

Supplemental Material-Table 2. Apoptosis-related genes whose expression is altered in trauma/HS by two-fold or more.

mRNA Probeset Number	Gene Name*	Gene Symbol	SBR50 vs. Sham		SBR50/IL-6 vs. SBR50		SBR50/IL-6/G vs. SBR50/IL-6	
			Fold P/Sham	FDR ⁺	Fold IL-6/P	FDR ⁺	Fold G/IL-6	FDR ⁺
GROUP IA GENES INCREASED IN SBR50 vs. SHAM AND DECREASED IN SBR50/IL-6 vs. SBR50								
1369191_at	interleukin 6	Il6	96.34	0.0000	0.19	0.0000	3.77	0.0000
1367973_at	chemokine (C-C motif) ligand 2	Ccl2	47.34	0.0000	0.10	0.0000	3.03	0.0000
1371237_at	metallothionein 1a	Mt1a	25.94	0.0000	0.77	0.0029	1.09	0.3554
1368519_at	serine (or cysteine) peptidase inhibitor, clade E, member 1	Serpine1	16.75	0.0000	0.48	0.0001	1.04	0.8259
1368108_at	ATPase, Ca ⁺⁺ transporting, cardiac muscle, fast twitch 1	Atp2a1	11.92	0.0000	0.12	0.0000	23.02	0.0000
1368254_at	sphingosine kinase 1	Sphk1	11.54	0.0000	0.53	0.0012	1.15	0.4820
1368290_at	cysteine rich protein 61	Cyr61	11.29	0.0000	0.08	0.0000	4.76	0.0000
1368545_at	CASP8 and FADD-like apoptosis regulator	Cflar	10.68	0.0000	0.37	0.0005	1.48	0.1384
1369737_at	cAMP responsive element modulator	Crem	10.27	0.0000	0.59	0.0001	1.90	0.0001
1367712_at	tissue inhibitor of metalloproteinase 1	Timp1	10.10	0.0000	0.22	0.0000	2.01	0.0000
1368300_at	adenosine A2a receptor	Adora2a	9.36	0.0000	0.40	0.0003	2.23	0.0019
1370173_at	superoxide dismutase 2, mitochondrial	Sod2	8.53	0.0000	0.54	0.0000	1.48	0.0033
1368490_at	CD14 antigen	Cd14	7.85	0.0000	0.78	0.0043	1.33	0.0030
1369577_at	suppressor of cytokine signaling 2	Socs2	7.44	0.0000	0.71	0.0656	1.12	0.6008
1368731_at	orosomucoid 1	Orm1	7.32	0.0000	0.50	0.0365	1.16	0.6906
1368308_at	myelocytomatosis viral oncogene homolog (avian)	Myc	6.46	0.0000	0.49	0.0000	1.19	0.0763
1370113_at	baculoviral IAP repeat-containing 3	Birc3	5.83	0.0000	0.54	0.0002	2.10	0.0001
1370080_at	heme oxygenase (decycling) 1	Hmox1	5.17	0.0000	0.34	0.0000	2.15	0.0000
1367800_at	plasminogen activator, tissue	Plat	4.21	0.0000	0.79	0.0016	1.28	0.0019
1383426_at	proline-serine-threonine phosphatase-interacting protein 1 (predicted)	Pstpip1_predicted	4.18	0.0000	0.51	0.0000	1.15	0.2254
1370848_at	solute carrier family 2 (facilitated glucose transporter), member 1	Slc2a1	4.16	0.0000	0.54	0.0000	1.69	0.0001
1388924_at	angiopoietin-like 4	Angptl4	4.06	0.0000	0.38	0.0000	2.13	0.0002
1387219_at	Adrenomedullin	Adm	3.99	0.0000	0.60	0.0001	0.80	0.0471
1386908_at	glutaredoxin 1 (thioltransferase)	Glrx1	3.93	0.0000	0.57	0.0000	1.38	0.0012
1368238_at	pancreatitis-associated protein	Pap	3.47	0.0000	0.53	0.0003	1.24	0.1749
1370174_at	myeloid differentiation primary response gene 116	Myd116	3.35	0.0000	0.75	0.0245	1.11	0.4506
1369862_at	proviral integration site 1	Pim1	3.28	0.0000	0.76	0.0693	1.34	0.0691
1387354_at	signal transducer and activator of transcription 1	Stat1	3.26	0.0000	0.27	0.0000	1.41	0.0008
1390704_at	SDA1 domain containing 1	Sdad1	3.14	0.0000	0.37	0.0001	1.13	0.5990
1368856_at	Janus kinase 2	Jak2	2.91	0.0000	0.50	0.0000	1.52	0.0006
1370224_at	signal transducer and activator of transcription 3	Stat3	2.84	0.0000	0.76	0.0456	1.34	0.0500
1369181_at	cytochrome b-245, beta polypeptide	Cybb	2.76	0.0000	0.48	0.0000	1.14	0.3116
1372009_at	tyrosyl-tRNA synthetase	Yars	2.64	0.0000	0.51	0.0000	1.27	0.0041
1370265_at	arrestin, beta 2	Arrb2	2.62	0.0000	0.40	0.0000	1.19	0.0401
1387871_at	cofilin 1, non-muscle	Cfl1	2.61	0.0000	0.67	0.0013	1.03	0.8569
1370346_at	cyclin B1	Ccnb1	2.60	0.0000	0.34	0.0000	1.05	0.6727
1370688_at	glutamate-cysteine ligase, catalytic subunit	Gclc	2.60	0.0000	0.88	0.0912	0.92	0.2948
1368973_at	adenosine deaminase, RNA-specific	Adar	2.52	0.0000	0.36	0.0000	1.26	0.0066
1398756_at	nucleophosmin 1 /// similar to Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Numatrin) (Nucleolar protein NO38)	Npm1 /// LOC300303	2.45	0.0000	0.46	0.0000	1.27	0.0233
1374468_at	myeloid differentiation primary response gene 88	Myd88	2.38	0.0000	0.74	0.0002	1.08	0.2890

1369204_at	hemopoietic cell kinase	Hck	2.30	0.0000	0.49	0.0000	1.78	0.0000
1369688_at	protein tyrosine kinase 2 beta	Ptk2b	2.23	0.0000	0.77	0.0054	1.07	0.5298
1372601_at	activating transcription factor 5	Atf5	2.22	0.0000	0.36	0.0000	1.60	0.0001
1369104_at	protein kinase, AMP-activated, alpha 1 catalytic subunit	Prkaa1	2.18	0.0000	0.64	0.0058	1.13	0.4705
1387566_at	phospholipase A2, group IVA (cytosolic, calcium-dependent)	Pla2g4a	2.13	0.0000	0.74	0.0020	1.07	0.4977
1367943_at	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, beta	Nfkbib	2.05	0.0000	0.73	0.0039	1.20	0.0832
1368482_at	B-cell leukemia/lymphoma 2 related protein A1	Bcl2a1	2.02	0.0000	0.57	0.0000	1.56	0.0000
1370869_at	branched chain aminotransferase 1, cytosolic	Bcat1	17.72	0.0000	0.32	0.0001	2.60	0.0008
1388792_at	growth arrest and DNA-damage-inducible 45 gamma	Gadd45g	16.85	0.0000	0.72	0.0143	0.91	0.5561
1368683_at	oxidized low density lipoprotein (lectin-like) receptor 1	Oldlr1	15.78	0.0000	0.19	0.0000	2.55	0.0001
1370628_at	granzyme B	Gzmb	12.93	0.0000	0.07	0.0000	3.89	0.0000
1387134_at	schlafen 3	Slfn3	11.77	0.0000	0.16	0.0000	2.21	0.0000
1368017_at	lectin, galactose binding, soluble 7	Lgals7	7.16	0.0000	0.13	0.0000	19.97	0.0000
1387818_at	caspase 4, apoptosis-related cysteine peptidase	Casp4	7.08	0.0000	0.22	0.0000	1.33	0.0008
1369173_at	complement component 3a receptor 1	C3ar1	6.79	0.0000	0.14	0.0000	1.62	0.0007
1391384_at	tumor necrosis factor (TNF superfamily, member 2)	Tnf	6.25	0.0000	0.44	0.0001	2.13	0.0004
1387242_at	Protein kinase, interferon-inducible double stranded RNA dependent	Prkr	6.25	0.0000	0.20	0.0000	1.67	0.0001
1370422_at	receptor-interacting serine-threonine kinase 3	Ripk3	6.11	0.0000	0.30	0.0000	1.91	0.0001
1387011_at	lipocalin 2	Lcn2	5.56	0.0000	0.39	0.0000	1.80	0.0000
1387221_at	GTP cyclohydrolase 1	Gch	4.74	0.0000	0.43	0.0000	1.36	0.0596
1398256_at	interleukin 1 beta	Il1b	4.18	0.0000	0.76	0.0038	2.05	0.0000
1370096_at	perforin 1 (pore forming protein)	Prf1	4.08	0.0000	0.11	0.0000	2.39	0.0000
1368558_at	allograft inflammatory factor 1	Aif1	3.81	0.0000	0.28	0.0000	1.23	0.1029
1392731_at	hypothetical gene supported by NM_130426	LOC497808	3.67	0.0000	0.52	0.0001	2.32	0.0000
1369182_at	coagulation factor III	F3	3.63	0.0000	0.65	0.0000	1.02	0.8569
1370928_at	LPS-induced TN factor	Litaf	3.41	0.0000	0.71	0.0001	1.40	0.0004
1368645_at	protein tyrosine phosphatase, non-receptor type 1	Ptpn1	3.05	0.0000	0.63	0.0010	1.91	0.0001
1393280_at	lymphocyte antigen 86 (predicted)	Ly86_predicted	2.91	0.0000	0.21	0.0000	1.69	0.0001
1369186_at	caspase 1	Casp1	2.85	0.0000	0.36	0.0000	1.35	0.0008
1369590_at	DNA-damage inducible transcript 3	Ddit3	2.79	0.0000	0.23	0.0000	1.89	0.0000
1369683_at	BH3 interacting domain death agonist	Bid	2.78	0.0000	0.50	0.0000	1.30	0.0216
1387591_at	interleukin 2 receptor, alpha chain	Il2ra	2.75	0.0000	0.44	0.0003	1.11	0.6562
1376327_at	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	Tnfrsf14	2.73	0.0000	0.50	0.0000	1.09	0.4992
1387605_at	caspase 12	Casp12	2.68	0.0000	0.37	0.0000	1.16	0.0397
1368124_at	dual specificity phosphatase 5	Dusp5	2.59	0.0000	0.74	0.0610	1.11	0.5568
1387800_at	Fas death domain-associated protein	Daxx	2.53	0.0000	0.35	0.0000	1.29	0.0016
1387394_at	interleukin 2 receptor, beta chain	Il2rb	2.45	0.0000	0.41	0.0000	1.09	0.5786
1388587_at	immediate early response 3	Ier3	2.34	0.0000	0.84	0.0054	0.87	0.0380
1387690_at	caspase 3, apoptosis related cysteine protease	Casp3	2.27	0.0000	0.43	0.0000	1.41	0.0076
1370987_at	Sialophorin	Spn	2.13	0.0000	0.47	0.0000	1.33	0.0027
1367715_at	tumor necrosis factor receptor superfamily, member 1a	Tnfrsf1a	2.13	0.0000	0.89	0.0934	1.16	0.0562
1368860_at	pleckstrin homology-like domain, family A, member 1	Phlda1	2.11	0.0000	0.75	0.0394	0.97	0.8625
1369003_at	death effector domain-containing	Dedd	2.06	0.0193	0.38	0.0045	1.57	0.1897
1388673_at	lymphocyte specific 1	Lsp1	2.05	0.0000	0.70	0.0038	1.22	0.1071
1367831_at	tumor protein p53	Tp53	2.04	0.0000	0.60	0.0000	1.18	0.0471

GROUP IB GENES INCREASED IN SBR50 vs. SHAM AND UNCHANGED IN SBR50/IL-6 vs. SBR50								
1368321_at	early growth response 1	Egr1	37.45	0.0000	1.19	0.1283	0.60	0.0004
1369268_at	activating transcription factor 3	Atf3	21.60	0.0000	0.94	0.7252	0.61	0.0086
1369584_at	suppressor of cytokine signaling 3	Socs3	12.91	0.0000	0.76	0.1088	0.91	0.6511
1369067_at	nuclear receptor subfamily 4, group A, member 3	Nr4a3	12.73	0.0000	1.27	0.1229	1.60	0.0080
1386935_at	nuclear receptor subfamily 4, group A, member 1	Nr4a1	7.42	0.0000	1.07	0.5943	0.85	0.2618
1367581_at	secreted phosphoprotein 1	Spp1	6.53	0.0000	1.25	0.4116	1.04	0.9000
1387391_at	cyclin-dependent kinase inhibitor 1A	Cdkn1a	5.63	0.0000	1.29	0.1249	0.87	0.4597
1387788_at	Jun-B oncogene	Junb	5.09	0.0000	1.10	0.4755	1.02	0.9273
1369393_at	mitogen-activated protein kinase kinase kinase 8	Map3k8	4.30	0.0000	1.09	0.4965	1.08	0.5656
1368813_at	CCAAT/enhancer binding protein (C/EBP), delta	Cebpd	3.51	0.0000	0.88	0.1907	1.25	0.0368
1370485_at	Bcl2-like 1	Bcl2l1	3.36	0.0000	1.22	0.1320	0.74	0.0418
1369006_at	hexokinase 2	Hk2	3.05	0.0000	0.96	0.6906	0.95	0.6832
1387701_at	hepatocyte growth factor	Hgf	2.62	0.0011	1.46	0.1641	0.77	0.4033
1368174_at	hypothetical gene supported by NM_019371	LOC497816	2.13	0.0005	0.76	0.1601	0.89	0.6323
1370690_at	heat shock 70kDa protein 9A (predicted)	Hspa9a_predicted	2.09	0.0000	0.90	0.1088	0.78	0.0012
1387269_at	<i>plasminogen activator, urokinase receptor</i>	<i>Plaur</i>	4.87	0.0000	1.05	0.6948	1.00	0.9923
1387530_at	<i>fos-like antigen 2 /// FBJ osteosarcoma oncogene B</i>	<i>Fosl2 /// Fosb</i>	4.03	0.0000	0.91	0.5739	1.14	0.4597
1371785_at	<i>tumor necrosis factor receptor superfamily, member 12a</i>	<i>Tnfrsf12a</i>	3.84	0.0000	0.89	0.5508	0.70	0.0840
1368947_at	<i>growth arrest and DNA-damage-inducible 45 alpha</i>	<i>Gadd45a</i>	3.76	0.0000	0.94	0.5540	1.05	0.6442
1387868_at	<i>lipopolysaccharide binding protein</i>	<i>Lbp</i>	2.50	0.0000	0.92	0.2390	1.05	0.5411
1368748_at	<i>testis-specific kinase 2</i>	<i>Tesk2</i>	2.31	0.0011	0.74	0.1985	1.22	0.4597
GROUP IIA GENES DECREASED IN SBR50 vs. SHAM AND INCREASED IN SBR50/IL-6 vs. SBR50								
1369699_at	glucagon-like peptide 1 receptor	Glp1r	0.08	0.0000	9.71	0.0000	0.49	0.0010
1370114_at	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1	Pik3r1	0.18	0.0000	1.28	0.0456	0.67	0.0046
1367628_at	lectin, galactose binding, soluble 1	Lgals1	0.19	0.0000	4.48	0.0000	0.64	0.0000
1370864_at	procollagen, type 1, alpha 1	Col1a1	0.25	0.0000	6.49	0.0000	0.92	0.7742
1370197_at	protein kinase C, zeta	Prkcz	0.29	0.0000	1.62	0.0002	0.75	0.0165
1387071_at	microtubule-associated protein tau /// hypothetical gene supported by NM_017212	Mapt /// LOC497674	0.30	0.0000	1.72	0.0000	1.22	0.0006
1368677_at	brain derived neurotrophic factor	Bdnf	0.30	0.0000	1.84	0.0020	0.48	0.0009
1368989_at	tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	Timp3	0.34	0.0000	2.45	0.0001	0.40	0.0001
1370427_at	platelet derived growth factor, alpha	Pdgfa	0.34	0.0000	1.58	0.0000	0.87	0.0524
1376711_at	claudin 11	Cldn11	0.34	0.0000	1.43	0.0190	0.61	0.0038
1370583_at	ATP-binding cassette, sub-family B (MDR/TAP), member 1 /// ATP-binding cassette, sub-family B (MDR/TAP), member 1A	Abcb1 /// Abcb1a	0.41	0.0000	1.52	0.0001	1.01	0.9021
1367823_at	tissue inhibitor of metalloproteinase 2	Timp2	0.42	0.0000	1.95	0.0000	0.76	0.0119
1370333_at	insulin-like growth factor 1	Igf1	0.42	0.0000	2.16	0.0000	0.93	0.4114
1387971_at	mitogen activated protein kinase 8 interacting protein	Mapk8ip	0.45	0.0000	1.85	0.0000	0.72	0.0080
1369654_at	protein kinase, AMP-activated, alpha 2 catalytic subunit	Prkaa2	0.46	0.0000	1.81	0.0001	0.91	0.4677
1399098_at	glyoxylase 1	Glo1	0.46	0.0000	1.93	0.0000	0.78	0.0014
1370331_at	interleukin 11 receptor, alpha chain 1	Il11ra1	0.46	0.0000	1.83	0.0000	0.82	0.0404
1387173_at	chymase 1, mast cell	Cma1	0.47	0.0011	2.62	0.0002	1.09	0.7451
1371668_at	Retinoid X receptor alpha	Rxra	0.47	0.0000	1.26	0.0223	1.07	0.5827
1370081_at	vascular endothelial growth factor A	Vegfa	0.48	0.0000	1.65	0.0002	0.65	0.0016
1387771_at	mitogen activated protein kinase 3	Mapk3	0.48	0.0000	1.26	0.0047	0.86	0.0620
1387769_at	inhibitor of DNA binding 3	Id3	0.48	0.0000	1.50	0.0005	0.59	0.0001
1387232_at	bone morphogenetic protein 4	Bmp4	0.50	0.0000	1.44	0.0000	0.74	0.0000

1370100_at	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2	Pik3r2	0.53	0.0000	1.39	0.0017	1.09	0.4116
1386862_at	annexin A5	Anxa5	0.54	0.0000	1.53	0.0000	0.91	0.0970
1367771_at	TSC22 domain family 3	Tsc22d3	0.55	0.0000	1.67	0.0000	1.06	0.1897
1387875_at	PTK2 protein tyrosine kinase 2	Ptk2	0.56	0.0000	1.13	0.0731	1.01	0.8568
1367651_at	cathepsin D	Ctsd	0.56	0.0000	1.34	0.0000	0.89	0.0245
1376569_at	Kruppel-like factor 2 (lung) (predicted)	Klf2_predicted	0.56	0.0000	1.10	0.0109	1.08	0.0419
1370026_at	crystallin, alpha B	Cryab	0.59	0.0000	2.48	0.0000	0.65	0.0001
1388459_at	procollagen, type XVIII, alpha 1	Col18a1	0.59	0.0001	1.76	0.0000	1.06	0.6296
1369159_at	androgen receptor	Ar	0.60	0.0004	1.24	0.0953	0.74	0.0345
1367871_at	cytochrome P450, family 2, subfamily e, polypeptide 1	Cyp2e1	0.12	0.0000	4.17	0.0000	0.48	0.0000
1372299_at	cyclin-dependent kinase inhibitor 1C (P57)	Cdkn1c	0.21	0.0000	2.40	0.0000	0.85	0.1255
1368897_at	MAD homolog 7 (Drosophila)	Madh7	0.23	0.0000	1.42	0.0585	0.62	0.0202
1368120_at	NEL-like 1 (chicken)	Nell1	0.24	0.0000	3.75	0.0000	0.56	0.0005
1388384_at	Dynein light chain LC8-type 1	Dynl1	0.25	0.0000	1.47	0.0139	0.81	0.1874
1368242_at	potassium voltage gated channel, Shab-related subfamily, member 1	Kcnb1	0.31	0.0000	2.02	0.0000	0.88	0.3317
1376285_at	GULP, engulfment adaptor PTB domain containing 1	Gulp1	0.33	0.0000	1.76	0.0002	0.83	0.1662
1369373_at	fibroblast growth factor receptor 3	Fgfr3	0.34	0.0000	1.45	0.0117	0.66	0.0085
1388193_at	huntingtin interacting protein 1	Hip1	0.42	0.0000	1.25	0.0142	1.18	0.0887
1377064_at	dual specificity phosphatase 6	Dusp6	0.42	0.0000	1.38	0.0002	1.10	0.1928
1368863_at	non-metastatic cell expressed protein 3	Nme3	0.45	0.0000	1.82	0.0000	0.63	0.0005
1372423_at	PERP, TP53 apoptosis effector (predicted)	Perp_predicted	0.46	0.0000	1.69	0.0000	0.82	0.0202
1370552_at	protein phosphatase 1F (PP2C domain containing)	Ppm1f	0.46	0.0035	1.78	0.0270	0.61	0.0743
1370301_at	matrix metalloproteinase 2	Mmp2	0.46	0.0000	2.14	0.0000	0.93	0.3072
1376689_at	similar to RIKEN cDNA 1700023M03	RGD1305457	0.47	0.0000	1.47	0.0023	0.90	0.4230
1369407_at	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	Tnfrsf11b	0.47	0.0000	2.08	0.0000	0.80	0.0883
1387022_at	aldehyde dehydrogenase family 1, member A1	Aldh1a1	0.47	0.0000	1.76	0.0000	0.84	0.0407
1388718_at	tropomodulin 1	Tmod1	0.49	0.0000	1.49	0.0001	0.90	0.2254
1388272_at	immunoglobulin heavy chain 1a (serum IgG2a)	Igh-1a	0.51	0.0008	1.89	0.0020	1.08	0.7171
1372503_at	tumor necrosis factor ligand superfamily member 12	Tnfsf12	0.53	0.0000	1.19	0.0335	0.88	0.1344
1390096_at	SH3-domain GRB2-like B1 (endophilin)	Sh3glb1	0.55	0.0000	1.40	0.0000	0.98	0.7369
1369179_at	peroxisome proliferator activated receptor gamma	Pparg	0.56	0.0000	1.94	0.0000	0.59	0.0001
1370091_at	guanine nucleotide binding protein, alpha q polypeptide	Gnaq	0.56	0.0014	1.61	0.0079	0.75	0.1143
1368403_at	retinoblastoma-like 2	Rbl2	0.58	0.0000	1.33	0.0000	0.84	0.0024
1372330_at	goliath	LOC652955	0.59	0.0000	1.17	0.0130	0.96	0.5970
1386978_at	BCL2/adenovirus E1B 19 kDa-interacting protein 3-like	Bnip3l	0.59	0.0000	1.30	0.0002	0.92	0.2008
1373479_at	Protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	0.59	0.0000	1.20	0.0027	0.79	0.0006
1387957_at	SH3-domain kinase binding protein 1	Sh3kbp1	0.60	0.0000	1.49	0.0000	0.80	0.0026
GROUP IIB GENES DECREASED IN SBR50 vs. SHAM AND UNCHANGED IN SBR50/IL-6 vs. SBR50								
1368375_at	interleukin 15	Il15	0.39	0.0000	1.12	0.4963	0.66	0.0202
1369816_at	RAB3A, member RAS oncogene family	Rab3a	0.52	0.0000	1.19	0.1708	0.76	0.0451
1368924_at	growth hormone receptor	Ghr	0.53	0.0004	1.28	0.1220	0.89	0.5114
1376692_at	homeodomain interacting protein kinase 2 (predicted)	Hipk2_predicted	0.56	0.0006	1.05	0.7744	1.62	0.0063
1371819_at	histone deacetylase 5	Hdac5	0.59	0.0000	1.05	0.5269	1.12	0.1559
1390627_at	T-box 3	Tbx3	0.33	0.0000	1.16	0.4537	0.89	0.5946
1368486_at	insulin receptor substrate 3	Irs3	0.40	0.0000	1.18	0.1039	1.13	0.2781
1369146_at	aryl hydrocarbon receptor	Ahr	0.44	0.0000	1.12	0.3783	0.86	0.2707

<i>1369115_at</i>	<i>adrenergic receptor, beta 2</i>	<i>Adrb2</i>	<i>0.54</i>	<i>0.0000</i>	<i>0.97</i>	<i>0.7842</i>	<i>1.08</i>	<i>0.5060</i>
<i>1368222_at</i>	<i>nuclear receptor subfamily 3, group C, member 1</i>	<i>Nr3c1</i>	<i>0.54</i>	<i>0.0007</i>	<i>1.13</i>	<i>0.4802</i>	<i>0.81</i>	<i>0.2313</i>
<i>1387675_at</i>	<i>plasminogen activator, urokinase</i>	<i>Plau</i>	<i>0.55</i>	<i>0.0000</i>	<i>1.04</i>	<i>0.7279</i>	<i>0.94</i>	<i>0.5786</i>
<i>1389431_at</i>	<i>protein kinase, DNA activated, catalytic polypeptide (predicted)</i>	<i>Prkdc_predicted</i>	<i>0.56</i>	<i>0.0000</i>	<i>1.07</i>	<i>0.4122</i>	<i>0.93</i>	<i>0.4116</i>
<i>1374786_at</i>	<i>Cytotoxic granule-associated RNA binding protein 1</i>	<i>Tial</i>	<i>0.57</i>	<i>0.0013</i>	<i>1.26</i>	<i>0.1484</i>	<i>0.76</i>	<i>0.1164</i>
<i>1370443_at</i>	<i>deoxyribonuclease II</i>	<i>Dnase2</i>	<i>0.59</i>	<i>0.0000</i>	<i>1.08</i>	<i>0.3836</i>	<i>0.93</i>	<i>0.4597</i>
<i>1368650_at</i>	<i>Kruppel-like factor 10</i>	<i>Klf10</i>	<i>0.59</i>	<i>0.0000</i>	<i>1.04</i>	<i>0.5065</i>	<i>1.14</i>	<i>0.0524</i>
GROUP III GENES INCREASED IN SBR50 vs. SHAM AND INCREASED IN SBR50/IL-6 vs. SBR50								
<i>1367555_at</i>	Albumin	Alb	3.87	0.0000	14.97	0.0000	1.52	0.0397
<i>1368592_at</i>	interleukin 1 alpha	Il1a	3.69	0.0000	1.47	0.0072	1.84	0.0004
<i>1386995_at</i>	B-cell translocation gene 2, anti-proliferative	Btg2	2.96	0.0000	1.34	0.0130	0.60	0.0004
<i>1370989_at</i>	ret proto-oncogene	Ret	2.36	0.0000	1.81	0.0002	1.15	0.3447
<i>1389179_at</i>	<i>cell death-inducing DNA fragmentation factor, alpha subunit-like effector A (predicted)</i>	<i>Cidea_predicted</i>	<i>3.96</i>	<i>0.0002</i>	<i>6.45</i>	<i>0.0000</i>	<i>0.28</i>	<i>0.0011</i>
<i>1398275_at</i>	<i>matrix metalloproteinase 9</i>	<i>Mmp9</i>	<i>2.53</i>	<i>0.0000</i>	<i>1.50</i>	<i>0.0049</i>	<i>1.08</i>	<i>0.6442</i>
<i>1387811_at</i>	<i>angiotensinogen (serpin peptidase inhibitor, clade A, member 8)</i>	<i>Agt</i>	<i>2.18</i>	<i>0.0012</i>	<i>3.61</i>	<i>0.0000</i>	<i>0.38</i>	<i>0.0007</i>

*Genes listed in regular type are anti-apoptotic, while genes listed in italics are pro-apoptotic.

+FDR: False discovery rate.