





























































Table S1. Gene Ontology analysis with DAVID for 100-bp genomic regions where H1.2 xChIP signal dominates over H1.5 xChIP.
















Annotation Cluster 1		Enrichment Score: 3.59	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	<b>RT</b>		60	8.5E-7	8.6E-4
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">ATP-binding</a>	<b>RT</b>		75	1.3E-6	1.2E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein serine/threonine kinase activity</a>	<b>RT</b>		30	2.6E-5	1.8E-2
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Serine/threonine-protein kinase</a>	<b>RT</b>		29	2.6E-5	1.2E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ATP binding</a>	<b>RT</b>		79	4.6E-5	1.5E-2
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Nucleotide-binding</a>	<b>RT</b>		83	8.9E-5	3.2E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase	<b>RT</b>		31	1.7E-4	8.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">peptidyl-serine phosphorylation</a>	<b>RT</b>		14	2.8E-4	5.0E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transferase</a>	<b>RT</b>		77	3.9E-4	1.1E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase-like domain</a>	<b>RT</b>		33	4.6E-4	7.0E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase, catalytic domain</a>	<b>RT</b>		31	4.8E-4	6.5E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein phosphorylation</a>	<b>RT</b>		30	7.3E-4	5.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Proton acceptor	<b>RT</b>		37	8.4E-4	1.7E-1












Annotation Cluster 1		Enrichment Score: 3.59			Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Kinase</a>	<a href="#">RT</a>		39	9.4E-4	2.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:ATP	<a href="#">RT</a>		32	1.1E-3	1.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Serine/threonine-protein kinase, active site</a>	<a href="#">RT</a>		22	1.1E-3	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase, ATP binding site</a>	<a href="#">RT</a>		25	1.3E-3	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">intracellular signal transduction</a>	<a href="#">RT</a>		26	2.3E-3	6.1E-1
<input type="checkbox"/>	SMART	<a href="#">S_TKc</a>	<a href="#">RT</a>		26	2.8E-3	1.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein kinase activity</a>	<a href="#">RT</a>		21	1.8E-2	4.6E-1
Annotation Cluster 2		Enrichment Score: 3.44			Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">SH3 domain</a>	<a href="#">RT</a>		19	9.8E-5	3.2E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Src homology-3 domain</a>	<a href="#">RT</a>		19	2.3E-4	8.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH3	<a href="#">RT</a>		16	3.2E-4	1.0E-1
<input type="checkbox"/>	SMART	<a href="#">SH3</a>	<a href="#">RT</a>		18	2.4E-3	4.9E-1
Annotation Cluster 3		Enrichment Score: 2.55			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">microtubule motor activity</a>	<a href="#">RT</a>		12	6.7E-5	1.5E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:AAA 6	<a href="#">RT</a>		5	5.0E-4	1.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:AAA 2	<a href="#">RT</a>		5	6.8E-4	1.6E-1

Annotation Cluster 1		Enrichment Score: 3.59			Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:AAA 3	<a href="#">RT</a>		5	6.8E-4	1.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:AAA 1	<a href="#">RT</a>		5	6.8E-4	1.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Stem	<a href="#">RT</a>		5	6.8E-4	1.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Stalk	<a href="#">RT</a>		5	6.8E-4	1.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:AAA 5	<a href="#">RT</a>		5	6.8E-4	1.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:AAA 4	<a href="#">RT</a>		5	6.8E-4	1.6E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Motor protein</a>	<a href="#">RT</a>		13	8.1E-4	1.8E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Dynein heavy chain, P-loop containing D4 domain</a>	<a href="#">RT</a>		5	1.1E-3	1.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ATPase activity</a>	<a href="#">RT</a>		16	1.2E-3	1.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Dynein heavy chain domain</a>	<a href="#">RT</a>		5	1.4E-3	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Dynein heavy chain, coiled coil stalk</a>	<a href="#">RT</a>		5	1.4E-3	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Dynein heavy chain</a>	<a href="#">RT</a>		5	1.4E-3	1.1E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Dynein heavy chain, domain-2</a>	<a href="#">RT</a>		5	1.4E-3	1.1E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Dynein</a>	<a href="#">RT</a>		6	2.9E-3	4.5E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">axonemal dynein complex</a>	<a href="#">RT</a>		4	3.3E-3	2.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">microtubule-based movement</a>	<a href="#">RT</a>		9	5.6E-3	8.6E-1

Annotation Cluster 1		Enrichment Score: 3.59			Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">ATPase, dynein-related, AAA domain</a>	<a href="#">RT</a>		4	9.0E-3	3.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Microtubule</a>	<a href="#">RT</a>		17	1.1E-2	1.2E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">microtubule</a>	<a href="#">RT</a>		19	1.2E-2	4.0E-1
<input type="checkbox"/>	INTERPRO	<a href="#">AAA+ ATPase domain</a>	<a href="#">RT</a>		11	1.2E-2	3.9E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Dynein heavy chain, domain-1</a>	<a href="#">RT</a>		3	3.2E-2	6.2E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">dynein complex</a>	<a href="#">RT</a>		4	3.2E-2	6.1E-1
<input type="checkbox"/>	SMART	<a href="#">AAA</a>	<a href="#">RT</a>		11	3.6E-2	6.8E-1
<input type="checkbox"/>	COG_ONTOLOGY	<a href="#">Cytoskeleton</a>	<a href="#">RT</a>		4	1.1E-1	7.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Huntington's disease</a>	<a href="#">RT</a>		10	1.7E-1	5.0E-1
Annotation Cluster 4		Enrichment Score: 2.52			Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Pleckstrin homology-like domain</a>	<a href="#">RT</a>		30	1.2E-4	1.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Pleckstrin homology domain</a>	<a href="#">RT</a>		19	2.8E-3	1.7E-1
<input type="checkbox"/>	SMART	<a href="#">PH</a>	<a href="#">RT</a>		19	1.3E-2	4.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PH	<a href="#">RT</a>		15	1.9E-2	7.2E-1
Annotation Cluster 5		Enrichment Score: 2.37			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">zinc ion binding</a>	<a href="#">RT</a>		59	1.5E-3	1.6E-1

Annotation Cluster 1		Enrichment Score: 3.59	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Zinc</a>	RT		94	3.6E-3	5.2E-2
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Zinc-finger</a>	RT		73	6.6E-3	7.7E-2
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Metal-binding</a>	RT		134	8.9E-3	1.0E-1
Annotation Cluster 6		Enrichment Score: 2.33	G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">WW domain</a>	RT		9	2.6E-4	6.8E-2
<input type="checkbox"/>	SMART	<a href="#">WW</a>	RT		8	2.4E-3	2.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 2	RT		5	1.1E-2	6.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 1	RT		5	1.1E-2	6.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW	RT		4	2.8E-2	7.9E-1
Annotation Cluster 7		Enrichment Score: 2.29	G		Count	P_Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Ubiquitin mediated proteolysis</a>	RT		13	1.6E-3	1.1E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ubiquitin-protein transferase activity</a>	RT		23	1.6E-3	1.5E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Ubl conjugation pathway</a>	RT		32	1.5E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein ubiquitination</a>	RT		21	1.8E-2	9.5E-1
Annotation Cluster 8		Enrichment Score: 2.27	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Cell junction</a>	RT		38	3.7E-4	1.1E-2

Annotation Cluster 1		Enrichment Score: 3.59			Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Synapse</a>	<a href="#">RT</a>		23	1.3E-3	2.5E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">postsynaptic density</a>	<a href="#">RT</a>		15	2.5E-3	2.5E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">cell junction</a>	<a href="#">RT</a>		25	1.3E-2	4.1E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Postsynaptic cell membrane</a>	<a href="#">RT</a>		12	2.0E-2	1.8E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">postsynaptic membrane</a>	<a href="#">RT</a>		12	7.8E-2	6.8E-1
Annotation Cluster 9		Enrichment Score: 2.2			Count	P_Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Morphine addiction</a>	<a href="#">RT</a>		12	1.6E-4	1.8E-2
<input type="checkbox"/>	INTERPRO	<a href="#">3'5'-cyclic nucleotide phosphodiesterase, conserved site</a>	<a href="#">RT</a>		6	4.3E-4	7.7E-2
<input type="checkbox"/>	INTERPRO	<a href="#">3'5'-cyclic nucleotide phosphodiesterase, catalytic domain</a>	<a href="#">RT</a>		6	5.4E-4	6.5E-2
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">cAMP</a>	<a href="#">RT</a>		7	6.6E-4	1.7E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">3',5'-cyclic-AMP phosphodiesterase activity</a>	<a href="#">RT</a>		5	1.2E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cAMP catabolic process</a>	<a href="#">RT</a>		5	1.3E-3	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 2	<a href="#">RT</a>		6	1.4E-3	2.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 1	<a href="#">RT</a>		6	1.4E-3	2.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">3'5'-cyclic nucleotide phosphodiesterase</a>	<a href="#">RT</a>		5	2.7E-3	1.7E-1

Annotation Cluster 1		Enrichment Score: 3.59			Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">HD/PDEase domain</a>	<a href="#">RT</a>		5	5.6E-3	2.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">3',5'-cyclic-nucleotide phosphodiesterase activity</a>	<a href="#">RT</a>		5	6.5E-3	3.6E-1
<input type="checkbox"/>	SMART	<a href="#">HDc</a>	<a href="#">RT</a>		5	1.1E-2	4.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cAMP-mediated signaling</a>	<a href="#">RT</a>		5	3.7E-2	9.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Catalytic	<a href="#">RT</a>		5	7.4E-2	9.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Purine metabolism</a>	<a href="#">RT</a>		10	1.2E-1	4.2E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">cGMP</a>	<a href="#">RT</a>		3	1.3E-1	5.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">cAMP binding</a>	<a href="#">RT</a>		3	1.9E-1	9.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Proton donor	<a href="#">RT</a>		8	4.1E-1	1.0E0