

# Olmeda et al. Supplementary Table S3

	MDK/NEG	shM1/shC	shM5/shC	
MDK/NEG UP & shM1/shC DOWN & shM5/shC DOWN	MTOR_UP.N4.V1_UP	<0.001	<0.001	<0.001
	HINATA_NFKB_IMMUNO_INF	<0.001	<0.001	<0.001
	LTE2_UP.V1_DN	<0.001	0.001	0.026
	STK33_UP	<0.001	0.006	<0.001
	EGFR_UP.V1_UP	<0.001	<0.001	<0.001
	CAMP_UP.V1_UP	<0.001	0.001	<0.001
	BMI1_DN_MEL18_DN.V1_UP	<0.001	<0.001	0.002
	E2F1_UP.V1_DN	<0.001	0.003	<0.001
	HOXA9_DN.V1_UP	0.001	0.009	<0.001
	ALK_DN.V1_UP	0.002	0.003	0.016
	MEL18_DN.V1_UP	0.004	0.001	0.022
	RB_P107_DN.V1_DN	0.012	0.200	<0.001
	ESC_J1_UP_EARLY.V1_DN	0.012	0.197	0.004
	KRAS.300_UP.V1_DN	0.025	0.007	0.034
	RPS14_DN.V1_UP	0.028	0.014	0.026
	SIRNA_EIF4GI_UP	0.029	0.022	0.002
	DCA_UP.V1_UP	0.066	0.199	0.206
	P53_DN.V2_UP	0.120	0.022	0.165
	IL15_UP.V1_DN	0.123	0.198	0.130
	VEGF_A_UP.V1_UP	0.140	<0.001	<0.001
CAHOY_ASTROGLIAL	0.220	0.003	0.093	
HINATA_NFKB_MATRIX	0.249	0.001	0.034	
MDK/NEG DOWN & shM1/shC UP & shM5/shC UP	RB_P107_DN.V1_UP	<0.001	<0.001	<0.001
	PRC2_EDD_UP.V1_UP	<0.001	<0.001	<0.001
	CSR_LATE_UP.V1_UP	<0.001	<0.001	<0.001
	HOXA9_DN.V1_DN	<0.001	0.003	0.002
	E2F3_UP.V1_UP	<0.001	<0.001	<0.001
	E2F1_UP.V1_UP	<0.001	<0.001	<0.001
	MEK_UP.V1_UP	<0.001	0.002	<0.001
	LTE2_UP.V1_UP	<0.001	0.004	<0.001
	RPS14_DN.V1_DN	<0.001	<0.001	<0.001
	EGFR_UP.V1_DN	<0.001	<0.001	<0.001
	KRAS.DF.V1_UP	<0.001	<0.001	<0.001
	GCNP_SHH_UP_EARLY.V1_UP	<0.001	<0.001	<0.001
	TBK1.DF_UP	<0.001	0.002	0.012
	RB_DN.V1_UP	<0.001	0.005	<0.001
	ERB2_UP.V1_UP	<0.001	0.002	0.001
	GCNP_SHH_UP_LATE.V1_UP	<0.001	<0.001	<0.001
	PRC2_EZH2_UP.V1_UP	<0.001	0.004	<0.001
	VEGF_A_UP.V1_DN	<0.001	<0.001	<0.001
	ESC_V6.5_UP_LATE.V1_UP	<0.001	0.229	0.172
	RAF_UP.V1_UP	0.001	0.008	0.033
	PDGF_UP.V1_UP	0.001	<0.001	0.002
	P53_DN.V1_UP	0.001	0.001	0.001
	IL21_UP.V1_DN	0.004	0.168	0.020
	CRX_NRL_DN.V1_UP	0.005	0.215	0.017
	KRAS.AMP.LUNG_UP.V1_UP	0.008	0.012	0.042
	PRC2_SUZ12_UP.V1_UP	0.009	0.046	<0.001
	PRC1_BMI_UP.V1_UP	0.013	0.008	0.001
	ALK_DN.V1_DN	0.013	0.047	0.023
	ATF2_UP.V1_UP	0.016	0.132	0.051
	SRC_UP.V1_DN	0.031	0.024	0.042
	PRC2_EZH2_UP.V1_DN	0.034	0.054	0.027
	SIRNA_EIF4GI_DN	0.040	0.143	0.126
ATM_DN.V1_DN	0.043	0.228	0.011	
TBK1.DN.48HRS_UP	0.055	0.116	0.052	
PDGF_ERK_DN.V1_DN	0.085	0.106	<0.001	
LEF1_UP.V1_UP	0.100	0.054	0.041	
NRL_DN.V1_UP	0.148	0.171	0.010	

**Table S3. Signaling pathways identified by RNA seq to be controlled by MDK in lymphatic endothelial cells (LEC).** Transcriptomic analyses were performed in MDK gain or loss of function studies (LoF and GoF) as indicated in Fig. 5a,b. Shown are Oncogenic Signatures found by gene set enrichment analyses (GSEA) to show a consistent (opposed) alterations in both settings. FDR for each gene set are shown. MDK/Neg, stands for comparative analyses of WM164 overexpressing MDK vs the parental (MDK negative control). shM1/shC and shM2/shC correspond to data from SK-Mel-147 expressing MDK sh1 or sh5, respectively, and analyzed with respect to the parental MDK-expressing cells transduced with shRNA control.