

Suppl. Table 1a. qPCR primers and reactions for which qPCR values are reported in this study

Gene	LocusLink ID	Gene Name	PrimerBank ID	Primer Name	Sequence	Amplicon Size	Intron Spanning	Tm Found	Predicted Tm
Adora2a	11540	Adenosine A2a receptor	33859500a1	Adora2a F166-184 Adora2a R287-266	GCCATCCCATTGCGCCATCA GCAATAGCCAAGAGGCTGAAGA	122	N	84.6	83
Bmpr1a	12166	Bone morphogenetic protein receptor, type 1A	primer3	Bmpr1a (B) F1674-1694 Bmpr1a (B) R1831-1811	AGCCCTACATCATGGCTGAC ACACACAACCTCACGCATGT	158	Y	78.7	79
Bmpr2	12168	Bone morphogenetic protein receptor, type II	6680804a2	Bmpr2 F254-273 Bmpr2 R405-385	GGTCTCACATCGGTGATCCC GTCAGGGGGTGGAAAGTTCTC	152	N	78.8	80
Lifr	16880	Leukemia inhibitory factor receptor	7305235a1	Lifr F90-108 Lifr R270-250	AGCTCTGACCCTCTGCAT TGGGTGACAAGAATGGAACCT	181	Y	84.0	82
Prkar2b	19088	Protein kinase, cAMP dependent regulatory, type II beta	26334123a2	Prkar2b F445-467 Prkar2b R545-525	GACATCTGTGTTTAAAGAACCT TGGTCAATTACGTGTTCCCT	101	Y	76.5	76
Prkcc	18752	Protein kinase C, gamma	6755080a1	Prkcc F119-139 Prkcc R222-201	CTCGTTTCTTCAAGCAGCCAA GTGAACCACAAGCTACAGACT	104	Y	81.3	79
Prkcz	18762	Protein kinase C, zeta	6679355a1	Prkcz F89-107 Prkcz R279-259	GCGTGGATGCCATGACAAC AATGATGAGCACTTCGTCCCT	191	Y	84.8	85
Rgs1	50778	Regulator of G-protein signaling 1	7657512a1	Rgs1 F148-168 Rgs1 R395-374	TCTGGGATGAAATCGGCCAAG GCATCTGAATGCACAAATGCTT	248	Y	78.1	78
Rgs10	67865	Regulator of G-protein signaling 10	13385914a1	Rgs10 F53-71 Rgs10 R209-187	TCCATGACGGAGATGGGAG AACAAGACATTCTTCGCTGAA	157	Y	82.7	82
Rgs12	71729	Regulator of G-protein signaling 12	27777689a2	Rgs12 F913-933 Rgs12 R1077-1059	CCGGATGATAGGCGGTTCTTC CCCAAACTCCGCGCAATG	165	N	83.1	84
Rgs13	246709	Regulator of G-protein signaling 13	23346630a1	Rgs13 F34-56 Rgs13 R207-186	TGCAGAGATGAATCTAAGAGGCT GGTTTCACATGCCATCCAGAAT	174	Y	76.9	77
Rgs18	64214	Regulator of G-protein signaling 18	12738845a2	Rgs18 F514-535 Rgs18 R630-610	AGTTTGTATACGGCACAAGCA TGTTGGTCTCTGAGGCTTCC	117	N	76.3	78
Rgs2	19735	Regulator of G-protein signaling 2	31543586a2	Rgs2 F364-385 Rgs2 R504-484	ACCAAATCACCCAAAACTGT GCCACTTGATGCCTCTGGAT	141	Y	76.6	77
Smad1	17125	MAD homolog 1 (Drosophila)	31543220a1	Smad1 F1244-1262 Smad1 R1390-1369	GCTTCGTGAAGGGTTGGGG CGGATGAAATAGGATTGTGGGG	147	N	83.5	84
Smad4	17128	MAD homolog 4 (Drosophila)	31543220a2	Smad4 F546-564 Smad4 R798-776	ACACCCGCCAAGTAATCGC GGTGGTAGTGCTTATGATGGT	253	Y	86.4	86
Smad6	17130	MAD homolog 6 (Drosophila)	12836011a2	Smad6 F266-285 Smad6 R421-401	GCAACCCTACCACTTCAGC GAGCAGTGATGAGGGAGTTGG	156	Y	84.6	85
Smad7	17131	MAD homolog 7 (Drosophila)	6678778a1	Smad7 F494-512 Smad7 R646-625	GGCCGGATCTCAGGCATTC TTGGGTATCTGGAGTAAGGAGG	153	Y	82.4	83

Suppl. Table Ib. Expression values of genes referred to herein, generated by second generation microarray screen comparing murine naïve and memory B cells

Affymetrix ID	Gene	Fold M/N ^b	T- Test ^c	Expression Value ^a									
				Av Nve	Av Mem	Naïve A	Naïve B	Naïve C	Naïve D	Mem A	Mem B	Mem C	Mem D
1427519_at	Adora2a	4.83	0.0000	18	88	23	23	13	14	91	94	76	93
1460710_at	Adora2a	5.71	0.0000	49	282	44	49	57	49	284	284	280	278
1420577_at	Aicda	0.19	0.2562	719	139	212	2103	246	314	158	106	162	131
1418279_a_at	Akap1	1.50	0.0272	14	21	15	13	14	13	25	23	15	18
1449019_at	Akap1	2.17	0.0017	23	51	26	26	18	23	56	61	39	47
1430774_at	Akap10	0.93	0.5001	302	281	339	288	344	237	258	251	296	318
1441829_s_at	Akap10	1.32	0.1093	218	288	214	171	224	263	355	245	223	329
1441830_x_at	Akap10	1.30	0.2066	135	175	127	92	124	197	209	153	137	202
1447570_s_at	Akap10	1.00	0.9942	24	24	28	18	25	26	27	17	34	18
1421121_at	Akap10	1.04	0.7352	154	160	140	136	173	166	154	165	126	193
1428482_at	Akap10	1.01	0.3698	316	320	319	319	306	319	319	324	326	312
1434764_at	Akap11	0.88	0.0080	696	614	735	644	699	705	613	636	594	614
1419706_a_at	Akap12	0.22	0.0028	64	14	39	88	59	67	12	13	13	17
1443923_at	Akap13	2.02	0.0010	583	1177	549	526	654	601	1389	1092	956	1271
1455870_at	Akap2	0.93	0.3110	412	383	380	404	456	410	419	368	415	330
1449168_a_at	Akap2	0.91	0.3621	383	348	345	466	401	319	357	377	331	329
1433669_at	Akap8	0.87	0.0192	1765	1539	1859	1808	1818	1575	1461	1521	1576	1598
1450983_at	Akap8	0.90	0.1168	1370	1232	1310	1428	1397	1346	1171	1131	1187	1441
1428814_at	Akap8l	1.01	0.8699	40	41	41	40	44	37	40	39	42	41
1417734_at	Akap8l	0.86	0.0209	997	853	985	955	1088	959	764	898	836	914
1435769_at	Akap9	0.95	0.2284	857	812	916	872	841	800	782	827	871	768
1437082_at	Akap9	1.15	0.2097	548	632	519	540	598	534	657	557	530	782
1446237_at	Akap9	1.03	0.5283	14	15	14	13	15	15	14	15	16	14
1447912_x_at	Akap9	1.02	0.8471	49	50	47	46	56	47	60	45	48	47
1447913_x_at	Akap9	1.06	0.0249	25	27	25	24	26	26	27	27	27	26
1455151_at	Akap9	1.33	0.1063	695	923	682	626	746	726	1116	642	819	1116
1438967_x_at	Amhr2	1.01	0.1861	3	3	3	3	3	3	3	3	4	3
1457021_x_at	Amhr2	1.01	0.4388	4	4	4	4	4	4	4	4	4	4
1427989_at	Amhr2	1.00	0.8493	4	4	4	4	4	4	4	4	4	4
1457687_at	Bcl2	0.55	0.0000	5037	2760	5325	4571	5312	4939	2429	2764	2893	2953

1427818_at	Bcl2	1.01	0.4036	11	11	11	11	11	11	11	11	11	11
1427819_at	Bcl2	0.90	0.7107	77	70	70	58	111	70	75	44	48	112
1437122_at	Bcl2	0.54	0.0001	1609	869	1710	1468	1725	1532	751	882	918	923
1440770_at	Bcl2	0.81	0.3392	1202	979	1161	996	1688	965	1053	772	762	1330
1443837_x_at	Bcl2	0.69	0.0473	1237	848	1292	1144	1586	928	772	752	801	1066
1422938_at	Bcl2	0.59	0.0151	251	148	230	211	317	248	119	132	135	208
1425491_at	Bmpr1a	1.92	0.0632	22	43	11	44	18	15	41	30	53	46
1425492_at	Bmpr1a	2.12	0.0185	148	315	99	266	113	115	395	236	337	291
1425493_at	Bmpr1a	2.56	0.0064	17	44	10	34	12	13	53	37	42	45
1425494_s_at	Bmpr1a	2.63	0.0126	17	44	9	40	7	12	46	44	44	45
1445413_at	Bmpr1a	1.01	0.1082	3	3	3	3	3	3	3	3	4	3
1451729_at	Bmpr1a	1.07	0.2056	8	9	8	8	8	8	10	8	8	8
1437312_at	Bmpr1b	1.01	0.8004	6	6	6	6	6	6	6	6	6	6
1443720_s_at	Bmpr1b	1.13	0.1240	9	10	7	9	9	10	9	10	11	10
1422872_at	Bmpr1b	1.01	0.9602	23	23	27	22	16	26	18	24	31	19
1419616_at	Bmpr2	0.97	0.5601	13	12	13	13	13	12	12	11	12	13
1450357_a_at	Ccr6	1.53	0.0078	2232	3411	2139	1939	2264	2586	3559	3537	2646	3902
1420404_at	Cd86	1.01	0.9448	1087	1096	1176	1348	1039	785	1068	1085	1084	1146
1449858_at	Cd86	1.06	0.3025	851	905	825	928	836	815	853	834	921	1012
1417409_at	Jun	0.85	0.1389	493	419	478	515	547	433	374	524	404	374
1448694_at	Jun	0.87	0.1434	163	142	189	166	147	150	132	153	157	126
1425107_a_at	Lifr	25.40	0.0012	15	368	13	17	13	14	511	410	330	222
1447098_at	Lifr	1.07	0.0151	11	11	11	10	10	11	11	11	12	11
1450207_at	Lifr	1.53	0.0063	6	8	7	6	5	5	9	9	9	7
1434178_at	Mil3	1.03	0.7665	1172	1202	1140	1160	1300	1088	1202	1025	1156	1424
1434179_at	Mil3	0.99	0.9320	3516	3495	3681	3606	3711	3065	3241	3240	3510	3989
1457193_at	Mil3	1.51	0.0499	188	285	143	191	188	232	320	217	237	366
1427150_at	Mil3	1.25	0.0602	1115	1398	1116	1133	1150	1060	1473	1588	1043	1486
1448757_at	Pml	1.53	0.0003	1470	2247	1367	1438	1377	1697	2186	2276	2107	2419
1459137_at	Pml	2.57	0.0386	43	109	41	39	53	37	96	83	75	183
1447635_at	Prkar1a	0.91	0.0839	13	12	12	14	14	12	12	12	12	11
1452032_at	Prkar1a	0.83	0.0063	4393	3629	4522	4407	4431	4213	3392	3951	3271	3904
1425550_a_at	Prkar1a	0.84	0.0640	1190	1003	1163	1272	1222	1101	892	991	912	1214
1434325_x_at	Prkar1b	0.96	0.7939	12	12	11	11	10	17	13	12	11	11
1440132_s_at	Prkar1b	0.93	0.3587	20	19	18	24	18	20	19	19	19	19
1440133_x_at	Prkar1b	1.02	0.0524	48	49	48	48	47	48	48	49	49	48

1416753_at	Prkar1b	1.03	0.4397	19	19	19	19	18	19	19	21	19	19
1416754_at	Prkar1b	1.03	0.0805	18	19	18	18	18	18	18	19	19	18
1427414_at	Prkar2a	1.53	0.0464	13	20	13	11	14	14	21	20	13	26
1428783_at	Prkar2a	1.82	0.0002	147	268	141	174	144	129	262	292	241	278
1432409_at	Prkar2a	0.97	0.5219	17	16	16	16	17	19	16	17	17	16
1452915_at	Prkar2a	1.69	0.0001	416	704	436	481	368	378	749	659	688	718
1430640_a_at	Prkar2b	21.83	0.0003	24	518	32	23	15	25	541	445	395	692
1438664_at	Prkar2b	39.86	0.0000	101	4045	146	74	78	108	5006	3737	3745	3692
1456475_s_at	Prkar2b	34.83	0.0000	164	5715	234	148	127	148	6384	5309	4964	6201
1455758_at	Prkcc	14.28	0.0000	18	258	18	21	10	23	301	258	208	263
1421446_at	Prkcc	30.84	0.0001	13	392	14	14	9	14	480	393	275	419
1449692_at	Prkcz	1.06	0.0772	6	7	6	6	6	6	6	7	7	6
1454902_at	Prkcz	3.62	0.0009	35	126	23	37	38	41	135	112	95	161
1418085_at	Prkcz	6.38	0.0000	43	272	35	61	33	42	269	290	231	299
1417601_at	Rgs1	0.65	0.0824	38	25	29	40	28	55	23	22	29	25
1416882_at	Rgs10	0.14	0.0000	910	125	842	1112	885	800	117	117	136	131
1457511_at	Rgs12	0.89	0.1342	12	11	14	11	13	11	10	11	12	11
1459566_at	Rgs12	1.05	0.1295	19	20	19	20	19	19	19	21	20	19
1429380_at	Rgs12	1.02	0.1394	8	8	8	8	8	8	8	8	8	8
1453129_a_at	Rgs12	0.51	0.0007	46	23	48	38	44	52	21	20	28	24
1442263_at	Rgs13	0.44	0.0000	14680	6407	14280	14782	14375	15283	6221	4890	7634	6883
1420398_at	Rgs18	0.62	0.0008	1850	1141	1949	1518	1912	2020	1138	1088	1164	1174
1449856_at	Rgs18	0.59	0.0005	482	285	537	408	463	518	278	280	291	292
1419247_at	Rgs2	0.28	0.0000	989	273	936	935	1083	1002	248	244	294	304
1419248_at	Rgs2	0.30	0.0000	3801	1152	4073	3450	3948	3734	974	1017	1353	1264
1450265_at	Samd9 (8)	1.02	0.0902	6	6	6	6	6	6	6	6	6	6
1419480_at	Sell	1.00	0.9921	2535	2536	2768	2542	2493	2335	2398	2856	2368	2524
1419481_at	Sell	0.95	0.2347	5355	5094	5338	5139	5468	5477	4674	5551	5005	5146
1459843_s_at	Smad1	0.50	0.0019	49	25	59	43	40	53	27	23	28	20
1416081_at	Smad1	1.02	0.2036	5	5	5	5	5	5	5	5	5	5
1448208_at	Smad1	0.78	0.0572	76	59	85	70	71	80	43	57	69	69
1444205_at	Smad4	1.01	0.6835	12	12	12	12	12	12	11	12	12	12
1422485_at	Smad4	1.07	0.1499	635	680	633	617	685	603	676	709	622	712
1422486_a_at	Smad4	0.87	0.0661	1364	1187	1450	1452	1395	1158	1104	1143	1257	1242
1422487_at	Smad4	0.96	0.2764	2988	2854	3118	2848	3111	2874	2656	2822	3065	2873
1433641_at	Smad5	0.91	0.0906	299	273	300	300	301	294	258	265	260	311

1421047_at	Smad5	1.04	0.4817	27	28	26	27	27	27	28	28	25	31
1451873_a_at	Smad5	1.05	0.4398	90	94	93	91	83	93	89	91	108	89
1422771_at	Smad6	1.01	0.6563	5	5	5	5	5	5	5	5	5	5
1422771_at	Smad6	1.01	0.6563	5	5	5	5	5	5	5	5	5	5
1422771_at	Smad6	1.01	0.6563	5	5	5	5	5	5	5	5	5	5
1423389_at	Smad7	0.59	0.0001	322	190	316	306	337	327	191	191	218	159
1440952_at	Smad7	0.57	0.0156	35	20	31	44	40	26	18	18	18	26
1443771_x_at	Smad7	0.60	0.0010	400	242	390	384	432	395	282	205	285	196
1416723_at	Tcf4	1.00	0.9804	5117	5111	5454	4999	5127	4887	4916	4756	5232	5541
1416724_x_at	Tcf4	1.09	0.1383	3167	3461	3135	3184	3122	3227	3564	3500	2986	3794
1416725_at	Tcf4	1.08	0.4483	164	177	138	144	169	204	198	160	180	171
1434148_at	Tcf4	0.95	0.3784	4077	3876	4270	3804	4180	4054	4137	3474	4241	3653
1434149_at	Tcf4	1.06	0.3155	2230	2363	2205	1996	2262	2457	2291	2223	2364	2575
1439336_at	Tcf4	1.34	0.1349	158	211	163	140	187	143	230	181	152	283
1440106_at	Tcf4	1.33	0.1759	6	9	7	6	9	4	7	9	7	11
1442903_at	Tcf4	0.39	0.0017	184	72	198	223	188	126	64	78	74	74
1446386_at	Tcf4	0.67	0.0662	65	43	56	92	60	50	37	47	42	47
1446953_at	Tcf4	1.05	0.6902	542	569	607	530	596	434	572	433	580	693
1458201_at	Tcf4	0.91	0.3281	482	438	448	422	585	474	469	382	432	470
1421983_s_at	Tcf4	1.02	0.0930	5	5	5	5	5	5	5	5	5	5
1450447_at	Tcf4	0.91	0.5372	22	20	25	19	21	23	18	26	22	13
1424089_a_at	Tcf4	1.10	0.0701	4600	5080	4513	4126	4768	4991	5258	5040	4769	5254

^aExpression values generated after GCRMA normalization of Affymetrix .cel files. A-D refer to replicates of naïve (Nve) or memory (Mem) samples. The averages (Av) of these values are also listed.

^bFold difference between the average memory and average naïve expression values.

^cStudent's t-test p values of naïve versus memory expression values.