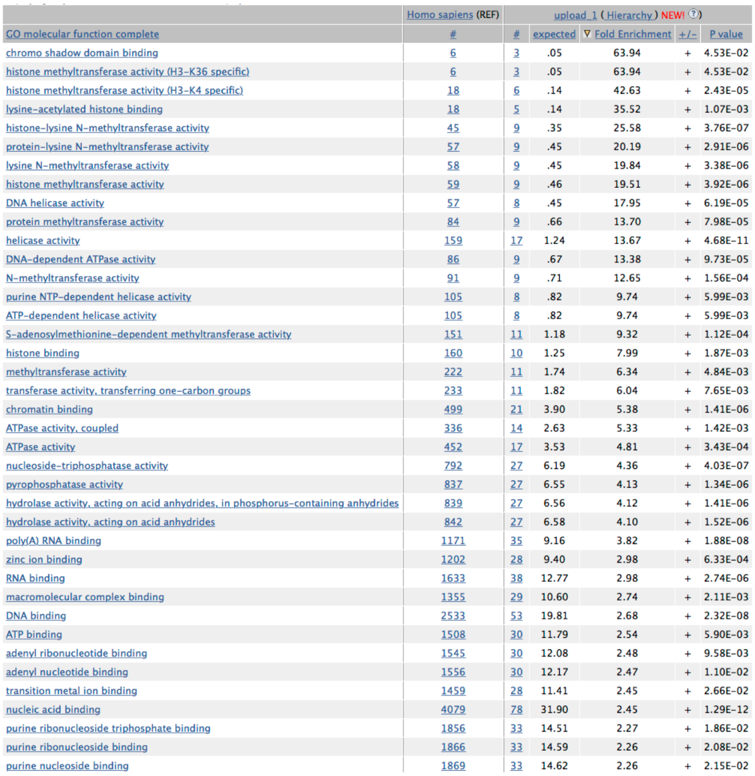
GENESDEV-2017-304782, Xiao_Supplemental Table S2.pdf

Cellular component

	Homo sapiens (REF)	upload_1 (Hierarchy) NEW! ?)				
GO cellular component complete	#	#	expected	▽ Fold Enrichment	+/-	P value
pericentric heterochromatin	18	4	.14	28.42	+	1.84E-02
nuclear transcriptional repressor complex	32	6	.25	23.98	+	3.30E-04
SWI/SNF superfamily-type complex	76	9	.59	15.14	+	1.60E-05
heterochromatin	72	6	.56	10.66	+	3.31E-02
histone methyltransferase complex	72	6	.56	10.66	+	3.31E-02
transcriptional repressor complex	87	7	.68	10.29	+	8.68E-03
nuclear speck	198	13	1.55	8.40	+	1.00E-05
nuclear body	355	17	2.78	6.12	+	5.07E-06
nucleoplasm part	739	30	5.78	5.19	+	2.02E-10
chromosome	905	31	7.08	4.38	+	5.91E-09
chromatin	442	15	3.46	4.34	+	3.23E-03
nucleolus	879	22	6.87	3.20	+	2.17E-03
chromosomal part	793	19	6.20	3.06	+	2.14E-02
nucleoplasm	2943	67	23.01	2.91	+	4.90E-14
nuclear lumen	3532	77	27.62	2.79	+	5.25E-16
nuclear part	3929	83	30.72	2.70	+	5.16E-17
intracellular organelle lumen	4397	78	34.38	2.27	+	4.27E-11
organelle lumen	4398	78	34.39	2.27	+	4.32E-11
membrane-enclosed lumen	4398	78	34.39	2.27	+	4.32E-11
intracellular non-membrane-bounded organelle	3890	67	30.42	2.20	+	3.88E-08
non-membrane-bounded organelle	3890	67	30.42	2.20	+	3.88E-08
nucleus	7006	106	54.79	1.93	+	4.20E-13
macromolecular complex	4908	66	38.38	1.72	+	1.57E-03
intracellular organelle part	8198	98	64.11	1.53	+	9.35E-05
organelle part	8402	99	65.70	1.51	+	1.62E-04
intracellular membrane-bounded organelle	10464	113	81.83	1.38	+	8.25E-04
membrane-bounded organelle	12169	128	95.16	1.35	+	7.11E-05
intracellular organelle	12048	125	94.21	1.33	+	5.17E-04
organelle	13117	134	102.57	1.31	+	1.00E-04
intracellular part	13838	133	108.21	1.23	+	1.82E-02
Unclassified	2678	8	20.94	.38	-	0.00E00

Molecular function



	Homo sapiens (REF)	upload_1 (Hierarchy) NEW! ?)				
GO molecular function complete	#	#	expected	▽ Fold Enrichment	+/-	P value
chromo shadow domain binding	6	3	.05	63.94	+	4.53E-02
histone methyltransferase activity (H3-K36 specific)	6	3	.05	63.94	+	4.53E-02
histone methyltransferase activity (H3-K4 specific)	18	6	.14	42.63	+	2.43E-05
lysine-acetylated histone binding	18	5	.14	35.52	+	1.07E-03
histone-lysine N-methyltransferase activity	45	9	.35	25.58	+	3.76E-07
protein-lysine N-methyltransferase activity	57	9	.45	20.19	+	2.91E-06
lysine N-methyltransferase activity	58	9	.45	19.84	+	3.38E-06
histone methyltransferase activity	59	9	.46	19.51	+	3.92E-06
DNA helicase activity	57	8	.45	17.95	+	6.19E-05
protein methyltransferase activity	84	9	.66	13.70	+	7.98E-05
helicase activity	159	17	1.24	13.67	+	4.68E-11
DNA-dependent ATPase activity	86	9	.67	13.38	+	9.73E-05
N-methyltransferase activity	91	9	.71	12.65	+	1.56E-04
purine NTP-dependent helicase activity	105	8	.82	9.74	+	5.99E-03
ATP-dependent helicase activity	105	8	.82	9.74	+	5.99E-03
S-adenosylmethionine-dependent methyltransferase activity	151	11	1.18	9.32	+	1.12E-04
histone binding	160	10	1.25	7.99	+	1.87E-03
methyltransferase activity	222	11	1.74	6.34	+	4.84E-03
transferase activity, transferring one-carbon groups	233	11	1.82	6.04	+	7.65E-03
chromatin binding	499	21	3.90	5.38	+	1.41E-06
ATPase activity, coupled	336	14	2.63	5.33	+	1.42E-03
ATPase activity	452	17	3.53	4.81	+	3.43E-04
nucleoside-triphosphatase activity	792	27	6.19	4.36	+	4.03E-07
pyrophosphatase activity	837	27	6.55	4.13	+	1.34E-06
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	839	27	6.56	4.12	+	1.41E-06
hydrolase activity, acting on acid anhydrides	842	27	6.58	4.10	+	1.52E-06
poly(A) RNA binding	1171	35	9.16	3.82	+	1.88E-08
zinc ion binding	1202	28	9.40	2.98	+	6.33E-04
RNA binding	1633	38	12.77	2.98	+	2.74E-06
macromolecular complex binding	1355	29	10.60	2.74	+	2.11E-03
DNA binding	2533	53	19.81	2.68	+	2.32E-08
ATP binding	1508	30	11.79	2.54	+	5.90E-03
adenyl ribonucleotide binding	1545	30	12.08	2.48	+	9.58E-03
adenyl nucleotide binding	1556	30	12.17	2.47	+	1.10E-02
transition metal ion binding	1459	28	11.41	2.45	+	2.66E-02
nucleic acid binding	4079	78	31.90	2.45	+	1.29E-12
purine ribonucleoside triphosphate binding	1856	33	14.51	2.27	+	1.86E-02
purine ribonucleoside binding	1866	33	14.59	2.26	+	2.08E-02
purine nucleoside binding	1869	33	14.62	2.26	+	2.15E-02