

Table S4

Enrichment Score: 22.21679332120849

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
nucleus	6.55E-38	2.970245353	1.15E-35	1.15E-35	8.03E-35
Transcription	1.85E-34	4.275328995	3.24E-32	1.62E-32	2.27E-31
transcription regulation	1.86E-33	4.269822989	3.25E-31	1.08E-31	2.28E-30
GO:0006350~transcription	3.37E-30	3.545436471	2.15E-27	2.15E-27	5.02E-27
zinc-finger	6.14E-30	4.44291997	1.07E-27	2.68E-28	7.52E-27
zinc finger region:C2H2-type 9	9.39E-29	10.7581898	5.88E-26	5.88E-26	1.40E-25
zinc finger region:C2H2-type 8	3.58E-28	9.942940885	2.24E-25	1.12E-25	5.32E-25
zinc finger region:C2H2-type 7	5.85E-28	9.41759054	3.66E-25	1.22E-25	8.69E-25
zinc finger region:C2H2-type 6	1.08E-27	8.910779339	6.79E-25	1.70E-25	1.61E-24
IPR007087:Zinc finger, C2H2-type	1.99E-27	6.291521776	6.09E-25	6.09E-25	2.67E-24
GO:0045449~regulation of transcription	3.43E-27	3.028474929	2.18E-24	1.09E-24	5.10E-24
IPR015880:Zinc finger, C2H2-like	4.34E-27	6.188899715	1.33E-24	6.64E-25	5.82E-24
zinc finger region:C2H2-type 4	6.67E-27	7.914285714	4.17E-24	8.35E-25	9.91E-24
zinc finger region:C2H2-type 3	1.68E-26	7.478844485	1.05E-23	1.76E-24	2.50E-23
zinc finger region:C2H2-type 5	5.54E-25	7.894671623	3.47E-22	4.96E-23	8.23E-22
GO:0003677~DNA binding	6.08E-25	3.128194731	1.42E-22	1.42E-22	7.81E-22
zinc	8.28E-25	3.579936721	1.45E-22	2.90E-23	1.02E-21
IPR013087:Zinc finger, C2H2-type/integrase, DNA-binding	3.13E-24	6.743988341	9.59E-22	3.20E-22	4.20E-21
zinc finger region:C2H2-type 2	6.22E-24	7.152072891	3.89E-21	4.86E-22	9.23E-21
zinc finger region:C2H2-type 1	7.48E-24	7.649827213	4.68E-21	5.20E-22	1.11E-20
domain:KRAB	9.03E-24	10.35637789	5.65E-21	5.65E-22	1.34E-20
dna-binding	9.21E-24	3.813744151	1.61E-21	2.69E-22	1.13E-20
zinc finger region:C2H2-type 10	1.09E-23	10.29436365	6.84E-21	6.22E-22	1.62E-20
GO:0008270~zinc ion binding	6.44E-23	3.039830353	1.51E-20	7.53E-21	8.28E-20
IPR001909:Krueppel-associated box	6.81E-23	9.175623574	2.08E-20	5.21E-21	9.13E-20
SM00355:ZnF_C2H2	4.61E-22	4.539457175	4.06E-20	4.06E-20	4.99E-19
metal-binding	3.81E-21	2.876476746	6.66E-19	9.52E-20	4.67E-18
zinc finger region:C2H2-type 11	8.36E-20	10.00915543	5.24E-17	4.36E-18	1.24E-16
SM00349:KRAB	3.24E-19	6.730170497	2.85E-17	1.42E-17	3.51E-16
GO:0046914~transition metal ion binding	3.97E-19	2.586318585	9.29E-17	3.10E-17	5.11E-16
zinc finger region:C2H2-type 12	4.55E-17	10.0324389	2.85E-14	2.19E-15	6.77E-14
zinc finger region:C2H2-type 13	5.15E-17	11.57174445	3.22E-14	2.30E-15	7.65E-14
GO:0051252~regulation of RNA metabolic process	2.79E-13	2.73909249	1.77E-10	5.91E-11	4.15E-10
GO:0006355~regulation of transcription, DNA-dependent	1.55E-12	2.704305797	9.89E-10	2.47E-10	2.31E-09
GO:0046872~metal ion binding	2.41E-12	1.890185957	5.64E-10	1.41E-10	3.10E-09
zinc finger region:C2H2-type 14	3.56E-12	10.95005561	2.23E-09	1.48E-10	5.29E-09

GO:0043169~cation binding	4.28E-12	1.872546031	1.00E-09	2.00E-10	5.50E-09
GO:0043167~ion binding	1.04E-11	1.845170918	2.44E-09	4.07E-10	1.34E-08
zinc finger region:C2H2-type 15	8.94E-08	9.056147832	5.60E-05	3.50E-06	1.33E-04

Enrichment Score: 7.901711245751855

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0031981~nuclear lumen	5.67E-11	3.547569386	8.95E-09	8.95E-09	6.83E-08
GO:0043228~non-membrane-bounded organelle	4.58E-09	2.461864407	7.24E-07	3.62E-07	5.52E-06
GO:0043232~intracellular non-membrane-bounded organelle	4.58E-09	2.461864407	7.24E-07	3.62E-07	5.52E-06
GO:0070013~intracellular organelle lumen	1.05E-08	2.891498375	1.66E-06	5.53E-07	1.27E-05
GO:0043233~organelle lumen	1.84E-08	2.826360225	2.91E-06	7.27E-07	2.22E-05
GO:0031974~membrane-enclosed lumen	2.97E-08	2.771538583	4.69E-06	9.38E-07	3.58E-05
GO:0005730~nucleolus	4.94E-08	4.466419736	7.80E-06	1.30E-06	5.95E-05
GO:0005654~nucleoplasm	1.82E-06	3.534649632	2.87E-04	4.10E-05	0.002187243

Enrichment Score: 7.222013089662222

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
chromatin regulator	3.27E-10	8.122686738	5.73E-08	6.36E-09	4.01E-07
GO:0016568~chromatin modification	1.19E-07	5.312205488	7.56E-05	1.51E-05	1.77E-04
GO:0006325~chromatin organization	3.95E-07	4.303663519	2.52E-04	4.19E-05	5.88E-04
GO:0051276~chromosome organization	8.44E-07	3.707268694	5.37E-04	7.68E-05	0.001256098

Enrichment Score: 7.160509555746129

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
zinc finger region:C2H2-type 12	4.55E-17	10.0324389	2.85E-14	2.19E-15	6.77E-14
zinc finger region:C2H2-type 13	5.15E-17	11.57174445	3.22E-14	2.30E-15	7.65E-14
zinc finger region:C2H2-type 14	3.56E-12	10.95005561	2.23E-09	1.48E-10	5.29E-09
zinc finger region:C2H2-type 15	8.94E-08	9.056147832	5.60E-05	3.50E-06	1.33E-04
zinc finger region:C2H2-type 16	8.06E-07	9.818153799	5.05E-04	2.97E-05	0.001197551
zinc finger region:C2H2-type 19	1.62E-05	12.87070707	0.010116411	5.65E-04	0.02412557
zinc finger region:C2H2-type 17	1.76E-05	9.747179193	0.010960886	5.80E-04	0.026150343
zinc finger region:C2H2-type 18	4.65E-05	10.72558923	0.028719093	0.001455917	0.069124222
zinc finger region:C2H2-type 20	4.18E-04	14.04541446	0.230039257	0.010402149	0.618419055
zinc finger region:C2H2-type 21	0.002061302	15.55799756	0.725198611	0.046714641	3.018716537
zinc finger region:C2H2-type 22	0.02489012	12.1352381	0.99999986	0.325956132	31.23128575

Enrichment Score: 3.3107824634939407

Term	PValue	Fold	Bonferroni	Benjamini	FDR
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		Enrichment			
domain:SCAN box	2.42E-04	10.6449457	0.140325717	0.006552426	0.358158493
IPR003309:Transcriptional regulator SCAN	3.52E-04	9.796530432	0.102036025	0.013363077	0.470309493
SM00431:SCAN	0.001375961	7.185595568	0.11411481	0.029837776	1.480343682

Enrichment Score: 3.2230796608798102

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0005694~chromosome	3.03E-05	4.405249205	0.004776254	5.98E-04	0.036503859
GO:0044427~chromosomal part	1.56E-04	4.442120561	0.024344546	0.002734673	0.187769831
GO:0000228~nuclear chromosome	0.003629998	5.773261066	0.437060511	0.050894038	4.287106481
GO:0044454~nuclear chromosome part	0.007468967	6.388444622	0.694108852	0.087089455	8.63711235

Enrichment Score: 2.3130380263222956

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0044427~chromosomal part	1.56E-04	4.442120561	0.024344546	0.002734673	0.187769831
GO:0000775~chromosome, centromeric region	0.001127328	7.542486231	0.163240251	0.017663959	1.349882119
GO:0000793~condensed chromosome	0.048527052	4.833427869	0.999613955	0.353797258	45.08382775
GO:0000779~condensed chromosome, centromeric region	0.065578614	7.085365854	0.99997783	0.431094842	55.83564827

Enrichment Score: 1.9942403821216887

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0006730~one-carbon metabolic process	0.001932511	5.351265823	0.708349823	0.142749434	2.839237976
GO:0043414~biopolymer methylation	0.008414554	6.204366171	0.995404831	0.450135455	11.82301673
GO:0032259~methylation	0.011735525	5.632911392	0.999457726	0.495209975	16.11952629
methyltransferase	0.055256448	3.485359136	0.999952144	0.407581843	50.18492728

Enrichment Score: 1.9292045235495077

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
hsa00310:Lysine degradation	0.001367962	17.12121212	0.072524979	0.072524979	1.337401931
GO:0018024~histone-lysine N-methyltransferase activity	0.00533937	11.11558219	0.714284898	0.117746643	6.651022219
GO:0016278~lysine N-methyltransferase activity	0.00533937	11.11558219	0.714284898	0.117746643	6.651022219
GO:0016279~protein-lysine N-methyltransferase activity	0.00533937	11.11558219	0.714284898	0.117746643	6.651022219
GO:0042054~histone methyltransferase activity	0.009295436	9.120477696	0.887556518	0.166489278	11.31312122
domain:Post-SET	0.010547965	18.96130952	0.998690483	0.182213892	14.57419346
domain:SET	0.012385353	8.25526401	0.999590938	0.205037338	16.90061692
IPR003616:Post-SET zinc-binding region	0.013895822	16.42359514	0.986184186	0.378594396	17.10181228
IPR001214:SET	0.015422278	7.597309315	0.991399939	0.351025833	18.80536576

GO:0008276~protein methyltransferase activity	0.0182432	7.113972603	0.986543973	0.264891907	21.0767893
GO:0008170~N-methyltransferase activity	0.021285153	6.711294908	0.993490535	0.285114721	24.16344823
SM00508:PostSET	0.024737543	12.04643963	0.889670275	0.356514882	23.76250072
SM00317:SET	0.034063996	5.572502685	0.952635261	0.398490454	31.29841131
methyltransferase	0.055256448	3.485359136	0.999952144	0.407581843	50.18492728

Enrichment Score: 1.8300576056858162

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
IPR019786:Zinc finger, PHD-type, conserved site	6.82E-06	9.006487655	0.002085425	4.17E-04	0.009143667
IPR001965:Zinc finger, PHD-type	5.01E-05	8.272625698	0.015199861	0.002549505	0.067066893
IPR019787:Zinc finger, PHD-finger	2.98E-04	7.664344397	0.087026693	0.012922723	0.398015745
SM00249:PHD	3.21E-04	6.067836257	0.027866551	0.009376494	0.347264263
GO:0032452~histone demethylase activity	0.001211765	53.35479452	0.247026288	0.034844085	1.54666813
zinc finger region:PHD-type 2	0.003127356	13.48359788	0.859253173	0.067632572	4.546367355
zinc finger region:PHD-type 3	0.004111709	30.33809524	0.924168093	0.085098781	5.93698306
zinc finger region:PHD-type 1	0.004112952	12.25781626	0.924227289	0.082406291	5.938726185
GO:0032451~demethylase activity	0.005256475	26.67739726	0.708658534	0.128054894	6.550958771
IPR013129:Transcription factor jumonji domain:JmjC	0.026859363	11.63337989	0.999759156	0.473168162	30.57540997
IPR003347:Transcription factor jumonji/aspartyl beta-hydroxylase	0.043113413	9.006487655	0.999998609	0.52725392	44.60560967
SM00558:JmjC	0.074197614	6.606112054	0.998868616	0.492587686	56.61496085
zinc finger region:PHD-type dioxygenase	0.092751415	5.834249084	1	0.697231248	76.44812883
GO:0016702~oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	0.136146605	4.626022126	1	0.574172612	83.3740831
GO:0016701~oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	0.168029077	4.042029888	1	0.846118205	90.60419375
iron	0.172001719	3.981701084	1	0.84122322	91.16491495
GO:0005506~iron ion binding	0.529790313	1.428385779	1	0.93977053	99.99039599
oxidoreductase	0.672693158	1.154865682	1	0.995680773	99.99994187
GO:0055114~oxidation reduction	0.915406538	0.724359336	1	0.999256298	100
	0.942781936	0.669955033	1	0.999999091	100