Table S1: Zebrafish transcripts recognized by Affymetrix probe sets that are differentially expressed in CONVD compared to GF zebrafish larvae at 6dpf

Probe set ID	Gene name[a]	Gene symbol[a]	ZFIN ID[a]	Ensembl ID[a]	Fold-difference[b]	SAM[c]	Mean intensity[d]	GI enrichment[e]	GI development[f]	Compugen probe ID[g]
Dr.18756.1.S1_at	hypothetical protein, weakly similar to XP_001638848.1 predicted protein (Nematostella vectensis)	--	--	--	24.19	+	639.06	GI	late	--
Dr.8591.1.A1_at	similar to hemopexin (HPX)	zgc:152945	ZDB-GENE-060929-800	ENSDARG00000051912	9.04	+	142.06	GI	late	--
Dr.13131.1.S1_at	serum amyloid A	saa	ZDB-GENE-040927-15	ENSDARG00000045999	8.96	+	113.88	--	--	CGENXEB_456005085_0
Dr.9478.3.S1_a_at	myeloperoxidase (myeloid-specific peroxidase)	mpo	ZDB-GENE-030131-9460	ENSDARG00000019521	8.01	+	71.70	--	--	CGENXEB_456000173_0
Dr.967.1.S1_at	matrix metalloproteinase 9	mmp9	ZDB-GENE-040426-2132	ENSDARG00000042816	7.17	--	305.77	non-GI	--	CGENXEB_456008310_0
Dr.18835.2.S1_at	similar to microfibrillar-associated protein 4 (MFAP4)	zgc:171687	ZDB-GENE-071004-9	ENSDARG00000038682	6.41	+	113.98	--	--	CGENXEB_456015134_0
Dr.3585.1.S1_at	angiotensinogen	agt	ZDB-GENE-030131-1205	ENSDARG00000016412	5.97	+	100.11	GI	late	--
Dr.4863.1.A1_at	similar to apical early endosomal glycoprotein (novel MAM domain containing protein)	wu:fb63a08	ZDB-GENE-030131-1216	ENSDARG00000020994	5.97	+	319.20	GI	late	CGENXEB_456003284_0
Dr.21005.1.S1_s_at	complement component C3b /// complement component C3c	c3b /// c3c	ZDB-GENE-990415-37	ENSDARG00000052207	5.88	+	269.81	GI	late	CGENXEB_456000236_0 /// CGENXEB_456000237_0 /// CGENXEB_456015311_0
Dr.7722.1.A1_at	complement component C3a	c3a	ZDB-GENE-030131-9749	ENSDARG00000012694	5.53	+	438.71	GI	late	CGENXEB_456000235_0 /// CGENXEB_456012358_0
Dr.190.1.S1_at	complement factor B	cfb	ZDB-GENE-980526-487	ENSDARG00000055278	5.06	+	211.71	GI	late	CGENXEB_456000406_0
Dr.10314.1.S1_a_at	matrix metalloproteinase 13	mmp13	ZDB-GENE-031202-2	ENSDARG00000012395	5.05	+	304.60	non-GI	--	CGENXEB_456003294_0
Dr.4863.2.S1_at	similar to apical early endosomal glycoprotein (novel MAM domain containing protein)	wu:fb63a08	ZDB-GENE-030131-1216	ENSDARG00000020994	4.92	+	525.46	--	--	--
Dr.12491.1.A1_at	complement C4	c4	--	ENSDARG00000038424	4.90	+	162.15	GI	--	CGENXEB_456008645_0
Dr.15281.1.A1_at	tissue inhibitor of metalloproteinase 2b	timp2b	ZDB-GENE-040426-2655	ENSDARG00000075261	4.89	--	85.38	--	--	CGENXEB_456014703_0
Dr.25195.1.S1_at	similar to putative galactose-binding protein	LOC561528	--	ENSDARG00000068465	4.80	+	37.98	--	--	CGENXEB_456007984_0
Dr.23731.1.A1_at	similar to complement component C3	zgc:103710	ZDB-GENE-041212-2	ENSDARG00000043719	4.33	+	121.27	GI	late	--
Dr.17591.1.S1_at	similar to complement component 1, q subcomponent-like 4	LOC100149559	--	--	4.19	--	168.81	GI	late	--
Dr.20291.1.A1_at	complement component C3b /// complement component C3c	c3b /// c3c	ZDB-GENE-990415-37	ENSDARG00000052207	4.09	+	399.86	GI	late	CGENXEB_456000236_0 /// CGENXEB_456000237_0 /// CGENXEB_456015311_0
Dr.6431.1.S1_at	suppressor of cytokine signaling 3a	socs3a	ZDB-GENE-030131-7349	ENSDARG00000025428	3.66	+	342.76	non-GI	--	CGENXEB_456010175_0
Dr.4937.1.A1_at	similar to Deleted in malignant brain tumors 1 protein precursor (CRP-ductin)	wu:fb66a12	--	--	3.50	+	116.46	--	late	CGENXEB_456011892_0
Dr.22145.1.A1_at	complement factor B	cfb	ZDB-GENE-980526-487	ENSDARG00000055278	3.48	+	131.85	GI	late	CGENXEB_456000406_0
Dr.8000.1.S1_at	glutathione peroxidase 1b	gpx1b	ZDB-GENE-040912-60	ENSDARG00000006207	3.29	--	450.20	GI	--	CGENXEB_456009641_0
Dr.13972.1.S1_at	similar to DNA-damage-inducible transcript 4 (DDIT4)	zgc:64114	ZDB-GENE-031002-35	ENSDARG00000037618	3.25	+	71.28	--	--	--
Dr.4676.1.A1_at	unknown	--	--	--	3.14	+	28.65	GI	--	--
Dr.6845.1.S1_at	complement component C3a	c3a	ZDB-GENE-030131-9749	ENSDARG00000012694	3.12	+	25.25	GI	late	CGENXEB_456000235_0 /// CGENXEB_456012358_0
Dr.2452.2.A1_a_at	complement component 9	c9	ZDB-GENE-050522-442	ENSDARG00000016319	3.11	+	96.03	GI	late	CGENXEB_456004336_0
Dr.22217.1.A1_at	similar to complement factor H-related 1	--	--	--	3.09	+	122.30	GI	late	--
Dr.18429.1.A1_at	coagulation factor V	f5	ZDB-GENE-030131-5531	ENSDARG00000055705	3.04	+	231.17	GI	late	--
Dr.2973.1.A1_at	neutrophil cytosolic factor 1	ncf1	ZDB-GENE-031006-6	ENSDARG00000033735	2.99	+	43.12	--	--	CGENXEB_456008385_0
Dr.2452.2.A1_x_at	complement component 9	c9	ZDB-GENE-050522-442	ENSDARG00000016319	2.93	+	198.53	GI	late	CGENXEB_456004336_0
Dr.17470.1.S1_at	nephrosin	npsn	ZDB-GENE-040420-2	ENSDARG00000010423	2.87	+	170.03	non-GI	late	--
Dr.10376.1.S1_at	similar to cornifelin	--	--	--	2.87	+	139.57	non-GI	--	--
Dr.8090.1.A1_at	N-myc downstream regulated gene 1, like	ndrg1l	ZDB-GENE-040426-1648	ENSDARG00000010420	2.86	+	188.63	non-GI	--	--
Dr.2452.1.A1_at	complement component 9	c9	ZDB-GENE-050522-442	ENSDARG00000016319	2.86	+	463.16	GI	late	CGENXEB_456004336_0
Dr.10624.1.S1_at	similar to peroxiredoxin 1	zgc:110343	ZDB-GENE-050320-35	--	2.85	--	193.79	GI	late	--
Dr.9457.1.A1_at	egl nine homolog 3 (C. elegans)	egln3	ZDB-GENE-040426-2541	ENSDARG00000032553	2.85	+	35.20	GI	--	--
Dr.5461.1.A1_at	similar to cytochrome c oxidase subunit IV isoform 2 (COX4L1)	Q6PBK2_DANRE	--	ENSDARG00000012388	2.85	+	104.87	GI	--	CGENXEB_456006757_0
Dr.19799.1.A1_at	lipin 1	lpin1	--	ENSDARG00000020239	2.63	--	1096.44	GI	late	CGENXEB_456015908_0
Dr.1889.2.A1_a_at	transferrin a	tfa	ZDB-GENE-980526-35	ENSDARG00000016771	2.60	+	3166.85	GI	--	--
Dr.5462.1.S1_at	fibrinogen, B beta polypeptide	fgb	ZDB-GENE-030131-9261	ENSDARG00000008969	2.60	+	343.58	GI	late	--
Dr.7368.1.A1_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha a	ikbaa	ZDB-GENE-040426-2227	ENSDARG00000005481	2.54	+	215.48	non-GI	--	--
Dr.12770.1.S1_at	unknown	--	--	--	2.50	+	78.34	non-GI	--	--
Dr.12725.1.A1_at	similar to six transmembrane prostate protein 4 (STEAP4)	zgc:112143	ZDB-GENE-050417-240	ENSDARG00000055901	2.50	--	134.26	GI	late	--
Dr.22129.1.A1_at	si:ch1073-126c3.2	si:ch1073-126c3.2	--	ENSDARG00000077600	2.48	--	17.57	GI	late	--
Dr.15942.1.S1_at	novel protein similar to vertebrate transmembrane 4 L six family member 5 (TM4SF5)	CH211-137I24.10	--	ENSDARG00000057706	2.41	+	280.77	GI	--	--
Dr.1280.1.A1_at	CCAAT/enhancer binding protein (C/EBP), delta	cebpd	ZDB-GENE-020111-4	--	2.40	+	768.22	GI	late	--

Dr.16392.1.A1_at	complement component 6	c6	ZDB-GENE-040426-1358	ENSDARG00000057113	2.36	--	62.12	--	--	--
Dr.23512.1.A1_at	unknown	wu:fb05h10	--	--	2.33	--	45.26	--	--	--
Dr.3444.2.S1_at	similar to lysozyme G	zgc:162941	ZDB-GENE-030131-8517	ENSDARG00000071701	2.33	+	40.70	--	--	--
Dr.2655.1.S1_at	proteoglycan 4	prg4	ZDB-GENE-041014-324	ENSDARG00000028163	2.32	--	73.69	GI	late	--
Dr.20270.1.S1_at	novel pentraxin-related gene	si:ch211-234p6.12	ZDB-GENE-060503-220	ENSDARG00000042613	2.31	--	511.86	GI	late	CGENXEB_456015990_0
Dr.8723.1.S1_at	novel thioredoxin domain-containing protein	zgc:92903	ZDB-GENE-040718-162	ENSDARG00000044125	2.29	--	235.22	GI	late	--
Dr.20030.1.S1_at	melanocortin 4 receptor	mc4r	ZDB-GENE-021223-2	ENSDARG00000015515	2.29	--	28.19	--	late	--
Dr.17437.1.S1_at	similar to C1q-like protein	zgc:136272	ZDB-GENE-040724-112	ENSDARG00000023157	2.25	+	44.59	GI	late	--
Dr.5356.1.A1_at	similar to platelet receptor GI24	zgc:153073	ZDB-GENE-060929-716	ENSDARG00000068784	2.24	+	54.00	non-GI	--	--
Dr.845.1.A1_at	fibrinogen alpha chain	fga	ZDB-GENE-031010-21	ENSDARG00000020741	2.23	+	506.69	GI	--	--
Dr.1280.1.A2_at	CCAAT/enhancer binding protein (C/EBP), delta	cebpd	ZDB-GENE-020111-4	--	2.20	--	23.47	--	--	--
Dr.8109.1.S1_at	lymphocyte cytosolic plastin 1	lcp1	ZDB-GENE-991213-5	ENSDARG00000023188	2.17	+	127.97	--	--	--
Dr.9478.1.S1_at	cytochrome P450, family 1, subfamily A	cyp1a	ZDB-GENE-011219-1	ENSDARG00000026039	2.15	--	743.29	GI	late	CGENXEB_456000434_0 /// CGENXEB_456011738_0
Dr.9617.1.A1_at	suppressor of cytokine signaling 3b	socs3b	ZDB-GENE-040426-2528	ENSDARG00000026611	2.09	--	183.74	--	late	CGENXEB_456004003_0
Dr.827.1.A1_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	ndufa4	ZDB-GENE-040426-1962	ENSDARG00000056108	2.08	+	96.04	GI	late	--
DrAffx.1.32.S1_at	transforming growth factor, beta 1	tgfb1	ZDB-GENE-030618-1	ENSDARG00000041502	2.08	--	34.11	--	late	--
Dr.6575.1.S1_at	CCAAT/enhancer binding protein (C/EBP), beta	cebpb	ZDB-GENE-020111-3	ENSDARG00000042725	2.06	--	471.78	--	late	--
Dr.20821.1.A1_at	plasminogen	plg	ZDB-GENE-030131-1411	ENSDARG00000023111	2.06	--	319.30	GI	--	--
Dr.17761.1.S1_at	similar to Thrombospondin 1	LOC100151346	--	--	2.06	--	66.70	GI	--	--
Dr.20185.1.S1_at	lipoprotein lipase	lpl	ZDB-GENE-990415-139	ENSDARG00000071472	2.04	+	292.56	GI	--	--
Dr.12399.1.S1_at	macrophage stimulating 1 (hepatocyte growth factor-like)	mst1	ZDB-GENE-020806-3	ENSDARG00000031855	2.04	+	68.88	GI	--	--
Dr.4907.1.S1_at	fibrinogen, gamma polypeptide	fgg	ZDB-GENE-040426-1998	ENSDARG00000037281	2.02	+	1073.75	GI	--	--
Dr.14963.1.A1_at	similar to immune-related lectin-like receptor 4 (illr4)	si:ch211-154o6.6	ZDB-GENE-060503-576	ENSDARG00000056379	2.00	+	140.85	GI	late	--
Dr.2999.1.S1_at	serglycin (secretory granule proteoglycan core peptide)	B8A5H9_DANRE	--	ENSDARG00000077069	1.99	--	65.43	non-GI	--	--
Dr.7365.1.A1_at	ATP-binding cassette, sub-family A (ABC1), member 1A	abca1a	ZDB-GENE-031006-12	ENSDARG00000074635	1.99	+	622.55	GI	late	--
Dr.3645.1.S1_at	plasminogen	plg	ZDB-GENE-030131-1411	ENSDARG00000023111	1.98	--	577.06	GI	late	--
Dr.22133.1.S1_at	unknown	--	--	--	1.97	--	33.42	GI	--	--
Dr.19902.1.S1_at	cathepsin L1, a	ctsl1a	ZDB-GENE-030131-106	ENSDARG00000007836	1.96	+	1644.33	GI	late	CGENXEB_456012788_0
Dr.10250.1.A1_at	L-threonine dehydrogenase	tdh	ZDB-GENE-040426-2379	ENSDARG00000002745	1.96	+	1736.29	GI	late	--
Dr.9515.1.A1_at	coronin, actin binding protein, 1A	coro1a	ZDB-GENE-030131-9512	ENSDARG00000054610	1.96	+	68.14	non-GI	--	--
Dr.16095.1.S1_at	insulin-like growth factor binding protein 1b	igfbp1b	ZDB-GENE-081210-3	ENSDARG00000038666	1.93	+	839.42	GI	late	--
Dr.25219.1.A1_at	novel serine protease	zgc:153968	ZDB-GENE-061027-211	ENSDARG00000061858	1.92	+	380.02	GI	late	--
Dr.17438.1.S1_at	similar to TRAF2 binding protein (TIFA)	LOC560548	--	ENSDARG00000022134	1.92	--	295.40	--	--	--
Dr.18834.1.S1_at	urate oxidase	uox	ZDB-GENE-040718-17	ENSDARG00000007024	1.91	--	591.96	GI	late	--
Dr.26268.1.A1_at	similar to Macrophage receptor with collagenous structure (Scavenger receptor class A member 2)	LOC571584	--	ENSDARG00000059294	1.91	--	76.06	--	--	--
Dr.24507.1.S1_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha b	ikbab	ZDB-GENE-030131-1819	ENSDARG00000007693	1.91	--	294.00	non-GI	--	--
Dr.4103.1.A1_at	novel protein similar to vertebrate complement component (3d/Epstein Barr virus) receptor 2 (CR2)	A8E7E1_DANRE	--	ENSDARG00000075761	1.91	+	660.21	GI	late	--
Dr.8587.1.A1_at	insulin-like growth factor binding protein 1a	igfbp1a	ZDB-GENE-021231-1	ENSDARG00000014947	1.90	--	653.43	GI	late	CGENXEB_456000336_0
Dr.11290.1.A1_at	midnolin	midn	ZDB-GENE-030131-2433	ENSDARG00000018524	1.86	--	609.63	non-GI	early	--
Dr.8587.1.A2_at	insulin-like growth factor binding protein 1a	igfbp1a	ZDB-GENE-021231-1	ENSDARG00000014947	1.86	+	1156.50	GI	late	CGENXEB_456000336_0
Dr.26483.1.S1_at	ERO1-like (S. cerevisiae)	ero1l	ZDB-GENE-040426-1312	ENSDARG00000015228	1.85	+	34.36	--	--	--
DrAffx.2.58.A1_at	cytochrome P450, family 24, subfamily A, polypeptide 1, like	cyp24a1l	ZDB-GENE-060825-1	ENSDARG00000070420	1.83	+	184.99	GI	late	--
Dr.14944.1.A1_at	similar to Mitogen-activated protein kinase kinase kinase 5 (MAPK/ERK kinase kinase 5) (MEK kinase 5) (MEKK 5) (Apoptosis signal-regulating kinase 1) (ASK-1)	LOC555662	--	--	1.82	--	79.99	--	--	--
Dr.25449.1.A1_at	similar to ATP-dependent DNA helicase Q5	LOC100150325	--	ENSDARG00000059556	1.82	+	41.35	--	--	--
Dr.5573.1.S1_at	ADP-ribosylation factor-like 11	arl11	ZDB-GENE-030131-3410	ENSDARG00000036637	1.82	+	25.58	GI	late	--
Dr.20479.1.S1_at	similar to Uncharacterized protein C16orf7	zgc:113159	ZDB-GENE-050306-57	ENSDARG00000019195	1.81	--	16.89	--	--	--
Dr.1889.1.S1_at	transferrin a	tfa	ZDB-GENE-980526-35	ENSDARG00000016771	1.78	--	2671.34	GI	--	--
Dr.4654.2.S1_at	similar to Protein phosphatase 1 regulatory subunit 15A (Growth arrest and DNA damage-inducible protein GADD34)(Myeloid differentiation primary response protein MyD116 homolog)	zgc:162126	ZDB-GENE-030131-4408	ENSDARG00000069135	1.77	--	281.38	--	--	--
Dr.15004.1.A1_at	unknown	--	--	--	1.77	+	11.31	--	--	--
Dr.25944.1.A1_at	unknown	--	--	--	1.77	+	48.59	GI	late	--

Dr.4748.1.S1_at	granulin 2 /// similar to granulin	grn2 /// zgc:136318	ZDB-GENE-050522-264 /// ZDB-GENE-060512-171	ENSDARG00000035817 /// ENSDARG00000035818	1.77	+	273.75	GI	late	--
Dr.14415.1.A1_at	LMBR1 domain containing 2a	lmbrd2a	ZDB-GENE-050417-32	ENSDARG00000034710	1.76	+	33.55	--	--	--
Dr.25155.1.S1_s_at	ba2 globin	ba2	ZDB-GENE-990415-19	ENSDARG00000077603 /// ENSDARG00000078255	1.75	+	27.84	--	late	--
Dr.148.1.A1_at	wu:fa03e10	wu:fa03e10	--	--	1.74	+	534.32	non-GI	--	--
Dr.4868.1.A1_at	hypothetical protein LOC558116	zgc:174888	ZDB-GENE-030328-33	ENSDARG00000077176	1.70	--	173.50	non-GI	--	--
Dr.1605.1.S1_at	serine proteinase inhibitor, clade A, member 1 /// serine proteinase inhibitor, clade A, member 1, like	serpina1 /// serpina1l	ZDB-GENE-030131-1421 /// ZDB-GENE-040721-3	ENSDARG00000078556 /// ENSDARG00000079619	1.70	+	2243.65	GI	late	--
Dr.4654.1.A1_at	similar to Protein phosphatase 1 regulatory subunit 15A (Growth arrest and DNA damage-inducible protein GADD34)(Myeloid differentiation primary response protein MyD116 homolog)	zgc:162126	ZDB-GENE-030131-4408	ENSDARG00000069135	1.69	+	226.30	non-GI	early	--
Dr.19560.1.S1_at	insulin induced gene 1	insig1	ZDB-GENE-030131-6121	ENSDARG00000010658	1.69	+	120.79	GI	--	--
Dr.4957.1.S1_at	myeloid cell leukemia sequence 1a	mcl1a	ZDB-GENE-000511-7	ENSDARG00000009779	1.69	+	1297.48	--	--	--
Dr.360.1.A1_at	phospholipase A2, group XV	pla2g15	ZDB-GENE-030131-6948	--	1.69	+	277.71	GI	late	--
Dr.2829.1.A1_at	unknown	--	--	--	1.68	--	12.11	--	--	--
Dr.24483.1.S1_at	unknown	--	--	--	1.68	+	1014.18	--	late	--
Dr.12369.1.A1_at	sulfotransferase family 2, cytosolic sulfotransferase 1	sult2st1	ZDB-GENE-061117-5	ENSDARG00000033170	1.67	+	117.74	non-GI	--	--
Dr.24729.1.S1_x_at	unknown	--	--	--	1.67	--	1290.50	--	late	--
Dr.956.1.S1_at	cytochrome c oxidase subunit VIb-like	zgc:92631	ZDB-GENE-040718-448	ENSDARG00000045230	1.66	+	483.51	GI	--	--
Dr.737.1.A1_at	jun B proto-oncogene, like	junbl	ZDB-GENE-040426-2666	--	1.65	--	242.46	non-GI	early	--
Dr.10728.1.S1_at	glucagon a	gcga	ZDB-GENE-010219-1	ENSDARG00000042999	1.65	+	88.62	non-GI	early	CGENXEB_456000240_0
Dr.10713.1.S1_at	ATPase, Na+/K+ transporting, alpha 1a.3 polypeptide	atp1a1a.3	ZDB-GENE-001212-3	ENSDARG00000039131	1.65	+	184.80	non-GI	--	--
Dr.17570.2.A1_at	MAP kinase-interacting serine/threonine kinase 2b	mknk2b	ZDB-GENE-030829-2	ENSDARG00000015164	1.64	+	2475.97	--	late	CGENXEB_456015226_0 /// CGENXEB_456005195_0
Dr.25214.1.A1_at	cytochrome P450, family 24, subfamily A, polypeptide 1, like	cyp24a1l	ZDB-GENE-060825-1	ENSDARG00000070420	1.64	--	270.41	GI	late	--
Dr.17459.1.S1_a_at	inter-alpha (globulin) inhibitor H4 (itih4)	zgc:112265	ZDB-GENE-050626-133	ENSDARG00000036573	1.62	+	733.99	GI	late	--
Dr.4654.2.S1_a_at	similar to Protein phosphatase 1 regulatory subunit 15A (Growth arrest and DNA damage-inducible protein GADD34)(Myeloid differentiation primary response protein MyD116 homolog)	zgc:162126	ZDB-GENE-030131-4408	ENSDARG00000069135	1.62	+	64.63	--	--	--
Dr.25727.1.A1_at	mitogen-activated protein kinase 14b	mapk14b	ZDB-GENE-021007-1	ENSDARG00000028721	1.62	+	49.41	--	--	--
Dr.1368.4.A1_at	unknown	--	--	--	1.62	+	2269.42	non-GI	late	--
Dr.1659.1.A1_at	wu:fc02a12	wu:fc02a12	--	--	1.62	+	590.37	--	late	--
Dr.6604.2.A1_a_at	similar to Protein phosphatase 1 regulatory subunit 3C (Protein phosphatase 1 regulatory subunit 5)(Protein targeting to glycogen)	zgc:77112	ZDB-GENE-040426-2219	ENSDARG00000015657	1.61	--	36.14	non-GI	--	--
Dr.1082.1.S1_at	prostaglandin-endoperoxide synthase 2a	ptgs2a	ZDB-GENE-020530-2	ENSDARG00000004539	1.60	+	82.14	--	--	--
Dr.26478.1.S1_at	similar to cAMP-dependent protein kinase catalytic subunit beta	zgc:64054	ZDB-GENE-040426-1351	ENSDARG00000001782	1.60	--	23.25	--	--	--
Dr.3789.1.A1_at	similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8)	LOC100007704	--	ENSDARG00000075831	1.60	+	432.81	non-GI	early	--
Dr.9665.1.S1_at	ras homolog gene family, member Gb	rhogb	ZDB-GENE-030131-8877	ENSDARG00000004301	1.59	--	74.67	--	--	--
Dr.26324.1.A1_at	acyl-CoA synthetase short-chain family member 1	zgc:113194	ZDB-GENE-050320-139	ENSDARG00000044142	1.59	--	84.98	GI	late	--
Dr.7977.1.S1_at	glutathione peroxidase 1a	gpx1a	ZDB-GENE-030410-1	ENSDARG00000018146	1.59	--	706.52	GI	late	--
Dr.2960.1.A1_at	inter-alpha (globulin) inhibitor H4 isoform 2	zgc:112265	ZDB-GENE-050626-133	ENSDARG00000036573	1.59	--	1231.00	GI	late	--
Dr.10345.1.A1_at	wu:fb14a07	wu:fb14a07	ZDB-GENE-030131-8516	--	1.58	+	345.38	--	--	--
Dr.8014.1.S1_at	B-cell translocation gene 1	btg1	ZDB-GENE-010726-1	ENSDARG00000027249	1.57	--	788.65	non-GI	early	--
Dr.1372.1.S1_at	keratin 18	krt18	ZDB-GENE-030411-6	ENSDARG00000018404	1.56	+	501.76	GI	--	--
Dr.6531.2.S1_at	suppressor of cytokine signaling 1	socs1	ZDB-GENE-040801-205	ENSDARG00000038095	1.55	--	108.68	GI	early	--
Dr.9288.1.S1_at	insulin-like growth factor 2b	igf2b	ZDB-GENE-030131-2935	ENSDARG00000033307	1.54	+	187.74	GI	late	--
Dr.9890.1.A1_at	hypothetical protein LOC564090	zgc:193593	ZDB-GENE-080723-21	ENSDARG00000075096	1.54	+	445.14	non-GI	--	--
Dr.1259.1.A1_at	similar to peptidyl-glycine alpha-amidating monooxygenase (PAM) precursor	LOC100148119	--	--	1.54	--	380.84	--	--	--
Dr.9492.1.A1_at	sulfide quinone reductase-like (yeast)	sqrdl	ZDB-GENE-050417-436	ENSDARG00000017034	1.54	--	224.10	GI	late	--
Dr.15644.1.A1_at	unknown	--	--	--	1.54	--	12.17	GI	--	--
Dr.14396.1.A1_at	similar to mucin 2 (MUC2)	LOC100148804	--	ENSDARG00000039253	1.54	+	443.47	--	early	--
Dr.15382.1.A1_at	unknown	--	--	--	1.54	--	477.73	non-GI	early	--
Dr.96.1.A1_at	similar to complement protein component C7-1	LOC570832	--	ENSDARG00000057121	1.53	+	113.12	--	late	CGENXEB_456003701_0
Dr.23886.1.A1_at	spondin 2a, extracellular matrix protein	spon2a	ZDB-GENE-990415-160	ENSDARG00000025465	1.53	--	11.91	GI	--	--
Dr.22629.1.A1_x_at	unknown	wu:fj29c05	--	--	1.52	--	214.46	--	--	--
Dr.25133.5.A1_at	hypothetical protein LOC561590	wu:fd20f07	--	ENSDARG00000045424	1.52	--	79.65	--	--	--

Dr.3563.2.S1_at	transmembrane 4 superfamily member 4	zgc:92479	ZDB-GENE-040801-231	ENSDARG00000040747	1.52	+	770.73	GI	late	--
Dr.18812.1.S1_at	similar to Upstream stimulatory factor 2 (USF2)	si:dkey-211g8.3	ZDB-GENE-030131-8475	ENSDARG00000020228	1.51	--	23.30	--	--	--
Dr.6064.1.A1_at	novel mucin protein	A1L1X2_DANRE	--	ENSDARG00000069841	1.51	--	57.13	non-GI	--	--
Dr.12596.1.S1_at	claudin c	cldnc	ZDB-GENE-010328-3	ENSDARG00000015955	1.51	--	185.43	GI	--	--
Dr.681.1.A1_at	similar to Dexamethasone-induced Ras-related protein 1 (RASD1)	zgc:65909	ZDB-GENE-040426-1473	ENSDARG00000019274	1.51	--	91.76	--	early	--
Dr.3804.2.A1_a_at	similar to vacuolar proton translocating ATPase 116 kDa subunit a isoform 2 (ATP6V0A2)	zgc:55891	ZDB-GENE-040426-2022	ENSDARG00000076003	1.50	--	138.60	GI	--	--
Dr.8654.2.A1_a_at	septin 7a	sept7a	ZDB-GENE-040426-1008	ENSDARG00000052673	0.66	--	371.43	non-GI	early	--
Dr.2045.1.A1_at	hydroxyacyl-Coenzyme A dehydrogenase	hadh	ZDB-GENE-040801-261	ENSDARG00000030765	0.66	--	349.50	GI	--	--
Dr.7343.1.S1_at	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	acadm	ZDB-GENE-040426-1945	ENSDARG00000038900	0.66	+	720.77	GI	late	--
Dr.23526.1.A1_at	synovial sarcoma, X breakpoint 2 interacting protein	ssx2ip	ZDB-GENE-040426-1756	ENSDARG00000039521	0.66	--	11.63	GI	--	--
Dr.13114.1.A1_at	ras homolog gene family, member V	rhov	ZDB-GENE-031002-10	ENSDARG00000070434	0.66	+	53.91	--	--	--
Dr.16053.1.S1_at	similar to Heparin-binding EGF-like growth factor (HBEGF)	zgc:175091	--	--	0.66	--	146.16	--	early	--
Dr.26381.1.A1_at	tubulin, alpha 2	tuba2	ZDB-GENE-040426-1970	ENSDARG00000045014	0.65	+	695.29	--	late	--
Dr.548.1.S1_at	odorant receptor, family C, subfamily 103, member 4	or103-4	ZDB-GENE-000329-12	ENSDARG00000003090	0.65	--	16.50	GI	--	--
Dr.16609.2.A1_at	TRNA-yW synthesizing protein 3 homolog (S. cerevisiae)	tyw3	ZDB-GENE-040718-355	ENSDARG00000038222	0.65	--	33.09	--	--	--
Dr.16257.1.A1_at	unknown	--	--	--	0.64	--	73.87	--	--	--
Dr.16229.1.A1_at	unknown	--	--	--	0.64	--	133.06	GI	--	--
Dr.8097.1.S1_at	opsin 1 (cone pigments), short-wave-sensitive 2	opn1sw2	ZDB-GENE-990604-40	ENSDARG00000017274	0.63	--	1821.51	non-GI	--	--
Dr.558.1.S1_at	visual system homeobox 1 homolog, chx10-like	vsx1	ZDB-GENE-990415-205	ENSDARG00000056292	0.63	--	107.65	non-GI	--	--
Dr.24284.1.A1_at	novel protein similar to gastrin-releasing peptide (GRP)	B8A4X5_DANRE	ZDB-GENE-090313-9	ENSDARG00000060656	0.63	--	25.29	non-GI	--	--
Dr.6928.3.S1_at	similar to Quinoid dihydropteridine reductase (QDPR)(Dihydropteridine reductase)	zgc:171517	ZDB-GENE-080219-12	ENSDARG00000070071	0.63	--	354.85	--	--	--
Dr.3521.1.A1_at	unknown	--	--	--	0.63	--	135.59	non-GI	early	--
Dr.15054.1.S1_at	retinol binding protein 2a, cellular	rbp2a	ZDB-GENE-020320-2	ENSDARG00000070038	0.62	--	894.29	--	--	--
Dr.21859.1.A1_at	similar to serine protease 36 (PRSS36)	zgc:100868	ZDB-GENE-040801-33	ENSDARG00000004748	0.61	--	153.16	non-GI	--	--
Dr.7853.1.A1_at	dynein, cytoplasmic 1, heavy chain 1	dync1h1	ZDB-GENE-030131-7050	ENSDARG00000014717	0.60	--	54.37	--	--	--
Dr.18599.1.S1_at	fatty acid binding protein 6, ileal (gastrotropin)	fabp6	ZDB-GENE-040625-49	ENSDARG00000044566	0.60	--	888.83	GI	late	--
Dr.15733.1.S1_at	unknown	--	--	--	0.59	+	55.08	GI	late	--
Dr.4060.1.S1_at	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	hadhb	ZDB-GENE-030131-8550	ENSDARG00000057147	0.59	--	487.05	GI	--	--
Dr.17493.1.S1_s_at	hypothetical protein LOC560538	LOC560538	--	--	0.58	--	13.69	GI	--	--
Dr.23038.1.A1_at	unknown	--	--	--	0.57	--	10.40	--	--	--
Dr.11310.3.S1_at	tubulin, alpha 1, like 2	tuba1l2	ZDB-GENE-051127-7	ENSDARG00000001889	0.57	--	140.22	non-GI	early	--
Dr.12478.1.S1_at	unknown	--	--	--	0.57	--	149.13	non-GI	--	--
Dr.11252.1.A1_at	similar to creatine kinase, mitochondrial 2 sarcomeric (CKMT2)	zgc:56085	ZDB-GENE-030131-5717	ENSDARG00000069615	0.57	--	330.56	non-GI	--	--
Dr.15687.2.S1_a_at	2,4-dienoyl-CoA reductase, mitochondrial precursor	decr1 (zgc:92356)	ZDB-GENE-040718-142	ENSDARG00000003869	0.56	--	44.40	GI	--	--
Dr.467.1.A1_at	similar to Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial precursor	zgc:92093	ZDB-GENE-040912-168	ENSDARG00000038834	0.56	--	128.99	GI	late	--
Dr.2188.1.S1_at	glycerol-3-phosphate dehydrogenase 1 (soluble)	gpd1	ZDB-GENE-040426-2576	ENSDARG00000036942	0.56	--	142.20	--	--	CGENXEB_456002354_0
Dr.8102.1.S1_at	opsin 1 (cone pigments), medium-wave-sensitive, 1	opn1mw1	ZDB-GENE-990604-42	ENSDARG00000044280	0.55	--	1155.42	non-GI	--	--
AFFX-Dr-NM_131175-1_s_at	opsin 1 (cone pigments), long-wave-sensitive, 1	opn1lw1	ZDB-GENE-990604-41	ENSDARG00000044862	0.53	--	889.89	non-GI	--	--
Dr.12733.1.A1_at	similar to cytochrome P450, family 2, subfamily W, polypeptide 1 (CYP2W1)	zgc:66268	ZDB-GENE-040426-1584	ENSDARG00000038366	0.52	--	196.40	GI	late	--
Dr.16372.1.A1_at	similar to Inositol polyphosphate 5-phosphatase K (SKIP)	zgc:162883	--	--	0.52	--	19.96	non-GI	early	--
Dr.24261.1.S1_at	fatty acid binding protein 1b	fabp1b	ZDB-GENE-050522-96	ENSDARG00000059227	0.52	--	468.69	GI	--	--
Dr.1254.1.A1_at	collagen, type V, alpha 2-like	col5a2l	ZDB-GENE-030616-13	--	0.52	--	12.54	--	--	--
Dr.25442.1.A1_at	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	elovl4	ZDB-GENE-030131-7672	ENSDARG00000027495	0.50	+	164.36	non-GI	--	--
Dr.9876.1.S1_at	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2	gngt2	ZDB-GENE-030131-7595	ENSDARG00000010680	0.47	--	98.61	non-GI	--	--
Dr.18459.1.S1_at	novel trypsin-like serine protease	zgc:92590	ZDB-GENE-041024-15	ENSDARG00000040282	0.47	+	509.61	GI	late	--
Dr.8153.1.S1_at	claudin g	cldng	ZDB-GENE-060421-5306	ENSDARG00000003701	0.46	--	85.31	GI	late	--
Dr.8143.1.S1_at	fatty acid binding protein 2, intestinal	fabp2	ZDB-GENE-991019-5	ENSDARG00000006427	0.45	+	1565.21	GI	--	--
Dr.11305.1.A1_at	guanylate kinase 1	guk1	ZDB-GENE-020916-1	ENSDARG00000005776	0.44	--	41.82	non-GI	--	--

Dr.765.1.A1_at	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, alpha subunit	hadha	--	--	0.43	--	187.21	GI	--	--
Dr.6143.1.A1_at	gamma-butyrobetaine hydroxylase	bbox1	ZDB-GENE-050417-218	ENSDARG00000036135	0.43	--	170.02	GI	late	--
Dr.3238.1.A1_at	kruppel-like factor 11a	klf11a	ZDB-GENE-060825-95	ENSDARG00000030844	0.41	--	224.04	--	early	--
Dr.12241.1.A1_at	carnitine palmitoyltransferase 1B (muscle)	cpt1b	ZDB-GENE-041010-9	ENSDARG00000058285	0.38	--	42.16	GI	--	CGENXEB_456010085_0
Dr.12817.1.A1_at	angiopoietin-like factor 4 (fasting-induced adipose factor)	angptl4	ZDB-GENE-041111-222	ENSDARG00000035859	0.35	+	647.14	--	--	CGENXEB_456004079_0
Dr.9448.1.A1_at	kruppel-like factor 11b	klf11b	ZDB-GENE-061103-82	ENSDARG00000013794	0.24	--	48.58	--	--	CGENXEB_456013370_0
Dr.14719.1.A1_at	hypothetical protein LOC550402	zgc:112199	ZDB-GENE-050417-205	--	0.17	--	26.50	--	--	--

[a] If a probe set represents multiple zebrafish transcripts, those genes are listed together separated by "///".

[b] Fold difference of transcript level in 6dpf zebrafish larvae is shown as CONVD/GF.

[c] Probe sets with <5% false discovery rate using Significance Analysis for Microarrays software (SAM) are indicated by "+".

[d] Relative expression level for each probe set is shown as mean intensity across all microarrays after normalization.

[e] Probe sets previously found to be enriched in the transcriptomes of FAC-sorted cells from the gastrointestinal tract (GI) vs. other tissues (non-GI) in conventionally-raised zebrafish larvae at 4dpf or 6dpf (Stuckenholz et al., 2009).

[f] Probe sets previously found to display increased expression in FAC-sorted gastrointestinal tract cells from conventionally-raised zebrafish during early (2dpf-3dpf) vs. late developmental stages (4dpf-6dpf; Stuckenholz et al., 2009).

[g] Compugen probe IDs that were previously found to display differential expression in gastrointestinal tracts from GF compared to CONVD or CONV-R zebrafish at 6dpf (Rawls et al., 2004) are shown next to their corresponding zebrafish transcript.