

## Supplementary Material

**Table 1.** List of genes selected for the hierarchical cluster analysis shown in Fig. 3B\*.

No.	Genes**			HUC-1						MC-T2
				Arsenicals ( $\mu\text{M}$ )						
	Full name	Symbol	Sequence ID	MMA <sup>III</sup>			DMA <sup>III</sup>		iAs <sup>III</sup>	None
0.05				0.1	0.2	0.2	0.5	0.5		
1	S100 calcium binding protein A8	<i>S100A8</i>	NM_002964	1.60	1.41	1.01	2.02	2.41	1.90	3.13
2	OC0727-S-0096 <sup>#</sup>			1.05	0.92	1.12	1.94	1.68	1.76	2.82
3	Growth factor, augments liver regeneration	<i>GFER</i>	NM_005262	0.93	1.18	1.06	0.65	1.54	2.61	3.14
4	Homeodomain interacting protein kinase 3	<i>HIPK3</i>	NM_005734	0.87	1.09	1.15	1.05	1.64	2.21	2.05
5	SRY (sex determining region Y)-box 15	<i>SOX15</i>	NM_006942	0.77	1.05	1.58	1.14	1.34	2.02	1.59
6	Glycerol-3-phosphate dehydrogenase 1	<i>GPD1</i>	NM_005276	1.30	1.31	1.15	0.55	1.25	1.67	2.26
7	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	<i>NFATC2</i>	NM_012340	1.32	1.49	1.21	0.83	1.32	1.57	1.93
8	Fem-1 homolog c	<i>FEM1C</i>	NM_020177	1.25	1.20	1.16	0.82	1.14	1.66	1.84
9	CDC2-related protein kinase 7	<i>CRK7</i>	NM_016507	1.11	1.11	1.10	0.80	1.33	1.55	1.62
10	Lipopolysaccharide-induced TNF factor	<i>LITAF</i>	NM_004862	1.30	1.40	1.06	0.91	1.38	1.17	1.52
11	Kruppel-like factor 5	<i>KLF5</i>	NM_001730	0.74	0.85	0.89	1.32	0.99	1.13	1.88
12	TAP binding protein	<i>TAPBP</i>	NM_003190	0.88	0.88	0.80	1.03	1.33	1.29	1.73
13	GDP-mannose 4,6-dehydratase	<i>GMDS</i>	NM_001500	0.87	0.90	0.74	1.02	1.21	1.06	1.51
14	Laminin, alpha 3	<i>LAMA3</i>	NM_000227	1.03	1.01	0.98	1.37	1.78	1.49	1.83
15	NPC440-S-0005 <sup>#</sup>			1.02	1.29	1.07	1.48	1.23	1.23	1.93
16	NPC440-S-0006 <sup>#</sup>			1.01	1.18	1.10	1.52	1.33	1.23	1.62
17	Cadherin 1, type 1, E-cadherin	<i>CDH1</i>	NM_004360	1.04	1.18	1.12	1.12	1.14	1.70	1.82
18	Myeloid/lymphoid or mixed-lineage leukemia 3	<i>MLL3</i>	NM_021230	0.97	1.09	1.06	1.17	1.15	1.19	1.54
19	Ladinin 1	<i>LAD1</i>	NM_005558	1.04	1.07	1.18	1.11	1.42	1.31	1.52
20	Phosphoinositide-3-kinase, regulatory subunit 1	<i>PIK3R1</i>	NM_181504	1.14	0.85	0.83	0.60	1.57	0.99	1.97

21	Transducin (beta)-like 1X-linked receptor 1	<i>TBL1XR1</i>	NM_024665	1.07	1.07	1.10	0.67	1.57	0.93	1.70
22	OC0727-S-0467 <sup>#</sup>			1.03	1.23	1.17	0.46	1.01	0.77	1.15
23	Hect domain and RLD 6	<i>HERC6</i>	NM_017912	1.90	1.16	1.53	0.60	0.57	2.22	4.73
24	Cyclin D2	<i>CCND2</i>	NM_001759	1.30	1.64	1.50	0.81	0.67	2.82	4.22
25	NPC493-S-0591 <sup>#</sup>			1.04	1.17	0.56	1.36	0.60	1.78	2.67
26	TSC22 domain family 1	<i>TGFB114</i>	NM_006022	1.10	1.02	0.94	1.57	0.75	2.56	2.86
27	Tubulin-specific chaperone d	<i>TBCD</i>	NM_005993	1.09	0.85	1.07	0.99	0.87	2.35	1.90
28	Zinc finger protein 286	<i>ZNF286</i>	NM_020652	0.99	0.87	0.53	1.01	0.55	1.00	1.65
29	NPC493-S-0328 <sup>#</sup>			0.98	0.77	0.45	0.88	0.60	1.82	1.19
30	Ring finger protein 141	<i>RNF141</i>	NM_016422	0.97	1.01	0.93	0.71	0.69	1.60	1.68
31	Ubiquitin specific protease 21	<i>USP21</i>	NM_012475	0.98	0.99	0.92	0.80	0.85	1.16	1.53
32	Polymerase (DNA directed), beta	<i>POLB</i>	NM_002690	1.08	1.06	1.04	0.86	0.92	1.55	1.02
33	Cisplatin resistance related protein CRR9p	<i>CRR9</i>	NM_030782	1.01	0.91	0.95	1.15	0.85	1.57	0.85
34	SG09G03 <sup>#</sup>			1.00	1.27	1.19	1.06	0.72	1.72	0.86
35	NPC445-S-0233 <sup>#</sup>			1.61	1.87	2.79	0.57	0.87	1.15	1.28
36	Thrombomodulin	<i>THBD</i>	NM_000361	1.45	2.13	1.95	0.80	0.65	1.49	1.60
37	Interleukin 8	<i>IL8</i>	NM_000584	1.57	1.49	1.78	1.22	0.69	1.98	1.26
38	Heparin-binding EGF-like growth factor	<i>HBEGF</i>	NM_001945	1.39	1.71	1.95	0.89	0.41	2.23	0.92
39	DNA-damage-inducible transcript 3	<i>DDIT3</i>	NM_004083	1.00	1.75	1.44	1.13	0.33	1.25	1.65
40	OC0727-S-0822 <sup>#</sup>			0.74	1.34	1.25	0.66	0.27	1.05	0.94
41	CCAAT/enhancer binding protein (C/EBP), beta	<i>CEBPB</i>	NM_005194	0.90	1.13	1.19	0.82	0.45	1.08	1.05
42	Ornithine decarboxylase 1	<i>ODC1</i>	NM_002539	1.01	1.26	1.21	0.78	0.45	1.29	0.87
43	NPC440-S-0703 <sup>#</sup>			0.44	0.36	0.36	10.73	3.16	1.12	3.54
44	V-myc myelocytomatosis viral oncogene homolog 1	<i>MYCL1</i>	NM_005376	1.19	0.21	0.30	1.10	4.15	1.09	0.85
45	A kinase (PRKA) anchor protein 5	<i>AKAP5</i>	NM_004857	0.74	0.13	0.43	1.63	1.98	1.40	0.79
46	Vav 3 oncogene	<i>VAV3</i>	NM_006113	0.29	0.52	0.55	1.70	2.91	0.59	2.03
47	Involucrin	<i>IVL</i>	NM_005547	0.83	0.56	0.98	1.82	4.66	1.53	1.10
48	Mitogen-activated protein kinase kinase kinase 11	<i>MAP3K11</i>	NM_002419	0.88	0.58	0.77	2.07	2.95	1.52	1.10
49	OC0717-S-0282 <sup>#</sup>			0.94	0.98	0.38	1.22	2.92	2.30	1.03
50	Protocadherin 1	<i>PCDH1</i>	NM_002587	1.15	1.00	1.11	1.50	1.69	1.39	1.09
51	NPC445-S-0362 <sup>#</sup>			0.91	0.82	0.89	1.23	1.60	1.58	1.09

52	Xeroderma pigmentosum, complementation group A	<i>XPA</i>	NM_000380	0.91	0.93	0.90	1.34	1.60	1.09	1.07
53	Glucose phosphate isomerase	<i>GPI</i>	NM_000175	0.79	0.75	0.76	1.30	1.66	1.77	0.73
54	Integrin beta 1 binding protein 1	<i>ITGB1BP1</i>	NM_004763	0.97	1.08	0.84	0.79	1.54	1.48	0.72
55	RNA, U70 small nucleolar	<i>RNU70</i>	BF670618	1.06	0.75	0.90	0.74	1.63	1.14	0.67
56	CD22 antigen	<i>CD22</i>	NM_001771	0.96	1.05	1.29	1.30	1.64	0.96	0.81
57	Keratin 15	<i>KRT15</i>	NM_002275	0.98	0.94	0.81	1.51	2.08	0.79	0.82
58	Connective tissue growth factor	<i>CTGF</i>	NM_001901	0.84	0.71	0.95	1.32	1.65	0.68	0.78
59	Guanine nucleotide binding protein (G protein), beta polypeptide 2	<i>GNB2</i>	NM_005273	0.73	0.75	0.55	1.36	2.05	0.92	0.68
60	CDC-like kinase 3	<i>CLK3</i>	NM_001292	0.66	1.00	0.47	1.37	1.33	0.80	0.63
61	E2F transcription factor 1	<i>E2F1</i>	NM_005225	0.77	0.62	0.62	2.12	2.22	1.01	0.52
62	Cadherin 13, H-cadherin	<i>CDH13</i>	NM_001257	1.70	1.14	1.03	0.76	1.07	1.01	0.70
63	Hemoglobin, gamma G	<i>HBG2</i>	NM_000184	1.52	1.44	1.02	1.22	1.05	0.93	0.63
64	Annexin A8	<i>ANXA8</i>	NM_001630	1.06	1.05	1.08	0.88	1.15	1.01	0.47
65	Ring-box 1	<i>RBX1</i>	NM_014248	0.97	1.19	0.83	1.02	0.75	0.97	0.46
66	S100 calcium binding protein P	<i>S100P</i>	NM_005980	1.09	1.76	1.49	1.84	0.90	2.08	0.36
67	Keratin 13	<i>KRT13</i>	NM_002274	0.93	0.90	0.87	1.35	1.68	0.59	0.36
68	Keratin 14	<i>KRT14</i>	NM_000526	1.17	0.65	0.86	1.39	2.72	0.49	0.25
69	A disintegrin and metalloproteinase domain 17	<i>ADAM17</i>	NM_003183	0.75	0.71	0.87	0.29	0.99	0.50	0.32
70	Ataxin 1	<i>ATXN1</i>	NM_000332	0.94	0.87	0.97	0.90	1.62	1.04	0.27
71	Protein kinase C, theta	<i>PRKCQ</i>	NM_006257	0.61	0.77	0.79	0.70	1.00	1.27	0.23
72	Interleukin 1 receptor, type II	<i>IL1R2</i>	NM_173343 NM_004633	2.09	2.24	1.79	3.61	1.91	7.22	0.20
73	Arachidonate 5-lipoxygenase-activating protein	<i>ALOX5AP</i>	NM_001629	0.30	1.44	1.63	0.15	0.21	0.29	0.66
74	Thioredoxin-like 5	<i>TXNL5</i>	NM_032731	0.29	0.35	1.20	2.43	0.36	0.75	0.72
75	Discoidin domain receptor family, member 2	<i>DDR2</i>	NM_006182	0.88	0.43	0.61	0.56	0.86	0.84	1.29
76	Protein kinase C, eta	<i>PRKCH</i>	NM_006255	0.85	0.44	0.48	0.59	0.41	0.65	0.93
77	Peroxisomal biogenesis factor 14	<i>PEX14</i>	NM_004565	0.70	0.55	0.66	0.72	0.70	0.48	1.05
78	Nedd4 family interacting protein 2	<i>NDFIP2</i>	NM_019080	0.70	0.59	0.80	0.69	0.71	0.34	0.86

79	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	<i>HMGCS1</i>	NM_002130	0.35	0.46	0.93	0.71	0.53	0.44	0.57
80	Serine/threonine kinase 4	<i>STK4</i>	NM_006282	0.67	0.62	0.47	0.89	0.66	0.65	0.55
81	Myristoylated alanine-rich protein kinase C substrate	<i>MARCKS</i>	NM_002356	0.72	0.76	0.69	0.92	0.59	0.45	0.57
82	Tubulin, beta 6	<i>TUBB6</i>	NM_032525	0.77	0.79	0.65	0.81	0.75	0.57	0.43
83	Fibroblast growth factor receptor 1	<i>FGFR1</i>	NM_015850 NM_000604 NM_023105 NM_023106 NM_023107 NM_023108 NM_023109 NM_023110 NM_023111	0.76	0.30	0.71	0.66	0.17	0.57	0.69
84	Thrombospondin 1	<i>THBS1</i>	NM_003246	0.87	0.64	0.76	0.88	0.29	0.61	0.48
85	Transcription factor 12	<i>TCF12</i>	NM_003205 NM_207040 NM_207038 NM_207037 NM_207036	0.71	0.53	0.60	0.69	0.35	0.45	0.37
86	NPC440-S-0223 <sup>#</sup>			0.97	0.94	0.68	0.88	0.35	0.69	0.90
87	N-ethylmaleimide-sensitive factor	<i>NSF</i>	NM_006178	0.89	0.98	1.01	0.85	0.49	0.76	0.73
88	Cyclin A1	<i>CCNA1</i>	NM_003914	0.98	0.81	0.83	0.78	0.34	0.60	0.65
89	Proteasome (prosome, macropain) subunit, alpha type, 3	<i>PSMA3</i>	NM_002788 NM_152132	0.94	0.83	0.76	0.90	0.47	0.61	0.59
90	Chromosome 2 open reading frame 23	<i>C2orf23</i>	NM_022912	0.74	0.86	0.74	0.70	0.44	0.51	0.62
91	Chromosome 21 open reading frame 4	<i>C21orf4</i>	NM_006134	0.95	0.93	0.97	0.50	0.47	0.84	0.82
92	TAF9-like RNA polymerase II	<i>TAF9L</i>	NM_015975	0.83	0.96	0.84	0.45	0.57	0.63	0.74
93	RNA pseudouridylate synthase domain containing 4	<i>RPUSD4</i>	NM_032795	0.93	1.26	1.11	0.49	0.48	1.25	0.50
94	Arrestin domain containing 4	<i>ARRDC4</i>	NM_183376	0.94	1.01	0.90	0.67	0.56	0.81	0.50
95	Peroxisome proliferative activated receptor, gamma	<i>PPARG</i>	NM_005037 NM_015869 NM_138712 NM_138711	1.03	1.22	0.97	0.64	0.75	1.06	0.48
96	Hypothetical protein FLJ11712	<i>FLJ11712</i>	NM_024570	0.80	1.03	1.70	1.04	0.50	0.78	0.56

97	Proteasome (prosome, macropain) subunit, beta type, 1	<i>PSMB1</i>	NM_003518	0.81	0.95	0.97	1.12	0.64	0.46	0.40
98	Ring finger protein 127	<i>RNF127</i>	NM_024778	0.58	0.77	1.03	0.87	0.67	0.93	0.46
99	Methionine adenosyltransferase II, alpha	<i>MAT2A</i>	NM_005911	0.62	0.95	1.01	0.92	0.77	0.76	0.28
100	Insulin-like growth factor binding protein 5	<i>IGFBP5</i>	NM_000599	0.35	0.31	0.34	0.81	0.29	0.22	1.14
101	Insulin-like growth factor binding protein 5	<i>IGFBP5</i>	NM_000599	0.43	0.23	0.22	0.86	0.31	0.19	1.14
102	Protein kinase C, alpha	<i>PRKCA</i>	NM_002737	0.52	0.12	0.41	0.49	0.32	0.28	0.56
103	SMAD, mothers against DPP homolog 7	<i>SMAD7</i>	NM_005904	0.57	0.31	0.51	0.92	0.25	0.20	0.53
104	Nucleoporin 88kDa	<i>NUP88</i>	NM_002532	0.44	0.31	0.42	0.56	0.41	0.40	0.45
105	Myosin, light polypeptide kinase	<i>MYLK</i>	NM_005965 NM_053032 NM_053031 NM_053030 NM_053029 NM_053028 NM_053027 NM_053026 NM_053025	0.38	0.31	0.32	0.73	0.33	0.33	0.38
106	GATA binding protein 6	<i>GATA6</i>	NM_005257	0.17	0.15	0.32	0.98	0.33	0.35	0.44
107	Matrix metalloproteinase 2	<i>MMP2</i>	NM_004530	0.53	0.22	0.29	0.36	0.05	0.05	0.42
108	Chemokine (C-C motif) ligand 2	<i>CCL2</i>	NM_002982	0.38	0.45	0.40	1.13	0.12	0.17	0.20
109	Protease, serine, 11 (IGF binding)	<i>PRSS11</i>	NM_002775	0.51	0.35	0.33	0.64	0.59	0.14	0.20
110	Protease, serine, 11 (IGF binding)	<i>PRSS11</i>	NM_002775	0.57	0.32	0.35	0.56	0.46	0.11	0.15
111	OC0717-S-0504 <sup>#</sup>			0.15	0.05	0.15	0.35	0.10	0.09	0.41
112	Collagen, type I, alpha 1	<i>COL1A1</i>	NM_000088	0.17	0.08	0.18	0.46	0.07	0.11	0.32
113	Integrin, beta 3	<i>ITGB3</i>	NM_000212	0.06	0.06	0.12	0.46	0.09	0.06	0.28
114	Connexin 43	<i>GJA1</i>	NM_000165	0.10	0.06	0.12	0.51	0.32	0.08	0.28

\*The data shown are the ratios of the expression in arsenical-treated HUC-1 or MC-T2 cells compared to that in untreated HUC-1 cells. The ratios are the mean values for 4 independent experiments.

\*\*Gene names and symbols are from Unigene

(<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=unigene>), and sequence IDs are from Cancer Genomic Anatomy Project (<http://cgap.nci.nih.gov/Genes/BatchGeneFinder>).

<sup>#</sup> Indicates the clone ID from original subtraction library.