SUPPLEMENTARY INFORMATION

The MHC I immunopeptidome conveys to the cell surface an integrative view of cellular regulation

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- **Table S5.** List of components from a comprehensive mTOR interactome and signalling network.

- **Table S6.** Relative expression of DEM source genes at multiple regulatory layers.

- **Table S7.** List of primers for quantitative real-time PCR analyses.

Supplementary methods

1. Label-free quantitative proteomics approach

Label-free quantitative proteomics analyses were performed using ProteoProfile an in-house software that comprises three different modules. The peptide detection module generates an exportable .csv file that includes peptide features (m/z value, charge, retention time, intensity, score) subsequently used for clustering analyses. Intensity threshold was typically set to 10,000 counts for Orbitrap LC-MS experiments. Peptide identified by Mascot are then aligned with their corresponding peptide maps and their intensities across replicates and conditions are correlated by the clustering module using a complete linkage hierarchical clustering algorithm similar to that of Bellew et al (Bellew M., Coram M., Fitzgibbon M., Igra M., Randolph T., Wang P., May D., Eng J., Fang R., Lin C., Chen J., Goodlett, D., Whiteaker J., Paulovich A., McIntosh M. (2006) A suite of algorithms for the comprehensive analysis of complex protein mixtures using high-resolution LC-MS Bioinformatics 22 1902-1909). Initially, m/z tolerance of ±0.035 Th and a time difference of 1 min are used for clustering. Normalization of retention time is then performed on the initial peptide cluster list using a dynamic and nonlinear correction. A moving-average time-window interpolation scheme is used to compute the time shifts for each peptide across the different data sets. This alignment confines the retention time distribution to less than ± 0.1 min (< 0.3% RSD) on average. Following normalization, peptides are then re-clustered using the complete linkage hierarchical clustering algorithm but with a tighter time tolerance (typically 30 seconds). This clustering analysis enables the comparison of abundance distribution for peptide ions sharing the same m/z, time, charge coordinates. We required confident peptide detection in at least two out of three replicate LC-MS analyses to consider a cluster for subsequent analysis. A simple heuristic function referred to as missing peaks was developed to retrieve missing peptide ions. After clustering, missing peaks will query the raw data for any replicates missing within a given cluster due to low intensity or false negative detection errors. The m/z and retention time of the average peptide clusters are used as a starting point in searching the raw data of the missing peptide. By using the time normalisation function, adjustment of target time is performed to efficiently locate the coordinates of missing peptide. Peak apex located within ± 0.035 Th and ±1 min of the target peptide coordinates is then considered. The RSD value of the retrieved peak must be within typically ± 25 % of the average cluster intensity to be considered. In 2D LC-MS data, clustering is performed across salt fractions to combine the intensities of the same peptide found over adjacent fractions (typically £ 2). Differentially abundant peptides were selected on the basis of their statistical significance ($p \leq 0.05$ using a paired t-test) and reproducibility of the control to challenge peptide-intensity ratio (at least 2-fold in 2 out of 3 replicate runs). The data generated by the clustering program and the peptide maps are available as Excel .csv file and can be included in downstream programs for further analysis. Peptide ions of interest were manually validated using the validation module that enables the verification of all ions assigned to a specific peptide cluster.

2. PHP script for MHC class I peptide selection

```
function isMHCpeptide($pepseq) {
$peplength = strlen($pepseq);
$poslast = substr($pepseq, $peplength -1, 1);
if ($peplength >= 8 && $peplength <= 9) {
$pos3 = substr($pepseq, 2, 1);
$pos5 = substr($pepseq, 4, 1);
$pos7 = substr($pepseq, 6, 1);
if (preg_match('/[ILVMF]/', $poslast) && ((preg_match('/[YF]/', $pos3) && $peplength == 8) ||
preg_match('/[YF]/', $pos5) ||
(preg_match('/[H]/', $pos7) && $peplength == 9) || (preg_match('/[N]/', $pos5) && $peplength
== 9))) {
return 1;
} else
if ($peplength == 9 && preg_match('/LLL$/', $pepseq)) {
return 1;
}
} else
if ($peplength >= 10 && $peplength <= 13) {
$pos5 = substr($pepseq, 4, 1);
if (preg_match('/[N]/', $pos5) && preg_match('/[ILVMF]/', $poslast)) {
return 1;
}
}
return 0;
}
```

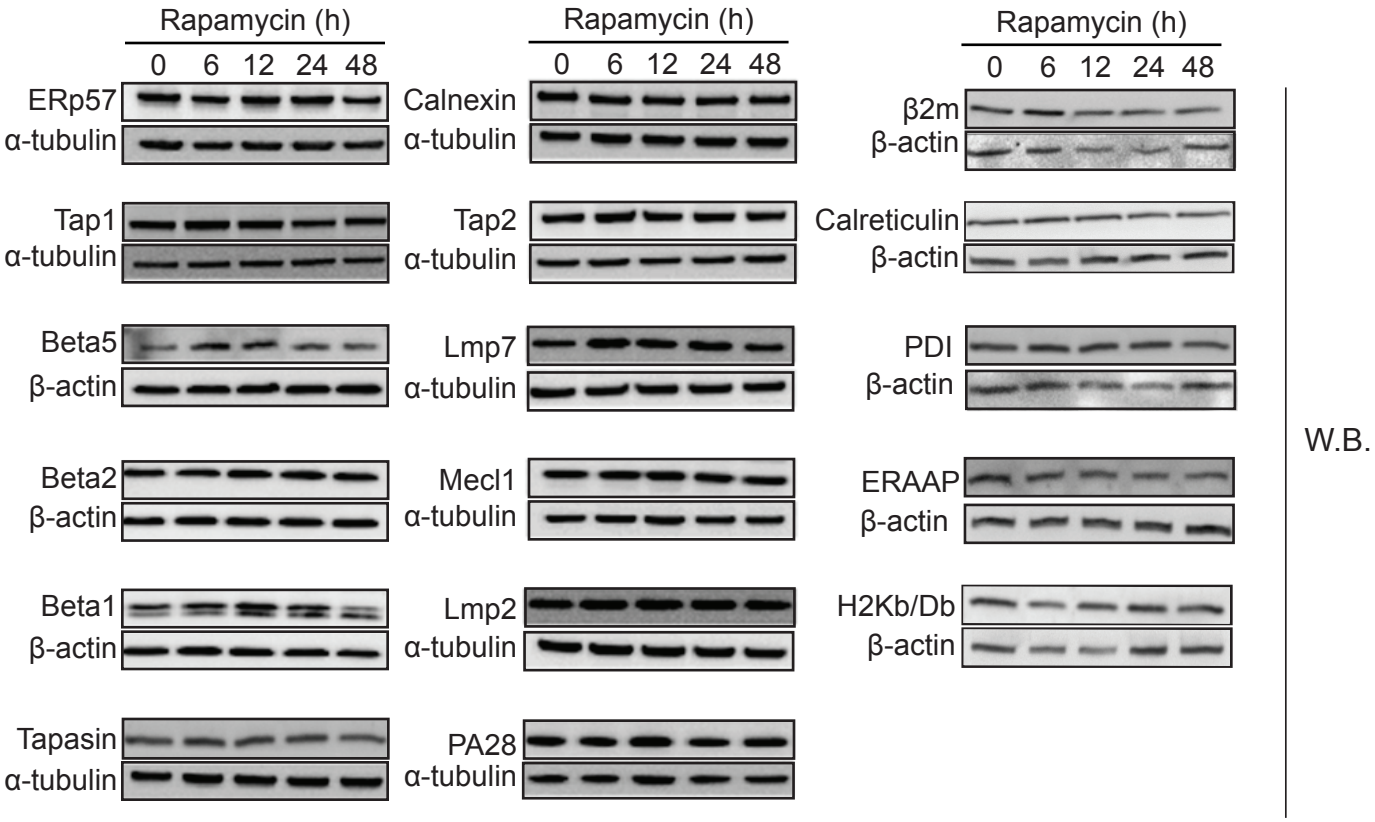

Figure S1. Rapamycin does not affect levels of proteins involved in the antigen processing and presentation pathway (Jensen *et al.,* 2007). Levels of the indicated proteins were determined by western blotting. β-actin and α-tubulin served as loading controls. Data are representative of three independent experiments.

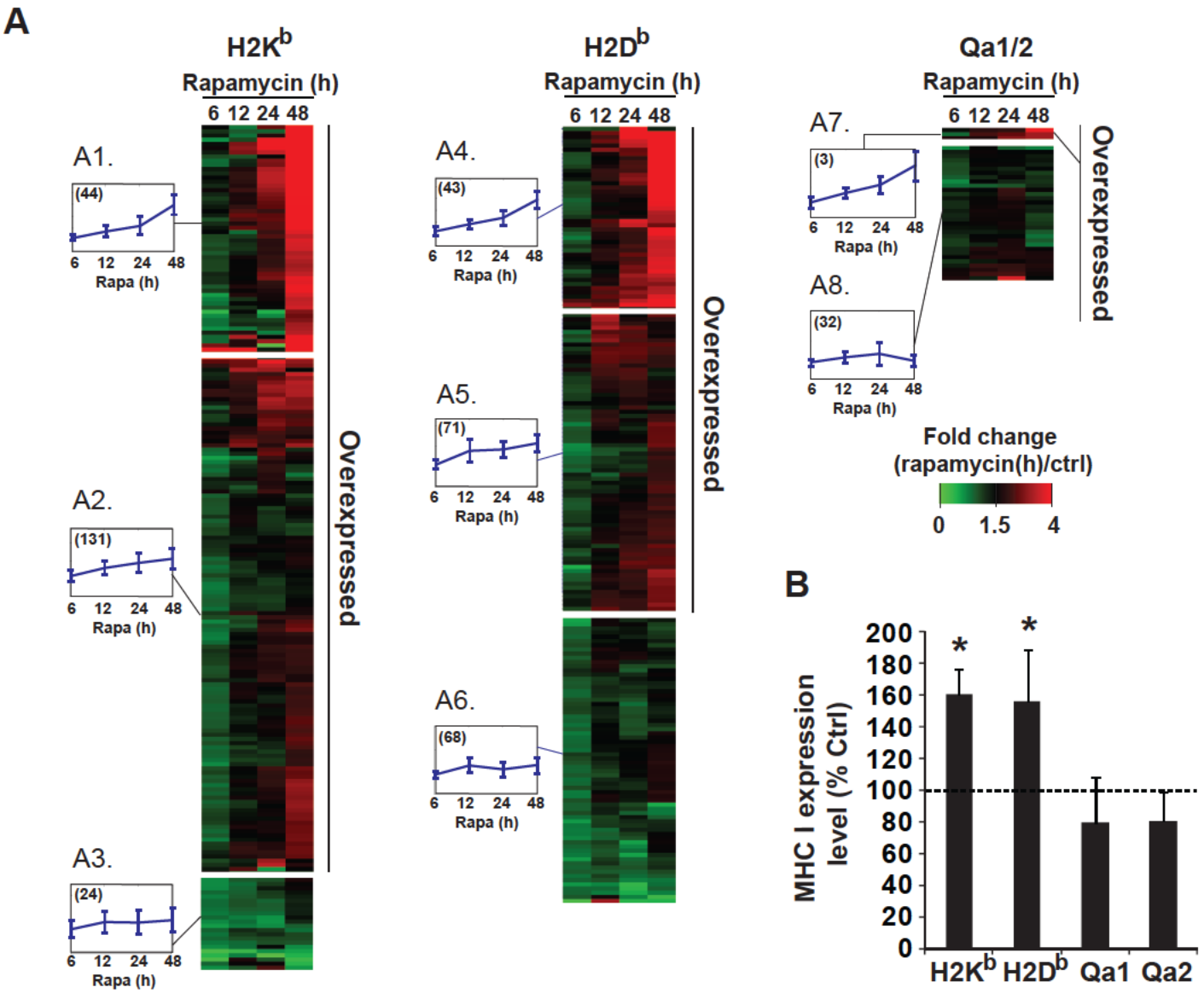

Figure S2. Rapamycin increases the abundance of MIPs presented by MHC Ia molecules. (**A**) Representation of unsupervised hierarchical clustering of 416 MIPs detected and quantified at different time points. 6 MIPs were detected exclusively after 48h of rapamycin treatment and were not included in the clustering analysis. MIPs are represented vertically, and experimental conditions (i.e., rapamycin time course) are displayed horizontally. Clusters for $H2K^b$-, $H2D^b$-, and Qa1/2-associated peptides are shown with the mean temporal profile in A1-A8. The number of MIPs per cluster is indicated in parenthesis. Clusters A1,2,4,5 and 7 show MIPs that were progressively overexpressed upon rapamycin treatment. (**B**) Cell surface expression of MHC I allelic products was evaluated by flow cytometry after 48h of rapamycin treatment. Histogram shows the rapamycin/ctrl mean fluorescence intensity ratio for $H2K^b$, $H2D^b$, Qa1, and Qa2. (n=6, $*P < 0.005$, Student *t*-test).

A

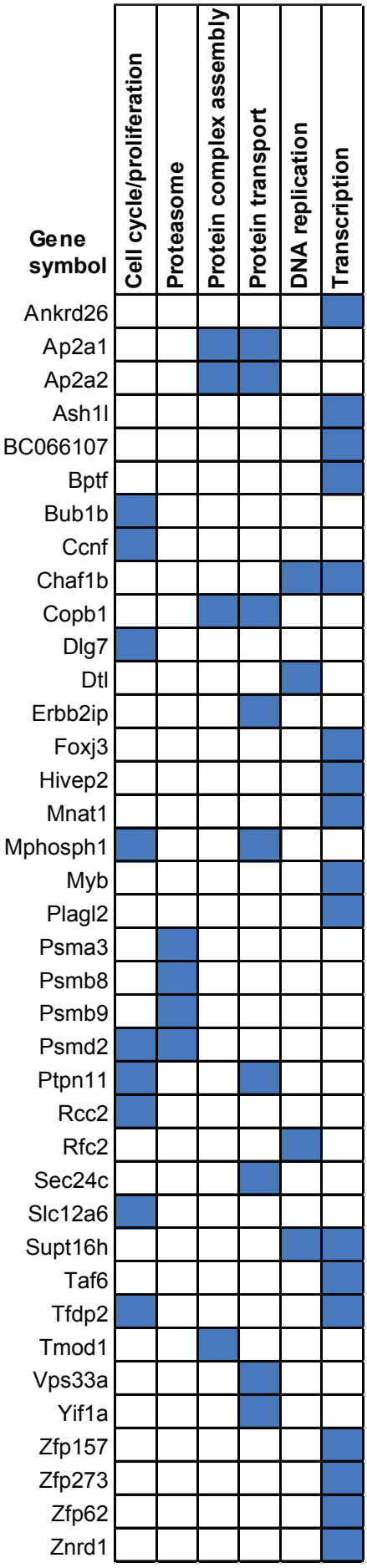

Figure S3. Cellular processes enriched in the DEM source genes or the DEGs. (**A**) Representation of 38 genes encoding DEMs (rows) in 6 cellular processes (columns) that were enriched in the GO analysis. See also Supplementary Table S2.

B

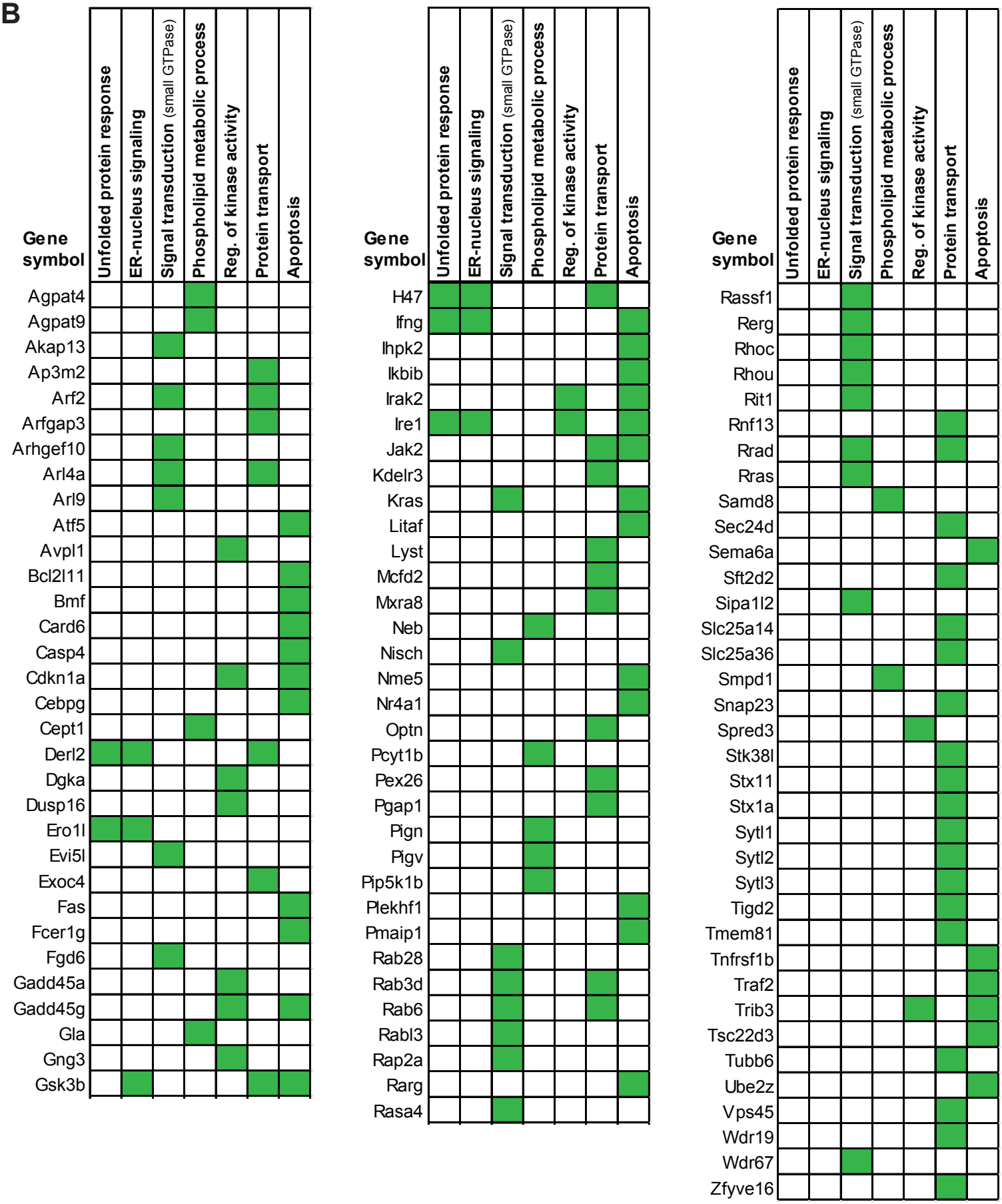

Figure S3 continued. Cellular processes enriched in the DEM source genes or the DEGs. (**B**) Representation of 101 underexpressed genes (rows) in 7 cellular processes (columns) that were enriched in the GO analysis. See also Supplementary Table S2.

C

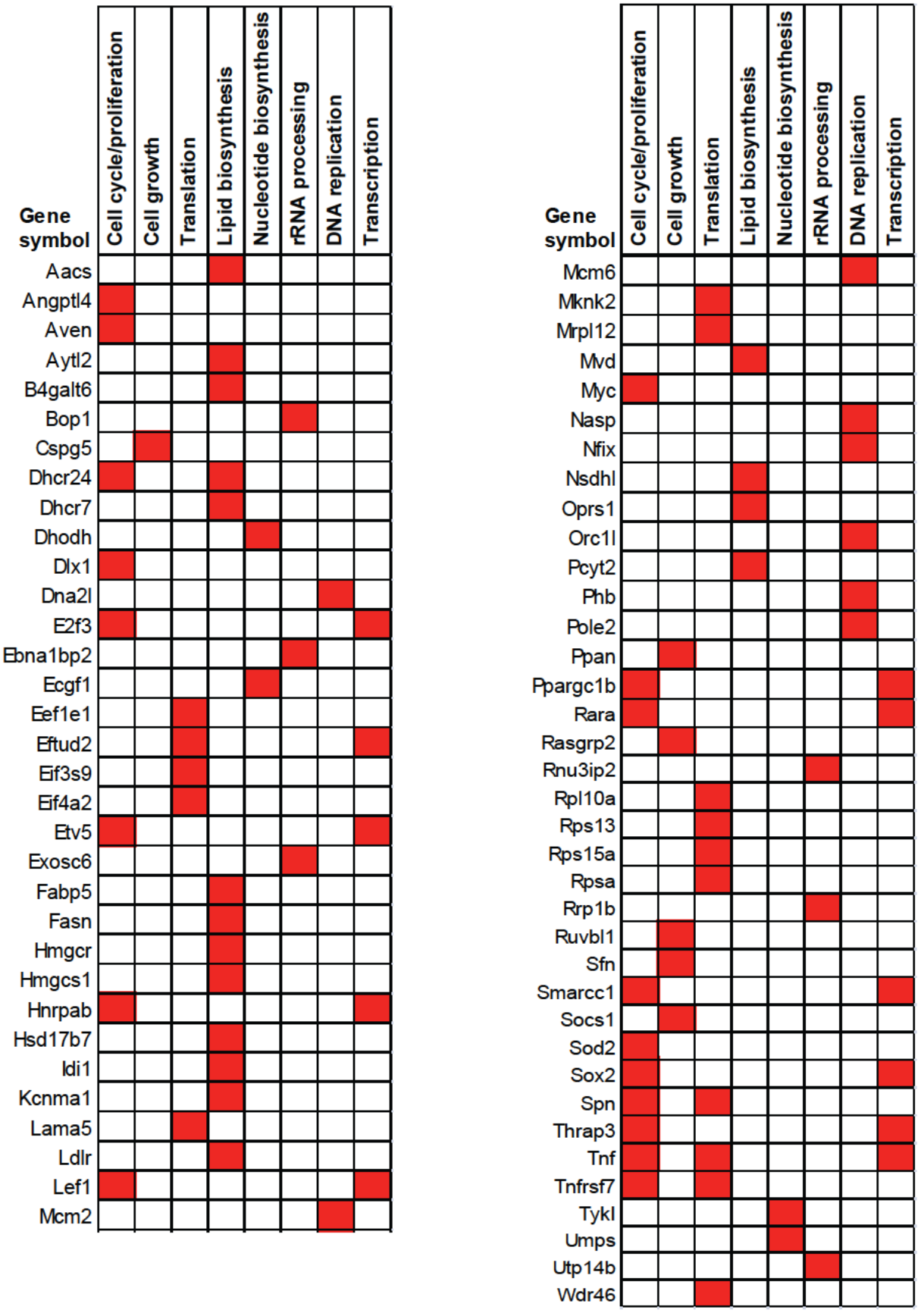

Figure S3 continued. Cellular processes enriched in the DEM source genes or the DEGs. (**C**) Representation of 70 overexpressed genes (rows) in 8 functional classes (columns) that were enriched in the GO analysis. See also Supplementary Table S2.

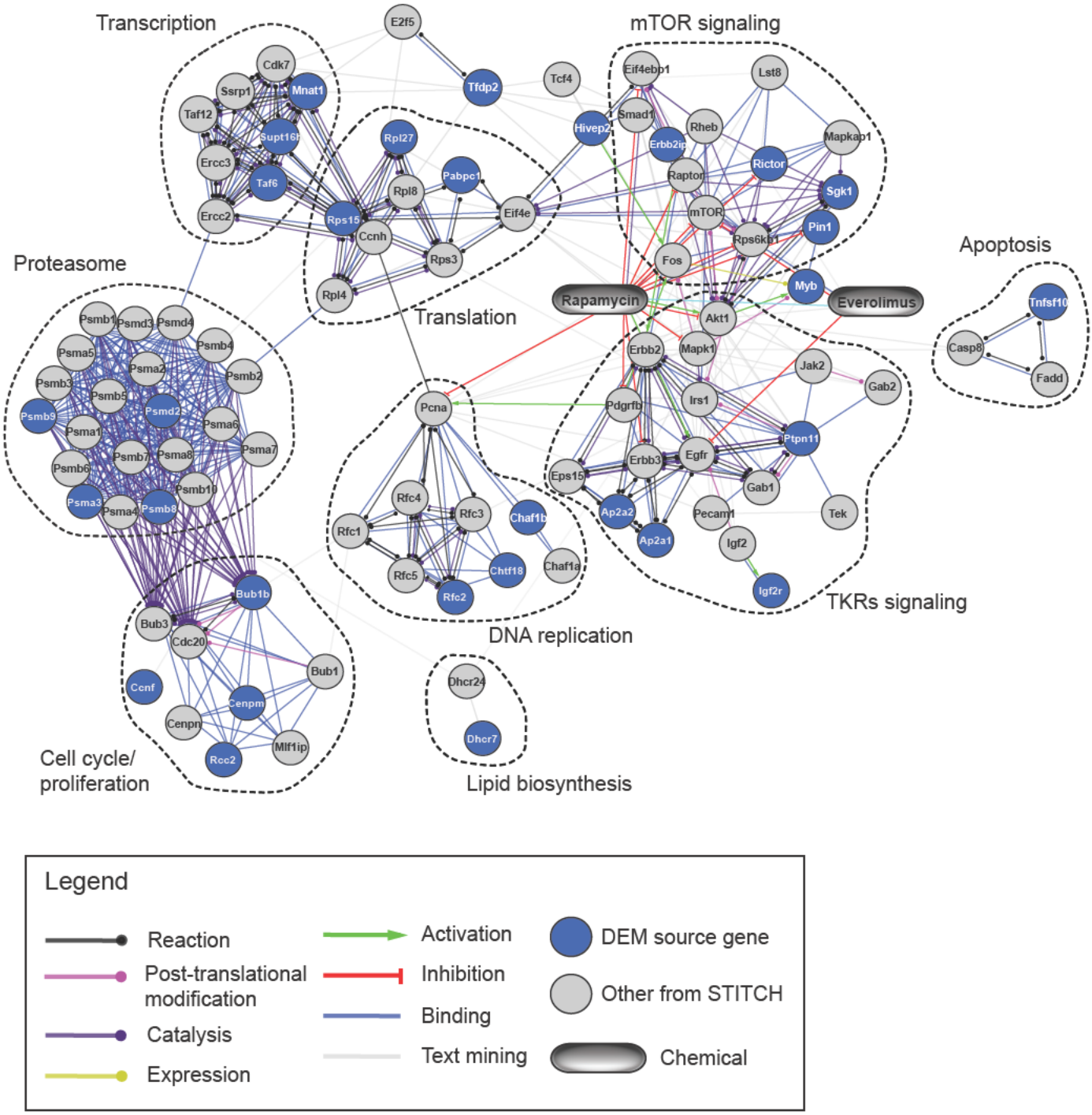

Figure S4. DEM source genes are involved in cellular processes and signaling events governed by the mTOR network. Source genes encoding DEMs were analyzed with the STITCH database (http://stitch.embl.de/) and the network was elucidated based upon protein-protein interactions, protein-chemical associations, and functional associations. The emerging network elucidates a total of 30 DEM source genes distributed within different subnetworks, such as apoptosis, cell cycle/proliferation, DNA replication, lipid biosynthesis, proteasome, transcription, translation, mTOR signaling and tyrosine kinase receptors (TKRs) signaling. Rapamycin and everolimus (rapamycin analog) are the 2 unique chemicals that were revealed in the network. Symbols and arrows in the network are illustrated in the legend.

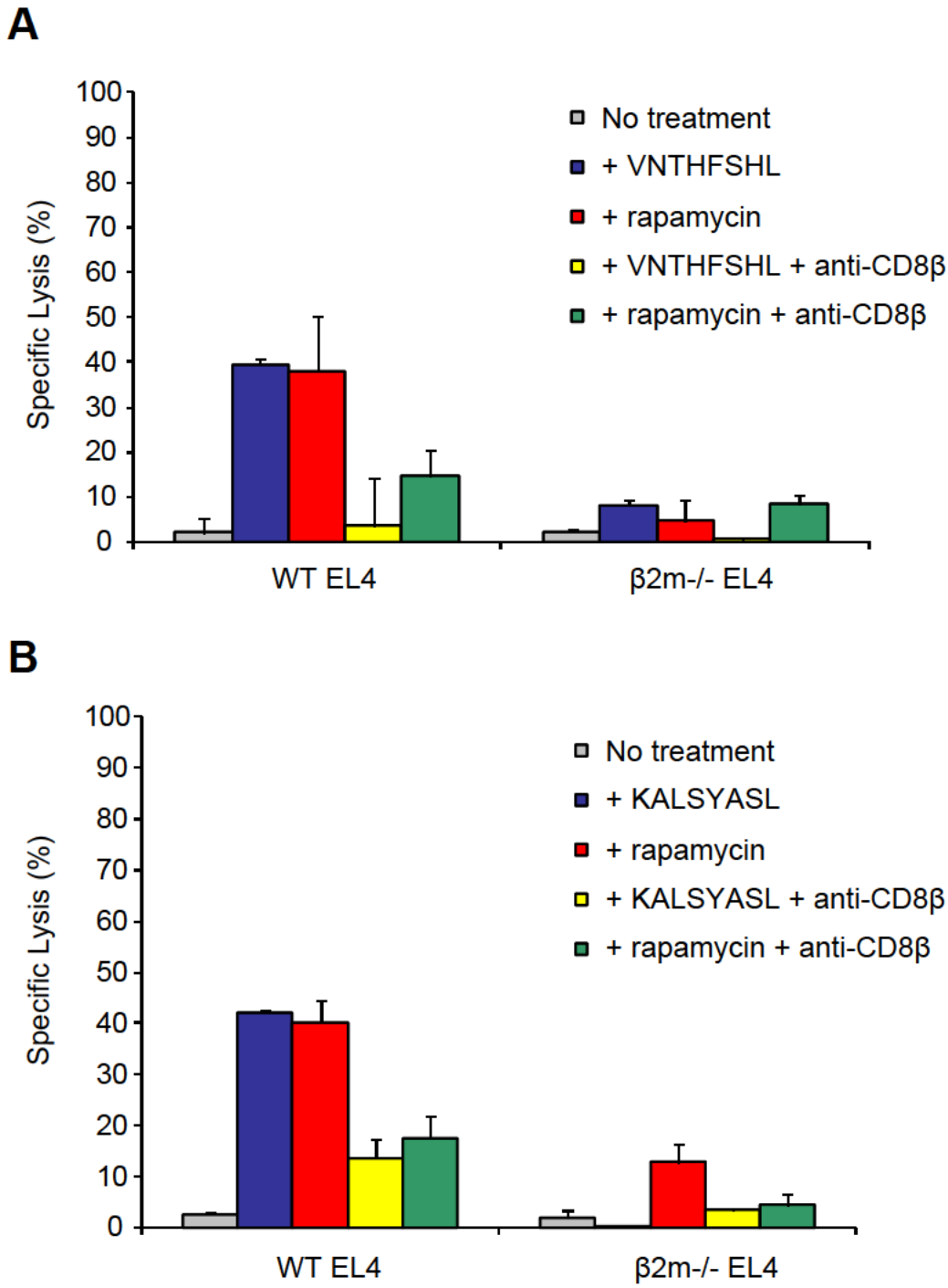

Figure S5. Cytotoxic activity against VNTHFSHL and KALSYASL is MHC-I restricted. Specific lysis against wild-type and β2-microglobullin deficient CFSE-labeled EL4 cells (Fortier *et al.*, 2008) was estimated as in figure 7 at E:T ratio of 200:1 in the presence or absence of 5mg/ml of anti-CD8β antibody (clone H35-17.2). Data represent the mean ± SD for three mice per group.

Table S3. GO terms enriched in DEM source genes and DEGs. DAVID bioinformatics resources (http://david.abcc.ncifcrf.gov/) were used to identify enriched biological processes (P<0.05) associated to DEGs and to genes coding for DEMs. Functionally related GO terms were annoted within unique cellular processes (last column). Biological processes enriched in DEM source genes are highlighted in blue. Biological processes enriched in over- and underexpressed mRNAs are highlighted in red and green, respectively.

	GO term	GO number	Genes in sample	p value	Gene symbol	Cellular processes in Figure 3 and Supplementary Figure S3
Biological processes enriched in DEM source genes	Regulation of progression through cell cycle	GO:0000074	7	0.007	Bub1b, Ccnf, Ptpn11, Psmd2, Slc12a6, Tfdp2, Dlg7	Cell cycle/proliferation
	M phase of mitotic cell cycle	GO:0000087	5	0.012	Bub1b, Ccnf, Rcc2, Dlg7, Mphosph1	
	DNA replication	GO:0006260	4	0.044	Rfc2, Dtl, Chaf1b, Supt16h	DNA replication
	Transcription, DNA-dependent	GO:0006351	17	0.042	Hivep2, Mnat1, Myb, Taf6, Zfp62, Plagl2, Znrd1, Zfp157, Chaf1b, Supt16h, Ash1l, Bptf, Tfdp2, Zfp273, Foxj3, Ankrd26, BC066107	Transcription
	Regulation of transcription, DNA-dependent	GO:0006355	17	0.038	Hivep2, Mnat1, Myb, Taf6, Zfp62, Plagl2, Znrd1, Zfp157, Chaf1b, Supt16h, Ash1l, Bptf, Tfdp2, Zfp273, Foxj3, Ankrd26, BC066107	
	Protein complex assembly	GO:0006461	4	0.047	Ap2a1, Ap2a2, Tmod1, Copb1	Protein complex assembly
	Intracellular transport	GO:0046907	8	0.048	Ptpn11, Erbb2ip, Sec24c, Mphosph1, Ap2a1, Ap2a2, Yif1a, Copb1	Protein transport
	Protein transport	GO:0015031	8	0.043	Ptpn11, Erbb2ip, Sec24c, Vps33a, Ap2a1, Ap2a2, Yif1a, Copb1	
	Proteasome complex	GO:0000502	4	0.011	Psma3, Psmb8, Psmb9, Psmd2	Proteasome
Biological processes enriched in DEGs (overexpressed mRNAs)	Translation	GO:0006412	15	0.012	Lama5, Rpl10a, Eif3s9, Mknk2, Wdr46, Rpsa, Eif4a2, Rps15a, Mrpl12, Eftud2, Tnf, Eef1e1, Spn, Tnfrsf7, Rps13	Translation
	DNA replication	GO:0006260	8	0.010	Pole2, Mcm2, Mcm6, Dna2l, Nfix, Orc1l, Phb, Nasp	DNA replication
	Positive regulation of cellular metabolic process	GO:0031325	19	0.037	E2f3, Lef1, Ppargc1b, Smarcc1, Etv5, Hnrpab, Thrap3, Tnf, Tnfrsf7, Rara, Spn, Sox2, Myc, Dhcr24, Aven, Sod2, Tnfrsf7, Dlx1, Angptl4	Cell cycle/proliferation
	Steroid biosynthetic process	GO:0006694	9	0.00001	Dhcr7, Dhcr24, Hmgcr, Idi1, Oprs1, Hsd17b7, Mvd, Nsdhl, Hmgcs1	Lipid biosynthesis (sterol)
	Steroid metabolic process	GO:0008202	11	0.00006	Kcnma1, Ldlr, Dhcr7, Dhcr24, Hmgcr, Idi1, Oprs1, Hsd17b7, Mvd, Nsdhl, Hmgcs1	
	Cholesterol metabolic process	GO:0008203	9	0.00001	Dhrc7, Hmgcr, Hsd17b7, Ldlr, Nsdhl, Dhcr24, Mvd, Hmgcs1, Idi1	
	Lipid biosynthetic process	GO:0008610	15	0.00001	Dhcr7, Fasn, Hmgcr, Hsd17b7, Fabp5, Nsdhl, Oprs1, B4galt6, Pcyt2, Dhcr24, Aacs, Mvd, Hmgcs1, Aytl2, Idi1	
	Sterol metabolic process	GO:0016125	10	0.000001	Dhrc7, Hmgcr, Hsd17b7, Ldlr, Nsdhl, Oprs1, Dhcr24, Mvd, Hmgcs1, Idi1	
	Sterol biosynthetic process	GO:0016126	9	0.00000001	Dhrc7, Hmgcr, Hsd17b7, Nsdhl, Oprs1, Dhcr24, Mvd, Hmgcs1, Idi1	
	rRNA processing	GO:0006364	6	0.001	Rrp1b, Exosc6, Utp14b, Bop1, Rnu3ip2, Ebna1bp2	rRNA processing
	RNA processing	GO:0006396	17	0.0001	Sf3b3, Rrp1b, Ppih, 6720458F09Rik, Syncrip, Hnrpab, Magoh, Bop1, Rnu3ip2, Ddx54, Pusl1, Lsm7, Exosc6, Eftud2, Utp14b, Lsm2, Ebna1bp2	Transcription
	Positive regulation of transcription, DNA-dependent	GO:0045893	9	0.043	E2f3, Hnrpab, Lef1, Rara, Smarcc1, Eftud2, Tnf, Ppargc1b, Thrap3	
	Positive regulation of transcription	GO:0045941	10	0.047	Etv5, E2f3, Hnrpab, Lef1, Rara, Smarcc1, Eftud2, Tnf, Ppargc1b, Thrap3	

	Pyrimidine base metabolic process	GO:0006206	3	0.008	Dhodh, Ecgf1, Umps	Nucleotide biosynthesis
	Pyrimidine nucleotide biosynthetic process	GO:0006221	4	0.003	Tyki, Dhodh, Ecgf1, Umps	
	Nucleobase metabolic process	GO:0009112	3	0.026	Dhodh, Ecgf1, Umps	
	Regulation of cell size	GO:0008361	6	0.044	Cspg5, Sfn, Ruvbl1, Socs1, Rasgrp2, Ppan	Cell growth
	Regulation of cell growth	GO:0001558	6	0.015	Cspg5, Sfn, Ruvbl1, Socs1, Rasgrp2, Ppan	
	rRNA metabolic process	GO:0016072	6	0.001	Ebna1bp2, Rrp1b, Exosc6, Utp14b, Bop1, Rnu3ip2	rRNA processing
Biological processes enriched in DEGs (underexpressed mRNAs)	Apoptosis	GO:0006915	29	0.038	1200009F10Rik, Atf5, Bcl2l11, Bmf, Card6, Casp4, Cdkn1a, Cebpg, Ern1, Fas, Fcer1g, Gadd45g, Gsk3b, Ifng, Ihpk2, Irak2, Jak2, Kras, Litaf, Nme5, Nr4a1, Plekhf1, Pmaip1, Rarg, Sema6a, Traf2, Trib3, Tsc22d3, Ube2z	Apoptosis
	Cell death	GO:0008219	30	0.044	1200009F10Rik, Atf5, Bcl2l11, Bmf, Card6, Casp4, Cdkn1a, Cebpg, Ern1, Fas, Fcer1g, Gadd45g, Gsk3b, Ifng, Ihpk2, Irak2, Jak2, Kras, Litaf, Nme5, Nr4a1, Plekhf1, Pmaip1, Rarg, Sema6a, Tnfrsf1b, Traf2,	
	Regulation of apoptosis	GO:0042981	22	0.025	Bcl2l11, Casp4, Cdkn1a, Cebpg, Fas, Fcer1g, Tsc22d3, Nr4a1, Kras, Rarg, Traf2, Gsk3b, Pmaip1, 1200009F10Rik, Plekhf1, Nme5, Ihpk2, Ern1, Atf5, Irak2, Bmf, Card6	
	Positive regulation of programmed cell death	GO:0043068	12	0.040	Bcl2l11, 1200009F10Rik, Casp4, Cdkn1a, Cebpg, Ern1, Fas, Ihpk2, Nr4a1, Plekhf1, Pmaip1, Rarg	
	Intracellular protein transport	GO:0006886	26	0.002	Ap3m2, Arf2, Arl4a, Jak2, Rab6, Snap23, Stx1a, Rnf13, Gsk3b, Arfgap3, Tigd2, Sec24d, Optn, Pex26, Tmem81, Stx11, Mxra8, Sytl2, Sytl3, Kdelr3, H47, Derl2, Wdr19, Zfyve16, Stk38l, Sytl1	Protein transport
	Protein transport	GO:0015031	37	0.004	Arf2, Arl4a, Jak2, Lyst, Rab3d, Rab6, Exoc4, Snap23, Stx1a, Vps45, Rnf13, Gsk3b, Ap3m2, Arfgap3, Tigd2, Sec24d, Optn, Pex26, Tmem81, Stx11, Mxra8, Sytl2, Sytl3, Kdelr3, H47, Derl2, Mcfd2, Wdr19, Zfyve16, Stk38l, Pgap1, Sytl1, Sft2d2, Rrad, Slc25a14, Slc25a36, Tubb6	
	Membrane lipid metabolic process	GO:0006643	11	0.036	A230097K15Rik, Agpat4, Cept1, Neb, Pcyt1b, Pign, Pigv, Pip5k1b, Samd8, Smpd1, Gla	Phospholipid metabolic process
	Phospholipid metabolic process	GO:0006644	10	0.020	A230097K15Rik, Agpat4, Cept1, Neb, Pcyt1b, Pign, Pigv, Pip5k1b, Samd8, Smpd1	
	ER-nuclear signaling pathway	GO:0006984	6	0.0005	Derl2, Ern1, Ero1l, H47, Ifng, Gsk3b	ER-nucleus signaling
	Small GTPase mediated signal transduction	GO:0007264	24	0.001	Akap13, Arf2, Arhgef10, Arl4a, Arl9, Evi5l, Fgd6, Kras, Nisch, Rab28, Rab3d, Rab6, Rabl3, Rap2a, Rasa4, Rassf1, Rerg, Rhoc, Rhou, Rit1, Rrad, Rras, Sipa1l2, Wdr67	Signal transduction (small GTPase)
	Unfolded protein response	GO:0030968	5	0.001	Derl2, Ern1, Ero1l, H47, Ifng	Unfolded protein response
	Regulation of kinase activity	GO:0043549	11	0.027	Gadd45g, Gng3, Gadd45a, Trib3, Cdkn1a, Irak2, Spred3, Ern1, Avpi1, Dgka, Dusp16	Regulation of kinase activity

Table S6. Relative expression of DEM source genes (blue) at multiple regulatory layers (see also Fig. 3b). Fold change (FC) represents the rapamycin/ctrl abundance ratio. Overexpressed (red) and underexpressed (green): $P<0.05$, no change (grey). n.d.: not determined. (n=3, Student *t*-test).

	mRNA		Normalized polysomal mRNA		Protein		MIP	
Gene symbol	FC	p value	FC	p value	FC	p value	FC	p value
Ap2a2	0.77	0.09	0.78	0.17	n.d.	n.d.	3.39	0.007
Ap2a1	1.17	0.18	0.64	0.047	n.d.	n.d.	2.58	0.01
Bptf	1.42	0.06	1.12	0.12	n.d.	n.d.	4.70	0.004
Bub1b	1.66	0.02	0.64	0.002	n.d.	n.d.	3.62	0.05
Ccnf	3.07	0.01	0.92	0.04	n.d.	n.d.	6.05	0.02
Cenpm	1.15	0.16	1.25	0.21	n.d.	n.d.	3.90	0.01
Chaf1b	1.71	0.01	0.66	0.02	n.d.	n.d.	2.62	0.03
Chtf18	2.46	0.004	0.61	0.002	n.d.	n.d.	4.47	0.04
Dhcr7	3.74	0.01	0.75	0.07	n.d.	n.d.	3.81	0.009
Dtl	1.47	0.048	0.80	0.03	n.d.	n.d.	2.52	0.02
Erbb2ip	0.95	0.83	0.81	0.13	n.d.	n.d.	4.64	0.03
Hivep2	0.87	0.30	1.17	0.47	n.d.	n.d.	2.94	0.03
Igf2r	1.08	0.61	1.40	0.67	n.d.	n.d.	3.18	0.002
Mnat1	0.65	0.04	0.79	0.002	n.d.	n.d.	3.56	0.01
Myb	1.54	0.04	0.98	0.08	2.16	0.01	4.34	0.01
Nsmaf	0.98	0.88	1.05	0.81	n.d.	n.d.	3.47	0.004
Pabpc1	1.25	0.06	1.77	0.03	0.96	0.23	3.41	0.001
Pin1	0.92	0.08	1.21	0.23	n.d.	n.d.	3.02	0.02
Psma3	0.89	0.053	1.02	0.61	n.d.	n.d.	2.60	0.02
Psmb8	1.05	0.34	0.96	0.54	1.01	0.44	5.39	0.02
Psmb9	0.96	0.11	1.00	0.46	0.97	0.24	4.67	0.01
Psmd2	0.98	0.92	0.54	0.001	n.d.	n.d.	3.46	0.02
Ptpn11	0.84	0.22	1.20	0.42	n.d.	n.d.	2.79	0.02
Rcc2	1.09	0.43	0.76	0.02	n.d.	n.d.	3.24	0.07
Rfc2	1.25	0.19	0.88	0.03	1.06	0.18	5.31	0.02
Rictor	1.26	0.02	1.15	0.17	1.06	0.28	9.73	0.003
Rpl27	0.91	0.47	1.10	0.53	n.d.	n.d.	4.63	0.001
Rps15	1.07	0.64	1.14	0.44	n.d.	n.d.	2.52	0.02
Sgk1	2.30	0.04	1.16	0.07	0.9	0.13	9.21	0.03
Supt16h	1.31	0.09	0.59	0.004	n.d.	n.d.	8.91	0.01
Taf6	1.08	0.42	0.77	0.04	n.d.	n.d.	4.07	0.003
Tfdp2	2.65	0.03	1.11	0.87	1.29	0.04	7.92	0.004
Tnfsf10	4.58	0.02	2.03	0.04	n.d.	n.d.	8.97	0.01

Table S7. List of primers for quantitative real-time PCR analyses

Gene symbol	Gene ID	Primer A	Primer B	Probe
Ap2a1	11772	CCTGGCTGTGTCTCGCTTA	TGTAGTCCTGGAGGTCAGTGG	Universal Library probe: #73
Ap2a2	11771	CTGTCTCGCTAGCTGTCTCG	CCTGAAGATCTGTTGATGCAGA	Universal Library probe: #15
Bptf	207165	CACCGTACGATGAGTCCAAA	CCCGTGGTACCAATTCTGAC	Universal Library probe: #76
Bub1b	12236	GTGTCGGAGGTGCTCTGAA	TGGGGAACTGCATTTAGGAA	Universal Library probe: #85
Ccnf	12449	GGCTTTCTGTTGGGGACAT	CCAGGTACTTGAGGTGGGAGT	Universal Library probe: #56
Cenpm	66570	TTGTGTTTGTGATTAACCTGCAC	AGCTGCTGTCCACGTGCT	Universal Library probe: #25
Chaf1b	110749	GCAGATCGCCTTTCAGGA	TTGCCCAGCAAATATCATACA	Universal Library probe: #63
Chtf18	214901	CACCTGATGGGCAGTACCTC	CTTTCGGGCAGGTAGTTCAG	Universal Library probe: #78
Dhcr7	13360	CCTTGTGGGTCAGCTTCC	CCACATAACCTGGCAGAAATC	Universal Library probe: #29
Dtl	76843	GCTGCCTACATTTGGAAGGT	AGAATGACCCAGGAGCACAG	Universal Library probe: #88
Erbb2ip	59079	AAATGGTGCTTACTAATTACATGTTCC	GCAGGATTAAAACTTTCATTATCTGA	Universal Library probe: #66
Hivep2	15273	ATTGATTTCATTGGAACATTCTCTC	ATGATTGTCCTGACGCTTCC	Universal Library probe: #20
Igf2r	16004	TCAGTATGCAAAGTTCCTGTGG	TTGAATATTGGAGGGCCTGT	Universal Library probe: #53
Mnat1	17420	TGCAGCAGGCTCTGAAAAG	AGCAGAGCAACAGGGAGGT	Universal Library probe: #78
Myb*	17863	Mm00501741		
Nsmaf	18201	CTTGCAATGGCTCTTCAGTCT	TCTTTGTAGCATTTTGGATTCCT	Universal Library probe: #10
Pabpc1	18458	GGTGCCAGACCTCATCCA	TGTGAGGAAGCTGGTCTCATC	Universal Library probe: #68
Pin1**	23988	ACAGTTCAGTGATTGCAGCTCTGCCA	AAAGATCACCAGGAGCAAGGAGGA	TGGTTTCTGCATCTGACCTCTGCT
Psma3	19167	GAAGCAGAGAAATATGCCAAGG	GCAACTGTTACAGAAATGTAAACCA	Universal Library probe: #60
Psmb8	16913	CACACTCGCCTTCAAGTTCC	TCTCGATCACTTTGTTCATCCTT	Universal Library probe: #81
Psmb9	16912	GCCCAAGCCATAGCTGAC	GATGTTCTTCACCACGTTTGC	Universal Library probe: #78
Psmd2	21762	AATGGGAGATTCCAAGTCCA	TGACATCTCCATTGCAGGAC	Universal Library probe: #10
Ptpn11	19247	GAACATGACATCGCGGAGA	AACTGCCATCGACTCCTCTG	Universal Library probe: #18
Rcc2	108911	CTATCAGTTGGGGTCCATCG	AGAAGATGCCATCCAGAGTCTT	Universal Library probe: #79
Rfc2	19718	TTGAAGCTCAACGAAATAGTGG	GGGCACATTGCCTTCTCTT	Universal Library probe: #100
Rictor	78757	TTCCACTACAGACACAGTCCAGA	TGGCTAGAAATCGTGCTTCTC	Universal Library probe: #41
Rpl27	19942	TGAAAGGTTAGCGGAAGTGC	TTTCATGAACTTGCCCATCTC	Universal Library probe: #40
Rps15	20054	TCGACCAACTGCTCGACAT	GCGCTTGAGCAGTGAGTGT	Universal Library probe: #82
Sgk1	20393	TGCCAGCAACACCTATGC	GAGGGGTTAGCGTTCATAAGC	Universal Library probe: #92
Supt16h	114741	TCATGAAGACCATTGTTGATGAC	CGTCCTCAGCGTCACTCC	Universal Library probe: #83
Taf6	21343	GGATGTCTGCCTCAAAGCTC	CTCAGCCTTCTGCTGCTCTT	Universal Library probe: #20
Tfdp2	211586	CGCAATGGTCACTCAGACTC	TCTCTAGCTCGTTTTCTATCACTGG	Universal Library probe: #66
Tnfsf10	22035	TGAGAACCTTTCAGGACACCA	GAGCTGCCACTTTCTGAGGT	Universal Library probe: #52

* Pre-designed Taqman gene expression assay from Applied Biosystems

** Custom Taqman probe (Integrated DNA Technologies) specific assay