

SUPPLEMENTAL DATA

(Tables S1-S2, Figures S1-S3)

Early transcriptional responses of HepG2-A16 liver cells to infection by *Plasmodium falciparum* sporozoites

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Running title: Early hepatocyte responses following malarial sporozoite infection
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Supplementary Table S1

Table S1: Genes which are differentially expressed between *Spor* vs *SalGld*. A total of 742 genes were found to be significant at $p < 0.001$ level using a univariate pairwise test; the genes are listed in ranked order by their parametric p-values. Datasets representing the three time points within each experimental group have been grouped together and were regarded as experimental replicates. Genes whose expression in *Spor* showed >5-fold change in either direction relative to *SalGld* values are indicated in bold.

	Gene symbol	Description	Parametric p-value	Fold-change
1	KIF20A	kinesin family member 20A	< 1e-07	6.25
2	HSPA1A	heat shock 70kDa protein 1A	< 1e-07	0.33
3	TK1	thymidine kinase 1, soluble	< 1e-07	3.03
4	CDC20	cell division cycle 20 homolog (S. cerevisiae)	< 1e-07	4.00
5	AZGP1	alpha-2-glycoprotein 1, zinc-binding	< 1e-07	0.18
6	S100P	S100 calcium binding protein P	< 1e-07	0.20
7	CSE1L	CSE1 chromosome segregation 1-like (yeast)	< 1e-07	2.70
8	C6orf173	chromosome 6 open reading frame 173	< 1e-07	3.70
9	UBE2C	ubiquitin-conjugating enzyme E2C	< 1e-07	2.63
10	OTC	ornithine carbamoyltransferase	< 1e-07	2.86
11	AURKA	aurora kinase A	1e-07	4.00
12	LGALS2	lectin, galactoside-binding, soluble, 2	1e-07	3.13
13	TMED4	transmembrane emp24 protein transport domain containing 4	1e-07	2.94
14	KLHL5	kelch-like 5 (Drosophila)	1e-07	0.37
15	RBP1	retinol binding protein 1, cellular	1e-07	2.38
16	PTTG1	pituitary tumor-transforming 1	1e-07	3.33
17	AIMP1	aminoacyl tRNA synthetase complex-interacting multifunctional protein 1	1e-07	2.38
18	ACOT13	acyl-CoA thioesterase 13	1e-07	2.86
19	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	1e-07	2.17
20	LRRN4	leucine rich repeat neuronal 4	1e-07	3.33
21	ADH4	alcohol dehydrogenase 4 (class II), pi polypeptide	1e-07	2.70
22	GAS2L1	growth arrest-specific 2 like 1	1e-07	2.38
23	CD36	CD36 molecule (thrombospondin receptor)	1e-07	2.70
24	CENPF	centromere protein F, 350/400ka (mitosin)	2e-07	4.17
25	MYCBP	c-myc binding protein	2e-07	2.27
26	IL1RN	interleukin 1 receptor antagonist	2e-07	0.33
27	MKI67	antigen identified by monoclonal antibody Ki-67	2e-07	4.76
28	DKK1	dickkopf homolog 1 (Xenopus laevis)	2e-07	5.00
29	NASP	nuclear autoantigenic sperm protein (histone-binding)	2e-07	2.27
30	POLA1	polymerase (DNA directed), alpha 1, catalytic subunit	2e-07	2.63
31	TRIP13	thyroid hormone receptor interactor 13	2e-07	2.38
32	ADH6	alcohol dehydrogenase 6 (class V)	2e-07	2.17
33	IDS	iduronate 2-sulfatase	2e-07	0.41

34	SPC24	SPC24, NDC80 kinetochore complex component, homolog (<i>S. cerevisiae</i>)	3e-07	2.78
35	EPN3	epsin 3	3e-07	2.13
36	G6PD	glucose-6-phosphate dehydrogenase	3e-07	3.45
37	DHDPSL	dihydrodipicolinate synthase-like, mitochondrial	3e-07	3.03
38	RABGAP1L	RAB GTPase activating protein 1-like	3e-07	2.78
39	WHSC1	Wolf-Hirschhorn syndrome candidate 1	3e-07	2.27
40	IDI2	isopentenyl-diphosphate delta isomerase 2	3e-07	0.47
41	ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	4e-07	2.44
42	C12orf48	chromosome 12 open reading frame 48	4e-07	2.33
43	PTTG3P	pituitary tumor-transforming 3 (pseudogene)	4e-07	3.13
44	SMC4	structural maintenance of chromosomes 4	4e-07	3.45
45	WDR20	WD repeat domain 20	4e-07	2.78
46	C15orf23	chromosome 15 open reading frame 23	4e-07	2.22
47	HIST1H2BK	histone cluster 1, H2bk	4e-07	0.41
48	RHOB	ras homolog gene family, member B	4e-07	0.38
49	FOXRED2	FAD-dependent oxidoreductase domain containing 2	4e-07	2.17
50	KIF15	kinesin family member 15	4e-07	3.23
51	SLC30A7	solute carrier family 30 (zinc transporter), member 7	4e-07	0.47
52	AMBP	alpha-1-microglobulin/bikunin precursor	4e-07	0.47
53	NCAPH	non-SMC condensin I complex, subunit H	5e-07	2.94
54	CENPE	centromere protein E, 312kDa	5e-07	2.78
55	CSDE1	cold shock domain containing E1, RNA-binding	5e-07	0.44
56	DNAJC12	DnaJ (Hsp40) homolog, subfamily C, member 12	5e-07	0.33
57	FAM3C	family with sequence similarity 3, member C	5e-07	0.40
58	GTSE1	G-2 and S-phase expressed 1	5e-07	3.70
59	SLC38A6	solute carrier family 38, member 6	6e-07	2.33
60	C7orf58	chromosome 7 open reading frame 58	6e-07	2.70
61	HIST2H2BE	histone cluster 2, H2be	6e-07	0.32
62	HMOX1	heme oxygenase (decycling) 1	6e-07	2.63
63	C19orf69	chromosome 19 open reading frame 69	6e-07	3.03
64	IQGAP3	IQ motif containing GTPase activating protein 3	7e-07	3.03
65	KPNB1	karyopherin (importin) beta 1	7e-07	1.92
66	CCNB1	cyclin B1	7e-07	3.45
67	RPN2	ribophorin II	7e-07	0.49
68	CDC25C	cell division cycle 25 homolog C (<i>S. pombe</i>)	7e-07	2.50
69	ITIH3	inter-alpha (globulin) inhibitor H3	8e-07	0.18
70	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	8e-07	0.32
71	ELP4	elongation protein 4 homolog (<i>S. cerevisiae</i>)	8e-07	2.38
72	LMNB1	lamin B1	9e-07	2.50
73	KRT19	keratin 19	9e-07	4.76
74	ZWILCH	Zwilch, kinetochore associated, homolog (<i>Drosophila</i>)	9e-07	2.33
75	ZC3H4	zinc finger CCCH-type containing 4	9e-07	2.33
76	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	1e-06	3.85

77	CD302	CD302 molecule	1e-06	0.39
78	MCCC2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	1e-06	1.92
79	FGL1	fibrinogen-like 1	1e-06	0.37
80	SEMA3G	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	1.1e-06	0.38
81	DNMT1	DNA (cytosine-5-)-methyltransferase 1	1.1e-06	2.04
82	ATP5G1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9)	1.1e-06	2.00
83	DDX39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	1.1e-06	1.96
84	PPAPDC1B	phosphatidic acid phosphatase type 2 domain containing 1B	1.2e-06	0.50
85	CCL20	chemokine (C-C motif) ligand 20	1.2e-06	0.13
86	CDC2	cell division cycle 2, G1 to S and G2 to M	1.2e-06	4.17
87	KLF10	Kruppel-like factor 10	1.3e-06	0.21
88	LRRC40	leucine rich repeat containing 40	1.3e-06	2.04
89	G6PC	glucose-6-phosphatase, catalytic subunit	1.3e-06	0.25
90	ANKRD57	ankyrin repeat domain 57	1.3e-06	0.44
91	ISG20	interferon stimulated exonuclease gene 20kDa	1.3e-06	0.49
92	CDCA3	cell division cycle associated 3	1.3e-06	3.85
93	TP53INP2	tumor protein p53 inducible nuclear protein 2	1.3e-06	0.45
94	FXYD1	FXYD domain containing ion transport regulator 1	1.3e-06	0.49
95	TGFB1	transforming growth factor, beta 1	1.3e-06	0.38
96	SEC23IP	SEC23 interacting protein	1.3e-06	0.46
97	FIGNL1	fidgetin-like 1	1.4e-06	2.63
98	SRPRB	signal recognition particle receptor, B subunit	1.4e-06	0.40
99	RBMS1	RNA binding motif, single stranded interacting protein 1	1.4e-06	0.48
100	SEC24D	SEC24 family, member D (<i>S. cerevisiae</i>)	1.4e-06	0.51
101	CRLS1	cardiolipin synthase 1	1.4e-06	2.00
102	SSR1	signal sequence receptor, alpha	1.4e-06	0.56
103	RBP2	retinol binding protein 2, cellular	1.5e-06	2.44
104	HLA-C	major histocompatibility complex, class I, C	1.5e-06	0.45
105	H2AFX	H2A histone family, member X	1.5e-06	2.70
106	SKP2	S-phase kinase-associated protein 2 (p45)	1.5e-06	2.13
107	CLU	clusterin	1.6e-06	0.30
108	TMEM107	transmembrane protein 107	1.6e-06	1.96
109	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	1.6e-06	0.48
110	CALML4	calmodulin-like 4	1.6e-06	3.03
111	VTN	vitronectin	1.6e-06	0.39
112	SLC2A2	solute carrier family 2 (facilitated glucose transporter), member 2	1.7e-06	1.96
113	TM4SF5	transmembrane 4 L six family member 5	1.7e-06	0.36
114	MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	1.7e-06	2.13
115	CPE	carboxypeptidase E	1.7e-06	0.45
116	C5	complement component 5	1.7e-06	0.22
117	RNF138	ring finger protein 138	1.8e-06	2.63
118	ATPIF1	ATPase inhibitory factor 1	1.8e-06	1.75

119	C12orf44	chromosome 12 open reading frame 44	1.8e-06	0.55
120	CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	1.9e-06	1.92
121	PSPC1	paraspeckle component 1	2e-06	2.38
122	HIST1H1C	histone cluster 1, H1c	2e-06	0.21
123	FST	follistatin	2e-06	0.31
124	SGK493	protein kinase-like protein Sgk493	2e-06	2.13
125	NCAPG	non-SMC condensin I complex, subunit G	2e-06	6.67
126	CLIP2	CAP-GLY domain containing linker protein 2	2e-06	0.43
127	MCM5	minichromosome maintenance complex component 5	2.1e-06	3.85
128	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	2.1e-06	0.18
129	CRYBG3	beta-gamma crystallin domain containing 3	2.1e-06	1.82
130	CCNE2	cyclin E2	2.1e-06	2.13
131	IER3	immediate early response 3	2.1e-06	0.44
132	NDUFB1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa	2.2e-06	2.00
133	AHSG	alpha-2-HS-glycoprotein	2.2e-06	0.28
134	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	2.2e-06	2.56
135	VDAC3	voltage-dependent anion channel 3	2.2e-06	1.75
136	C2orf68	chromosome 2 open reading frame 68	2.2e-06	0.47
137	TOP2A	topoisomerase (DNA) II alpha 170kDa	2.3e-06	3.45
138	F5	coagulation factor V (proaccelerin, labile factor)	2.3e-06	0.37
139	LYPLA1	lysophospholipase I	2.3e-06	0.57
140	SDC4	syndecan 4	2.3e-06	0.47
141	RPP30	ribonuclease P/MRP 30kDa subunit	2.3e-06	2.44
142	TMEM59	transmembrane protein 59	2.4e-06	0.42
143	PNRC2	proline-rich nuclear receptor coactivator 2	2.4e-06	1.69
144	C12orf57	chromosome 12 open reading frame 57	2.4e-06	0.41
145	CD109	CD109 molecule	2.4e-06	0.39
146	LOXL4	lysyl oxidase-like 4	2.5e-06	0.38
147	SEC11C	SEC11 homolog C (S. cerevisiae)	2.5e-06	0.39
148	DTL	denticleless homolog (Drosophila)	2.5e-06	2.94
149	KIF22	kinesin family member 22	2.6e-06	2.13
150	ULK4	unc-51-like kinase 4 (C. elegans)	2.7e-06	2.13
151	ARV1	ARV1 homolog (S. cerevisiae)	2.7e-06	1.96
152	NUSAP1	nucleolar and spindle associated protein 1	2.7e-06	3.57
153	TTR	transthyretin	2.7e-06	0.20
154	SARS	seryl-tRNA synthetase	2.8e-06	0.45
155	ORC3L	origin recognition complex, subunit 3-like (yeast)	2.8e-06	1.96
156	NEK2	NIMA (never in mitosis gene a)-related kinase 2	2.8e-06	3.23
157	UHRF1	ubiquitin-like with PHD and ring finger domains 1	2.9e-06	2.78
158	ZMAT3	zinc finger, matrin type 3	2.9e-06	0.40
159	NIPBL	Nipped-B homolog (Drosophila)	2.9e-06	1.79
160	CTSB	cathepsin B	3e-06	0.47

161	C20orf108	chromosome 20 open reading frame 108	3e-06	0.44
162	FN1	fibronectin 1	3e-06	0.56
163	PPIH	peptidylprolyl isomerase H (cyclophilin H)	3.1e-06	2.22
164	SHMT1	serine hydroxymethyltransferase 1 (soluble)	3.1e-06	1.75
165	ABCC6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	3.1e-06	1.72
166	NUP107	nucleoporin 107kDa	3.1e-06	2.00
167	ZNF207	zinc finger protein 207	3.2e-06	0.36
168	WSB2	WD repeat and SOCS box-containing 2	3.2e-06	0.56
169	MANF	mesencephalic astrocyte-derived neurotrophic factor	3.2e-06	0.57
170	KITLG	KIT ligand	3.2e-06	2.63
171	CMBL	carboxymethylenebutenolidase homolog (Pseudomonas)	3.3e-06	1.85
172	CPD	carboxypeptidase D	3.4e-06	0.58
173	JAG1	jagged 1 (Alagille syndrome)	3.4e-06	0.53
174	SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	3.4e-06	0.51
175	PTTG1IP	pituitary tumor-transforming 1 interacting protein	3.5e-06	0.52
176	DNLZ	DNL-type zinc finger	3.5e-06	0.52
177	C2	complement component 2	3.5e-06	0.40
178	TMEM33	transmembrane protein 33	3.5e-06	0.54
179	TACC3	transforming, acidic coiled-coil containing protein 3	3.7e-06	3.23
180	LOC285943	hypothetical protein LOC285943	3.7e-06	2.13
181	PEX3	peroxisomal biogenesis factor 3	3.7e-06	1.79
182	BOK	BCL2-related ovarian killer	3.8e-06	0.44
183	C20orf19	chromosome 20 open reading frame 19	3.8e-06	1.75
184	CP	ceruloplasmin (ferroxidase)	3.9e-06	0.12
185	HLA-B	major histocompatibility complex, class I, B	3.9e-06	0.40
186	BCCIP	BRCA2 and CDKN1A interacting protein	3.9e-06	2.04
187	THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	3.9e-06	1.82
188	GDF15	growth differentiation factor 15	4e-06	0.18
189	AURKB	aurora kinase B	4.1e-06	3.23
190	ALKBH7	alkB, alkylation repair homolog 7 (E. coli)	4.1e-06	0.60
191	BPIL1	bactericidal/permeability-increasing protein-like 1	4.1e-06	0.25
192	DLGAP5	discs, large (Drosophila) homolog-associated protein 5	4.1e-06	3.45
193	RNF115	ring finger protein 115	4.2e-06	1.72
194	PDS5A	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	4.3e-06	1.75
195	HSPB11	heat shock protein family B (small), member 11	4.5e-06	2.27
196	C12orf75	chromosome 12 open reading frame 75	4.5e-06	1.79
197	NUDT15	nudix (nucleoside diphosphate linked moiety X)-type motif 15	4.5e-06	1.69
198	MLF1IP	MLF1 interacting protein	4.7e-06	3.33
199	GINS3	GINS complex subunit 3 (Psf3 homolog)	4.7e-06	2.56
200	RAB22A	RAB22A, member RAS oncogene family	4.7e-06	0.49
201	RPA1	replication protein A1, 70kDa	4.8e-06	2.08
202	SMPDL3A	sphingomyelin phosphodiesterase, acid-like 3A	4.8e-06	0.54

203	AKR1D1	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)	4.9e-06	2.94
204	FOXN3	forkhead box N3	4.9e-06	0.43
205	FAM171A1	family with sequence similarity 171, member A1	5e-06	0.52
206	OPTN	optineurin	5.1e-06	0.46
207	LIG1	ligase I, DNA, ATP-dependent	5.1e-06	1.85
208	VAMP5	vesicle-associated membrane protein 5 (myobrevin)	5.2e-06	0.48
209	TRIM50	tripartite motif-containing 50	5.2e-06	2.27
210	CENPN	centromere protein N	5.3e-06	2.94
211	CDT1	chromatin licensing and DNA replication factor 1	5.4e-06	2.94
212	CCPG1	cell cycle progression 1	5.5e-06	0.54
213	RB1	retinoblastoma 1	5.5e-06	1.96
214	ZNRF1	zinc and ring finger 1	5.6e-06	0.47
215	CDCA2	cell division cycle associated 2	5.6e-06	2.86
216	SYTL2	synaptotagmin-like 2	5.6e-06	2.86
217	GTPBP4	GTP binding protein 4	5.7e-06	0.49
218	C19orf10	chromosome 19 open reading frame 10	5.7e-06	0.46
219	C21orf45	chromosome 21 open reading frame 45	5.9e-06	2.86
220	SLC35E1	solute carrier family 35, member E1	5.9e-06	0.58
221	CCNI	cyclin I	6e-06	0.50
222	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	6e-06	4.76
223	C18orf10	chromosome 18 open reading frame 10	6e-06	2.08
224	KIF2C	kinesin family member 2C	6e-06	2.63
225	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	6.1e-06	2.04
226	DNAJC3	DnaJ (Hsp40) homolog, subfamily C, member 3	6.1e-06	0.58
227	RPL10L	ribosomal protein L10-like	6.1e-06	0.58
228	TGFBI	transforming growth factor, beta-induced, 68kDa	6.2e-06	0.57
229	ETFB	electron-transfer-flavoprotein, beta polypeptide	6.2e-06	0.48
230	HJURP	Holliday junction recognition protein	6.3e-06	2.33
231	EPPK1	epiplakin 1	6.4e-06	0.53
232	ZBTB2	zinc finger and BTB domain containing 2	6.6e-06	2.38
233	RBM15	RNA binding motif protein 15	6.6e-06	2.33
234	FAM148A	family with sequence similarity 148, member A	6.7e-06	2.38
235	MTAP	methylthioadenosine phosphorylase	6.8e-06	1.92
236	PPP2CB	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	6.8e-06	0.56
237	L1CAM	L1 cell adhesion molecule	6.8e-06	0.52
238	ZNF367	zinc finger protein 367	6.8e-06	2.08
239	SEZ6L2	seizure related 6 homolog (mouse)-like 2	6.9e-06	0.49
240	TRIM24	tripartite motif-containing 24	6.9e-06	1.79
241	RTN3	reticulon 3	7e-06	0.62
242	CXCL2	chemokine (C-X-C motif) ligand 2	7.1e-06	0.15
243	JUNB	jun B proto-oncogene	7.1e-06	0.50
244	SNRPF	small nuclear ribonucleoprotein polypeptide F	7.2e-06	1.85
245	PHF19	PHD finger protein 19	7.2e-06	1.75

246	REEP4	receptor accessory protein 4	7.5e-06	1.69
247	BHMT2	betaine-homocysteine methyltransferase 2	7.5e-06	1.72
248	KIF4A	kinesin family member 4A	7.5e-06	2.78
249	DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	7.6e-06	1.67
250	SERPIND1	serpin peptidase inhibitor, clade D (heparin cofactor), member 1	7.6e-06	0.39
251	F10	coagulation factor X	7.7e-06	0.46
252	SF3B3	splicing factor 3b, subunit 3, 130kDa	7.9e-06	1.59
253	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	8e-06	1.85
254	FNDC3B	fibronectin type III domain containing 3B	8.2e-06	0.42
255	VKORC1	vitamin K epoxide reductase complex, subunit 1	8.4e-06	0.53
256	GNAZ	guanine nucleotide binding protein (G protein), alpha z polypeptide	8.4e-06	0.60
257	DUSP1	dual specificity phosphatase 1	8.4e-06	0.27
258	DBF4	DBF4 homolog (S. cerevisiae)	8.4e-06	2.22
259	RFX5	regulatory factor X, 5 (influences HLA class II expression)	8.5e-06	1.82
260	SLC39A10	solute carrier family 39 (zinc transporter), member 10	8.5e-06	0.50
261	TTK	TTK protein kinase	8.6e-06	3.85
262	PAM	peptidylglycine alpha-amidating monooxygenase	8.6e-06	0.52
263	MCAM	melanoma cell adhesion molecule	8.7e-06	1.92
264	SGOL2	shugoshin-like 2 (S. pombe)	8.8e-06	3.03
265	CKAP2L	cytoskeleton associated protein 2-like	8.8e-06	1.92
266	GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	9e-06	0.49
267	NEIL3	nei endonuclease VIII-like 3 (E. coli)	9.1e-06	2.22
268	AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	9.3e-06	0.47
269	DIAPH3	diaphanous homolog 3 (Drosophila)	9.4e-06	2.63
270	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	9.5e-06	1.85
271	DGAT1	diacylglycerol O-acyltransferase homolog 1 (mouse)	9.5e-06	1.96
272	REEP6	receptor accessory protein 6	9.5e-06	2.17
273	FAM64A	family with sequence similarity 64, member A	9.6e-06	1.72
274	ITGB3BP	integrin beta 3 binding protein (beta3-endonexin)	9.7e-06	2.17
275	HSPH1	heat shock 105kDa/110kDa protein 1	9.9e-06	0.40
276	PNMA1	paraneoplastic antigen MA1	9.9e-06	0.56
277	ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	1.01e-05	1.85
278	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	1.04e-05	3.45
279	RBM24	RNA binding motif protein 24	1.05e-05	0.48
280	TMCO3	transmembrane and coiled-coil domains 3	1.06e-05	0.48
281	VRK1	vaccinia related kinase 1	1.07e-05	2.63
282	KIAA0101	KIAA0101	1.08e-05	3.03
283	OSR2	odd-skipped related 2 (Drosophila)	1.08e-05	1.61
284	APPL2	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	1.09e-05	0.59
285	IGFBP2	insulin-like growth factor binding protein 2, 36kDa	1.09e-05	0.43
286	NTAN1	N-terminal asparagine amidase	1.1e-05	0.52
287	SSR3	signal sequence receptor, gamma (translocon-associated protein gamma)	1.11e-05	0.48
288	C14orf28	chromosome 14 open reading frame 28	1.11e-05	0.36

289	NCOR1	nuclear receptor co-repressor 1	1.13e-05	1.61
290	APOC1	apolipoprotein C-I	1.13e-05	0.55
291	PGC	progastricsin (pepsinogen C)	1.14e-05	0.55
292	ATRN	attractin	1.14e-05	0.49
293	C22orf32	chromosome 22 open reading frame 32	1.16e-05	0.46
294	APOE	apolipoprotein E	1.17e-05	0.56
295	FLNA	filamin A, alpha	1.19e-05	0.50
296	NHSL1	NHS-like 1	1.19e-05	1.61
297	POR	P450 (cytochrome) oxidoreductase	1.2e-05	0.55
298	IQCG	IQ motif containing G	1.21e-05	0.50
299	RHBDD2	rhomboid domain containing 2	1.22e-05	0.49
300	PIGK	phosphatidylinositol glycan anchor biosynthesis, class K	1.22e-05	2.27
301	SPC25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	1.22e-05	7.14
302	WDFY2	WD repeat and FYVE domain containing 2	1.25e-05	0.56
303	FAM54A	family with sequence similarity 54, member A	1.25e-05	4.55
304	KIF18B	kinesin family member 18B	1.25e-05	3.85
305	MATN3	matrilin 3	1.27e-05	0.28
306	HSPA13	heat shock protein 70kDa family, member 13	1.3e-05	0.46
307	ZBED3	zinc finger, BED-type containing 3	1.3e-05	1.64
308	VPS28	vacuolar protein sorting 28 homolog (S. cerevisiae)	1.31e-05	0.53
309	ALDH7A1	aldehyde dehydrogenase 7 family, member A1	1.31e-05	1.92
310	SOD2	superoxide dismutase 2, mitochondrial	1.31e-05	0.43
311	CCDC53	coiled-coil domain containing 53	1.35e-05	2.13
312	SSR2	signal sequence receptor, beta (translocon-associated protein beta)	1.36e-05	0.54
313	CENPL	centromere protein L	1.36e-05	2.13
314	F2	coagulation factor II (thrombin)	1.36e-05	0.52
315	PRC1	protein regulator of cytokinesis 1	1.37e-05	2.63
316	HMGXB4	HMG box domain containing 4	1.4e-05	1.72
317	CTHRC1	collagen triple helix repeat containing 1	1.4e-05	0.39
318	CUGBP1	CUG triplet repeat, RNA binding protein 1	1.41e-05	1.54
319	IGF2BP1	insulin-like growth factor 2 mRNA binding protein 1	1.42e-05	1.75
320	PDIA3	protein disulfide isomerase family A, member 3	1.43e-05	0.45
321	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	1.43e-05	3.45
322	SPON2	spondin 2, extracellular matrix protein	1.45e-05	0.49
323	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	1.46e-05	1.82
324	QSOX1	quiescin Q6 sulfhydryl oxidase 1	1.46e-05	0.46
325	PALLD	palladin, cytoskeletal associated protein	1.47e-05	0.25
326	C14orf143	chromosome 14 open reading frame 143	1.48e-05	2.38
327	DARS	aspartyl-tRNA synthetase	1.48e-05	1.75
328	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	1.49e-05	2.70
329	METAP2	methionyl aminopeptidase 2	1.49e-05	1.96
330	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10	1.5e-05	0.44
331	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	1.51e-05	0.54

332	ATF3	activating transcription factor 3	1.51e-05	0.23
333	DDX20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	1.53e-05	2.13
334	SAMHD1	SAM domain and HD domain 1	1.54e-05	2.04
335	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	1.54e-05	2.78
336	ERCC6L	excision repair cross-complementing rodent repair deficiency, complementation group 6-like	1.54e-05	1.82
337	DEPDC1	DEP domain containing 1	1.57e-05	1.89
338	ARSD	arylsulfatase D	1.58e-05	0.49
339	NGRN	neugrin, neurite outgrowth associated	1.59e-05	0.51
340	ATF4	activating transcription factor 4 (tax-responsive enhancer element B67)	1.6e-05	1.64
341	CA9	carbonic anhydrase IX	1.61e-05	0.24
342	IL8	interleukin 8	1.62e-05	0.36
343	TIMM44	translocase of inner mitochondrial membrane 44 homolog (yeast)	1.65e-05	1.69
344	CCDC34	coiled-coil domain containing 34	1.65e-05	2.44
345	hCG_1811732	hypothetical LOC151534	1.65e-05	2.08
346	NR2F2	nuclear receptor subfamily 2, group F, member 2	1.68e-05	2.22
347	TMEM117	transmembrane protein 117	1.7e-05	0.64
348	SERP1	stress-associated endoplasmic reticulum protein 1	1.72e-05	0.61
349	TOMM20	translocase of outer mitochondrial membrane 20 homolog (yeast)	1.73e-05	0.41
350	ODAM	odontogenic, ameloblast associated	1.74e-05	2.44
351	TMEM64	transmembrane protein 64	1.74e-05	0.42
352	FUNDC2	FUN14 domain containing 2	1.74e-05	0.33
353	STXBP1	syntaxin binding protein 1	1.75e-05	0.58
354	DBF4B	DBF4 homolog B (<i>S. cerevisiae</i>)	1.76e-05	1.96
355	TF	transferrin	1.79e-05	0.49
356	STMN1	stathmin 1	1.8e-05	2.33
357	MED25	mediator complex subunit 25	1.8e-05	2.27
358	TXNIP	thioredoxin interacting protein	1.82e-05	0.36
359	CCDC138	coiled-coil domain containing 138	1.84e-05	2.33
360	STOM	stomatin	1.85e-05	0.60
361	BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	1.9e-05	2.63
362	TERF1	telomeric repeat binding factor (NIMA-interacting) 1	1.93e-05	1.56
363	IQCK	IQ motif containing K	1.95e-05	2.08
364	BAG1	BCL2-associated athanogene	1.95e-05	0.58
365	CXCL16	chemokine (C-X-C motif) ligand 16	1.96e-05	0.43
366	PGCP	plasma glutamate carboxypeptidase	1.97e-05	0.48
367	ARFGAP3	ADP-ribosylation factor GTPase activating protein 3	1.98e-05	0.47
368	SOX4	SRY (sex determining region Y)-box 4	1.98e-05	0.57
369	C13orf34	chromosome 13 open reading frame 34	1.99e-05	2.17
370	PDGFA	platelet-derived growth factor alpha polypeptide	2.02e-05	0.35
371	TROAP	trophinin associated protein (tastin)	2.05e-05	1.69
372	CDKN3	cyclin-dependent kinase inhibitor 3	2.05e-05	2.27
373	POLD1	polymerase (DNA directed), delta 1, catalytic subunit 125kDa	2.06e-05	1.85
374	LARS2	leucyl-tRNA synthetase 2, mitochondrial	2.06e-05	1.72

375	ANLN	anillin, actin binding protein	2.07e-05	3.23
376	SNRNP48	small nuclear ribonucleoprotein 48kDa (U11/U12)	2.1e-05	2.04
377	BLM	Bloom syndrome, RecQ helicase-like	2.11e-05	2.08
378	CPN2	carboxypeptidase N, polypeptide 2	2.12e-05	1.89
379	SEC23B	Sec23 homolog B (<i>S. cerevisiae</i>)	2.12e-05	0.45
380	ASB9	ankyrin repeat and SOCS box-containing 9	2.13e-05	3.13
381	SQSTM1	sequestosome 1	2.15e-05	0.51
382	CHAF1A	chromatin assembly factor 1, subunit A (p150)	2.16e-05	2.13
383	GM2A	GM2 ganglioside activator	2.17e-05	1.72
384	PLEKHA1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	2.17e-05	0.54
385	CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	2.17e-05	0.15
386	RNASET2	ribonuclease T2	2.17e-05	0.41
387	SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	2.18e-05	1.85
388	TMPO	thymopoietin	2.24e-05	1.96
389	HIST1H2AC	histone cluster 1, H2ac	2.27e-05	0.31
390	CNOT8	CCR4-NOT transcription complex, subunit 8	2.28e-05	0.44
391	TPP1	tripeptidyl peptidase I	2.29e-05	0.53
392	C20orf199	chromosome 20 open reading frame 199	2.3e-05	0.58
393	THBS1	thrombospondin 1	2.3e-05	0.23
394	PARN	poly(A)-specific ribonuclease (deadenylation nuclease)	2.31e-05	1.67
395	PIR	pirin (iron-binding nuclear protein)	2.31e-05	2.27
396	PDZD8	PDZ domain containing 8	2.32e-05	2.17
397	SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	2.32e-05	0.36
398	SKA3	spindle and kinetochore associated complex subunit 3	2.33e-05	1.75
399	KIF20B	kinesin family member 20B	2.33e-05	2.27
400	C12orf11	chromosome 12 open reading frame 11	2.34e-05	1.96
401	ITPRIPL2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	2.34e-05	0.52
402	EXOC5	exocyst complex component 5	2.36e-05	1.59
403	MXRA7	matrix-remodelling associated 7	2.38e-05	0.52
404	PCGF5	polycomb group ring finger 5	2.44e-05	0.52
405	PPARG	peroxisome proliferator-activated receptor gamma	2.45e-05	0.58
406	NDC80	NDC80 homolog, kinetochore complex component (<i>S. cerevisiae</i>)	2.45e-05	5.88
407	PLK4	polo-like kinase 4 (<i>Drosophila</i>)	2.49e-05	2.86
408	LAMP2	lysosomal-associated membrane protein 2	2.51e-05	0.60
409	CDCA4	cell division cycle associated 4	2.52e-05	1.92
410	SERPINA5	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5	2.53e-05	0.35
411	CDC45L	CDC45 cell division cycle 45-like (<i>S. cerevisiae</i>)	2.55e-05	2.04
412	ALCAM	activated leukocyte cell adhesion molecule	2.59e-05	0.52
413	GAB1	GRB2-associated binding protein 1	2.63e-05	1.75
414	SPAG5	sperm associated antigen 5	2.63e-05	3.03
415	HIST1H4C	histone cluster 1, H4c	2.67e-05	2.50
416	TUBA1A	tubulin, alpha 1a	2.7e-05	0.34
417	RIOK3	RIO kinase 3 (yeast)	2.75e-05	0.36

418	UBASH3B	ubiquitin associated and SH3 domain containing, B	2.76e-05	0.66
419	CENPM	centromere protein M	2.76e-05	2.04
420	UBFD1	ubiquitin family domain containing 1	2.76e-05	0.51
421	HNRNPL	heterogeneous nuclear ribonucleoprotein L	2.78e-05	1.72
422	RNF14	ring finger protein 14	2.8e-05	0.41
423	RPL3	ribosomal protein L3	2.81e-05	0.51
424	SH3RF2	SH3 domain containing ring finger 2	2.86e-05	2.27
425	IFI30	interferon, gamma-inducible protein 30	2.87e-05	1.72
426	ETV4	ets variant 4	2.87e-05	0.41
427	UPF3B	UPF3 regulator of nonsense transcripts homolog B (yeast)	2.89e-05	1.92
428	PLG	plasminogen	2.9e-05	0.52
429	POLR1D	polymerase (RNA) I polypeptide D, 16kDa	2.93e-05	0.49
430	FANCM	Fanconi anemia, complementation group M	2.96e-05	2.22
431	MRE11A	MRE11 meiotic recombination 11 homolog A (<i>S. cerevisiae</i>)	2.98e-05	1.96
432	MKLN1	muskelin 1, intracellular mediator containing kelch motifs	3.03e-05	0.60
433	EPAS1	endothelial PAS domain protein 1	3.05e-05	0.40
434	TFF3	trefoil factor 3 (intestinal)	3.07e-05	0.51
435	SMPX	small muscle protein, X-linked	3.07e-05	2.17
436	OS9	osteosarcoma amplified 9, endoplasmic reticulum lectin	3.08e-05	0.47
437	C5orf53	chromosome 5 open reading frame 53	3.09e-05	0.62
438	GEN1	Gen homolog 1, endonuclease (<i>Drosophila</i>)	3.1e-05	2.00
439	C9orf40	chromosome 9 open reading frame 40	3.1e-05	2.17
440	HMGN4	high mobility group nucleosomal binding domain 4	3.11e-05	0.47
441	SMC2	structural maintenance of chromosomes 2	3.14e-05	2.50
442	AKAP12	A kinase (PRKA) anchor protein 12	3.22e-05	0.48
443	ST6GALNAC4	ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylglactosaminide alpha-2,6-sialyltransferase 4	3.24e-05	0.56
444	AKIRIN2	akirin 2	3.26e-05	2.13
445	CTSD	cathepsin D	3.29e-05	0.37
446	MAGOHB	mago-nashi homolog B (<i>Drosophila</i>)	3.3e-05	1.92
447	C4orf46	chromosome 4 open reading frame 46	3.3e-05	2.27
448	BNIP2	BCL2/adenovirus E1B 19kDa interacting protein 2	3.31e-05	0.59
449	SPTBN1	spectrin, beta, non-erythrocytic 1	3.37e-05	0.45
450	HRSP12	heat-responsive protein 12	3.37e-05	1.92
451	IFRD1	interferon-related developmental regulator 1	3.41e-05	0.47
452	RFXAP	regulatory factor X-associated protein	3.41e-05	1.92
453	ERLEC1	endoplasmic reticulum lectin 1	3.41e-05	0.56
454	IGFBP1	insulin-like growth factor binding protein 1	3.46e-05	0.11
455	SFRS2B	splicing factor, arginine/serine-rich 2B	3.49e-05	0.64
456	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	3.54e-05	0.52
457	CCNB2	cyclin B2	3.62e-05	2.22
458	SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	3.68e-05	0.54
459	CDCA8	cell division cycle associated 8	3.76e-05	1.92

460	HELLS	helicase, lymphoid-specific	3.82e-05	2.27
461	PINK1	PTEN induced putative kinase 1	3.83e-05	0.58
462	KIF14	kinesin family member 14	3.85e-05	4.35
463	ZDHHC4	zinc finger, DHHC-type containing 4	3.94e-05	0.41
464	DSCC1	defective in sister chromatid cohesion 1 homolog (<i>S. cerevisiae</i>)	4.03e-05	2.22
465	MCM3	minichromosome maintenance complex component 3	4.09e-05	2.00
466	CRYAA	crystallin, alpha A	4.13e-05	0.40
467	MFSD6	major facilitator superfamily domain containing 6	4.28e-05	0.58
468	BRCA1	breast cancer 1, early onset	4.28e-05	3.70
469	IL1R1	interleukin 1 receptor, type I	4.29e-05	1.92
470	HLA-F	major histocompatibility complex, class I, F	4.32e-05	0.53
471	NCAPG2	non-SMC condensin II complex, subunit G2	4.52e-05	2.94
472	PHF10	PHD finger protein 10	4.58e-05	0.53
473	HAUS1	HAUS augmin-like complex, subunit 1	4.61e-05	1.92
474	LMO4	LIM domain only 4	4.61e-05	1.64
475	HMGB2	high-mobility group box 2	4.62e-05	2.50
476	PTGR2	prostaglandin reductase 2	4.62e-05	1.96
477	ZWINT	ZW10 interactor	4.65e-05	3.03
478	ESPL1	extra spindle pole bodies homolog 1 (<i>S. cerevisiae</i>)	4.77e-05	2.38
479	BHMT	betaine-homocysteine methyltransferase	4.81e-05	2.00
480	RFC3	replication factor C (activator 1) 3, 38kDa	4.83e-05	2.38
481	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	4.84e-05	0.50
482	ALDOA	aldolase A, fructose-bisphosphate	4.88e-05	0.53
483	HPS3	Hermansky-Pudlak syndrome 3	4.88e-05	0.42
484	C9orf3	chromosome 9 open reading frame 3	4.94e-05	0.62
485	HMMR	hyaluronan-mediated motility receptor (RHAMM)	4.95e-05	3.45
486	TST	thiosulfate sulfurtransferase (rhodanese)	4.98e-05	0.41
487	PTPRF	protein tyrosine phosphatase, receptor type, F	5.02e-05	0.59
488	CTGF	connective tissue growth factor	5.03e-05	0.16
489	SERINC1	serine incorporator 1	5.04e-05	0.50
490	STIL	SCL/TAL1 interrupting locus	5.07e-05	2.04
491	L3MBTL	l(3)mbt-like (<i>Drosophila</i>)	5.08e-05	0.47
492	UPRT	uracil phosphoribosyltransferase (FUR1) homolog (<i>S. cerevisiae</i>)	5.09e-05	1.82
493	GPSM2	G-protein signaling modulator 2 (AGS3-like, <i>C. elegans</i>)	5.2e-05	2.22
494	PRIM2	primase, DNA, polypeptide 2 (58kDa)	5.2e-05	2.78
495	UBE2Q2	ubiquitin-conjugating enzyme E2Q family member 2	5.24e-05	0.46
496	SMC3	structural maintenance of chromosomes 3	5.26e-05	2.04
497	CCDC91	coiled-coil domain containing 91	5.55e-05	0.51
498	FANCI	Fanconi anemia, complementation group I	5.56e-05	2.94
499	KIF23	kinesin family member 23	5.57e-05	2.50
500	HIST1H2BD	histone cluster 1, H2bd	5.62e-05	0.32
501	SPTLC3	serine palmitoyltransferase, long chain base subunit 3	5.71e-05	2.56
502	ORC5L	origin recognition complex, subunit 5-like (yeast)	5.8e-05	1.61

503	IL18	interleukin 18 (interferon-gamma-inducing factor)	5.82e-05	2.27
504	LOC645722	hypothetical LOC645722	5.84e-05	1.96
505	MAP1LC3B	microtubule-associated protein 1 light chain 3 beta	5.85e-05	0.56
506	TIMP2	TIMP metalloproteinase inhibitor 2	5.88e-05	0.60
507	FLJ12993	hypothetical LOC441027	5.92e-05	1.92
508	C14orf145	chromosome 14 open reading frame 145	5.94e-05	1.69
509	CEP55	centrosomal protein 55kDa	6.03e-05	2.86
510	KIF18A	kinesin family member 18A	6.12e-05	2.00
511	SMURF2	SMAD specific E3 ubiquitin protein ligase 2	6.16e-05	0.38
512	TMX4	thioredoxin-related transmembrane protein 4	6.17e-05	0.49
513	CPN1	carboxypeptidase N, polypeptide 1	6.18e-05	0.52
514	CENPH	centromere protein H	6.37e-05	2.04
515	TTYH1	tweety homolog 1 (Drosophila)	6.41e-05	0.57
516	THOC2	THO complex 2	6.48e-05	1.64
517	TMPRSS3	transmembrane protease, serine 3	6.51e-05	0.32
518	KLF11	Kruppel-like factor 11	6.6e-05	0.38
519	H2BFS	H2B histone family, member S	6.74e-05	0.28
520	CPB2	carboxypeptidase B2 (plasma)	6.77e-05	1.82
521	CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 2	6.8e-05	0.50
522	SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	6.88e-05	0.61
523	HIST1H2BC	histone cluster 1, H2bc	6.9e-05	0.50
524	NRTN	neurturin	7.01e-05	0.42
525	ASXL1	additional sex combs like 1 (Drosophila)	7.05e-05	1.79
526	DIO1	deiodinase, iodothyronine, type I	7.07e-05	2.22
527	CENPK	centromere protein K	7.08e-05	2.63
528	TRIM22	tripartite motif-containing 22	7.11e-05	0.56
529	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	7.19e-05	2.50
530	CAMTA1	calmodulin binding transcription activator 1	7.2e-05	0.50
531	LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	7.24e-05	0.52
532	HPCAL1	hippocalcin-like 1	7.31e-05	0.52
533	WWTR1	WW domain containing transcription regulator 1	7.36e-05	0.51
534	ERP27	endoplasmic reticulum protein 27	7.4e-05	2.70
535	RNASE4	ribonuclease, RNase A family, 4	7.54e-05	0.38
536	TUBB2B	tubulin, beta 2B	7.67e-05	0.18
537	C20orf72	chromosome 20 open reading frame 72	7.69e-05	2.00
538	MCM7	minichromosome maintenance complex component 7	7.77e-05	1.79
539	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	7.82e-05	0.44
540	N4BP2L1	NEDD4 binding protein 2-like 1	7.82e-05	0.56
541	APOM	apolipoprotein M	8.02e-05	0.47
542	CD9	CD9 molecule	8.08e-05	0.44
543	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	8.26e-05	0.43
544	RBM3	RNA binding motif (RNP1, RRM) protein 3	8.29e-05	0.47
545	NUF2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	8.4e-05	4.17

546	TPM1	tropomyosin 1 (alpha)	8.43e-05	0.49
547	DIS3	DIS3 mitotic control homolog (<i>S. cerevisiae</i>)	8.53e-05	0.34
548	C1orf135	chromosome 1 open reading frame 135	8.54e-05	1.67
549	40240	membrane-associated ring finger (C3HC4) 3	8.57e-05	0.62
550	MIXL1	Mix1 homeobox-like 1 (<i>Xenopus laevis</i>)	8.77e-05	0.53
551	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	8.84e-05	2.27
552	DCLRE1B	DNA cross-link repair 1B (PSO2 homolog, <i>S. cerevisiae</i>)	8.88e-05	2.08
553	HIST1H2BE	histone cluster 1, H2be	9.02e-05	0.40
554	SRP72	signal recognition particle 72kDa	9.37e-05	0.47
555	PHF17	PHD finger protein 17	9.38e-05	2.13
556	SCLT1	sodium channel and clathrin linker 1	9.4e-05	2.56
557	DEPDC1B	DEP domain containing 1B	9.56e-05	2.13
558	E2F8	E2F transcription factor 8	9.62e-05	4.00
559	FOXM1	forkhead box M1	9.62e-05	2.44
560	SAT1	spermidine/spermine N1-acetyltransferase 1	9.63e-05	0.39
561	SDCCAG10	serologically defined colon cancer antigen 10	9.76e-05	1.54
562	BRWD1	bromodomain and WD repeat domain containing 1	0.000101	0.38
563	JMJD6	jumonji domain containing 6	0.0001024	0.60
564	ZSCAN16	zinc finger and SCAN domain containing 16	0.0001026	1.92
565	LEAP2	liver expressed antimicrobial peptide 2	0.0001068	0.53
566	TM4SF1	transmembrane 4 L six family member 1	0.0001094	0.51
567	ARRDC4	arrestin domain containing 4	0.0001105	0.35
568	HIST1H2BF	histone cluster 1, H2bf	0.0001108	0.44
569	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	0.0001115	0.54
570	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	0.000112	0.54
571	TUBB2A	tubulin, beta 2A	0.0001127	0.59
572	MAL2	mal, T-cell differentiation protein 2	0.0001128	0.56
573	CREBZF	CREB/ATF bZIP transcription factor	0.0001135	0.58
574	C14orf106	chromosome 14 open reading frame 106	0.0001192	2.27
575	NCAPD2	non-SMC condensin I complex, subunit D2	0.0001201	1.72
576	SMAD4	SMAD family member 4	0.0001208	0.49
577	MELK	maternal embryonic leucine zipper kinase	0.0001227	2.63
578	NT5E	5'-nucleotidase, ecto (CD73)	0.000123	0.43
579	DLK1	delta-like 1 homolog (<i>Drosophila</i>)	0.0001246	0.58
580	AQP3	aquaporin 3 (Gill blood group)	0.0001257	0.43
581	SLC17A2	solute carrier family 17 (sodium phosphate), member 2	0.0001261	0.53
582	ARL6IP6	ADP-ribosylation-like factor 6 interacting protein 6	0.0001275	2.04
583	TNNC1	troponin C type 1 (slow)	0.0001286	0.47
584	LOC730101	hypothetical LOC730101	0.0001289	1.96
585	LSM5	LSM5 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>)	0.0001299	1.79
586	MCM8	minichromosome maintenance complex component 8	0.0001309	2.50
587	PBK	PDZ binding kinase	0.000132	3.45
588	ERAP1	endoplasmic reticulum aminopeptidase 1	0.0001334	0.44

589	BAMBI	BMP and activin membrane-bound inhibitor homolog (<i>Xenopus laevis</i>)	0.000134	1.72
590	NANOS1	nanos homolog 1 (<i>Drosophila</i>)	0.0001358	0.50
591	S100A11	S100 calcium binding protein A11	0.0001407	1.96
592	KLF6	Kruppel-like factor 6	0.0001416	0.46
593	C19orf6	chromosome 19 open reading frame 6	0.0001421	0.53
594	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	0.0001429	0.48
595	HIST1H2BH	histone cluster 1, H2bh	0.0001431	0.39
596	TCOF1	Treacher Collins-Franceschetti syndrome 1	0.000146	2.86
597	GINS2	GINS complex subunit 2 (Psf2 homolog)	0.0001465	2.44
598	KIAA0430	KIAA0430	0.0001472	0.45
599	PHTF2	putative homeodomain transcription factor 2	0.0001473	1.89
600	LDLR	low density lipoprotein receptor	0.0001488	0.46
601	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	0.0001515	0.44
602	C1orf104	chromosome 1 open reading frame 104	0.0001516	0.48
603	FLJ39632	hypothetical LOC642477	0.0001536	0.52
604	DUSP6	dual specificity phosphatase 6	0.0001537	0.53
605	SALL1	sal-like 1 (<i>Drosophila</i>)	0.0001538	1.79
606	RETSAT	retinol saturase (all-trans-retinol 13,14-reductase)	0.0001565	0.57
607	IL11	interleukin 11	0.0001571	0.55
608	MRPS23	mitochondrial ribosomal protein S23	0.0001572	0.53
609	SGMS2	sphingomyelin synthase 2	0.0001624	0.49
610	CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	0.000165	0.57
611	BTBD3	BTB (POZ) domain containing 3	0.0001673	0.52
612	ARHGAP18	Rho GTPase activating protein 18	0.0001683	1.89
613	CHPT1	choline phosphotransferase 1	0.0001697	0.53
614	RAD51AP1	RAD51 associated protein 1	0.0001711	3.13
615	CENPA	centromere protein A	0.0001734	3.45
616	MDK	midkine (neurite growth-promoting factor 2)	0.0001754	0.53
617	ESCO2	establishment of cohesion 1 homolog 2 (<i>S. cerevisiae</i>)	0.0001793	2.94
618	EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	0.0001823	0.65
619	TIMM17A	translocase of inner mitochondrial membrane 17 homolog A (yeast)	0.0001842	0.39
620	SYNJ2	synaptojanin 2	0.0001862	0.56
621	DRAM2	DNA-damage regulated autophagy modulator 2	0.0001865	0.47
622	RACGAP1	Rac GTPase activating protein 1	0.0001879	2.63
623	HINT3	histidine triad nucleotide binding protein 3	0.0001896	0.36
624	TFR2	transferrin receptor 2	0.0001957	0.41
625	LIMA1	LIM domain and actin binding 1	0.0001997	1.75
626	PERP	PERP, TP53 apoptosis effector	0.0002007	0.32
627	MRPS31	mitochondrial ribosomal protein S31	0.0002092	1.69
628	TIMP3	TIMP metalloproteinase inhibitor 3	0.0002102	0.44
629	FBXL22	F-box and leucine-rich repeat protein 22	0.0002132	1.85
630	WIPI1	WD repeat domain, phosphoinositide interacting 1	0.0002148	0.39
631	C10orf78	chromosome 10 open reading frame 78	0.0002163	2.00

632	GHITM	growth hormone inducible transmembrane protein	0.0002224	0.51
633	RPA3	replication protein A3, 14kDa	0.0002235	2.56
634	UNG	uracil-DNA glycosylase	0.000227	2.08
635	SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	0.0002282	0.50
636	HSPD1	heat shock 60kDa protein 1 (chaperonin)	0.0002292	0.47
637	E2F7	E2F transcription factor 7	0.000232	2.08
638	C10orf10	chromosome 10 open reading frame 10	0.0002327	0.23
639	PIF1	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	0.0002346	2.70
640	MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	0.0002349	3.45
641	BIRC5	baculoviral IAP repeat-containing 5	0.0002361	2.44
642	SYNE2	spectrin repeat containing, nuclear envelope 2	0.0002361	2.22
643	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	0.0002376	2.63
644	GPBP1L1	GC-rich promoter binding protein 1-like 1	0.0002412	0.48
645	GLB1	galactosidase, beta 1	0.00026	0.47
646	FAM83D	family with sequence similarity 83, member D	0.0002653	2.33
647	LOC729887	hypothetical protein LOC729887	0.0002678	1.82
648	C5orf34	chromosome 5 open reading frame 34	0.0002753	1.49
649	DERL1	Der1-like domain family, member 1	0.000276	0.50
650	NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	0.0002772	2.13
651	TTC14	tetratricopeptide repeat domain 14	0.0002774	0.44
652	PPIL5	peptidylprolyl isomerase (cyclophilin)-like 5	0.0002774	1.96
653	PBLD	phenazine biosynthesis-like protein domain containing	0.0002782	2.70
654	YME1L1	YME1-like 1 (S. cerevisiae)	0.0002791	0.53
655	IFI6	interferon, alpha-inducible protein 6	0.0002821	0.51
656	EHHADH	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	0.0002847	2.17
657	RASD1	RAS, dexamethasone-induced 1	0.0002902	0.41
658	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	0.0002924	0.19
659	C1D	C1D nuclear receptor co-repressor	0.0002957	0.44
660	ABCA5	ATP-binding cassette, sub-family A (ABC1), member 5	0.0002974	0.47
661	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	0.0003047	0.53
662	RNASEH2A	ribonuclease H2, subunit A	0.0003068	1.96
663	SNRPN	small nuclear ribonucleoprotein polypeptide N	0.0003106	0.59
664	DOK6	docking protein 6	0.000315	0.49
665	RSRC1	arginine/serine-rich coiled-coil 1	0.000315	1.61
666	C8orf4	chromosome 8 open reading frame 4	0.0003161	0.21
667	PCYT1B	phosphate cytidyltransferase 1, choline, beta	0.0003214	3.03
668	ZSWIM7	zinc finger, SWIM-type containing 7	0.0003234	0.49
669	C5orf26	chromosome 5 open reading frame 26	0.0003242	0.56
670	BRP44	brain protein 44	0.0003264	1.92
671	MYO10	myosin X	0.0003268	2.38
672	C16orf75	chromosome 16 open reading frame 75	0.000334	2.44
673	KIF11	kinesin family member 11	0.0003364	3.23
674	SELS	selenoprotein S	0.0003415	0.50

675	CCNA2	cyclin A2	0.0003548	2.22
676	DNAJC14	DnaJ (Hsp40) homolog, subfamily C, member 14	0.0003561	0.57
677	DUT	deoxyuridine triphosphatase	0.0003779	1.92
678	ANKRD32	ankyrin repeat domain 32	0.0003975	1.89
679	TGOLN2	trans-golgi network protein 2	0.0003991	0.51
680	DNA2	DNA replication helicase 2 homolog (yeast)	0.0004034	2.27
681	C6orf211	chromosome 6 open reading frame 211	0.000408	2.04
682	DHFR	dihydrofolate reductase	0.0004244	2.86
683	MTIF2	mitochondrial translational initiation factor 2	0.0004349	1.82
684	ERO1LB	ERO1-like beta (<i>S. cerevisiae</i>)	0.0004458	0.49
685	C6orf130	chromosome 6 open reading frame 130	0.0004499	1.52
686	WWC2	WW and C2 domain containing 2	0.0004528	1.49
687	DSG2	desmoglein 2	0.0004532	0.50
688	C8orf40	chromosome 8 open reading frame 40	0.0004793	0.56
689	APP	amyloid beta (A4) precursor protein	0.0004807	0.47
690	FANCD2	Fanconi anemia, complementation group D2	0.0004826	2.44
691	HNF4G	hepatocyte nuclear factor 4, gamma	0.0004976	0.52
692	LRP10	low density lipoprotein receptor-related protein 10	0.0005019	0.56
693	ORC6L	origin recognition complex, subunit 6 like (yeast)	0.0005148	1.92
694	TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1	0.0005178	0.35
695	SKP1	S-phase kinase-associated protein 1	0.0005248	0.38
696	TNFSF14	tumor necrosis factor (ligand) superfamily, member 14	0.0005274	0.43
697	RSC1A1	regulatory solute carrier protein, family 1, member 1	0.0005356	2.08
698	RMI1	RMI1, RecQ mediated genome instability 1, homolog (<i>S. cerevisiae</i>)	0.0005435	2.33
699	RRM1	ribonucleotide reductase M1	0.000546	2.17
700	P4HB	prolyl 4-hydroxylase, beta polypeptide	0.0005492	0.27
701	DNAJB1	DnaJ (Hsp40) homolog, subfamily B, member 1	0.000551	0.52
702	CD24	CD24 molecule	0.0005564	0.48
703	C1orf112	chromosome 1 open reading frame 112	0.0005609	1.64
704	LYZ	lysozyme (renal amyloidosis)	0.0005661	0.28
705	PDIA2	protein disulfide isomerase family A, member 2	0.0005767	0.45
706	C3orf23	chromosome 3 open reading frame 23	0.0005815	0.53
707	CBX4	chromobox homolog 4 (Pc class homolog, <i>Drosophila</i>)	0.0005863	0.56
708	UHRF1BP1	UHRF1 binding protein 1	0.0005872	1.75
709	RAD54B	RAD54 homolog B (<i>S. cerevisiae</i>)	0.0005949	1.96
710	GAS2L3	growth arrest-specific 2 like 3	0.000627	2.56
711	PTP4A1	protein tyrosine phosphatase type IVA, member 1	0.0006275	0.51
712	USP31	ubiquitin specific peptidase 31	0.000628	0.60
713	SLC16A3	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	0.0006287	0.50
714	IPP	intracisternal A particle-promoted polypeptide	0.000634	1.85
715	HPN	hepsin	0.0006356	0.51
716	ANXA3	annexin A3	0.0006373	0.58
717	PGK1	phosphoglycerate kinase 1	0.0006434	0.53

718	EFR3A	EFR3 homolog A (<i>S. cerevisiae</i>)	0.0006466	0.54
719	WDYHV1	WDYHV motif containing 1	0.0006628	0.42
720	CHST9	carbohydrate (N-acetylgalactosamine 4-O) sulfotransferase 9	0.0006716	4.00
721	HSPA8	heat shock 70kDa protein 8	0.0006842	0.52
722	MASTL	microtubule associated serine/threonine kinase-like	0.0007025	2.17
723	FAM19A5	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	0.0007071	0.52
724	PSAP	prosaposin	0.0007121	0.47
725	ALB	albumin	0.0007186	0.28
726	INSIG2	insulin induced gene 2	0.0007311	0.56
727	RSL1D1	ribosomal L1 domain containing 1	0.0007596	0.41
728	PSMD7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	0.0007666	0.59
729	NCRNA00204	non-protein coding RNA 204	0.0007757	0.57
730	ARF1	ADP-ribosylation factor 1	0.0007858	0.43
731	LOC729680	hypothetical protein LOC729680	0.0008121	0.48
732	C8G	complement component 8, gamma polypeptide	0.000827	0.47
733	PPP3R1	protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform	0.0008358	0.49
734	TRIB1	tribbles homolog 1 (<i>Drosophila</i>)	0.0008563	0.46
735	ACSL3	acyl-CoA synthetase long-chain family member 3	0.0008615	0.50
736	RHOBTB1	Rho-related BTB domain containing 1	0.0008666	2.63
737	INHBE	inhibin, beta E	0.000874	0.46
738	PLEKHA6	pleckstrin homology domain containing, family A member 6	0.0008786	1.82
739	NEK7	NIMA (never in mitosis gene a)-related kinase 7	0.0009124	0.54
740	SKA1	spindle and kinetochore associated complex subunit 1	0.0009765	2.63
741	JUN	jun oncogene	0.0009798	0.42
742	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	0.0009851	1.39

Supplementary Table S2

Table S2: Functional classification of genes differentially expressed between the *Spor* and *SalGld* groups using KEGG and Biocarta pathways. Gene expression changes were expressed as fold change between *Spor* to *SalGld*, and represent the ratio of the geometric mean intensities of *Spor* to those of *SalGld*. Datasets representing the three time points within each experimental group have been grouped together and were regarded as experimental replicates.

Gene symbol	Description	Parametric p-value	Fold-change
	<u>Antigen processing and presentation (Kegg Pathway hsa04612)</u>		
HSPA1A	heat shock 70kDa protein 1A	< 1e-07	0.33
NA	NA	< 1e-07	0.16
CTSB	cathepsin B	9e-07	0.31
HLA-C	major histocompatibility complex, class I, C	1.5e-06	0.45
HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	1.6e-06	0.48
CTSB	cathepsin B	3e-06	0.47
HLA-B	major histocompatibility complex, class I, B	3.9e-06	0.40
RFX5	regulatory factor X, 5 (influences HLA class II expression)	8.5e-06	1.82
PDIA3	protein disulfide isomerase family A, member 3	1.43e-05	0.45
IFI30	interferon, gamma-inducible protein 30	2.87e-05	1.72
RFXAP	regulatory factor X-associated protein	3.41e-05	1.92
HLA-F	major histocompatibility complex, class I, F	4.32e-05	0.53
HSPA8	heat shock 70kDa protein 8	6.844e-04	0.52
	<u>Ubiquitin mediated proteolysis (Kegg Pathway hsa04120)</u>		
CDC20	cell division cycle 20 homolog (S. cerevisiae)	< 1e-07	4.00
UBE2C	ubiquitin-conjugating enzyme E2C	< 1e-07	2.63
SKP2	S-phase kinase-associated protein 2 (p45)	1.5e-06	2.13
SMURF2	SMAD specific E3 ubiquitin protein ligase 2	6.17e-05	0.38
SKP1	S-phase kinase-associated protein 1	5.249e-04	0.38
	<u>Glycerolipid metabolism (Kegg Pathway hsa00561)</u>		
ADH4	alcohol dehydrogenase 4 (class II), pi polypeptide	1e-07	2.70
ADH6	alcohol dehydrogenase 6 (class V)	2e-07	2.17
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	9e-06	0.49
DGAT1	diacylglycerol O-acyltransferase homolog 1 (mouse)	9.5e-06	1.96
ALDH7A1	aldehyde dehydrogenase 7 family, member A1	1.31e-05	1.92
GLB1	galactosidase, beta 1	2.6e-04	0.47
	<u>Cell cycle (Kegg Pathway hsa04110)</u>		
CDC20	cell division cycle 20 homolog (S. cerevisiae)	< 1e-07	4.00
PTTG1	pituitary tumor-transforming 1	< 1e-07	3.33
CCNB1	cyclin B1	7e-07	3.45
CDC25C	cell division cycle 25 homolog C (S. pombe)	7e-07	2.50
BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	1e-06	3.85
CDC2	cell division cycle 2, G1 to S and G2 to M	1.2e-06	4.17

TGFB1	transforming growth factor, beta 1	1.3e-06	0.38
SKP2	S-phase kinase-associated protein 2 (p45)	1.5e-06	2.13
MCM5	minichromosome maintenance complex component 5	2.1e-06	3.85
CCNE2	cyclin E2	2.1e-06	2.13
ORC3L	origin recognition complex, subunit 3-like (yeast)	2.8e-06	1.96
RB1	retinoblastoma 1	5.5e-06	1.96
DBF4	DBF4 homolog (S. cerevisiae)	8.4e-06	2.22
CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	1.43e-05	3.45
CDC45L	CDC45 cell division cycle 45-like (S. cerevisiae)	2.55e-05	2.04
CCNB2	cyclin B2	3.62e-05	2.22
MCM3	minichromosome maintenance complex component 3	4.1e-05	2.00
ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	4.77e-05	2.38
ORC5L	origin recognition complex, subunit 5-like (yeast)	5.81e-05	1.61
MCM7	minichromosome maintenance complex component 7	7.77e-05	1.79
YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	8.26e-05	0.43
SMAD4	SMAD family member 4	1.20e-04	0.49
MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	2.37e-04	2.63
CCNA2	cyclin A2	3.54e-04	2.22
ORC6L	origin recognition complex, subunit 6 like (yeast)	5.14e-04	1.92
SKP1	S-phase kinase-associated protein 1	5.24e-04	0.38
	<u>ECM-receptor interaction (Kegg Pathway hsa04512)</u>		
CD36	CD36 molecule (thrombospondin receptor)	1e-07	2.70
VTN	vitronectin	1.6e-06	0.39
SDC4	syndecan 4	2.3e-06	0.47
FN1	fibronectin 1	3e-06	0.56
THBS1	thrombospondin 1	2.3e-05	0.23
HMMR	hyaluronan-mediated motility receptor (RHAMM)	4.96e-05	3.45
ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	1.51e-04	0.44
	<u>Cell Communication (Kegg Pathway hsa01430)</u>		
LMNB1	lamin B1	9e-07	2.50
KRT19	keratin 19	9e-07	4.76
VTN	vitronectin	1.6e-06	0.39
FN1	fibronectin 1	3e-06	0.56
THBS1	thrombospondin 1	2.3e-05	0.23
DSG2	desmoglein 2	4.53e-04	0.50
	<u>MAPK signaling pathway (Kegg Pathway hsa04010)</u>		
HSPA1A	heat shock 70kDa protein 1A	< 1e-07	0.33
NA	NA	< 1e-07	0.16
TGFB1	transforming growth factor, beta 1	1.3e-06	0.38
HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	1.6e-06	0.48
DUSP1	dual specificity phosphatase 1	8.4e-06	0.27
FLNA	filamin A, alpha	1.19e-05	0.50
ATF4	activating transcription factor 4 (tax-responsive enhancer element B67)	1.6e-05	1.64

STMN1	stathmin 1	1.8e-05	2.33
IL1R1	interleukin 1 receptor, type I	4.3e-05	1.92
DUSP6	dual specificity phosphatase 6	1.53e-04	0.53
HSPA8	heat shock 70kDa protein 8	6.84e-04	0.52
PPP3R1	protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform	8.36e-04	0.49
JUN	jun oncogene	9.8e-04	0.42
	<u>Fatty acid metabolism (Kegg Pathway hsa00071)</u>		
ADH4	alcohol dehydrogenase 4 (class II), pi polypeptide	1e-07	2.70
ADH6	alcohol dehydrogenase 6 (class V)	2e-07	2.17
ALDH7A1	aldehyde dehydrogenase 7 family, member A1	1.31e-05	1.92
EHHADH	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	2.84e-04	2.17
ACSL3	acyl-CoA synthetase long-chain family member 3	8.61e-04	0.50
	<u>Type I diabetes mellitus (Kegg Pathway hsa04940)</u>		
HLA-C	major histocompatibility complex, class I, C	1.5e-06	0.45
CPE	carboxypeptidase E	1.7e-06	0.45
HLA-B	major histocompatibility complex, class I, B	3.9e-06	0.40
HLA-F	major histocompatibility complex, class I, F	4.32e-05	0.53
HSPD1	heat shock 60kDa protein 1 (chaperonin)	2.29e-04	0.47
	<u>Metabolism of xenobiotics by cytochrome P450 (Kegg Pathway hsa00980)</u>		
GSTA2	Glutathione S-transferase A2	<1 x 10 ⁻⁷	5.88
ADH4	alcohol dehydrogenase 4 (class II), pi polypeptide	1.0 x 10 ⁻⁷	2.70
ADH6	alcohol dehydrogenase 6 (class V)	2.0 x 10 ⁻⁷	2.17
UGT1A6	UDP glucuronosyltransferase 1 family, polypeptide A6	1.2 x 10 ⁻⁶	2.22
CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	2.2 x 10 ⁻⁵	0.15
AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	1.5 x 10 ⁻³	0.42
CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	7.9 x 10 ⁻²	0.66
	<u>Cell adhesion molecules (CAMs) (Kegg Pathway hsa04514)</u>		
HLA-C	major histocompatibility complex, class I, C	1.5e-06	0.45
SDC4	syndecan 4	2.3e-06	0.47
HLA-B	major histocompatibility complex, class I, B	3.9e-06	0.40
L1CAM	L1 cell adhesion molecule	6.8e-06	0.52
ALCAM	activated leukocyte cell adhesion molecule	2.59e-05	0.52
HLA-F	major histocompatibility complex, class I, F	4.32e-05	0.53
ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	4.84e-05	0.50
PTPRF	protein tyrosine phosphatase, receptor type, F	5.02e-05	0.59
	<u>Glycolysis/Gluconeogenesis (Kegg Pathway hsa00010)</u>		
ADH4	alcohol dehydrogenase 4 (class II), pi polypeptide	1e-07	2.70
ADH6	alcohol dehydrogenase 6 (class V)	2e-07	2.17
G6PC	glucose-6-phosphatase, catalytic subunit	1.3e-06	0.25
ALDH7A1	aldehyde dehydrogenase 7 family, member A1	1.31e-05	1.92
PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	1.46e-05	1.82
ALDOA	aldolase A, fructose-bisphosphate	4.88e-05	0.53

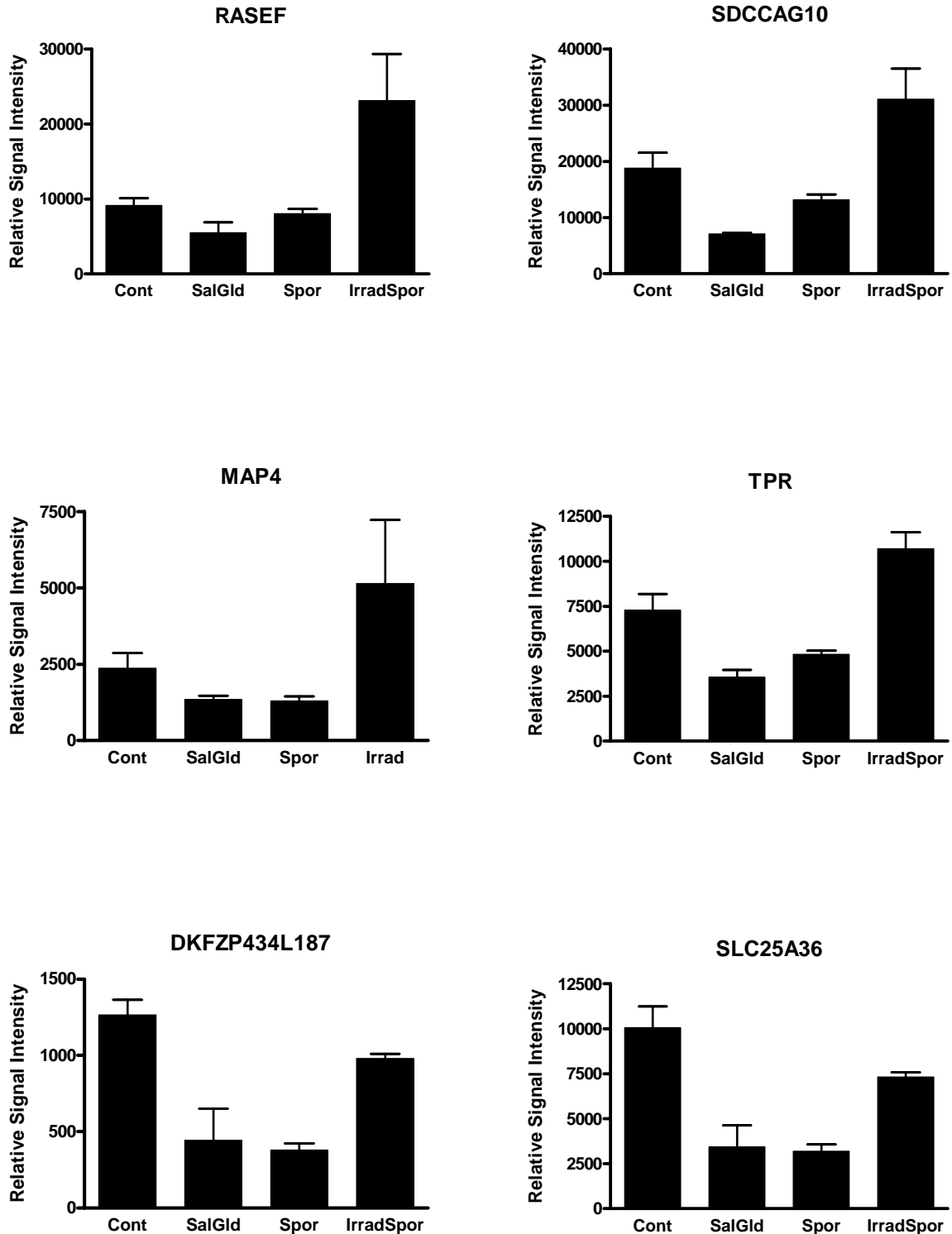
PGK1	phosphoglycerate kinase 1	6.43e-04	0.53
PGK1	phosphoglycerate kinase 1	1.31e-04	0.39
	<u>Complement and coagulation cascades (Kegg Pathway hsa04610)</u>		
C5	complement component 5	1.7e-06	0.22
SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	2.1e-06	0.18
F5	coagulation factor V (proaccelerin, labile factor)	2.3e-06	0.37
C2	complement component 2	3.5e-06	0.40
SERPIND1	serpin peptidase inhibitor, clade D (heparin cofactor), member 1	7.6e-06	0.39
F10	coagulation factor X	7.7e-06	0.46
F2	coagulation factor II (thrombin)	1.36e-05	0.52
SERPINA5	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5	2.54e-05	0.35
PLG	plasminogen	2.9e-05	0.52
CPB2	carboxypeptidase B2 (plasma)	6.77e-05	1.82
C8G	complement component 8, gamma polypeptide	8.27e-04	0.47
	<u>Regulation of actin cytoskeleton (Kegg Pathway hsa04810)</u>		
IQGAP3	IQ motif containing GTPase activating protein 3	7e-07	3.03
FN1	fibronectin 1	3e-06	0.56
DIAPH3	diaphanous homolog 3 (Drosophila)	9.4e-06	2.63
F2	coagulation factor II (thrombin)	1.36e-05	0.52
BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	1.9e-05	2.63
ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	4.84e-05	0.50
ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	1.51e-04	0.44
	<u>Natural killer cell mediated cytotoxicity (Kegg Pathway hsa04650)</u>		
TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	8e-07	0.32
HLA-C	major histocompatibility complex, class I, C	1.5e-06	0.45
HLA-B	major histocompatibility complex, class I, B	3.9e-06	0.40
ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	4.84e-05	0.50
PPP3R1	protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform	8.36e-04	0.49
	<u>Pyrimidine metabolism (Kegg Pathway hsa00240)</u>		
TK1	thymidine kinase 1, soluble	< 1e-07	3.03
POLA1	polymerase (DNA directed), alpha 1, catalytic subunit	2e-07	2.63
WSB2	WD repeat and SOCS box-containing 2	3.2e-06	0.56
POLD1	polymerase (DNA directed), delta 1, catalytic subunit 125kDa	2.06e-05	1.85
POLR1D	polymerase (RNA) I polypeptide D, 16kDa	2.93e-05	0.49
PRIM2	primase, DNA, polypeptide 2 (58kDa)	5.2e-05	2.78
NT5E	5'-nucleotidase, ecto (CD73)	1.23e-04	0.43
DUT	deoxyuridine triphosphatase	3.78e-04	1.92
RRM1	ribonucleotide reductase M1	5.46e-04	2.17
	<u>Hematopoietic cell lineage (Kegg Pathway hsa04640)</u>		
CD36	CD36 molecule (thrombospondin receptor)	1e-07	2.70
KITLG	KIT ligand	3.3e-06	2.63
IL1R1	interleukin 1 receptor, type I	4.3e-05	1.92
CD9	CD9 molecule	8.08e-05	0.44

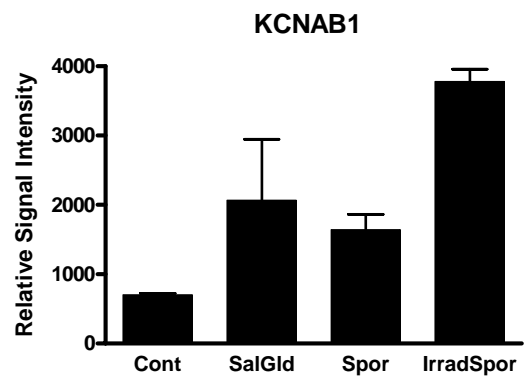
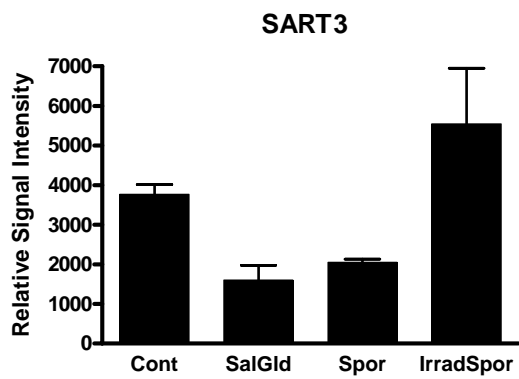
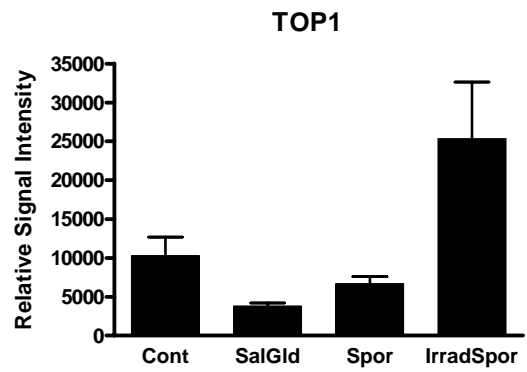
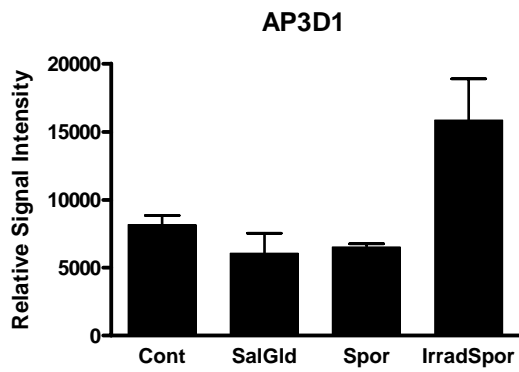
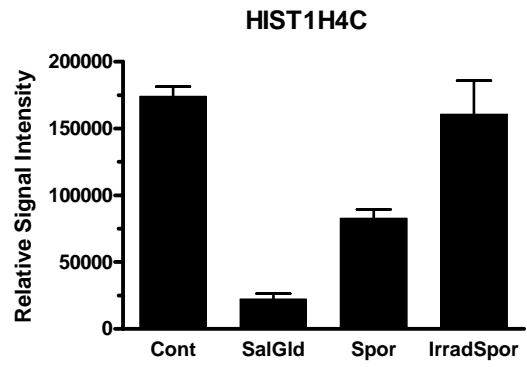
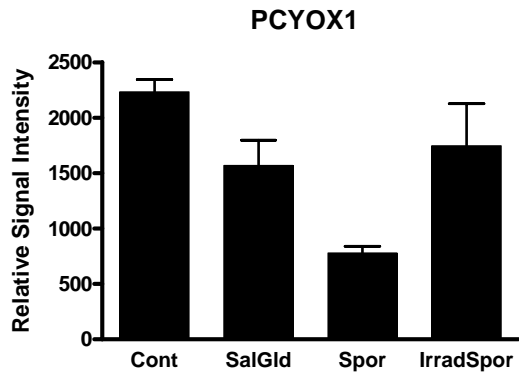
ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	1.51e-04	0.44
IL11	interleukin 11	1.57e-04	0.55
	Cytokine-cytokine receptor interaction (Kegg Pathway hsa04060)		
TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	8e-07	0.32
CCL20	chemokine (C-C motif) ligand 20	1.2e-06	0.13
TGFB1	transforming growth factor, beta 1	1.3e-06	0.38
KITLG	KIT ligand	3.3e-06	2.63
CXCL2	chemokine (C-X-C motif) ligand 2	7.1e-06	0.15
IL8	interleukin 8	1.62e-05	0.36
CXCL16	chemokine (C-X-C motif) ligand 16	1.96e-05	0.43
IL1R1	interleukin 1 receptor, type I	4.3e-05	1.92
IL18	interleukin 18 (interferon-gamma-inducing factor)	5.82e-05	2.27
IL11	interleukin 11	1.57e-04	0.55
TNFSF14	tumor necrosis factor (ligand) superfamily, member 14	5.27e-04	0.43
INHBE	inhibin, beta E	8.74e-04	0.46
	Purine metabolism (Kegg Pathway hsa00230)		
POLA1	polymerase (DNA directed), alpha 1, catalytic subunit	2e-07	2.63
WSB2	WD repeat and SOCS box-containing 2	3.2e-06	0.56
POLD1	polymerase (DNA directed), delta 1, catalytic subunit 125kDa	2.06e-05	1.85
POLR1D	polymerase (RNA) I polypeptide D, 16kDa	2.93e-05	0.49
PRIM2	primase, DNA, polypeptide 2 (58kDa)	5.2e-05	2.78
NT5E	5'-nucleotidase, ecto (CD73)	1.23e-04	0.43
RRM1	ribonucleotide reductase M1	5.46e-04	2.17
	Focal adhesion (Kegg Pathway hsa04510)		
VTN	vitronectin	1.6e-06	0.39
FN1	fibronectin 1	3e-06	0.56
FLNA	filamin A, alpha	1.19e-05	0.50
BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	1.9e-05	2.63
THBS1	thrombospondin 1	2.3e-05	0.23
ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	1.51e-04	0.44
JUN	jun oncogene	9.8e-04	0.42
	Gap junction (Kegg Pathway hsa04540)		
CDC2	cell division cycle 2, G1 to S and G2 to M	1.2e-06	4.17
TUBA1A	tubulin, alpha 1a	2.7e-05	0.34
PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	3.55e-05	0.52
TUBB2B	tubulin, beta 2B	7.67e-05	0.18
TUBB2A	tubulin, beta 2A	1.12e-04	0.59
	TGF-beta signaling pathway (Kegg Pathway hsa04350)		
TGFB1	transforming growth factor, beta 1	1.3e-06	0.38
FST	follistatin	2e-06	0.31
PPP2CB	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	6.8e-06	0.56
THBS1	thrombospondin 1	2.3e-05	0.23
SMURF2	SMAD specific E3 ubiquitin protein ligase 2	6.17e-05	0.38

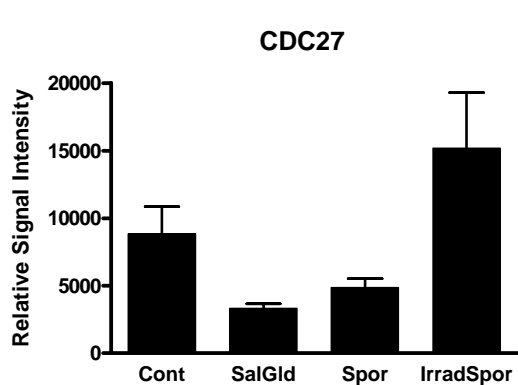
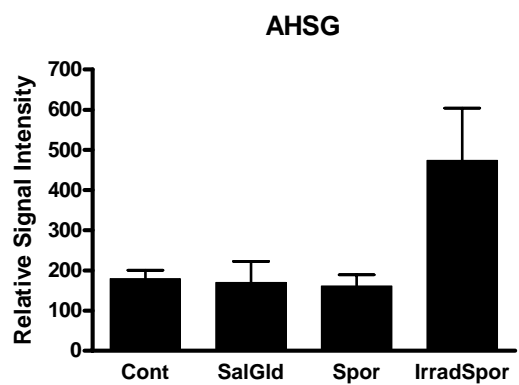
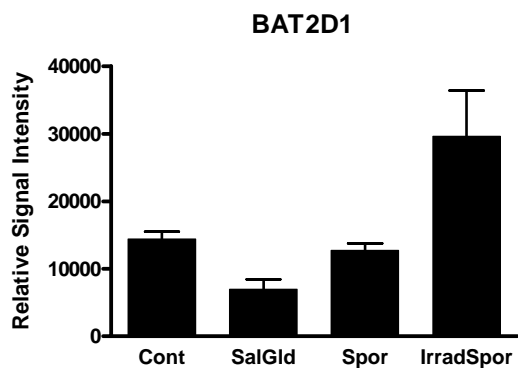
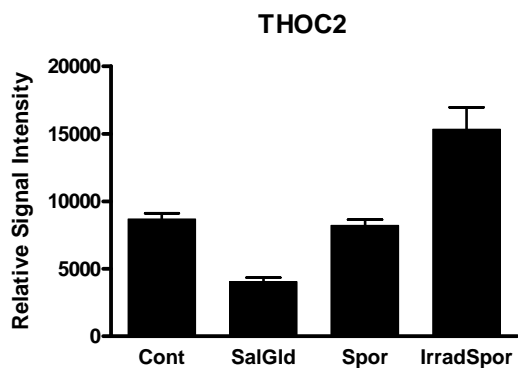
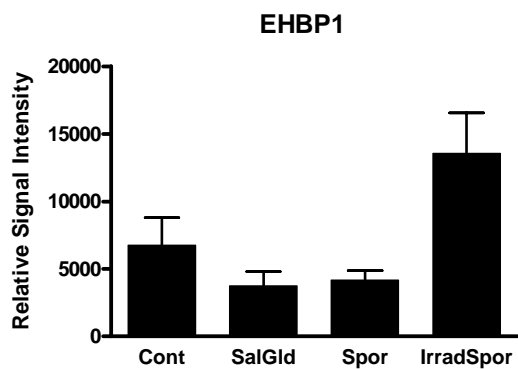
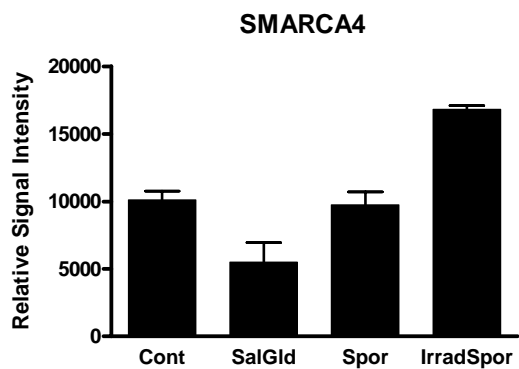
SMAD4	SMAD family member 4	1.20e-04	0.49
SKP1	S-phase kinase-associated protein 1	5.24e-04	0.38
INHBE	inhibin, beta E	8.74e-04	0.46
	<u>Glycerophospholipid metabolism (Kegg Pathway hsa00564)</u>		
LYPLA1	lysophospholipase I	2.3e-06	0.57
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	9e-06	0.49
CDS2	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 2	1.65e-04	0.57
CHPT1	choline phosphotransferase 1	1.69e-04	0.53
ESCO2	establishment of cohesion 1 homolog 2 (<i>S. cerevisiae</i>)	1.79e-04	2.94
PCYT1B	phosphate cytidyltransferase 1, choline, beta	3.21e-04	3.03
	<u>Wnt signaling pathway (Kegg Pathway hsa04310)</u>		
DKK1	dickkopf homolog 1 (<i>Xenopus laevis</i>)	2e-07	5.00
PPP2CB	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	6.8e-06	0.56
PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	3.55e-05	0.52
SMAD4	SMAD family member 4	1.20e-04	0.49
SKP1	S-phase kinase-associated protein 1	5.24e-04	0.38
PPP3R1	protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform	8.36e-04	0.49
JUN	jun oncogene	9.8e-04	0.42
	<u>Cell Cycle: G1/S Check Point (Biocarta h_g1Pathway)</u>		
CDC2	cell division cycle 2, G1 to S and G2 to M	1.2e-06	4.17
TGFB1	transforming growth factor, beta 1	1.3e-06	0.38
SKP2	S-phase kinase-associated protein 2 (p45)	1.5e-06	2.13
RB1	retinoblastoma 1	5.5e-06	1.96
SMAD4	SMAD family member 4	1.20e-04	0.49
DHFR	dihydrofolate reductase	4.24e-04	2.86
	<u>CDK Regulation of DNA Replication h_mcmPathway</u>		
MCM5	minichromosome maintenance complex component 5	2.1e-06	3.85
ORC3L	origin recognition complex, subunit 3-like (yeast)	2.8e-06	1.96
KITLG	KIT ligand	3.3e-06	2.63
CDT1	chromatin licensing and DNA replication factor 1	5.4e-06	2.94
MCM3	minichromosome maintenance complex component 3	4.1e-05	2.00
ORC5L	origin recognition complex, subunit 5-like (yeast)	5.81e-05	1.61
MCM7	minichromosome maintenance complex component 7	7.77e-05	1.79
ORC6L	origin recognition complex, subunit 6 like (yeast)	5.14 e-04	1.92
	<u>Mechanism of Gene Regulation by Peroxisome Proliferators via PPARα (h_pparaPathway)</u>		
HSPA1A	heat shock 70kDa protein 1A	< 1e-07	0.33
RB1	retinoblastoma 1	5.5e-06	1.96
DUSP1	dual specificity phosphatase 1	8.4e-06	0.27
NCOR1	nuclear receptor co-repressor 1	1.13e-05	1.61
PDGFA	platelet-derived growth factor alpha polypeptide	2.02e-05	0.35
EHHADH	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	2.84e-04	2.17
DUT	deoxyuridine triphosphatase	3.78e-04	1.92
JUN	jun oncogene	9.8e-04	0.42

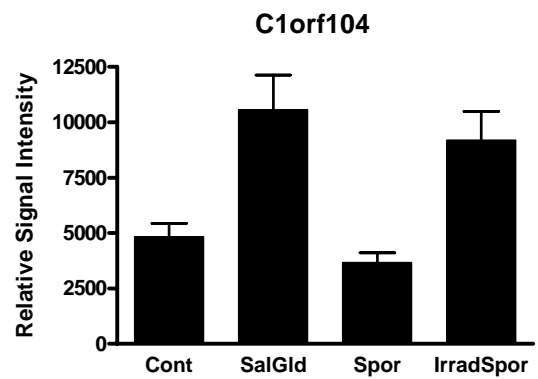
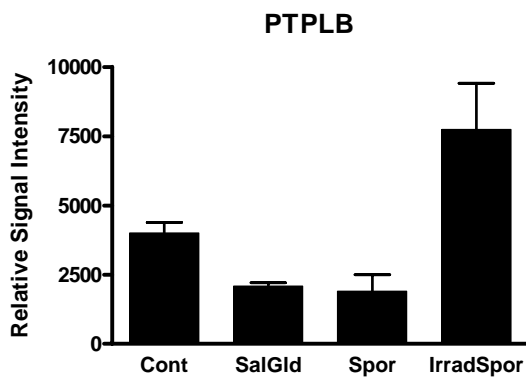
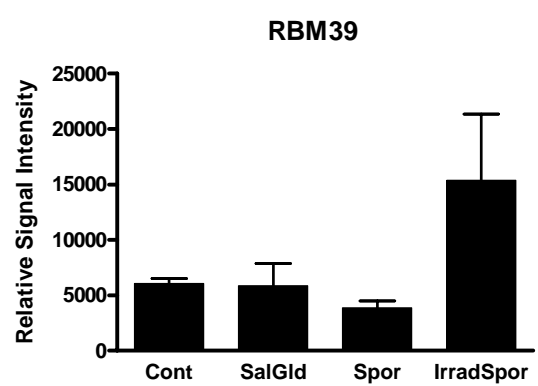
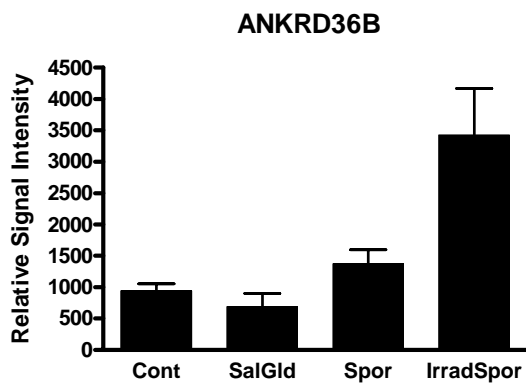
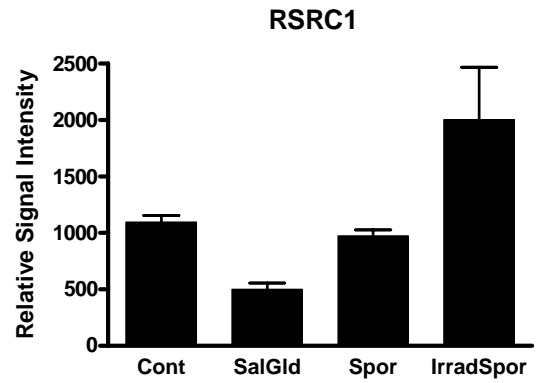
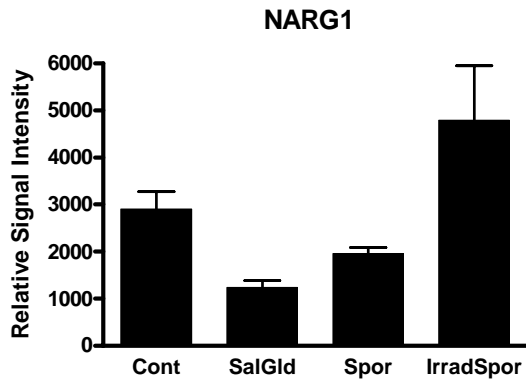
Supplementary Figure S1

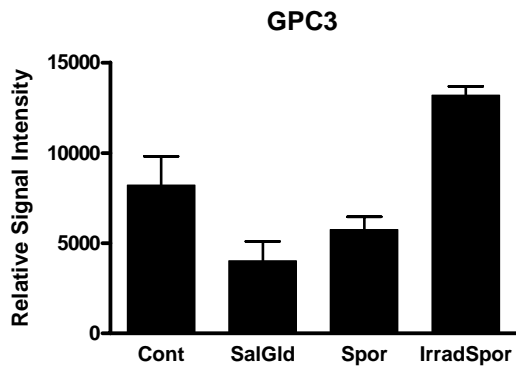
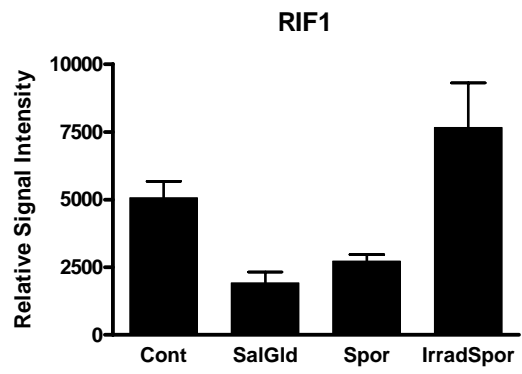
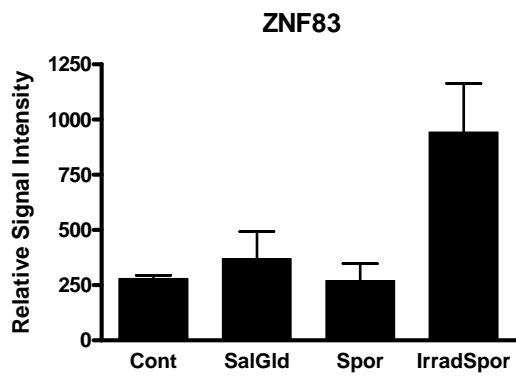
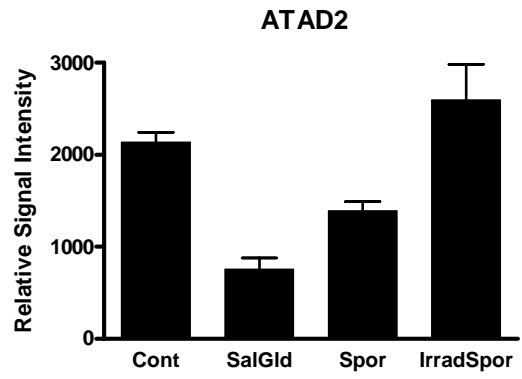
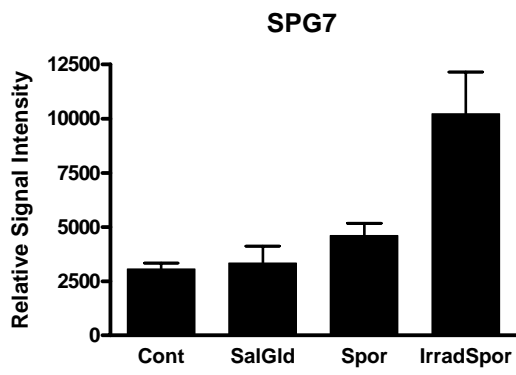
Figure S1: Relative expression of genes from the *Spor* vs. *Irrad* DEGs to demonstrate the differential gene expression among the four study groups. The expression (mean \pm SE) of the 29 *Spor/Irrad* DEGs listed in Table 2 was plotted.





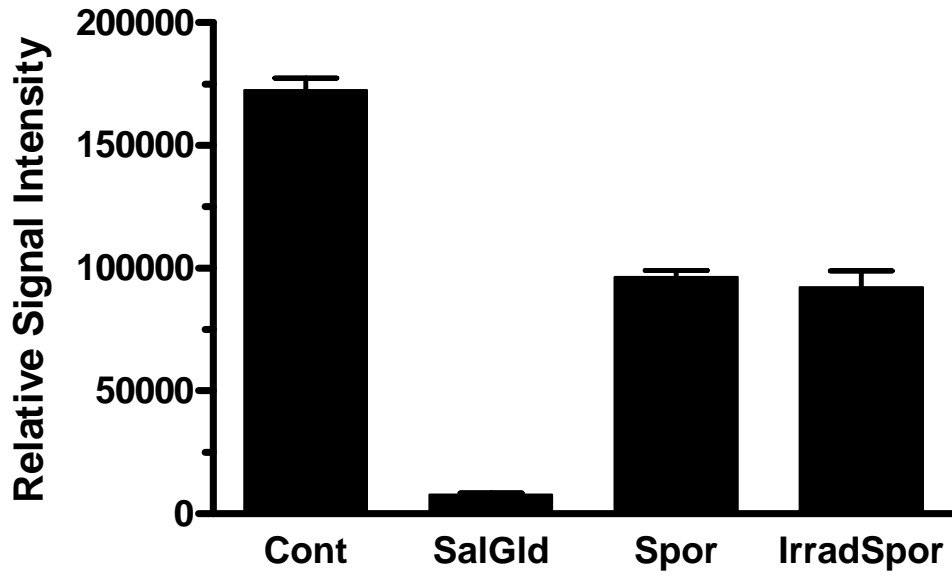






Supplementary Figure S2

Figure S2: Expression of glutathione S-transferase A2 gene, *GSTA2*, among the four study groups.



Supplementary Figure S3

Figure S3: Expression of some Ras subfamily genes among the four study groups.

