

TABLE 3 Reactome pathways enrichments of histone H1 subtypes-partner proteins interaction network derived from STRING database

Histone H1	Pathway	Description	Count in gene set	False discovery rate
H1.1	HSA-74160	Gene expression (Transcription)	42 of 1366	3.52e-15
	HSA-2559583	Cellular senescence	19 of 161	3.52e-15
	HSA-73857	RNA polymerase II Transcription	39 of 1233	1.74e-14
	HSA-2262752	Cellular responses to stress	23 of 384	2.50e-13
	HSA-453279	Mitotic G1-G1/S phases	15 of 145	1.26e-11
H1.2	HSA-597592	Post-translational protein modification	33 of 1366	1.06e-13
	HSA-392499	Metabolism of proteins	38 of 1948	1.14e-13
	HSA-8951664	Neddylation	16 of 227	1.53e-12
	HSA-3214841	PKMTs methylate histone lysines	7 of 47	4.54e-07
	HSA-453279	E3 ubiquitin ligases ubiquitinate target proteins	7 of 53	7.76e-07
H1.3	HSA-6791312	TP53 regulates transcription of cell cycle genes	4 of 49	0.00045
	HSA-8849470	PTK6 regulates cell cycle	2 of 6	0.0049
	HSA-8848021	Signaling by PTK6	3 of 51	0.0049
	HSA-69278	Cell cycle Mitotic	6 of 483	0.0049
	HSA-69242	S-phase	4 of 156	0.0049
H1.4	HSA-8953854	Metabolism of RNA	17 of 625	5.54 e-06
	HSA-8868773	rRNA processing of the nucleus and cytosol	8 of 189	0.00079
	HSA-6790901	rRNA modification of the nucleus and cytosol	5 of 60	0.0012
	HSA-74160	Gene expression (Transcription)	19 of 1366	0.0017
	HSA-8864260	Transcriptional regulation of the AP-2 (TFAP2 family)	19 of 1233	7.34 e-09
H1.5	HSA-73857	RNA polymerase II Transcription	19 of 1233	7.34 e-09
	HSA-6791312	TP53 regulates transcription of cell cycle genes	7 of 49	7.34 e-09
	HSA-212436	Genetic transcription pathway	18 of 1112	7.34 e-09
	HSA-2559583	Cellular senescence	9 of 161	1.55 e-08
	HSA-69273	Cyclin A/B1/B2 associated events during G2/M	5 of 25	4.89 e-07