

Transcriptome Analysis of Thiram-treated Zebrafish (*Danio rerio*) Embryos Reveals Disruption of Reproduction Signaling Pathways

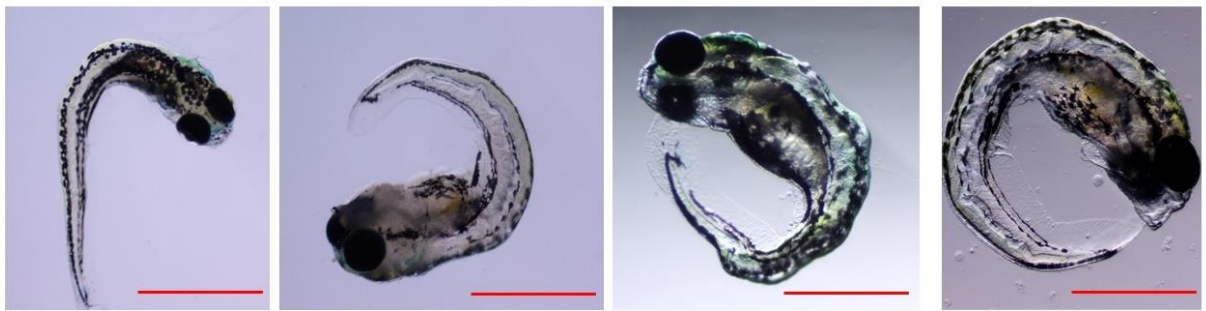
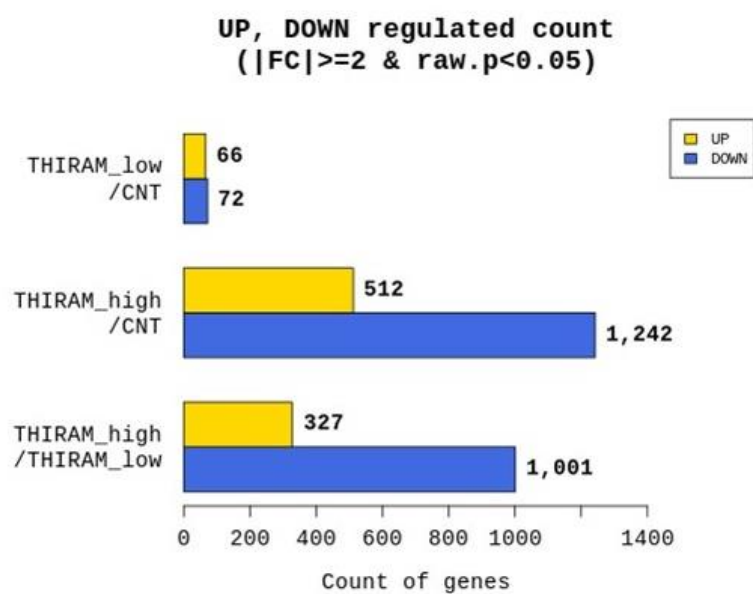
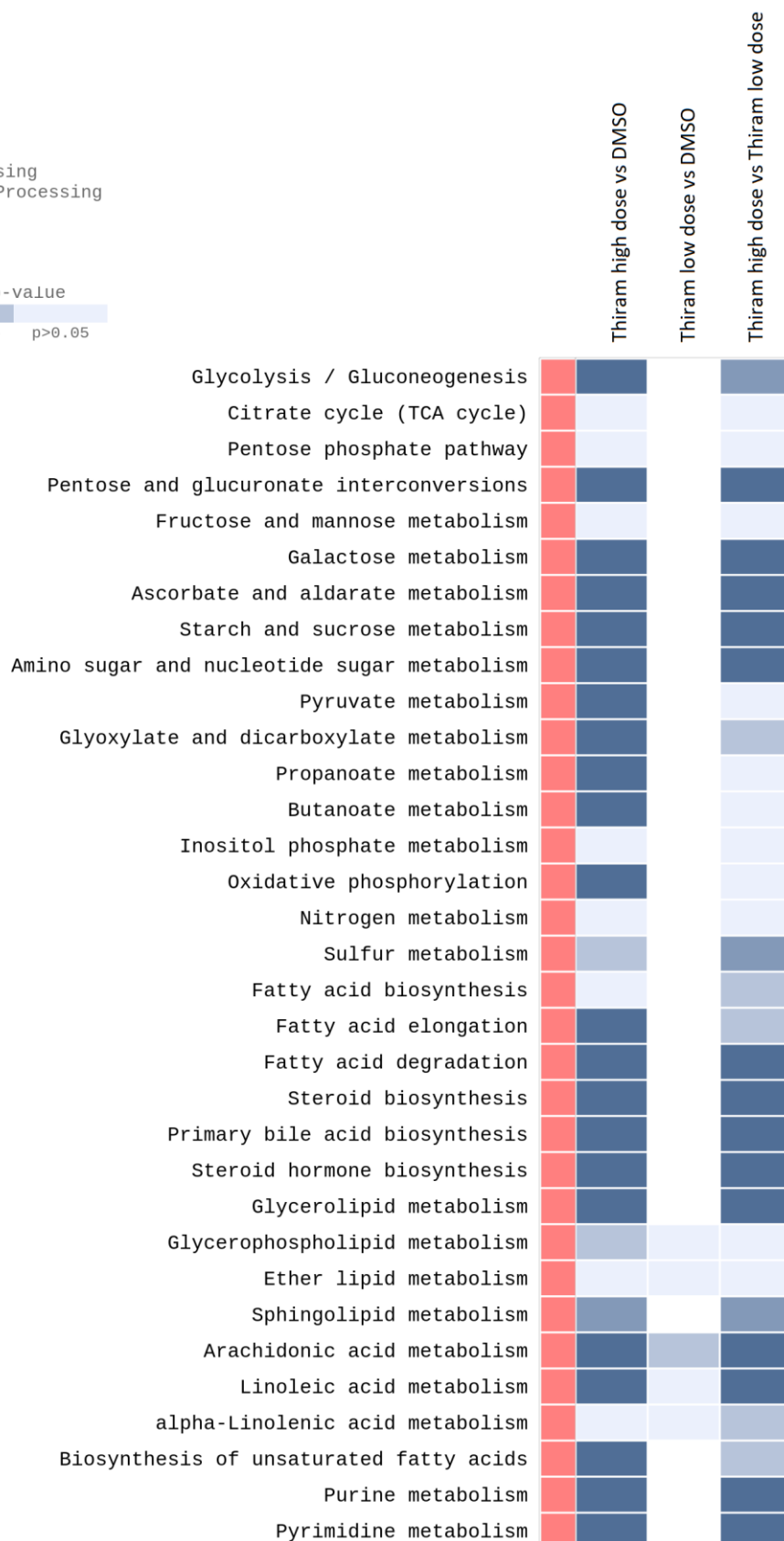
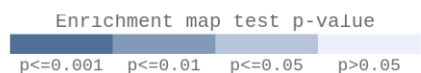
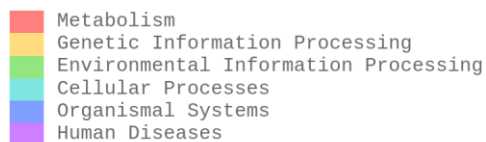


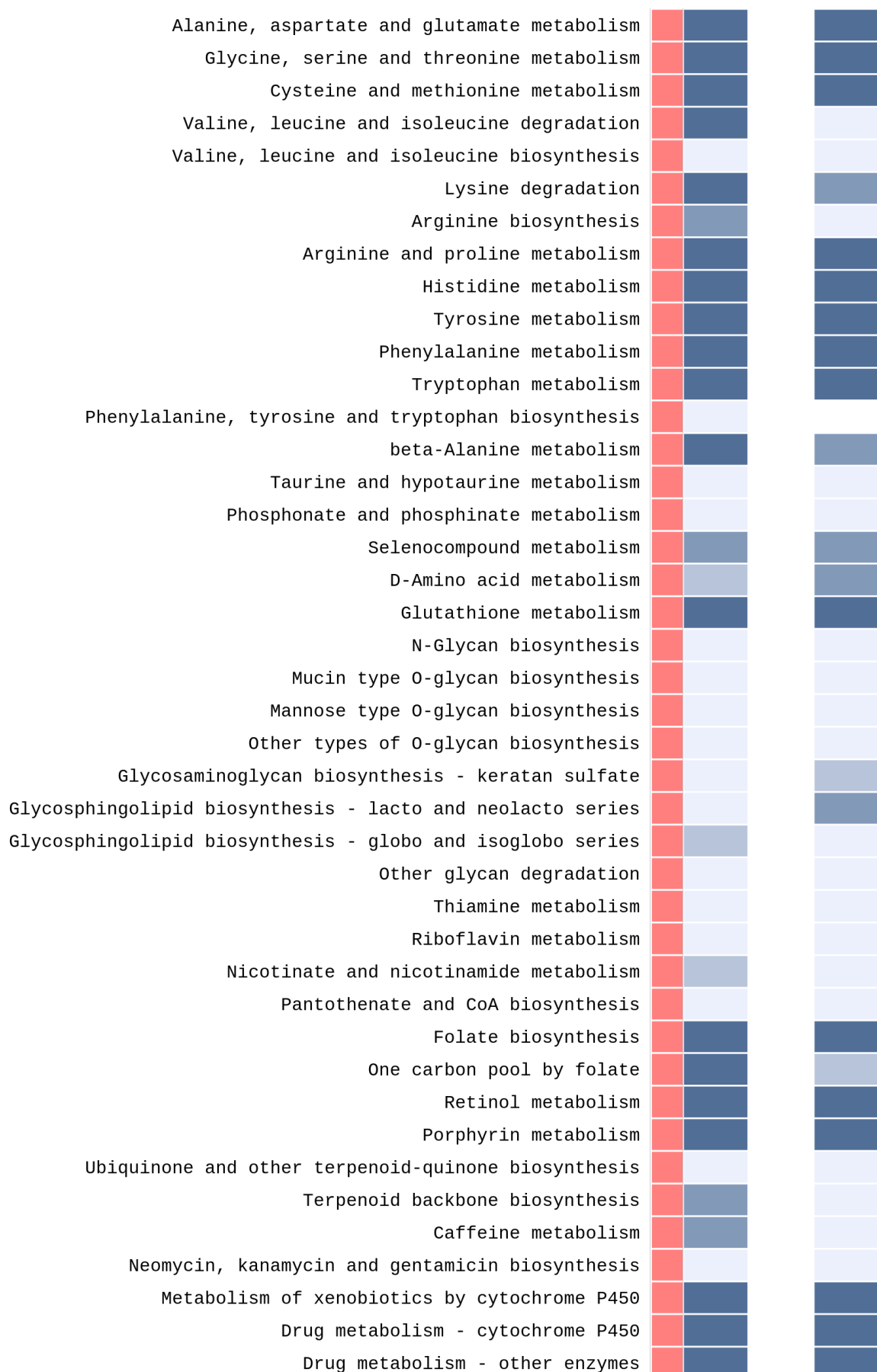
Figure S1. Representative images showing spinal curves observed in HTZF (zebrafish treated with 4.0 $\mu\text{g/L}$ thiram); Scale = 0.5mm.

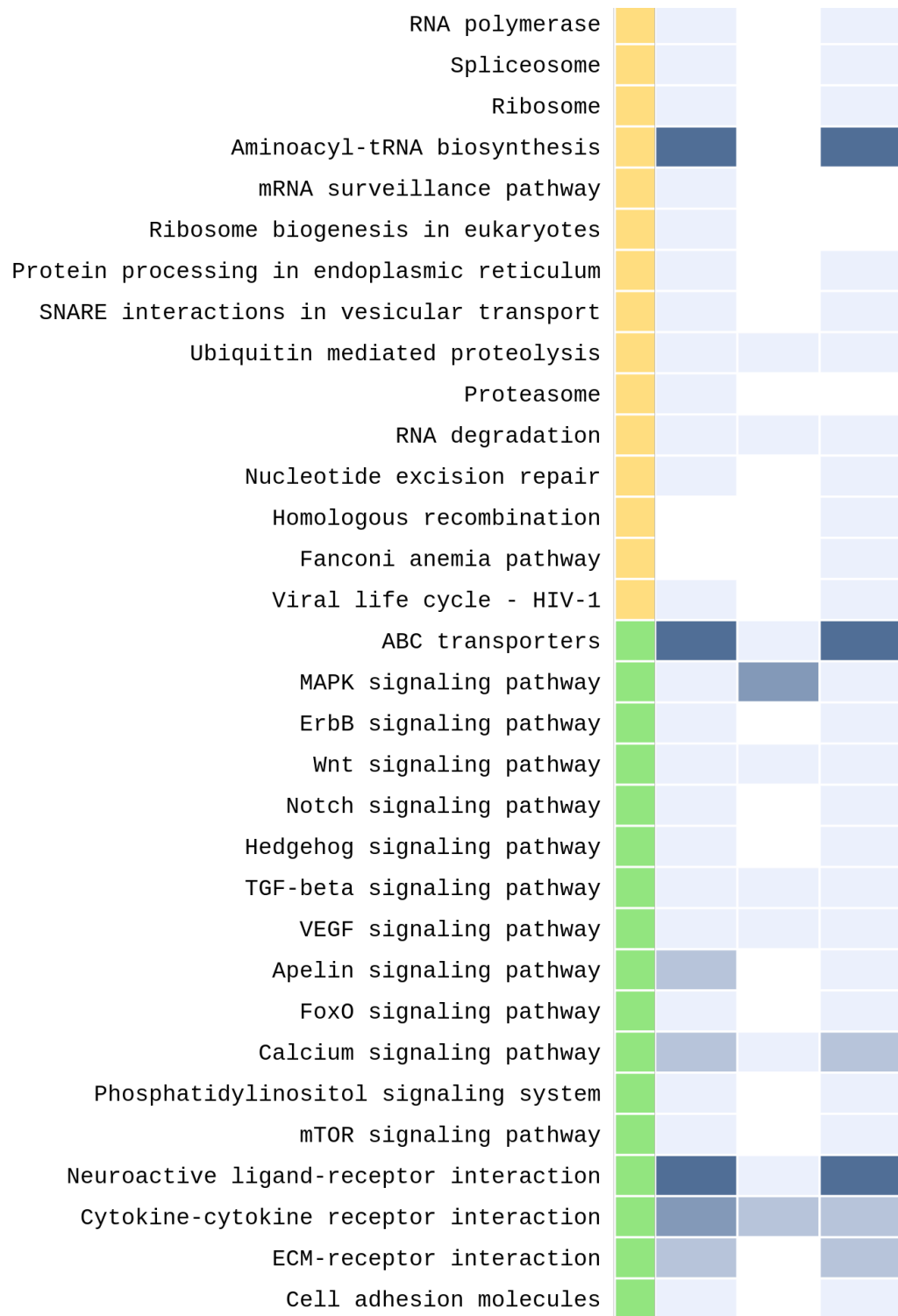


CNT, DMSO-treated fish
 THIRAM_high, 4.0 $\mu\text{g/L}$ thiram-treated fish
 THIRAM_low, 0.4 $\mu\text{g/L}$ thiram-treated fish

Figure S2. Up and down-regulated count of Differentially Expressed Genes. Yellow bar, upregulated DEGs; blue bar, downregulated DEGs.







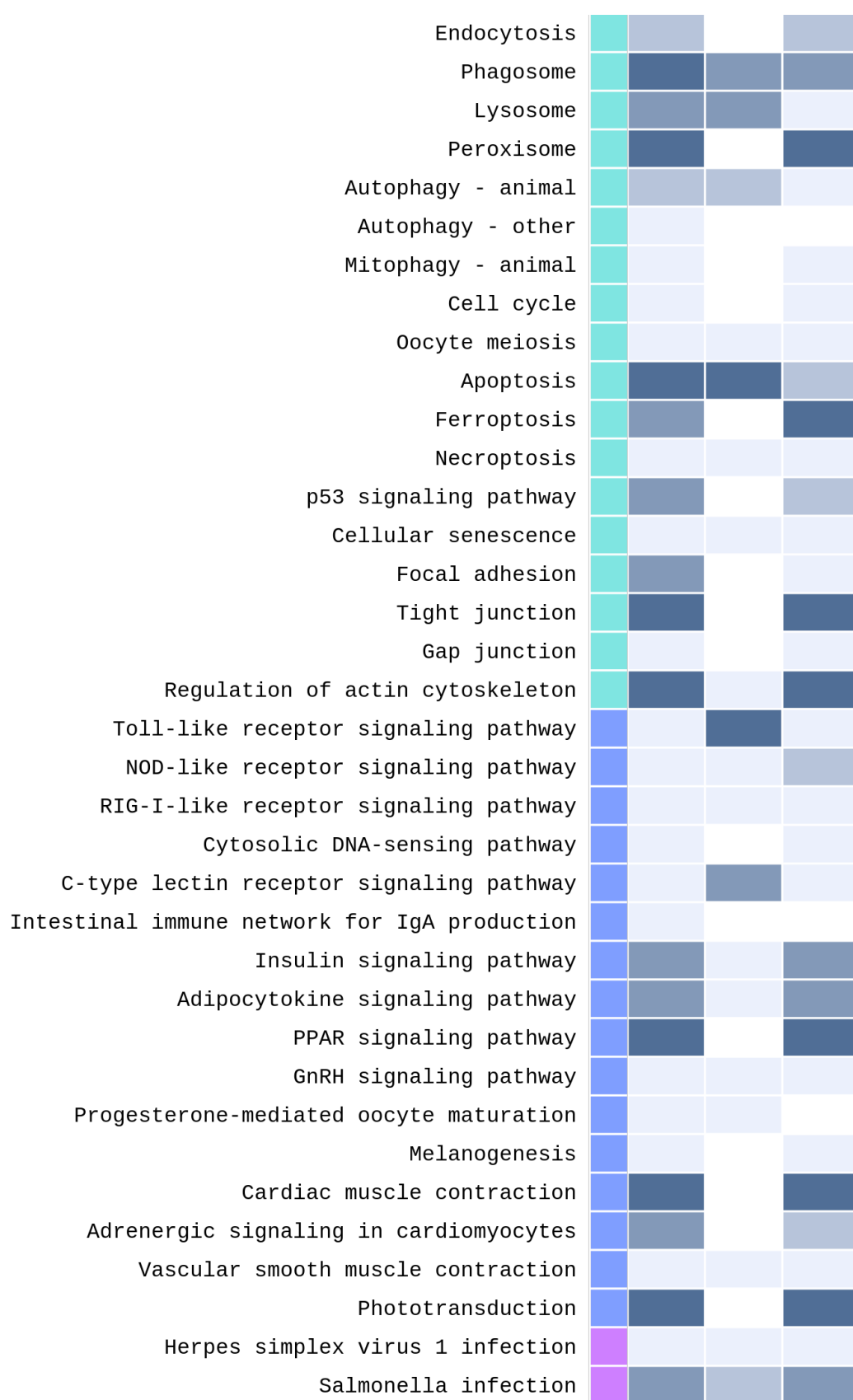


Figure S3. List of enriched pathway in KEGG pathway analysis

Supplementary Table 1. List of top upregulated ($Fc > 5$) and top downregulated ($Fc < -10$) gens after 4.0 $\mu\text{g/L}$ thiram treatment

Transcript_ID	Gene_Symbol	Description	THIRAM_high vs DMSO.fc
NM_001045282	zgc:136461	zgc:136461	-136.787033
NM_001024408,XM_005171867,XM_021476165	ela3l	elastase 3 like	-88.746940
NM_001139464	ela2	elastase 2	-57.165890
NR_015620	sycn.2	syncollin, tandem duplicate 2	-43.916148
NM_213249	chia.2	chitinase, acidic.2	-38.589898
NM_199886	ela2l	elastase 2 like	-37.621427
XM_021479024	LOC559107	lactase-phlorizin hydrolase	-36.644986
NM_001020482	cpa1	carboxypeptidase A1 (pancreatic)	-28.059968
NM_001077598	aoc1	amine oxidase, copper containing 1	-27.596219
NM_001076723	ugt5a2	UDP glucuronosyltransferase 5 family, polypeptide A2	-27.102873
XM_005162727,XM_009297410	si:ch211-161h7.5	si:ch211-161h7.5, transcript variant X2	-26.339568
NM_001177498	ugt5a4	UDP glucuronosyltransferase 5 family, polypeptide A4	-24.675914
XM_017352058	si:ch211-219a15.4	si:ch211-219a15.4	-21.130032
NM_001040175,XM_005164755	slc26a3.2	solute carrier family 26 (anion exchanger), member 3, tandem duplicate 2	-18.275764
XM_001921697,XM_021477806	LOC100147904	zonadhesin, transcript variant X1	-18.156202
NM_001099240	zgc:154142	zgc:154142	-17.294006
NM_001007356	cyp2n13	cytochrome P450, family 2, subfamily N, polypeptide 13	-17.191939
NM_001030281	mep1a.1	mep1a, alpha (PABA peptide hydrolase), tandem duplicate 1	-16.950245
XM_021470771	muc2.1	mucin 2.1	-16.764632
NM_001017724	zgc:112160	zgc:112160	-16.346380
NM_205643	pnp4b	purine nucleoside phosphorylase 4b	-16.264116

NM_001045385	Gck	glucokinase (hexokinase 4)	-16.146532
XM_017351817	si:ch211 - 214p16. 3	si:ch211-214p16.3	-16.082961
NM_001089325	Anpepb	alanyl (membrane) aminopeptidase b	-16.059259
NM_001003729	zgc:921 37	zgc:92137	-15.900719
XM_001343386	Eevs	2-epi-5-epi-valiolone synthase	-15.859847
XM_021468040	LOC11 043812 5	zonadhesin-like	-15.817021
XM_009297092, XM_021470 040	si:ch107 3- 138d10. 2	si:ch1073-138d10.2, transcript variant X2	-15.301128
NM_001002076	fabp6	fatty acid binding protein 6, ileal (gastrotropin)	-14.773093
XM_021478559	LOC10 033141 7	glycosyltransferase family 92 protein F13G3.3-like	-14.299863
NM_001007297, XM_005169 359, XM_005169360	ace2	angiotensin I converting enzyme 2	-14.111774
NM_001109843	rhcg11	Rh family, C glycoprotein, like 1	-13.463241
NM_131788, XM_005155405	cry5	cryptochrome circadian clock 5	-13.403722
NM_001033097	plac8.1	placenta-specific 8, tandem duplicate 1	-13.187097
NM_001102388	ankrd1b	ankyrin repeat domain 1b (cardiac muscle)	-13.039337
NM_199736	slc6a19 b	solute carrier family 6 (neutral amino acid transporter), member 19b	-12.814183
XM_009293262, XM_021476 927	vwa11	von Willebrand factor A domain containing 11, transcript variant X1	-12.745574
XM_003199562	si:ch107 3- 13h15.3	si:ch1073-13h15.3	-12.563861
NM_001002368, XM_005158 777	ctsl.1	cathepsin L.1	-12.497900
XM_005156429	LOC10 188249 6	sushi, nidogen and EGF-like domain-containing protein 1	-12.385683

XM_021466343	LOC110437898	uncharacterized LOC110437898	-12.273213
NM_001320118	dpep1	dipeptidase 1 (renal)	-12.225874
XM_021468039	wu:fb63a08	wu:fb63a08	-12.221217
NM_001025188	alpi.2	alkaline phosphatase, intestinal, tandem duplicate 2	-11.771664
NM_001159584	itln3	intelectin 3	-11.634496
rna-trnD	trnD	tRNA-Asp	-11.555799
NM_198064	slc15a1b	solute carrier family 15 (oligopeptide transporter), member 1b	-11.453348
NM_001098772	zgc:165502	zgc:165502	-11.362849
XM_003200878	si:dkey-22f5.9	si:dkey-22f5.9	-11.275452
rna-trnE	trnE	tRNA-Glu	-11.168690
NM_212618	ctrb1	chymotrypsinogen B1	-10.778630
XR_223934	si:dkey-104n9.1	si:dkey-104n9.1	-10.663062
NM_131624	slc34a2a	solute carrier family 34 (type II sodium/phosphate cotransporter), member 2a	-10.561936
NM_199605	prss59.1	protease, serine, 59, tandem duplicate 1	-10.274042
NM_001077456	zgc:153968	zgc:153968	-10.265950
NM_001002349	aqp10a	aquaporin 10a	-10.257251
NM_001083007, XM_021480002	zgc:153932	zgc:153932	-10.194839
NM_001081497, XM_005159300	slc28a1	solute carrier family 28 (concentrative nucleoside transporter), member 1	-10.131767
NM_001037438	cyp3a65	cytochrome P450, family 3, subfamily A, polypeptide 65	-10.105329
NM_183347	sult1st2	sulfotransferase family 1, cytosolic sulfotransferase 2	-10.041400
XM_021467200, XM_021467205, XM_021467206	myo7bb	myosin VIIBb, transcript variant X2	-10.020172
XM_021468701, XR_002456254	LOC110438198	uncharacterized LOC110438198, transcript variant X1	5.094741
NM_001037674	Smtlb	somatolactin beta	5.095720
XM_003198188, XM_021474762	sdr42e2	short chain dehydrogenase/reductase family 42E, member 2, transcript variant X2	5.129626

NM_001145614	ankrd37	ankyrin repeat domain 37	5.165035
XM_017351489	si:dkey-34k9.3	si:dkey-34k9.3	5.256805
NM_205569	Fosab	v-fos FBJ murine osteosarcoma viral oncogene homolog Ab	5.429473
NM_001327818	LOC557301	cocaine- and amphetamine-regulated transcript protein-like	5.447309
NM_001113589	hsp70l	heat shock cognate 70-kd protein, like	5.453033
XM_005164772	LOC101882092	podocan-like protein 1	5.472315
NM_001002493, XM_005160857	jdp2b	Jun dimerization protein 2b	5.731857
gene-LOC110438683	LOC110438683	.	6.012371
XM_682306, XR_658820	tgm2l	transglutaminase 2, like, transcript variant X1	6.096538
NM_213310, XM_005169814	egln3	egl-9 family hypoxia-inducible factor 3	6.141942
XR_002456031	LOC110438090	uncharacterized LOC110438090	6.472505
XM_017352961, XM_021469064, XR_002456325	LOC798694	complement component C6-like, transcript variant X1	6.477369
XR_002459390, XR_002459391, XR_002459392, XR_002459393, XR_002459394	im:7152855	im:7152855, transcript variant X1	6.669534
XR_002458203, XR_002458204	LOC110439372	uncharacterized LOC110439372, transcript variant X1	6.796486
XM_001919491	si:ch73-265d7.2	si:ch73-265d7.2	6.819292
XR_002455919	LOC110438028	uncharacterized LOC110438028	6.836930
XM_021478389, XM_021478390	si:dkey-21p1.3	si:dkey-21p1.3, transcript variant X2	7.556664
NM_001305571	Tcap	titin-cap (telethonin)	7.685431
NM_199950	socs3a	suppressor of cytokine signaling 3a	8.215998
NM_001033740, XM_005165183	dao.1	D-amino-acid oxidase, tandem duplicate 1	11.262813
NM_001326701	hbae5	hemoglobin, alpha embryonic	15.261024

Supplementary Table 2. List of oligo primers used in qPCR validation

Gene (Sequence ID)	Orientation	Oligo sequence
<i>hbae5</i> (NM_001326701)	Forward	TGAATTGCACGCCTTTCAGC
	Reverse	GCGGTGAAGTCATCAGGGAA
<i>socs3a</i> (NM_199950)	Forward	ATGGAGTTGTCCAGCCACTG
	Reverse	GCAAGAATGGCGCTTCAACA
<i>tcap</i> (NM_001305571)	Forward	TGACTGGCGCAGCATCAATA
	Reverse	GAGGACGCACCTGCCAATAA
<i>egln3</i> (NM_213310)	Forward	TTTGGCTTTTGCGCAGGTTG
	Reverse	GGAATGCATGCGTTTGACCT
<i>jdp2b</i> (NM_001002493)	Forward	CTGGCGGAACCTTACCGTCT
	Reverse	CAAACGGTCTTTTGGCGTGT

<i>smtlb</i> (NM_001037674)	Forward	CTGCTTCCGAAAAGACGCAC
	Reverse	GGGAGCAGTTTTCCCTGTCA
<i>ela2</i> (NM_001139464)	Forward	TGATCGACAAGCAGTGGGTC
	Reverse	AGGTTGTGCTTGCCCAGTAA
<i>chia.2</i> (NM_213249)	Forward	TGGATAATTGCGGAGCAGGC
	Reverse	AATGTGCAGTGTCCCATTTC
<i>aoc1</i> (NM_001077598)	Forward	GACTCCAGGAAACTCGGTGG
	Reverse	TGACCCTTTTCATCGGGACG
<i>ugt5a4</i> (NM_001177498)	Forward	TTTGATGCTGACTTCGGGGA
	Reverse	CAGCAAGTGCCATTTCAGTCC
β -actin (Housekeeping gene)	Forward	CGAGCTGTCTTCCCATCCA
	Reverse	TCACCAACGTAGCTGTCTTTCTG