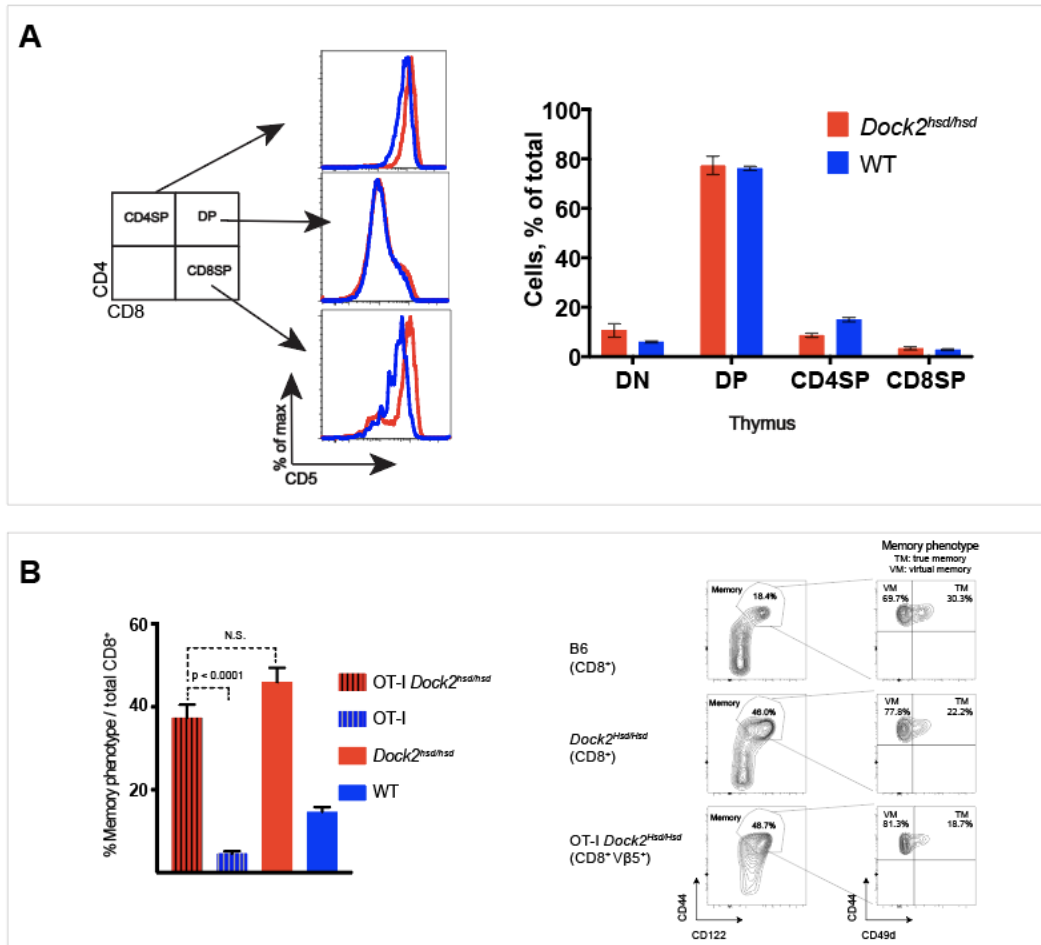


SUPPLEMENTAL DATA

Supplementary Figure 1

A) Flow cytometric analysis of the CD5 expression levels (left) on thymic T cell subsets and their respective proportions (right) in the thymi of WT and *Dock2*^{h^{sd}/h^{sd}} mice.

B) The proportion of CD8⁺ memory phenotype cells (MP) in the spleens of OT-I TCR transgenic mice in the *Dock2*^{h^{sd}/h^{sd}} and WT backgrounds, as well as *Dock2*^{h^{sd}/h^{sd}} and WT mice lacking the OT-I TCR transgene. The proportion of true memory (TM) and virtual memory (VM) as determined by flow cytometric analysis of CD49d staining is shown on the right.



Supplementary Table 1:

Gene set enrichment analysis of MSigDB immunological gene signatures comparing *Dock2*-deficient and wild-type naïve CD8⁺ T cells.

Significantly enriched gene sets in *Dock2*-deficient CD8⁺ T cells (FDR < 0.25) are shown.

Memory-linked gene sets are marked with an asterisk.

	GENE SET	FDR < 0.25	SIZE	ES	NES	NOM p val	FDR q val	FWER p val	RANK AT MAX	LEADING EDGE
MSIGDB IMMUNOLOGICAL GENE SIGNATURES	GSE7218_UNSTIM_VS_ANTIGEN_STIM_THROUGH_IGG_BCELL_DN	Yes	137	0.449	1.927	0	0.014	0	2719	tags=28%, list=13%, signal=32%
	GSE15330_LYMPHOID_MULTIPOTENT_VS_MEGAKARYOCYTE_ERYTHROID_PROGENITOR_IKAROS_KO_DN	Yes	163	0.470	1.727	0	0.172	0.256	3161	tags=34%, list=15%, signal=40%
	GSE46606_IRF4HIGH_VS_WT_CD40L_IL2_IL5_DAY3_STIMULATED_BCELL_DN	Yes	130	0.447	1.733	0	0.180	0.256	2302	tags=31%, list=11%, signal=34%
	GSE39820_CTRL_VS_IL1B_IL6_IL23A_CD4_TCELL_DN	Yes	165	0.406	1.694	0	0.192	0.309	3729	tags=33%, list=18%, signal=39%
	GSE40443_INDUCED_VS_TOTAL_TREG_DN	Yes	160	0.364	1.738	0	0.193	0.245	2589	tags=26%, list=12%, signal=30%
	GSE3337_CTRL_VS_4H_IFNG_IN_CD8POS_DC_DN	Yes	168	0.384	1.700	0	0.197	0.289	2267	tags=24%, list=11%, signal=27%
	KAECH_NAIVE_VS_MEMORY_CD8_TCELL_DN*	Yes	184	0.432	1.743	0	0.201	0.225	2683	tags=33%, list=13%, signal=38%
	KAECH_NAIVE_VS_DAY15_EFF_CD8_TCELL_DN*	Yes	174	0.397	1.686	0	0.202	0.309	2683	tags=30%, list=13%, signal=35%
	GSE24972_MARGINAL_ZONE_BCELL_VS_FOLLICULAR_BCELL_DN	Yes	126	0.330	1.680	0	0.202	0.322	2610	tags=24%, list=12%, signal=27%
	GSE9650_NAIVE_VS_MEMORY_CD8_TCELL_DN*	Yes	185	0.418	1.700	0	0.213	0.289	2683	tags=33%, list=13%, signal=37%
	GSE37605_TREG_VS_TCONV_C57BL6_FOXP3_FUSION_GFP_DN	Yes	132	0.410	1.703	0	0.219	0.289	2373	tags=28%, list=11%, signal=31%
	GSE20715_OH_VS_GH_OZONE_LUNG_UP	Yes	144	0.354	1.655	0	0.220	0.413	4967	tags=41%, list=24%, signal=53%
	GOLDRATH_NAIVE_VS_MEMORY_CD8_TCELL_DN*	Yes	183	0.409	1.657	0	0.229	0.413	2633	tags=32%, list=13%, signal=36%
	GSE21063_WT_VS_NFATC1_KO_3H_ANTI_IGM_STIM_BCELL_DN	Yes	150	0.421	1.746	0	0.235	0.212	2719	tags=30%, list=13%, signal=34%
	GSE38304_MYC_NEG_VS_POS_GC_BCELL_DN	Yes	174	0.427	1.658	0	0.240	0.413	2948	tags=33%, list=14%, signal=38%
GSE2826_XID_VS_BTK_KO_BCELL_DN	Yes	153	0.387	1.638	0	0.246	0.469	3875	tags=35%, list=18%, signal=43%	
GSE3039_NKT_CELL_VS_ALPHAALPHA_CD8_TCELL_DN	Yes	172	0.360	1.644	0	0.248	0.469	2724	tags=27%, list=13%, signal=30%	
INTERSECTIONS AMONG THE MEMORY-LINKED GENE SETS(*) WITH > 15 GENES	GOLDRATH_NAIVE_VS_MEMORY_CD8_TCELL_DN GSE9650_NAIVE_VS_MEMORY_CD8_TCELL_DN KAECH_NAIVE_VS_DAY15_EFF_CD8_TCELL_DN KAECH_NAIVE_VS_MEMORY_CD8_TCELL_DN	Yes	66	0.486	1.780	0.000	0.006	0.000	2220	tags=39%, list=11%, signal=44%
	GOLDRATH_NAIVE_VS_MEMORY_CD8_TCELL_DN GSE9650_NAIVE_VS_MEMORY_CD8_TCELL_DN KAECH_NAIVE_VS_MEMORY_CD8_TCELL_DN	Yes	17	0.499	1.436	0.030	0.139	0.157	2273	tags=41%, list=11%, signal=46%
	GSE9650_NAIVE_VS_MEMORY_CD8_TCELL_DN KAECH_NAIVE_VS_MEMORY_CD8_TCELL_DN	no	51	0.407	1.277	0.176	0.280	0.381	2492	tags=27%, list=12%, signal=31%
	GOLDRATH_NAIVE_VS_MEMORY_CD8_TCELL_DN GSE9650_NAIVE_VS_MEMORY_CD8_TCELL_DN KAECH_NAIVE_VS_DAY15_EFF_CD8_TCELL_DN KAECH_NAIVE_VS_MEMORY_CD8_TCELL_DN	no	76	0.318	1.188	0.070	0.332	0.546	2598	tags=26%, list=12%, signal=30%
	GSE9650_NAIVE_VS_MEMORY_CD8_TCELL_DN KAECH_NAIVE_VS_DAY15_EFF_CD8_TCELL_DN KAECH_NAIVE_VS_MEMORY_CD8_TCELL_DN	no	31	0.360	1.079	0.383	0.337	0.688	2683	tags=29%, list=13%, signal=33%
	KAECH_NAIVE_VS_DAY15_EFF_CD8_TCELL_DN KAECH_NAIVE_VS_MEMORY_CD8_TCELL_DN	no	54	0.270	1.138	0.244	0.341	0.598	2629	tags=22%, list=13%, signal=25%

Supplementary Table 2:

Genes shared among or unique to the memory-linked gene immunological gene signatures in Dock2-deficient naïve CD8+ T cells. All possible intersections are shown below.

Gene set intersection	Number of genes	Genes
GOLDRATH_NAIVE_VS_MEMORY_CD8_TCELL_DN GSE9650_NAIVE_VS_MEMORY_CD8_TCELL_DN KAECH_NAIVE_VS_DAY15_EFF_CD8_TCELL_DN KAECH_NAIVE_VS_MEMORY_CD8_TCELL_DN	71	EMP1 KRTCAP2 CHPT1 CD44 ANXA2 ATF6 FASLG FGL2 CRTAM DOCK5 MDFIC CCL5 ANXA1 GZMM DENND5A KLRK1 PHF13 AQP9 CCR2 MCART6 ITGB1 MYO1F NRP1 UNC119B CLDND1 PGLYRP1 FCGR2B S100A4 CASP1 CCR5 ST3GAL6 CD160 CXCR3 CAPN2 LGALS1 CCL4 KLRG1 DAPK2 PRF1 ELL2 IFNG TXNDC5 ERRF1 PLSCR1 CASP4 S100A6 EOMES IL18R1 RECK F2R GZMB ACOT7 GABARAPL2 PTPN13 EEA1 KCNJ8 CCND3 BHLHE40 ID2 SNX10 IL18RAP S100A13 GZMK GLRX AHNAK BCL2A1 ITGAX MAPRE2 S100A10 IFITM10 KLRC1
GOLDRATH_NAIVE_VS_MEMORY_CD8_TCELL_DN KAECH_NAIVE_VS_DAY15_EFF_CD8_TCELL_DN KAECH_NAIVE_VS_MEMORY_CD8_TCELL_DN	3	GGH FCGRT STARD10
GSE9650_NAIVE_VS_MEMORY_CD8_TCELL_DN KAECH_NAIVE_VS_DAY15_EFF_CD8_TCELL_DN KAECH_NAIVE_VS_MEMORY_CD8_TCELL_DN	34	XDH IL10RA POLR2L PRR13 FGR SH2D1A RORA RNF19B HLA-A ETFB EFHD2 TRAPPC1 GSG2 CTLA4 TXN KLF10 LYPLA2 CTSD NUCB1 COX17 MAP7D1 MBD2 TSPAN31 CSDA GBP4 SNTB2 S100A11 HMGB2 TTC7B TSMN1 H1FO MX2 HOPX ITGA4
GOLDRATH_NAIVE_VS_MEMORY_CD8_TCELL_DN GSE9650_NAIVE_VS_MEMORY_CD8_TCELL_DN KAECH_NAIVE_VS_MEMORY_CD8_TCELL_DN	17	PGAM1 GATA3 GSTO1 PRSS12 N4BP1 RPGR VKORC1 HCFC1R1 CST7 CTSW TNFRSF1B RNF138 POU6F1 TMEM37 ST3GAL4 ODC1 PPP3CC
GOLDRATH_NAIVE_VS_MEMORY_CD8_TCELL_DN GSE9650_NAIVE_VS_MEMORY_CD8_TCELL_DN KAECH_NAIVE_VS_DAY15_EFF_CD8_TCELL_DN	4	NBEAL2 ENPP1 SLC35E4 LPIN1
KAECH_NAIVE_VS_DAY15_EFF_CD8_TCELL_DN KAECH_NAIVE_VS_MEMORY_CD8_TCELL_DN	5	PON1 MTMR7 RACGAP1 RPAP1 TMED10
GOLDRATH_NAIVE_VS_MEMORY_CD8_TCELL_DN KAECH_NAIVE_VS_MEMORY_CD8_TCELL_DN	4	CTNNA1 BAG3 CISH ARL6
GSE9650_NAIVE_VS_MEMORY_CD8_TCELL_DN KAECH_NAIVE_VS_MEMORY_CD8_TCELL_DN	54	HS1BP3 MOGS PFKP DPM3 JUND RBMX FGF13 SORL1 SHC1 RDBP PCNA GDNF CD7 DPP7 CDC34 ATN1 SEPT1 LRRC8C XRCC5 UNC119 CAPNS1 ST8SIA2 FOSB FAM46C PACS1 IGF2R FRMD5 CDK4 FOS TNFSF10 BCL2 SLC03A1 ADAM19 CRIP2 TBL2 CYFIP2 YES1 TNFAIP3 LYSDM2 ZMAT3 TOB1 DYM WEE1 CYB5R3 GADD45B UBC FGF19 PIM1 PRDX2 KLF6 SH2D2A KLF4 ITGB7 IQGAP2
GOLDRATH_NAIVE_VS_MEMORY_CD8_TCELL_DN KAECH_NAIVE_VS_DAY15_EFF_CD8_TCELL_DN	11	SOCS2 VMP1 GZMA SERPINB9 DSTN LGALS3 BCL2L2 SMYD1 LITAF PRDM1 MYADM
GSE9650_NAIVE_VS_MEMORY_CD8_TCELL_DN KAECH_NAIVE_VS_DAY15_EFF_CD8_TCELL_DN	1	PTTG1
GOLDRATH_NAIVE_VS_MEMORY_CD8_TCELL_DN GSE9650_NAIVE_VS_MEMORY_CD8_TCELL_DN	2	AIM1 GPC1
KAECH_NAIVE_VS_MEMORY_CD8_TCELL_DN*	12	IL7R RAD51D CECR5 SH3YL1 SF3A1 CD97 BCHE TOM1 ITGB2 KIAA0101 SYT9 OPRK1
KAECH_NAIVE_VS_DAY15_EFF_CD8_TCELL_DN*	71	ACTB CARHSP1 MED12L IL13RA2 GALNT3 ENTPD1 CHL1 MTM1 C7orf73 SLA ODZ3 CD4 LXN NR4A2 ARF6 SSPN GJA1 CR1L INSM1 LAPTM5 C16orf61 CD47 DNMT1 RAB33B RALY SORBS1 GPM6B NT5E CCNB2 FAM89B DNAJC1 ALG2 FANCM ZNF821 RPA2 LPIN2 TERF1 MAN2A1 IDE RRBP1 SRGN CASP7 ALCAM C17orf79 UBE2K SEC61G C9orf16 HK2 ALAD HIST1H1C ADORA2A EMP3 ZNF398 ANXA4 GMFG H2AFX CYP3A43 PRDX1 LRP10 PRDX4 C10orf58 KCTD9 LAMC1 KLRD1 ITGAL GSTM3 RAB5C RHOQ PERP RSU1 CASP3
GOLDRATH_NAIVE_VS_MEMORY_CD8_TCELL_DN*	88	CHCHD7 EI24 GPHN KIAA1737 TK1 RASA4 TRAF3IP2 IER3 MAP3K8 ABHD5 MS4A1 GOLM1 GK DENND4C GCAT SEMA4F PTPN22 CYB5R4 ACY1 FHIT TMEM55A ART3 CAPG CD22 ANKH POLR1B SEMA4A SAMHD1 EYA4 DBNDD2 PLAT SSX2IP PLP2 STX7 IRF8 OSTF1 EVI2A TMEM159 LPGAT1 CYFIP1 DNAJC5 TMEM141 RAB3D IL15 ITM2C PLCD1 MAPK12 MGST3 KCTD12 TSPAN4 SERPINB6 MYL1 IL15RA GCLM XIST KIAA1274 PLEKHB2 HSD17B11 LIMD1 SOS2 PLEKHA5 CPNE3 ECH1 PLBD1 IL10RB CCDC130 MED10 CYBB AIF1 TKTL1 TRAF1 PRKCA MCOLN2 ANTXR2 TUSC2 RNASE4 PBX3 KLHL7 GOLIM4 ASAH1 PQLC3 ABCB1 NOTCH4 SOAT2 CYP4V2 NCKAP1 SKAP2 HIP1R
GSE9650_NAIVE_VS_MEMORY_CD8_TCELL_DN*	17	TNNI1 PAM FAM207A MNS1 TULP4 KITLG RPS6KA4 PHYH FRAT1 C9orf3 EPN1 MID2 AARS GNPTG CNR1 NFKBIB ZFP36L2
* genes unique to the particular gene set		

Supplementary Table 3:

TCR repertoire sequencing metrics

Replicate	Genotype	Cells (CD8 naïve vs memory)	Total sequencing reads	Successfully aligned reads	Successfully aligned, percent	Total reads used in CDR3 clonotypes	Final CDR3 clonotype count
1	WT	CD44lo	3439	3153	91.68%	3068	2109
2	WT	CD44lo	3638	3009	82.71%	2913	2344
3	WT	CD44lo	2881	2693	93.47%	2618	1900
4	WT	CD44lo	2745	2590	94.35%	2507	1662
1	Harlan	CD44lo	3851	3761	97.66%	3630	2698
2	Harlan	CD44lo	4646	4486	96.56%	4345	3111
3	Harlan	CD44lo	2565	2503	97.58%	2411	1853
1	WT	CD44hi	17152	16576	96.64%	16438	2729
2	WT	CD44hi	19629	17809	90.73%	17660	3238
3	WT	CD44hi	13017	12765	98.06%	12613	2510
4	WT	CD44hi	18465	17983	97.39%	17839	2609
1	Harlan	CD44hi	5964	5322	89.24%	5209	2758
2	Harlan	CD44hi	7673	6848	89.25%	6706	2966
3	Harlan	CD44hi	3470	3211	92.54%	3170	1525