

SUPPLEMENTARY FIGURE LEGENDS

Supplementary Figure 1: Tabular representation of gene expression determined from RNA sequence analysis. Purified splenic T cells from WT and TKO mouse were activated using anti-CD3 and anti-CD28 (2µg/ml each) in presence of IL2 (50 IU/ml) for three days before RNA was prepared for sequencing. Gene ID, and p-values of the significant genes is listed.

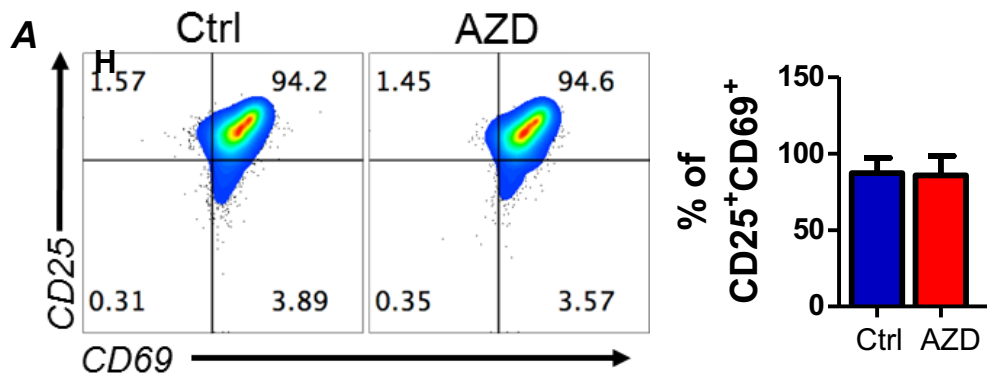
Supplementary Figure 2:

A). pMel T cells activated with the cognate antigen either in presence of vehicle control (DMSO) or AZD1208 (3 µM) were used to determine cell surface expression of CD25 and CD69. The adjacent scatter plot represents the cumulative data of MFI from there independent experiments.

B). Tabular representation of gene expression determined from RNA sequence analysis. Purified splenic T cells from WT mouse were activated using anti-CD3 and anti-CD28 (2µg/ml each) with IL2 (50 IU/ml) for three days either alone or in presence of pan-PIM inhibitor AZD1208 (3 µM) before RNA was prepared for sequencing. Fold changes listed as ratio of AZD1208 treated to untreated T cells in the significantly different genes.

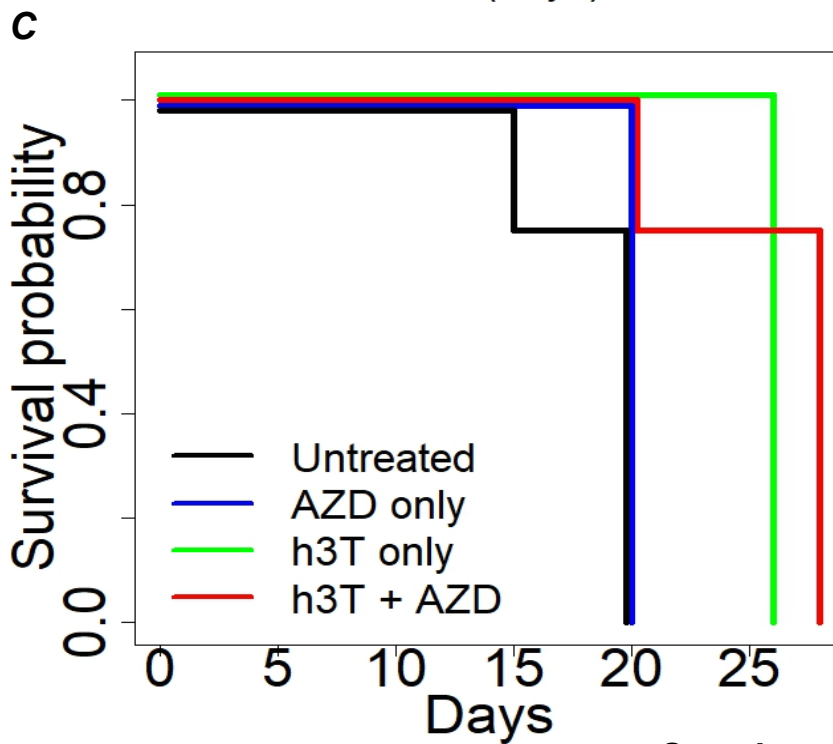
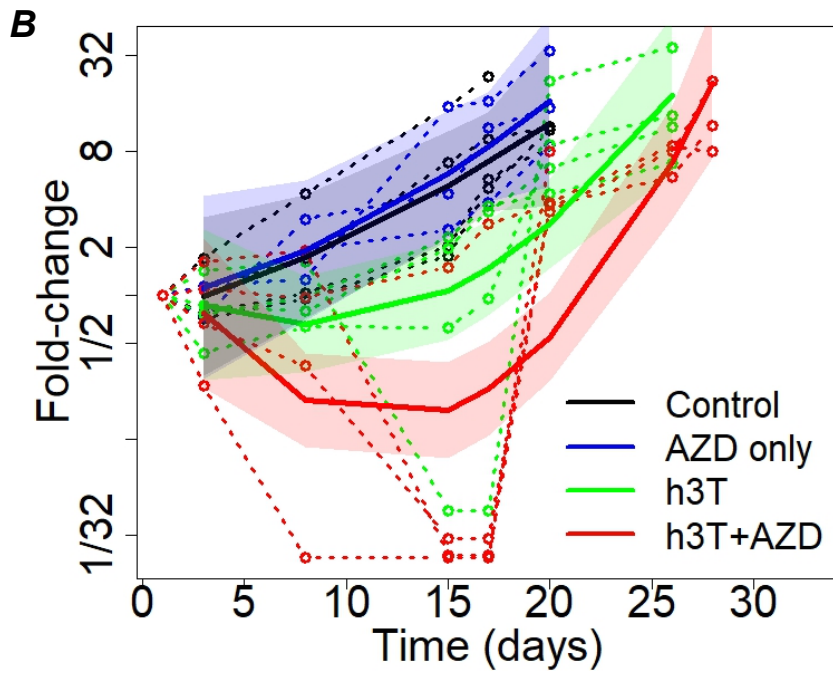
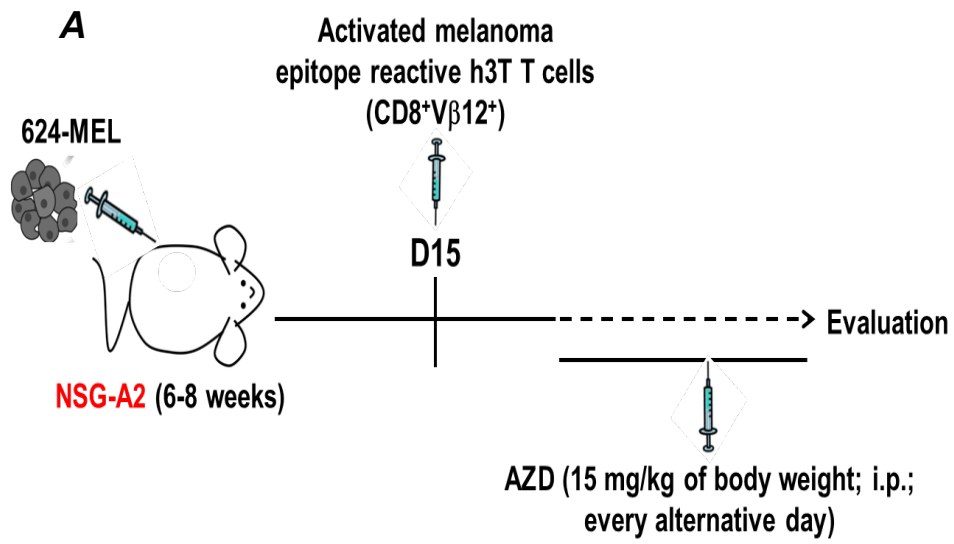
Supplementary Figure 3: NSG-A2 mice (n=4 mice/group) were inoculated with 2.5×10^6 HLA-A2⁺ human melanoma 624-MEL cells and after fifteen days mice either injected via intraperitoneal route (i.p) with vehicle (methyl acetate) or administered (i.p) AZD1208 or adoptively transferred with three-day-activated human tyrosinase epitope reactive h3T CD8 T cells (1×10^6 cells/mouse). Cohorts that received adoptive T cell therapy were further subdivided in two groups and either injected *i.p* with vehicle (methyl acetate) or AZD1208 every other day until day 21. Tumor growth was measured using digital calipers every three days. (A) Schematic diagram for the experiment, (B) mean tumor size at each time point is shown, (C) Kaplan-Meier curves were generated from data in B.

Gene ID	Fold Change	p value
<i>Eno2</i>	-30.91	4.48E-94
<i>Selenbp1</i>	-5.99	8.78E-10
<i>Pygl</i>	-5.83	4.36E-13
<i>Mcf2l</i>	-5.80	7.05E-10
<i>Ppp1r3b</i>	-3.49	0.0015554
<i>Bmp7</i>	-3.26	0.0005673
<i>Gbe1</i>	-2.82	1.70E-07
<i>Cadm1</i>	6.09	1.69E-08
<i>Il2</i>	4.95	3.94E-11
<i>Bcl2a1d</i>	3.05	3.87E-17
<i>Afp</i>	3.01	8.52E-06
<i>Tnfsf4</i>	2.99	1.53E-05
<i>Tgfb2</i>	2.82	0.004829
<i>Slc12a2</i>	2.78	6.21E-11
<i>Stat4</i>	2.69	9.76E-09
<i>Txnrd1</i>	2.64	2.21E-09
<i>Csf1</i>	2.64	2.44E-05
<i>Cxcl13</i>	2.30	0.01005
<i>mt-cytb</i>	2.30	0.000137
<i>Cd8a</i>	2.26	3.24E-05
<i>Slc15a3</i>	2.26	0.000824
<i>Nudt1</i>	2.25	0.000578
<i>Dusp1</i>	2.24	0.028118
<i>Hmgb1</i>	2.23	8.28E-09
<i>Slc25a10</i>	2.21	0.000127
<i>Slc7a11</i>	2.17	0.0011
<i>Nudc</i>	2.17	9.23E-06
<i>Timm10</i>	2.17	0.002127
<i>Glul</i>	2.16	6.95E-06
<i>Mt-ND1</i>	2.14	8.47E-07
<i>Kif4</i>	1.98	0.043843



B

Gene ID	Fold Change	<i>p</i> value
<i>Pygl</i>	-2.45	1.27E-30
<i>Ppp1r3b</i>	-2.37	1.82E-34
<i>Gbe1</i>	-1.74	6.72E-29
<i>Abca1</i>	3.17	1.82E-46
<i>Sell</i>	2.44	1.31E-169
<i>Klf4</i>	2.01	3.65E-13
<i>Socs2</i>	1.84	1.25E-68
<i>Ccl5</i>	1.80	3.60E-11
<i>Ccl3</i>	1.73	6.46E-08
<i>Il6ra</i>	1.64	1.33E-06
<i>CD27</i>	1.63	9.66E-24
<i>Cxcr3</i>	1.54	2.23E-06



Supplementary Figure 3