Atg5-KO vs ctrl-KO Rnf31/Atg5-dKO vs ctrl-KO O IFN signaling B2M CXCL10 OAS1 BST2 ISG15 FN1 • 300 300 VEGFA O NFkB signaling CDKN1A STAT1 ----IRF9 CDKNIA CEBPD HLA-A-COKNIA HLA-A-COKNIA HLA-A-COKNIA COLO COLO COLO STATT-B2M-PLK2 PLK2 COLO STATT-PLK2 COLO STATT-PLK2 COKNIA COLO STATT-PLK2 COKNIA CORNIA COR O Cytokine-mediated signaling 10010FDR 100 HLA-A RSAD2 200 log10FDR FN1 CCL5 Without $\mathsf{TNF}\alpha$ 100 $\frac{1}{2}$ 14 See 0 0 2 log2FoldChange 4 -2 4 å log2FoldChange B2M STAT1 HLA-A ISG15 CEBPD 300 300 ISG15 BST2 RSAD2 B2M IRF9 CXCL10 STAT1 IFIT3 TRIM25 100 100 100 100 100 100 100 100 ITGB1 VIM CSF1 NFKBIA VIM CSF1 NFKBIA PLK2IRF9 GBP2 STAT3 - IFI35 IRF1 2ng/ml TNF α VEGFA CCL5 TRIM5 HLA-A. CDRN FAN1 XAF1 100 100 4 105 1 1. 1 0 0 4 -2.5 0.0 2.1 log2FoldChange 2.5 5.0 ò 8 log2FoldChange

Comparison of gene expression by RNA sequencing

Supplementary Fig. S4. Differentially expressed genes revealed by RNA-seq analysis.

Volcano plots of differentially expressed genes by RNA-seq analysis. B16 *B2m-/-* ctrl-KO cells, B16 *B2m-/- Atg5-*KO cells, and B16 *B2m-/- Rnf31/Atg5-*dKO cells were cultured for 24h with or without 2ng/ml TNF α . False discovery rate (FDR) (log₁₀ adjusted FDR) was plotted against log₂ fold change of gene expression levels (B16 *B2m-/-* exp-KO cells / B16 *B2m-/-* ctrl-KO cells).