

Ratio log2	TTEST	Gene Name	Function
1.421	0.00048	Chac1	UPR
1.263	0.00081	Derl3	UPR
1.256	0.03297	Rtp4	opiod receptor
1.252	0.00047	Trib3	UPR
1.241	0.04811	Esm1	Immunity/sepsis
1.195	0.00045	Nupr1	ER-stress/DNA-repair
1.188	0.00563	Slc7a1	cationic amino acid transporter
1.172	0.03451	Upk3b	
1.162	0.01369	Slc7a3	cationic amino acid transporter
1.161	0.00227	Ddit3	ER-stress
1.143	0.00288	Aldh1l2	
1.142	0.02999	Slc1a4	glutamate/neutral amino acid transporter
1.135	0.01323	Insig1	HMG-Coa regulation
1.125	0.01359	Idi1	isopentenyl-diphosphate isomerase
1.124	0.00284	Herpud1	ER-stress
1.124	0.01424	Lss	lanosterol synthase
1.122	0.00574	Slc2a6	facilitated glucose transporter
1.122	0.00105	Ttc17	
1.118	0.00186	Kcnj8	potassium inwardly-rectifying channel
1.117	0.00571	Hmgcs1	HMG-Coa 2
1.117	0.00472	Slc6a9	neurotransmitter transporter
1.113	0.00589	Bhlhb8	seminal vesicle epithelium differentiation
1.113	0.00875	Ero1b	UPR
1.112	0.04184	Cep135	centriole biogenesis
1.112	0.00052	Olf430	olfactory receptor
1.110	0.00096	Sdf2l1	ER-stress
1.110	0.04832	Cyp51	cholesterol biosynthesis
1.107	0.01452	Lpin1	glycerolipid biosynthesis
1.105	0.00926	AK138790	
1.105	0.00416	CJ042244	
1.105	0.00046	9030617O03Rik	
1.103	0.04668	Sc4mol	cholesterol biosynthesis
1.103	0.04538	Rsad2	
1.102	0.01337	Gpt2	
1.101	0.00301	Cng2	
1.101	0.03025	Prkg1	protein kinase
1.100	0.03283	Robo4	guidance receptor/angiogenesis
1.100	0.00092	Nucb2	
1.100	0.00002	D12Erd647e	
1.099	0.01947	Dusp26	
1.099	0.01222	Hyou1	UPR-ER Stress
1.098	0.00733	Afp	fetal counterpart of serum albumin
1.098	0.00601	Ppp1r3c	glycogen metabolism.
1.098	0.01834	Kcne3	potassium voltage-gated channel
1.097	0.00786	Mbnl2	
1.095	0.01065	Lama4	basement membranes
1.095	0.00509	Armcx3	
1.094	0.00229	Dnajb9	ER stress-UPR
1.094	0.01227	Ldlr	Cholesterol transport
1.093	0.01125	Sc5d	sterol-C5-desaturase
1.093	0.00128	H2-M3	histocompatibility 2, M region locus 3
1.092	0.01341	AI595406	
1.091	0.00326	Sesn2	
1.091	0.00083	Idh1	isocitrate dehydrogenase 1
1.091	0.01825	Dnajc3	ER-stress- UPR
1.091	0.02041	Gsbs	
1.090	0.00043	Vldlr	Cholesterol transport

Table S1. Related to Figure 4

Transcripts ranked by the order of expressions most increase in E8.5 *Srd5a3*^{Gt/Gt}. Ratio of log2 of the expression are means of 4 replicates experiment. All transcripts listed here were significantly increased (P<0.05). Genes involved in ER stress or UPR are in green, genes involved in the mevalonate pathway are in yellow.

Ratio log2	TTEST	Gene Name	Gene title
0.73	0.00041	Srd5a3	steroid 5 alpha-reductase 3
0.82	0.00345	Pi4k2b	Phosphatidylinositol 4-kinase type 2 beta
0.84	0.03075	Abhd1	Abhydrolase domain containing 1
0.85	0.00339	Hspa1a	Heat shock protein 1A
0.85	0.00124	Hspa1b	Heat shock protein 1B
0.90	0.01162	T	Brachyury
0.90	0.00992	3732412D22Rik	
0.90	0.00772	A230097K15Rik	Interferon stimulated exonuclease gene 20-like 1
0.91	0.00016	Isg20l1	
0.91	0.00604	5730593N15Rik	
0.91	0.03364	5730437N04Rik	
0.92	0.03754	C330024D21Rik	
0.92	0.02911	Ubap2l	Ubiquitin associated protein 2-like
0.92	0.00005	Rangap1	RAN GTPase activating protein 1
0.92	0.01860	Tagln	Transgelin
0.92	0.02285	Cldn4	Claudin 4
0.93	0.02943	Pnpla6	Patatin-like phospholipase domain containing 6
0.93	0.00934	Trip10	Thyroid hormone receptor interactor 10
0.93	0.02331	Fgf3	Fibroblast growth factor 3
0.93	0.00528	E030010A14Rik	
0.93	0.00216	Smo	Smoothened
0.93	0.00663	Cpa2	Carboxypeptidase A2
0.93	0.02163	Evx1	Even skipped homeotic gene 1
0.93	0.04052	Tomm40	Translocase of outer mitochondrial membrane 40 homolog
0.93	0.00535	Strn4	Striatin, calmodulin binding protein 4
0.93	0.00050	Tnfrsf19l	Tumor necrosis factor receptor superfamily, member 19-like
0.93	0.04161	Rnd2	Rho family GTPase 2
0.93	0.00516	Ttll4	Tubulin tyrosine ligase-like family, member 4
0.93	0.00023	E2f1	E2F transcription factor 1
0.93	0.00369	Pim1	Proviral integration site 1

Table S2. Related to Figure 4

Transcripts ranked by the order of expressions most decrease in E8.5 *Srd5a3*^{Giv/Gt}. Ratio of log2 of the expression are means of 4 replicates experiment. All transcripts listed here were significantly increased (P<0.05).

Biological Process associated with over-expressed genes according to their gene ontology (GO) category

GO Term	P-value	Sample frequency
GO:0051789 response to protein stimulus	8.25E-10	23/923 (2.5%)
GO:0006986 response to unfolded protein	1.66E-08	16/923 (1.7%)
GO:0016126 sterol biosynthetic process	8.88E-08	15/923 (1.6%)
GO:0006695 cholesterol biosynthetic process	4.88E-07	13/923 (1.4%)
GO:0008610 lipid biosynthetic process	2.54E-04	37/923 (4.0%)
GO:0006694 steroid biosynthetic process	8.13E-04	17/923 (1.8%)
GO:0016125 sterol metabolic process	9.91E-04	17/923 (1.8%)
GO:0044237 cellular metabolic process	5.78E-03	372/923 (40.3%)
GO:0008203 cholesterol metabolic process	8.00E-03	428/923 (46.4%)

Biological Process associated with under-expressed genes according to their GO category

GO Term	P-value	Sample frequency
GO:0044237 cellular metabolic process	2.72E-12	362/775 (46.7%)
GO:0008152 metabolic process	2.49E-11	407/775 (52.5%)
GO:0044238 primary metabolic process	2.45E-10	364/775 (47.0%)
GO:0034960 cellular biopolymer metabolic process	3.99E-09	284/775 (36.6%)
GO:0044260 cellular macromolecule metabolic process	5.97E-09	289/775 (37.3%)
GO:0043170 macromolecule metabolic process	5.46E-08	310/775 (40.0%)
GO:0043283 biopolymer metabolic process	1.13E-07	301/775 (38.8%)
GO:0006807 nitrogen compound metabolic process	4.68E-06	213/775 (27.5%)
GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.39E-05	196/775 (25.3%)
GO:0009792 embryonic development ending in birth or egg hatching	1.22E-04	45/775 (5.8%)
GO:0034470 ncRNA processing	2.03E-04	22/775 (2.8%)
GO:0043009 chordate embryonic development	2.55E-04	44/775 (5.7%)
GO:0048519 negative regulation of biological process	3.12E-04	88/775 (11.4%)
GO:0006396 RNA processing	3.49E-04	42/775 (5.4%)
GO:0034660 ncRNA metabolic process	5.30E-04	25/775 (3.2%)
GO:0048523 negative regulation of cellular process	9.38E-04	79/775 (10.2%)
GO:0009888 tissue development	2.51E-03	58/775 (7.5%)
GO:0009790 embryonic development	4.13E-03	57/775 (7.4%)
GO:0003002 regionalization	4.24E-03	27/775 (3.5%)
GO:0040007 growth	6.70E-03	36/775 (4.6%)

Table S3. Related to Figure 4

Enrichment of Gene Ontology (GO) categories by differentially expressed genes in *Srd5a3*^{Gt/Gt} embryos compared to wt litter mates.

Genes enriched in the GO category Response to unfolded protein (2nd line of the GO term) are also present in the GO category Response to protein stimulus (1st line of the GO term) where they represent 70% of the genes enriched in this last category.