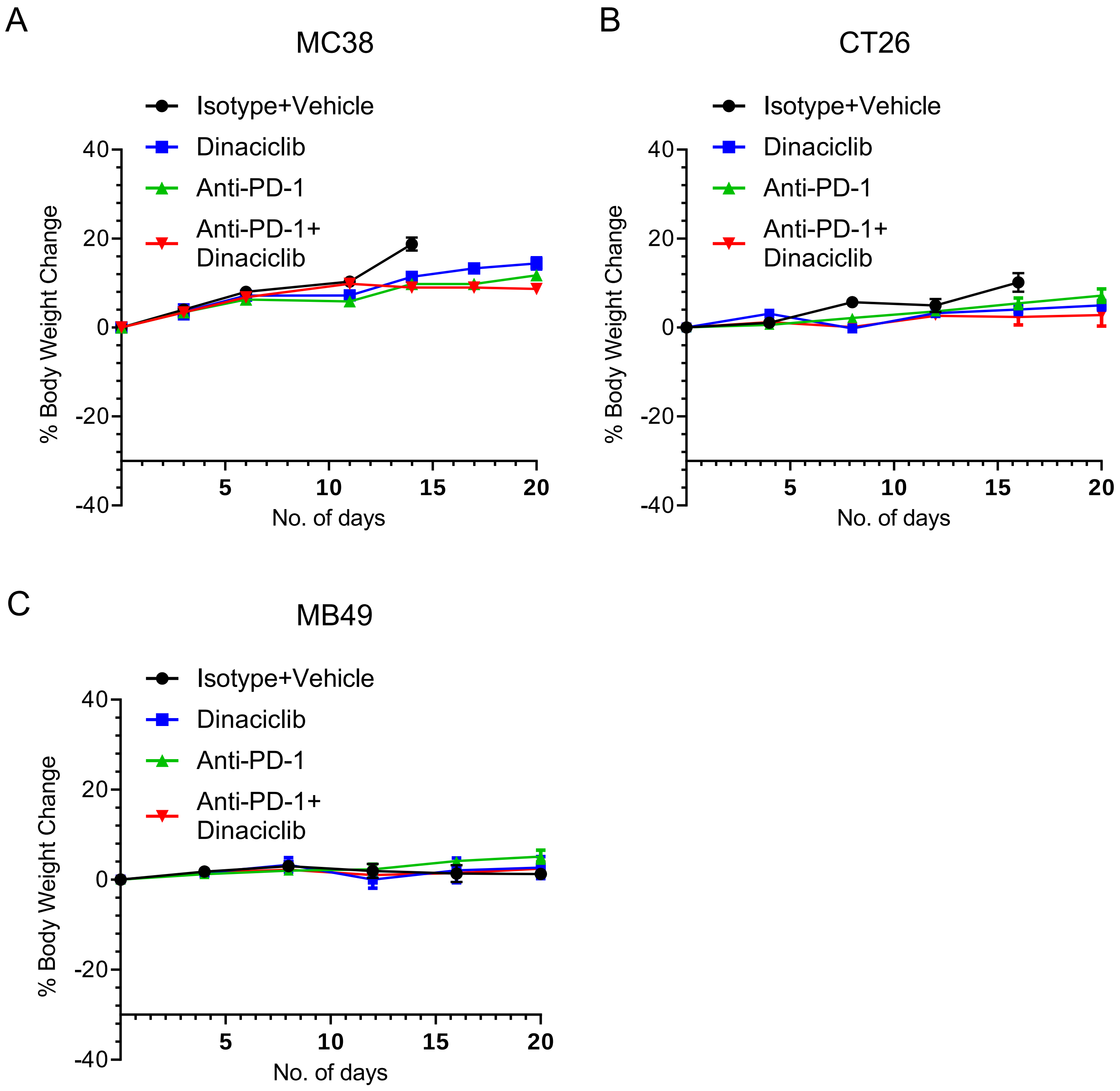
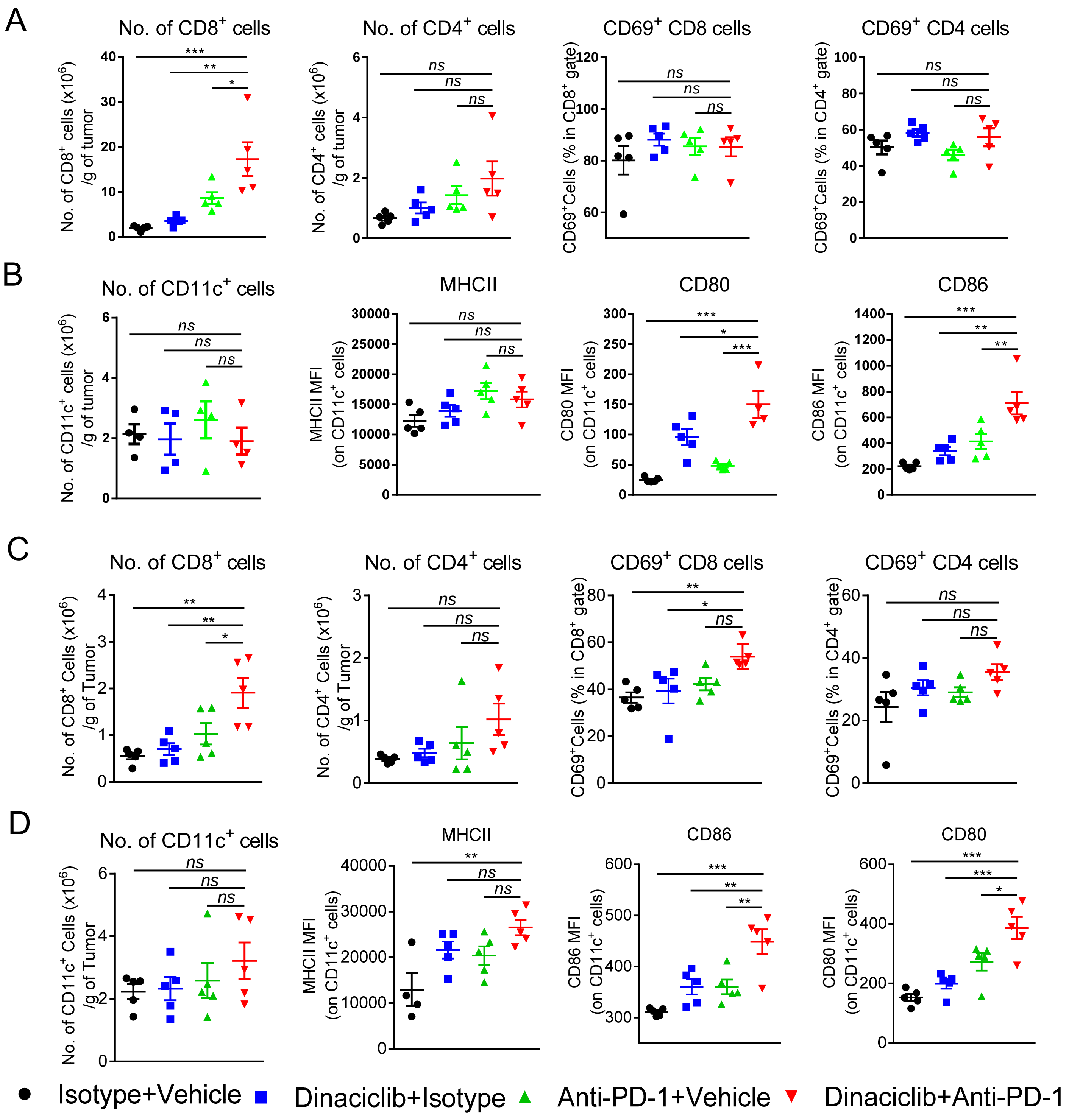
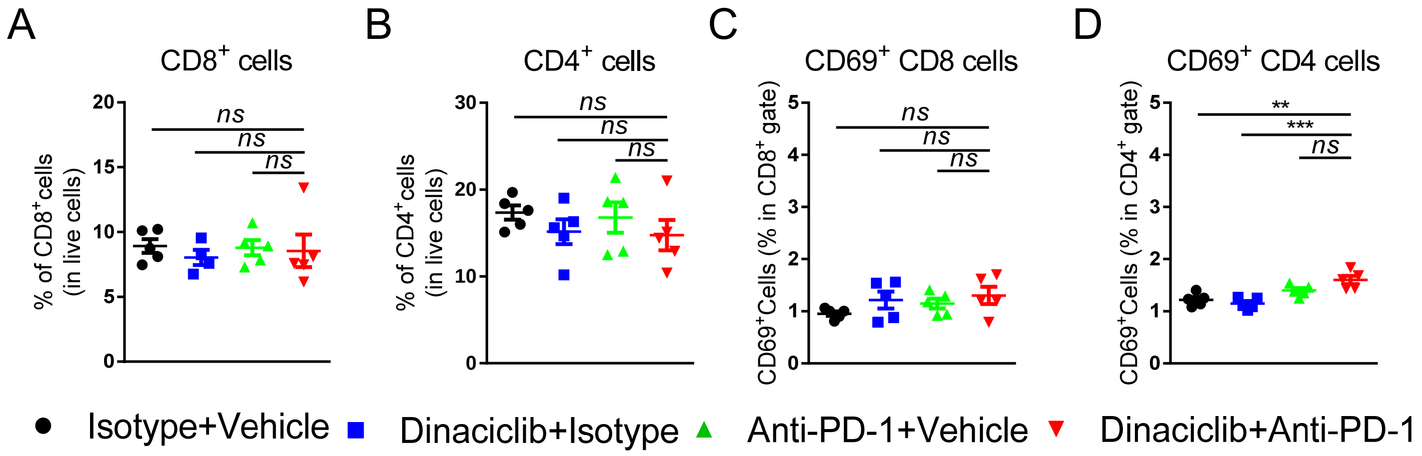


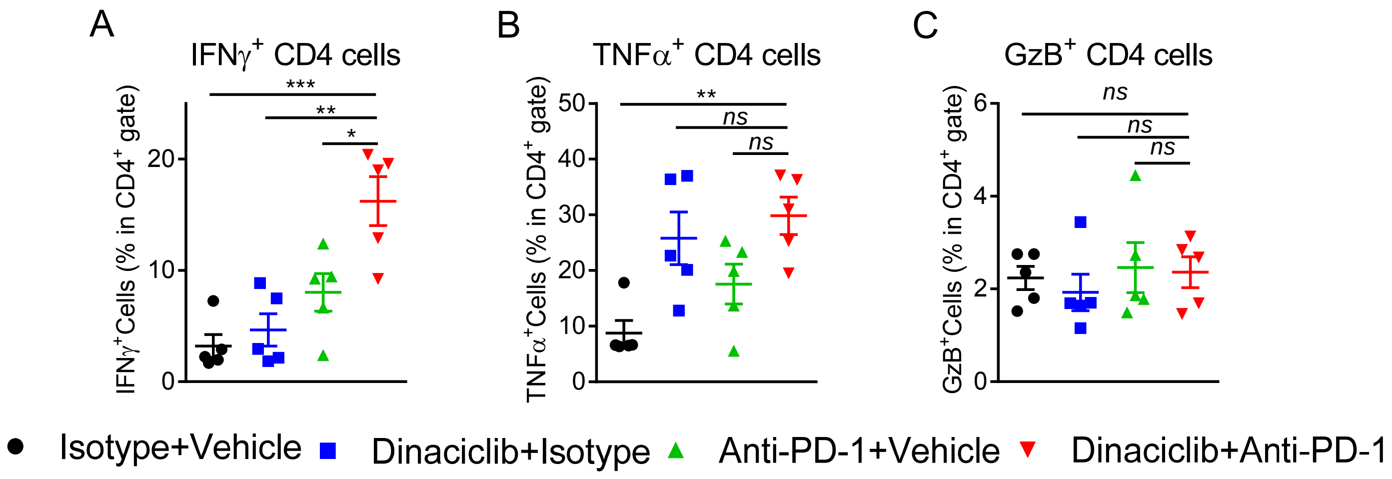
Supplementary Figure 1. No significant change in the body weight of mice treated with dinaciclib and/or anti-PD-1. Mice bearing (A) MC38 (n=12), (B) CT26 (n=10) and (C) MB49 (n=10) tumors were treated with dinaciclib and anti-PD-1 alone or in combination. Dinaciclib (10 mg/kg) or vehicle control (2 Hydroxypropyl)-β-cyclodextrin (HPbCD) was administered intraperitoneally (i.p.) in 2 doses, 2 hours apart on days 0, 4, 8, and 12. Anti-PD-1 or isotype control (mIgG1) mAb was administered i.p. at 5 mg/kg on days 0, 4, 8 and 12. Body weight was assessed every 4-5 days and represented as percentage body weight change, mean ± SEM.



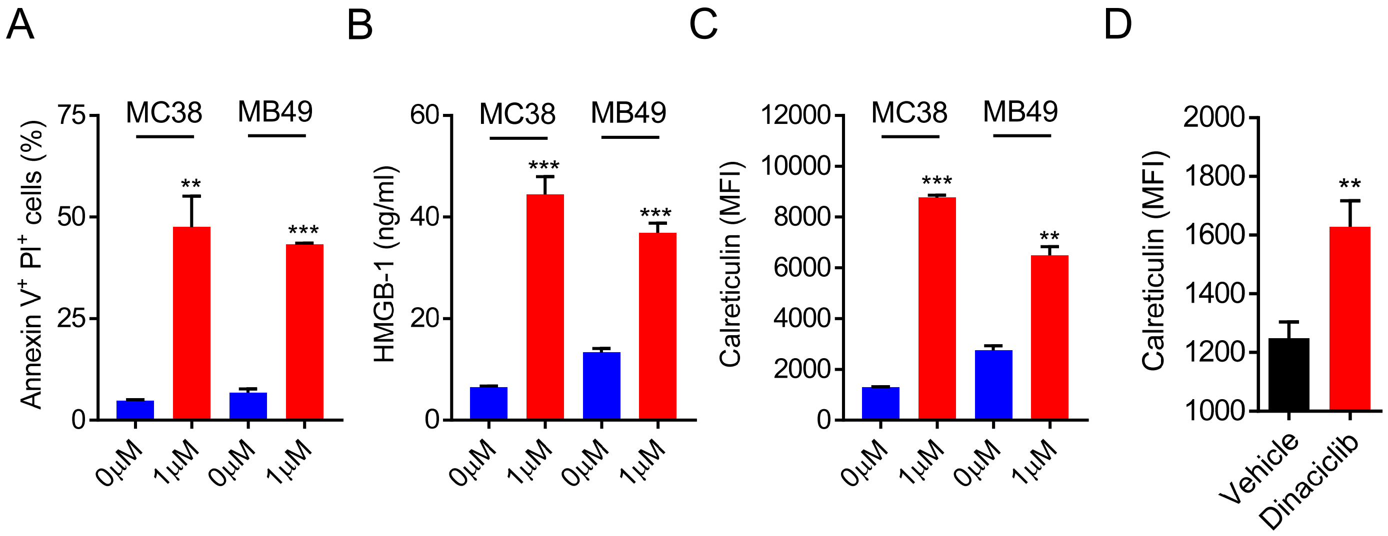
Supplementary Figure 2. Dinaciclib and anti-PD-1 combination therapy increases CD8^{+} T cell infiltration and dendritic cell activation in the tumor. Mice with established MC38 and MB49 tumors were treated with dinaciclib and/or anti-PD-1 mAb as described earlier. Tumors were isolated on day 14 and immune cells were analyzed by flow cytometry (n=5 mice per group). Shown are scatter plots for the number of tumor-infiltrating CD8+ , CD4+ T cells and CD11c+ dendritic cells in (A, B) MC38 and (C, D) and MB49 tumors. Also shown is the activation status of these populations as measured by %CD69+ CD4 and CD8 T cells (A, in MC38 and C, in MB49 tumor model) or MHC II, CD80, and CD86 mean fluorescence intensity (MFI) on DCs (B, in MC38 and D, in MB49). Statistically significant differences between groups are indicated with asterisks: ***P < 0.001; **P < 0.01; *P < 0.05.



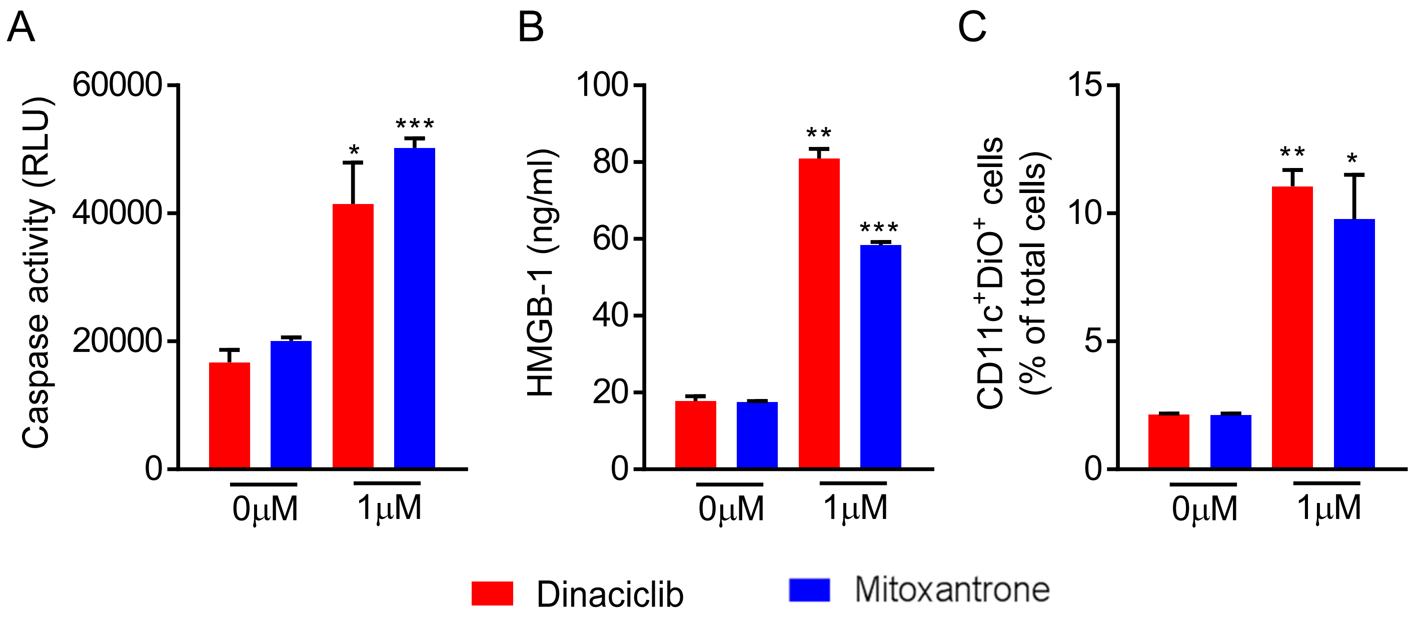
Supplementary Figure 3. No effect of dinaciclib treatment on splenic T cells. Mice with established CT26 tumors were treated with dinaciclib and anti-PD-1 mAb as described earlier. Spleens were isolated on day 14 and immune cells were analyzed by flow cytometry (n=5 mice per group). Shown are the percentages of (A) CD8+ T cells and (B) CD4+ T cells. Also shown is the activation status of these populations as measured by %CD69+ CD4 and CD8 T cells (C, D) Statistically significant differences between groups are indicated with asterisks: ***P < 0.001; **P < 0.01.



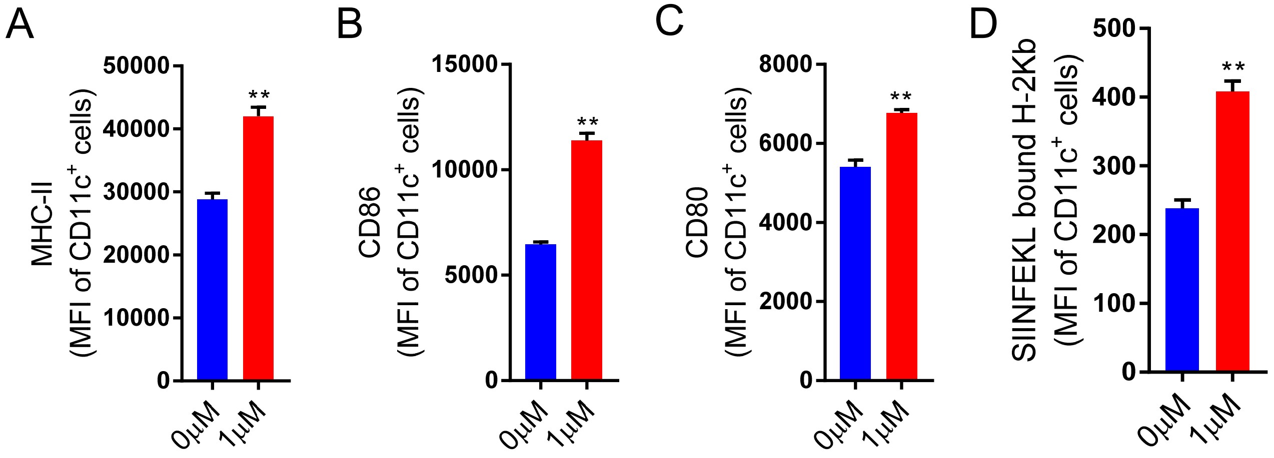
Supplementary Figure 4. Dinaciclib and anti-PD-1 combination therapy increases tumor infiltrating T cell function. Mice with established CT26 tumors were treated with dinaciclib and/or anti-PD-1 mAb as described earlier. TILs were isolated from dissociated tumors using density gradient centrifugation. For the detection of intracellular cytokines, harvested TILs were stimulated with PMA and ionomycin in presence of brefeldin A for 4h before staining. Shown are the percentages of (A) IFNγ$^+$, (B) TNFα$^+$ and (C) granzyme-B$^+$ CD4$^+$ T cells (n=5 mice per group). Statistically significant differences between groups are indicated with asterisks: ***$P < 0.001$; **$P < 0.01$; *$P < 0.05$.



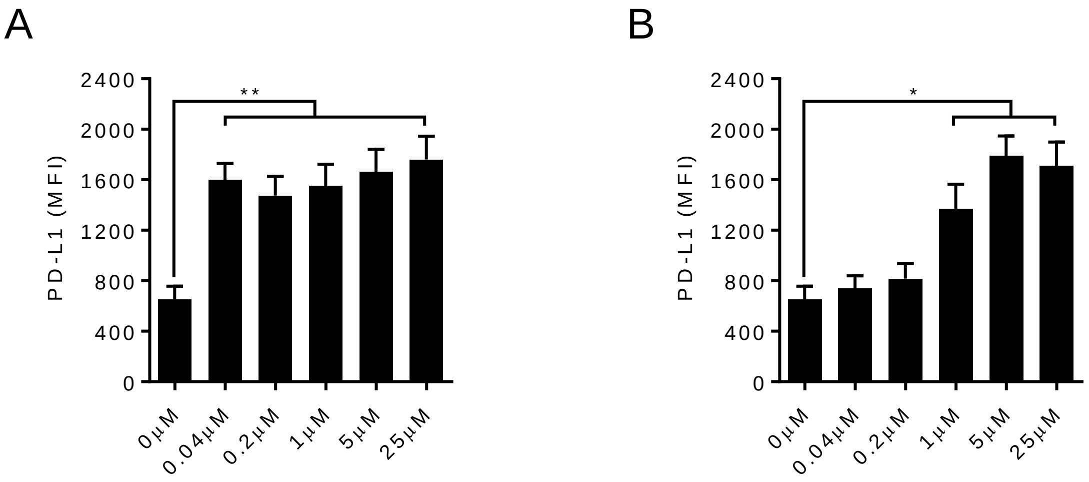
Supplementary Figure 5. Dinaciclib induces immunogenic cancer cell death *in vivo* and *in vitro*. (A-C) MC38 and MB49 cells were treated *in vitro* with 1μM dinaciclib for 24h. Graphical data showing (A) percentage of tumor cell apoptosis, (B) HMGB1 release in culture supernatant and (C) expression of calreticulin on the tumor cell surface. (D) To check *in vivo* calreticulin expression, mice with established MC38 tumors were treated with dinaciclib (10mg/kg, 2 doses, 2h apart) for two consecutive days. 24h after the last dose, calreticulin expression on live $CD45^-$ tumor cells (n=3) was assessed by flow cytometry. Statistically significant differences between groups are indicated with asterisks: ***P < 0.001; **P < 0.01; *P < 0.05.



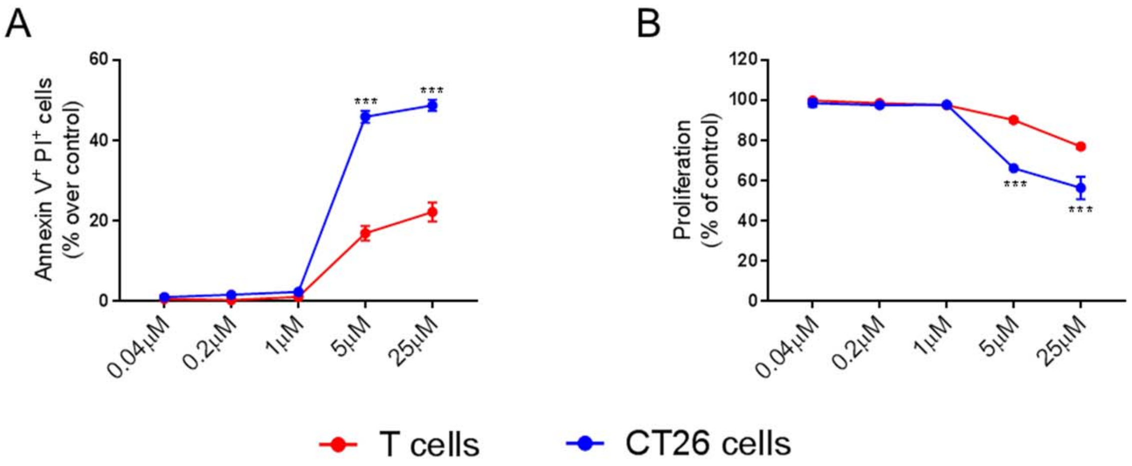
Supplementary Figure 6. Immunogenic nature of dinaciclib is comparable to known ICD-inducer mitoxantrone. CT26 cells were treated *in vitro* with 1μM dinaciclib or mitoxantrone. After 24h, (A) tumor cell apoptosis and (B) HMGB1 release into the culture supernatant were measured by caspase activity and ELISA, respectively. To detect phagocytosis, DiO-labeled CT26 cells were treated with 1μM of dinaciclib or mitoxantrone for 24h. Then cells were co-cultured with bone marrow derived dendritic cells for additional 24h. (C) Tumor cell phagocytosis by DCs is shown as the percent of double positive cells (DiO/tumor cell+ CD11c/dendritic cell+) using flow cytometry. Statistically significant differences between treatment groups and corresponding control groups are indicated with asterisks: ***$P < 0.001$; **$P < 0.01$; *$P < 0.05$.



Supplementary Figure 7. Dinaciclib treatment enhances processing and presentation of tumor antigens by DCs. MC38-OVA cells were treated with the indicated concentrations of dinaciclib for 24h, and then co-cultured with bone marrow-derived dendritic cells for an additional 24h. Expression of (A) MHCII, (B) CD86, (C) CD80 and (D) OVA peptide SIINFEKL bound to H-2K^b on CD11c+ dendritic cells were measured by flow cytometry. Data represents mean value ± SEM of replicates of one representative experiment. ** indicates p< 0.01, for comparison between individual dinaciclib dose group and the untreated group (0 μM).



Supplementary Figure 8. Dinaciclib induces PD-L1 expression on tumor cells *in vitro*. CT26 cells were treated *in vitro* with dinaciclib at the indicated concentrations for 24h either continuously (A) or washing and replacing medium after 2h (B). Shown is the expression of PD-L1 on live tumor cells after 24h in both the treatment conditions. Data represents mean value ± SEM of triplicates of one representative experiment. ** indicates p< 0.01, and * indicates p<0.05 for comparison between individual dinaciclib dose group and the untreated group (0 µM).



Supplementary Figure 9. Differential effect of dinaciclib on T cells versus tumor cells. Mouse splenic T cells (stimulated 2 days with 10ug/ml plate bound anti-CD3 and 1ug/ml soluble anti-CD28) and CT26 tumor cells were treated with different concentrations of dinaciclib as indicated. After 2h of treatment medium was replaced and cells were cultured for another 24h. Comparative data showing percentage of T cell and tumor cell (A) apoptosis and (B) proliferation. Data represents mean value ± SEM of 2 replicates of one representative experiment. *** indicates $p<0.001$ for comparison between T cells and tumor cells.

Supplementary Table-1: List of type I interferon response genes in CT26, MB49 and MC38 tumor cells after *in vitro* dinaciclib treatemnt for 24h or 2h pulse.

			CT26				MB49				MC38			
			2h pulse		24h		2h pulse		24h		2h pulse		24h	
Gene Symbol	**Description***	**Assay ID****	**FC (Log10)**	***p* value**	**FC (Log10)**	***p* value**	**FC (Log10)**	***p* value**	**FC (Log10)**	***p* value**	**FC (Log10)**	***p* value**	**FC (Log10)**	***p* value**
Bst2	bone marrow stromal cell antigen 2	Mm01609165_g1	0.763955	2.33E-05	0.734152	6.11E-06	1.310436	8.58E-08	1.4149383	8.88E-06	0.716795	0.000228	0.9393549	0.000186
Cav1	caveolin 1, caveolae protein	Mm00483057_m1	0.580232	0.002681	0.529059	0.000201	1.080793	4.62E-06	1.2007396	1.77E-06	0.432755	0.000314	0.7482968	0.000228
Jak1	Janus kinase 1	Mm00600614_m1	0.571424	0.001836	0.464512	0.000848	1.028914	1.17E-05	1.133685	7.27E-05	0.418275	0.000113	0.7327187	0.001383
Ifnar2	interferon (alpha and beta) receptor 2	Mm00494916_m1	0.49796	0.003265	0.516174	9.15E-05	0.778706	9.91E-06	1.026764	9.68E-06	0.352564	0.000649	0.5918989	0.000513
Ifitm2	interferon induced transmembrane protein 2	Mm00850080_g1	0.420506	0.002498	0.447785	0.000807	1.059991	6.01E-06	1.206264	5.2E-05	0.532804	0.000226	0.7835555	0.000207
H2-D1	histocompatibility 2, D region locus 1	Mm01612937_g1	0.818326	0.004481	0.729136	0.003679	1.089563	0.000216	1.2346506	0.000272	0.86394	7.58E-05	0.7656901	0.00287
Ifitm3	interferon induced transmembrane protein 3	Mm00847057_s1	0.66015	0.000214	0.618676	0.000439	1.094982	1.84E-06	1.3254928	1.47E-05	0.677895	0.000216	0.9852393	9.47E-05
Timp1	tissue inhibitor of metalloproteinase 1	Mm00441818_m1	0.707708	0.002115	0.729039	4.71E-05	1.057466	6.98E-07	1.2375523	5.81E-07	0.711395	2.24E-05	0.9280839	0.000122
H2-T23	histocompatibility 2, T region locus 23	Mm00439246_g1	0.541593	0.000762	0.549684	4.67E-05	0.961003	8.85E-06	1.0839764	1.87E-05	0.279781	0.01043	0.4793494	0.036767
Isg20	interferon stimulated exonuclease gene 20	Mm00469585_m1	0.478249	0.008396	0.382366	0.000246	0.813537	5.1E-05	1.0364373	5.8E-05	0.270757	0.005767	0.4978722	0.000406
Myd88	myeloid differentiation primary response gene 88	Mm00440338_m1	0.326668	0.021545	-0.020267	0.741092	0.697213	1.45E-05	0.9040395	0.002777	0.415531	0.049867	0.6618325	0.000734
Samhd1	SAM domain and HD domain, 1	Mm01250767_m1	0.367883	0.007524	0.218789	0.013189	0.812825	2.08E-07	0.9967069	3.77E-05	0.496005	7.38E-05	0.6428532	0.000424
Ccl5	C-C motif chemokine ligand 5	Mm01302428_m1	0.610901	0.000897	0.553805	9.93E-06	0.993588	0.016428	0.3371414	0.600969	0.450242	0.003794	0.7466995	0.000283
Cxcl10	chemokine (C-X-C motif) ligand 10	Mm00445235_m1	0.404564	0.006321	0.681325	2.3E-05	0.281609	0.199449	0.4329817	0.029715	1.041201	4.08E-05	1.1250865	0.000108
Oas1a	2'-5' oligoadenylate synthetase 1A	Mm00836412_m1	0.438259	0.023841	0.328233	0.001288	0.830613	0.001417	0.5616247	0.436581	0.152866	0.66911	0.3247195	0.488865
Ccl2	chemokine (C-C motif) ligand 2	Mm00441242_m1	0.905974	3.04E-05	-0.506035	5.65E-05	1.049307	7.81E-05	1.1823384	1.08E-05	0.165045	0.074404	0.4259168	0.001802
Nmi	N-myc (and STAT) interactor	Mm00803857_m1	0.269081	0.024749	0.12839	0.02541	0.763066	7.06E-05	0.756071	0.001381	0.209154	0.003151	0.3735657	0.000102
Ifi204	interferon activated gene 204	Mm00492602_m1	-0.11256	0.331261	-0.1444	0.153334	0.563055	0.000102	0.6447386	0.011694	0.029595	0.599221	0.3429896	0.004435
Gbp2	guanylate binding protein 2	Mm00494576_g1	0.128455	0.04501	-0.002458	0.984388	0.576796	0.000386	0.8579964	0.000507	0.061413	0.430052	0.3259058	0.019813
Stat1	signal transducer and activator of transcription 1	Mm00439518_m1	0.26775	0.043464	0.132948	0.052905	0.992676	0.000163	1.0461073	7.4E-05	0.35255	0.000164	0.3554357	0.024454
H2-K1	histocompatibility 2, K1, K region	Mm01612247_mH	0		0		1.338949	9.26E-06	1.4418496	3.11E-06	0.734028	7.28E-05	0.9170778	6E-05
Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	Mm01235646_g1	-0.237061	0.112029	-0.14521	0.01142	0.327207	0.018	0.5797877	0.005019	-0.130719	0.1198	0.2738306	0.029064
Ifi35	interferon-induced protein 35	Mm01260550_g1	-0.050101	0.551848	-0.07574	0.452965	0.473007	0.011774	0.7855224	2.64E-06	-0.046753	0.69575	0.2082568	0.001729
Casp1	caspase 1	Mm00438023_m1	0.194375	0.050137	0.228331	0.002885	0.729404	0.001768	0.8543297	0.000504	0.088548	0.233517	0.1504504	0.118768
Stat3	signal transducer and activator of transcription 3	Mm00456961_m1	-0.047033	0.576104	-0.168013	0.125979	0.564198	0.008918	0.545612	0.005184	-0.163982	0.013256	-0.15127	0.103872
H2-M3	histocompatibility 2, M region locus 3	Mm00469263_m1	0.35222	0.003	0.355273	0.000443	0.972125	3.57E-05	1.114201	6.53E-06	0.045212	0.491865	0.1485955	0.515518
Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	Mm00554529_m1	-0.182799	0.028513	-0.3112	0.026215	0.473682	0.003593	0.5467006	0.000329	-0.05597	0.118676	0.2453494	0.001788
Cd80	CD80 antigen	Mm00711660_m1	0.318593	0.101868	-0.096551	0.484221	0.740617	0.001817	0.5083231	0.132056	0		0	
H2-T10	histocompatibility 2, T region locus 10	Mm02393403_m1	0		0		0.002108	0.997356	0.4634514	0.001402	-0.025278	0.878392	0.3620287	0.045353
Ifnar1	interferon (alpha and beta) receptor 1	Mm00439544_m1	0.1964	0.067404	-0.248208	0.114557	0.19359	0.009492	0.3922773	0.044032	-0.146798	0.043895	0.1956917	0.166937
Ifi30	interferon gamma inducible protein 30	Mm00499131_m1	-0.061683	0.028214	-0.444396	5.39E-05	0.298366	0.007392	0.3507517	0.002402	-0.169193	0.029318	0.012237	0.888606
Ifnb1	interferon beta 1, fibroblast	Mm00439546_s1	0.168314	0.799686	0.866583	3.4E-05	0.464979	0.373901	0		0.738042	0.125731	0.4751427	0.373901
Ifna2	interferon alpha 2	Mm00833961_s1	0.397746	0.373901	0.466131	0.373901	0		0		0.968374	0.01073	0.5413593	0.373901
Irf7	interferon regulatory factor 7	Mm00516788_m1	0.881616	0.000733	0.718153	6.88E-05	0.272049	0.6262	-0.755137	5.4E-05	-0.763499	0.045537	-0.587871	0.253865
Ifitm1	interferon induced transmembrane protein 1	Mm00850040_g1	0.751666	0.004114	0.707069	6.63E-06	0.457269	0.529728	-0.189649	0.290364	0.165568	0.142561	0.3763174	0.098479
Oas1g	2'-5' oligoadenylate synthetase 1G	Mm01730198_m1	0.646922	0.00187	0.52644	0.000323	0.153117	0.777211	0.3175188	0.658619	0.077977	0.693966	-0.099429	0.117109
Traf3	TNF receptor-associated factor 3	Mm00495752_m1	0.564753	0.006566	0.340842	0.010382	0.943515	0.124575	0		0.277597	0.012298	0.5338484	0.000318
Ptpn5	protein tyrosine phosphatase, non-receptor type 5	Mm00479066_m1	0.474194	0.020688	-0.303787	0.448917	0.17308	0.72076	-0.260109	0.587423	0.298908	0.378572	-0.135206	0.775495

FC: Fold change (Log10); *Source: https://www.ncbi.nlm.nih.gov/gene/; **Source: Applied Biosystems (Thermo Fisher Scientific)

Supplementary Table 2: List of upregulated genes in whole MC38 tumor isolated from mice 24 hours after treatment with dinaciclib and anti-PD-1 alone or in combination.

Dinaciclib

Gene Symbol	Description*	FC (Log10)	*p* value
RP24-492O4.5	*retinitis pigmentosa 24 (X-linked recessive,*	1.221	5.87E-03
D630023F18Rik	RIKEN cDNA D630023F18 gene	1.177	1.03E-06
Ifnb1	interferon beta 1, fibroblast	0.982	5.33E-03
Speer3	spermatogenesis associated glutamate (E)-rich protein 3	0.923	6.79E-03
Gm7970	predicted gene 7970	0.885	6.70E-03
Gm5447	predicted gene 5447	0.871	4.55E-03
Olfr1193	olfactory receptor 1193	0.865	7.36E-03
Tacr2	tachykinin receptor 2	0.848	9.31E-03
Pdzd9	PDZ domain containing 9	0.842	3.71E-03
Ankmy1	ankyrin repeat and MYND domain containing 1	0.829	6.09E-03
Adam1b	a disintegrin and metallopeptidase domain 1b	0.736	4.39E-03
Oas1d	2'-5' oligoadenylate synthetase 1D	0.634	7.77E-03
Grid1	glutamate receptor, ionotropic, delta 1	0.623	2.99E-03
Teddm1b	transmembrane epididymal protein 1B	0.603	7.43E-03
Igsf21	immunoglobulin superfamily, member 21	0.59	5.39E-03
F11	coagulation factor XI	0.587	8.47E-03
Plekhb1	pleckstrin homology domain containing, family B (evectins) member 1	0.558	6.89E-03
Tshb	thyroid stimulating hormone, beta subunit	0.523	7.62E-03
Aldh8a1	aldehyde dehydrogenase 8 family, member A1	0.504	3.99E-03
Gm5615	predicted gene 5615	0.491	3.98E-03
Ccdc81	coiled-coil domain containing 81	0.477	4.24E-03
Pax5	paired box 5	0.468	1.42E-03
Dcdc2c	doublecortin domain containing 2C	0.454	4.46E-03
Rimbp3	RIMS binding protein 3	0.432	1.47E-04
Oas3	2'-5' oligoadenylate synthetase 3	0.428	2.53E-03
Ifi44	interferon-induced protein 44	0.423	6.09E-04
Syngr4	synaptogyrin 4	0.392	1.58E-05
Il1rl1	interleukin 1 receptor-like 1	0.391	2.50E-04
Rsad2	radical S-adenosyl methionine domain containing 2	0.391	2.03E-03
Oasl1	2'-5' oligoadenylate synthetase-like 1	0.389	1.45E-03
Ifit3b	interferon-induced protein with tetratricopeptide repeats 3B	0.383	7.83E-03
Prl2c3	prolactin family 2, subfamily c, member 3	0.38	8.22E-03
Slc47a1	solute carrier family 47, member 1	0.377	1.84E-03
Prl2c5	prolactin family 2, subfamily c, member 5	0.369	2.33E-03
Cmpk2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	0.358	4.79E-03
Ifit3	interferon-induced protein with tetratricopeptide repeats 3	0.358	8.24E-03
Oas1g	2'-5' oligoadenylate synthetase 1G	0.357	6.16E-04
Oas1a	2'-5' oligoadenylate synthetase 1A	0.335	5.12E-04
Isg15	ISG15 ubiquitin-like modifier	0.331	2.15E-03
Apol9a	apolipoprotein L 9a	0.329	1.56E-04
Usp18	ubiquitin specific peptidase 18	0.329	7.56E-03
Lgr6	leucine-rich repeat-containing G protein-coupled receptor 6	0.326	1.55E-03
Dlk2	delta-like 2 homolog (Drosophila)	0.325	3.43E-03
Nxf7	nuclear RNA export factor 7	0.324	8.45E-03
Gm6904	predicted gene 6904	0.322	3.58E-03
Ces2e	carboxylesterase 2E	0.322	3.04E-03
Phf11d	PHD finger protein 11D	0.321	1.73E-03
Phf11a	PHD finger protein 11A	0.307	8.52E-03
Apol9b	apolipoprotein L 9b	0.303	6.80E-04
Ddx60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	0.301	9.67E-04

Anti-PD-1

Gene Symbol	Description*	FC (Log10)	*p* value
Ifne	nterferon epsilon	0.958	4.51E-03
Slc27a5	solute carrier family 27 (fatty acid transporter), member 5	0.849	9.48E-03
Cartpt	CART prepropeptide	0.834	5.99E-03
Spata17	spermatogenesis associated 17	0.802	7.45E-03
Ppil6	peptidylprolyl isomerase (cyclophilin)-like 6	0.793	5.13E-03
Sun3	Sad1 and UNC84 domain containing 3	0.768	3.06E-03
Fam163a	family with sequence similarity 163, member A	0.664	2.03E-04
Tm4sf4	transmembrane 4 superfamily member 4	0.587	3.96E-03

Nkx2-3	NK2 homeobox 3	0.553	5.03E-03
Pnoc	prepronociceptin	0.536	5.47E-03
Lrrc38	leucine rich repeat containing 38	0.527	5.55E-03
Fcrl6	Fc receptor-like 6	0.481	8.43E-03
Gbp6	guanylate binding protein 6	0.45	9.11E-03
Gzmc	granzyme C	0.438	5.21E-03
Tmc1	transmembrane channel-like gene family 1	0.427	5.61E-03
Trpm1	transient receptor potential cation channel, subfamily M, member 1	0.421	5.85E-03
Gzmb	granzyme B	0.406	6.43E-03
Gbp10	guanylate-binding protein 10	0.391	7.78E-03
Dyrk4	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	0.372	8.79E-04
S100a3	S100 calcium binding protein A3	0.371	8.66E-03
Tgtp1	T cell specific GTPase 1	0.342	6.97E-03
Serpina3f	serine (or cysteine) peptidase inhibitor, clade A, member 3F	0.337	7.24E-03
Apol6	apolipoprotein L 6	0.334	6.83E-03
Gm12185	predicted gene 12185	0.331	4.85E-03
Igtp	interferon gamma induced GTPase	0.331	7.08E-03
Ubd	ubiquitin D	0.314	2.50E-03
Batf2	basic leucine zipper transcription factor, ATF-like 2	0.313	7.38E-03
Cst7	cystatin F (leukocystatin)	0.312	6.38E-03
Anti-PD-1+Dinaciclib			
Gene Symbol	**Description***	**FC (Log10)**	***p* value**
Mup19	major urinary protein 19	1.54	5.04E-03
Myf6	myogenic factor 6	1.468	4.97E-03
Prm1	protamine 1	1.384	4.64E-03
Gm7325	predicted gene 7325	1.269	1.26E-03
Hspb3	heat shock protein 3	1.232	6.74E-03
Gck	glucokinase	1.224	5.83E-03
Rasd2	radical S-adenosyl methionine domain containing 2	1.216	5.22E-03
Gm3448	predicted gene 3448	1.203	4.38E-03
Ifnb1	interferon beta 1, fibroblast	1.151	5.20E-03
Myod1	myogenic differentiation 1	1.146	6.82E-03
Gm13305	predicted gene 13305	1.138	2.73E-03
Pdk4	pyruvate dehydrogenase kinase, isoenzyme 4	1.118	4.24E-03
Krt20	keratin 20	1.116	5.17E-04
Trim63	tripartite motif-containing 63	1.082	3.86E-03
1700015F17Rik	RIKEN cDNA 1700015F17 gene	1.041	7.35E-03
2300005B03Rik	RIKEN cDNA 2300005B03 gene	1.02	4.76E-03
Myog	myogenin	1.019	4.79E-03
Nmrk2	nicotinamide riboside kinase 2	1.019	8.44E-03
Khdc1a	KH domain containing 1A	1.011	2.55E-04
Sgcg	sarcoglycan, gamma (dystrophin-associated glycoprotein)	1.005	5.22E-03
Krt24	keratin 24	0.997	7.55E-03
Hspb7	heat shock protein family, member 7 (cardiovascular)	0.997	8.09E-03
Rbm24	RNA binding motif protein 24	0.988	8.26E-03
Ninj2	ninjurin 2	0.976	3.93E-03
Abcb11	ATP-binding cassette, sub-family B (MDR/TAP), member 11	0.975	2.00E-04
D630023F18Rik	RIKEN cDNA D630023F18 gene	0.974	2.50E-06
2310007B03Rik	RIKEN cDNA 2310007B03 gene	0.963	7.63E-07
Gm19345	predicted gene, 19345	0.952	7.71E-03
Gm21655	predicted gene, 21655	0.95	4.31E-03
1700014D04Rik	RIKEN cDNA 1700014D04 gene	0.949	9.38E-04
Msln	mesothelin	0.941	4.80E-03
Fabp12	fatty acid binding protein 12	0.935	5.63E-03
Mylk2	myosin light chain kinase 2	0.925	6.83E-03
Eef1a2	eukaryotic translation elongation factor 1 alpha 2	0.915	9.52E-03
Mybph	myosin binding protein H	0.912	5.75E-03
Hrc	histidine rich calcium binding protein	0.908	3.44E-03
Tmod4	tropomodulin 4	0.9	2.79E-03
Tnnt3	troponin T3, skeletal, fast	0.894	9.93E-03
Gzmf	granzyme F	0.89	9.19E-03
Myo18b	myosin XVIIIb	0.89	4.68E-03
Smtnl1	smoothelin-like 1	0.882	9.68E-03
Gm15401	predicted gene 15401	0.882	6.67E-03

Pdlim3	PDZ and LIM domain 3	0.881	8.00E-03
Myh4	myosin, heavy polypeptide 4, skeletal muscle	0.878	8.60E-03
Rhox8	reproductive homeobox 8	0.85	5.13E-03
Asb16	ankyrin repeat and SOCS box-containing 16	0.847	7.55E-04
Pygm	glycogen phosphorylase, muscle associated	0.847	9.83E-03
Mybpc1	myosin binding protein C, slow-type	0.842	8.44E-03
Ano5	anoctamin 5	0.817	1.90E-03
Ddo	D-aspartate oxidase	0.806	4.12E-03
Zfp641	zinc finger protein 641	0.805	6.05E-03
Klhl41	kelch-like 41	0.797	8.83E-03
Cmya5	cardiomyopathy associated 5	0.79	4.47E-03
Neb	nebulin	0.786	8.92E-03
Dusp27	dual specificity phosphatase 27 (putative)	0.784	4.17E-03
Nrap	nebulin-related anchoring protein	0.782	6.38E-03
Nxf2	nuclear RNA export factor 2	0.779	6.22E-03
Coro6	coronin 6	0.773	7.06E-03
Des	desmin	0.767	8.46E-03
Hspb1	heat shock protein 1	0.756	6.35E-03
Ryr1	ryanodine receptor 1, skeletal muscle	0.756	5.99E-03
Mboat4	membrane bound O-acyltransferase domain containing 4	0.742	4.70E-03
Vmn1r42	vomeronasal 1 receptor 42	0.74	4.15E-03
Nos1	nitric oxide synthase 1, neuronal	0.737	4.08E-03
Cryab	crystallin, alpha B	0.734	6.65E-03
Angptl4	angiopoietin-like 4	0.72	4.04E-04
Sgca	sarcoglycan, alpha (dystrophin-associated glycoprotein)	0.704	9.29E-03
Cap2	CAP, adenylate cyclase-associated protein, 2 (yeast)	0.704	6.52E-03
Dynap	dynactin associated protein	0.685	2.83E-04
4930548H24Rik	RIKEN cDNA 4930548H24 gene	0.677	8.27E-03
Fbxo40	F-box protein 40	0.666	9.72E-03
Hspb2	heat shock protein 2	0.665	9.96E-03
Prl2c3	prolactin family 2, subfamily c, member 3	0.653	2.92E-04
Klhl30	kelch-like 30	0.646	9.79E-03
Arg1	arginase, liver	0.642	4.42E-03
Tmem182	transmembrane protein 182	0.628	5.00E-03
Wfdc3	WAP four-disulfide core domain 3	0.579	6.77E-03
Myh7	myosin, heavy polypeptide 7, cardiac muscle, beta	0.578	1.73E-03
Ifit1bl1	interferon induced protein with tetratricpeptide repeats 1B like 1	0.574	1.99E-06
Ffar1	free fatty acid receptor 1	0.572	2.50E-03
Oasl1	2'-5' oligoadenylate synthetase-like 1	0.568	1.48E-05
Gm5415	predicted gene 5415	0.567	2.36E-04
Rsad2	radical S-adenosyl methionine domain containing 2	0.56	1.54E-06
A530064D06Rik	RIKEN cDNA A530064D06 gene	0.56	1.40E-04
Stra6l	STRA6-like	0.553	5.12E-04
Htr2b	5-hydroxytryptamine (serotonin) receptor 2B	0.549	3.28E-03
Tnnt1	troponin T1, skeletal, slow	0.549	4.95E-03
Cdhr3	cadherin-related family member 3	0.54	9.89E-03
Ms4a4a	membrane-spanning 4-domains, subfamily A, member 4A	0.538	4.62E-04
Clca3a1	chloride channel accessory 3A1	0.537	5.42E-04
Gzmc	granzyme C	0.535	7.68E-03
Ifit3	interferon-induced protein with tetratricopeptide repeats 3	0.533	9.26E-06
Ifit3b	interferon-induced protein with tetratricopeptide repeats 3B	0.524	8.42E-06
Gzmb	granzyme B	0.518	2.67E-03
BC094916	interferon activated gene 214	0.516	7.21E-04
Tal2	T cell acute lymphocytic leukemia 2	0.512	9.48E-03
1700123I01Rik	RIKEN cDNA 1700123I01 gene	0.508	7.94E-03
Il21	interleukin 21	0.504	3.79E-03
Ttn	titin	0.503	9.50E-03
Prl2c5	prolactin family 2, subfamily c, member 5	0.489	1.72E-04
Il1rn	interleukin 1 receptor antagonist	0.488	8.27E-03
Ppbp	pro-platelet basic protein	0.486	7.74E-03
Cmpk2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	0.481	6.64E-06
Il1rl1	interleukin 1 receptor-like 1	0.48	3.40E-04
Isg15	ISG15 ubiquitin-like modifier	0.48	1.17E-05
Il7r	interleukin 7 receptor	0.478	4.85E-03

Fam189a2	family with sequence similarity 189, member A2	0.476	7.71E-03
Oas3	2'-5' oligoadenylate synthetase 3	0.476	1.70E-04
Plin2	perilipin 2	0.471	2.69E-04
B430306N03Rik	RIKEN cDNA B430306N03 gene	0.47	9.02E-04
Slc9a2	solute carrier family 9 (sodium/hydrogen exchanger), member 2	0.459	4.17E-04
Clic5	chloride intracellular channel 5	0.457	4.27E-03
Ifit1	interferon-induced protein with tetratricopeptide repeats 1	0.449	1.33E-04
Srgn	serglycin	0.448	2.31E-03
C5ar2	complement component 5a receptor 2	0.448	4.94E-04
Gm4955	predicted gene 4955	0.446	1.27E-04
Ksr2	kinase suppressor of ras 2	0.442	1.91E-03
Ms4a4c	membrane-spanning 4-domains, subfamily A, member 4C	0.438	1.07E-04
Il18bp	interleukin 18 binding protein	0.436	1.10E-03
Usp18	ubiquitin specific peptidase 18	0.435	1.01E-04
Oas1g	2'-5' oligoadenylate synthetase 1G	0.434	4.35E-05
Ifi44	interferon-induced protein 44	0.433	2.84E-05
Gprc5a	G protein-coupled receptor, family C, group 5, member A	0.431	2.42E-04
Gpr55	G protein-coupled receptor 55	0.428	2.58E-03
Slfn4	schlafen 4	0.426	5.16E-04
Rhbg	Rhesus blood group-associated B glycoprotein	0.426	3.55E-03
Spink2	serine peptidase inhibitor, Kazal type 2	0.425	9.14E-03
Apol9a	apolipoprotein L 9a	0.419	1.52E-06
Prl2c2	prolactin family 2, subfamily c, member 2	0.411	2.95E-03
Oas1a	2'-5' oligoadenylate synthetase 1A	0.411	7.64E-06
Fam195a	family with sequence similarity 195, member A	0.41	2.54E-05
Slfn1	schlafen 1	0.409	1.30E-05
Phf11a	PHD finger protein 11A	0.409	7.42E-04
Mx1	MX dynamin-like GTPase 1	0.4	3.22E-04
Oasl2	2'-5' oligoadenylate synthetase-like 2	0.397	1.16E-05
Adssl1	adenylosuccinate synthetase like 1	0.395	3.98E-03
Zdbf2	zinc finger, DBF-type containing 2	0.394	1.81E-03
Apol9b	apolipoprotein L 9b	0.394	4.51E-07
Myh3	myosin, heavy polypeptide 3, skeletal muscle, embryonic	0.393	4.87E-03
AA467197	expressed sequence AA467197	0.393	2.45E-03
Pyhin1	pyrin and HIN domain family member 1	0.391	9.30E-05
Irf7	interferon regulatory factor 7	0.39	2.04E-04
Phf11d	PHD finger protein 11D	0.388	7.61E-06
Abcc3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	0.384	4.63E-04
Dhx58	DEXH (Asp-Glu-X-His) box polypeptide 58	0.384	5.47E-05
Omp	olfactory marker protein	0.383	9.69E-03
Ocstamp	osteoclast stimulatory transmembrane protein	0.378	1.61E-03
Syngr4	synaptogyrin 4	0.378	1.91E-03
Pax5	paired box 5	0.377	3.63E-03
Ttll9	tubulin tyrosine ligase-like family, member 9	0.376	2.18E-03
Oas2	2'-5' oligoadenylate synthetase 2	0.371	1.25E-04
Slc37a2	solute carrier family 37 (glycerol-3-phosphate transporter), member 2	0.371	3.74E-04
Aldh1b1	aldehyde dehydrogenase 1 family, member B1	0.37	3.67E-03
Hsh2d	hematopoietic SH2 domain containing	0.368	1.11E-03
Ces2e	carboxylesterase 2E	0.368	4.28E-03
Cd22	CD22 antigen	0.366	5.97E-03
Ptger2	prostaglandin E receptor 2 (subtype EP2)	0.365	3.35E-03
Car7	carbonic anhydrase 7	0.365	9.47E-03
Nr1h3	nuclear receptor subfamily 1, group H, member 3	0.364	9.94E-03
Adh1	alcohol dehydrogenase 1 (class I)	0.364	7.15E-03
Lag3	lymphocyte-activation gene 3	0.363	7.63E-03
Gja8	gap junction protein, alpha 8	0.361	6.91E-03
Fcgr4	Fc receptor, IgG, low affinity IV	0.357	6.06E-03
Gm4841	predicted gene 4841	0.357	2.75E-03
Nkg7	natural killer cell group 7 sequence	0.357	6.54E-03
Guca1b	guanylate cyclase activator 1B	0.356	1.97E-03
Dlk2	delta-like 2 homolog (Drosophila) [Mus musculus	0.354	7.91E-03
Gm5431	predicted gene 5431	0.353	1.72E-04
Tfec	transcription factor EC	0.353	2.53E-03
Dnah6	dynein, axonemal, heavy chain 6	0.353	8.32E-03

Csf2rb2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)	0.351	3.02E-03
Xaf1	XIAP associated factor 1	0.349	4.15E-06
Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D	0.348	9.01E-04
Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	0.348	6.73E-03
Ankrd55	ankyrin repeat domain 55	0.347	7.93E-03
Bst2	bone marrow stromal cell antigen 2	0.346	3.14E-06
Fam110c	family with sequence similarity 110, member C	0.345	3.60E-04
AC132444.1	-	0.345	4.04E-03
Gm5150	predicted gene 5150	0.343	1.35E-03
Nrip3	nuclear receptor interacting protein 3	0.343	9.26E-03
Ccl5	C-C motif chemokine ligand 5	0.342	9.88E-04
Tmem220	transmembrane protein 220	0.34	1.58E-03
Hap1	huntingtin-associated protein 1	0.34	7.06E-05
Ifi35	interferon-induced protein 35	0.339	4.03E-06
Slc7a8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	0.339	3.20E-04
Gpr171	G protein-coupled receptor 171	0.338	2.70E-03
Tbx21	T-box 21	0.334	6.01E-04
Tnfrsf11a	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	0.333	1.08E-03
Zbp1	Z-DNA binding protein 1	0.33	2.53E-05
Igsf6	immunoglobulin superfamily, member 6	0.33	5.63E-03
Adap2	ArfGAP with dual PH domains 2	0.329	7.39E-04
Aldh3b1	aldehyde dehydrogenase 3 family, member B1	0.327	4.98E-04
Tnfrsf19	tumor necrosis factor receptor superfamily, member 19	0.326	4.05E-03
Acrbp	proacrosin binding protein	0.324	4.02E-04
Lgr6	leucine-rich repeat-containing G protein-coupled receptor 6	0.322	2.25E-03
Grrp1	glycine/arginine rich protein 1	0.322	9.61E-03
Pnma5	paraneoplastic Ma antigen family member 5	0.322	6.85E-03
Ribc1	RIB43A domain with coiled-coils 1	0.322	7.65E-04
Misp	mitotic spindle positioning	0.321	1.38E-03
Gm9913	predicted gene 9913	0.321	2.36E-03
Pydc3	interferon activated gene 208	0.319	1.17E-04
Rtp4	receptor transporter protein 4	0.318	1.61E-06
Trex1	three prime repair exonuclease 1	0.318	6.14E-05
Rasl11a	RAS-like, family 11, member A	0.314	4.30E-04
Pydc4	interferon activated gene 213	0.313	3.36E-04
Col11a2	collagen, type XI, alpha 2	0.313	3.25E-03
Pira2	paired-Ig-like receptor A2	0.31	7.69E-04
Galnt6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6	0.308	2.52E-03
Tnfsf13	tumor necrosis factor (ligand) superfamily, member 13	0.307	6.07E-03
Slamf7	SLAM family member 7	0.305	3.92E-03
Gm10146	predicted gene 10146	0.305	8.98E-03
Enho	energy homeostasis associated	0.305	8.29E-03
Cpt1a	carnitine palmitoyltransferase 1A	0.302	5.73E-04

FC: Fold change (Log10); *Source: https://www.ncbi.nlm.nih.gov/gene/