Figure S1. The H&E stain of mouse liver tissue. After euthanization, the livers were harvested for H&E staining and examined by light microscopy at magnifications of (A) x100, (B) x200 and (C) x400. Arrowheads, normal hepatocytes (black) and patent sinusoidal capillary space (white); Arrow, swollen hepatocytes with narrowed sinusoidal capillary spaces.

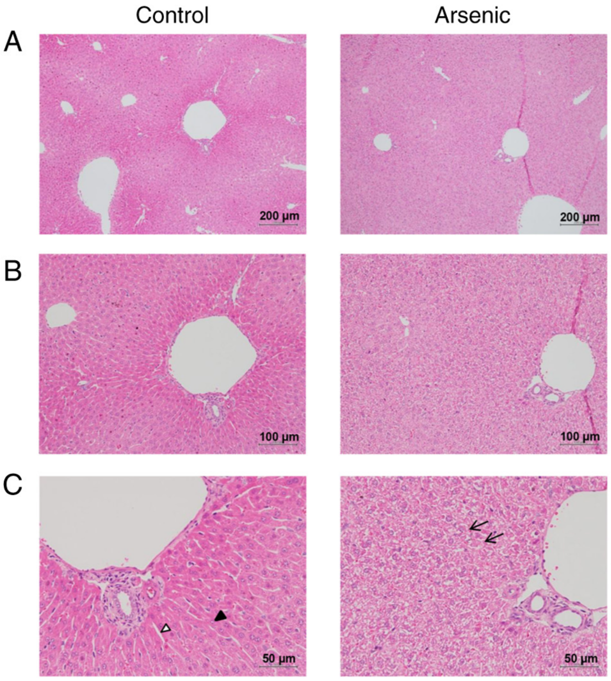


Figure S2. The putative CpG island location of mouse *Cbs*, *Malat1*, *Adora1* and *Wif1* genes. The CpG island was predicted by EMBOSS Cpgplot (https://www.ebi.ac.uk/Tools/seqstats/emboss_cpgplot/). The 500-bp sequence region before and after transcription start site (TSS) (-500 to +500 bp) of *Cbs*, *Adora1* and *Wif1* were assayed, and the -250 to +100 bp region of *Malat1* was analyzed. The putative CpG island was indicated by 2 lines in the lower image of each gene. *Cbs*, cystathionine β-synthase; *Adora1*, adenosine A1 receptor; *Wif1*, Wnt inhibitory factor 1; *Malat1*, metastasis-associated lung adenocarcinoma transcript 1; *WIF1*, Wnt inhibitory factor 1.

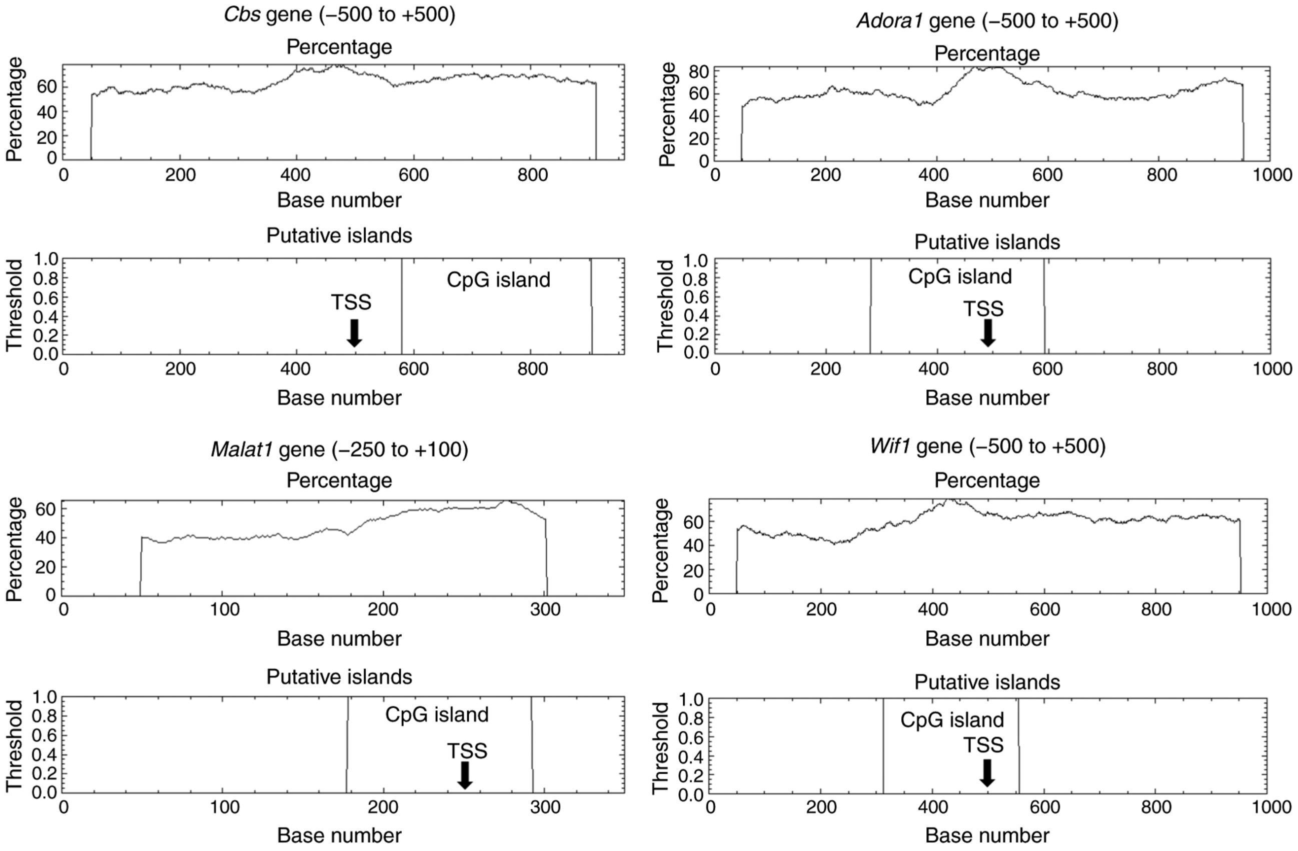
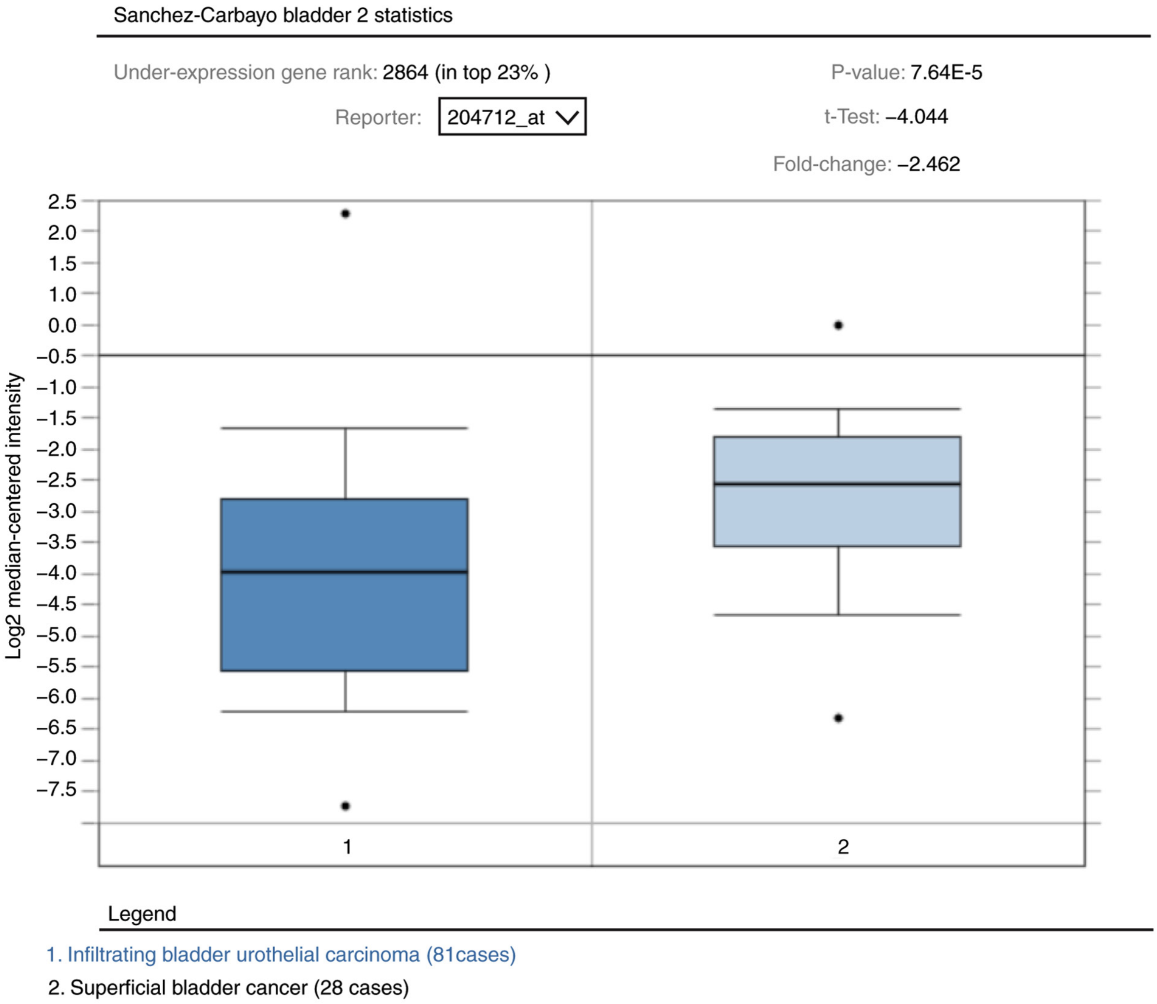


Figure S3. The result of Oncomine database (http://www.oncomine.org) search of the *WIF1* gene. Primary filters: differential analysis and bladder cancer. Threshold by: P-value (1E-4), fold change (1.5) and gene rank (all). The differential analysis result is from Sanchez-Carbayo Bladder 2, fold change=2.462, P=7.64E-5. *WIF1*, Wnt inhibitory factor 1.



Sanchez-Carbayo bladder 2 statistics

Under-expression gene rank: 2864 (in top 23%)

Reporter: 204712_at

P-value: 7.64E-5

t-Test: –4.044

Fold-change: –2.462

Legend

1. Infiltrating bladder urothelial carcinoma (81cases)
2. Superficial bladder cancer (28 cases)

Table SI. Normalized intensities of upregulated genes and downregulated genes in control and arsenic-treated mouse bladder from DNA microarray chip analysis.

A, Upregulated genes

Normalized intensity		Log$_2$ (ratio)	P-value (differentially expressed)	Annotation	
Control (C)	Arsenic (A)	A/C	A/C	Gene_symbol	Entrez_gene
153.485535	1036.77869	2.746921	5.74949E-14	Rnu11	353373
395.941101	2607.92529	2.646373	1.65899E-18	Rn7sk	19817
359.535034	1817.66797	2.265185	2.34224E-06	Fosb	14282
34.984741	126.803871	2.16917	0.006034087	Rnu12	104307
3769.73877	17352.2539	2.097754	4.30274E-16	Fos	14281
15.989611	22.479181	1.947264	0.044331357	Gm10743	100038546
42.509399	129.80954	1.878069	0.003601267	Ibsp	15891
936.258789	3540.99121	1.822469	6.26443E-12	Rnu2-10	19848
38.520142	107.812469	1.798473	0.010967372	Mmp10	17384
485.036041	1329.93628	1.373896	7.68319E-07	Tcap	21393
1129.51733	3140.69141	1.363321	1.16534E-05	Socs3	12702
8192.96875	21538.9609	1.295025	2.08289E-08	Ttr	22139
201.459778	490.625916	1.272628	0.00058669	Mybpc1	109272
1396.37097	3719.51392	1.212231	0.037542097	Clec4e	56619
91.494553	192.407654	1.191006	0.005159843	Dhrs7c	68460
86.921112	94.882675	1.187354	0.027968194	NA	NA
8121.84766	19472.3359	1.164074	2.40878E-09	Egr1	13653
2255.12646	5376.09668	1.149773	3.52351E-06	Zfp36	22695
119.538826	251.563416	1.147271	0.006744966	Cbs	12411
3981.85132	9069.32812	1.064651	0.002077494	Malat1	72289
185.605942	371.309631	1.012777	0.007683907	Scarna17	100217466
3973.00098	8301.45703	0.960877	1.45229E-06	Junb	16477
602.702759	1228.66467	0.942128	0.001716867	Klf15	66277
439.072693	874.21521	0.926631	7.29423E-05	Plk5	216166
3180.61206	6389.47363	0.903116	2.22309E-05	Adamts1	11504
303.794067	579.398682	0.897292	0.022352822	Cebpd	12609
128.041794	225.209045	0.889885	0.034369335	Tat	234724
920.280029	1809.25562	0.871417	0.002074455	Adamdec1	58860
556.703735	1070.8042	0.86606	0.000579368	Clec2d	93694
3075.29004	6080.85107	0.863064	0.001731373	Rbp4	19662
5333.5625	10411.2383	0.861113	8.13888E-06	Junb	16477
1247.68225	2434.2688	0.859713	0.027991001	Dgkg	110197
393.498047	738.08606	0.845484	0.001502705	Fetub	59083
398.585083	771.472168	0.838087	0.047943927	Arhgap33	233071
185.054337	326.266266	0.835007	0.021149697	Usp2	53376
393.606628	722.708008	0.815195	0.004435451	Slitrk6	239250
144.506973	242.022766	0.798585	0.023139855	Sprr2g	20761
156.950317	261.537842	0.7792	0.044738293	Pcdh9	211712
125.014549	201.293228	0.767894	0.037883788	Txlnb	378431
356.037659	625.528931	0.764461	0.001694825	Bend5	67621
468.554565	831.699219	0.758096	0.001003372	Fkbp5	14229
9253.59375	16599.5508	0.744607	1.55619E-05	Rbp4	19662
1084.28723	1940.88538	0.744371	0.000749457	Serpina3n	20716
149.485413	241.368698	0.741597	0.037141141	Rn45s	100861531
15192.4678	26981.7676	0.738061	5.64203E-05	Id3|LOC101056296|LOC101056300	15903|101056296|101056300
294.576569	501.074707	0.735905	0.012214851	Ndp	17986
697.555908	1227.27148	0.728774	0.000442648	Actr3b	242894
180.470032	292.072662	0.720932	0.036786776	Lin7a	108030
135.506714	212.83667	0.718884	0.04100243	Serpina3m	20717
1370.76587	2409.66675	0.718413	0.002684748	Cytl1	231162

Table SI. Continued.

A, Upregulated genes

Normalized intensity		Log$_2$ (ratio) A/C	P-value (differentially expressed) A/C	Annotation	
Control (C)	Arsenic (A)			Gene_symbol	Entrez_gene
4767.77344	8416.74512	0.717124	2.76778E-05	Dusp1	19252
1243.83582	2167.35132	0.702907	0.000929946	Mtfp1	67900
2486.36963	4334.47656	0.698241	0.000212627	Snord13	100217422
275.52713	451.37262	0.690226	0.01485487	Adora1	11539
57401.1836	99647.4219	0.686216	0.000431261	Inmt	21743
2717.72095	4696.84912	0.685559	0.000622338	Cxcl14	57266
220.066223	350.661285	0.677038	0.0370434	2900060B14Rik	68204
1475.69287	2520.45117	0.672433	0.000223106	Adamdec1	58860
369.643951	609.668762	0.66952	0.029570961	Ch25h	12642
238.017883	378.84552	0.666936	0.0202254	Fxyd2	11936
518.102173	865.545044	0.665476	0.004683108	Abcb1a	18671
599.082886	1005.32996	0.665054	0.003155256	Snord118	100216530
2007.12744	3441.54126	0.653193	0.027642824	Gata2	14461
1011.32855	1695.54956	0.652501	0.003362621	Trdn	76757
1006.87762	1687.66113	0.650644	0.002822923	Rasgef1b	320292
410.022949	665.166748	0.637393	0.012258762	Rasl10a	75668
1197.83667	1968.66663	0.619752	0.004075403	Cldn1	12737
20457.5781	33419.6484	0.616783	0.002667355	Akr1b8	14187
340.539917	534.311829	0.60876	0.020731846	Zbtb16	235320
290.500427	449.109924	0.605549	0.032752112	NA	NA
3201.81982	5218.00098	0.599564	0.001631009	St8sia6	241230
3507.01123	5693.85693	0.594263	0.001465738	Ccl11	20292
341.534515	530.086914	0.593726	0.020579733	Ebf1	13591
612.661987	977.324463	0.592875	0.012493176	Sprr2f	20760
521.691895	822.505432	0.587228	0.03414515	Pln	18821

B, Downregulated genes

Normalized intensity		Log$_2$ (ratio) A/C	P-value (differentially expressed) A/C	Annotation	
Control (C)	Arsenic (A)			Gene_symbol	Entrez_gene
1914.3877	36.155842	-6.405718	0.003595377	Gpr110	77596
30.509045	5.314735	-3.715784	0.048019603	NA	NA
1699.06104	217.584259	-2.998247	1.23615E-21	Myh2	17882
728.994385	124.582718	-2.524884	1.03799E-12	Ankrd1	107765
629.964294	111.124405	-2.460865	1.20796E-07	Spp1	20750
351.458771	69.652855	-2.202048	2.00502E-06	NA	NA
915.598022	231.089935	-2.005796	1.33911E-07	Myl7	17898
743.416016	220.025726	-1.861317	0.009790109	Cxcl9	17329
63.191933	20.081207	-1.672153	0.040939804	4930579G18Rik	75913
31567.2363	10633.502	-1.665745	1.14711E-09	Myl4	17896
10237.5244	3756.19873	-1.538292	1.90209E-08	Npy6r	18169
16166.2754	6054.1499	-1.516723	4.35213E-10	Actc1	11464
573.962646	207.609863	-1.481053	2.02036E-06	Ptprz1	19283
1299.08484	495.281738	-1.469969	1.57932E-06	4930550L24Rik	75352
3797.87061	1525.40576	-1.411951	8.58834E-09	Msln	56047
299.49527	107.855942	-1.395203	6.49299E-05	Ccna2	12428
3935.02612	1613.60742	-1.385206	6.30632E-12	NA	NA
3060.07617	1271.18164	-1.363406	3.58031E-11	Mfap4	76293
5628.4209	2354.21997	-1.357813	2.75966E-09	Aldh3a2	11671
3790.3772	1579.23804	-1.357584	4.29882E-09	Col8a2	329941

Table SI. Continued.

B, Downregulated genes

Normalized intensity		$\log_2$ (ratio) A/C	P-value (differentially expressed) A/C	Annotation	
Control (C)	Arsenic (A)			Gene_symbol	Entrez_gene
997.143433	412.210144	-1.336443	4.44963E-06	Itgbl1	223272
239.012482	88.688705	-1.318805	0.002132823	Lamc2	16782
119.495377	39.248451	-1.282041	0.021120226	Nkx2-1	21869
215.384171	81.546043	-1.280585	0.03067179	Cilp	214425
767.031128	327.580261	-1.253426	0.005115786	Pilra	231805
354.064758	147.452209	-1.228663	0.000195902	Hcrtr1	230777
4011.35498	1854.1936	-1.21401	9.39427E-10	C1qtnf3	81799
222.764526	89.21138	-1.192589	0.038304966	Calm4	80796
274.744324	111.427765	-1.192149	0.010099172	Troap	78733
470.456848	207.042725	-1.190463	0.000182393	NA	NA
23861.4727	11405.7812	-1.162101	8.65714E-07	Ctgf	14219
670.240112	308.020752	-1.156681	0.004795406	Rnf212	671564
475.491943	211.699493	-1.151799	0.032885071	Gm8140	666504
338.490967	151.154449	-1.128236	0.001012222	Nts	67405
528.550903	246.292145	-1.123275	0.000305395	NA	NA
2565.49146	1268.26392	-1.119616	9.75541E-05	Tnnt3	21957
165.939728	68.694443	-1.094632	0.035931412	Slc26a3	13487
1190.12744	589.718994	-1.09381	1.51391E-05	Pck1	18534
19350.2832	9785.77441	-1.077605	5.75037E-10	Ccnd1	12443
203.704224	88.166023	-1.075845	0.049914289	Trpm5	56843
794.238281	398.014709	-1.050786	0.001042764	Fgf9	14180
513.080322	251.43103	-1.050308	0.000123996	Arc	11838
1024.49487	546.424316	-0.982049	9.51398E-05	Clca2	80797
315.965881	156.122345	-0.978843	0.014549288	Kif26a	668303
548.983643	285.321289	-0.97501	0.000353746	Igj	16069
18552.4316	10232.7598	-0.953051	2.8041E-07	Optc	269120
2830.12695	1594.22388	-0.927684	8.6092E-07	Tgfb3	21809
853.44104	471.932068	-0.925456	0.000794824	Wif1	24117
350.042908	182.692139	-0.921286	0.004668062	H60c	670558
200.027618	98.228363	-0.917324	0.034402076	Fam150a	620393
208.02243	102.542191	-0.916796	0.0316476	Med1	19014
562.179504	311.587708	-0.886199	0.001602161	Cyp1a1	13076
837.630615	475.032471	-0.883015	0.010627735	Gm6557|2310042E22Rik	625123|66561
2518.53027	1464.32349	-0.880711	3.33803E-05	Bdh1	71911
973.406494	566.50647	-0.860589	0.001162811	Pmaip1	58801
1110.69836	657.242432	-0.839553	0.000447285	Angptl7	654812
1083.0614	637.472412	-0.839186	0.016063986	Ush1c	72088
20711.6719	12566.5938	-0.831693	0.01297027	Gbp2	14469
4639.85205	2817.79883	-0.830224	0.000419801	D0H4S114	27528
408.531067	231.046463	-0.828766	0.0150002	Prss12	19142
1952.20349	1171.6217	-0.826702	0.034708113	Ly9	17085
299.932831	165.530609	-0.823636	0.025340134	Cmah	12763
532.572754	309.628387	-0.816553	0.002017579	Fmod	14264
1209.2312	729.55127	-0.814549	0.000157314	Ern2	26918
324.177917	180.82074	-0.813161	0.038676731	Pirt	193003
810.423462	494.244141	-0.804451	0.023405904	NA	NA
23916.1992	14666.9004	-0.797319	1.1134E-06	Pi16	74116
497.664032	291.549988	-0.796916	0.005954845	NA	NA
830.766174	501.860168	-0.796409	0.001313661	Wisp2	22403
2621.63135	1618.13965	-0.795047	5.3017E-05	Diras2	68203
14586.3652	9008.46875	-0.794666	6.44409E-05	Krt4	16682
49674.9727	31111.9414	-0.767447	0.000537027	Ank1	11733

Table SI. Continued.

B, Downregulated genes

Normalized intensity		Log$_2$ (ratio)	P-value (differentially expressed)	Annotation	
Control (C)	Arsenic (A)	A/C	A/C	Gene_symbol	Entrez_gene
899.308899	559.795654	-0.758247	0.007493428	Ms4a8a	64381
2783.21777	1779.79321	-0.7459	2.23722E-05	Tpm1	22003
2105.80371	1346.31824	-0.743338	0.000466877	Col3a1	12825
3427.62866	2200.94116	-0.740452	0.000356835	Cdk5r1	12569
2591.42407	1665.75195	-0.73773	6.92538E-05	Mmp17	23948
1991.34888	1275.42407	-0.737293	0.021628581	Cib3	234421
760.514282	480.38385	-0.730935	0.002586799	Il1r2	16178
1931.67139	1246.44849	-0.728007	0.006150825	Itga1	109700
1991.37683	1288.25427	-0.725593	0.000500811	1500015O10Rik	78896
767.487366	488.828857	-0.723628	0.039193843	Gnat1	14685
11536.957	7521.60449	-0.718262	8.17324E-05	Spon2	100689
489.009003	305.491394	-0.708889	0.020198081	Gbp1	14468
4831.72607	3244.00171	-0.706416	0.021084402	Jub	16475
547.146484	344.999695	-0.705599	0.010139853	Rspo1	192199
978.547852	635.856079	-0.702984	0.008429675	Cntnap2	66797
272.008026	162.697876	-0.701483	0.042324562	Folr1	14275
9966.65527	6586.2915	-0.699184	2.83333E-05	Cyp2e1	13106
1565.45117	1031.4292	-0.695128	0.003282167	Cck	12424
943.0224	616.209595	-0.693895	0.007732067	NA	NA
7354.54736	4885.90967	-0.689811	0.00615911	Angptl4	57875
231.514984	137.912537	-0.683121	0.044621166	Vstm5	69137
333.966431	206.128754	-0.683085	0.032027572	Smpd3	58994
720.388184	468.84433	-0.682884	0.019377662	Rnd3	74194
1501.94885	997.877075	-0.682236	0.006110414	Dlk2	106565
739.831787	482.912262	-0.680466	0.012043689	Kcnf1	382571
17346.7969	11590.1182	-0.677572	7.10318E-05	Nr4a1	15370
449.515991	285.932861	-0.675417	0.033560619	NA	NA
559.486633	362.204712	-0.672117	0.010414192	Gdf15	23886
1696.32703	1137.10266	-0.671259	0.000740886	Cnn1	12797
853.932861	566.940308	-0.667129	0.006158834	Kcnj15	16516
16119.7383	10902.0801	-0.661791	5.12121E-05	Synm	233335
37001.3125	24872.9023	-0.657317	0.001368895	Ogn	18295
2580.6333	1758.14868	-0.654683	0.001239567	S100a8	20201
7946.46777	5427.271	-0.653866	0.000202307	Synm	233335
12346.7451	8431.80371	-0.650212	0.000257113	Acta1	11459
603.607422	399.405945	-0.648742	0.008173375	Flrt1	396184
4090.82739	2803.98779	-0.648551	0.001530082	Amotl2	56332
3470.1062	2401.8584	-0.646529	0.040920261	Atg12	67526
2181.34131	1494.16846	-0.644822	0.00069364	Prss23	76453
1648.61646	1131.1377	-0.638084	0.002860422	Tnfrsf12a	27279
3036.94531	2099.7583	-0.63414	0.00632641	Ppp2r2b	72930
423.493469	276.304321	-0.633701	0.022227325	Cd3d	12500
560.432373	373.228394	-0.633283	0.034886446	Insc	233752
3394.40967	2354.09644	-0.629854	0.000452636	Gpm6a	234267
1413.7019	975.787292	-0.629571	0.029339576	Pgm5	226041
2680.83472	1860.85718	-0.628052	0.001128397	Fgf1	14164
16280.9141	11242.8457	-0.627968	0.001421577	Serpinf1	20317
2160.18311	1498.74902	-0.627068	0.005879942	Gls	14660
5660.77344	3974.41162	-0.623978	0.007879104	Eno3	13808
1961.66138	1361.27124	-0.623905	0.009681475	Dusp8	18218
900.958313	616.511963	-0.622448	0.018653993	Tnnc2	21925
3418.03809	2400.7168	-0.616811	0.02503904	Plekhh2	213556

Table SI. Continued.

B, Downregulated genes

Normalized intensity		Log_2 (ratio)	P-value (differentially expressed)	Annotation	
Control (C)	Arsenic (A)	A/C	A/C	Gene_symbol	Entrez_gene
1257.48779	870.860718	-0.616797	0.007756962	Ncapd2	68298
5946.74121	4173.57471	-0.615261	0.001212917	Gm11627	100040792
1175.2085	815.627502	-0.6141	0.004568187	Ccbp2	59289
577.190796	390.736755	-0.61207	0.023669234	Ccl17	20295
5196.88184	3659.41553	-0.610044	0.00128898	Cfb	14962
387.503296	255.831818	-0.60785	0.048117422	Grip1	74053
1959.50305	1370.66968	-0.607413	0.010486256	Bcas1	76960
15384.9375	10849.7812	-0.60444	0.029953726	Flnc	68794
15080.3555	10613.5117	-0.604429	0.001522034	Adipoq	11450
24050.127	16882.2832	-0.600867	0.000330164	Cyp2f2	13107
6341.31738	4511.24902	-0.59527	0.000266698	Smoc2	64074
12860.1279	9114.61328	-0.593077	0.002557868	Dpt	56429
853.500732	598.479004	-0.590876	0.014802474	Lass3	545975
555.567993	381.806702	-0.589164	0.021848679	Wfdc10	629756
752.921387	524.380859	-0.588112	0.035533104	Frzb	20378

Table SII. Twelve enriched KEGG pathways identified following microarray analysis.

A, mmu04151:PI3K-Akt signaling pathway; Q-value: 4.666E-01

Gene_ symbol	Description	Entrez_ gene_id	log2 (ratio)	P-value (differentially expressed)
Itga1	Integrin alpha 1	109700	-0.728006555	0.006150825
Ccnd1	Cyclin D1	12443	-1.077605284	5.75037E-10
Col3a1	Collagen, type III, alpha 1	12825	-0.743337828	0.000466877
Fgf1	Fibroblast growth factor 1	14164	-0.628052346	0.001128397
Fgf9	Fibroblast growth factor 9	14180	-1.050785867	0.001042764
Nr4a1	Nuclear receptor subfamily 4, group A, member 1	15370	-0.677572388	7.10318E-05
Ibsp	Integrin binding sialoprotein	15891	1.878069263	0.003601267
Lamc2	Laminin, gamma 2	16782	-1.318804613	0.002132823
Pck1	Phosphoenolpyruvate carboxykinase 1, cytosolic	18534	-1.093810094	1.51391E-05
Spp1	Secreted phosphoprotein 1	20750	-2.46086461	1.20796E-07
Ppp2r2b	Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	72930	-0.634139583	0.00632641

B, mmu04261:Adrenergic signaling in cardiomyocytes; Q-value: 3.48218E-01

Gene_ symbol	Description	Entrez_ gene_id	log2 (ratio)	P-value (differentially expressed)
Actc1	Actin, alpha, cardiac muscle 1	11464	-1.516723299	4.35213E-10
Fxyd2	FXYD domain-containing ion transport regulator 2	11936	0.66693585	0.0202254
Myl4	Myosin, light polypeptide 4	17896	-1.665745408	1.14711E-09
Pln	Phospholamban	18821	0.587228275	0.03414515
Tpm1	Tropomyosin 1, alpha	22003	-0.745899579	2.23722E-05
Ppp2r2b	Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	72930	-0.634139583	0.00632641
Calm4	Calmodulin 4	80796	-1.192588809	0.038304966

C, mmu04010:MAPK signaling pathway; Q-value: 2.51979E-01

Gene_ symbol	Description	Entrez_ gene_id	log2 (ratio)	P-value (differentially expressed)
Fgf1	Fibroblast growth factor 1	14164	-0.628052346	0.001128397
Fgf9	Fibroblast growth factor 9	14180	-1.050785867	0.001042764
Fos	FBJ osteosarcoma oncogene	14281	2.097754447	4.30274E-16
Nr4a1	Nuclear receptor subfamily 4, group A, member 1	15370	-0.677572388	7.10318E-05
Il1r2	Interleukin 1 receptor, type II	16178	-0.730935456	0.002586799
Dusp8	Dual specificity phosphatase 8	18218	-0.623904643	0.009681475
Dusp1	Dual specificity phosphatase 1	19252	0.717123898	2.76778E-05
Tgfb3	Transforming growth factor, beta 3	21809	-0.927684244	8.6092E-07
Flnc	Filamin C, gamma	68794	-0.604439776	0.029953726

D, mmu04510:Focal adhesion; Q-value: 2.30786E-01

Gene_ symbol	Description	Entrez_ gene_id	log2 (ratio)	P-value (differentially expressed)
Itga1	Integrin alpha 1	109700	-0.728006555	0.006150825
Ccnd1	Cyclin D1	12443	-1.077605284	5.75037E-10
Col3a1	Collagen, type III, alpha 1	12825	-0.743337828	0.000466877
Ibsp	Integrin binding sialoprotein	15891	1.878069263	0.003601267
Lamc2	Laminin, gamma 2	16782	-1.318804613	0.002132823

Table SII. Continued.

D, mmu04510:Focal adhesion; Q-value: 2.30786E-01

Gene_ symbol	Description	Entrez_ gene_id	log2 (ratio)	P-value (differentially expressed)
Myl7	Myosin, light polypeptide 7, regulatory	17898	-2.005796219	1.33911E-07
Spp1	Secreted phosphoprotein 1	20750	-2.46086461	1.20796E-07
Flnc	Filamin C, gamma	68794	-0.604439776	0.029953726

E, mmu05414:Dilated cardiomyopathy; Q-value: 3.28022E-01

Gene_ symbol	Description	Entrez_ gene_id	log2 (ratio)	P-value (differentially expressed)
Itga1	Integrin alpha 1	109700	-0.728006555	0.006150825
Actc1	Actin, alpha, cardiac muscle 1	11464	-1.516723299	4.35213E-10
Pln	Phospholamban	18821	0.587228275	0.03414515
Tgfb3	Transforming growth factor, beta 3	21809	-0.927684244	8.6092E-07
Tpm1	Tropomyosin 1, alpha	22003	-0.745899579	2.23722E-05

F, mmu04512:ECM-receptor interaction; Q-value: 3.32824E-01

Gene_ symbol	Description	Entrez_ gene_id	log2 (ratio)	P-value (differentially expressed)
Itga1	Integrin alpha 1	109700	-0.728006555	0.006150825
Col3a1	Collagen, type III, alpha 1	12825	-0.743337828	0.000466877
Ibsp	Integrin binding sialoprotein	15891	1.878069263	0.003601267
Lamc2	Laminin, gamma 2	16782	-1.318804613	0.002132823
Spp1	Secreted phosphoprotein 1	20750	-2.46086461	1.20796E-07

G, mmu04390:Hippo signaling pathway; Q-value: 4.17219E-01

Gene_ symbol	Description	Entrez_ gene_id	log2 (ratio)	P-value (differentially expressed)
Ccnd1	Cyclin D1	12443	-1.077605284	5.75037E-10
Fgf1	Fibroblast growth factor 1	14164	-0.628052346	0.001128397
Ctgf	Connective tissue growth factor	14219	-1.162100608	8.65714E-07
Jub	Ajuba LIM protein	16475	-0.706416327	0.021084402
Tgfb3	Transforming growth factor, beta 3	21809	-0.927684244	8.6092E-07
Ppp2r2b	Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	72930	-0.634139583	0.00632641

H, mmu04964:Proximal tubule bicarbonate reclamation; Q-value: 3.91079E-01

Gene_ symbol	Description	Entrez_ gene_id	log2 (ratio)	P-value (differentially expressed)
Fxyd2	FXYD domain-containing ion transport regulator 2	11936	0.66693585	0.0202254
Gls	Glutaminase	14660	-0.627068474	0.005879942
Pck1	Phosphoenolpyruvate carboxykinase 1, cytosolic	18534	-1.093810094	1.51391E-05

I, mmu05031:Amphetamine addiction; Q-value: 4.86761E-01

Gene_ symbol	Description	Entrez_ gene_id	log2 (ratio)	P-value (differentially expressed)
Arc	Activity regulated cytoskeletal-associated protein	11838	-1.050307792	0.000123996

Table SII. Continued.

I, mmu05031:Amphetamine addiction; Q-value: 4.86761E-01

Gene_ symbol	Description	Entrez_ gene_id	log2 (ratio)	P-value (differentially expressed)
Fos	FBJ osteosarcoma oncogene	14281	2.097754447	4.30274E-16
Fosb	FBJ osteosarcoma oncogene B	14282	2.265185031	2.34224E-06
Calm4	Calmodulin 4	80796	-1.192588809	0.038304966

J, mmu04152:AMPK signaling pathway; Q-value: 5.53642E-01

Gene_ symbol	Description	Entrez_ gene_id	log2 (ratio)	P-value (differentially expressed)
Adipoq	Adiponectin, C1Q and collagen domain containing	11450	-0.604428986	0.001522034
Ccna2	Cyclin A2	12428	-1.395203322	6.49299E-05
Ccnd1	Cyclin D1	12443	-1.077605284	5.75037E-10
Pck1	Phosphoenolpyruvate carboxykinase 1, cytosolic	18534	-1.093810094	1.51391E-05
Ppp2r2b	Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	72930	-0.634139583	0.00632641

K, mmu04260:Cardiac muscle contraction; Q-value: 5.41416E-01

Gene_ symbol	Description	Entrez_ gene_id	log2 (ratio)	P-value (differentially expressed)
Actc1	Actin, alpha, cardiac muscle 1	11464	-1.516723299	4.35213E-10
Fxyd2	FXYD domain-containing ion transport regulator 2	11936	0.66693585	0.0202254
Myl4	Myosin, light polypeptide 4	17896	-1.665745408	1.14711E-09
Tpm1	Tropomyosin 1, alpha	22003	-0.745899579	2.23722E-05

L, mmu05410:Hypertrophic cardiomyopathy (HCM); Q-value: 5.335E-01

Gene_ symbol	Description	Entrez_ gene_id	log2 (ratio)	P-value (differentially expressed)
Itga1	Integrin alpha 1	109700	-0.728006555	0.006150825
Actc1	Actin, alpha, cardiac muscle 1	11464	-1.516723299	4.35213E-10
Tgfb3	Transforming growth factor, beta 3	21809	-0.927684244	8.6092E-07
Tpm1	Tropomyosin 1, alpha	22003	-0.745899579	2.23722E-05