

Supplementary Table S4: Significant GO terms (p < 0.01) related to the 5hmC-containing probes in Fantom5 Enhancer Regions

Category = Gene ontology category

Over_represented pvalue = p-value of the overrepresented gene ontology term

Number DE In Cat = The number of differentially expressed genes in the gene ontology category

Number In Cat = The total number of genes in the gene ontology category

GO term = Specific gene ontology term in the category

Category	over_represented pvalue	number DE In Cat	number In Cat	GO term
GO:0009306	8.64E-05	141	164	protein secretion
GO:0002252	1.88E-04	213	256	immune effector process
GO:0065003	2.04E-04	347	431	macromolecular complex assembly
GO:0006897	2.28E-04	199	236	endocytosis
GO:0009611	3.02E-04	324	396	response to wounding
GO:0050708	3.02E-04	114	132	regulation of protein secretion
GO:0098602	3.35E-04	269	326	single organism cell adhesion
GO:0001775	3.37E-04	307	375	cell activation
GO:0016337	4.21E-04	248	300	single organismal cell-cell adhesion
GO:0034622	4.93E-04	176	212	cellular macromolecular complex assembly
GO:0022607	4.98E-04	580	737	cellular component assembly
GO:0006461	5.54E-04	312	387	protein complex assembly
GO:0070271	5.54E-04	312	387	protein complex biogenesis
GO:0022610	7.15E-04	466	584	biological adhesion
GO:0007155	7.94E-04	465	583	cell adhesion
GO:0030155	8.08E-04	230	278	regulation of cell adhesion
GO:0098609	8.18E-04	285	350	cell-cell adhesion
GO:0044085	8.28E-04	595	760	cellular component biogenesis
GO:0051234	1.02E-03	1067	1399	establishment of localization
GO:0009617	1.89E-03	132	157	response to bacterium
GO:0045321	2.09E-03	232	284	leukocyte activation
GO:0060627	2.12E-03	126	150	regulation of vesicle-mediated transport
GO:0016323	2.12E-03	72	83	basolateral plasma membrane
GO:0016020	2.40E-03	1880	2506	membrane
GO:0009064	2.46E-03	18	18	glutamine family amino acid metabolic process
GO:0006810	2.67E-03	1034	1361	transport
GO:0016192	2.77E-03	382	482	vesicle-mediated transport
GO:0071702	2.80E-03	575	747	organic substance transport
GO:0051179	2.93E-03	1355	1788	localization
GO:0002521	2.96E-03	167	201	leukocyte differentiation
GO:0072593	3.14E-03	67	76	reactive oxygen species metabolic process
GO:0031099	3.42E-03	58	65	regeneration
GO:0071216	3.42E-03	59	66	cellular response to biotic stimulus
GO:0032940	3.50E-03	261	327	secretion by cell
GO:0010876	3.52E-03	87	102	lipid localization
GO:0071219	3.59E-03	55	61	cellular response to molecule of bacterial origin
GO:0006909	3.81E-03	83	96	phagocytosis
GO:0002274	3.84E-03	57	64	myeloid leukocyte activation
GO:0030097	4.03E-03	233	286	hemopoiesis
GO:0071222	4.21E-03	54	60	cellular response to lipopolysaccharide
GO:0044765	4.28E-03	911	1200	single-organism transport
GO:0032101	4.51E-03	251	312	regulation of response to external stimulus
GO:1902578	4.58E-03	955	1259	single-organism localization
GO:0019439	4.79E-03	73	86	aromatic compound catabolic process
GO:0044425	4.94E-03	1382	1839	membrane part
GO:1901564	4.95E-03	421	542	organonitrogen compound metabolic process
GO:2000377	5.39E-03	44	49	regulation of reactive oxygen species metabolic process
GO:0006890	5.43E-03	15	15	retrograde vesicle-mediated transport Golgi to ER
GO:0001817	5.48E-03	156	191	regulation of cytokine production
GO:0097529	5.55E-03	53	60	myeloid leukocyte migration
GO:0002433	5.56E-03	38	41	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis
GO:0038094	5.56E-03	38	41	Fc-gamma receptor signaling pathway
GO:0038096	5.56E-03	38	41	Fc-gamma receptor signaling pathway involved in phagocytosis
GO:0043623	5.64E-03	130	157	cellular protein complex assembly

GO:1903530	5.68E-03	168	207	regulation of secretion by cell
GO:0007169	5.69E-03	311	390	transmembrane receptor protein tyrosine kinase signaling pathway
GO:0042060	5.77E-03	232	286	wound healing
GO:0051345	5.78E-03	271	335	positive regulation of hydrolase activity
GO:0061695	6.06E-03	48	54	transferase complex transferring phosphorus-containing groups
GO:0002520	6.09E-03	250	309	immune system development
GO:0000784	6.20E-03	15	15	nuclear chromosome telomeric region
GO:0033036	6.33E-03	635	827	macromolecule localization
GO:0034655	6.34E-03	57	66	nucleobase-containing compound catabolic process
GO:0002429	6.50E-03	116	138	immune response-activating cell surface receptor signaling pathway
GO:0002444	6.73E-03	29	31	myeloid leukocyte mediated immunity
GO:0044281	6.78E-03	523	678	small molecule metabolic process
GO:0005070	6.92E-03	30	32	SH3/SH2 adaptor activity
GO:0043207	7.06E-03	210	260	response to external biotic stimulus
GO:0051707	7.06E-03	210	260	response to other organism
GO:0007167	7.06E-03	394	499	enzyme linked receptor protein signaling pathway
GO:0043933	7.27E-03	525	677	macromolecular complex subunit organization
GO:0010811	7.35E-03	41	45	positive regulation of cell-substrate adhesion
GO:0099568	7.48E-03	94	111	cytoplasmic region
GO:0002250	7.51E-03	106	128	adaptive immune response
GO:0031102	7.59E-03	18	18	neuron projection regeneration
GO:0006869	8.13E-03	78	92	lipid transport
GO:1901361	8.21E-03	77	92	organic cyclic compound catabolic process
GO:0009607	8.27E-03	217	270	response to biotic stimulus
GO:0046649	8.28E-03	198	244	lymphocyte activation
GO:0002431	8.33E-03	41	45	Fc receptor mediated stimulatory signaling pathway
GO:0006954	8.39E-03	168	207	inflammatory response
GO:0019637	8.44E-03	232	291	organophosphate metabolic process
GO:0015711	8.60E-03	107	130	organic anion transport
GO:0002237	8.81E-03	100	119	response to molecule of bacterial origin
GO:0048534	8.89E-03	242	300	hematopoietic or lymphoid organ development
GO:0050778	8.91E-03	190	235	positive regulation of immune response
GO:0051046	9.24E-03	181	225	regulation of secretion
GO:0002263	9.64E-03	69	80	cell activation involved in immune response
GO:0006950	9.88E-03	909	1192	response to stress