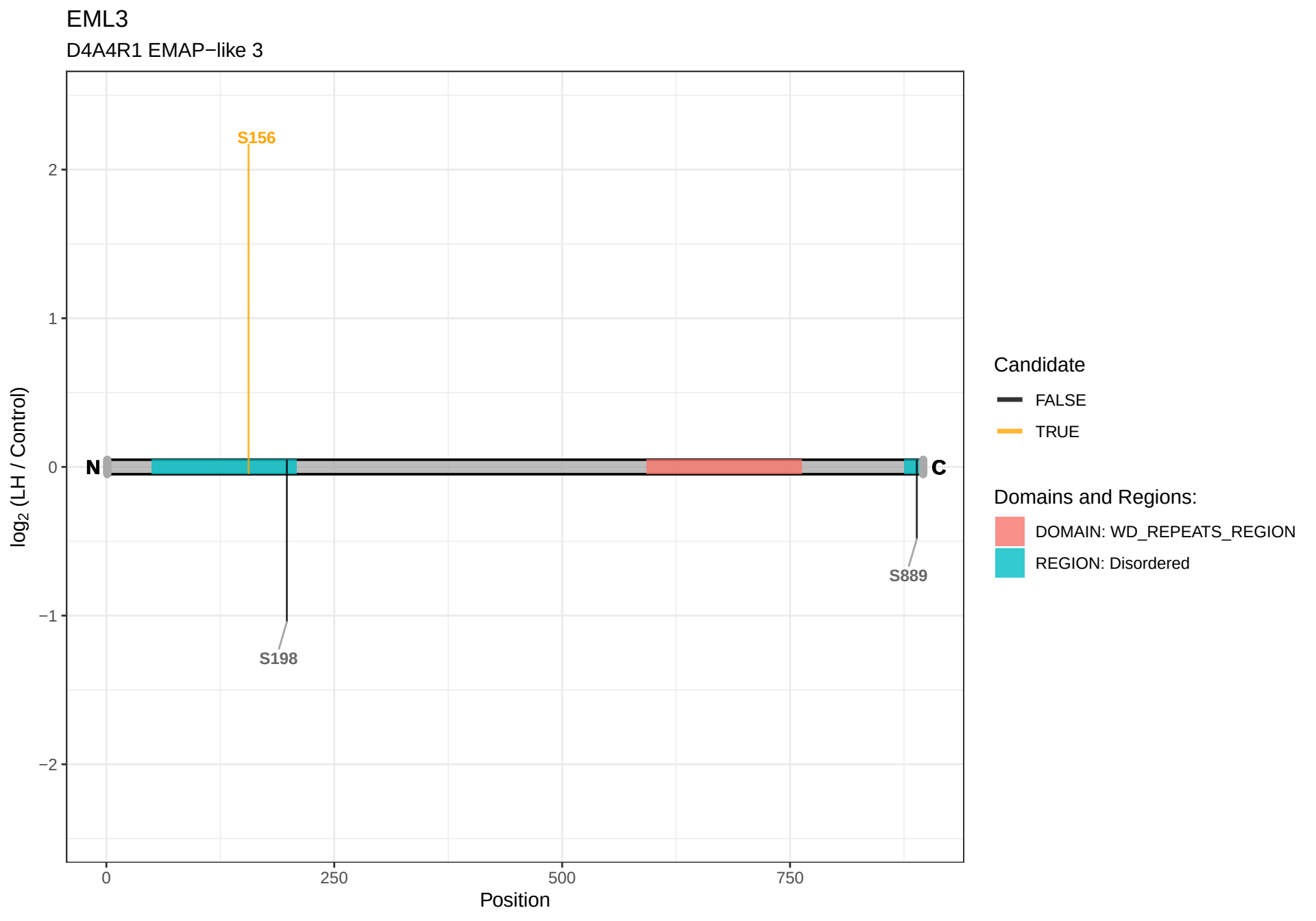

EIF4B
Q5RKG9 Eukaryotic translation initiation factor 4B
log2 (LH / Control)
Position
N
C
S16
S93
S263
S406
S409
S422
S424
S425
S442
S445
S459
S488
S489
S495
S497
S498
T500
S504
T506
S597
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RRM
REGION: Disordered

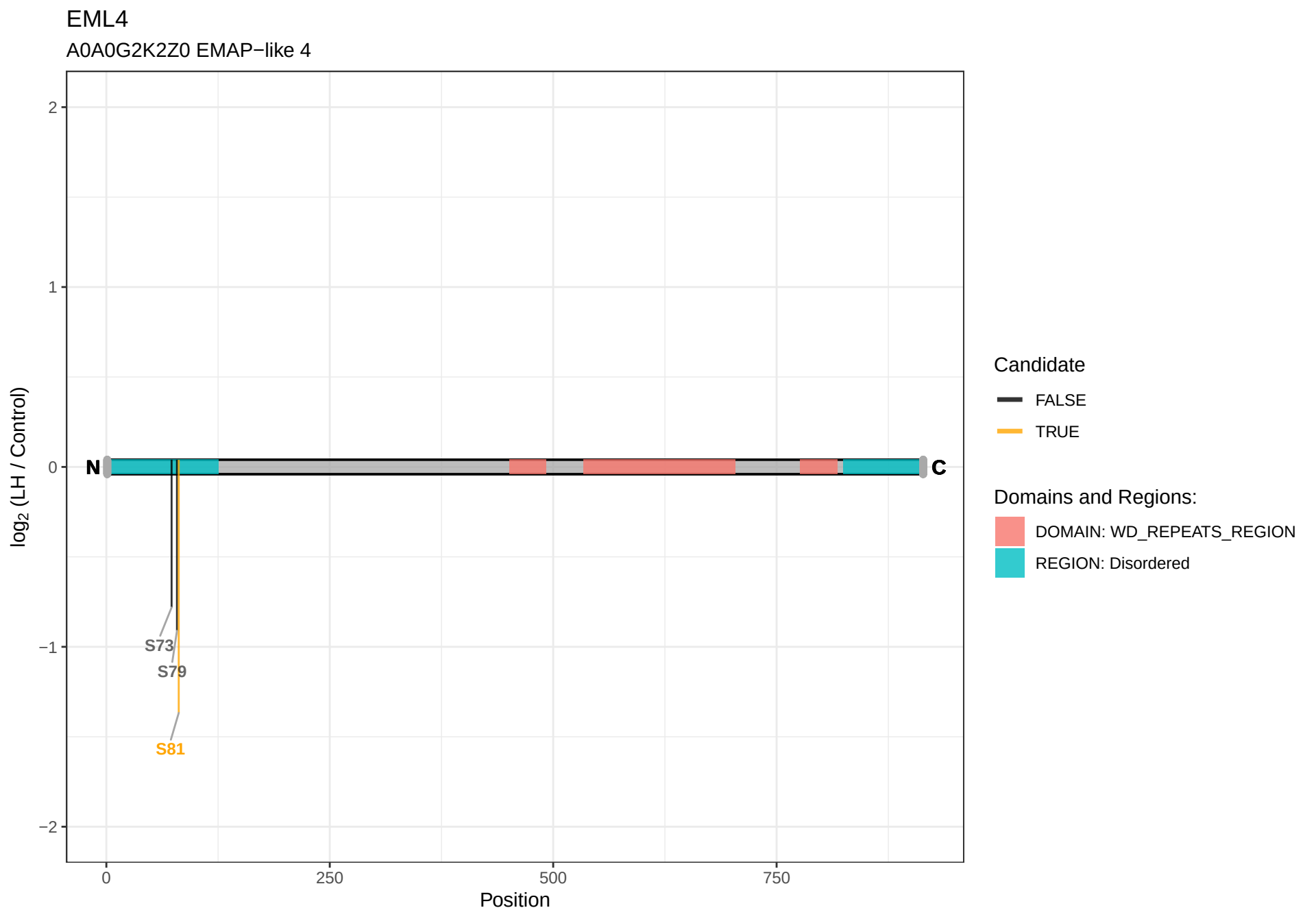

EIF4G2
F1LN59 Eukaryotic translation initiation factor 4, gamma 2
log2 (LH / Control)
2
0
−2
N
C
S394
T507
0
250
500
750
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: MI
DOMAIN: W2
REGION: Disordered

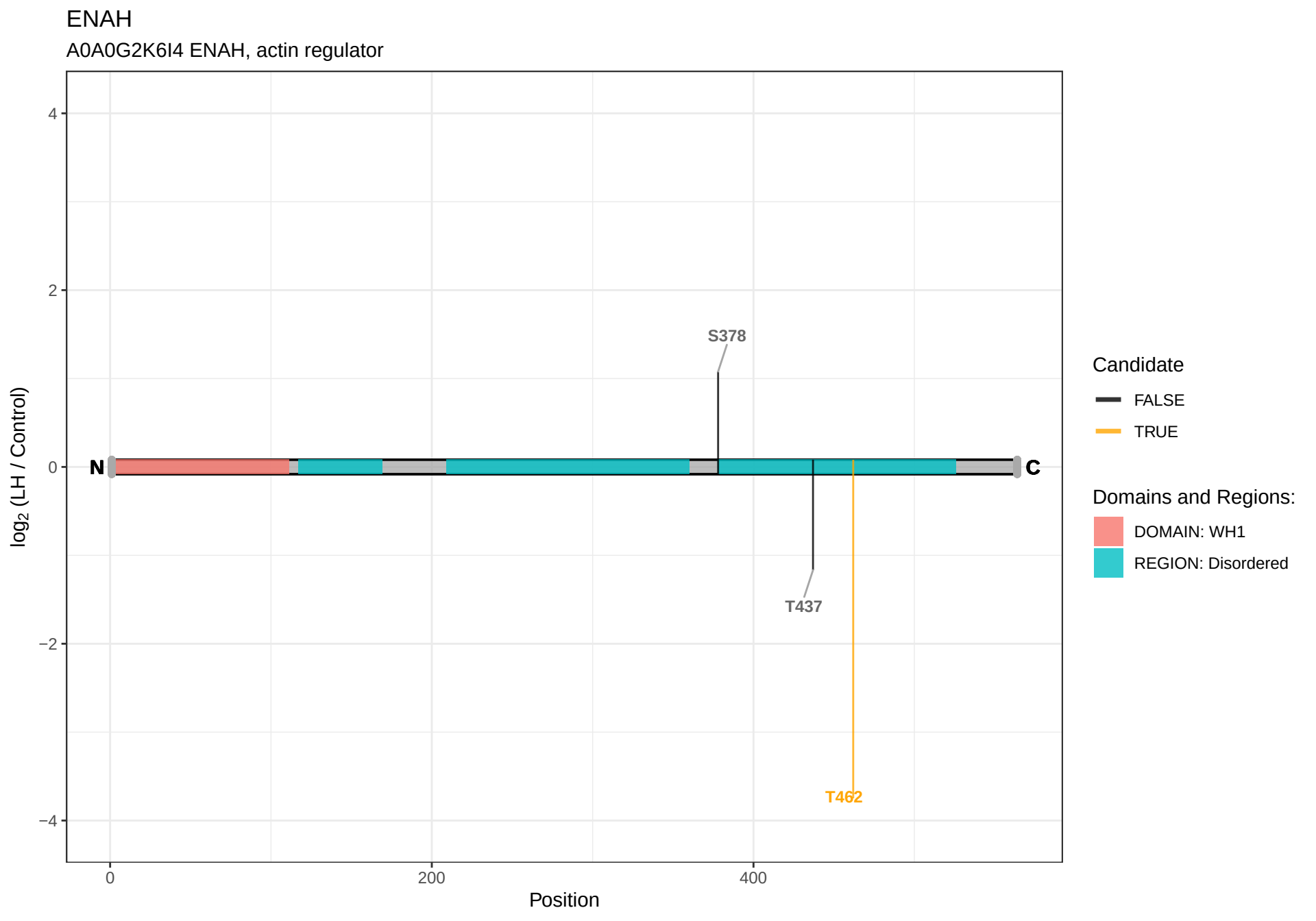

EIF4G3
A0A0G2JY73 Eukaryotic translation initiation factor 4 gamma, 3
S336
S322
S314
S544
S526
S1185
S1186
S1441
N
C
2
0
−2
log2 (LH / Control)
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: MI
DOMAIN: W2
REGION: Disordered

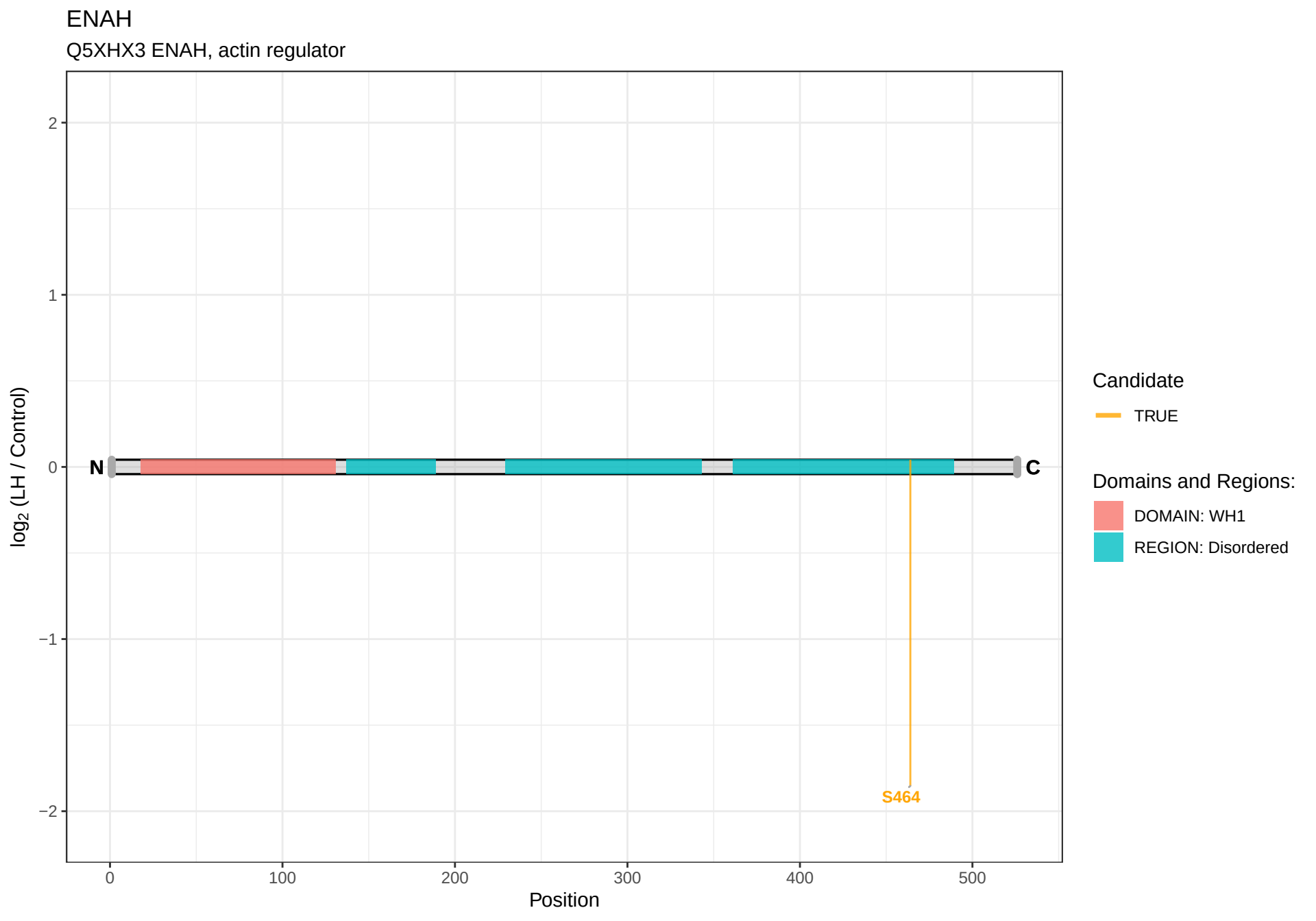

EIF5B
B2GUV7 Eukaryotic translation initiation factor 5B
log2 (LH / Control)
2
0
−2
N
C
S9
S209
S108
S183
S184
S132
S223
S187
T303
S66
S137
S139
S215
S114
S165
T287
S1164
0
250
500
750
1000
1250
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: tr−type G
REGION: Disordered
REGION: G1
REGION: G2
REGION: G3
REGION: G4
REGION: G5

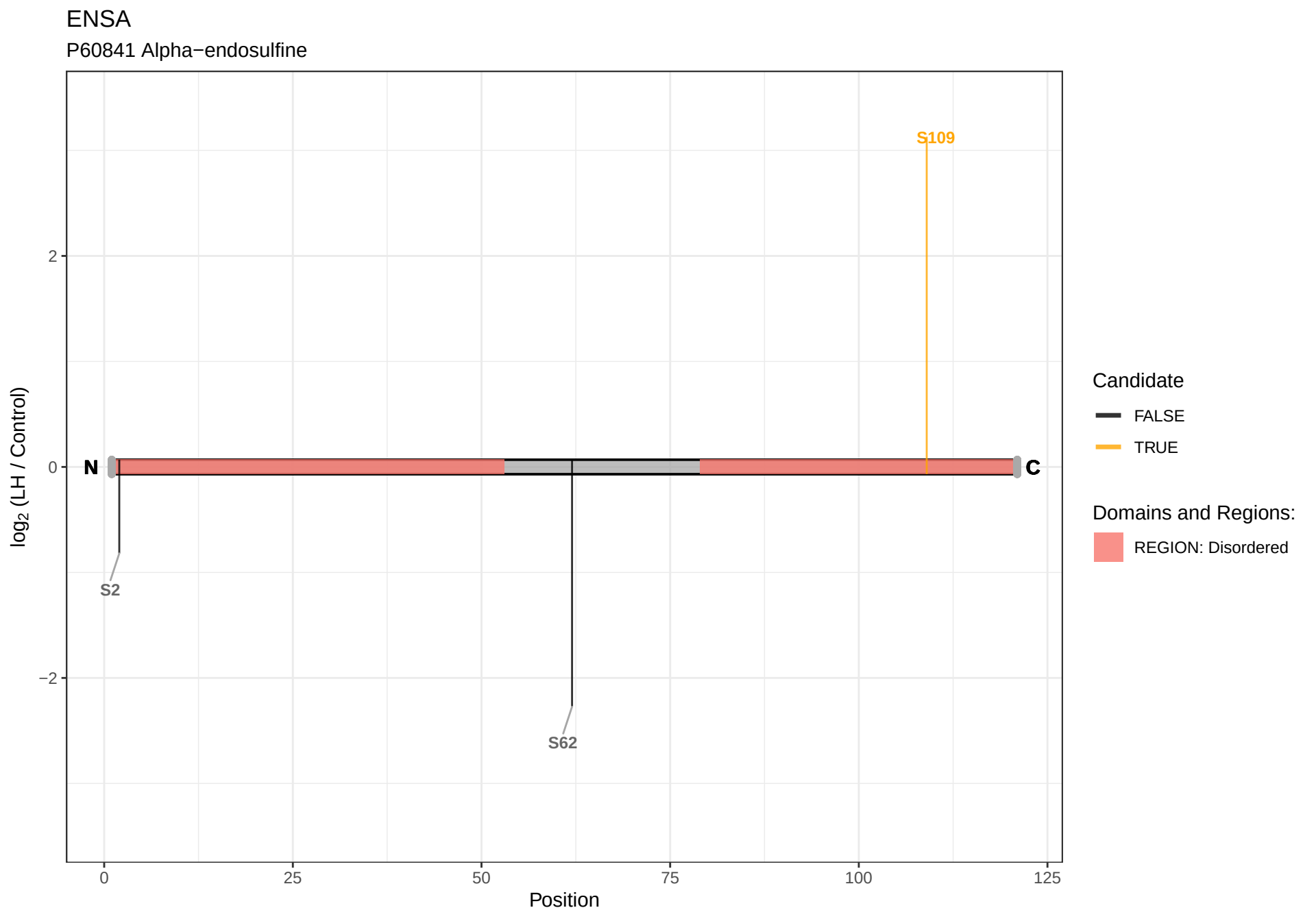

EMD
Q6PCU4 Emd protein
2
1
0
−1
−2
log2 (LH / Control)
S142
S49
S143
N
C
S88
S144
0
100
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: LEM
REGION: Disordered

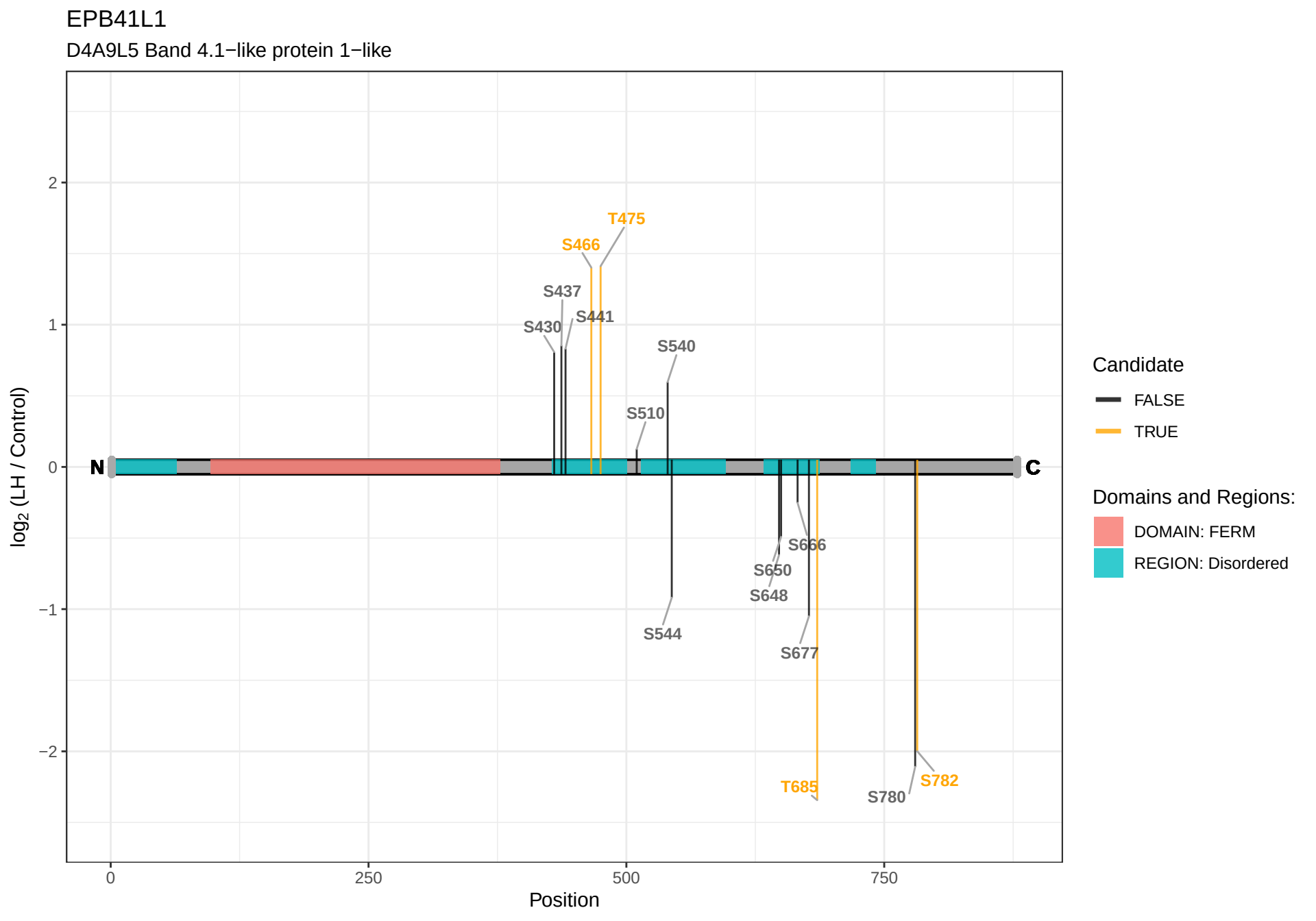

EML3
D4A4R1 EMAP−like 3
S156
S198
S889
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WD_REPEATS_REGION
REGION: Disordered

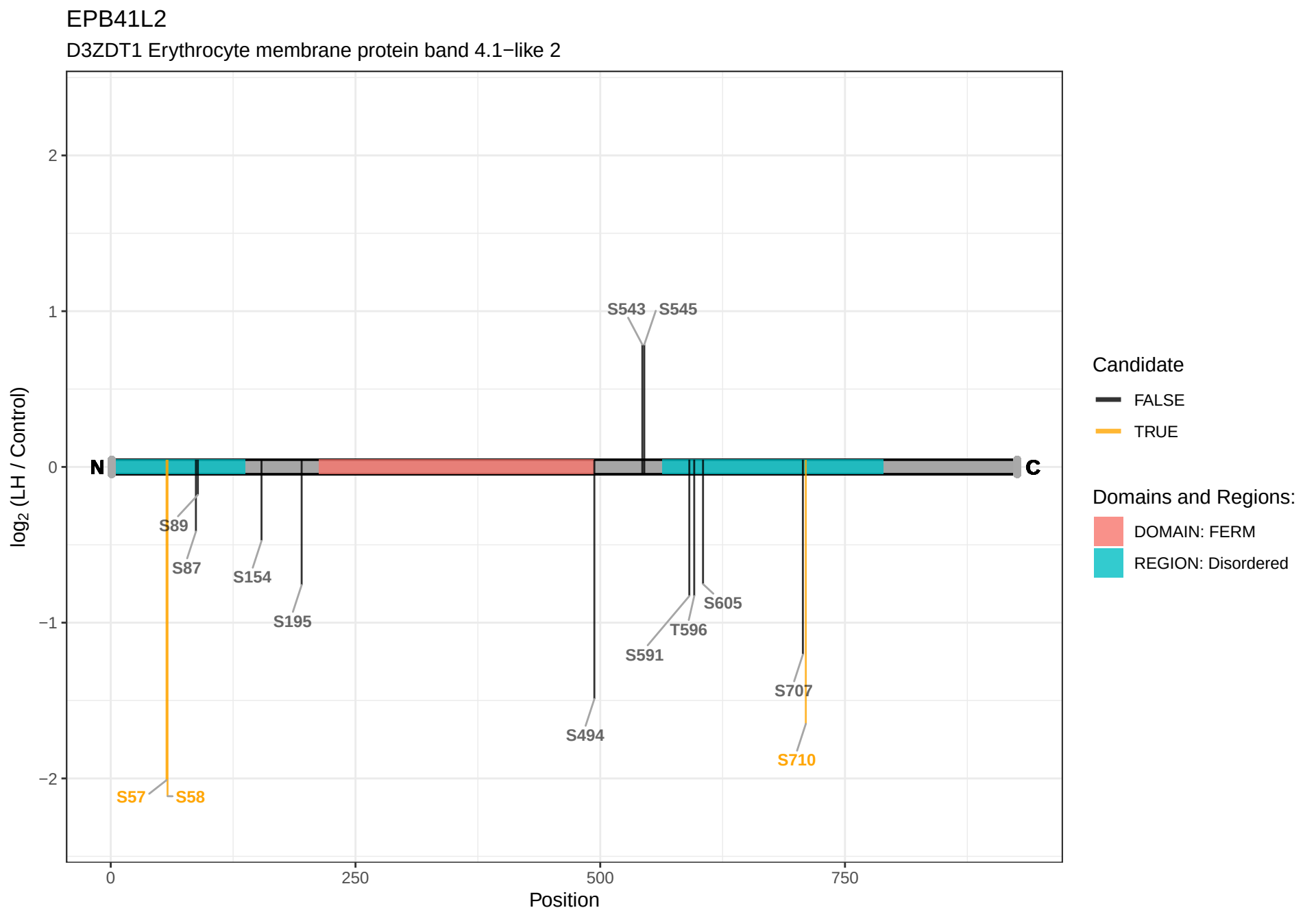

EML4
A0A0G2K2Z0 EMAP−like 4
2
1
0
−1
−2
log2 (LH / Control)
N
C
S73
S79
S81
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WD_REPEATS_REGION
REGION: Disordered

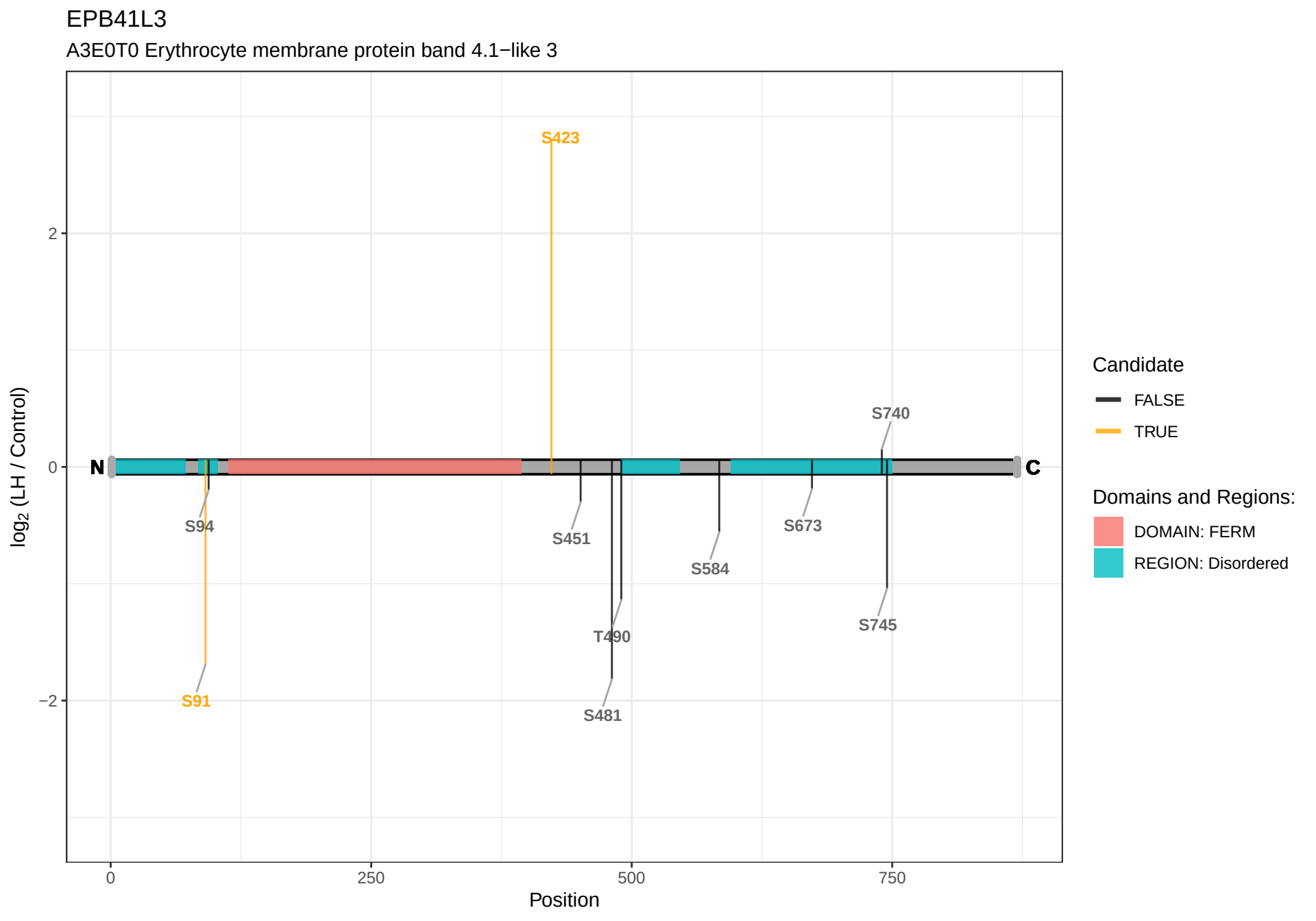

ENAH
A0A0G2K6I4 ENAH, actin regulator
4
2
0
−2
−4
log2 (LH / Control)
N
C
S378
T437
T462
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WH1
REGION: Disordered

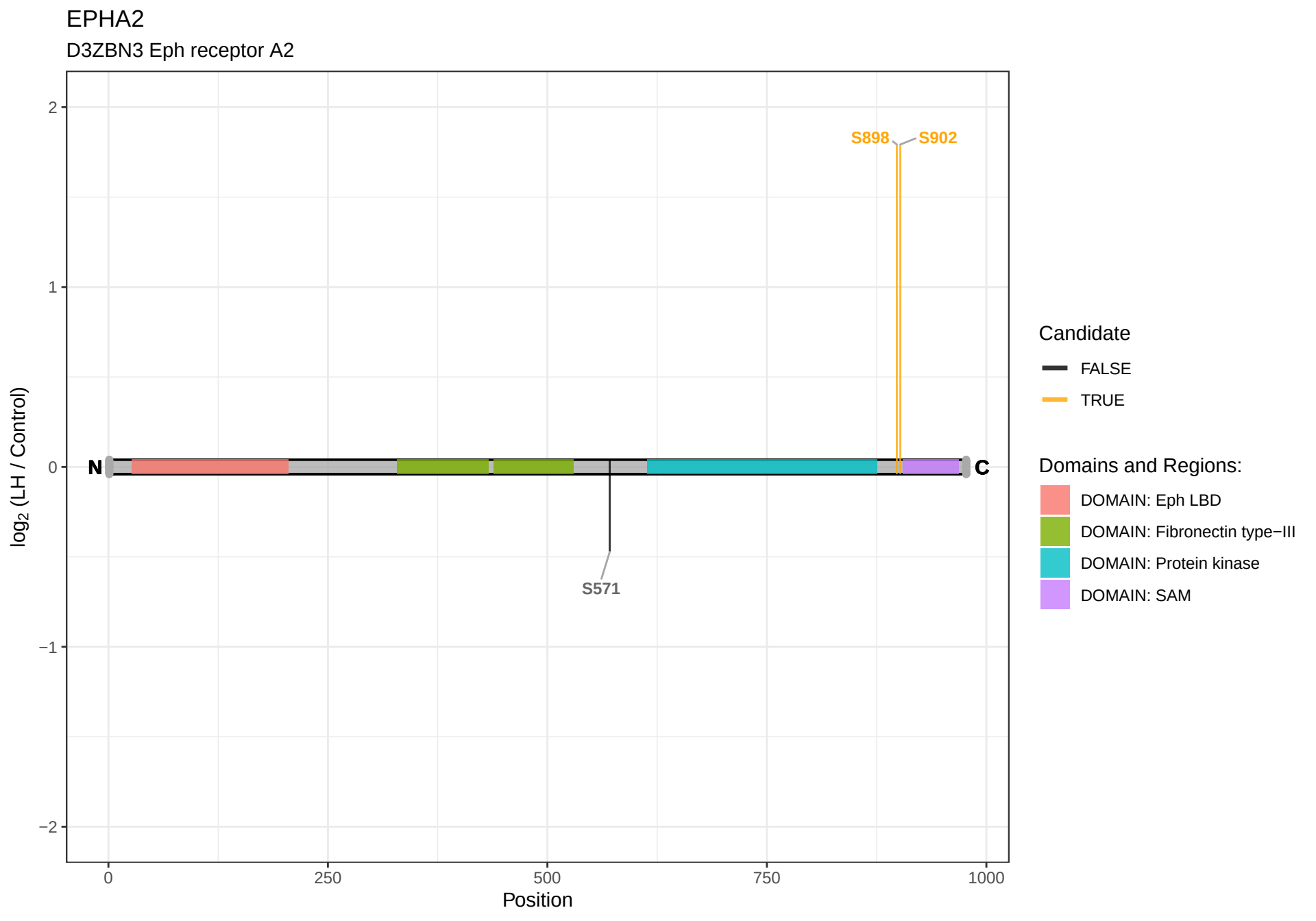

ENAH
Q5XHX3 ENAH, actin regulator
log2 (LH / Control)
2
1
0
−1
−2
N
C
S464
0
100
200
300
400
500
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: WH1
REGION: Disordered

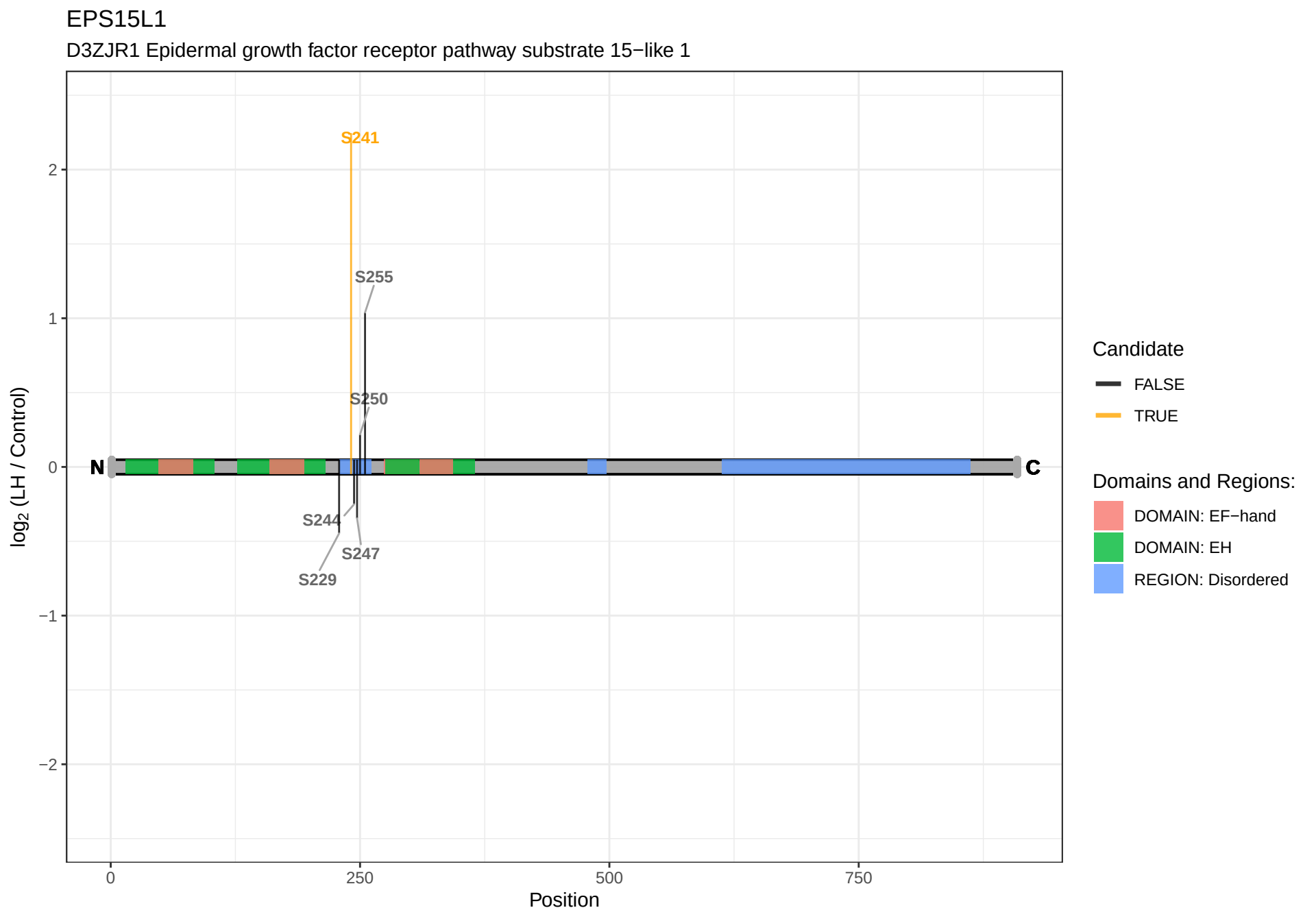

ENSA
P60841 Alpha−endosulfine
S109
N
C
S2
S62
2
0
−2
log2 (LH / Control)
0
25
50
75
100
125
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

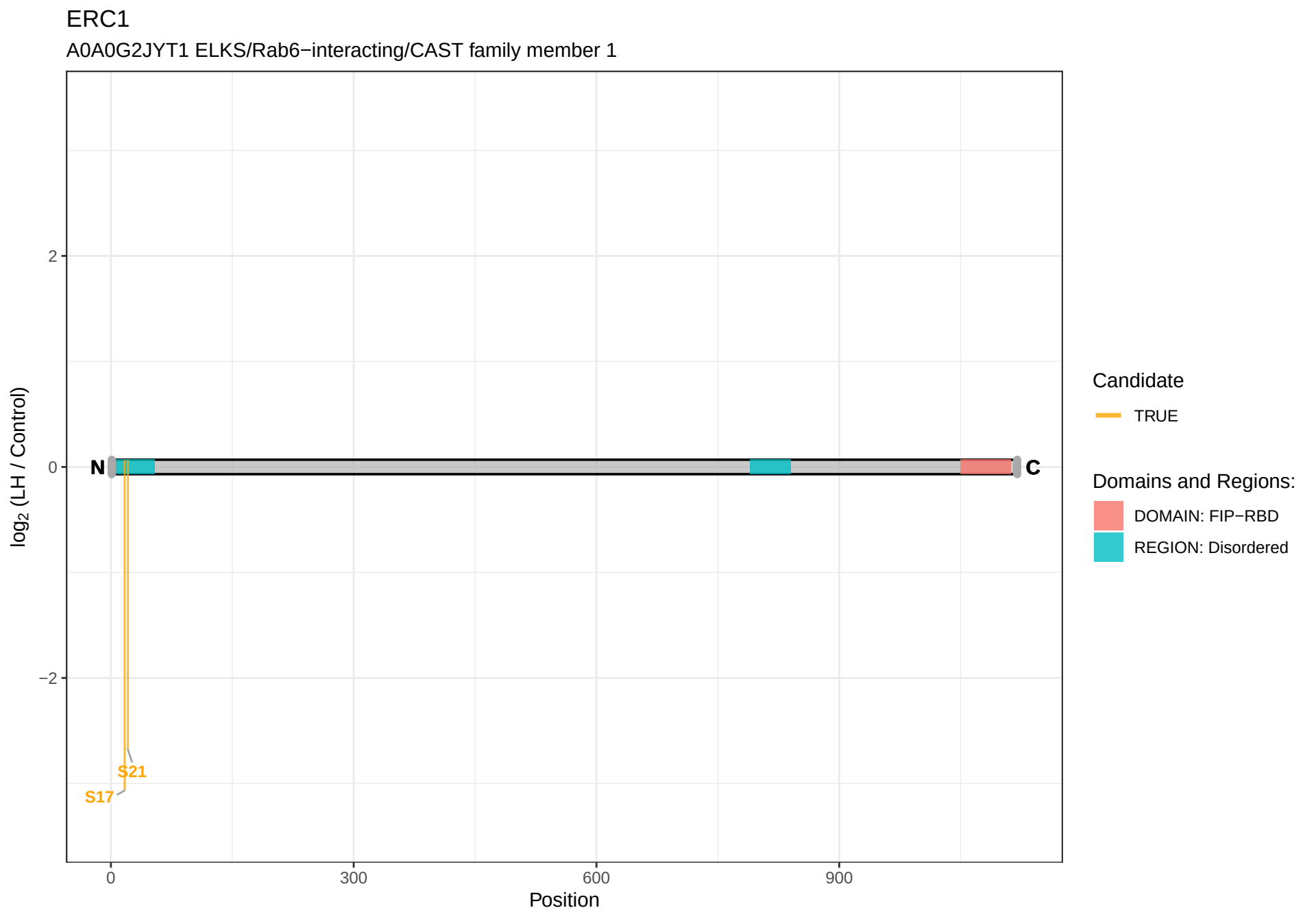

EPB41L1
D4A9L5 Band 4.1−like protein 1−like
log2 (LH / Control)
Position
N
C
T475
S466
S437
S441
S430
S540
S510
S544
S666
S650
S648
S677
T685
S780
S782
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: FERM
REGION: Disordered

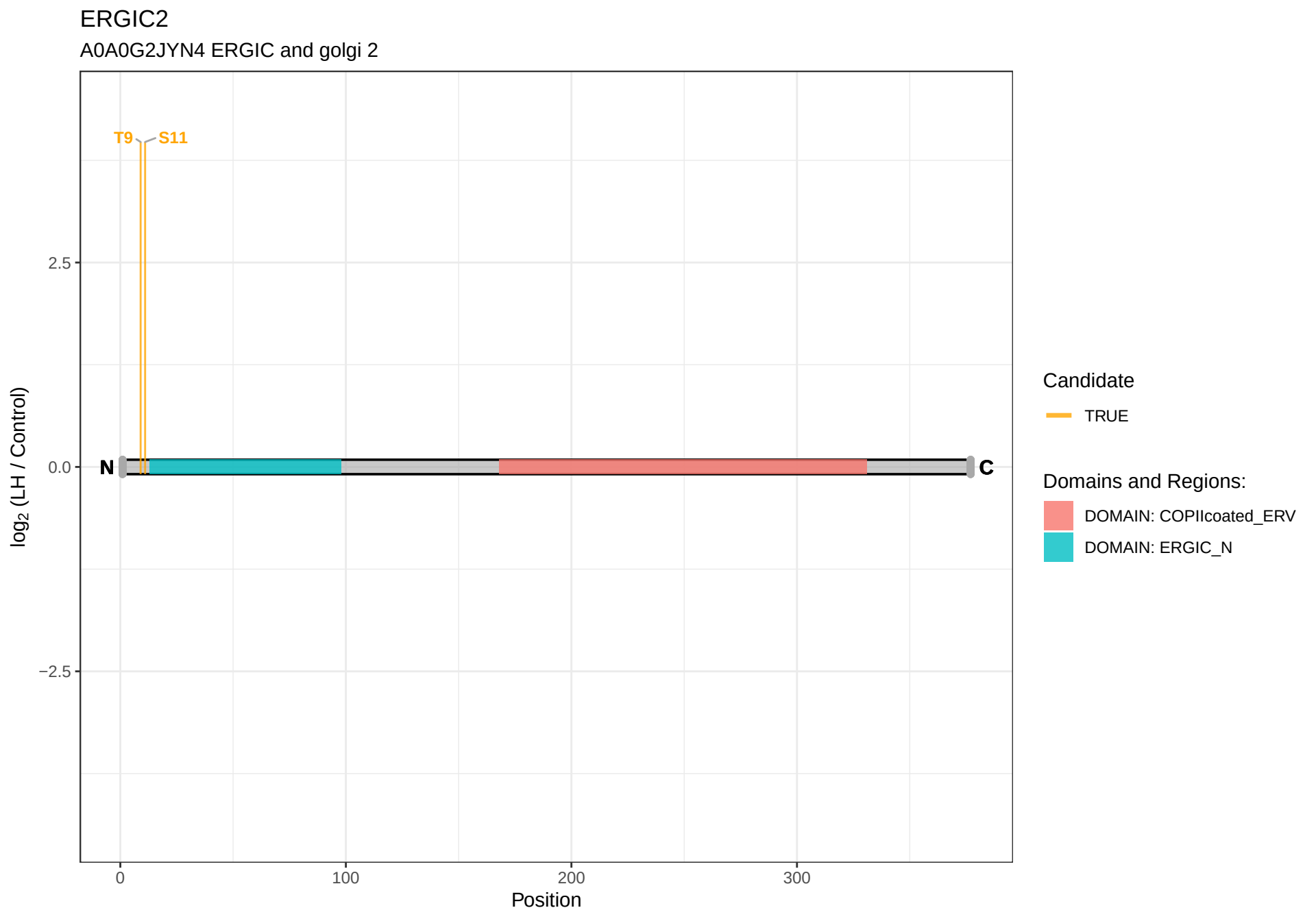

EPB41L2
D3ZDT1 Erythrocyte membrane protein band 4.1−like 2
log2 (LH / Control)
2
1
0
−1
−2
0
250
500
750
Position
N
C
S543
S545
S89
S87
S154
S195
S605
T596
S591
S707
S494
S710
S57
S58
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: FERM
REGION: Disordered

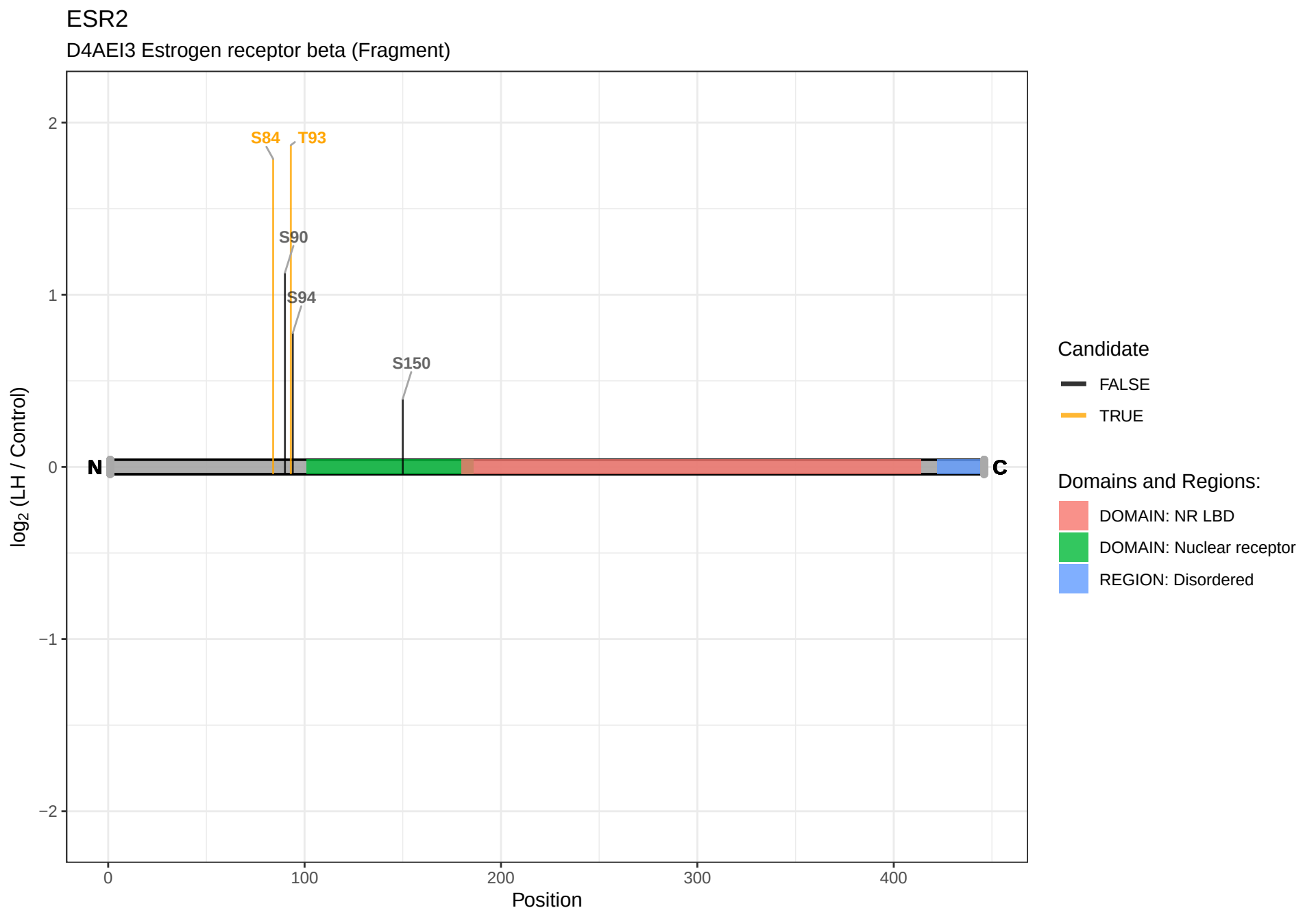

EPB41L3
A3E0T0 Erythrocyte membrane protein band 4.1−like 3
S423
S740
N
C
S94
S451
S673
S584
S745
T490
S91
S481
2
0
−2
log2 (LH / Control)
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: FERM
REGION: Disordered

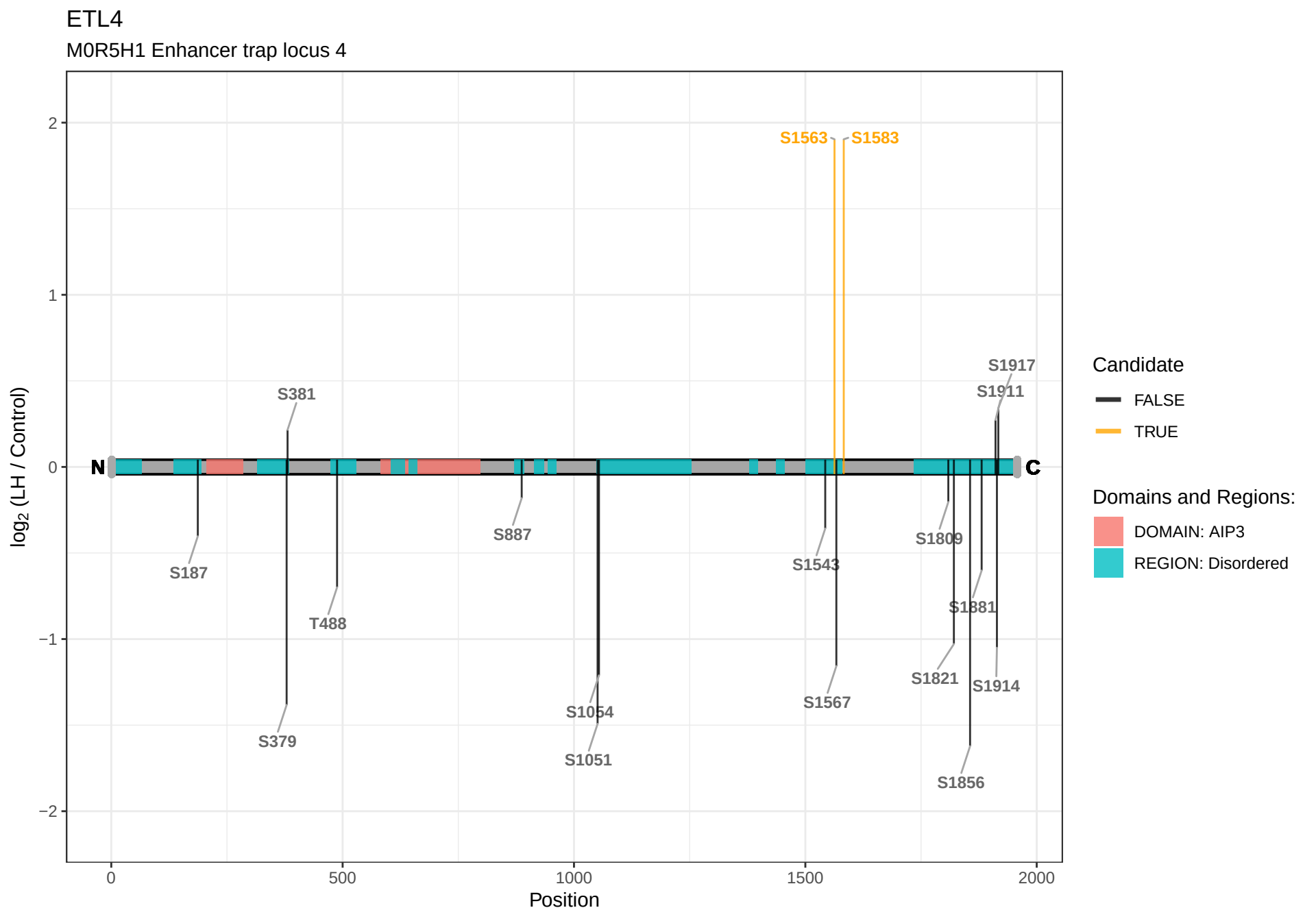

EPHA2
D3ZBN3 Eph receptor A2
2
1
0
−1
−2
log2 (LH / Control)
S898
S902
S571
N
C
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Eph LBD
DOMAIN: Fibronectin type−III
DOMAIN: Protein kinase
DOMAIN: SAM

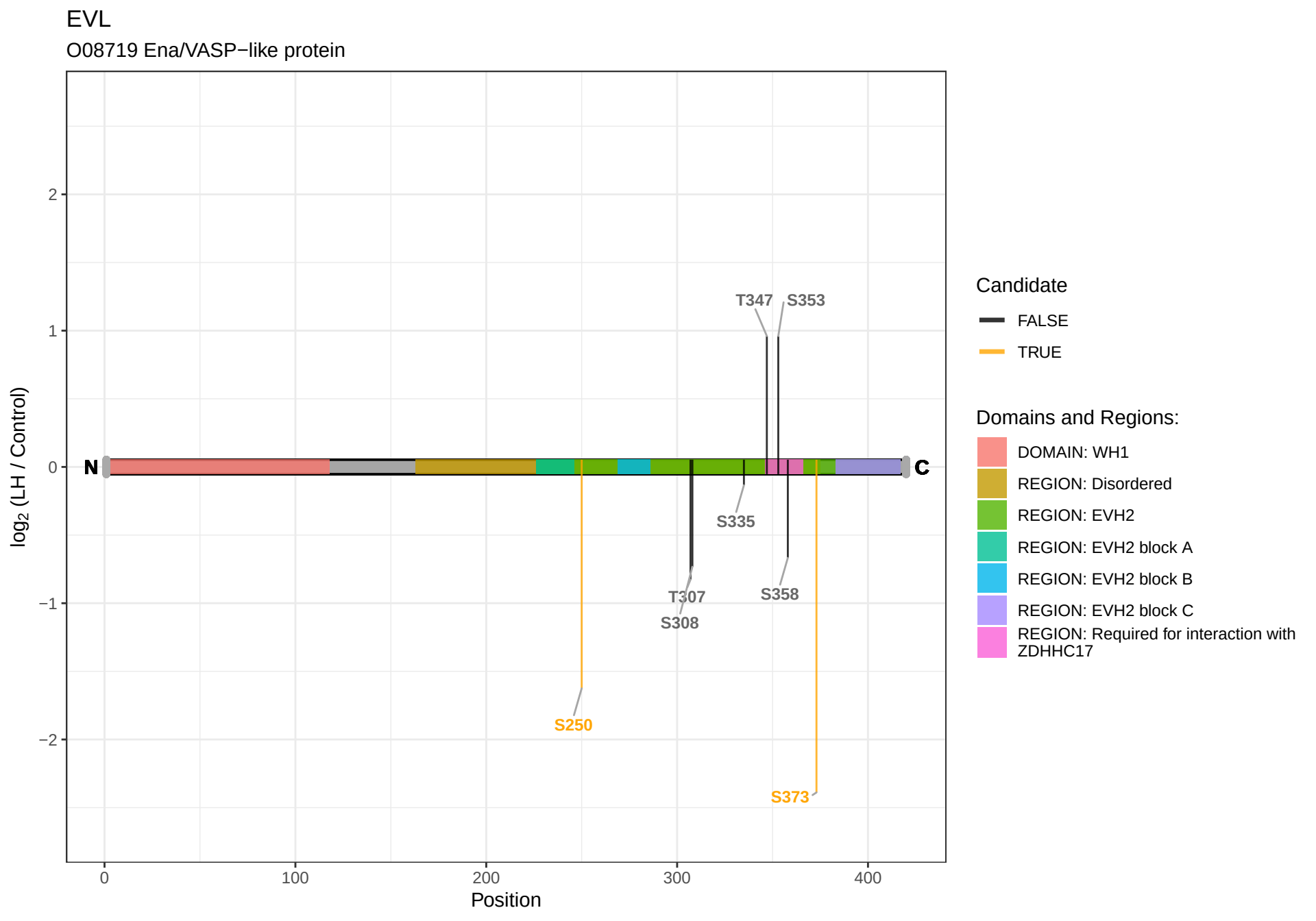

EPS15L1
D3ZJR1 Epidermal growth factor receptor pathway substrate 15−like 1
S241
S255
S250
S244
S247
S229
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: EF−hand
DOMAIN: EH
REGION: Disordered

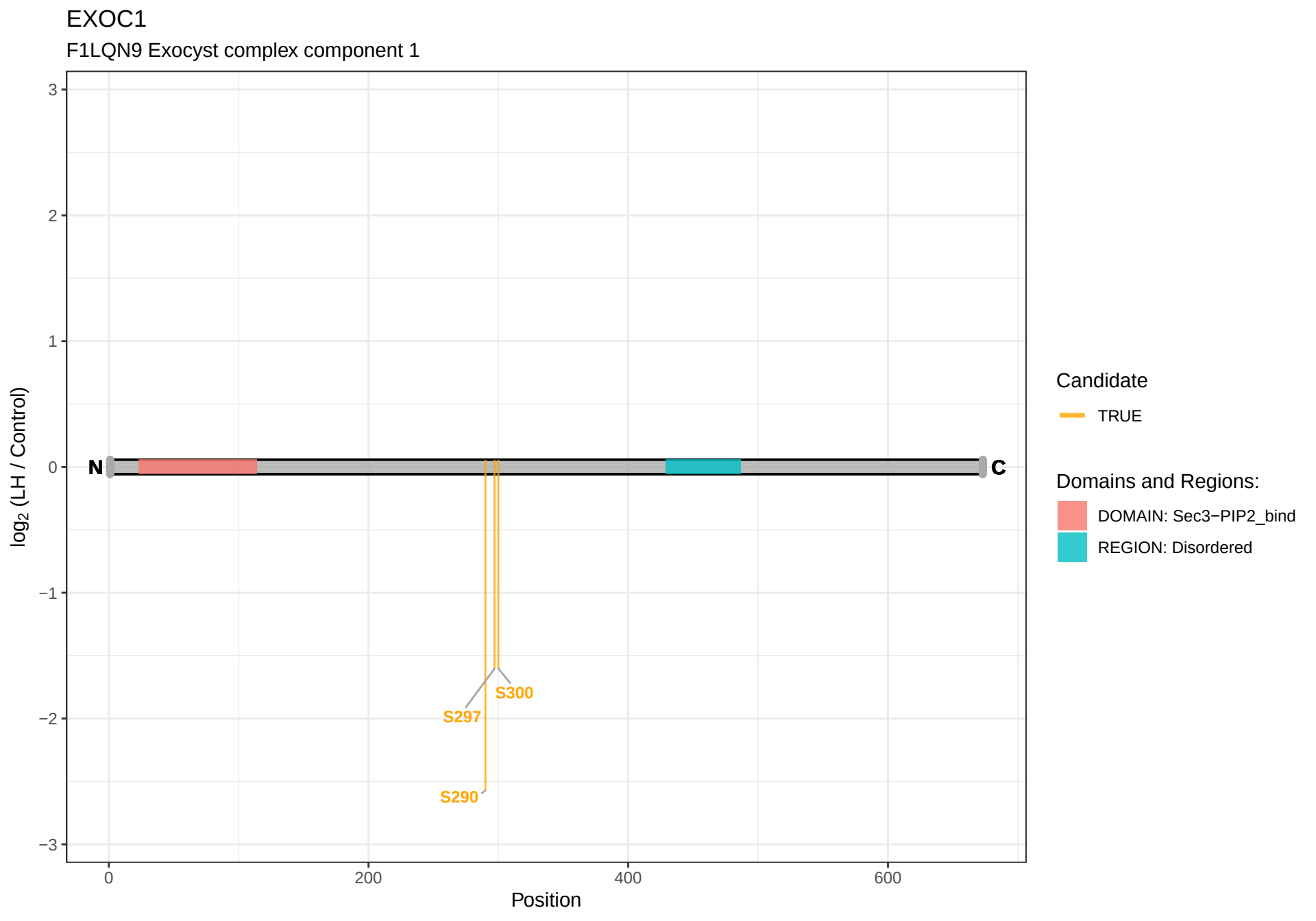

ERC1
A0A0G2JYT1 ELKS/Rab6−interacting/CAST family member 1
log2 (LH / Control)
2
0
−2
N
C
S21
S17
0
300
600
900
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: FIP−RBD
REGION: Disordered

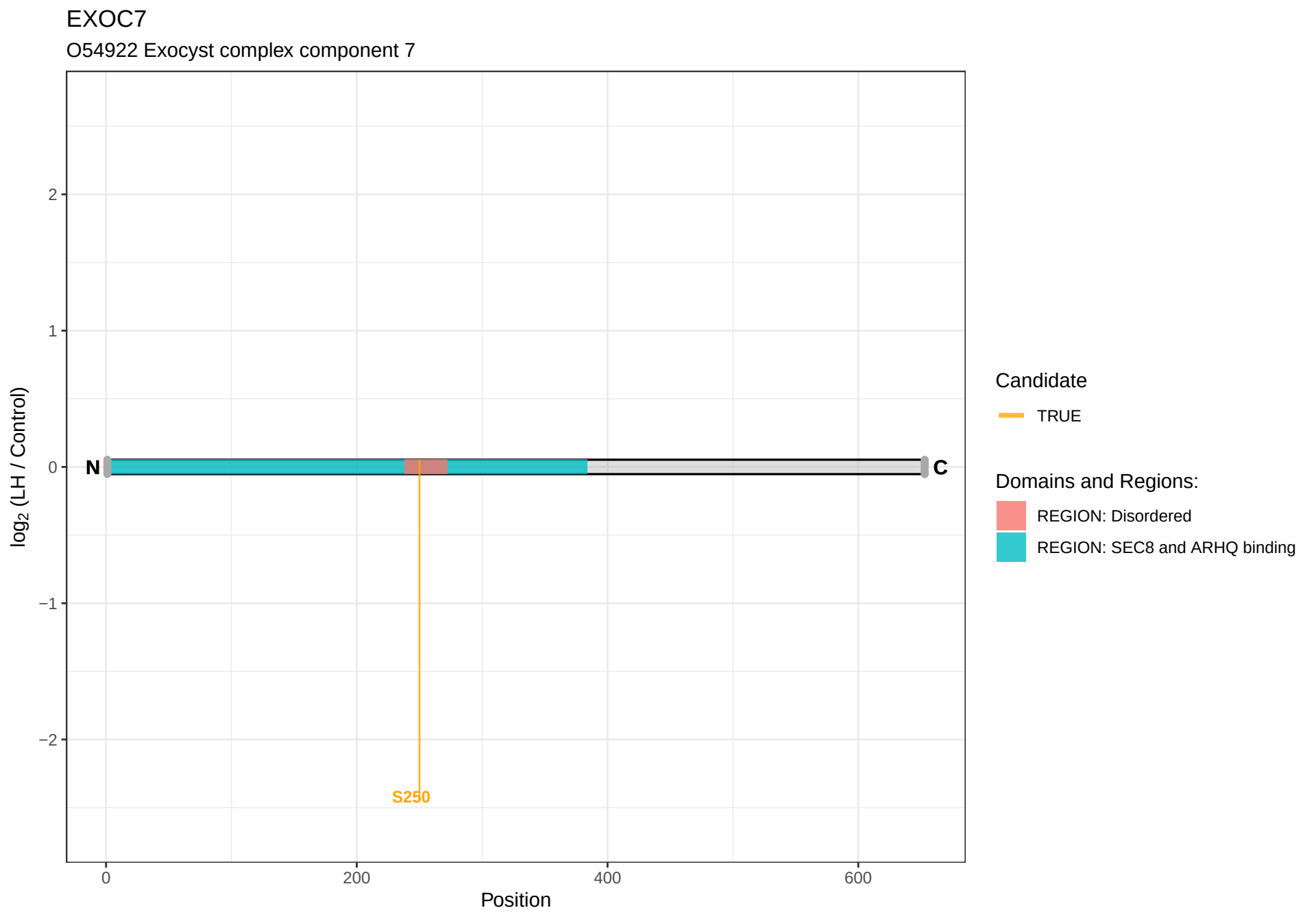

ERGIC2
A0A0G2JYN4 ERGIC and golgi 2
T9
S11
N
C
2.5
0.0
−2.5
log2 (LH / Control)
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: COPIIcoated_ERV
DOMAIN: ERGIC_N

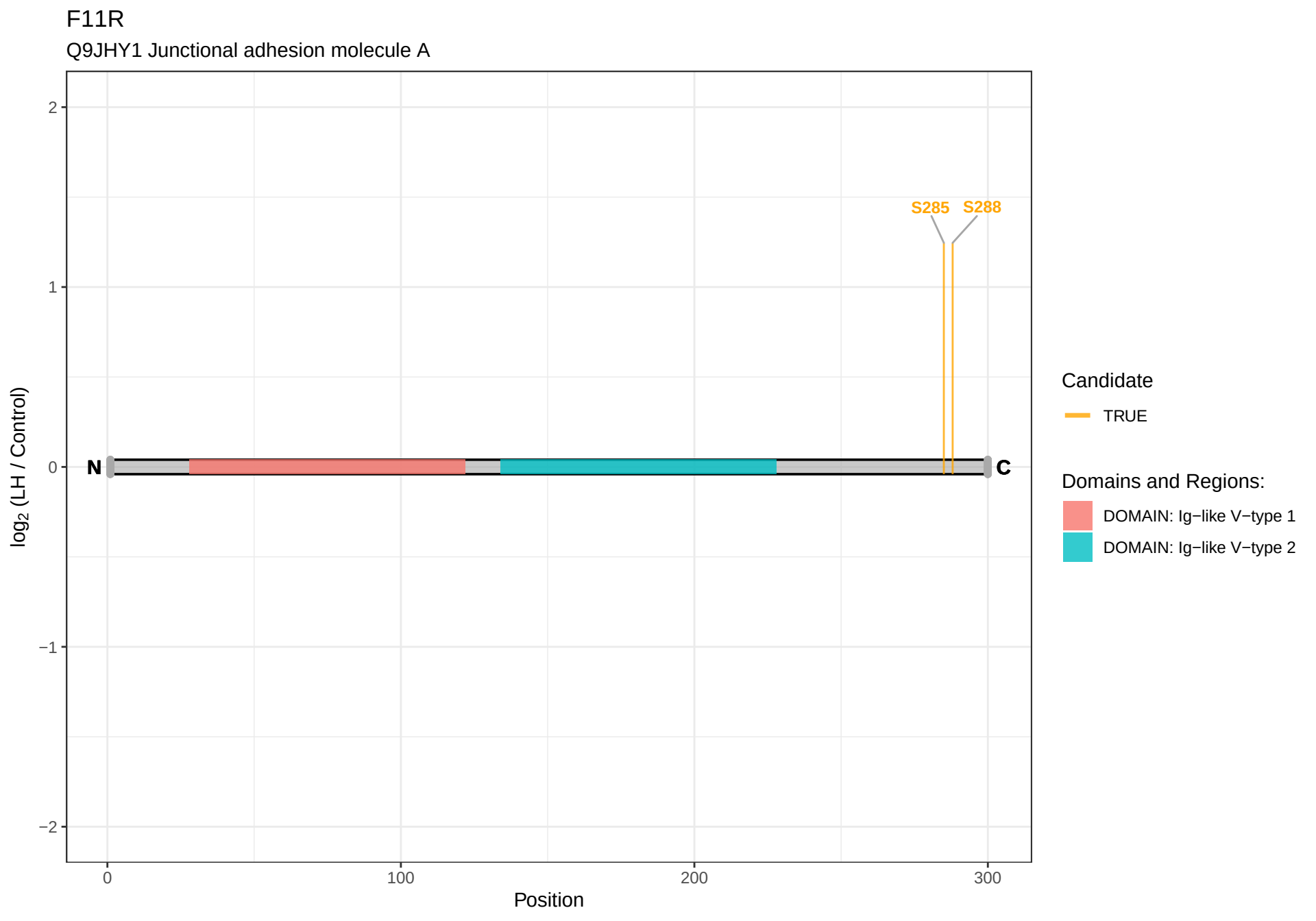

ESR2
D4AEI3 Estrogen receptor beta (Fragment)
S84
T93
S90
S94
S150
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: NR LBD
DOMAIN: Nuclear receptor
REGION: Disordered

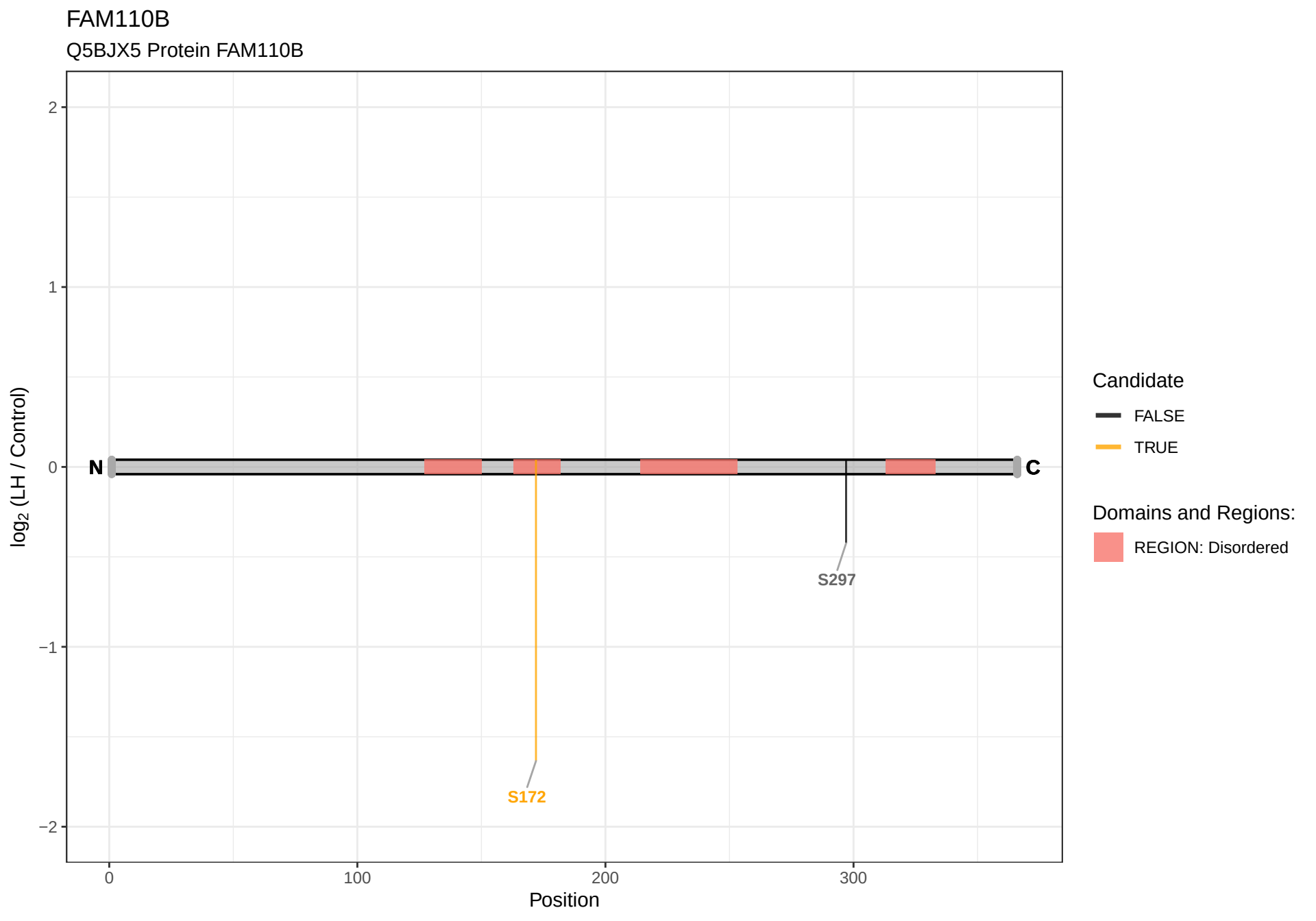

ETL4
M0R5H1 Enhancer trap locus 4
log2 (LH / Control)
Position
N
C
S1563
S1583
S381
S1917
S1911
S187
S887
S1809
S1543
S1881
T488
S1821
S1914
S1567
S1054
S379
S1051
S1856
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AIP3
REGION: Disordered

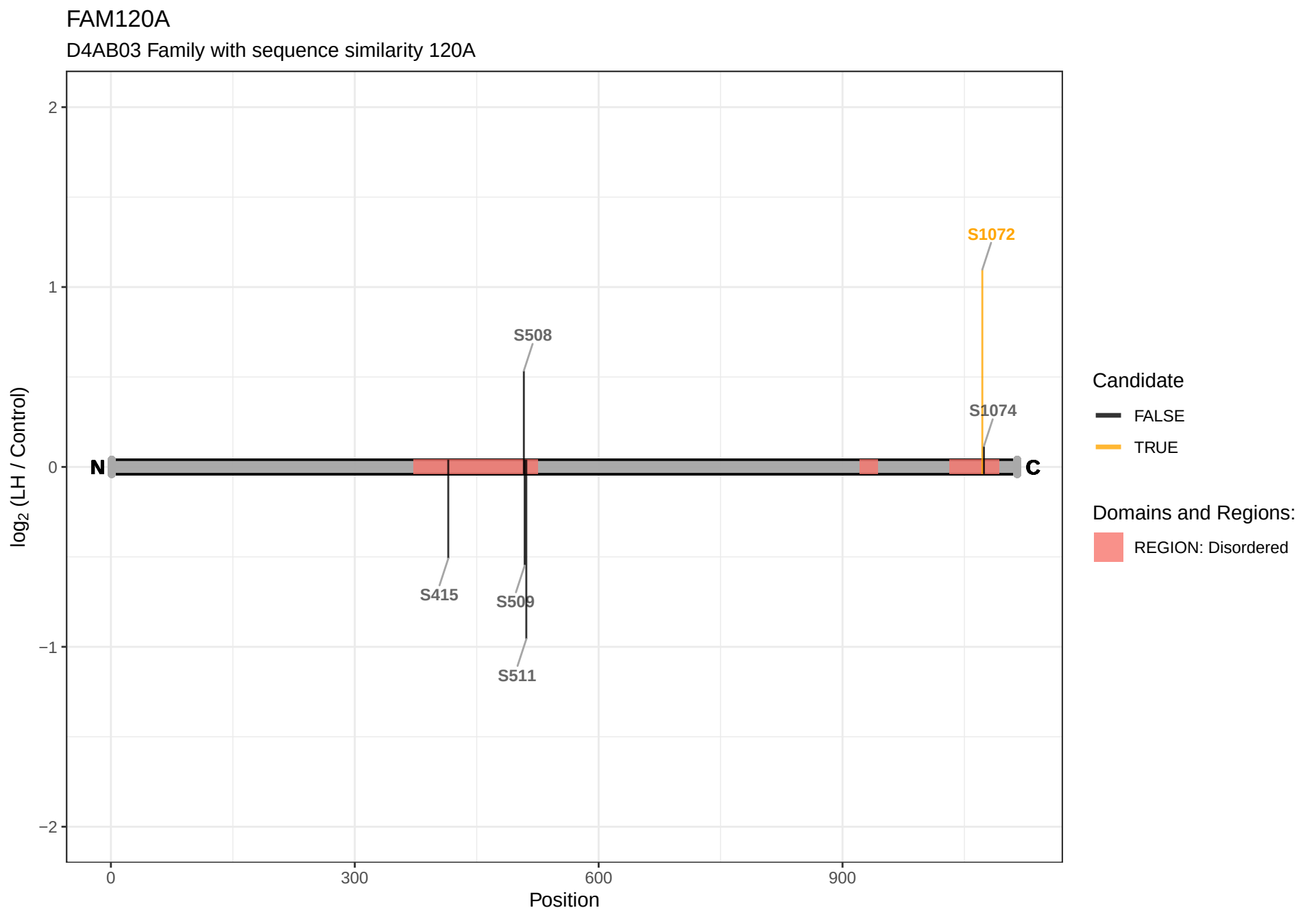

EVL
O08719 Ena/VASP−like protein
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
400
Position
N
C
T347
S353
S335
T307
S308
S358
S250
S373
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WH1
REGION: Disordered
REGION: EVH2
REGION: EVH2 block A
REGION: EVH2 block B
REGION: EVH2 block C
REGION: Required for interaction with ZDHHC17

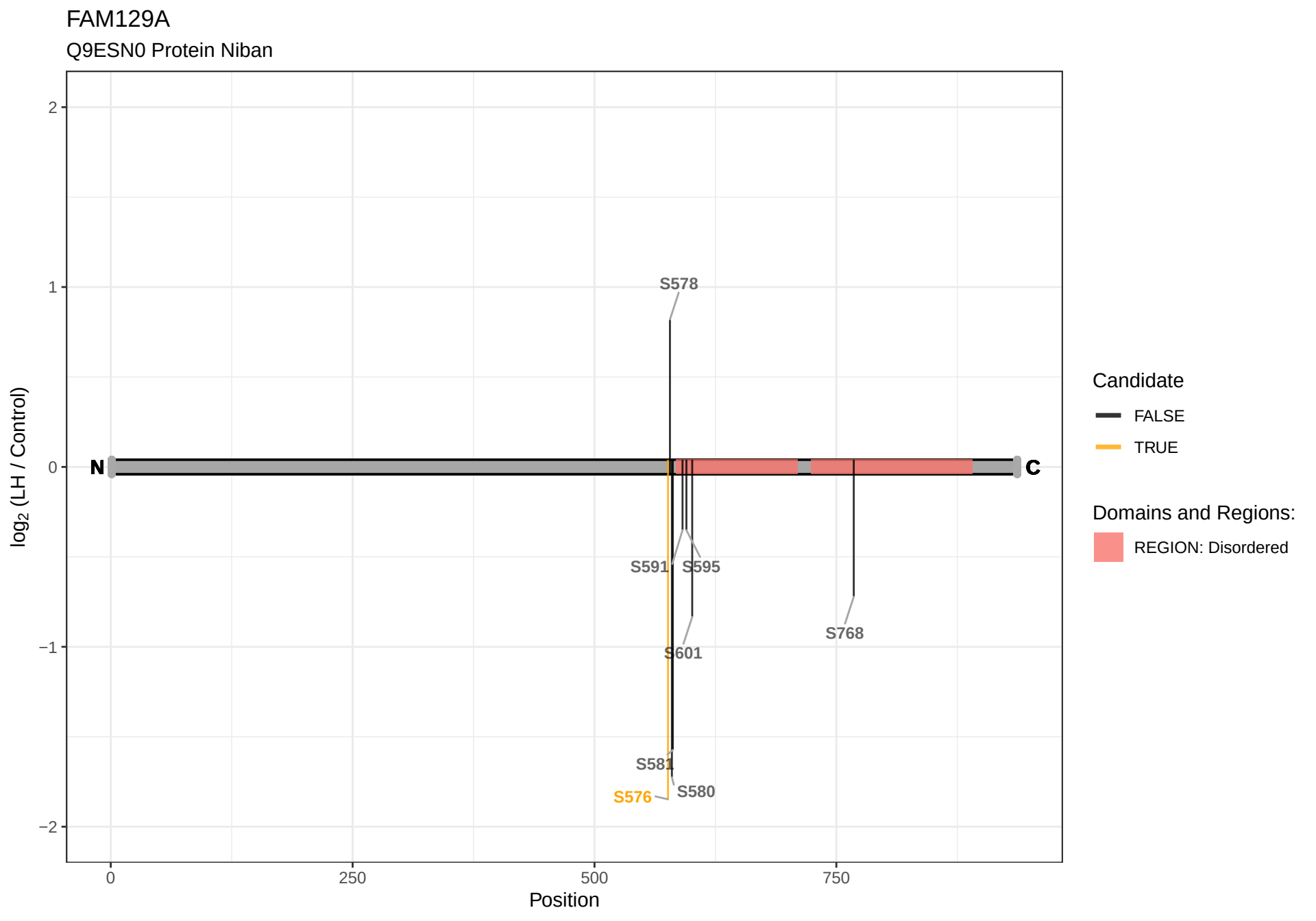

EXOC1
F1LQN9 Exocyst complex component 1
log2 (LH / Control)
3
2
1
0
−1
−2
−3
N
C
S300
S297
S290
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Sec3−PIP2_bind
REGION: Disordered

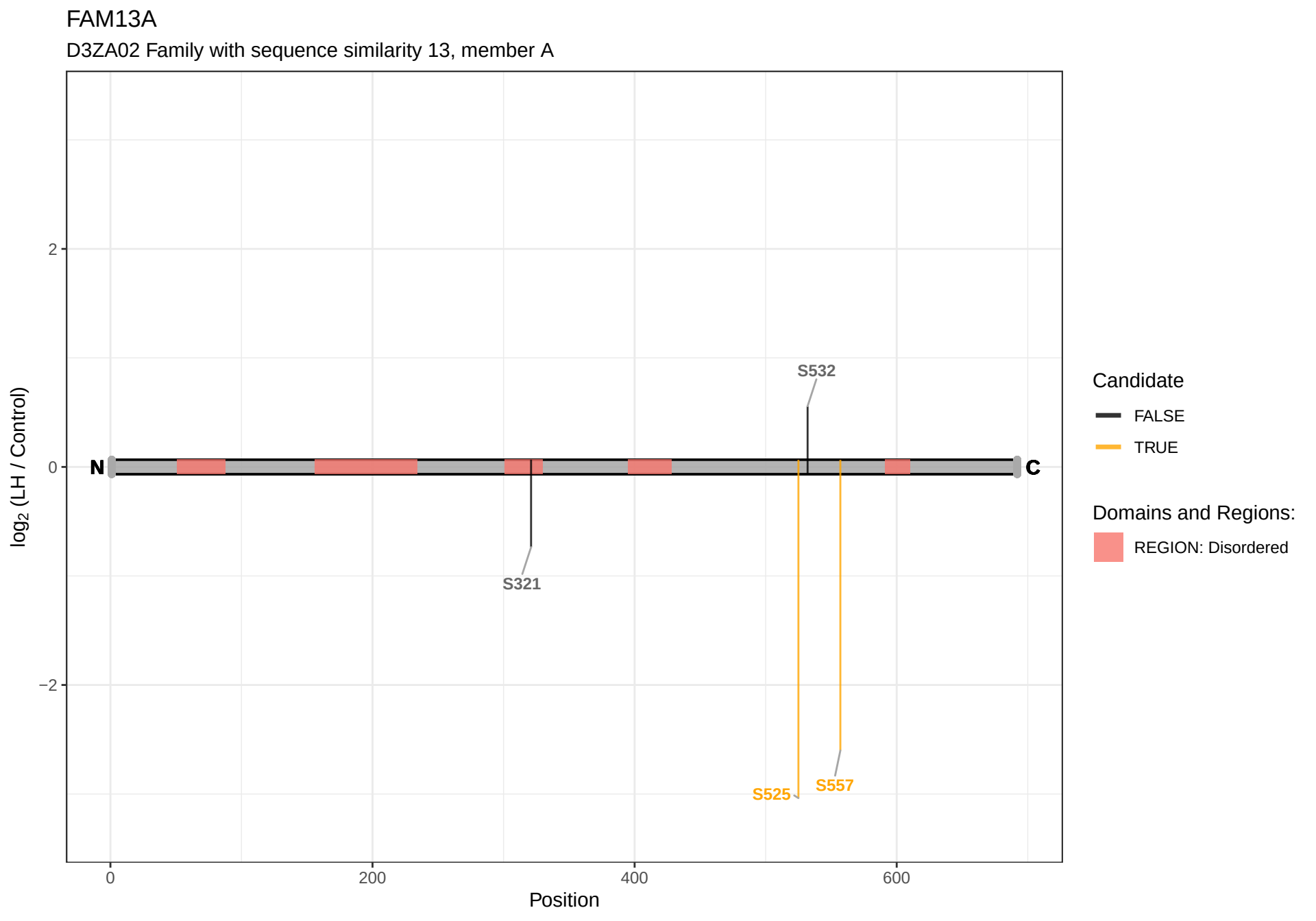

EXOC7
O54922 Exocyst complex component 7
log2 (LH / Control)
2
1
0
−1
−2
N
C
S250
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered
REGION: SEC8 and ARHQ binding

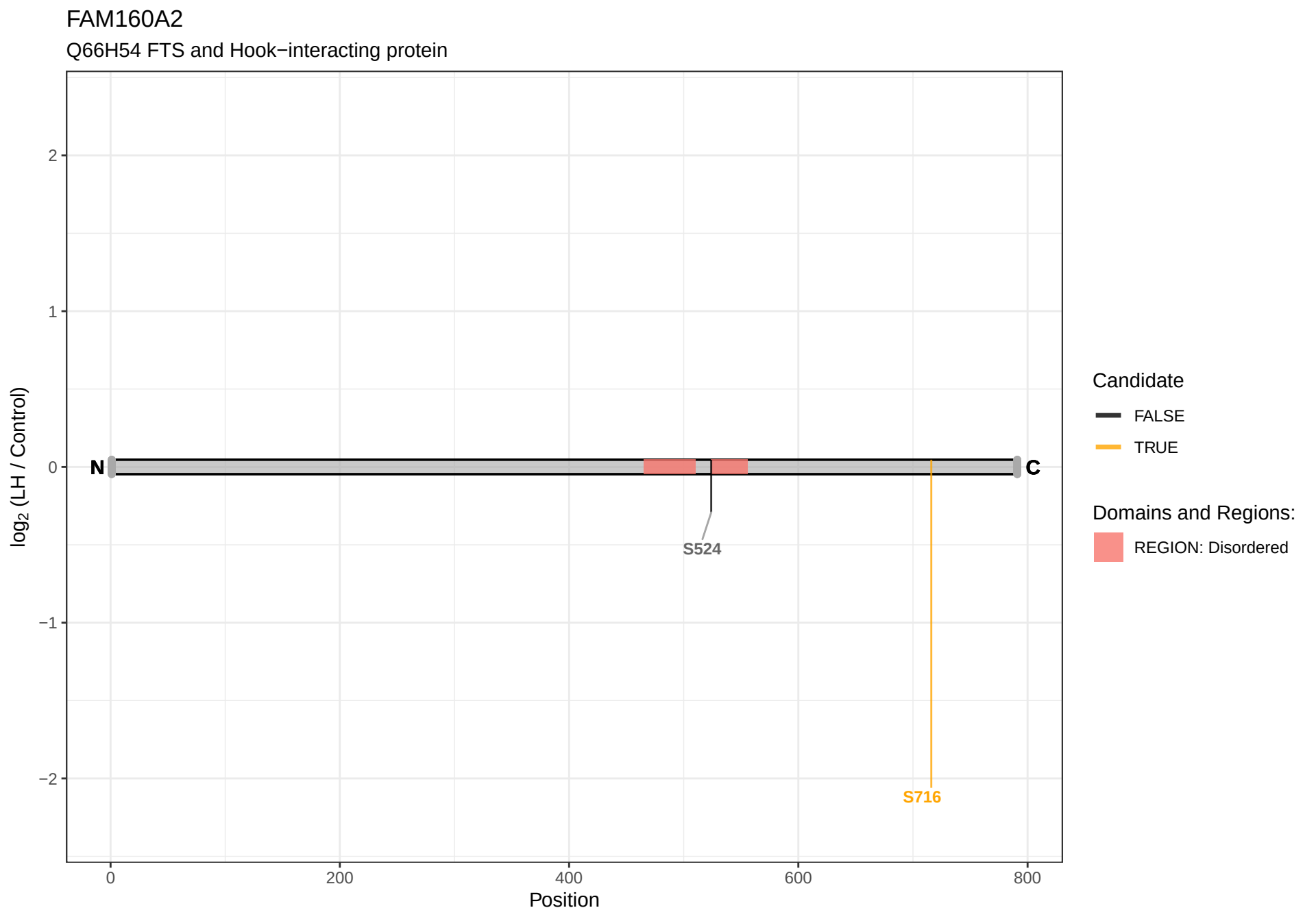

F11R
Q9JHY1 Junctional adhesion molecule A
2
1
0
−1
−2
log2 (LH / Control)
S285
S288
N
C
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Ig−like V−type 1
DOMAIN: Ig−like V−type 2

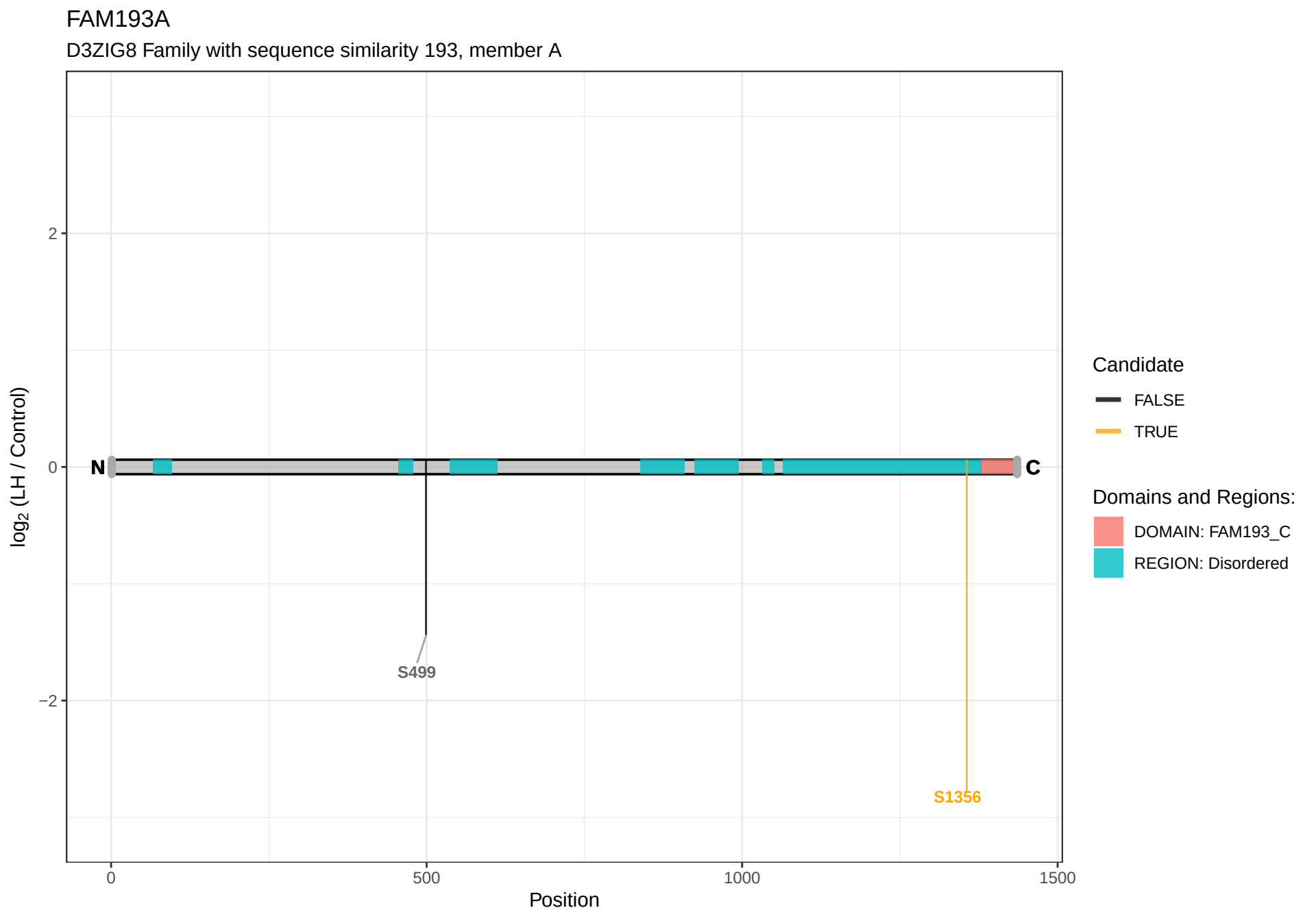

FAM110B
Q5BJX5 Protein FAM110B
2
1
0
−1
−2
log2 (LH / Control)
N
C
S297
S172
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

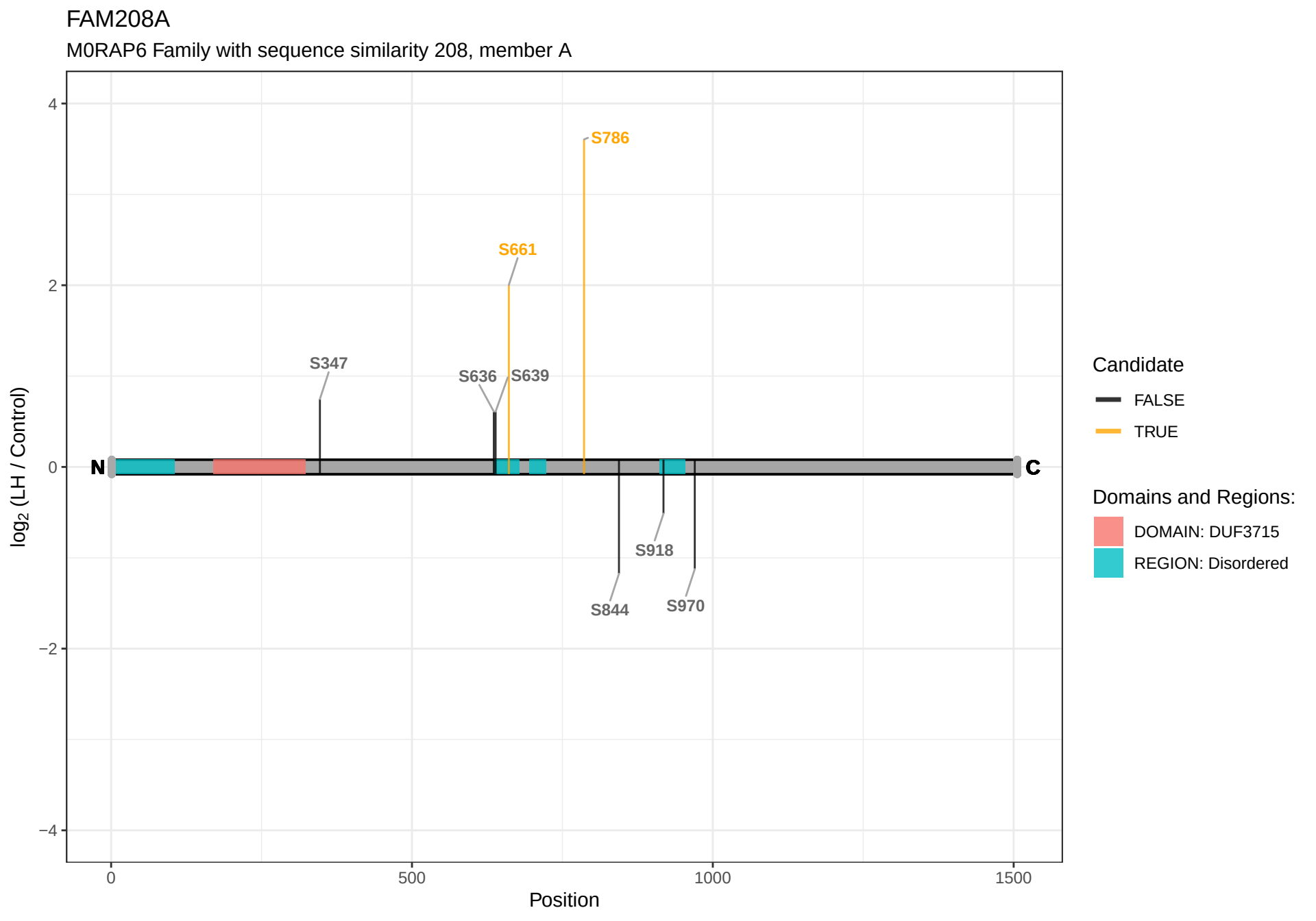

FAM120A
D4AB03 Family with sequence similarity 120A
log2 (LH / Control)
2
1
0
−1
−2
N
C
S1072
S508
S1074
S415
S509
S511
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

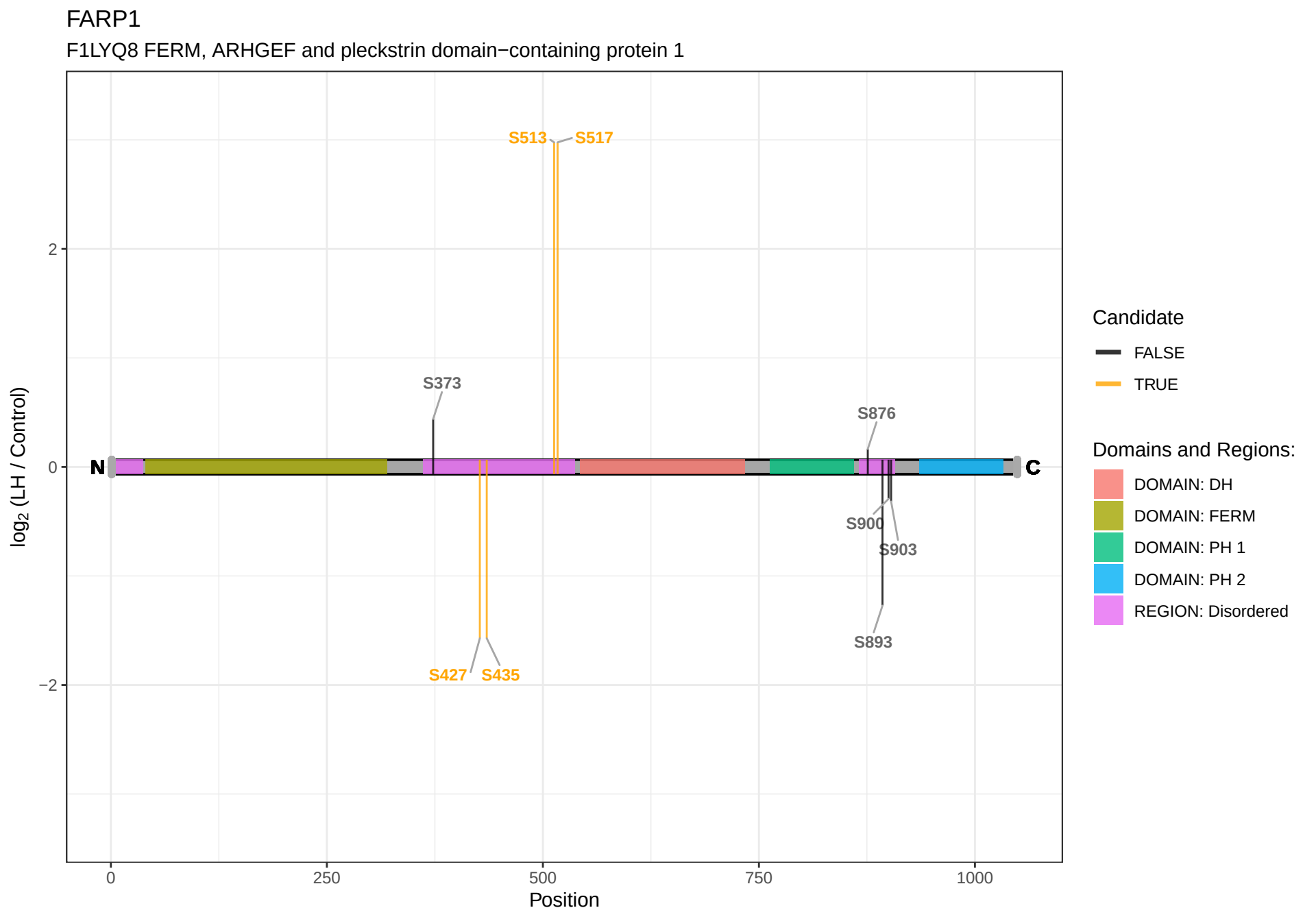

FAM129A
Q9ESN0 Protein Niban
log2 (LH / Control)
2
1
0
−1
−2
N
C
S578
S591
S595
S601
S768
S581
S580
S576
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

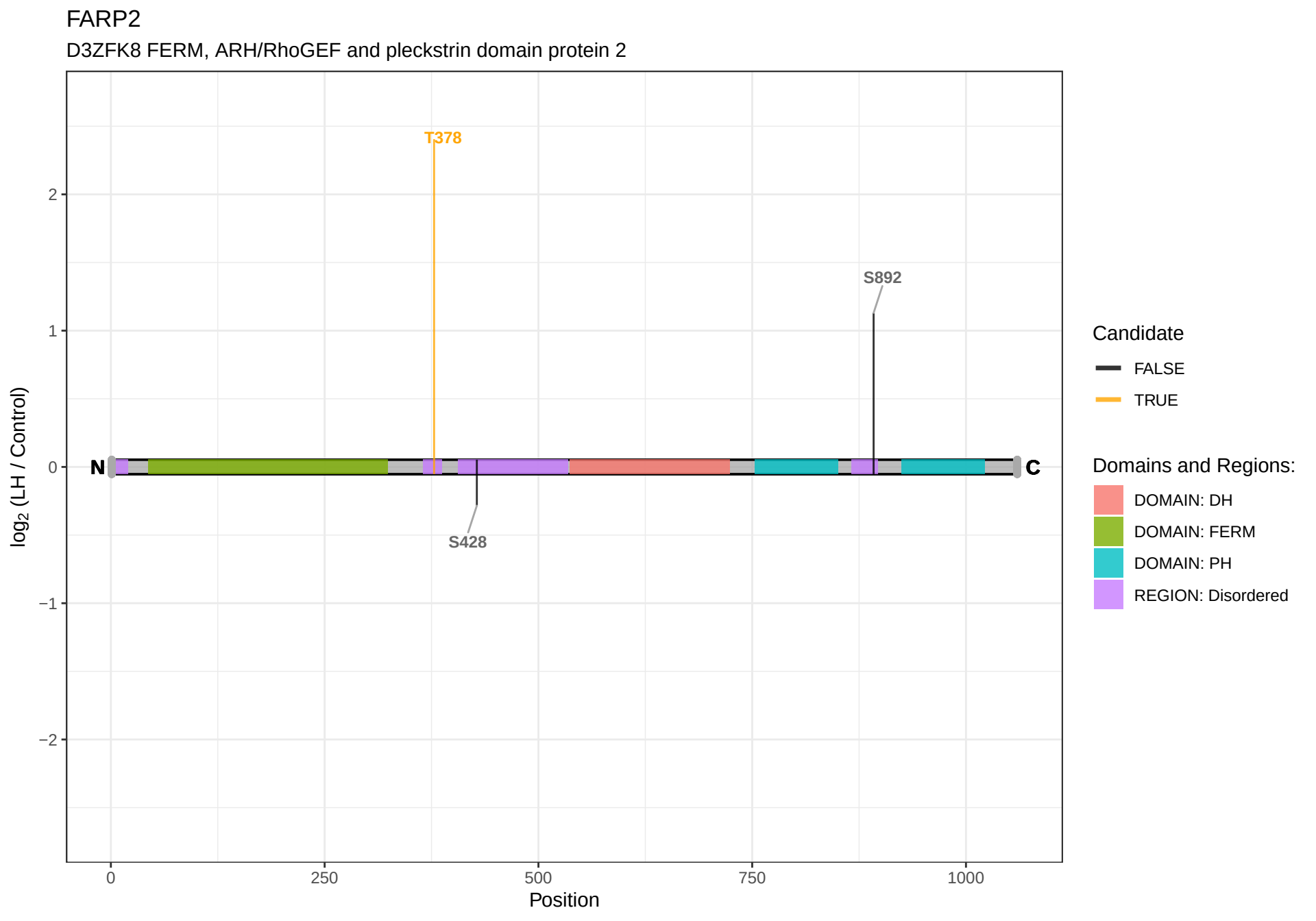

FAM13A
D3ZA02 Family with sequence similarity 13, member A
log2 (LH / Control)
2
0
−2
N
C
S532
S321
S525
S557
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

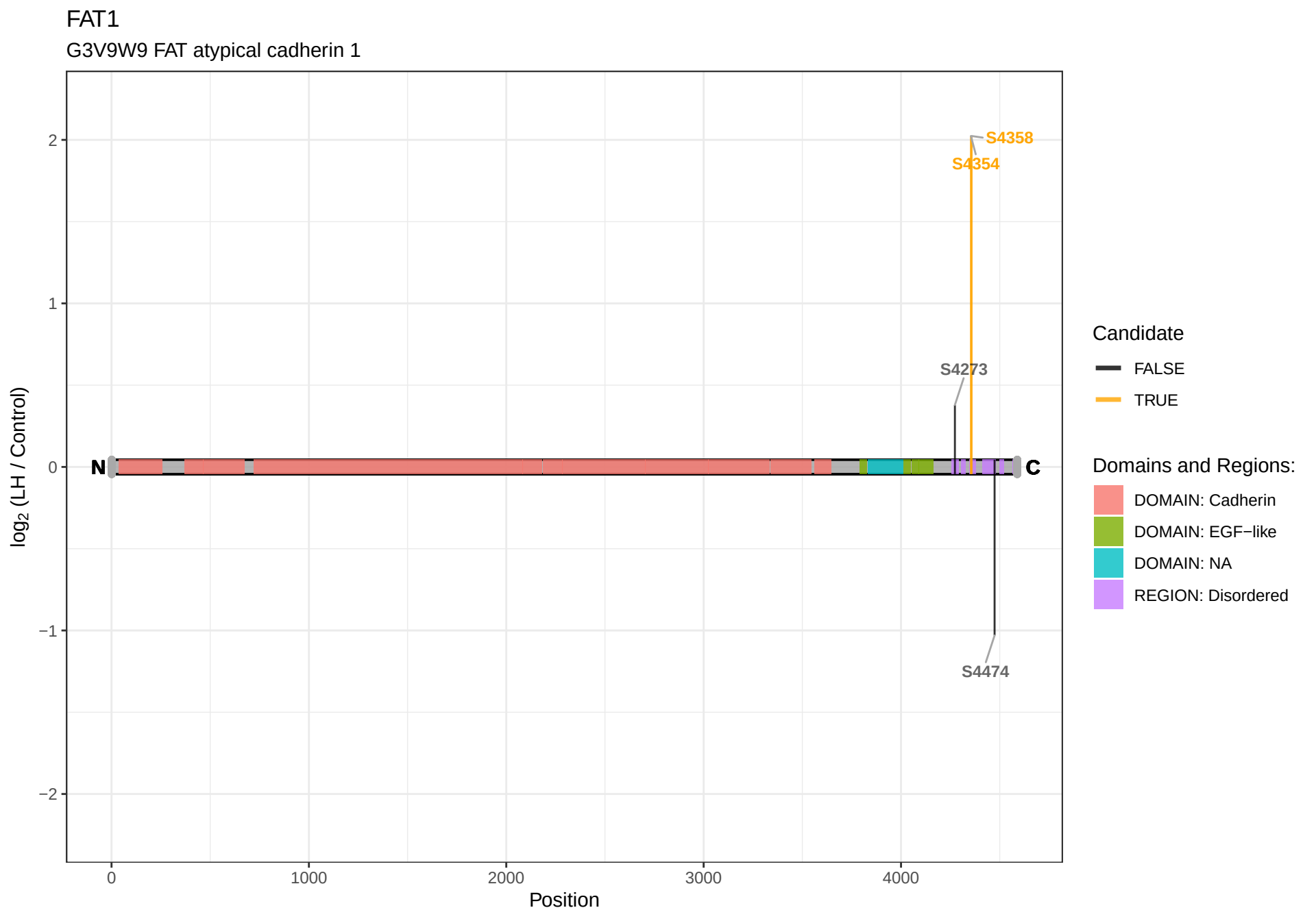

FAM160A2
Q66H54 FTS and Hook−interacting protein
log2 (LH / Control)
2
1
0
−1
−2
N
C
S524
S716
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

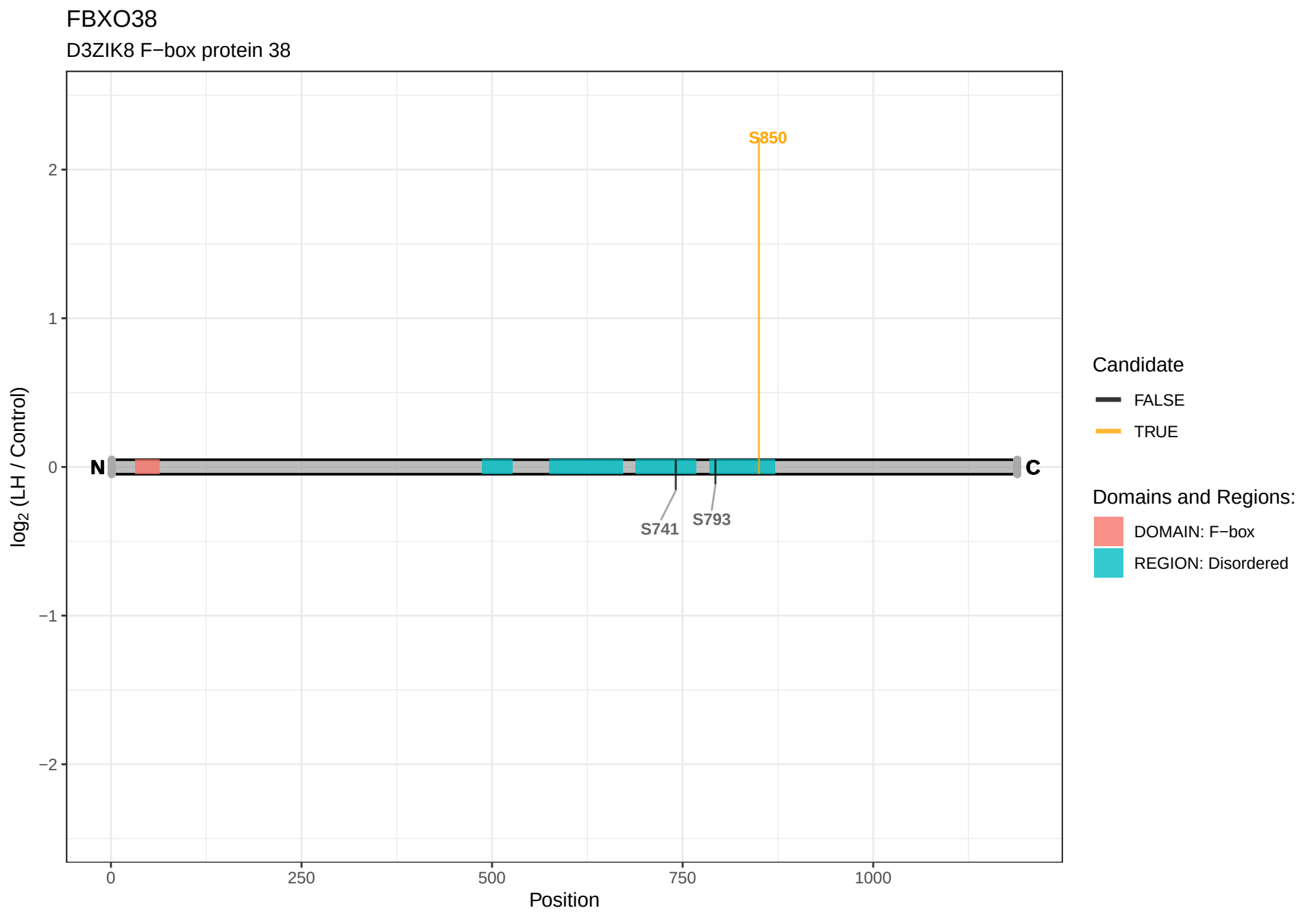

FAM193A
D3ZIG8 Family with sequence similarity 193, member A
log2 (LH / Control)
2
0
−2
N
C
S499
S1356
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: FAM193_C
REGION: Disordered

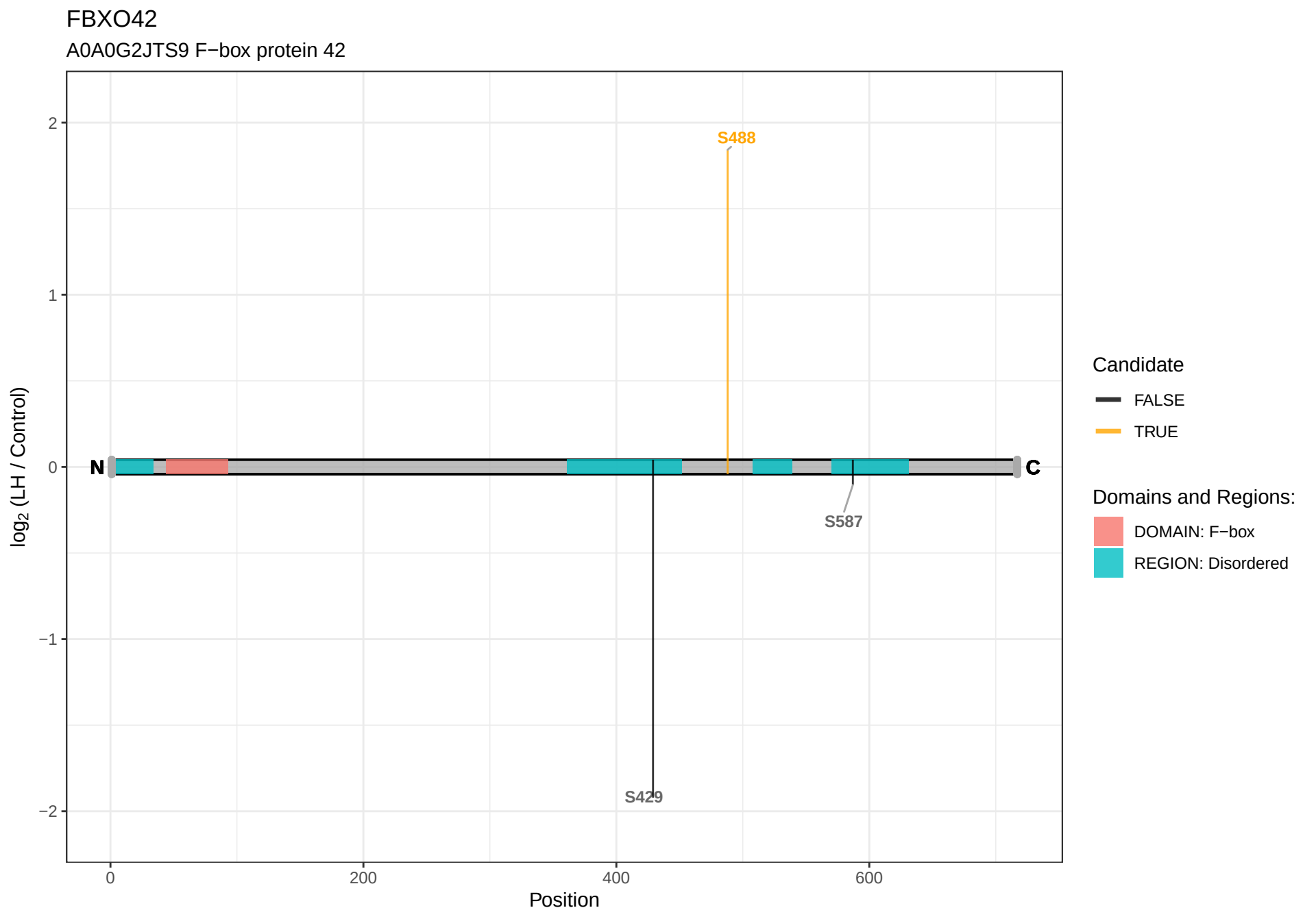

FAM208A
M0RAP6 Family with sequence similarity 208, member A
log2 (LH / Control)
4
2
0
−2
−4
0
500
1000
1500
Position
N
C
S786
S661
S347
S636
S639
S918
S844
S970
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DUF3715
REGION: Disordered

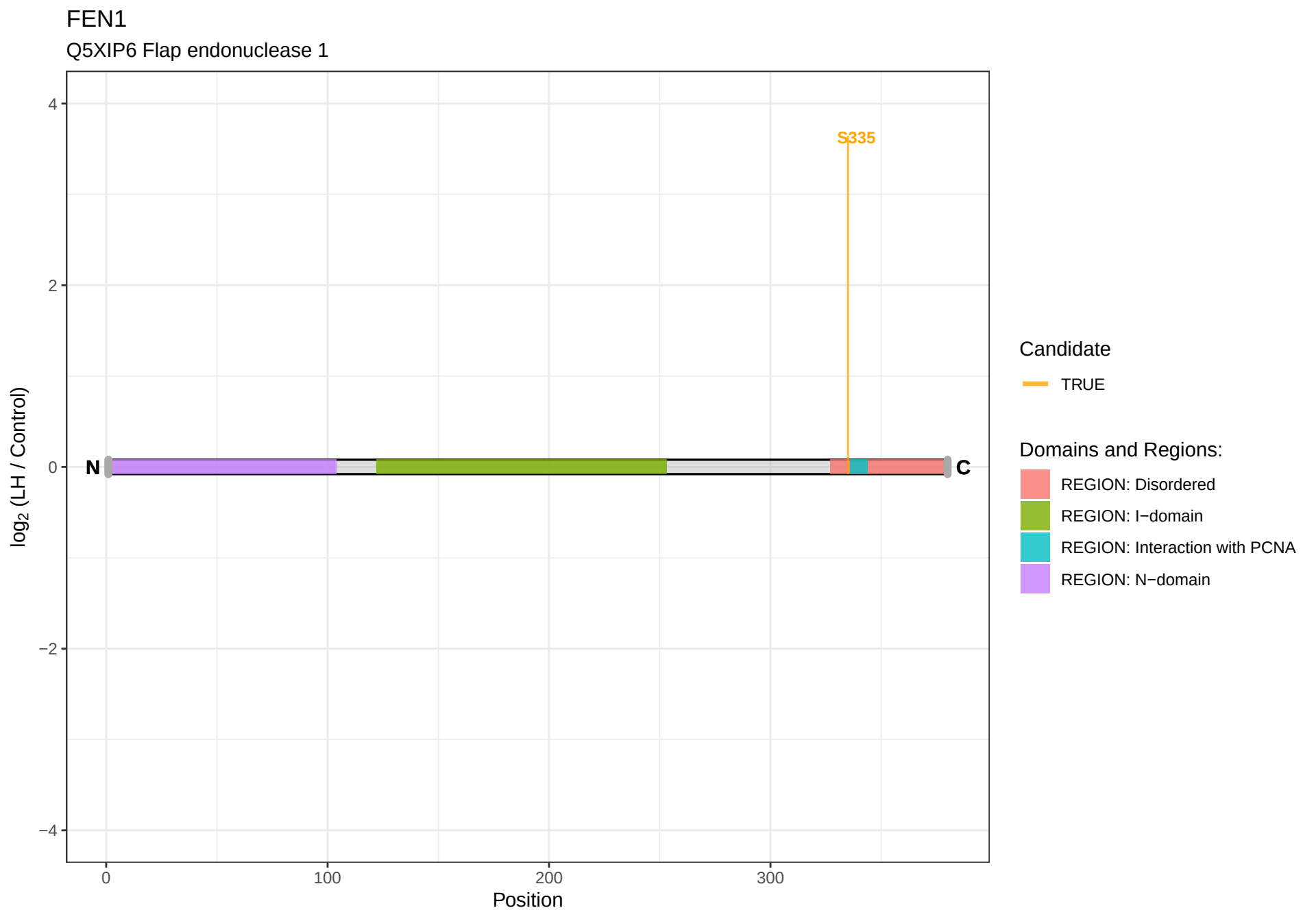

FARP1
F1LYQ8 FERM, ARHGEF and pleckstrin domain−containing protein 1
S513
S517
S373
S876
S900
S903
S893
S427
S435
N
C
2
0
−2
log2 (LH / Control)
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DH
DOMAIN: FERM
DOMAIN: PH 1
DOMAIN: PH 2
REGION: Disordered

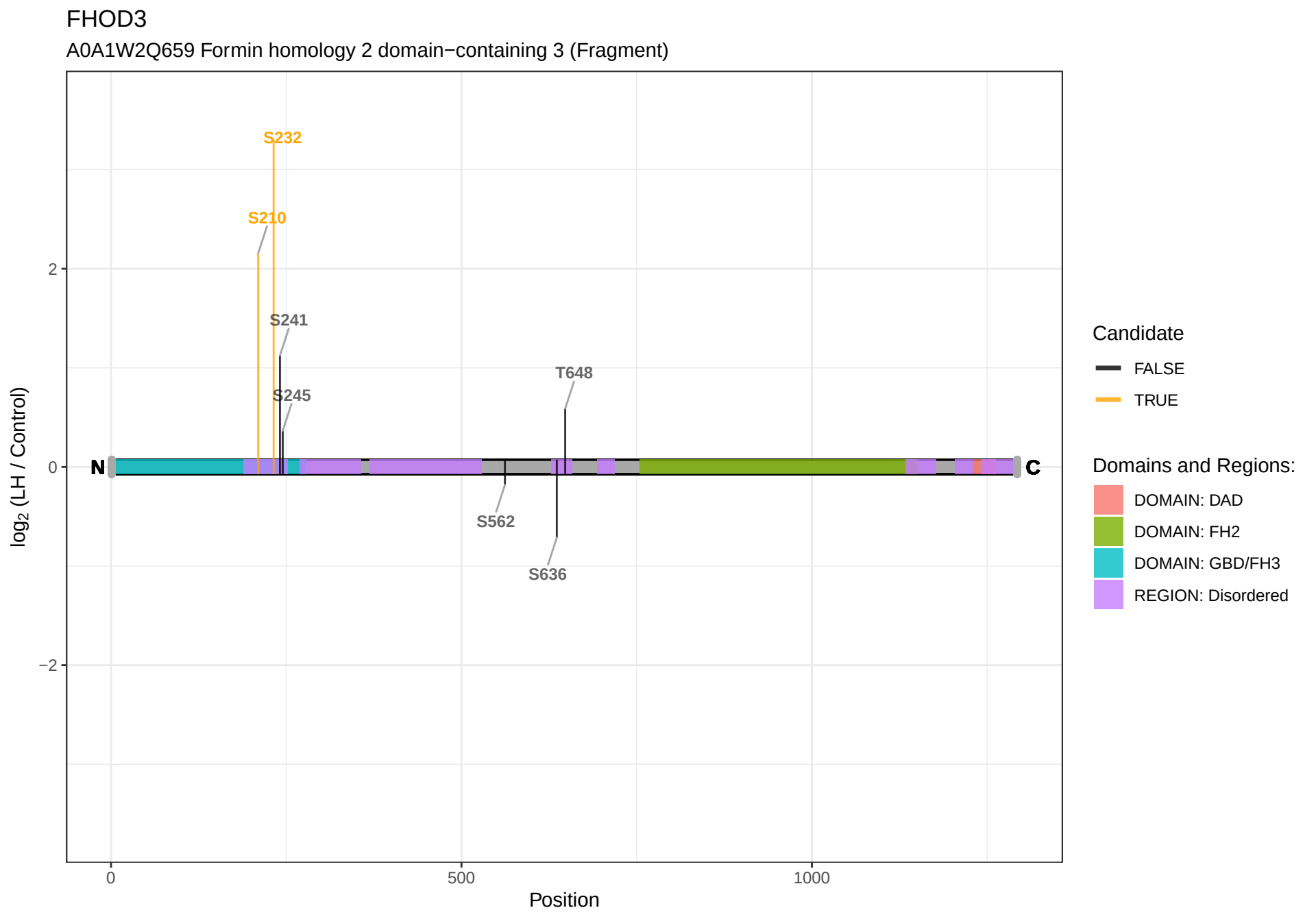

FARP2
D3ZFK8 FERM, ARH/RhoGEF and pleckstrin domain protein 2
T378
S892
S428
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DH
DOMAIN: FERM
DOMAIN: PH
REGION: Disordered

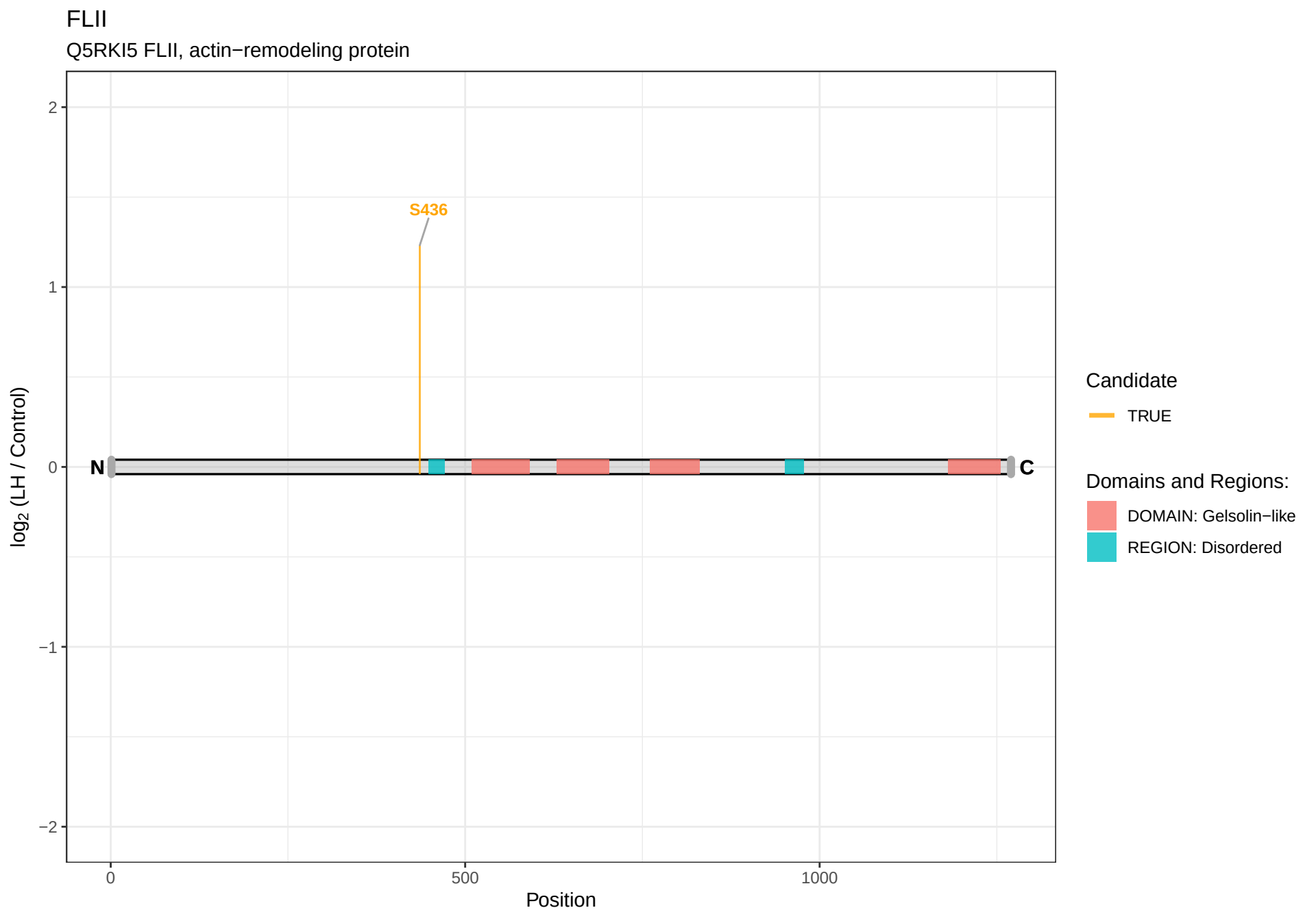

FAT1
G3V9W9 FAT atypical cadherin 1
S4358
S4354
S4273
S4474
N
C
log2 (LH / Control)
Position
0
1000
2000
3000
4000
2
1
0
−1
−2
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Cadherin
DOMAIN: EGF−like
DOMAIN: NA
REGION: Disordered

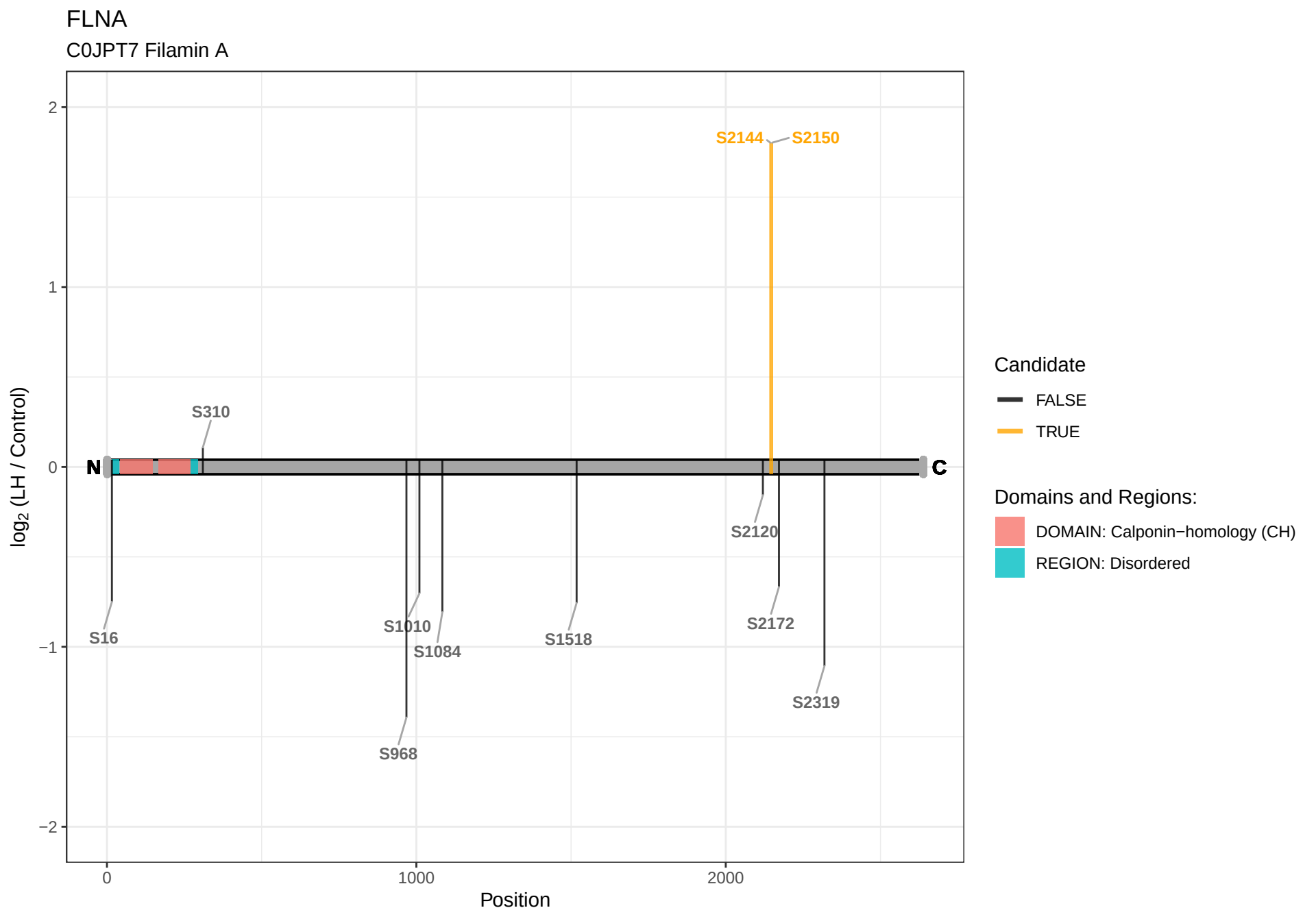

FBXO38
D3ZIK8 F−box protein 38
S850
S741
S793
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: F−box
REGION: Disordered

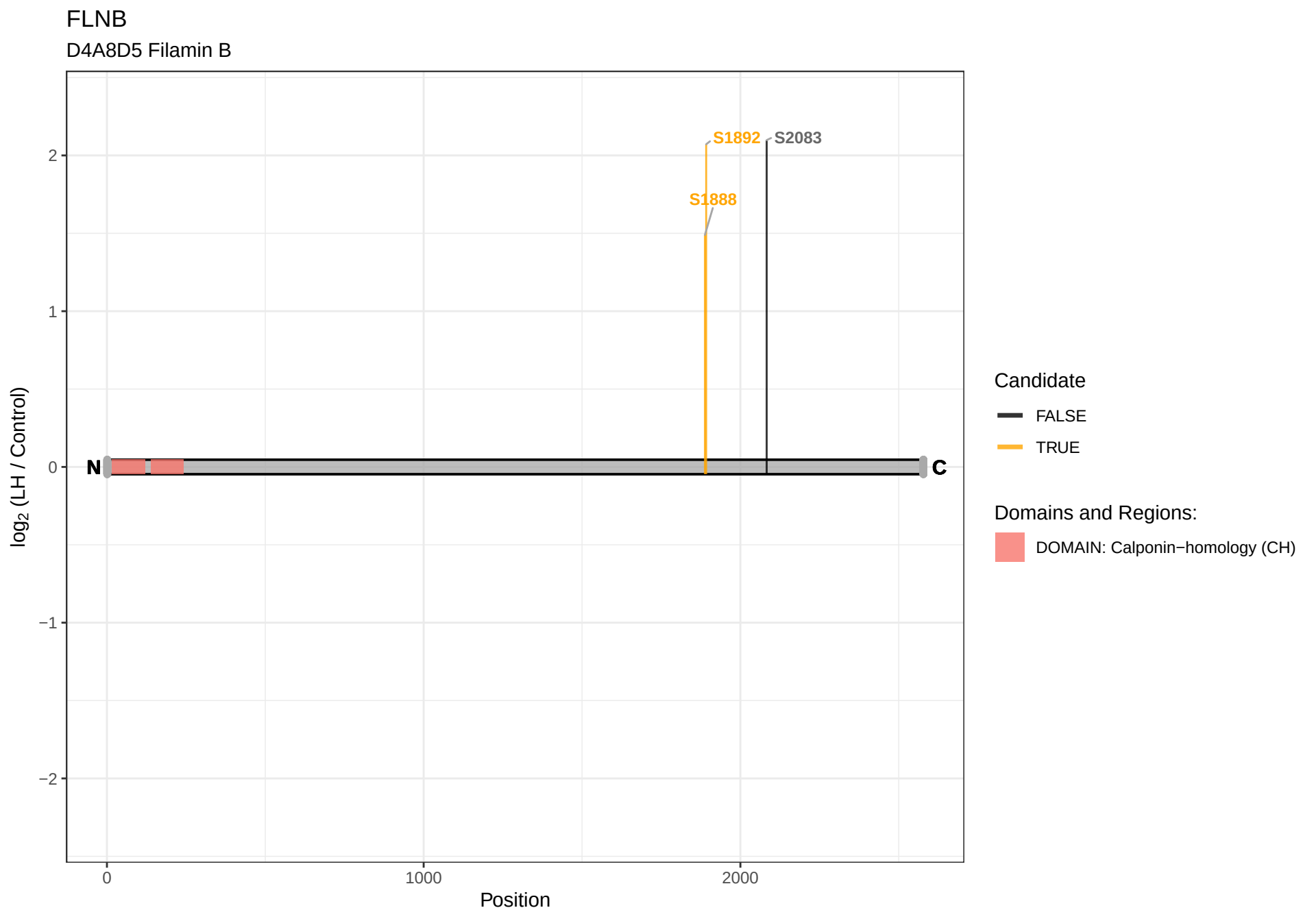

FBXO42
A0A0G2JTS9 F−box protein 42
S488
S587
S429
N
C
log2 (LH / Control)
Position
0
200
400
600
2
1
0
−1
−2
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: F−box
REGION: Disordered

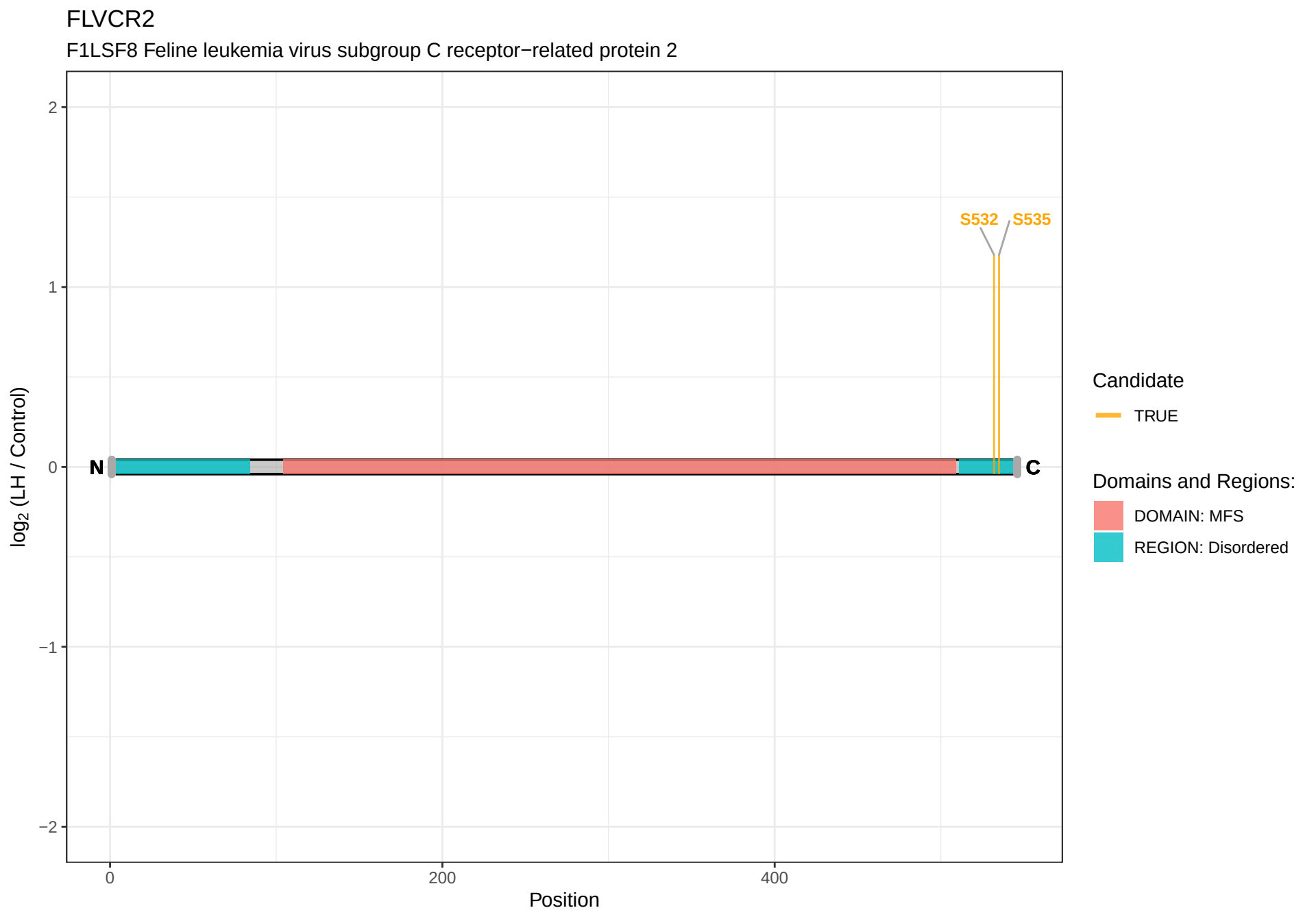

FEN1
Q5XIP6 Flap endonuclease 1
S335
N
C
4
2
0
−2
−4
0
100
200
300
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
REGION: Disordered
REGION: I−domain
REGION: Interaction with PCNA
REGION: N−domain

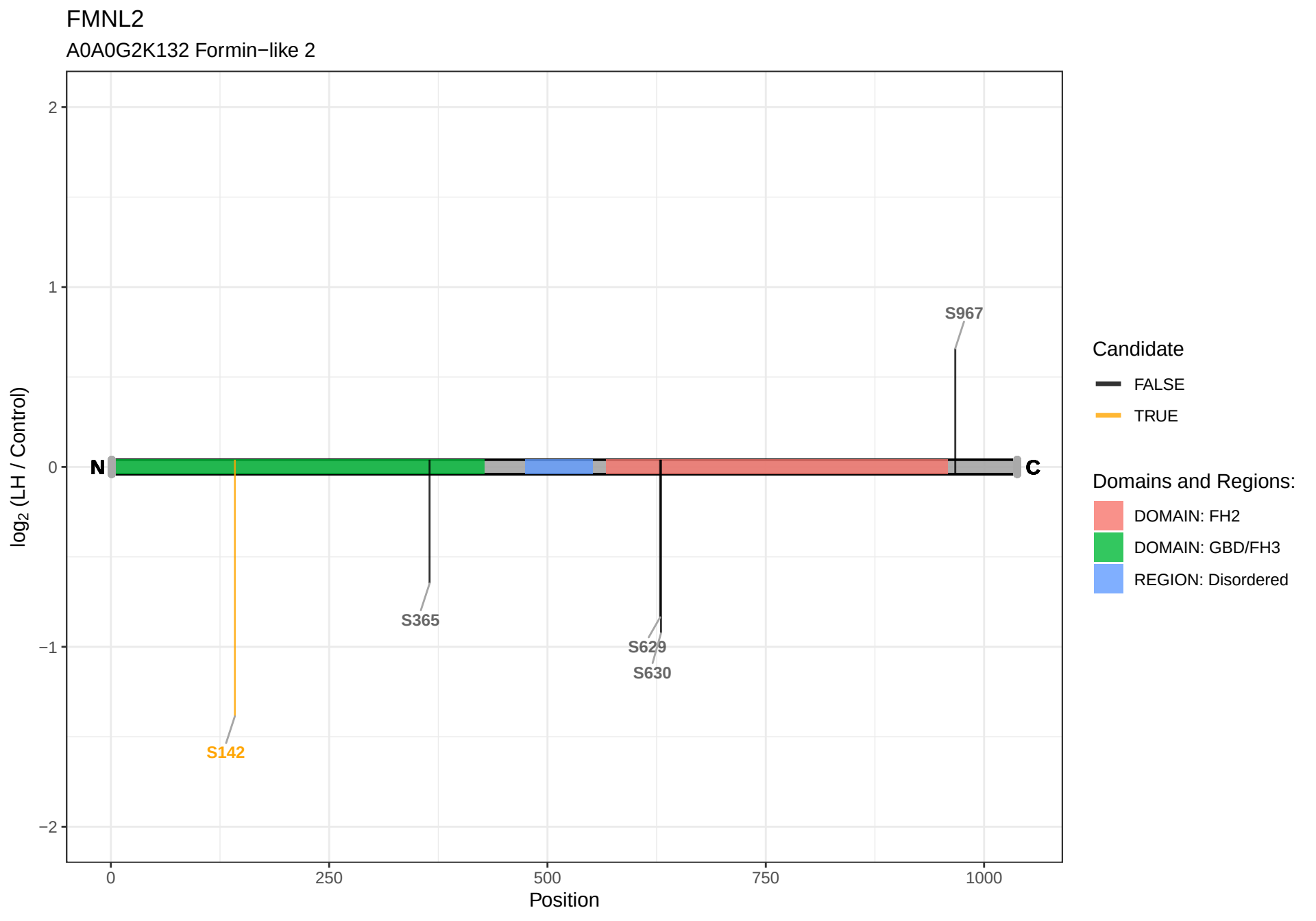

FHOD3
A0A1W2Q659 Formin homology 2 domain−containing 3 (Fragment)
S232
S210
S241
S245
T648
S562
S636
N
C
2
0
−2
log2 (LH / Control)
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DAD
DOMAIN: FH2
DOMAIN: GBD/FH3
REGION: Disordered

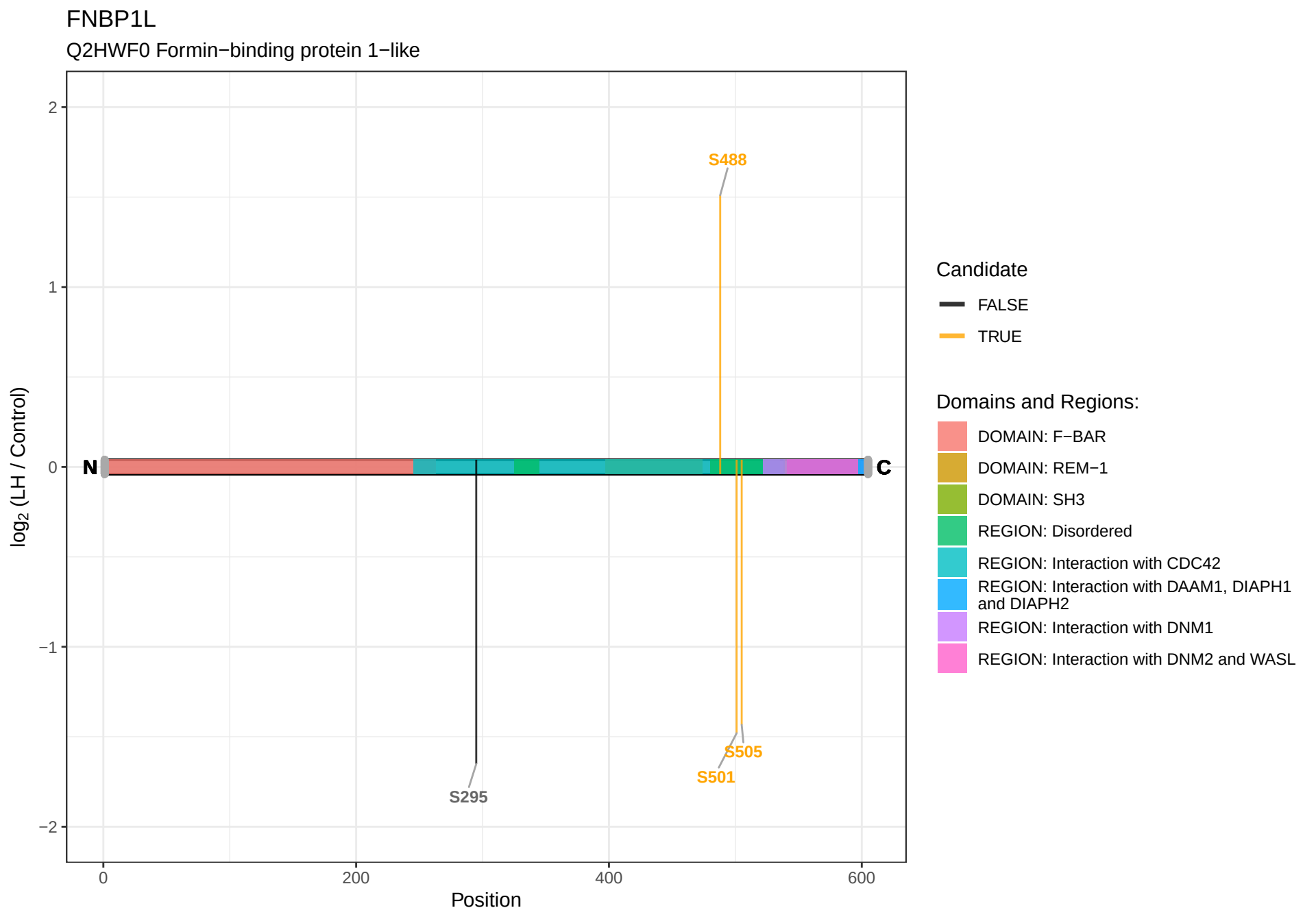

FLII
Q5RKI5 FLII, actin−remodeling protein
S436
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Gelsolin−like
REGION: Disordered

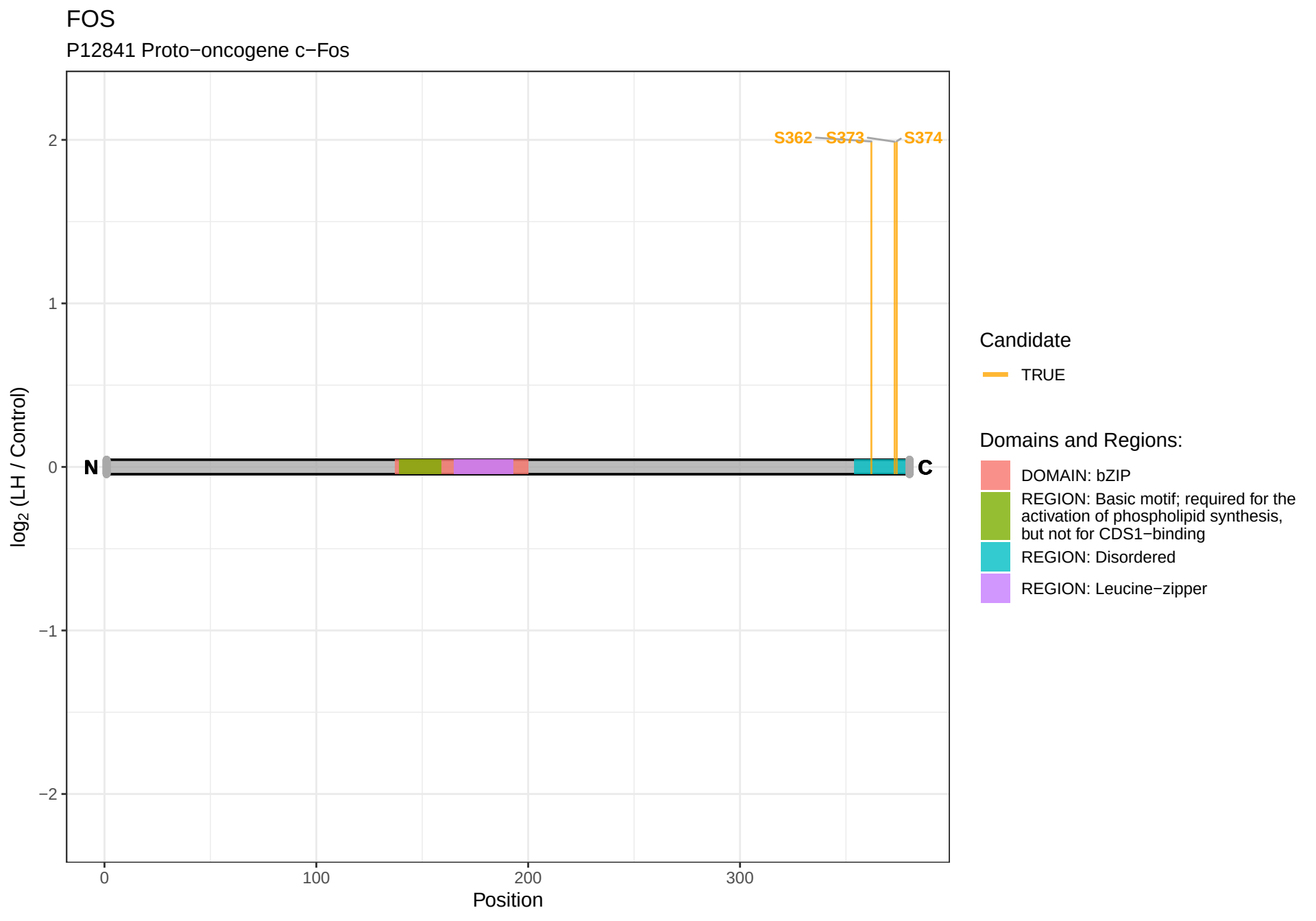

FLNA
C0JPT7 Filamin A
log2 (LH / Control)
Position
N
C
S16
S310
S968
S1010
S1084
S1518
S2120
S2144
S2150
S2172
S2319
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Calponin−homology (CH)
REGION: Disordered

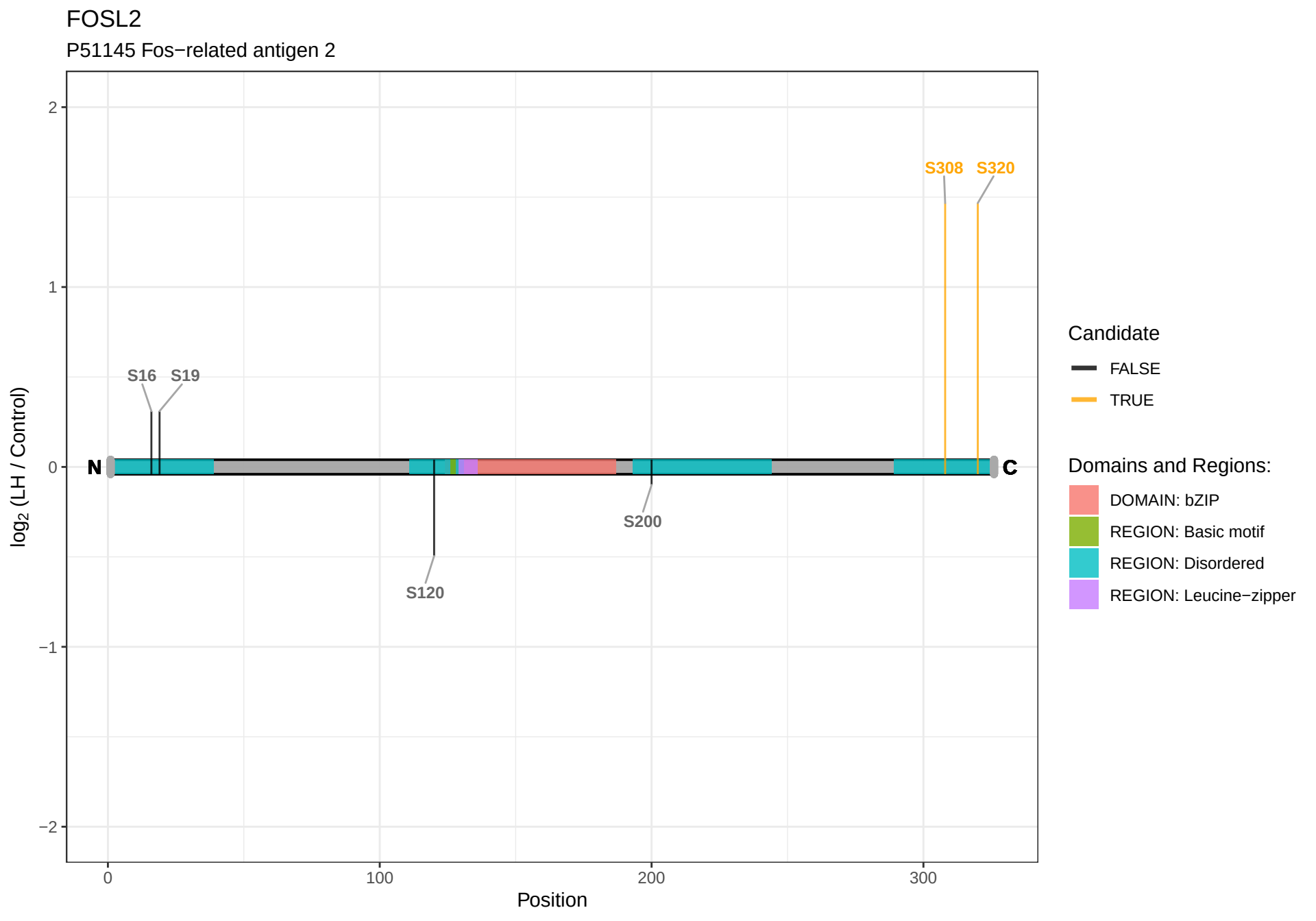

FLNB
D4A8D5 Filamin B
S1892
S2083
S1888
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
1000
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Calponin−homology (CH)

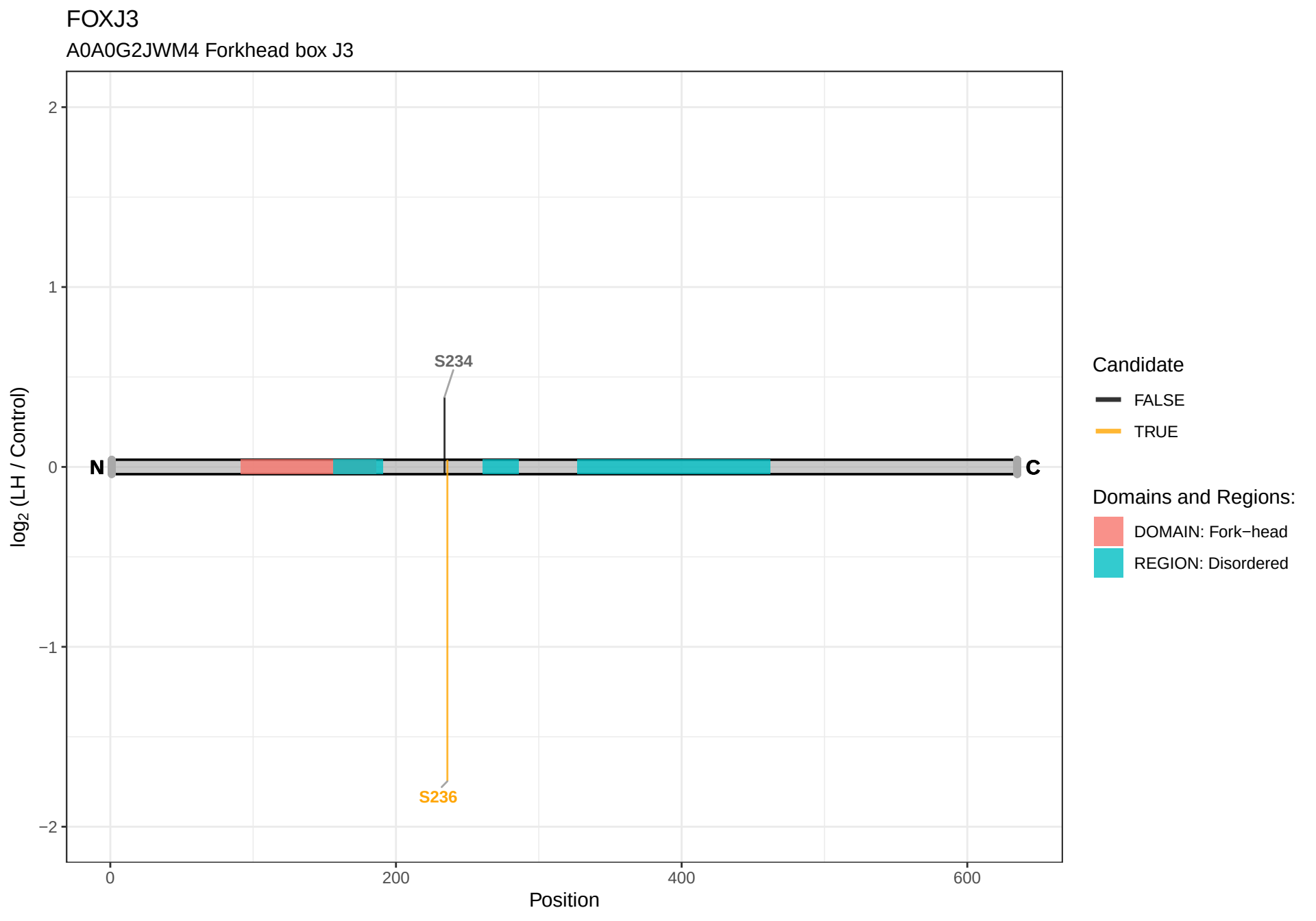

FLVCR2
F1LSF8 Feline leukemia virus subgroup C receptor−related protein 2
log2 (LH / Control)
2
1
0
−1
−2
N
C
S532
S535
0
200
400
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: MFS
REGION: Disordered

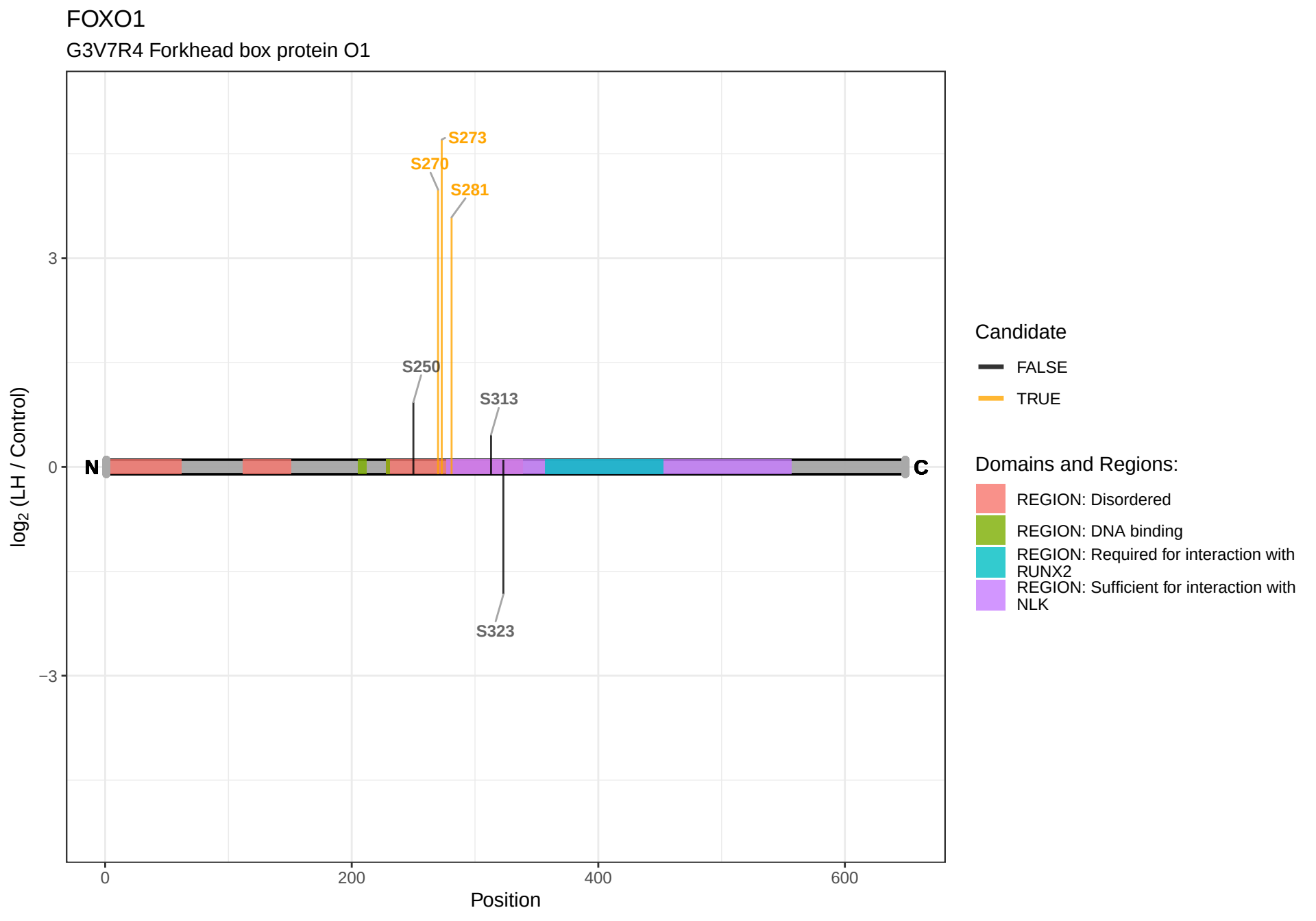

FMNL2
A0A0G2K132 Formin−like 2
log2 (LH / Control)
2
1
0
−1
−2
0
250
500
750
1000
Position
N
C
S967
S365
S629
S630
S142
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: FH2
DOMAIN: GBD/FH3
REGION: Disordered

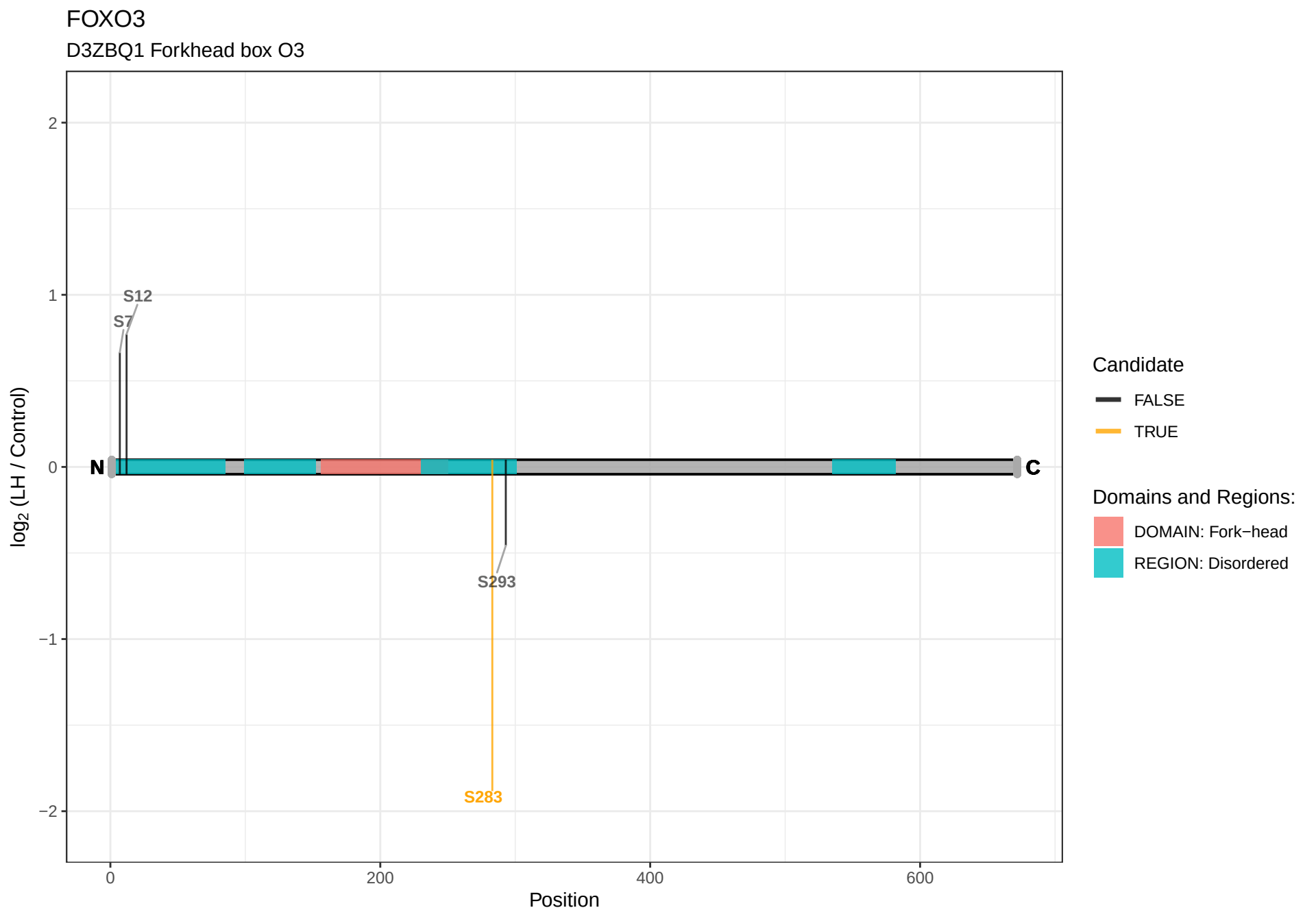

FNBP1L
Q2HWF0 Formin−binding protein 1−like
log2 (LH / Control)
2
1
0
−1
−2
N
C
S488
S295
S505
S501
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: F−BAR
DOMAIN: REM−1
DOMAIN: SH3
REGION: Disordered
REGION: Interaction with CDC42
REGION: Interaction with DAAM1, DIAPH1 and DIAPH2
REGION: Interaction with DNM1
REGION: Interaction with DNM2 and WASL

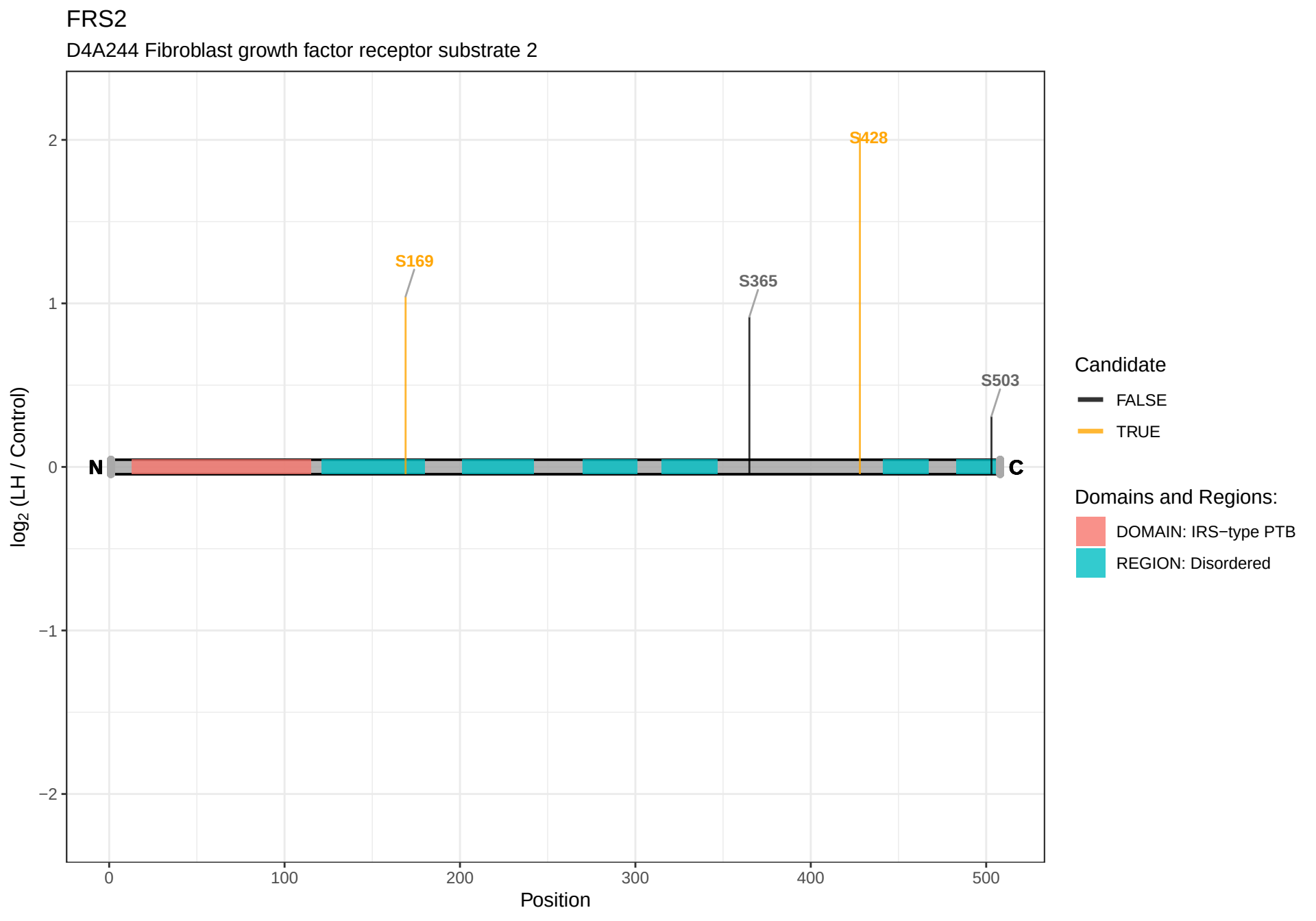

FOS
P12841 Proto−oncogene c−Fos
S362
S373
S374
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: bZIP
REGION: Basic motif; required for the activation of phospholipid synthesis, but not for CDS1−binding
REGION: Disordered
REGION: Leucine−zipper

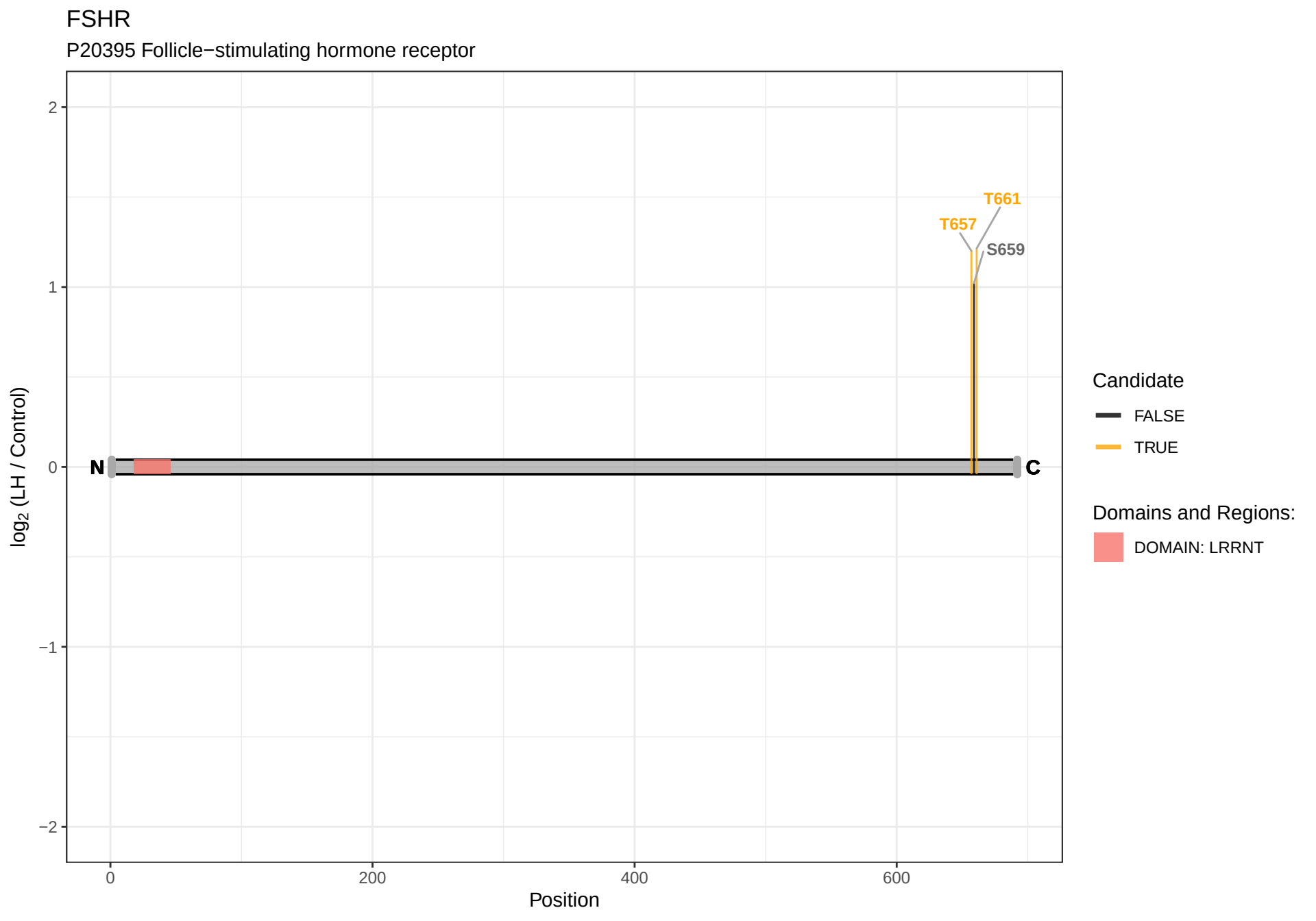

FOSL2
P51145 Fos−related antigen 2
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
Position
N
C
S16
S19
S120
S200
S308
S320
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: bZIP
REGION: Basic motif
REGION: Disordered
REGION: Leucine−zipper

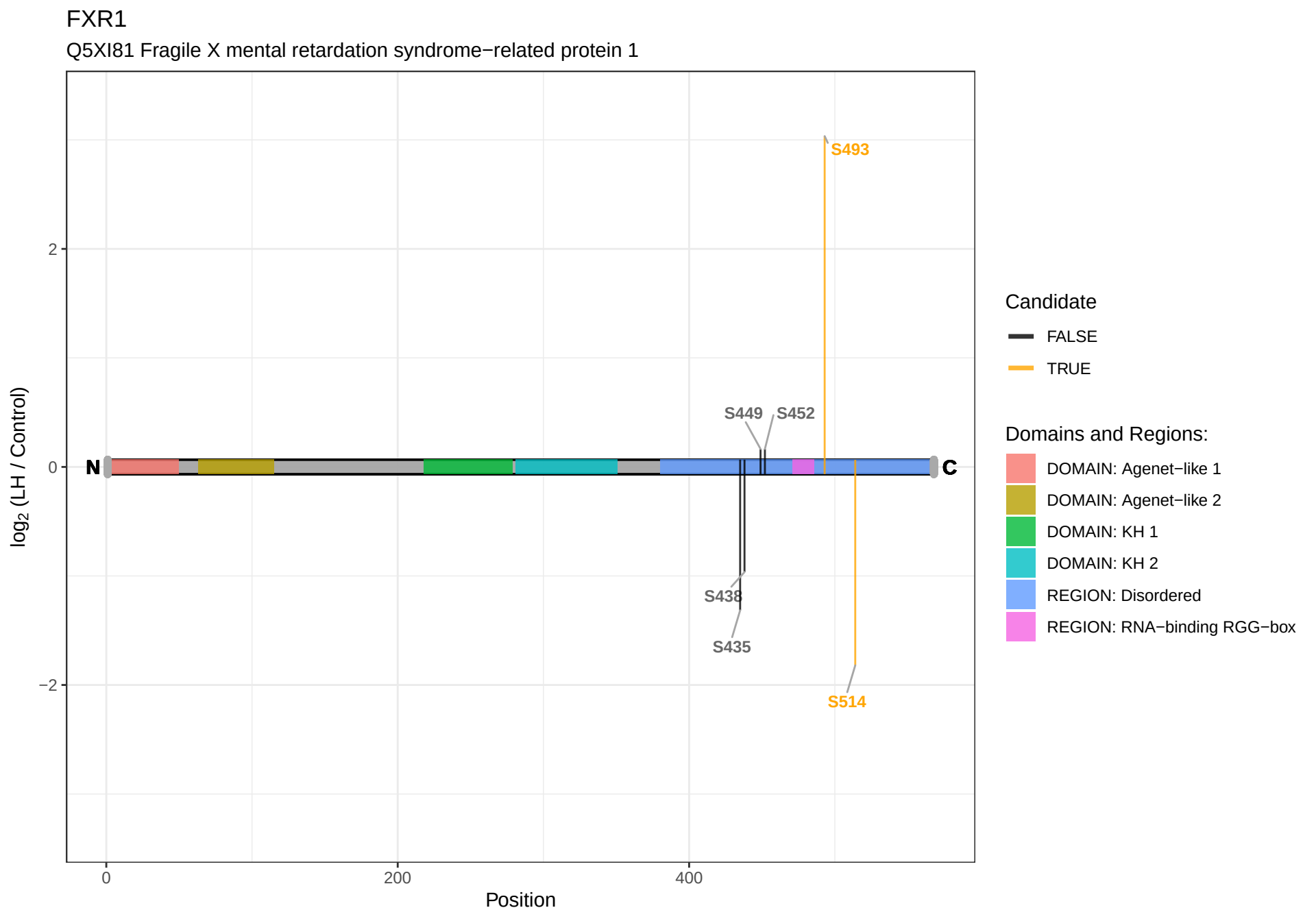

FOXJ3
A0A0G2JWM4 Forkhead box J3
2
1
0
−1
−2
log2 (LH / Control)
S234
S236
N
C
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Fork−head
REGION: Disordered

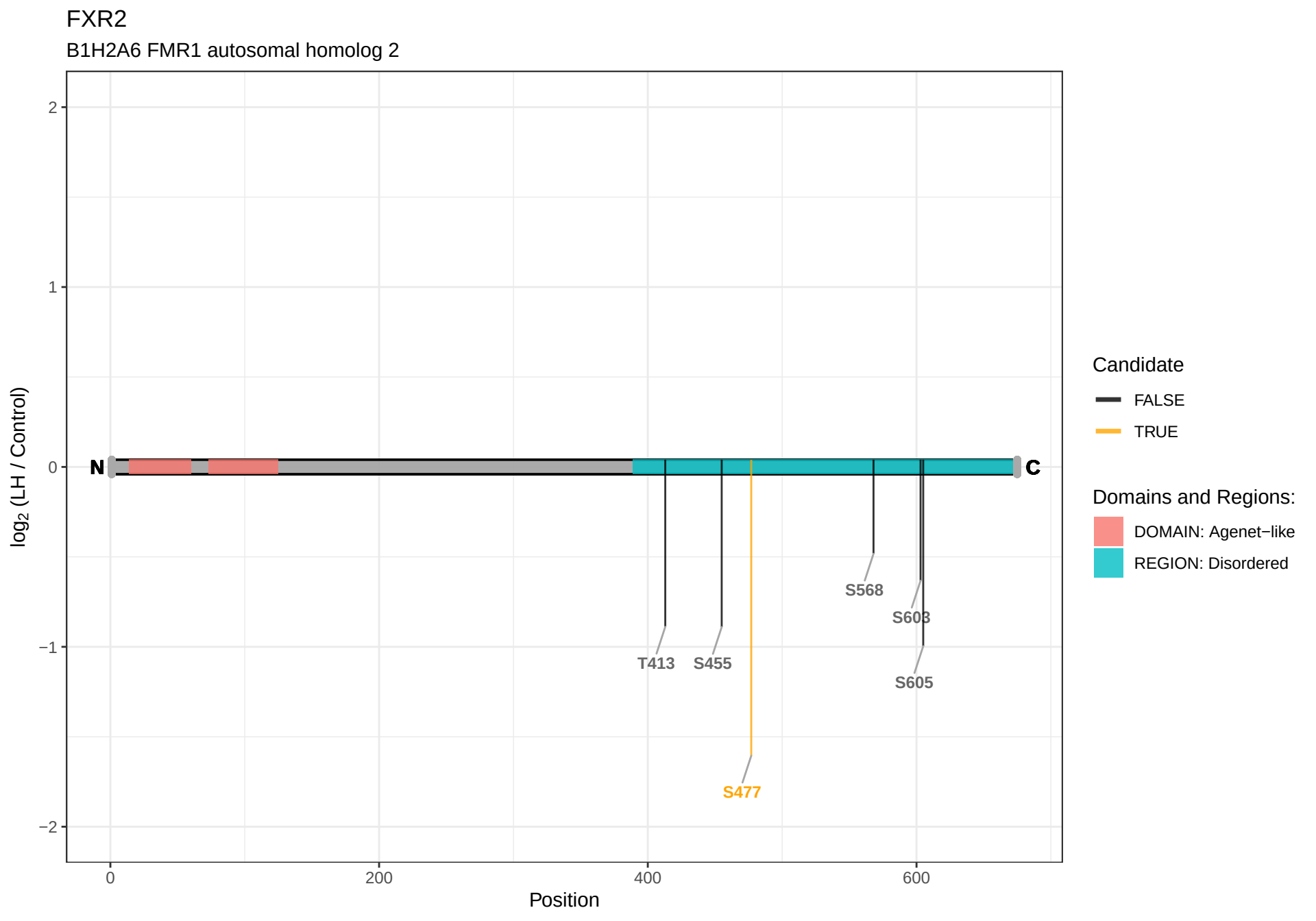

FOXO1
G3V7R4 Forkhead box protein O1
S273
S270
S281
S250
S313
S323
N
C
3
0
−3
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: DNA binding
REGION: Required for interaction with RUNX2
REGION: Sufficient for interaction with NLK

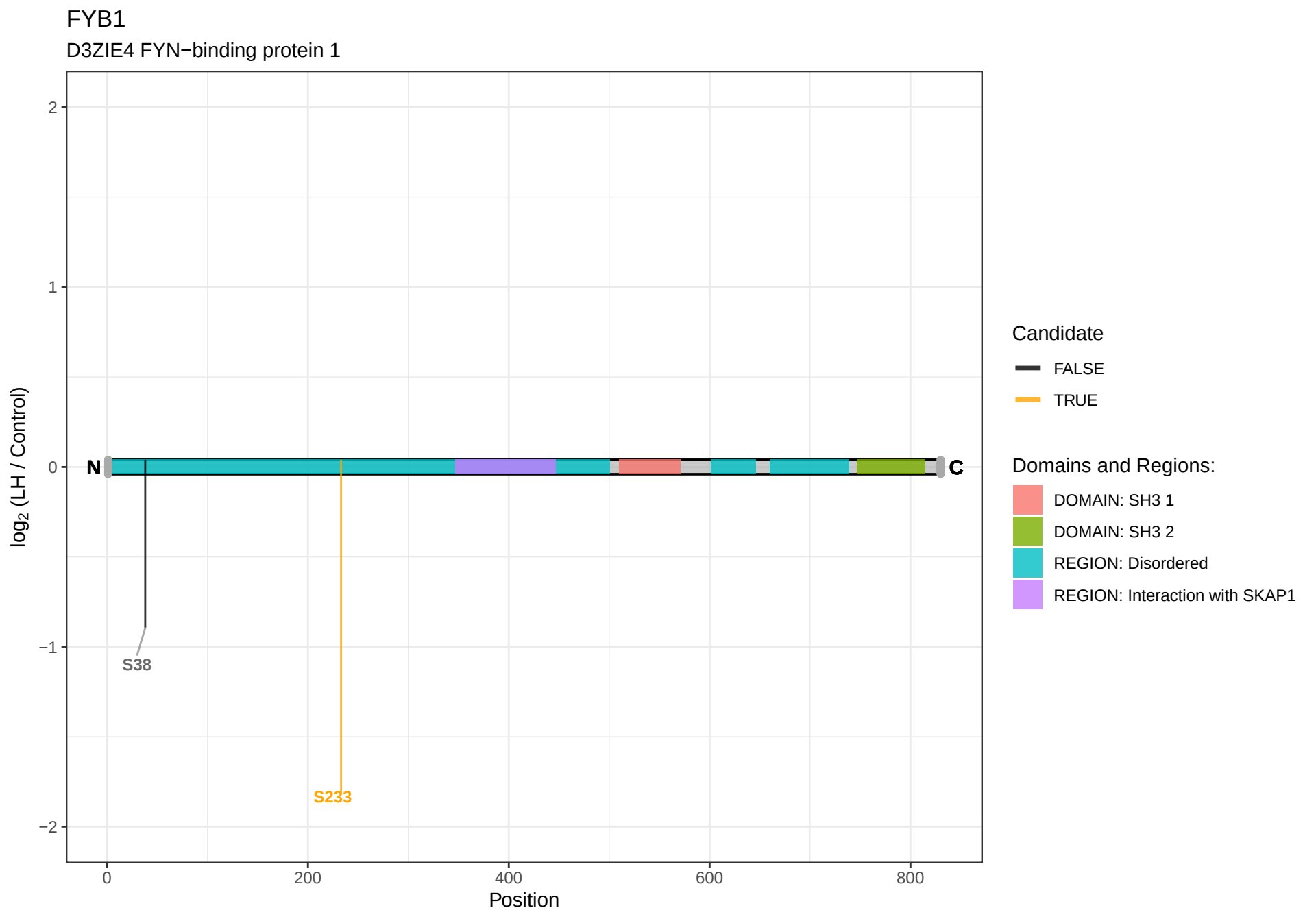

FOXO3
D3ZBQ1 Forkhead box O3
2
1
0
−1
−2
log2 (LH / Control)
S12
S7
S293
S283
N
C
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Fork−head
REGION: Disordered

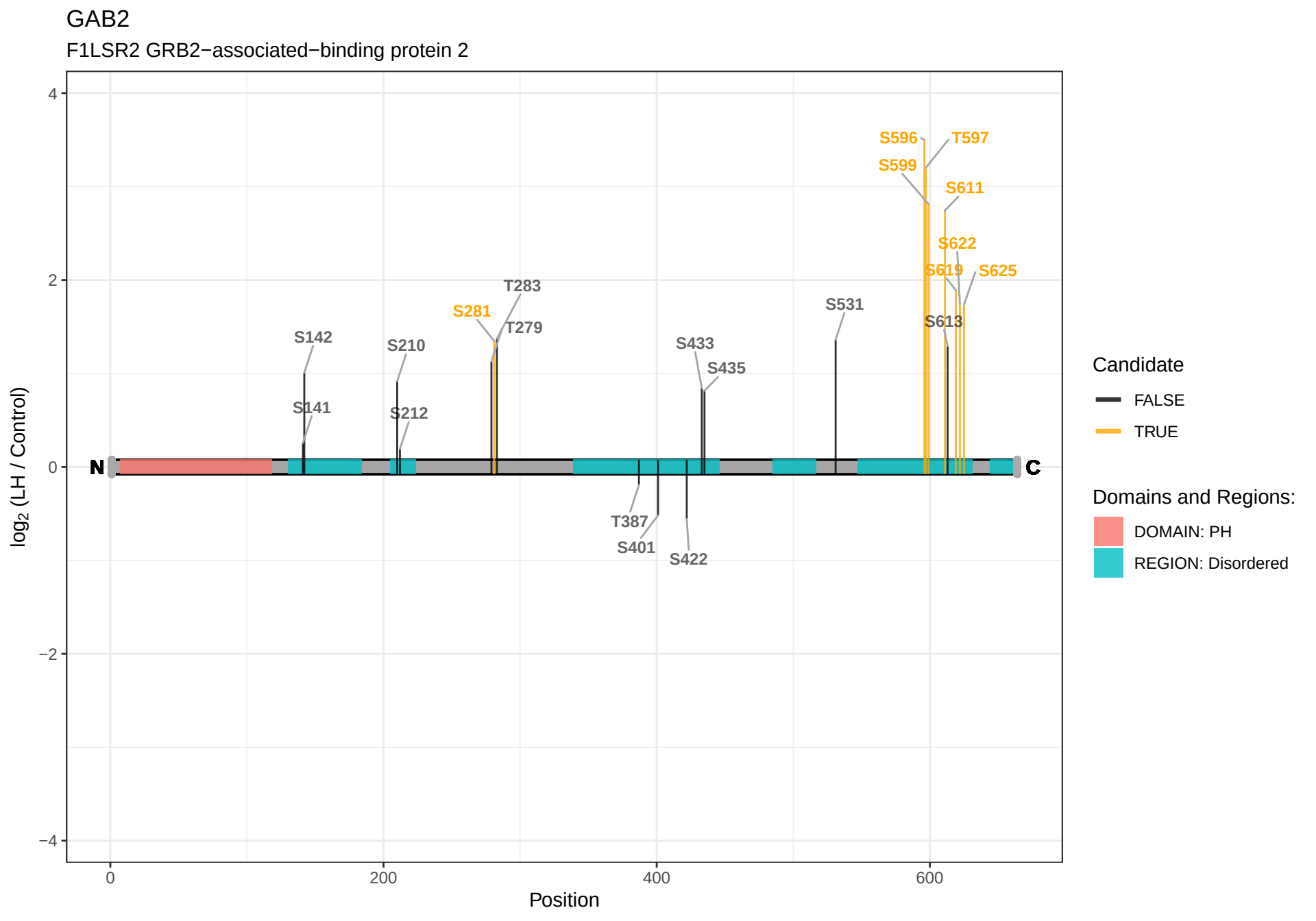

FRS2
D4A244 Fibroblast growth factor receptor substrate 2
S169
S365
S428
S503
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: IRS−type PTB
REGION: Disordered

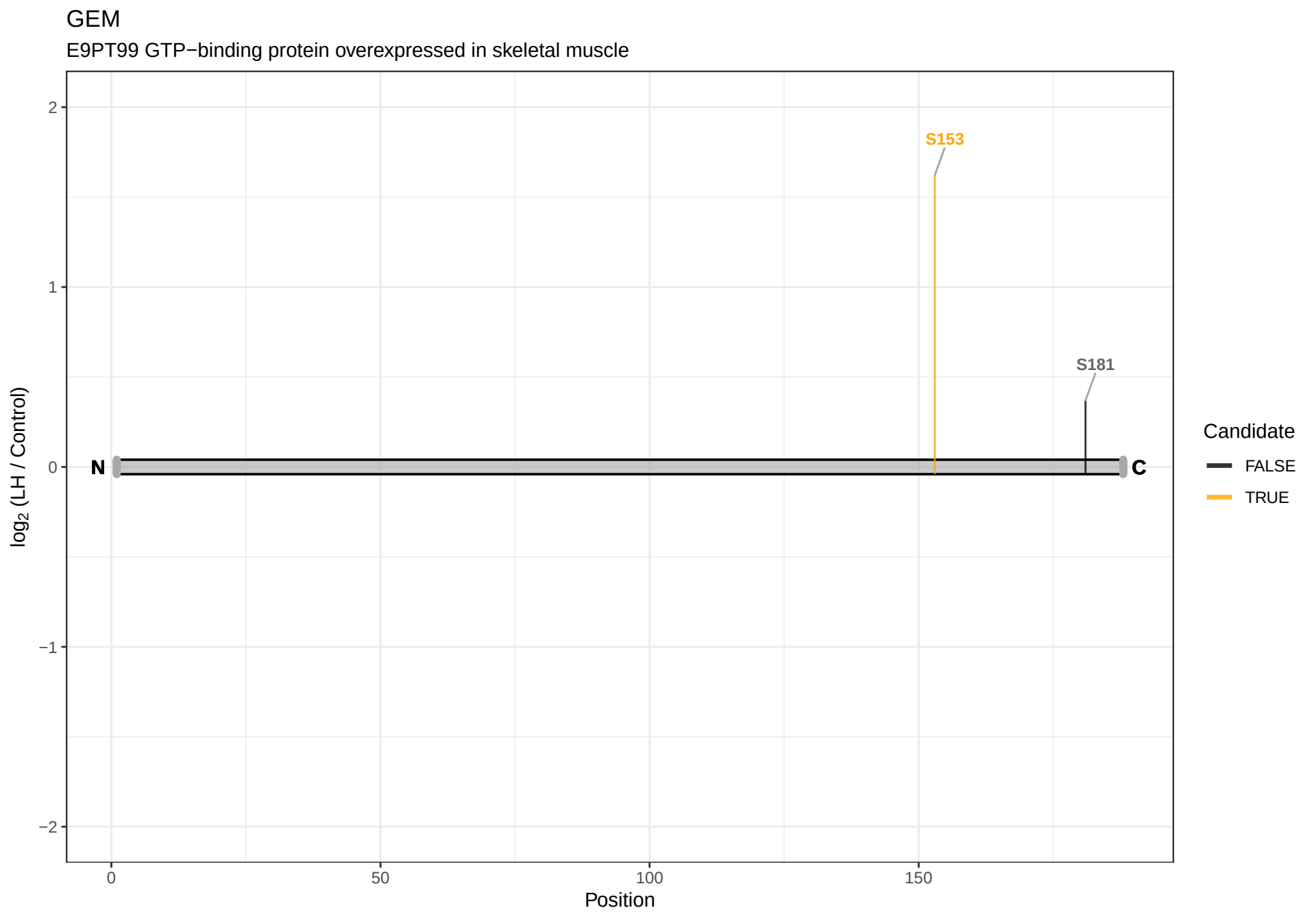

FSHR
P20395 Follicle−stimulating hormone receptor
2
1
0
−1
−2
log2 (LH / Control)
T661
T657
S659
N
C
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: LRRNT

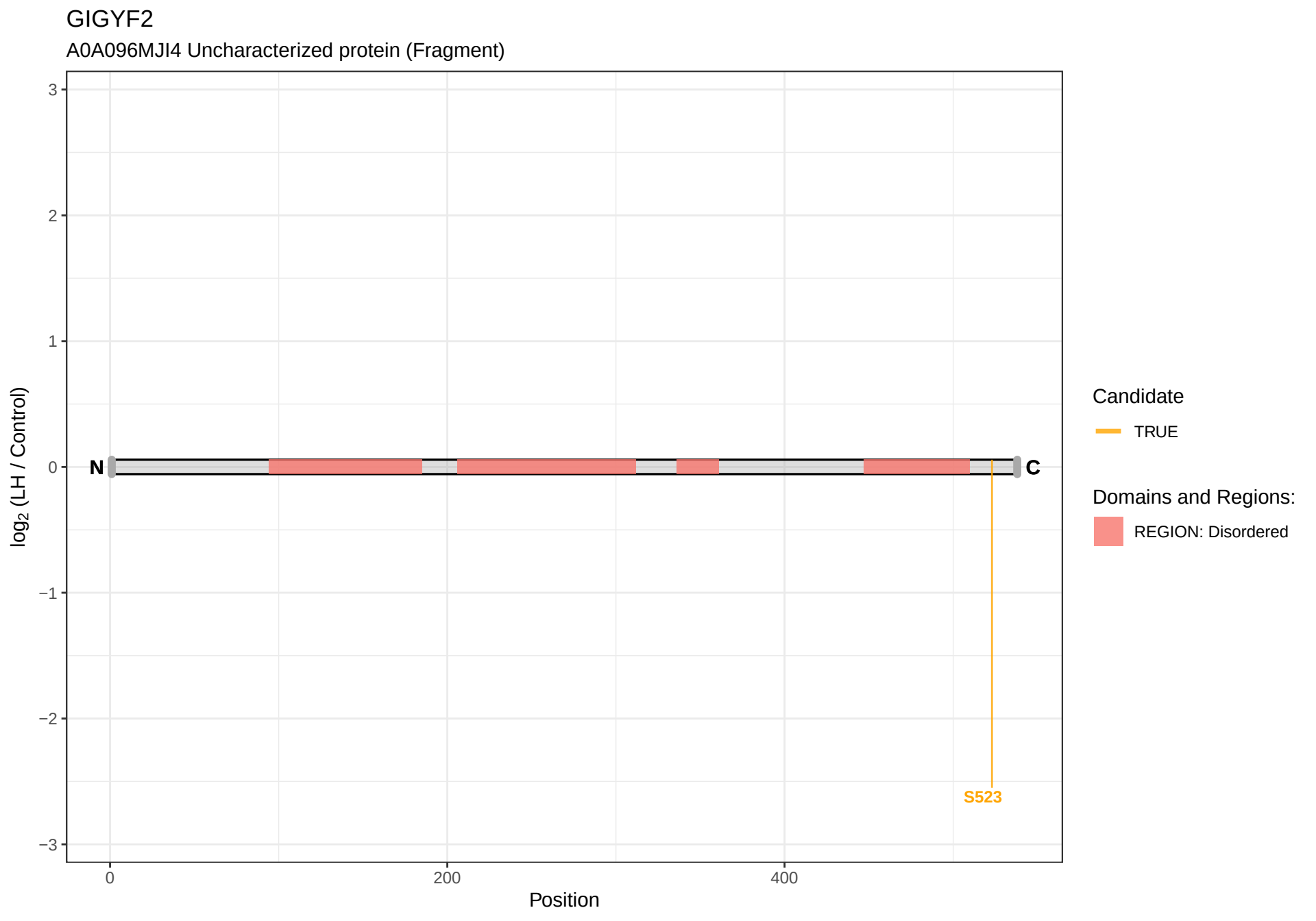

FXR1
Q5XI81 Fragile X mental retardation syndrome−related protein 1
S493
S449
S452
S438
S435
S514
N
C
2
0
−2
log2 (LH / Control)
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Agenet−like 1
DOMAIN: Agenet−like 2
DOMAIN: KH 1
DOMAIN: KH 2
REGION: Disordered
REGION: RNA−binding RGG−box

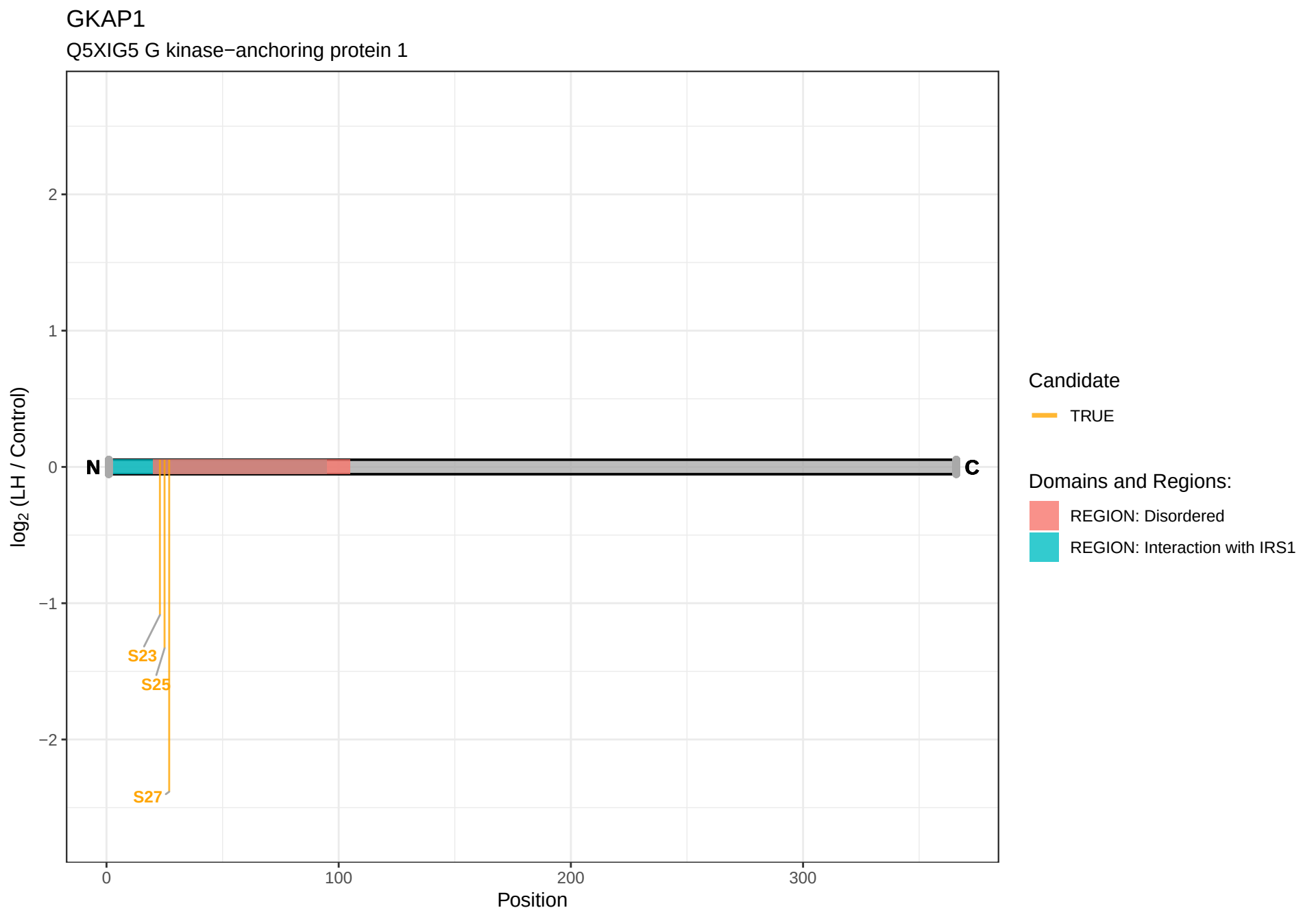

FXR2
B1H2A6 FMR1 autosomal homolog 2
log2 (LH / Control)
2
1
0
−1
−2
N
C
T413
S455
S477
S568
S603
S605
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Agenet−like
REGION: Disordered

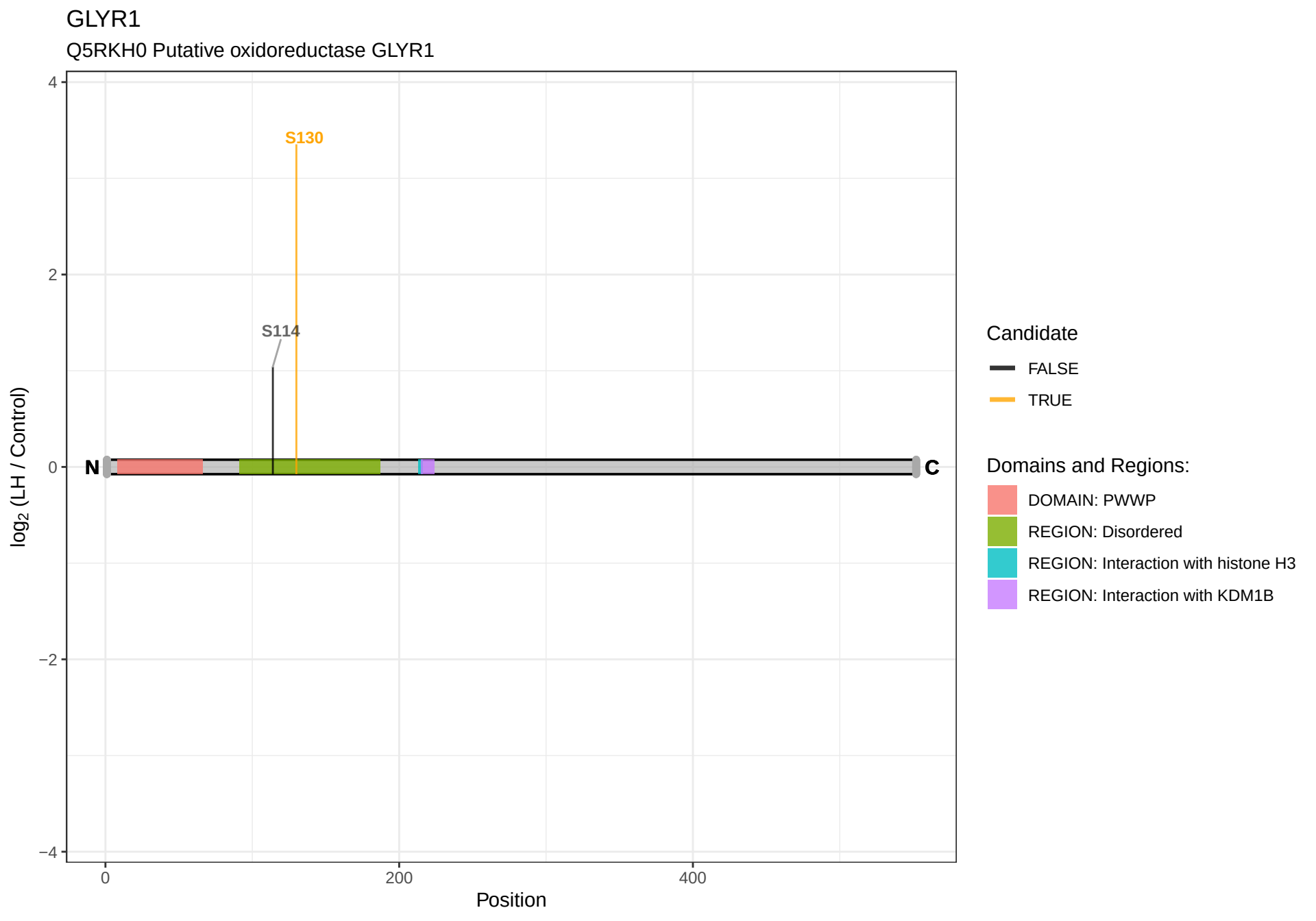

FYB1
D3ZIE4 FYN−binding protein 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S38
S233
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SH3 1
DOMAIN: SH3 2
REGION: Disordered
REGION: Interaction with SKAP1

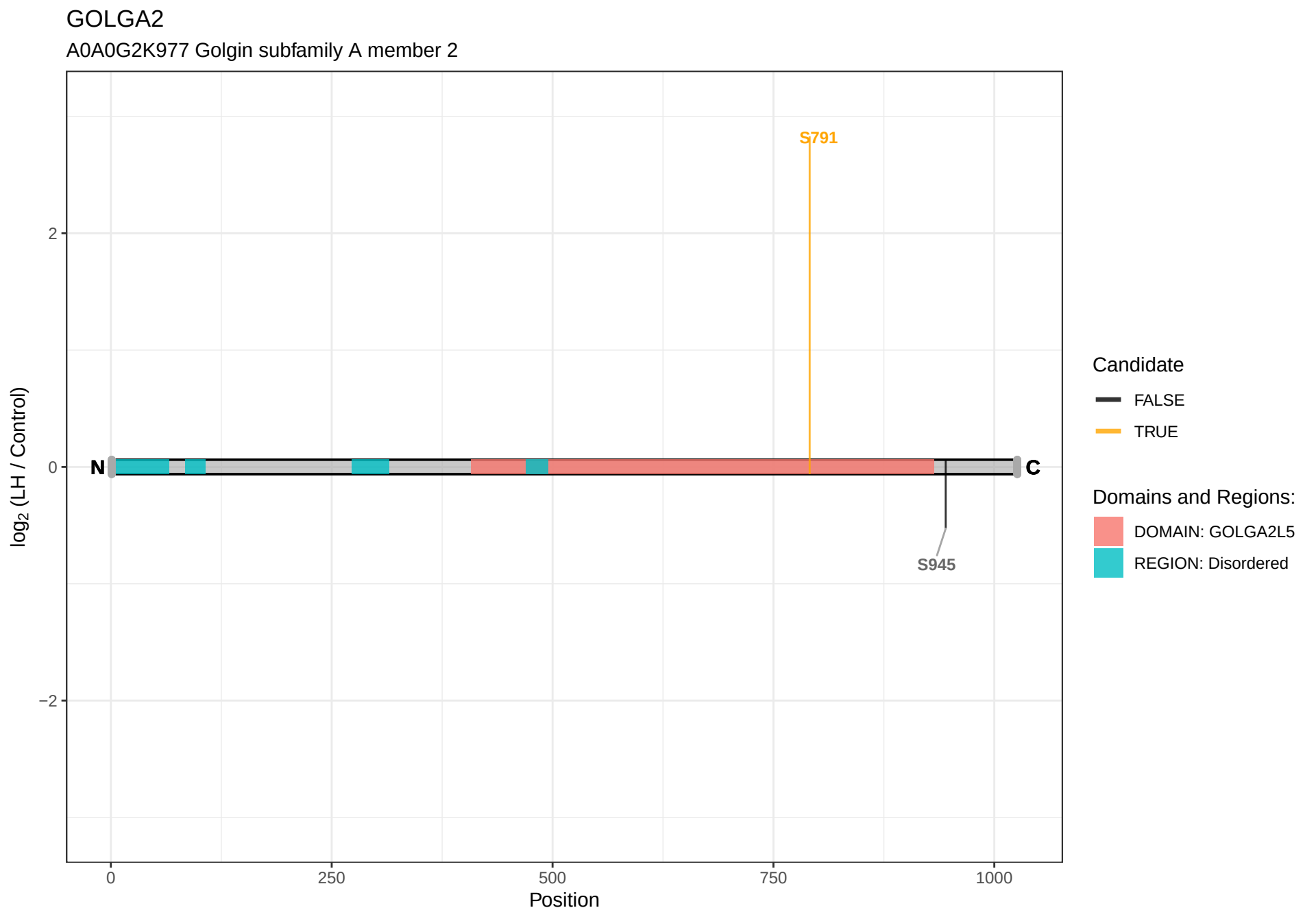

GAB2
F1LSR2 GRB2−associated−binding protein 2
log2 (LH / Control)
Position
N
C
S142
S141
S210
S212
S281
T283
T279
S433
S435
S531
T387
S401
S422
S596
T597
S599
S611
S622
S619
S625
S613
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PH
REGION: Disordered

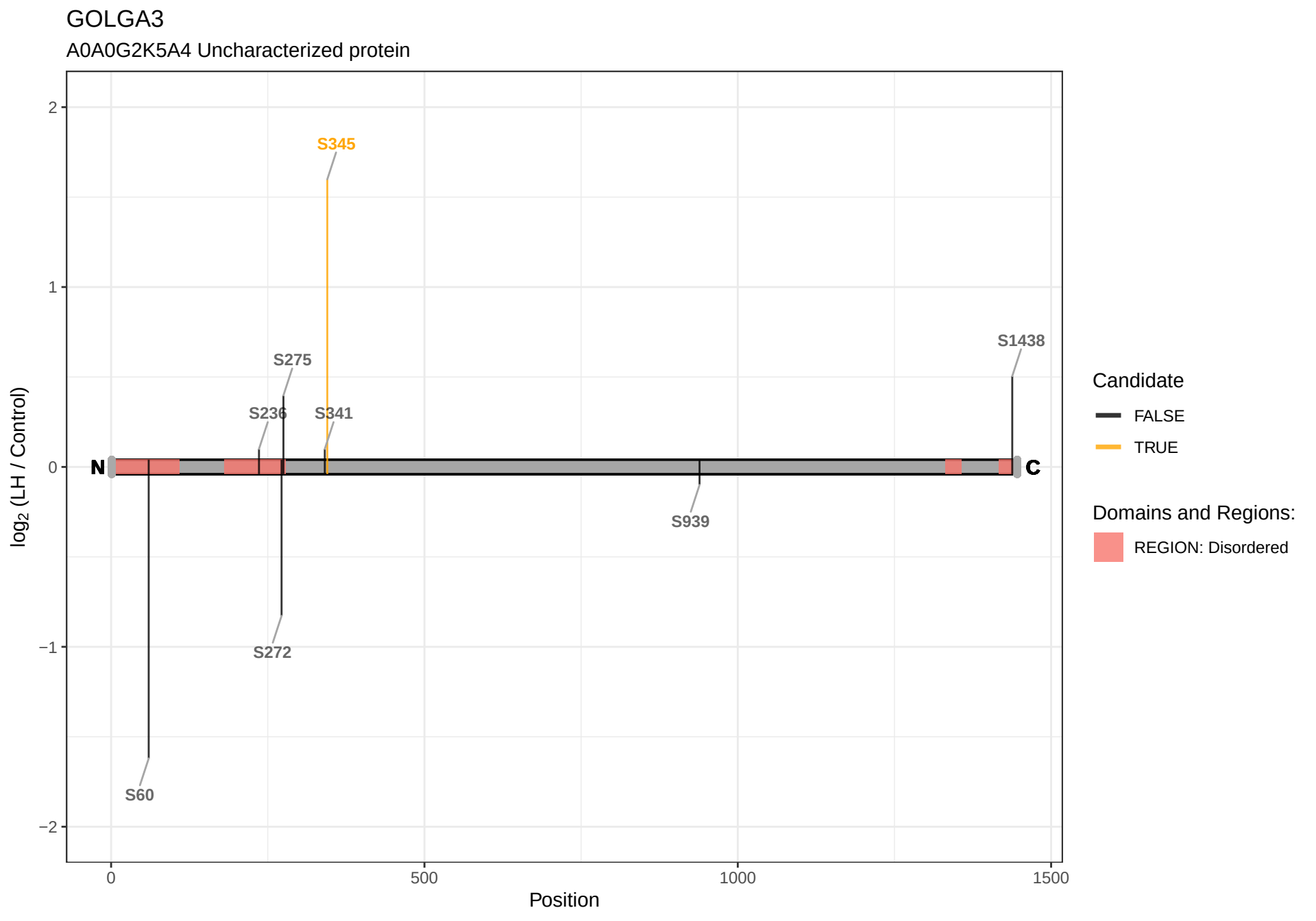

GEM
E9PT99 GTP−binding protein overexpressed in skeletal muscle
S153
S181
N
C
log2 (LH / Control)
Position
Candidate
FALSE
TRUE

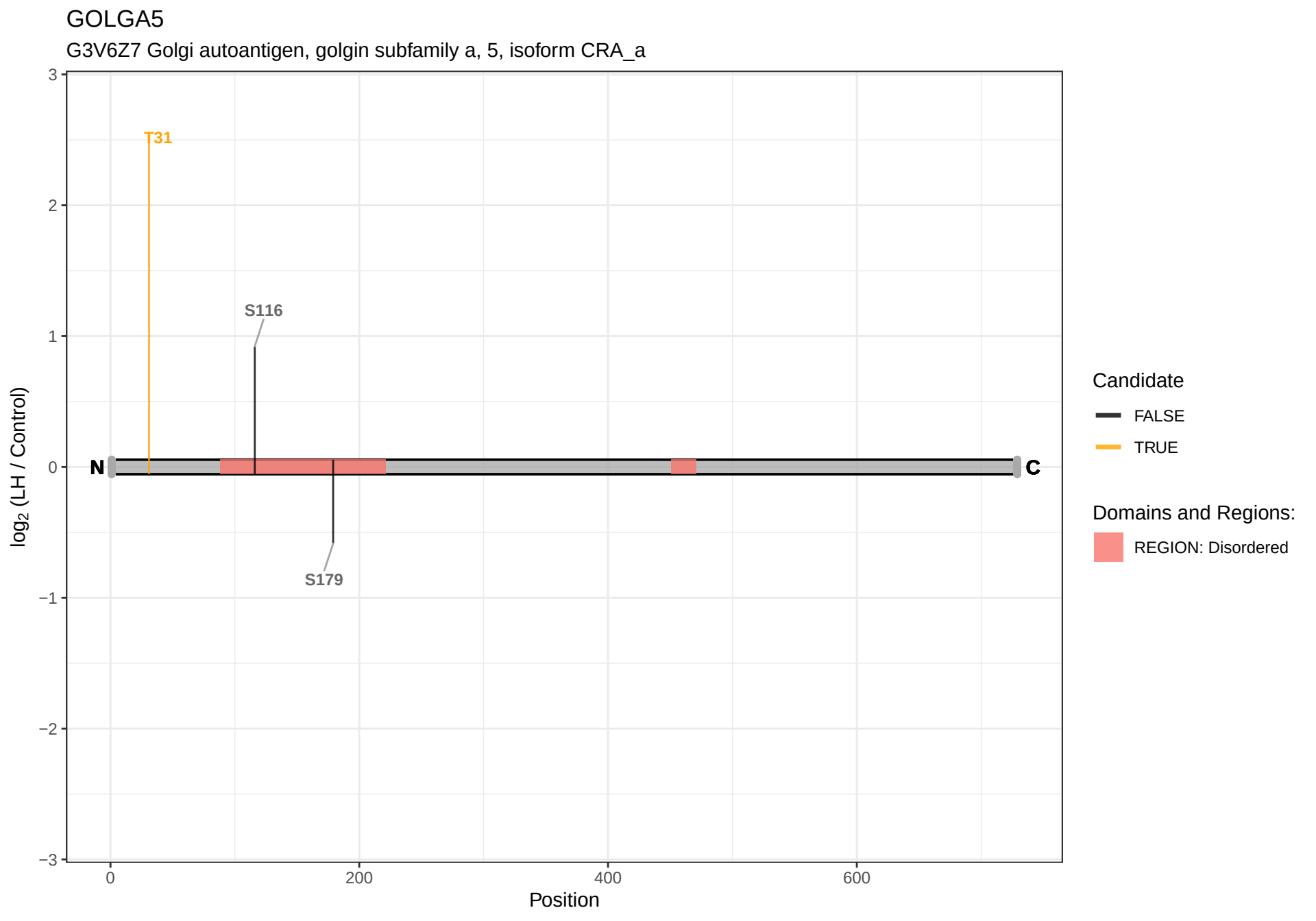

GIGYF2
A0A096MJI4 Uncharacterized protein (Fragment)
log2 (LH / Control)
3
2
1
0
−1
−2
−3
N
C
S523
0
200
400
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

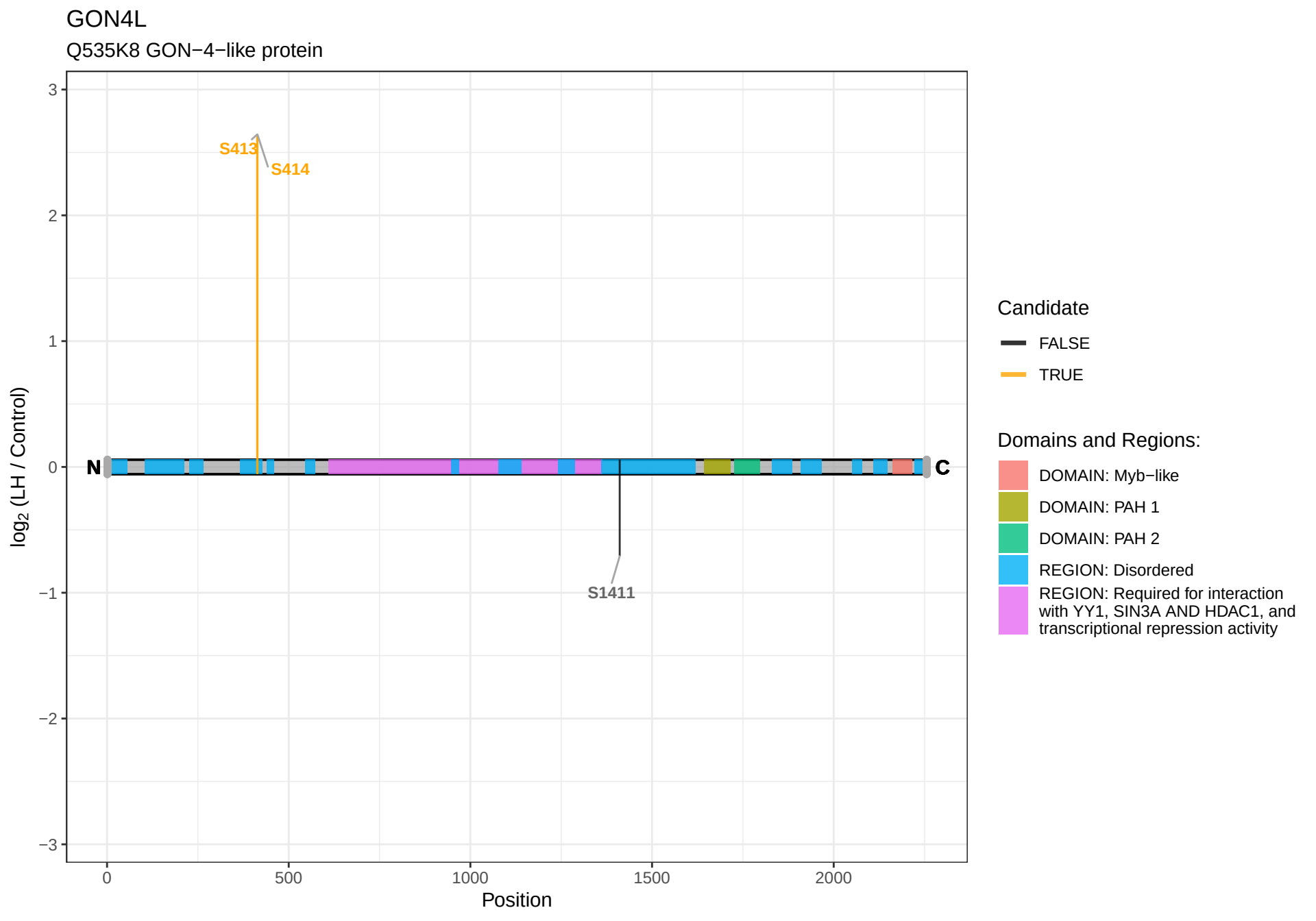

GKAP1
Q5XIG5 G kinase−anchoring protein 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S23
S25
S27
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered
REGION: Interaction with IRS1

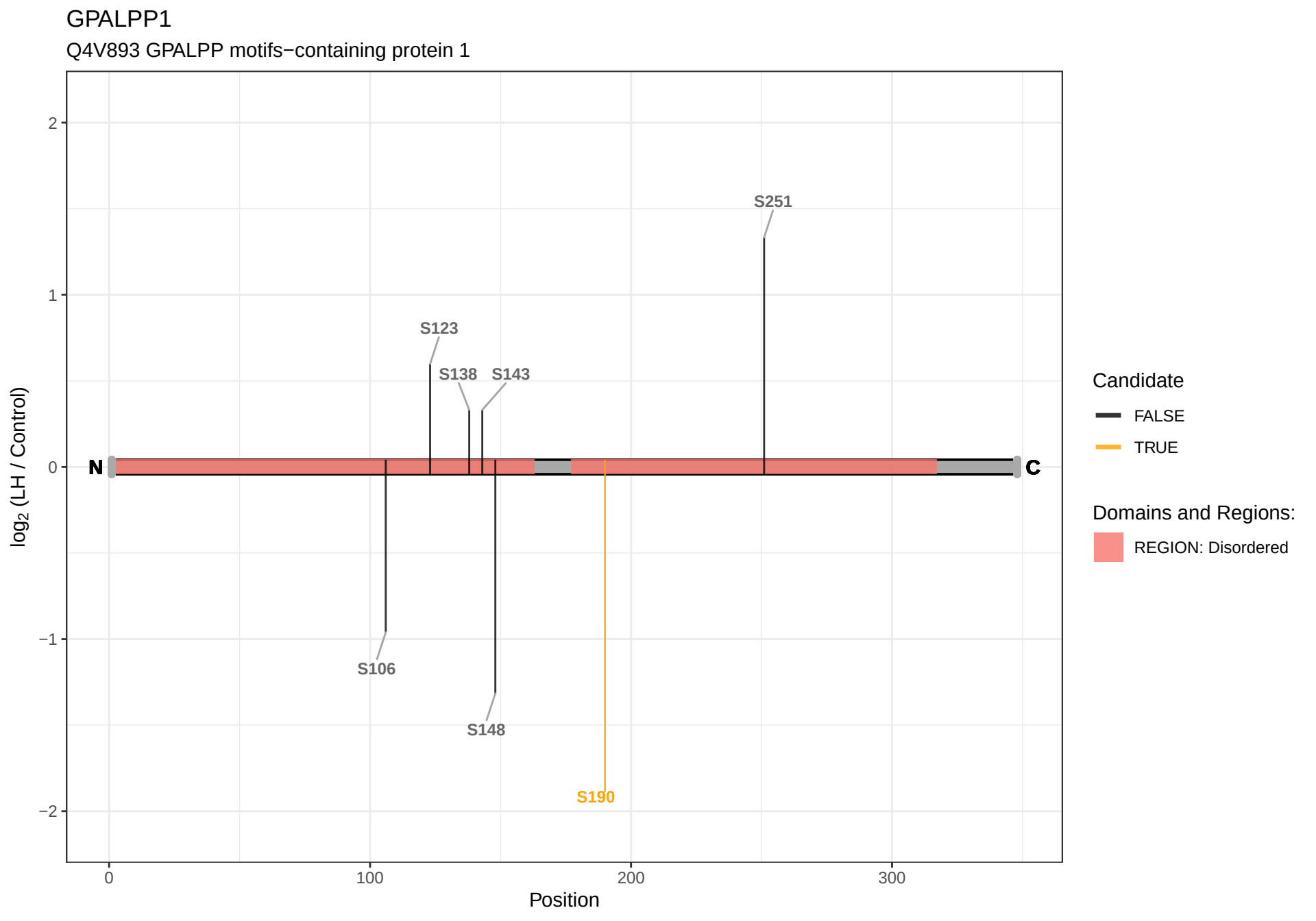

GLYR1
Q5RKH0 Putative oxidoreductase GLYR1
S130
S114
N
C
4
2
0
−2
−4
0
200
400
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PWWP
REGION: Disordered
REGION: Interaction with histone H3
REGION: Interaction with KDM1B

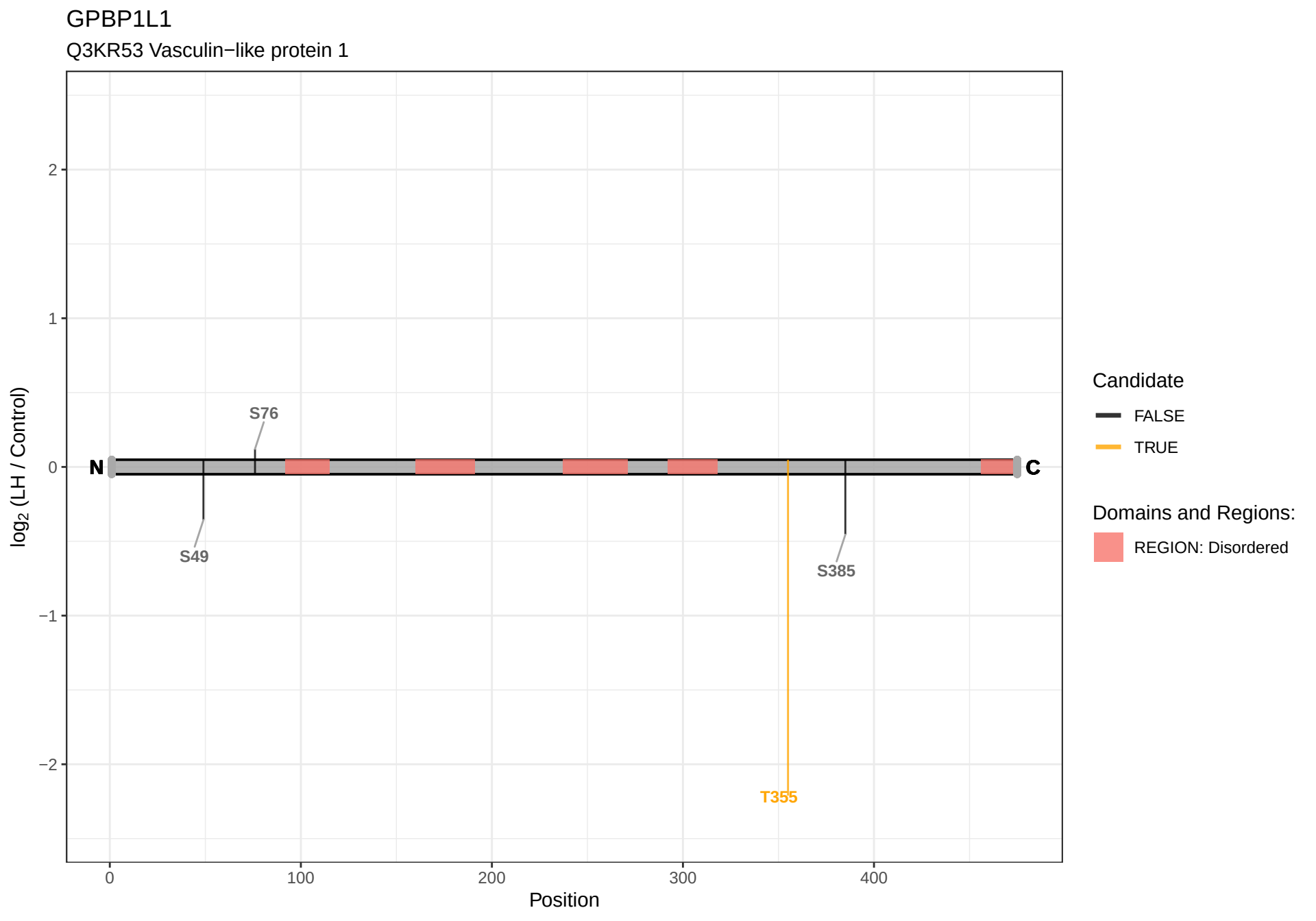

GOLGA2
A0A0G2K977 Golgin subfamily A member 2
S791
S945
N
C
2
0
−2
log2 (LH / Control)
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: GOLGA2L5
REGION: Disordered

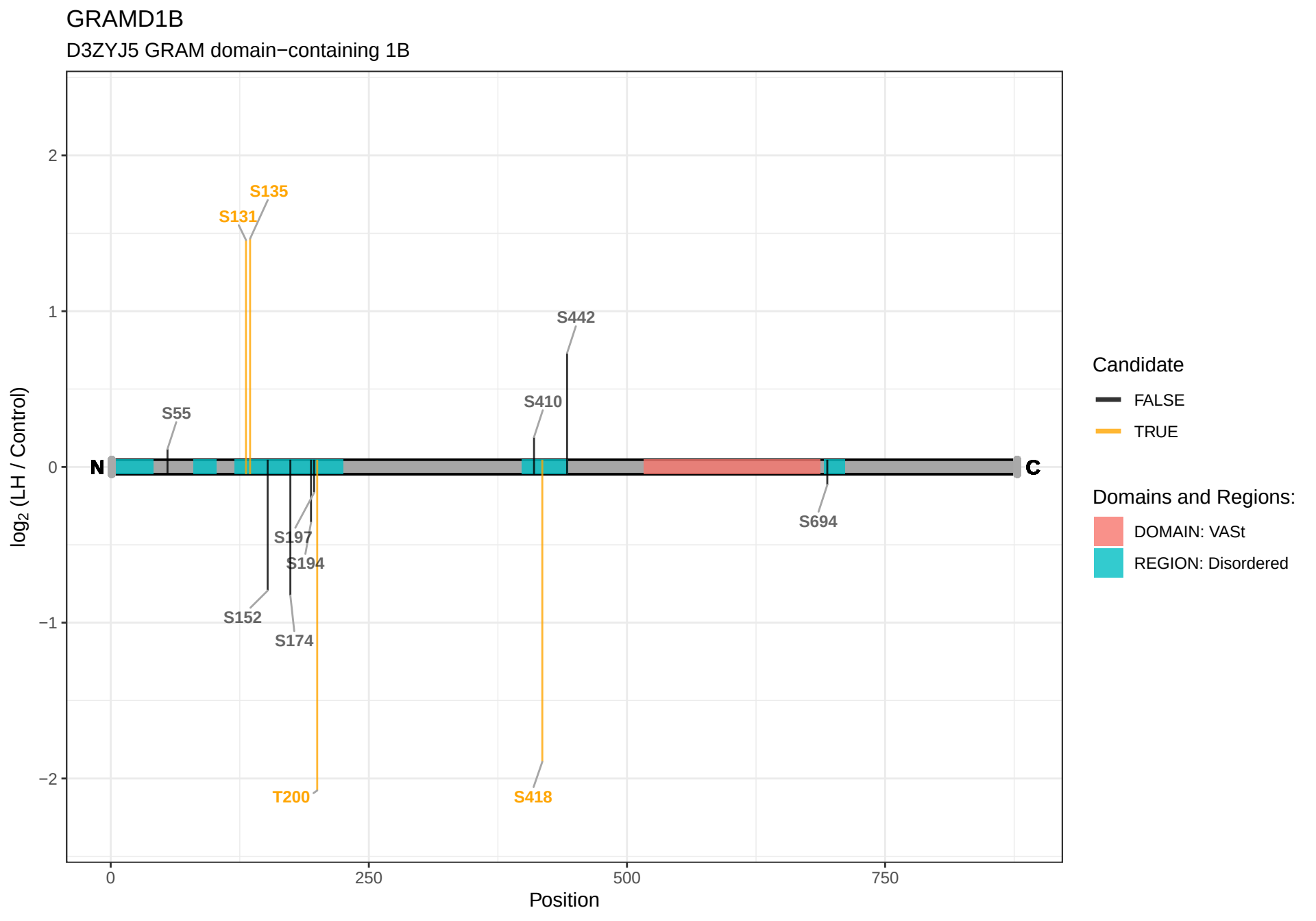

GOLGA3
A0A0G2K5A4 Uncharacterized protein
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
Position
N
C
S345
S275
S236
S341
S1438
S939
S272
S60
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

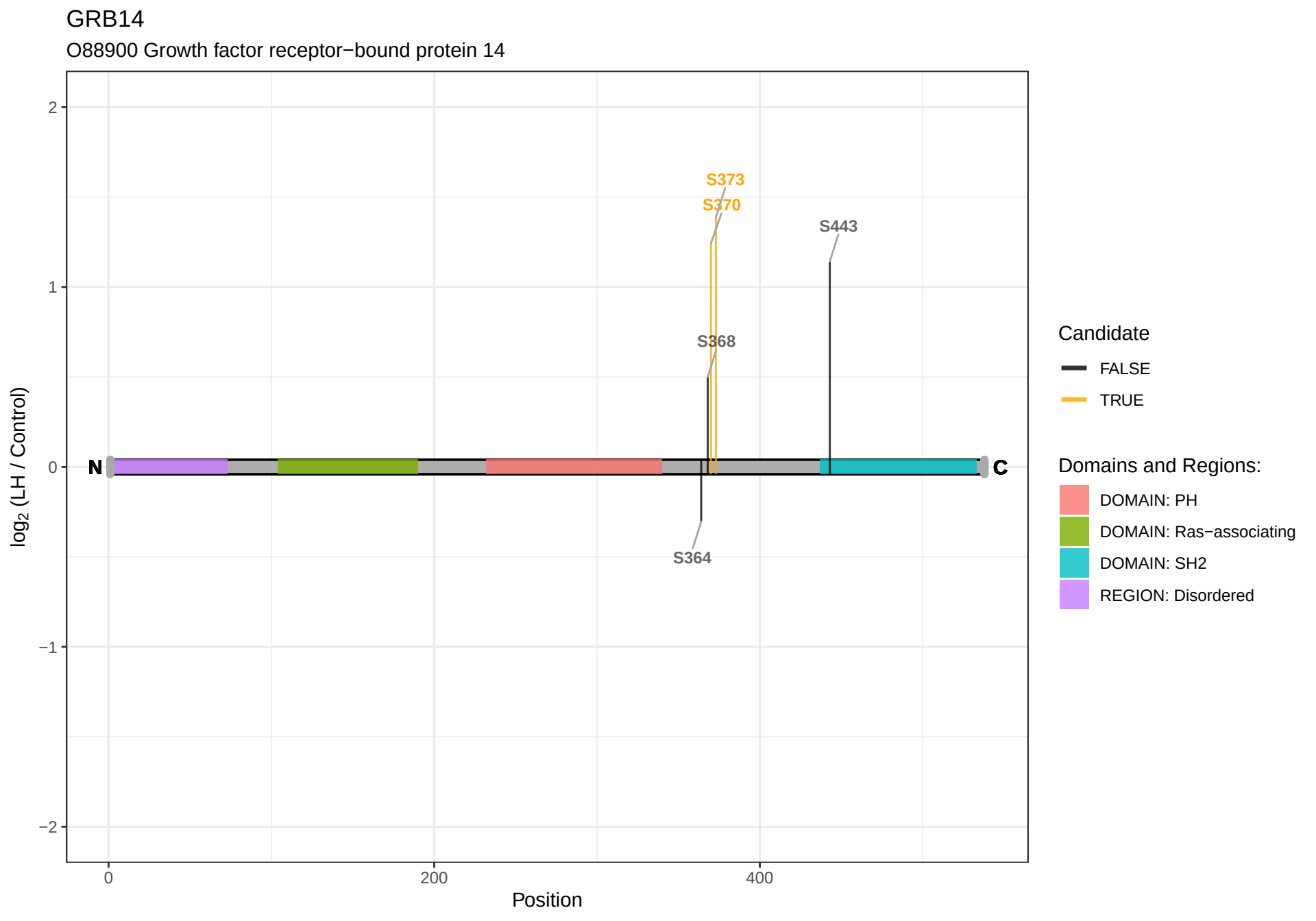

GOLGA5
G3V6Z7 Golgi autoantigen, golgin subfamily a, 5, isoform CRA_a
log2 (LH / Control)
3
2
1
0
−1
−2
−3
T31
S116
S179
N
C
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

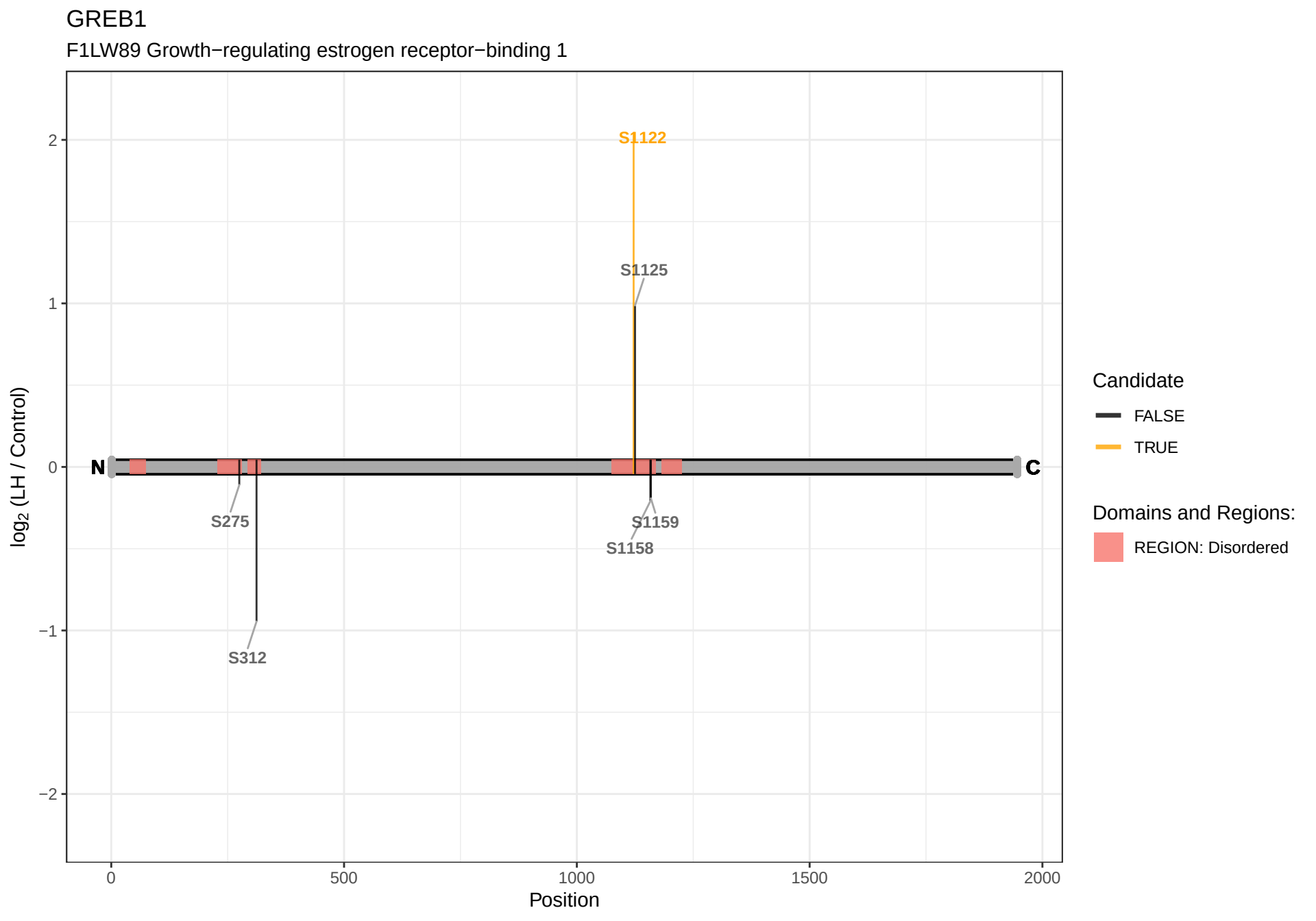

GON4L
Q535K8 GON−4−like protein
S413
S414
S1411
N
C
log2 (LH / Control)
Position
3
2
1
0
−1
−2
−3
0
500
1000
1500
2000
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Myb−like
DOMAIN: PAH 1
DOMAIN: PAH 2
REGION: Disordered
REGION: Required for interaction with YY1, SIN3A AND HDAC1, and transcriptional repression activity

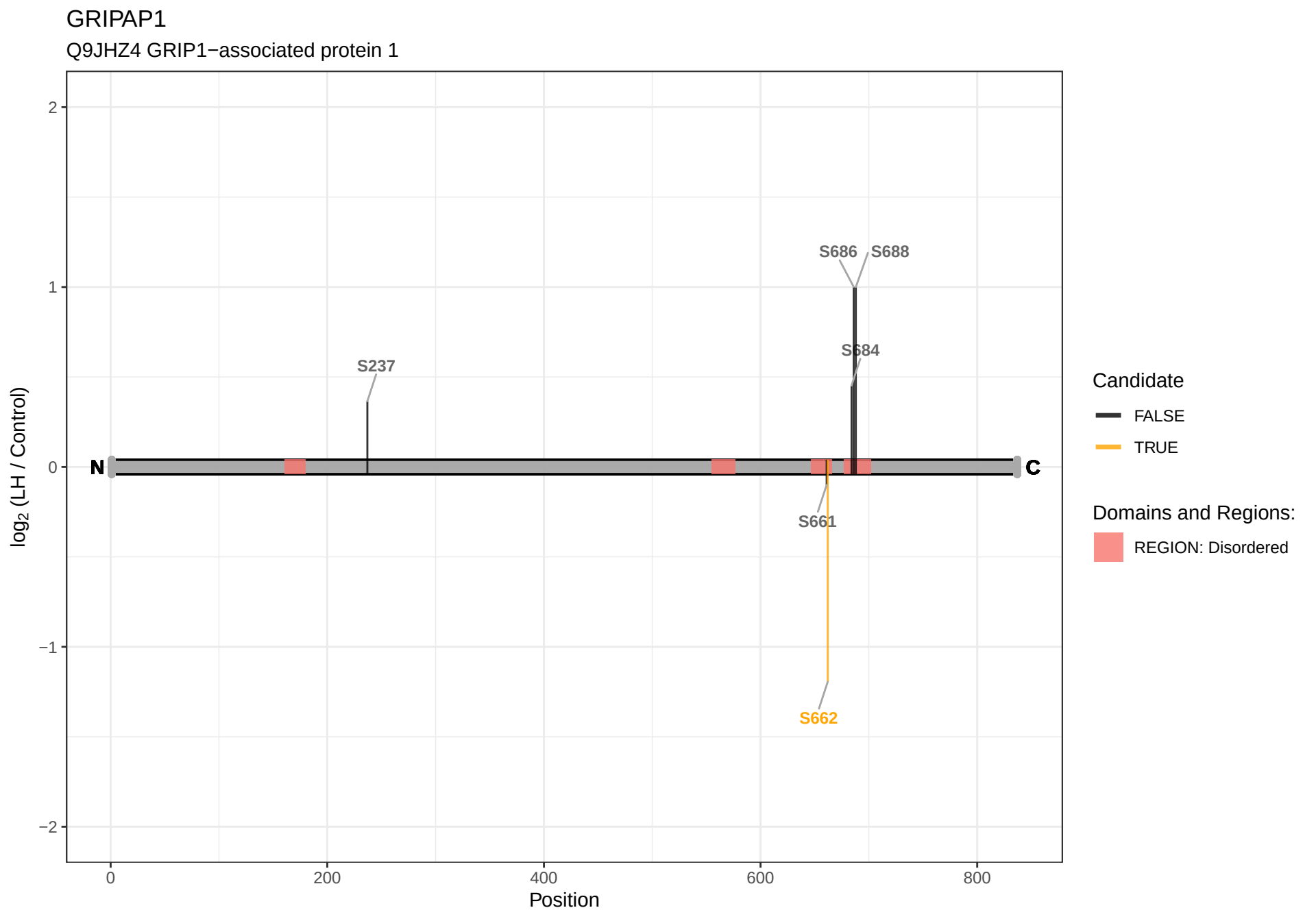

GPALPP1
Q4V893 GPALPP motifs−containing protein 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S251
S123
S138
S143
S106
S148
S190
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

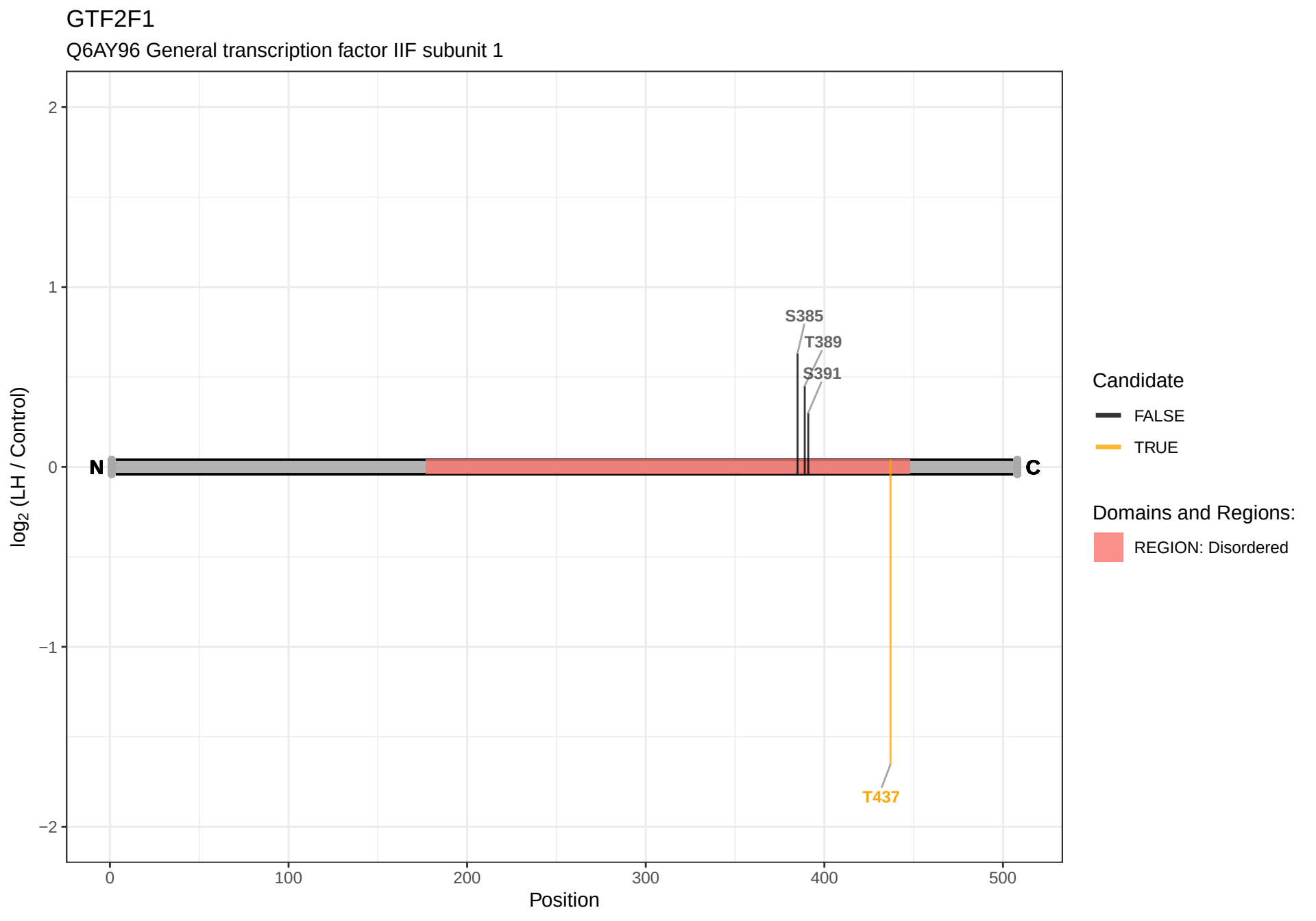

GPBP1L1
Q3KR53 Vasculin−like protein 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S76
S49
S385
T355
0
100
200
300
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

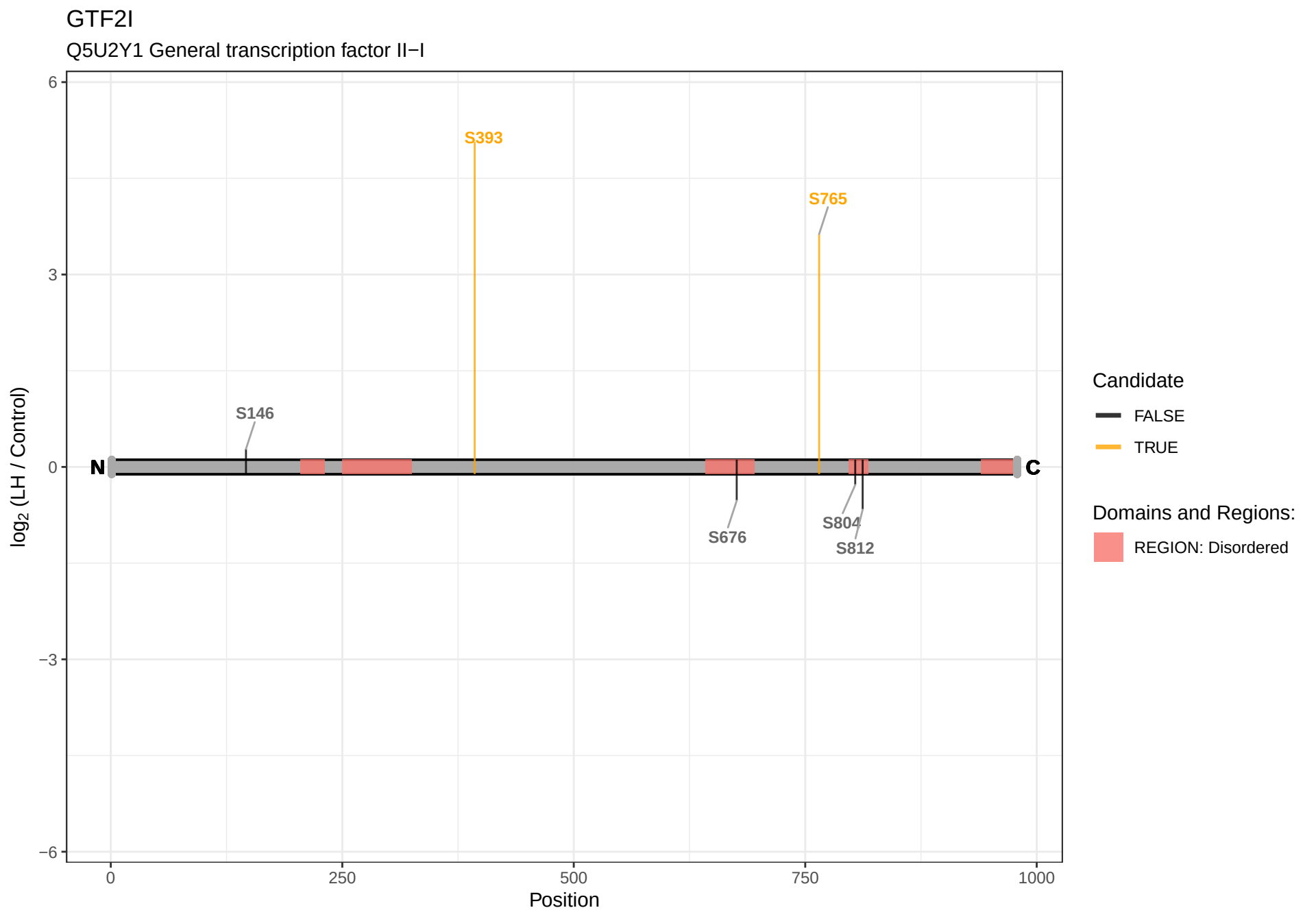

GRAMD1B
D3ZYJ5 GRAM domain−containing 1B
log2 (LH / Control)
2
1
0
−1
−2
0
250
500
750
Position
N
C
S135
S131
S442
S55
S410
S694
S197
S194
S152
S174
T200
S418
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: VASt
REGION: Disordered

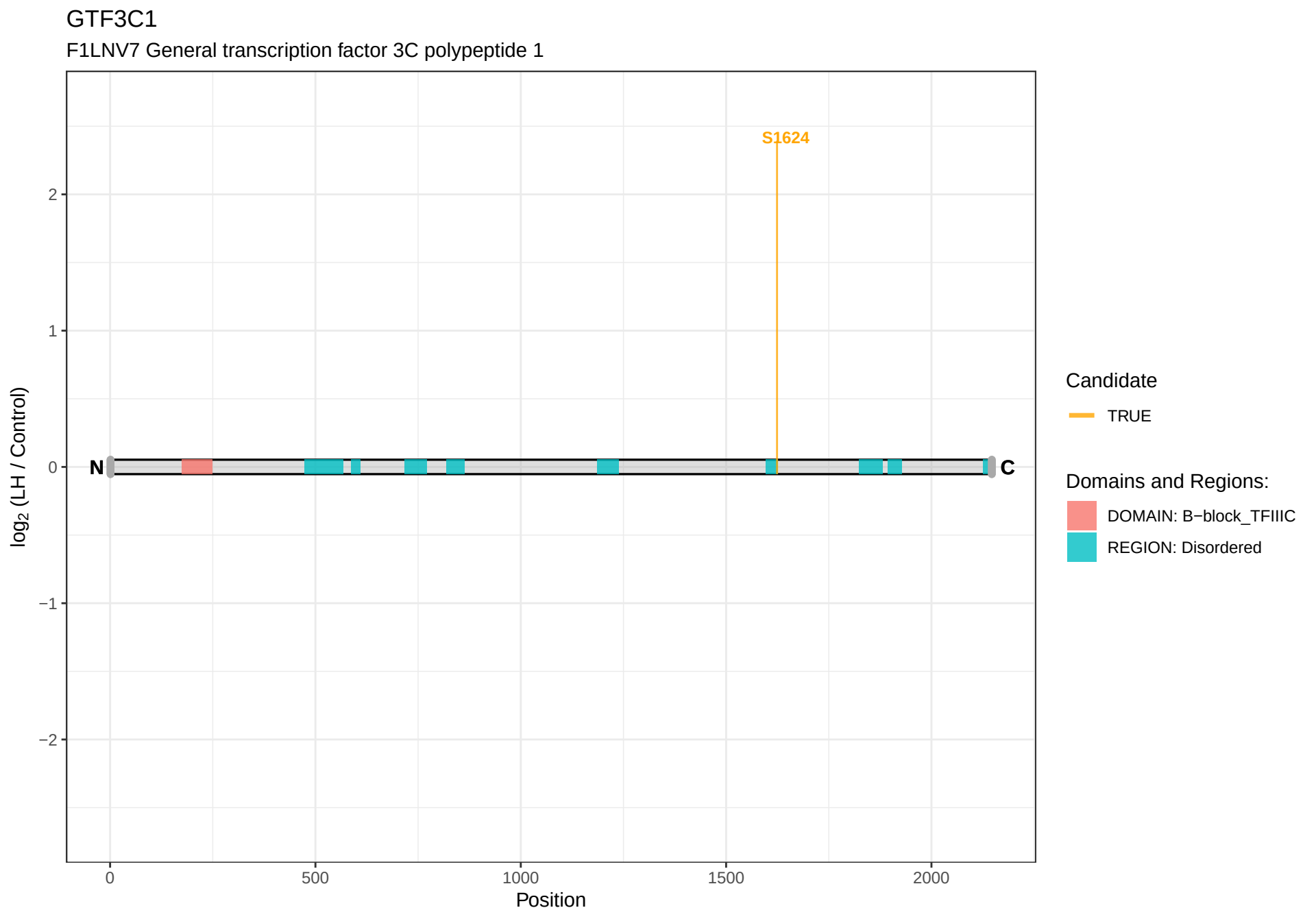

GRB14
O88900 Growth factor receptor−bound protein 14
log2 (LH / Control)
Position
N
C
S373
S370
S443
S368
S364
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PH
DOMAIN: Ras−associating
DOMAIN: SH2
REGION: Disordered

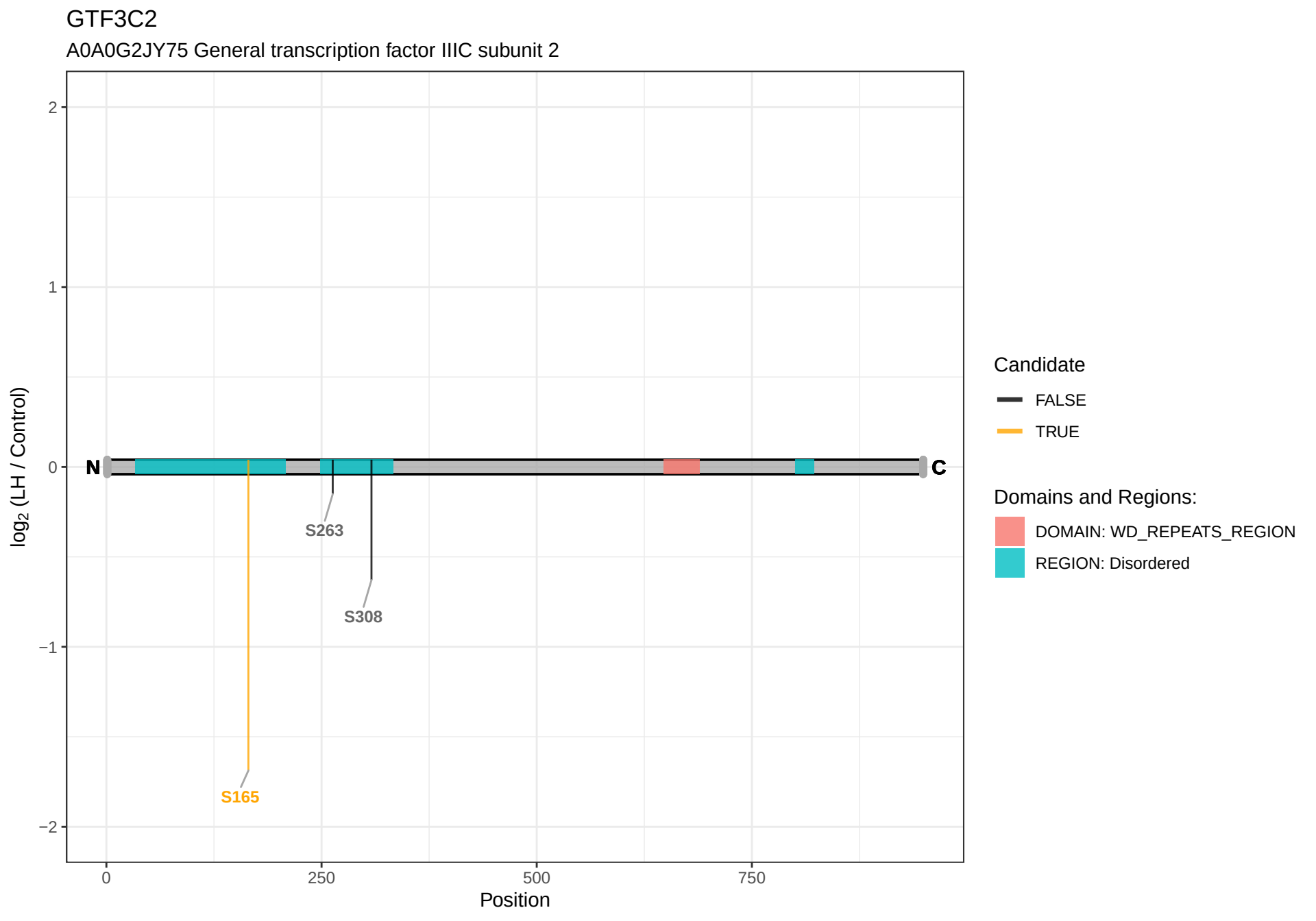

GREB1
F1LW89 Growth−regulating estrogen receptor−binding 1
S1122
S1125
S275
S312
S1159
S1158
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
1500
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

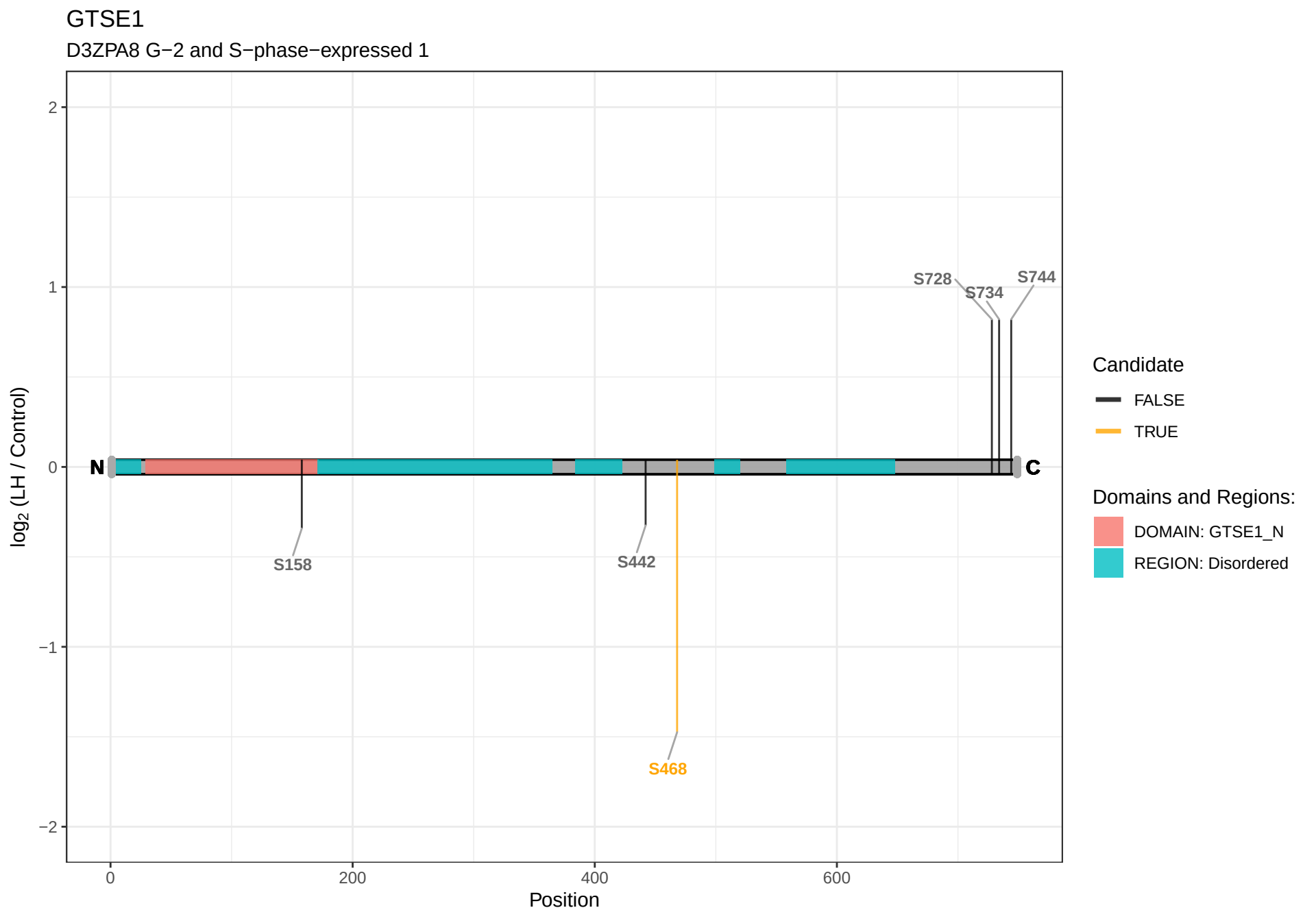

GRIPAP1
Q9JHZ4 GRIP1−associated protein 1
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
800
Position
N
C
S237
S686
S688
S684
S661
S662
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

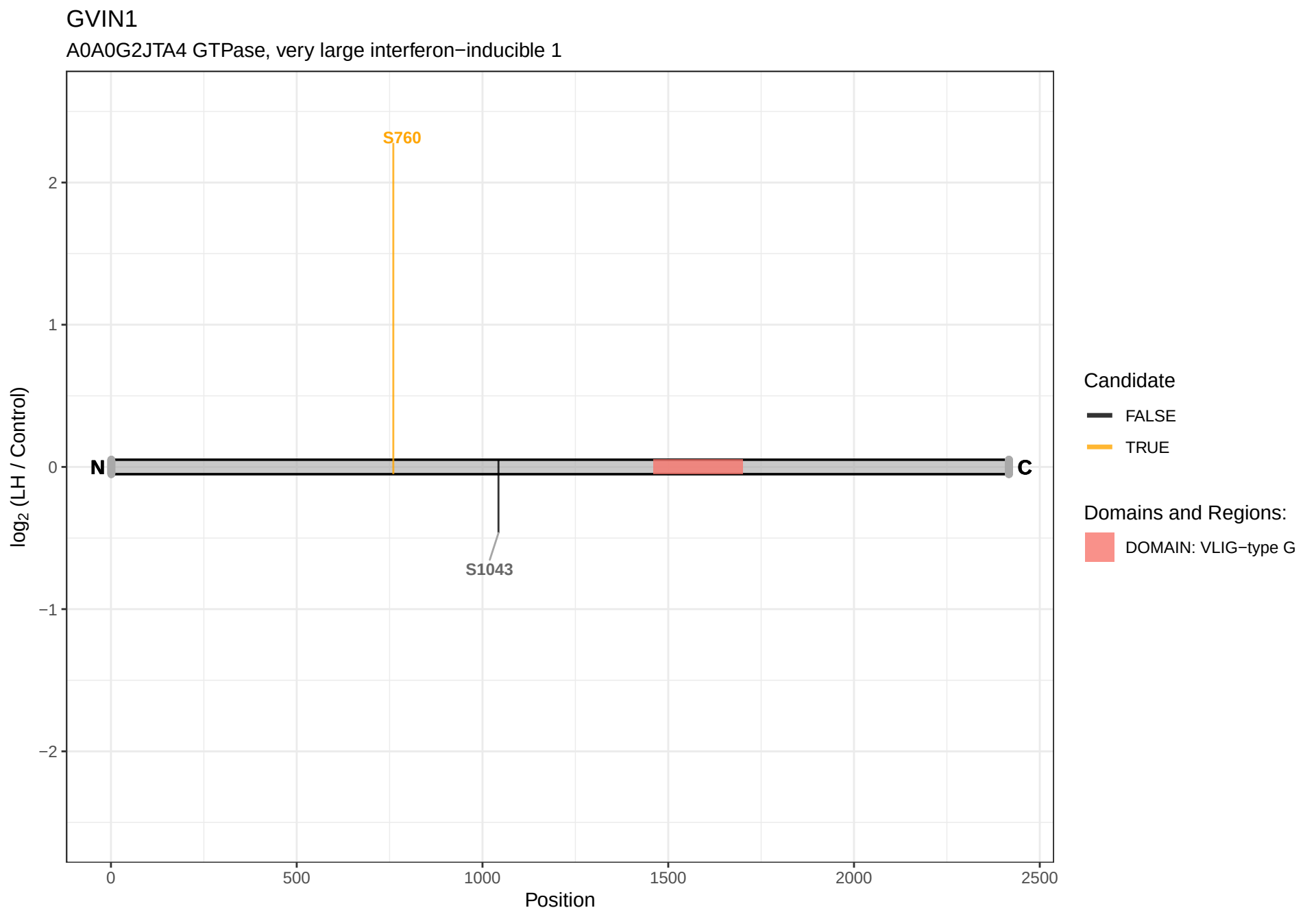

GTF2F1
Q6AY96 General transcription factor IIF subunit 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S385
T389
S391
T437
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

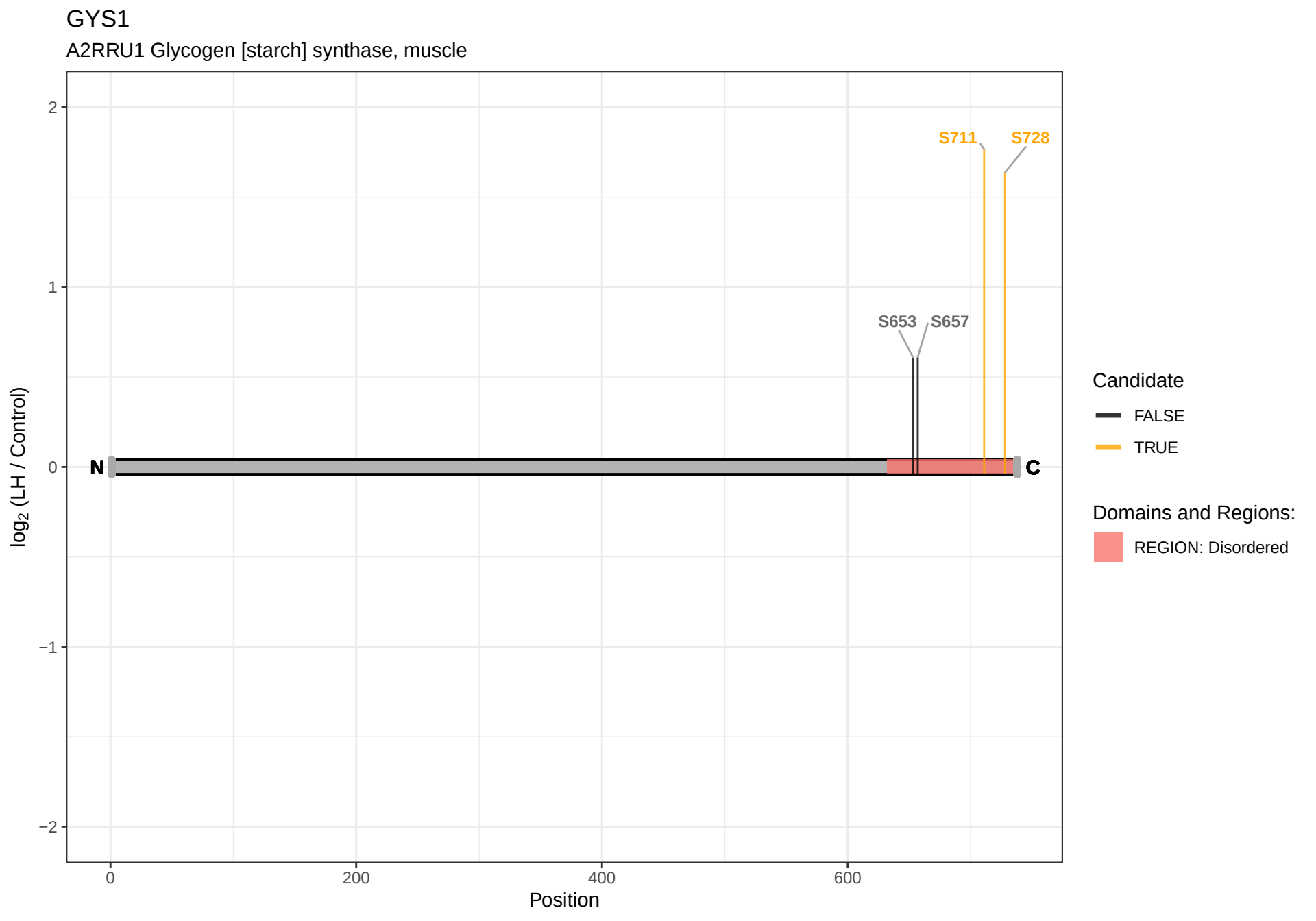

GTF2I
Q5U2Y1 General transcription factor II−I
6
3
0
−3
−6
log2 (LH / Control)
S393
S765
S146
S676
S804
S812
N
C
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

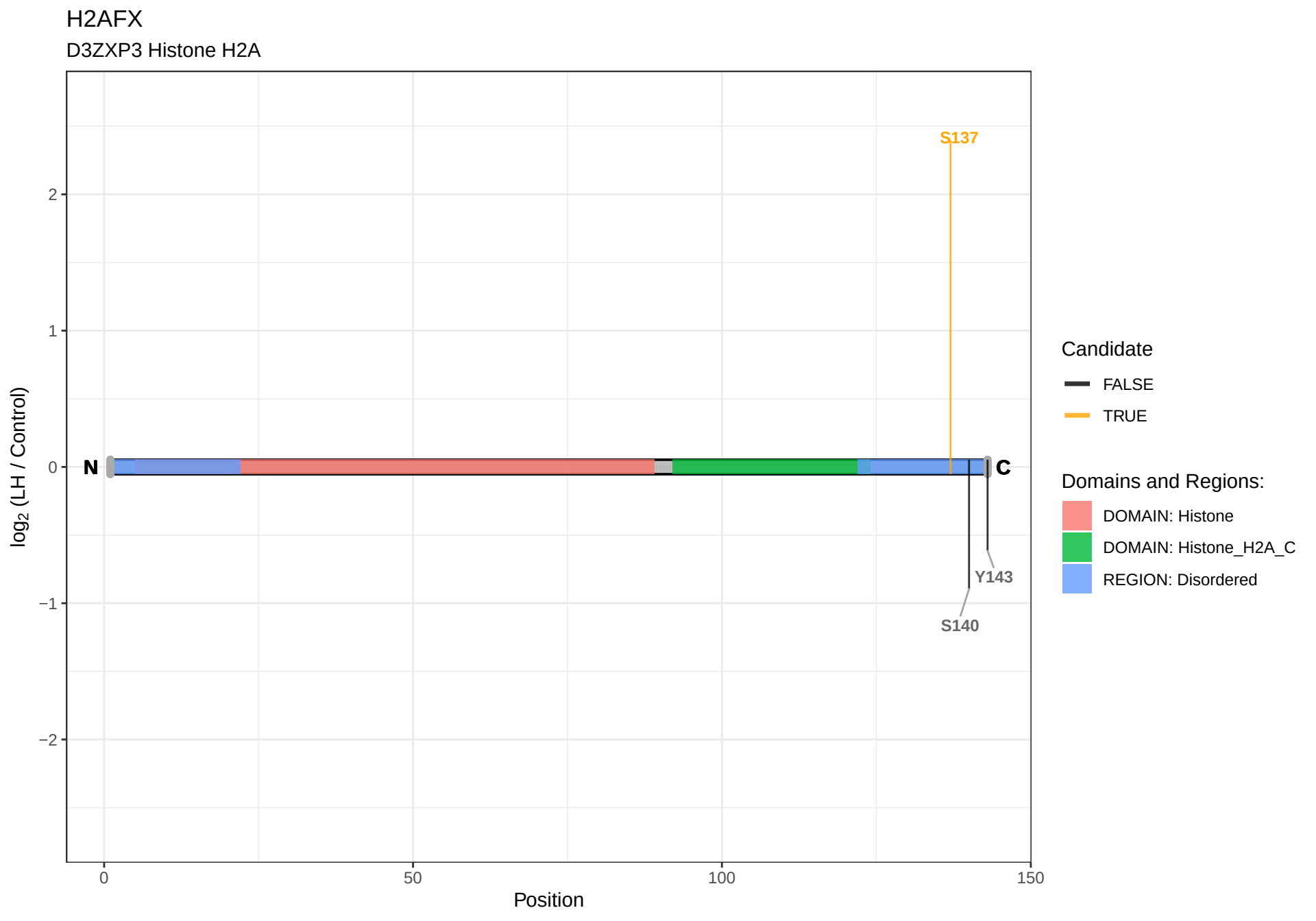

GTF3C1
F1LNV7 General transcription factor 3C polypeptide 1
S1624
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
2000
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: B−block_TFIIIC
REGION: Disordered

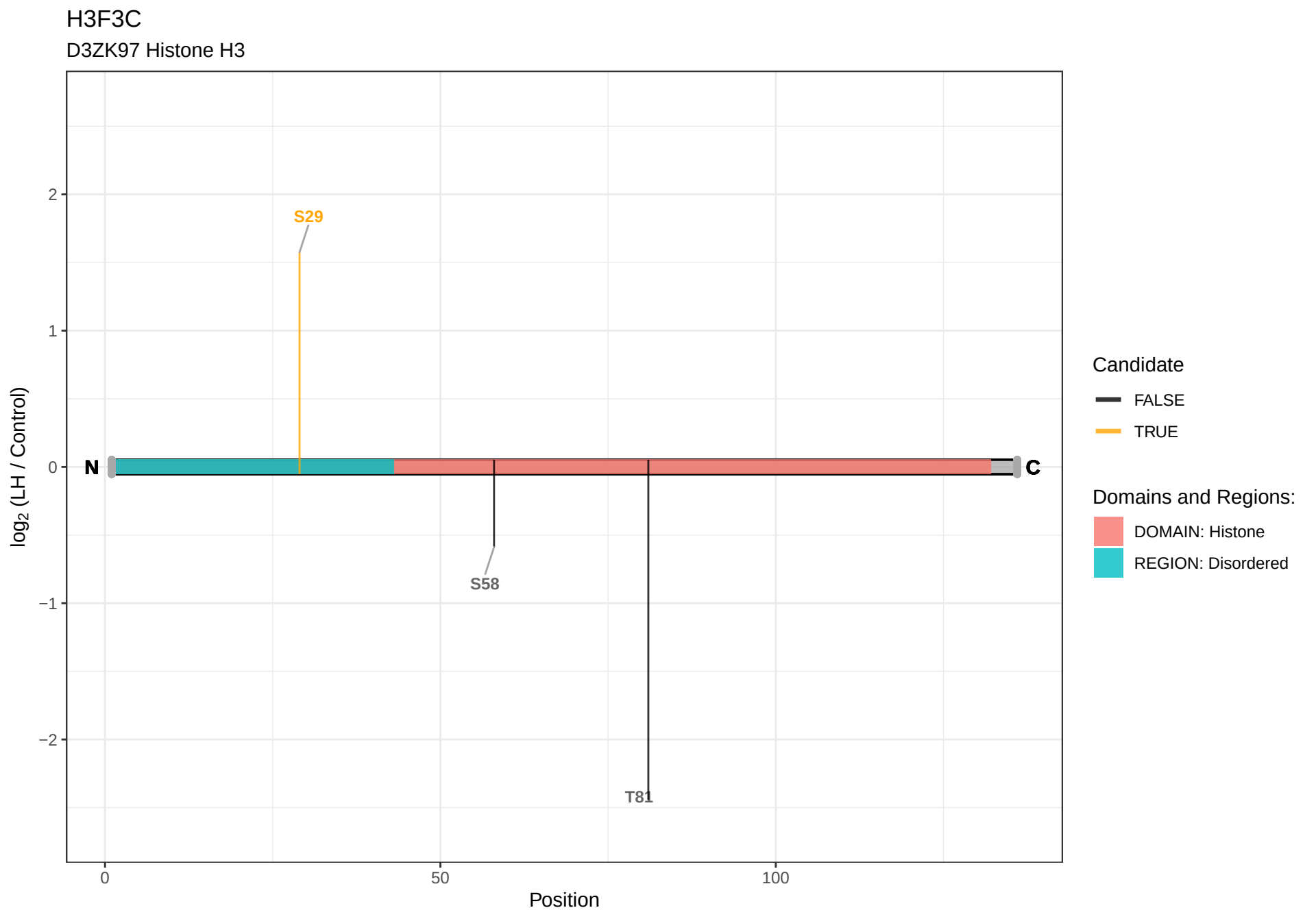

GTF3C2
A0A0G2JY75 General transcription factor IIIC subunit 2
log2 (LH / Control)
2
1
0
−1
−2
N
C
S263
S308
S165
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WD_REPEATS_REGION
REGION: Disordered

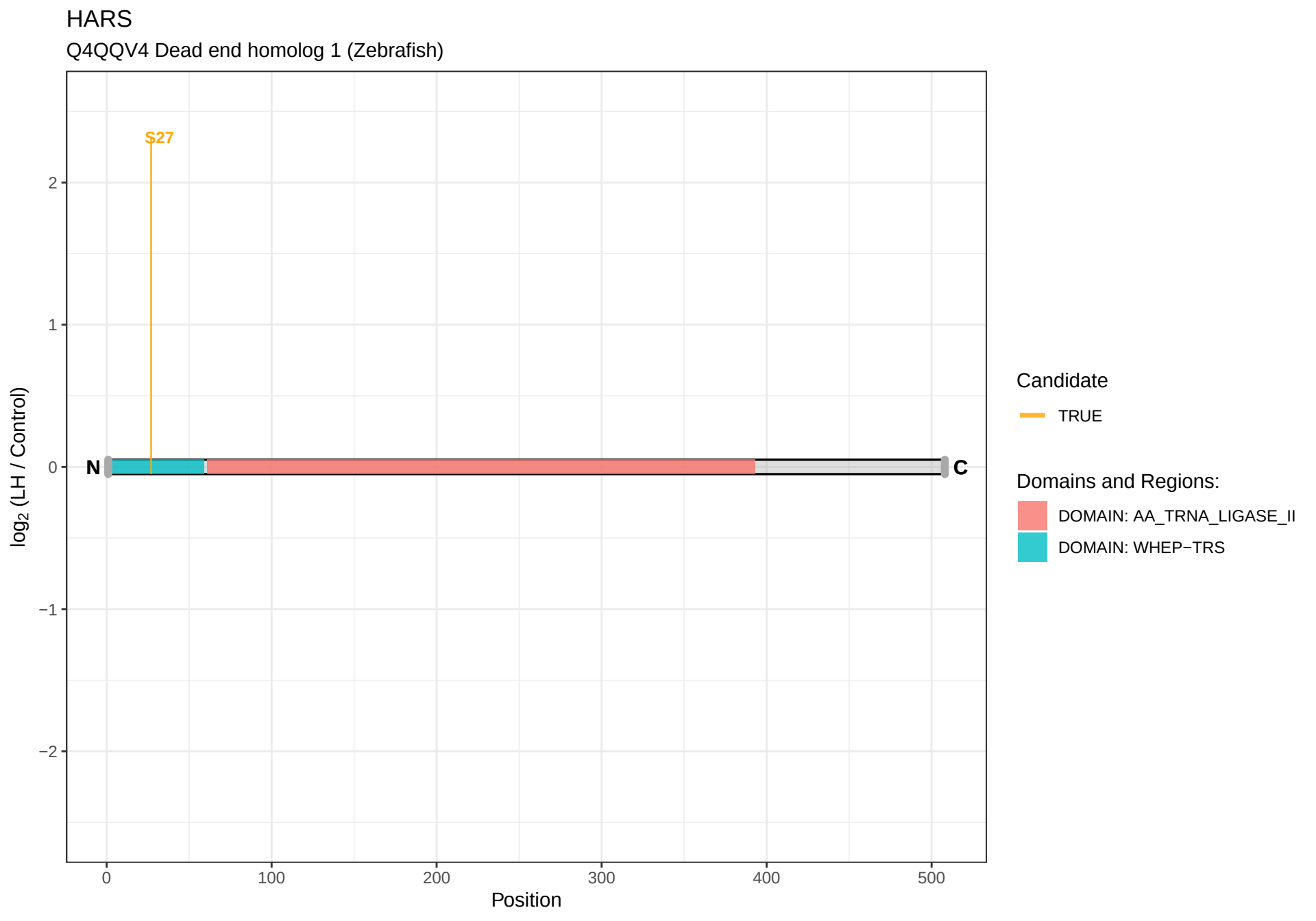

GTSE1
D3ZPA8 G−2 and S−phase−expressed 1
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
N
C
S158
S442
S468
S728
S734
S744
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: GTSE1_N
REGION: Disordered

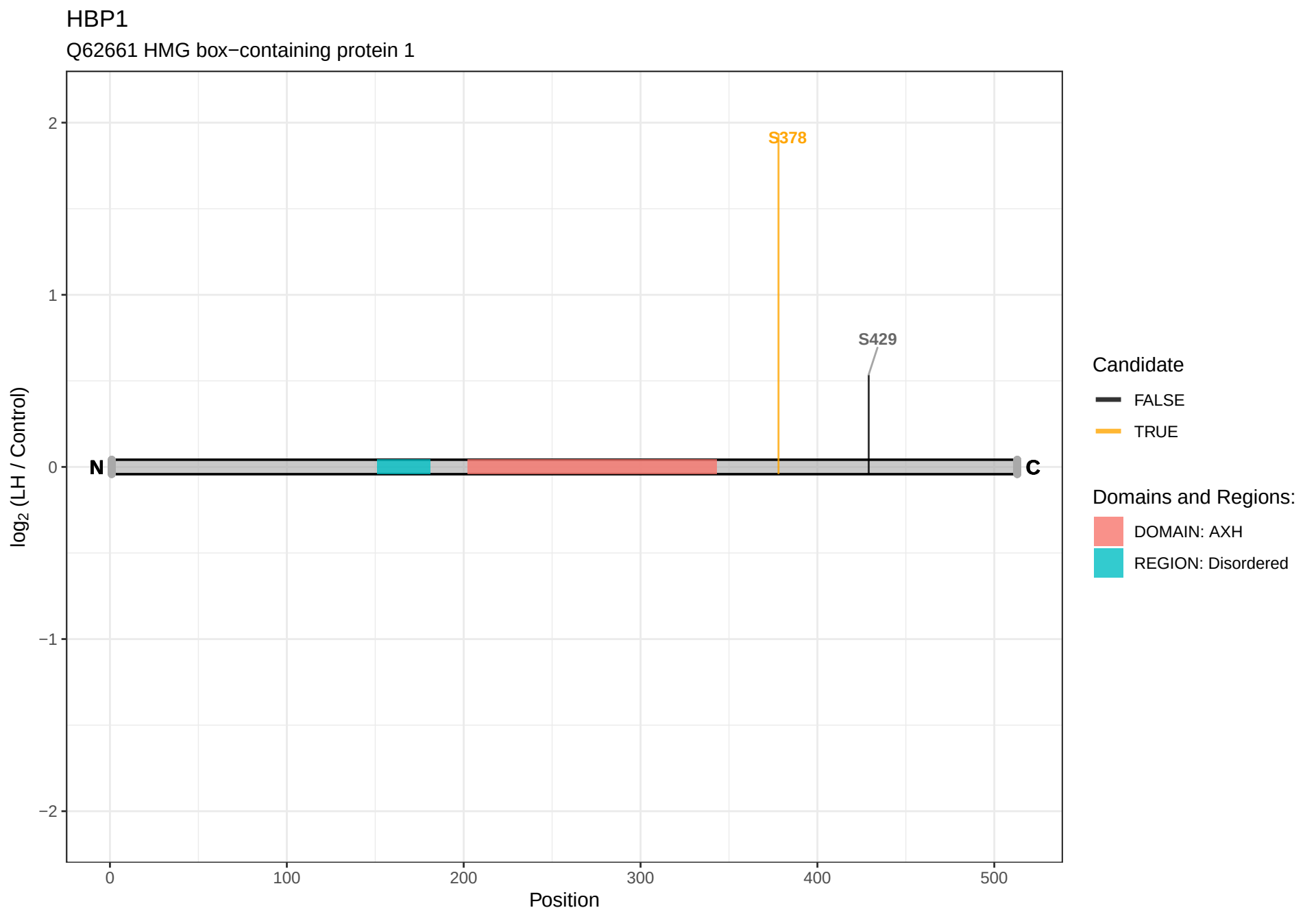

GVIN1
A0A0G2JTA4 GTPase, very large interferon−inducible 1
S760
S1043
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
1500
2000
2500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: VLIG−type G

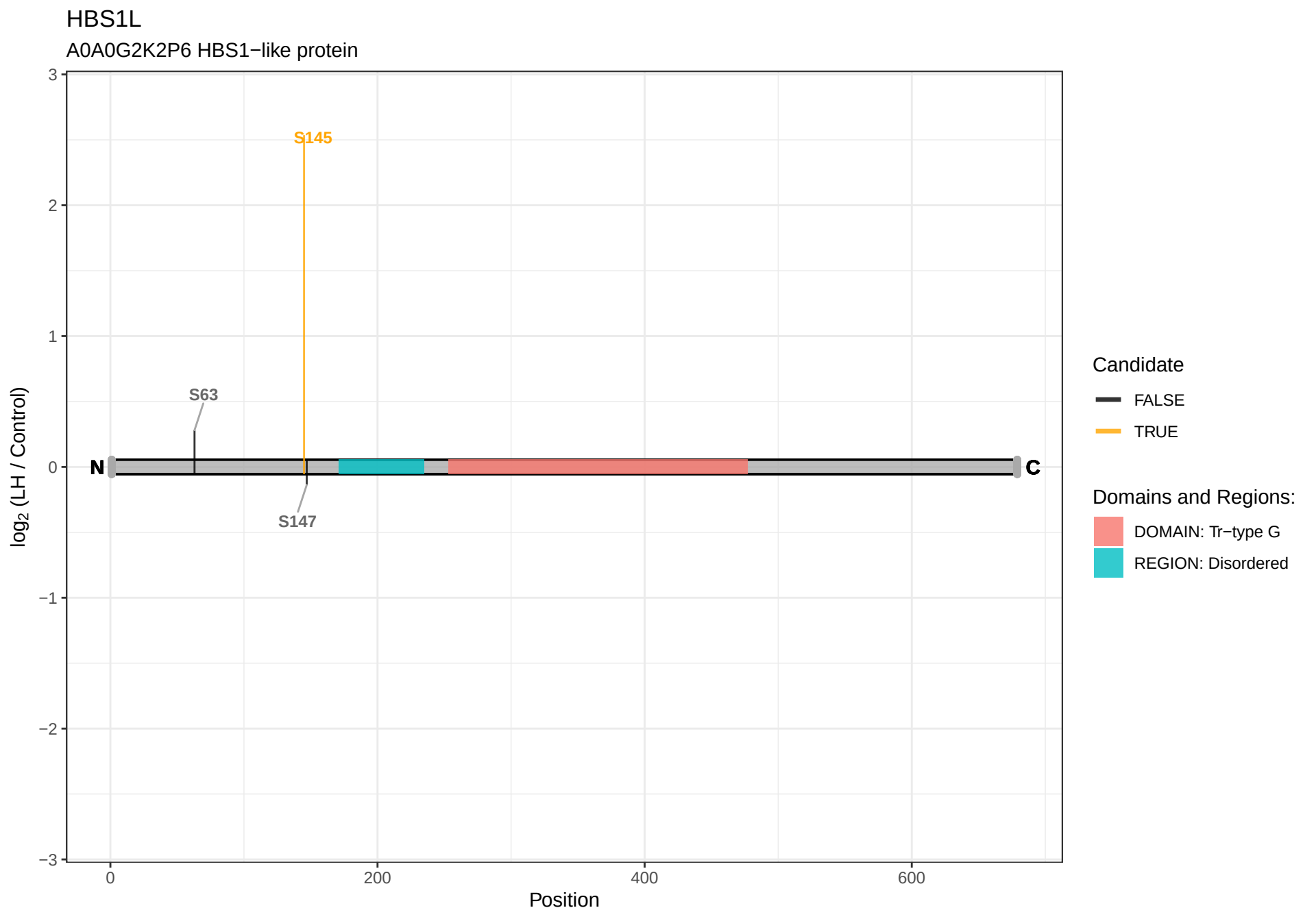

GYS1
A2RRU1 Glycogen [starch] synthase, muscle
2
1
0
−1
−2
log2 (LH / Control)
S711
S728
S653
S657
N
C
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

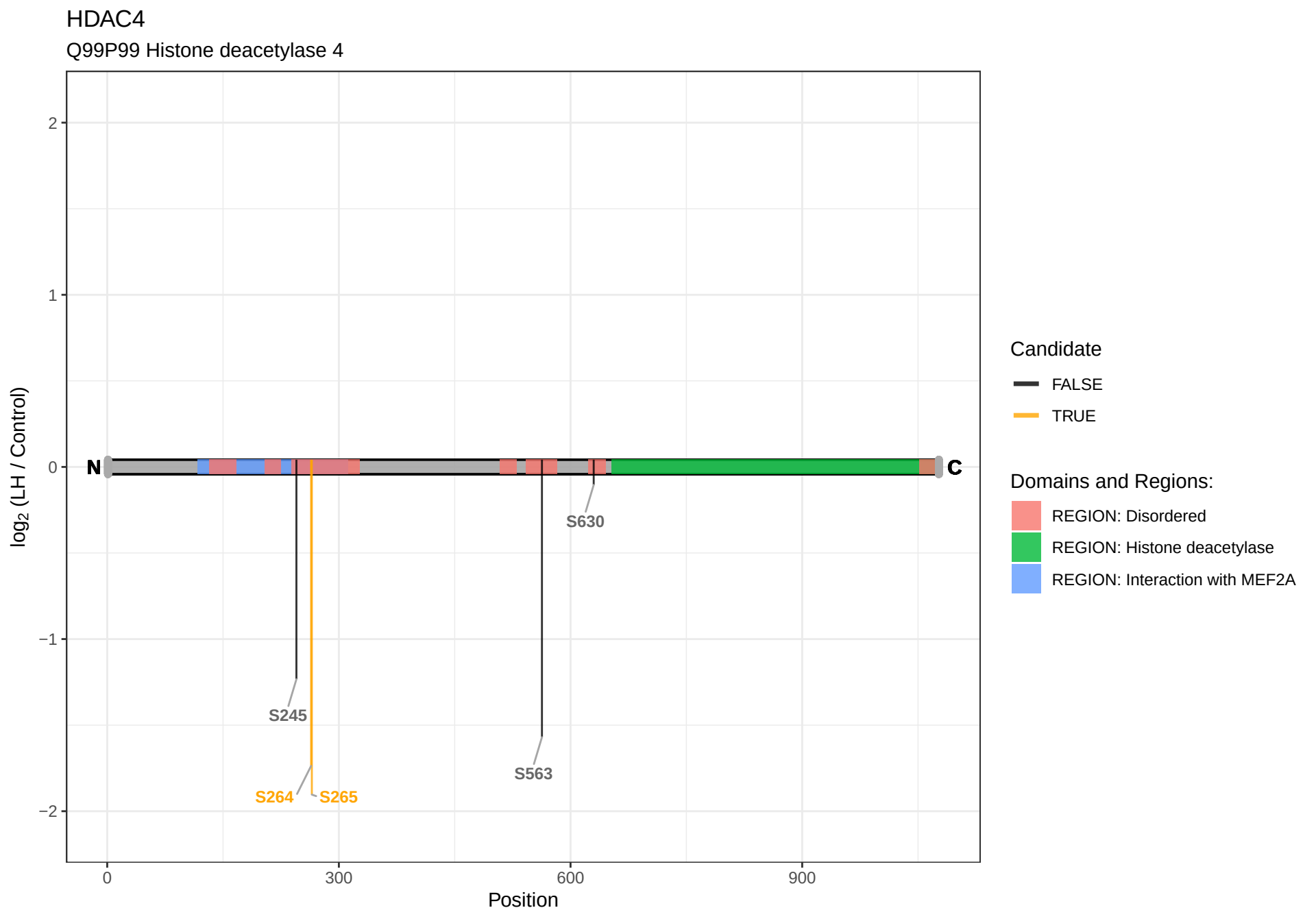

H2AFX
D3ZXP3 Histone H2A
S137
N
C
Y143
S140
2
1
0
−1
−2
log2 (LH / Control)
0
50
100
150
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Histone
DOMAIN: Histone_H2A_C
REGION: Disordered

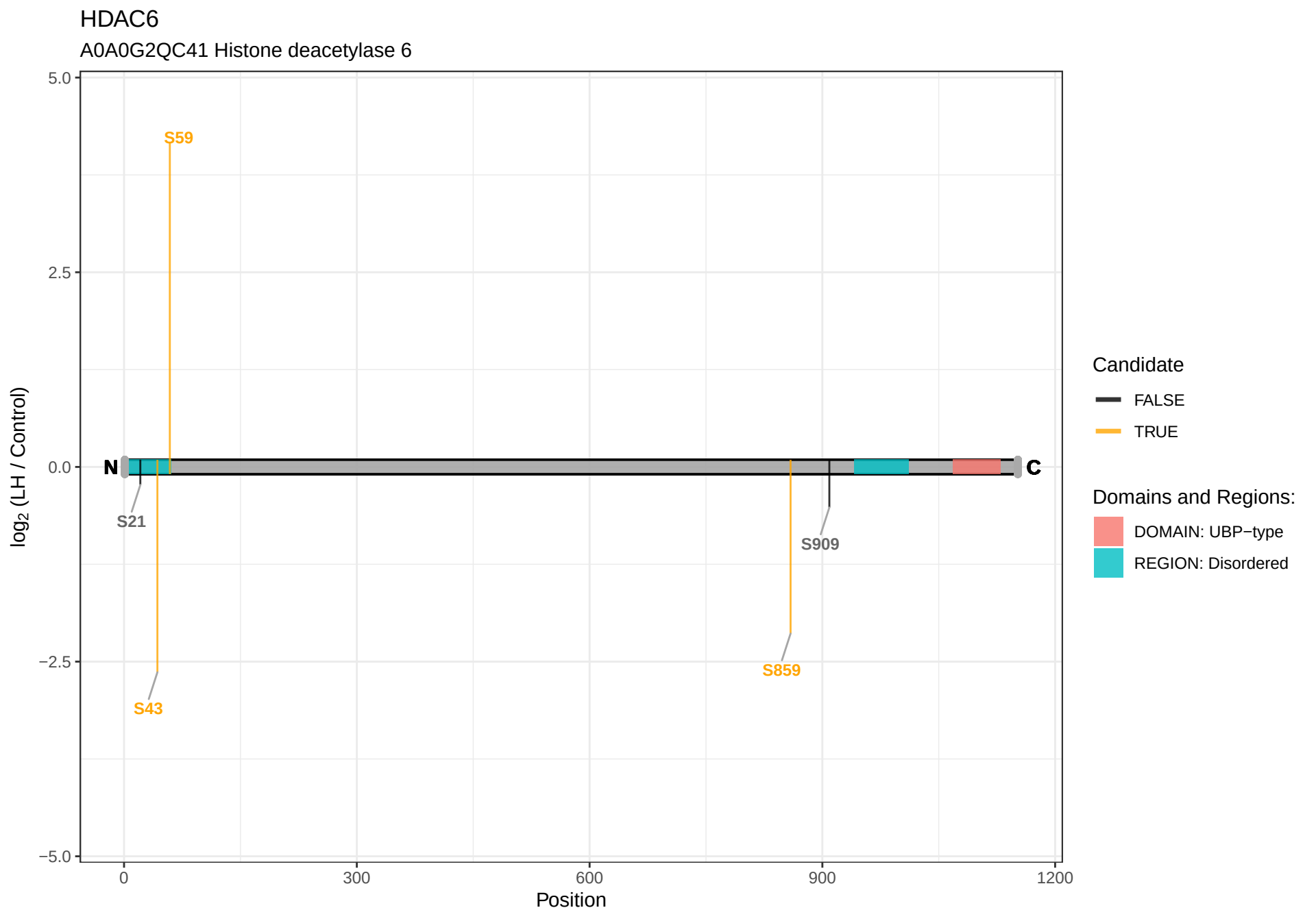

H3F3C
D3ZK97 Histone H3
S29
S58
T81
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
50
100
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Histone
REGION: Disordered

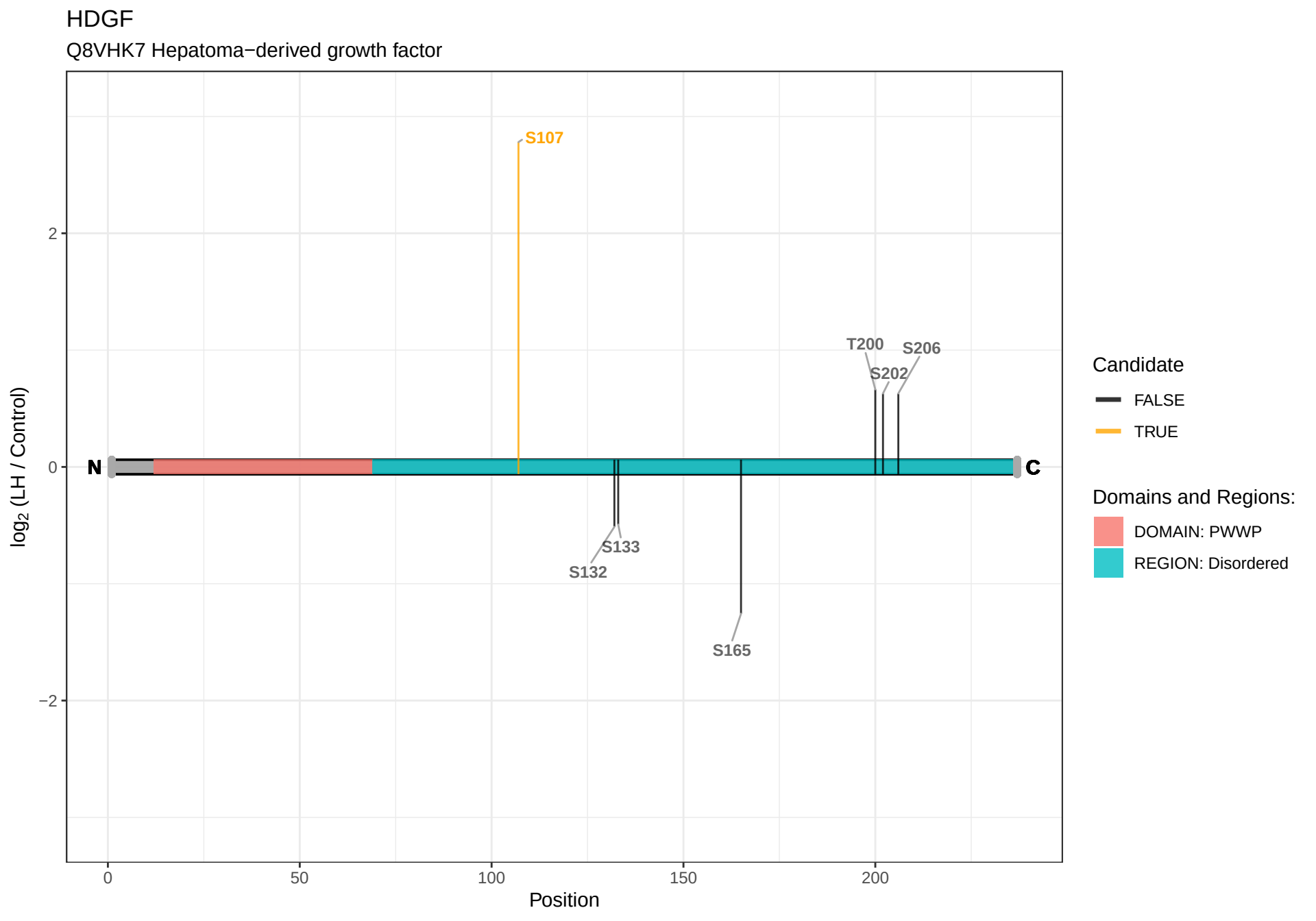

HARS
Q4QQV4 Dead end homolog 1 (Zebrafish)
S27
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
400
500
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: AA_TRNA_LIGASE_II
DOMAIN: WHEP−TRS

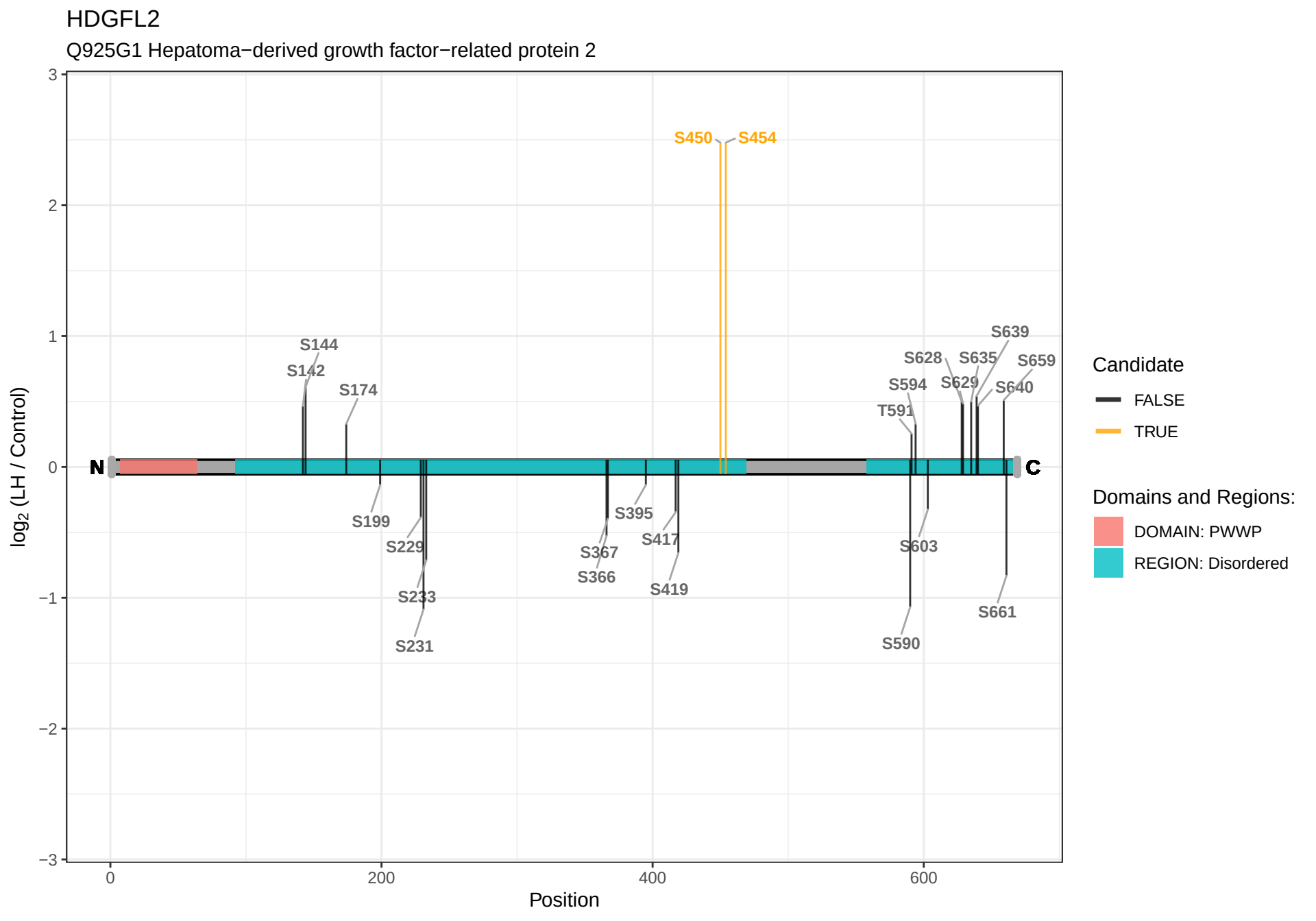

HBP1
Q62661 HMG box−containing protein 1
S378
S429
N
C
log2 (LH / Control)
Position
0
100
200
300
400
500
2
1
0
−1
−2
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AXH
REGION: Disordered

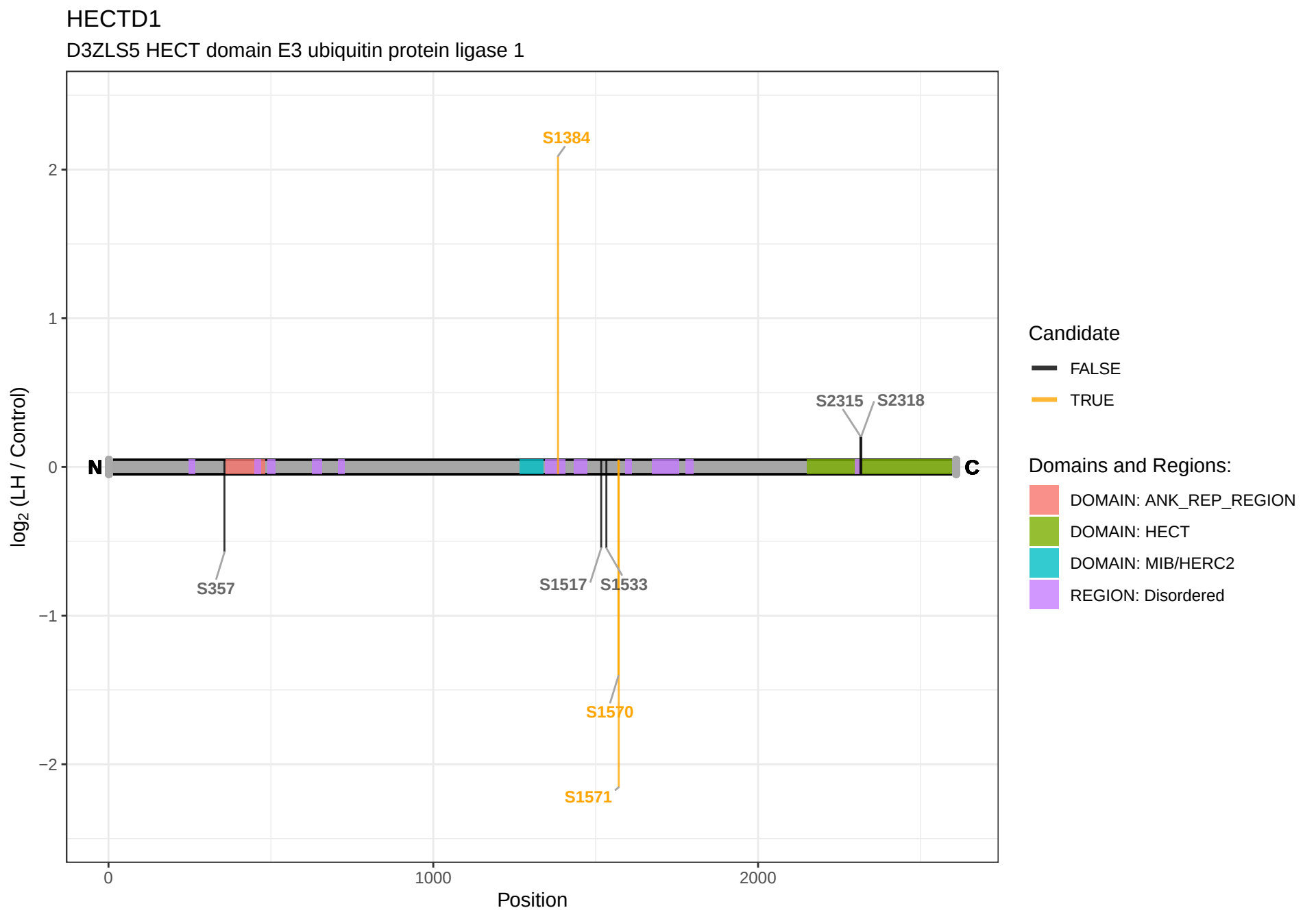

HBS1L
A0A0G2K2P6 HBS1−like protein
log2 (LH / Control)
3
2
1
0
−1
−2
−3
S145
S63
S147
N
C
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Tr−type G
REGION: Disordered

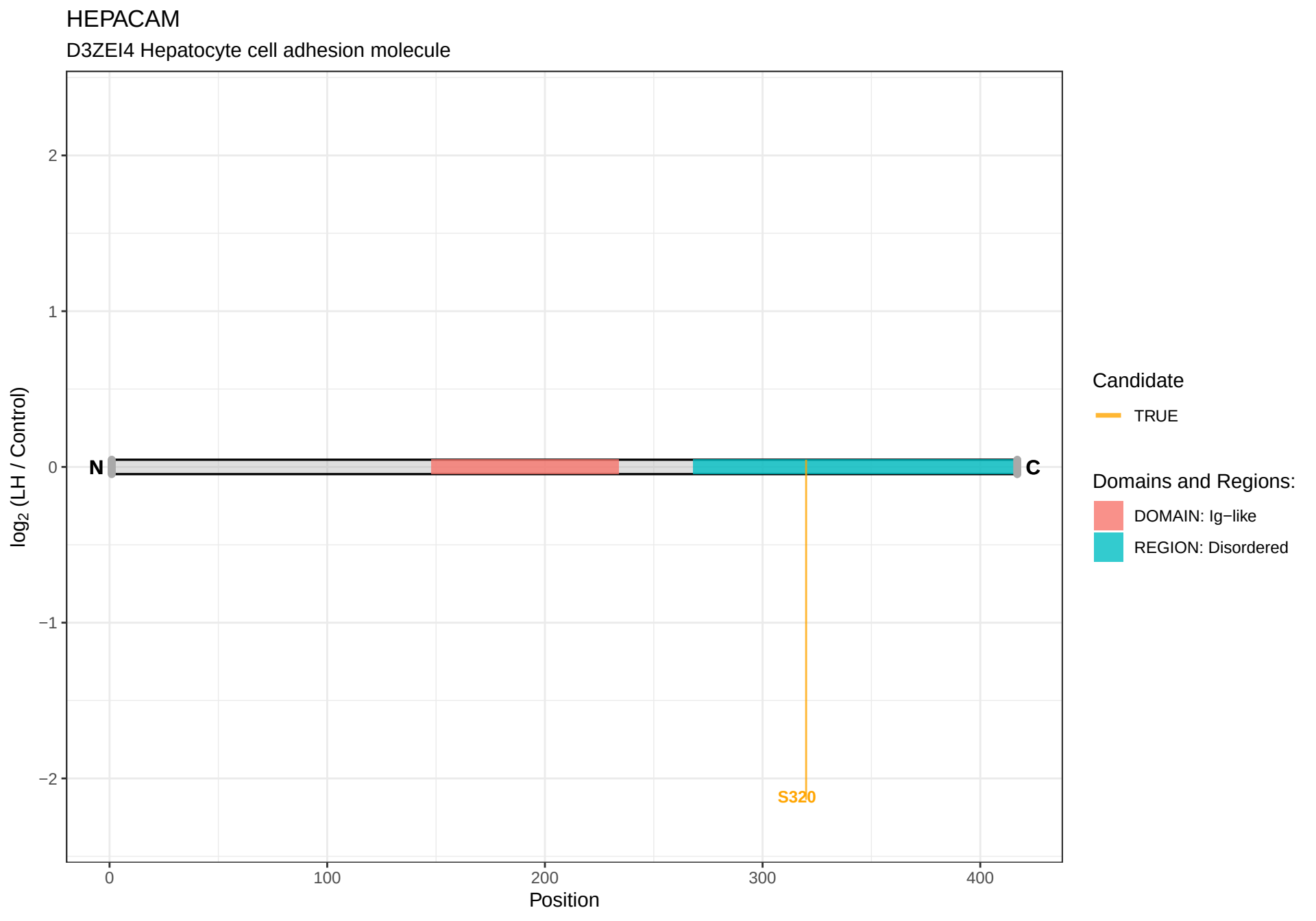

HDAC4
Q99P99 Histone deacetylase 4
log2 (LH / Control)
2
1
0
−1
−2
N
C
S630
S245
S563
S264
S265
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Histone deacetylase
REGION: Interaction with MEF2A

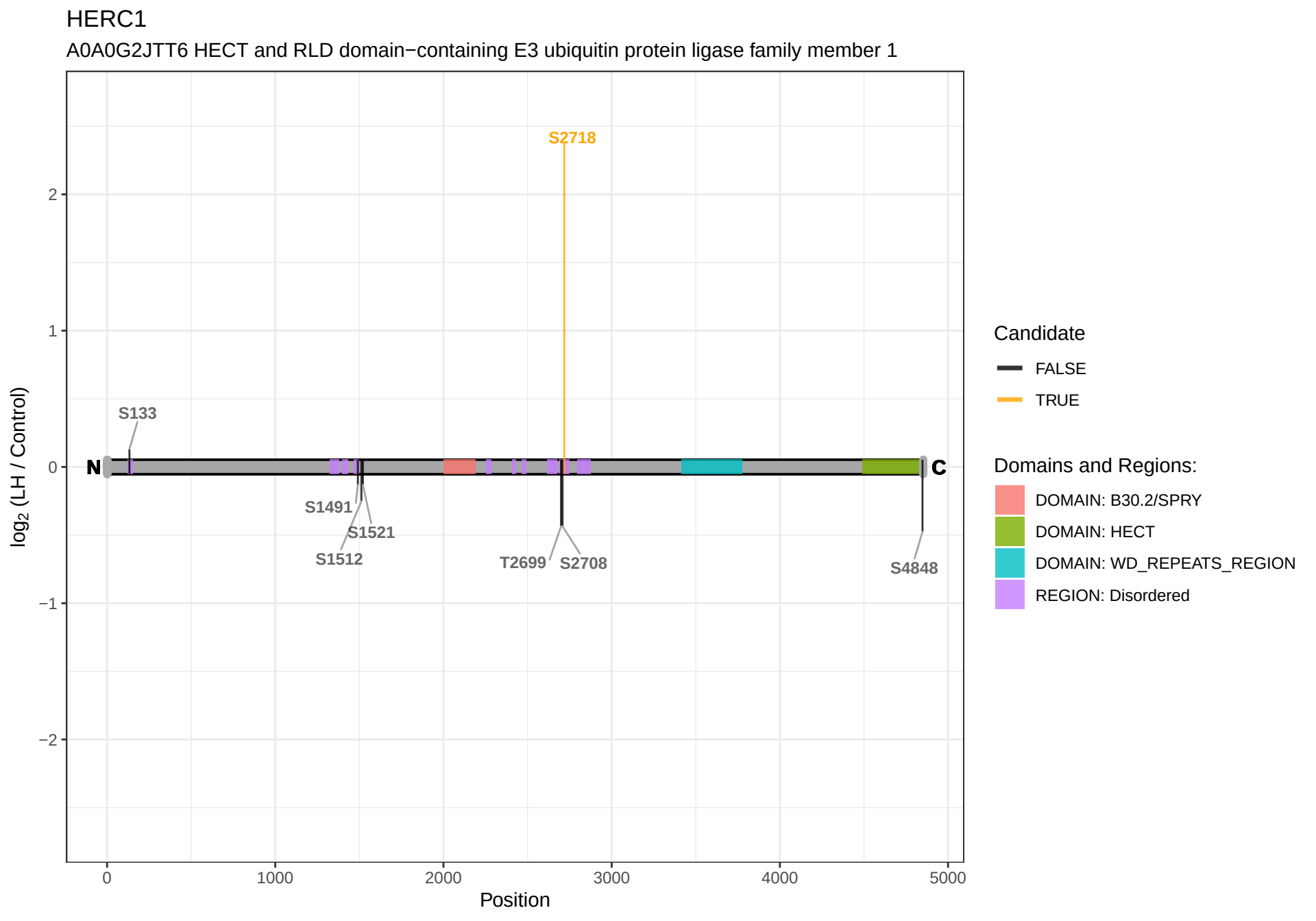

HDAC6
A0A0G2QC41 Histone deacetylase 6
5.0
2.5
0.0
−2.5
−5.0
log2 (LH / Control)
S59
S21
S43
S909
S859
N
C
0
300
600
900
1200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: UBP−type
REGION: Disordered

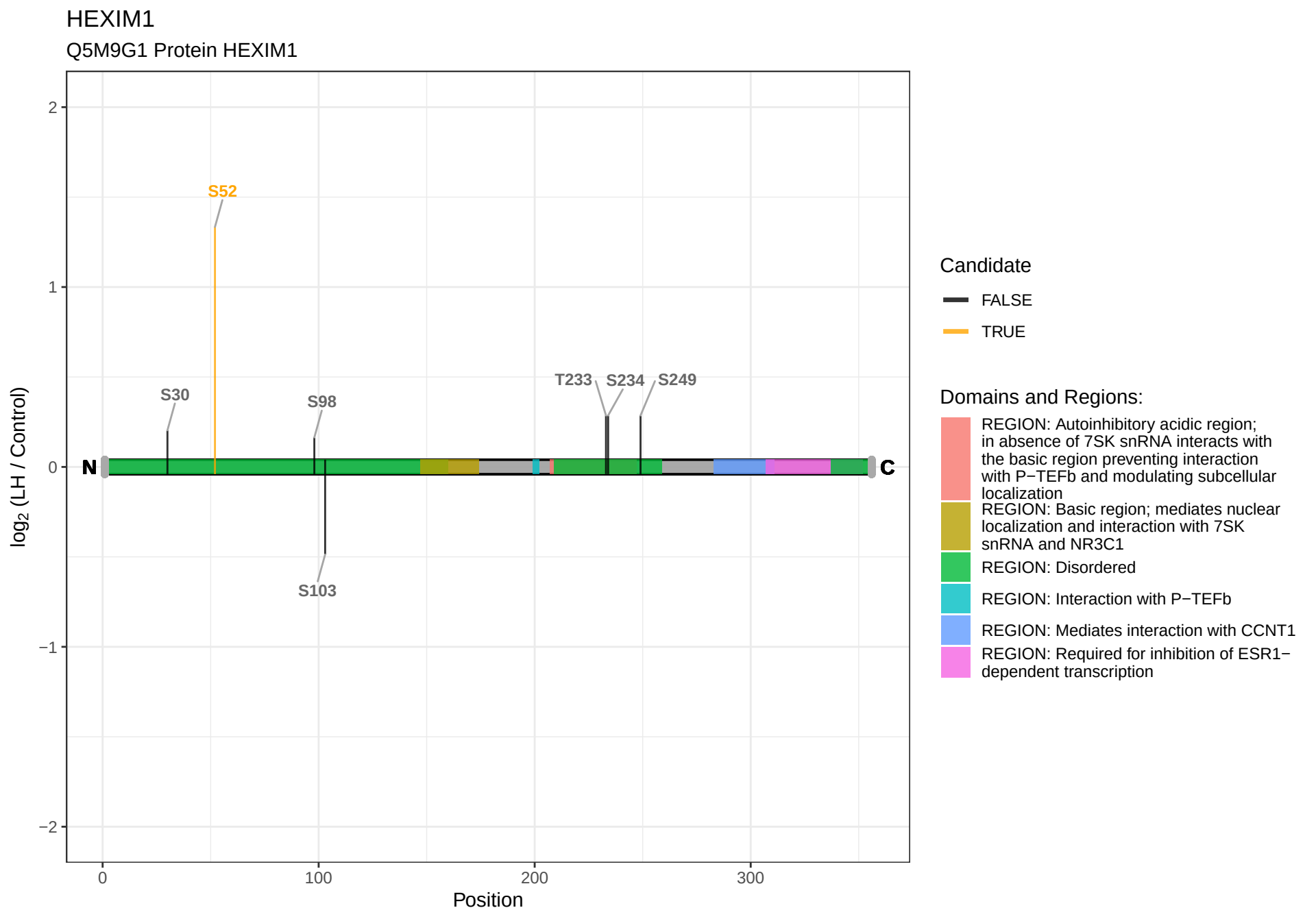

HDGF
Q8VHK7 Hepatoma−derived growth factor
S107
T200
S206
S202
N
C
S133
S132
S165
2
0
−2
log2 (LH / Control)
0
50
100
150
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PWWP
REGION: Disordered

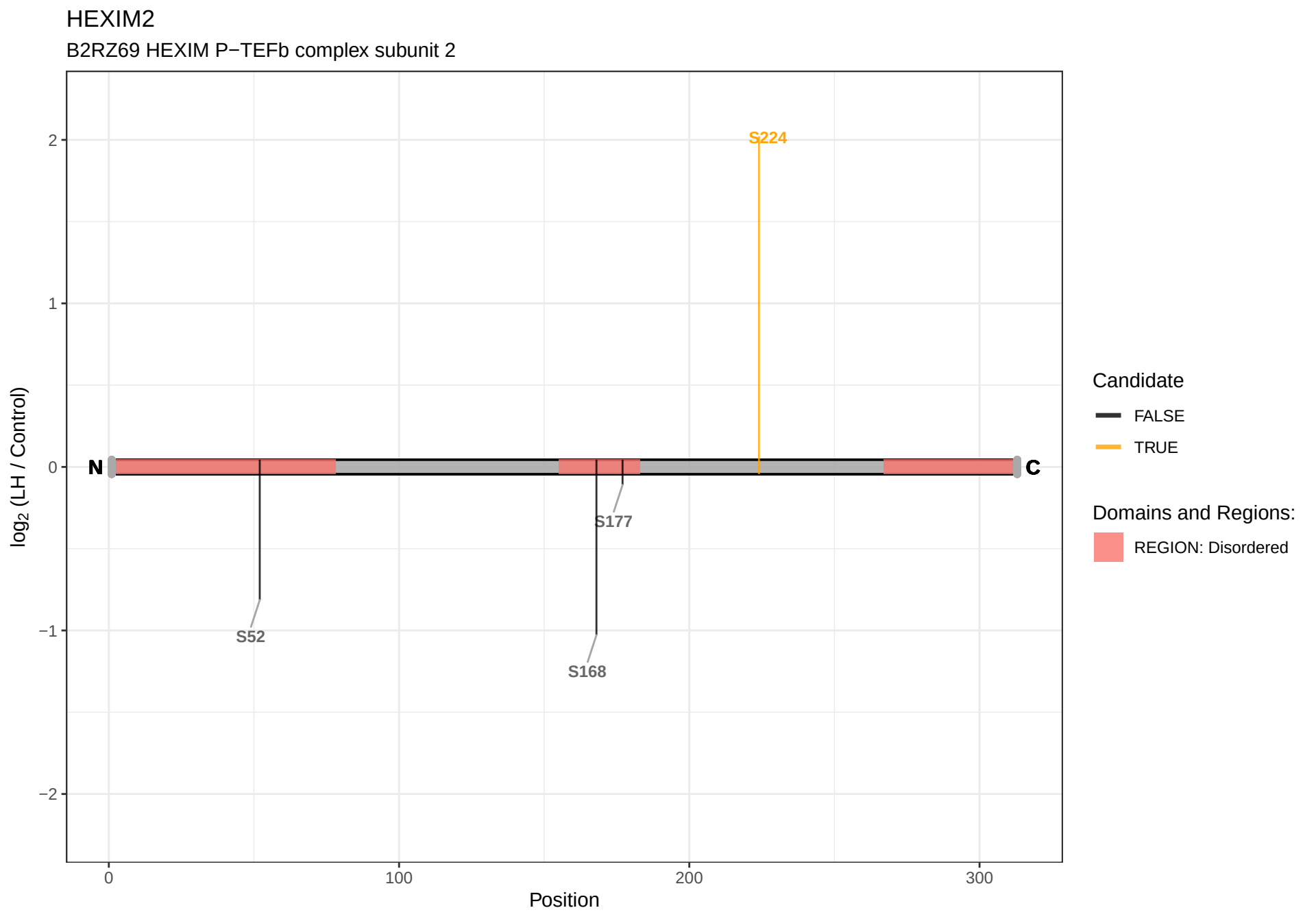

HDGFL2
Q925G1 Hepatoma−derived growth factor−related protein 2
log2 (LH / Control)
Position
N
C
S450
S454
S144
S142
S174
S199
S229
S233
S231
S395
S367
S366
S417
S419
S639
S628
S635
S659
S594
S629
S640
T591
S603
S590
S661
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PWWP
REGION: Disordered

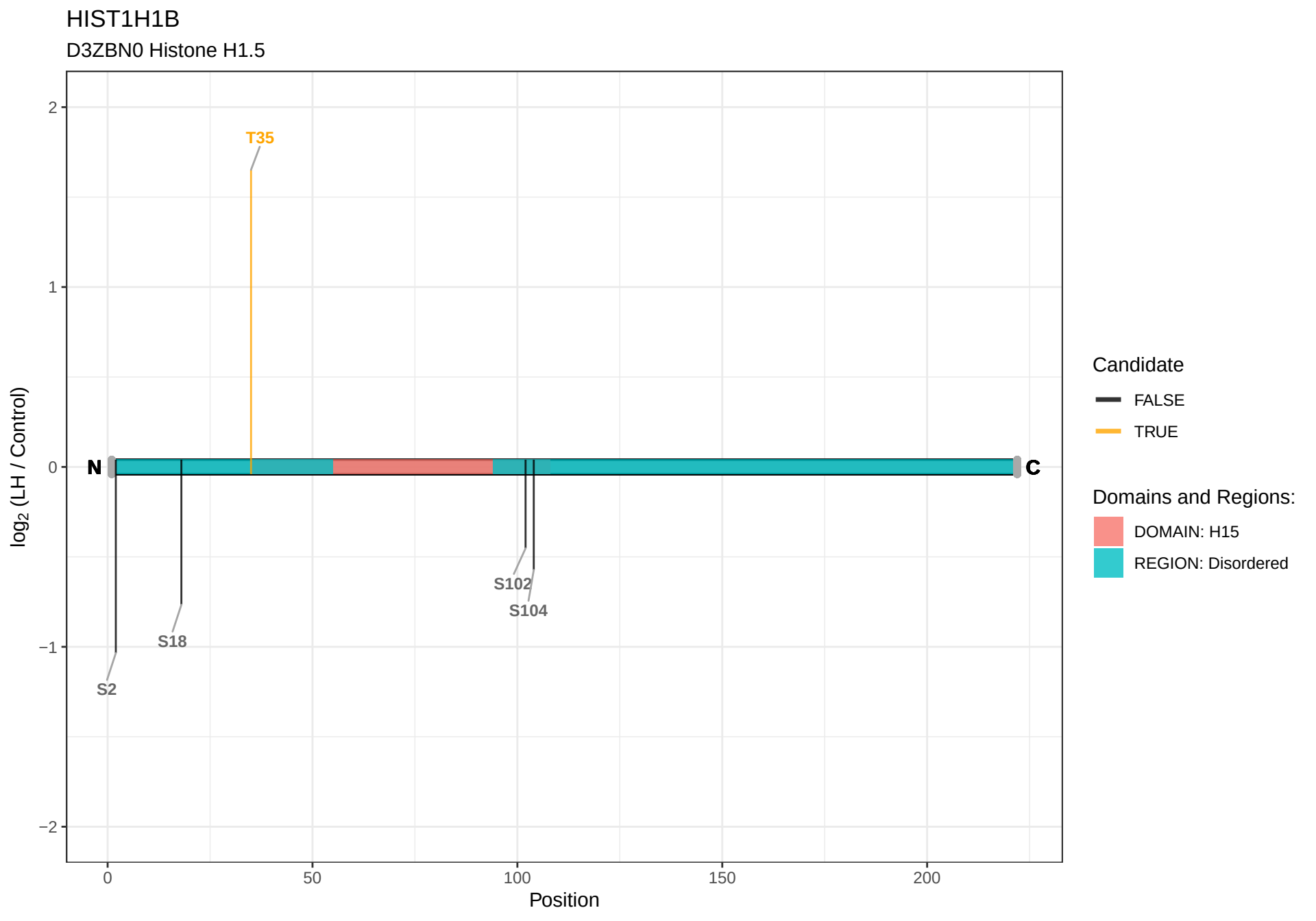

HECTD1
D3ZLS5 HECT domain E3 ubiquitin protein ligase 1
S1384
S2315
S2318
N
C
S357
S1517
S1533
S1570
S1571
2
1
0
−1
−2
log2 (LH / Control)
0
1000
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ANK_REP_REGION
DOMAIN: HECT
DOMAIN: MIB/HERC2
REGION: Disordered

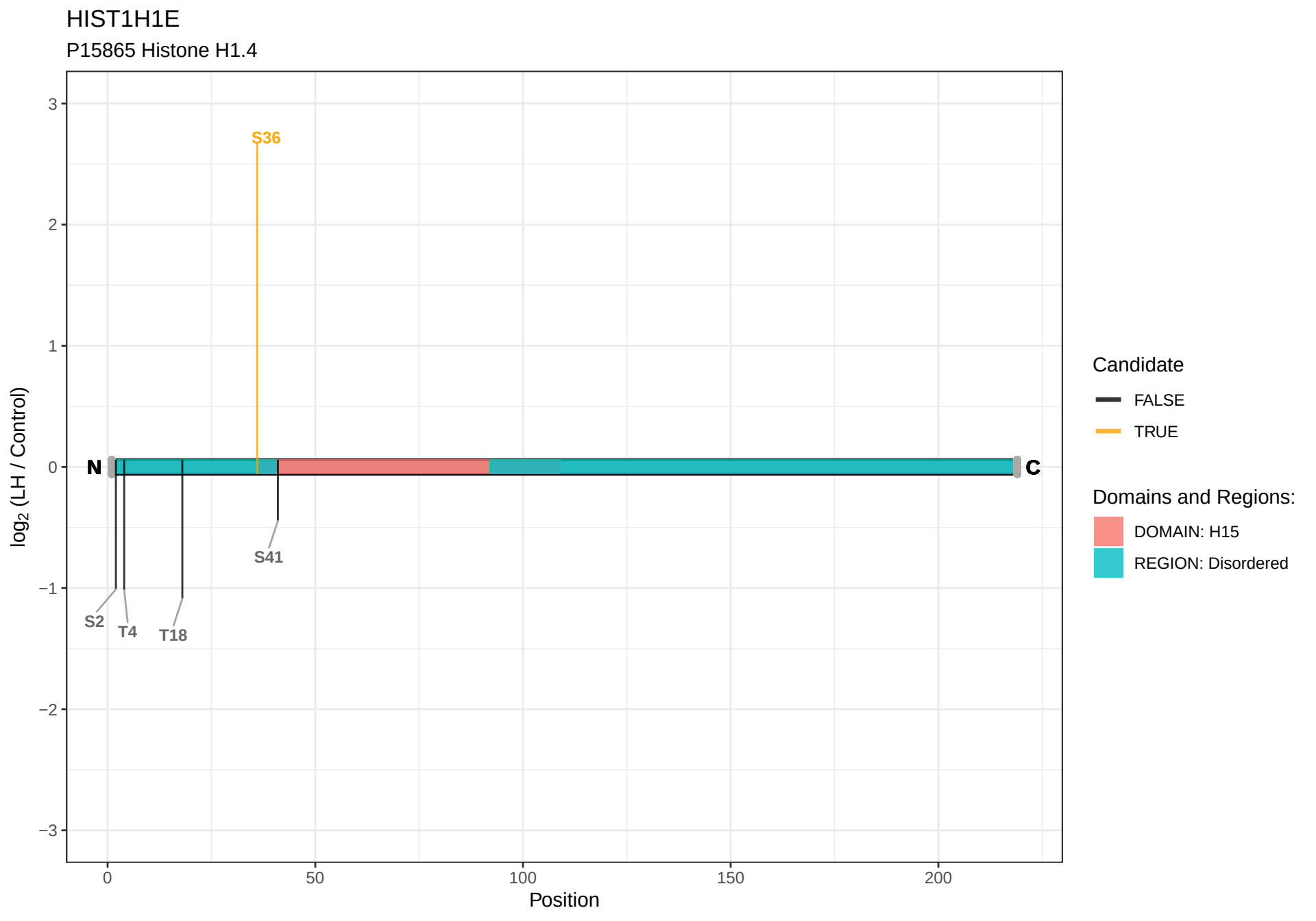

HEPACAM
D3ZEI4 Hepatocyte cell adhesion molecule
log2 (LH / Control)
2
1
0
−1
−2
N
C
S320
0
100
200
300
400
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Ig−like
REGION: Disordered

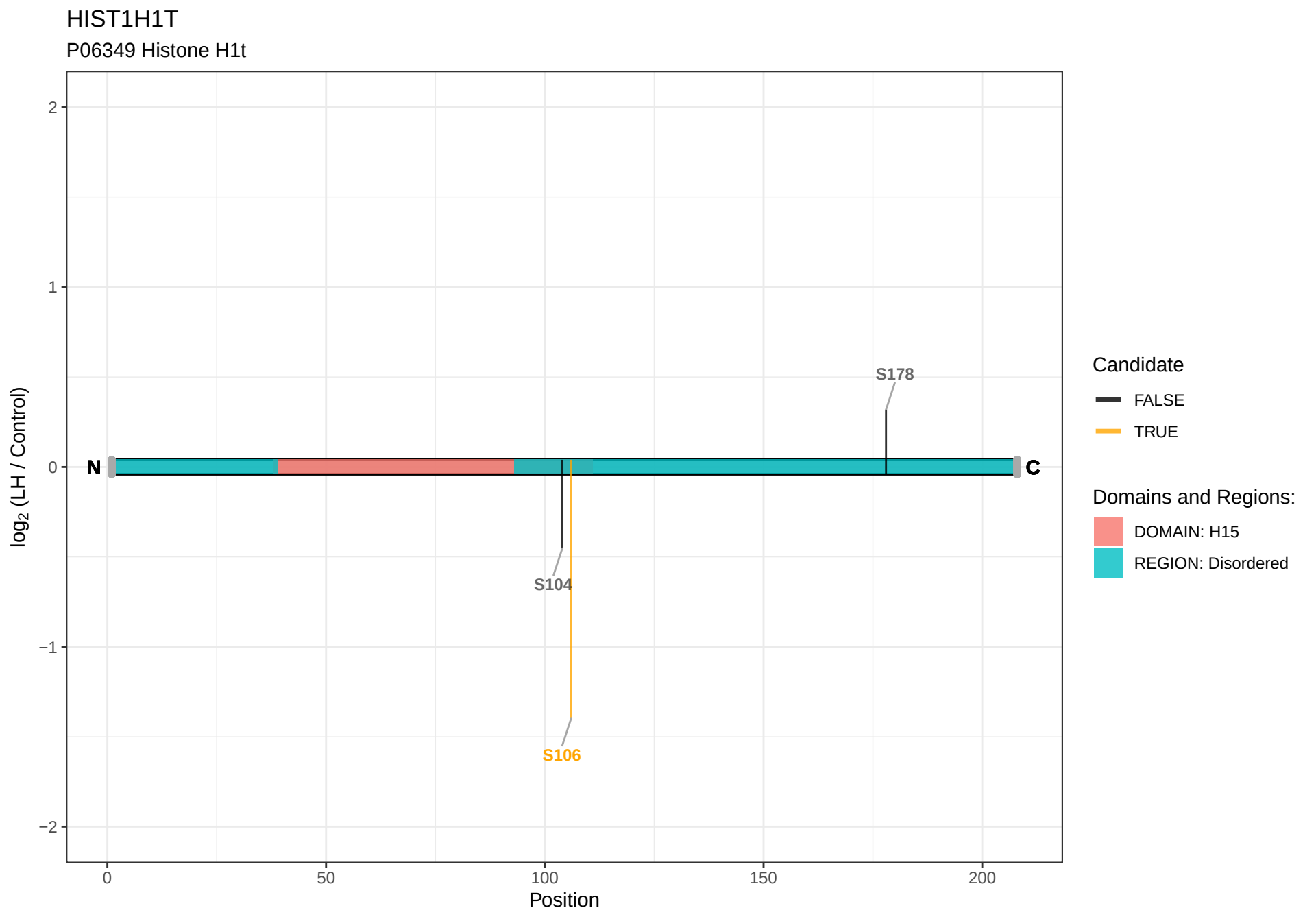

HERC1
A0A0G2JTT6 HECT and RLD domain−containing E3 ubiquitin protein ligase family member 1
S2718
S133
N
C
S1491
S1521
S1512
T2699
S2708
S4848
log2 (LH / Control)
2
1
0
−1
−2
0
1000
2000
3000
4000
5000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: B30.2/SPRY
DOMAIN: HECT
DOMAIN: WD_REPEATS_REGION
REGION: Disordered

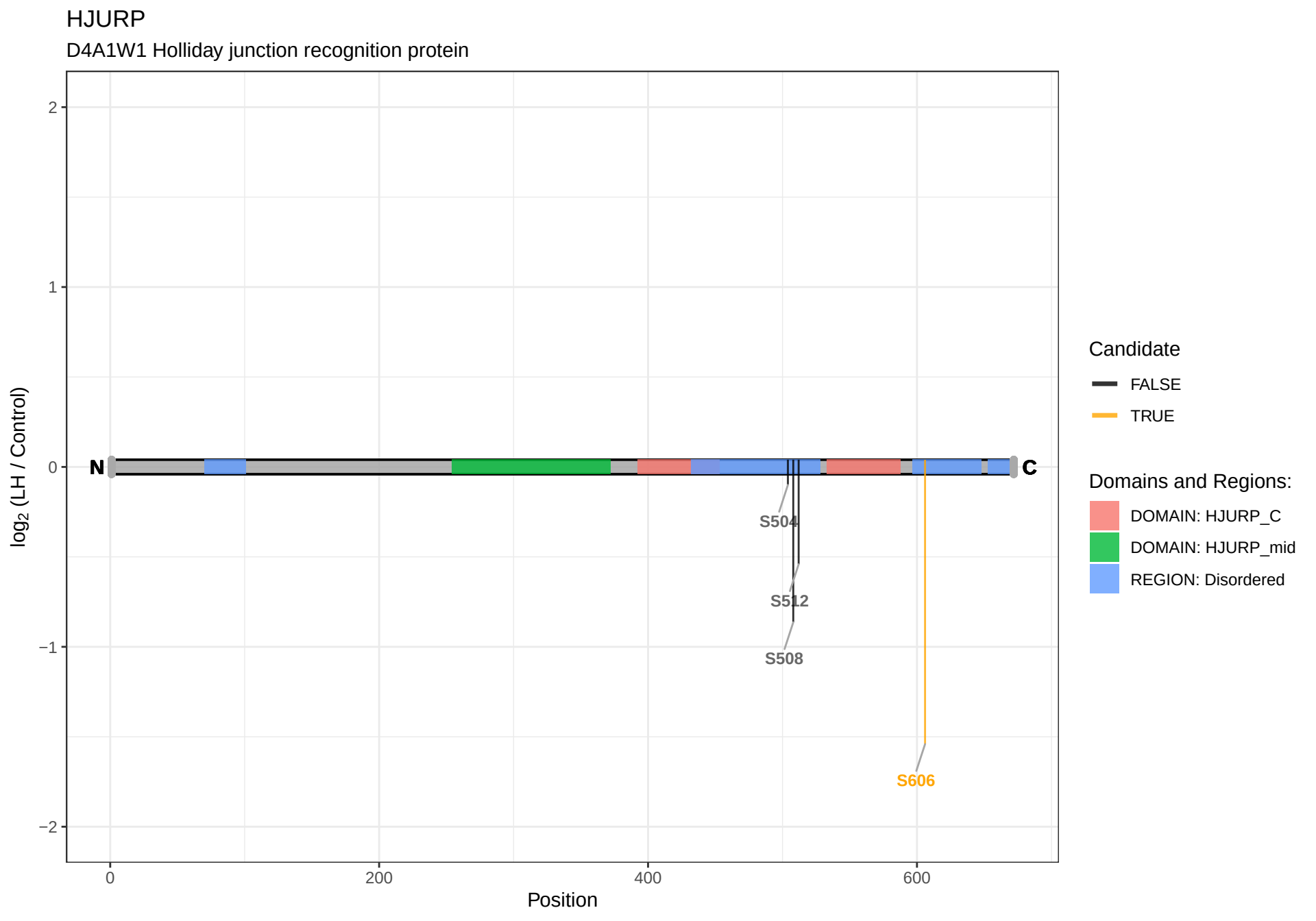

HEXIM1
Q5M9G1 Protein HEXIM1
S52
S30
S98
S103
T233
S234
S249
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Autoinhibitory acidic region; in absence of 7SK snRNA interacts with the basic region preventing interaction with P−TEFb and modulating subcellular localization
REGION: Basic region; mediates nuclear localization and interaction with 7SK snRNA and NR3C1
REGION: Disordered
REGION: Interaction with P−TEFb
REGION: Mediates interaction with CCNT1
REGION: Required for inhibition of ESR1−dependent transcription

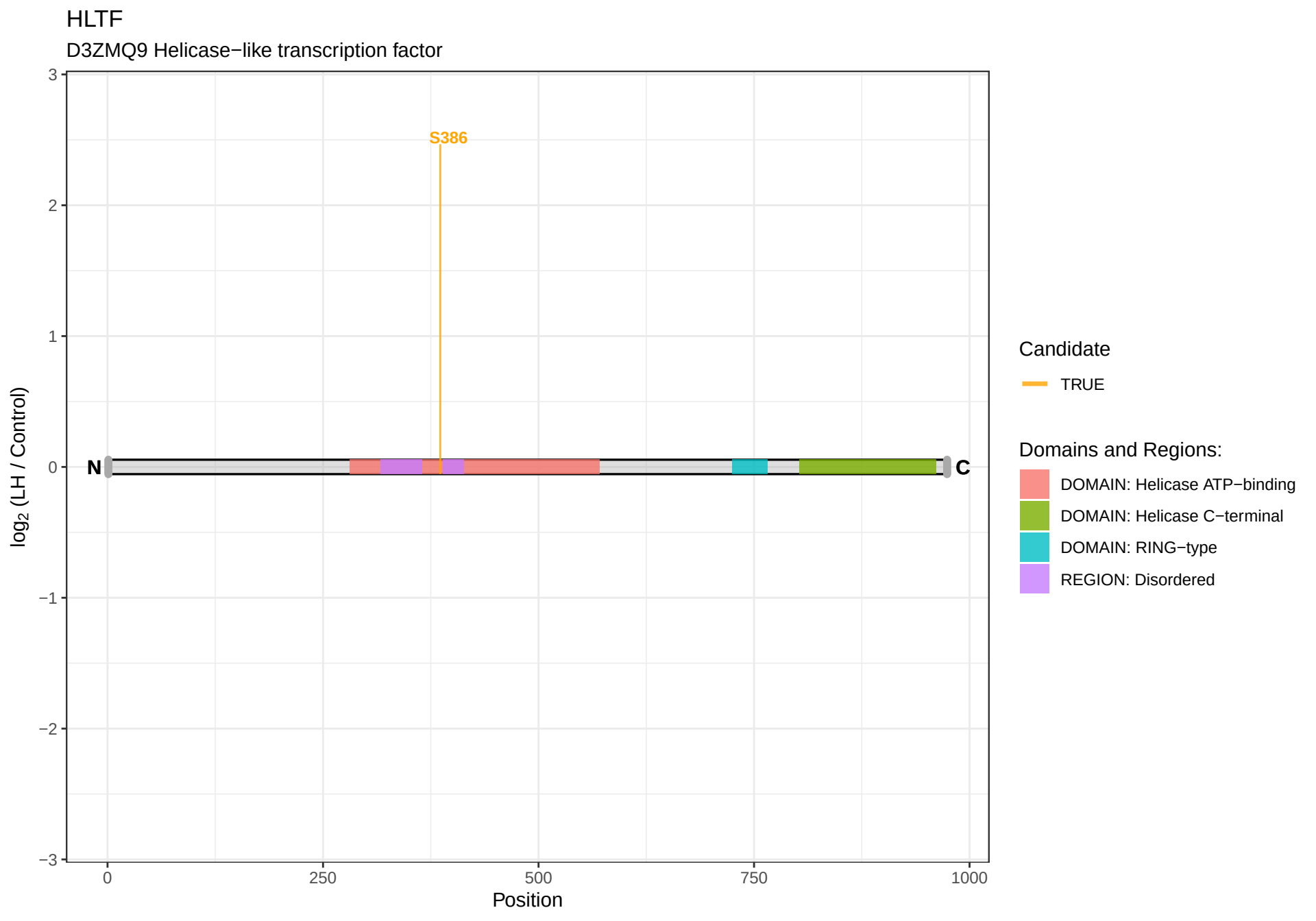

HEXIM2
B2RZ69 HEXIM P−TEFb complex subunit 2
log2 (LH / Control)
2
1
0
−1
−2
N
C
S224
S177
S52
S168
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

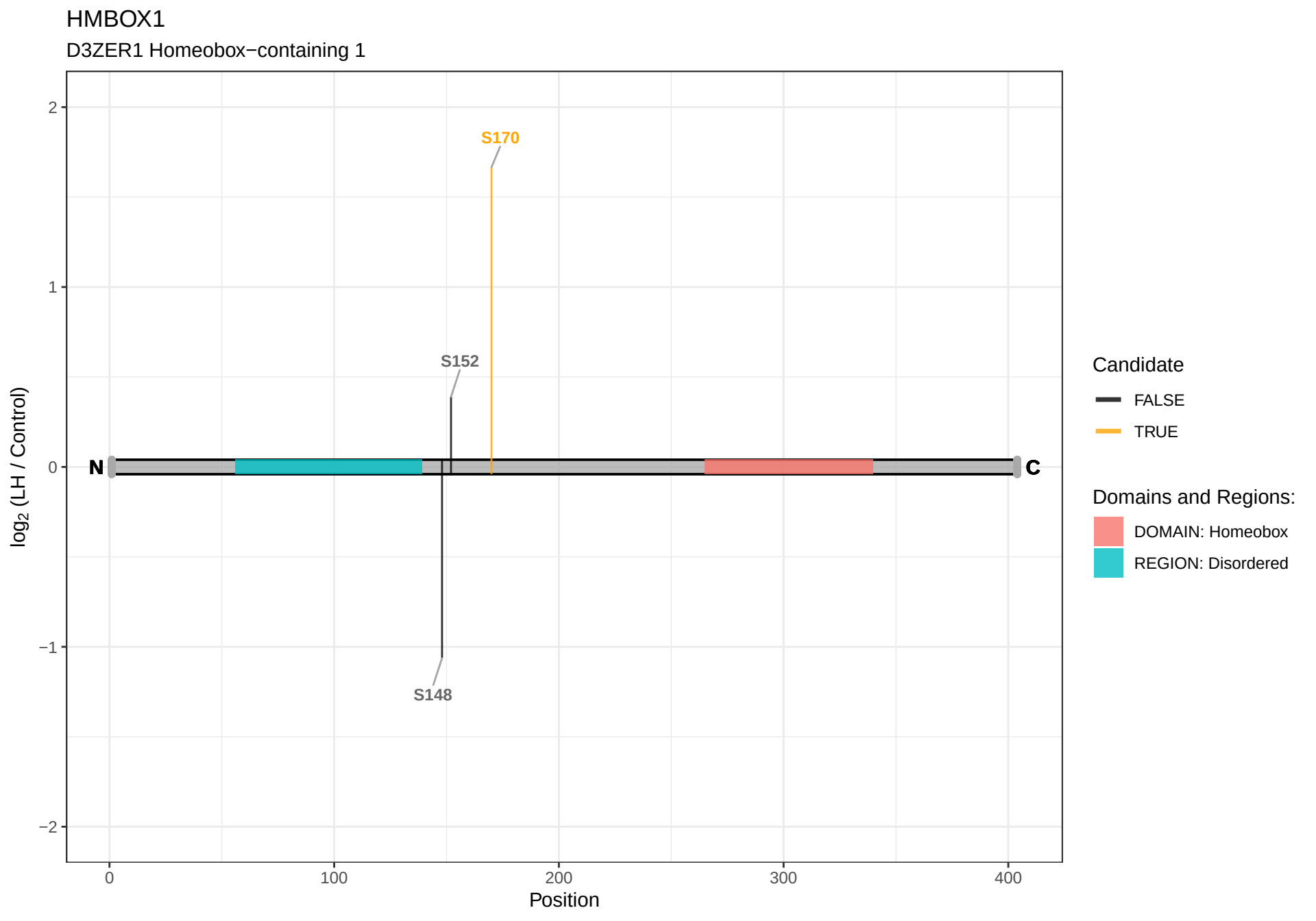

HIST1H1B
D3ZBN0 Histone H1.5
T35
N
C
S2
S18
S102
S104
log2 (LH / Control)
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: H15
REGION: Disordered

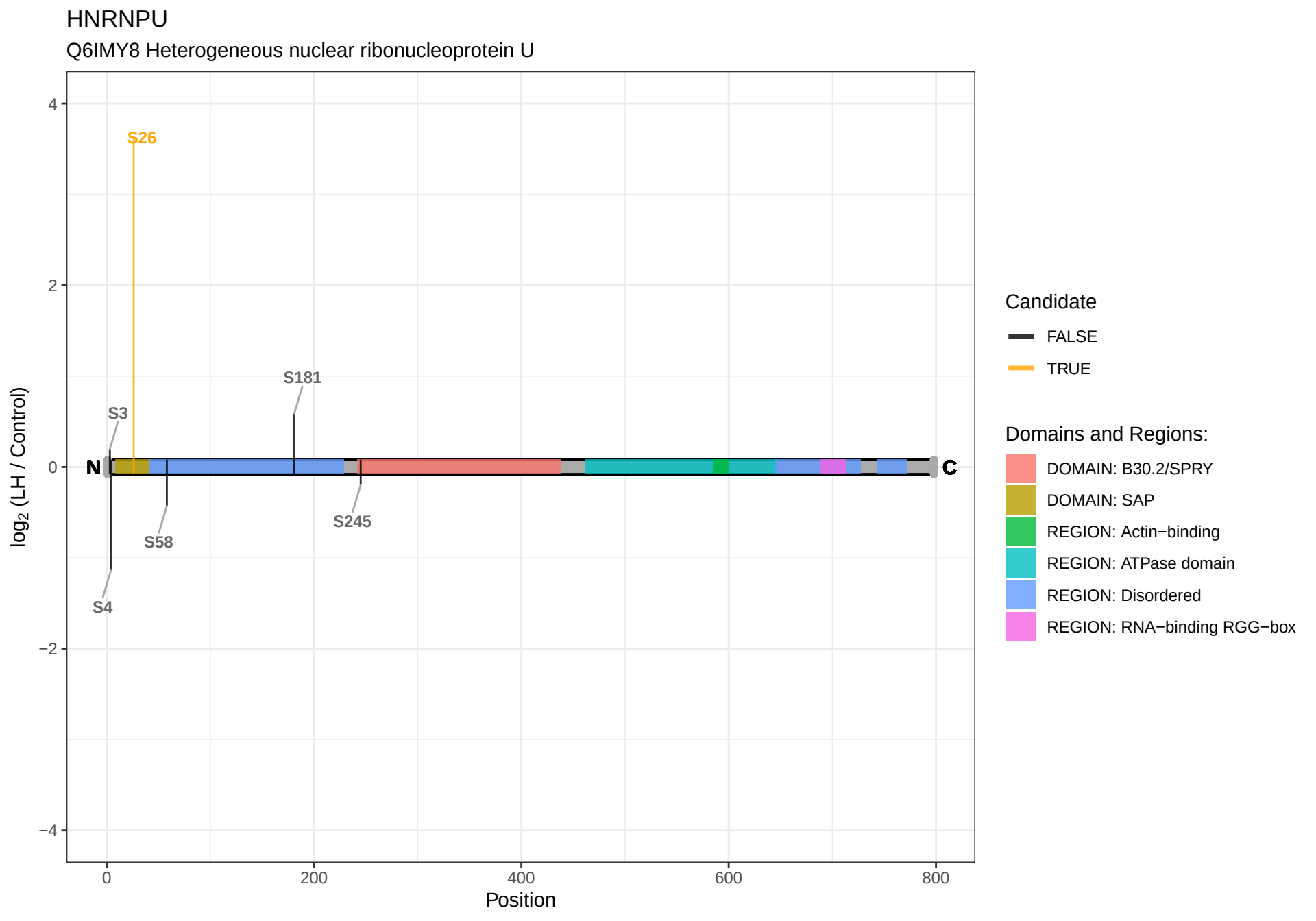

HIST1H1E
P15865 Histone H1.4
log2 (LH / Control)
3
2
1
0
−1
−2
−3
S36
N
C
S41
S2
T4
T18
0
50
100
150
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: H15
REGION: Disordered

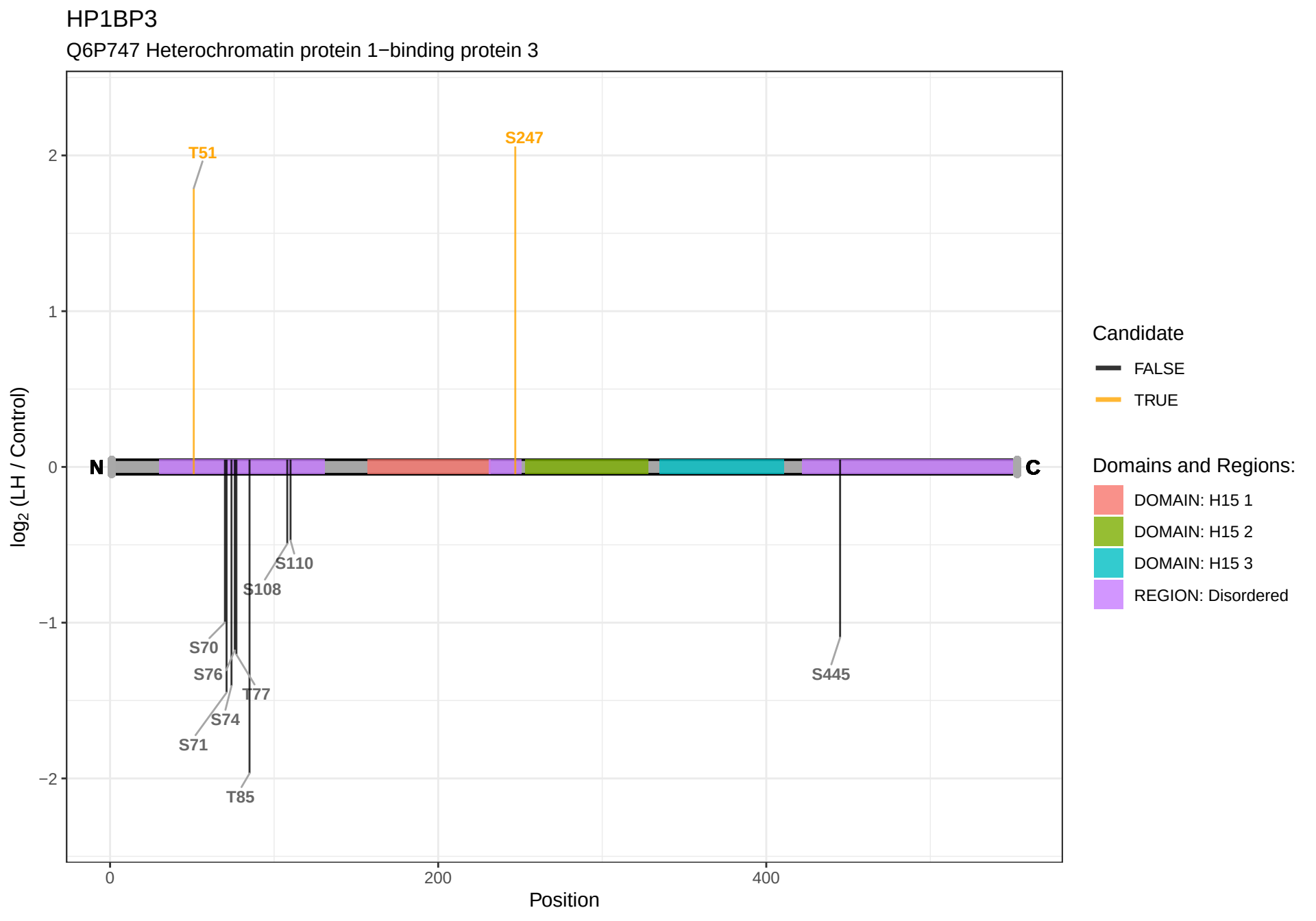

HIST1H1T
P06349 Histone H1t
log2 (LH / Control)
2
1
0
−1
−2
N
C
S178
S104
S106
0
50
100
150
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: H15
REGION: Disordered

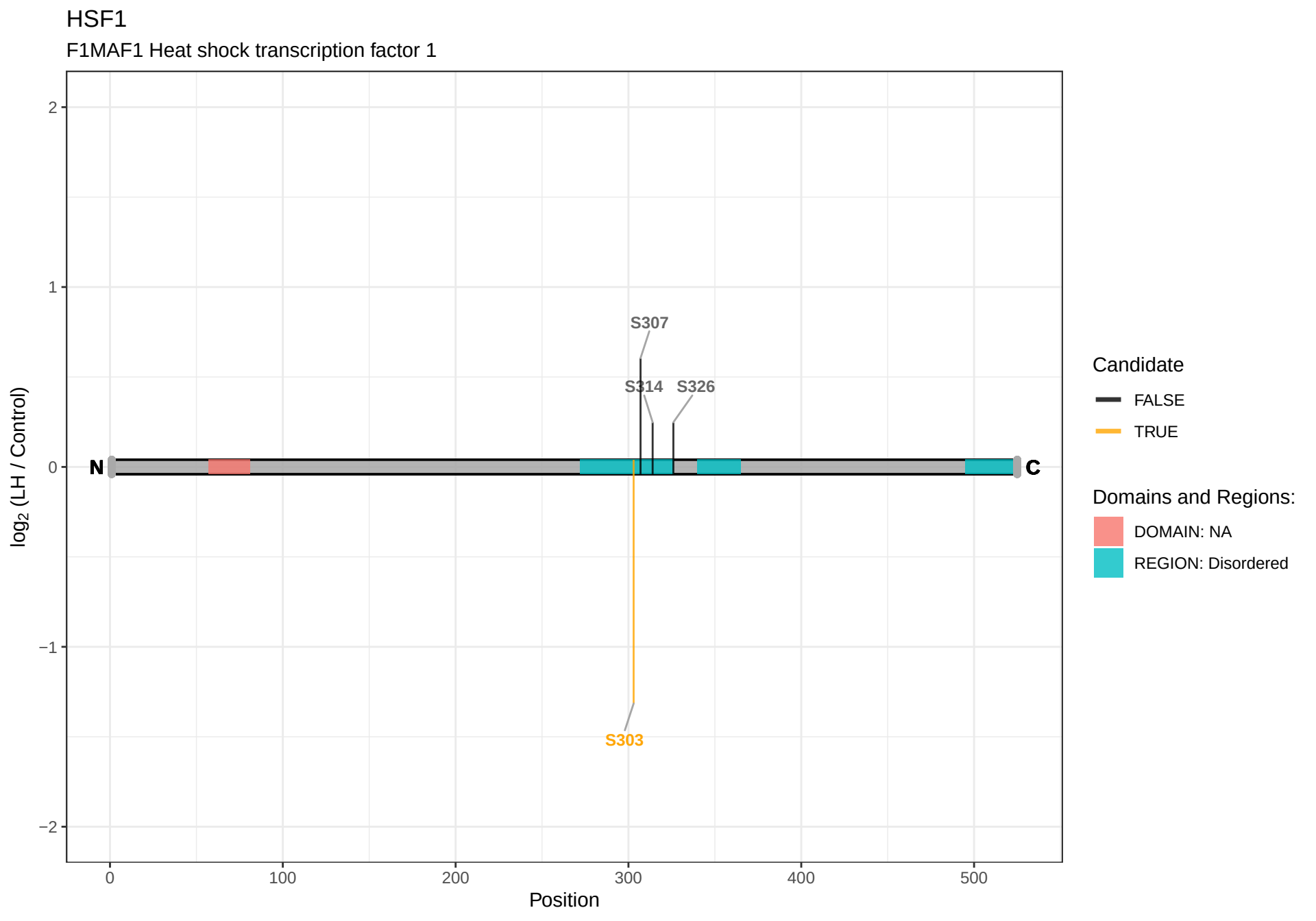

HJURP
D4A1W1 Holliday junction recognition protein
log2 (LH / Control)
2
1
0
−1
−2
N
C
S504
S512
S508
S606
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: HJURP_C
DOMAIN: HJURP_mid
REGION: Disordered

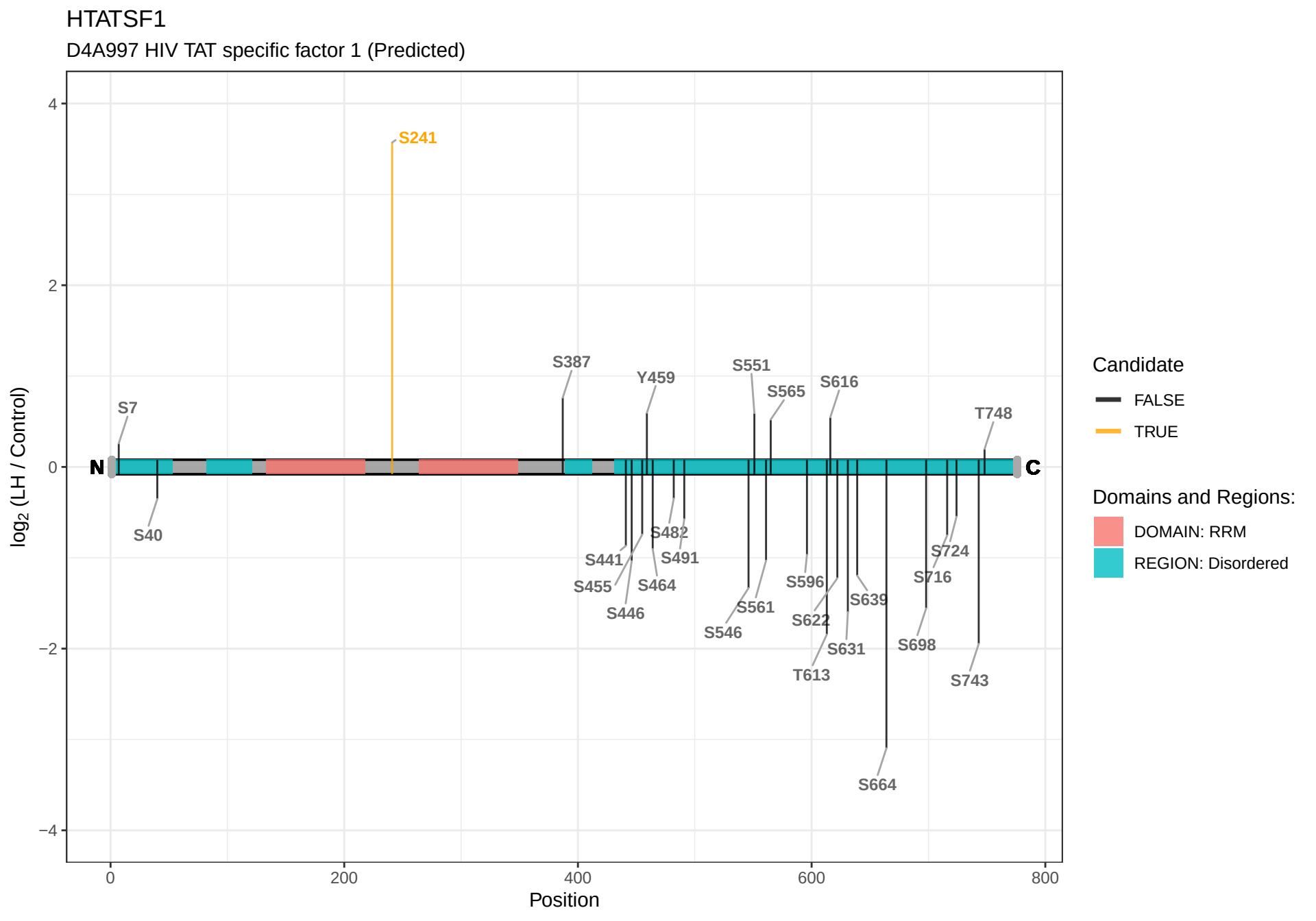

HLTF
D3ZMQ9 Helicase−like transcription factor
S386
N
C
log2 (LH / Control)
Position
3
2
1
0
−1
−2
−3
0
250
500
750
1000
Candidate
TRUE
Domains and Regions:
DOMAIN: Helicase ATP−binding
DOMAIN: Helicase C−terminal
DOMAIN: RING−type
REGION: Disordered

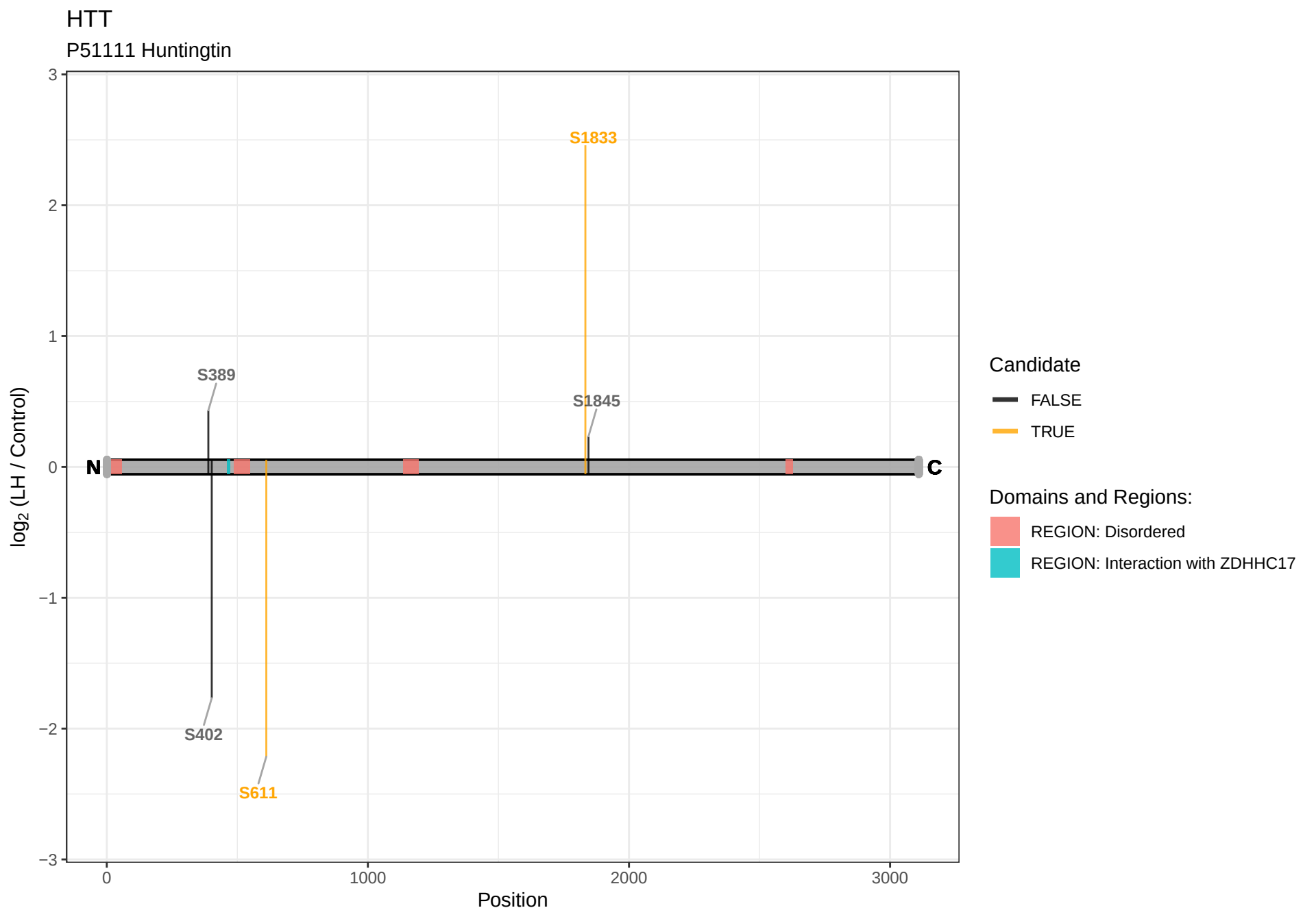

HMBOX1
D3ZER1 Homeobox−containing 1
S170
S152
S148
N
C
2
1
0
−1
−2
0
100
200
300
400
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Homeobox
REGION: Disordered

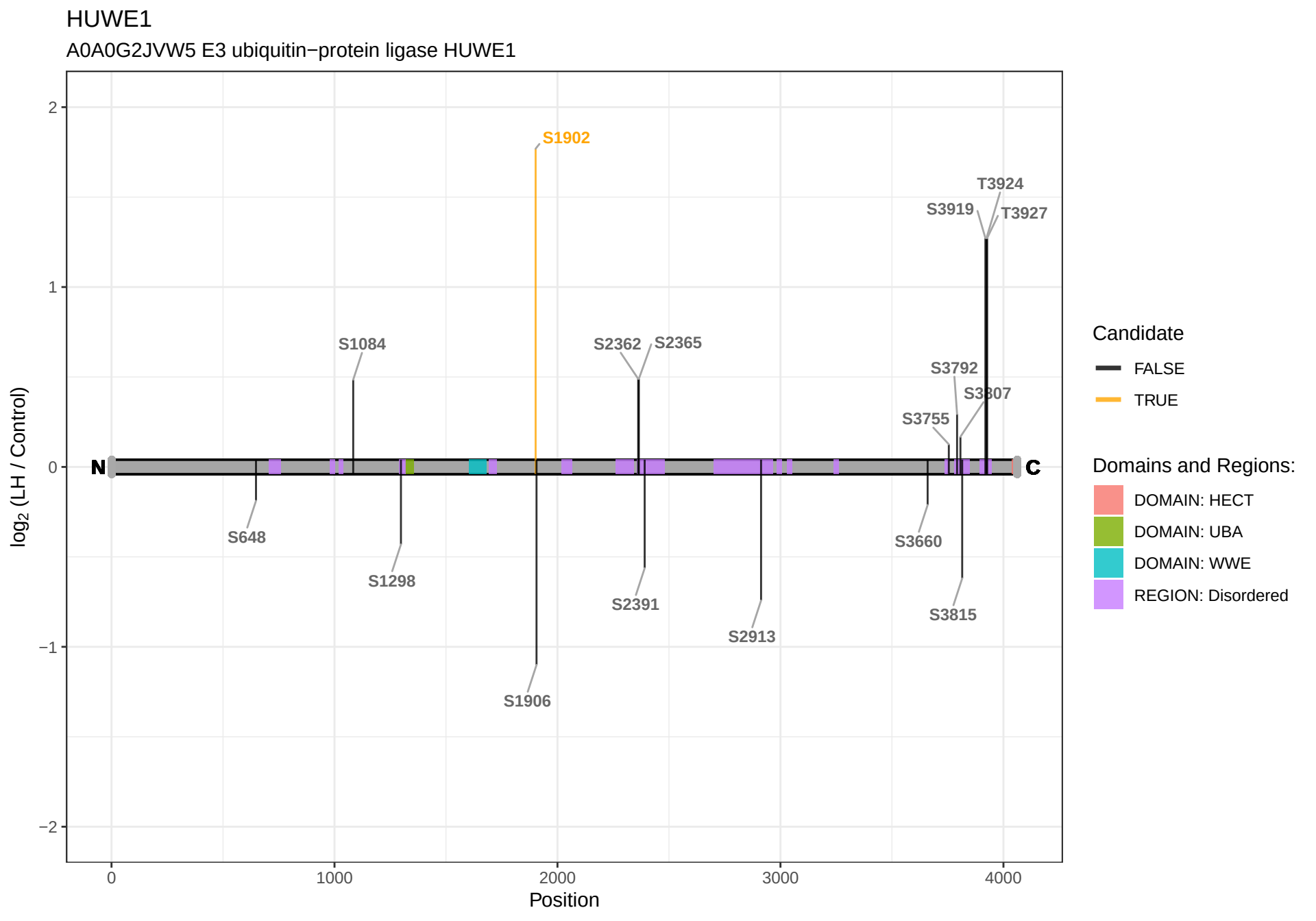

HNRNPU
Q6IMY8 Heterogeneous nuclear ribonucleoprotein U
log2 (LH / Control)
4
2
0
−2
−4
S26
S3
S181
S4
S58
S245
N
C
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: B30.2/SPRY
DOMAIN: SAP
REGION: Actin−binding
REGION: ATPase domain
REGION: Disordered
REGION: RNA−binding RGG−box

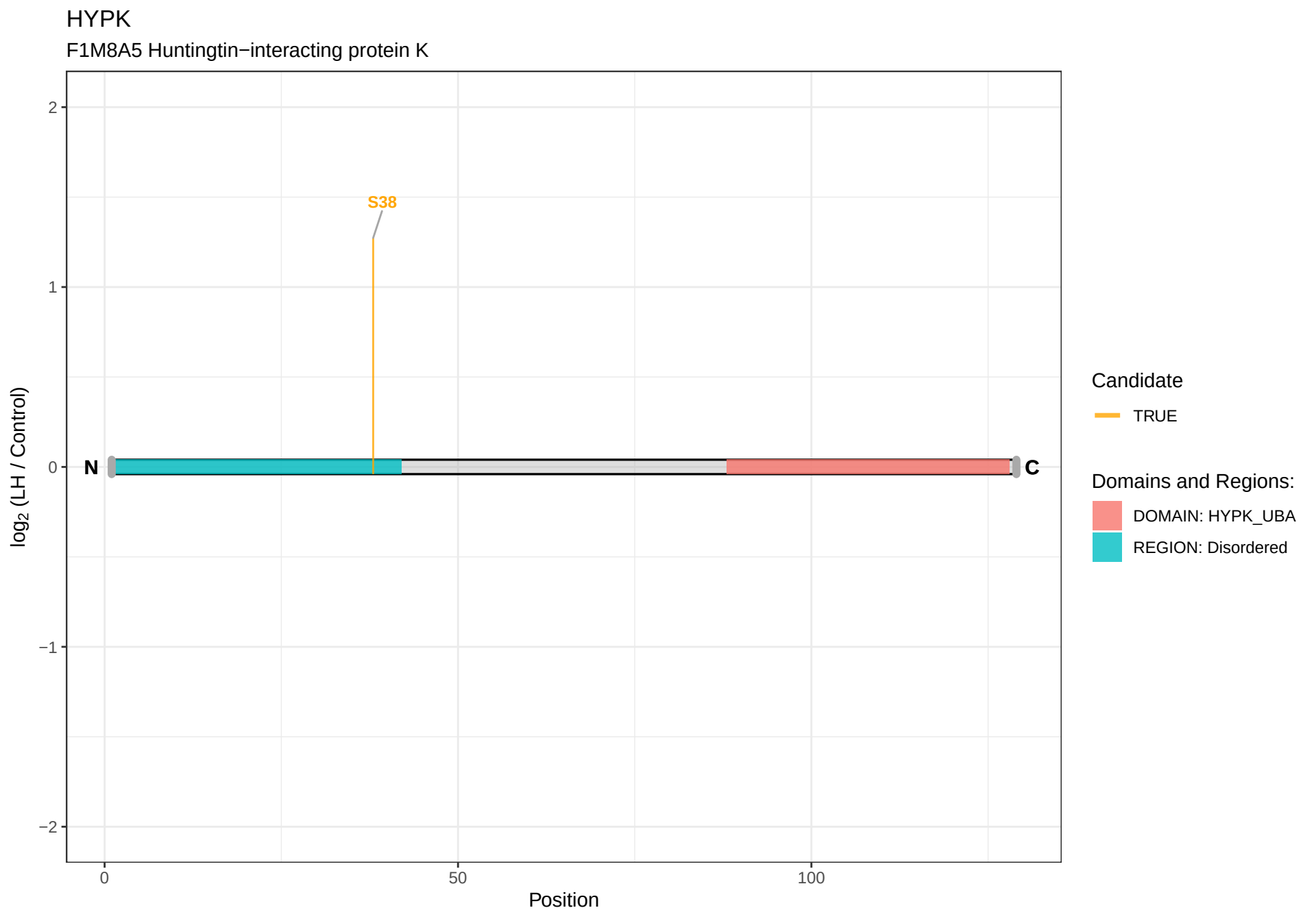

HP1BP3
Q6P747 Heterochromatin protein 1−binding protein 3
T51
S247
N
C
S110
S108
S70
S76
T77
S74
S71
T85
S445
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: H15 1
DOMAIN: H15 2
DOMAIN: H15 3
REGION: Disordered

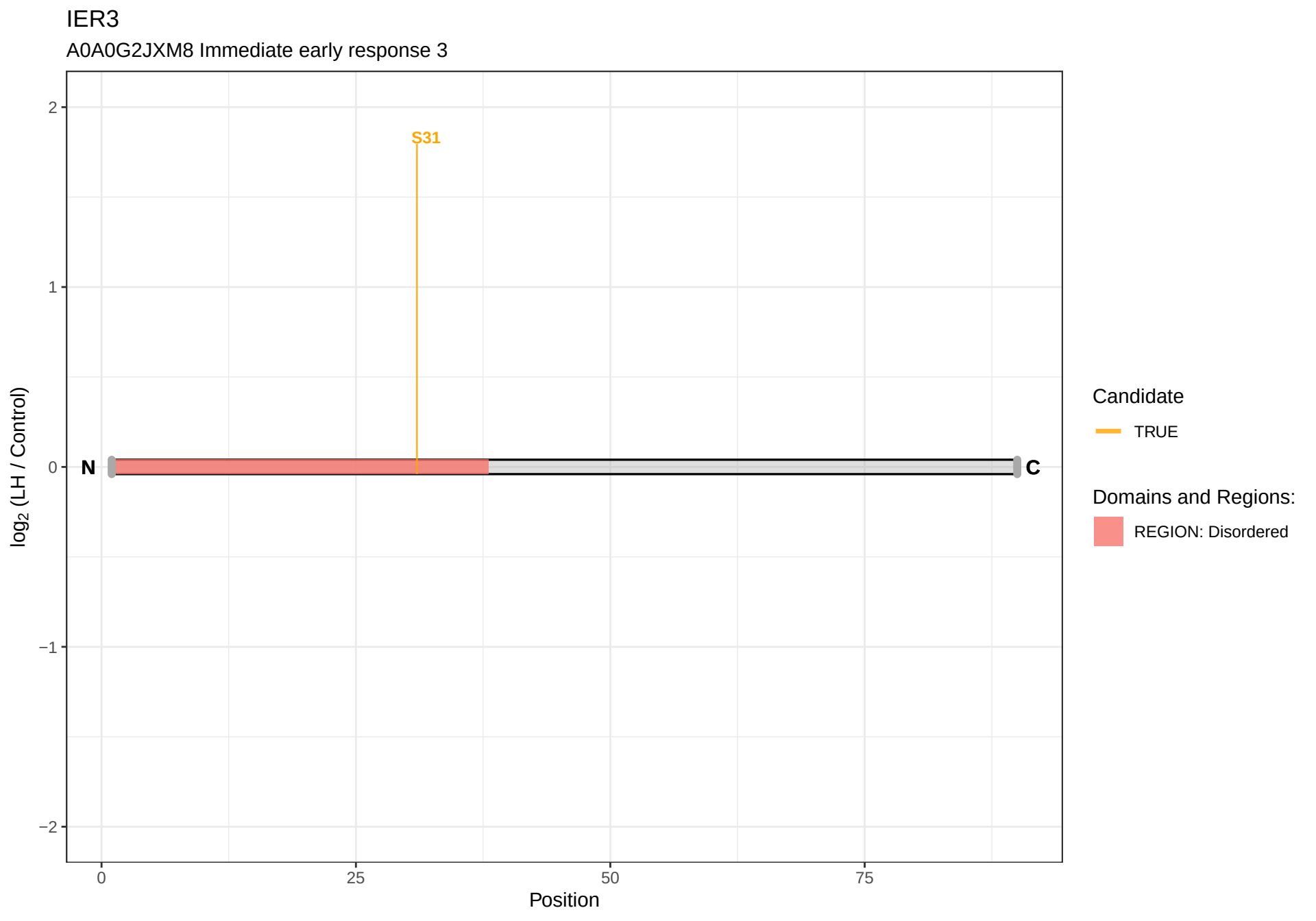

HSF1
F1MAF1 Heat shock transcription factor 1
2
1
0
−1
−2
log2 (LH / Control)
S307
S314
S326
S303
N
C
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: NA
REGION: Disordered

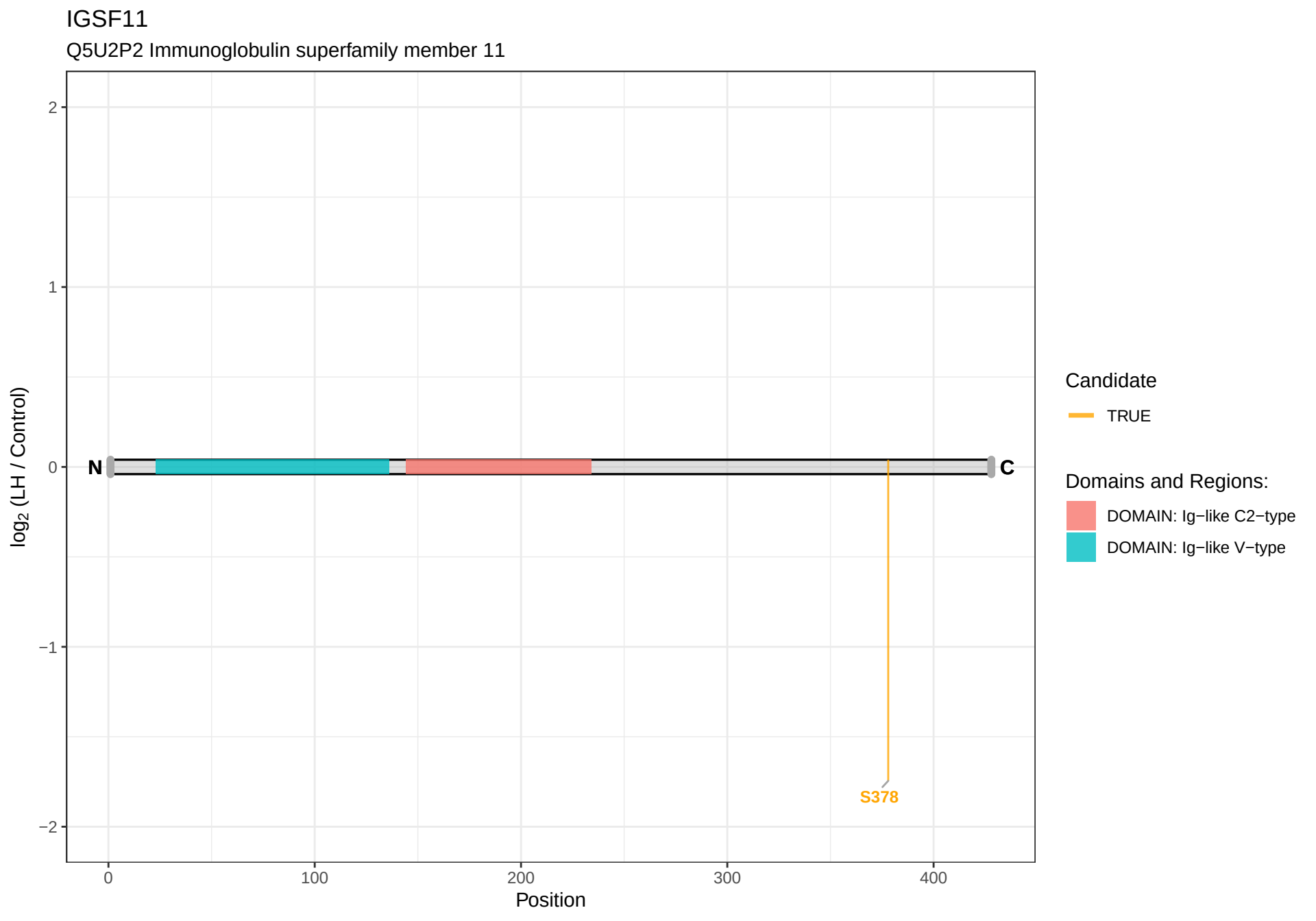

HTATSF1
D4A997 HIV TAT specific factor 1 (Predicted)
log2 (LH / Control)
Position
N
C
S241
S7
S40
S387
Y459
S551
S565
S616
T748
S482
S441
S491
S455
S464
S446
S561
S546
S596
S622
S639
S631
T613
S698
S724
S716
S743
S664
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RRM
REGION: Disordered

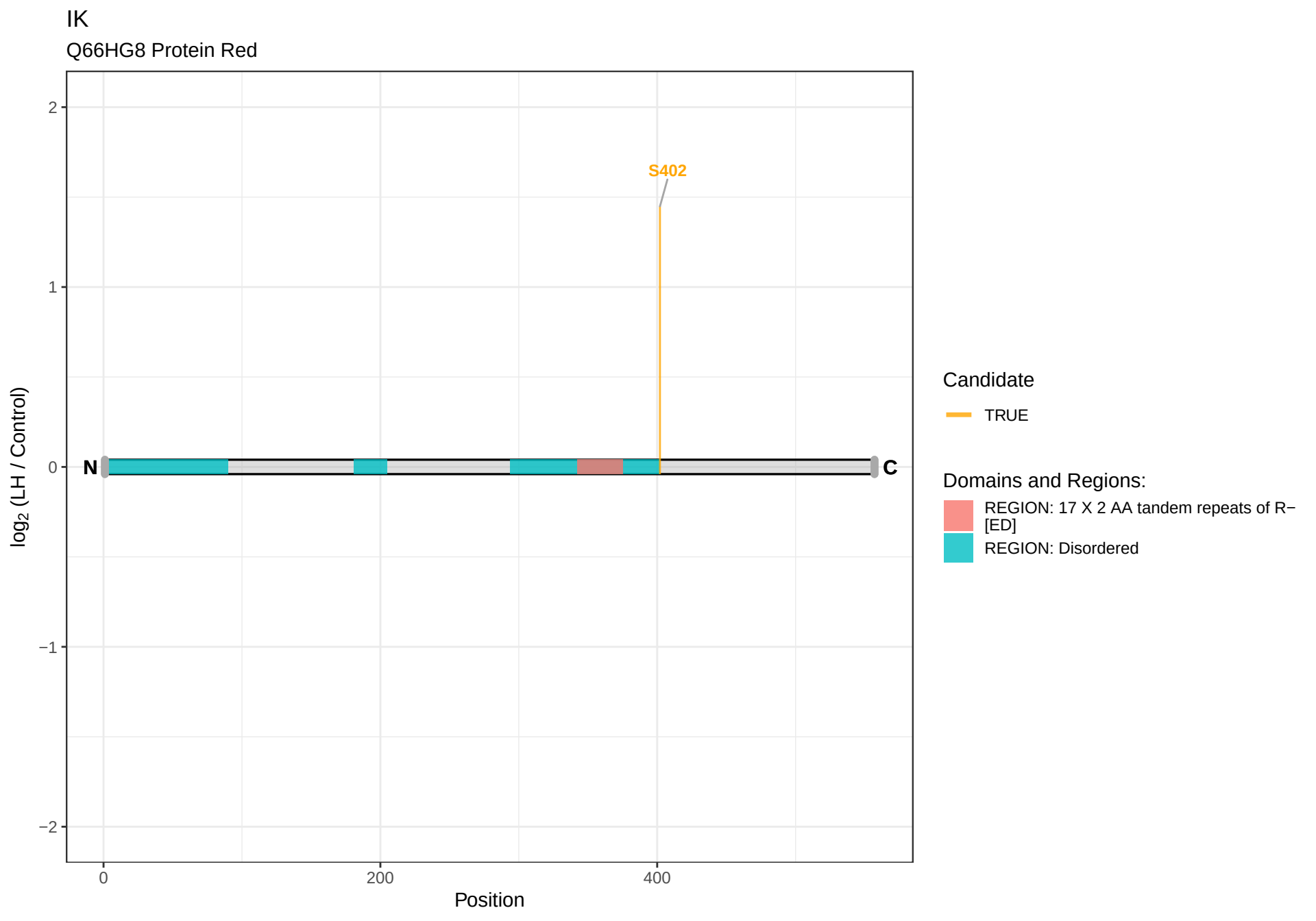

HTT
P51111 Huntingtin
S1833
S389
S1845
S402
S611
N
C
log2 (LH / Control)
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Interaction with ZDHHC17

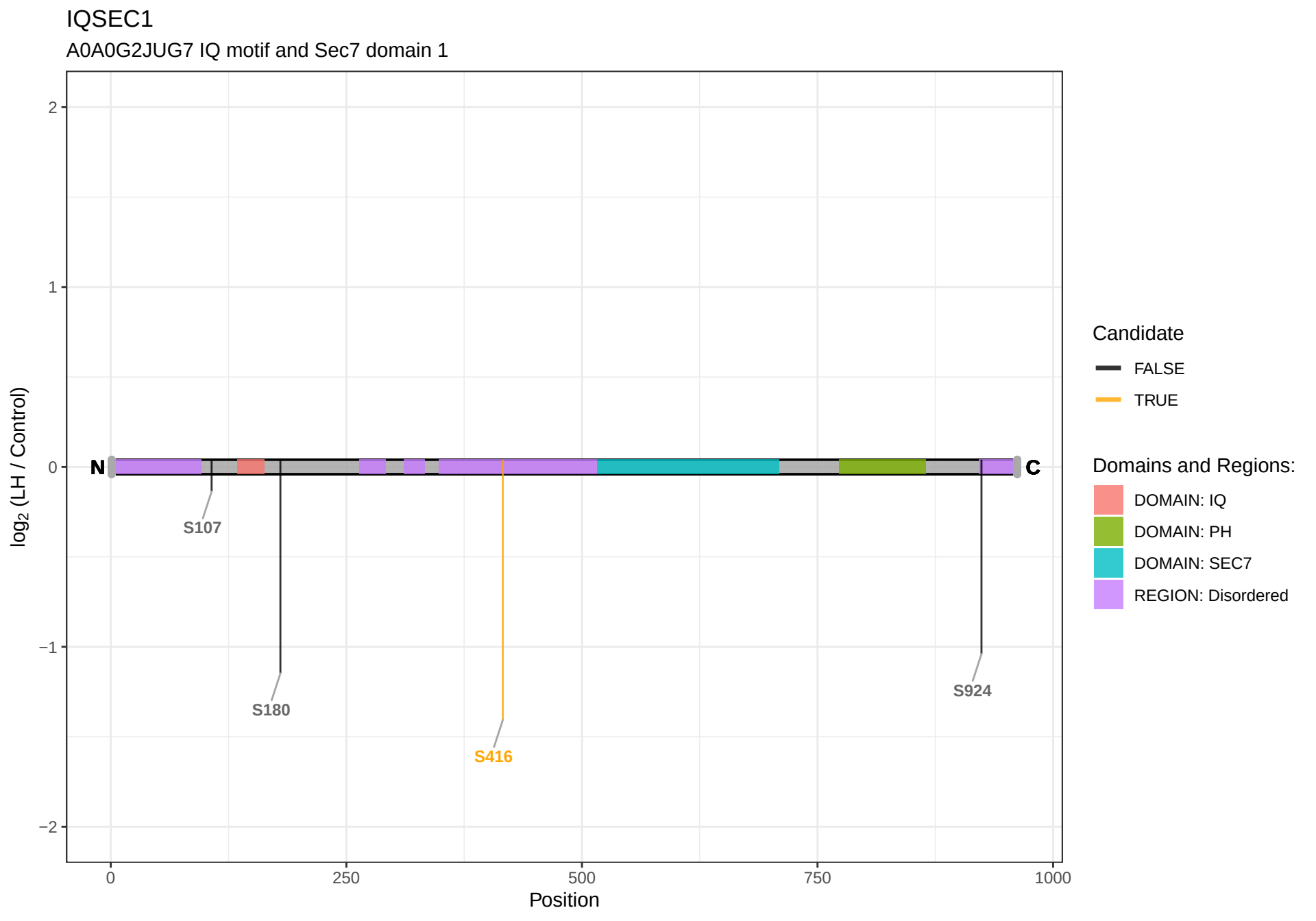

HUWE1
A0A0G2JVW5 E3 ubiquitin−protein ligase HUWE1
log2 (LH / Control)
Position
N
C
S1902
T3924
S3919
T3927
S1084
S2362
S2365
S3792
S3807
S3755
S648
S1298
S2391
S2913
S3660
S3815
S1906
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: HECT
DOMAIN: UBA
DOMAIN: WWE
REGION: Disordered

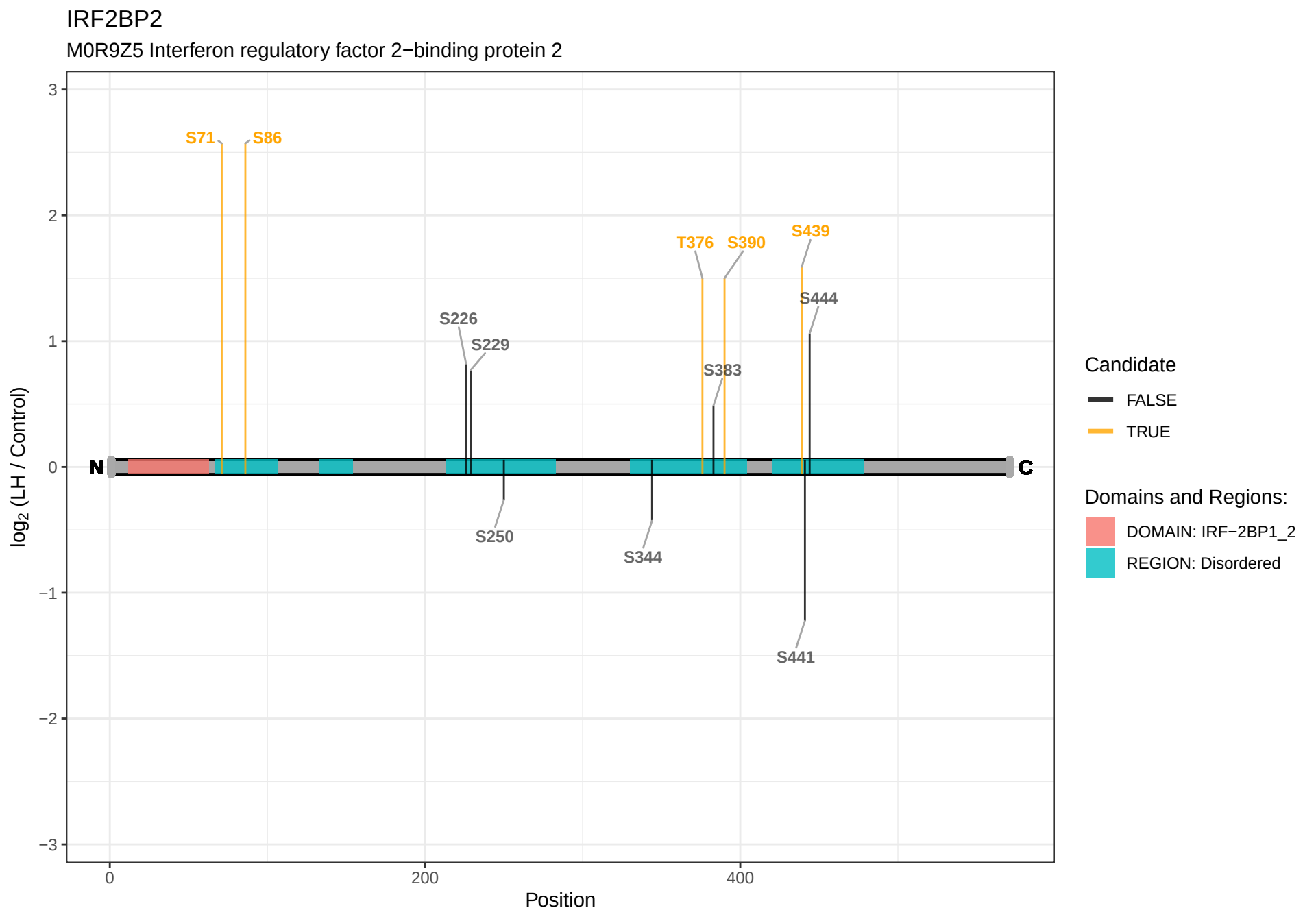

HYPK
F1M8A5 Huntingtin−interacting protein K
S38
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
50
100
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: HYPK_UBA
REGION: Disordered

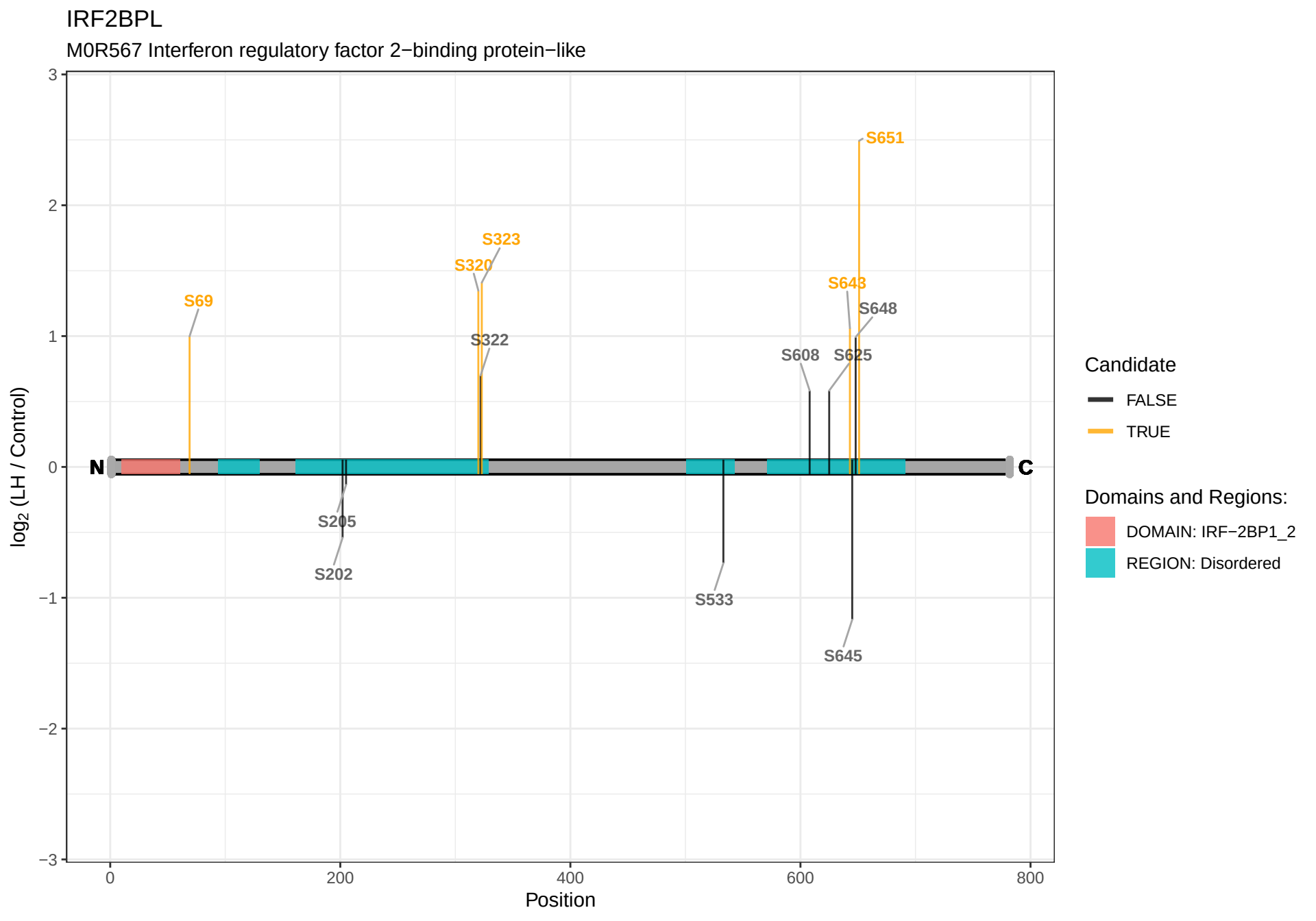

IER3
A0A0G2JXM8 Immediate early response 3
S31
N
C
2
1
0
−1
−2
0
25
50
75
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
REGION: Disordered

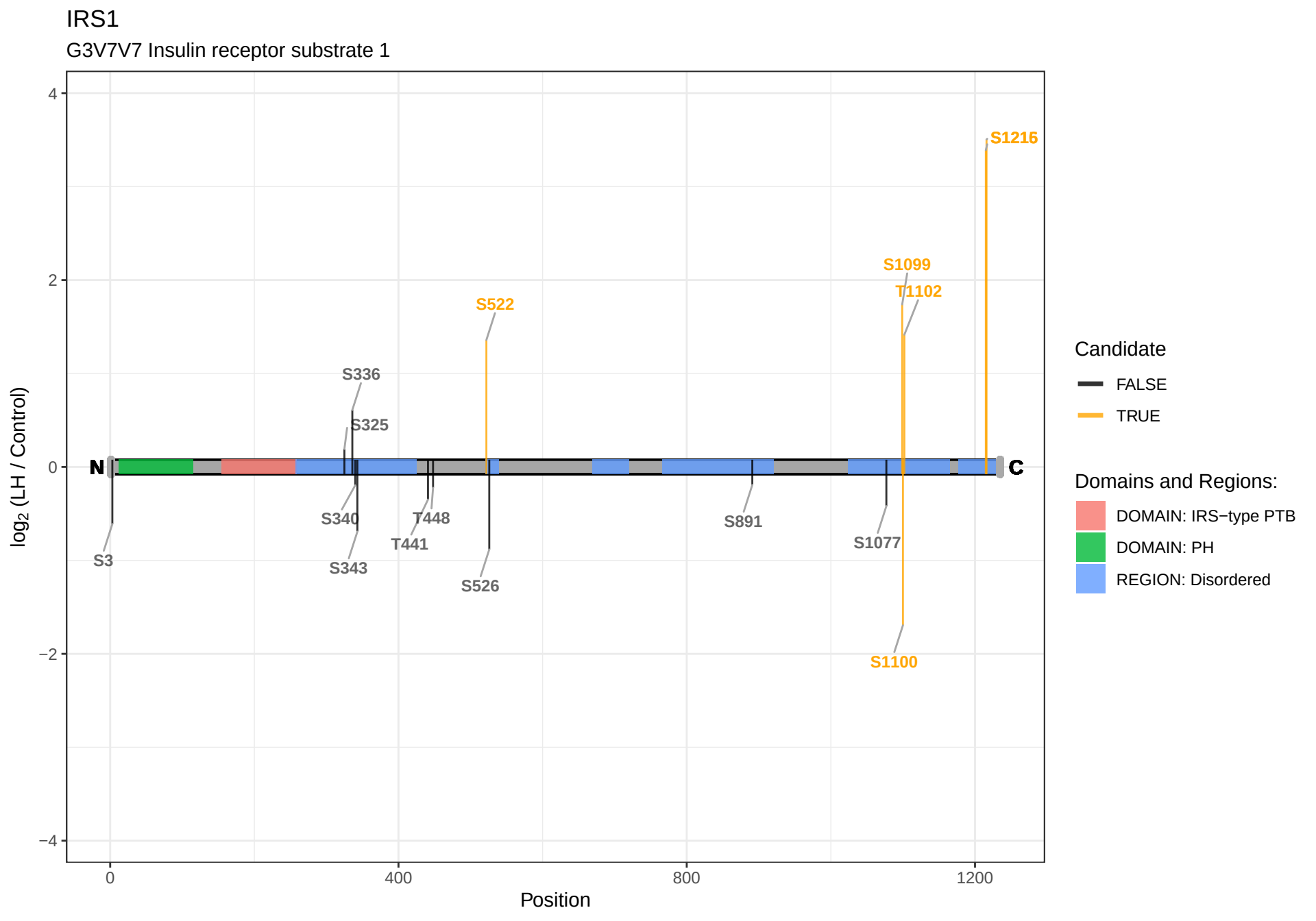

IGSF11
Q5U2P2 Immunoglobulin superfamily member 11
log2 (LH / Control)
2
1
0
−1
−2
N
C
S378
0
100
200
300
400
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Ig−like C2−type
DOMAIN: Ig−like V−type

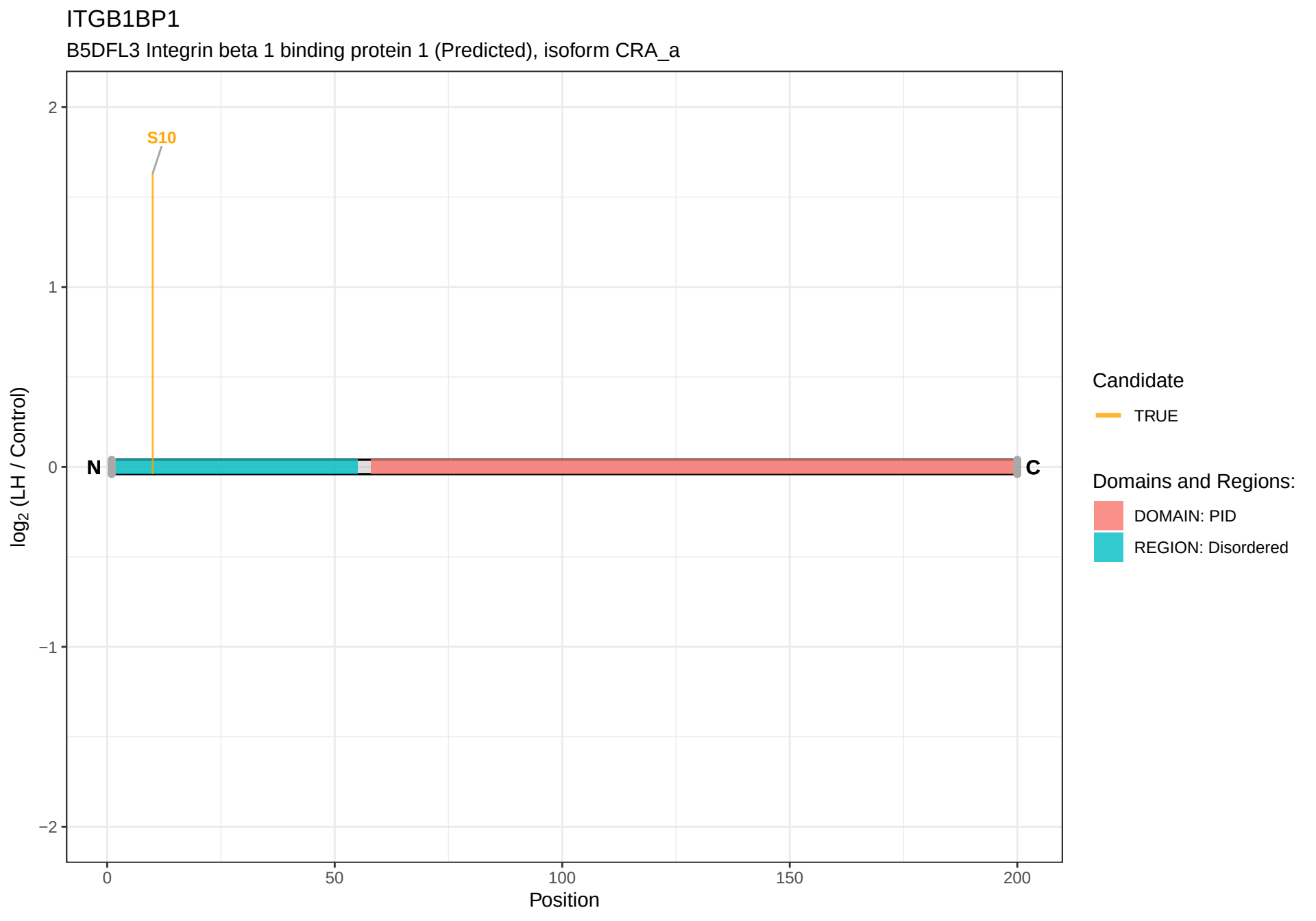

IK
Q66HG8 Protein Red
S402
N
C
2
1
0
−1
−2
0
200
400
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
REGION: 17 X 2 AA tandem repeats of R−[ED]
REGION: Disordered

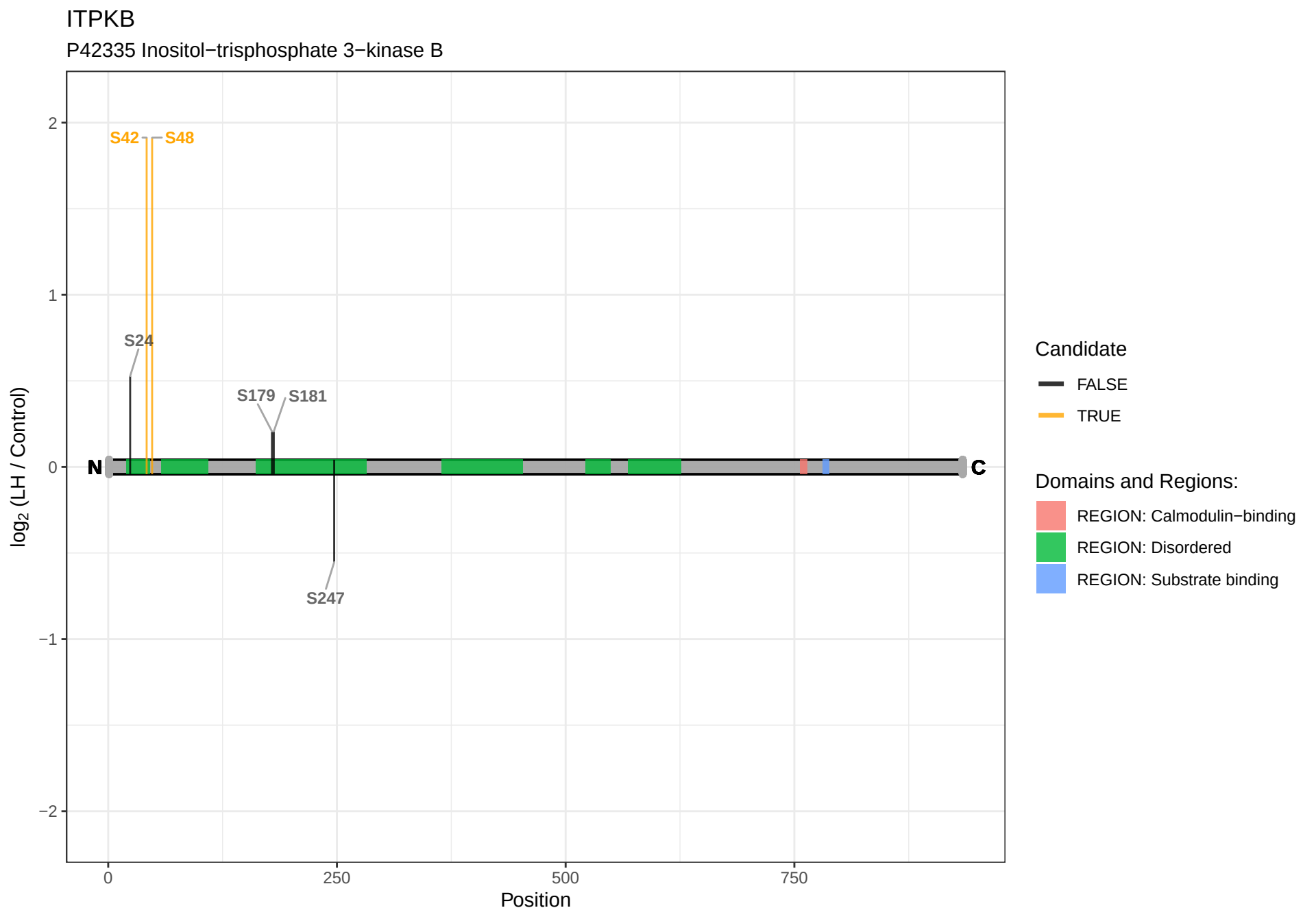

IQSEC1
A0A0G2JUG7 IQ motif and Sec7 domain 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S107
S180
S416
S924
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: IQ
DOMAIN: PH
DOMAIN: SEC7
REGION: Disordered

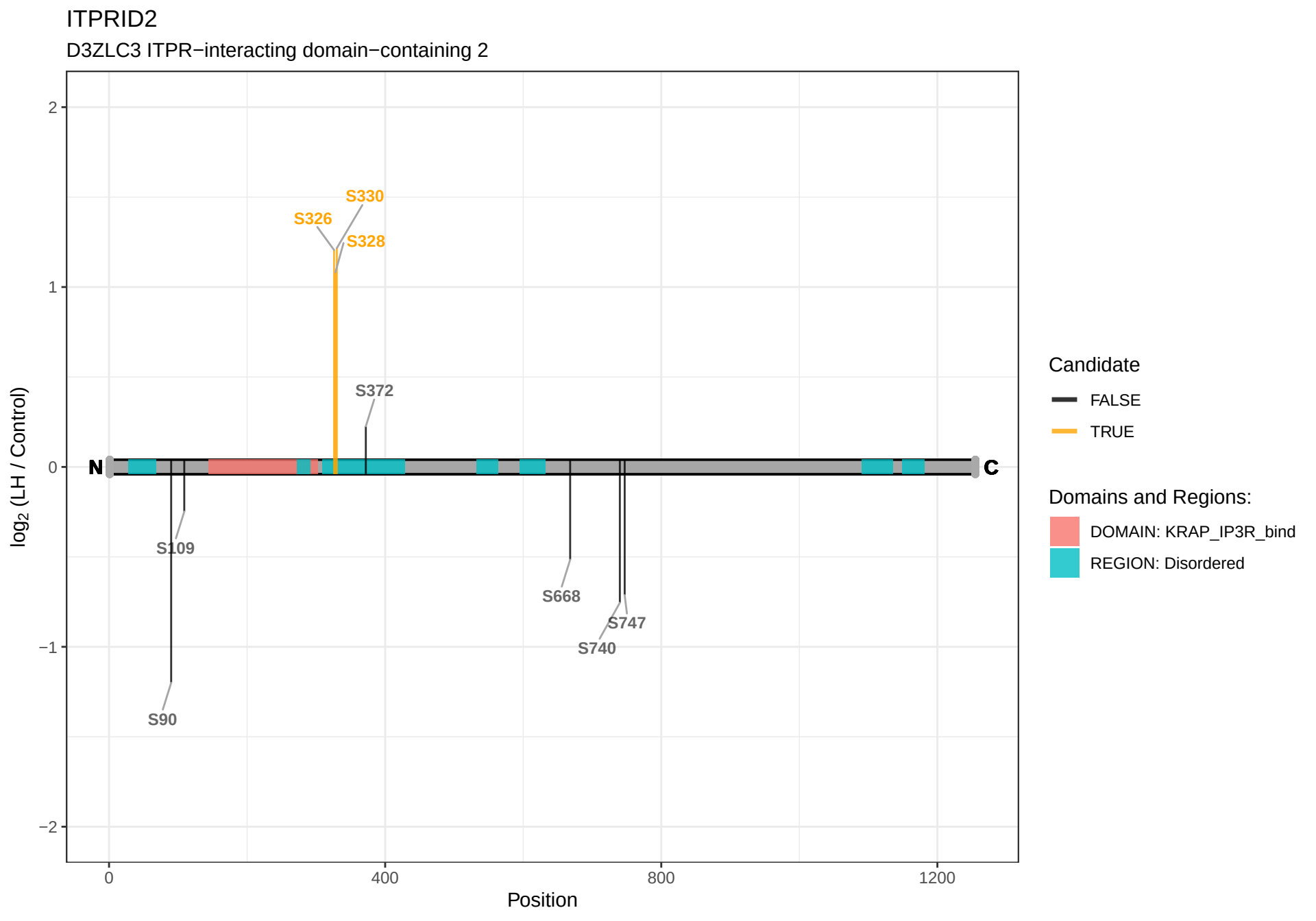

IRF2BP2
M0R9Z5 Interferon regulatory factor 2−binding protein 2
log2 (LH / Control)
Position
N
C
S71
S86
S226
S229
S250
S344
T376
S383
S390
S439
S444
S441
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: IRF−2BP1_2
REGION: Disordered

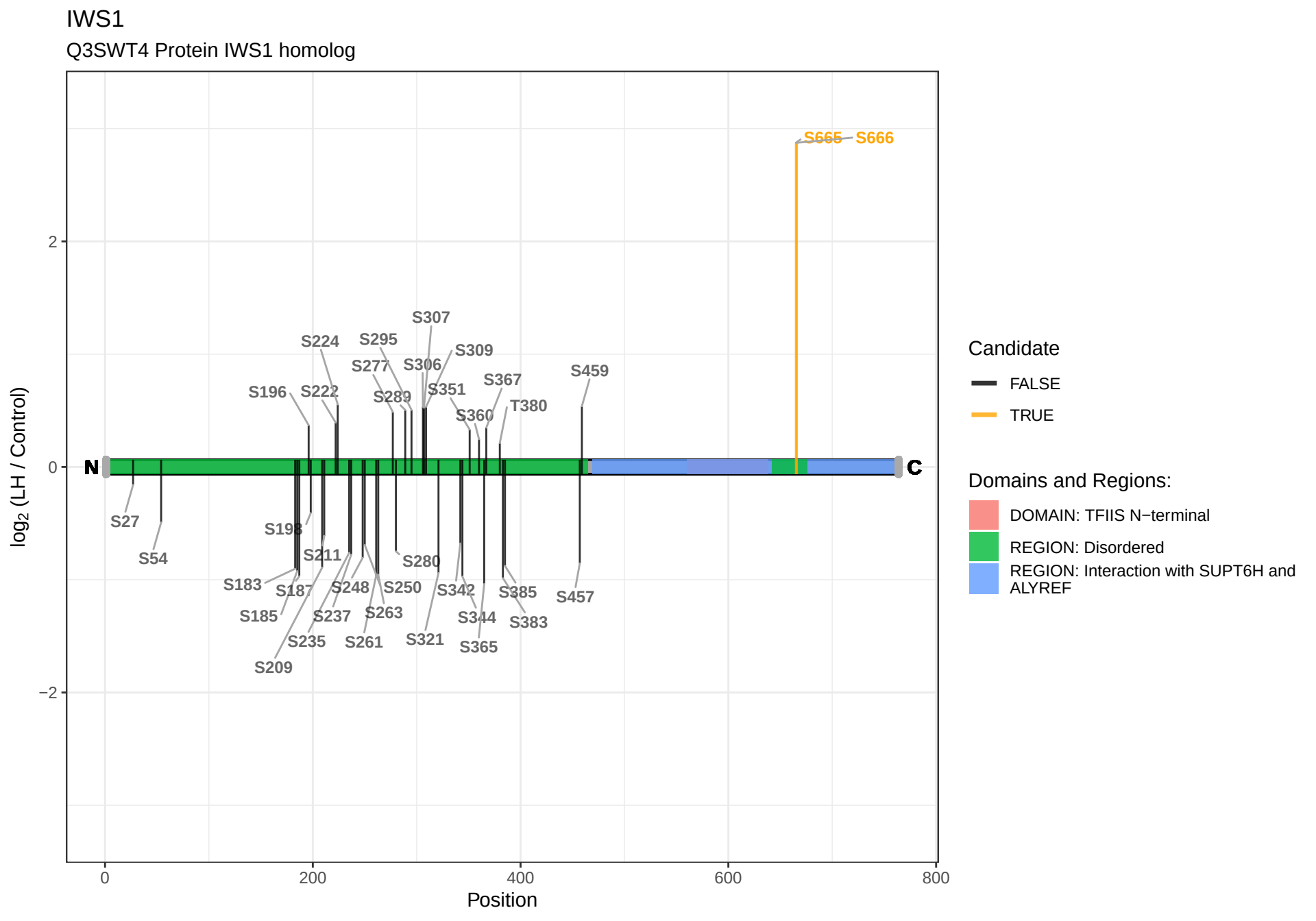

IRF2BPL
M0R567 Interferon regulatory factor 2−binding protein−like
log2 (LH / Control)
Position
N
C
S69
S205
S202
S320
S323
S322
S533
S608
S625
S643
S648
S651
S645
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: IRF−2BP1_2
REGION: Disordered

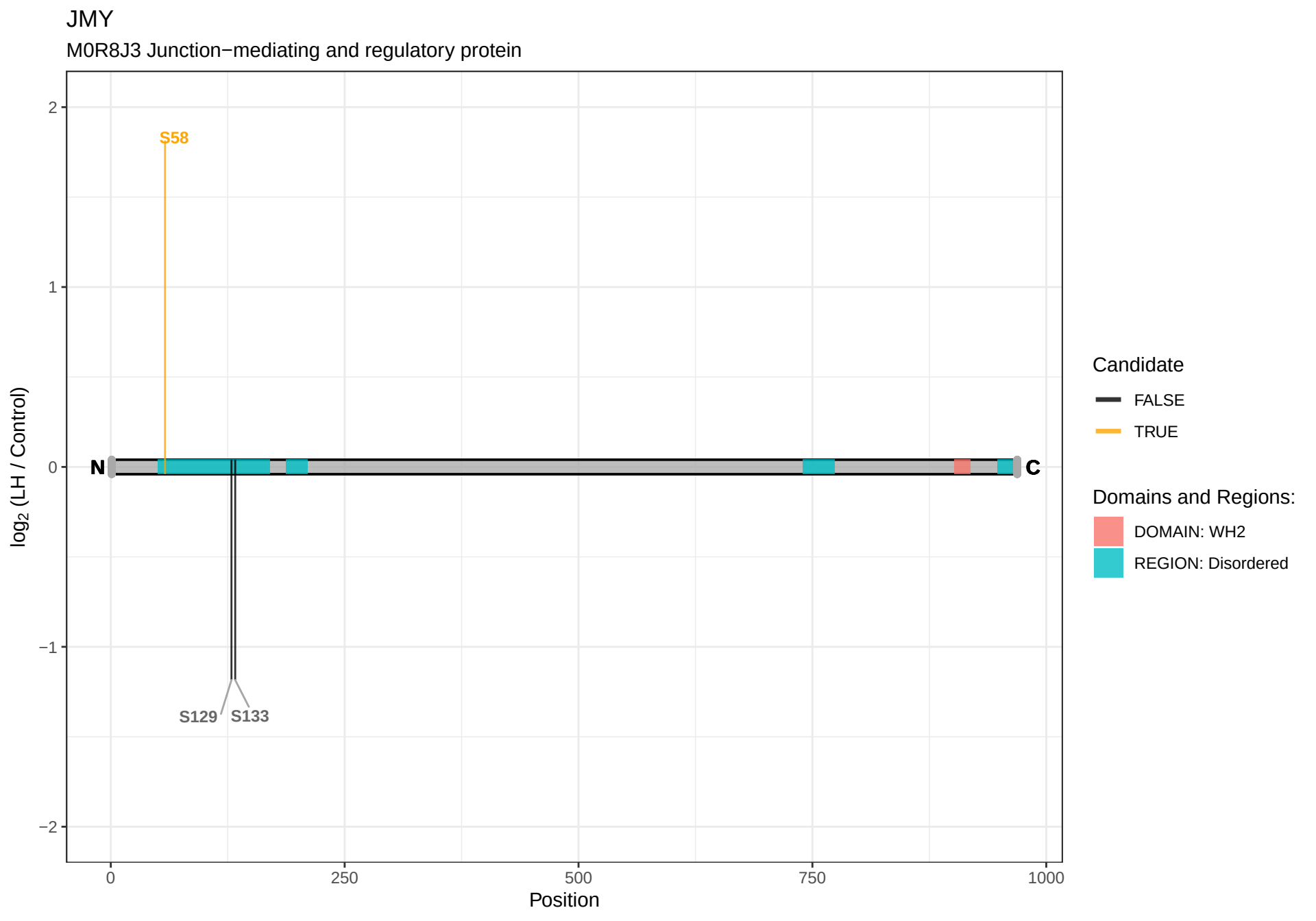

IRS1
G3V7V7 Insulin receptor substrate 1
log2 (LH / Control)
4
2
0
−2
−4
0
400
800
1200
Position
N
C
S1216
S1099
T1102
S522
S336
S325
S340
T448
T441
S343
S3
S526
S891
S1077
S1100
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: IRS−type PTB
DOMAIN: PH
REGION: Disordered

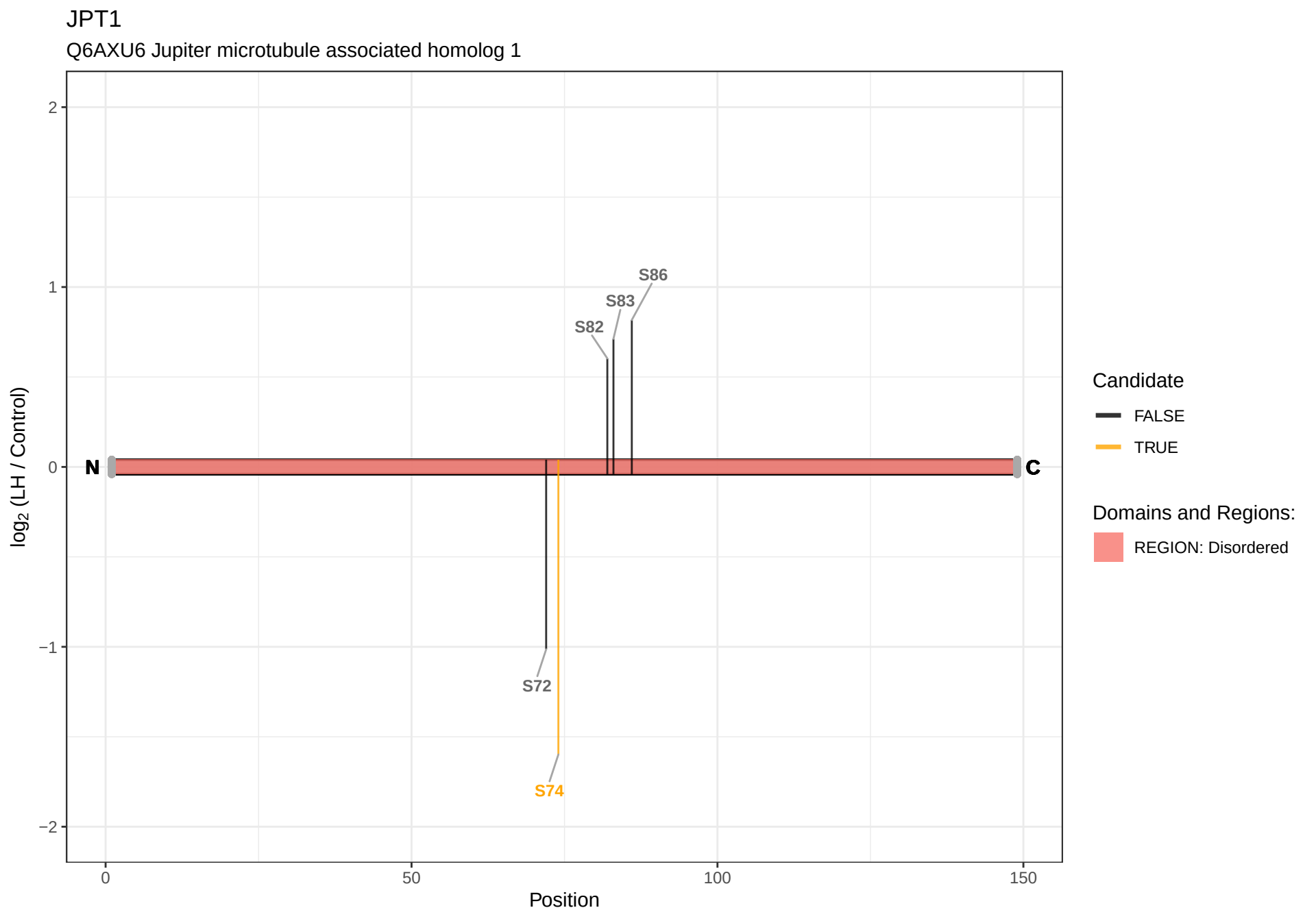

ITGB1BP1
B5DFL3 Integrin beta 1 binding protein 1 (Predicted), isoform CRA_a
S10
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
50
100
150
200
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: PID
REGION: Disordered

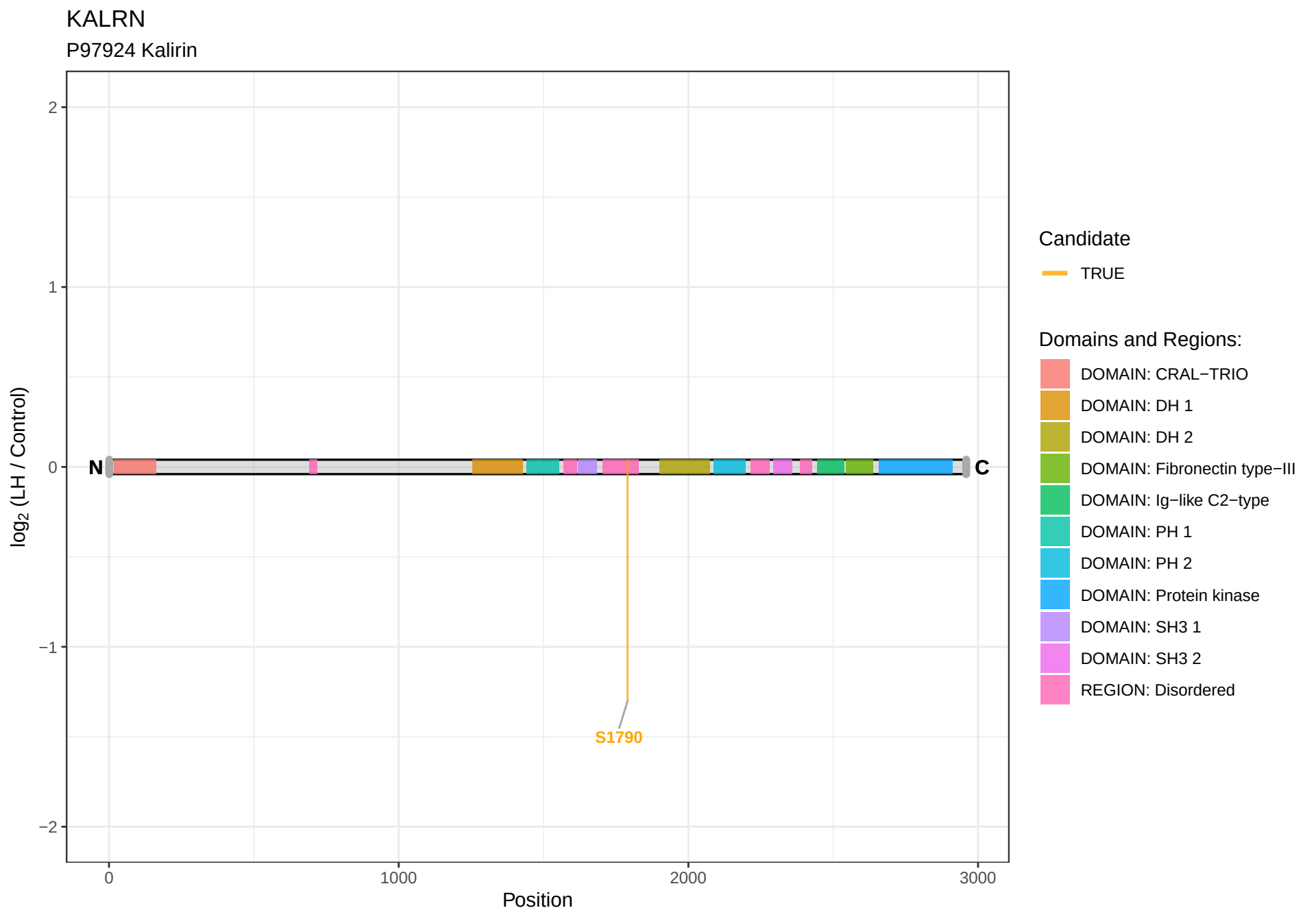

ITPKB
P42335 Inositol−trisphosphate 3−kinase B
S42
S48
S24
S179
S181
S247
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Calmodulin−binding
REGION: Disordered
REGION: Substrate binding

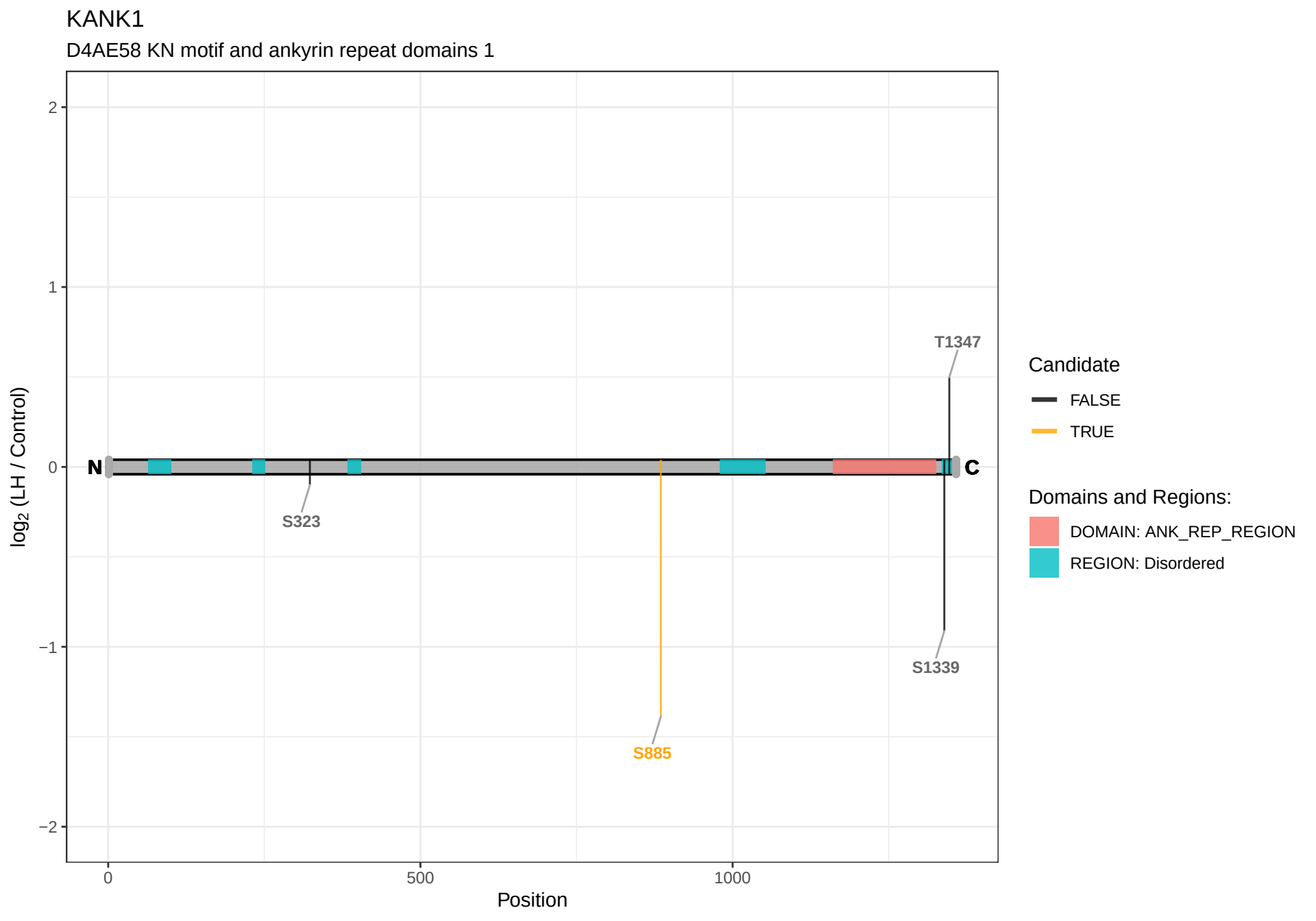

ITPRID2
D3ZLC3 ITPR−interacting domain−containing 2
log2 (LH / Control)
2
1
0
−1
−2
0
400
800
1200
Position
N
C
S330
S326
S328
S372
S109
S90
S668
S747
S740
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: KRAP_IP3R_bind
REGION: Disordered

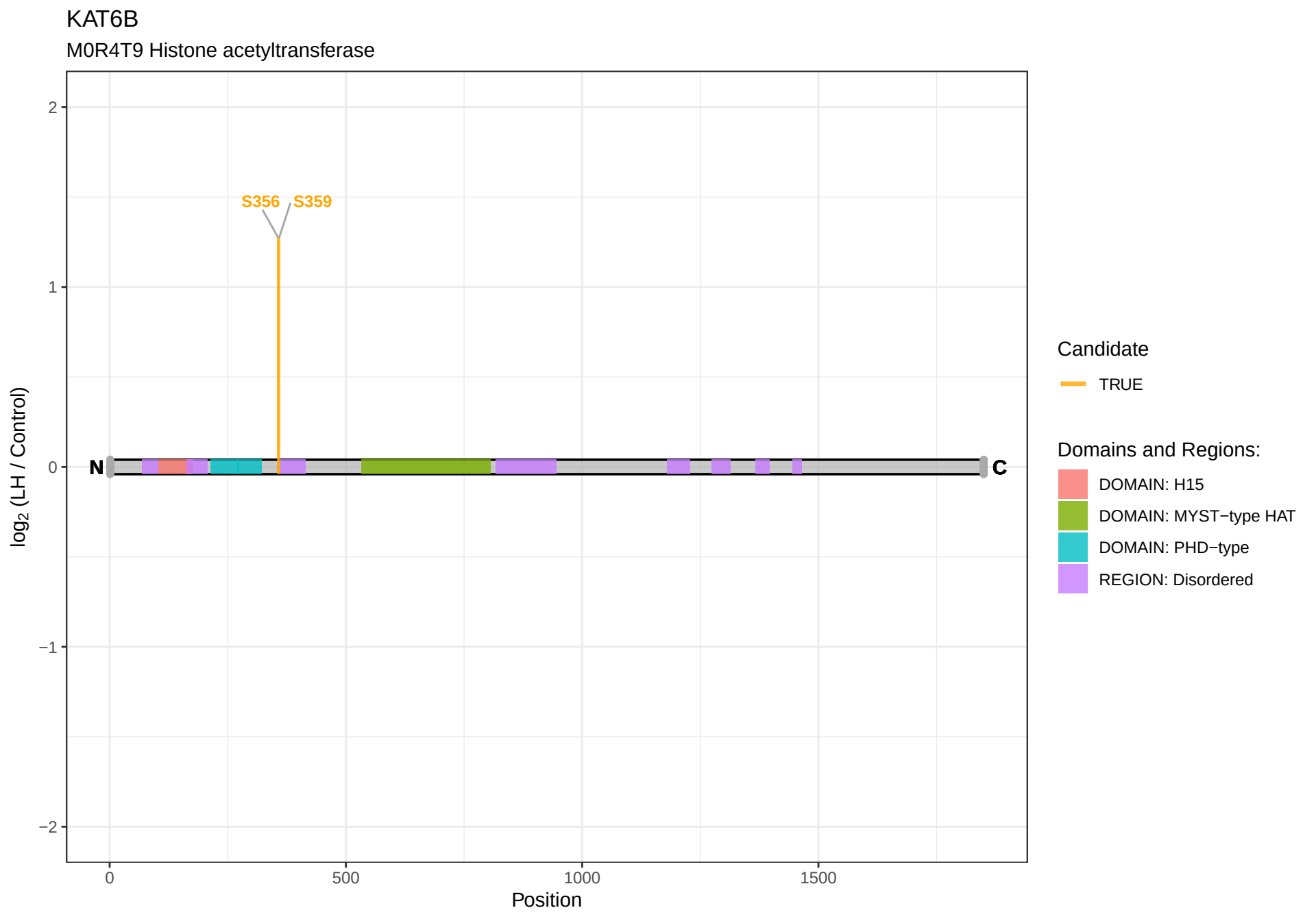

IWS1
Q3SWT4 Protein IWS1 homolog
log2 (LH / Control)
Position
N
C
S665
S666
S307
S224
S295
S309
S277
S306
S367
S459
S196
S222
S289
S351
T380
S360
S27
S54
S198
S211
S280
S183
S187
S248
S250
S342
S385
S457
S185
S237
S263
S344
S383
S235
S261
S321
S365
S209
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: TFIIS N−terminal
REGION: Disordered
REGION: Interaction with SUPT6H and ALYREF

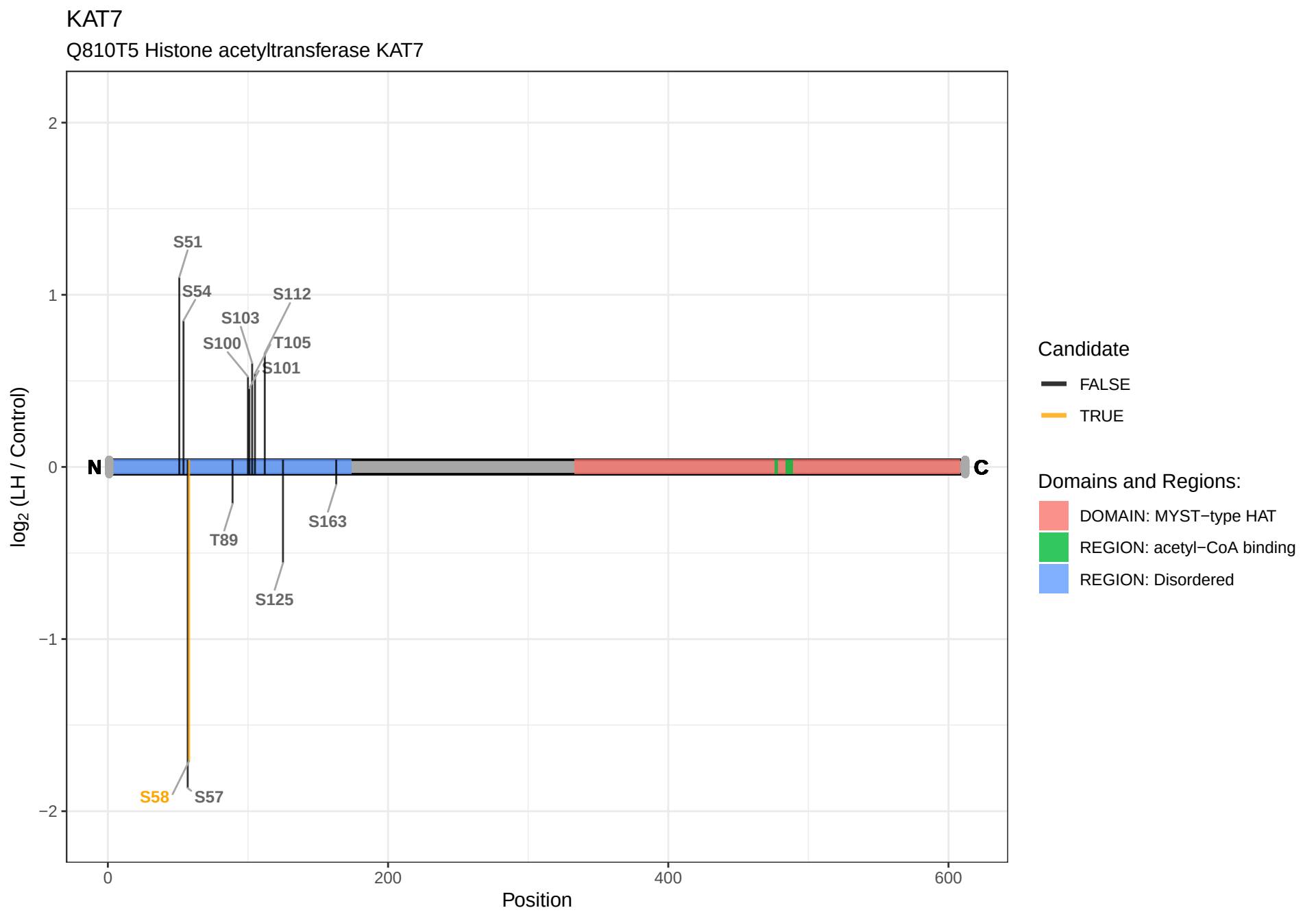

JMY
M0R8J3 Junction−mediating and regulatory protein
2
1
0
−1
−2
log2 (LH / Control)
S58
N
C
S129
S133
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WH2
REGION: Disordered

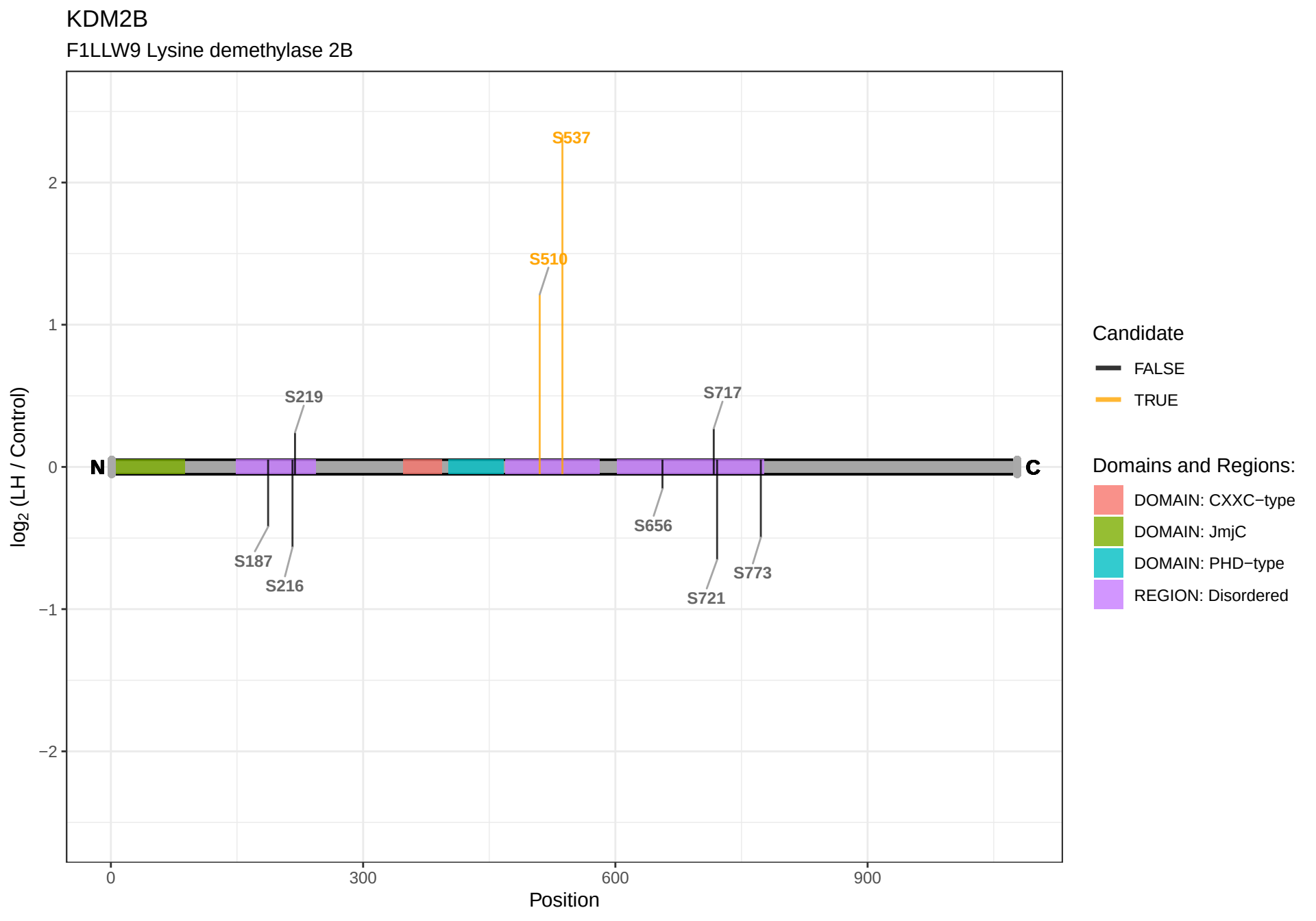

JPT1
Q6AXU6 Jupiter microtubule associated homolog 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S86
S83
S82
S72
S74
0
50
100
150
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

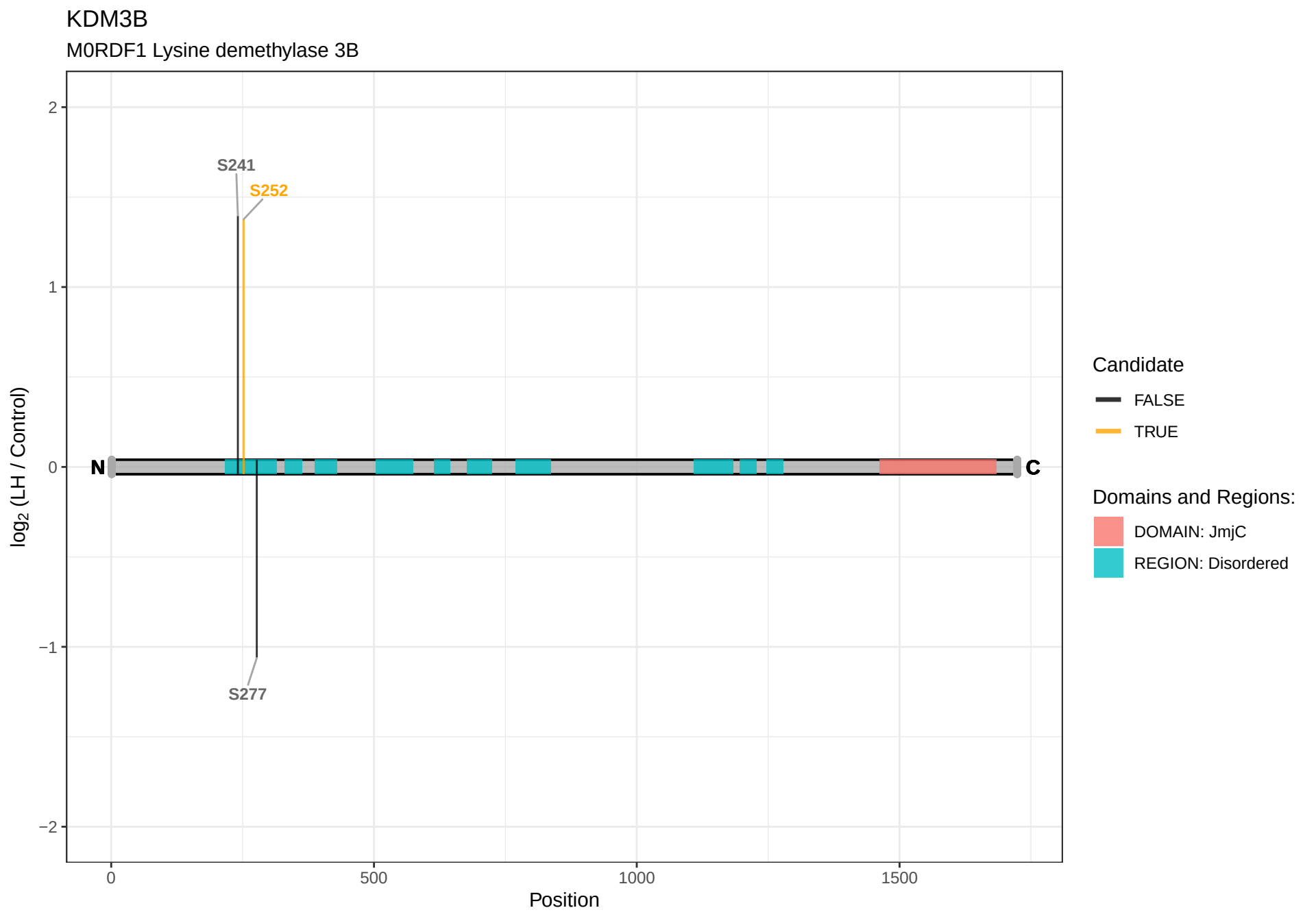

KALRN
P97924 Kalirin
2
1
0
−1
−2
log2 (LH / Control)
N
C
S1790
0
1000
2000
3000
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: CRAL−TRIO
DOMAIN: DH 1
DOMAIN: DH 2
DOMAIN: Fibronectin type−III
DOMAIN: Ig−like C2−type
DOMAIN: PH 1
DOMAIN: PH 2
DOMAIN: Protein kinase
DOMAIN: SH3 1
DOMAIN: SH3 2
REGION: Disordered

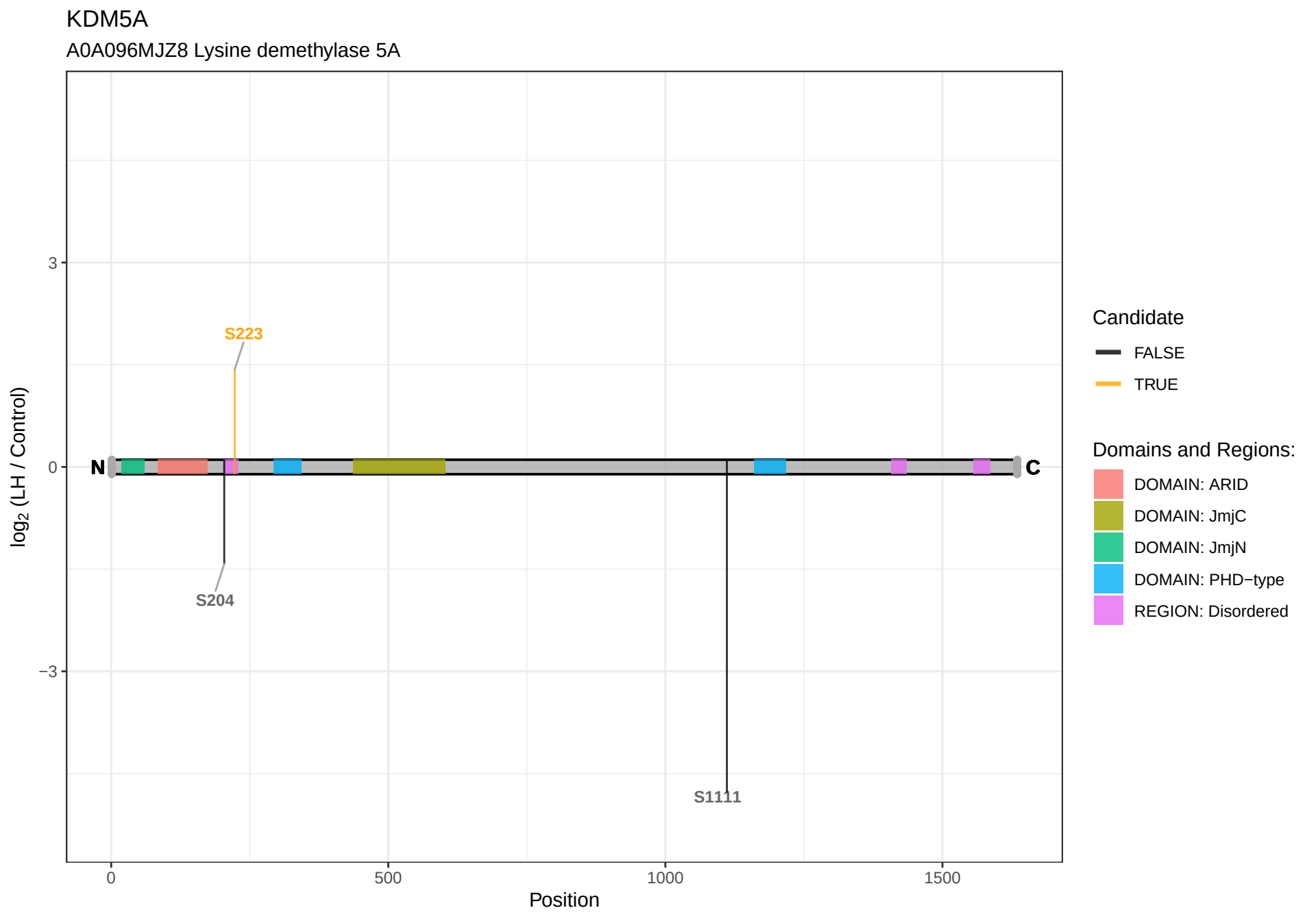

KANK1
D4AE58 KN motif and ankyrin repeat domains 1
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
Position
N
C
S323
S885
S1339
T1347
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ANK_REP_REGION
REGION: Disordered

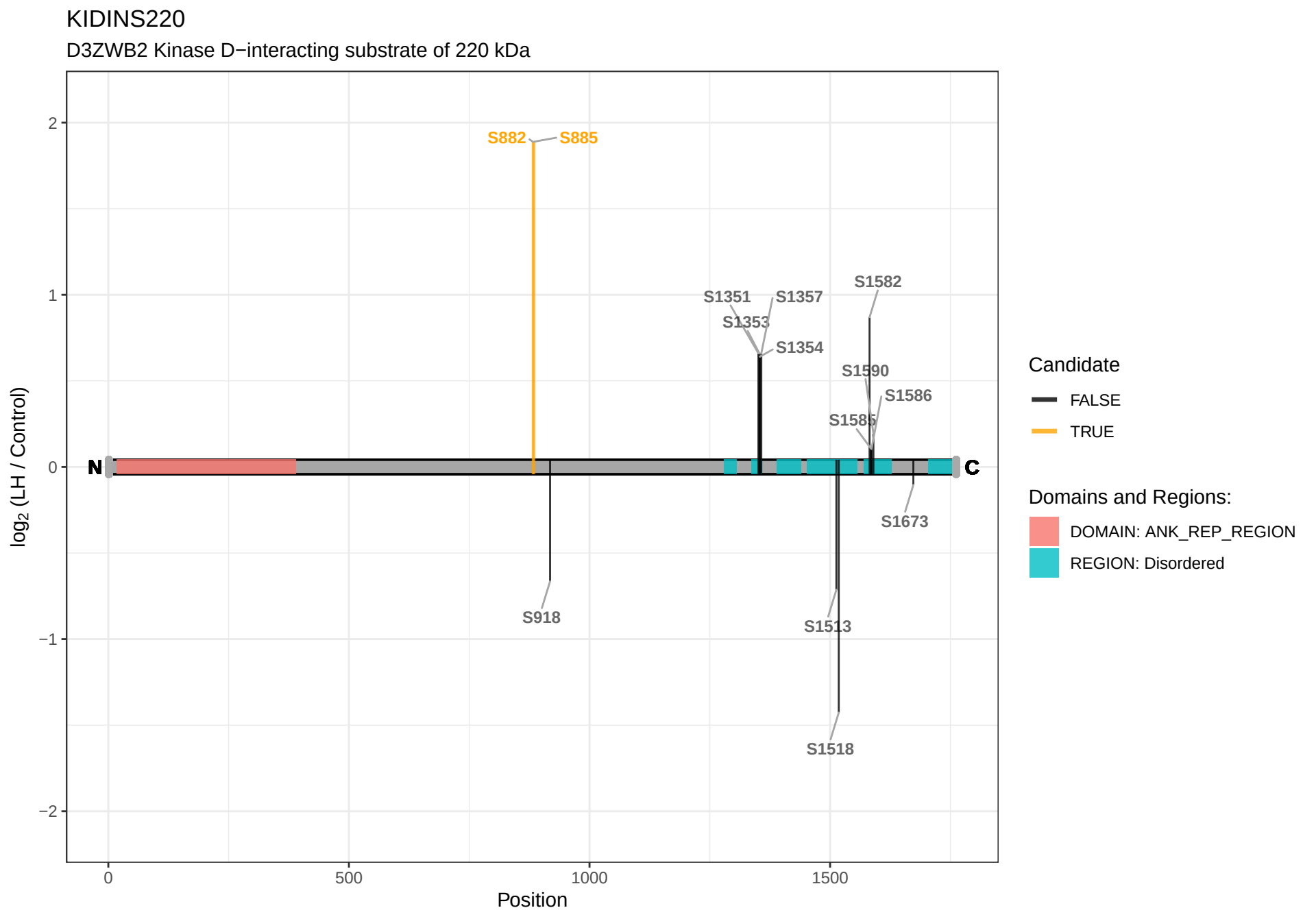

KAT6B
M0R4T9 Histone acetyltransferase
S356
S359
N
C
2
1
0
−1
−2
0
500
1000
1500
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
DOMAIN: H15
DOMAIN: MYST−type HAT
DOMAIN: PHD−type
REGION: Disordered

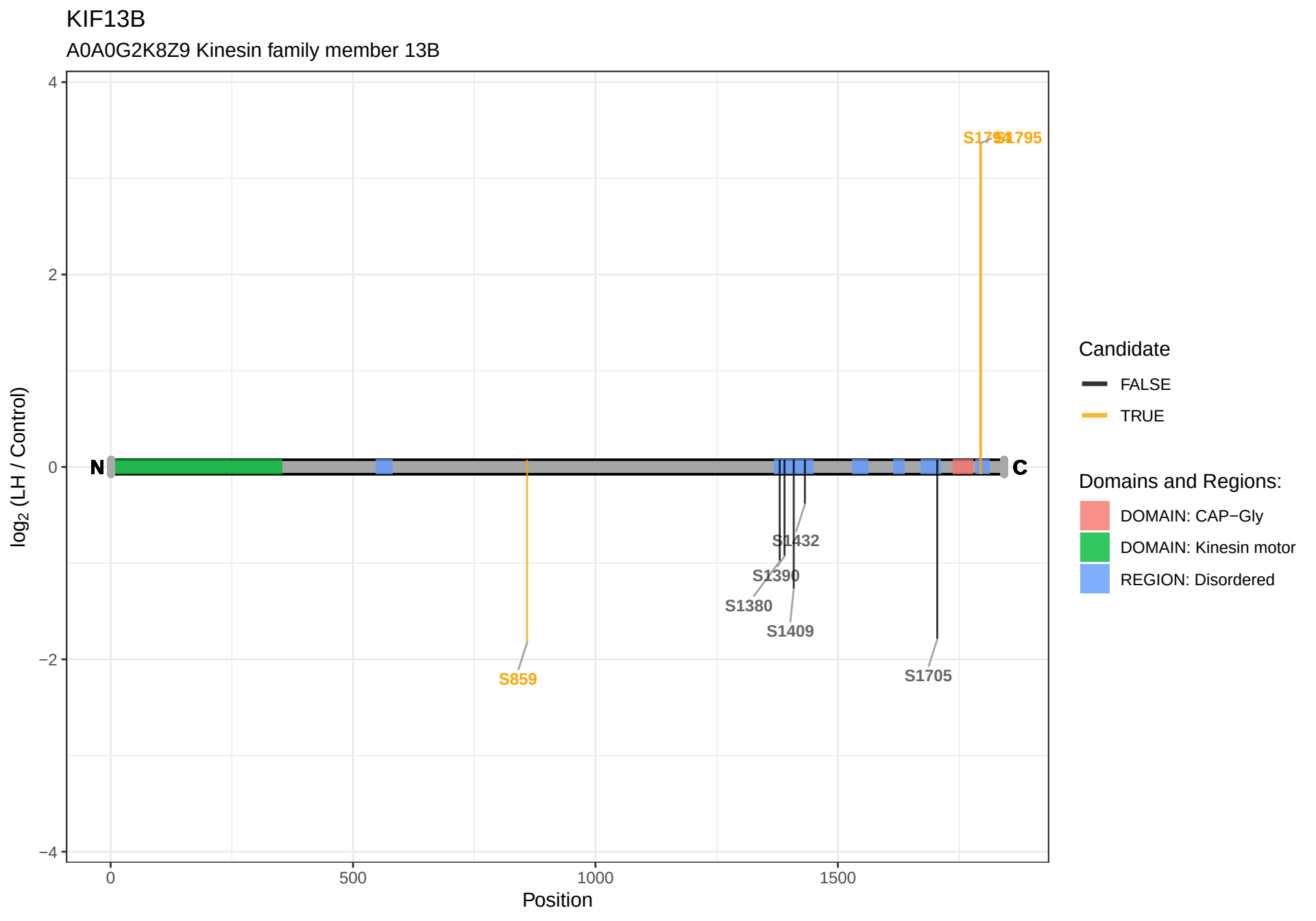

KAT7
Q810T5 Histone acetyltransferase KAT7
log2 (LH / Control)
2
1
0
−1
−2
N
C
S51
S54
S112
S103
S100
T105
S101
T89
S163
S125
S58
S57
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: MYST−type HAT
REGION: acetyl−CoA binding
REGION: Disordered

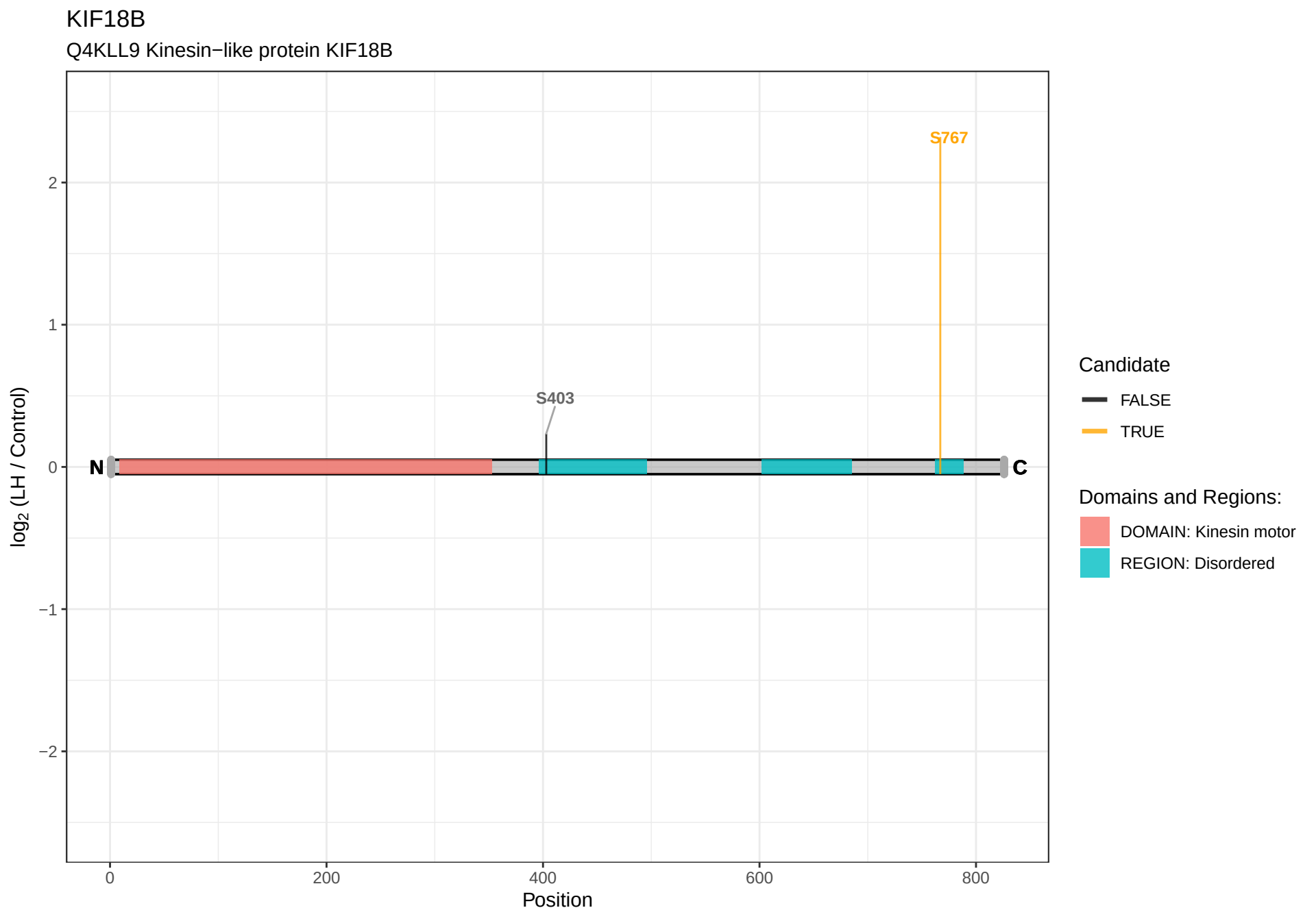

KDM2B
F1LLW9 Lysine demethylase 2B
S537
S510
S219
S717
N
C
S187
S216
S656
S721
S773
2
1
0
−1
−2
log2 (LH / Control)
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CXXC−type
DOMAIN: JmjC
DOMAIN: PHD−type
REGION: Disordered

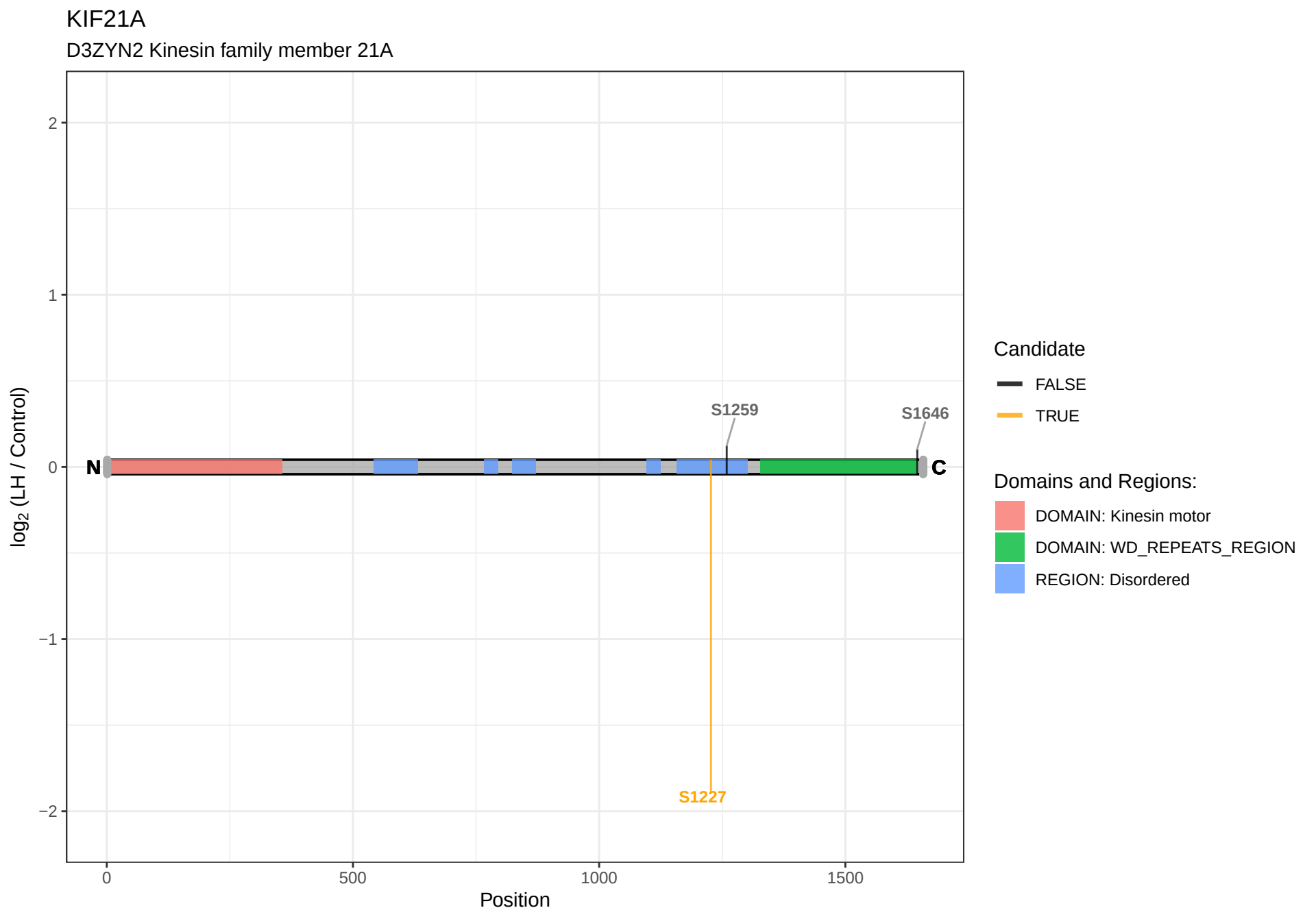

KDM3B
M0RDF1 Lysine demethylase 3B
S241
S252
S277
N
C
2
1
0
−1
−2
0
500
1000
1500
log2 (LH / Control)
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: JmjC
REGION: Disordered

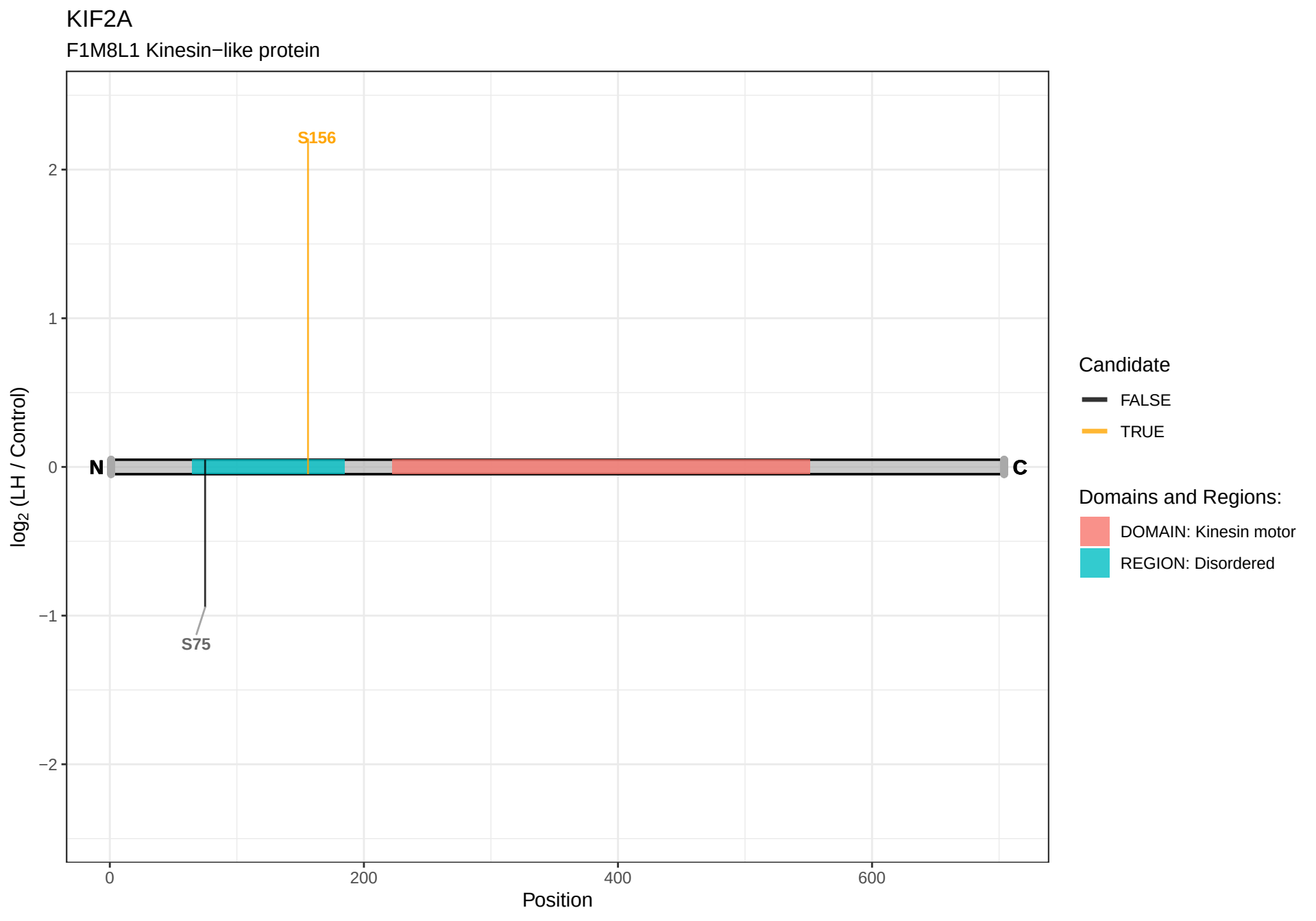

KDM5A
A0A096MJZ8 Lysine demethylase 5A
3
0
−3
log2 (LH / Control)
S223
S204
S1111
N
C
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ARID
DOMAIN: JmjC
DOMAIN: JmjN
DOMAIN: PHD−type
REGION: Disordered

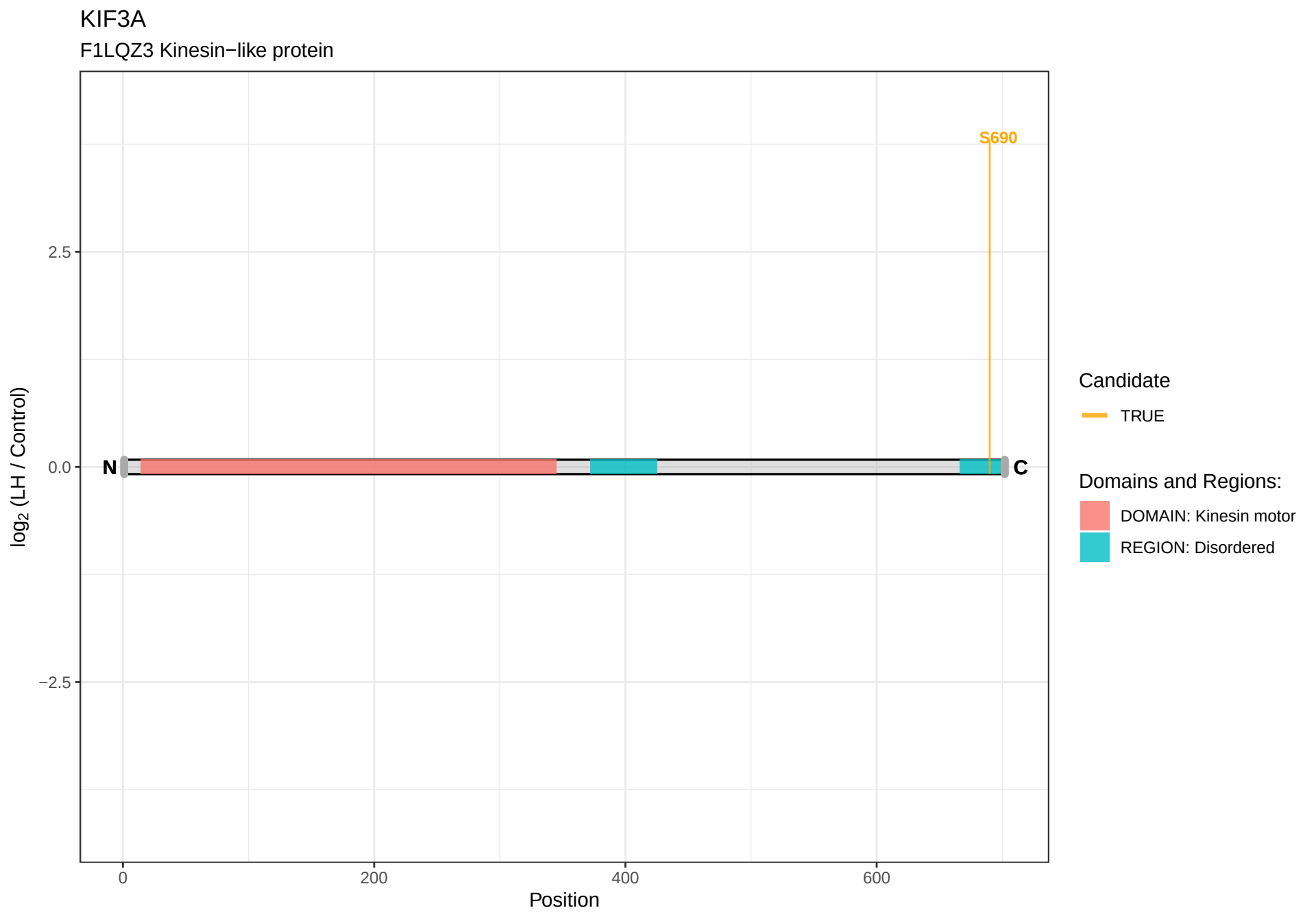

KIDINS220
D3ZWB2 Kinase D−interacting substrate of 220 kDa
S882
S885
S1351
S1357
S1353
S1354
S1582
S1590
S1586
S1585
S1673
S918
S1513
S1518
N
C
log2 (LH / Control)
Position
0
500
1000
1500
2
1
0
−1
−2
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ANK_REP_REGION
REGION: Disordered

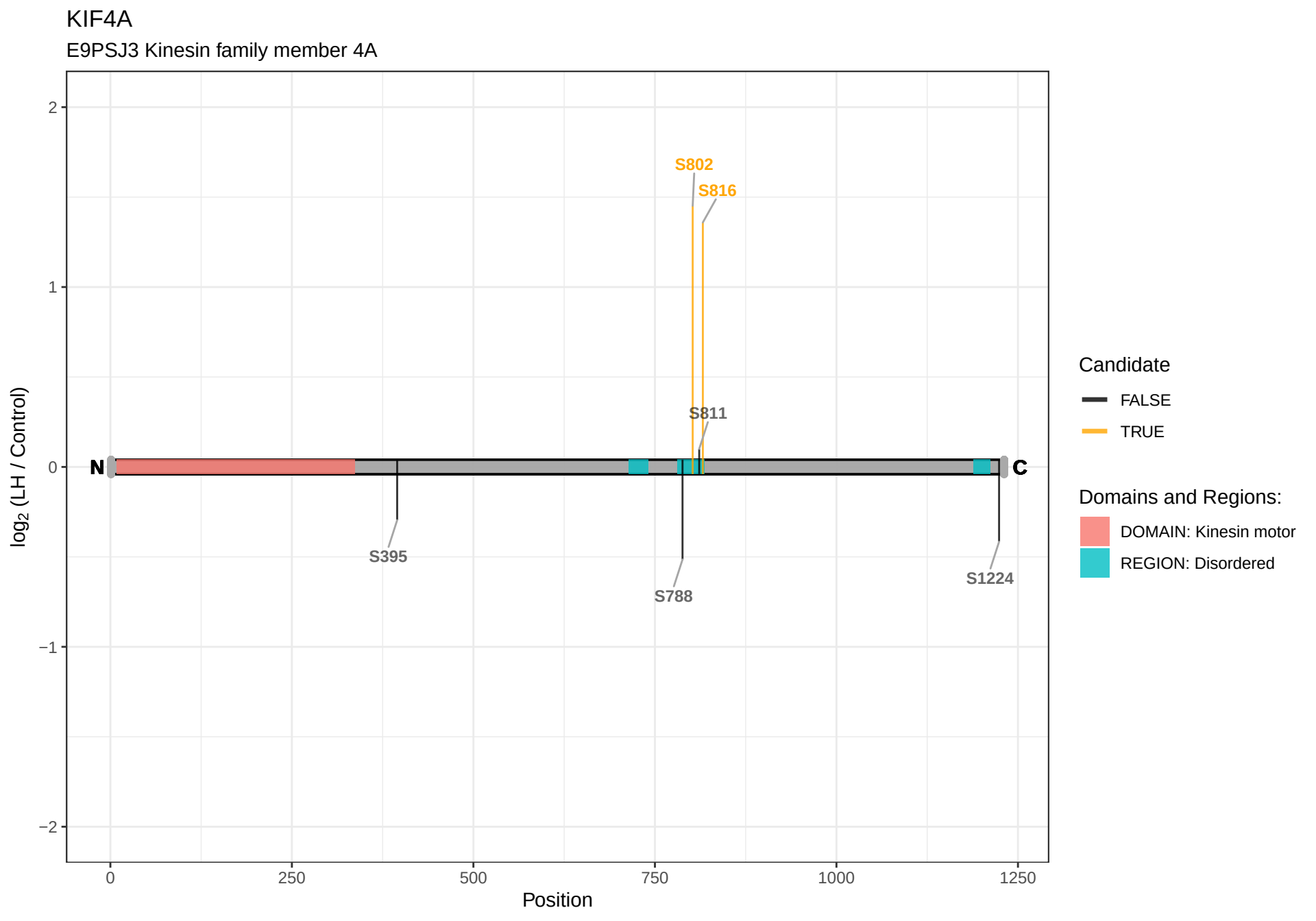

KIF13B
A0A0G2K8Z9 Kinesin family member 13B
log2 (LH / Control)
4
2
0
−2
−4
0
500
1000
1500
Position
N
C
S1795
S1795
S859
S1432
S1390
S1380
S1409
S1705
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CAP−Gly
DOMAIN: Kinesin motor
REGION: Disordered

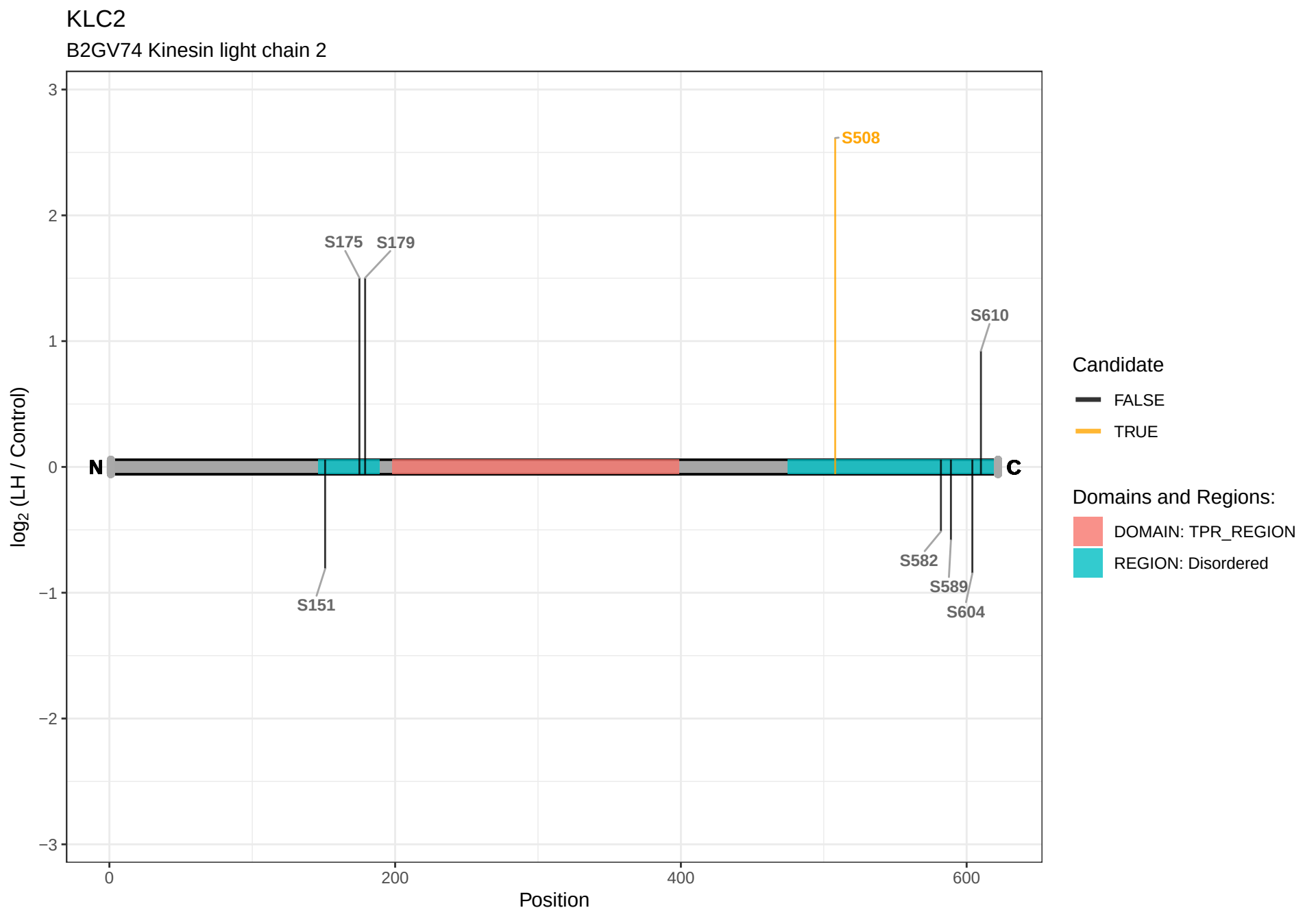

KIF18B
Q4KLL9 Kinesin−like protein KIF18B
S767
S403
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Kinesin motor
REGION: Disordered

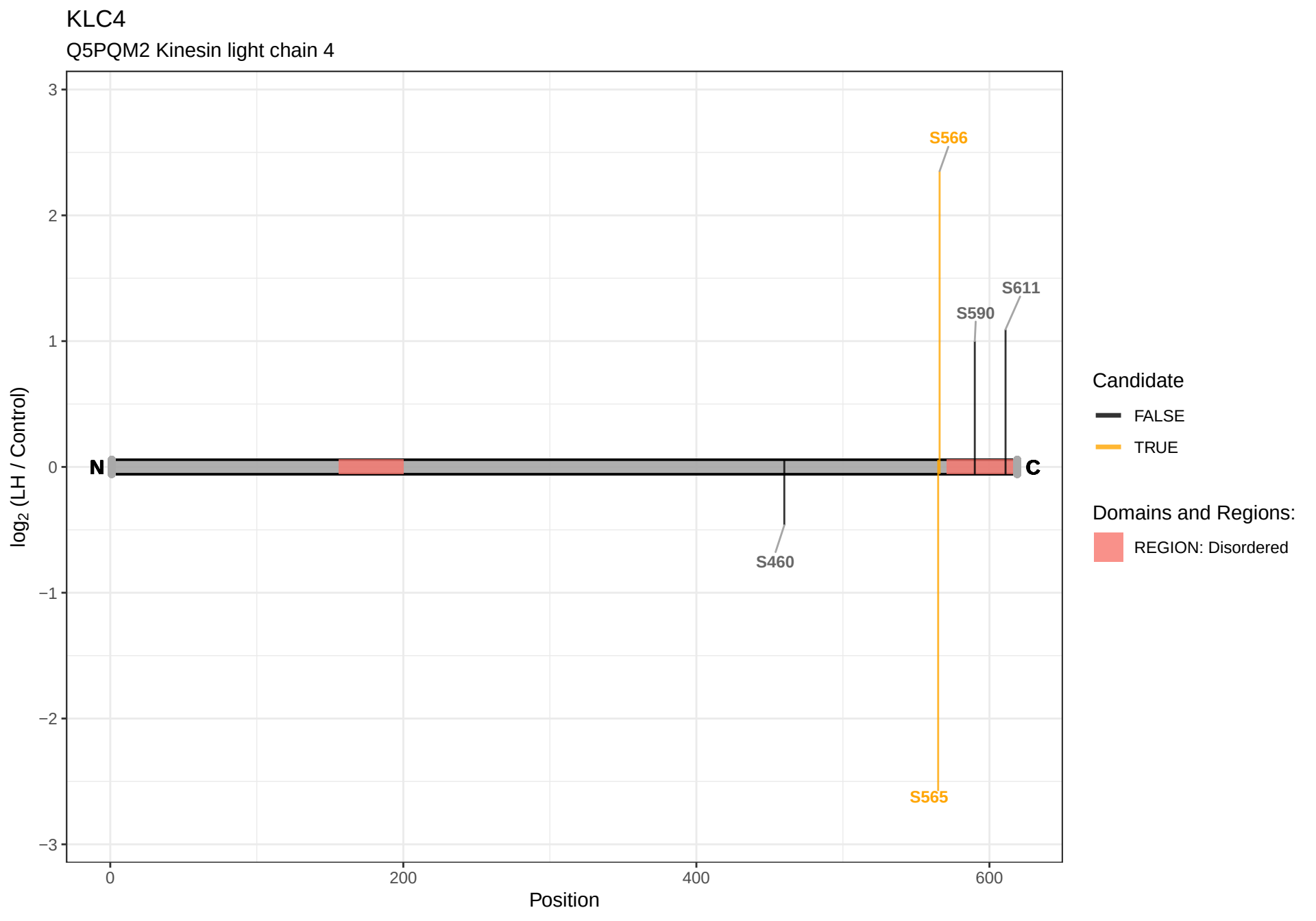

KIF21A
D3ZYN2 Kinesin family member 21A
log2 (LH / Control)
2
1
0
−1
−2
N
C
S1259
S1646
S1227
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Kinesin motor
DOMAIN: WD_REPEATS_REGION
REGION: Disordered

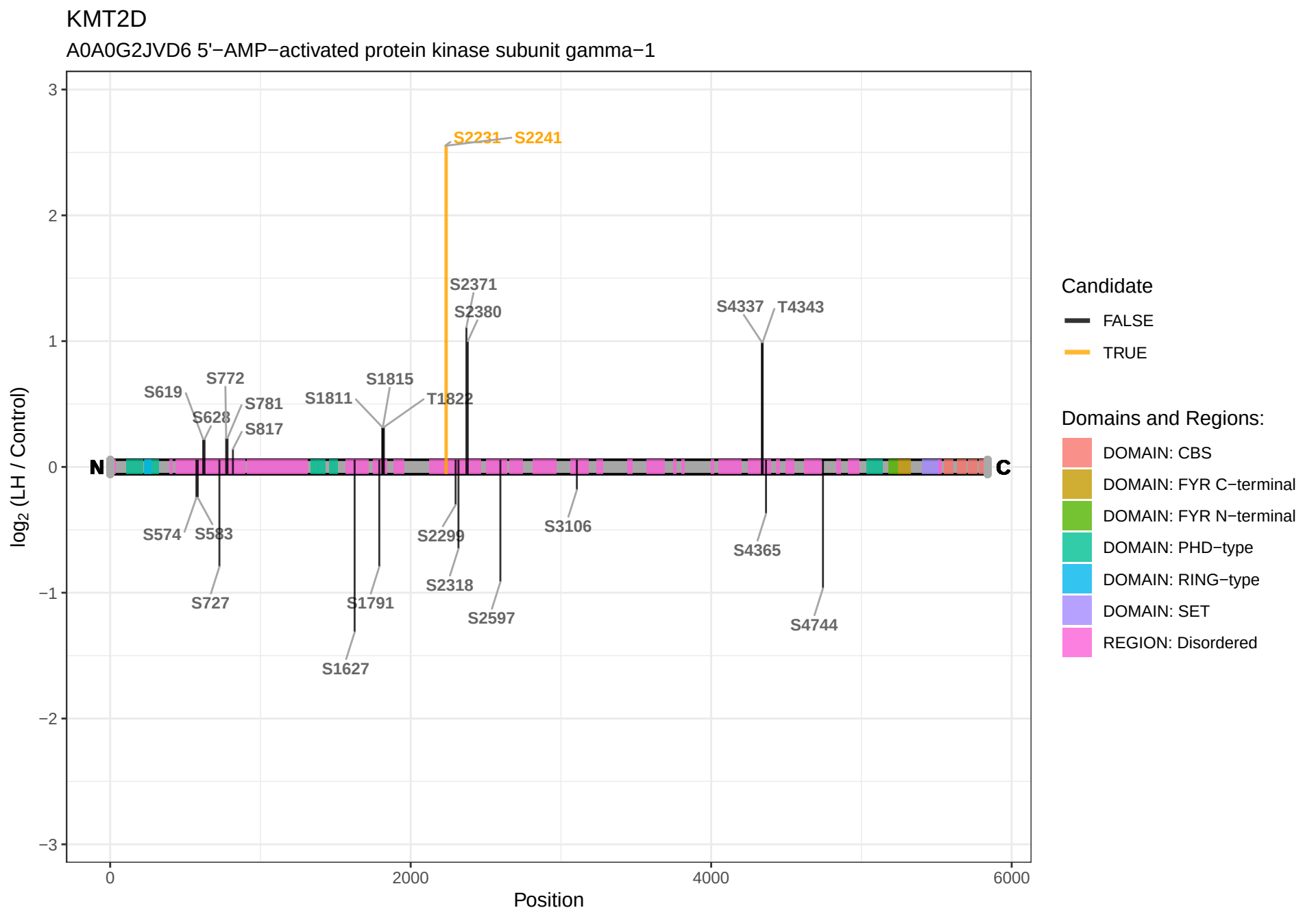

KIF2A
F1M8L1 Kinesin−like protein
S156
S75
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Kinesin motor
REGION: Disordered

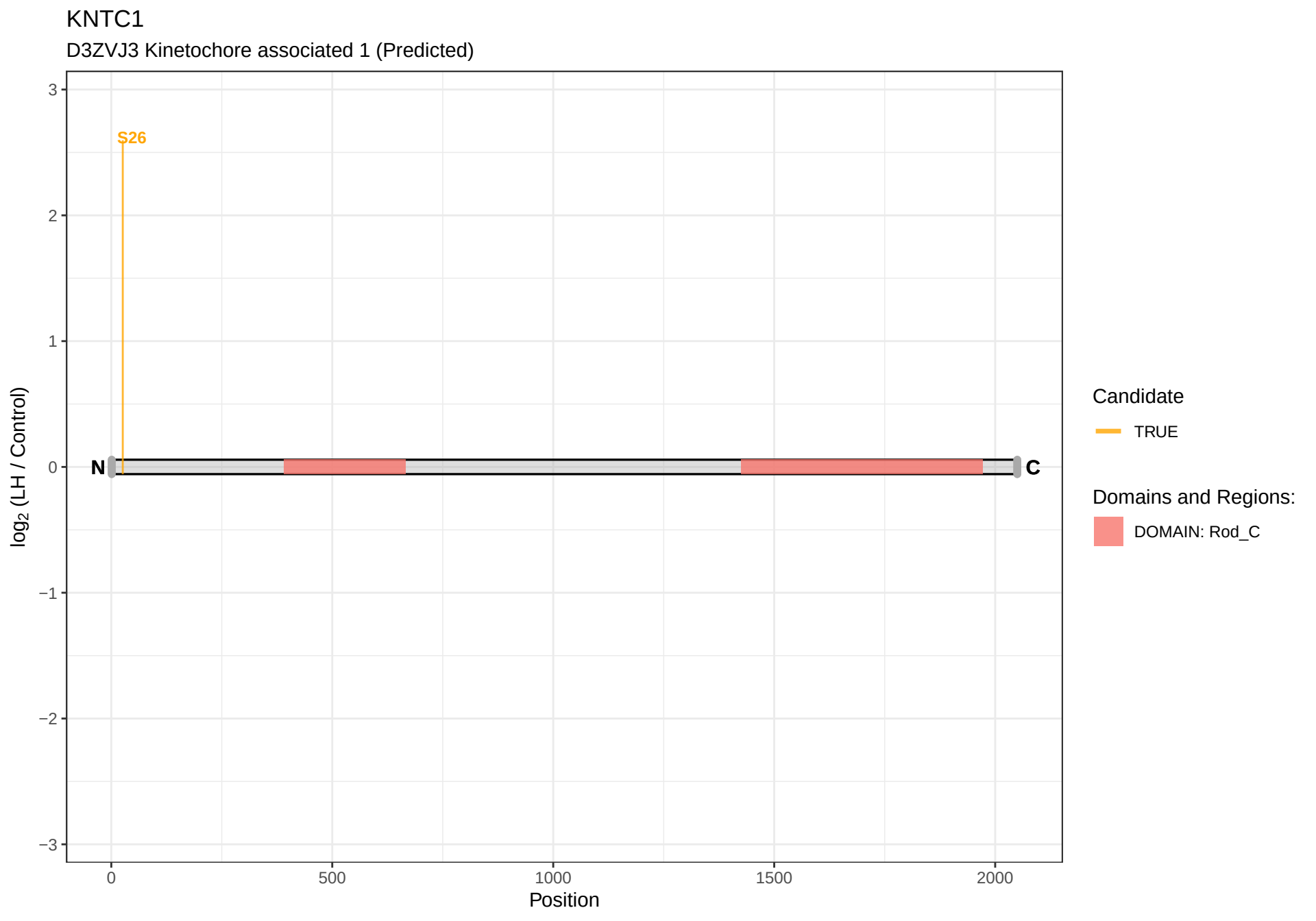

KIF3A
F1LQZ3 Kinesin−like protein
S690
N
C
2.5
0.0
−2.5
log2 (LH / Control)
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Kinesin motor
REGION: Disordered

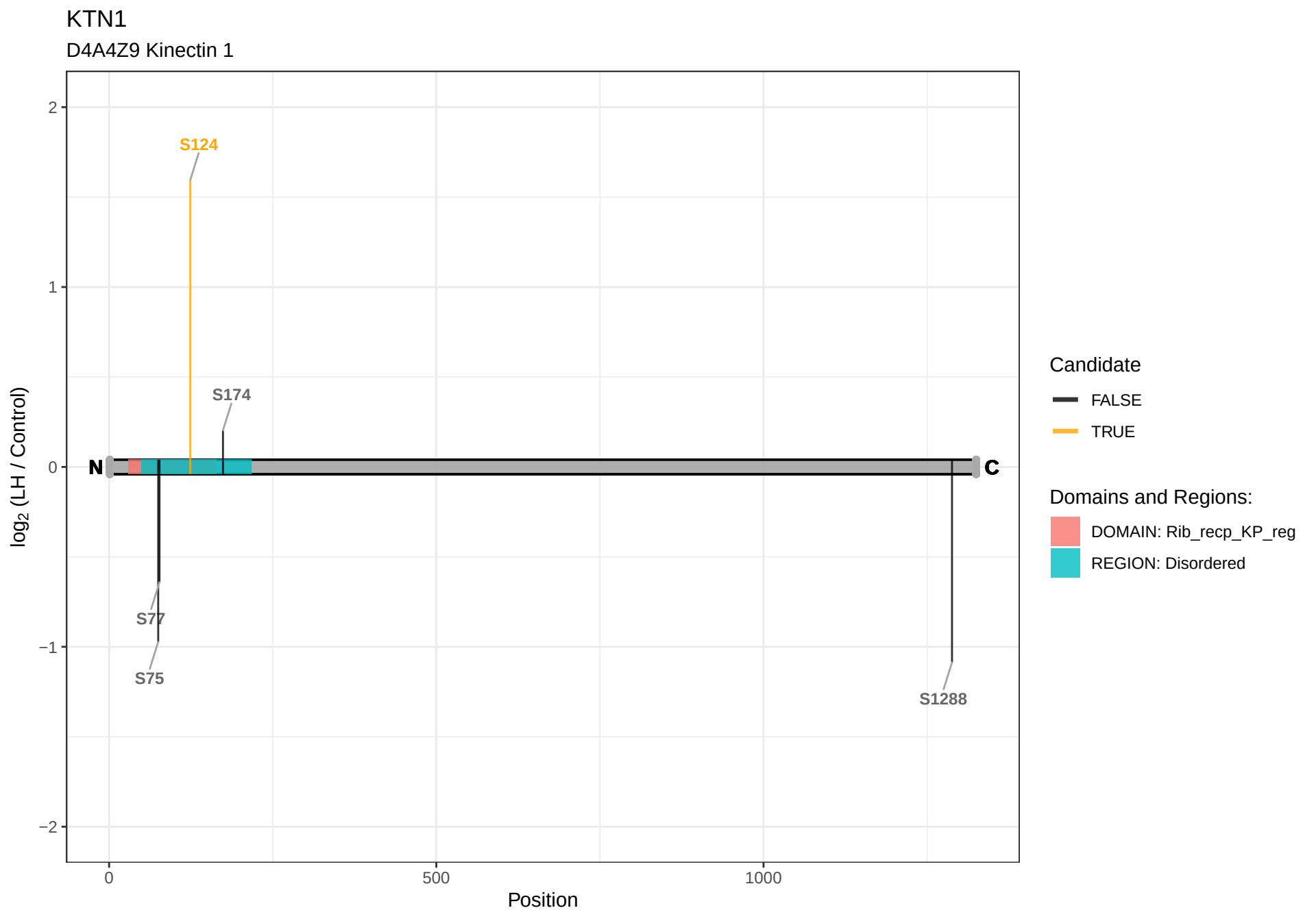

KIF4A
E9PSJ3 Kinesin family member 4A
log2 (LH / Control)
2
1
0
−1
−2
0
250
500
750
1000
1250
Position
N
C
S802
S816
S811
S395
S788
S1224
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Kinesin motor
REGION: Disordered

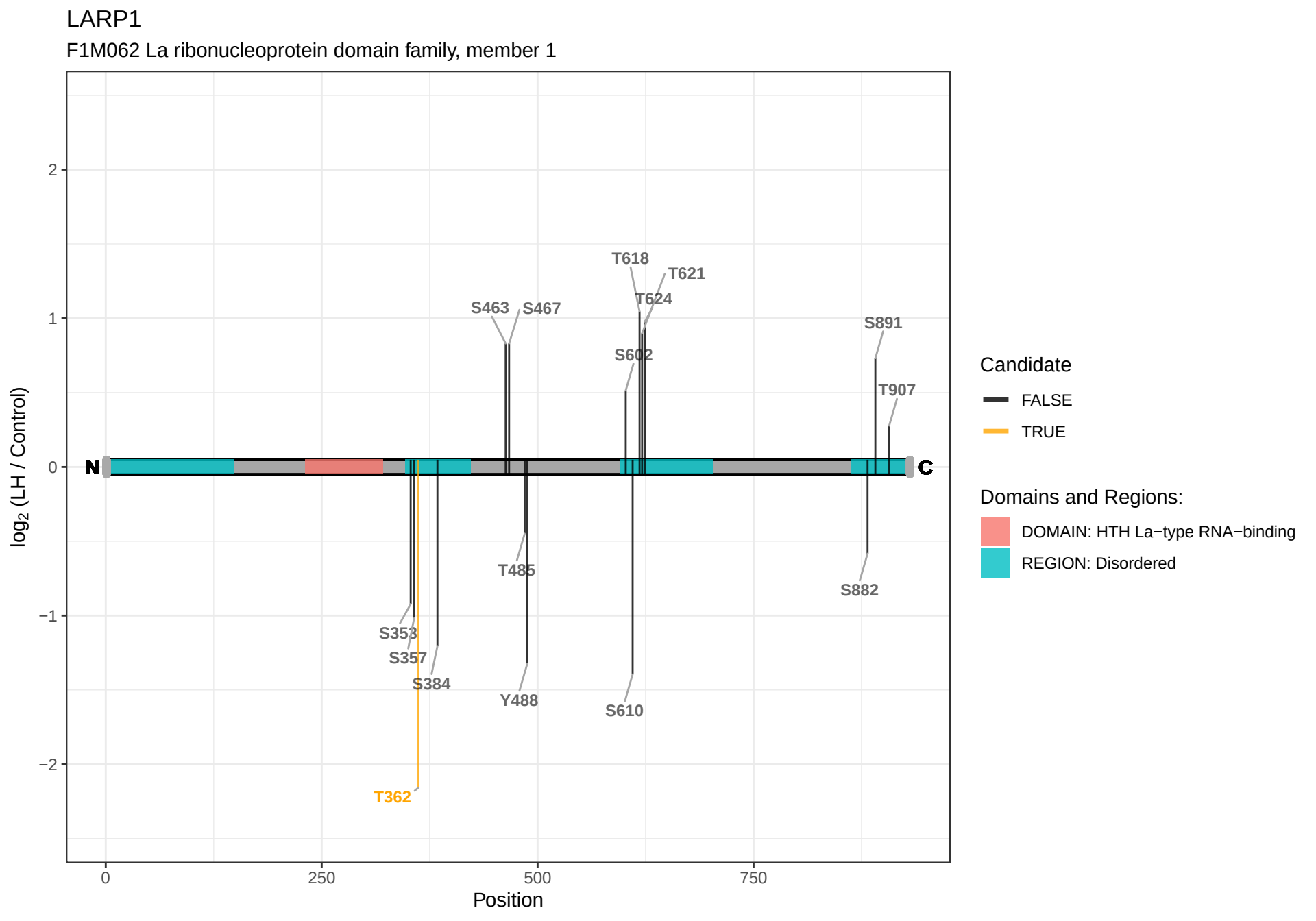

KLC2
B2GV74 Kinesin light chain 2
log2 (LH / Control)
Position
N
C
S508
S175
S179
S610
S151
S582
S589
S604
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: TPR_REGION
REGION: Disordered

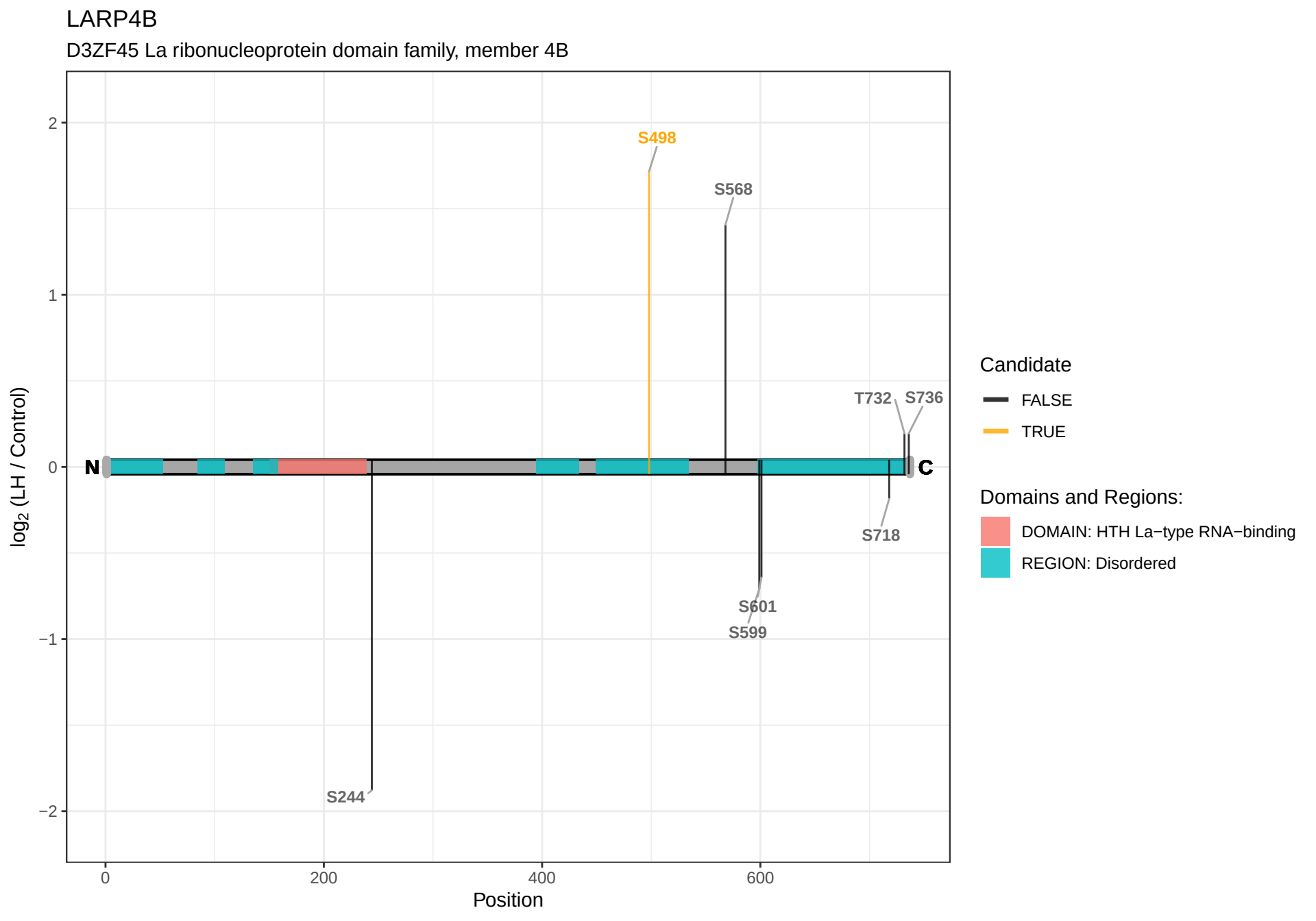

KLC4
Q5PQM2 Kinesin light chain 4
log2 (LH / Control)
3
2
1
0
−1
−2
−3
0
200
400
600
Position
N
C
S566
S611
S590
S460
S565
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

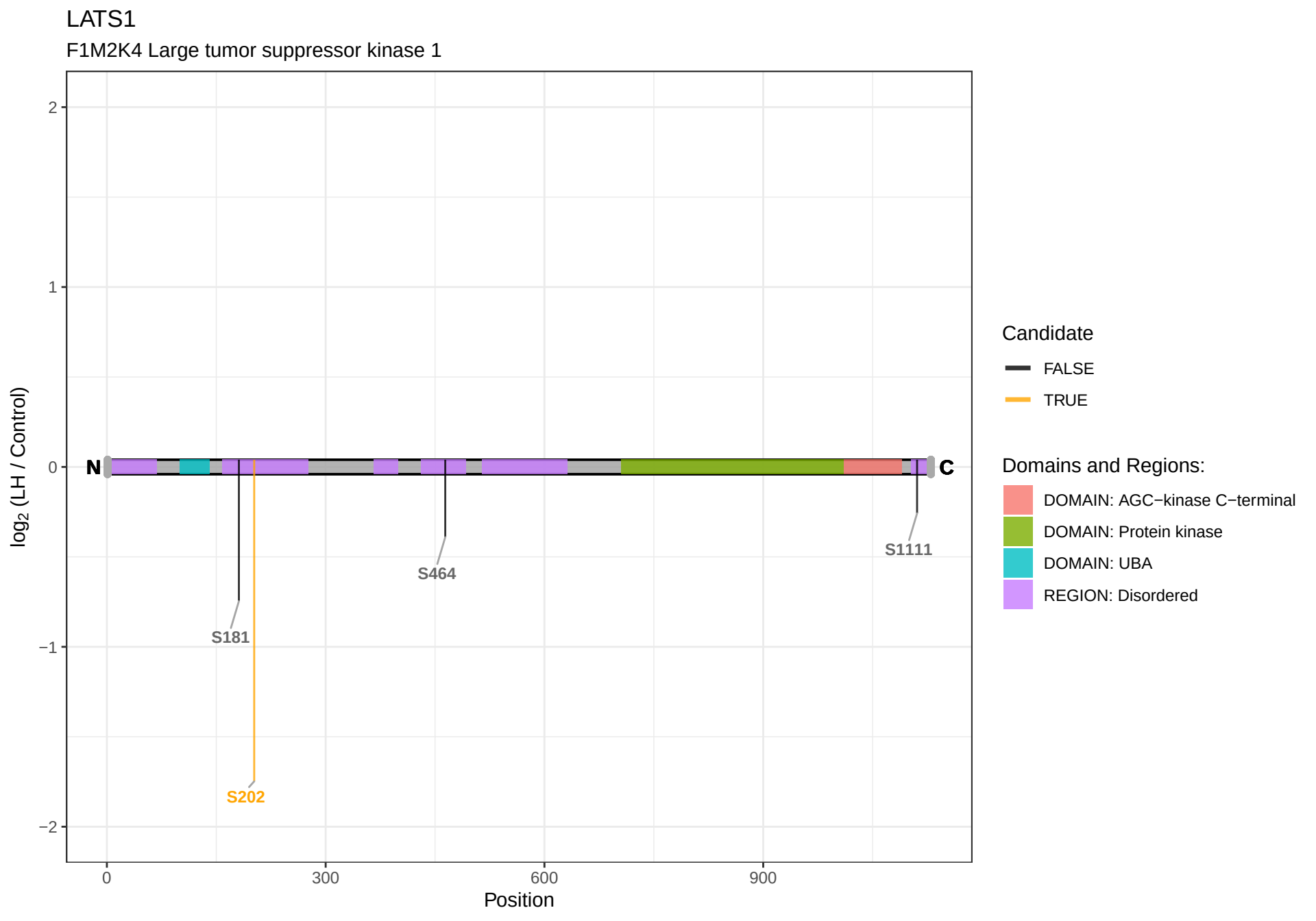

KMT2D
A0A0G2JVD6 5'−AMP−activated protein kinase subunit gamma−1
log2 (LH / Control)
Position
N
C
S2231
S2241
S2371
S2380
S4337
T4343
S619
S772
S781
S628
S817
S1811
S1815
T1822
S574
S583
S727
S1627
S1791
S2299
S2318
S2597
S3106
S4365
S4744
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CBS
DOMAIN: FYR C−terminal
DOMAIN: FYR N−terminal
DOMAIN: PHD−type
DOMAIN: RING−type
DOMAIN: SET
REGION: Disordered

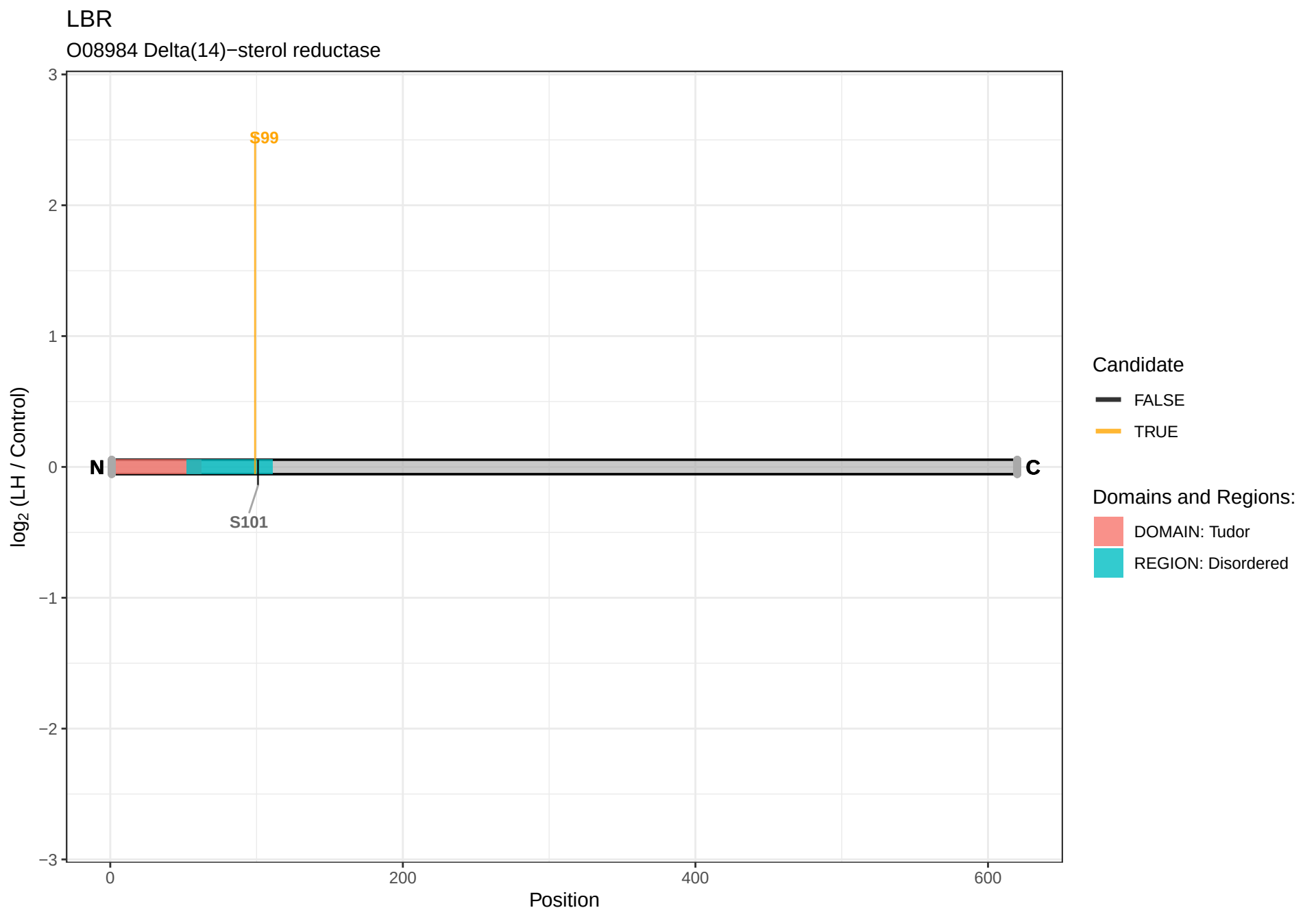

KNTC1
D3ZVJ3 Kinetochore associated 1 (Predicted)
S26
N
C
log2 (LH / Control)
Position
3
2
1
0
−1
−2
−3
0
500
1000
1500
2000
Candidate
TRUE
Domains and Regions:
DOMAIN: Rod_C

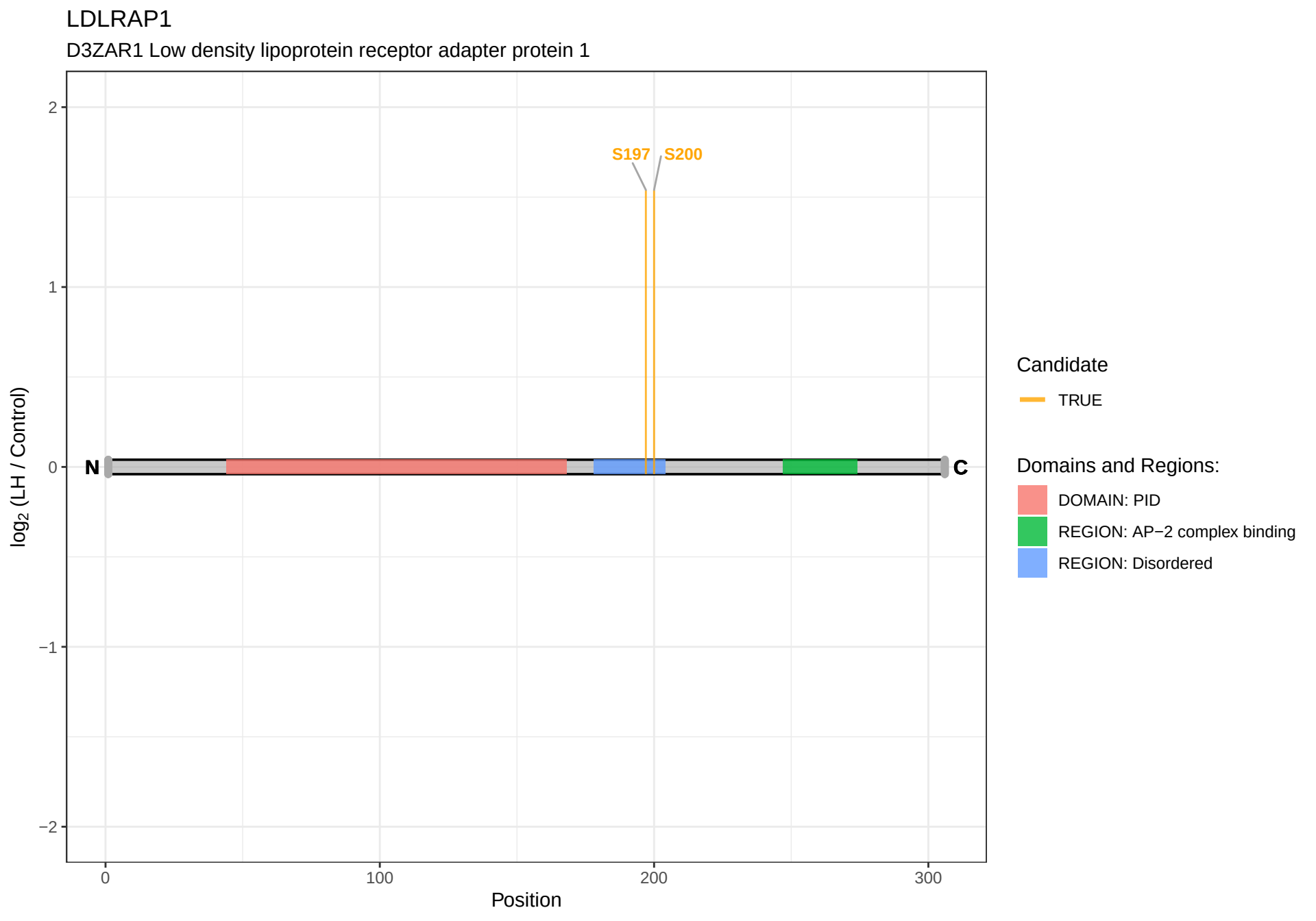

KTN1
D4A4Z9 Kinectin 1
2
1
0
−1
−2
log2 (LH / Control)
S124
S174
N
C
S77
S75
S1288
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Rib_recp_KP_reg
REGION: Disordered

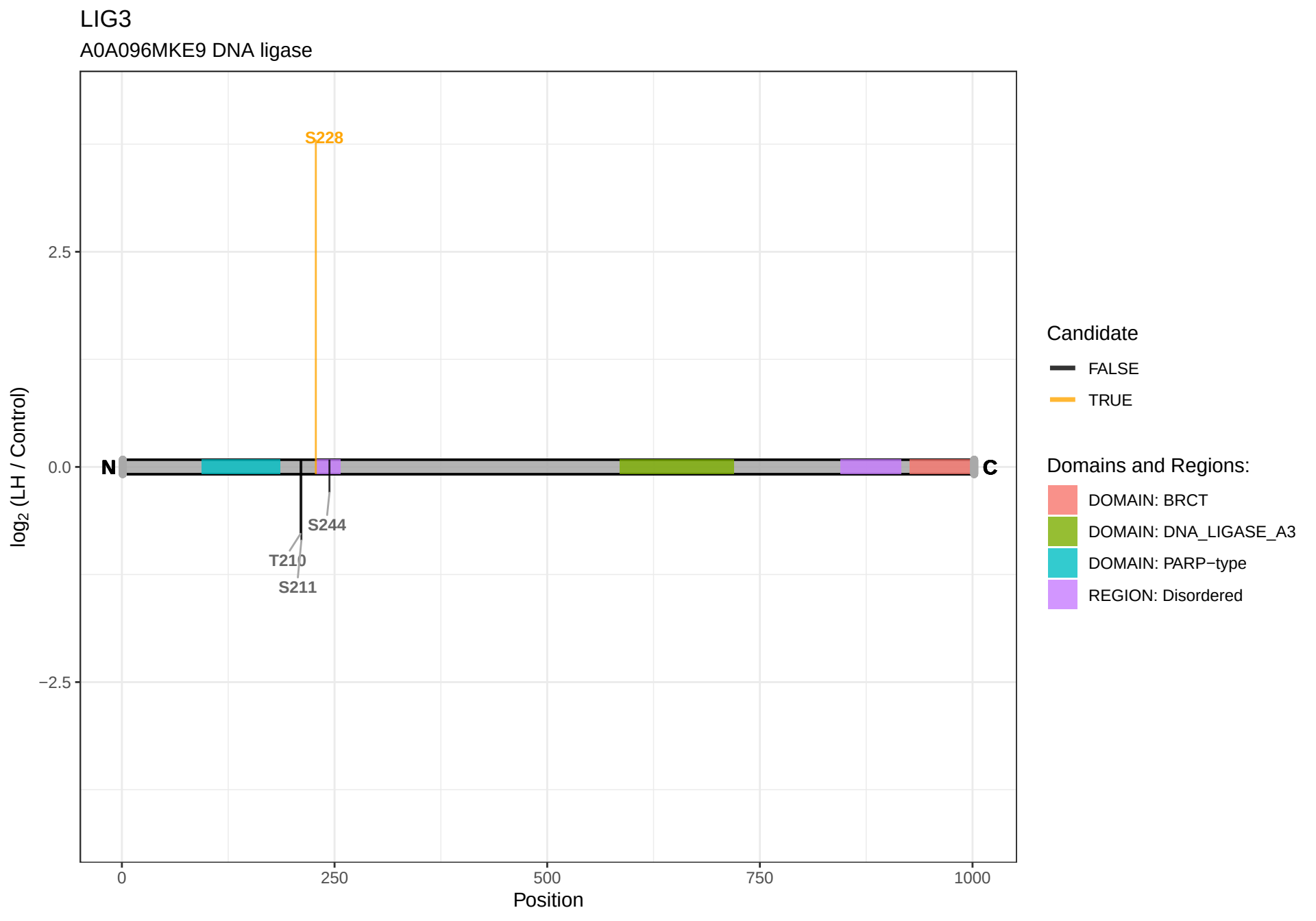

LARP1
F1M062 La ribonucleoprotein domain family, member 1
log2 (LH / Control)
Position
N
C
T618
T621
T624
S463
S467
S891
S602
T907
T485
S882
S353
S357
S384
Y488
S610
T362
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: HTH La−type RNA−binding
REGION: Disordered

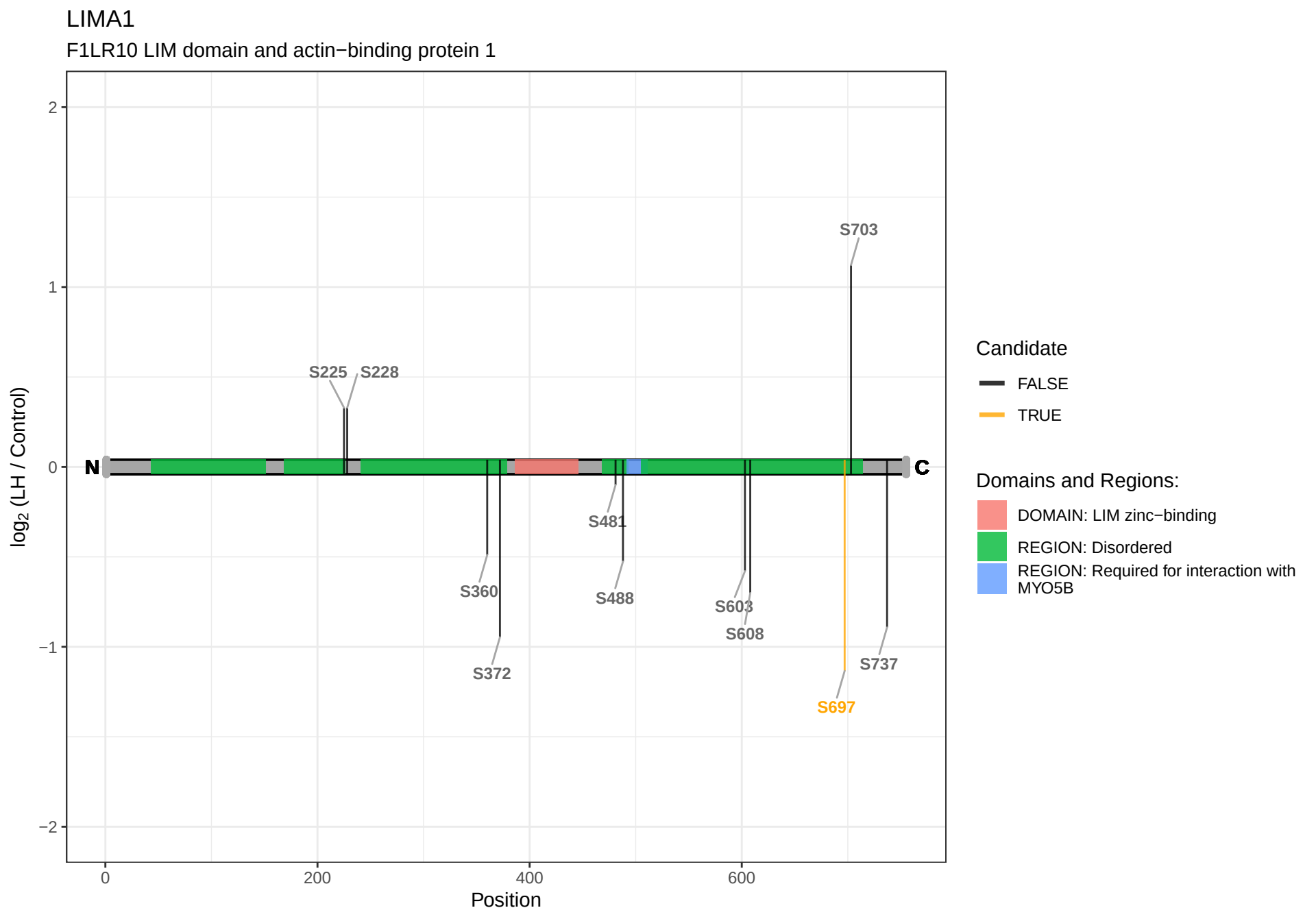

LARP4B
D3ZF45 La ribonucleoprotein domain family, member 4B
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
N
C
S498
S568
T732
S736
S718
S601
S599
S244
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: HTH La−type RNA−binding
REGION: Disordered

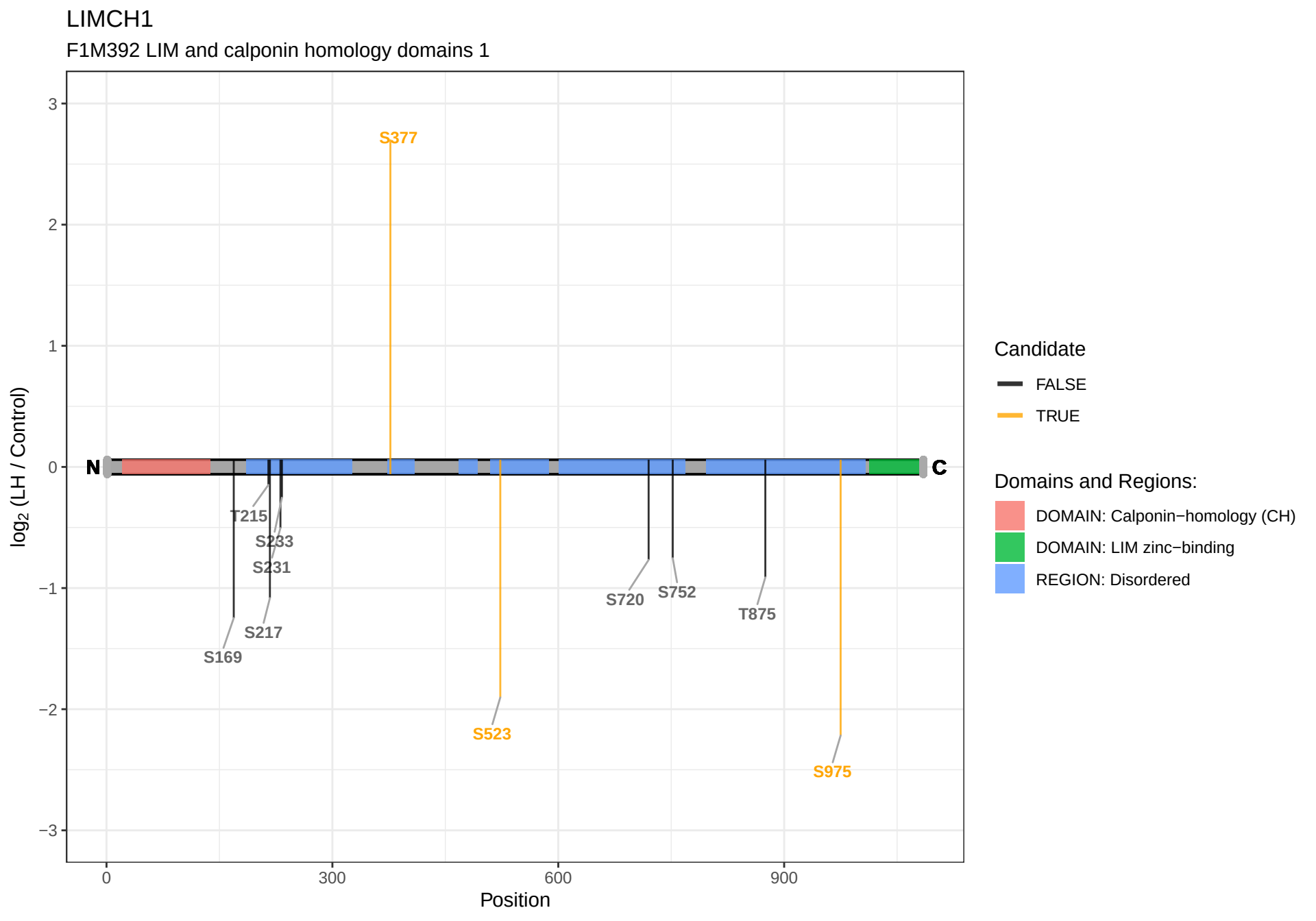

LATS1
F1M2K4 Large tumor suppressor kinase 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S181
S202
S464
S1111
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AGC−kinase C−terminal
DOMAIN: Protein kinase
DOMAIN: UBA
REGION: Disordered

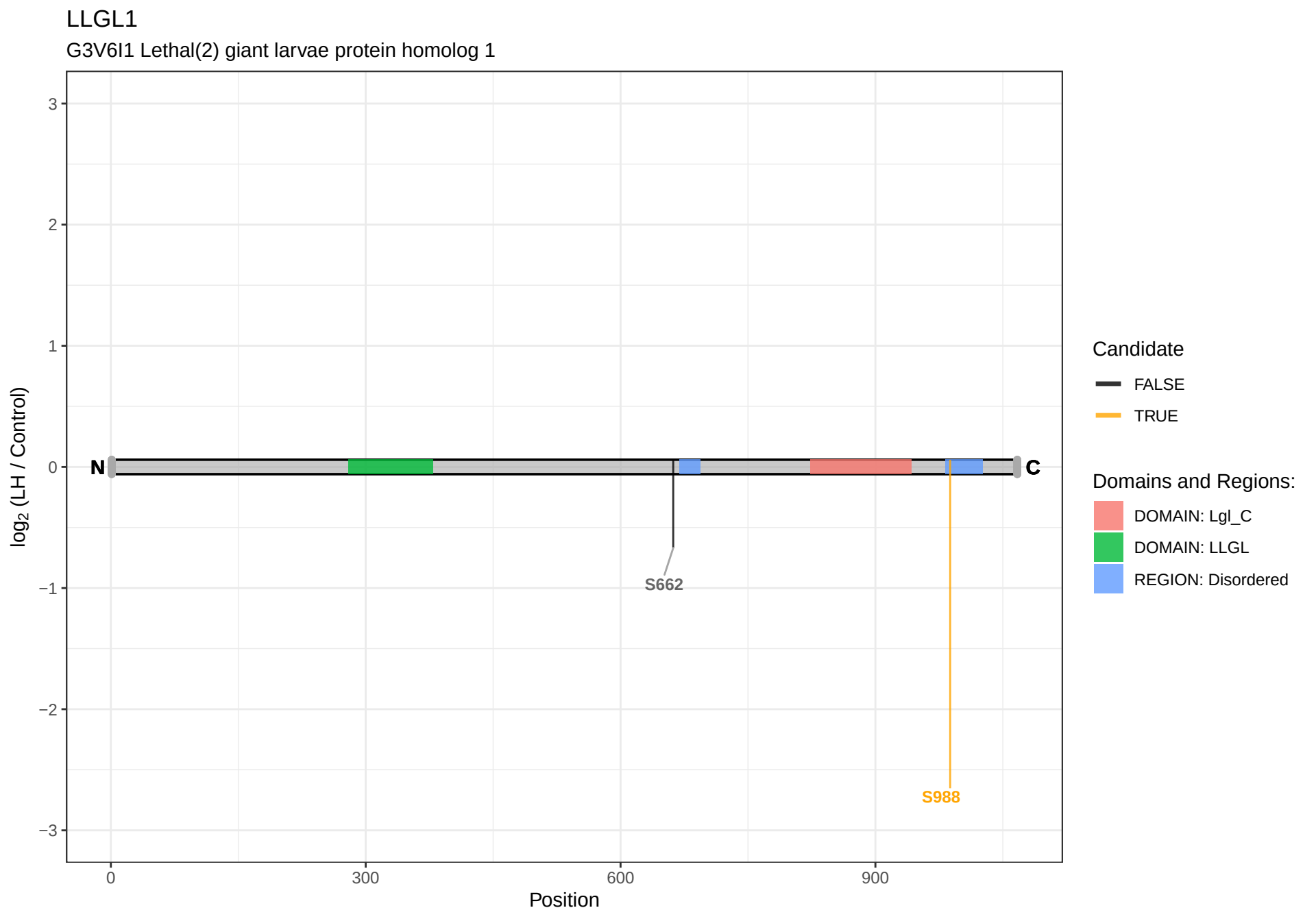

LBR
O08984 Delta(14)−sterol reductase
S99
S101
N
C
log2 (LH / Control)
Position
3
2
1
0
−1
−2
−3
0
200
400
600
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Tudor
REGION: Disordered

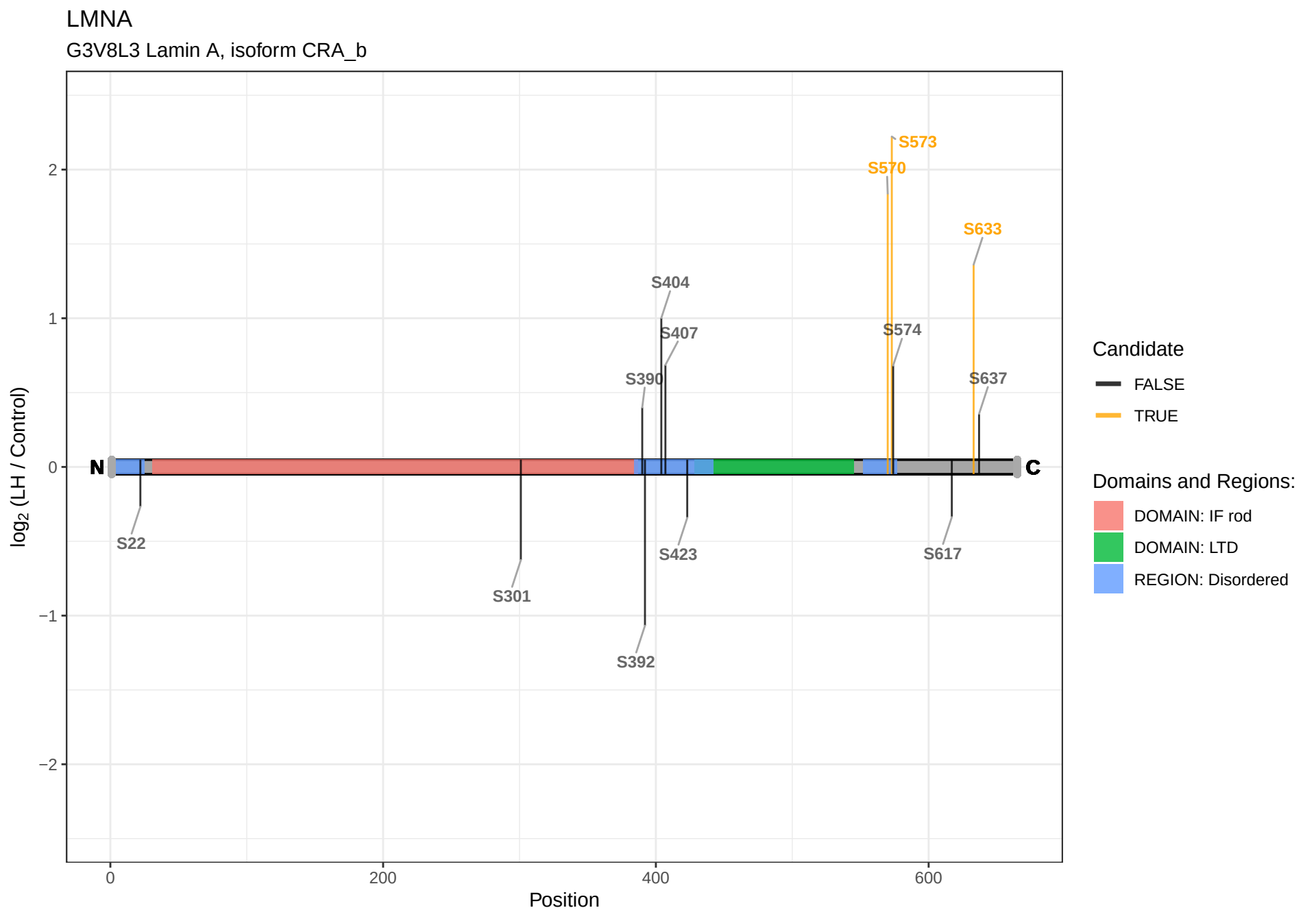

LDLRAP1
D3ZAR1 Low density lipoprotein receptor adapter protein 1
S197
S200
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: PID
REGION: AP−2 complex binding
REGION: Disordered

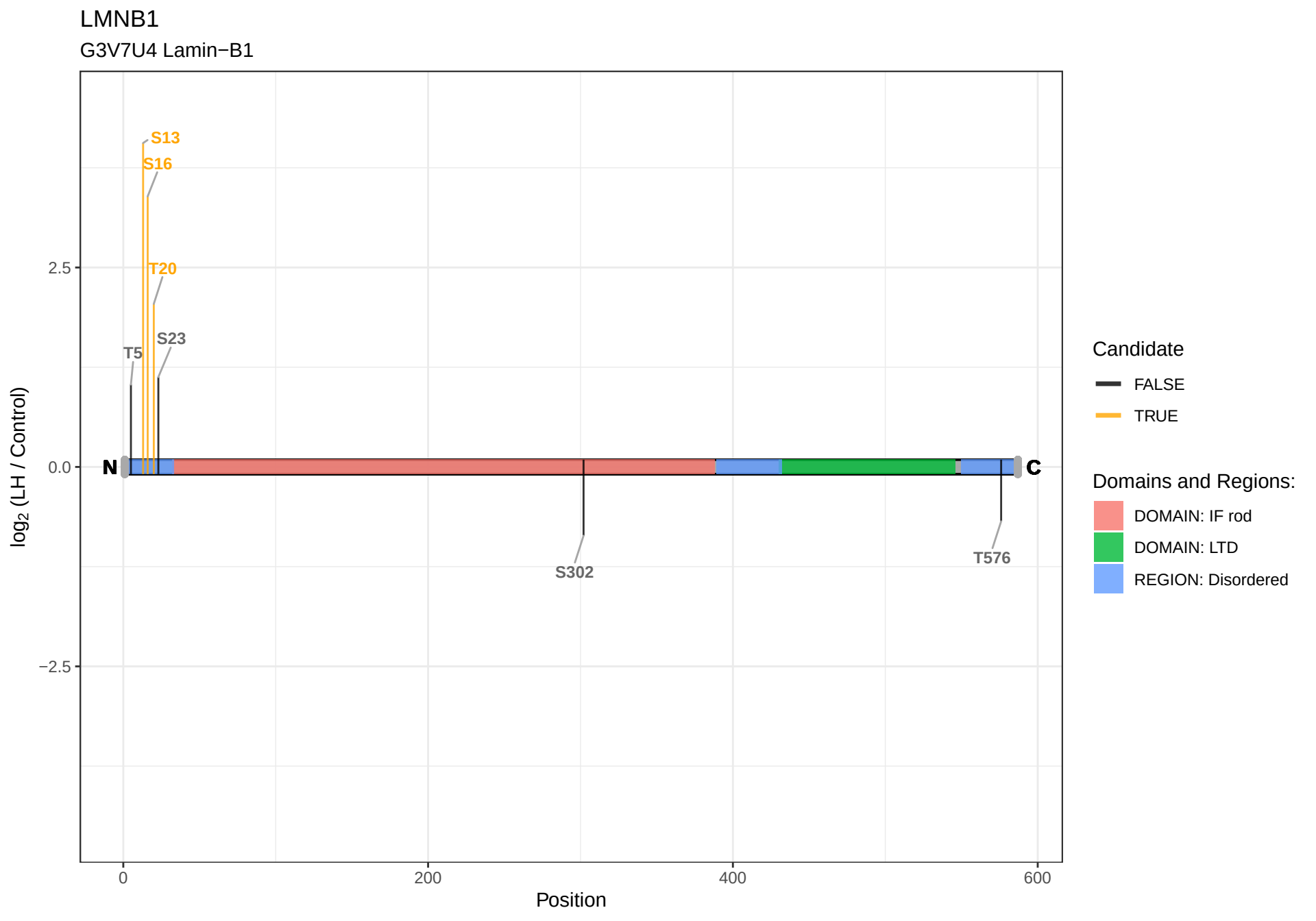

LIG3
A0A096MKE9 DNA ligase
S228
S244
T210
S211
N
C
2.5
0.0
−2.5
log2 (LH / Control)
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: BRCT
DOMAIN: DNA_LIGASE_A3
DOMAIN: PARP−type
REGION: Disordered

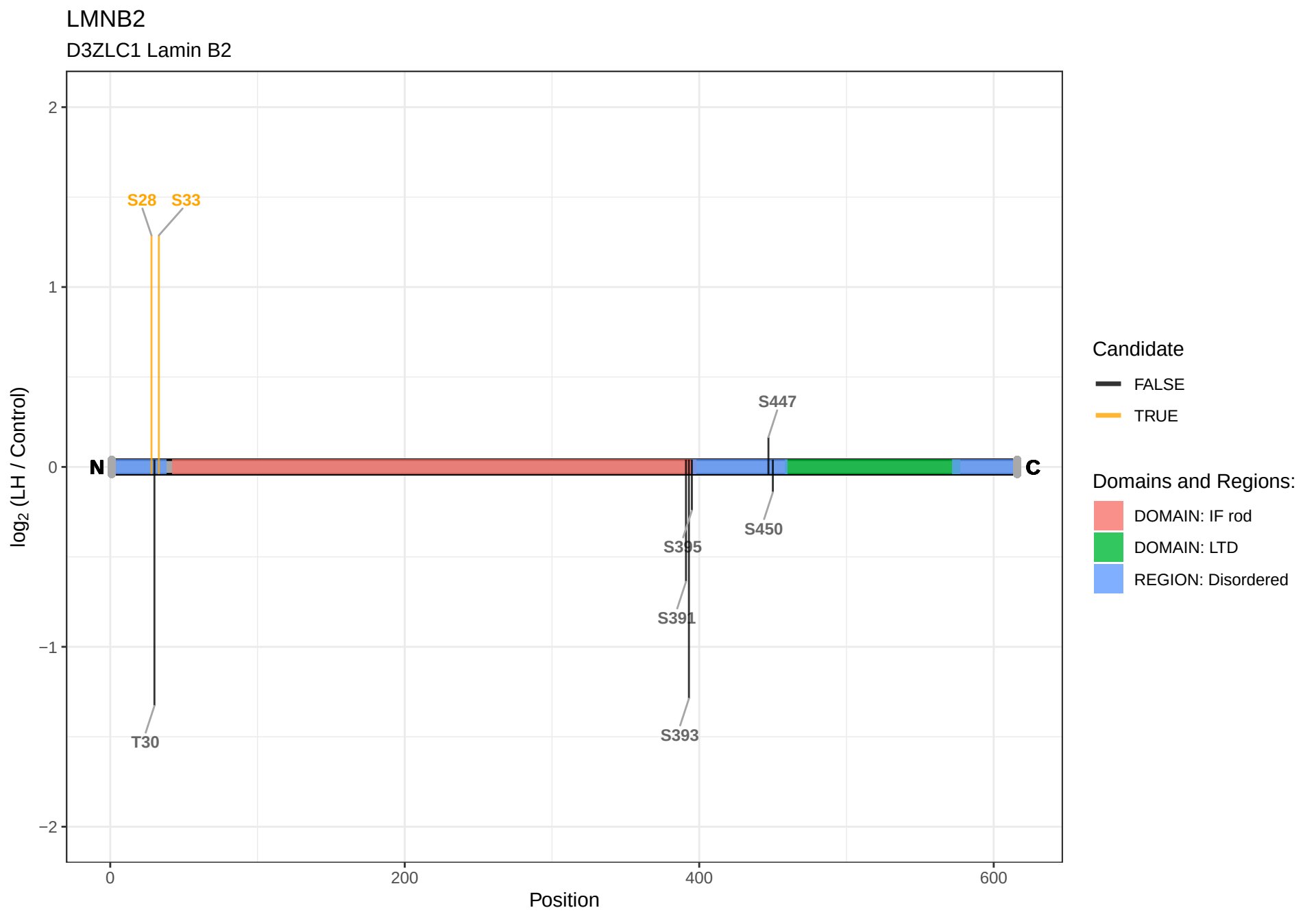

LIMA1
F1LR10 LIM domain and actin−binding protein 1
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
N
C
S225
S228
S703
S481
S360
S488
S603
S608
S372
S737
S697
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: LIM zinc−binding
REGION: Disordered
REGION: Required for interaction with MYO5B

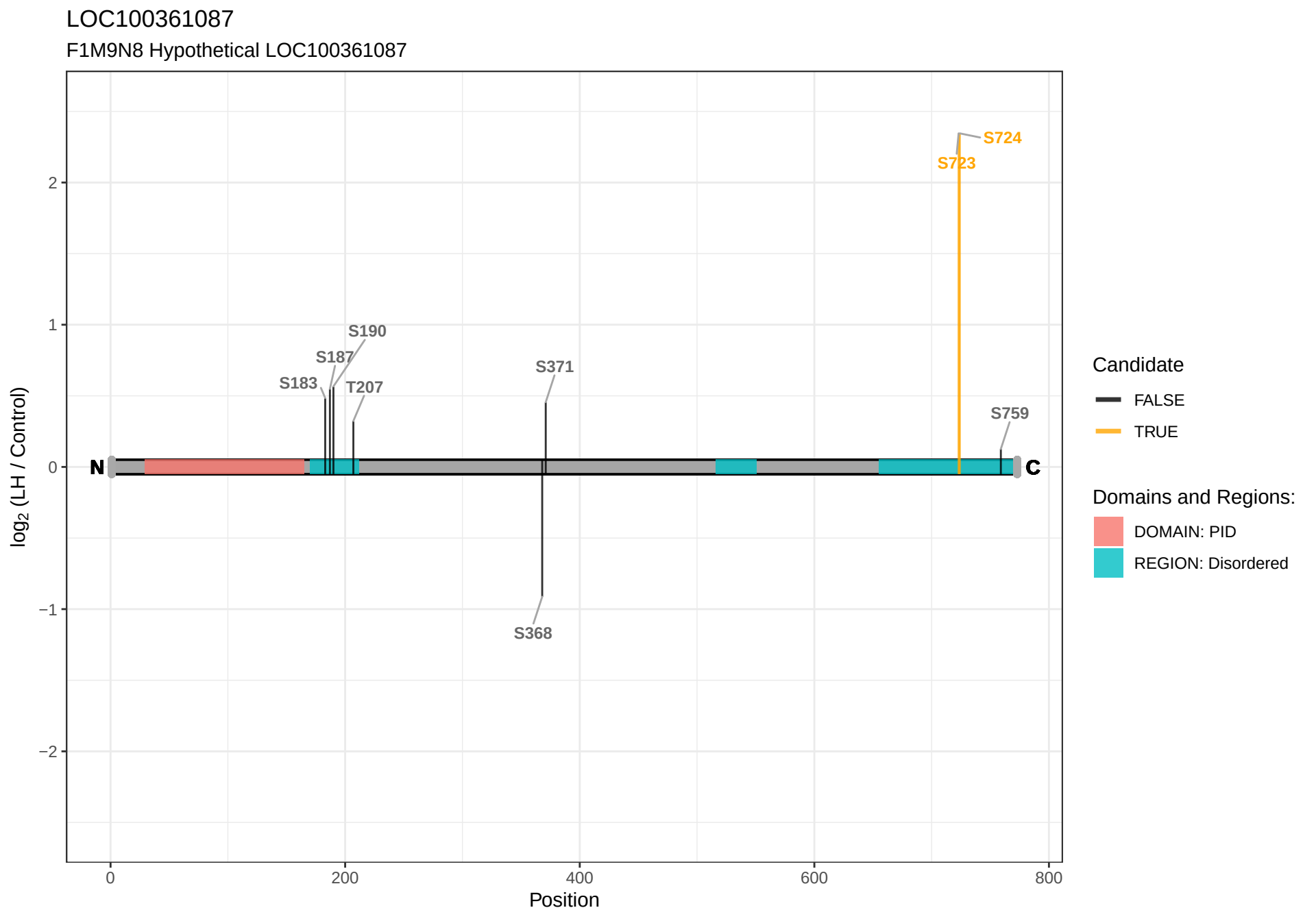

LIMCH1
F1M392 LIM and calponin homology domains 1
log2 (LH / Control)
3
2
1
0
−1
−2
−3
0
300
600
900
Position
N
C
S377
T215
S233
S231
S217
S169
S720
S752
T875
S523
S975
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Calponin−homology (CH)
DOMAIN: LIM zinc−binding
REGION: Disordered

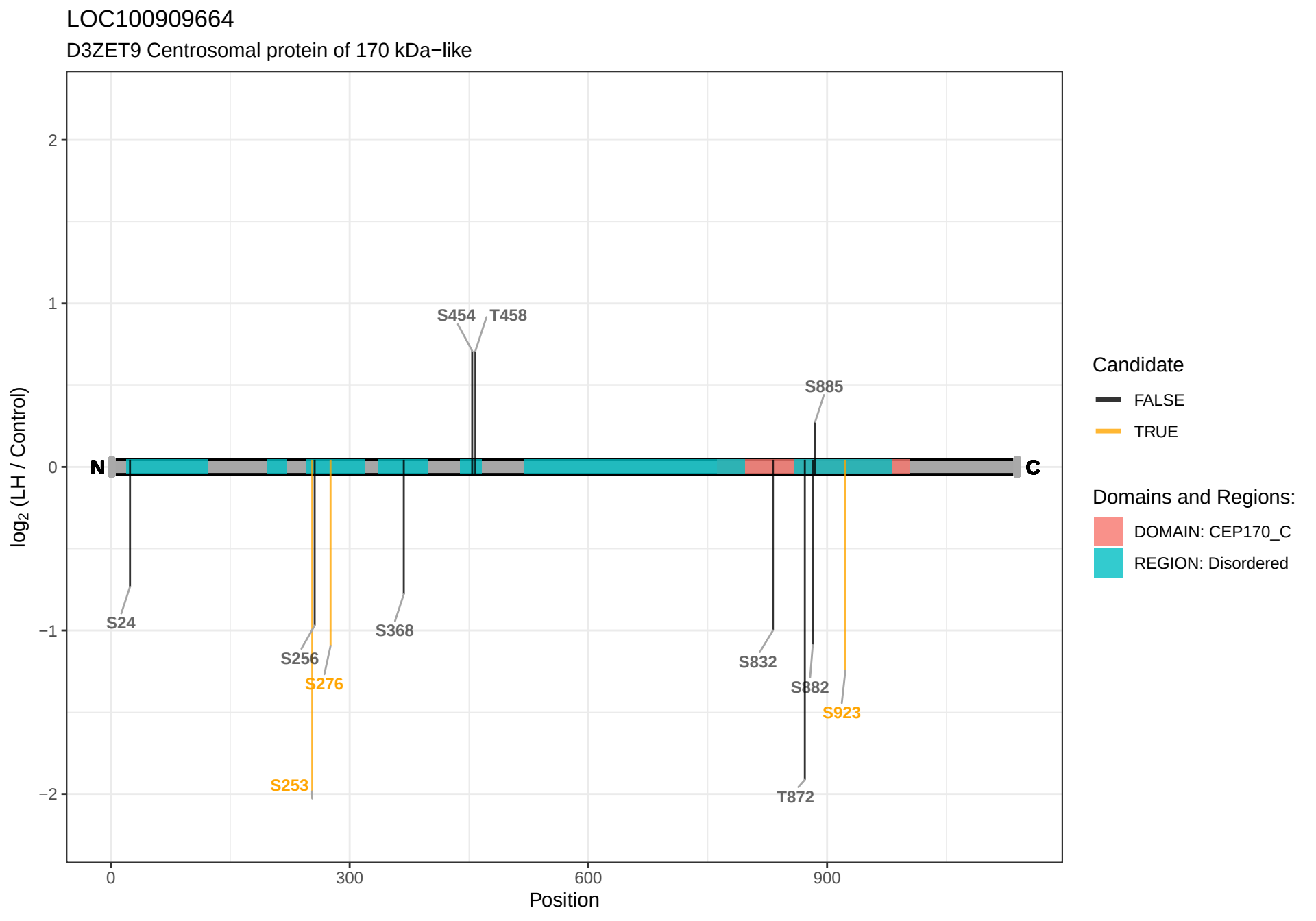

LLGL1
G3V6I1 Lethal(2) giant larvae protein homolog 1
log2 (LH / Control)
3
2
1
0
−1
−2
−3
N
C
S662
S988
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Lgl_C
DOMAIN: LLGL
REGION: Disordered

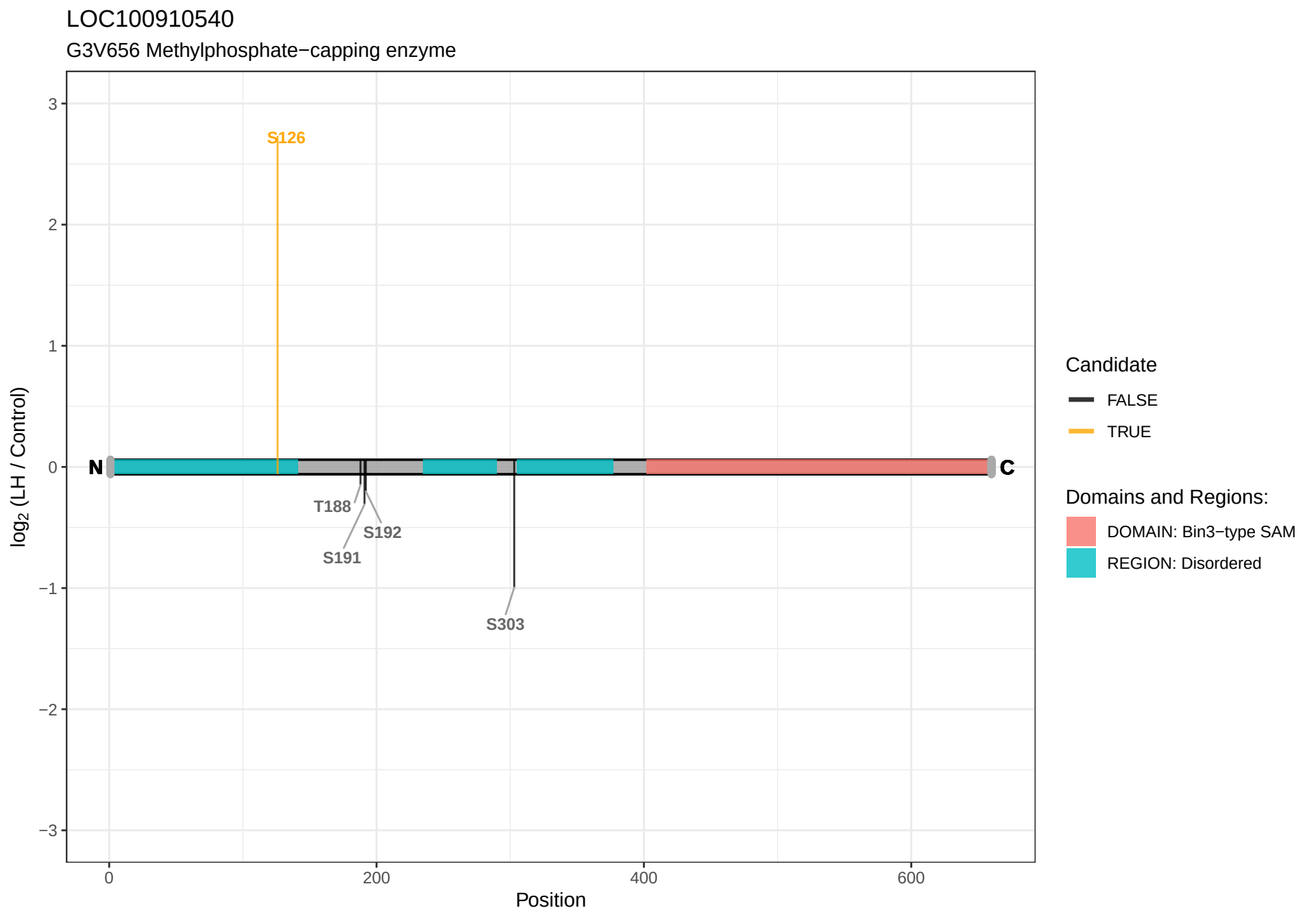

LMNA
G3V8L3 Lamin A, isoform CRA_b
log2 (LH / Control)
Position
0
200
400
600
2
1
0
−1
−2
N
C
S573
S570
S633
S404
S407
S574
S390
S637
S22
S301
S423
S617
S392
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: IF rod
DOMAIN: LTD
REGION: Disordered

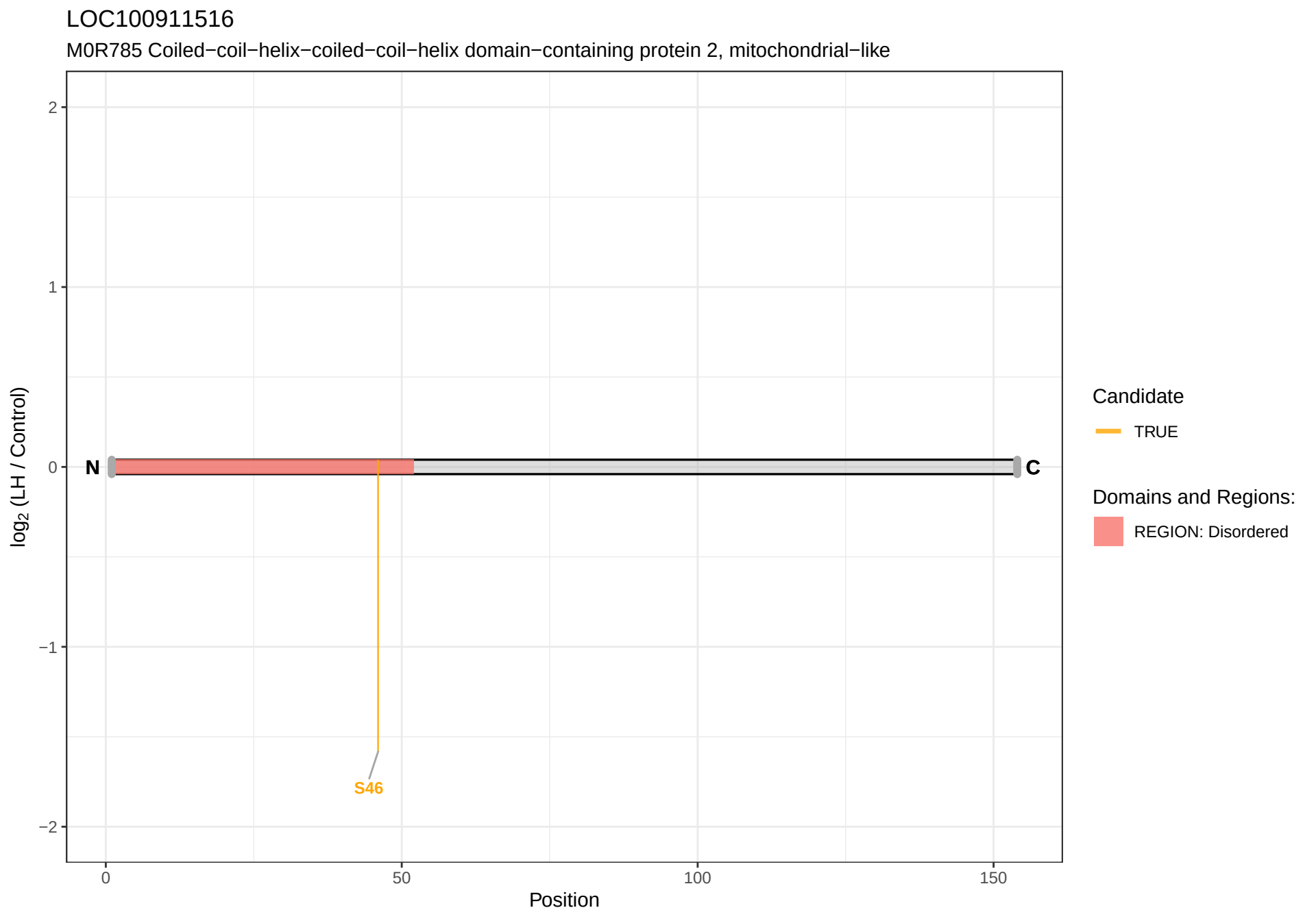

LMNB1
G3V7U4 Lamin−B1
S13
S16
T20
S23
T5
N
C
S302
T576
2.5
0.0
−2.5
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: IF rod
DOMAIN: LTD
REGION: Disordered

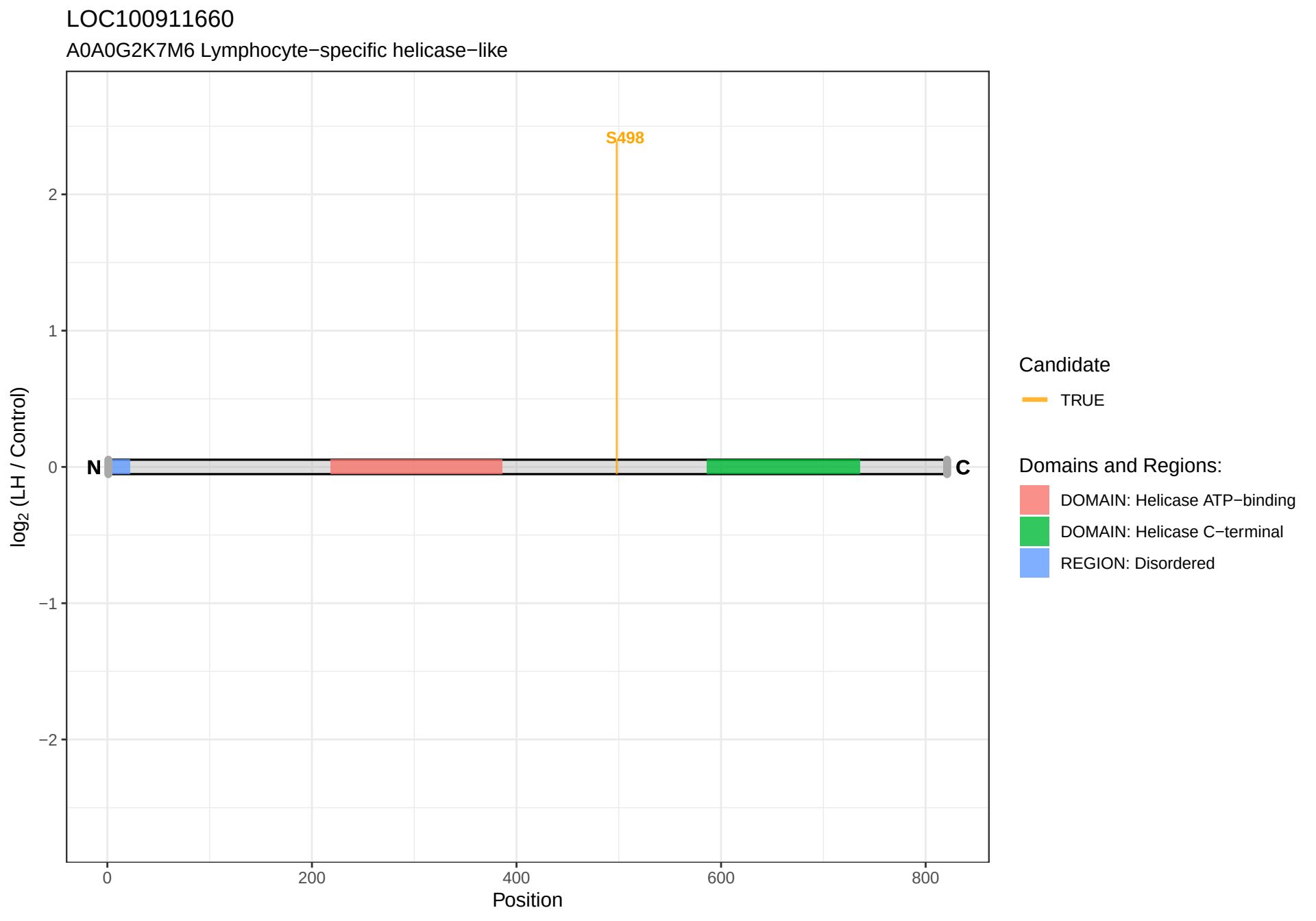

LMNB2
D3ZLC1 Lamin B2
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
N
C
S28
S33
T30
S395
S391
S393
S447
S450
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: IF rod
DOMAIN: LTD
REGION: Disordered

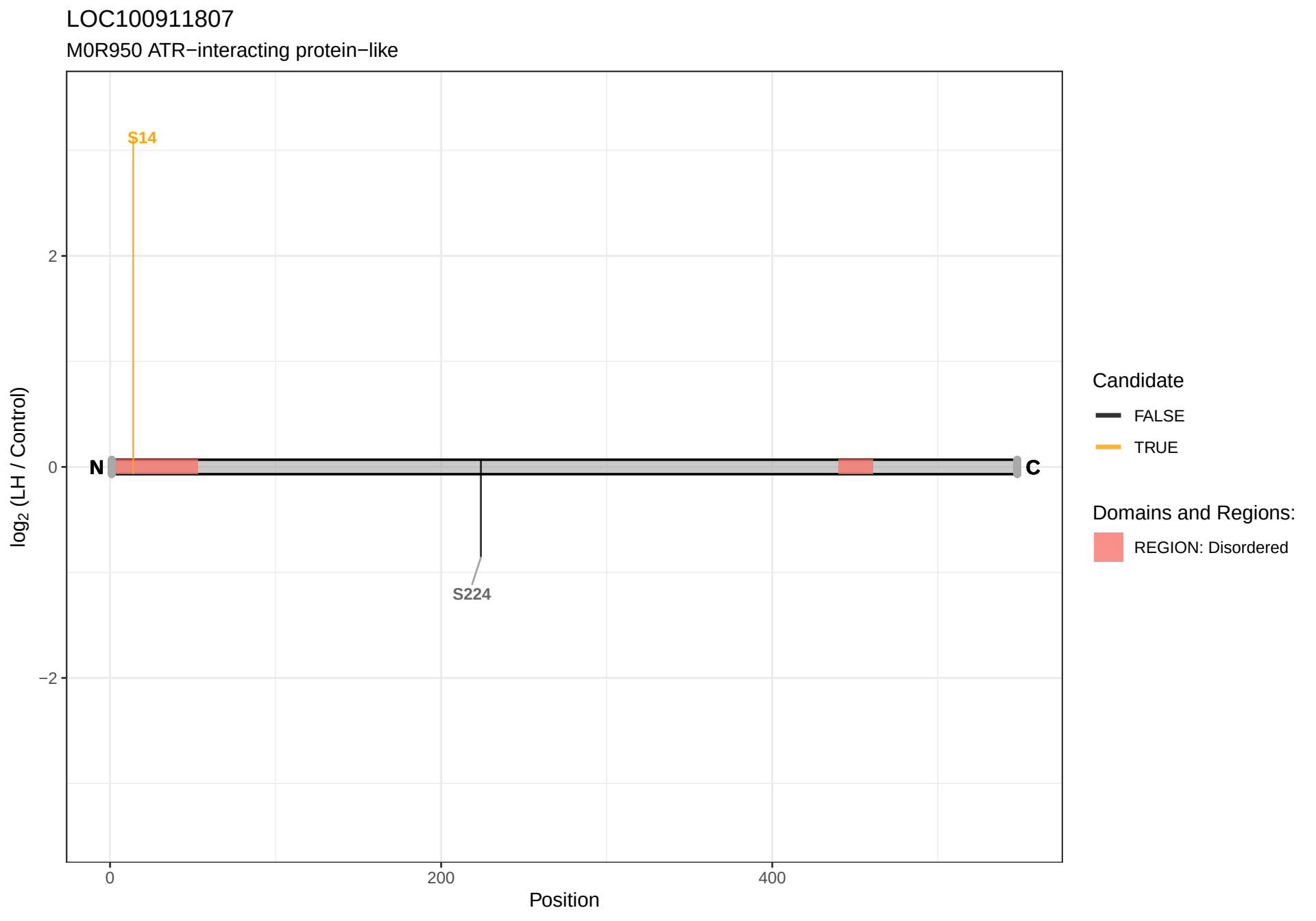

LOC100361087
F1M9N8 Hypothetical LOC100361087
S724
S723
S190
S187
S183
T207
S371
S759
S368
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PID
REGION: Disordered

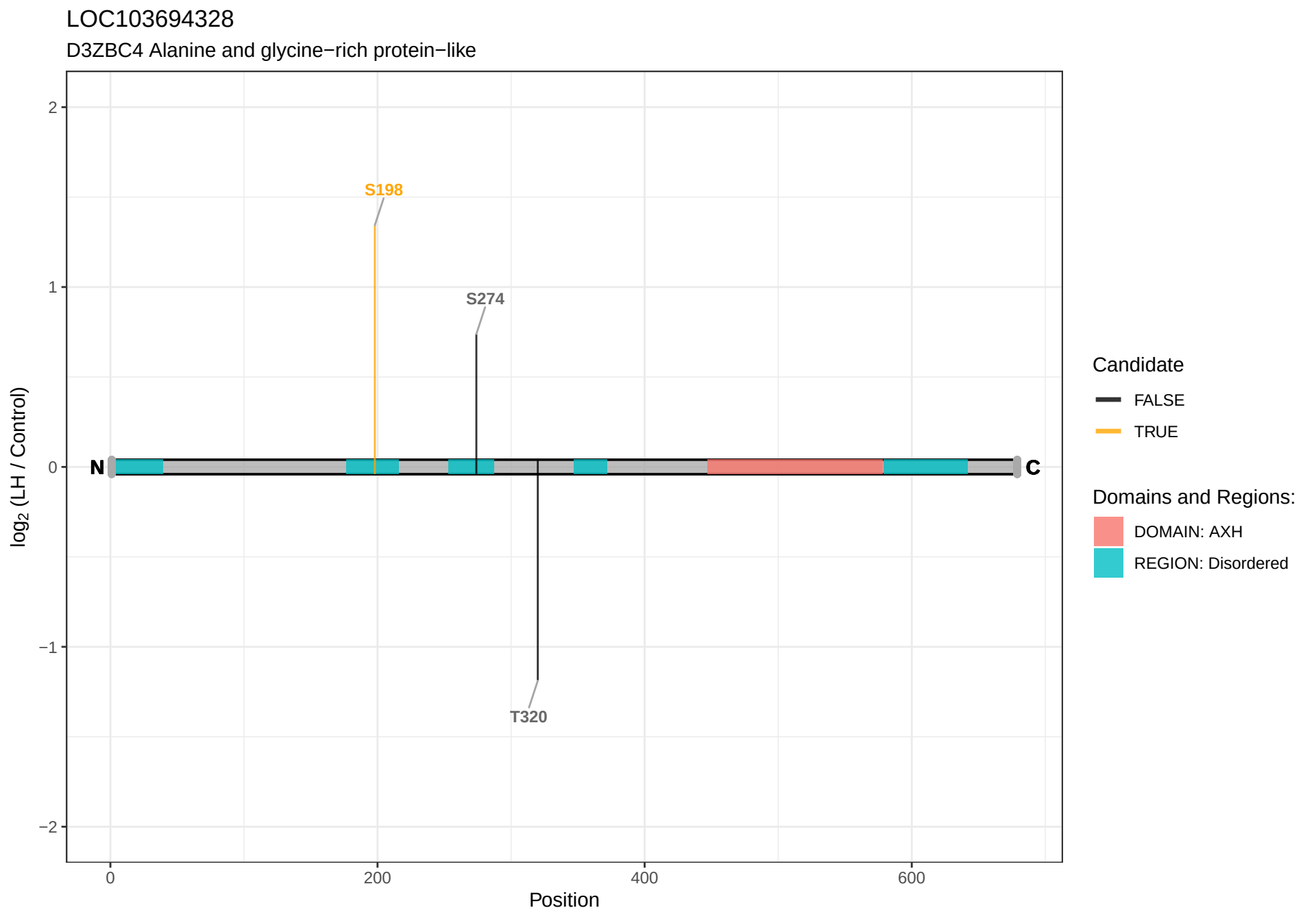

LOC100909664
D3ZET9 Centrosomal protein of 170 kDa−like
log2 (LH / Control)
2
1
0
−1
−2
N
C
S454
T458
S885
S24
S256
S276
S253
S368
S832
S882
S923
T872
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CEP170_C
REGION: Disordered

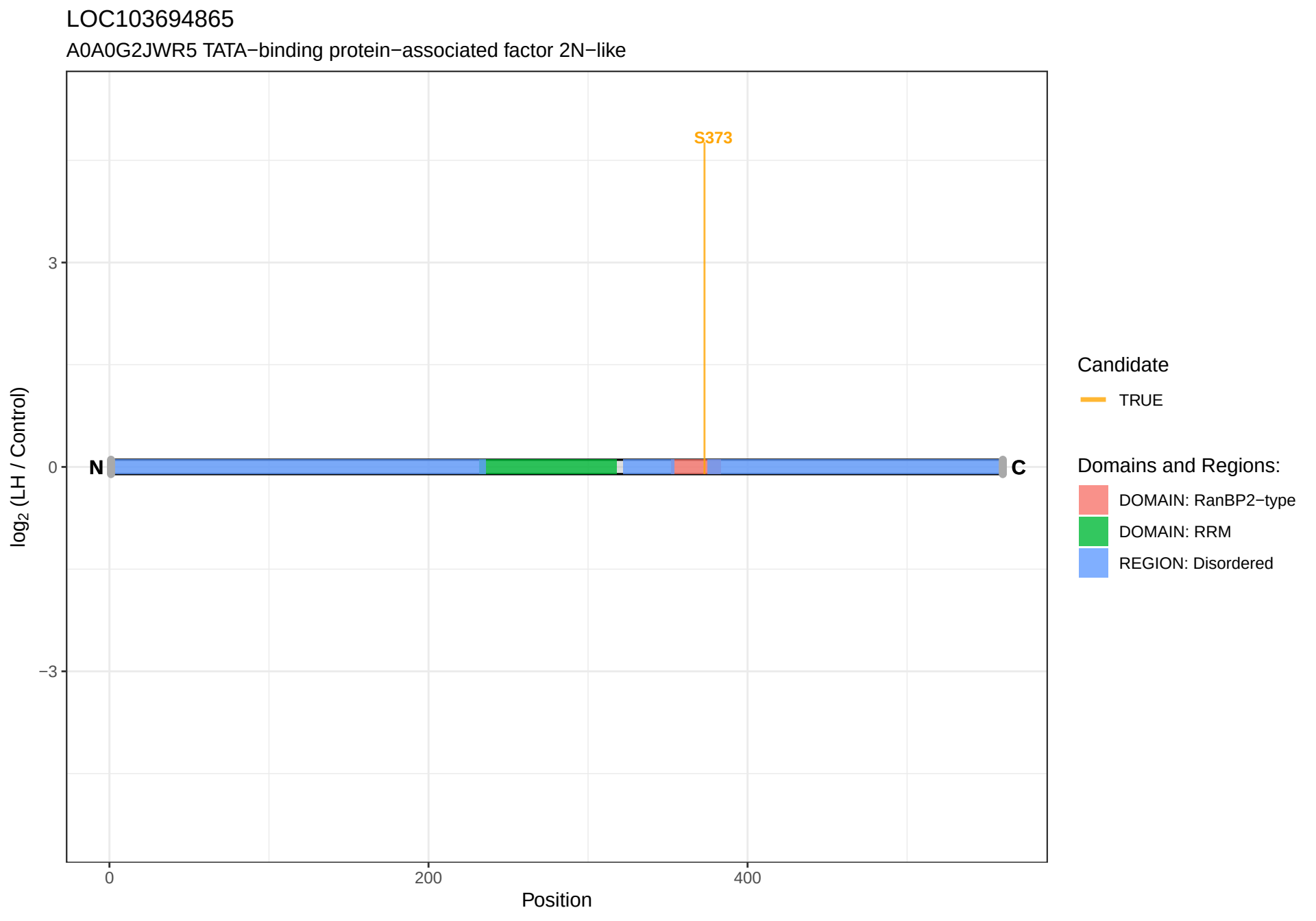

LOC100910540
G3V656 Methylphosphate−capping enzyme
S126
T188
S192
S191
S303
N
C
log2 (LH / Control)
Position
0
200
400
600
3
2
1
0
−1
−2
−3
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Bin3−type SAM
REGION: Disordered

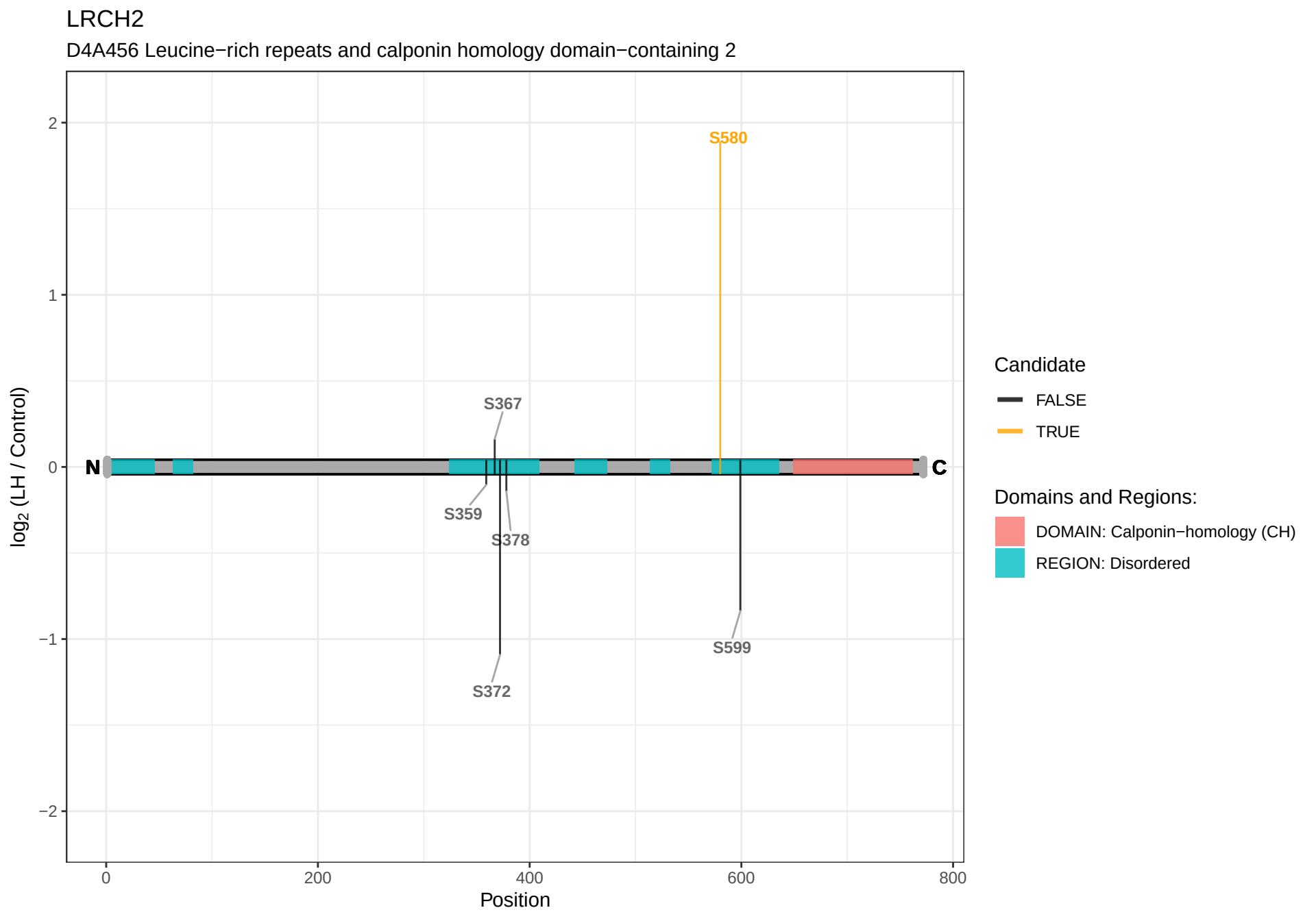

LOC100911516
M0R785 Coiled−coil−helix−coiled−coil−helix domain−containing protein 2, mitochondrial−like
log2 (LH / Control)
2
1
0
−1
−2
N
C
S46
0
50
100
150
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

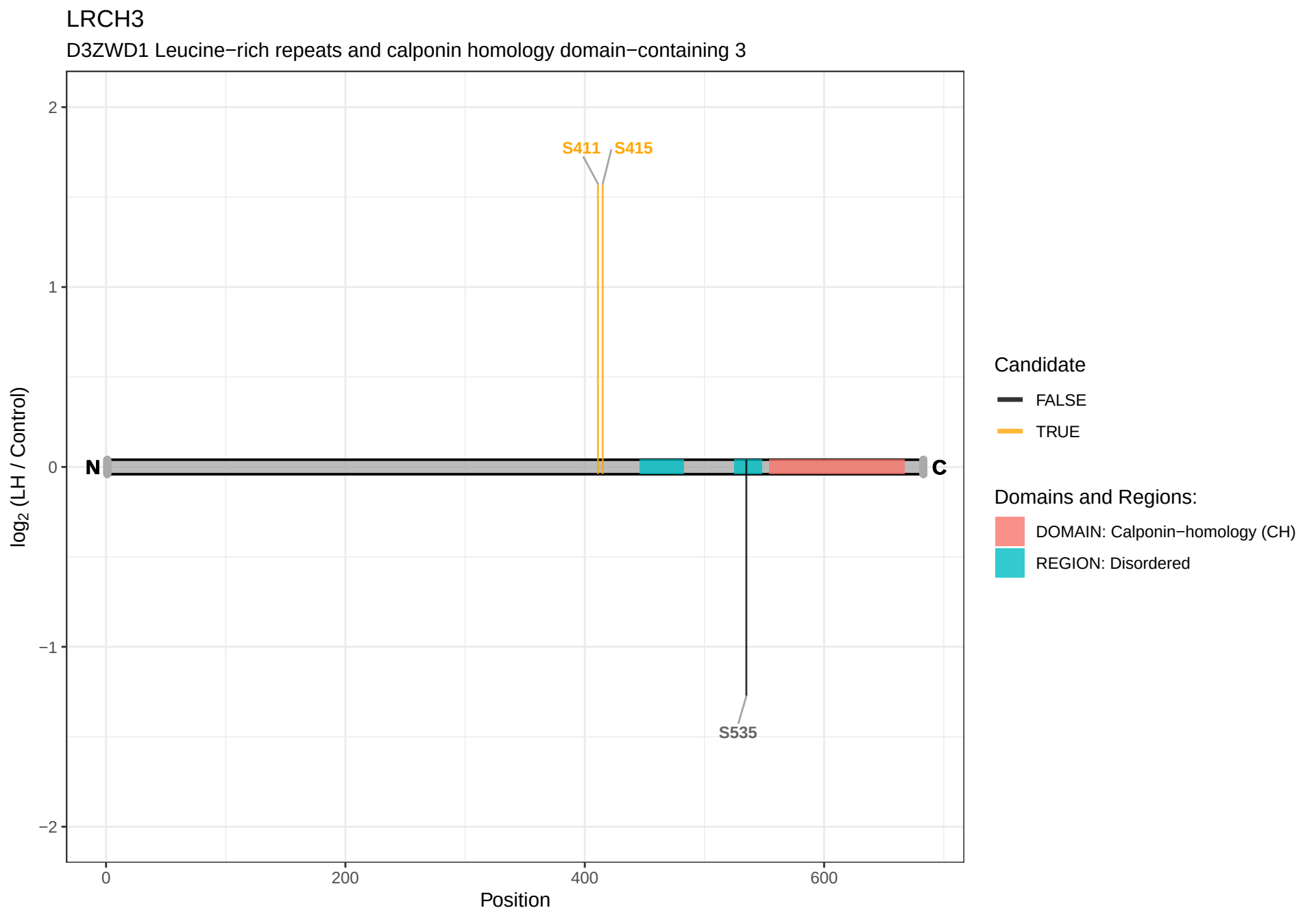

LOC100911660
A0A0G2K7M6 Lymphocyte−specific helicase−like
S498
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
800
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Helicase ATP−binding
DOMAIN: Helicase C−terminal
REGION: Disordered

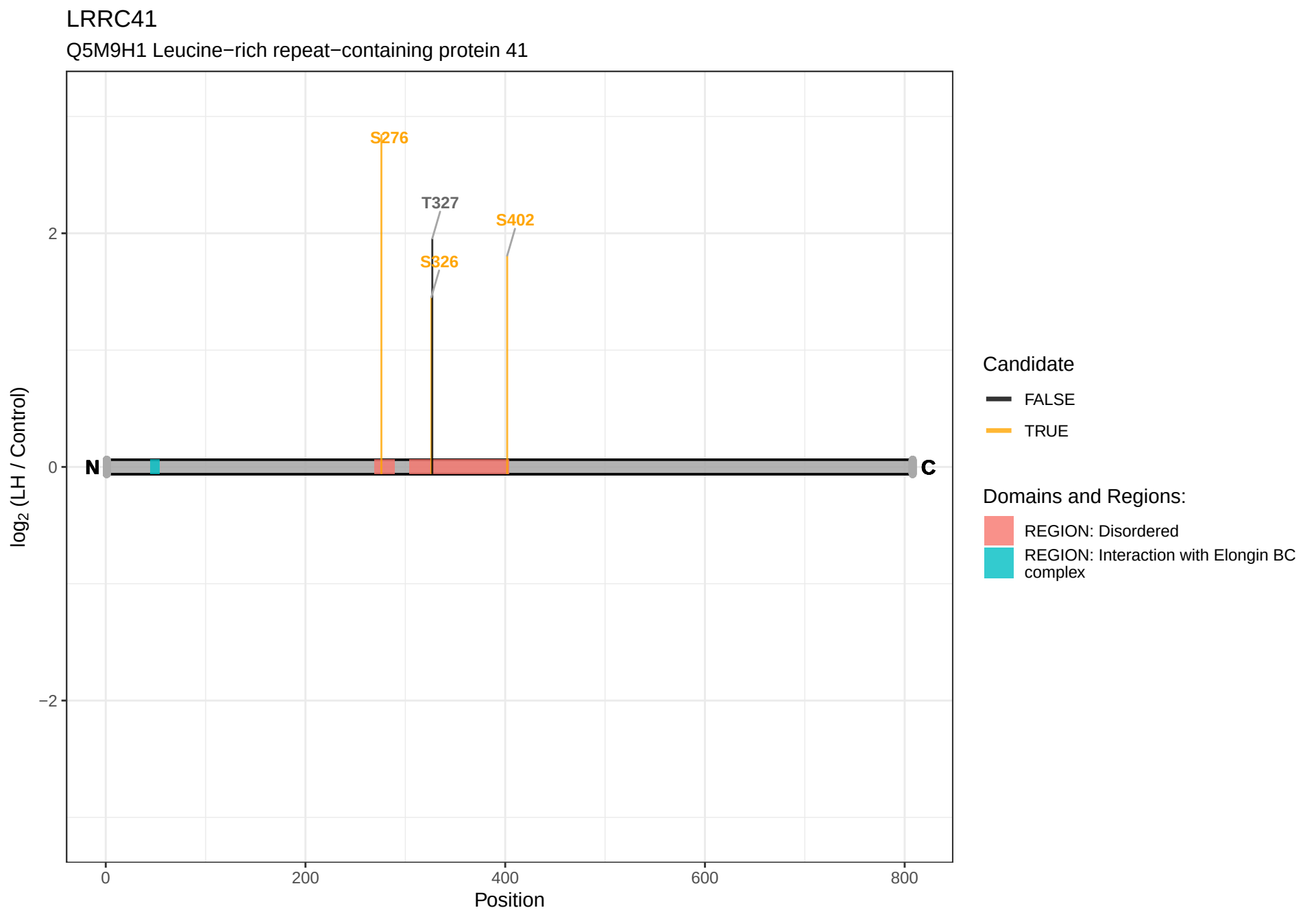

LOC100911807
M0R950 ATR−interacting protein−like
S14
S224
N
C
2
0
−2
log2 (LH / Control)
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

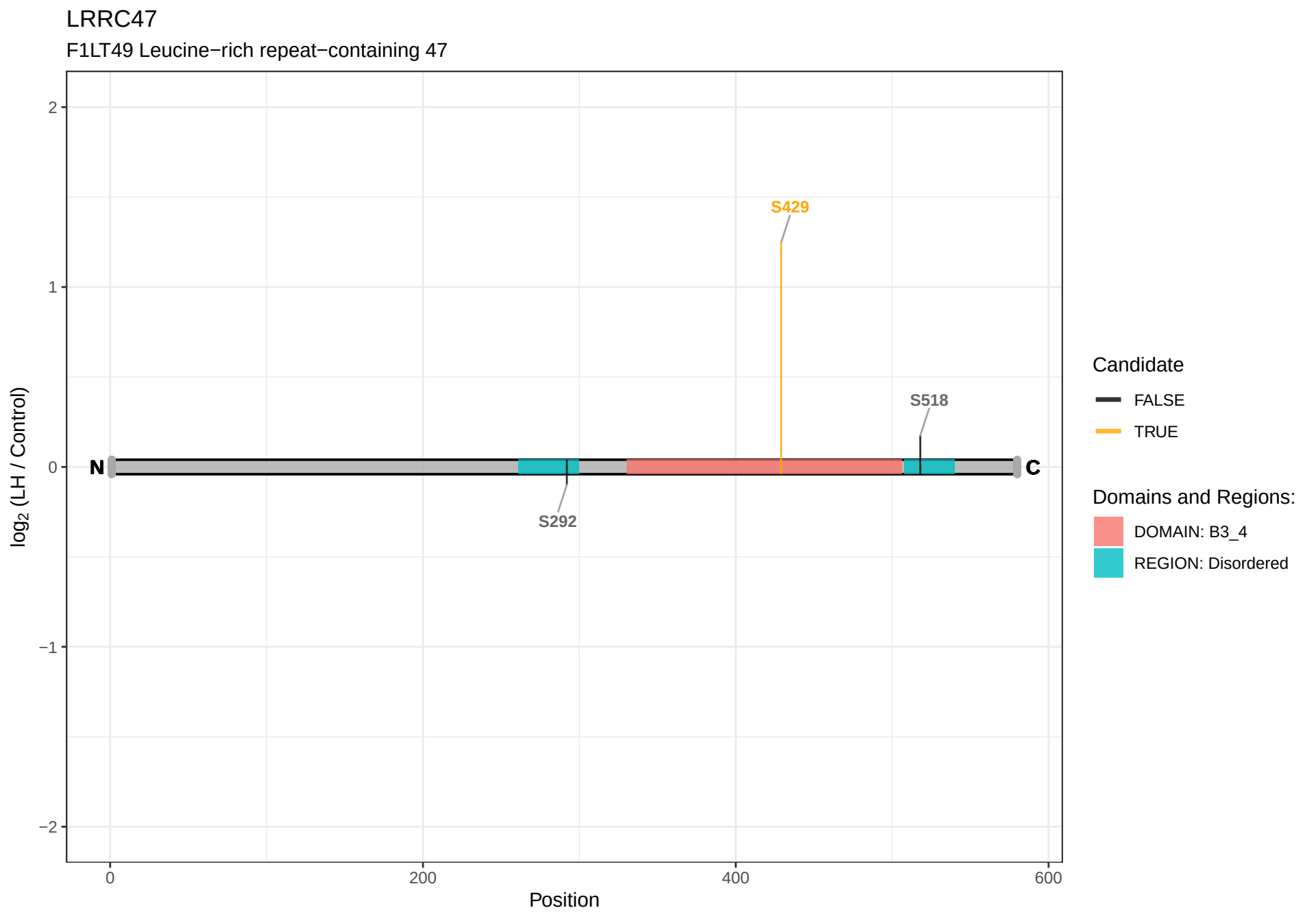

LOC103694328
D3ZBC4 Alanine and glycine−rich protein−like
S198
S274
T320
N
C
log2 (LH / Control)
Position
0
200
400
600
2
1
0
−1
−2
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AXH
REGION: Disordered

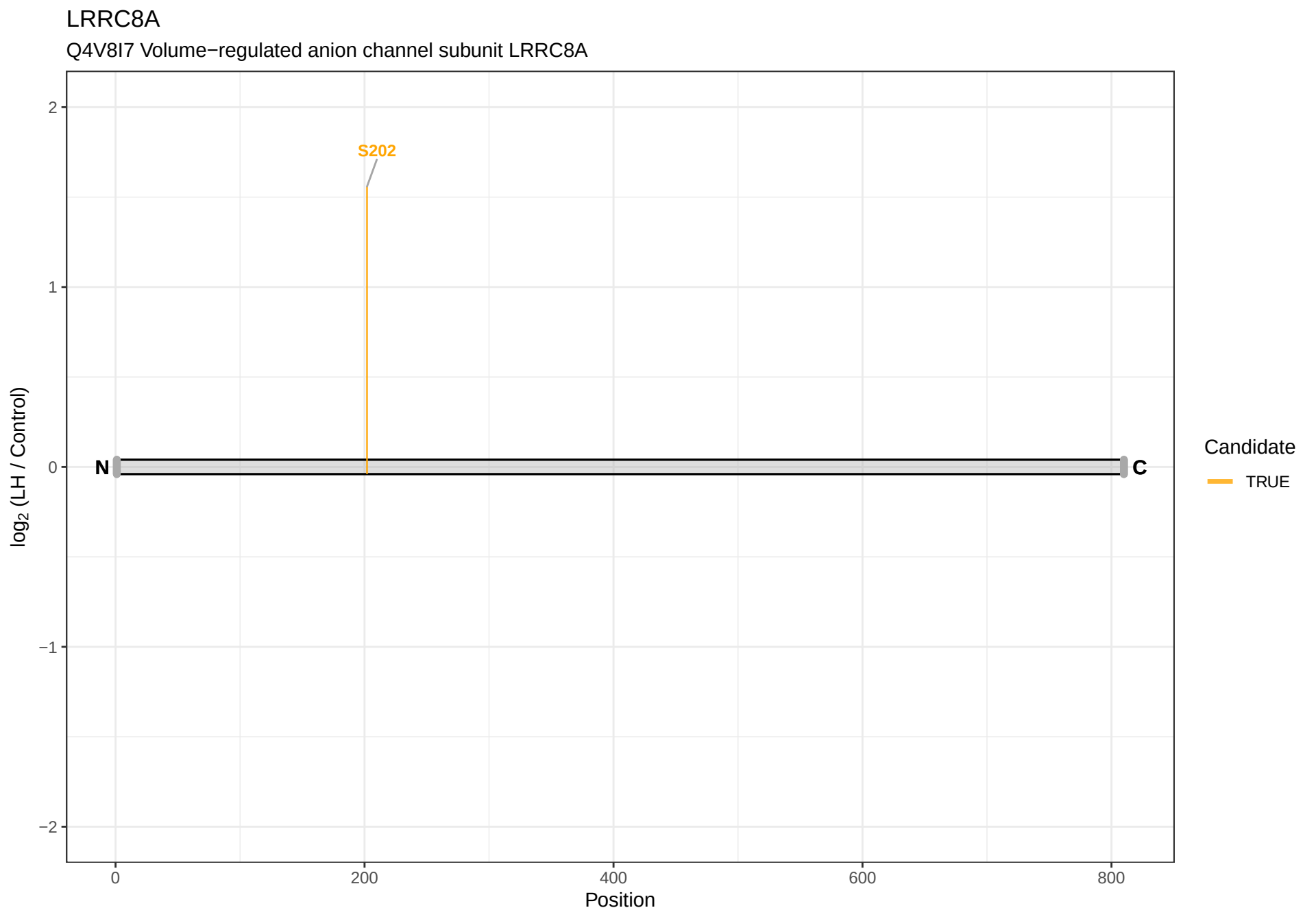

LOC103694865
A0A0G2JWR5 TATA−binding protein−associated factor 2N−like
S373
N
C
3
0
−3
log2 (LH / Control)
0
200
400
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: RanBP2−type
DOMAIN: RRM
REGION: Disordered

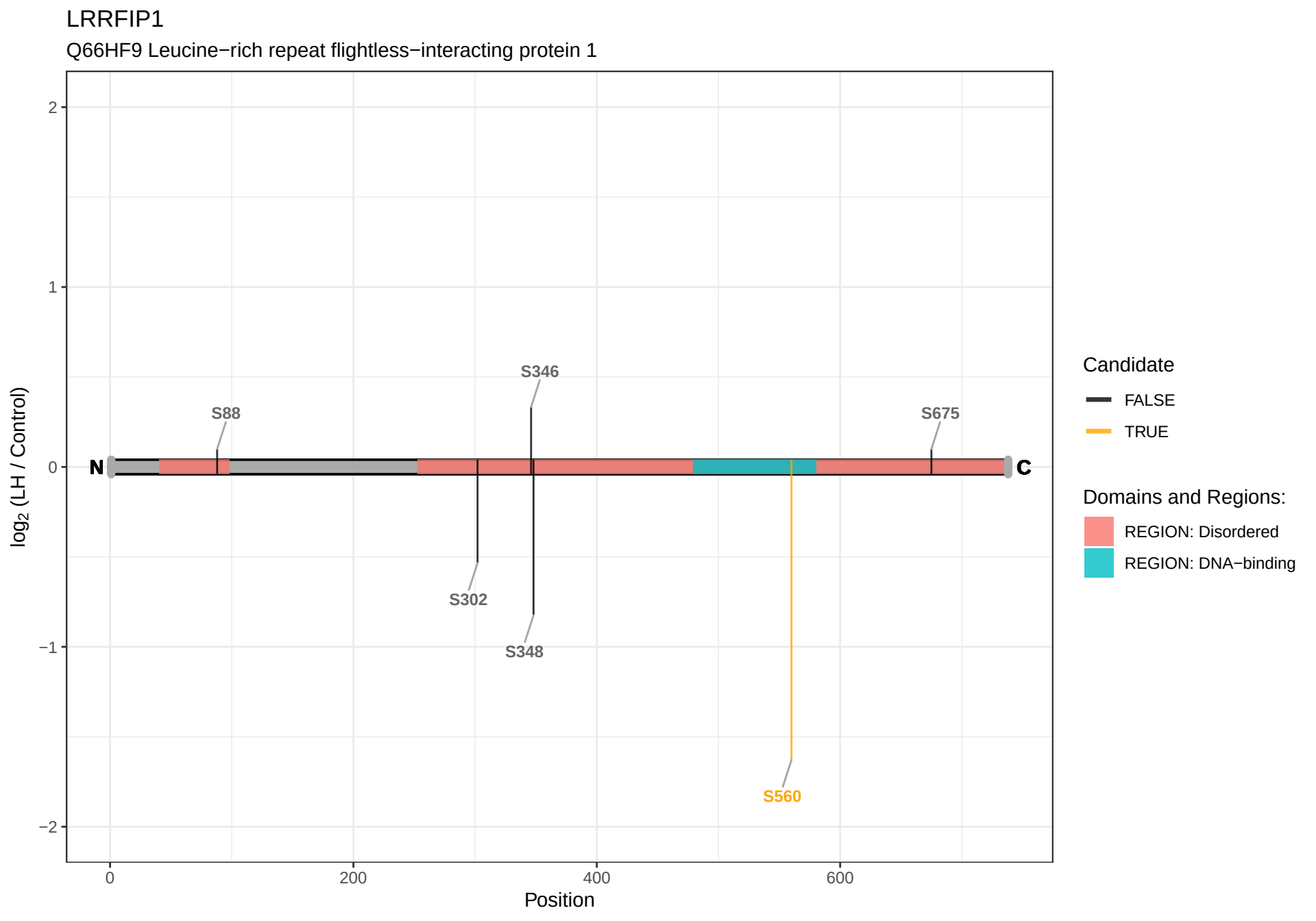

LRCH2
D4A456 Leucine−rich repeats and calponin homology domain−containing 2
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
800
Position
N
C
S580
S367
S359
S378
S372
S599
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Calponin−homology (CH)
REGION: Disordered

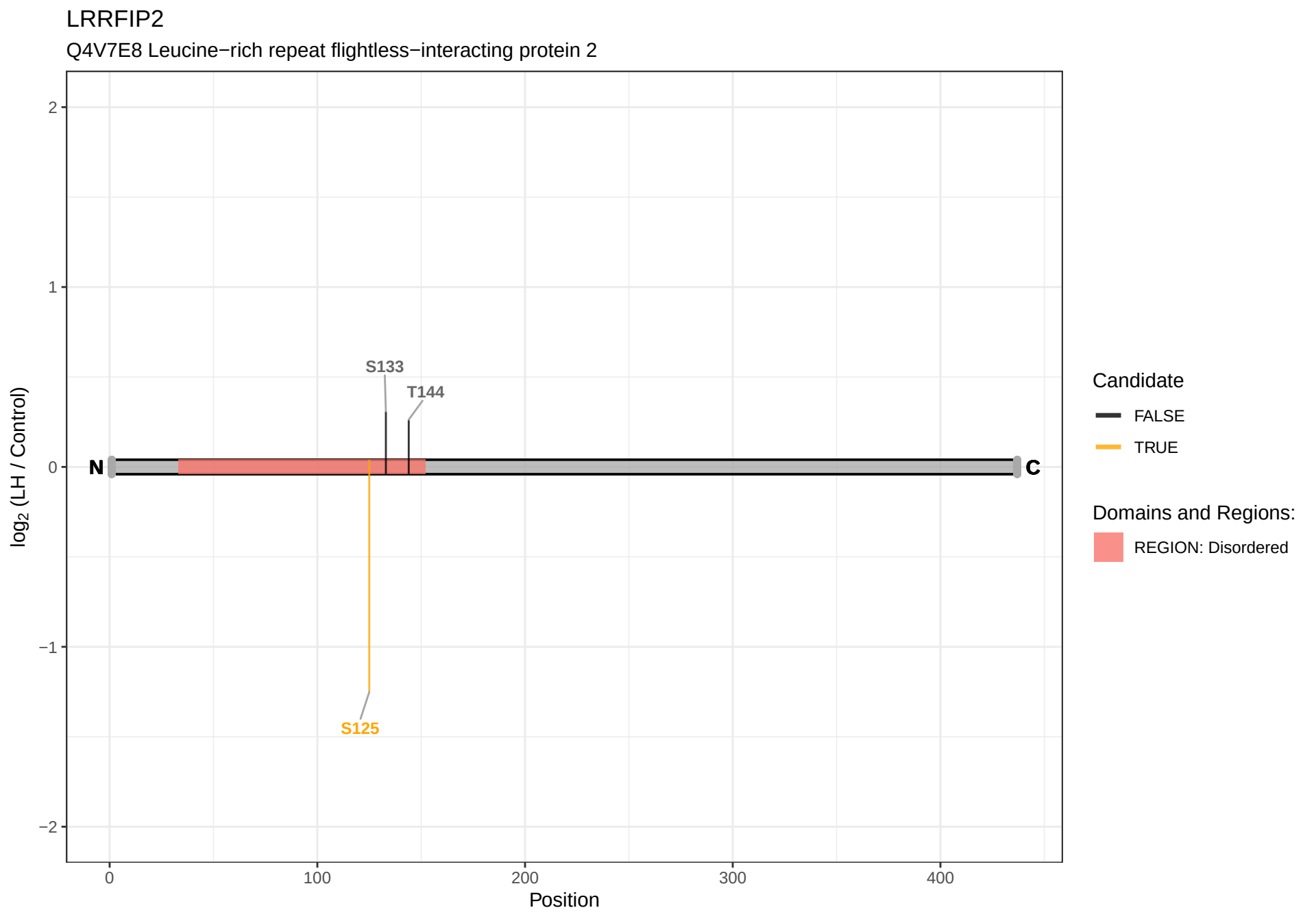

LRCH3
D3ZWD1 Leucine−rich repeats and calponin homology domain−containing 3
2
1
0
−1
−2
log2 (LH / Control)
S411
S415
S535
N
C
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Calponin−homology (CH)
REGION: Disordered

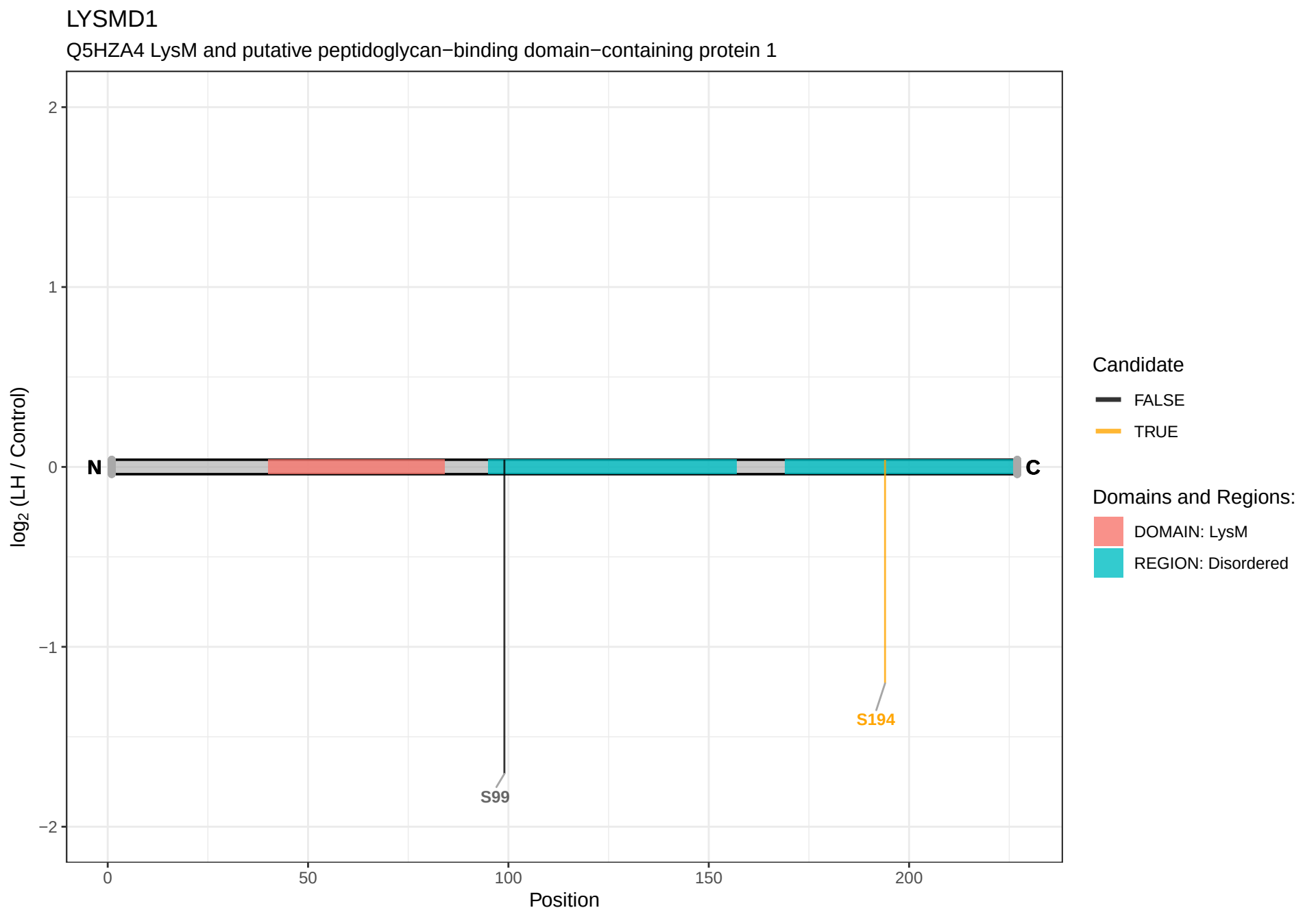

LRRC41
Q5M9H1 Leucine−rich repeat−containing protein 41
S276
T327
S402
S326
N
C
2
0
−2
log2 (LH / Control)
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Interaction with Elongin BC complex

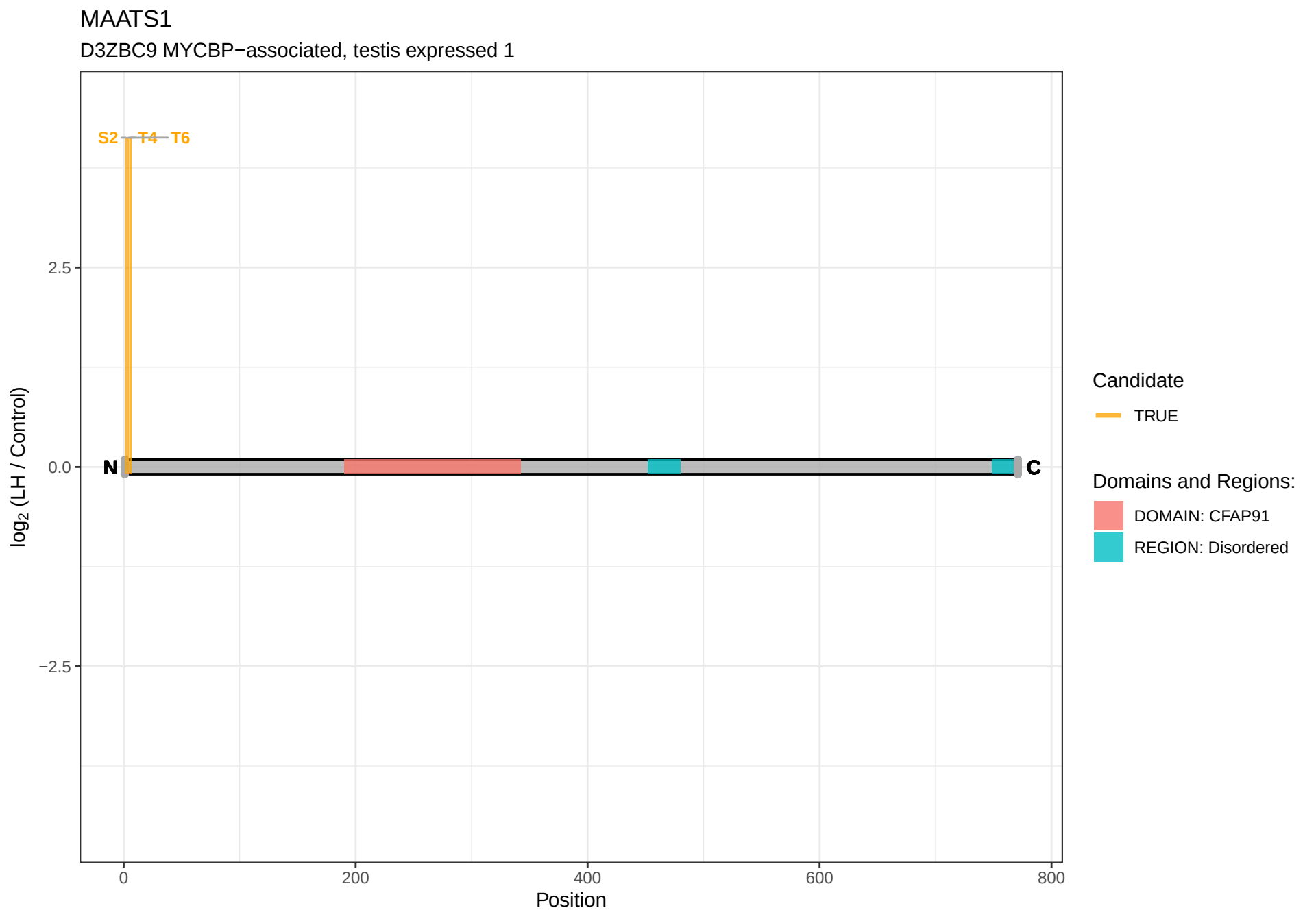

LRRC47
F1LT49 Leucine−rich repeat−containing 47
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
N
C
S429
S518
S292
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: B3_4
REGION: Disordered

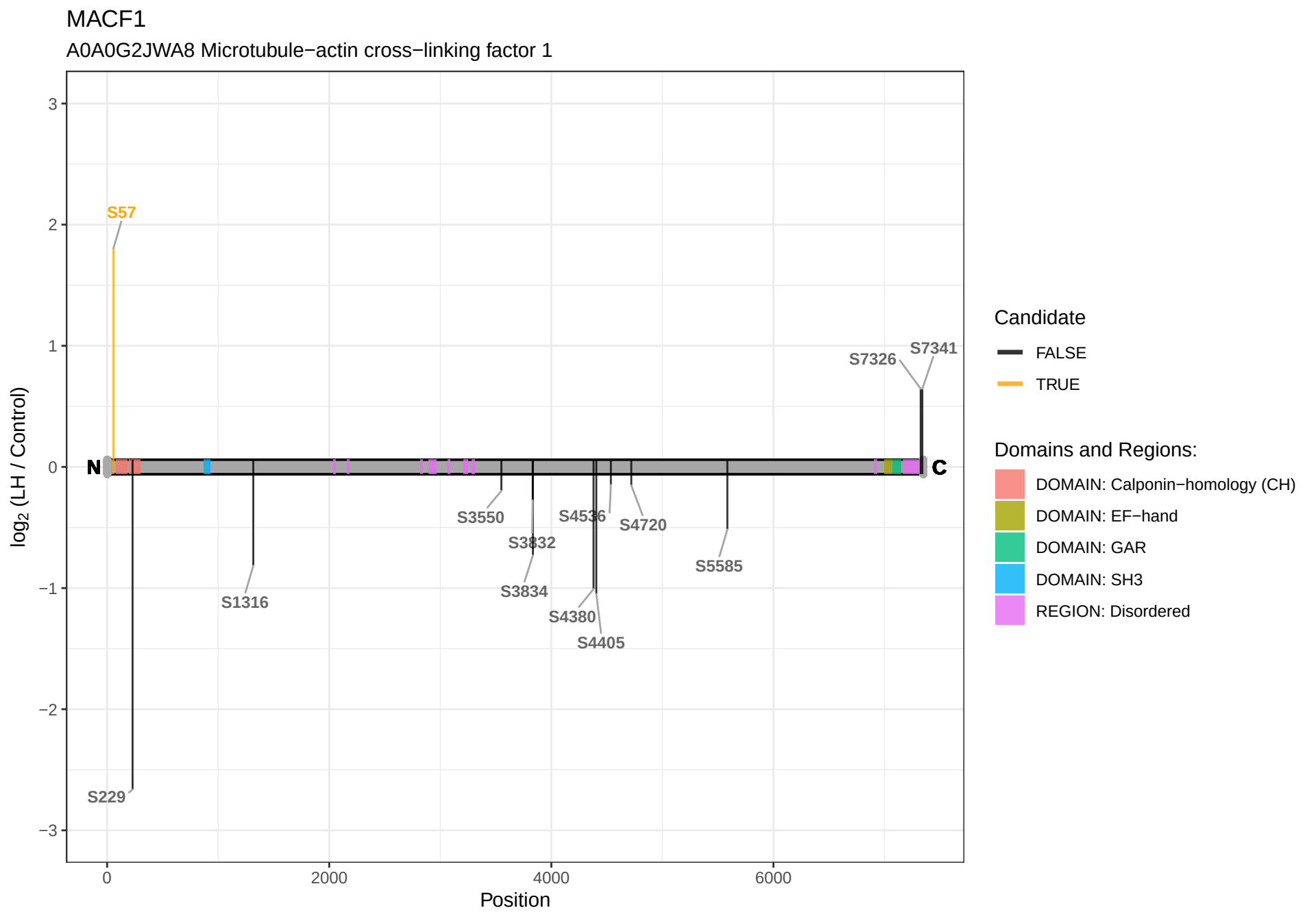

LRRC8A
Q4V8I7 Volume−regulated anion channel subunit LRRC8A
S202
N
C
2
1
0
−1
−2
0
200
400
600
800
Position
log2 (LH / Control)
Candidate
TRUE

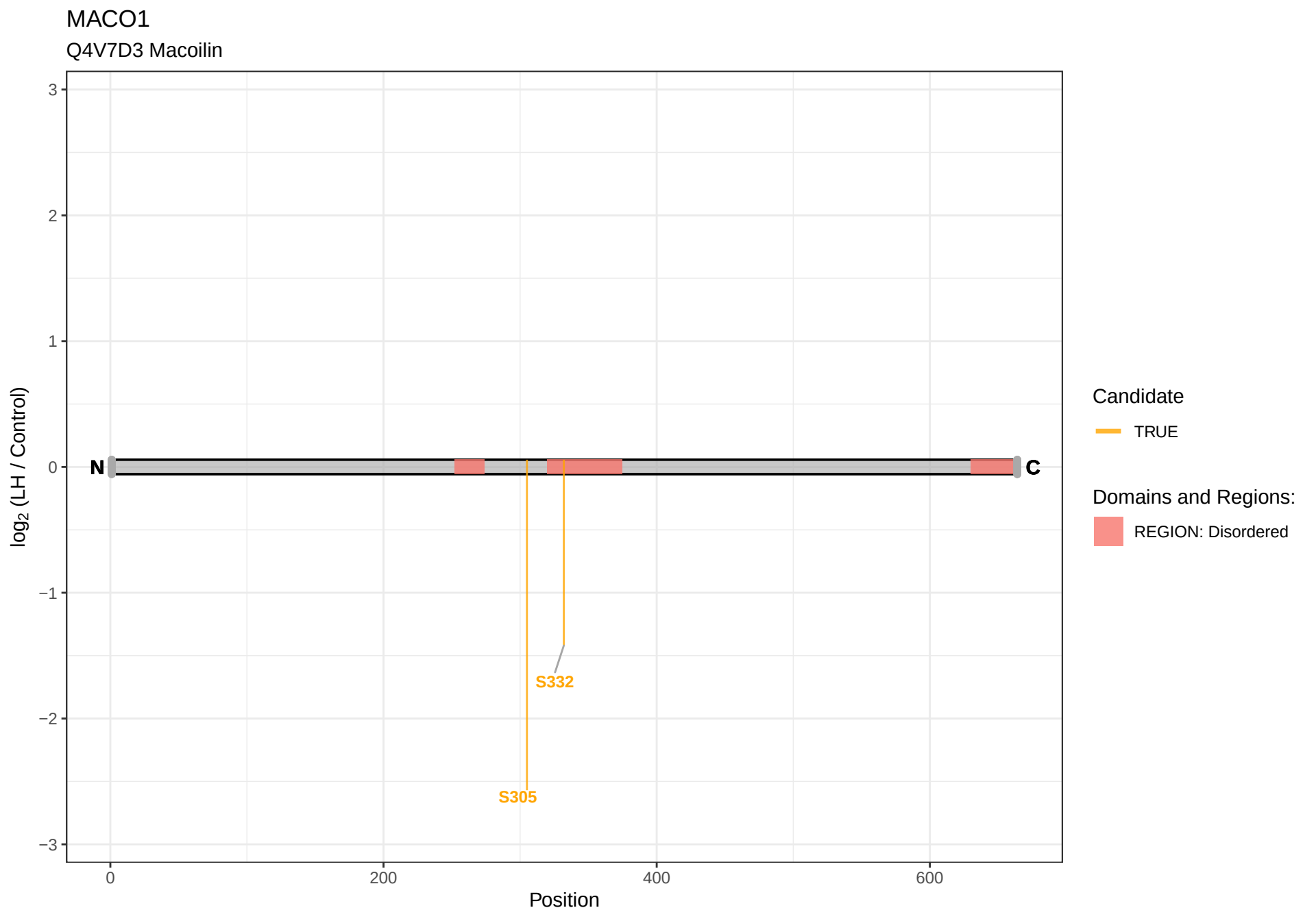

LRRFIP1
Q66HF9 Leucine−rich repeat flightless−interacting protein 1
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
N
C
S88
S346
S675
S302
S348
S560
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: DNA−binding

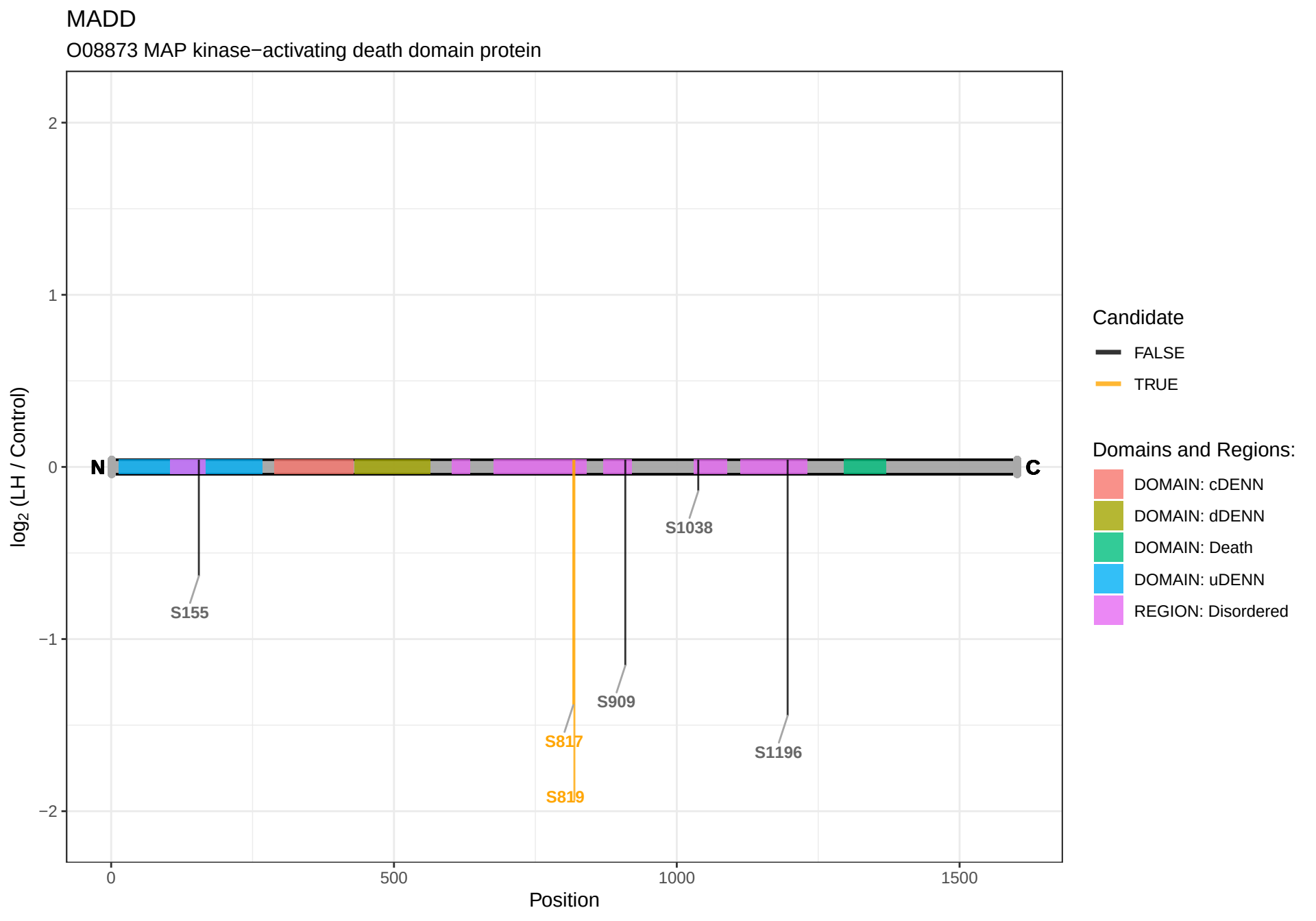

LRRFIP2
Q4V7E8 Leucine−rich repeat flightless−interacting protein 2
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
400
Position
N
C
S133
T144
S125
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

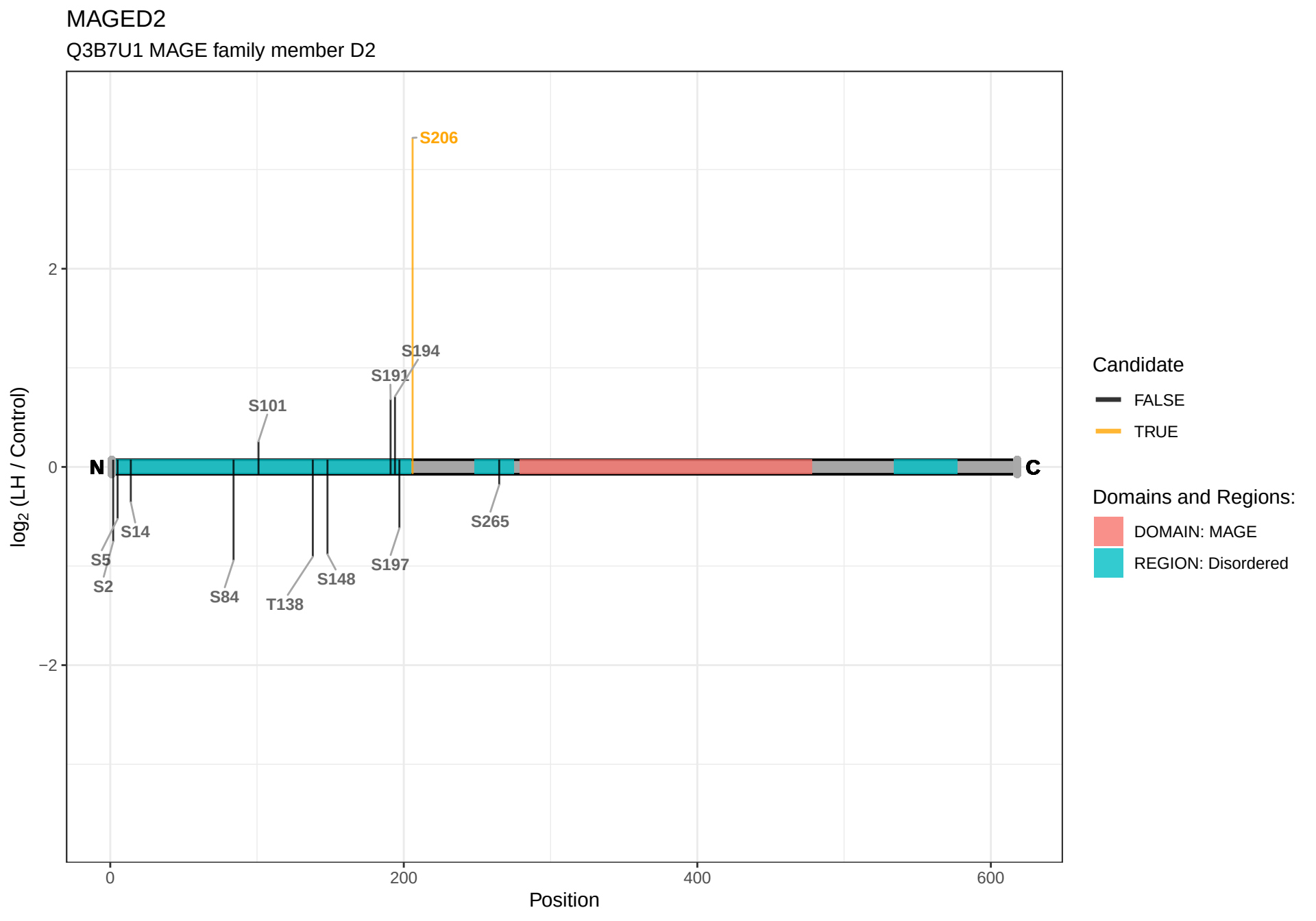

LYSMD1
Q5HZA4 LysM and putative peptidoglycan−binding domain−containing protein 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S99
S194
0
50
100
150
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: LysM
REGION: Disordered

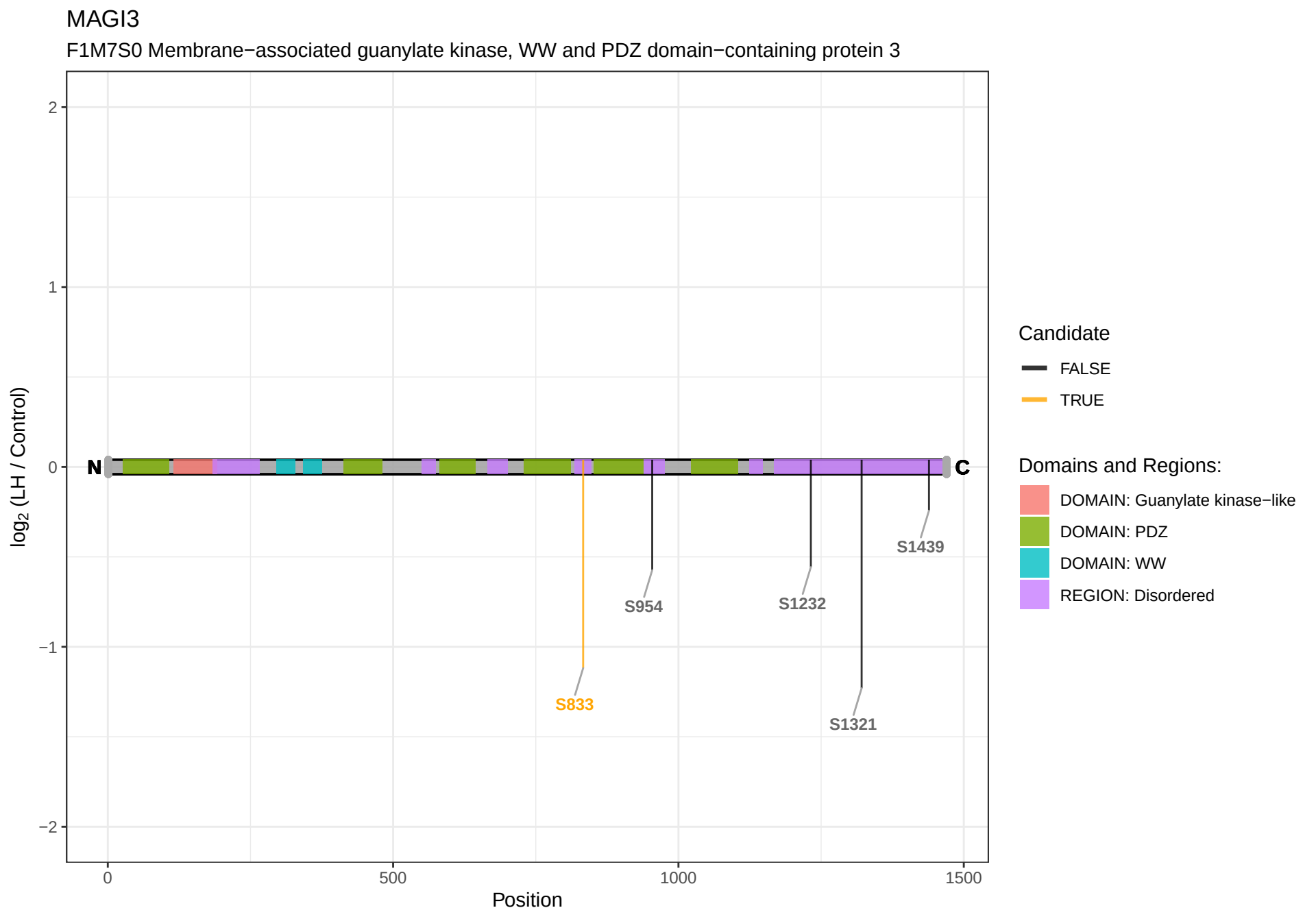

MAATS1
D3ZBC9 MYCBP−associated, testis expressed 1
S2
T4
T6
N
C
2.5
0.0
−2.5
log2 (LH / Control)
0
200
400
600
800
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: CFAP91
REGION: Disordered

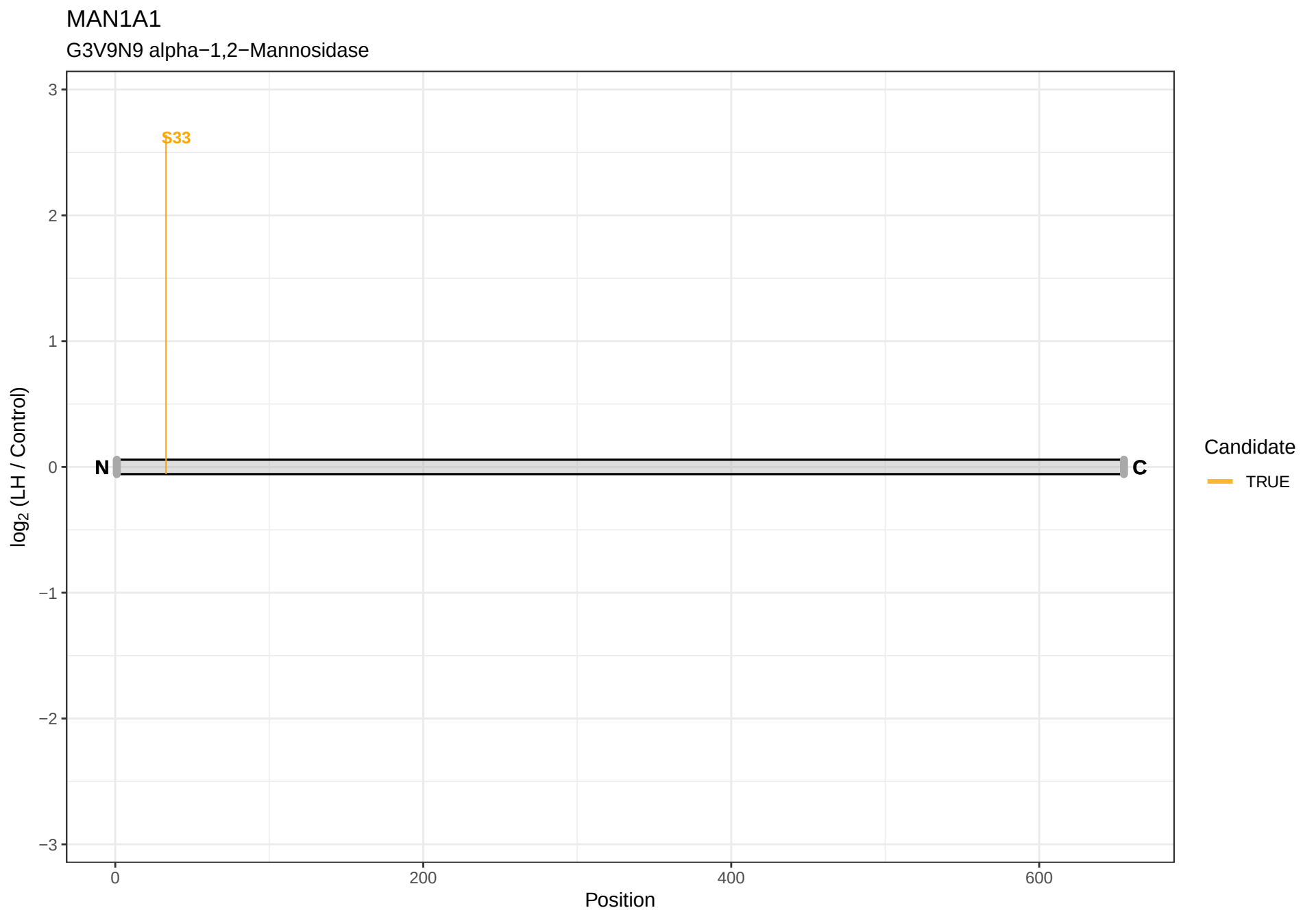

MACF1
A0A0G2JWA8 Microtubule−actin cross−linking factor 1
log2 (LH / Control)
Position
N
C
S57
S229
S1316
S3550
S3832
S3834
S4380
S4405
S4536
S4720
S5585
S7326
S7341
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Calponin−homology (CH)
DOMAIN: EF−hand
DOMAIN: GAR
DOMAIN: SH3
REGION: Disordered

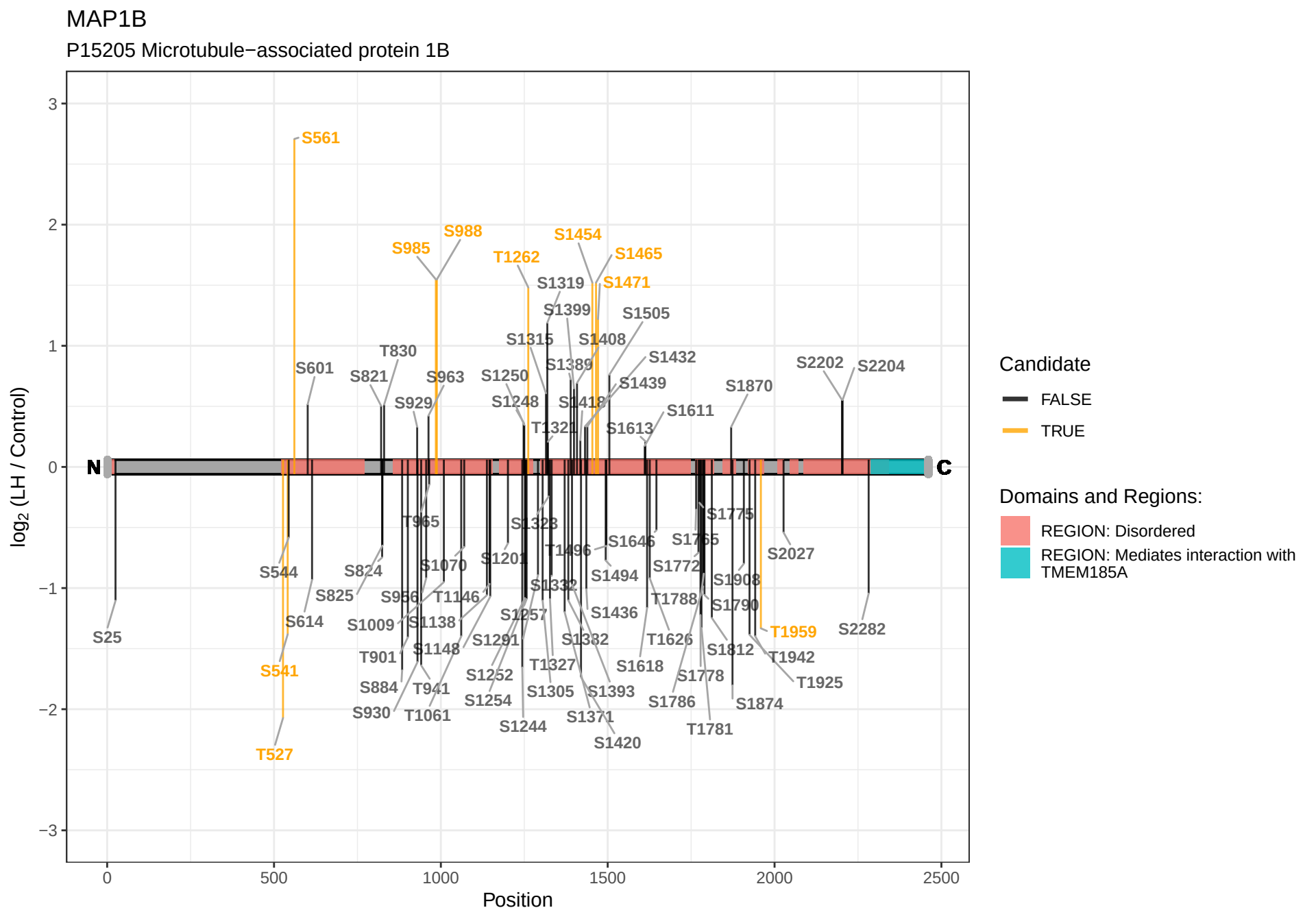

MACO1
Q4V7D3 Macoilin
3
2
1
0
−1
−2
−3
log2 (LH / Control)
N
C
S332
S305
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

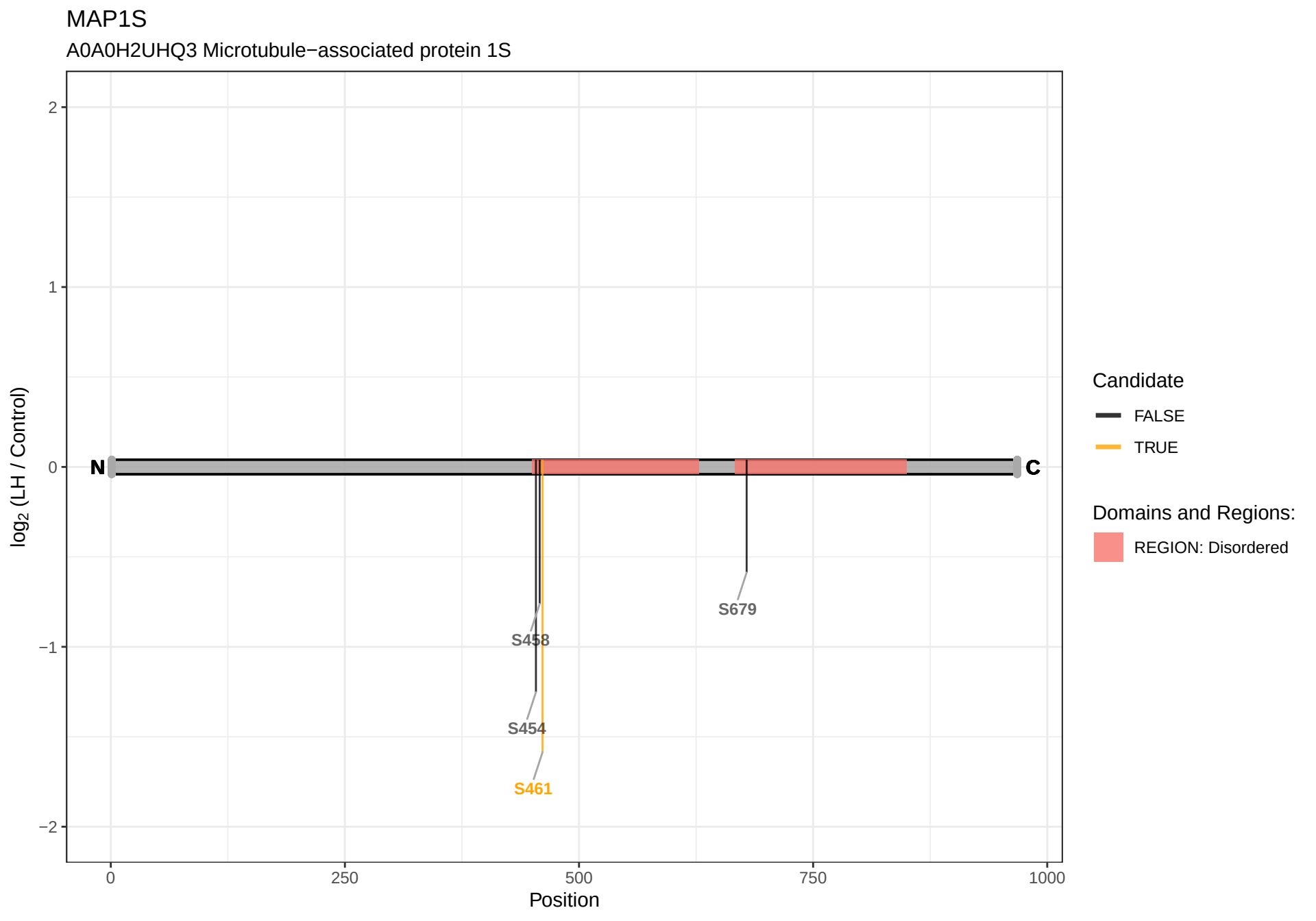

MADD
O08873 MAP kinase−activating death domain protein
log2 (LH / Control)
2
1
0
−1
−2
N
C
S155
S1038
S909
S817
S819
S1196
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: cDENN
DOMAIN: dDENN
DOMAIN: Death
DOMAIN: uDENN
REGION: Disordered

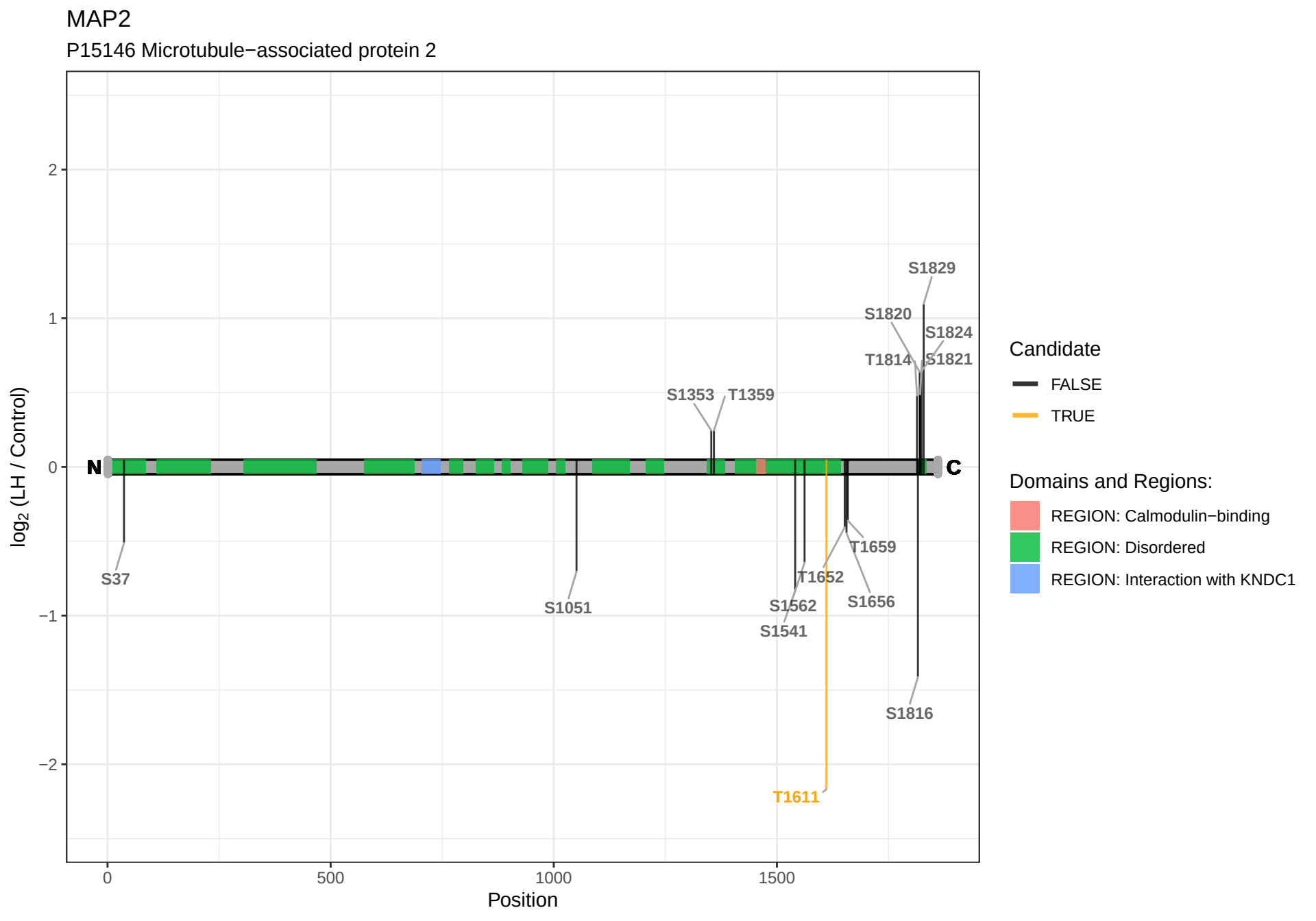

MAGED2
Q3B7U1 MAGE family member D2
S206
S194
S191
S101
N
C
S14
S5
S2
S84
T138
S148
S197
S265
2
0
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: MAGE
REGION: Disordered

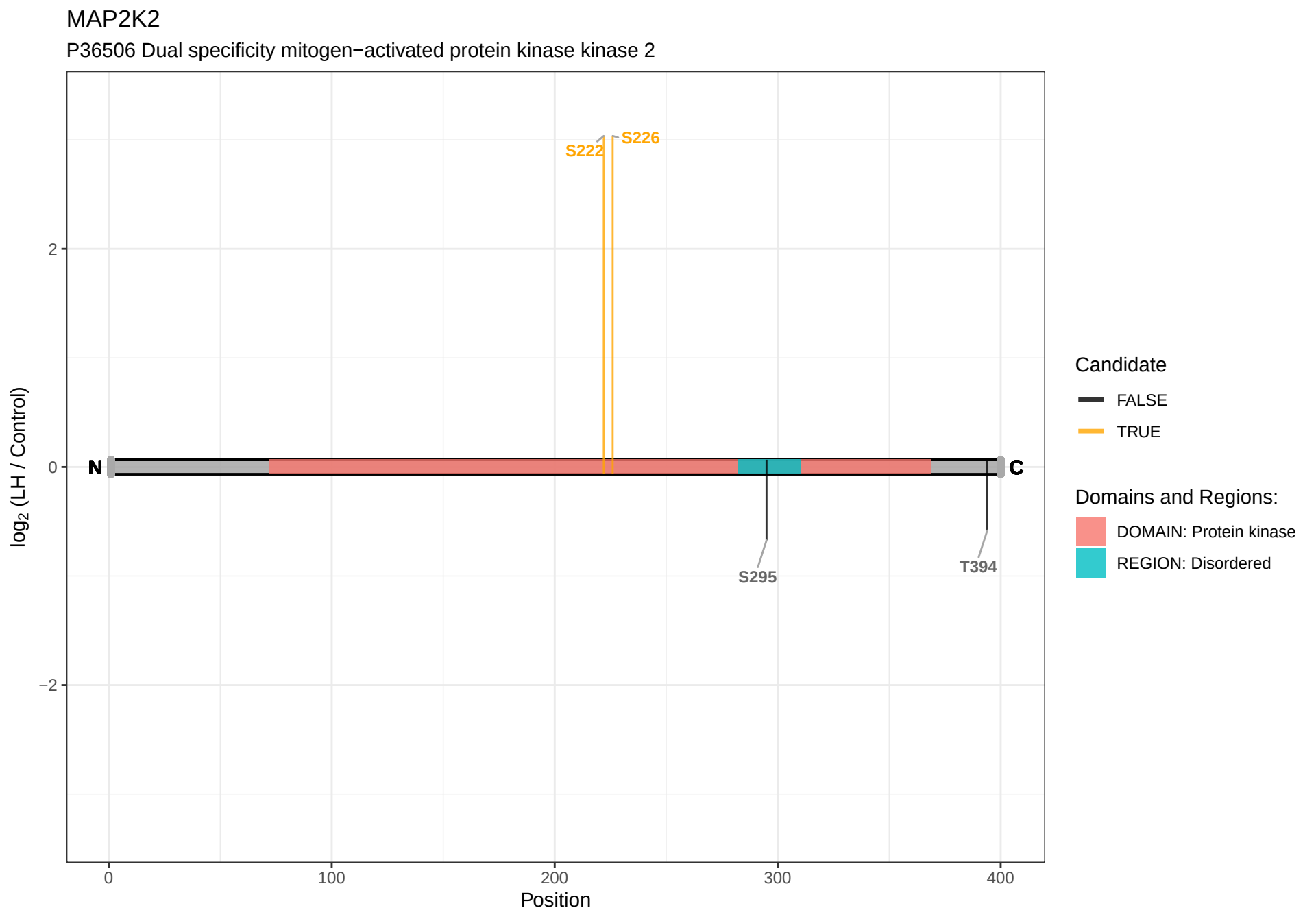

MAGI3
F1M7S0 Membrane−associated guanylate kinase, WW and PDZ domain−containing protein 3
log2 (LH / Control)
2
1
0
−1
−2
N
C
S833
S954
S1232
S1321
S1439
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Guanylate kinase−like
DOMAIN: PDZ
DOMAIN: WW
REGION: Disordered

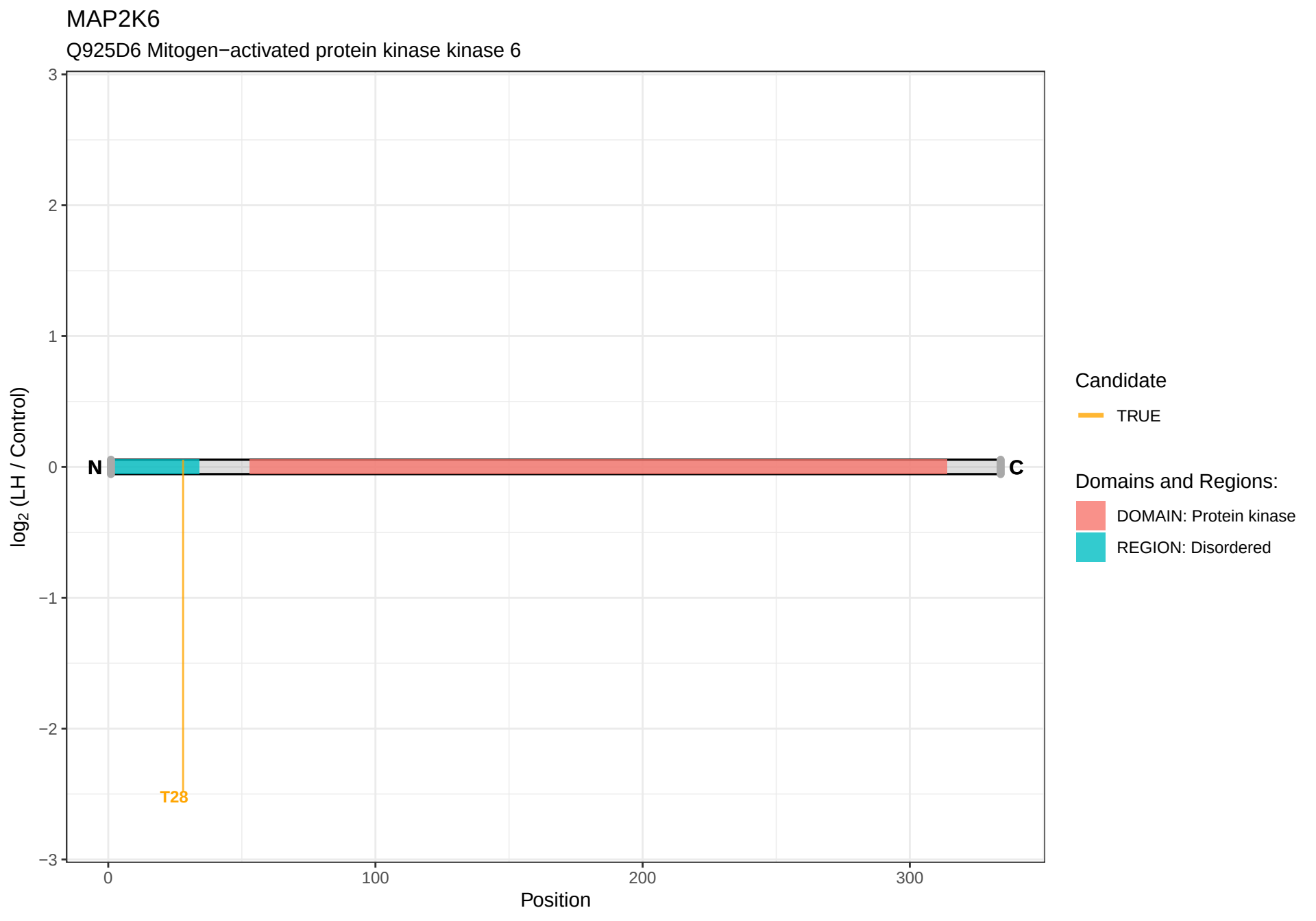

MAN1A1
G3V9N9 alpha−1,2−Mannosidase
S33
N
C
log2 (LH / Control)
Position
0
200
400
600
3
2
1
0
−1
−2
−3
Candidate
TRUE

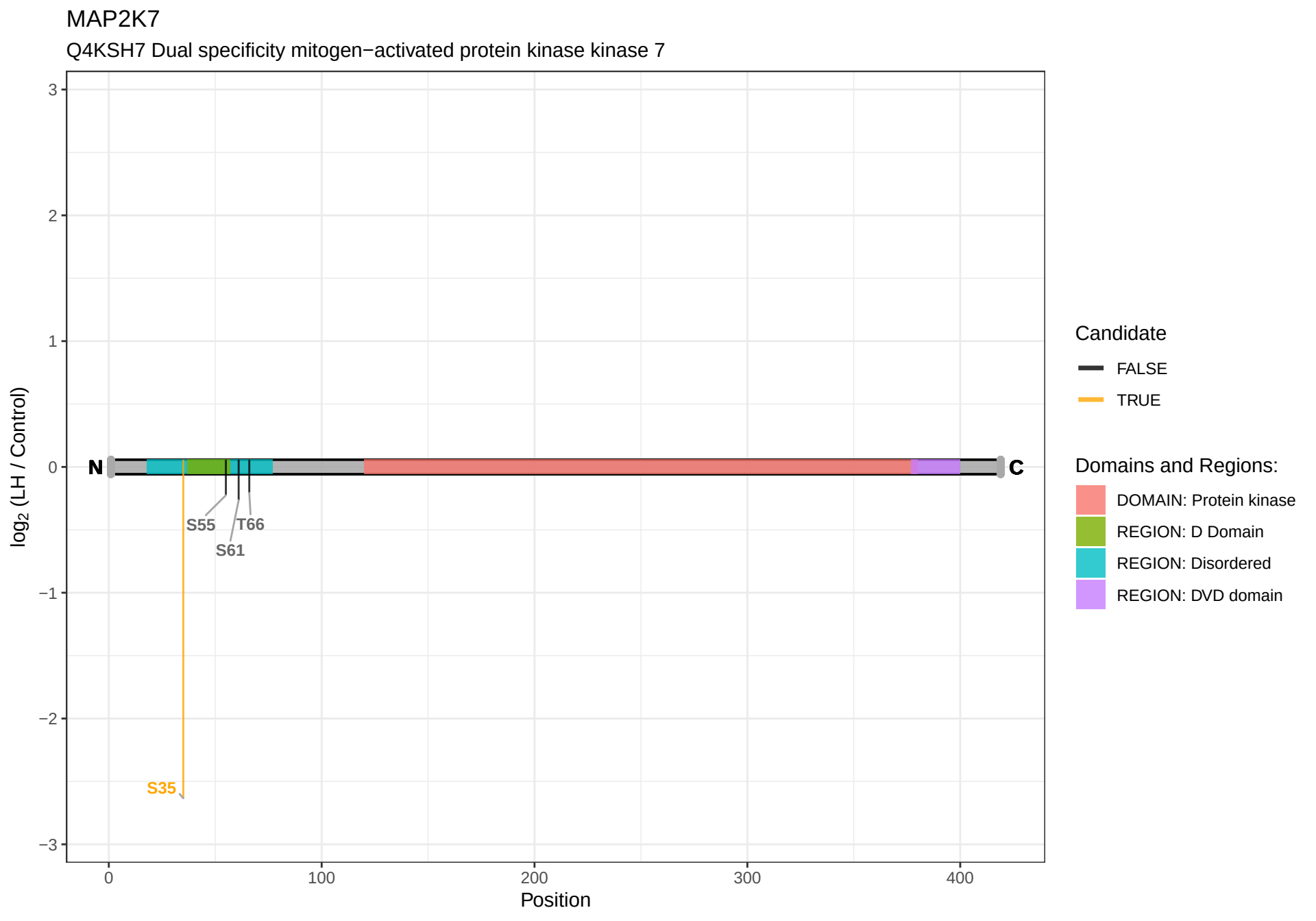

MAP1B
P15205 Microtubule−associated protein 1B
log2 (LH / Control)
Position
N
C
S561
S985
S988
T1262
S1454
S1465
S1471
S1319
S1399
S1505
S1315
S1408
S1432
S1389
S1439
S1250
S1248
S1418
S1611
S1613
T1321
S601
S821
T830
S963
S929
S1870
S2202
S2204
S1775
S1765
S1646
S1496
S1323
S1201
S1070
S1772
S1908
S1494
S1332
S1790
S1788
S1436
S1257
S1291
S1382
T1626
S1812
T1959
S2282
T1942
T1925
S1778
S1618
T1327
S1393
S1305
S1254
S1252
S1244
S1371
S1420
S1786
S1874
T1781
S1148
S1138
S1009
S956
T1146
S824
S825
S544
S614
S25
S541
T527
T965
T901
S884
T941
S930
T1061
S2027
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Mediates interaction with TMEM185A

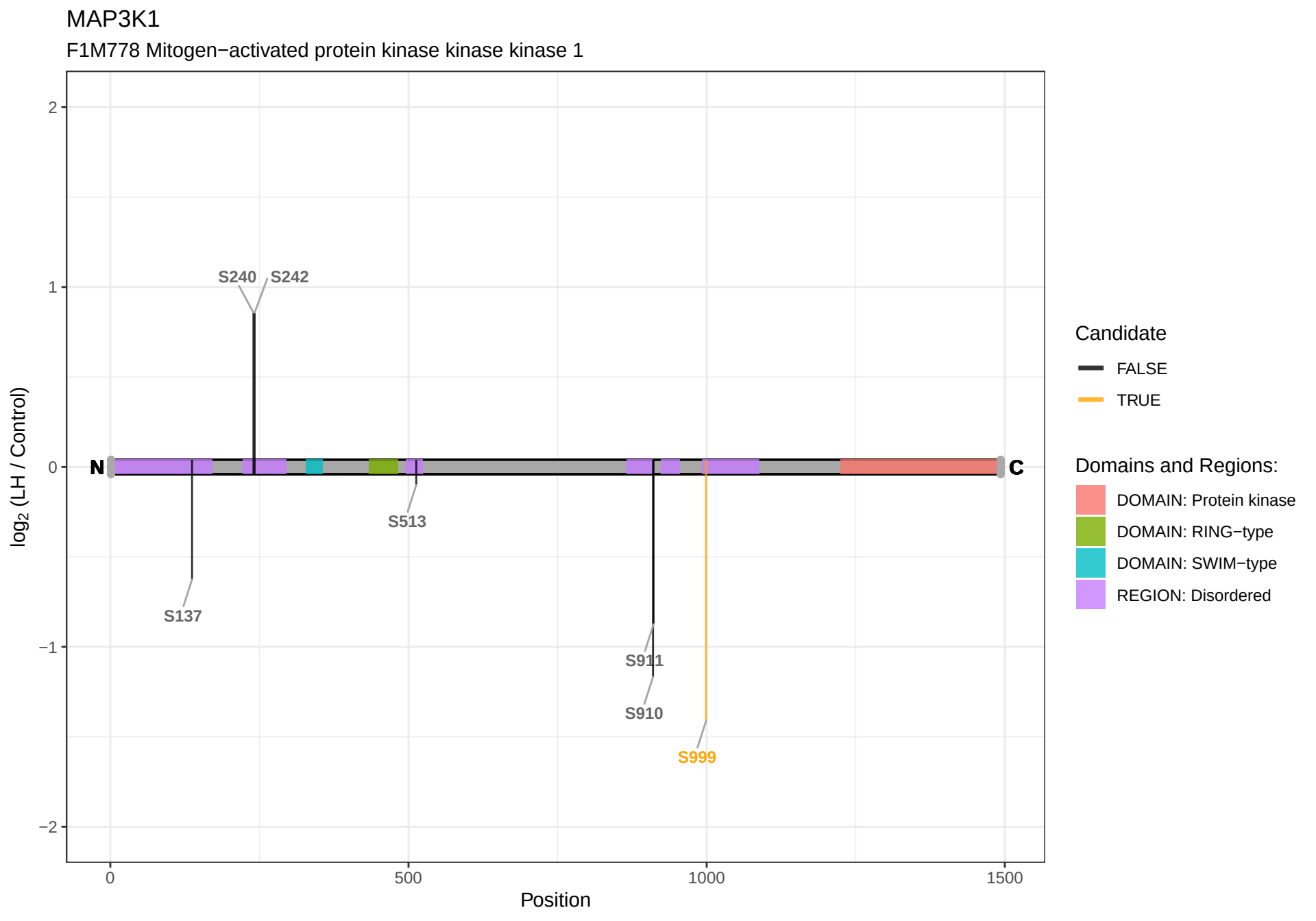

MAP1S
A0A0H2UHQ3 Microtubule−associated protein 1S
log2 (LH / Control)
2
1
0
−1
−2
N
C
S458
S454
S461
S679
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

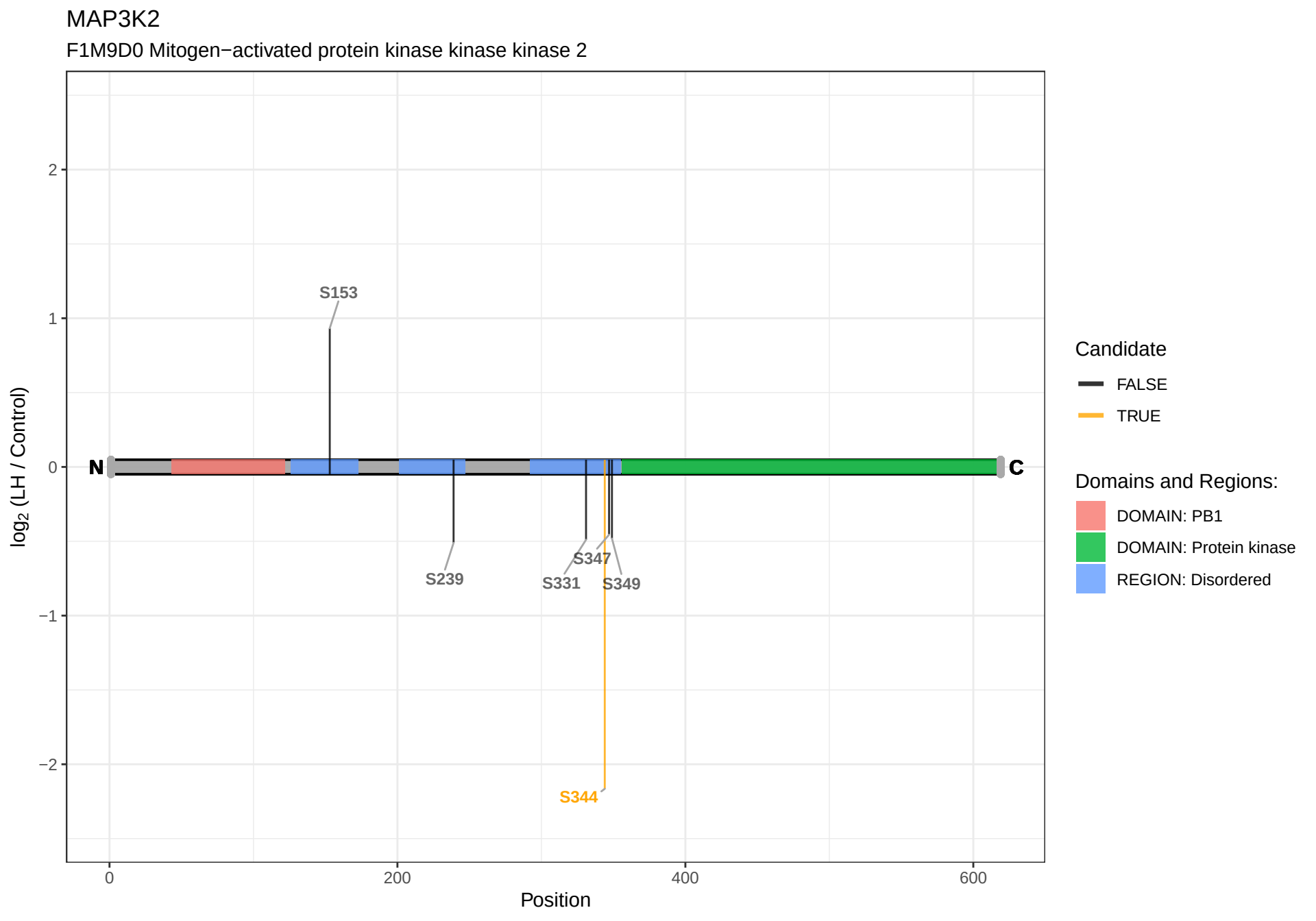

MAP2
P15146 Microtubule−associated protein 2
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
Position
N
C
S37
S1051
S1353
T1359
S1562
S1541
T1652
T1659
S1656
T1611
S1816
S1829
S1820
S1824
T1814
S1821
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Calmodulin−binding
REGION: Disordered
REGION: Interaction with KNDC1

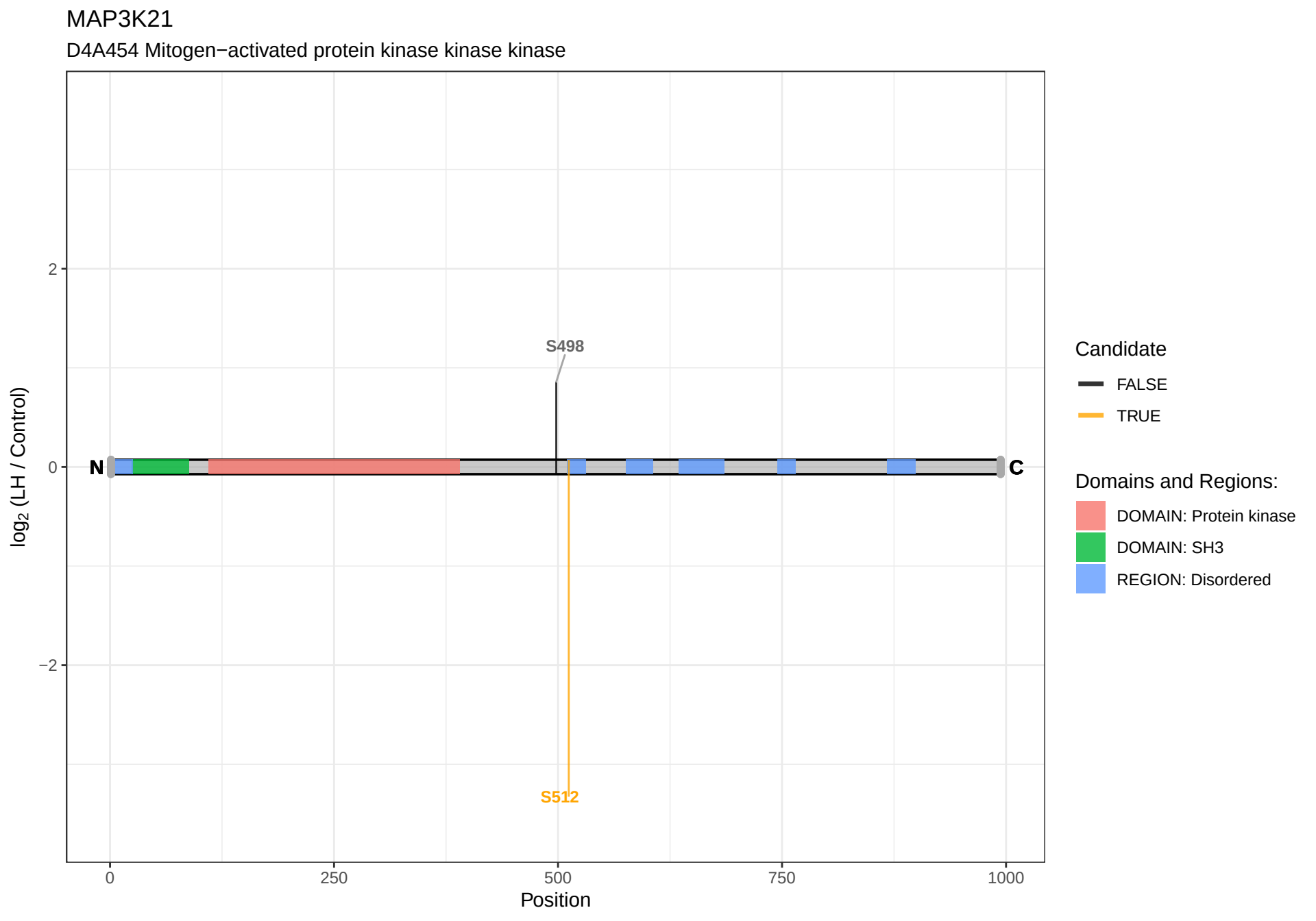

MAP2K2
P36506 Dual specificity mitogen−activated protein kinase kinase 2
S222
S226
S295
T394
N
C
2
0
−2
log2 (LH / Control)
0
100
200
300
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered

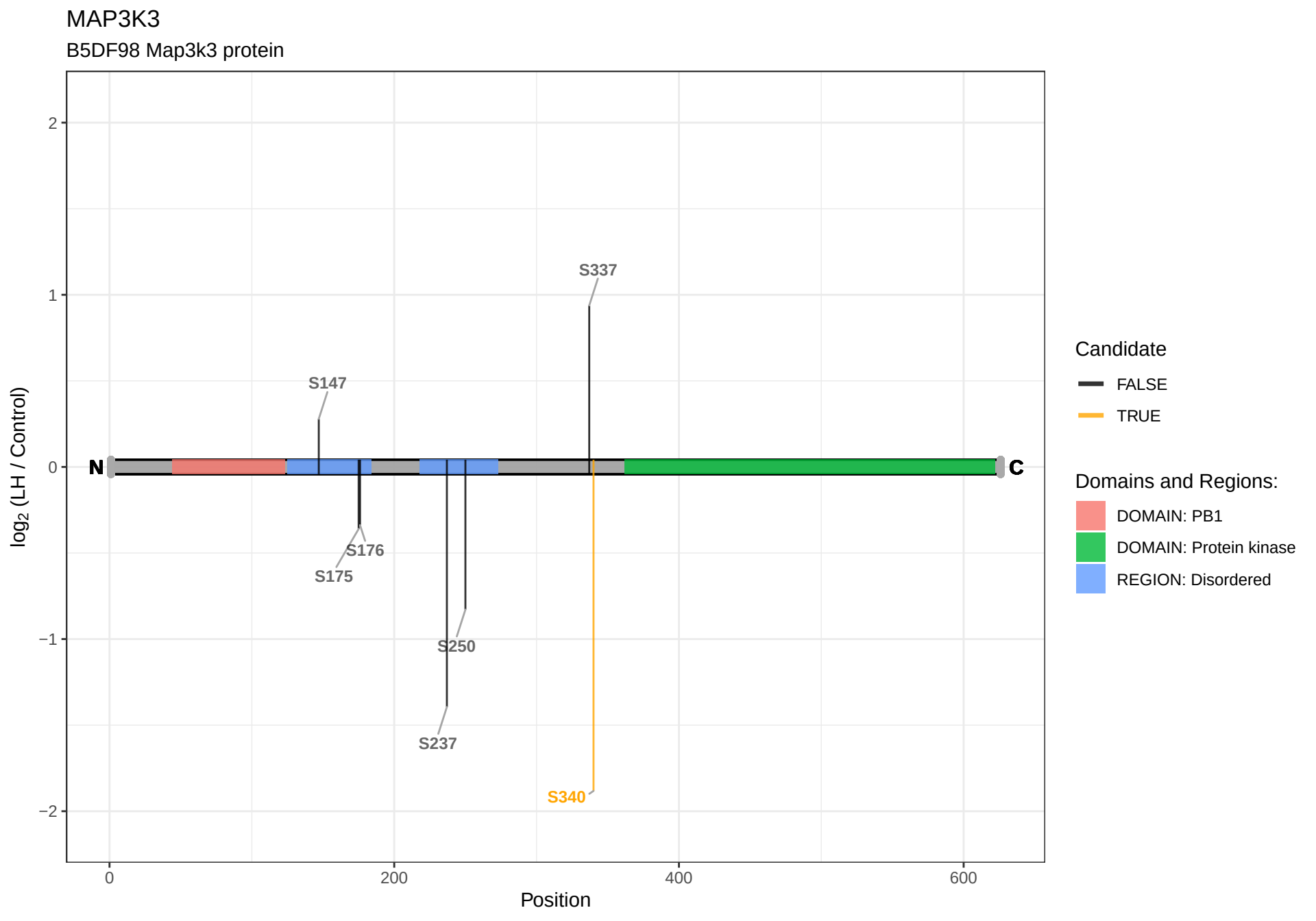

MAP2K6
Q925D6 Mitogen−activated protein kinase kinase 6
log2 (LH / Control)
3
2
1
0
−1
−2
−3
N
C
T28
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered

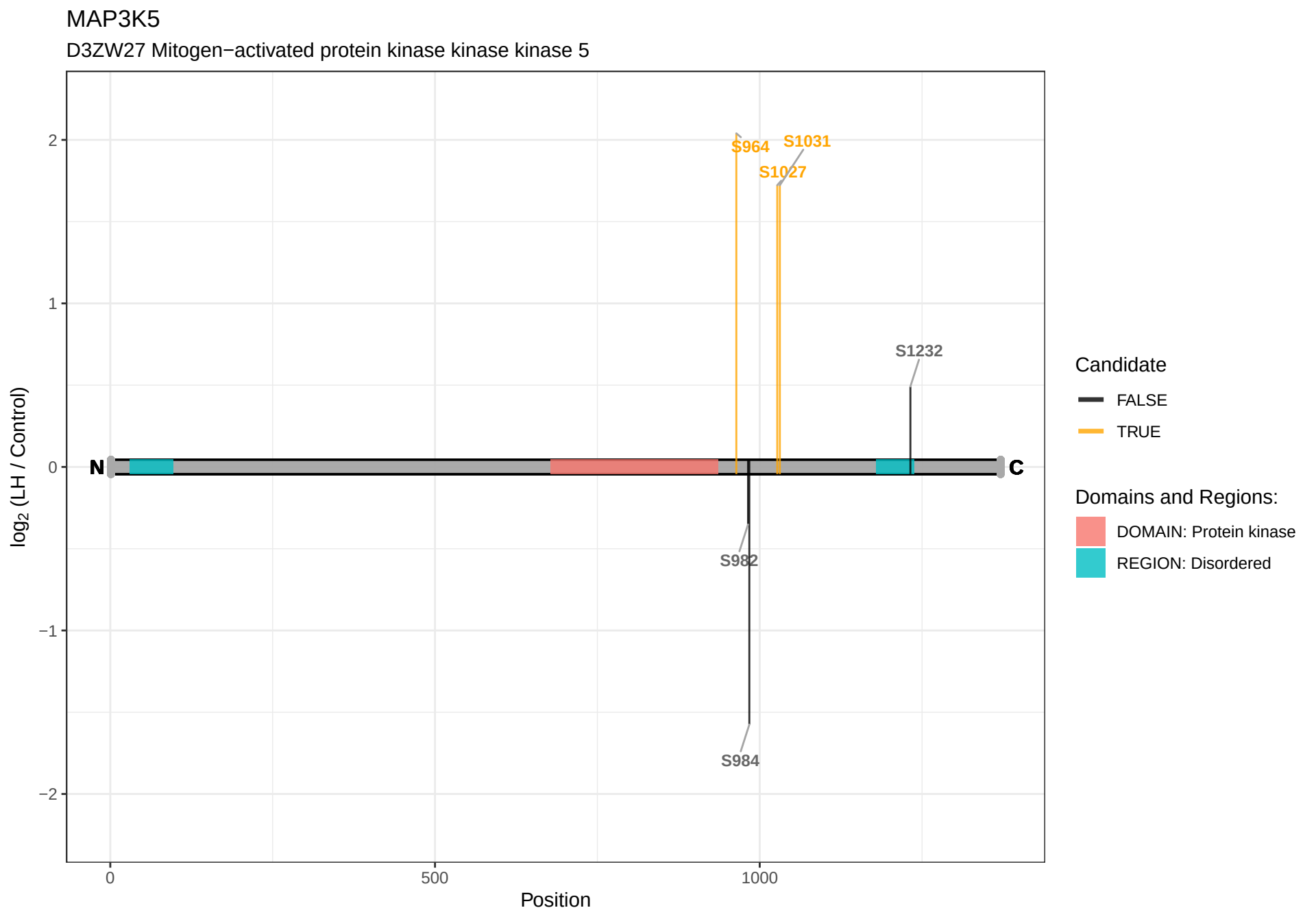

MAP2K7
Q4KSH7 Dual specificity mitogen−activated protein kinase kinase 7
log2 (LH / Control)
3
2
1
0
−1
−2
−3
N
C
S55
T66
S61
S35
0
100
200
300
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: D Domain
REGION: Disordered
REGION: DVD domain

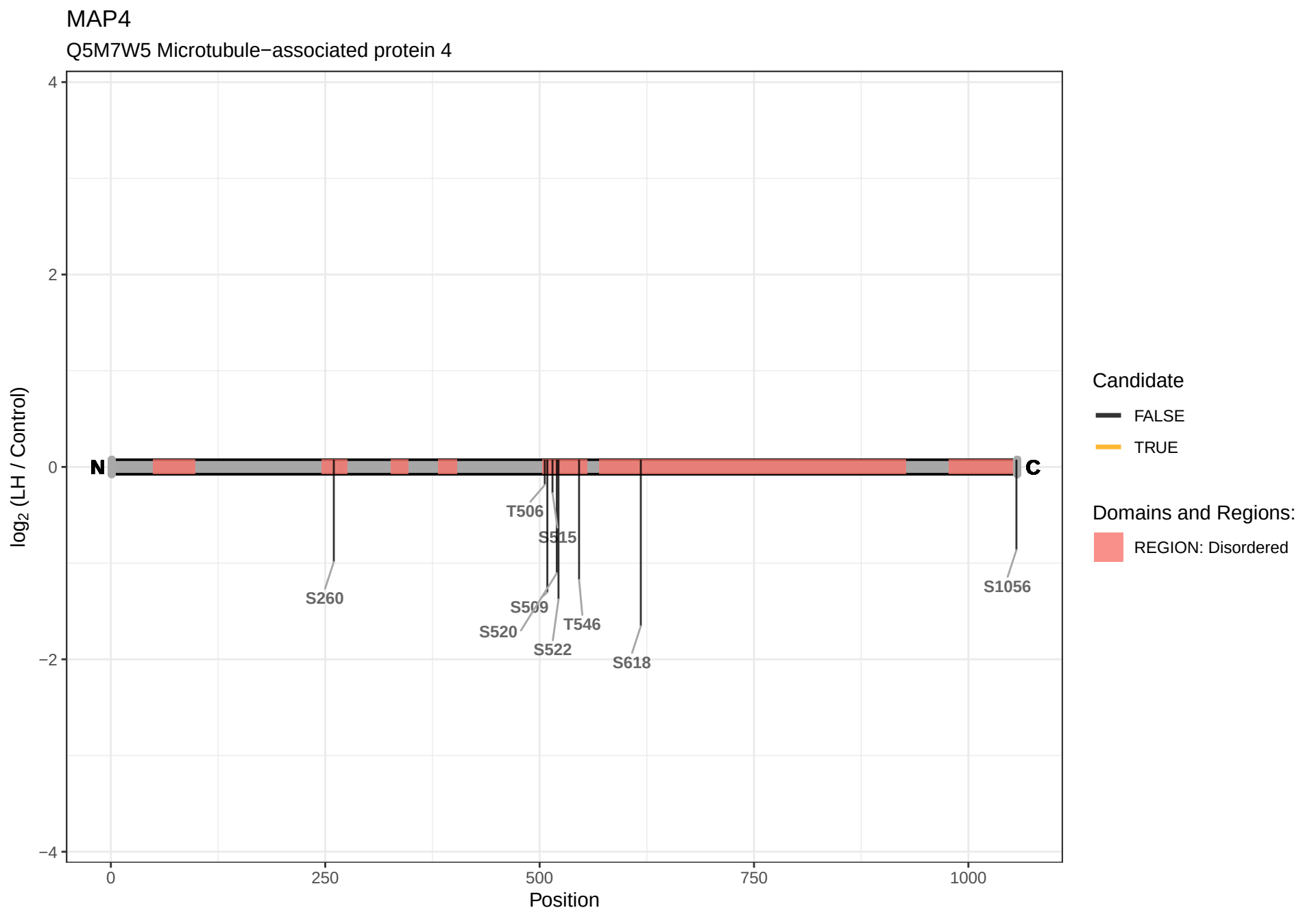

MAP3K1
F1M778 Mitogen−activated protein kinase kinase kinase 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S240
S242
S513
S137
S911
S910
S999
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
DOMAIN: RING−type
DOMAIN: SWIM−type
REGION: Disordered

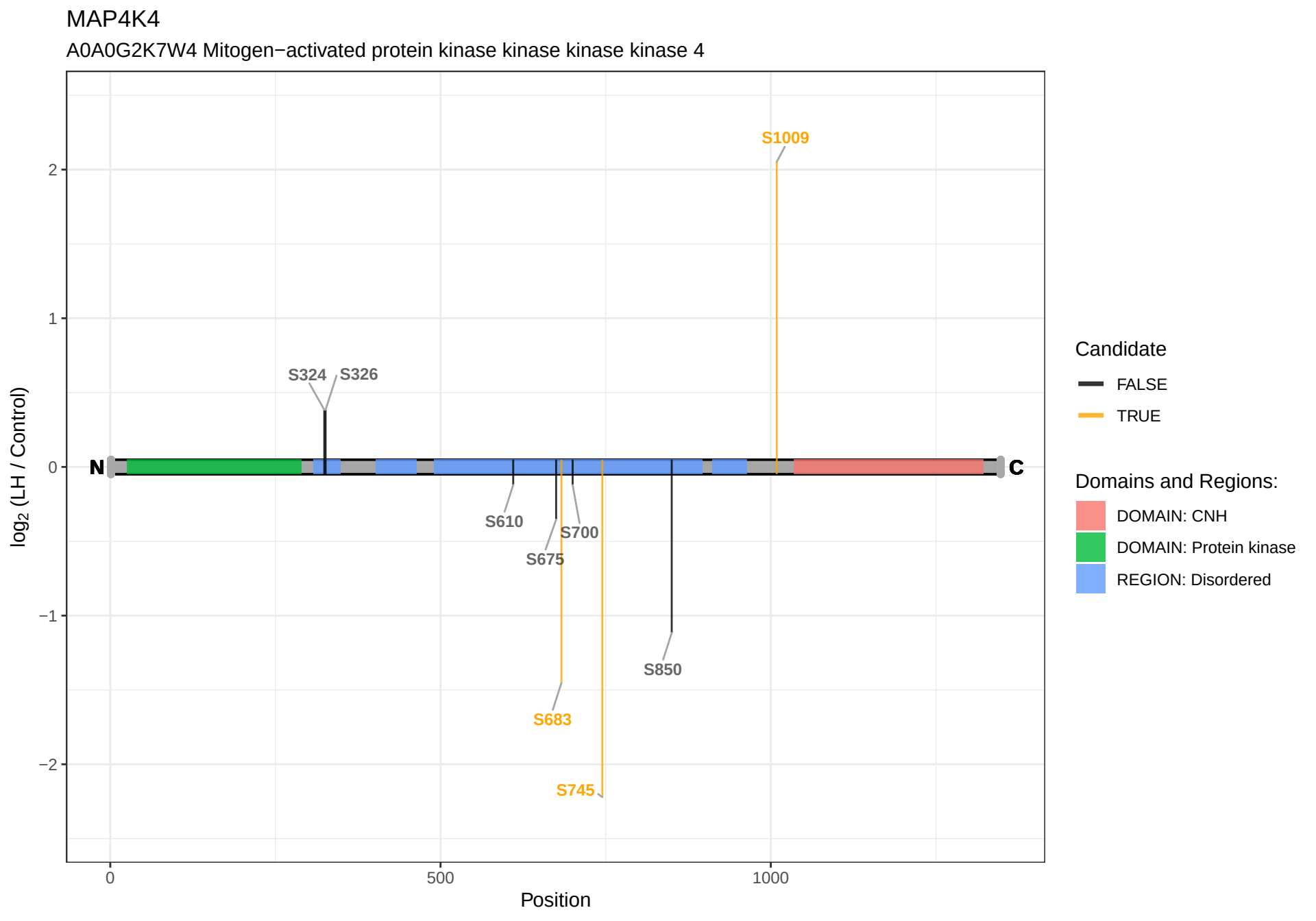

MAP3K2
F1M9D0 Mitogen−activated protein kinase kinase kinase 2
log2 (LH / Control)
2
1
0
−1
−2
N
C
S153
S239
S331
S347
S349
S344
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PB1
DOMAIN: Protein kinase
REGION: Disordered

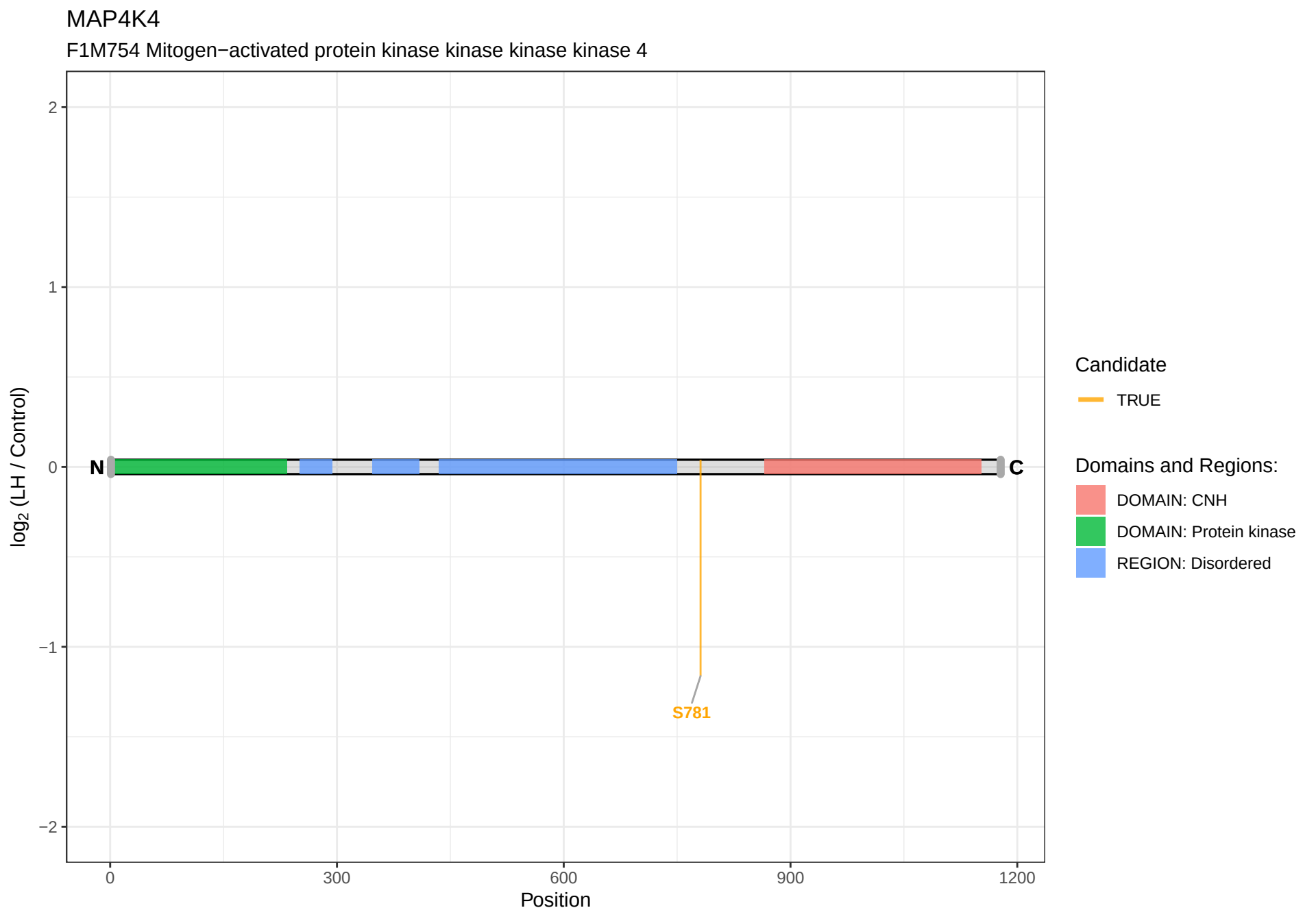

MAP3K21
D4A454 Mitogen−activated protein kinase kinase kinase
log2 (LH / Control)
2
0
−2
S498
S512
N
C
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
DOMAIN: SH3
REGION: Disordered

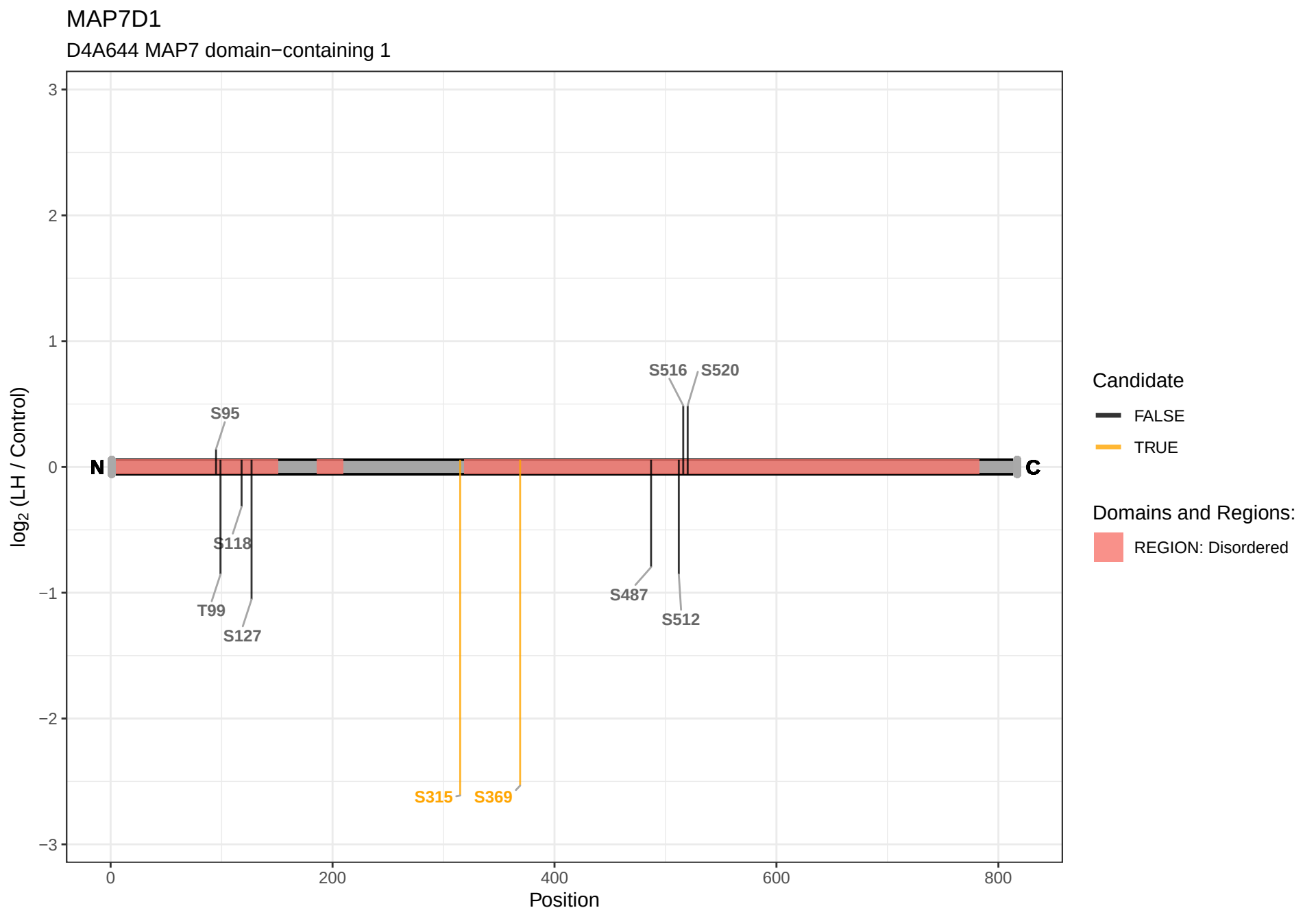

MAP3K3
B5DF98 Map3k3 protein
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
N
C
S337
S147
S176
S175
S250
S237
S340
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PB1
DOMAIN: Protein kinase
REGION: Disordered

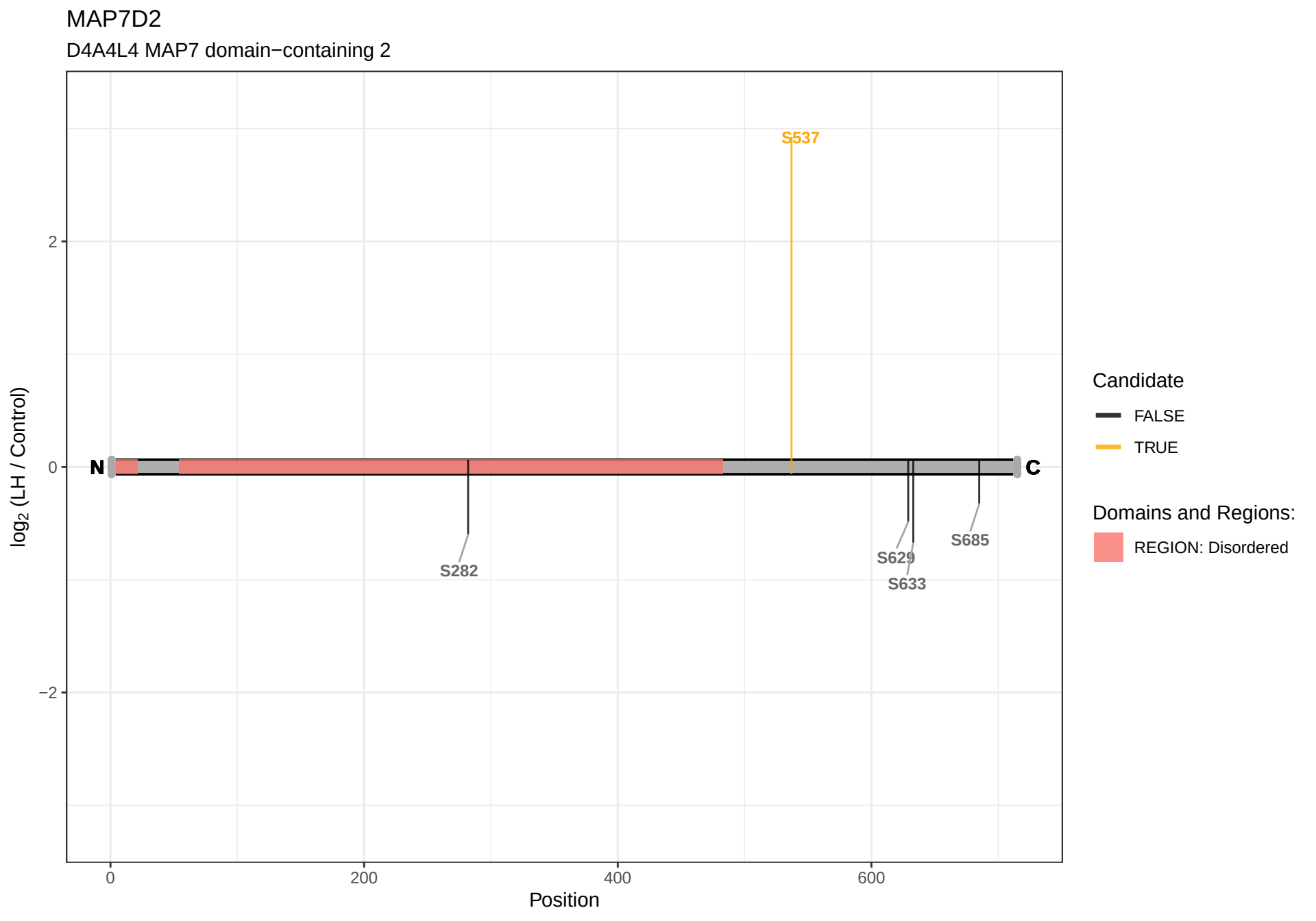

MAP3K5
D3ZW27 Mitogen−activated protein kinase kinase kinase 5
S964
S1031
S1027
S1232
S982
S984
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered

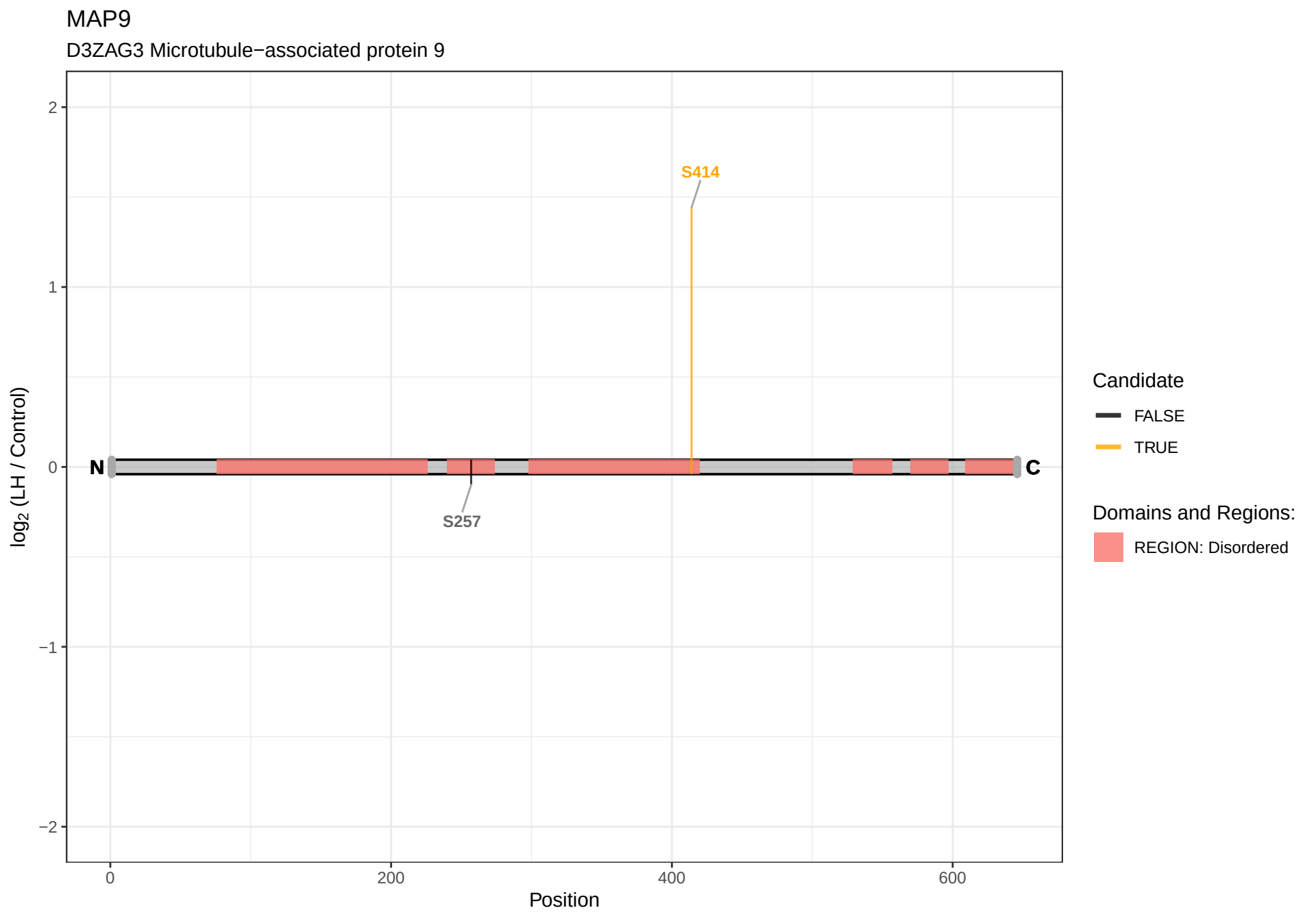

MAP4
Q5M7W5 Microtubule−associated protein 4
log2 (LH / Control)
4
2
0
−2
−4
N
C
T506
S515
S260
S509
S520
T546
S522
S618
S1056
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

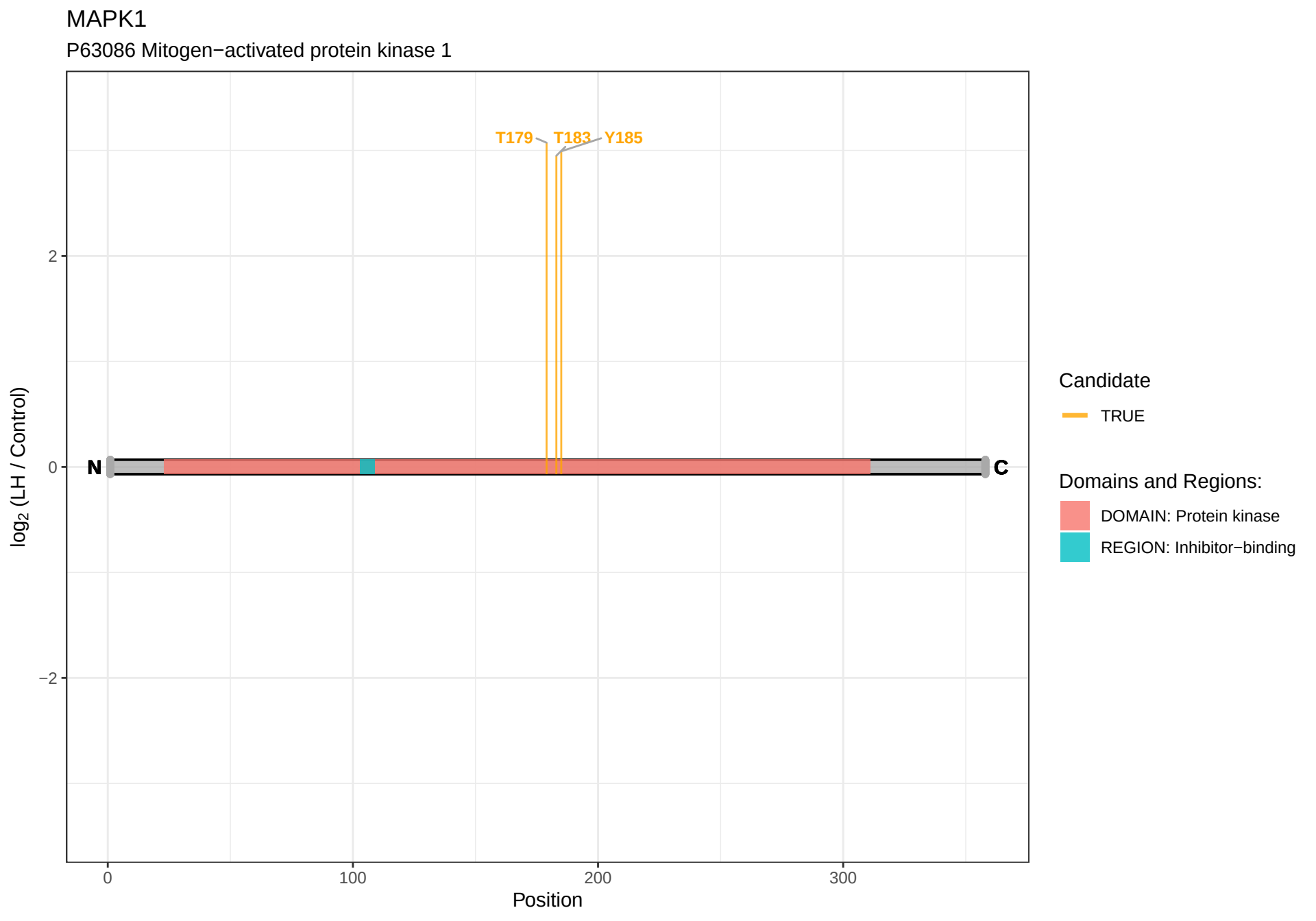

MAP4K4
A0A0G2K7W4 Mitogen−activated protein kinase kinase kinase kinase 4
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
Position
N
C
S1009
S324
S326
S610
S675
S700
S683
S745
S850
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CNH
DOMAIN: Protein kinase
REGION: Disordered

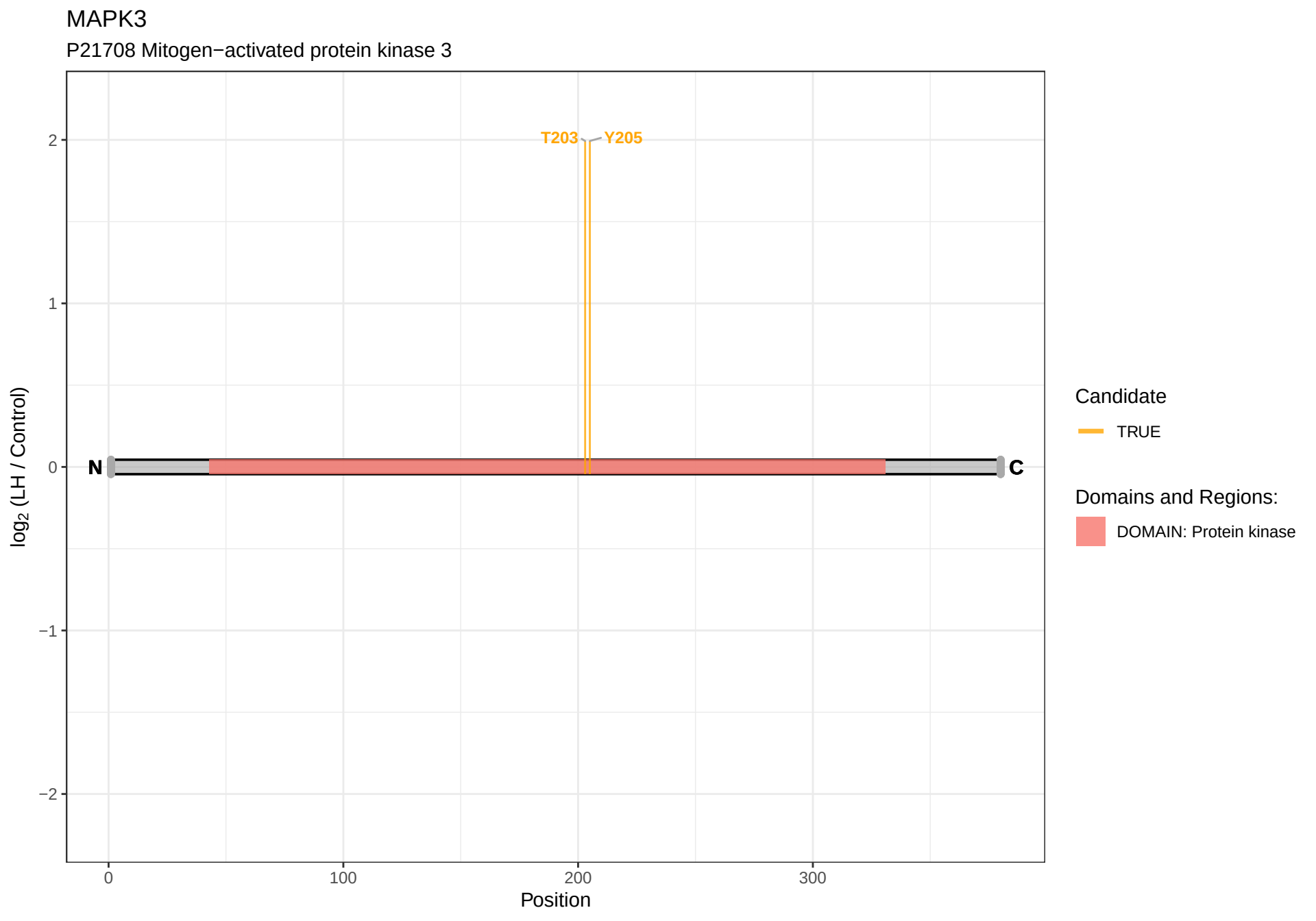

MAP4K4
F1M754 Mitogen−activated protein kinase kinase kinase kinase 4
log2 (LH / Control)
2
1
0
−1
−2
N
C
S781
0
300
600
900
1200
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: CNH
DOMAIN: Protein kinase
REGION: Disordered

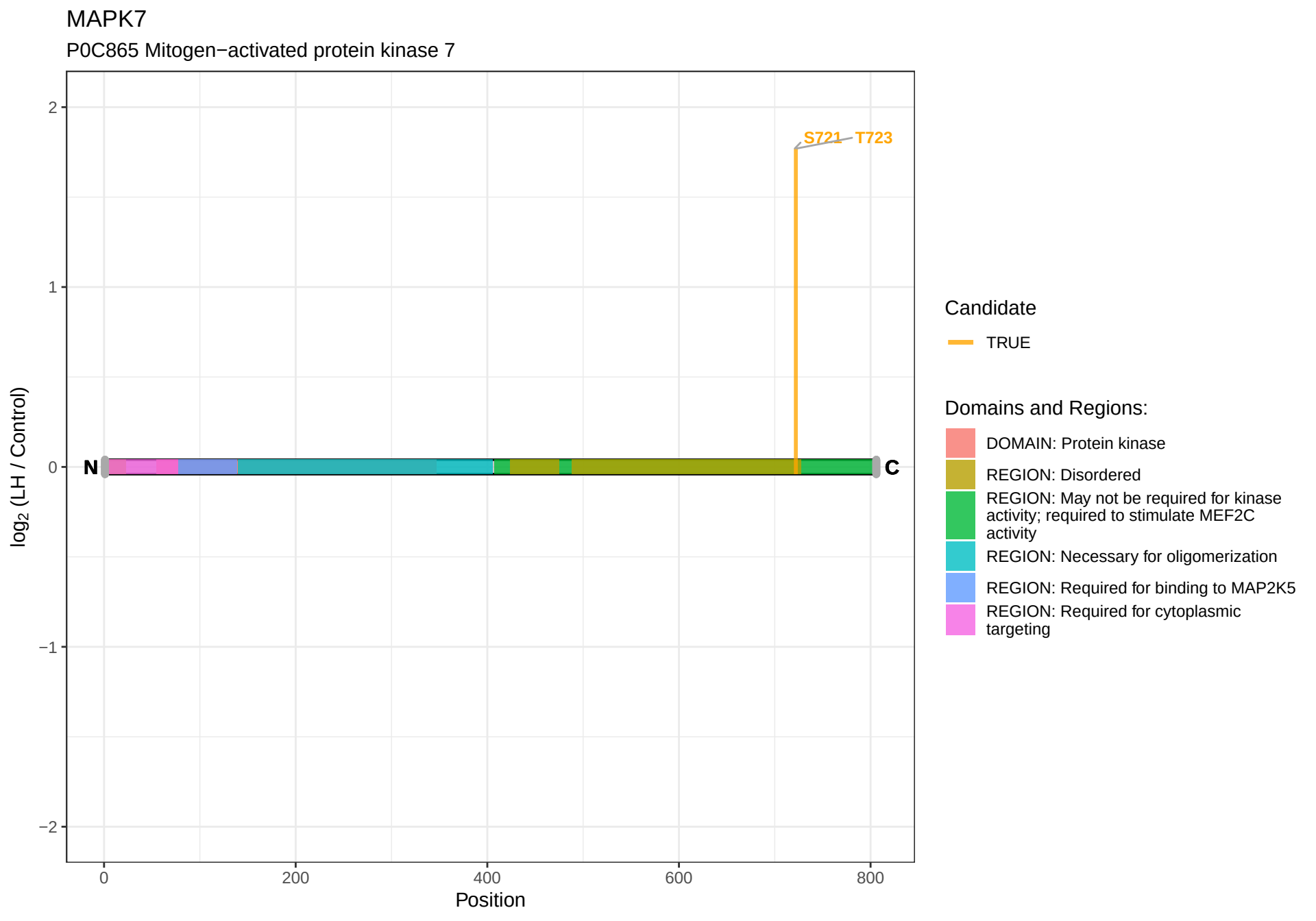

MAP7D1
D4A644 MAP7 domain−containing 1
log2 (LH / Control)
3
2
1
0
−1
−2
−3
0
200
400
600
800
Position
N
C
S95
S118
T99
S127
S315
S369
S516
S520
S487
S512
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

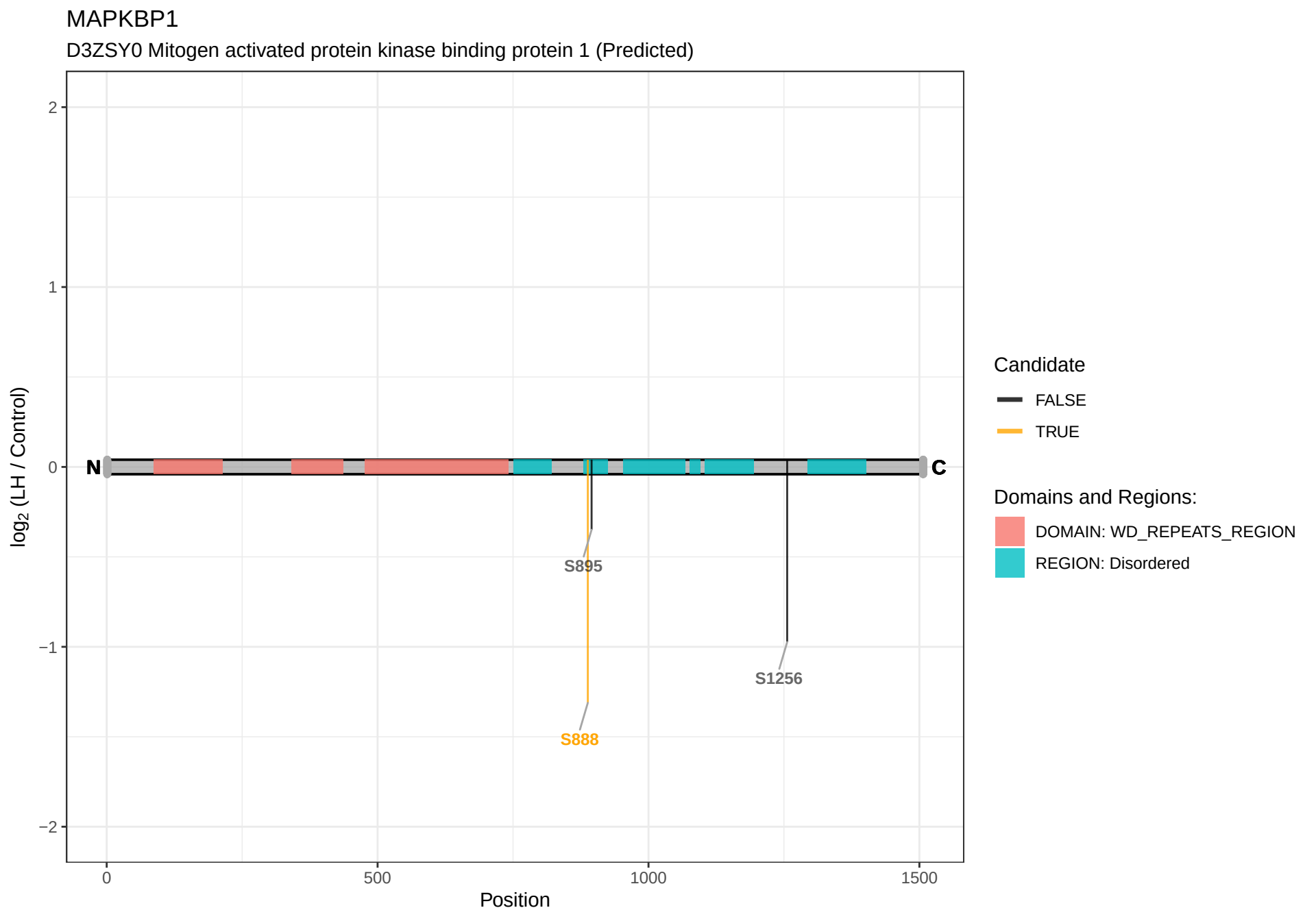

MAP7D2
D4A4L4 MAP7 domain−containing 2
S537
S282
S629
S633
S685
N
C
2
0
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

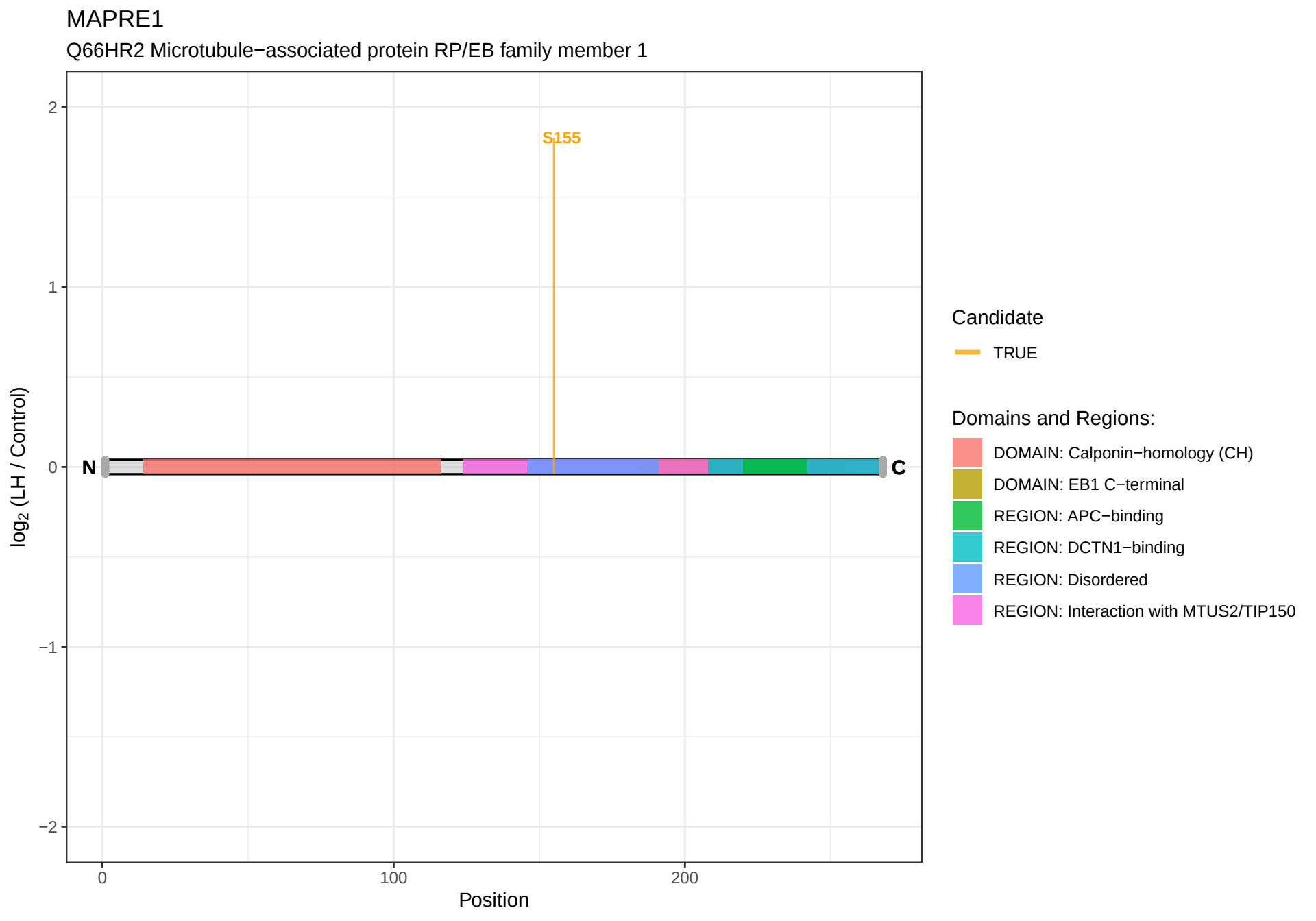

MAP9
D3ZAG3 Microtubule−associated protein 9
S414
S257
N
C
log2 (LH / Control)
Position
0
200
400
600
2
1
0
−1
−2
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

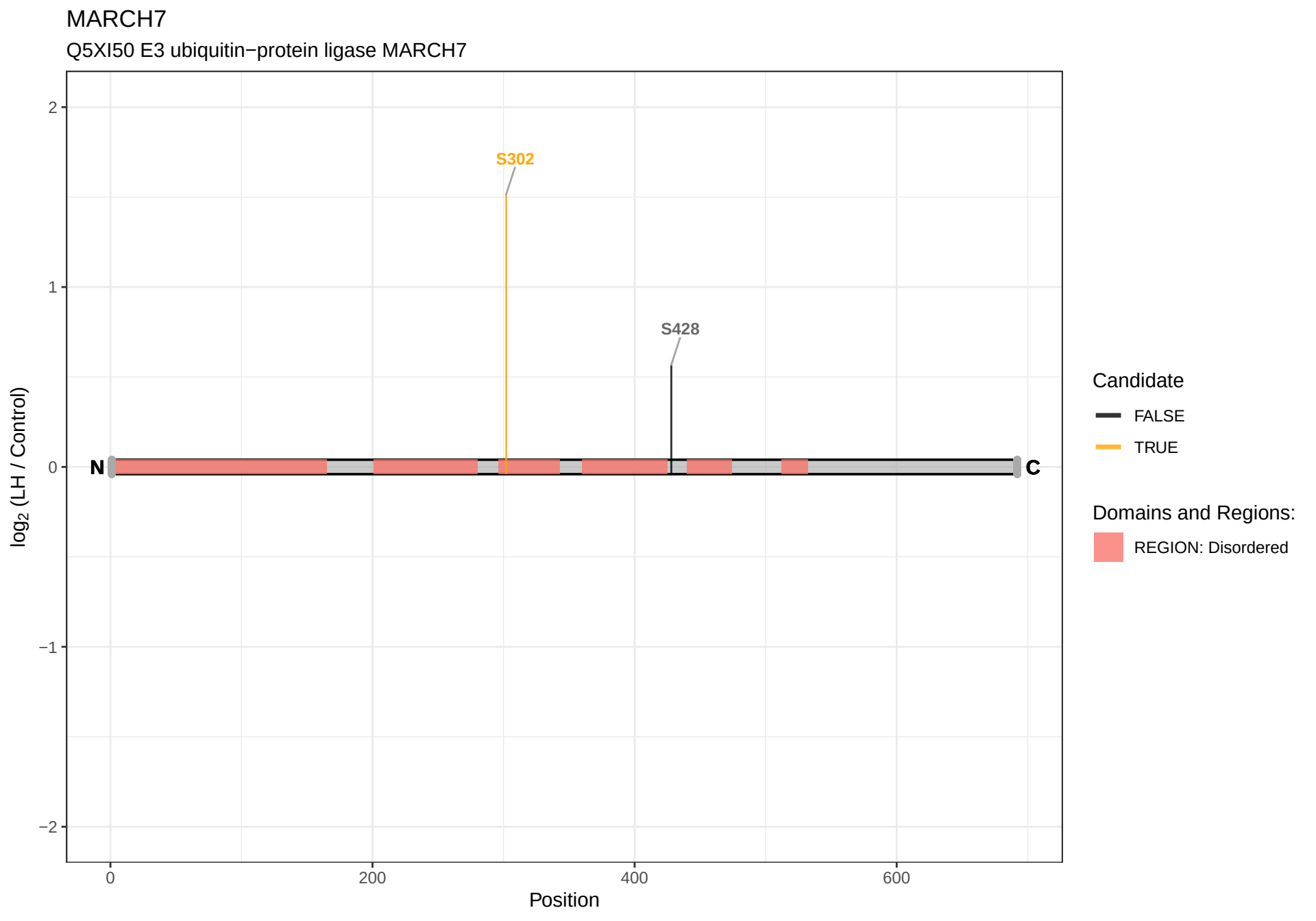

MAPK1
P63086 Mitogen−activated protein kinase 1
T179
T183
Y185
N
C
2
0
−2
log2 (LH / Control)
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Inhibitor−binding

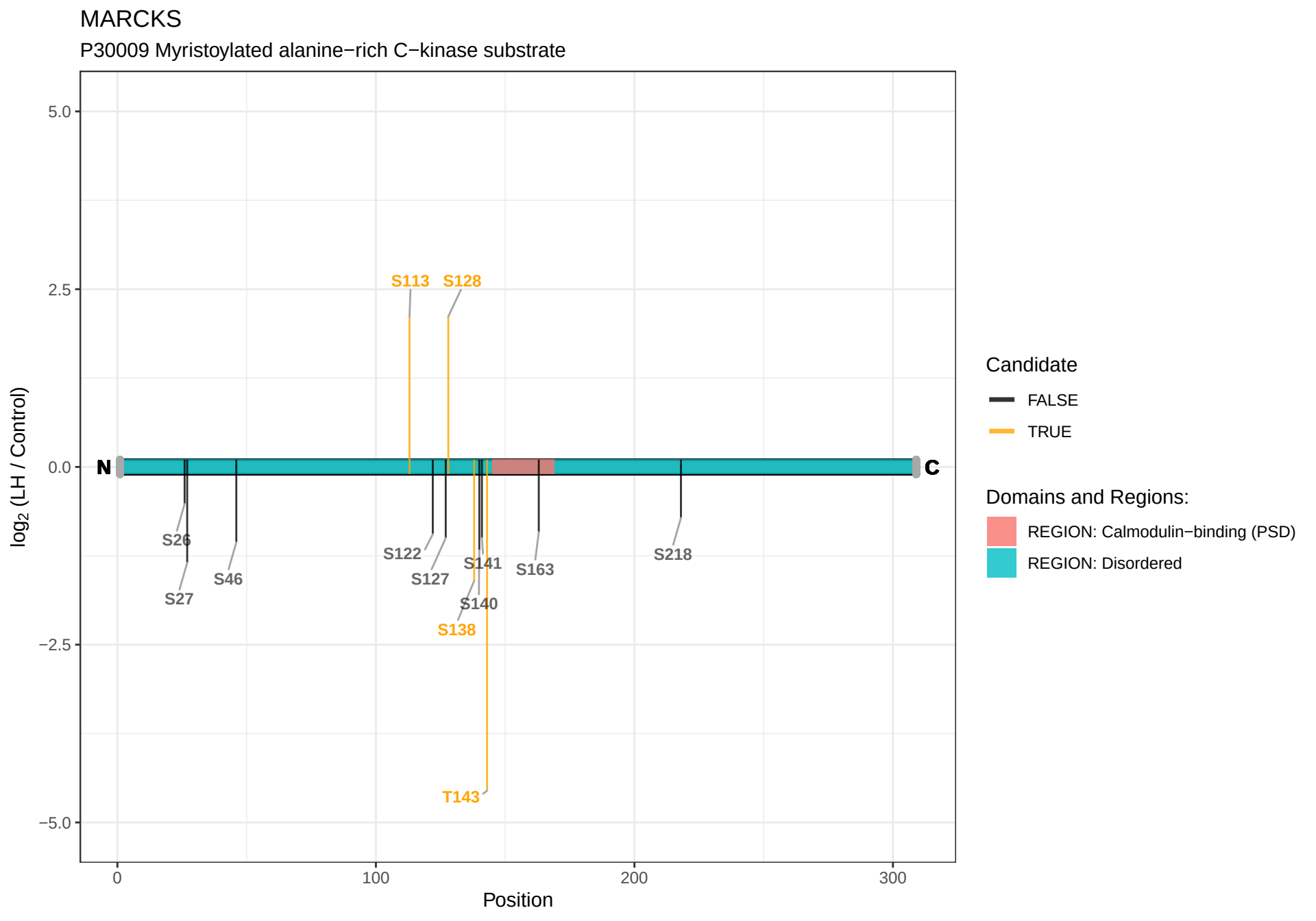

MAPK3
P21708 Mitogen−activated protein kinase 3
T203
Y205
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Protein kinase

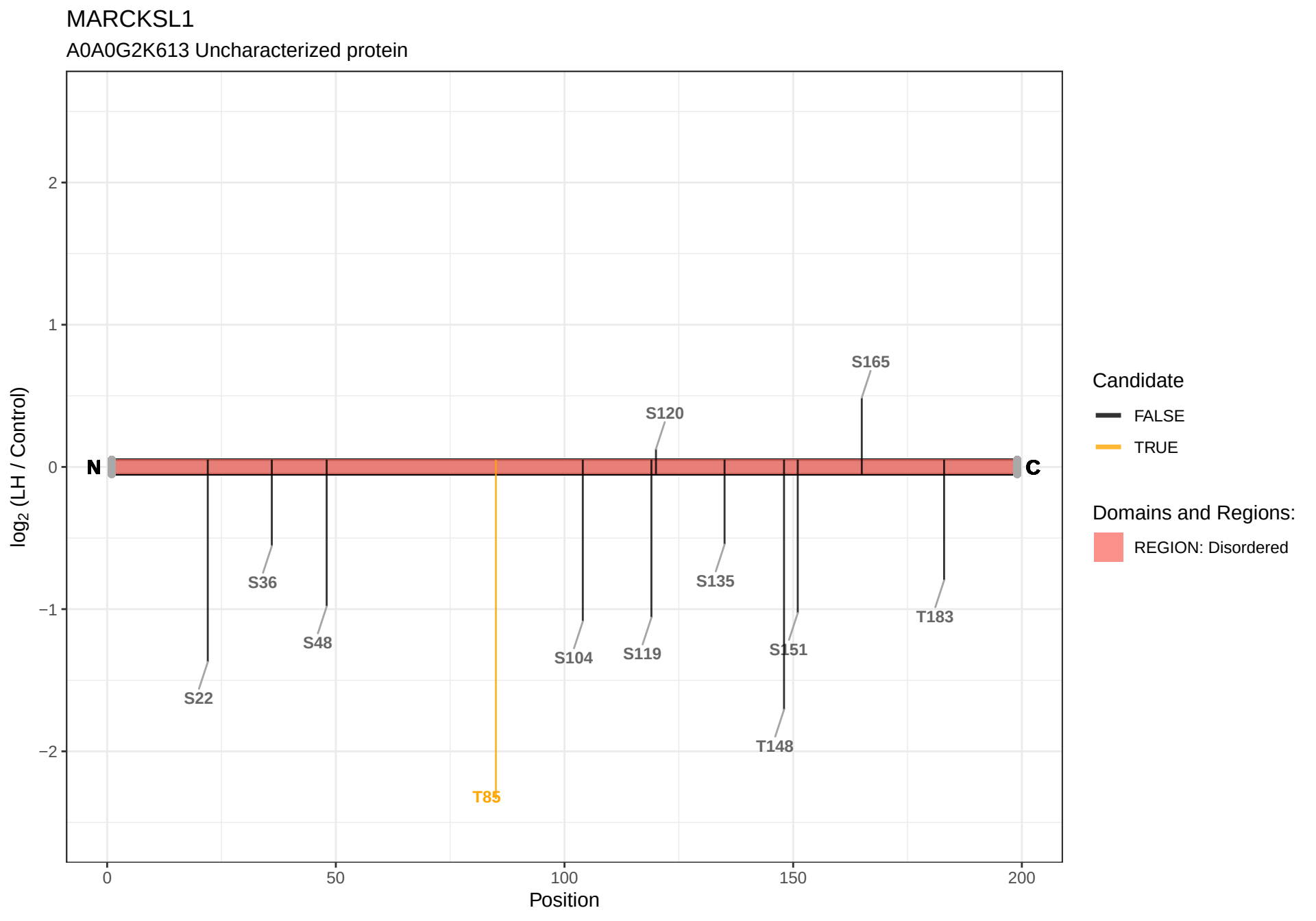

MAPK7
P0C865 Mitogen−activated protein kinase 7
S721
T723
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
800
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered
REGION: May not be required for kinase activity; required to stimulate MEF2C activity
REGION: Necessary for oligomerization
REGION: Required for binding to MAP2K5
REGION: Required for cytoplasmic targeting

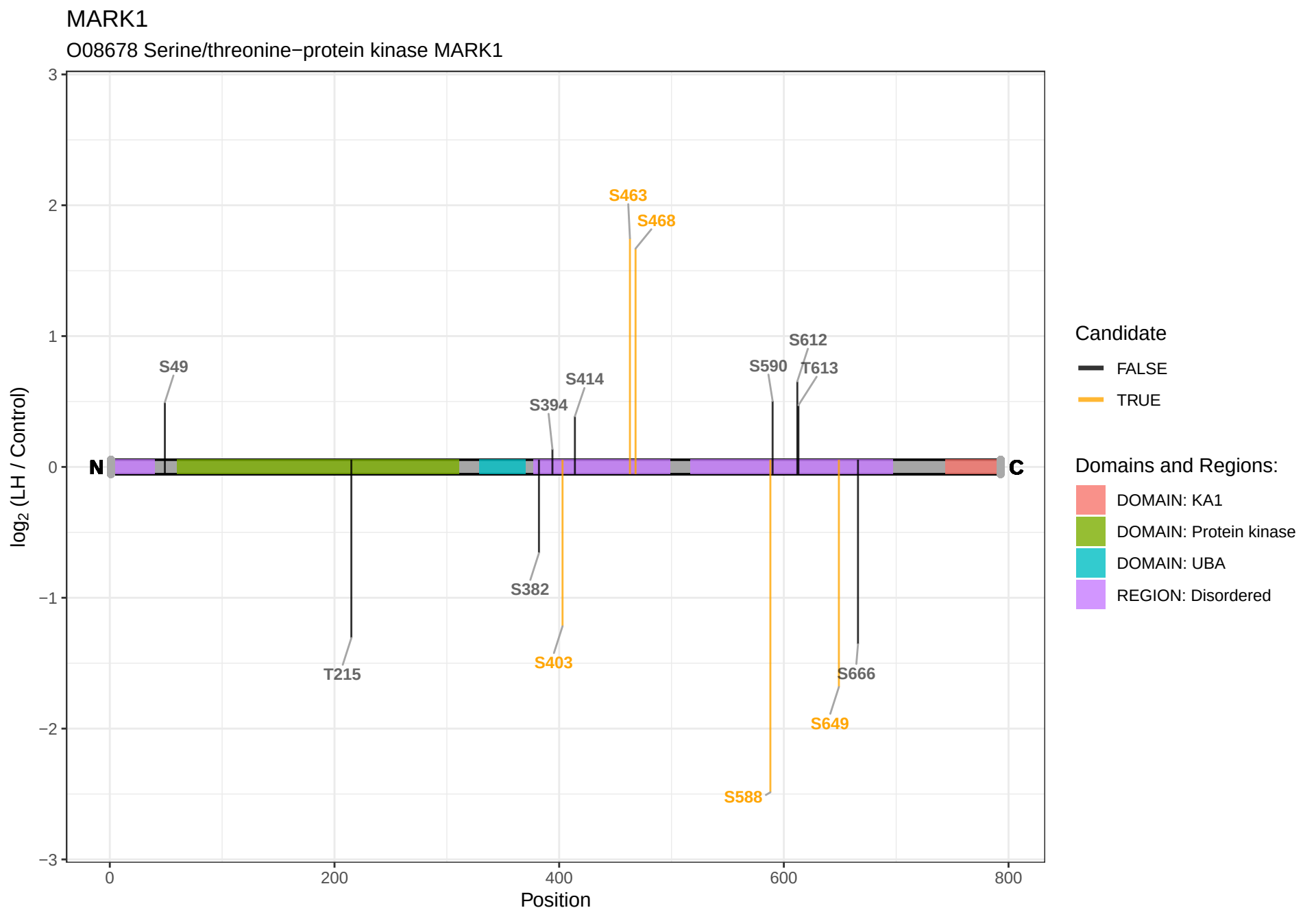

MAPKBP1
D3ZSY0 Mitogen activated protein kinase binding protein 1 (Predicted)
log2 (LH / Control)
2
1
0
−1
−2
N
C
S895
S888
S1256
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WD_REPEATS_REGION
REGION: Disordered

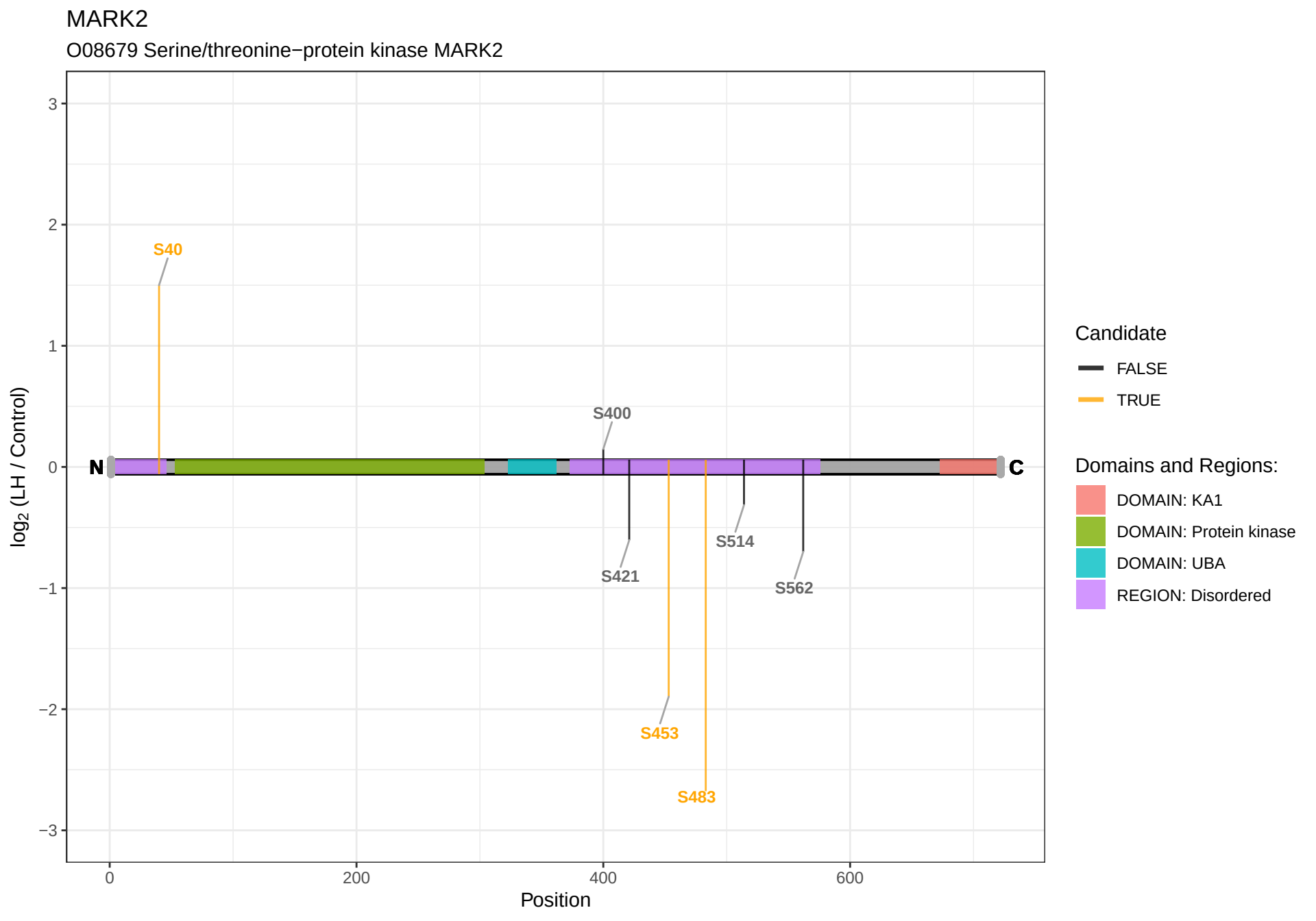

MAPRE1
Q66HR2 Microtubule−associated protein RP/EB family member 1
S155
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
100
200
Candidate
TRUE
Domains and Regions:
DOMAIN: Calponin−homology (CH)
DOMAIN: EB1 C−terminal
REGION: APC−binding
REGION: DCTN1−binding
REGION: Disordered
REGION: Interaction with MTUS2/TIP150

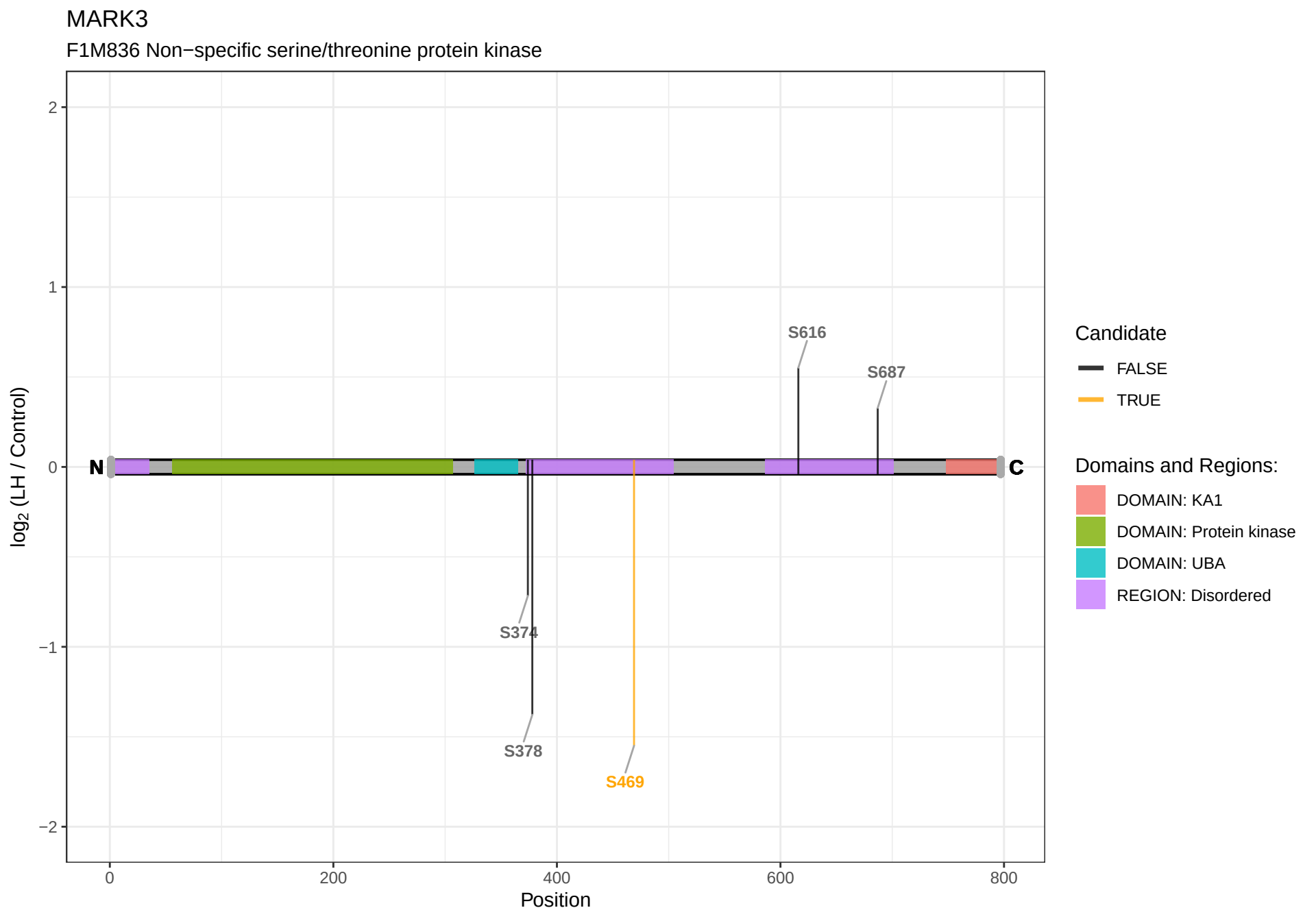

MARCH7
Q5XI50 E3 ubiquitin−protein ligase MARCH7
S302
S428
N
C
2
1
0
−1
−2
0
200
400
600
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

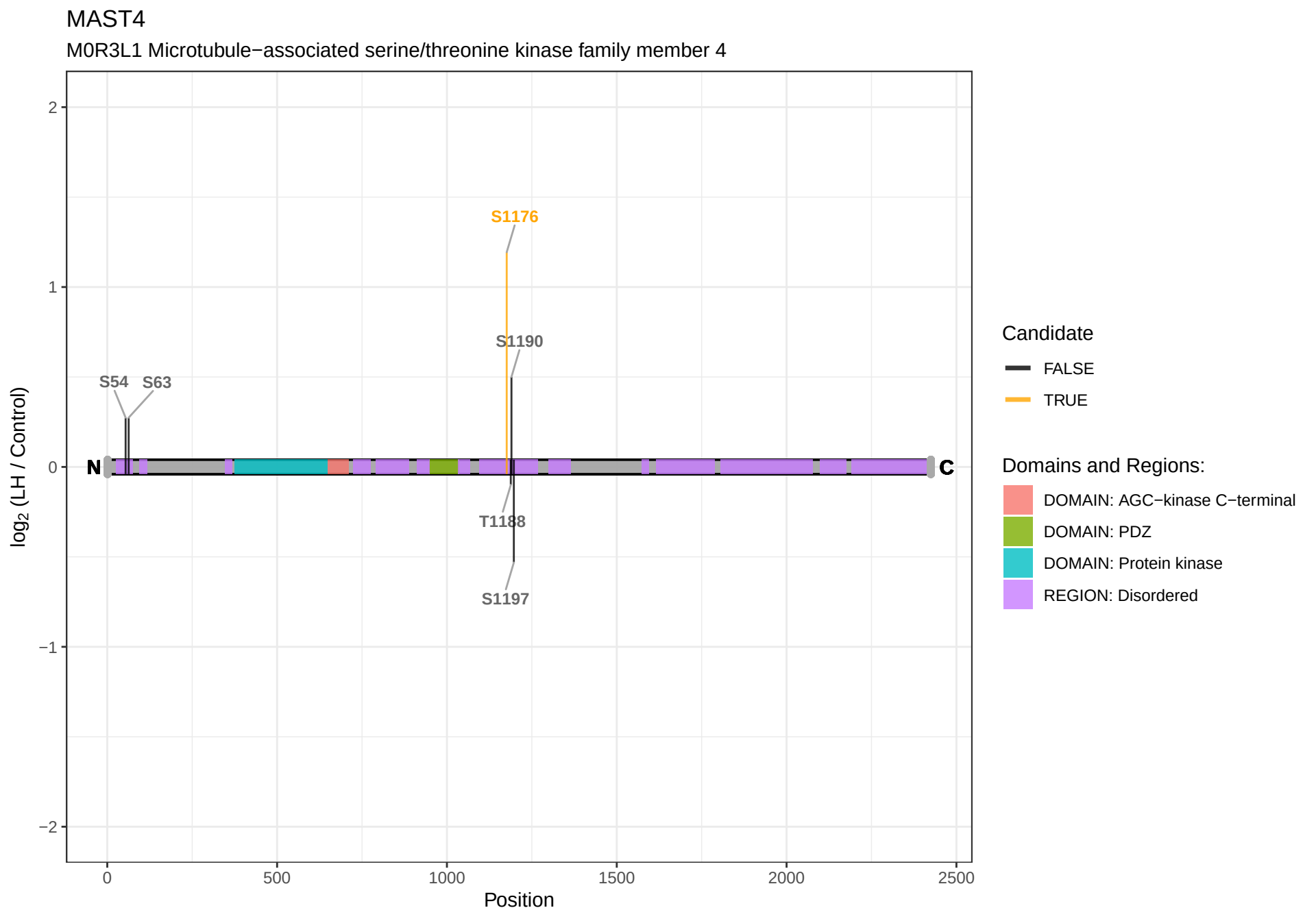

MARCKS
P30009 Myristoylated alanine−rich C−kinase substrate
log2 (LH / Control)
5.0
2.5
0.0
−2.5
−5.0
0
100
200
300
Position
N
C
S113
S128
S26
S27
S46
S122
S127
S141
S140
S138
S163
S218
T143
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Calmodulin−binding (PSD)
REGION: Disordered

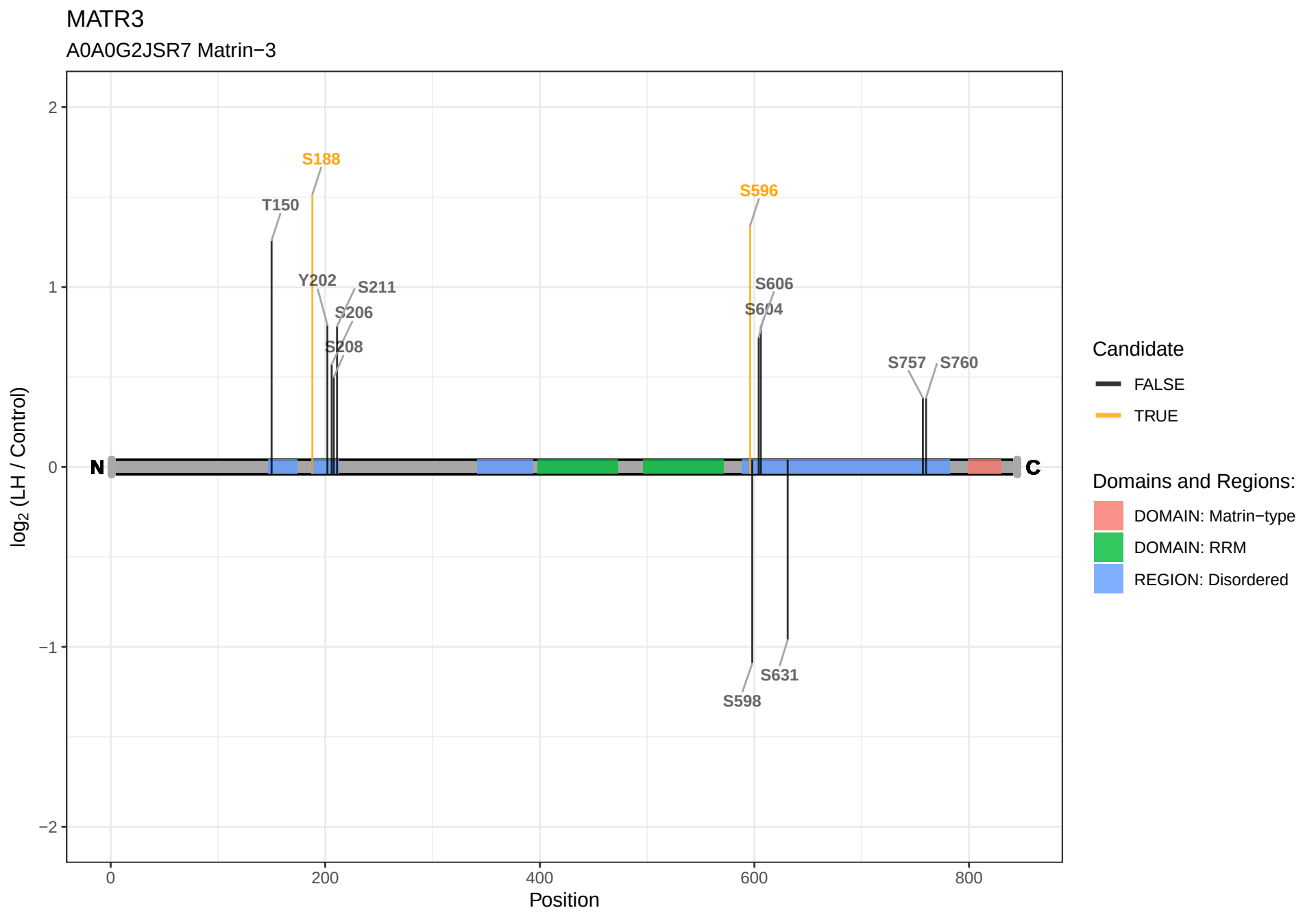

MARCKSL1
A0A0G2K613 Uncharacterized protein
log2 (LH / Control)
2
1
0
−1
−2
N
C
S165
S120
S36
S135
S48
S104
S119
S151
T183
S22
T85
T148
0
50
100
150
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

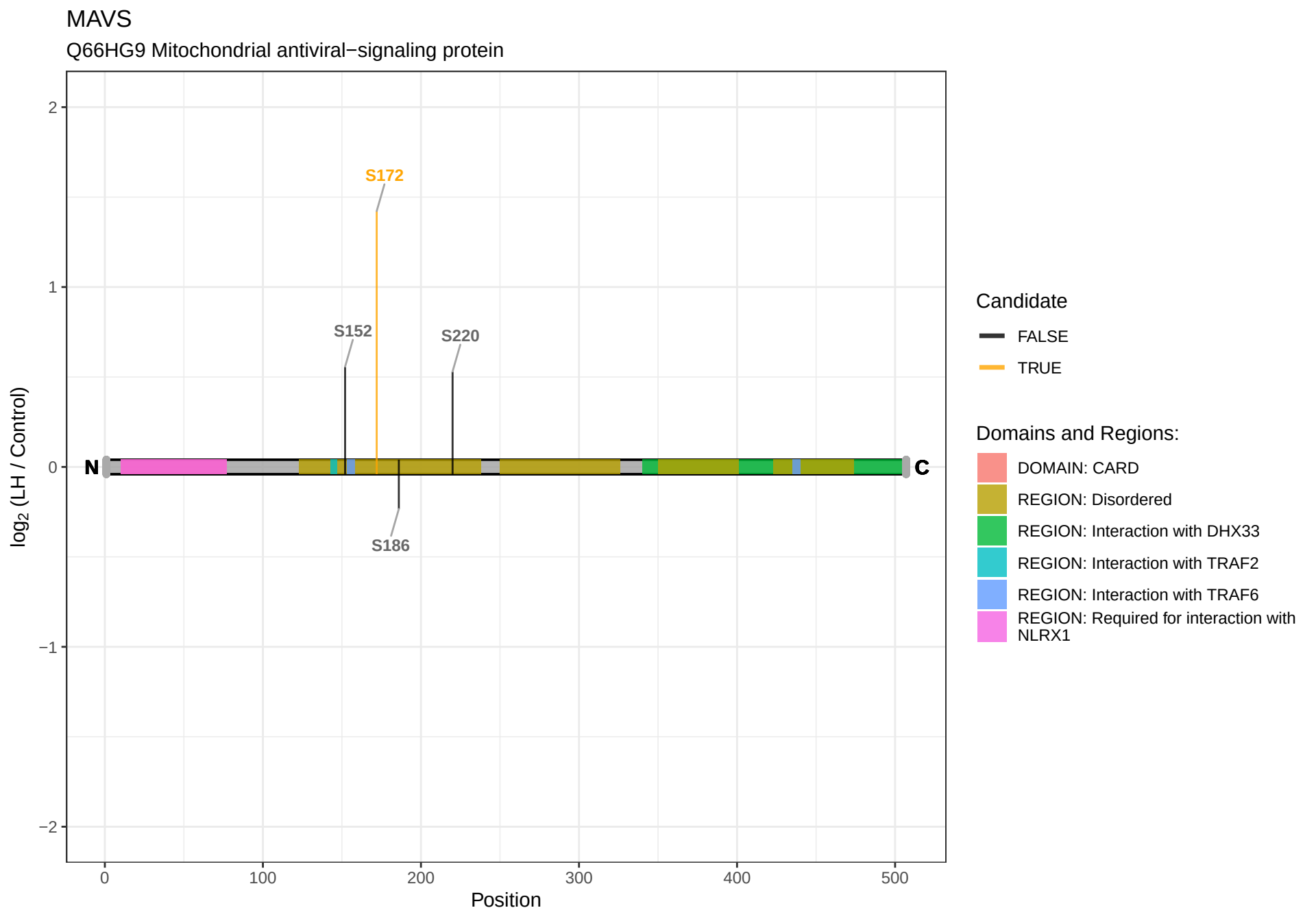

MARK1
O08678 Serine/threonine−protein kinase MARK1
log2 (LH / Control)
Position
N
C
S49
T215
S382
S394
S403
S414
S463
S468
S588
S590
S612
T613
S649
S666
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: KA1
DOMAIN: Protein kinase
DOMAIN: UBA
REGION: Disordered

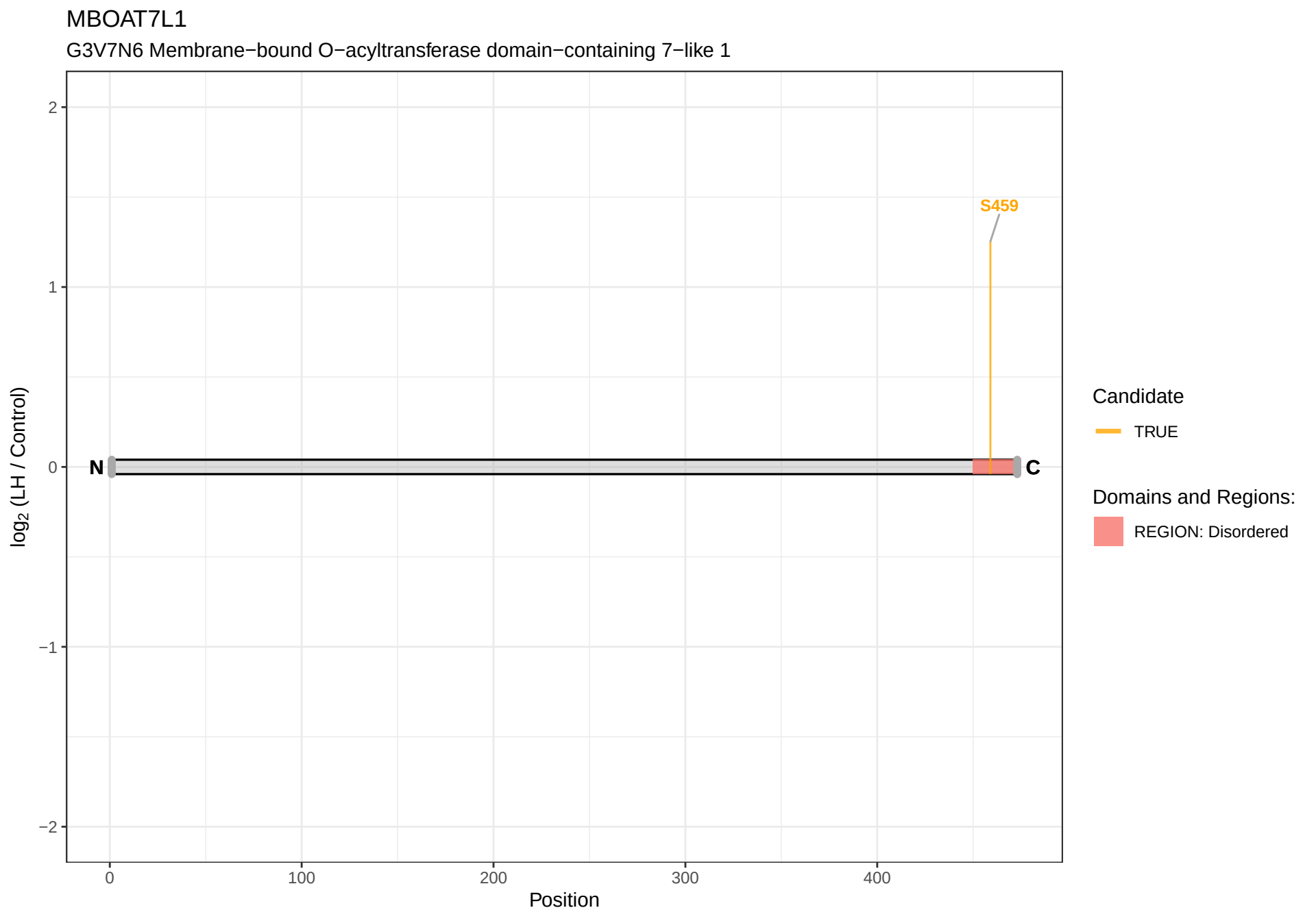

MARK2
O08679 Serine/threonine−protein kinase MARK2
log2 (LH / Control)
3
2
1
0
−1
−2
−3
0
200
400
600
Position
N
C
S40
S400
S421
S453
S483
S514
S562
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: KA1
DOMAIN: Protein kinase
DOMAIN: UBA
REGION: Disordered

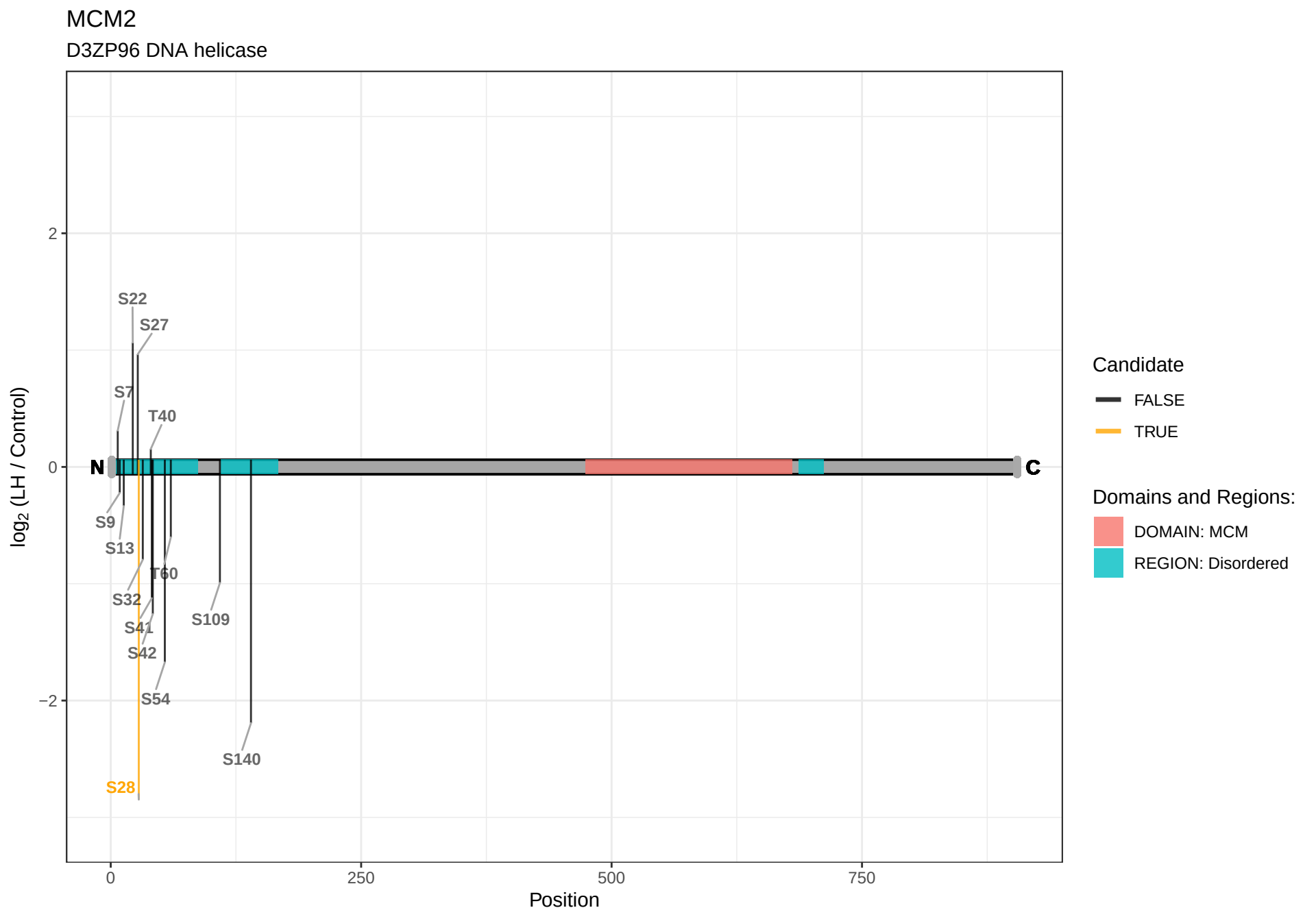

MARK3
F1M836 Non−specific serine/threonine protein kinase
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
800
Position
N
C
S616
S687
S374
S378
S469
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: KA1
DOMAIN: Protein kinase
DOMAIN: UBA
REGION: Disordered

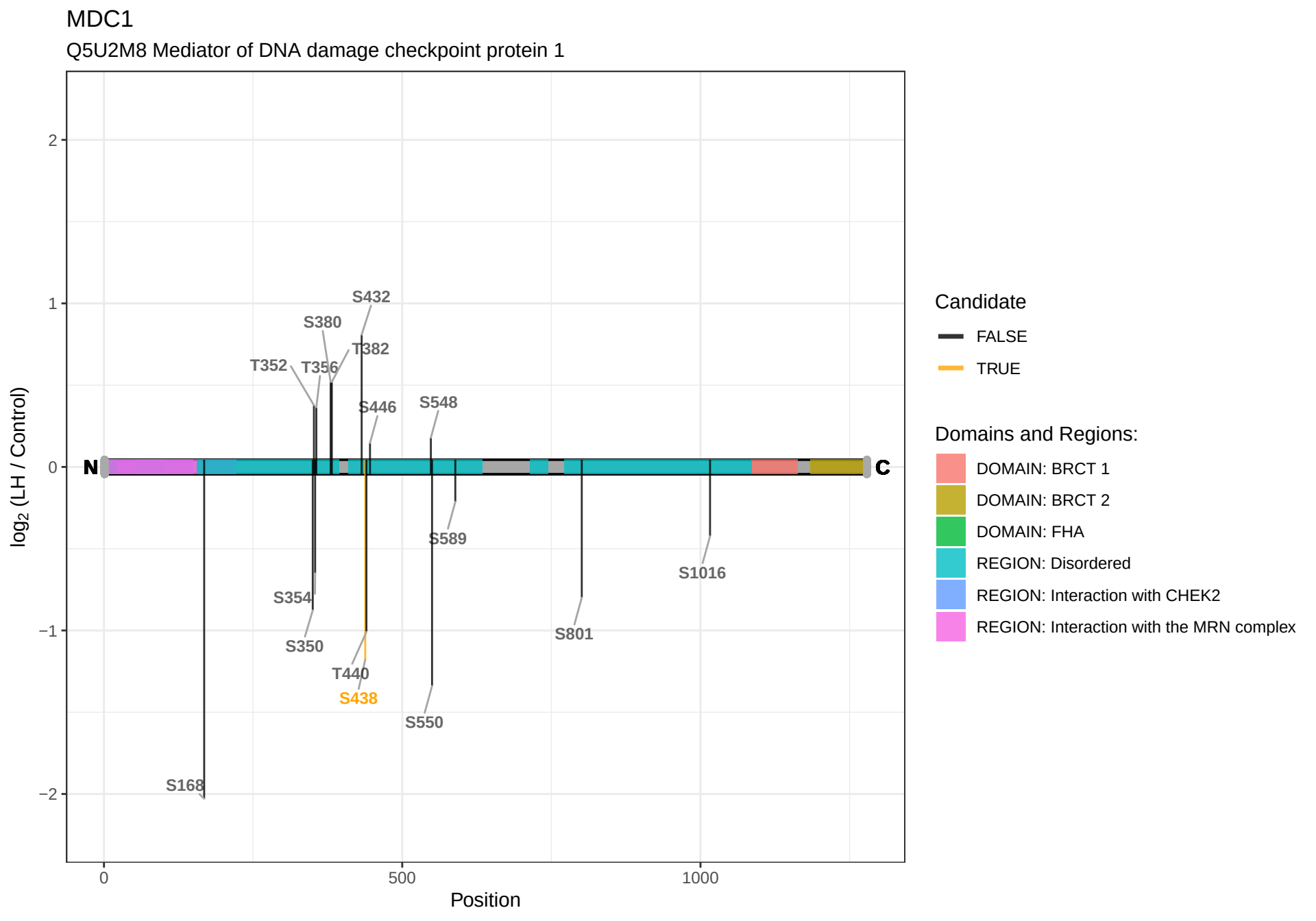

MAST4
M0R3L1 Microtubule−associated serine/threonine kinase family member 4
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
2000
2500
Position
N
C
S54
S63
S1176
S1190
T1188
S1197
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AGC−kinase C−terminal
DOMAIN: PDZ
DOMAIN: Protein kinase
REGION: Disordered

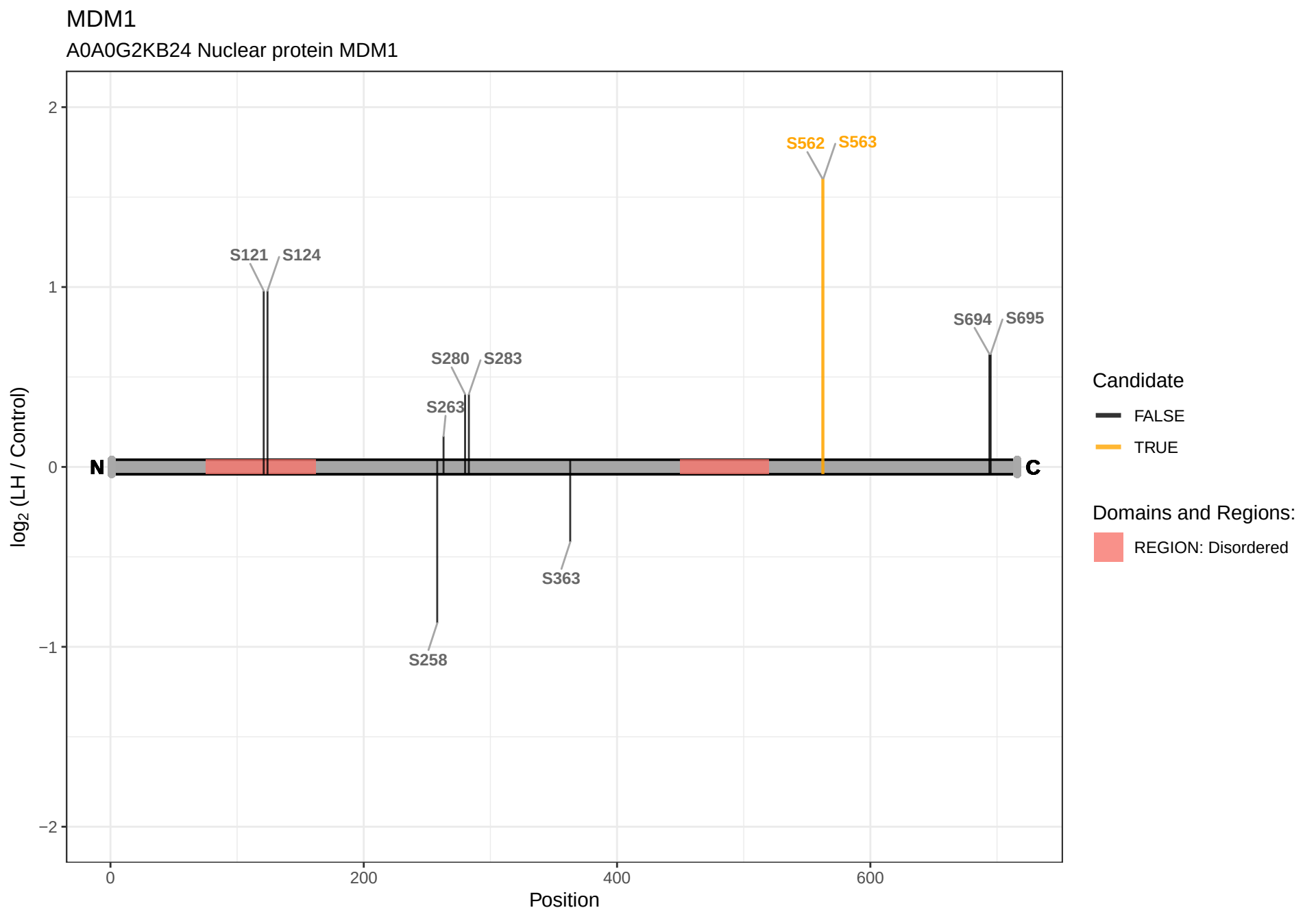

MATR3
A0A0G2JSR7 Matrin−3
log2 (LH / Control)
2
1
0
−1
−2
S188
T150
S596
Y202
S211
S606
S206
S604
S208
S757
S760
N
C
S631
S598
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Matrin−type
DOMAIN: RRM
REGION: Disordered

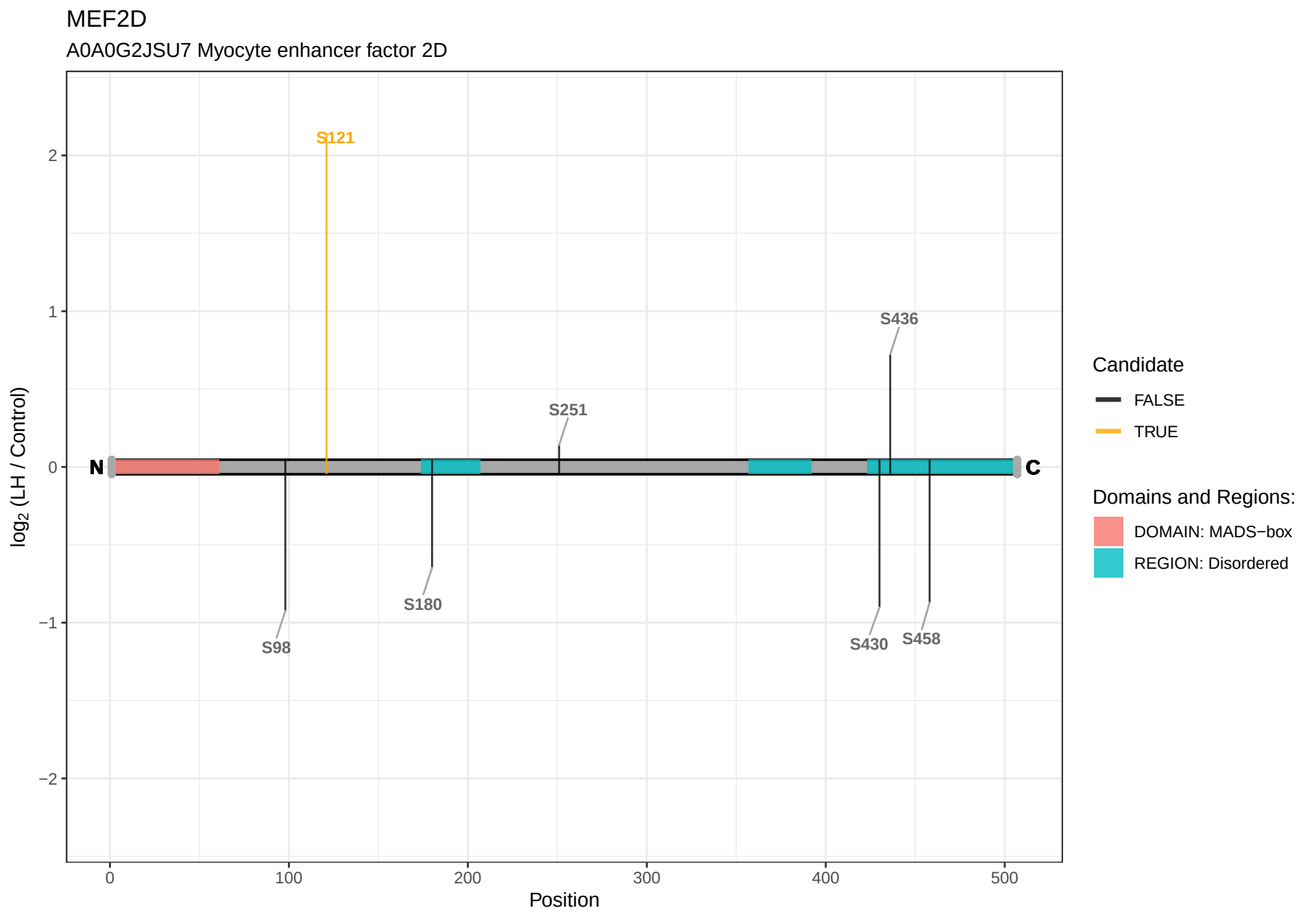

MAVS
Q66HG9 Mitochondrial antiviral−signaling protein
log2 (LH / Control)
2
1
0
−1
−2
S172
S152
S220
S186
N
C
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CARD
REGION: Disordered
REGION: Interaction with DHX33
REGION: Interaction with TRAF2
REGION: Interaction with TRAF6
REGION: Required for interaction with NLRX1

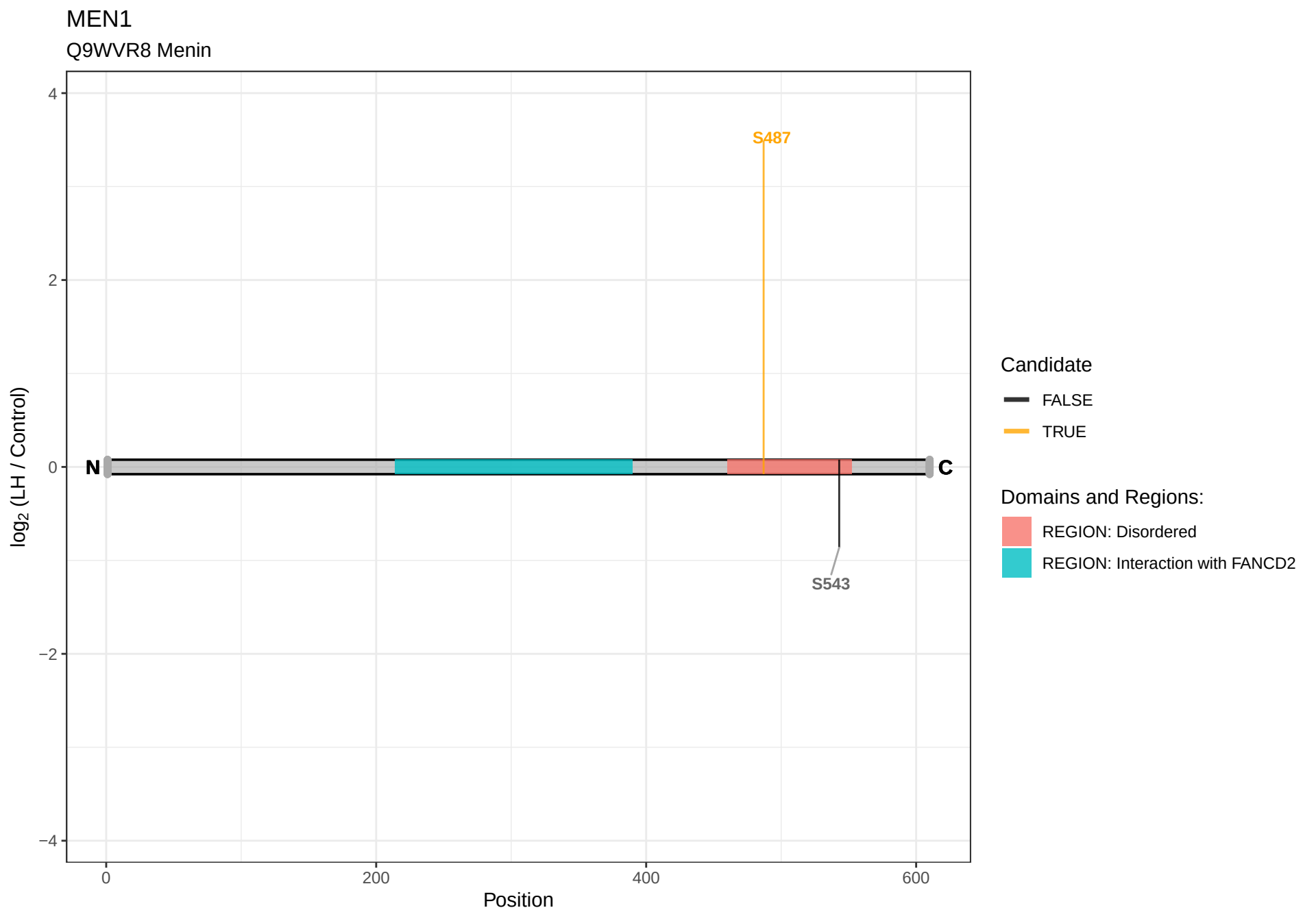

MBOAT7L1
G3V7N6 Membrane−bound O−acyltransferase domain−containing 7−like 1
2
1
0
−1
−2
log2 (LH / Control)
S459
N
C
0
100
200
300
400
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

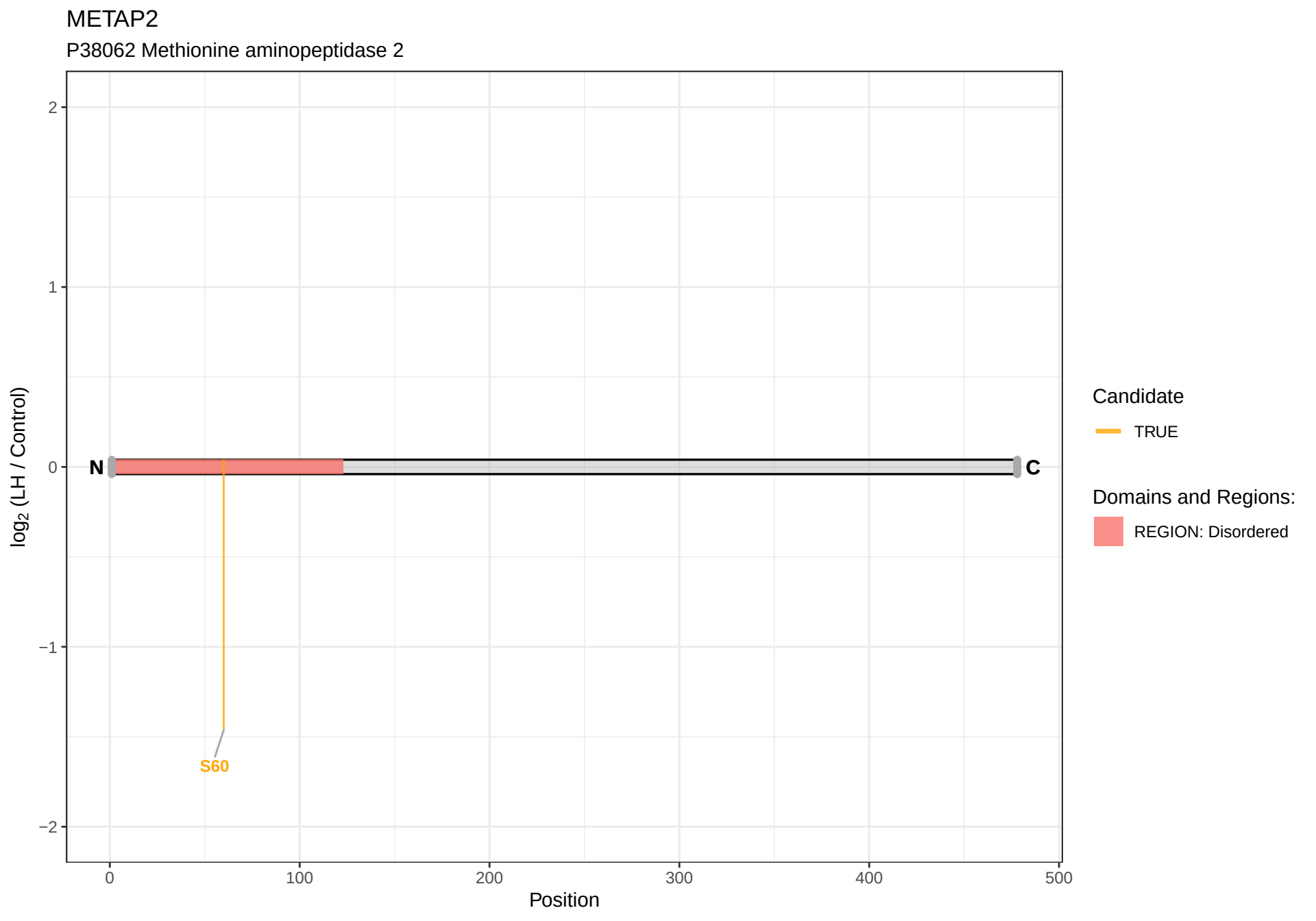

MCM2
D3ZP96 DNA helicase
log2 (LH / Control)
2
0
−2
N
C
S22
S27
S7
T40
S9
S13
T60
S32
S41
S42
S54
S109
S140
S28
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: MCM
REGION: Disordered

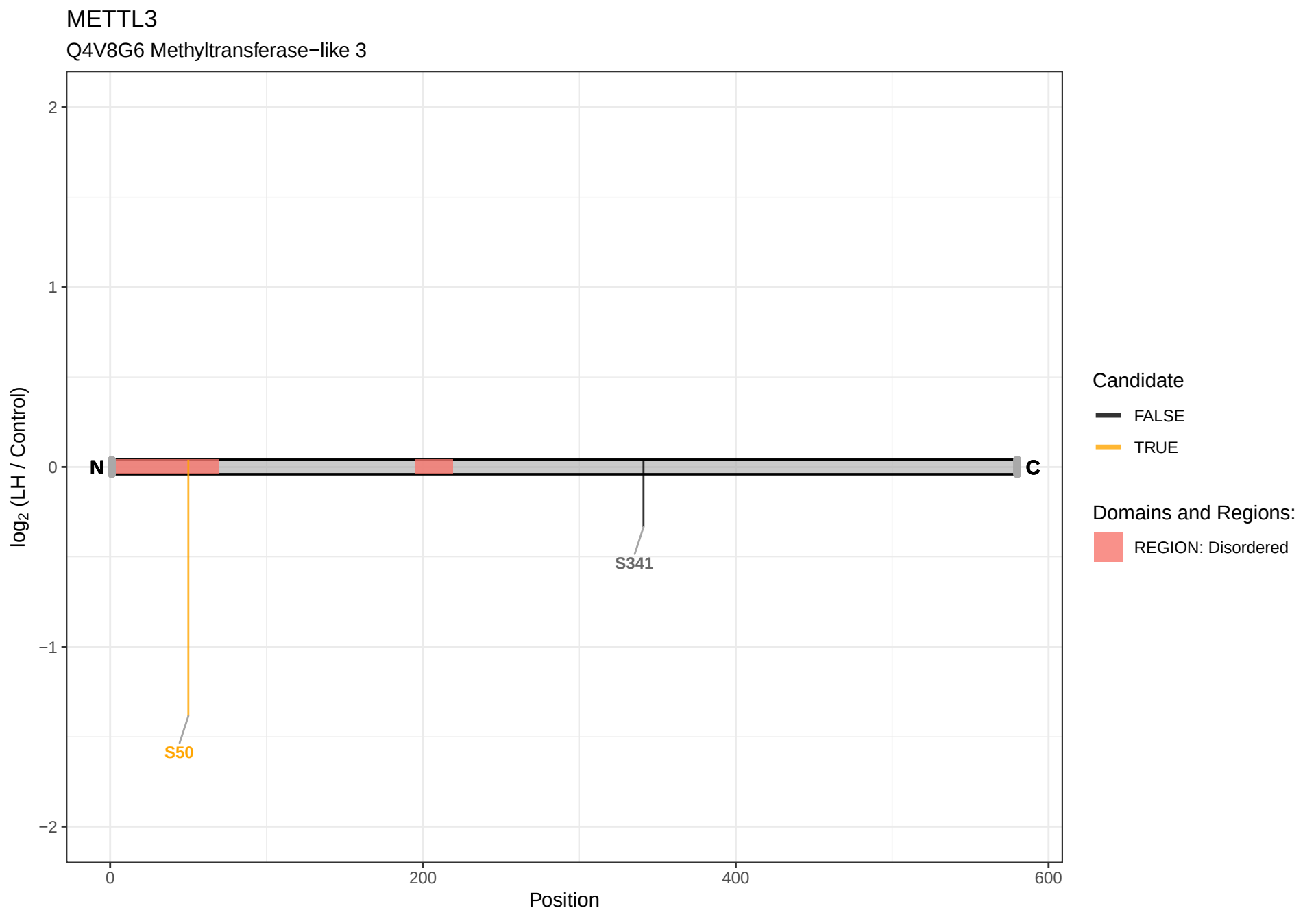

MDC1
Q5U2M8 Mediator of DNA damage checkpoint protein 1
log2 (LH / Control)
Position
N
C
S168
S354
S350
T440
S438
S550
S589
S801
S1016
S548
S446
S432
S380
T382
T352
T356
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: BRCT 1
DOMAIN: BRCT 2
DOMAIN: FHA
REGION: Disordered
REGION: Interaction with CHEK2
REGION: Interaction with the MRN complex

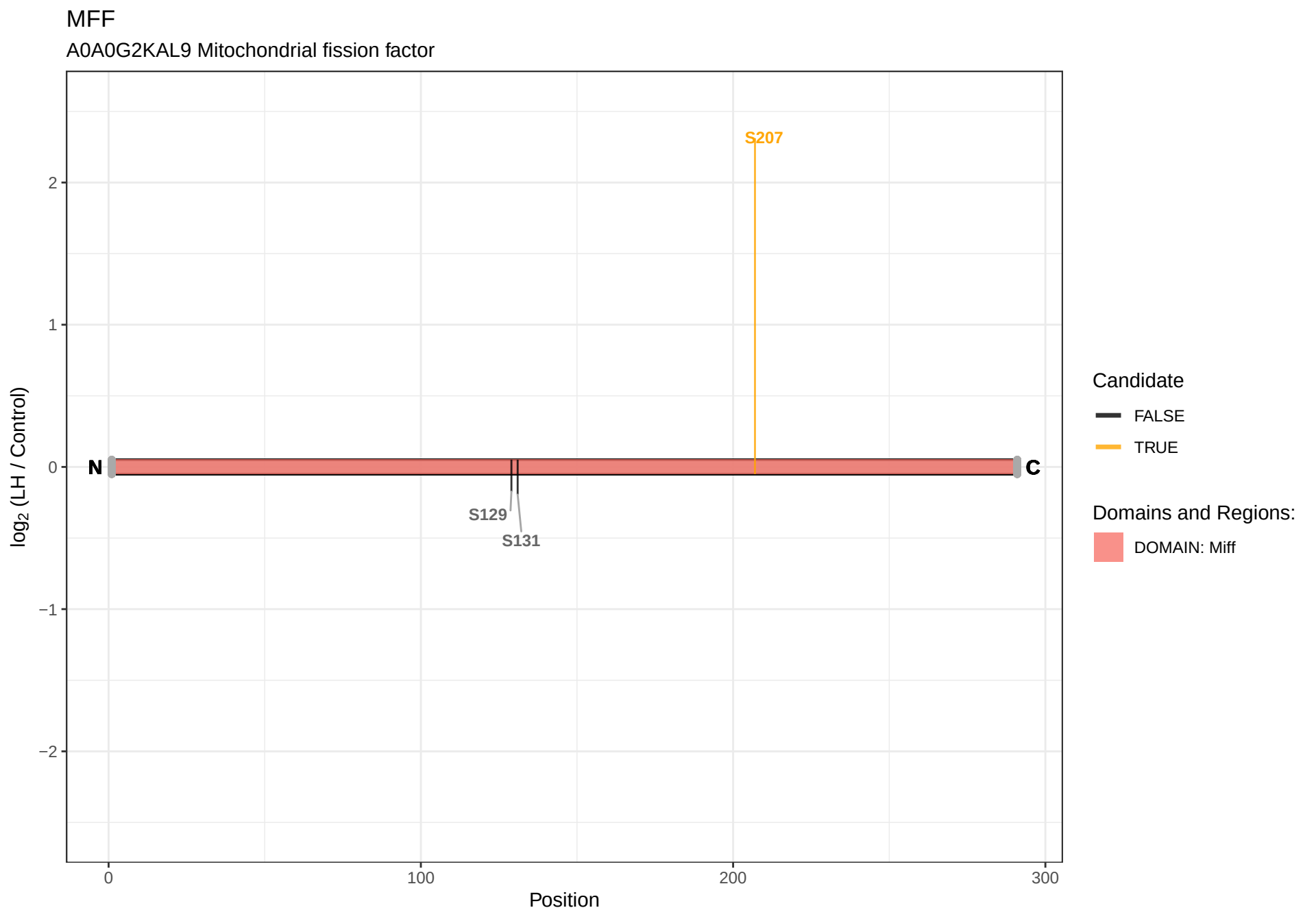

MDM1
A0A0G2KB24 Nuclear protein MDM1
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
N
C
S562
S563
S121
S124
S694
S695
S280
S283
S263
S363
S258
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

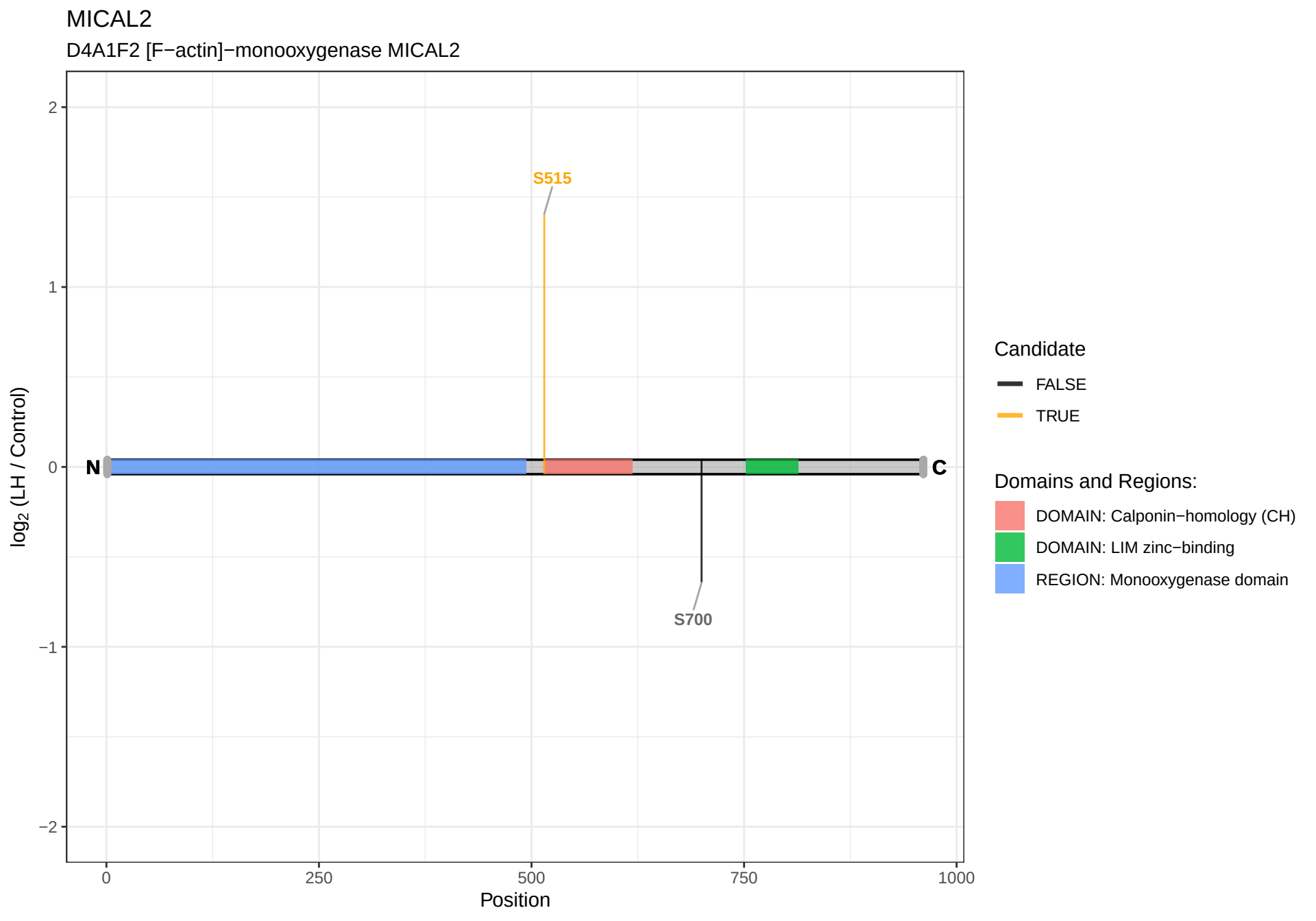

MEF2D
A0A0G2JSU7 Myocyte enhancer factor 2D
S121
S436
S251
N
C
S180
S98
S430
S458
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: MADS−box
REGION: Disordered

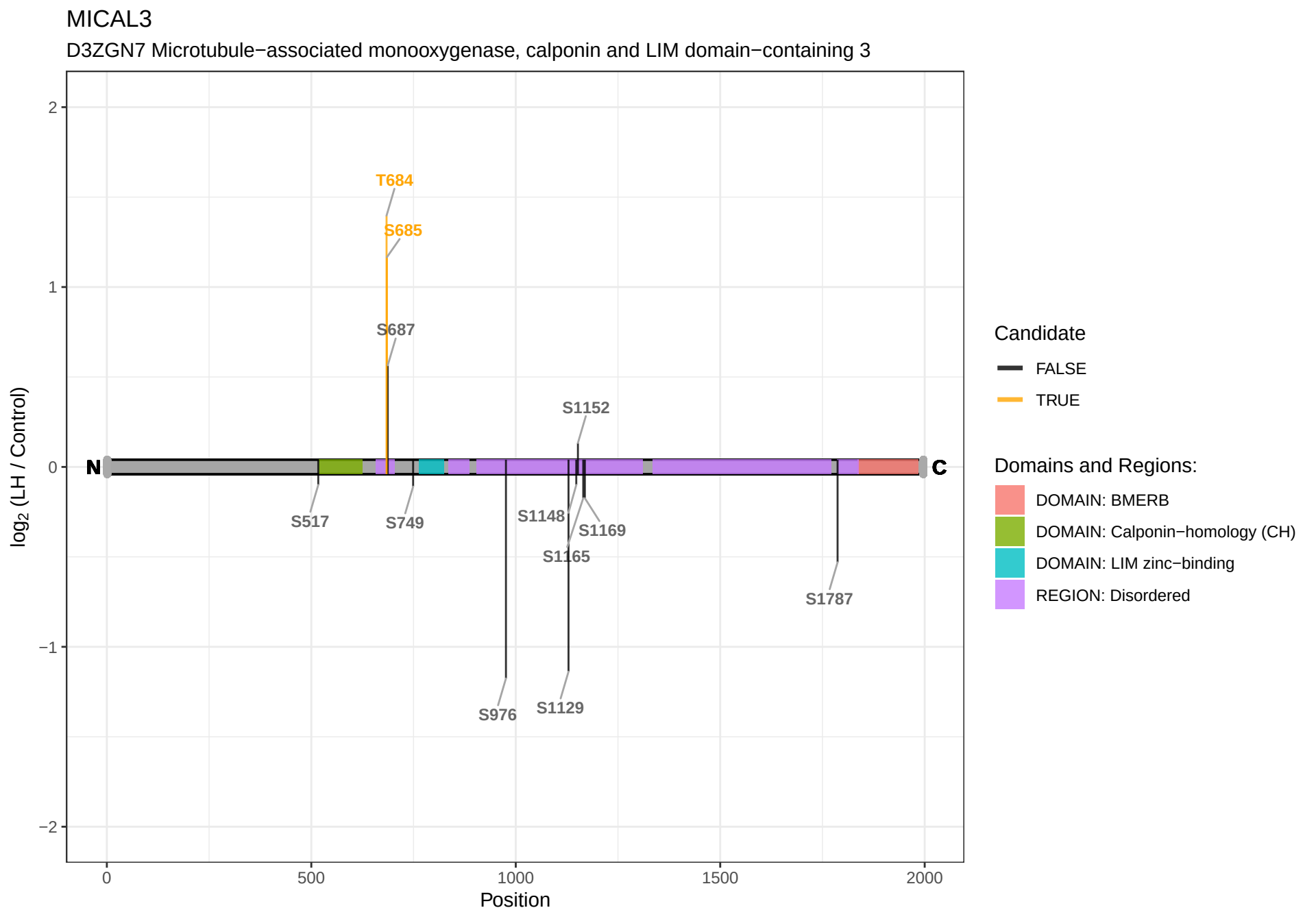

MEN1
Q9WVR8 Menin
S487
S543
N
C
log2 (LH / Control)
Position
4
2
0
−2
−4
0
200
400
600
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Interaction with FANCD2

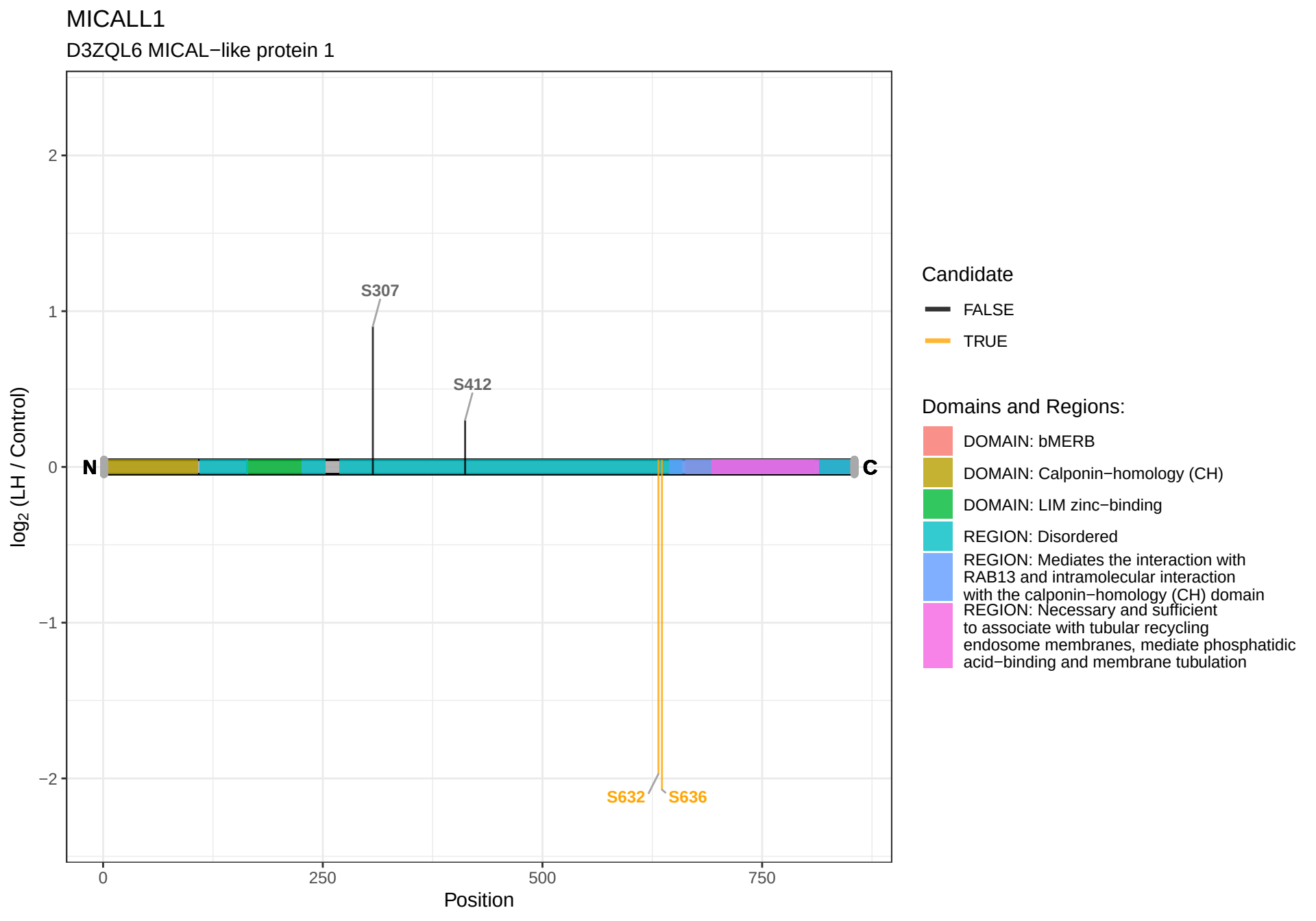

METAP2
P38062 Methionine aminopeptidase 2
log2 (LH / Control)
2
1
0
−1
−2
N
C
S60
0
100
200
300
400
500
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

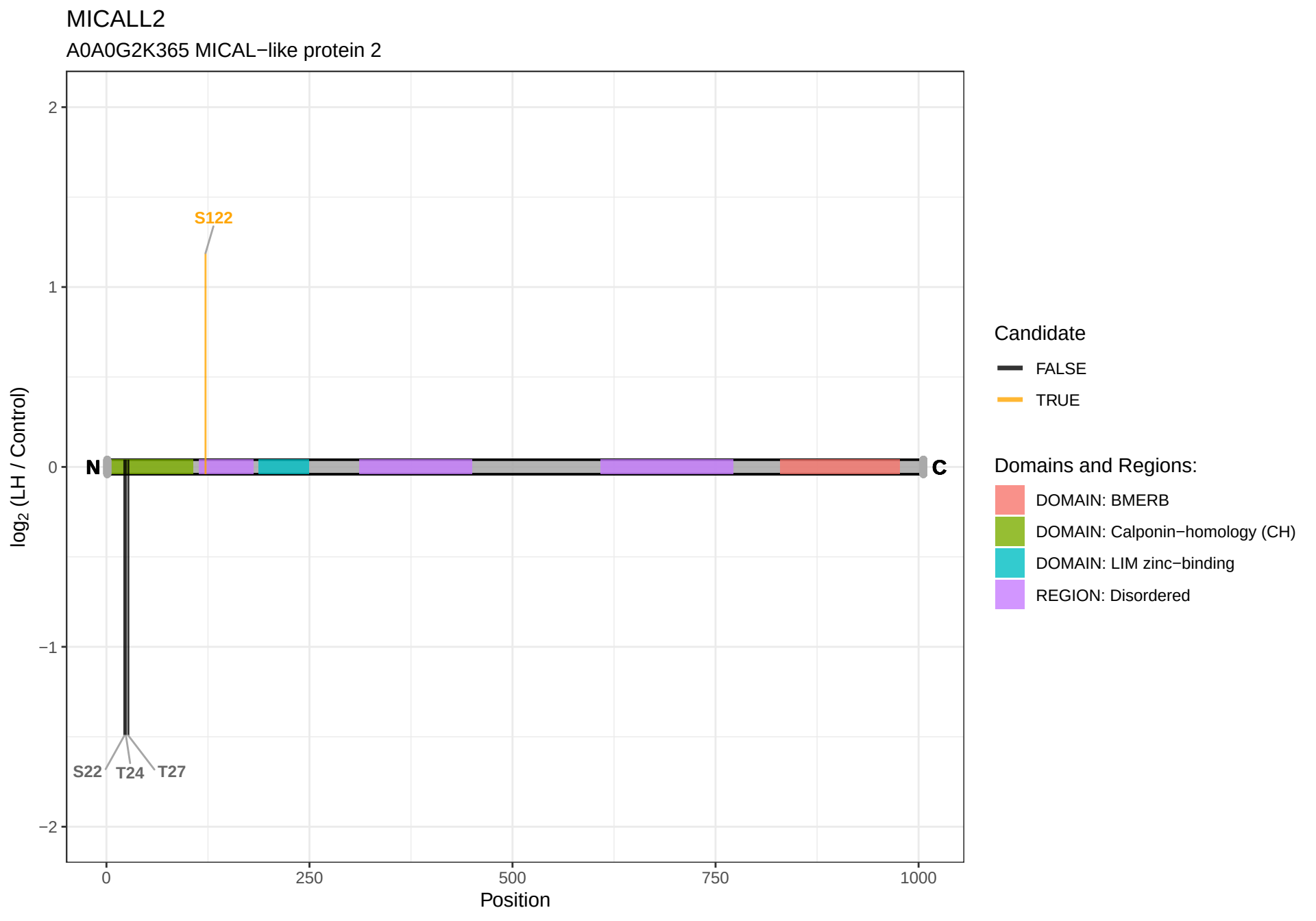

METTL3
Q4V8G6 Methyltransferase−like 3
2
1
0
−1
−2
log2 (LH / Control)
N
C
S341
S50
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

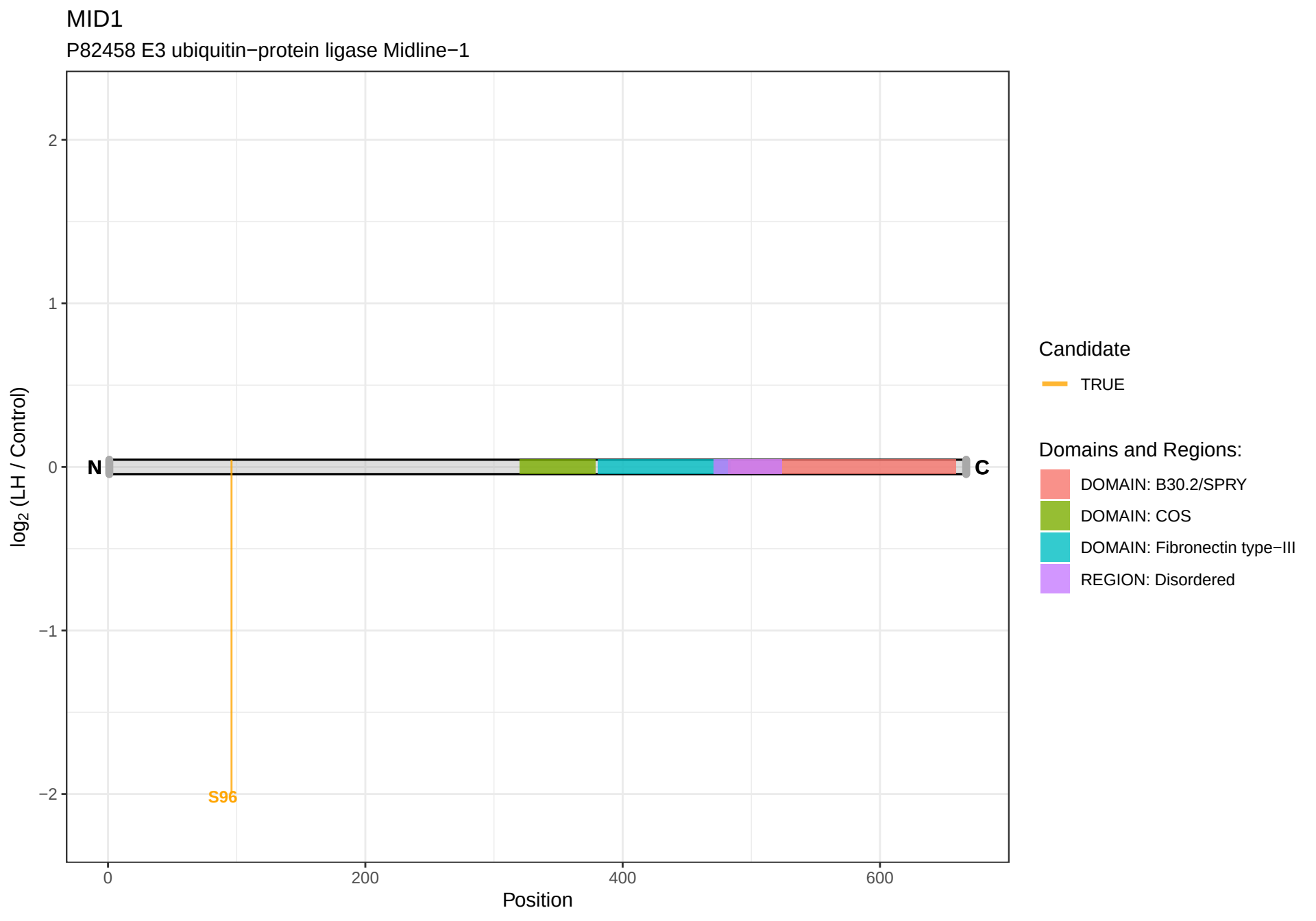

MFF
A0A0G2KAL9 Mitochondrial fission factor
S207
N
C
S129
S131
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Miff

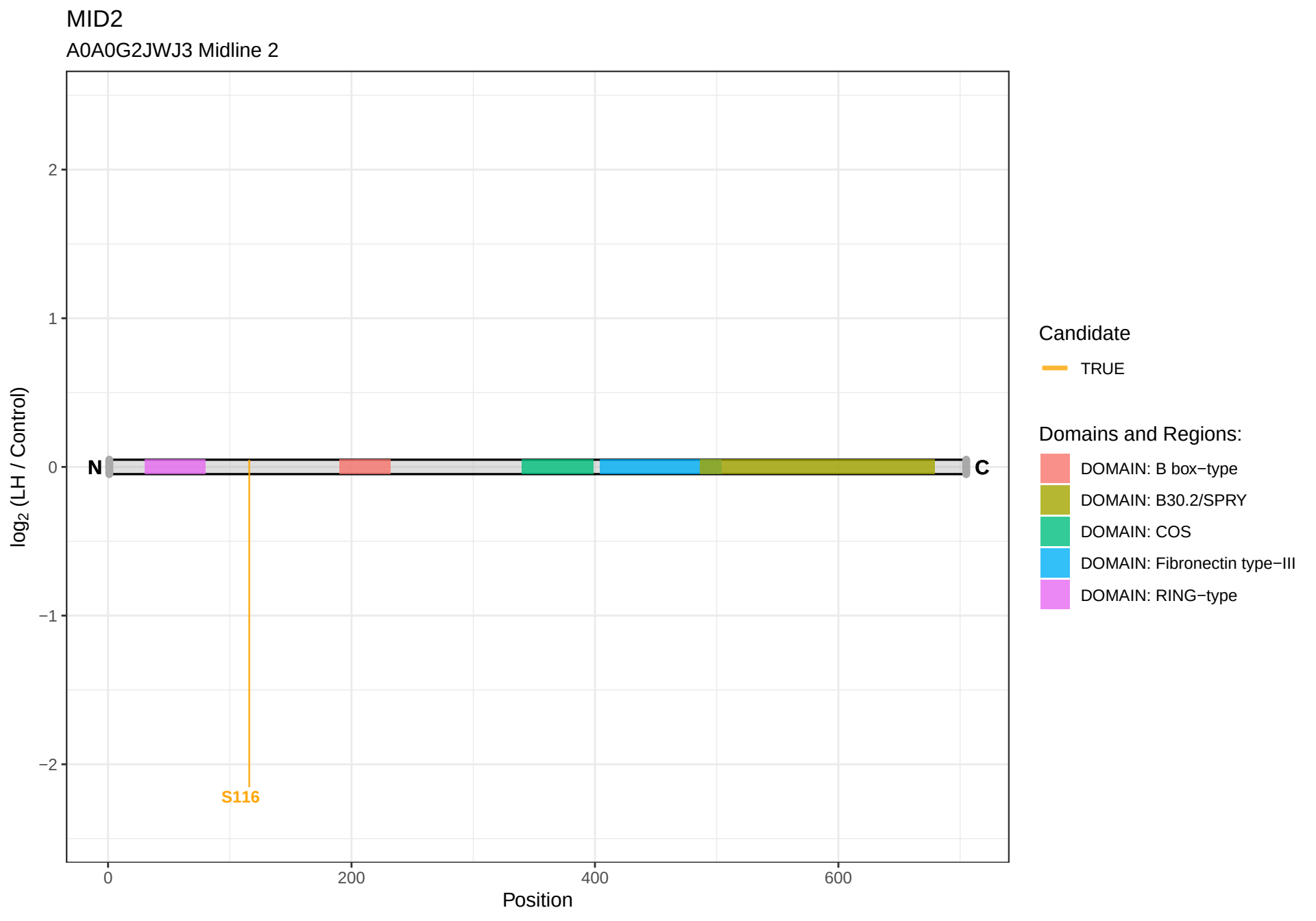

MICAL2
D4A1F2 [F−actin]−monooxygenase MICAL2
log2 (LH / Control)
2
1
0
−1
−2
S515
S700
N
C
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Calponin−homology (CH)
DOMAIN: LIM zinc−binding
REGION: Monooxygenase domain

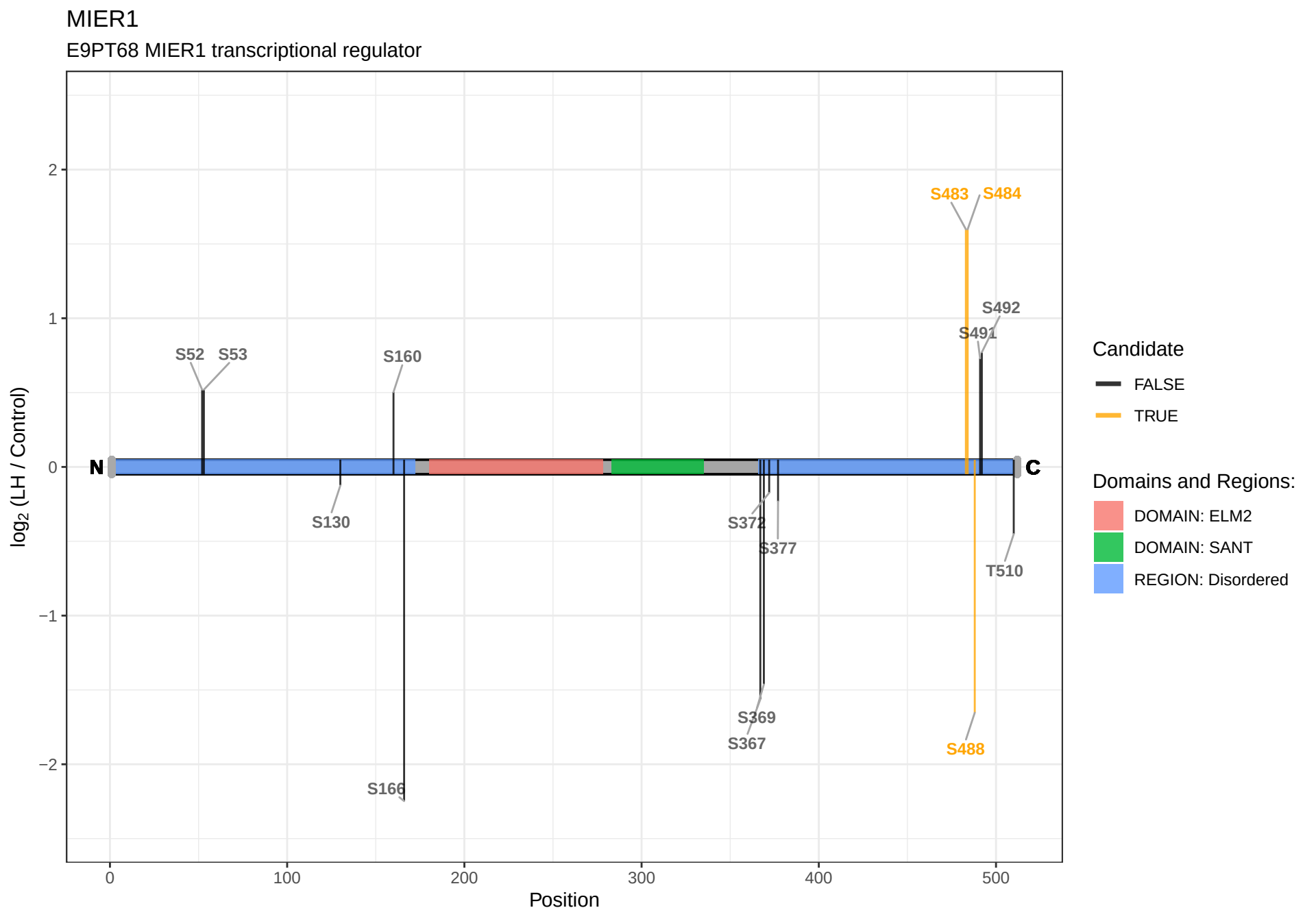

MICAL3
D3ZGN7 Microtubule−associated monooxygenase, calponin and LIM domain−containing 3
log2 (LH / Control)
Position
N
C
T684
S685
S687
S1152
S517
S749
S1148
S1169
S1165
S1787
S976
S1129
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: BMERB
DOMAIN: Calponin−homology (CH)
DOMAIN: LIM zinc−binding
REGION: Disordered

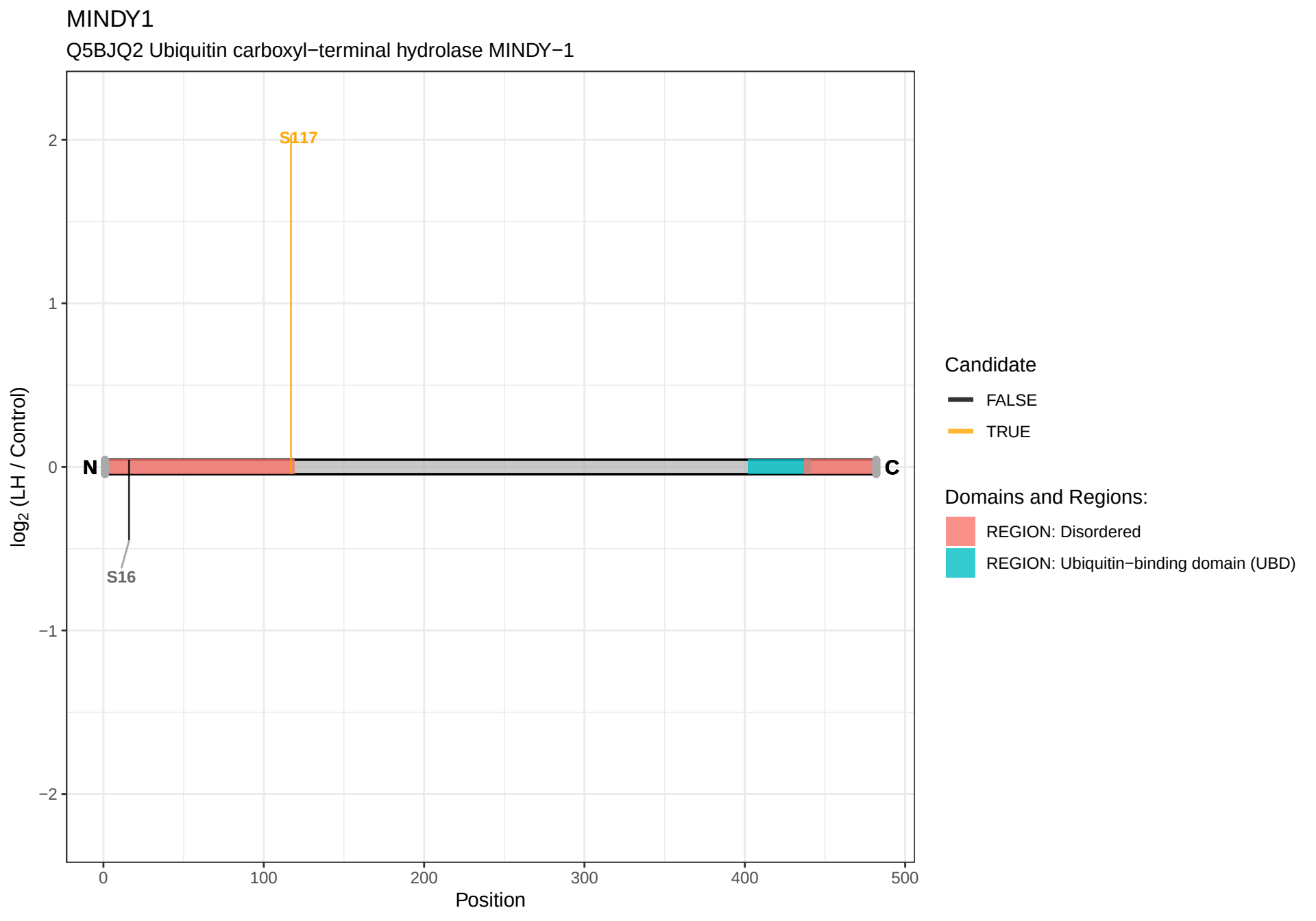

MICALL1
D3ZQL6 MICAL−like protein 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S307
S412
S632
S636
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: bMERB
DOMAIN: Calponin−homology (CH)
DOMAIN: LIM zinc−binding
REGION: Disordered
REGION: Mediates the interaction with RAB13 and intramolecular interaction with the calponin−homology (CH) domain
REGION: Necessary and sufficient to associate with tubular recycling endosome membranes, mediate phosphatidic acid−binding and membrane tubulation

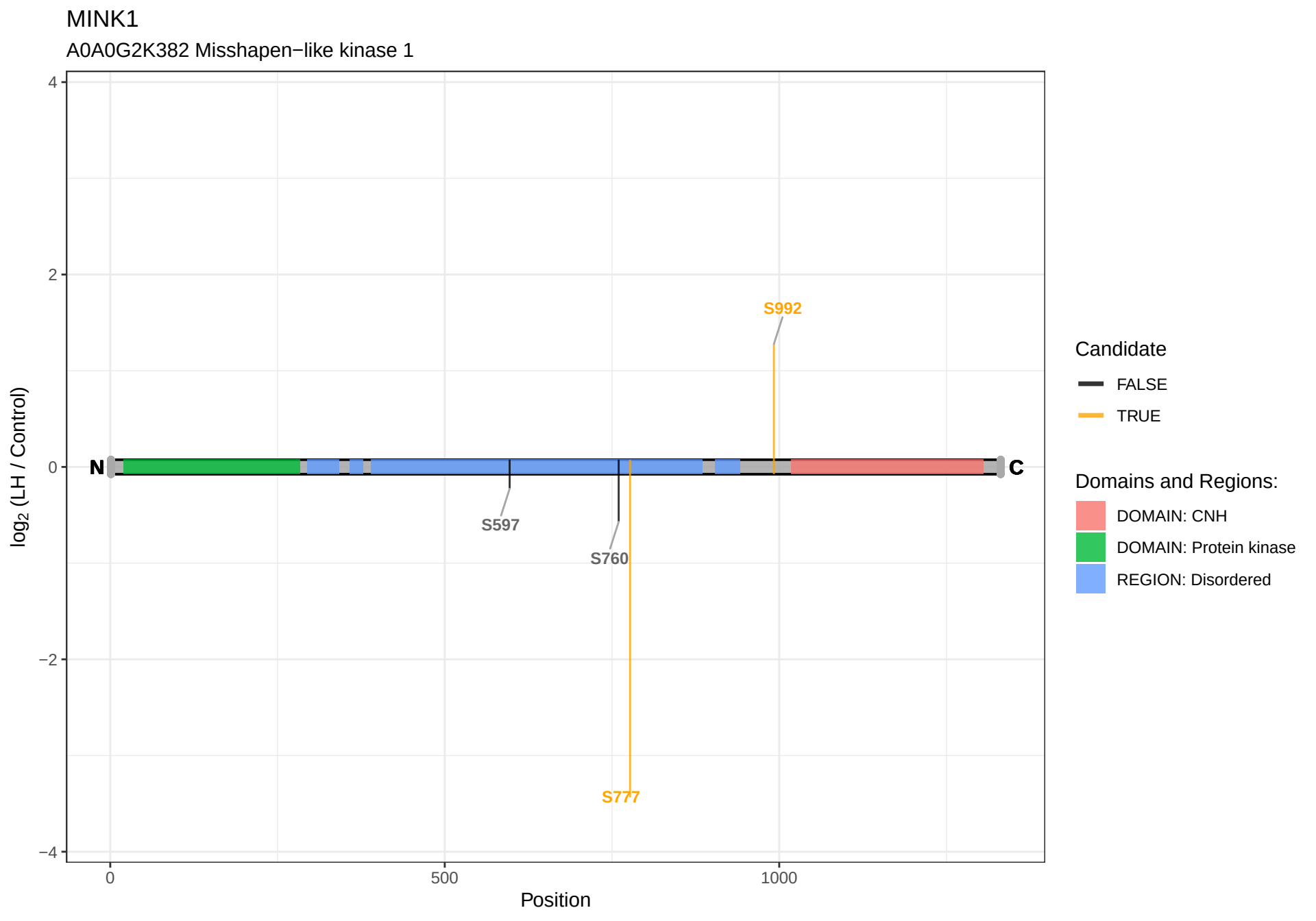

MICALL2
A0A0G2K365 MICAL−like protein 2
log2 (LH / Control)
2
1
0
−1
−2
S122
N
C
S22
T24
T27
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: BMERB
DOMAIN: Calponin−homology (CH)
DOMAIN: LIM zinc−binding
REGION: Disordered

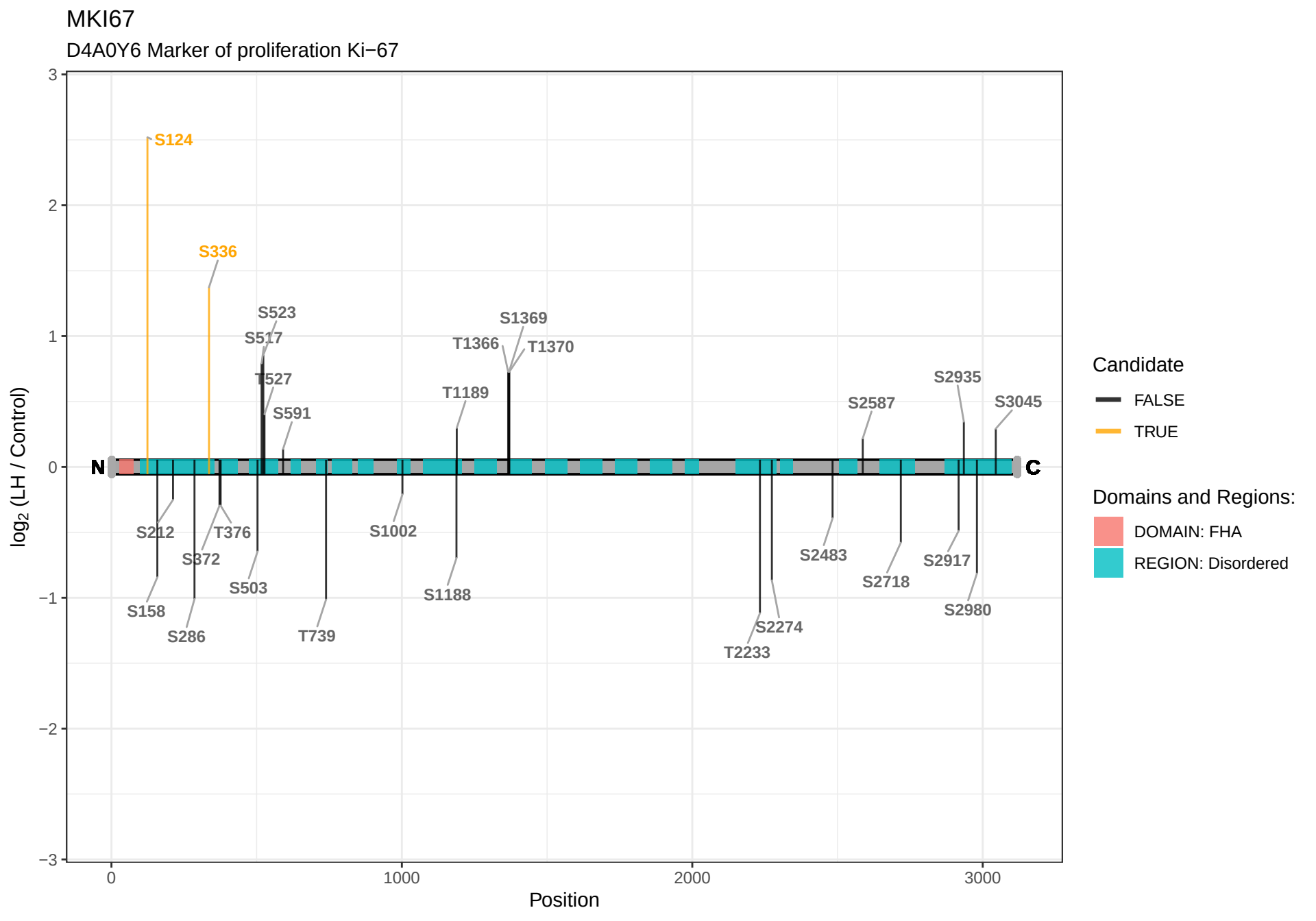

MID1
P82458 E3 ubiquitin−protein ligase Midline−1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S96
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: B30.2/SPRY
DOMAIN: COS
DOMAIN: Fibronectin type−III
REGION: Disordered

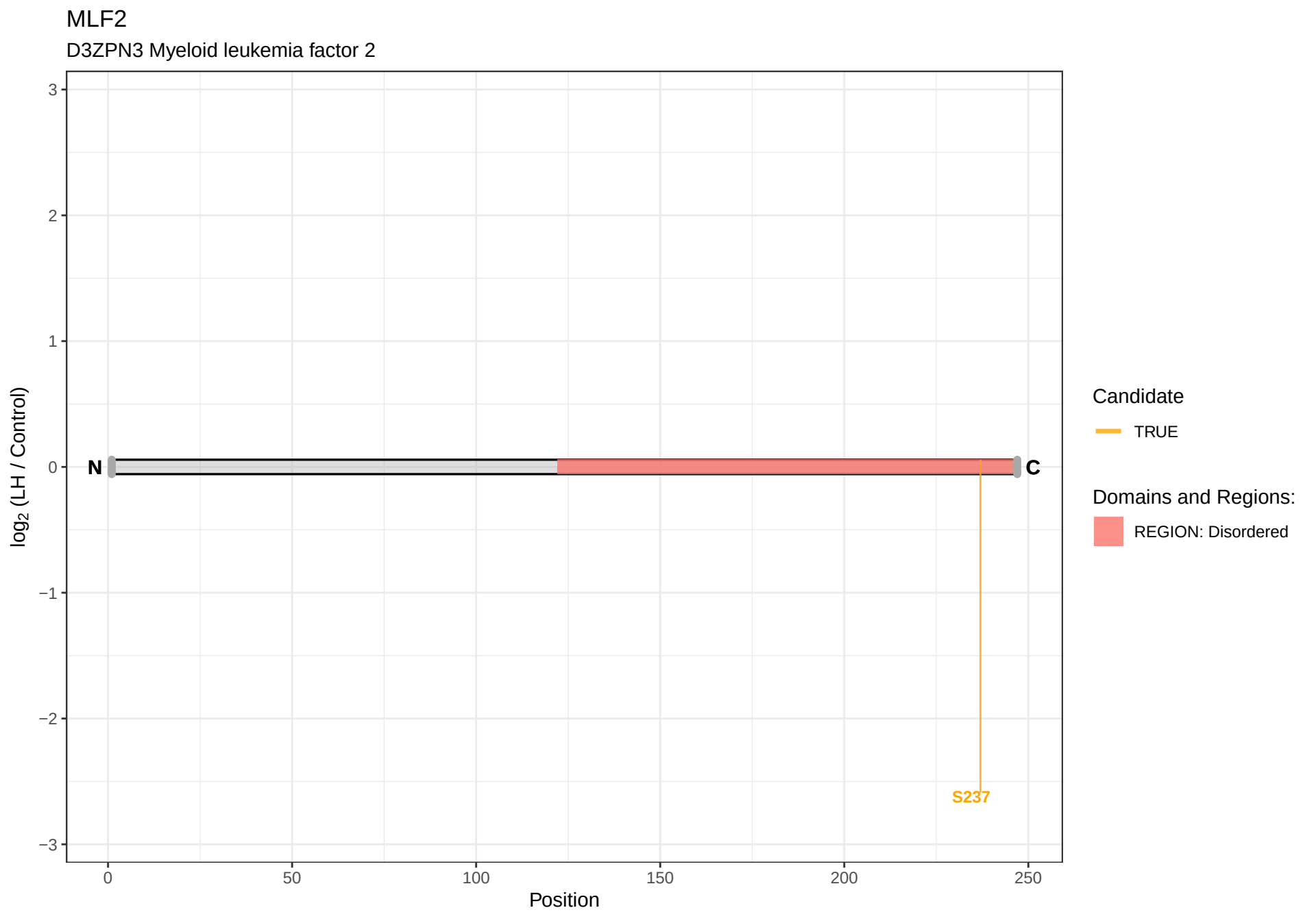

MID2
A0A0G2JWJ3 Midline 2
log2 (LH / Control)
2
1
0
−1
−2
N
C
S116
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: B box−type
DOMAIN: B30.2/SPRY
DOMAIN: COS
DOMAIN: Fibronectin type−III
DOMAIN: RING−type

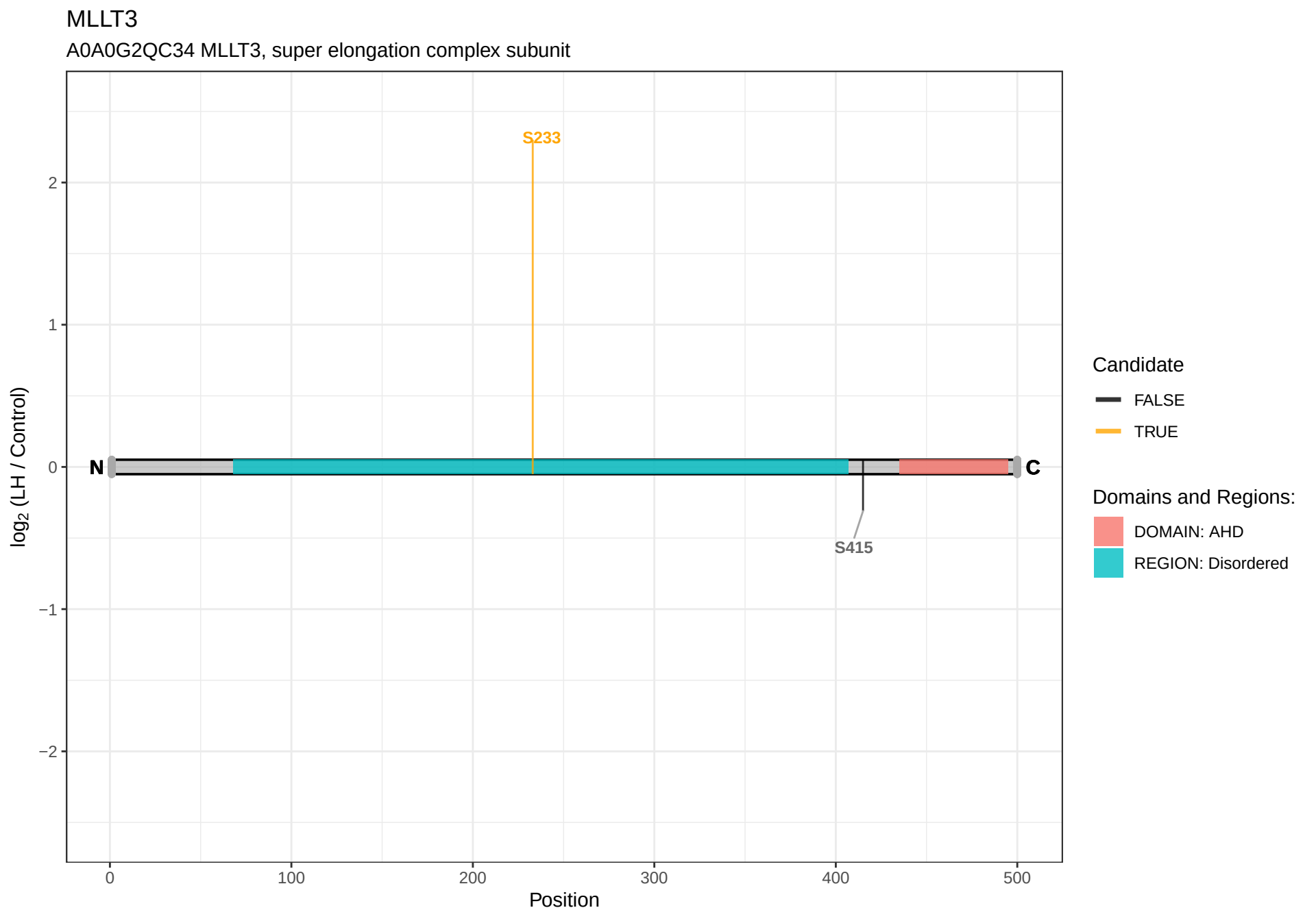

MIER1
E9PT68 MIER1 transcriptional regulator
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
400
500
Position
N
C
S52
S53
S160
S130
S166
S372
S377
S369
S367
S483
S484
S492
S491
T510
S488
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ELM2
DOMAIN: SANT
REGION: Disordered

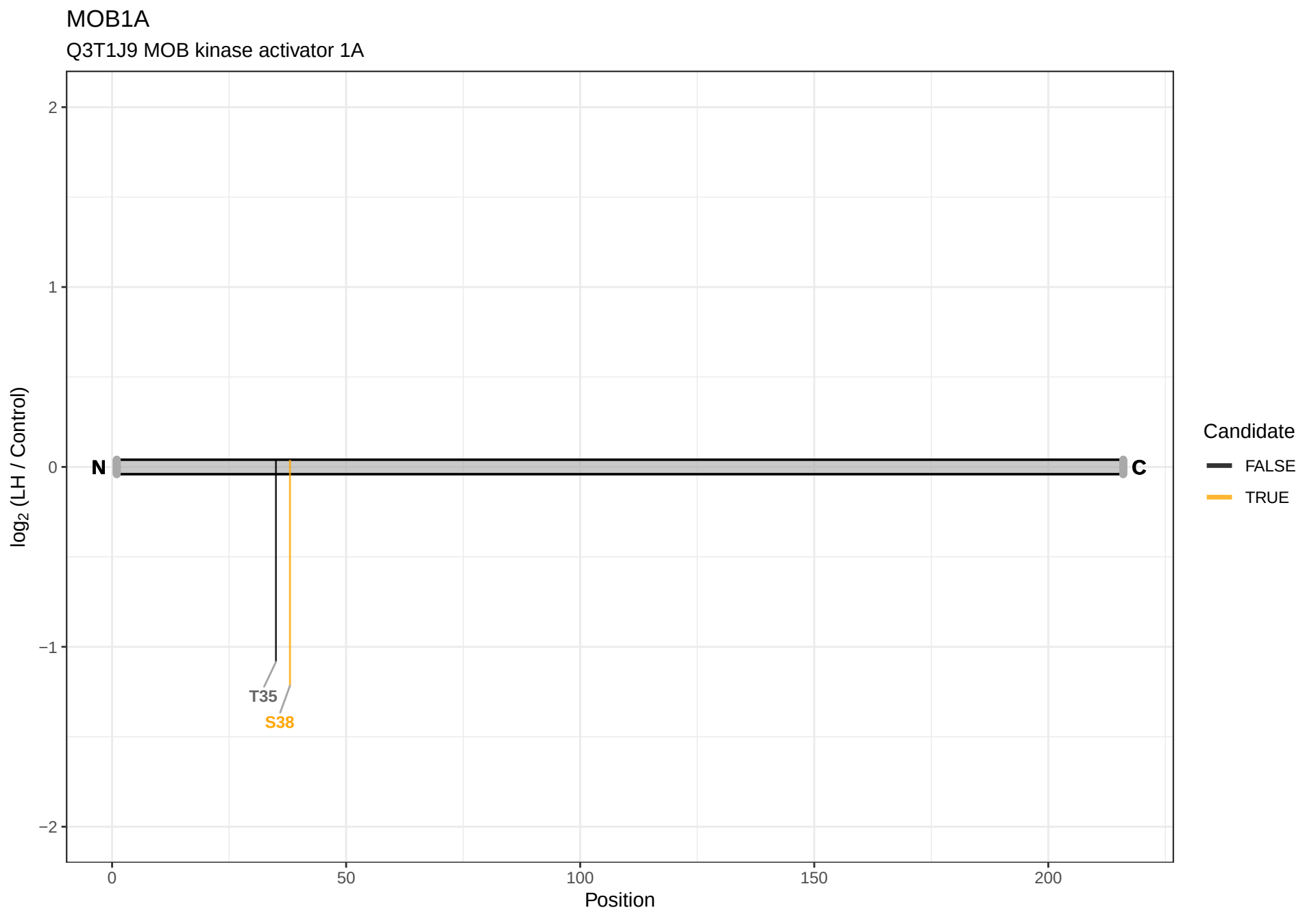

MINDY1
Q5BJQ2 Ubiquitin carboxyl−terminal hydrolase MINDY−1
S117
S16
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Ubiquitin−binding domain (UBD)

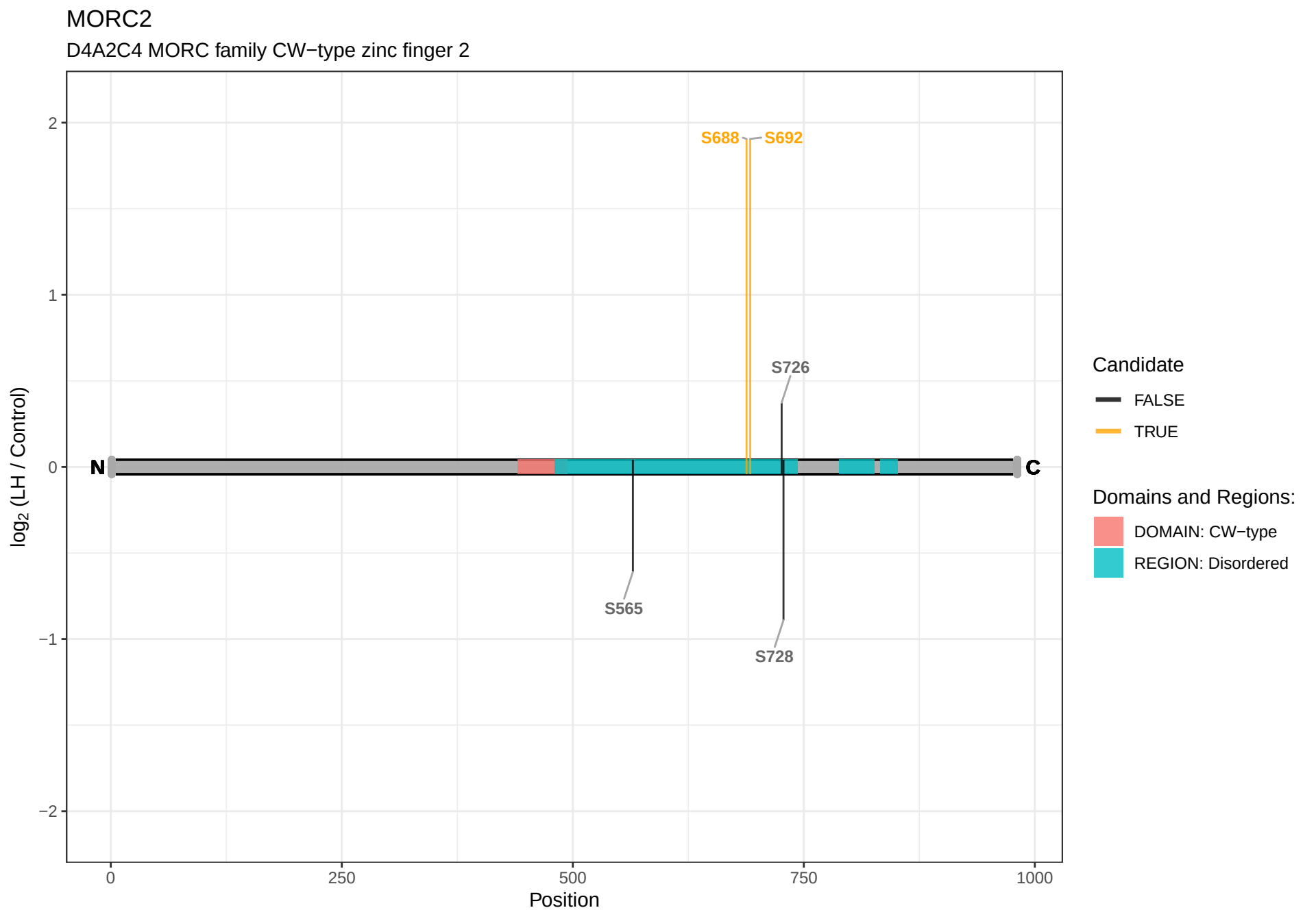

MINK1
A0A0G2K382 Misshapen−like kinase 1
4
2
0
−2
−4
log2 (LH / Control)
N
C
S992
S597
S760
S777
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CNH
DOMAIN: Protein kinase
REGION: Disordered

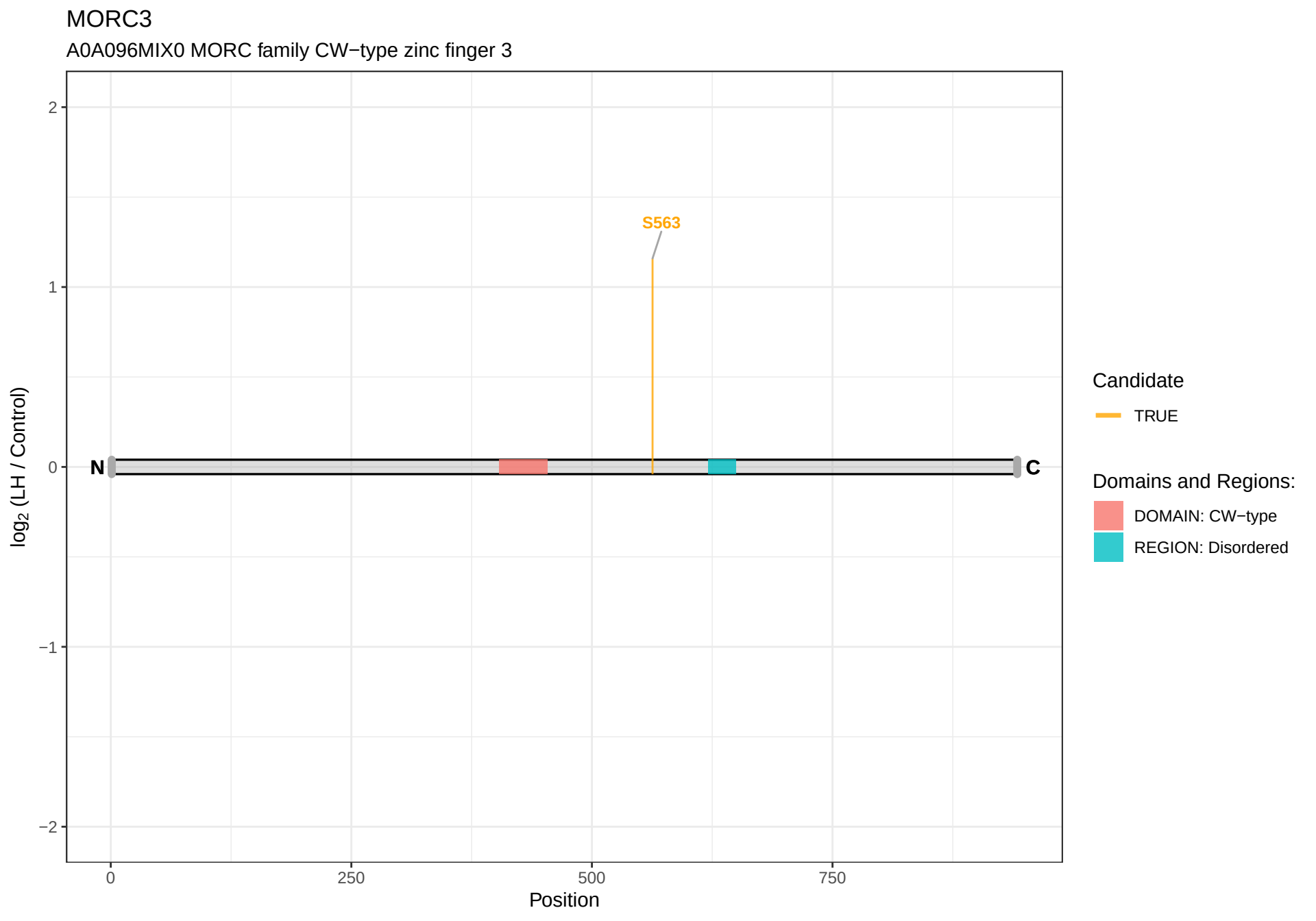

MKI67
D4A0Y6 Marker of proliferation Ki−67
log2 (LH / Control)
Position
3
2
1
0
−1
−2
−3
0
1000
2000
3000
N
C
S124
S336
S523
S517
T527
S591
T1366
S1369
T1370
T1189
S2587
S2935
S3045
S212
T376
S372
S158
S286
S503
T739
S1002
S1188
S2483
S2718
S2917
S2980
T2233
S2274
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: FHA
REGION: Disordered

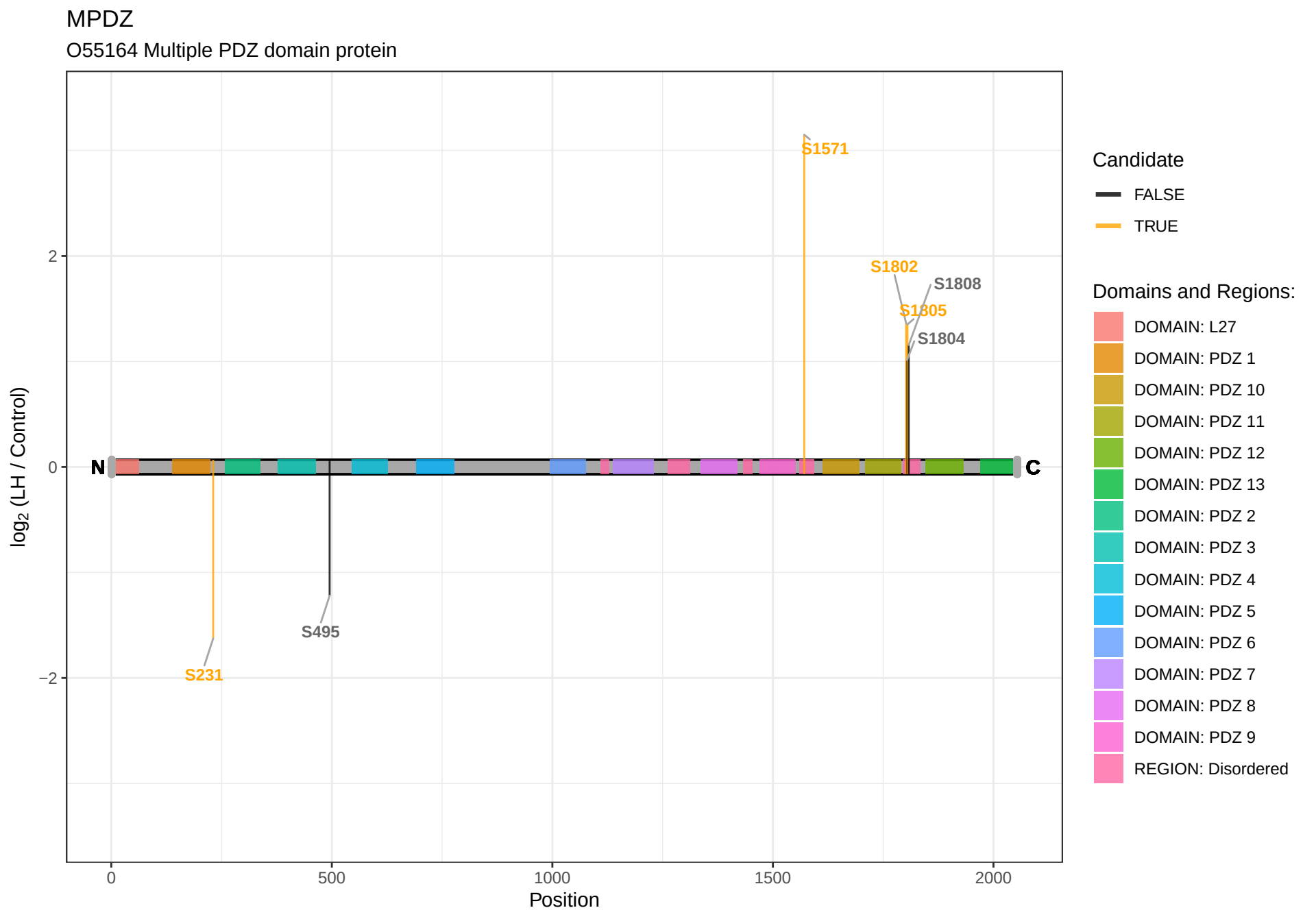

MLF2
D3ZPN3 Myeloid leukemia factor 2
log2 (LH / Control)
3
2
1
0
−1
−2
−3
N
C
S237
0
50
100
150
200
250
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

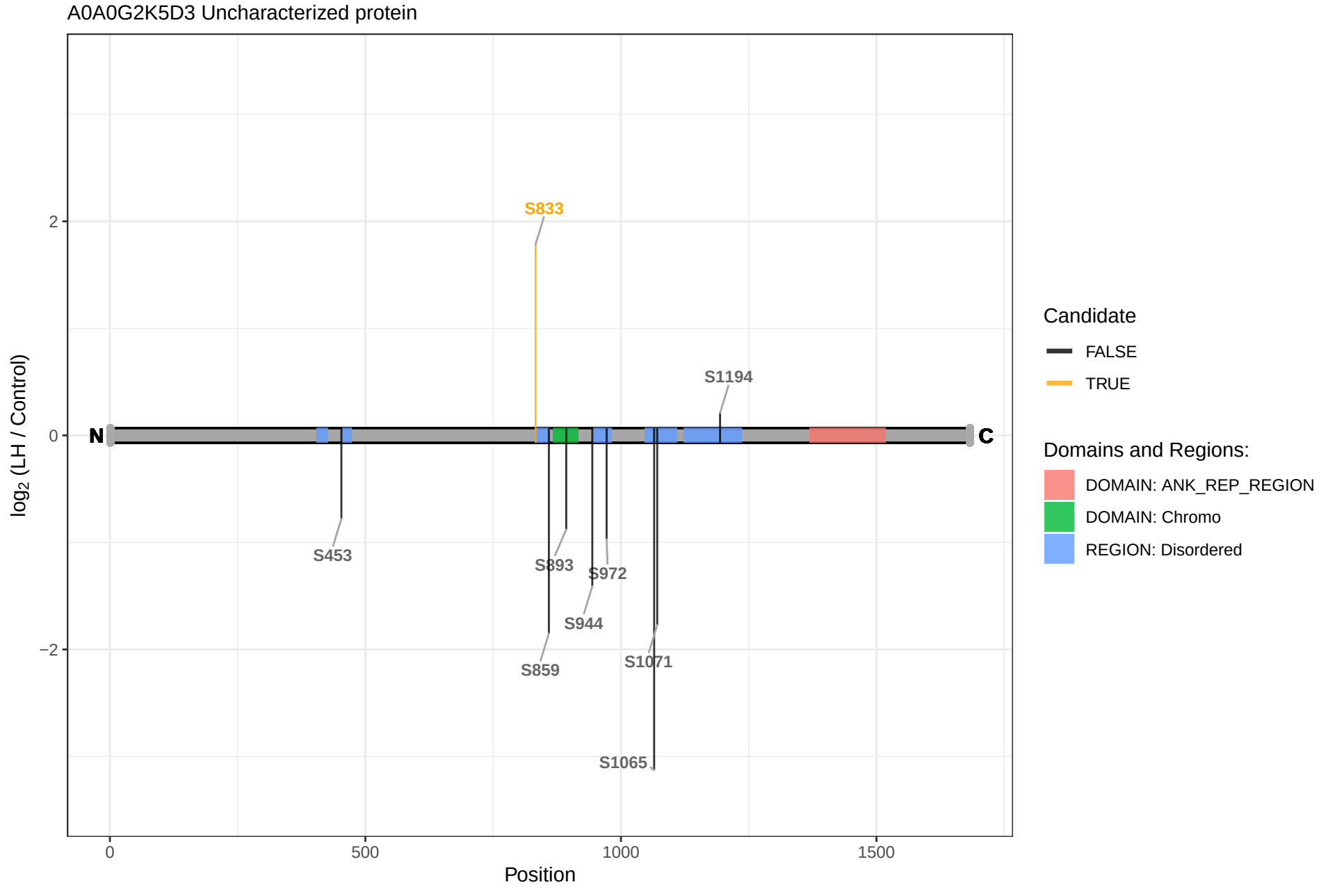

MLLT3
A0A0G2QC34 MLLT3, super elongation complex subunit
S233
S415
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AHD
REGION: Disordered

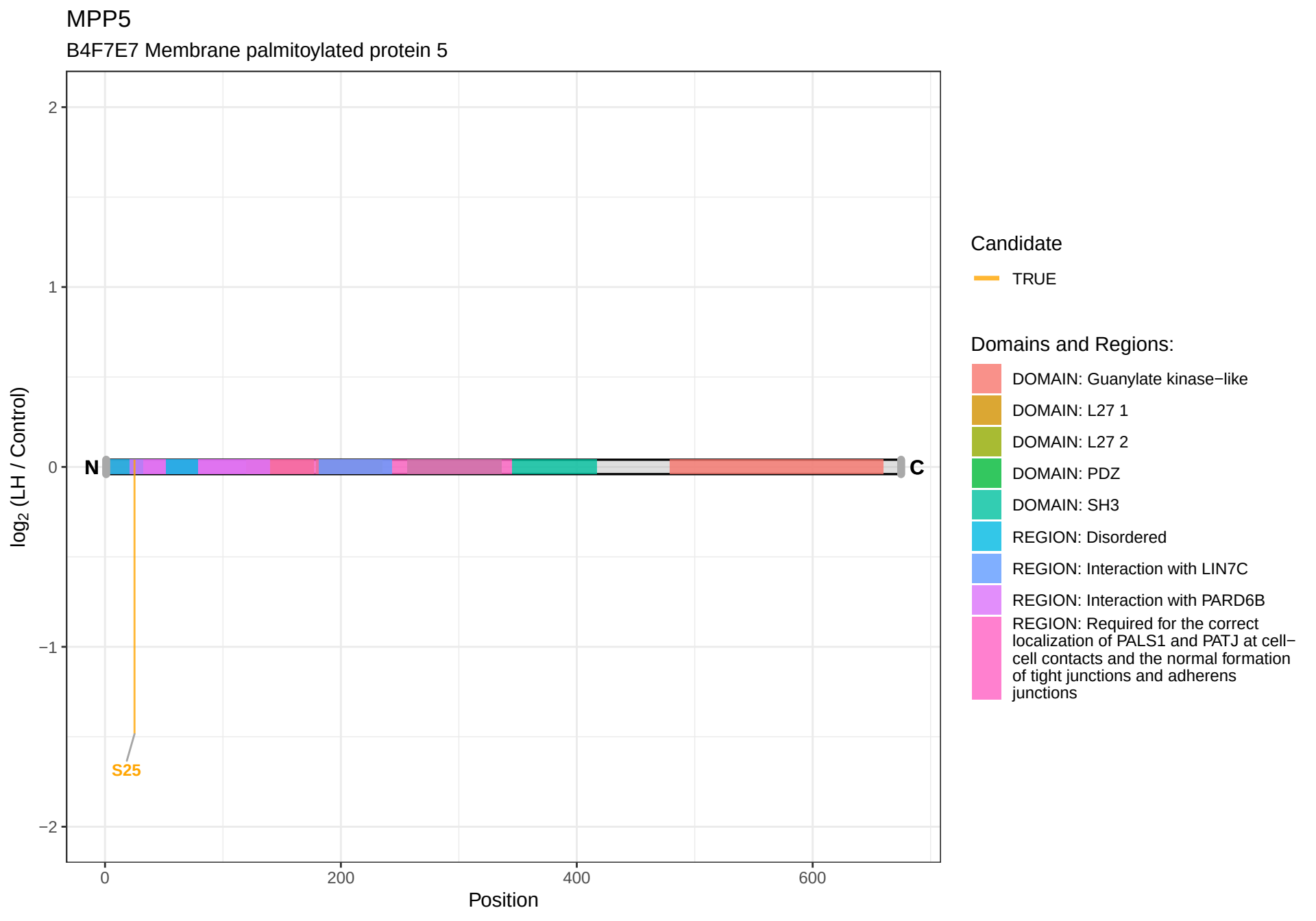

MOB1A
Q3T1J9 MOB kinase activator 1A
2
1
0
−1
−2
log2 (LH / Control)
N
C
T35
S38
0
50
100
150
200
Position
Candidate
FALSE
TRUE

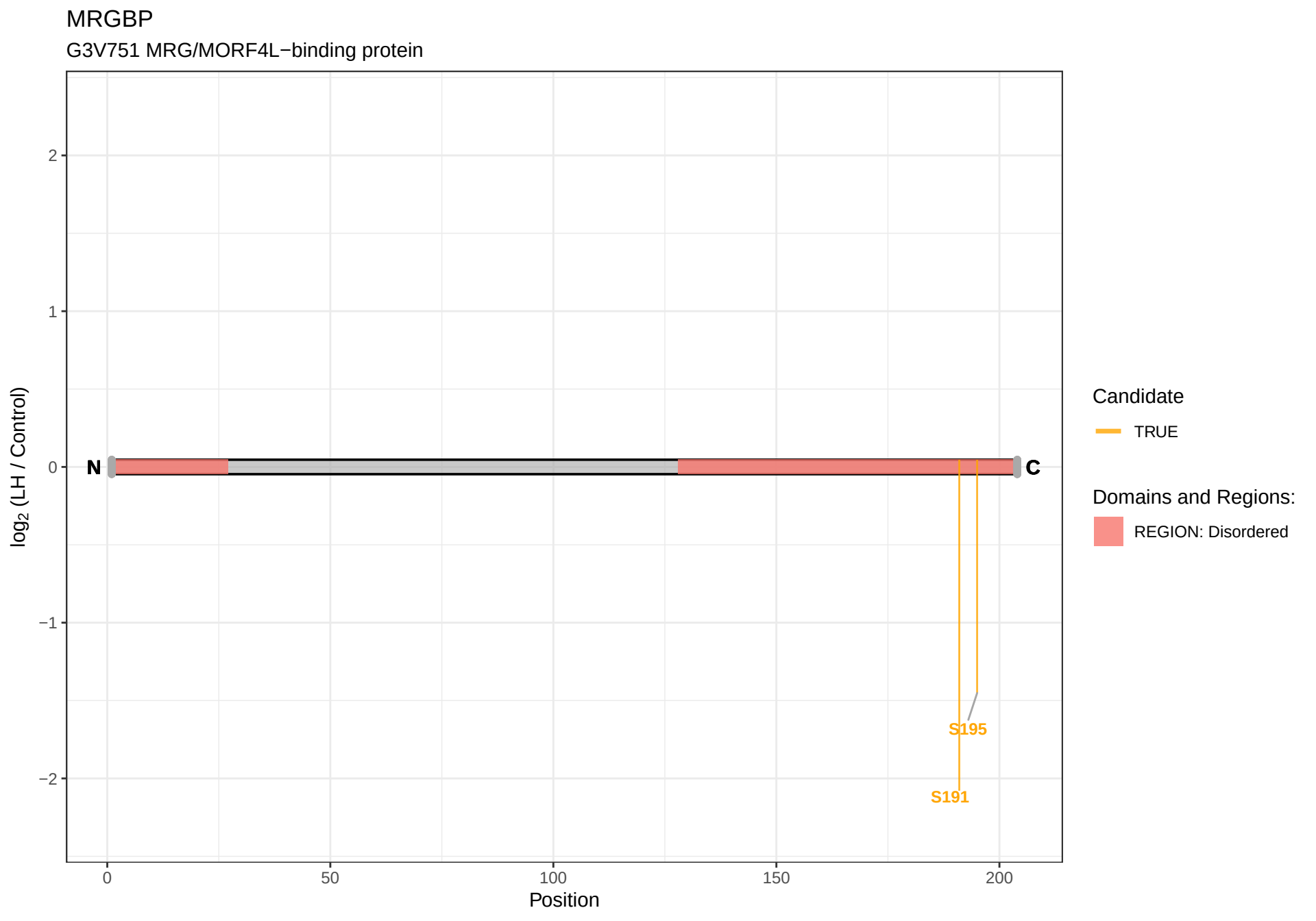

MORC2
D4A2C4 MORC family CW−type zinc finger 2
log2 (LH / Control)
2
1
0
−1
−2
S688
S692
S726
S565
S728
N
C
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CW−type
REGION: Disordered

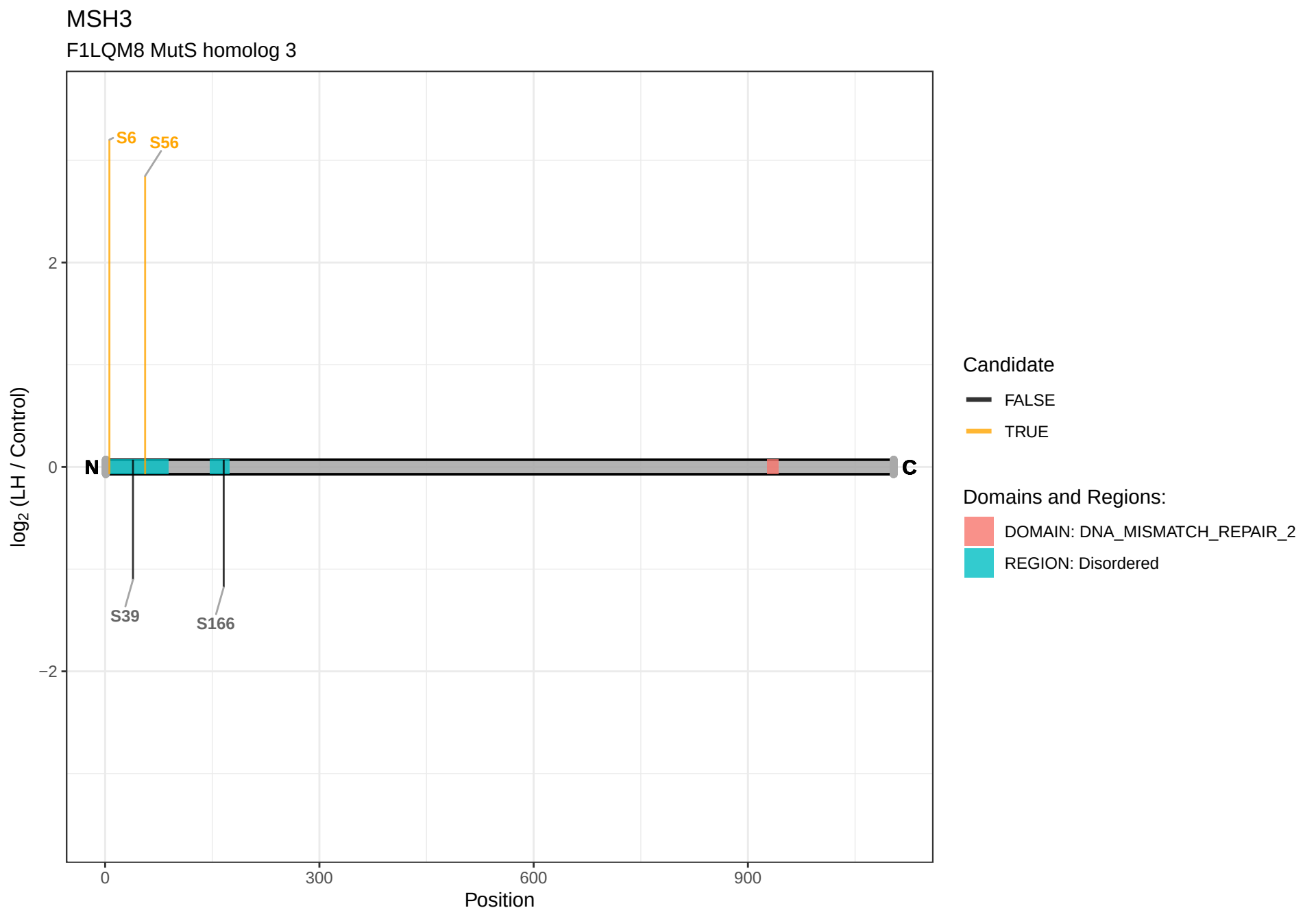

MORC3
A0A096MIX0 MORC family CW−type zinc finger 3
S563
N
C
log2 (LH / Control)
Position
0
250
500
750
2
1
0
−1
−2
Candidate
TRUE
Domains and Regions:
DOMAIN: CW−type
REGION: Disordered

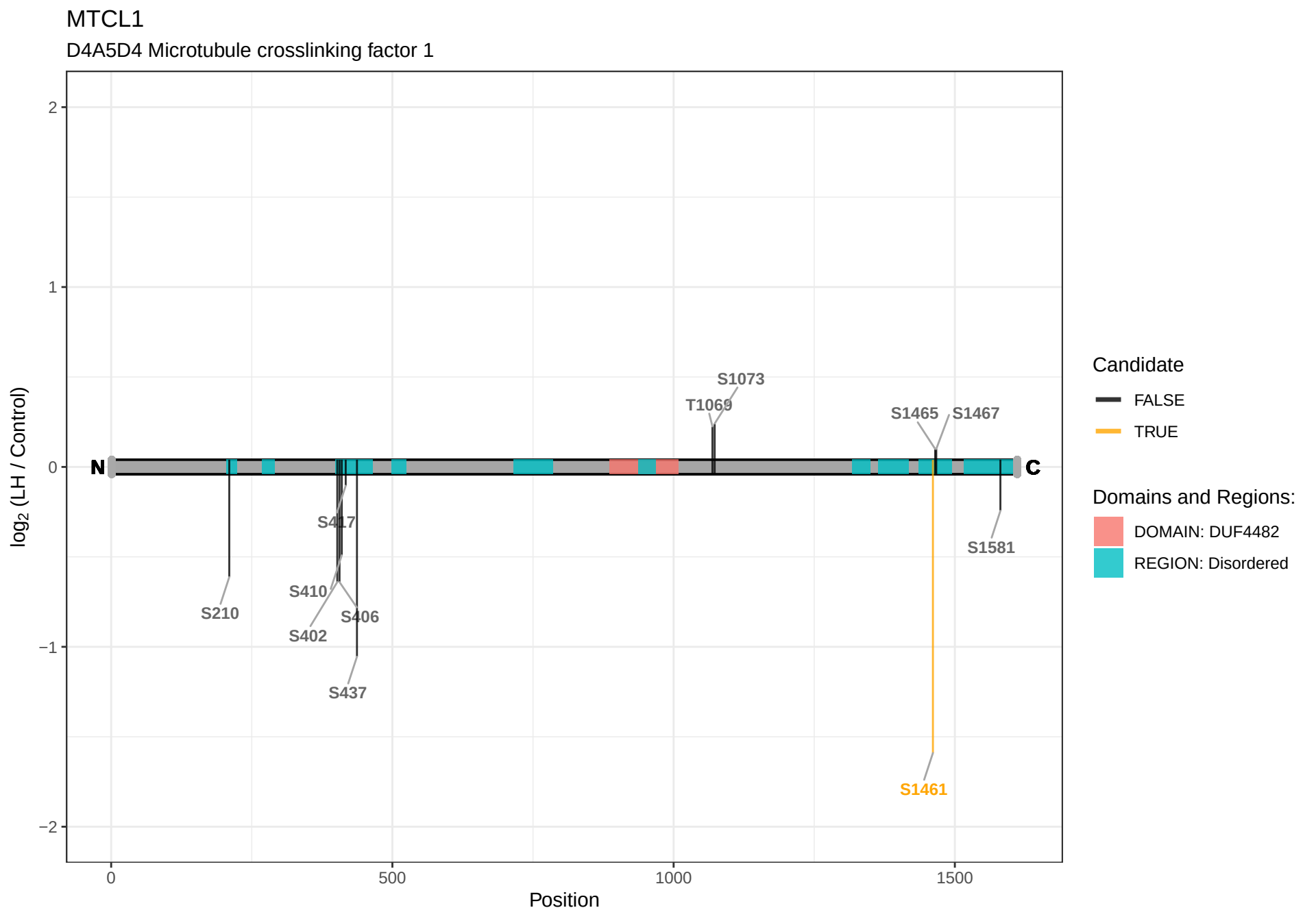

MPDZ
O55164 Multiple PDZ domain protein
S1571
S1802
S1808
S1805
S1804
S495
S231
N
C
2
0
−2
log2 (LH / Control)
0
500
1000
1500
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: L27
DOMAIN: PDZ 1
DOMAIN: PDZ 10
DOMAIN: PDZ 11
DOMAIN: PDZ 12
DOMAIN: PDZ 13
DOMAIN: PDZ 2
DOMAIN: PDZ 3
DOMAIN: PDZ 4
DOMAIN: PDZ 5
DOMAIN: PDZ 6
DOMAIN: PDZ 7
DOMAIN: PDZ 8
DOMAIN: PDZ 9
REGION: Disordered

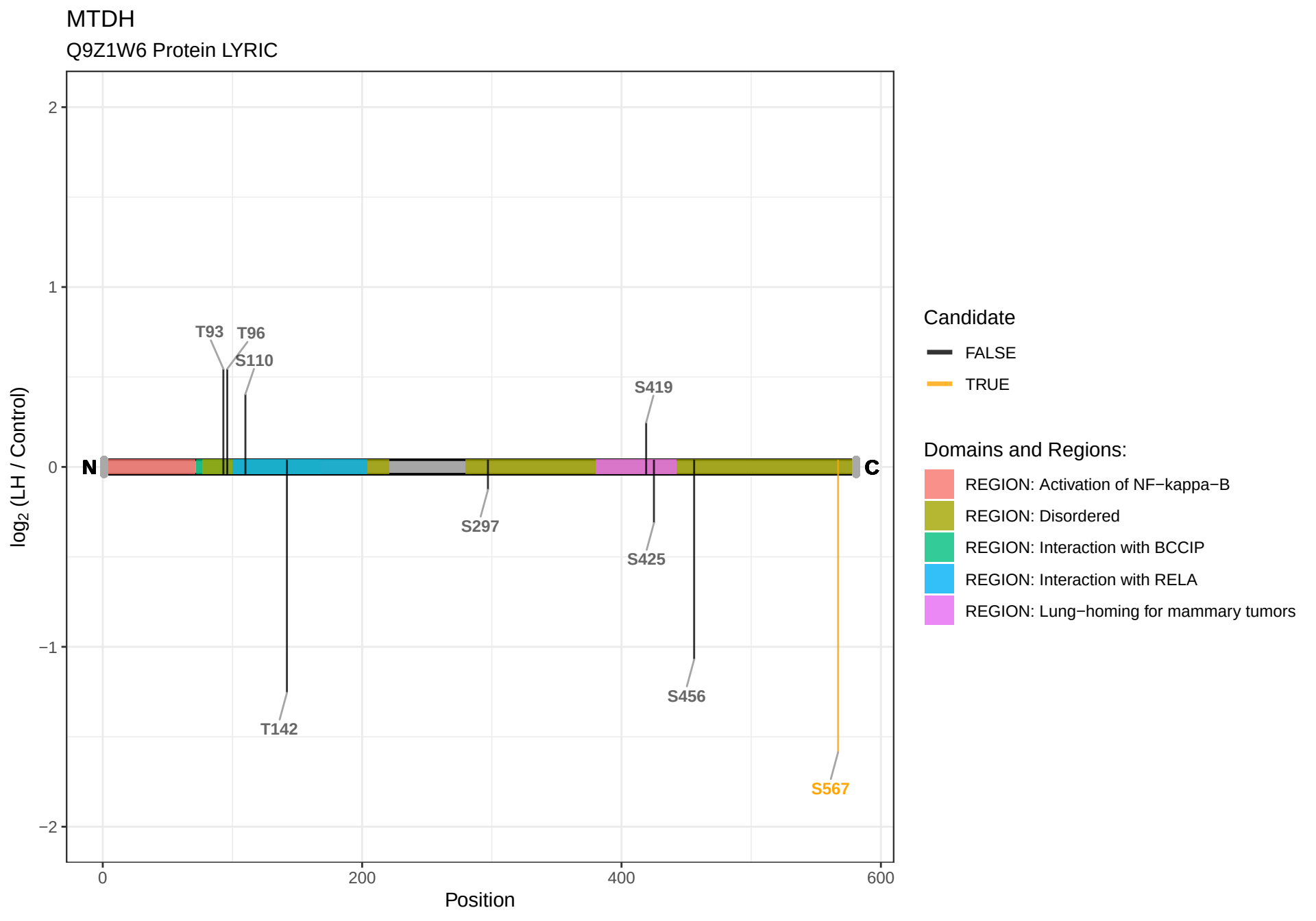

A0A0G2K5D3 Uncharacterized protein
log2 (LH / Control)
2
0
−2
N
C
S833
S1194
S453
S893
S972
S944
S859
S1071
S1065
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ANK_REP_REGION
DOMAIN: Chromo
REGION: Disordered

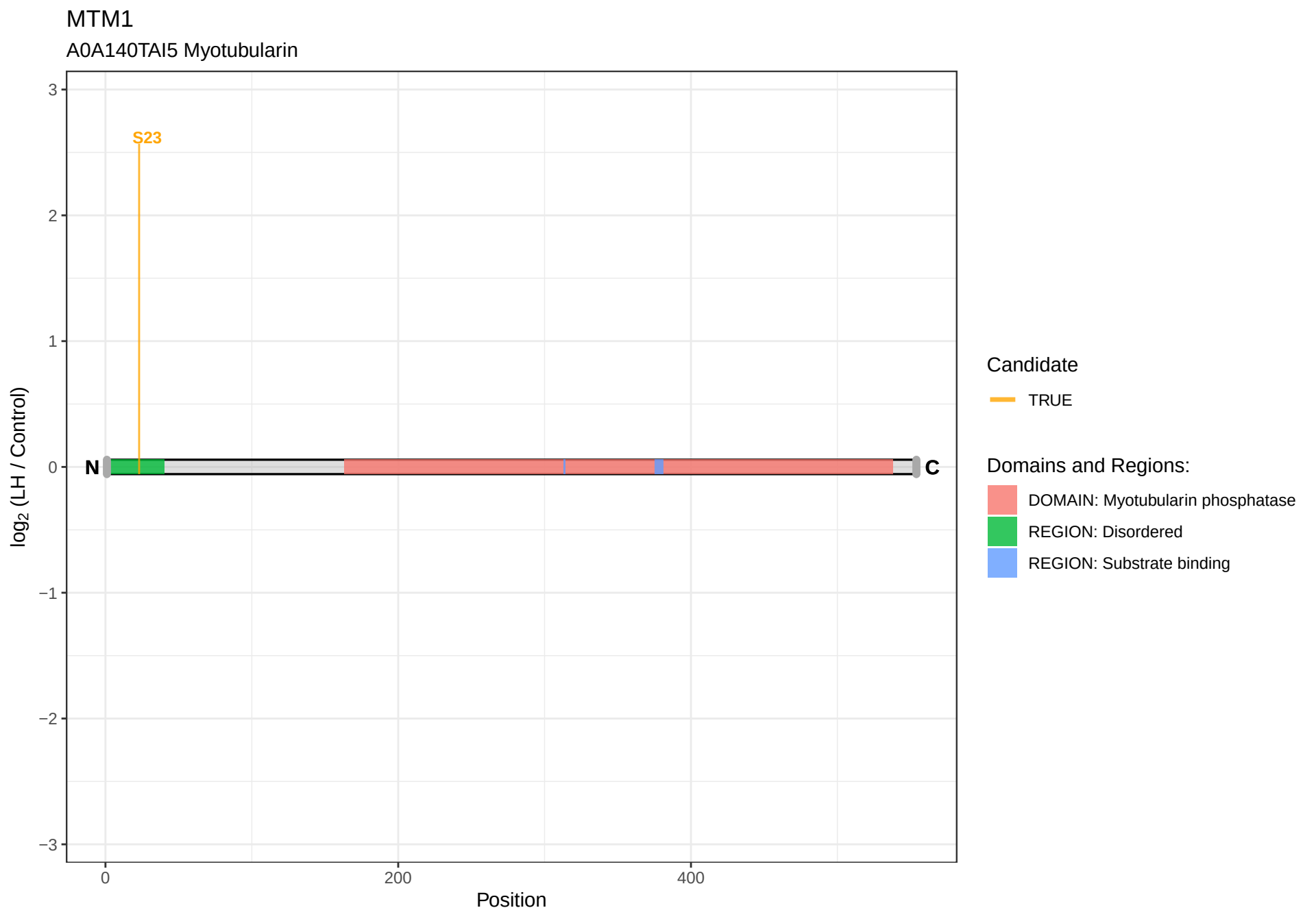

MPP5
B4F7E7 Membrane palmitoylated protein 5
log2 (LH / Control)
2
1
0
−1
−2
N
C
S25
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Guanylate kinase−like
DOMAIN: L27 1
DOMAIN: L27 2
DOMAIN: PDZ
DOMAIN: SH3
REGION: Disordered
REGION: Interaction with LIN7C
REGION: Interaction with PARD6B
REGION: Required for the correct localization of PALS1 and PATJ at cell−cell contacts and the normal formation of tight junctions and adherens junctions

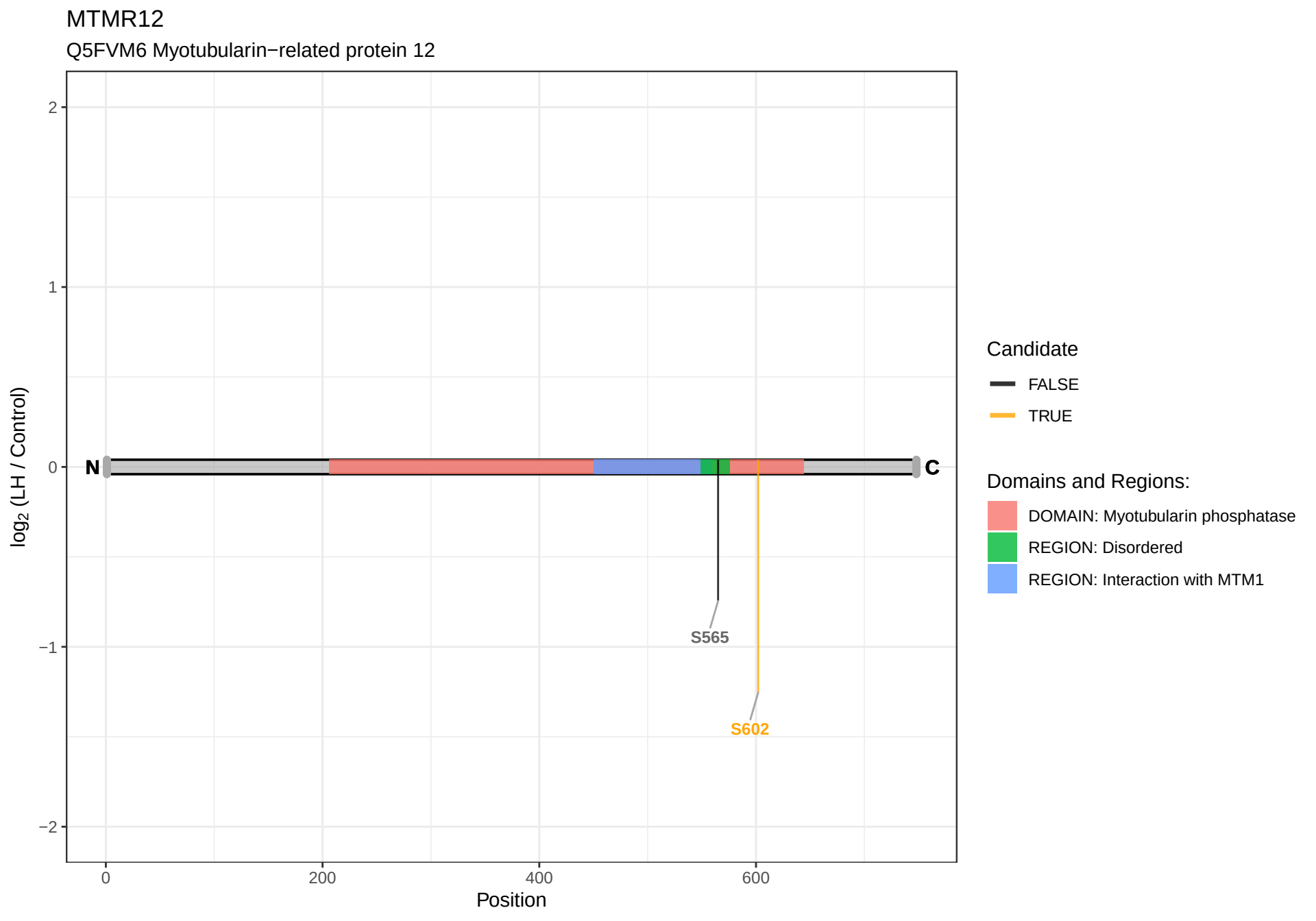

MRGBP
G3V751 MRG/MORF4L−binding protein
log2 (LH / Control)
2
1
0
−1
−2
N
C
S195
S191
0
50
100
150
200
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

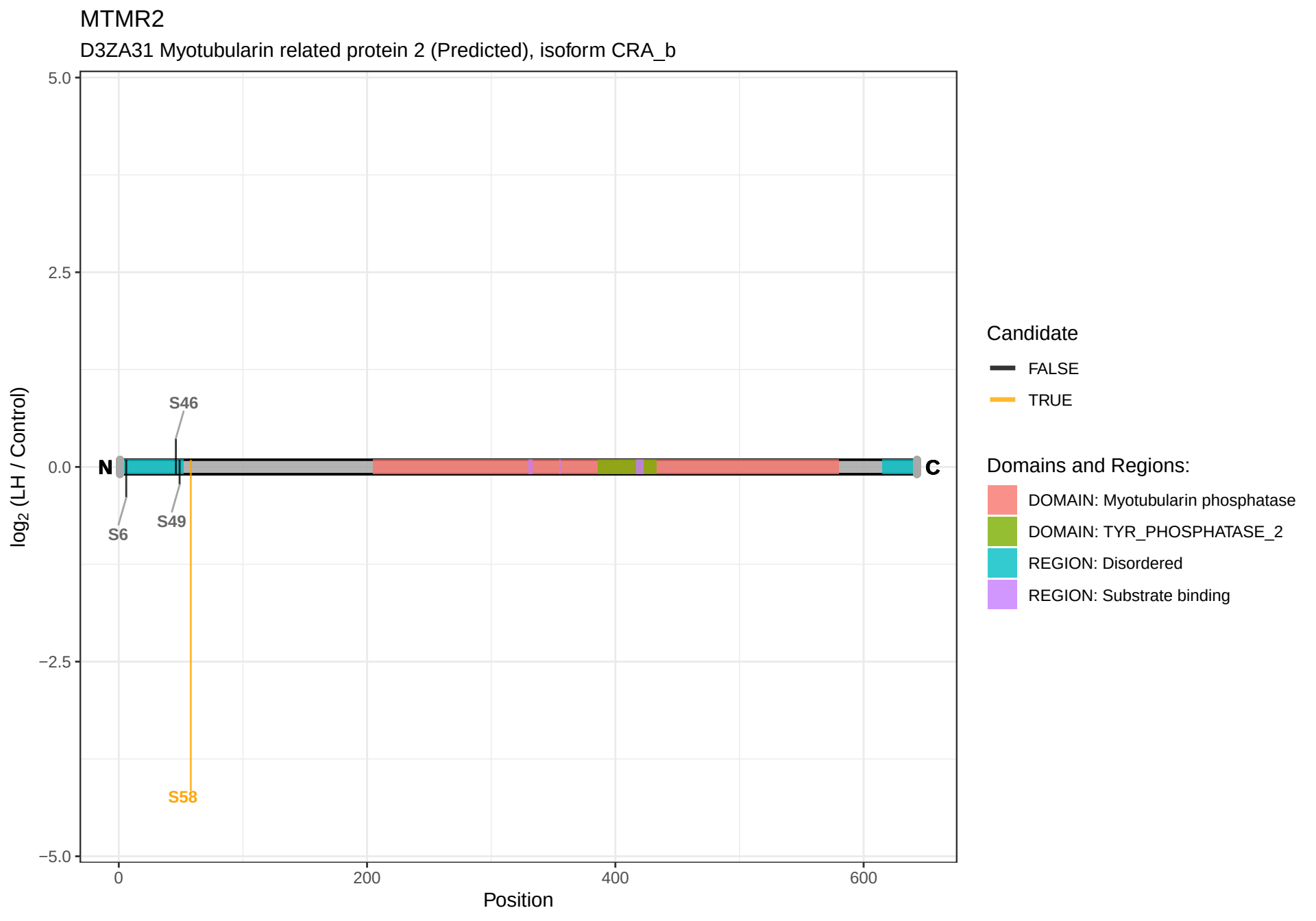

MSH3
F1LQM8 MutS homolog 3
S6
S56
S39
S166
N
C
2
0
−2
log2 (LH / Control)
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DNA_MISMATCH_REPAIR_2
REGION: Disordered

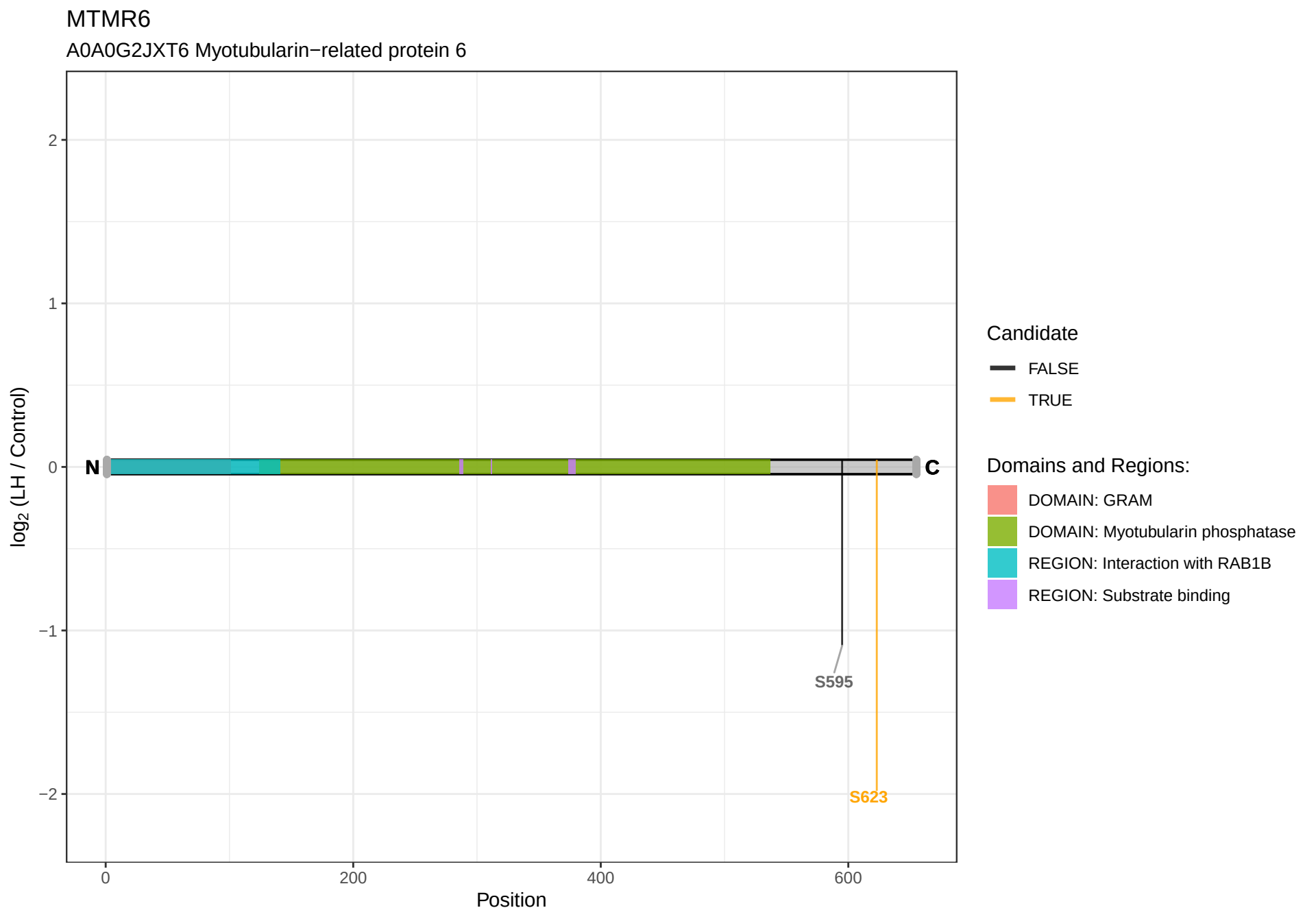

MTCL1
D4A5D4 Microtubule crosslinking factor 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S1073
T1069
S1465
S1467
S417
S1581
S210
S410
S406
S402
S437
S1461
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DUF4482
REGION: Disordered

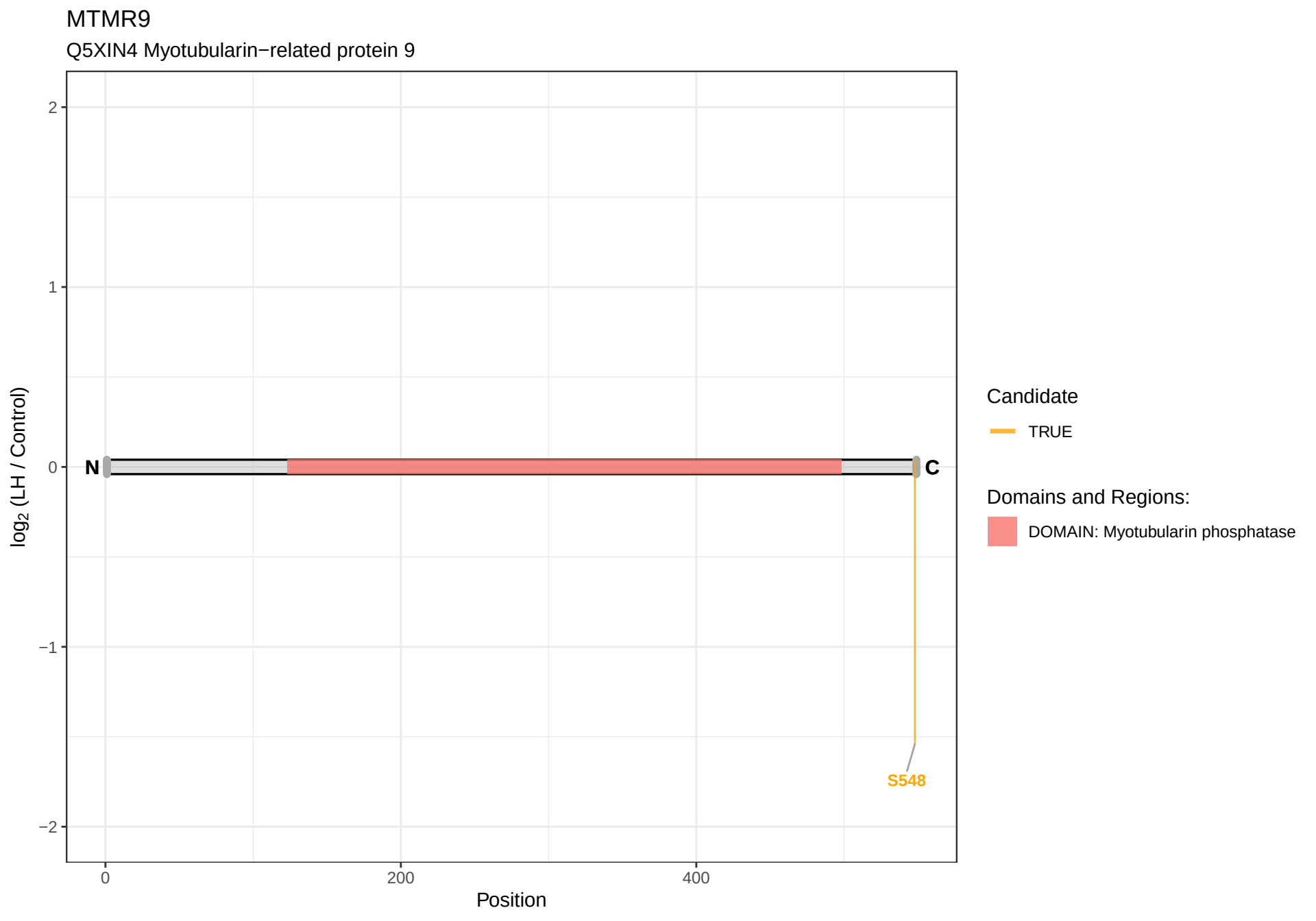

MTDH
Q9Z1W6 Protein LYRIC
log2 (LH / Control)
Position
N
C
T93
T96
S110
T142
S297
S419
S425
S456
S567
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Activation of NF−kappa−B
REGION: Disordered
REGION: Interaction with BCCIP
REGION: Interaction with RELA
REGION: Lung−homing for mammary tumors

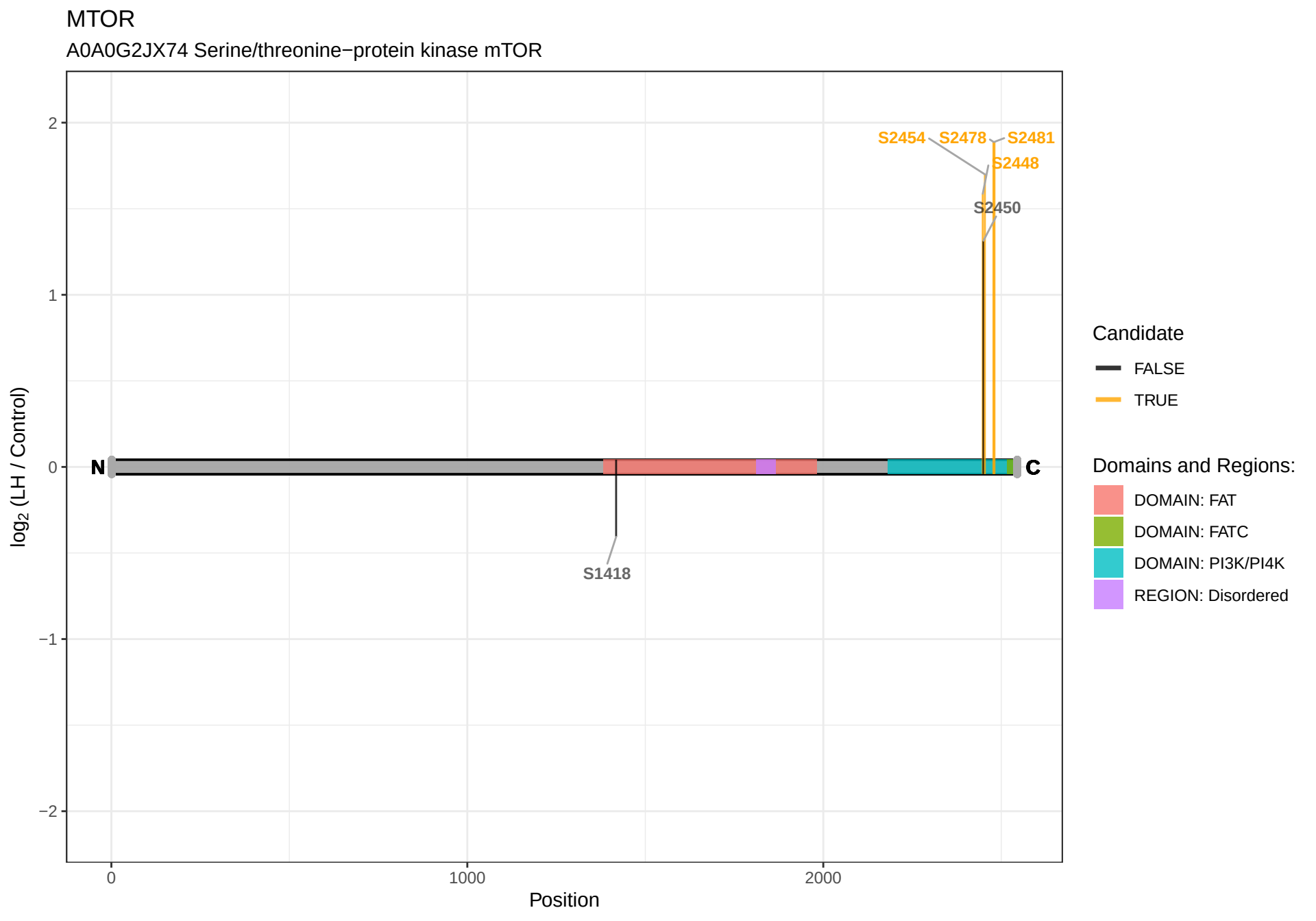

MTM1
A0A140TAI5 Myotubularin
S23
N
C
3
2
1
0
−1
−2
−3
0
200
400
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
DOMAIN: Myotubularin phosphatase
REGION: Disordered
REGION: Substrate binding

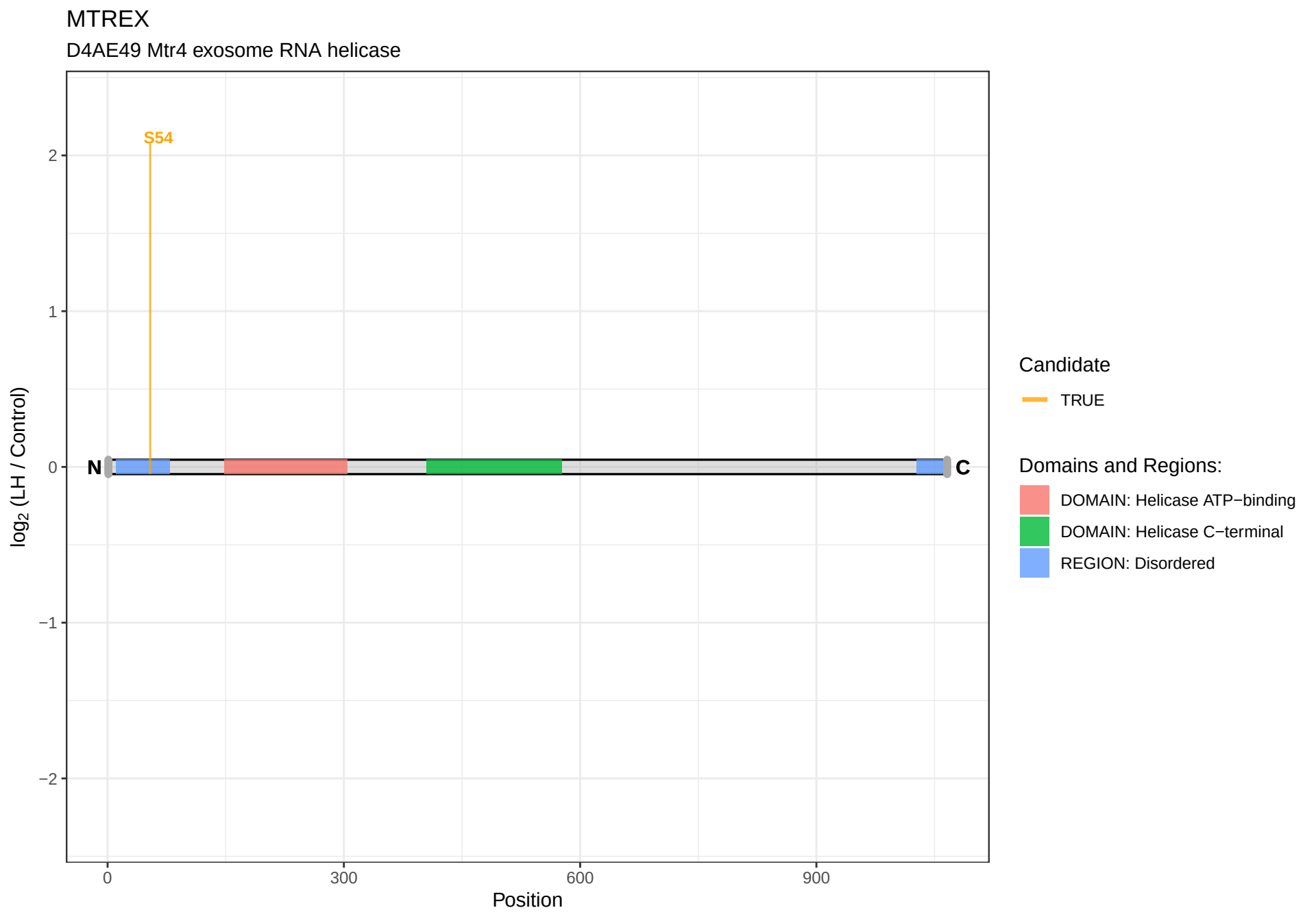

MTMR12
Q5FVM6 Myotubularin−related protein 12
log2 (LH / Control)
2
1
0
−1
−2
N
C
S565
S602
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Myotubularin phosphatase
REGION: Disordered
REGION: Interaction with MTM1

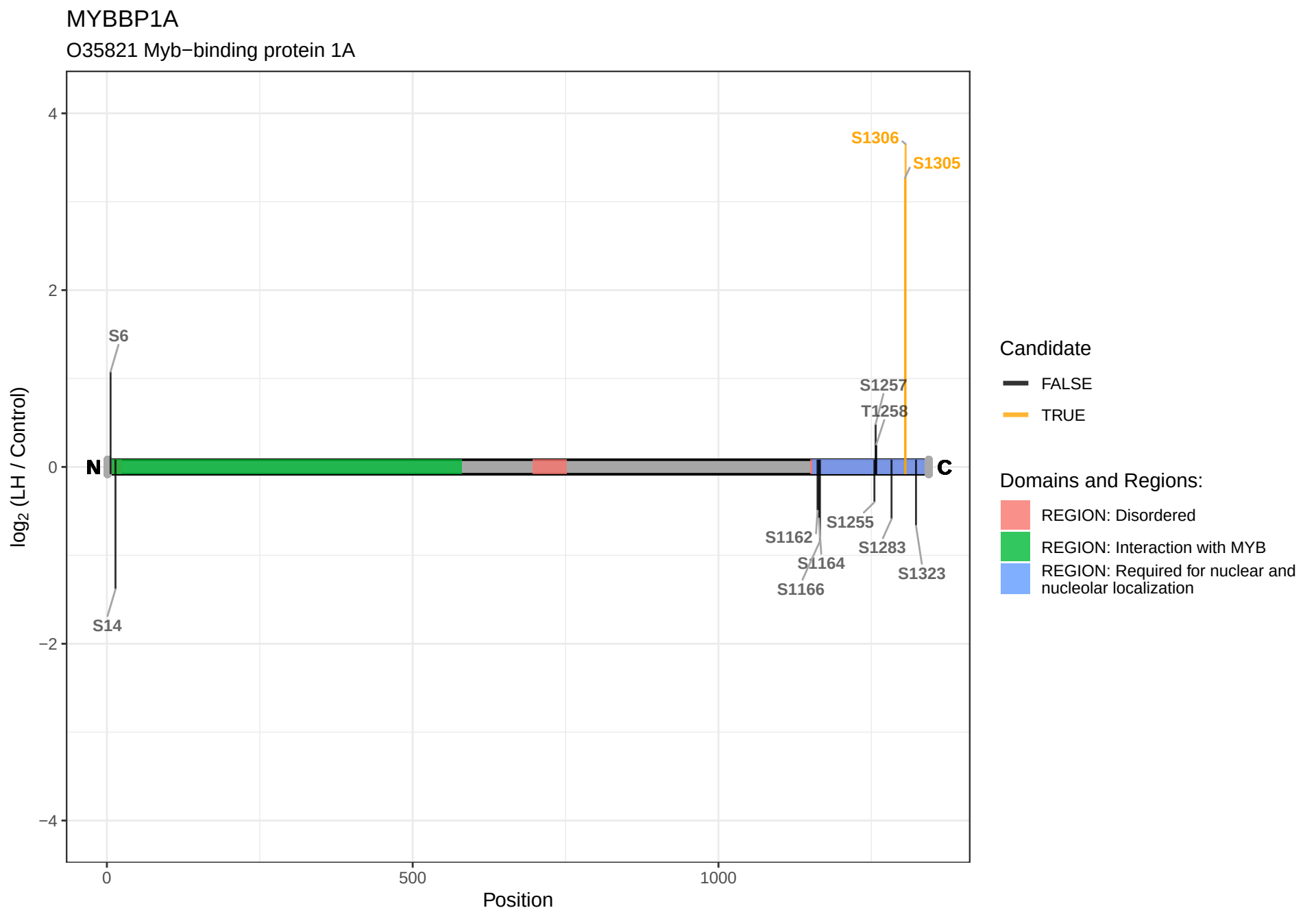

MTMR2
D3ZA31 Myotubularin related protein 2 (Predicted), isoform CRA_b
5.0
2.5
0.0
−2.5
−5.0
log2 (LH / Control)
0
200
400
600
Position
N
C
S46
S6
S49
S58
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Myotubularin phosphatase
DOMAIN: TYR_PHOSPHATASE_2
REGION: Disordered
REGION: Substrate binding

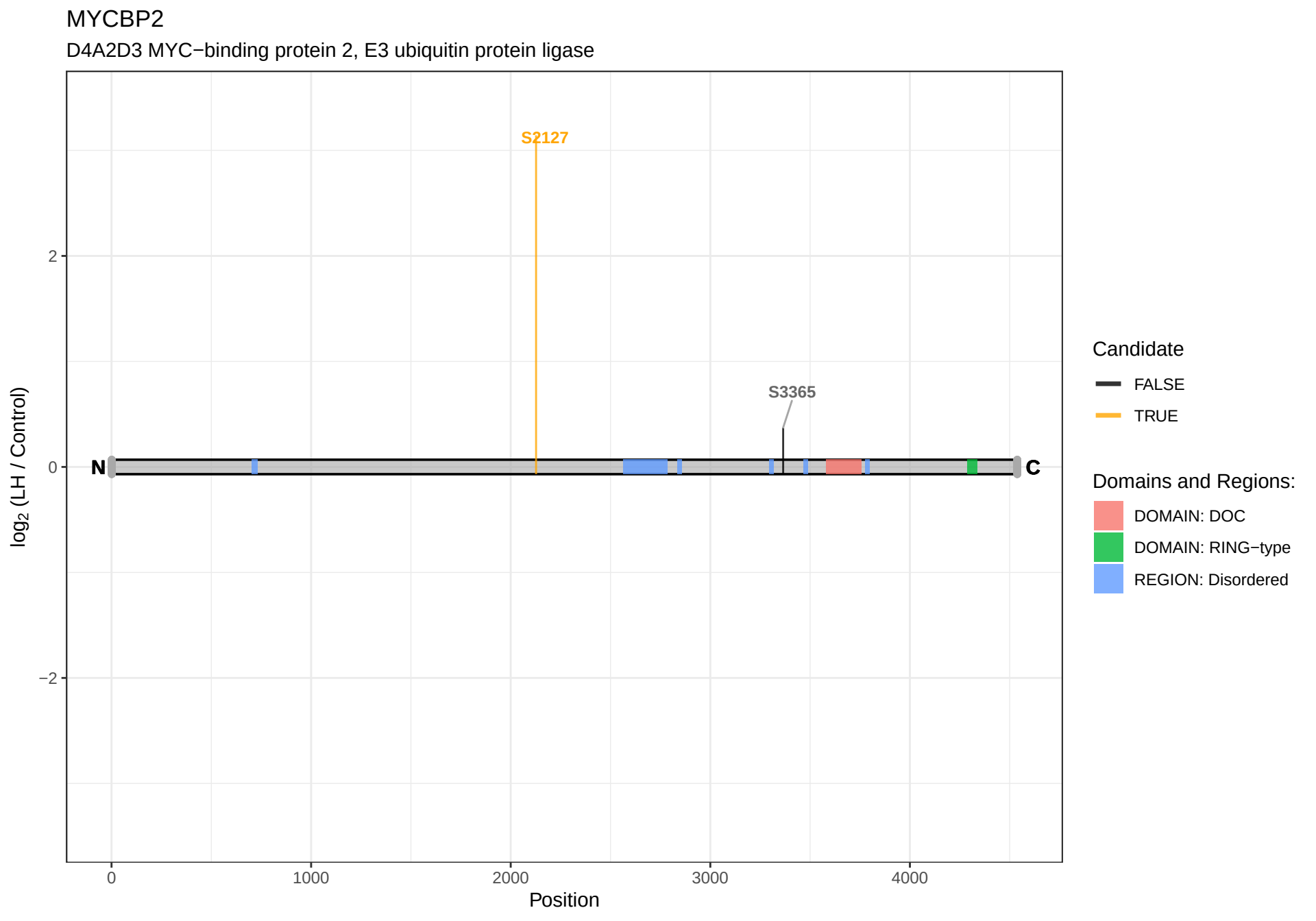

MTMR6
A0A0G2JXT6 Myotubularin−related protein 6
log2 (LH / Control)
2
1
0
−1
−2
N
C
S595
S623
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: GRAM
DOMAIN: Myotubularin phosphatase
REGION: Interaction with RAB1B
REGION: Substrate binding

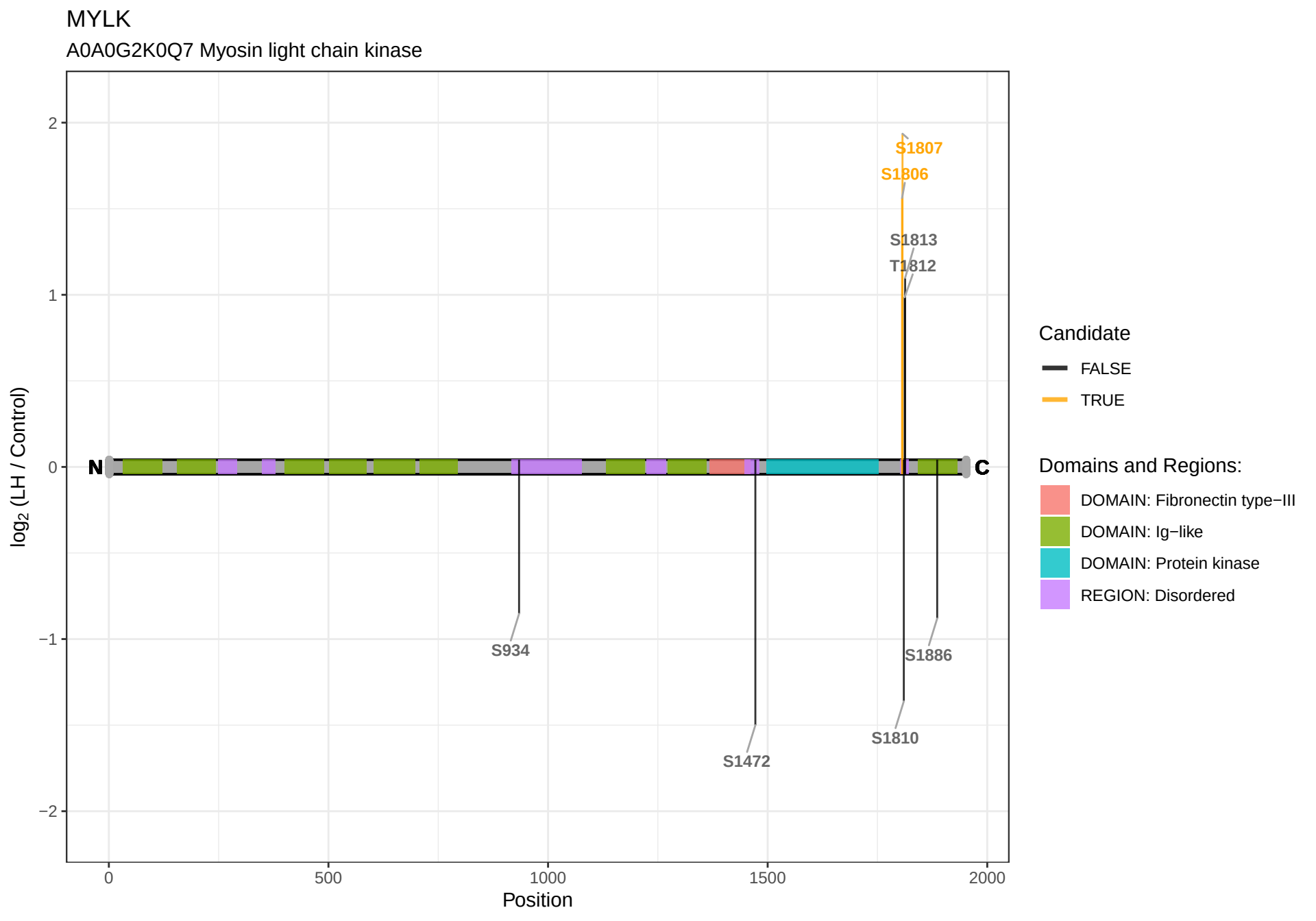

MTMR9
Q5XIN4 Myotubularin−related protein 9
log2 (LH / Control)
2
1
0
−1
−2
N
C
S548
0
200
400
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Myotubularin phosphatase

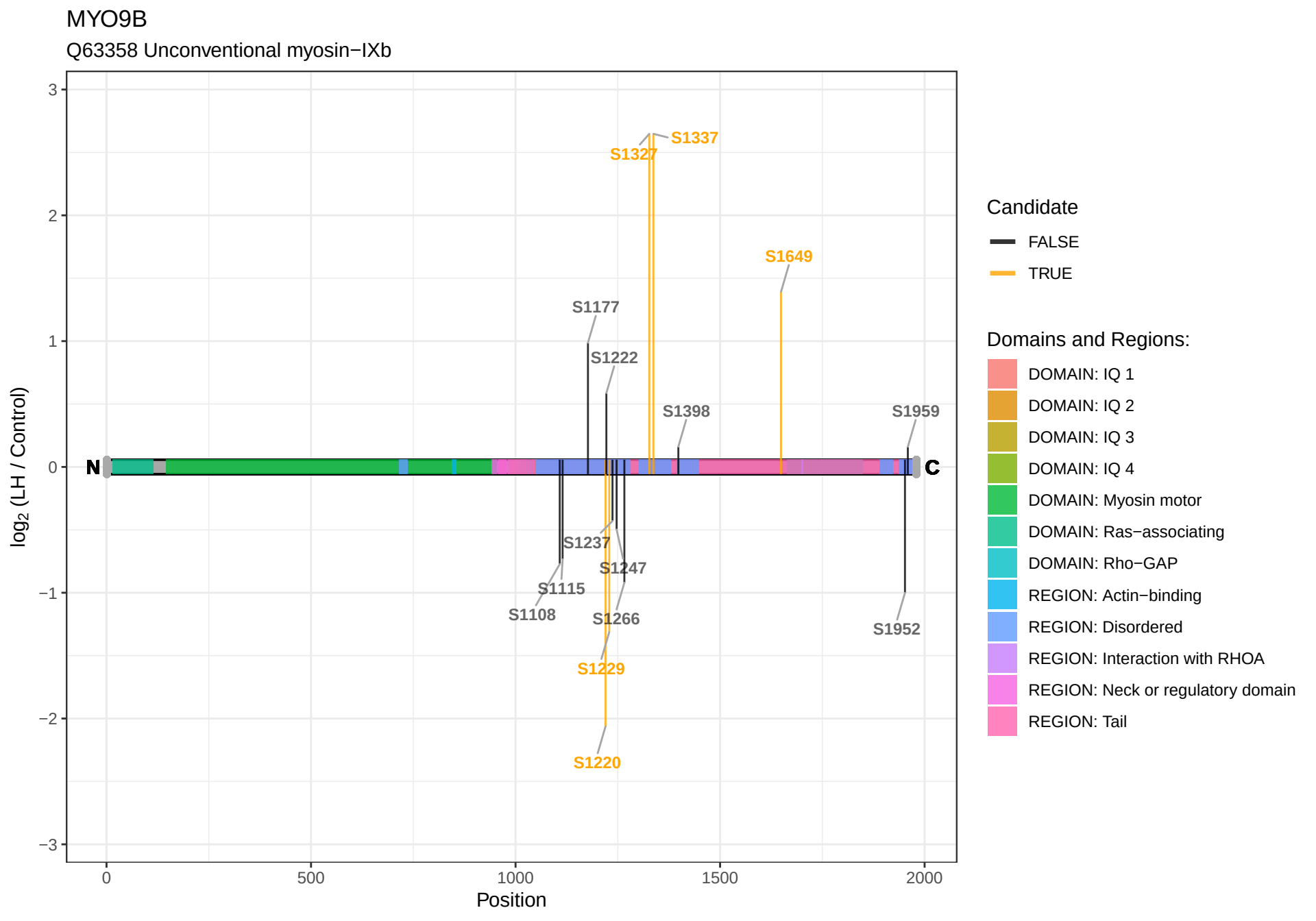

MTOR
A0A0G2JX74 Serine/threonine−protein kinase mTOR
log2 (LH / Control)
2
1
0
−1
−2
0
1000
2000
Position
N
C
S2454
S2478
S2481
S2448
S2450
S1418
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: FAT
DOMAIN: FATC
DOMAIN: PI3K/PI4K
REGION: Disordered

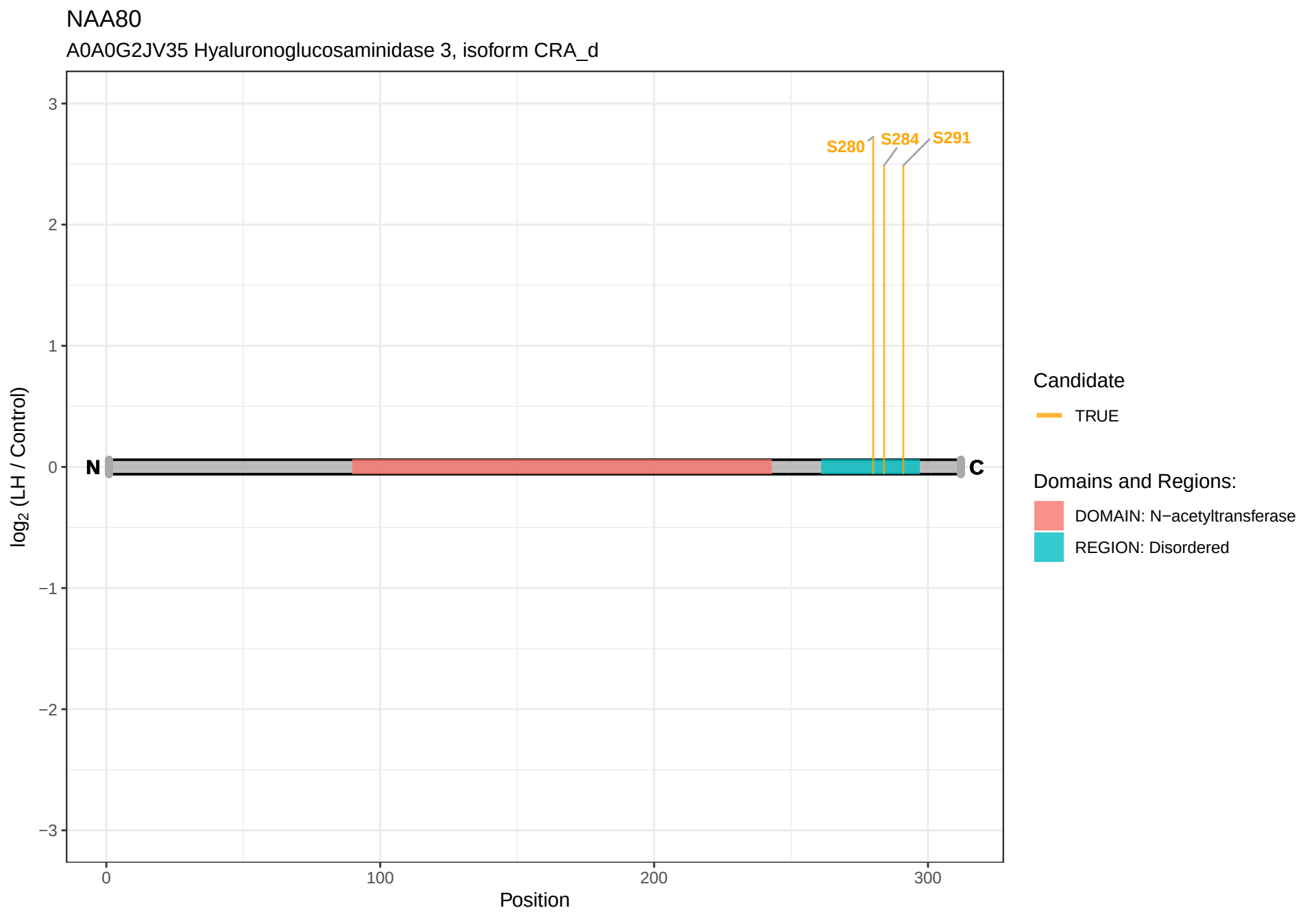

MTREX
D4AE49 Mtr4 exosome RNA helicase
S54
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
300
600
900
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Helicase ATP−binding
DOMAIN: Helicase C−terminal
REGION: Disordered

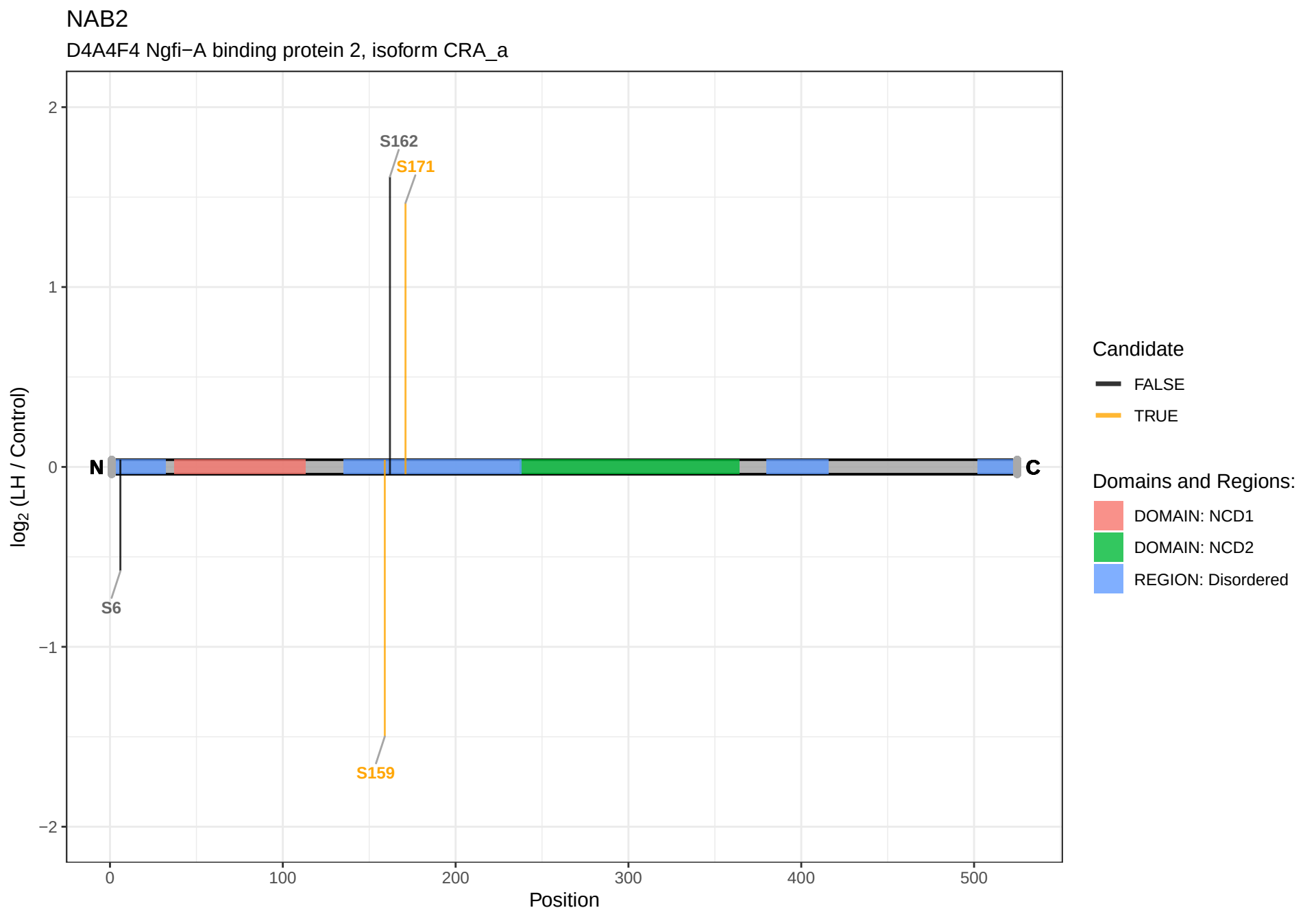

MYBBP1A
O35821 Myb−binding protein 1A
log2 (LH / Control)
4
2
0
−2
−4
0
500
1000
Position
N
C
S1306
S1305
S6
S1257
T1258
S1162
S1255
S1283
S1164
S1323
S1166
S14
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Interaction with MYB
REGION: Required for nuclear and nucleolar localization

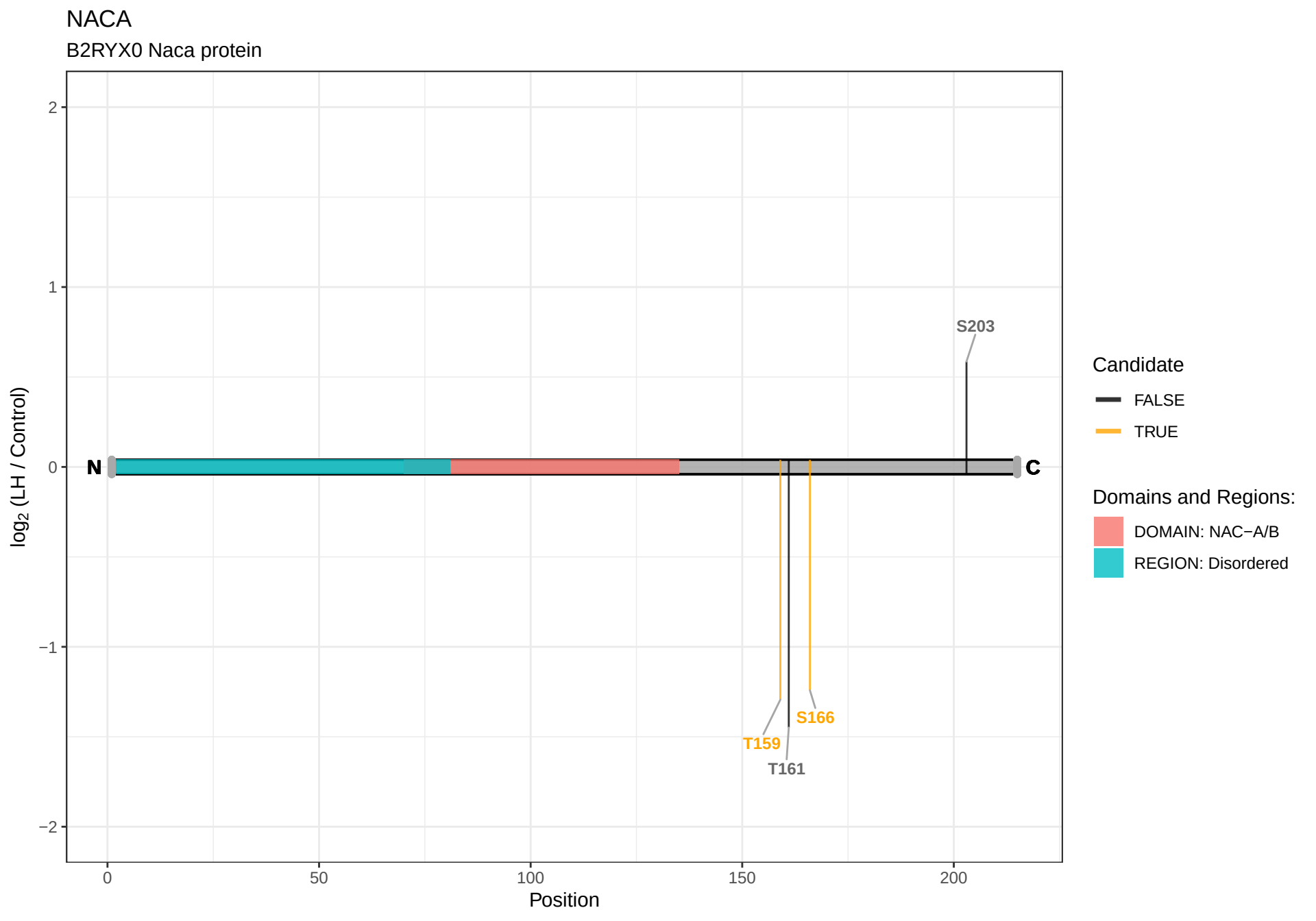

MYCBP2
D4A2D3 MYC−binding protein 2, E3 ubiquitin protein ligase
S2127
S3365
N
C
2
0
−2
log2 (LH / Control)
0
1000
2000
3000
4000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DOC
DOMAIN: RING−type
REGION: Disordered

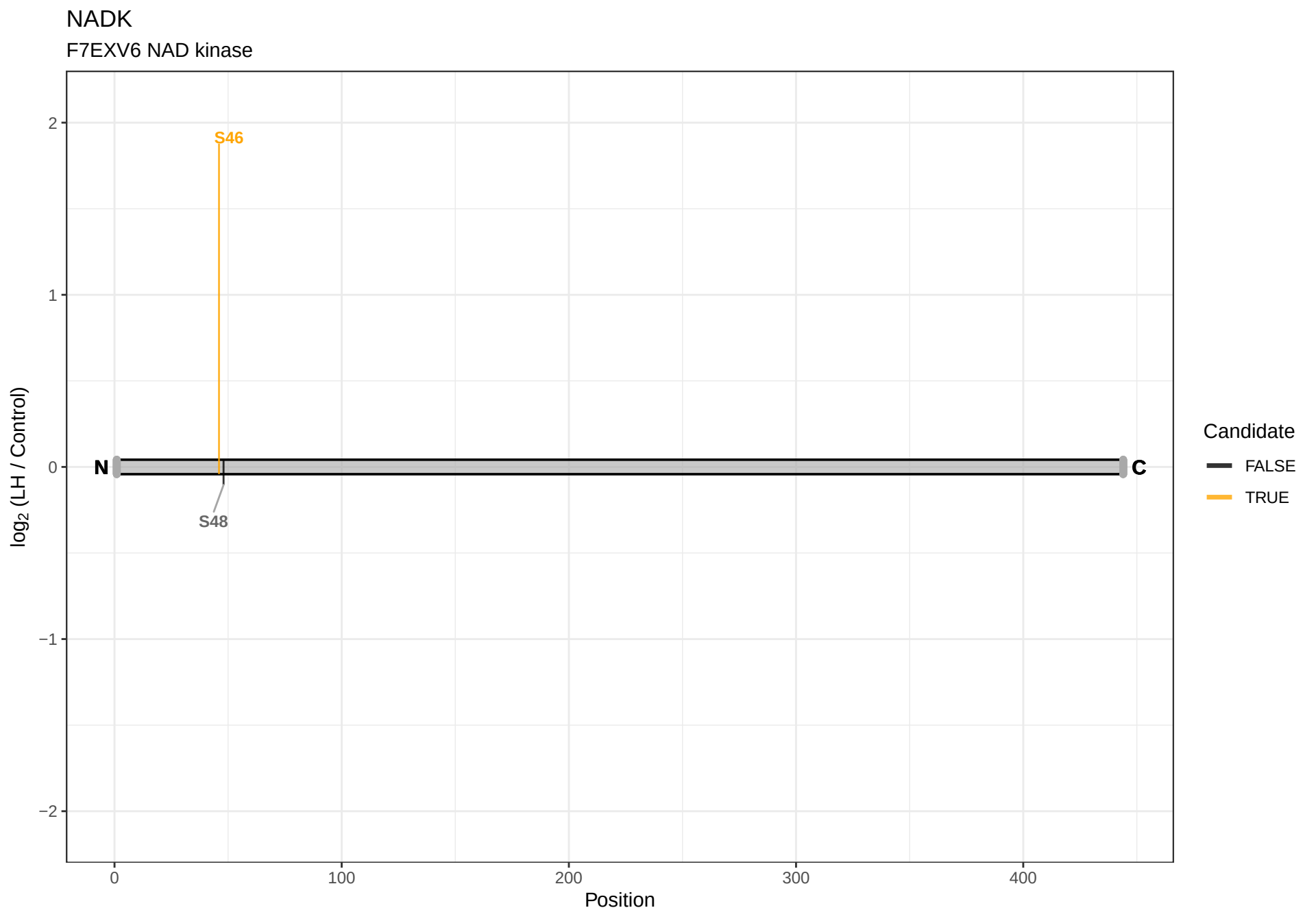

MYLK
A0A0G2K0Q7 Myosin light chain kinase
log2 (LH / Control)
2
1
0
−1
−2
N
C
S1807
S1806
S1813
T1812
S934
S1472
S1886
S1810
0
500
1000
1500
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Fibronectin type−III
DOMAIN: Ig−like
DOMAIN: Protein kinase
REGION: Disordered

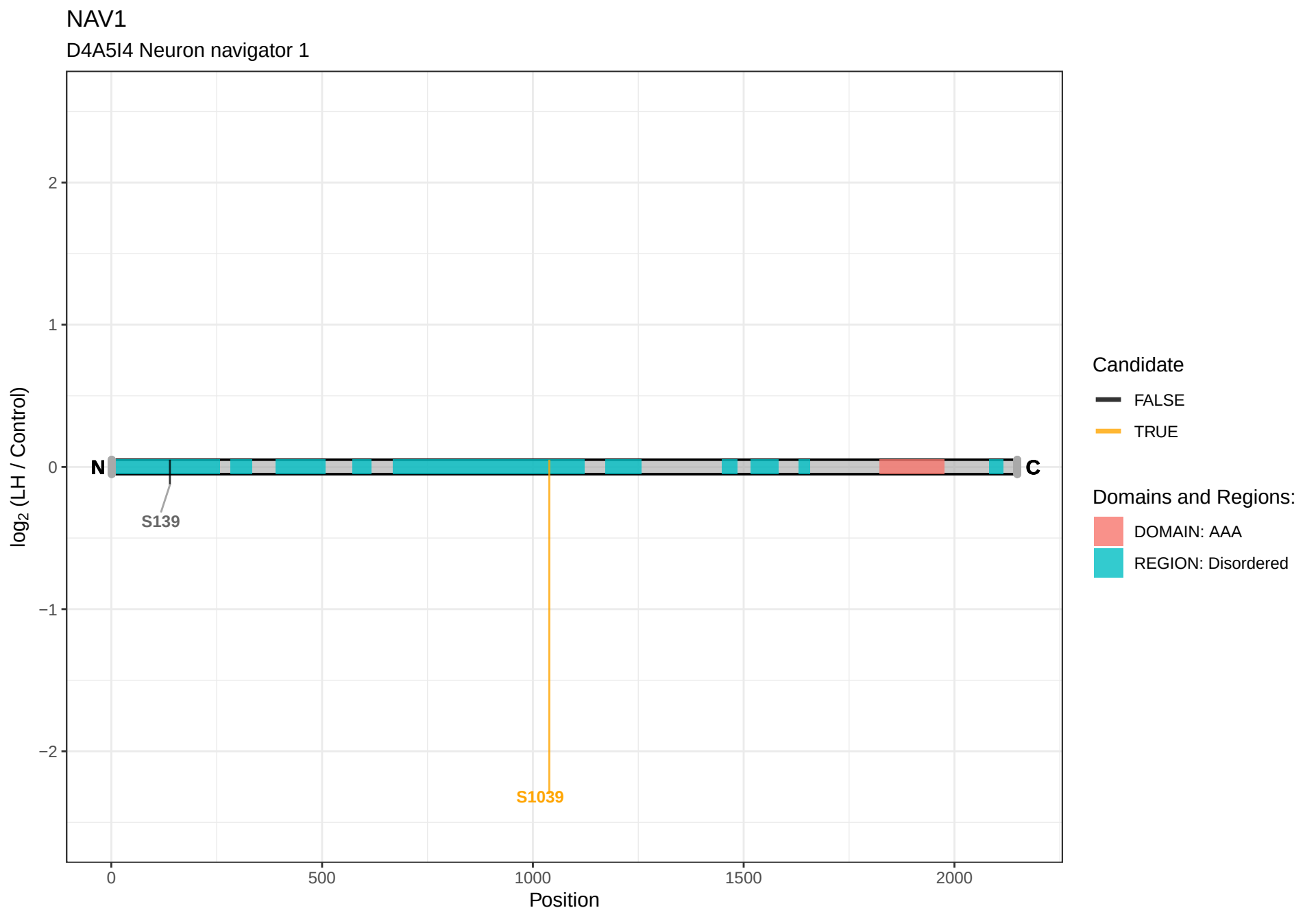

MYO9B
Q63358 Unconventional myosin−IXb
log2 (LH / Control)
Position
N
C
S1337
S1327
S1649
S1177
S1222
S1398
S1959
S1237
S1247
S1115
S1108
S1266
S1952
S1229
S1220
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: IQ 1
DOMAIN: IQ 2
DOMAIN: IQ 3
DOMAIN: IQ 4
DOMAIN: Myosin motor
DOMAIN: Ras−associating
DOMAIN: Rho−GAP
REGION: Actin−binding
REGION: Disordered
REGION: Interaction with RHOA
REGION: Neck or regulatory domain
REGION: Tail

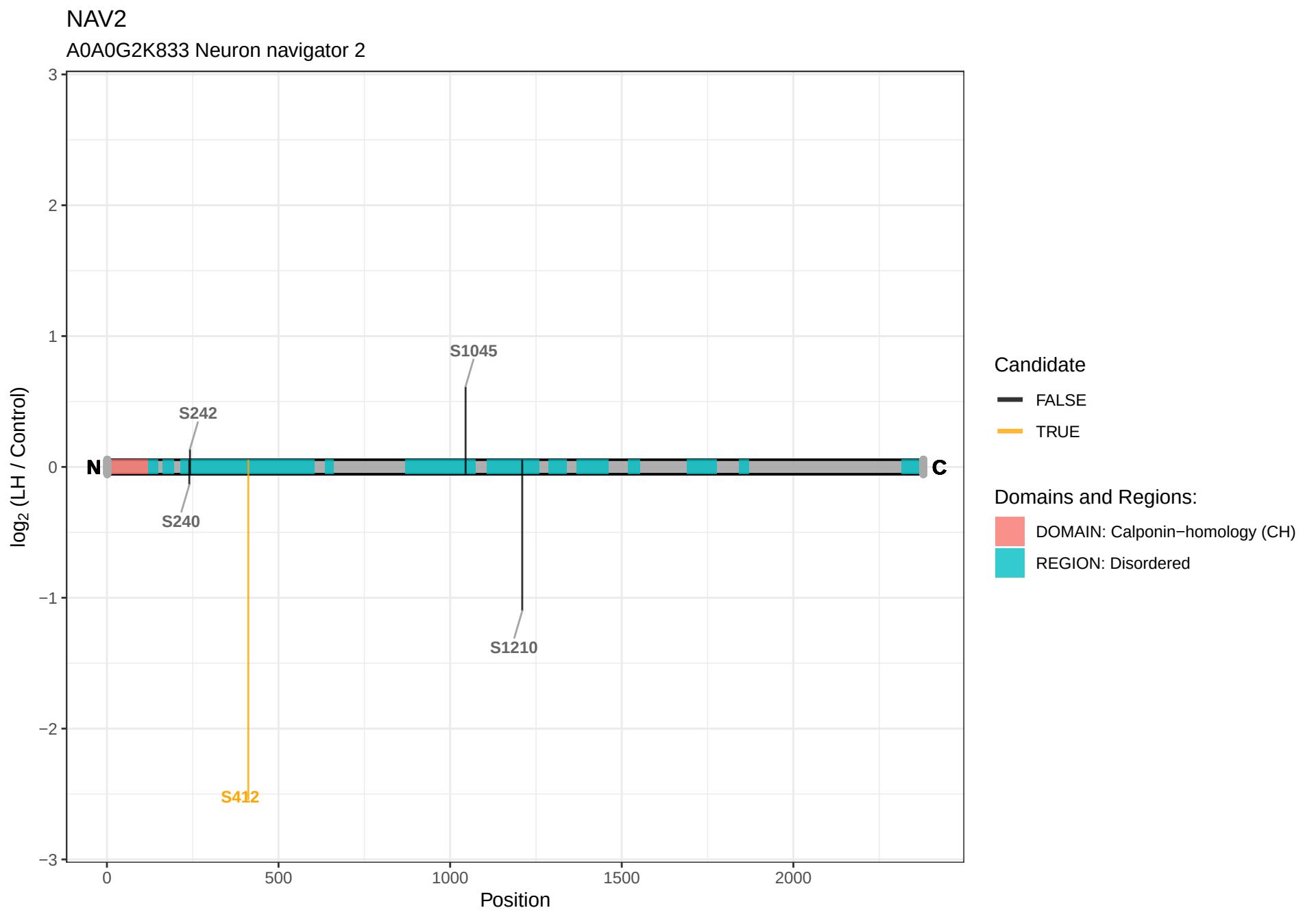

NAA80
A0A0G2JV35 Hyaluronoglucosaminidase 3, isoform CRA_d
S280
S284
S291
N
C
log2 (LH / Control)
Position
3
2
1
0
−1
−2
−3
0
100
200
300
Candidate
TRUE
Domains and Regions:
DOMAIN: N−acetyltransferase
REGION: Disordered

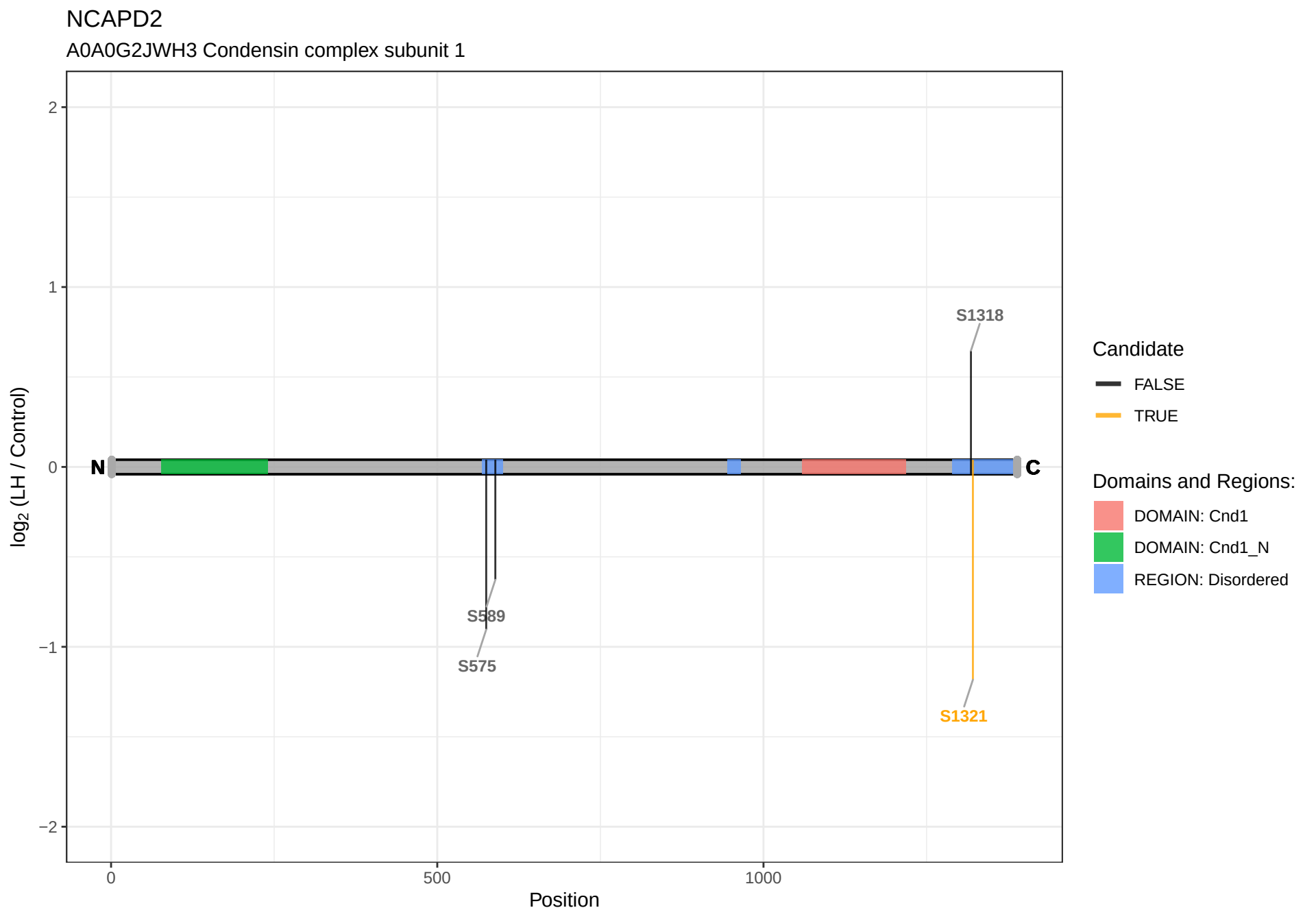

NAB2
D4A4F4 Ngfi−A binding protein 2, isoform CRA_a
S162
S171
S6
S159
N
C
2
1
0
−1
−2
0
100
200
300
400
500
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: NCD1
DOMAIN: NCD2
REGION: Disordered

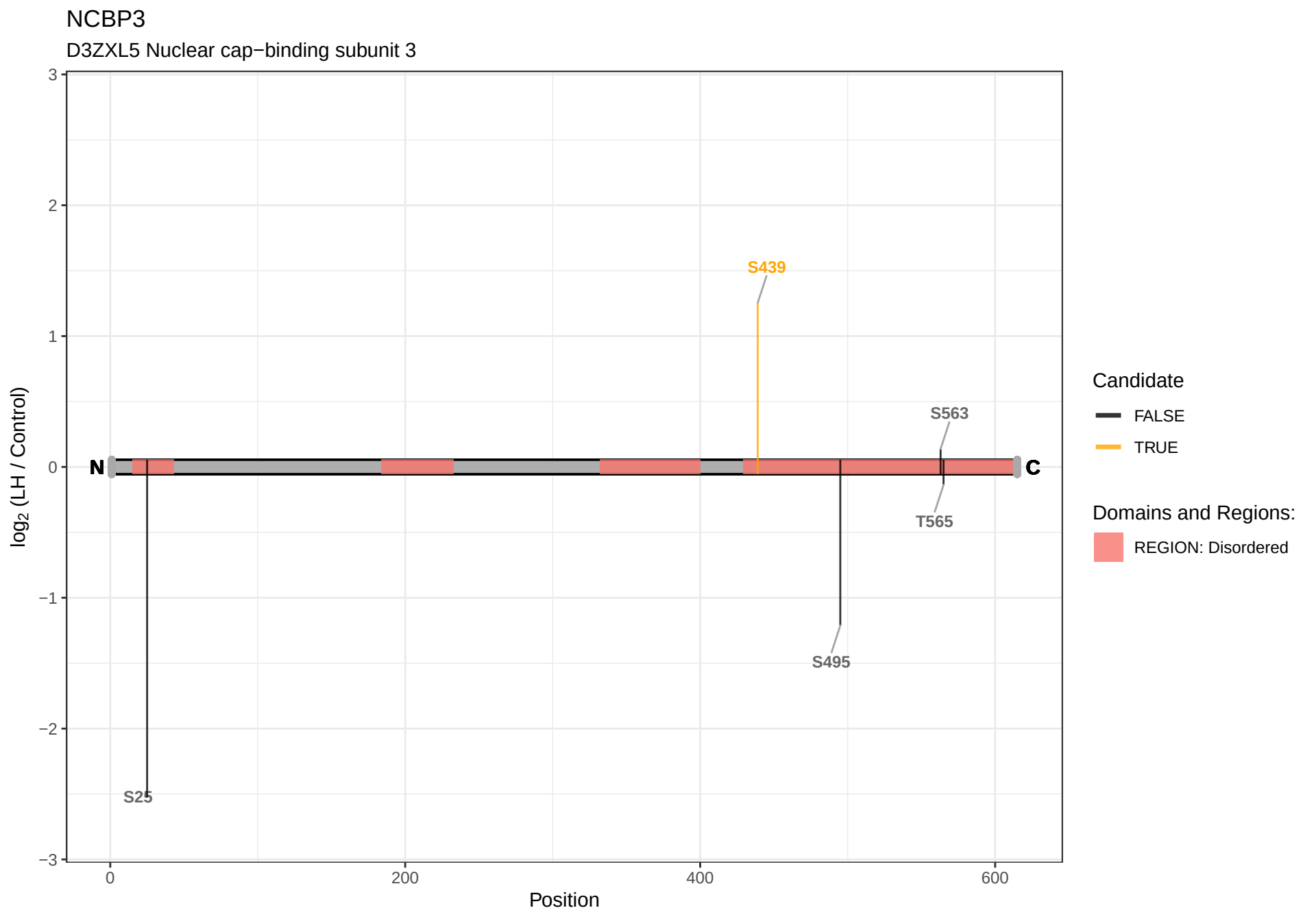

NACA
B2RYX0 Naca protein
log2 (LH / Control)
2
1
0
−1
−2
N
C
S203
T159
S166
T161
0
50
100
150
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: NAC−A/B
REGION: Disordered

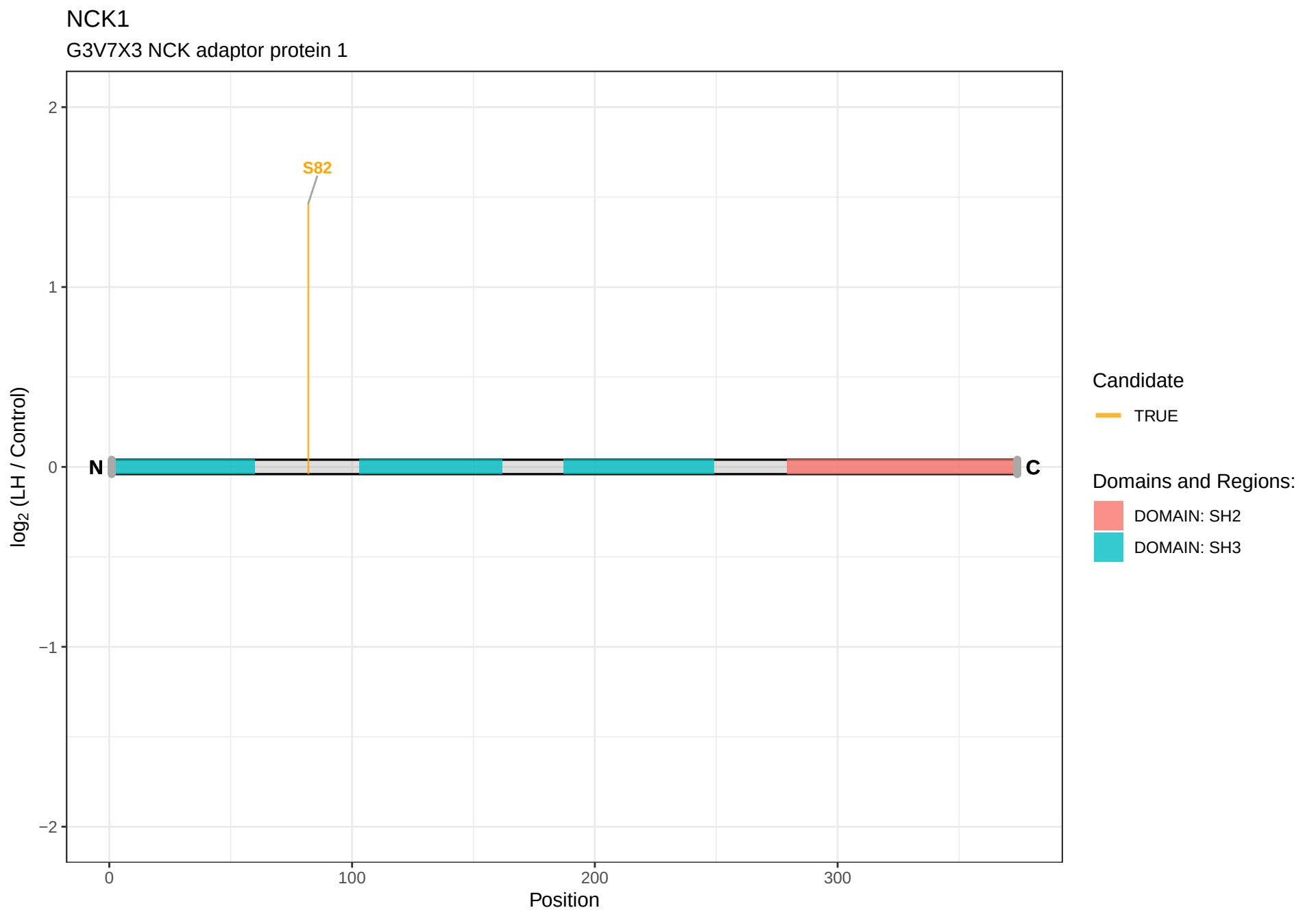

NADK
F7EXV6 NAD kinase
S46
S48
N
C
2
1
0
−1
−2
0
100
200
300
400
Position
log2 (LH / Control)
Candidate
FALSE
TRUE

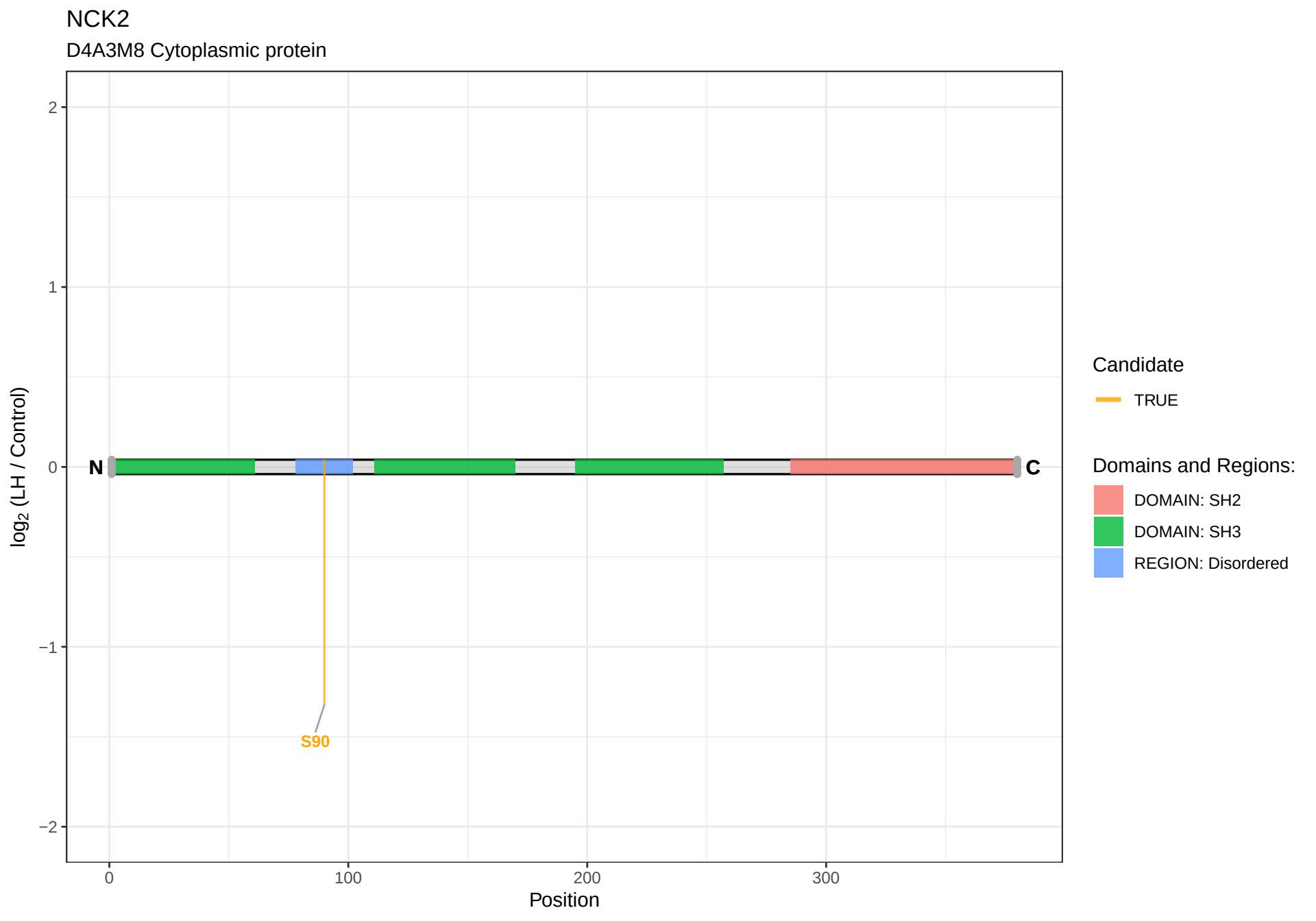

NAV1
D4A5I4 Neuron navigator 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S139
S1039
0
500
1000
1500
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AAA
REGION: Disordered

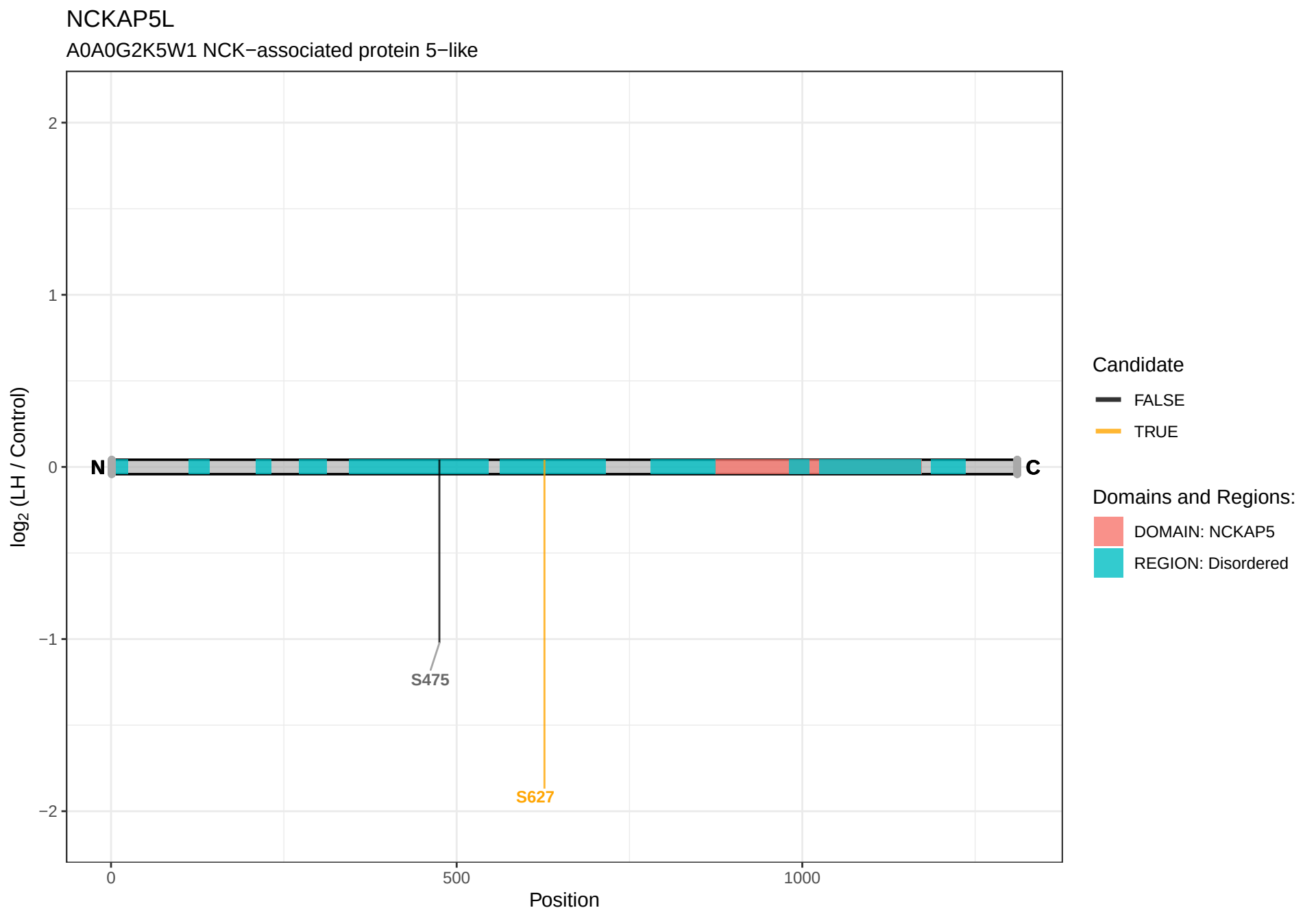

NAV2
A0A0G2K833 Neuron navigator 2
log2 (LH / Control)
Position
3
2
1
0
−1
−2
−3
0
500
1000
1500
2000
N
C
S1045
S242
S240
S1210
S412
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Calponin−homology (CH)
REGION: Disordered

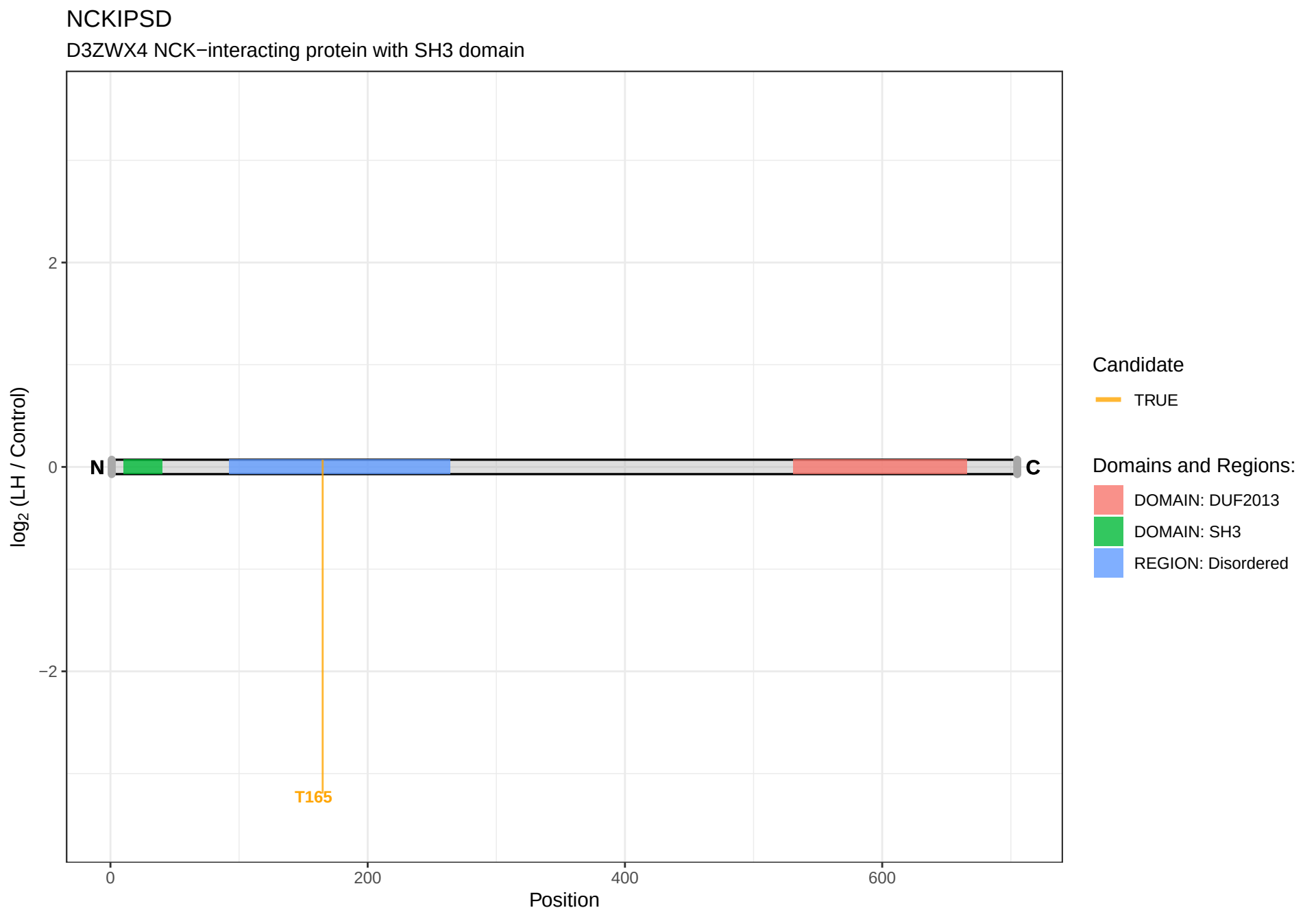

NCAPD2
A0A0G2JWH3 Condensin complex subunit 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S1318
S589
S575
S1321
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Cnd1
DOMAIN: Cnd1_N
REGION: Disordered

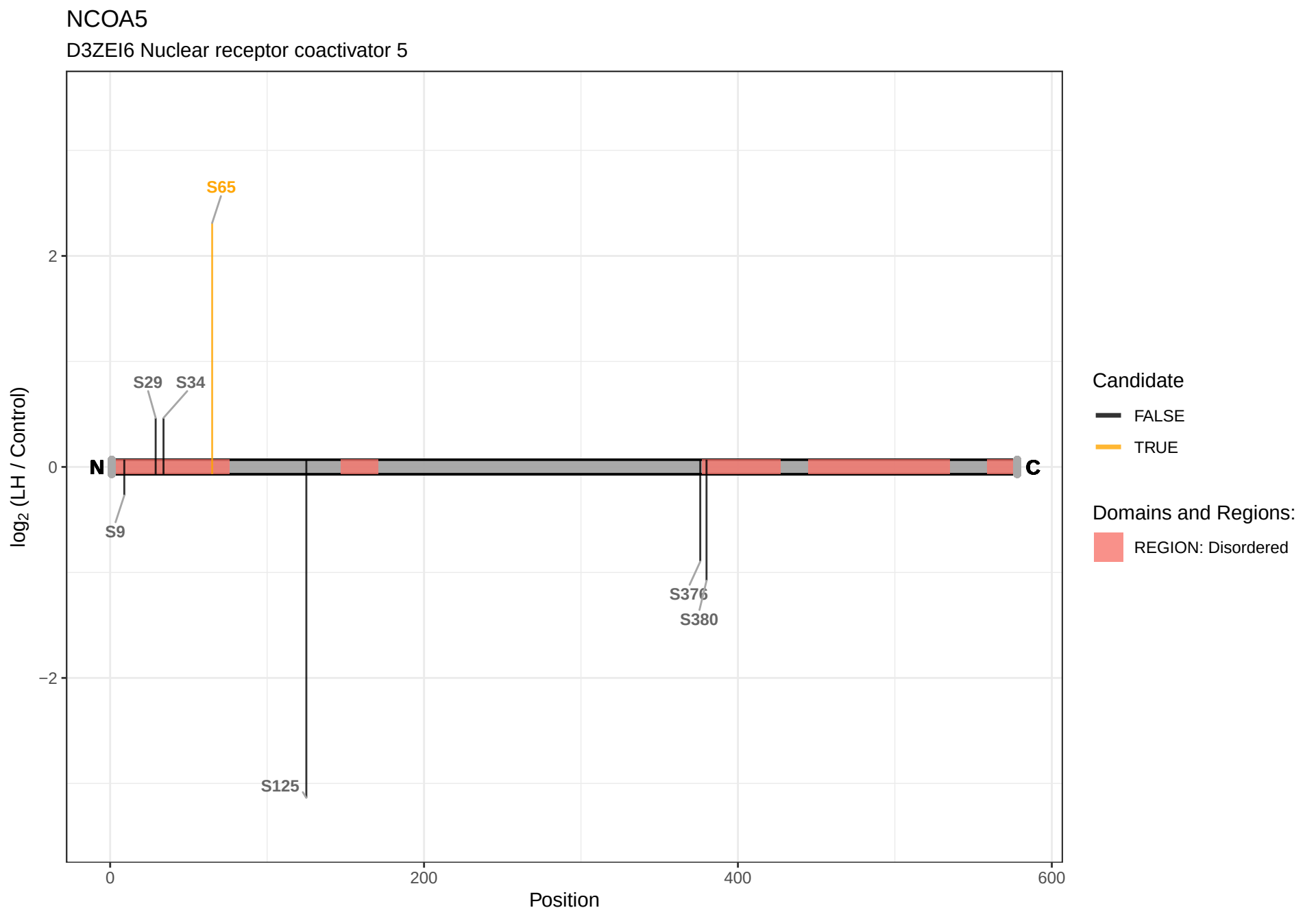

NCBP3
D3ZXL5 Nuclear cap−binding subunit 3
log2 (LH / Control)
3
2
1
0
−1
−2
−3
0
200
400
600
Position
N
C
S439
S563
T565
S495
S25
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

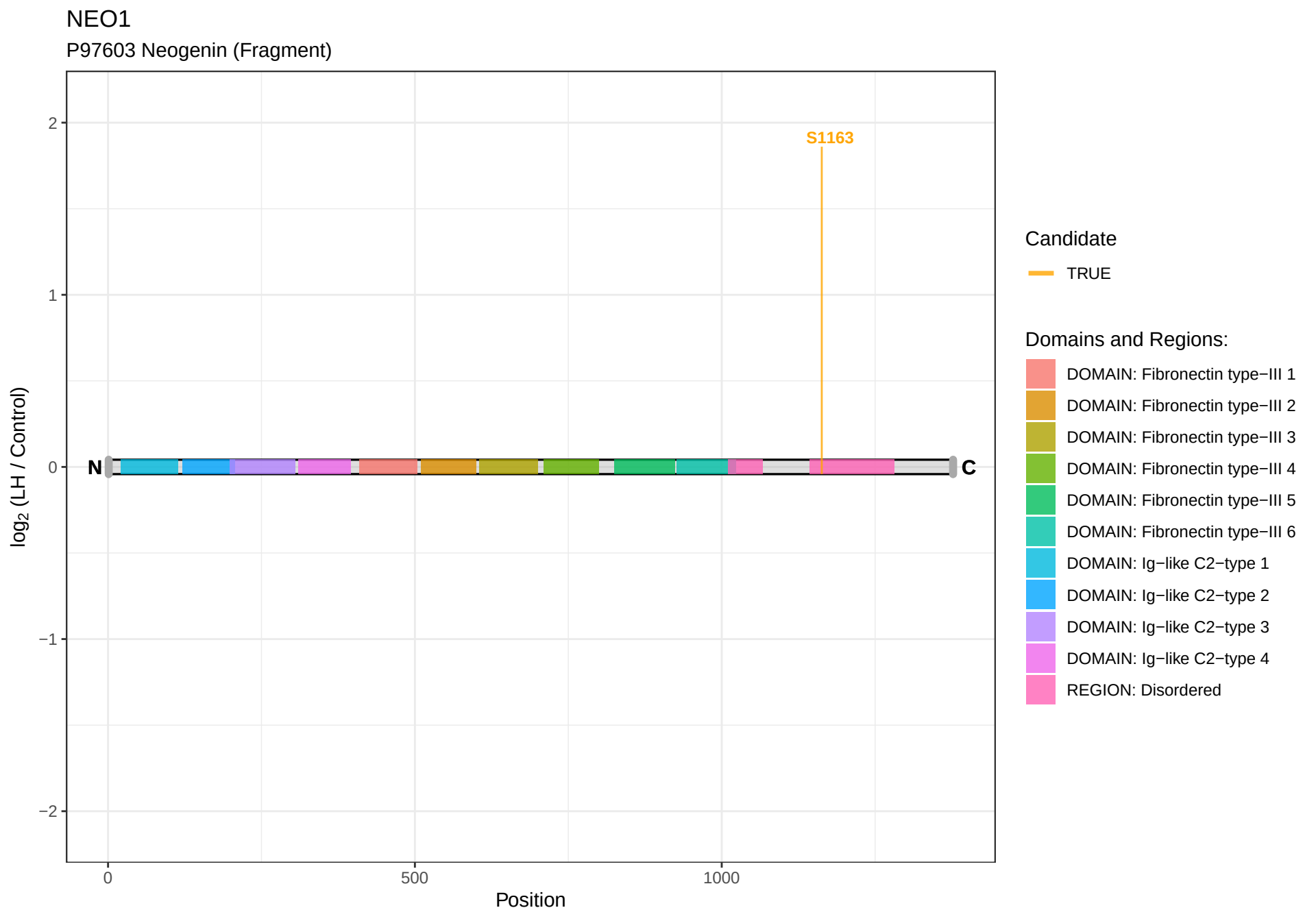

NCK1
G3V7X3 NCK adaptor protein 1
S82
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
100
200
300
Candidate
TRUE
Domains and Regions:
DOMAIN: SH2
DOMAIN: SH3

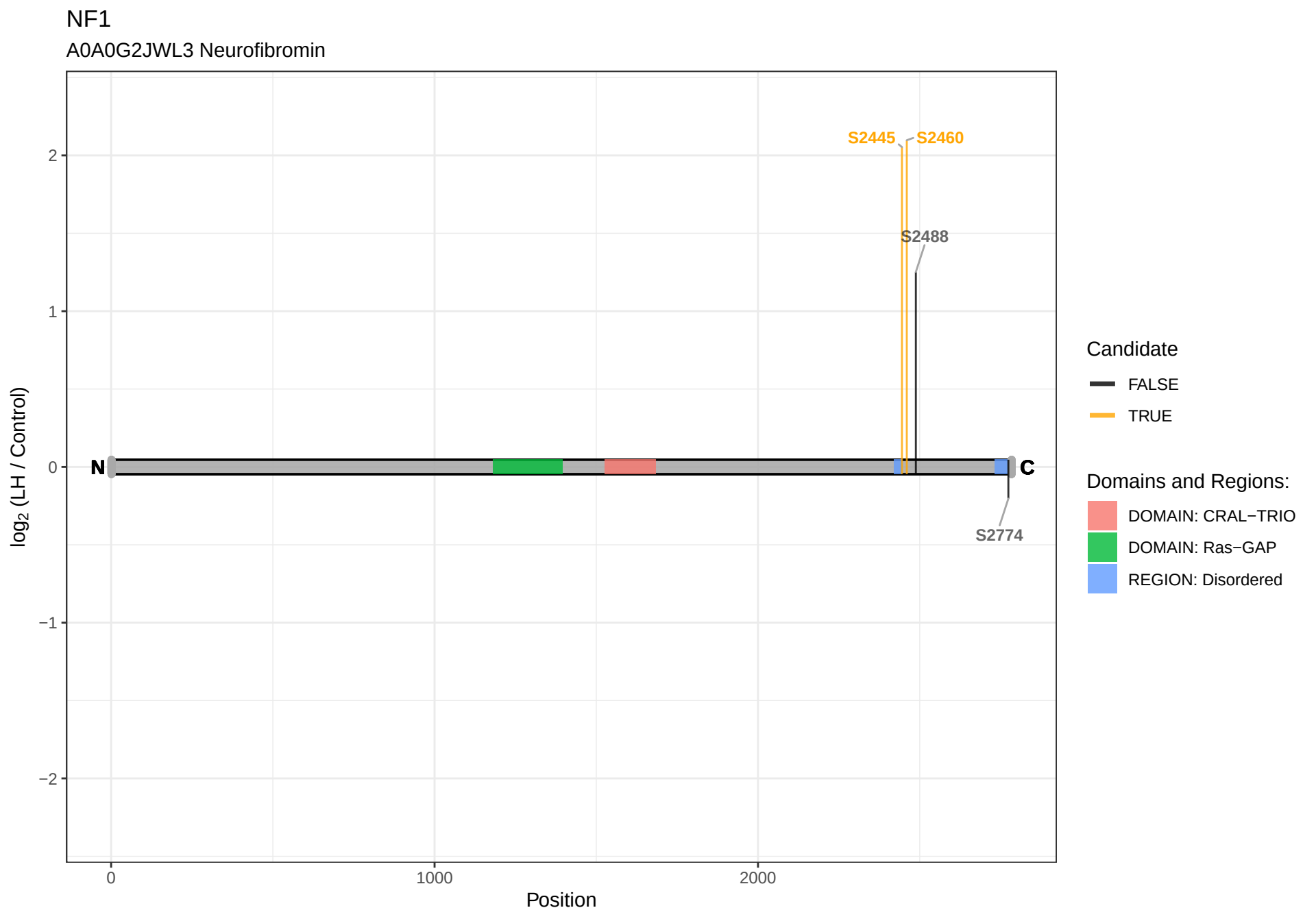

NCK2
D4A3M8 Cytoplasmic protein
log2 (LH / Control)
2
1
0
−1
−2
N
C
S90
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: SH2
DOMAIN: SH3
REGION: Disordered

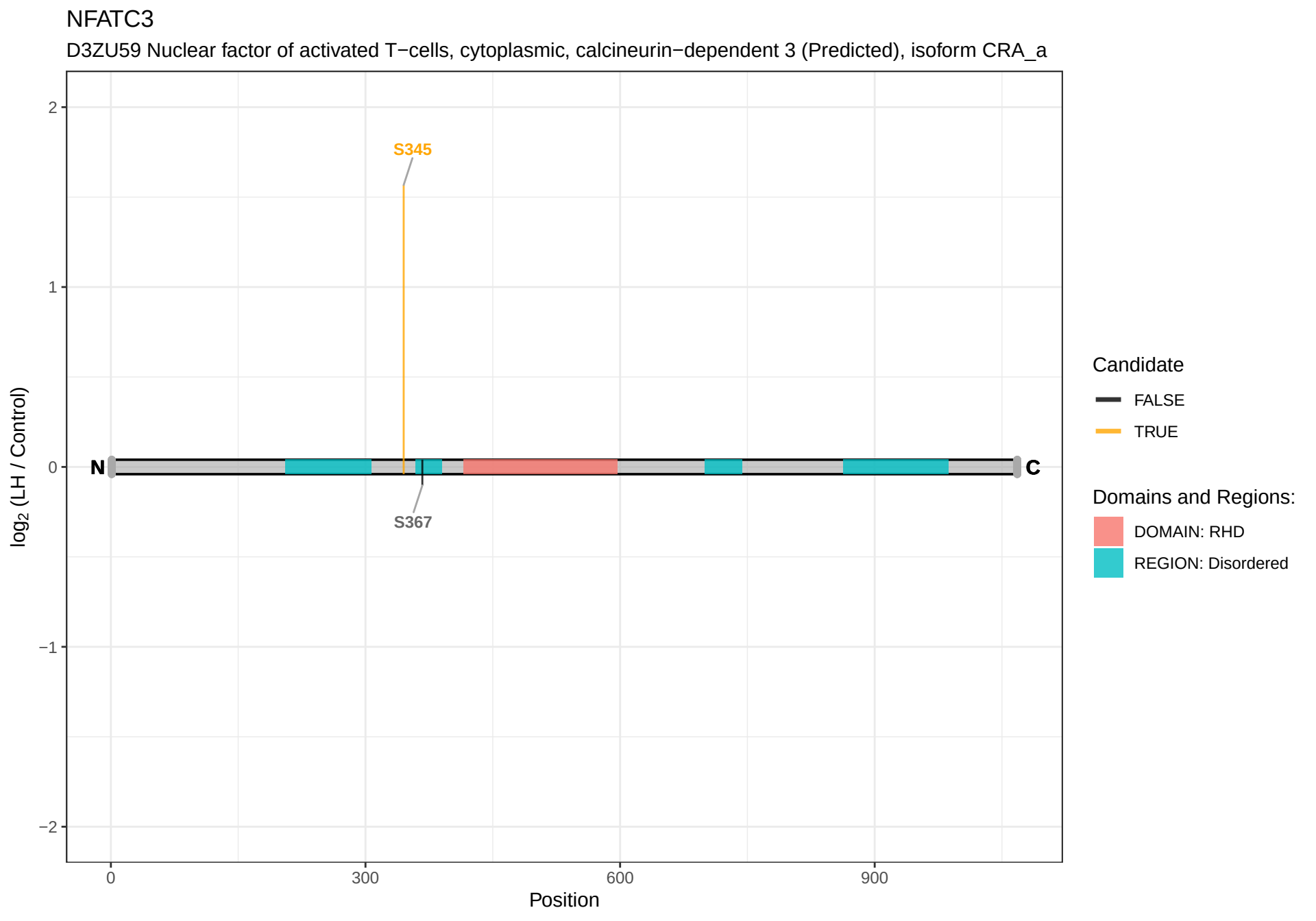

NCKAP5L
A0A0G2K5W1 NCK−associated protein 5−like
log2 (LH / Control)
2
1
0
−1
−2
N
C
S475
S627
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: NCKAP5
REGION: Disordered

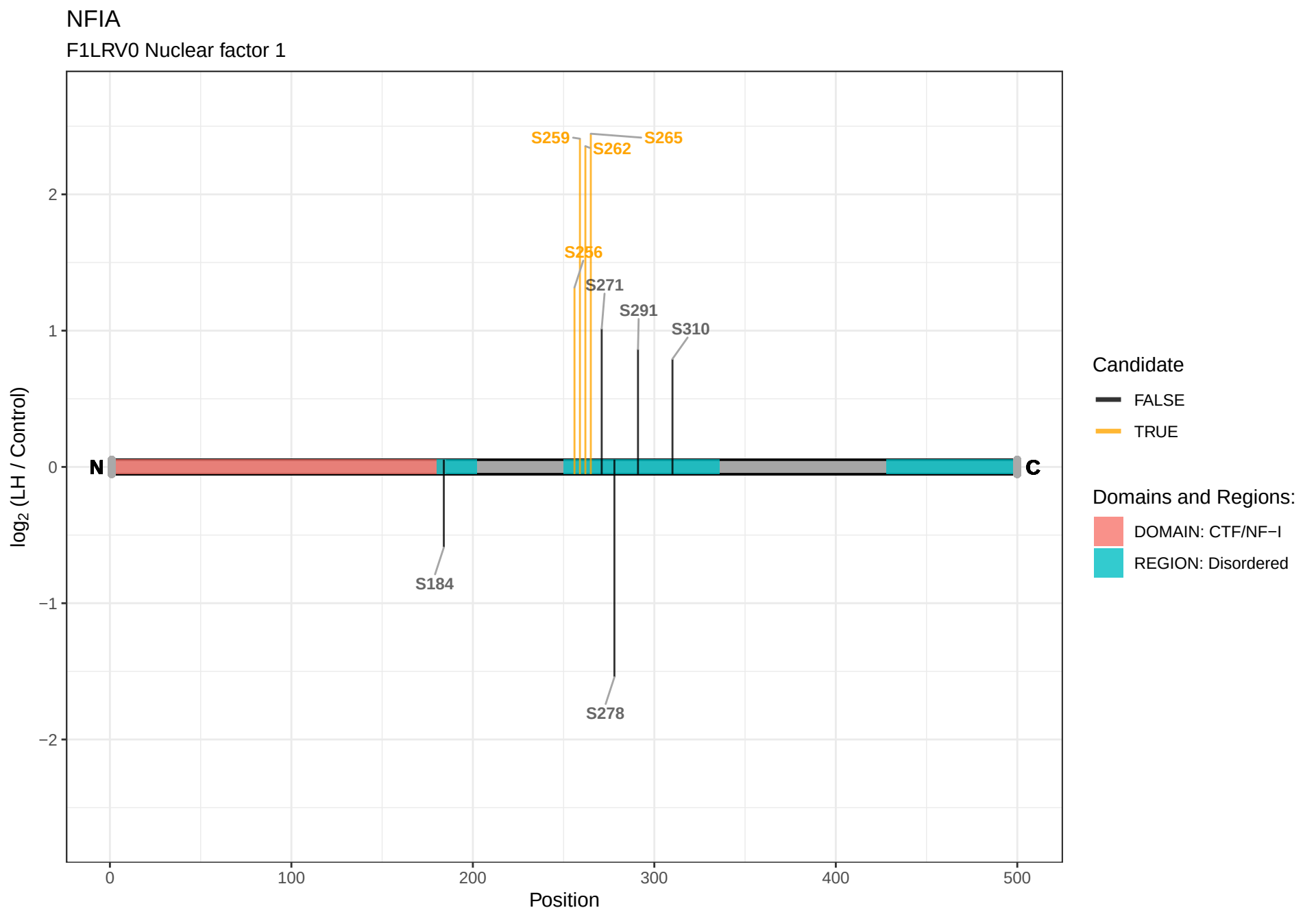

NCKIPSD
D3ZWX4 NCK−interacting protein with SH3 domain
log2 (LH / Control)
2
0
−2
N
C
T165
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: DUF2013
DOMAIN: SH3
REGION: Disordered

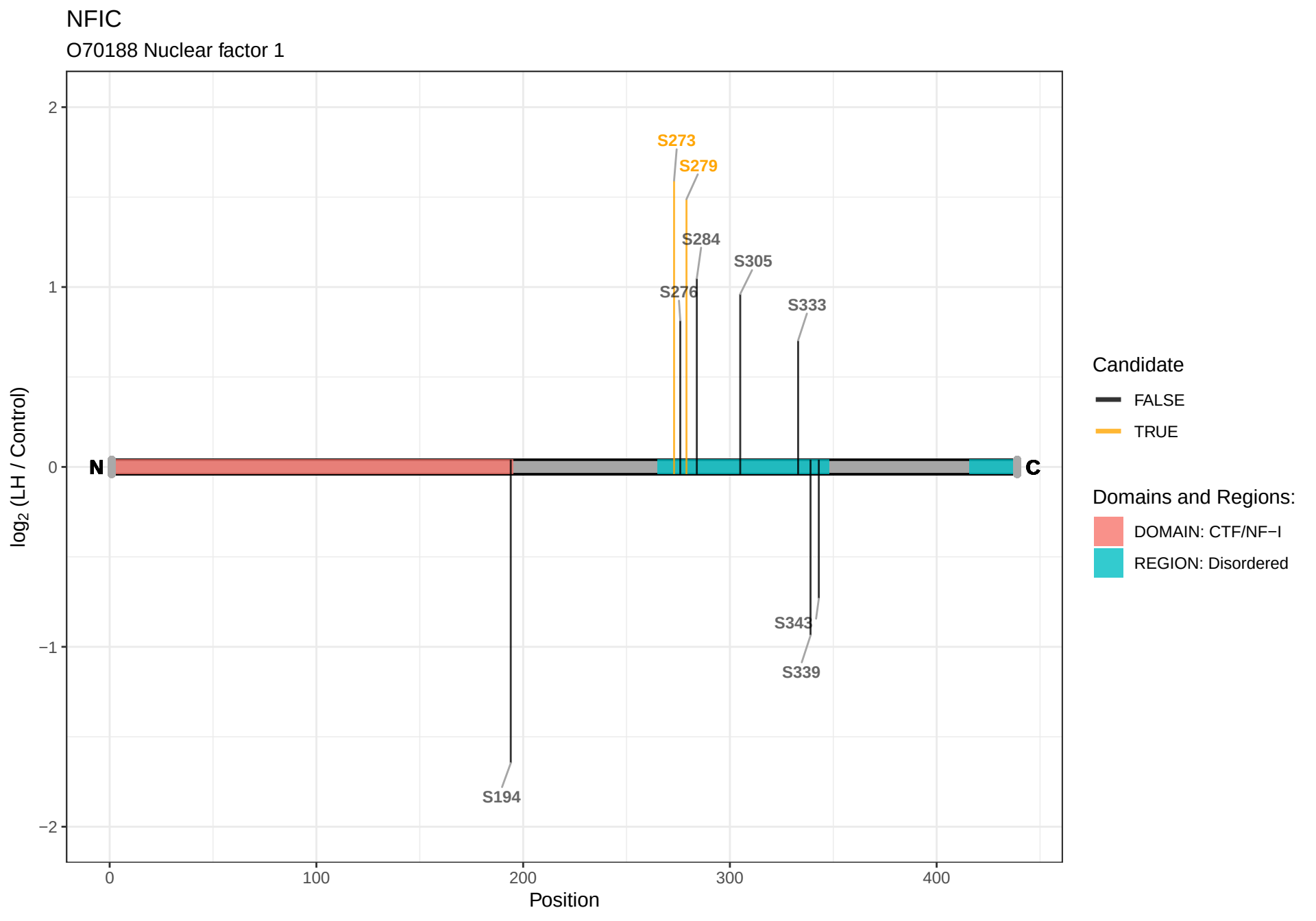

NCOA5
D3ZEI6 Nuclear receptor coactivator 5
S65
S29
S34
N
C
S9
S376
S380
S125
2
0
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

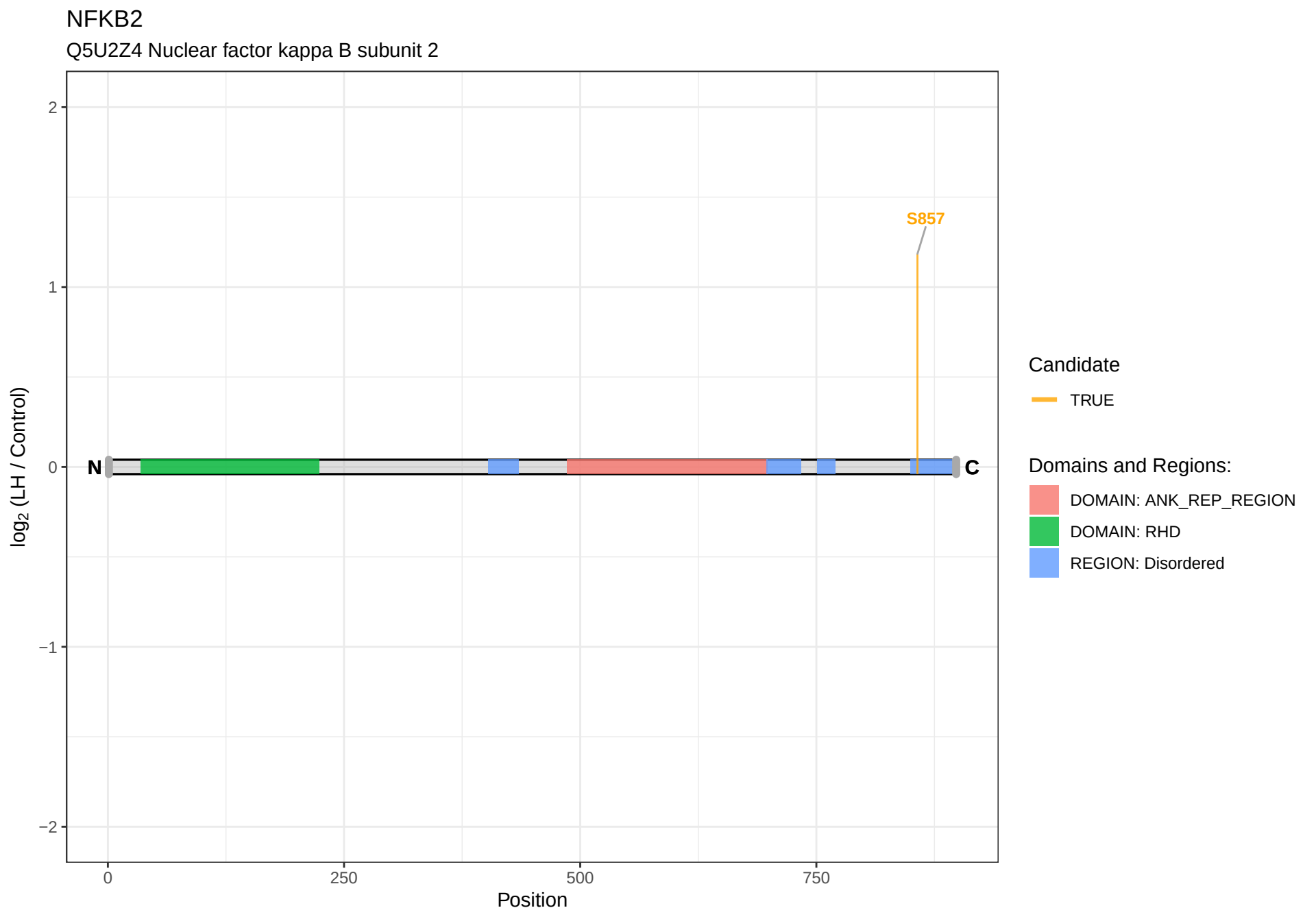

NEO1
P97603 Neogenin (Fragment)
S1163
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Fibronectin type−III 1
DOMAIN: Fibronectin type−III 2
DOMAIN: Fibronectin type−III 3
DOMAIN: Fibronectin type−III 4
DOMAIN: Fibronectin type−III 5
DOMAIN: Fibronectin type−III 6
DOMAIN: Ig−like C2−type 1
DOMAIN: Ig−like C2−type 2
DOMAIN: Ig−like C2−type 3
DOMAIN: Ig−like C2−type 4
REGION: Disordered

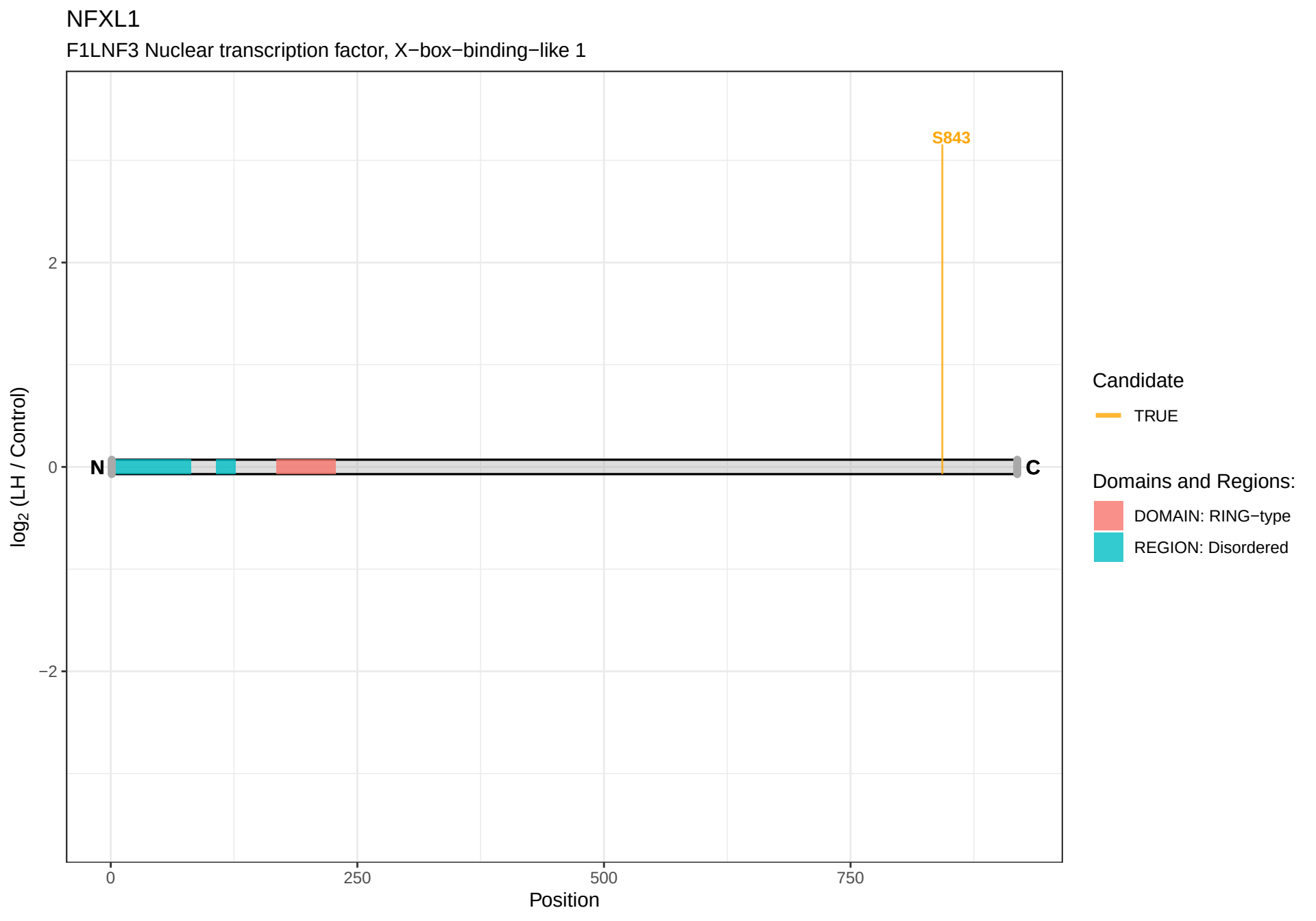

NF1
A0A0G2JWL3 Neurofibromin
S2445
S2460
S2488
S2774
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
1000
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CRAL−TRIO
DOMAIN: Ras−GAP
REGION: Disordered

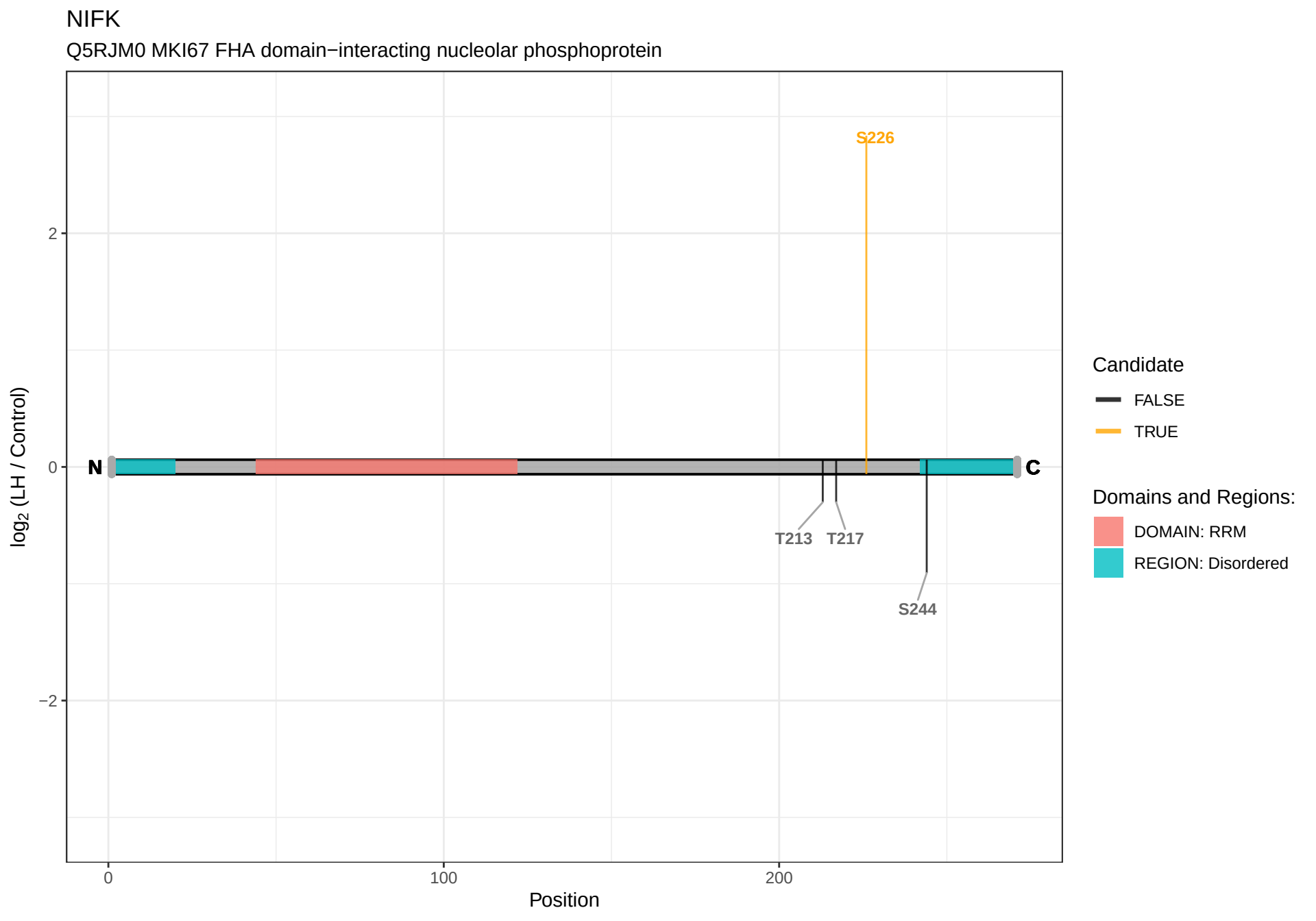

NFATC3
D3ZU59 Nuclear factor of activated T−cells, cytoplasmic, calcineurin−dependent 3 (Predicted), isoform CRA_a
S345
S367
N
C
log2 (LH / Control)
Position
0
300
600
900
2
1
0
−1
−2
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RHD
REGION: Disordered

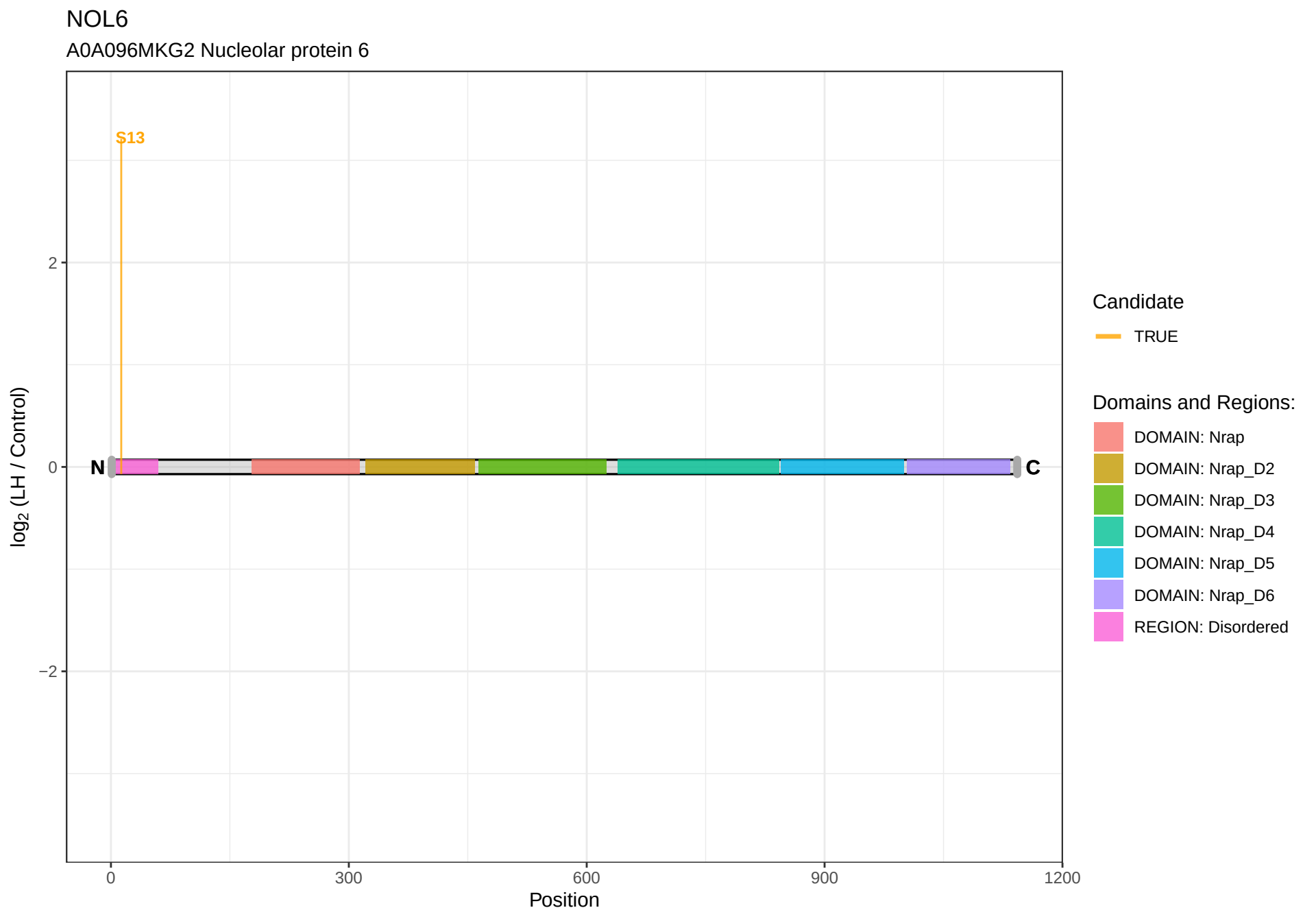

NFIA
F1LRV0 Nuclear factor 1
S259
S262
S265
S256
S271
S291
S310
S184
S278
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CTF/NF−I
REGION: Disordered

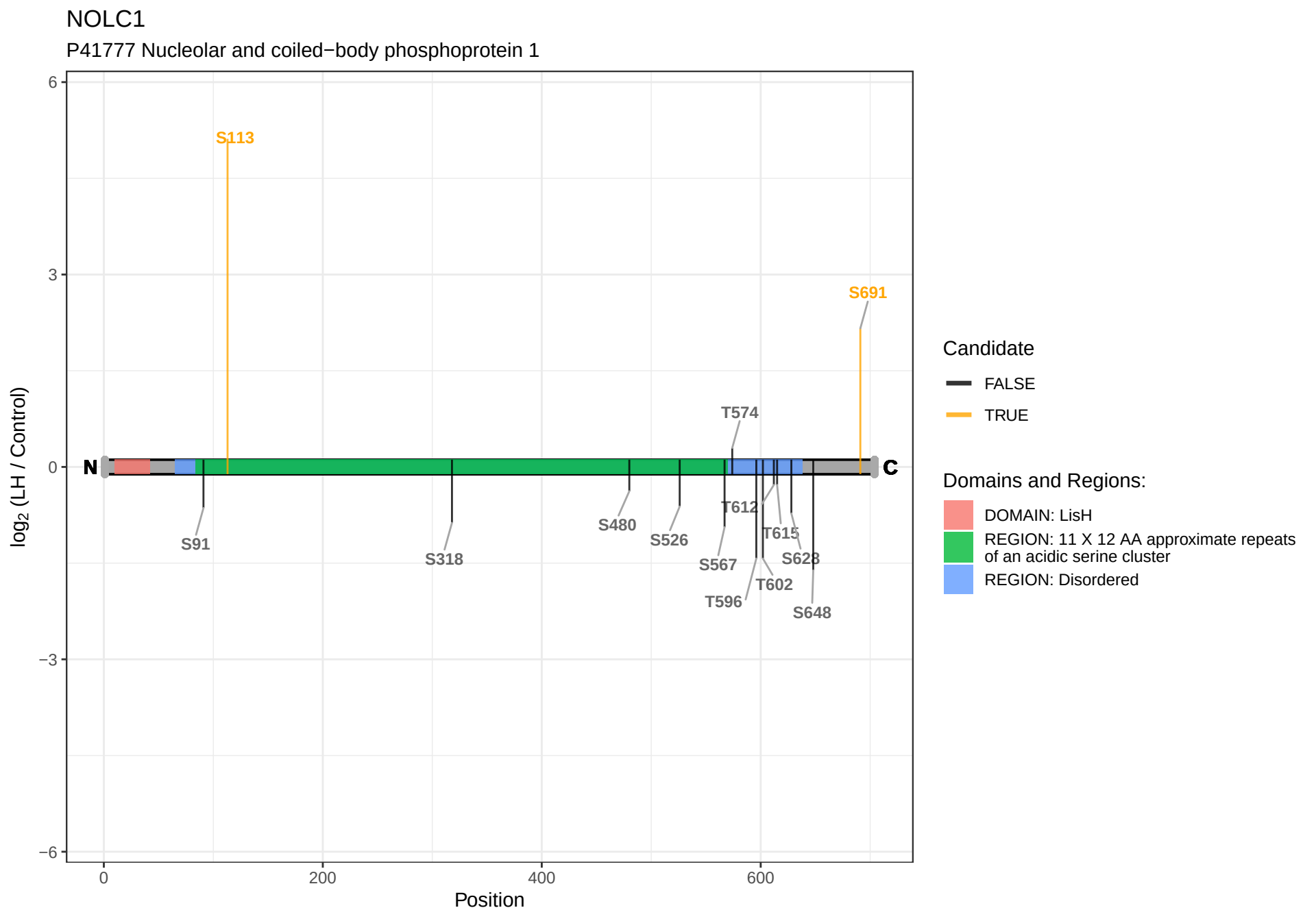

NFIC
O70188 Nuclear factor 1
S273
S279
S284
S305
S276
S333
S343
S339
S194
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CTF/NF−I
REGION: Disordered

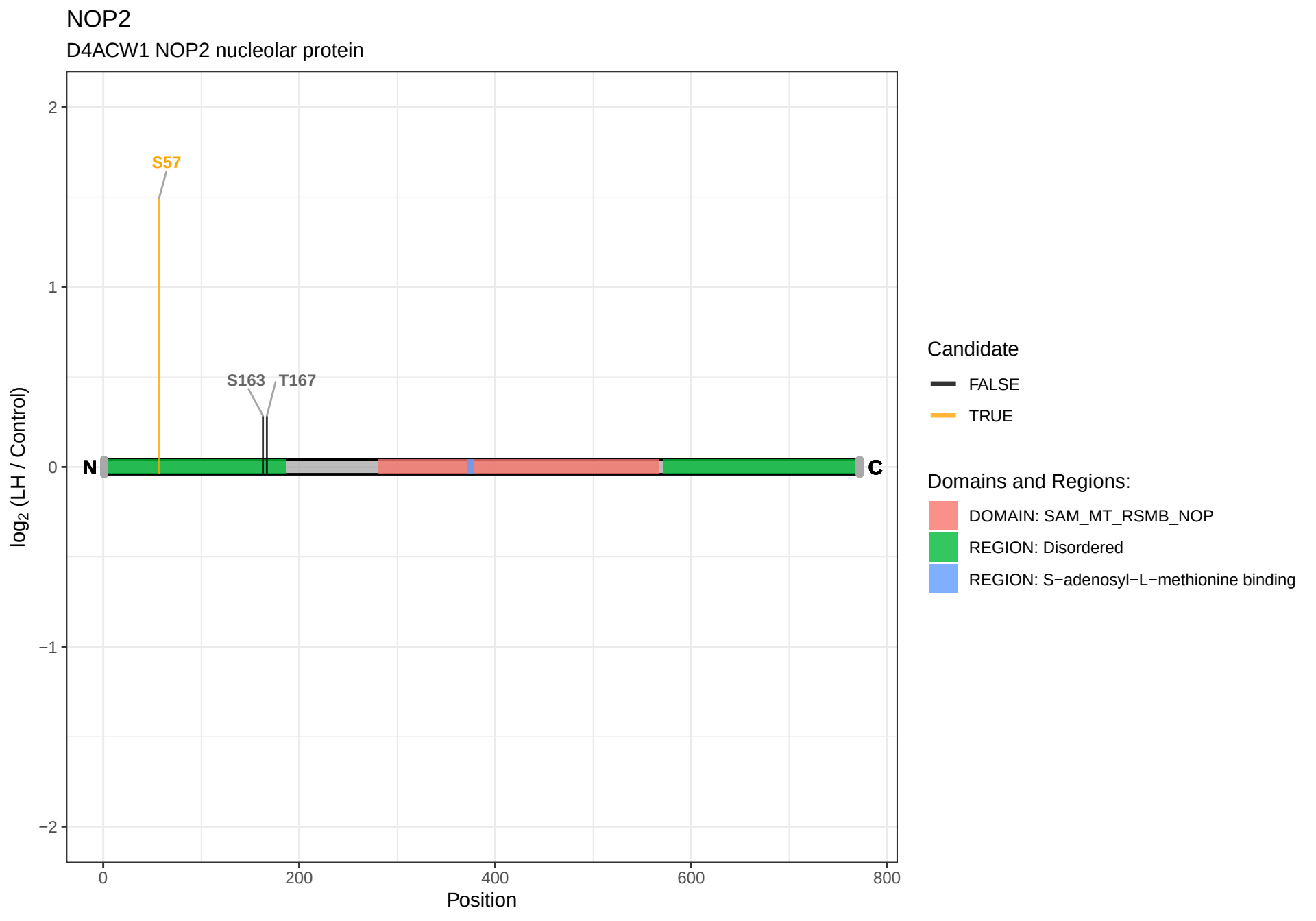

NFKB2
Q5U2Z4 Nuclear factor kappa B subunit 2
2
1
0
−1
−2
log2 (LH / Control)
S857
N
C
0
250
500
750
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: ANK_REP_REGION
DOMAIN: RHD
REGION: Disordered

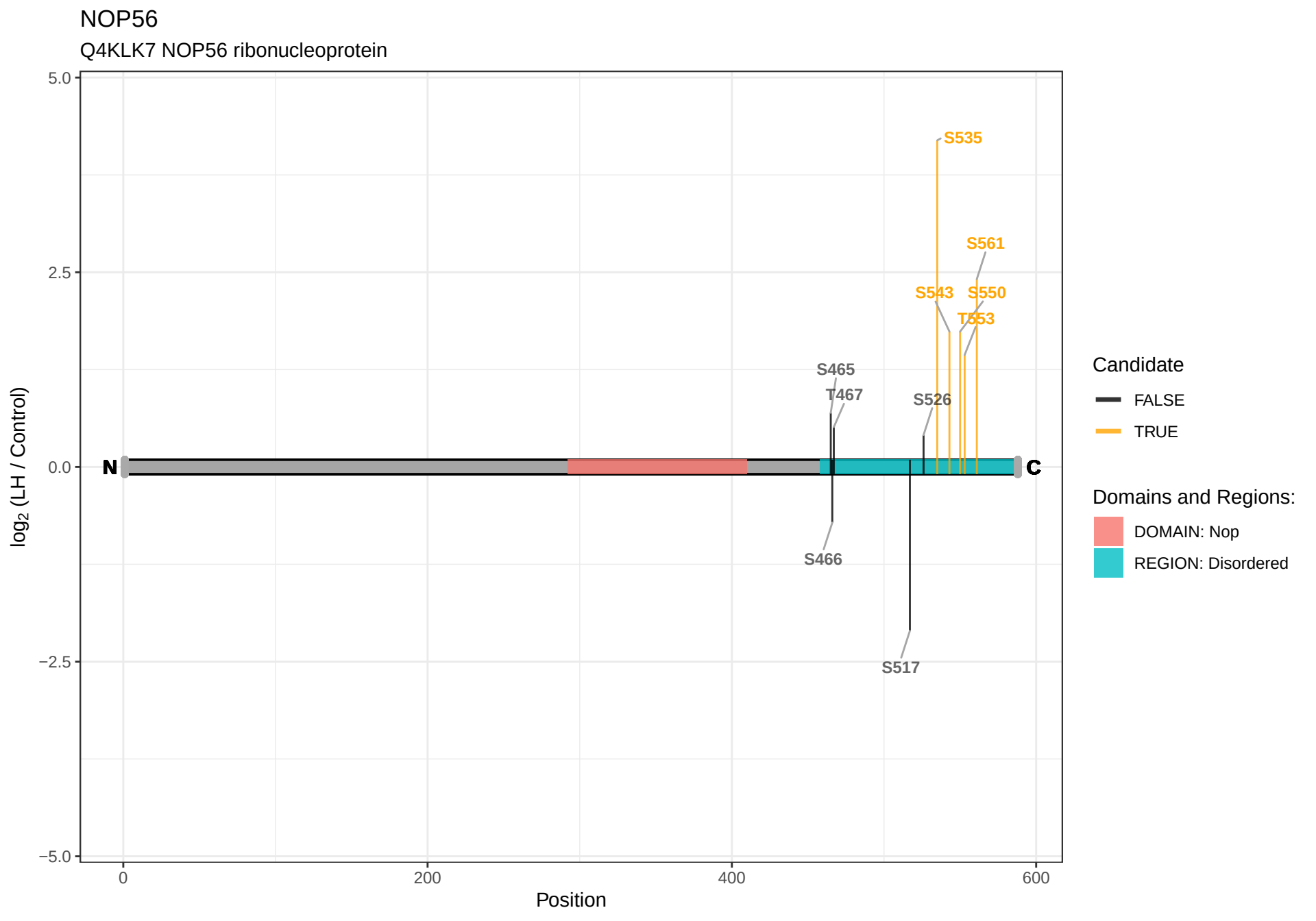

NFXL1
F1LNF3 Nuclear transcription factor, X−box−binding−like 1
S843
N
C
2
0
−2
log2 (LH / Control)
0
250
500
750
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: RING−type
REGION: Disordered

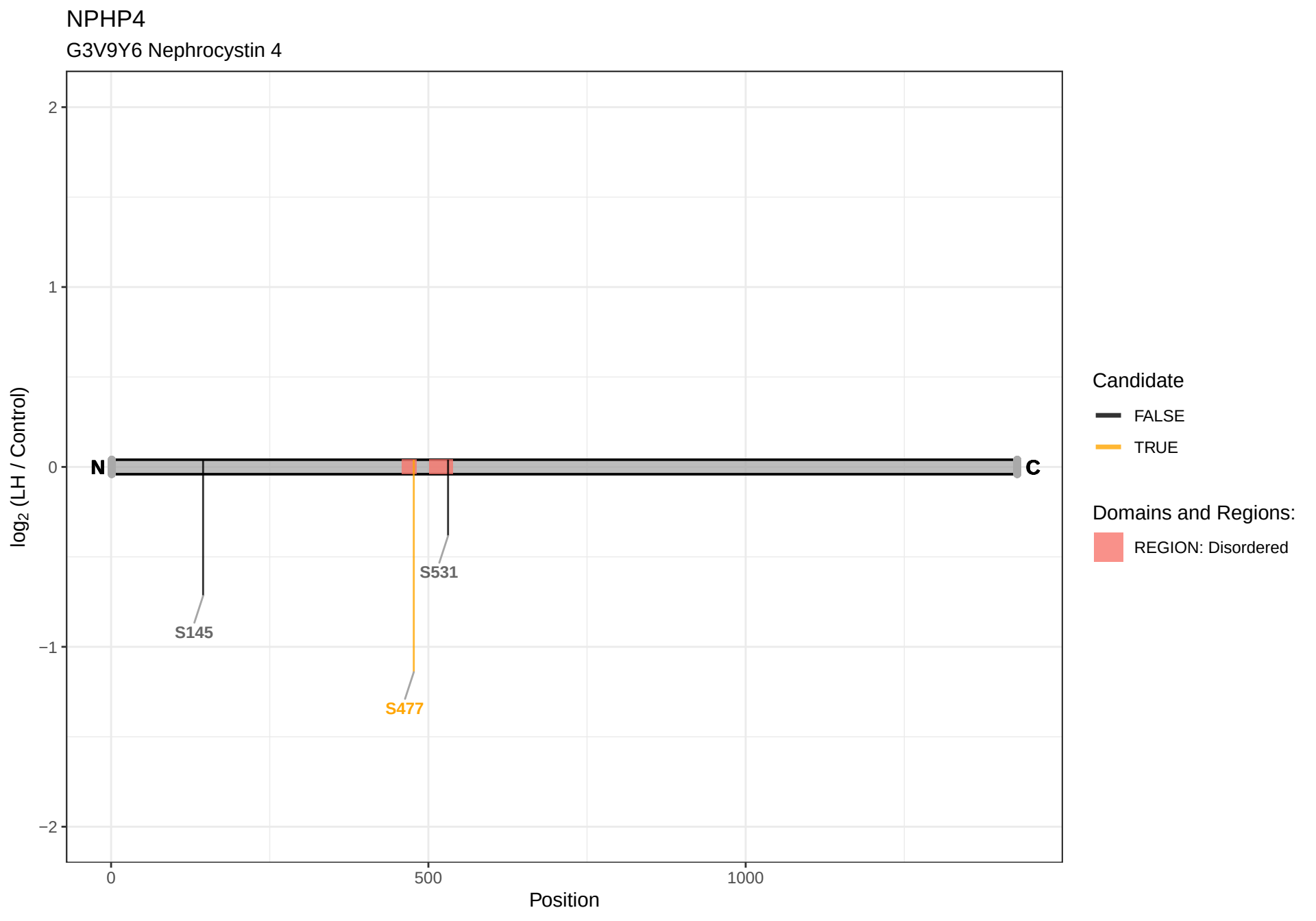

NIFK
Q5RJM0 MKI67 FHA domain−interacting nucleolar phosphoprotein
S226
T213
T217
S244
N
C
2
0
−2
log2 (LH / Control)
0
100
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RRM
REGION: Disordered

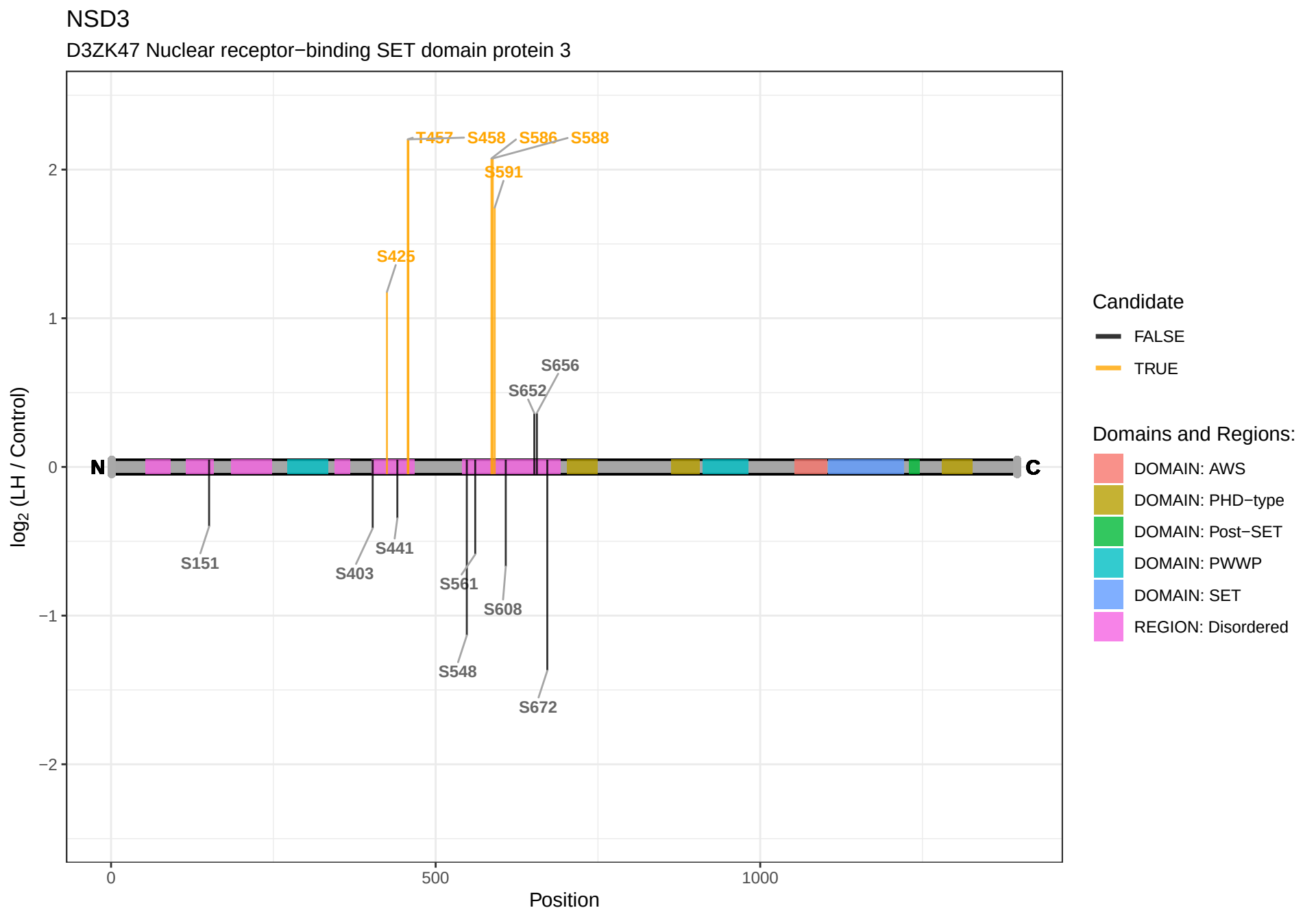

NOL6
A0A096MKG2 Nucleolar protein 6
S13
N
C
2
0
−2
log2 (LH / Control)
0
300
600
900
1200
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Nrap
DOMAIN: Nrap_D2
DOMAIN: Nrap_D3
DOMAIN: Nrap_D4
DOMAIN: Nrap_D5
DOMAIN: Nrap_D6
REGION: Disordered

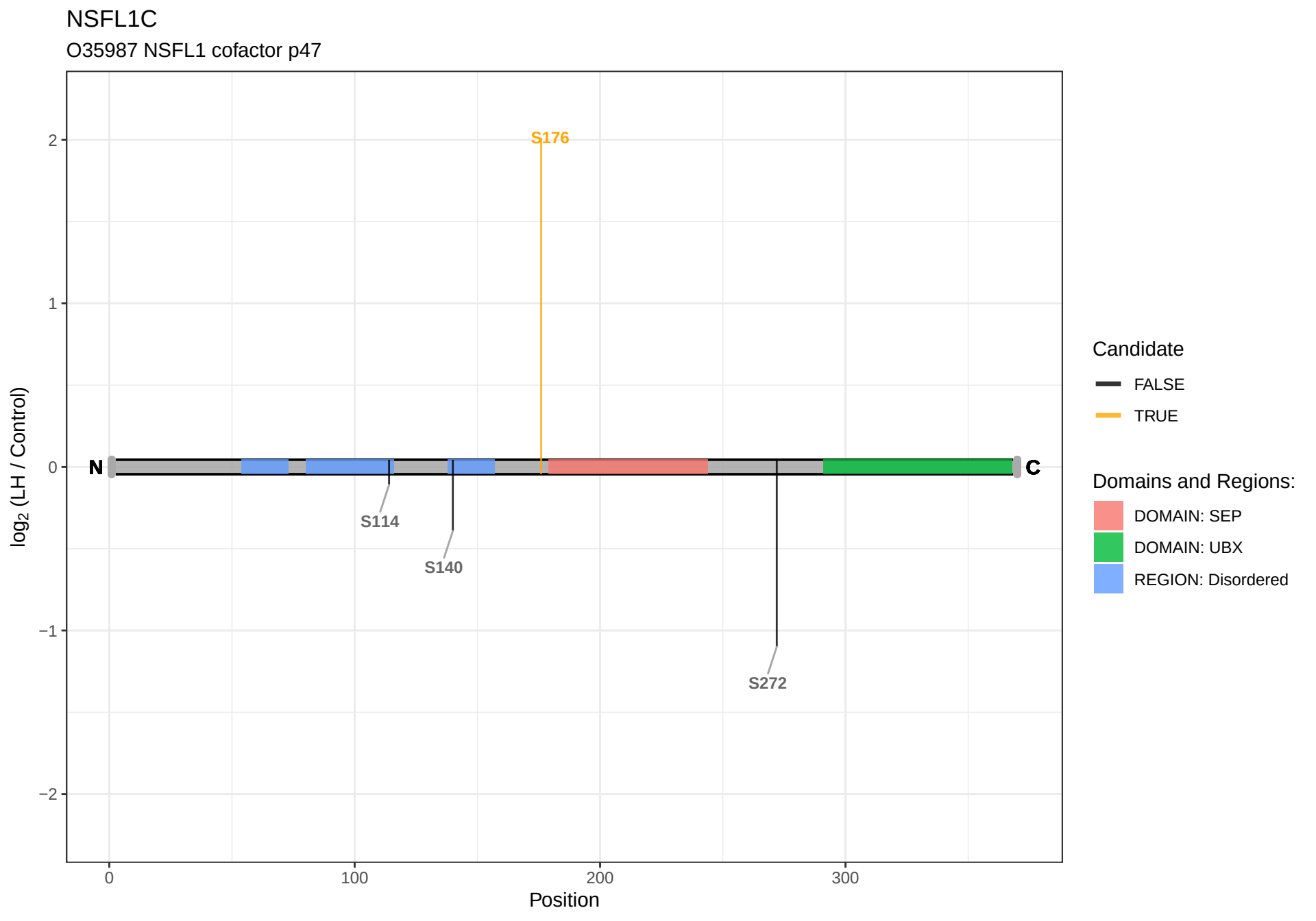

NOLC1
P41777 Nucleolar and coiled−body phosphoprotein 1
log2 (LH / Control)
6
3
0
−3
−6
0
200
400
600
Position
N
C
S113
S691
T574
S91
S318
S480
S526
T612
T615
S567
S628
T602
T596
S648
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: LisH
REGION: 11 X 12 AA approximate repeats of an acidic serine cluster
REGION: Disordered

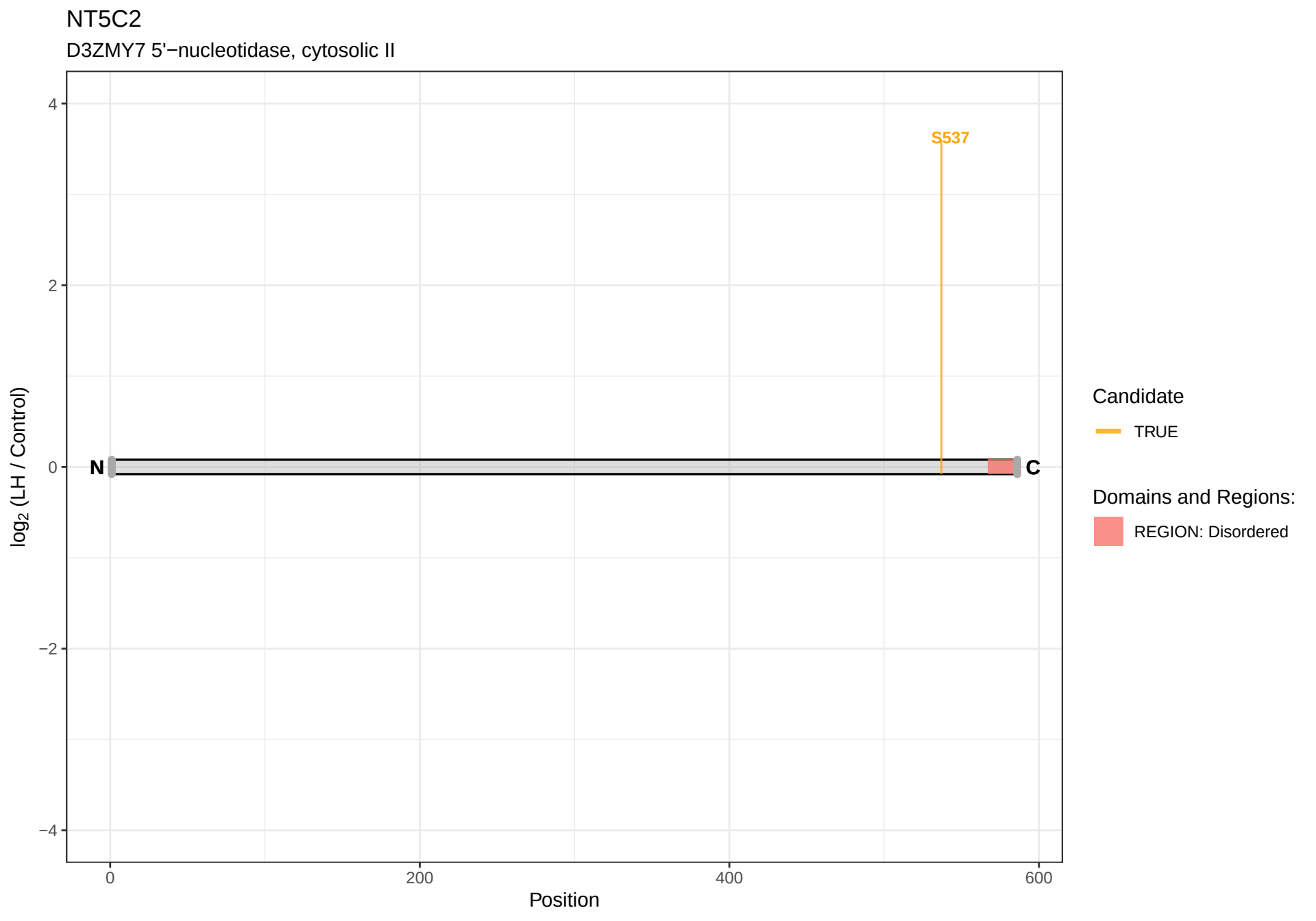

NOP2
D4ACW1 NOP2 nucleolar protein
S57
S163
T167
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SAM_MT_RSMB_NOP
REGION: Disordered
REGION: S−adenosyl−L−methionine binding

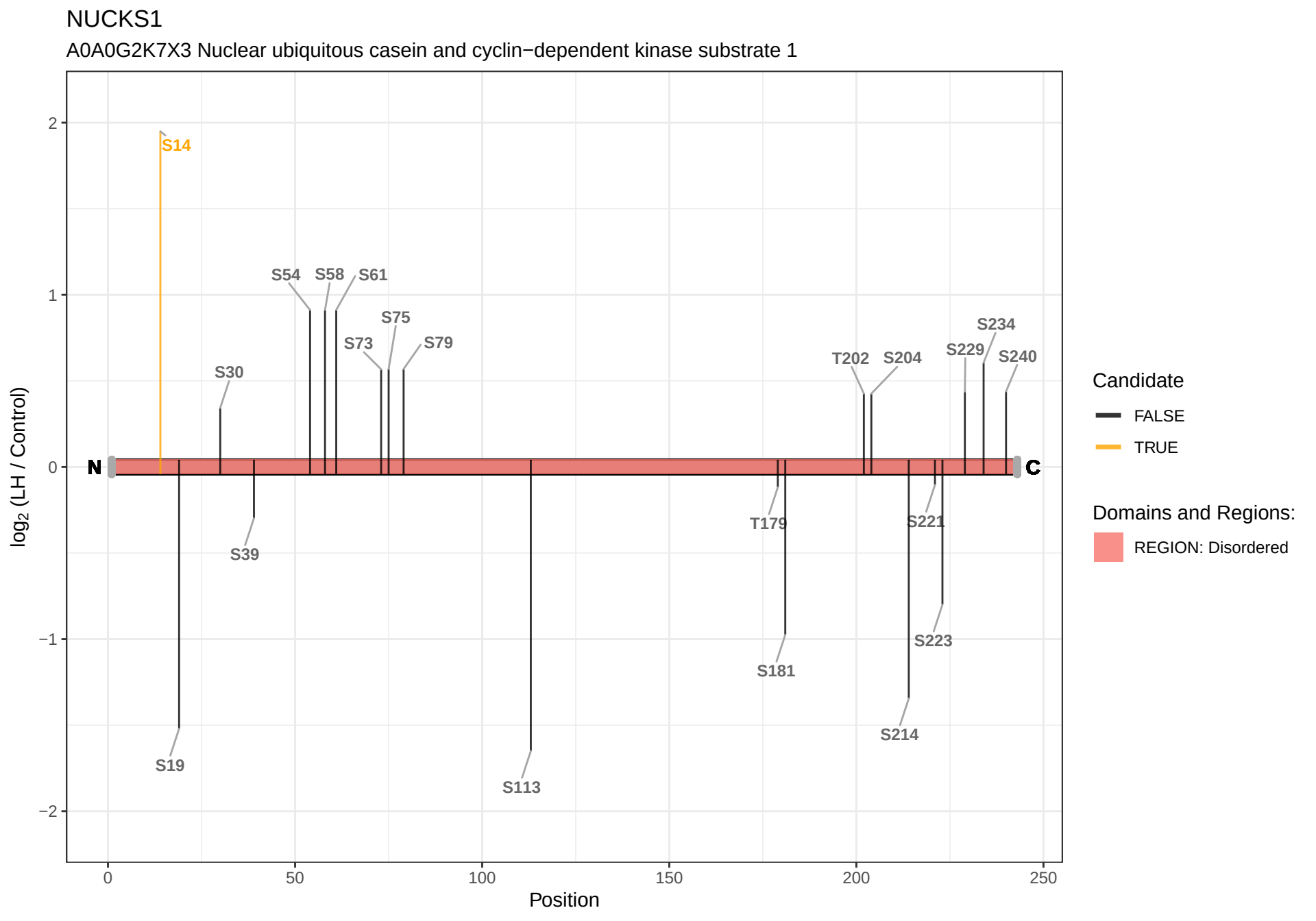

NOP56
Q4KLK7 NOP56 ribonucleoprotein
5.0
2.5
0.0
−2.5
−5.0
log2 (LH / Control)
0
200
400
600
Position
N
C
S535
S561
S543
S550
T553
S465
T467
S526
S466
S517
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Nop
REGION: Disordered

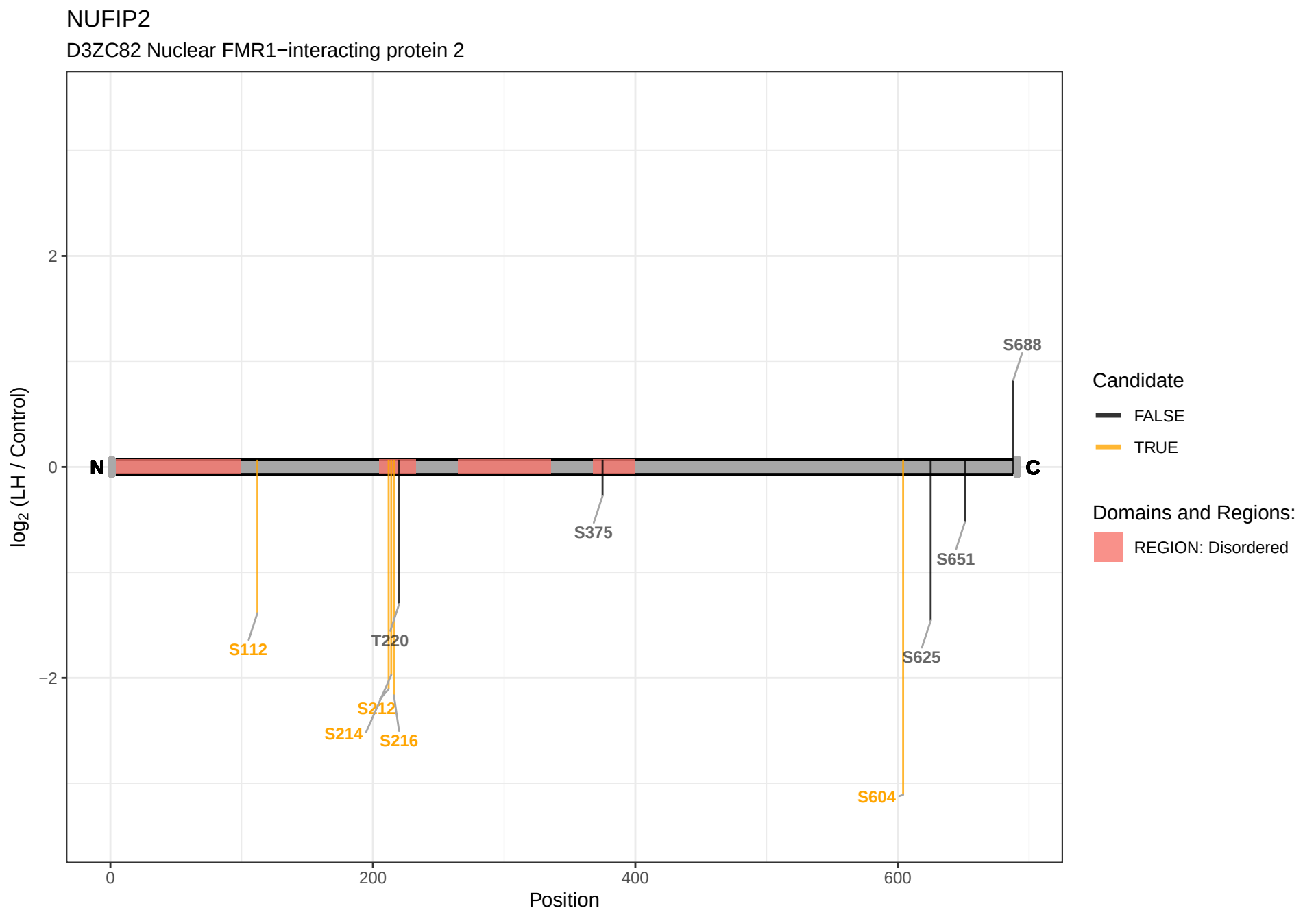

NPHP4
G3V9Y6 Nephrocystin 4
2
1
0
−1
−2
log2 (LH / Control)
N
C
S145
S531
S477
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

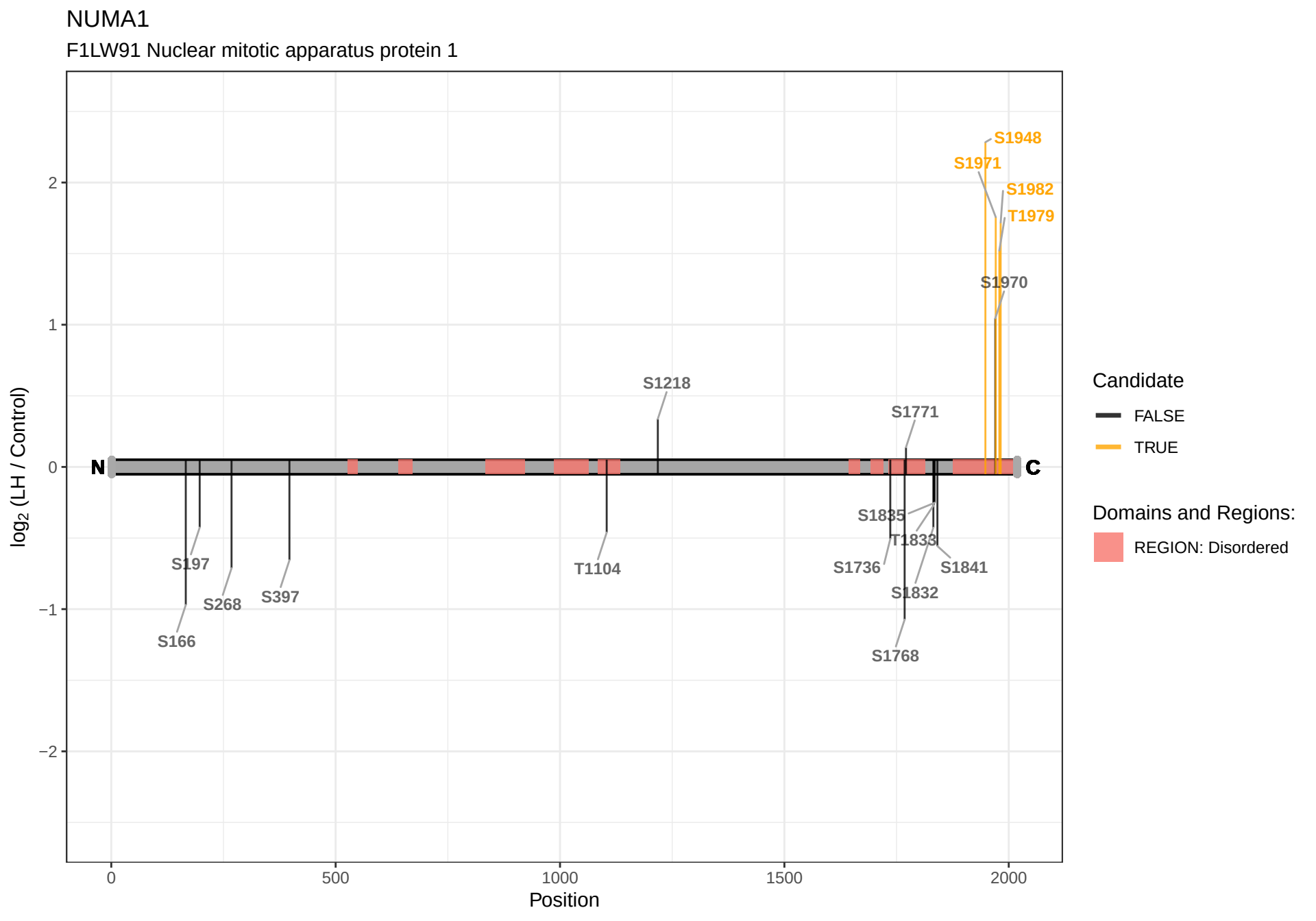

NSD3
D3ZK47 Nuclear receptor−binding SET domain protein 3
T457
S458
S586
S588
S591
S425
S656
S652
N
C
S151
S403
S441
S561
S608
S548
S672
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AWS
DOMAIN: PHD−type
DOMAIN: Post−SET
DOMAIN: PWWP
DOMAIN: SET
REGION: Disordered

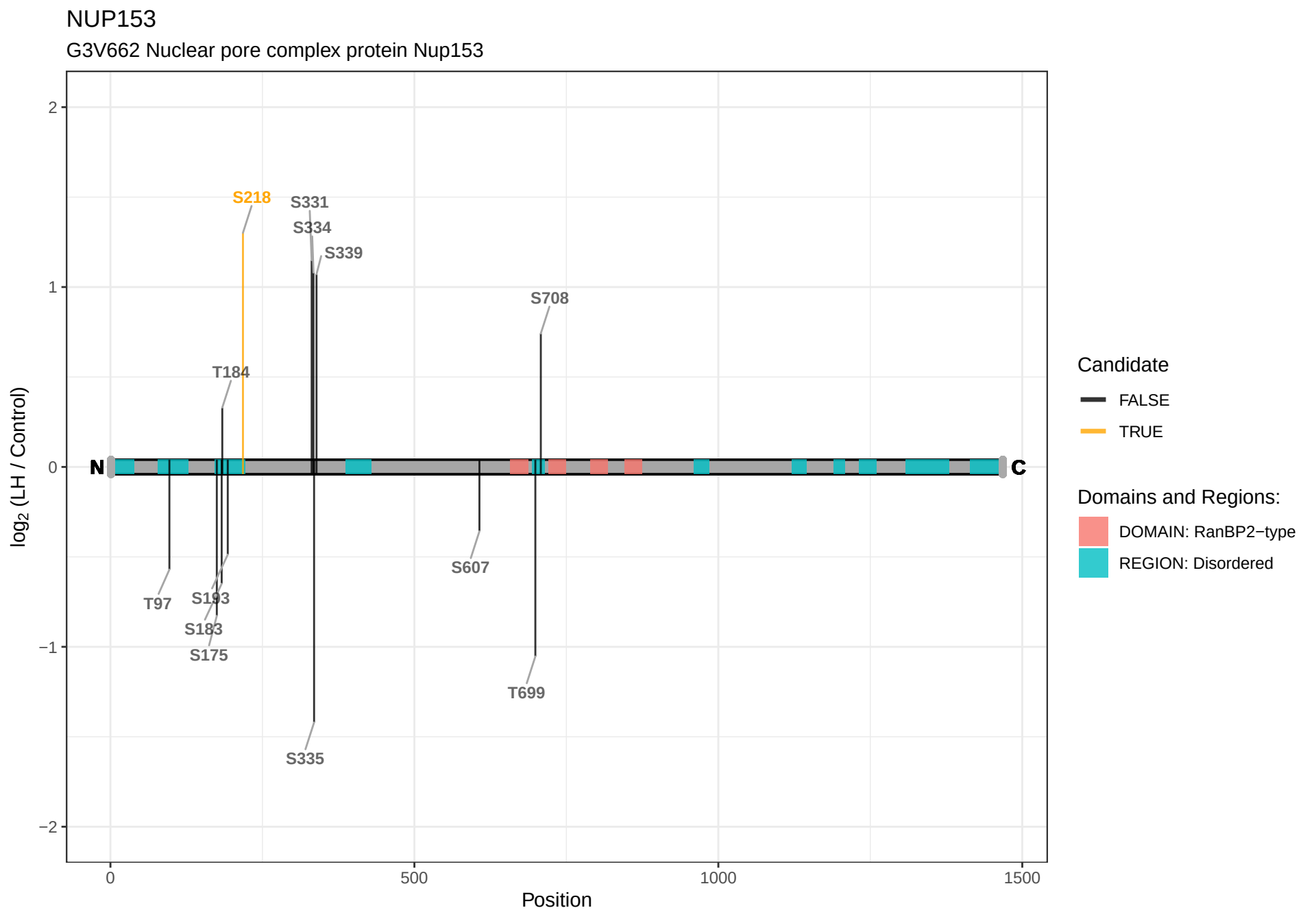

NSFL1C
O35987 NSFL1 cofactor p47
S176
S114
S140
S272
N
C
log2 (LH / Control)
Position
0
100
200
300
2
1
0
−1
−2
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SEP
DOMAIN: UBX
REGION: Disordered

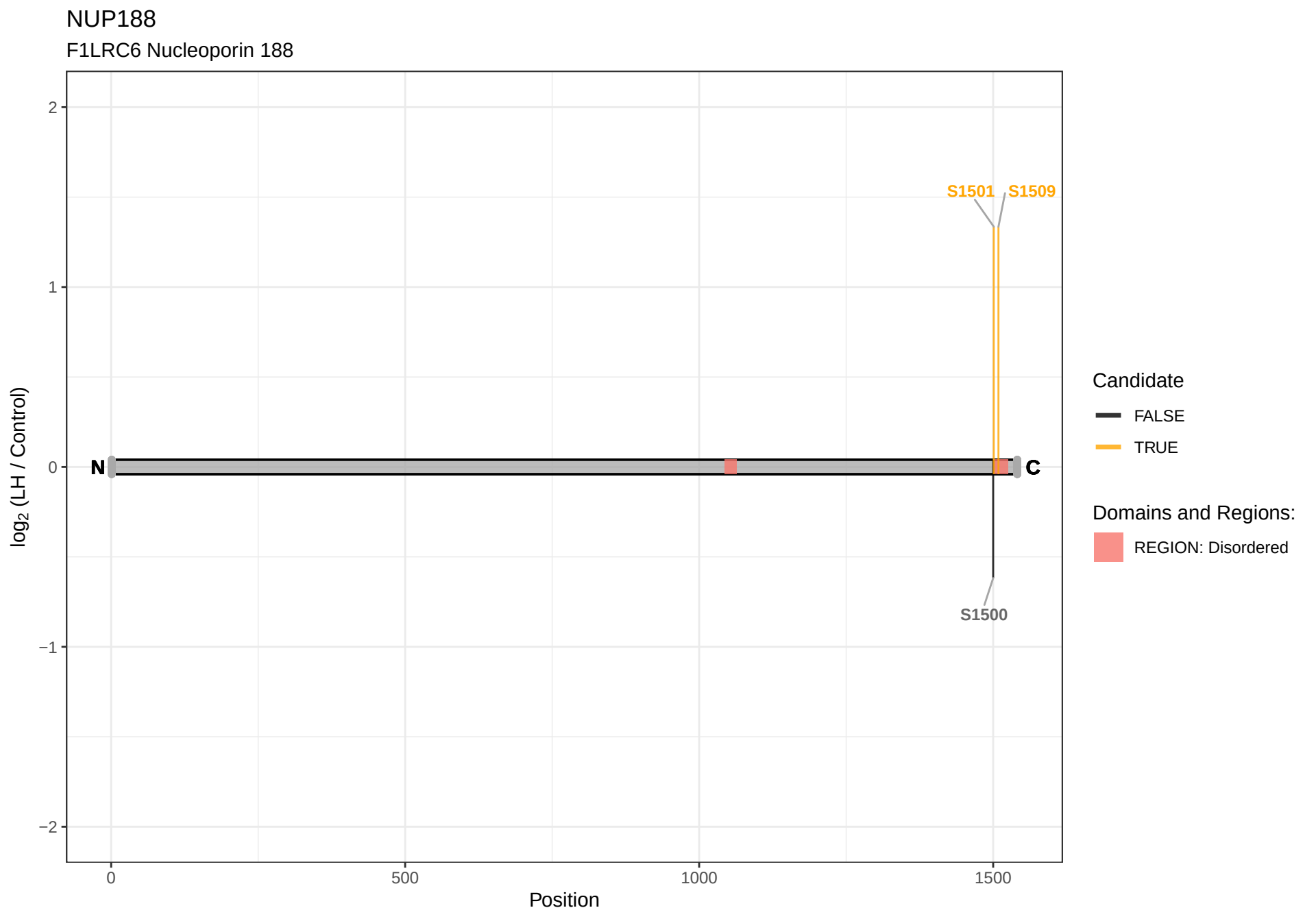

NT5C2
D3ZMY7 5'−nucleotidase, cytosolic II
S537
N
C
4
2
0
−2
−4
0
200
400
600
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
REGION: Disordered

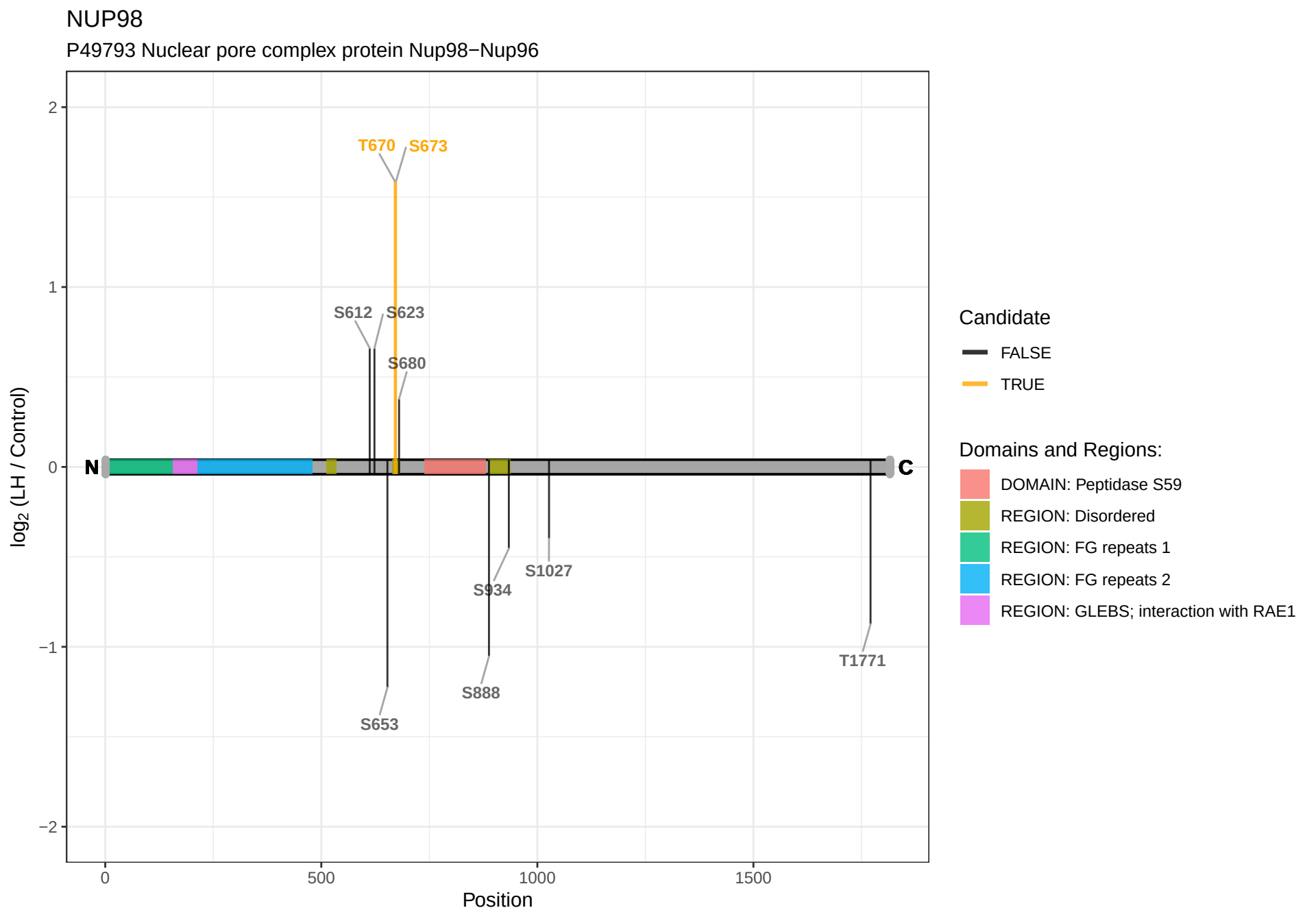

NUCKS1
A0A0G2K7X3 Nuclear ubiquitous casein and cyclin−dependent kinase substrate 1
log2 (LH / Control)
2
1
0
−1
−2
0
50
100
150
200
250
Position
N
C
S14
S54
S58
S61
S75
S73
S79
S30
T202
S204
S234
S229
S240
S39
T179
S221
S223
S181
S19
S113
S214
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

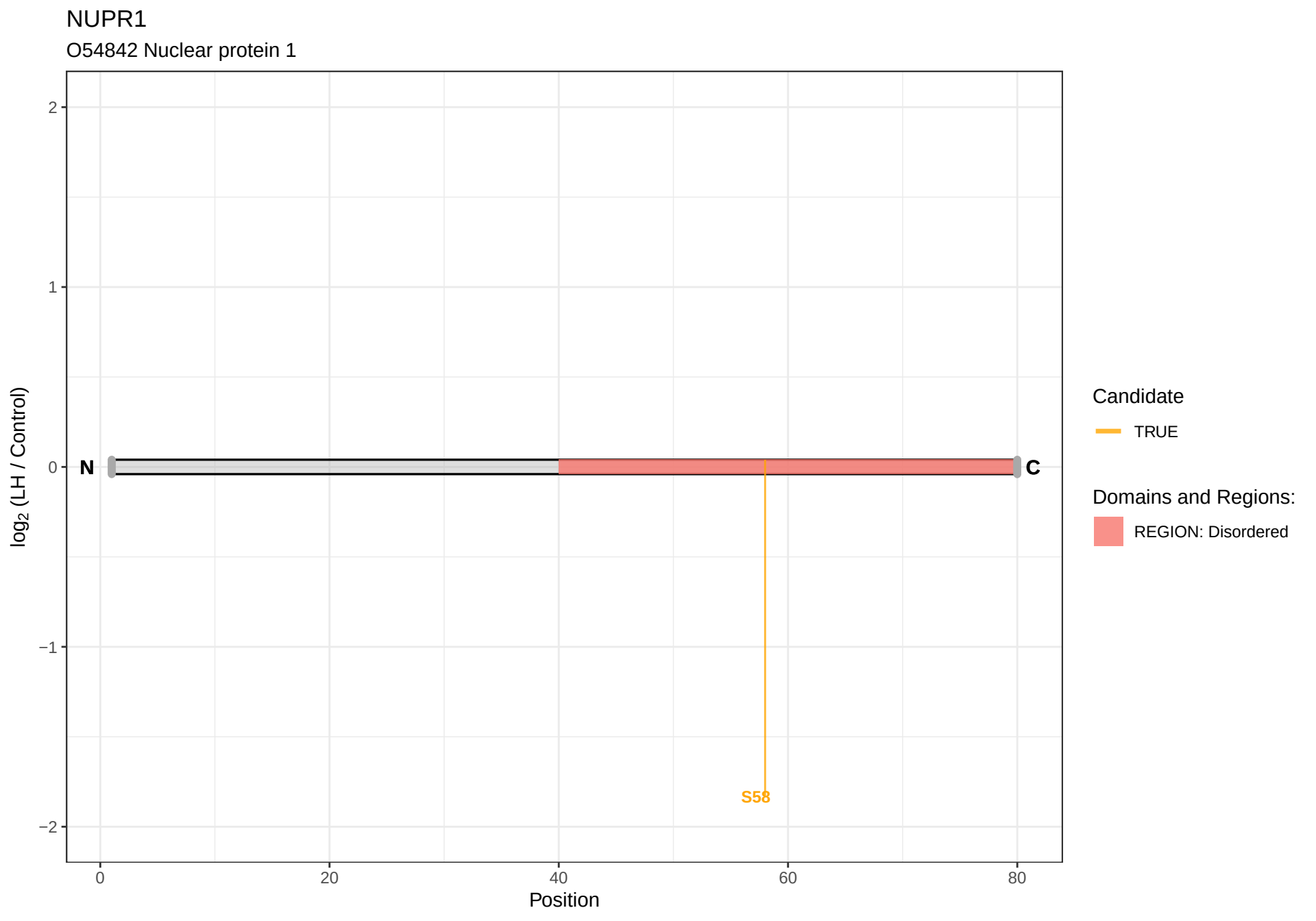

NUFIP2
D3ZC82 Nuclear FMR1−interacting protein 2
log2 (LH / Control)
2
0
−2
N
C
S688
S375
S651
S112
T220
S625
S212
S214
S216
S604
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

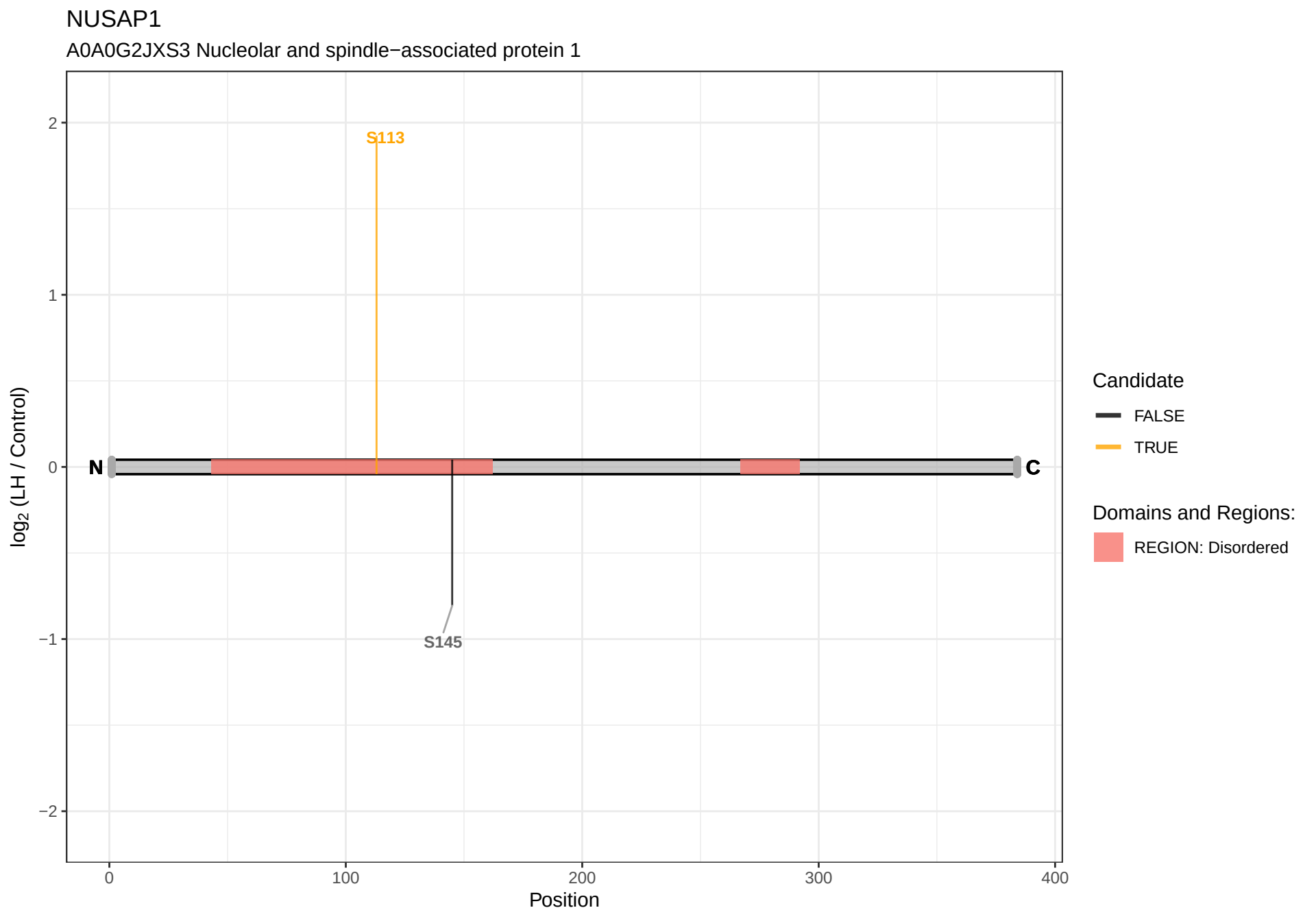

NUMA1
F1LW91 Nuclear mitotic apparatus protein 1
log2 (LH / Control)
Position
N
C
S1948
S1971
S1982
T1979
S1970
S1218
S1771
S197
S166
S268
S397
T1104
S1835
T1838
S1736
S1841
S1832
S1768
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

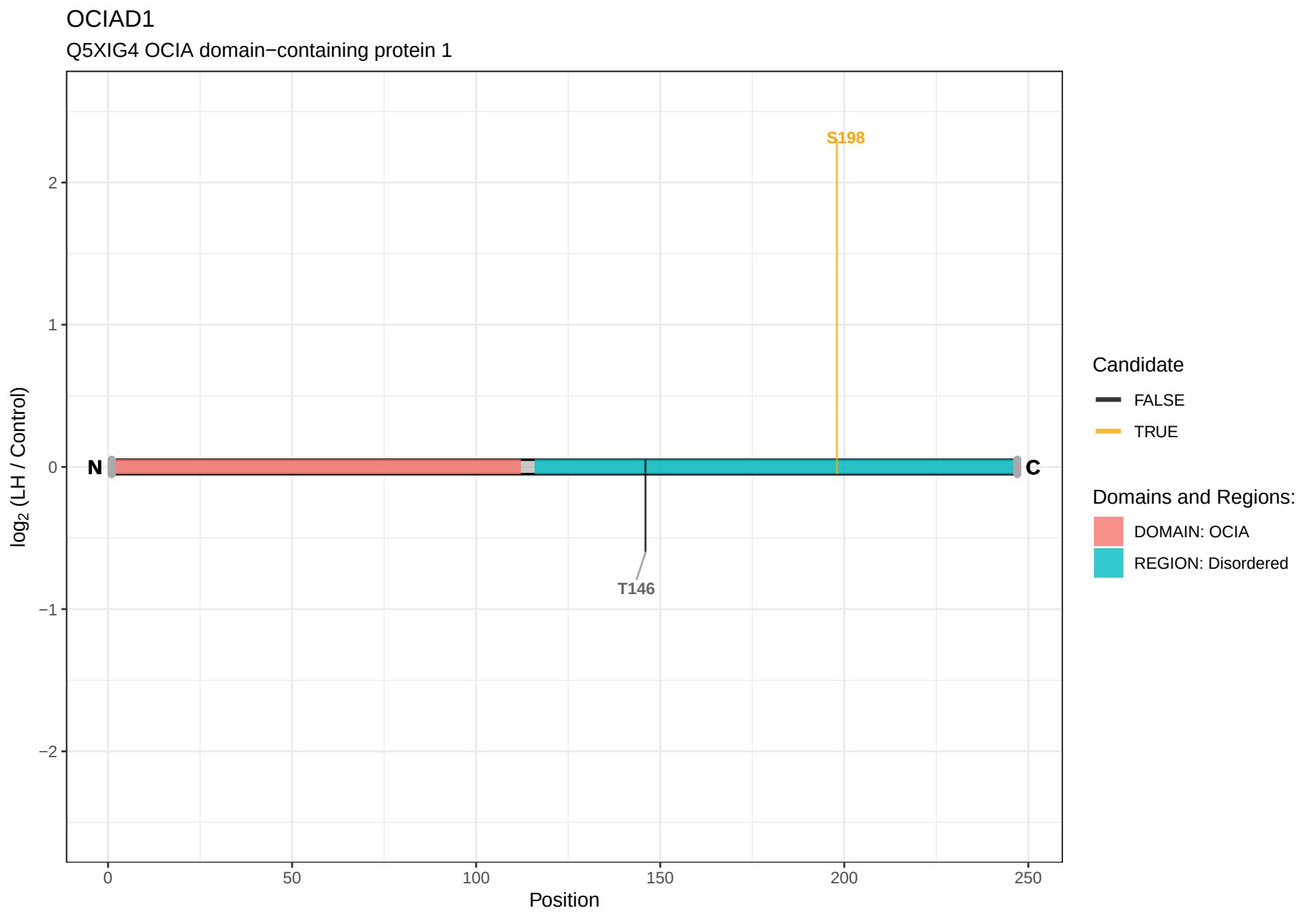

NUP153
G3V662 Nuclear pore complex protein Nup153
log2 (LH / Control)
Position
2
1
0
−1
−2
0
500
1000
1500
N
C
S218
S331
S334
S339
S708
T184
T97
S193
S183
S175
S607
T699
S335
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RanBP2−type
REGION: Disordered

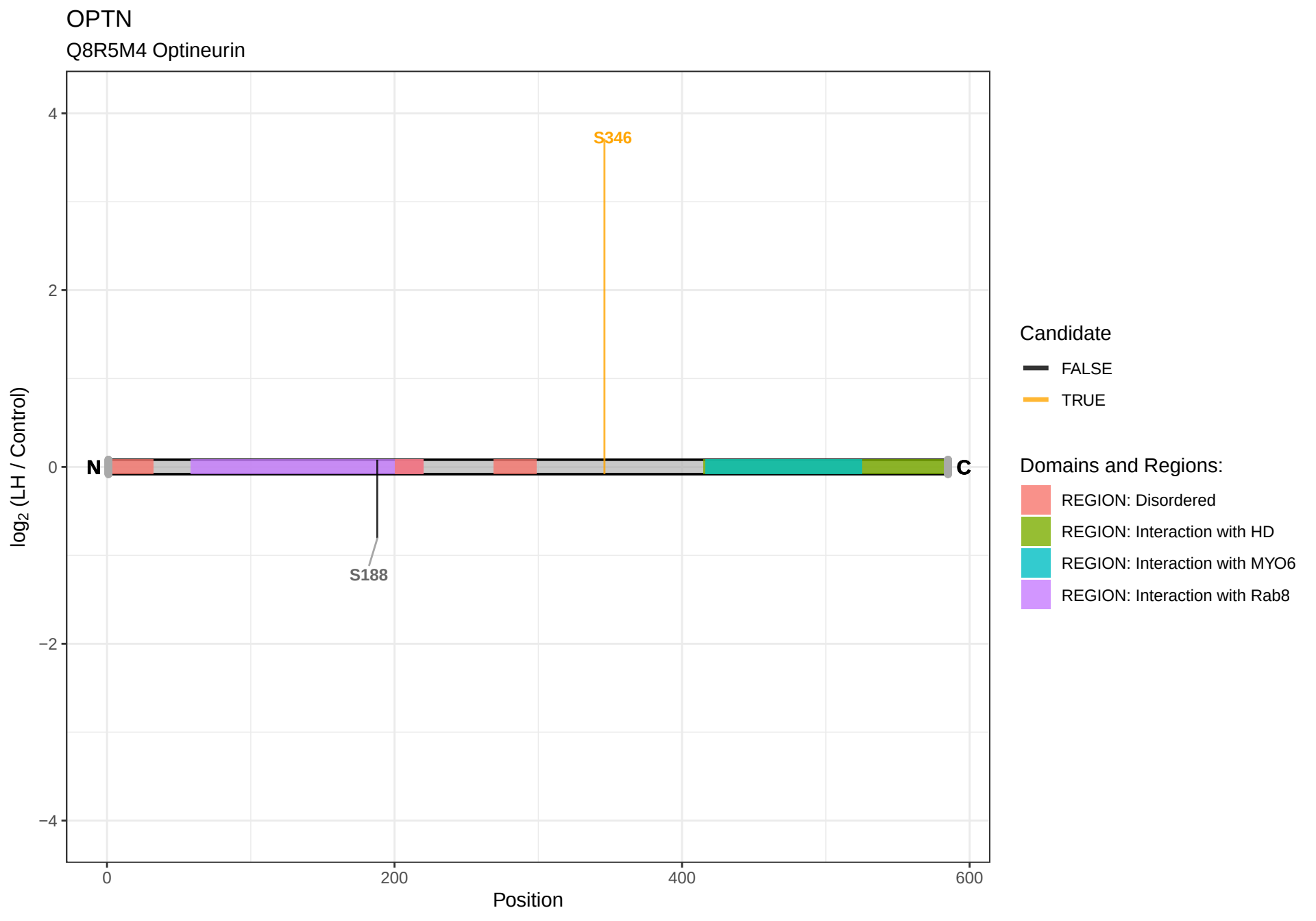

NUP188
F1LRC6 Nucleoporin 188
2
1
0
−1
−2
log2 (LH / Control)
N
C
S1501
S1509
S1500
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

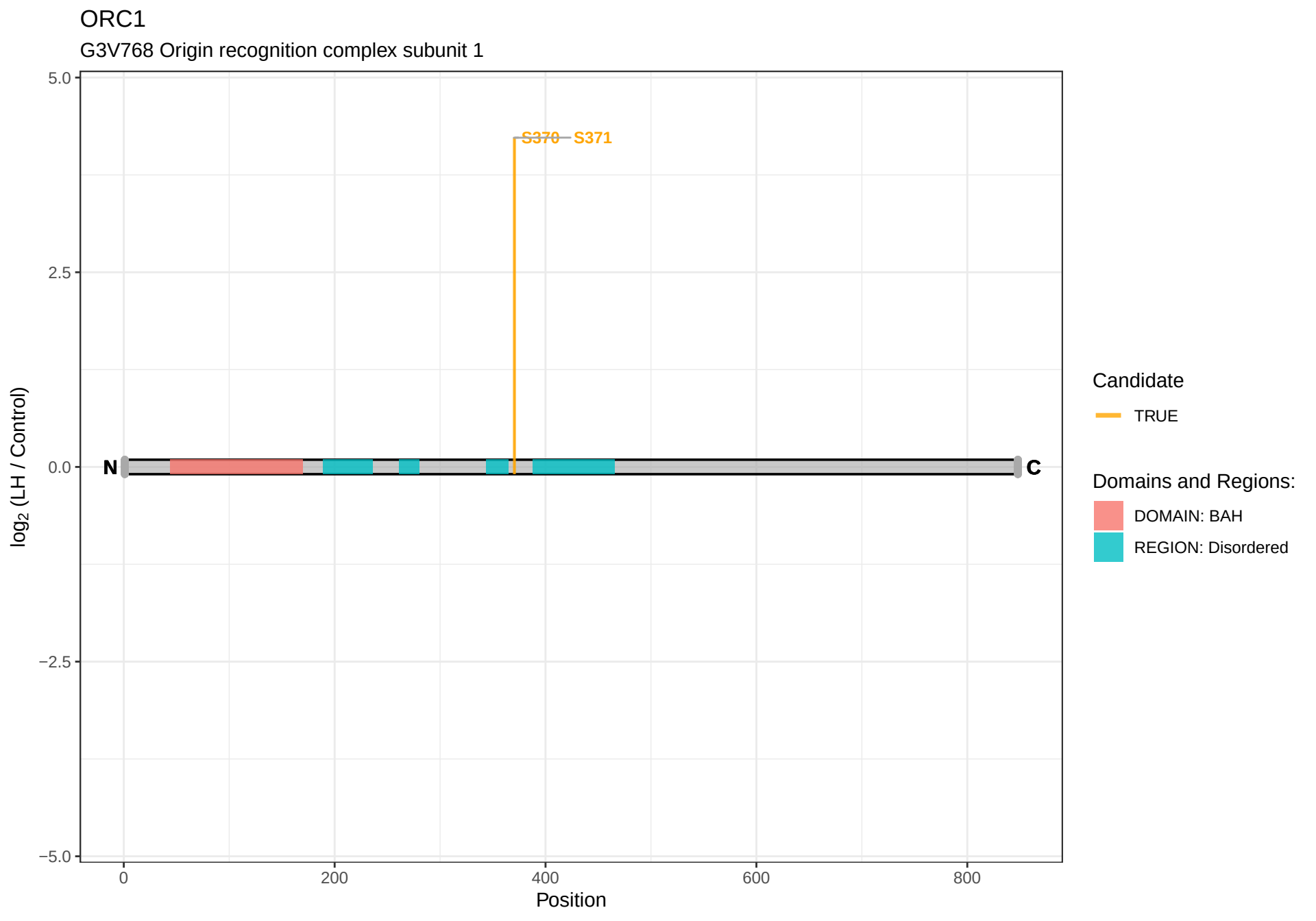

NUP98
P49793 Nuclear pore complex protein Nup98−Nup96
T670
S673
S612
S623
S680
S934
S1027
S888
S653
T1771
N
C
log2 (LH / Control)
Position
0
500
1000
1500
2
1
0
−1
−2
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Peptidase S59
REGION: Disordered
REGION: FG repeats 1
REGION: FG repeats 2
REGION: GLEBS; interaction with RAE1

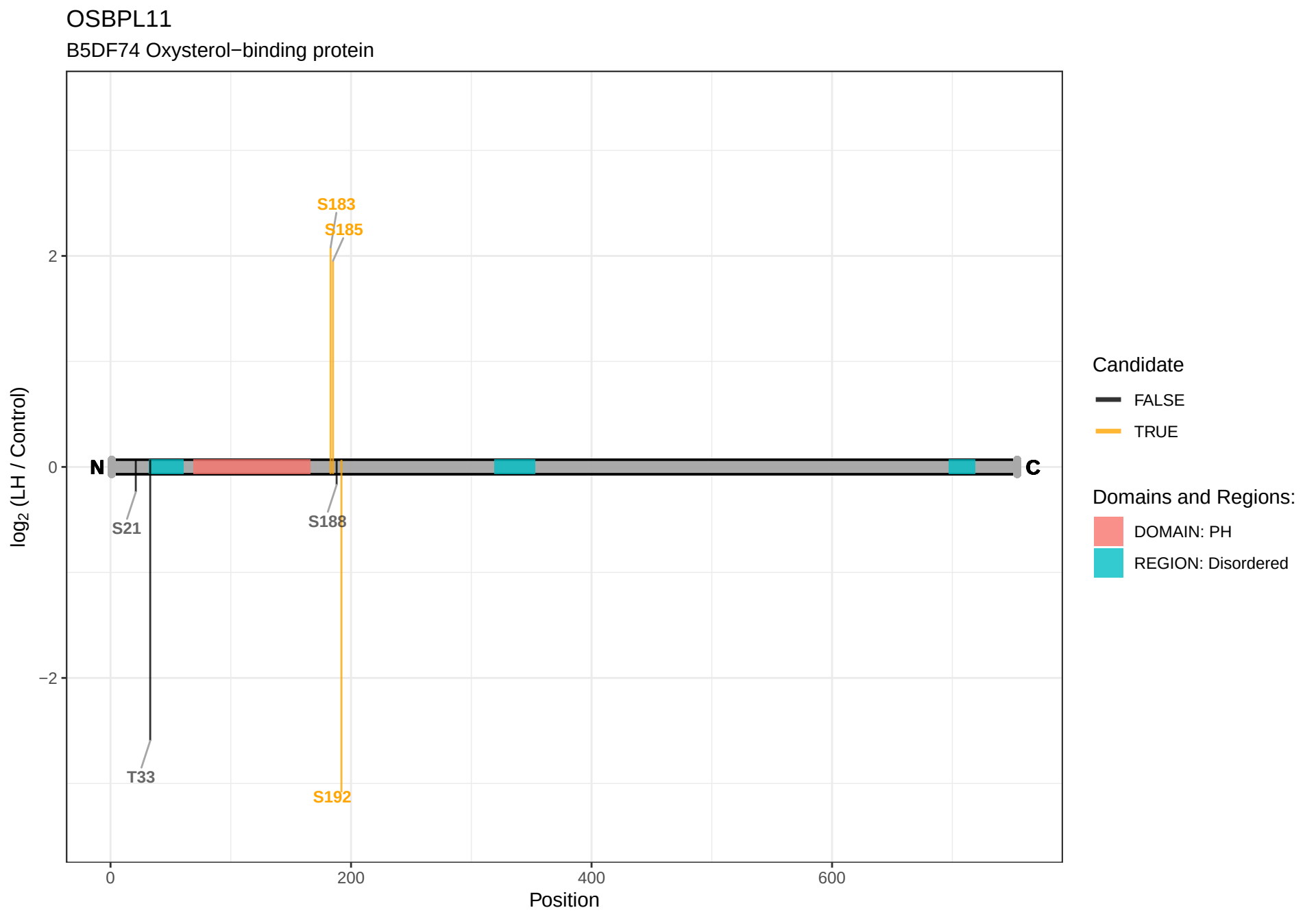

NUPR1
O54842 Nuclear protein 1
2
1
0
−1
−2
log2 (LH / Control)
N
C
S58
0
20
40
60
80
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

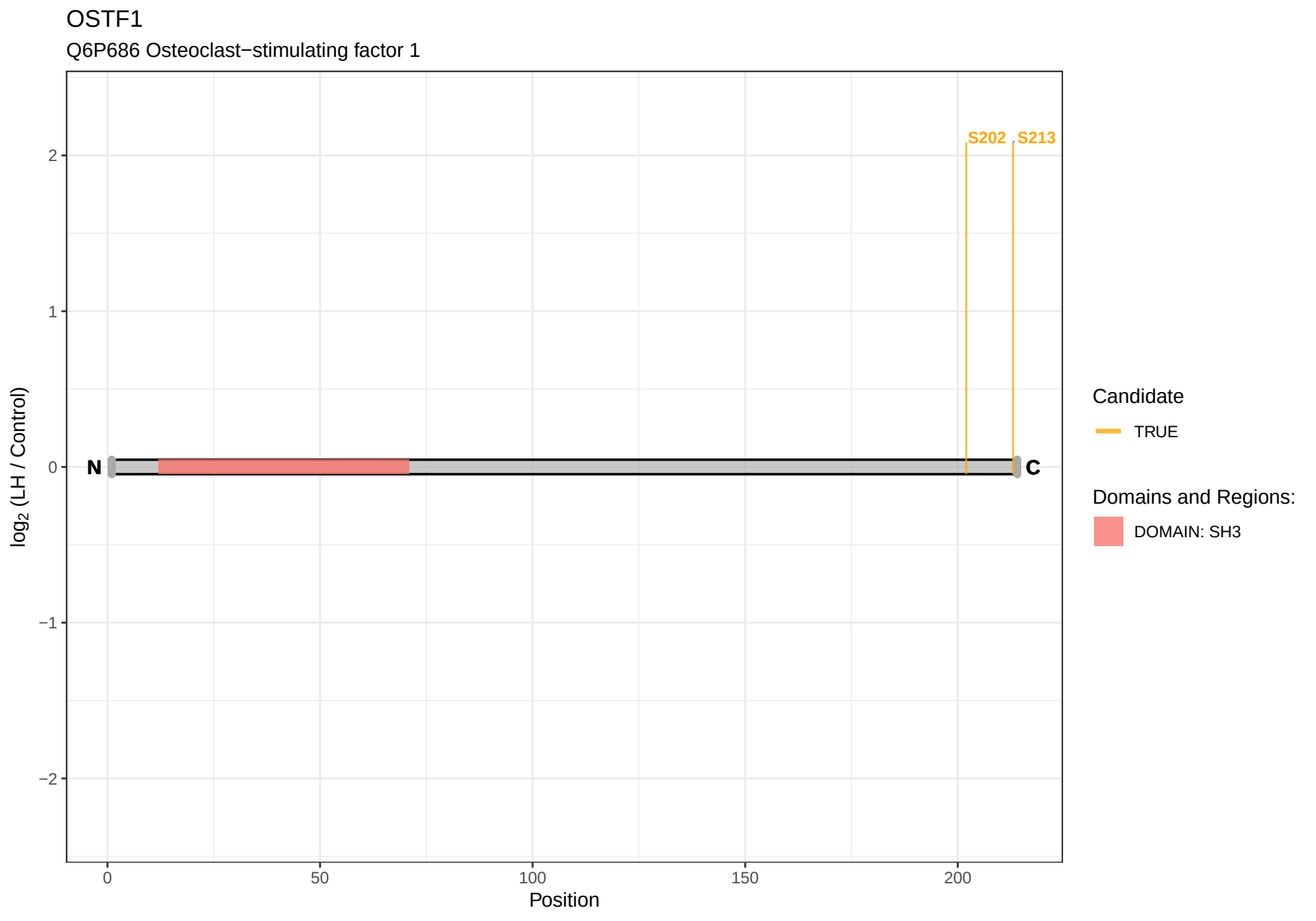

NUSAP1
A0A0G2JXS3 Nucleolar and spindle−associated protein 1
S113
S145
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
100
200
300
400
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

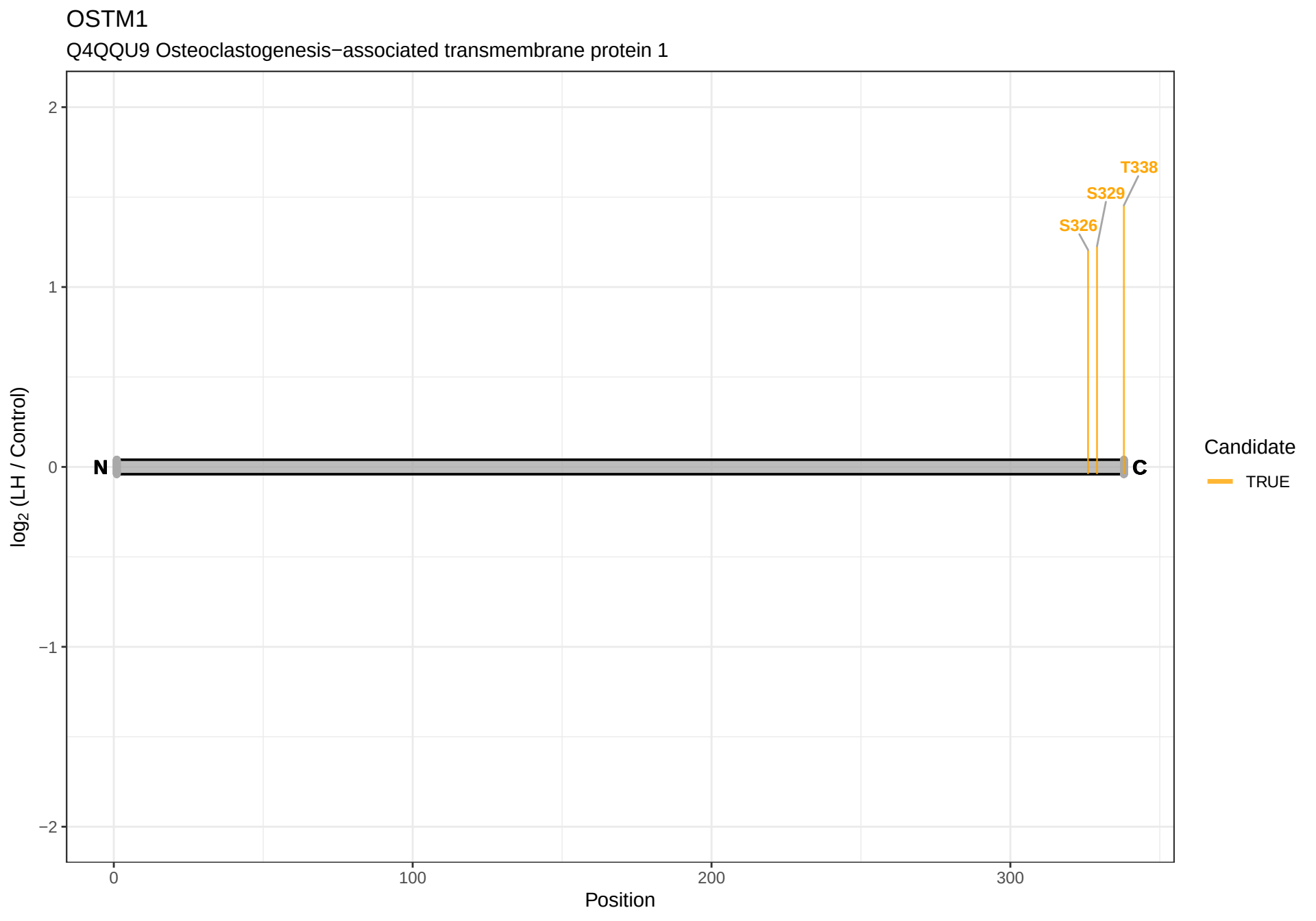

OCIAD1
Q5XIG4 OCIA domain−containing protein 1
S198
T146
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
50
100
150
200
250
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: OCIA
REGION: Disordered

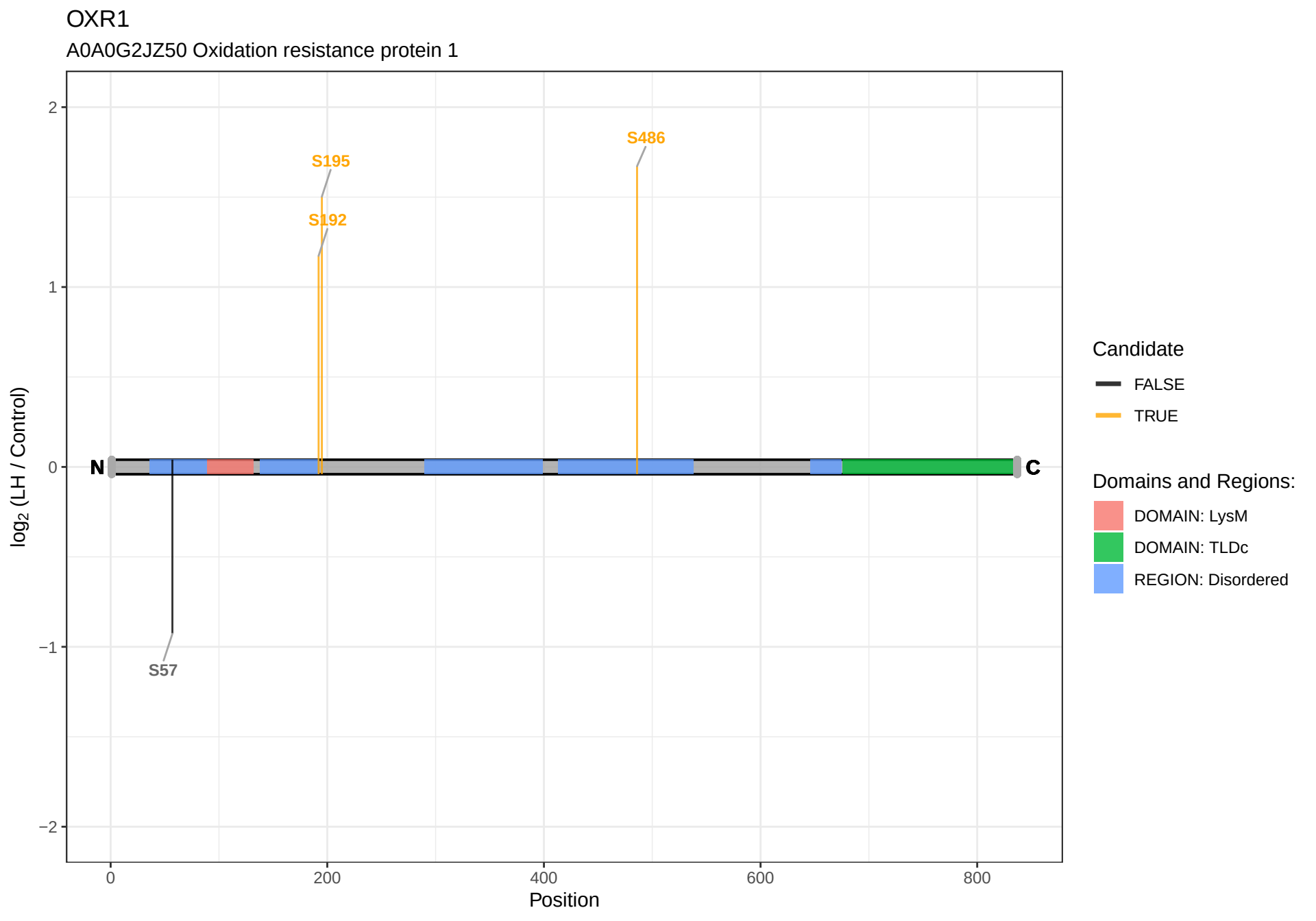

OPTN
Q8R5M4 Optineurin
S346
S188
N
C
4
2
0
−2
−4
0
200
400
600
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Interaction with HD
REGION: Interaction with MYO6
REGION: Interaction with Rab8

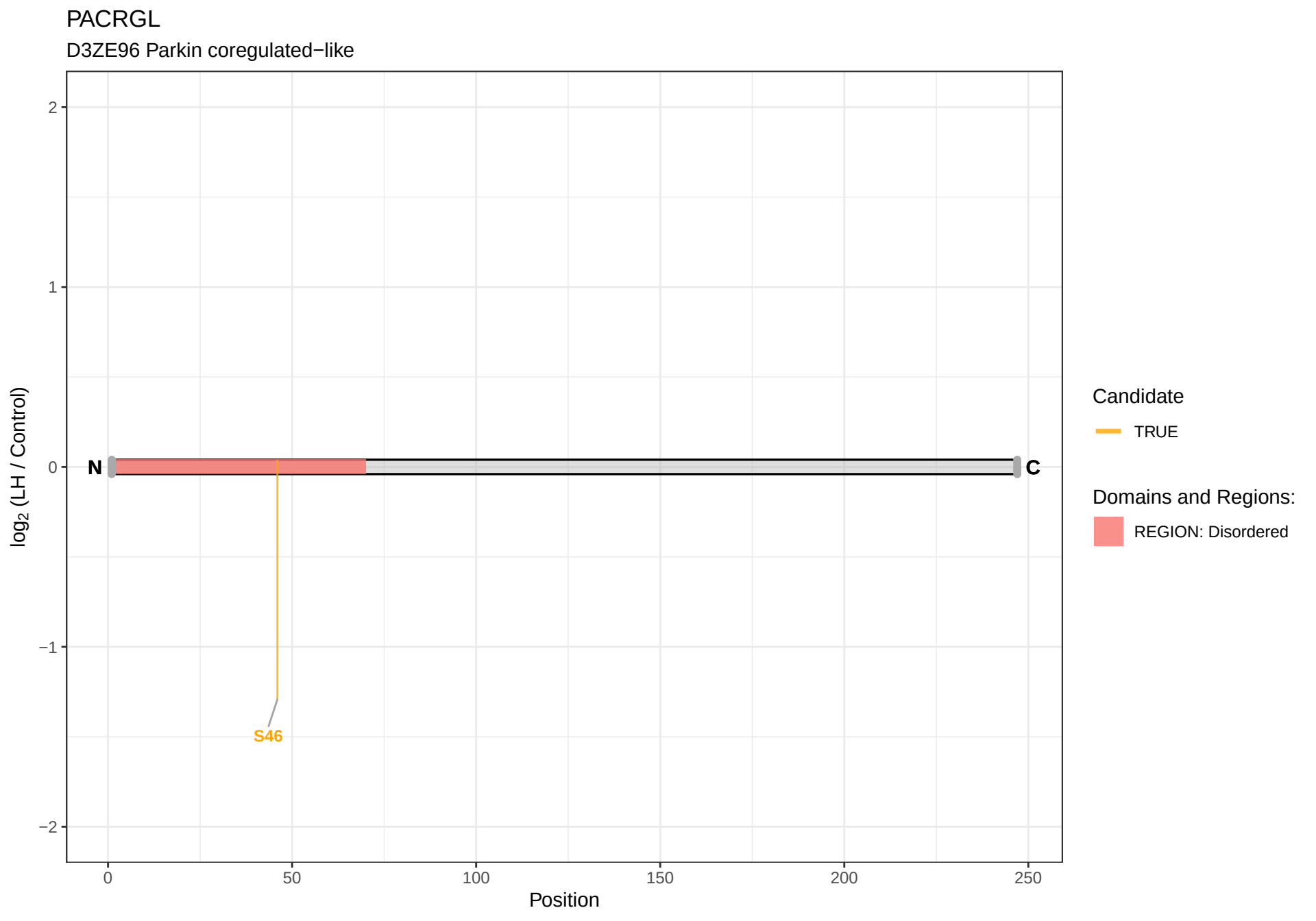

ORC1
G3V768 Origin recognition complex subunit 1
5.0
2.5
0.0
−2.5
−5.0
log2 (LH / Control)
S370
S371
N
C
0
200
400
600
800
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: BAH
REGION: Disordered

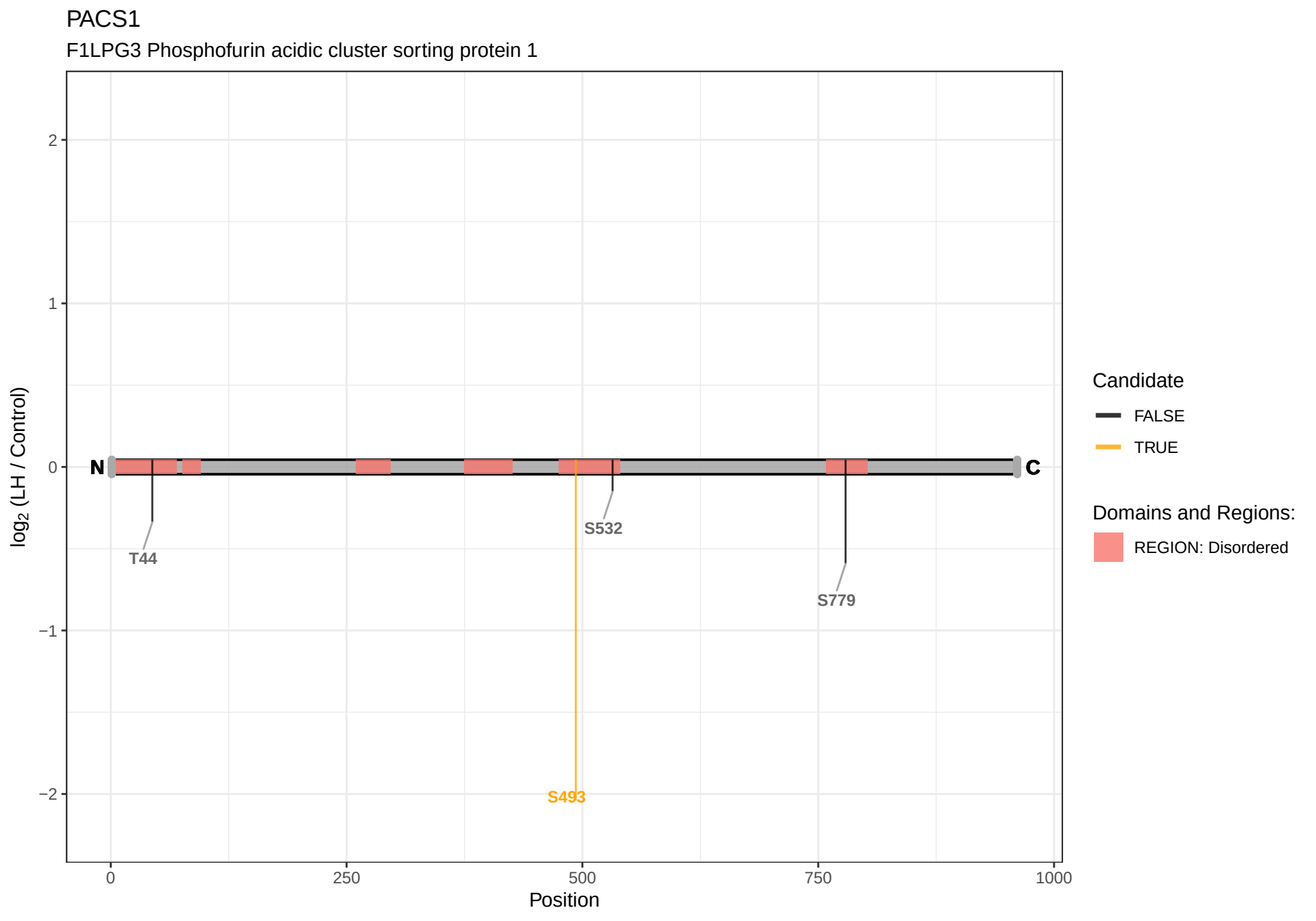

OSBPL11
B5DF74 Oxysterol−binding protein
S183
S185
S21
S188
T33
S192
N
C
2
0
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PH
REGION: Disordered

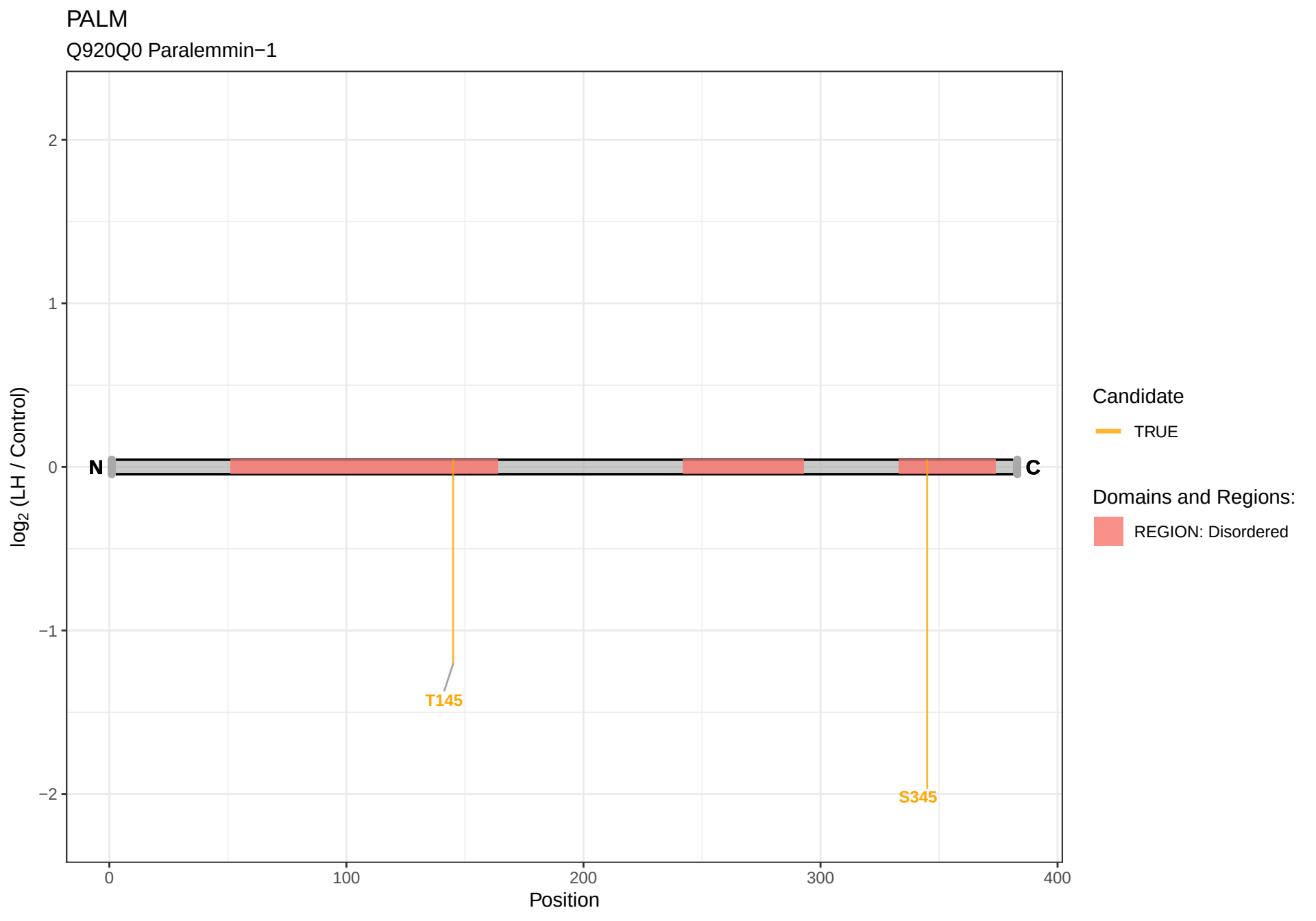

OSTF1
Q6P686 Osteoclast−stimulating factor 1
S202
S213
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
50
100
150
200
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: SH3

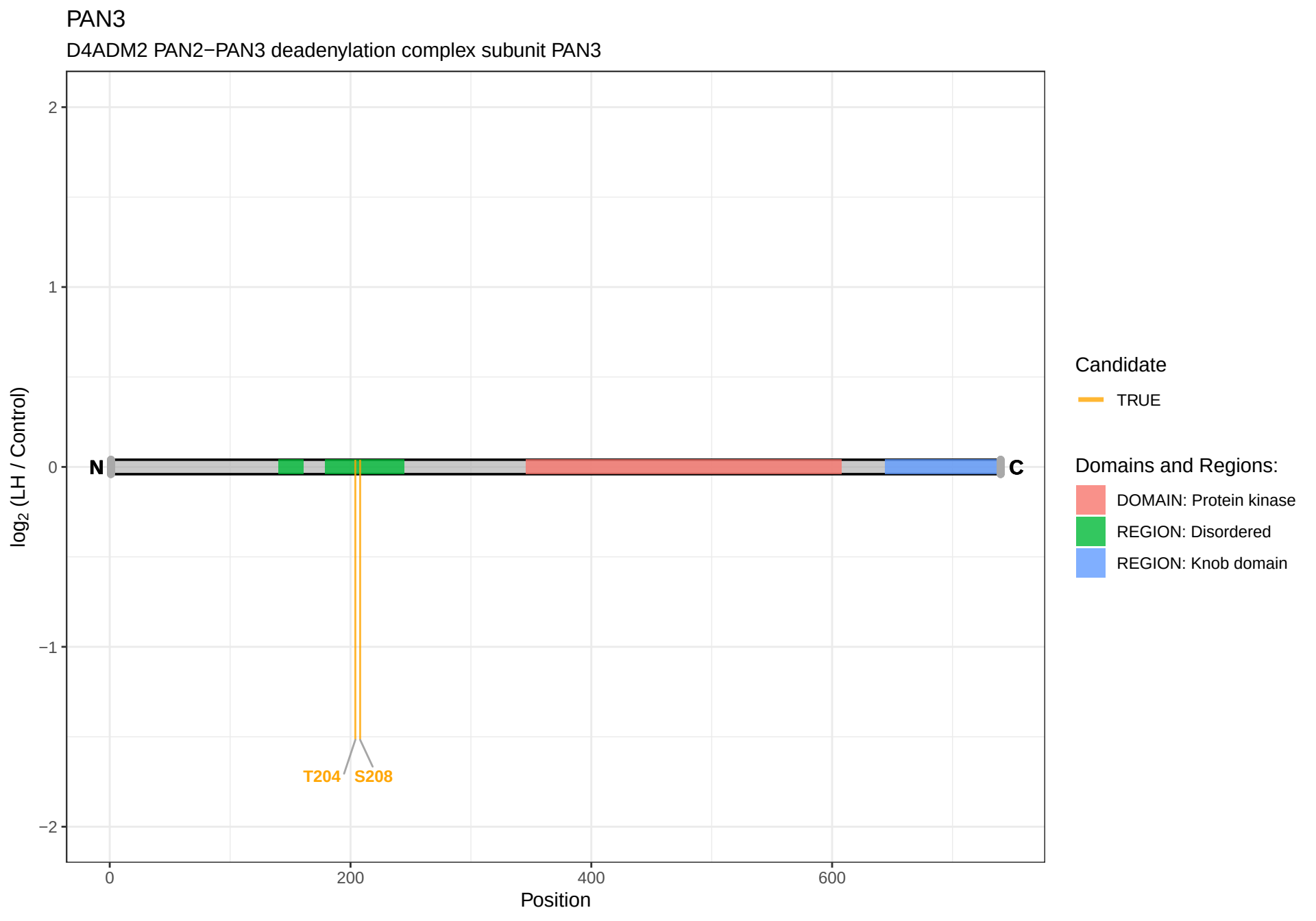

OSTM1
Q4QQU9 Osteoclastogenesis−associated transmembrane protein 1
T338
S329
S326
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
Position
Candidate
TRUE

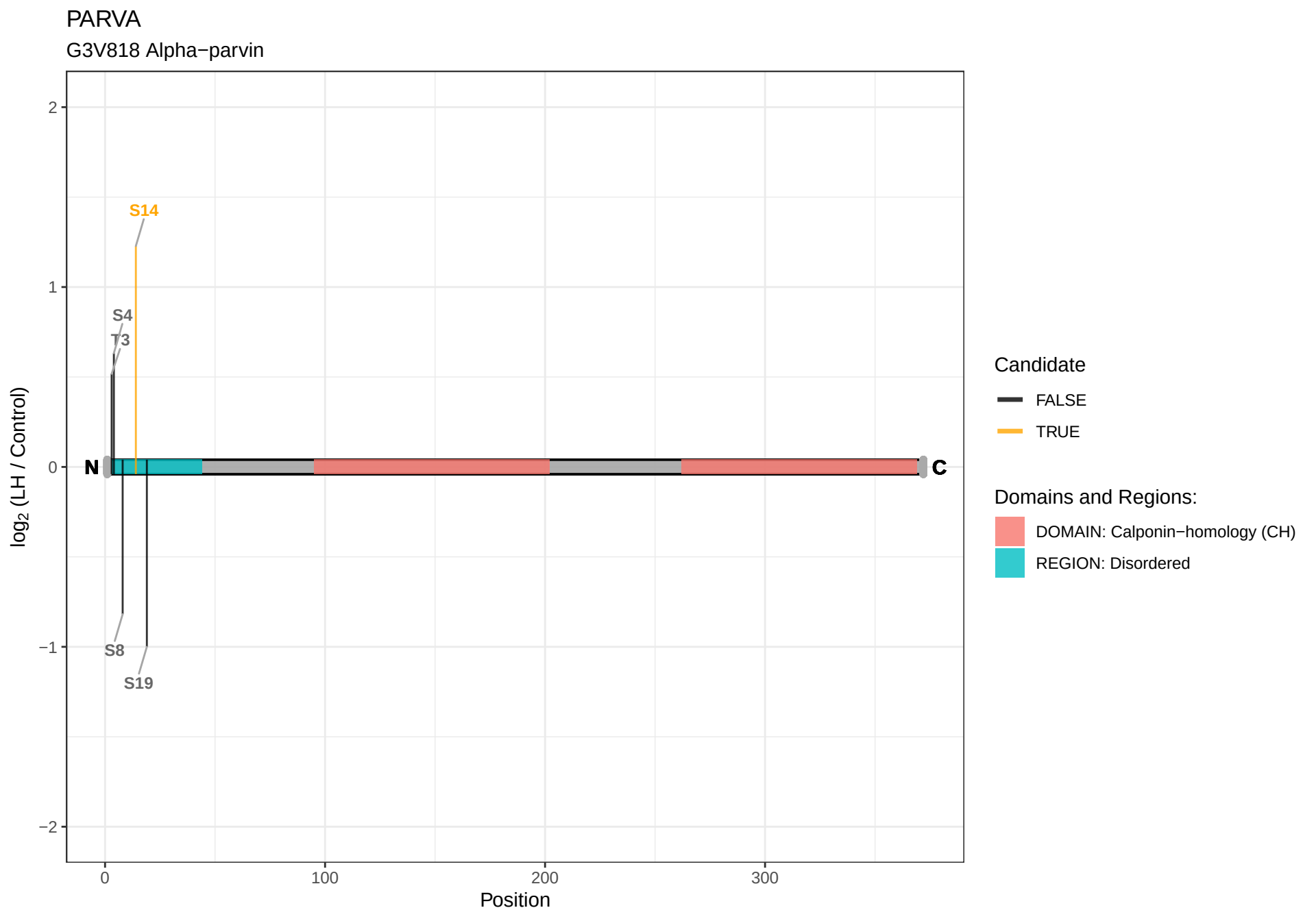

OXR1
A0A0G2JZ50 Oxidation resistance protein 1
S195
S192
S486
S57
N
C
2
1
0
−1
−2
0
200
400
600
800
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: LysM
DOMAIN: TLDc
REGION: Disordered

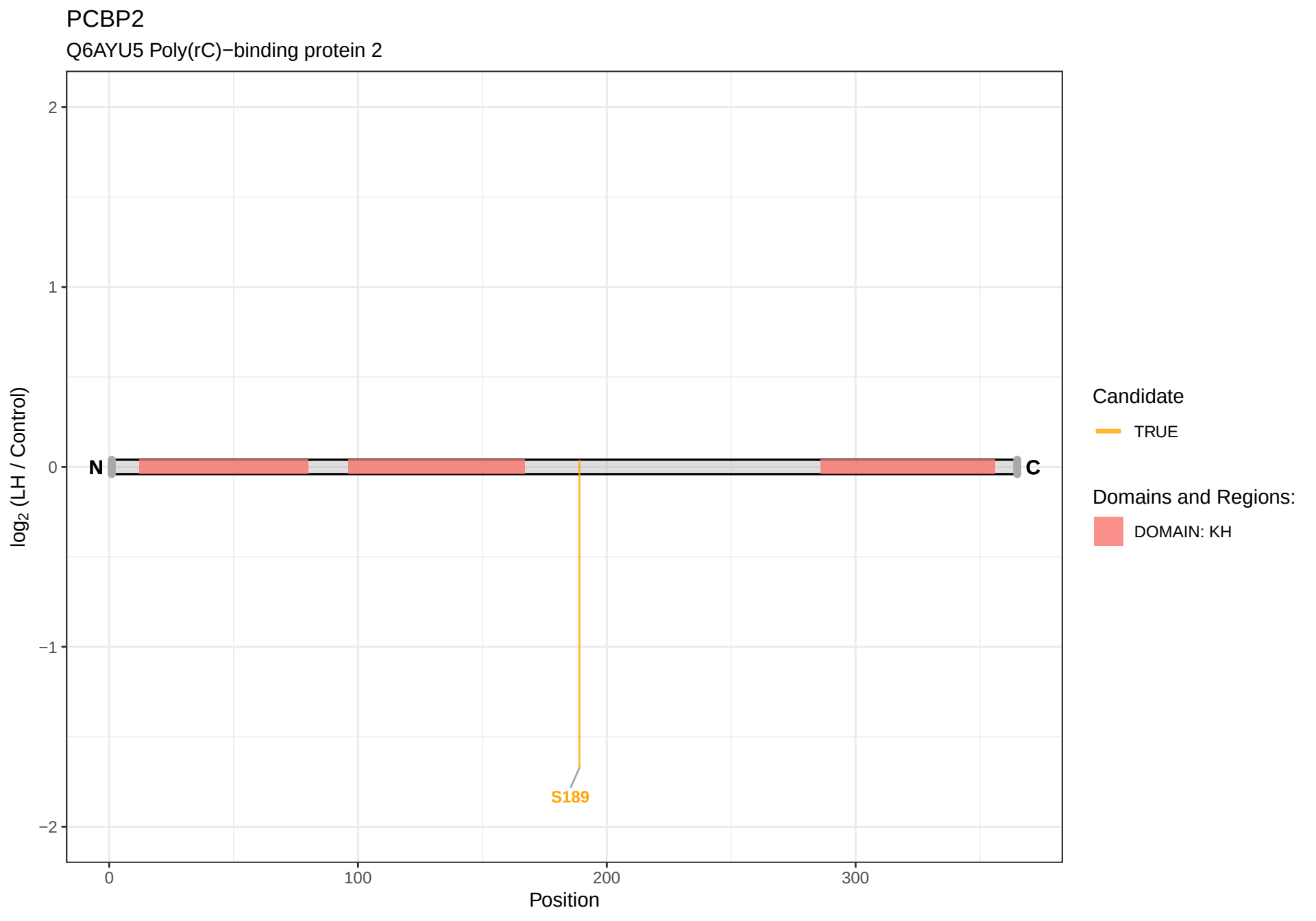

PACRGL
D3ZE96 Parkin coregulated−like
2
1
0
−1
−2
log2 (LH / Control)
N
C
S46
0
50
100
150
200
250
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

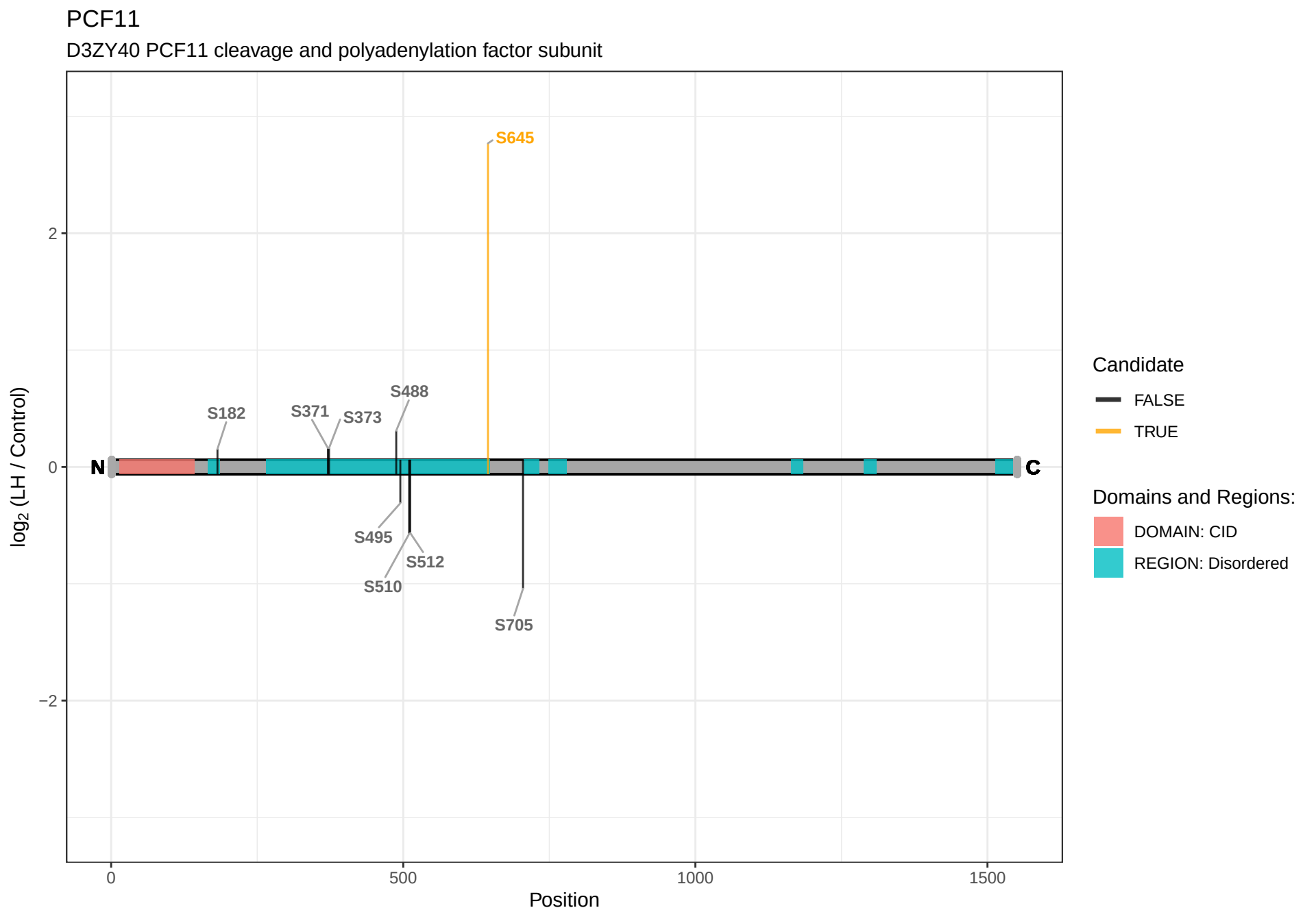

PACS1
F1LPG3 Phosphofurin acidic cluster sorting protein 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
T44
S532
S779
S493
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

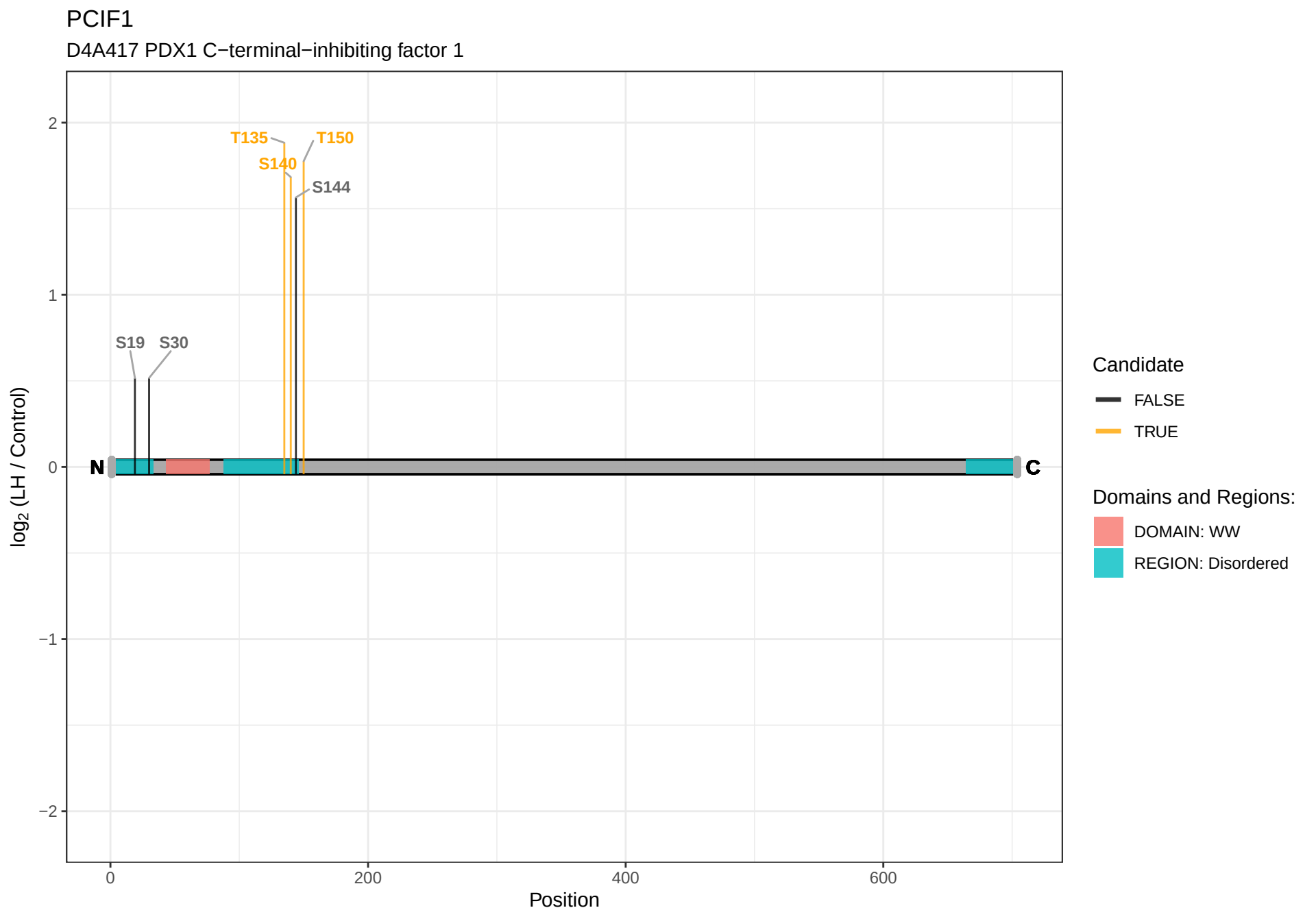

PALM
Q920Q0 Paralemmin−1
2
1
0
−1
−2
log2 (LH / Control)
N
C
T145
S345
0
100
200
300
400
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

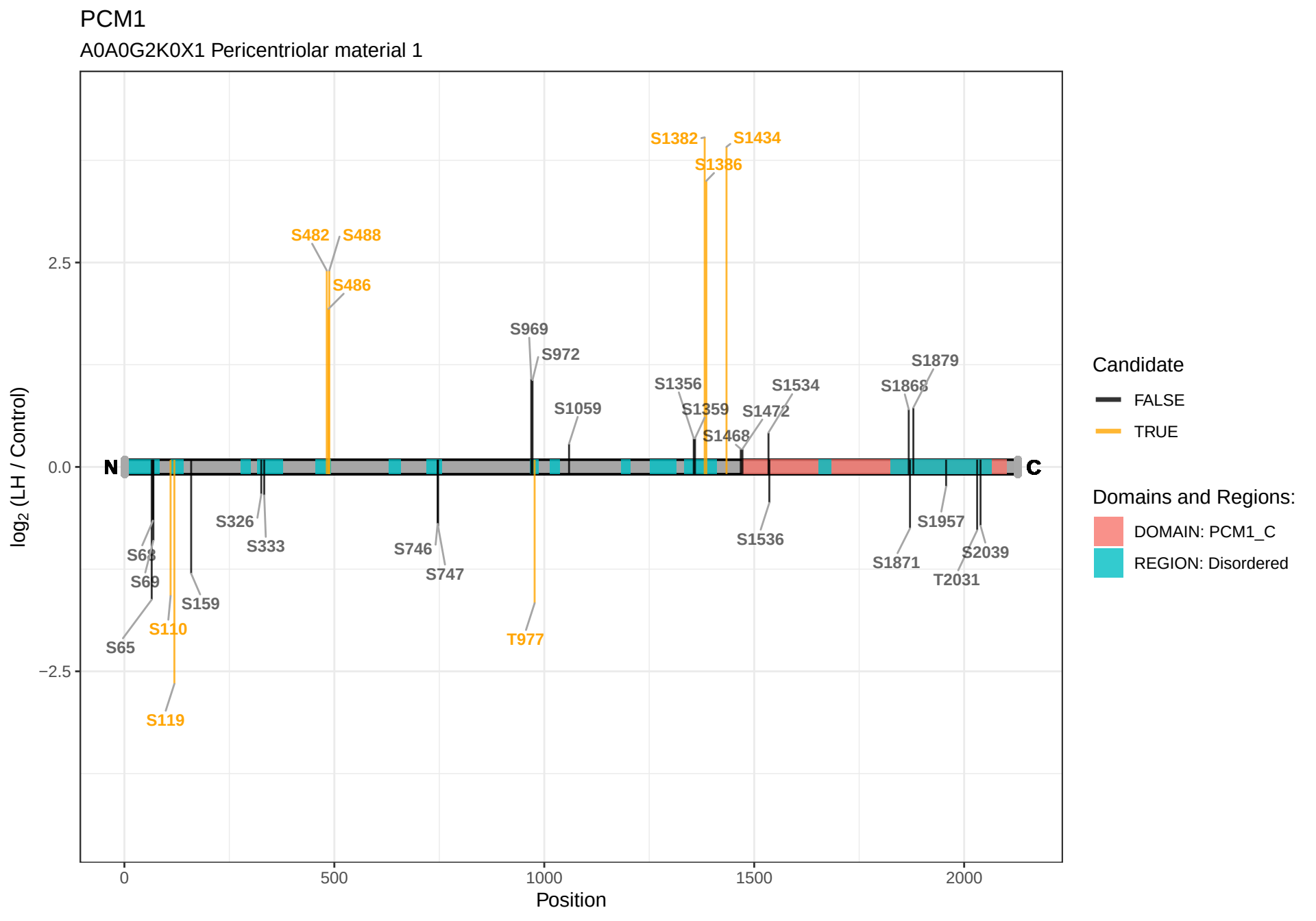

PAN3
D4ADM2 PAN2−PAN3 deadenylation complex subunit PAN3
log2 (LH / Control)
2
1
0
−1
−2
N
C
T204
S208
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered
REGION: Knob domain

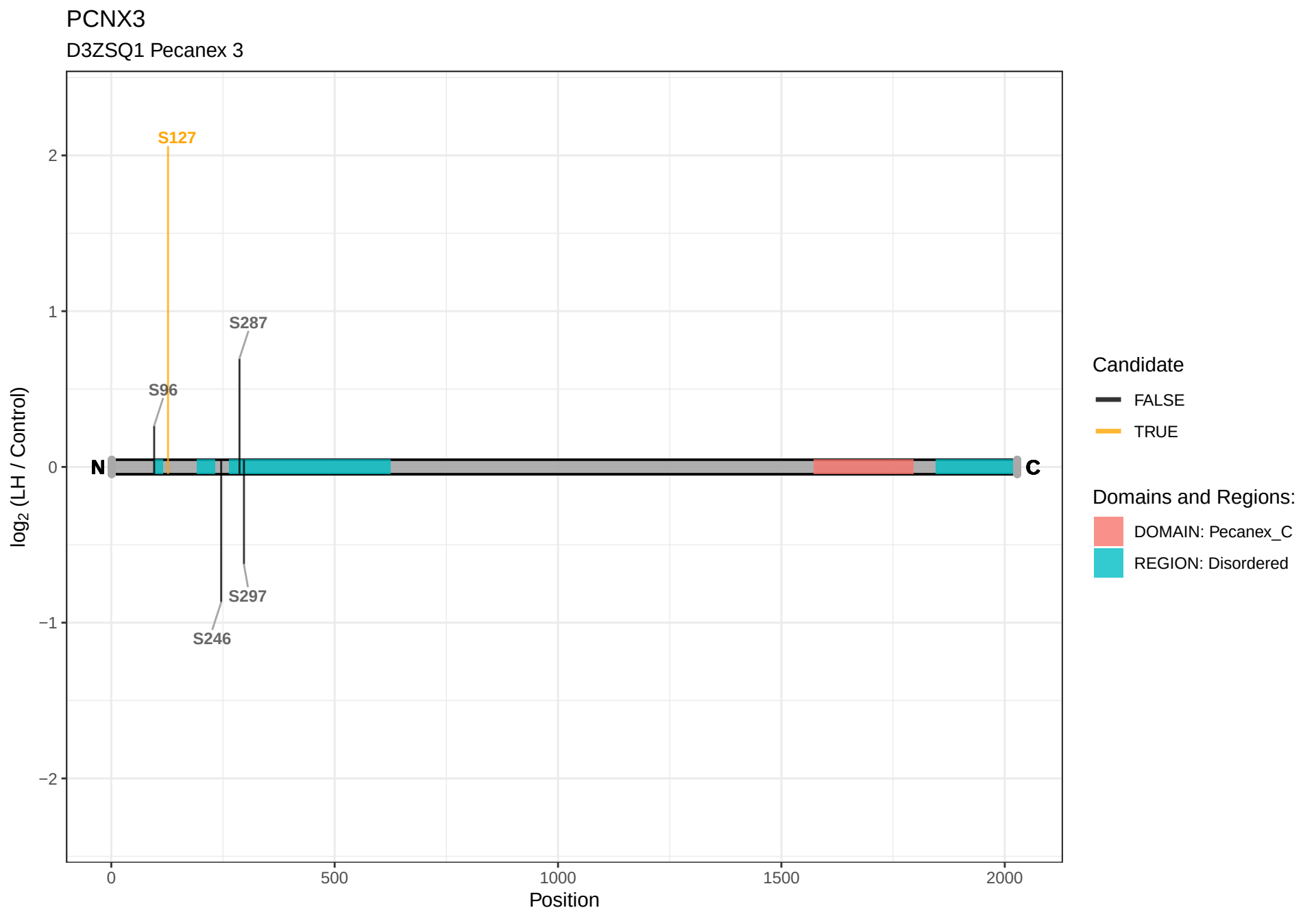

PARVA
G3V818 Alpha−parvin
2
1
0
−1
−2
log2 (LH / Control)
S14
S4
T3
S8
S19
N
C
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Calponin−homology (CH)
REGION: Disordered

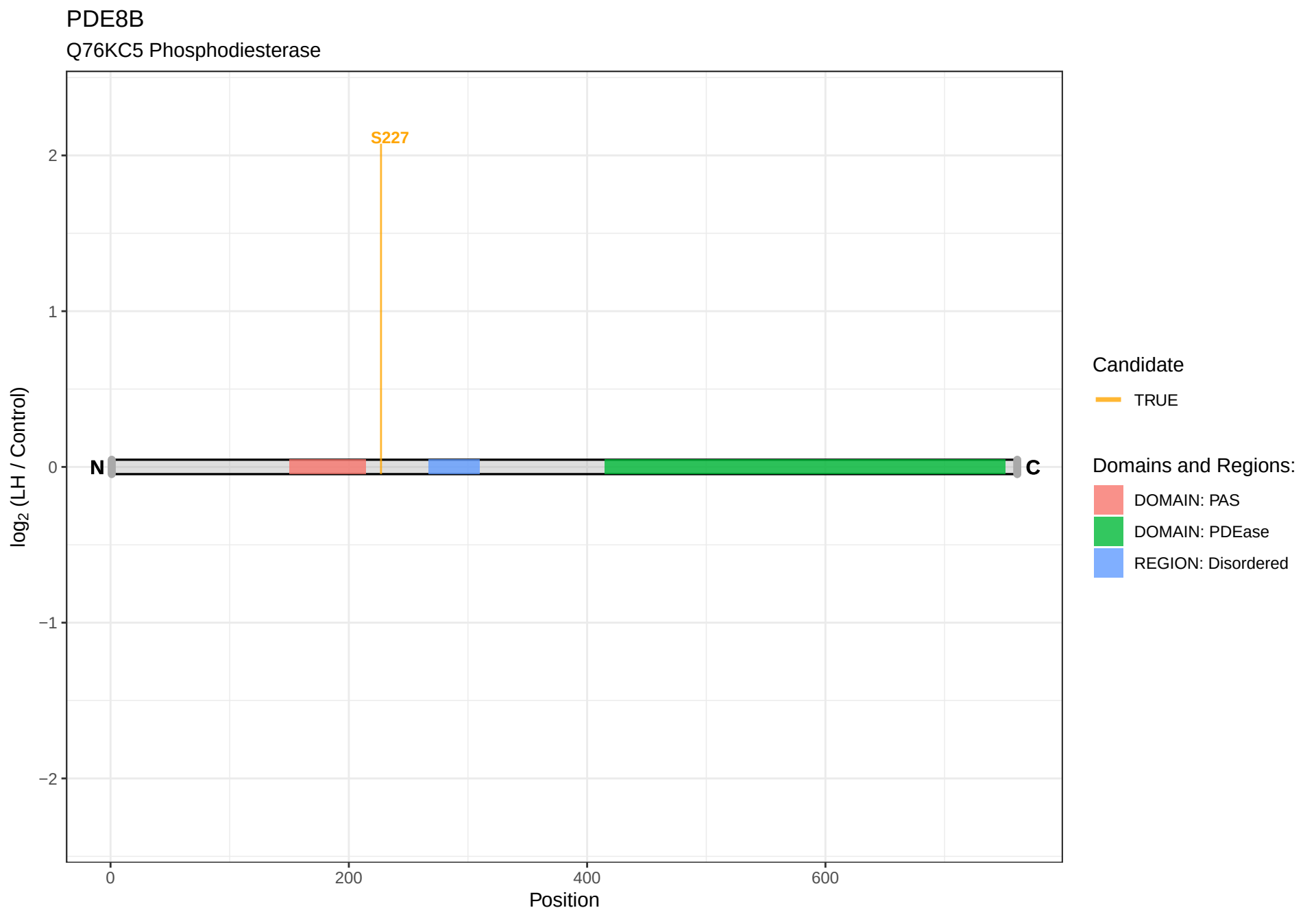

PCBP2
Q6AYU5 Poly(rC)−binding protein 2
log2 (LH / Control)
2
1
0
−1
−2
N
C
S189
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: KH

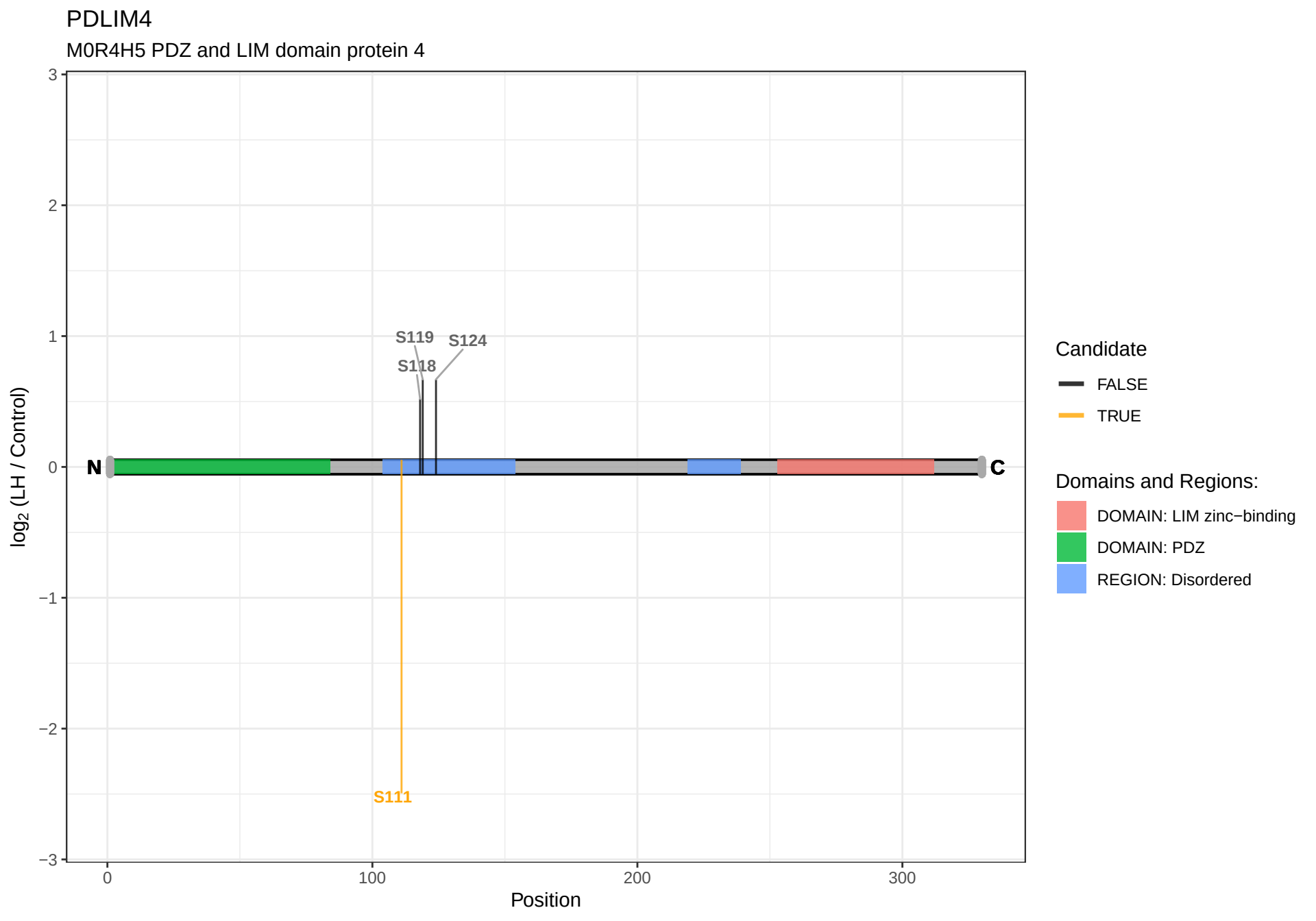

PCF11
D3ZY40 PCF11 cleavage and polyadenylation factor subunit
S645
S182
S371
S373
S488
S495
S512
S510
S705
N
C
2
0
−2
log2 (LH / Control)
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CID
REGION: Disordered

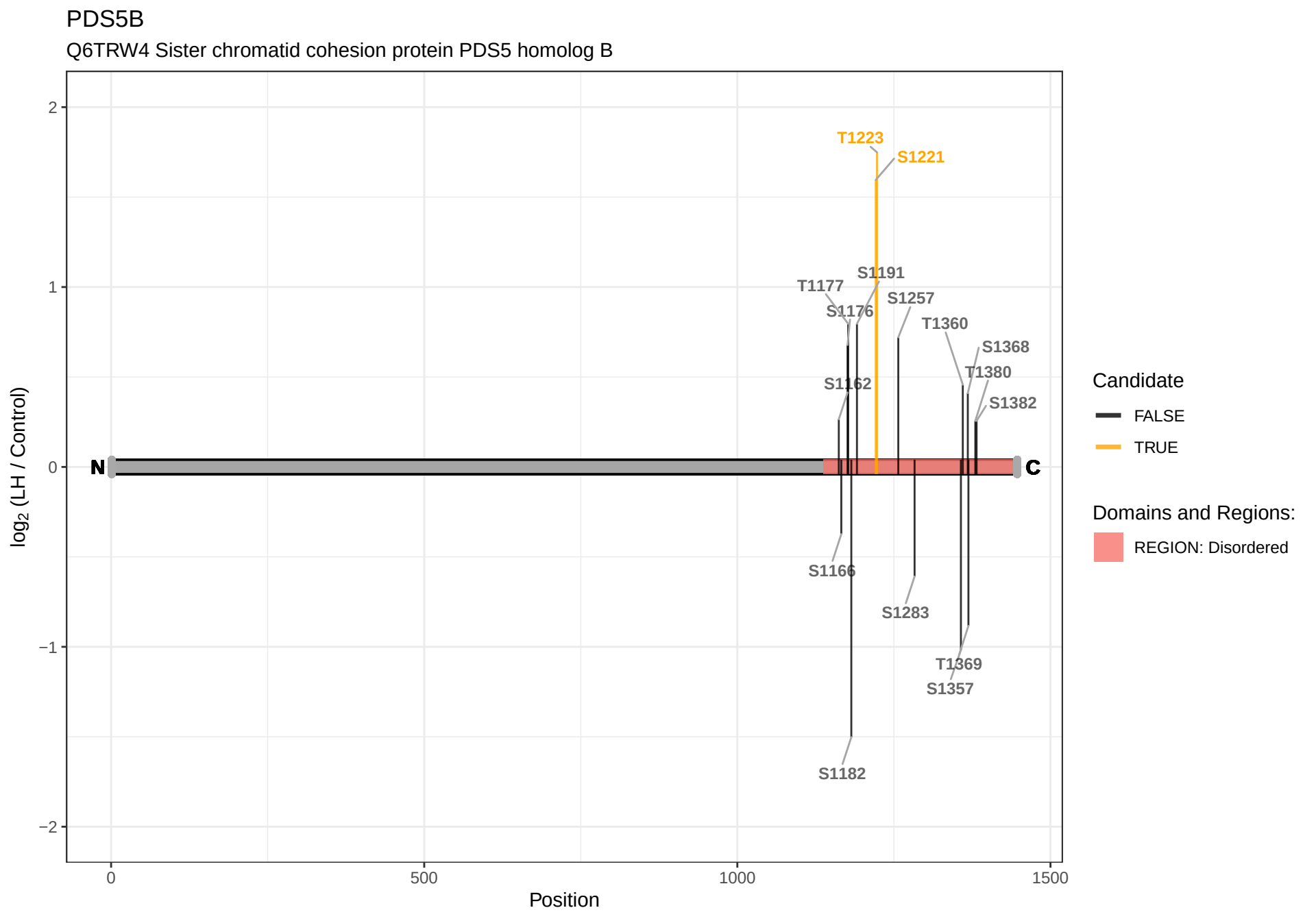

PCIF1
D4A417 PDX1 C−terminal−inhibiting factor 1
T135
T150
S140
S144
S19
S30
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WW
REGION: Disordered

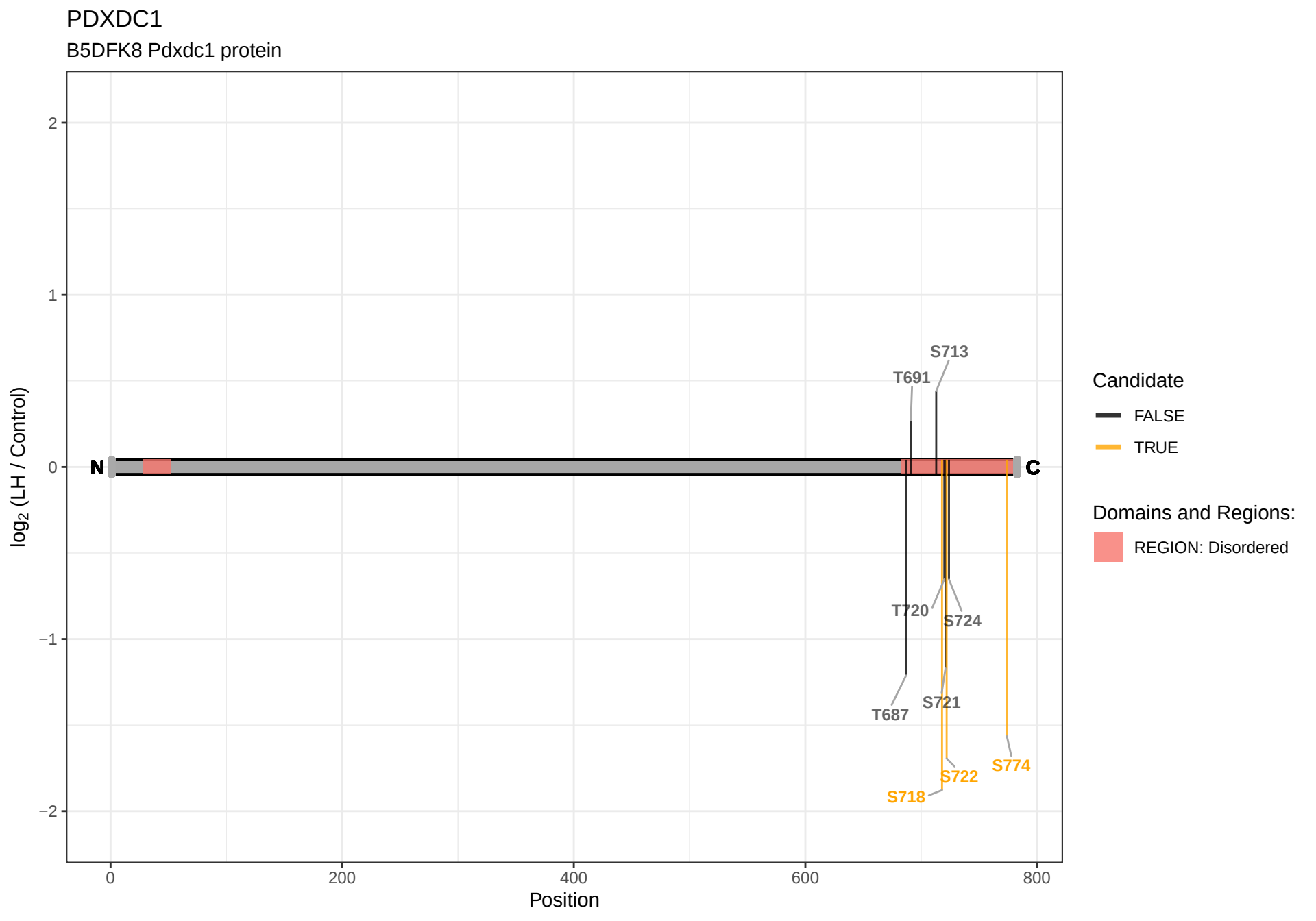

PCM1
A0A0G2K0X1 Pericentriolar material 1
log2 (LH / Control)
2.5
0.0
−2.5
N
C
S1382
S1434
S1386
S482
S488
S486
S969
S972
S1059
S1356
S1359
S1468
S1472
S1534
S1879
S1868
S326
S333
S746
S747
S1536
S1957
S1871
S2039
T2031
S63
S69
S159
S65
S110
S119
T977
0
500
1000
1500
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PCM1_C
REGION: Disordered

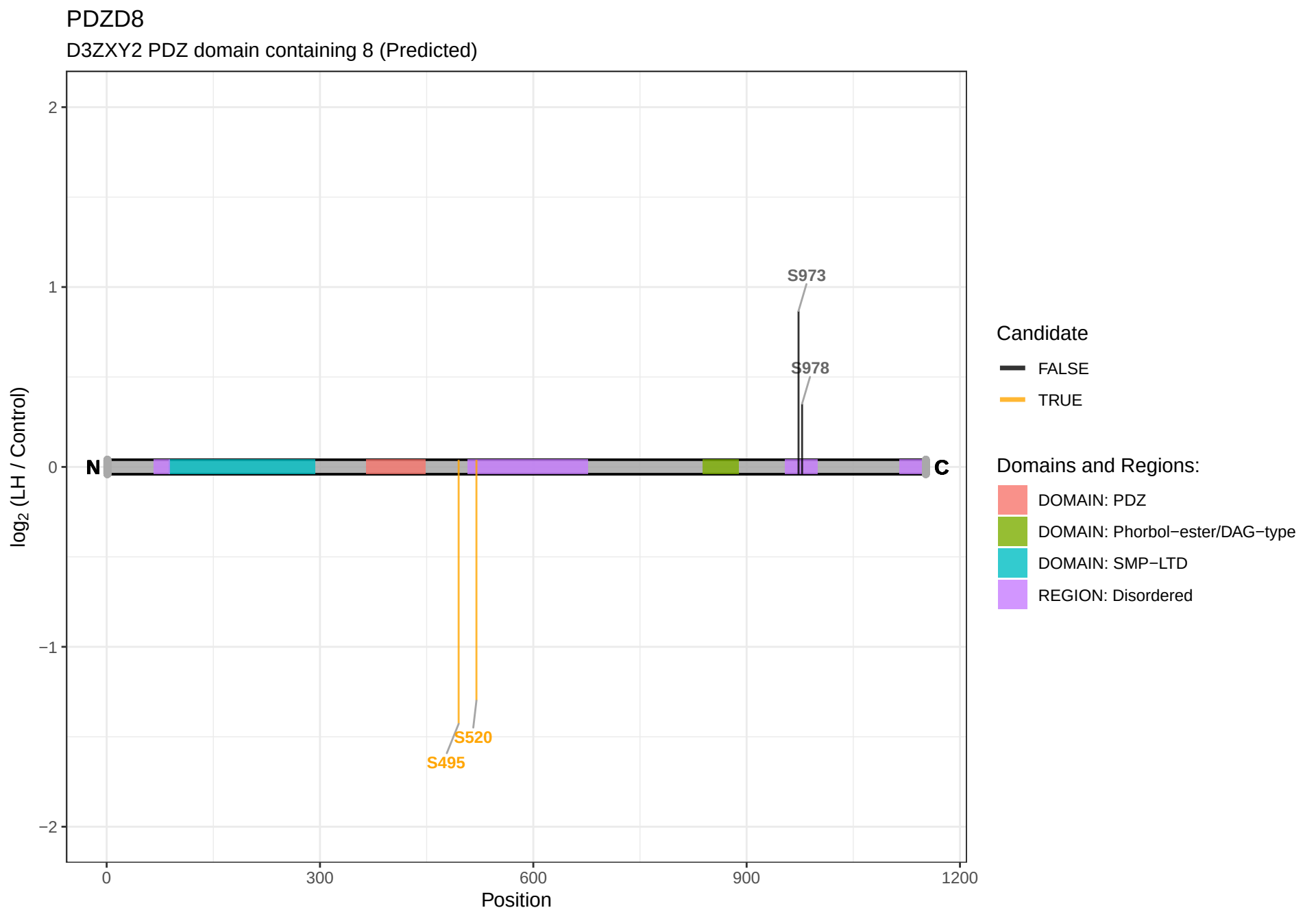

PCNX3
D3ZSQ1 Pecanex 3
S127
S287
S96
S297
S246
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
1500
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Pecanex_C
REGION: Disordered

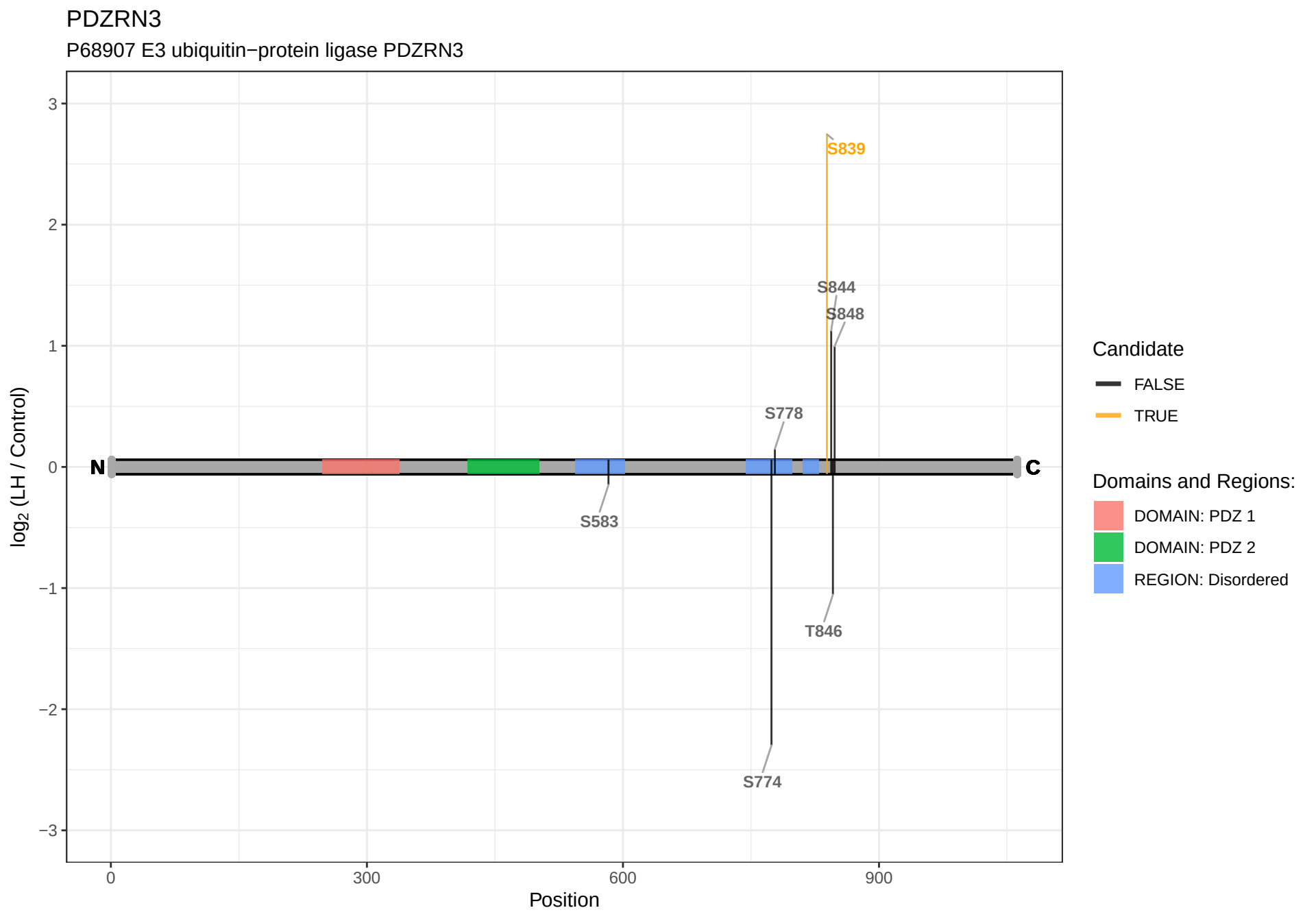

PDE8B
Q76KC5 Phosphodiesterase
S227
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: PAS
DOMAIN: PDEase
REGION: Disordered

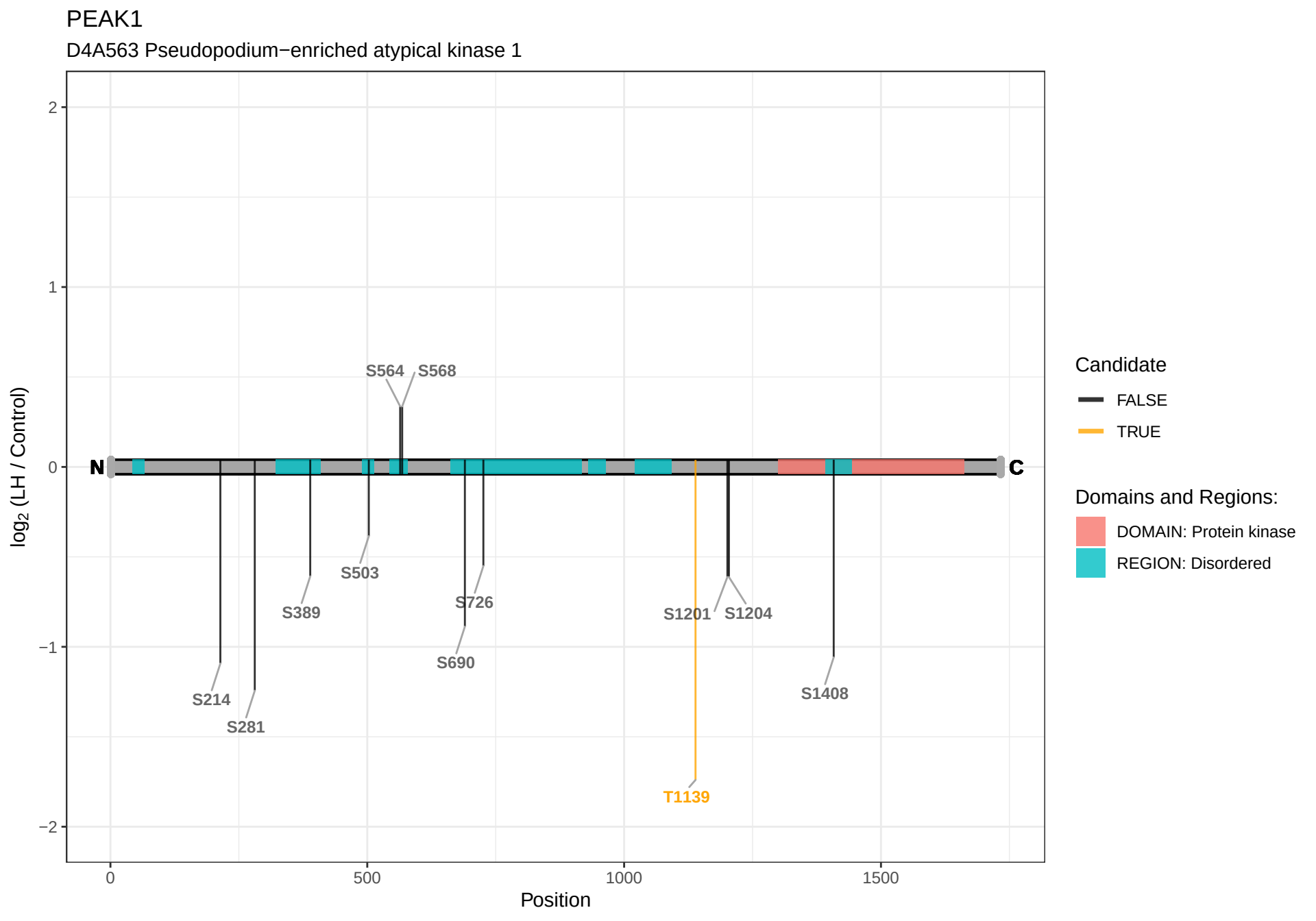

PDLIM4
M0R4H5 PDZ and LIM domain protein 4
log2 (LH / Control)
3
2
1
0
−1
−2
−3
0
100
200
300
Position
N
C
S119
S124
S118
S111
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: LIM zinc−binding
DOMAIN: PDZ
REGION: Disordered

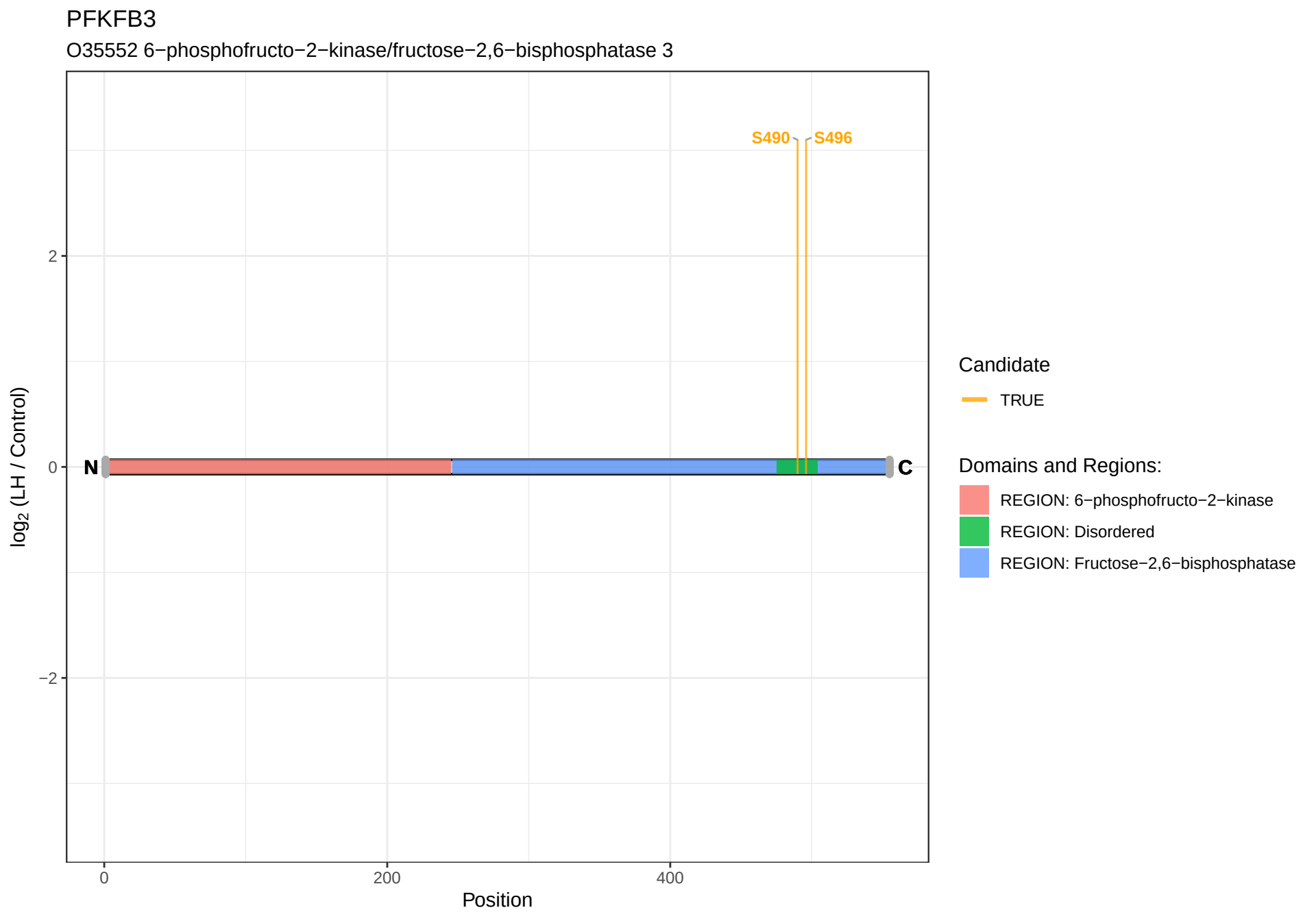

PDS5B
Q6TRW4 Sister chromatid cohesion protein PDS5 homolog B
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
Position
N
C
T1223
S1221
S1191
T1177
S1176
S1257
T1360
S1368
T1380
S1162
S1382
S1166
S1283
T1369
S1357
S1182
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

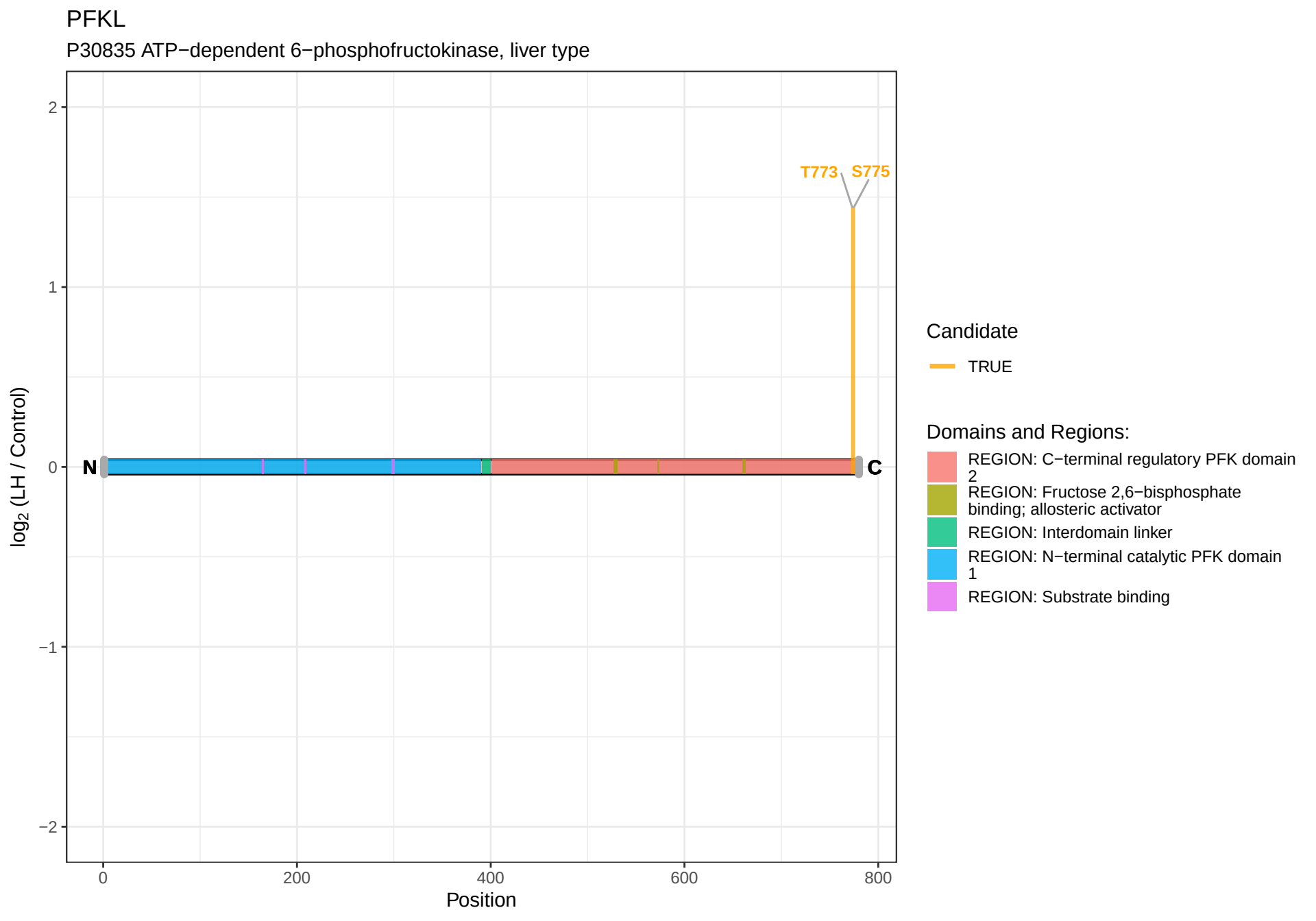

PDXDC1
B5DFK8 Pdxdc1 protein
log2 (LH / Control)
2
1
0
−1
−2
N
C
S713
T691
T720
S724
T687
S721
S722
S774
S718
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

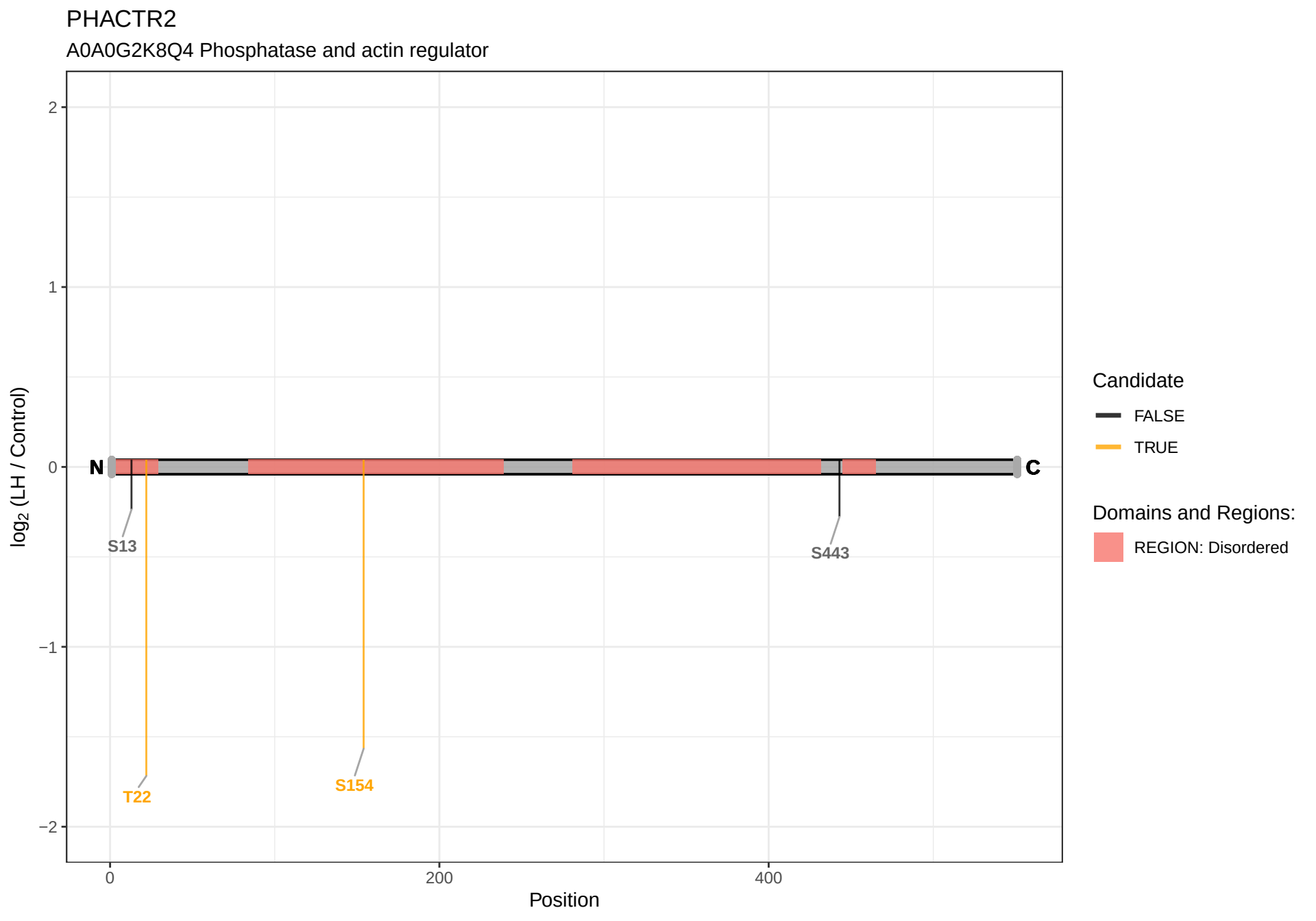

PDZD8
D3ZXY2 PDZ domain containing 8 (Predicted)
log2 (LH / Control)
2
1
0
−1
−2
0
300
600
900
1200
Position
N
C
S973
S978
S520
S495
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PDZ
DOMAIN: Phorbol−ester/DAG−type
DOMAIN: SMP−LTD
REGION: Disordered

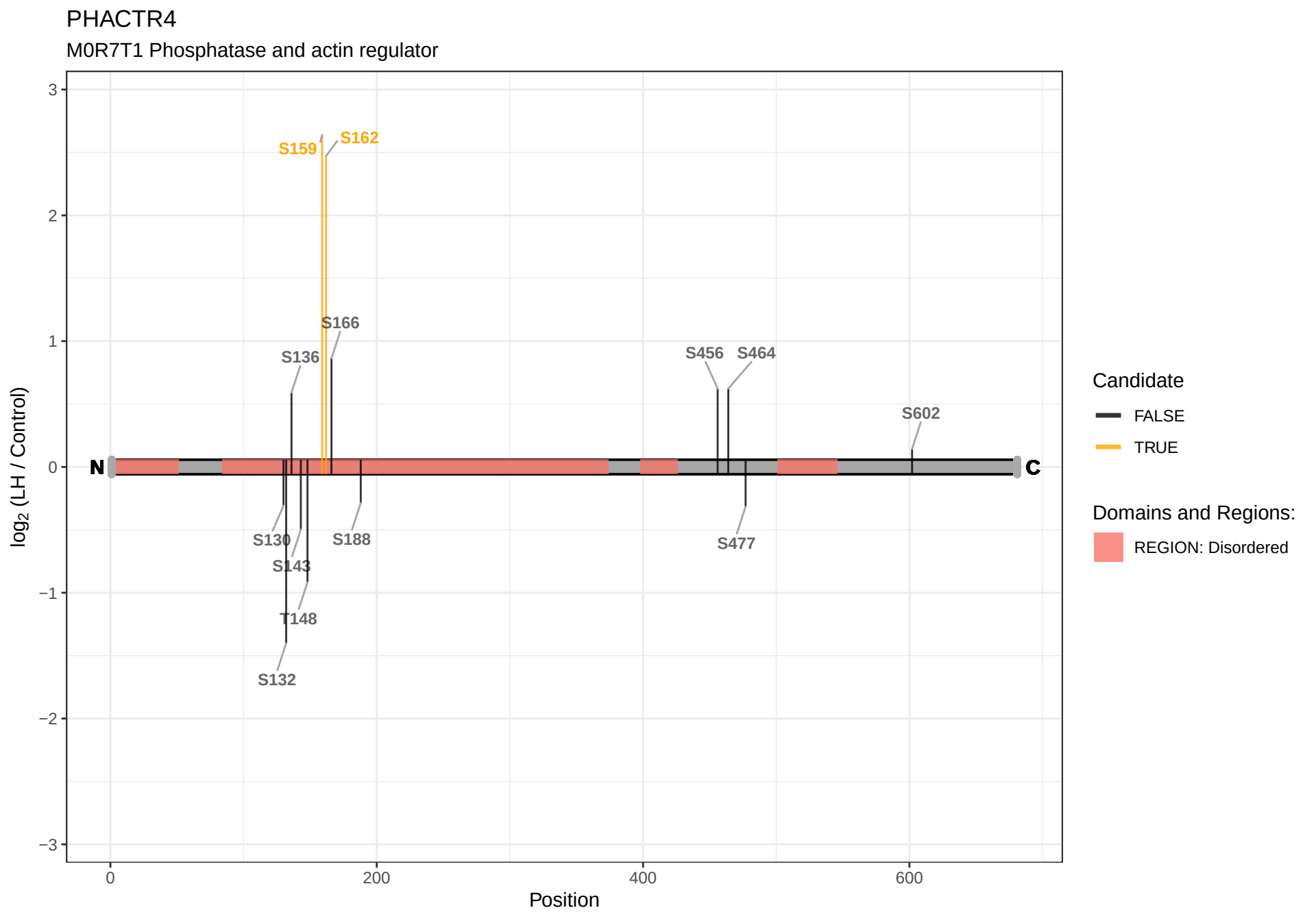

PDZRN3
P68907 E3 ubiquitin−protein ligase PDZRN3
log2 (LH / Control)
3
2
1
0
−1
−2
−3
0
300
600
900
Position
N
C
S839
S844
S848
S778
S583
T846
S774
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PDZ 1
DOMAIN: PDZ 2
REGION: Disordered

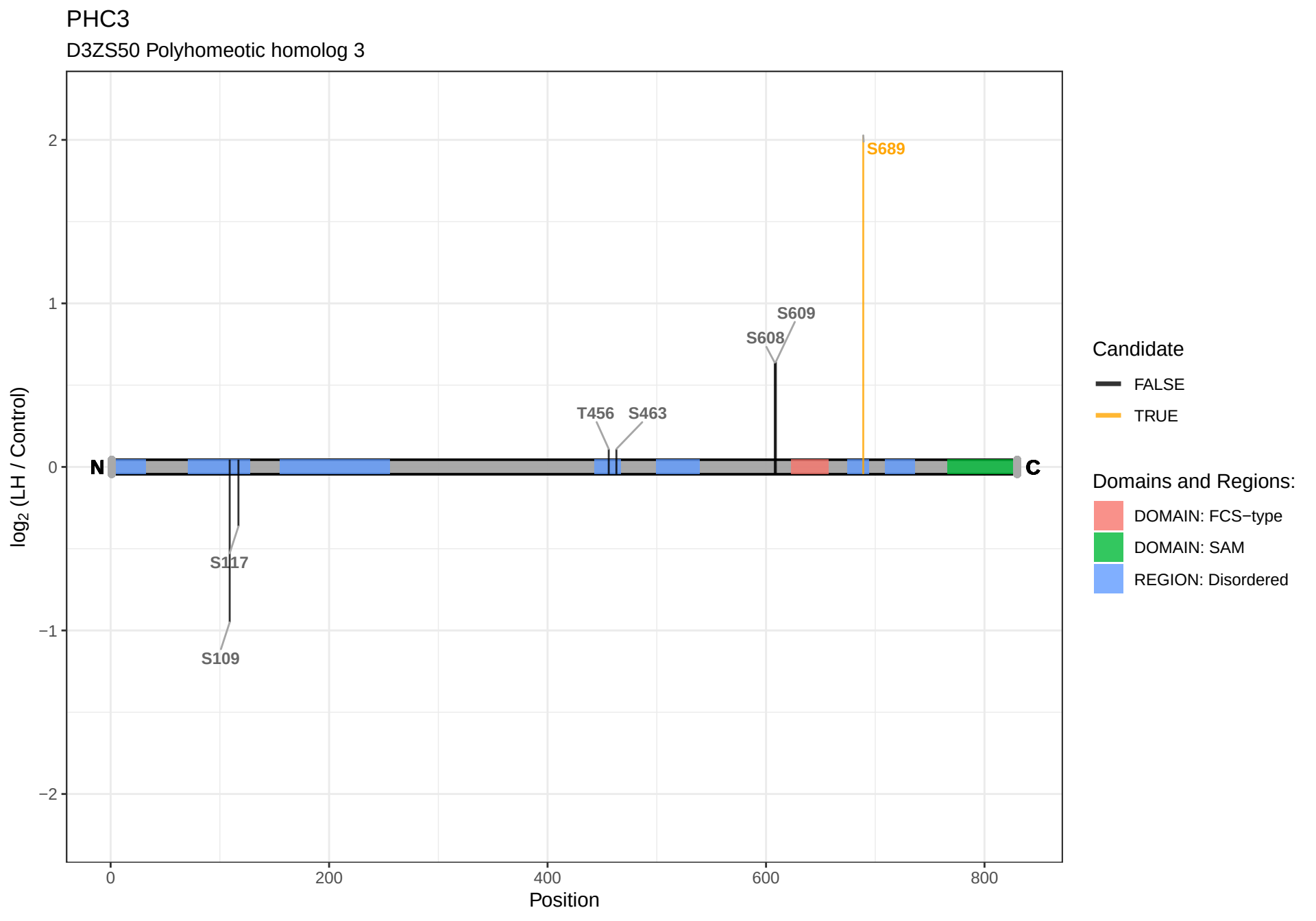

PEAK1
D4A563 Pseudopodium−enriched atypical kinase 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S564
S568
S503
S389
S726
S690
S214
S281
S1201
S1204
S1408
T1139
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered

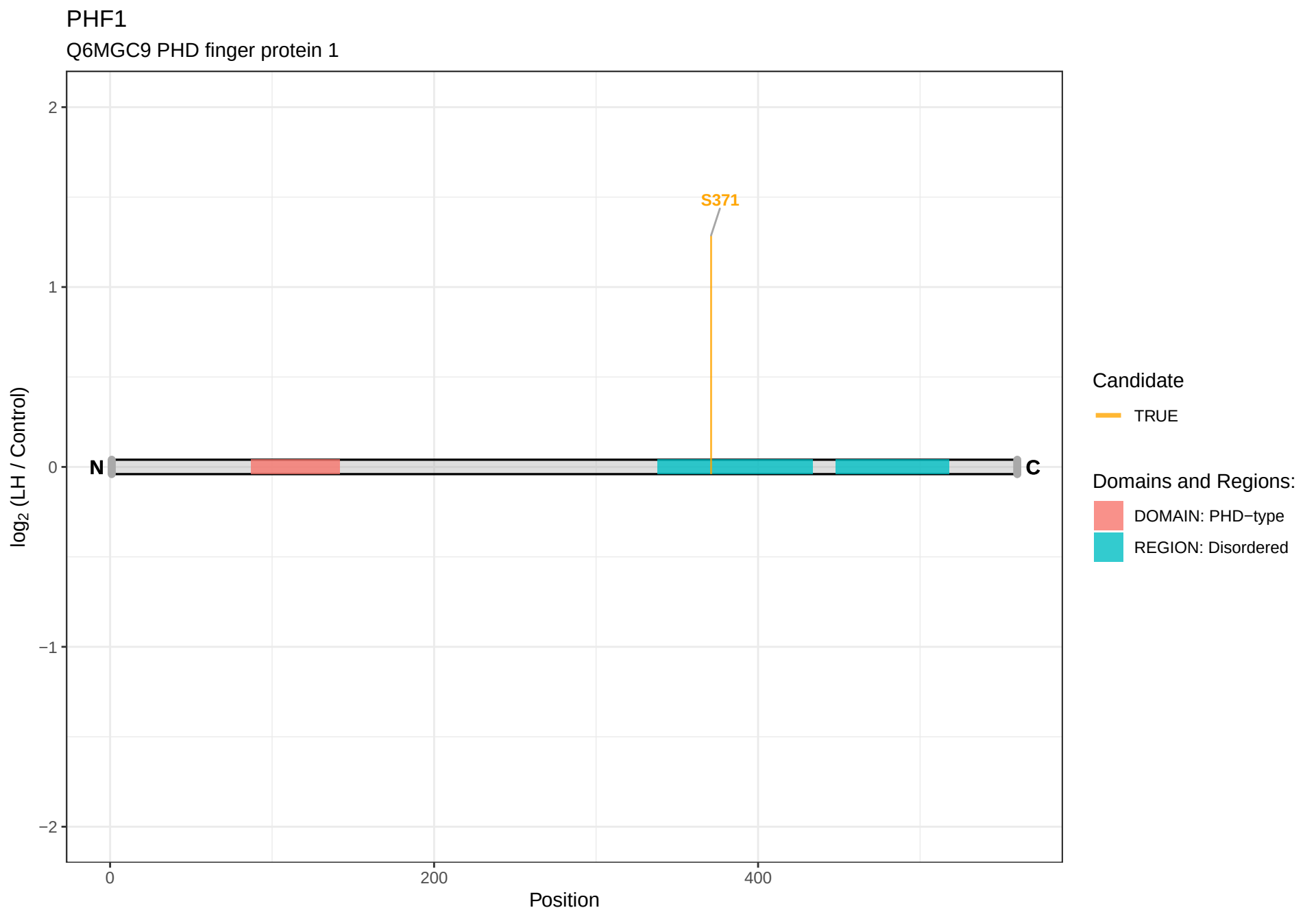

PFKFB3
O35552 6−phosphofructo−2−kinase/fructose−2,6−bisphosphatase 3
S490
S496
N
C
2
0
−2
log2 (LH / Control)
0
200
400
Position
Candidate
TRUE
Domains and Regions:
REGION: 6−phosphofructo−2−kinase
REGION: Disordered
REGION: Fructose−2,6−bisphosphatase

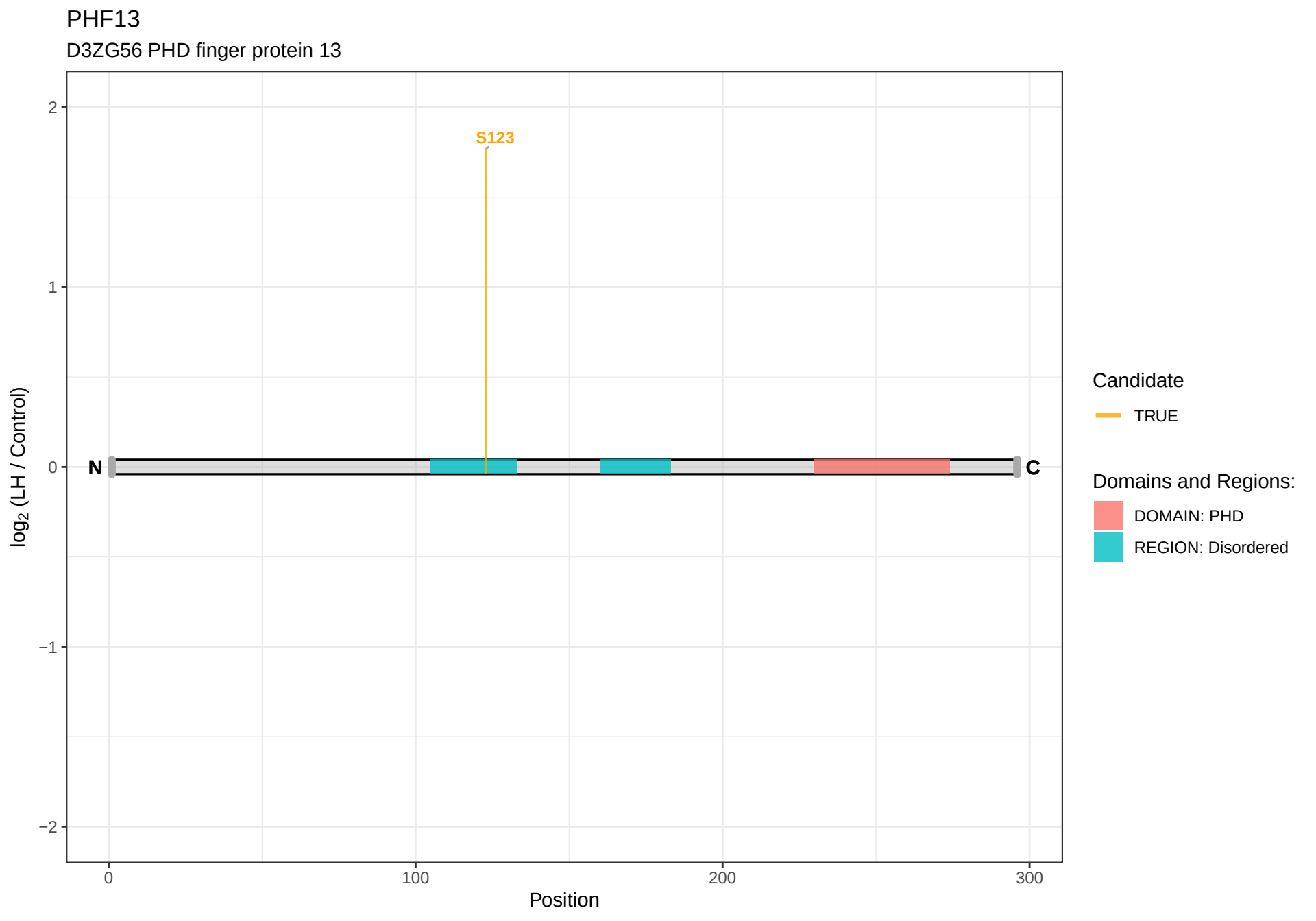

PFKL
P30835 ATP−dependent 6−phosphofructokinase, liver type
T773
S775
N
C
2
1
0
−1
−2
0
200
400
600
800
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
REGION: C−terminal regulatory PFK domain 2
REGION: Fructose 2,6−bisphosphate binding; allosteric activator
REGION: Interdomain linker
REGION: N−terminal catalytic PFK domain 1
REGION: Substrate binding

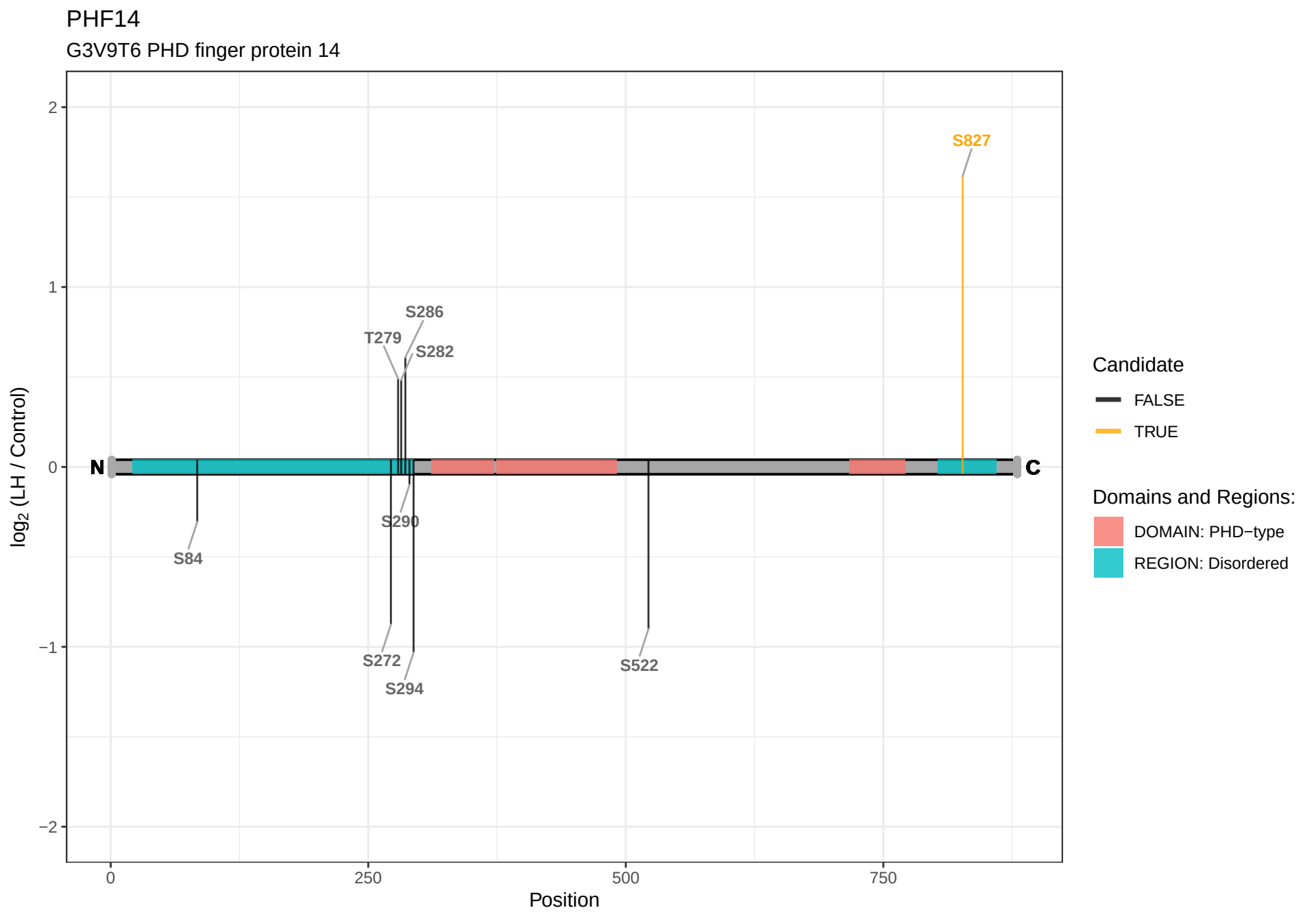

PHACTR2
A0A0G2K8Q4 Phosphatase and actin regulator
2
1
0
−1
−2
log2 (LH / Control)
N
C
S13
T22
S154
S443
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

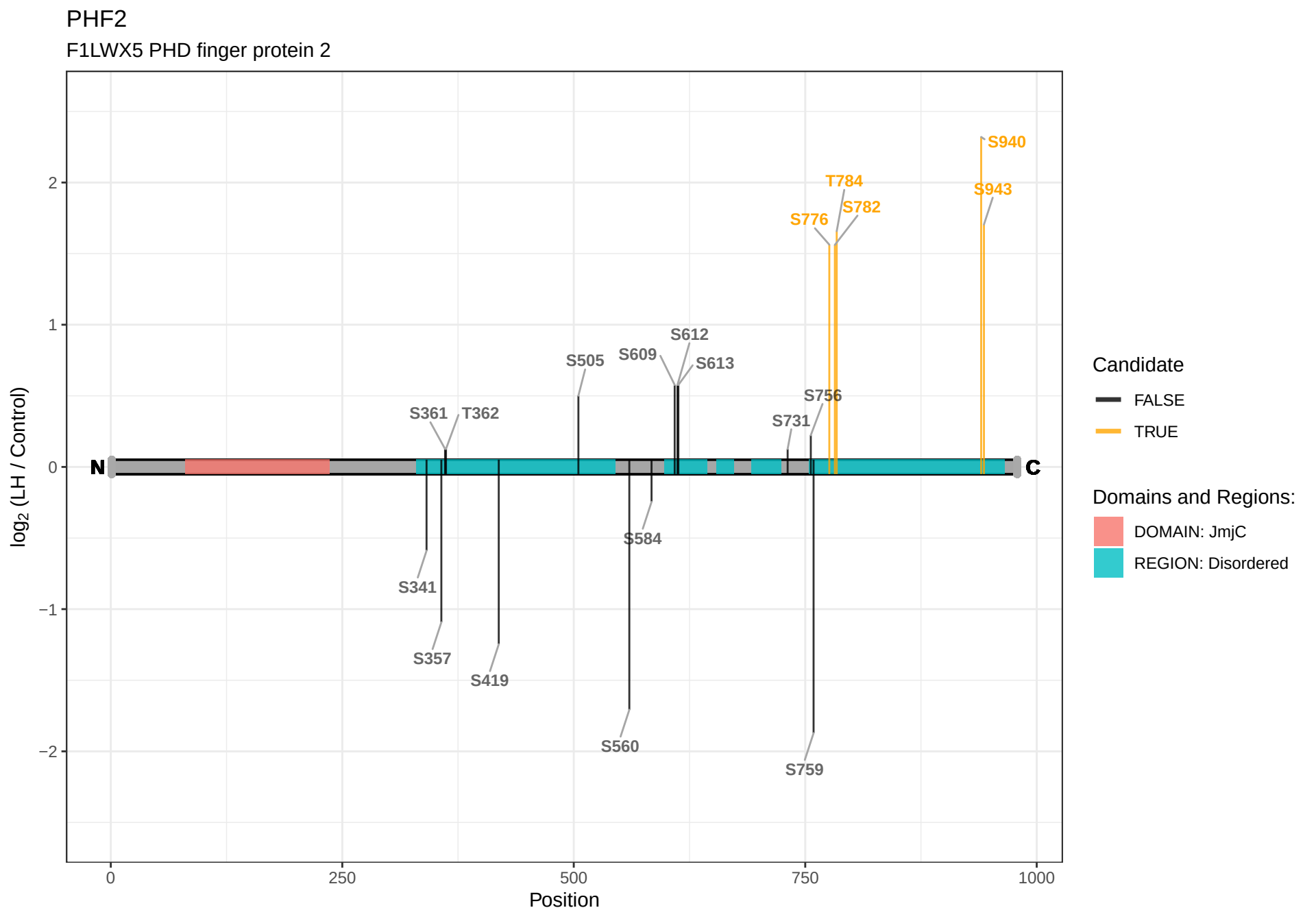

PHACTR4
M0R7T1 Phosphatase and actin regulator
log2 (LH / Control)
3
2
1
0
−1
−2
−3
0
200
400
600
Position
N
C
S159
S162
S166
S136
S456
S464
S602
S130
S188
S143
S477
T148
S132
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

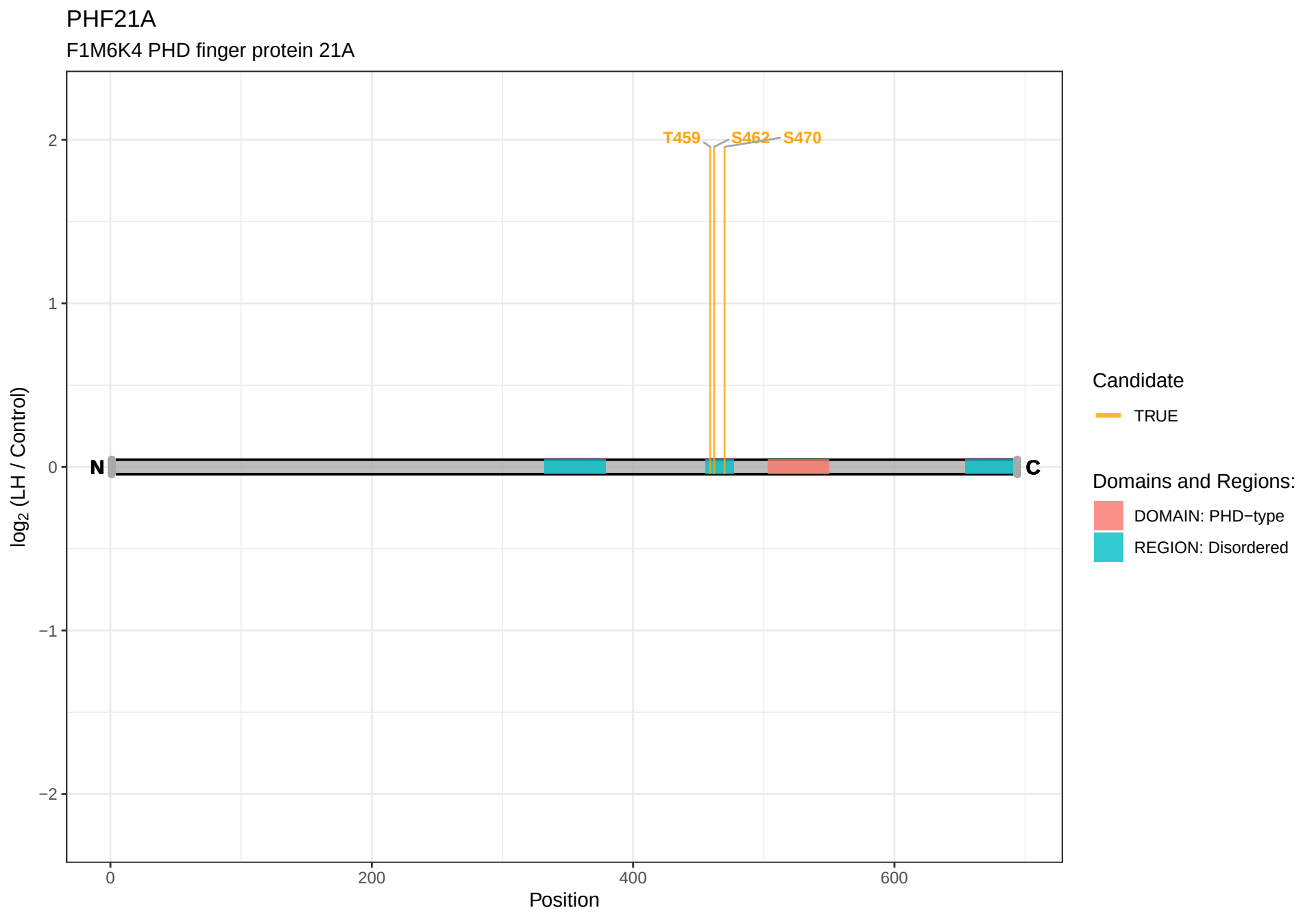

PHC3
D3ZS50 Polyhomeotic homolog 3
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
800
Position
N
C
S689
S609
S608
T456
S463
S117
S109
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: FCS−type
DOMAIN: SAM
REGION: Disordered

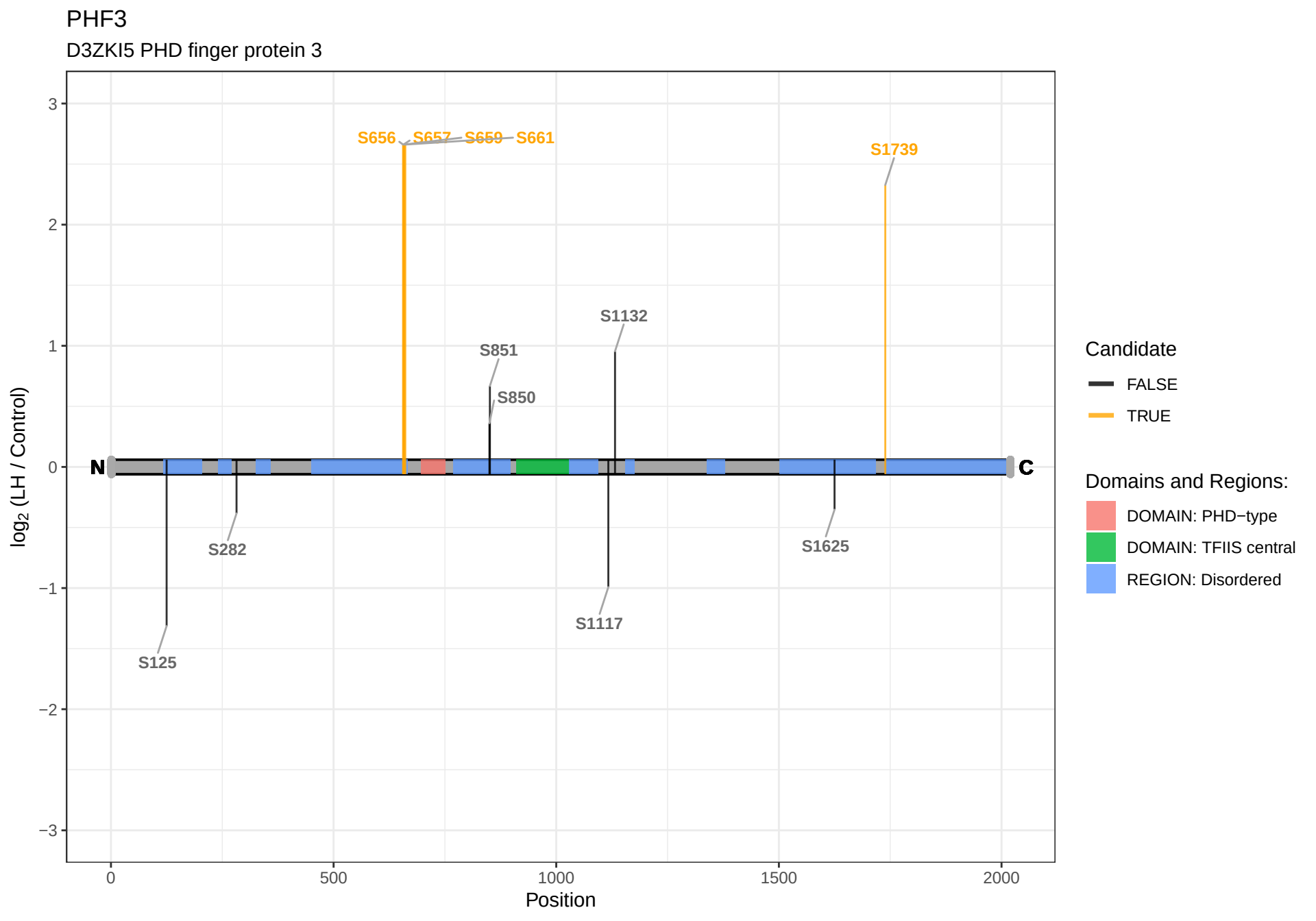

PHF1
Q6MGC9 PHD finger protein 1
S371
N
C
log2 (LH / Control)
Position
0
200
400
2
1
0
−1
−2
Candidate
TRUE
Domains and Regions:
DOMAIN: PHD−type
REGION: Disordered


PHF13
D3ZG56 PHD finger protein 13
S123
N
C
2
1
0
−1
−2
0
100
200
300
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
DOMAIN: PHD
REGION: Disordered


PHF14
G3V9T6 PHD finger protein 14
2
1
0
−1
−2
log2 (LH / Control)
0
250
500
750
Position
N
C
S827
S286
T279
S282
S290
S84
S272
S294
S522
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PHD−type
REGION: Disordered

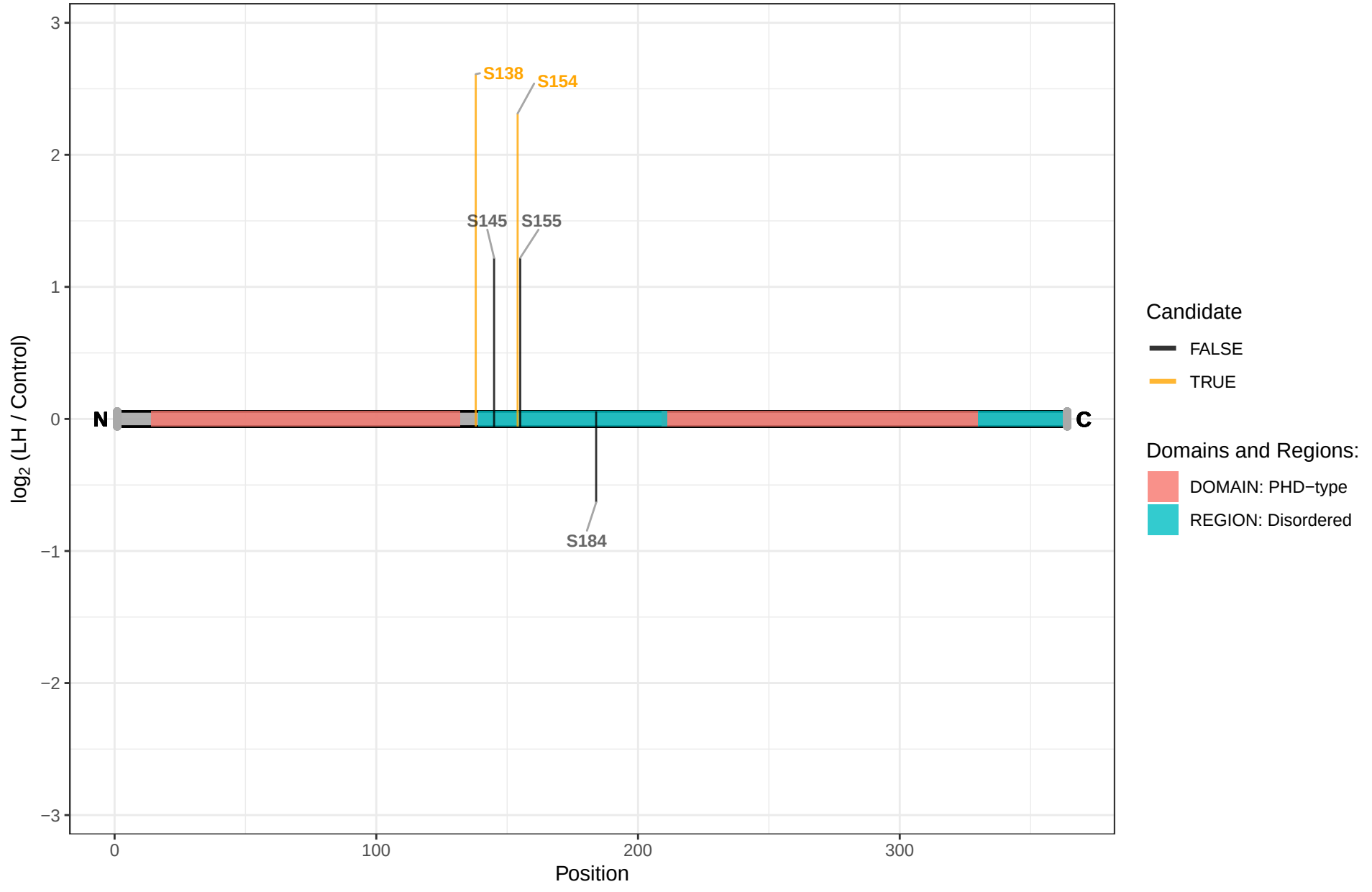

PHF2
F1LWX5 PHD finger protein 2
log2 (LH / Control)
Position
N
C
S940
T784
S943
S782
S776
S612
S505
S609
S613
S756
S361
T362
S731
S584
S341
S357
S419
S560
S759
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: JmjC
REGION: Disordered

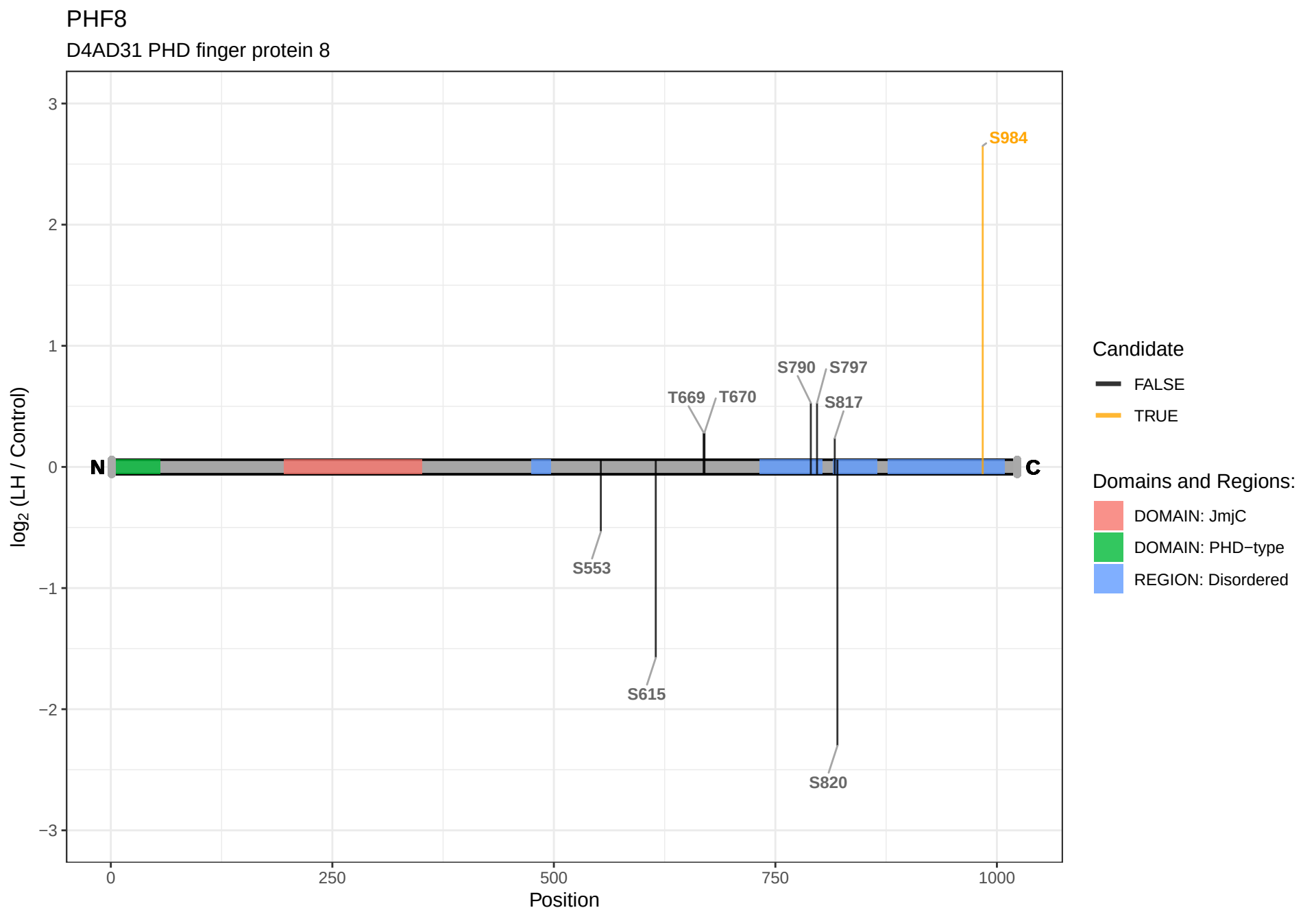

PHF21A
F1M6K4 PHD finger protein 21A
T459
S462
S470
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: PHD−type
REGION: Disordered

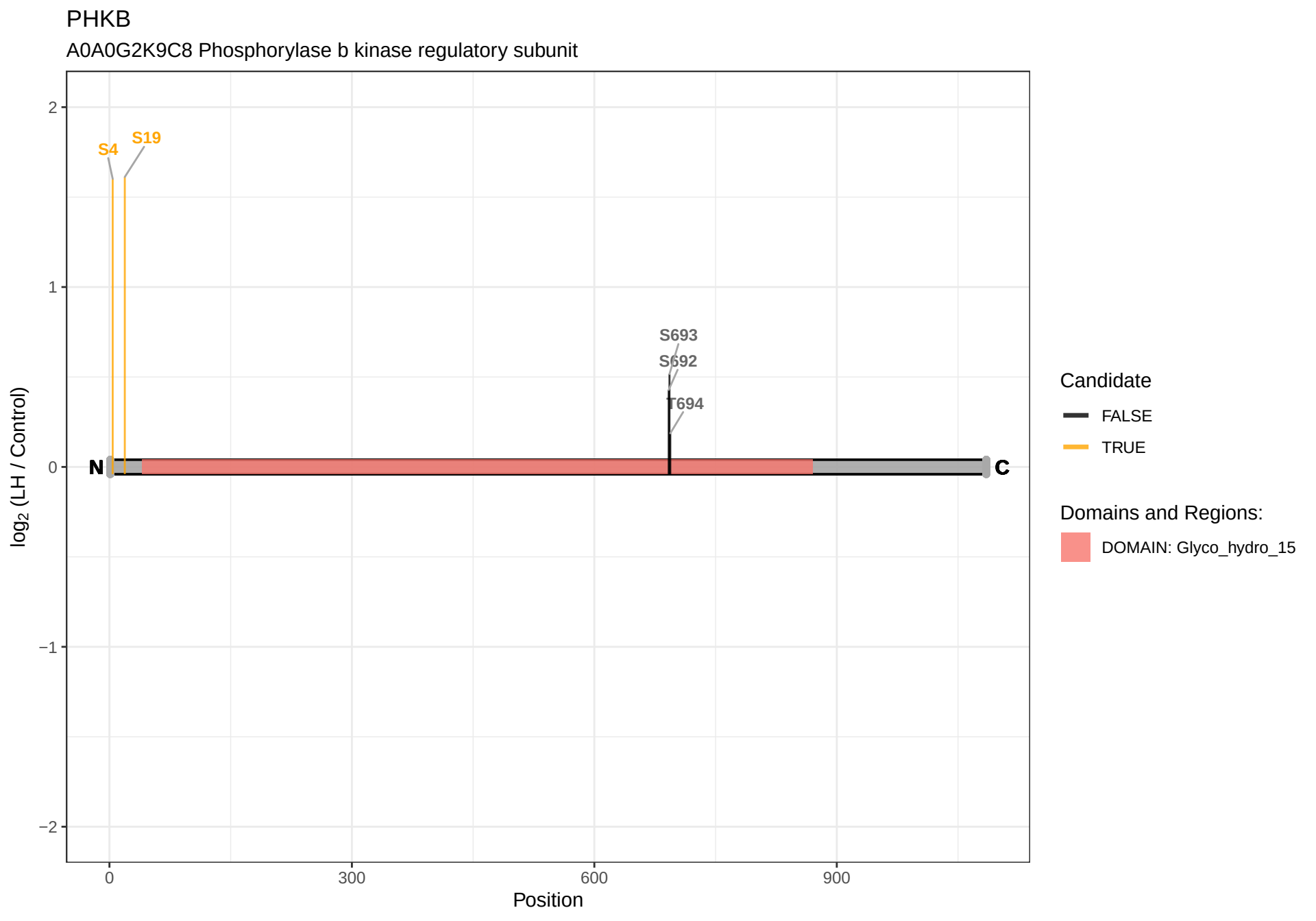

PHF3
D3ZKI5 PHD finger protein 3
S656
S657
S659
S661
S1739
S1132
S851
S850
N
C
S282
S125
S1117
S1625
3
2
1
0
−1
−2
−3
log2 (LH / Control)
0
500
1000
1500
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PHD−type
DOMAIN: TFIIS central
REGION: Disordered

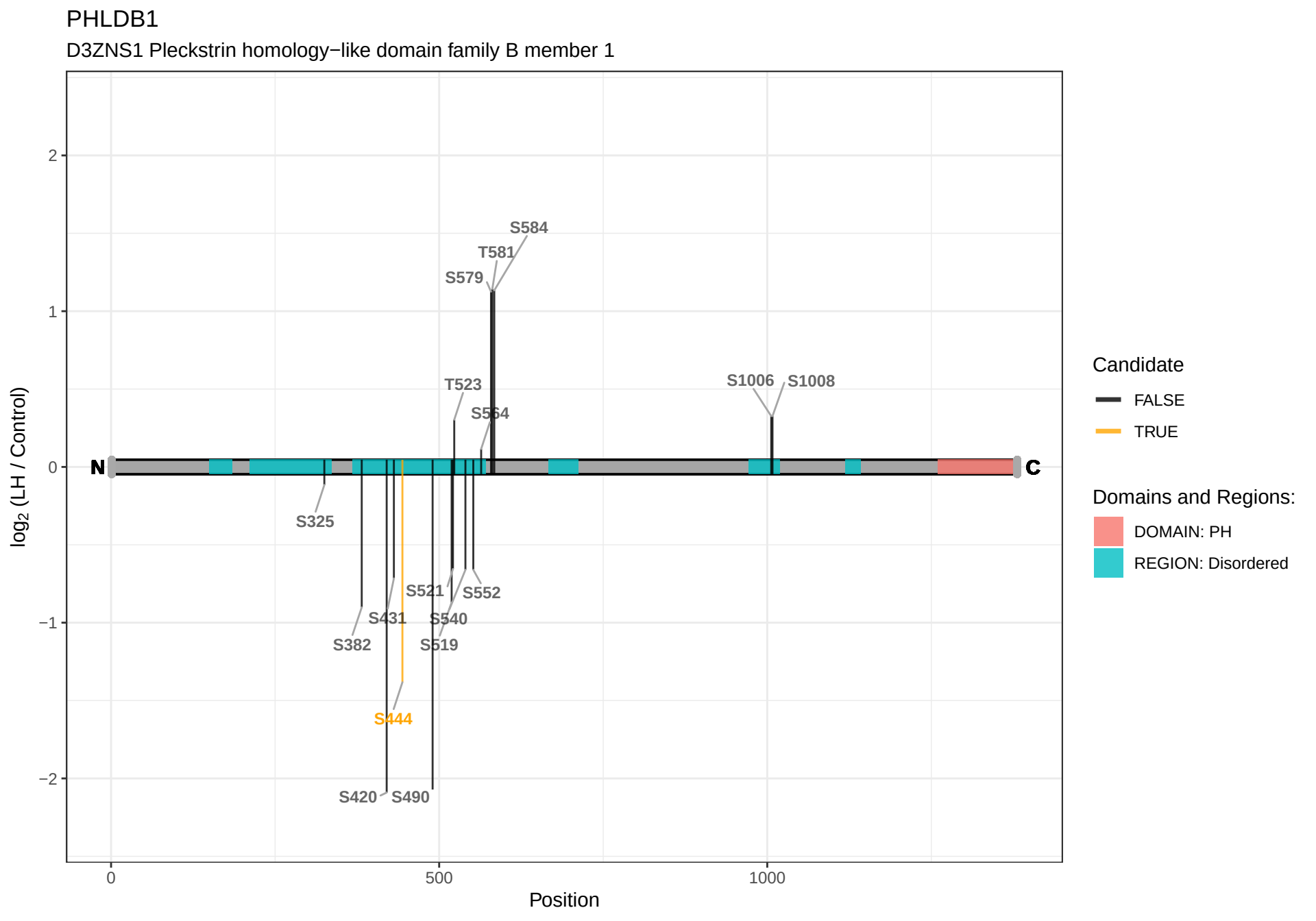
PHF6

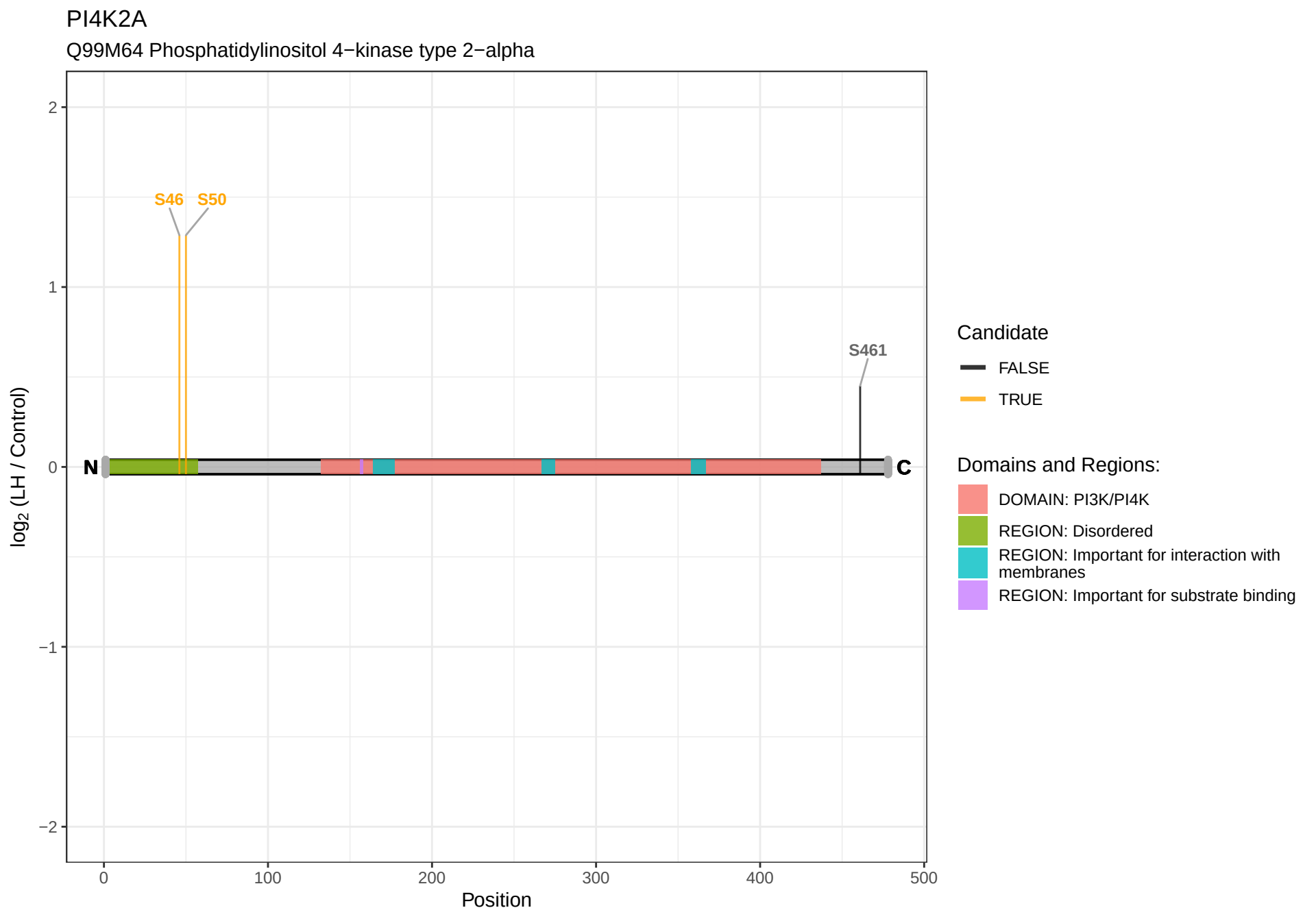
D3ZQV8 PHD finger protein 6

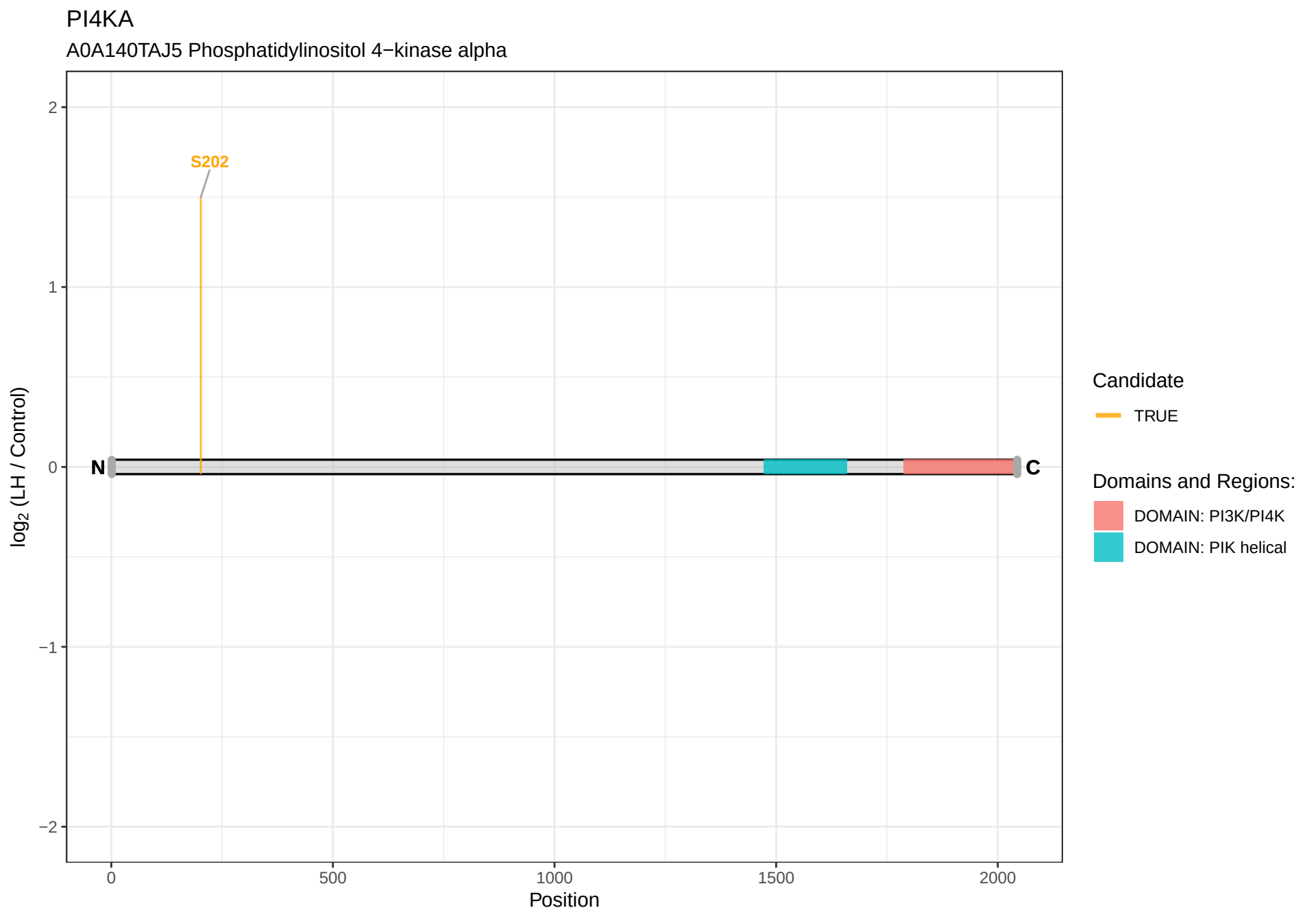


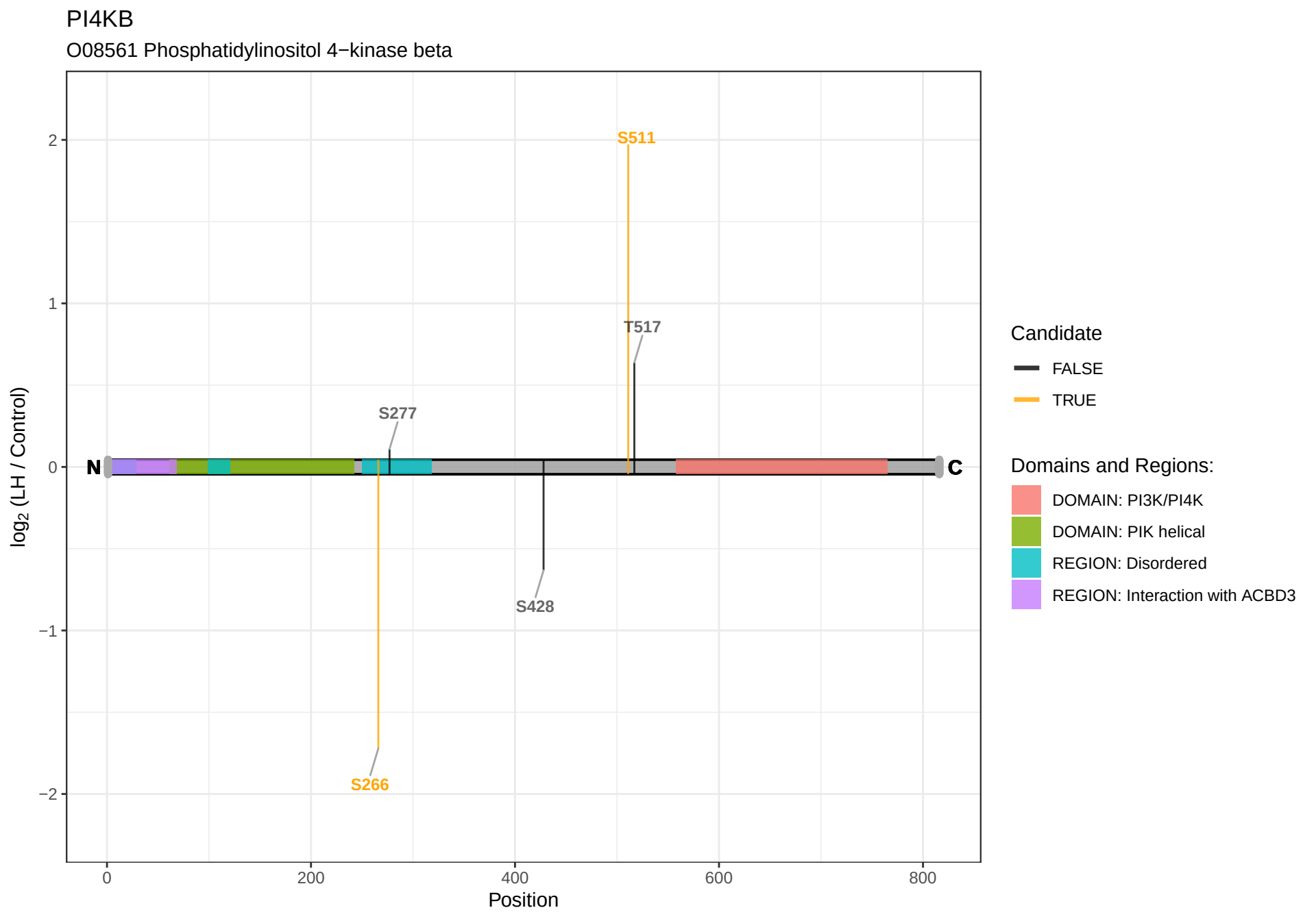

PHF8
D4AD31 PHD finger protein 8
log2 (LH / Control)
3
2
1
0
−1
−2
−3
0
250
500
750
1000
Position
N
C
S984
S790
S797
T669
T670
S817
S553
S615
S820
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: JmjC
DOMAIN: PHD−type
REGION: Disordered

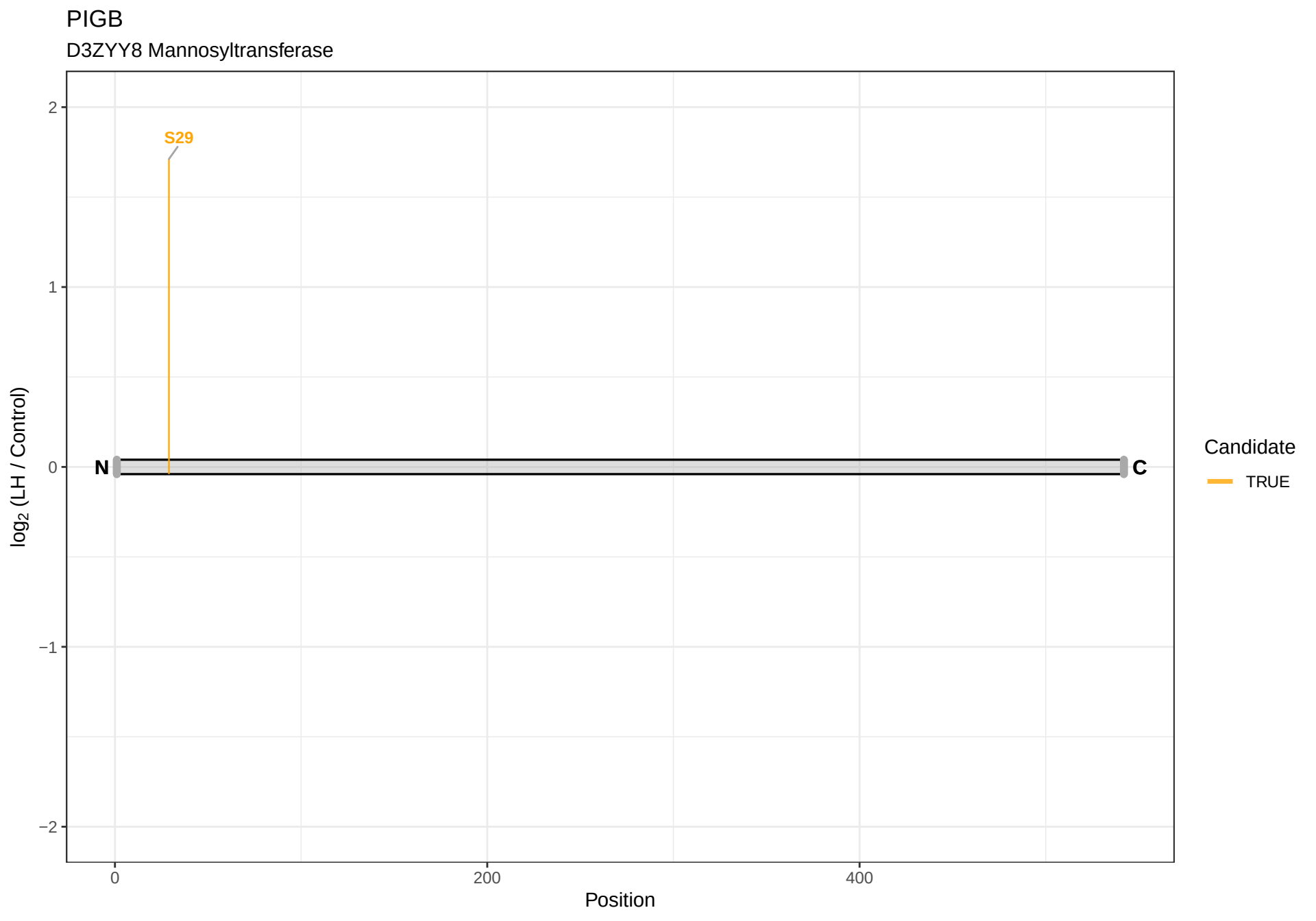

PHKB
A0A0G2K9C8 Phosphorylase b kinase regulatory subunit
S4
S19
S693
S692
T694
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Glyco_hydro_15

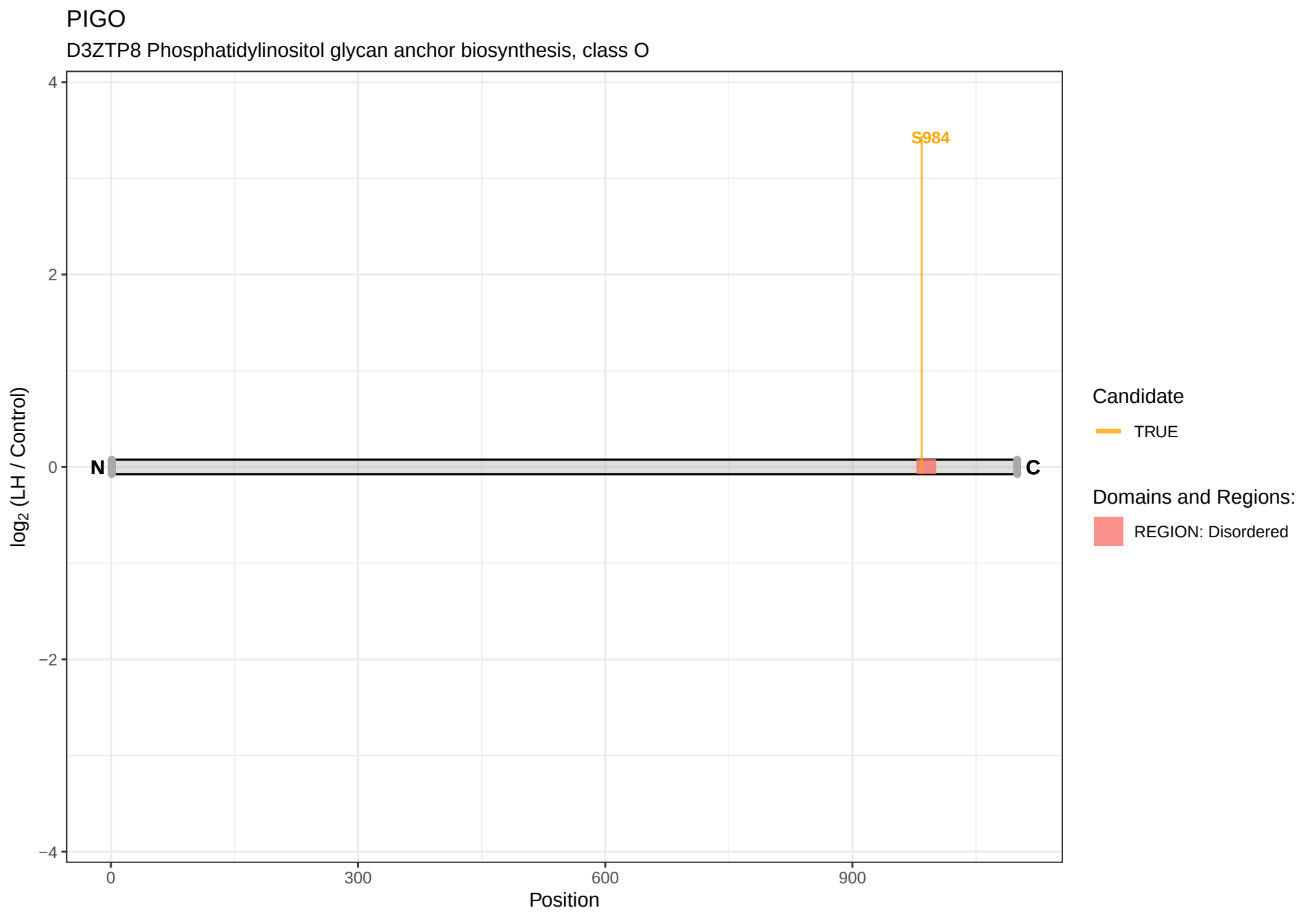

PHLDB1
D3ZNS1 Pleckstrin homology−like domain family B member 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S584
T581
S579
T523
S564
S1006
S1008
S325
S521
S552
S431
S540
S382
S519
S444
S420
S490
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PH
REGION: Disordered

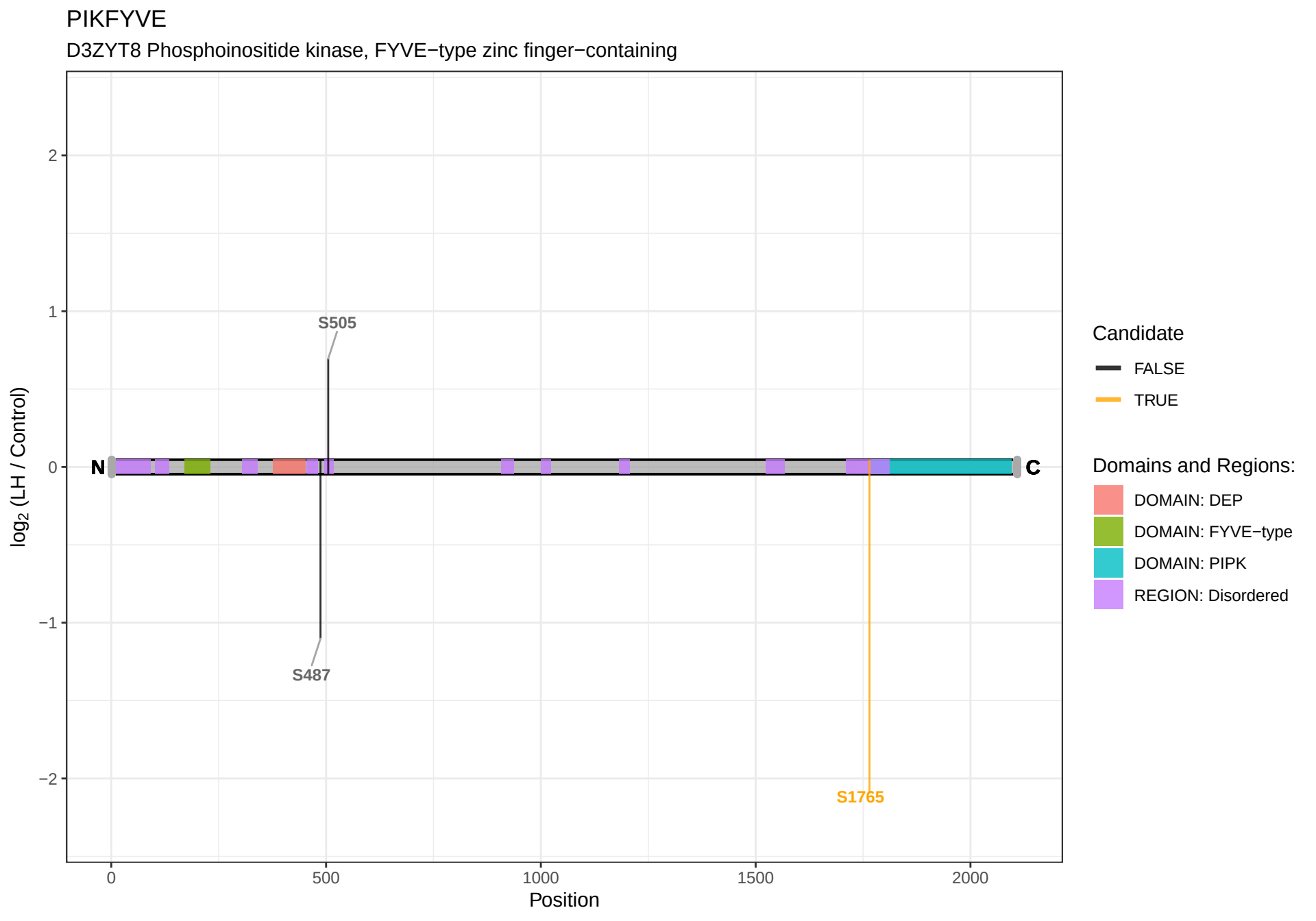

PI4K2A
Q99M64 Phosphatidylinositol 4−kinase type 2−alpha
S46
S50
S461
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
100
200
300
400
500
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PI3K/PI4K
REGION: Disordered
REGION: Important for interaction with membranes
REGION: Important for substrate binding

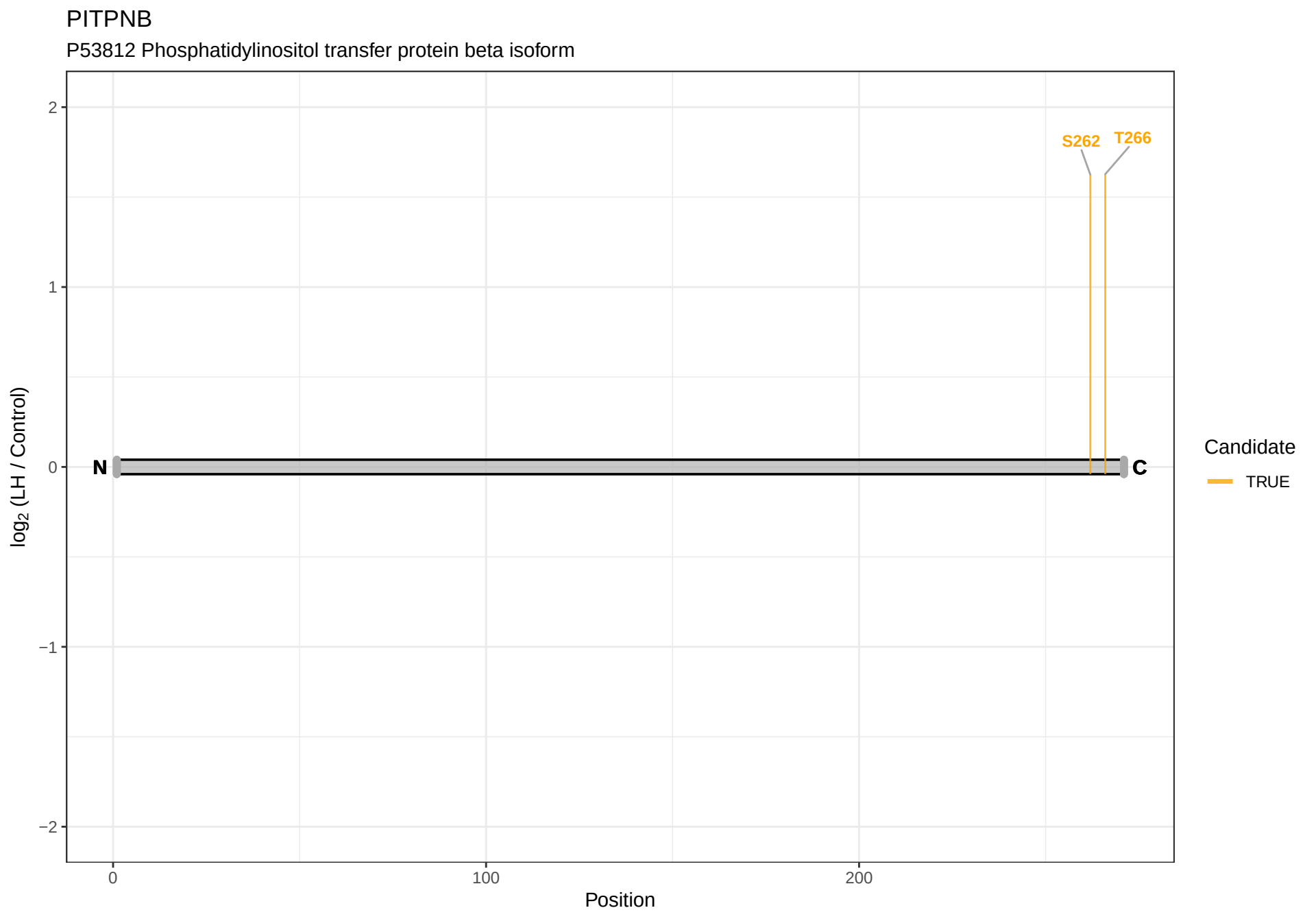

PI4KA
A0A140TAJ5 Phosphatidylinositol 4−kinase alpha
S202
N
C
2
1
0
−1
−2
0
500
1000
1500
2000
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
DOMAIN: PI3K/PI4K
DOMAIN: PIK helical

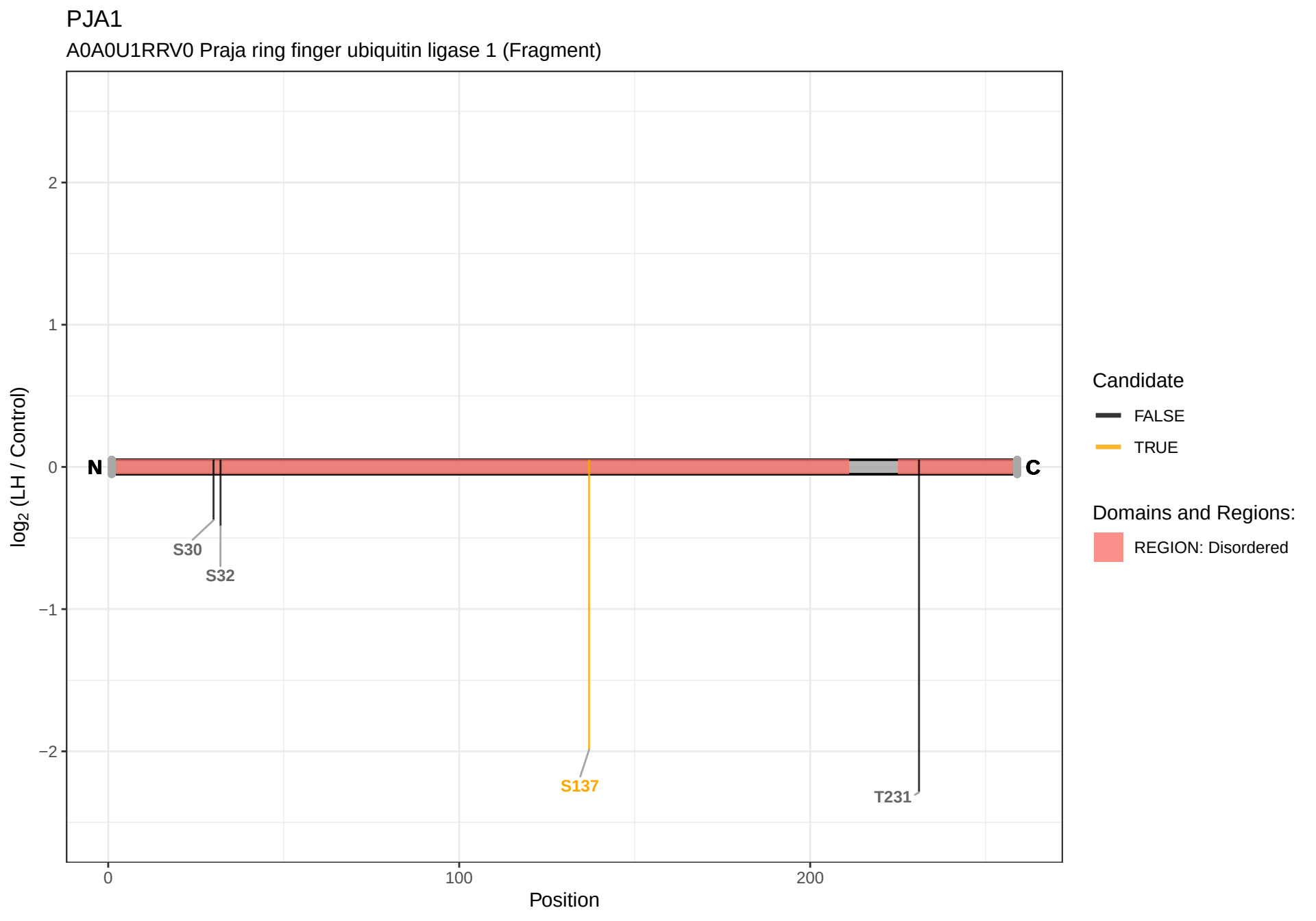

PI4KB
O08561 Phosphatidylinositol 4−kinase beta
S511
T517
S277
N
C
S428
S266
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PI3K/PI4K
DOMAIN: PIK helical
REGION: Disordered
REGION: Interaction with ACBD3

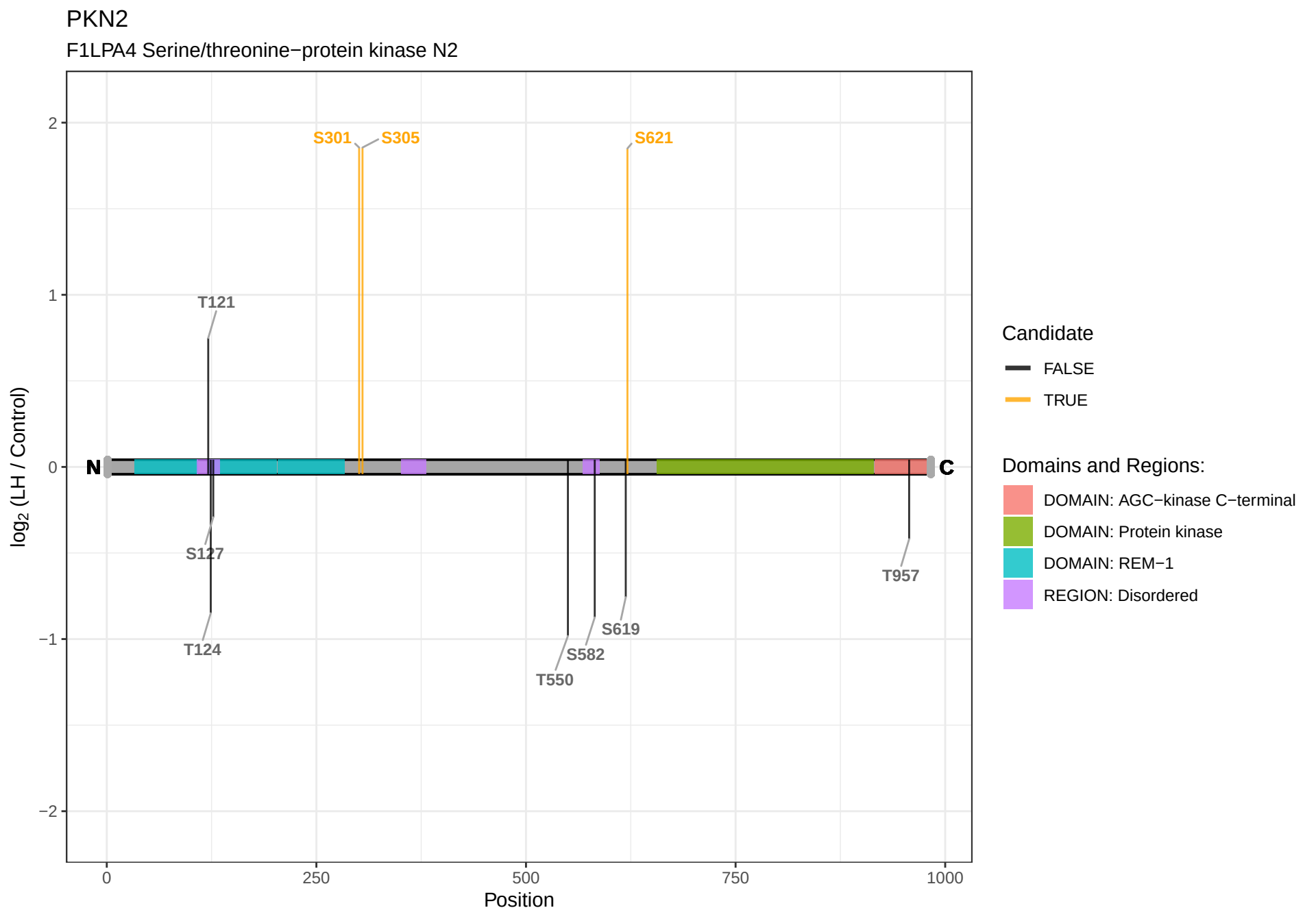

PIGB
D3ZYY8 Mannosyltransferase
S29
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
Position
Candidate
TRUE

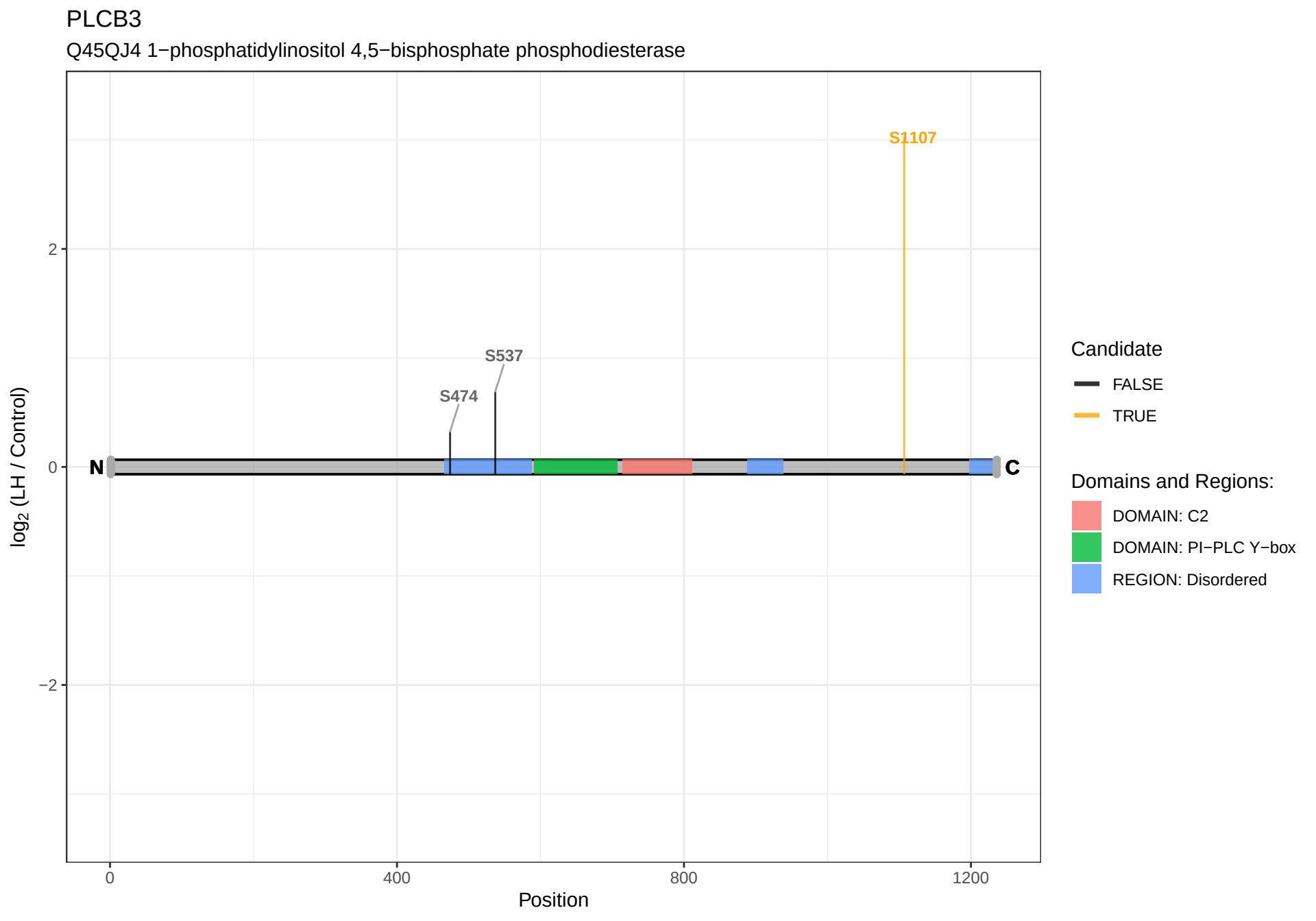

PIGO
D3ZTP8 Phosphatidylinositol glycan anchor biosynthesis, class O
S984
N
C
log2 (LH / Control)
4
2
0
−2
−4
0
300
600
900
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

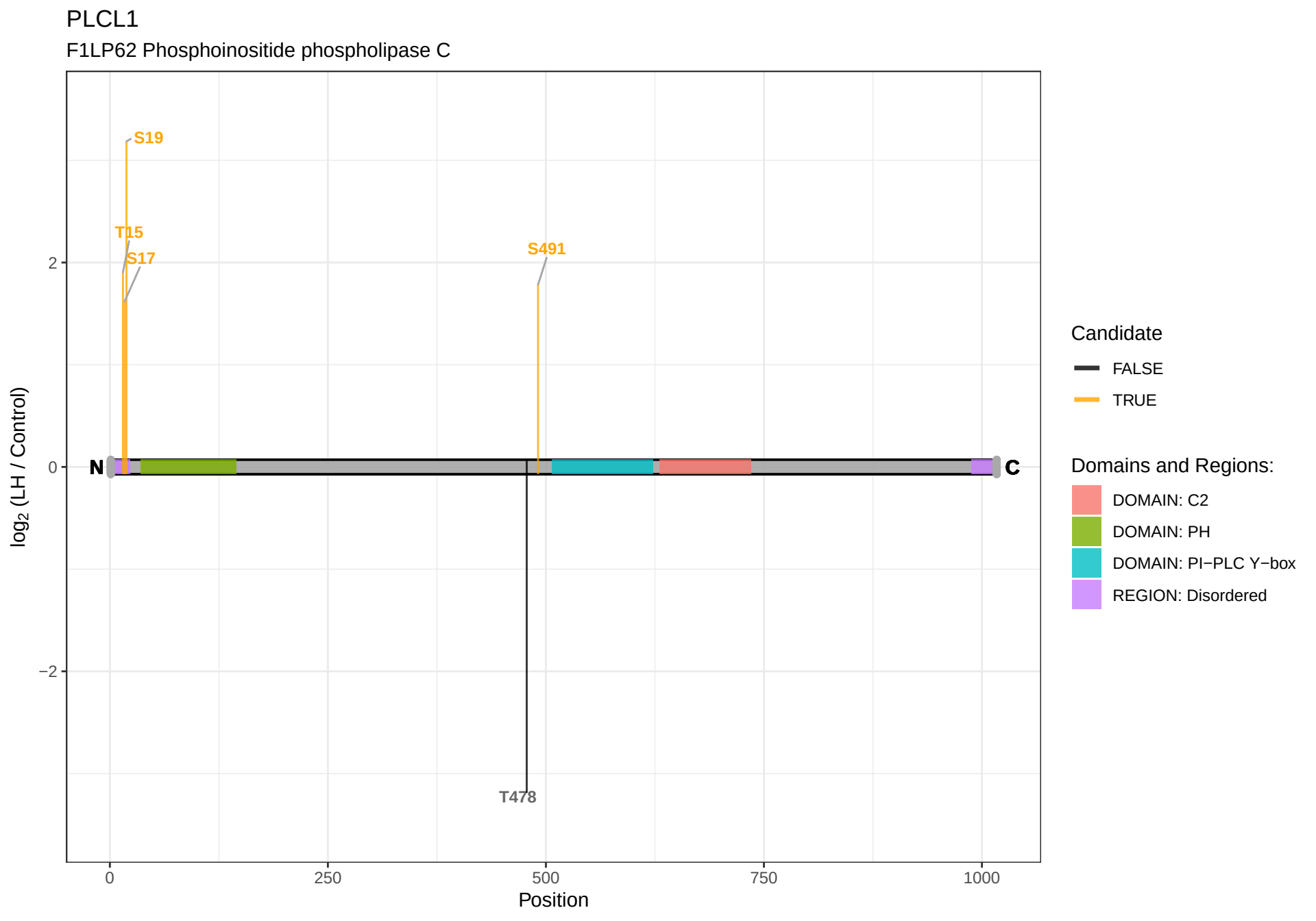

PIKFYVE
D3ZYT8 Phosphoinositide kinase, FYVE−type zinc finger−containing
log2 (LH / Control)
2
1
0
−1
−2
N
C
S505
S487
S1765
0
500
1000
1500
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DEP
DOMAIN: FYVE−type
DOMAIN: PIPK
REGION: Disordered

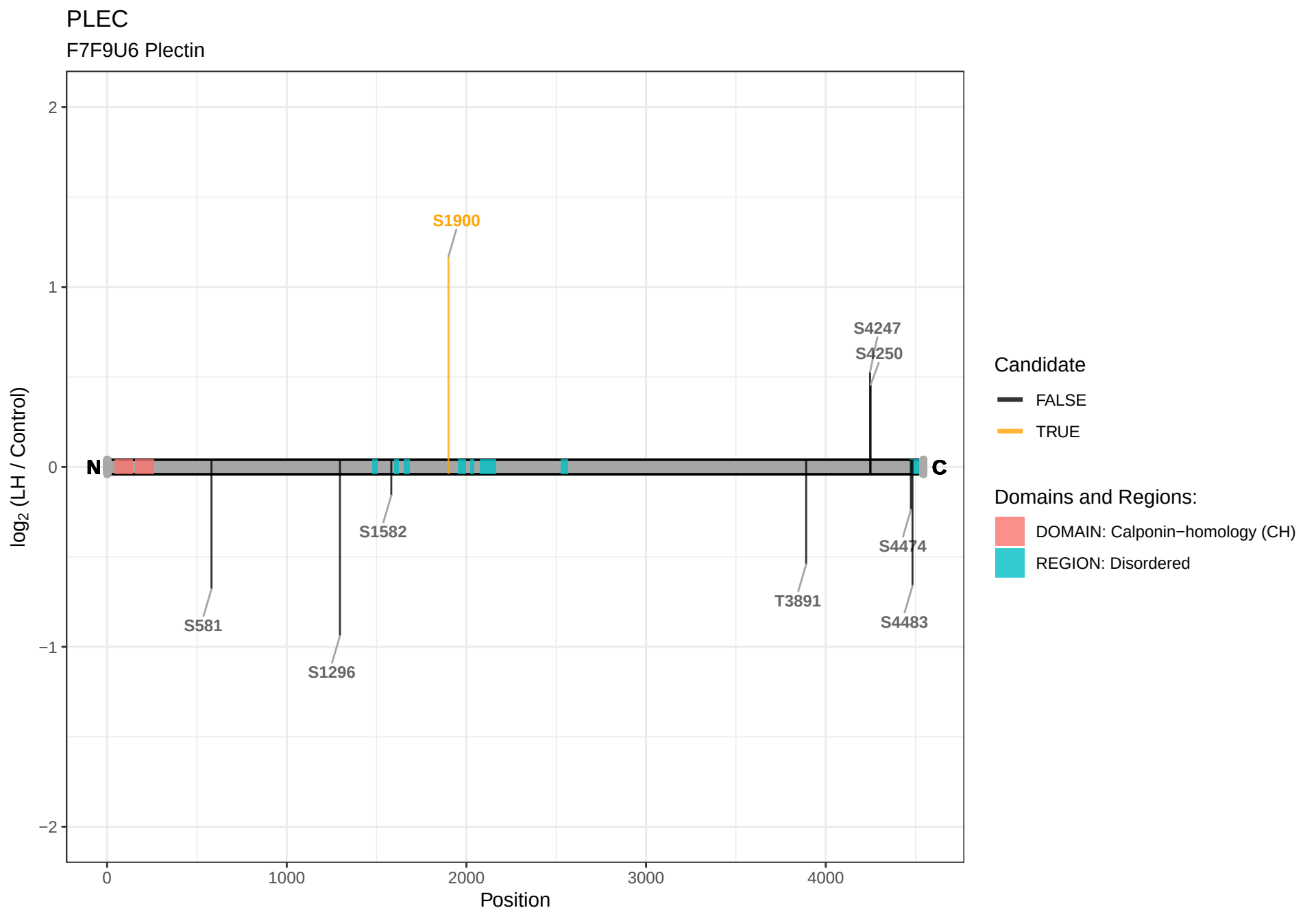

PITPNB
P53812 Phosphatidylinositol transfer protein beta isoform
S262
T266
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
Position
Candidate
TRUE

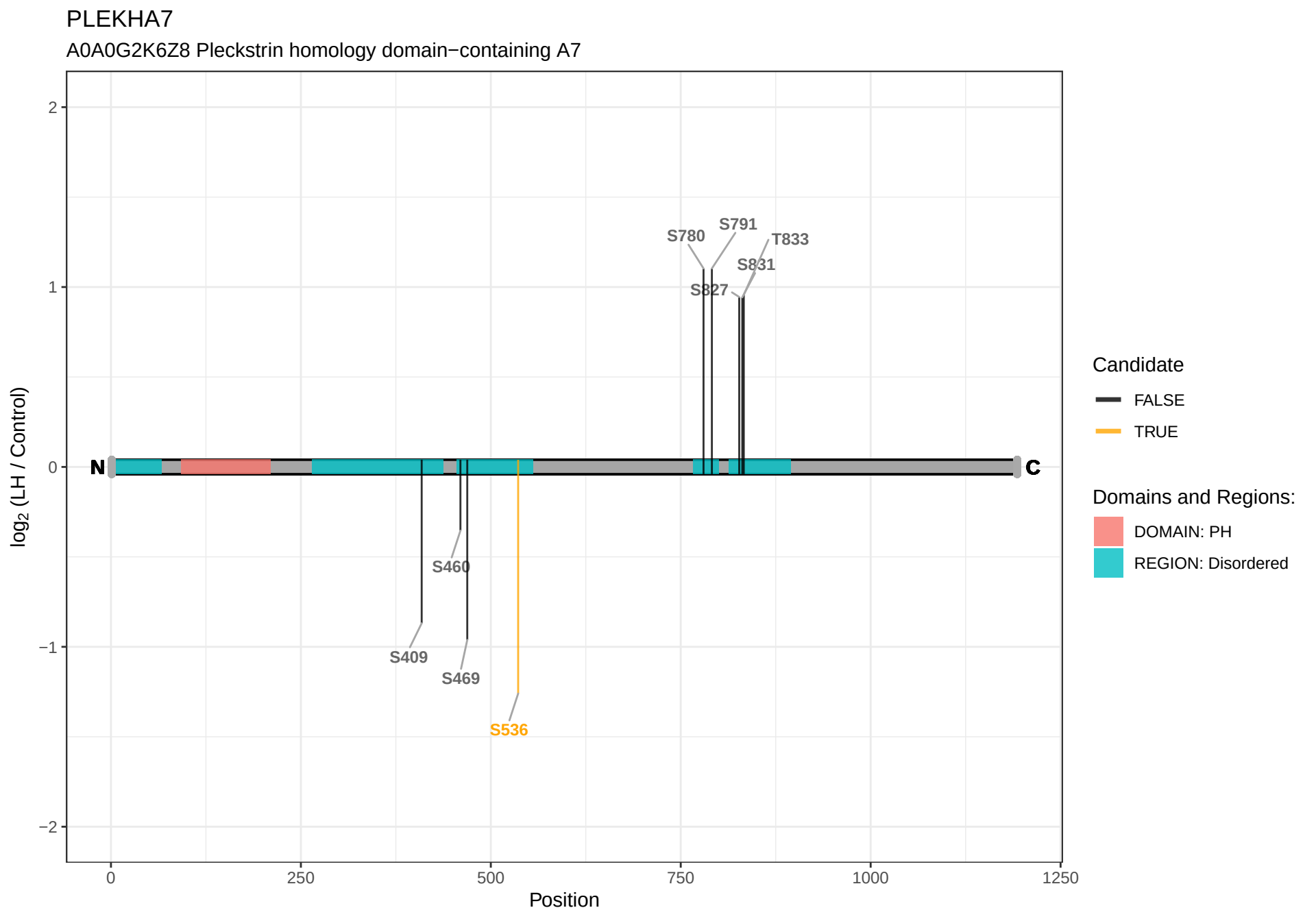

PJA1
A0A0U1RRV0 Praja ring finger ubiquitin ligase 1 (Fragment)
log2 (LH / Control)
2
1
0
−1
−2
N
C
S30
S32
S137
T231
0
100
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

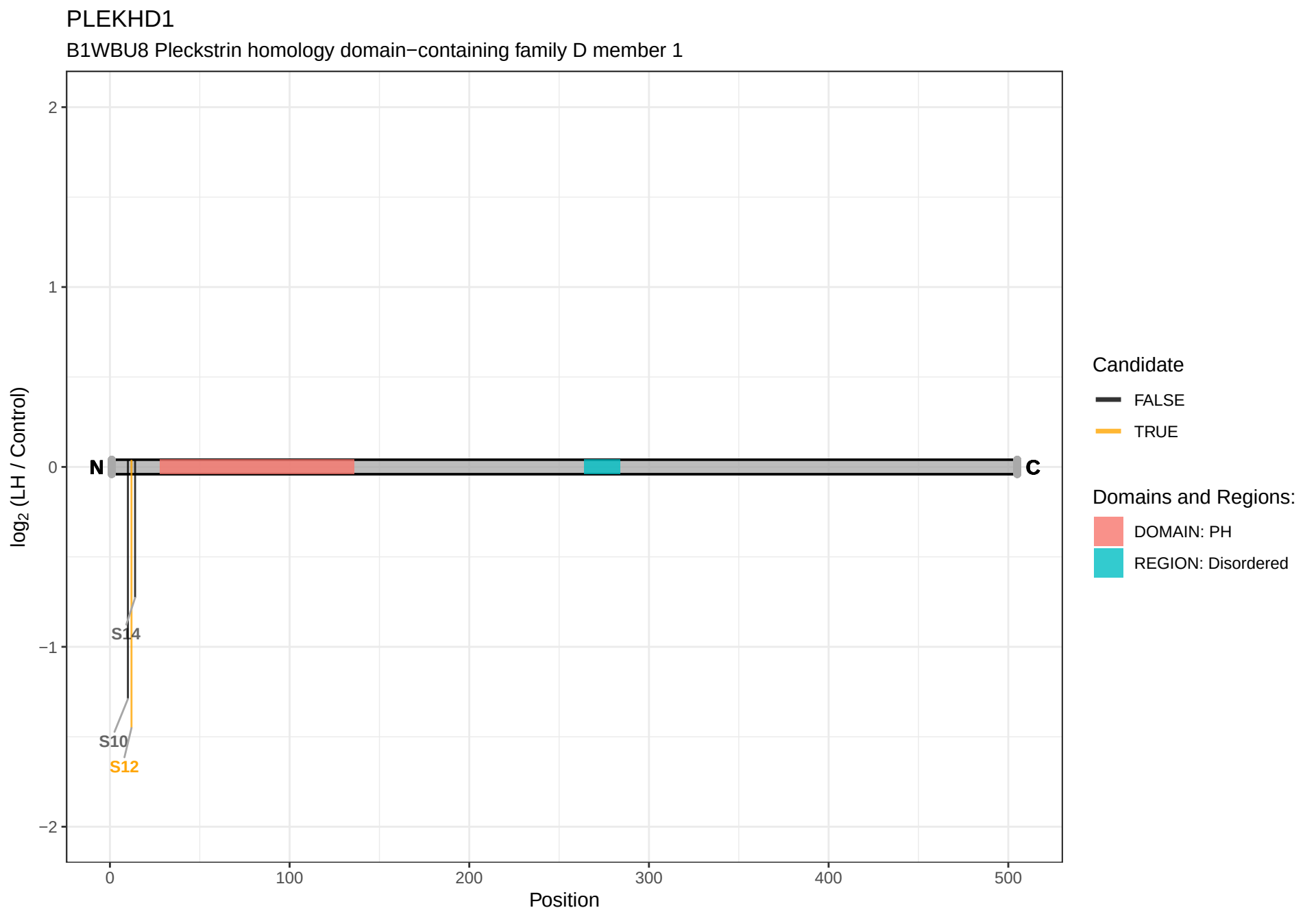

PKN2
F1LPA4 Serine/threonine−protein kinase N2
log2 (LH / Control)
2
1
0
−1
−2
S301
S305
S621
T121
N
C
S127
T124
T550
S582
S619
T957
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AGC−kinase C−terminal
DOMAIN: Protein kinase
DOMAIN: REM−1
REGION: Disordered

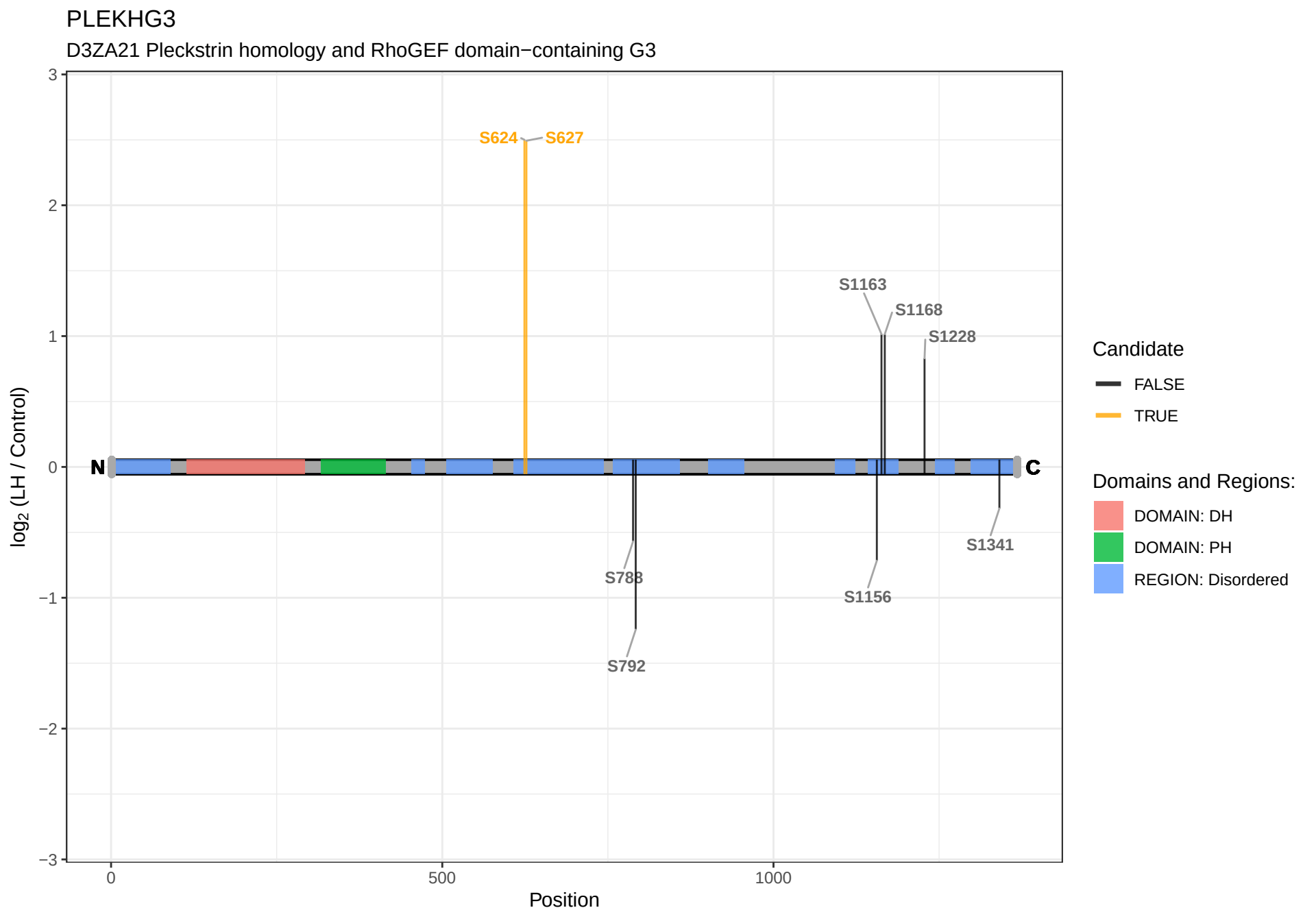

PLCB3
Q45QJ4 1−phosphatidylinositol 4,5−bisphosphate phosphodiesterase
S1107
S537
S474
N
C
2
0
−2
log2 (LH / Control)
0
400
800
1200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2
DOMAIN: PI−PLC Y−box
REGION: Disordered

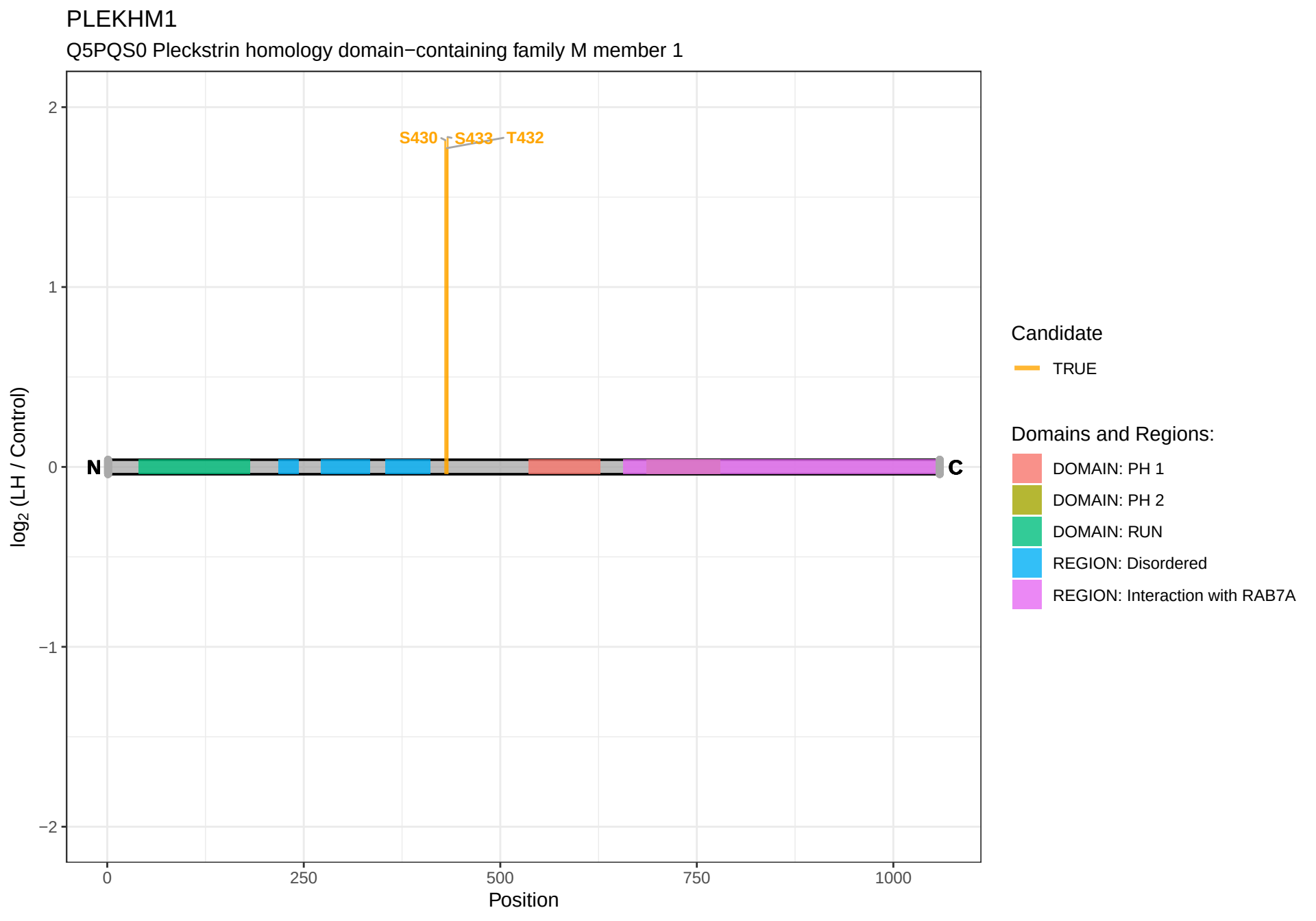

PLCL1
F1LP62 Phosphoinositide phospholipase C
S19
T15
S17
S491
T478
N
C
2
0
−2
log2 (LH / Control)
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2
DOMAIN: PH
DOMAIN: PI−PLC Y−box
REGION: Disordered

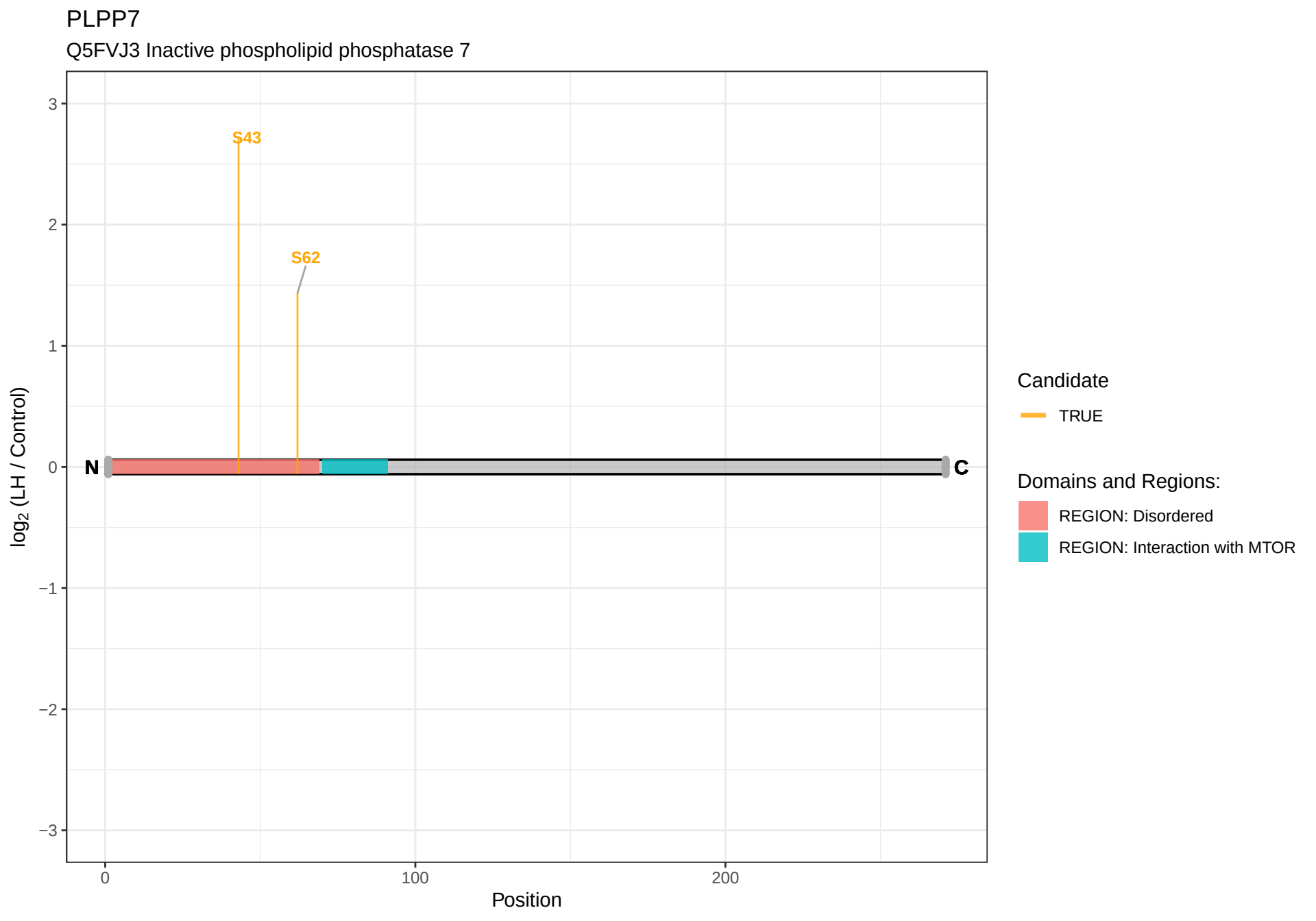

PLEC
F7F9U6 Plectin
log2 (LH / Control)
2
1
0
−1
−2
0
1000
2000
3000
4000
Position
N
C
S1900
S4247
S4250
S1582
S581
S1296
T3891
S4474
S4483
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Calponin−homology (CH)
REGION: Disordered

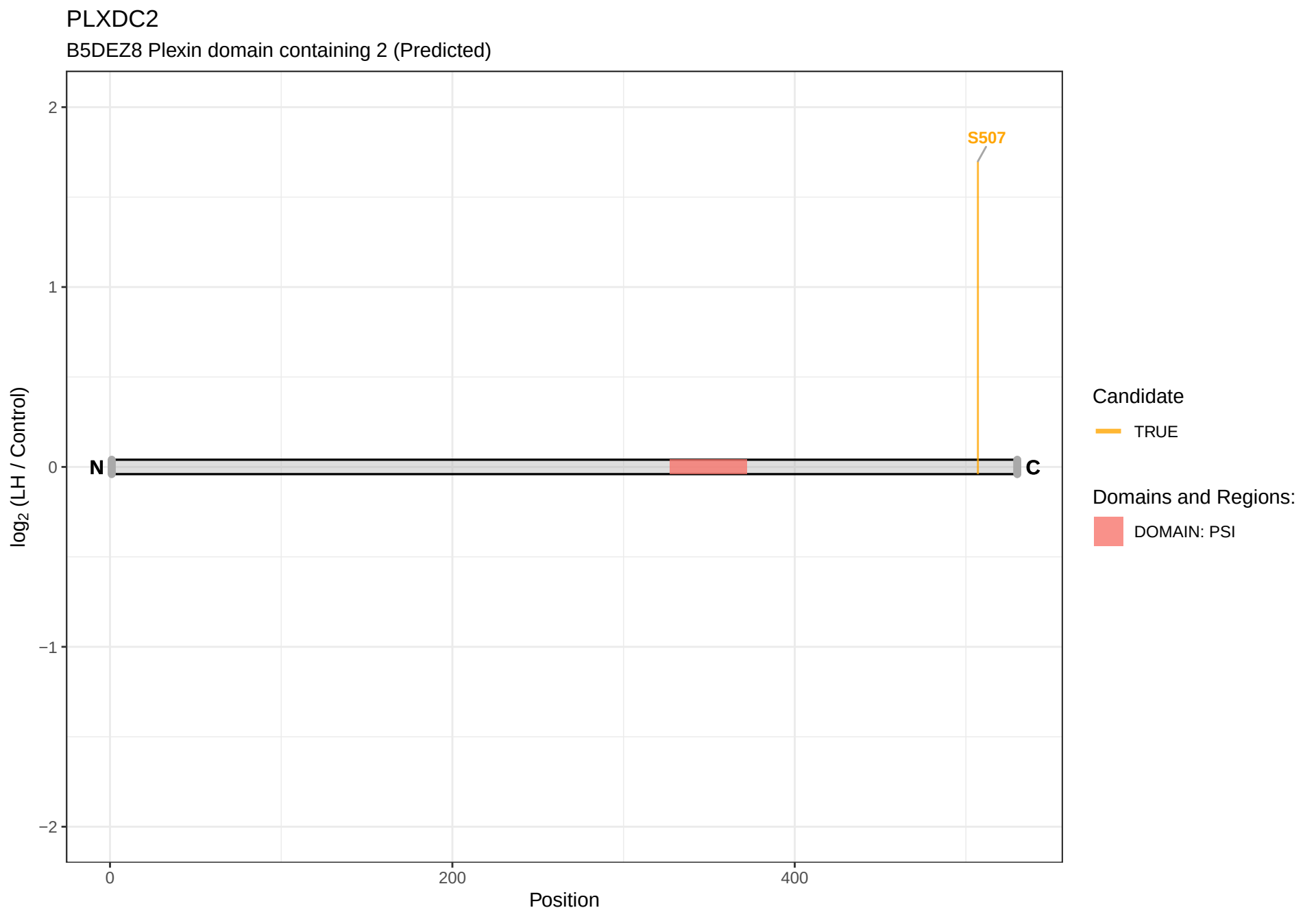

PLEKHA7
A0A0G2K6Z8 Pleckstrin homology domain−containing A7
log2 (LH / Control)
2
1
0
−1
−2
0
250
500
750
1000
1250
Position
N
C
S780
S791
T833
S831
S827
S460
S409
S469
S536
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PH
REGION: Disordered

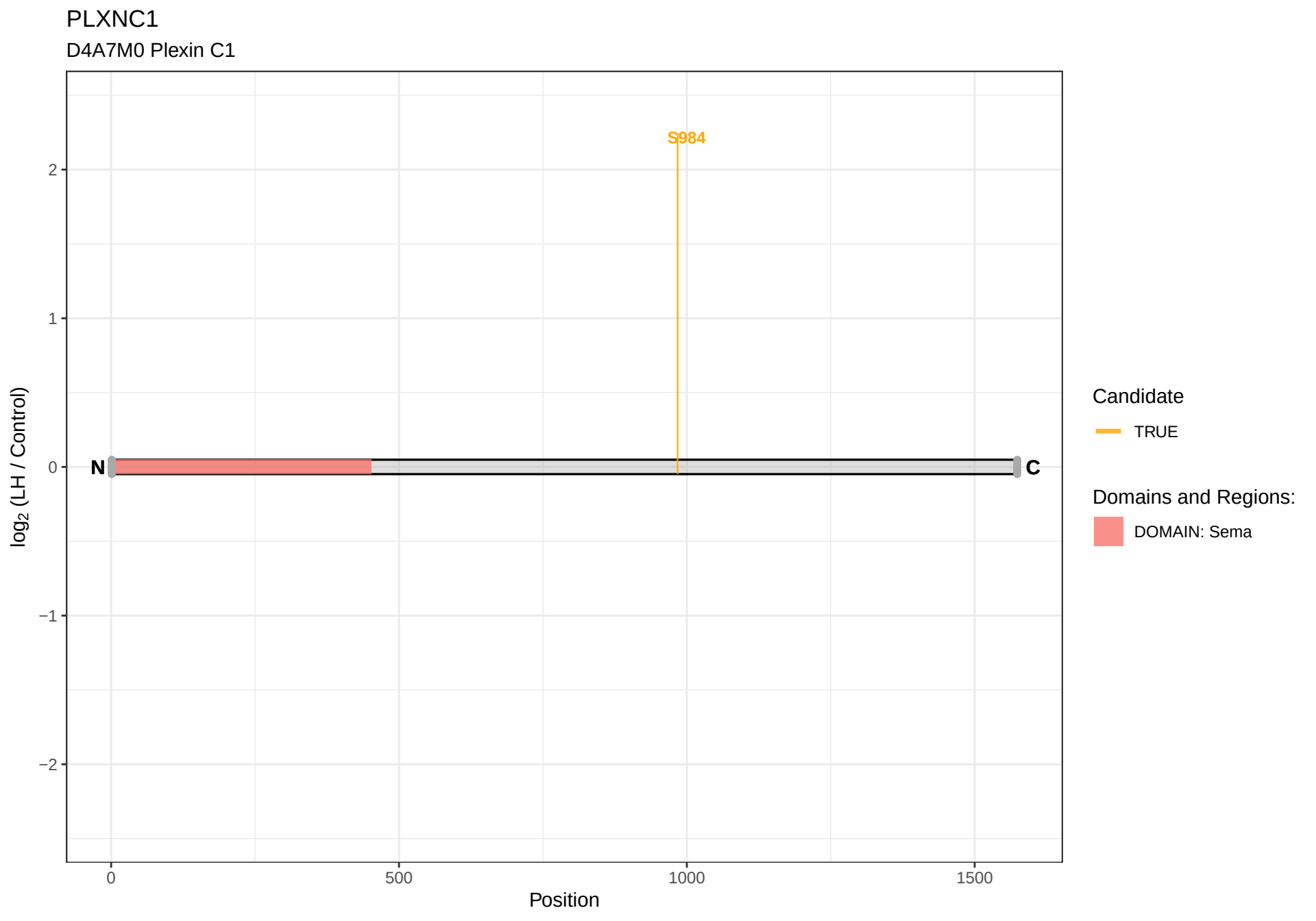

PLEKHD1
B1WBU8 Pleckstrin homology domain−containing family D member 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S14
S10
S12
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PH
REGION: Disordered

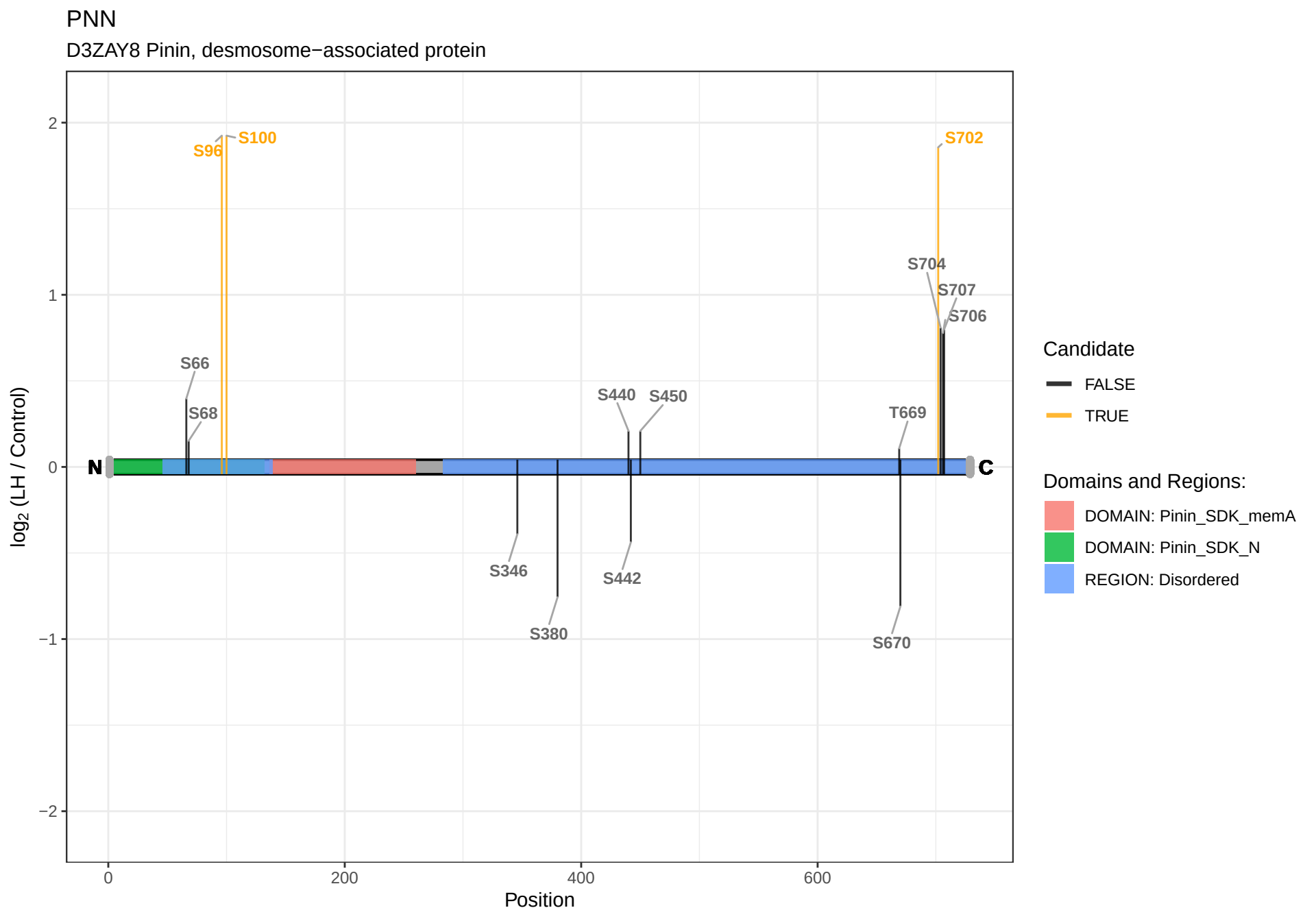

PLEKHG3
D3ZA21 Pleckstrin homology and RhoGEF domain−containing G3
log2 (LH / Control)
Position
N
C
S624
S627
S1163
S1168
S1228
S788
S792
S1156
S1341
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DH
DOMAIN: PH
REGION: Disordered

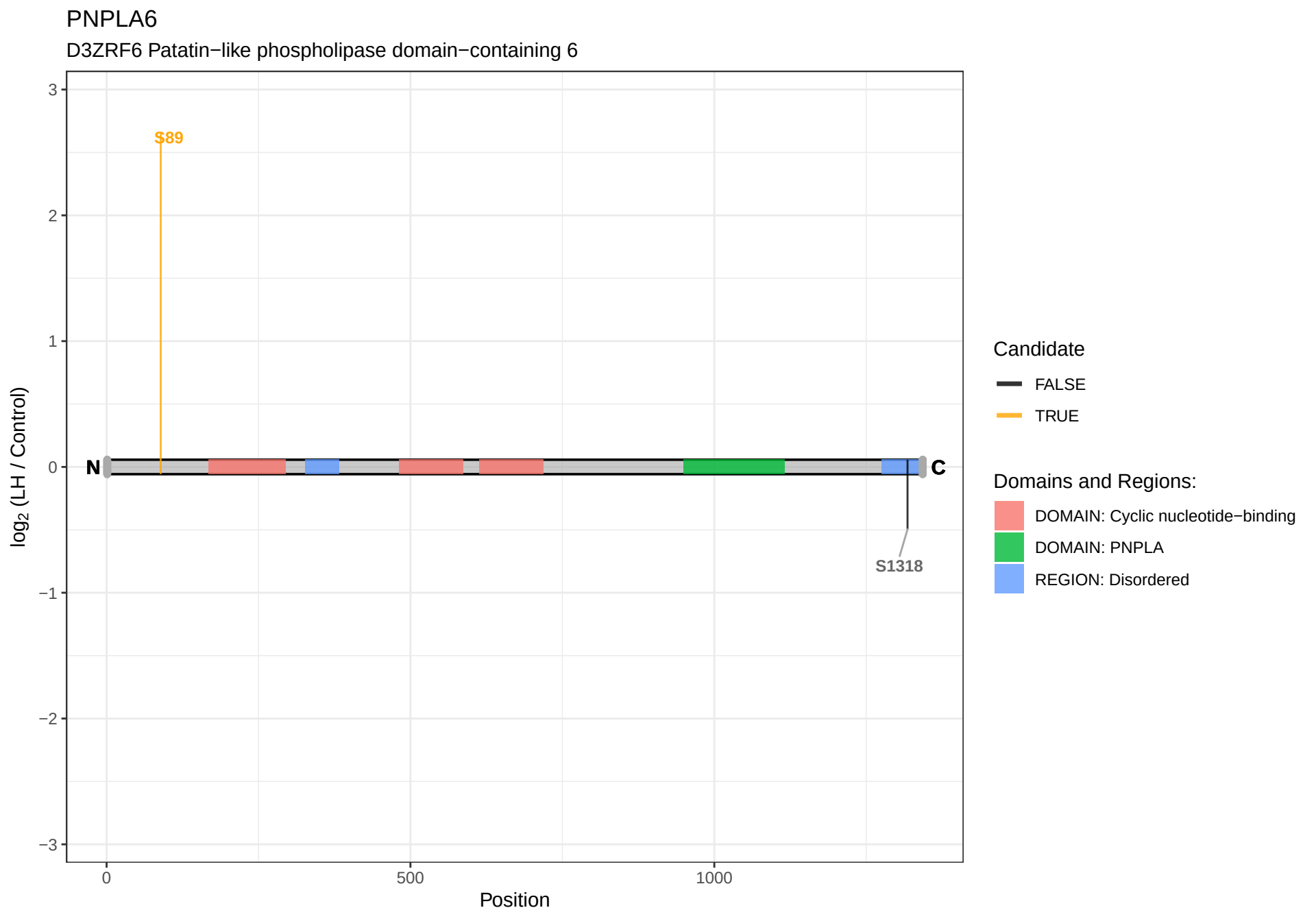

PLEKHM1
Q5PQS0 Pleckstrin homology domain−containing family M member 1
S430
S433
T432
N
C
2
1
0
−1
−2
0
250
500
750
1000
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
DOMAIN: PH 1
DOMAIN: PH 2
DOMAIN: RUN
REGION: Disordered
REGION: Interaction with RAB7A

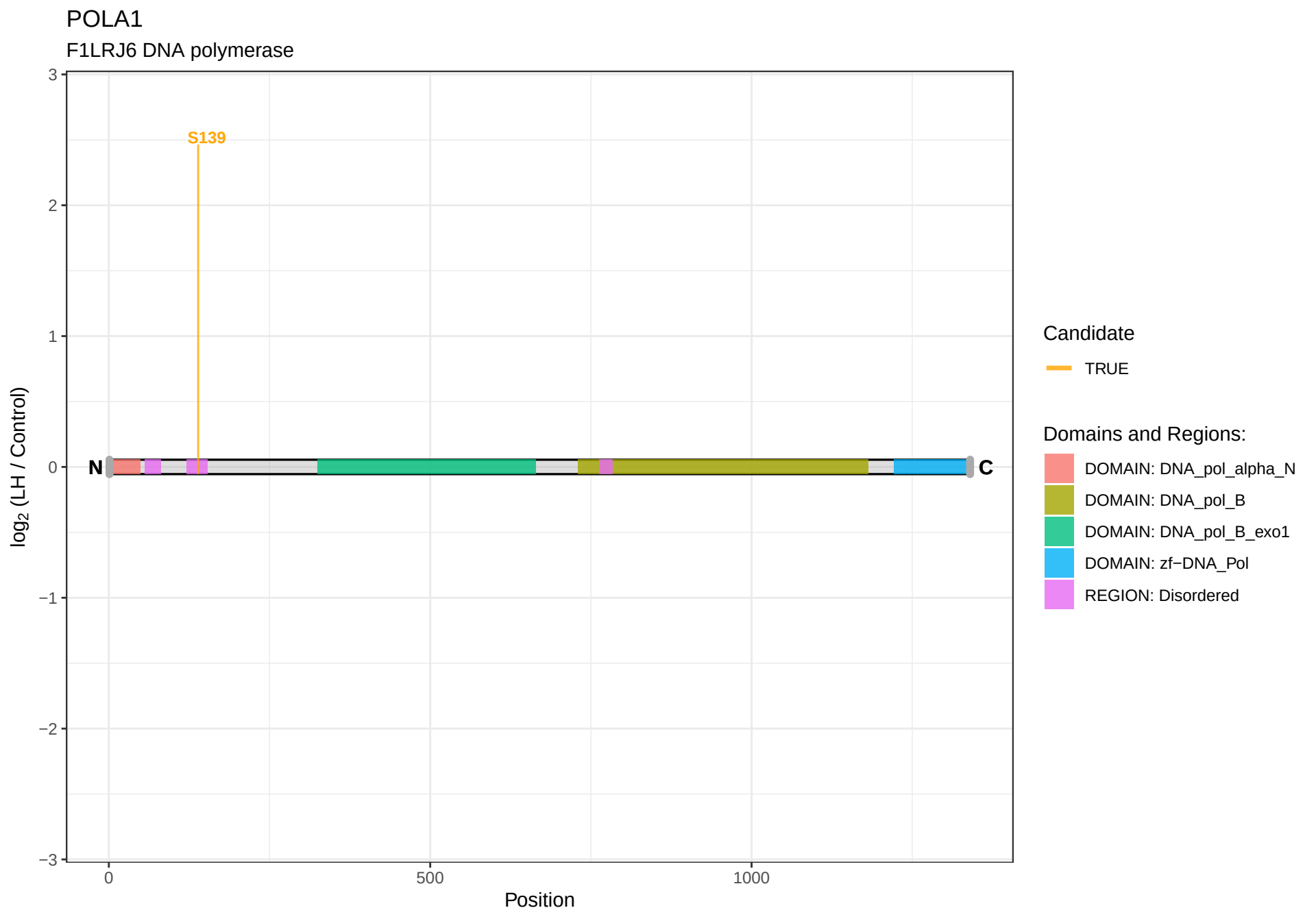

PLPP7
Q5FVJ3 Inactive phospholipid phosphatase 7
S43
S62
N
C
log2 (LH / Control)
Position
0
100
200
3
2
1
0
−1
−2
−3
Candidate
TRUE
Domains and Regions:
REGION: Disordered
REGION: Interaction with MTOR

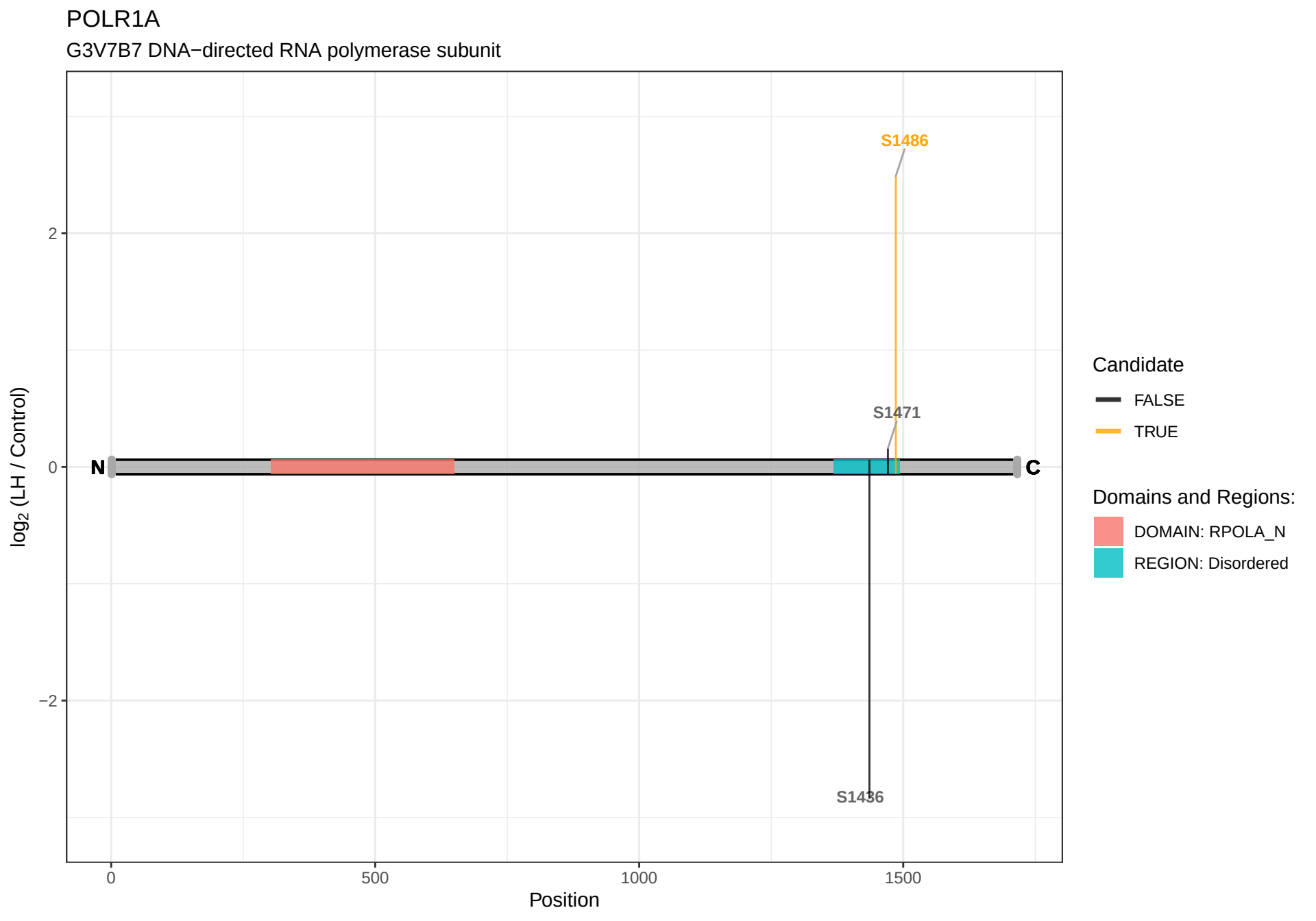

PLXDC2
B5DEZ8 Plexin domain containing 2 (Predicted)
S507
N
C
log2 (LH / Control)
Position
0
200
400
2
1
0
−1
−2
Candidate
TRUE
Domains and Regions:
DOMAIN: PSI

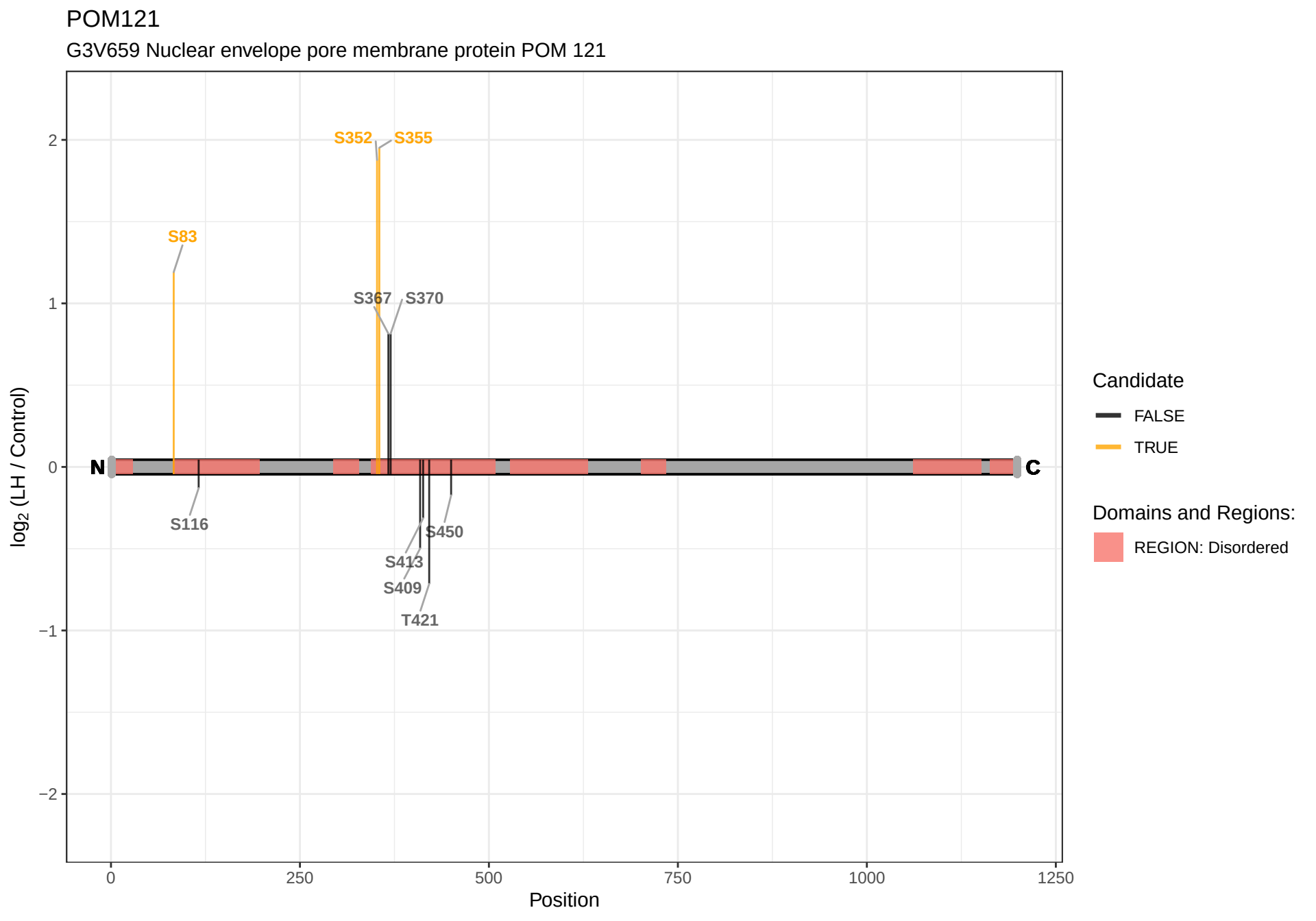

PLXNC1
D4A7M0 Plexin C1
S984
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Sema


PNN
D3ZAY8 Pinin, desmosome−associated protein
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
N
C
S96
S100
S66
S68
S346
S380
S440
S450
S442
S702
S704
S707
S706
T669
S670
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Pinin_SDK_memA
DOMAIN: Pinin_SDK_N
REGION: Disordered


PNPLA6
D3ZRF6 Patatin−like phospholipase domain−containing 6
log2 (LH / Control)
3
2
1
0
−1
−2
−3
S89
S1318
N
C
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Cyclic nucleotide−binding
DOMAIN: PNPLA
REGION: Disordered

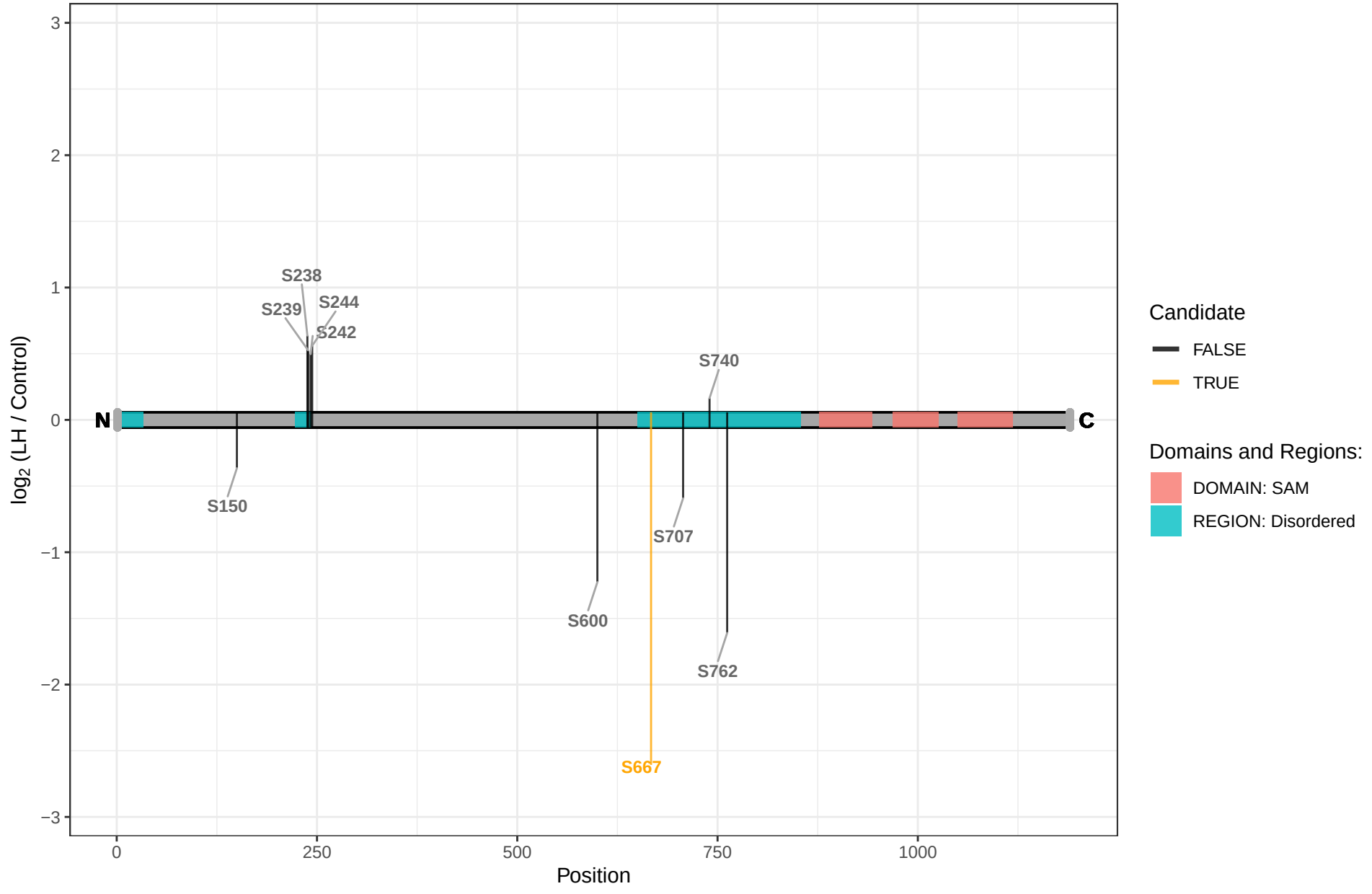

POLA1
F1LRJ6 DNA polymerase
S139
N
C
log2 (LH / Control)
Position
3
2
1
0
−1
−2
−3
0
500
1000
Candidate
TRUE
Domains and Regions:
DOMAIN: DNA_pol_alpha_N
DOMAIN: DNA_pol_B
DOMAIN: DNA_pol_B_exo1
DOMAIN: zf−DNA_Pol
REGION: Disordered

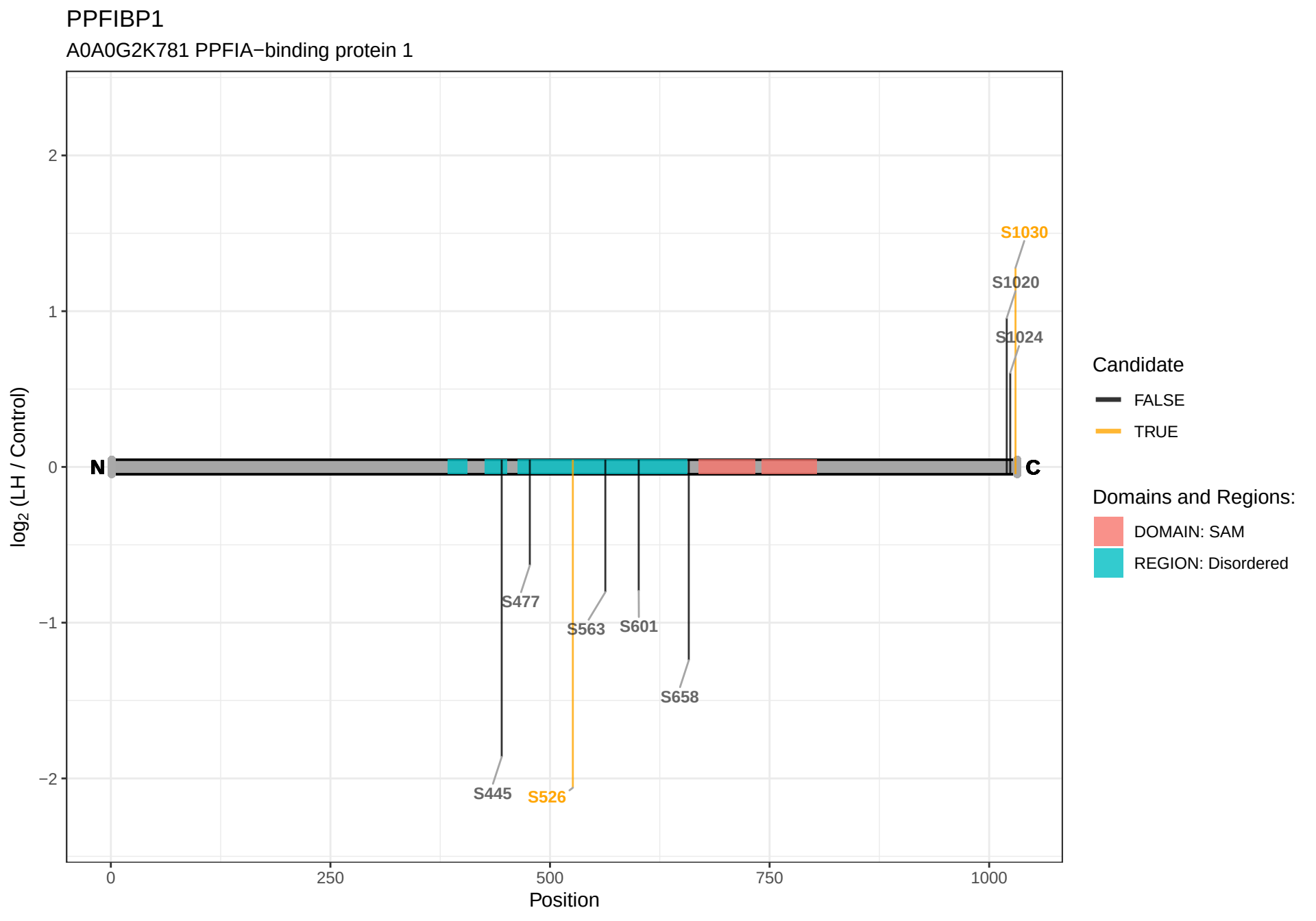

POLR1A
G3V7B7 DNA−directed RNA polymerase subunit
S1486
S1471
S1436
N
C
2
0
−2
0
500
1000
1500
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RPOLA_N
REGION: Disordered

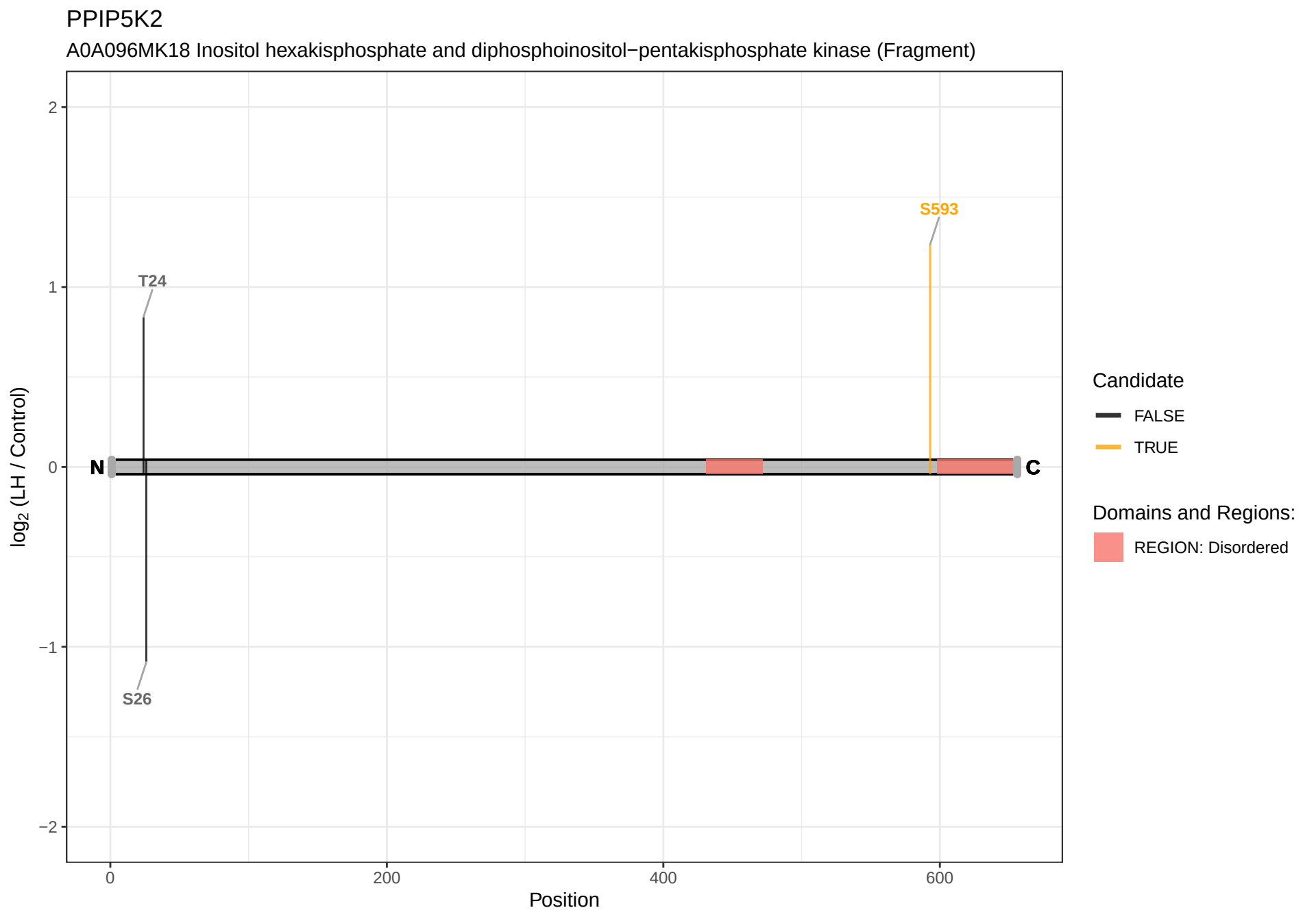

POM121
G3V659 Nuclear envelope pore membrane protein POM 121
S352
S355
S83
S367
S370
S116
S450
S413
S409
T421
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
250
500
750
1000
1250
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

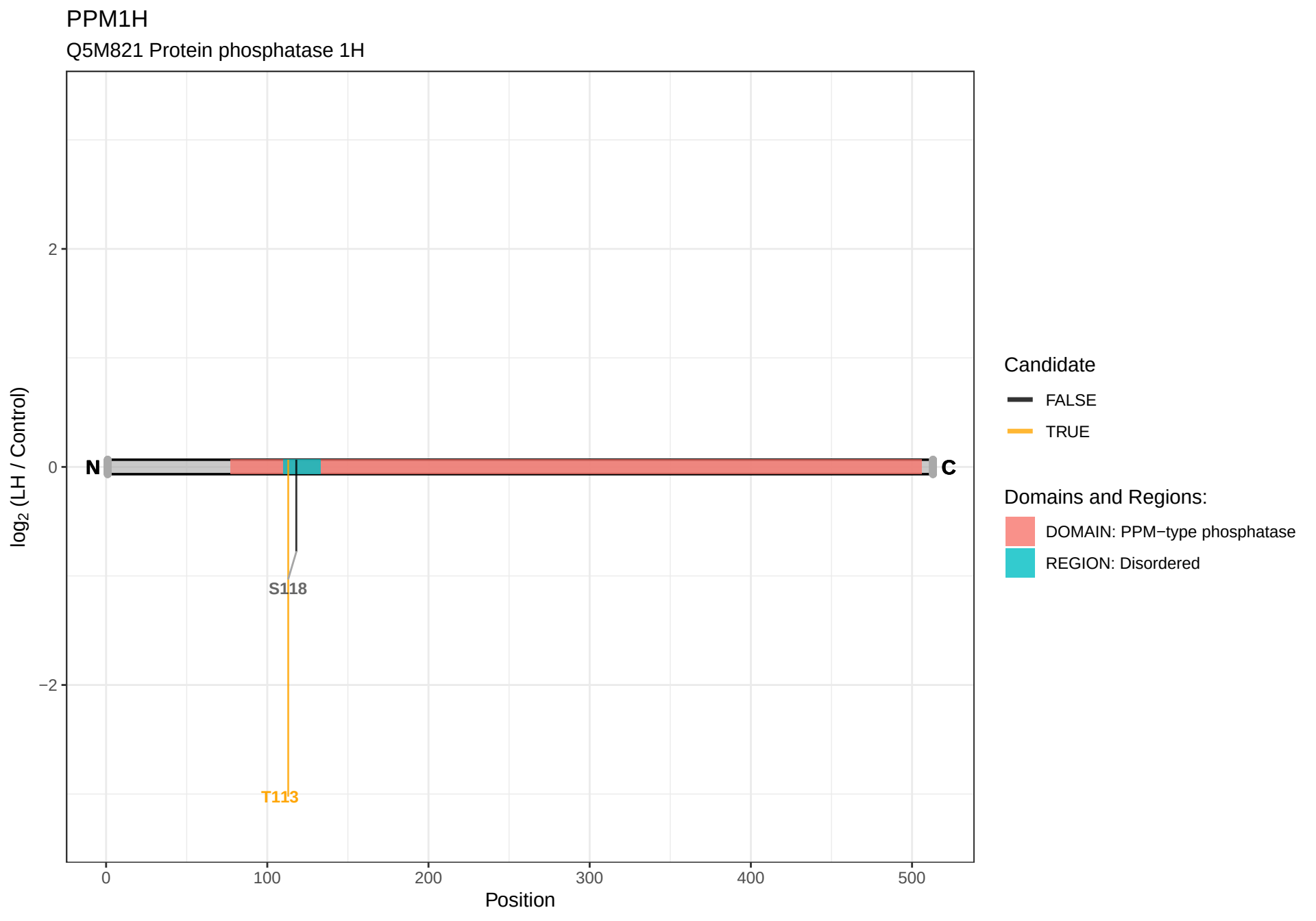
PPFIA1

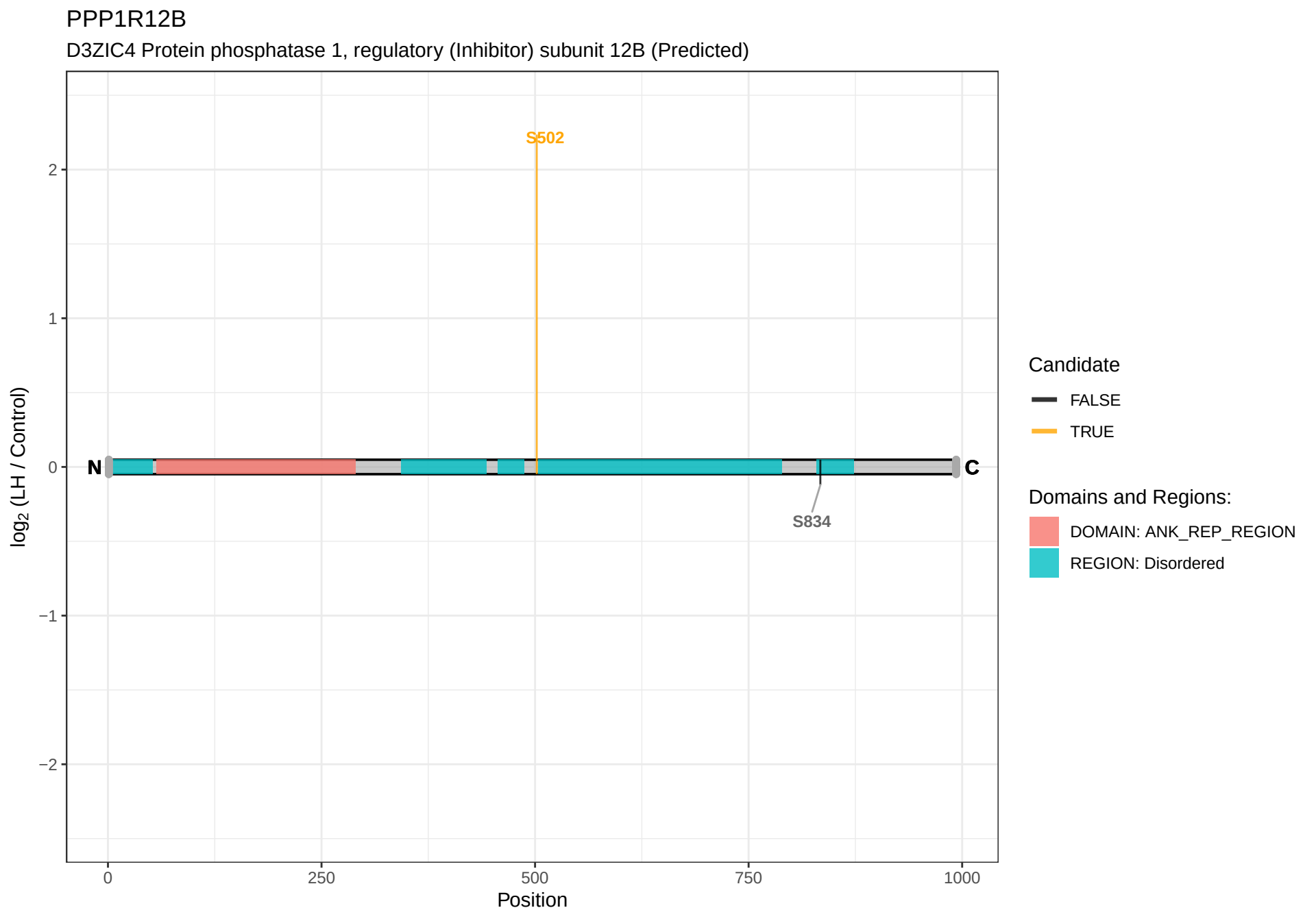
D3ZZ81 PTPRF−interacting protein alpha 1

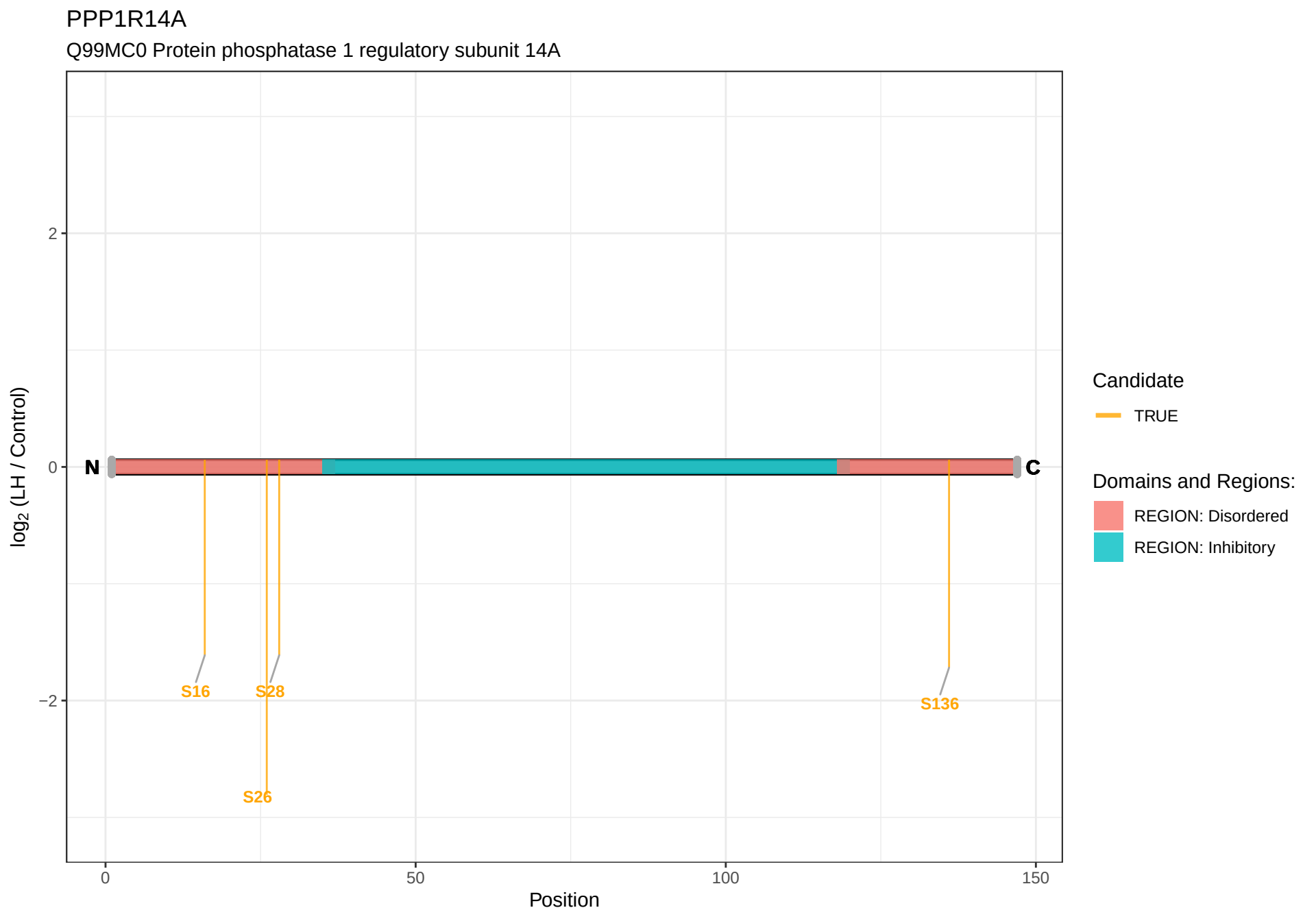


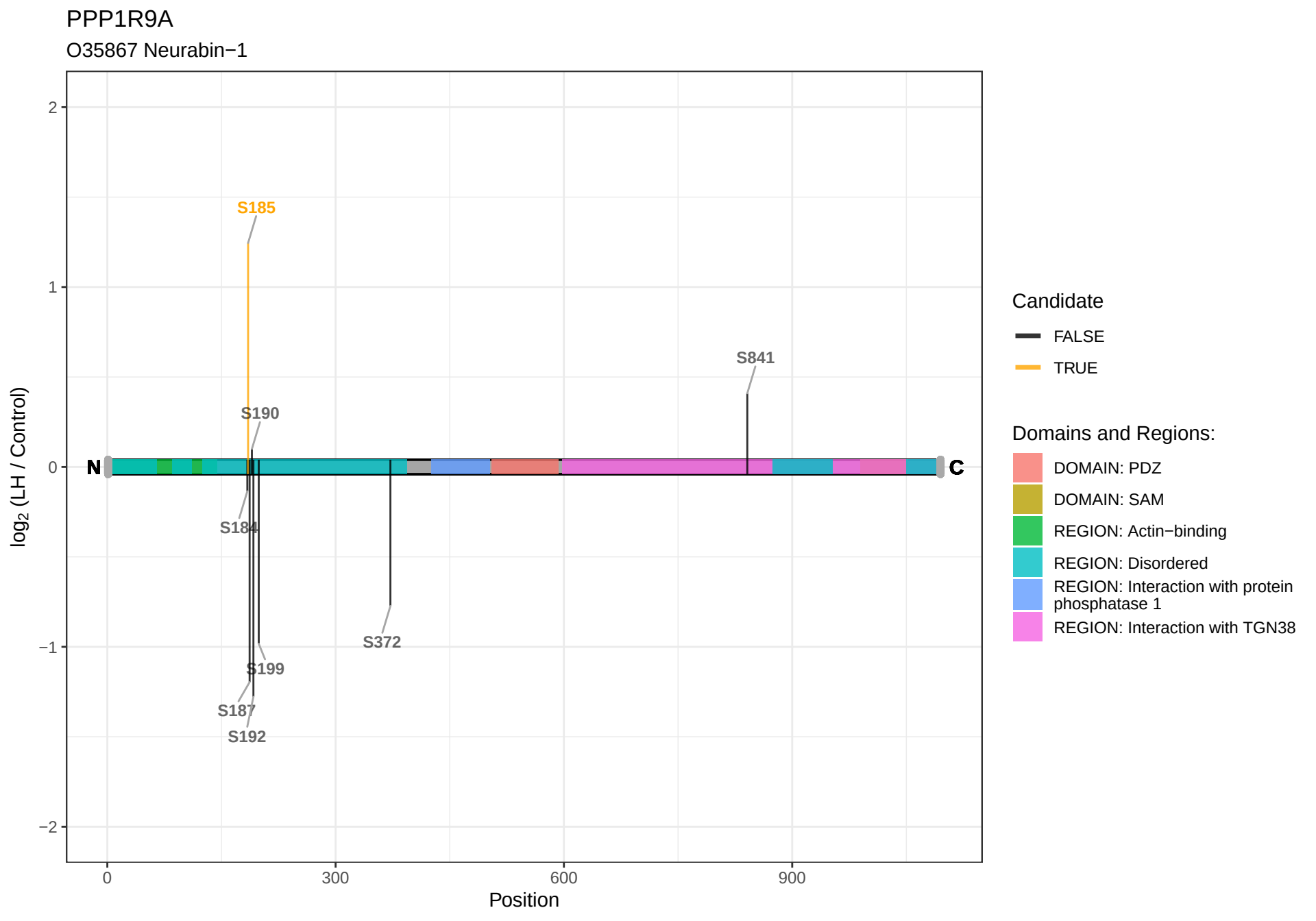

PPFIBP1
A0A0G2K781 PPFIA−binding protein 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S1030
S1020
S1024
S477
S563
S601
S658
S445
S526
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SAM
REGION: Disordered

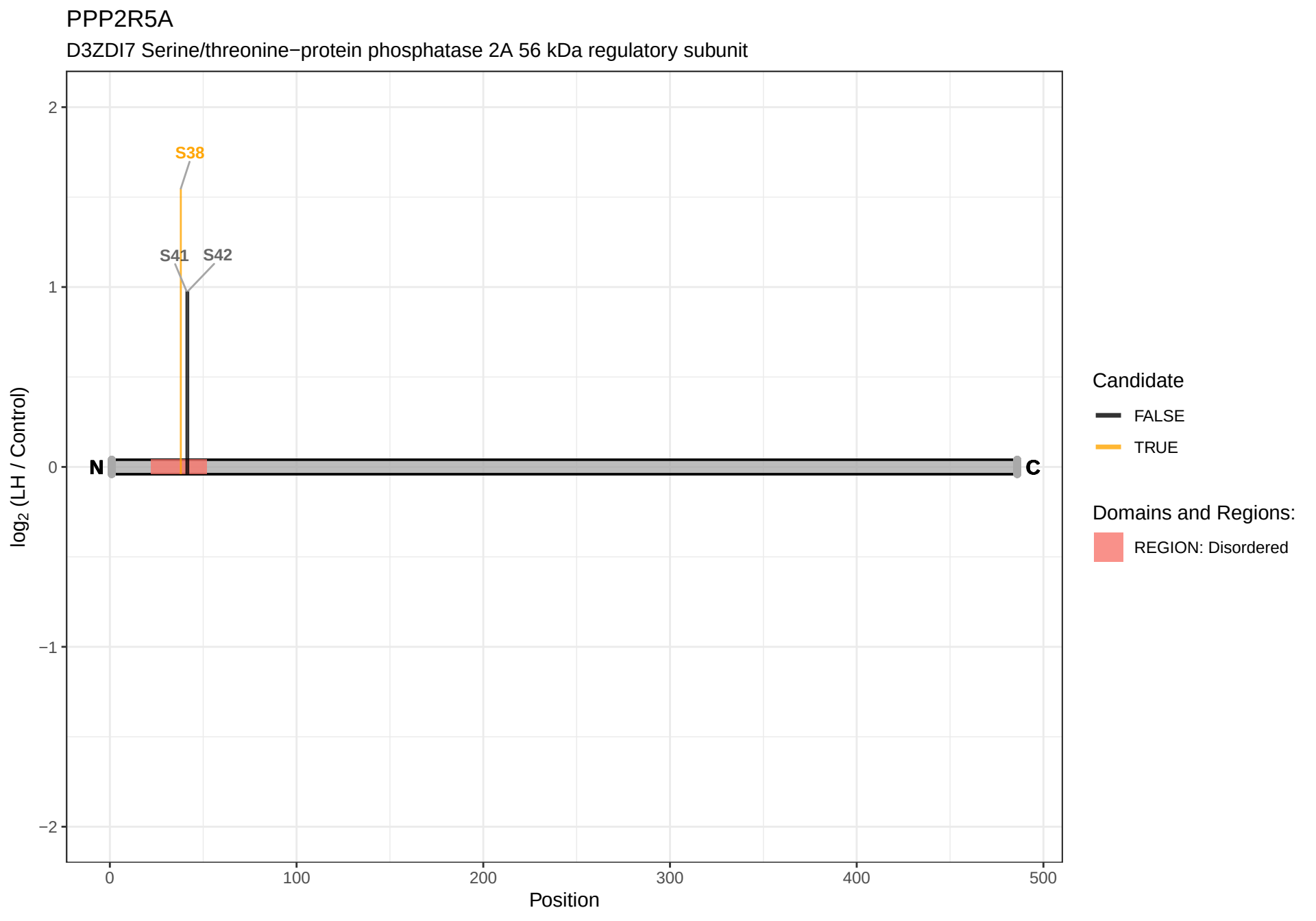

PPIP5K2
A0A096MK18 Inositol hexakisphosphate and diphosphoinositol−pentakisphosphate kinase (Fragment)
log2 (LH / Control)
2
1
0
−1
−2
T24
S26
S593
N
C
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

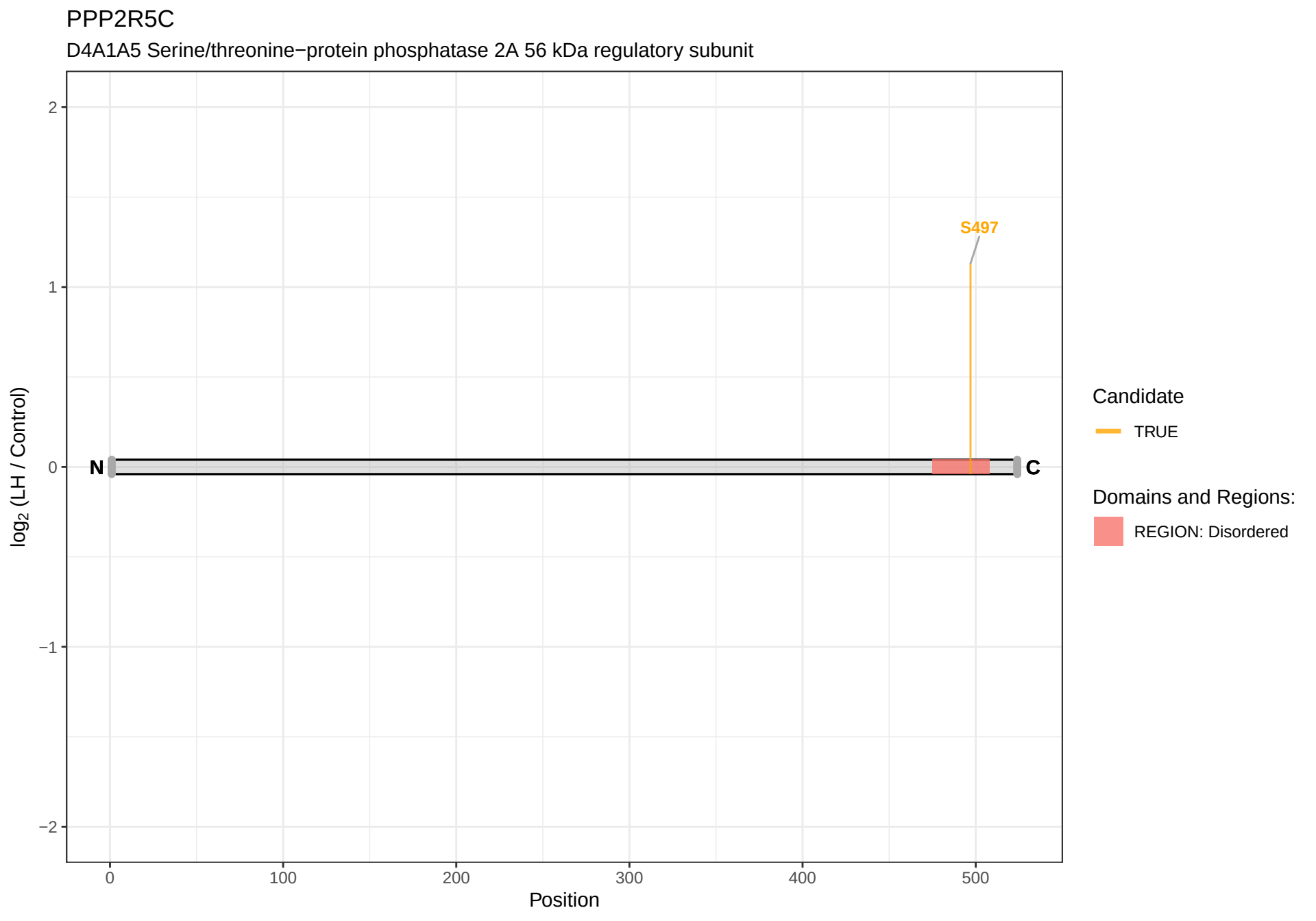

PPM1H
Q5M821 Protein phosphatase 1H
log2 (LH / Control)
2
0
−2
N
C
S118
T113
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PPM−type phosphatase
REGION: Disordered

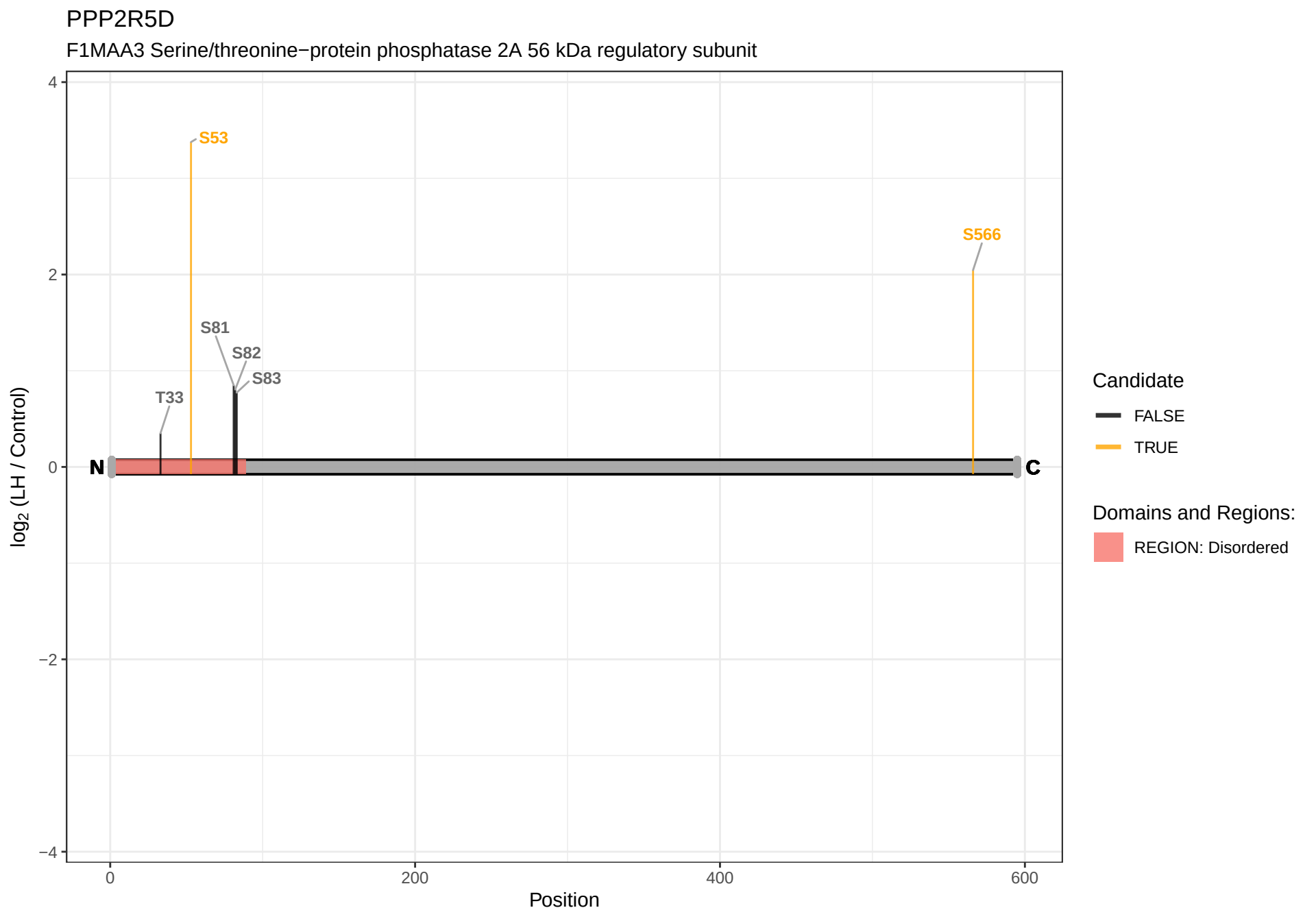

PPP1R12B
D3ZIC4 Protein phosphatase 1, regulatory (Inhibitor) subunit 12B (Predicted)
S502
S834
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ANK_REP_REGION
REGION: Disordered

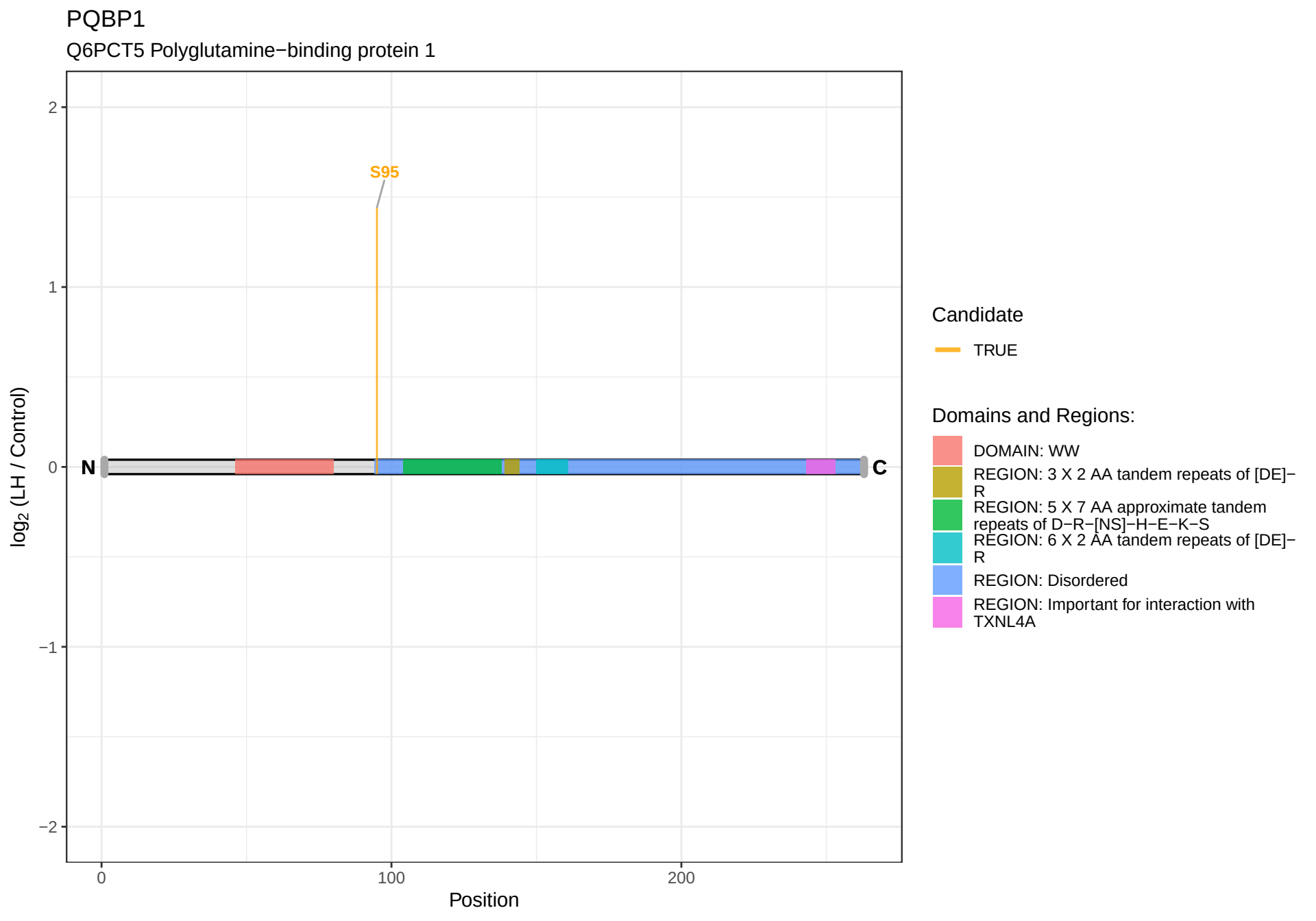

PPP1R14A
Q99MC0 Protein phosphatase 1 regulatory subunit 14A
log2 (LH / Control)
2
0
−2
N
C
S16
S28
S26
S136
0
50
100
150
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered
REGION: Inhibitory

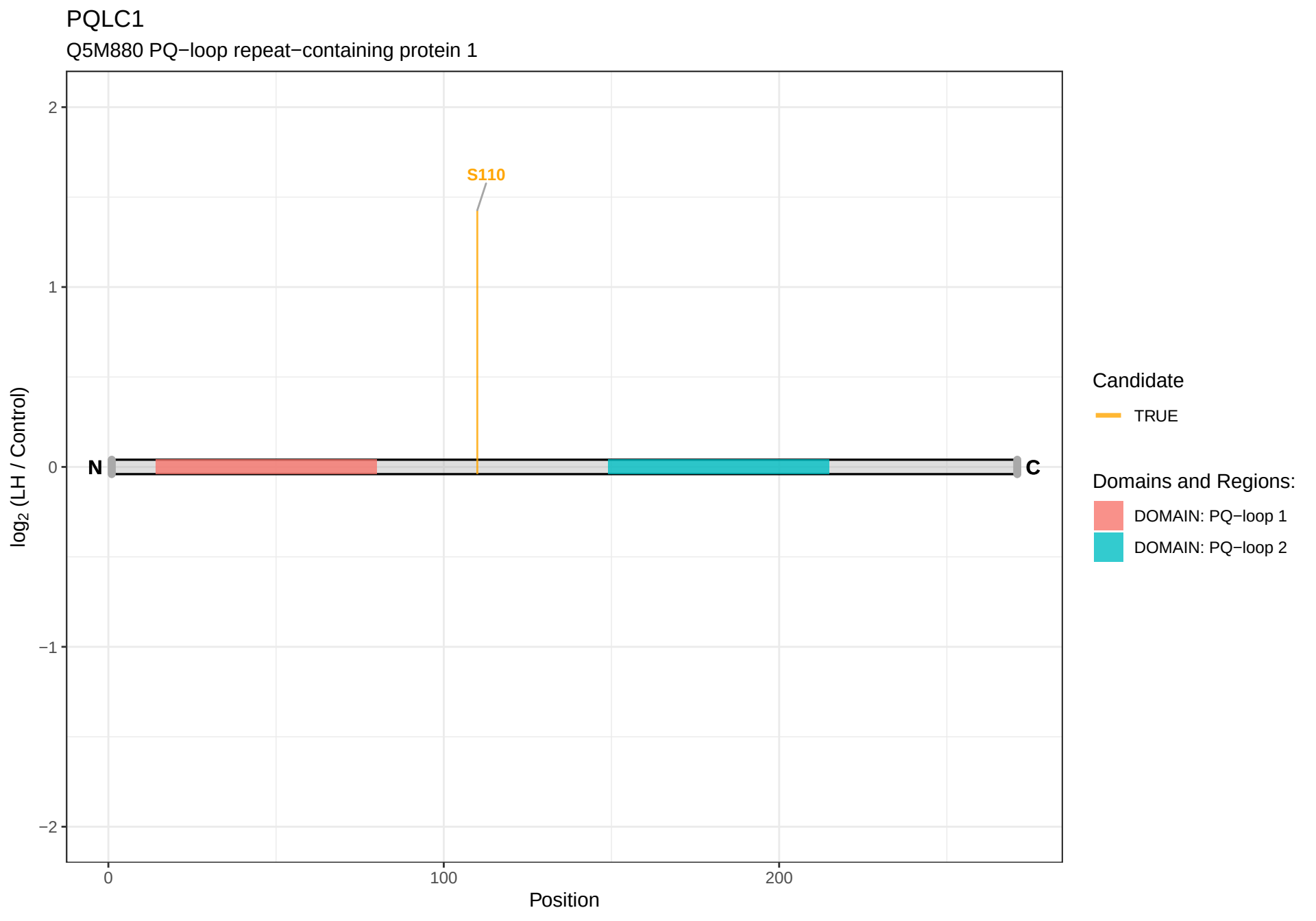

PPP1R9A
O35867 Neurabin−1
log2 (LH / Control)
2
1
0
−1
−2
0
300
600
900
Position
N
C
S185
S190
S184
S187
S192
S199
S372
S841
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PDZ
DOMAIN: SAM
REGION: Actin−binding
REGION: Disordered
REGION: Interaction with protein phosphatase 1
REGION: Interaction with TGN38

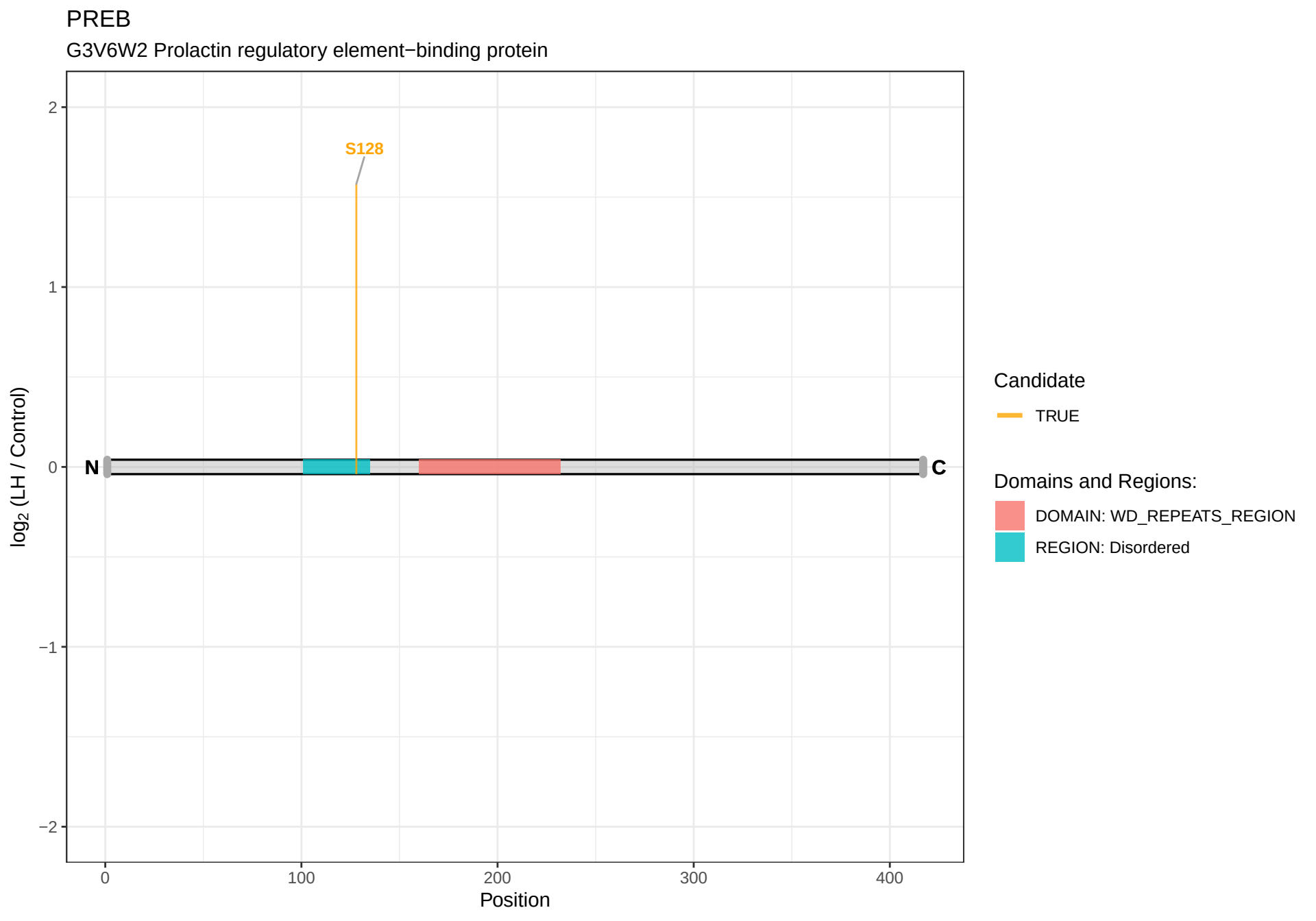

PPP2R5A
D3ZDI7 Serine/threonine−protein phosphatase 2A 56 kDa regulatory subunit
S38
S41
S42
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

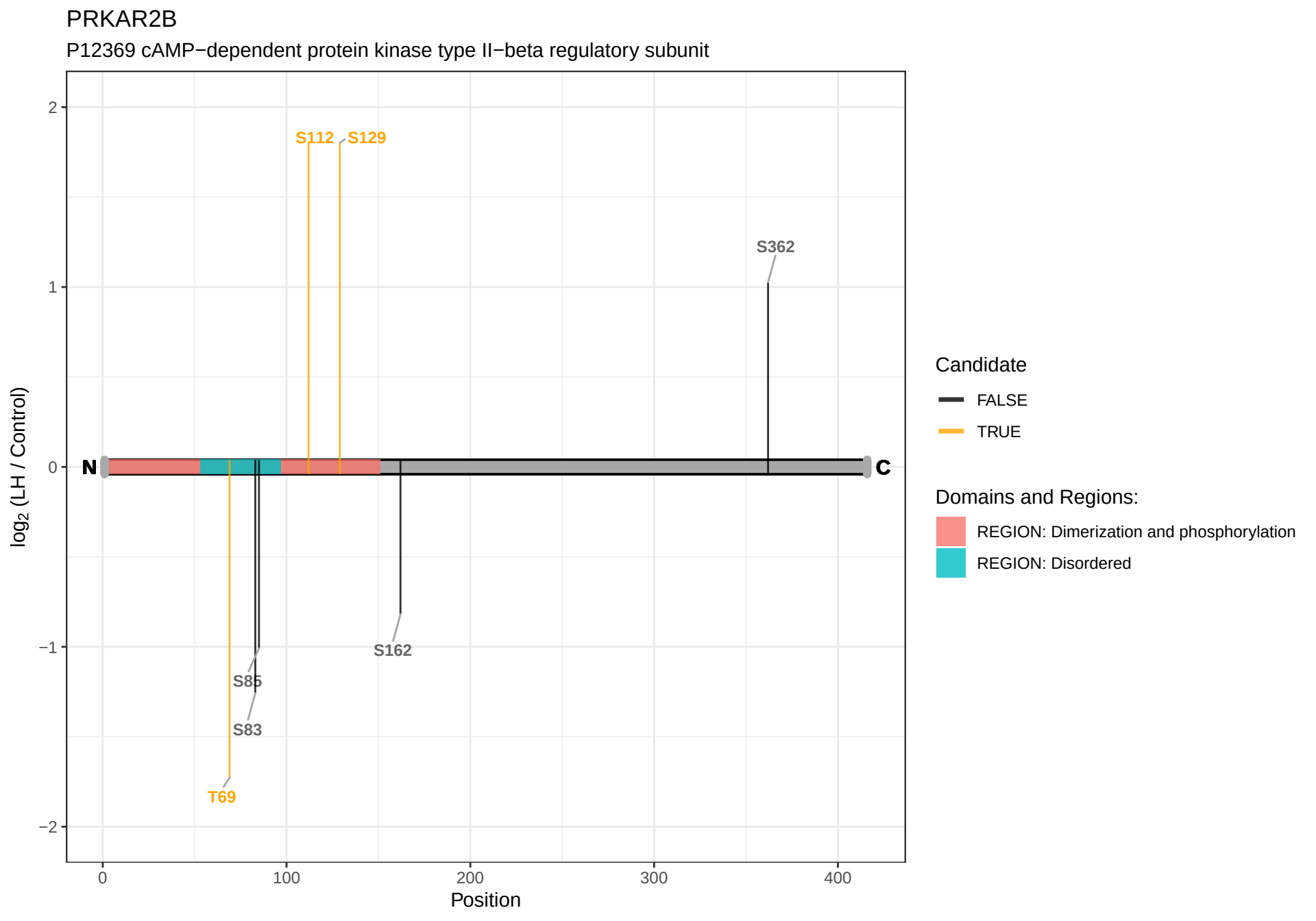

PPP2R5C
D4A1A5 Serine/threonine−protein phosphatase 2A 56 kDa regulatory subunit
S497
N
C
log2 (LH / Control)
Position
0
100
200
300
400
500
2
1
0
−1
−2
Candidate
TRUE
Domains and Regions:
REGION: Disordered

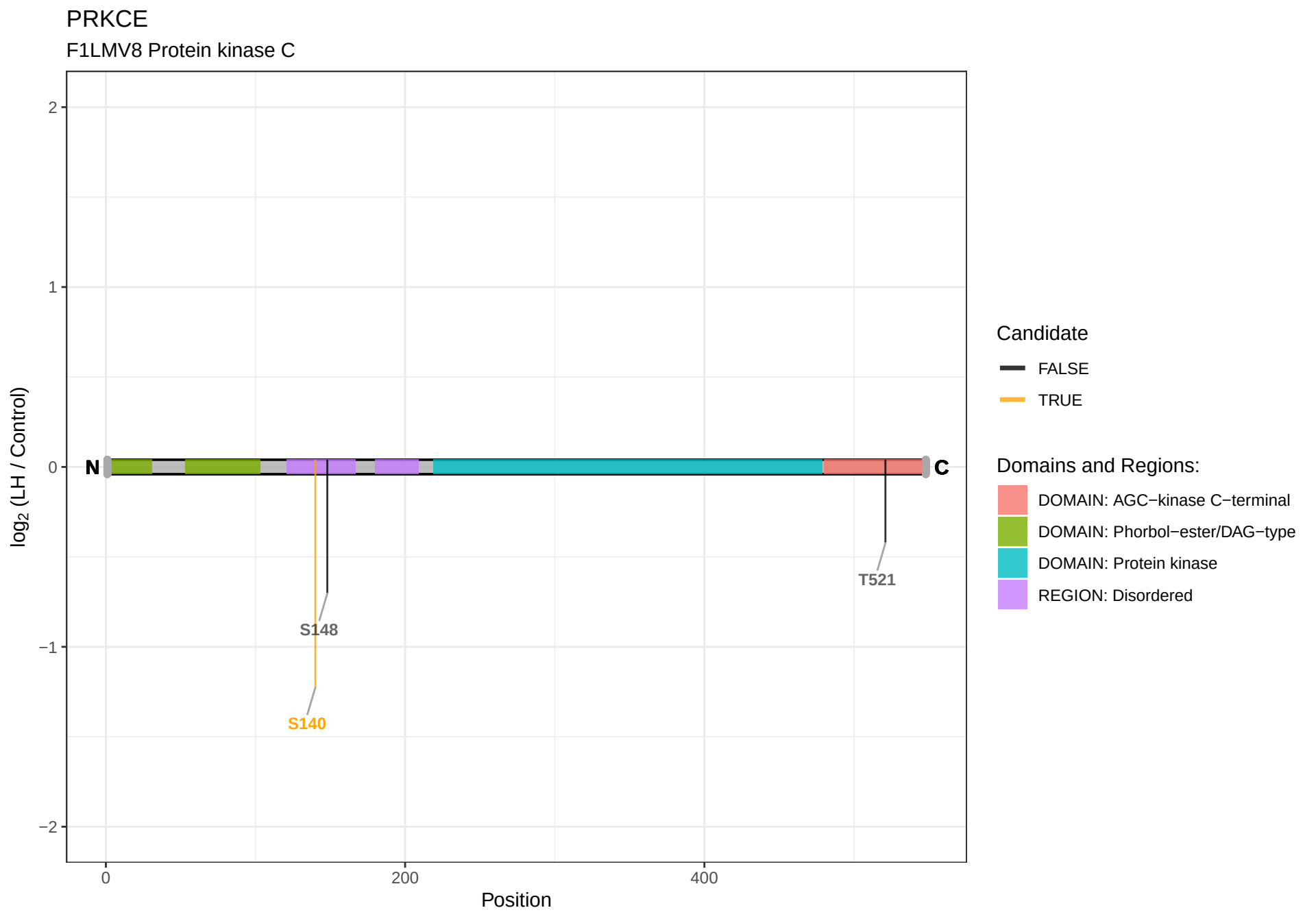

PPP2R5D
F1MAA3 Serine/threonine−protein phosphatase 2A 56 kDa regulatory subunit
log2 (LH / Control)
4
2
0
−2
−4
S53
S566
S81
S82
S83
T33
N
C
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

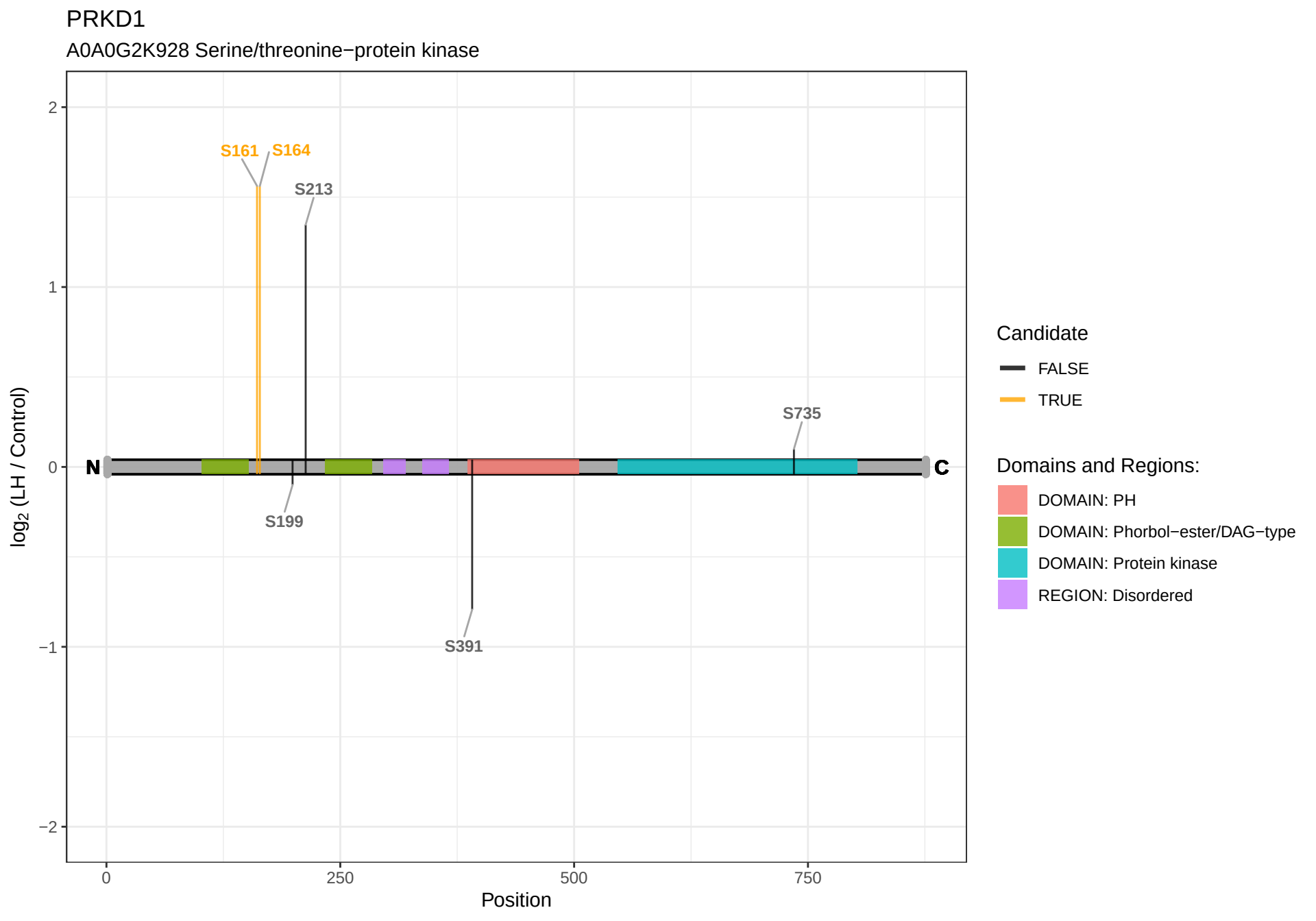

PQBP1
Q6PCT5 Polyglutamine−binding protein 1
S95
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
100
200
Candidate
TRUE
Domains and Regions:
DOMAIN: WW
REGION: 3 X 2 AA tandem repeats of [DE]−R
REGION: 5 X 7 AA approximate tandem repeats of D−R−[NS]−H−E−K−S
REGION: 6 X 2 AA tandem repeats of [DE]−R
REGION: Disordered
REGION: Important for interaction with TXNL4A

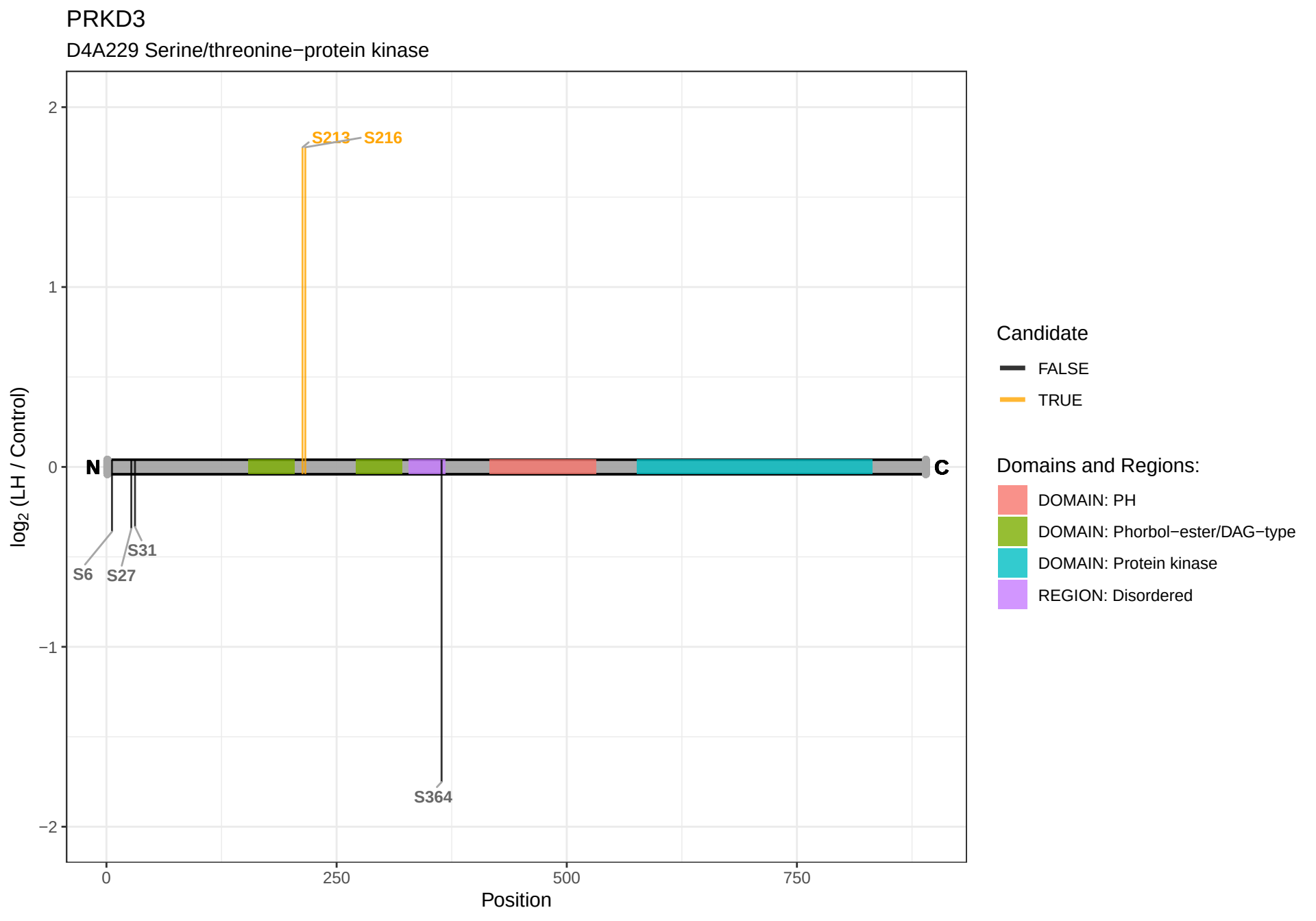

PQLC1
Q5M880 PQ−loop repeat−containing protein 1
S110
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: PQ−loop 1
DOMAIN: PQ−loop 2

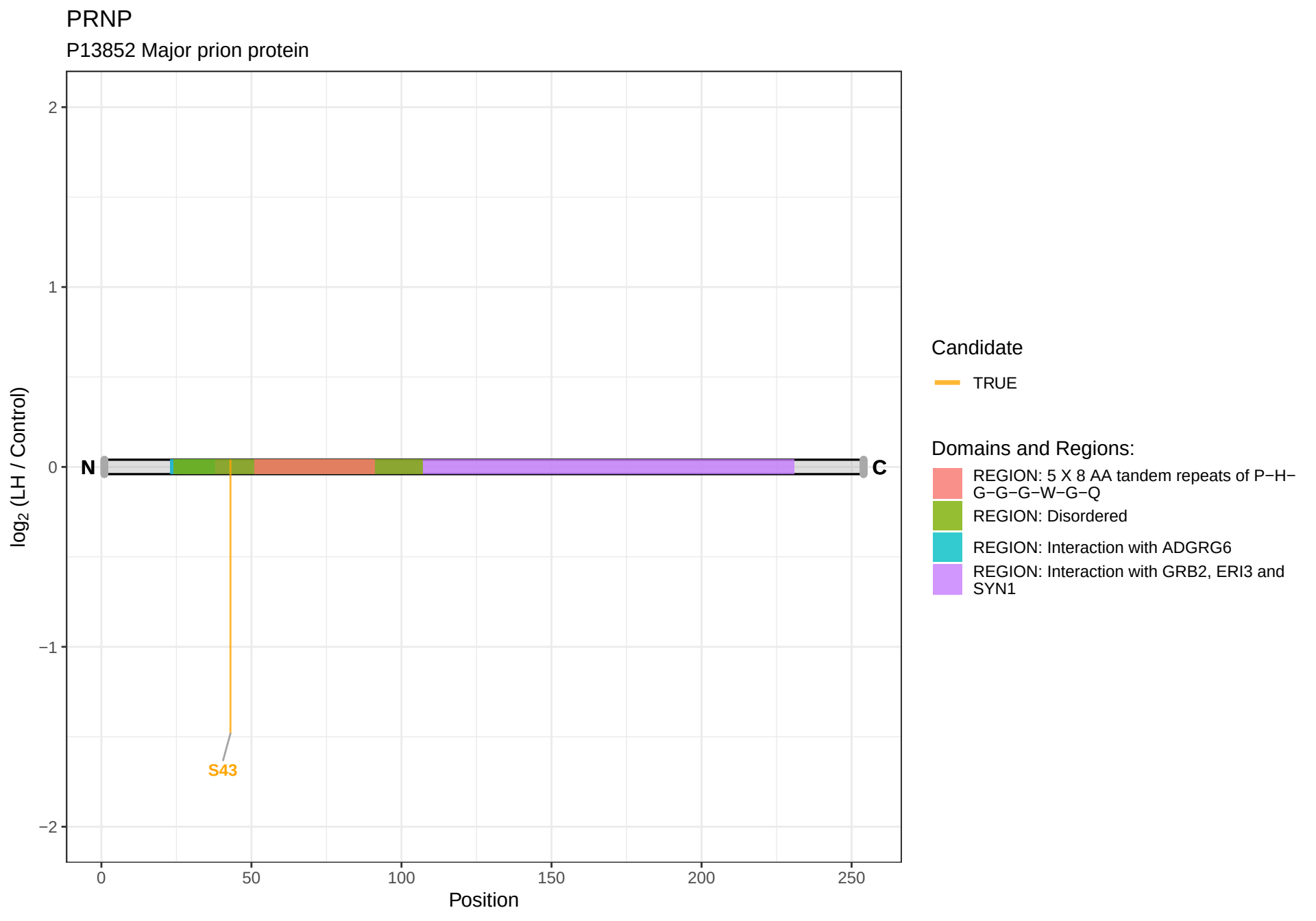

PREB
G3V6W2 Prolactin regulatory element−binding protein
S128
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
100
200
300
400
Candidate
TRUE
Domains and Regions:
DOMAIN: WD_REPEATS_REGION
REGION: Disordered

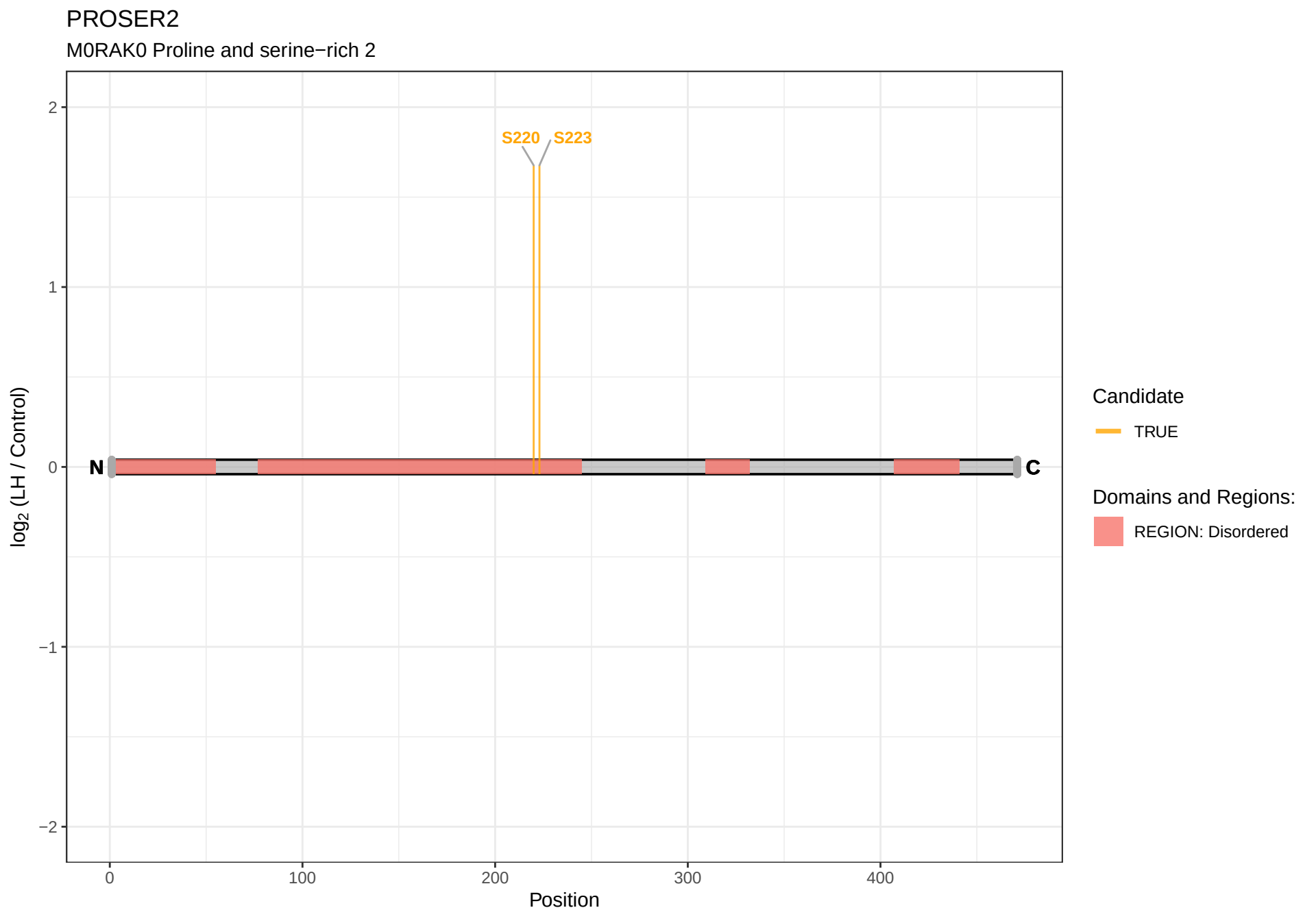

PRKAR2B
P12369 cAMP−dependent protein kinase type II−beta regulatory subunit
log2 (LH / Control)
2
1
0
−1
−2
S112
S129
S362
N
C
S162
S85
S83
T69
0
100
200
300
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Dimerization and phosphorylation
REGION: Disordered

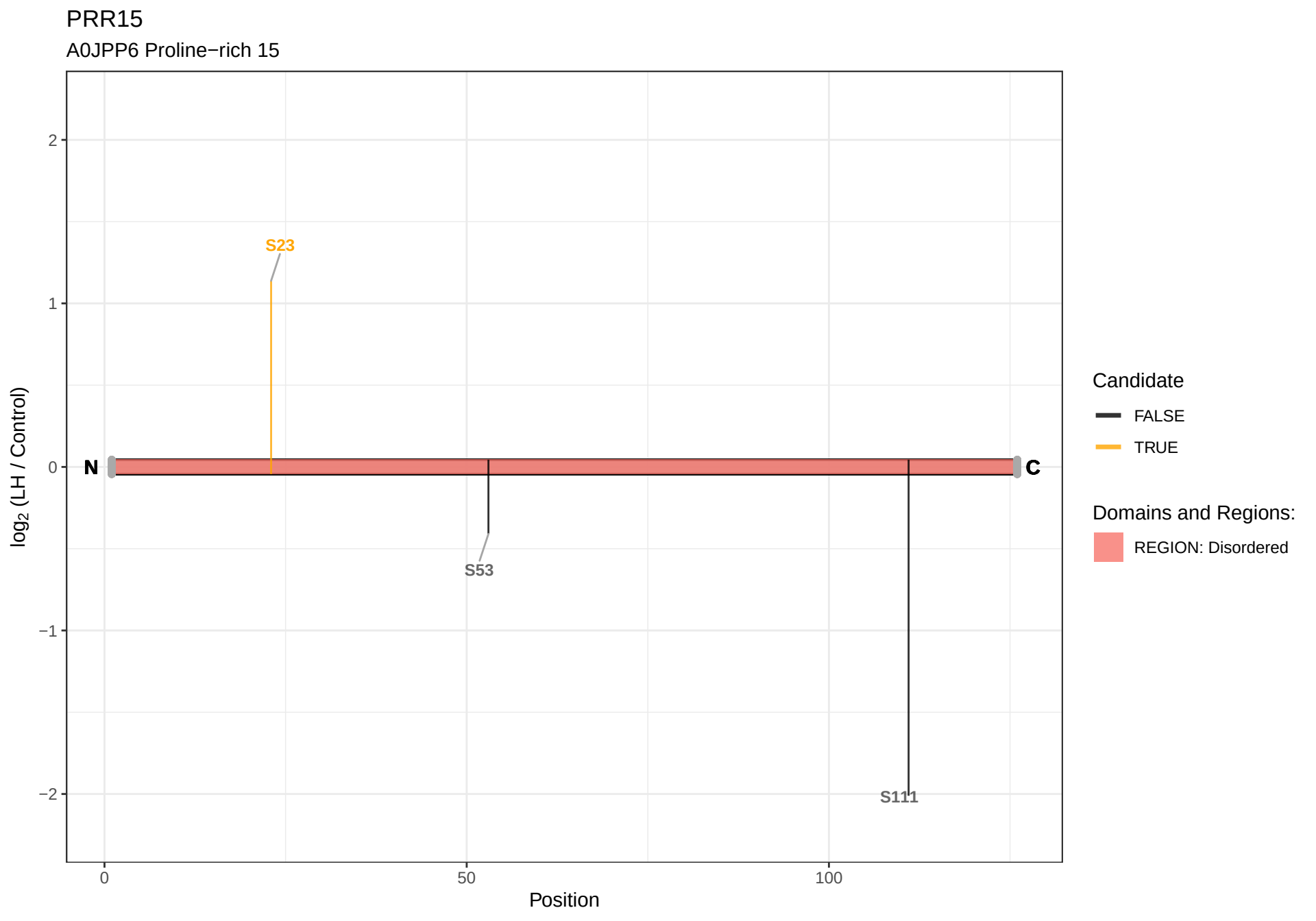

PRKCE
F1LMV8 Protein kinase C
log2 (LH / Control)
2
1
0
−1
−2
N
C
S148
S140
T521
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AGC−kinase C−terminal
DOMAIN: Phorbol−ester/DAG−type
DOMAIN: Protein kinase
REGION: Disordered

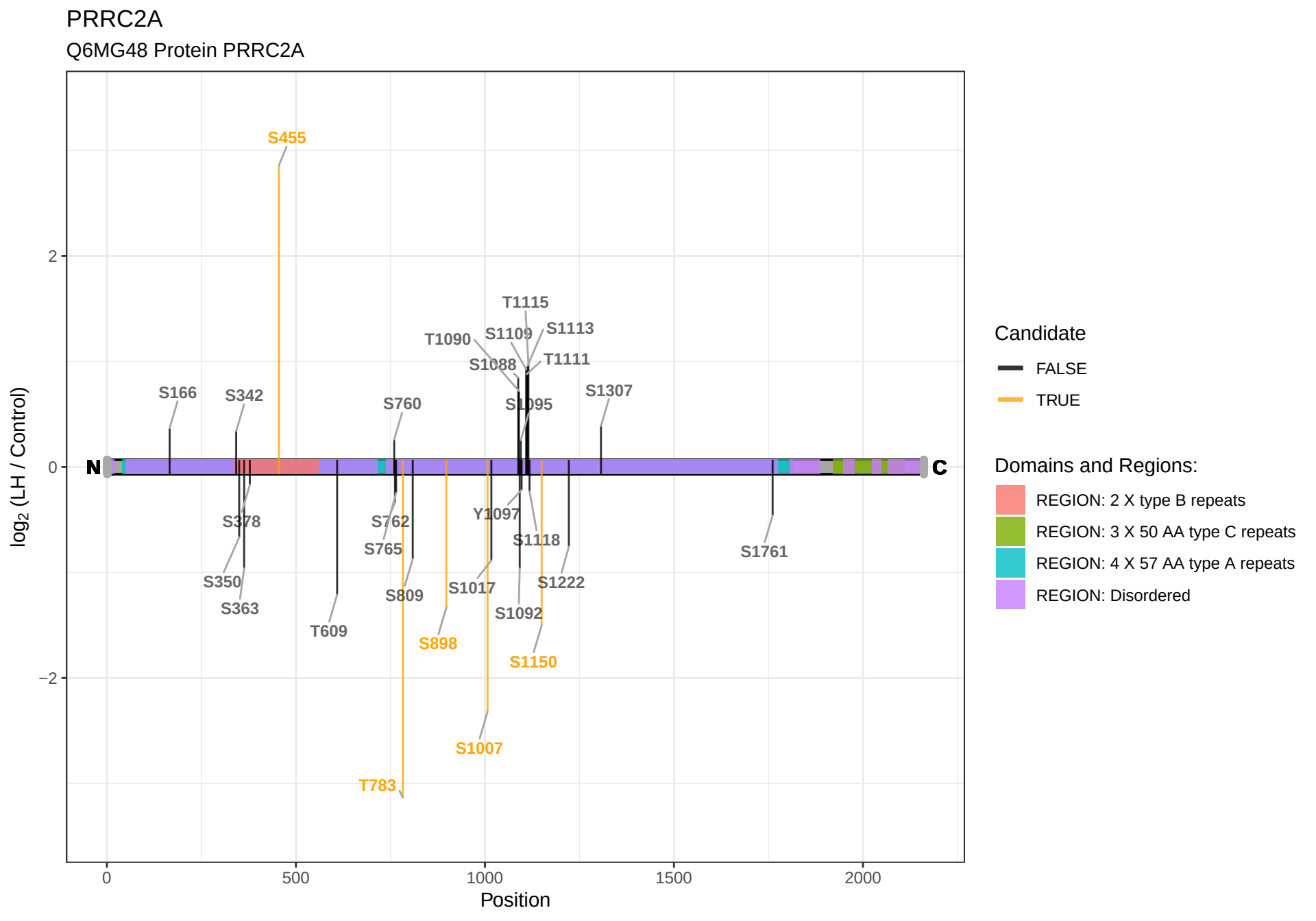

PRKD1
A0A0G2K928 Serine/threonine−protein kinase
S161
S164
S213
S735
S199
S391
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PH
DOMAIN: Phorbol−ester/DAG−type
DOMAIN: Protein kinase
REGION: Disordered

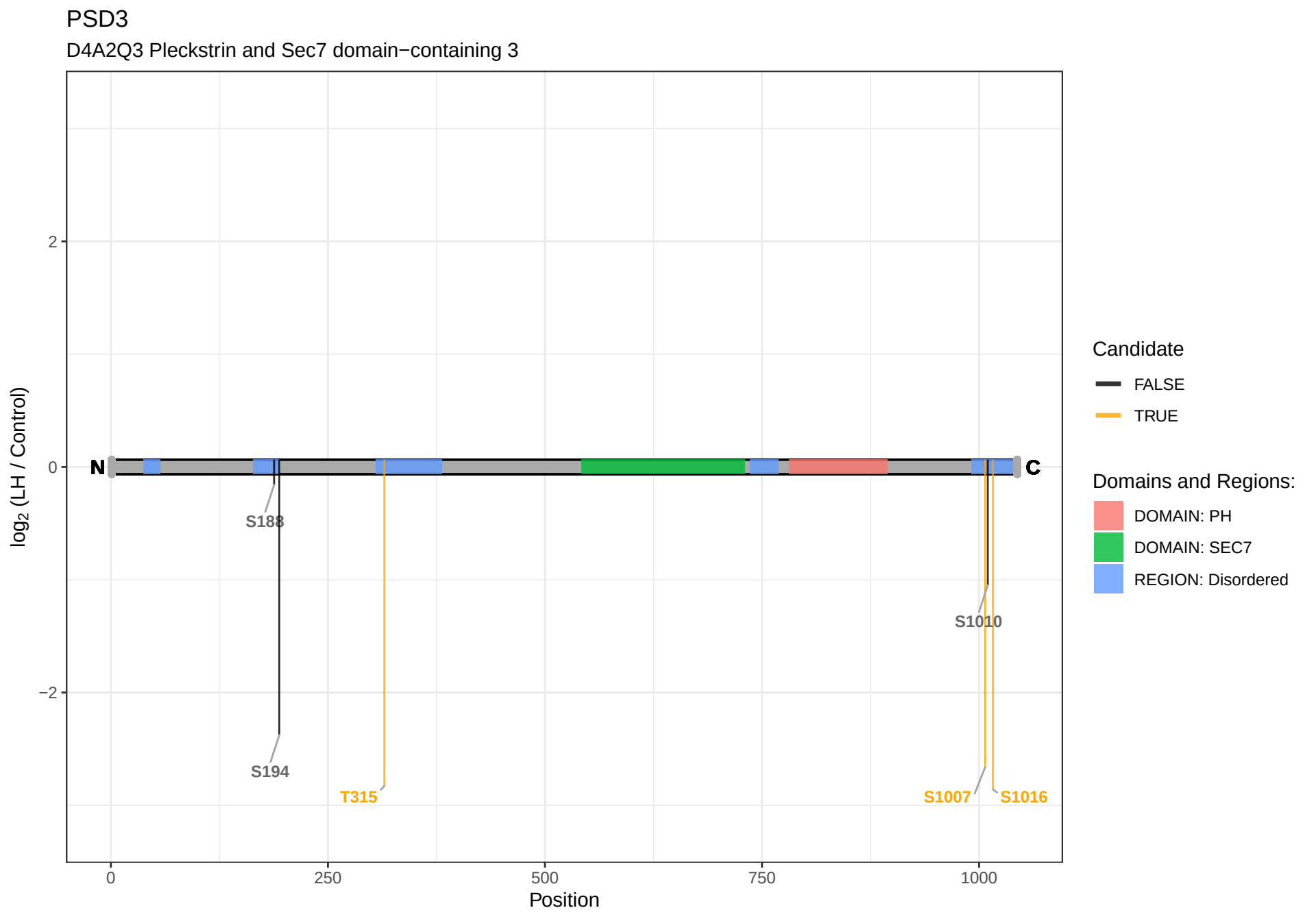

PRKD3
D4A229 Serine/threonine−protein kinase
log2 (LH / Control)
2
1
0
−1
−2
S213
S216
N
C
S6
S27
S31
S364
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PH
DOMAIN: Phorbol−ester/DAG−type
DOMAIN: Protein kinase
REGION: Disordered

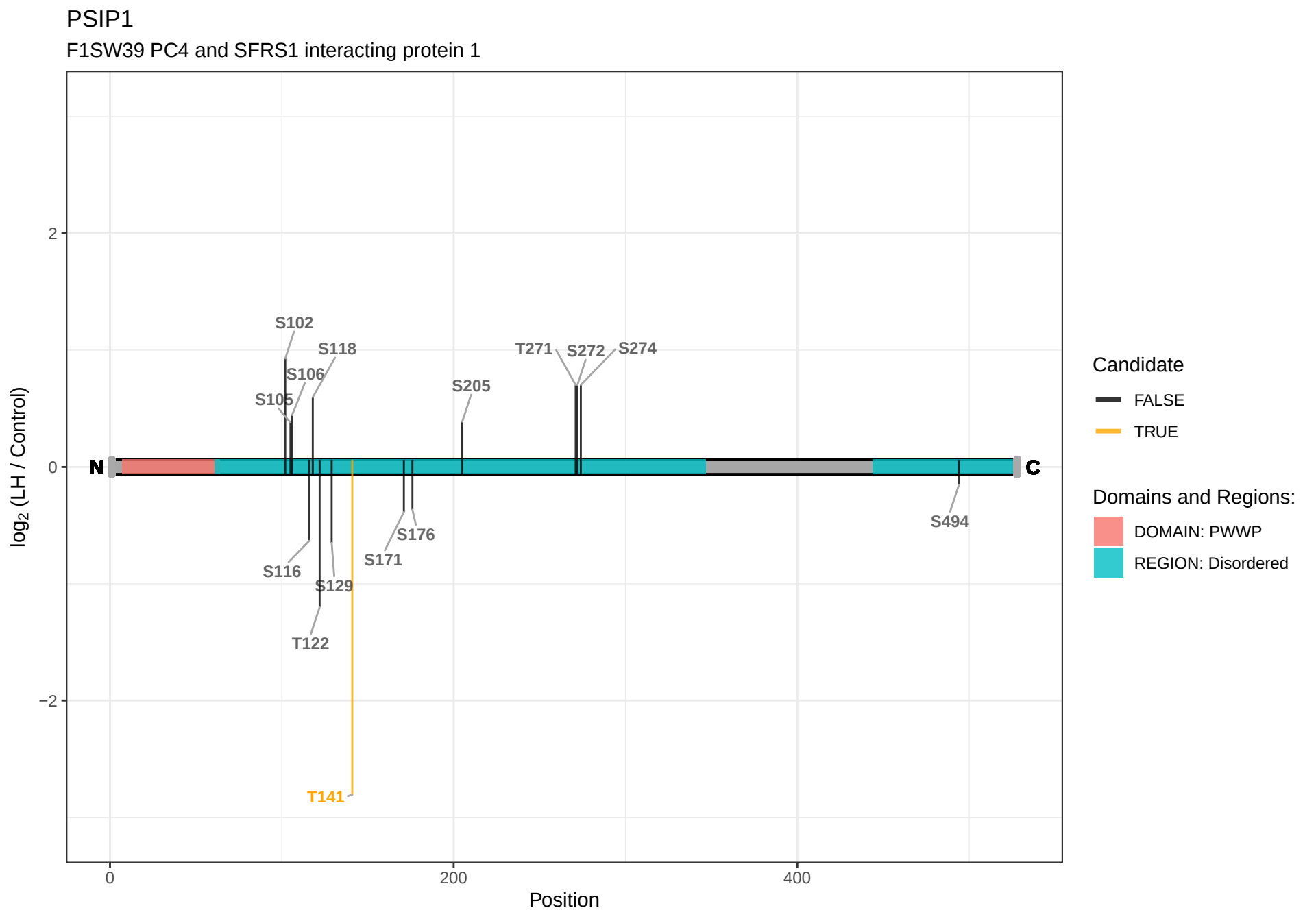

PRNP
P13852 Major prion protein
2
1
0
−1
−2
log2 (LH / Control)
N
C
S43
0
50
100
150
200
250
Position
Candidate
TRUE
Domains and Regions:
REGION: 5 X 8 AA tandem repeats of P−H−G−G−G−W−G−Q
REGION: Disordered
REGION: Interaction with ADGRG6
REGION: Interaction with GRB2, ERI3 and SYN1

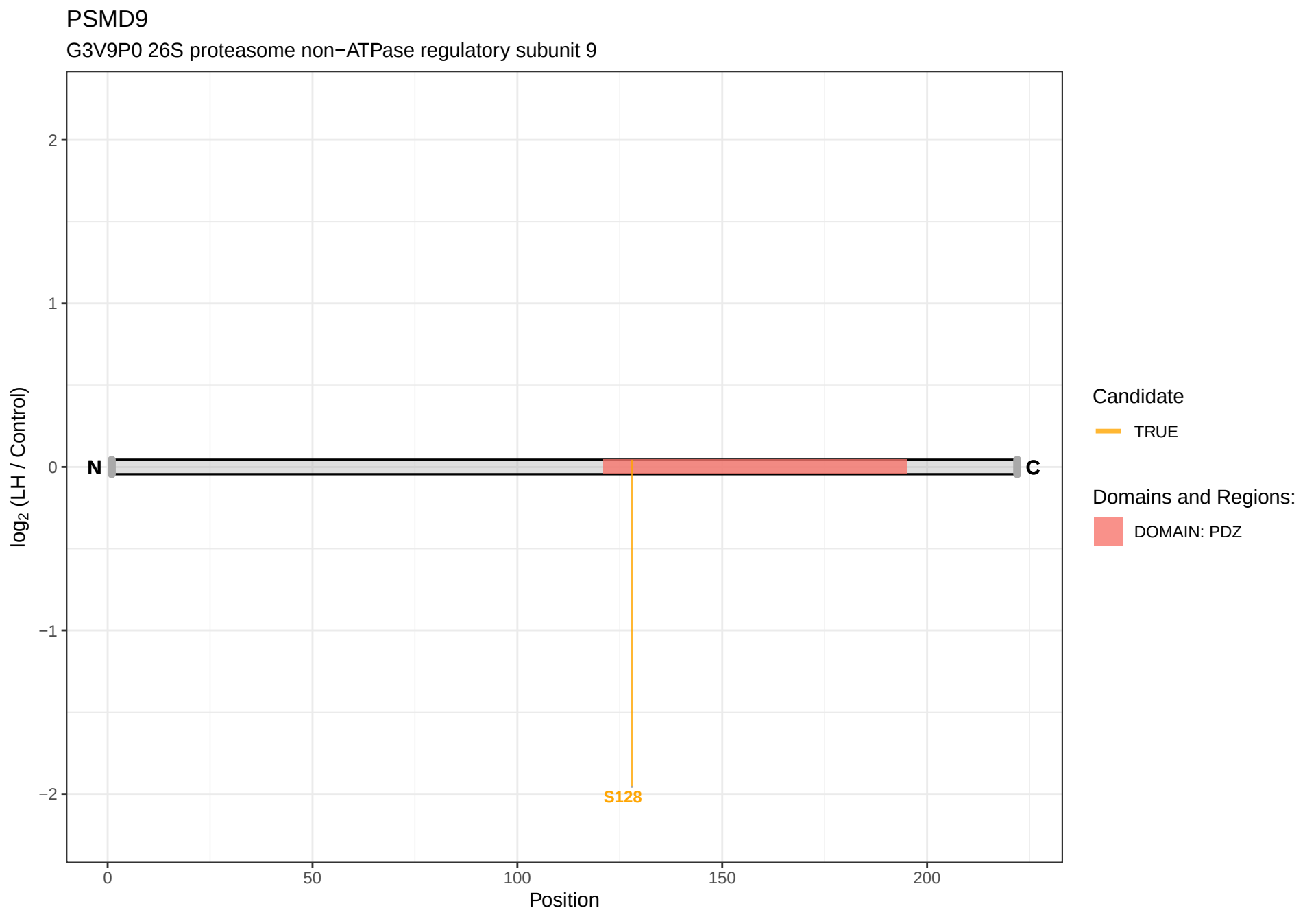

PROSER2
M0RAK0 Proline and serine−rich 2
S220
S223
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
400
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

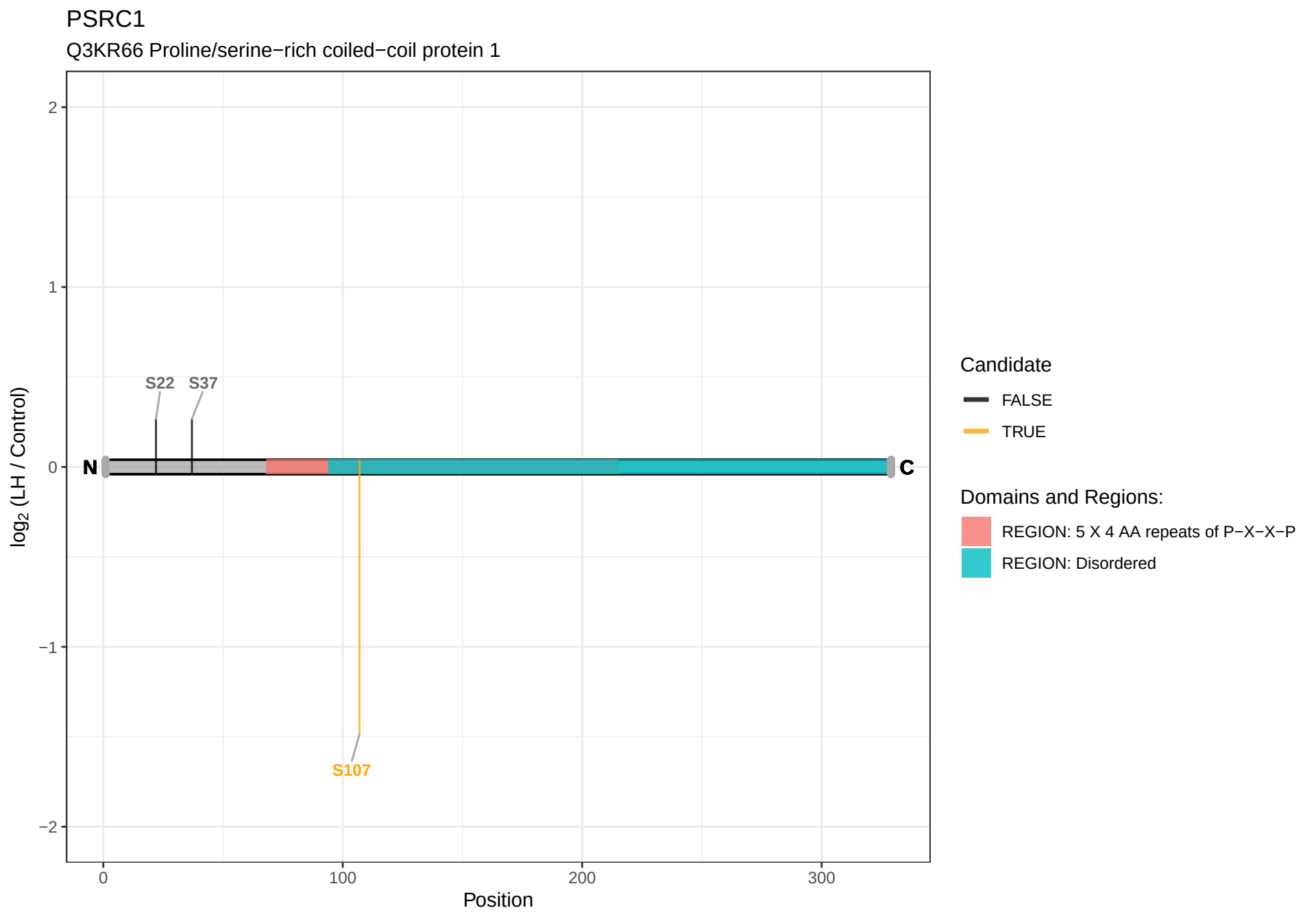

PRR15
A0JPP6 Proline−rich 15
log2 (LH / Control)
2
1
0
−1
−2
S23
S53
S111
N
C
0
50
100
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

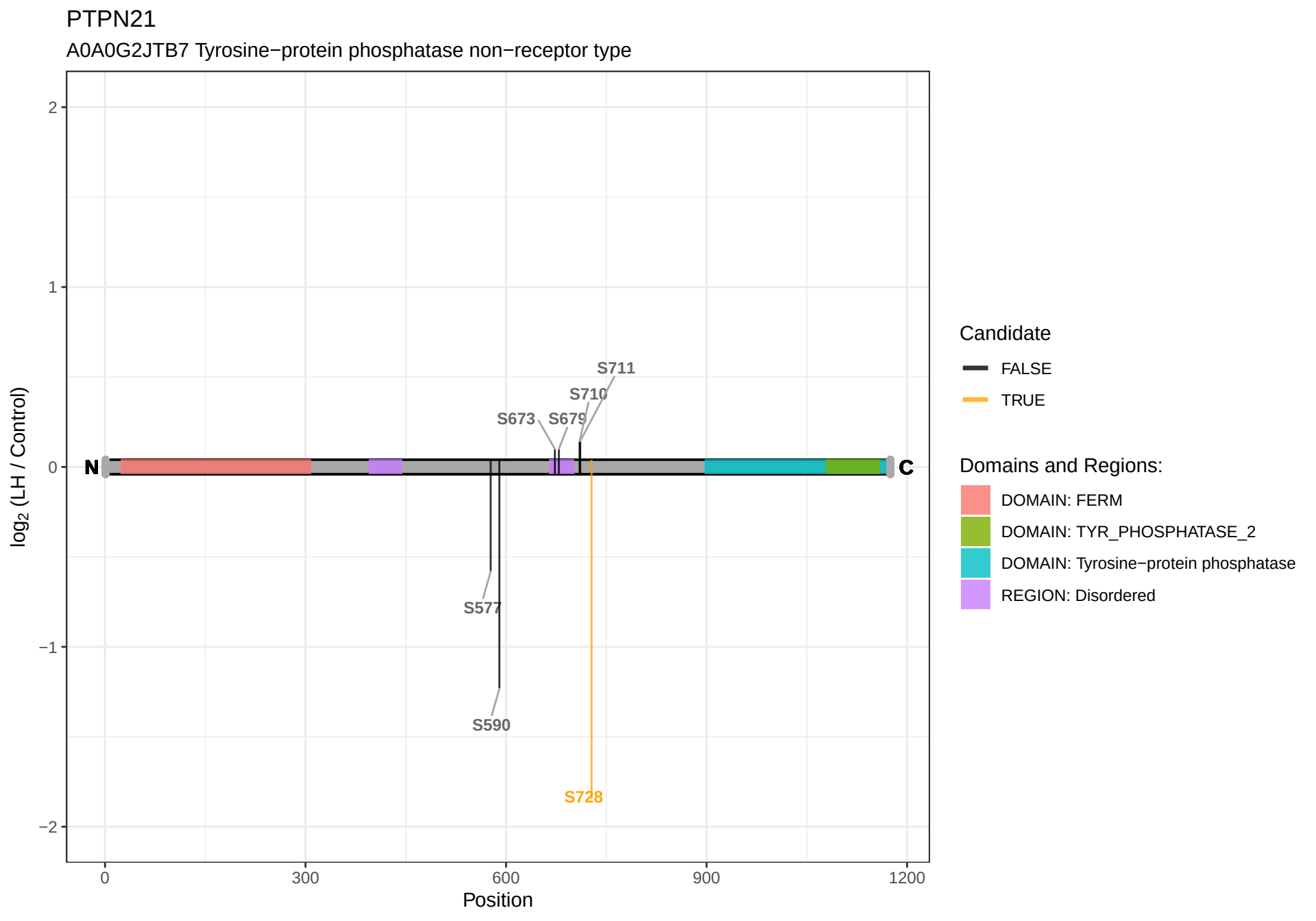

PRRC2A
Q6MG48 Protein PRRC2A
S455
T1115
T1090
S1109
S1113
S1088
T1111
S166
S342
S760
S1095
S1307
N
C
S378
S762
Y1097
S765
S1118
S1761
S350
S809
S1017
S1222
S363
S1092
T609
S898
S1150
S1007
T783
2
0
−2
log2 (LH / Control)
0
500
1000
1500
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: 2 X type B repeats
REGION: 3 X 50 AA type C repeats
REGION: 4 X 57 AA type A repeats
REGION: Disordered

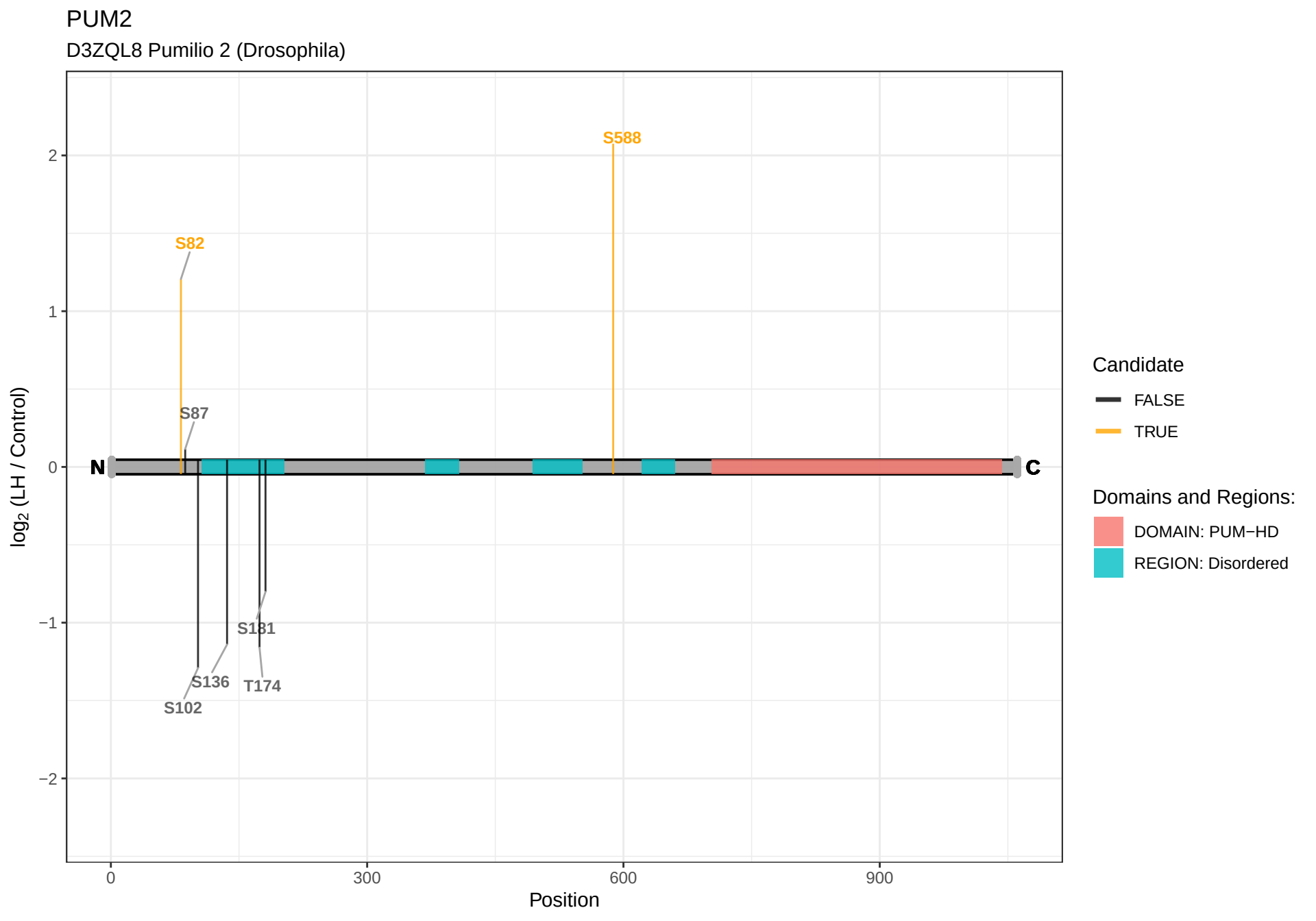

PSD3
D4A2Q3 Pleckstrin and Sec7 domain−containing 3
log2 (LH / Control)
2
0
−2
N
C
S188
S194
T315
S1010
S1007
S1016
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PH
DOMAIN: SEC7
REGION: Disordered

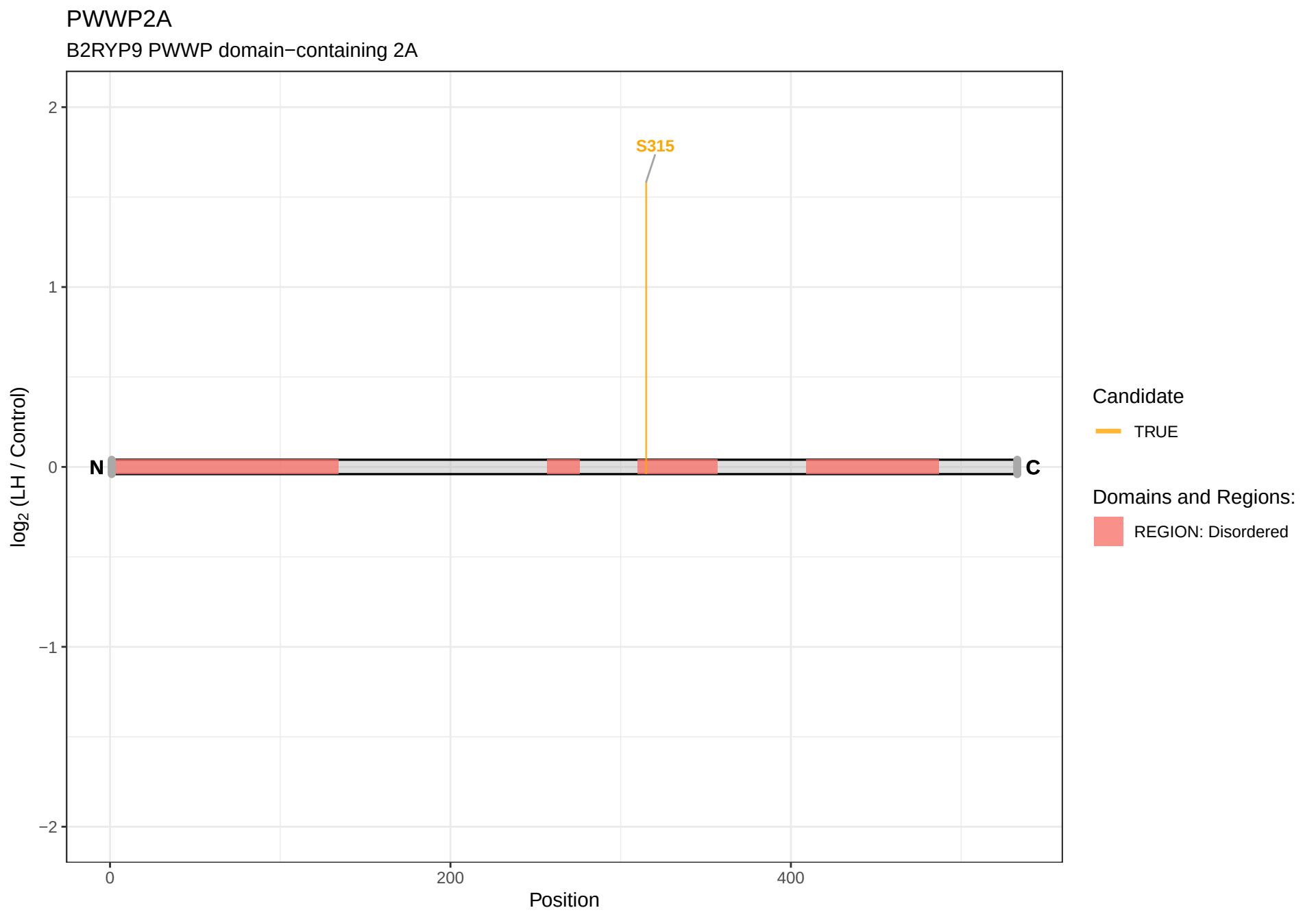

PSIP1
F1SW39 PC4 and SFRS1 interacting protein 1
log2 (LH / Control)
2
0
−2
0
200
400
Position
N
C
S102
S118
S106
S105
S205
T271
S272
S274
S494
S176
S171
S116
S129
T122
T141
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PWWP
REGION: Disordered

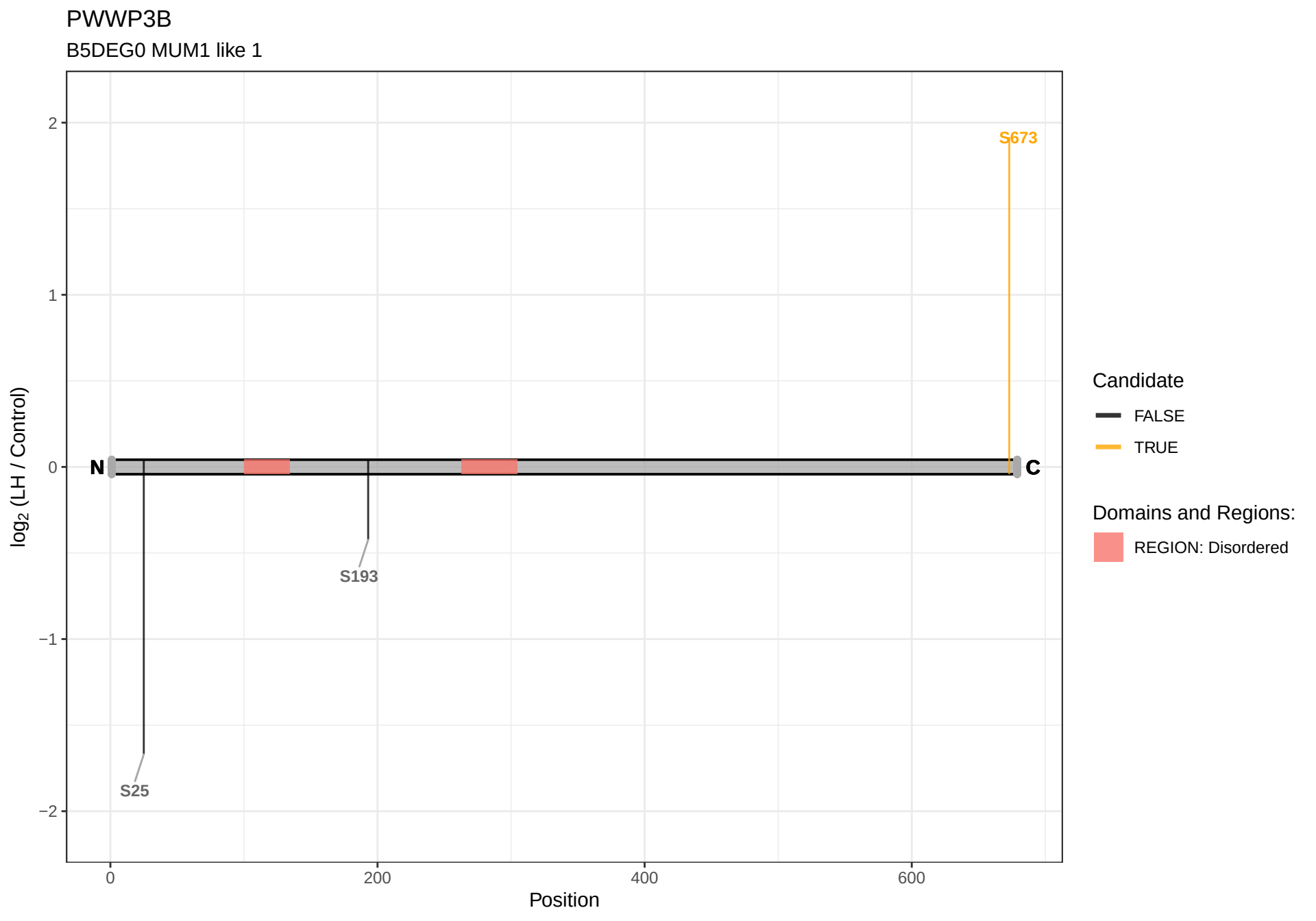

PSMD9
G3V9P0 26S proteasome non−ATPase regulatory subunit 9
log2 (LH / Control)
2
1
0
−1
−2
N
C
S128
0
50
100
150
200
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: PDZ

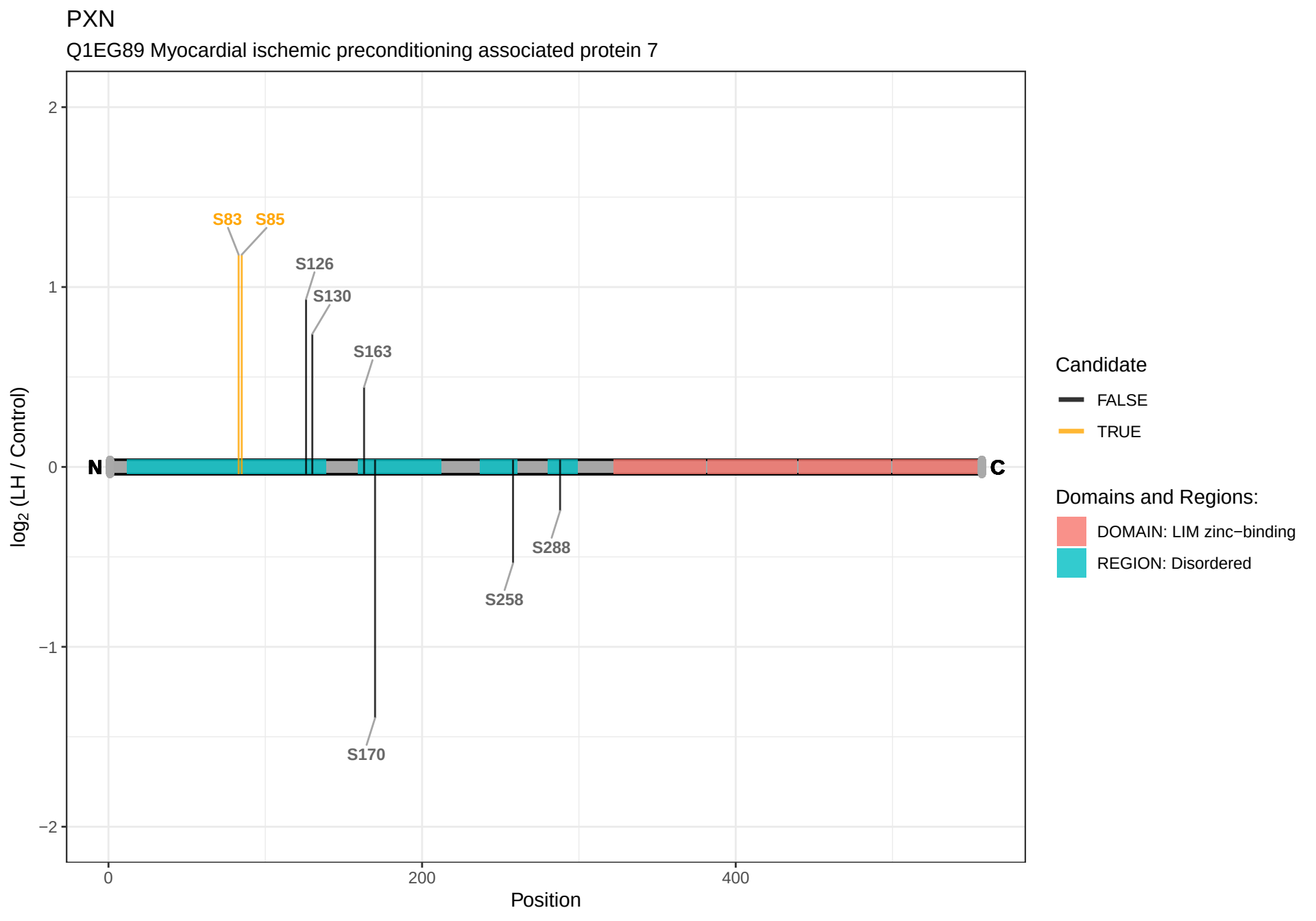

PSRC1
Q3KR66 Proline/serine−rich coiled−coil protein 1
log2 (LH / Control)
2
1
0
−1
−2
S22
S37
S107
N
C
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: 5 X 4 AA repeats of P−X−X−P
REGION: Disordered

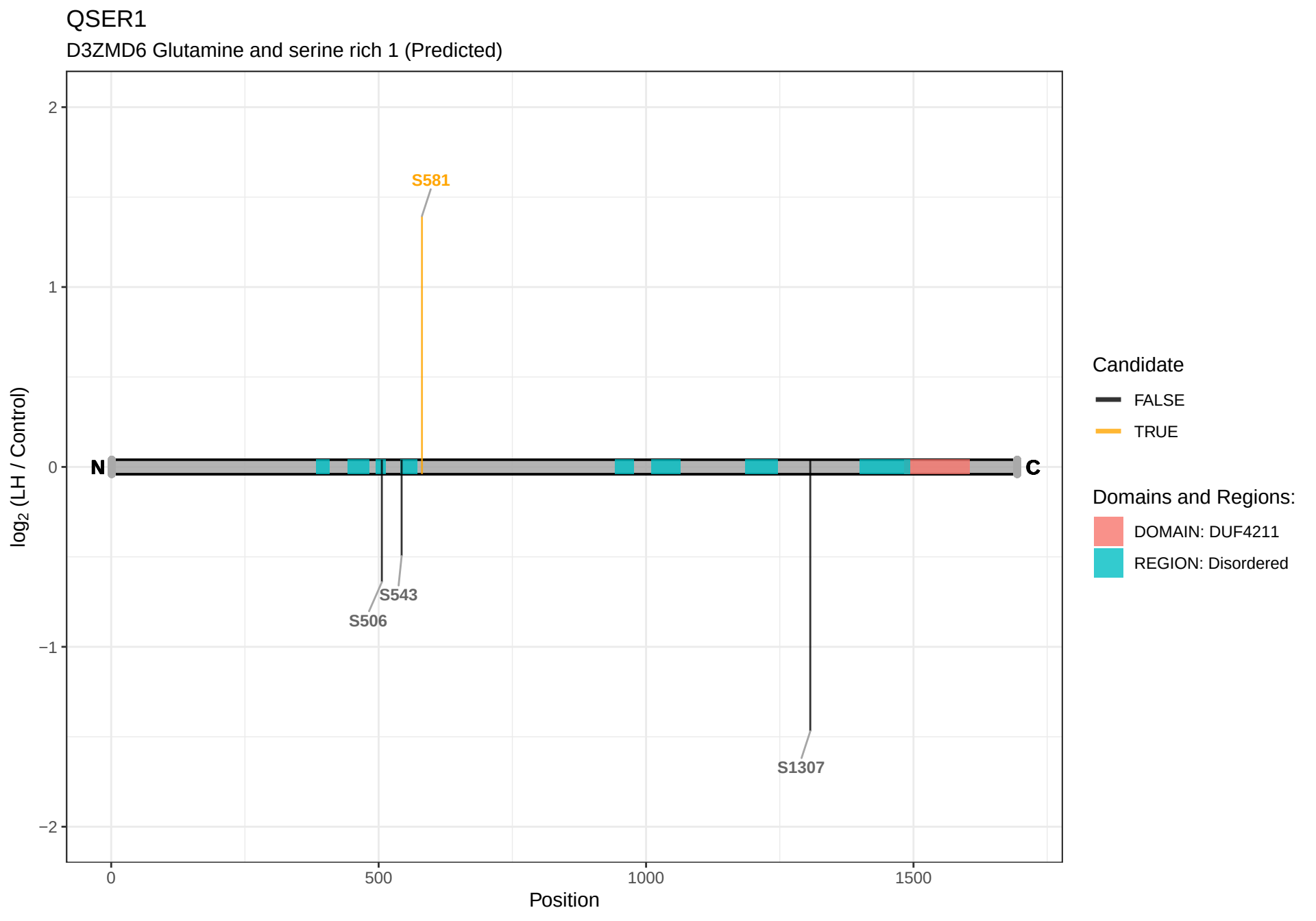

PTPN21
A0A0G2JTB7 Tyrosine−protein phosphatase non−receptor type
log2 (LH / Control)
2
1
0
−1
−2
N
C
S711
S710
S673
S679
S577
S590
S728
0
300
600
900
1200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: FERM
DOMAIN: TYR_PHOSPHATASE_2
DOMAIN: Tyrosine−protein phosphatase
REGION: Disordered

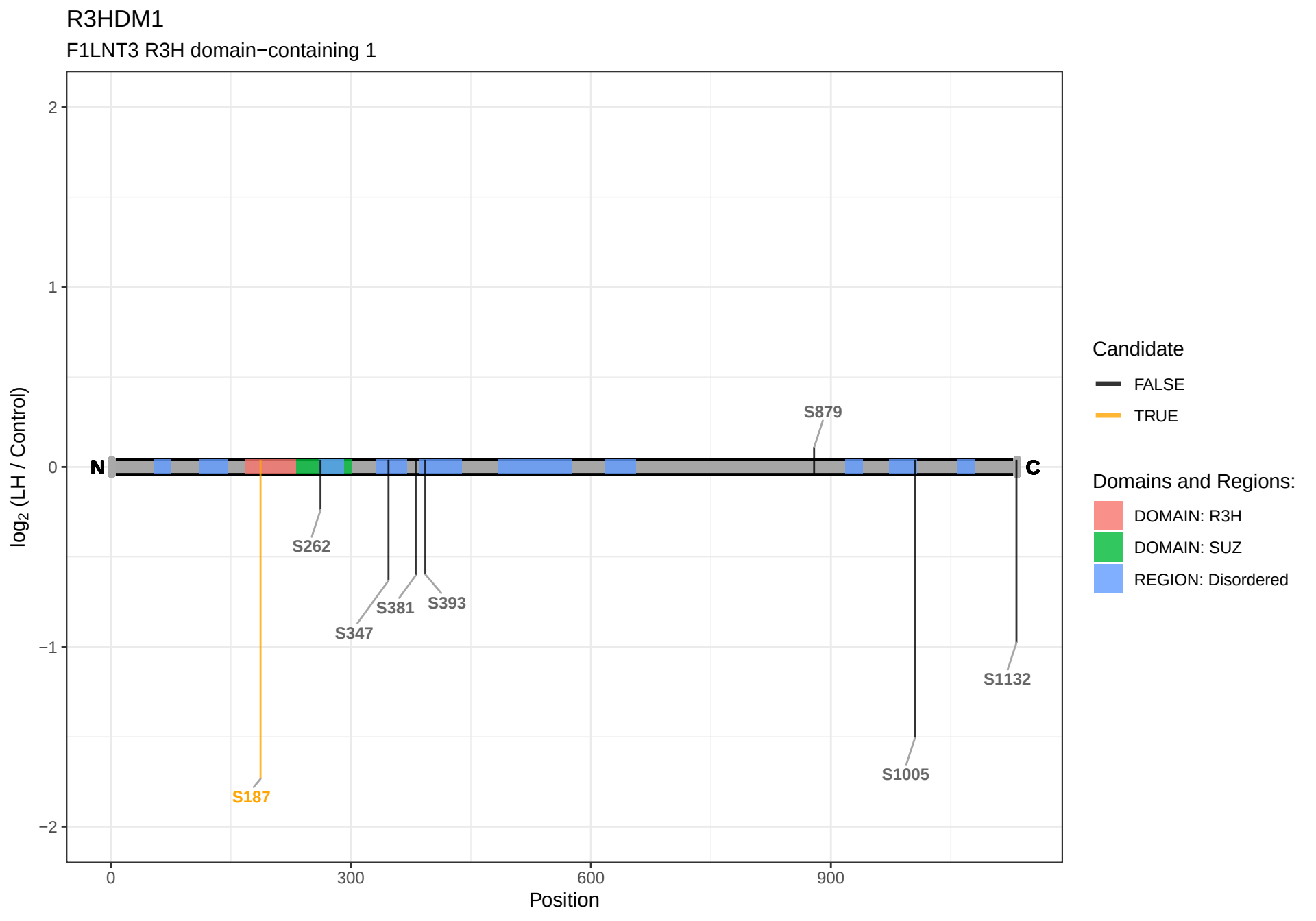

PUM2
D3ZQL8 Pumilio 2 (Drosophila)
S588
S82
S87
N
C
S181
S136
T174
S102
2
1
0
−1
−2
log2 (LH / Control)
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PUM−HD
REGION: Disordered

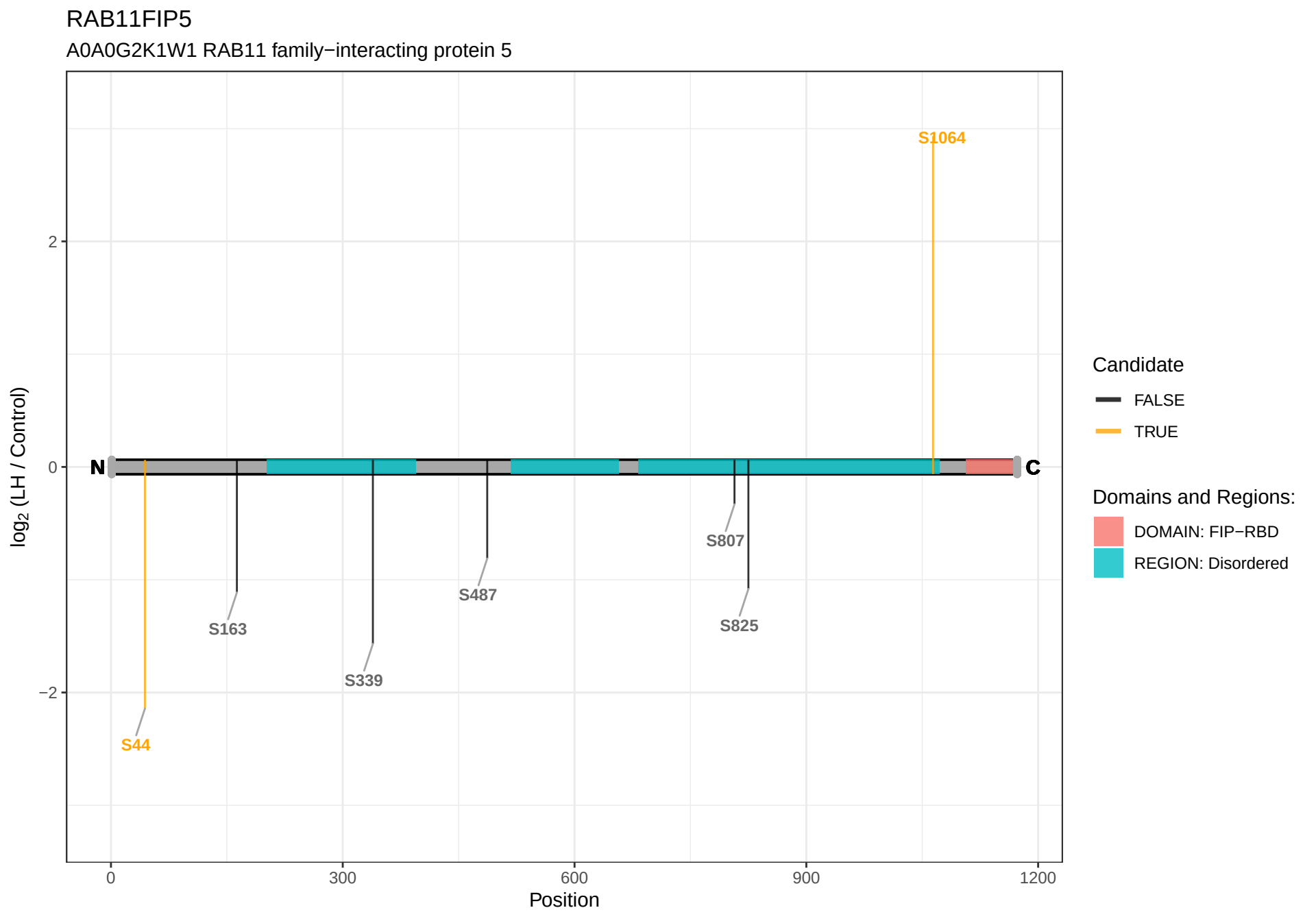

PWWP2A
B2RYP9 PWWP domain−containing 2A
S315
N
C
2
1
0
−1
−2
0
200
400
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
REGION: Disordered

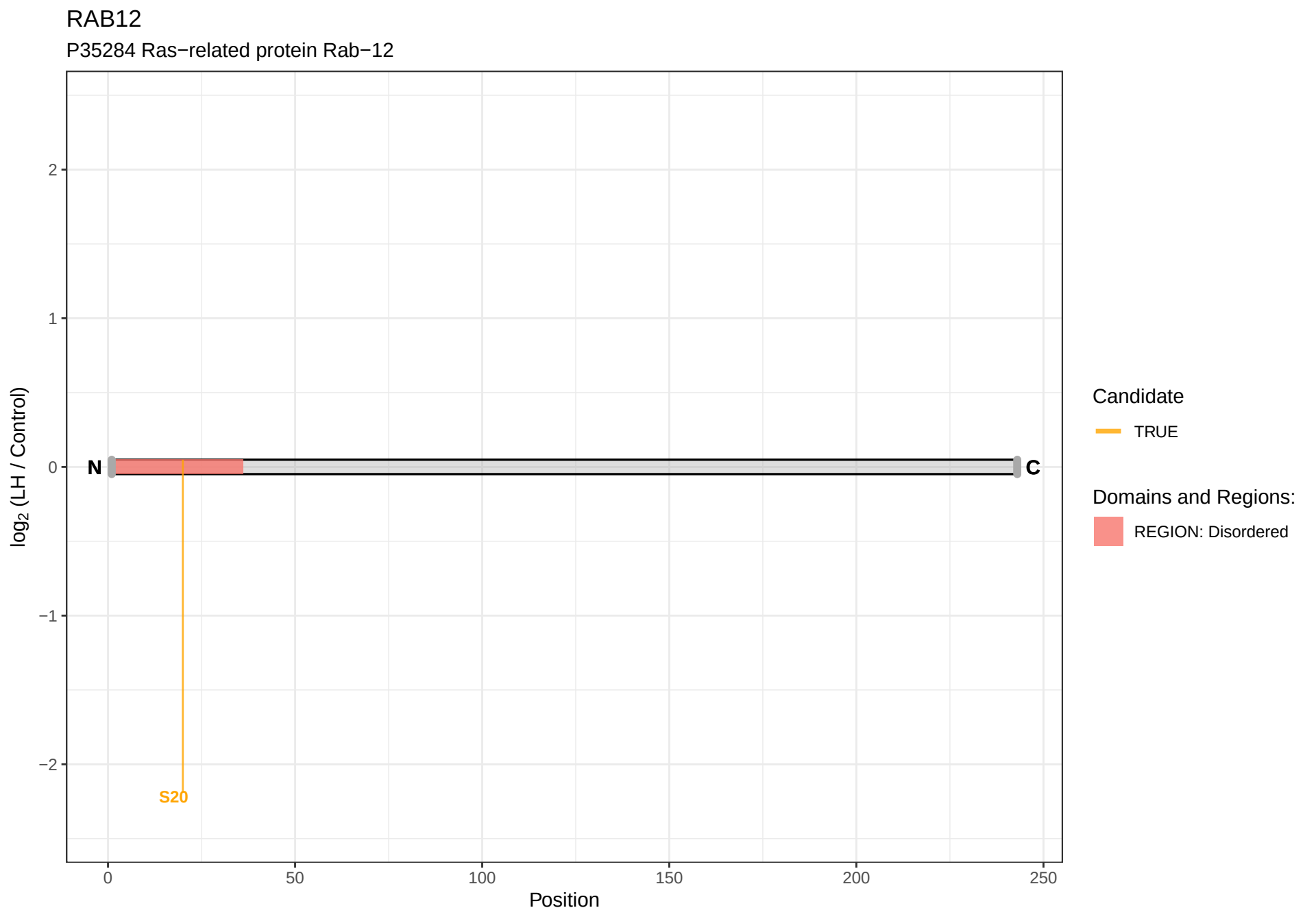

PWWP3B
B5DEG0 MUM1 like 1
2
1
0
−1
−2
log2 (LH / Control)
N
C
S673
S193
S25
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

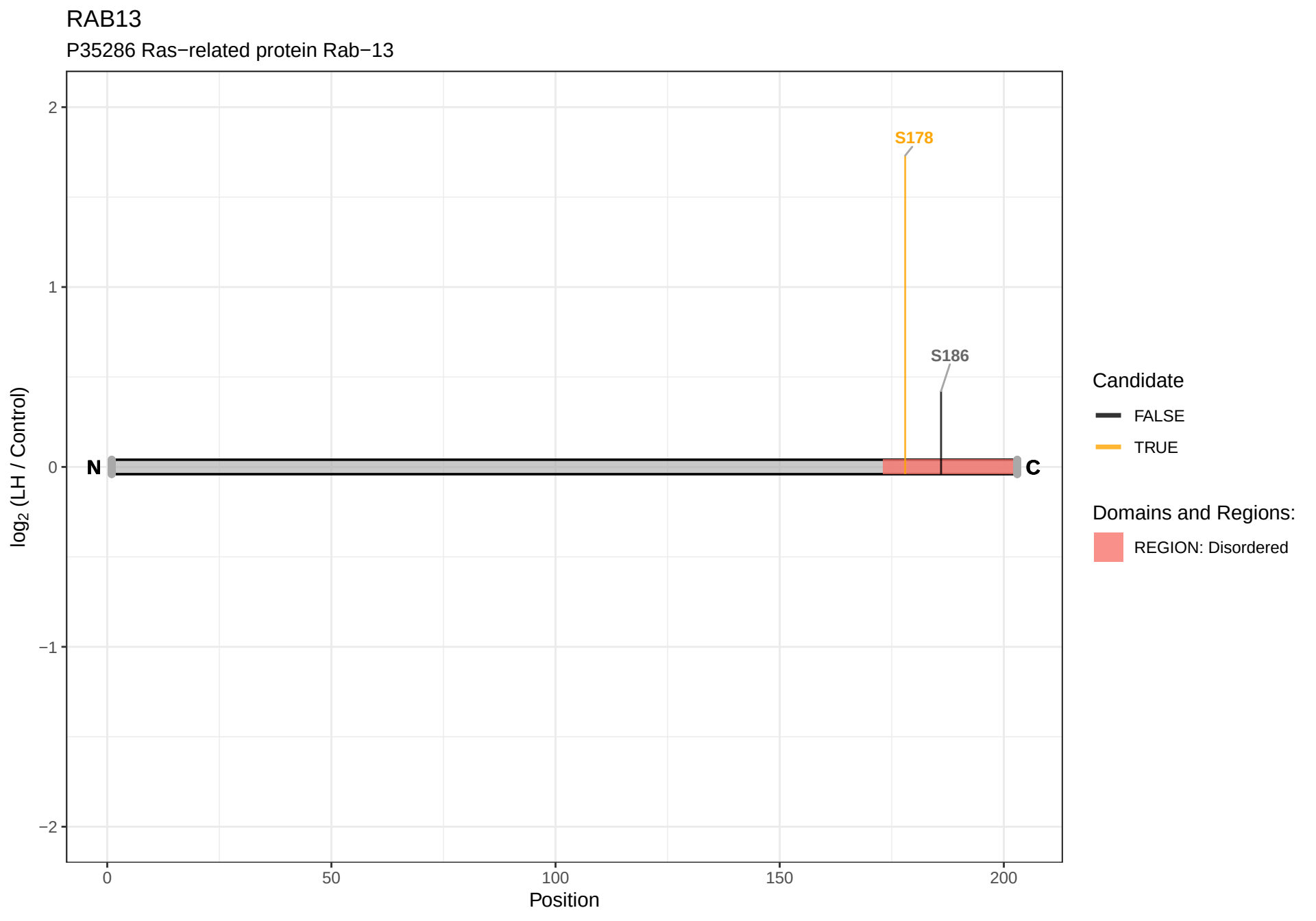

PXN
Q1EG89 Myocardial ischemic preconditioning associated protein 7
log2 (LH / Control)
2
1
0
−1
−2
S83
S85
S126
S130
S163
S288
S258
S170
N
C
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: LIM zinc−binding
REGION: Disordered

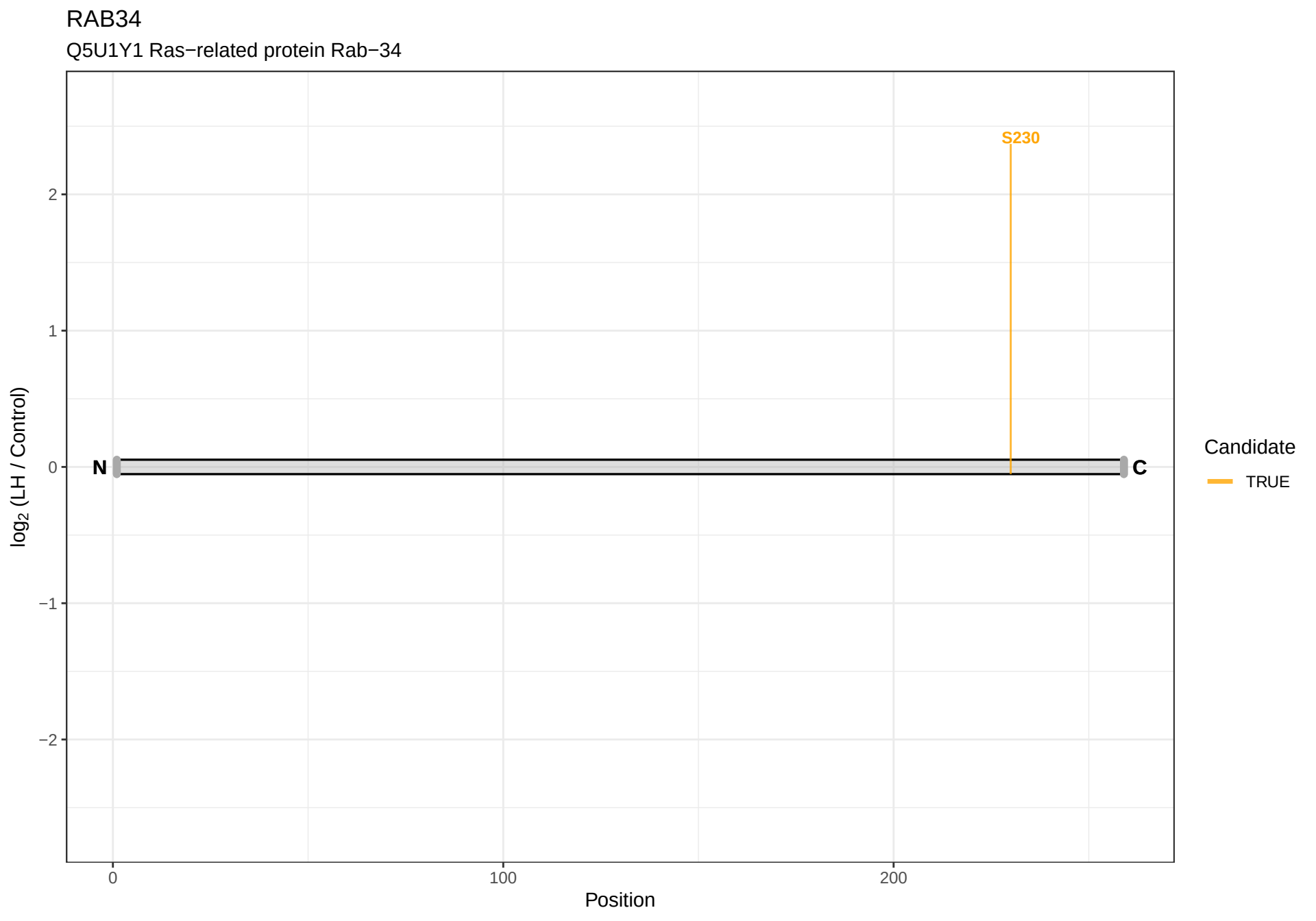

QSER1
D3ZMD6 Glutamine and serine rich 1 (Predicted)
2
1
0
−1
−2
log2 (LH / Control)
S581
N
C
S543
S506
S1307
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DUF4211
REGION: Disordered

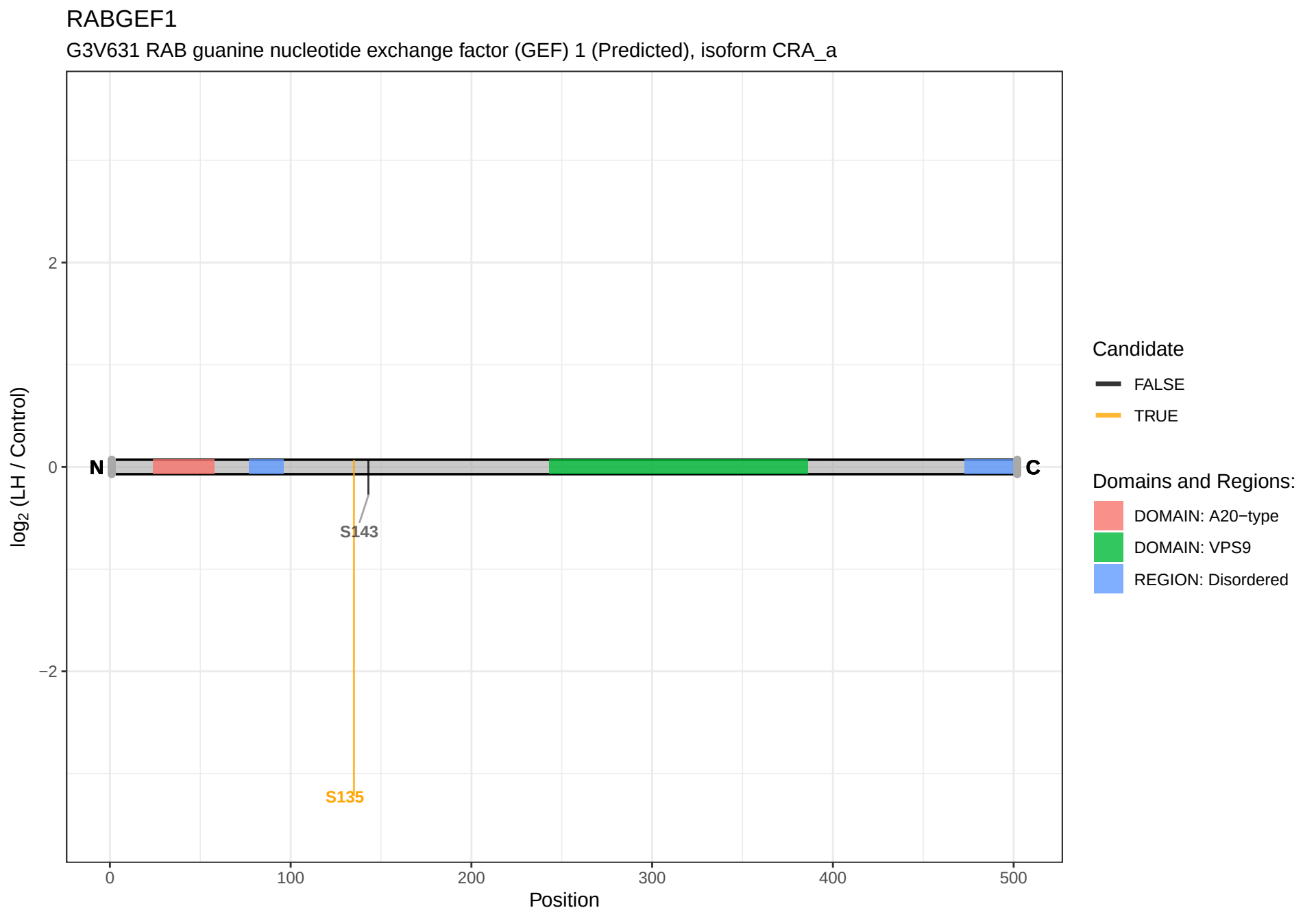

R3HDM1
F1LNT3 R3H domain−containing 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S879
S262
S381
S393
S347
S1132
S187
S1005
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: R3H
DOMAIN: SUZ
REGION: Disordered

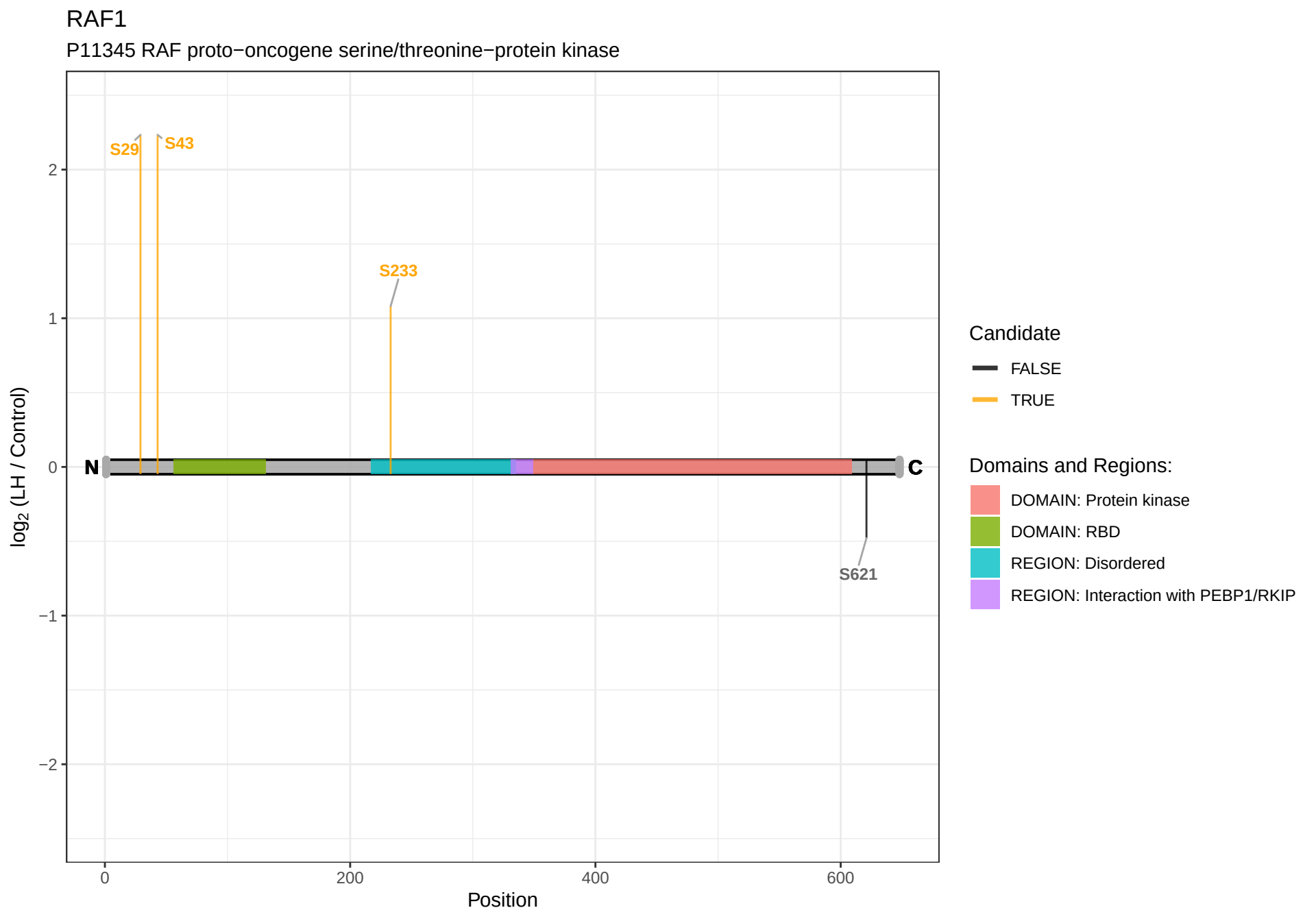

RAB11FIP5
A0A0G2K1W1 RAB11 family−interacting protein 5
log2 (LH / Control)
2
0
−2
N
C
S1064
S807
S487
S163
S825
S339
S44
0
300
600
900
1200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: FIP−RBD
REGION: Disordered

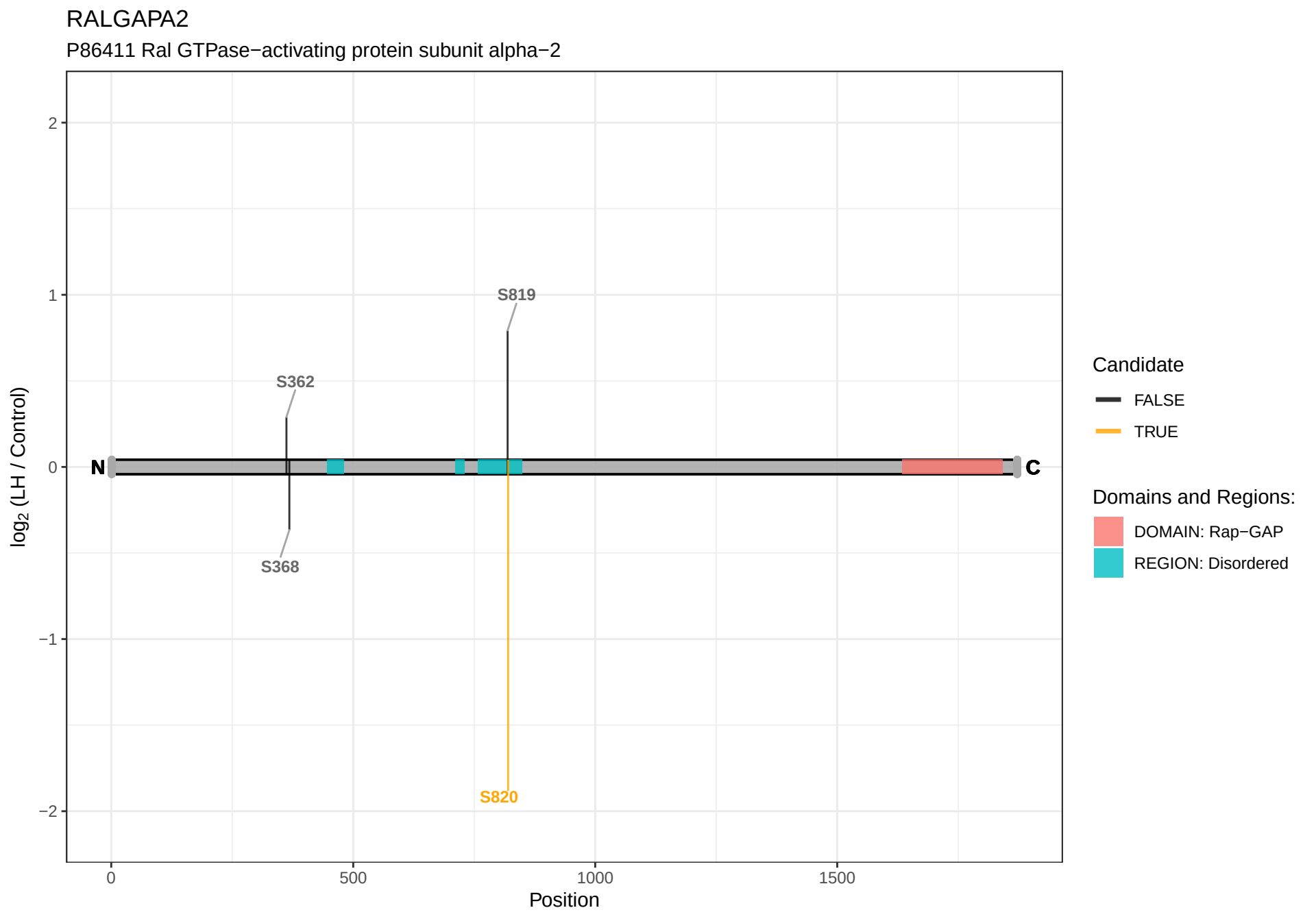

RAB12
P35284 Ras−related protein Rab−12
log2 (LH / Control)
2
1
0
−1
−2
N
C
S20
0
50
100
150
200
250
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

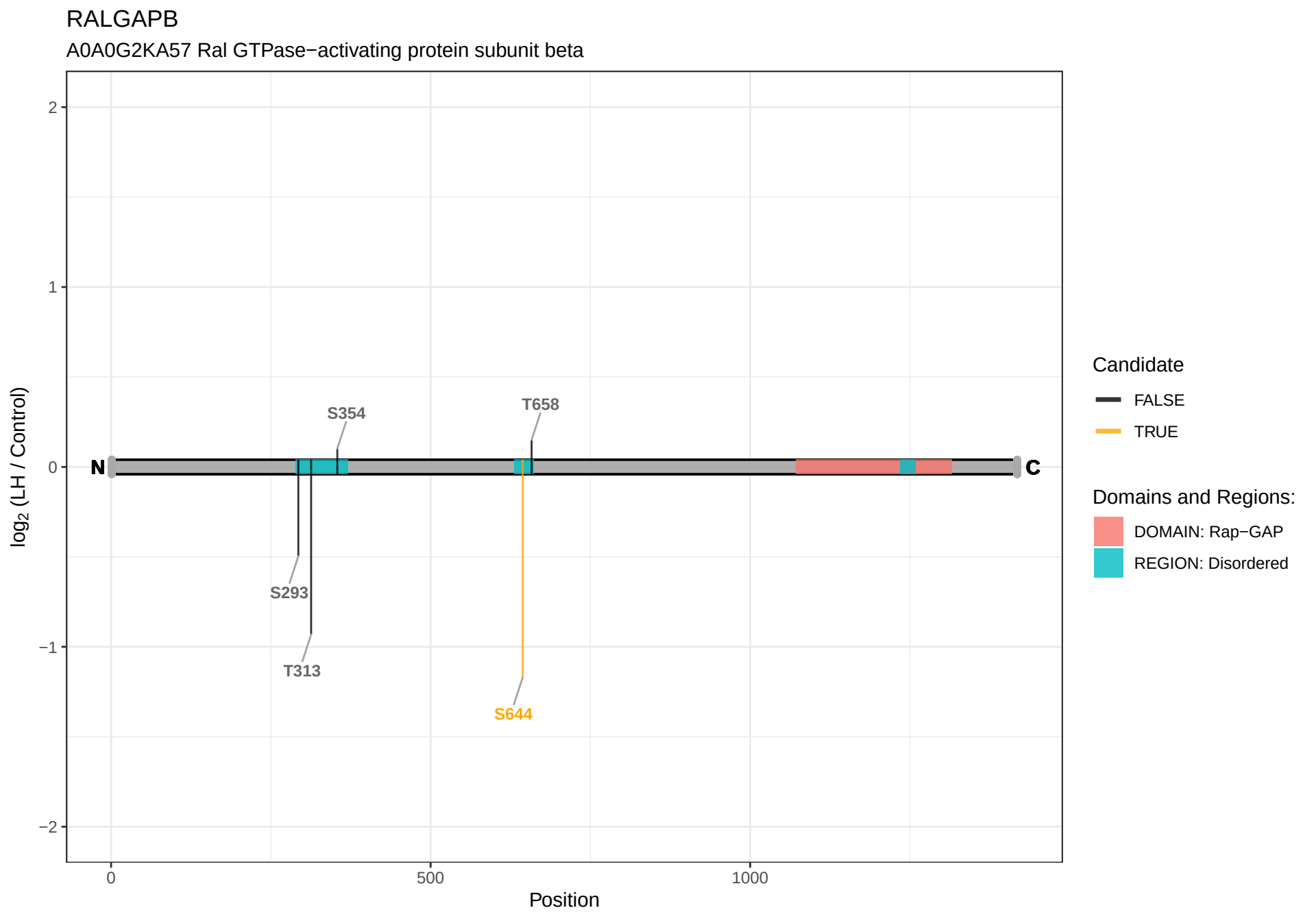

RAB13
P35286 Ras−related protein Rab−13
S178
S186
N
C
2
1
0
−1
−2
0
50
100
150
200
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

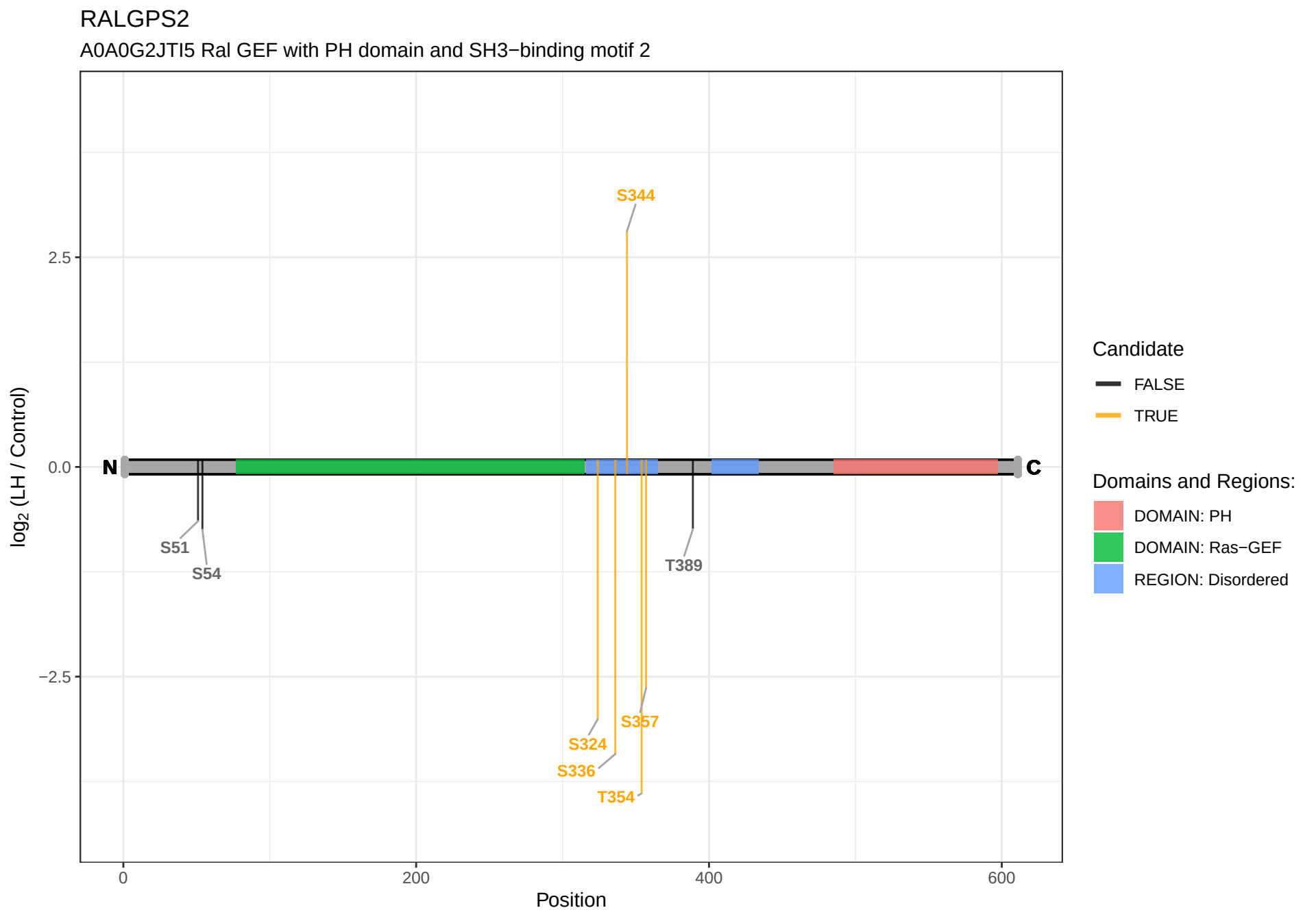

RAB34
Q5U1Y1 Ras−related protein Rab−34
S230
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
Position
Candidate
TRUE

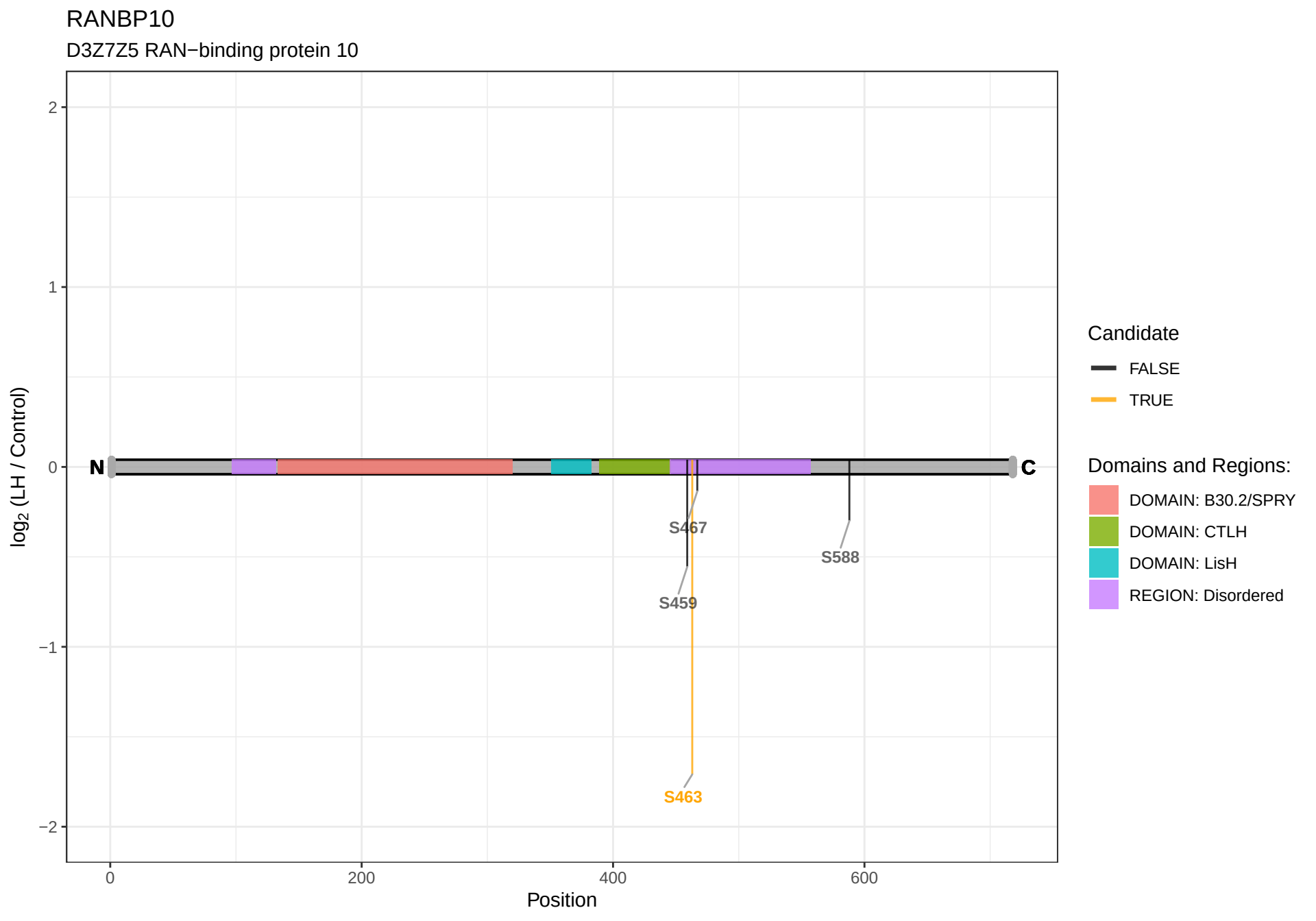

RABGEF1
G3V631 RAB guanine nucleotide exchange factor (GEF) 1 (Predicted), isoform CRA_a
log2 (LH / Control)
2
0
−2
N
C
S143
S135
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: A20−type
DOMAIN: VPS9
REGION: Disordered

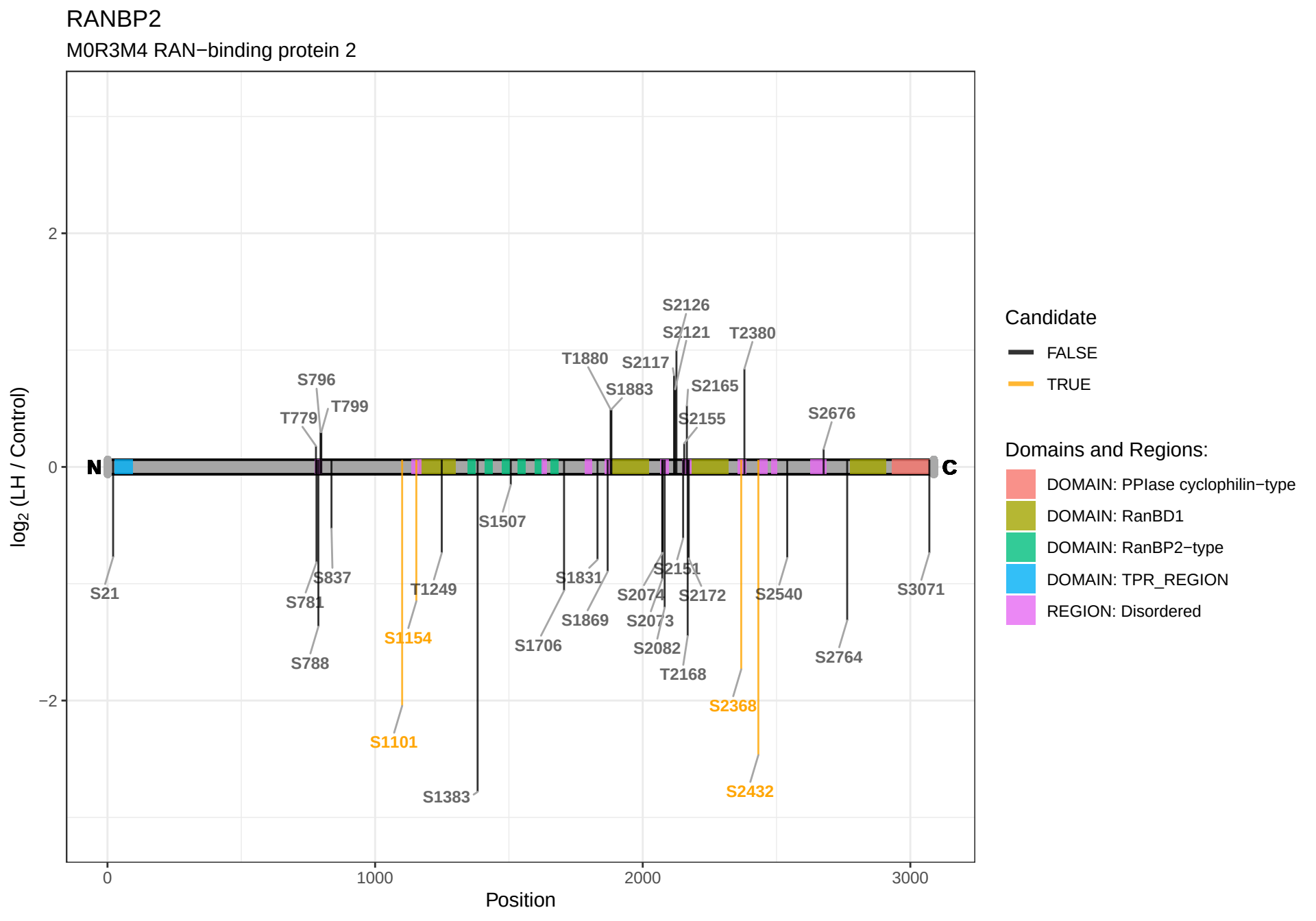

RAF1
P11345 RAF proto−oncogene serine/threonine−protein kinase
S29
S43
S233
S621
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
DOMAIN: RBD
REGION: Disordered
REGION: Interaction with PEBP1/RKIP

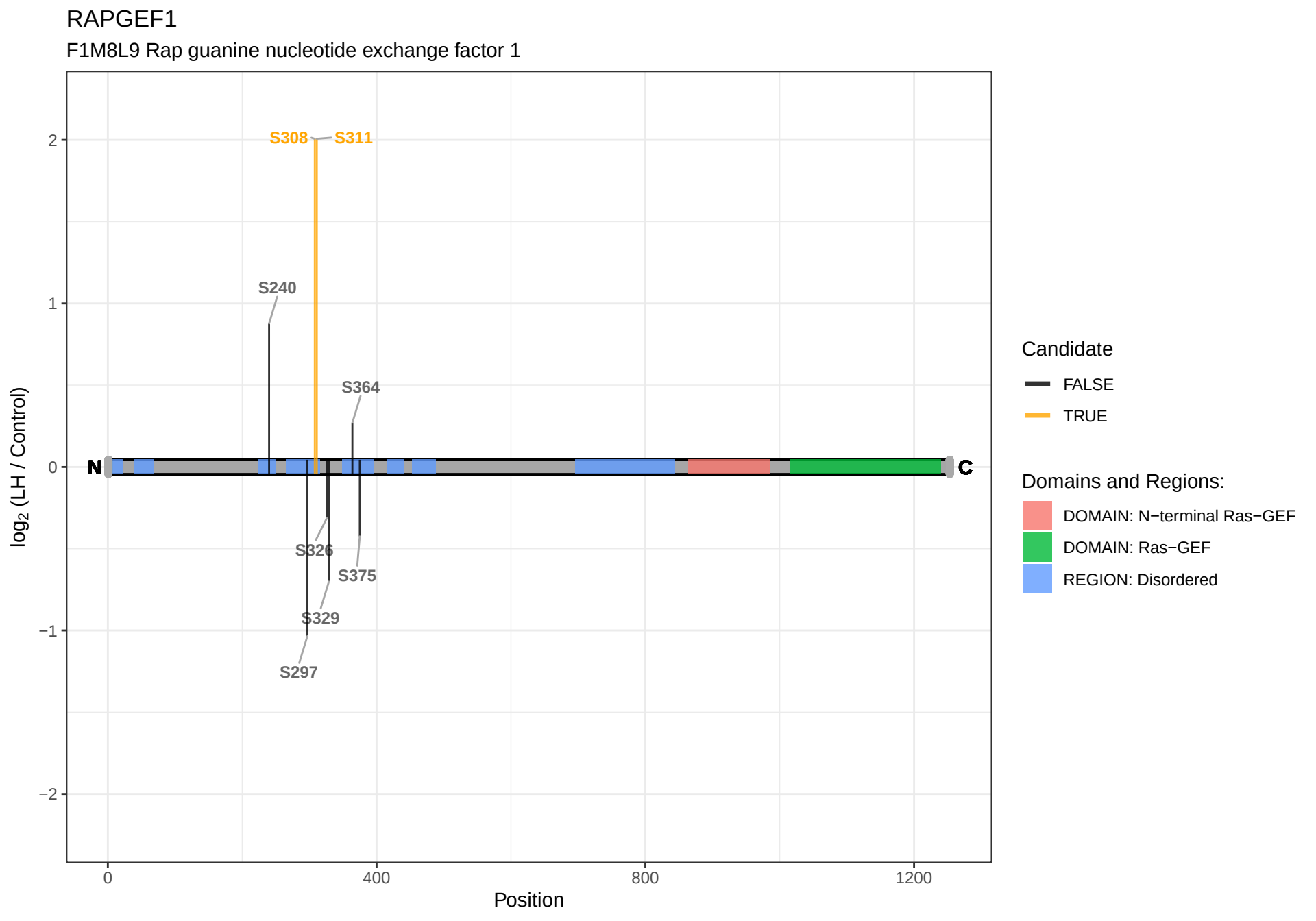

RALGAPA2
P86411 Ral GTPase−activating protein subunit alpha−2
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
Position
N
C
S362
S368
S819
S820
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Rap−GAP
REGION: Disordered

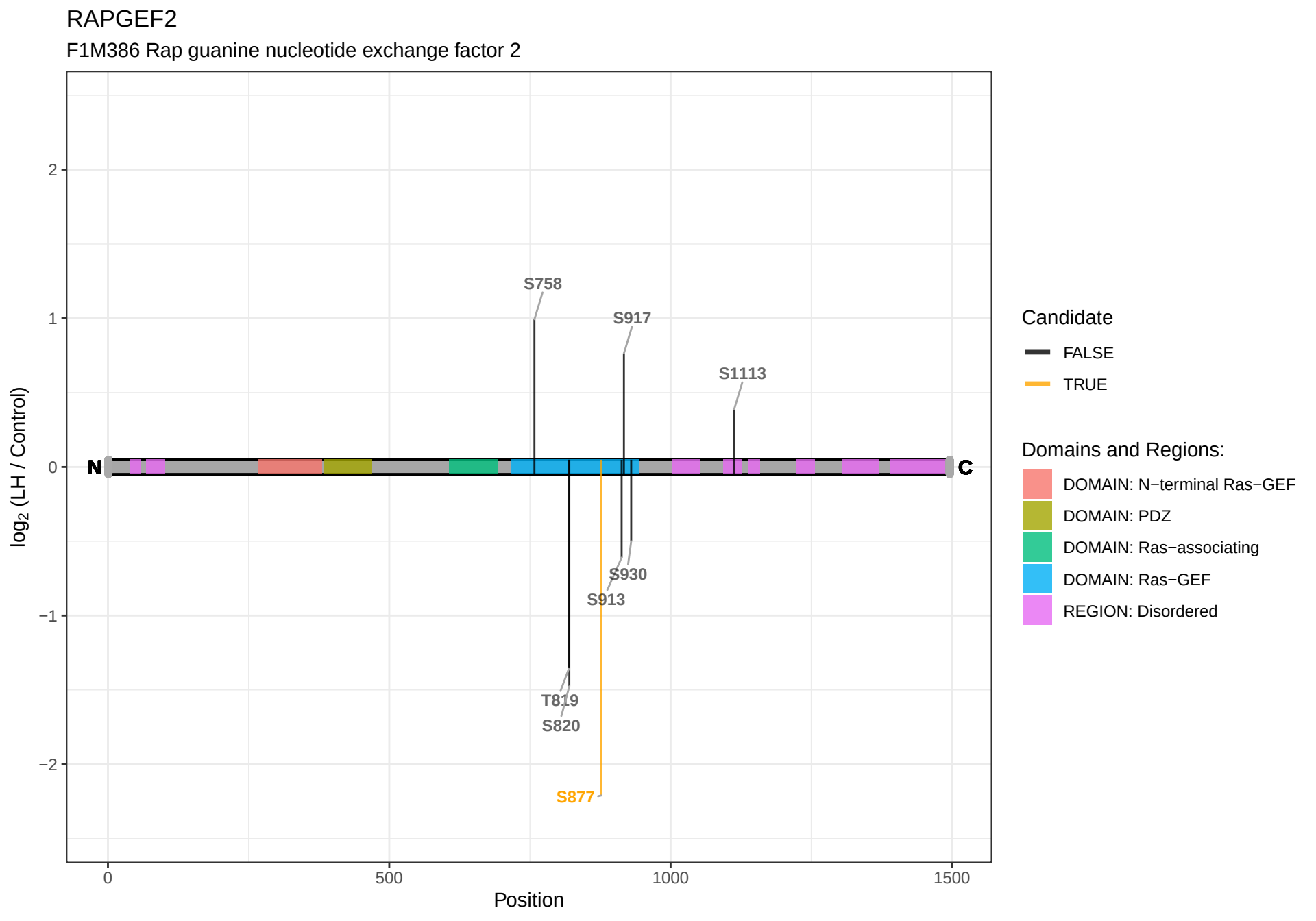

RALGAPB
A0A0G2KA57 Ral GTPase−activating protein subunit beta
log2 (LH / Control)
2
1
0
−1
−2
N
C
S354
T658
S293
T313
S644
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Rap−GAP
REGION: Disordered

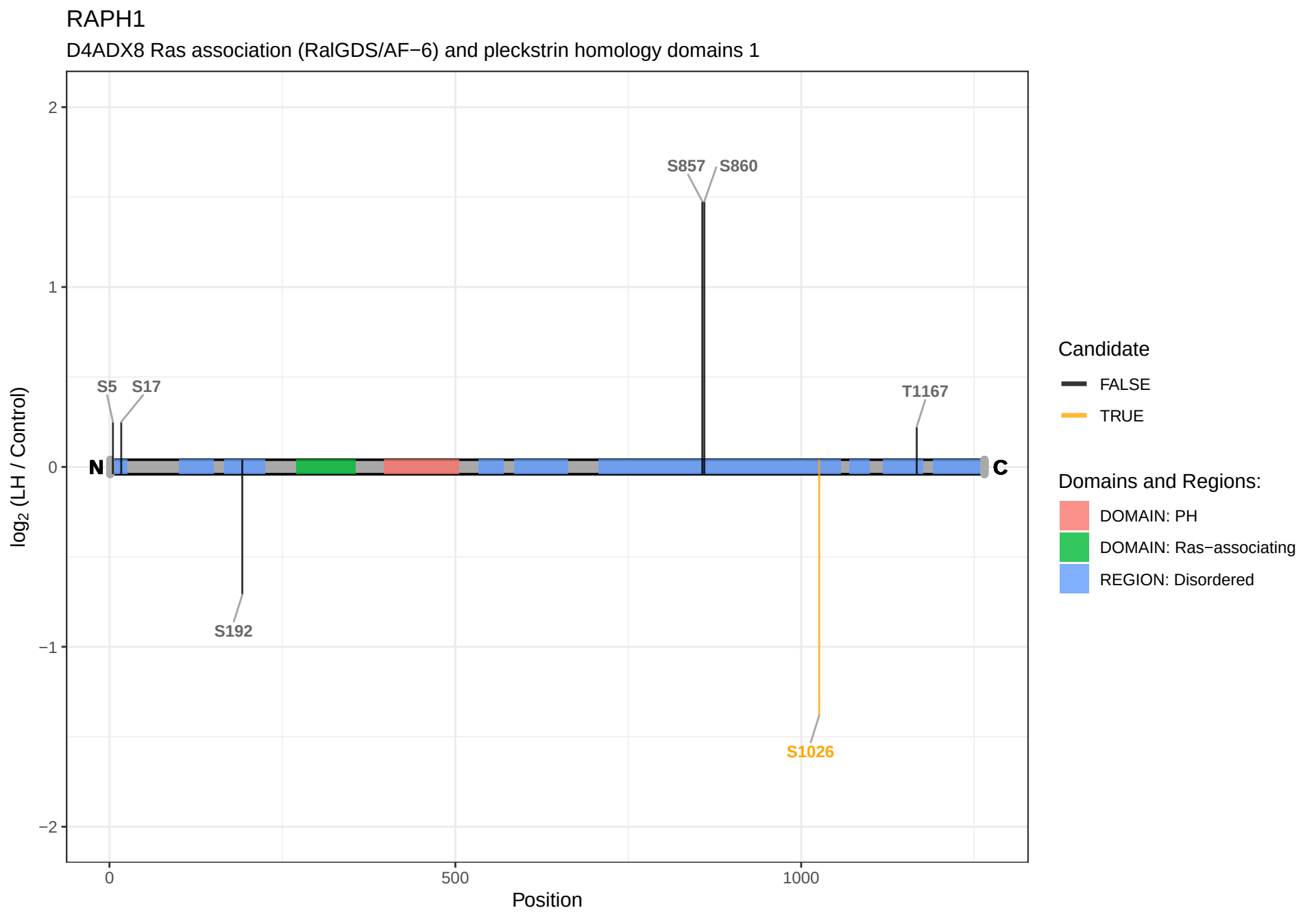

RALGPS2
A0A0G2JTI5 Ral GEF with PH domain and SH3−binding motif 2
log2 (LH / Control)
2.5
0.0
−2.5
N
C
S344
S51
S54
T389
S357
S324
S336
T354
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PH
DOMAIN: Ras−GEF
REGION: Disordered

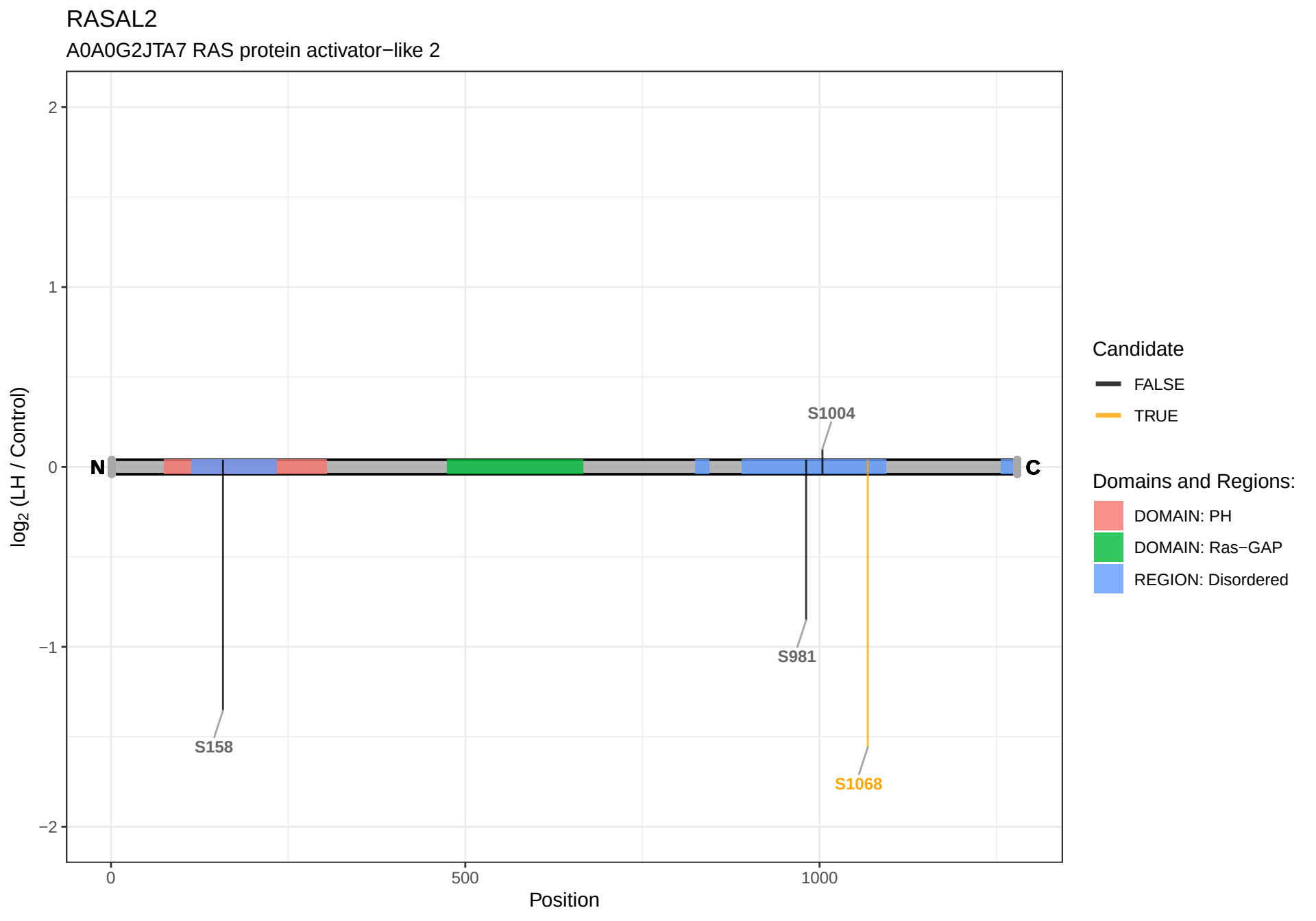

RANBP10
D3Z7Z5 RAN−binding protein 10
log2 (LH / Control)
2
1
0
−1
−2
N
C
S467
S459
S463
S588
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: B30.2/SPRY
DOMAIN: CTLH
DOMAIN: LisH
REGION: Disordered

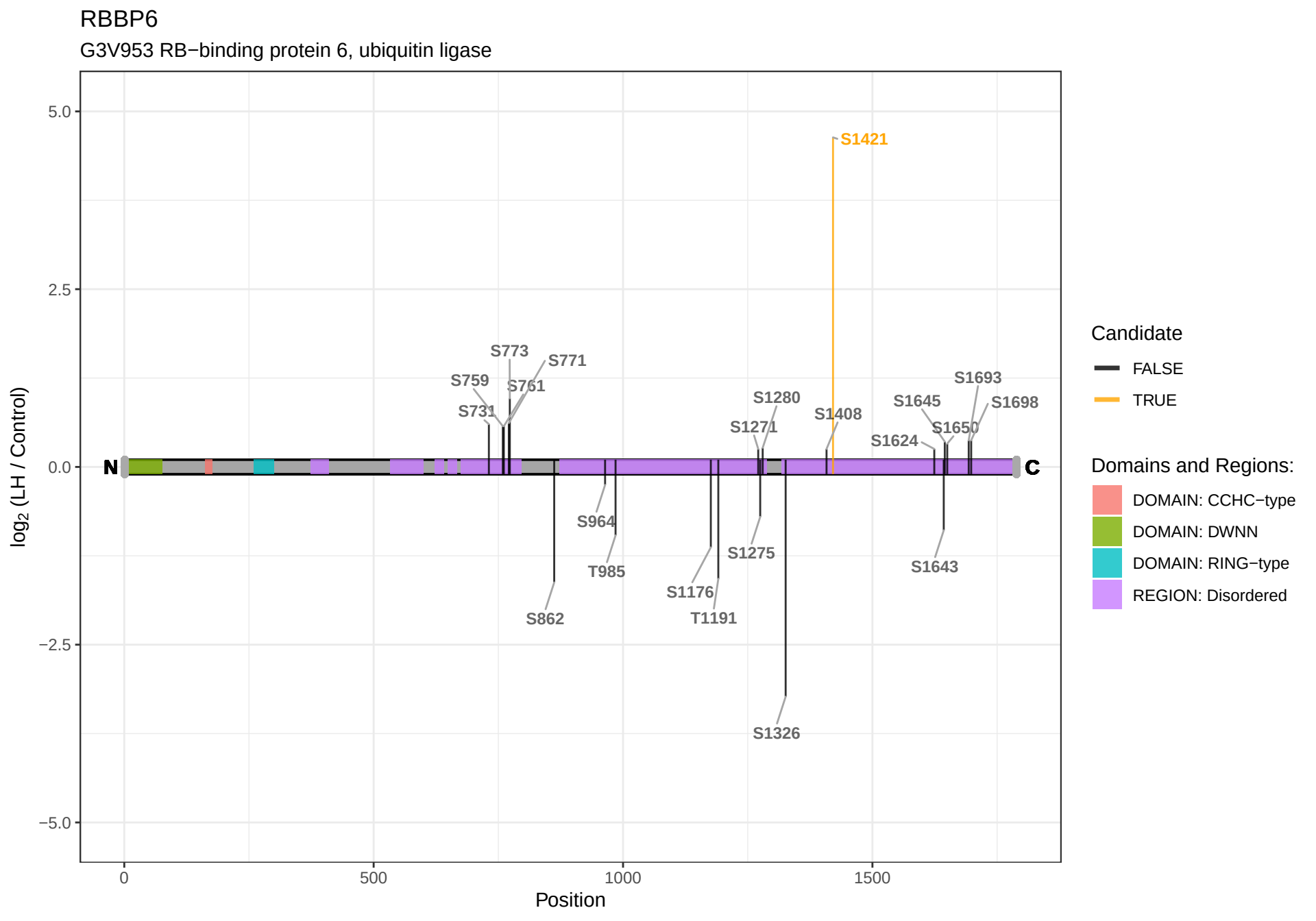

RANBP2
M0R3M4 RAN−binding protein 2
log2 (LH / Control)
Position
N
C
S21
S796
T779
T799
S781
S837
S788
T1249
S1154
S1101
S1507
S1383
S1706
T1880
S1883
S1831
S1869
S2126
S2121
S2117
T2380
S2165
S2155
S2151
S2074
S2073
S2082
S2172
T2168
S2368
S2432
S2540
S2676
S2764
S3071
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PPIase cyclophilin−type
DOMAIN: RanBD1
DOMAIN: RanBP2−type
DOMAIN: TPR_REGION
REGION: Disordered

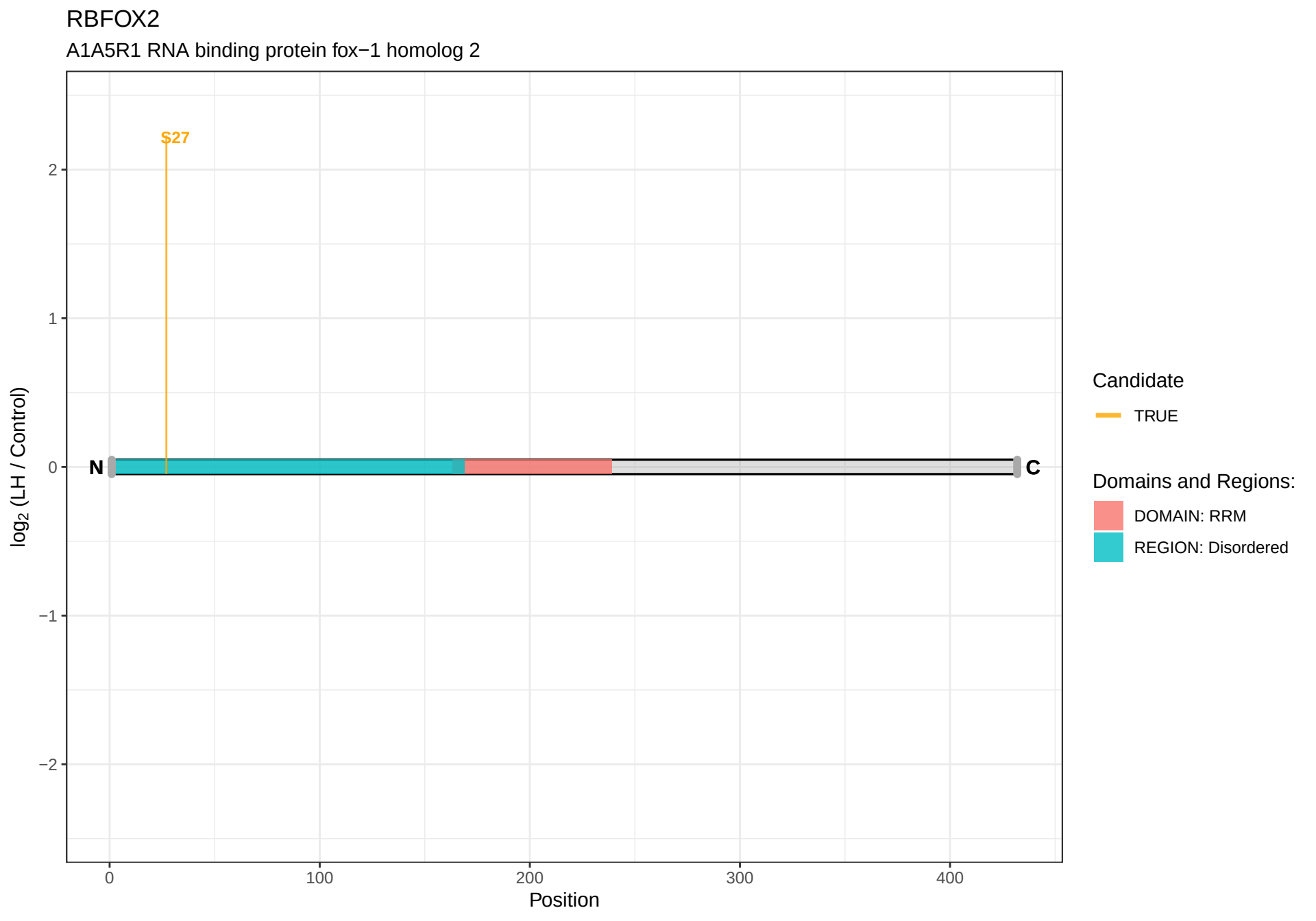

RAPGEF1
F1M8L9 Rap guanine nucleotide exchange factor 1
S308
S311
S240
S364
S326
S375
S329
S297
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
400
800
1200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: N−terminal Ras−GEF
DOMAIN: Ras−GEF
REGION: Disordered

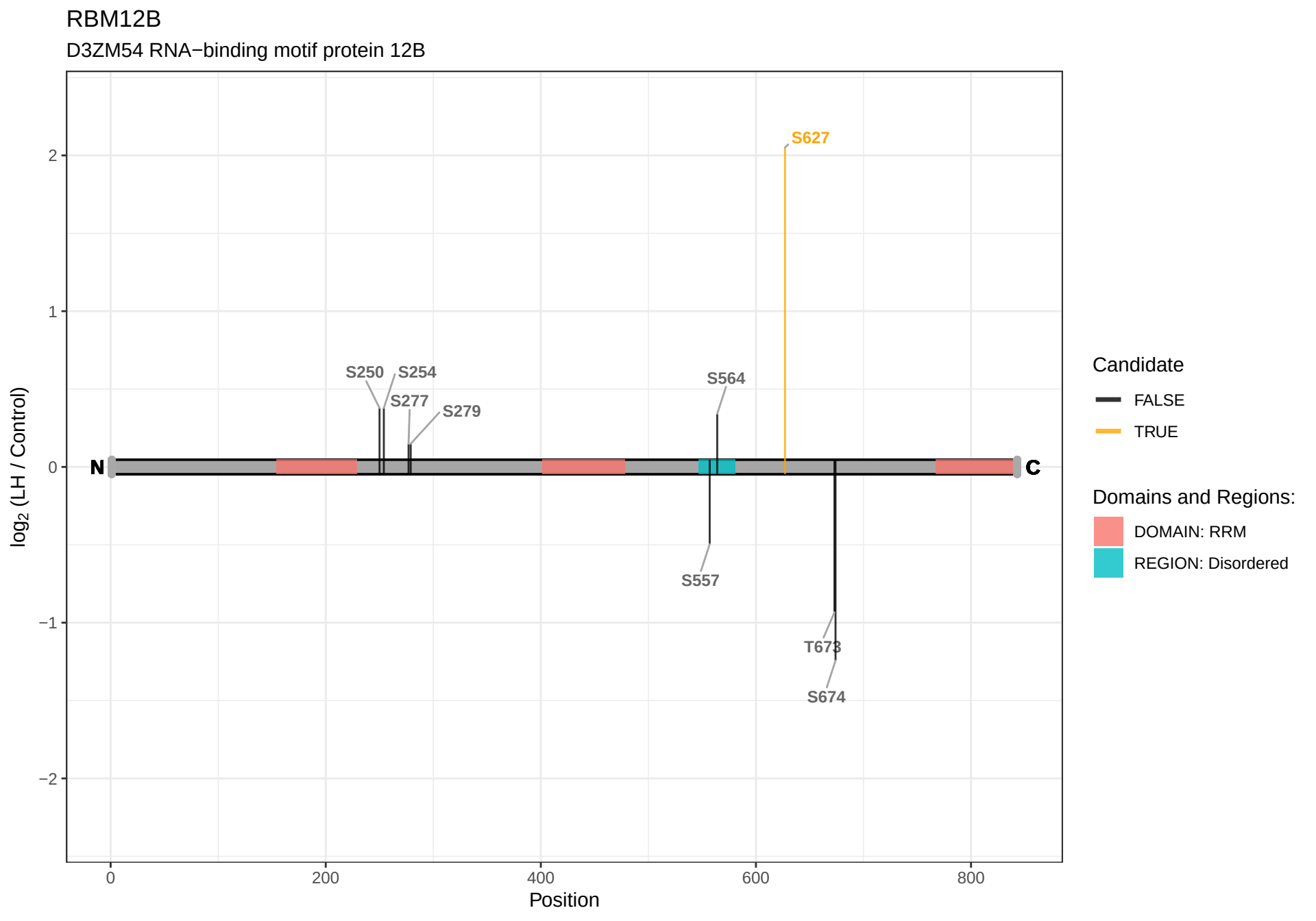

RAPGEF2
F1M386 Rap guanine nucleotide exchange factor 2
log2 (LH / Control)
2
1
0
−1
−2
N
C
S758
S917
S1113
S930
S913
T819
S820
S877
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: N−terminal Ras−GEF
DOMAIN: PDZ
DOMAIN: Ras−associating
DOMAIN: Ras−GEF
REGION: Disordered

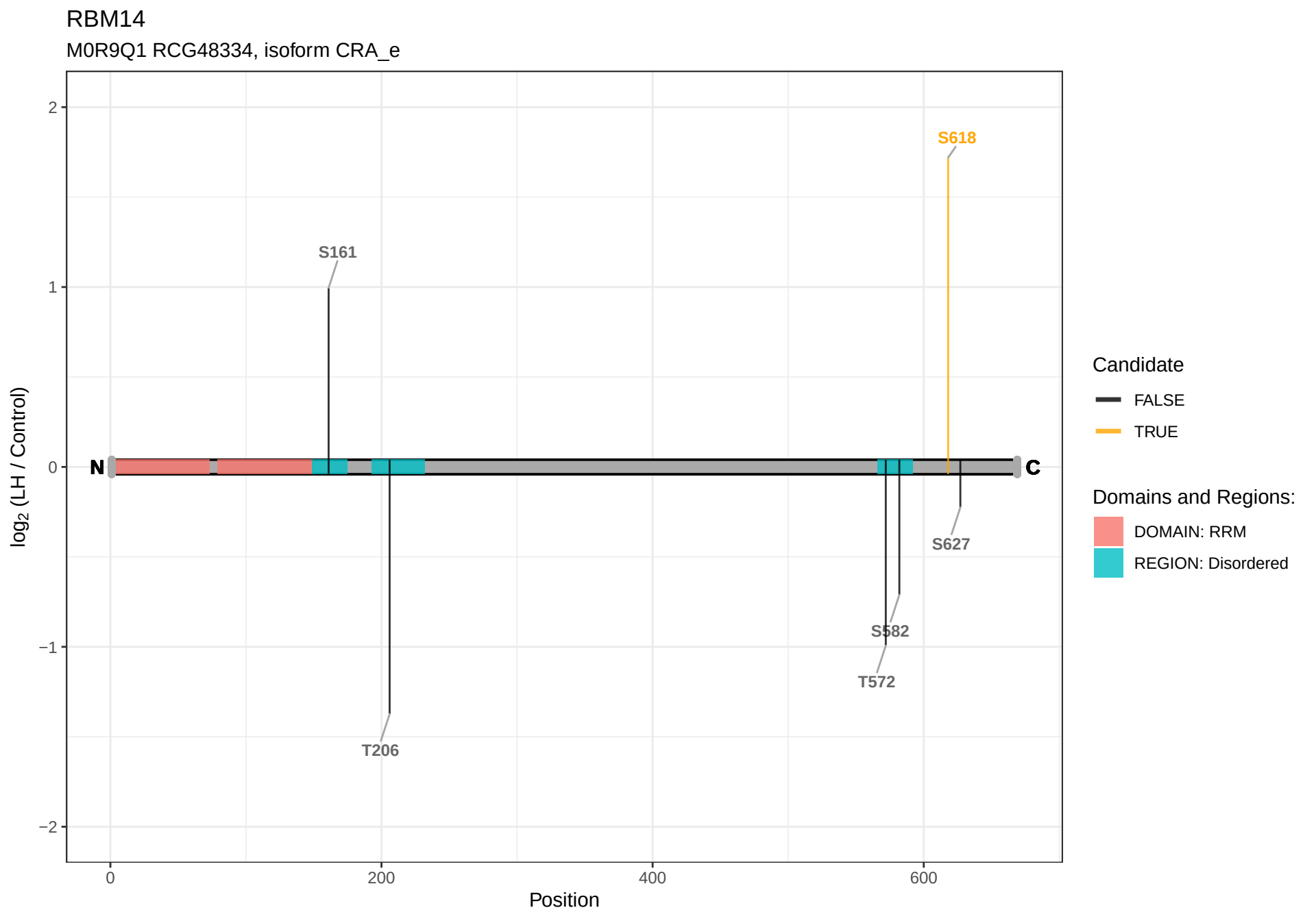

RAPH1
D4ADX8 Ras association (RalGDS/AF−6) and pleckstrin homology domains 1
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
Position
S857
S860
S5
S17
T1167
N
C
S192
S1026
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PH
DOMAIN: Ras−associating
REGION: Disordered

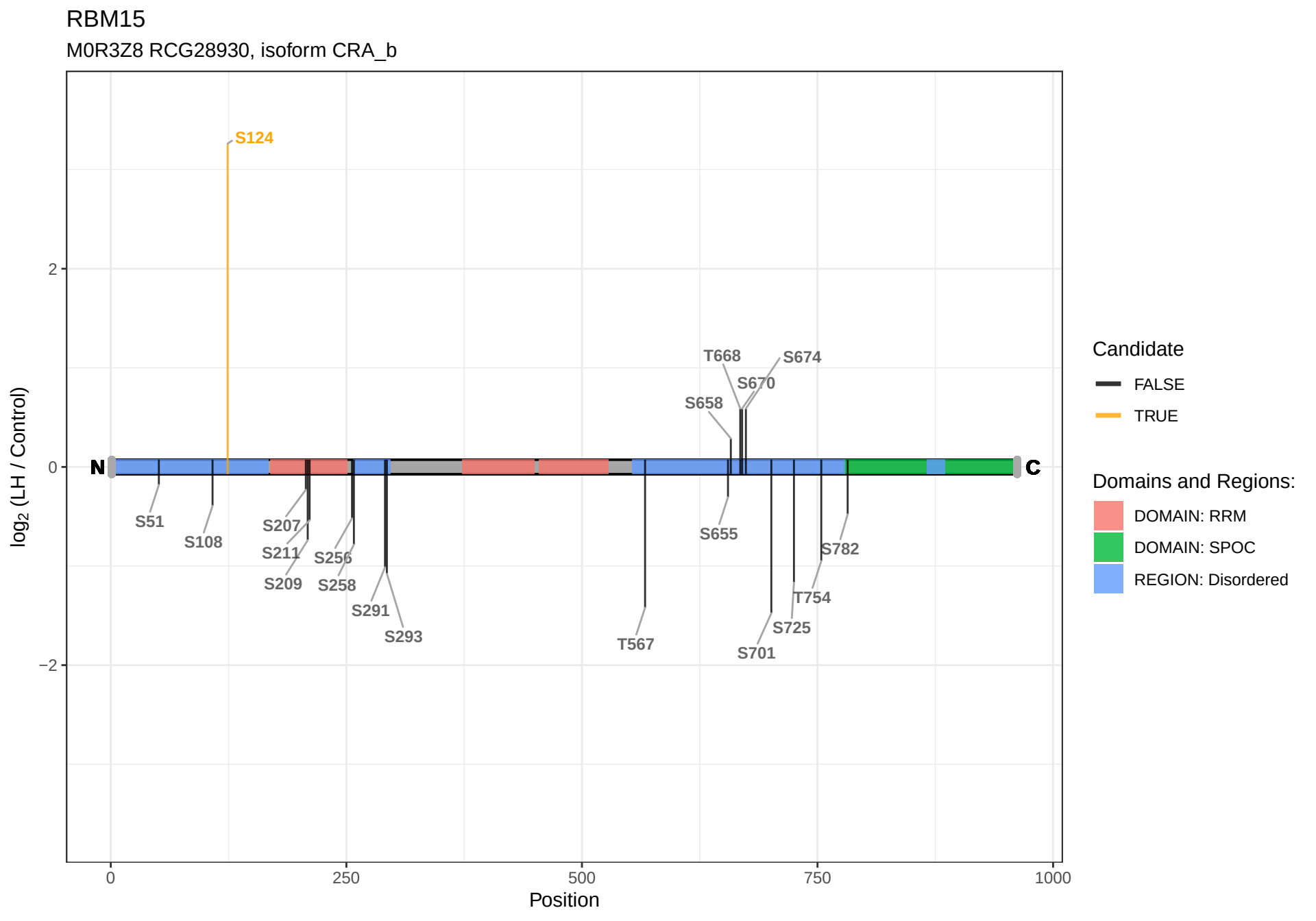

RASAL2
A0A0G2JTA7 RAS protein activator−like 2
2
1
0
−1
−2
log2 (LH / Control)
N
C
S1004
S981
S158
S1068
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PH
DOMAIN: Ras−GAP
REGION: Disordered

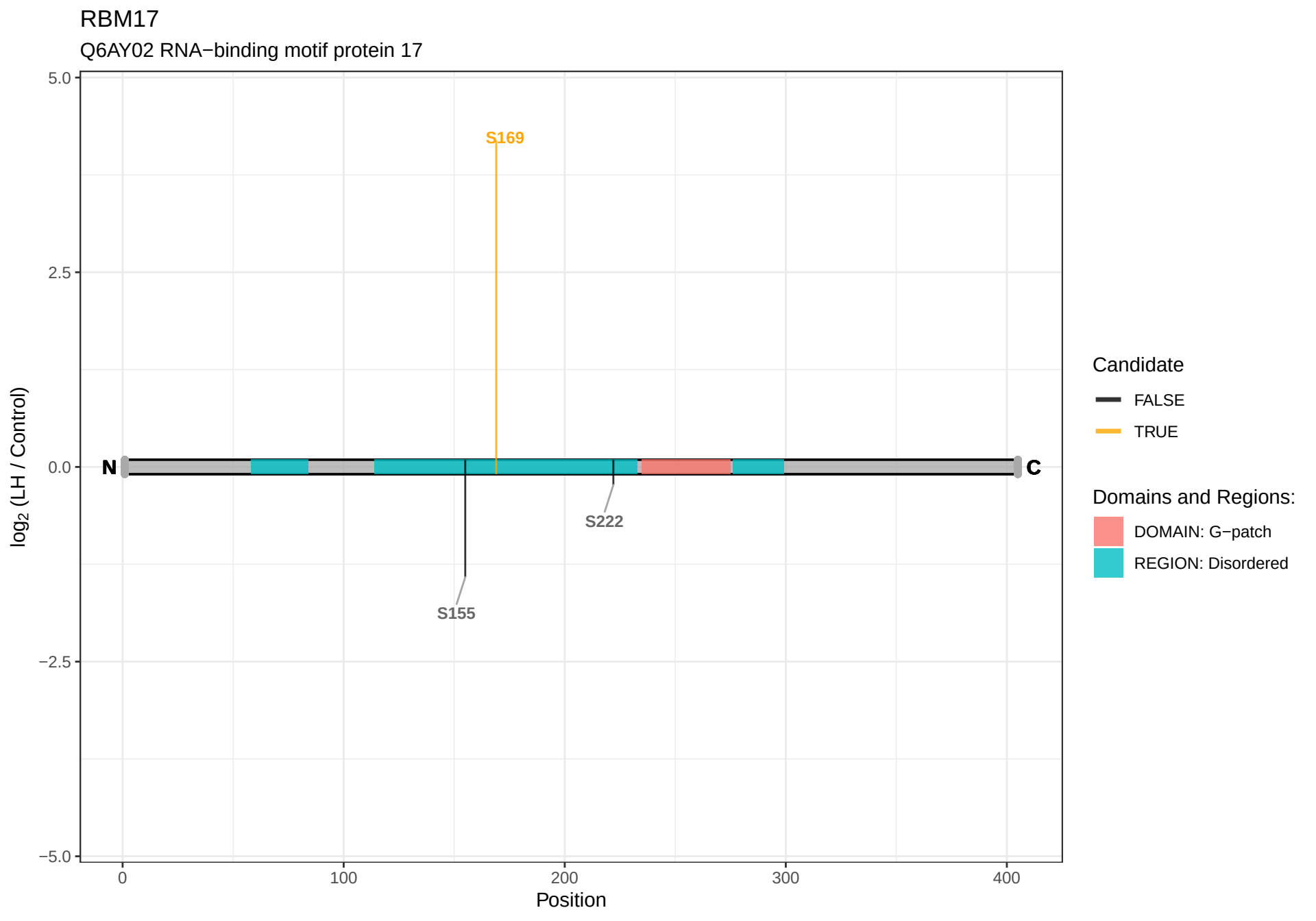

RBBP6
G3V953 RB−binding protein 6, ubiquitin ligase
log2 (LH / Control)
5.0
2.5
0.0
−2.5
−5.0
0
500
1000
1500
Position
N
C
S1421
S773
S771
S759
S761
S731
S1280
S1271
S1408
S1645
S1693
S1698
S1650
S1624
S964
T985
S862
S1176
T1191
S1275
S1643
S1326
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CCHC−type
DOMAIN: DWNN
DOMAIN: RING−type
REGION: Disordered

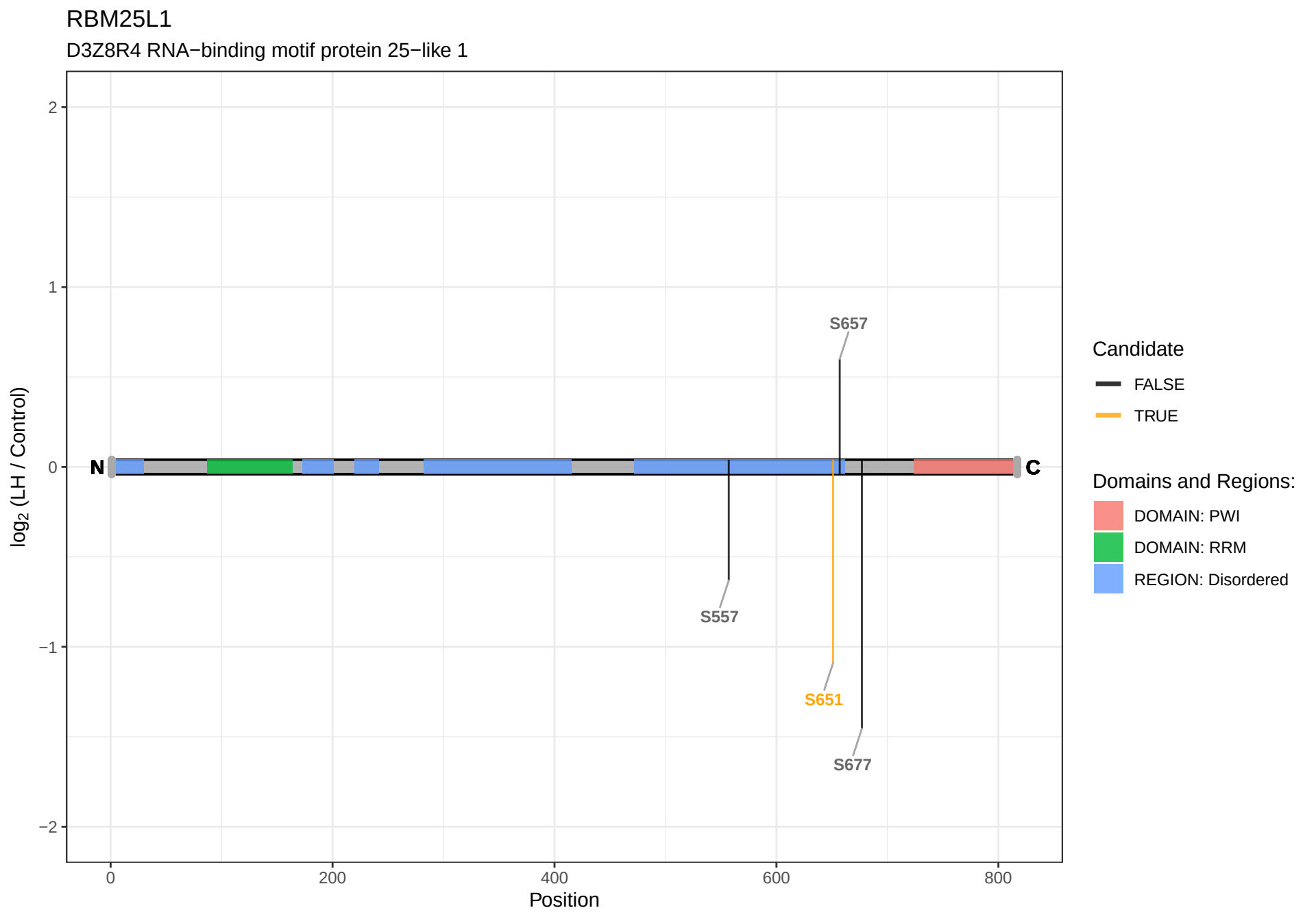

RBFOX2
A1A5R1 RNA binding protein fox−1 homolog 2
S27
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
400
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: RRM
REGION: Disordered

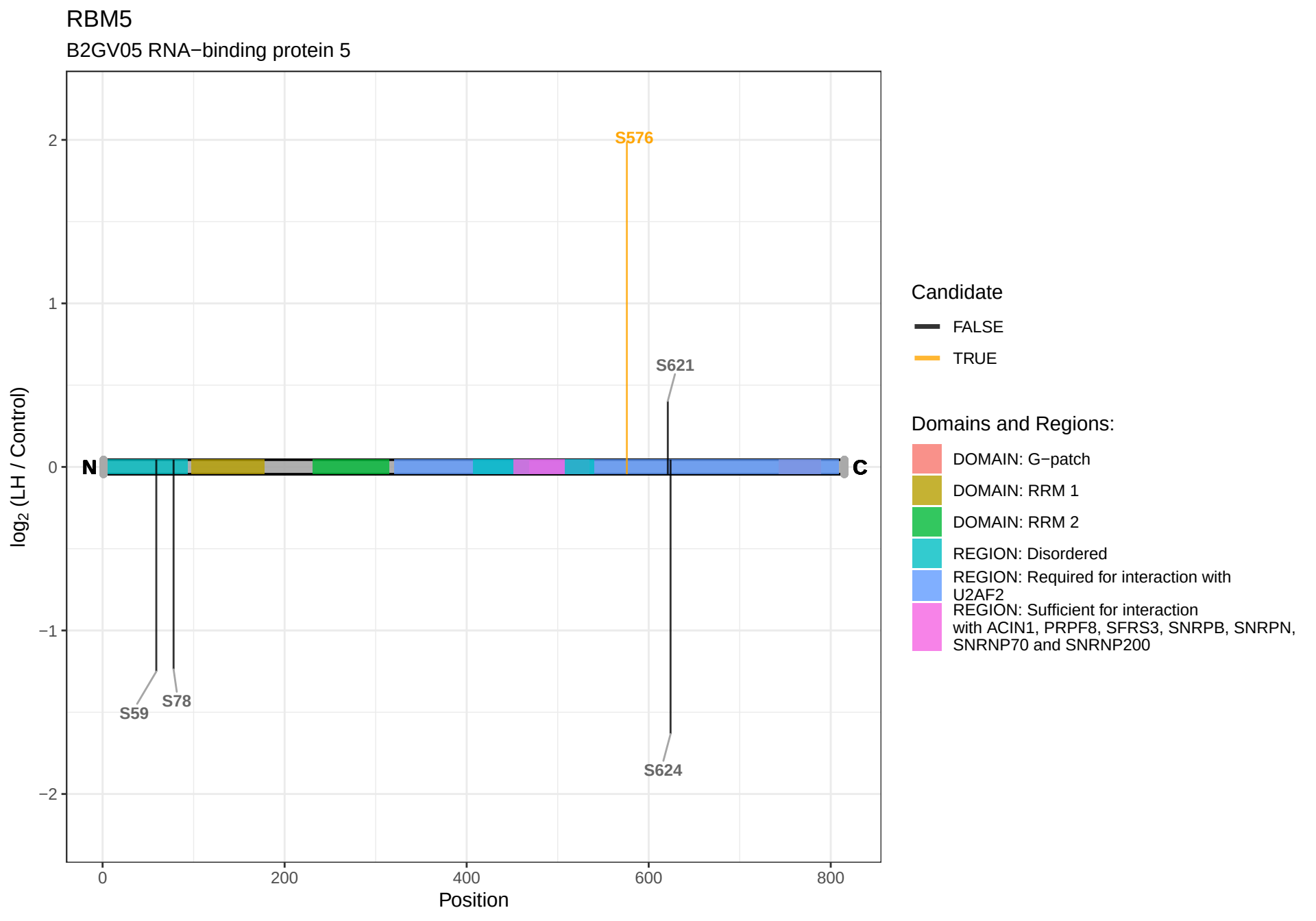

RBM12B
D3ZM54 RNA−binding motif protein 12B
S627
S250
S254
S277
S279
S564
S557
T673
S674
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RRM
REGION: Disordered

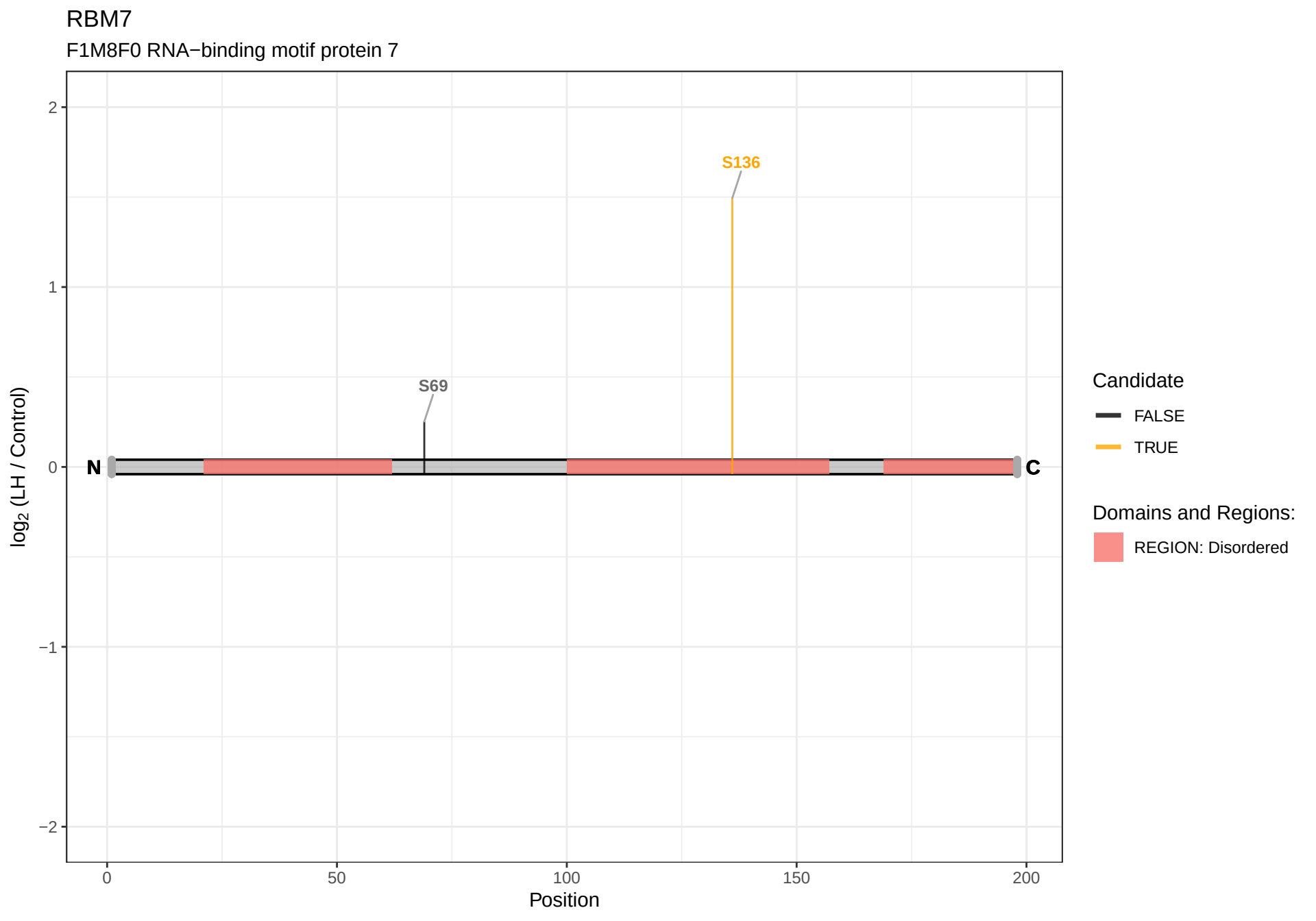

RBM14
M0R9Q1 RCG48334, isoform CRA_e
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
N
C
S618
S161
S627
S582
T572
T206
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RRM
REGION: Disordered

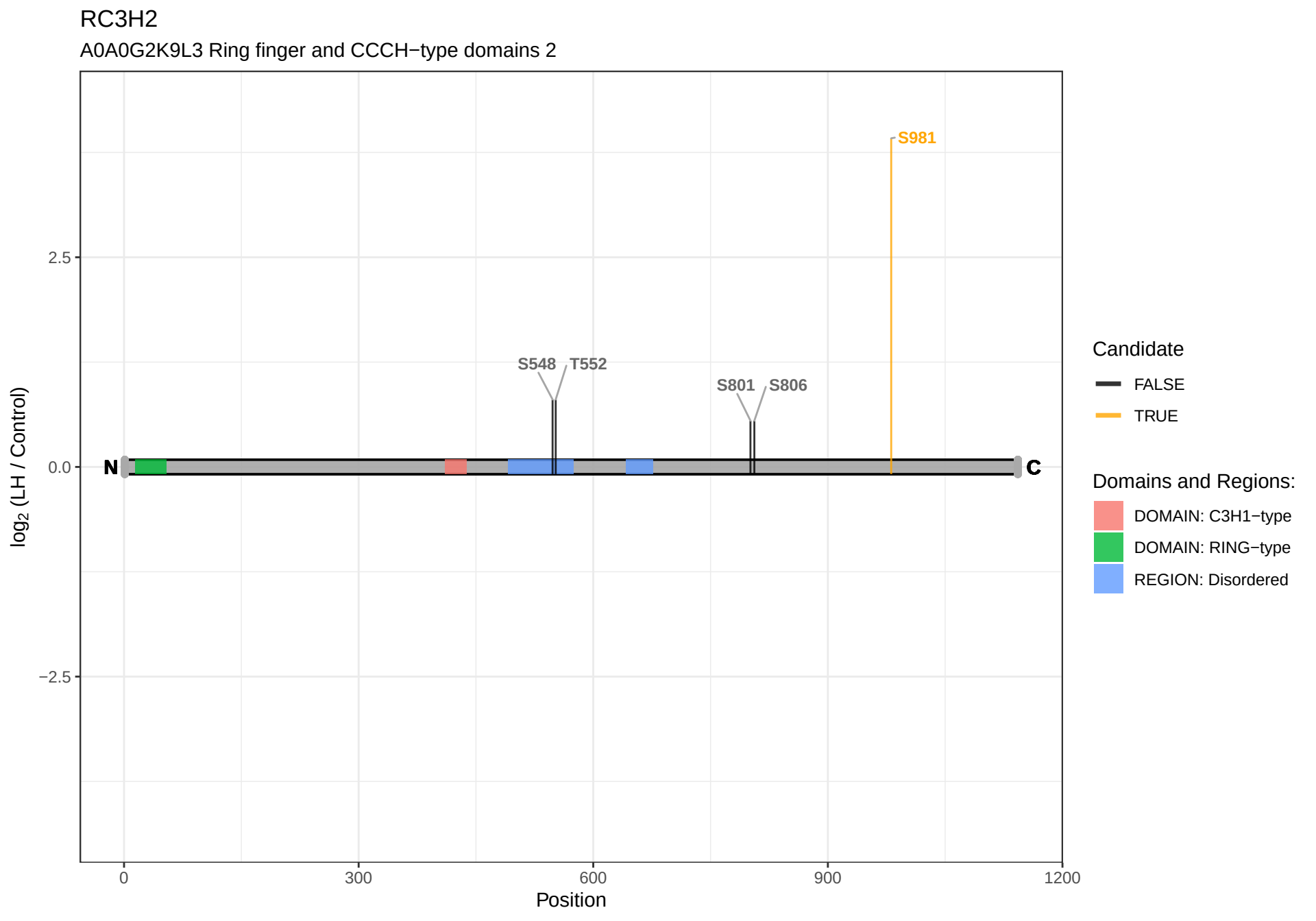

RBM15
M0R3Z8 RCG28930, isoform CRA_b
S124
T668
S674
S670
S658
N
C
S51
S108
S207
S211
S209
S256
S258
S291
S293
T567
S655
S782
T754
S725
S701
2
0
−2
log2 (LH / Control)
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RRM
DOMAIN: SPOC
REGION: Disordered

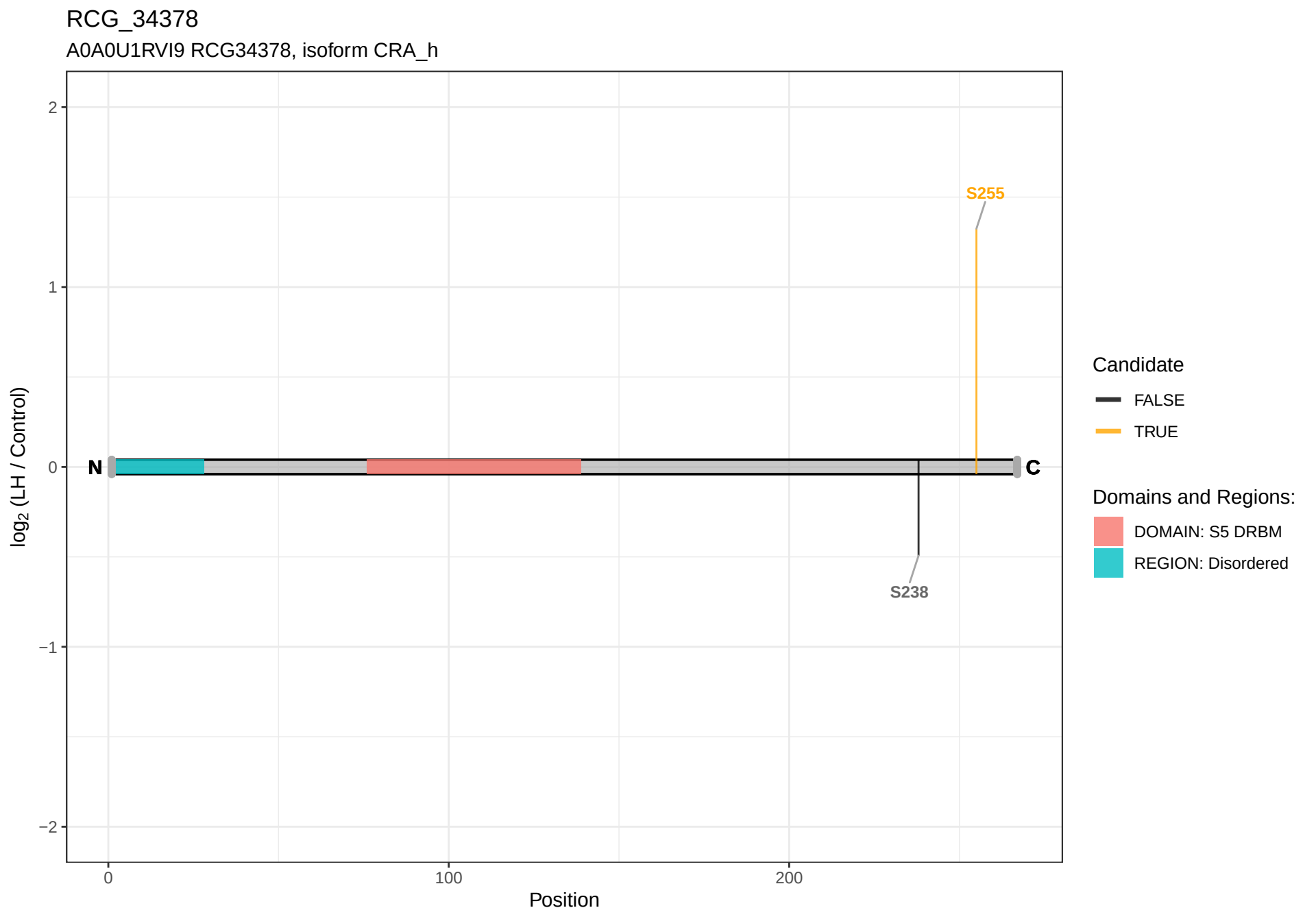

RBM17
Q6AY02 RNA−binding motif protein 17
5.0
2.5
0.0
−2.5
−5.0
log2 (LH / Control)
S169
S222
S155
N
C
0
100
200
300
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: G−patch
REGION: Disordered

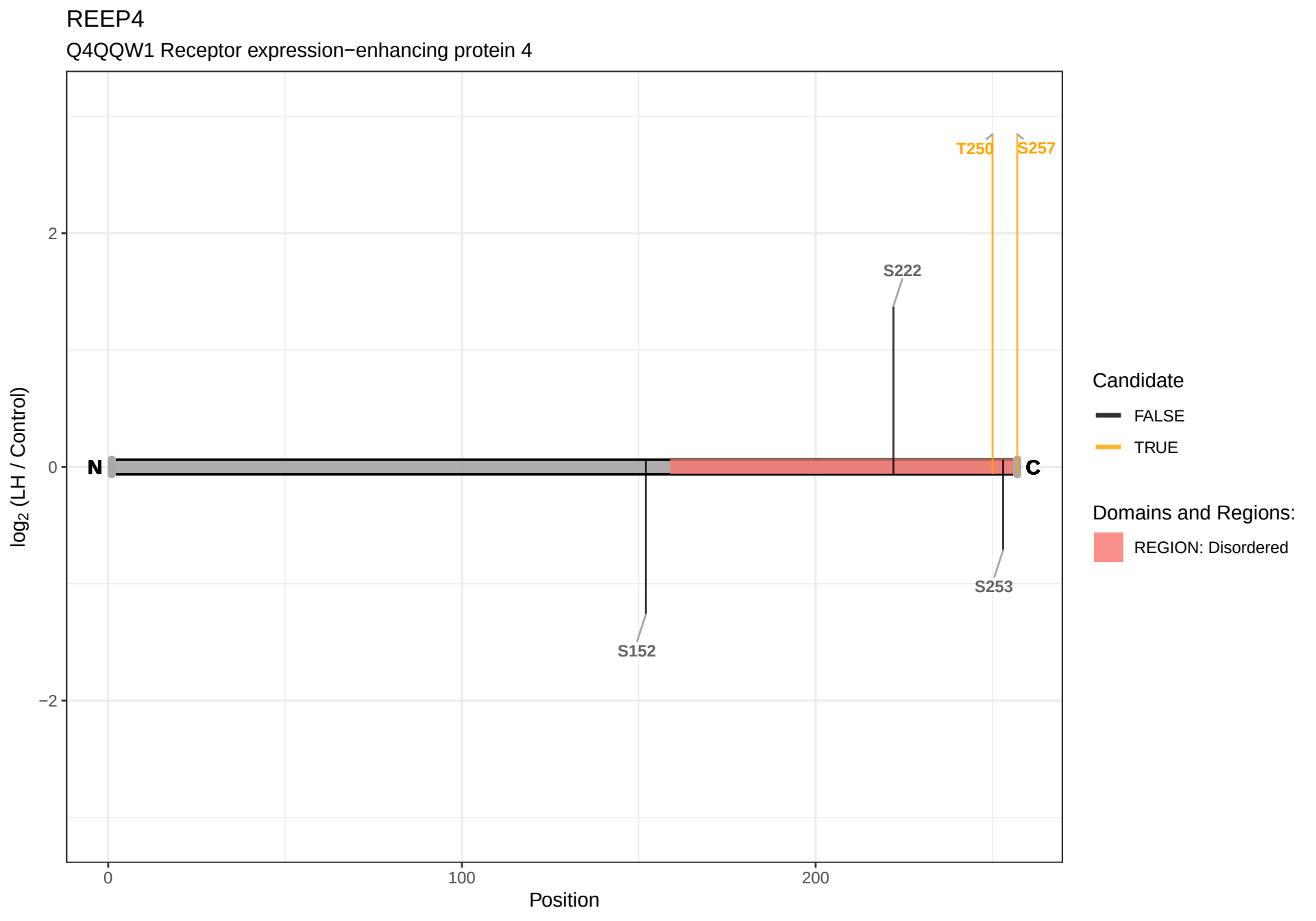

RBM25L1
D3Z8R4 RNA−binding motif protein 25−like 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S657
S557
S651
S677
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PWI
DOMAIN: RRM
REGION: Disordered

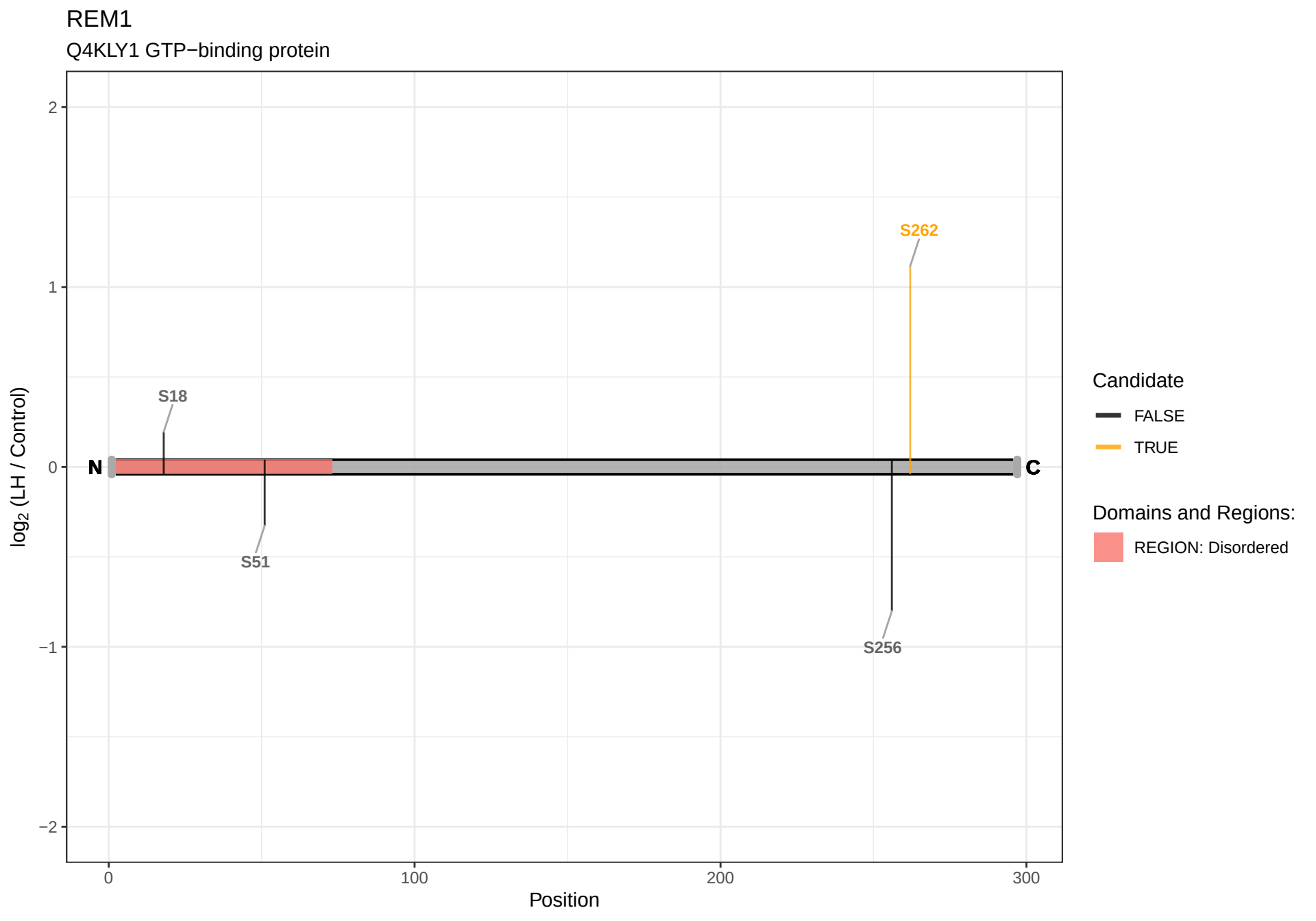

RBM5
B2GV05 RNA−binding protein 5
S576
S621
S59
S78
S624
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: G−patch
DOMAIN: RRM 1
DOMAIN: RRM 2
REGION: Disordered
REGION: Required for interaction with U2AF2
REGION: Sufficient for interaction with ACIN1, PRPF8, SFRS3, SNRPB, SNRPN, SNRNP70 and SNRNP200

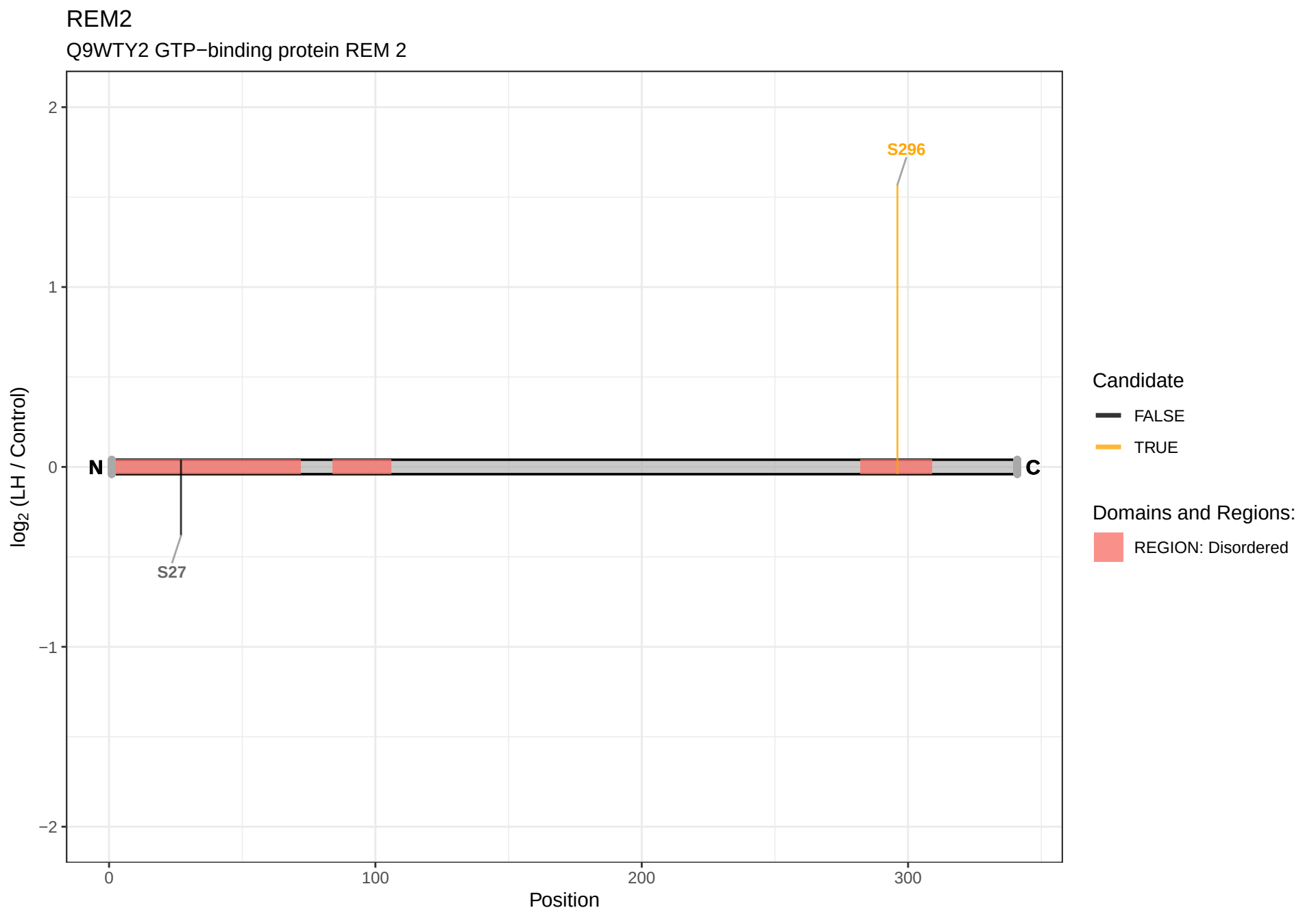

RBM7
F1M8F0 RNA−binding motif protein 7
S136
S69
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
50
100
150
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

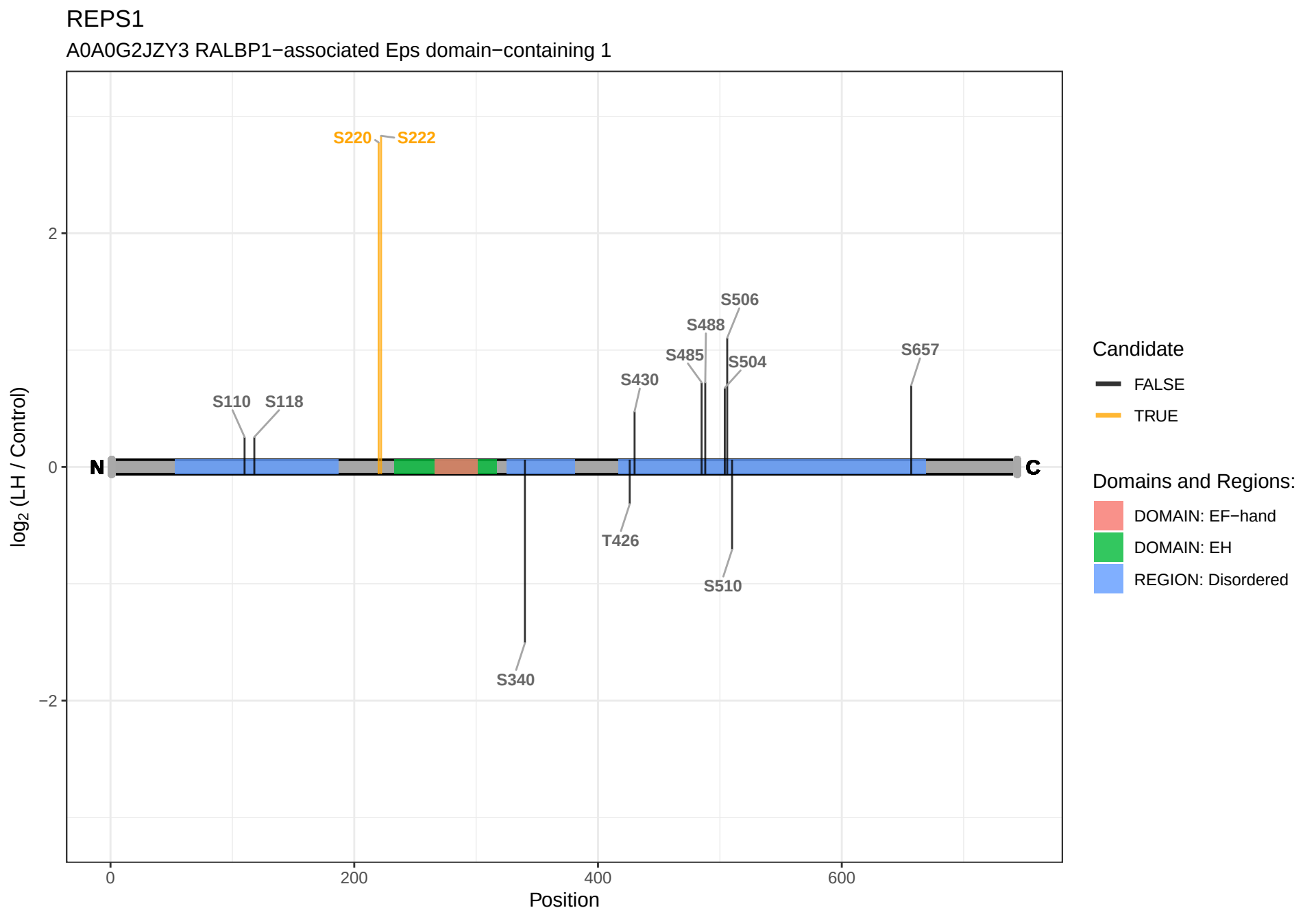

RC3H2
A0A0G2K9L3 Ring finger and CCCH−type domains 2
S981
S548
T552
S801
S806
N
C
2.5
0.0
−2.5
log2 (LH / Control)
0
300
600
900
1200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C3H1−type
DOMAIN: RING−type
REGION: Disordered

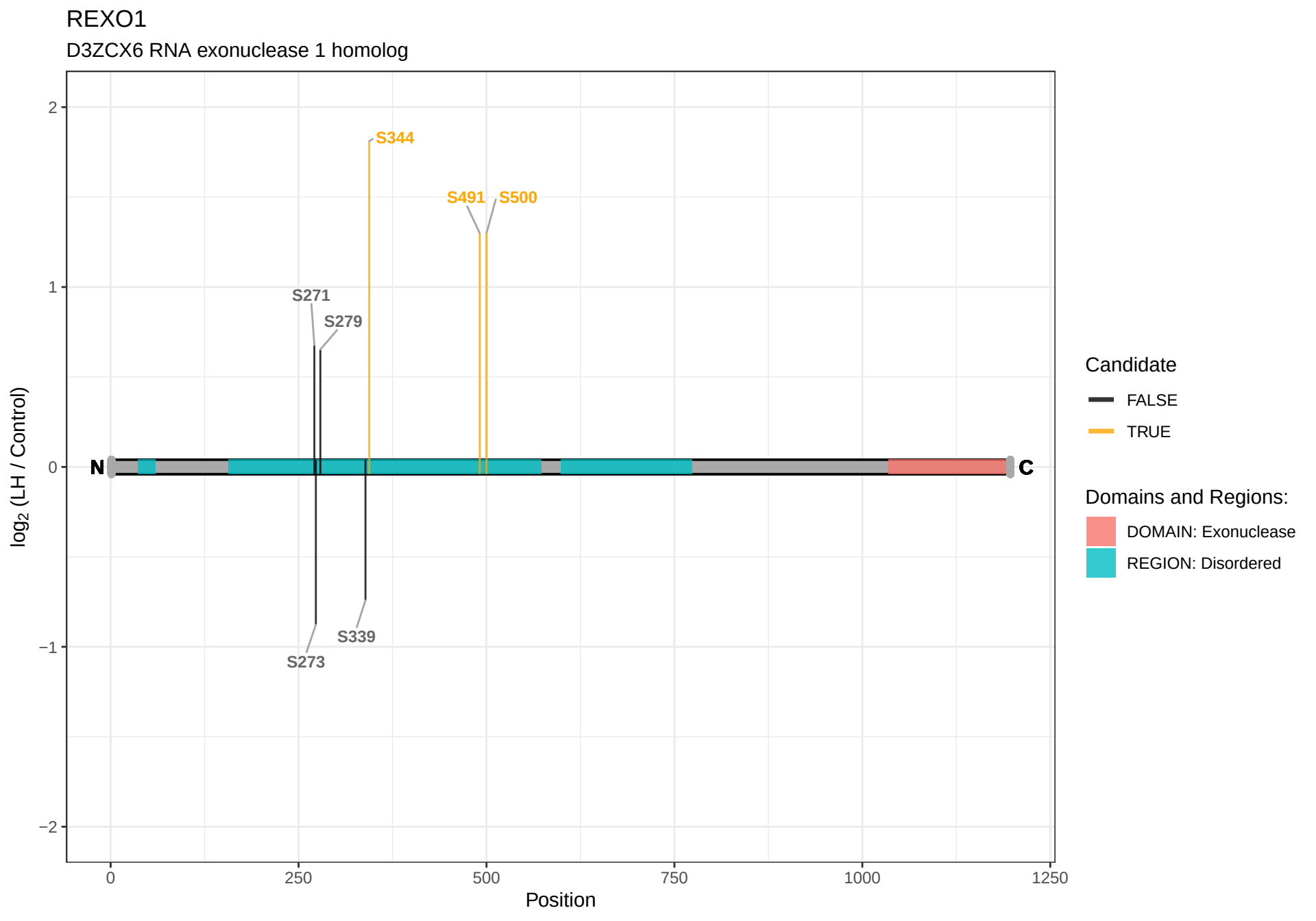

RCG_34378
A0A0U1RVI9 RCG34378, isoform CRA_h
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
Position
N
C
S255
S238
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: S5 DRBM
REGION: Disordered

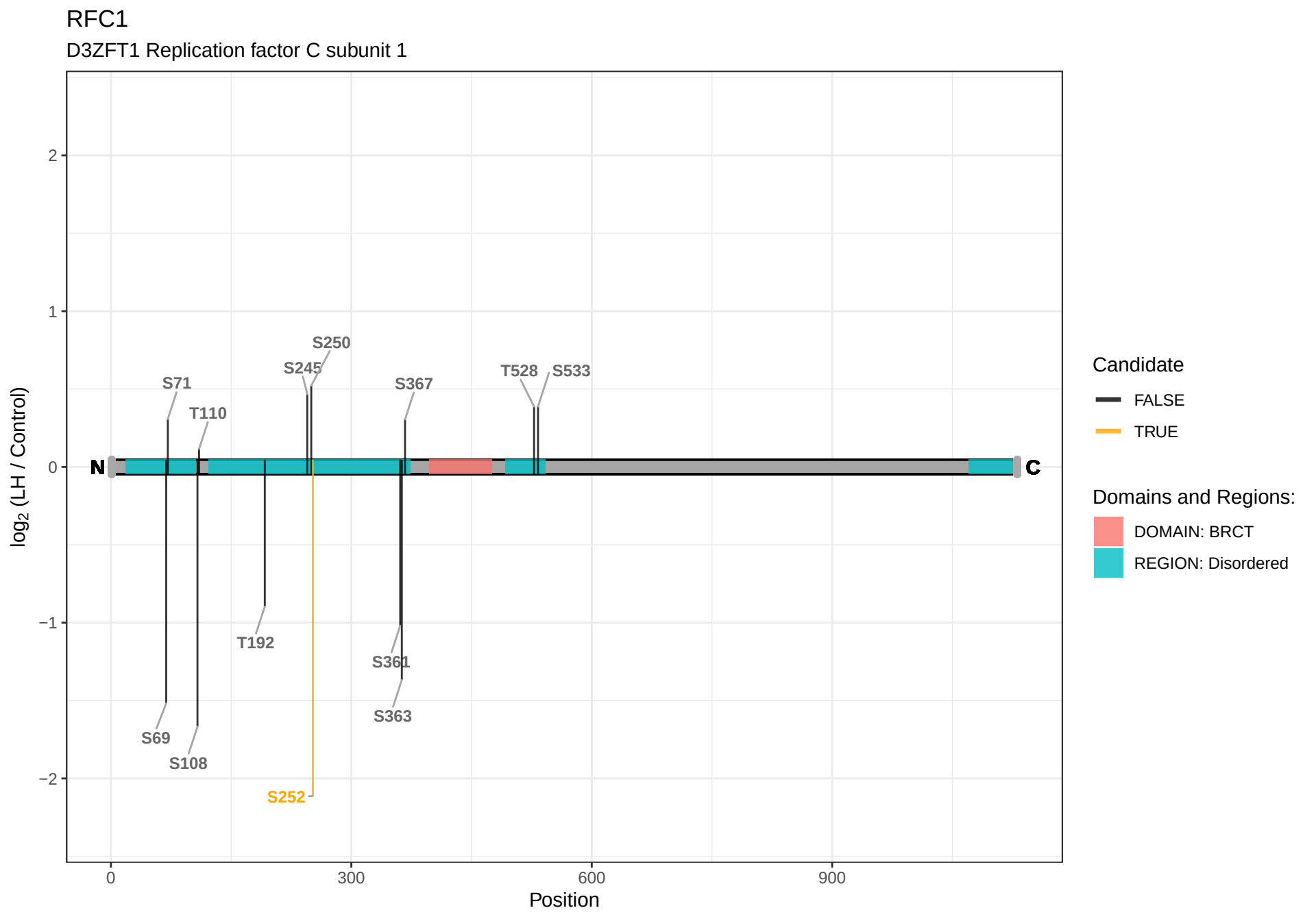

REEP4
Q4QQW1 Receptor expression−enhancing protein 4
T250
S257
S222
S253
S152
N
C
2
0
−2
log2 (LH / Control)
0
100
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

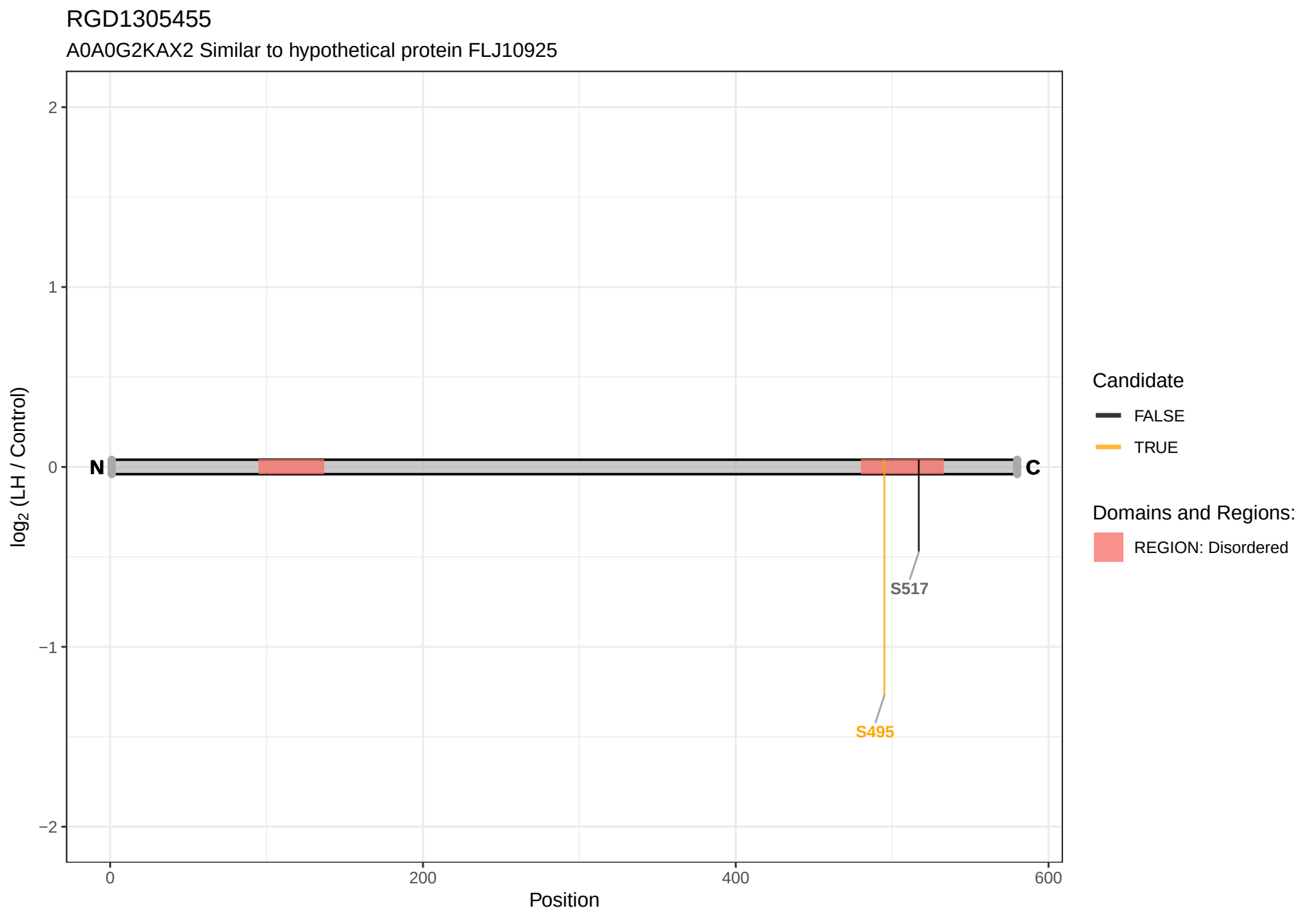

REM1
Q4KLY1 GTP−binding protein
2
1
0
−1
−2
log2 (LH / Control)
S18
S51
S256
S262
N
C
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

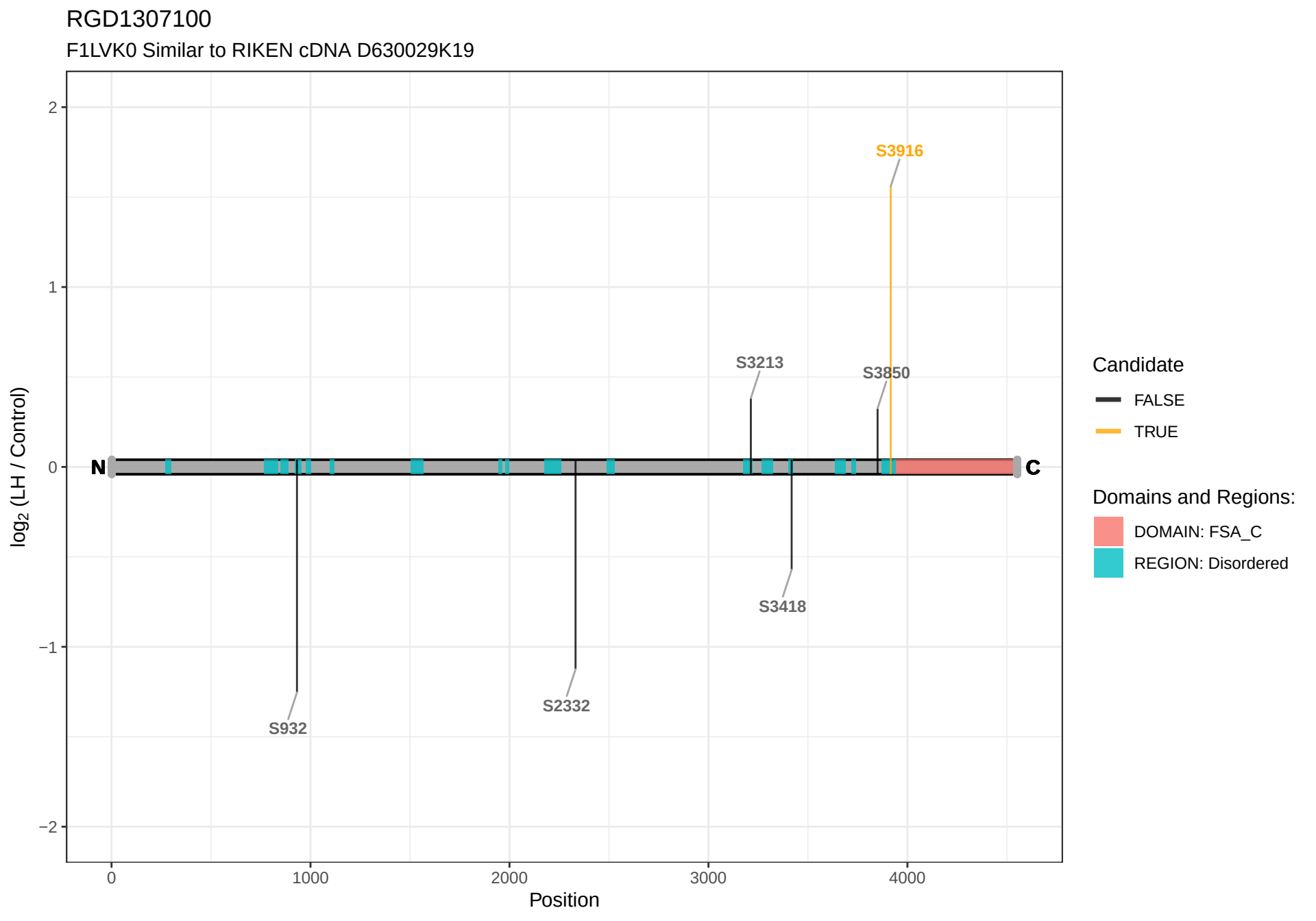

REM2
Q9WTY2 GTP−binding protein REM 2
2
1
0
−1
−2
log2 (LH / Control)
S296
S27
N
C
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered


REPS1
A0A0G2JZY3 RALBP1−associated Eps domain−containing 1
S220
S222
S506
S488
S485
S504
S657
S430
S110
S118
N
C
T426
S510
S340
2
0
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: EF−hand
DOMAIN: EH
REGION: Disordered


REXO1
D3ZCX6 RNA exonuclease 1 homolog
S344
S491
S500
S271
S279
S339
S273
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
250
500
750
1000
1250
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Exonuclease
REGION: Disordered

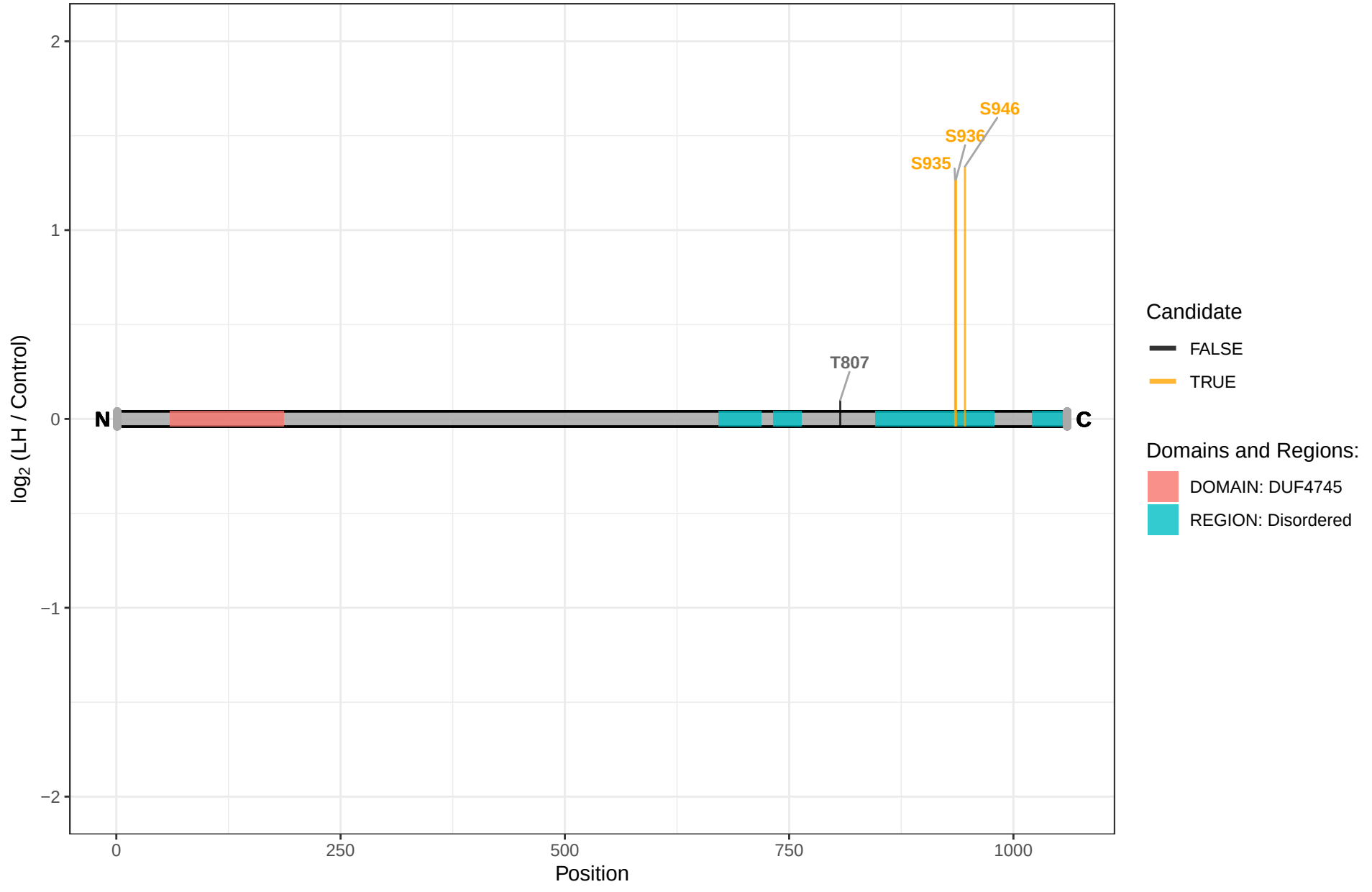

RFC1
D3ZFT1 Replication factor C subunit 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S71
T110
S250
S245
S367
T528
S533
T192
S361
S363
S69
S108
S252
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: BRCT
REGION: Disordered

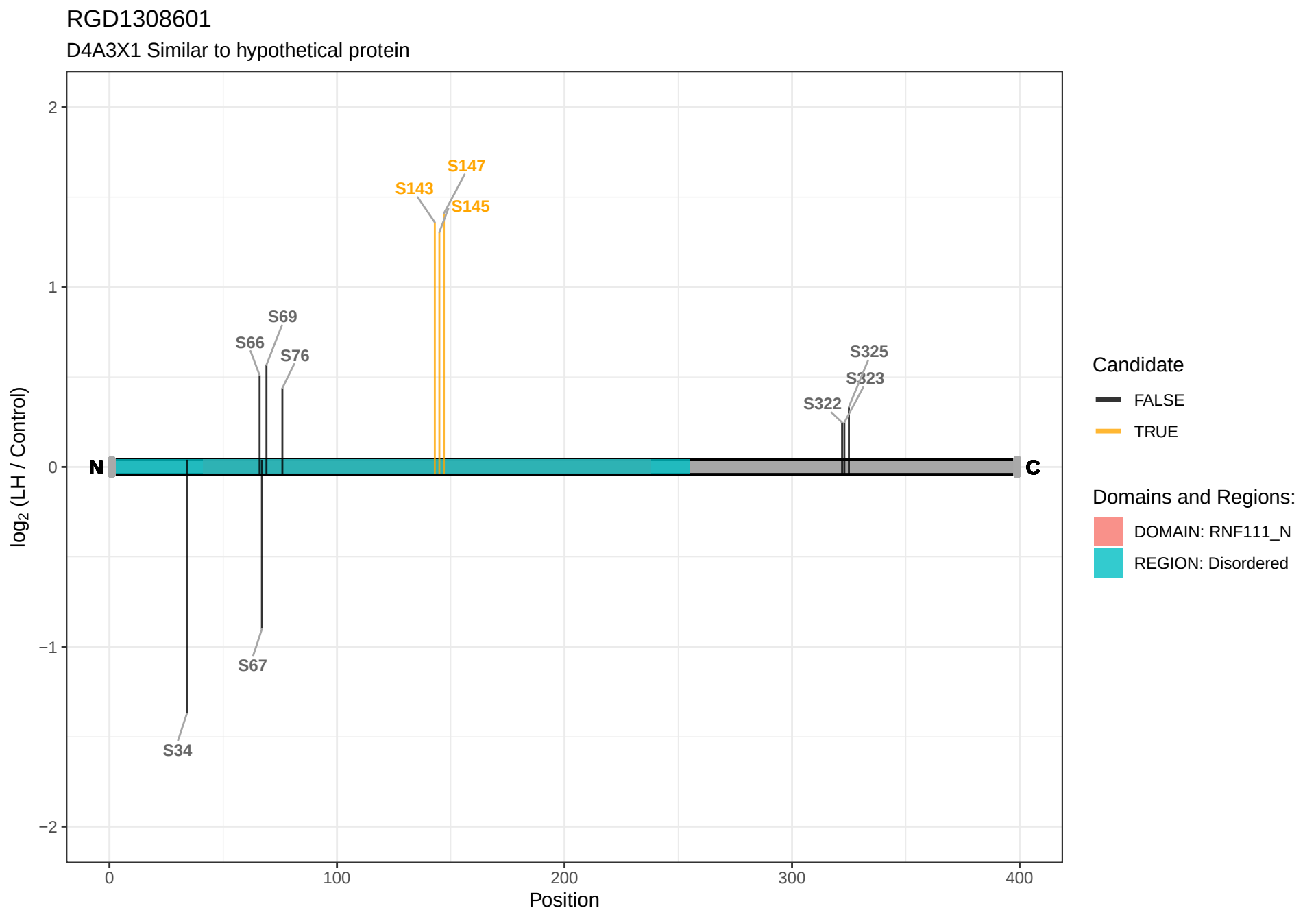

RGD1305455
A0A0G2KAX2 Similar to hypothetical protein FLJ10925
log2 (LH / Control)
2
1
0
−1
−2
N
C
S517
S495
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

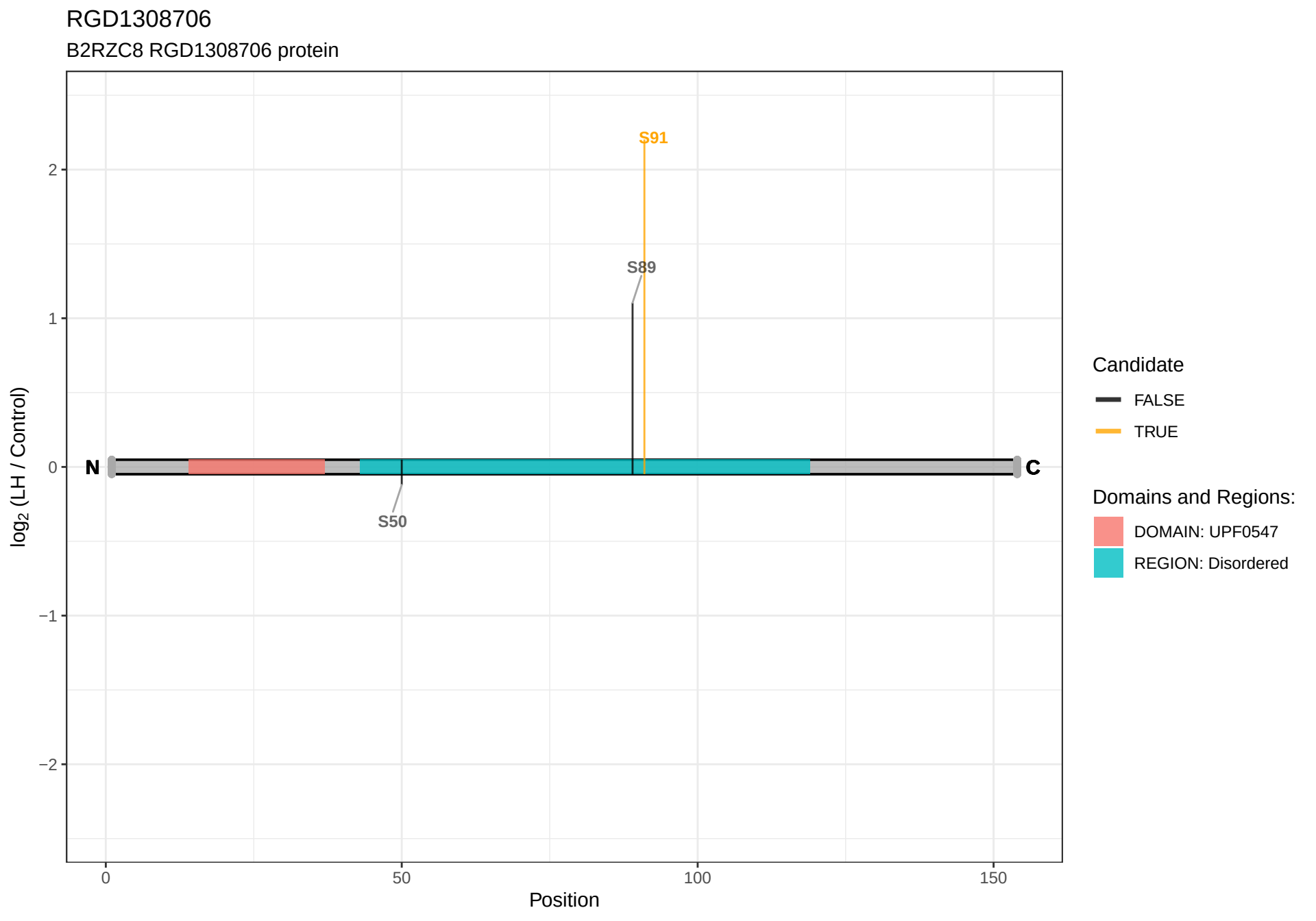

RGD1307100
F1LVK0 Similar to RIKEN cDNA D630029K19
log2 (LH / Control)
2
1
0
−1
−2
0
1000
2000
3000
4000
Position
N
C
S3916
S3213
S3850
S3418
S2332
S932
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: FSA_C
REGION: Disordered

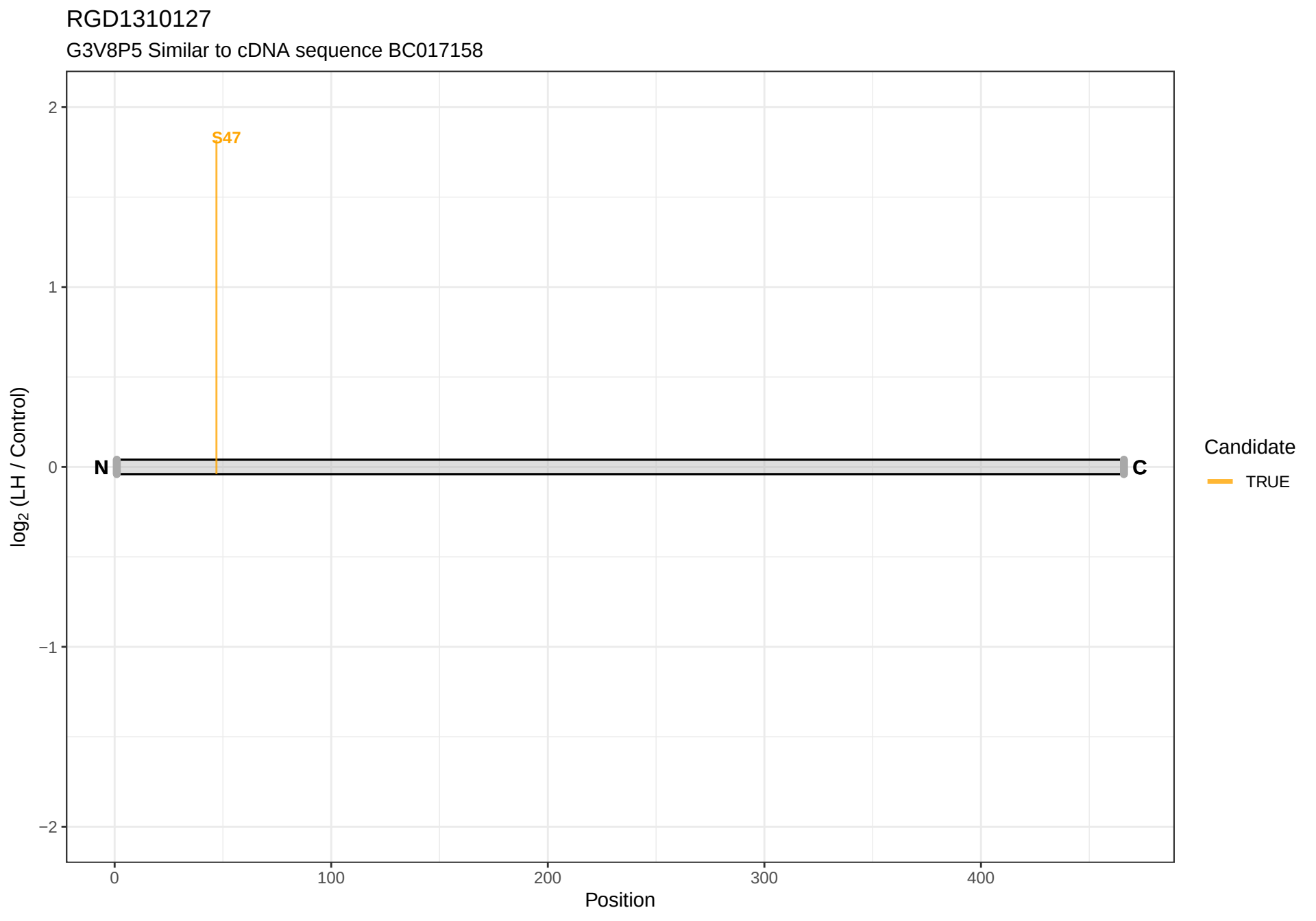
RGD1308428

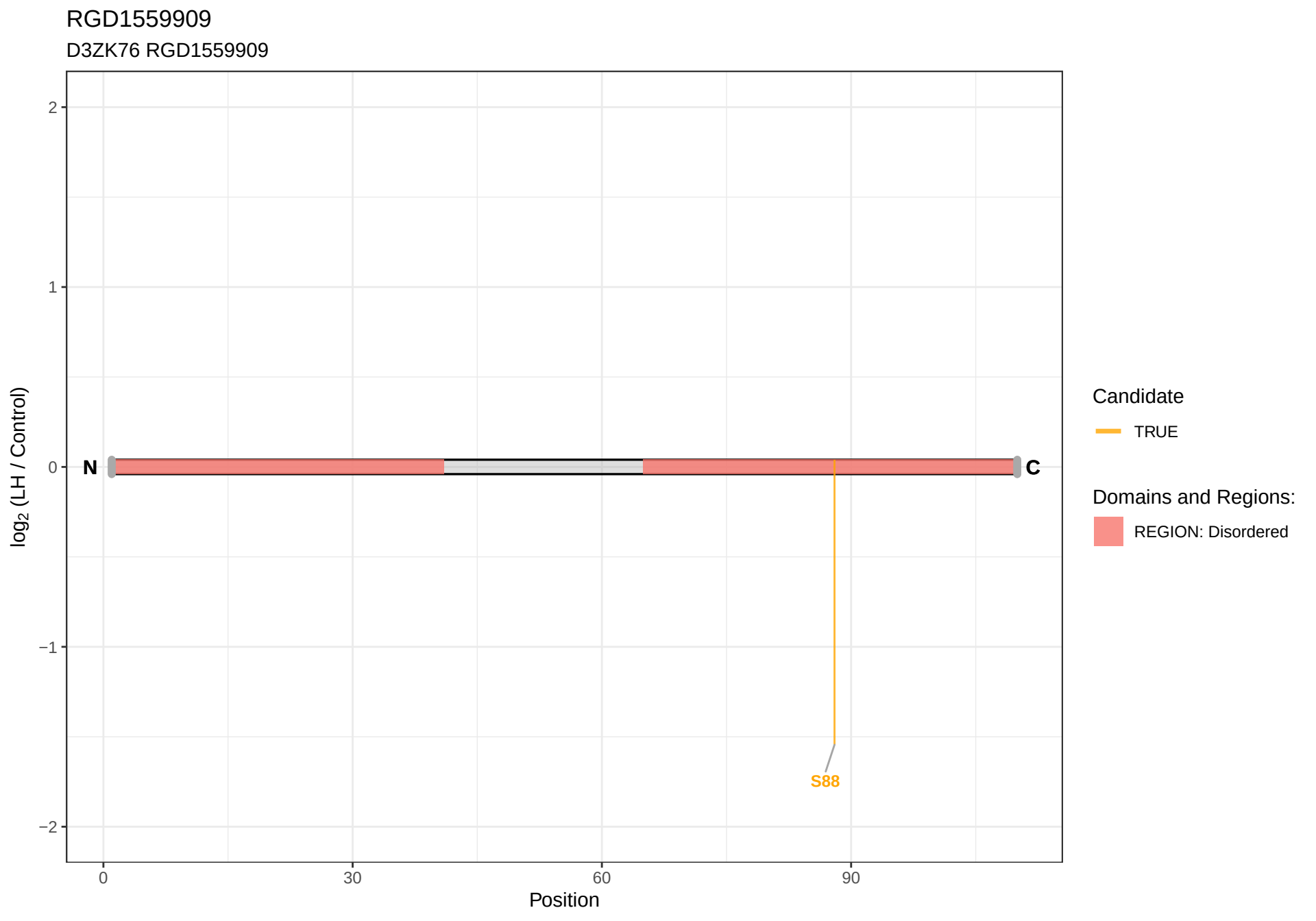
F1M037 Similar to RIKEN cDNA 4931406P16

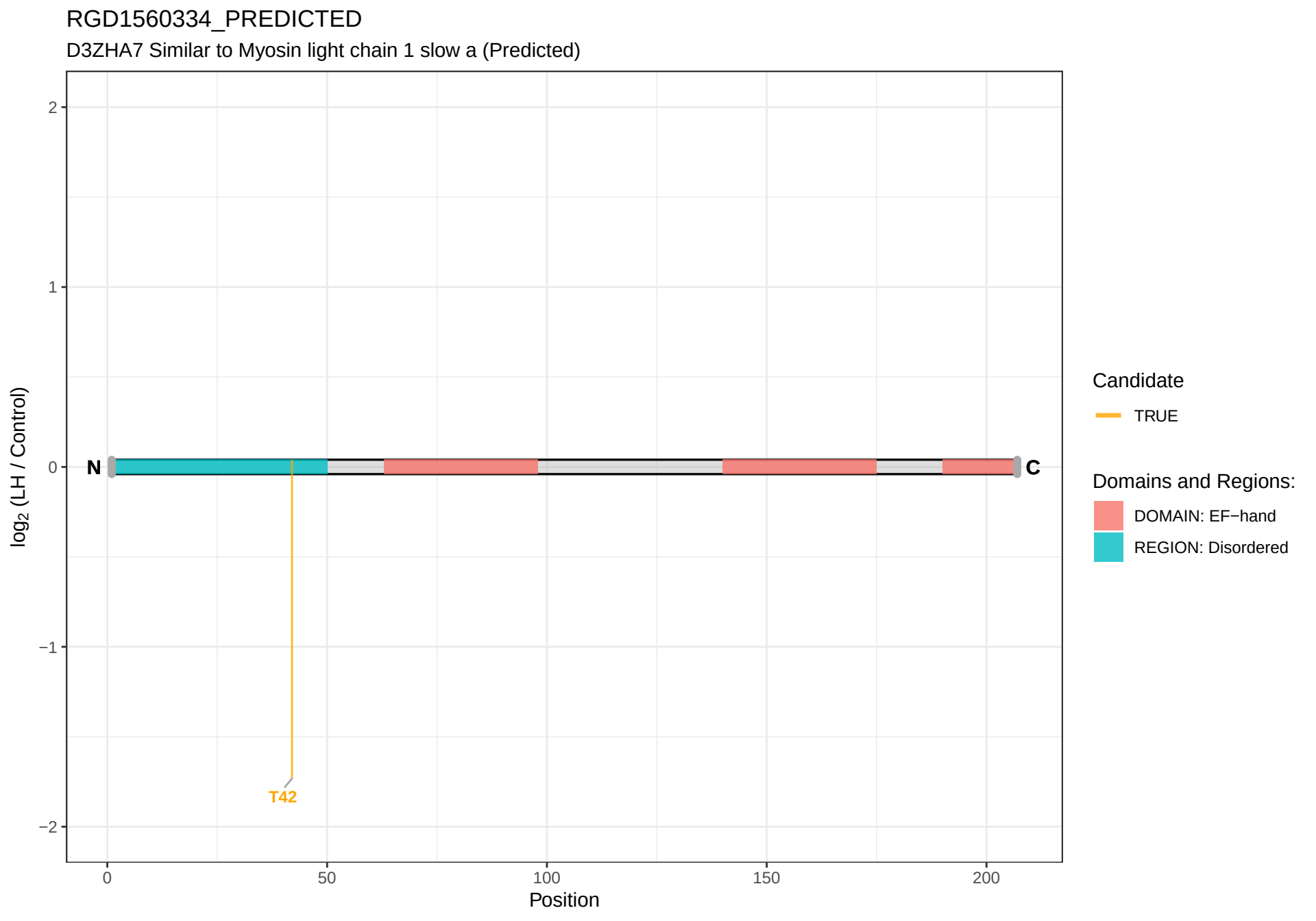


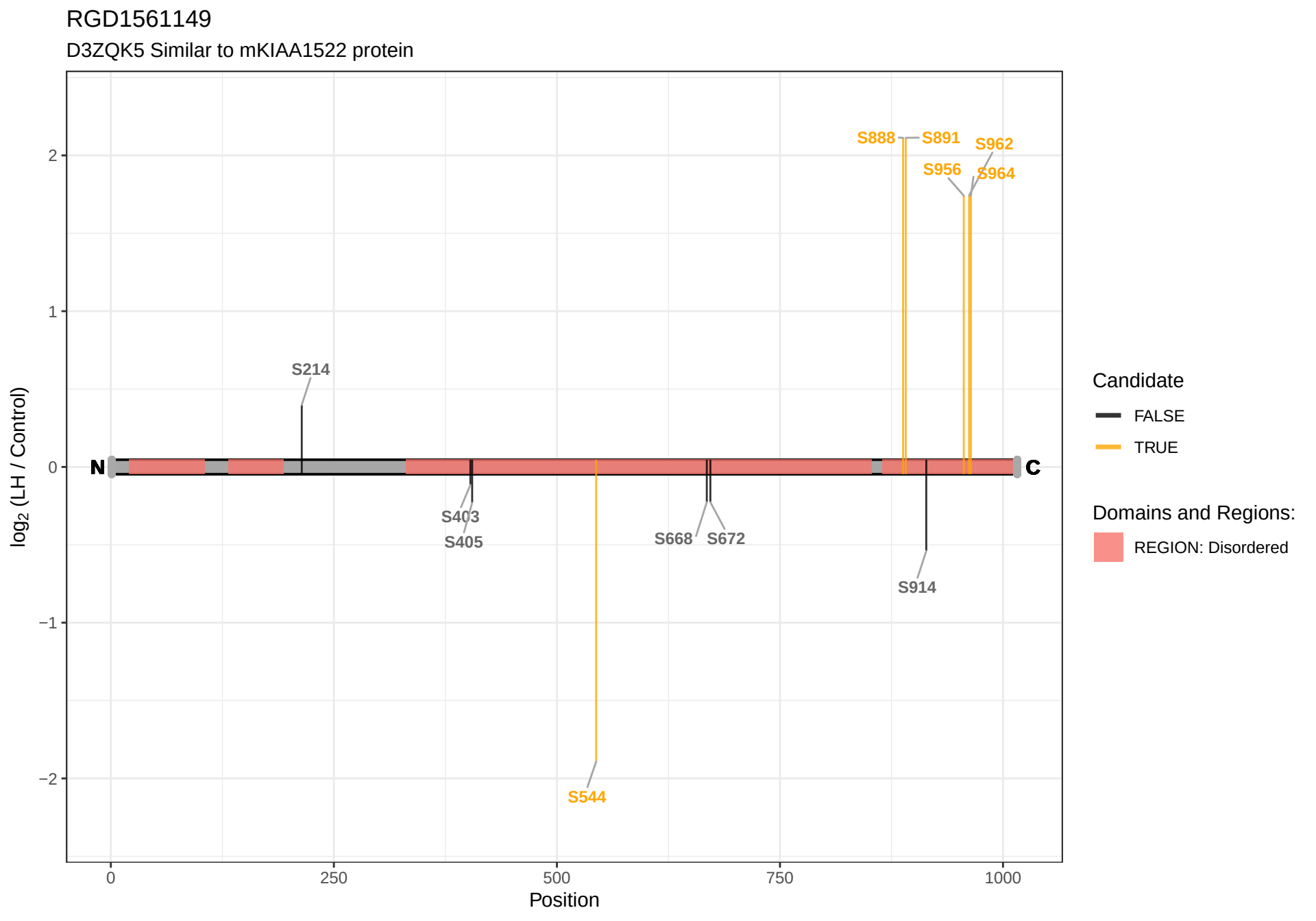

RGD1308601
D4A3X1 Similar to hypothetical protein
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
400
Position
N
C
S147
S143
S145
S69
S66
S76
S325
S323
S322
S67
S34
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RNF111_N
REGION: Disordered

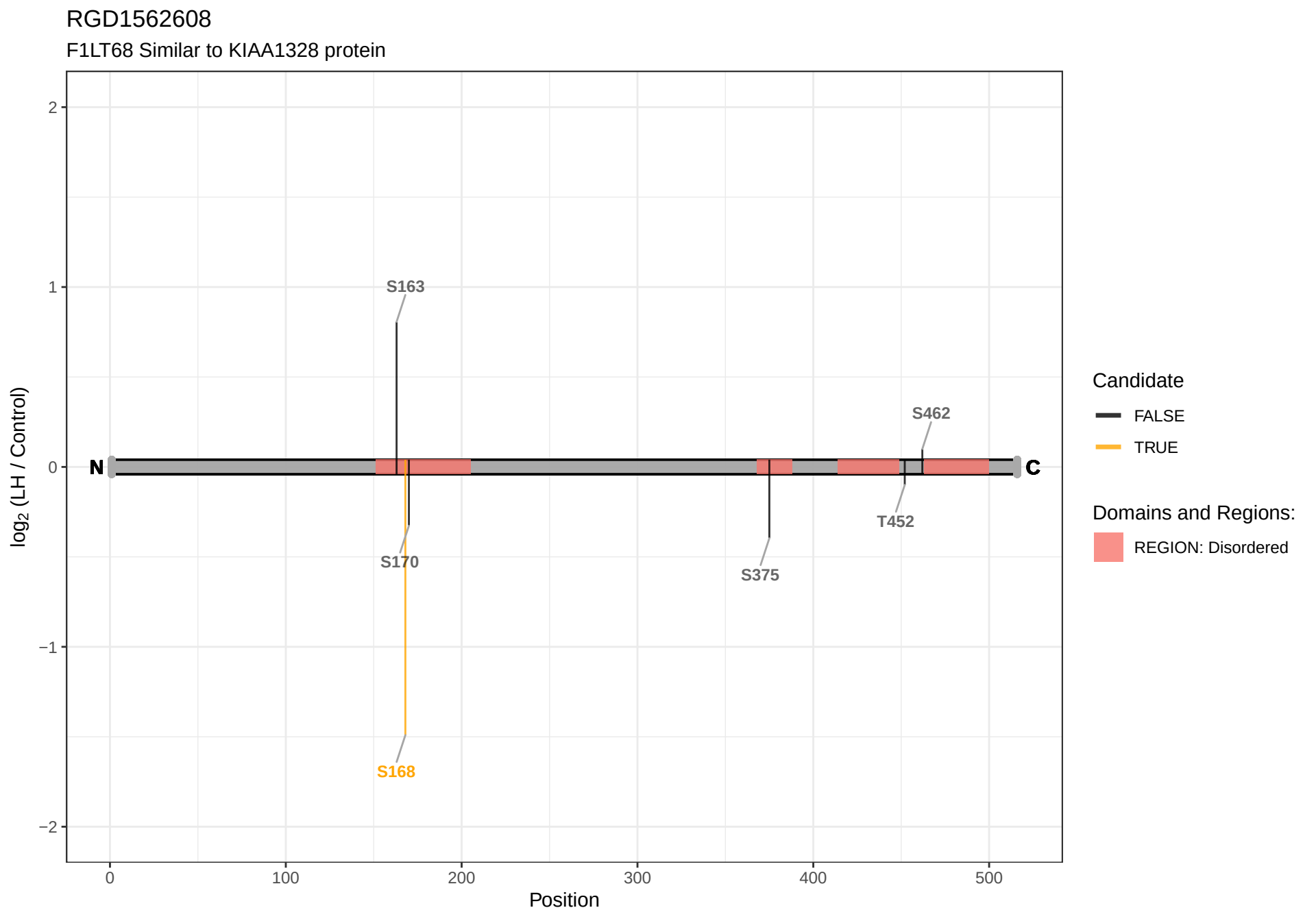

RGD1308706
B2RZC8 RGD1308706 protein
S91
S89
S50
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
50
100
150
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: UPF0547
REGION: Disordered

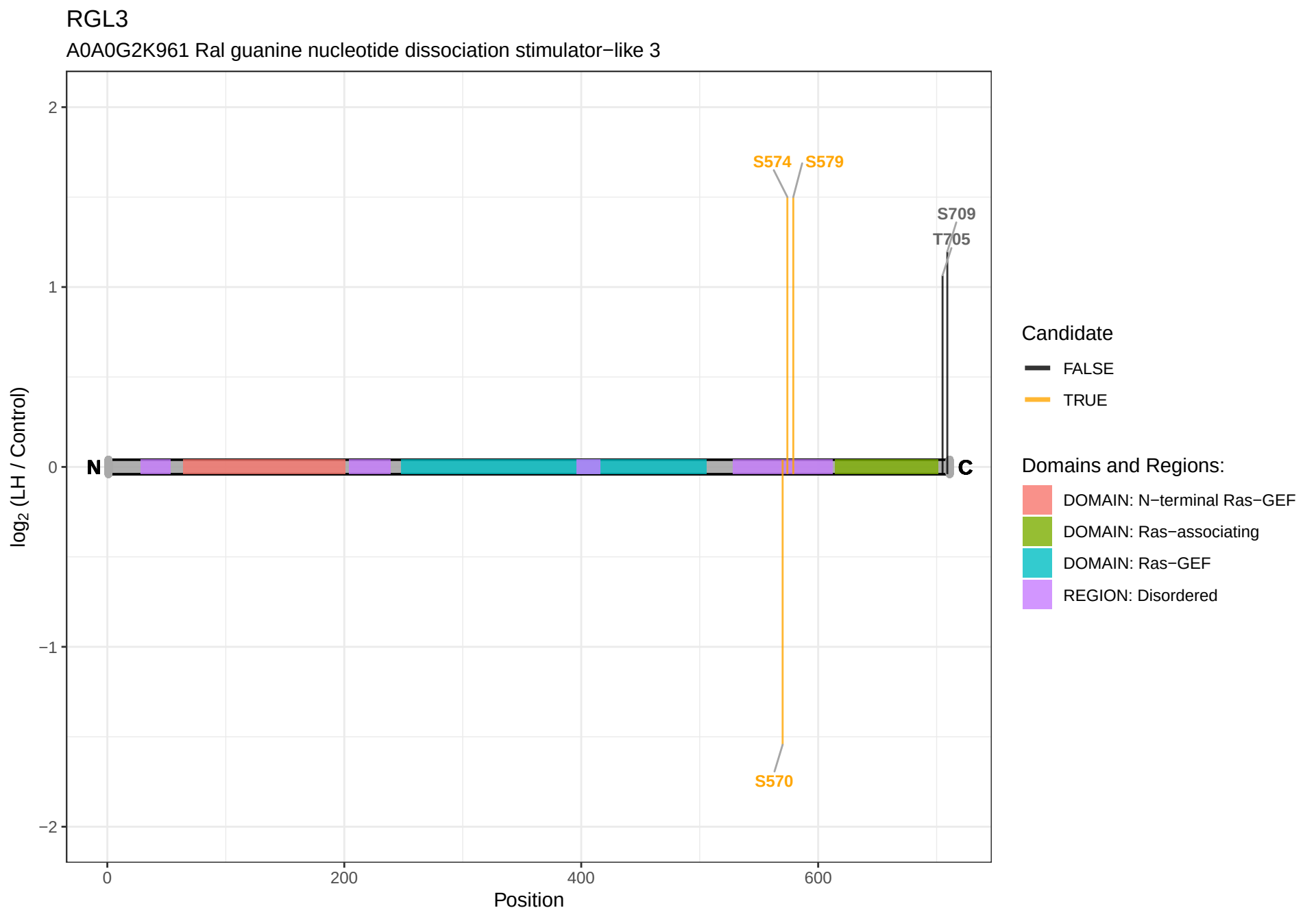

RGD1310127
G3V8P5 Similar to cDNA sequence BC017158
S47
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
400
Position
Candidate
TRUE

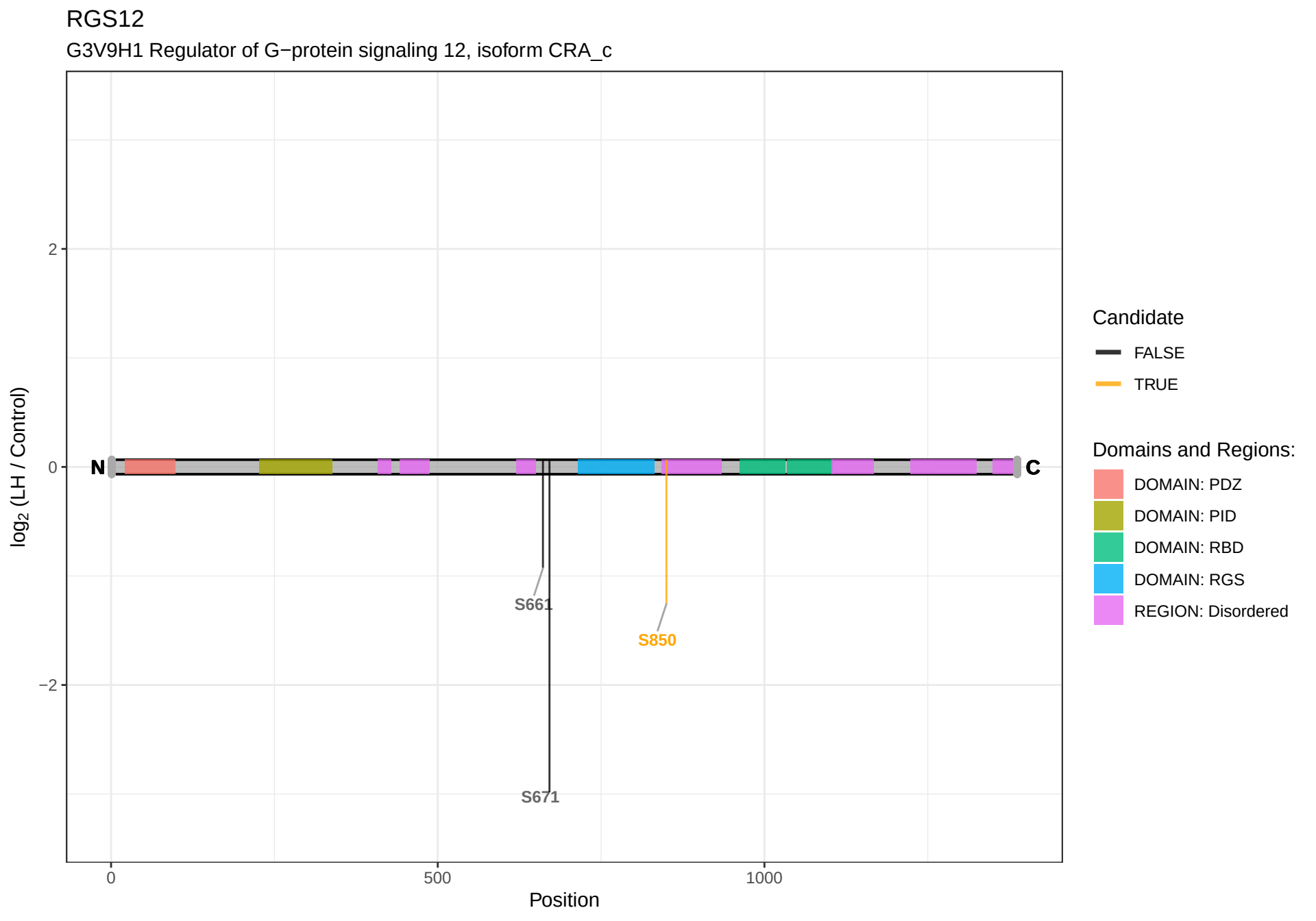

RGD1559909
D3ZK76 RGD1559909
2
1
0
−1
−2
log2 (LH / Control)
N
C
S88
0
30
60
90
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

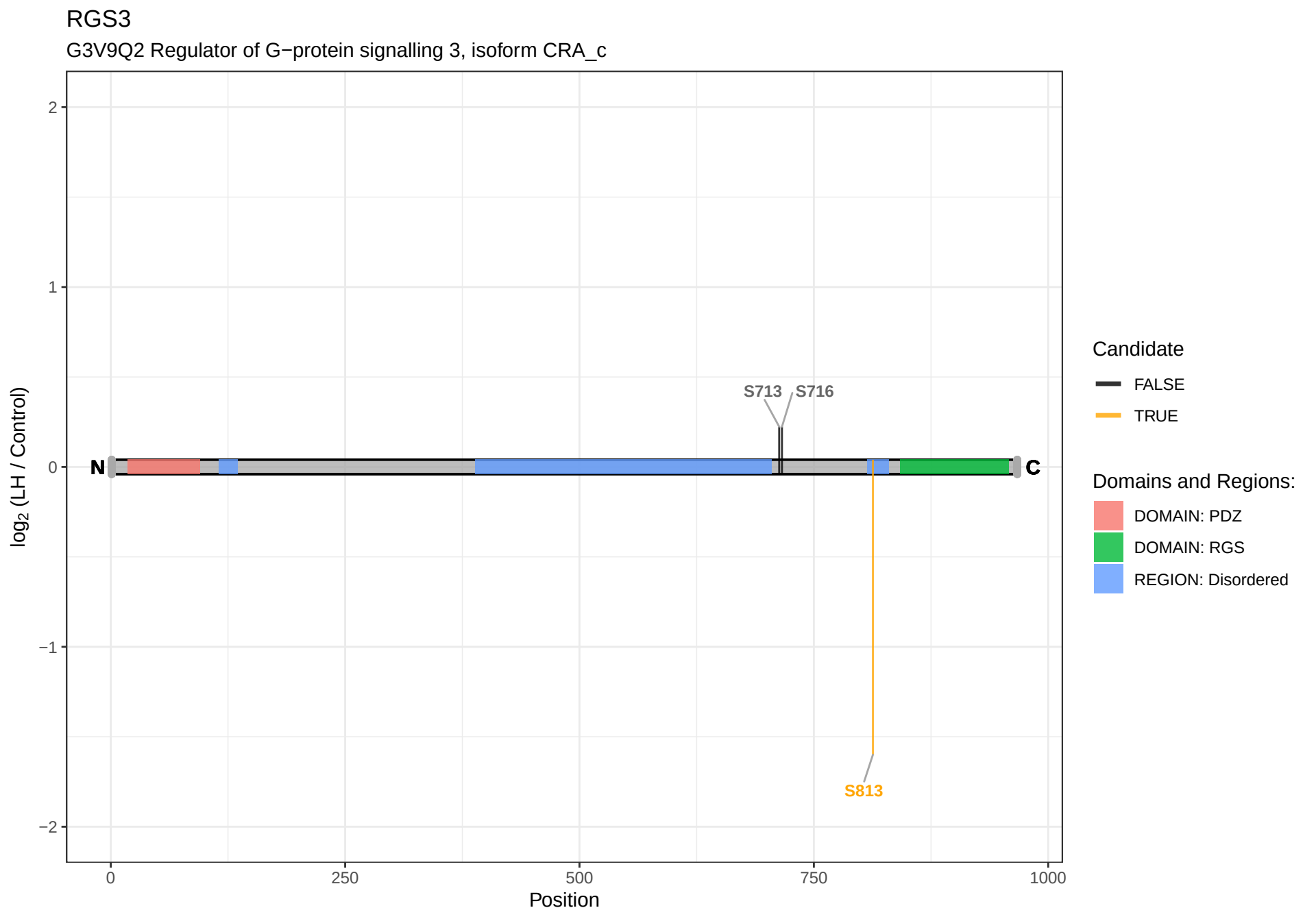

RGD1560334_PREDICTED
D3ZHA7 Similar to Myosin light chain 1 slow a (Predicted)
log2 (LH / Control)
2
1
0
−1
−2
N
C
T42
0
50
100
150
200
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: EF−hand
REGION: Disordered

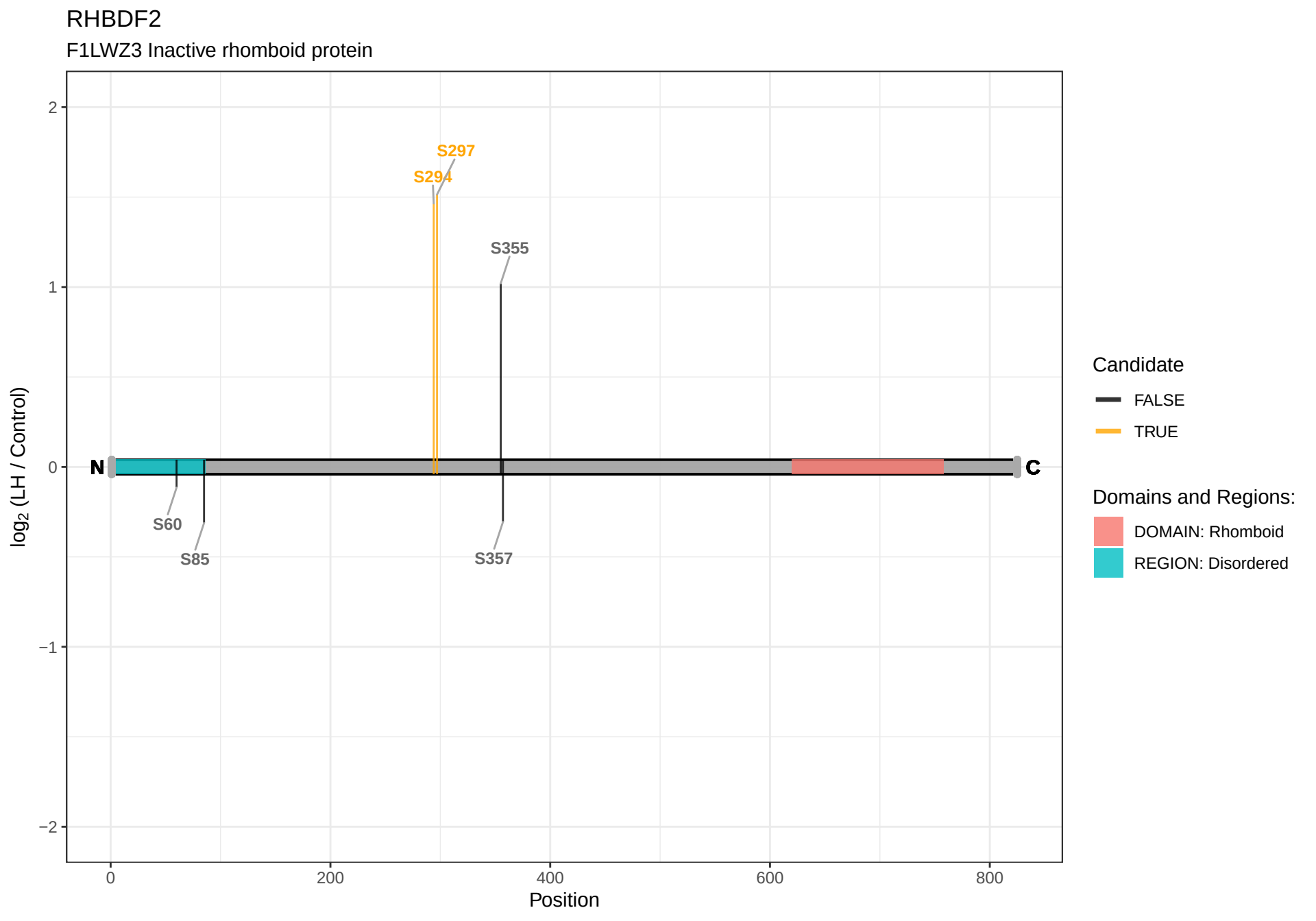

RGD1561149
D3ZQK5 Similar to mKIAA1522 protein
log2 (LH / Control)
2
1
0
−1
−2
N
C
S214
S403
S405
S544
S668
S672
S888
S891
S914
S956
S962
S964
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

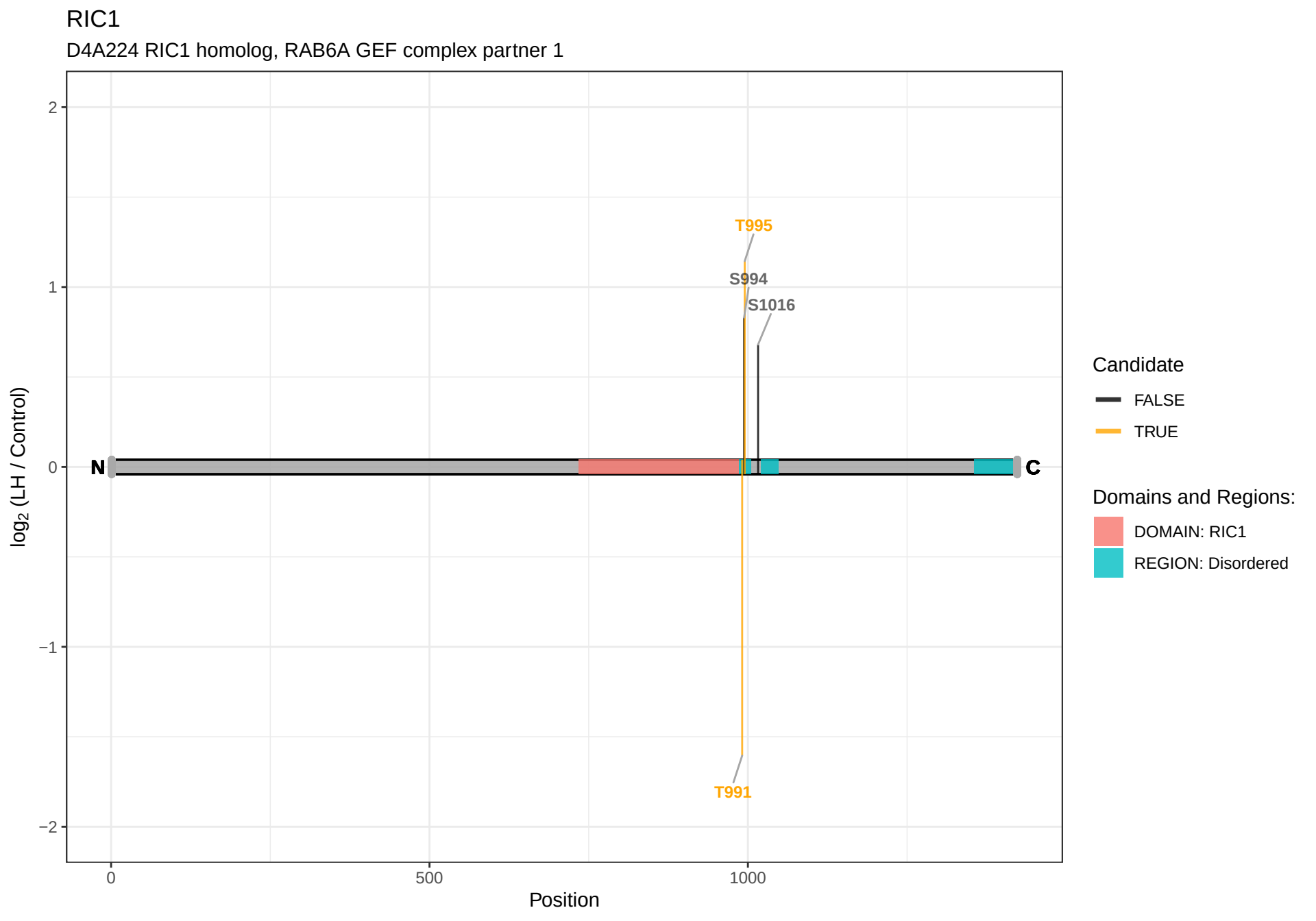

RGD1562608
F1LT68 Similar to KIAA1328 protein
log2 (LH / Control)
2
1
0
−1
−2
N
C
S163
S170
S168
S375
T452
S462
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

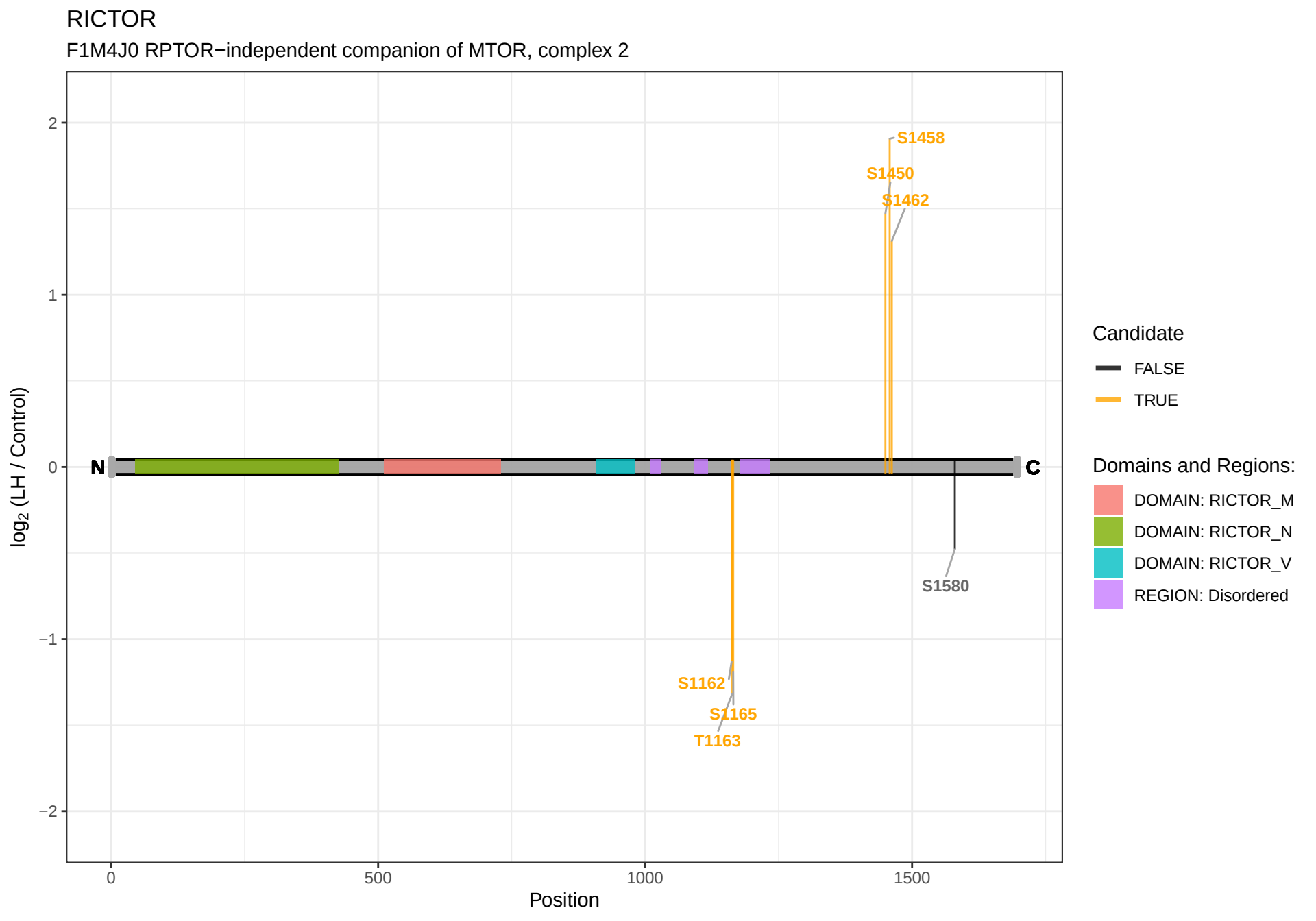

RGL3
A0A0G2K961 Ral guanine nucleotide dissociation stimulator−like 3
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
Position
S574
S579
S709
T705
S570
N
C
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: N−terminal Ras−GEF
DOMAIN: Ras−associating
DOMAIN: Ras−GEF
REGION: Disordered

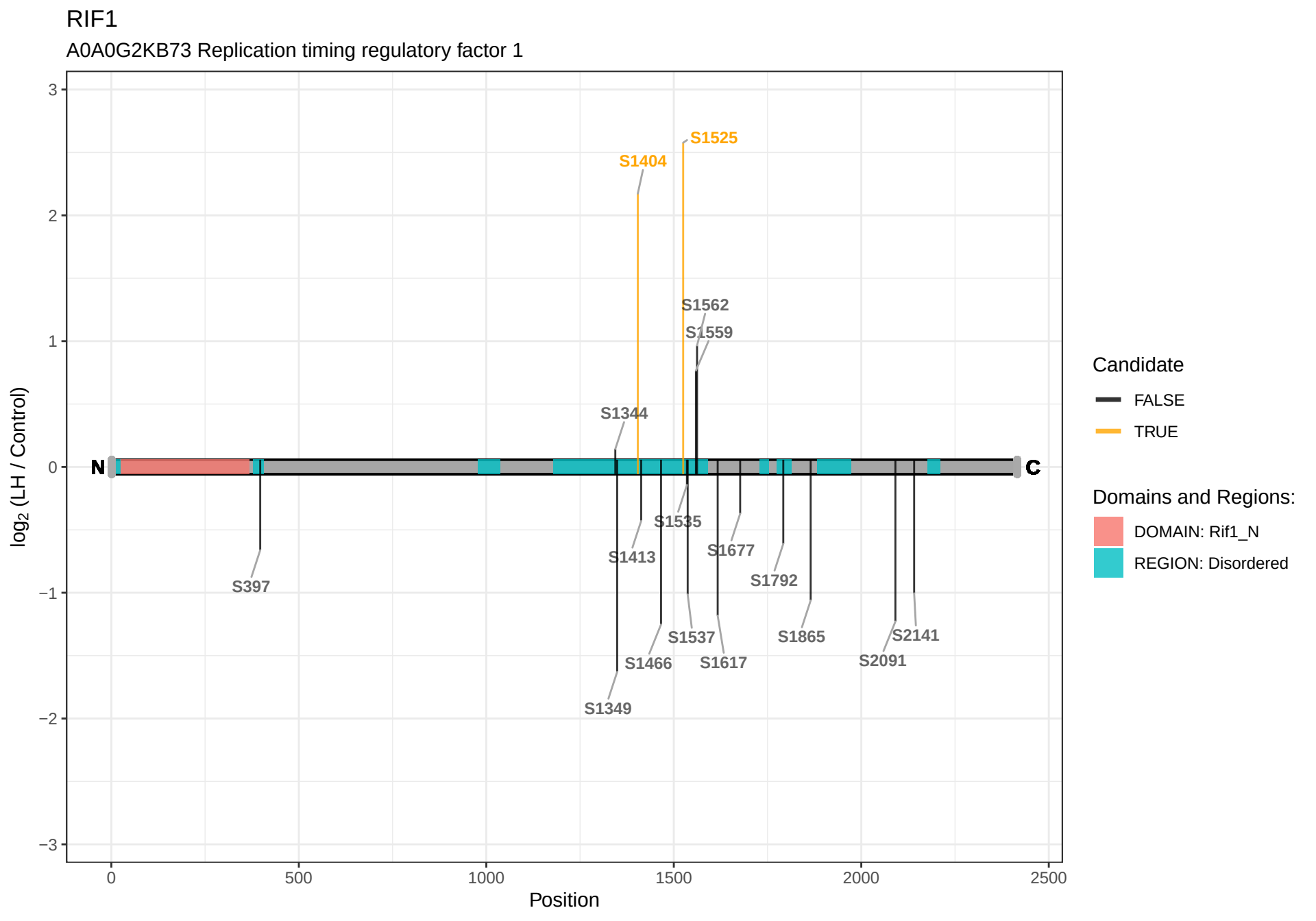

RGS12
G3V9H1 Regulator of G−protein signaling 12, isoform CRA_c
log2 (LH / Control)
2
0
−2
N
C
S661
S850
S671
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PDZ
DOMAIN: PID
DOMAIN: RBD
DOMAIN: RGS
REGION: Disordered

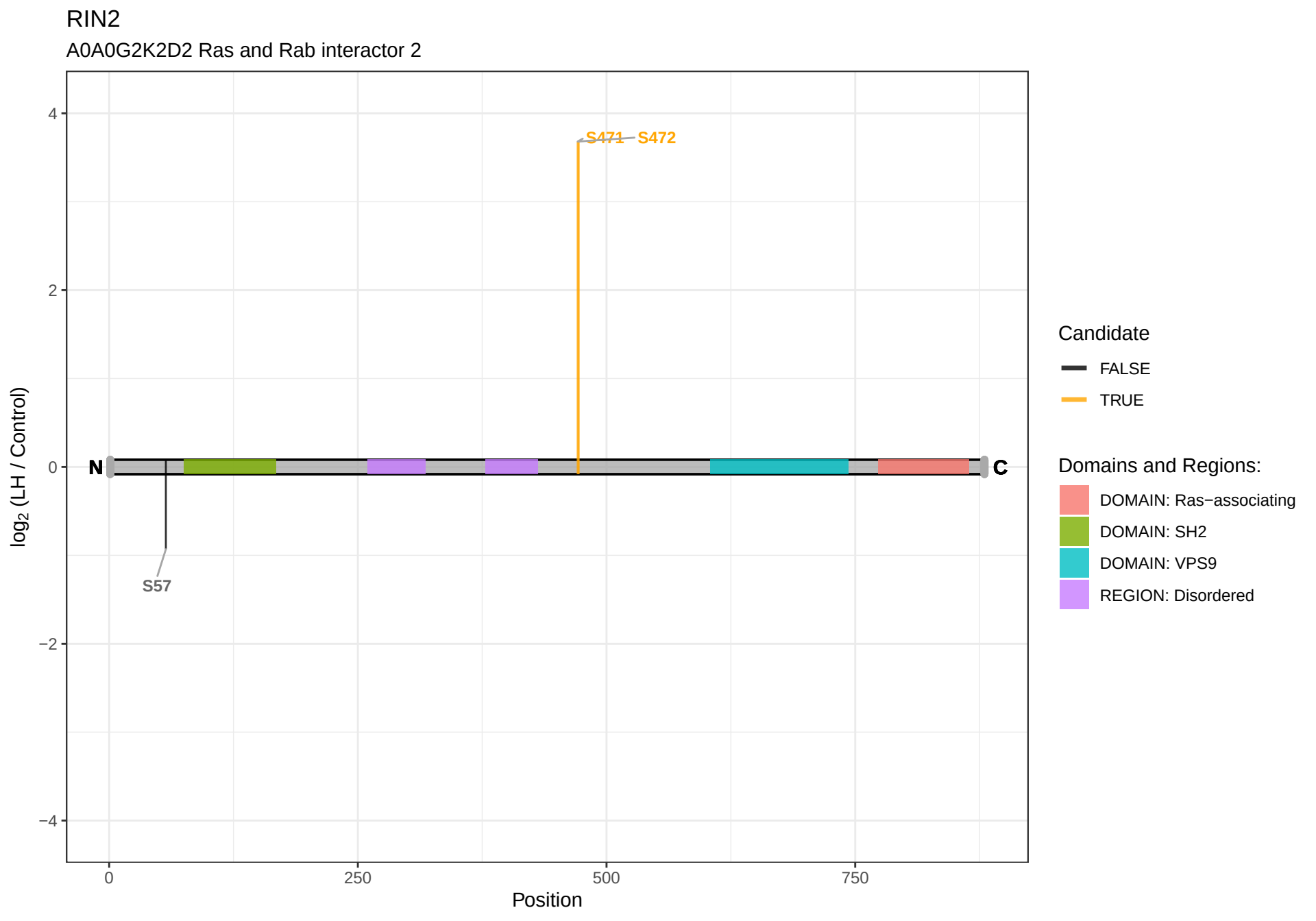

RGS3
G3V9Q2 Regulator of G−protein signalling 3, isoform CRA_c
log2 (LH / Control)
2
1
0
−1
−2
N
C
S713
S716
S813
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PDZ
DOMAIN: RGS
REGION: Disordered

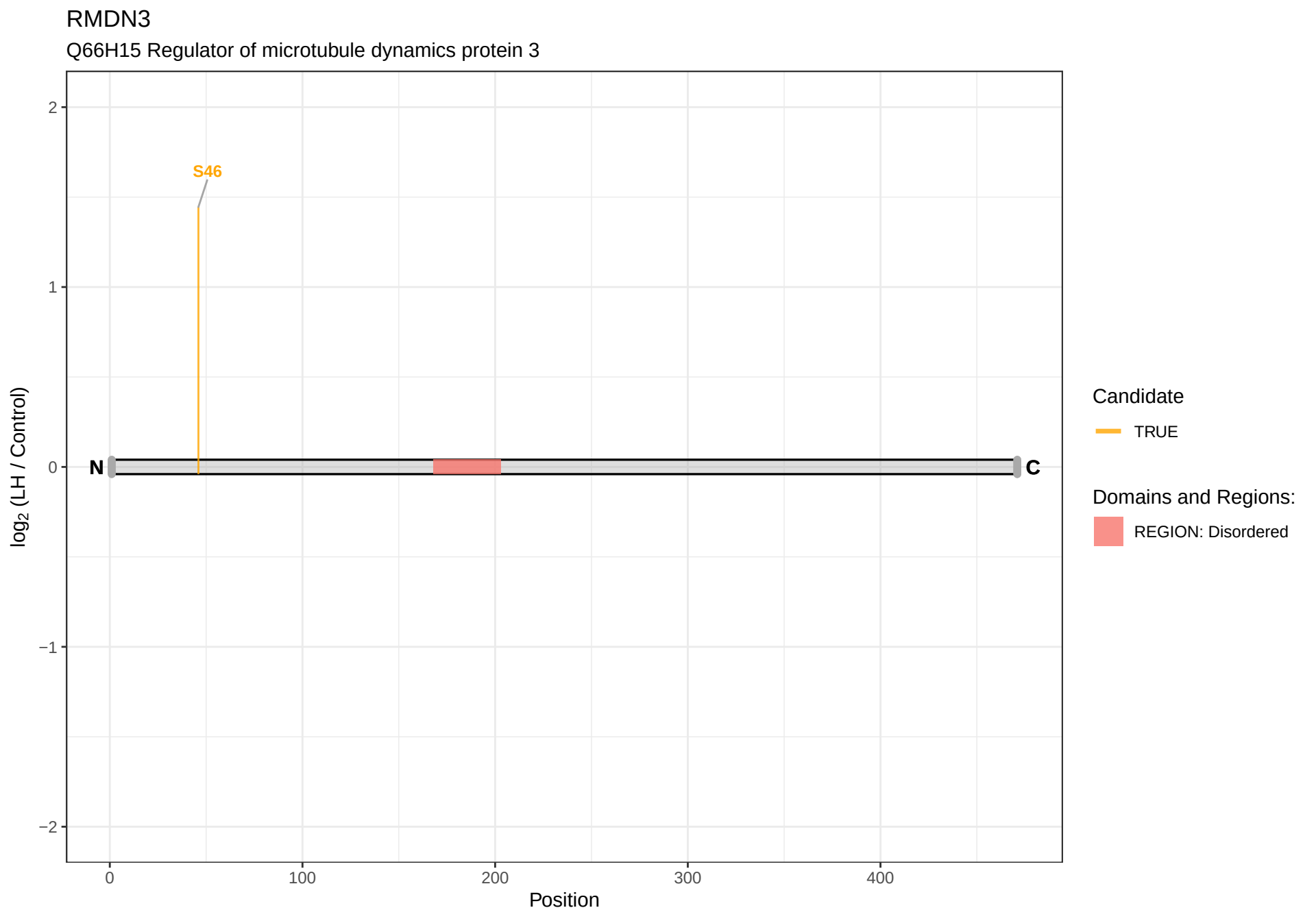

RHBDF2
F1LWZ3 Inactive rhomboid protein
log2 (LH / Control)
2
1
0
−1
−2
S297
S294
S355
N
C
S60
S85
S357
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Rhomboid
REGION: Disordered

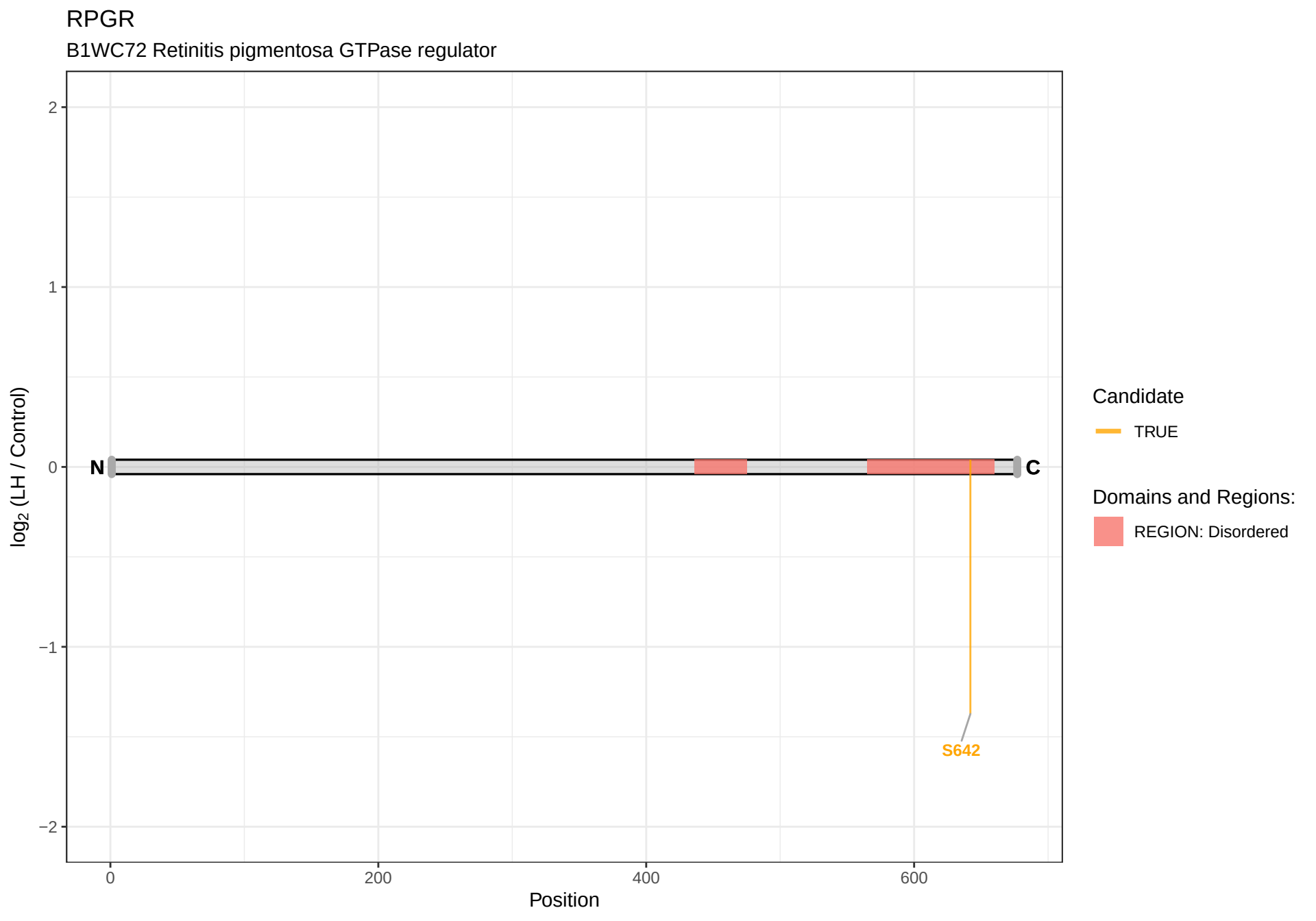

RIC1
D4A224 RIC1 homolog, RAB6A GEF complex partner 1
2
1
0
−1
−2
log2 (LH / Control)
T995
S994
S1016
T991
N
C
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RIC1
REGION: Disordered

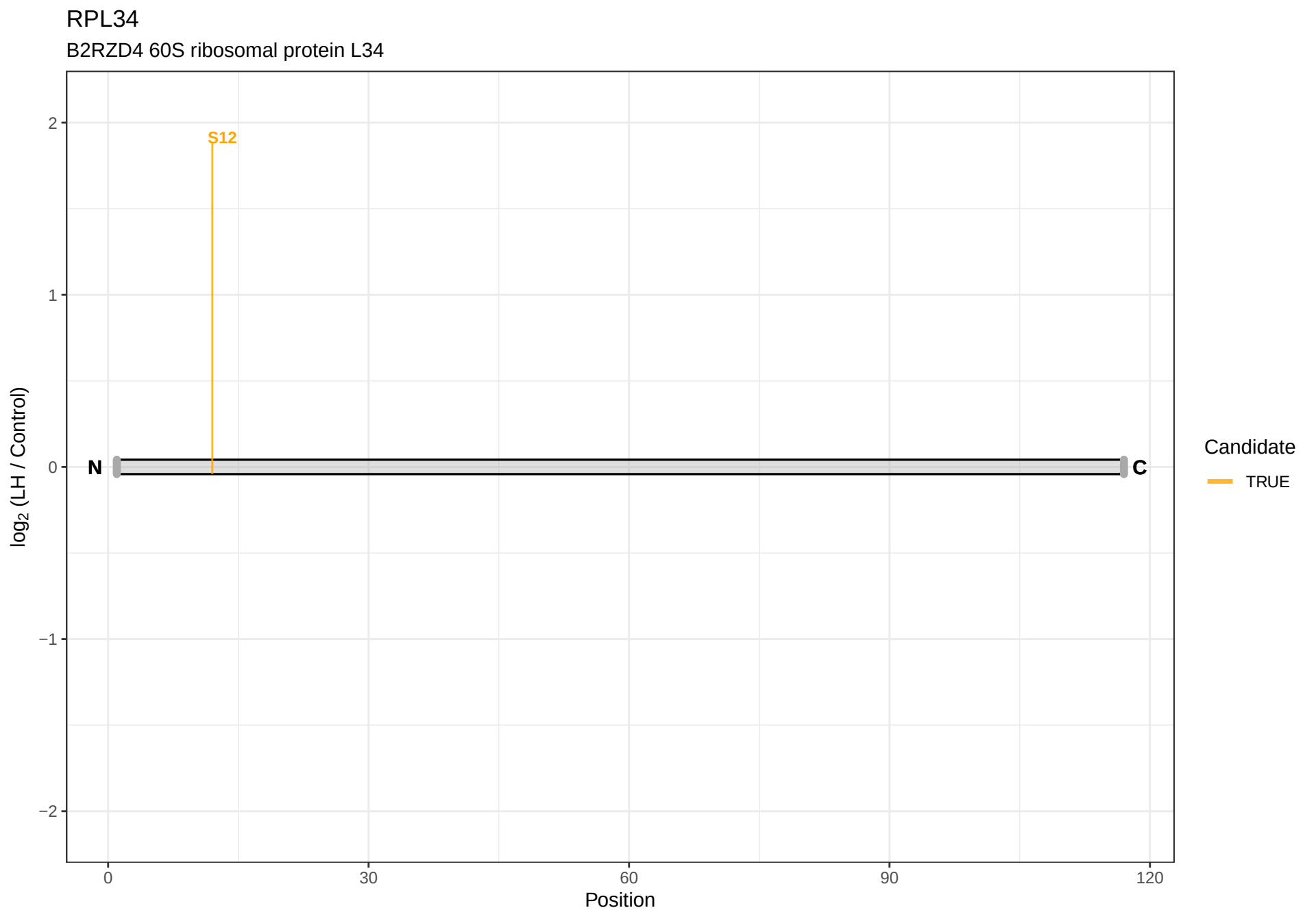

RICTOR
F1M4J0 RPTOR−independent companion of MTOR, complex 2
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
Position
N
C
S1458
S1450
S1462
S1580
S1162
S1165
T1163
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RICTOR_M
DOMAIN: RICTOR_N
DOMAIN: RICTOR_V
REGION: Disordered

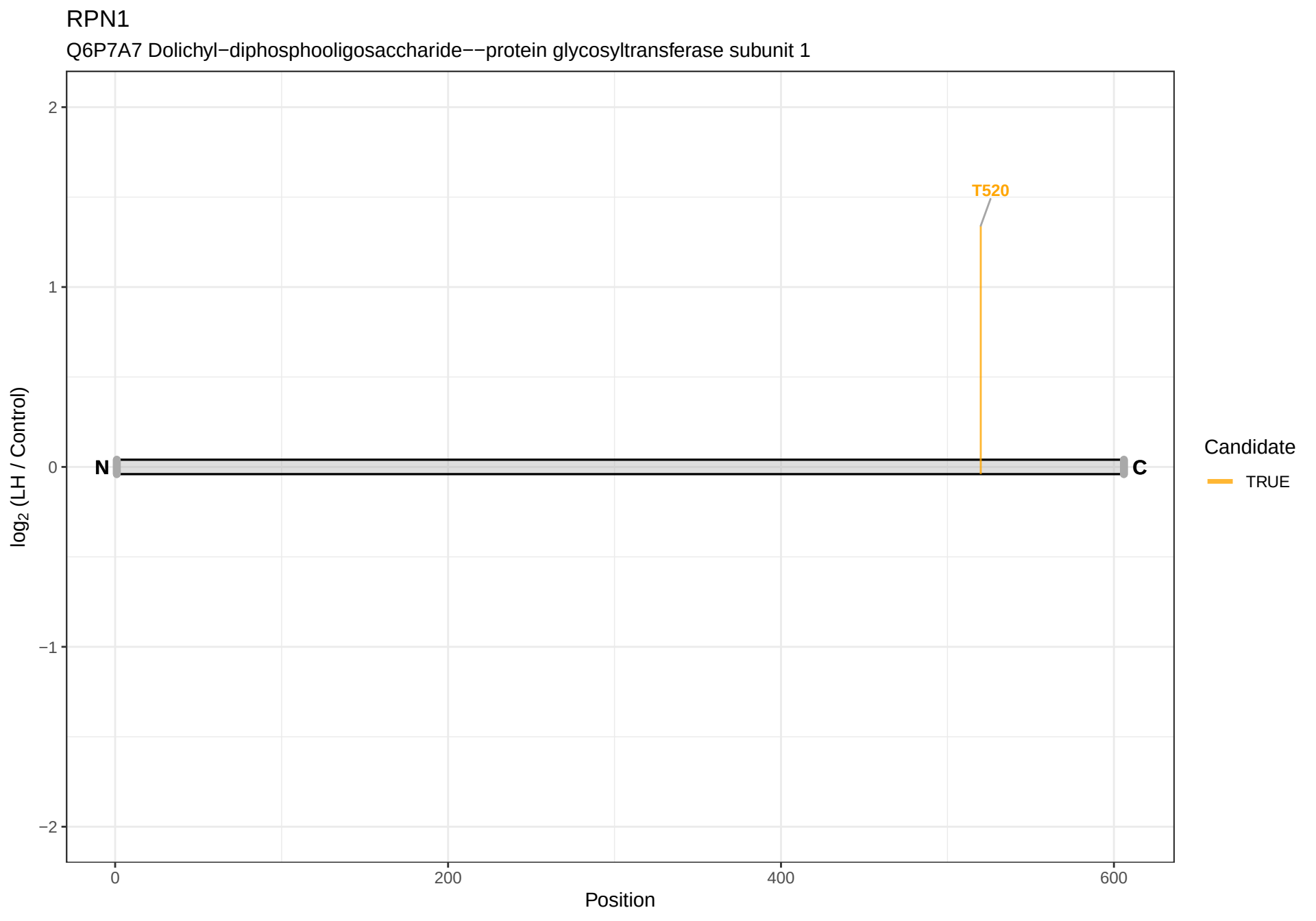

RIF1
A0A0G2KB73 Replication timing regulatory factor 1
log2 (LH / Control)
Position
N
C
S1525
S1404
S1562
S1559
S1344
S1535
S1413
S1677
S1792
S397
S1537
S1865
S2141
S1466
S1617
S2091
S1349
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Rif1_N
REGION: Disordered

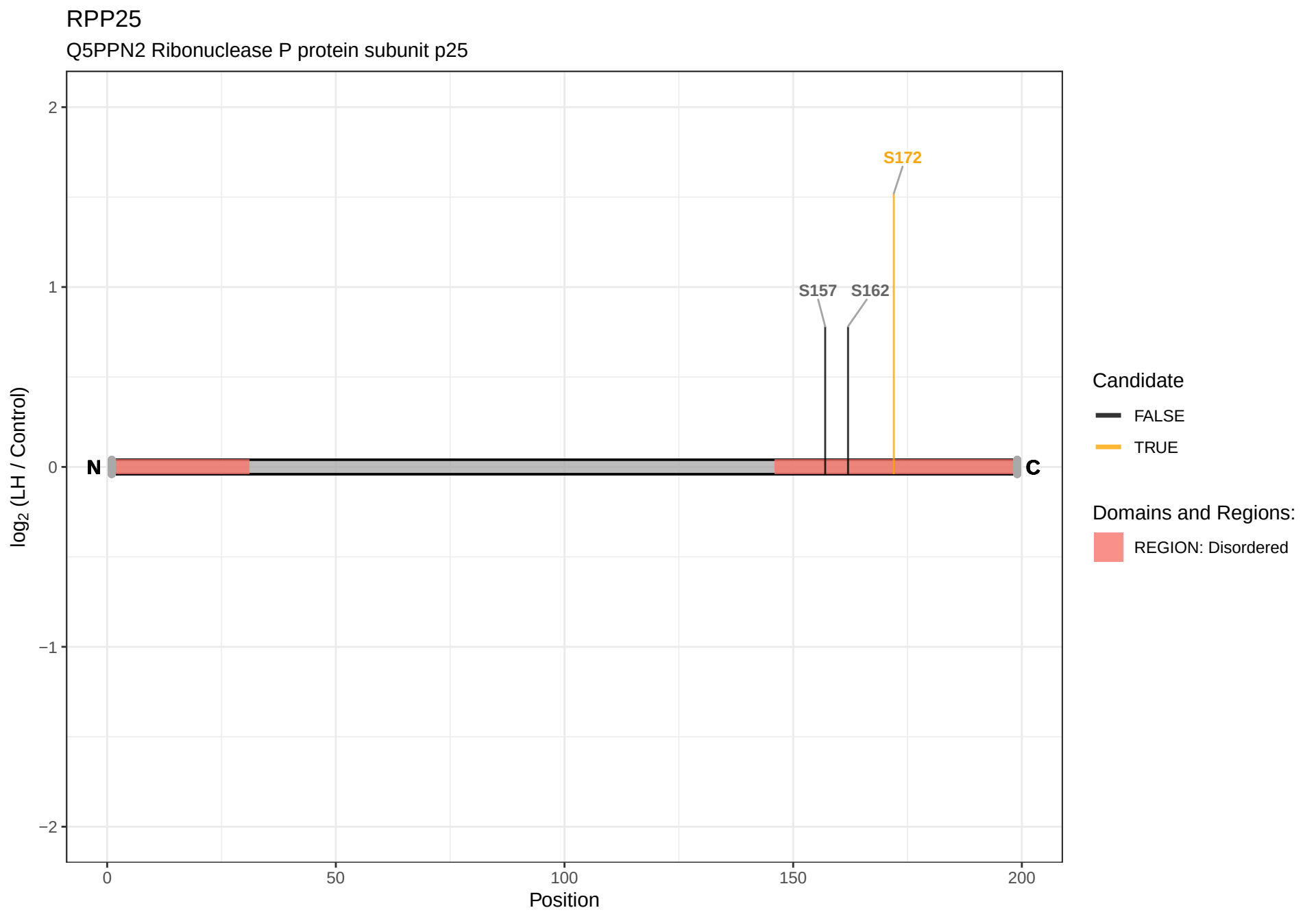

RIN2
A0A0G2K2D2 Ras and Rab interactor 2
S471
S472
S57
N
C
4
2
0
−2
−4
log2 (LH / Control)
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Ras−associating
DOMAIN: SH2
DOMAIN: VPS9
REGION: Disordered

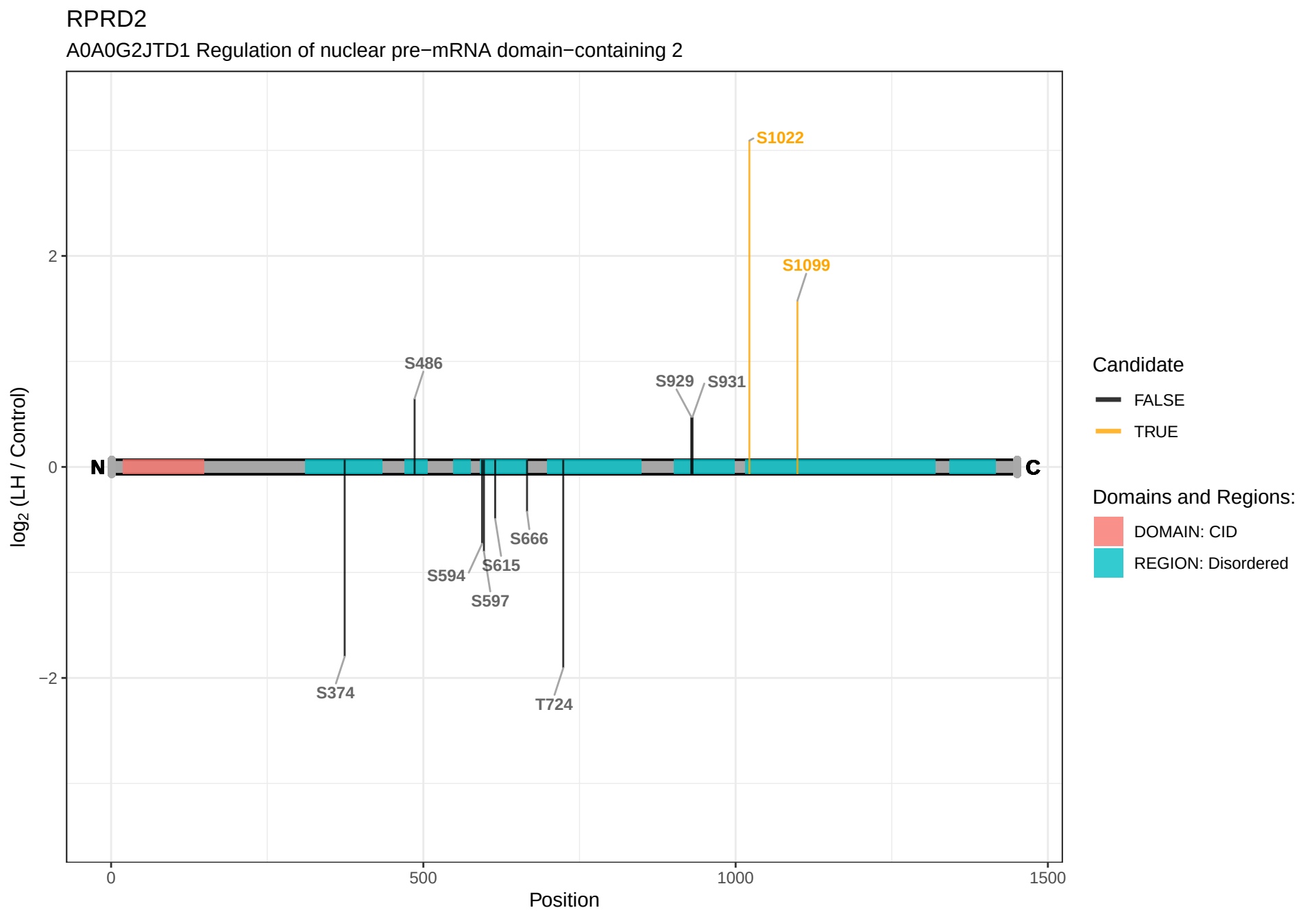

RMDN3
Q66H15 Regulator of microtubule dynamics protein 3
S46
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
400
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

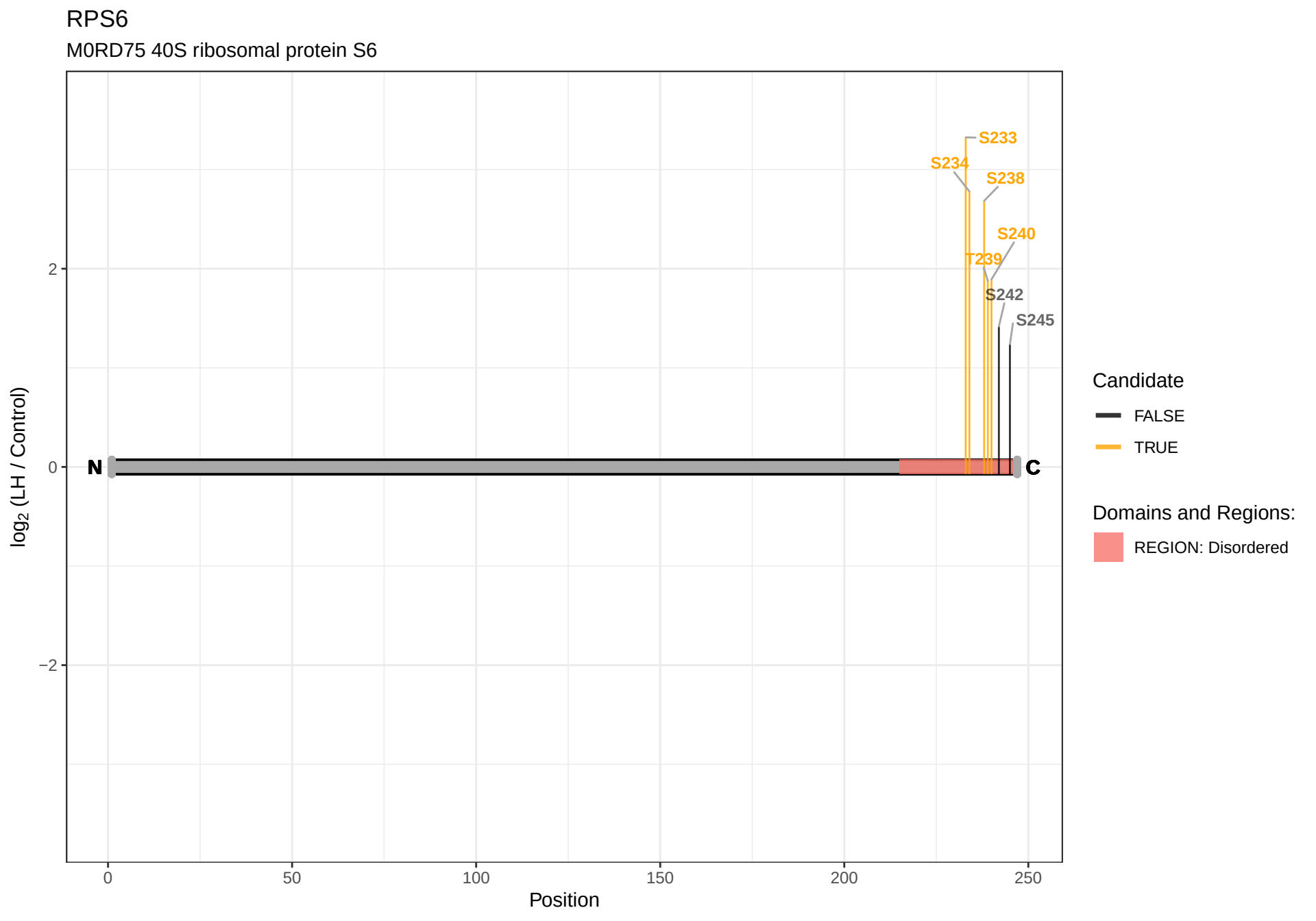

RPGR
B1WC72 Retinitis pigmentosa GTPase regulator
2
1
0
−1
−2
log2 (LH / Control)
N
C
S642
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

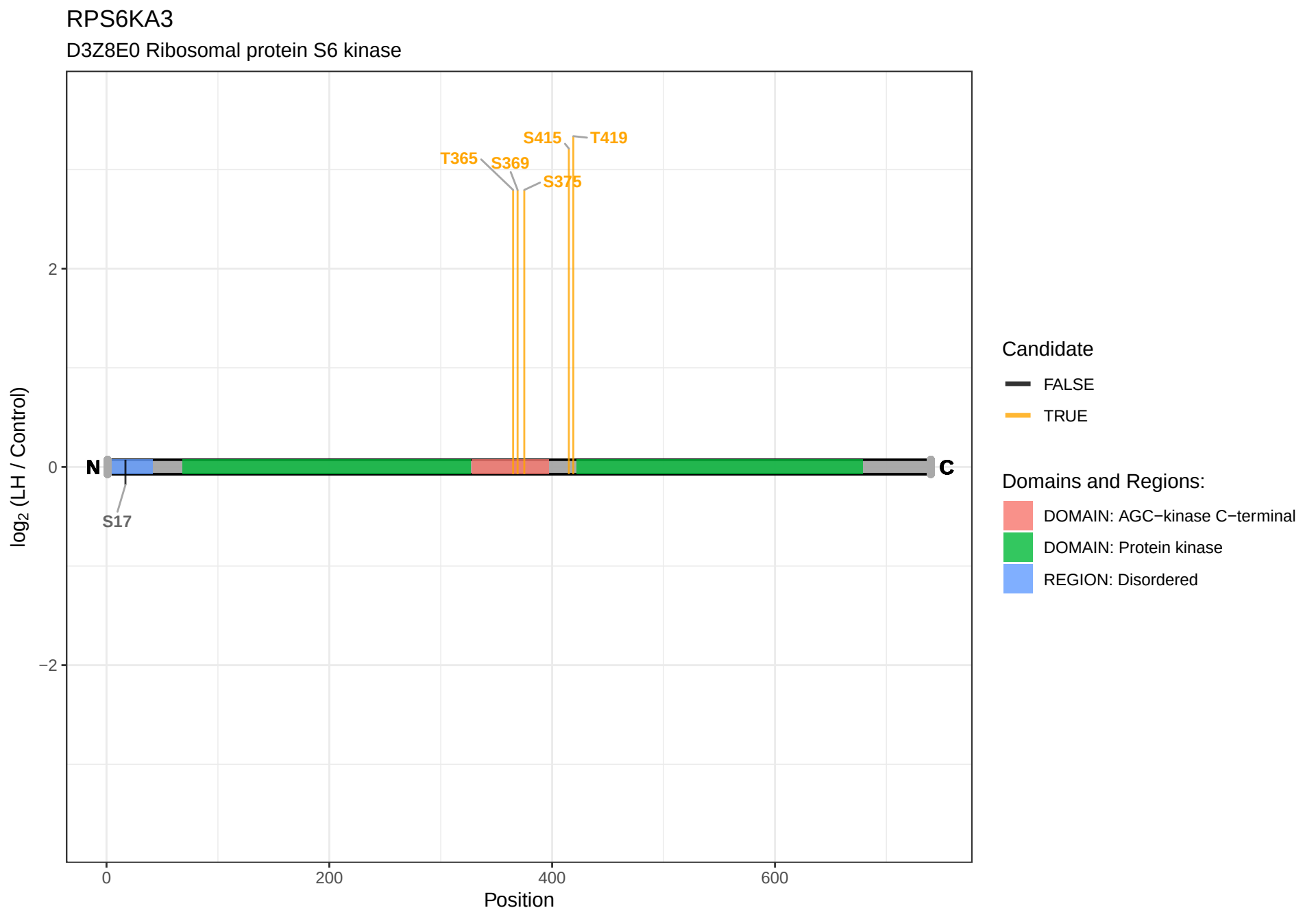

RPL34
B2RZD4 60S ribosomal protein L34
S12
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
30
60
90
120
Position
Candidate
TRUE

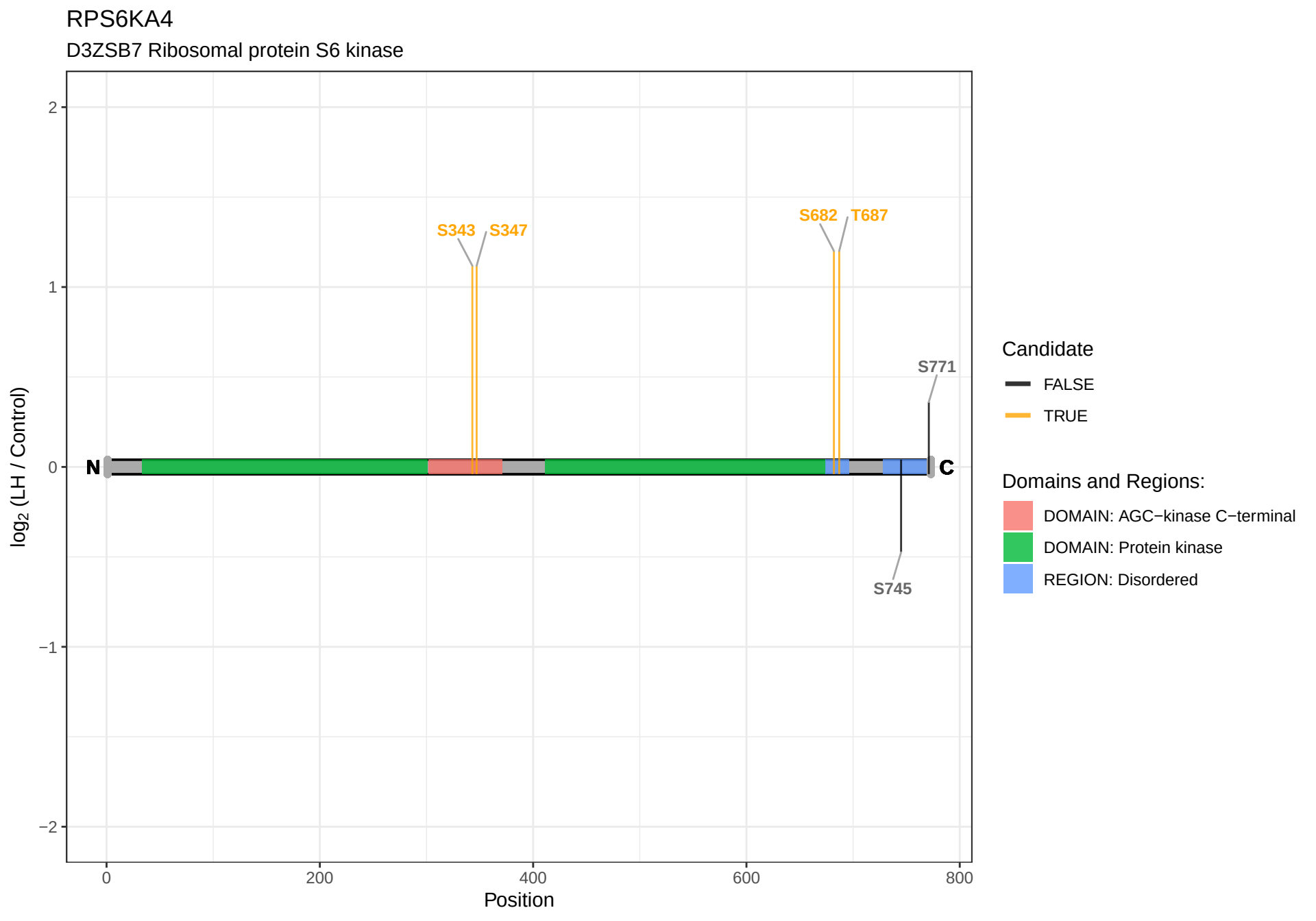

RPN1
Q6P7A7 Dolichyl−diphosphooligosaccharide−−protein glycosyltransferase subunit 1
T520
N
C
log2 (LH / Control)
Position
Candidate
TRUE
2
1
0
−1
−2
0
200
400
600

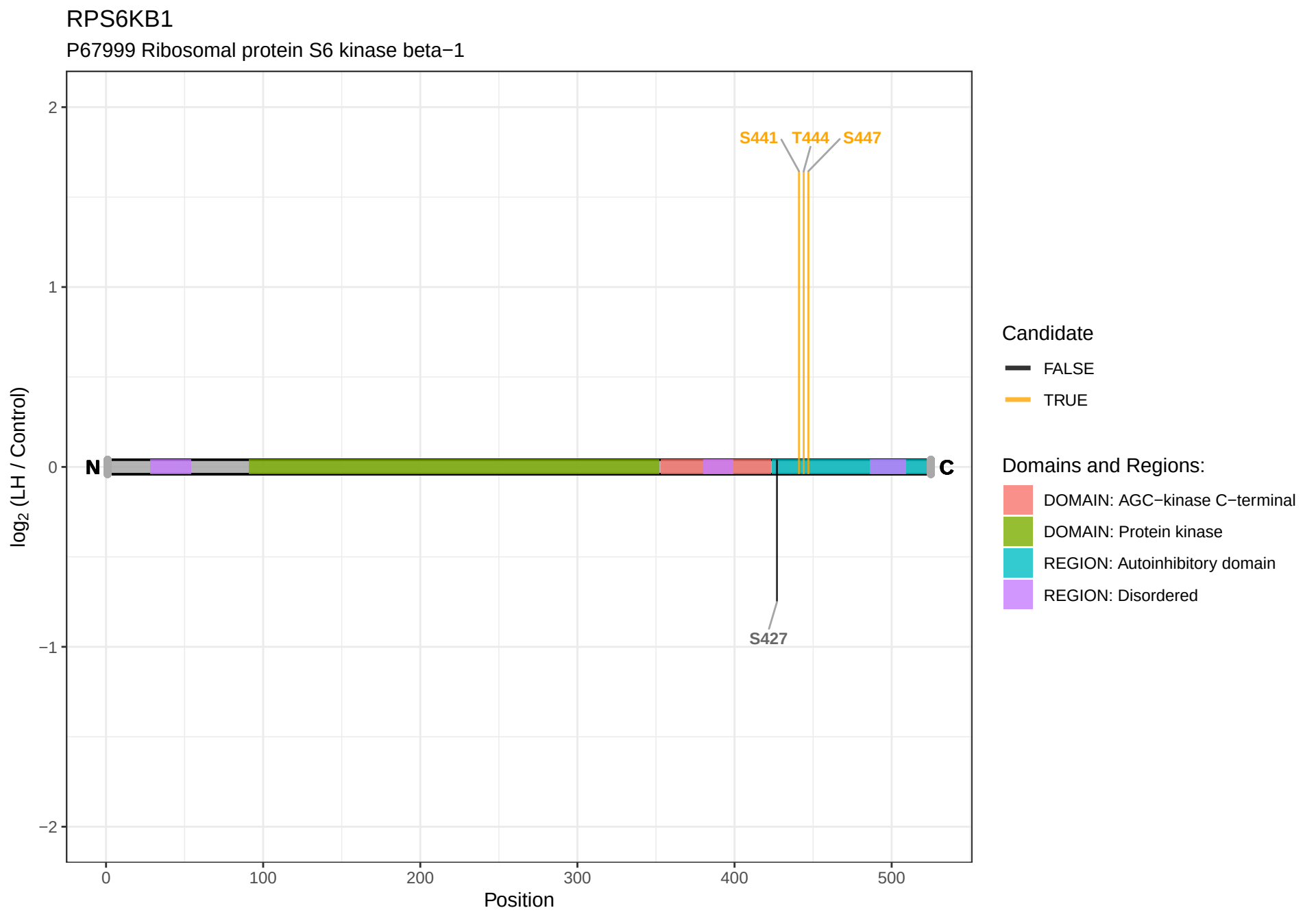

RPP25
Q5PPN2 Ribonuclease P protein subunit p25
log2 (LH / Control)
2
1
0
−1
−2
S172
S157
S162
N
C
0
50
100
150
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

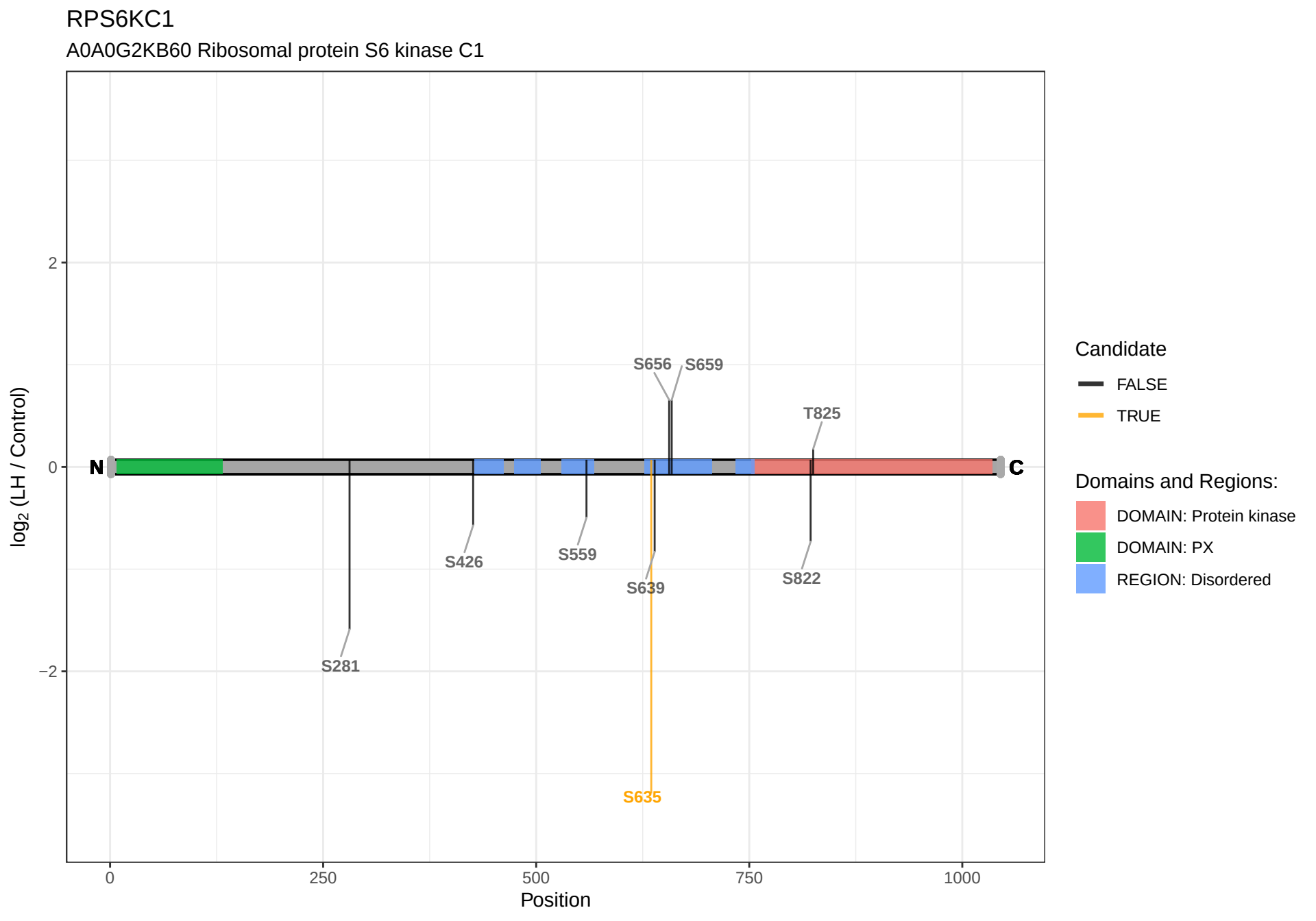

RPRD2
A0A0G2JTD1 Regulation of nuclear pre−mRNA domain−containing 2
log2 (LH / Control)
2
0
−2
N
C
S1022
S1099
S486
S929
S931
S666
S594
S615
S597
S374
T724
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CID
REGION: Disordered

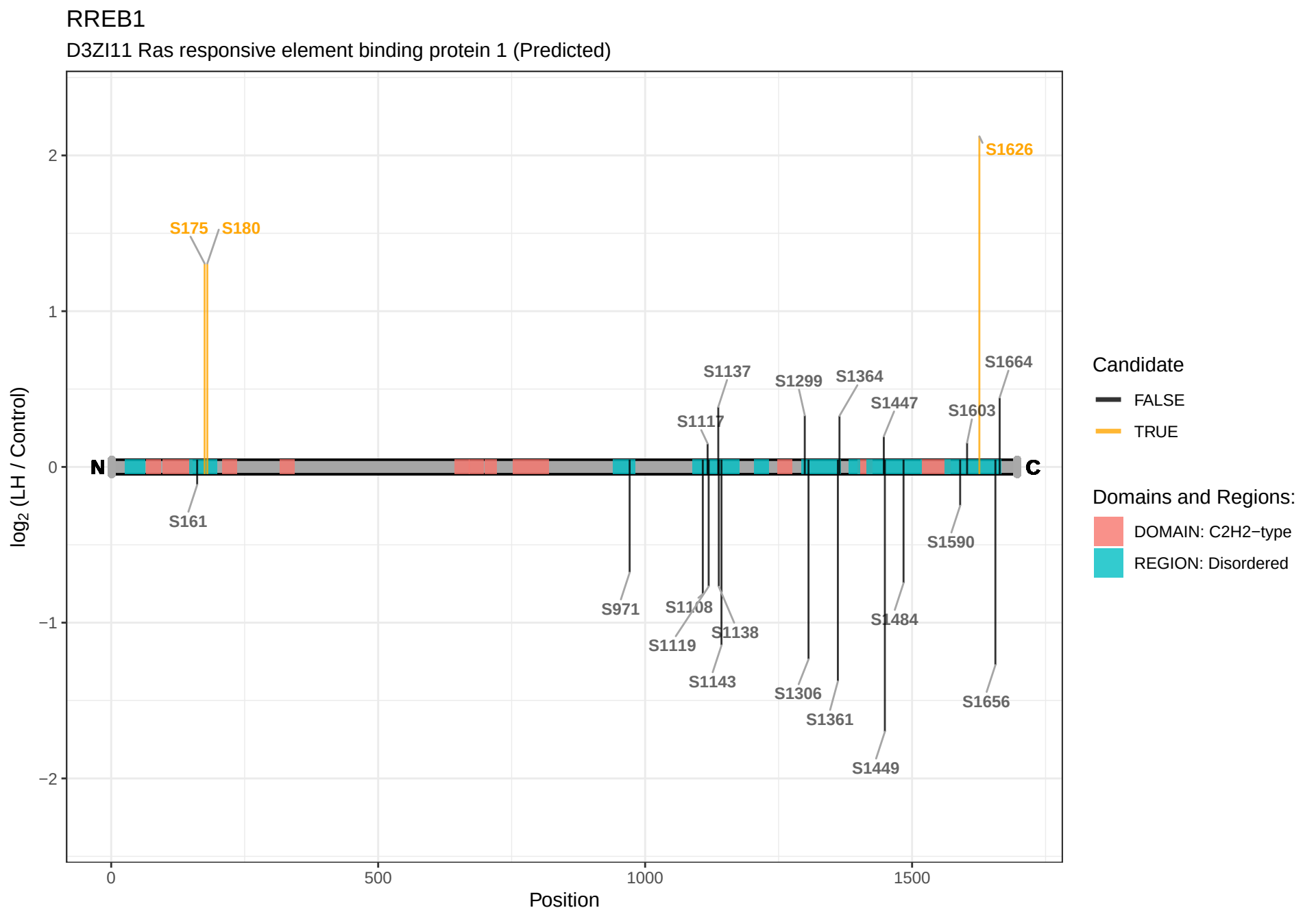

RPS6
M0RD75 40S ribosomal protein S6
S233
S234
S238
S240
T239
S242
S245
N
C
2
0
−2
log2 (LH / Control)
0
50
100
150
200
250
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

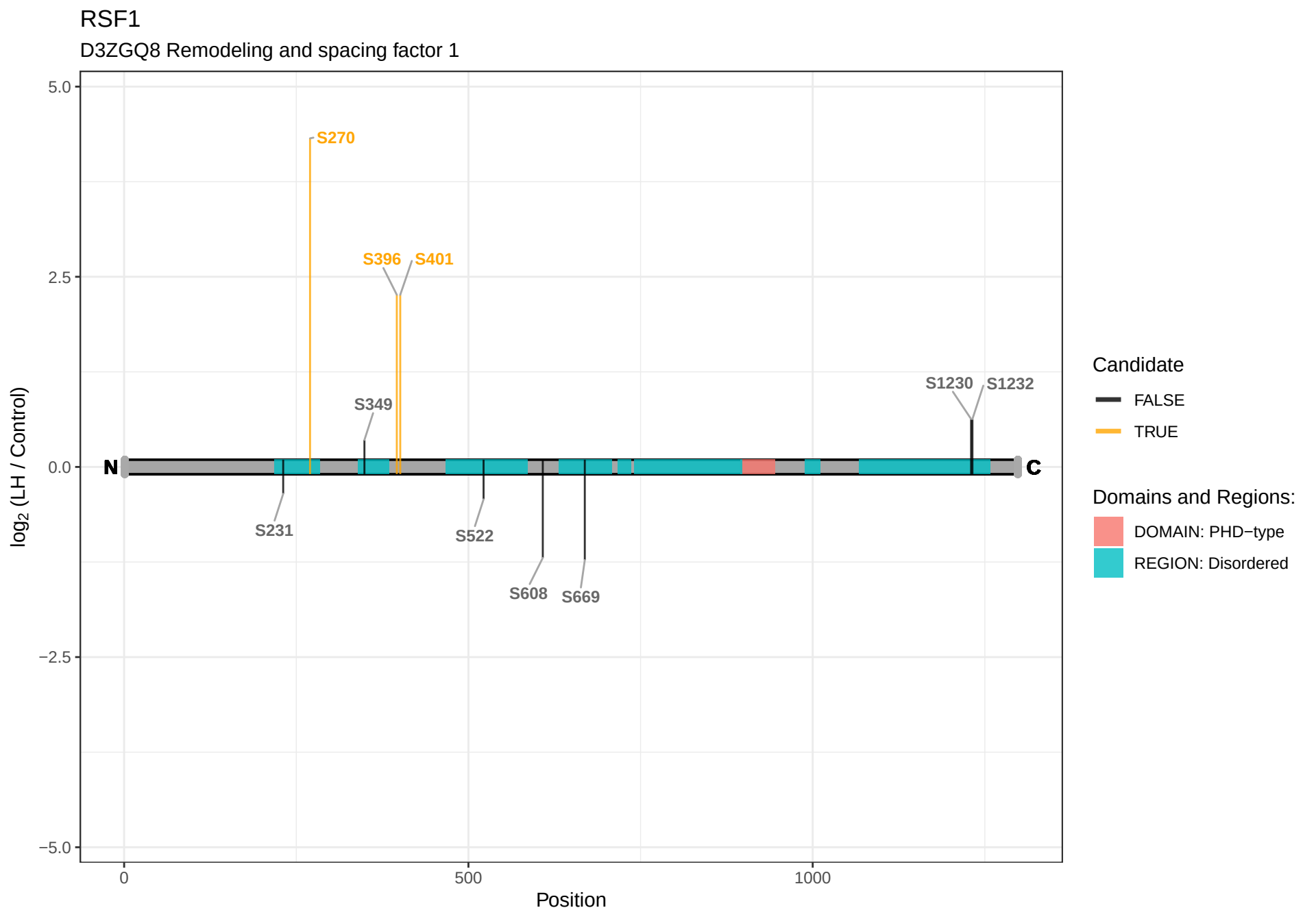

RPS6KA3
D3Z8E0 Ribosomal protein S6 kinase
S415
T419
T365
S369
S375
N
C
S17
2
0
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AGC−kinase C−terminal
DOMAIN: Protein kinase
REGION: Disordered

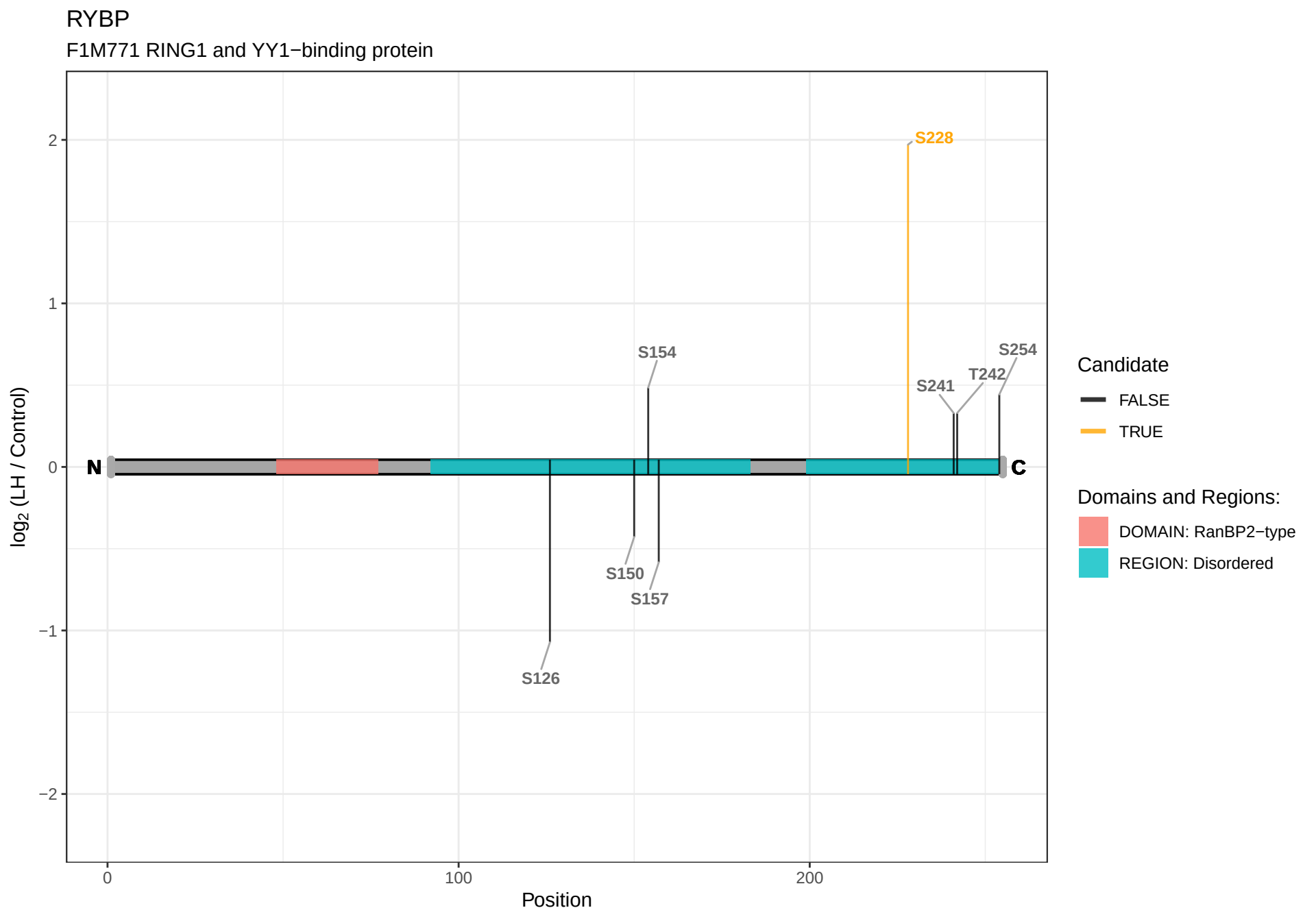

RPS6KA4
D3ZSB7 Ribosomal protein S6 kinase
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
800
Position
N
C
S343
S347
S682
T687
S771
S745
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AGC−kinase C−terminal
DOMAIN: Protein kinase
REGION: Disordered


RPS6KB1
P67999 Ribosomal protein S6 kinase beta−1
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
400
500
Position
N
C
S441
T444
S447
S427
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AGC−kinase C−terminal
DOMAIN: Protein kinase
REGION: Autoinhibitory domain
REGION: Disordered


RPS6KC1
A0A0G2KB60 Ribosomal protein S6 kinase C1
log2 (LH / Control)
2
0
−2
N
C
S656
S659
T825
S426
S559
S639
S822
S281
S635
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
DOMAIN: PX
REGION: Disordered

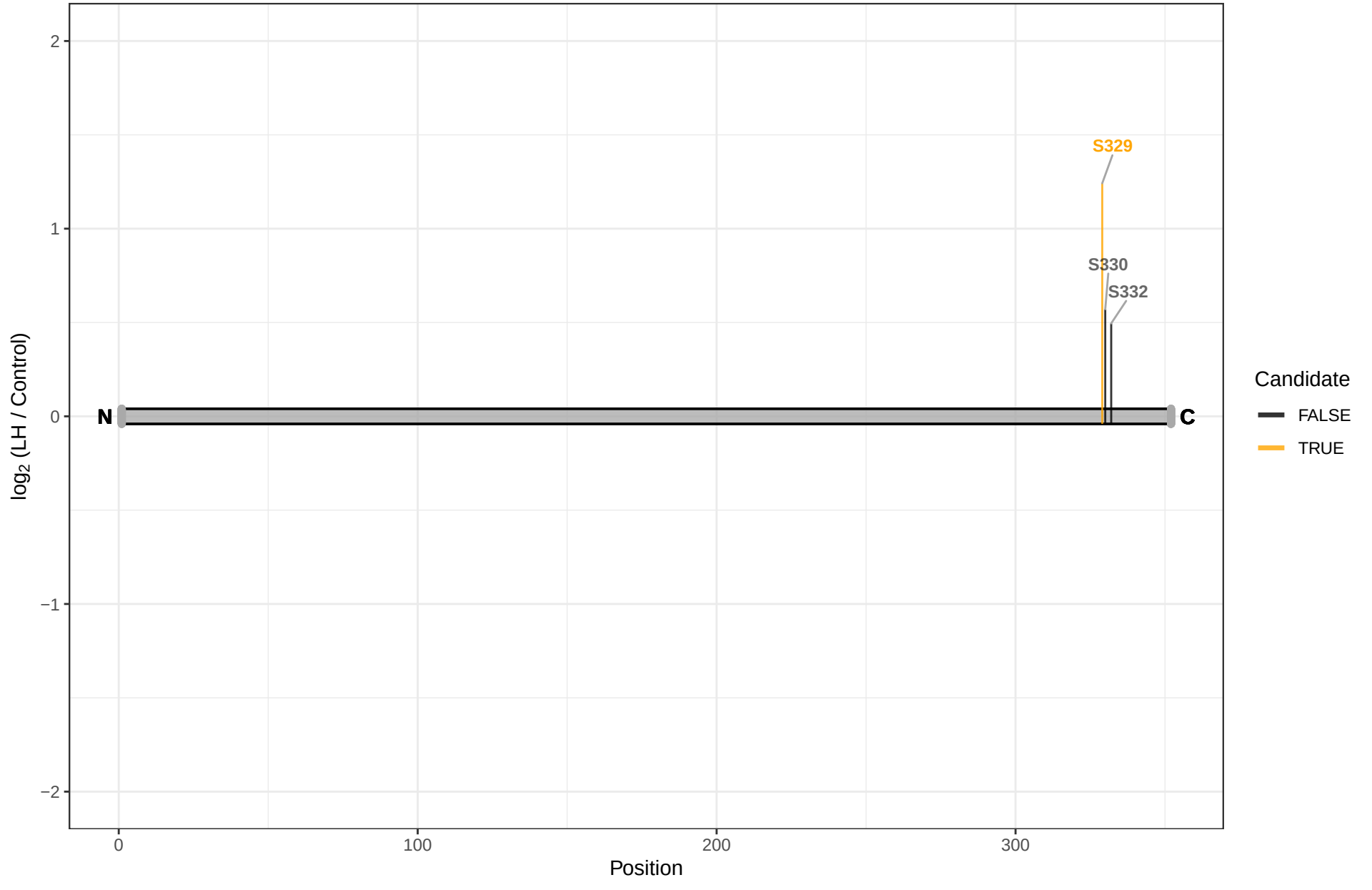

RREB1
D3ZI11 Ras responsive element binding protein 1 (Predicted)
log2 (LH / Control)
Position
0
500
1000
1500
2
1
0
−1
−2
N
C
S1626
S175
S180
S161
S1137
S1299
S1364
S1447
S1603
S1664
S1117
S971
S1108
S1119
S1138
S1143
S1306
S1361
S1449
S1484
S1590
S1656
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2H2−type
REGION: Disordered

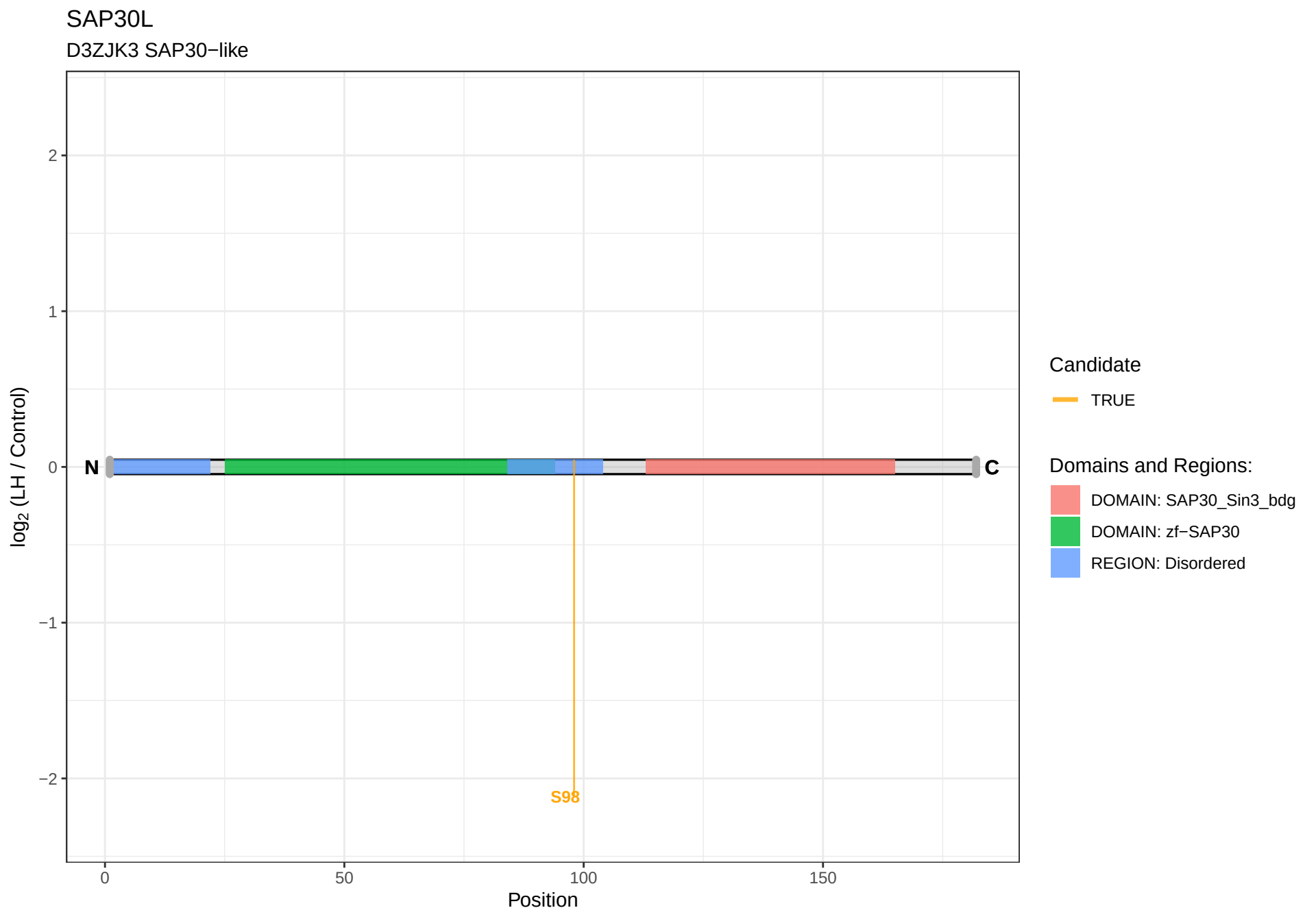

RSF1
D3ZGQ8 Remodeling and spacing factor 1
5.0
2.5
0.0
−2.5
−5.0
log2 (LH / Control)
S270
S396
S401
S349
S1230
S1232
N
C
S231
S522
S608
S669
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PHD−type
REGION: Disordered

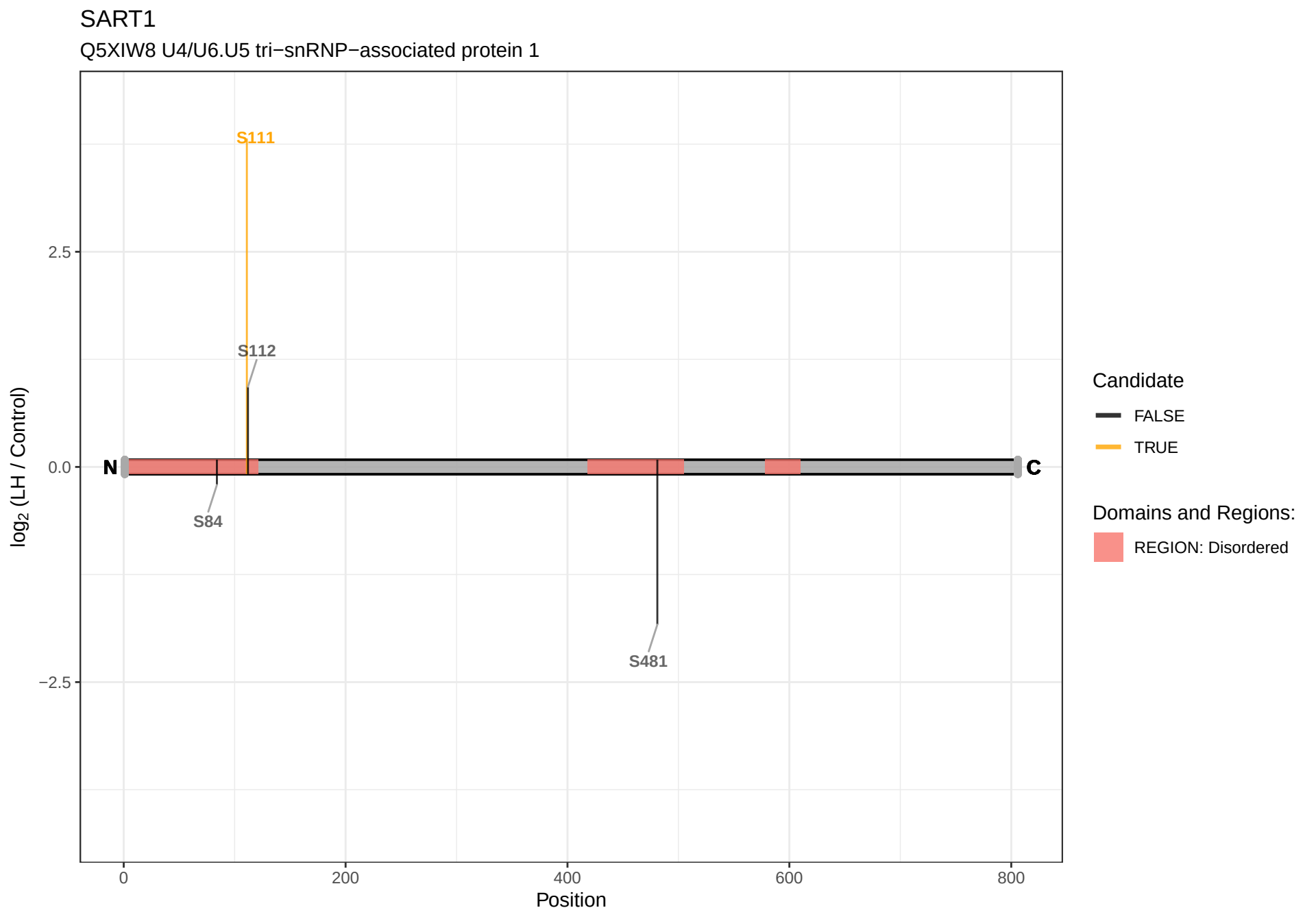

RYBP
F1M771 RING1 and YY1−binding protein
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
Position
N
C
S228
S154
S254
T242
S241
S150
S157
S126
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RanBP2−type
REGION: Disordered

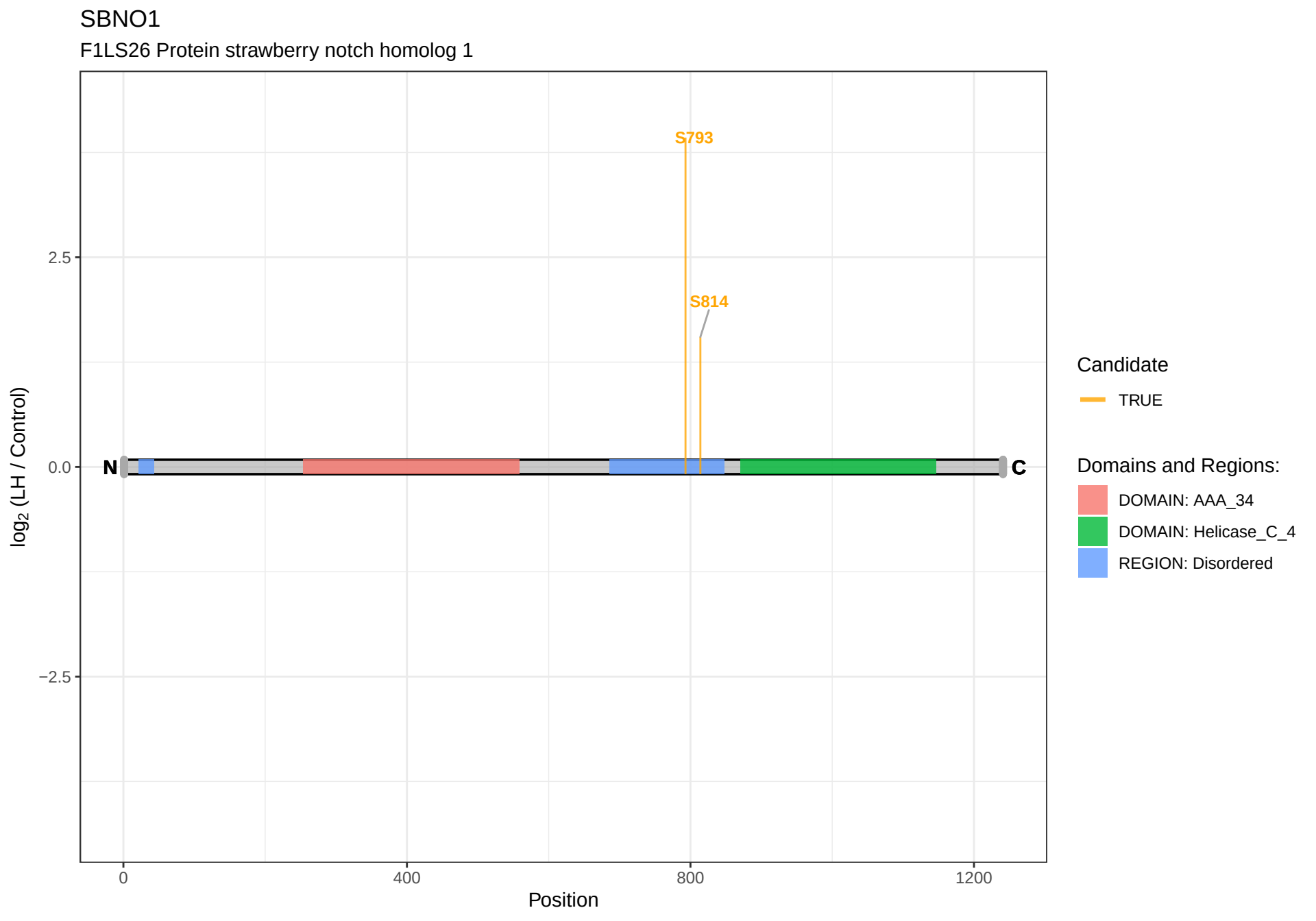
S1PR2

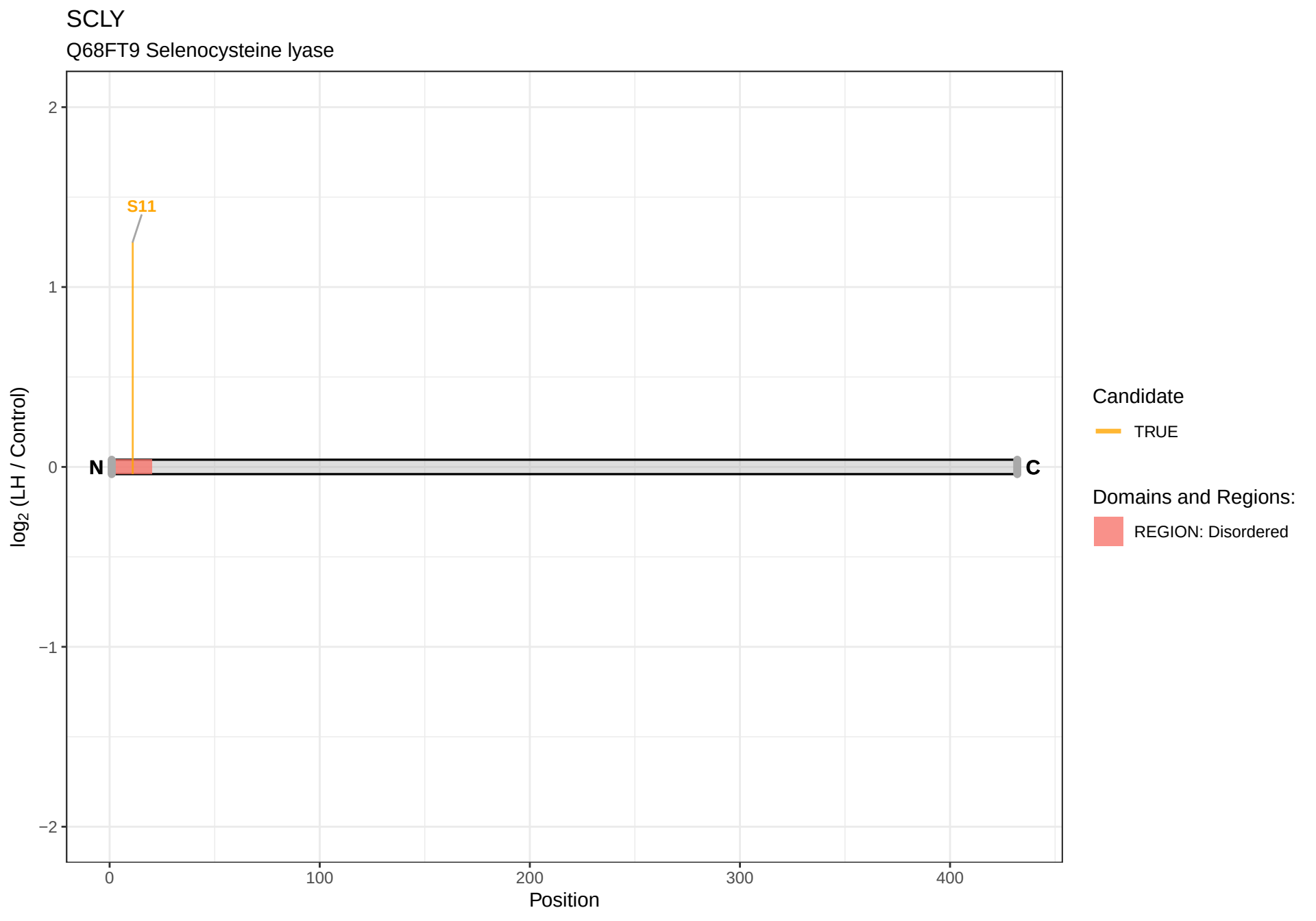
P47752 Sphingosine 1−phosphate receptor 2

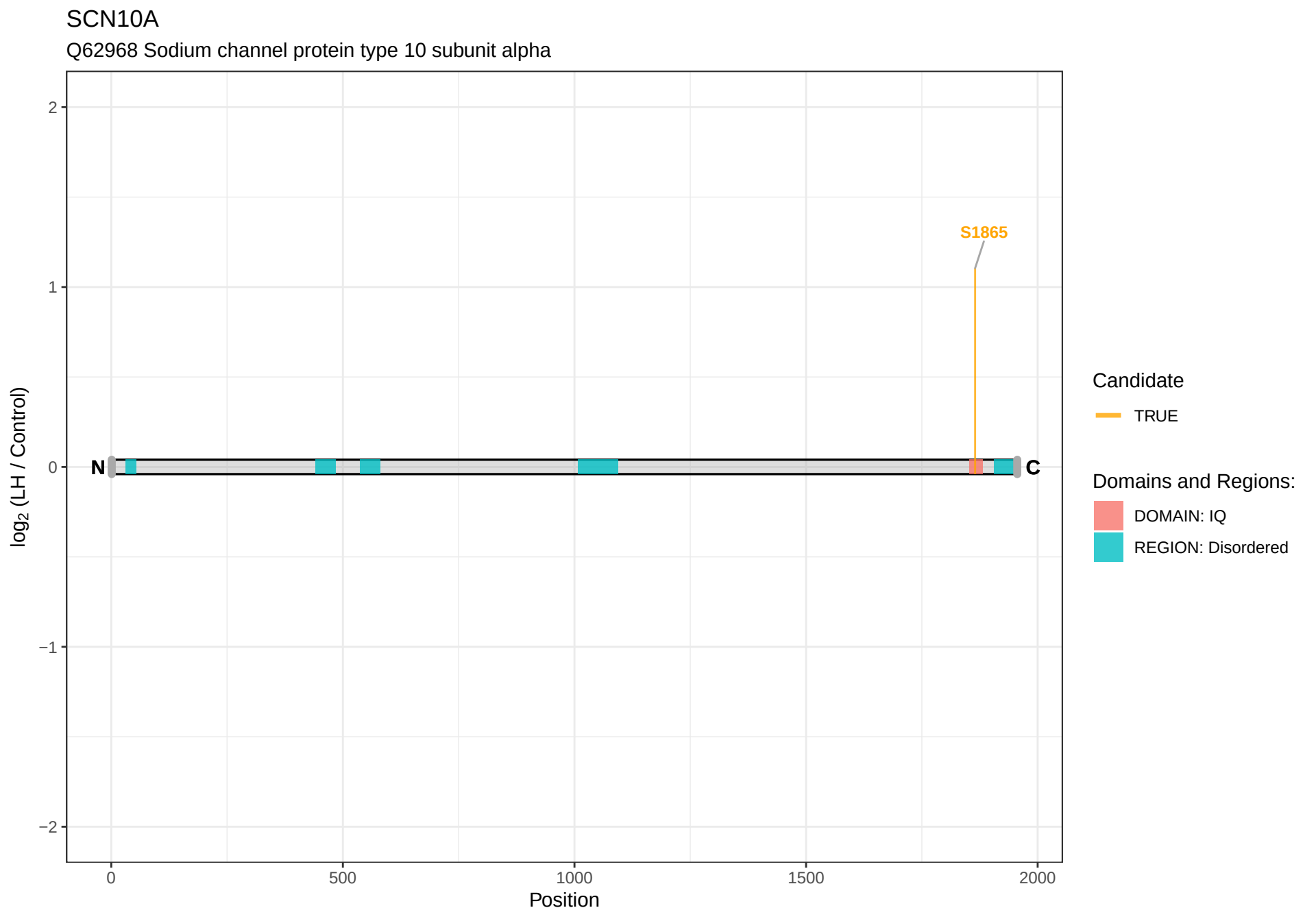


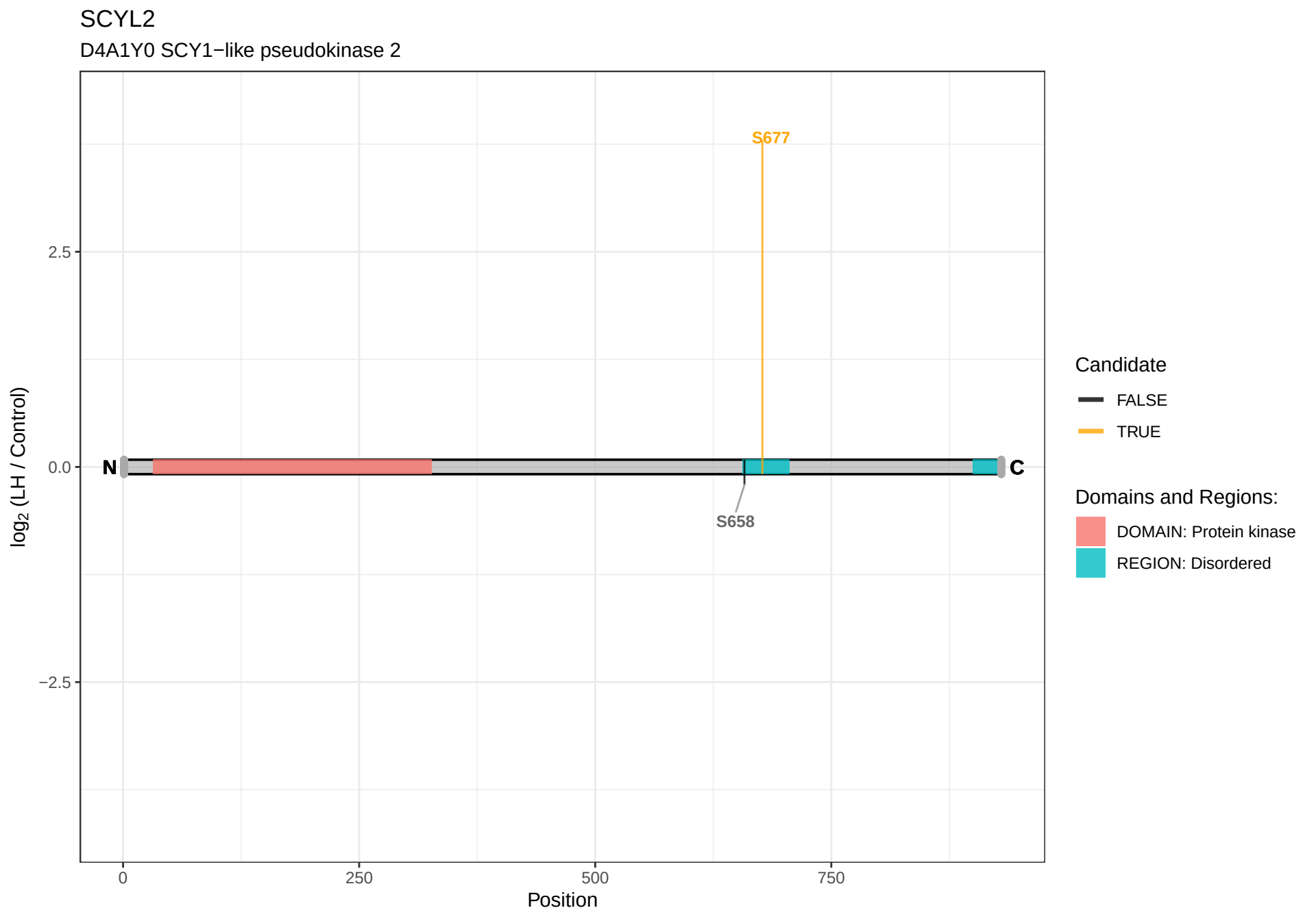

SAP30L
D3ZJK3 SAP30−like
log2 (LH / Control)
2
1
0
−1
−2
N
C
S98
0
50
100
150
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: SAP30_Sin3_bdg
DOMAIN: zf−SAP30
REGION: Disordered

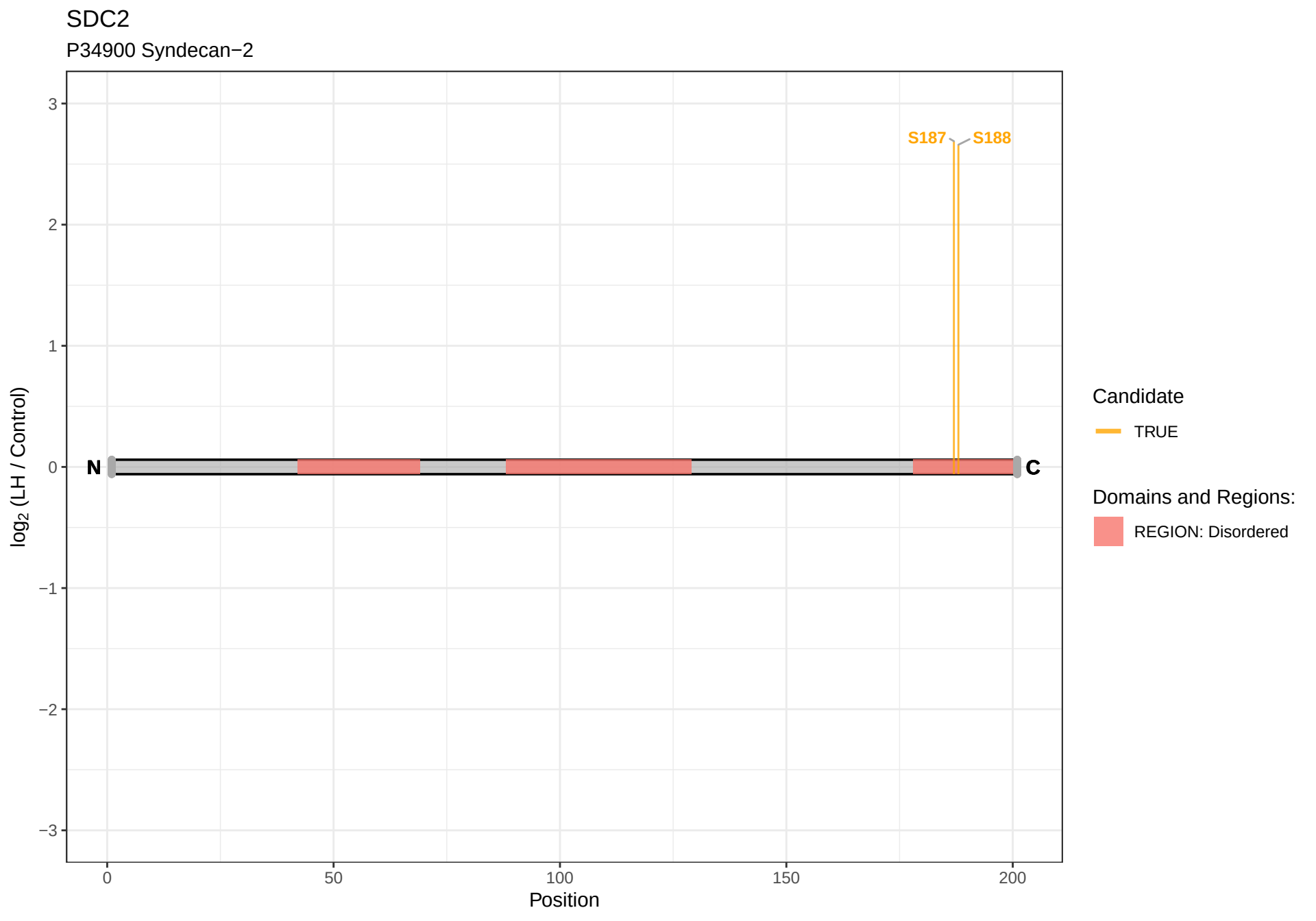

SART1
Q5XIW8 U4/U6.U5 tri−snRNP−associated protein 1
S111
S112
S84
S481
N
C
2.5
0.0
−2.5
log2 (LH / Control)
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

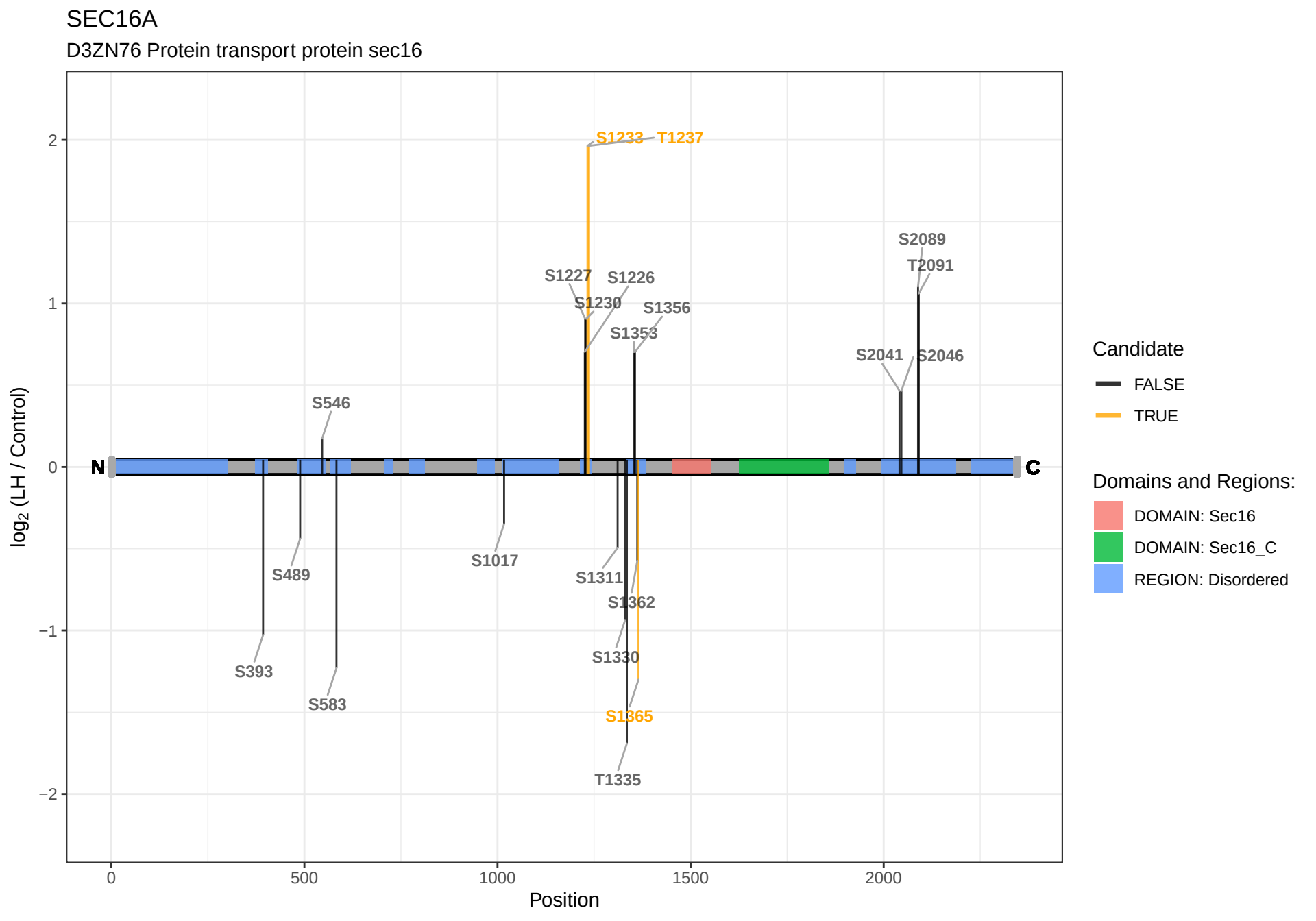

SBNO1
F1LS26 Protein strawberry notch homolog 1
S793
S814
N
C
2.5
0.0
−2.5
log2 (LH / Control)
0
400
800
1200
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: AAA_34
DOMAIN: Helicase_C_4
REGION: Disordered

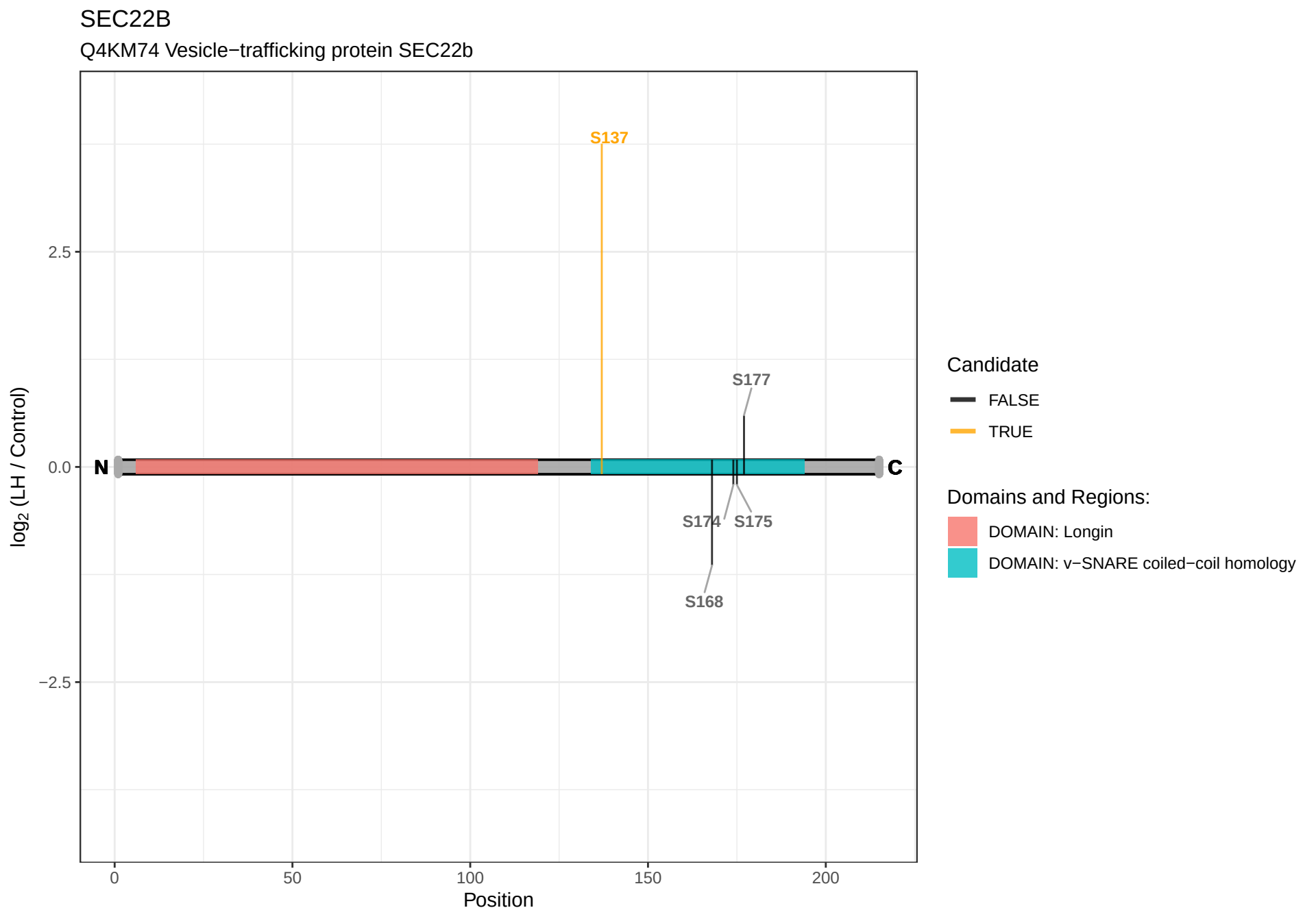

SCLY
Q68FT9 Selenocysteine lyase
S11
N
C
2
1
0
−1
−2
0
100
200
300
400
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
REGION: Disordered

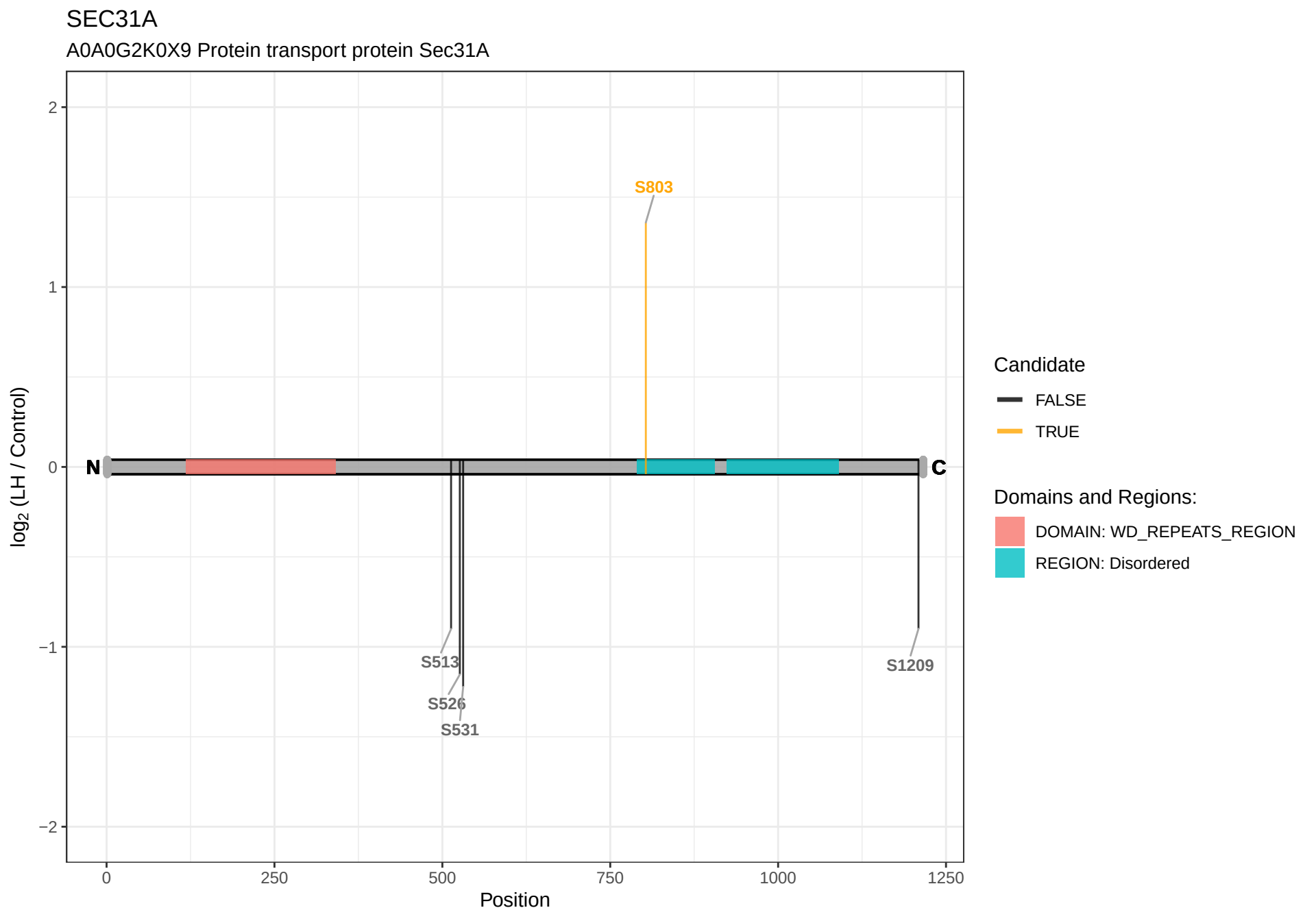

SCN10A
Q62968 Sodium channel protein type 10 subunit alpha
S1865
N
C
log2 (LH / Control)
Position
0
500
1000
1500
2000
2
1
0
−1
−2
Candidate
TRUE
Domains and Regions:
DOMAIN: IQ
REGION: Disordered

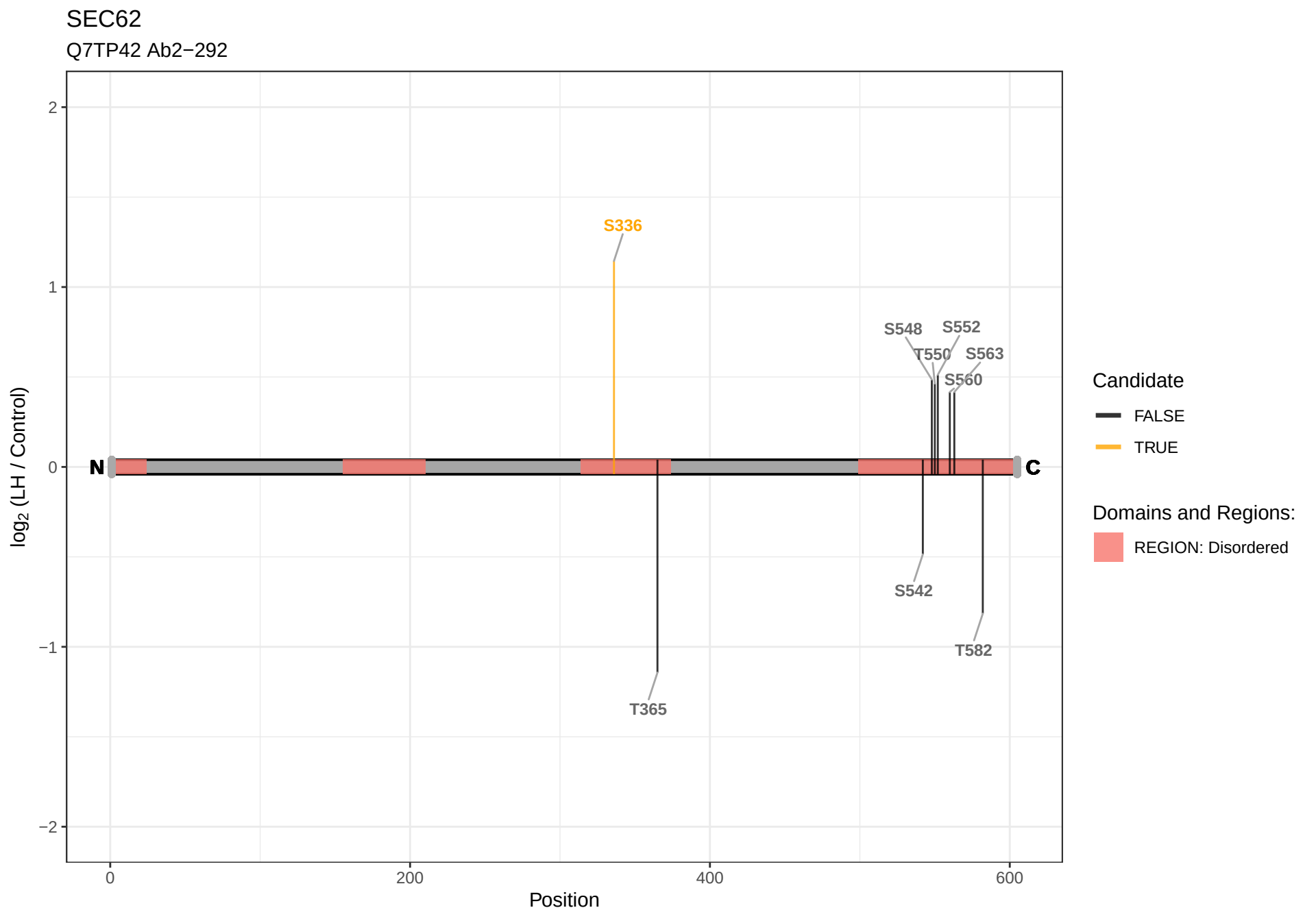

SCYL2
D4A1Y0 SCY1−like pseudokinase 2
S677
S658
N
C
2.5
0.0
−2.5
log2 (LH / Control)
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered

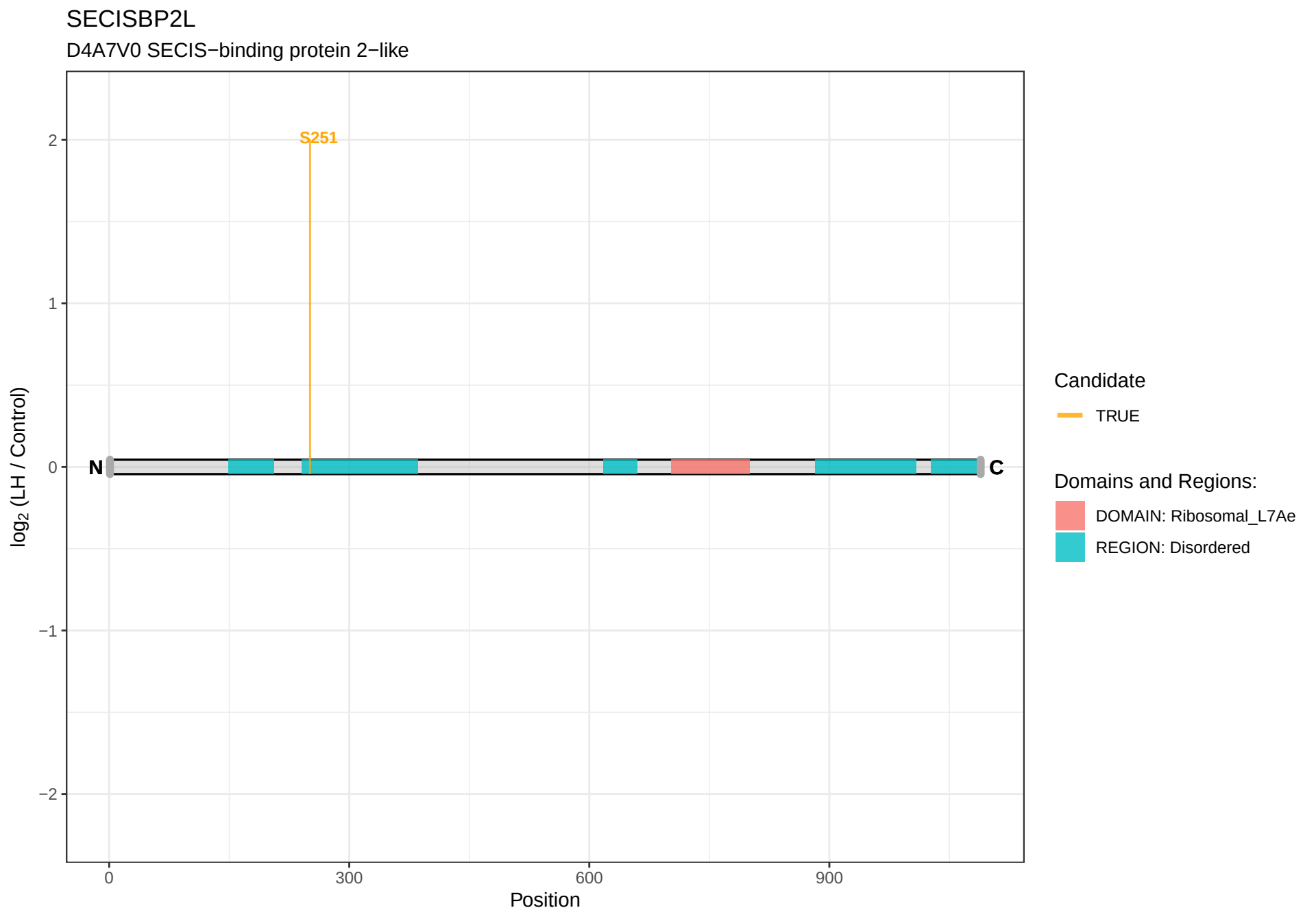

SDC2
P34900 Syndecan−2
S187
S188
N
C
log2 (LH / Control)
Position
3
2
1
0
−1
−2
−3
0
50
100
150
200
Candidate
TRUE
Domains and Regions:
REGION: Disordered

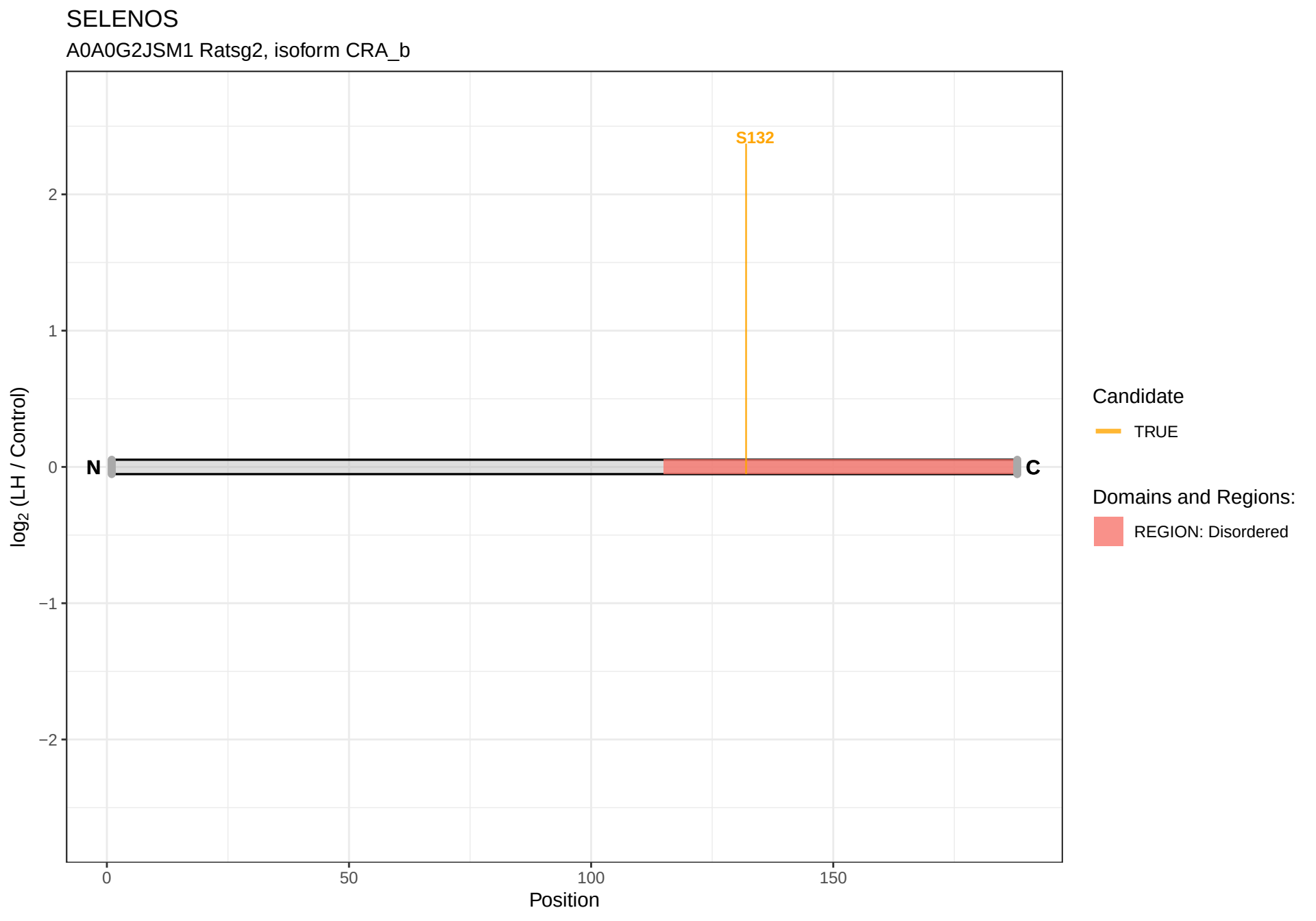

SEC16A
D3ZN76 Protein transport protein sec16
log2 (LH / Control)
Position
N
C
S1233
T1237
S1227
S1226
S1230
S1356
S1353
S2089
T2091
S2041
S2046
S546
S489
S393
S583
S1017
S1311
S1362
S1330
S1365
T1335
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Sec16
DOMAIN: Sec16_C
REGION: Disordered

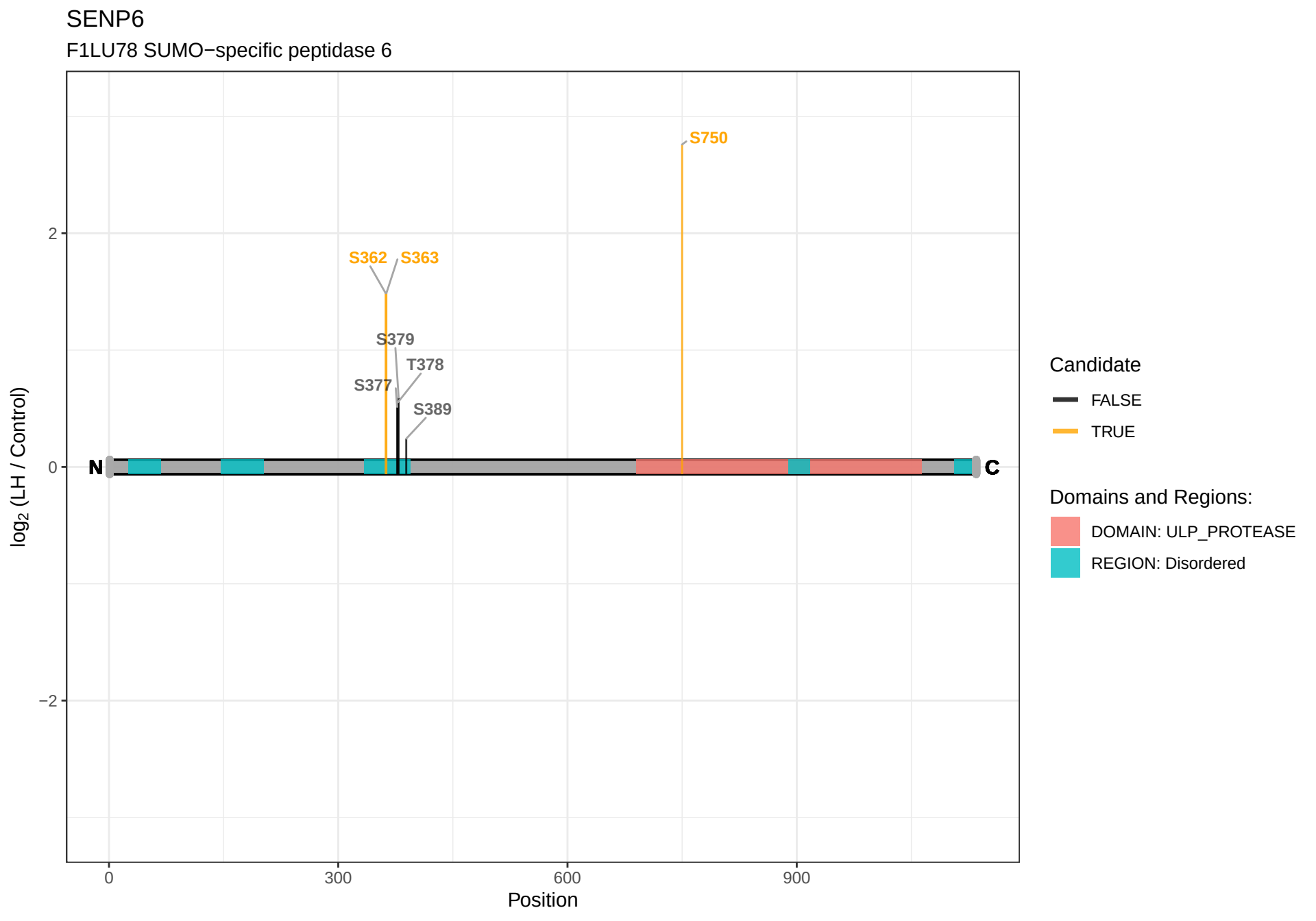

SEC22B
Q4KM74 Vesicle−trafficking protein SEC22b
S137
S177
S174
S175
S168
N
C
2.5
0.0
−2.5
log2 (LH / Control)
0
50
100
150
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Longin
DOMAIN: v−SNARE coiled−coil homology

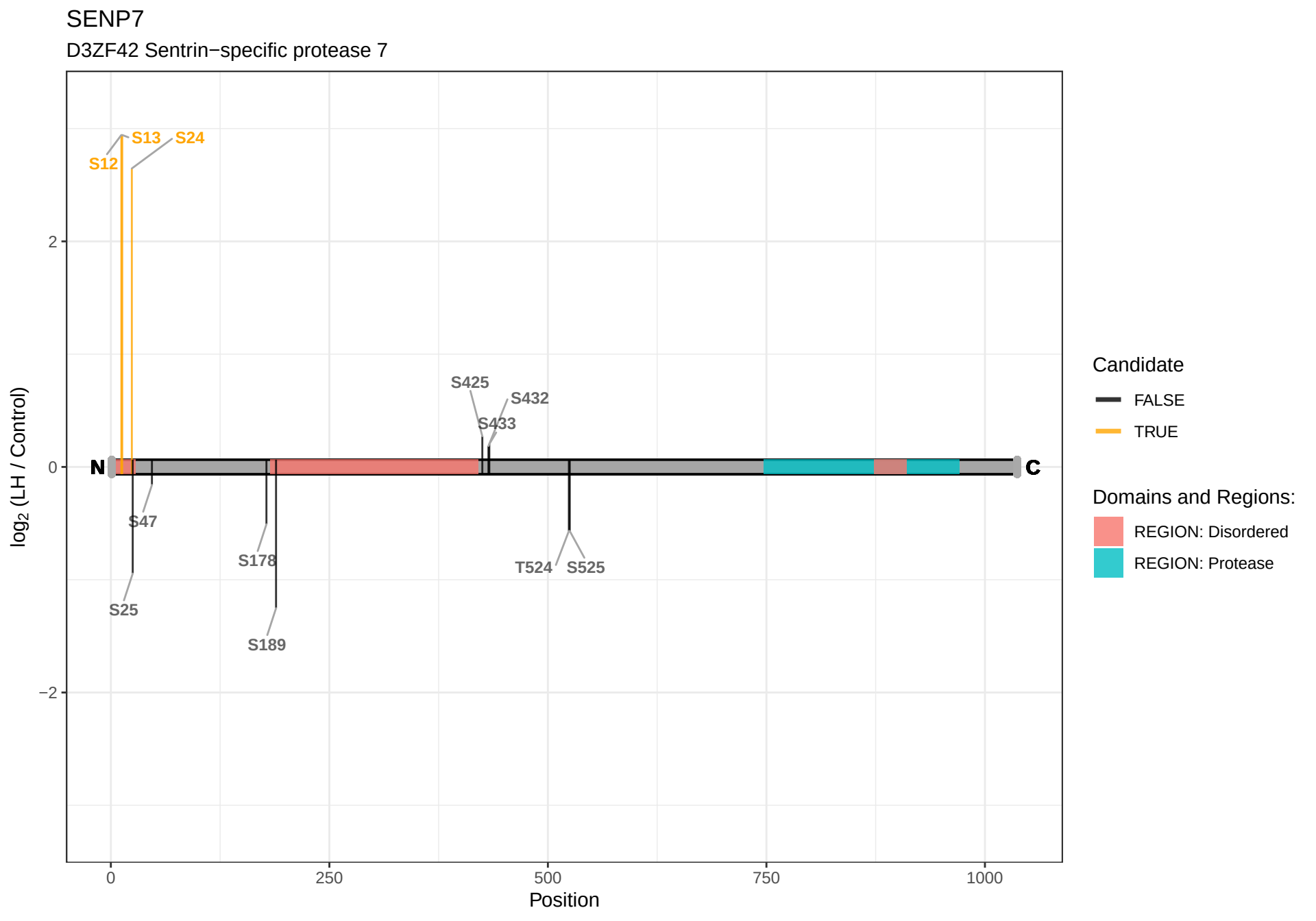

SEC31A
A0A0G2K0X9 Protein transport protein Sec31A
log2 (LH / Control)
2
1
0
−1
−2
N
C
S803
S513
S526
S531
S1209
0
250
500
750
1000
1250
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WD_REPEATS_REGION
REGION: Disordered

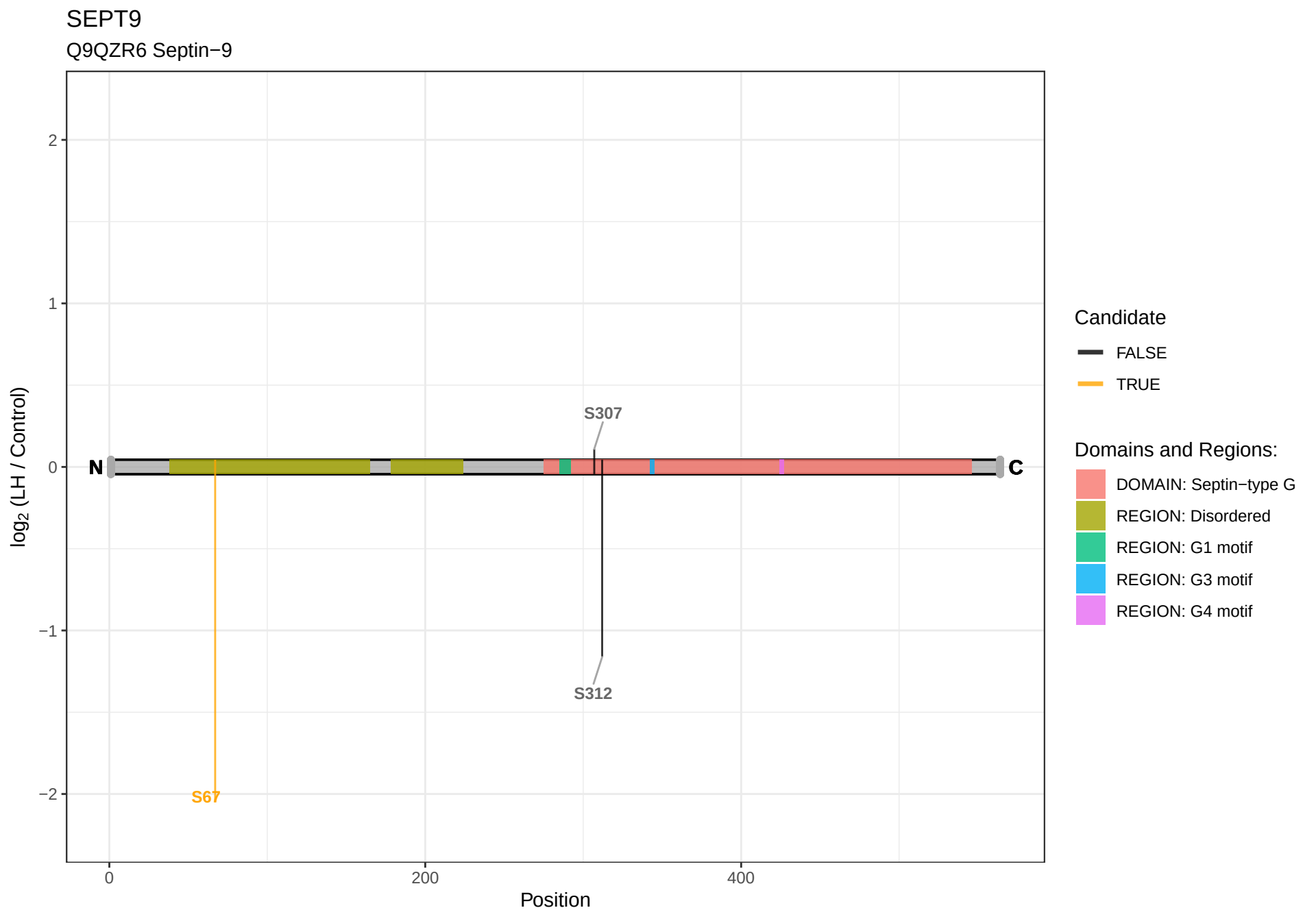

SEC62
Q7TP42 Ab2−292
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
Position
N
C
S336
S548
S552
T550
S563
S560
S542
T582
T365
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

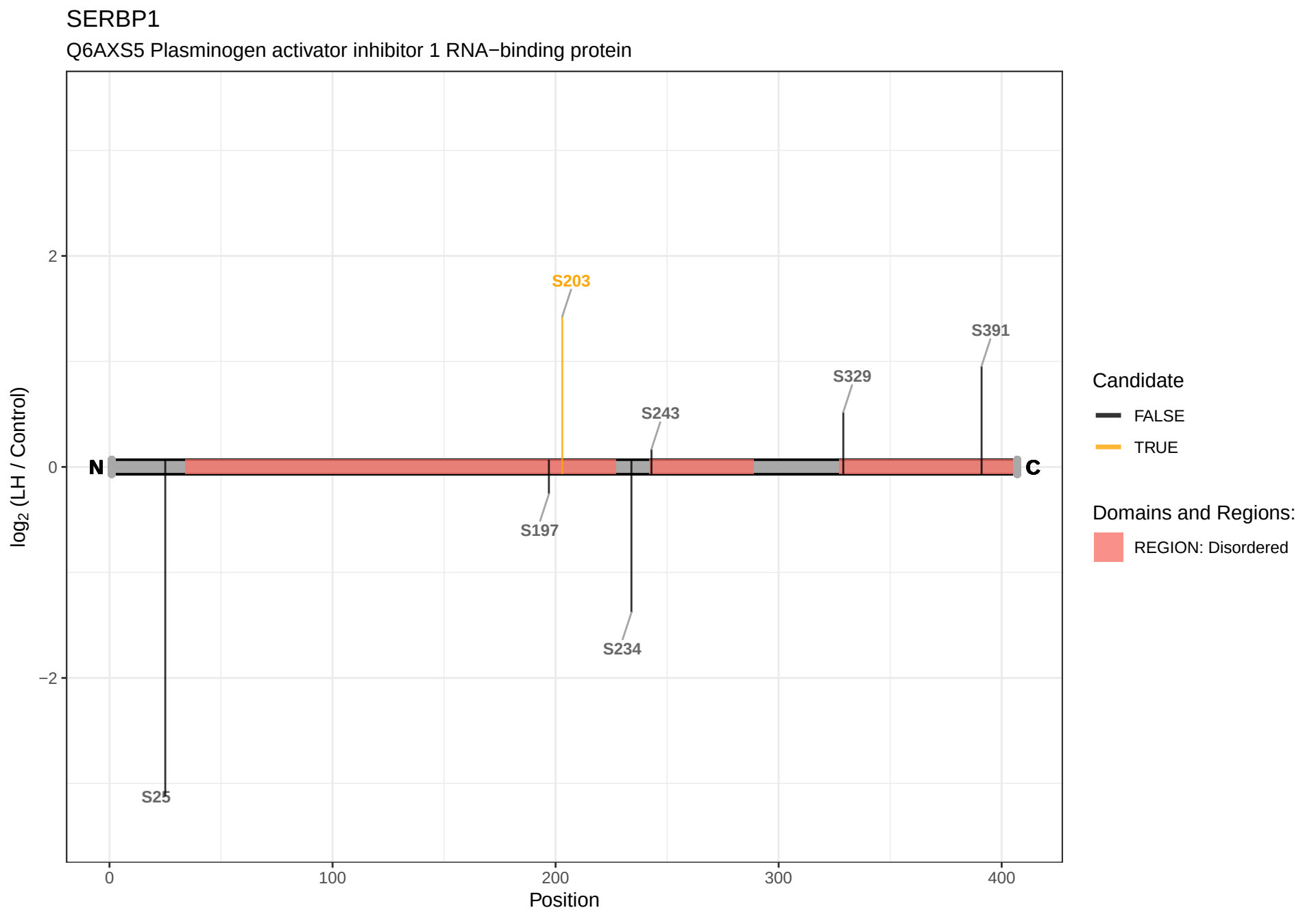

SECISBP2L
D4A7V0 SECIS−binding protein 2−like
S251
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
300
600
900
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Ribosomal_L7Ae
REGION: Disordered

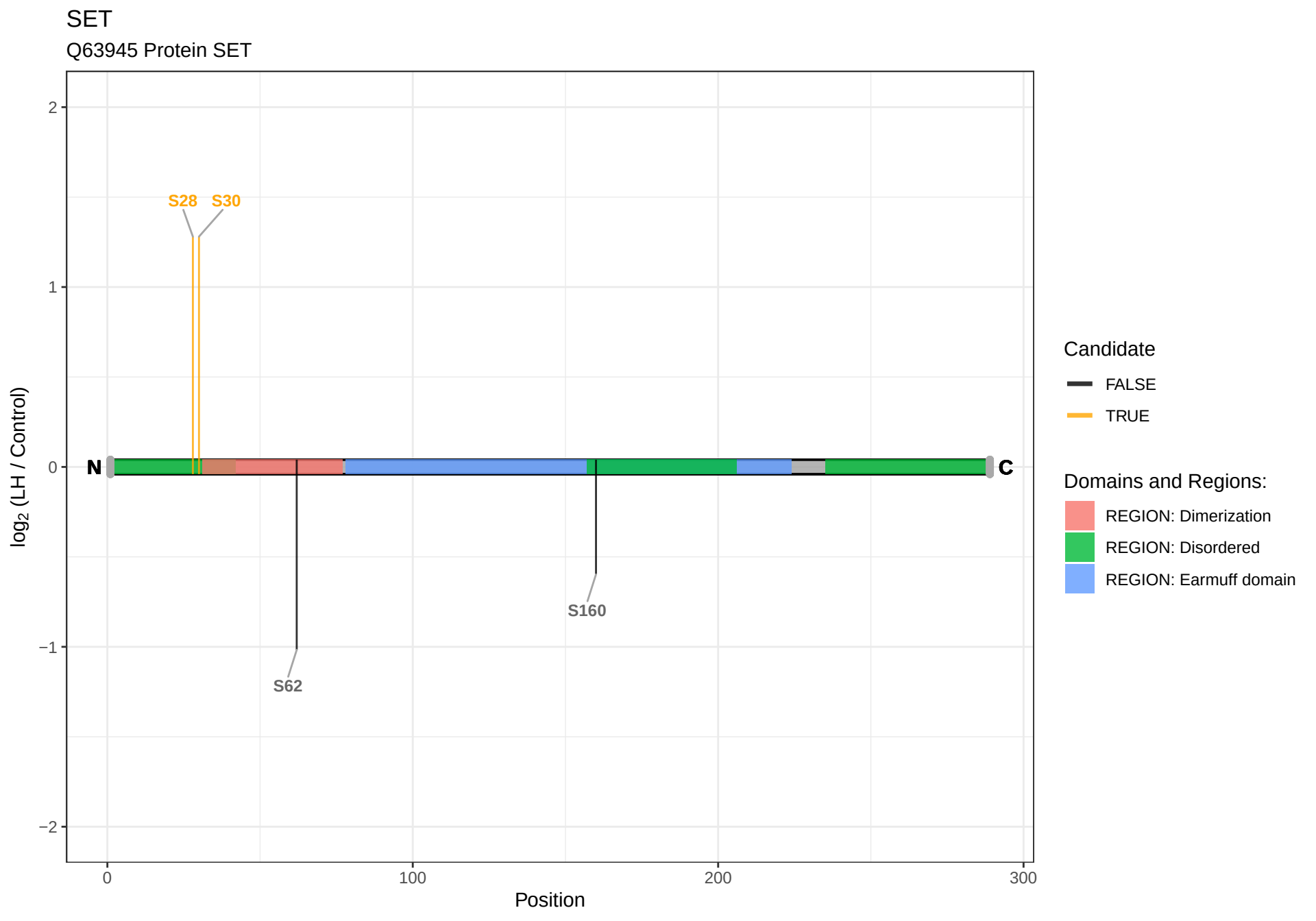

SELENOS
A0A0G2JSM1 Ratsg2, isoform CRA_b
S132
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
50
100
150
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

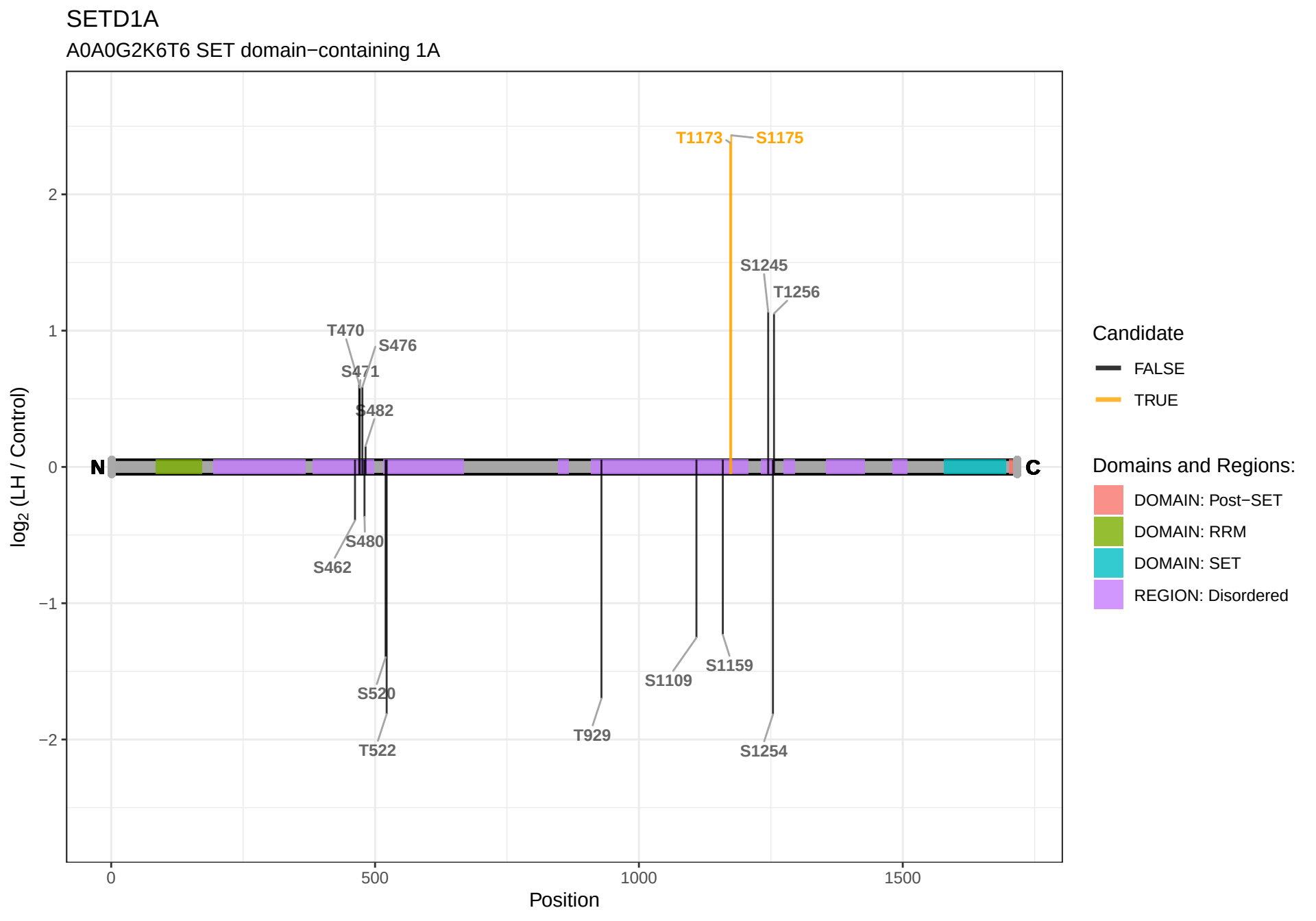

SENP6
F1LU78 SUMO−specific peptidase 6
S750
S362
S363
S379
T378
S377
S389
N
C
2
0
−2
log2 (LH / Control)
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ULP_PROTEASE
REGION: Disordered

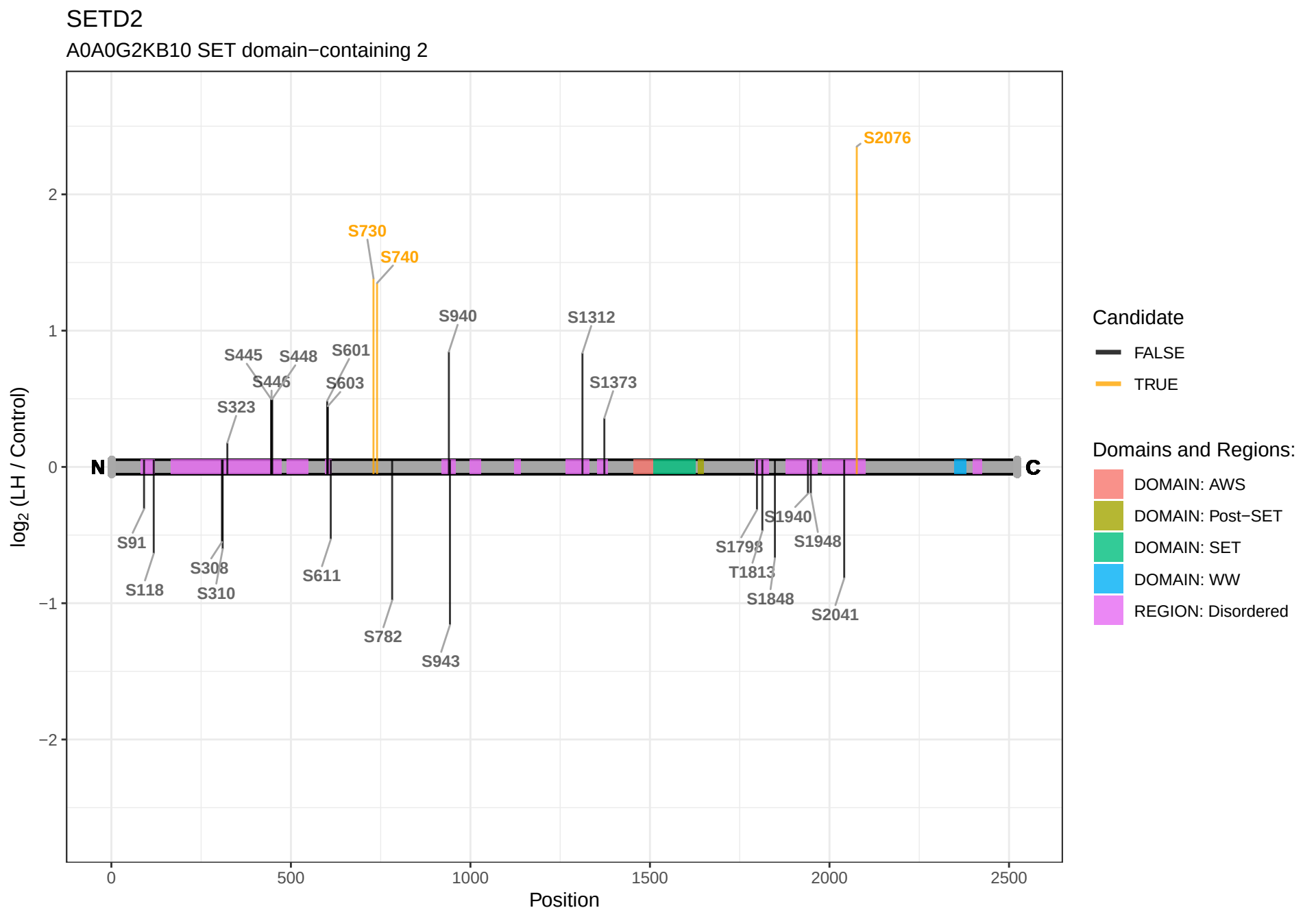

SENP7
D3ZF42 Sentrin−specific protease 7
S13
S24
S12
S425
S432
S433
N
C
S47
S178
S25
S189
T524
S525
2
0
−2
log2 (LH / Control)
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Protease

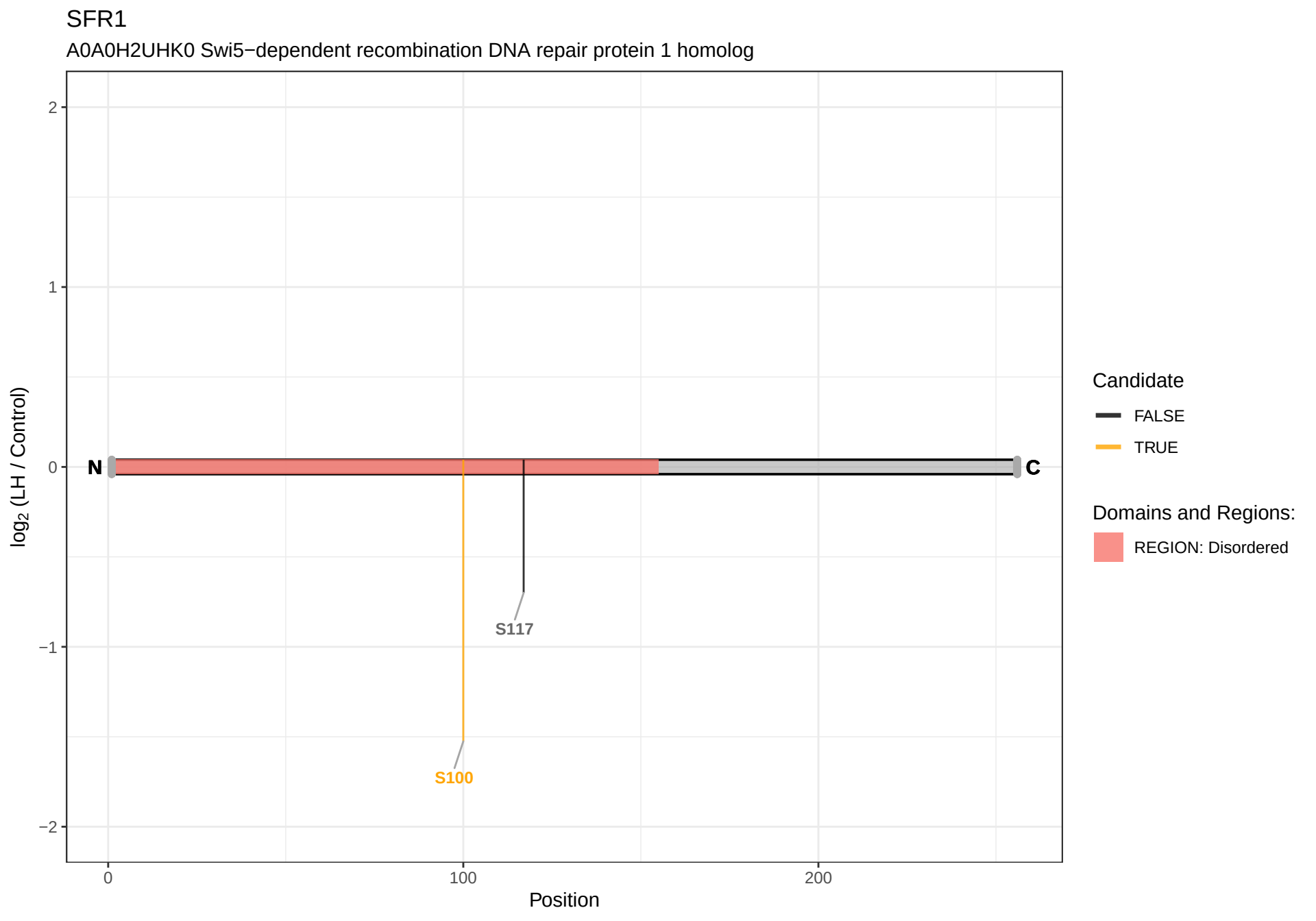

SEPT9
Q9QZR6 Septin−9
log2 (LH / Control)
2
1
0
−1
−2
N
C
S307
S312
S67
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Septin−type G
REGION: Disordered
REGION: G1 motif
REGION: G3 motif
REGION: G4 motif

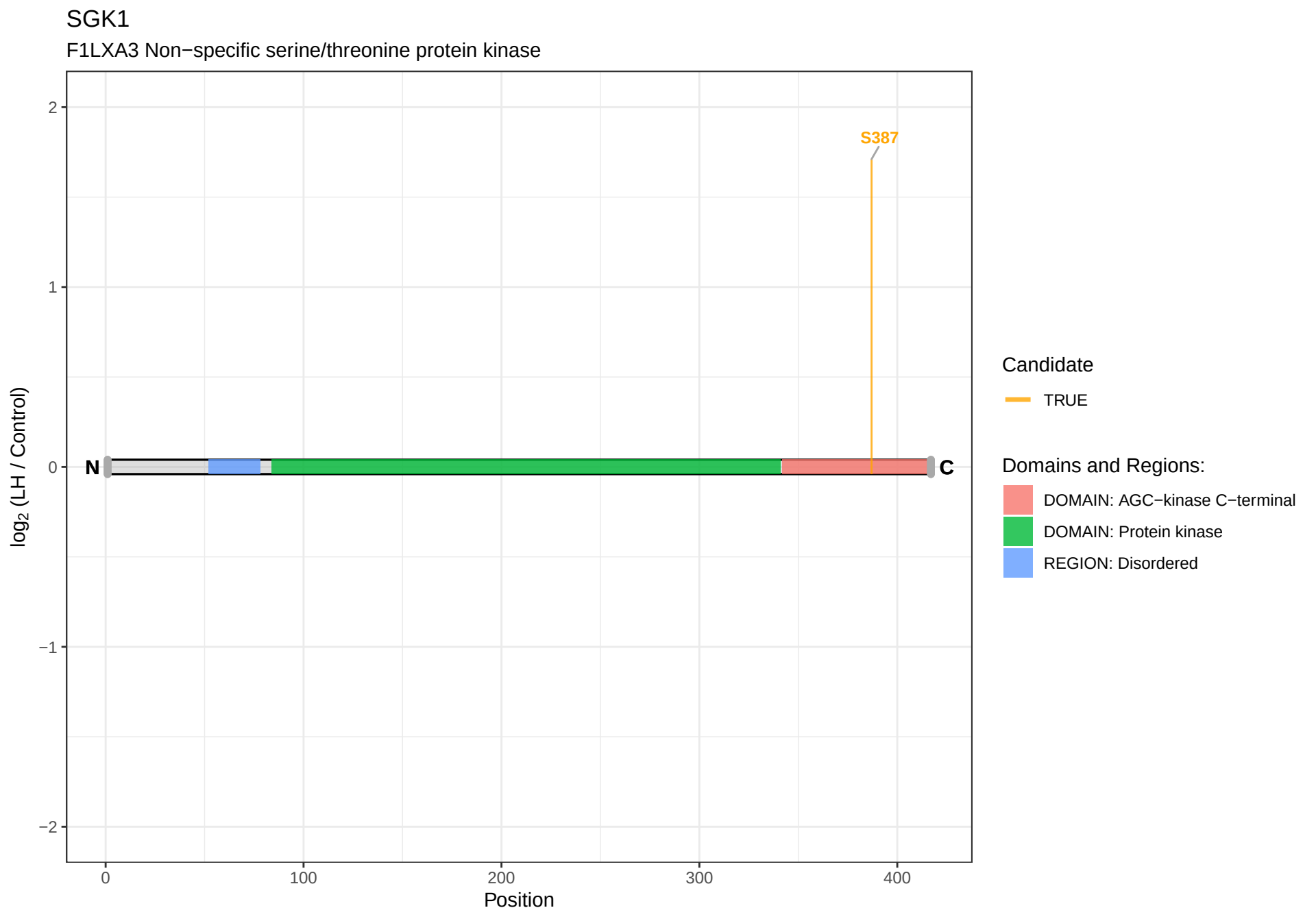

SERBP1
Q6AXS5 Plasminogen activator inhibitor 1 RNA−binding protein
log2 (LH / Control)
2
0
−2
N
C
S203
S391
S329
S243
S197
S234
S25
0
100
200
300
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

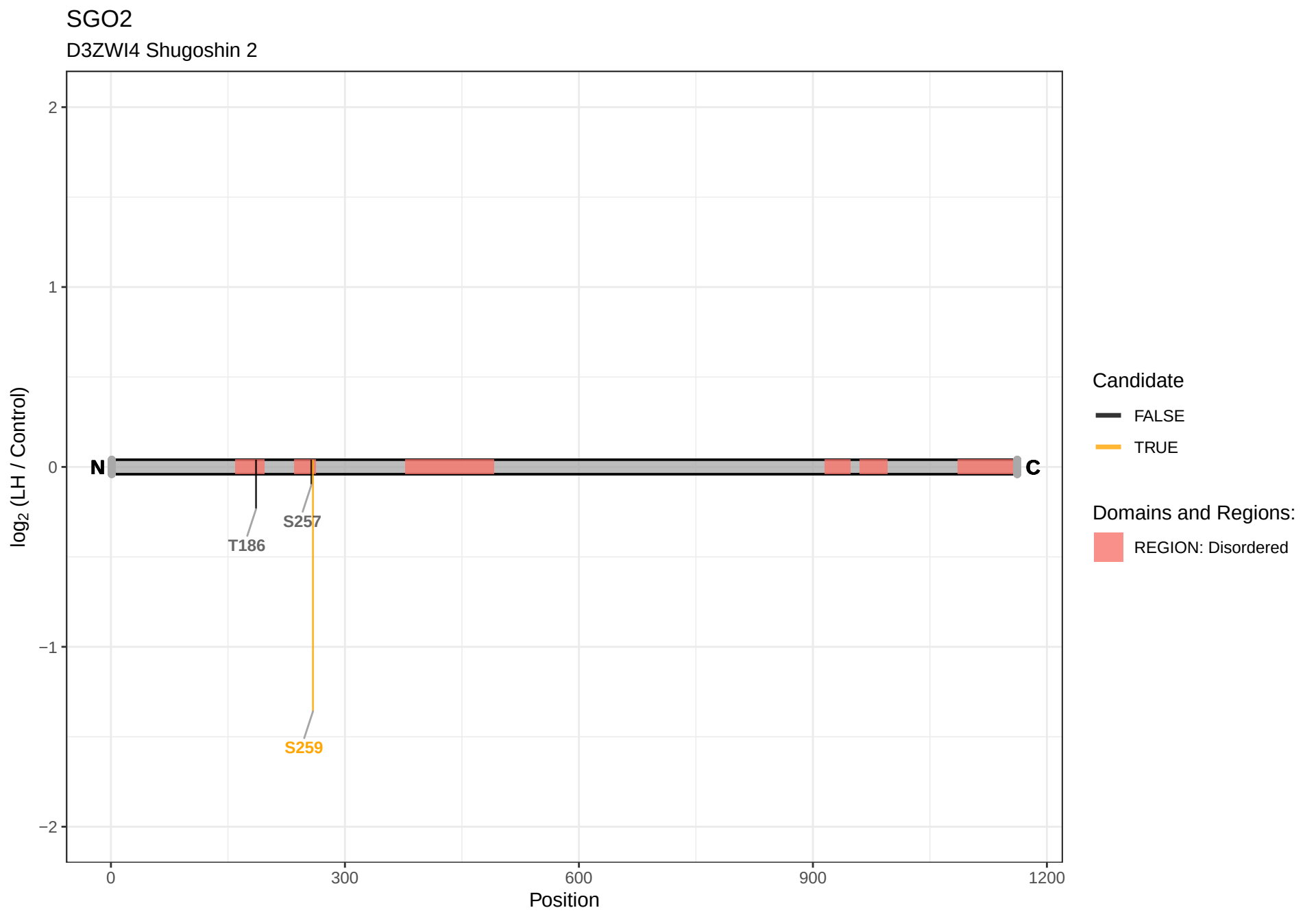

SET
Q63945 Protein SET
log2 (LH / Control)
2
1
0
−1
−2
S28
S30
N
C
S160
S62
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Dimerization
REGION: Disordered
REGION: Earmuff domain

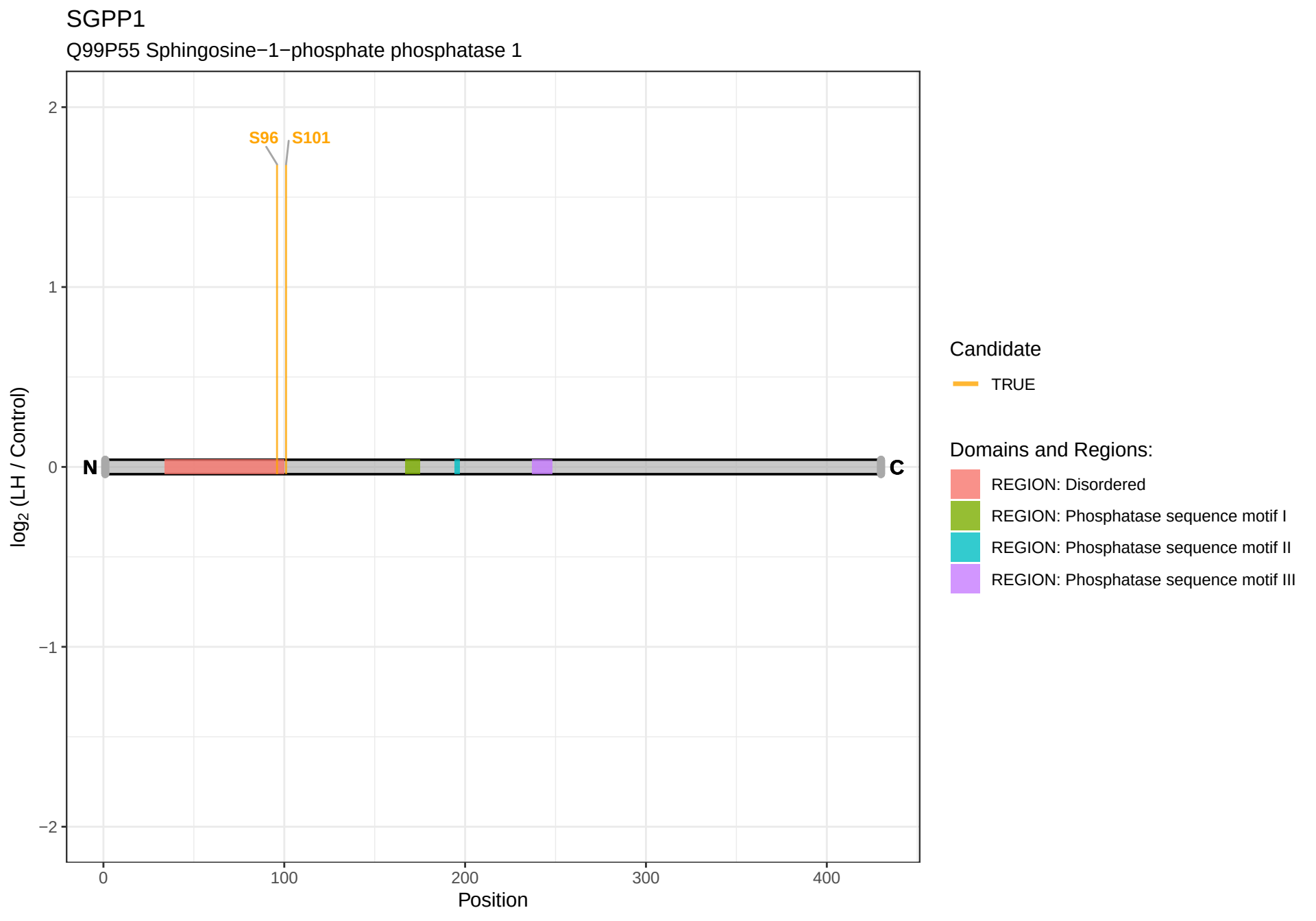

SETD1A
A0A0G2K6T6 SET domain−containing 1A
T1173
S1175
S1245
T1256
T470
S476
S471
S482
N
C
S480
S462
S520
T522
T929
S1109
S1159
S1254
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Post−SET
DOMAIN: RRM
DOMAIN: SET
REGION: Disordered

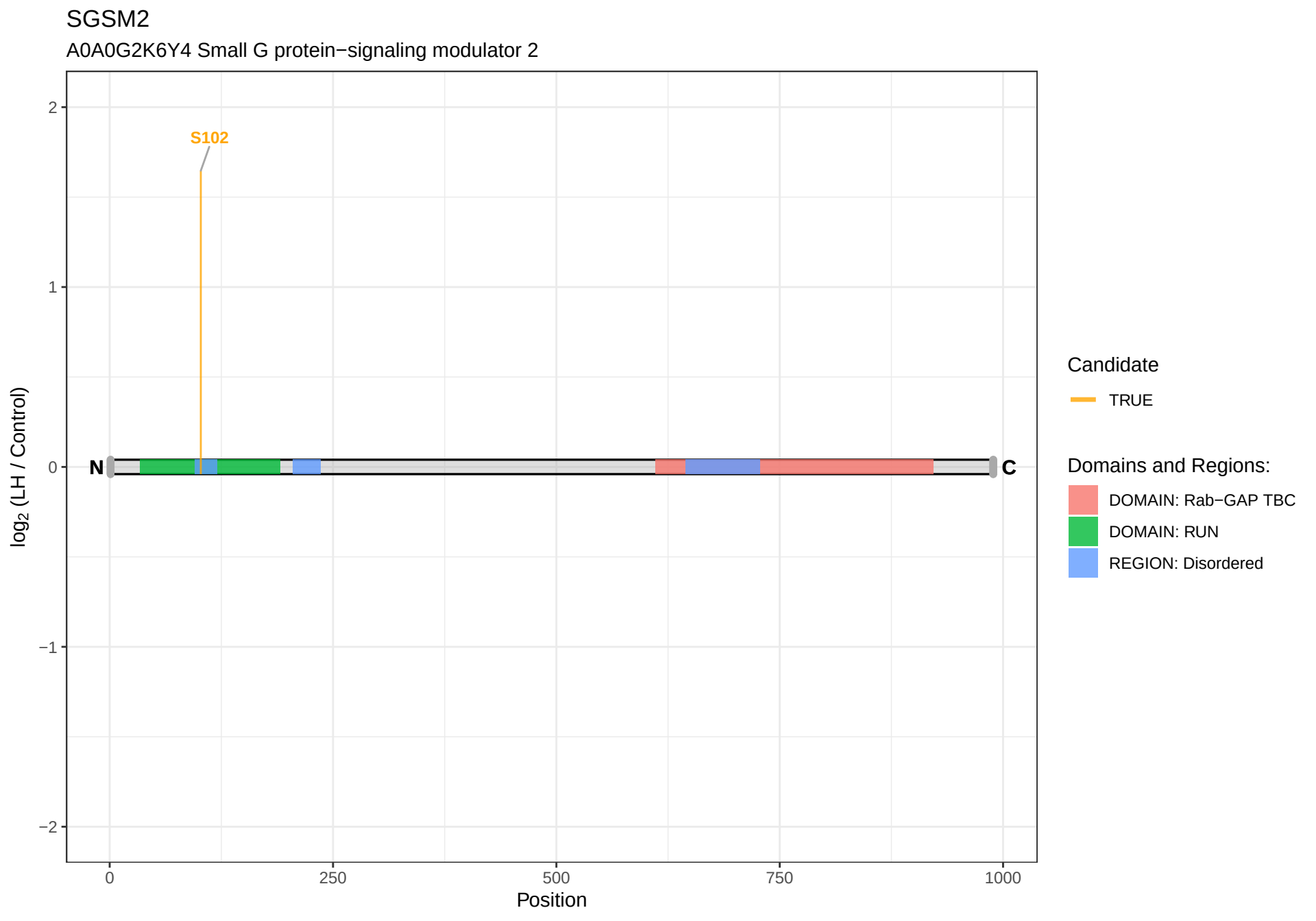

SETD2
A0A0G2KB10 SET domain−containing 2
S2076
S730
S740
S940
S1312
S445
S448
S601
S446
S603
S1373
S323
N
C
S91
S118
S308
S310
S611
S782
S943
S1940
S1798
S1948
T1813
S1848
S2041
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
2000
2500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AWS
DOMAIN: Post−SET
DOMAIN: SET
DOMAIN: WW
REGION: Disordered

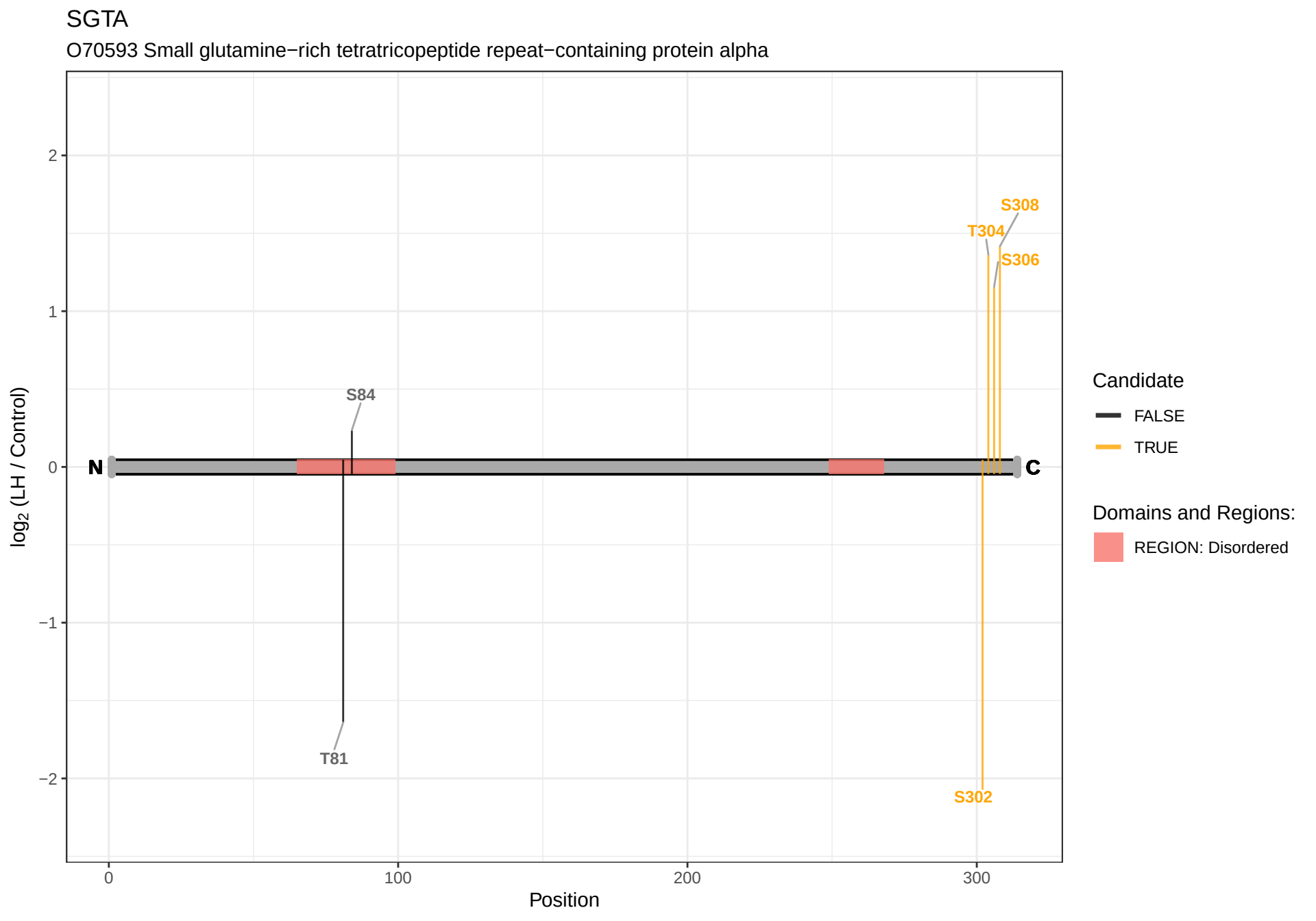

SFR1
A0A0H2UHK0 Swi5−dependent recombination DNA repair protein 1 homolog
2
1
0
−1
−2
log2 (LH / Control)
N
C
S117
S100
0
100
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

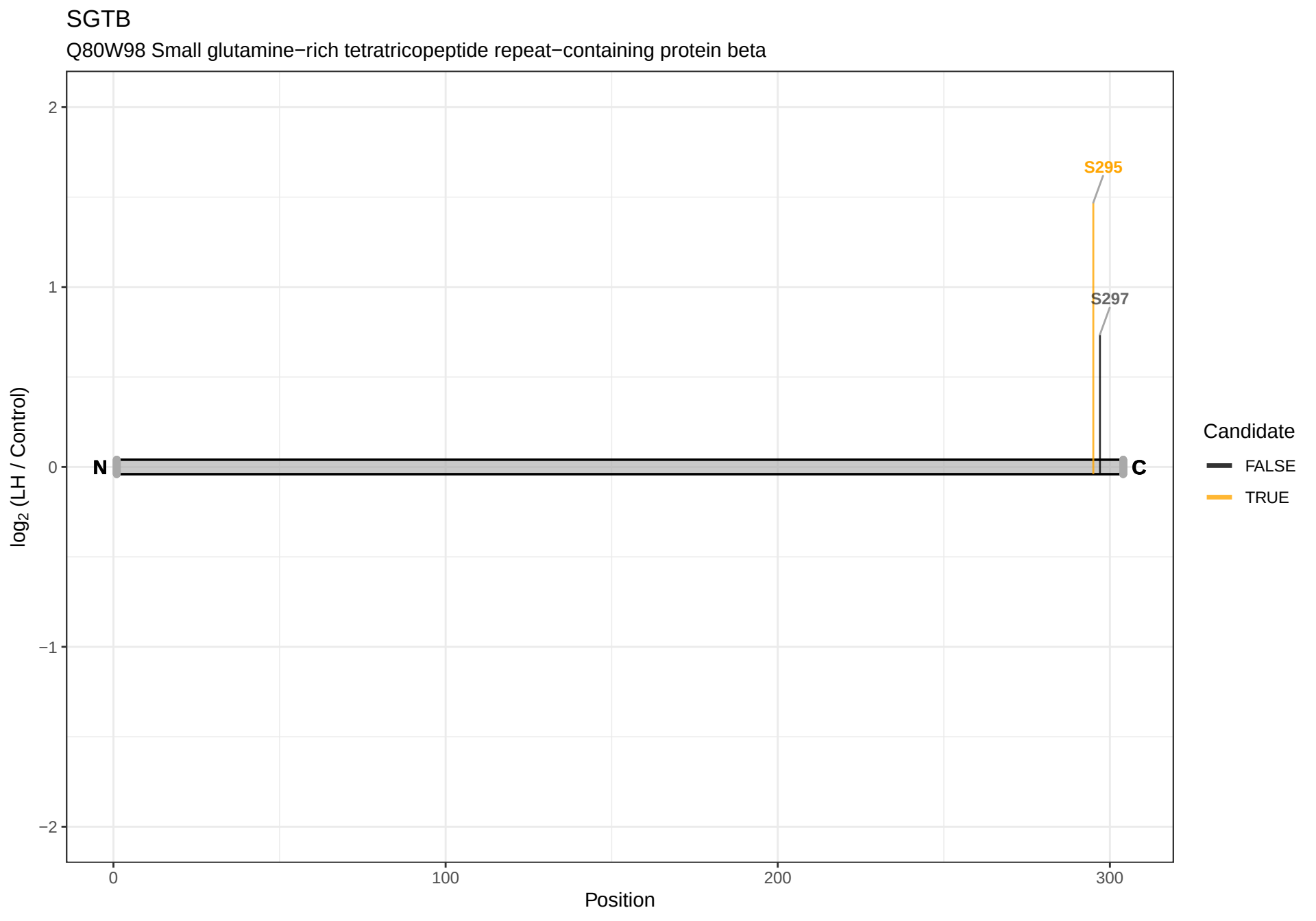

SGK1
F1LXA3 Non−specific serine/threonine protein kinase
S387
N
C
2
1
0
−1
−2
0
100
200
300
400
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
DOMAIN: AGC−kinase C−terminal
DOMAIN: Protein kinase
REGION: Disordered

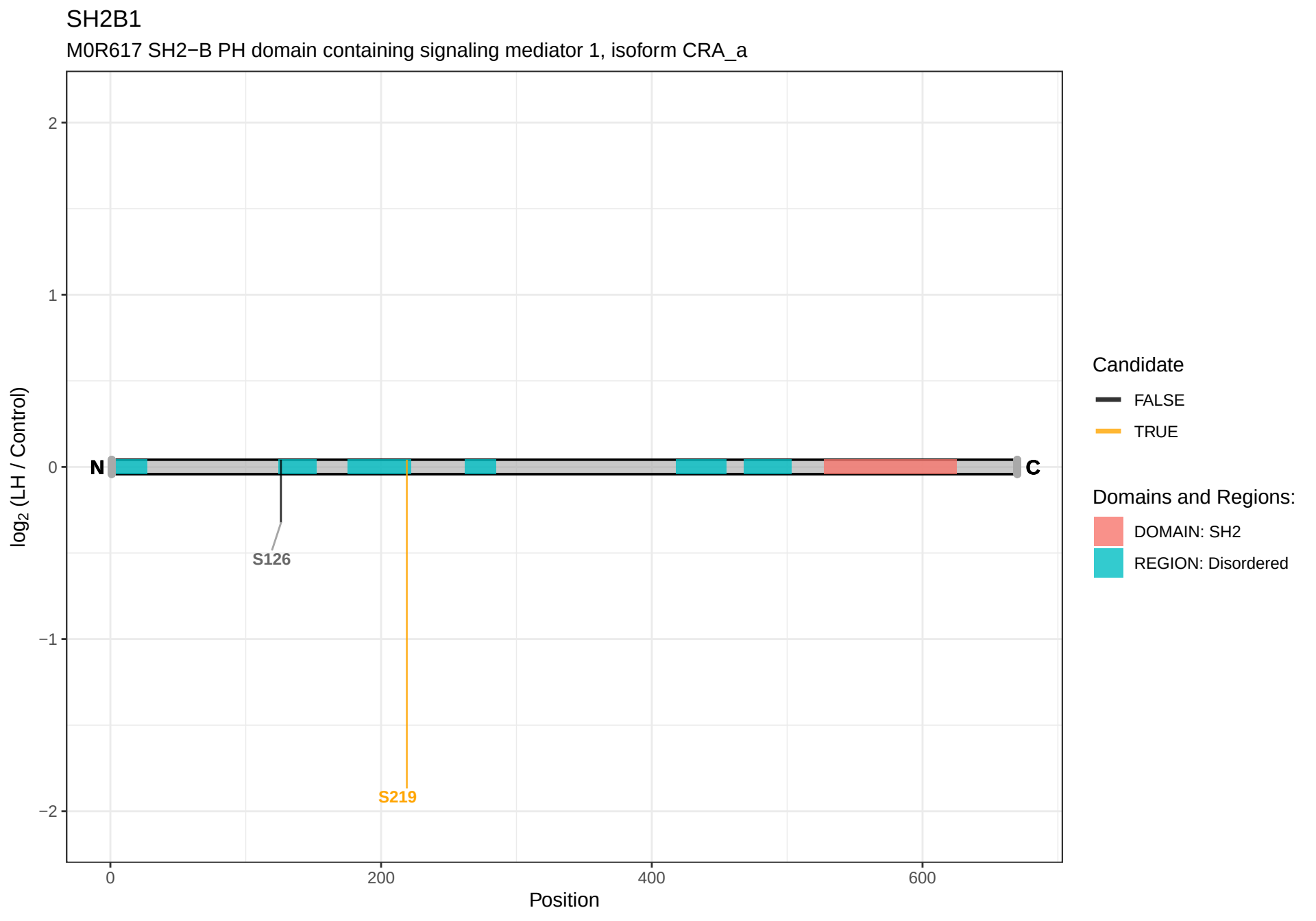

SGO2
D3ZWI4 Shugoshin 2
2
1
0
−1
−2
log2 (LH / Control)
N
C
T186
S257
S259
0
300
600
900
1200
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

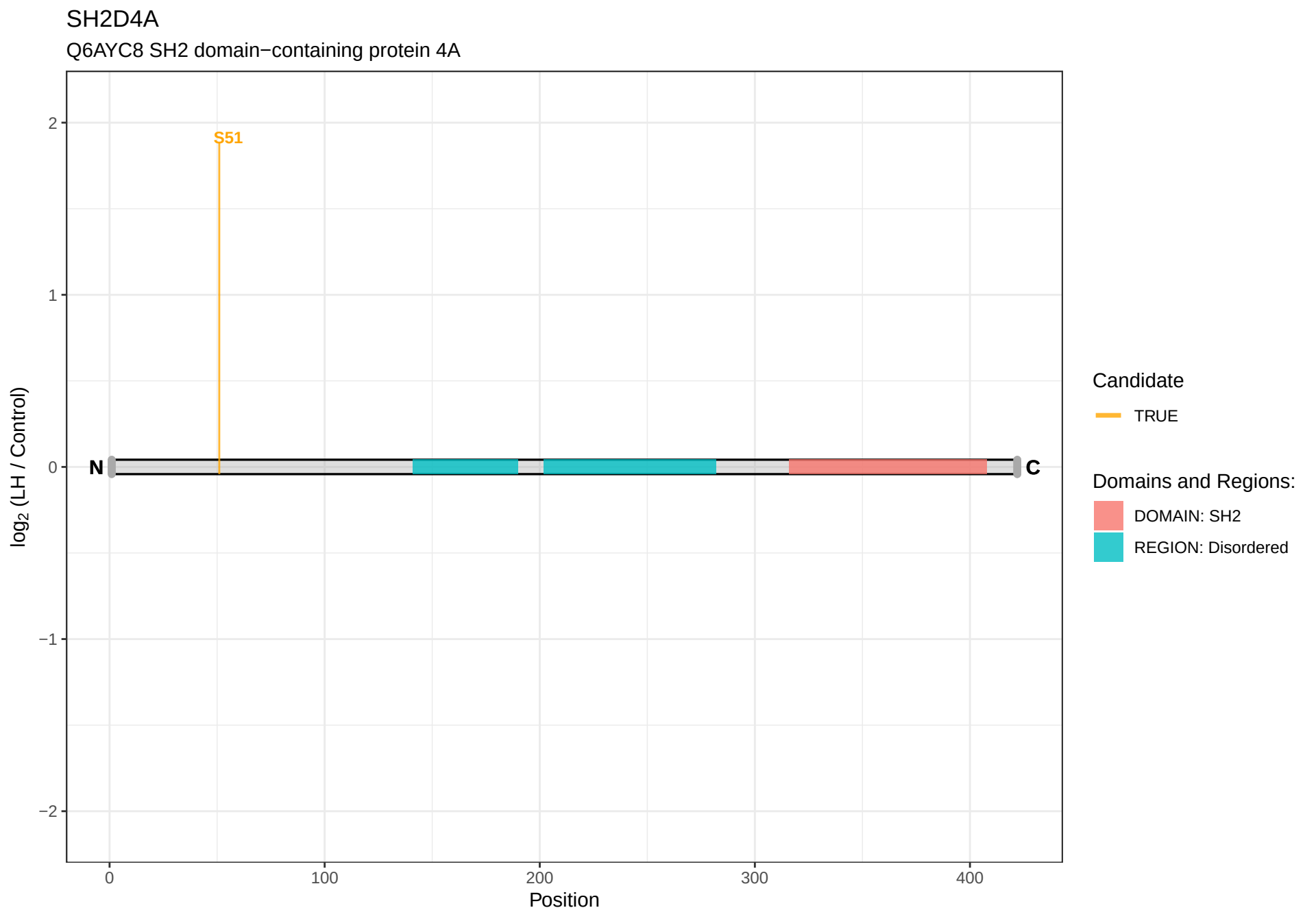

SGPP1
Q99P55 Sphingosine−1−phosphate phosphatase 1
S96
S101
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
100
200
300
400
Candidate
TRUE
Domains and Regions:
REGION: Disordered
REGION: Phosphatase sequence motif I
REGION: Phosphatase sequence motif II
REGION: Phosphatase sequence motif III

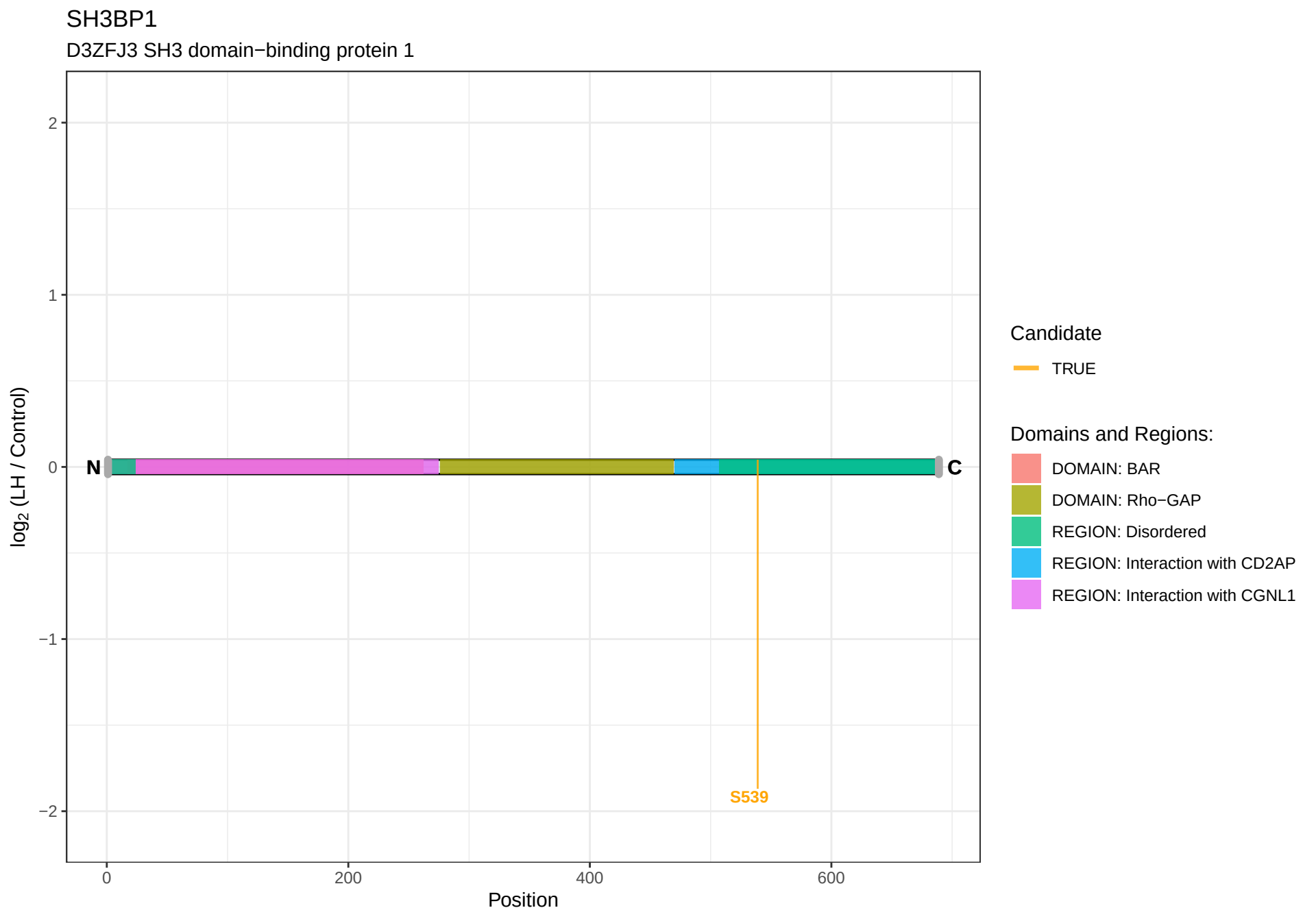

SGSM2
A0A0G2K6Y4 Small G protein−signaling modulator 2
S102
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
250
500
750
1000
Candidate
TRUE
Domains and Regions:
DOMAIN: Rab−GAP TBC
DOMAIN: RUN
REGION: Disordered

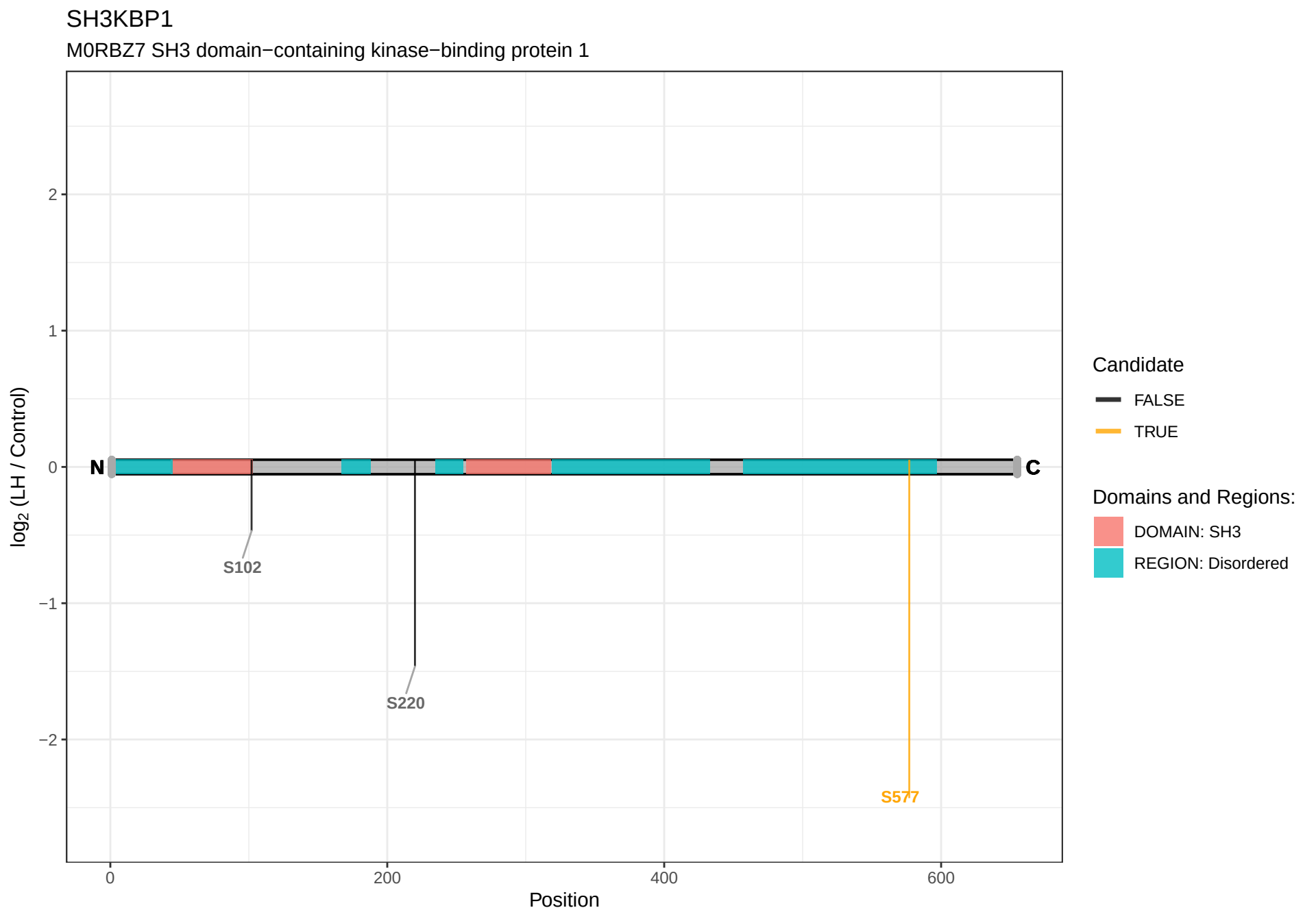

SGTA
O70593 Small glutamine−rich tetratricopeptide repeat−containing protein alpha
log2 (LH / Control)
2
1
0
−1
−2
N
C
S84
T81
S308
T304
S306
S302
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

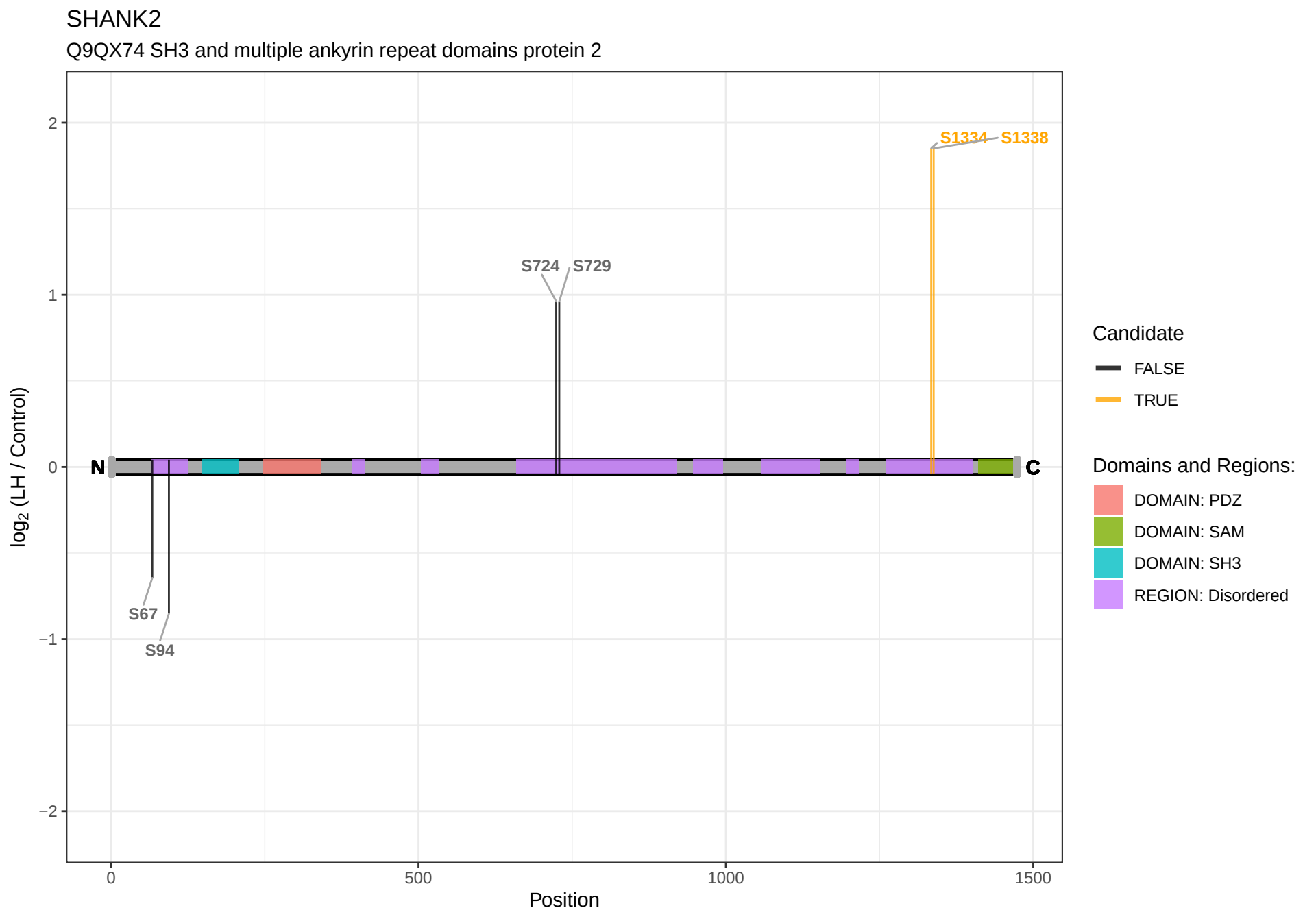

SGTB
Q80W98 Small glutamine−rich tetratricopeptide repeat−containing protein beta
S295
S297
N
C
log2 (LH / Control)
Position
Candidate
FALSE
TRUE
2
1
0
−1
−2
0
100
200
300

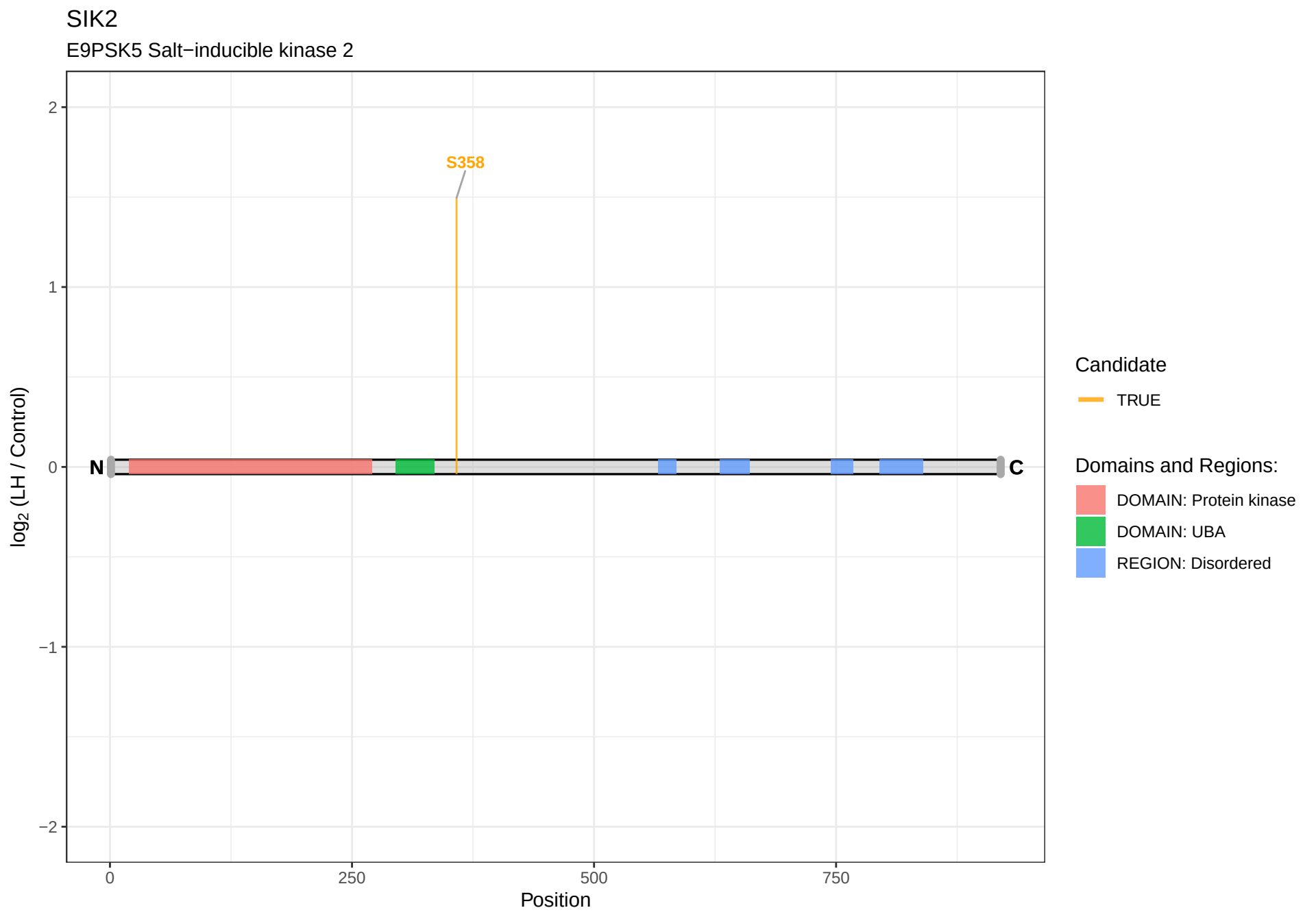

SH2B1
M0R617 SH2−B PH domain containing signaling mediator 1, isoform CRA_a
2
1
0
−1
−2
log2 (LH / Control)
N
C
S126
S219
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SH2
REGION: Disordered

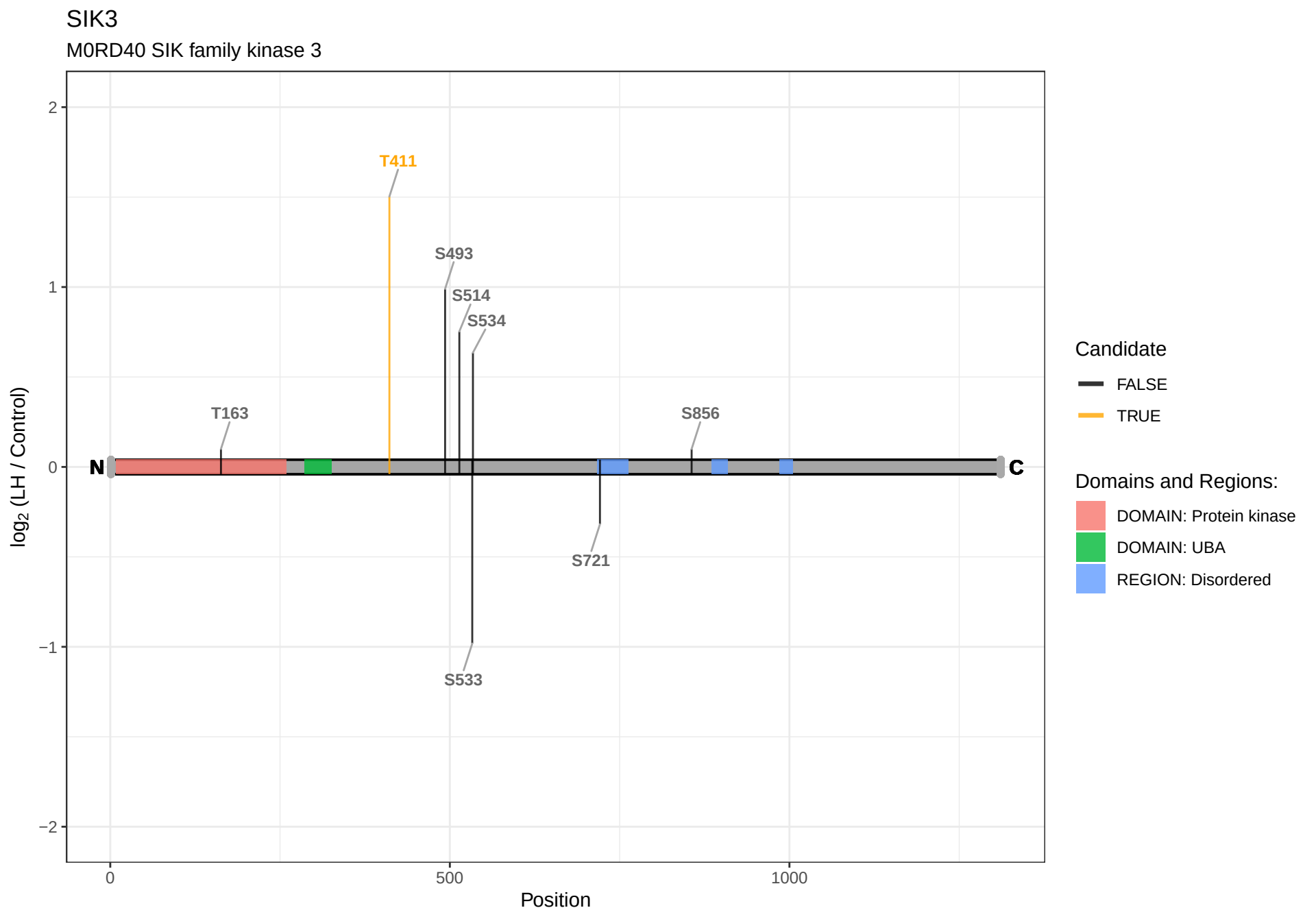

SH2D4A
Q6AYC8 SH2 domain−containing protein 4A
S51
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
400
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: SH2
REGION: Disordered

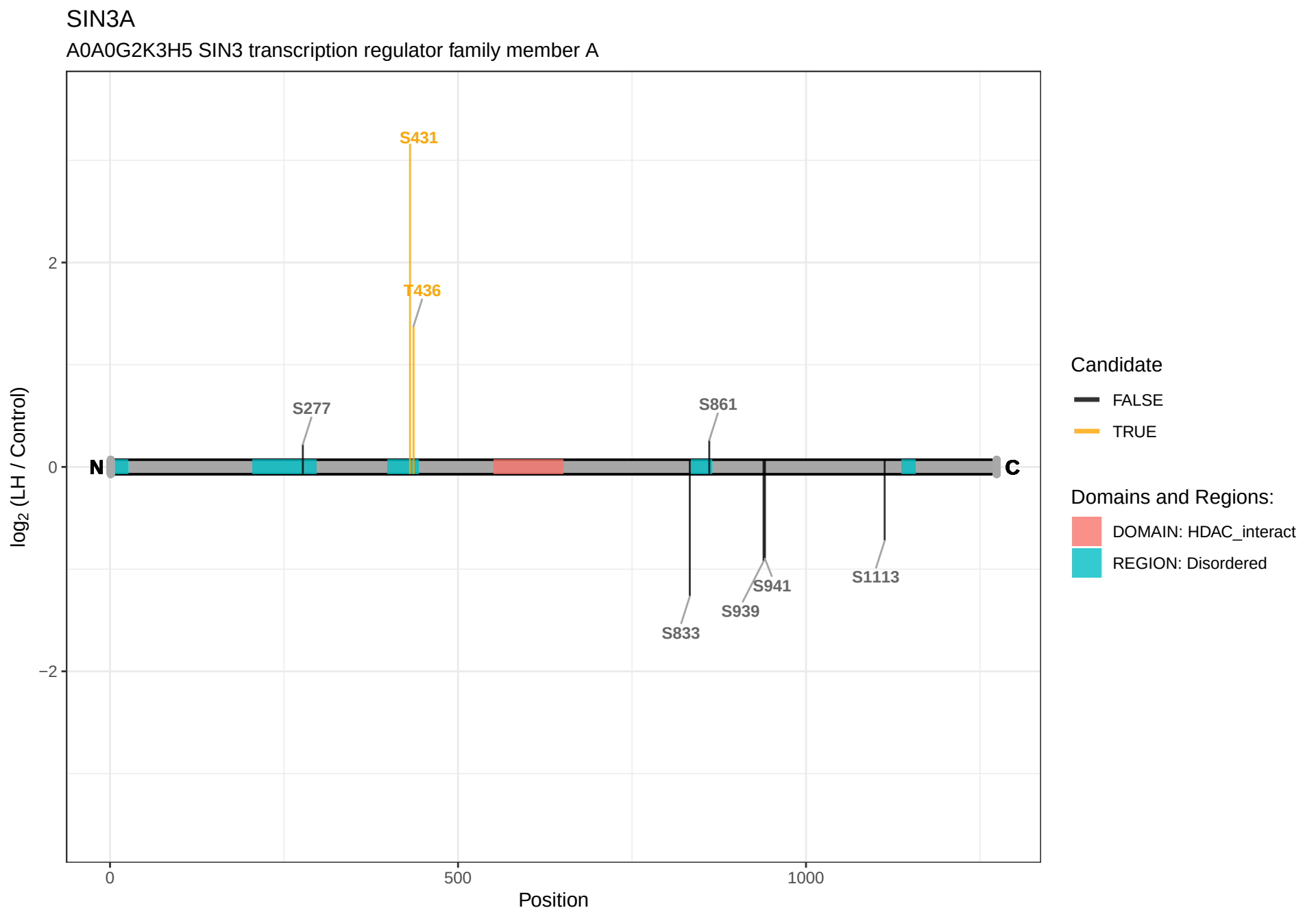

SH3BP1
D3ZFJ3 SH3 domain−binding protein 1
2
1
0
−1
−2
log2 (LH / Control)
N
C
S539
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: BAR
DOMAIN: Rho−GAP
REGION: Disordered
REGION: Interaction with CD2AP
REGION: Interaction with CGNL1

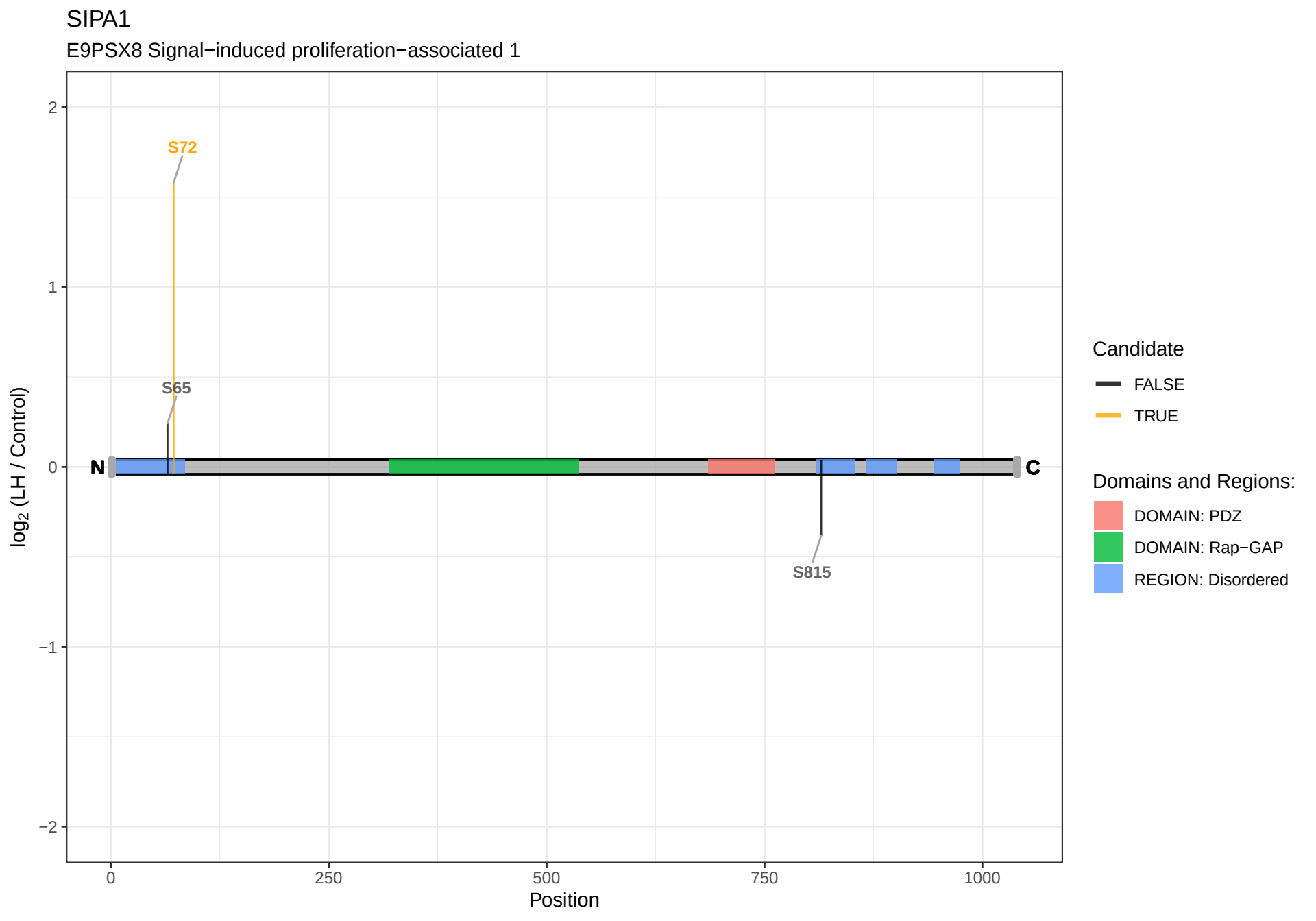

SH3KBP1
M0RBZ7 SH3 domain−containing kinase−binding protein 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S102
S220
S577
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SH3
REGION: Disordered

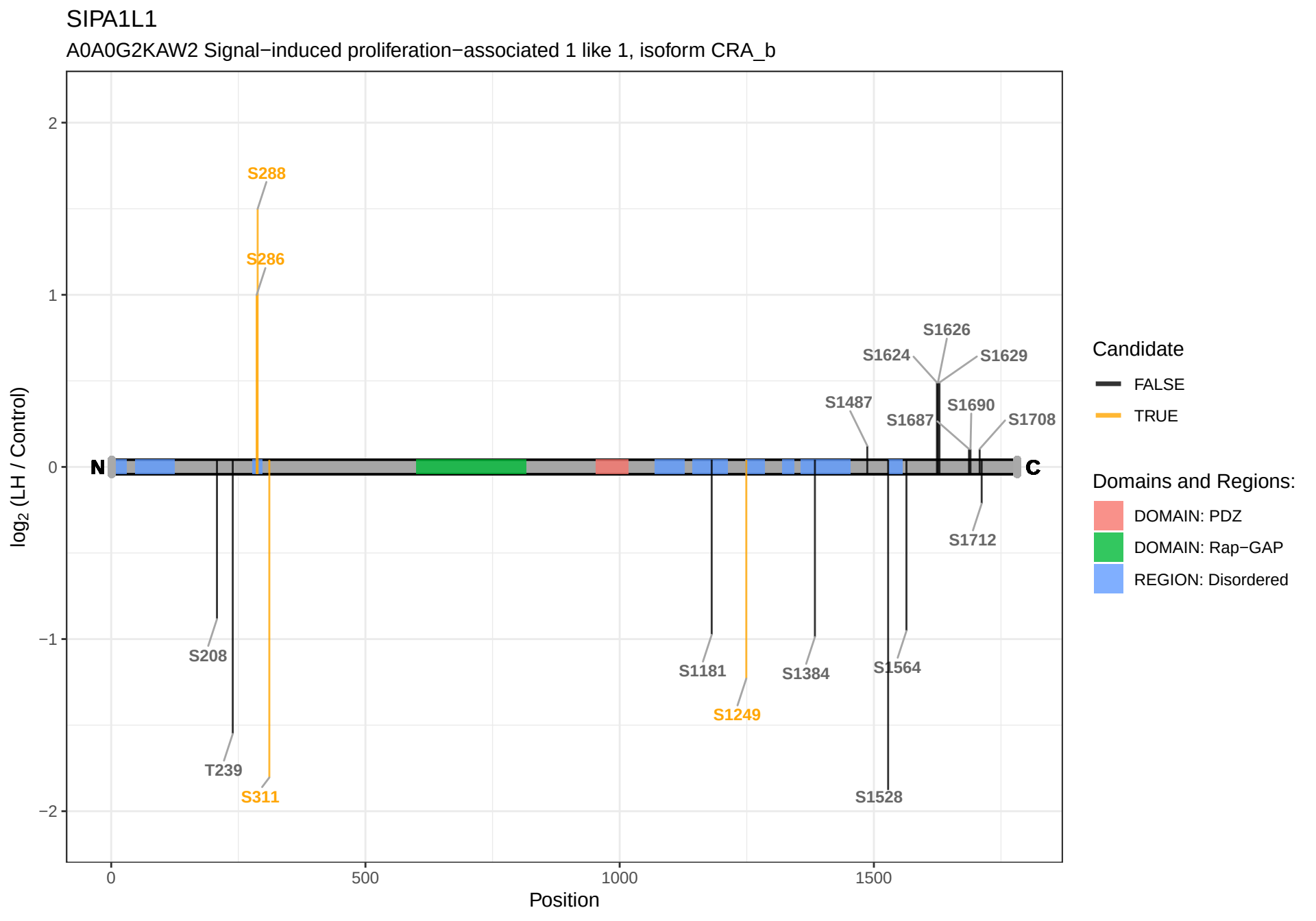

SHANK2
Q9QX74 SH3 and multiple ankyrin repeat domains protein 2
S1334
S1338
S724
S729
S67
S94
N
C
2
1
0
−1
−2
0
500
1000
1500
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PDZ
DOMAIN: SAM
DOMAIN: SH3
REGION: Disordered

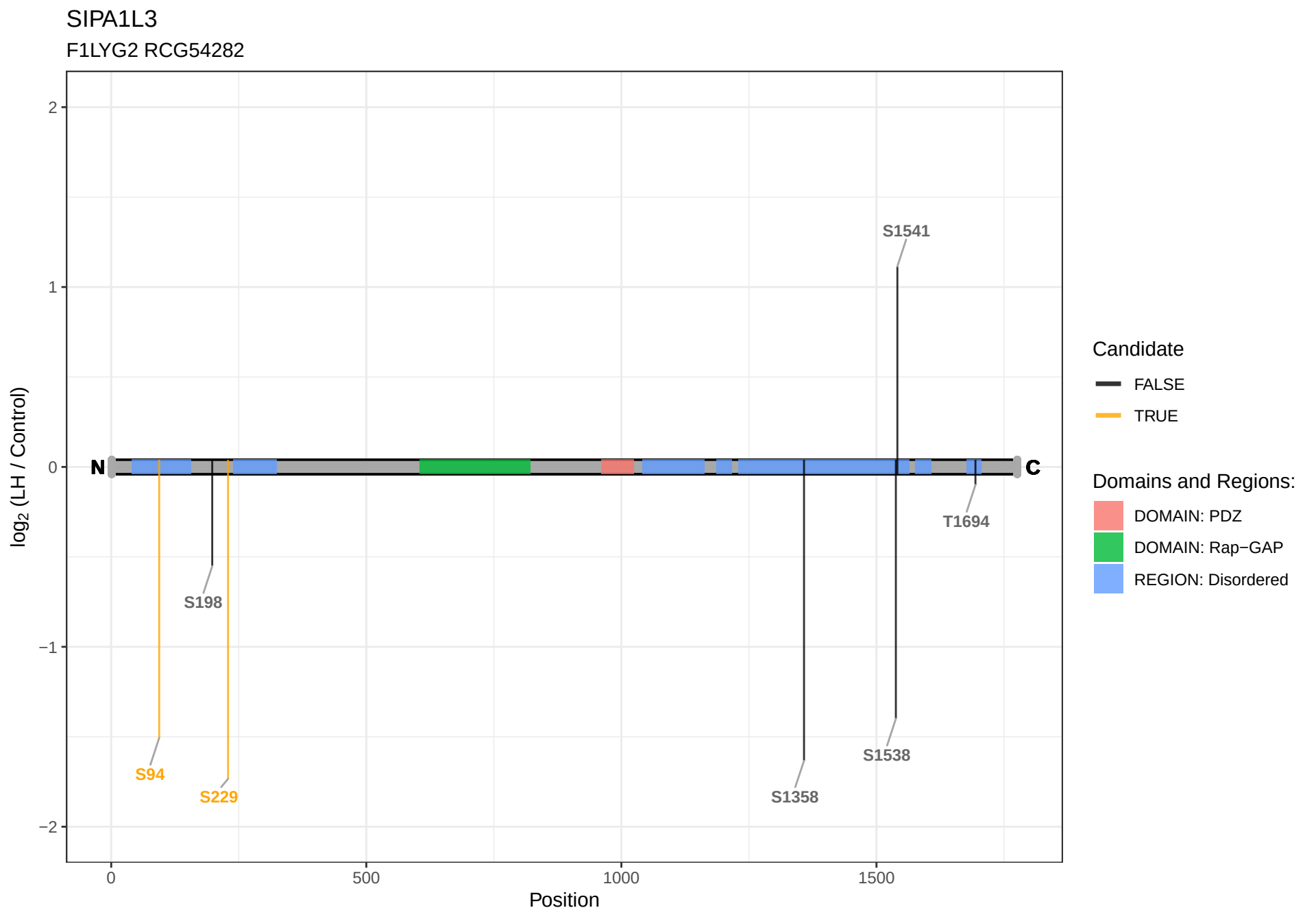

SIK2
E9PSK5 Salt−inducible kinase 2
S358
N
C
2
1
0
−1
−2
0
250
500
750
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
DOMAIN: Protein kinase
DOMAIN: UBA
REGION: Disordered

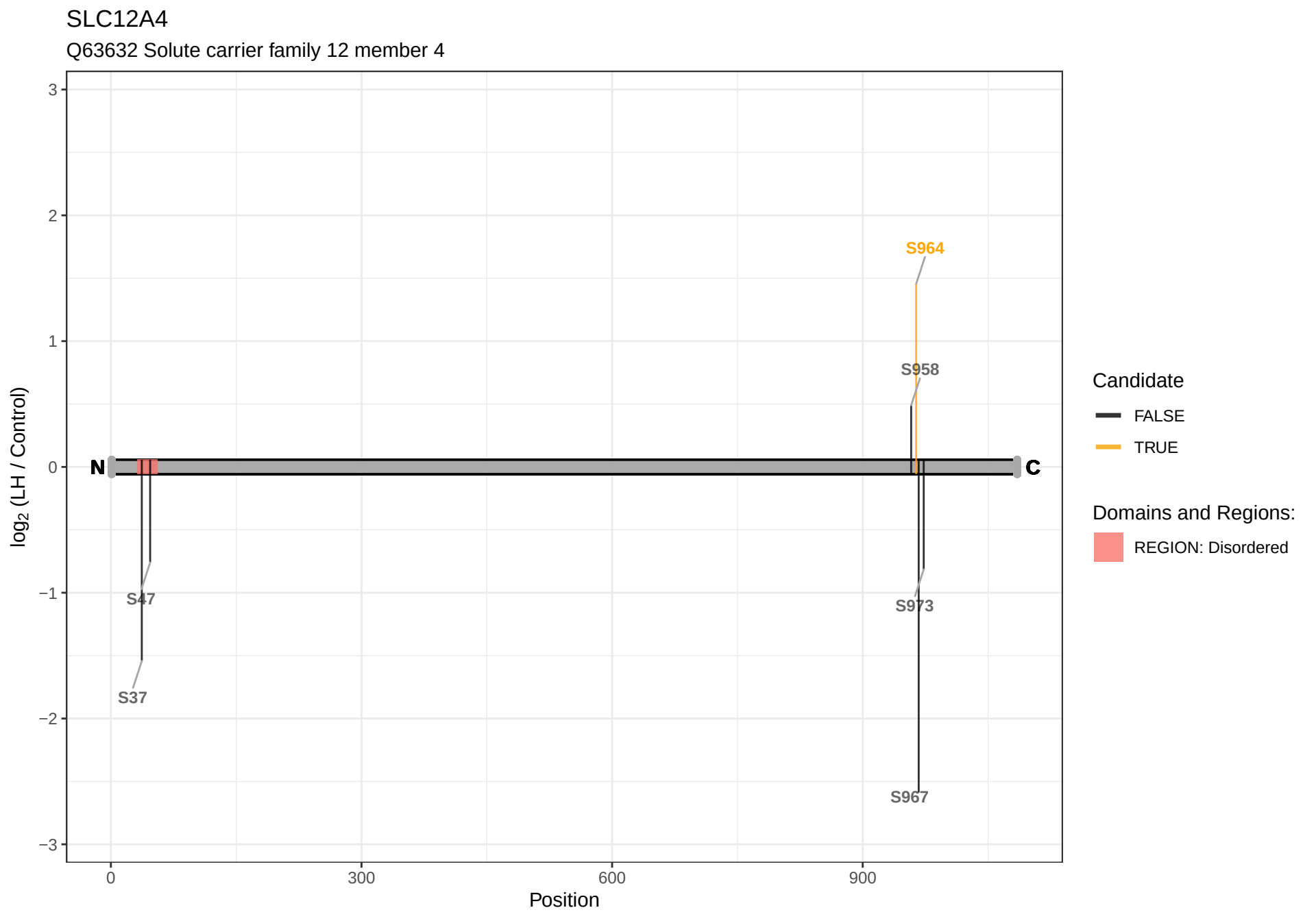

SIK3
M0RD40 SIK family kinase 3
T411
S493
S514
S534
T163
S856
S721
S533
N
C
2
1
0
−1
−2
0
500
1000
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
DOMAIN: UBA
REGION: Disordered

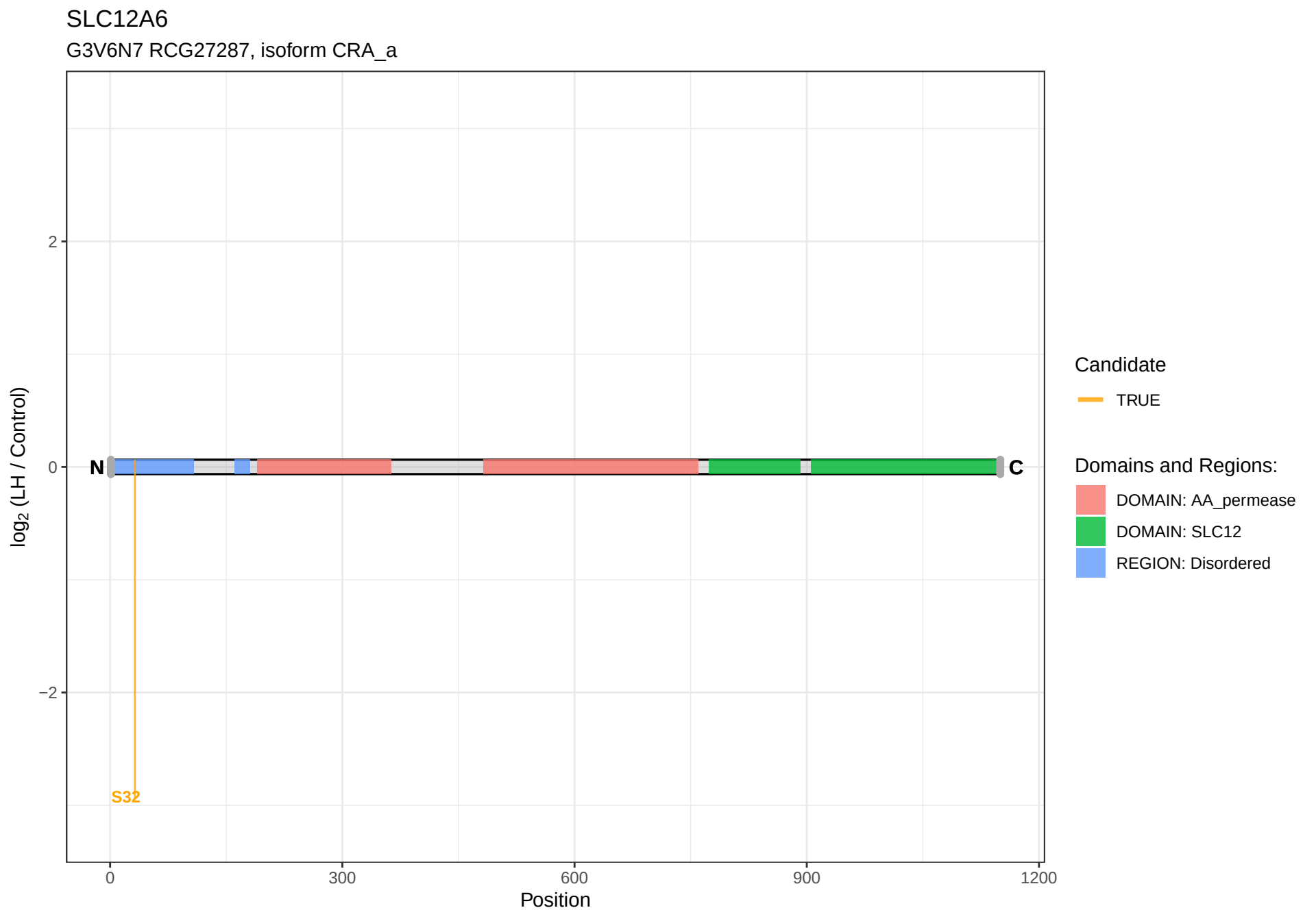

SIN3A
A0A0G2K3H5 SIN3 transcription regulator family member A
S431
T436
S277
S861
S941
S939
S833
S1113
N
C
2
0
−2
0
500
1000
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: HDAC_interact
REGION: Disordered

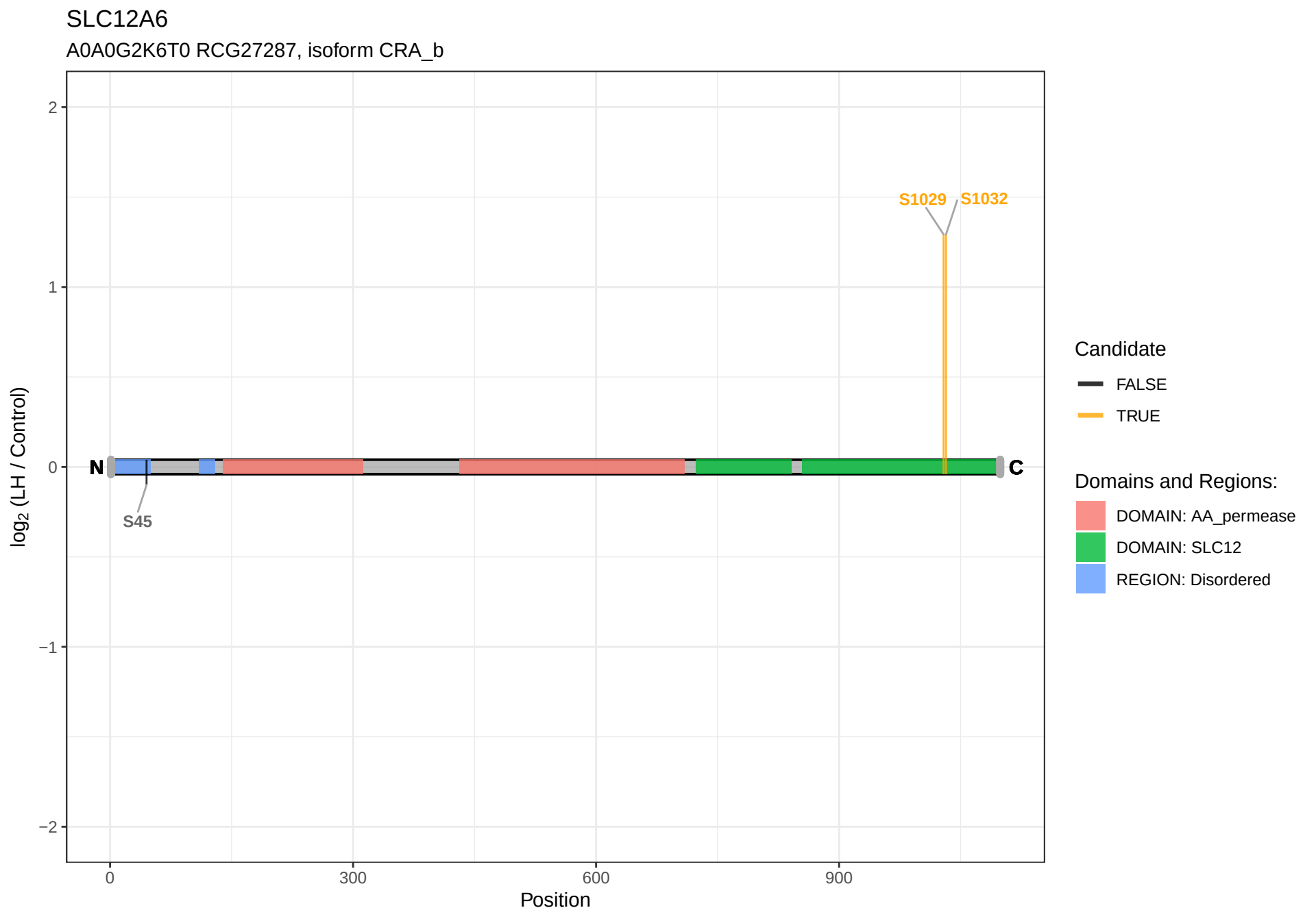

SIPA1
E9PSX8 Signal−induced proliferation−associated 1
log2 (LH / Control)
2
1
0
−1
−2
S72
S65
S815
N
C
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PDZ
DOMAIN: Rap−GAP
REGION: Disordered


SIPA1L1
A0A0G2KAW2 Signal−induced proliferation−associated 1 like 1, isoform CRA_b
log2 (LH / Control)
2
1
0
−1
−2
N
C
S288
S286
S208
T239
S311
S1181
S1249
S1384
S1564
S1528
S1487
S1624
S1626
S1629
S1687
S1690
S1708
S1712
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PDZ
DOMAIN: Rap−GAP
REGION: Disordered


SIPA1L3
F1LYG2 RCG54282
log2 (LH / Control)
2
1
0
−1
−2
N
C
S1541
T1694
S198
S94
S229
S1538
S1358
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PDZ
DOMAIN: Rap−GAP
REGION: Disordered

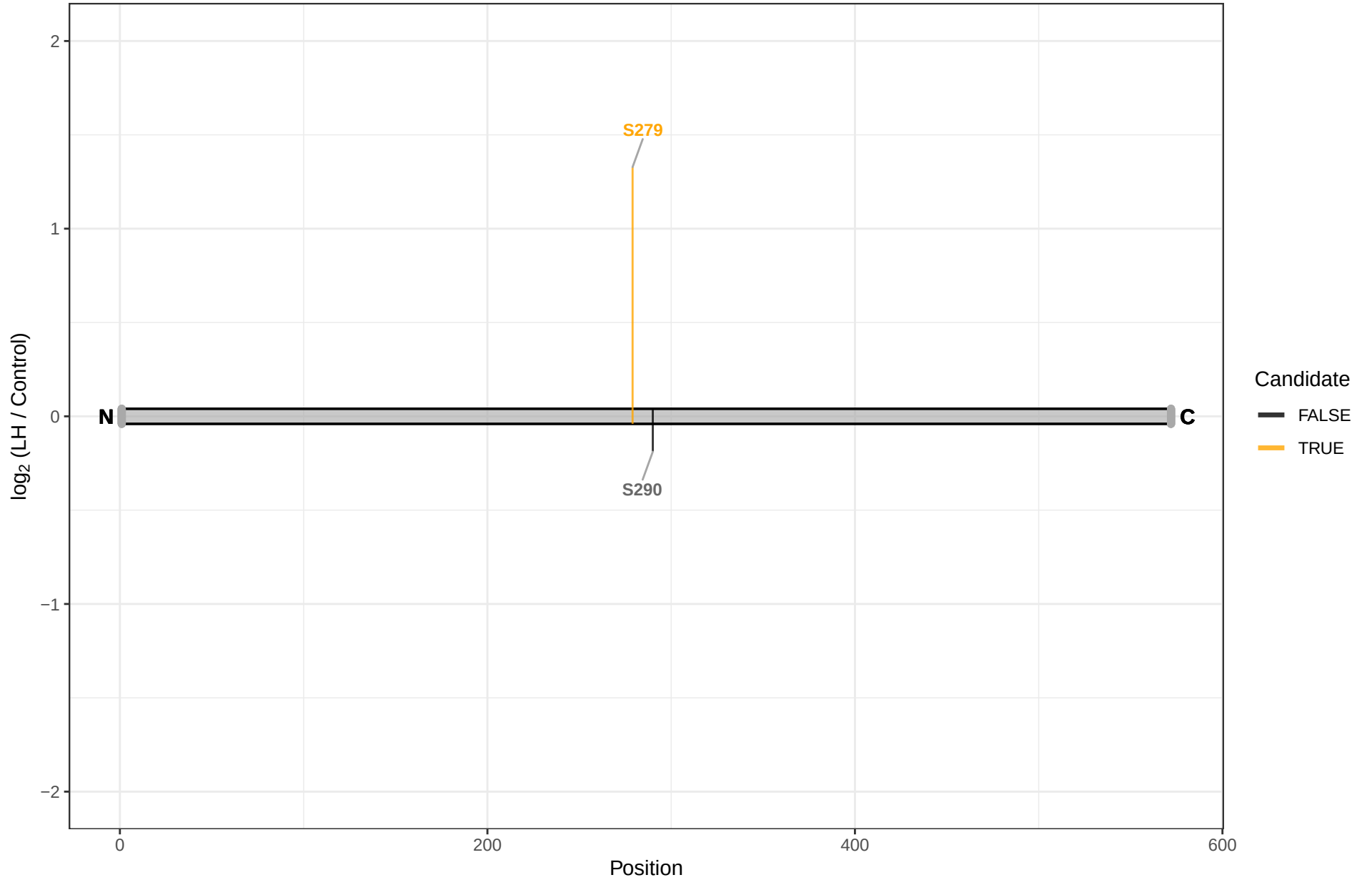

SLC12A4
Q63632 Solute carrier family 12 member 4
log2 (LH / Control)
3
2
1
0
−1
−2
−3
N
C
S964
S958
S47
S37
S973
S967
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

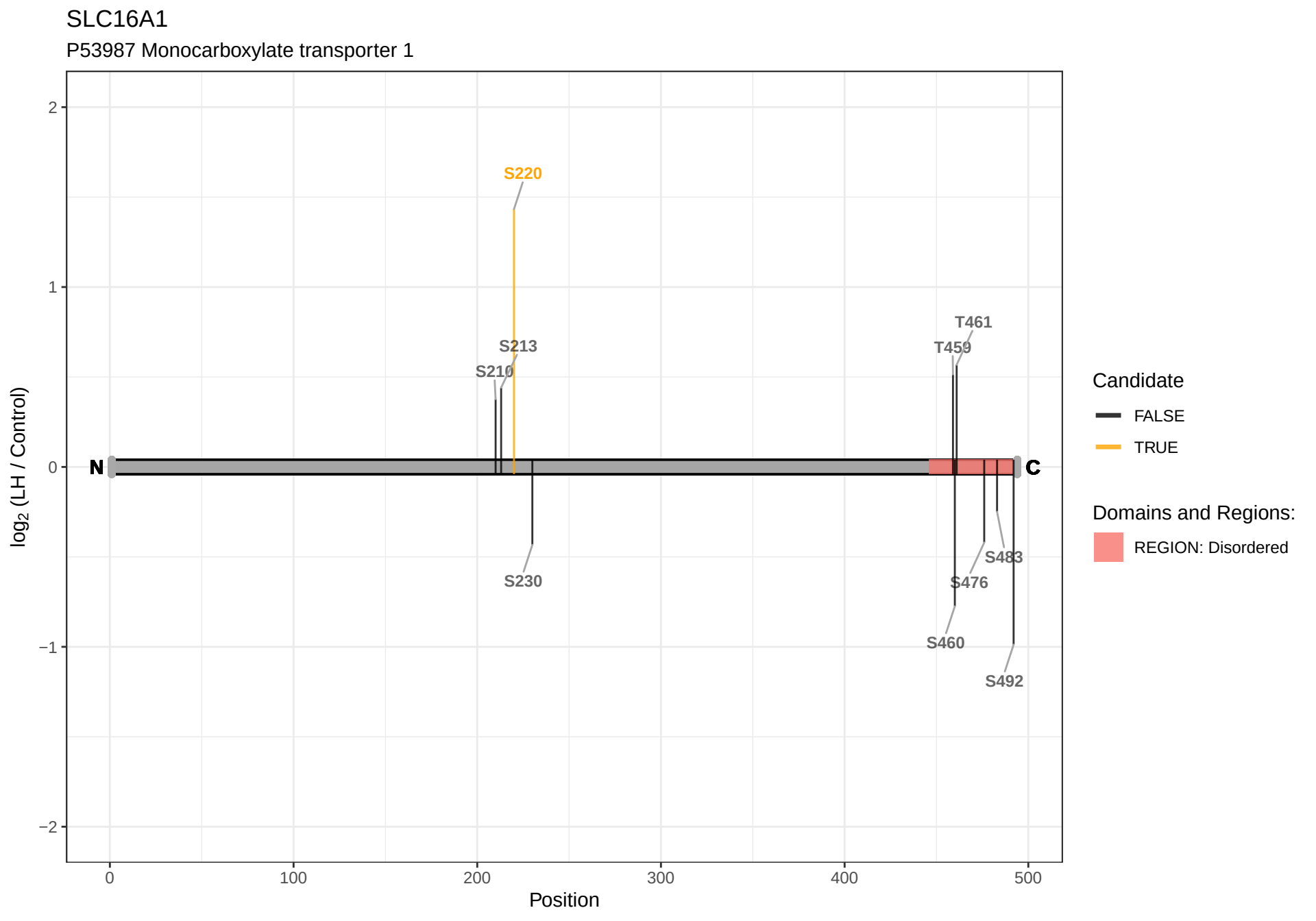

SLC12A6
G3V6N7 RCG27287, isoform CRA_a
log2 (LH / Control)
2
0
−2
N
C
S32
0
300
600
900
1200
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: AA_permease
DOMAIN: SLC12
REGION: Disordered

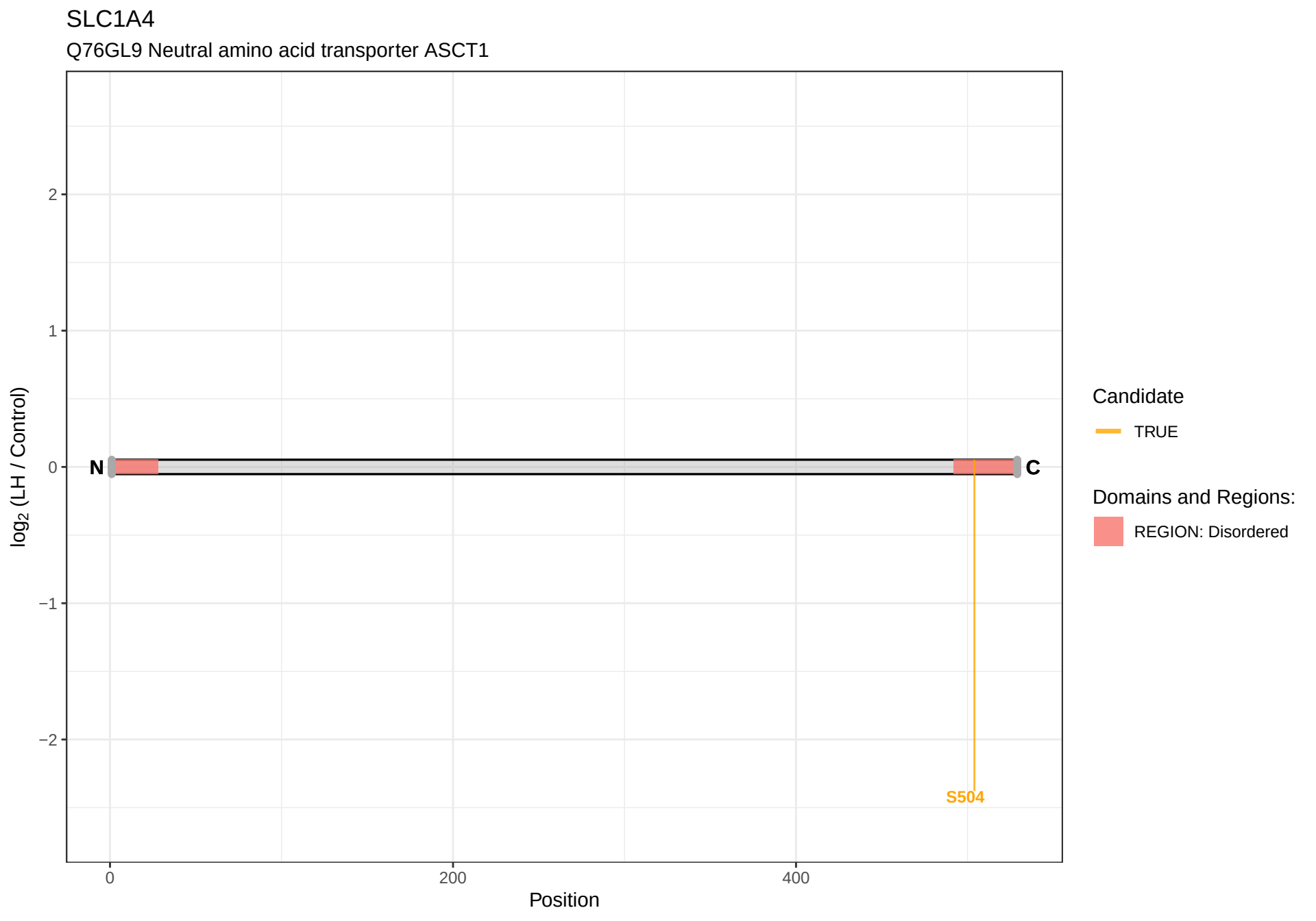

SLC12A6
A0A0G2K6T0 RCG27287, isoform CRA_b
2
1
0
−1
−2
log2 (LH / Control)
S1029
S1032
N
C
S45
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: AA_permease
DOMAIN: SLC12
REGION: Disordered

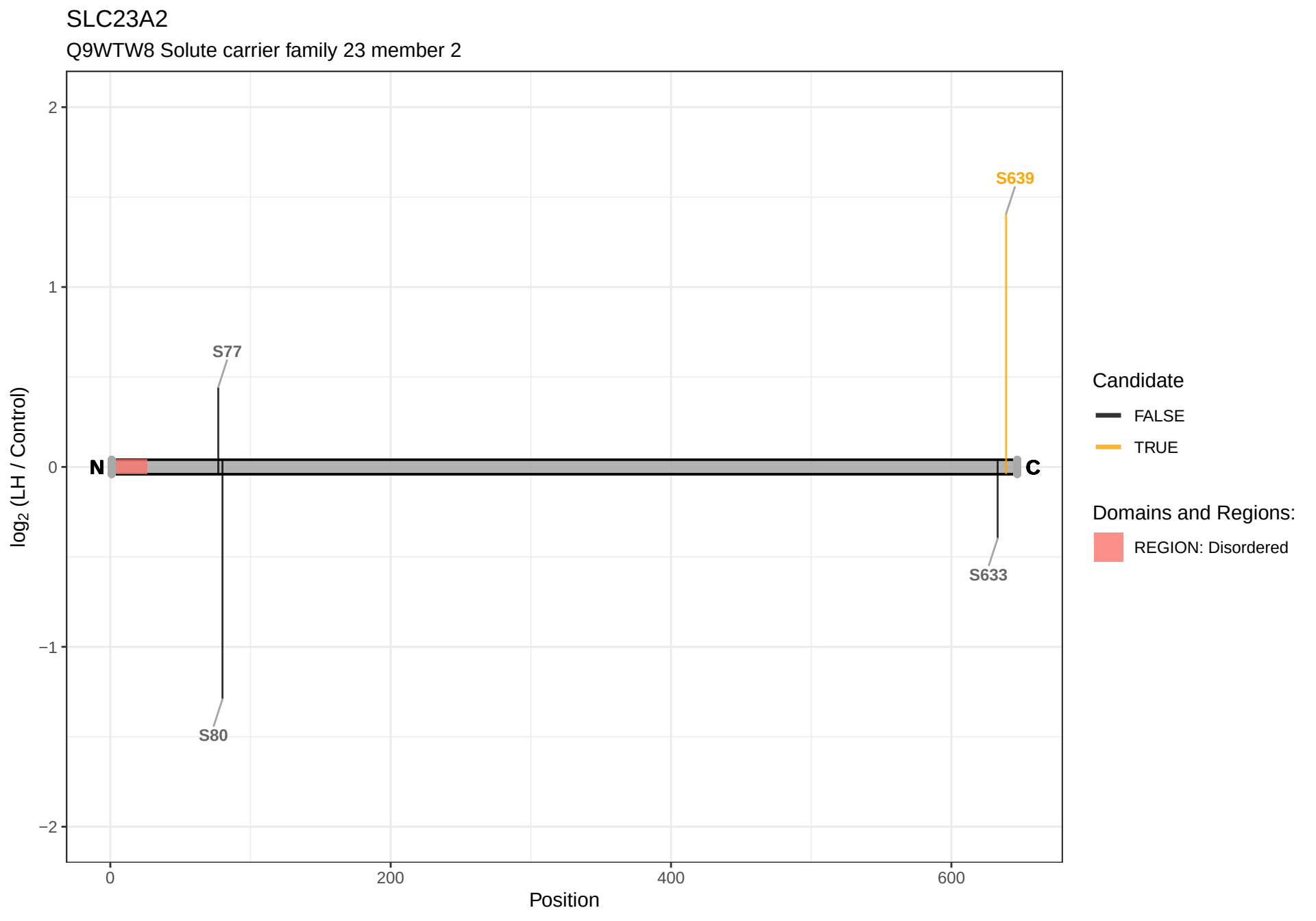
SLC15A4

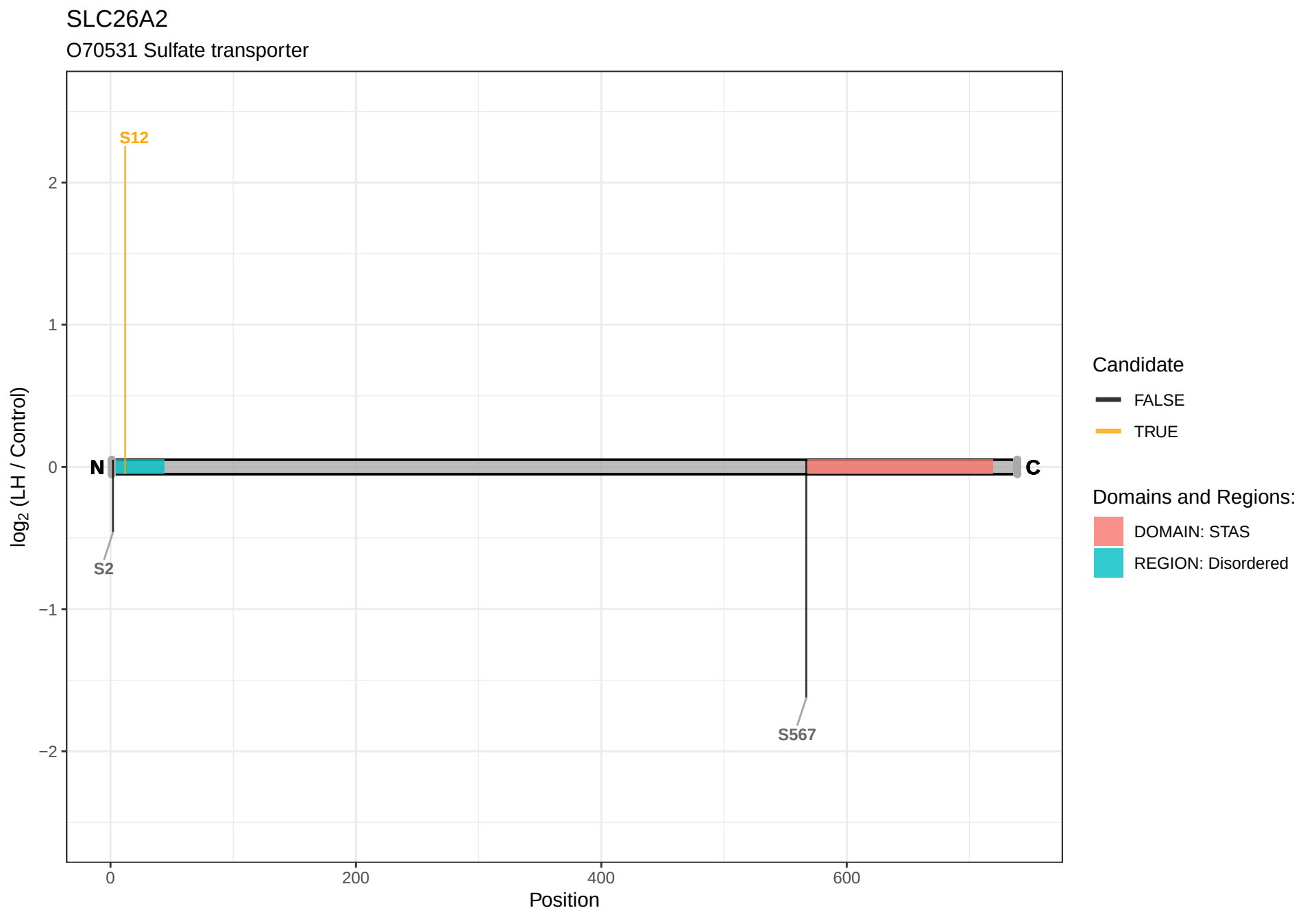
A0A0G2JSH0 Solute carrier family 15 member 4

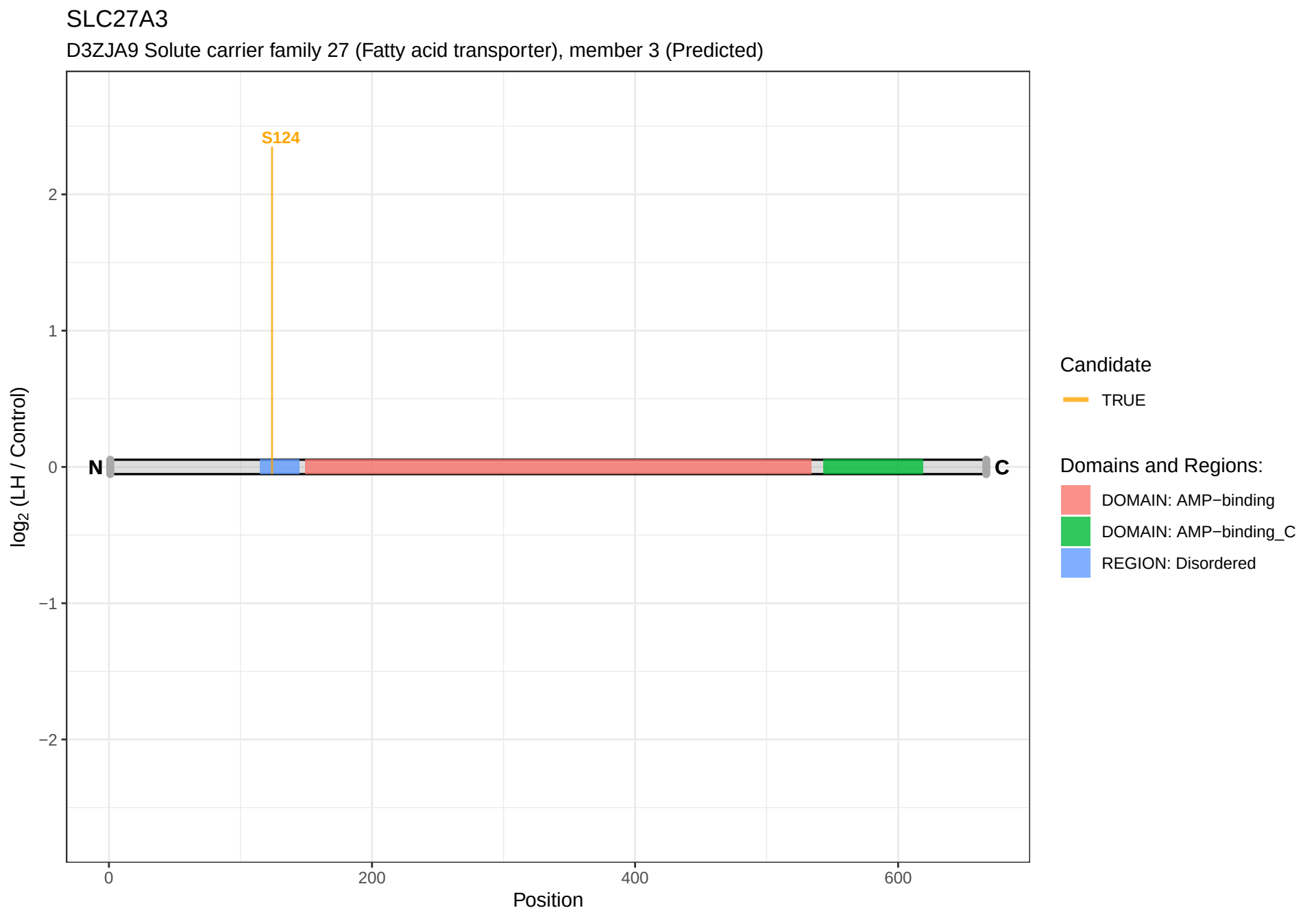


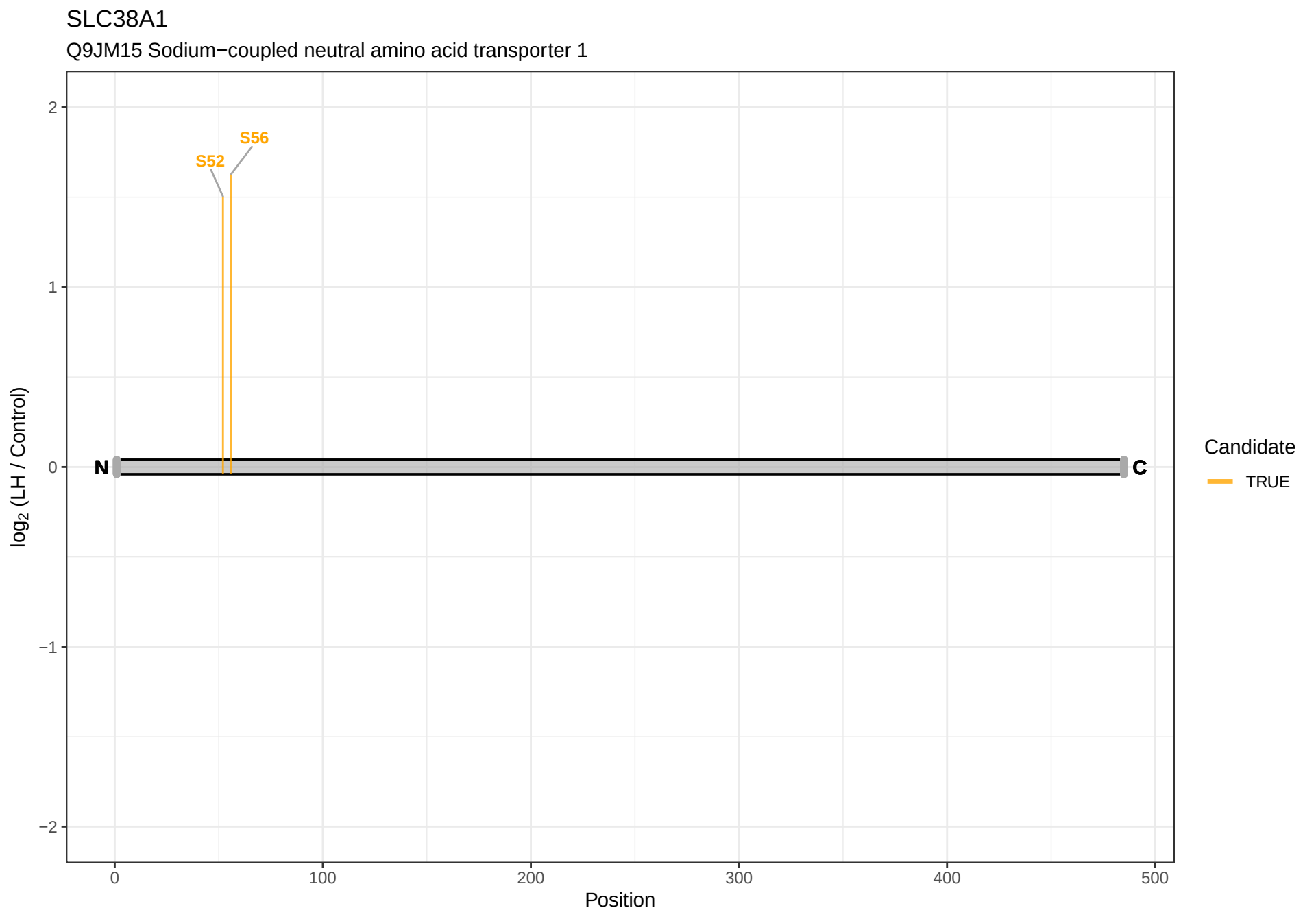

SLC16A1
P53987 Monocarboxylate transporter 1
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
400
500
Position
N
C
S220
S213
S210
S230
T461
T459
S483
S476
S460
S492
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

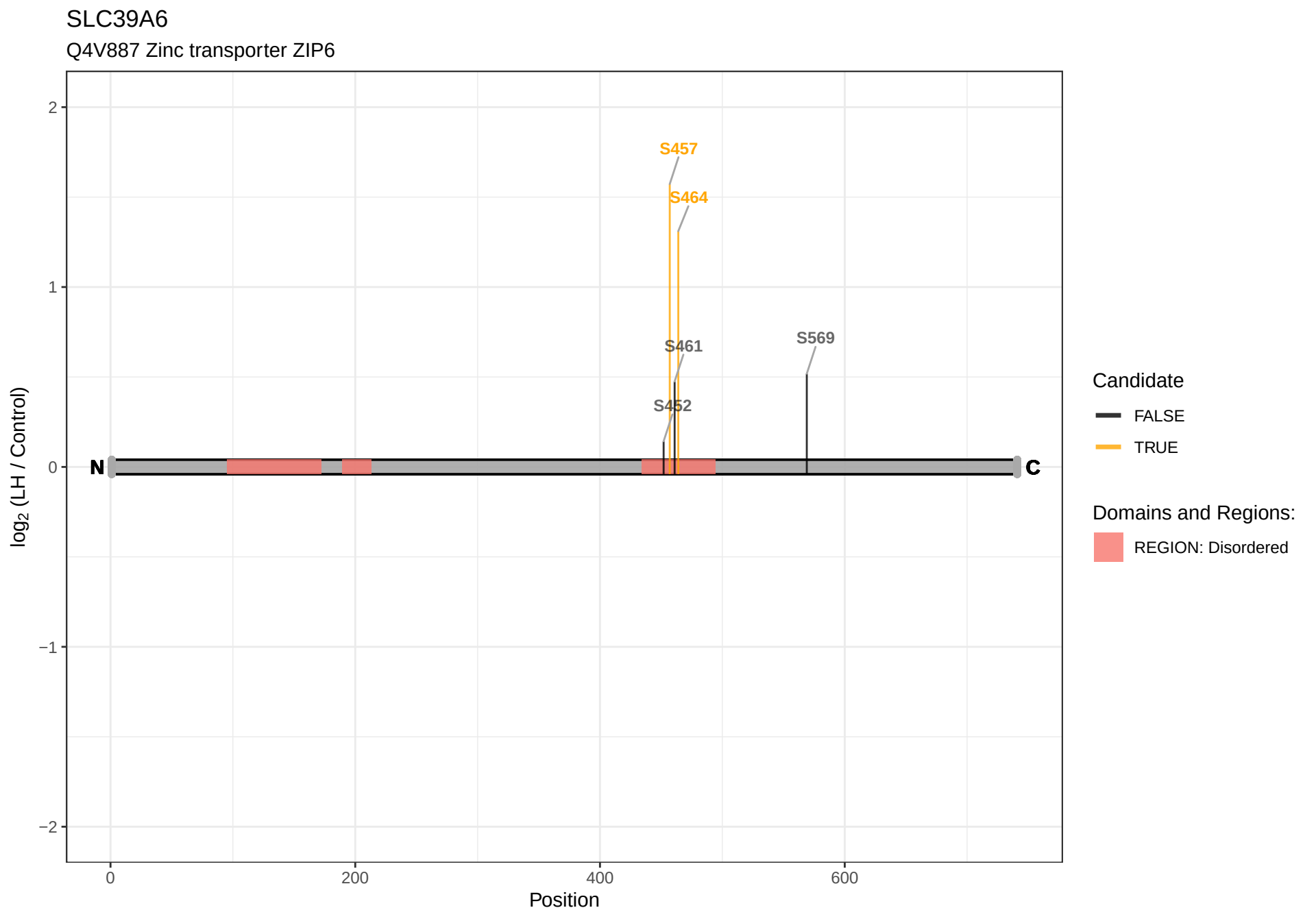

SLC1A4
Q76GL9 Neutral amino acid transporter ASCT1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S504
0
200
400
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

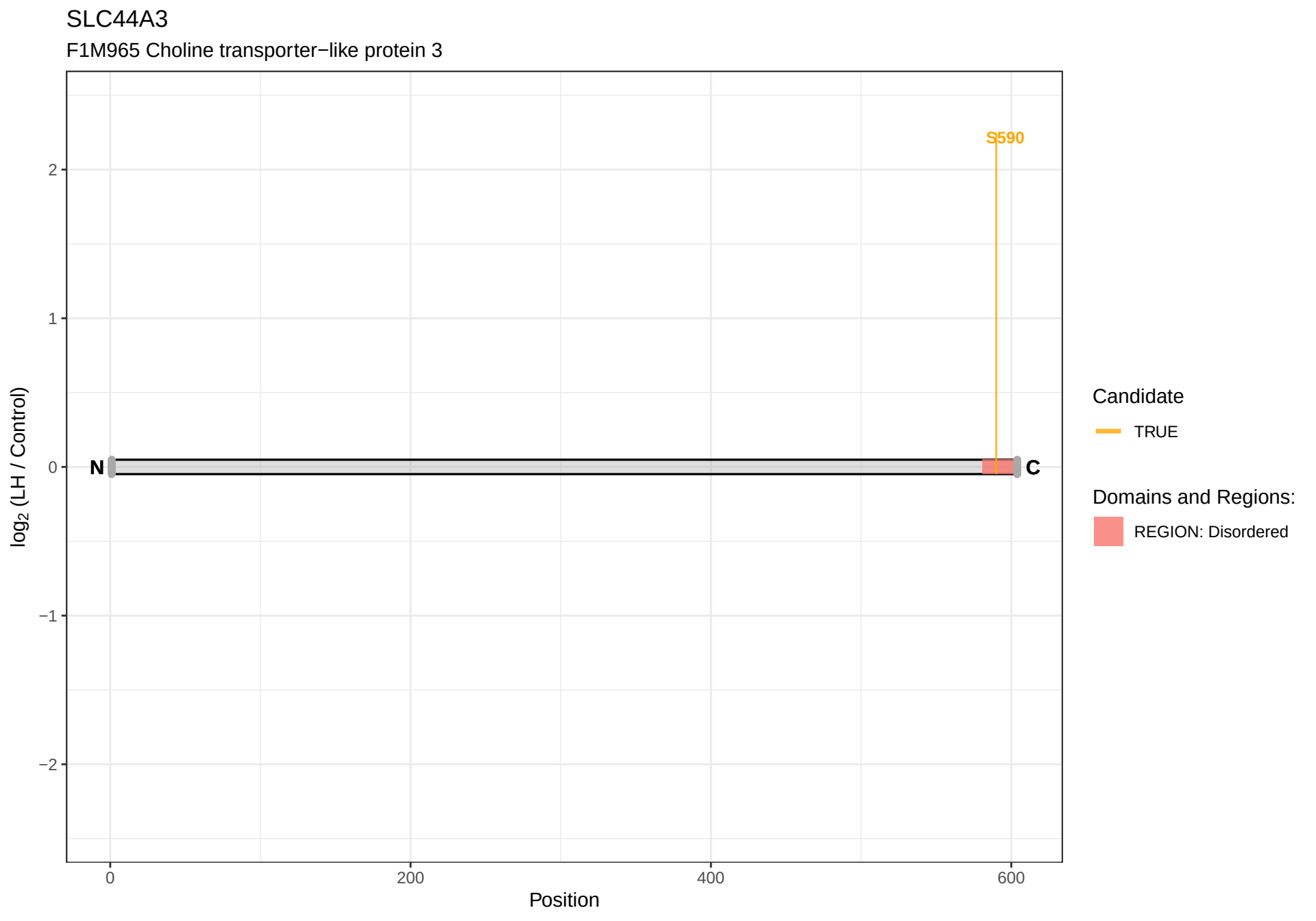

SLC23A2
Q9WTW8 Solute carrier family 23 member 2
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
N
C
S639
S77
S633
S80
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

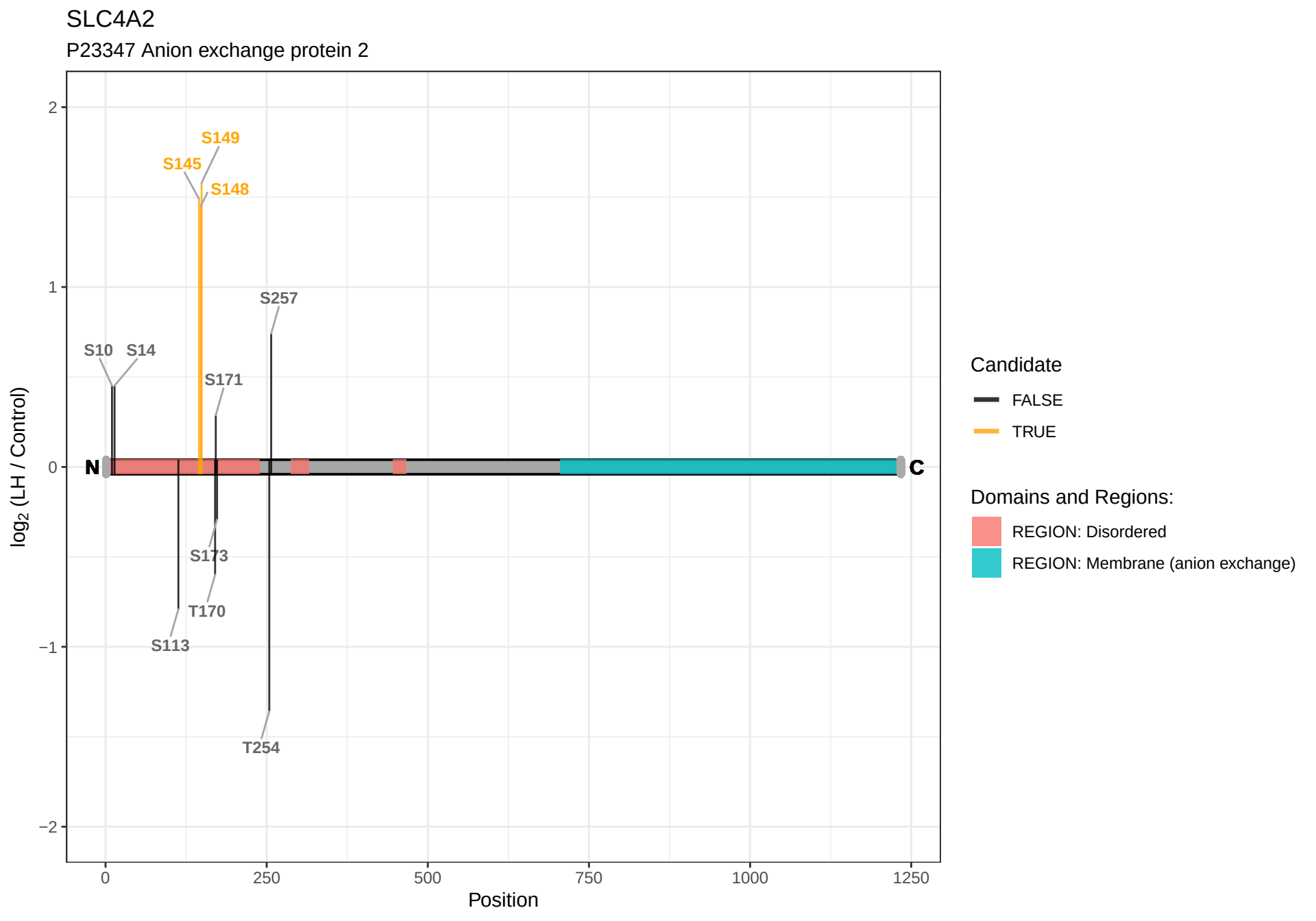

SLC26A2
O70531 Sulfate transporter
S12
S2
S567
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: STAS
REGION: Disordered

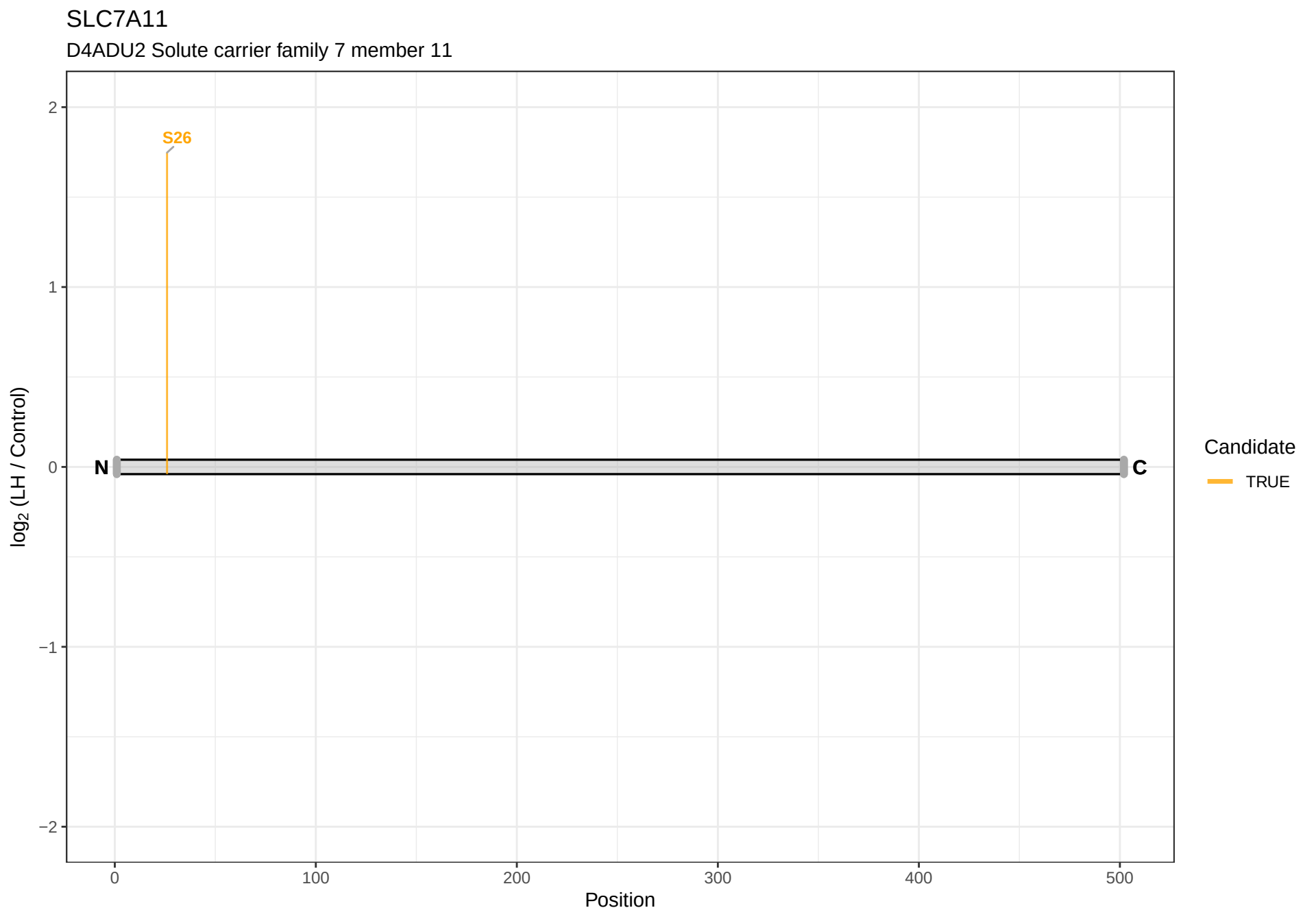

SLC27A3
D3ZJA9 Solute carrier family 27 (Fatty acid transporter), member 3 (Predicted)
S124
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: AMP−binding
DOMAIN: AMP−binding_C
REGION: Disordered

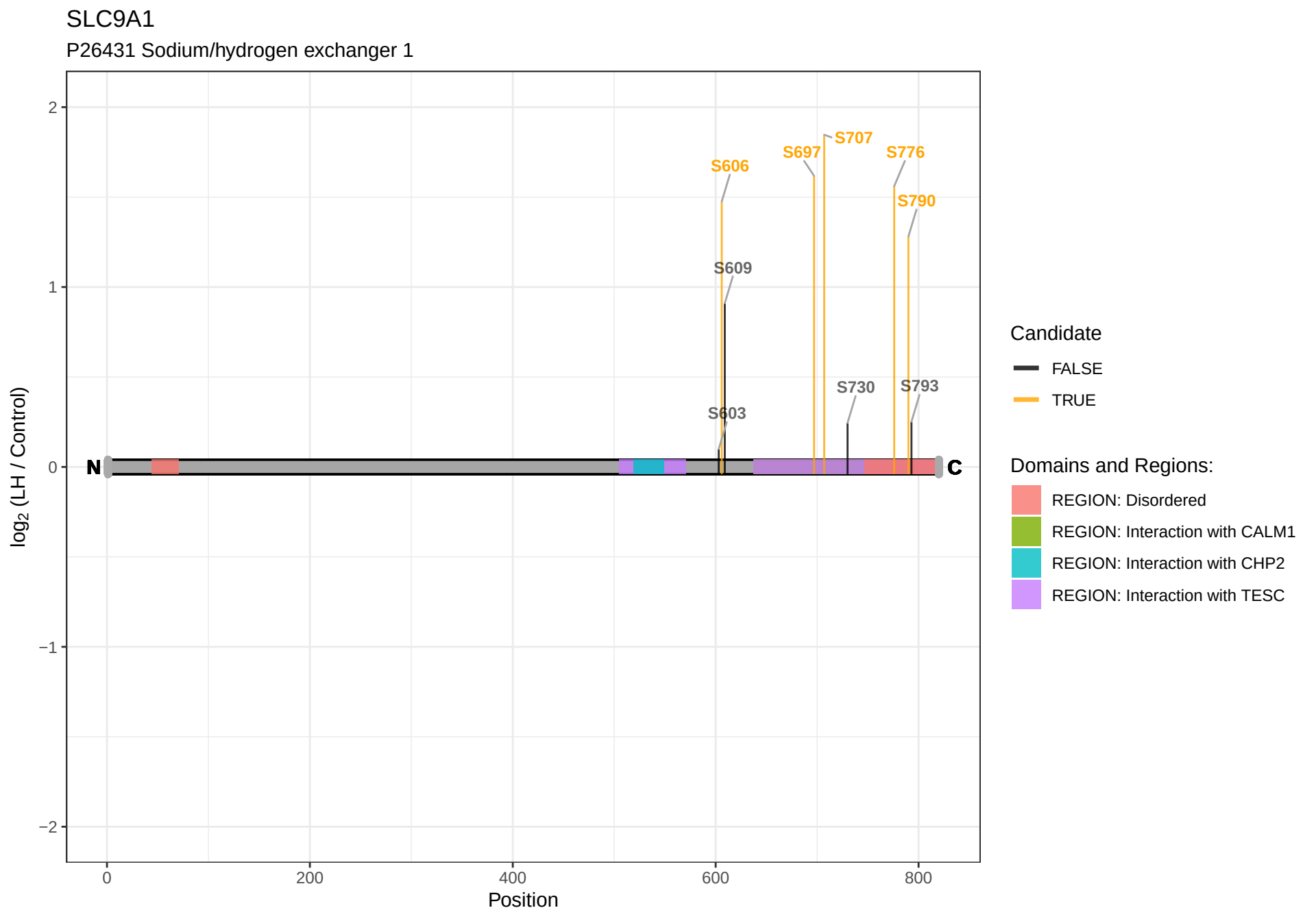

SLC38A1
Q9JM15 Sodium−coupled neutral amino acid transporter 1
S56
S52
N
C
log2 (LH / Control)
Position
Candidate
TRUE
2
1
0
−1
−2
0
100
200
300
400
500

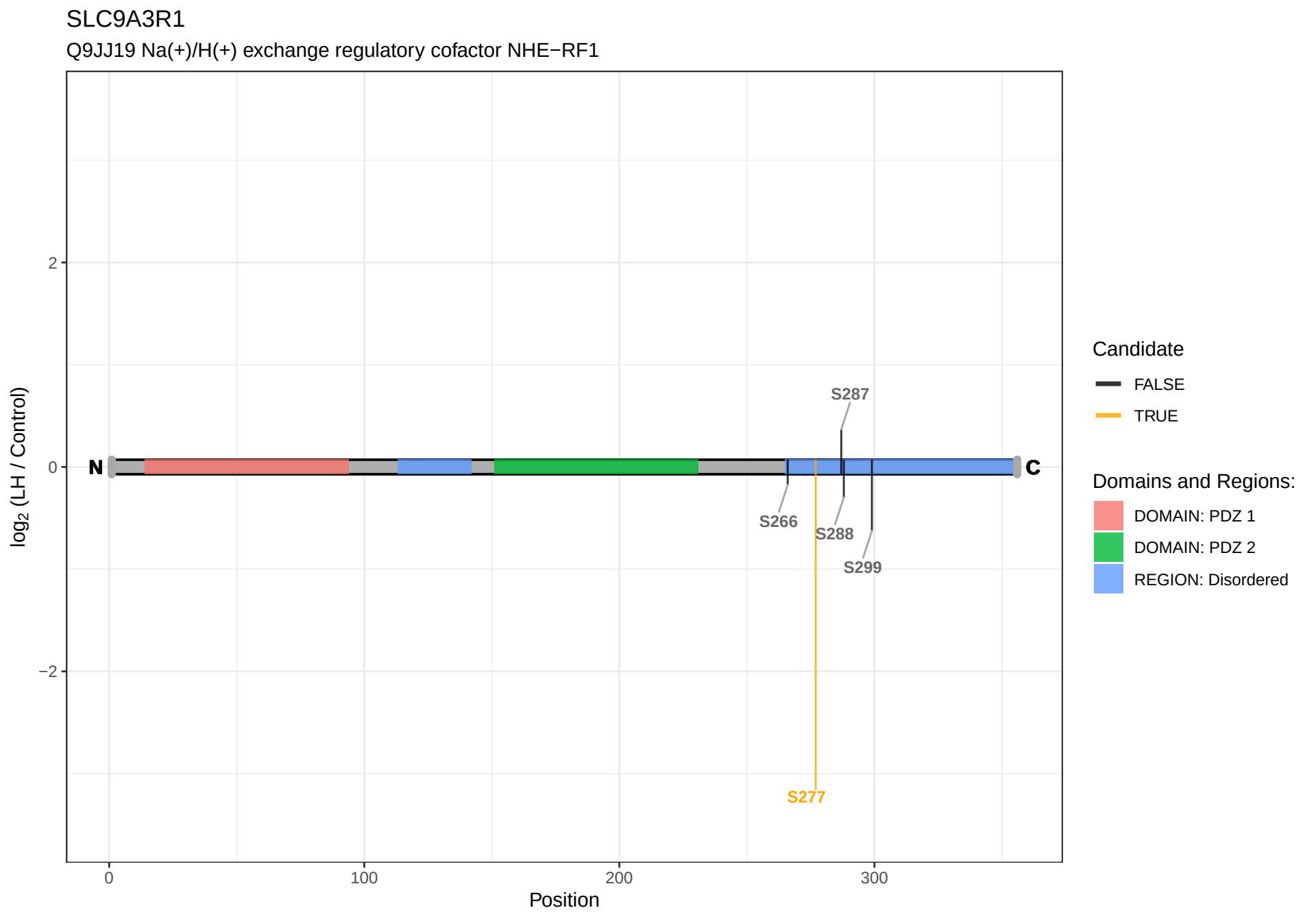

SLC39A6
Q4V887 Zinc transporter ZIP6
S457
S464
S461
S452
S569
N
C
log2 (LH / Control)
Position
0
200
400
600
2
1
0
−1
−2
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

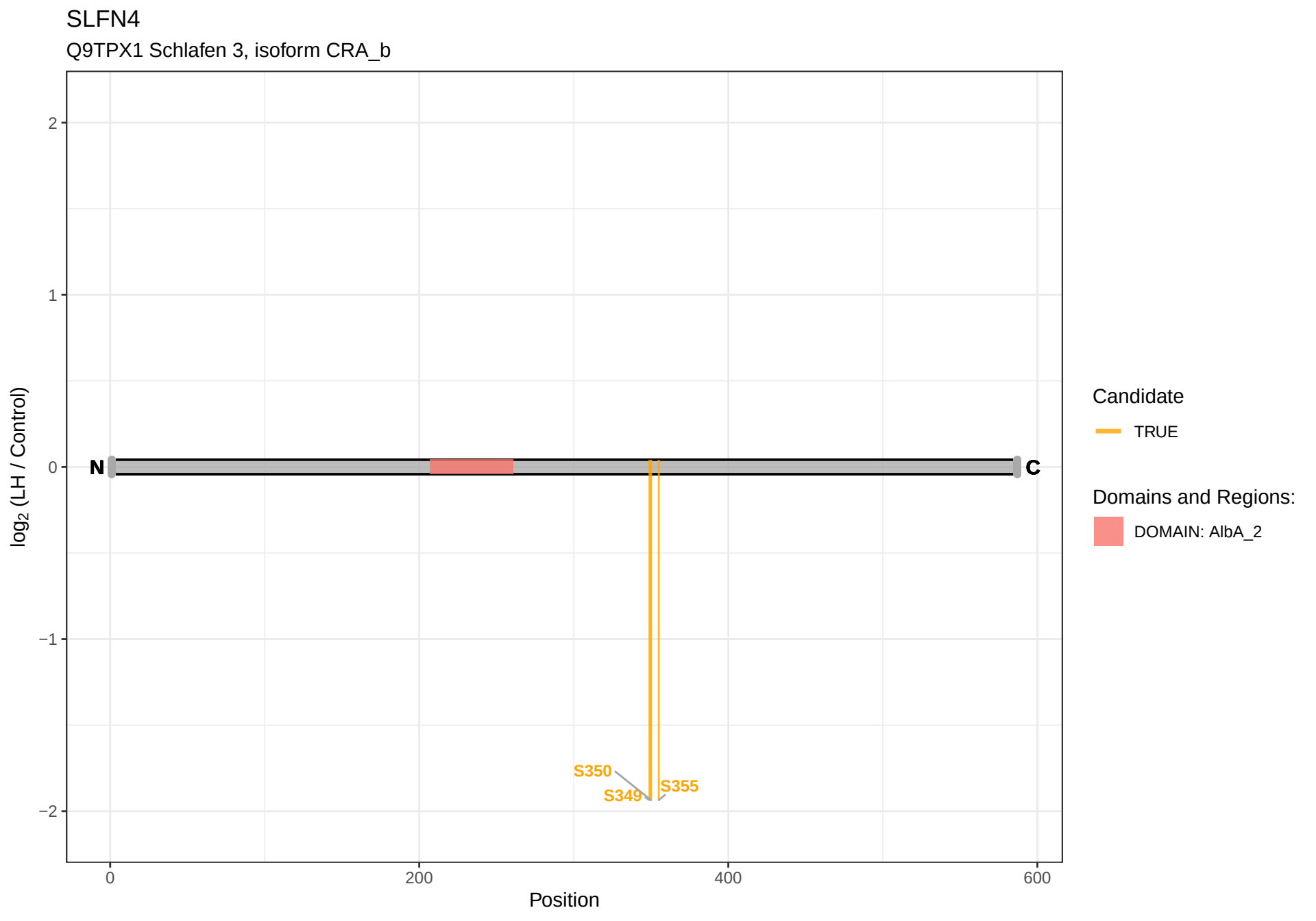

SLC44A3
F1M965 Choline transporter−like protein 3
S590
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

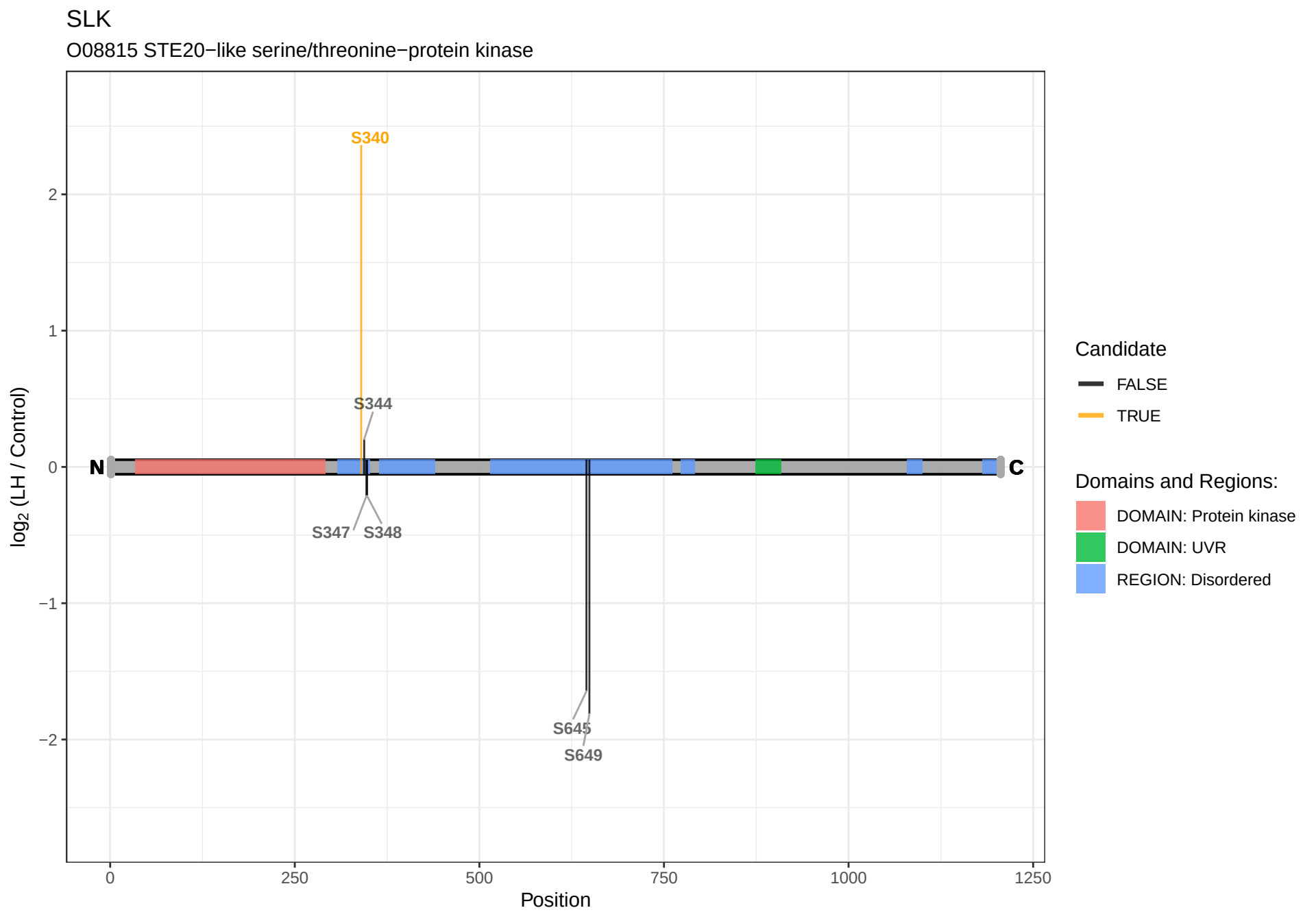

SLC4A2
P23347 Anion exchange protein 2
log2 (LH / Control)
Position
S149
S145
S148
S257
S10
S14
S171
S173
T170
S113
T254
N
C
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Membrane (anion exchange)

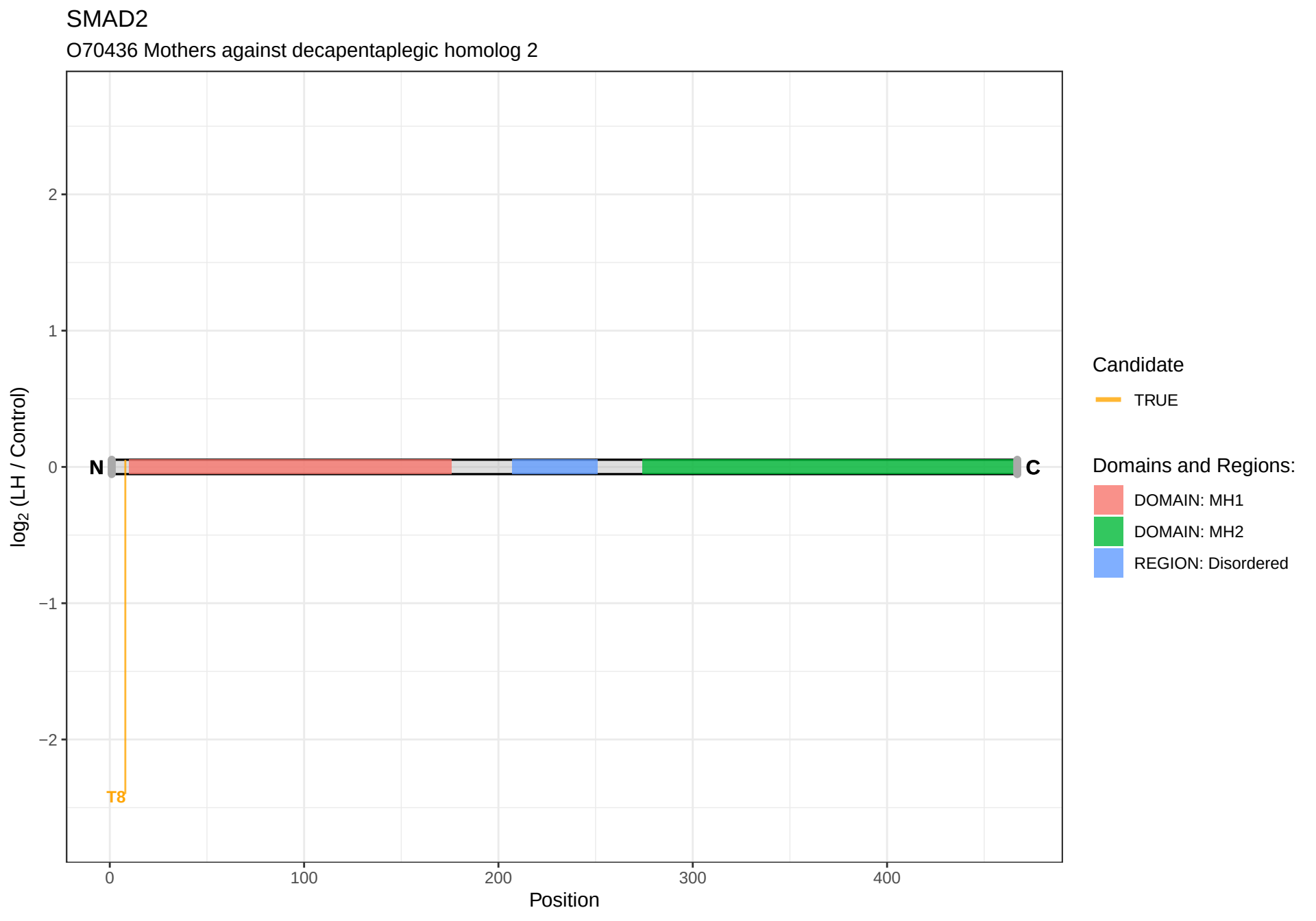

SLC7A11
D4ADU2 Solute carrier family 7 member 11
S26
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
400
500
Position
Candidate
TRUE

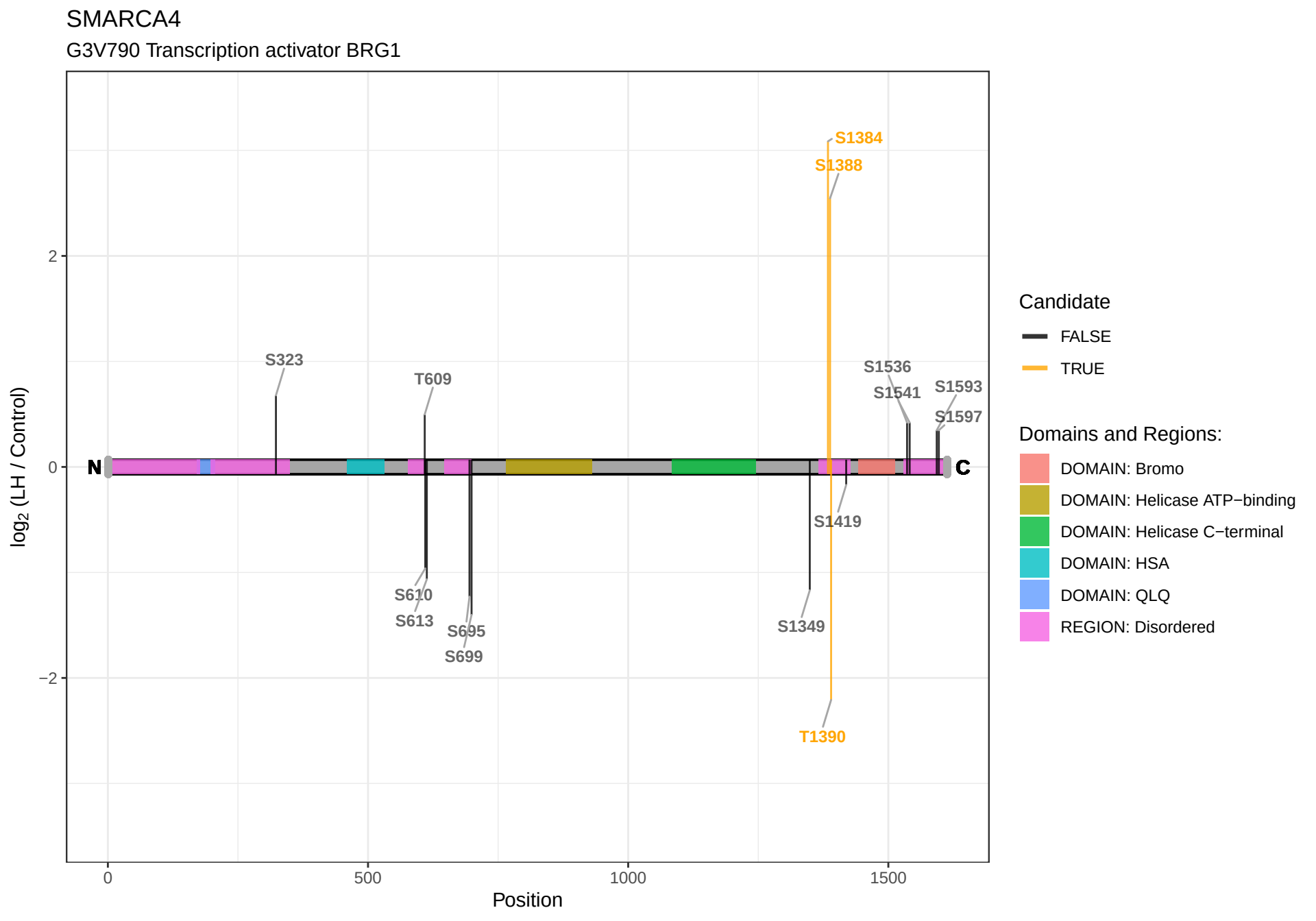

SLC9A1
P26431 Sodium/hydrogen exchanger 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S606
S697
S707
S776
S790
S609
S730
S793
S603
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Interaction with CALM1
REGION: Interaction with CHP2
REGION: Interaction with TESC

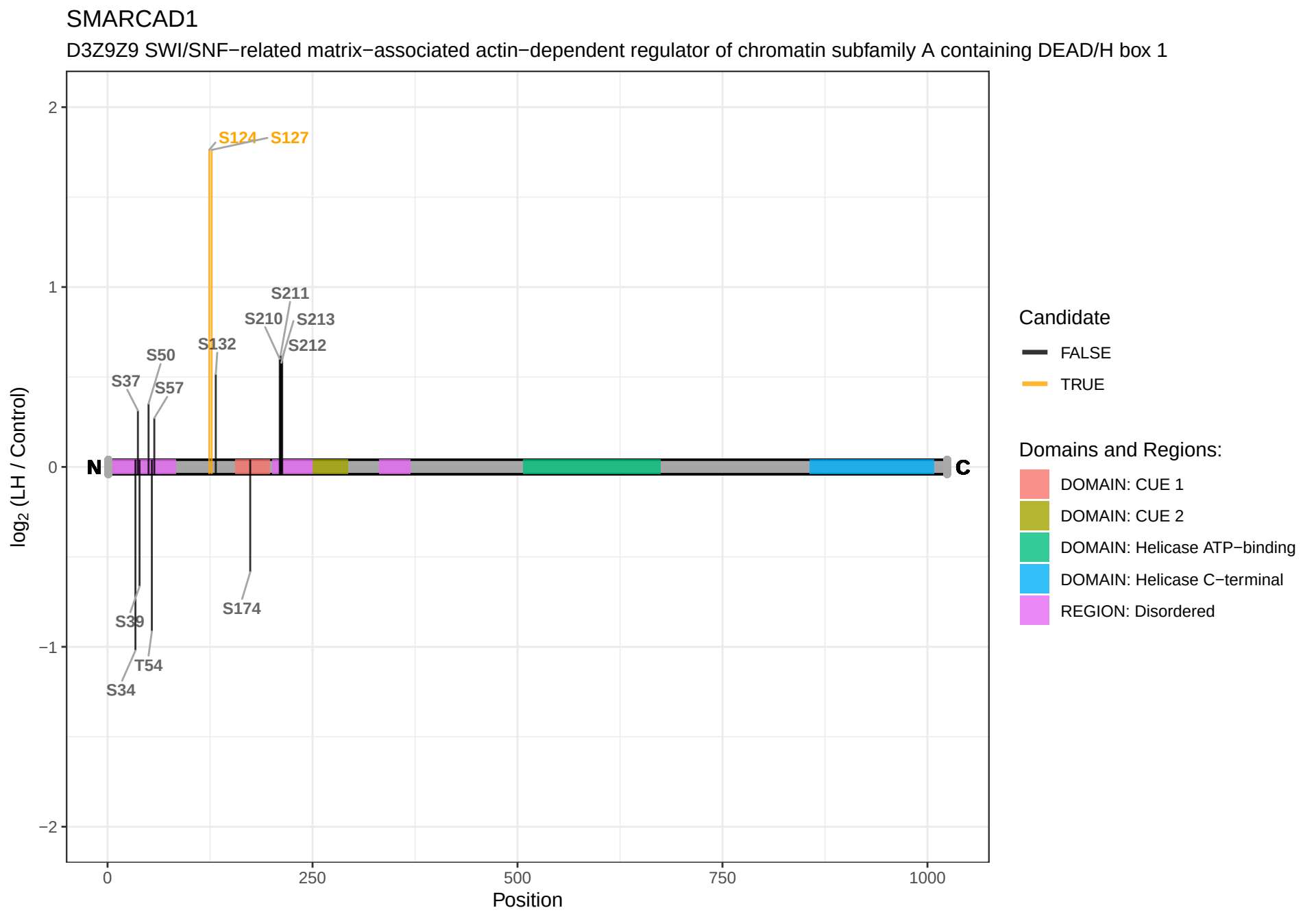

SLC9A3R1
Q9JJ19 Na(+)/H(+) exchange regulatory cofactor NHE−RF1
log2 (LH / Control)
2
0
−2
N
C
S287
S266
S288
S299
S277
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PDZ 1
DOMAIN: PDZ 2
REGION: Disordered

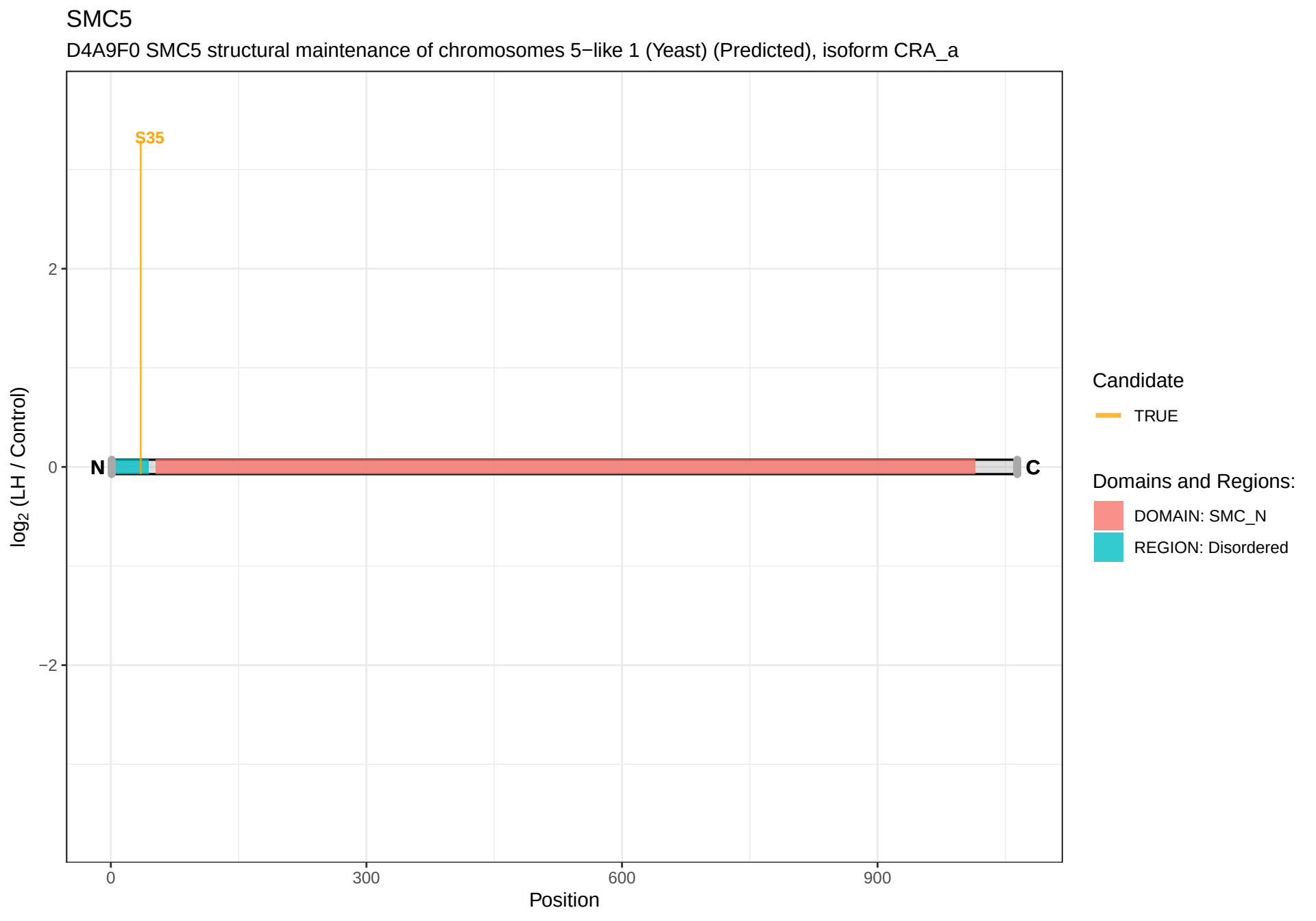

SLFN4
Q9TPX1 Schlafen 3, isoform CRA_b
log2 (LH / Control)
2
1
0
−1
−2
N
C
S350
S349
S355
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: AlbA_2

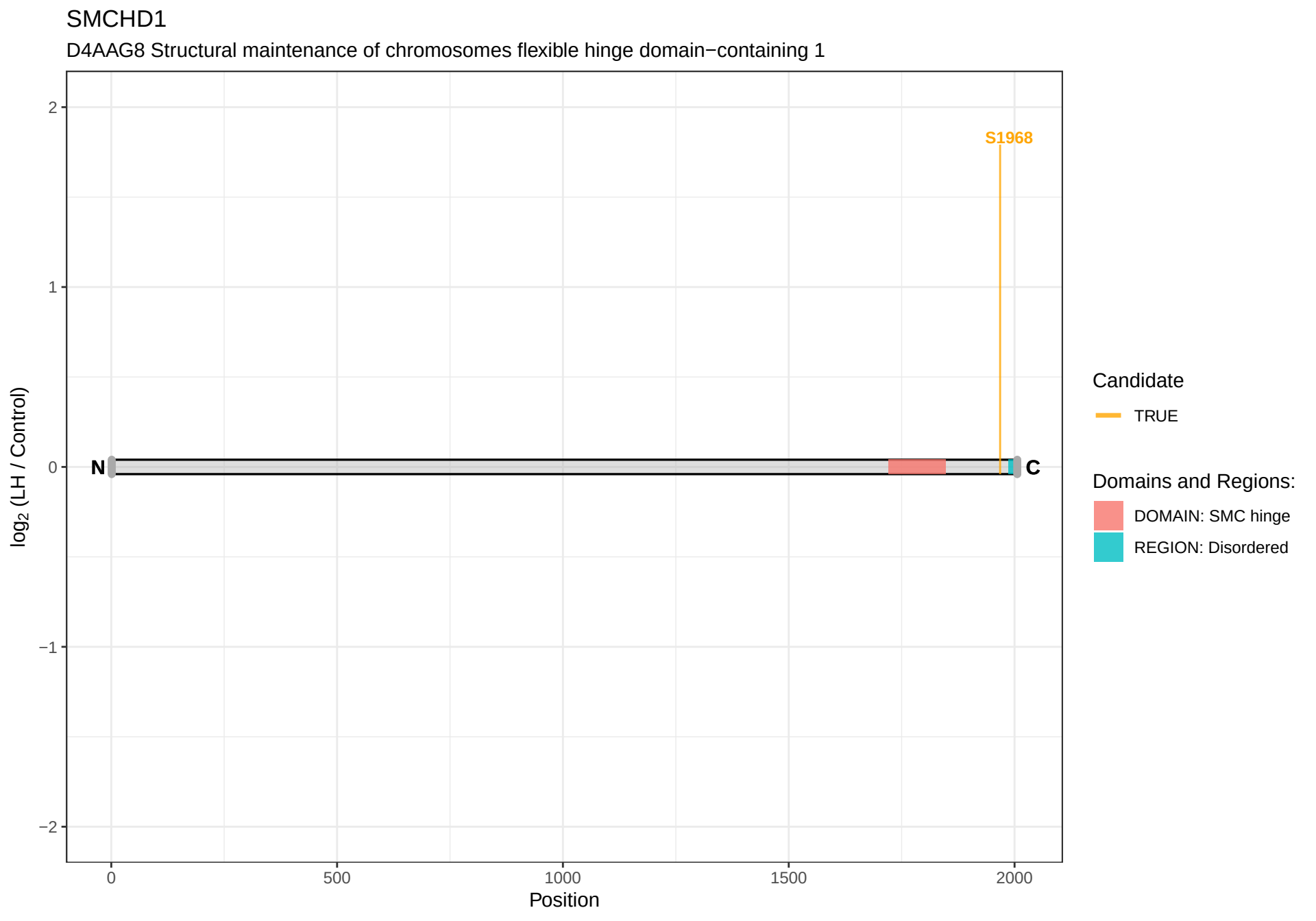

SLK
O08815 STE20−like serine/threonine−protein kinase
S340
S344
S347
S348
S645
S649
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
250
500
750
1000
1250
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
DOMAIN: UVR
REGION: Disordered

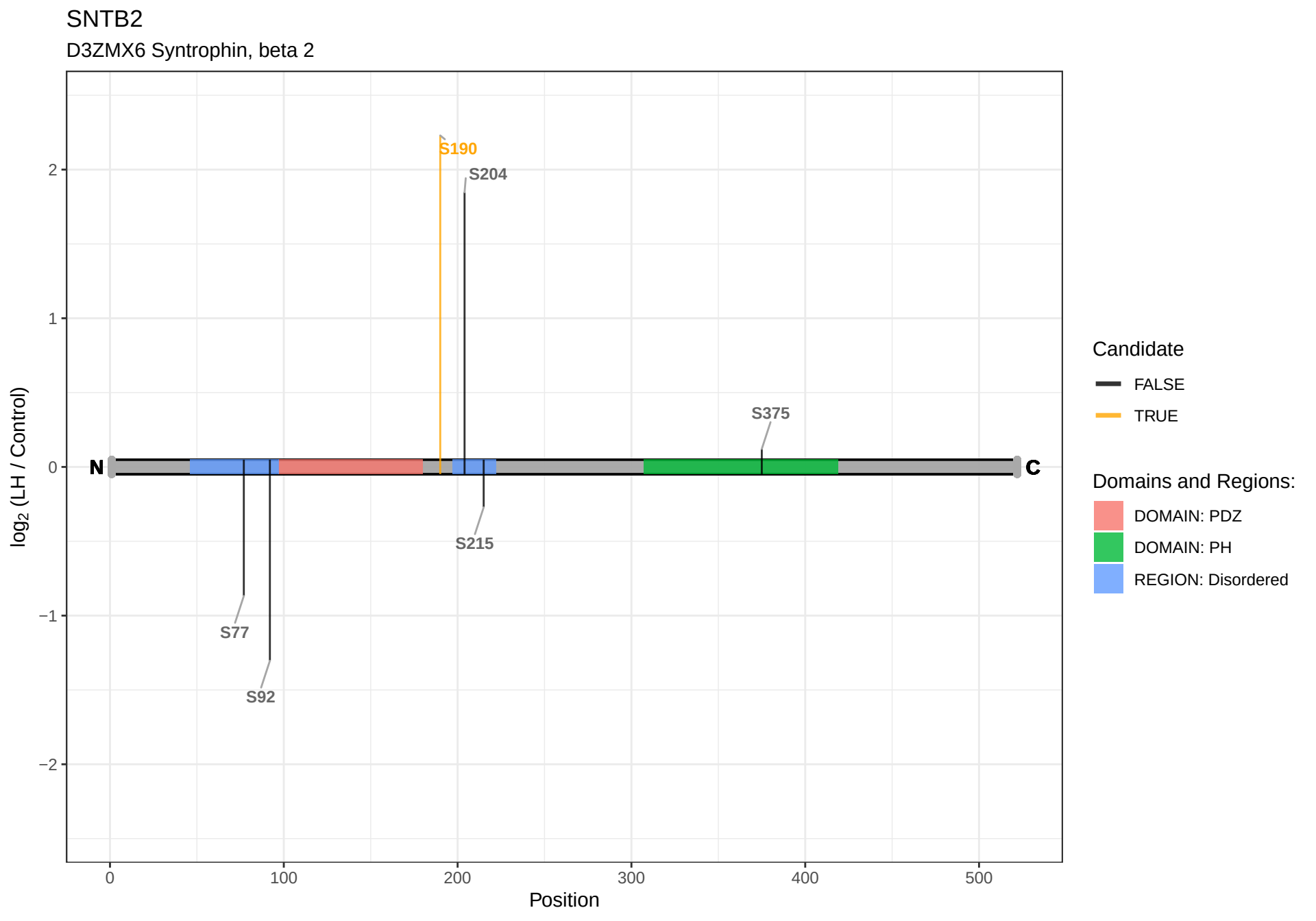

SMAD2
O70436 Mothers against decapentaplegic homolog 2
log2 (LH / Control)
2
1
0
−1
−2
N
C
T8
0
100
200
300
400
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: MH1
DOMAIN: MH2
REGION: Disordered

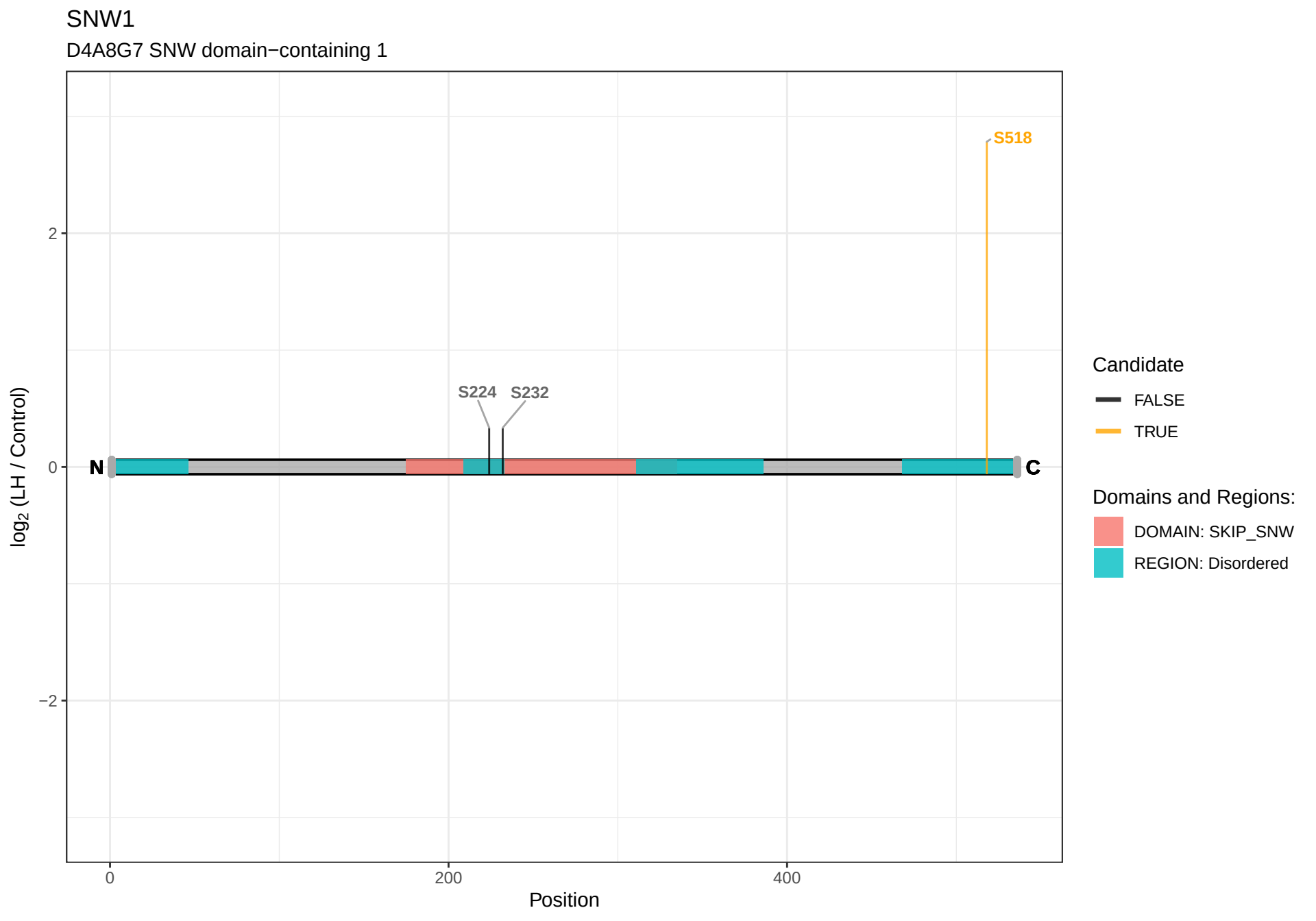

SMARCA4
G3V790 Transcription activator BRG1
log2 (LH / Control)
2
0
−2
0
500
1000
1500
Position
N
C
S323
T609
S610
S613
S695
S699
S1349
S1384
S1388
S1390
S1419
S1536
S1541
S1593
S1597
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Bromo
DOMAIN: Helicase ATP−binding
DOMAIN: Helicase C−terminal
DOMAIN: HSA
DOMAIN: QLQ
REGION: Disordered

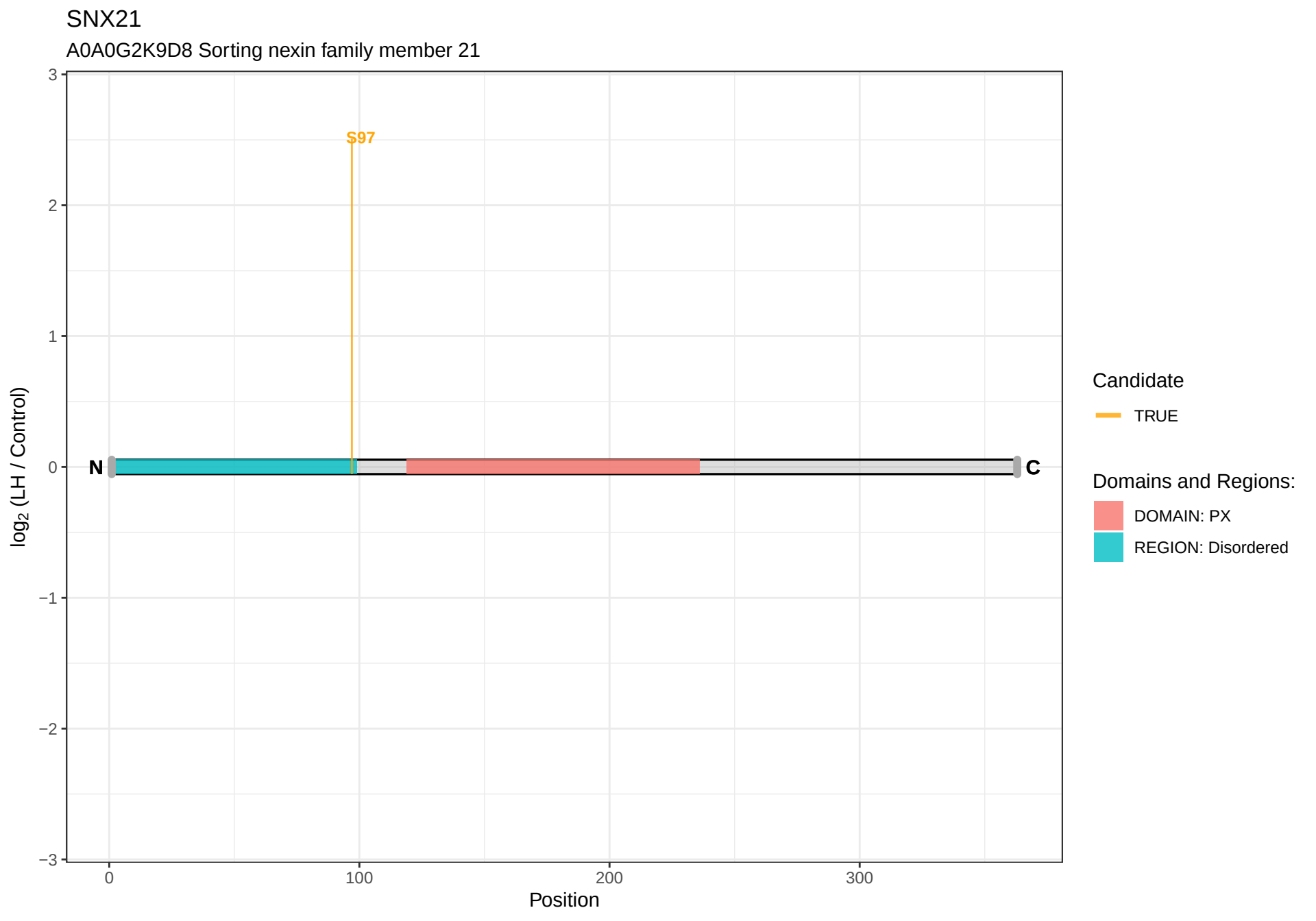

SMARCAD1
D3Z9Z9 SWI/SNF−related matrix−associated actin−dependent regulator of chromatin subfamily A containing DEAD/H box 1
log2 (LH / Control)
2
1
0
−1
−2
S124
S127
S211
S210
S213
S212
S132
S50
S37
S57
N
C
S39
S174
T54
S34
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CUE 1
DOMAIN: CUE 2
DOMAIN: Helicase ATP−binding
DOMAIN: Helicase C−terminal
REGION: Disordered

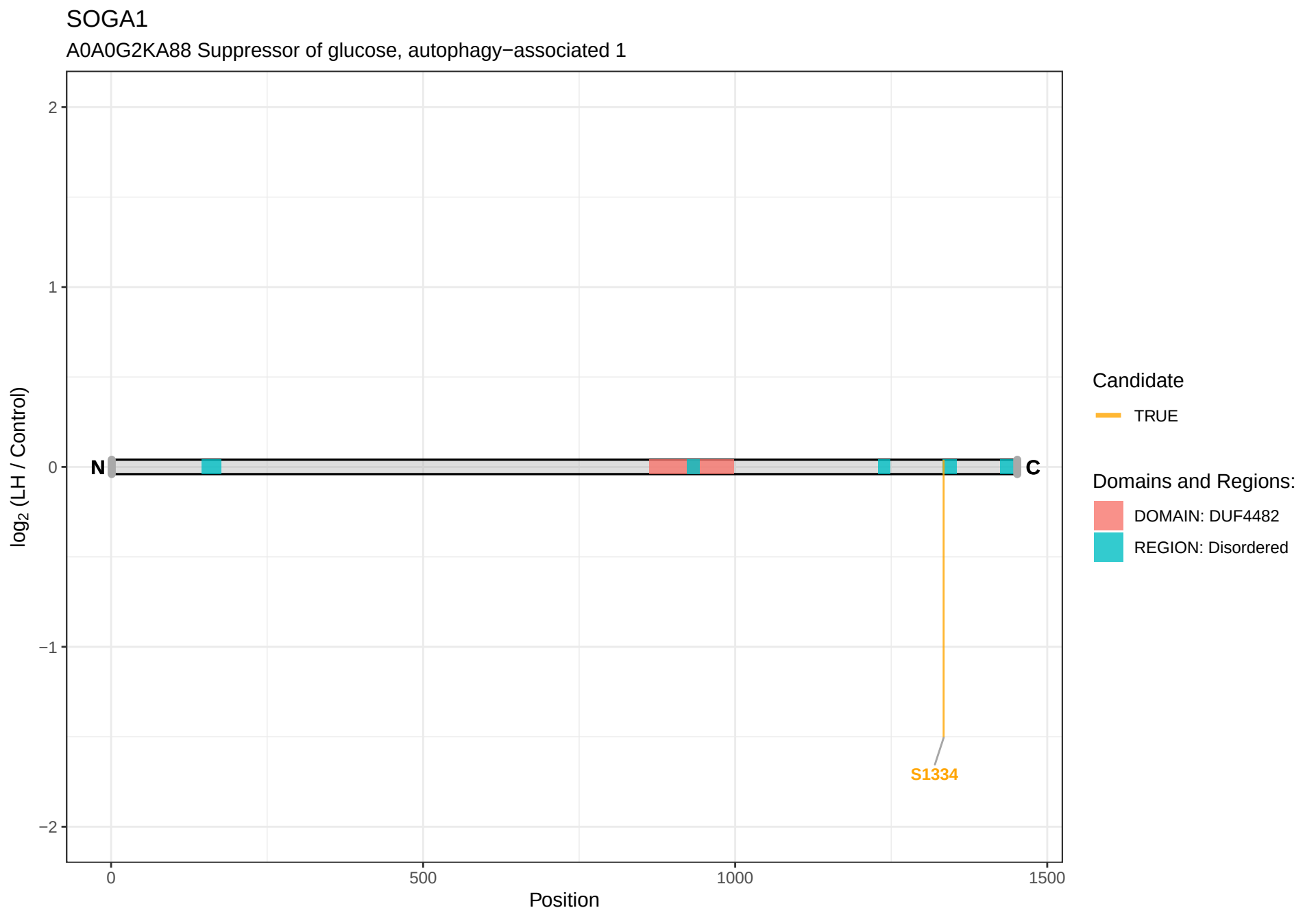

SMC5
D4A9F0 SMC5 structural maintenance of chromosomes 5−like 1 (Yeast) (Predicted), isoform CRA_a
S35
N
C
2
0
−2
log2 (LH / Control)
0
300
600
900
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: SMC_N
REGION: Disordered

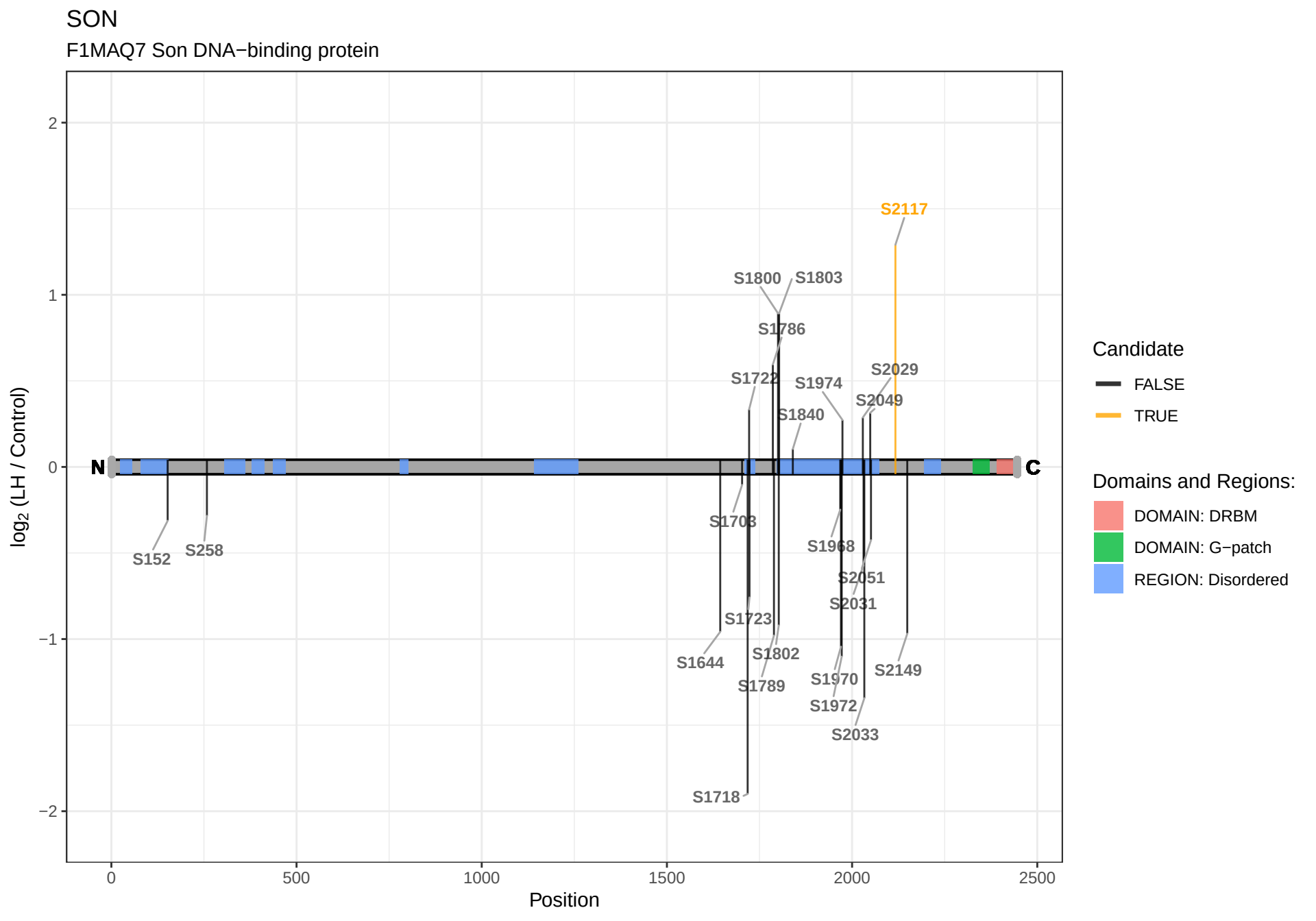

SMCHD1
D4AAG8 Structural maintenance of chromosomes flexible hinge domain−containing 1
S1968
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
500
1000
1500
2000
Candidate
TRUE
Domains and Regions:
DOMAIN: SMC hinge
REGION: Disordered

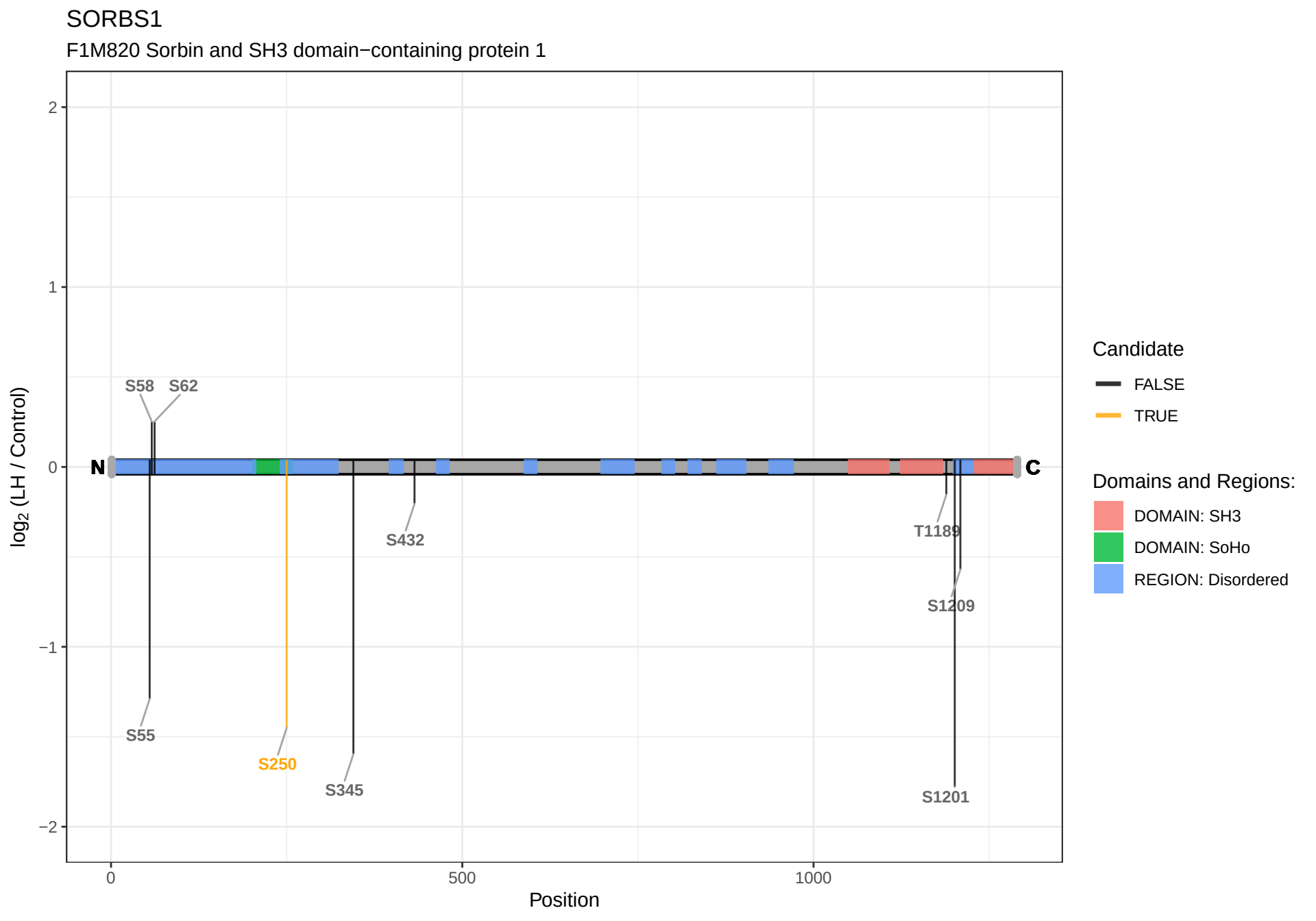

SNTB2
D3ZMX6 Syntrophin, beta 2
S190
S204
S375
S215
S77
S92
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PDZ
DOMAIN: PH
REGION: Disordered

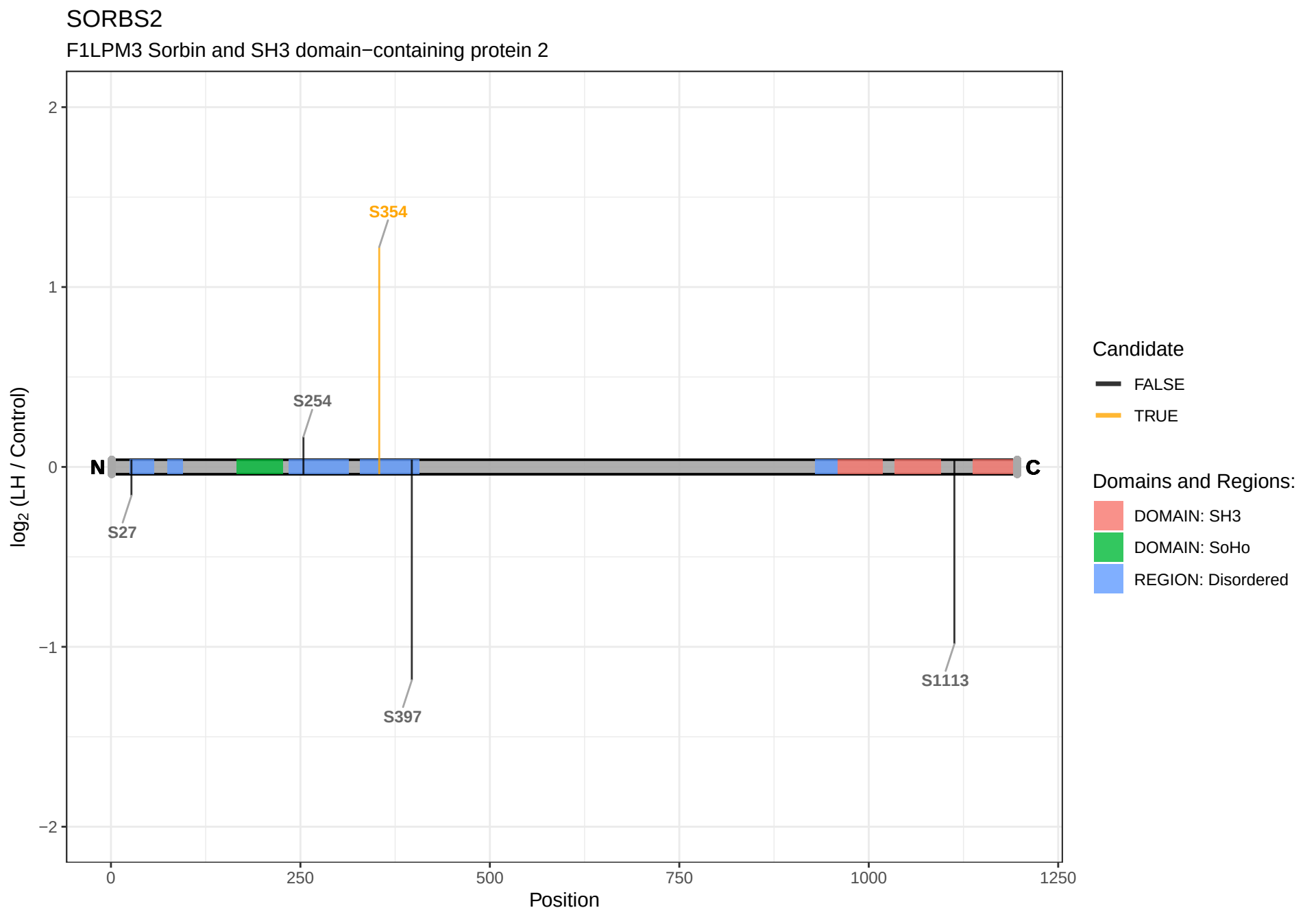

SNW1
D4A8G7 SNW domain−containing 1
S518
S224
S232
N
C
2
0
−2
log2 (LH / Control)
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SKIP_SNW
REGION: Disordered

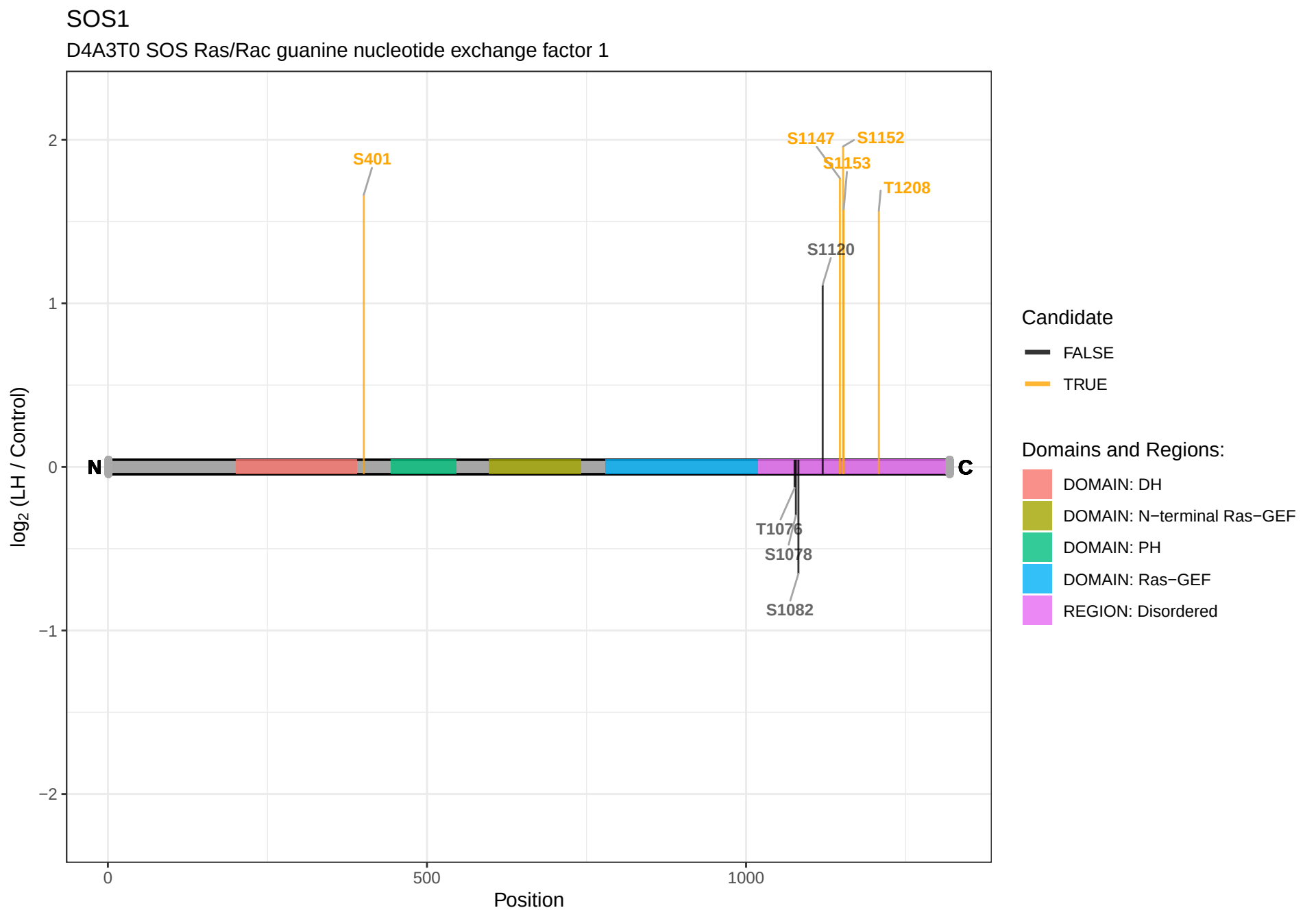

SNX21
A0A0G2K9D8 Sorting nexin family member 21
S97
N
C
log2 (LH / Control)
Position
3
2
1
0
−1
−2
−3
0
100
200
300
Candidate
TRUE
Domains and Regions:
DOMAIN: PX
REGION: Disordered

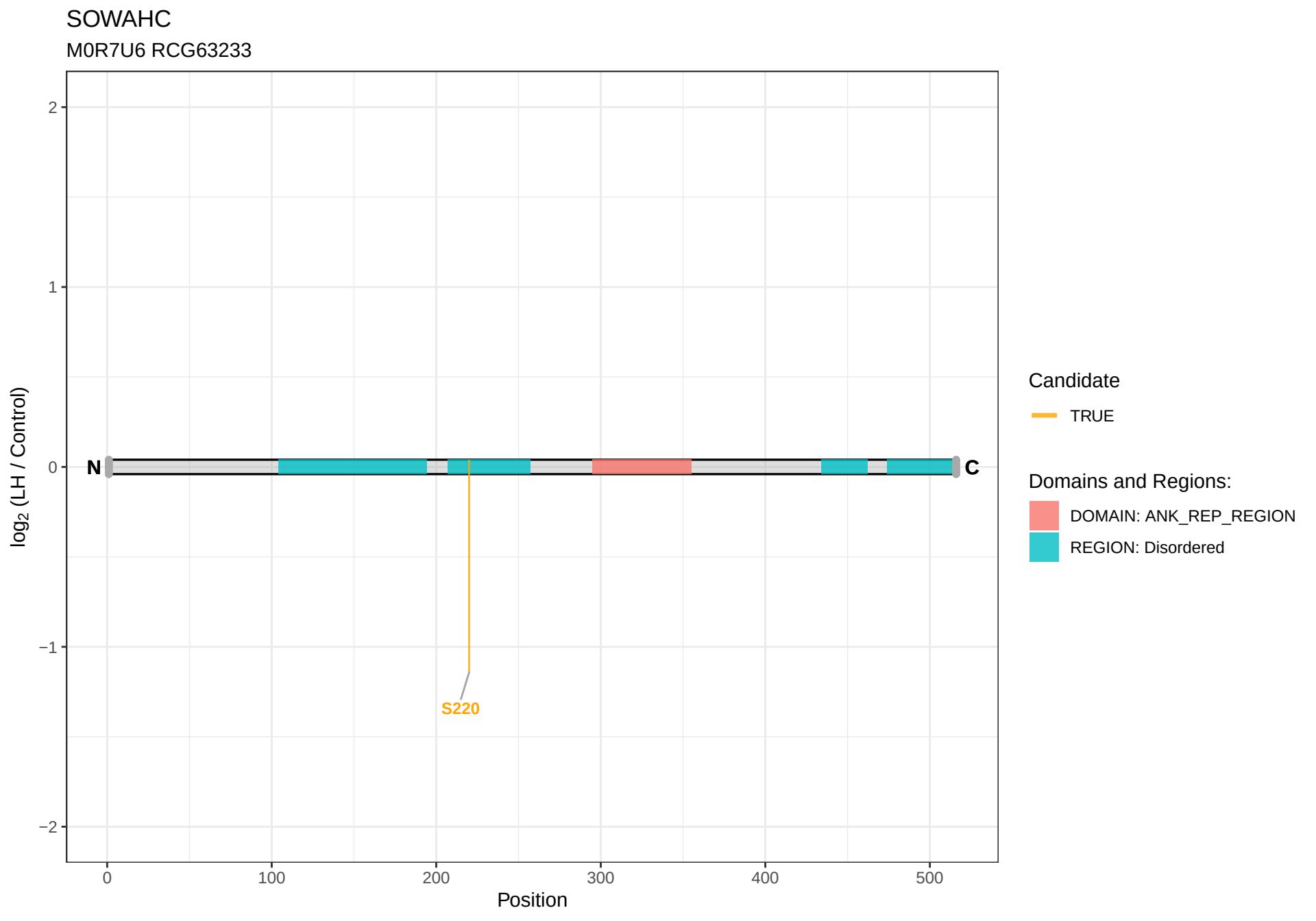

SOGA1
A0A0G2KA88 Suppressor of glucose, autophagy−associated 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S1334
0
500
1000
1500
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: DUF4482
REGION: Disordered

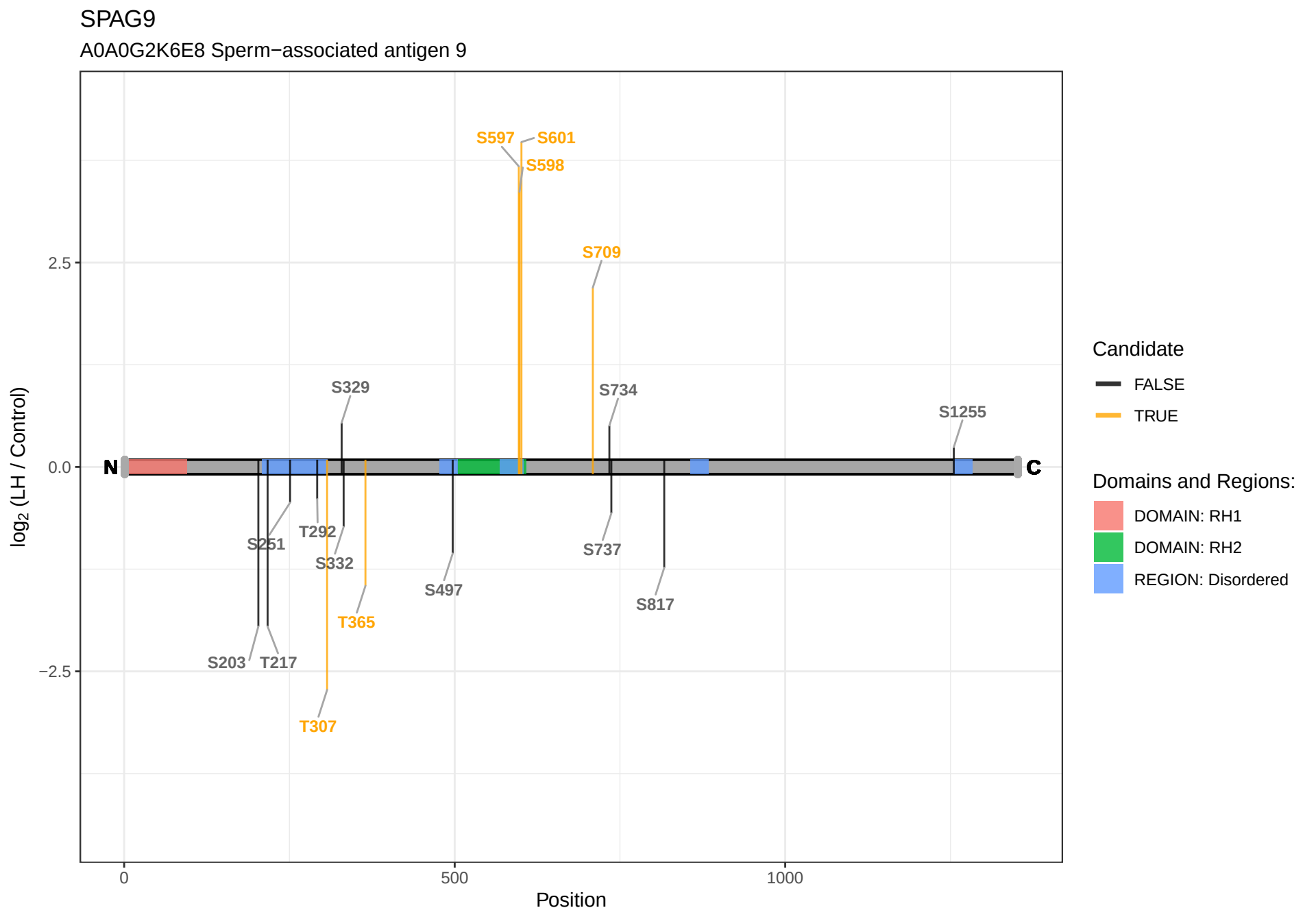

SON
F1MAQ7 Son DNA−binding protein
log2 (LH / Control)
Position
N
C
S152
S258
S1703
S1718
S1722
S1723
S1644
S1786
S1789
S1800
S1802
S1803
S1840
S1968
S1970
S1972
S1974
S2029
S2031
S2033
S2049
S2051
S2117
S2149
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DRBM
DOMAIN: G−patch
REGION: Disordered

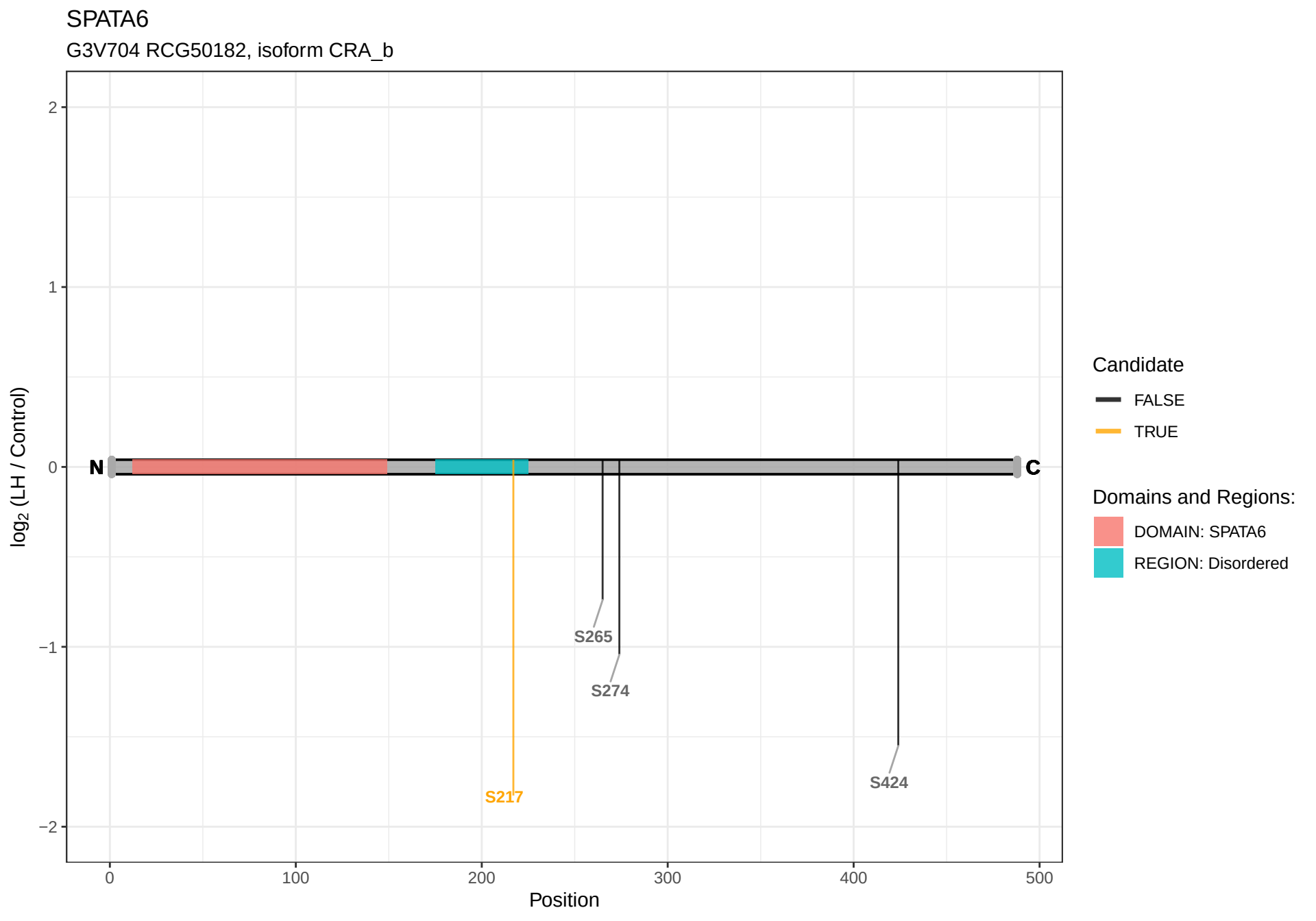

SORBS1
F1M820 Sorbin and SH3 domain−containing protein 1
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
Position
N
C
S58
S62
S55
S250
S345
S432
T1189
S1209
S1201
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SH3
DOMAIN: SoHo
REGION: Disordered

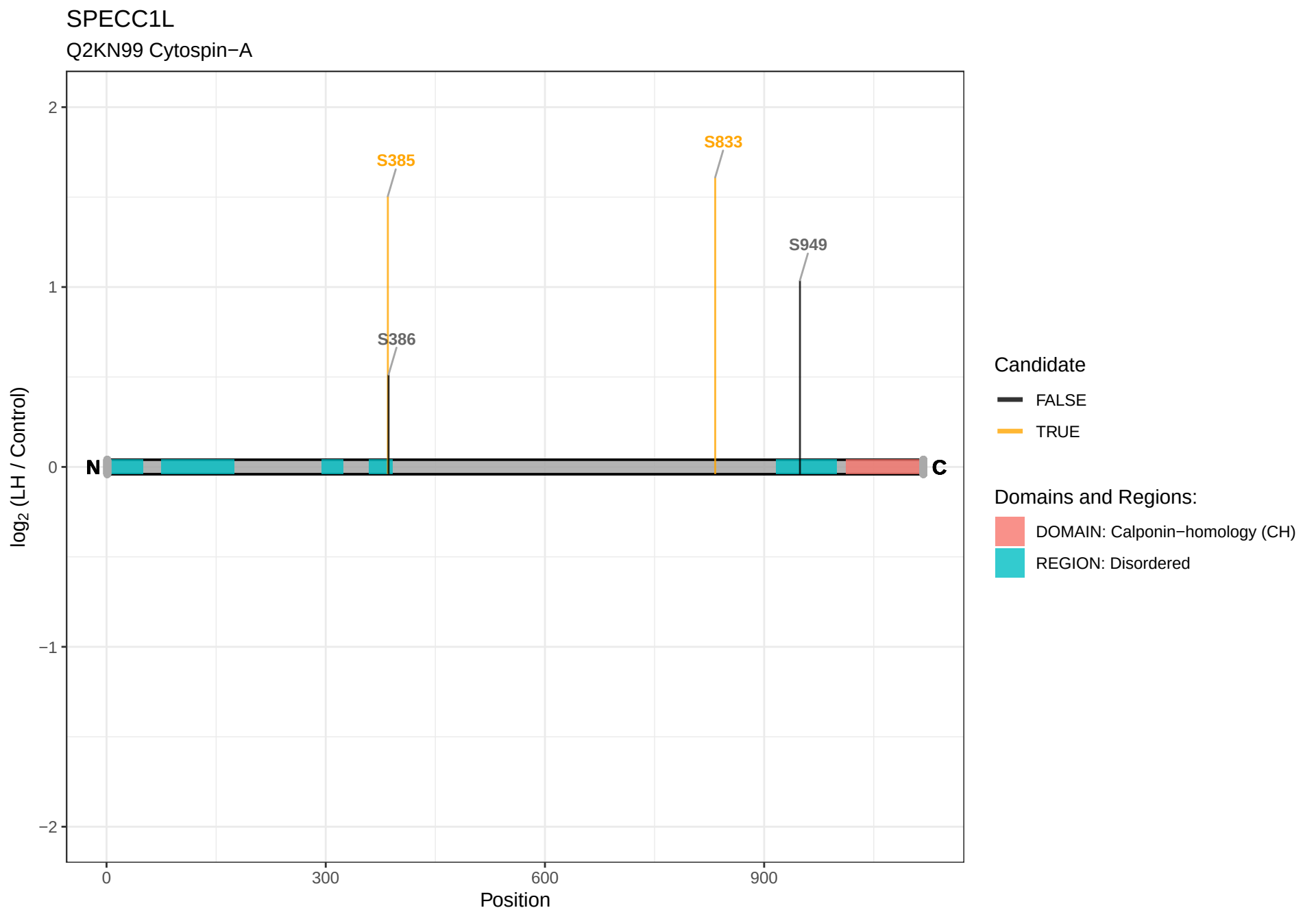

SORBS2
F1LPM3 Sorbin and SH3 domain−containing protein 2
log2 (LH / Control)
2
1
0
−1
−2
0
250
500
750
1000
1250
Position
N
C
S354
S254
S27
S397
S1113
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SH3
DOMAIN: SoHo
REGION: Disordered

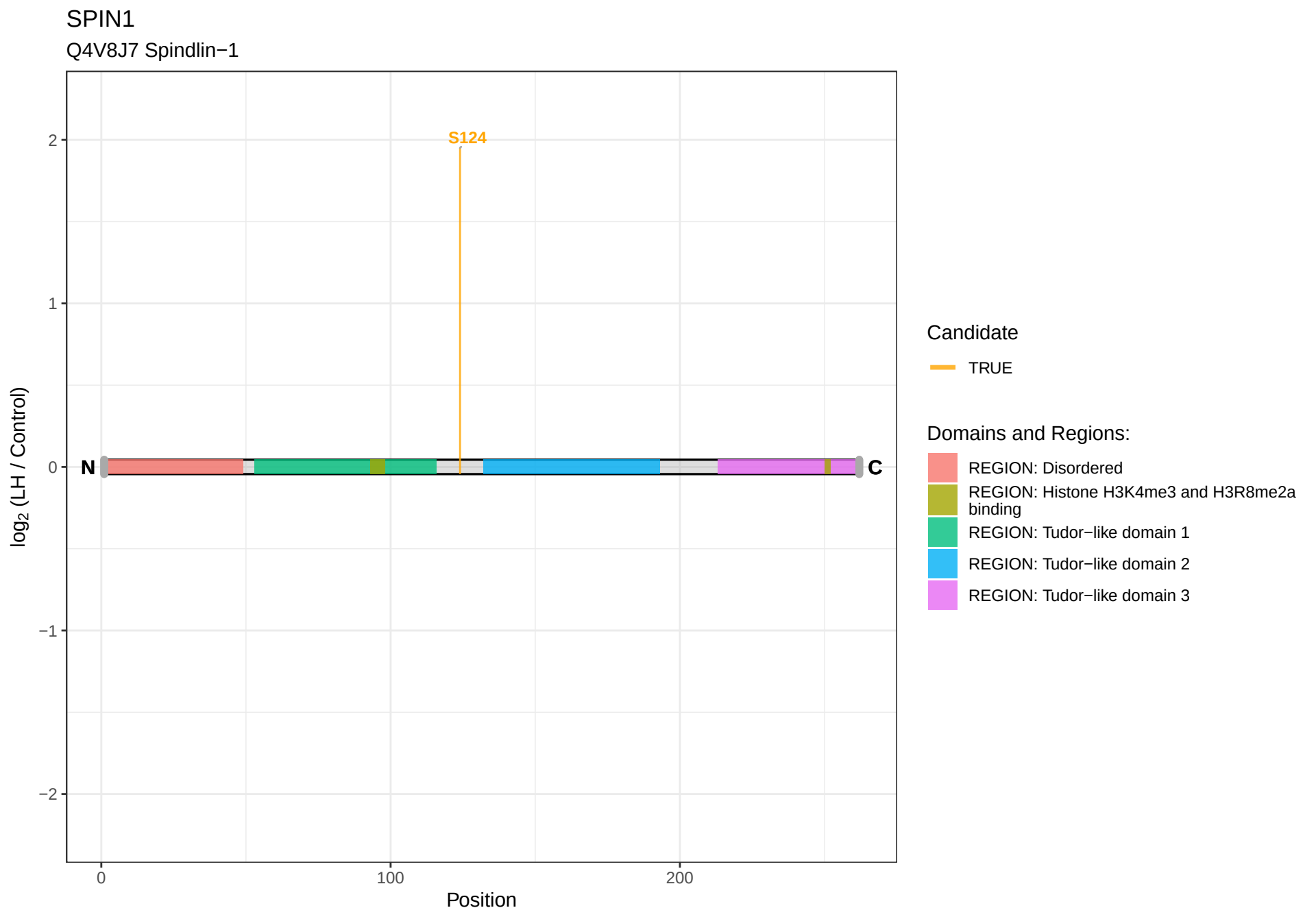

SOS1
D4A3T0 SOS Ras/Rac guanine nucleotide exchange factor 1
S401
S1147
S1152
S1153
T1208
S1120
T1076
S1078
S1082
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DH
DOMAIN: N−terminal Ras−GEF
DOMAIN: PH
DOMAIN: Ras−GEF
REGION: Disordered

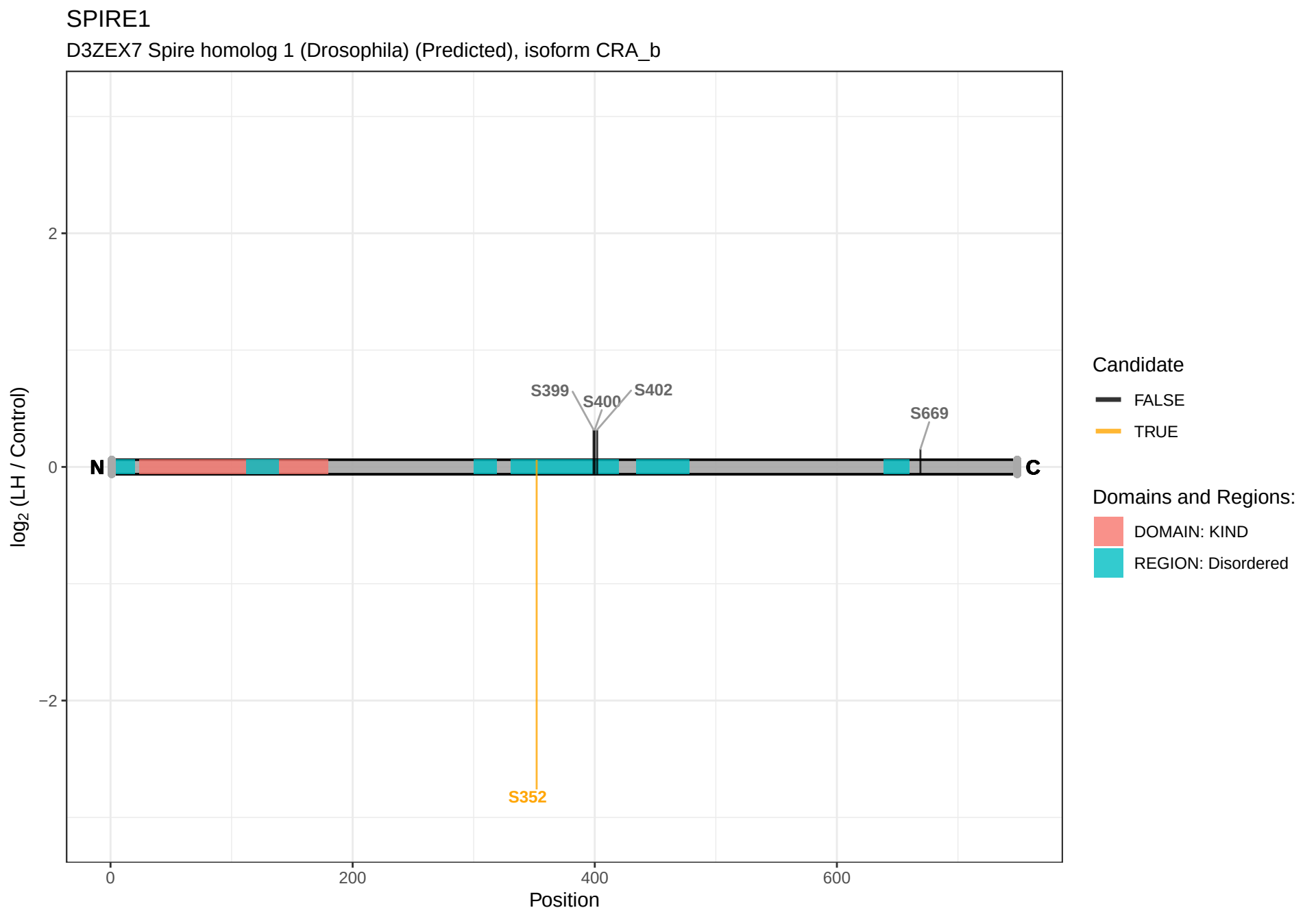

SOWAHC
M0R7U6 RCG63233
log2 (LH / Control)
2
1
0
−1
−2
N
C
S220
0
100
200
300
400
500
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: ANK_REP_REGION
REGION: Disordered

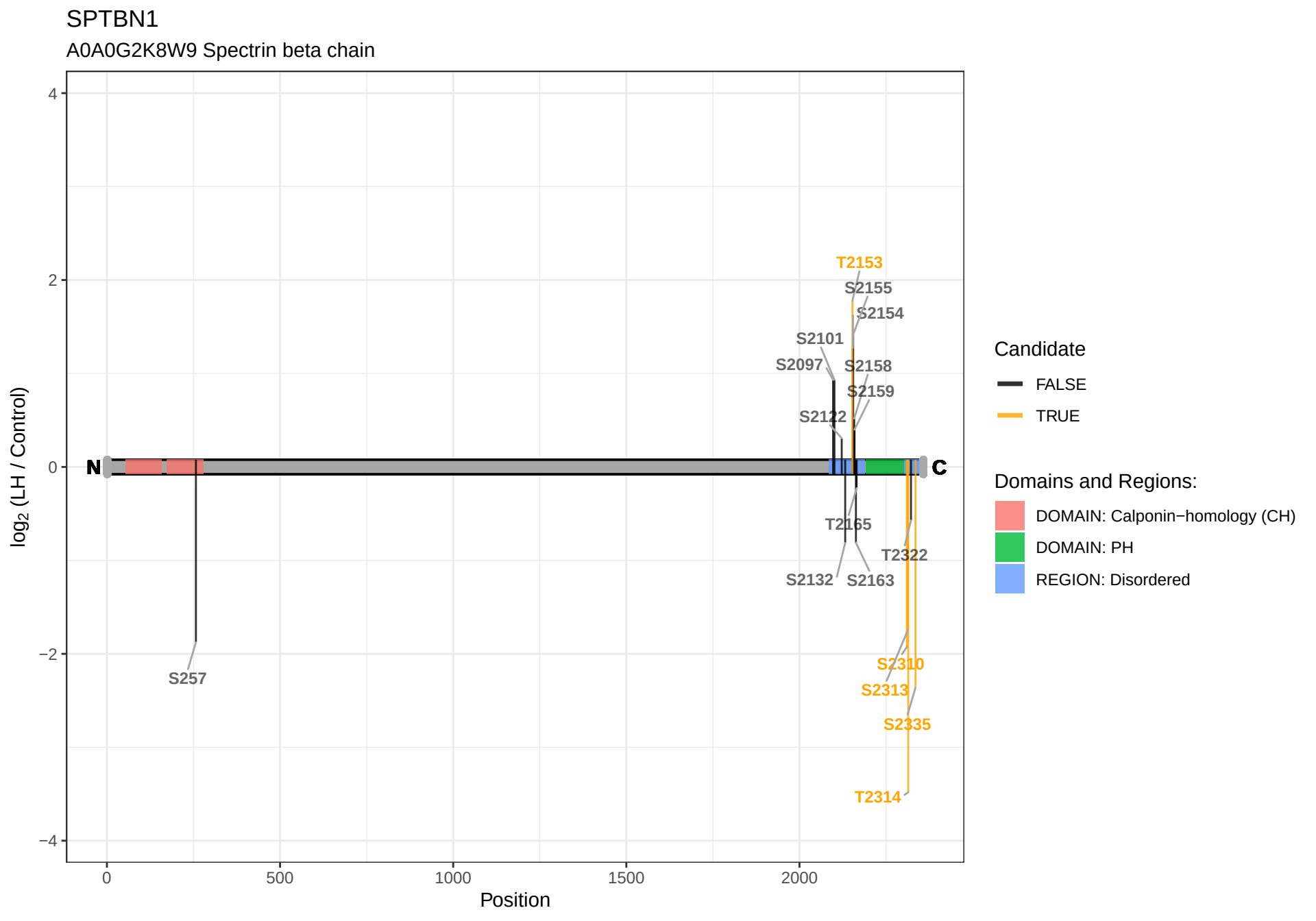

SPAG9
A0A0G2K6E8 Sperm−associated antigen 9
S597
S601
S598
S709
S329
S734
S1255
N
C
S251
T292
S332
S497
S737
S817
T365
S203
T217
T307
2.5
0.0
−2.5
log2 (LH / Control)
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RH1
DOMAIN: RH2
REGION: Disordered

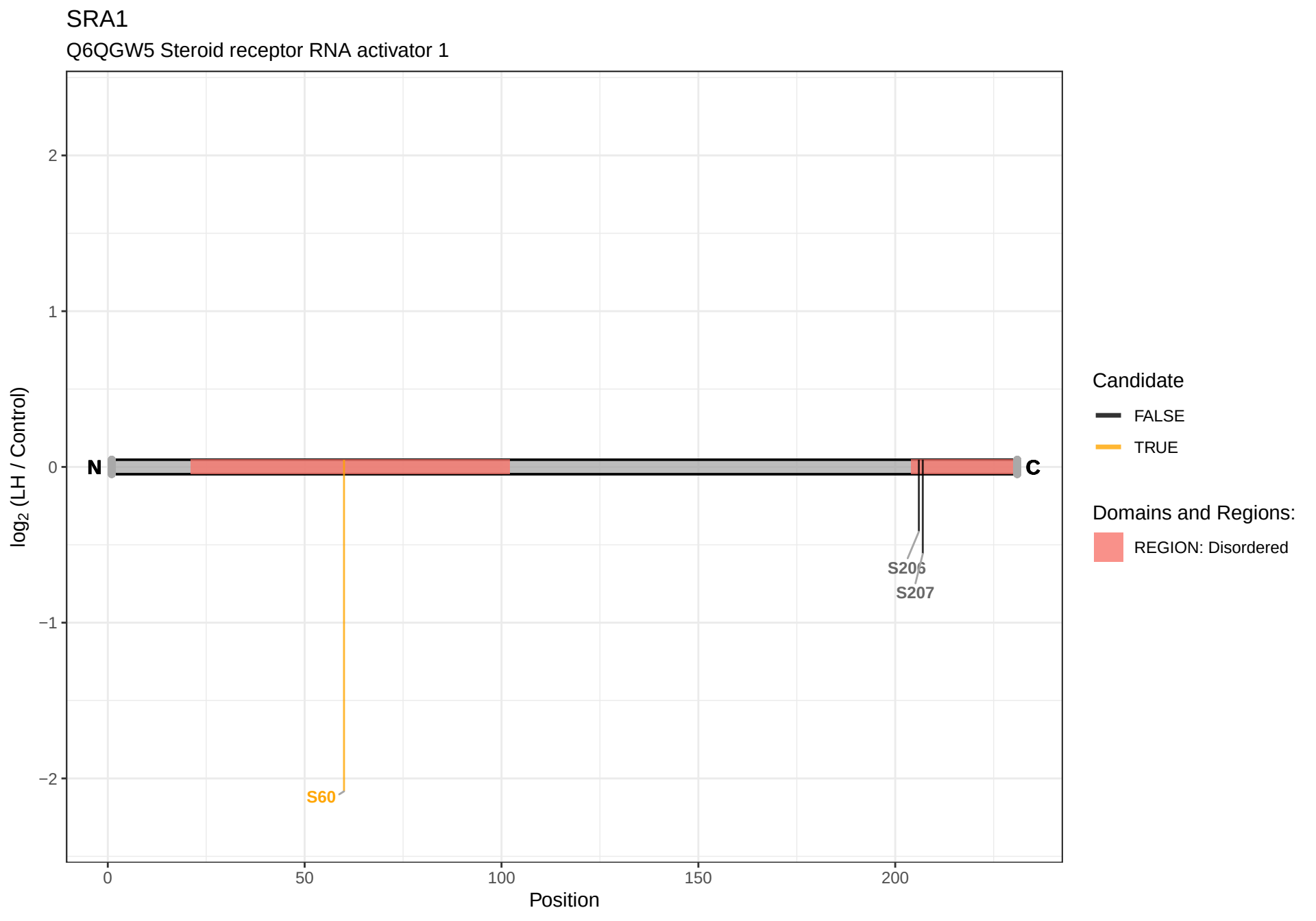

SPATA6
G3V704 RCG50182, isoform CRA_b
log2 (LH / Control)
2
1
0
−1
−2
N
C
S265
S274
S217
S424
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SPATA6
REGION: Disordered

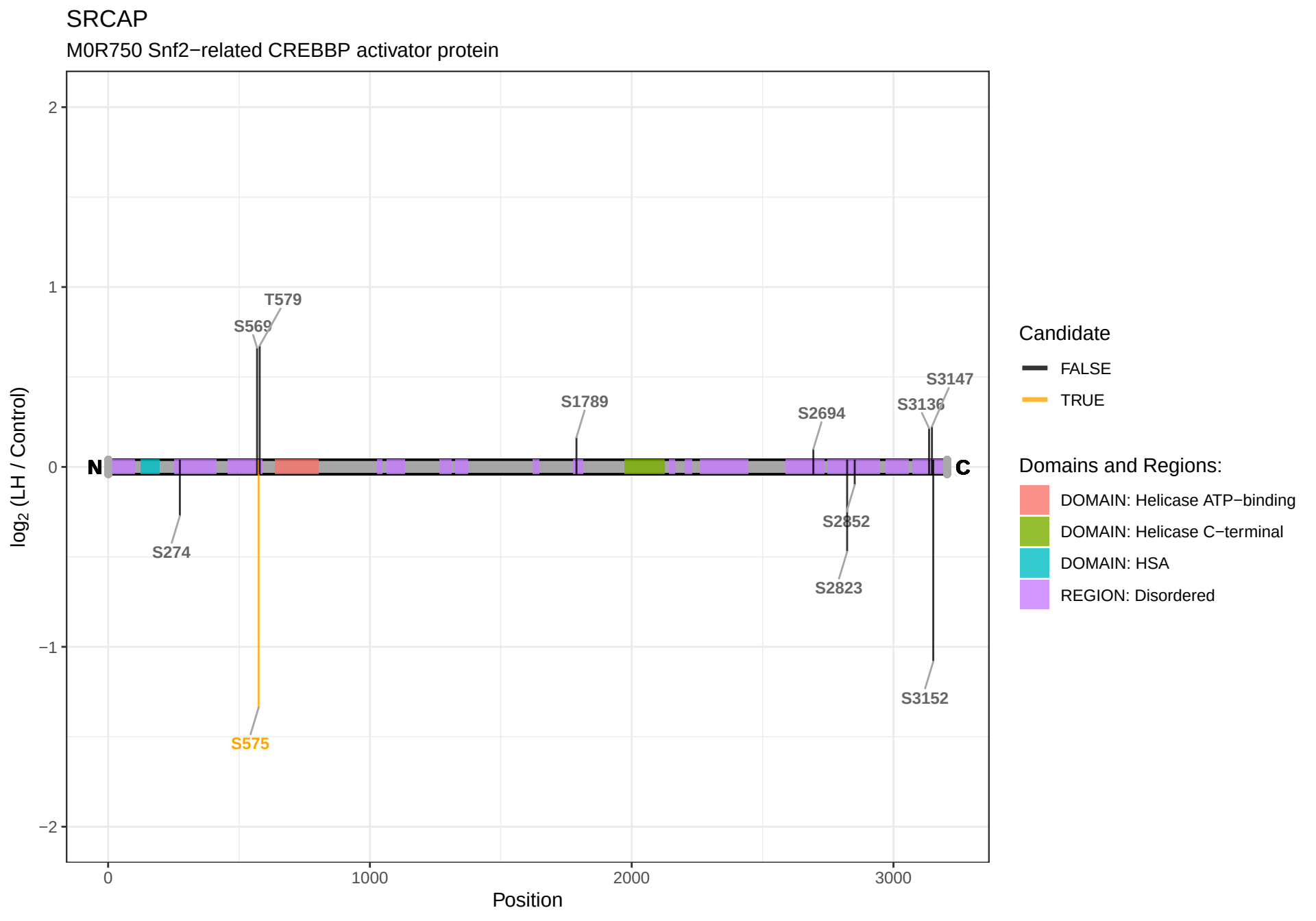

SPECC1L
Q2KN99 Cytospin−A
S385
S833
S949
S386
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Calponin−homology (CH)
REGION: Disordered

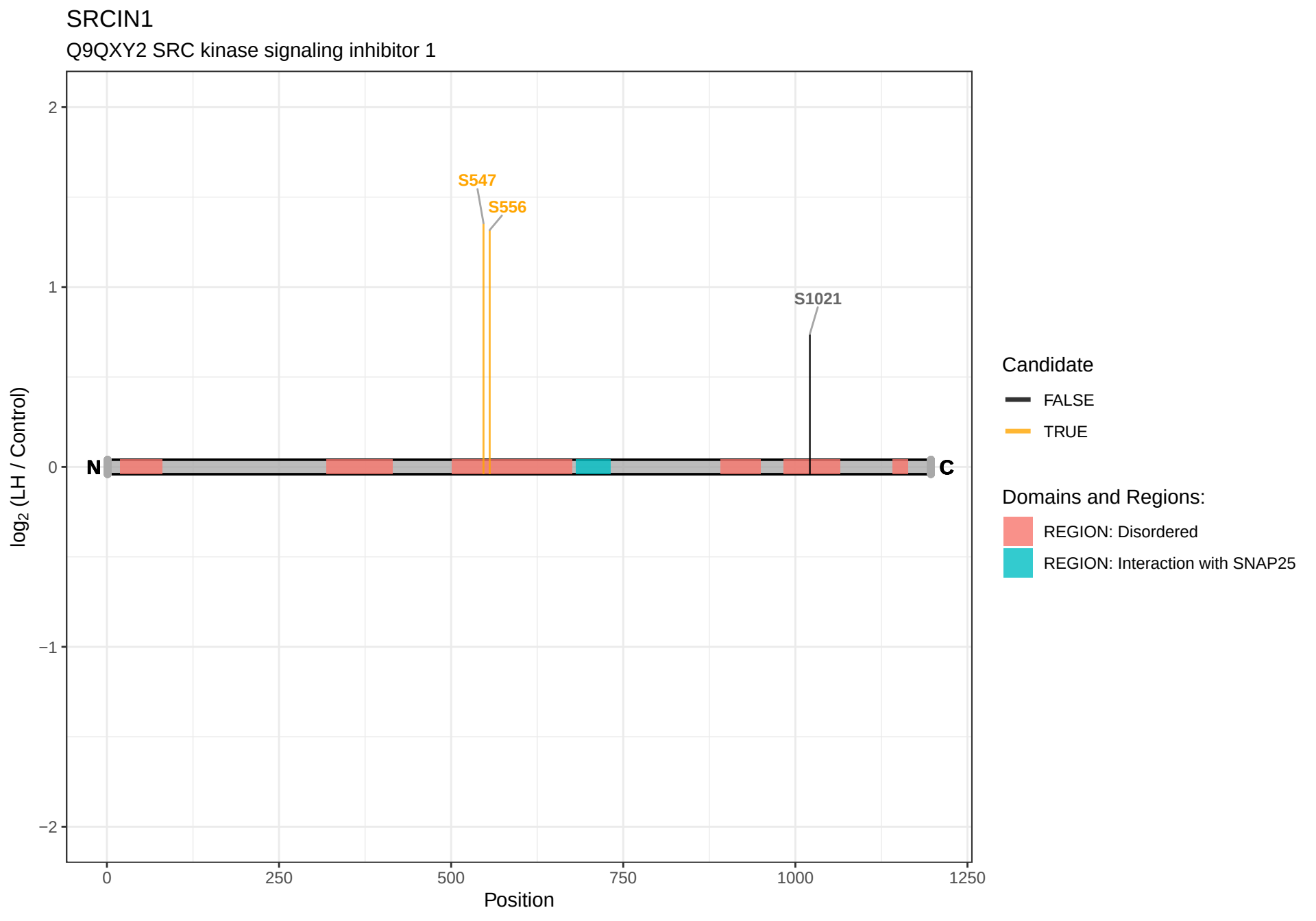

SPIN1
Q4V8J7 Spindlin−1
S124
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered
REGION: Histone H3K4me3 and H3R8me2a binding
REGION: Tudor−like domain 1
REGION: Tudor−like domain 2
REGION: Tudor−like domain 3

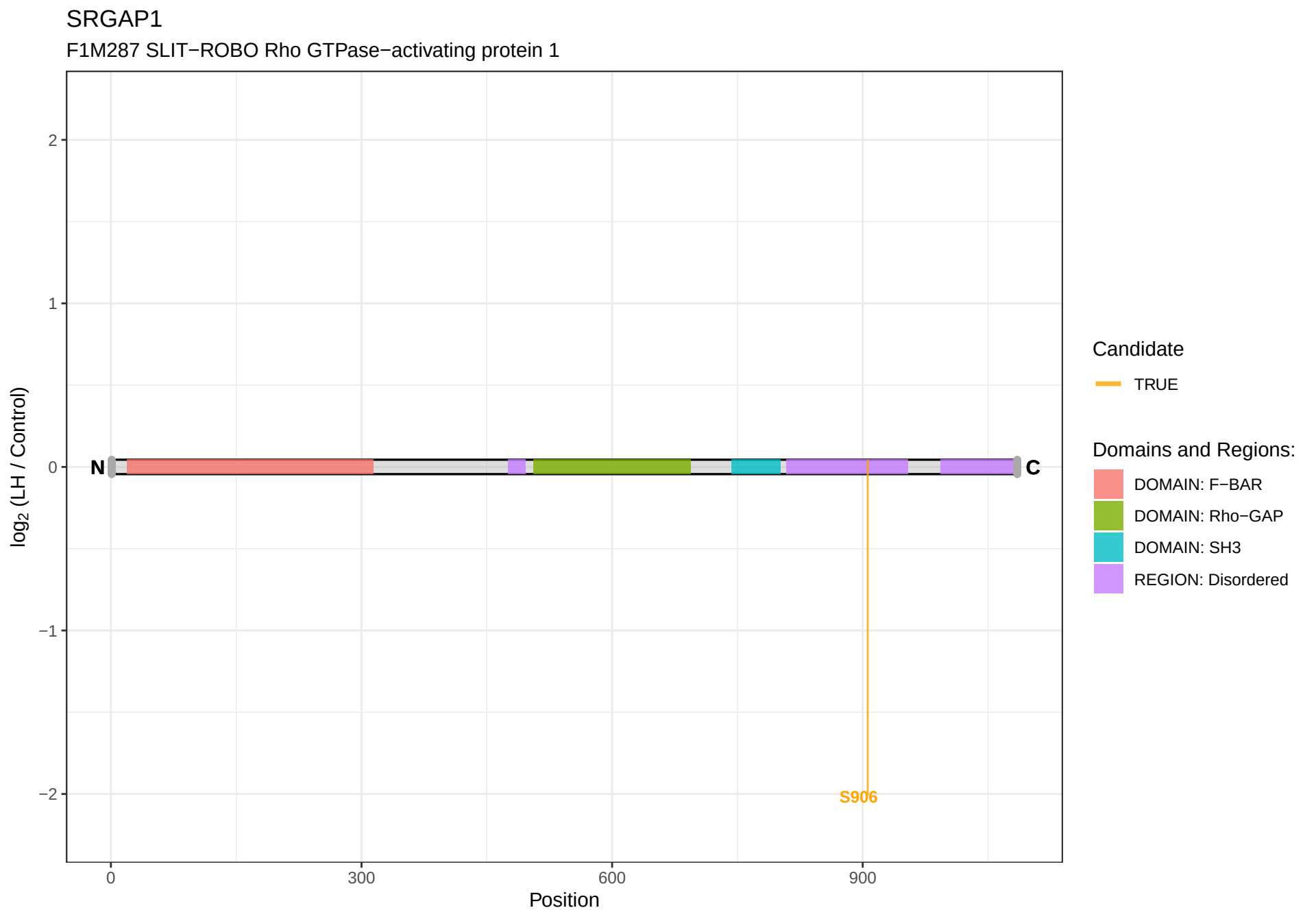

SPIRE1
D3ZEX7 Spire homolog 1 (Drosophila) (Predicted), isoform CRA_b
log2 (LH / Control)
2
0
−2
N
C
S399
S400
S402
S669
S352
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: KIND
REGION: Disordered

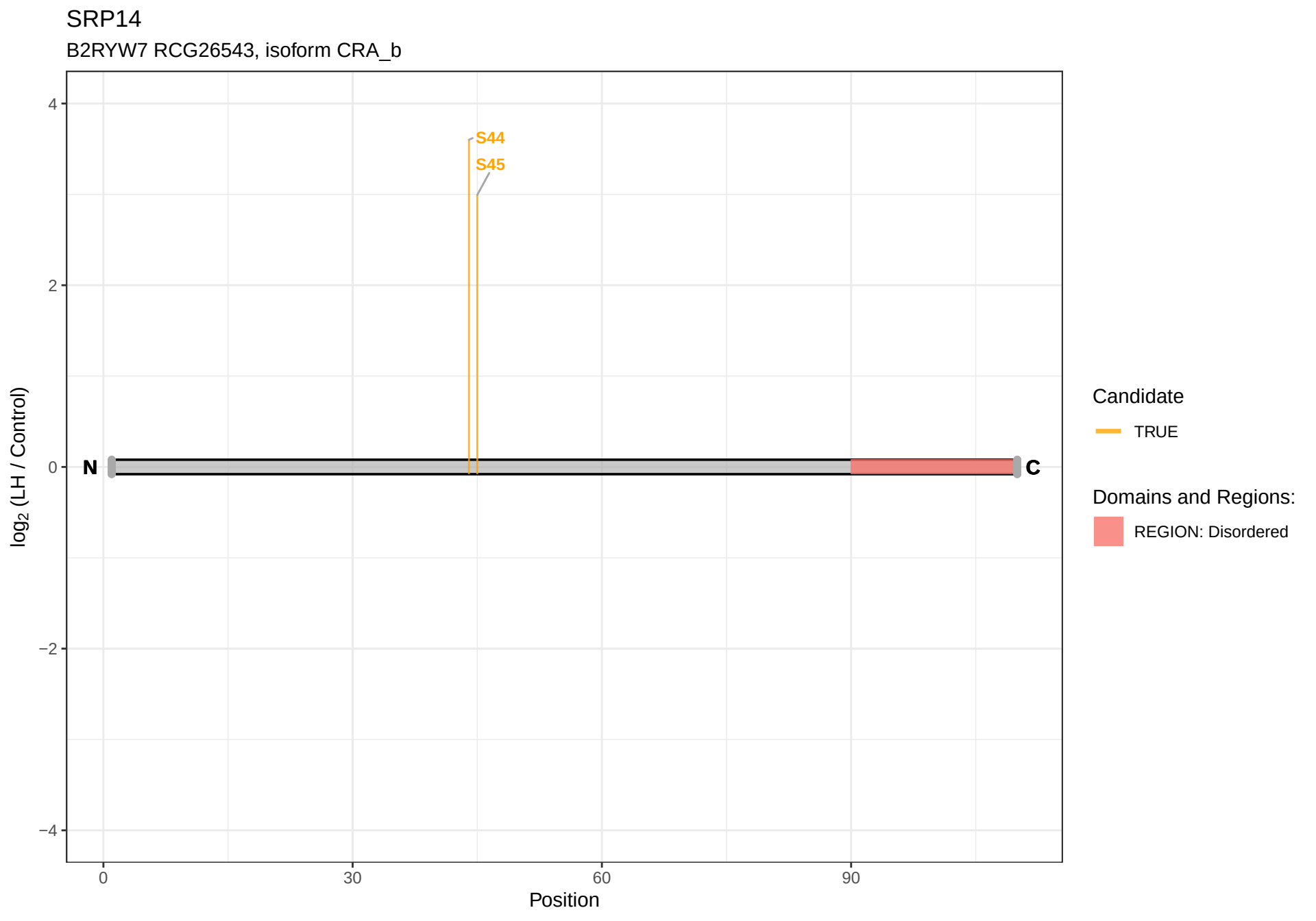

SPTBN1
A0A0G2K8W9 Spectrin beta chain
log2 (LH / Control)
Position
N
C
T2153
S2155
S2154
S2101
S2097
S2158
S2159
S2122
T2165
T2322
S2132
S2163
S257
S2310
S2313
S2335
T2314
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Calponin−homology (CH)
DOMAIN: PH
REGION: Disordered

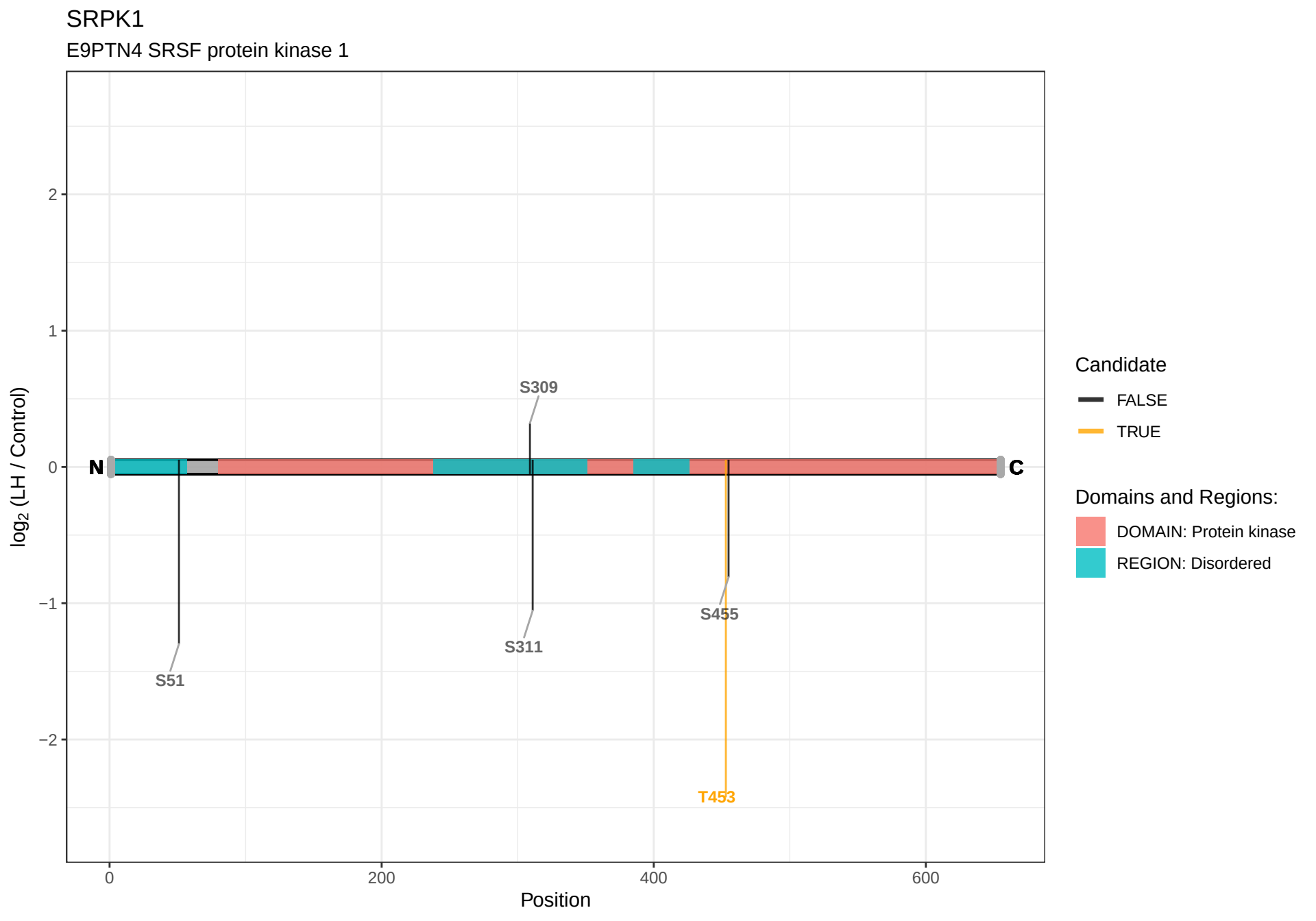

SRA1
Q6QGW5 Steroid receptor RNA activator 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S60
S206
S207
0
50
100
150
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

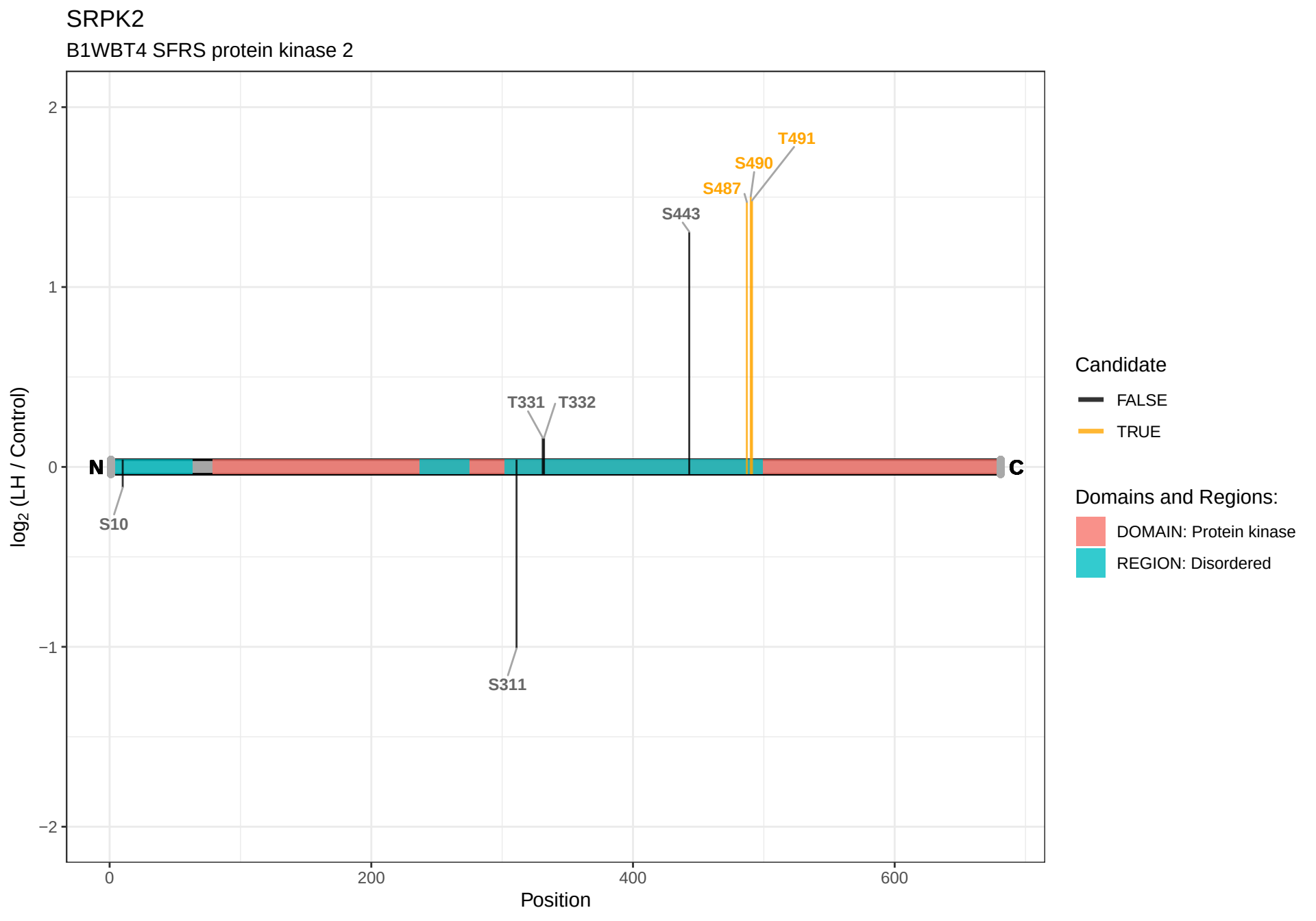

SRCAP
M0R750 Snf2−related CREBBP activator protein
log2 (LH / Control)
2
1
0
−1
−2
0
1000
2000
3000
Position
N
C
T579
S569
S1789
S2694
S3147
S3136
S274
S2852
S2823
S3152
S575
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Helicase ATP−binding
DOMAIN: Helicase C−terminal
DOMAIN: HSA
REGION: Disordered

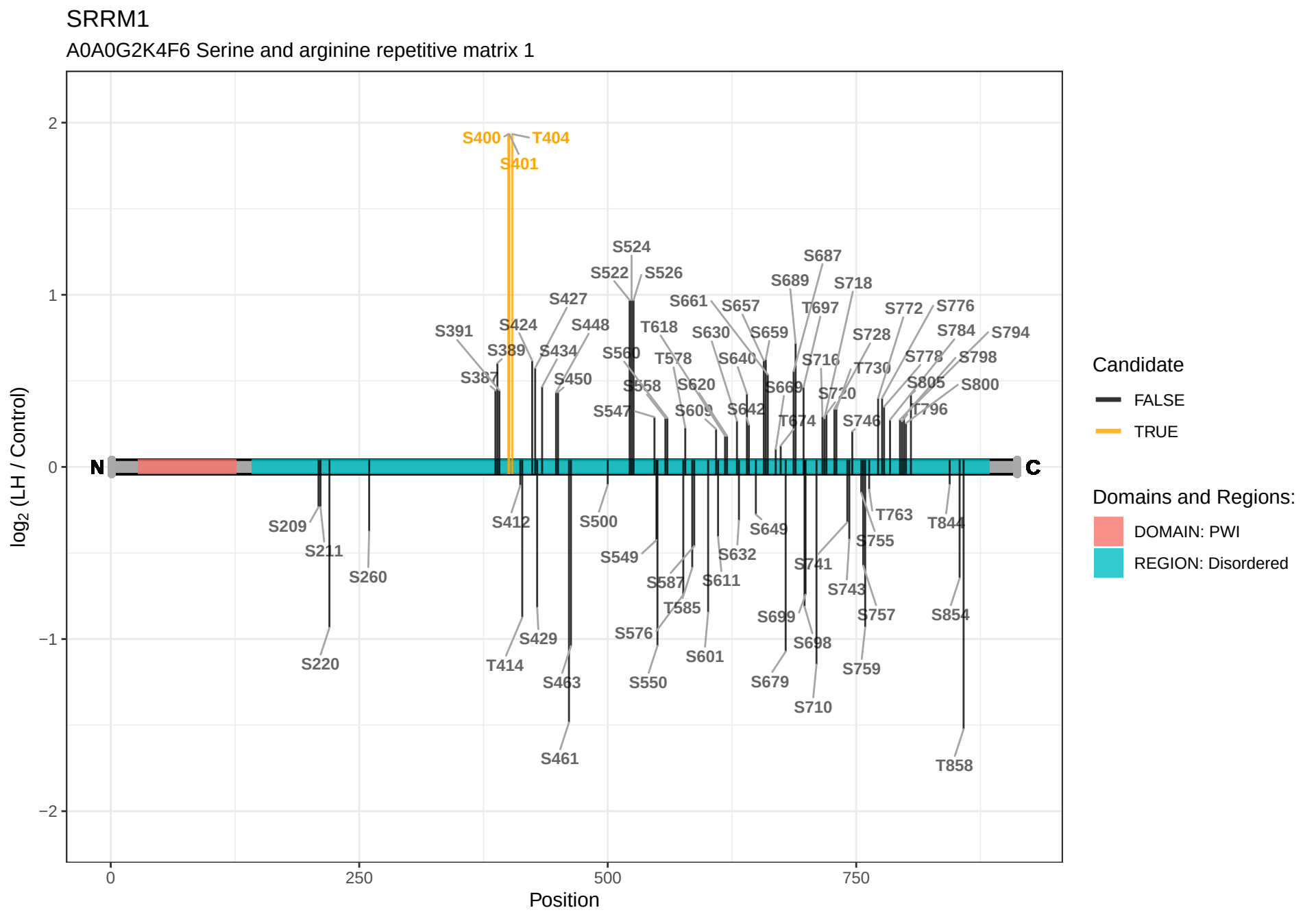

SRCIN1
Q9QXY2 SRC kinase signaling inhibitor 1
S547
S556
S1021
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
250
500
750
1000
1250
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Interaction with SNAP25

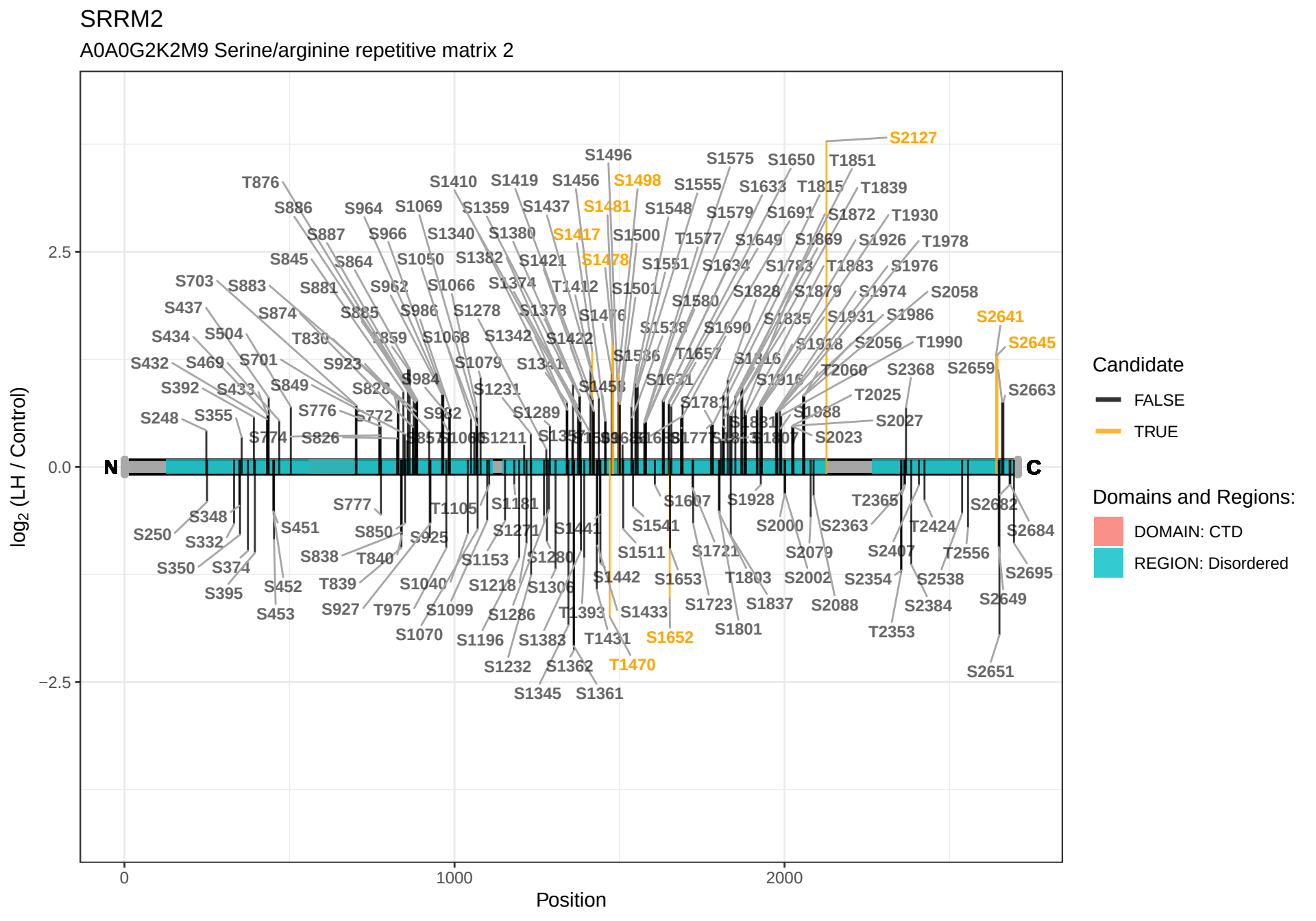

SRGAP1
F1M287 SLIT−ROBO Rho GTPase−activating protein 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S906
0
300
600
900
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: F−BAR
DOMAIN: Rho−GAP
DOMAIN: SH3
REGION: Disordered

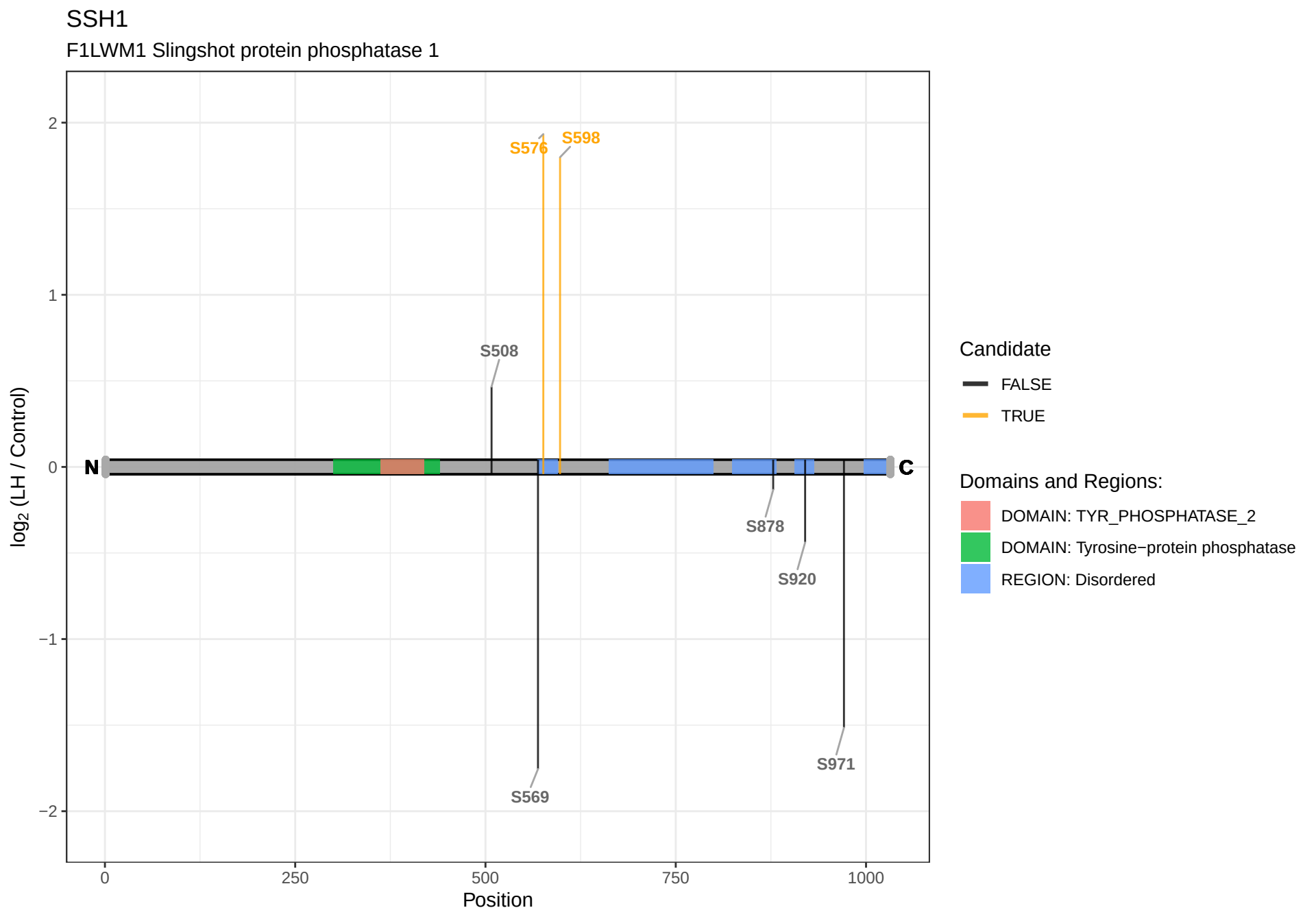

SRP14
B2RYW7 RCG26543, isoform CRA_b
S44
S45
N
C
4
2
0
−2
−4
log2 (LH / Control)
0
30
60
90
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

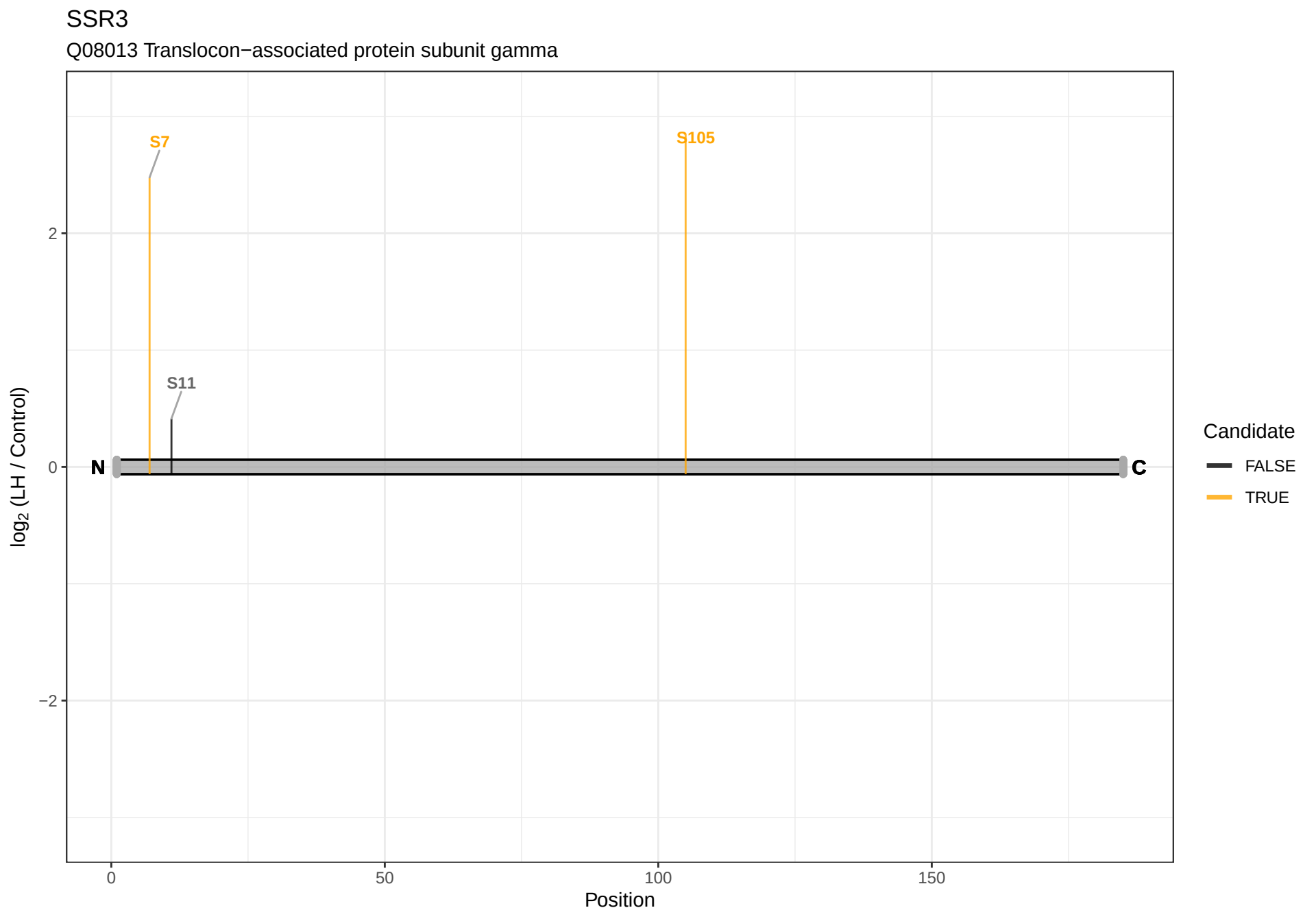

SRPK1
E9PTN4 SRSF protein kinase 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S309
S51
S311
S455
T453
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered

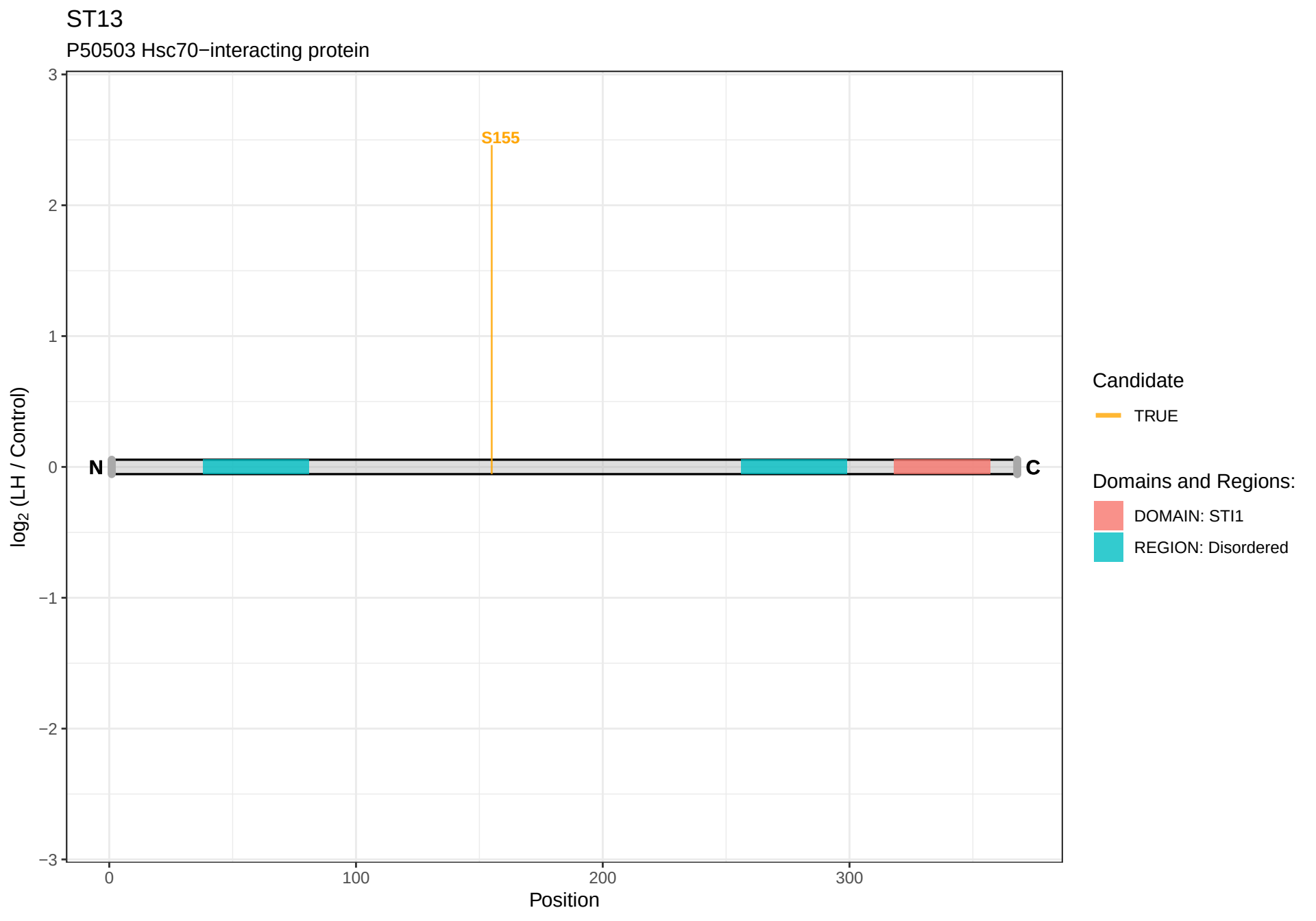

SRPK2
B1WBT4 SFRS protein kinase 2
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
Position
N
C
S10
S311
T331
T332
S443
S487
S490
T491
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered


SRRM1
A0A0G2K4F6 Serine and arginine repetitive matrix 1
log2 (LH / Control)
Position
N
C
S400
T404
S401
S524
S522
S526
S687
S689
S718
S427
S661
S657
T697
S772
S776
S391
S424
S448
T618
S630
S659
S728
S784
S794
S389
S434
S560
T578
S640
S716
S778
S798
S387
S450
S558
S620
T730
S805
S800
S669
S720
S547
S609
S642
T674
S746
T796
S209
S412
S500
S649
T763
T844
S211
S549
S632
S755
S260
S587
S611
S741
S743
T585
S699
S757
S854
S220
S429
S576
S698
T414
S601
S759
S463
S550
S679
S710
S461
T858
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PWI
REGION: Disordered


SRRM2
A0A0G2K2M9 Serine/arginine repetitive matrix 2
log2 (LH / Control)
2.5
0.0
−2.5
0
1000
2000
Position
N
C
S2127
S1496
S1575
S1650
T1851
T876
S1410
S1419
S1456
S1498
S1555
S1633
T1815
T1839
S886
S964
S1069
S1359
S1437
S1481
S1548
S1579
S1691
S1872
T1930
S887
S966
S1340
S1380
S1417
S1500
T1577
S1649
S1869
S1926
T1978
S845
S864
S1050
S1382
S1421
S1478
S1551
S1634
S1783
T1883
S1976
S703
S883
S881
S962
S1066
S1374
T1412
S1501
S1828
S1879
S1974
S2058
S437
S874
S885
S986
S1278
S1378
S1476
S1580
S1538
S1690
S1835
S1931
S1986
S2641
S434
S504
T830
T859
S1068
S1342
S1422
S1690
S1918
S2056
T1990
S2645
S432
S469
S701
S923
S1079
S1341
S1536
T1657
S1816
T2060
S2368
S2659
S392
S433
S849
S828
S984
S1231
S1456
S1631
S1916
T2025
S2663
S248
S355
S776
S772
S932
S1289
S1781
S1988
S2027
S774
S826
S1211
S1807
S2023
S777
T1105
S1181
S1607
S1928
T2365
S2682
S348
S250
S451
S850
S925
S1271
S1441
S1541
S2000
S2363
T2424
S2684
S332
S838
T840
S1153
S1280
S1511
S1721
S2079
S2407
T2556
S350
S374
S1442
S1653
T1803
S2002
S2354
S2538
S2695
S395
S452
T839
S1040
S1218
S1306
S1723
S1837
S2088
S2384
S2649
S453
S927
T975
S1099
S1286
T1393
S1433
S1801
T2353
S1070
S1196
S1383
T1431
S1652
S1232
S1362
T1470
S2651
S1345
S1361
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CTD
REGION: Disordered

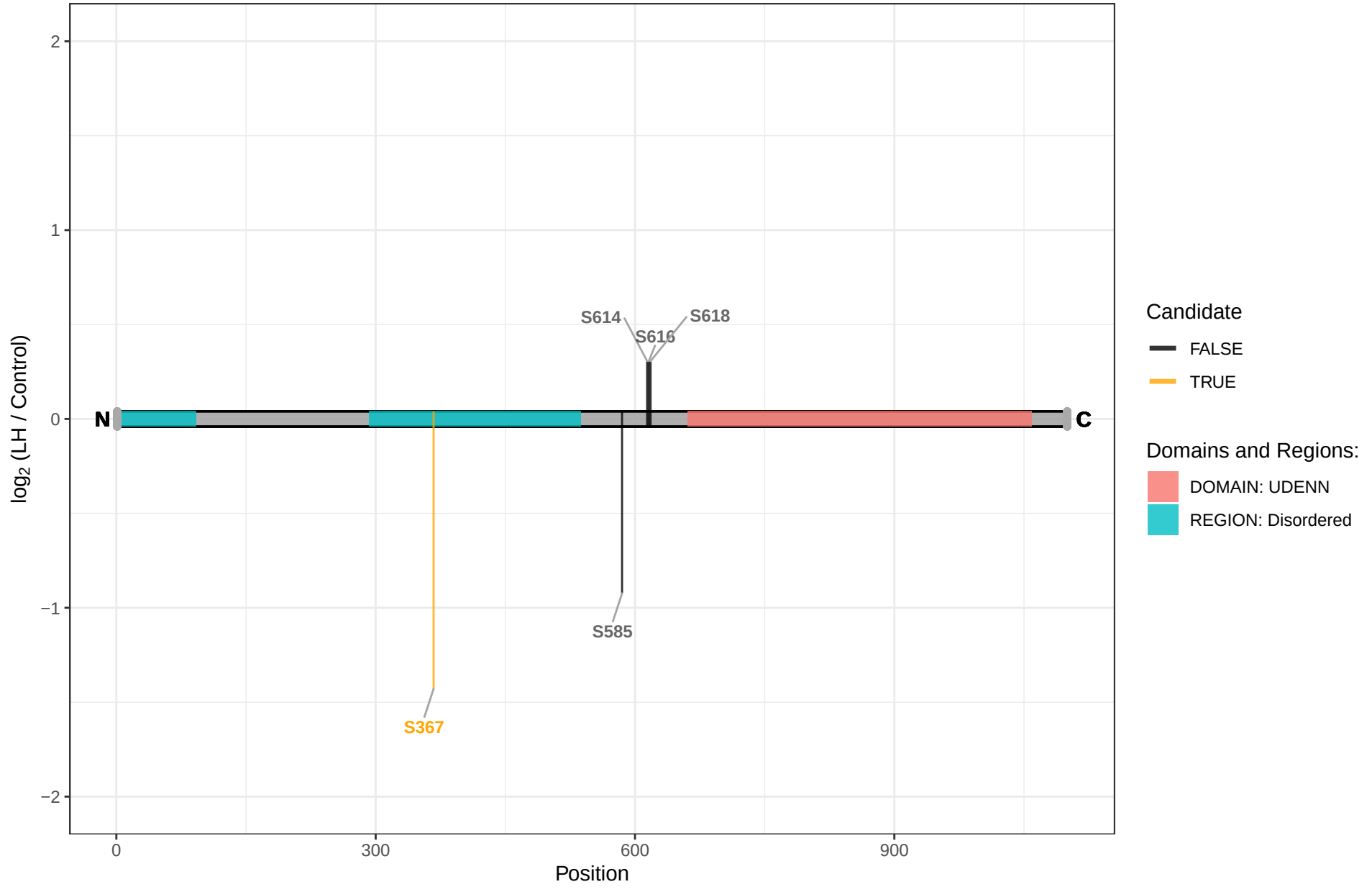

SSH1
F1LWM1 Slingshot protein phosphatase 1
log2 (LH / Control)
Position
N
C
S576
S598
S508
S878
S920
S569
S971
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: TYR_PHOSPHATASE_2
DOMAIN: Tyrosine−protein phosphatase
REGION: Disordered

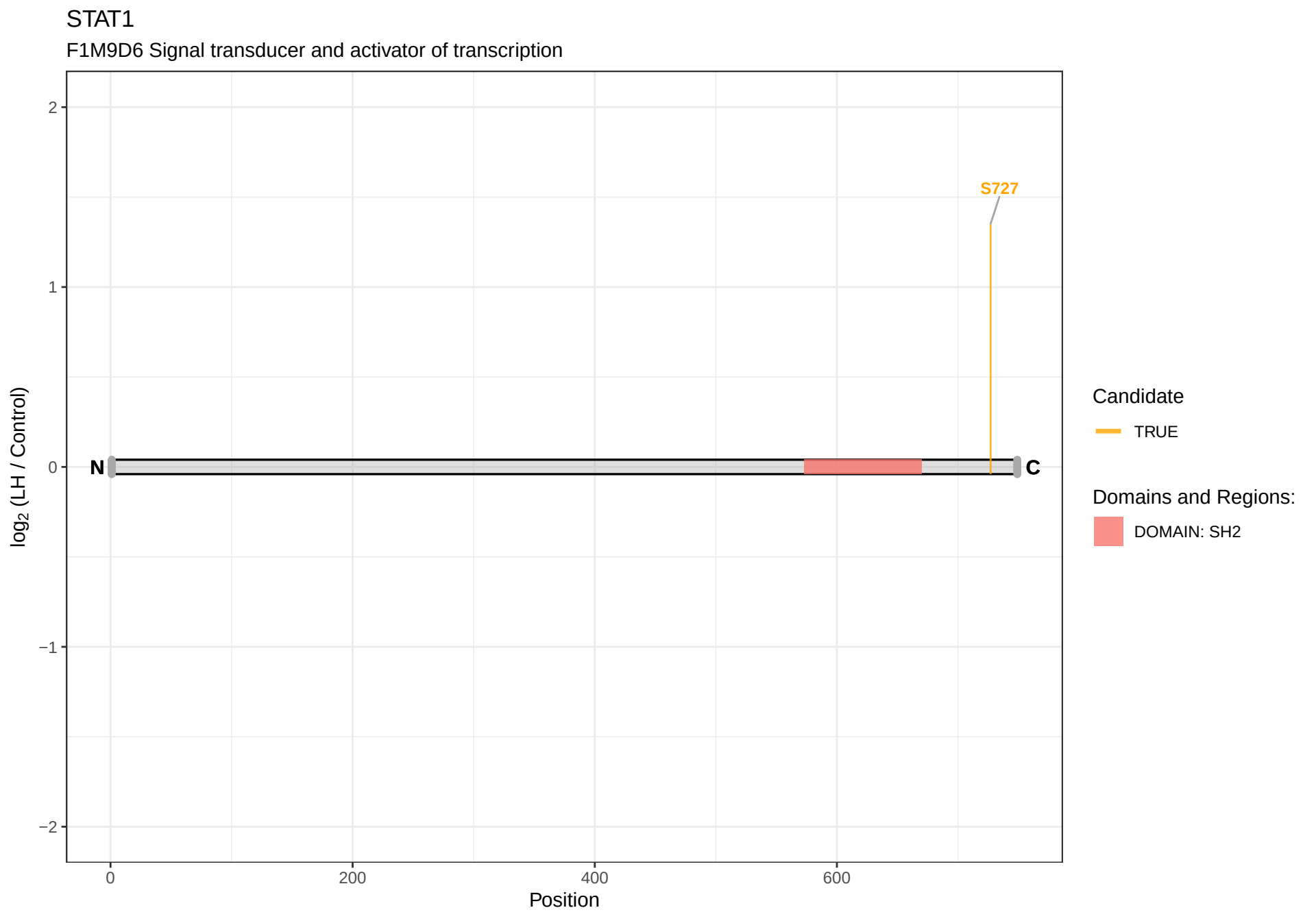

SSR3
Q08013 Translocon−associated protein subunit gamma
S7
S105
S11
N
C
2
0
−2
log2 (LH / Control)
0
50
100
150
Position
Candidate
FALSE
TRUE

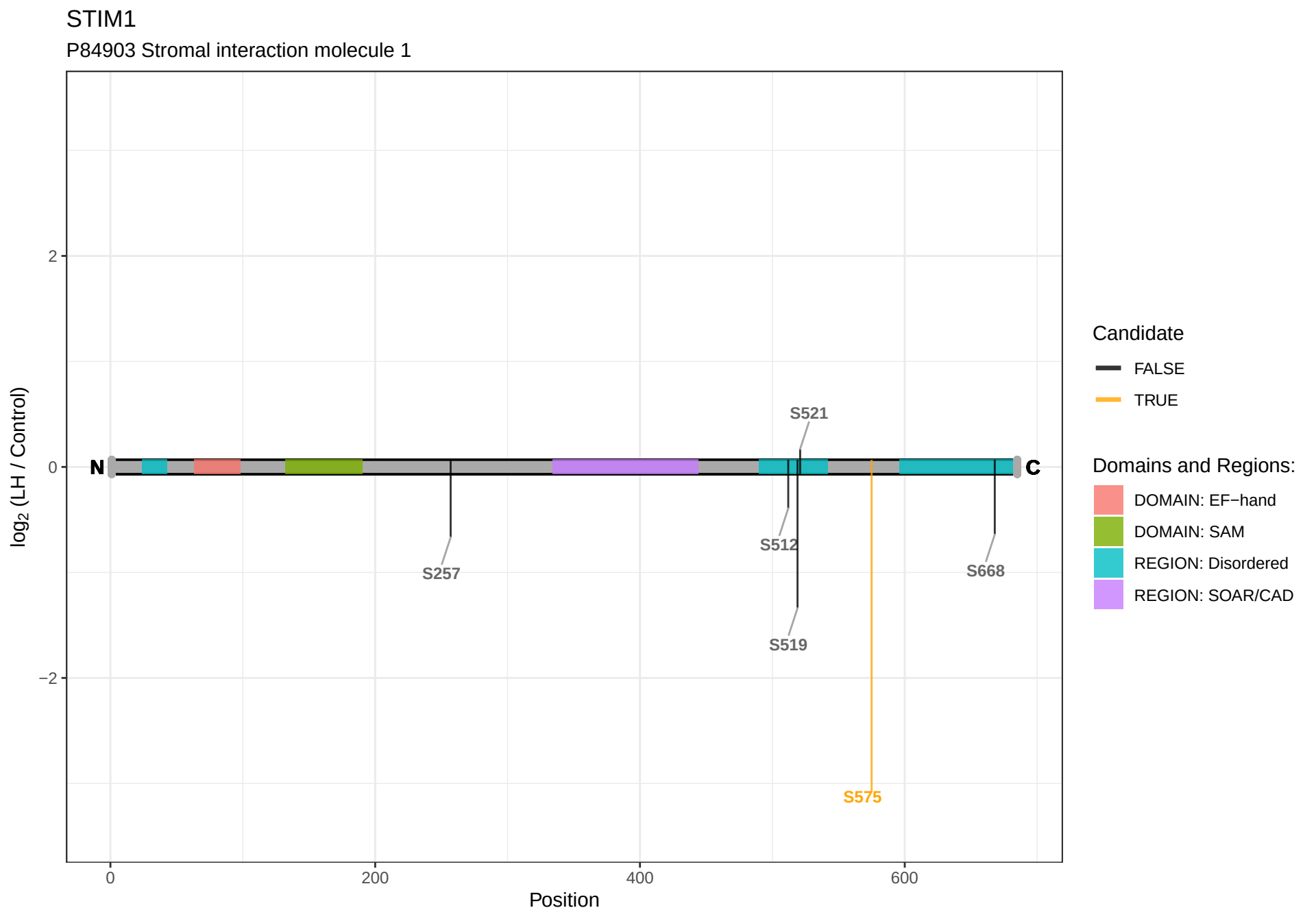

ST13
P50503 Hsc70−interacting protein
S155
N
C
log2 (LH / Control)
Position
3
2
1
0
−1
−2
−3
0
100
200
300
Candidate
TRUE
Domains and Regions:
DOMAIN: STI1
REGION: Disordered

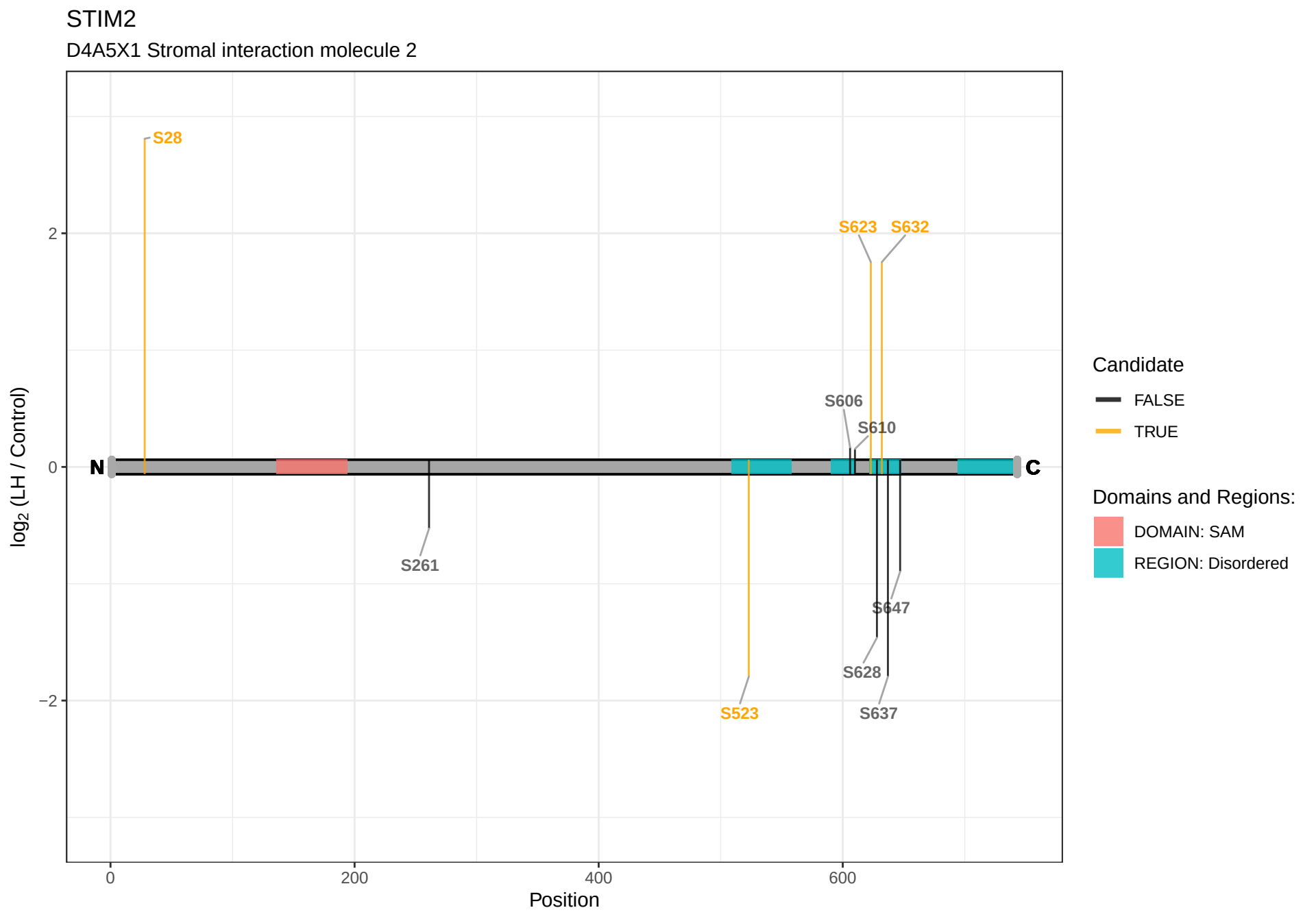
ST5

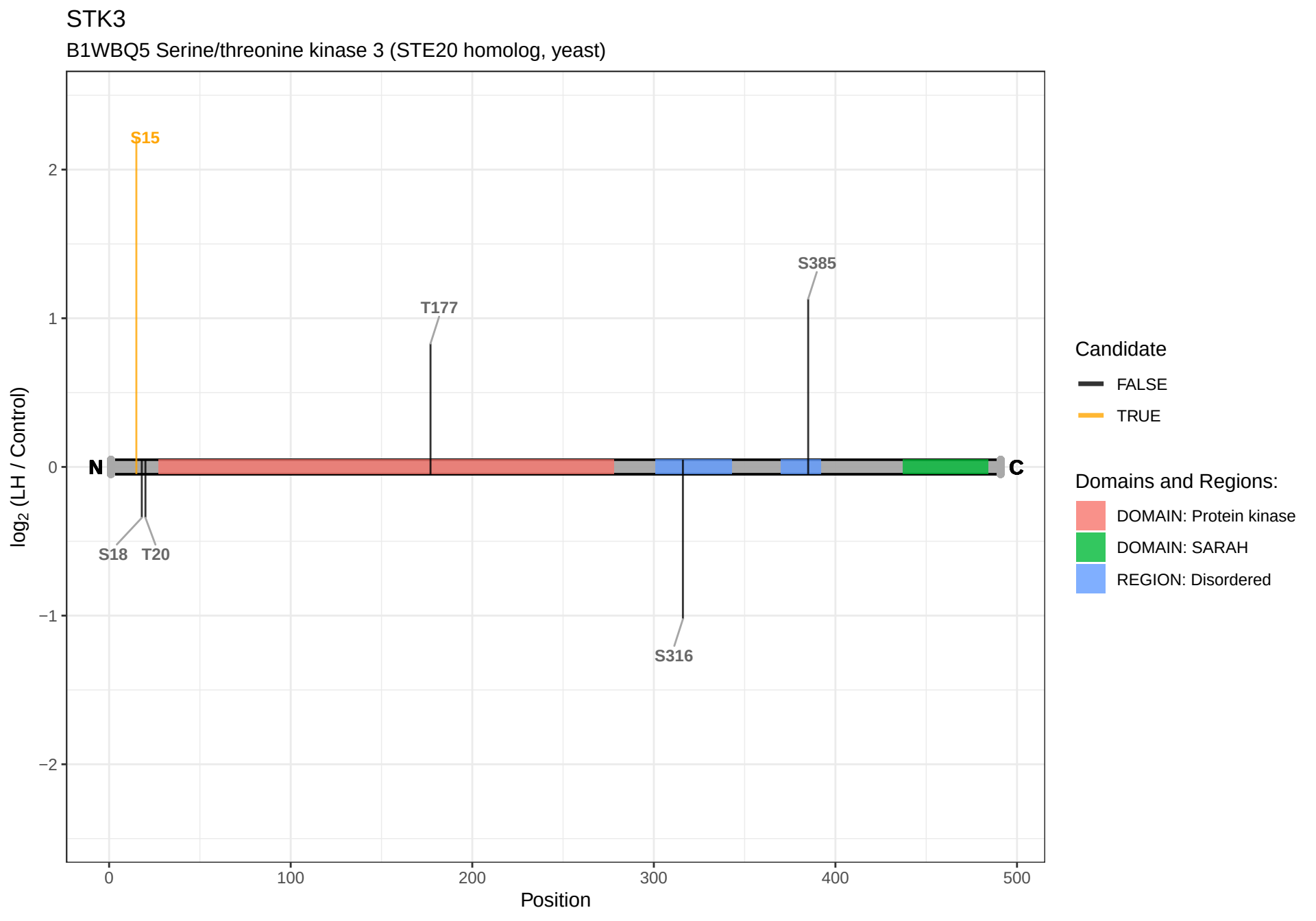
D4A9H6 Suppression of tumorigenicity 5

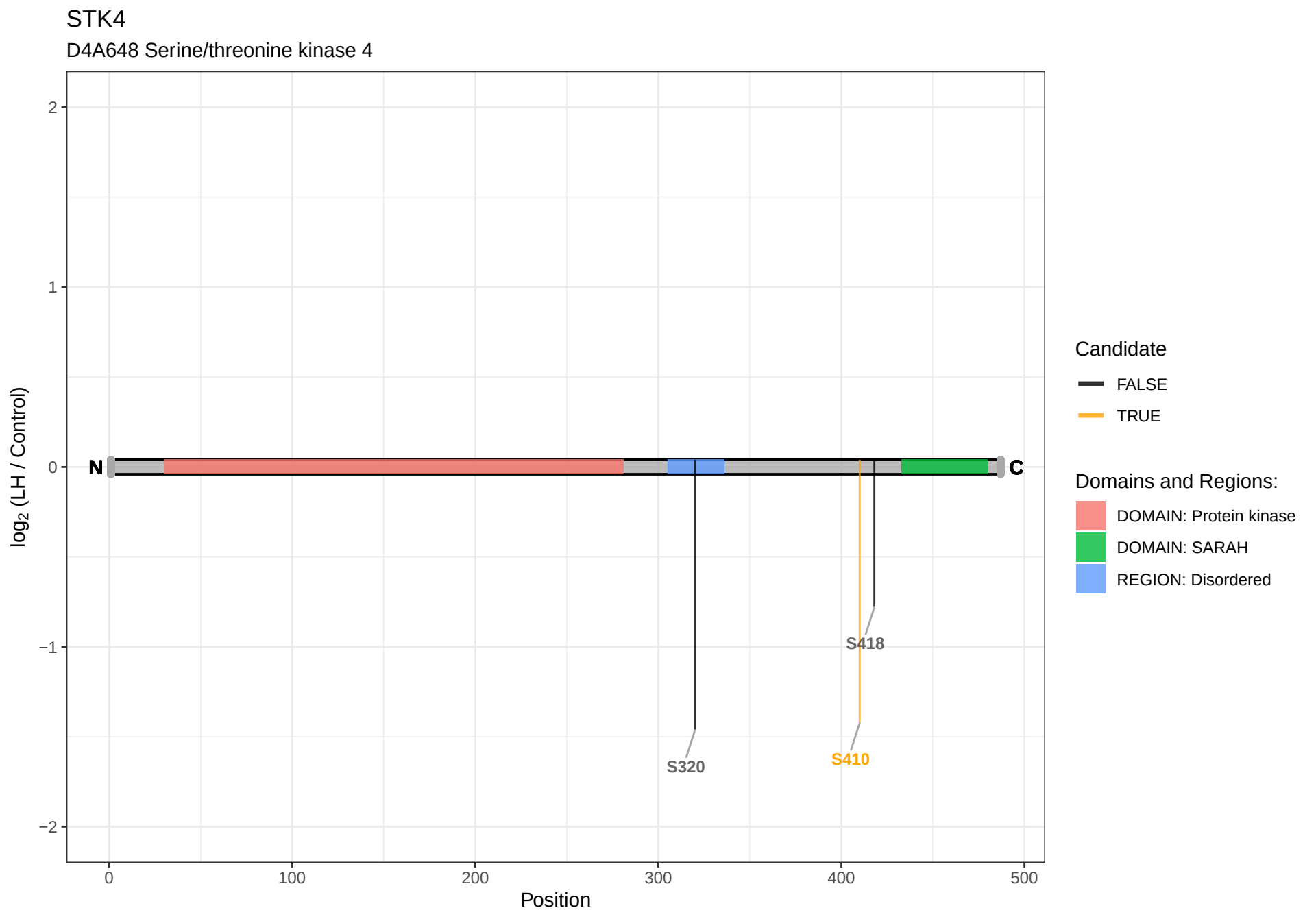


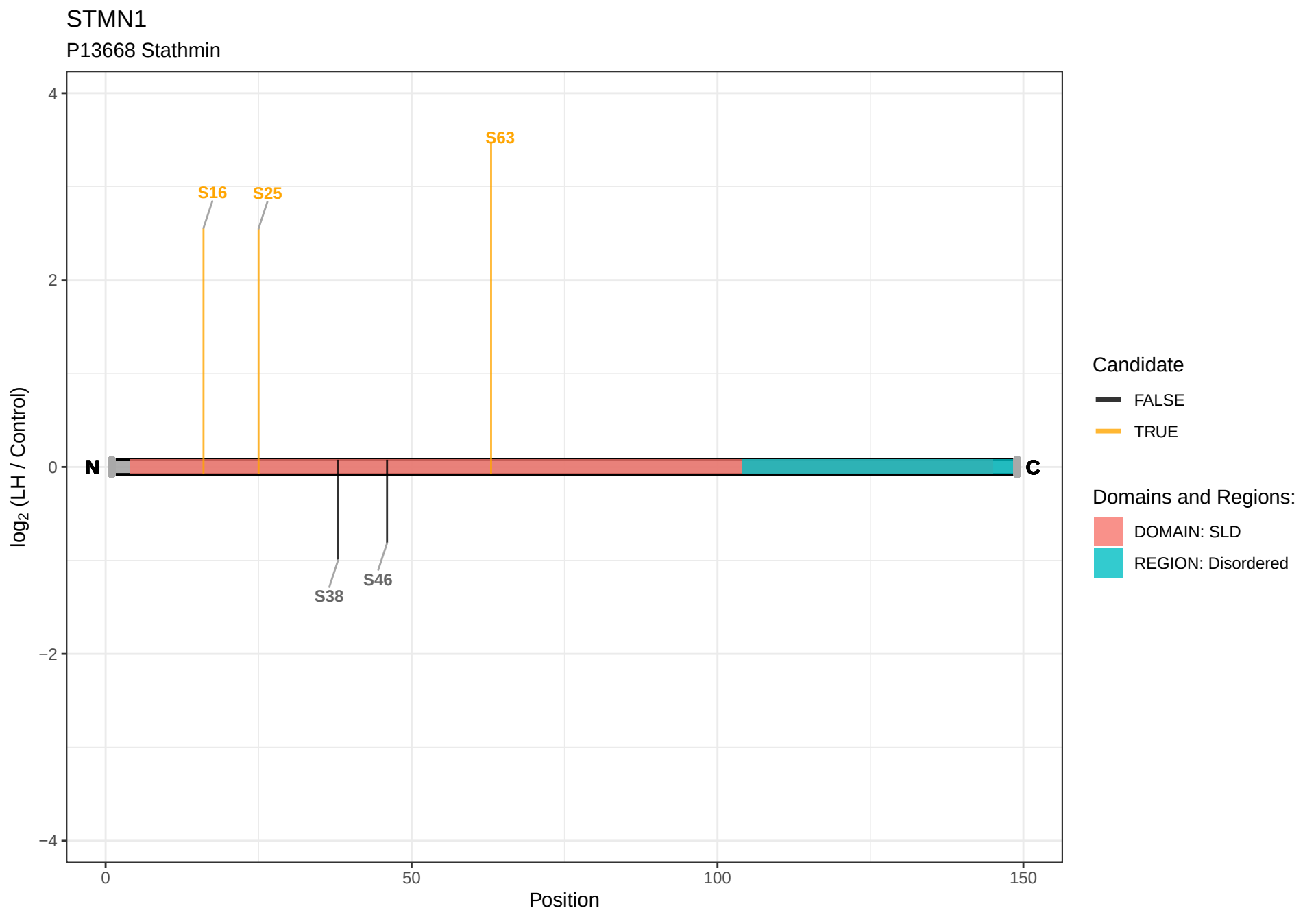

STAT1
F1M9D6 Signal transducer and activator of transcription
2
1
0
−1
−2
log2 (LH / Control)
S727
N
C
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: SH2

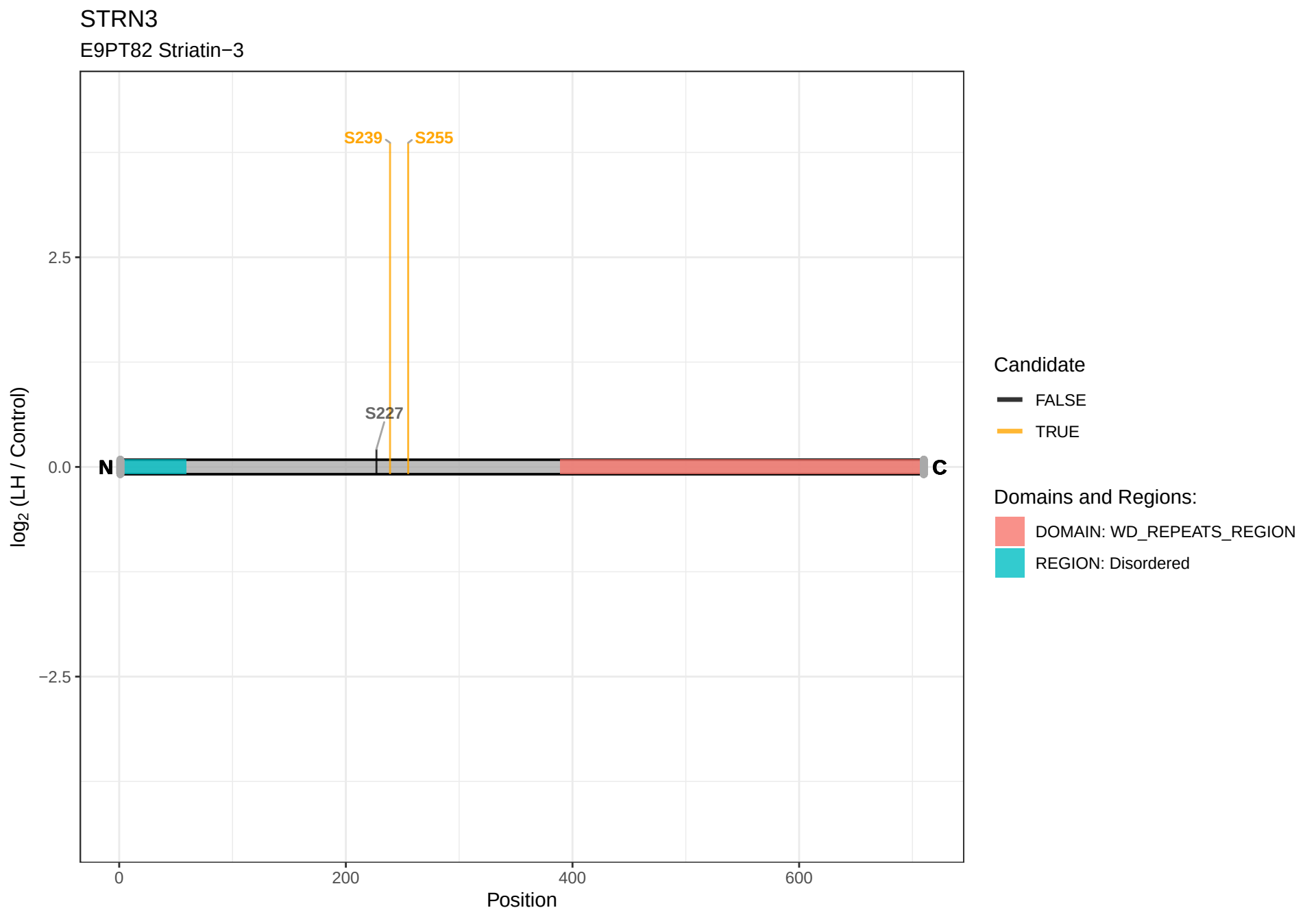

STIM1
P84903 Stromal interaction molecule 1
log2 (LH / Control)
2
0
−2
N
C
S257
S512
S519
S521
S575
S668
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: EF−hand
DOMAIN: SAM
REGION: Disordered
REGION: SOAR/CAD

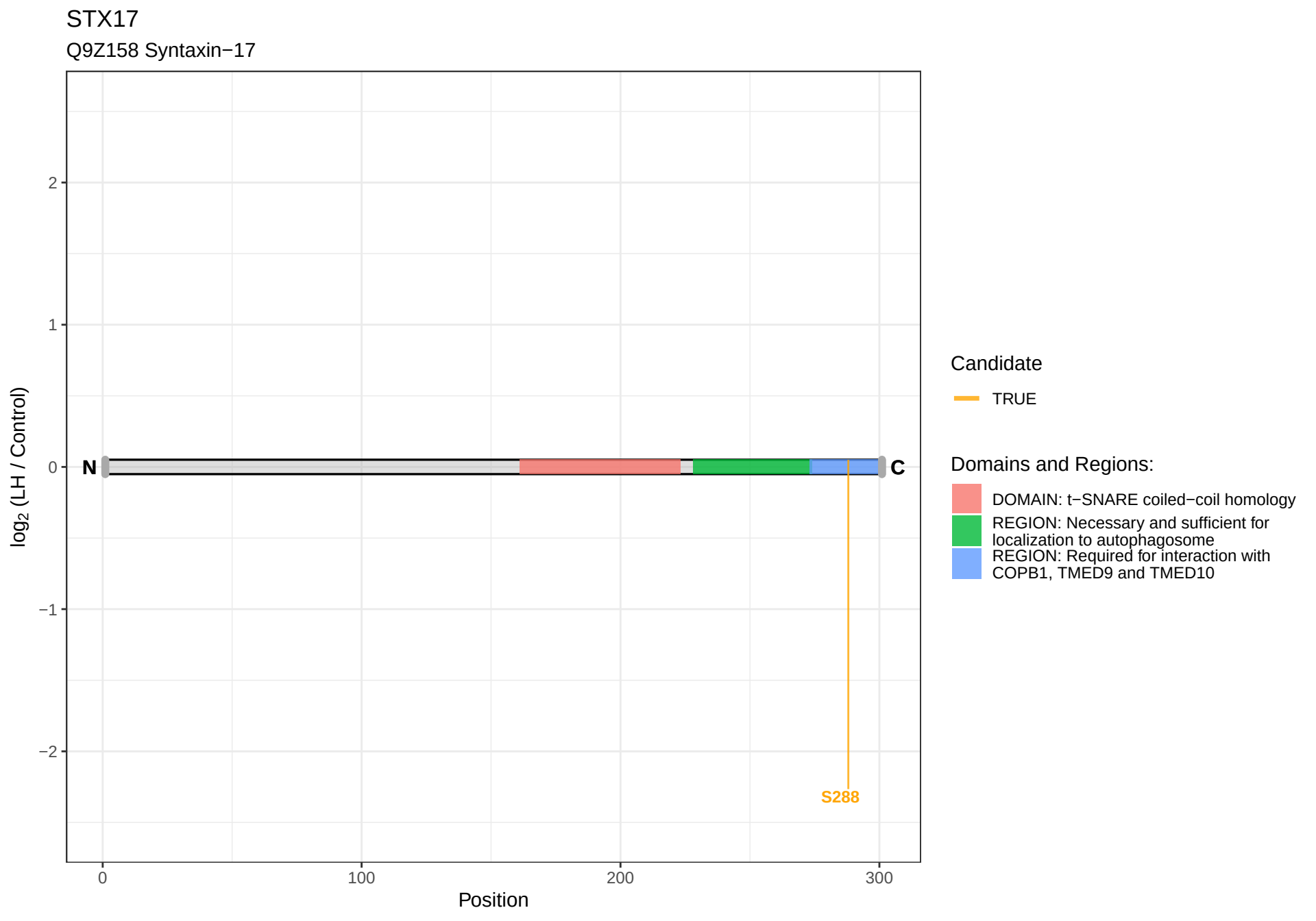

STIM2
D4A5X1 Stromal interaction molecule 2
S28
S623
S632
S606
S610
S261
S647
S628
S523
S637
N
C
2
0
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SAM
REGION: Disordered

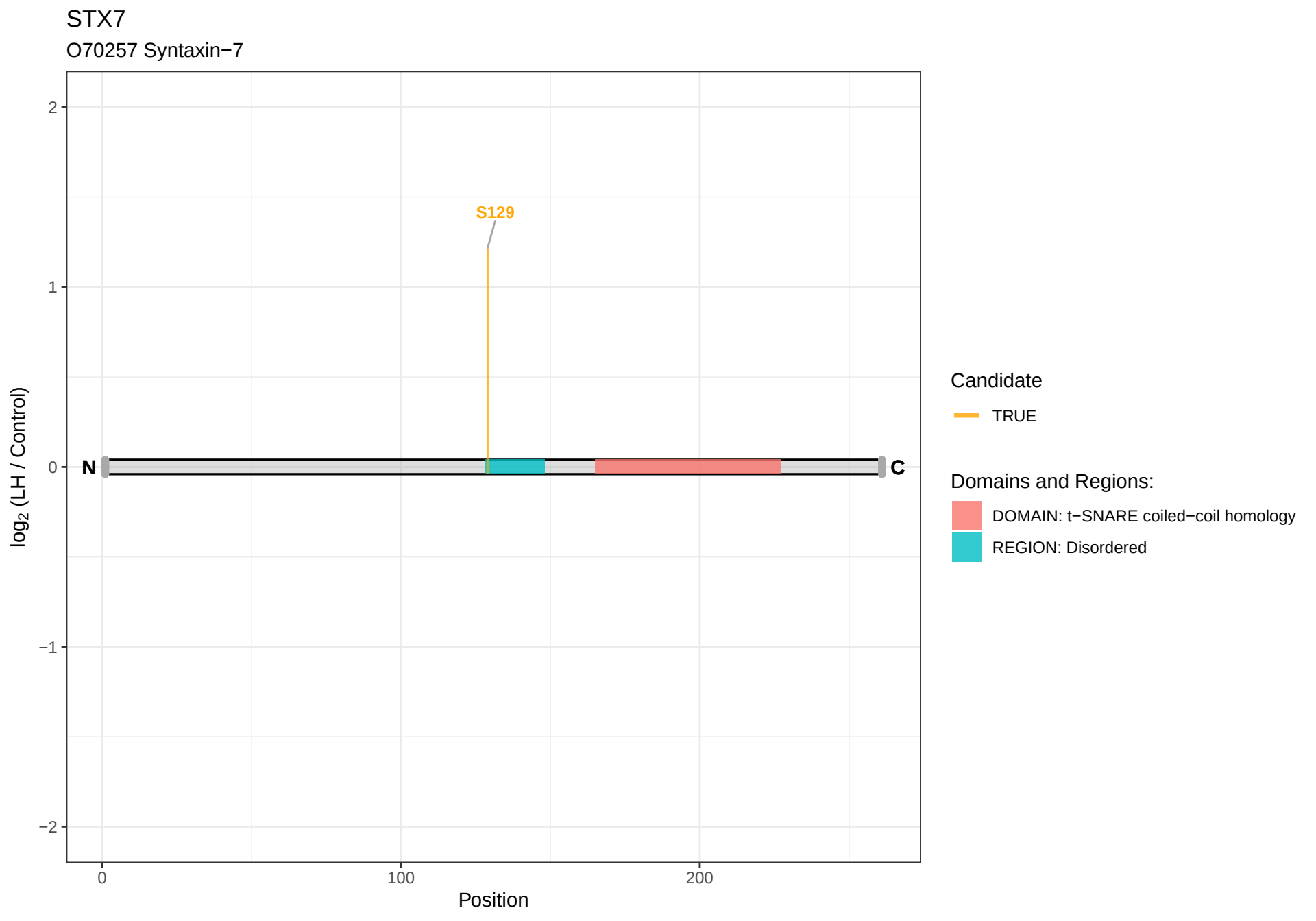

STK3
B1WBQ5 Serine/threonine kinase 3 (STE20 homolog, yeast)
S15
T177
S385
S316
S18
T20
N
C
log2 (LH / Control)
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
DOMAIN: SARAH
REGION: Disordered

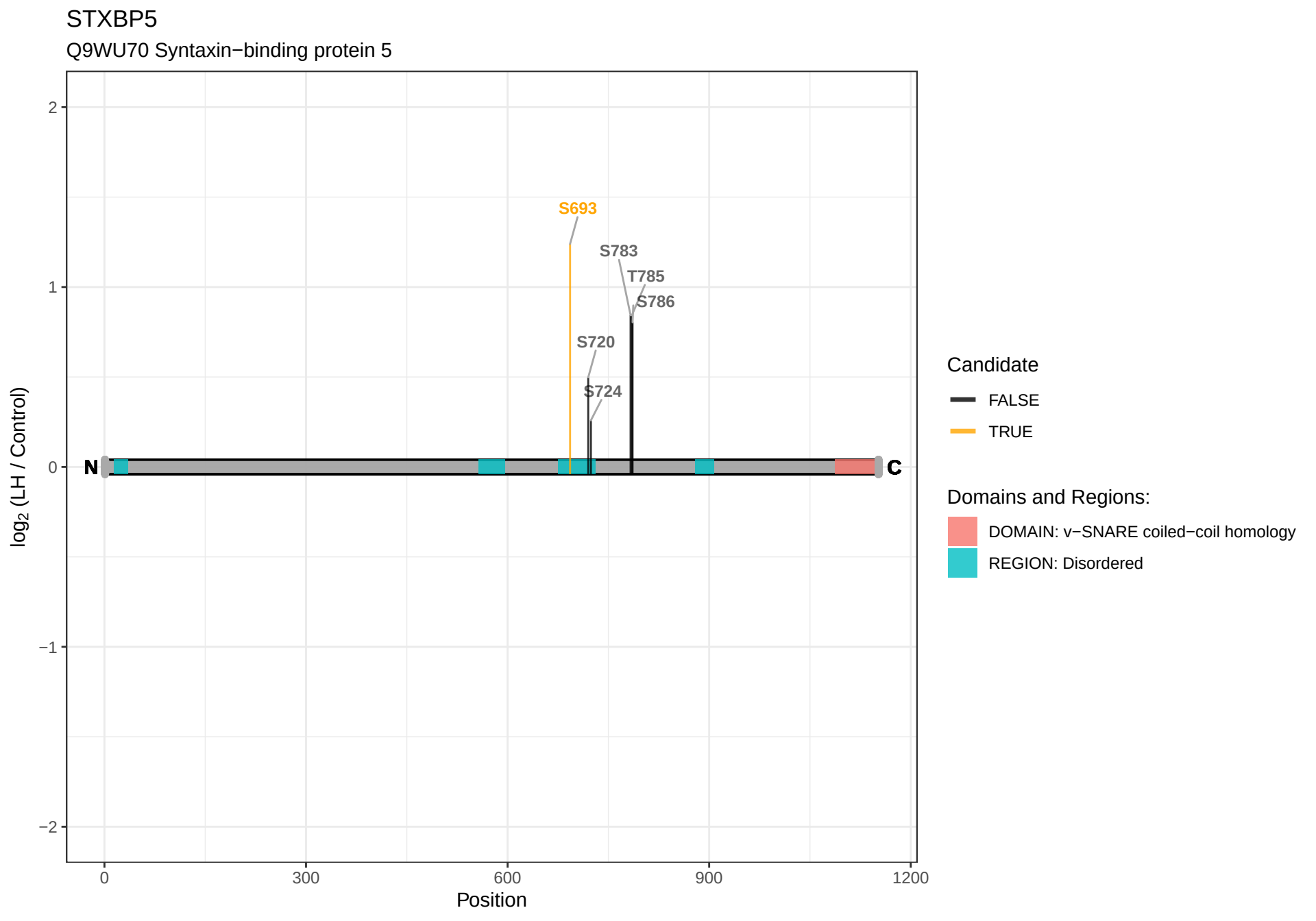

STK4
D4A648 Serine/threonine kinase 4
log2 (LH / Control)
2
1
0
−1
−2
N
C
S320
S418
S410
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
DOMAIN: SARAH
REGION: Disordered

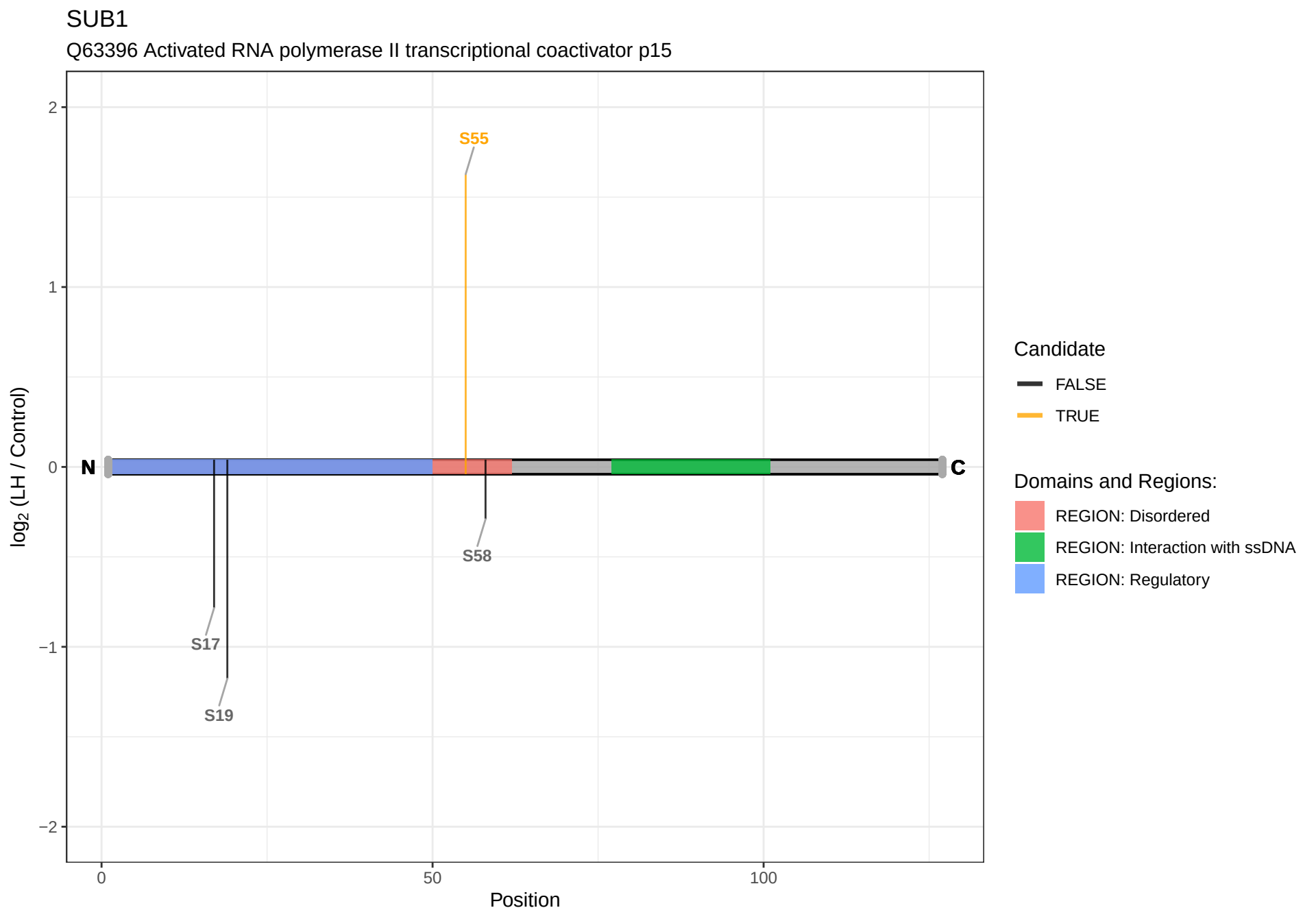

STMN1
P13668 Stathmin
S16
S25
S63
S38
S46
N
C
log2 (LH / Control)
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SLD
REGION: Disordered

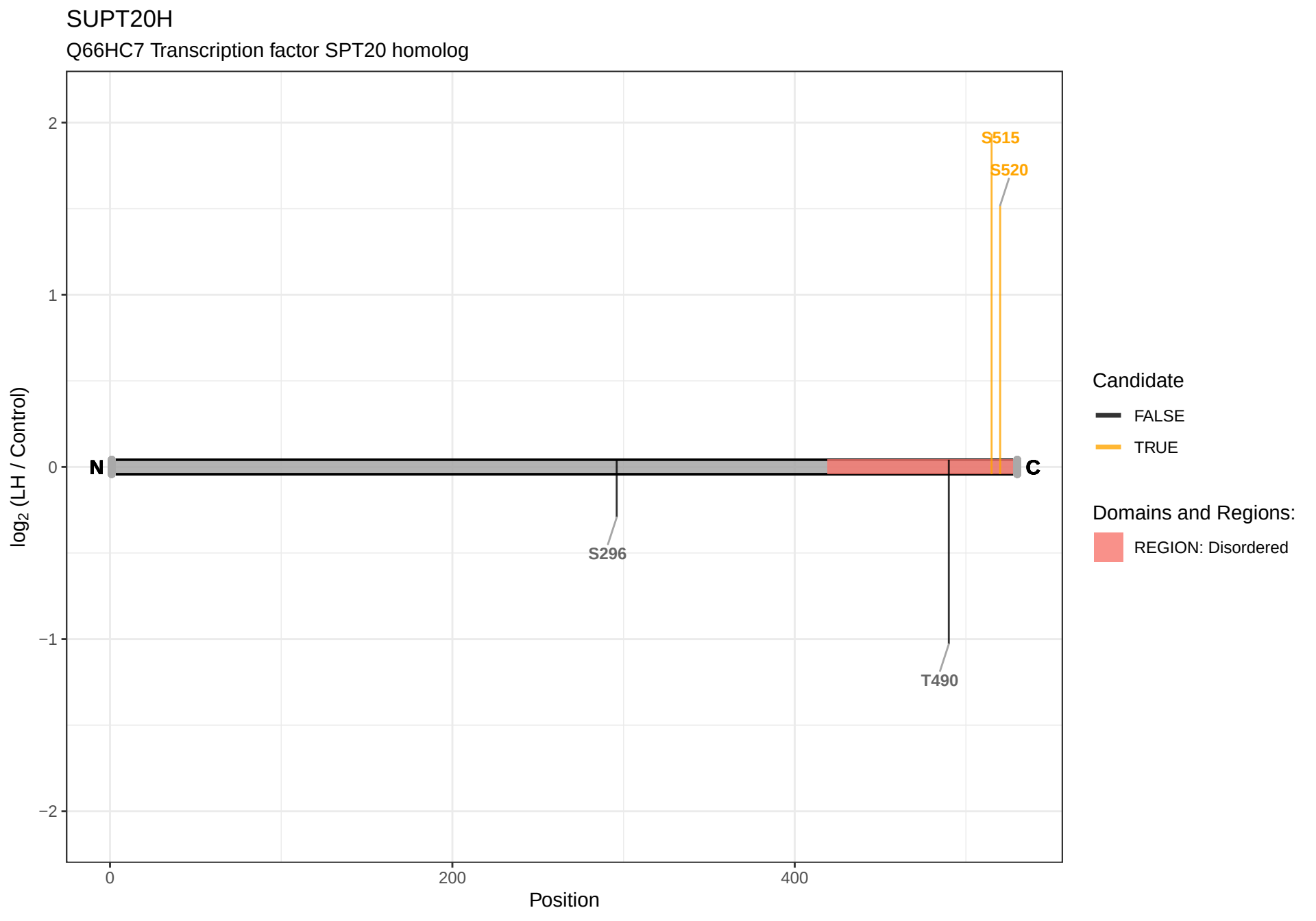

STRN3
E9PT82 Striatin−3
S239
S255
S227
N
C
2.5
0.0
−2.5
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WD_REPEATS_REGION
REGION: Disordered

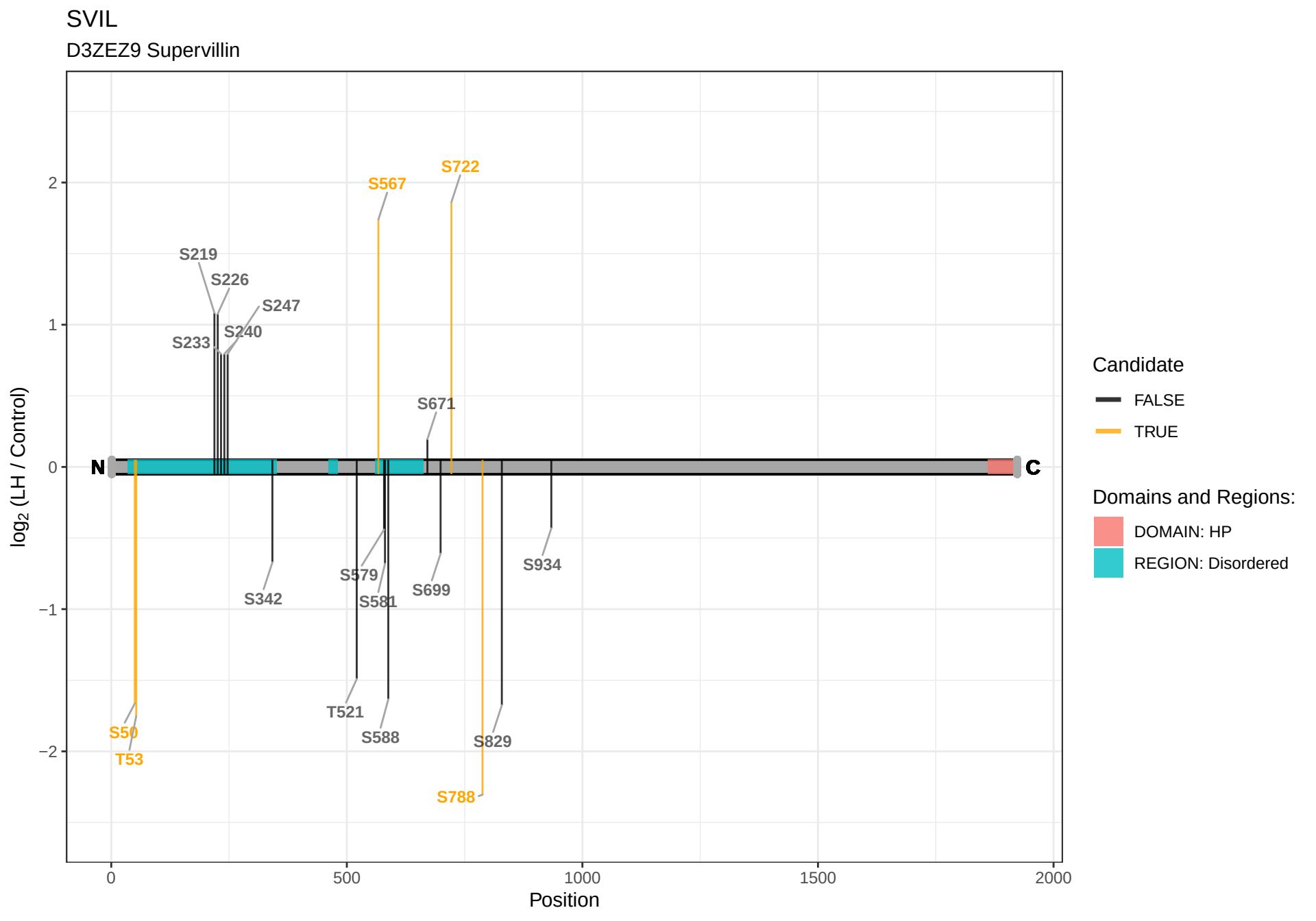

STX17
Q9Z158 Syntaxin−17
log2 (LH / Control)
2
1
0
−1
−2
N
C
S288
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: t−SNARE coiled−coil homology
REGION: Necessary and sufficient for localization to autophagosome
REGION: Required for interaction with COPB1, TMED9 and TMED10

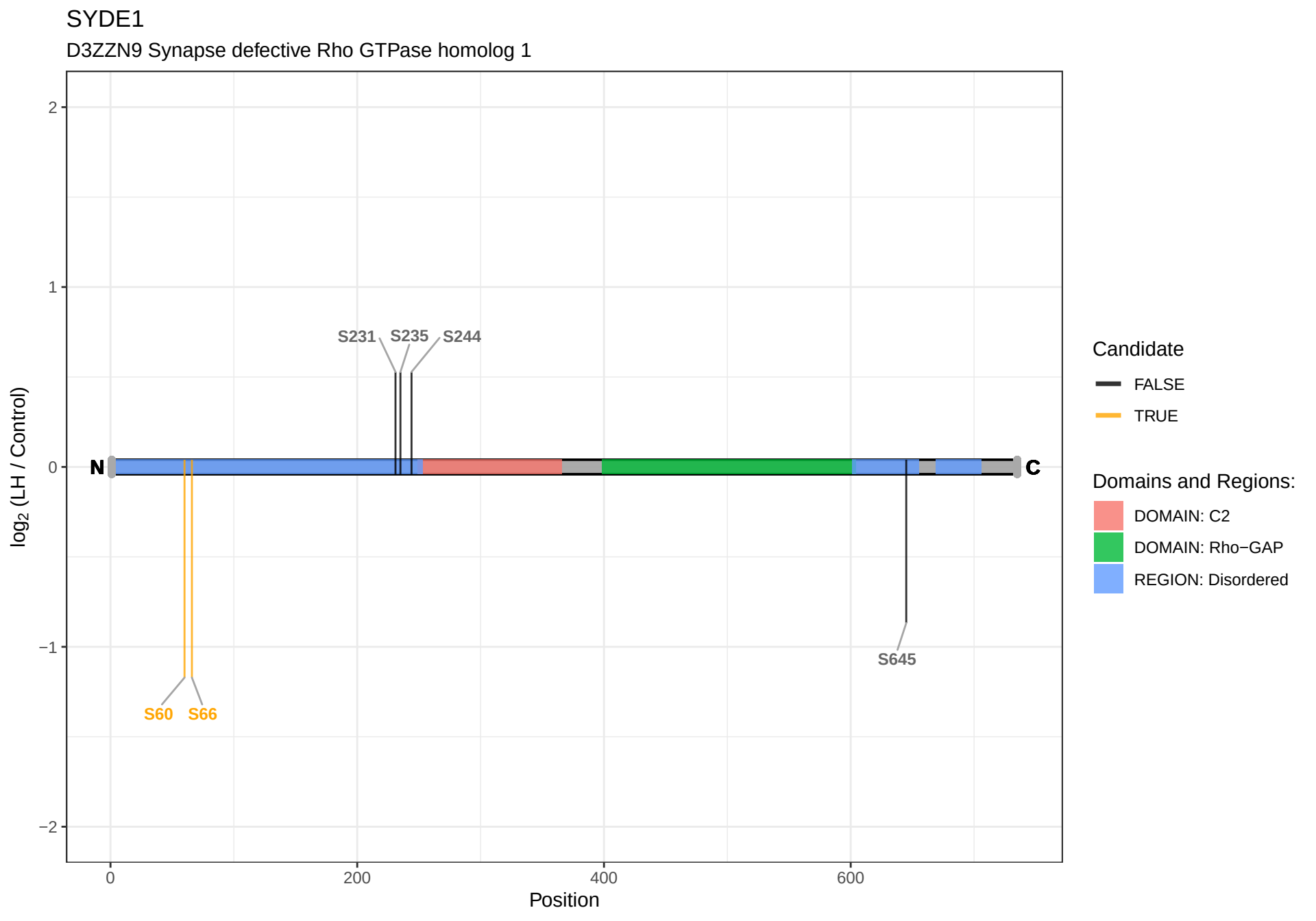

STX7
O70257 Syntaxin−7
S129
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
100
200
Candidate
TRUE
Domains and Regions:
DOMAIN: t−SNARE coiled−coil homology
REGION: Disordered

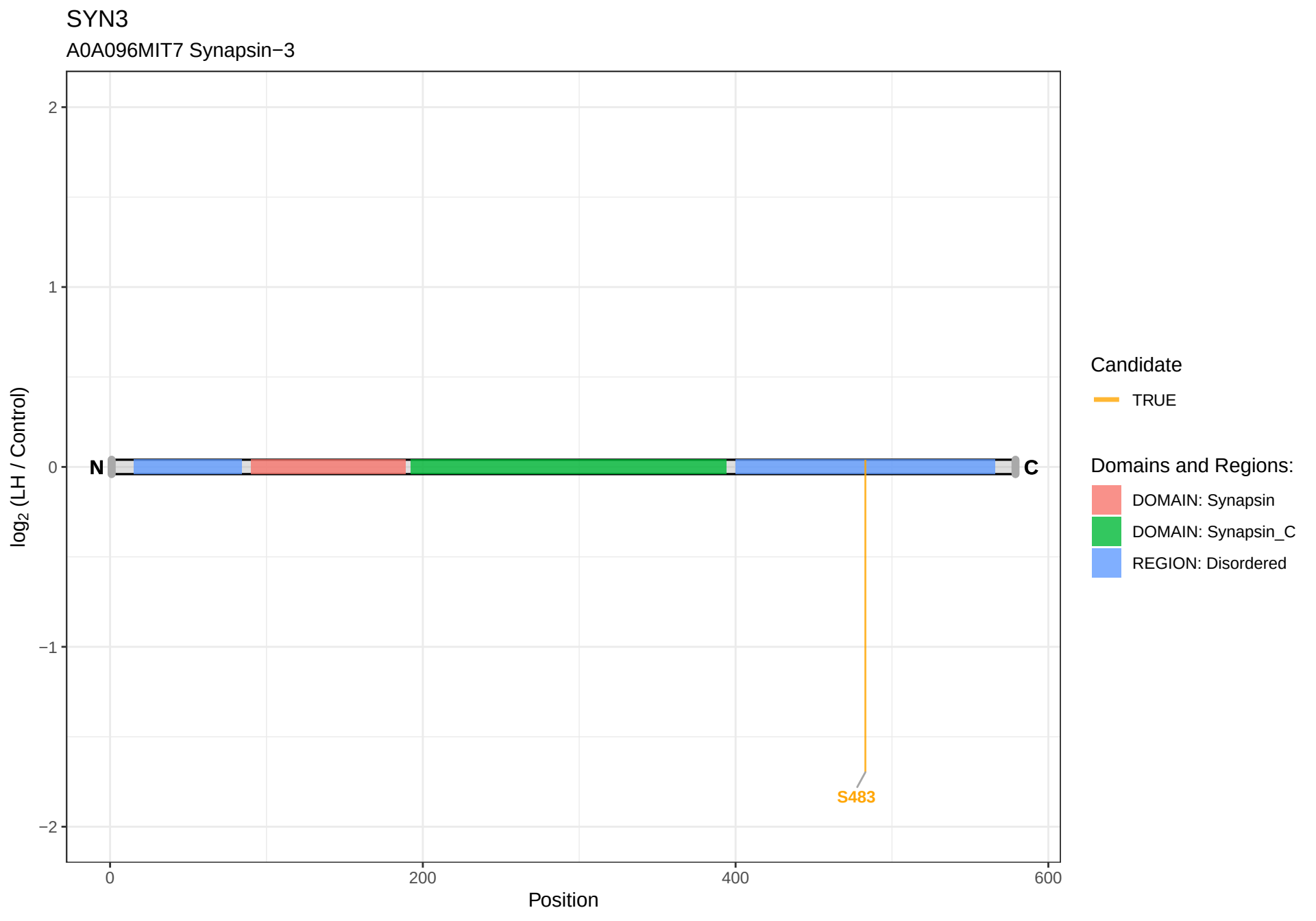

STXBP5
Q9WU70 Syntaxin−binding protein 5
S693
S783
T785
S786
S720
S724
N
C
2
1
0
−1
−2
0
300
600
900
1200
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: v−SNARE coiled−coil homology
REGION: Disordered

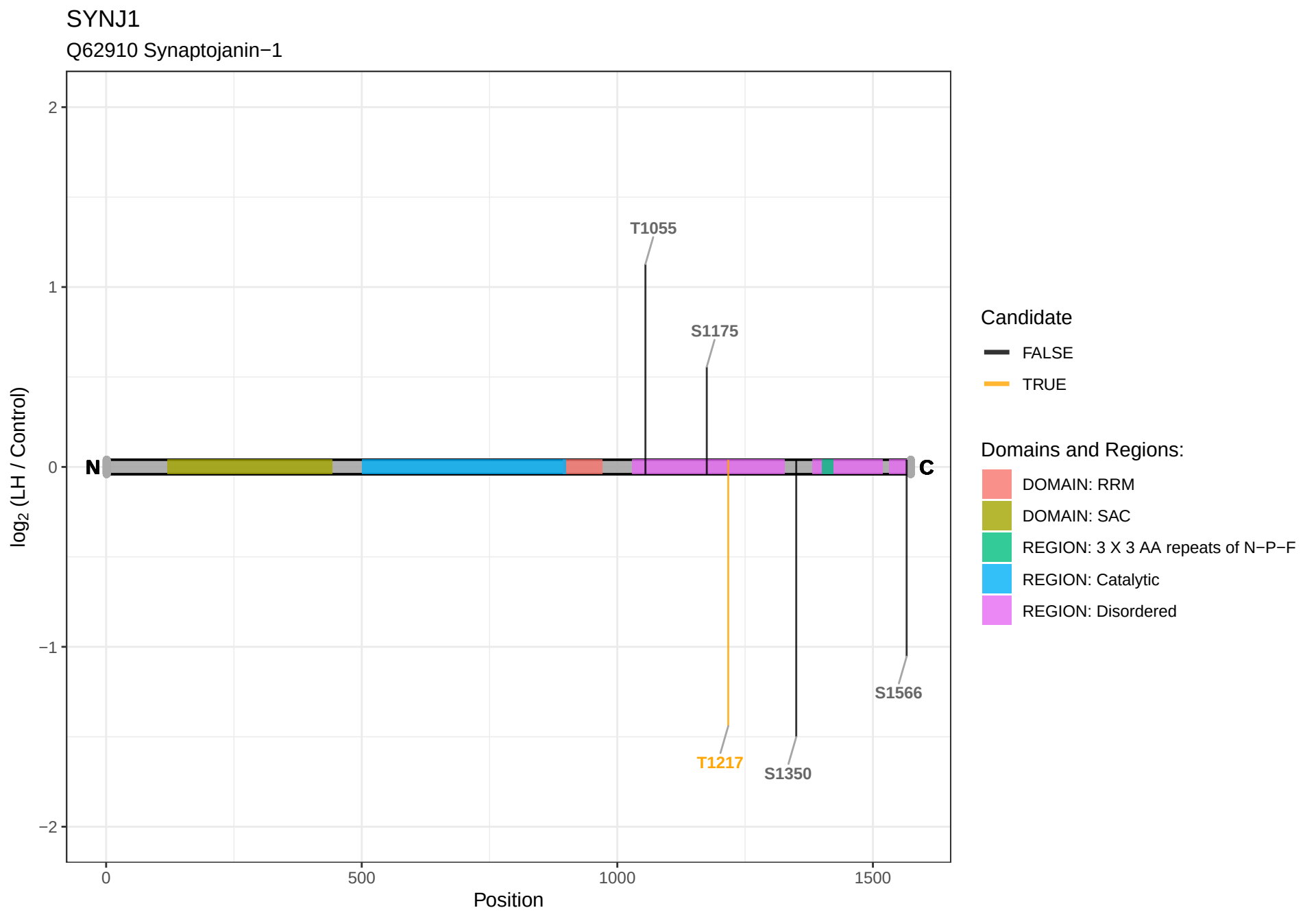

SUB1
Q63396 Activated RNA polymerase II transcriptional coactivator p15
log2 (LH / Control)
2
1
0
−1
−2
0
50
100
Position
N
C
S55
S58
S17
S19
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Interaction with ssDNA
REGION: Regulatory

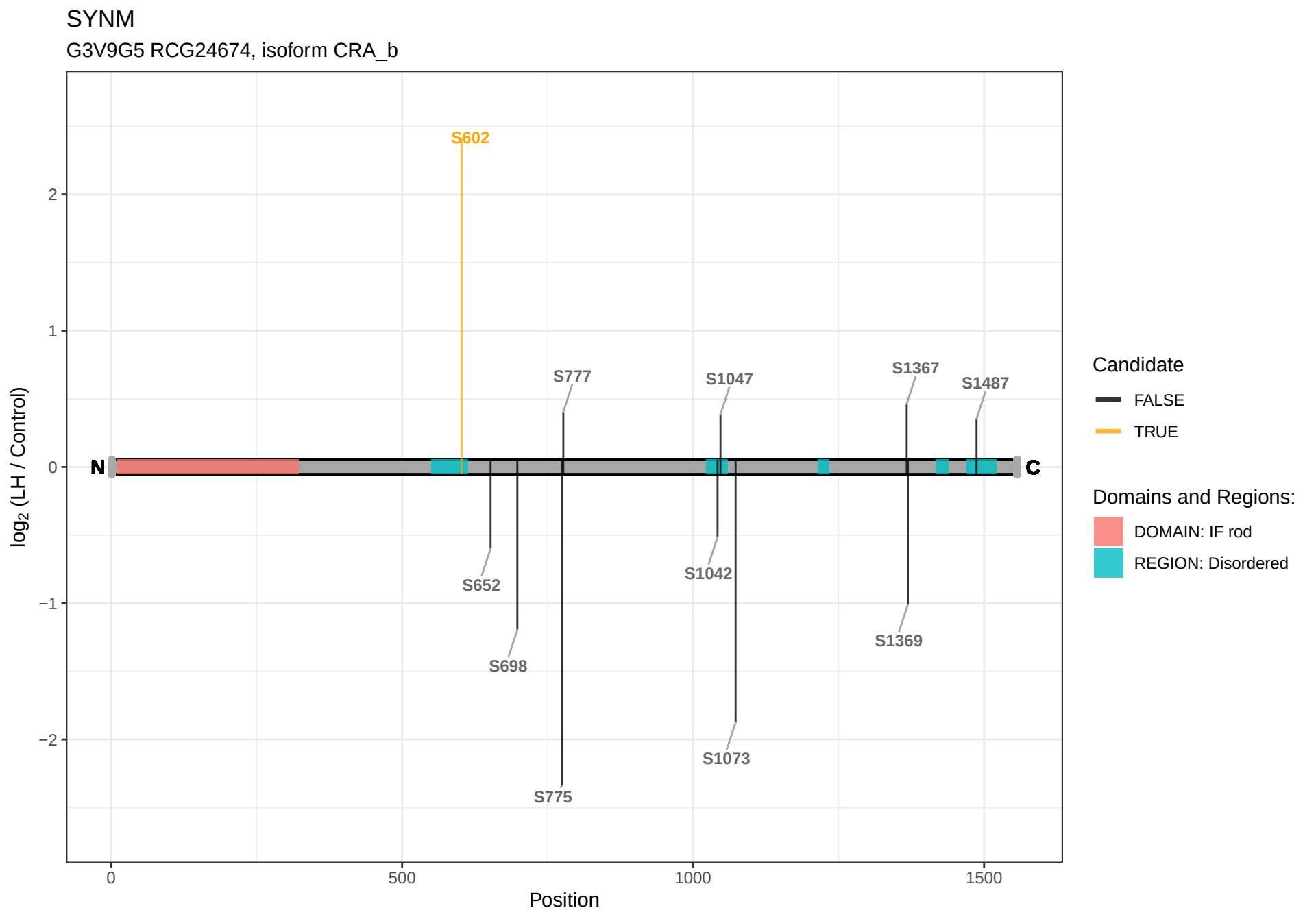

SUPT20H
Q66HC7 Transcription factor SPT20 homolog
2
1
0
−1
−2
log2 (LH / Control)
N
C
S515
S520
S296
T490
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

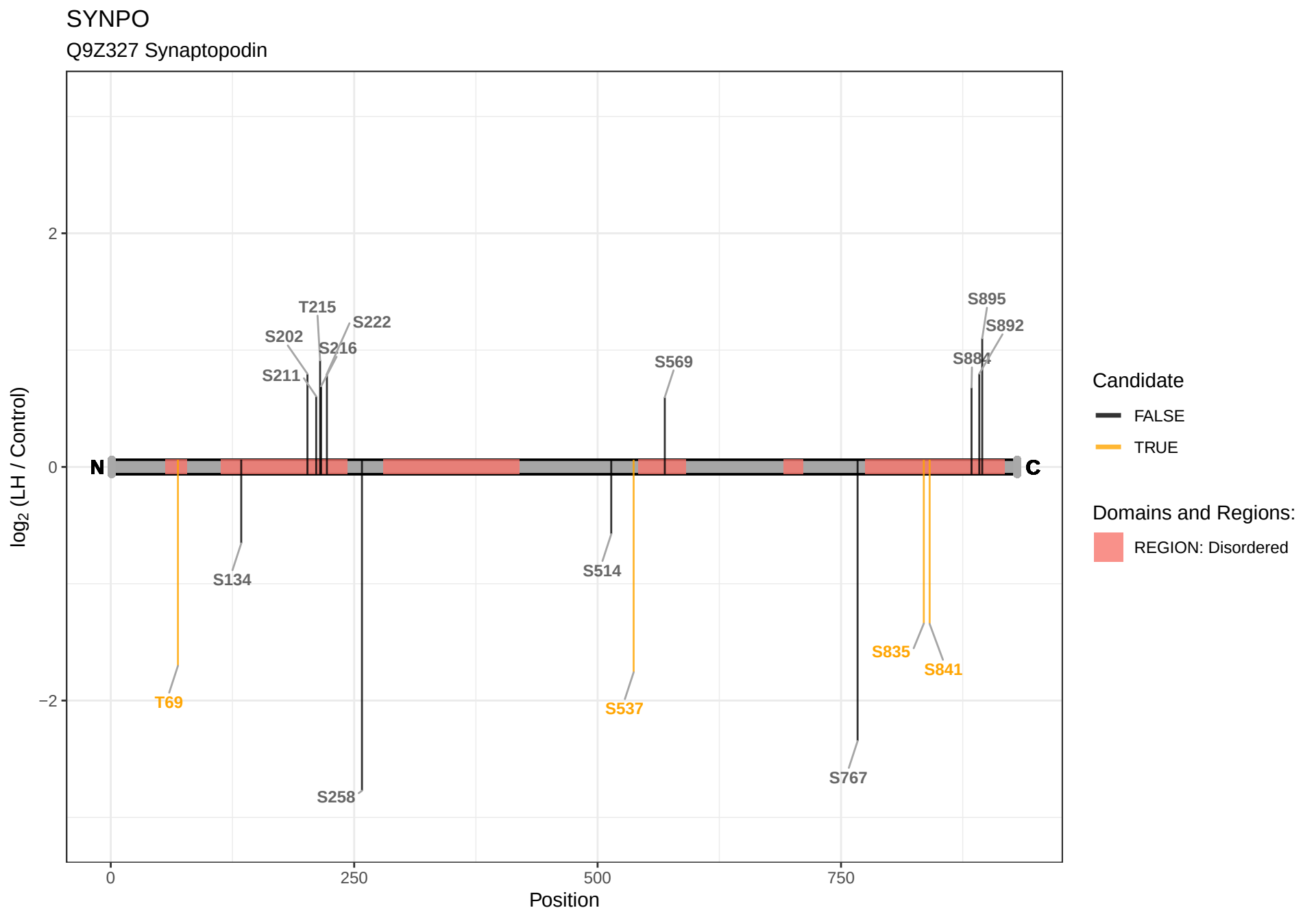

SVIL
D3ZEZ9 Supervillin
log2 (LH / Control)
Position
0
500
1000
1500
2000
2
1
0
−1
−2
N
C
S567
S722
S219
S226
S247
S233
S240
S671
S342
S579
S581
S699
S934
T521
S588
S829
S50
T53
S788
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: HP
REGION: Disordered

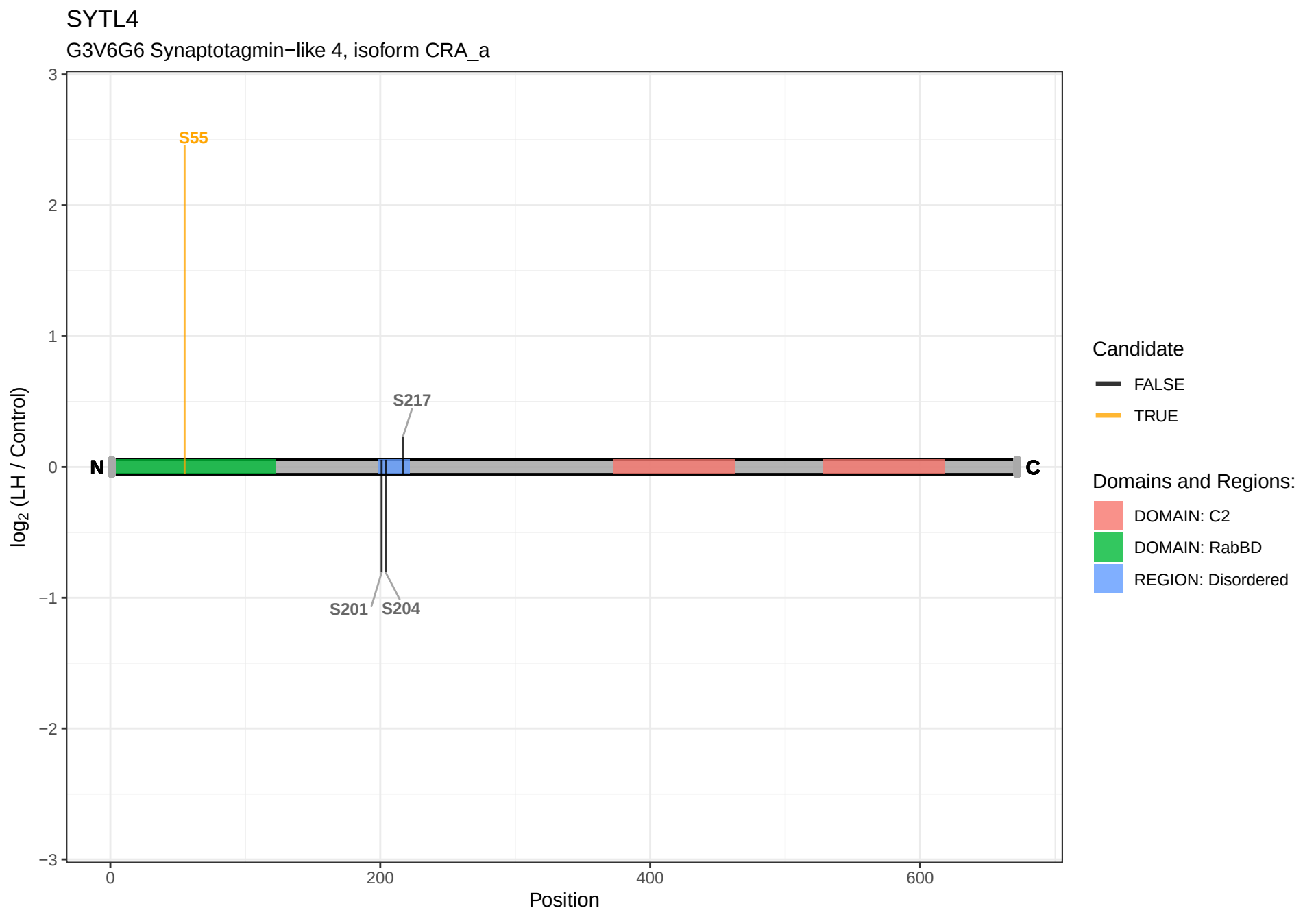

SYDE1
D3ZZN9 Synapse defective Rho GTPase homolog 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S231
S235
S244
S60
S66
S645
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2
DOMAIN: Rho−GAP
REGION: Disordered

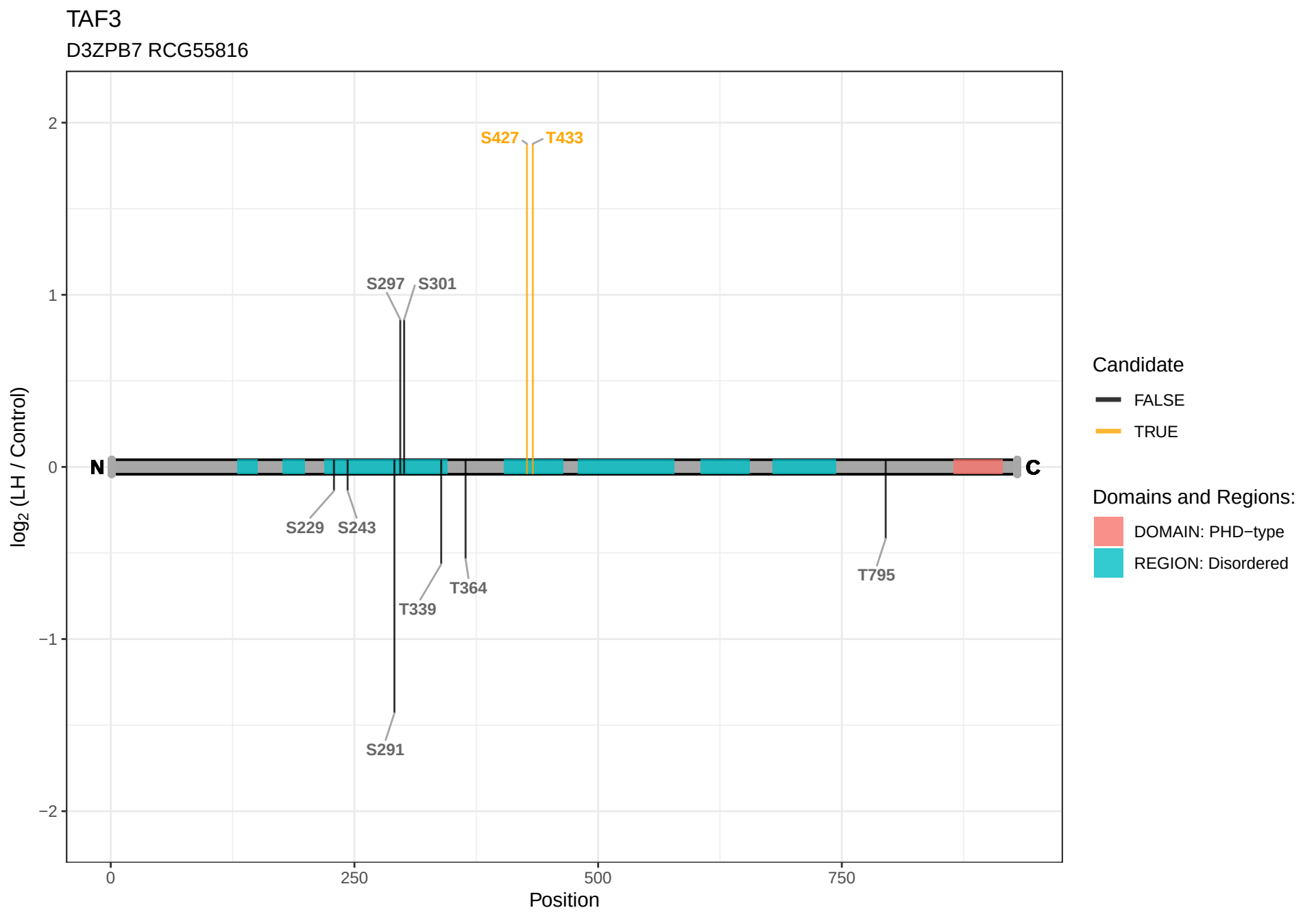

SYN3
A0A096MIT7 Synapsin−3
2
1
0
−1
−2
log2 (LH / Control)
N
C
S483
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Synapsin
DOMAIN: Synapsin_C
REGION: Disordered

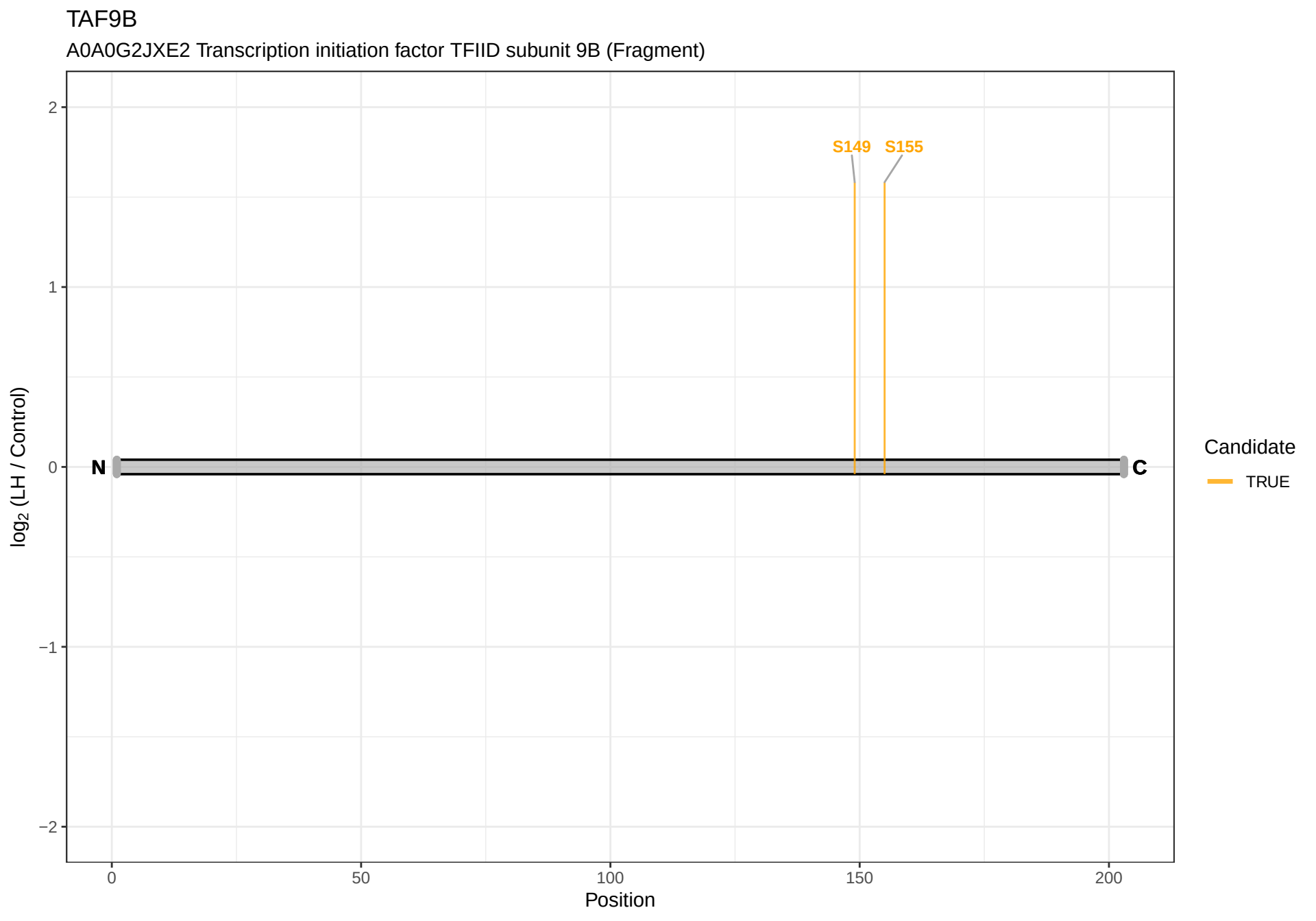

SYNJ1
Q62910 Synaptojanin−1
2
1
0
−1
−2
log2 (LH / Control)
N
C
T1055
S1175
T1217
S1350
S1566
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RRM
DOMAIN: SAC
REGION: 3 X 3 AA repeats of N−P−F
REGION: Catalytic
REGION: Disordered

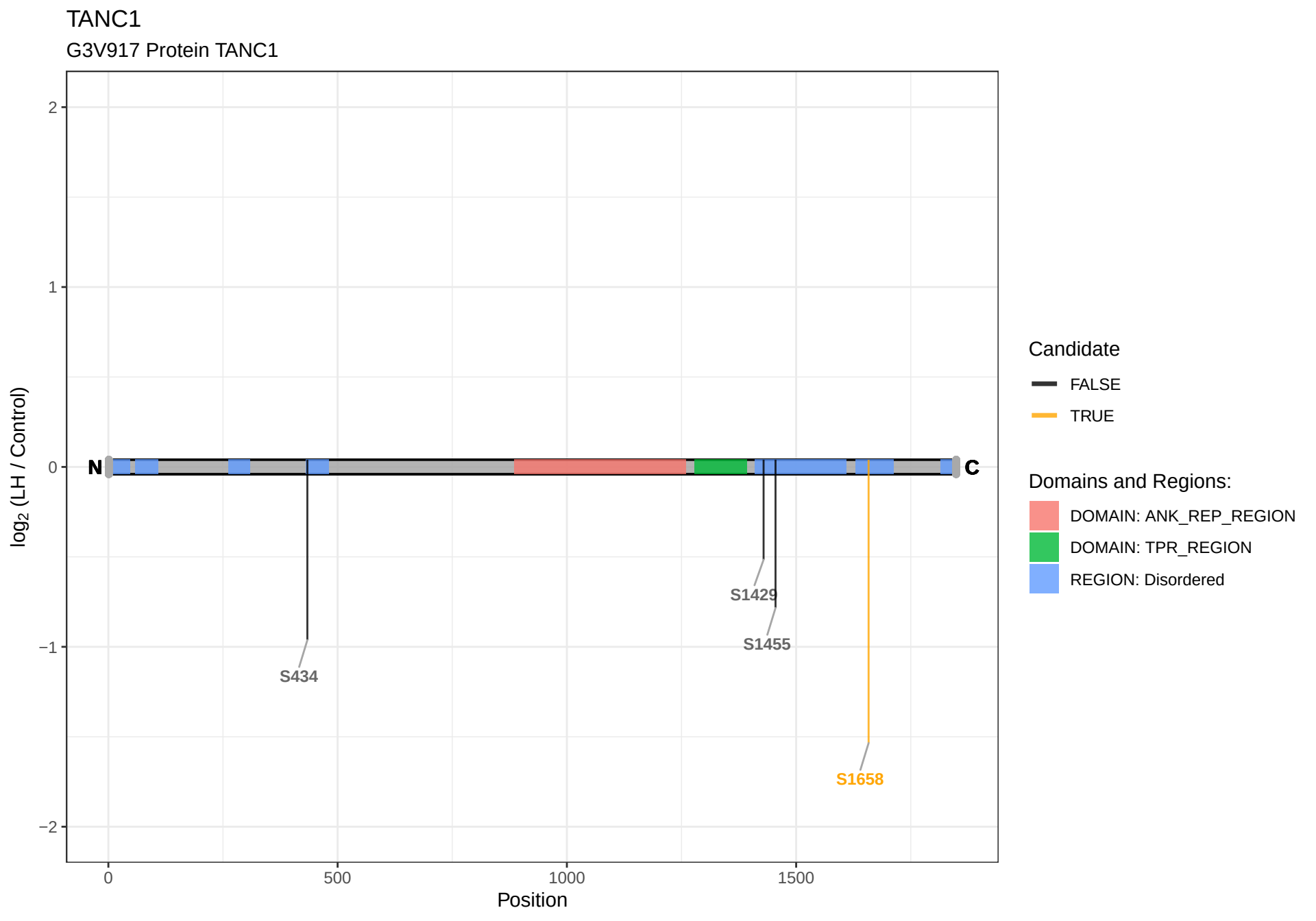

SYNM
G3V9G5 RCG24674, isoform CRA_b
S602
S777
S1047
S1367
S1487
S652
S698
S775
S1042
S1073
S1369
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: IF rod
REGION: Disordered

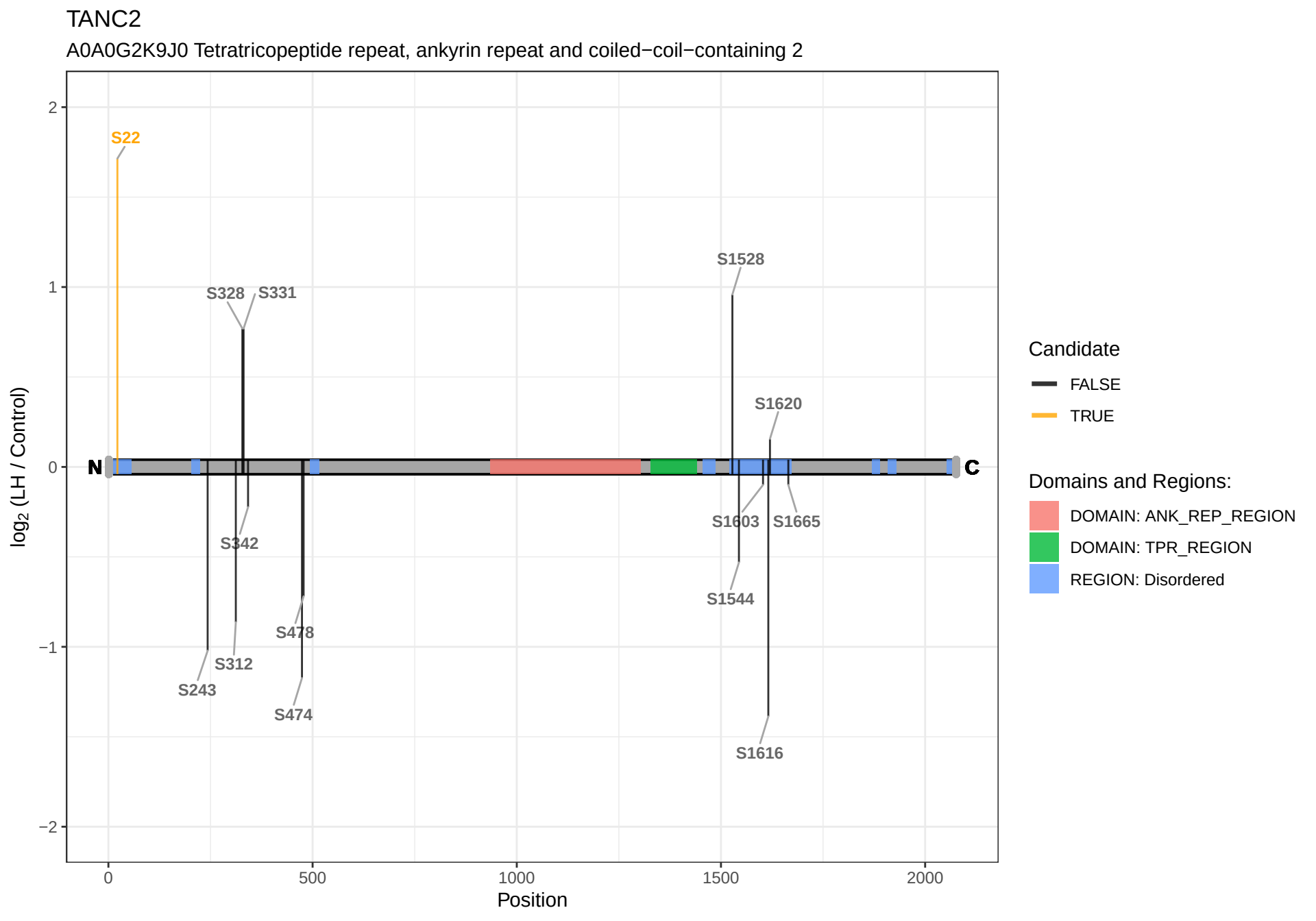

SYNPO
Q9Z327 Synaptopodin
log2 (LH / Control)
2
0
−2
N
C
T215
S222
S202
S216
S211
S569
S895
S892
S884
S134
S514
T69
S537
S835
S841
S258
S767
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

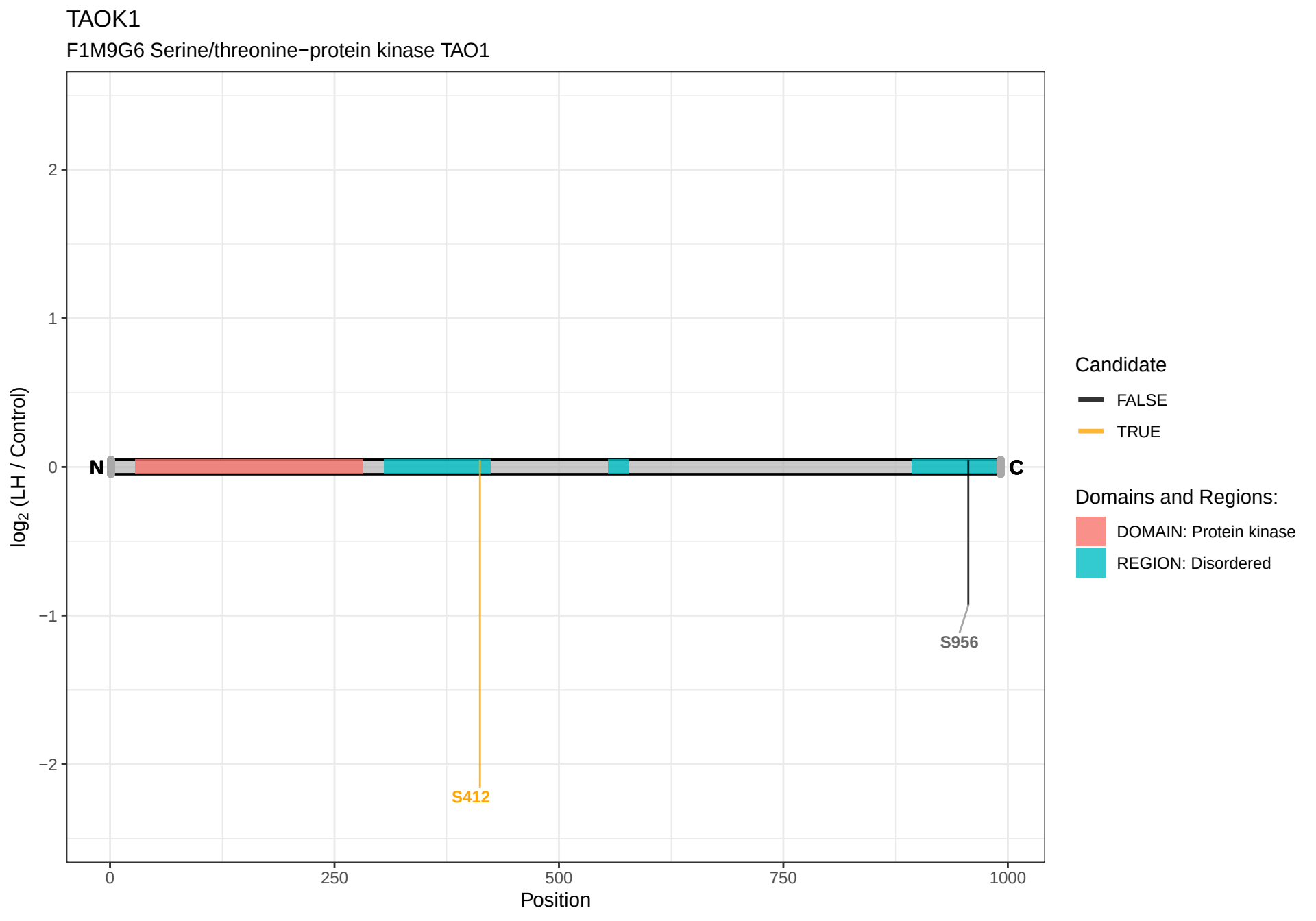

SYTL4
G3V6G6 Synaptotagmin−like 4, isoform CRA_a
S55
S217
S201
S204
N
C
log2 (LH / Control)
Position
3
2
1
0
−1
−2
−3
0
200
400
600
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2
DOMAIN: RabBD
REGION: Disordered

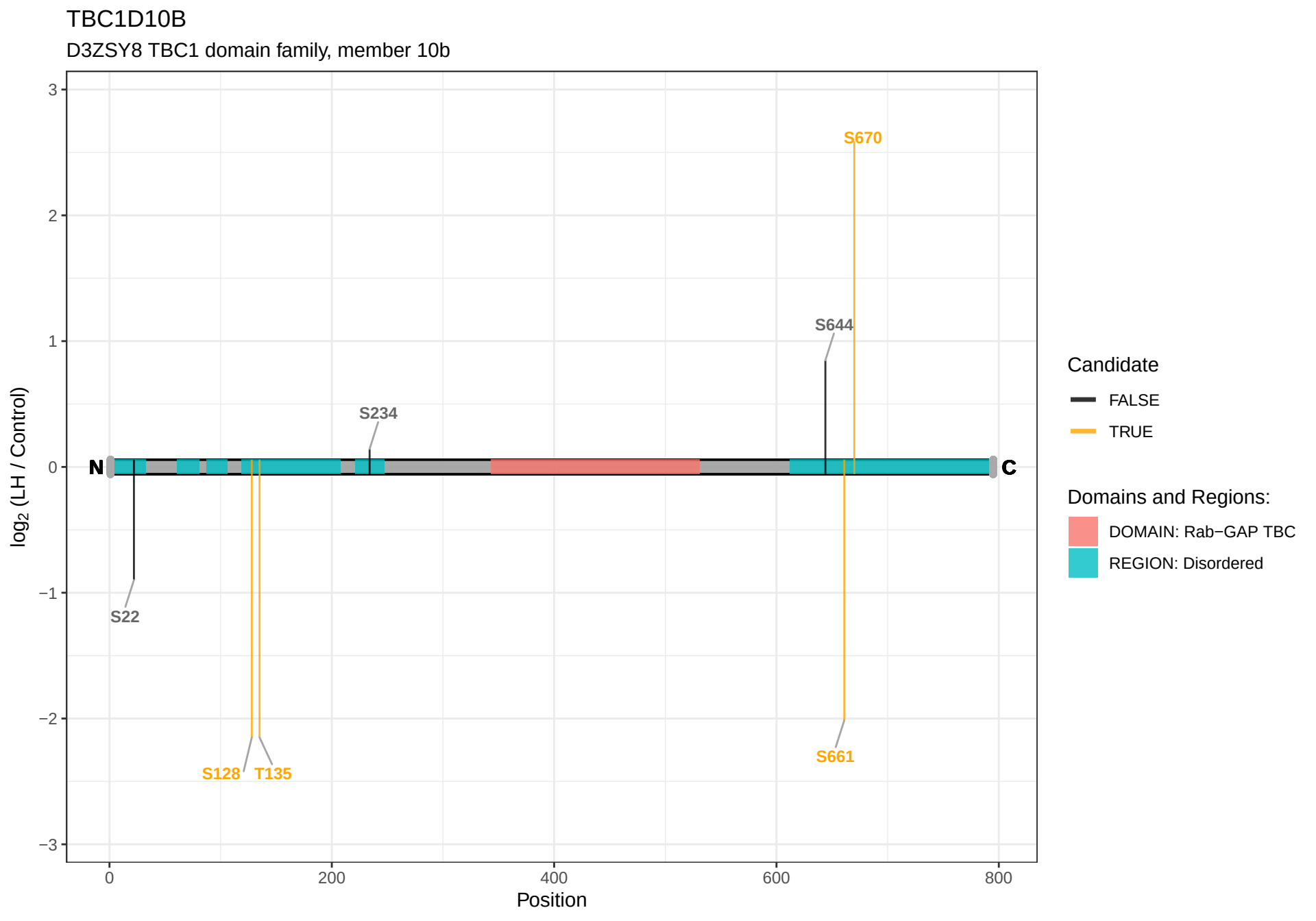

TAF3
D3ZPB7 RCG55816
S427
T433
S297
S301
S229
S243
T339
T364
T795
S291
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PHD−type
REGION: Disordered

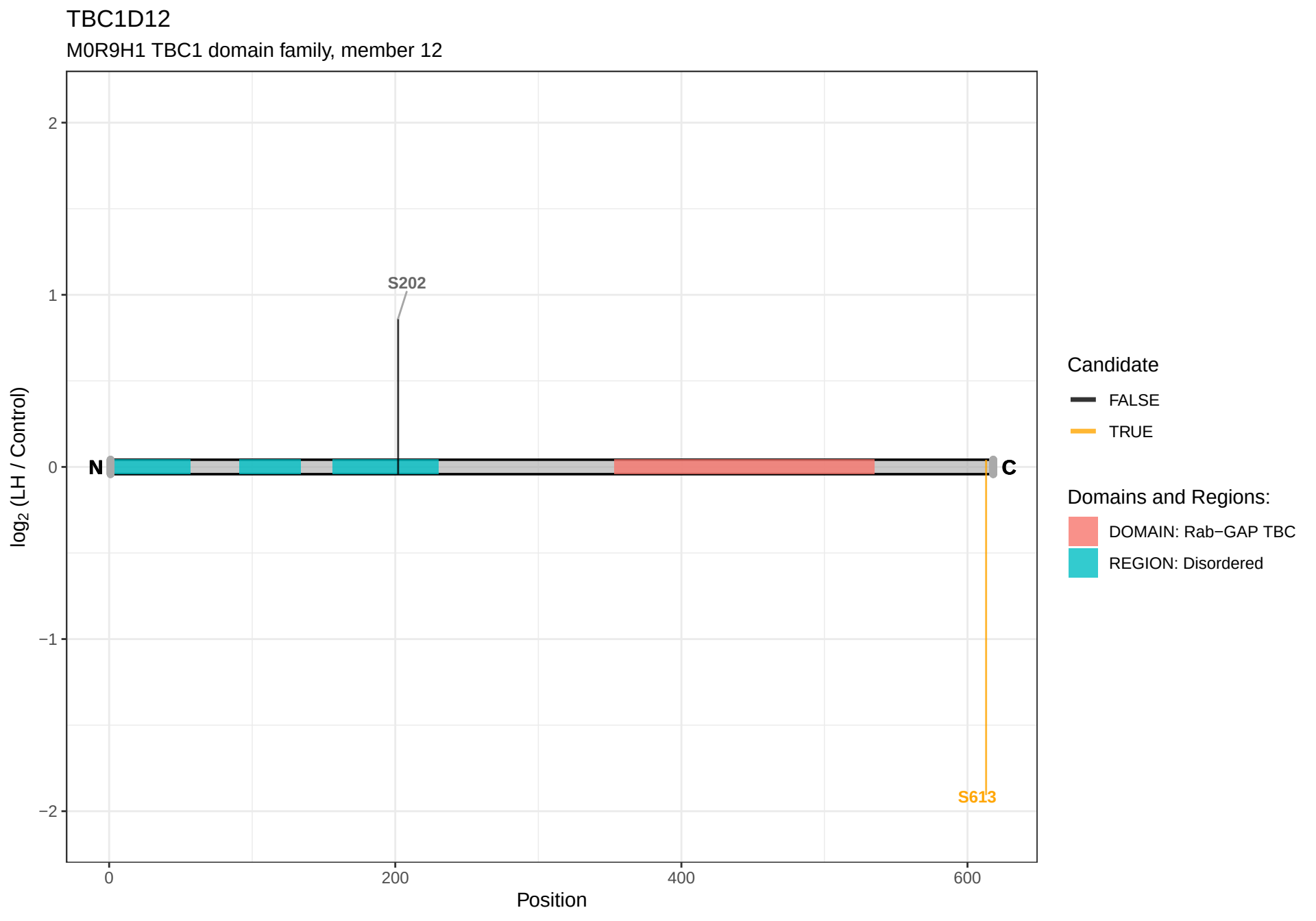

TAF9B
A0A0G2JXE2 Transcription initiation factor TFIID subunit 9B (Fragment)
S149
S155
N
C
log2 (LH / Control)
Position
Candidate
TRUE
2
1
0
−1
−2
0
50
100
150
200

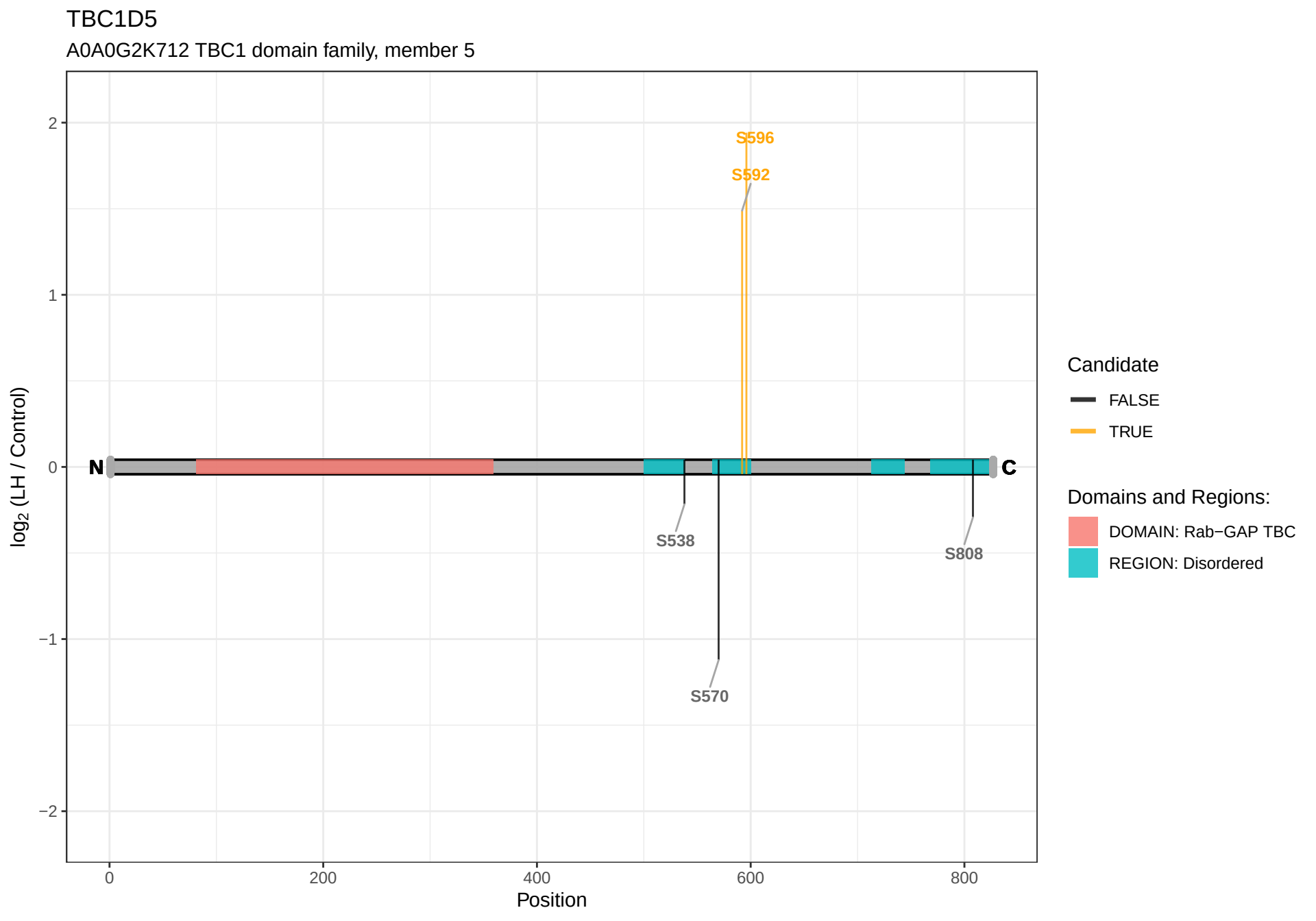

TANC1
G3V917 Protein TANC1
2
1
0
−1
−2
log2 (LH / Control)
N
C
S434
S1429
S1455
S1658
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ANK_REP_REGION
DOMAIN: TPR_REGION
REGION: Disordered

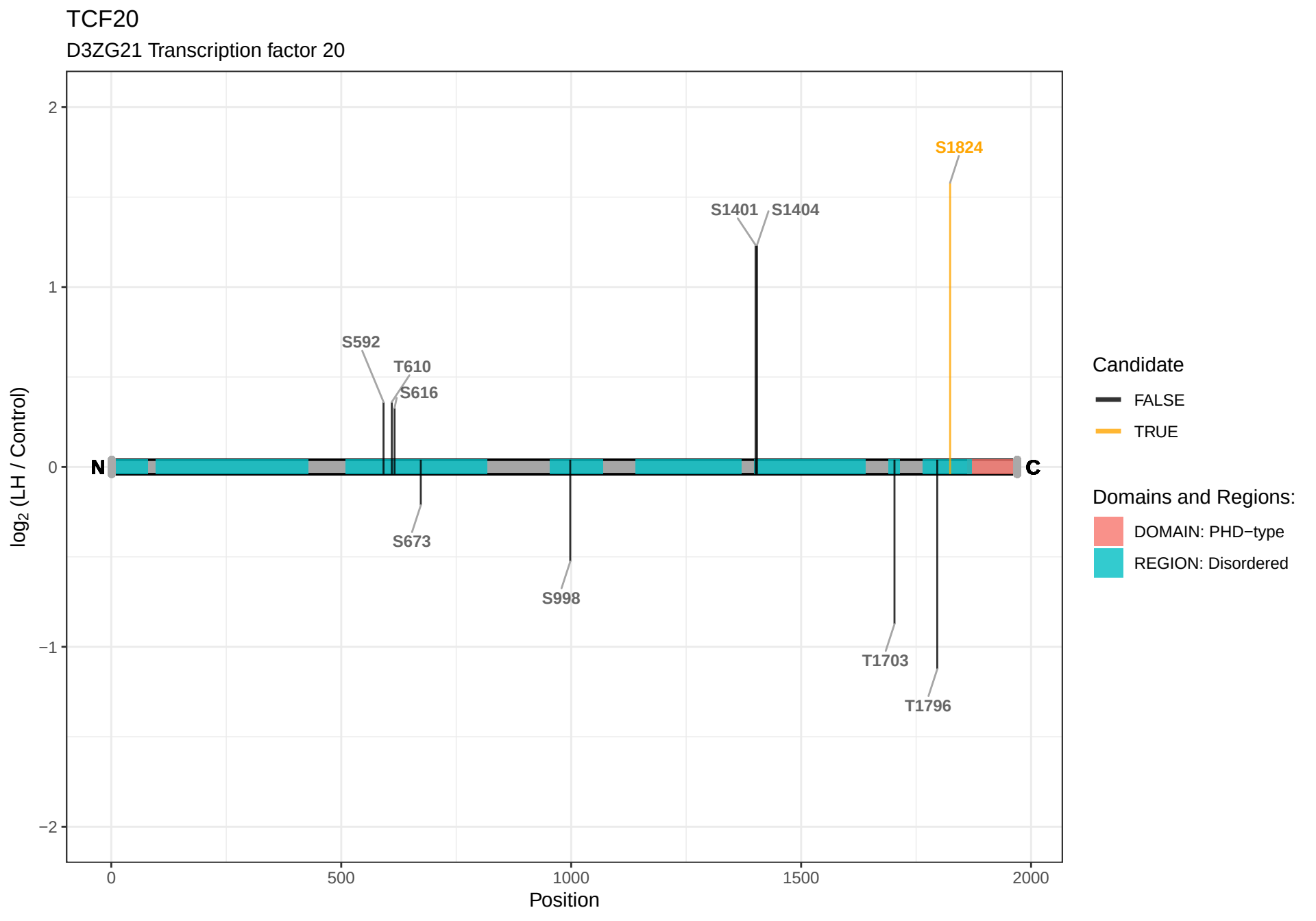

TANC2
A0A0G2K9J0 Tetratricopeptide repeat, ankyrin repeat and coiled−coil−containing 2
log2 (LH / Control)
Position
N
C
S22
S328
S331
S1528
S1620
S342
S1603
S1665
S1544
S478
S312
S243
S474
S1616
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ANK_REP_REGION
DOMAIN: TPR_REGION
REGION: Disordered

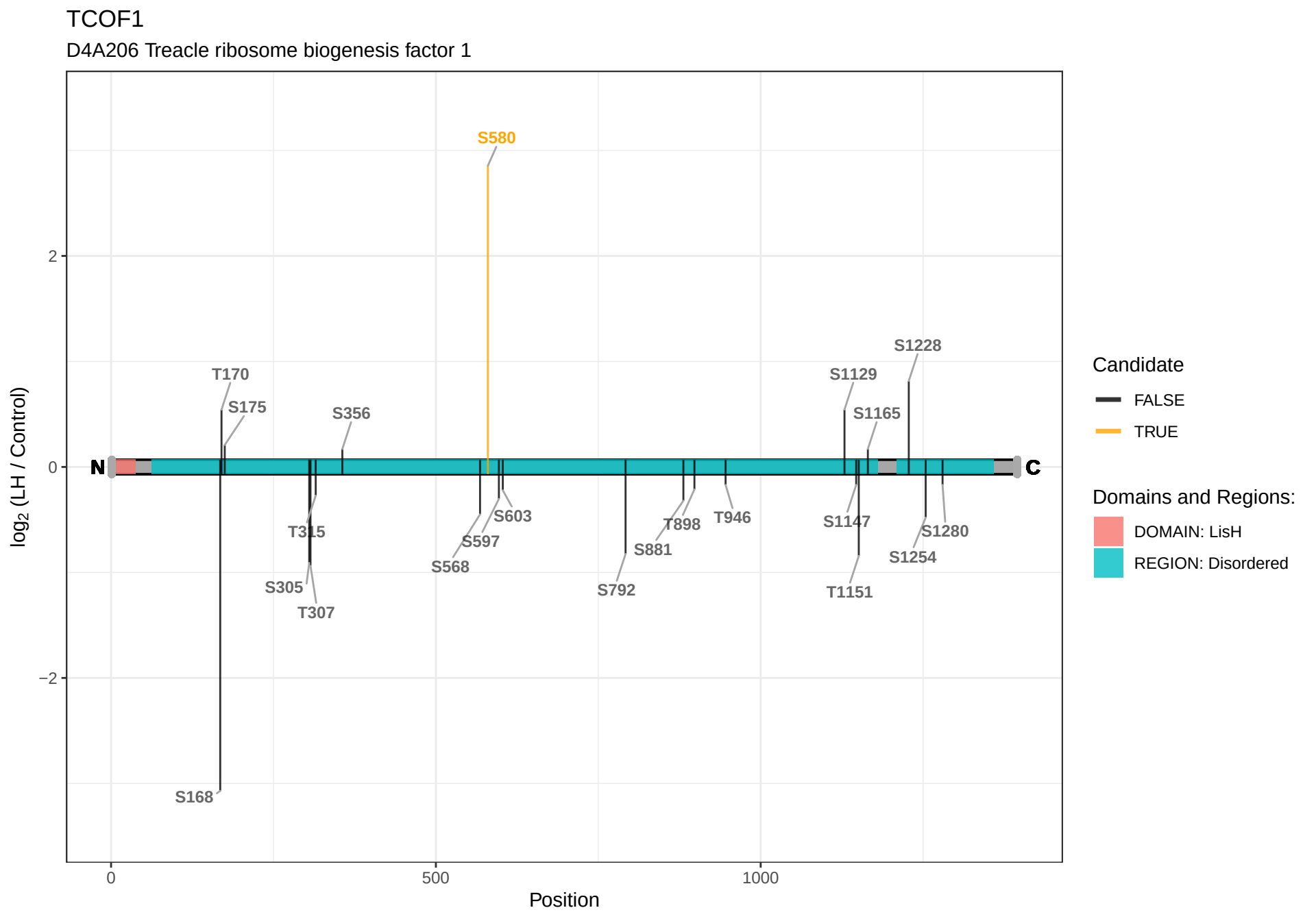

TAOK1
F1M9G6 Serine/threonine−protein kinase TAO1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S412
S956
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered

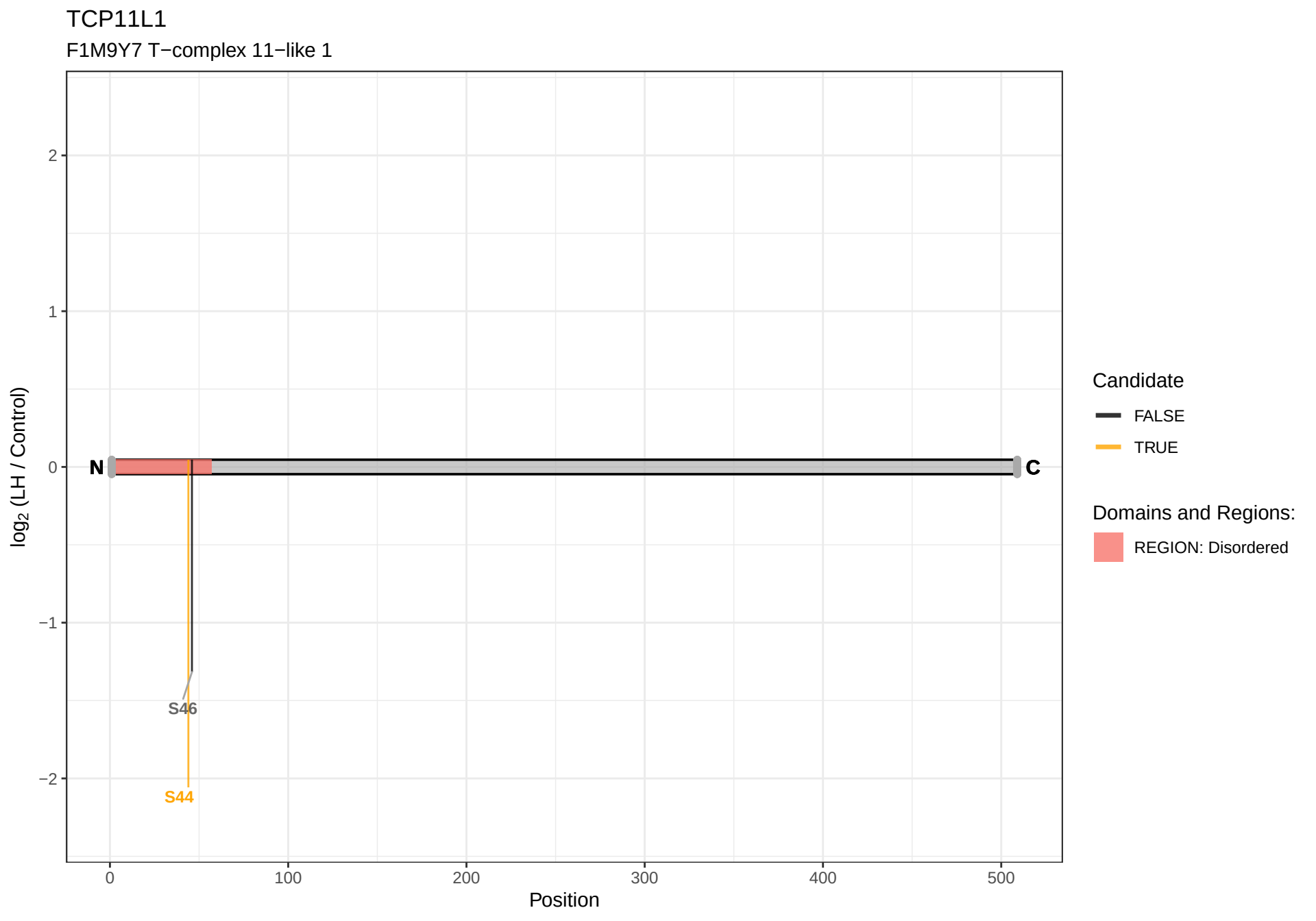

TBC1D10B
D3ZSY8 TBC1 domain family, member 10b
log2 (LH / Control)
3
2
1
0
−1
−2
−3
0
200
400
600
800
Position
N
C
S670
S644
S234
S22
S128
T135
S661
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Rab−GAP TBC
REGION: Disordered

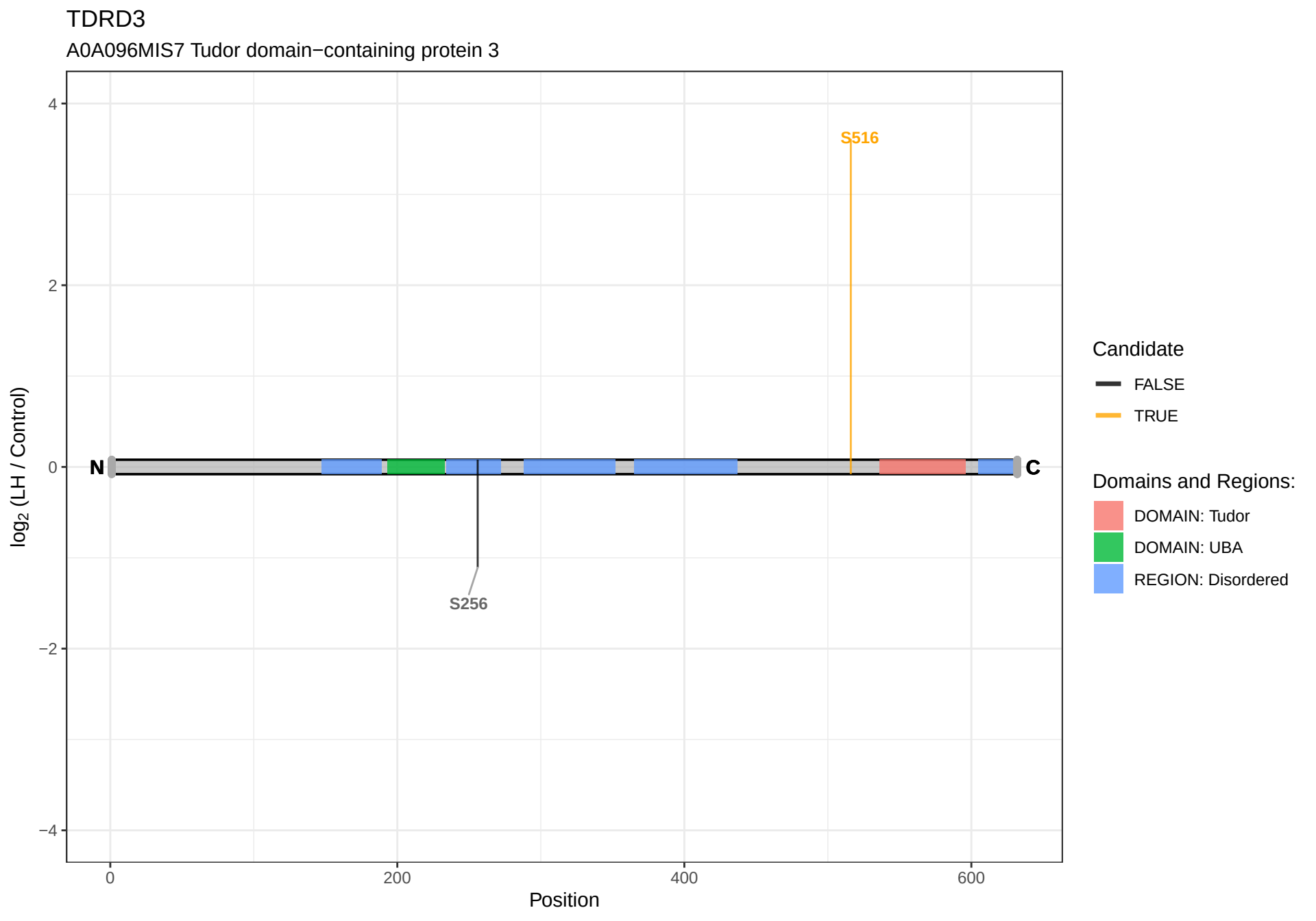

TBC1D12
M0R9H1 TBC1 domain family, member 12
log2 (LH / Control)
2
1
0
−1
−2
S202
S613
N
C
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Rab−GAP TBC
REGION: Disordered

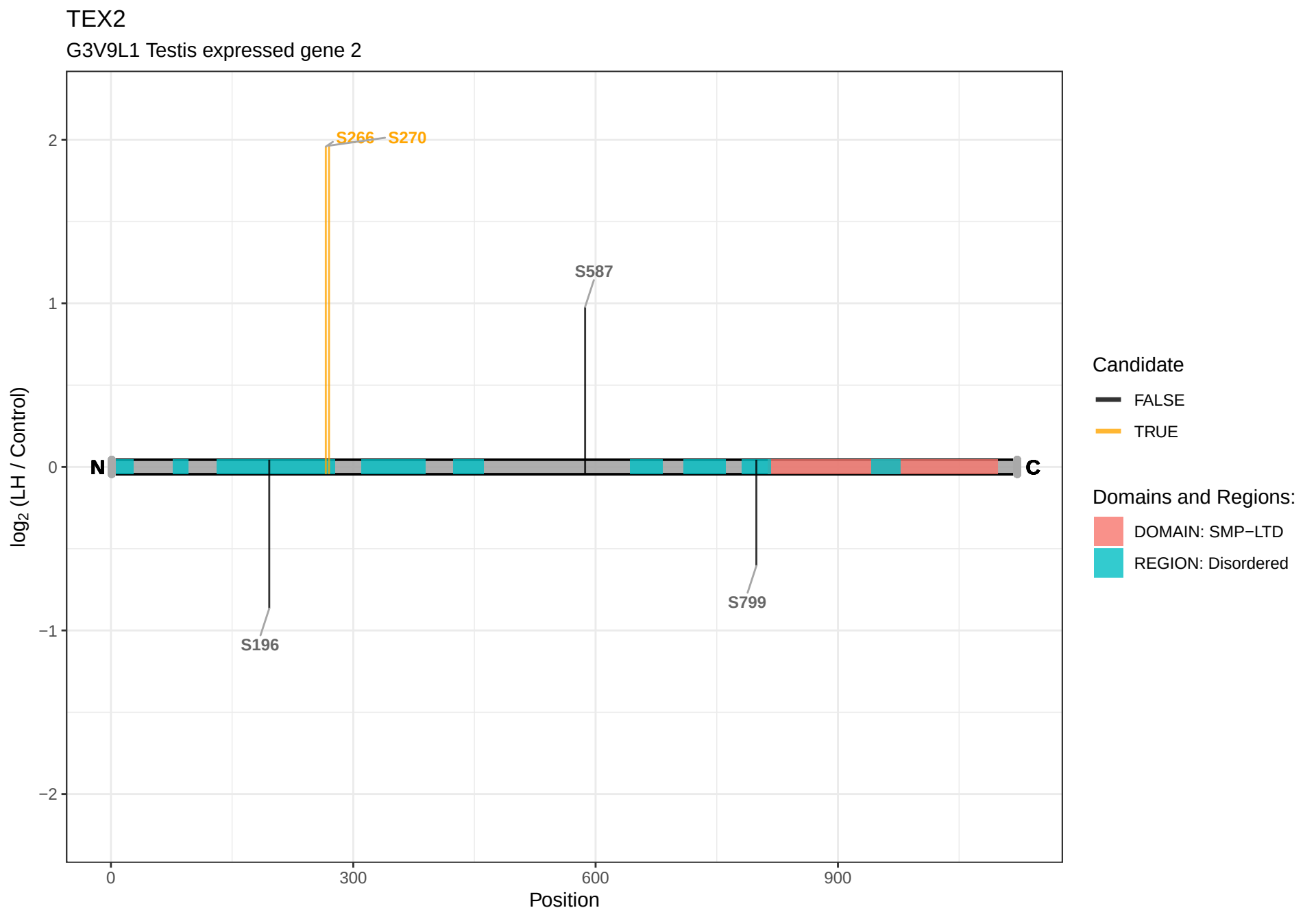

TBC1D5
A0A0G2K712 TBC1 domain family, member 5
log2 (LH / Control)
2
1
0
−1
−2
N
C
S596
S592
S538
S570
S808
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Rab−GAP TBC
REGION: Disordered

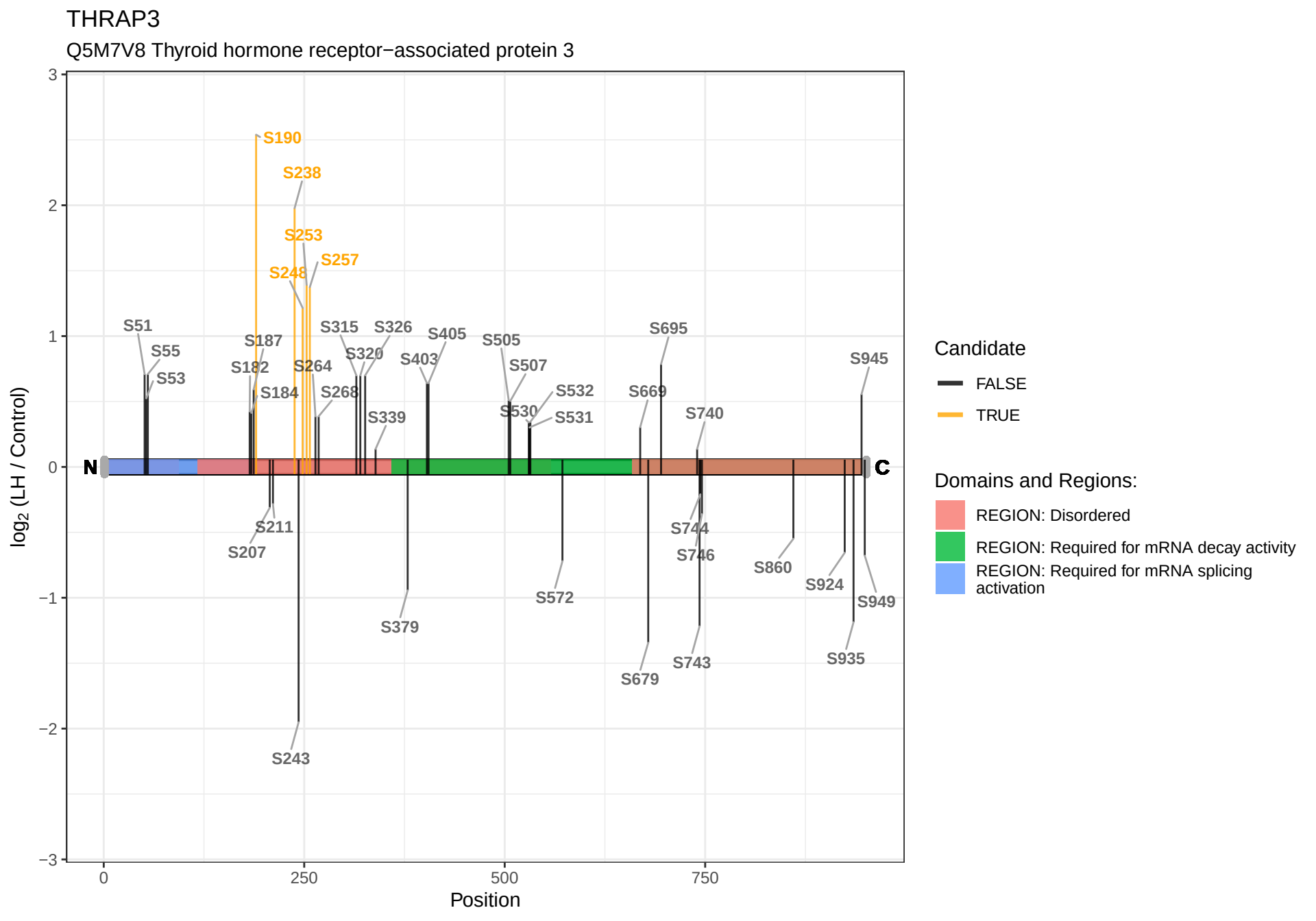

TCF20
D3ZG21 Transcription factor 20
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
2000
Position
N
C
S1824
S1401
S1404
S592
T610
S616
S673
S998
T1703
T1796
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PHD−type
REGION: Disordered

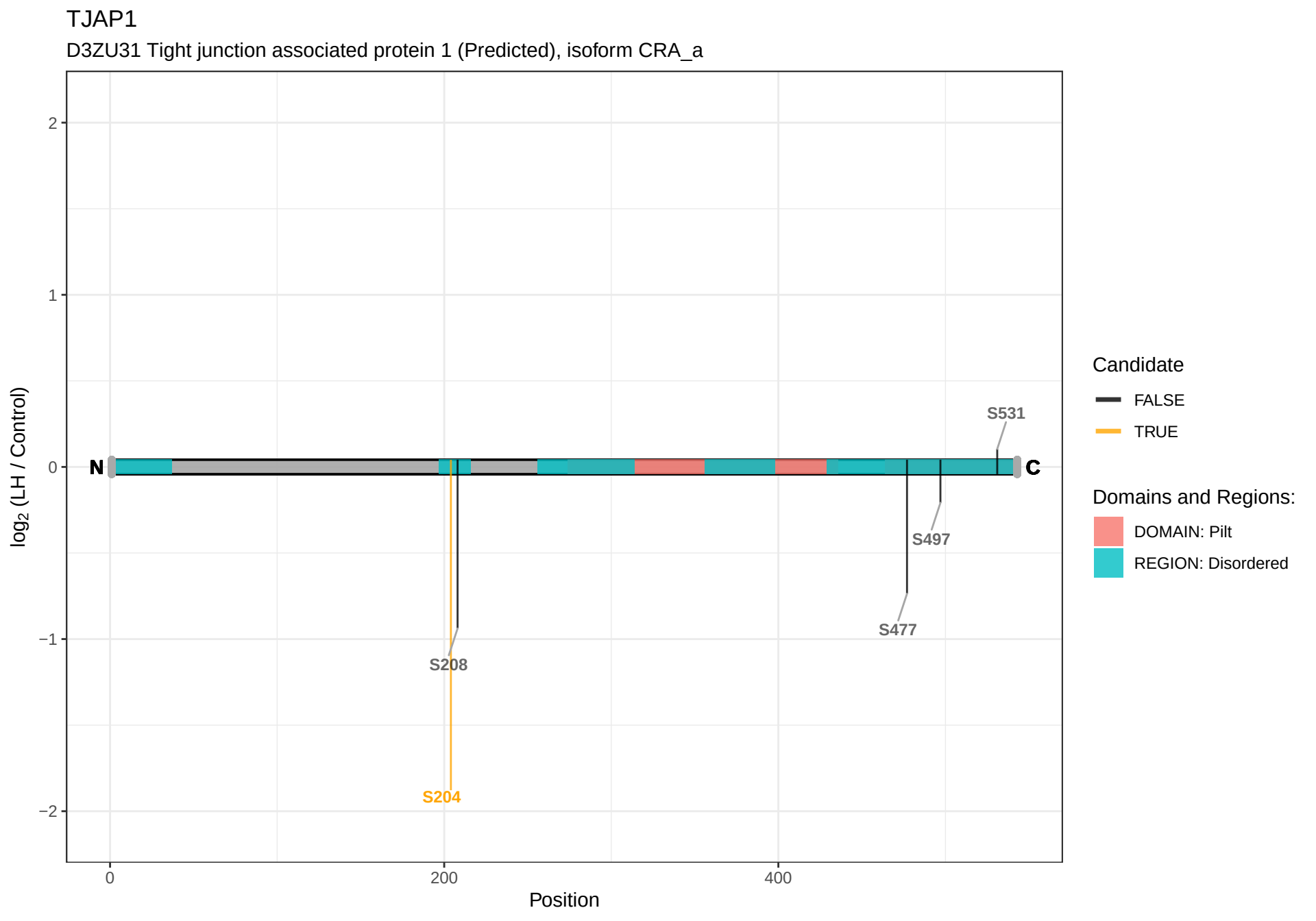

TCOF1
D4A206 Treacle ribosome biogenesis factor 1
S580
T170
S175
S356
S1228
S1129
S1165
N
C
T315
S603
S597
S568
T898
T946
S881
S1147
S1280
S1254
S305
T307
S792
T1151
S168
2
0
−2
log2 (LH / Control)
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: LisH
REGION: Disordered

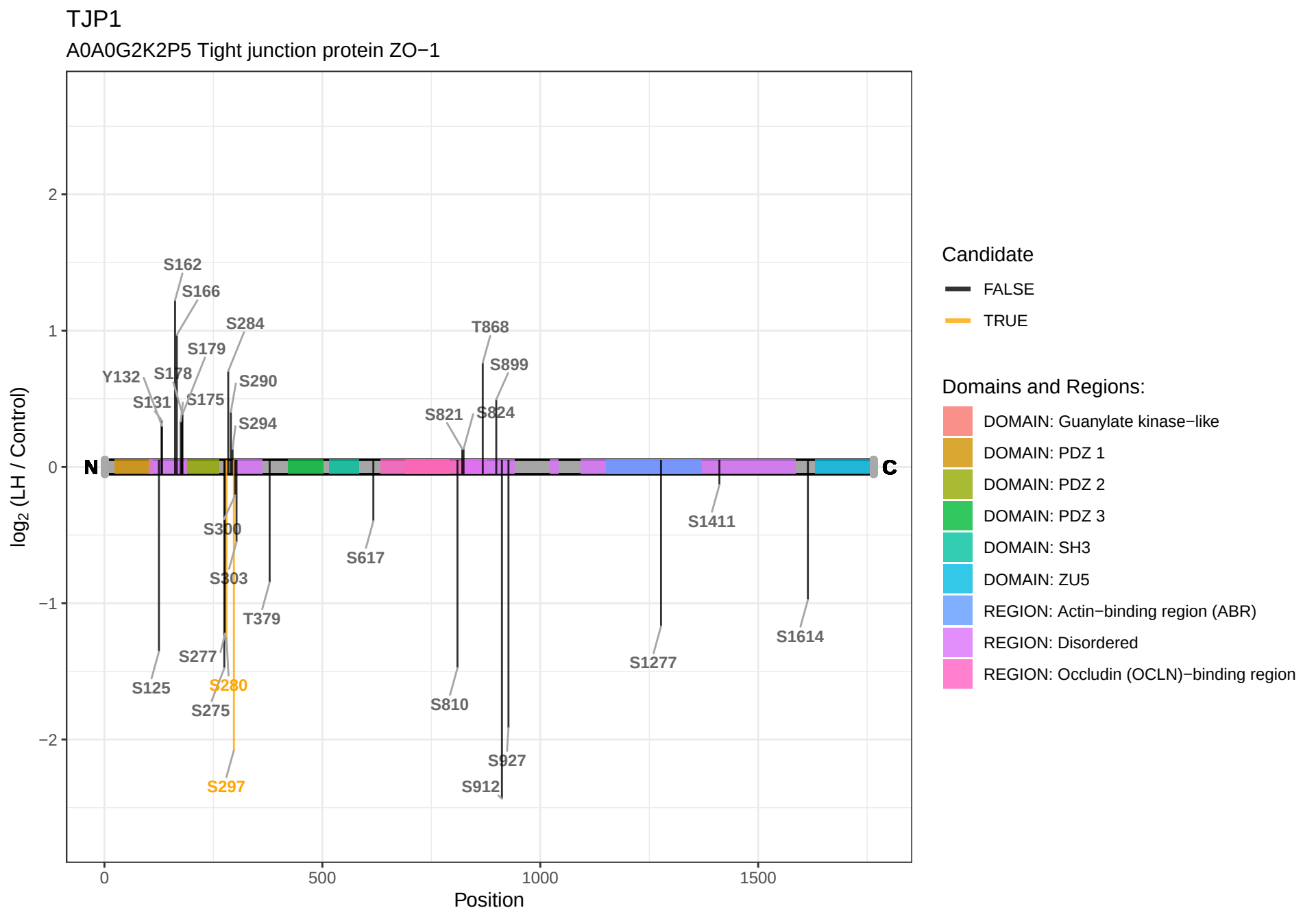

TCP11L1
F1M9Y7 T−complex 11−like 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S46
S44
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

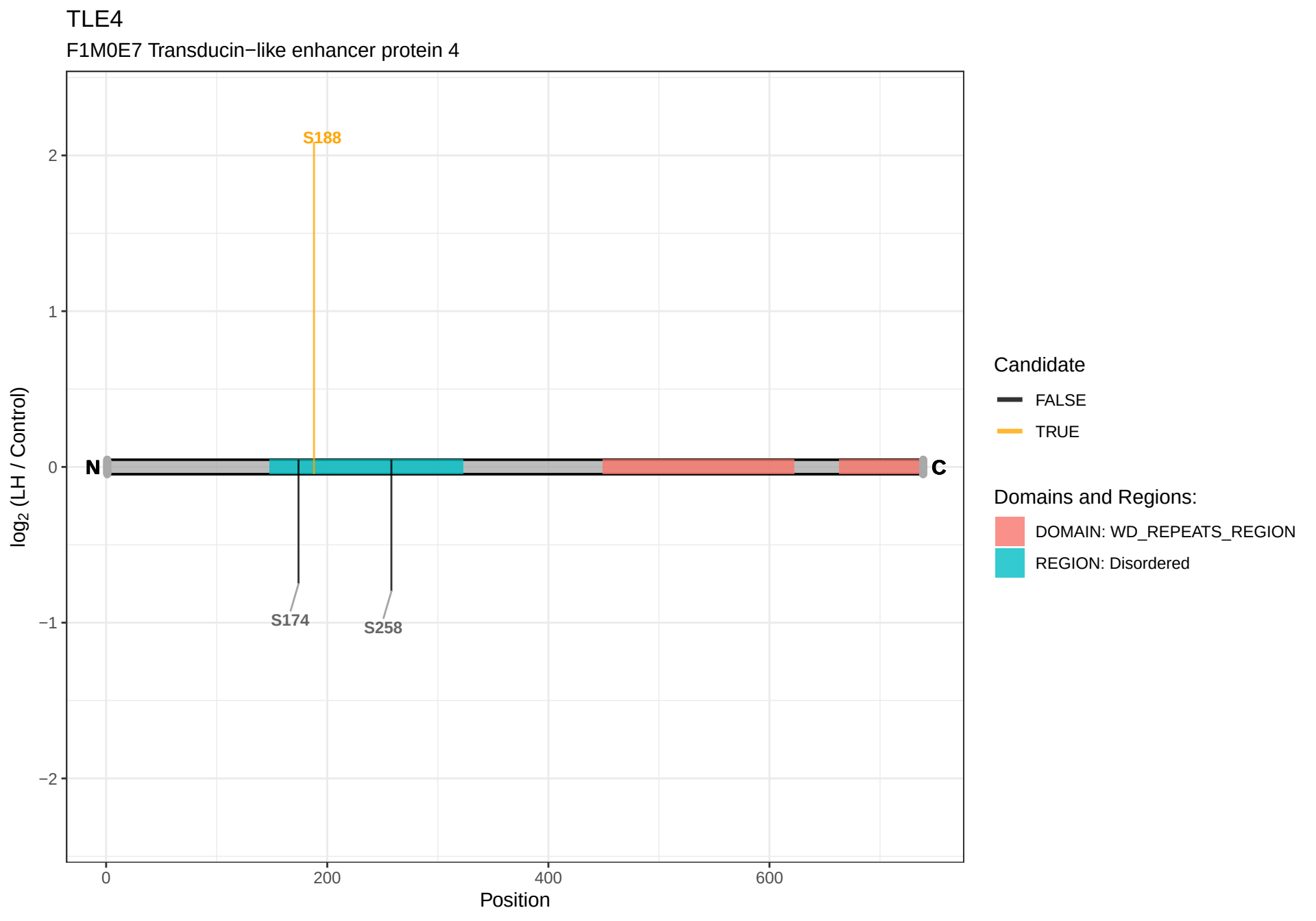

TDRD3
A0A096MIS7 Tudor domain−containing protein 3
log2 (LH / Control)
4
2
0
−2
−4
S516
S256
N
C
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Tudor
DOMAIN: UBA
REGION: Disordered

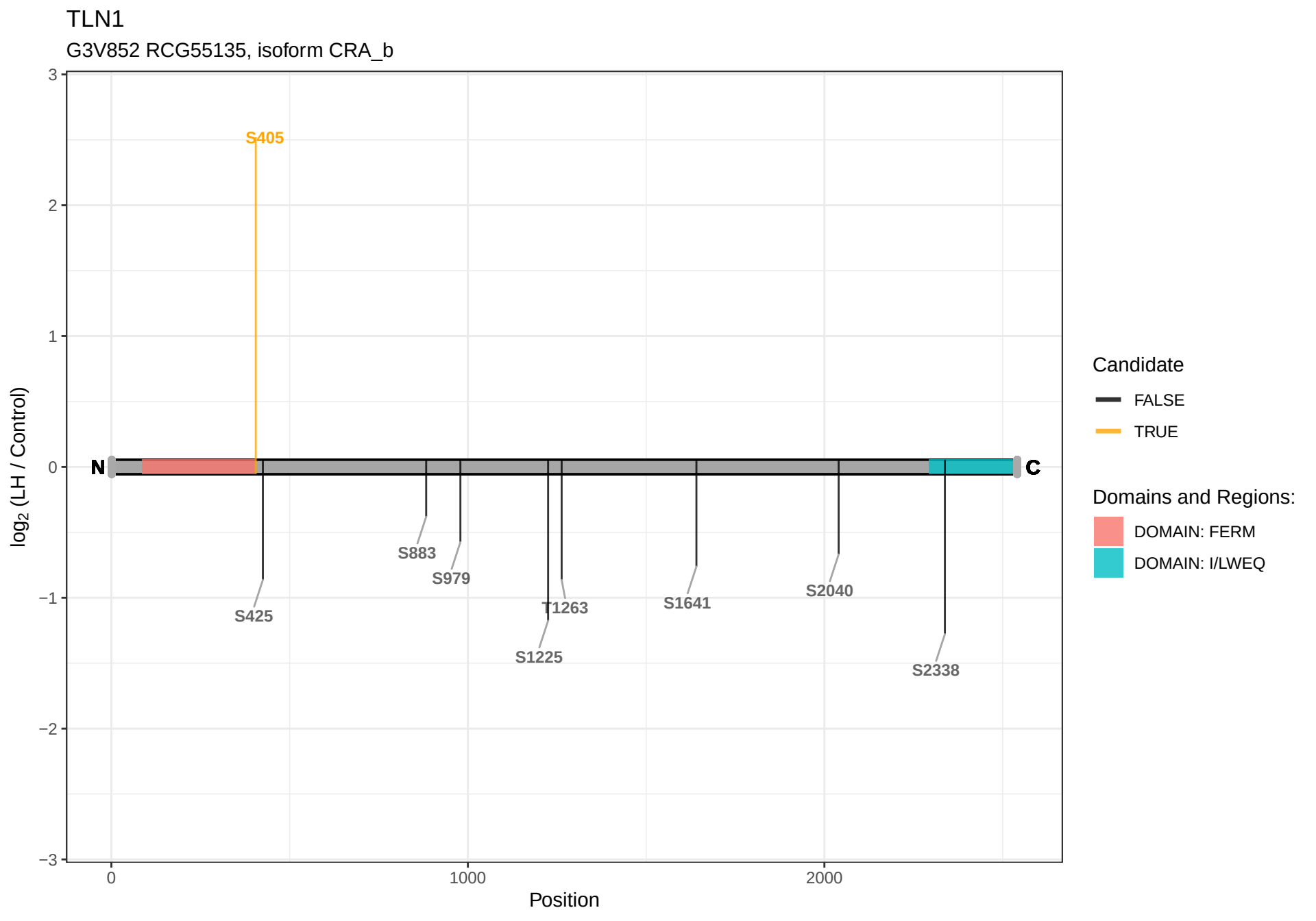

TEX2
G3V9L1 Testis expressed gene 2
S266
S270
S587
S196
S799
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SMP−LTD
REGION: Disordered

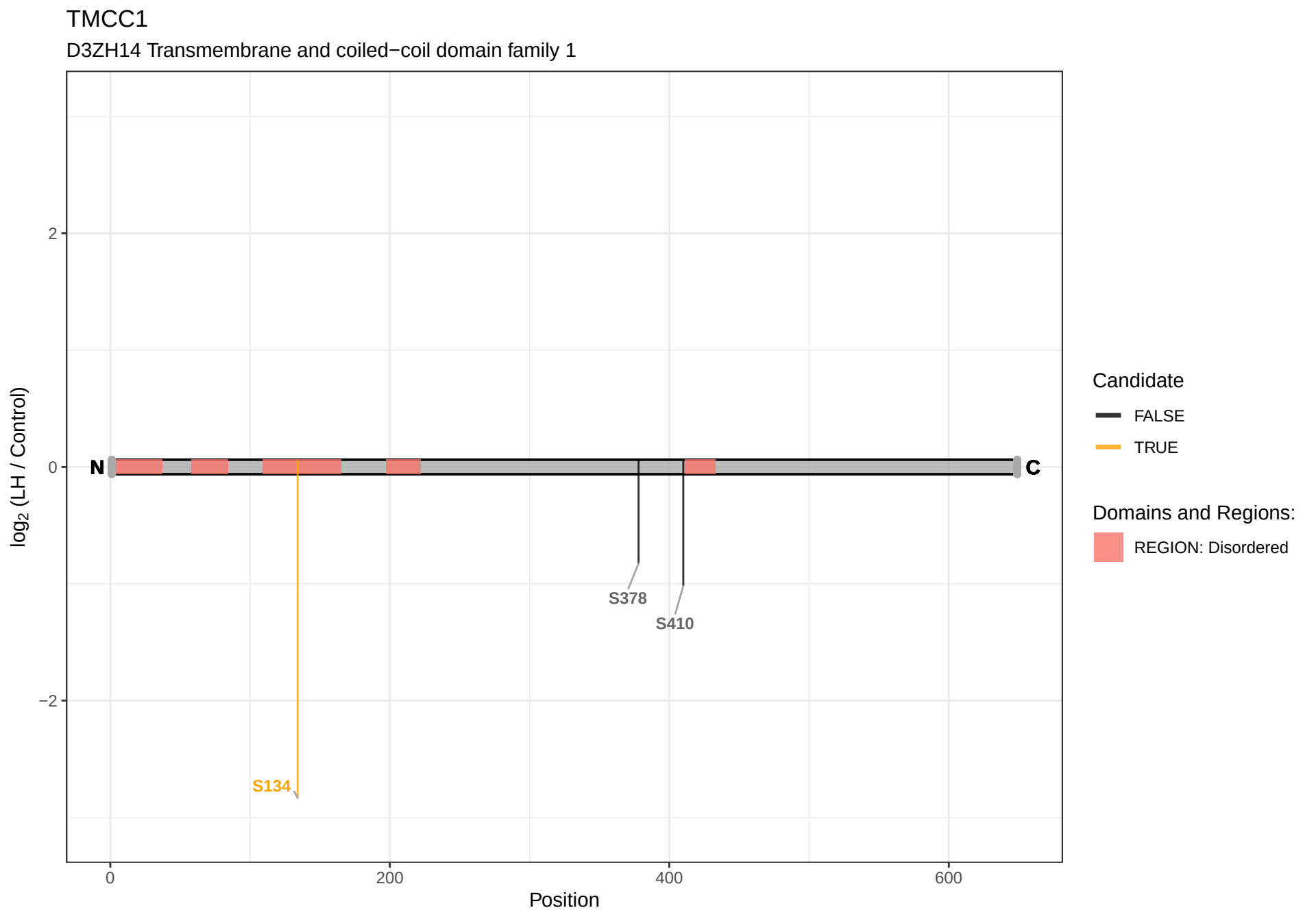

THRAP3
Q5M7V8 Thyroid hormone receptor−associated protein 3
log2 (LH / Control)
Position
N
C
S190
S238
S253
S257
S248
S51
S55
S53
S187
S182
S184
S315
S326
S320
S264
S268
S339
S405
S403
S505
S507
S530
S532
S531
S695
S669
S740
S945
S211
S207
S379
S572
S744
S746
S860
S924
S949
S935
S679
S743
S243
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Required for mRNA decay activity
REGION: Required for mRNA splicing activation

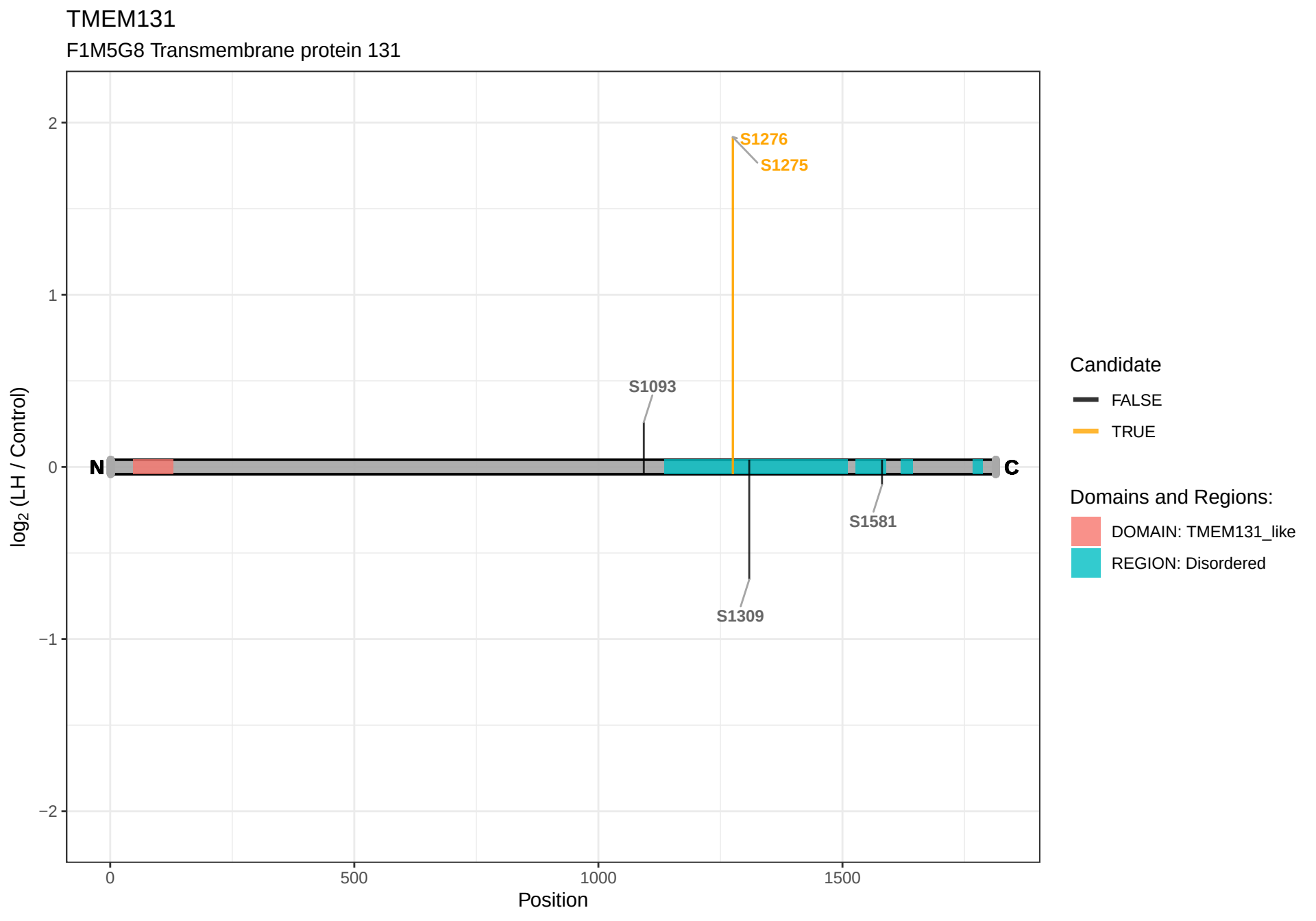

TJAP1
D3ZU31 Tight junction associated protein 1 (Predicted), isoform CRA_a
log2 (LH / Control)
2
1
0
−1
−2
N
C
S531
S497
S477
S208
S204
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Pilt
REGION: Disordered

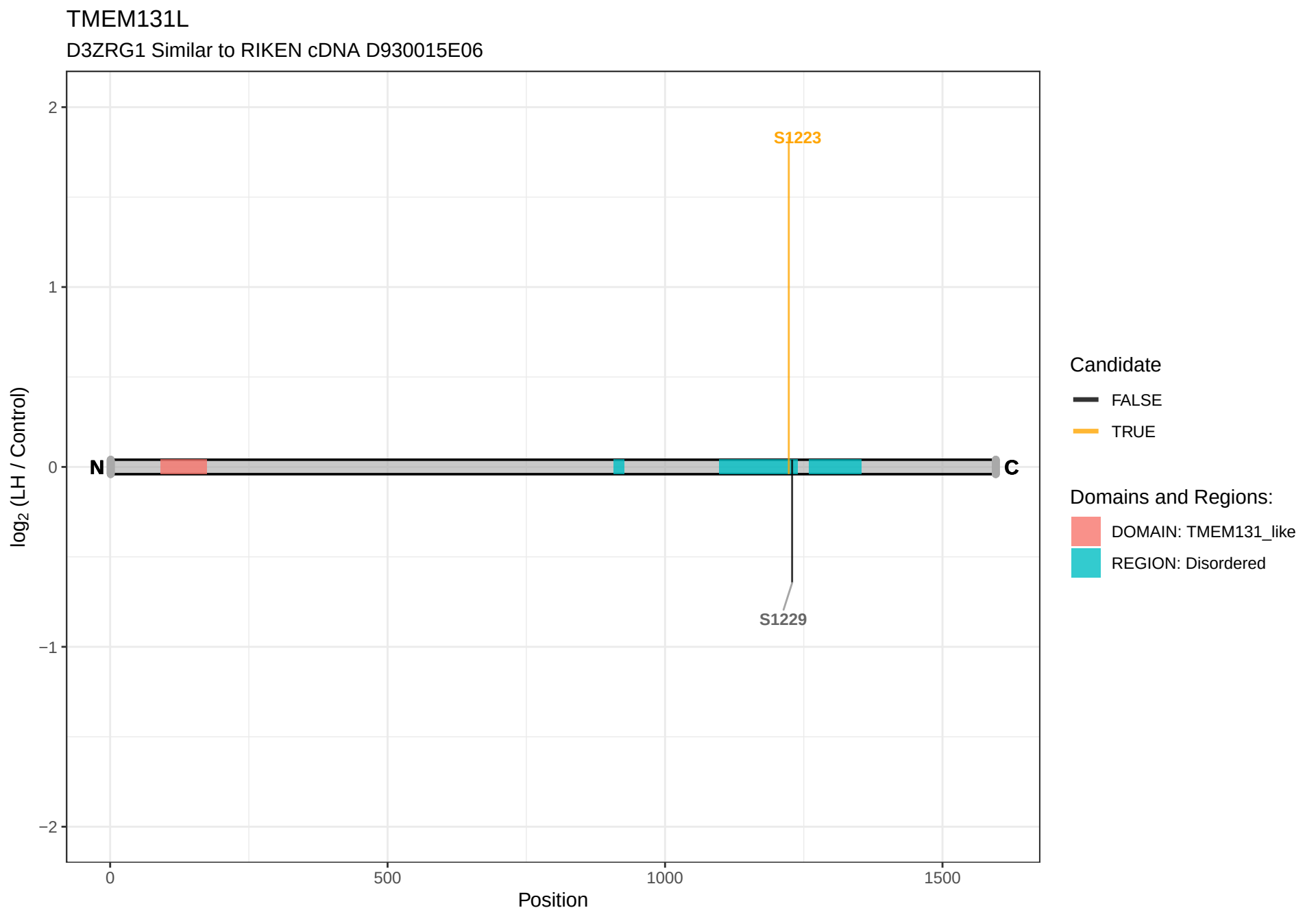

TJP1
A0A0G2K2P5 Tight junction protein ZO−1
log2 (LH / Control)
Position
N
C
S162
S166
S284
S179
Y132
S178
S290
S131
S175
S294
T868
S899
S821
S824
S300
S303
S617
T379
S1411
S277
S125
S280
S275
S297
S810
S927
S912
S1277
S1614
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Guanylate kinase−like
DOMAIN: PDZ 1
DOMAIN: PDZ 2
DOMAIN: PDZ 3
DOMAIN: SH3
DOMAIN: ZU5
REGION: Actin−binding region (ABR)
REGION: Disordered
REGION: Occludin (OCLN)−binding region

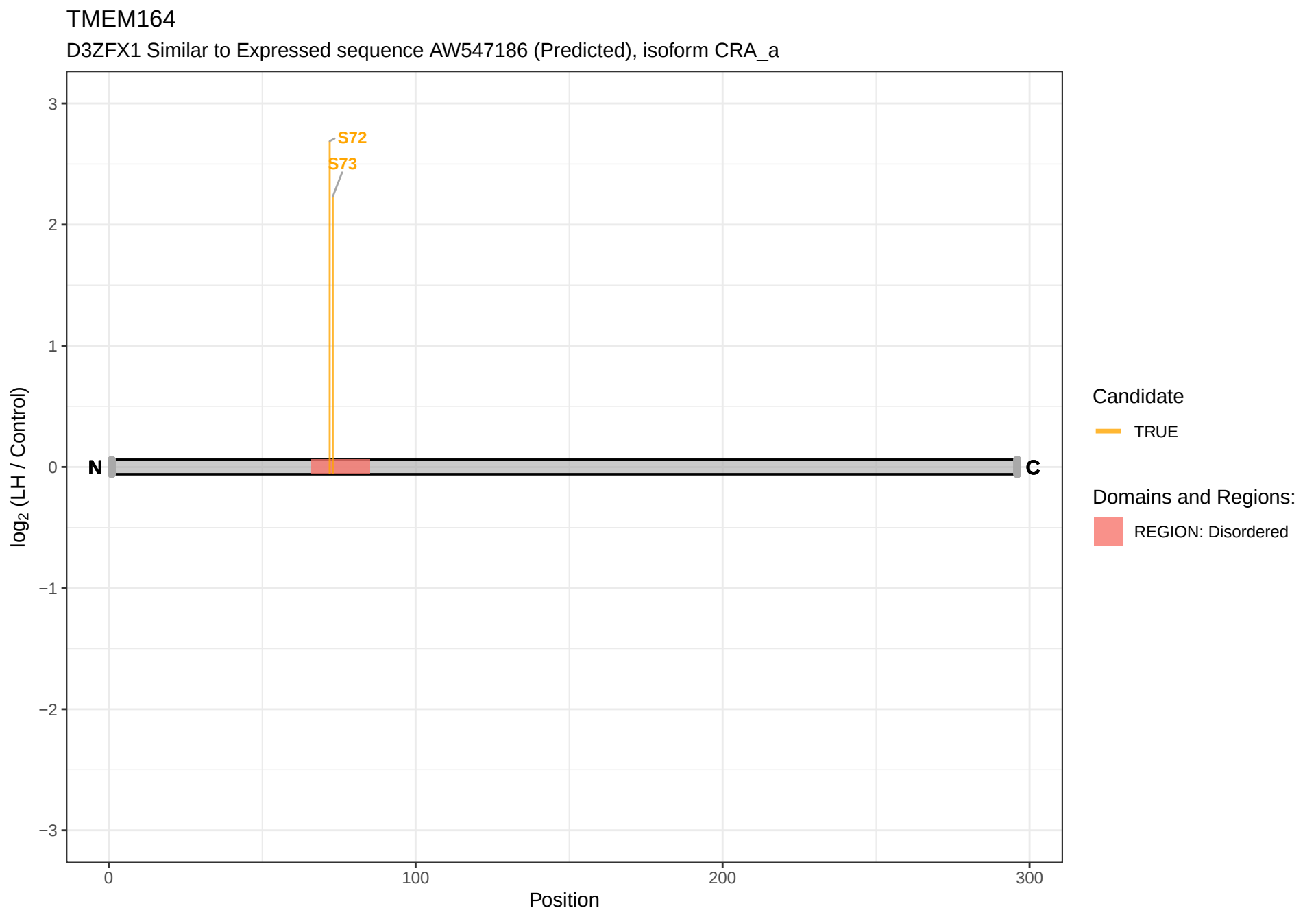

TLE4
F1M0E7 Transducin−like enhancer protein 4
S188
S174
S258
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WD_REPEATS_REGION
REGION: Disordered

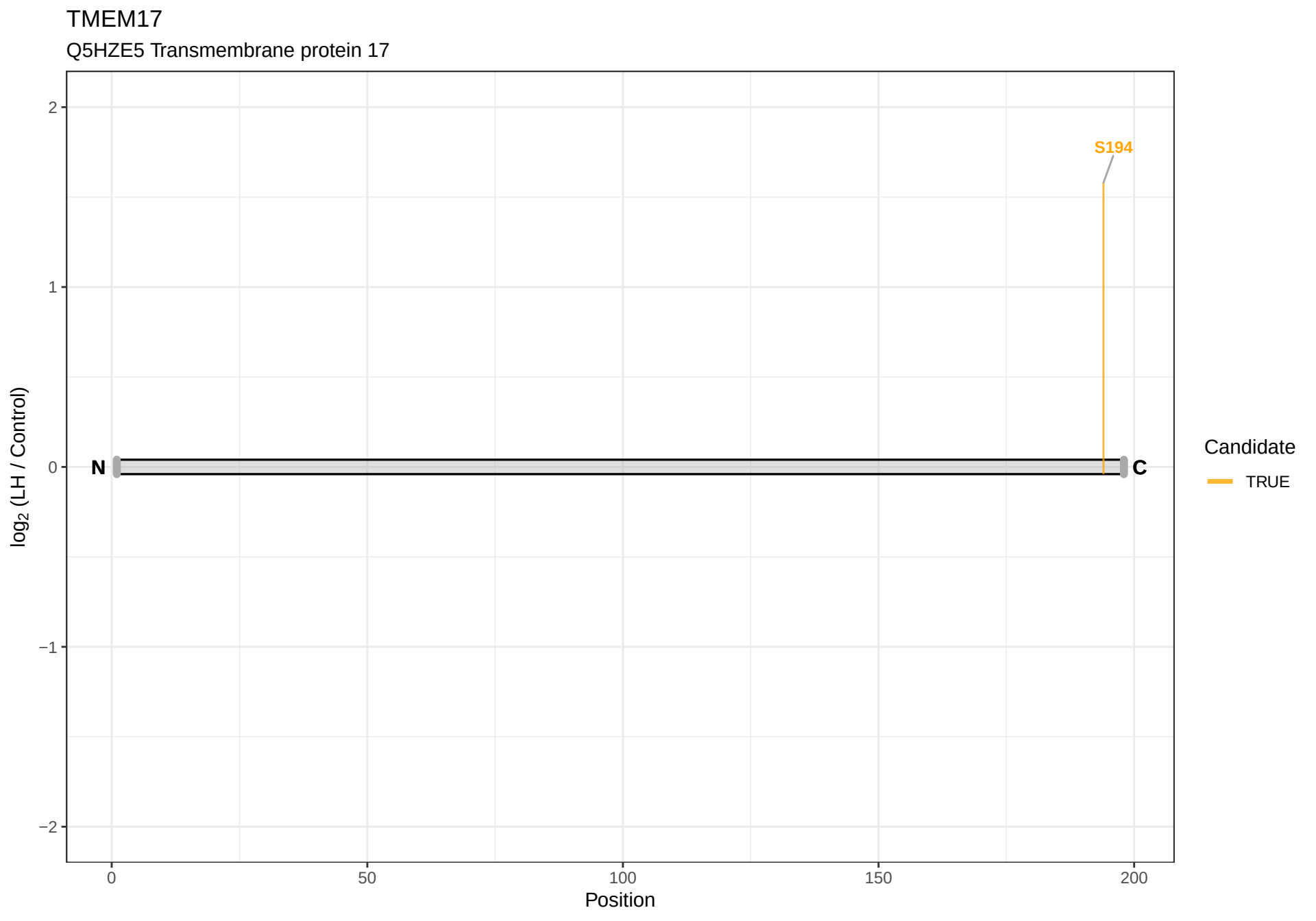

TLN1
G3V852 RCG55135, isoform CRA_b
log2 (LH / Control)
Position
N
C
S405
S425
S883
S979
T1263
S1225
S1641
S2040
S2338
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: FERM
DOMAIN: I/LWEQ

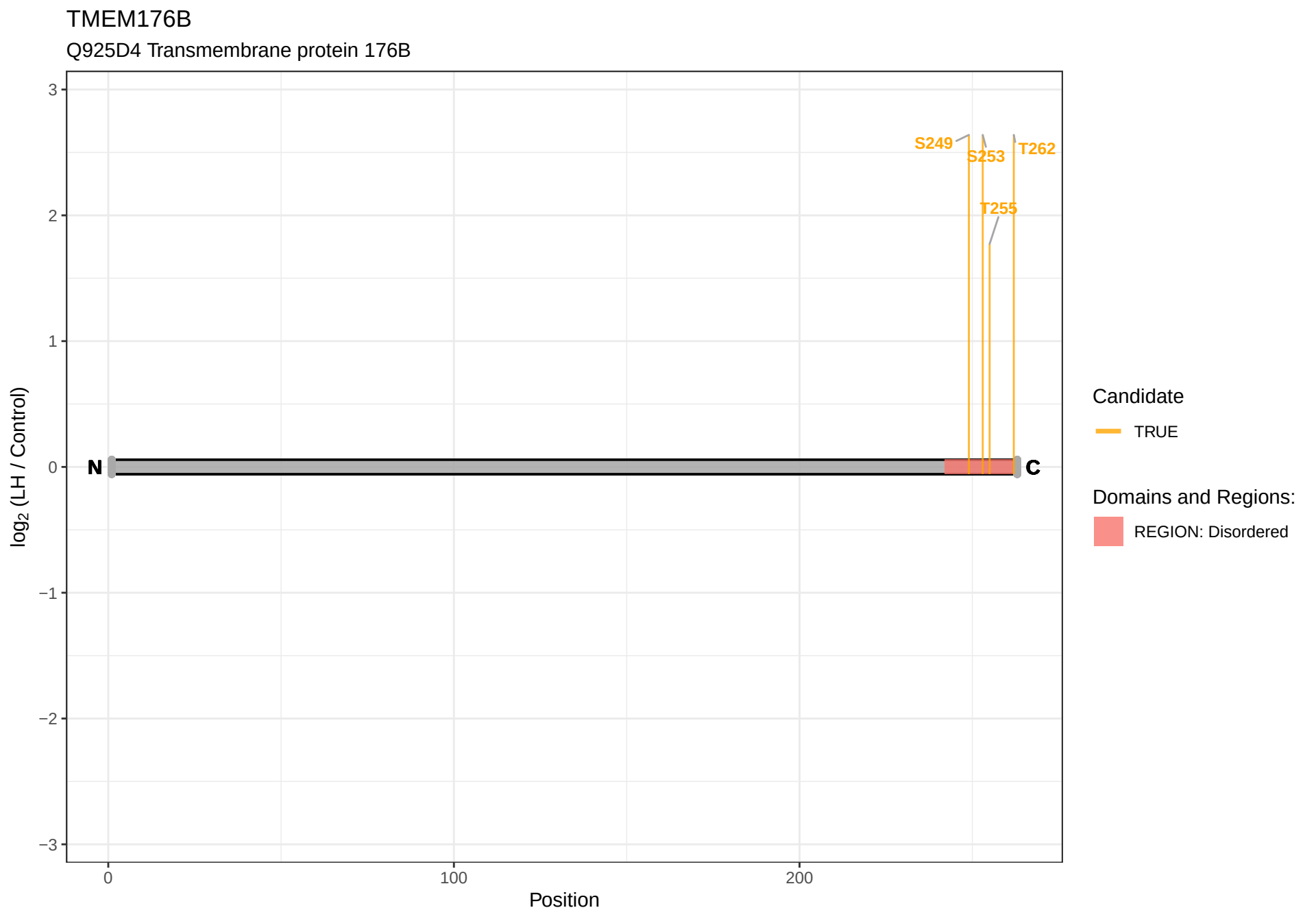

TMCC1
D3ZH14 Transmembrane and coiled−coil domain family 1
log2 (LH / Control)
2
0
−2
N
C
S378
S410
S134
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

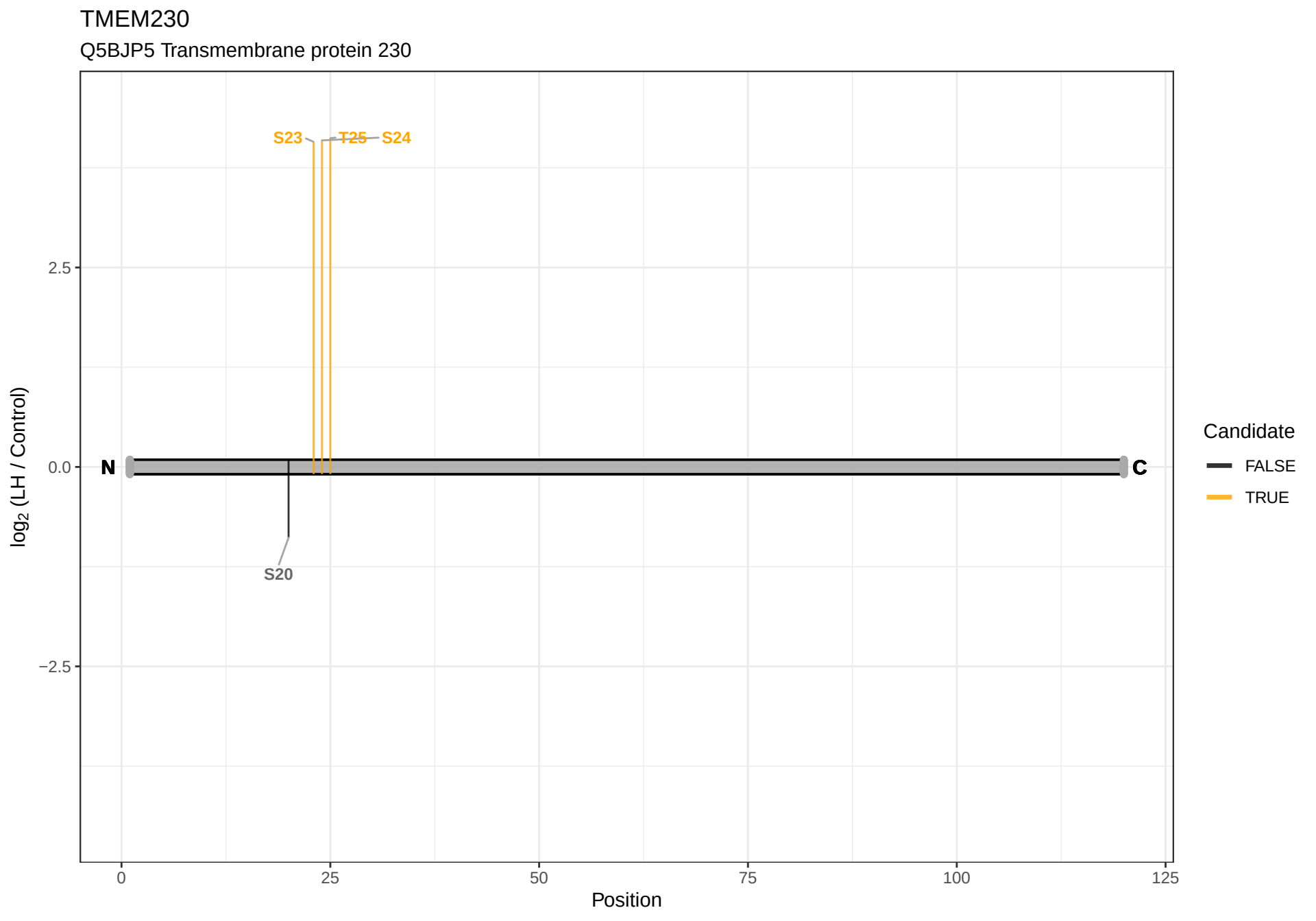

TMEM131
F1M5G8 Transmembrane protein 131
S1276
S1275
S1093
S1581
S1309
N
C
log2 (LH / Control)
Position
0
500
1000
1500
2
1
0
−1
−2
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: TMEM131_like
REGION: Disordered

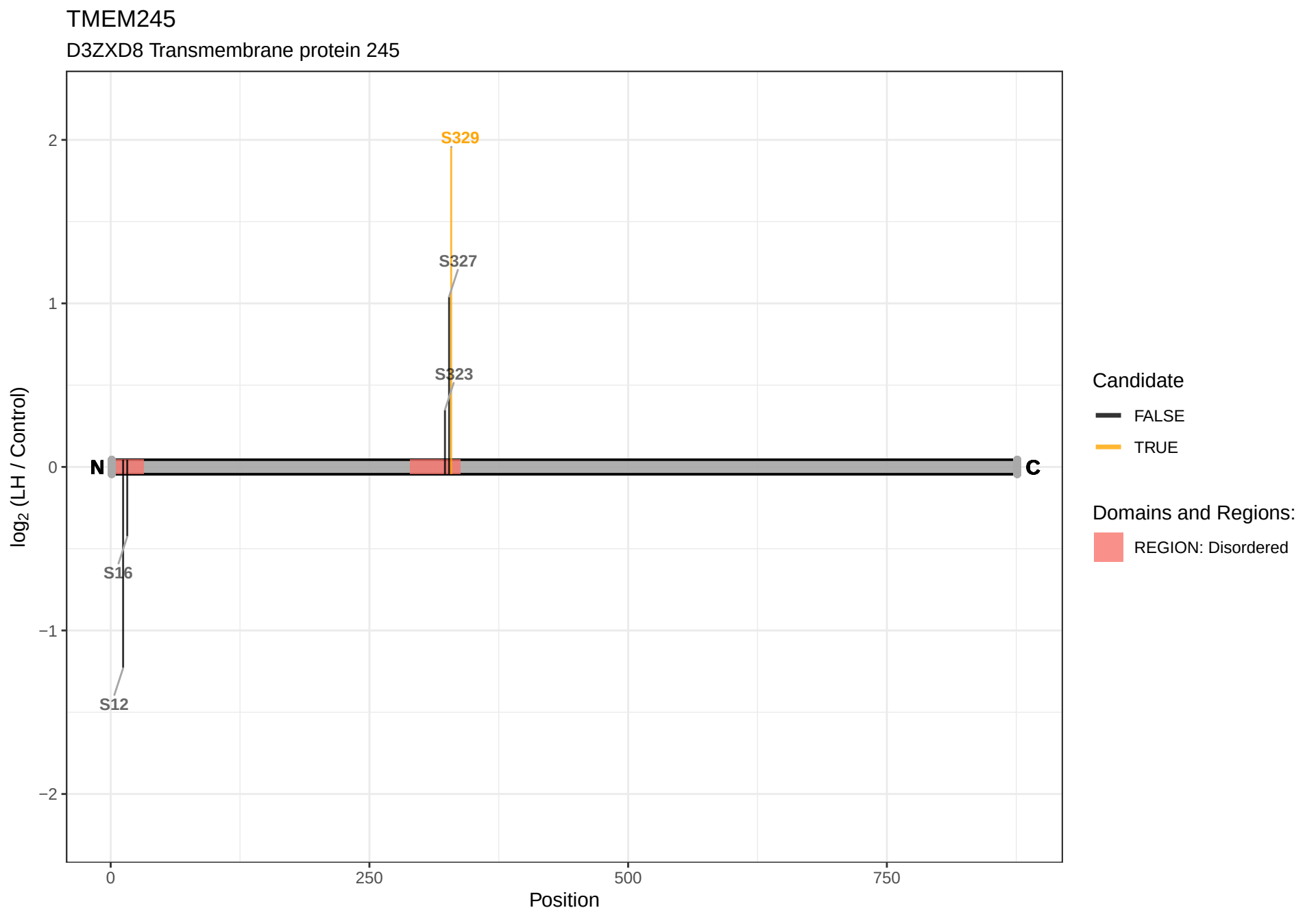

TMEM131L
D3ZRG1 Similar to RIKEN cDNA D930015E06
log2 (LH / Control)
2
1
0
−1
−2
S1223
S1229
N
C
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: TMEM131_like
REGION: Disordered

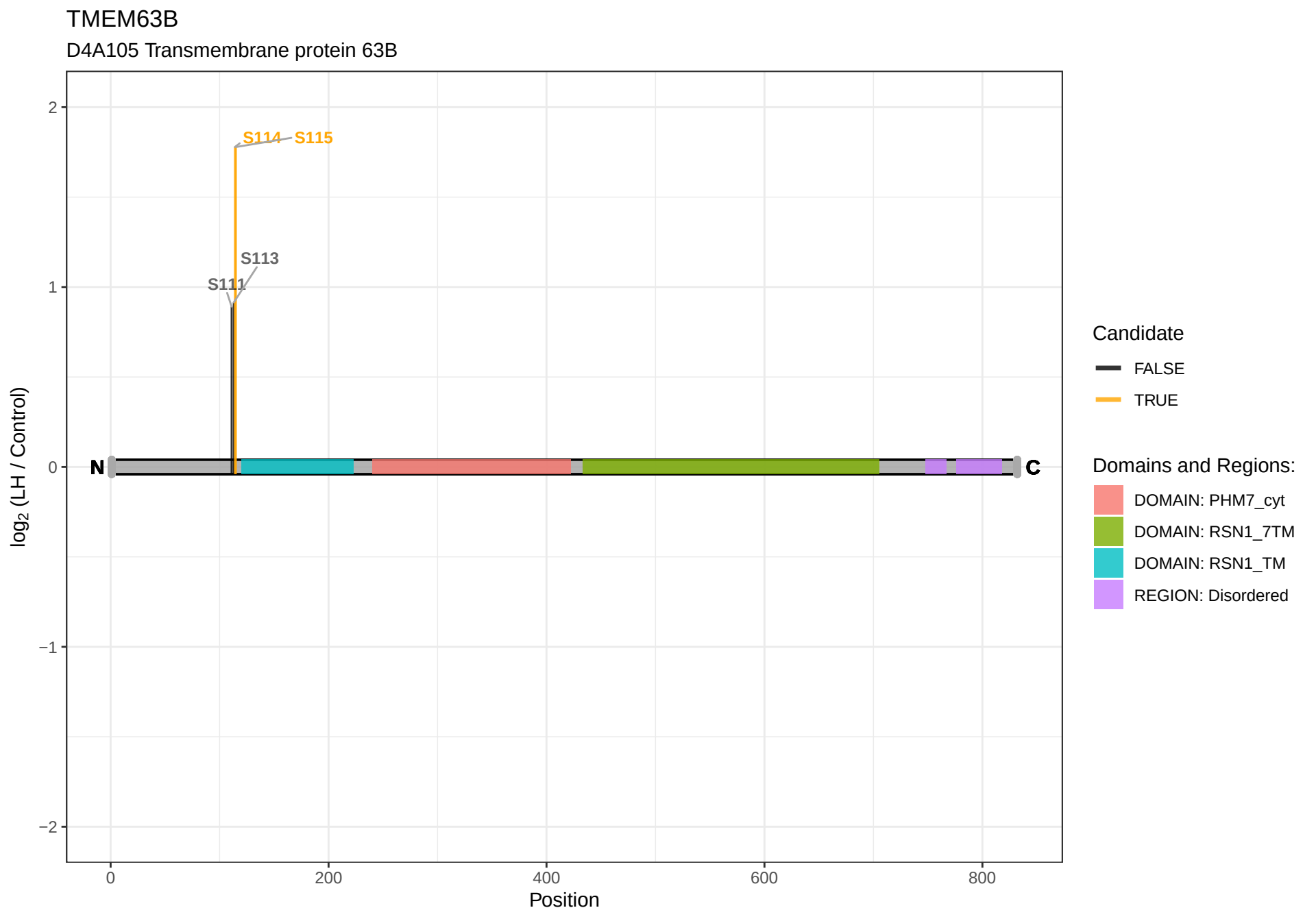

TMEM164
D3ZFX1 Similar to Expressed sequence AW547186 (Predicted), isoform CRA_a
S72
S73
N
C
log2 (LH / Control)
3
2
1
0
−1
−2
−3
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

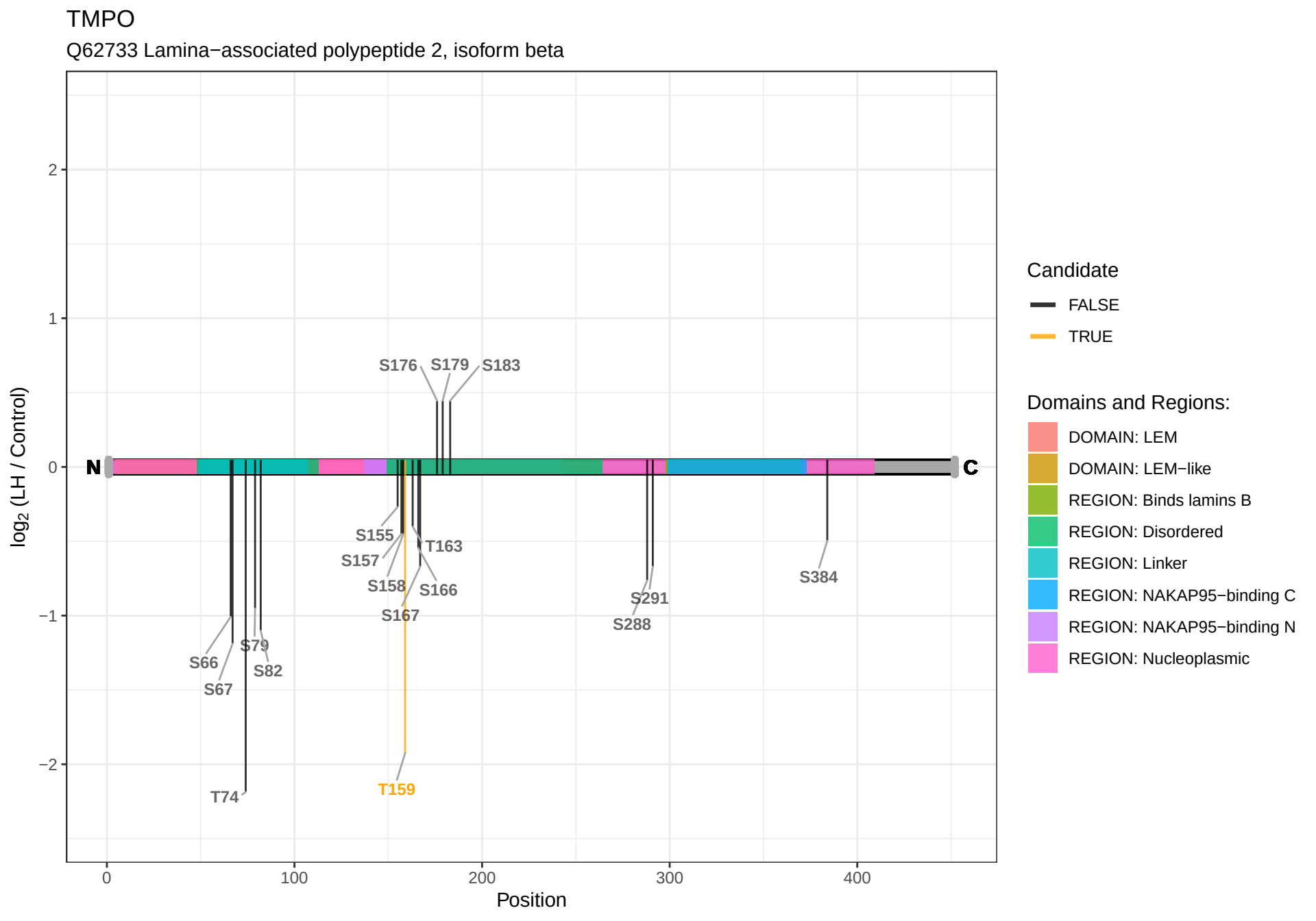

TMEM17
Q5HZE5 Transmembrane protein 17
S194
N
C
log2 (LH / Control)
Position
Candidate
TRUE
2
1
0
−1
−2
0
50
100
150
200

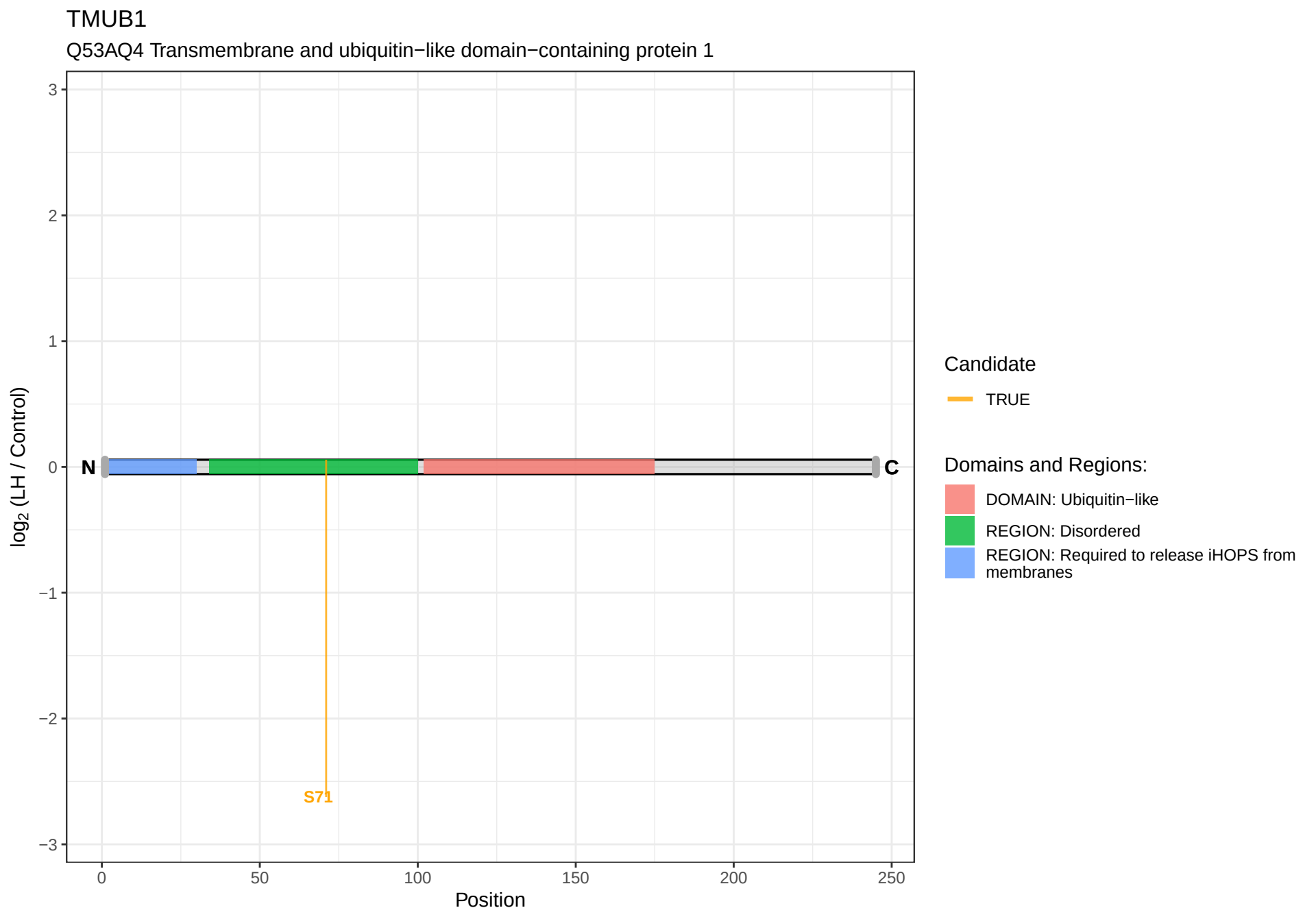

TMEM176B
Q925D4 Transmembrane protein 176B
S249
S253
T262
T255
N
C
log2 (LH / Control)
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

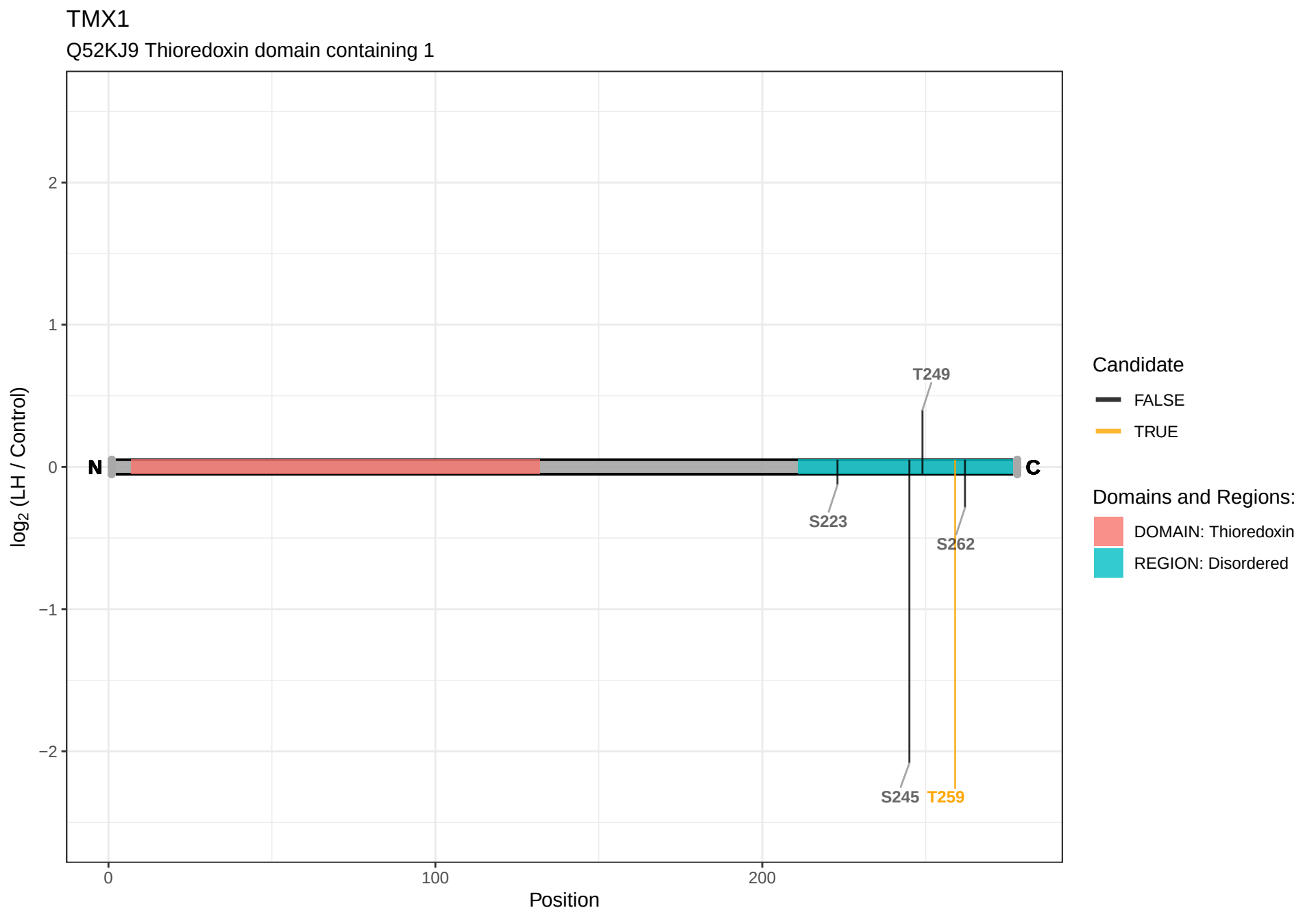

TMEM230
Q5BJP5 Transmembrane protein 230
S23
T25
S24
S20
N
C
2.5
0.0
−2.5
log2 (LH / Control)
0
25
50
75
100
125
Position
Candidate
FALSE
TRUE

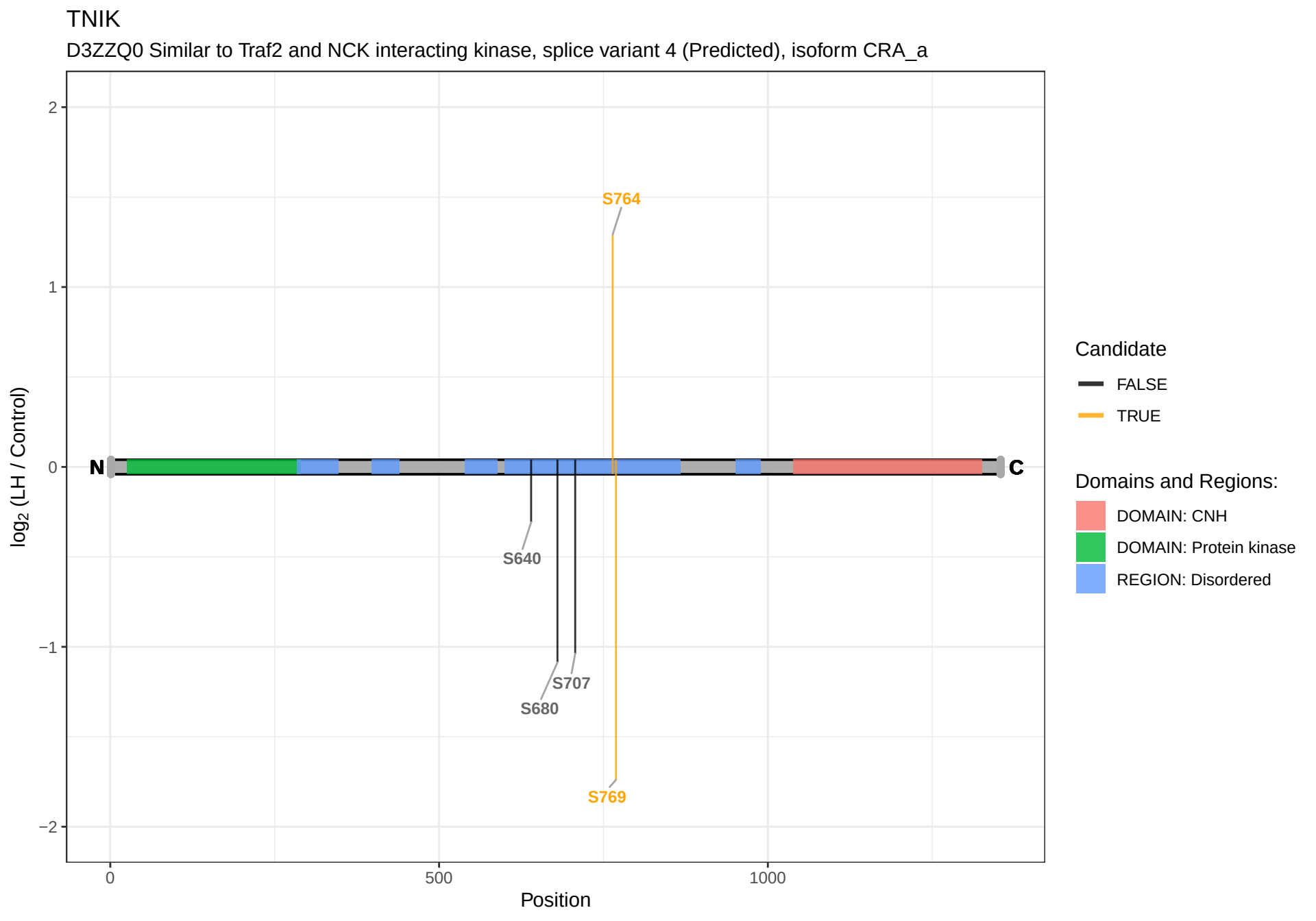

TMEM245
D3ZXD8 Transmembrane protein 245
S329
S327
S323
S16
S12
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

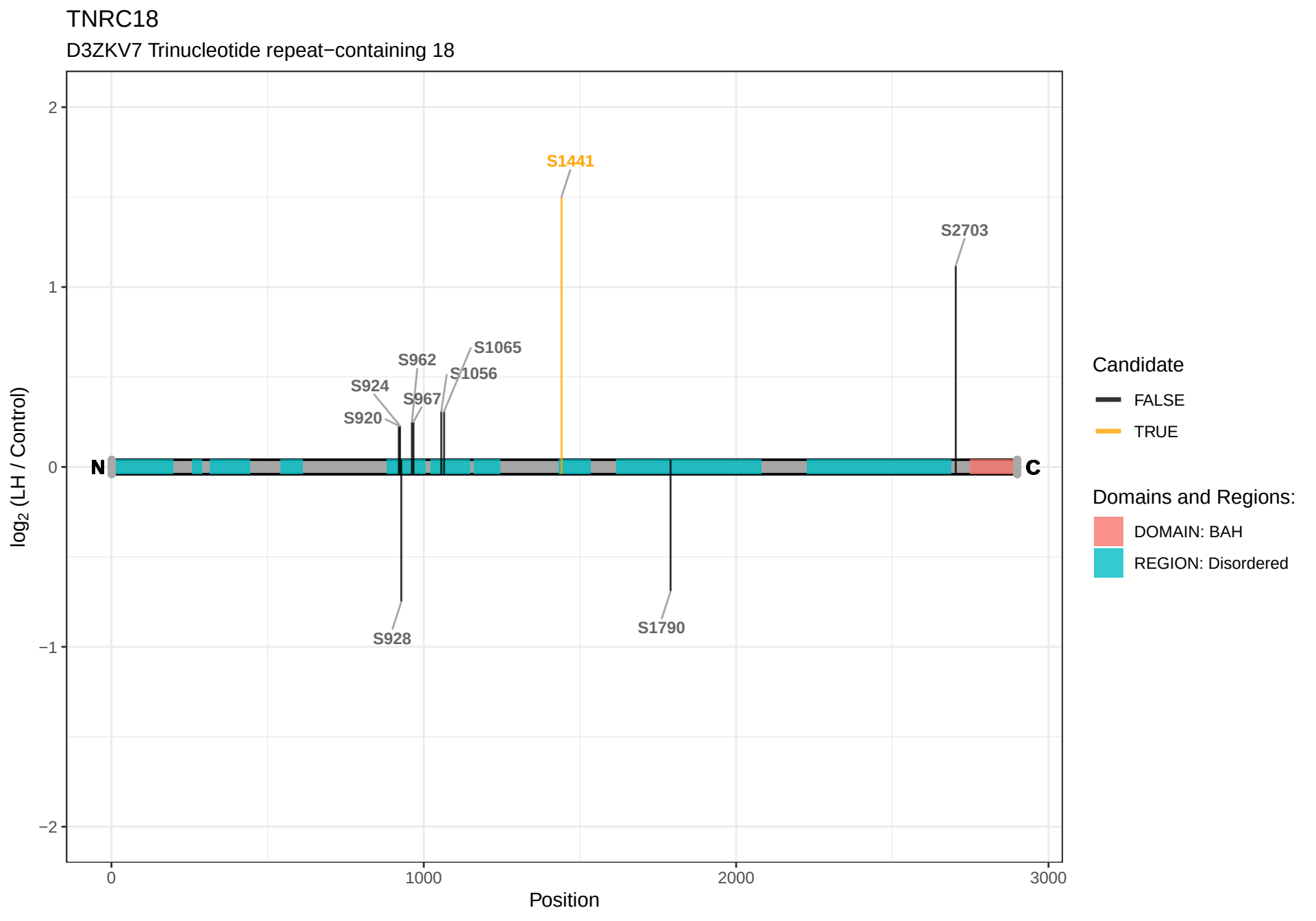

TMEM63B
D4A105 Transmembrane protein 63B
S114
S115
S113
S111
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PHM7_cyt
DOMAIN: RSN1_7TM
DOMAIN: RSN1_TM
REGION: Disordered

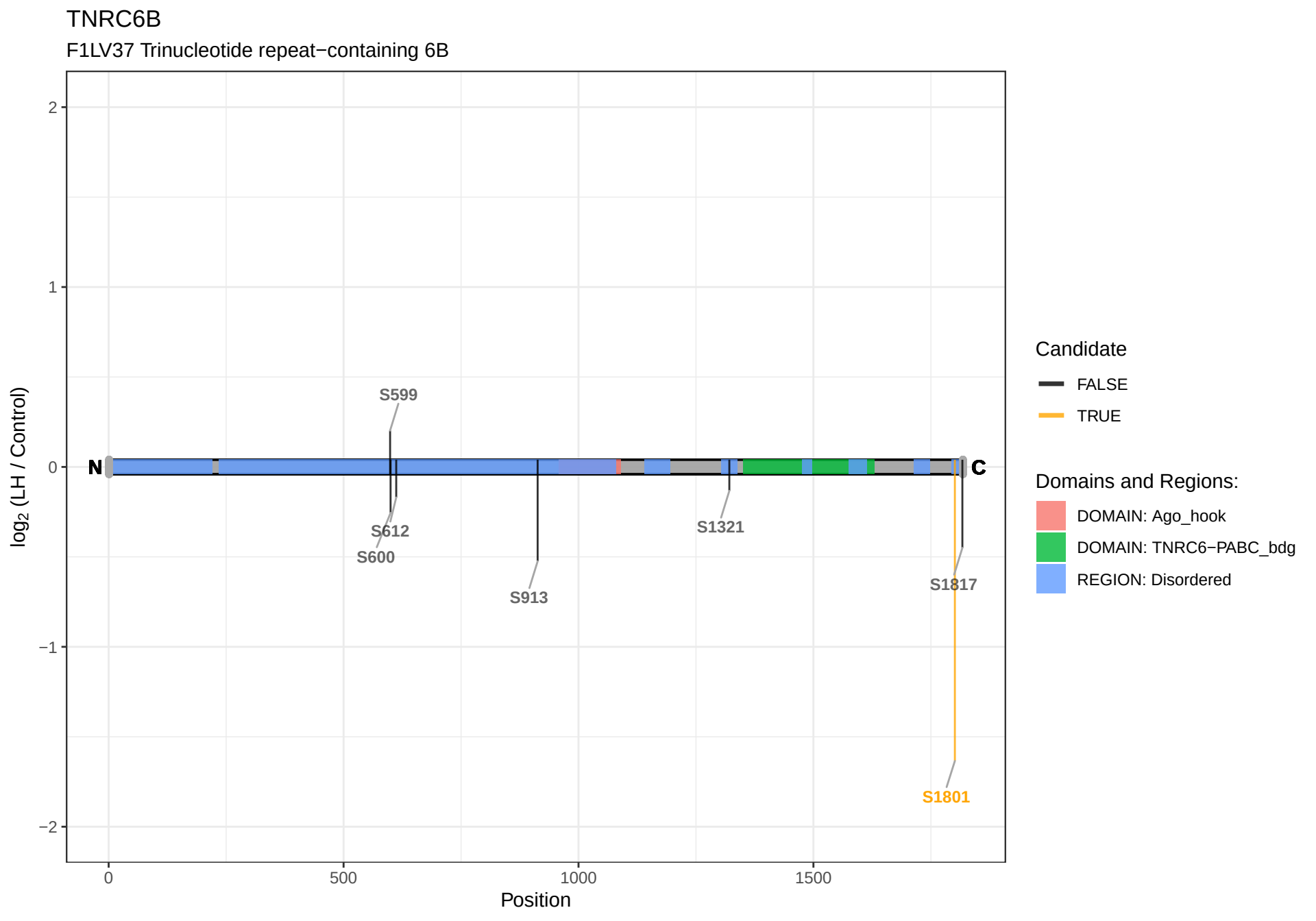

TMPO
Q62733 Lamina−associated polypeptide 2, isoform beta
log2 (LH / Control)
Position
N
C
S176
S179
S183
S155
S157
S158
S167
T163
S166
S66
S67
S79
S82
T74
T159
S288
S291
S384
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: LEM
DOMAIN: LEM−like
REGION: Binds lamins B
REGION: Disordered
REGION: Linker
REGION: NAKAP95−binding C
REGION: NAKAP95−binding N
REGION: Nucleoplasmic

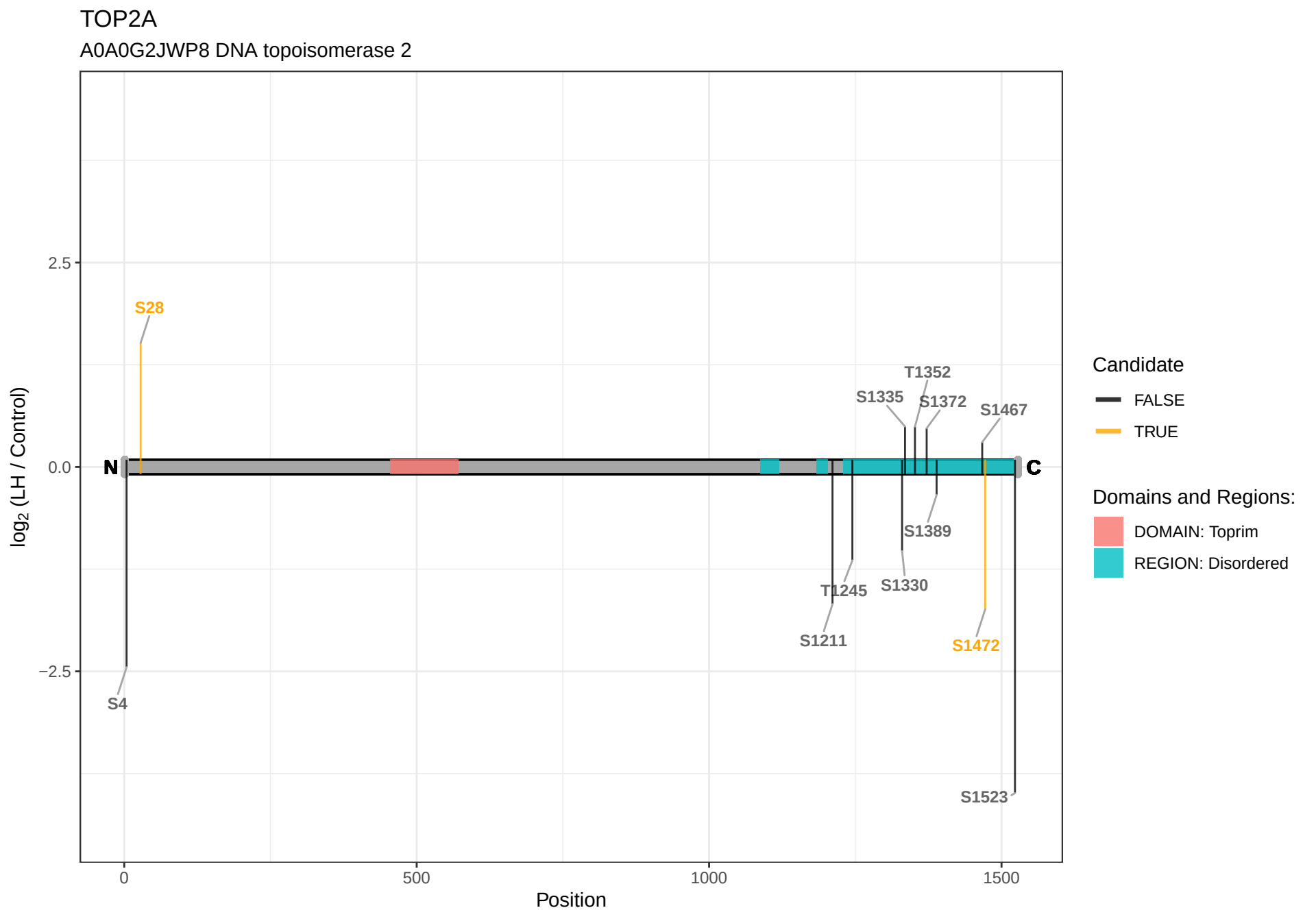

TMUB1
Q53AQ4 Transmembrane and ubiquitin−like domain−containing protein 1
log2 (LH / Control)
3
2
1
0
−1
−2
−3
N
C
S71
0
50
100
150
200
250
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: Ubiquitin−like
REGION: Disordered
REGION: Required to release iHOPS from membranes

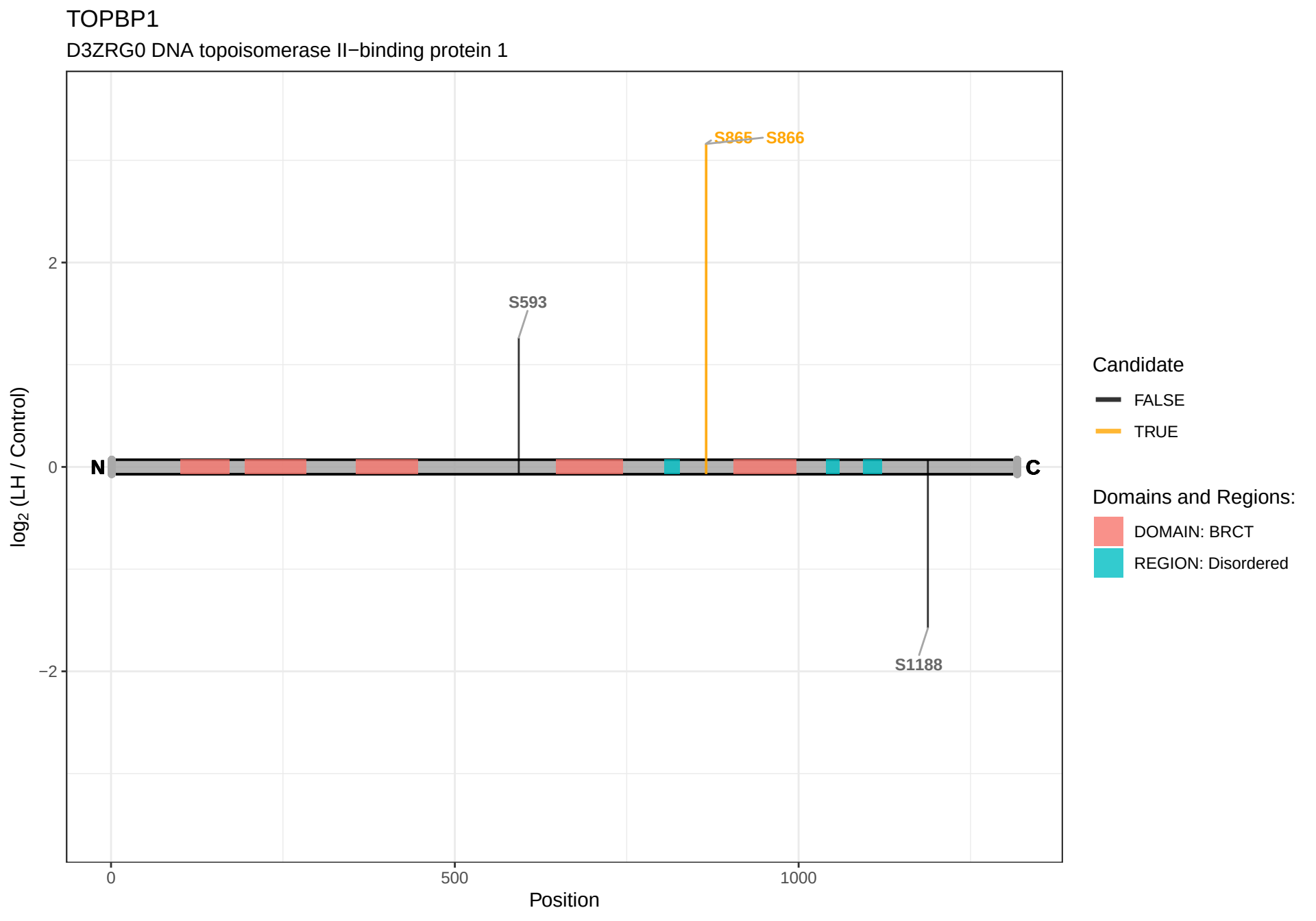

TMX1
Q52KJ9 Thioredoxin domain containing 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
T249
S223
S262
S245
T259
0
100
200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Thioredoxin
REGION: Disordered

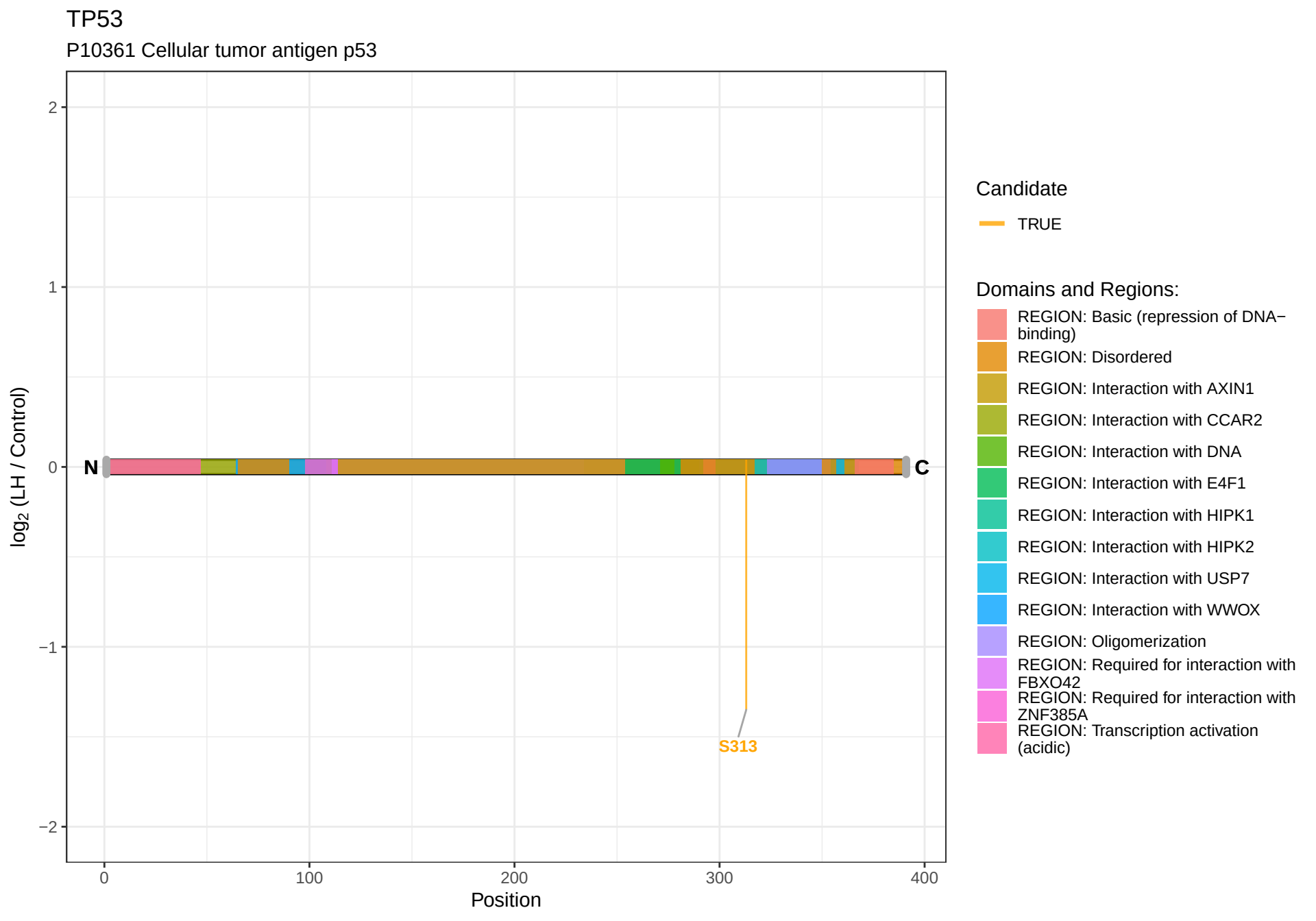

TNIK
D3ZZQ0 Similar to Traf2 and NCK interacting kinase, splice variant 4 (Predicted), isoform CRA_a
log2 (LH / Control)
2
1
0
−1
−2
N
C
S764
S640
S707
S680
S769
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CNH
DOMAIN: Protein kinase
REGION: Disordered

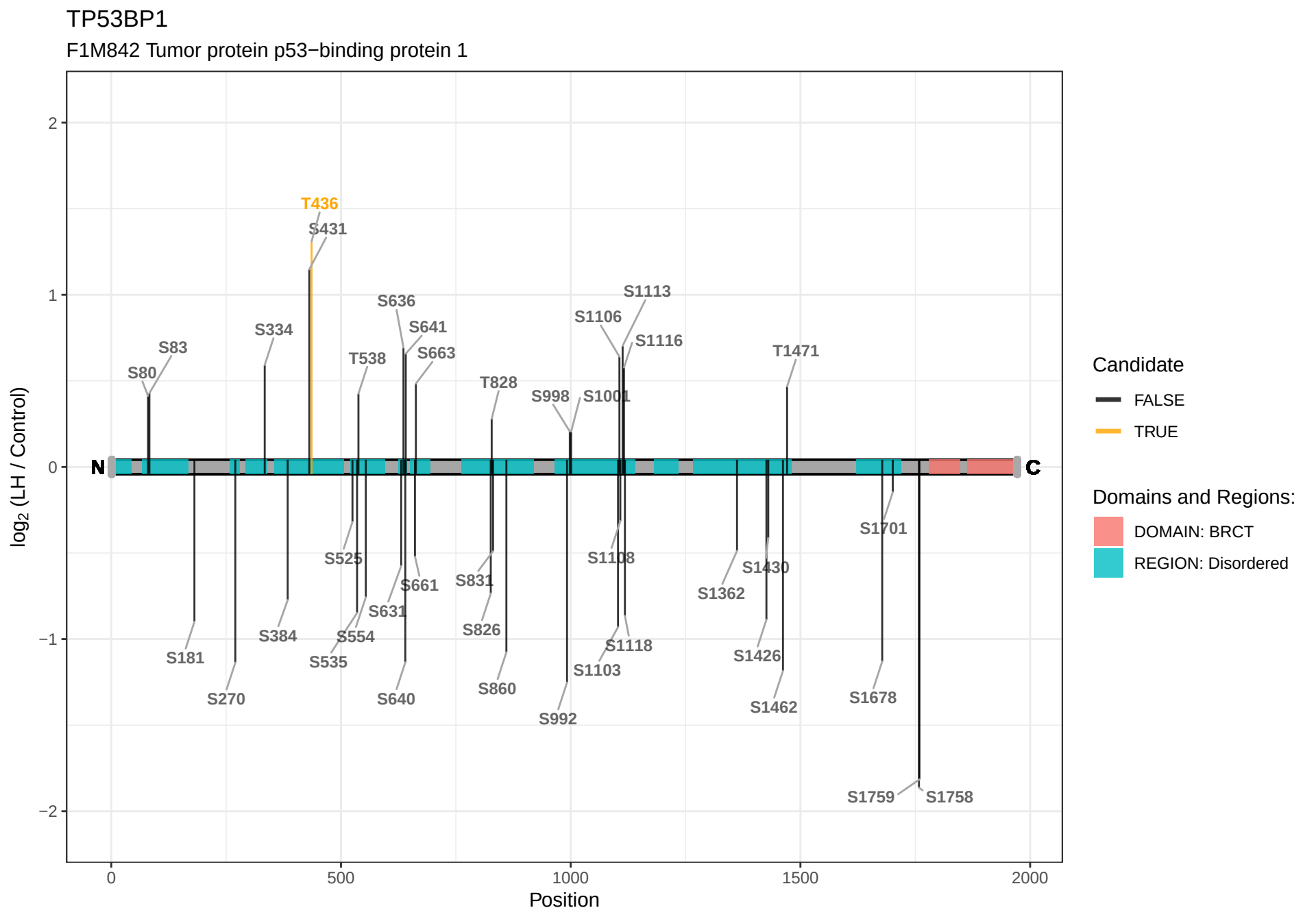

TNRC18
D3ZKV7 Trinucleotide repeat−containing 18
log2 (LH / Control)
2
1
0
−1
−2
0
1000
2000
3000
Position
N
C
S1441
S2703
S1065
S962
S1056
S924
S967
S920
S928
S1790
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: BAH
REGION: Disordered

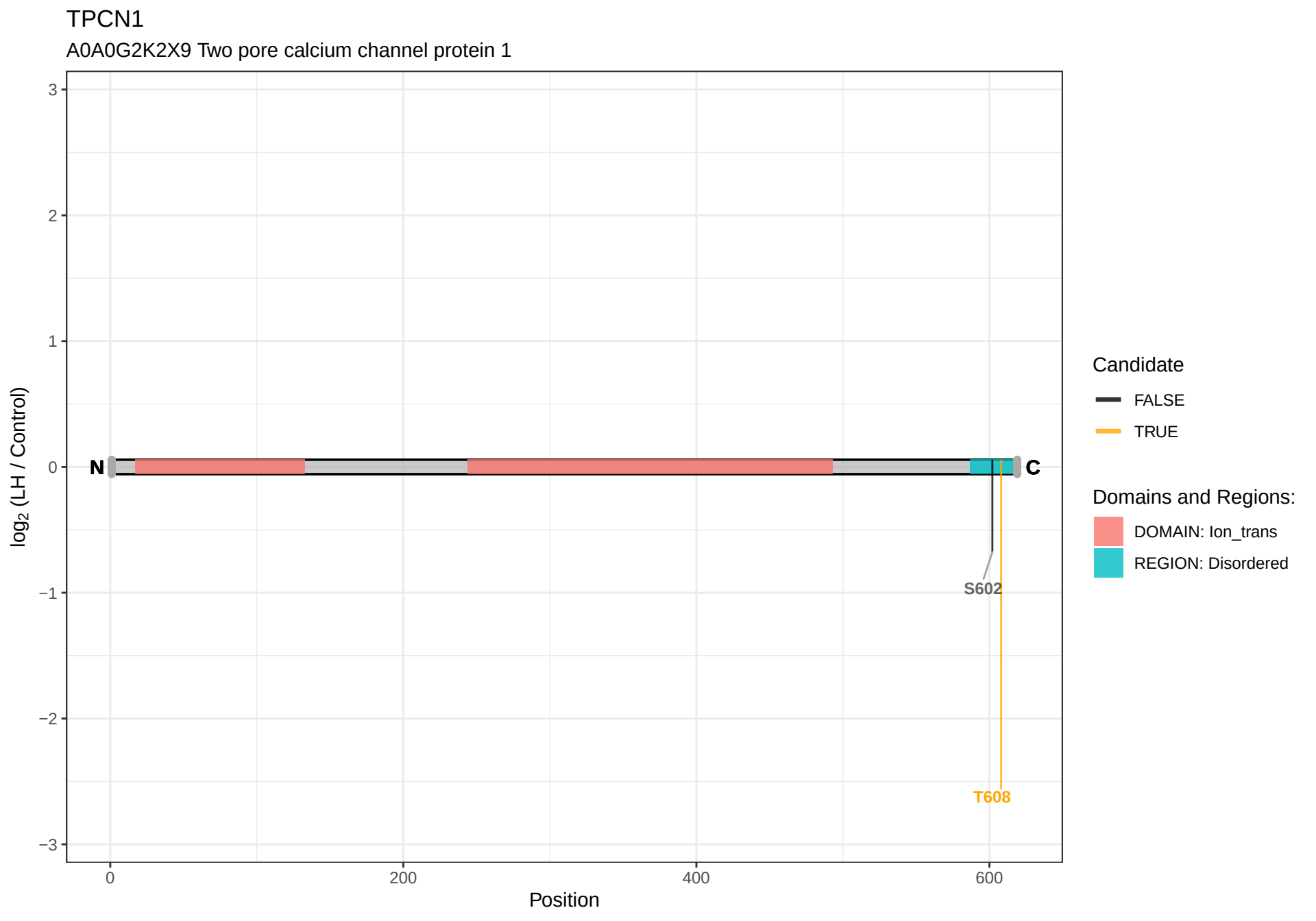

TNRC6B
F1LV37 Trinucleotide repeat−containing 6B
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
Position
N
C
S599
S612
S600
S913
S1321
S1817
S1801
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Ago_hook
DOMAIN: TNRC6−PABC_bdg
REGION: Disordered

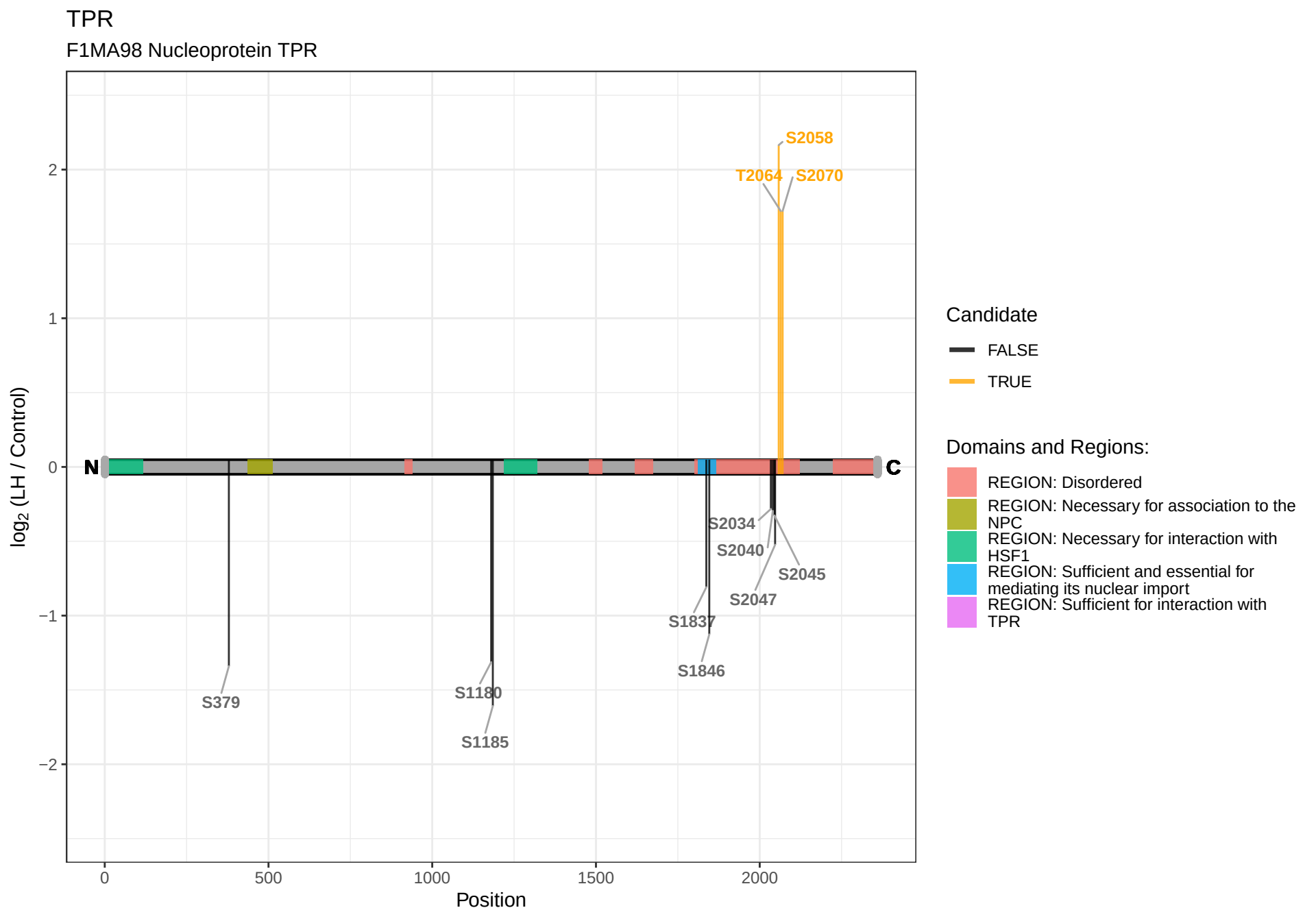

TOP2A
A0A0G2JWP8 DNA topoisomerase 2
2.5
0.0
−2.5
log2 (LH / Control)
N
C
S28
S4
T1352
S1335
S1372
S1467
S1389
S1330
T1245
S1211
S1472
S1523
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Toprim
REGION: Disordered

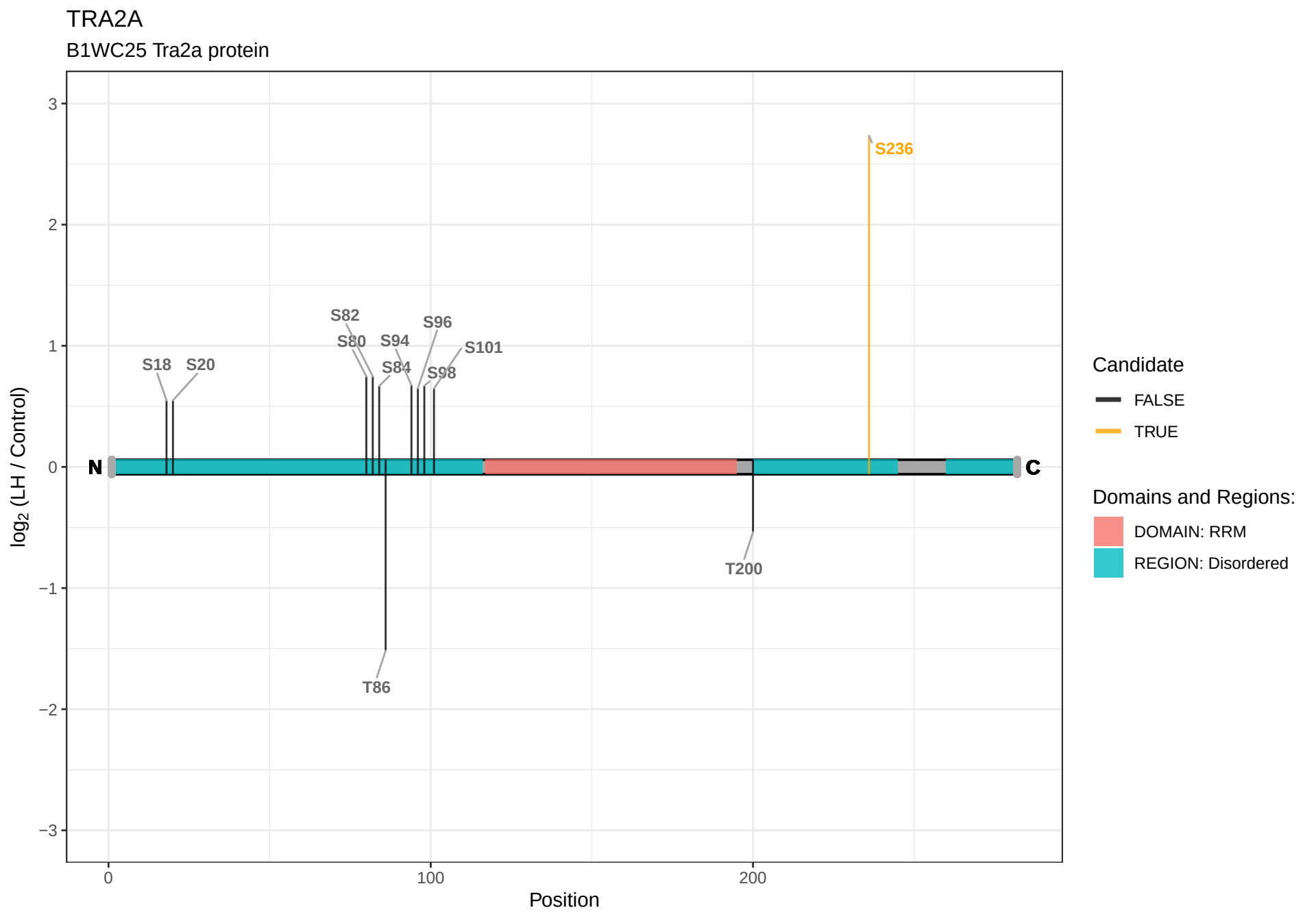

TOPBP1
D3ZRG0 DNA topoisomerase II−binding protein 1
S865
S866
S593
S1188
N
C
2
0
−2
log2 (LH / Control)
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: BRCT
REGION: Disordered

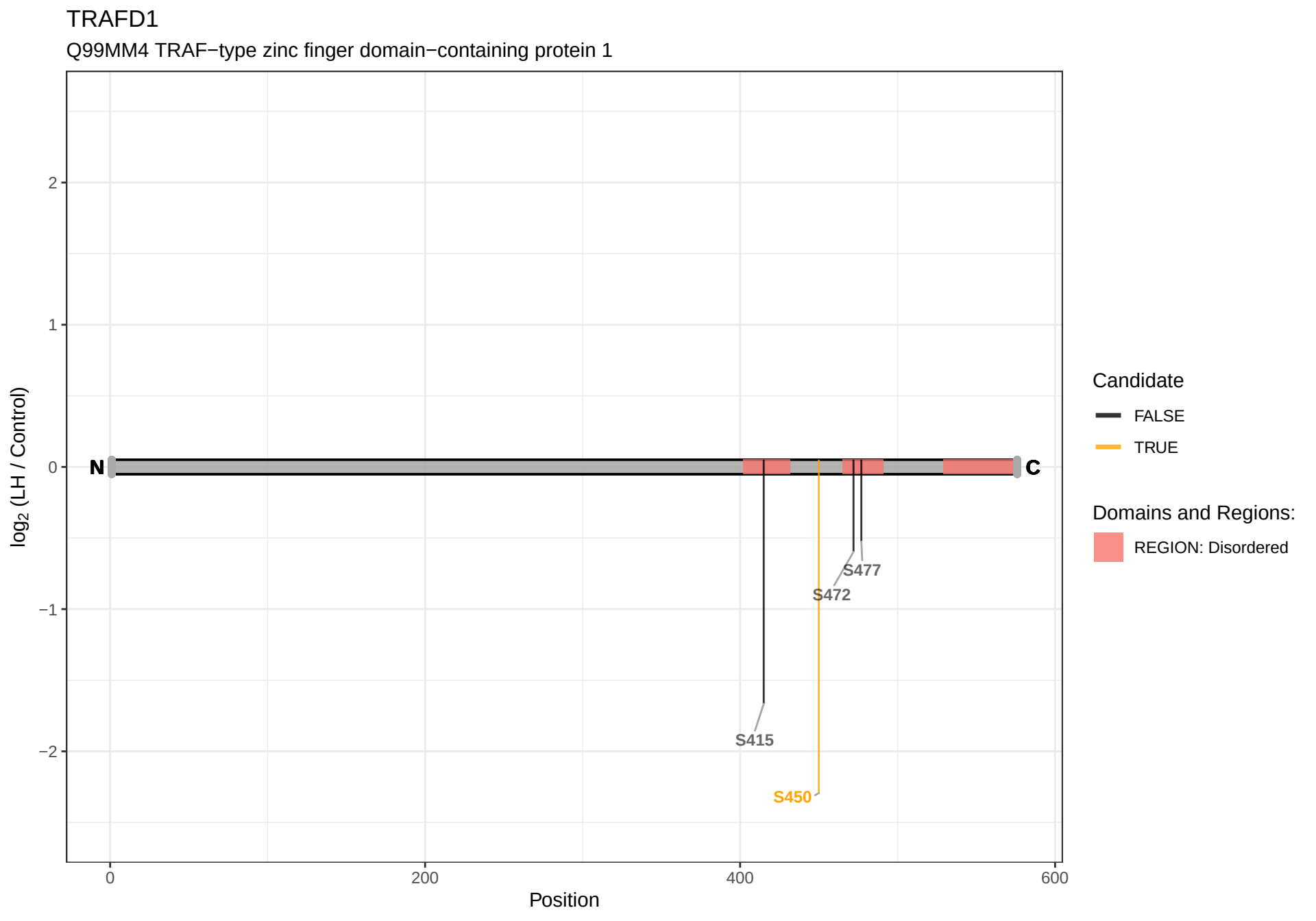

TP53
P10361 Cellular tumor antigen p53
log2 (LH / Control)
2
1
0
−1
−2
N
C
S313
0
100
200
300
400
Position
Candidate
TRUE
Domains and Regions:
REGION: Basic (repression of DNA−binding)
REGION: Disordered
REGION: Interaction with AXIN1
REGION: Interaction with CCAR2
REGION: Interaction with DNA
REGION: Interaction with E4F1
REGION: Interaction with HIPK1
REGION: Interaction with HIPK2
REGION: Interaction with USP7
REGION: Interaction with WWOX
REGION: Oligomerization
REGION: Required for interaction with FBXO42
REGION: Required for interaction with ZNF385A
REGION: Transcription activation (acidic)

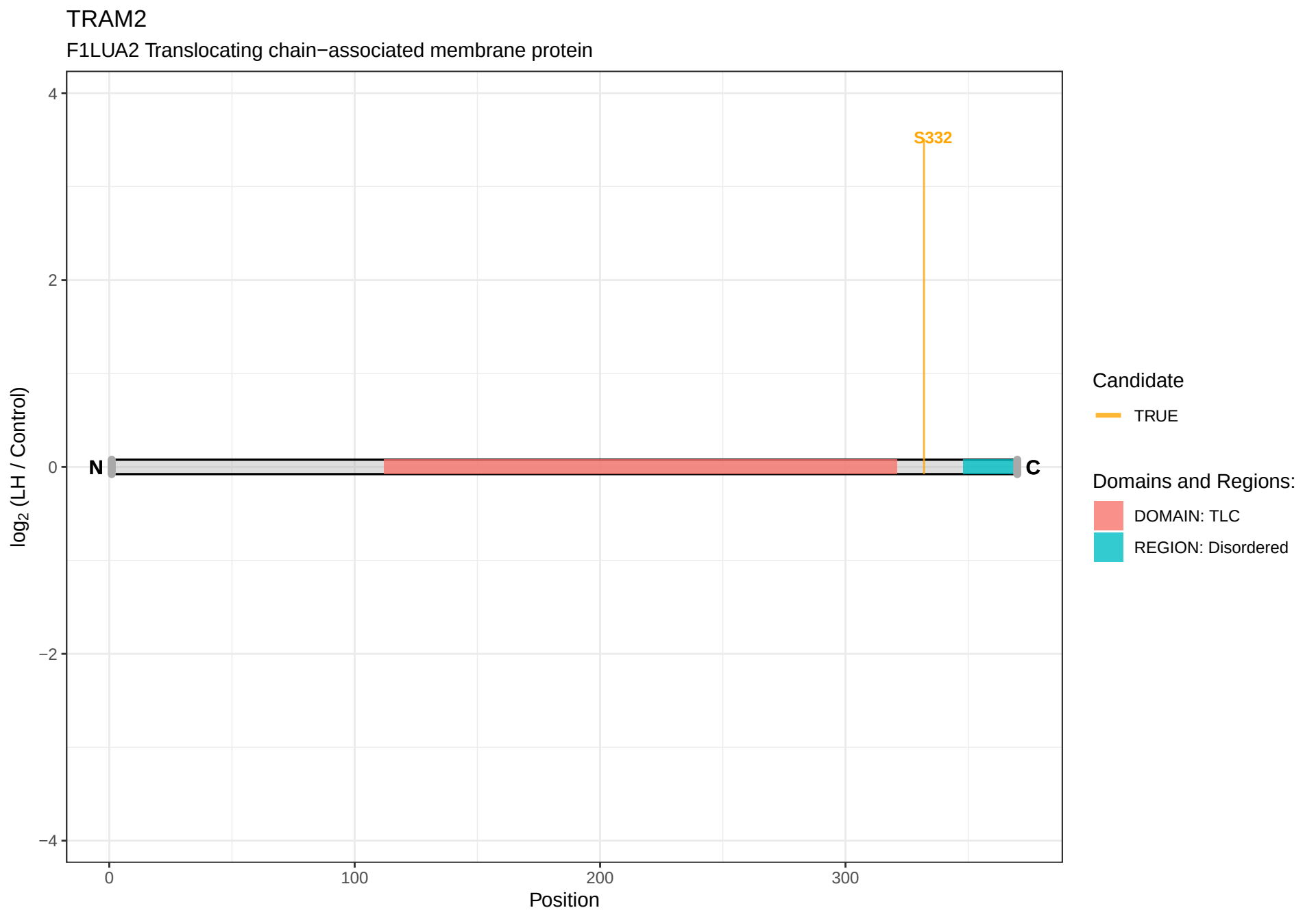

TP53BP1
F1M842 Tumor protein p53−binding protein 1
log2 (LH / Control)
Position
N
C
T436
S431
S636
S641
S663
S1113
S1106
S1116
S334
S83
S80
T538
T828
S998
S1001
T1471
S525
S661
S831
S1108
S1701
S1430
S1362
S631
S384
S554
S826
S1118
S1426
S181
S535
S1103
S270
S640
S860
S1678
S992
S1462
S1759
S1758
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: BRCT
REGION: Disordered

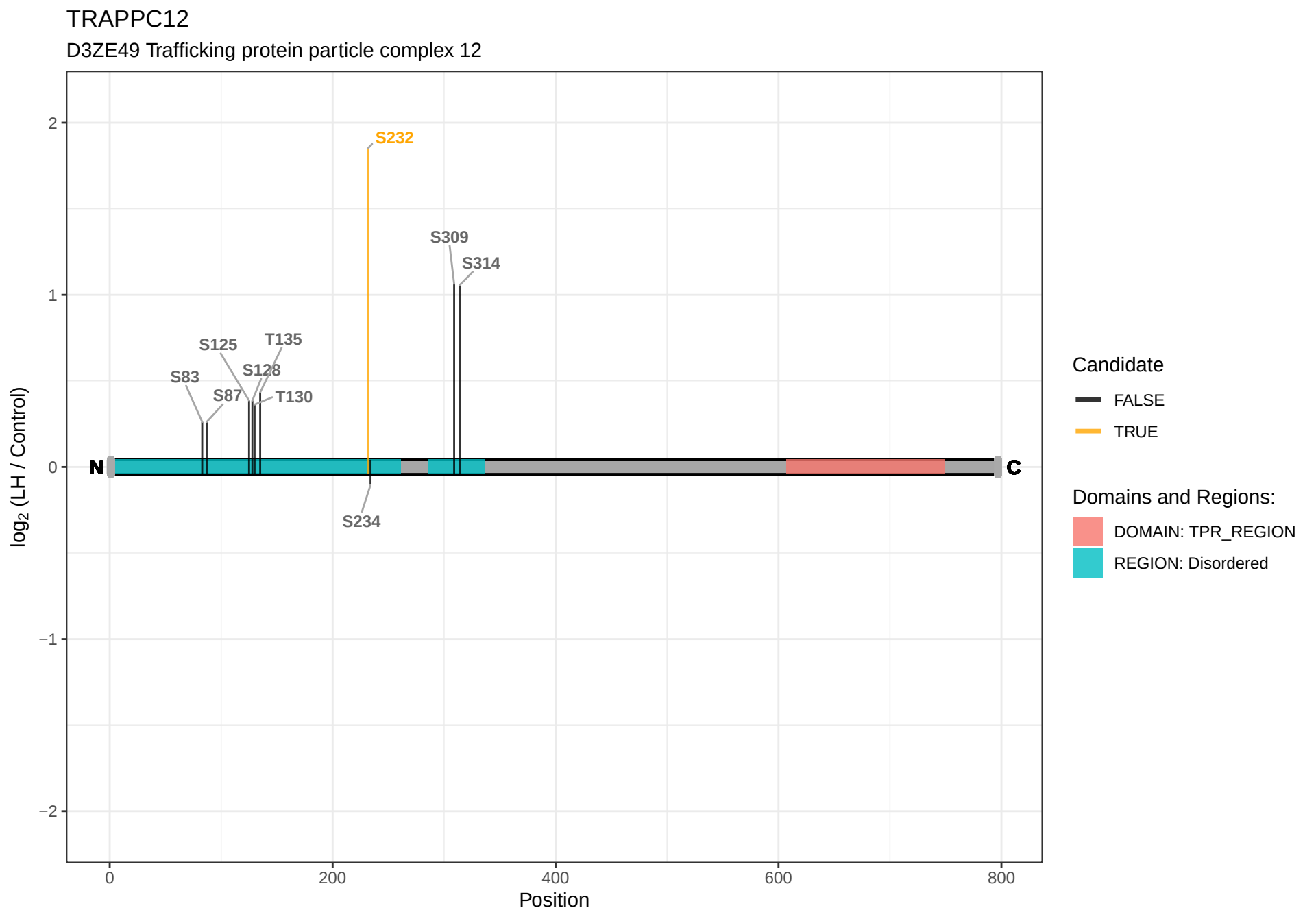

TPCN1
A0A0G2K2X9 Two pore calcium channel protein 1
log2 (LH / Control)
3
2
1
0
−1
−2
−3
N
C
S602
T608
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Ion_trans
REGION: Disordered

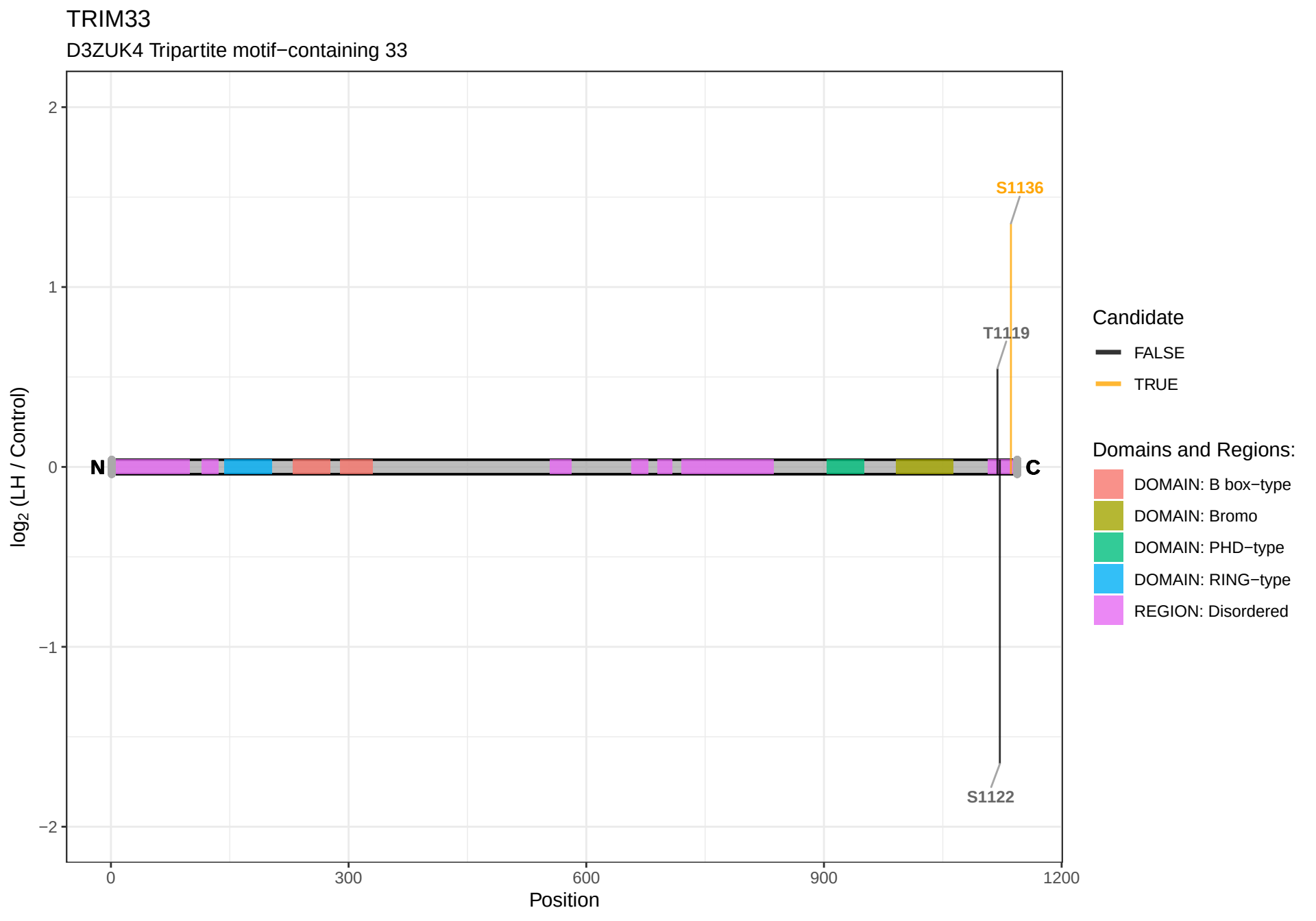

TPR
F1MA98 Nucleoprotein TPR
S2058
T2064
S2070
S2034
S2040
S2045
S2047
S1837
S1846
S379
S1180
S1185
N
C
log2 (LH / Control)
Position
0
500
1000
1500
2000
2
1
0
−1
−2
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Necessary for association to the NPC
REGION: Necessary for interaction with HSF1
REGION: Sufficient and essential for mediating its nuclear import
REGION: Sufficient for interaction with TPR

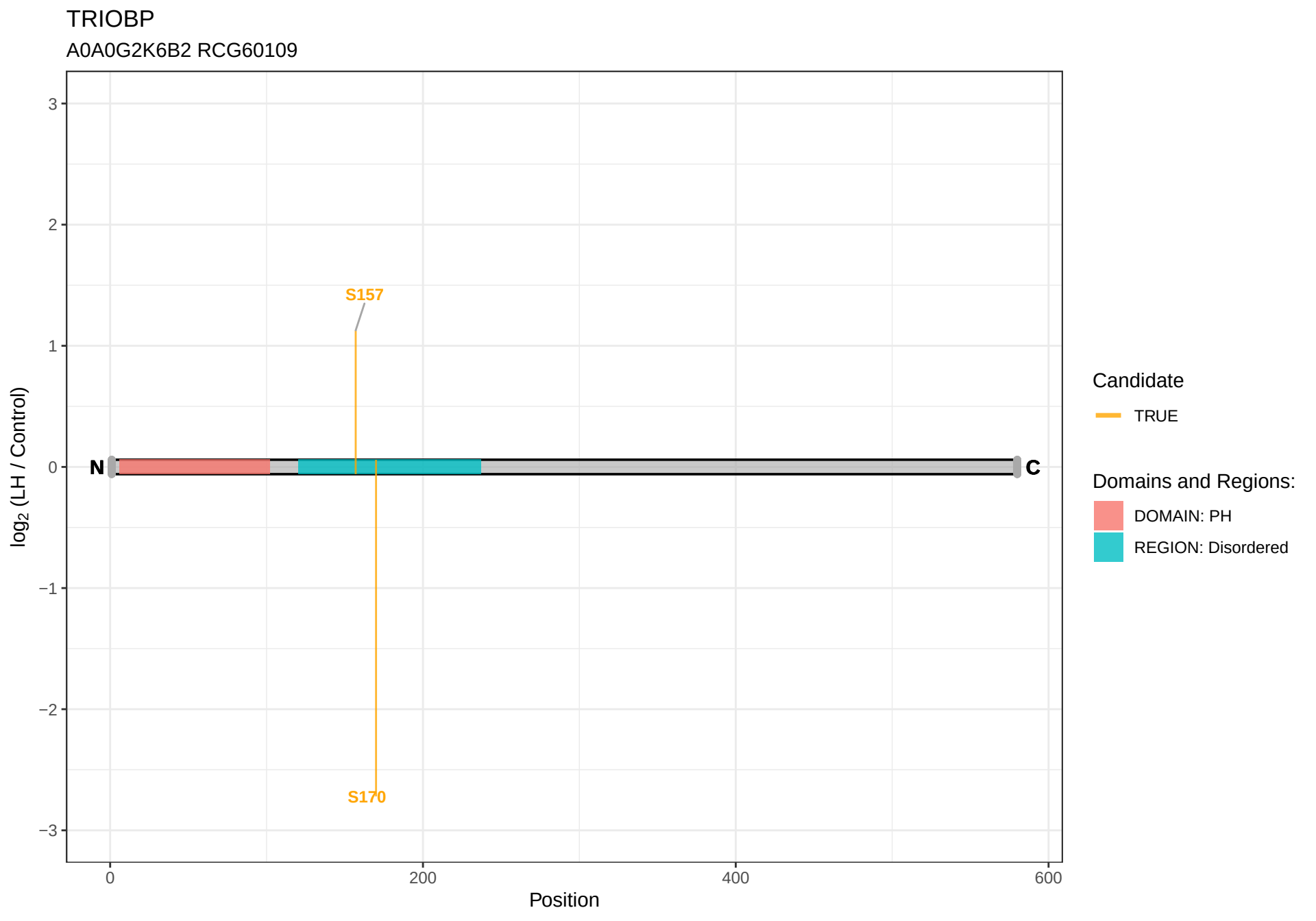

TRA2A
B1WC25 Tra2a protein
log2 (LH / Control)
Position
N
C
S18
S20
S82
S80
S94
S84
S96
S98
S101
T86
T200
S236
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RRM
REGION: Disordered

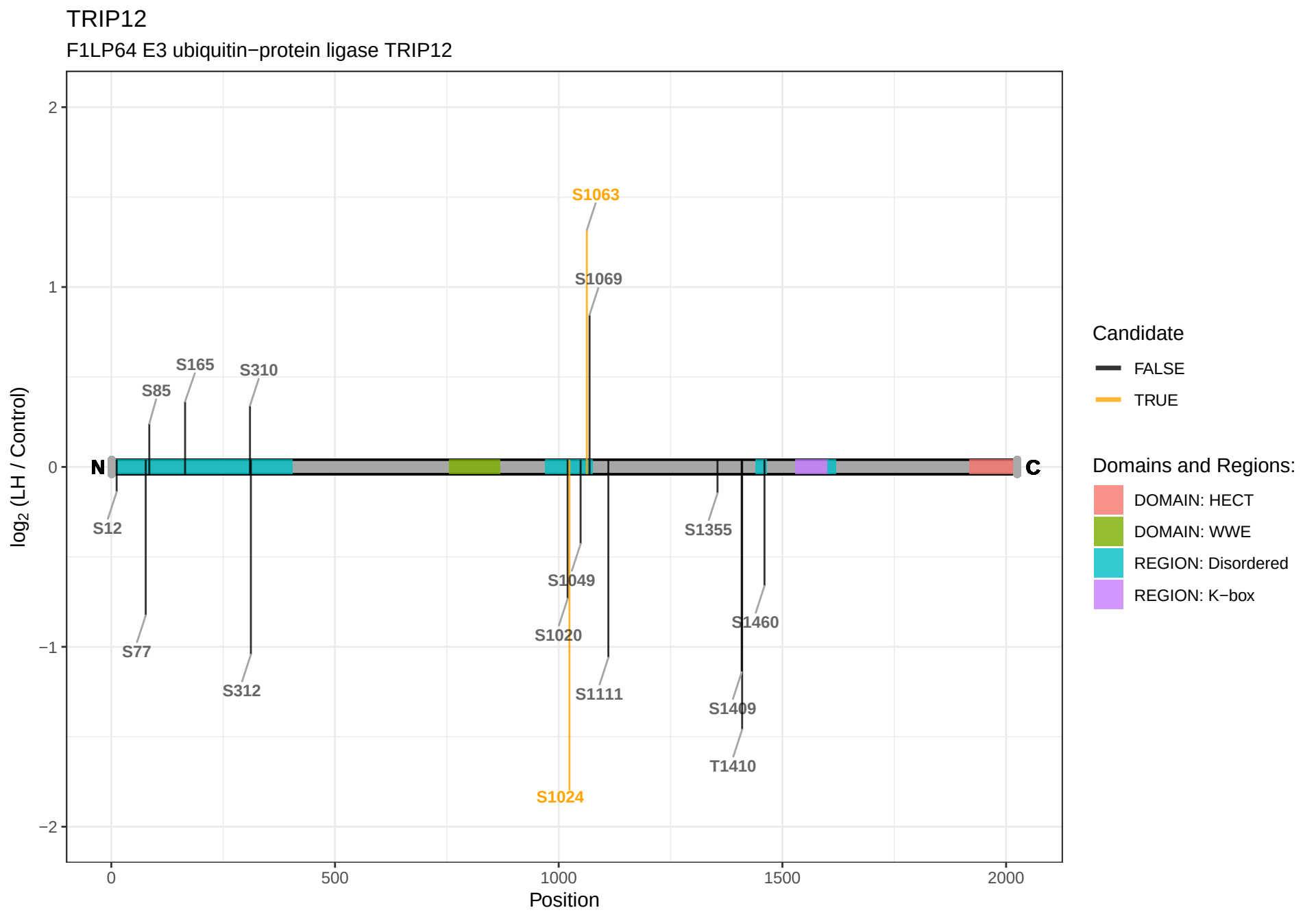

TRAFD1
Q99MM4 TRAF−type zinc finger domain−containing protein 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S415
S450
S472
S477
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

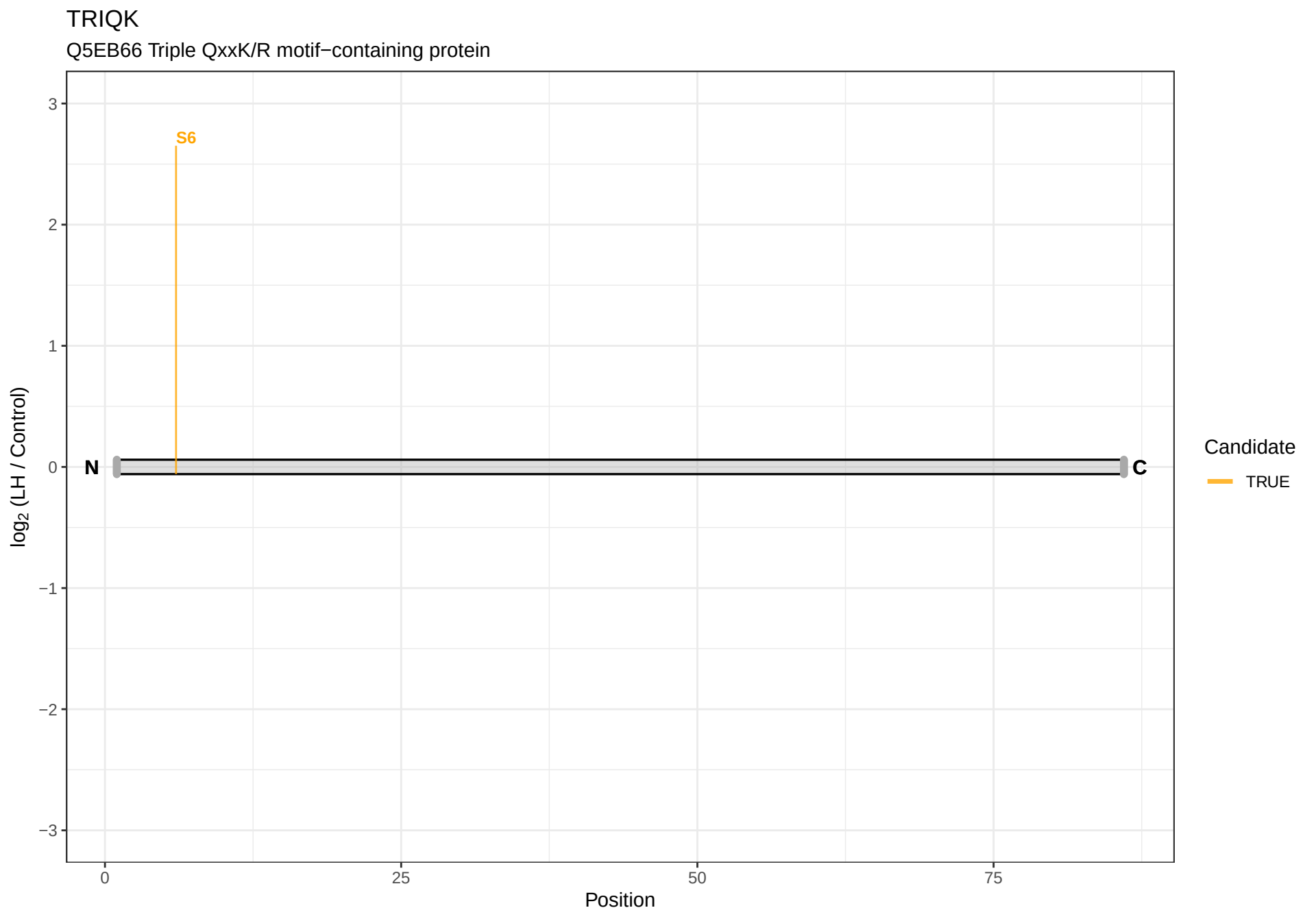

TRAM2
F1LUA2 Translocating chain−associated membrane protein
S332
N
C
4
2
0
−2
−4
0
100
200
300
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
DOMAIN: TLC
REGION: Disordered

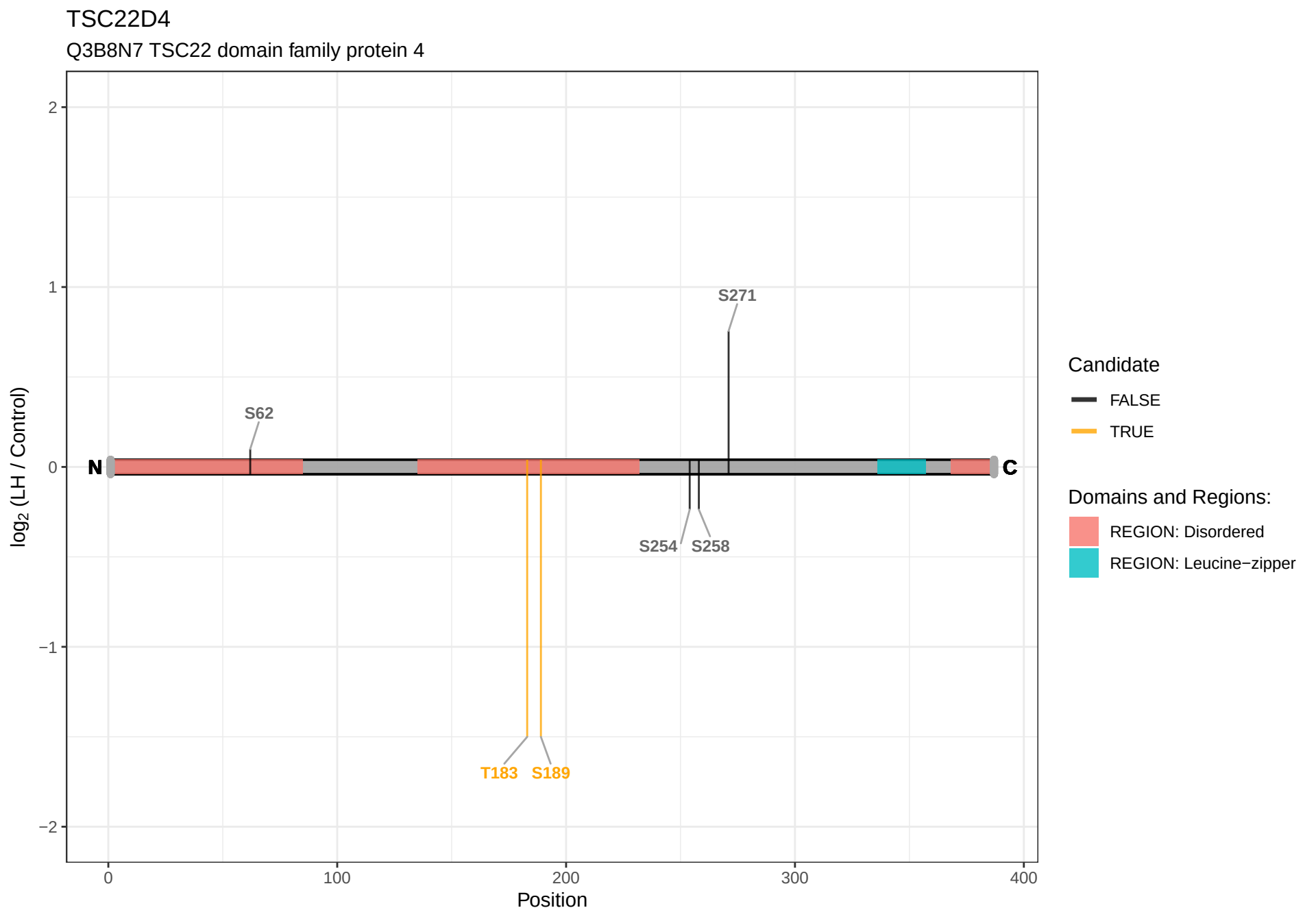

TRAPPC12
D3ZE49 Trafficking protein particle complex 12
S232
S309
S314
S125
T135
S83
S128
S87
T130
S234
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: TPR_REGION
REGION: Disordered

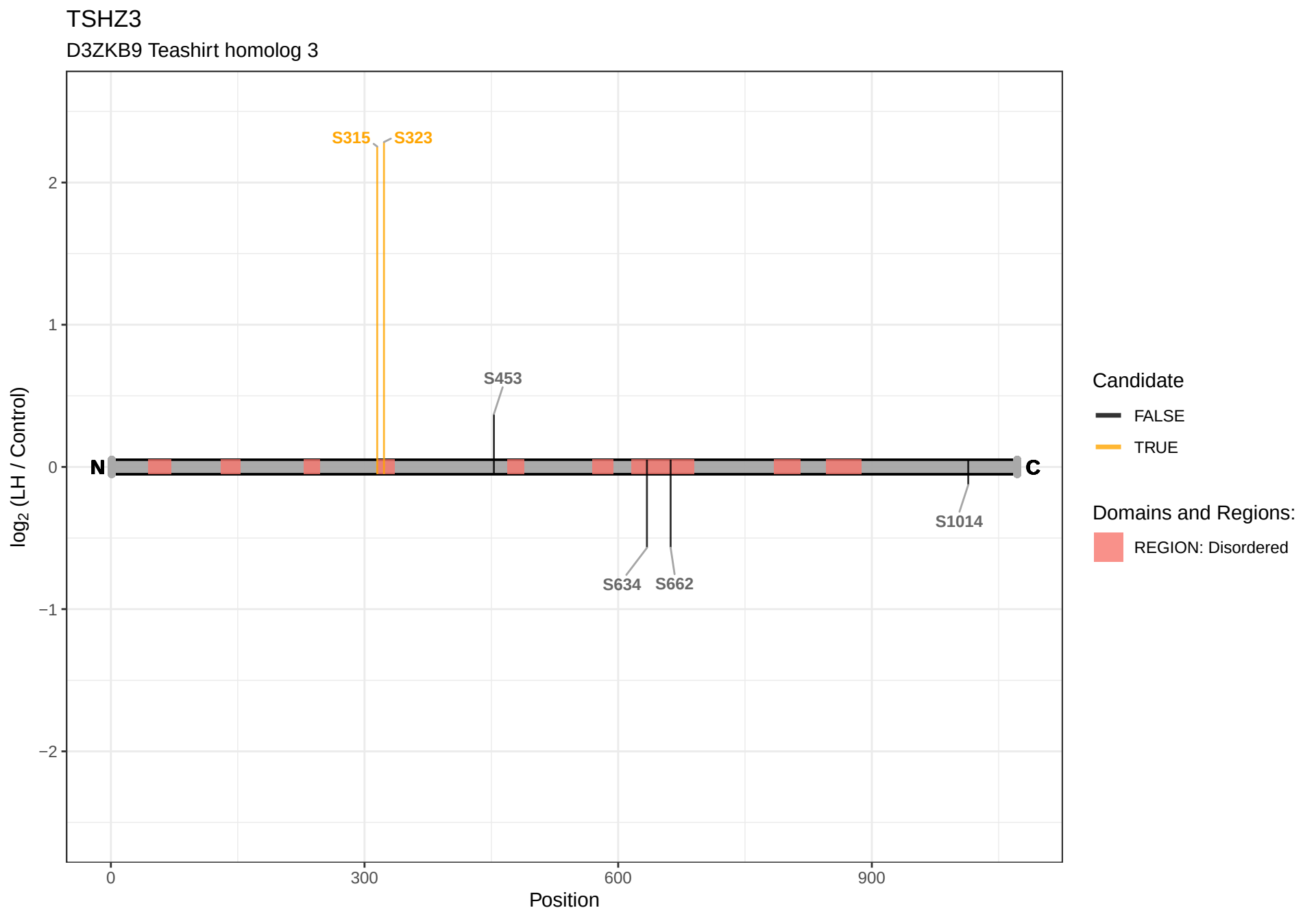

TRIM33
D3ZUK4 Tripartite motif−containing 33
2
1
0
−1
−2
log2 (LH / Control)
S1136
T1119
S1122
N
C
0
300
600
900
1200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: B box−type
DOMAIN: Bromo
DOMAIN: PHD−type
DOMAIN: RING−type
REGION: Disordered

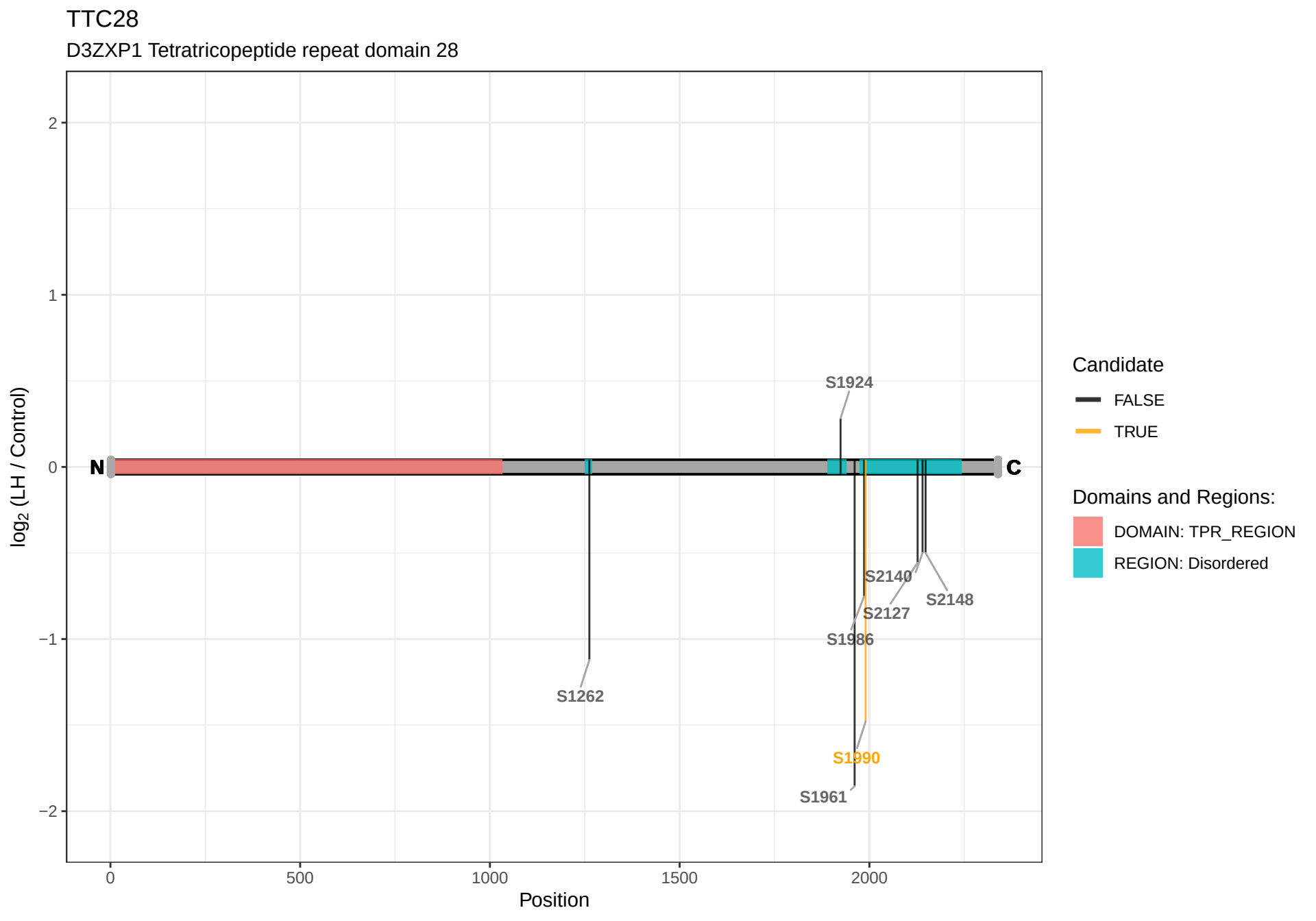

TRIOBP
A0A0G2K6B2 RCG60109
3
2
1
0
−1
−2
−3
log2 (LH / Control)
S157
S170
N
C
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: PH
REGION: Disordered

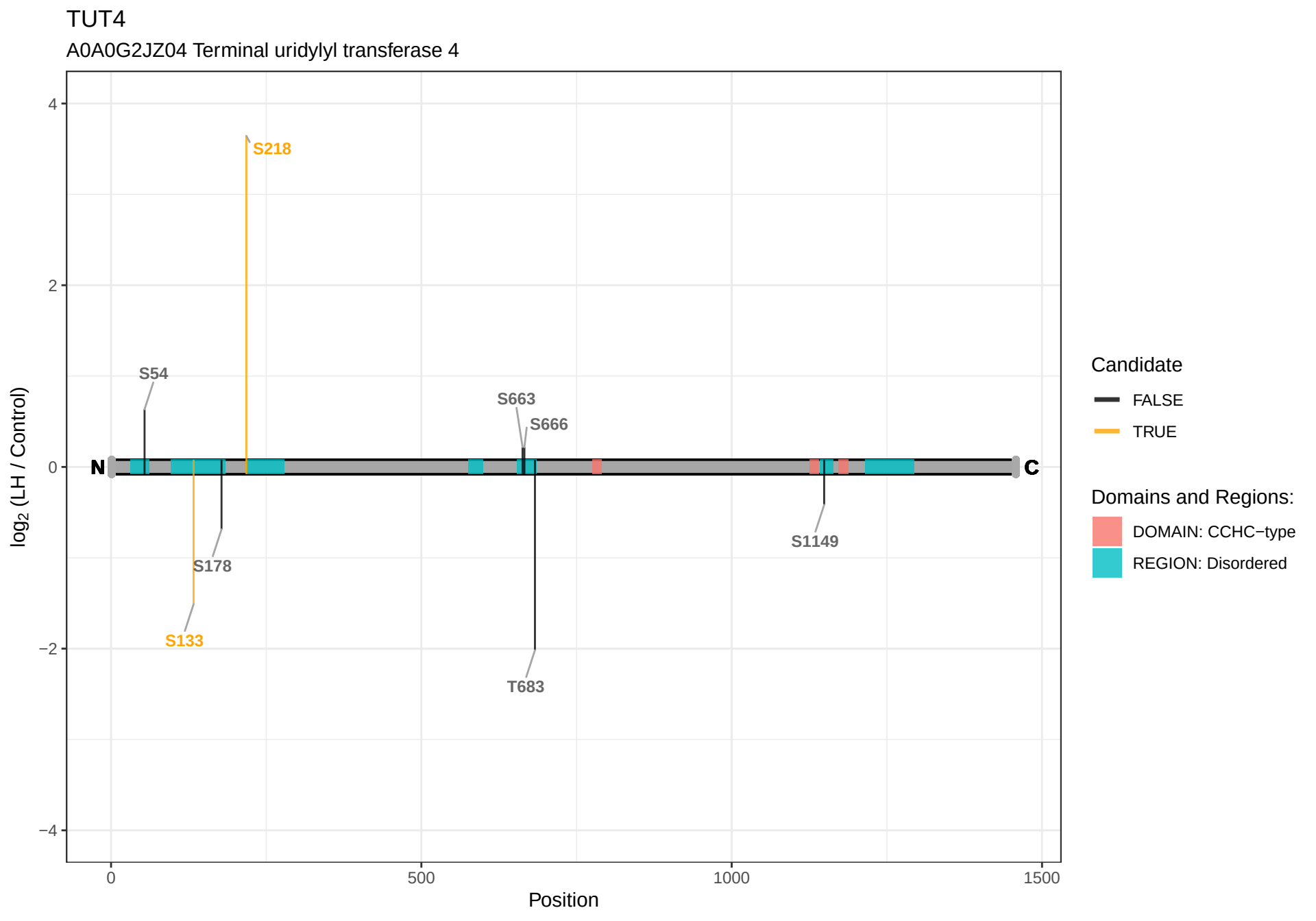

TRIP12
F1LP64 E3 ubiquitin−protein ligase TRIP12
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
2000
Position
N
C
S12
S85
S165
S310
S77
S312
S1063
S1069
S1049
S1020
S1024
S1111
S1355
S1460
S1409
T1410
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: HECT
DOMAIN: WWE
REGION: Disordered
REGION: K−box

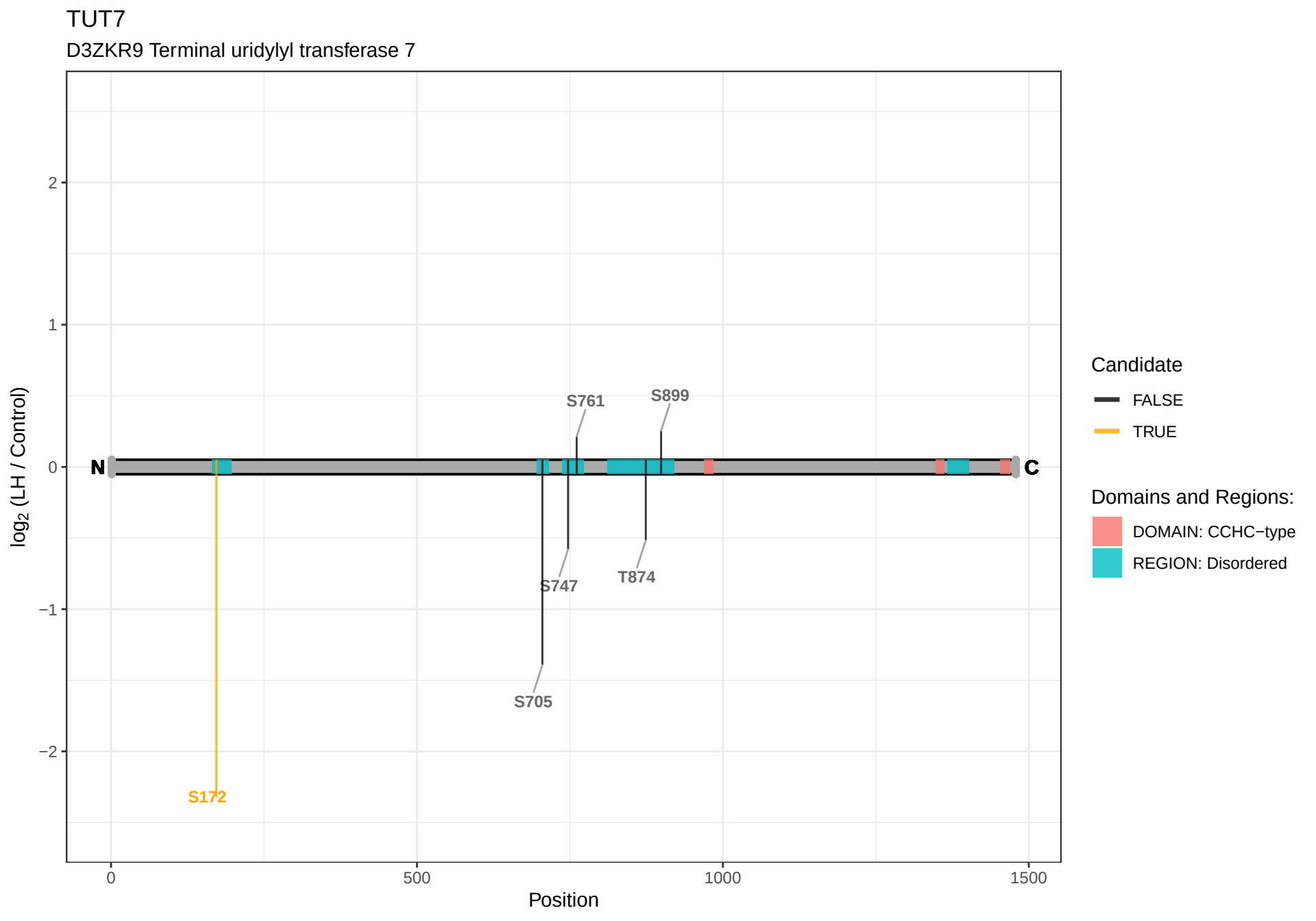

TRIQK
Q5EB66 Triple QxxK/R motif−containing protein
S6
N
C
3
2
1
0
−1
−2
−3
0
25
50
75
Position
log2 (LH / Control)
Candidate
TRUE

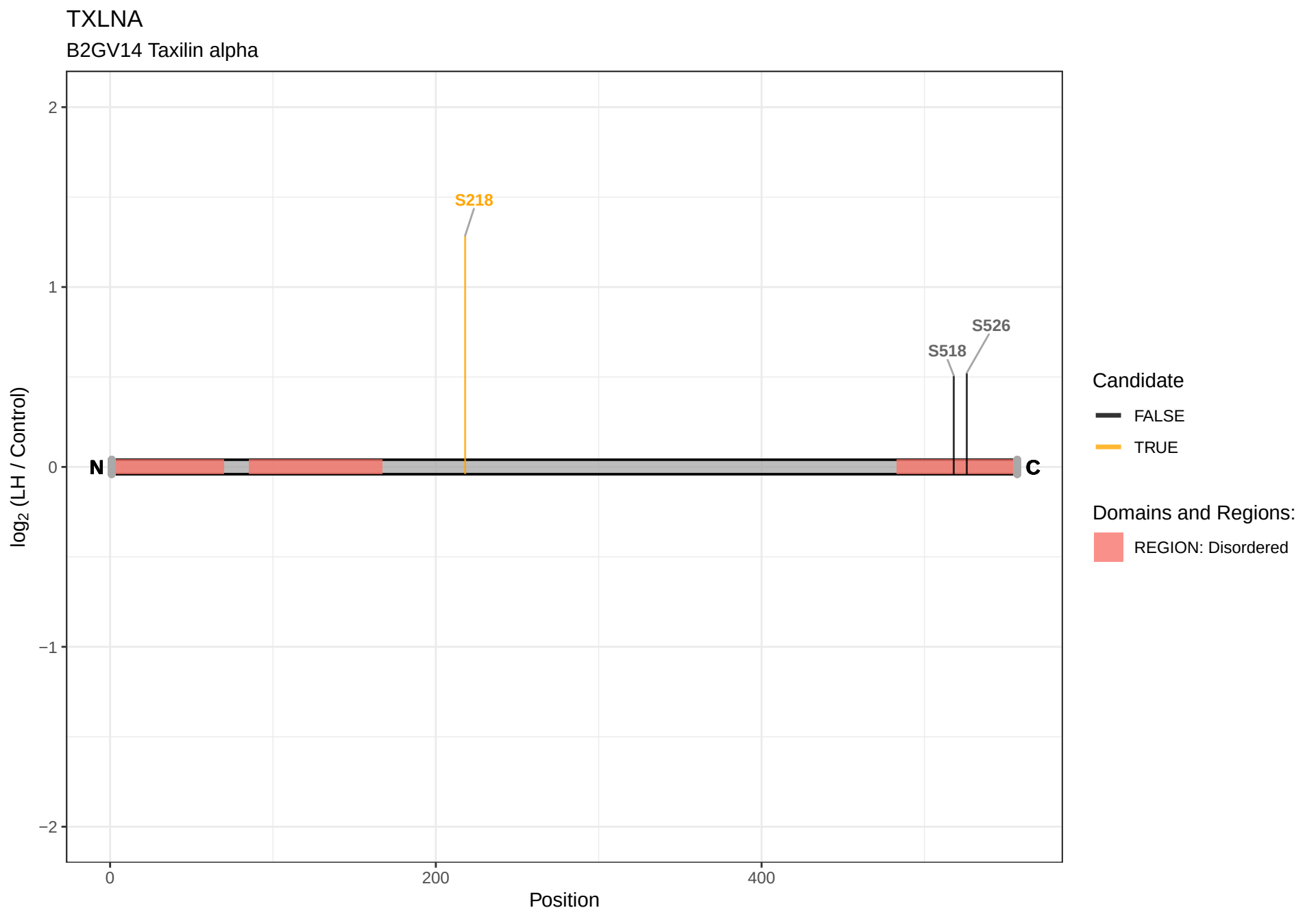

TSC22D4
Q3B8N7 TSC22 domain family protein 4
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
400
Position
N
C
S62
S271
S254
S258
T183
S189
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Leucine−zipper

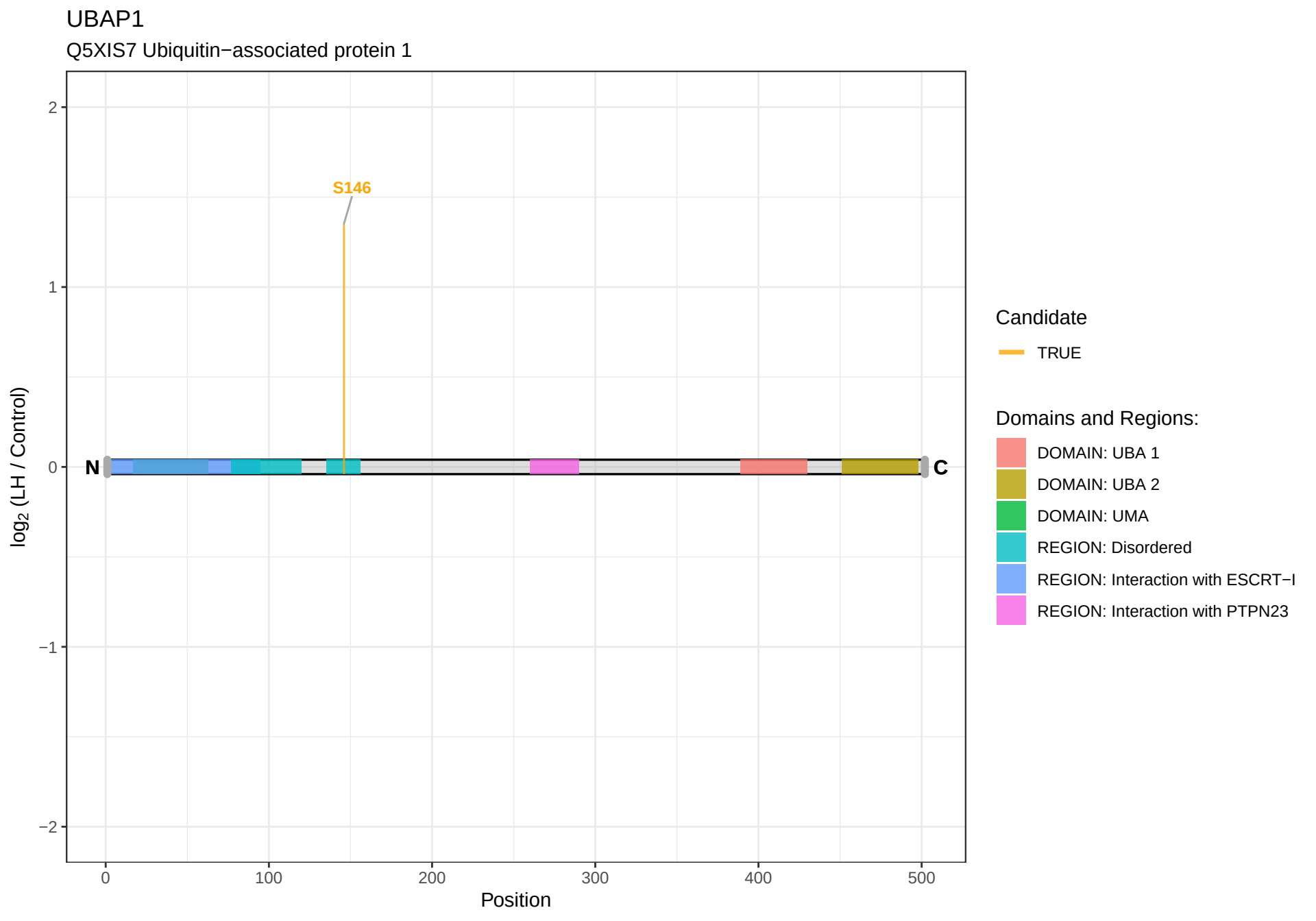

TSHZ3
D3ZKB9 Teashirt homolog 3
S315
S323
S453
S634
S662
S1014
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

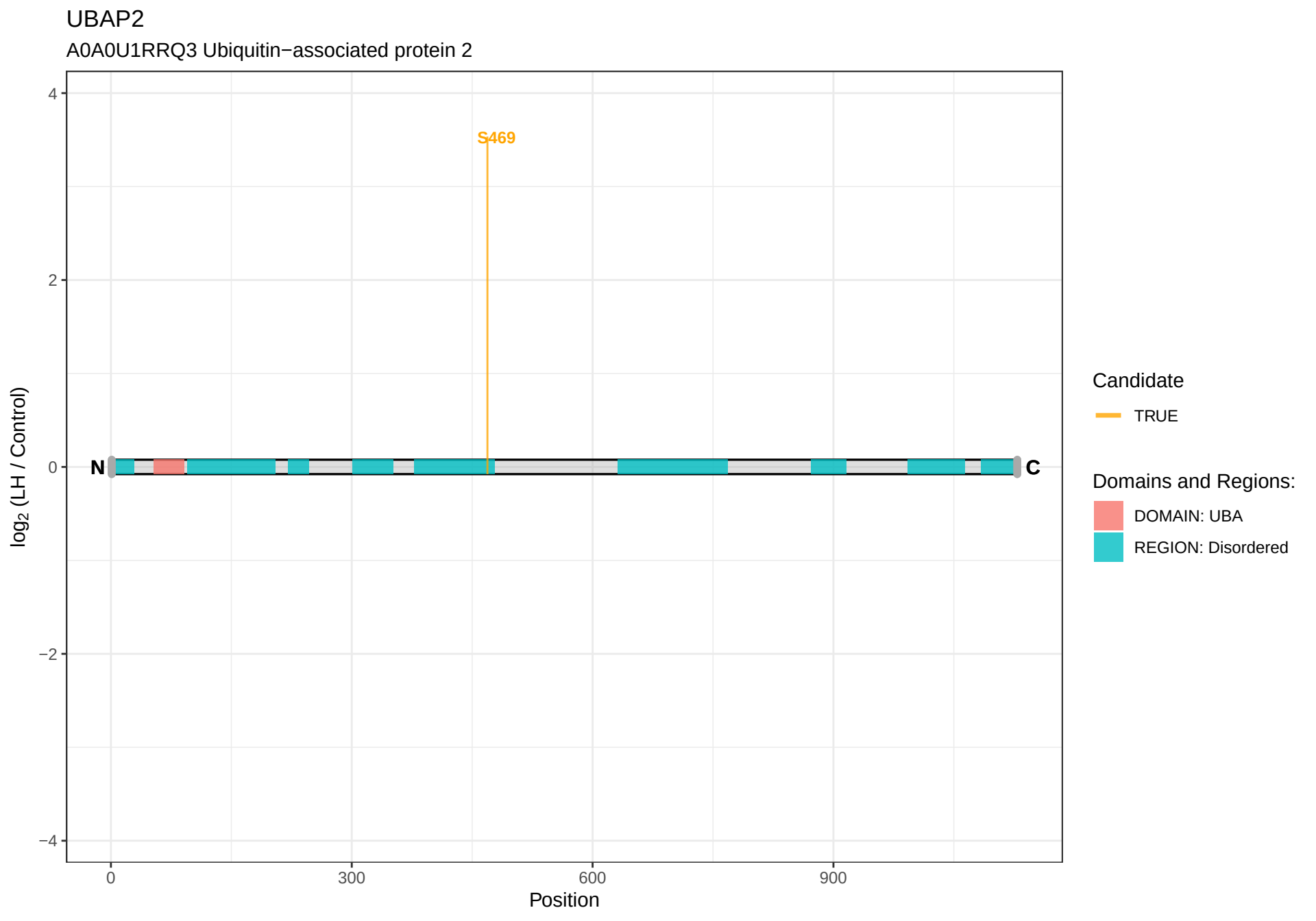

TTC28
D3ZXP1 Tetratricopeptide repeat domain 28
log2 (LH / Control)
2
1
0
−1
−2
N
C
S1924
S2140
S2148
S2127
S1986
S1262
S1990
S1961
0
500
1000
1500
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: TPR_REGION
REGION: Disordered

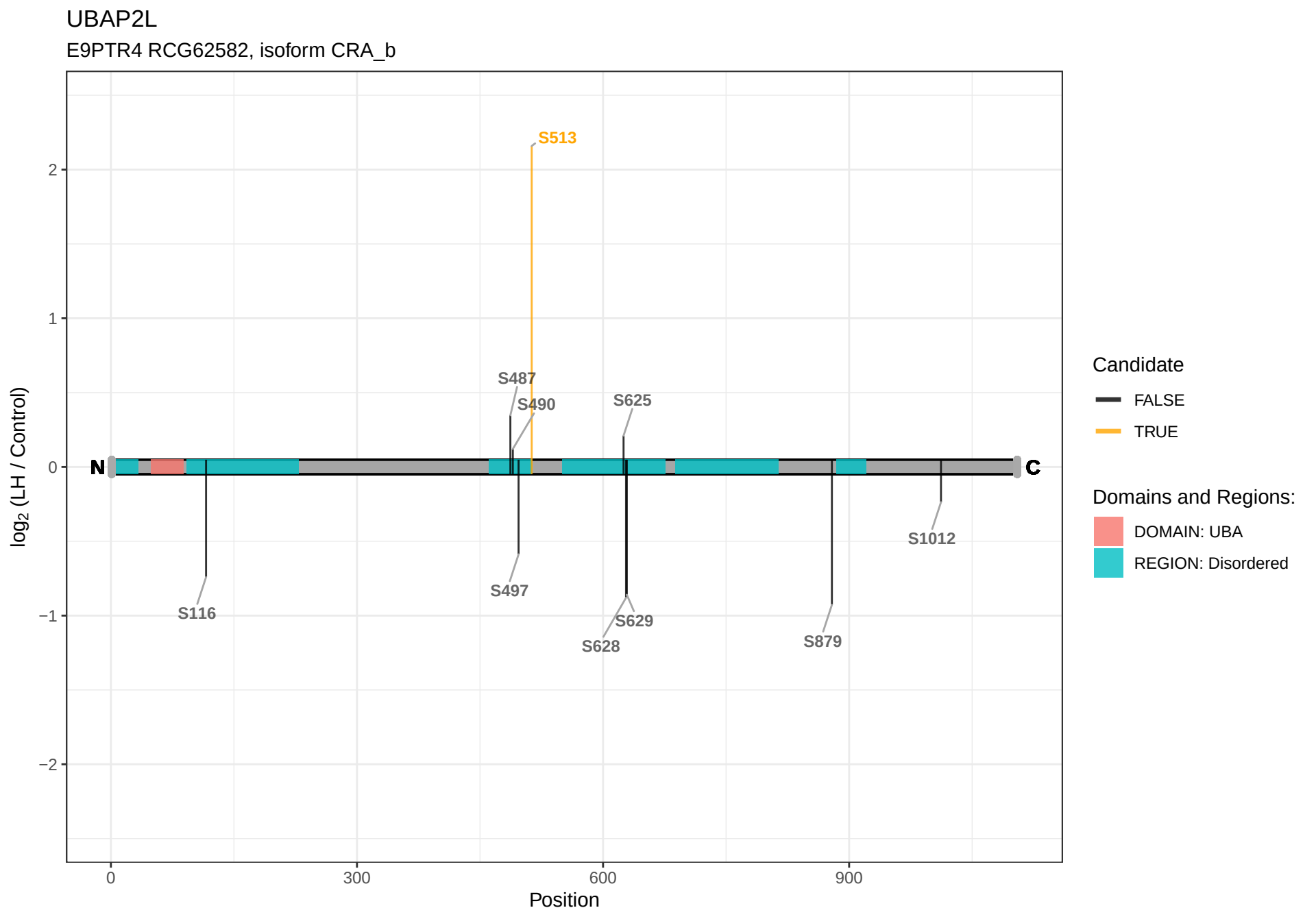

TUT4
A0A0G2JZ04 Terminal uridylyl transferase 4
log2 (LH / Control)
4
2
0
−2
−4
0
500
1000
1500
Position
N
C
S218
S54
S663
S666
S178
S133
T683
S1149
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CCHC−type
REGION: Disordered

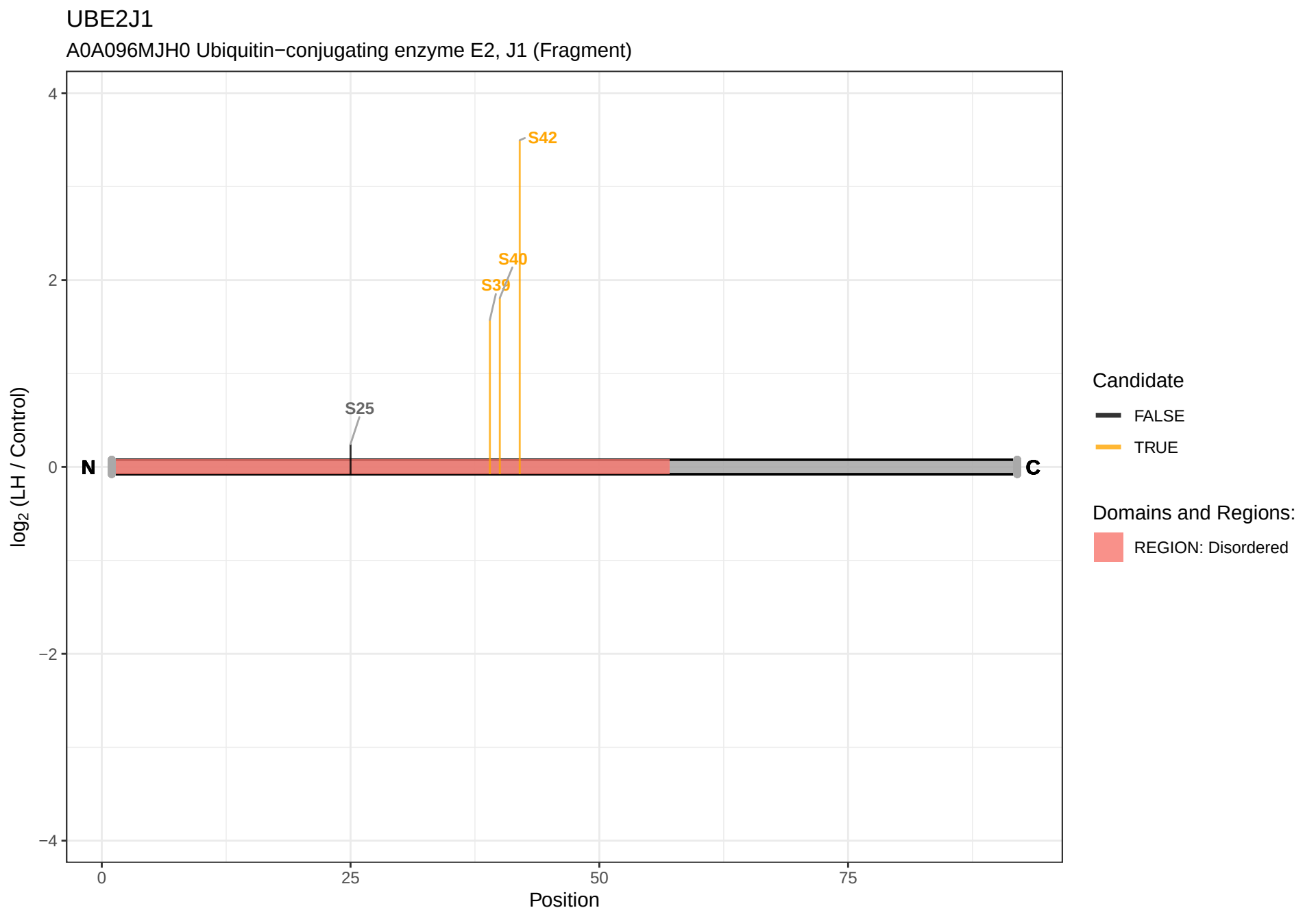

TUT7
D3ZKR9 Terminal uridylyl transferase 7
log2 (LH / Control)
2
1
0
−1
−2
N
C
S761
S899
S747
T874
S705
S172
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CCHC−type
REGION: Disordered

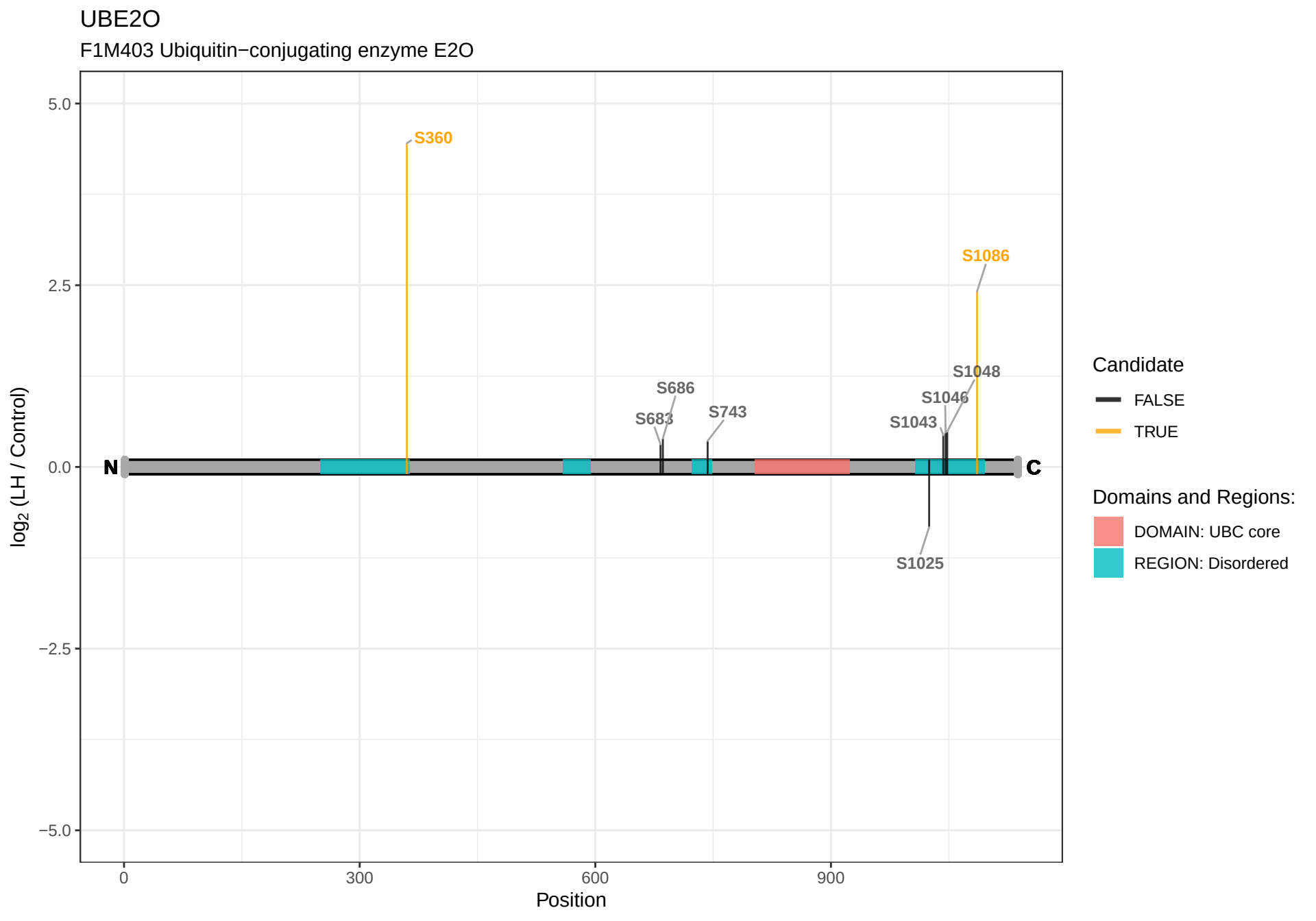

TXLNA
B2GV14 Taxilin alpha
S218
S526
S518
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

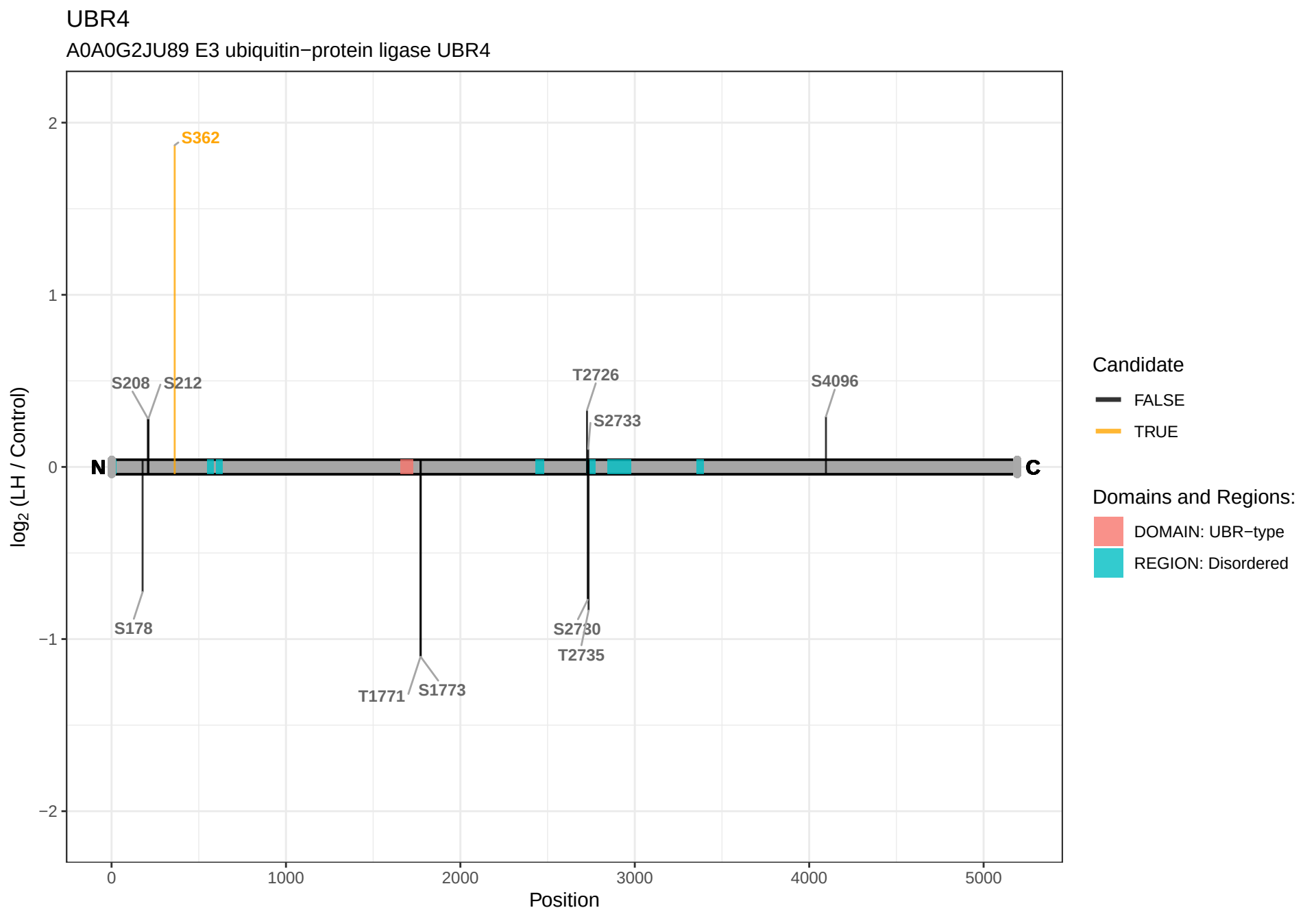

UBAP1
Q5XIS7 Ubiquitin−associated protein 1
S146
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
100
200
300
400
500
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: UBA 1
DOMAIN: UBA 2
DOMAIN: UMA
REGION: Disordered
REGION: Interaction with ESCRT−I
REGION: Interaction with PTPN23

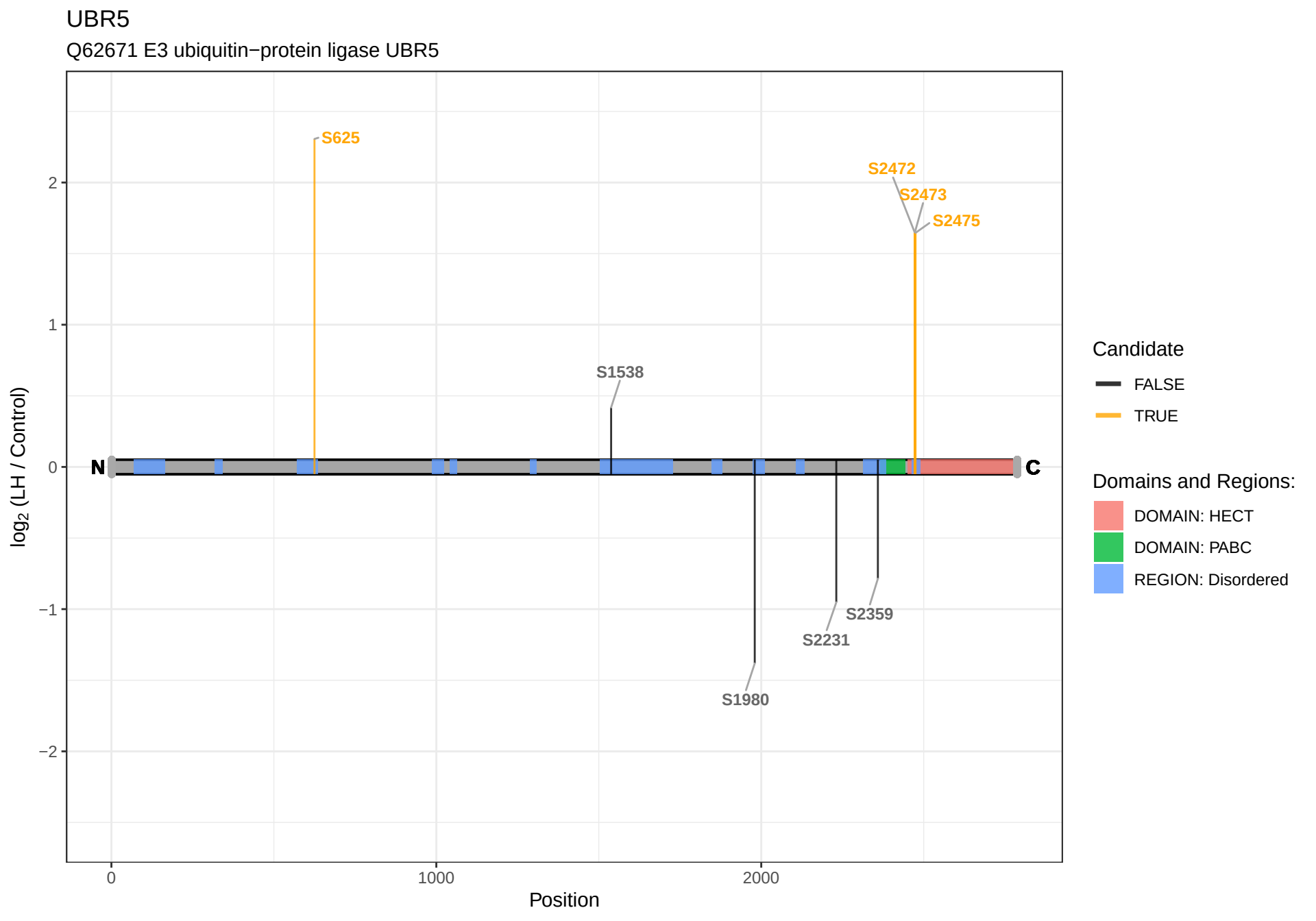

UBAP2
A0A0U1RRQ3 Ubiquitin−associated protein 2
S469
N
C
4
2
0
−2
−4
0
300
600
900
Position
log2 (LH / Control)
Candidate
TRUE
Domains and Regions:
DOMAIN: UBA
REGION: Disordered

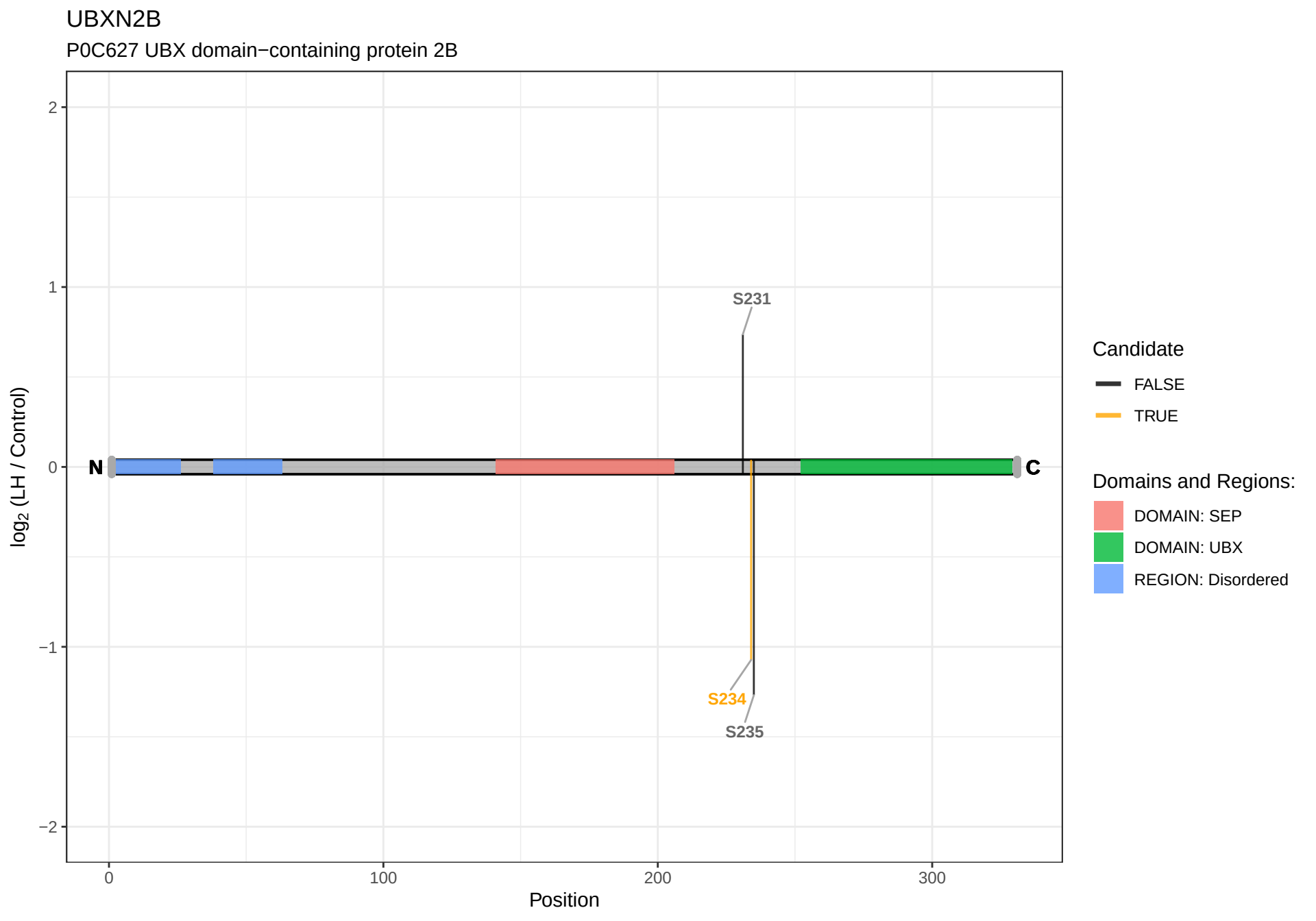

UBAP2L
E9PTR4 RCG62582, isoform CRA_b
S513
S487
S490
S625
S116
S497
S628
S629
S879
S1012
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: UBA
REGION: Disordered

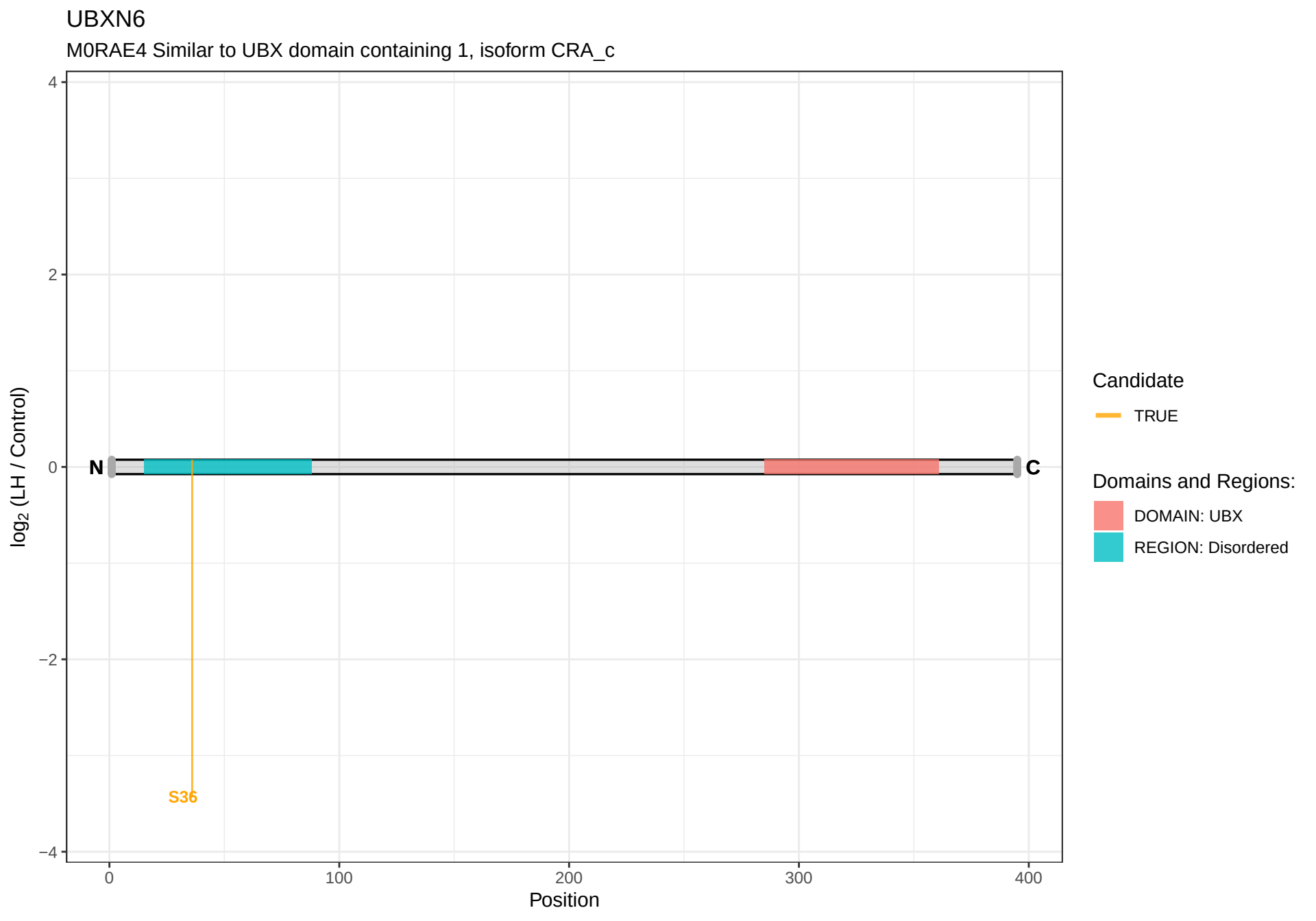

UBE2J1
A0A096MJH0 Ubiquitin−conjugating enzyme E2, J1 (Fragment)
log2 (LH / Control)
4
2
0
−2
−4
S42
S40
S39
S25
N
C
0
25
50
75
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

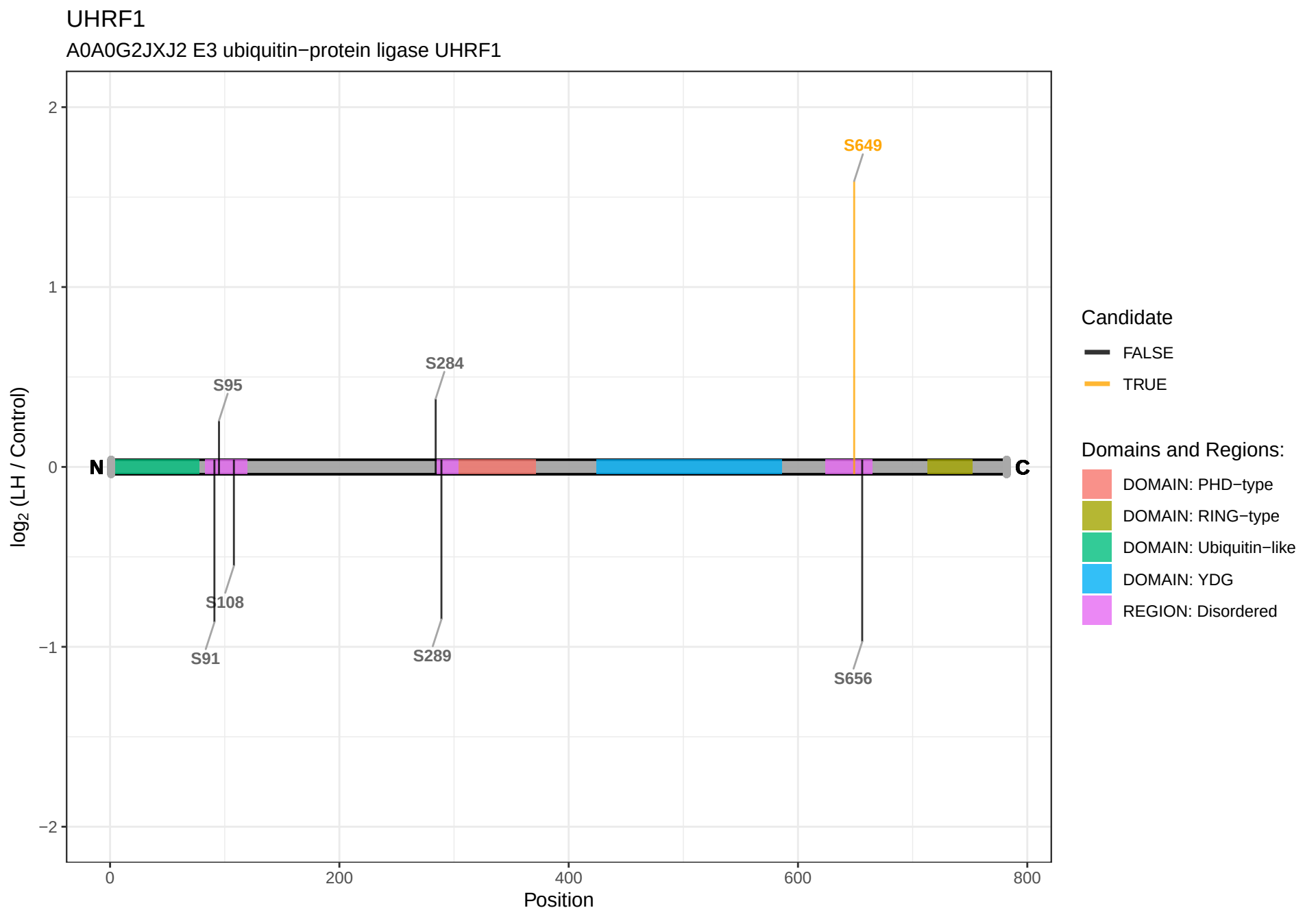

UBE2O
F1M403 Ubiquitin−conjugating enzyme E2O
5.0
2.5
0.0
−2.5
−5.0
log2 (LH / Control)
S360
S1086
S686
S683
S743
S1048
S1046
S1043
S1025
N
C
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: UBC core
REGION: Disordered

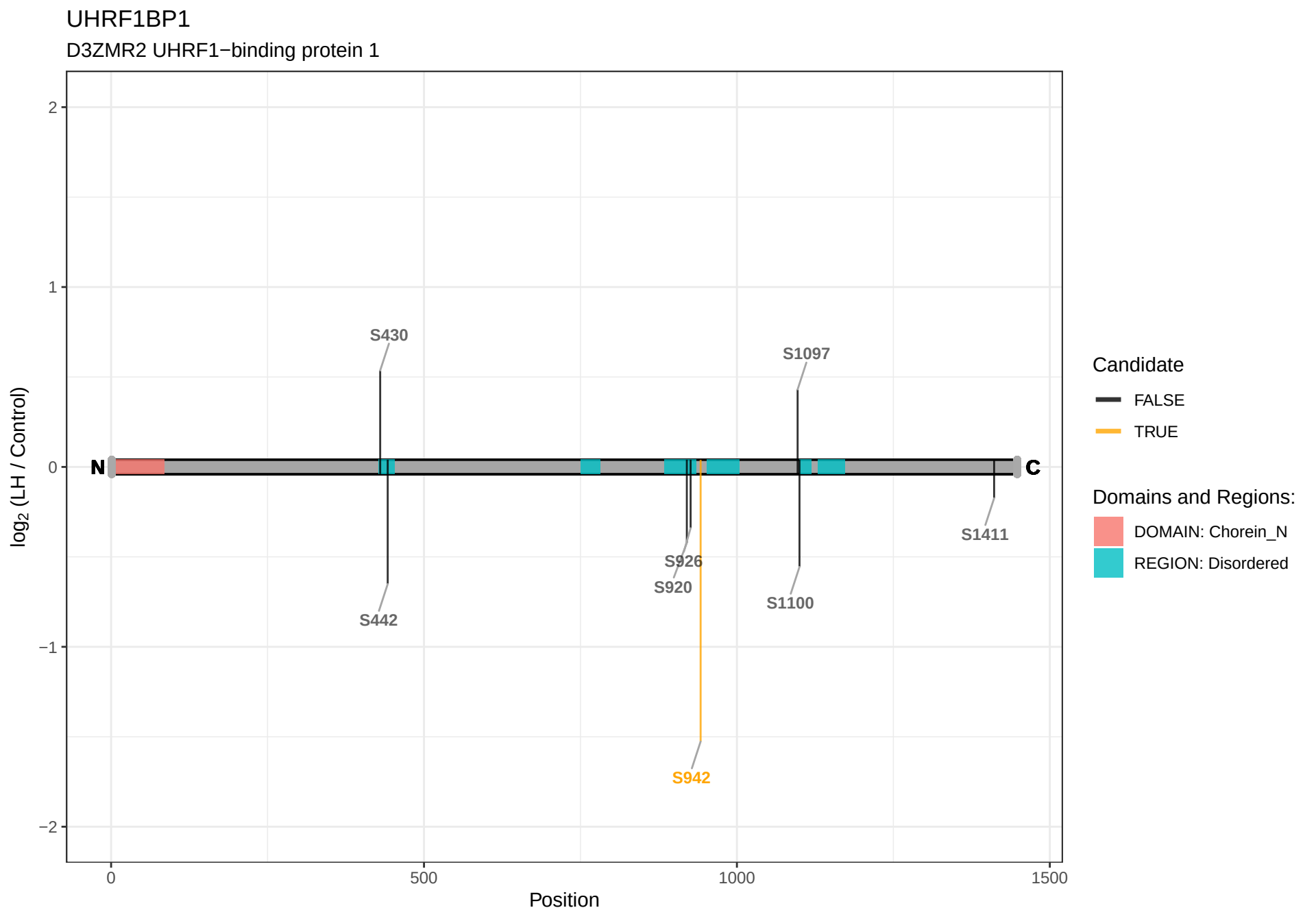

UBR4
A0A0G2JU89 E3 ubiquitin−protein ligase UBR4
S362
S208
S212
T2726
S2733
S4096
N
C
S178
T1771
S1773
S2730
T2735
2
1
0
−1
−2
log2 (LH / Control)
0
1000
2000
3000
4000
5000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: UBR−type
REGION: Disordered

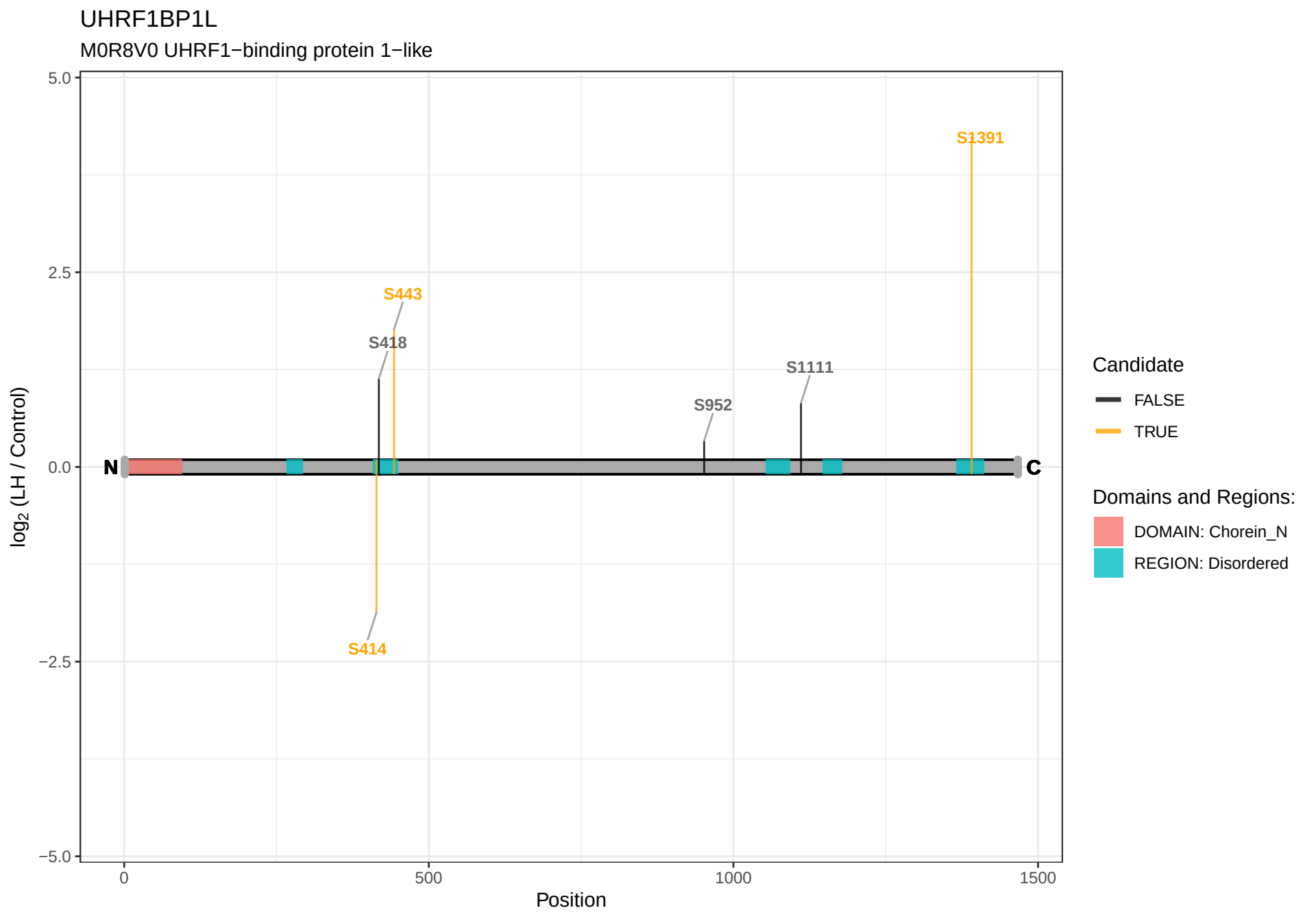

UBR5
Q62671 E3 ubiquitin−protein ligase UBR5
S625
S2472
S2473
S2475
S1538
S2359
S2231
S1980
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
1000
2000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: HECT
DOMAIN: PABC
REGION: Disordered

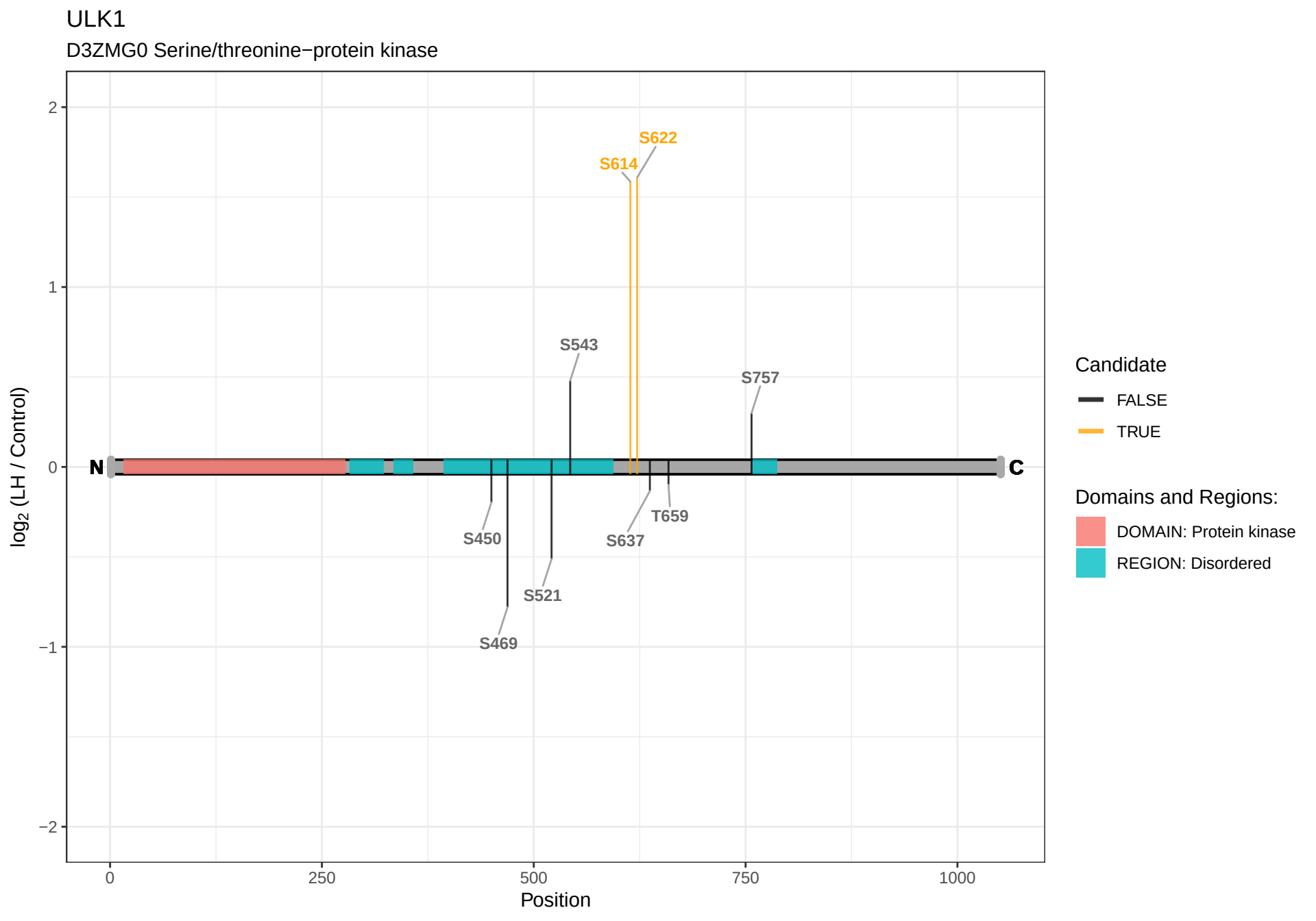

UBXN2B
P0C627 UBX domain−containing protein 2B
2
1
0
−1
−2
log2 (LH / Control)
N
C
S231
S234
S235
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SEP
DOMAIN: UBX
REGION: Disordered

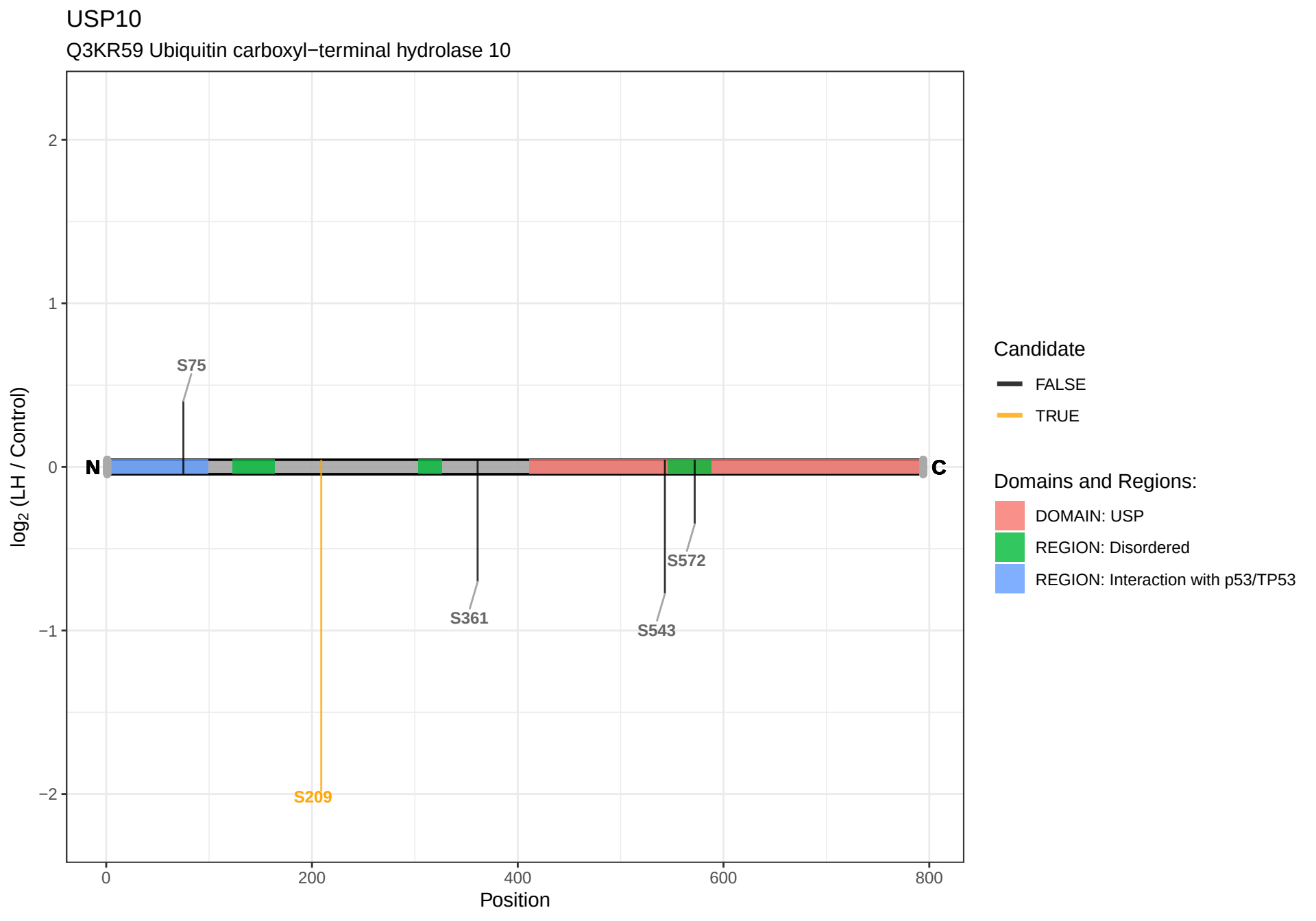

UBXN6
M0RAE4 Similar to UBX domain containing 1, isoform CRA_c
4
2
0
−2
−4
log2 (LH / Control)
N
C
S36
0
100
200
300
400
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: UBX
REGION: Disordered

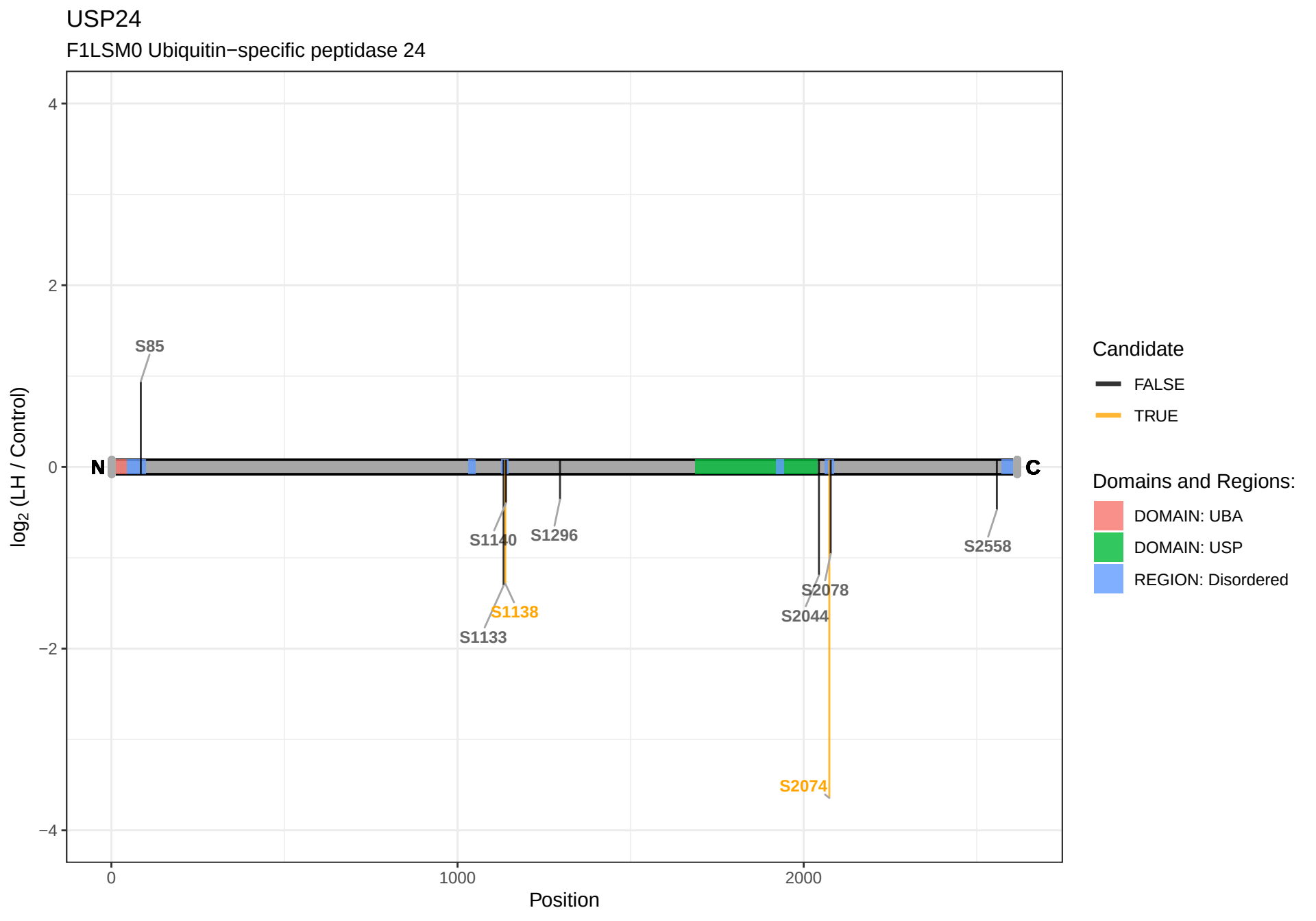

UHRF1
A0A0G2JXJ2 E3 ubiquitin−protein ligase UHRF1
log2 (LH / Control)
2
1
0
−1
−2
0
200
400
600
800
Position
N
C
S649
S284
S95
S108
S91
S289
S656
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: PHD−type
DOMAIN: RING−type
DOMAIN: Ubiquitin−like
DOMAIN: YDG
REGION: Disordered

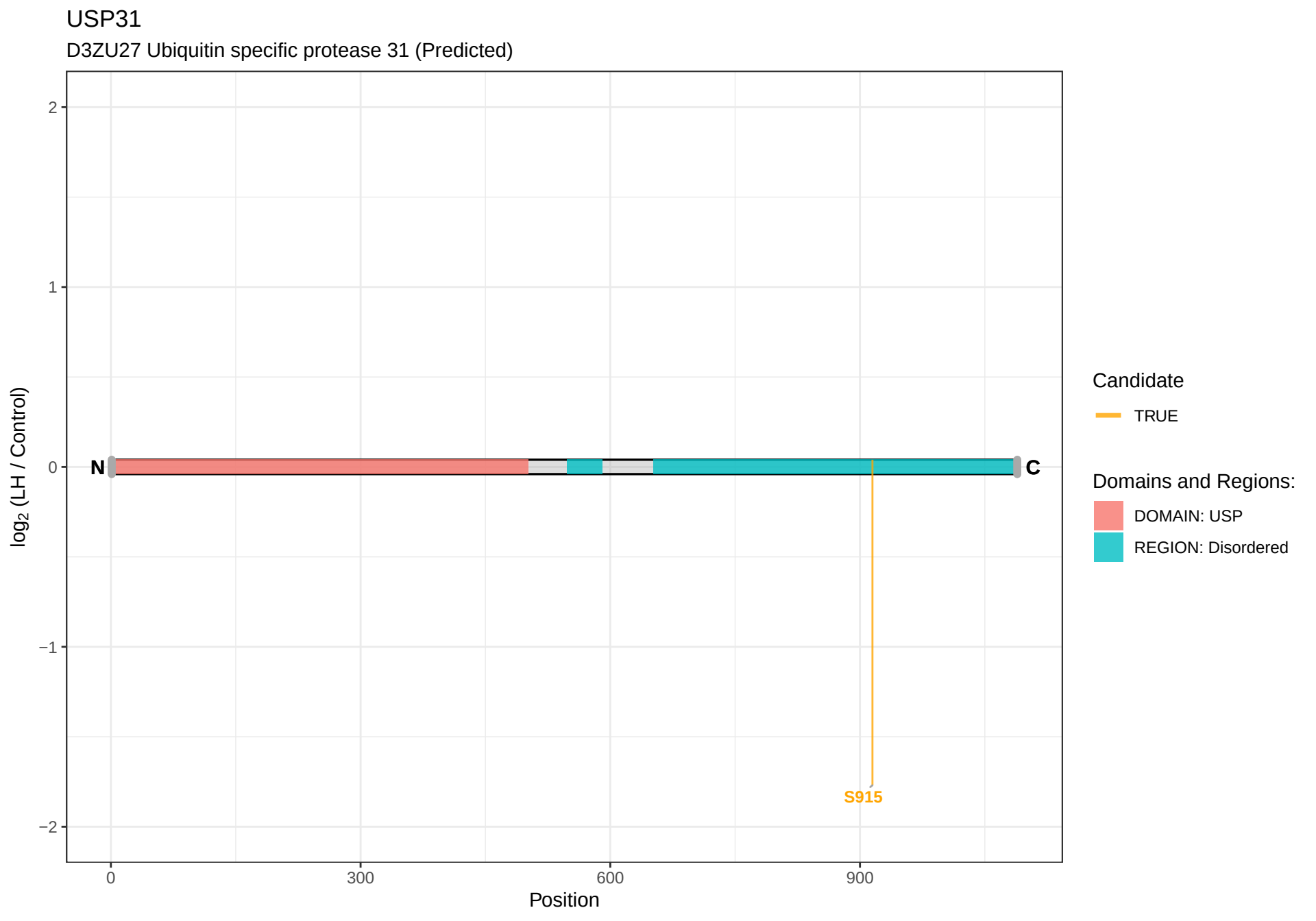

UHRF1BP1
D3ZMR2 UHRF1−binding protein 1
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
1500
Position
N
C
S430
S442
S926
S920
S942
S1097
S1100
S1411
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Chorein_N
REGION: Disordered

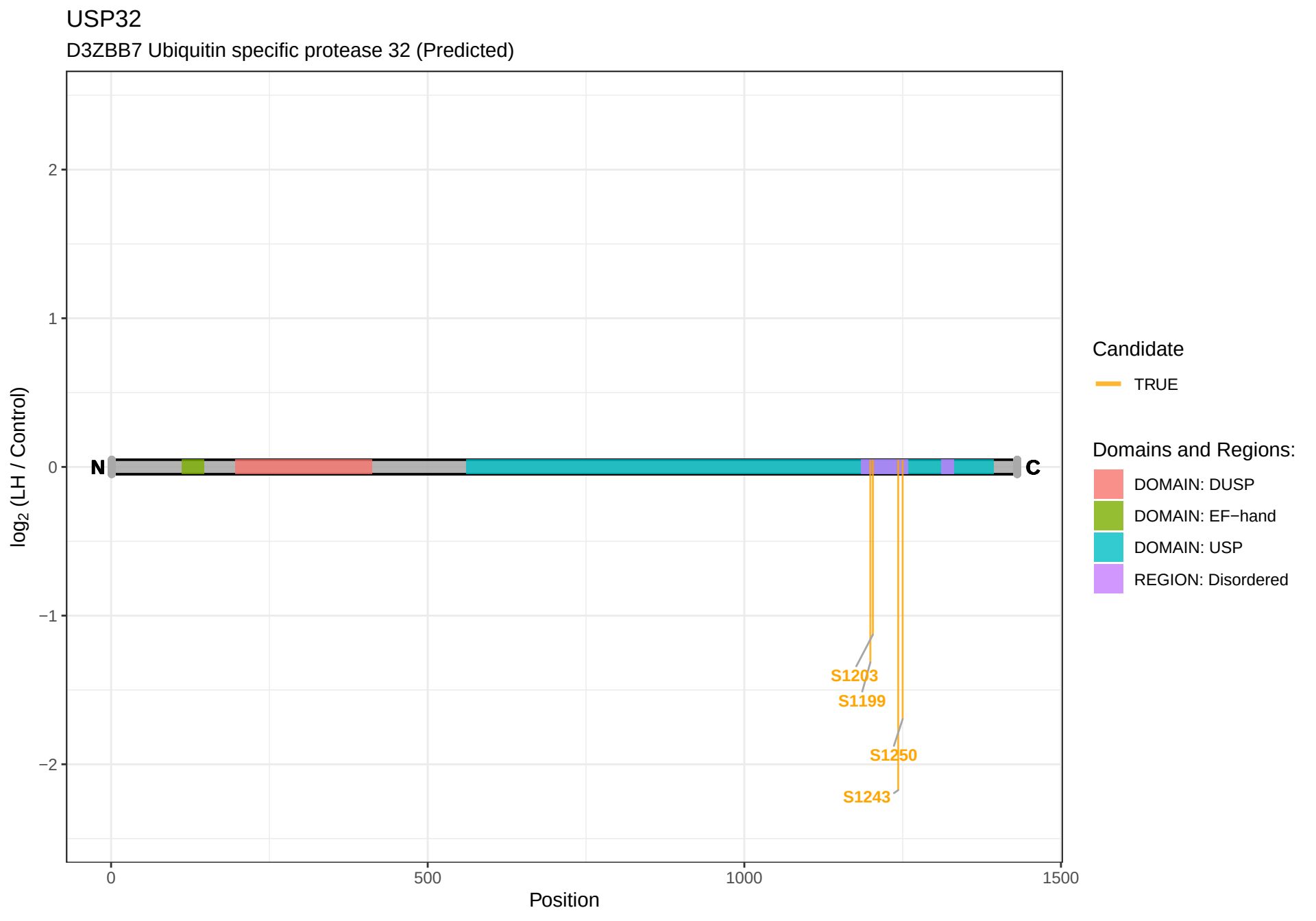

UHRF1BP1L
M0R8V0 UHRF1−binding protein 1−like
5.0
2.5
0.0
−2.5
−5.0
log2 (LH / Control)
S1391
S443
S418
S1111
S952
S414
N
C
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Chorein_N
REGION: Disordered

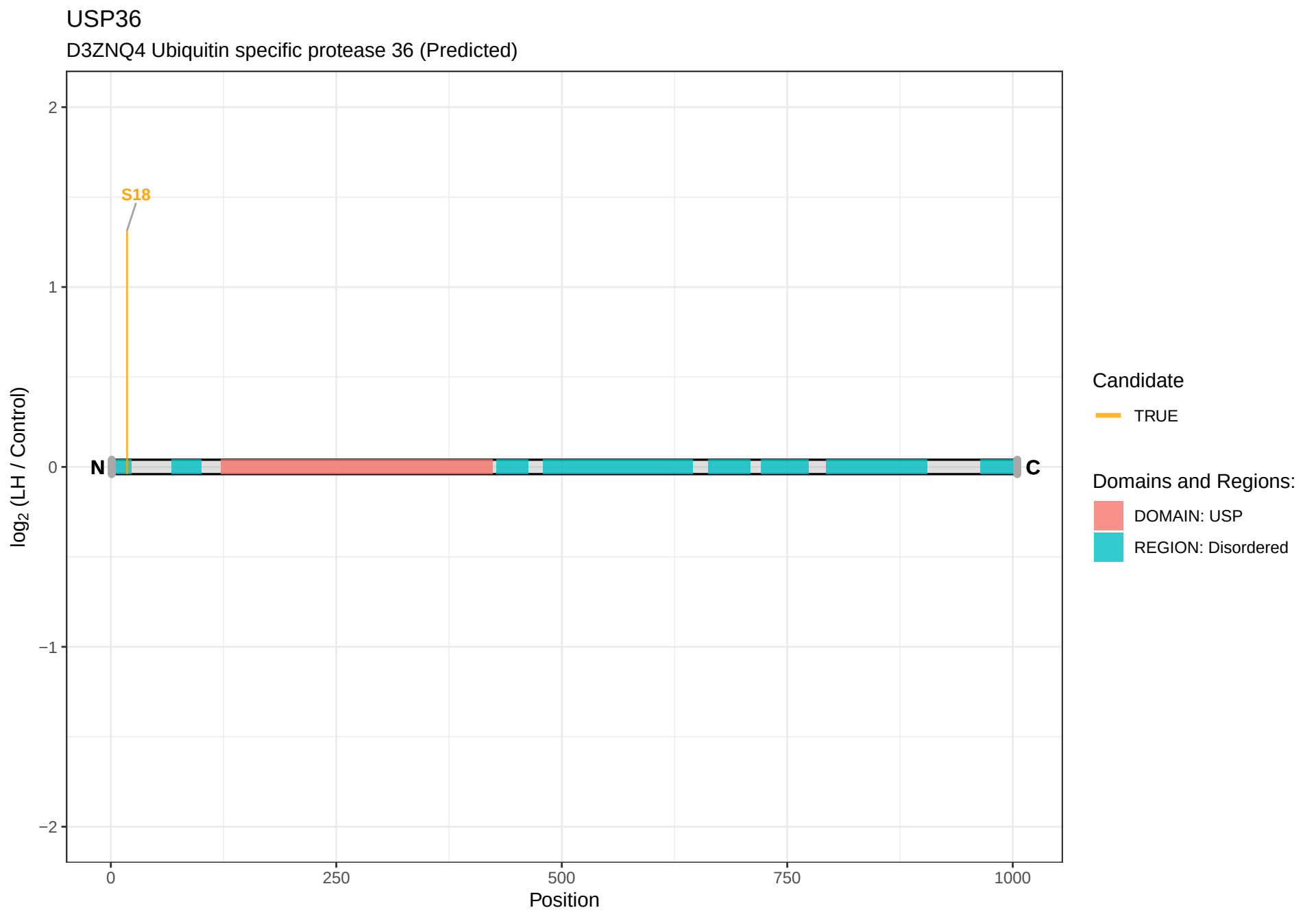

ULK1
D3ZMG0 Serine/threonine−protein kinase
log2 (LH / Control)
2
1
0
−1
−2
0
250
500
750
1000
Position
N
C
S622
S614
S543
S757
S450
S469
S521
S637
T659
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Protein kinase
REGION: Disordered

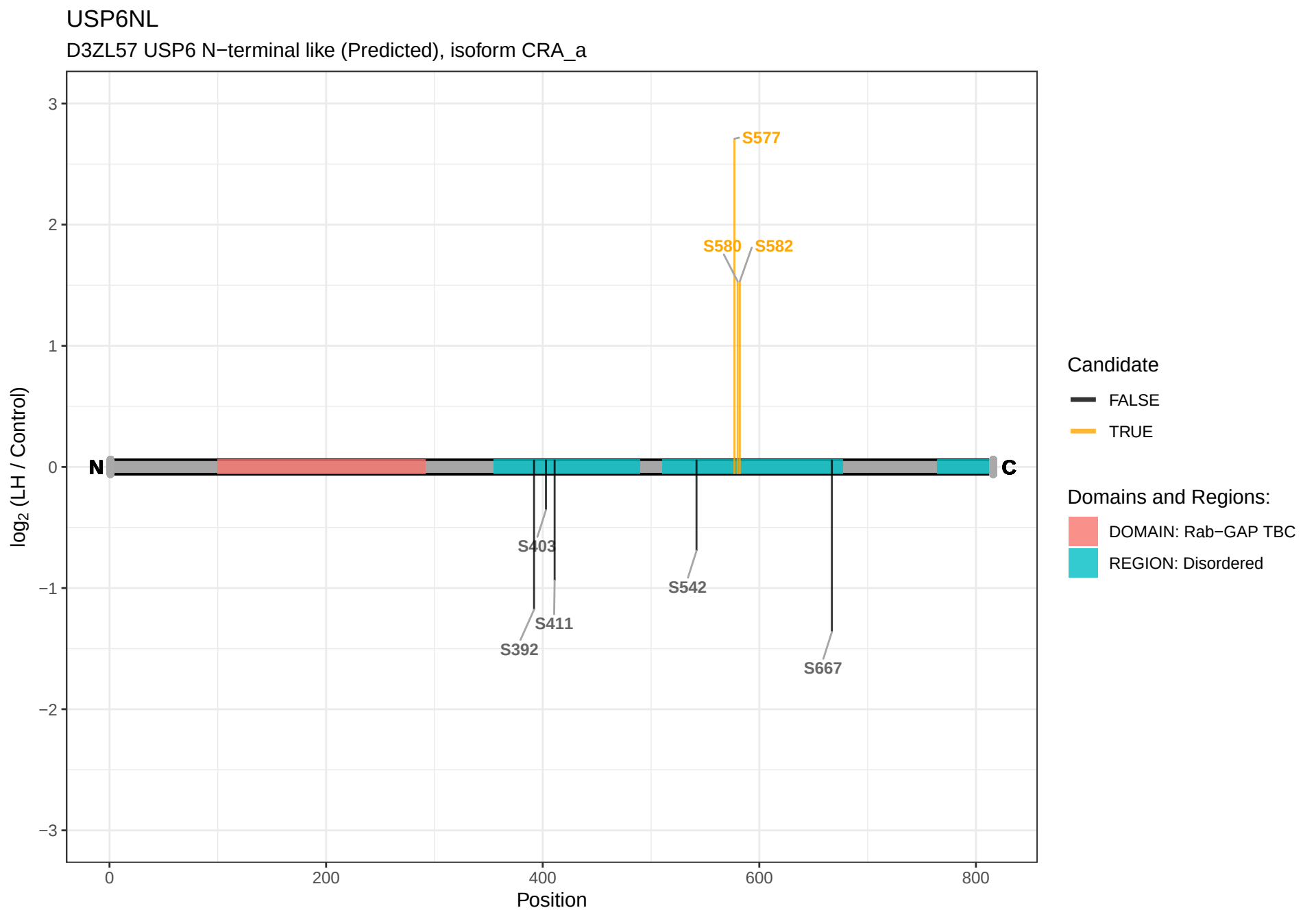

USP10
Q3KR59 Ubiquitin carboxyl−terminal hydrolase 10
log2 (LH / Control)
2
1
0
−1
−2
N
C
S75
S209
S361
S543
S572
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: USP
REGION: Disordered
REGION: Interaction with p53/TP53

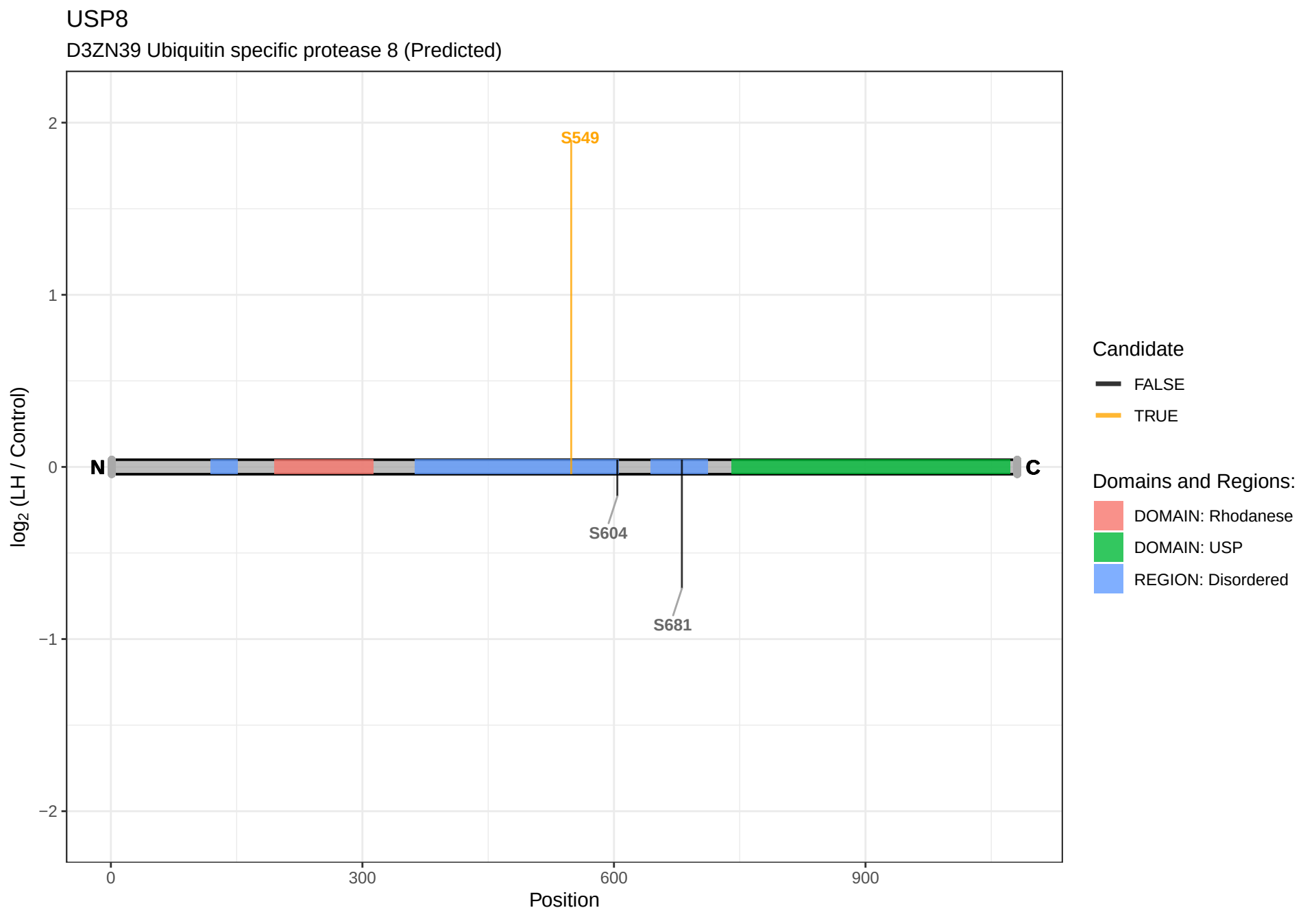

USP24
F1LSM0 Ubiquitin−specific peptidase 24
log2 (LH / Control)
4
2
0
−2
−4
0
1000
2000
Position
N
C
S85
S1140
S1296
S1138
S1133
S2078
S2044
S2074
S2558
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: UBA
DOMAIN: USP
REGION: Disordered

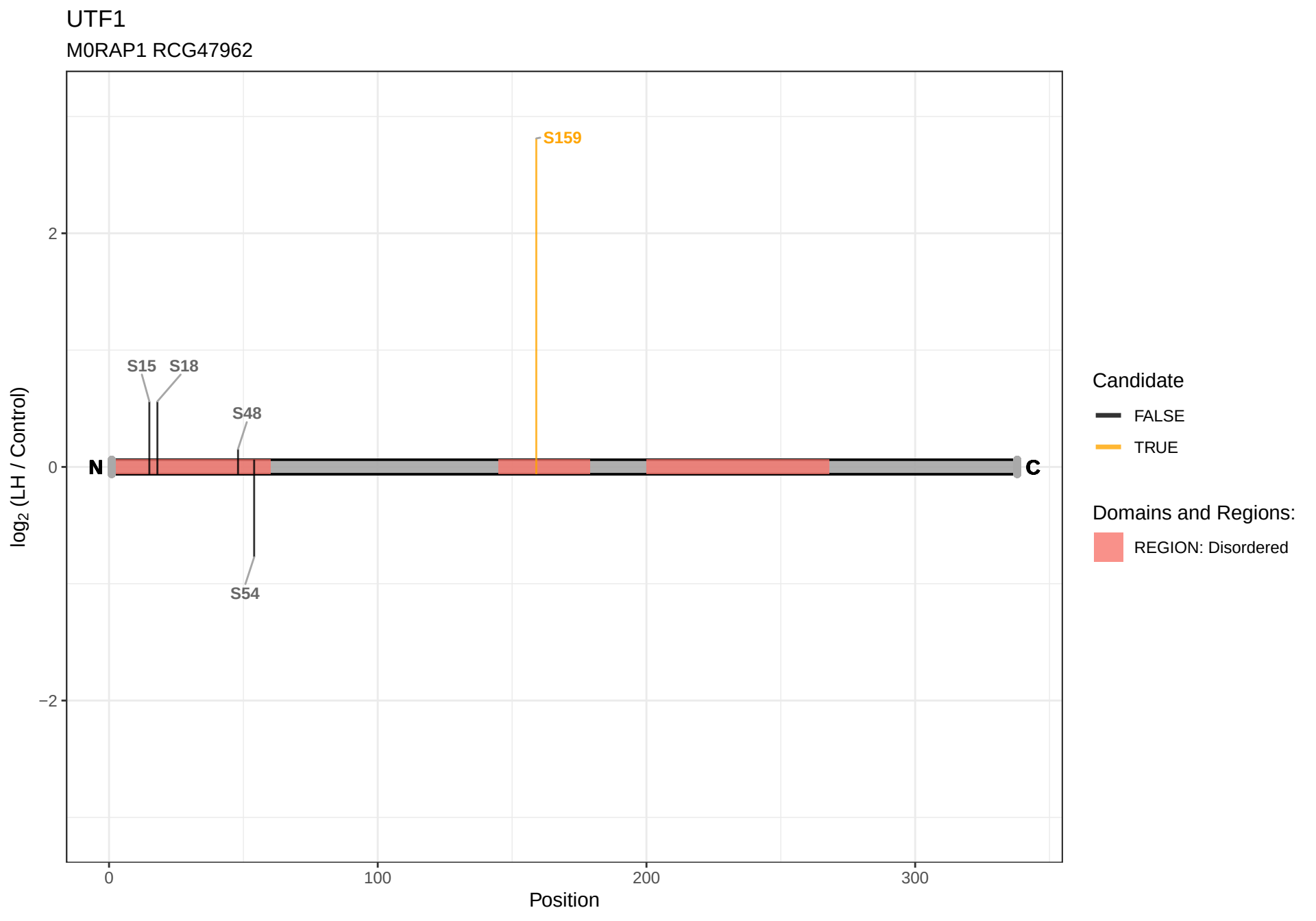

USP31
D3ZU27 Ubiquitin specific protease 31 (Predicted)
2
1
0
−1
−2
log2 (LH / Control)
N
C
S915
0
300
600
900
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: USP
REGION: Disordered

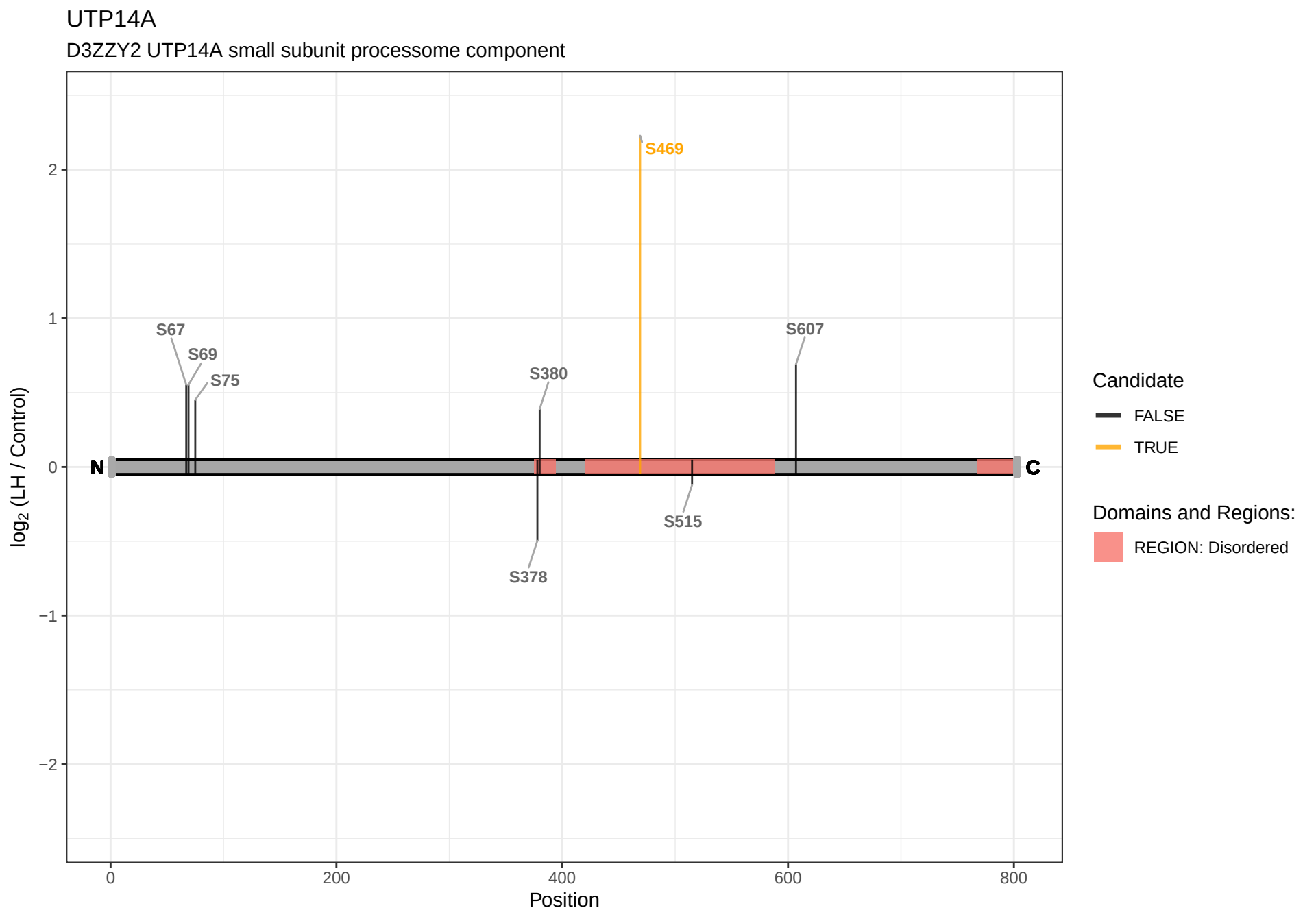

USP32
D3ZBB7 Ubiquitin specific protease 32 (Predicted)
log2 (LH / Control)
2
1
0
−1
−2
N
C
S1203
S1199
S1250
S1243
0
500
1000
1500
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: DUSP
DOMAIN: EF−hand
DOMAIN: USP
REGION: Disordered

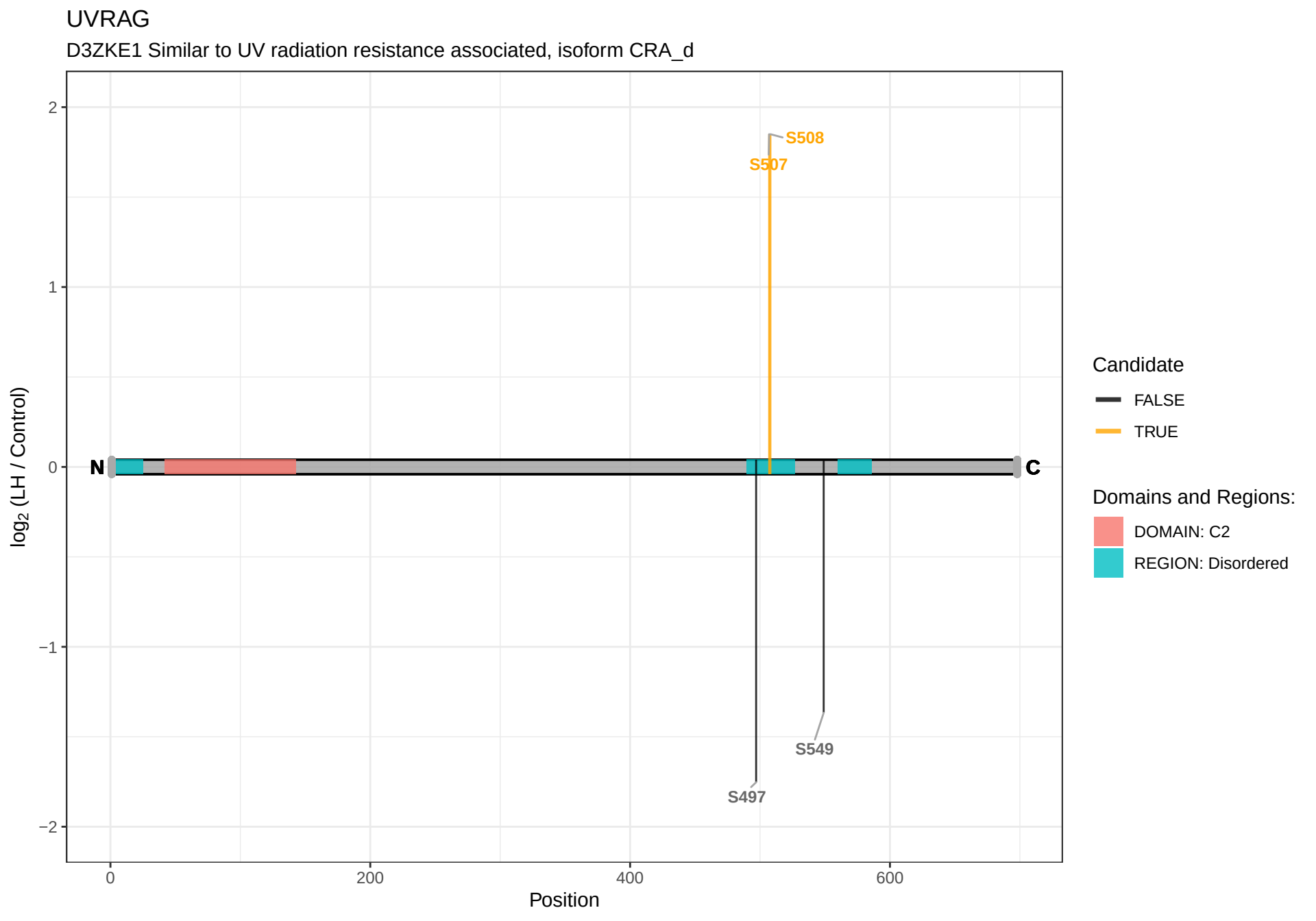

USP36
D3ZNQ4 Ubiquitin specific protease 36 (Predicted)
S18
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
250
500
750
1000
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: USP
REGION: Disordered

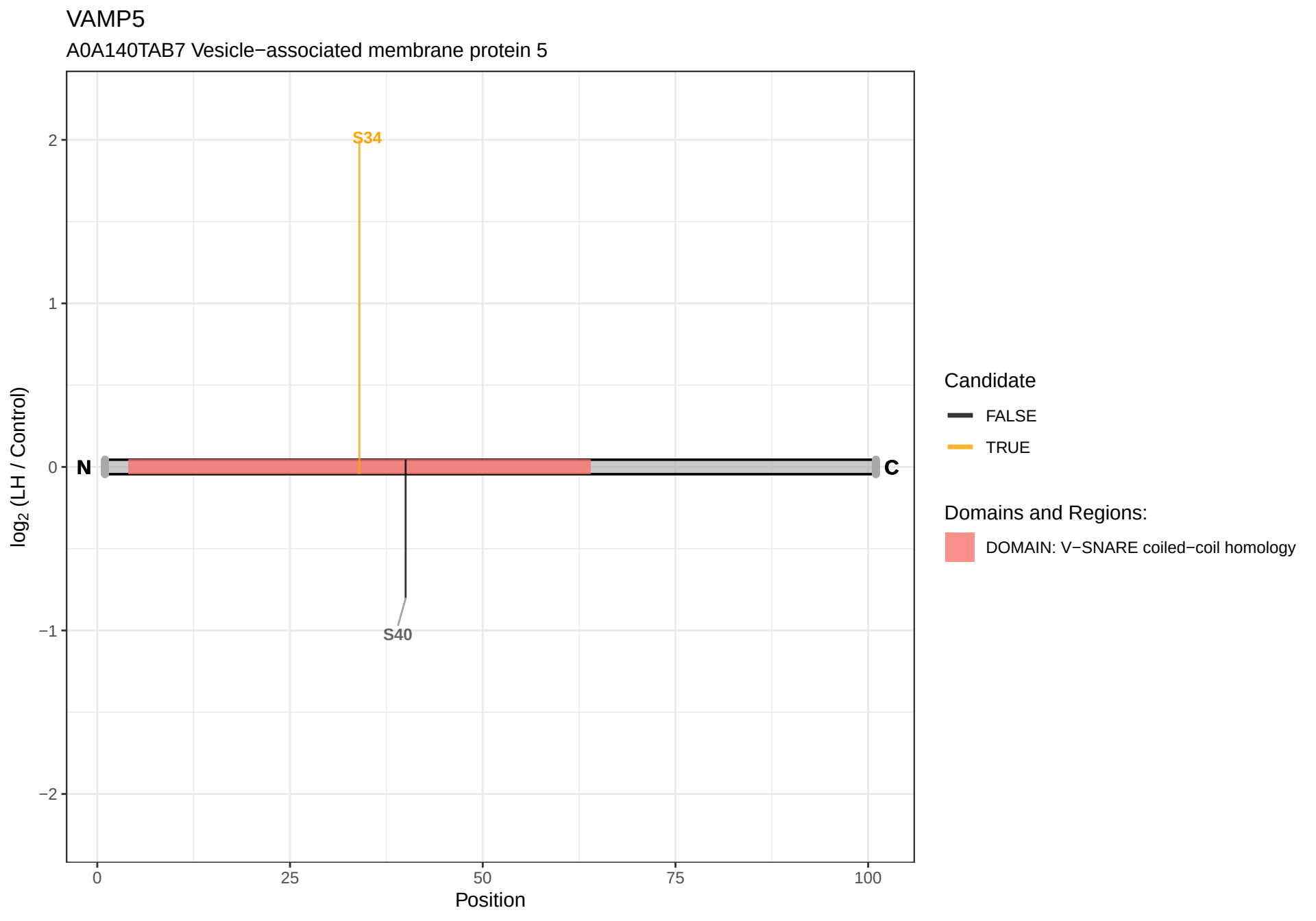

USP6NL
D3ZL57 USP6 N−terminal like (Predicted), isoform CRA_a
log2 (LH / Control)
Position
N
C
S577
S580
S582
S403
S411
S392
S542
S667
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Rab−GAP TBC
REGION: Disordered

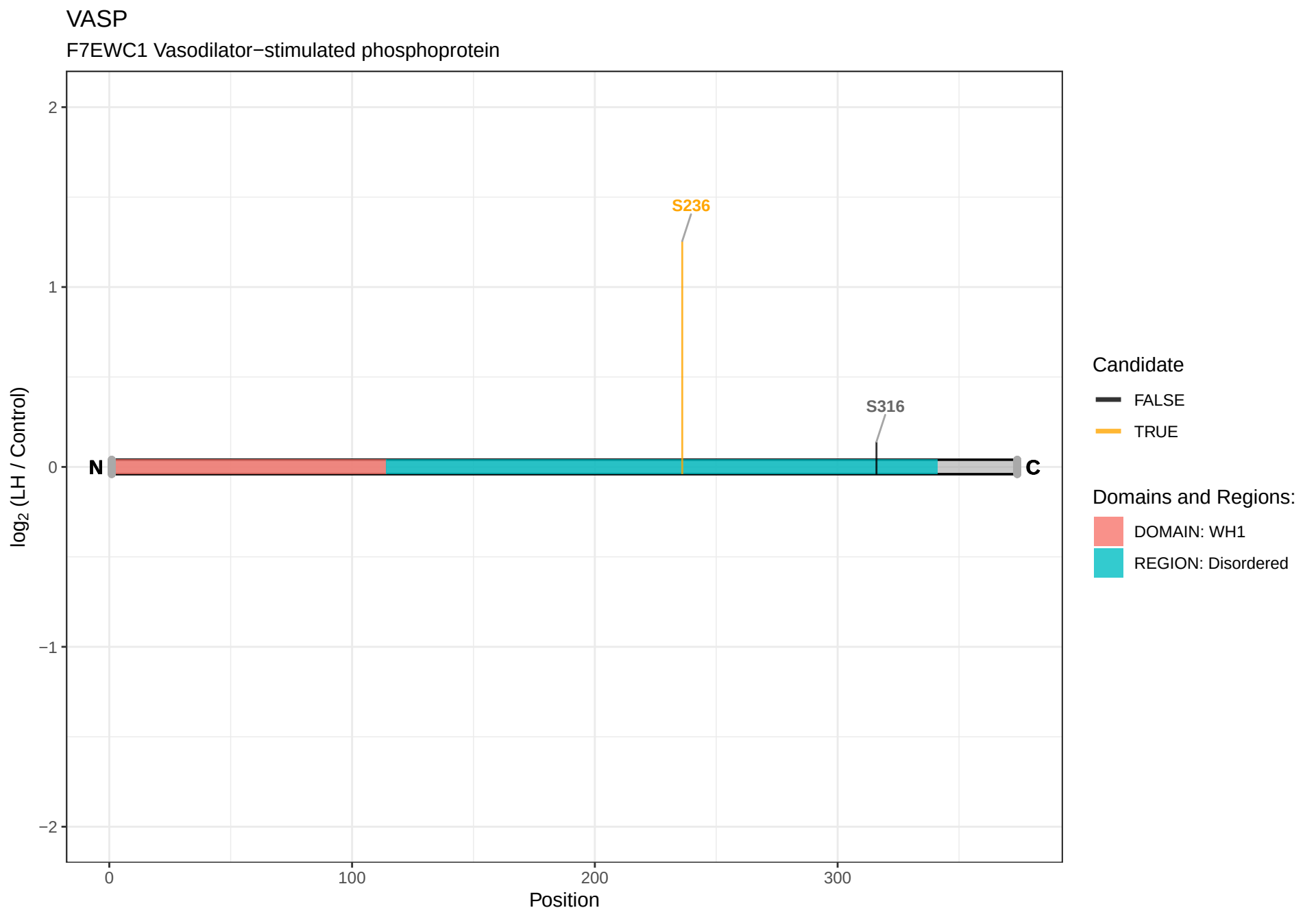

USP8
D3ZN39 Ubiquitin specific protease 8 (Predicted)
S549
S604
S681
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
300
600
900
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: Rhodanese
DOMAIN: USP
REGION: Disordered

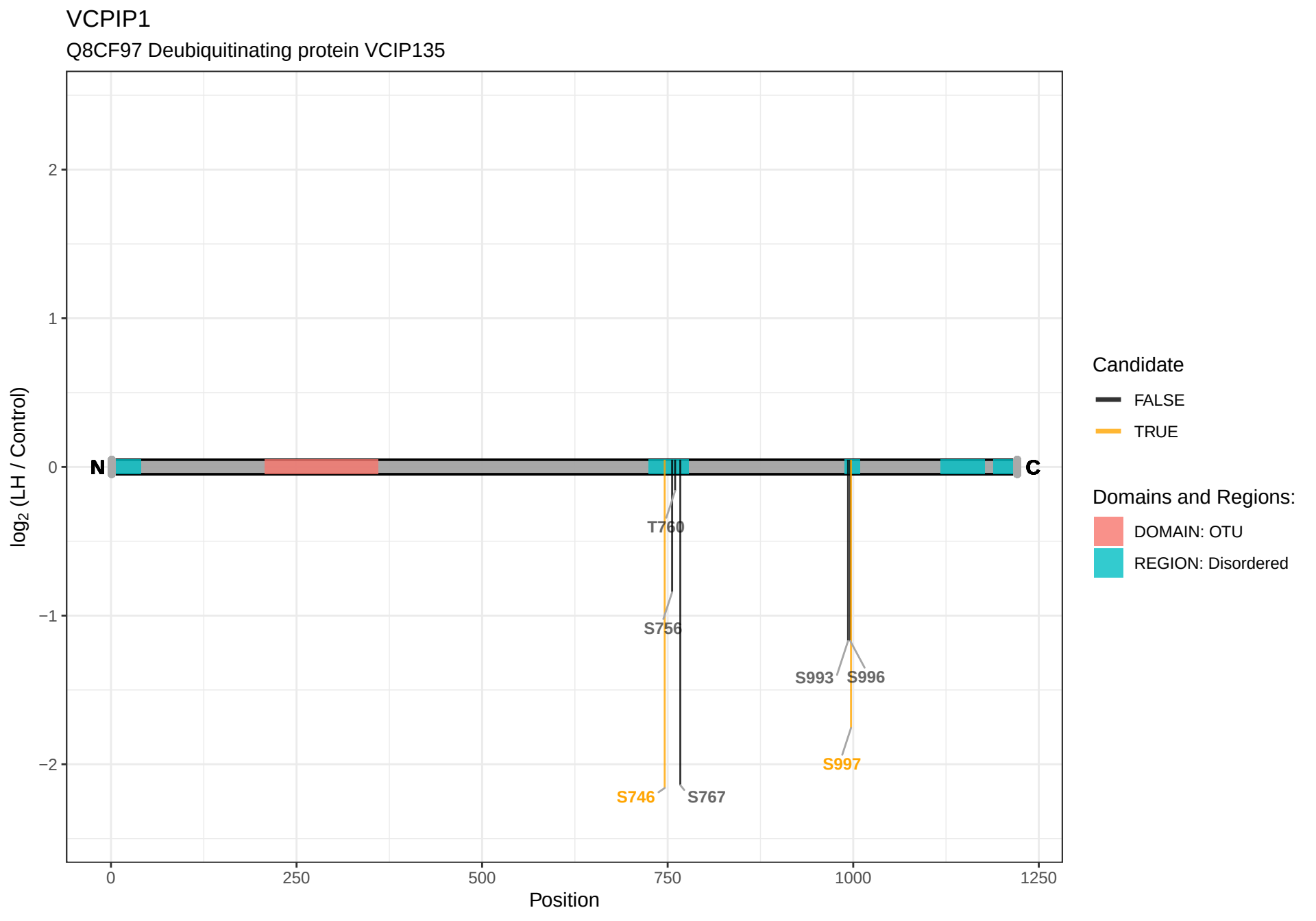

UTF1
M0RAP1 RCG47962
S159
S15
S18
S48
S54
N
C
2
0
−2
log2 (LH / Control)
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered


UTP14A
D3ZZY2 UTP14A small subunit processome component
S469
S67
S69
S75
S380
S607
S515
S378
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered


UVRAG
D3ZKE1 Similar to UV radiation resistance associated, isoform CRA_d
log2 (LH / Control)
2
1
0
−1
−2
S508
S507
S549
S497
N
C
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2
REGION: Disordered

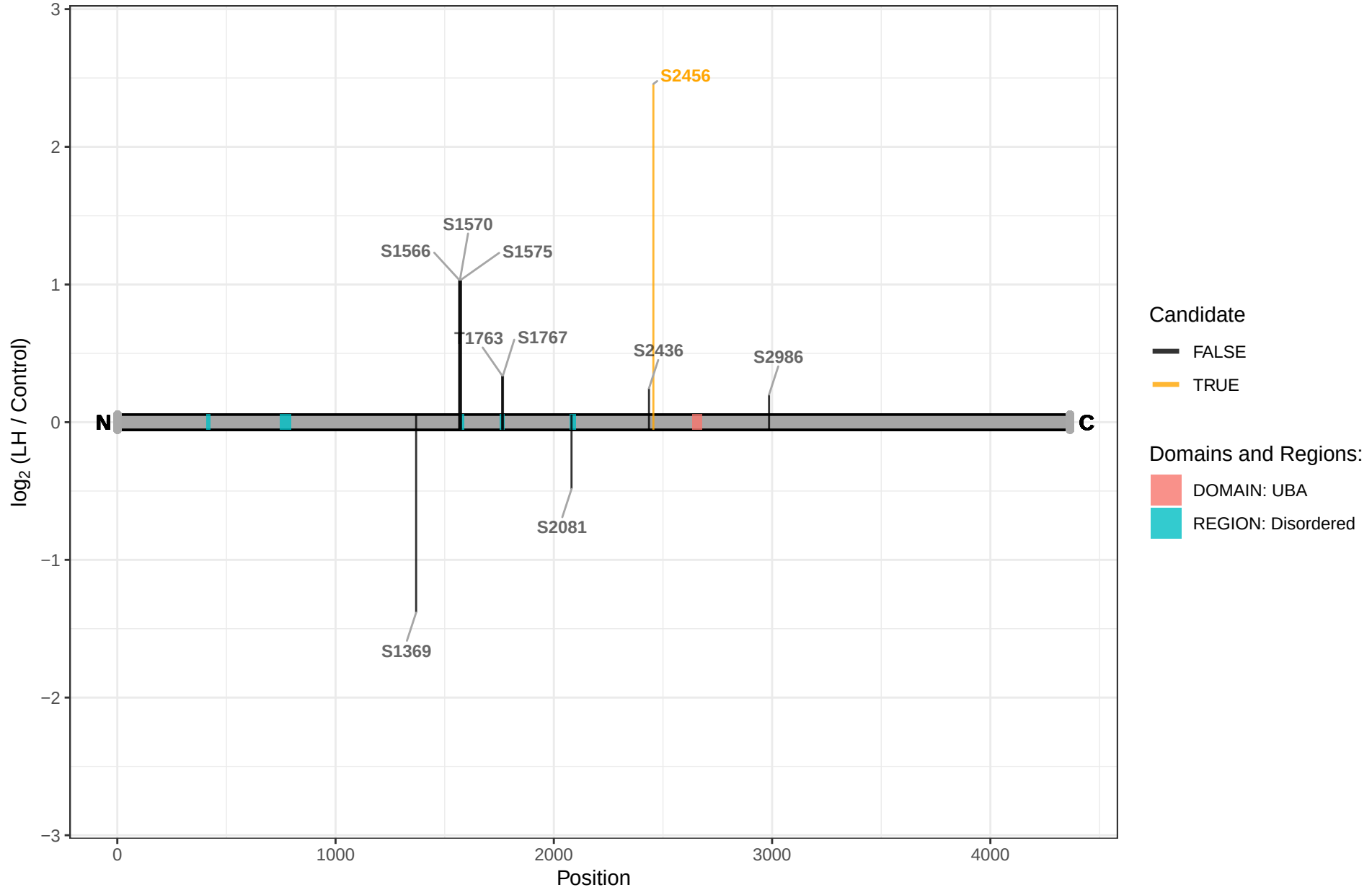

VAMP5
A0A140TAB7 Vesicle−associated membrane protein 5
S34
S40
N
C
2
1
0
−1
−2
0
25
50
75
100
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: V−SNARE coiled−coil homology

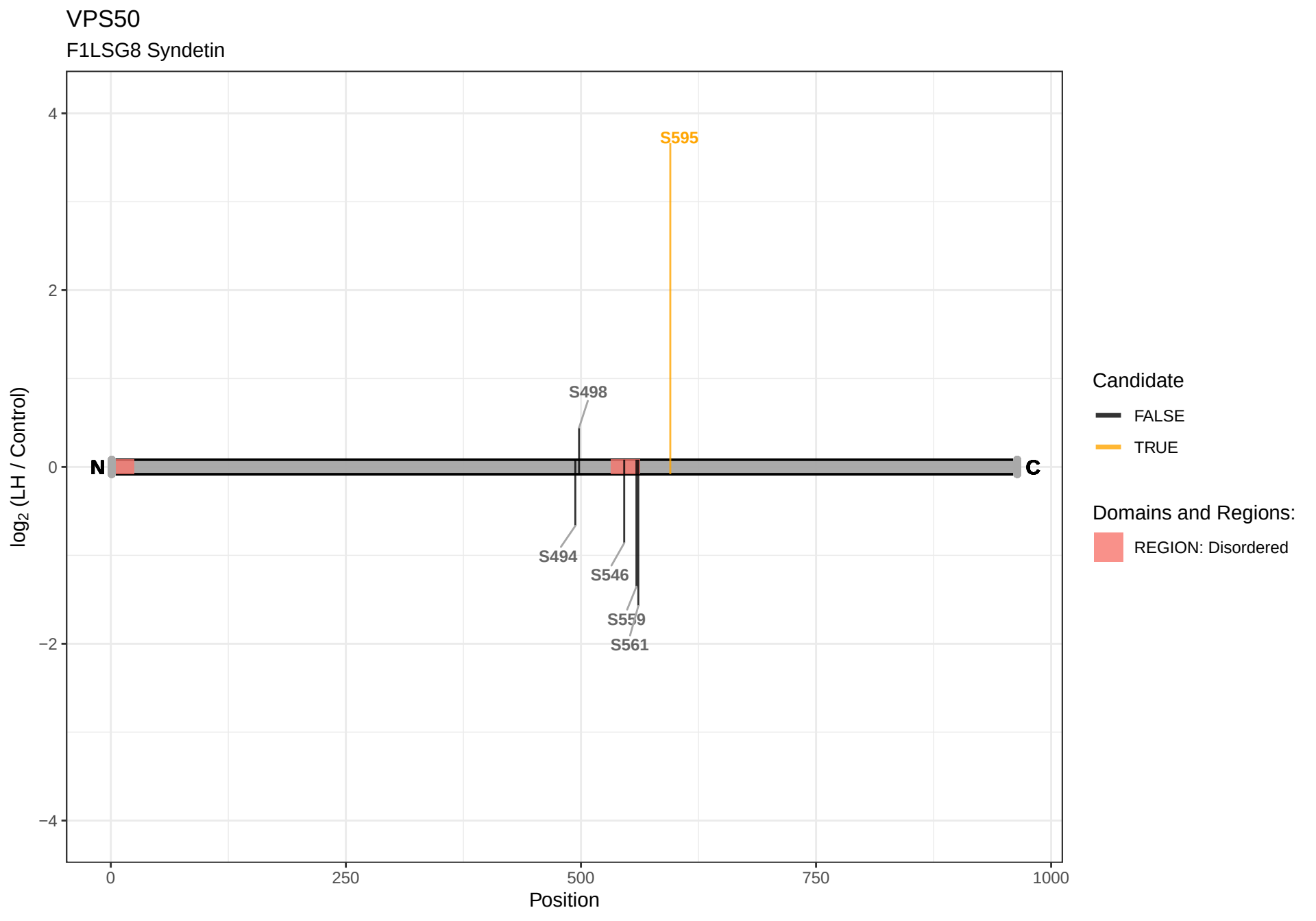

VASP
F7EWC1 Vasodilator−stimulated phosphoprotein
2
1
0
−1
−2
log2 (LH / Control)
S236
S316
N
C
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WH1
REGION: Disordered

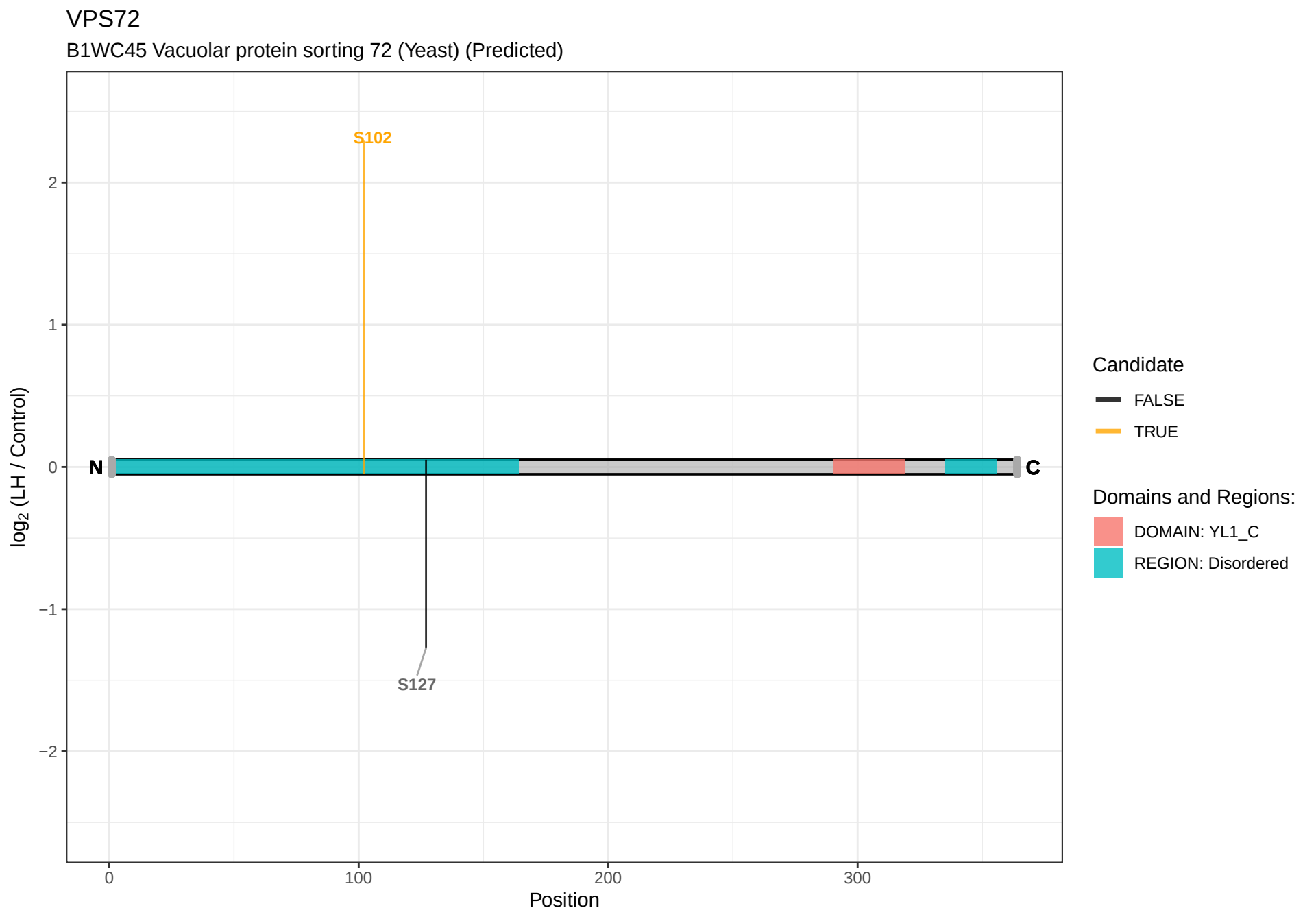

VCPIP1
Q8CF97 Deubiquitinating protein VCIP135
log2 (LH / Control)
2
1
0
−1
−2
N
C
T760
S756
S993
S996
S997
S746
S767
0
250
500
750
1000
1250
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: OTU
REGION: Disordered

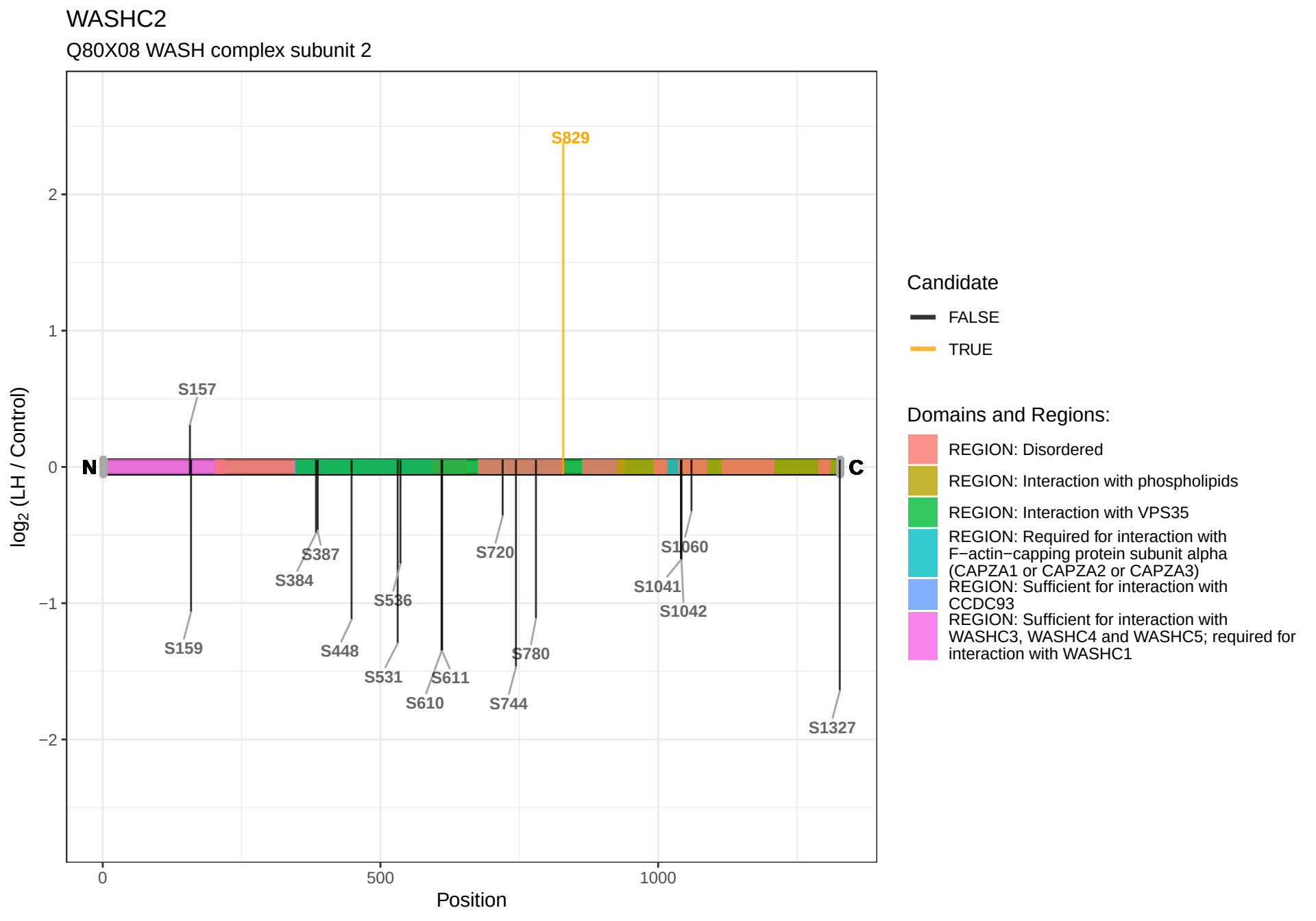
VPS13D

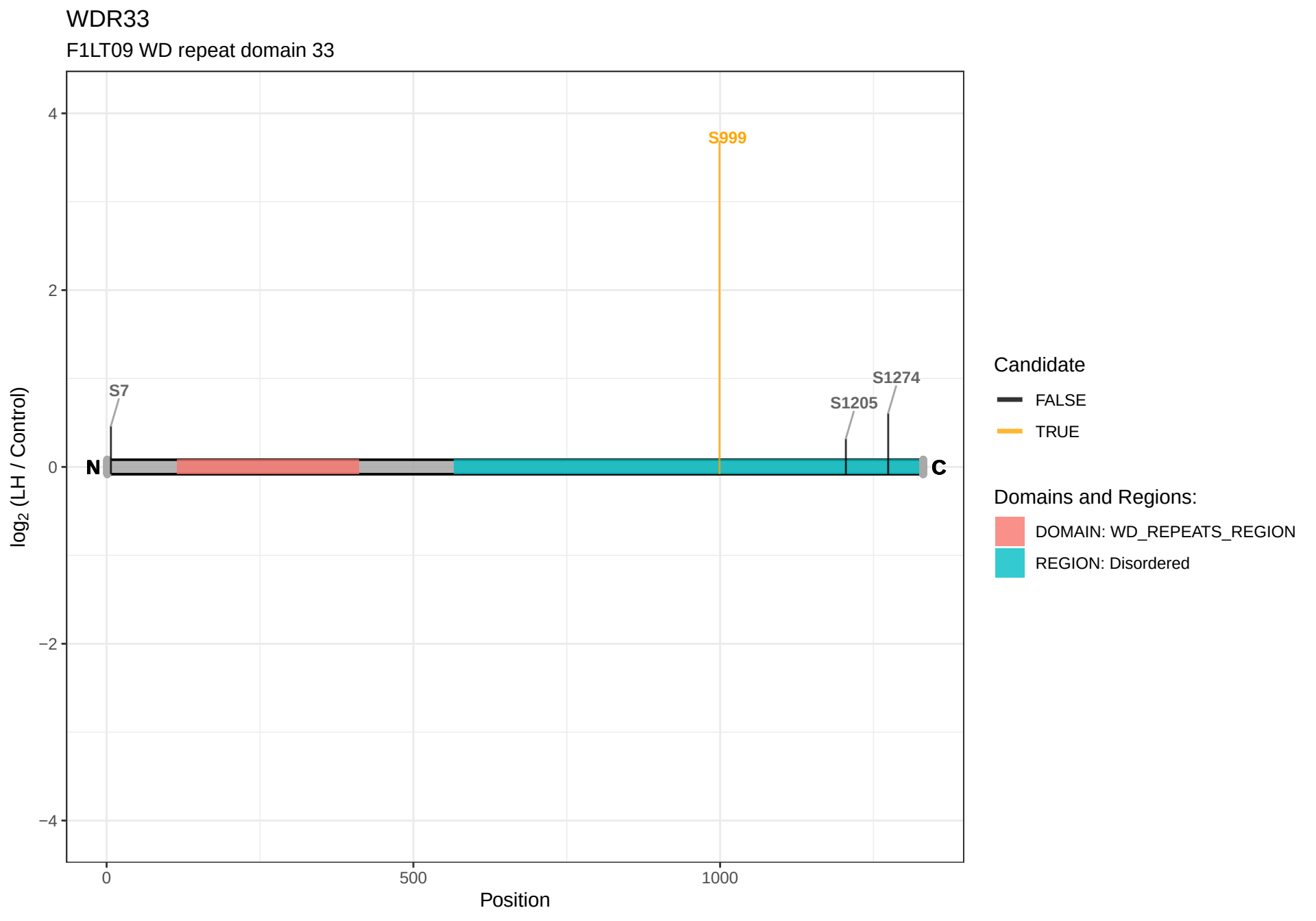
A0A0G2JYD4 Vacuolar protein sorting 13 homolog D

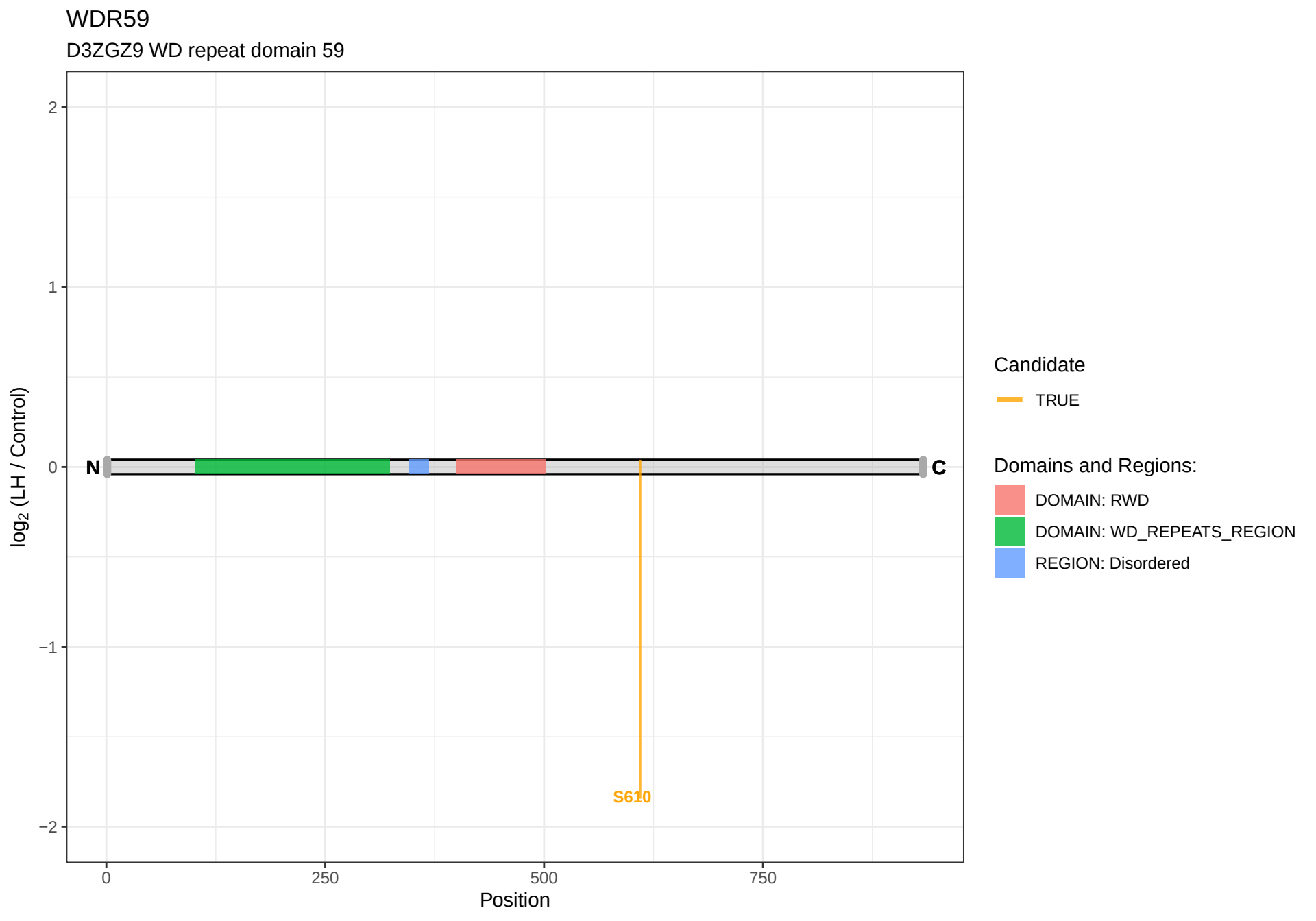


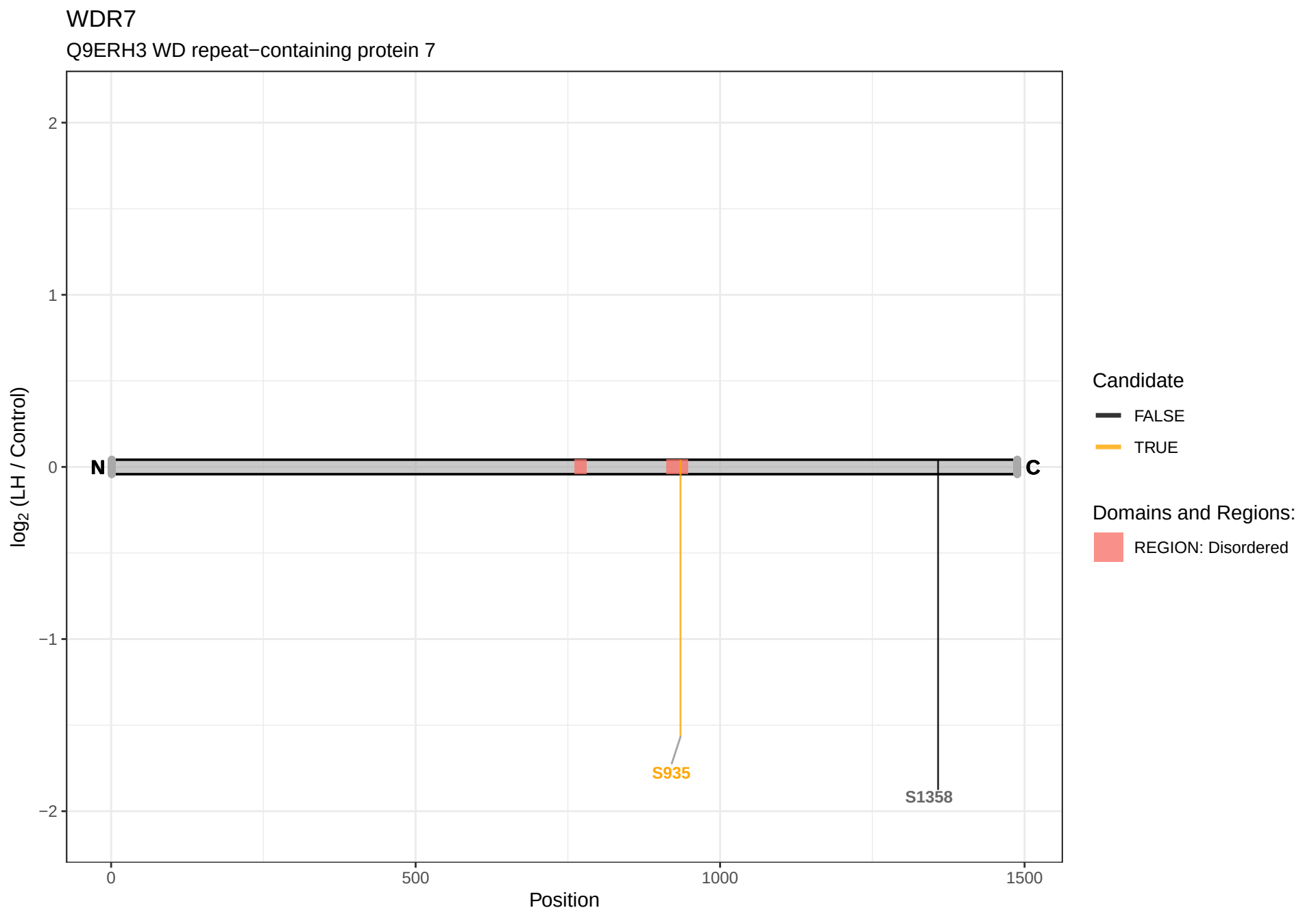

VPS50
F1LSG8 Syndetin
S595
S498
S494
S546
S559
S561
N
C
4
2
0
−2
−4
0
250
500
750
1000
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

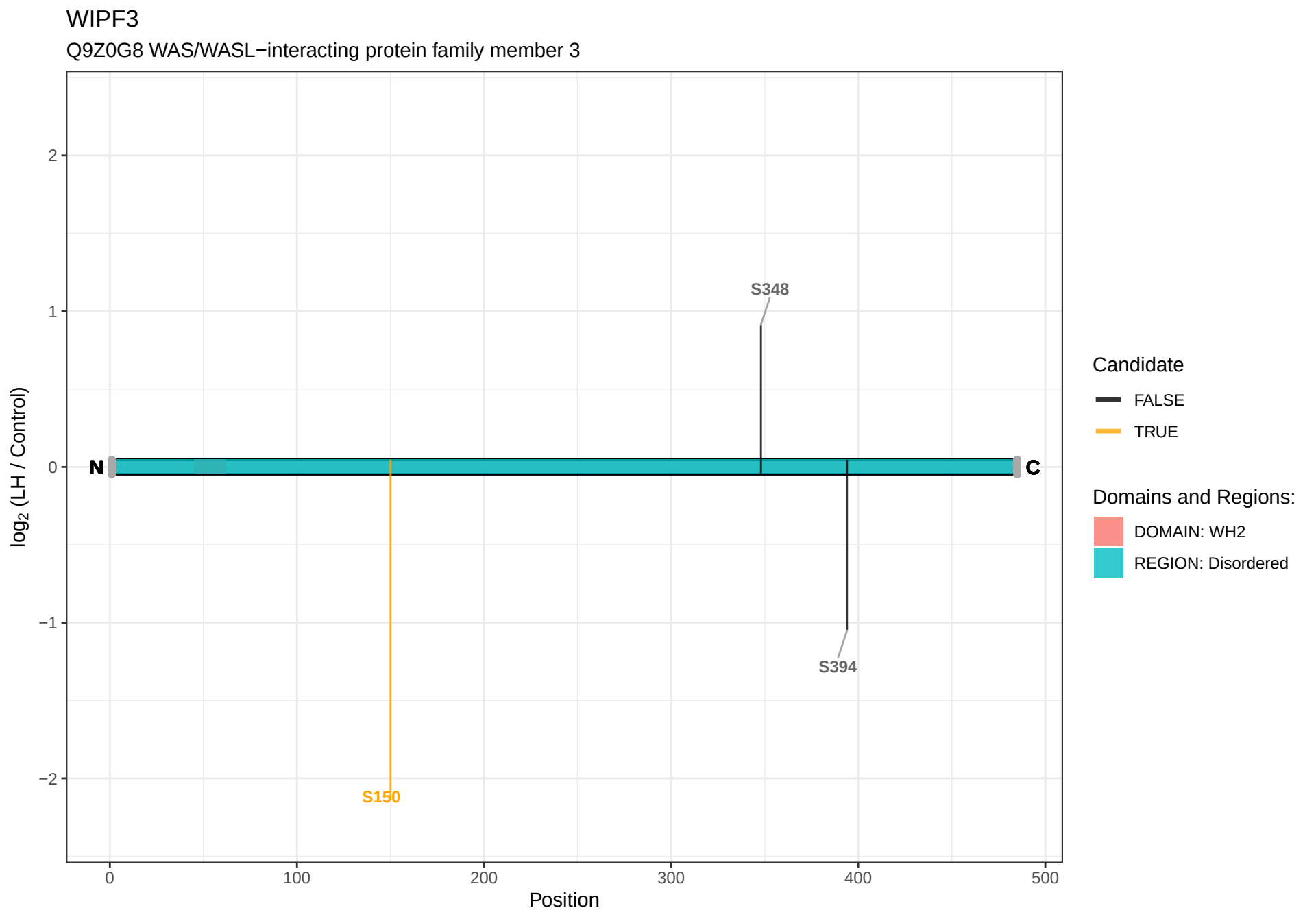

VPS72
B1WC45 Vacuolar protein sorting 72 (Yeast) (Predicted)
S102
S127
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: YL1_C
REGION: Disordered

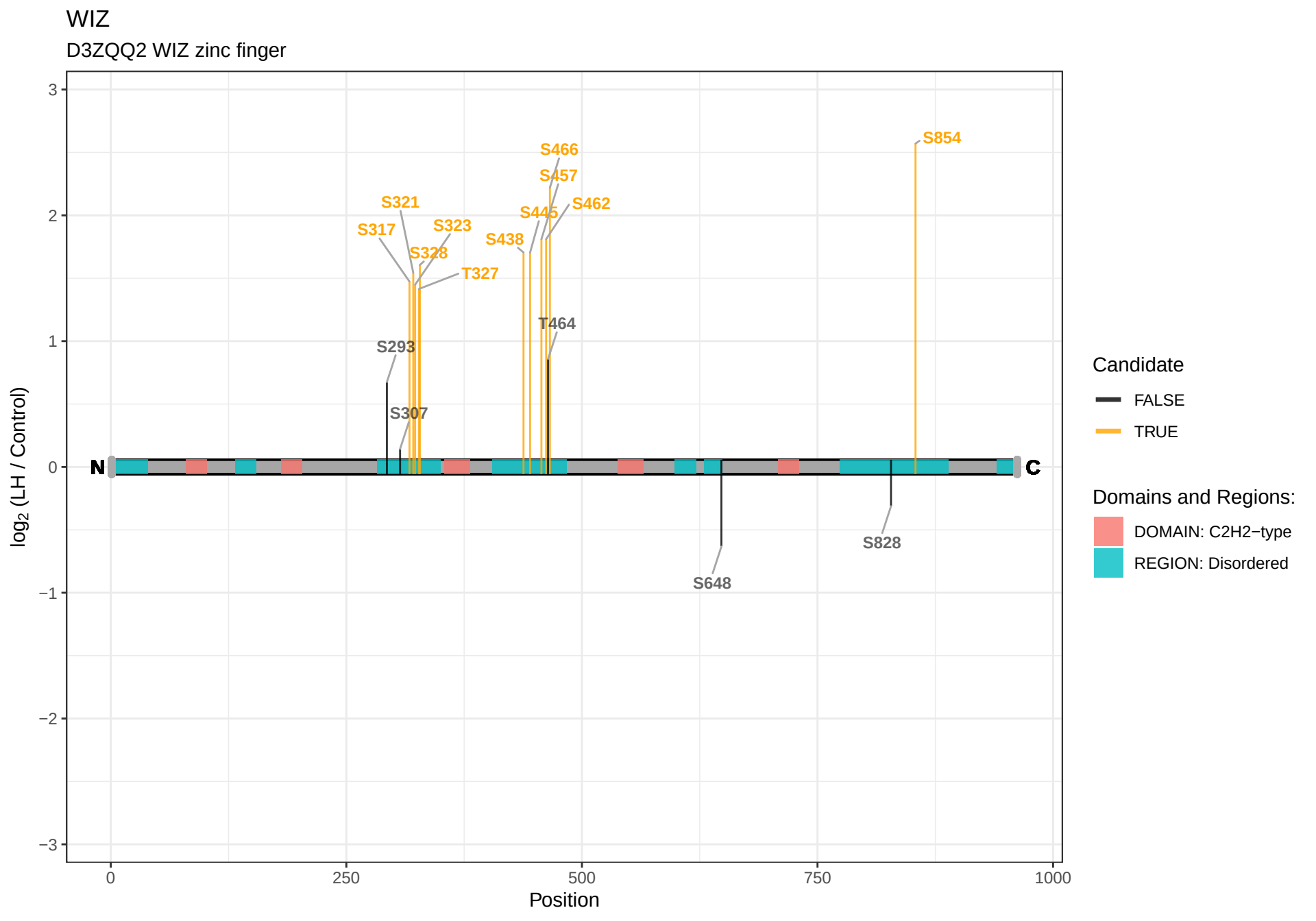

WASHC2
Q80X08 WASH complex subunit 2
S829
S157
N
C
S387
S384
S720
S1060
S1041
S1042
S536
S159
S448
S780
S531
S611
S610
S744
S1327
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Interaction with phospholipids
REGION: Interaction with VPS35
REGION: Required for interaction with F−actin−capping protein subunit alpha (CAPZA1 or CAPZA2 or CAPZA3)
REGION: Sufficient for interaction with CCDC93
REGION: Sufficient for interaction with WASHC3, WASHC4 and WASHC5; required for interaction with WASHC1

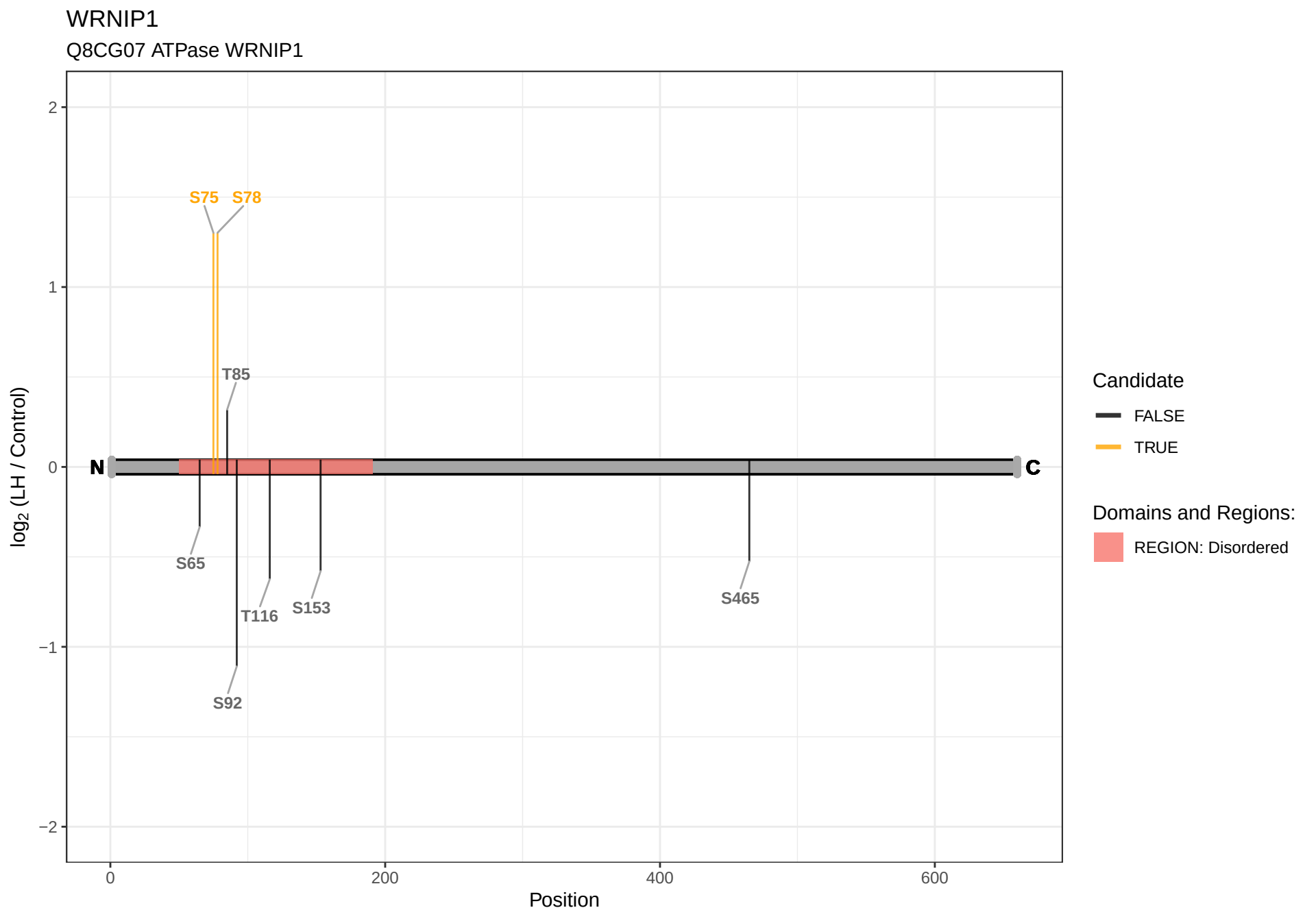

WDR33
F1LT09 WD repeat domain 33
S999
S7
S1205
S1274
N
C
4
2
0
−2
−4
log2 (LH / Control)
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WD_REPEATS_REGION
REGION: Disordered

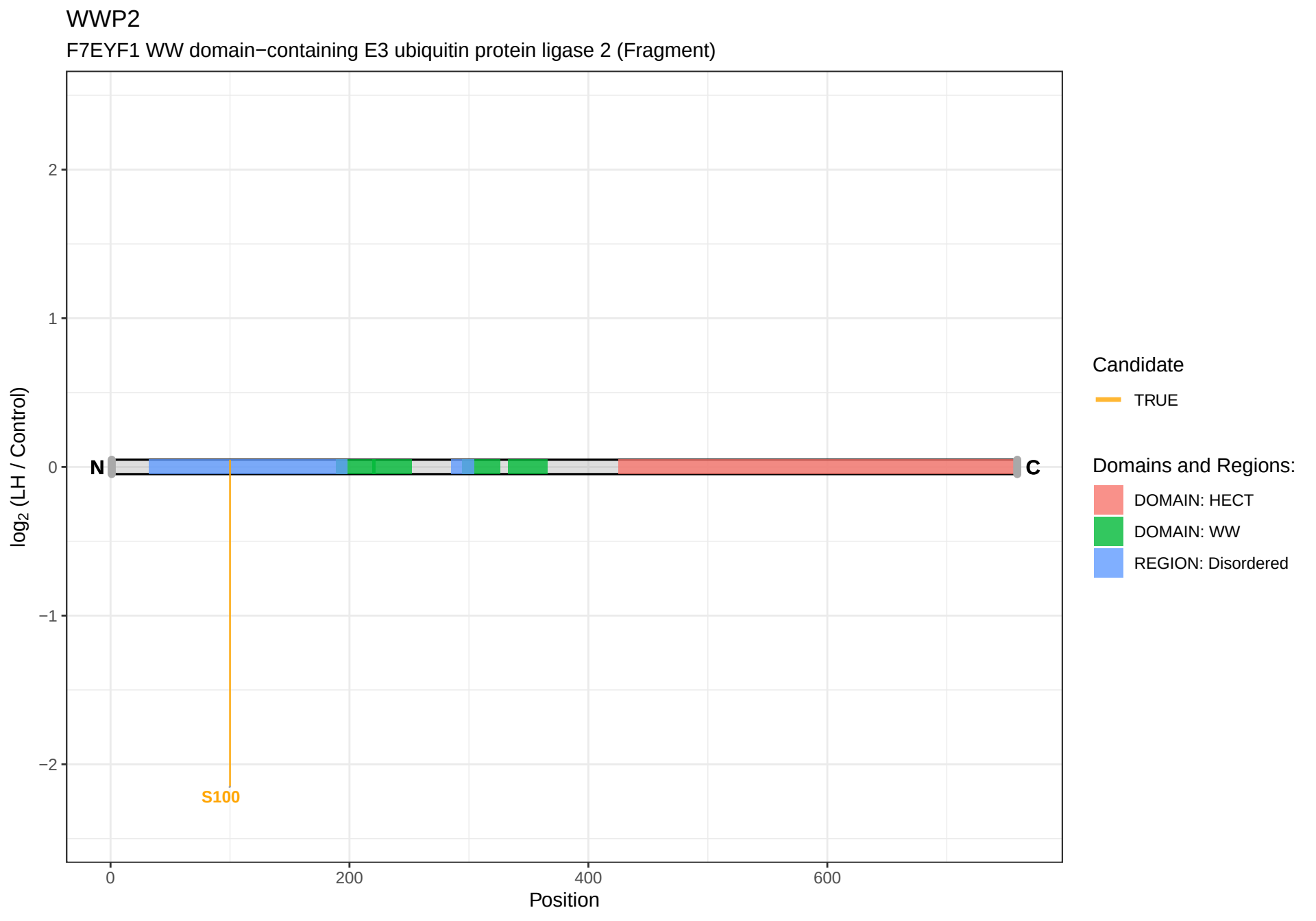

WDR59
D3ZGZ9 WD repeat domain 59
2
1
0
−1
−2
log2 (LH / Control)
N
C
S610
0
250
500
750
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: RWD
DOMAIN: WD_REPEATS_REGION
REGION: Disordered

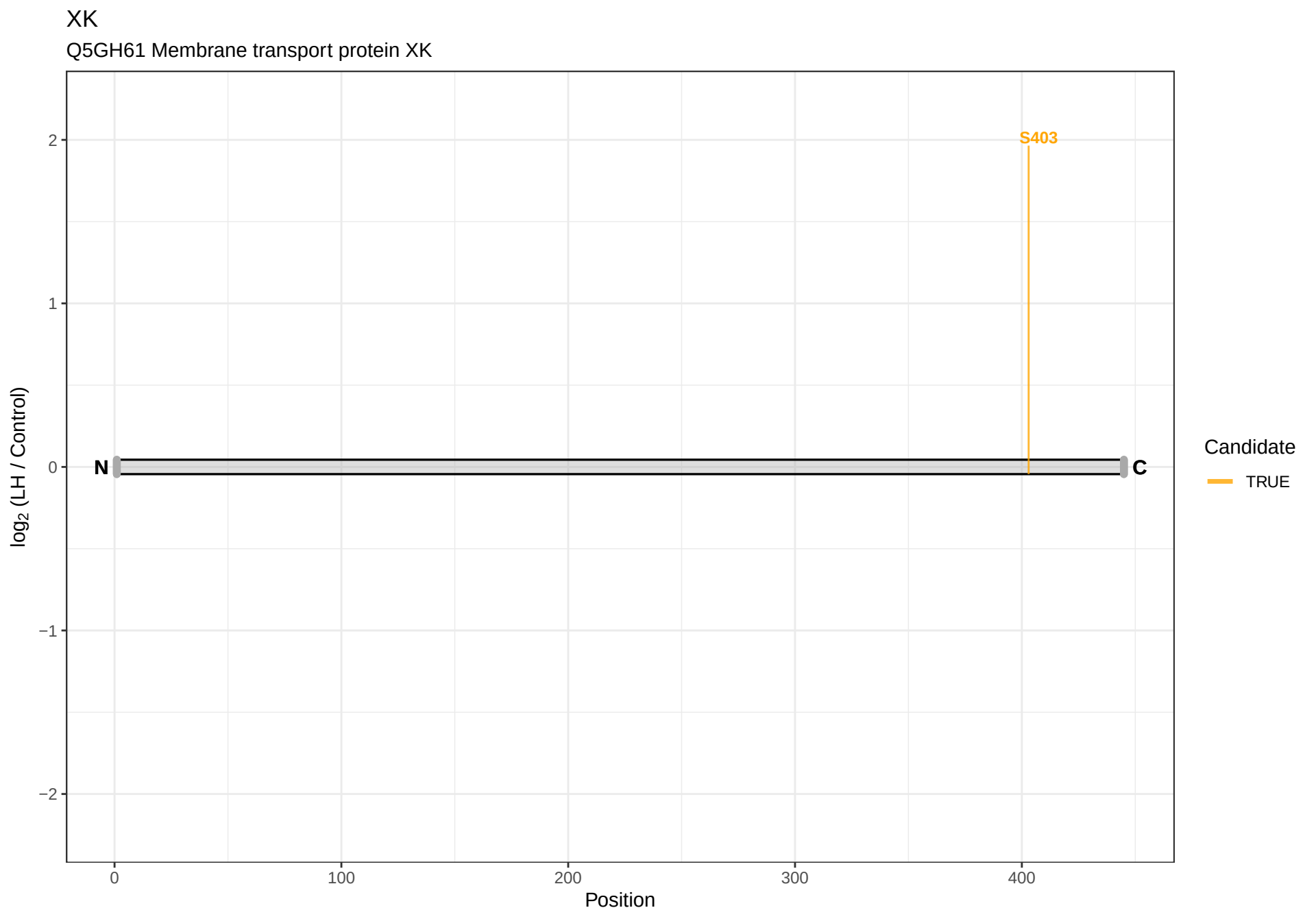

WDR7
Q9ERH3 WD repeat−containing protein 7
log2 (LH / Control)
2
1
0
−1
−2
N
C
S935
S1358
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

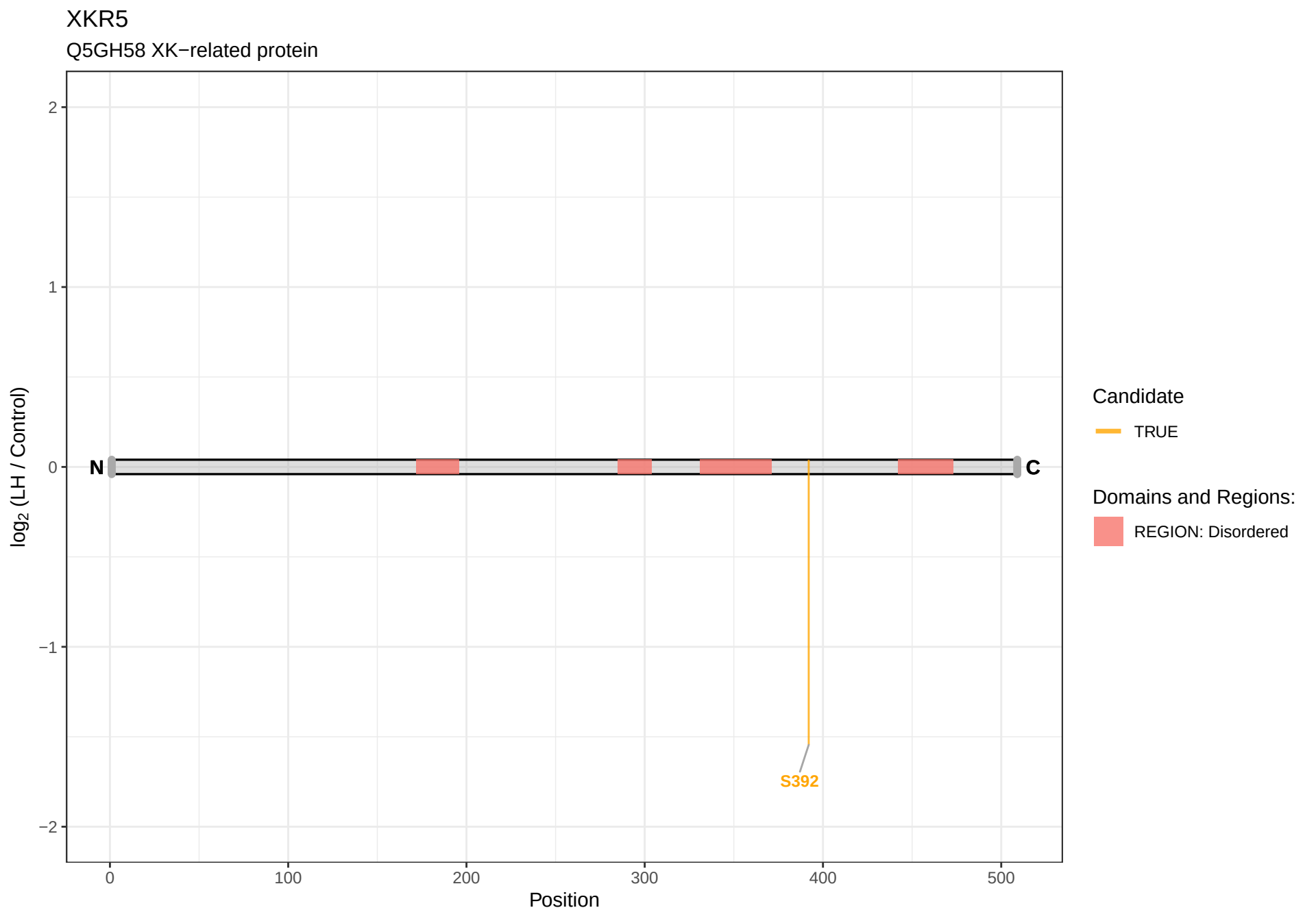

WIPF3
Q9Z0G8 WAS/WASL−interacting protein family member 3
log2 (LH / Control)
2
1
0
−1
−2
N
C
S348
S394
S150
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WH2
REGION: Disordered

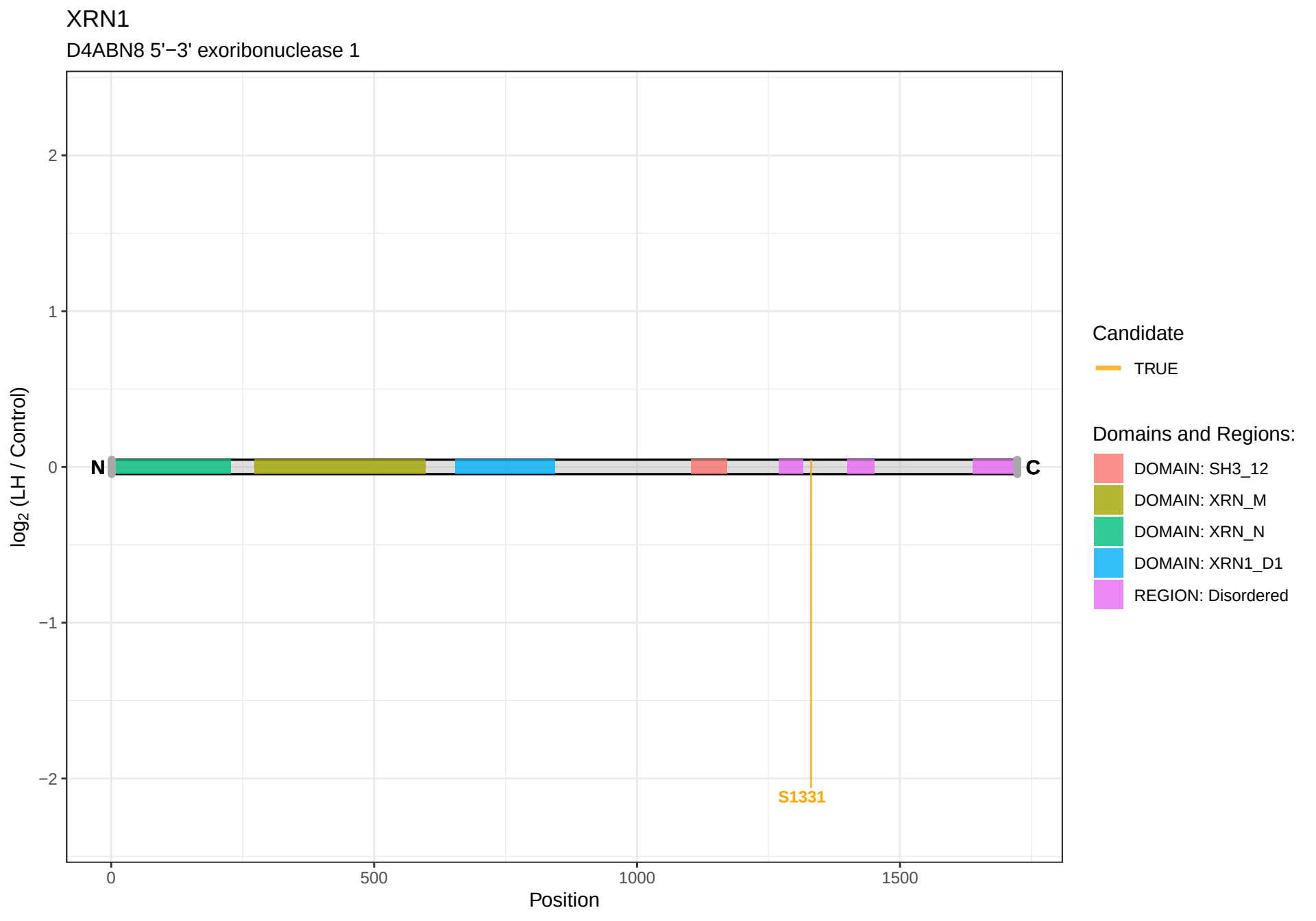

WIZ
D3ZQQ2 WIZ zinc finger
log2 (LH / Control)
Position
N
C
S854
S466
S457
S462
S445
S321
S317
S323
S438
S328
T327
T464
S293
S307
S828
S648
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2H2−type
REGION: Disordered

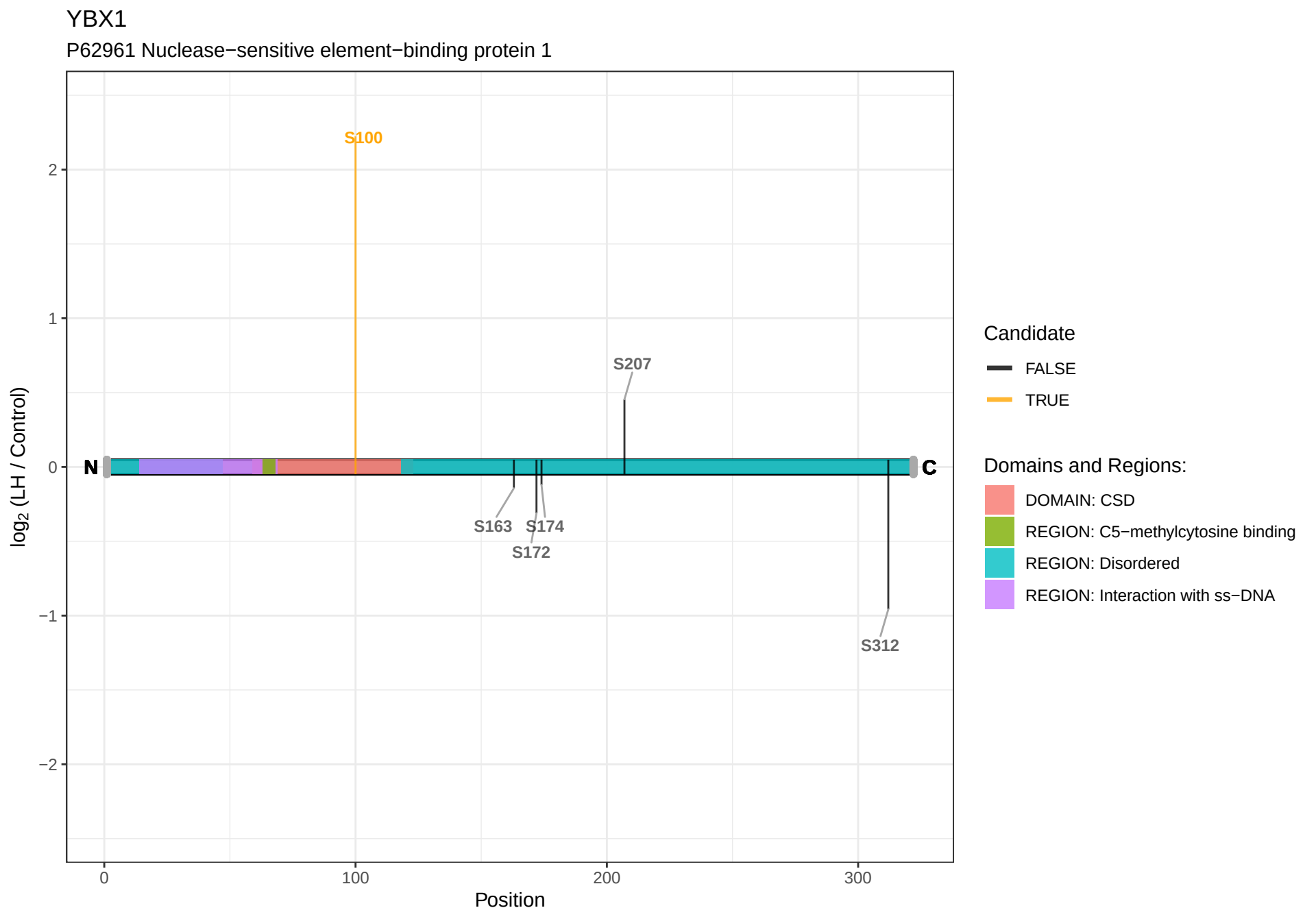

WRNIP1
Q8CG07 ATPase WRNIP1
log2 (LH / Control)
2
1
0
−1
−2
S75
S78
T85
N
C
S65
T116
S153
S92
S465
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered

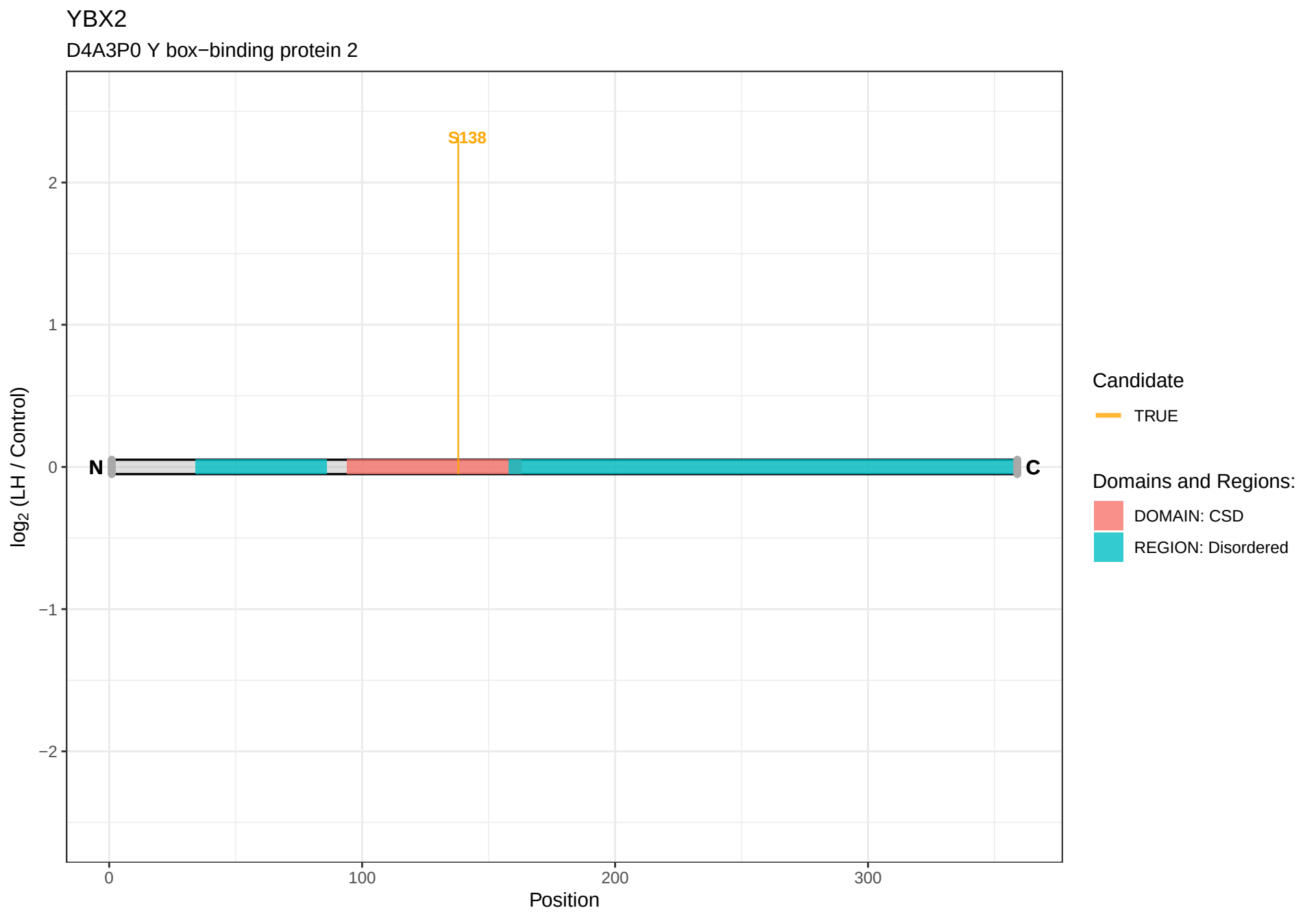

WWP2
F7EYF1 WW domain−containing E3 ubiquitin protein ligase 2 (Fragment)
log2 (LH / Control)
2
1
0
−1
−2
N
C
S100
0
200
400
600
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: HECT
DOMAIN: WW
REGION: Disordered

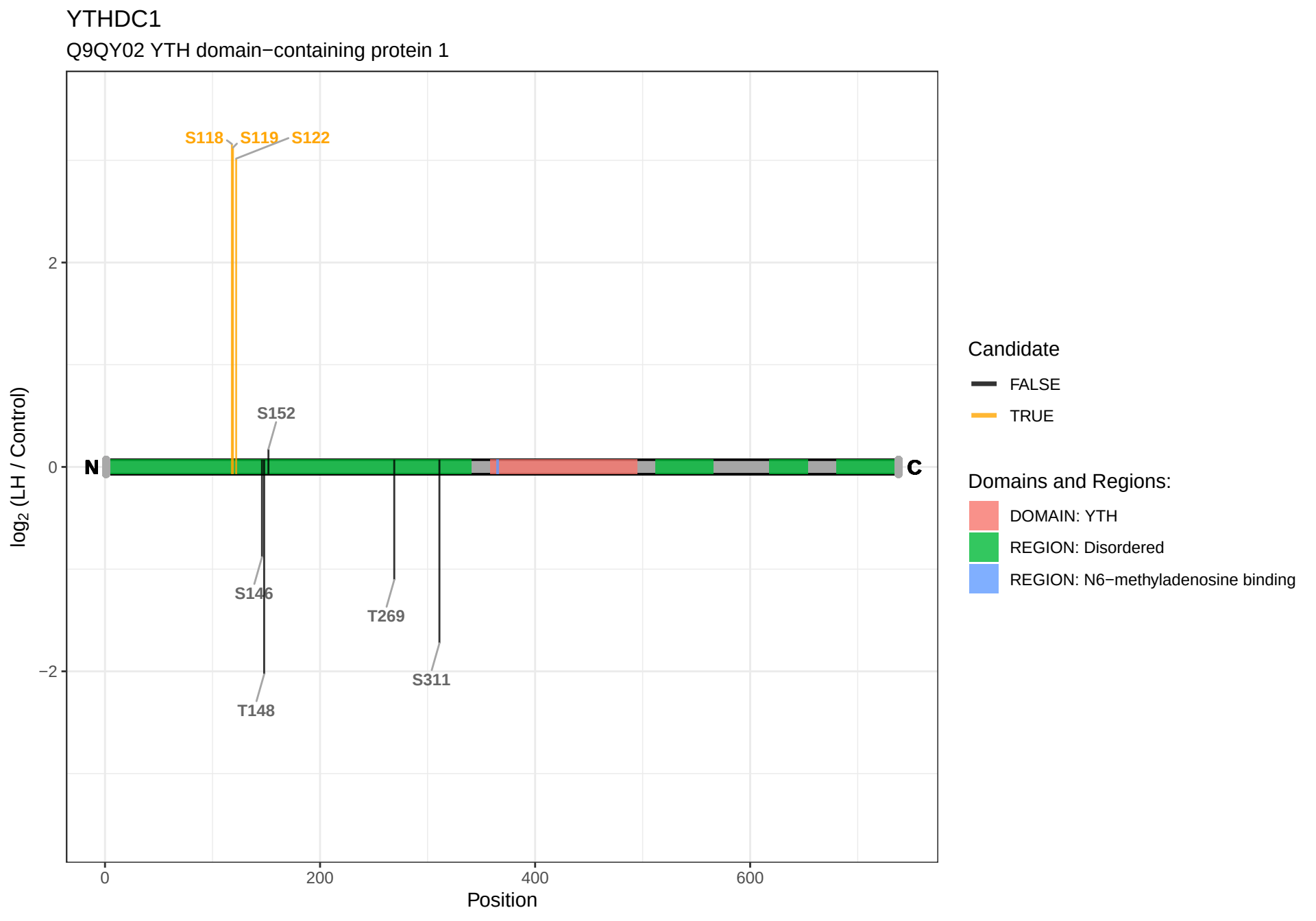

XK
Q5GH61 Membrane transport protein XK
S403
N
C
2
1
0
−1
−2
0
100
200
300
400
Position
log2 (LH / Control)
Candidate
TRUE

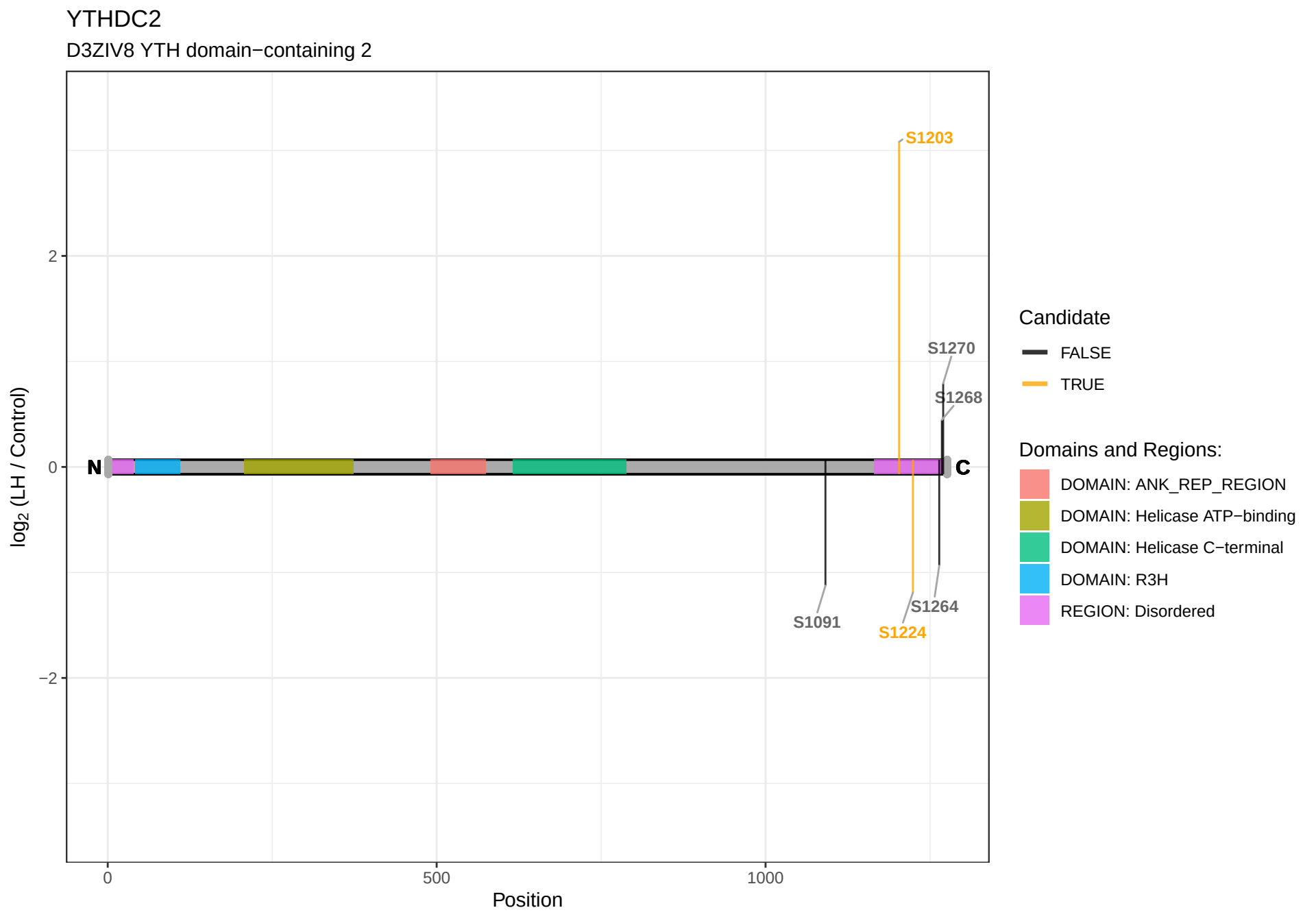

XKR5
Q5GH58 XK−related protein
2
1
0
−1
−2
log2 (LH / Control)
N
C
S392
0
100
200
300
400
500
Position
Candidate
TRUE
Domains and Regions:
REGION: Disordered

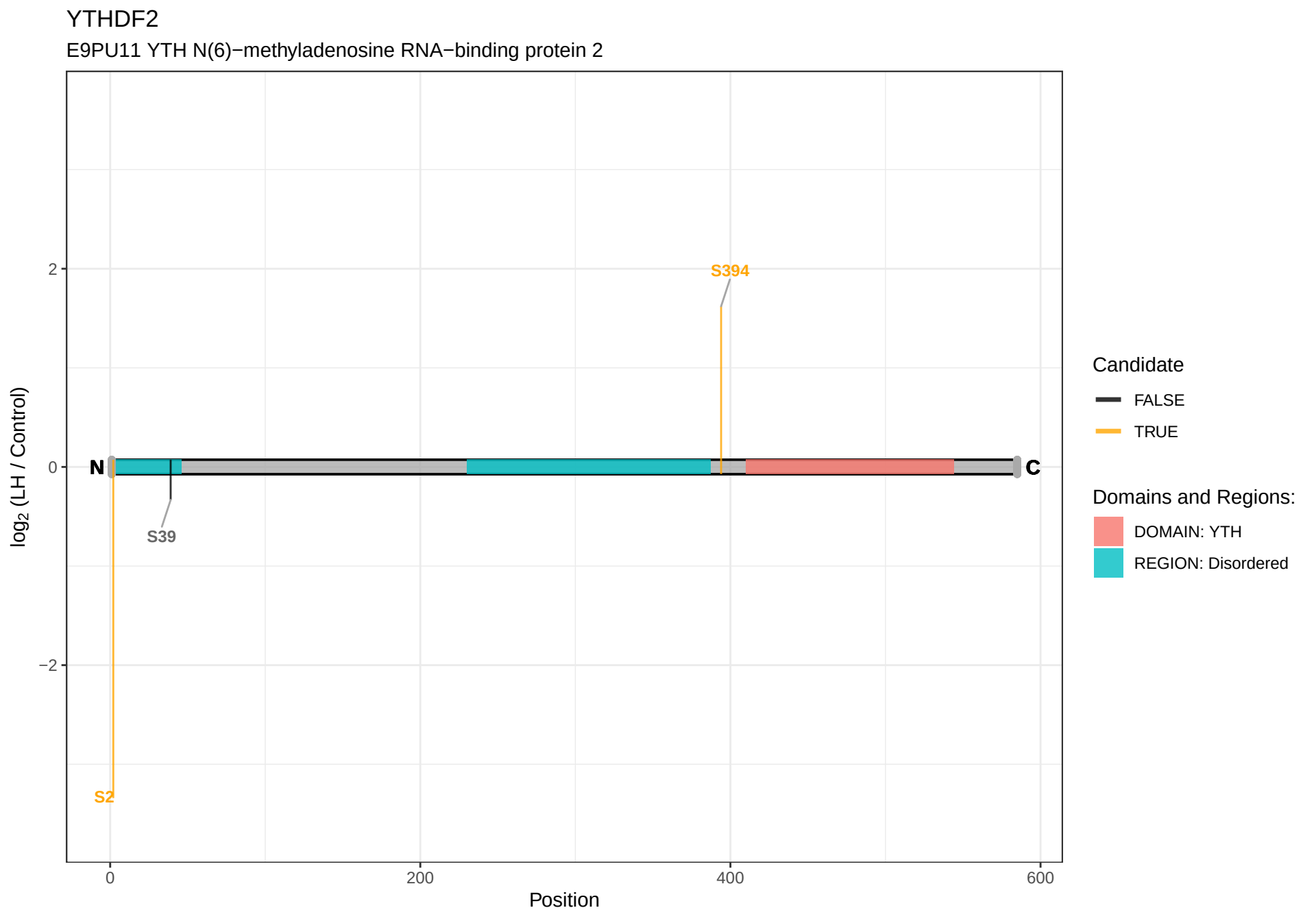

XRN1
D4ABN8 5'−3' exoribonuclease 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S1331
0
500
1000
1500
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: SH3_12
DOMAIN: XRN_M
DOMAIN: XRN_N
DOMAIN: XRN1_D1
REGION: Disordered

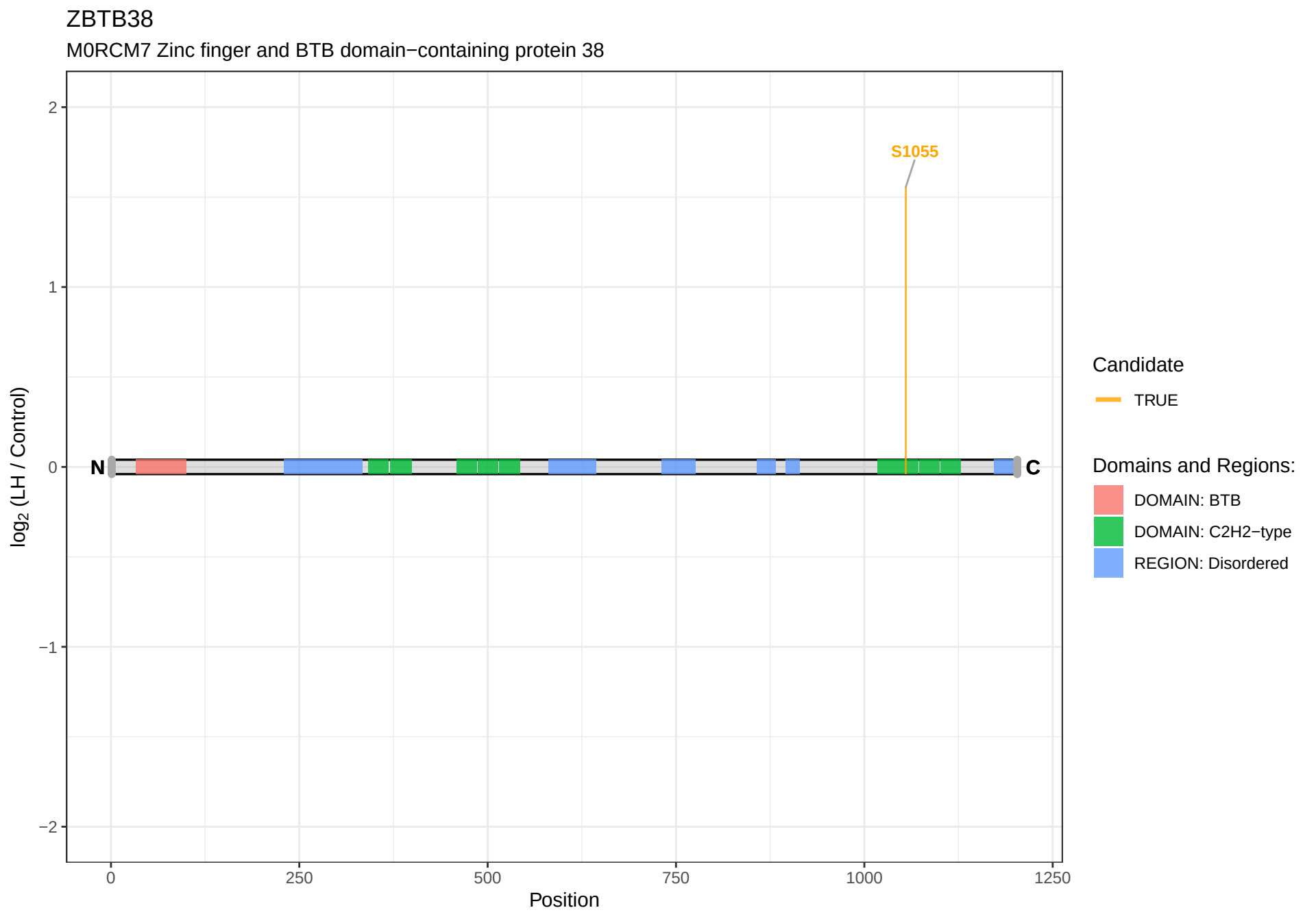

YBX1
P62961 Nuclease−sensitive element−binding protein 1
S100
S207
S163
S174
S172
S312
N
C
2
1
0
−1
−2
0
100
200
300
Position
log2 (LH / Control)
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: CSD
REGION: C5−methylcytosine binding
REGION: Disordered
REGION: Interaction with ss−DNA

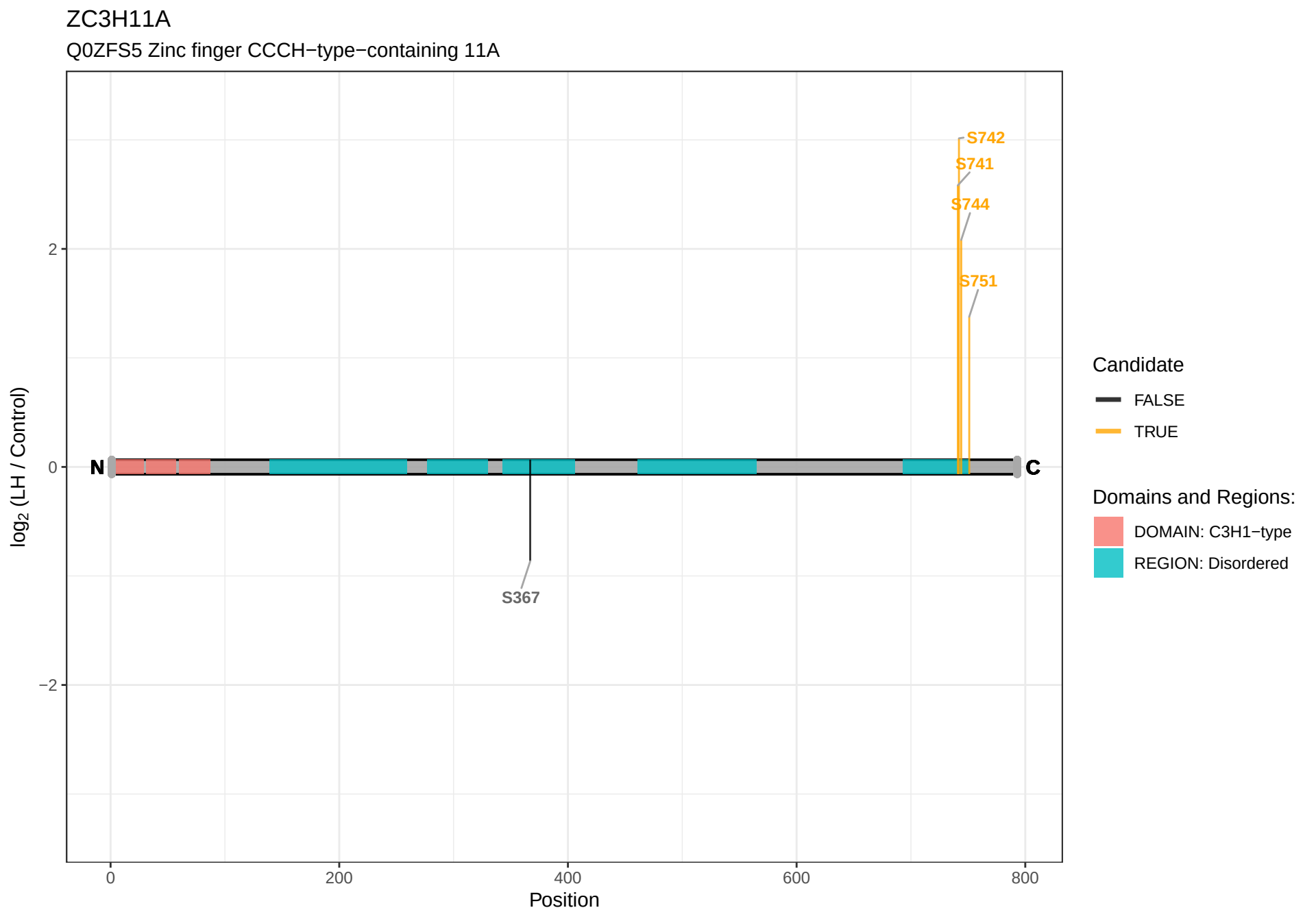

YBX2
D4A3P0 Y box−binding protein 2
S138
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
100
200
300
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: CSD
REGION: Disordered

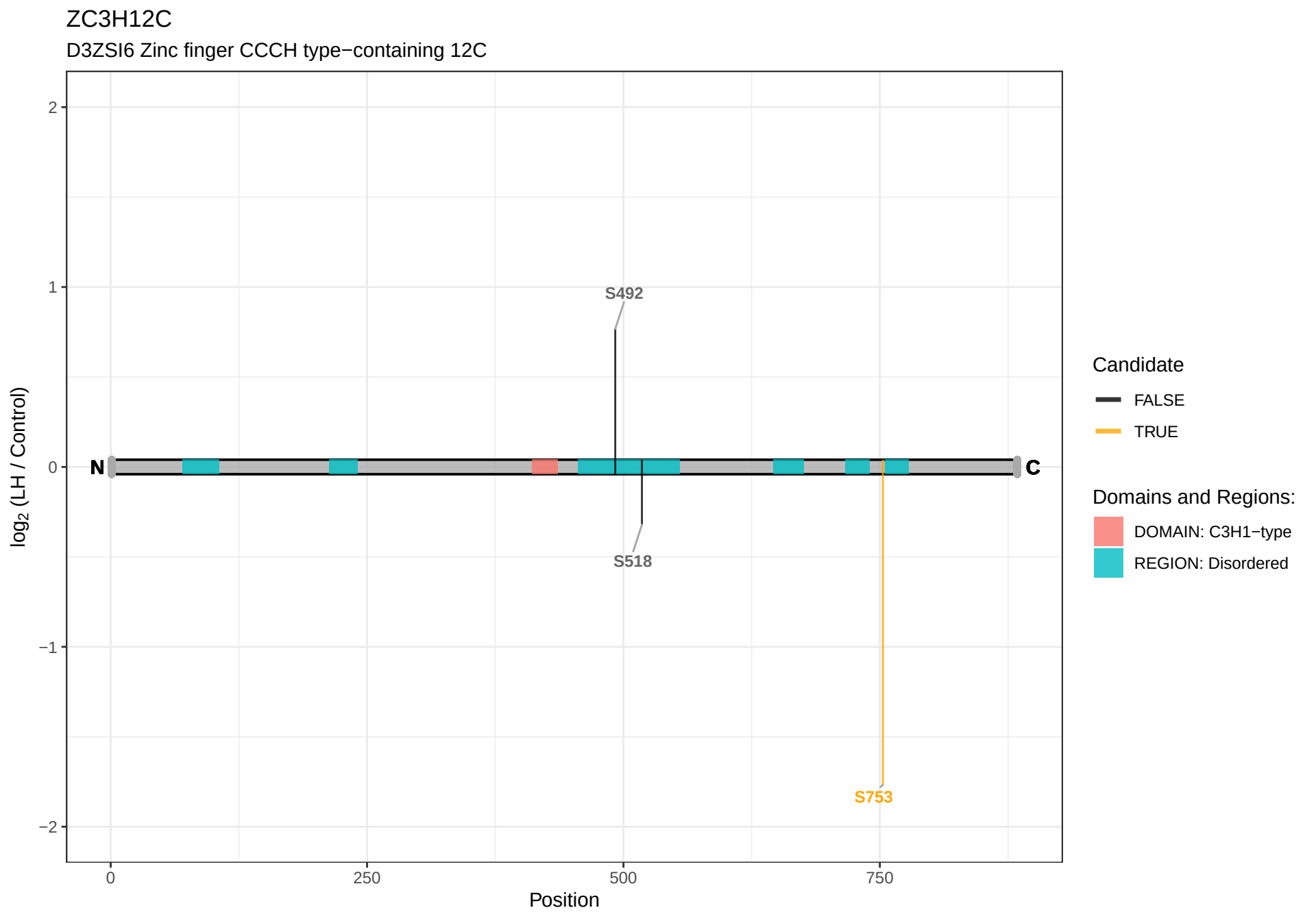

YTHDC1
Q9QY02 YTH domain−containing protein 1
S118
S119
S122
S152
S146
T148
T269
S311
N
C
2
0
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: YTH
REGION: Disordered
REGION: N6−methyladenosine binding

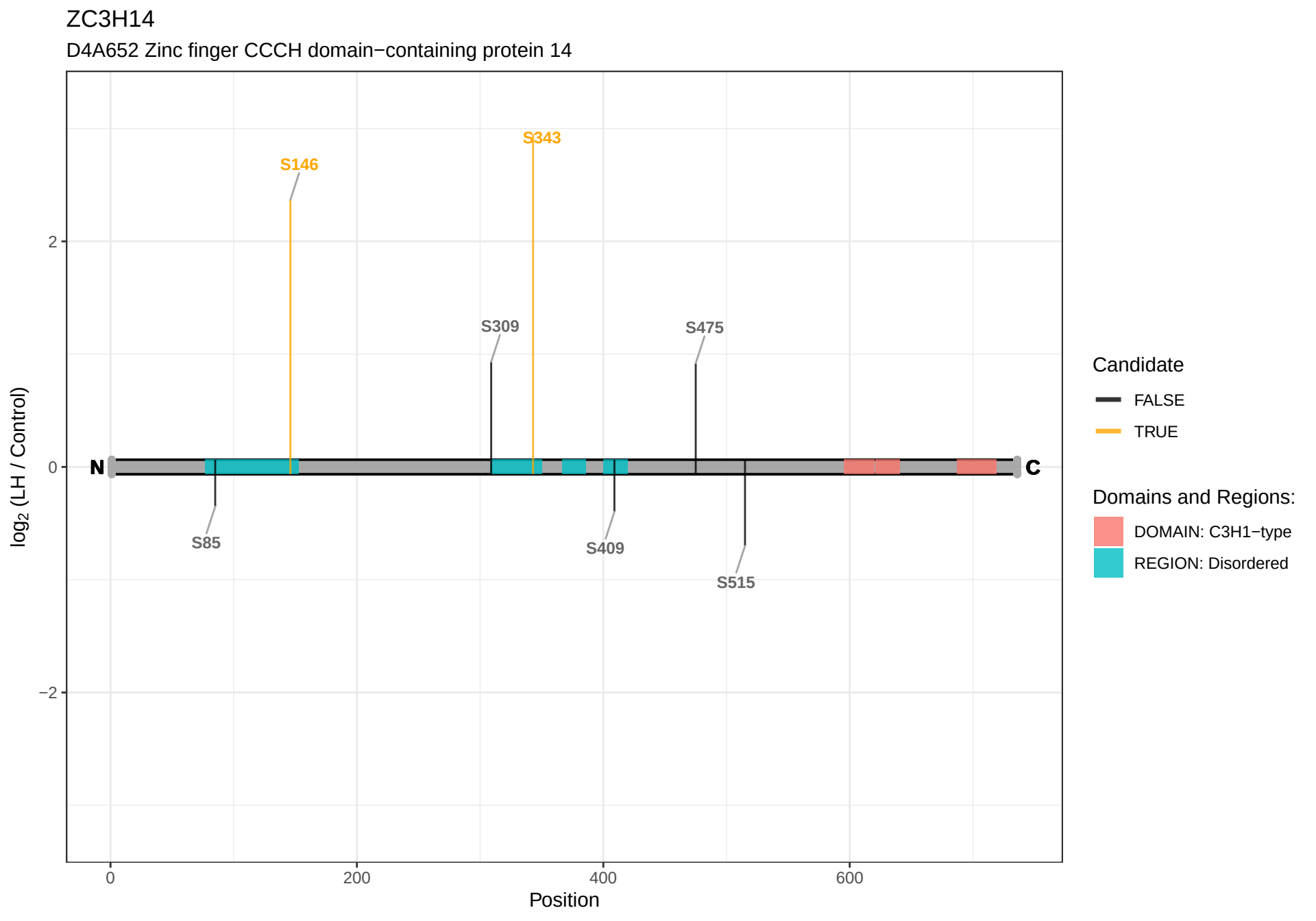

YTHDC2
D3ZIV8 YTH domain−containing 2
S1203
S1270
S1268
S1264
S1224
S1091
N
C
2
0
−2
log2 (LH / Control)
0
500
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: ANK_REP_REGION
DOMAIN: Helicase ATP−binding
DOMAIN: Helicase C−terminal
DOMAIN: R3H
REGION: Disordered

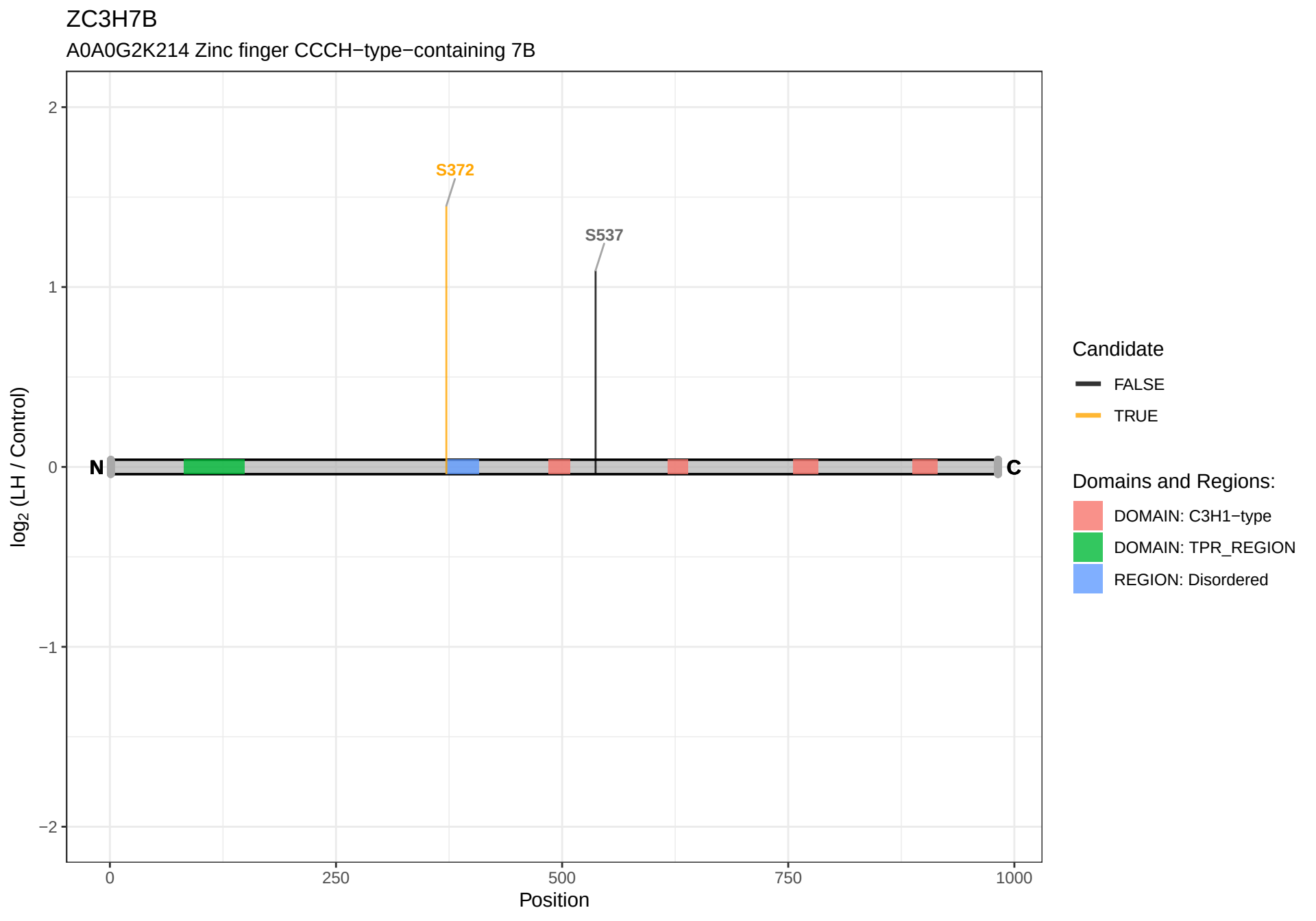

YTHDF2
E9PU11 YTH N(6)−methyladenosine RNA−binding protein 2
log2 (LH / Control)
2
0
−2
N
C
S394
S39
S2
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: YTH
REGION: Disordered

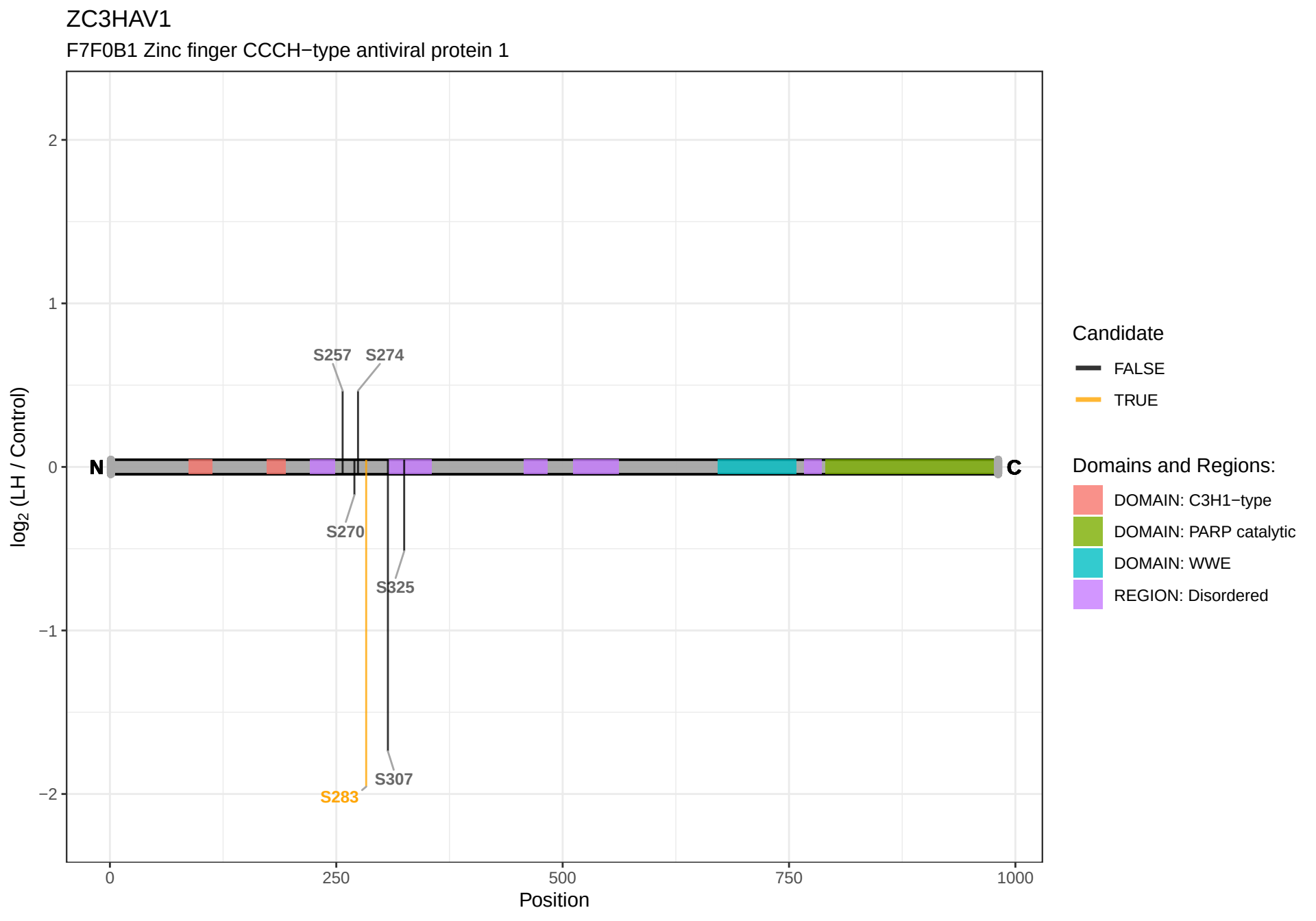

ZBTB38
M0RCM7 Zinc finger and BTB domain−containing protein 38
S1055
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
250
500
750
1000
1250
Candidate
TRUE
Domains and Regions:
DOMAIN: BTB
DOMAIN: C2H2−type
REGION: Disordered

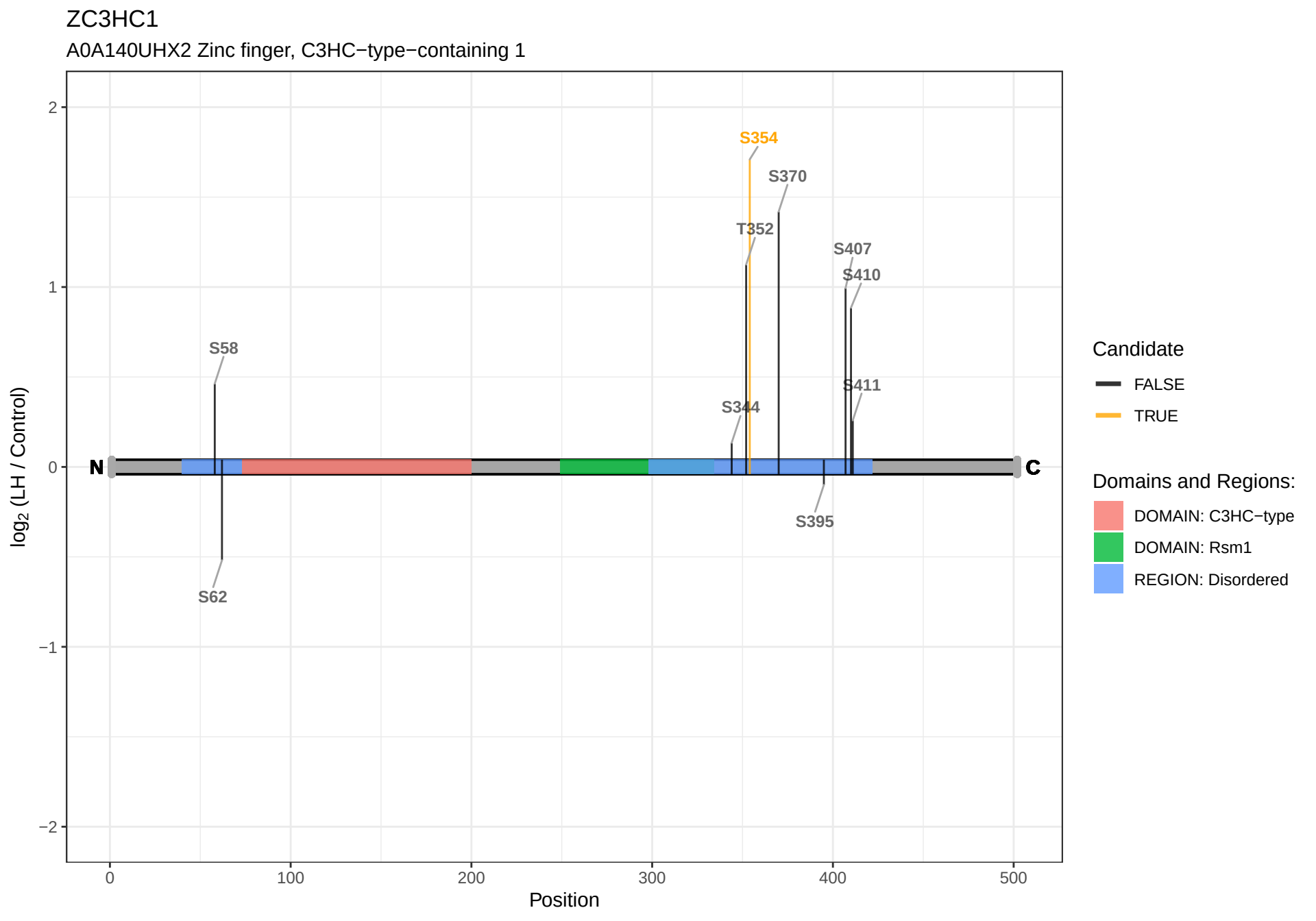

ZC3H11A
Q0ZFS5 Zinc finger CCCH−type−containing 11A
S742
S741
S744
S751
S367
N
C
2
0
−2
log2 (LH / Control)
0
200
400
600
800
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C3H1−type
REGION: Disordered

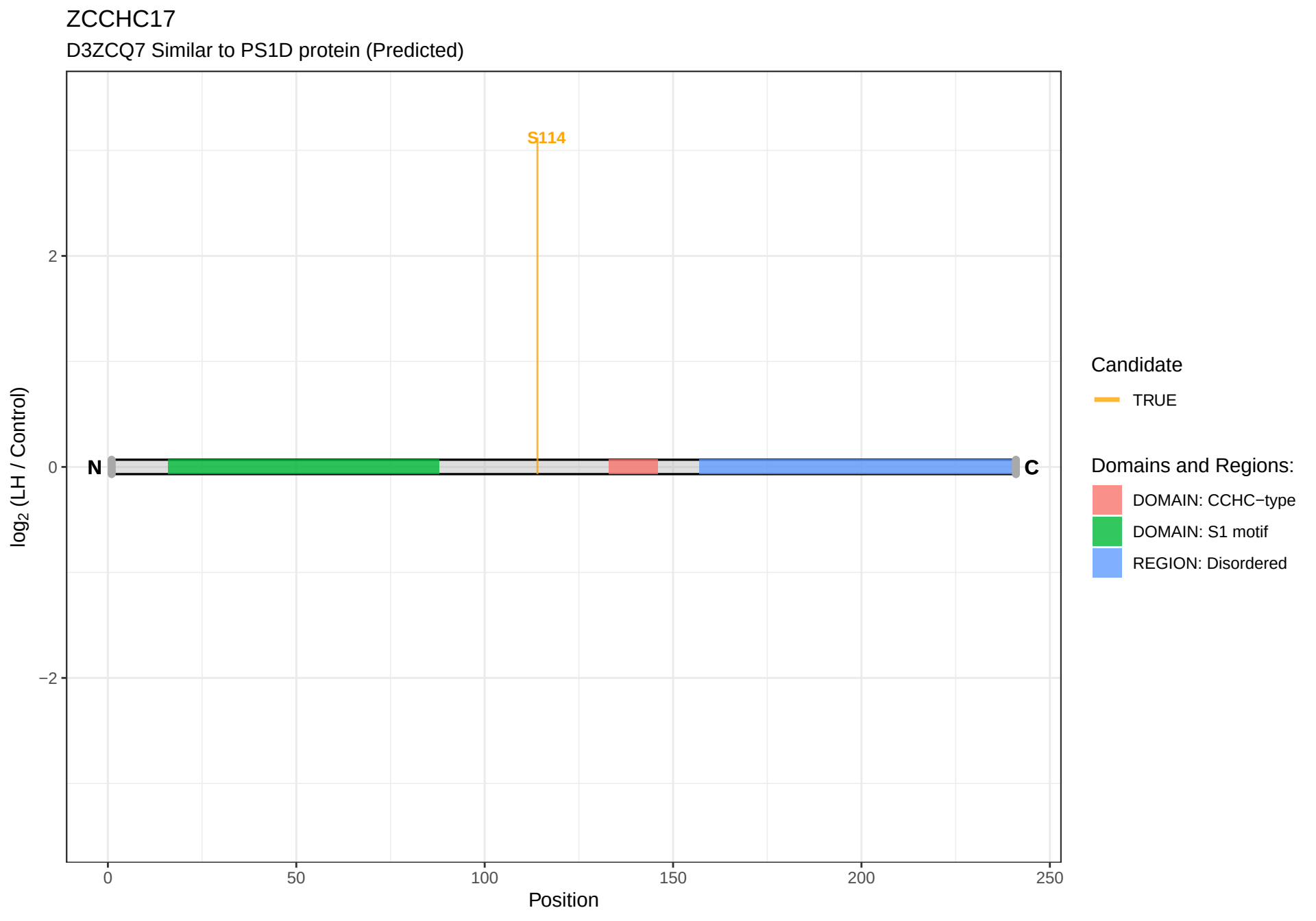

ZC3H12C
D3ZSI6 Zinc finger CCCH type−containing 12C
log2 (LH / Control)
2
1
0
−1
−2
N
C
S492
S518
S753
0
250
500
750
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C3H1−type
REGION: Disordered

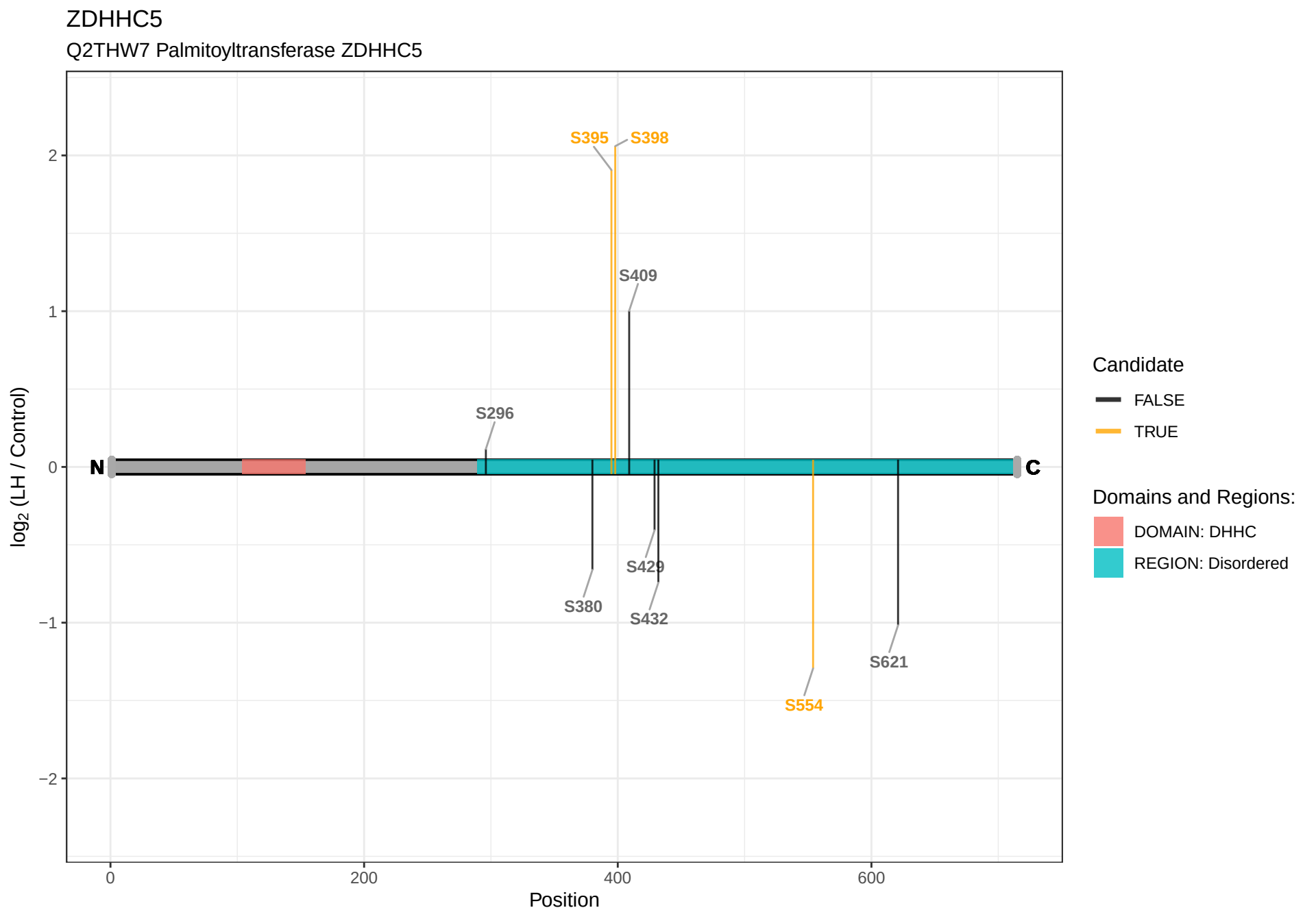

ZC3H14
D4A652 Zinc finger CCCH domain−containing protein 14
S146
S343
S309
S475
S85
S409
S515
N
C
2
0
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C3H1−type
REGION: Disordered

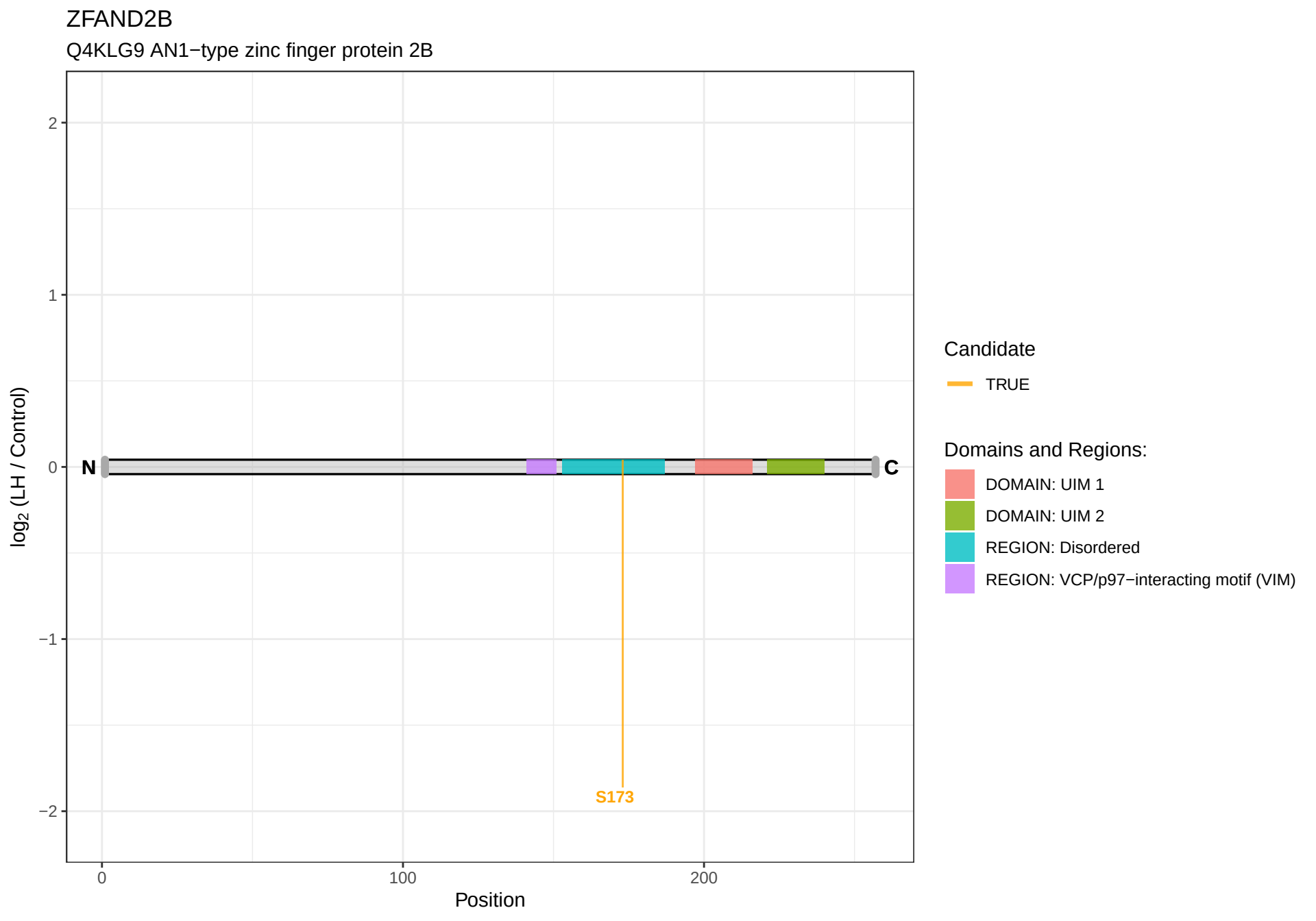

ZC3H7B
A0A0G2K214 Zinc finger CCCH−type−containing 7B
S372
S537
N
C
log2 (LH / Control)
2
1
0
−1
−2
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C3H1−type
DOMAIN: TPR_REGION
REGION: Disordered

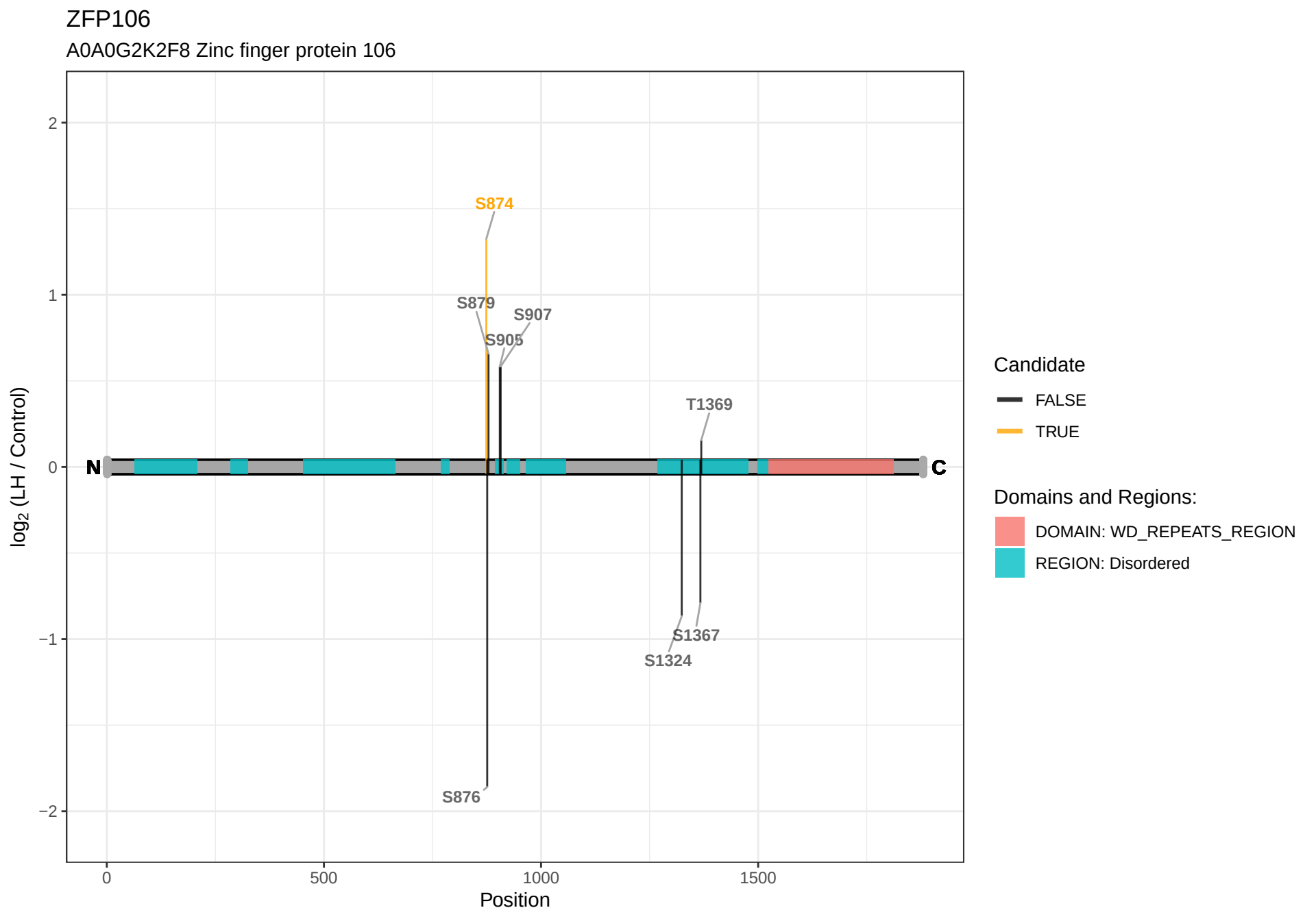

ZC3HAV1
F7F0B1 Zinc finger CCCH−type antiviral protein 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S257
S274
S270
S325
S307
S283
0
250
500
750
1000
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C3H1−type
DOMAIN: PARP catalytic
DOMAIN: WWE
REGION: Disordered

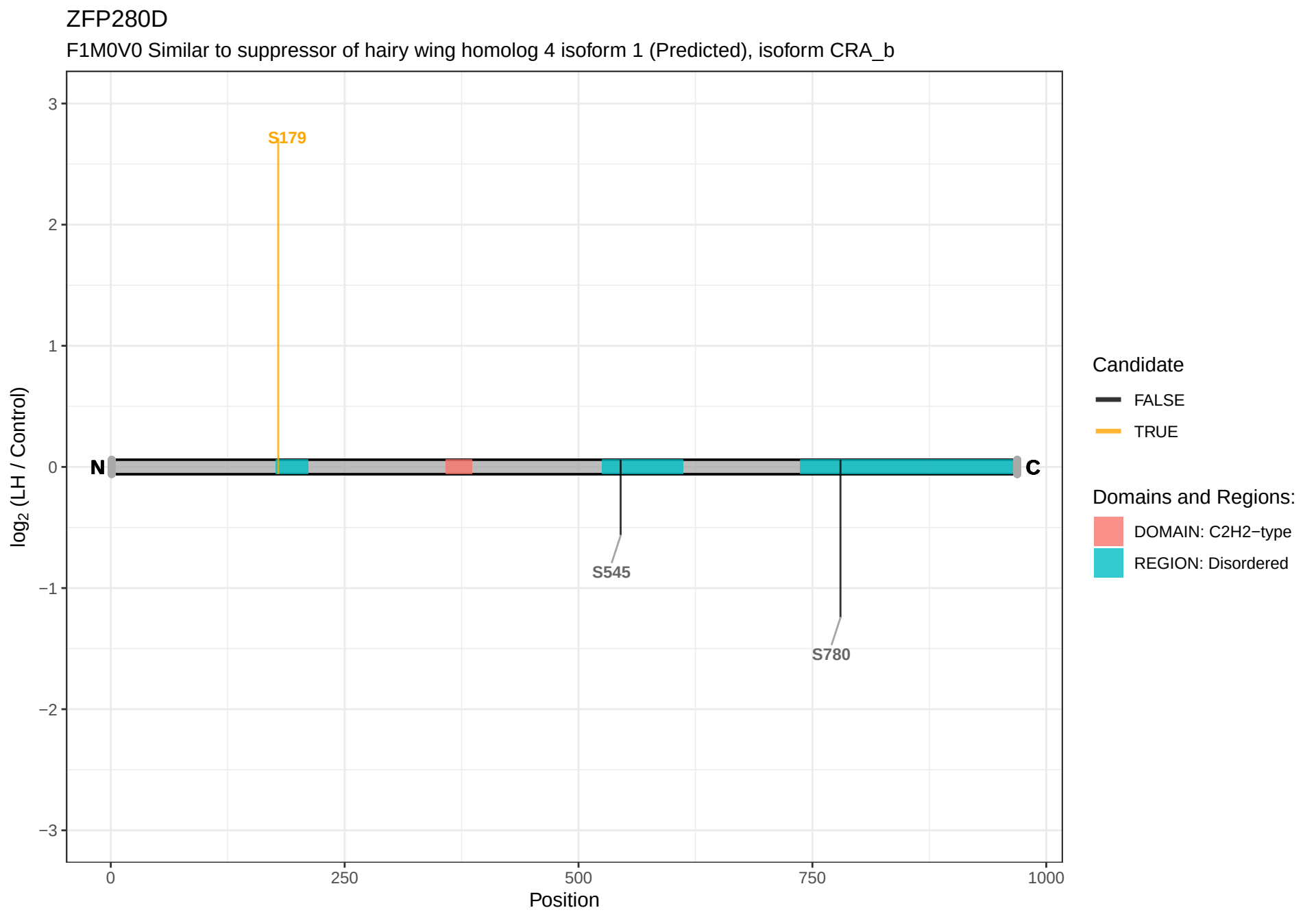

ZC3HC1
A0A140UHX2 Zinc finger, C3HC−type−containing 1
log2 (LH / Control)
2
1
0
−1
−2
N
C
S354
S370
T352
S407
S410
S58
S411
S344
S395
S62
0
100
200
300
400
500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C3HC−type
DOMAIN: Rsm1
REGION: Disordered

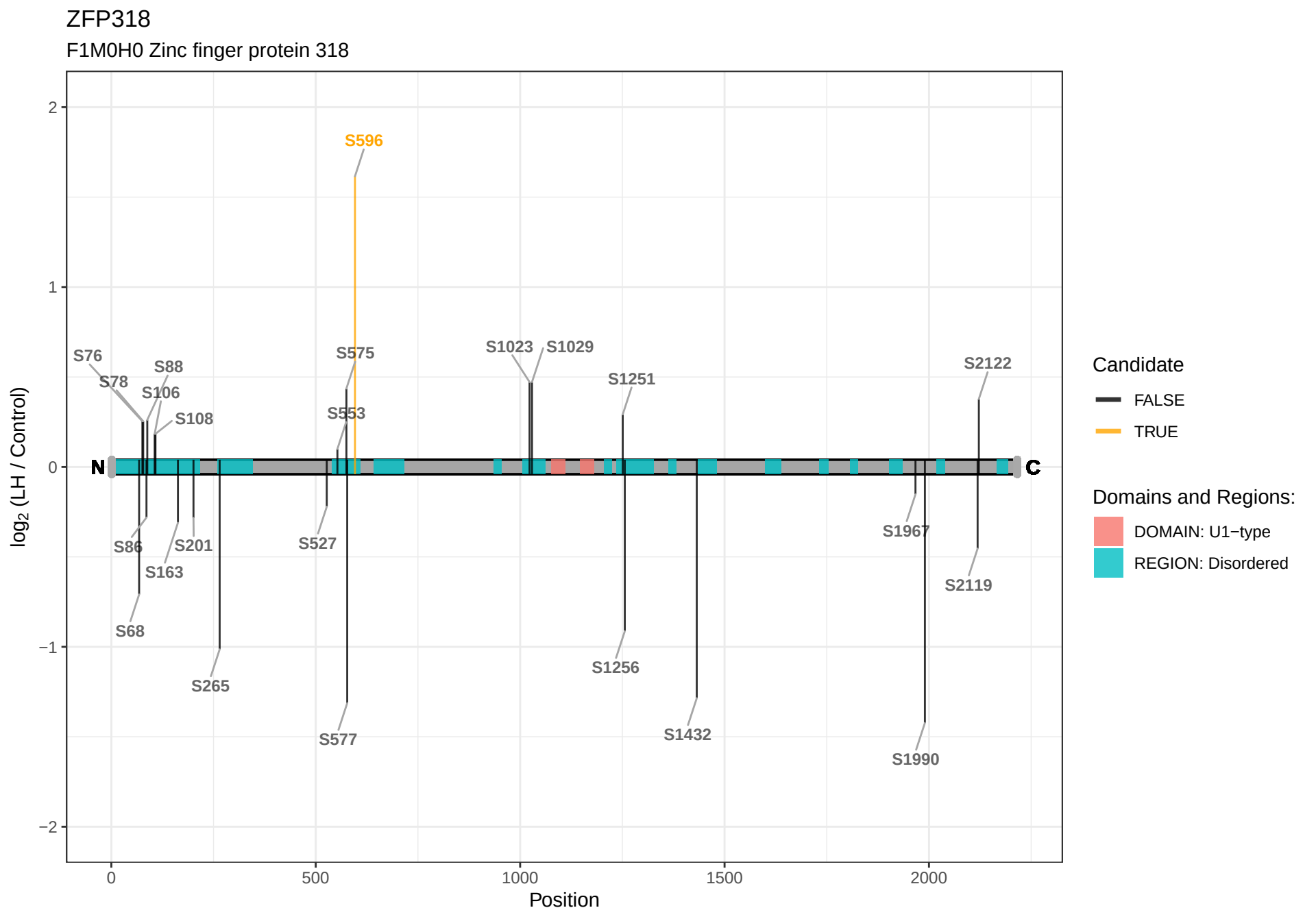

ZCCHC17
D3ZCQ7 Similar to PS1D protein (Predicted)
S114
N
C
2
0
−2
log2 (LH / Control)
0
50
100
150
200
250
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: CCHC−type
DOMAIN: S1 motif
REGION: Disordered

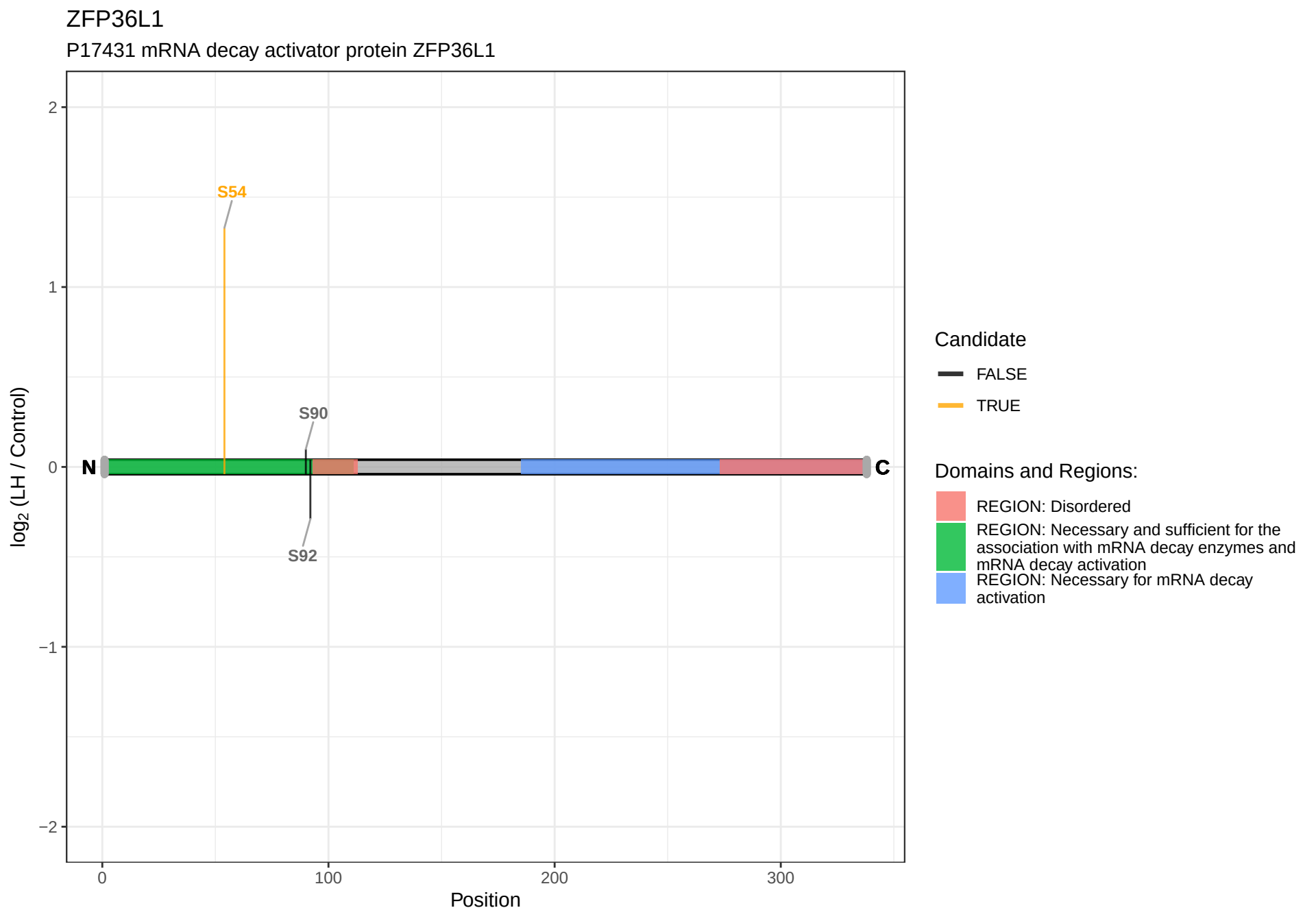

ZDHHC5
Q2THW7 Palmitoyltransferase ZDHHC5
S395
S398
S409
S296
N
C
S380
S429
S432
S621
S554
2
1
0
−1
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DHHC
REGION: Disordered

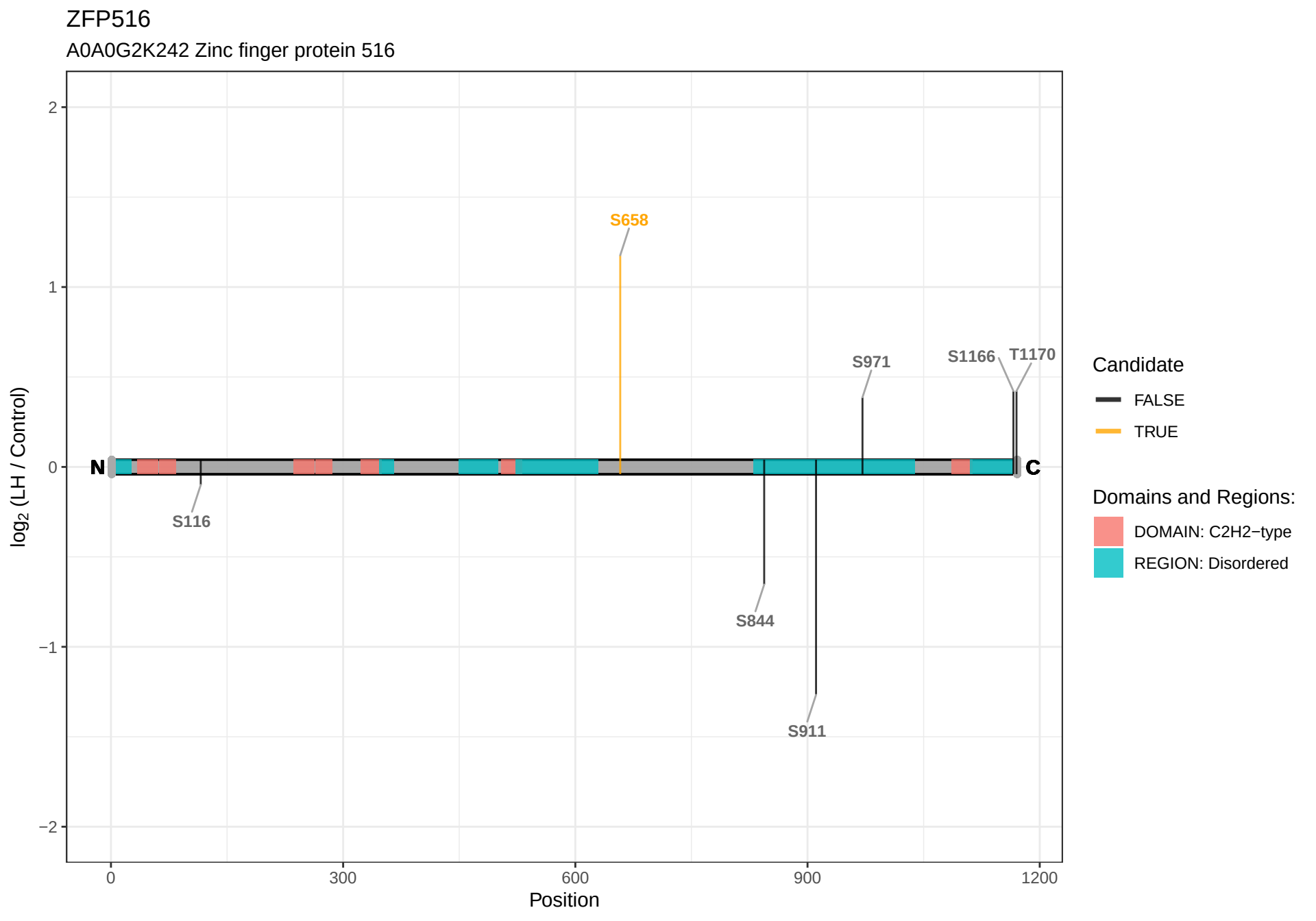

ZFAND2B
Q4KLG9 AN1−type zinc finger protein 2B
log2 (LH / Control)
2
1
0
−1
−2
N
C
S173
0
100
200
Position
Candidate
TRUE
Domains and Regions:
DOMAIN: UIM 1
DOMAIN: UIM 2
REGION: Disordered
REGION: VCP/p97−interacting motif (VIM)

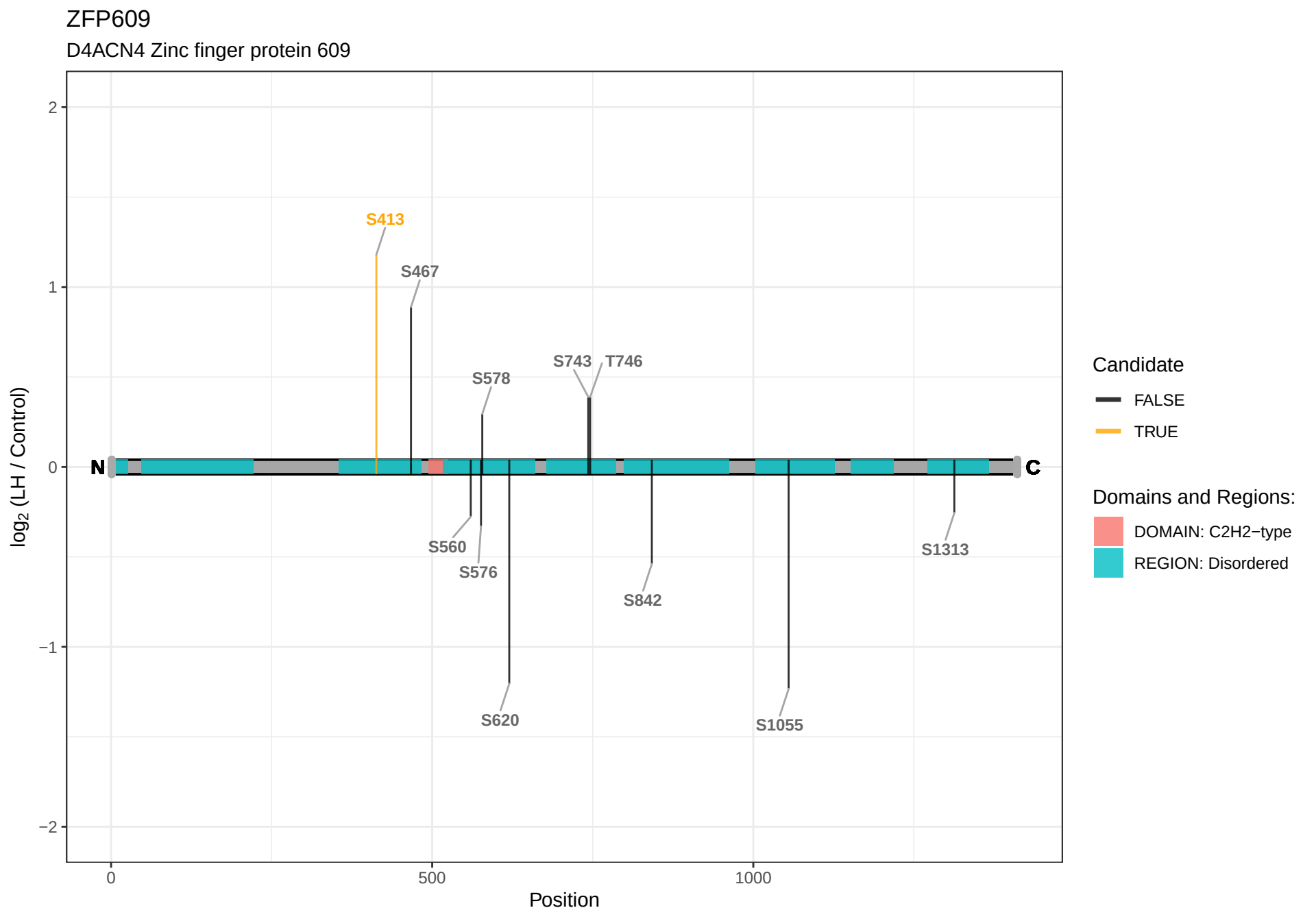

ZFP106
A0A0G2K2F8 Zinc finger protein 106
log2 (LH / Control)
2
1
0
−1
−2
N
C
S874
S879
S907
S905
T1369
S1367
S1324
S876
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: WD_REPEATS_REGION
REGION: Disordered

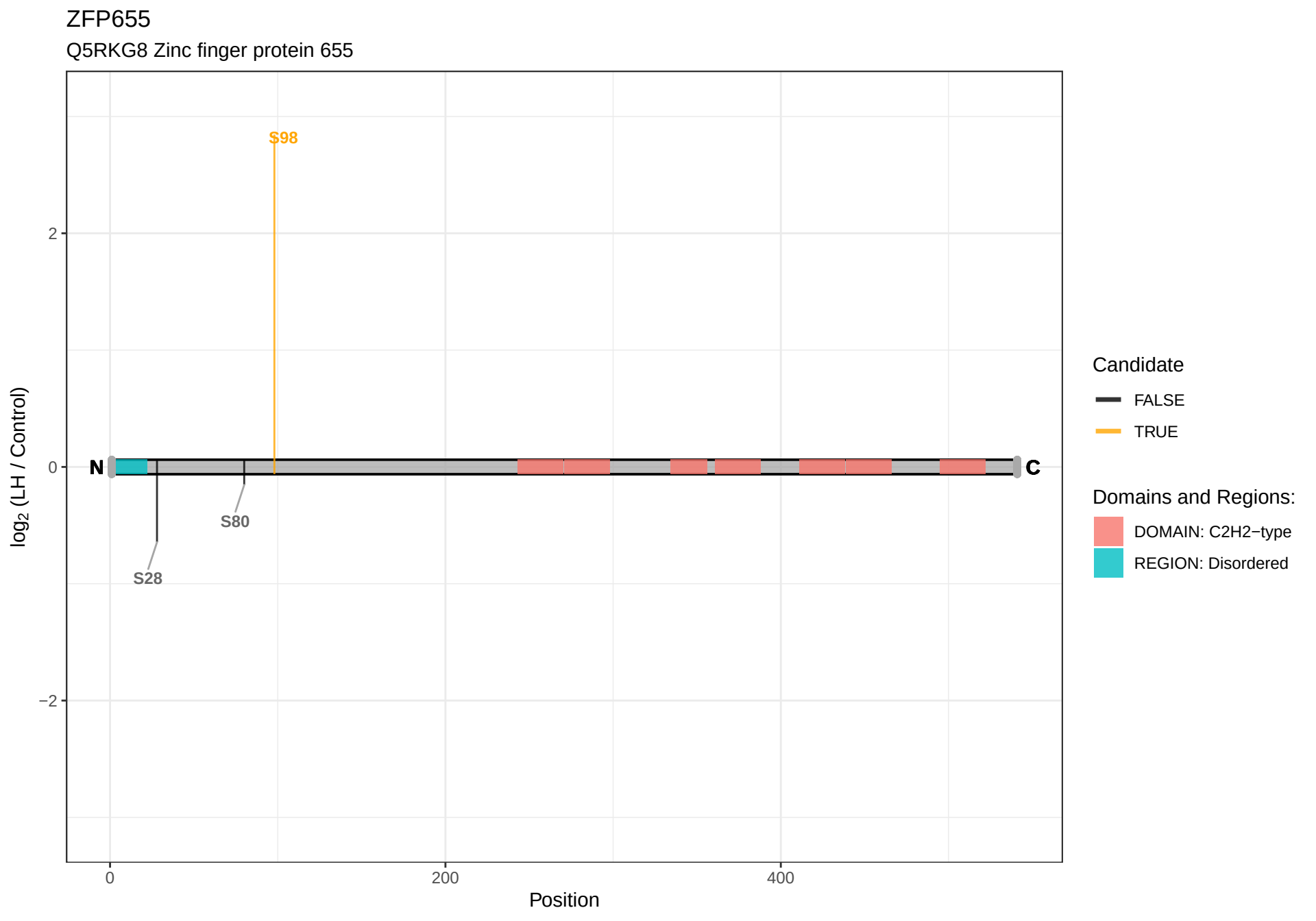

ZFP280D
F1M0V0 Similar to suppressor of hairy wing homolog 4 isoform 1 (Predicted), isoform CRA_b
S179
S545
S780
N
C
log2 (LH / Control)
Position
0
250
500
750
1000
3
2
1
0
−1
−2
−3
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2H2−type
REGION: Disordered

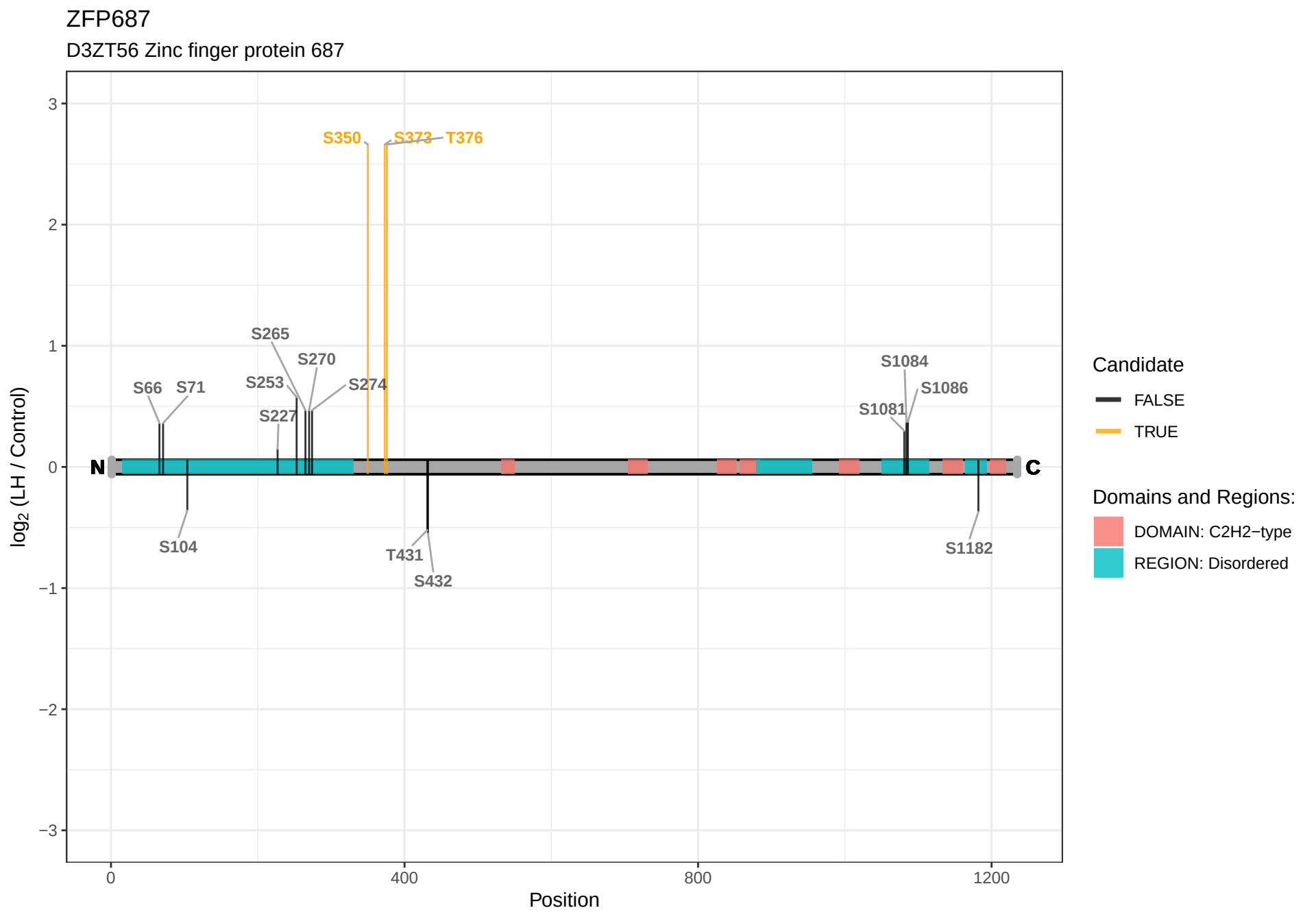

ZFP318
F1M0H0 Zinc finger protein 318
log2 (LH / Control)
Position
N
C
S596
S76
S78
S88
S106
S108
S575
S553
S1023
S1029
S1251
S2122
S86
S201
S163
S68
S265
S527
S577
S1256
S1432
S1967
S2119
S1990
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: U1−type
REGION: Disordered

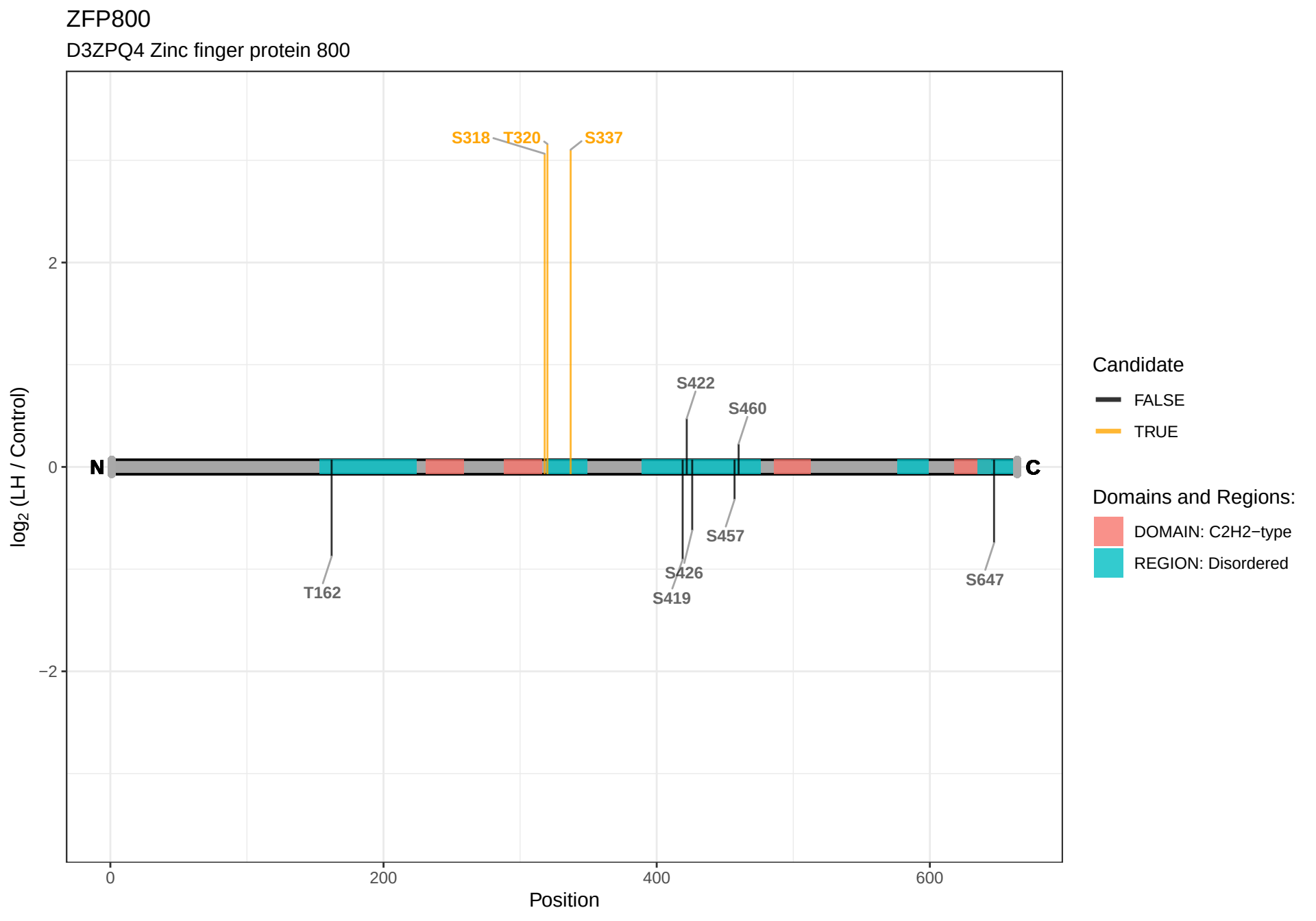

ZFP36L1
P17431 mRNA decay activator protein ZFP36L1
log2 (LH / Control)
2
1
0
−1
−2
S54
S90
S92
N
C
0
100
200
300
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered
REGION: Necessary and sufficient for the association with mRNA decay enzymes and mRNA decay activation
REGION: Necessary for mRNA decay activation

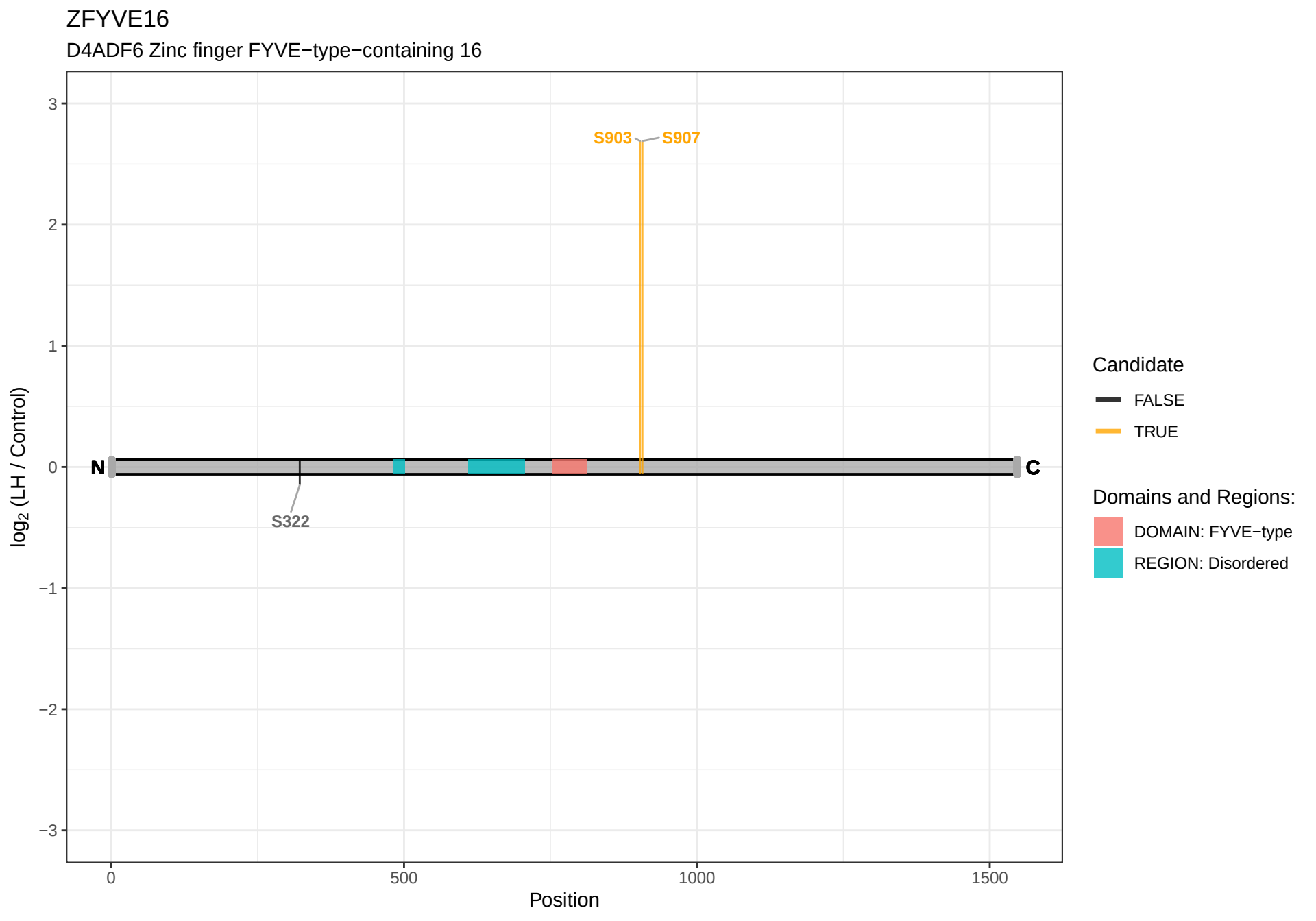

ZFP516
A0A0G2K242 Zinc finger protein 516
log2 (LH / Control)
2
1
0
−1
−2
N
C
S658
S971
S1166
T1170
S116
S844
S911
0
300
600
900
1200
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2H2−type
REGION: Disordered

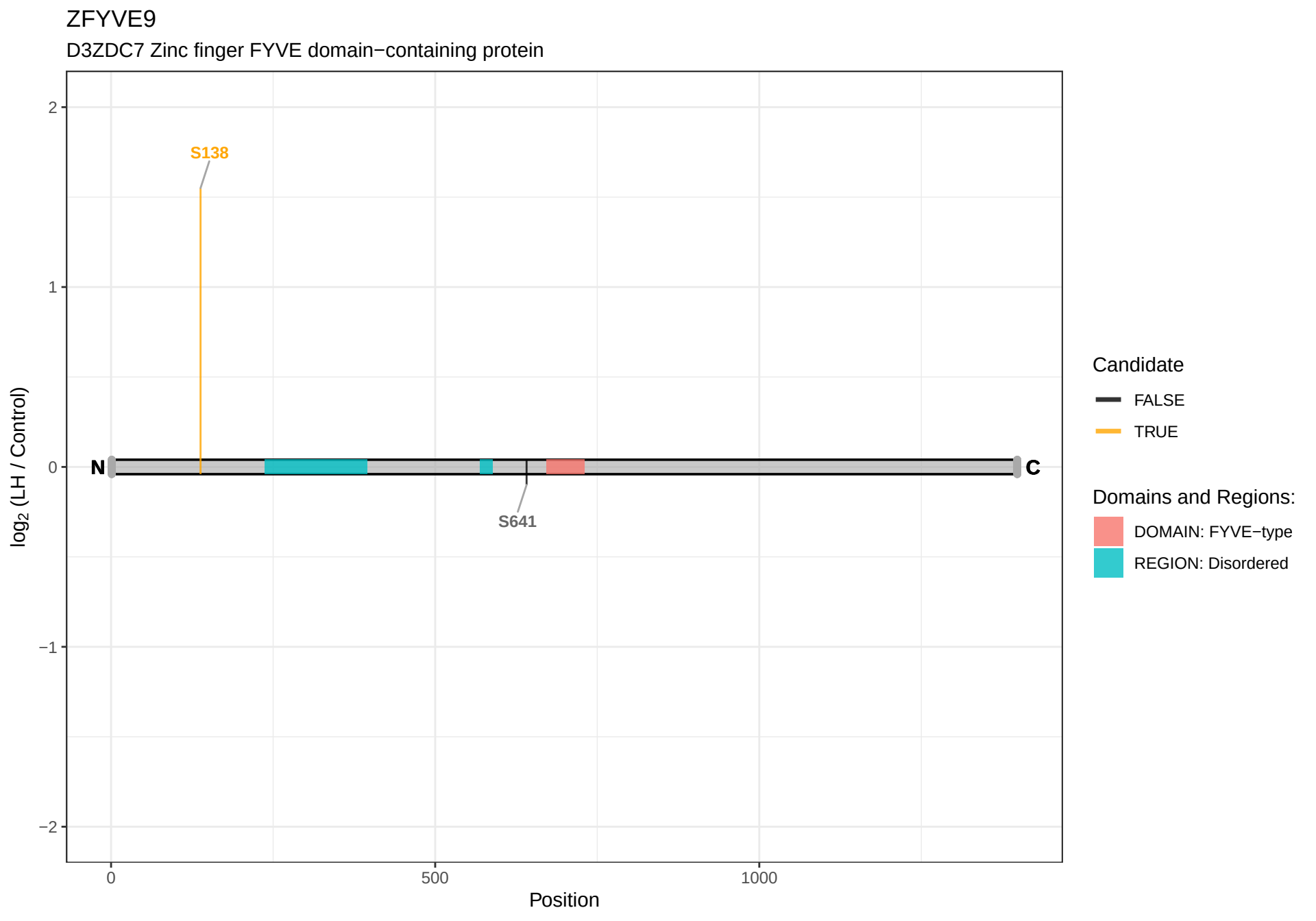

ZFP609
D4ACN4 Zinc finger protein 609
log2 (LH / Control)
2
1
0
−1
−2
0
500
1000
Position
N
C
S413
S467
S578
S743
T746
S560
S576
S620
S842
S1055
S1313
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2H2−type
REGION: Disordered

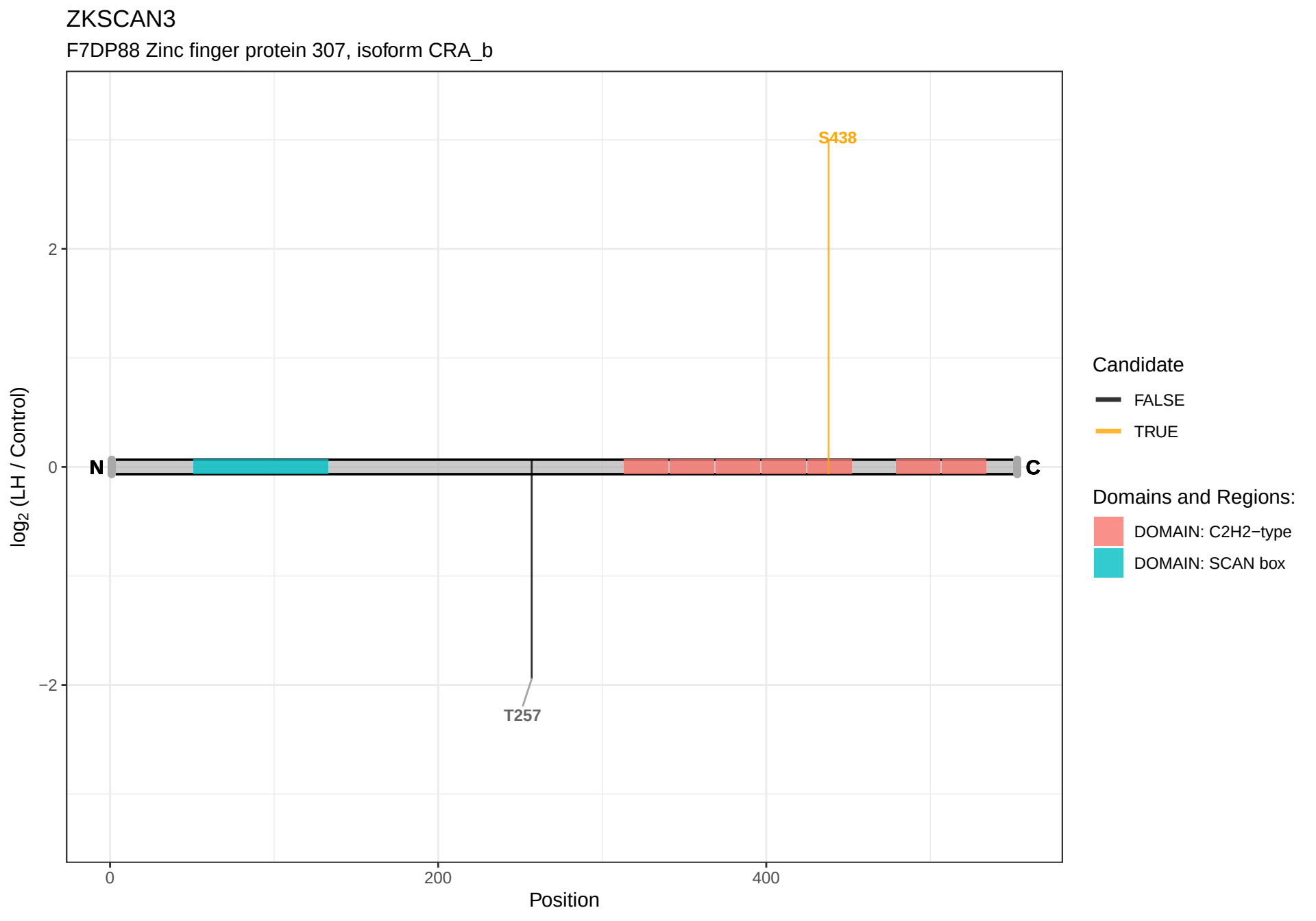

ZFP655
Q5RKG8 Zinc finger protein 655
S98
S80
S28
N
C
2
0
−2
log2 (LH / Control)
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2H2−type
REGION: Disordered

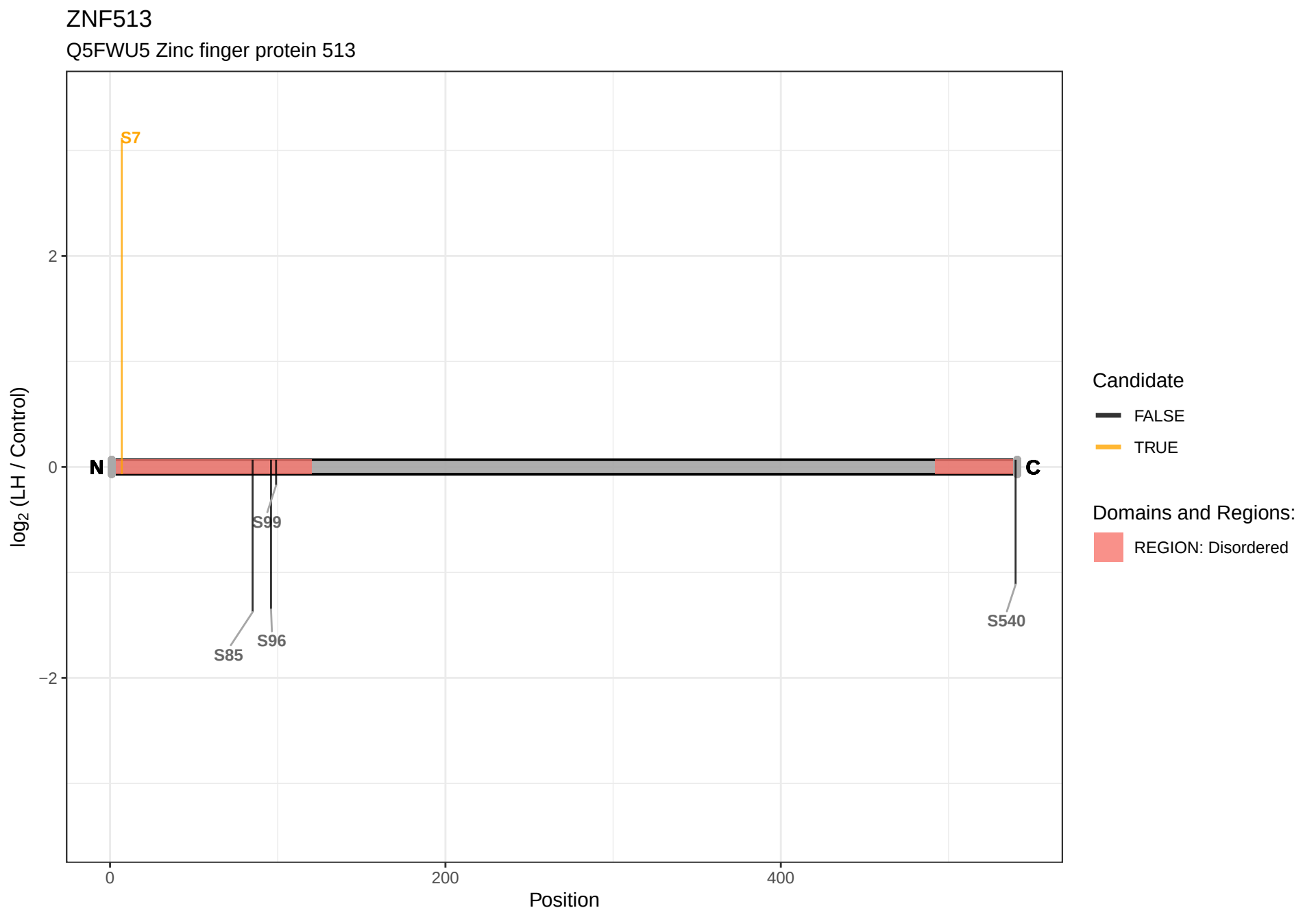

ZFP687
D3ZT56 Zinc finger protein 687
log2 (LH / Control)
Position
N
C
S350
S373
T376
S265
S270
S253
S274
S227
S66
S71
S104
T431
S432
S1084
S1086
S1081
S1182
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2H2−type
REGION: Disordered

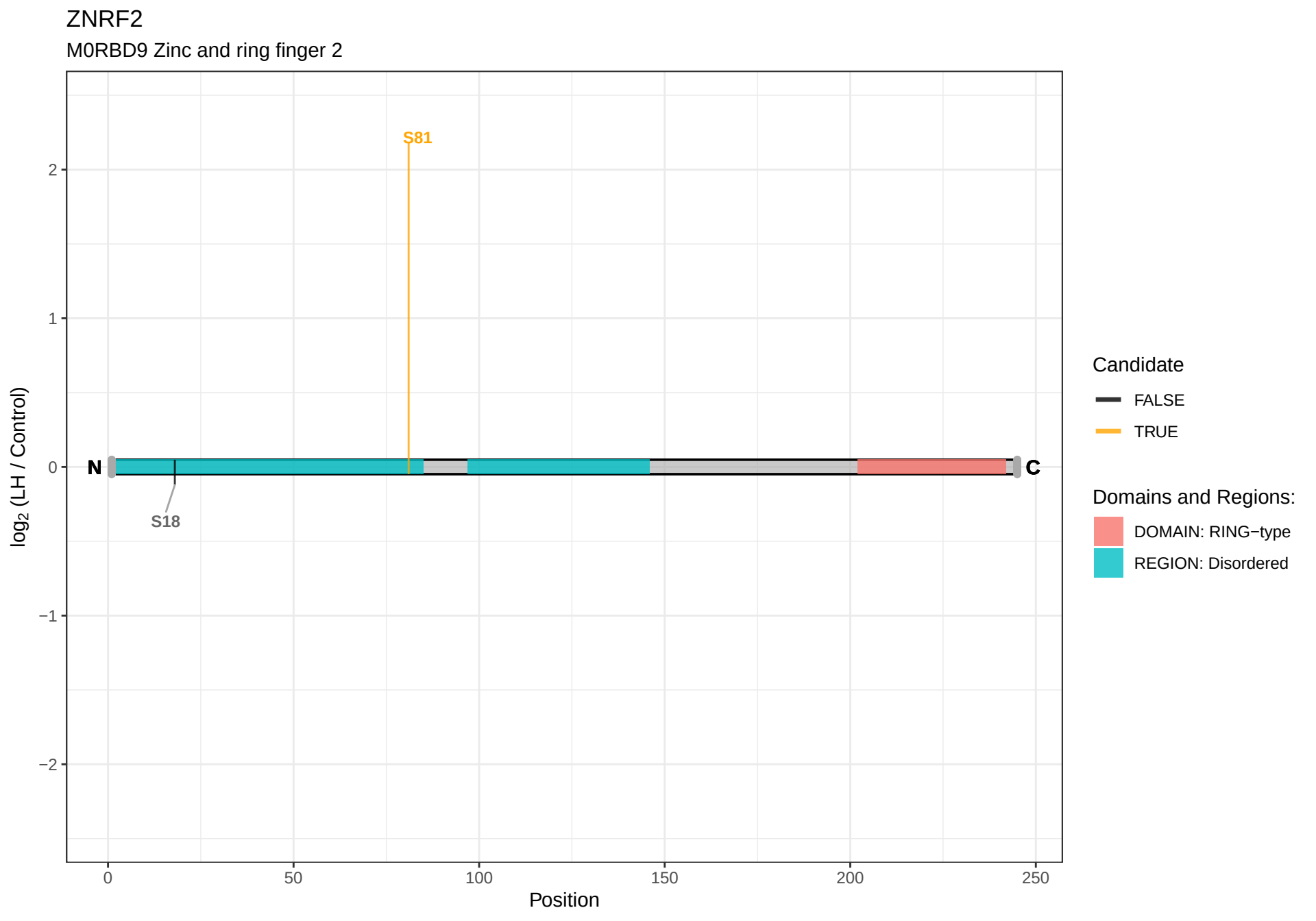

ZFP800
D3ZPQ4 Zinc finger protein 800
S318
T320
S337
S422
S460
S457
S426
S419
T162
S647
N
C
2
0
−2
log2 (LH / Control)
0
200
400
600
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2H2−type
REGION: Disordered

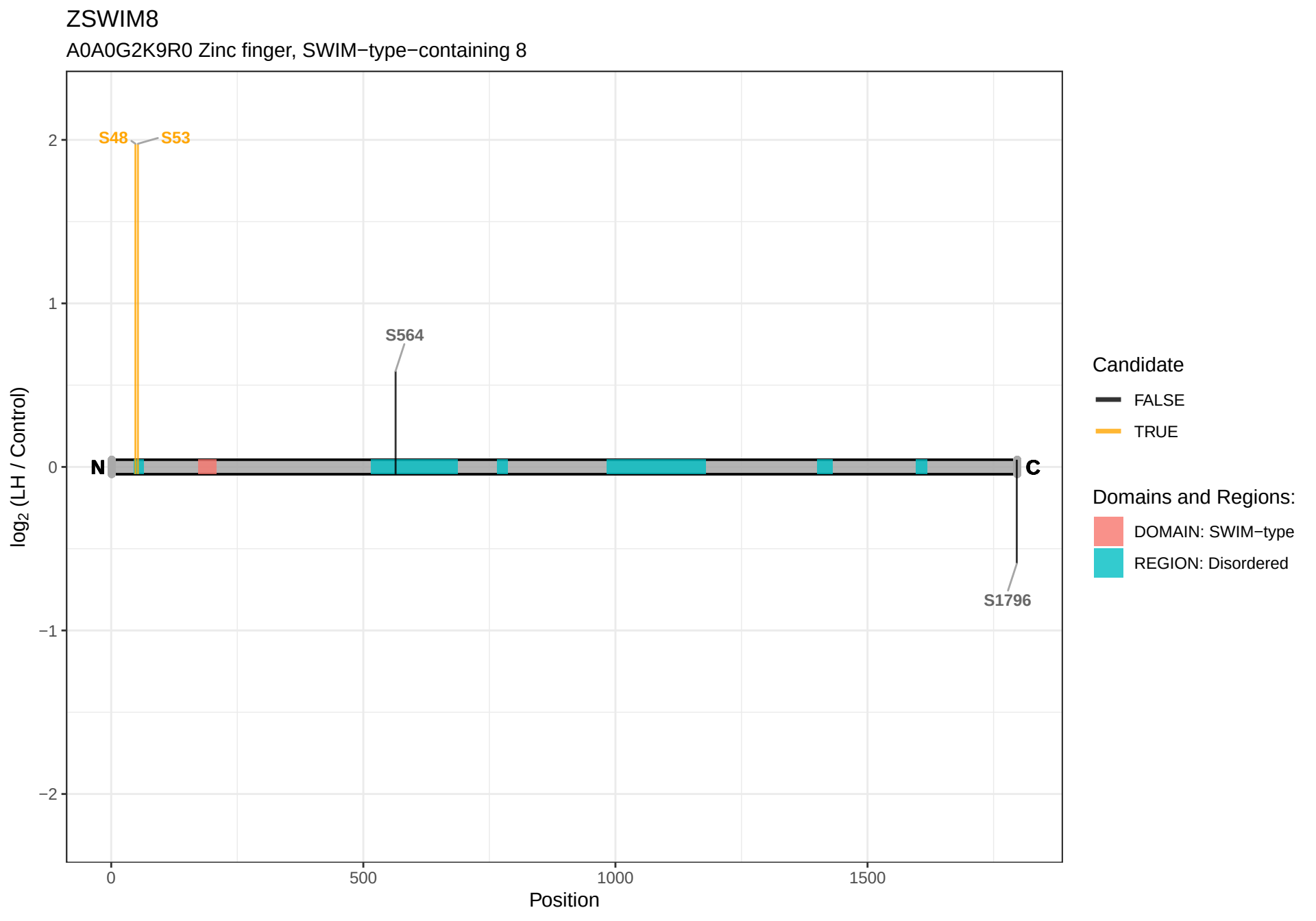

ZFYVE16
D4ADF6 Zinc finger FYVE−type−containing 16
S903
S907
S322
N
C
log2 (LH / Control)
Position
0
500
1000
1500
3
2
1
0
−1
−2
−3
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: FYVE−type
REGION: Disordered

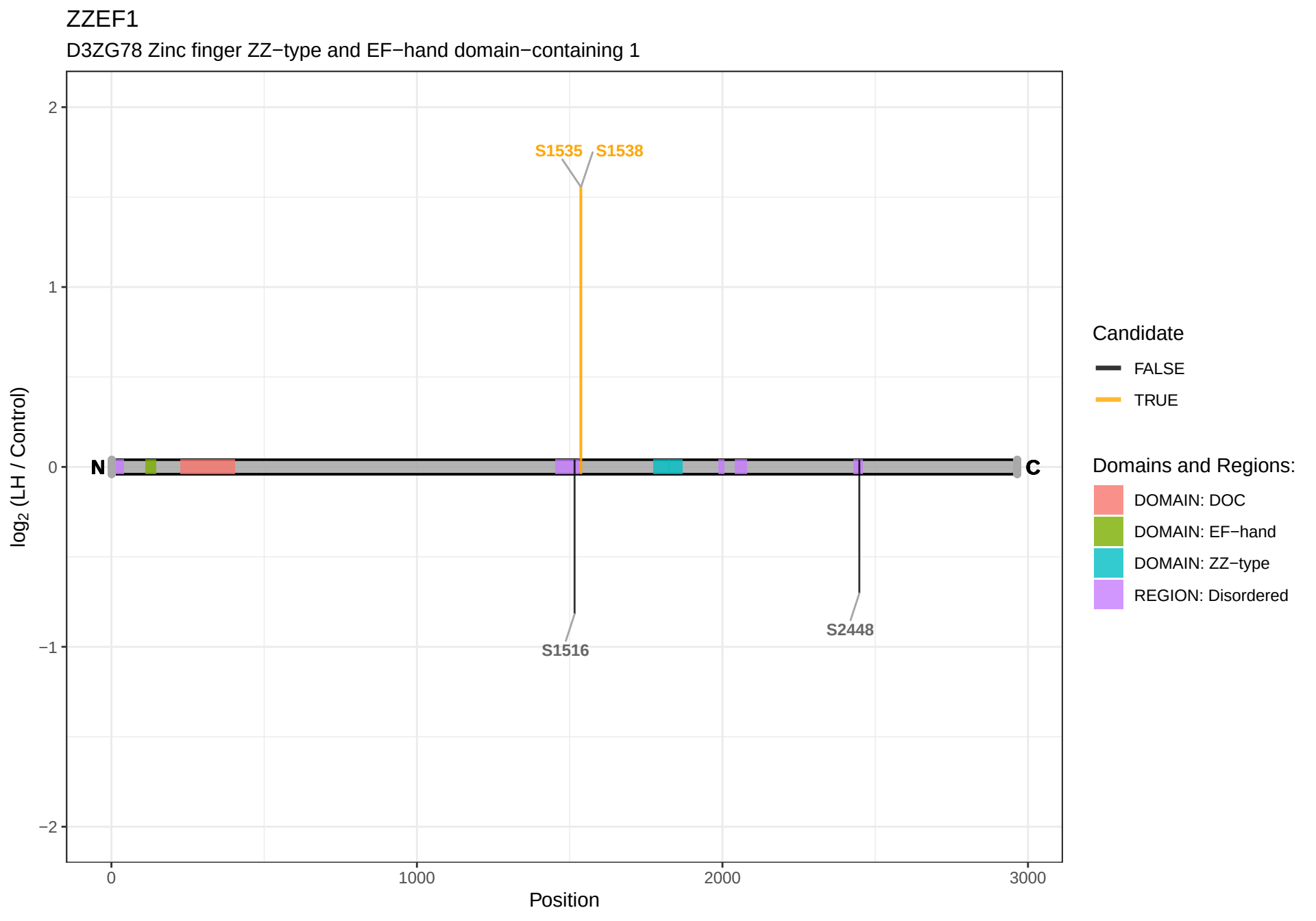

ZFYVE9
D3ZDC7 Zinc finger FYVE domain−containing protein
S138
S641
N
C
log2 (LH / Control)
Position
0
500
1000
2
1
0
−1
−2
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: FYVE−type
REGION: Disordered

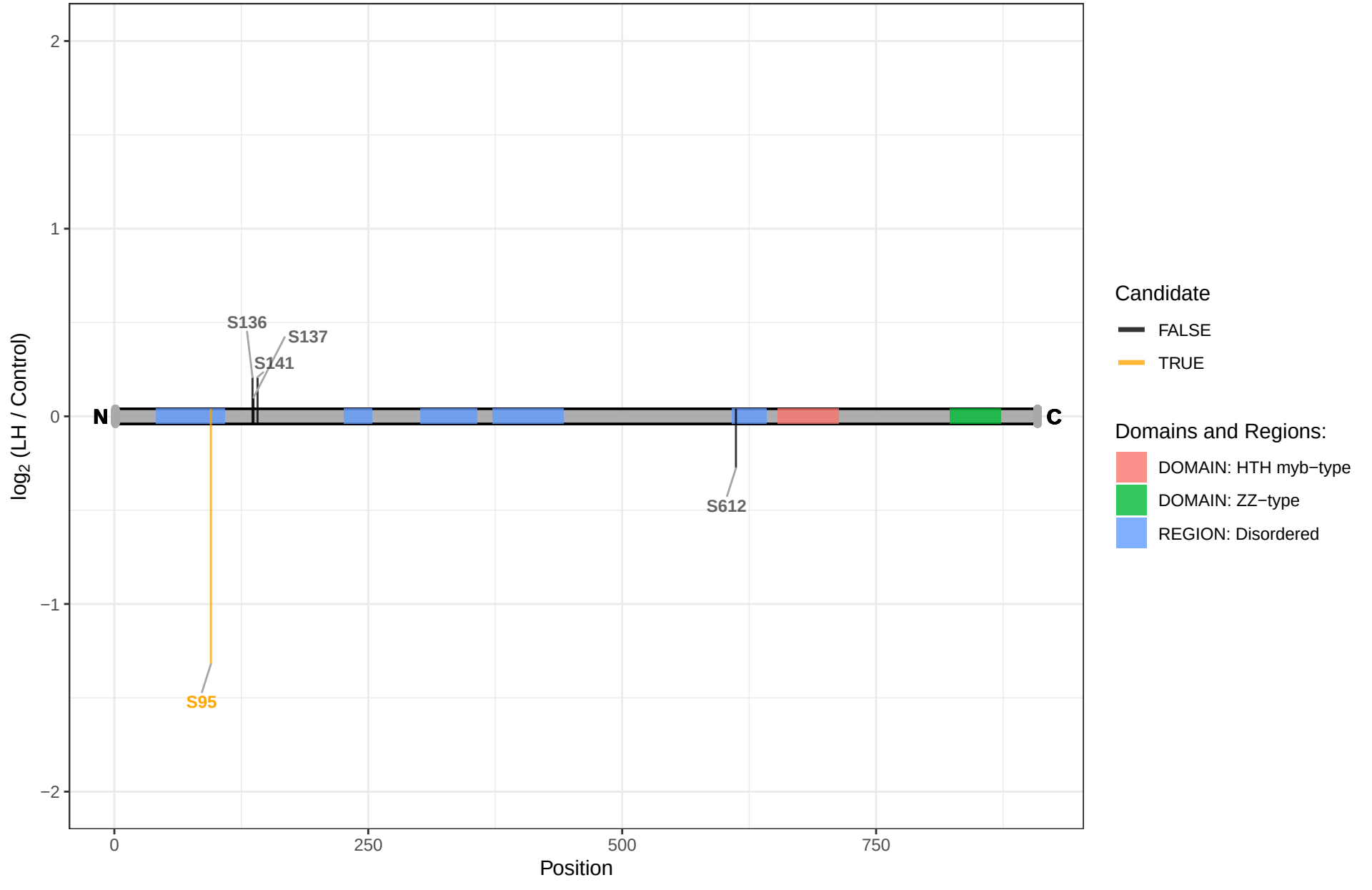

ZKSCAN3
F7DP88 Zinc finger protein 307, isoform CRA_b
S438
T257
N
C
2
0
−2
log2 (LH / Control)
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: C2H2−type
DOMAIN: SCAN box


ZNF513
Q5FWU5 Zinc finger protein 513
S7
N
C
S99
S85
S96
S540
2
0
−2
log2 (LH / Control)
0
200
400
Position
Candidate
FALSE
TRUE
Domains and Regions:
REGION: Disordered


ZNRF2
M0RBD9 Zinc and ring finger 2
S81
S18
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
50
100
150
200
250
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: RING−type
REGION: Disordered


ZSWIM8
A0A0G2K9R0 Zinc finger, SWIM−type−containing 8
S48
S53
S564
S1796
N
C
2
1
0
−1
−2
log2 (LH / Control)
0
500
1000
1500
Position
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: SWIM−type
REGION: Disordered


ZZEF1
D3ZG78 Zinc finger ZZ−type and EF−hand domain−containing 1
S1535
S1538
S1516
S2448
N
C
log2 (LH / Control)
Position
2
1
0
−1
−2
0
1000
2000
3000
Candidate
FALSE
TRUE
Domains and Regions:
DOMAIN: DOC
DOMAIN: EF−hand
DOMAIN: ZZ−type
REGION: Disordered

ZZZ3

M0R9X4 Zinc finger, ZZ−type−containing 3