

Table S1. Significantly upregulated genes in LMP2A/λ-MYC pretumor B cells

Symbol	Definition	Fold change	p-value	false discovery rate
Tubb6	tubulin, beta 6 (Tubb6)	7.2761	9.28E-06	0.0070
Nfkbid	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, delta (Nfkbid)	5.5403	4.53E-07	0.0013
Gpr176	G protein-coupled receptor 176 (Gpr176)	4.5664	1.23E-07	0.0004
Reln	reelin (Reln)	4.0695	9.42E-07	0.0019
Rhbdf1	rhomboid family 1 (Drosophila) (Rhbdf1)	3.3097	2.66E-05	0.0095
Foxf2	forkhead box F2 (Foxf2)	3.2704	1.56E-06	0.0021
Ehd3	EH-domain containing 3 (Ehd3)	3.0876	3.33E-08	0.0003
Egr1	early growth response 1 (Egr1)	2.9477	3.26E-05	0.0102
Gramd3	GRAM domain containing 3 (Gramd3)	2.9327	5.38E-04	0.0383
Slc27a3	solute carrier family 27 (fatty acid transporter), member 3	2.8373	3.91E-04	0.0318
Ryk	receptor-like tyrosine kinase (Ryk), transcript variant 2	2.8041	7.15E-06	0.0060
Acaa2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) (Acaa2), nuclear gene encoding mitochondrial protein	2.7839	2.33E-04	0.0256
Cd69	CD69 antigen (Cd69)	2.5919	6.61E-05	0.0122
6430550H21Rik	RIKEN cDNA 6430550H21 gene (6430550H21Rik)	2.5138	2.88E-04	0.0290
Glipr2	GLI pathogenesis-related 2 (Glipr2)	2.4801	3.37E-04	0.0309
Ebi3	Epstein-Barr virus induced gene 3 (Ebi3)	2.4276	3.08E-04	0.0302
Asns	asparagine synthetase (Asns)	2.3896	5.49E-04	0.0383
Dlk1	delta-like 1 homolog (Drosophila) (Dlk1)	2.2525	1.63E-04	0.0212
Chst7	carbohydrate (N-acetylglucosamino) sulfotransferase 7 (Chst7)	2.2365	1.96E-05	0.0087
Gng10	guanine nucleotide binding protein (G protein), gamma 10 (Gng10)	2.1966	3.47E-05	0.0105
Slc2a6	solute carrier family 2 (facilitated glucose transporter), member 6 (Slc2a6)	2.1744	2.03E-04	0.0245
Adarb1	adenosine deaminase, RNA-specific, B1 (Adarb1), transcript variant 1	2.1662	5.48E-05	0.0114
Lrig3	leucine-rich repeats and immunoglobulin-like domains 3 (Lrig3)	2.1424	1.26E-04	0.0182
Zfhx3	zinc finger homeobox 3 (Zfhx3)	2.1011	3.77E-05	0.0108
Ets2	E26 avian leukemia oncogene 2, 3' domain (Ets2)	2.0975	6.82E-05	0.0123
Zmat3	zinc finger matrin type 3 (Zmat3)	2.0682	1.77E-04	0.0224
Gpx7	glutathione peroxidase 7 (Gpx7)	2.0619	5.14E-05	0.0113
Ruvbl1	RuvB-like protein 1 (Ruvbl1)	2.0402	7.79E-04	0.0455
Ahnak	AHNAK nucleoprotein (desmoyokin) (Ahnak), transcript variant 1	2.0390	5.40E-04	0.0383
Stac	src homology three (SH3) and cysteine rich domain (Stac)	2.0150	2.42E-04	0.0262
Casp4	caspase 4, apoptosis-related cysteine peptidase (Casp4)	2.0036	8.19E-04	0.0463
Tmem33	transmembrane protein 33 (Tmem33), transcript variant 2	1.9981	2.81E-04	0.0288
Lysmd2	LysM, putative peptidoglycan-binding, domain containing 2 (Lysmd2)	1.9601	2.09E-05	0.0088
Evi5	ecotropic viral integration site 5 (Evi5)	1.9329	4.87E-04	0.0375
Mapk12	mitogen-activated protein kinase 12 (Mapk12)	1.9183	1.78E-06	0.0021
D12Ert553e	DNA segment, Chr 12, ERATO Doi 553, expressed (D12Ert553e)	1.9131	2.44E-05	0.0094
Alg5	asparagine-linked glycosylation 5 homolog (yeast, dolichyl-phosphate beta-glucosyltransferase) (Alg5)	1.8984	4.23E-04	0.0332
Prr7	proline rich 7 (synaptic) (Prr7)	1.8955	9.53E-05	0.0149
LOC233529		1.8953	7.95E-04	0.0459
Cebpb	CCAAT/enhancer binding protein (C/EBP), beta (Cebpb)	1.8699	7.57E-04	0.0451
Tmem49	transmembrane protein 49 (Tmem49)	1.8455	7.17E-04	0.0441
Cd80	CD80 antigen (Cd80)	1.8391	1.76E-05	0.0084
Cdc14b	CDC14 cell division cycle 14 homolog B (S. cerevisiae) (Cdc14b)	1.8206	1.03E-04	0.0158
Uba1	ubiquitin-like modifier activating enzyme 1 (Uba1)	1.8190	3.29E-04	0.0308
Rin3	Ras and Rab interactor 3 (Rin3)	1.7937	7.85E-04	0.0455
Nt5e	5' nucleotidase, ecto (Nt5e)	1.7728	6.89E-05	0.0123
Rps6kl1	ribosomal protein S6 kinase-like 1 (Rps6kl1)	1.7687	1.76E-04	0.0224
Bag3	BCL2-associated athanogene 3 (Bag3)	1.7406	1.56E-04	0.0207

Fcgr2b	Fc receptor, IgG, low affinity IIb (Fcgr2b), transcript variant 1	1.7341	6.72E-04	0.0431
Sas	Sarcoma-amplified sequence (Sas)	1.7179	4.22E-04	0.0332
Smpd13b	sphingomyelin phosphodiesterase, acid-like 3B (Smpd13b)	1.7128	3.02E-05	0.0098
Rrp1b	ribosomal RNA processing 1 homolog B (<i>S. cerevisiae</i>) (Rrp1b)	1.7074	6.88E-04	0.0436
Wrb	tryptophan rich basic protein (wrb)	1.6765	6.11E-04	0.0409
Kctd14	potassium channel tetramerisation domain containing 14 (Kctd14)	1.6612	2.36E-04	0.0258
Nme7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase) (Nme7), transcript variant 1	1.6509	4.29E-04	0.0334
Amd2	S-adenosylmethionine decarboxylase 2 (Amd2)	1.6480	7.07E-04	0.0440
Krr1	KRR1, small subunit (SSU) processome component, homolog (yeast) (Krr1)	1.6468	7.08E-04	0.0440
Wnt10b	wingless related MMTV integration site 10b (Wnt10b)	1.6459	7.11E-04	0.0440
Tnfaip3	tumor necrosis factor, alpha-induced protein 3 (Tnfaip3)	1.6330	7.85E-04	0.0455
Tlr2	toll-like receptor 2 (Tlr2)	1.6326	5.38E-04	0.0383
Tmed3	transmembrane emp24 domain containing 3 (Tmed3)	1.6311	4.82E-05	0.0113
Spire1	spire homolog 1 (<i>Drosophila</i>) (Spire1), transcript variant 2	1.6306	2.84E-04	0.0288
Cd86	CD86 antigen (Cd86)	1.6260	1.54E-04	0.0206
Rassf4	Ras association (RalGDS/AF-6) domain family member 4 (Rassf4)	1.6144	5.96E-04	0.0403
Trub1	TruB pseudouridine (psi) synthase homolog 1 (<i>E. coli</i>) (Trub1), transcript variant 1	1.5861	3.65E-04	0.0316
Aldh3b1	aldehyde dehydrogenase 3 family, member B1 (Aldh3b1)	1.5645	5.39E-04	0.0383
Mpp6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6) (Mpp6)	1.5542	1.67E-05	0.0084
Lrp11	low density lipoprotein receptor-related protein 11 (Lrp11)	1.5538	2.93E-05	0.0097
Sh3bgrl2	SH3 domain binding glutamic acid-rich protein like 2 (Sh3bgrl2)	1.5504	3.23E-04	0.0308
Cdkn2a	cyclin-dependent kinase inhibitor 2A (Cdkn2a), transcript variant 1	1.5485	1.33E-05	0.0083
Cdc42bbp	CDC42 binding protein kinase beta (Cdc42bbp)	1.5456	3.88E-04	0.0318
LOC100046608	PREDICTED: <i>Mus musculus</i> similar to Bcl2-like protein (LOC100046608)	1.5320	5.47E-04	0.0383
Dctd	dCMP deaminase (Dctd)	1.5312	5.63E-05	0.0115
BC048355	cDNA sequence BC048355	1.5300	9.22E-04	0.0495
Arl5c	ADP-ribosylation factor-like 5C (Arl5c)	1.5262	3.76E-04	0.0316
Gpr120	G protein-coupled receptor 120 (Gpr120)	1.5202	7.51E-04	0.0451
2700062C07Rik	RIKEN cDNA 2700062C07 gene (2700062C07Rik)	1.5171	8.44E-04	0.0468

Table S2. Significantly downregulated genes in LMP2A/λ-MYC pretumor B cells

Symbol	Definition	Fold change	p-value	false discovery rate
Vpreb1	pre-B lymphocyte gene 1 (Vpreb1)	-7.7424	6.13E-05	0.0120
Rsph1	radial spoke head 1 homolog (Chlamydomonas) (Rsph1)	-7.4494	3.65E-06	0.0033
Myl4	myosin, light polypeptide 4 (Myl4)	-3.8564	5.12E-05	0.0113
Tnfrsf19	tumor necrosis factor receptor superfamily, member 19 (Tnfrsf19)	-3.2686	6.08E-05	0.0120
Atp1b1	ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide (Atp1b1)	-3.2529	1.57E-05	0.0083
Il7r	interleukin 7 receptor (Il7r)	-3.1715	7.84E-05	0.0135
Bach2	BTB and CNC homology 2 (Bach2)	-3.0149	3.90E-05	0.0109
Laptm5	lysosomal-associated protein transmembrane 5 (Laptm5)	-2.9751	3.59E-04	0.0316
Tmem132e	transmembrane protein 132E (Tmem132e)	-2.9319	3.20E-06	0.0031
Tes	testis derived transcript (Tes), transcript variant 1	-2.8828	4.60E-08	0.0003
Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast) (Elovl6)	-2.8645	2.92E-05	0.0097
Sertad4	SERTA domain containing 4 (Sertad4)	-2.8603	9.04E-06	0.0070
Btrc	beta-transducin repeat containing protein (Btrc), transcript variant 1	-2.8491	1.32E-04	0.0186
Satb1	special AT-rich sequence binding protein 1 (Satb1)	-2.7133	4.15E-05	0.0112
Plcd3	phospholipase C, delta 3 (Plcd3)	-2.6771	9.95E-06	0.0071
1700027N10Rik	RIKEN cDNA 1700027N10 gene (1700027N10Rik)	-2.6412	4.24E-05	0.0112
Zcchc18	zinc finger, CCHC domain containing 18 (Zcchc18), transcript variant 3	-2.5319	7.19E-08	0.0003
Emid1	EMI domain containing 1 (Emid1)	-2.4252	2.43E-04	0.0262
Marcks	myristoylated alanine rich protein kinase C substrate (Marcks)	-2.3969	5.43E-05	0.0114
Hvcn1	hydrogen voltage-gated channel 1 (Hvcn1)	-2.3613	7.25E-05	0.0127
Dntt	deoxynucleotidyltransferase, terminal (Dntt), transcript variant 2	-2.3599	6.27E-04	0.0412
Arpp21	cyclic AMP-regulated phosphoprotein, 21 (Arpp21), transcript variant 2	-2.3511	2.24E-04	0.0256
D230007K08Rik	PREDICTED: RIKEN cDNA D230007K08 gene, transcript variant 5 (D230007K08Rik)	-2.3456	1.75E-06	0.0021
Fgf13	fibroblast growth factor 13 (Fgf13)	-2.3338	1.56E-05	0.0083
Ell3	elongation factor RNA polymerase II-like 3 (Ell3)	-2.3034	2.01E-05	0.0087
9630015D15Rik	RIKEN cDNA 9630015D15 gene (9630015D15Rik)	-2.2662	6.24E-04	0.0412
Palm	paralemmin (Palm)	-2.2504	8.77E-05	0.0142
Islr2	immunoglobulin superfamily containing leucine-rich repeat 2 (Islr2)	-2.2048	1.32E-05	0.0083
9830002I17Rik	RIKEN cDNA 9830002I17 gene (9830002I17Rik)	-2.1742	5.13E-04	0.0383
Hvcn1	hydrogen voltage-gated channel 1 (Hvcn1), transcript variant 1	-2.1615	5.79E-05	0.0117
Coq7	demethyl-Q 7 (Coq7)	-2.1427	4.95E-05	0.0113
Arntl	aryl hydrocarbon receptor nuclear translocator-like (Arntl)	-2.1333	2.05E-04	0.0245
Slpi	secretory leukocyte peptidase inhibitor (Slpi)	-2.1154	2.92E-06	0.0030
Wwc2	WW, C2 and coiled-coil domain containing 2 (Wwc2)	-2.1105	6.16E-04	0.0410
Cnp	2',3'-cyclic nucleotide 3' phosphodiesterase (Cnp)	-2.0918	5.30E-04	0.0383
Axl	AXL receptor tyrosine kinase (Axl)	-2.0663	1.71E-04	0.0221
Rem2	rad and gem related GTP binding protein 2 (Rem2)	-2.0658	4.30E-05	0.0112
Inpp5d	inositol polyphosphate-5-phosphatase D (Inpp5d)	-2.0513	8.59E-05	0.0141
Cfp	complement factor properdin (Cfp)	-2.0184	1.39E-05	0.0083
D930015E06Rik	RIKEN cDNA D930015E06 gene (D930015E06Rik)	-2.0101	5.16E-05	0.0113
Tmc7	transmembrane channel-like gene family 7 (Tmc7)	-2.0005	6.63E-04	0.0430
Tmem108	transmembrane protein 108 (Tmem108)	-1.9843	1.36E-04	0.0188
Rasgrp3	RAS, guanyl releasing protein 3 (Rasgrp3)	-1.9760	7.99E-04	0.0459
Dtx1	deltex 1 homolog (Drosophila) (Dtx1)	-1.9409	9.55E-05	0.0149
Zfp608	zinc finger protein 608 (Zfp608)	-1.9343	1.27E-06	0.0021
Nrarp	Notch-regulated ankyrin repeat protein (Nrarp)	-1.9133	1.59E-04	0.0209
Socs2	suppressor of cytokine signaling 2 (Socs2)	-1.9105	5.17E-04	0.0383
Capsl	calcyphosine-like (Capsl)	-1.8892	1.70E-05	0.0084
Fam101a	family with sequence similarity 101, member A (Fam101a)	-1.8892	1.64E-06	0.0021
Abi3	ABI family member 3 (Abi3)	-1.8833	6.83E-04	0.0435

Rgs12	regulator of G-protein signaling 12 (Rgs12)	-1.8795	2.55E-05	0.0095
Tax1bp3	Tax1 (human T-cell leukemia virus type I) binding protein 3 (Tax1bp3)	-1.8517	1.34E-04	0.0187
Lxn	latexin (Lxn)	-1.8513	3.53E-05	0.0105
Smtn	smoothelin (Smtn)	-1.8487	1.22E-04	0.0180
Otub2	OTU domain, ubiquitin aldehyde binding 2 (Otub2)	-1.8374	3.79E-04	0.0316
Btrc	beta-transducin repeat containing protein (Btrc), transcript variant 2	-1.8347	7.71E-04	0.0455
Serpina3g	serine (or cysteine) peptidase inhibitor, clade A, member 3G (Serpina3g)	-1.8213	4.30E-04	0.0334
Sdc3	syndecan 3 (Sdc3)	-1.8147	8.08E-04	0.0461
Pde2a	phosphodiesterase 2A, cGMP-stimulated (Pde2a)	-1.8130	4.12E-04	0.0328
Pik3cd	phosphatidylinositol 3-kinase catalytic delta polypeptide (Pik3cd), transcript variant 1	-1.7952	9.24E-04	0.0495
Dpp4	dipeptidylpeptidase 4 (Dpp4)	-1.7768	2.29E-04	0.0256
Marcksl1	MARCKS-like 1 (Marcksl1)	-1.7610	2.23E-04	0.0256
Skil	SKI-like (Skil), transcript variant 2	-1.7539	5.39E-04	0.0383
Axud1	AXIN1 up-regulated 1 (Axud1)	-1.7426	8.20E-05	0.0139
Spnb2	spectrin beta 2 (Spnb2), transcript variant 2	-1.7370	1.16E-04	0.0174
Ccr6	chemokine (C-C motif) receptor 6 (Ccr6)	-1.7219	5.22E-05	0.0113
Fam169b	family with sequence similarity 169, member B (Fam169b)	-1.7169	2.97E-04	0.0294
Tspan6	tetraspanin 6 (Tspan6)	-1.7141	2.92E-04	0.0292
Pip5k1b	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta (Pip5k1b)	-1.7043	4.10E-04	0.0328
Stk17b	serine/threonine kinase 17b (apoptosis-inducing) (Stk17b)	-1.6932	7.05E-04	0.0440
Atp2a3	ATPase, Ca ⁺⁺ transporting, ubiquitous (Atp2a3)	-1.6857	8.81E-05	0.0142
Abcb4	ATP-binding cassette, sub-family B (MDR/TAP), member 4 (Abcb4)	-1.6821	3.17E-04	0.0308
Sord	sorbitol dehydrogenase (Sord)	-1.6788	1.42E-04	0.0193
Ptk2b	PTK2 protein tyrosine kinase 2 beta (Ptk2b)	-1.6725	3.36E-04	0.0309
Dyrk1b	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1b (Dyrk1b), transcript variant 1	-1.6705	2.19E-06	0.0024
Plekha2	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 2 (Plekha2)	-1.6678	1.44E-05	0.0083
Insl6	insulin-like 6 (Insl6)	-1.6587	6.67E-05	0.0122
Amz2	archaelysin family metallopeptidase 2 (Amz2)	-1.6552	1.15E-05	0.0078
Dusp23	dual specificity phosphatase 23 (Dusp23)	-1.6485	4.87E-05	0.0113
Lgr5	leucine rich repeat containing G protein coupled receptor 5 (Lgr5)	-1.6437	2.57E-04	0.0271
Rdm1	RAD52 motif 1 (Rdm1)	-1.6433	3.59E-04	0.0316
Zkscan17	zinc finger with KRAB and SCAN domains 17 (Zkscan17)	-1.6422	6.46E-05	0.0122
Smarca4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 (Smarca4)	-1.6348	5.70E-04	0.0392
Cc2d1b	coiled-coil and C2 domain containing 1B (Cc2d1b)	-1.6346	3.83E-04	0.0317
9530077C05Rik	RIKEN cDNA 9530077C05 gene (9530077C05Rik)	-1.6173	2.31E-04	0.0256
Parp8	poly (ADP-ribose) polymerase family, member 8 (Parp8)	-1.6172	7.29E-05	0.0127
Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1 (Enpp1)	-1.6124	3.72E-04	0.0316
Sft2d2	SFT2 domain containing 2 (Sft2d2)	-1.6095	2.59E-04	0.0271
LOC675228	PREDICTED: Mus musculus similar to vacuolar ATPase subunit F (LOC675228)	-1.5997	2.10E-04	0.0248
Ffar2	free fatty acid receptor 2 (Ffar2)	-1.5953	6.18E-05	0.0120
Xrcc6	X-ray repair complementing defective repair in Chinese hamster cells 6 (Xrcc6)	-1.5828	5.18E-04	0.0383
Lck	lymphocyte protein tyrosine kinase (Lck)	-1.5824	2.72E-05	0.0095
Msh5	mutS homolog 5 (E. coli) (Msh5)	-1.5785	1.22E-04	0.0180
Epsti1	epithelial stromal interaction 1 (breast) (Epsti1), transcript variant a	-1.5781	3.18E-04	0.0308
Dusp6	dual specificity phosphatase 6 (Dusp6)	-1.5771	3.22E-04	0.0308
Col18a1	procollagen, type XVIII, alpha 1 (Col18a1)	-1.5710	2.31E-04	0.0256
Fmnl3	formin-like 3 (Fmnl3)	-1.5701	1.31E-04	0.0186
Slamf9	SLAM family member 9 (Slamf9)	-1.5673	5.85E-04	0.0397
Ulk1	Unc-51 like kinase 1 (C. elegans) (Ulk1)	-1.5634	6.61E-04	0.0430
Itgad	integrin, alpha D (Itgad)	-1.5609	3.33E-04	0.0309
St8sia4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4 (St8sia4)	-1.5571	2.15E-05	0.0088

Csrp2	cysteine and glycine-rich protein 2 (Csrp2)	-1.5460	7.56E-04	0.0451
Tap1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) (Tap1)	-1.5434	8.62E-04	0.0469
Zfp428	zinc finger protein 428 (Zfp428)	-1.5410	2.68E-05	0.0095
BC057627	cDNA sequence BC057627 (BC057627)	-1.5392	3.93E-04	0.0318
Bhlhb2	basic helix-loop-helix domain containing, class B2 (Bhlhb2)	-1.5344	5.81E-04	0.0396
Pard6g	par-6 partitioning defective 6 homolog gamma (C. elegans) (Pard6g)	-1.5199	5.43E-04	0.0383
4933428G20Rik	RIKEN cDNA 4933428G20 gene (4933428G20Rik)	-1.5132	3.76E-04	0.0316
Gstp2	glutathione S-transferase, pi 2 (Gstp2)	-1.5036	3.75E-05	0.0108
Rnf31	ring finger protein 31 (Rnf31)	-1.5007	8.52E-05	0.0141