

Table 4: Genes with a gender-differentiated expression pattern that were also affected in male rats continuously infused with GH.

Unigene	Accession	Name	F/M	GH/untreated
Female predominant and up-regulated by continuous infusion of GH				
Rn.3211	AW917574	similar to TNF ligand superfamily member 12	4.61	8.14
Rn.14535	AI070587	carboxylesterase 2 (intestine, liver)	3.54	4.57
Rn.53990	AJ302031	alpha-1-B glycoprotein	7.08	3.60
Rn.2586	NM_031572	Cytochrom P450 15-beta gene	4.72	3.08
Rn.115975	AW916713	EST sequence	5.61	2.85
Rn.2011	AA818134	peroxiredoxin 3	8.75	2.78
Rn.107116	AW142960	EST sequence	4.66	2.77
Rn.101709	AA819200	similar to Alcohol sulfotransferase (Hydroxysteroid sulfotransferase)	9.73	2.71
Rn.92406	AA819605	rat senescence marker protein 2A gene, exons 1 and 2	9.17	2.67
Rn.11377	AA875291	HRAS like suppressor	2.13	2.61
Rn.3790	LI9658	cd36 antigen	5.81	2.39
Rn.91378	AA818024	sulfotransferase, hydroxysteroid preferring 2	7.53	2.35
Rn.32282	AI045872	arginine vasopressin receptor 1A	1.86	1.99
Rn.1292	AA858662	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	2.20	1.99
Rn.102325	AW917611	EST sequence	5.41	1.94
Rn.4000	X74402	guanosine diphosphate dissociation inhibitor 1	2.38	1.84
Rn.91122	AA858966	Cytochrome P450, subfamily IIC6	2.28	1.84
Rn.6946	AW140722	ferredoxin 1	2.28	1.79
Rn.8195	AW917572	EST sequence	3.61	1.68
Rn.106771	AA996745	similar to stromal interaction molecule 1	1.94	1.55
Rn.2180	CFI08424	Atp5g3: ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	1.86	1.53
Male predominant and down-regulated by continuous infusion of GH				
Rn.1647	AF037072	carbonic anhydrase 3	0.06	0.09
Rn.37424	X79320	testosterone 6-beta-hydroxylase	0.10	0.15
Rn.23348	NM_031332	solute carrier family 22, member 8	0.10	0.16
Rn.103016	J00737	alpha-2u globulin PGCLI	0.01	0.18
Rn.106677	AA851893	similar to nucleoporin 37; nucleoporin Nup37	0.15	0.18
Rn.103770	CA504514	similar to Gelsolin precursor, plasma	0.19	0.22
Rn.888	AA819595	hydroxysteroid 11-beta dehydrogenase 1	0.12	0.31
Rn.7279	AF121345	phytanoyl-CoA hydroxylase (Refsum disease)	0.44	0.34
Rn.11320	CFI10333	phosphoribosyl pyrophosphate synthetase 2	0.33	0.35
Rn.20403	CB805116	ectonucleotide pyrophosphatase/phosphodiesterase 2	0.22	0.36
Rn.106064	AW141056	similar to another partner for ARF 1	0.61	0.43
Rn.43232	AI045953	cysteine-sulfinate decarboxylase	0.27	0.54
Rn.22952	AW140875	putative homeodomain transcription factor 1	0.59	0.59
Rn.801	AW144321	EST sequence	0.48	0.59
Rn.6835	AA963739	similar to Putative lysophosphatidic acid acyltransferase	0.48	0.59
Rn.12345	AW916917	similar to RIKEN cDNA 6330575P11	0.48	0.64
Rn.93760	AA998734	glutathione S-transferase, mu 1	0.45	0.65
Male predominant but up-regulated by continuous infusion of GH				
Rn.29771	AA900486	ATP citrate lyase	0.46	2.61
Rn.10992	AA964628	glucose-6-phosphatase, catalytic	0.48	2.10
Rn.98269	NM_145878	fatty acid binding protein 5, epidermal	0.63	2.03
Rn.9486	X62888	fatty acid synthase	0.56	2.36

Differentially expressed genes were defined using SAM statistics, with a 5% false discovery rate as cutoff. An additional criterion was for the gene to have a mean ratio of at least 1.5. The table shows UniGene ID, GenBank accession number, gene name, and the median expression ratio (female/male or GH treated/untreated male).

sion in 3 month old males. Similarly, around 34% of the male-enriched transcripts were down-regulated in males by the same treatment. Few genes (less than 4% of the male-enriched and none of the female-enriched) were

affected in the opposite direction by continuous treatment with GH. On the other hand, estrogen treatment in 3 month old male rats induced the expression of 27% of the female-enriched genes, and repressed the expression