Table S1 Validation of the DYRK1A-depletion array data by RT-qPCR on a series of genes mostly involved in immune response. The genes listed in column 1 were designated by Affimetrix Exon 1.0 array analysis as regulated by DYRK1A (columns 2 and 3). To confirm this, total RNA was prepared from Hela cells either transfected with non-targeting control siRNAs or two different DYRK1A siRNAs (columns 4-5 and 6-7). Variations in mRNA levels for the indicated genes were then assessed by RT-qPCR. To further document that these genes are under the control of DYRK1A, total RNA was prepared from HEK293T cells containing inducible constructs for DYRK1A either WT or with a K188R mutation, before and after induction with ponasterone. Variations in mRNA levels for the indicated genes were then assessed by RT-qPCR (column 8-9). Data shown are means from three independent experiments. For each data set, the significance of the differences was estimated using Student's *t*-test.

1	2	3	4	5	6	7	8	9
	Fold change in mRNA levels in HeLa cells upon depletion of DYRK1A with siRNA #1 (Microarray data)	**p-Values**	**Fold change in mRNA levels in HeLa cells upon depletion of DYRK1A with siRNA #1 (RT-qPCR data)**	**p-Values**	**Fold change in mRNA levels in HeLa cells upon depletion of DYRK1A with siRNA #2 (RT-qPCR data)**	**p-Values**	**Fold change in mRNA levels in HEK293T cells upon over-expression of WT DYRK1A (RT-qPCR data)**	**p-Values**
CXCL1	**-2.77**	1.77 E-04	**-1.88**	1.11 E-02	**-2.08**	4.97 E-02	**+1.56**	2.00 E-02
CXCL2	**-2.01**	2.35 E-02	**-1.81**	9.35 E-03	**-1.81**	9.36 E-02	**+1.92**	5.48 E-04
CCL13	**-1.65**	2.85 E-03	**-1.85**	1.57 E-03	**-1.31**	2.09 E-02	**+1.28**	6.22 E-02
CHUK	**-1.63**	7.20 E-03	**-2.38**	1.42 E-02	**-1.85**	2.14 E-01	**+1.63**	1.96 E-01
MICB	**-1.87**	4.40 E-04	**-2.17**	2.67 E-05	**-1.28**	1.22 E-01	**+1.28**	
FAS	**-1.68**	1.43 E-03	**-1.78**	1.08 E-03	**-1.88**	1.77 E-01	**+1.13**	2.91 E-01
TPD52	**-3.68**	8.38 E-05	**-6.25**	8.69 E-07	**-1.47**	4.66 E-03	**+1.12**	2.46 E-03
NOTCH2	**-2.07**	8.84 E-04	**-2.43**	2.10 E-04	**-1.28**	2.63 E-02	**+1.72**	8.89 E-02
OSTM1	**-1.71**	3.76 E-02	**-1.92**	5.48 E-03	**-1.53**	5.84 E-04	**+1.78**	3.84 E-03
BNIP3L	**-1.78**	2.76 E-03	**-2.22**	1.85 E-03	**-1.35**	5.38 E-02	**+1.15**	2.01 E-01
JMJD6	**-1.75**	3.96 E-03	**-1.58**	4.72 E-04	**-1.47**	3.88 E-03	**+1.66**	4.86 E-02
TLR6	**-1.75**	1.31 E-02	**-1.61**	7.15 E-03	**-1.47**	1.30 E-02	**+1.15**	1.98 E-01
MAPK1	**-1.77**	1.80 E-03	**-1.75**	3.27 E-04	**-1.42**	2.51 E-03	**+1.33**	1.69 E-02
EREG	**-1.66**	3.54 E-02	**-2.70**	2.51 E-05	**-2.12**	1.31 E-04	**+1.61**	6.63 E-04
CCNB2	**-1.6**	2.45 E-03	**-1.75**	2.81 E-03	**-1.23**	1.69 E-02	**+1.05**	1.27 E-01
CCL2	**-1.59**	5.52 E-11	**-2.27**	1.00 E-04	**-1.40**	3.02 E-03	**+1.20**	3.39 E-02
IL18	**-1.61**	3.78 E-04	**-1.26**	5.66 E-02	**+1.92**	5.34 E-02	**+1.23**	4.30 E-03
PTMS	**+1.72**	1.62 E-03	**+1.58**	1.02 E-02	**+1.04**	3.73 E-01	**-1.25**	2.60 E-02
ATP6V1C1	**-1.75**	4.98 E-02	**-1.61**	1.90 E-03	**-1.35**	9.89 E-03	**+1.23**	1.18 E-01
B3GNT5	**-1.87**	4.00 E-02	**-2.63**	4.42 E-05	**-2.12**	1.04 E-05	**+1.13**	3.63 E-01
LYAR	**-1.87**	8.36 E-03	**-2.08**	4.17 E-04	**-1.92**	2.82 E-03	**+1.20**	2.73 E-01
MDM2	**-1.62**	1.76 E-02	**-2.12**	2.47 E-02	**+1.01**	4.57 E-01	**+1.22**	2.42 E-01
RGS2	**-1.53**	2.02 E-02	**-1.42**	5.26 E-04	**-1.11**	8.93 E-02	**+1.11**	2.59 E-01