Supplemental Material

Global Gene Expression Analysis Reveals Dynamic and Developmental Stage Dependent Enrichment of Lead (Pb)-Induced Neurological Gene Alterations

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Supplemental Material, Table 1. Comparison of gene expression results with qPCR

		72hpf		120hpf	
Gene	Primer Sequence	Array	qPCR[a]	Array	qPCR[a]
CHIT1	AACGAAGGTCCGTTATCTGAAA AGCATGAGTGGTGGTAGTTGTG	0.03	1.51	-0.98[†]	-0.64[††]
FRYL	CAACGAGGAGAAGATGCACA GTCTTCTGTCCCGCTCTGTC	-1.62[†]	-1.44[††]	-0.42	-0.79
GAPDH	TCTGACAGTCCGTCTTGAGAAA ACAAAGTGATCGTTGAGAGCAA	xxx	xxx	xxx	xxx
HPX	GAACGAGGAGGGAGTTCCTTAT TCCAAGAAAAAGAACTGGTGGT	0.00	0.13	0.97[†]	0.89[††]
MT2	TGTGCCAAGACTGGAACTTG CAGGAATTGCCTTTGCAGAC	0.87[†]	1.11[††]	0.35	0.65
NAV3	GGTGTTGTCAACCAGTACCTCA TGTGTTGGGATGGTTATGTTGT	-0.77[†]	-0.90	-0.33	0.33
NRXN2	CTCCCTACGGTAAACAAACTGC TCTTTAAGGCAACCCATGAAGT	-1.29[†]	-1.28[††]	-0.31	*
RELN	TTCTACTGCCCCTACCAGAGAG AATCTCGAGAAAACTCCAGACG	-1.32[†]	-3.91[††]	0.20	*
ROBO2	CAATTGGACATGGCTAAACAGA GCTGTCTAAGTTGTCCATGCTG	-1.36[†]	-1.04	-0.65	*
TXN1	CACAATGGTTCTCGAAATTGAA TCTCTGGTTTTTCAGACAGCAA	0.58	-0.18	1.29[†]	2.11

[a]Expression values for given genes were normalized to *GAPDH* expression. Values are reported as the mean $\log_2$ expression ratio of treated compared to controls.

*Expression of given gene was undetectable.

[†] Gene determined to be differentially expressed according to described microarray criteria.

[††] Gene determined to be differentially expressed according to two-sided *t*-test ($p \leq 0.05$).

Supplemental Material, Table 2. Probes altered due to lead exposure at 72 hpf

SEQ_ID	Symbol	Entrez Gene Name	Log_2 Expression Ratio	P-value
AF427524.1	*RELN*	reelin	-1.32	0.132
BC057445.1	*MLL5*	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	-1.45	0.117
BC121719.1			-0.99	0.038
BI882297			0.59	0.029
ENSDART00000003080			-1.15	0.089
ENSDART00000004619			-0.60	0.033
ENSDART00000004986	*IGSF9*	immunoglobulin superfamily, member 9	-0.69	0.043
ENSDART00000005300	*AP3D1*	adaptor-related protein complex 3, delta 1 subunit	-0.97	0.077
ENSDART00000006221			-0.74	0.009
ENSDART00000006657			-1.61	0.070
ENSDART00000008532	*MBIP*	MAP3K12 binding inhibitory protein 1	0.60	0.059
ENSDART00000008968			0.63	0.021
ENSDART00000013709			-0.65	0.039
ENSDART00000015054			0.86	0.098
ENSDART00000015126			-0.79	0.052
ENSDART00000015938	*LARP1*	La ribonucleoprotein domain family, member 1	-1.24	0.068
ENSDART00000016208			-0.99	0.077
ENSDART00000017244			-0.68	0.073
ENSDART00000017620			0.71	0.513
ENSDART00000023669			-1.31	0.036

ENSDART00000027547			-0.73	0.046
ENSDART00000028010			0.64	0.061
ENSDART00000031188			-0.94	0.039
ENSDART00000033970	*UBR4*	ubiquitin protein ligase E3 component n-recognin 4	-0.90	0.066
ENSDART00000035877			-0.65	0.099
ENSDART00000036779			-0.91	0.087
ENSDART00000039791			-0.67	0.055
ENSDART00000040203			-0.59	0.058
ENSDART00000046613			-0.85	0.076
ENSDART00000050672			-0.86	0.075
ENSDART00000052029			0.67	0.047
ENSDART00000052971			-1.21	0.053
ENSDART00000053529	*PLEKHO2*	pleckstrin homology domain containing, family O member 2	-0.96	0.051
ENSDART00000053768	*PTCHD2*	patched domain containing 2	-0.88	0.057
ENSDART00000053863			-0.74	0.059
ENSDART00000053865			-0.61	0.084
ENSDART00000054959			-1.31	0.035
ENSDART00000055168	*UBR4*	ubiquitin protein ligase E3 component n-recognin 4	-1.44	0.026
ENSDART00000055837	*ZBTB47*	zinc finger and BTB domain containing 47	-0.77	0.032
ENSDART00000056681	*MOBP*	myelin-associated oligodendrocyte basic protein	-0.66	0.090
ENSDART00000057304			-1.02	0.071
ENSDART00000058370	*ARHGAP33*	Rho GTPase activating protein 33	-1.02	0.087

ENSDART00000058498	*FRYL*	FRY-like	-1.62	0.058
ENSDART00000058537			-0.85	0.271
ENSDART00000059370	*VPS13B*	vacuolar protein sorting 13 homolog B (yeast)	-0.61	0.531
ENSDART00000059586			-0.77	0.079
ENSDART00000060194			-0.94	0.001
ENSDART00000061293	*NEB*	nebulin	-1.57	0.076
ENSDART00000062667			-0.66	0.029
ENSDART00000062848			-0.98	0.028
ENSDART00000066734			-0.83	0.111
ENSDART00000067030			-1.39	0.030
ENSDART00000074870			-1.16	0.037
ENSDART00000075629	*TLN1*	talin 1	-1.19	0.033
ENSDART00000076539			-1.03	0.065
ENSDART00000077495	*POLR2A*	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa	-1.50	0.067
ENSDART00000078334	*CELSR3*	cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Drosophila)	-1.47	0.022
ENSDART00000079193	*DCHS1*	dachsous 1 (Drosophila)	-0.68	0.081
ENSDART00000079875			-0.60	0.001
ENSDART00000079941	*NEB*	nebulin	-1.98	0.024
ENSDART00000079974			-0.61	0.030
ENSDART00000080190	*MEF2A* (includes EG:4205)	myocyte enhancer factor 2A	-0.82	0.059
ENSDART00000080432			-0.79	0.084

ENSDART00000080780			-0.69	0.071
ENSDART00000080924			1.04	0.321
ENSDART00000080987			-0.88	0.162
ENSDART00000082074	*FAM179B*	family with sequence similarity 179, member B	-0.77	0.063
ENSDART00000082127	*HEATR5B*	HEAT repeat containing 5B	-0.91	0.006
ENSDART00000082421	*WDR7*	WD repeat domain 7	-1.09	0.029
ENSDART00000083484	*SHANK1*	SH3 and multiple ankyrin repeat domains 1	-0.94	0.019
ENSDART00000083605			-0.59	0.089
ENSDART00000083777			-0.92	0.084
ENSDART00000084070			-1.02	0.061
ENSDART00000084551			-1.52	0.138
ENSDART00000085327	*SHANK1*	SH3 and multiple ankyrin repeat domains 1	-0.97	0.024
ENSDART00000085330			-0.62	0.031
ENSDART00000085804			-0.99	0.084
ENSDART00000085939			-0.78	0.076
ENSDART00000086389	*ANKFN1*	ankyrin-repeat and fibronectin type III domain containing 1	-0.83	0.099
ENSDART00000086790			-1.31	0.041
ENSDART00000087665			-0.82	0.063
ENSDART00000088009			-0.68	0.028
ENSDART00000088100			-1.26	0.057
ENSDART00000088273			-0.85	0.094
ENSDART00000088403	*KIF1A*	kinesin family member 1A	-0.99	0.082

ENSDART00000088484	*AHNAK*	AHNAK nucleoprotein	-1.02	0.001
ENSDART00000088668	*NFIC*	nuclear factor I/C (CCAAT-binding transcription factor)	-0.68	0.058
ENSDART00000089997			-1.06	0.051
ENSDART00000090000			-1.01	0.025
ENSDART00000090174	*DOCK9*	dedicator of cytokinesis 9	-0.87	0.092
ENSDART00000090499			-0.86	0.046
ENSDART00000092665	*SREBF1*	sterol regulatory element binding transcription factor 1	-0.97	0.070
ENSDART00000092701	*TOX4*	TOX high mobility group box family member 4	-0.81	0.022
ENSDART00000092784			-0.60	0.049
ENSDART00000093173			-2.07	0.096
ENSDART00000093328			-1.14	0.078
ENSDART00000093412	*OSBPL6*	oxysterol binding protein-like 6	-0.62	0.017
ENSDART00000097159			-1.00	0.065
ENSDART00000097524			-1.39	0.038
ENSDART00000097564	*ENPP5*	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)	-0.74	0.054
ENSDART00000097661	*ANO3* (includes EG:63982)	anoctamin 3	-0.90	0.029
ENSDART00000097856	*FRAS1*	Fraser syndrome 1	-1.18	0.050
ENSDART00000097946			-1.78	0.013
ENSDART00000098338			-0.96	0.096
ENSDART00000098492			-0.94	0.047
ENSDART00000098524			0.65	0.034

ENSDART0 0000099310			0.63	0.050
ENSDART0 0000099431			-1.01	0.078
ENSDART0 0000099444			-1.15	0.004
ENSDART0 0000099461			-1.35	0.061
ENSDART0 0000099521			-0.65	0.053
ENSDART0 0000100154	*MADD*	MAP-kinase activating death domain	-0.89	0.066
ENSDART0 0000100510			-0.67	0.093
ENSDART0 0000100722			-0.63	0.013
ENSDART0 0000100747	*SLC7A1*	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	-1.08	0.087
ENSDART0 0000100858			-0.95	0.084
ENSDART0 0000100947			0.70	0.025
ENSDART0 0000101003			-0.74	0.098
ENSDART0 0000102649			-0.81	0.056
ENSDART0 0000102745	*WDR7*	WD repeat domain 7	-1.17	0.182
ENSDART0 0000103040			-0.62	0.080
ENSDART0 0000103222			0.68	0.047
ENSDART0 0000103380			-0.85	0.064
ENSDART0 0000104066	*BAT2*	HLA-B associated transcript 2	-1.74	0.046
ENSDART0 0000104179			0.81	0.252
ENSDART0 0000104228	*UBR4*	ubiquitin protein ligase E3 component n-recognin 4	-0.83	0.025
ENSDART0 0000104312			-1.78	0.099
ENSDART0 0000104313			-1.96	0.098

NM_001018134			-0.91	0.029
NM_001030097			-0.89	0.063
NM_001034986	*LAMA1*	laminin, alpha 1	-0.81	0.076
NM_001080577	*CELSR2*	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	-0.80	0.077
NM_001082992	*MBD5*	methyl-CpG binding domain protein 5	-0.83	0.416
NM_001083540	*ZSWIM7*	zinc finger, SWIM-type containing 7	0.67	0.074
NM_198360	*GRIA3*	glutamate receptor, ionotrophic, AMPA 3	-0.75	0.098
NM_199941	*SERPINB6*	serpin peptidase inhibitor, clade B (ovalbumin), member 6	0.76	0.029
NM_200804	*TIMM16*	mitochondria-associated protein involved in granulocyte-macrophage colony-stimulating factor signal transduction	0.60	0.062
NM_207080	*RALBP1*	ralA binding protein 1	-0.62	0.073
OTTDART00000001485	*NCOR2*	nuclear receptor co-repressor 2	-1.21	0.092
OTTDART00000001874			-2.08	0.198
OTTDART00000001875	*MYCBP2*	MYC binding protein 2	-1.62	0.035
OTTDART00000004353			-1.22	0.032
OTTDART00000004361			-0.71	0.003
OTTDART00000004904	*CACNA1A*	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	-1.05	0.065
OTTDART00000004925	*CACNA1A*	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	-1.14	0.087
OTTDART00000005817	*SYNE1*	spectrin repeat containing, nuclear envelope 1	-0.67	0.079
OTTDART00000006174	*NCOA1*	nuclear receptor coactivator 1	-0.82	0.086
OTTDART00000006630	*HIVEP2*	human immunodeficiency virus type I enhancer binding protein 2	-0.84	0.088

OTTDART0 0000007423			-1.17	0.058
OTTDART0 0000007739	*RYR3*	ryanodine receptor 3	-1.34	0.097
OTTDART0 0000007851	*GABRR2*	gamma-aminobutyric acid (GABA) receptor, rho 2	0.66	0.074
OTTDART0 0000008696	*PCLO*	piccolo (presynaptic cytomatrix protein)	-1.01	0.069
OTTDART0 0000008954	*HMGA2*	high mobility group AT-hook 2	-0.62	0.029
OTTDART0 0000009736	*CACNA1C*	calcium channel, voltage-dependent, L type, alpha 1C subunit	-1.18	0.076
OTTDART0 0000010814	*ROBO2*	roundabout, axon guidance receptor, homolog 2 (Drosophila)	-1.36	0.096
OTTDART0 0000010968			0.79	0.348
OTTDART0 0000011499	*COL11A2*	collagen, type XI, alpha 2	-1.99	0.024
OTTDART0 0000013208	*MAPK6*	mitogen-activated protein kinase 6	-1.30	0.008
OTTDART0 0000013300	*LRP1B*	low density lipoprotein receptor-related protein 1B	-0.77	0.056
OTTDART0 0000014265			-0.66	0.085
OTTDART0 0000014895			-0.81	0.073
OTTDART0 0000015431	*MT2A*	metallothionein 2A	0.87	0.026
OTTDART0 0000015896			-0.99	0.152
OTTDART0 0000017071	*PKHD1L1*	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	-0.62	0.021
OTTDART0 0000017190	*MLL5*	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	-1.52	0.128
OTTDART0 0000017232	*KCNH8*	potassium voltage-gated channel, subfamily H (eag-related), member 8	-0.72	0.037
OTTDART0 0000018601	*SYNE1*	spectrin repeat containing, nuclear envelope 1	-0.59	0.092
OTTDART0 0000018796	*MACF1*	microtubule-actin crosslinking factor 1	-1.22	0.009
OTTDART0 0000020590			-0.95	0.098

OTTDART0 0000021634			-1.30	0.068
OTTDART0 0000021748	*NTRK2*	neurotrophic tyrosine kinase, receptor, type 2	-0.80	0.083
OTTDART0 0000021816	*MINK1*	misshapen-like kinase 1 (zebrafish)	-1.23	0.087
OTTDART0 0000022442	*WDFY3*	WD repeat and FYVE domain containing 3	-1.22	0.118
OTTDART0 0000022501	*FCGBP* (includes EG:8857)	Fc fragment of IgG binding protein	-1.18	0.074
OTTDART0 0000022729	*KCMF1*	potassium channel modulatory factor 1	-0.63	0.091
OTTDART0 0000023373			-0.63	0.035
OTTDART0 0000023625			-0.63	0.006
OTTDART0 0000023881	*FAT1*	FAT tumor suppressor homolog 1 (Drosophila)	-1.00	0.021
OTTDART0 0000024880	*HIPK3*	homeodomain interacting protein kinase 3	-0.85	0.080
OTTDART0 0000025923	*MAPK8*	mitogen-activated protein kinase 8	-0.87	0.024
OTTDART0 0000026198			-1.18	0.018
OTTDART0 0000026514	*MYCBP2*	MYC binding protein 2	-1.06	0.024
OTTDART0 0000027103	*KIF1B*	kinesin family member 1B	-1.17	0.085
OTTDART0 0000027927	*C17ORF62*	chromosome 17 open reading frame 62	1.64	0.233
OTTDART0 0000027995			-1.62	0.141
OTTDART0 0000028508	*PICALM*	phosphatidylinositol binding clathrin assembly protein	-0.78	0.072
OTTDART0 0000028640	*ANK2*	ankyrin 2, neuronal	-0.67	0.020
OTTDART0 0000029506	*ERAP1*	endoplasmic reticulum aminopeptidase 1	0.59	0.066
OTTDART0 0000030170			-0.65	0.084
OTTDART0 0000030337			-0.82	0.067

OTTDART00000030339	*GRM3*	glutamate receptor, metabotropic 3	-0.70	0.055
OTTDART00000030520			-0.82	0.089
OTTDART00000030529			-0.93	0.065
OTTDART00000030789	*MACF1*	microtubule-actin crosslinking factor 1	-1.58	0.038
OTTDART00000030796			-0.75	0.096
OTTDART00000031305	*ABI1*	abl-interactor 1	-0.84	0.088
OTTDART00000031533	*MLL3*	myeloid/lymphoid or mixed-lineage leukemia 3	-0.69	0.027
OTTDART00000031535	*MLL3*	myeloid/lymphoid or mixed-lineage leukemia 3	-1.32	0.014
OTTDART00000031536	*MLL3*	myeloid/lymphoid or mixed-lineage leukemia 3	-1.28	0.065
OTTDART00000031537	*MLL3*	myeloid/lymphoid or mixed-lineage leukemia 3	-1.32	0.014
OTTDART00000032689			-0.91	0.044
TC235438	*NAV3*	neuron navigator 3	-0.77	0.083
TC236736	*SALL4*	sal-like 4 (Drosophila)	-0.59	0.073
TC237872	*CTSL2*	cathepsin L2	0.61	0.057
TC239115	*DNAJC13*	DnaJ (Hsp40) homolog, subfamily C, member 13	-1.66	0.093
TC239967	*TNRC18*	trinucleotide repeat containing 18	-1.22	0.051
TC245351	*HOXC12*	homeobox C12	-0.71	0.052
TC245623			-0.95	0.058
TC246849	*PDE4DIP*	phosphodiesterase 4D interacting protein	-1.94	0.103
TC252900			-0.81	0.102
TC253435	*DYNC1H1*	dynein, cytoplasmic 1, heavy chain 1	-0.81	0.058
TC254762	*NRXN2*	neurexin 2	-1.29	0.096
TC254869	*LRP1*	low density lipoprotein receptor-related protein 1	-1.54	0.022
TC260965			0.79	0.012
TC261325			0.61	0.071
TC263188	*DYNC1H1*	dynein, cytoplasmic 1, heavy chain 1	-2.39	0.128
ZV700S00000010	*SAMD4B*	sterile alpha motif domain containing 4B	-1.04	0.070
ZV700S00000109	*CSF1R*	colony stimulating factor 1 receptor	0.90	0.049

ZV700S0000 0121	*DYNC1H1*	dynein, cytoplasmic 1, heavy chain 1	-1.09	0.160
ZV700S0000 1340	*TNRC18*	trinucleotide repeat containing 18	-1.34	0.088
ZV700S0000 1605			-0.68	0.040
ZV700S0000 2076	*ZNF567*	zinc finger protein 567	-0.73	0.006
ZV700S0000 2250	*PDE4DIP*	phosphodiesterase 4D interacting protein	-2.04	0.142
ZV700S0000 2273			-0.60	0.092
ZV700S0000 2926	*MLL3*	myeloid/lymphoid or mixed-lineage leukemia 3	-0.96	0.021
ZV700S0000 3107	*POU2F1*	POU class 2 homeobox 1	-0.78	0.045
ZV700S0000 3244	*SIK3*	SIK family kinase 3	-1.44	0.096
ZV700S0000 3301	*ELAVL3*	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	-0.71	0.054
ZV700S0000 3335	*POU2F1*	POU class 2 homeobox 1	-0.69	0.071
ZV700S0000 6220	*DYNC1H1*	dynein, cytoplasmic 1, heavy chain 1	-2.32	0.129
ZV700S0000 6501	*TANC2*	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	-0.95	0.093

Supplemental Material, Table 3. Probes altered due to lead exposure at 120 hpf

SEQ_ID	Symbol	Entrez Gene Name	Log_2 Expression Ratio	P-value
AW279987	*PTER*	phosphotriesterase related	-0.63	0.040
BC045331.1	*CHIA*	chitinase, acidic	-0.98	0.040
BC056563.1	*HPX*	hemopexin	0.97	0.383
BG727638	*SMARCAD1*	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1	1.53	0.048
BG728531			1.63	0.088
BI884441			-0.90	0.069
ENSDART00000009476	*CCDC39*	coiled-coil domain containing 39	0.62	0.078
ENSDART00000050942			0.69	0.099
ENSDART00000052904			0.74	0.005
ENSDART00000053099			0.85	0.192
ENSDART00000058017			-0.74	0.033
ENSDART00000059617			0.91	0.274
ENSDART00000060844			0.60	0.014
ENSDART00000063704			0.64	0.088
ENSDART00000074302			-0.65	0.063
ENSDART00000076069			0.82	0.073
ENSDART00000077671			-1.25	0.174
ENSDART00000078873			1.73	0.023
ENSDART00000080259			-0.81	0.071
ENSDART00000081362			-1.36	0.248
ENSDART00000083850			-0.72	0.084

ENSDART00000087926			-0.58	0.088
ENSDART00000088042			0.61	0.035
ENSDART00000097616			-0.99	0.081
ENSDART00000097761			-0.87	0.097
ENSDART00000097909			-0.83	0.042
ENSDART00000098122			-0.73	0.034
ENSDART00000098720			-0.74	0.042
ENSDART00000099194			0.60	0.033
ENSDART00000100748			-0.60	0.097
ENSDART00000101785			1.01	0.079
ENSDART00000101932	*CYBASC3*	cytochrome b, ascorbate dependent 3	0.90	0.347
ENSDART00000102978			-0.94	0.047
ENSDART00000103983			2.65	0.035
ENSDART00000106080			-0.67	0.021
ENSDART00000106083			-0.65	0.084
ENSDART00000106462			-0.67	0.066
ENSDART00000106676			-0.64	0.096
NM_001002569			0.78	0.053
NM_001025557			-0.61	0.039
NM_001076602	*SLC25A38*	solute carrier family 25, member 38	0.76	0.030
NM_001080700			1.10	0.089
NM_001098731	*IQCA1*	IQ motif containing with AAA domain 1	0.62	0.025

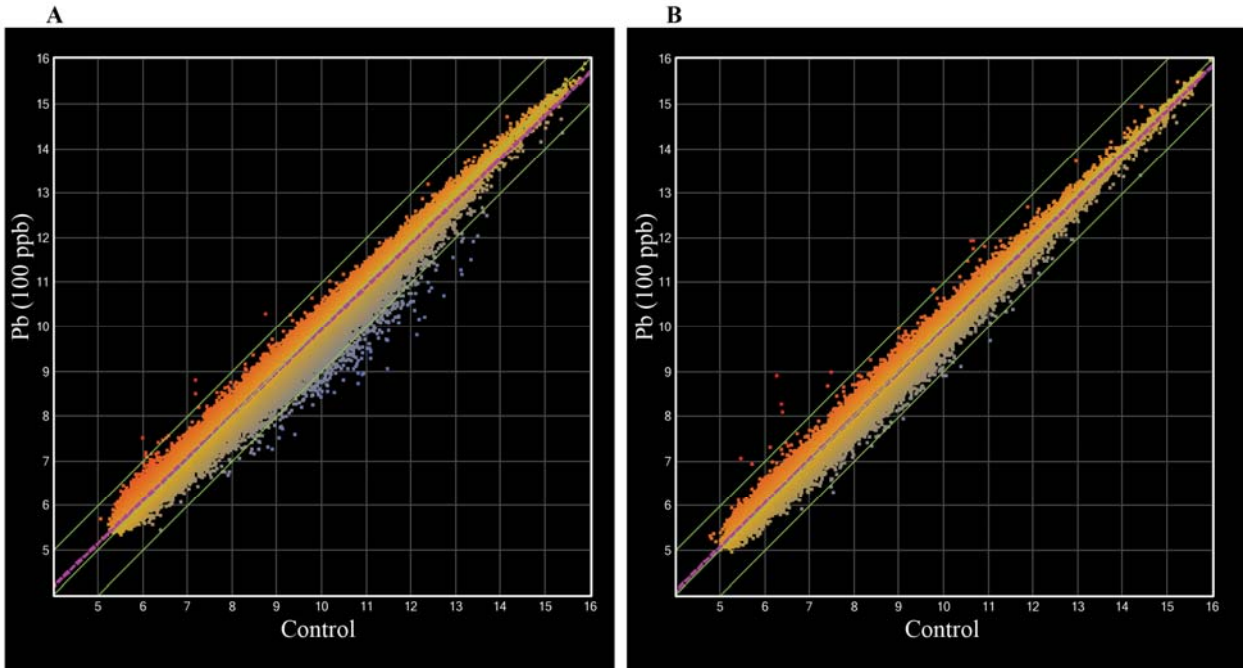
NM_178293	*AVP*	arginine vasopressin	0.68	0.169
NM_207077	*SLC22A20* (includes EG:381203)	solute carrier family 22 (organic anion transporter), member 20	0.91	0.159
OTTDART00000001892	*PSMB11*	proteasome (prosome, macropain) subunit, beta type, 11	0.61	0.042
OTTDART00000006798	*PLA2G4A*	phospholipase A2, group IVA (cytosolic, calcium-dependent)	0.95	0.034
OTTDART00000007191	*POMC*	proopiomelanocortin	0.83	0.003
OTTDART00000009952			0.60	0.092
OTTDART00000013519			-0.94	0.628
OTTDART00000014313			-0.97	0.098
OTTDART00000014811			-0.62	0.007
OTTDART00000017412			-0.71	0.082
OTTDART00000018095			-0.64	0.060
OTTDART00000018113	*LIN28*	lin-28 homolog (C. elegans)	0.69	0.051
OTTDART00000019826	*HIST1H4H* (includes EG:8365)	histone cluster 1, H4h	-1.13	0.085
OTTDART00000024968	*TLX1*	T-cell leukemia homeobox 1	0.64	0.079
OTTDART00000025660	*ASAH2*	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2	-0.62	0.038
OTTDART00000027046			0.58	0.075
OTTDART00000028561			0.64	0.031
OTTDART00000029487			-0.88	0.046
OTTDART00000029880			-0.64	0.060
OTTDART00000030461	*PPIL4*	peptidylprolyl isomerase (cyclophilin)-like 4	-0.63	0.087
OTTDART00000032376			-0.73	0.039

OTTDART00000032489			-0.78	0.099
TC237078	*MYOF*	myoferlin	-0.83	0.296
TC243686			0.61	0.092
TC245053			-0.67	0.049
ZV700S00000194	*FMO6*	flavin containing monooxygenase 6 pseudogene	-1.21	0.078
ZV700S00000569	*SLC22A6*	solute carrier family 22 (organic anion transporter), member 6	1.91	0.018
ZV700S00000778			-0.81	0.055
ZV700S00001053	*KCNK12*	potassium channel, subfamily K, member 12	-0.91	0.085
ZV700S00001159	*DNAH1*	dynein, axonemal, heavy chain 1	0.62	0.006
ZV700S00002986			0.63	0.078
ZV700S00003266	*AVP*	arginine vasopressin	0.69	0.214
ZV700S00004390			-0.85	0.006
ZV700S00004824	*XYLB*	xylulokinase homolog (H. influenzae)	0.65	0.084
ZV700S00005844	*AGL*	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase	0.80	0.059
ZV700S00006167	*HPX*	hemopexin	1.07	0.336
ZV700S00006269	*PAX7*	paired box 7	0.73	0.077
ZV700S00006452	*TXN*	thioredoxin	1.29	0.045
ZV700S00006543	*KRT13*	keratin 13	-0.68	0.038

Supplemental Material, Table 4. Gene ontology of altered genes at 120 hpf

Function Category	*p*-value[a]	# of Genes[b]
RENAL AND UROLOGICAL DISORDER		
Renal and Urological disorder	2.20E-02	3
CANCER		
Tumorigenesis	2.17E-02	9
Cancer	3.29E-02	8
HEMATOLOGICAL DISORDER		
Hematological disorder	3.72E-02	4
LIPID METABOLISM		
Synthesis of phosphatidic acid	2.30E-04	3
Release of eicosanoid	1.26E-03	3
Hydrolysis of lipid	2.53E-03	3
Quantity of lipid	3.82E-03	4
Accumulation of lipid	2.00E-03	3
Metabolism of lipid	2.97E-02	3
TISSUE DEVELOPMENT		
Developmental process of muscle	6.91E-04	4
CARDIOVASCULAR SYSTEM DEVELOPMENT AND FUNCTION		
Blood pressure	1.62E-03	3

[a] *p*-values are derived from the chance of observing the degree of enrichment in a gene set of a given size by chance alone.

[b] Number of genes classified as being differentially expressed that relate to the specified functional category. A gene may be present in more than one category.

Supplemental Material, Figure 1. 72 and 120 hpf Scatter Plot – Mean intensity values for each gene are represented by dots with Pb treated embryos being plotted against controls. The two treatment groups displayed similar expression patterns at (**A**) 72 and (**B**) 120 hpf with R^2 correlation of 0.9813 and 0.9918, respectively. Applying set criteria 231 probes were altered at 72 hpf while 82 probes were differentially expressed at 120 hpf. Diagonal white lines represent a $\log_2$ expression ratio of 1 or -1 between treated and controls (200% or 50% alteration in expression).