

**Supplemental Table S1.** Change in mRNA transcripts between 15 days and 20 days of pregnancy

Gene Symbol	Description	Gene ID	Fold Change d15/d20
<i>Hamp</i>	hepcidin antimicrobial peptide	84604	-11.26
<i>Rnf186</i>	ring finger protein 186	690433	-7.32
<i>Gsta2</i>	glutathione S-transferase A2	24422	-4.37
<i>Xpnpep2</i>	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	117522	-4.00
<i>Cyp3a18</i>	cytochrome P450, family 3, subfamily a, polypeptide 18	252931	-3.25
<i>Gdf15</i>	growth differentiation factor 15	29455	-3.24
<i>Nrep</i>	neuronal regeneration related protein	338475	-3.08
<i>Idi1</i>	isopentenyl-diphosphate delta isomerase 1	89784	-2.90
<i>Acss2</i>	acyl-CoA synthetase short-chain family member 2	311569	-2.89
<i>Cadps</i>	Cadependent secretion activator	26989	-2.75
<i>Mt1a</i>	metallothionein 1a	24567	-2.73
<i>LOC100911107</i>	leukocyte elastase inhibitor A-like	100911107	-2.71
<i>RGD1310209</i>	similar to KIAA1324 protein	362019	-2.66
<i>Kcnj15</i>	potassium inwardly-rectifying channel, subfamily J, member 15	170847	-2.52
<i>Acat3</i>	acetyl-Coenzyme A acetyltransferase 3	308100	-2.46
<i>Cml2</i>	camello-like 2	500237	-2.45
<i>Acsm2a</i>	acyl-CoA synthetase medium-chain family member 2A	246263	-2.42
<i>Dhcr7</i>	7-dehydrocholesterol reductase	64191	-2.42
<i>Ces1f, Cesl1</i>	carboxylesterase 1F, carboxylesterase-like 1	100125372	-2.36
<i>LOC689064, LOC100134871</i>	beta-globin, beta globin minor gene	100134871	-2.31
<i>Cyp51</i>	cytochrome P450, family 51	25427	-2.29
<i>Echdc1</i>	enoyl CoA hydratase domain containing 1	361465	-2.22
<i>Tmtc4</i>	transmembrane and tetratricopeptide repeat containing 4	290501	-2.22
<i>Cd300lf</i>	Cd300 molecule-like family member F	287818	-2.09
<i>Sult1c2a</i>	sulfotransferase family, cytosolic, 1C, member 2a	316153	-2.06
<i>Ppp2r2b</i>	protein phosphatase 2, regulatory subunit B, beta	60660	-2.04
<i>Hmgcs1</i>	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	29637	-2.04
<i>Osgin1</i>	oxidative stress induced growth inhibitor 1	171493	-2.02
<i>Aass</i>	aminoadipate-semialdehyde synthase	296925	2.04
<i>LOC691221</i>	similar to CG1998-PA	691221	2.05
<i>Tfrc</i>	transferrin receptor	64678	2.05
<i>Hsd11b1</i>	hydroxysteroid 11-beta dehydrogenase 1	25116	2.08
<i>Tox3</i>	TOX high mobility group box family member 3	291908	2.08
<i>Nqo1</i>	NAD(P)H dehydrogenase, quinone 1	24314	2.16
<i>Foxa3</i>	forkhead box A3	25100	2.19
<i>LOC689408, LOC685909, LOC685069, RGD1560813</i>	similar to H2A histone family, member V isoform 1	498894	2.19
<i>Aig1</i>	androgen-induced 1	292486	2.20
<i>Igfbp2</i>	insulin-like growth factor binding protein 2	25662	2.37

<i>Tp53i11</i>	tumor protein p53 inducible protein 11	311209	2.43
<i>Cpa1</i>	carboxypeptidase A1 (pancreatic)	24269	2.54
<i>RGD1311946</i>	similar to RIKEN cDNA 1810055G02	309145	2.56
<i>Enpp2</i>	ectonucleotide pyrophosphatase/phosphodiesterase 2	84050	2.61
<i>Cyp17a1</i>	cytochrome P450, family 17, subfamily a, polypeptide 1	25146	2.77
<i>RGD1562284</i>	similar to Glutaminy-peptide cyclotransferase precursor (QC)	313837	2.78
<i>Slc16a6</i>	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	303772	2.81
<i>Fam134b, Zfp622</i>	family with sequence similarity 134, member B, zinc finger protein 622	294846	2.91
<i>Anxa13</i>	annexin A13	362915	3.11
<i>Fam134b, Zfp622</i>	family with sequence similarity 134, member B, zinc finger protein 622	294846	3.51
<i>Mustn1</i>	musculoskeletal, embryonic nuclear protein 1	290553	3.72
<i>Got1</i>	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	24401	3.76
<i>Nov</i>	nephroblastoma overexpressed gene	81526	4.11
<i>Rnase1</i>	ribonuclease, RNase A family, 1 (pancreatic)	364304	4.32
<i>RGD1565709</i>	similar to ovostatin-2	362442	4.77
<i>Insrr</i>	insulin receptor-related receptor	60663	5.08
<i>Sds</i>	serine dehydratase	25044	6.78
<i>Gpr113</i>	G protein-coupled receptor 113	298857	6.98
<i>A2m</i>	alpha-2-macroglobulin	24153	9.17

Changes in day 20 of pregnancy as compared with day 15 of pregnancy (n = 4 for each group). Analysis of variance was used to identify differentially expressed genes with a false discovery rate of 0.05 to control for multiple testing.