Supplemental Table 2. Differentially expressed transcript isoforms in the host tumor microenvironment of 231^{Luc+} tumors implanted in $SS.BN3^{IL2R\gamma}$ and $SS^{IL2R\gamma}$ rats.

			Position		Transcript Abundance*					
Gene Symbol	Transcript ID	Chromosome	Start	End	$SS^{IL2R\gamma}$	SD	$SSBN3^{IL2R\gamma}$	SD	Fold Change (Log2)	FDR
Aasdhppt	XM_006242473.1	chr8	1,427,205	1,428,351	47	14	100	24	0.8	0.098
Abcg1	NM_053502.1	chr20	12,018,966	12,020,646	3114	149	4099	322	0.4	0.008
Abhd4	NM_001108866.1	chr15	36,716,010	36,717,401	1070	76	1337	17	0.3	0.053
Acbd5	XM_006254349.1	chr17	91,547,979	91,549,938	37	11	7	5	-1.1	0.041
Acp5	NM_001270889.1	chr8	23,197,094	23,197,657	202	25	353	41	0.7	0.001
Acsl1	XM_006253123.1	chr16	48,653,030	48,654,711	1617	289	2531	477	0.6	0.063
Acvr1	NM_024486.1	chr3	49,552,457	49,552,695	36	21	0	0	-1.4	0.000
Acvrl1	XM_006242303.1	chr7	140,586,100	140,588,083	353	45	171	34	-0.9	0.000
Adamts12	NM_001106420.2	chr2	83,352,797	83,356,508	919	88	558	124	-0.7	0.021
Adamts14	XM_006256449.1	chr20	32,601,730	32,605,456	418	22	307	17	-0.4	0.033
Adamts15	NM_001106810.1	chr8	32,003,563	32,007,228	1150	330	356	75	-1.4	0.000
Adamts4	NM_023959.1	chr13	94,258,141	94,259,351	523	234	235	69	-0.9	0.086
Adamts5	NM_198761.1	chr11	29,035,107	29,035,675	238	50	131	33	-0.7	0.084
Adamts9	XM_006236916.1	chr4	188,602,368	188,604,223	122	38	37	19	-1.1	0.021
Adamts9	XM_006236915.1	chr4	188,602,368	188,604,223	282	64	143	43	-0.8	0.074
Adra2a	NM_012739.3	chr1	282,178,474	282,181,275	129	14	67	16	-0.8	0.022
Adrm1	NM_031708.1	chr3	181,565,739	181,565,984	648	98	0	1	-6.1	0.000
Adrm1	XM_006235822.1	chr3	181,565,739	181,565,984	525	66	1134	238	1.0	0.000
Agmat	NM_001048185.1	chr5	164,033,139	164,033,407	3	2	55	3	2.4	0.000
Agtr1a	NM_030985.4	chr17	37,218,831	37,220,804	328	40	176	15	-0.8	0.000
Ak4	XM_006238445.1	chr5	124,186,037	124,189,606	1022	98	1462	183	0.5	0.027
Alas2	NM_013197.1	chrX	23,587,682	23,587,966	107	32	31	10	-1.3	0.001
Aldh1l2	NM_001191778.1	chr7	26,554,420	26,555,206	232	69	73	18	-1.3	0.000
Amotl2	NM_031717.1	chr8	110,618,112	110,619,840	505	47	349	45	-0.5	0.063
Angpt4	NM_001106526.1	chr3	153,804,930	153,805,765	184	100	50	18	-1.1	0.031
Ankrd23	XM_006244814.1	chr9	42,764,885	42,766,341	552	180	276	35	-0.9	0.015
Ano5	XM_006229266.1	chr1	108,010,318	108,013,421	37	22	8	5	-1.0	0.074
Aplnr	NM_031349.2	chr3	79,052,119	79,055,765	382	78	94	35	-1.6	0.000
Apoa1bp	NM_001106440.1	chr2	206,827,335	206,827,597	91	13	41	14	-0.9	0.077
App	XM_006248011.1	chr11	28,048,896	28,049,890	1182	117	725	134	-0.7	0.010
Aqp1	NM_012778.1	chr4	150,213,706	150,215,641	2526	810	1374	277	-0.8	0.032
Arap3	XM_006254648.1	chr18	30,800,118	30,801,133	386	76	206	27	-0.8	0.002
Arfgap1	XM_006235732.1	chr3	180,199,084	180,201,025	271	24	487	54	0.8	0.000
Arfgap1	NM_145090.3	chr3	180,199,084	180,199,752	412	59	157	46	-1.2	0.000
Arfgap2	NM_001033707.1	chr3	86,801,179	86,802,350	1296	58	376	49	-1.7	0.000
Arfgap2	XM_006234530.1	chr3	86,801,179	86,802,360	54	11	521	217	2.4	0.000
Arfgap2	XM_006234529.1	chr3	86,801,179	86,802,360	25	21	229	79	1.6	0.000
Arfgap2	XM_006234531.1	chr3	86,801,179	86,802,360	37	8	446	300	1.6	0.000
Arhgap15	NM_001013917.1	chr3	34,441,909	34,442,272	378	21	507	41	0.4	0.071
Arhgap22	XM_006252745.1	chr16	11,571,576	11,572,157	49	17	109	17	0.9	0.054
Arhgap5	XM_006240099.1	chr6	82,966,551	82,970,518	586	56	365	95	-0.6	0.098
Arhgef25	XM_006241454.1	chr7	70,646,944	70,647,400	207	83	81	18	-1.0	0.028
Armcx2	NM_001014274.1	chrX	105,506,648	105,509,483	155	33	78	15	-0.8	0.022
Arsi	XM_006254771.1	chr18	55,419,166	55,421,354	68	19	22	11	-1.1	0.023
Atp13a2	NM_001173432.1	chr5	163,243,504	163,243,883	838	169	2239	107	1.3	0.000
Atp13a2	XM_006239250.1	chr5	163,243,504	163,243,886	410	97	30	21	-2.4	0.000
Atp13a2	XM_006239246.1	chr5	163,243,504	163,243,886	371	135	22	15	-2.5	0.000
Atp13a2	XM_006239249.1	chr5	163,243,504	163,243,886	374	124	31	35	-1.4	0.002
Atp13a2	XM_006239247.1	chr5	163,243,504	163,243,886	245	58	102	44	-1.0	0.036
Atp1a3	NM_012506.1	chr1	83,104,724	83,105,127	606	94	1315	239	1.0	0.000
Atp9b	XM_006254983.1	chr18	76,447,175	76,448,226	617	27	787	46	0.3	0.063
Bag6	XM_006256090.1	chr20	7,211,176	7,211,343	74	25	25	11	-1.0	0.069
Bag6	XM_006256082.1	chr20	7,211,176	7,211,343	152	52	316	90	0.8	0.096
Bcl2l1	XM_006235265.1	chr3	154,662,585	154,664,213	667	107	988	138	0.5	0.088
Bdkrb2	NM_001270713.1	chr6	138,618,560	138,622,272	98	21	33	14	-1.1	0.007
Bloc1s6	NM_001025714.1	chr3	121,416,726	121,418,326	298	27	422	33	0.5	0.032
Blvra	NM_053850.1	chr3	126,102,917	126,103,270	360	65	0	0	-5.3	0.000
Blvra	XM_006234894.1	chr3	126,102,917	126,103,278	179	20	363	31	1.0	0.000
Bmf	XM_006234723.1	chr3	116,849,169	116,853,108	1178	166	1766	62	0.6	0.002
Bmper	NM_001135799.1	chr8	24,653,885	24,655,248	145	73	54	17	-1.0	0.050
Braf	XM_006236358.1	chr4	67,196,476	67,203,565	63	11	118	24	0.8	0.075
Btbd3	NM_001107782.1	chr3	137,830,139	137,831,600	18	7	2	1	-1.1	0.026
Cald1	XM_006236261.1	chr4	62,020,718	62,022,970	2784	462	1828	215	-0.6	0.022
Capg	XM_006236665.1	chr4	165,189,521	165,189,798	38	13	4	4	-1.1	0.025

Capn5	XM_006229731.1	chr1	169,278,329	169,280,626	162	30	307	92	0.8	0.099
Casq2	NM_017131.2	chr2	224,000,602	224,001,893	124	65	48	8	-0.9	0.088
Cass4	XM_006235680.1	chr3	176,512,058	176,513,806	47	29	9	4	-1.0	0.098
Cav1	NM_031556.2	chr4	45,234,247	45,236,458	1866	228	1019	244	-0.8	0.002
Ccbl1	NM_001013164.3	chr3	14,105,120	14,105,226	99	5	6	4	-2.4	0.000
Ccbl1	XM_006233813.1	chr3	14,104,784	14,105,226	40	6	92	28	0.9	0.039
Ccdc41	XM_006241277.1	chr7	35,911,000	35,911,633	189	16	90	30	-0.9	0.029
Ccdc8	NM_001009533.2	chr1	80,180,874	80,184,203	163	39	93	12	-0.7	0.100
Ccdc80	NM_022543.2	chr11	64,747,814	64,749,020	4276	628	2694	323	-0.6	0.003
Ccl22	NM_057203.1	chr19	10,668,402	10,669,927	604	61	1104	320	0.8	0.032
Cd244	XM_006250259.1	chr13	94,617,716	94,618,284	200	12	342	61	0.7	0.005
Cd248	NM_001106325.1	chr1	227,377,519	227,380,084	666	84	374	99	-0.7	0.021
Cd34	XM_006250486.1	chr13	118,550,879	118,550,907	56	19	21	7	-0.9	0.088
Cd44	NM_012924.2	chr3	99,339,456	99,341,202	747	184	0	0	-6.0	0.000
Cd69	NM_134327.1	chr4	211,685,114	211,686,163	462	50	712	157	0.6	0.088
Cd83	NM_001108410.1	chr17	26,382,447	26,384,002	1386	173	1876	105	0.4	0.054
Cd8b	NM_031539.1	chr4	163,979,800	163,980,405	760	88	1073	96	0.5	0.033
Cd96	NM_001025032.1	chr11	60,347,375	60,347,696	46	11	92	13	0.8	0.048
Cdc25b	NM_133572.1	chr3	130,238,050	130,239,028	134	64	50	6	-1.0	0.037
Cdc42	NM_171994.4	chr5	159,447,271	159,447,644	1618	74	2212	256	0.4	0.018
Cdh11	XM_006255059.1	chr19	2,528,768	2,531,010	424	79	216	81	-0.8	0.063
Cdh5	NM_001107407.1	chr19	1,022,709	1,023,385	710	107	436	94	-0.6	0.054
Cdr2l	XM_006247771.1	chr10	104,330,245	104,333,134	209	35	73	21	-1.3	0.000
Cdr2l	XM_006247772.1	chr10	104,330,245	104,333,137	53	24	10	7	-1.1	0.027
Cept1	XM_006233117.1	chr2	228,528,574	228,529,339	171	21	454	272	1.0	0.028
Cercam	XM_006233771.1	chr3	13,787,709	13,788,193	95	29	27	9	-1.3	0.002
Cfb	NM_212466.3	chr20	6,616,004	6,616,217	2770	1014	1392	412	-0.8	0.088
Chsy3	XM_225912.6	chr18	53,729,196	53,731,655	123	44	53	12	-0.9	0.037
Clec12a	NM_001134716.1	chr4	211,774,854	211,774,947	2649	268	3448	183	0.4	0.048
Clec14a	NM_001014077.1	chr6	88,832,645	88,835,788	509	83	322	62	-0.6	0.084
Clec7a	NM_001173386.1	chr4	211,859,713	211,861,491	2352	251	3692	620	0.6	0.008
Clec7a	XM_006237100.1	chr4	211,859,713	211,861,491	1766	222	2575	388	0.5	0.059
Clmp	NM_173154.1	chr8	46,020,804	46,023,795	1012	223	545	36	-0.8	0.000
Col14a1	NM_001130548.1	chr7	95,895,271	95,896,126	2307	509	835	256	-1.2	0.000
Col16a1	XM_006238947.1	chr5	152,029,705	152,030,103	411	67	197	44	-1.0	0.000
Col18a1	NM_053489.2	chr20	14,494,045	14,495,241	2772	307	1734	396	-0.6	0.027
Col1a1	NM_053304.1	chr10	82,578,864	82,580,364	101038	27094	57937	12070	-0.7	0.031
Col1a2	XM_006236080.1	chr4	29,477,612	29,478,616	63197	15911	37856	6162	-0.7	0.027
Col3a1	NM_032085.1	chr9	51,724,998	51,725,418	92827	11982	46567	7551	-0.9	0.000
Col4a1	NM_001135009.1	chr16	83,095,986	83,097,435	10980	3112	5840	1937	-0.8	0.077
Col4a2	XM_006253476.1	chr16	82,852,229	82,853,463	6227	1511	3332	933	-0.8	0.028
Col5a1	XM_006233874.1	chr3	11,935,586	11,937,880	3831	657	1888	597	-0.9	0.003
Col5a2	NM_053488.1	chr9	51,757,495	51,759,062	7533	882	5058	505	-0.6	0.003
Col5a3	NM_021760.1	chr8	21,842,412	21,843,339	4294	1665	1957	578	-0.9	0.017
Col6a1	XM_215375.7	chr20	14,834,436	14,835,868	13619	1673	9185	1992	-0.5	0.098
Col6a3	XM_003750732.2	chr9	97,607,495	97,608,243	6316	1038	4301	509	-0.5	0.040
Commd9	XM_006234637.1	chr3	98,136,038	98,136,423	218	53	754	105	1.6	0.000
Commd9	NM_001033692.1	chr3	98,135,720	98,136,421	1130	170	660	51	-0.7	0.000
Cpne8	NM_001108750.1	chr7	131,298,536	131,300,242	411	37	255	43	-0.6	0.016
Cr2	XM_006250475.1	chr13	118,586,945	118,587,665	1	1	20	8	1.1	0.015
Creb3l1	NM_001005562.1	chr3	87,591,102	87,591,822	572	182	209	90	-1.1	0.004
Cry2	NM_133405.1	chr3	88,020,047	88,020,378	34	24	0	0	-1.5	0.000
Csnk1g2	XM_006241000.1	chr7	12,112,481	12,113,207	73	28	267	55	1.5	0.000
Cthrc1	NM_172333.2	chr7	78,271,769	78,272,276	429	74	189	83	-0.9	0.035
Ctnnb1	XM_006244134.1	chr8	128,824,603	128,825,828	1733	93	1358	126	-0.3	0.098
Ctsd	NM_134334.2	chr1	222,436,921	222,437,743	17711	1498	22769	1791	0.4	0.072
Ctss	NM_017320.1	chr2	217,168,648	217,169,058	15805	1980	23078	3272	0.5	0.034
Cxcl12	NM_001033882.1	chr4	215,206,033	215,208,536	1228	230	598	68	-1.0	0.000
Cxcl13	XM_006250711.1	chr14	15,193,471	15,194,269	1802	229	2590	234	0.5	0.015
Cxcl13	XM_006250710.1	chr14	15,193,473	15,194,269	40406	6993	59972	9864	0.5	0.080
Cybrd1	NM_001011954.1	chr3	64,237,321	64,240,184	407	22	292	26	-0.5	0.044
Daam2	XM_236909.7	chr9	12,423,336	12,426,043	190	20	121	17	-0.6	0.069
Dab2ip	NM_138710.3	chr3	20,368,374	20,371,268	456	25	149	35	-1.4	0.000
Dab2ip	XM_006234062.1	chr3	20,368,374	20,371,268	62	38	249	77	1.2	0.015
Defb52	NM_001037524.1	chr16	75,175,520	75,175,695	53	46	1	1	-1.3	0.003
Dido1	XM_006235805.1	chr3	179,862,993	179,867,617	2	0	33	24	1.2	0.009
Dlk1	NM_053744.1	chr6	142,748,331	142,749,166	62	54	11	3	-1.1	0.054
Dll4	XM_006234765.1	chr3	117,694,726	117,695,772	301	58	175	27	-0.7	0.036
Dock6	XM_006242659.1	chr8	22,876,906	22,877,148	202	39	112	26	-0.7	0.073

Dut	NM_053592.2	chr3	124,048,804	124,049,162	82	22	0	0	-3.2	0.000
Dut	NM_001040271.1	chr3	124,048,804	124,049,162	661	167	98	28	-2.3	0.000
Dut	XM_006234923.1	chr3	124,048,804	124,049,168	0	0	315	227	2.3	0.000
Ebf3	XR_350798.1	chr1	216,447,385	216,450,064	18	4	1	1	-1.3	0.004
Efemp1	NM_001012039.1	chr14	112,984,216	112,984,803	868	234	481	122	-0.7	0.074
Efnb1	NM_017089.2	chrX	69,775,238	69,777,121	775	159	473	67	-0.7	0.025
Efr3b	XM_006239853.1	chr6	38,199,580	38,203,575	36	15	11	3	-1.1	0.049
Ehd2	NM_001024897.1	chr1	79,112,278	79,113,143	1042	60	681	130	-0.6	0.028
Elac1	XM_006254926.1	chr18	68,848,765	68,853,249	97	33	43	5	-0.9	0.035
Eln	NM_012722.1	chr12	27,021,484	27,022,485	1953	570	764	258	-1.1	0.001
Epb41l1	XM_006235440.1	chr3	159,071,717	159,075,048	596	89	321	67	-0.8	0.005
Epb41l1	XM_006235430.1	chr3	159,071,717	159,075,048	48	18	15	5	-1.0	0.041
Epb41l2	XM_006227709.1	chr1	22,362,882	22,364,113	167	24	87	20	-0.8	0.023
Epha3	XM_006247976.1	chr11	420,517	423,212	44	21	4	5	-1.2	0.015
Ephx2	NM_022936.1	chr15	48,836,446	48,836,811	5	3	85	32	2.3	0.000
Ext2	XM_006234576.1	chr3	89,303,366	89,304,021	1320	206	922	115	-0.5	0.090
Fahd2a	NM_001134834.1	chr3	127,329,192	127,329,380	194	51	1	1	-4.0	0.000
Fahd2a	XM_006234960.1	chr3	127,329,192	127,329,383	2	2	182	32	3.9	0.000
Fam114a1	XM_006250991.1	chr14	44,754,795	44,756,393	1058	107	780	55	-0.4	0.039
Fam210b	XM_006235677.1	chr3	176,437,345	176,440,047	646	52	462	67	-0.5	0.098
Fat4	NM_001191705.1	chr2	145,474,467	145,477,455	65	19	13	13	-1.1	0.042
Fbn1	NM_031825.1	chr3	124,095,125	124,095,838	250	70	0	0	-4.6	0.000
Fbn1	XM_006234935.1	chr3	124,094,457	124,095,838	6787	877	4005	452	-0.7	0.000
Fcrla	NM_001100682.1	chr13	93,908,943	93,909,083	577	96	894	101	0.6	0.018
Fermt2	NM_001011915.1	chr15	23,771,815	23,773,066	1129	270	647	48	-0.7	0.008
Fgd5	XM_006236926.1	chr4	189,298,418	189,299,967	349	31	186	46	-0.8	0.006
Fgf7	XM_006234903.1	chr3	124,890,824	124,892,611	366	105	200	24	-0.8	0.031
Fgfr1	NM_024146.1	chr16	70,925,603	70,925,780	327	13	221	30	-0.5	0.043
Fibin	NM_001025042.2	chr3	108,150,071	108,152,343	674	242	287	51	-1.0	0.003
Figf	XM_006256863.1	chrX	32,190,232	32,192,171	263	63	137	18	-0.8	0.009
Fkbp14	NM_001013210.1	chr4	149,413,597	149,414,356	211	31	131	19	-0.6	0.077
Flrt2	XM_006240416.1	chr6	128,826,105	128,832,871	567	74	362	21	-0.6	0.002
Fn1	XM_006245151.1	chr9	78,674,436	78,675,198	529	118	236	87	-1.0	0.012
Fn1	XM_006245156.1	chr9	78,674,436	78,675,198	7348	2015	4039	1133	-0.7	0.082
Fn1	XM_006245155.1	chr9	78,674,436	78,675,198	6127	1222	3397	1280	-0.7	0.093
Fstl1	XM_006248402.1	chr11	68,884,409	68,886,712	7283	880	4987	672	-0.5	0.024
Fubp3	NM_001039337.1	chr3	15,581,980	15,582,115	79	19	0	0	-3.2	0.000
Fzd4	NM_022623.2	chr1	159,895,560	159,901,945	673	151	375	71	-0.7	0.027
G0s2	NM_001009632.1	chr13	116,559,386	116,560,048	169	69	69	20	-0.9	0.074
Galnt16	XM_006240288.1	chr6	112,419,955	112,422,114	120	31	52	15	-1.0	0.023
Galnt16	NM_001100863.1	chr6	112,419,955	112,422,114	181	48	83	23	-0.9	0.041
Galnt3	NM_001015032.3	chr3	58,806,678	58,807,536	64	37	2	2	-1.7	0.000
Galnt3	XM_006234290.1	chr3	58,806,435	58,807,536	29	13	101	47	1.1	0.023
Gbx2	NM_053708.1	chr9	96,754,121	96,754,977	55	17	18	7	-1.0	0.040
Gfpt2	NM_001002819.2	chr10	35,096,392	35,097,280	456	93	265	34	-0.7	0.018
Ggcx	NM_031756.1	chr4	165,063,025	165,063,604	650	20	477	25	-0.4	0.004
Ggta1p	NM_145674.1	chr3	19,927,252	19,928,035	302	64	41	37	-1.6	0.000
Ggta1p	XM_006234034.1	chr3	19,925,444	19,928,035	575	266	1405	257	1.0	0.035
Ggta1p	XM_006234037.1	chr3	19,925,444	19,928,035	18	12	78	37	1.0	0.077
Gja1	NM_012567.2	chr20	39,621,603	39,624,555	1459	790	641	101	-0.9	0.049
Gk	NM_024381.2	chrX	54,426,882	54,429,329	342	41	520	84	0.6	0.064
Gm2a	NM_172335.2	chr10	40,288,020	40,289,541	15880	1368	21090	1979	0.4	0.035
Gpatch2	XM_006250435.1	chr13	110,470,216	110,473,833	40	13	130	31	1.3	0.000
Gpatch8	XM_006247479.1	chr10	90,209,813	90,215,973	37	16	99	35	1.0	0.075
Gpc1	NM_030828.1	chr9	99,690,893	99,692,723	1077	166	717	47	-0.6	0.011
Gpnmb	NM_133298.1	chr4	143,403,475	143,404,104	19346	1510	27434	2918	0.5	0.004
Gpr116	NM_139110.1	chr9	18,970,747	18,971,544	424	68	275	36	-0.6	0.076
Gpr153	XM_006239485.1	chr5	173,014,721	173,017,217	474	93	257	43	-0.8	0.010
Gpr161	XM_006250191.1	chr13	88,450,500	88,455,575	44	10	11	6	-1.1	0.027
Gpx7	NM_001106673.1	chr5	131,847,355	131,847,935	325	86	174	47	-0.8	0.080
Grb10	XM_006251508.1	chr14	91,818,383	91,821,477	417	69	221	21	-0.9	0.000
Gtf3c4	XM_006233870.1	chr3	12,752,410	12,755,211	135	20	52	26	-1.0	0.029
Harbi1	XM_006234588.1	chr3	87,321,276	87,322,832	0	0	78	2	3.5	0.000
Harbi1	NM_001113793.3	chr3	87,321,276	87,321,896	85	34	12	8	-1.5	0.001
Has2	NM_013153.1	chr7	97,055,457	97,058,395	277	187	93	27	-1.0	0.046
Hba1	NM_013096.1	chr10	15,497,888	15,498,111	5565	1470	1865	612	-1.3	0.000
Hba2	NM_001007722.1	chr10	15,484,458	15,484,669	2193	526	751	191	-1.3	0.000
Hbb	NM_033234.1	chr1	175,134,671	175,134,929	4849	1429	1592	458	-1.4	0.000
Hbb-b1	NM_198776.1	chr1	175,104,281	175,104,537	594	182	168	58	-1.4	0.000

Hipk3	NM_031787.1	chr3	100,989,147	100,989,698	82	18	11	10	-1.2	0.012
Hnrnpa3	NM_198132.3	chr3	69,034,738	69,036,149	100	23	45	14	-0.9	0.053
Hoxb2	XM_002727806.3	chr10	84,004,661	84,005,718	76	12	34	6	-0.9	0.022
Hspa12b	NM_001107778.1	chr3	130,185,226	130,187,026	120	35	4	7	-1.2	0.011
Igf1	NM_001082479.1	chr7	28,601,396	28,602,541	516	59	913	284	0.7	0.062
Il1r1	XM_006244749.1	chr9	46,720,109	46,723,241	304	63	145	57	-0.9	0.054
Il1r1	XM_006244754.1	chr9	46,720,109	46,723,241	224	61	123	11	-0.7	0.054
Itga2b	XM_001063315.4	chr10	90,186,490	90,186,719	1048	136	1449	142	0.4	0.087
Itga6	NM_053725.1	chr3	65,000,843	65,003,370	484	132	96	37	-1.8	0.000
Itgb2	NM_001037780.2	chr20	13,944,189	13,944,853	5758	378	7567	677	0.4	0.024
Jak3	XM_006252823.1	chr16	19,980,594	19,981,132	406	33	581	86	0.5	0.079
Jazf1	XM_001065610.4	chr4	147,499,539	147,501,792	124	45	55	8	-0.9	0.061
Jph2	NM_001037974.1	chr3	165,907,932	165,908,021	113	23	0	0	-3.8	0.000
Jph2	XM_006235526.1	chr3	165,905,605	165,907,224	571	31	368	70	-0.6	0.022
Kcnn4	NM_001270701.1	chr1	82,508,011	82,508,496	2037	151	2644	104	0.4	0.011
Kctd14	XM_006229795.1	chr1	168,630,002	168,631,088	123	14	69	5	-0.8	0.013
Kdelr3	NM_001127546.1	chr7	120,752,576	120,753,160	683	167	379	91	-0.7	0.040
Klhl5	NM_001047093.1	chr14	44,618,837	44,620,005	25	9	6	3	-1.0	0.076
Lama4	XM_003751975.2	chr20	45,926,169	45,926,468	2991	581	2056	187	-0.5	0.090
Lamc1	NM_053966.2	chr13	75,622,194	75,625,016	4772	880	3059	370	-0.6	0.019
Lats2	NM_001107267.1	chr15	41,788,719	41,790,869	635	32	454	46	-0.5	0.019
Limch1	XM_006250945.1	chr14	42,558,731	42,561,641	36	10	7	2	-1.4	0.001
Lipe	XM_006228394.1	chr1	83,511,503	83,512,035	280	76	157	21	-0.7	0.063
Lmo2	NM_001244781.1	chr3	100,571,064	100,572,039	589	139	287	114	-0.8	0.087
LOC100909795	XM_003751815.2	chr18	77,647,321	77,651,983	244	33	98	15	-1.2	0.000
LOC100909901	XM_006257400.1	chrX	115,782,005	115,783,035	89	38	200	53	0.9	0.082
LOC100911324	XM_006250499.1	chr13	118,258,378	118,258,406	56	19	21	7	-0.9	0.088
LOC100911361	XR_146195.2	chr10	80,795,423	80,796,745	1921	299	1156	349	-0.6	0.098
LOC100911548	XM_003750655.2	chr9	19,092,914	19,093,595	5	1	40	39	1.0	0.080
LOC100911902	XM_003749317.2	chr2	206,729,478	206,729,811	266	100	118	37	-0.9	0.079
LOC100911932	XM_003749040.2	chr1	227,293,043	227,295,593	978	114	541	139	-0.8	0.010
LOC102546738	XR_352381.1	chr3	66,300,851	66,301,363	97	11	27	9	-1.4	0.000
LOC102548277	XR_352430.1	chr3	77,615,129	77,615,348	13	6	44	18	1.0	0.057
LOC102550017	XR_352230.1	chr3	17,857,651	17,858,959	24	7	7	1	-1.1	0.050
LOC102550124	XM_006244906.1	chr9	54,472,209	54,473,966	536	42	323	59	-0.7	0.005
LOC102551034	XM_006245573.1	chr9	100,031,020	100,033,051	113	65	30	18	-1.1	0.053
LOC102552208	XR_359154.1	chr13	102,807,803	102,809,019	1	1	19	11	1.0	0.040
LOC102555254	XR_355136.1	chr6	142,986,713	142,986,843	28	22	3	2	-1.0	0.061
LOC102555299	XR_352678.1	chr3	146,282,636	146,283,940	23	5	2	1	-1.5	0.001
LOC102555453	XM_006256635.1	chrX	2,160,610	2,161,312	5775	403	3	5	-1.1	0.009
LOC102555660	XR_352586.1	chr3	126,550,399	126,550,752	4	4	28	3	1.2	0.010
LOC287167	NM_001013853.1	chr10	15,472,342	15,472,471	62	20	19	8	-1.1	0.028
LOC313641	XR_354365.1	chr5	159,668,632	159,669,759	4878	344	3009	591	-0.7	0.004
LOC682571	XM_003749254.2	chr2	129,043,115	129,044,788	82	24	161	38	0.8	0.081
LOC685619	XR_352828.1	chr3	168,346,760	168,346,924	229	62	18	16	-1.6	0.000
LOC685619	XM_002729250.3	chr3	168,347,122	168,348,324	33	28	206	29	1.5	0.000
LOC685619	XM_006235633.1	chr3	168,347,122	168,348,324	33	28	206	29	1.5	0.000
LOC689064	NM_001111269.1	chr1	175,098,753	175,099,017	747	212	245	80	-1.3	0.000
LOC690097	XM_006237125.1	chr4	212,692,295	212,692,406	634	68	949	103	0.6	0.008
LOC691960	XM_003749565.2	chr3	121,185,532	121,186,281	882	200	2167	282	1.2	0.000
Loxl2	NM_001106047.2	chr15	55,092,789	55,092,980	891	169	465	50	-0.9	0.000
Lrp8	XM_006238565.1	chr5	131,320,216	131,324,785	214	65	77	40	-1.0	0.035
Lrrc17	NM_001025155.2	chr4	10,109,699	10,110,521	182	43	76	17	-1.0	0.003
Lrrc32	NM_001170434.1	chr1	169,657,283	169,661,088	607	84	342	45	-0.8	0.000
Lum	NM_031050.1	chr7	38,867,390	38,868,211	8131	958	5537	367	-0.5	0.001
Ly49si1	NM_001009497.1	chr4	212,391,501	212,391,637	25	14	90	14	1.3	0.002
Lyve1	NM_001106286.1	chr1	182,650,924	182,652,890	616	198	328	73	-0.8	0.065
Lyz2	NM_012771.3	chr7	60,337,949	60,338,730	250988	24881	419557	79564	0.7	0.001
Maged1	NM_053409.2	chrX	64,712,955	64,713,160	1048	154	602	136	-0.7	0.010
Map1a	NM_030995.1	chr3	119,809,946	119,811,427	104	36	6	4	-2.4	0.000
Map4k4	XM_006244776.1	chr9	46,466,226	46,469,618	365	94	127	30	-1.3	0.000
Map7d1	XM_006238901.1	chr5	148,018,365	148,018,957	256	86	109	16	-1.0	0.007
Mapk6	XM_006243409.1	chr8	81,931,197	81,933,534	331	46	211	36	-0.6	0.074
Mcpt2	NM_172044.1	chr15	38,922,256	38,922,403	182	38	439	182	1.0	0.029
Med13l	XM_006249419.1	chr12	45,257,714	45,260,435	223	48	97	26	-1.0	0.005
Med15	XM_006248704.1	chr11	90,606,468	90,607,496	187	78	56	15	-1.3	0.001
Medag	XM_341029.5	chr12	8,808,628	8,809,904	392	41	191	36	-0.9	0.000
Meis2	NM_001107758.1	chr3	114,124,746	114,126,196	29	15	0	1	-1.4	0.001
Mertk	XM_006234988.1	chr3	128,669,533	128,671,875	1379	55	2538	285	0.9	0.000

Mest	NM_001009617.1	chr4	57,821,677	57,821,884	238	67	113	28	-0.9	0.033
Mettl23	XM_006247798.1	chr10	105,450,831	105,451,857	63	19	24	8	-1.0	0.049
Mettl5	NM_001114181.1	chr3	62,736,604	62,736,825	327	16	194	40	-0.7	0.013
Mmp7	NM_012864.2	chr8	5,902,884	5,903,105	216	24	366	27	0.7	0.000
Mpdz	XM_006238343.1	chr5	103,442,805	103,444,104	73	25	25	11	-1.0	0.079
Mprip	NM_053814.2	chr10	45,889,368	45,890,069	1367	136	997	123	-0.4	0.087
Mrc2	XM_006247631.1	chr10	93,339,088	93,340,436	1172	80	737	99	-0.6	0.001
Mrgprf	XM_006230698.1	chr1	225,342,212	225,344,027	68	29	23	4	-1.1	0.029
Mrps2	NM_001108576.1	chr3	12,405,542	12,407,371	519	68	78	37	-2.1	0.000
Mrps2	XM_006233832.1	chr3	12,405,542	12,407,382	20	18	155	69	1.0	0.082
Mrvi1	XM_006230047.1	chr1	182,668,660	182,671,988	66	27	23	7	-1.0	0.085
Msln	NM_031658.1	chr10	14,932,447	14,932,667	771	381	161	104	-1.4	0.001
Msr1	XM_006253207.1	chr16	56,551,359	56,554,765	2133	282	3398	848	0.6	0.078
Mtg1	XM_006230584.1	chr1	219,533,460	219,533,912	47	5	6	8	-1.0	0.095
Myo10	XM_006232082.1	chr2	97,788,915	97,790,396	439	31	243	43	-0.8	0.001
Mypn	XM_006256374.1	chr20	28,913,445	28,914,644	90	49	26	12	-1.0	0.066
Myrf	XM_006231030.1	chr1	233,205,241	233,207,424	25	14	77	8	1.0	0.042
Mysm1	XM_006238409.1	chr5	117,848,660	117,853,513	53	6	175	133	1.1	0.033
Napg	XM_006254831.1	chr18	57,564,327	57,566,988	34	6	6	2	-1.5	0.000
Nckap1	NM_031618.1	chr3	74,284,276	74,285,160	1277	79	848	147	-0.6	0.016
Ndrg4	NM_031967.2	chr19	9,751,516	9,753,272	41	17	10	7	-1.0	0.067
Necap2	XM_006239179.1	chr5	163,302,180	163,303,311	267	87	851	58	1.5	0.000
Nedd4	NM_012986.1	chr8	73,679,011	73,681,737	5317	898	3527	395	-0.6	0.019
Nfe2l2	NM_031789.2	chr3	69,041,646	69,043,314	1682	203	303	69	-2.3	0.000
Nfe2l2	XM_006234396.1	chr3	69,041,640	69,043,314	1867	393	3437	959	0.8	0.035
Nfix	XM_006255308.1	chr19	36,794,503	36,797,612	139	20	47	18	-1.2	0.001
Nfix	XM_006255305.1	chr19	36,794,503	36,797,612	41	26	5	3	-1.2	0.016
Nfkbiz	XM_006248249.1	chr11	50,445,907	50,447,281	317	28	182	47	-0.7	0.033
Ngf	XM_006233053.1	chr2	224,368,758	224,369,663	24	12	4	3	-1.0	0.074
Nhsl1	XM_006227670.1	chr1	15,388,198	15,389,483	68	11	23	10	-1.1	0.012
Nid1	XM_213954.7	chr17	92,213,994	92,216,215	4145	636	2652	394	-0.6	0.016
Nid2	NM_001012005.2	chr15	8,984,787	8,985,338	912	211	515	103	-0.7	0.033
Nol3	XM_006255542.1	chr19	48,101,693	48,102,350	209	50	107	14	-0.8	0.012
Notch3	NM_020087.2	chr7	14,294,586	14,295,893	1008	162	560	131	-0.8	0.011
Npas2	NM_001108214.2	chr9	45,768,365	45,769,792	150	63	40	15	-1.3	0.001
Nqo2	XM_006253868.1	chr17	34,023,010	34,023,886	57	3	125	31	0.9	0.006
Nrep	XM_006254595.1	chr18	25,898,560	25,900,359	1089	386	586	117	-0.7	0.091
Nt5dc2	NM_001009271.1	chr16	7,148,770	7,149,110	158	40	70	17	-1.0	0.009
Ntn4	NM_001106780.1	chr7	34,705,555	34,705,741	285	54	170	26	-0.7	0.053
Nuak1	NM_001106774.1	chr7	25,251,156	25,253,032	221	37	140	13	-0.6	0.086
Ofd1	XM_006256853.1	chrX	29,996,095	29,996,224	27	16	98	16	1.2	0.008
Olfml3	NM_001107708.1	chr2	225,643,128	225,644,406	689	79	448	79	-0.6	0.035
Otud7b	XM_006232961.1	chr2	217,782,905	217,789,205	93	9	45	13	-0.9	0.035
Pacsin3	NM_001009966.2	chr3	86,789,302	86,789,807	184	56	28	12	-1.9	0.000
Pacsin3	XM_006234512.1	chr3	86,789,302	86,789,813	0	0	50	31	1.4	0.000
Pak6	XR_352523.1	chr3	117,027,353	117,027,426	25	16	5	2	-1.0	0.065
Pcdh18	XM_006232322.1	chr2	158,301,726	158,303,680	269	76	136	24	-0.8	0.024
Pcdh19	XM_006257222.1	chrX	104,230,785	104,236,495	87	16	15	7	-1.7	0.000
Pcdhgb7	NM_001012215.1	chr18	30,660,086	30,662,068	123	7	72	12	-0.7	0.049
Pdgfra	NM_012802.1	chr14	35,356,433	35,359,696	1336	310	735	222	-0.7	0.096
Pdgfrl	NM_001011921.1	chr16	54,098,418	54,098,887	384	57	257	30	-0.5	0.081
Pdk1	XM_006234352.1	chr3	65,045,962	65,049,739	334	60	531	84	0.6	0.054
Pds5b	XM_006248737.1	chr12	774,945	777,766	108	25	221	46	0.9	0.009
Pdzrn3	NM_001271251.1	chr4	198,194,464	198,194,746	507	77	273	33	-0.8	0.000
Pear1	XM_006232619.1	chr2	206,519,950	206,520,374	128	24	63	15	-0.8	0.031
Phyhd1	XM_006233778.1	chr3	14,198,871	14,198,959	89	38	30	13	-1.0	0.088
Pi16	XM_006256183.1	chr20	9,172,107	9,172,502	299	87	638	209	0.9	0.060
Pigw	XM_006247056.1	chr10	72,101,632	72,103,307	32	7	73	18	0.9	0.050
Pkp4	XM_006234217.1	chr3	50,530,156	50,531,152	0	0	20	12	1.2	0.005
Plat	NM_013151.2	chr16	73,730,260	73,731,151	2433	273	1358	154	-0.8	0.000
Plcb4	NM_024353.1	chr3	135,457,673	135,459,248	163	40	0	0	-4.2	0.000
Plcb4	XM_006235083.1	chr3	135,457,673	135,459,248	17	14	68	35	1.0	0.095
Plce1	NM_053758.2	chr1	264,955,769	264,956,664	143	20	62	15	-1.0	0.001
Plekhg1	XM_006227841.1	chr1	41,865,120	41,868,666	59	15	21	11	-1.0	0.091
Pmp22	XM_006246585.1	chr10	49,345,703	49,346,995	30	9	5	5	-1.0	0.069
Pofut1	XM_006235290.1	chr3	155,348,573	155,350,262	1164	66	832	103	-0.5	0.027
Ppap2b	NM_138905.2	chr5	128,624,288	128,626,138	1336	254	872	88	-0.6	0.042
Ppdpf	NM_001009316.1	chr3	180,402,135	180,402,453	59	28	14	8	-1.1	0.039
Pphln1	XM_006242231.1	chr7	134,358,204	134,361,038	23	12	4	2	-1.1	0.051

Ppig	NM_031793.1	chr3	62,598,074	62,600,509	327	63	11	9	-2.4	0.000
Ppp1r14a	XM_006228644.1	chr1	88,411,621	88,411,822	27	10	5	4	-1.0	0.061
Prg4	NM_001105962.2	chr13	72,637,408	72,637,796	458	325	137	34	-1.0	0.078
Prrx1	NM_153821.1	chr13	86,039,712	86,040,161	374	96	198	44	-0.8	0.048
Psca	NM_001172106.1	chr7	115,997,003	115,997,258	157	65	316	42	0.8	0.094
Pxdn	NM_001271261.1	chr6	57,661,282	57,663,427	3850	581	2578	246	-0.5	0.012
Rab14	NM_053589.1	chr3	19,693,754	19,694,043	109	25	0	0	-3.7	0.000
Ralgapb	NM_001271210.1	chr3	160,623,750	160,627,554	261	71	9	7	-2.8	0.000
Rasip1	XM_006229030.1	chr1	102,700,021	102,700,428	232	40	139	21	-0.6	0.069
Rassf2	NM_001037096.1	chr3	131,075,322	131,077,600	215	63	88	35	-1.0	0.035
Rbms1	XM_006234236.1	chr3	51,910,790	51,911,572	128	10	295	82	1.0	0.001
Rcn3	NM_001008694.2	chr1	102,141,918	102,142,352	923	98	572	169	-0.6	0.088
Rem1	XM_006235278.1	chr3	154,521,394	154,522,147	124	35	57	18	-0.9	0.093
Rffl	XM_006246977.1	chr10	69,788,329	69,790,694	43	10	10	6	-1.2	0.018
RGD1304929	XM_224403.7	chr15	60,820,889	60,821,362	87	20	153	13	0.7	0.067
RGD1307182	XM_006244483.1	chr9	13,566,787	13,567,921	495	69	878	153	0.8	0.001
RGD1310587	NM_001100857.1	chr13	107,456,592	107,458,977	469	92	236	78	-0.8	0.037
RGD1560464	XM_343883.5	chr10	34,098,536	34,100,361	211	32	93	22	-1.0	0.000
RGD1561055	XM_577041.4	chrX	139,523,380	139,524,288	22	21	1	1	-0.9	0.087
RGD1562161	XM_006256933.1	chrX	38,603,665	38,604,729	77	10	38	6	-0.8	0.041
RGD1562284	XM_006239632.1	chr6	1,679,166	1,679,764	293	10	442	24	0.6	0.000
RGD1566307	XM_006228230.1	chr1	74,935,763	74,936,423	669	122	1046	178	0.6	0.075
RGD735065	XM_006256176.1	chr20	9,149,289	9,149,347	6	4	28	10	1.0	0.098
Rhbdf1	NM_001030034.1	chr10	15,579,781	15,580,428	506	93	284	60	-0.7	0.020
Rhoj	NM_001008320.1	chr6	107,784,161	107,785,252	643	93	359	24	-0.8	0.000
Rin2	XM_006235150.1	chr3	146,508,338	146,510,343	246	54	524	173	0.9	0.018
Rnase4	NM_020082.2	chr15	31,865,116	31,866,405	1444	189	1017	130	-0.5	0.087
Rnd3	NM_001007641.1	chr3	41,757,185	41,758,519	261	15	184	17	-0.5	0.073
Rnf34	XM_006249361.1	chr12	41,057,288	41,058,198	15	4	42	14	1.0	0.088
Robo4	NM_181375.1	chr8	39,089,745	39,090,142	101	33	28	19	-1.0	0.064
Ror2	NM_001107339.1	chr17	14,226,627	14,228,982	256	10	171	18	-0.6	0.022
Rpl12	NM_001109198.1	chr3	17,348,441	17,348,585	3389	343	9674	1629	1.4	0.000
Rpn2	NM_031698.1	chr3	158,274,303	158,274,645	1486	246	778	27	-0.9	0.000
RT1-CE10	XM_006255845.1	chr20	131,703	131,874	493	19	730	105	0.5	0.012
RT1-DOa	XM_006255914.1	chr20	5,971,381	5,971,753	908	109	1258	148	0.4	0.088
RT1-M2	NM_001001717.1	chr20	1,328,648	1,328,788	157	43	319	99	0.8	0.052
RT1-T18	XM_006255987.1	chr20	5,230,566	5,231,707	5	2	21	6	1.0	0.088
S100a16	XM_006232718.1	chr2	209,361,144	209,361,935	115	30	37	29	-1.0	0.083
S1pr3	NM_001271143.1	chr17	15,871,250	15,874,681	478	51	330	21	-0.5	0.018
Scara3	NM_001108870.1	chr15	48,985,118	48,986,864	934	332	459	65	-0.9	0.010
Scn7a	NM_031686.1	chr3	59,395,440	59,397,939	27	11	1	3	-0.9	0.079
Sdk1	XM_006248908.1	chr12	16,470,369	16,474,063	207	28	119	23	-0.7	0.035
Sec23b	XM_006235126.1	chr3	145,186,439	145,186,903	72	12	147	31	0.9	0.010
Sec31a	XM_006250688.1	chr14	10,856,294	10,856,889	248	61	100	34	-1.0	0.009
Sec31a	XM_006250689.1	chr14	10,856,294	10,856,889	63	29	18	7	-1.1	0.024
Sema3f	NM_001108185.1	chr8	115,795,105	115,796,441	169	28	88	30	-0.8	0.099
Sema4c	XM_006244758.1	chr9	42,783,318	42,785,044	258	124	94	16	-1.0	0.046
Sema6d	XM_006234919.1	chr3	123,479,082	123,482,791	326	50	179	53	-0.7	0.065
Senp6	XM_006243436.1	chr8	87,100,815	87,106,345	189	22	275	22	0.5	0.088
Serping1	XM_006234448.1	chr3	78,681,812	78,682,301	47	15	6270	1597	5.9	0.000
Serping1	XM_006234447.1	chr3	78,681,812	78,682,301	1616	292	12708	1168	2.8	0.000
Serping1	NM_199093.1	chr3	78,681,825	78,682,301	23416	2054	3283	733	-2.6	0.000
Serpinh1	NM_017173.1	chr1	170,503,467	170,504,454	7836	1764	4562	855	-0.7	0.015
Sertad4	NM_001108351.1	chr13	116,126,510	116,128,840	527	75	343	55	-0.6	0.055
Setd1b	XR_350738.1	chr1	206,269,600	206,270,421	62	13	20	4	-1.2	0.002
Sfrp2	NM_001100700.1	chr2	202,142,593	202,143,778	1248	841	126	42	-2.1	0.000
Sfrp4	NM_053544.1	chr17	56,104,293	56,105,248	2123	819	894	297	-1.0	0.023
Sfswap	XR_358631.1	chr12	32,675,283	32,675,669	49	30	2	2	-1.2	0.006
Sgta	XM_006240996.1	chr7	11,705,105	11,706,055	143	36	269	48	0.8	0.027
Shank3	NM_021676.1	chr7	130,218,101	130,220,171	408	95	235	49	-0.7	0.064
Sirpa	XM_006234953.1	chr3	127,864,144	127,866,495	544	61	1885	109	1.7	0.000
Sirpa	NM_013016.2	chr3	127,864,144	127,866,495	3975	654	1190	106	-1.6	0.000
Sirpa	XM_006234954.1	chr3	127,864,144	127,866,495	335	86	764	229	1.0	0.003
Slc13a3	NM_022866.2	chr3	168,266,584	168,268,109	734	114	1161	159	0.6	0.014
Slc25a25	NM_145677.1	chr3	16,791,265	16,793,076	133	12	1	2	-3.8	0.000
Slc30a4	NM_172066.1	chr3	121,344,026	121,348,033	866	87	638	59	-0.4	0.076
Slc35c2	XM_006235593.1	chr3	167,986,125	167,986,813	4	5	70	15	1.5	0.000
Slc35c2	XM_006235594.1	chr3	167,986,125	167,986,813	9	8	103	60	1.4	0.002
Slc39a13	XM_006234501.1	chr3	86,593,276	86,594,479	870	123	554	70	-0.6	0.010

Slc6a12	NM_017335.1	chr4	221,028,728	221,029,242	253	27	365	25	0.5	0.037
Slc9a8	NM_001025281.1	chr3	170,372,578	170,373,074	38	8	0	0	-2.3	0.000
Slmap	XM_006252552.1	chr16	2,087,745	2,089,548	8	8	81	65	1.1	0.032
Slmap	XM_006252547.1	chr16	2,087,745	2,089,548	10	5	79	84	0.9	0.098
Smarca5	XM_006255401.1	chr19	41,872,699	41,873,893	152	21	276	83	0.7	0.096
Smoc2	XM_006227958.1	chr1	57,564,113	57,565,436	367	98	191	16	-0.8	0.008
Smoc2	NM_001106215.2	chr1	57,564,113	57,565,337	640	135	361	62	-0.7	0.021
Smpdl3a	NM_001005539.1	chr20	42,531,769	42,532,381	6048	414	8636	1010	0.5	0.004
Sned1	XR_357229.1	chr9	100,092,147	100,095,480	406	302	125	27	-1.1	0.018
Snrpb2	XM_006235116.1	chr3	143,589,590	143,589,947	24	13	94	44	1.1	0.049
Sparc	NM_012656.1	chr10	40,573,509	40,574,610	3149	600	1978	313	-0.6	0.027
Sparc	XM_006246375.1	chr10	40,573,510	40,574,610	36850	7102	23217	3986	-0.6	0.031
Spata7	NM_138862.3	chr6	131,862,259	131,862,960	49	25	3	4	-1.0	0.050
Spib	NM_001024286.1	chr1	101,596,928	101,598,971	174	14	272	48	0.6	0.072
Spn	NM_001271086.1	chr1	205,563,658	205,567,456	2245	337	3004	132	0.4	0.098
Spon1	NM_172067.1	chr1	185,901,264	185,902,809	3098	101	2193	208	-0.5	0.000
Spon2	NM_138533.3	chr14	83,509,643	83,510,376	270	222	55	16	-1.2	0.015
Sppl2a	XM_006234920.1	chr3	125,885,609	125,889,130	1466	175	2484	171	0.7	0.000
Sptan1	NM_171983.2	chr3	13,950,503	13,950,970	272	74	2	2	-4.2	0.000
Sqrdl	XM_006234887.1	chr3	121,477,035	121,477,304	231	53	432	46	0.8	0.005
Srpx	NM_022524.1	chrX	14,932,358	14,932,908	651	123	333	35	-0.9	0.000
Ssfa2	XM_006234421.1	chr3	73,188,985	73,190,286	78	10	216	61	1.2	0.000
Ssrp1	XM_006234482.1	chr3	78,967,793	78,968,279	2	1	19	2	1.4	0.001
Ssrp1	XM_006234479.1	chr3	78,967,793	78,968,279	2	1	24	14	1.1	0.022
St3gal3	XM_006238715.1	chr5	140,554,357	140,555,346	96	8	40	16	-1.0	0.031
Stab1	XM_002728378.3	chr16	7,149,002	7,149,179	2239	352	1385	297	-0.6	0.052
Svil	XM_006254041.1	chr17	52,915,518	52,916,506	864	105	588	89	-0.5	0.060
Syde1	XM_006241068.1	chr7	14,199,663	14,201,067	434	78	235	51	-0.8	0.009
Sync	XM_006238944.1	chr5	151,230,511	151,232,433	77	26	24	2	-1.2	0.001
Tal1	XM_006238616.1	chr5	137,666,881	137,670,144	34	14	4	2	-1.4	0.003
Tbx3	XM_006249418.1	chr12	44,326,927	44,329,023	101	34	40	9	-1.0	0.033
Tdp1	XM_006240433.1	chr6	133,186,789	133,187,083	41	24	10	4	-1.0	0.083
Tek	NM_001105737.1	chr5	117,798,402	117,799,345	435	71	286	33	-0.6	0.069
Tfpi	XM_006234440.1	chr3	78,373,807	78,374,128	255	64	127	8	-0.9	0.003
Tgm2	NM_019386.2	chr3	161,005,718	161,007,261	6462	1115	3845	386	-0.7	0.001
Thbs1	NM_001013062.1	chr3	116,421,911	116,422,101	1561	379	865	213	-0.7	0.041
Thbs2	NM_001169138.1	chr1	57,842,345	57,844,336	2577	927	1334	171	-0.8	0.029
Tjp1	XM_006229330.1	chr1	127,243,077	127,244,571	128	13	38	24	-1.0	0.062
Tjp1	XM_006229333.1	chr1	127,243,077	127,244,571	104	8	31	20	-1.0	0.077
Tln2	XM_006243398.1	chr8	77,342,735	77,347,018	257	73	116	28	-0.9	0.011
Tmcc3	XM_006241257.1	chr7	35,604,267	35,608,386	35	15	112	30	1.2	0.004
Tmem100	NM_001017479.1	chr10	77,404,104	77,405,343	198	46	108	17	-0.7	0.063
Tmem173	NM_001109122.1	chr18	28,242,118	28,242,856	1317	139	1710	52	0.4	0.074
Tmem255a	XM_006257479.1	chrX	124,486,032	124,488,797	89	2	39	13	-0.9	0.031
Tmem50a	XM_006239147.1	chr5	157,009,243	157,009,383	34	23	107	31	1.0	0.069
Tnfaip6	NM_053382.1	chr3	42,662,493	42,663,190	272	131	90	31	-1.1	0.009
Tnfsf14	NM_001191803.1	chr9	8,771,946	8,772,374	23	7	65	23	1.0	0.058
Tnip1	XM_006246305.1	chr10	40,028,045	40,028,828	131	18	226	47	0.7	0.056
Tns3	XM_006251462.1	chr14	88,471,108	88,473,931	185	110	485	127	1.0	0.074
Tom1l2	XM_006246508.1	chr10	46,354,435	46,357,620	84	35	7	7	-1.1	0.024
Tomm34	XM_006235585.1	chr3	166,632,889	166,633,829	38	22	167	52	1.4	0.001
Tp53i11	NM_001107749.1	chr3	88,797,489	88,799,475	550	117	187	23	-1.4	0.000
Tp53i11	XM_006234571.1	chr3	88,797,489	88,799,481	51	39	357	204	1.5	0.000
Traf2	NM_001107815.2	chr3	2,727,487	2,728,238	291	39	476	99	0.6	0.065
Trem2	NM_001106884.1	chr9	13,532,919	13,533,182	408	74	726	98	0.8	0.002
Trerf1	XM_006244453.1	chr9	14,574,700	14,577,270	22	6	79	38	1.2	0.010
Trpv2	NM_001270798.1	chr10	48,707,799	48,707,996	490	65	916	200	0.8	0.001
Tsc1	NM_021854.1	chr3	12,615,120	12,615,637	24	13	0	0	-1.3	0.002
Tshz2	XM_006235659.1	chr3	172,859,967	172,864,981	287	33	160	46	-0.7	0.047
Tsku	XM_006229759.1	chr1	169,524,024	169,526,459	274	49	150	40	-0.7	0.078
Tspan6	NM_001100672.1	chrX	104,555,373	104,556,194	419	49	238	54	-0.7	0.018
Tti1	XM_006235428.1	chr3	161,140,237	161,140,923	196	28	326	79	0.6	0.080
Ttyh3	XM_006248929.1	chr12	18,105,533	18,108,497	972	86	618	80	-0.6	0.001
Uap1	NM_001191930.1	chr13	93,089,457	93,090,026	90	27	32	17	-1.0	0.093
Ubap2	XM_006238052.1	chr5	62,064,691	62,065,625	804	47	587	63	-0.4	0.038
Vcan	NM_001170559.1	chr2	18,363,889	18,365,933	1026	388	475	207	-0.8	0.100
Wisp2	NM_031590.1	chr3	166,407,942	166,408,879	215	131	637	75	1.1	0.011
Wwtr1	NM_001024869.1	chr2	166,985,077	166,985,451	243	23	136	9	-0.8	0.000
Xirp2	NM_201989.1	chr3	60,272,765	60,274,635	812	395	147	68	-1.6	0.000

Xrn1	XM_006243595.1	chr8	103,328,931	103,334,089	76	20	20	6	-1.4	0.000
Yap1	XM_006242493.1	chr8	6,131,652	6,134,416	456	94	252	66	-0.7	0.069
Zc3h15	NM_001010963.1	chr3	77,569,665	77,570,544	265	30	1029	132	1.8	0.000
Zc3h15	XR_352424.1	chr3	77,570,421	77,570,544	490	55	171	30	-1.4	0.000
Zc3h15	XR_352425.1	chr3	77,570,355	77,570,544	490	55	171	30	-1.4	0.000
Zfp334	XM_230857.6	chr3	168,255,821	168,257,790	1366	122	2024	332	0.5	0.028
Zfp638	XM_006236750.1	chr4	180,273,076	180,273,387	185	90	48	12	-1.3	0.001
Zfp672	XM_006246390.1	chr10	43,545,157	43,547,611	90	11	47	11	-0.8	0.078
Zfyve19	XM_006234787.1	chr3	117,572,081	117,572,481	41	7	127	23	1.4	0.000
Zfyve19	NM_001034948.1	chr3	117,572,081	117,572,476	132	16	49	16	-1.2	0.000
Zmiz1	XM_006252539.1	chr16	1,928,370	1,932,187	651	107	1020	120	0.6	0.021

*Average values from $231^{\mathrm{Luc+}}$ tumors implanted in $\mathrm{SS.BN3}^{\mathrm{IL2R\gamma}}$ (n=4) and $\mathrm{SS}^{\mathrm{IL2R\gamma}}$ (n=4) rats. SD, standard deviation; FDR, false discovery rate