

Table 2

probe ID	Gene Symbol	Title	P value	meanSig placebo	meanSig 6h	meanSig 24h	maxFC	Location
1423232_at	Etv4	ets variant gene 4 (E1A enhancer binding pr	7.64E-11	8.72	4.34	4.37	20.79	Chr:11 60.0 cM
1417141_at	Igtp	interferon gamma induced GTPase	2.68E-09	12.96	11.41	10.92	4.11	Chr:11 32.0 cM
1419043_a_at	Iigp-pending	interferon-inducible GTPase	1.87E-08	14.03	12.03	12.09	3.99	Chr:18 E1
1415753_at	BC005632	cDNA sequence BC005632	2.17E-08	12.22	10.74	10.78	2.78	Chr:10 C1
1421204_a_at	2310041H06Rik	RIKEN cDNA 2310041H06 gene	2.57E-08	7.59	8.97	8.93	2.61	Chr:9 F1
1438761_a_at	Odc	ornithine decarboxylase, structural	2.64E-08	12.22	10.05	10.17	4.52	Chr:12 6.0 cM
1423358_at	1810009K13Rik	RIKEN cDNA 1810009K13 gene	5.15E-08	8.65	7.86	7.76	1.85	Chr:16 A1
1421260_a_at	Srm	spermidine synthase	9.59E-08	10.56	9.00	9.35	2.96	Chr:4 E2
1416048_at	Phc2	polyhomeotic-like 2 (Drosophila)	1.03E-07	10.94	9.81	10.01	2.20	Chr:4 61.0 cM
1422886_a_at	Clk4	CDC like kinase 4	1.09E-07	8.21	9.21	9.11	2.00	Chr:11 B1.3
1416699_at	1110008F13Rik	RIKEN cDNA 1110008F13 gene	1.11E-07	11.87	11.12	11.25	1.68	Chr:2 H1
1417040_a_at	Bok	Bcl-2-related ovarian killer protein	1.12E-07	11.34	9.25	9.29	4.27	Chr:1 D
1416366_at	1810004I06Rik	RIKEN cDNA 1810004I06 gene	1.26E-07	12.73	11.99	11.77	1.94	Chr:7 E1
1434380_at	---	Mus musculus diabetic nephropathy-related i	1.78E-07	11.46	9.81	9.52	3.85	---
1451083_s_at	Aars	alanyl-tRNA synthetase	1.92E-07	10.60	9.74	9.43	2.25	Chr:8 E1
1427312_at	2310076E16Rik	RIKEN cDNA 2310076E16 gene	2.16E-07	6.45	8.05	7.89	3.03	Chr:13 C3
1426546_at	Tesk2	testis-specific kinase 2	2.30E-07	6.76	7.73	7.64	1.97	Chr:4 D1
1419042_at	Iigp-pending	interferon-inducible GTPase	2.30E-07	12.24	9.83	9.67	5.94	Chr:18 E1
1460330_at	Anxa3	annexin A3	2.75E-07	12.95	11.78	11.76	2.28	Chr:5 54.0 cM
1449056_at	E330009J07Rik	RIKEN cDNA E330009J07 gene	3.58E-07	7.84	8.80	8.64	1.95	Chr:6 B1
1416584_at	Man2b2	mannosidase 2, alpha B2	3.84E-07	7.01	7.84	7.77	1.78	Chr:5 B2-13.3
1427894_at	Slit2	Slit-like 2 (Drosophila)	4.01E-07	9.37	8.18	8.50	2.28	Chr:16 A1
1448529_at	Thbd	thrombomodulin	4.55E-07	11.46	9.51	9.82	3.88	Chr:2 84.0 cM
1424464_s_at	AW212394	expressed sequence AW212394	4.87E-07	5.71	6.88	6.93	2.33	Chr:1 C1.1
1416488_at	Ccng2	cyclin G2	5.32E-07	8.88	9.88	9.89	2.01	Chr:5 E3.3-F1.3
1427364_a_at	Odc	ornithine decarboxylase, structural	5.54E-07	9.94	8.28	8.50	3.17	Chr:12 6.0 cM
1431591_s_at	G1p2	interferon, alpha-inducible protein	5.88E-07	11.07	8.96	9.02	4.31	Chr:4 E2
1433691_at	Ppp1r3c	protein phosphatase 1, regulatory (inhibitor)	5.98E-07	4.82	8.76	8.82	16.04	Chr:19 C2
1437711_x_at	Odc	ornithine decarboxylase, structural	6.17E-07	11.01	9.25	9.40	3.37	Chr:12 6.0 cM
1424182_at	Acat1	acetyl-Coenzyme A acetyltransferase 1	6.25E-07	9.79	9.07	8.68	2.15	Chr:9 30.0 cM
1429379_at	Xlkd1	extra cellular link domain-containing 1	6.65E-07	12.82	11.67	11.67	2.22	Chr:7 E3
1431086_s_at	Pcmt1	protein-L-isoaspartate (D-aspartate) O-meth	7.16E-07	8.60	7.87	7.86	1.66	Chr:10 7.0 cM
1418825_at	Ifi1	interferon inducible protein 1	7.75E-07	11.50	9.94	9.88	3.08	Chr:11 B1.2
1430127_a_at	Ccnd2	cyclin D2	8.08E-07	12.77	11.79	11.51	2.39	Chr:6 61.1 cM
1424737_at	Thrsp	thyroid hormone responsive SPOT14 homolo	8.55E-07	13.55	11.87	11.43	4.36	Chr:7 E1
1416949_s_at	H2-Ke4	H2-K region expressed gene 4	8.92E-07	10.50	9.96	9.92	1.49	Chr:17 18.48 cM
1426499_at	Sh3glb2	SH3-domain GRB2-like endophilin B2	9.37E-07	11.38	10.49	10.49	1.85	Chr:2 B
1430005_a_at	4933430F08Rik	RIKEN cDNA 4933430F08 gene	9.48E-07	10.55	8.69	8.64	3.76	Chr:19 A
1437239_x_at	Phc2	polyhomeotic-like 2 (Drosophila)	9.53E-07	11.72	10.69	10.91	2.04	Chr:4 61.0 cM
1452161_at	AW558171	expressed sequence AW558171	1.02E-06	7.70	9.26	9.19	2.94	Chr:3 E1
1422758_at	Chst2	carbohydrate sulfotransferase 2	1.04E-06	10.26	8.71	8.10	4.48	---
1422973_a_at	Thrsp	thyroid hormone responsive SPOT14 homolo	1.04E-06	12.19	10.37	9.79	5.29	Chr:7 E1
1421019_at	1700021F05Rik	RIKEN cDNA 1700021F05 gene	1.05E-06	9.74	9.11	8.87	1.83	Chr:10 B2
1421818_at	Bcl6	B-cell leukemia/lymphoma 6	1.12E-06	6.22	8.23	8.62	5.26	Chr:16 13.9 cM
1453128_at	Xlkd1	extra cellular link domain-containing 1	1.19E-06	12.69	11.38	11.49	2.49	Chr:7 E3
1415907_at	Ccnd3	cyclin D3	1.24E-06	11.74	10.65	10.69	2.14	Chr:17 28.8 cM
1429692_s_at	Gch	GTP cyclohydrolase 1	1.26E-06	8.12	6.97	6.91	2.32	Chr:14 19.5 cM
1428374_at	1110017N23Rik	RIKEN cDNA 1110017N23 gene	1.31E-06	7.62	8.42	8.36	1.74	Chr:9 B
1452178_at	Plec1	plectin 1	1.59E-06	10.85	10.14	10.04	1.75	Chr:15 44.0 cM
1429360_at	Klf3	Kruppel-like factor 3 (basic)	1.75E-06	8.79	9.48	9.72	1.90	Chr:5 C3.1
1423549_at	Slc1a4	solute carrier family 1 (glutamate/neutral an	1.75E-06	7.18	4.75	4.55	6.20	Chr:11 10.92 cM
1428710_at	Rit1	Ras-like without CAAX 1	1.78E-06	7.61	8.30	8.26	1.62	Chr:3 F1
1455271_at	1500011J06Rik	RIKEN cDNA 1500011J06 gene	1.81E-06	13.48	11.79	11.55	3.80	---
1418884_x_at	Tuba1	tubulin, alpha 1	1.89E-06	12.78	11.43	11.64	2.55	Chr:15 60.4 cM
1455019_x_at	5630400A09Rik	RIKEN cDNA 5630400A09 gene	1.97E-06	11.28	10.42	10.18	2.15	Chr:10 C1
1417053_at	Phb	prohibitin	2.05E-06	10.94	9.98	10.01	1.94	Chr:11 55.6 cM
1450911_at	Ppib	peptidylprolyl isomerase B	2.12E-06	13.16	12.76	12.70	1.37	Chr:9 C
1452209_at	Pkp4	plakophilin 4	2.13E-06	7.58	8.93	9.04	2.74	Chr:2 C1.1
1434954_at	Mpp5	membrane protein, palmitoylated 5 (MAGUK	2.46E-06	8.15	8.61	8.61	1.38	Chr:12 C3
1421217_a_at	Lgals9	lectin, galactose binding, soluble 9	2.67E-06	12.76	11.66	11.63	2.19	Chr:11 B5
1456107_x_at	Snrp116-pendir	U5 small nuclear ribonucleoprotein	2.68E-06	12.35	10.80	10.58	3.40	Chr:11 E1
1419905_s_at	Hpgd	hydroxyprostaglandin dehydrogenase 15 (NF	2.78E-06	9.46	11.74	11.75	4.88	Chr:8 B3.2
1423685_at	Aars	alanyl-tRNA synthetase	2.90E-06	10.33	9.64	9.52	1.75	Chr:8 E1
1416315_at	1110035H23Rik	RIKEN cDNA 1110035H23 gene	3.04E-06	9.53	10.05	10.09	1.48	Chr:14 C1
1422429_at	Rnf14	ring finger protein 14	3.05E-06	11.20	10.78	10.77	1.35	Chr:18 17.0 cM
1421082_s_at	Banf1	barrier to autointegration factor 1	3.11E-06	11.41	10.88	11.01	1.45	Chr:19 A
1423794_at	D2Erttd391e	DNA segment, Chr 2, ERATO Doi 391, expres	3.20E-06	7.18	8.09	8.10	1.90	Chr:2 E1
1452160_at	AW558171	expressed sequence AW558171	3.23E-06	7.03	8.82	9.16	4.37	Chr:3 E1
1426381_at	BC013720	cDNA sequence BC013720	3.27E-06	8.22	7.37	7.51	1.80	Chr:19 C3
1424775_at	Oas1g	2'-5' oligoadenylate synthetase 1G	3.42E-06	11.85	11.12	11.01	1.80	Chr:5 67.0 cM
1416541_at	Skd3	suppressor of K+ transport defect 3	3.65E-06	8.58	8.39	7.80	1.72	Chr:7 E1
1418571_at	Tnfrsf12a	tumor necrosis factor receptor superfamily, r	3.69E-06	9.98	4.78	5.84	36.67	Chr:17 A3.3
1425921_a_at	1810055G02Rik	RIKEN cDNA 1810055G02 gene	3.94E-06	9.34	8.07	7.96	2.61	Chr:19 A
1448442_a_at	Psma3	proteasome (prosome, macropain) subunit, i	3.96E-06	12.18	11.70	11.61	1.49	Chr:12 C2
1424050_s_at	Fgfr1	fibroblast growth factor receptor 1	4.05E-06	11.74	10.45	10.32	2.68	Chr:8 10.0 cM
1425780_a_at	0610041E09Rik	RIKEN cDNA 0610041E09 gene	4.09E-06	10.62	10.08	9.93	1.62	Chr:13 C3