Supplementary Information

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Table S1. All common enrichment terms in all ZnHDACs

Term ID Enrichment Component	Term description
GO:0000118	histone deacetylase complex
GO:0000790	nuclear chromatin
GO:0017053	transcriptional repressor complex
GO:0044451	nucleoplasm part
GO:1902494	catalytic complex
GO:0005654	nucleoplasm
GO:0032991	protein-containing complex
Term ID Enrichment Function	**Term description**
GO:0003677	DNA binding
GO:0003676	nucleic acid binding
GO:0003682	chromatin binding
GO:0003714	transcription corepressor activity
GO:0042826	histone deacetylase binding
GO:0044212	transcription regulatory region DNA binding

GO:0140110	transcription regulator activity
GO:0001085	RNA polymerase II transcription factor binding
GO:0061629	RNA polymerase II-specific DNA-binding transcription factor binding
GO:0003700	DNA-binding transcription factor activity
GO:0008134	transcription factor binding
GO:0000977	RNA polymerase II regulatory region sequence-specific DNA binding
GO:0000978	RNA polymerase II proximal promoter sequence-specific DNA binding
GO:0000981	DNA-binding transcription factor activity, RNA polymerase II-specific
GO:0032041	NAD-dependent histone deacetylase activity (H3-K14 specific)
GO:0033613	activating transcription factor binding
GO:0005515	protein binding
GO:0001102	RNA polymerase II activating transcription factor binding
GO:0047485	protein N-terminus binding
GO:0016922	nuclear receptor binding

Term ID Enrichment pathway	**Term description**
hsa04330	Notch signaling pathway
hsa04919	Thyroid hormone signaling pathway
hsa05202	Transcriptional misregulation in cancer
hsa05034	Alcoholism
hsa05169	Epstein-Barr virus infection
hsa05203	Viral carcinogenesis
hsa05220	Chronic myeloid leukemia
hsa05165	Human papillomavirus infection
hsa04110	Cell cycle
hsa05206	MicroRNAs in cancer

Term ID Enrichment biological Processes	**Term description**
GO:0006325	chromatin organization
GO:0016575	histone deacetylation
GO:0016570	histone modification

GO:0051253	negative regulation of RNA metabolic process
GO:0006351	transcription, DNA-templated
GO:0006355	regulation of transcription, DNA-templated
GO:0040029	regulation of gene expression, epigenetic
GO:0051252	regulation of RNA metabolic process
GO:0006357	regulation of transcription by RNA polymerase II
GO:0000122	negative regulation of transcription by RNA polymerase II
GO:0016070	RNA metabolic process
GO:0010605	negative regulation of macromolecule metabolic process
GO:0048523	negative regulation of cellular process
GO:0018205	peptidyl-lysine modification
GO:0048511	rhythmic process
GO:0006338	chromatin remodeling
GO:0007623	circadian rhythm
GO:1903799	negative regulation of production of miRNAs involved in gene silencing by miRNA
GO:0010604	positive regulation of macromolecule metabolic process
GO:0070932	histone H3 deacetylation
GO:0048518	positive regulation of biological process
GO:0010628	positive regulation of gene expression
GO:1903508	positive regulation of nucleic acid-templated transcription
GO:0051254	positive regulation of RNA metabolic process
GO:0048522	positive regulation of cellular process
GO:0045893	positive regulation of transcription, DNA-templated
GO:0045652	regulation of megakaryocyte differentiation

Table S2. Unique enrichment terms for each ZnHDACs and involvement of unique genes for each subtypes.

Term	PValue	Genes	Fold Enrichment	FDR
HDAC1				
GO:0008285~stem cell proliferation	0.023583	HDAC1, JARID2	42.40404	0.004325
GO:0045892~negative regulation of transcription	0.029717	HDAC1, JARID2	33.6513	0.008425
HDAC2				
GO:0006338~chromatin remodeling	1.30E-07	HDAC2, CHRAC1, BAZ1A, BPTF	195.2558	7.91E-06
GO:0045893~positive regulation of transcription, DNA-templated	0.08922	HDAC2, BPTF	16.30291	0.011
HDAC 3				
GO:0003714~transcription corepressor activity	0.023907	HDAC3, DMAP1	55.43842	0.00406416
GO:0043968~histone H2A acetylation	0.0001786	HDAC3, DMAP1	746.311	0.023
HDAC4				
hsa05203:Viral carcinogenesis	0.001307	HDAC4, SRF, YWHAG, YWHAH	14.91382	0.0032687
GO:0042826~histone deacetylase binding	0.001576	HDAC4, MYOCD, SRF	45.13636	0.0044841
GO:0051091~positive regulation of apoptosis	0.001687	HDAC4, MYOCD, SRF	43.61558	0.0097237
GO:0010832~negative regulation of differentiation	0.00949	HDAC4, MYOCD	190.8182	0.00206885
GO:0008134~transcription factor binding	0.01161	HDAC4, MYOCD, SRF	16.21095	0.0136385
GO:0005515~protein binding	0.014861	HDAC4, MYOCD, XRCC6, TADA2A, SRF, RFX5, FOXO1, YWHAG, ARNTL, YWHAH	1.746883	0.0140115

GO:0003682~chromatin binding	0.021294	HDAC4, TADA2A, FOXO1	11.7747	0.0156154
GO:0008285~negative regulation of cell proliferation	0.022025	HDAC4, MYOCD, SRF	11.56474	0.0300094
HDAC 5				
GO:0000122~negative regulation of transcription from RNA polymerase II promoter	4.58E-07	HDAC5, KAT5, NR1D1, SUDS3, PPARA, NKX2-5, SAP30	16.32556	8.33E-05
GO:0044212~transcription regulatory region DNA binding	1.57E-04	HDAC5, GATA4, NR1D1, NKX2-5	31.70141	0.004448
GO:0045944~positive regulation of transcription from RNA polymerase II promoter	0.001151	HDAC5, KAT5, GATA4, PPARA, NKX2-5	8.558614	0.041892
GO:0010871~negative regulation of receptor biosynthetic process	0.001607	NR1D1, PPARA	1119.467	0.046514
GO:0071222~cellular response to lipopolysaccharide	0.058973	HDAC5, NR1D1	29.72035	0.0564902
HDAC 6				
GO:0031625~ubiquitin protein ligase binding	3.64E-05	HSPA8, VCP, NPLOC4, DERL1, HDAC6	22.62262	0.001091
GO:0070842~aggresome assembly	0.003568	VCP, HDAC6	516.6769	0.053202
GO:0048156~tau protein binding	0.007794	HSP90AA1, HDAC6	236.0979	0.02598
GO:0098779~mitophagy in response to mitochondrial depolarization	0.008545	CDC37, HDAC6	215.2821	0.0582431
GO:0016234~inclusion	0.011792	HSP90AB1, HDAC6	155.7607	0.0573967

body				
GO:0031593~polyubiquitin binding	0.016233	VCP, HDAC6	112.9164	0.04638
GO:0051879~Hsp90 protein binding	0.019031	CDC37, HDAC6	96.18803	0.051904
GO:0043234~protein complex	0.028969	STIP1, HSP90AA1, HDAC6	10.20762	0.142778
GO:0048471~perinuclear region of cytoplasm	0.061036	VCP, HSP90AA1, HDAC6	6.772204	0.233973
GO:0031647~regulation of protein stability	0.048908	HSPA8, HDAC6	36.90549	0.000267366
HDAC 7				
GO:0030914~STAGA complex	0.00307	ATXN7, TAF10, HDAC7	520.68	0.01841
GO:0005654~nucleoplasm translocation	5.44E-04	KDM1A, ATXN7,TAF10,RCOR1,HDAC7	6.545	0.0079
HDAC 8				
GO:0005737~cytoplasm	0.001171	UPF1, CREBBP, MTA1, SUMO1, UPF3B, UPF3A, ARID4B, HDAC8, MTA3, SMG5	2.6845	0.010539
GO:0032204~regulation of telomere maintenance	0.003568	HDAC8, SMG5	516.6769	0.075651
GO:0006333~chromatin assembly or disassembly	0.004993	MTA2, HDAC8	369.0549	0.088202
GO:0000118~histone deacetylase complex	0.023456	MTA2, HDAC8	77.88034	0.0105553
HDAC9				
GO:0004407~histone deacetylase activity	7.76E-05	MBD3, RBBP7, HDAC9	185.5055	0.002715
GO:0035097~histone methyltransferase complex	0.00755	KMT2D, HDAC9	226.3851	0.035861
GO:0030183~B cell differentiation	0.023356	TCF3, HDAC9	72.69264	0.0206864

GO:0005667~transcription factor complex	0.041892	TCF3, HDAC9	26.97853	0.0195992
GO:0007507~heart development	0.043642	MBD3, HDAC9	26.21702	0.0493223
HDAC11				
hsa05034:Alcoholism	6.58E-04	HDAC11, HIST2H2BE, HIST2H2AC	38.86441	0.001317
GO:0070062~extracellular exosome	0.023785	HDAC11, HIST2H2BE, HIST2H2AC	6.483102	0.0118925
GO:0046982~protein heterodimerization activity	0.044334	HIST2H2BE, HIST2H2AC	24.20215	0.0326006