















































Table S2. Gene Ontology analysis with DAVID for 100-bp genomic regions where H1.5 xChIP signal dominates over H1.2 xChIP.










Annotation Cluster 1		Enrichment Score: 7.67			Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">ATP-binding</a>	<b>RT</b>		201	7.7E-14	6.4E-12
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Nucleotide-binding</a>	<b>RT</b>		242	2.4E-13	1.7E-11
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ATP binding</a>	<b>RT</b>		213	1.5E-11	1.0E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	<b>RT</b>		148	3.6E-11	7.8E-8
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Kinase</a>	<b>RT</b>		114	6.0E-10	3.7E-8
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Serine/threonine-protein kinase</a>	<b>RT</b>		69	1.7E-8	7.8E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein phosphorylation</a>	<b>RT</b>		80	2.0E-8	4.2E-5
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase-like domain</a>	<b>RT</b>		88	2.0E-8	2.3E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein serine/threonine kinase activity</a>	<b>RT</b>		68	6.9E-8	3.1E-5
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase, catalytic domain</a>	<b>RT</b>		80	1.4E-7	7.9E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:ATP	<b>RT</b>		85	3.1E-7	3.3E-4
<input type="checkbox"/>	INTERPRO	<a href="#">Serine/threonine-protein kinase, active site</a>	<b>RT</b>		57	3.5E-7	1.3E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase	<b>RT</b>		73	2.1E-6	1.3E-3
<input type="checkbox"/>	SMART	<a href="#">S_TKc</a>	<b>RT</b>		62	1.2E-5	2.8E-3

Annotation Cluster 1		Enrichment Score: 7.67	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein kinase activity</a>	<b>RT</b>		59	1.2E-5	3.4E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase, ATP binding site</a>	<b>RT</b>		60	2.2E-5	4.5E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Proton acceptor	<b>RT</b>		87	1.3E-4	4.2E-2
Annotation Cluster 2		Enrichment Score: 6.98	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Pleckstrin homology-like domain</a>	<b>RT</b>		79	8.0E-10	1.8E-6
<input type="checkbox"/>	INTERPRO	<a href="#">Pleckstrin homology domain</a>	<b>RT</b>		53	1.0E-7	7.9E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PH	<b>RT</b>		46	9.3E-7	6.7E-4
<input type="checkbox"/>	SMART	<a href="#">PH</a>	<b>RT</b>		52	1.5E-6	7.1E-4
Annotation Cluster 3		Enrichment Score: 4.94	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">AGC-kinase, C-terminal</a>	<b>RT</b>		18	4.6E-6	1.5E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase, C-terminal</a>	<b>RT</b>		13	4.7E-6	1.3E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:AGC-kinase C-terminal	<b>RT</b>		17	1.3E-5	7.0E-3
<input type="checkbox"/>	SMART	<a href="#">S TK X</a>	<b>RT</b>		17	1.3E-5	2.0E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">peptidyl-serine phosphorylation</a>	<b>RT</b>		27	5.5E-5	3.8E-2
Annotation Cluster 4		Enrichment Score: 3.91	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Ubl conjugation pathway</a>	<b>RT</b>		99	2.1E-7	8.1E-6


Annotation Cluster 1		Enrichment Score: 7.67	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ligase activity</a>	<b>RT</b>		47	2.5E-5	4.8E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ubiquitin-protein transferase activity</a>	<b>RT</b>		53	6.3E-5	8.4E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ubiquitin protein ligase activity</a>	<b>RT</b>		31	1.6E-3	1.2E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, RING-type</a>	<b>RT</b>		36	5.2E-2	7.9E-1
Annotation Cluster 5		Enrichment Score: 3.65	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">WW domain</a>	<b>RT</b>		16	4.2E-5	7.3E-3
<input type="checkbox"/>	SMART	<a href="#">WW</a>	<b>RT</b>		16	4.3E-5	4.0E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 2	<b>RT</b>		11	9.5E-5	3.4E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 1	<b>RT</b>		11	9.5E-5	3.4E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW	<b>RT</b>		6	3.6E-2	8.6E-1
Annotation Cluster 6		Enrichment Score: 3.31	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">SH3 domain</a>	<b>RT</b>		37	7.7E-5	1.8E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH3	<b>RT</b>		30	4.7E-4	8.2E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Src homology-3 domain</a>	<b>RT</b>		36	4.9E-4	4.9E-2
<input type="checkbox"/>	SMART	<a href="#">SH3</a>	<b>RT</b>		34	3.2E-3	1.0E-1
Annotation Cluster 7		Enrichment Score: 3.27	<b>G</b>		Count	P_Value	Benjamini

Annotation Cluster 1		Enrichment Score: 7.67	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Zinc finger, A20-type</a>	<b>RT</b>		6	2.5E-4	3.1E-2
<input type="checkbox"/>	SMART	<a href="#">ZnF_A20</a>	<b>RT</b>		6	3.9E-4	2.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:A20-type	<b>RT</b>		5	1.6E-3	1.8E-1
Annotation Cluster 8		Enrichment Score: 3.15	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Protein kinase C-like, phorbol ester/diacylglycerol binding</a>	<b>RT</b>		19	1.3E-5	3.3E-3
<input type="checkbox"/>	SMART	<a href="#">C1</a>	<b>RT</b>		19	3.5E-5	4.0E-3
<input type="checkbox"/>	INTERPRO	<a href="#">Diacylglycerol/phorbol-ester binding</a>	<b>RT</b>		10	2.0E-4	2.6E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 1	<b>RT</b>		9	3.2E-4	6.4E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 2	<b>RT</b>		9	3.2E-4	6.4E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein kinase C activity</a>	<b>RT</b>		6	8.7E-3	3.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type	<b>RT</b>		10	1.3E-2	6.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">platelet activation</a>	<b>RT</b>		17	6.0E-2	9.8E-1
Annotation Cluster 9		Enrichment Score: 2.93	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Guanine-nucleotide releasing factor</a>	<b>RT</b>		31	8.3E-6	2.6E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ras-GEF	<b>RT</b>		11	9.5E-5	3.4E-2
<input type="checkbox"/>	INTERPRO	<a href="#">Ras guanine nucleotide exchange factor, domain</a>	<b>RT</b>		11	1.8E-4	2.5E-2
















Annotation Cluster 1		Enrichment Score: 7.67			Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">Guanine-nucleotide dissociation stimulator CDC25</a>	RT		11	1.8E-4	2.5E-2
<input type="checkbox"/>	SMART	<a href="#">RasGEF</a>	RT		11	3.8E-4	2.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:N-terminal Ras-GEF	RT		8	1.9E-3	2.0E-1
<input type="checkbox"/>	SMART	<a href="#">RasGEFN</a>	RT		8	2.1E-3	7.8E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">guanyl-nucleotide exchange factor activity</a>	RT		22	2.2E-3	1.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ras-like guanine nucleotide exchange factor, N-terminal</a>	RT		8	2.3E-3	1.4E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ras guanine-nucleotide exchange factor, conserved site</a>	RT		6	5.7E-3	2.7E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">Rap guanyl-nucleotide exchange factor activity</a>	RT		3	6.9E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">small GTPase mediated signal transduction</a>	RT		30	9.5E-2	9.9E-1
Annotation Cluster 10		Enrichment Score: 2.88			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">GTPase activator activity</a>	RT		47	5.7E-5	9.6E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of small GTPase mediated signal transduction</a>	RT		26	4.5E-4	1.6E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Rho GTPase-activating protein domain</a>	RT		15	2.1E-3	1.3E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Rho GTPase activation protein</a>	RT		18	2.7E-3	1.6E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">GTPase activation</a>	RT		30	2.9E-3	3.4E-2

Annotation Cluster 1		Enrichment Score: 7.67	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SMART	<a href="#">RhoGAP</a>	RT		15	3.6E-3	1.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Rho-GAP	RT		14	4.9E-3	3.7E-1
Annotation Cluster 11		Enrichment Score: 2.8	G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Metal-binding</a>	RT		380	1.1E-5	3.2E-4
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Zinc-finger</a>	RT		187	2.3E-3	3.0E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">zinc ion binding</a>	RT		130	1.2E-2	3.8E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Zinc</a>	RT		229	2.2E-2	1.5E-1
Annotation Cluster 12		Enrichment Score: 2.66	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">3',5'-cyclic-AMP phosphodiesterase activity</a>	RT		9	1.7E-5	3.8E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cAMP catabolic process</a>	RT		9	1.7E-5	1.8E-2
<input type="checkbox"/>	INTERPRO	<a href="#">3'5'-cyclic nucleotide phosphodiesterase, conserved site</a>	RT		10	3.9E-5	7.3E-3
<input type="checkbox"/>	INTERPRO	<a href="#">3'5'-cyclic nucleotide phosphodiesterase, catalytic domain</a>	RT		10	6.1E-5	9.8E-3
<input type="checkbox"/>	INTERPRO	<a href="#">3'5'-cyclic nucleotide phosphodiesterase</a>	RT		9	1.2E-4	1.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 1	RT		10	3.9E-4	7.4E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 2	RT		10	3.9E-4	7.4E-2
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Morphine addiction</a>	RT		20	4.7E-4	1.2E-2

Annotation Cluster 1		Enrichment Score: 7.67				Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	<a href="#">HD/PDEase domain</a>	<a href="#">RT</a>			9	5.8E-4	5.3E-2
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">cAMP</a>	<a href="#">RT</a>			11	6.7E-4	1.1E-2
<input type="checkbox"/>	SMART	<a href="#">HDc</a>	<a href="#">RT</a>			9	1.1E-3	4.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Catalytic	<a href="#">RT</a>			13	1.3E-3	1.6E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">3',5'-cyclic-nucleotide phosphodiesterase activity</a>	<a href="#">RT</a>			8	3.4E-3	2.2E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">cAMP binding</a>	<a href="#">RT</a>			7	1.8E-2	4.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Proton donor	<a href="#">RT</a>			27	2.3E-2	7.4E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">cGMP</a>	<a href="#">RT</a>			6	2.9E-2	1.8E-1
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">3',5'-cyclic-GMP phosphodiesterase activity</a>	<a href="#">RT</a>			5	3.3E-2	5.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Binds AMP, but not cAMP	<a href="#">RT</a>			3	4.0E-2	8.7E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Purine metabolism</a>	<a href="#">RT</a>			24	5.0E-2	2.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:cAMP	<a href="#">RT</a>			3	8.8E-2	9.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cGMP catabolic process</a>	<a href="#">RT</a>			3	1.3E-1	9.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:cAMP	<a href="#">RT</a>			3	2.4E-1	1.0E0
Annotation Cluster 13		Enrichment Score: 2.63				Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">microtubule binding</a>	<a href="#">RT</a>			36	2.8E-4	3.1E-2

Annotation Cluster 1		Enrichment Score: 7.67	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">microtubule</a>	<b>RT</b>		43	4.8E-3	2.0E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Microtubule</a>	<b>RT</b>		37	9.4E-3	7.9E-2
Annotation Cluster 14		Enrichment Score: 2.49	<b>G</b>		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 10	<b>RT</b>		10	5.2E-4	8.7E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 23	<b>RT</b>		6	8.2E-4	1.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 22	<b>RT</b>		6	8.2E-4	1.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 11	<b>RT</b>		9	8.5E-4	1.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 13	<b>RT</b>		7	1.0E-3	1.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 14	<b>RT</b>		7	1.0E-3	1.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 15	<b>RT</b>		7	1.0E-3	1.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 20	<b>RT</b>		6	1.4E-3	1.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 21	<b>RT</b>		6	1.4E-3	1.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 8	<b>RT</b>		12	1.5E-3	1.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 17	<b>RT</b>		6	2.2E-3	2.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 18	<b>RT</b>		6	2.2E-3	2.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 19	<b>RT</b>		6	2.2E-3	2.3E-1



Annotation Cluster 1		Enrichment Score: 7.67			Count	P_Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 7	<a href="#">RT</a>		14	2.4E-3	2.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 24	<a href="#">RT</a>		5	2.9E-3	2.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 12	<a href="#">RT</a>		7	3.0E-3	2.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 16	<a href="#">RT</a>		6	3.4E-3	2.9E-1
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">ANK repeat</a>	<a href="#">RT</a>		37	3.7E-3	4.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 4	<a href="#">RT</a>		26	5.8E-3	4.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 9	<a href="#">RT</a>		10	7.1E-3	4.5E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ankyrin repeat</a>	<a href="#">RT</a>		36	7.2E-3	3.0E-1
<input type="checkbox"/>	INTERPRO	<a href="#">Ankyrin repeat-containing domain</a>	<a href="#">RT</a>		37	7.7E-3	3.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 5	<a href="#">RT</a>		22	1.0E-2	5.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 6	<a href="#">RT</a>		17	1.0E-2	5.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 1	<a href="#">RT</a>		33	1.1E-2	5.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 3	<a href="#">RT</a>		29	1.1E-2	5.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 2	<a href="#">RT</a>		33	1.2E-2	5.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 25	<a href="#">RT</a>		4	1.7E-2	6.9E-1
<input type="checkbox"/>	SMART	<a href="#">ANK</a>	<a href="#">RT</a>		35	2.9E-2	4.1E-1

