

Table S2. Major GO categories with GH responsive genes.

Categories	GOID	GO Name	Changed	Measured	In GO	Changed (%)	Present (%)	Z Score	PermuteP
up 6 hr	10001	glial cell differentiation	3	5	9	60.00	55.56	3.381	0.013
up 6 hr	7229	integrin-mediated signaling pathway	7	30	49	23.33	61.22	2.585	0.015
up 6 hr	6164	purine nucleotide biosynthesis	3	6	10	50.00	60.00	2.404	0.025
up 6 hr, 24 hr, comb	16338	calcium-independent cell-cell adhesion	4	10	20	40.00	50.00	3.287	0.011
up 6 hr, comb	5975	carbohydrate metabolism	9	74	177	12.16	41.81	2.868	0.013
up 6 hr, down 24 hr	16192	vesicle-mediated transport	6	31	48	19.35	64.58	2.284	0.027
down 6 hr	6338	chromatin remodeling	3	18	27	16.67	66.67	2.564	0.026
down 6 hr	7368	determination of left/right symmetry	3	10	23	30.00	43.48	2.952	0.027
down 6 hr	7186	G-protein coupled receptor protein signaling pathway	12	87	1360	13.79	6.40	2.267	0.029
down 6 hr	7507	heart development	7	39	68	17.95	57.35	2.259	0.032
down 6 hr	184	mRNA catabolism, nonsense-mediated decay	3	8	10	37.50	80.00	3.49	0.011
down 6 hr	42475	odontogenesis (sensu Vertebrata)	4	11	16	36.36	68.75	5.169	0.001
up 24 hr	6865	amino acid transport	7	17	42	41.18	40.48	2.613	0.016
up 24 hr	51085	chaperone cofactor dependent protein folding	4	9	10	44.44	90.00	2.906	0.023
up 24 hr	1755	neural crest cell migration	3	6	9	50.00	66.67	2.784	0.015
up 24 hr	8654	phospholipid biosynthesis	4	14	20	28.57	70.00	2.752	0.017
up 24 hr	42102	positive regulation of T cell proliferation	3	6	11	50.00	54.55	2.19	0.041
up 24 hr	8360	regulation of cell shape	6	20	34	30.00	58.82	2.377	0.033
up 24 hr	6885	regulation of pH	4	9	16	44.44	56.25	2.906	0.01
up 24 hr, comb	7411	axon guidance	6	22	44	27.27	50.00	2.585	0.015
up 24 hr, comb	1568	blood vessel development	3	9	15	33.33	60.00	2.582	0.013
up 24 hr, comb	7155	cell adhesion	20	114	261	17.54	43.68	2.352	0.021
down 24 hr	30183	B cell differentiation	3	7	15	42.86	46.67	2.673	0.009
down 24 hr	6888	ER to Golgi transport	9	32	52	28.13	61.54	2.736	0.009
down 24 hr	30520	estrogen receptor signaling pathway	3	6	7	50.00	85.71	2.815	0.036
down 24 hr	82	G1/S transition of mitotic cell cycle	5	14	19	35.71	73.68	2.673	0.032
down 24 hr	6406	mRNA export from nucleus	6	13	16	46.15	81.25	3.273	0.005
down 24 hr	7405	neuroblast proliferation	3	4	8	75.00	50.00	3.822	0.008
down 24 hr	6457	protein folding	22	114	183	19.30	62.30	2.036	0.028
down 24 hr	43087	regulation of GTPase activity	5	16	29	31.25	55.17	2.313	0.045
up comb	7409	axonogenesis	5	14	37	35.71	37.84	2.797	0.002
up comb	8643	carbohydrate transport	3	9	12	33.33	75.00	2.098	0.048
up comb	30154	cell differentiation	22	123	228	17.89	53.95	2.001	0.048
up comb	16477	cell migration	3	13	25	23.08	52.00	2.266	0.032
up comb	7275	development	22	136	300	16.18	45.33	2.948	0.008
up comb	6006	glucose metabolism	3	9	41	33.33	21.95	2.051	0.043
up comb	6096	glycolysis	6	23	88	26.09	26.14	2.098	0.038
up comb	6811	ion transport	19	89	258	21.35	34.50	1.968	0.05
up comb	7612	learning	3	8	11	37.50	72.73	2.596	0.04
up comb	16044	membrane organization and biogenesis	3	5	10	60.00	50.00	2.489	0.018

up comb	7517 muscle development	14	34	72	41.18	47.22	2.903	0.009
up comb	6468 protein amino acid phosphorylation	51	267	480	19.10	55.63	1.998	0.05
up comb	8360 regulation of cell shape	8	20	34	40.00	58.82	3.303	0.001
up comb	7169 transmembrane receptor protein tyrosine kinase signaling pathway	9	35	66	25.71	53.03	2.272	0.029
down comb	7049 cell cycle	14	166	219	8.43	75.80	3.157	0.005
down comb	51301 cell division	9	90	123	10.00	73.17	3.622	0.002
down comb	6397 mRNA processing	3	40	56	7.50	71.43	3.657	0
down comb	398 nuclear mRNA splicing, via spliceosome	6	68	92	8.82	73.91	3.189	0.003
down comb	6412 protein biosynthesis	12	162	443	7.41	36.57	3.299	0.002

up 6 hr = genes significantly up-regulated by GH at 6 hours.

down 6 hr = genes significantly up-regulated by GH at 6 hours.

up 24 hr = genes significantly up-regulated by GH at 6 hours.

down 24 hr = genes significantly up-regulated by GH at 6 hours.

up or down comb = combined analysis of the data at 6 and 24 hours.