



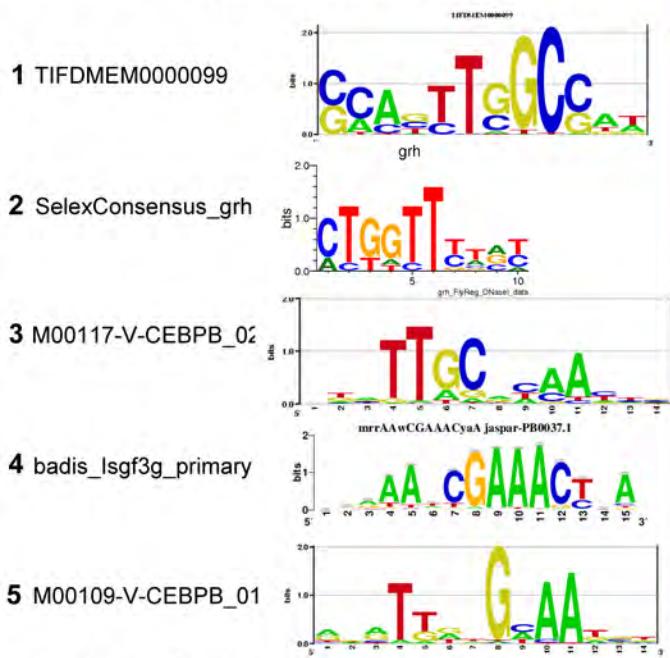
Menoret et al.; Figure S1A

Menoret et al.; Figure S1B



# cis-TargetX motifs detection

epidermal control genes



39 Svb downstream genes

1 ACCGTTA

2 M00968-P-ATMYB77\_01

3 M00993-V-TAL1\_Q6

4 M01101-I-OVO\_Q6

5 M00227-V-VMYB\_02



39 Svb downstream genes + SvbF7 & BM

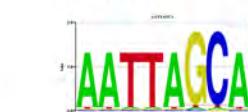
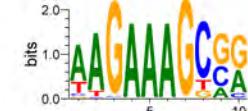
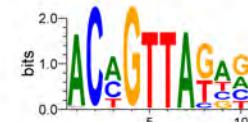
1 SvbF7

2 ACCGTTA

3 Blue Motif

4 nAACwGTw

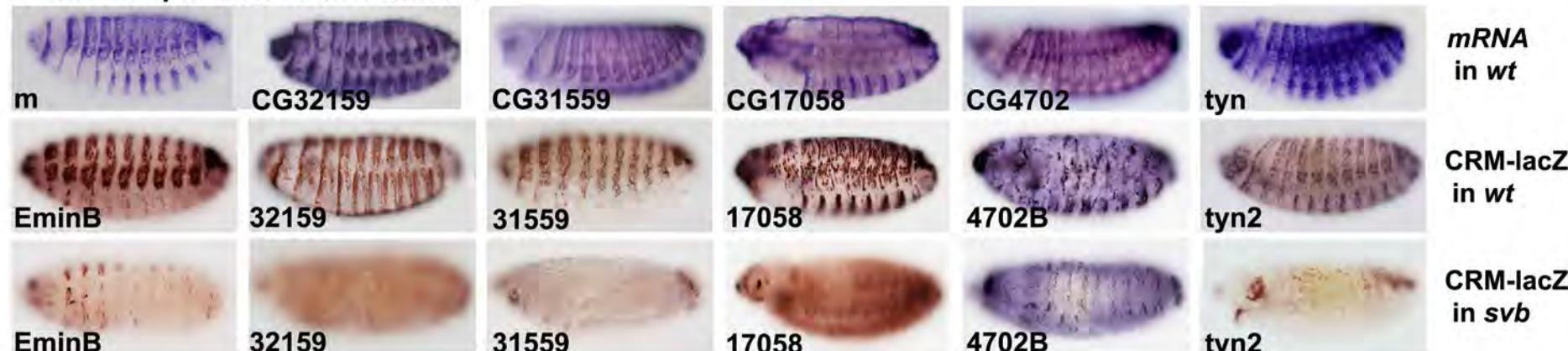
5 AATTAGCA

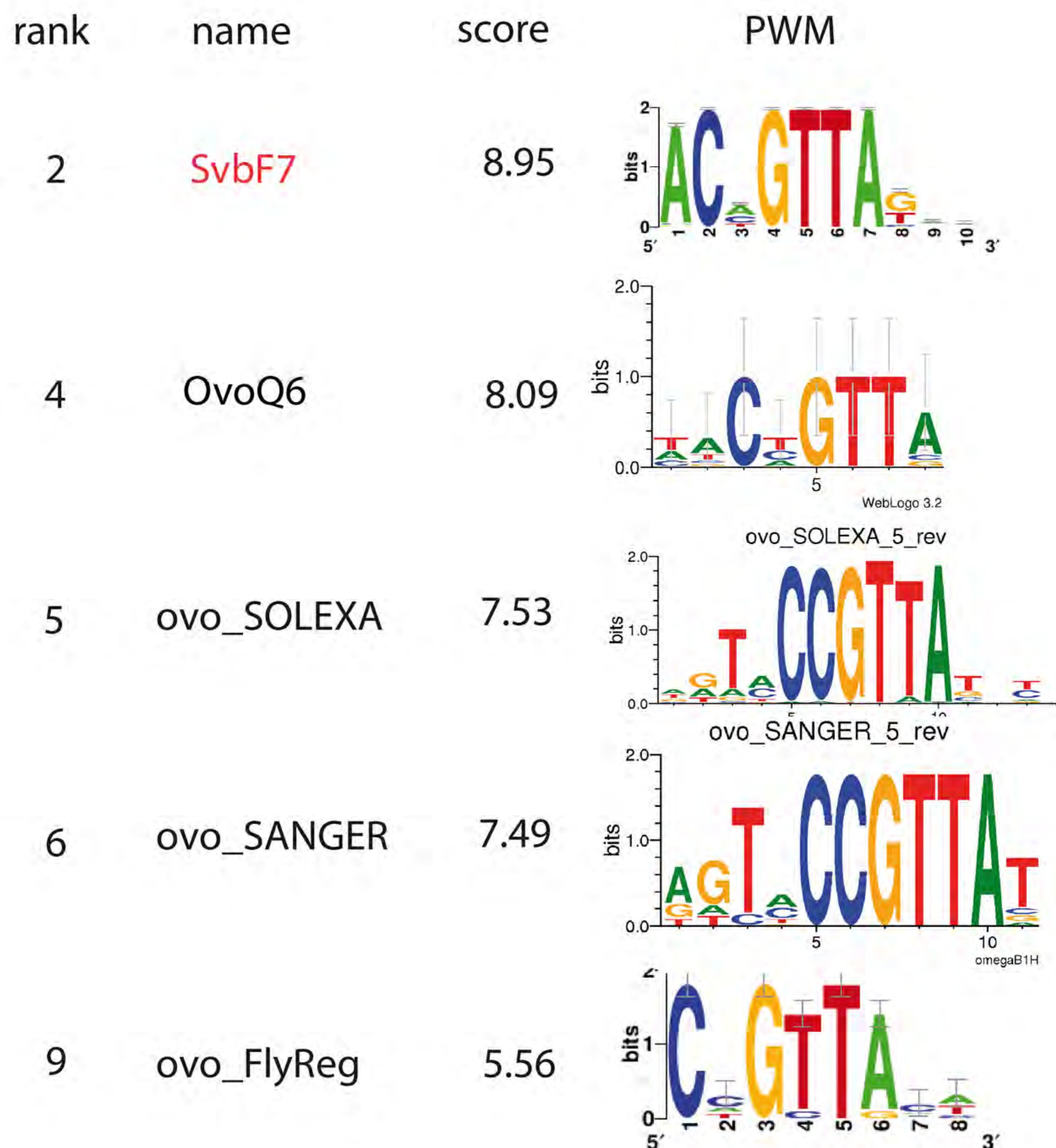


## Ranking of genomic predicted regions

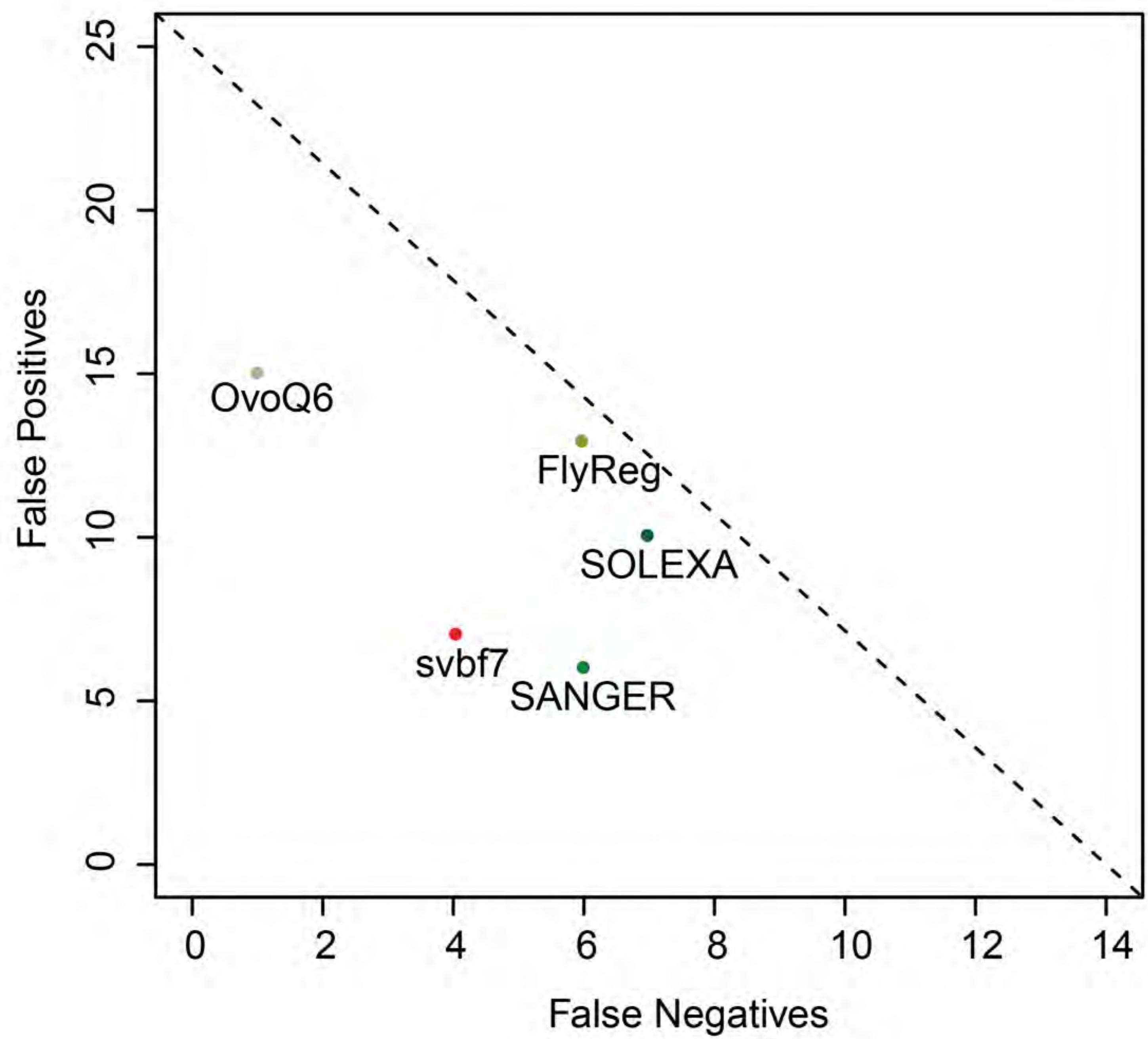
CisTargetX predicted CRMs	dy1	15589	cyrA	sne5	dy2	pmin	f2	32159	Emin	sox21b	sn-enh1	sha3	snH5	snB2	nyo3	sne1	sha-intron	EminB	f5	sha2	f4	cyrB	snP	nyo1	sne4
OvoQ6	1	3	4	5	8	ND	9	ND	ND	13	21	23	24	32	38	43	50	ND	55	63	73	77	79	80	82
svbF7	11	1	2	52	15	21	ND	24	26	104	34	ND	58	7	38	ND	55	ND	10	ND	ND	ND	97	ND	

## Additional epidermal CRMs identified

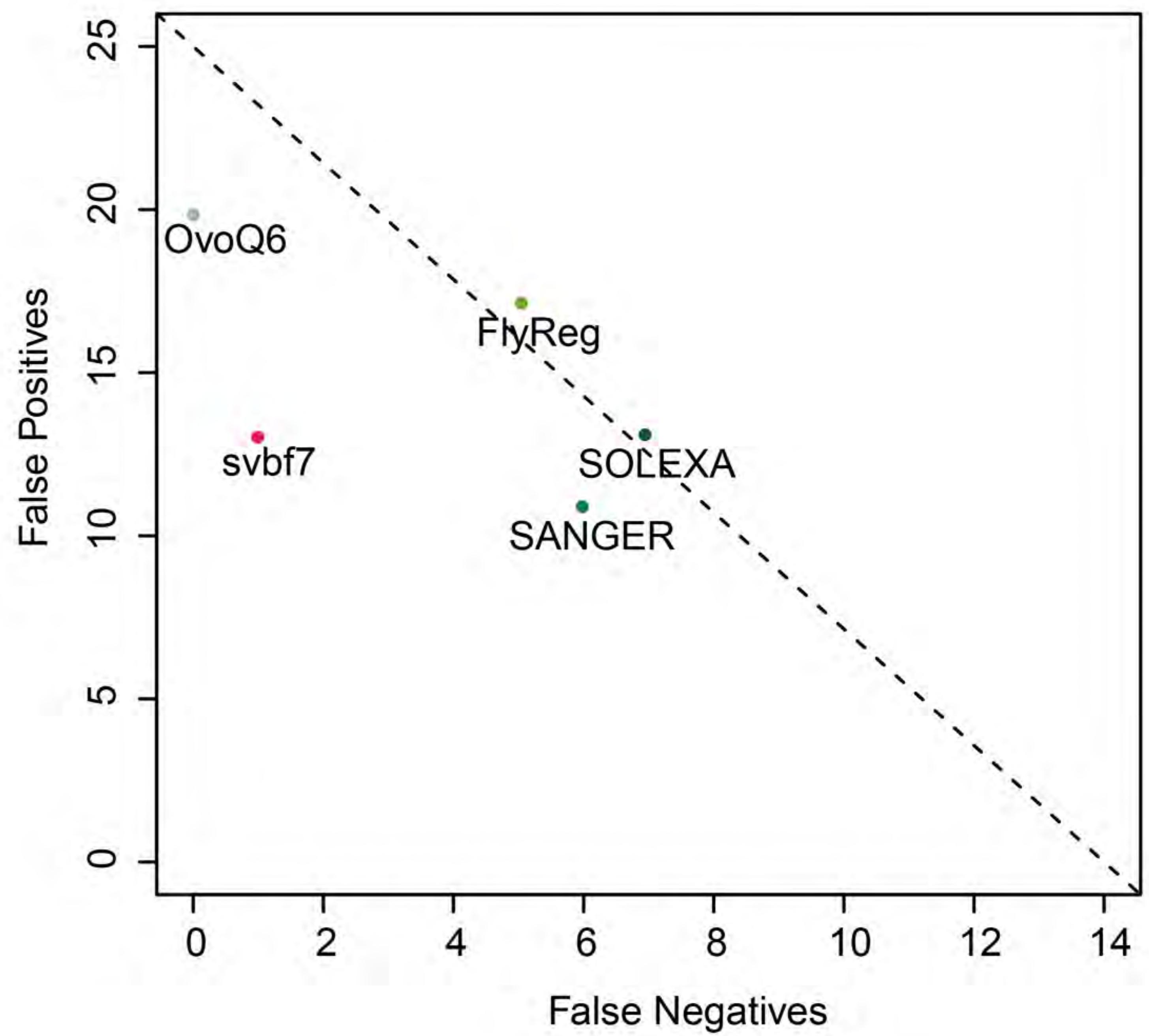


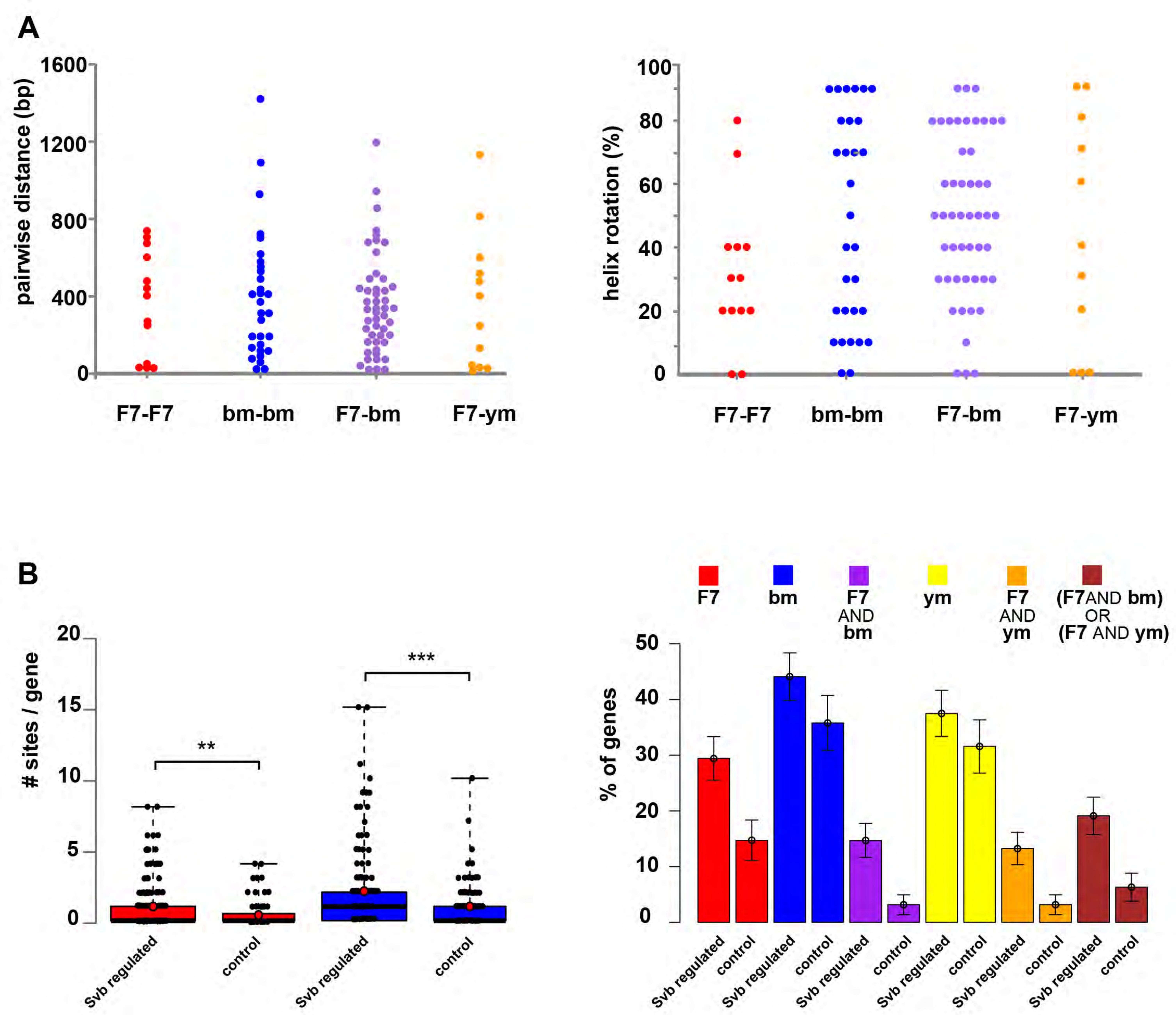


Conserved motifs



Non-conserved motifs





Menoret et al.; Figure S2


Gene symbol	Representative Public ID	Protein features/putative domains	epidermal expression	additional expression #	sub mutant microarrays (% of wt)	pri mutant microarrays (% of wt)	validated in svb mutant (in situ)	validated in svb estopic (in situ)	svbFT	blue motif	yellow motif	ChIP peaks in 5kb (12-14h)	ChIP intensity (12-14h)	ChIP peaks in 5kb (8-10h)	reference
CG15370	CG15370	unknown	no	ubiquitous	13.1	2.1	no	yes	no	yes	yes	yes	502	yes	this work
sha	CG13209	actin binding	stripes		24.6	6.6	yes	yes	yes	yes	yes	yes	92.92	yes	ref 1
CG14395	CG14395	PH like domain	stripes		41.2	3.0	yes	yes	yes	yes	yes	yes	135.174	yes	this work, FigS1
CG4386	CG4386	trypsin like protease	no	trachea	43.5	11.3	no	ND	no	yes	yes	no	no	no	this work
CG15818	CG15818	C-type lectin domain	no	midgut	47.9	17.8	no	ND	no	yes	yes	no	no	yes	this work
m	CG9369	ECM	stripes		48.5	6.2	yes	yes	yes	yes	yes	yes	173.768.69	yes	ref 1
CG32159	CG32159	Cuticle formation	stripes		50.1	12.6	yes	yes	yes	yes	yes	yes	56.789.69.54	yes	ref 2
dvo	CG1499	ECM	stripes	all gut	54.7	15.3	yes	yes	yes	yes	yes	yes	500	yes	ref 1
CG4914	CG4914	trypsin domain	stripes	hindgut	55.9	21.7	yes	ND	yes	yes	yes	yes	418.4.48	yes	this work, FigS4
nevo	CG7802	ECM	stripes	all gut	56.1	17.3	yes	yes	no	yes	yes	yes	59.14	yes	ref 1
myo	CG12063	ECM	stripes		57.1	7.8	yes	yes	yes	yes	yes	yes	654	yes	ref 1
CG16798	CG16798	unknown	stripes		57.1	18.4	yes	yes	no	yes	yes	yes	140	yes	ref 1
CHOP24	CG33564	protein secretion	stripes	salivary gland	59.0	27.0	ND	ND	no	yes	no	no	no	yes	this work, FigS4
CG11905	CG11905	unknown	stripes	trachea	59.3	20.1	yes	no	yes	yes	no	no	no	yes	this work, FigS4
CG14356	CG14356	unknown	no	foregut	60.3	27.1	ND	ND	yes	yes	no	yes	no	no	no
CG17211	CG17211	von Willebrand factor type C domain	ND	ND	60.5	26.4	ND	ND	no	yes	yes	yes	162	yes	no
CG17780	CG17780	unknown	no	hindgut & anal pad	61.0	27.1	no	ND	no	yes	yes	no	no	no	this work
rnwh	CG13913	actin binding	stripes		61.1	25.6	yes	yes	no	no	yes	yes	333	yes	ref 1
CG30283	CG30283	trypsin like protease	stripes	atrium & adult eye PR	62.0	18.3	ND	ND	no	yes	yes	no	no	yes	yes
CG4500	CG4500	blobbiemum like domain	ND	ND	65.2	30.3	ND	ND	no	no	yes	yes	956	yes	yes
sp26	CG9196	Toll signalling pathway	stripes	all gut & trachea	66.9	16.5	no	no	yes	no	yes	no	no	yes	this work, FigS1
CG1273	CG1273	unknown	ND	ND	67.7	20.8	yes	yes	yes	yes	yes	yes	98.98.52.84.	yes	this work, FigS4
CG6785	CG6785	unknown	stripes	gut & salivary gland	67.8	21.4	ND	ND	no	no	yes	yes	86	yes	this work, FigS4
CG10591	CG10591	ECM	stripes	gut & salivary gland	68.4	29.3	yes	yes	yes	yes	yes	yes	51.219.1214	yes	this work, FigS4
CG13698	CG13698	GmC oxidoreductase	stripes	oocytes	69.0	22.4	yes	yes	yes	yes	yes	yes	175.111	no	this work, FigS4
CG9514	CG9514	fatty acyl CoA reductase	no	oocytes	69.9	25.3	no	ND	no	no	no	no	no	no	this work
f	CG5424	actin binding	stripes		70.3	26.0	yes	yes	yes	yes	yes	yes	106.122.59.136.57	yes	ref 1
CG9184	CG9184	unknown	stripes	corpus cardiacum	70.9	15.7	yes	yes	yes	yes	yes	yes	100.59.303.	yes	this work, FigS4
CG12075	CG12075	PH like domain	stripes	gut & salivary gland	71.5	33.4	yes	yes	yes	yes	yes	yes	139.253.135.54.50.186	yes	this work, FigS4
lyn	CG17131	ECM	stripes		72.9	22.2	yes	yes	yes	yes	yes	yes	291.147.200.66.67.99.252	no	ref 1
CG4678	CG4678	metallocarboxypeptidase	no	foregut & anal pad	73.4	36.3	ND	ND	yes	no	yes	yes	52	yes	this work, FigS4
CG13616	CG13616	unknown	no	intestine & anal pad	73.4	12.7	ND	ND	yes	yes	yes	no	no	no	this work
CG14756	CG14756	unknown	no	salivary gland	74.0	12.3	ND	ND	no	yes	no	no	no	no	this work, FigS4
CG4666	CG4666	hot-dog domain	stripes	post spiracle	76.5	24.5	yes	yes	no	yes	yes	yes	66.136	yes	this work, FigS4
CG4686	CG4686	unknown	ND	ND	77.0	33.7	ND	ND	no	no	no	no	no	no	this work, FigS4
CG13082	CG13082	kethonehexokinase	stripes	all gut	77.7	20.7	ND	ND	yes	yes	yes	no	yes	yes	this work, FigS4
CG7173	CG7173	serine protease inhibitor	stripes		77.8	11.6	yes	yes	no	no	yes	yes	73.65	yes	this work, FigS4
CG14732	CG14732	trypsin like protease	ND	ND	78.0	18.9	ND	ND	no	yes	yes	yes	74.477.86.104.92	yes	no
Orct	CG63331	Major Facilitator Superfamily	no	midgut & fat body	78.1	35.5	ND	ND	no	no	yes	yes	70	yes	this work, FigS4
mas	CG15002	chymotrypsin, endopeptidase	stripes	foregut & hindgut & trachea	78.1	31.7	yes	yes	no	yes	yes	yes	57	yes	this work, FigS4
CG5039	CG5039	unknown	ND	ND	78.6	12.6	ND	ND	no	yes	yes	yes	109	yes	this work, FigS4
CG12017	CG12017	redox process	stripes		78.6	18.0	yes	yes	yes	yes	yes	yes	56.223.72.84.	yes	this work, FigS4
CG5873	CG5873	chitin metabolic process	stripes	all gut & trachea	78.7	36.1	ND	ND	yes	yes	yes	no	281	yes	this work, FigS4
CG8420	CG8420	isoprenoid biosynthesis	stripes		79.3	15.0	yes	no	yes	yes	yes	yes	190.86.170.	yes	this work, FigS4
CG11200	CG11200	metabolic process	stripes	trachea	79.8	32.0	ND	ND	yes	yes	yes	yes	104	yes	this work, FigS4
Cyp301al	Cyp301al	redox process	stripes	trachea	80.3	34.3	ND	ND	yes	yes	yes	yes	97.64.6.99	yes	no
CG42331	CG6879	redox process	ND	ND	80.4	9.8	ND	ND	yes	yes	yes	yes	181	yes	this work, FigS4
CG13822	CG13822	GLT domain, thiol reductase	stripes	lymph gland	80.8	34.3	yes	yes	no	yes	yes	yes	53.503	yes	ref 1
CG12009	CG12009	chitin metabolic process	no	trachea	82.4	17.3	ND	ND	yes	yes	no	no	no	no	this work
CG8239	CG8239	isoprenoid biosynthesis	stripes	hindgut & anal pad	82.9	12.7	ND	ND	no	no	no	no	no	yes	this work
SURNP-U1	CG5454	mRNA splicing	no	ubiquitous	83.2	38.9	ND	ND	yes	yes	yes	no	no	yes	this work
CG1140	CG1140	ketone body catabolism	no	midgut & fat body	83.4	39.7	ND	ND	yes	yes	yes	yes	74	no	this work
CG15013	CG15013	ECM	stripes		85.3	16.1	yes	yes	yes	yes	yes	yes	57.58.174.85.495.528.285.57	yes	ref 1
Hif6	CG33183	eddyson-pathway	no	ubiquitous	85.5	39.9	ND	ND	yes	yes	yes	yes	127.54.262.108.460.60.190.70	yes	this work
vri	CG14029	tracheal system development	stripes	hindgut	85.6	30.5	no	ND	yes	yes	yes	yes	78.187.54	yes	this work
wus	CG9098	ECM	stripes	all gut & trachea	86.1	12.6	no	ND	no	no	no	no	188	yes	this work

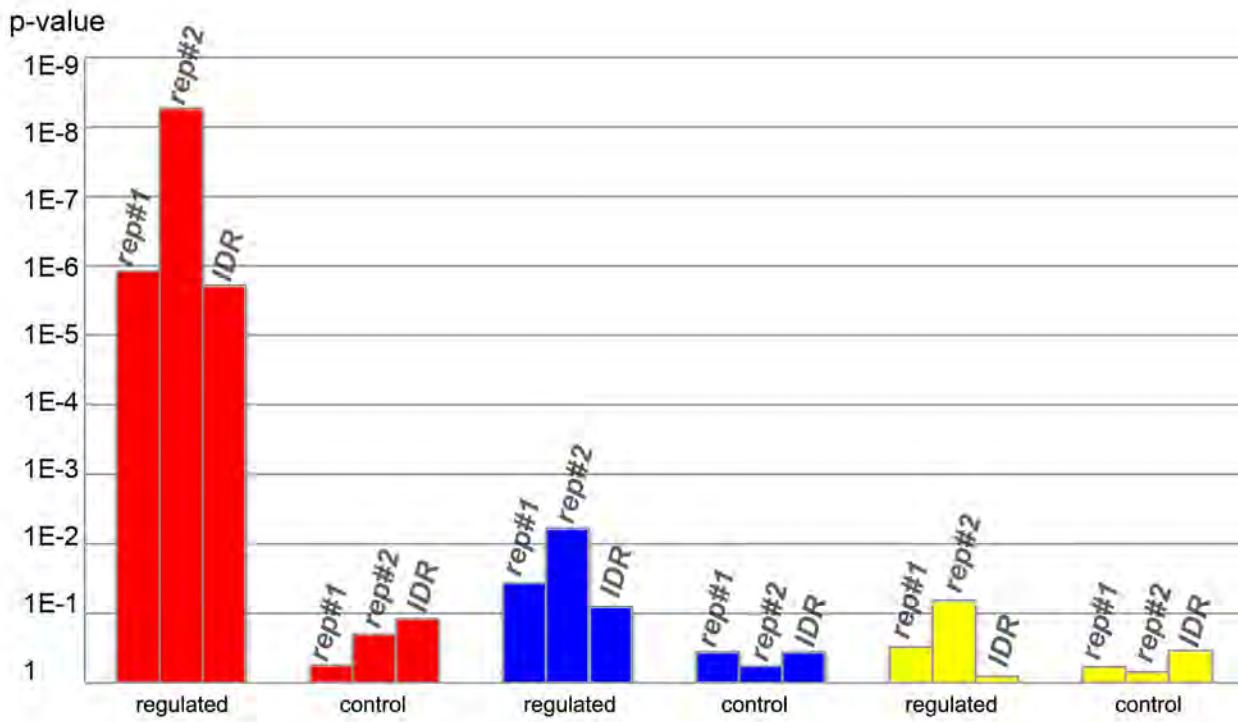
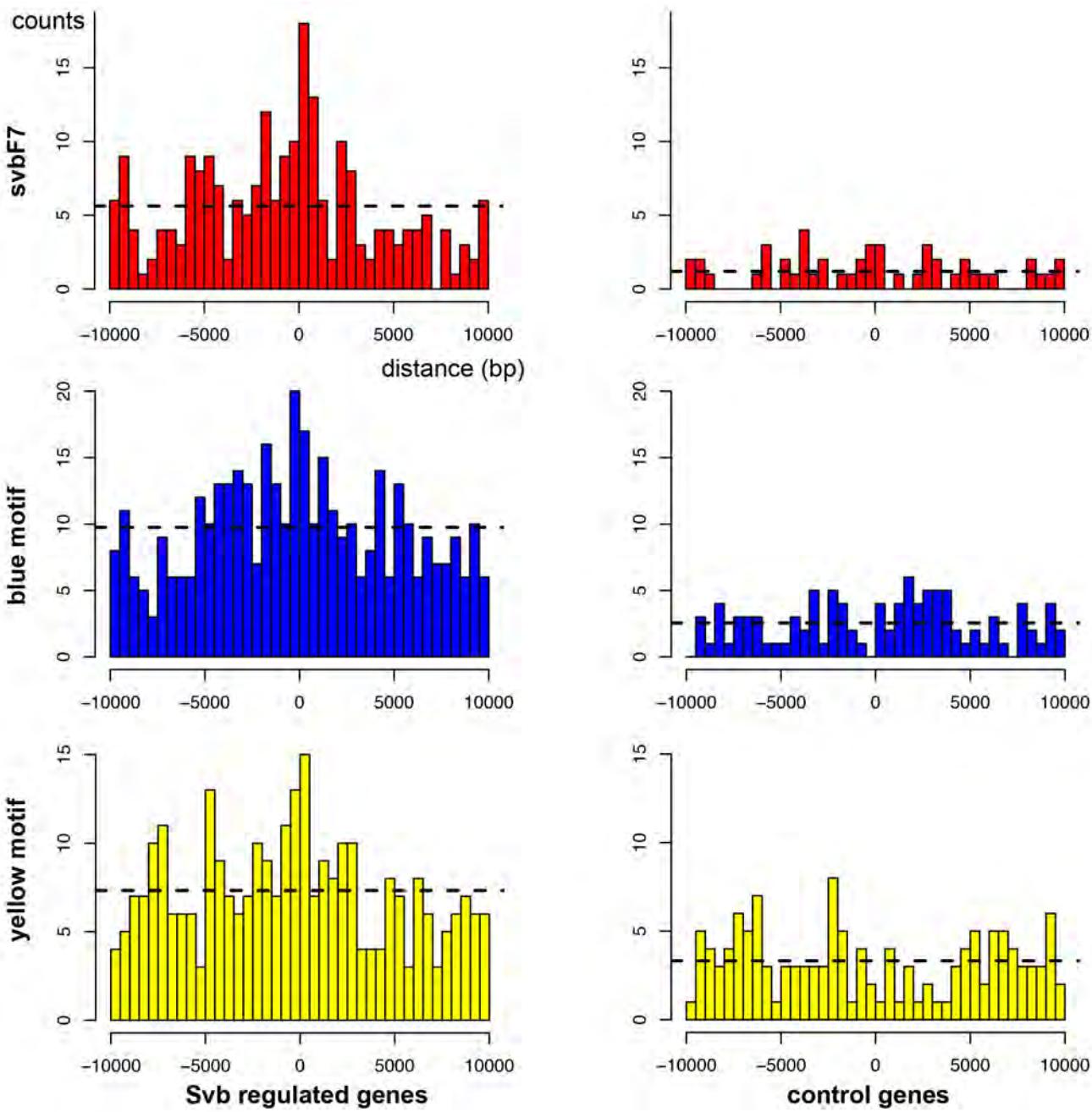
ImpEl	CG32356	ecdysone pathway	stripes	all gut	14.8	yes	yes	yes	yes	yes	67,251	yes
PilP	CG10371	protein dephosphorylation	ubiquitous	midgut & hindgut	86.7	32.5	ND	ND	no	no	239	yes
CG17672	CG11271	translational	no	ubiquitous	86.7	22.3	ND	ND	no	no	573,102	yes
CG32354	CG32354	unknown	stripes	all gut	86.8	42.3	ND	ND	no	yes	yes	yes
CG83016	CG83016	redox process	stripes	foregut & hindgut	86.8	41.3	ND	ND	no	no	no	yes
CG10585	CG10585	unknown	stripes	all gut	87.1	27.3	ND	ND	no	yes	no	yes
fw	CG1500	cell adhesion	no	fat body & amniocerosa	87.2	30.5	ND	ND	no	yes	463,156	yes
Dpp9c	CG7584	sensory perception	no	fat body & amniocerosa	87.3	27.4	ND	ND	no	yes	no	yes
CG5525	CG5525	microtubule organization	no	muscle system & hindgut	87.4	31.5	ND	ND	no	yes	yes	no
CG34007	Dm2L:1959.0	unknown	ND	ND	87.5	25.6	ND	ND	no	no	164	yes
CG14470	CG14470	unknown	no	hindgut	87.5	39.1	ND	ND	no	no	no	no
CG18249	CG18249	unknown	no	midgut & amniocerosa	87.6	28.4	ND	ND	no	no	59	yes
CG8386	CG8386	lateral inhibition	ubiquitous	salivary gland	87.9	41.5	ND	ND	no	no	no	no
DmW	CG11101	EGF-like calcium binding	ND	ND	88.0	29.8	ND	ND	no	yes	yes	yes
pHalphaSc51	CG31014	redox process	no	salivary gland	88.1	39.7	ND	ND	no	yes	51.5	no
CG6415	CG6415	glycan catabolic process	no	fat body	88.2	37.1	ND	ND	no	yes	yes	no
dher	CG39397	actin binding	stripes	muscle system	88.3	40.5	ND	ND	no	yes	103	yes
CG2016	CG2016	unknown	stripes	all gut & trachea	88.4	22.9	ND	ND	no	yes	no	no
Tb	CG35480	Cuticle formation	stripes	all gut & trachea	88.6	21.5	ND	ND	no	yes	309,53	no
CG10932	CG10932	mitotic spindle organization	no	midgut	88.8	34.6	ND	ND	no	yes	yes	yes
scu	CG7113	ecdysone pathway	no	midgut	89.1	39.8	ND	ND	no	yes	no	no
CG7860	CG7860	autophagic cell death	no	midgut & crystal cells	89.7	15.8	ND	ND	no	yes	yes	yes
CG9356	CG9356	unknown	no	midgut	89.7	39.8	ND	ND	no	no	no	yes
Himes	CG4311	hydroxymethylglutaryl-CoA synthase	stripes	foregut & hindgut	90.0	28.7	ND	ND	no	yes	286	yes
CG11836	CG11836	proteolysis	ubiquitous	midgut	90.3	32.3	ND	ND	no	no	111	no
CG9503	CG9503	redox process	no	dorsal trunk	90.4	22.4	ND	ND	no	yes	256	yes
CG1837	CG1837	apoptotic cell clearance	no	ubiquitous	90.4	39.5	ND	ND	no	yes	80,66	yes
tw	CG12311	somatic muscle development	ND	ND	90.5	38.0	ND	ND	no	no	no	yes
pHalphaEB	CG31022	procollagen dioxygenase	stripes	muscle system & plasmacytocytes	90.6	40.5	yes	yes	yes	yes	540,78	yes
amid	CG10501	chitin metabolic process	ND	ND	90.6	38.1	ND	ND	no	yes	yes	yes
Rab23	CG32108	GTPase, planar polarity	stripes	foregut	91.5	31.9	yes	yes	no	yes	289	yes
Smm	CG16725	neuromuscular junction	no	gonad	91.5	37.6	ND	ND	no	no	no	yes
Pros281	CG33422	protease	no	ubiquitous	91.6	28.1	ND	ND	no	yes	204,155	yes
CG9175	CG9175	unknown	no	midgut & hindgut & salivary gland	91.6	40.9	ND	ND	no	no	yes	yes
Ric1	CG69378	translation	ND	ND	91.8	45.2	ND	ND	no	yes	no	yes
Lip4	CG61113	lipid metabolism	no	amniocerosa	91.9	44.5	ND	ND	no	yes	240	no
CG7840	CG7840	lipid metabolism	no	midgut & hindgut & salivary gland	91.9	35.2	ND	ND	no	yes	no	no
Gtp-bp	CG2522	protein secretion	stripes	midgut & hindgut & salivary gland	92.1	39.0	ND	ND	no	no	no	yes
CG32250	CG32250	transport	ND	ND	92.2	41.7	ND	ND	no	no	no	no
CG15506	CG15506	unknown	ND	ND	92.2	13.6	ND	ND	no	yes	53,69	yes
TRAM	CG11642	protein targeting to membrane	stripes	salivary gland	92.3	36.0	ND	ND	no	yes	no	no
CG6704	CG6704	unknown	no	yolk nuclei	92.5	16.3	ND	ND	no	yes	yes	no
CG17218	CG17218	tracheal system development	stripes	all gut & anal pad	92.5	40.8	ND	ND	no	yes	no	no
CG4065	CG4065	unknown	no	midgut & muscle system	92.6	46.3	ND	ND	no	no	yes	322,66,
mRpL46	CG13922	unknown	no	midgut & muscle system	92.7	42.8	ND	ND	no	no	no	no
CG6180	CG6180	unknown	no	midgut	92.7	44.0	ND	ND	no	yes	no	yes
Tcf1	CG5374	protein folding	no	ubiquitous	92.9	41.1	ND	ND	no	yes	72	no
CG13585	CG13585	unknown	no	garland cell	93.0	45.3	ND	ND	no	yes	no	no
nimB3	Dm2L:8912.0	unknown	ND	ND	93.6	29.5	ND	ND	no	no	no	no
CG2663	CG2663	transport	head	post spiracle	93.7	41.8	ND	ND	no	yes	208	yes
CG11786	CG11786	unknown	no	dorsal trunk	93.8	27.0	ND	ND	no	yes	281	no
It	CG6097	synaptic activity	ND	ND	94.0	25.7	ND	ND	no	yes	61	yes
CG13627	CG13627	unknown	no	trachea	94.2	16.2	ND	ND	no	yes	no	no
Gma1	CG33206	protein targeting to Golgi	ND	ND	94.3	41.8	ND	ND	no	yes	yes	yes
CG6672	CG6672	transmembrane transport	ND	ND	94.4	42.0	ND	ND	no	yes	no	yes
CG4702	CG4702	unknown	stripes	all gut	94.5	16.9	yes	yes	no	yes	50,344	yes
CG3831	CG3831	unknown	no	corpus allatum	94.5	37.3	ND	ND	no	no	no	yes

<u>sec23</u>	CG1250	secretory pathway	stripes	salivary gland	94.5	41.8	ND	no	no	yes	136	yes	this work, FigS4
CG31559	CG31559	thioredoxin	stripes	foregut	94.8	14.3	yes	no	yes	yes	90,236,92	yes	this work, FigS1
<u>CG11771</u>	CG11771	proteolysis	no	all gut & muscle system	95.0	45.4	ND	ND	yes	no	yes	no	yes
<u>CG9095</u>	CG9095	cell adhesion	stripes		95.4	36.9	yes	yes	yes	yes	89,265,200,111	yes	this work, FigS4
—	GM01023	unknown	ND		95.6	42.4	ND	no	no	yes	79	no	
<u>CG32039</u>	CG32039	unknown	no	midgut	95.7	26.7	ND	no	no	yes	122	yes	
<u>CG1753</u>	CG1753	cystein biosynthesis	no	ND	96.0	26.3	ND	no	yes	no	154,93	yes	
<u>CG4422</u>	CG4422	unknown	ND	ND	96.3	43.6	ND	yes	yes	no	63	no	
<u>CG8112</u>	CG8112	unknown	no	yolk nuclei	96.8	30.2	ND	no	yes	yes	280	yes	
<u>ect</u>	CG6611	tube development	stripes	oesophagus & anal pad	96.9	19.7	yes	no	yes	yes	361	yes	this work, FigS4
<u>CG15239</u>	CG15239	unknown	stripes	salivary gland	97.0	19.4	ND	ND	yes	yes	yes	166	yes
<u>CG9689</u>	CG9689	unknown	stripes	oesophagus & post spiracle	97.1	43.7	ND	no	yes	no	no	no	yes
<u>mbtl45</u>	CG36949	translation & transport	no	ubiquitous	97.2	22.6	ND	ND	no	no	no	no	yes
<u>CG8213</u>	CG8213	proteolysis	ND	ND	97.3	13.7	ND	no	yes	yes	no	yes	
<u>CG2263</u>	CG2263	phenylalanine tRNA aminoacylation	no	ubiquitous	97.4	46.9	ND	no	no	yes	no	yes	109
<u>Rpl8</u>	CG11246	transcription	no	midgut	97.8	45.1	ND	ND	no	yes	yes	yes	yes
<u>qua</u>	CG6433	actin binding	stripes	all gut & lymph gland	97.8	43.1	no	no	yes	yes	no	yes	
<u>CG11227</u>	CG13630	proteolysis	ND	ND	97.8	47.0	ND	no	yes	no	no	no	yes
<u>CG9205</u>	CG9205	unknown	ND	ND	98.0	44.9	ND	no	yes	yes	no	yes	
<u>Nf-<i>ta</i></u>	CG33891	transcription & phagocytosis	no	ubiquitous	98.3	39.6	ND	no	yes	no	yes	yes	
<u>kar</u>	CG12286	transmembrane transport	no	midgut & amniogenesis	98.3	42.8	ND	no	no	yes	no	yes	
<u>CG31717</u>	CG31717	unknown	ND	ND	98.4	45.2	ND	yes	yes	yes	no	no	
<u>Past1</u>	CG6148	endocytosis	no	midgut & salivary gland	98.4	46.6	ND	no	yes	yes	66	yes	
<u>bw</u>	CG17632	eye pigment biosynthesis	no	malpighian tubule & fat body	98.4	37.4	ND	no	yes	no	no	yes	
<u>mRpL51</u>	CG13098	translation	no	midgut & muscle system	98.5	39.3	ND	no	no	no	no	yes	
<u>pk</u>	CG11084	planar polarity	no	ubiquitous	98.6	45.5	ND	yes	yes	yes	190,178,125	yes	
<u>CG5171</u>	CG5171	trehalose biosynthesis	no	amniogenesis & yolk nuclei	98.9	37.8	ND	no	yes	no	yes	351,159,153	yes
<u>CG13365</u>	CG13365	unknown	no	ubiquitous	98.9	43.2	ND	no	yes	no	518	yes	
<u>CG5742</u>	CG5742	neurogenesis	no	ND	98.9	43.8	ND	no	yes	no	yes	yes	
<u>PKD</u>	CG57125	intracellular signal transduction	ND	ND	99.0	46.5	ND	no	yes	yes	941,94	yes	
<u>CG11127</u>	CG11127	unknown	no	ubiquitous	99.1	47.2	ND	no	yes	yes	no	yes	
<u>Fib</u>	CG9888	centrosome organization	no	ubiquitous	99.1	49.2	ND	no	no	no	no	yes	
<u>CG30423</u>	CG30423	unknown	ND	ND	99.1	43.0	ND	yes	yes	yes	no	no	
<u>CG3842</u>	CG3842	redox process	stripes	foregut & anal pad	99.2	14.1	ND	no	no	yes	213,160,74	yes	
<u>CG15743</u>	CG15743	phosphatidylinositol phosphorylation	no	salivary gland	99.9	44.9	ND	no	no	yes	no	yes	

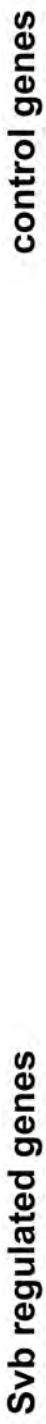
Menoret *et al.*; Figure S3

Menoret et al.; Figure S4





Menoret et al.; Figure S5



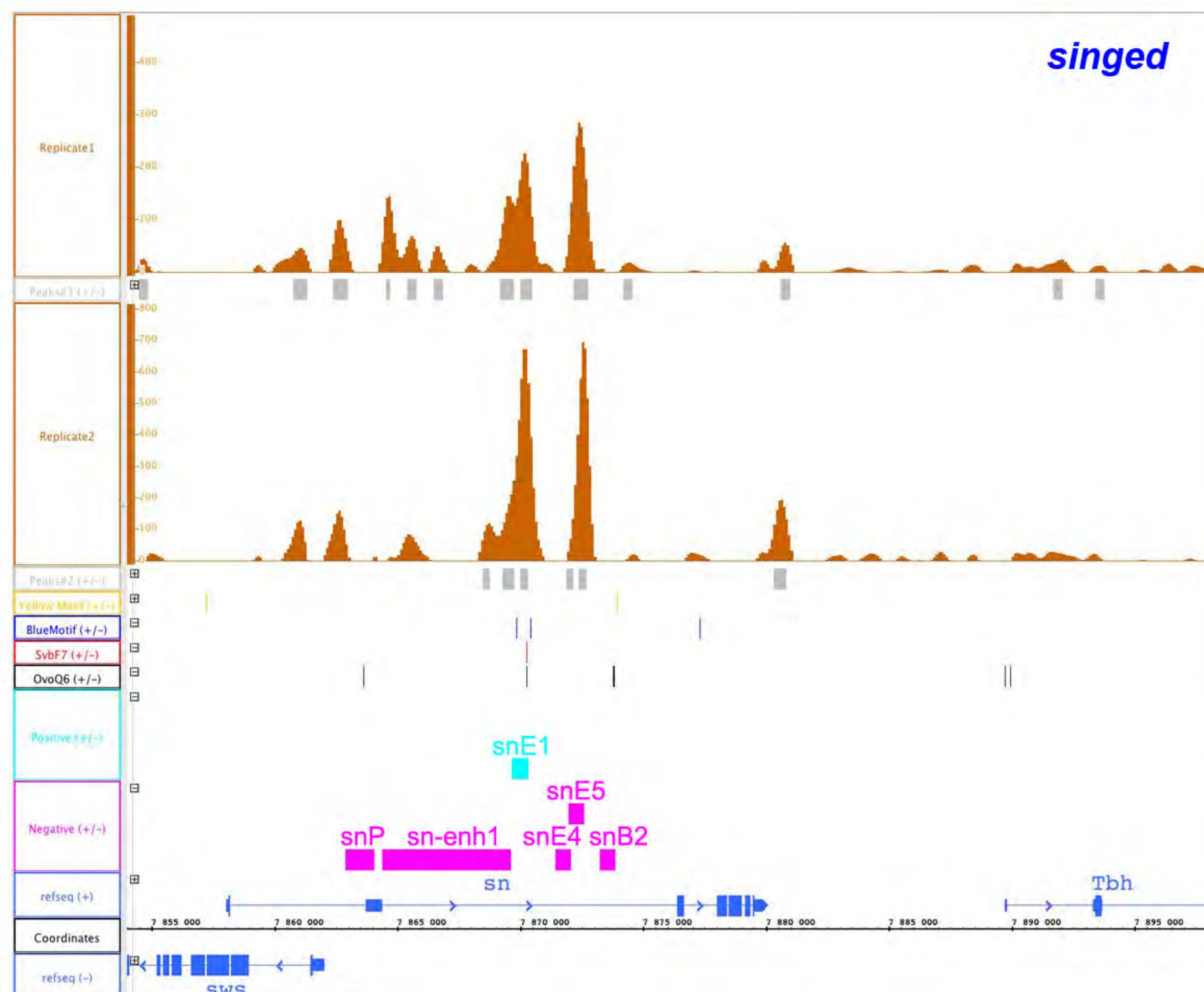
**predicted factor (>70% aligned)**

motif	predicted factor (>70% aligned)	logo	motif	predicted factor (>70% aligned)	logo
1	Klu		1	tayrTATGTayrt	
2	ND		2	rsAAAAAAyAAAAak	
3	ovo		3	straCAGCTGtys	
4	ND		4	wwwkCTAGTrccbt	
5	ND		5	rcGGCGCGCGcgy	
6	ELK4, ovo odd, grh		6	raCAGCTGty	
7	bab1		7	bataTACATACata	
8	klu		8	mmACAAAmAACAAac	
9	tll				

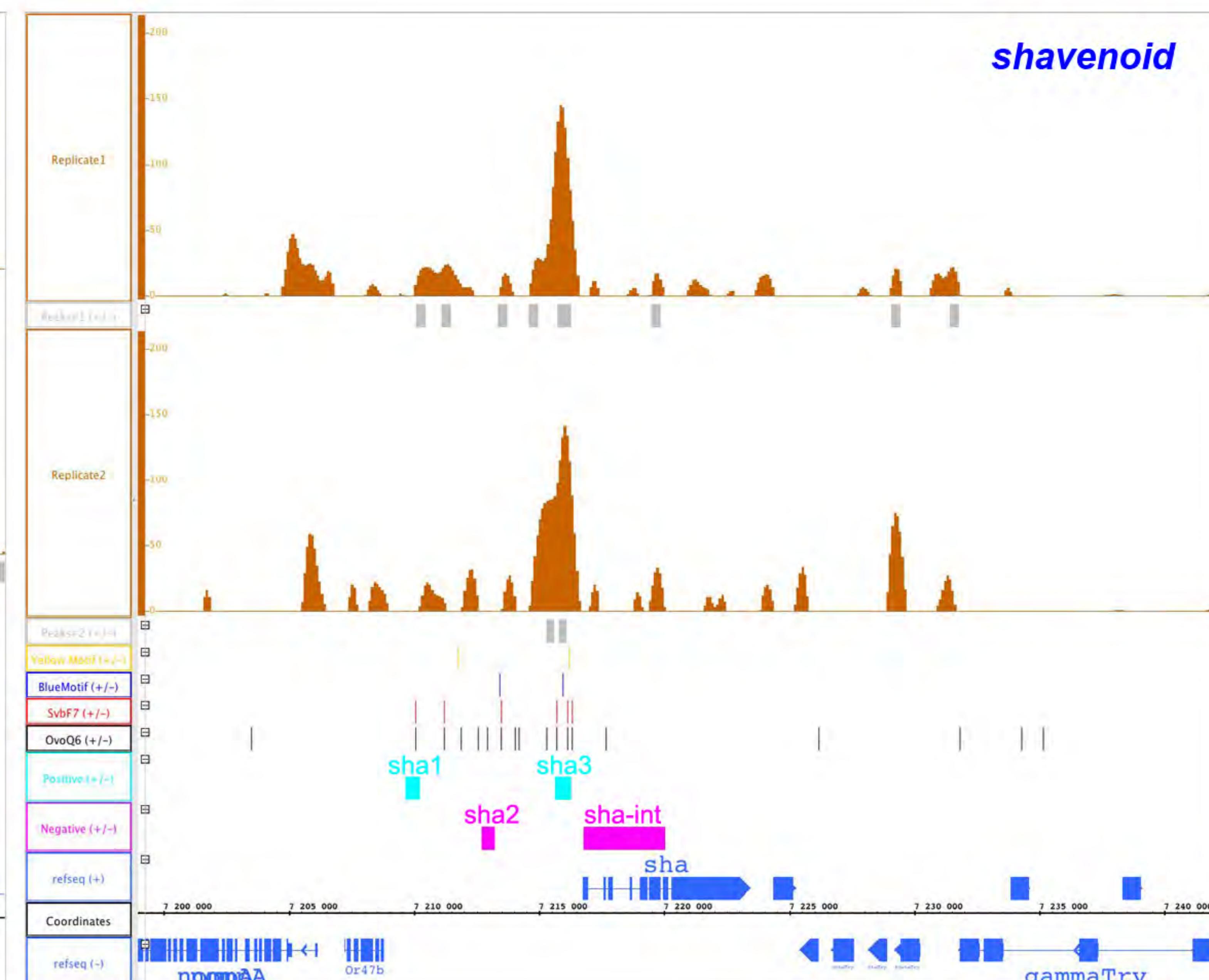
**predicted factor (>70% aligned)**

motif	predicted factor (>70% aligned)	logo	motif	predicted factor (>70% aligned)	logo
1	aCrCACACaCaC		1	aCrCACACaCaC	
2	atAwatAhhATATdTatwtat		2	atAwatAhhATATdTatwtat	
3	rktACCCTTAsck		3	rktACCCTTAsck	
4	srAGGCATGrg		4	srAGGCATGrg	
5	rgGGACTAcwa		5	rgGGACTAcwa	
6	wrcGGGwTAhv		6	wrcGGGwTAhv	
7	yaaATAwATAwATAwATA		7	yaaATAwATAwATAwATA	
8	cayaCACACACACAC		8	cayaCACACACACAC	
9	RSTGAAAAAGCW				

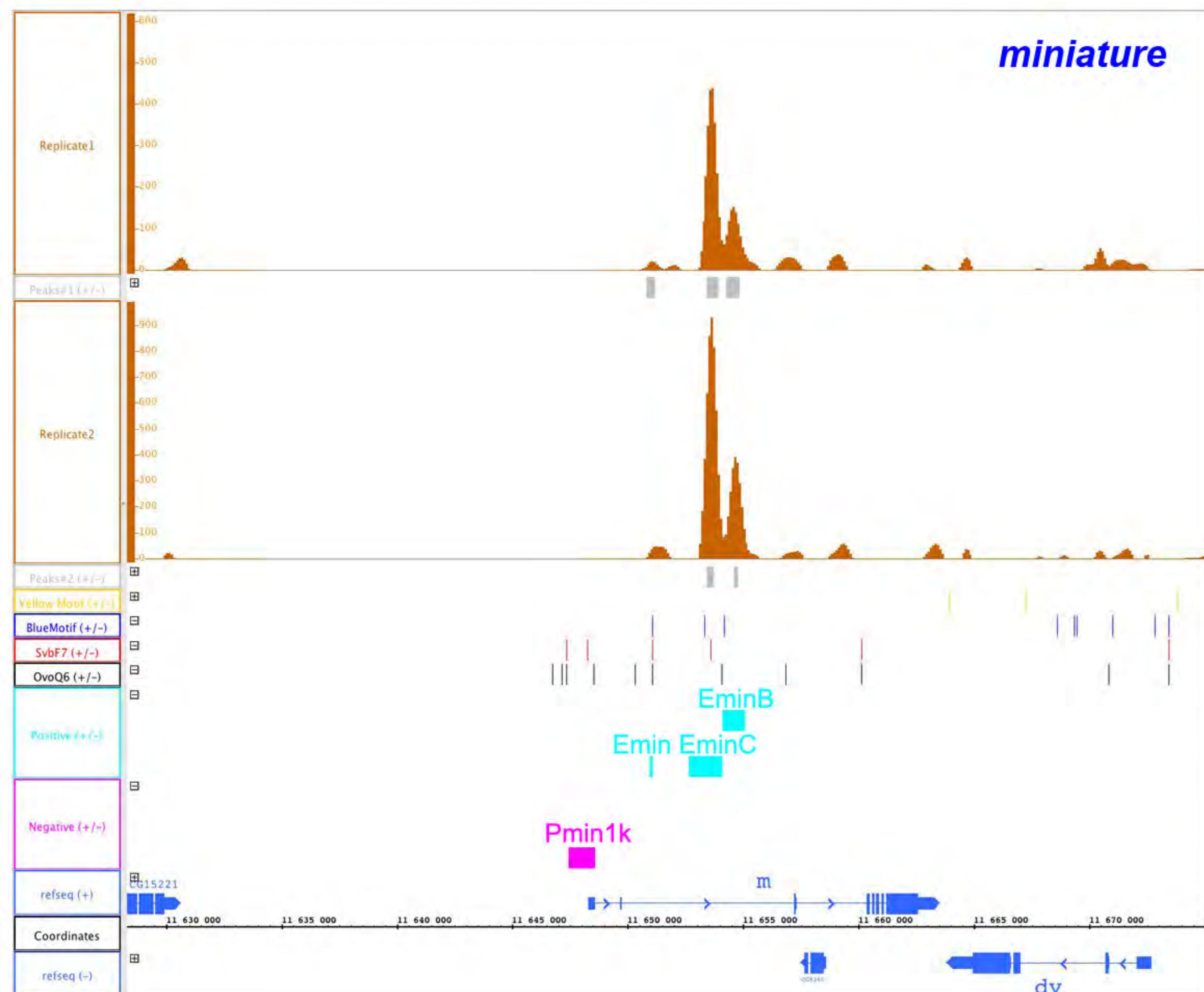
### singed



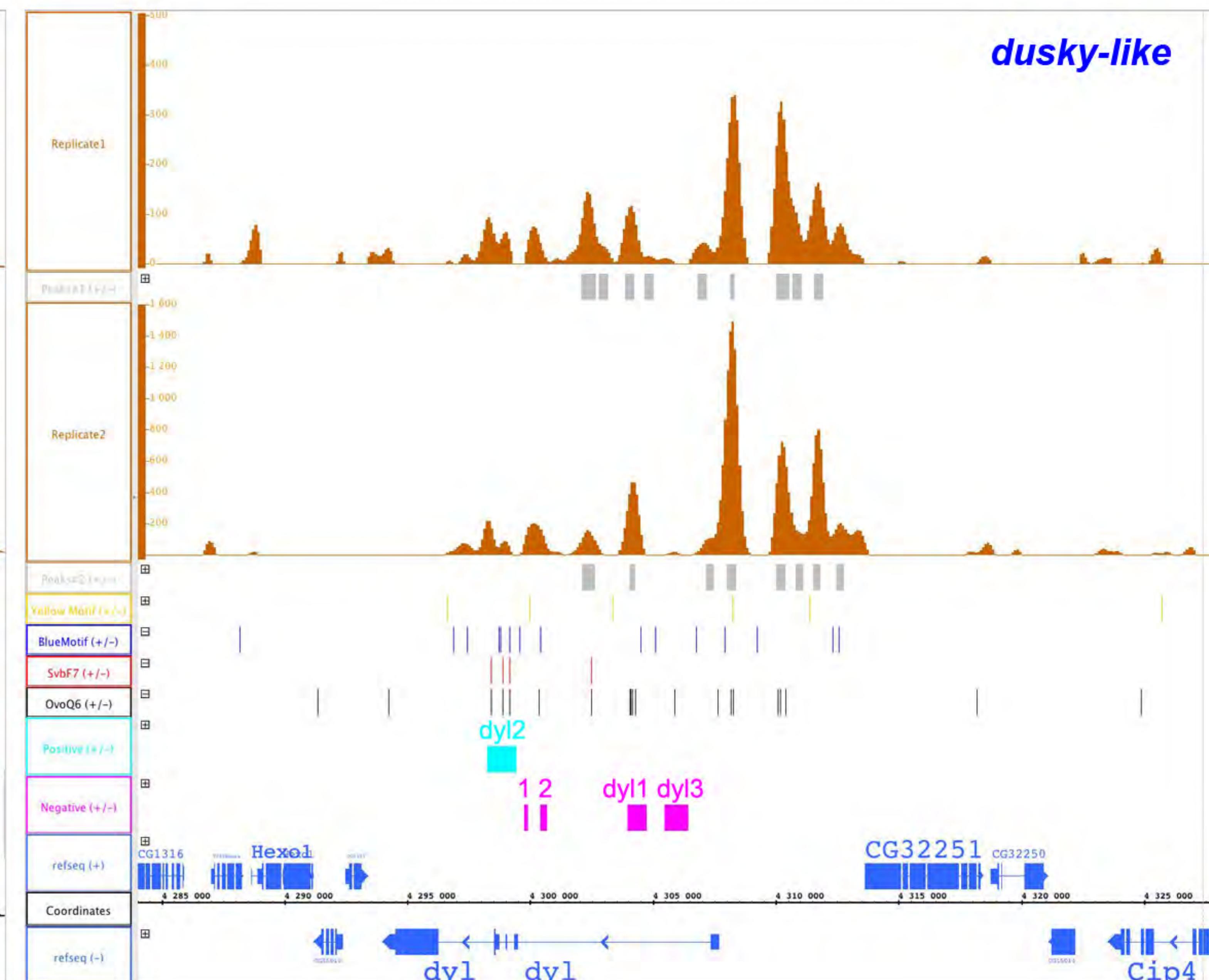
### shavenoid



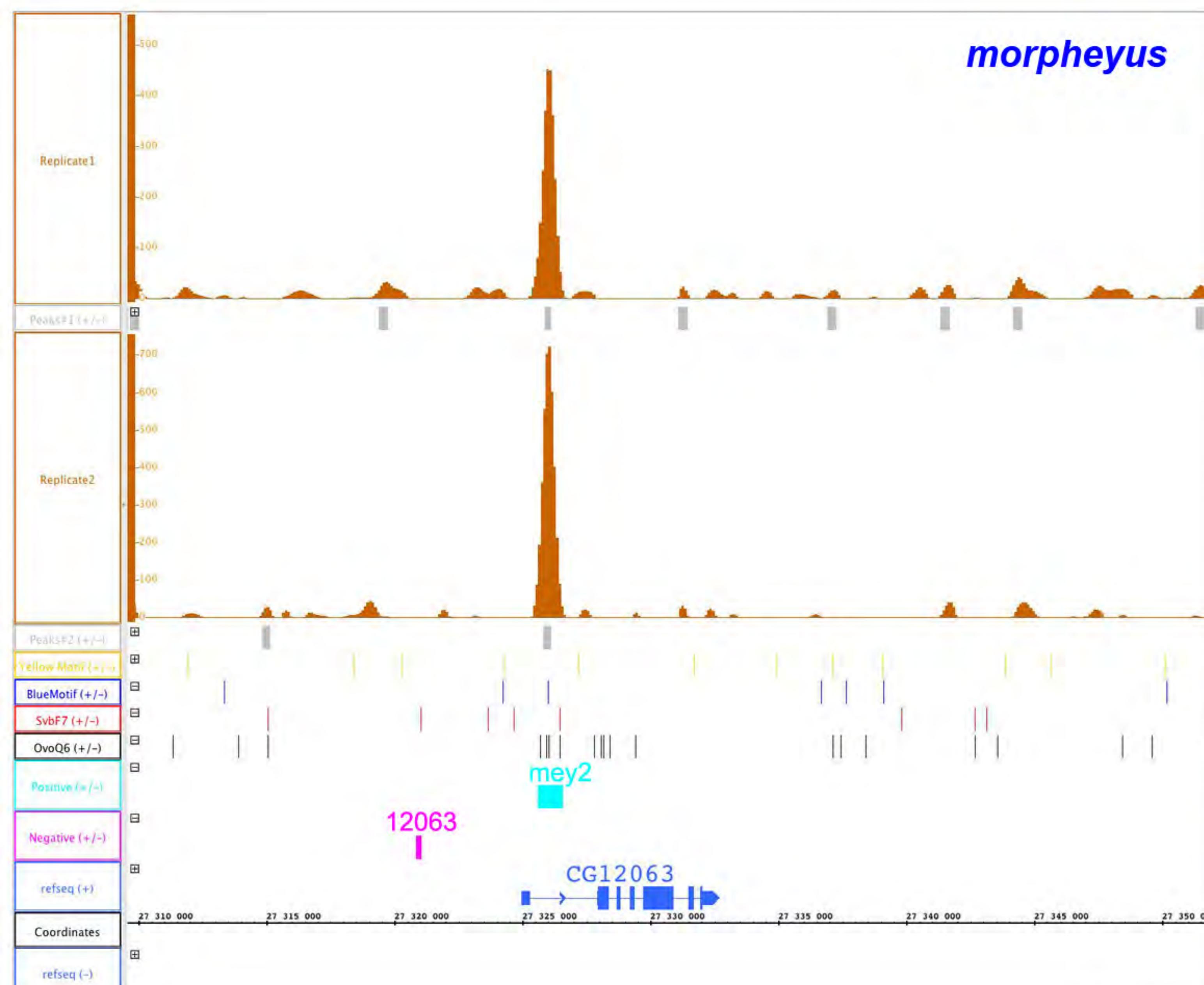
### miniature



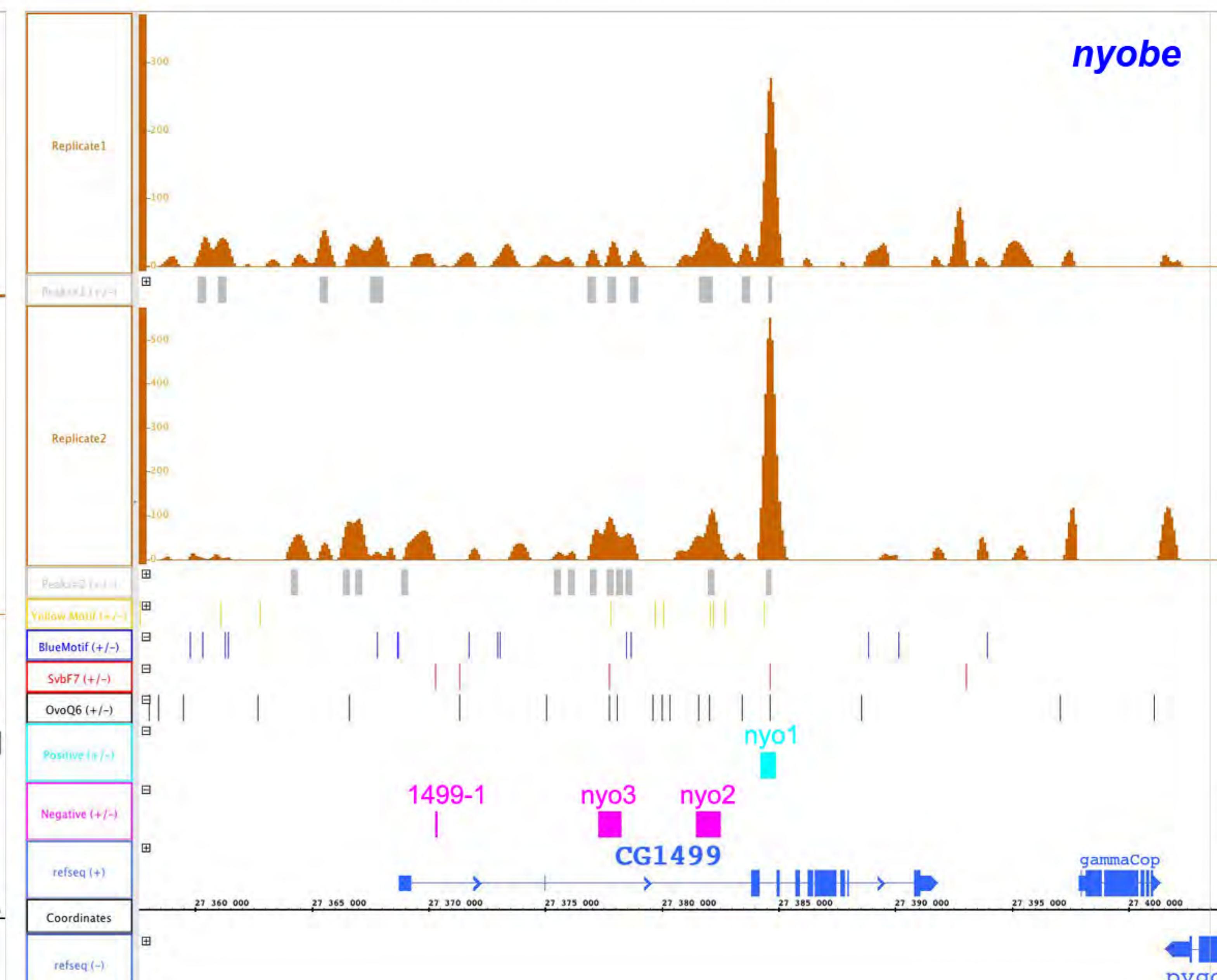
### dusky-like

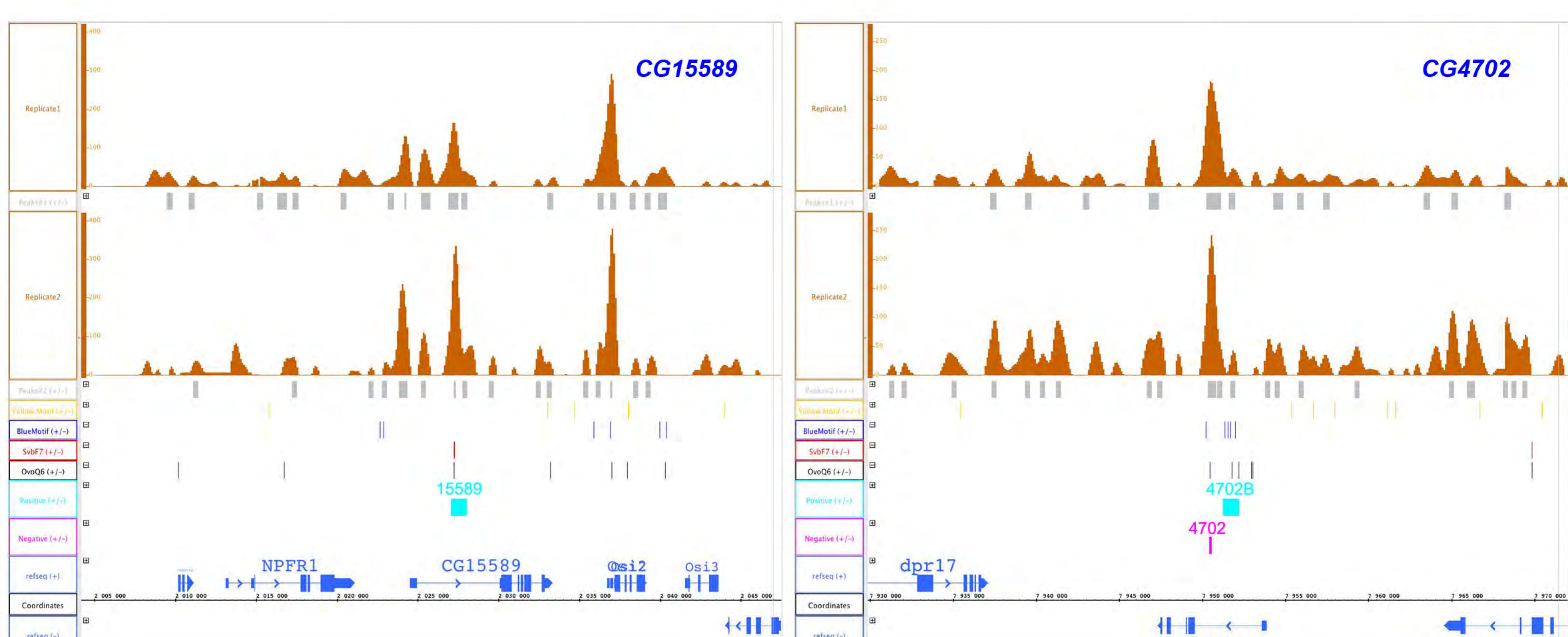
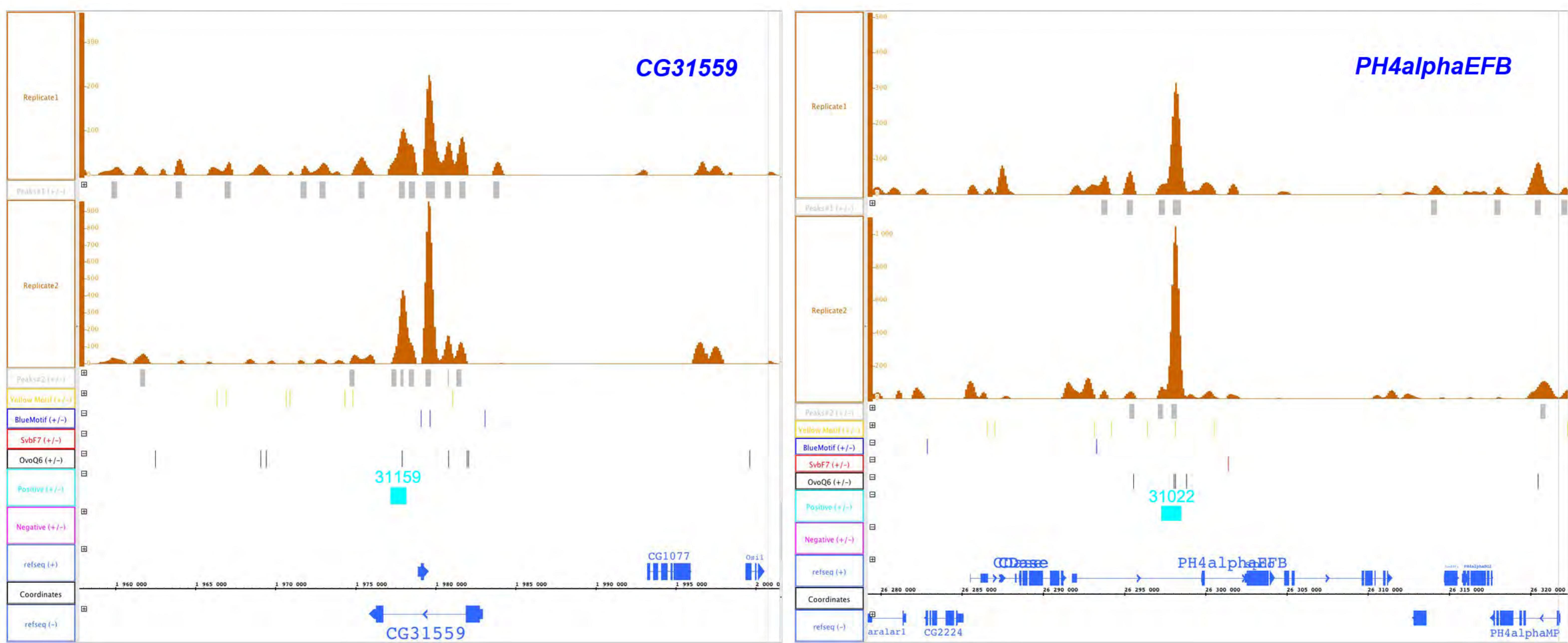
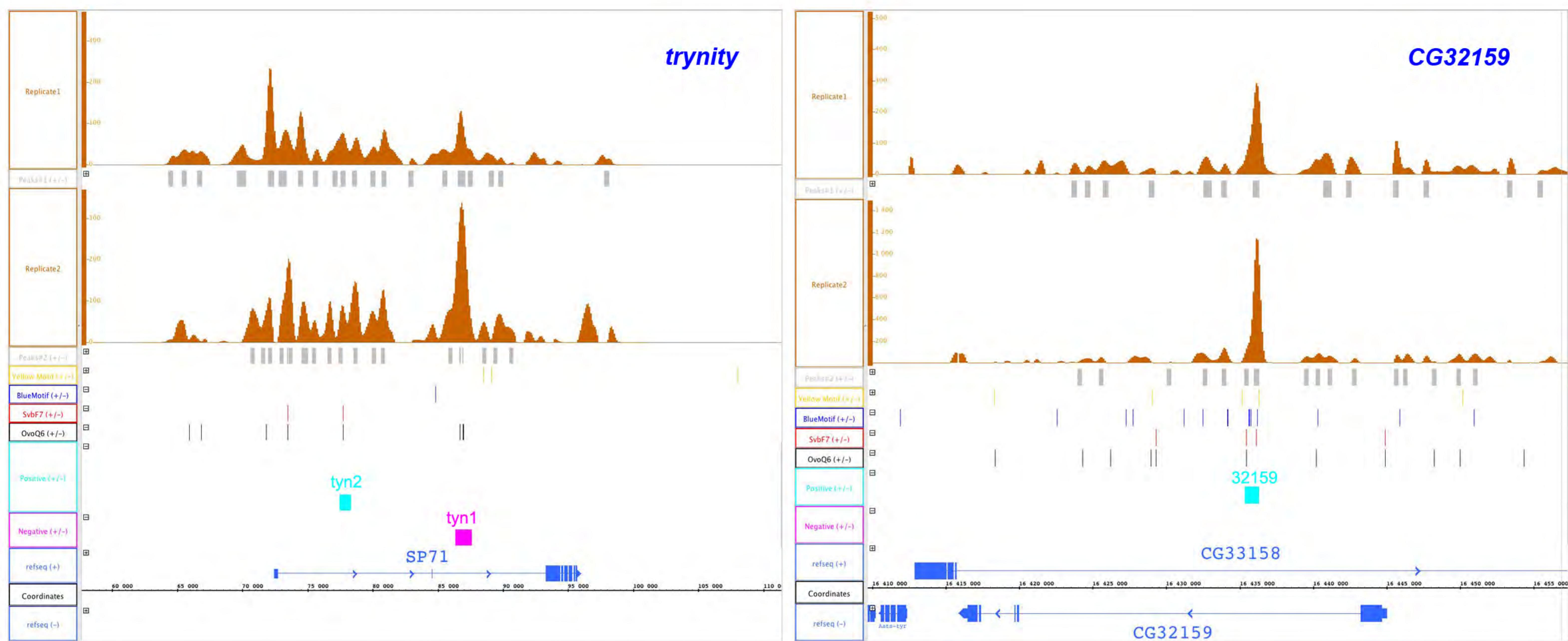


### morpheyus

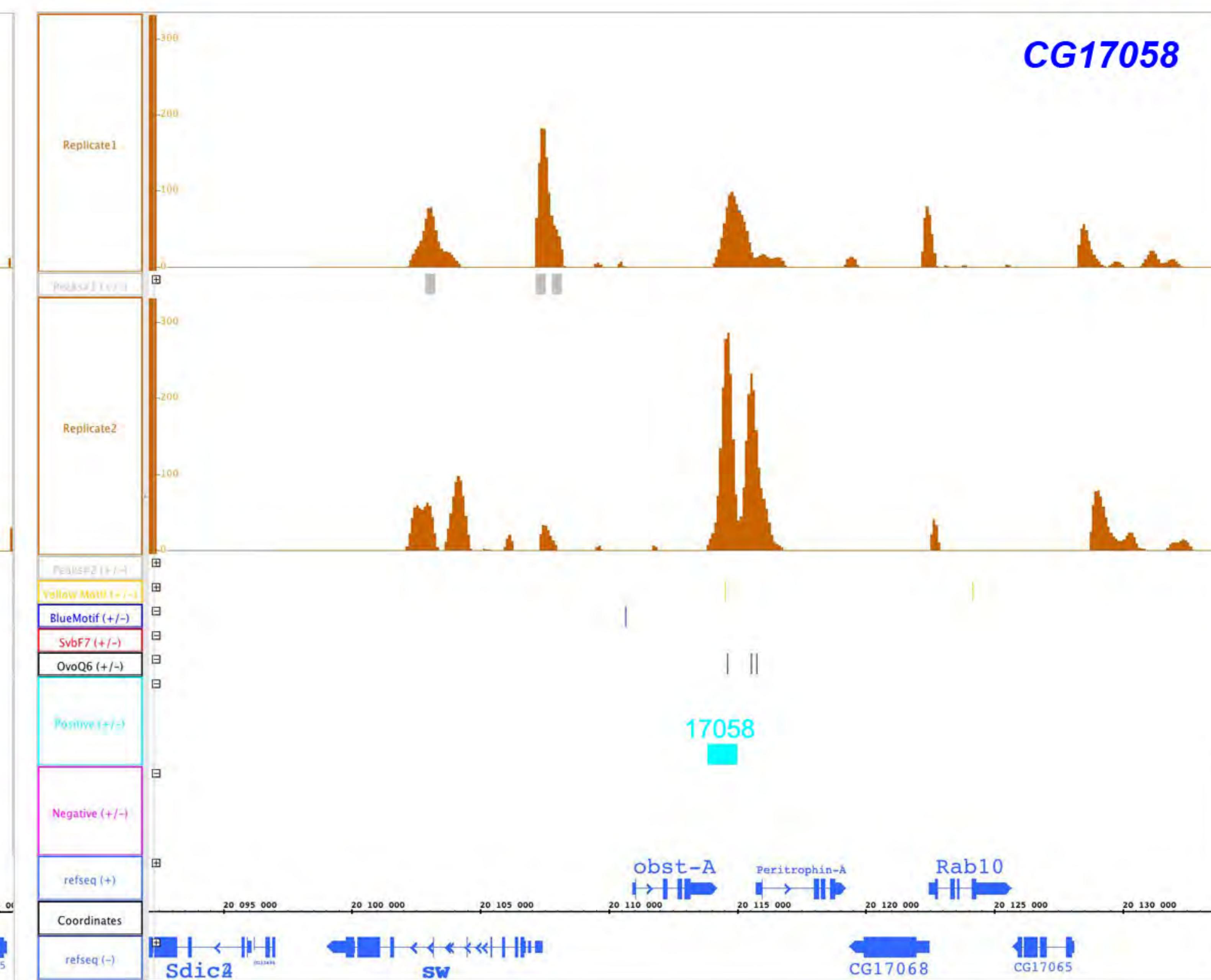
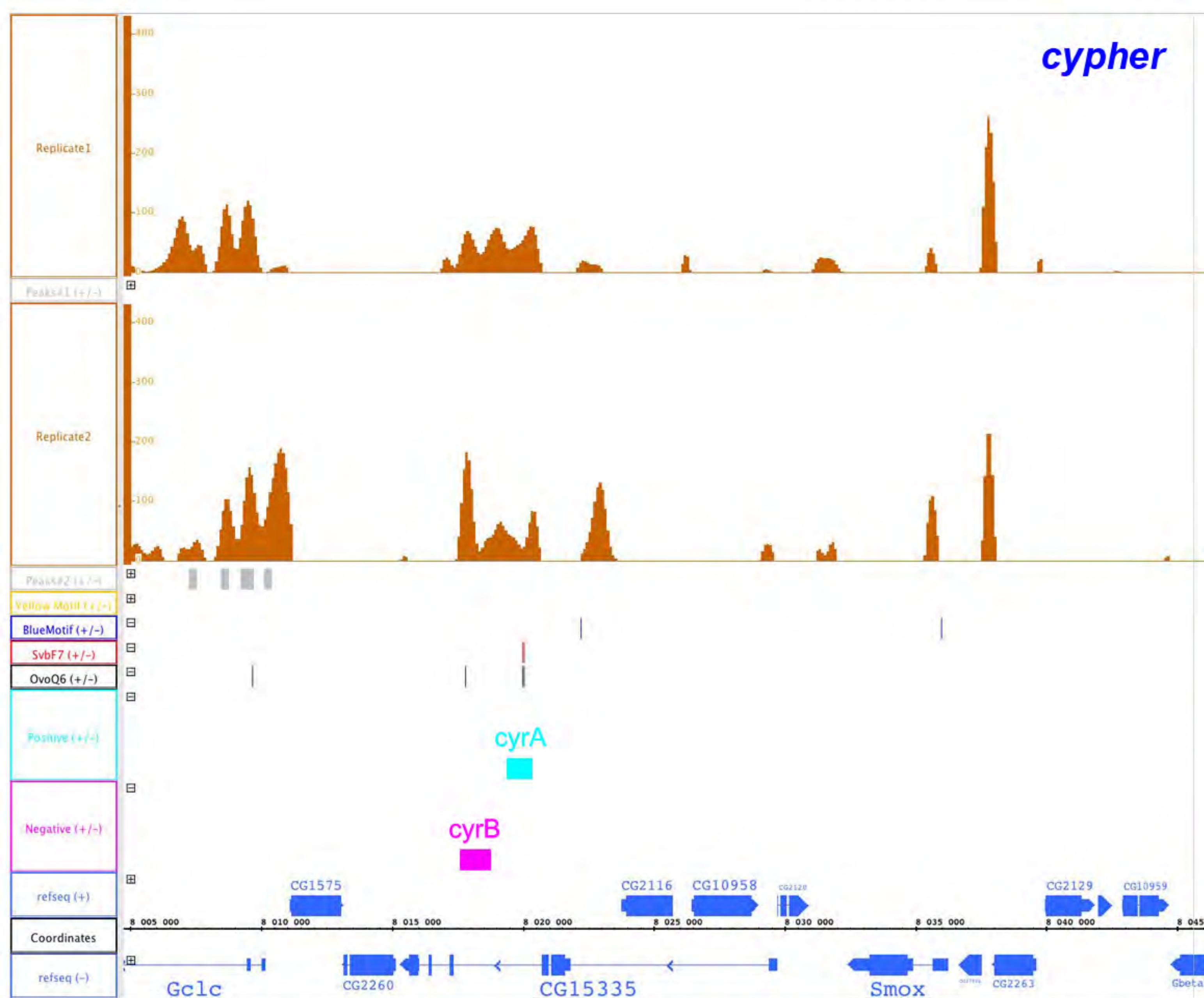


### nyobe



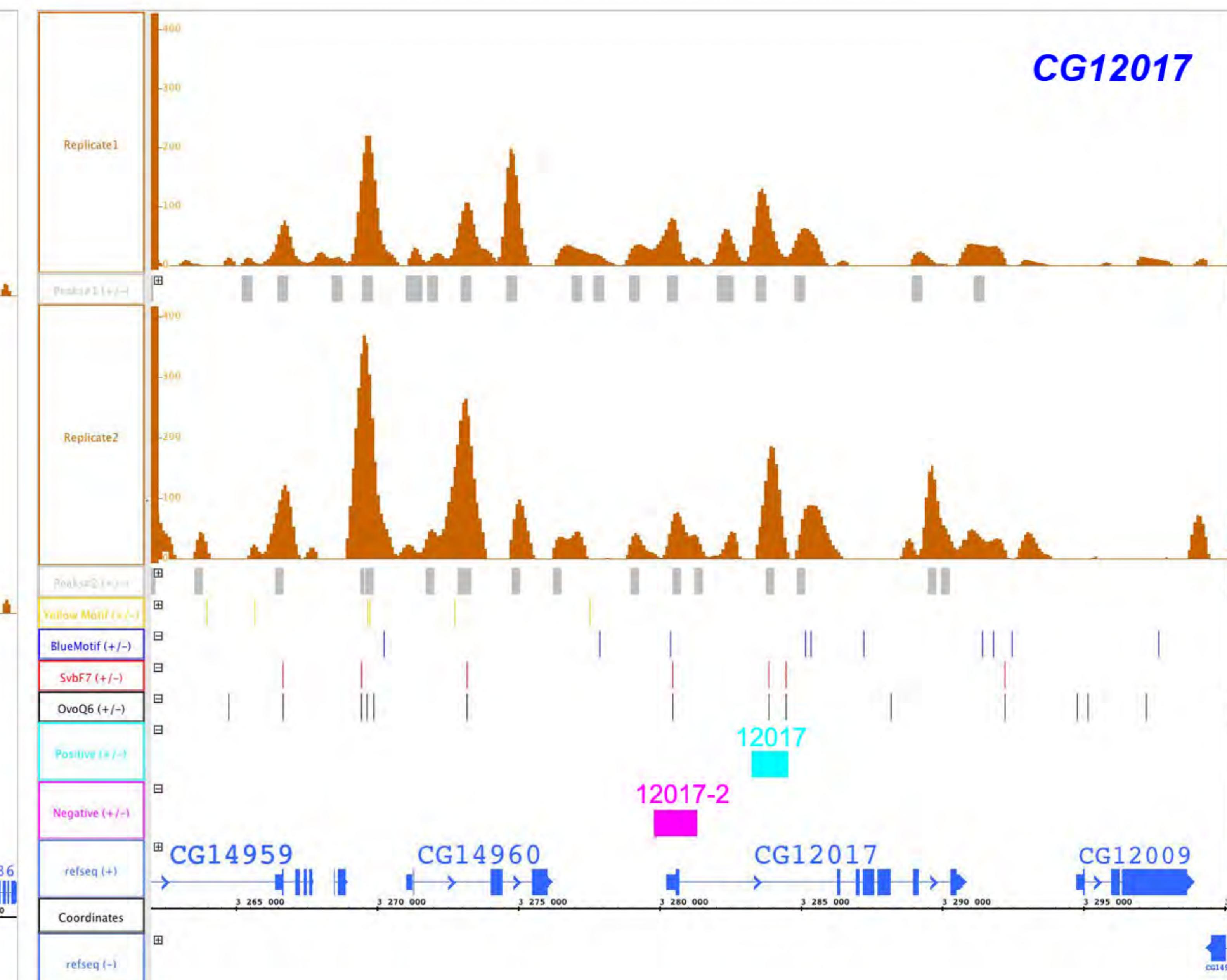
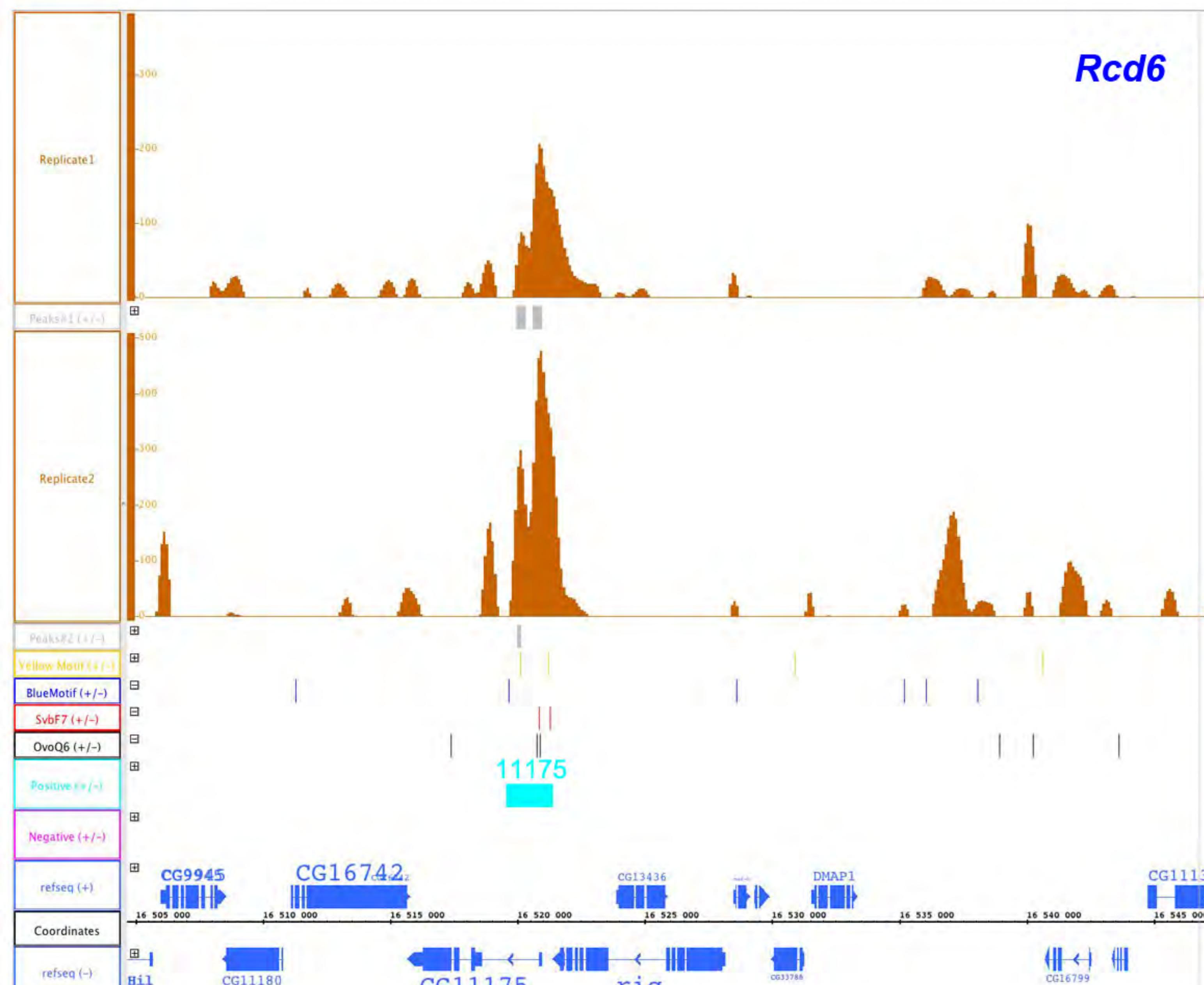


## cypher



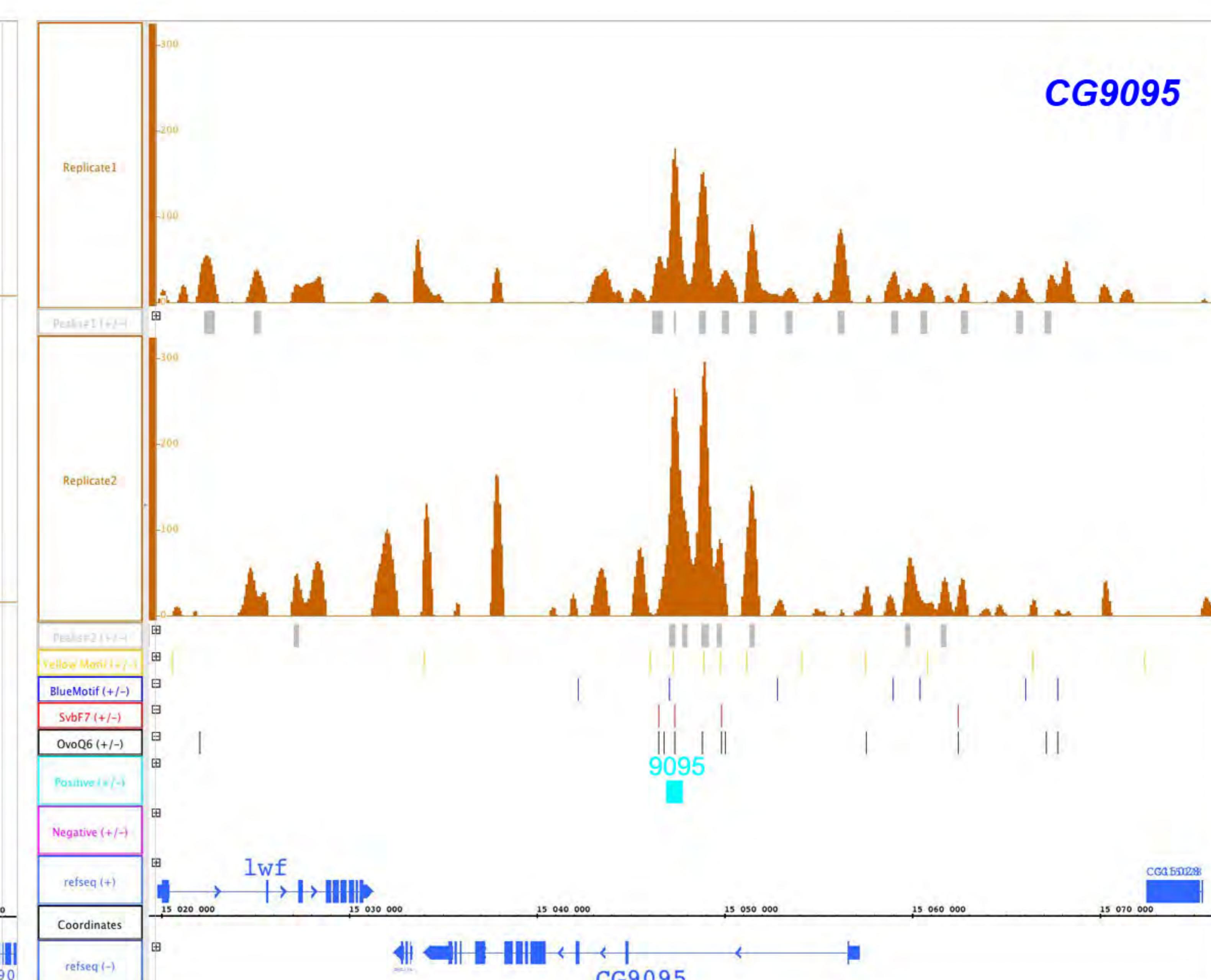
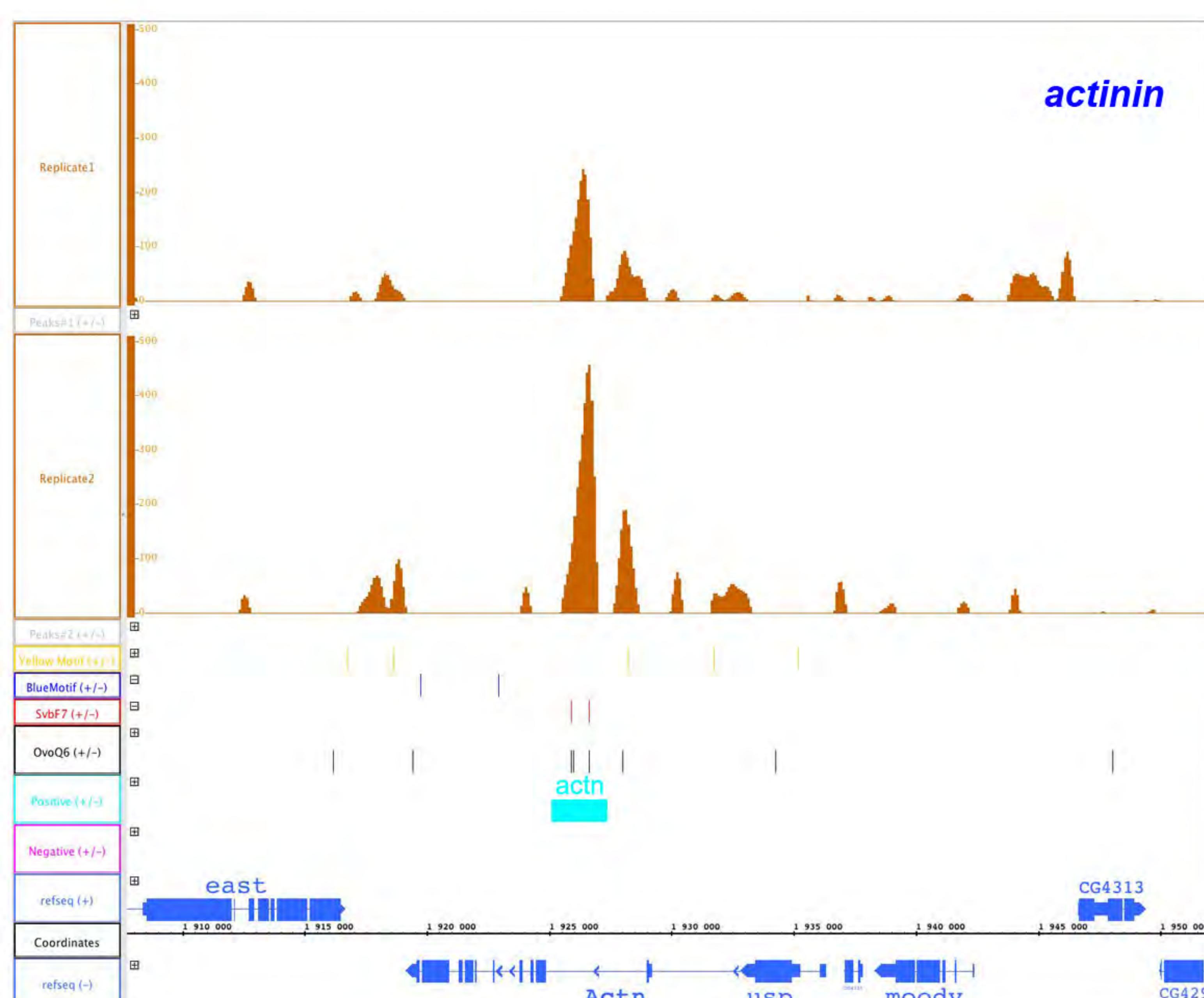
## CG12017

## Rcd6

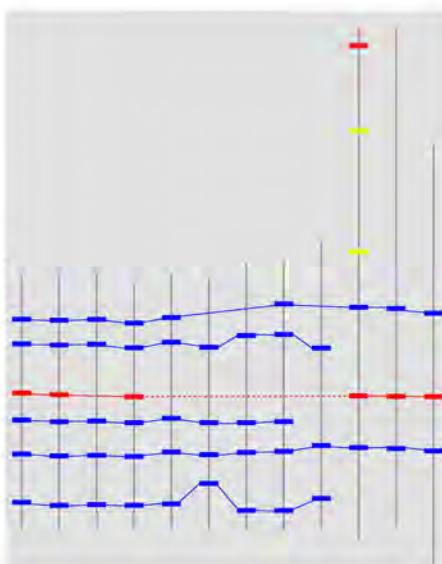


## CG9095

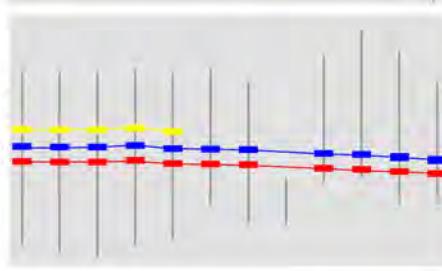
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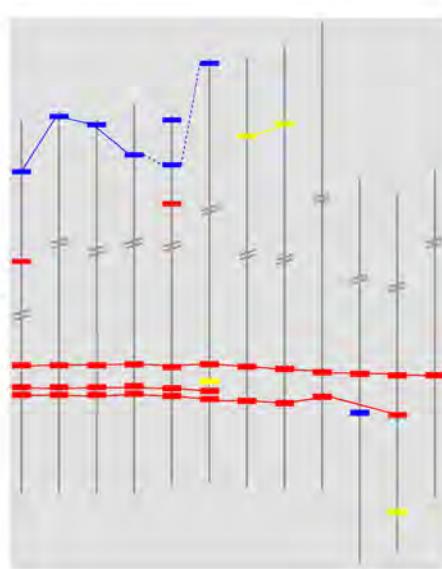
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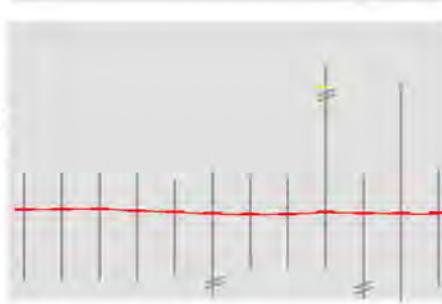
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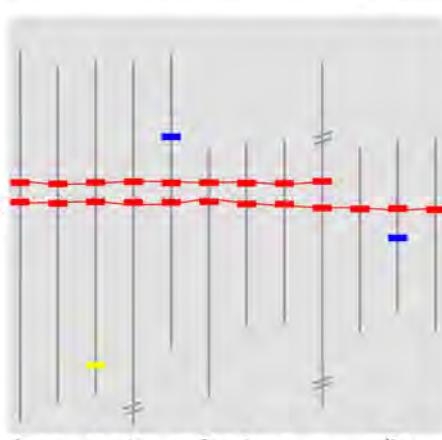
15589



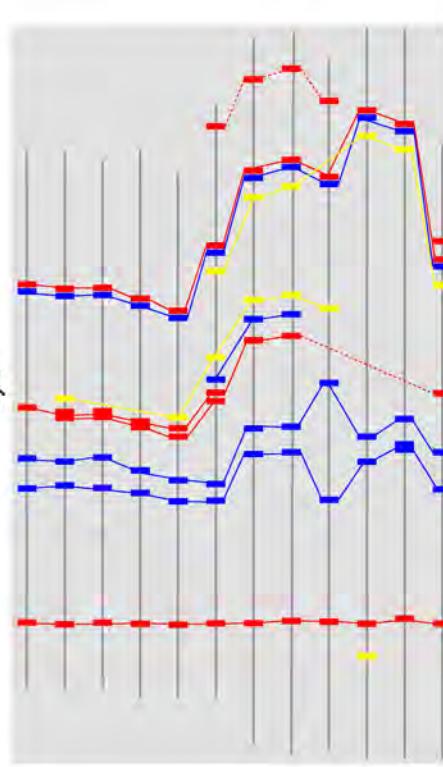
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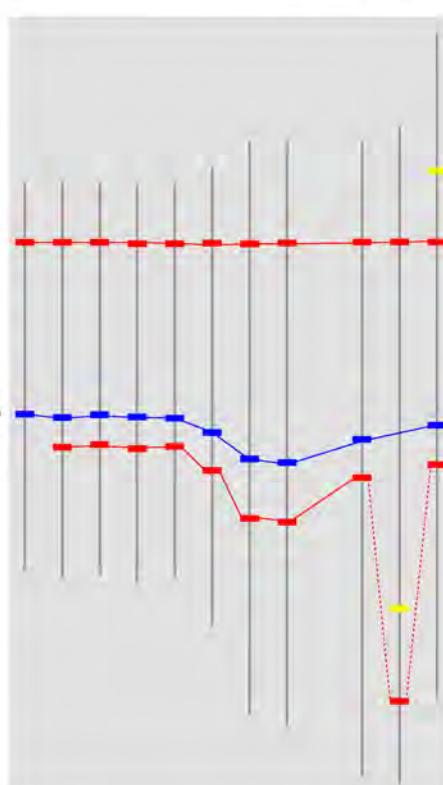
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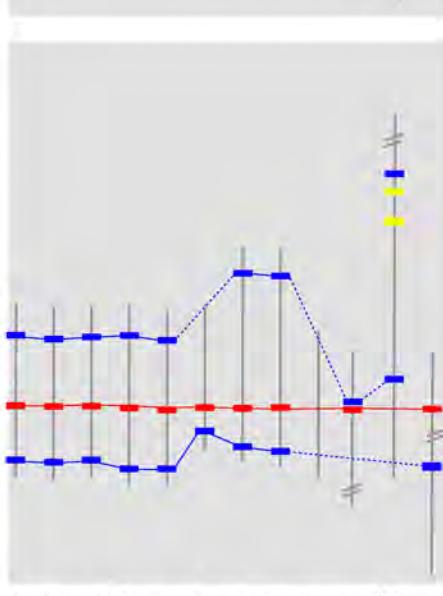
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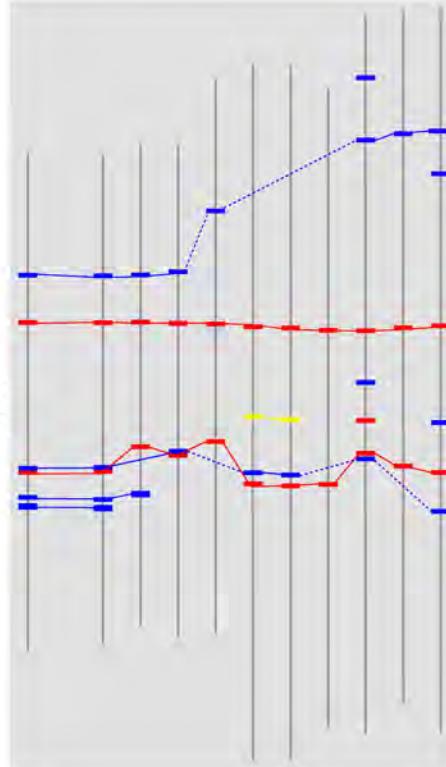
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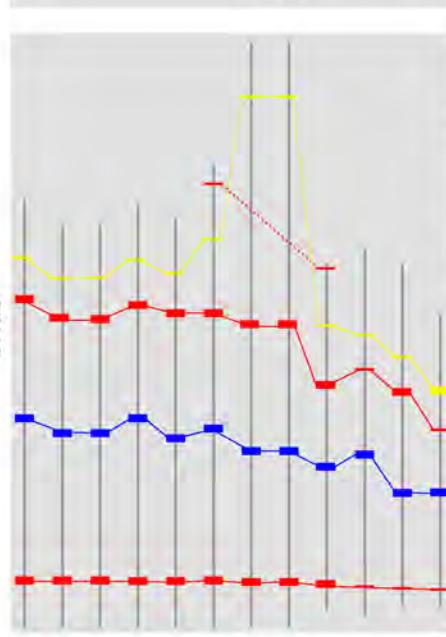
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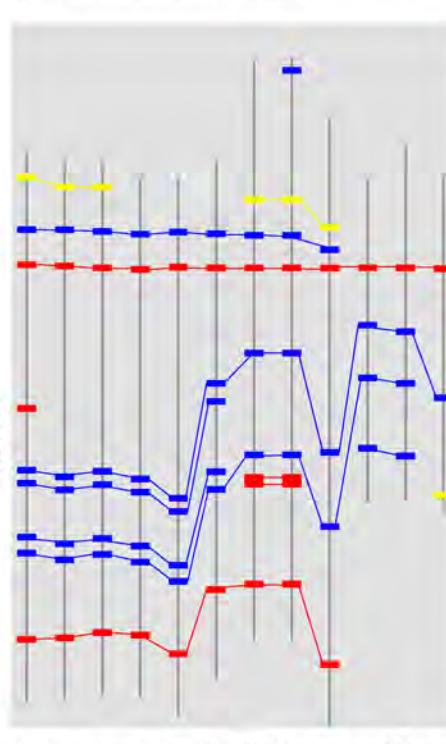
actn



sha3



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Menoret et al.; Figure S8B

