

Depleted 1		p-value 0.950.05		Enriched 1e-50		Differentially expressed in the trout			Correlated with mouse			Testis Specific			
		Somatic	Gonia	Meiotic/ p-meiotic	Somatic	Gonia	Meiotic/ p-meiotic	Somatic	Gonia	Meiotic/ p-meiotic					
Biological Process						4944	557	215	424	182	49	126	31	11	49
antigen processing and presentation						24	11 / 3	1 / 1	0 / 2	3 / 1	0 / 0	0 / 1	0 / 0	0 / 0	0 / 0
C21-steroid hormone metabolic process						10	6 / 1	1 / 0	1 / 1	1 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
positive regulation of cyclic nucleotide biosynthetic process						5	4 / 1	0 / 0	0 / 0	2 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
water homeostasis						3	3 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
glycosphingolipid catabolic process						3	3 / 0	0 / 0	0 / 0	1 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
cell-substrate junction assembly						3	3 / 0	0 / 0	0 / 0	2 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
oxygen transport						10	8 / 1	0 / 0	0 / 1	7 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
nitric oxide transport						4	4 / 1	0 / 0	0 / 0	4 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
skin morphogenesis						3	3 / 0	0 / 0	0 / 0	3 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
blood circulation						68	20 / 8	3 / 3	4 / 6	10 / 3	2 / 1	0 / 2	1 / 0	0 / 0	0 / 1
protein heterooligomerization						7	4 / 1	0 / 0	0 / 1	4 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
odontogenesis						16	6 / 2	0 / 1	0 / 1	6 / 1	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
erythrocyte maturation						8	4 / 1	1 / 0	0 / 1	4 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
cell junction assembly						6	4 / 1	0 / 0	0 / 1	3 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
transforming growth factor beta receptor signaling pathway						37	9 / 4	0 / 2	4 / 3	8 / 1	0 / 0	1 / 1	1 / 0	0 / 0	0 / 0
regulation of blood pressure						37	11 / 4	1 / 2	0 / 3	8 / 1	1 / 0	0 / 1	0 / 0	0 / 0	0 / 0
positive regulation of nitric oxide biosynthetic process						11	4 / 1	2 / 1	2 / 1	4 / 0	1 / 0	1 / 0	0 / 0	0 / 0	0 / 0
positive regulation of muscle contraction						7	3 / 1	0 / 0	1 / 1	3 / 0	0 / 0	1 / 0	0 / 0	0 / 0	0 / 0
glucose catabolic process						51	16 / 6	1 / 2	4 / 4	9 / 2	0 / 1	1 / 1	0 / 0	0 / 0	0 / 1
collagen catabolic process						8	4 / 1	0 / 0	0 / 1	3 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
negative regulation of cellular protein metabolic process						45	13 / 5	2 / 2	7 / 4	8 / 2	0 / 0	1 / 1	0 / 0	0 / 0	0 / 0
negative regulation of cellular component organization						28	10 / 3	0 / 1	2 / 2	6 / 1	0 / 0	0 / 1	0 / 0	0 / 0	0 / 0
system development						765	124 / 86	20 / 33	52 / 66	51 / 28	6 / 8	20 / 20	9 / 5	0 / 2	5 / 8
nucleotide-excision repair, DNA gap filling						10	0 / 1	5 / 0	4 / 1	0 / 0	1 / 0	0 / 0	0 / 0	0 / 0	0 / 0
DNA replication initiation						24	0 / 3	8 / 1	3 / 2	0 / 1	1 / 0	0 / 1	0 / 0	0 / 0	0 / 0
somatic hypermutation of immunoglobulin genes						4	0 / 1	3 / 0	0 / 0	0 / 0	1 / 0	0 / 0	0 / 0	0 / 0	0 / 0
nuclear mRNA splicing, via spliceosome						98	4 / 11	18 / 4	11 / 8	2 / 4	3 / 1	1 / 3	1 / 1	1 / 0	1 / 1
DNA unwinding during replication						8	0 / 1	4 / 0	0 / 1	0 / 0	1 / 0	0 / 0	0 / 0	0 / 0	0 / 0
rRNA processing						62	1 / 7	11 / 3	4 / 5	0 / 2	2 / 1	1 / 2	0 / 0	1 / 0	0 / 1
response to unfolded protein						37	1 / 4	8 / 2	8 / 3	1 / 1	1 / 0	4 / 1	0 / 0	1 / 0	1 / 0
RNA transport						38	2 / 4	8 / 2	3 / 3	2 / 1	1 / 0	1 / 1	1 / 0	1 / 0	0 / 0
somatic recombination of immunoglobulin gene segments						7	1 / 1	3 / 0	0 / 1	0 / 0	1 / 0	0 / 0	0 / 0	0 / 0	0 / 0
base-excision repair						12	0 / 1	4 / 1	0 / 1	0 / 0	1 / 0	0 / 0	0 / 0	0 / 0	0 / 0
response to ionizing radiation						15	0 / 2	4 / 1	2 / 1	0 / 1	3 / 0	0 / 0	0 / 0	0 / 0	0 / 0
response to UV						19	0 / 2	5 / 1	1 / 2	0 / 1	3 / 0	1 / 1	0 / 0	0 / 0	0 / 0
DNA-dependent DNA replication						47	0 / 5	15 / 2	6 / 4	0 / 2	4 / 1	0 / 1	0 / 0	0 / 0	0 / 1
cell cycle						293	22 / 33	32 / 13	56 / 25	11 / 11	7 / 3	21 / 8	0 / 2	3 / 1	8 / 3
cell division						90	5 / 10	6 / 4	31 / 8	3 / 3	0 / 1	6 / 2	0 / 1	0 / 0	3 / 1
regulation of cyclin-dependent protein kinase activity						23	0 / 3	1 / 1	9 / 2	0 / 1	1 / 0	2 / 1	0 / 0	0 / 0	1 / 0
chromosome condensation						6	0 / 1	0 / 0	4 / 1	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0	1 / 0
protein folding						105	11 / 12	11 / 5	23 / 9	3 / 4	3 / 1	7 / 3	0 / 1	1 / 0	2 / 1
meiosis						37	1 / 4	7 / 2	14 / 3	0 / 1	0 / 0	5 / 1	0 / 0	1 / 0	4 / 0
mitotic sister chromatid segregation						9	0 / 1	1 / 0	6 / 1	0 / 0	0 / 0	1 / 0	0 / 0	0 / 0	3 / 0
ciliary or flagellar motility						27	3 / 3	1 / 1	10 / 2	3 / 1	0 / 0	6 / 1	0 / 0	0 / 0	2 / 0
M phase						101	4 / 11	9 / 4	34 / 9	1 / 4	0 / 1	11 / 3	0 / 1	1 / 0	7 / 1
microtubule-based movement						52	2 / 6	2 / 2	20 / 5	1 / 2	0 / 1	9 / 1	0 / 0	0 / 0	4 / 1
spermatogenesis						86	12 / 10	6 / 4	19 / 7	4 / 3	2 / 1	14 / 2	0 / 1	1 / 0	8 / 1
sperm motility						13	4 / 2	0 / 1	4 / 1	2 / 1	0 / 0	4 / 0	1 / 0	0 / 0	1 / 0
fertilization						21	1 / 2	0 / 1	5 / 2	0 / 1	0 / 0	4 / 1	0 / 0	0 / 0	1 / 0
spermatid development						18	1 / 2	0 / 1	6 / 2	1 / 1	0 / 0	3 / 1	0 / 0	0 / 0	3 / 0
Molecular Function						5222	571	231	454	180	54	135	32	11	57
sodium:potassium-exchanging ATPase activity						3	3 / 0	0 / 0	0 / 0	2 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
oxygen transporter activity						11	8 / 1	0 / 1	0 / 1	7 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
hemoglobin alpha binding						4	4 / 0	0 / 0	0 / 0	4 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
hemoglobin beta binding						4	4 / 0	0 / 0	0 / 0	4 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
oxygen binding						17	9 / 2	0 / 1	0 / 2	7 / 1	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
structural constituent of cytoskeleton						21	10 / 2	0 / 1	2 / 2	7 / 1	0 / 0	0 / 1	0 / 0	0 / 0	0 / 0
cytoskeletal protein binding						196	42 / 21	5 / 9	17 / 17	19 / 7	3 / 2	3 / 5	1 / 1	0 / 0	1 / 2
platelet-derived growth factor binding						5	3 / 1	0 / 0	0 / 0	3 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
magnesium chelatase activity						4	0 / 0	4 / 0	0 / 0	0 / 0	1 / 0	0 / 0	0 / 0	0 / 0	0 / 0
unfolded protein binding						75	7 / 8	16 / 3	13 / 7	2 / 3	3 / 1	3 / 2	0 / 1	1 / 0	1 / 1
MutLalpha complex binding						4	0 / 0	3 / 0	0 / 0	0 / 0	1 / 0	0 / 0	0 / 0	0 / 0	0 / 0
single-stranded DNA binding						22	1 / 2	7 / 1	4 / 2	0 / 1	2 / 0	1 / 1	0 / 0	0 / 0	1 / 0
ubiquitin activating enzyme activity						5	0 / 1	3 / 0	0 / 0	0 / 0	1 / 0	0 / 0	0 / 0	0 / 0	0 / 0
RNA binding						351	16 / 38	38 / 16	35 / 31	6 / 12	4 / 4	7 / 9	1 / 2	4 / 1	2 / 4
threonine-type endopeptidase activity						19	0 / 2	6 / 1	1 / 2	0 / 1	0 / 0	0 / 1	0 / 0	0 / 0	0 / 0
ribonucleoprotein binding						25	0 / 3	7 / 1	0 / 2	0 / 1	2 / 0	0 / 1	0 / 0	0 / 0	0 / 0
nucleotide binding						1135	104 / 124	83 / 50	130 / 99	34 / 39	21 / 12	40 / 29	5 / 7	3 / 2	19 / 12
enzyme inhibitor activity						163	22 / 18	20 / 7	12 / 14	5 / 6	4 / 2	3 / 4	1 / 1	0 / 0	1 / 2
ATP-dependent DNA helicase activity						7	0 / 1	3 / 0</							