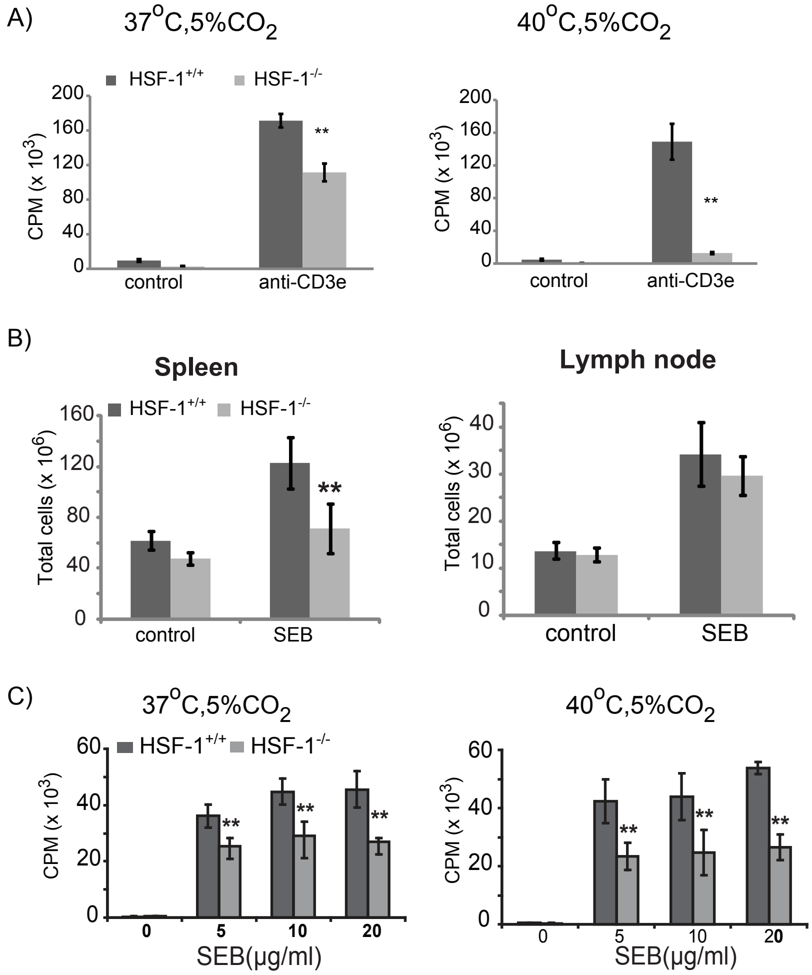

Figure S1. A) T cells from HSF1$^{-/-}$ mice proliferate normally under non-stressful conditions but poorly under stressful conditions in response to anti-CD3 stimulation. Purified T cells from HSF1$^{-/-}$ or HSF1$^{+/+}$mice were stimulated for three days in 96 well tissue culture plates in wells without (control) or with plate-bound anti-CD3 and pulsed with [3H] thymidine deoxyribose for the last 18h. T cell proliferation was estimated as a measure of [3H] thymidine incorporation. Data represents the average of two experiments with three replicates in each. **B) Spleen cell recovery in vivo in response to SEB is reduced in HSF1$^{-/-}$ mice compared to HSF1$^{+/+}$**: HSF1$^{-/-}$ or HSF1$^{+/+}$ mice were injected with PBS(control) or 150 µg SEB and the total number of spleen or draining lymph node lymphocytes after 48h was determined by hemocytometer counting . The data represent the average from 6-8 mice in each treatment. **C) HSF1$^{-/-}$ spleen cell proliferation in response to SEB is impaired both at non-stressful and stressful temperatures :** Spleen cells from HSF1$^{-/-}$ or HSF1$^{+/+}$ mice were cultured in media alone or with indicated concentrations of SEB for 72h in 96 well tissue culture plates at 37oC,5%[CO2] or 40oC, 5%[CO2] . The cells were then pulsed with 1µCi [3H] thymidine deoxyribose during the last 18h culture, harvested, and expansion of spleen cells were estimated as a measure of [3H] thymidine incorporation. Data represents the average (n=4) cpm values for each treatment and is a representative of three repeated experiments. Error bars represent the standard error calculated as ±1 standard deviation. P-values were estimated from student's T-test with one-tailed distribution and two-sample unequal variance. **represents P-value

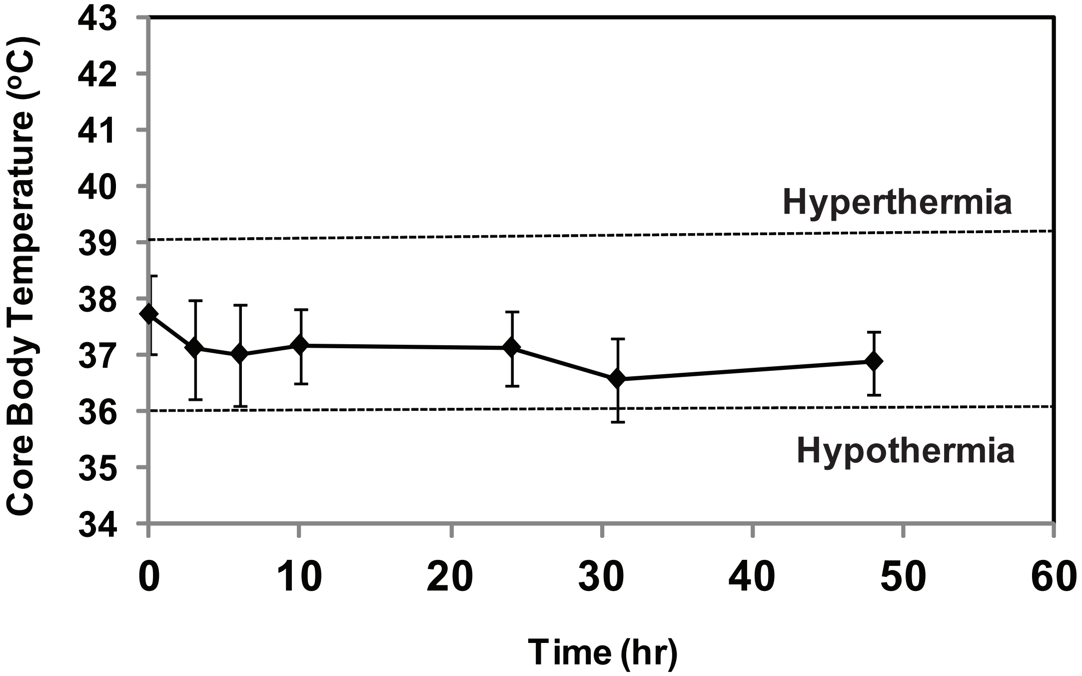

Figure S2: Core body temperature of sentinel mice treated with SEB. Mice were injected intravenously with 150 µg/mouse SEB and their core body temperatures were monitored over time using temperature transponders implanted in the peritoneal cavity. Data represented is combined average of two experiments with 6 mice in each group. There was no significant difference between HSF1-/- and HSF1+/+ mice.

Table S1: Genes regulated by HSF1 in T cells grouped by physiologic function.

Gene Title	**Gene Symbol**	**Fold change Log2 (KO37/ WT37)**	***p-value***	**Fold change Log2 (KO40/ WT40)**	***p-value***	**Alias**
Heat shock response						
heat shock protein 1B	Hspa1b	-4.00	*0.001*	-4.79	*<0.000*	Hsp 70.1, Hsp 70
heat shock protein 1A	Hspa1a	-3.55	*0.003*	-4.51	*0.001*	Hsp70.3, Hsp70
heat shock protein 110	Hsp110	-1.80	*0.001*	-1.64	*0.001*	ApG-2
DnaJ (Hsp40) homolog, subfamily A, member 1	Dnaja1	-0.99	*0.008*	-1.08	*0.006*	
DnaJ (Hsp40) homolog, subfamily B, member 1	Dnajb1	-0.91	*<0.000*	-1.04	*<0.000*	Hsp 40
heat shock protein 1 (chaperonin 10)	Hspe1	-0.77	*0.009*	-0.94	*0.004*	Hsp 10
stress-induced phosphoprotein 1	Stip1	-0.75	*0.005*	-0.79	*0.003*	Hop, mSTI1
activator of heat shock 90kDa protein ATPase homolog 1	Ahsa1	-0.74	*0.002*	-0.85	*0.001*	
heat shock factor 1	Hsf1	-0.70	*0.011*	-0.99	*0.003*	
DnaJ (Hsp40) homolog, subfamily A, member 4	Dnaja4	-0.69	*0.015*	-0.94	*0.006*	
heat shock protein 8	Hspa8	-0.54	*0.025*	-0.68	*0.009*	Hsc 70, Hsc71
heat shock protein 1, alpha	Hspca	-0.51	*0.011*	-0.61	*0.005*	Hsp 90 alpha
heat shock protein 1, beta	Hspcb	-0.38	*0.001*	-0.50	*<0.000*	Hsp 90 beta
heat-responsive protein 12	Hrsp12	1.14	*0.001*	1.16	*<0.000*	
heat shock factor 2	Hsf2	0.58	*0.014*	1.22	*0.001*	
Apoptosis						
Bcl2-associated athanogene 3	Bag3	-1.01	*0.005*	-1.41	*0.002*	
clusterin	Clu	-0.96	*0.004*	-0.72	*0.008*	ApoJ
caspase 6	Casp6	-0.50	*<0.000*	-0.75	*<0.000*	
BCL2-like 11 (apoptosis facilitator)	Bcl2l11	0.20	*0.117*	0.50	*0.003*	Bim, Bod
Tnf receptor-associated factor 1	Traf1	0.61	*0.005*	0.68	*0.004*	
Interferon regulatory factor 2, mRNA	Irf2	0.64	*0.023*	1.04	*0.006*	
caspase recruitment domain family, member 6	Card6	0.78	*0.002*	0.82	*0.002*	
caspase recruitment domain family, member 11	Card11	0.79	*<0.000*	0.65	*<0.000*	CARMA1
cell cycle						
minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	Mcm2	-0.36	*0.022*	-0.65	*0.001*	
G1 to S phase transition 1	Gspt1	0.44	*0.008*	0.66	*0.003*	Gst1
cell division cycle 2-like 6 (CDK8-like)	Cdc2l6	0.61	*0.001*	0.78	*0.001*	CDK11
cyclin G2	Ccng2	0.70	*0.009*	0.71	*0.016*	
histone deacetylase 5	Hdac5	0.76	*0.001*	0.25	*0.153*	
amyloid beta (A4) precursor protein-binding, family B, member 1	Apbb1	-1.24	0.007	-0.30	0.125	---
Ring-box 1, mRNA	Rbx1	0.10	0.463	0.74	0.005	
inflamation						
tumor necrosis factor (ligand) superfamily, member 8	Tnfsf8	-0.67	*0.005*	-0.69	*0.003*	
TRAF3 interacting protein 3	Traf3ip3	0.53	*0.006*	0.52	*0.009*	
CD86 antigen	Cd86	0.76	*0.001*	0.57	*0.003*	
inhibitor of kappaB kinase beta	Ikbkb	0.46	*0.206*	2.15	*0.006*	IKK2, IKKbeta
nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	Nfkbiz	0.48	0.007	0.59	0.006	---
nuclear factor of kappa light polypeptide gene enhancer in B-cells 2,	Nfkb2	0.51	*0.010*	0.29	*0.032*	p49/p100
cytokines and chemokines						
chemokine (C-X-C motif) receptor 6	Cxcr6	-0.58	*0.008*	-0.73	*0.006*	
chemokine (C-X-C motif) ligand 2	Cxcl2	-0.98	*0.002*	-0.63	*0.051*	
chemokine (C-C motif) ligand 3	Ccl3	-0.62	*0.002*	-0.50	*0.007*	
chemokine (C-C motif) receptor 9	Ccr9	0.52	*0.003*	0.59	*0.001*	

Gene Title	Gene Symbol	Log2 (KO37/ WT37)	p-value	Log2 (KO40/ WT40)	p-value	Alias
interleukin 13	Il13	-0.72	0.004	-0.75	0.004	
interleukin 4	Il4	-0.62	0.002	-0.67	0.001	
interleukin 16	Il16	0.79	<0.000	0.57	<0.000	
RAR-related orphan receptor gamma	Rorc	-0.31	0.099	-1.50	0.005	
Colony stimulating factor 1 receptor (Csf1r), mRNA	Csf1r	0.46	0.002	0.75	0.000	
transforming growth factor, beta receptor III	Tgfbr3	0.47	0.002	0.66	0.001	
Metabolism						
acyl-CoA thioesterase 7	Acot7	-1.43	0.001	-1.33	<0.000	
galactosylceramidase	Galc	-0.87	0.009	-0.60	0.026	
sterol-C5-desaturase	Sc5d	0.33	0.024	0.58	0.006	
alcohol dehydrogenase 1 (class I)	Adh1	0.34	0.005	0.95	<0.000	
hydroxysteroid 11-beta dehydrogenase 1	Hsd11b1	0.70	0.006	0.78	0.006	
cell signal						
cellular retinoic acid binding protein II	Crabp2	-1.68	0.013	-1.95	0.004	
ras homolog gene family, member f	Rhof	-0.71	0.002	-0.98	0.002	
protein kinase C, zeta	Prkcz	-0.69	0.002	-0.32	0.014	Pkcz
CD8 antigen, beta chain 1	Cd8b1	-0.45	0.006	-0.80	0.001	
IL2-inducible T-cell kinase	Itk	-0.30	0.033	-0.55	0.007	Tsk
RAN GTPase activating protein 1	Rangap1	-0.24	0.056	-0.55	0.004	
Protein kinase, cAMP dependent, catalytic, alpha,	Prkaca	0.29	0.050	0.54	0.007	PKA
interferon inducible GTPase 2	Iigp2	0.37	0.015	0.53	0.009	
dihydrolipoamide S-succinyltransferase	Dlst	0.45	0.033	0.78	0.010	
spectrin beta 2	Spnb2	0.54	0.005	0.38	0.023	---
diacylglycerol kinase, alpha	Dgka	0.55	<0.000	0.39	0.002	
Diacylglycerol kinase zeta	Dgkz	0.57	0.004	0.32	0.021	
phosphatidylinositol 3-kinase catalytic delta polypeptide	Pik3cd	0.62	0.009	0.47	0.019	
inositol polyphosphate-1-phosphatase	Inpp1	0.66	0.001	0.62	0.001	
mitogen activated protein kinase kinase kinase kinase 2	Map4k2	0.67	0.005	0.59	0.016	
Mitogen activated protein kinase kinase 2 (Map2k2)	Map2k2	0.71	0.006	0.19	0.193	
Rho GTPase activating protein 24	Arhgap24	0.71	0.005	0.64	0.012	
signal transducer and activator of transcription 2	Stat2	0.72	<0.000	0.81	<0.000	
phosphoinositide-3-kinase adaptor protein 1	Pik3ap1	0.77	0.001	0.89	0.001	BCAP
protein kinase inhibitor, gamma	Pkig	0.77	0.003	0.84	0.004	
RAS p21 protein activator 3	Rasa3	0.79	0.001	0.72	0.003	
diacylglycerol O-acyltransferase 1	Dgat1	0.80	0.003	0.61	0.009	
rho/rac guanine nucleotide exchange factor (GEF) 18	Arhgef18	0.80	0.007	1.02	0.010	
Protein tyrosine phosphatase, non-receptor type 22 (lymphoid) (Ptpn22), mRNA	Ptpn8	0.99	0.008	0.65	0.029	
Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (Ywhaz), mRNA	Ywhaz	3.93	<0.000	3.21	0.001	
Transcription and translation						
polymerase (RNA) II (DNA directed) polypeptide K	Polr2k	-1.66	0.002	-1.42	0.002	
general transcription factor II I	Gtf2i	-0.77	0.007	-0.35	0.114	
Eukaryotic translation initiation factor 2C, 1 (Eif2c1), mRNA	Eif2c1	-0.29	0.403	-2.71	0.008	
General transcription factor IIB (Gtf2b), mRNA	Gtf2b	0.78	0.099	2.69	0.006	
polymerase (DNA directed), gamma	Polg	1.46	0.009	1.42	0.007	
ubiquitin specific peptidase 11	Usp11	0.46	0.006	0.67	0.003	
proteasome (prosome, macropain) subunit, alpha type 1	Psma1	0.36	0.027	0.58	0.005	