A CRISPR-Cas9 delivery system for *in vivo* screening of genes in the immune system LaFleur et al.



## Supplementary Figure 1: Transduced immune cells are robustly recovered in CHIME-generated chimeras

(a) Representative flow cytometry plots for sorting of LSK cells (used for all chimera experiments). (b) Representative flow cytometry plots for gating of Vex<sup>+</sup> CD19<sup>+</sup> B cells for Figure 1b, Figure 1d, and Supplementary Figure 3d. (c) Representative flow cytometry plots for gating of Vex<sup>+</sup> red-pulp macrophages for Figure 1b. (d) Representative flow cytometry plots for gating of Vex<sup>+</sup> cross-presenting dendritic cells for Figure 1b. (e) Representative flow cytometry plots of Vex expression on major immune lineages in mice transduced with a non-targeting control sgRNA. All experiments had at least four biological replicate animals per group and are representative of two independent experiments.



(a) Day 30 kidney viral titer following LCMV Clone 13 infection of WT or Cas9 + sgRNA chimeras. (b) Representative flow cytometry plots of Granzyme B, Ki67, PD-1, GP<sub>33-41</sub> tetramer, and Tim-3 expression on CD8<sup>+</sup> T cells at day 30 post LCMV Clone 13 infection. (c) Quantification of (b). (d) Representative flow cytometry plots for gating of Vex<sup>+</sup> naive CD8<sup>+</sup> T cells for transfer experiments for Figure 1d, Figures 2b-i, and transfer experiments in Figures 3-5. (e) TIDE assay on naïve CD8<sup>+</sup> T cells containing *Batf* sgRNAs prior to transfer into the competitive assay. (f) Gating strategy for analyzing transferred CD8<sup>+</sup> T cells from the spleen following LCMV Clone 13 infection for Figures 3b-c, Figures 4b-h, Supplementary Figures 3h-j, and Figure 5. (g) Gating strategy for analyzing transferred CD8<sup>+</sup> T cells from the tumor following tumor challenge for Figures 3d and 3e. All experiments had five biological replicate animals per group and are representative of two independent experiments. Bar graphs represent mean and error bars represent standard deviation. Statistical significance was assessed among the replicate bone marrow chimeras by two-sided unpaired t-test (a), or one-way ANOVA (c) (ns p>.05, \* p<.05, \*\* p<.001, \*\*\*\* p<.001). Source data are provided as a source data file.



## Supplementary Figure 3: Bandwidth experiments increase the potential scale of in vivo CHIME screening

(a) Representative flow cytometry plots for gating of Vex<sup>+</sup> bone marrow subsets for Supplementary Figure 3d. (b) Representative flow cytometry plots for gating of Vex<sup>+</sup> macrophages and dendritic cells from the spleen for Supplementary Figure 3d. (c) Schematic of bandwidth experiments. (d) Quantification of detected barcodes per mouse in the different immune populations analyzed using a 25 read cutoff. (e) Plot of Monte Carlo simulation results following pooling of 11-80 chimeras to recover a 5000 sgRNA library. Magenta dotted lines depict 30 chimeras (x-axis) and 0.95 (y-axis). (f) Weight loss of animals from LCMV Clone 13 screen normalized to day 0. (g) Kidney viral titer of animals from LCMV Clone 13 screen normalized to kidney weight. (h) Representative flow cytometry plots analyzing CD44 expression on CD45.1<sup>+</sup> CD8<sup>+</sup> T cells from the spleen of mice from LCMV Clone 13 screen. (i) Quantification of (h). (j) Quantification of sgRNAs detected with 25 read cutoff from experiment in LCMV Clone 13 screen. (k) Plot of Pearson R correlation vs. the number of replicate mice analyzed in the lung from mice used in experiment in LCMV Clone 13 screen. The bandwidth experiment had five biological replicate animals per group and is representative of one experiment. The *in vivo* screen had thirty biological replicate animals per group and is representative of one experiment.

Supplementary Tat	Die 1: STARS anal	ysis of in vivo scre	sen, Related to Figures 40-n					
Spleen Enriched	Number of	Booko of		Mostoprished	STADE	Average		
Gene Symbol	nerturbations	nerturbations	Perturbations	nerturbation	Score	Score	p-value	FDR
Pdcd1	4	1:2:12:27	GCAATACAGGGATAC:GACACACGGCGCAAT:GCAGCTTGTCCAACT:GCACCCCAAGGCAAA	2	2,718512	2,23615	0.003794	0.075873
Kdr	4	6:10:11:63	GATACGTTTGAGAAC:GTTACCCGCTTAACG:GTCGGACTTGACTGC:GTTGTAAAGAATGGA	3	2.443697	1.383396	0.006477	0.06477
Adora2a	4	4;7;23;38	GGAGAGCCAACCCCT;GTGTCGATGGCAATA;GCTCCACAAAGACCT;GAAGCAGTTGATGAT	4	1.846436	1.485582	0.030627	0.204179
Ptpn2	4	9;16;41;44	GCACTCTATGAGGAT;GAATATGAGAAAGTA;GAAGAAGTTACATCT;GTGCAGTGATCCATT	4	1.59176	1.026825	0.058108	0.290539
Olfr5	3	21;22;65	GTGGGTCATACAAGC;GTACACTACCCAGTA;GACATGACAGGTTGA	2	1.017729	0.709741	0.211659	0.846634
Dgkz	4	20;37;42;95	GCAAGICITIGATCI;GACCCAGIGGIGICI;GAGCACATCCGAGIA;GATGGAGCCACIGAC	3	0.861254	0.595126	0.297432	0.991441
Socs3	4	30;39;43;70		3	0.837031	0.031124	0.30997	0.863628
Havcr2	4	30:33:100:104	GCTAAAGGGCGATCT:GTTACACTCTATCTA:GATCAGTTCTGAGCA:GTTCTCCAAGAACCC	2	0.57741	0.477265	0.571964	1
Cpt1a	4	55;59;75;79	GCACATTGTCGTGTA;GACGTTGGACGAATC;GCATACTGCTGTATC;GAGGAATACATCTAC	4	0.575062	0.500489	0.578395	1
Prkab2	4	13;73;83;94	GTACAAACTCTTTGT;GTCCTCACCTCTTTA;GAGGAGCACAAGATC;GTTCAGACCAGCGGA	2	0.52437	0.506811	0.672218	1
Lag3	4	15;72;86;102	GGGTGCGGGTTGTCT;GTCAGCAGCGTACAC;GATCCTAACTTTCTA;GAGAGAAGTCCCCGC	2	0.513187	0.483718	0.691696	1
Hk2	4	49;69;71;89	GGAGATGCGTCACAT;GAAGGCCATCCAGCG;GATCCGGAGTTGACC;GATTCCCGAGGACAT	2	0.484154	0.473383	0.754569	1
ll1r1	4	19;64;78;87	GCAGCAAGACCCCCCA;GCGTATGTCCTATAC;GAGCATACAATTGTA;GACTGTGTTAGAGAA	2	0.449544	0.413085	0.852972	1
Entrod 1	4	28;58;68;85		3	0.442735	0.415401	0.871108	1
Tnfrsf1a	4	32:50:82:99	GGATCCCGTGCCTGT GAGTTGCAAGACATG GATGGGGATACATCC GAGACCTAGCAAGAT	2	0.433177	0.396722	0.916216	1
Ifnar1	4	18:51:81:106	GTATGTGGAGCATAA:GTTCAGGGTGAAATA:GGTATTCCCAGCATA:GTATACCAATACGCA	2	0.430575	0.407703	0.930049	1
Tigit	4	40;53;74;107	GAGCCATGGTTCCTC;GTCTCTGACAATGAA;GCAGGCACGATAGAT;GCCTATCATACGTAT	2	0.427118	0.417596	0.956604	1
Olfr8	3	24;67;88	GAAGTACATGGGTGT;GATGTAGGATGCTAA;GTACAAGATTCATTA	2	0.361439	0.379644	0.990423	0.990423
Spleen Depleted	Numbers	Deales of		Mantaniahad	OTADO			
Gene Symbol	Number of	Ranks of	Perturbations	Most enriched	STARS	Average	p-value	FDR
7an70		1-2-3-20	GTOTGGOGCGTACCA:GGAGATCCCTGTGAG;GTCGACAACCCCTAC;GAACCCGACACAATCT	2 verturbation	4 102762	2 808/190	4 63E 05	0 000870
Cd28	4	6:8:18:21	GTCGGCATTCGAGCG;GCTTGTGGTAGATAG:GTTCCTACAACCTTC:GCAAGGGCGTGAACA	4	2.876694	1.752224	0.002082	0.019778
Dlat	4	10;13;14;64	GACTACCGCAACGGA;GCGACAAGGCCACCA;GCAGGCTCTCAAACC;GTTCAGAACCACACC	3	2.142855	1.208302	0.014573	0.092297
Entpd1	4	27;31;49;51	GTGGATGAAGTCATC;GCCAACCTGTACATC;GCTTGGATGTTGGTA;GAGCTATCACAGCCA	4	1.33529	0.756809	0.103817	0.49313
Havcr2	4	7;11;78;81	GTTCTCCAAGAACCC;GATCAGTTCTGAGCA;GTTACACTCTATCTA;GCTAAAGGGCGATCT	2	1.313364	0.726743	0.11034	0.419292
Cpt1a	4	32;36;52;56	GAGGAATACATCTAC;GCATACTGCTGTATC;GACGTTGGACGAATC;GCACATTGTCGTGTA	4	1.172819	0.68583	0.15059	0.476868
Hk2	4	22;40;42;62	GATTCCCGAGGACAT;GATCCGGAGTTGACC;GAAGGCCATCCAGCG;GGAGATGCGTCACAT	4	0.996004	0.6845	0.217164	0.589445
Prkab2	4	17;28;38;98		3	0.966827	0.686639	0.237474	0.564001
Lag3 Tigit	4	9,20,39,90 4-37-58-71		3	0.939059	0.700021	0.200072	0.040097
1r1	4	24:33:47:92	GACTGTGTTAGAGAA'GAGCATACAATTGTA'GCGTATGTCCTATAC'GCAGCAAGACCCCCCA	3	0.747877	0.568364	0.303340	0.651993
Rnf128	4	41:68:72:75	GTCACAATGGTCATC:GGGCAACCAGACGAT:GATAATTACGGCAGC:GCAACTACACCAAGA	4	0.665326	0.496785	0.457599	0.724532
Tnfrsf1a	4	12;29;61;79	GAGACCTAGCAAGAT;GATGGGGATACATCC;GAGTTGCAAGACATG;GGATCCCGTGCCTGT	2	0.645653	0.562173	0.476752	0.696792
Tnfrsf9	4	26;43;53;83	GACCAGGCTGACAGT;GTGCATACGTACTTC;GCCAAGTACCTTCTC;GTTGCTCCTCTACCC	3	0.634808	0.492947	0.488318	0.662718
lfngr1	4	5;30;60;93	GTATACCAATACGCA;GGTATTCCCAGCATA;GTTCAGGGTGAAATA;GTATGTGGAGCATAA	2	0.626997	0.652686	0.501457	0.635179
Olfr8	3	23;44;87	GTACAAGATTCATTA;GATGTAGGATGCTAA;GAAGTACATGGGTGT	2	0.540608	0.473449	0.630303	0.748485
Ptpn2	4	67;70;95;102	GIGCAGIGAICCAII;GAAGAAGIIACAICI;GAAIAIGAGAAAGIA;GCACICIAIGAGGAI	2	0.493103	0.665067	0.73796	0.824779
Dgkz Socs3	4	34:65:80:108		2	0.464154	0.441225	0.754569	0.796469
00000		01,00,00,100		-	0.100100	0.101200	0.000110	0.000110
Lung Enriched								
Lung Enriched Gene Symbol	Number of	Ranks of	Perturbations	Most enriched	STARS	Average	n-value	FDR
Lung Enriched Gene Symbol	Number of perturbations	Ranks of perturbations	Perturbations	Most enriched perturbation	STARS Score	Average Score	p-value	FDR
Lung Enriched Gene Symbol Pdcd1	Number of perturbations	Ranks of perturbations 1;2;11;18	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT	Most enriched perturbation	STARS Score 3.144481	Average Score 2.43948	p-value 0.001295	FDR 0.025908
Lung Enriched Gene Symbol Pdcd1 Adora2a	Number of perturbations 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAATA;GGAGAGCCAACCCCT;GCTCCACAAGACCT;GAGAGCAGTTGATGAT AUX ACTUTUTATALA ACTOCATTGATACA	Most enriched perturbation 4 2	STARS Score 3.144481 2.132688	Average Score 2.43948 1.559918	p-value 0.001295 0.016794	FDR 0.025908 0.167939
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Btrp2	Number of perturbations 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 0:12:44:46	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAATA;GCAGAGCCCCC;GCTCCCACAAGACCT;GAAGCAGTTGATGAT GATACGTTGACAAC;GCGGGACTGACCCC;GTTACCG;GTTGACAGAGAGC CCACCTATTGACCAACAATACTAAAAAAATACAAAAAATACAAAAAATACAAAAAA	Most enriched perturbation 4 2 3 4	STARS Score 3.144481 2.132688 1.768209	Average Score 2.43948 1.559918 1.224709	p-value 0.001295 0.016794 0.039648	FDR 0.025908 0.167939 0.264323
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Ptpn2 Socs3	Number of perturbations 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAATA;GGAGAGCCCAACCCCT;GCTCCACAAAGACCT;GAAGCAGTTGATGAT GATACGTTTGAGAAC;GTCGGACTTGACTGC;GTTTACCGCGTTAACGC;GTTGTAAAAAATGGA GCACTCTATGAGGAT;GAATATGAGAAAGTA;GAAGAAGTTACATCT;GTGCAGTGATCACATC GCGGGTAGCAGAAGGTCGGACTGGAGGCGTGAGGCCCTGACGCCGTTGAGTCACACTC	Most enriched perturbation 4 2 3 4 3	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144	p-value 0.001295 0.016794 0.039648 0.068749 0.133796	FDR 0.025908 0.167939 0.264323 0.343743 0.535184
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Ptpn2 Socs3 Rnf128	Number of perturbations 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 37;38;42:66	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAATA;GGAGAGCCAACCCCT;GCTCCACAAAGACCT;GAAGCAGTTGAT GATACGTTTGGAAA;GCGGACTGACTGCGCTCACCCCGCTTAAGCAATGGA GCACTCTATGAGAG;GAATATGAGAAAGTA;GAAGAAGTTACATCT;GTGCAGTGATCCACATC GCGACTAAGAAAGAGT;GACTTGGCACGAGG;GTGAGCCGTCAAGACC;GTTGAATACACAGT GCACATCACCCAAGA;GATATATGAGCAAGGCGCAGCGGCAACCCAGACGA;GCTGACTACGACAGT	Most enriched perturbation 4 2 3 4 3 4 4	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057 0.887395	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.27592	FDR 0.025908 0.167939 0.264323 0.343743 0.535184 0.919732
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Ptpn2 Socs3 Rnf128 Dgkz	Number of perturbations 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 37;38;42;66 20;35;43;95	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAATA;GGAGAGCCACCCCT;GCTCCACAAAGACCT;GAAGCAGTTGATGAT GATACGTTTGAGAAC;GTCGGACCTGACCCCC;GCTCACCG;GTTGTAAAGAATGGA GCACTCTATGAGGAT;GACTTCGGACGAGGG;GTGAGCGTCAAGACC;GTTGAGAAGACGAC GCACTCTAAGAAAGGT;GACTTCGGACGAGGG;GTGAGCGTCAAGACC;GTTGAGAAGACAAGT GCGACTAAGAAAGGT;GACTTCGGACGAGCG;GTGAGCGTCAAGACC;GTTGAGAACACAGT GCAACTACACCAAGG;GATAATACGGCAGC;GGGCAACCAGACGAT;GTCACAATGGTCAT GCAACTTTTGATC;AGCCAGTGGTGTGTGAGCACATCCGAGT;GATCACAATGGTCACAT	Most enriched perturbation 4 2 3 4 3 4 3 4 3 3	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057 0.887395 0.837031	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.595315	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.27592 0.30997	FDR 0.025908 0.167939 0.264323 0.343743 0.535184 0.919732 0.885628
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Ptpn2 Socs3 Rnf128 Dgkz Olfr5	Number of perturbations 4 4 4 4 4 4 4 3	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 37;38;42;66 20;35;43;95 28;34;74	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAATA;GGAGAGCCAACCCCT;GCTCCACCAAGACCCT;GAAGCAGTTGATGAT GATACGTTTGAGAAC;GTCGGACTTGACTGC;GTTACCCGCTTAACG;GTTGTAAAGAATGGA GCACTCTATGAGGAT;GAATATTGAGAAAGTA;GAAGAAGTTACATCT;GTGCAGTGATCCATT GCGGATAGAAAGGT;GACTTCGGACGGGGGGGCAGCAGCCGTGAGGTCACAATGGCACT GCAACTACACCAAGA;GATAATTACGGCAGC;GGGCAACCAGACGAT;GTCACAATGGTCATC GCAACTATCT;GACCCAGTGGTGTCT;GAGCACATCCGAGT;GAGCACCACTGGA	Most enriched perturbation 4 2 3 4 3 4 3 4 3 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057 0.887395 0.837031 0.703285	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.595315 0.53068	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.27592 0.30997 0.416933	FDR 0.025908 0.167939 0.264323 0.343743 0.535184 0.919732 0.885628 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Ptpn2 Socs3 Rrift28 Dgkz Olfr5 Cpt1a	Number of perturbations 4 4 4 4 4 4 3 3 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 37;38;42;66 20;35;43;95 28;34;74 60;68;73;79	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGGCTTGTCCAACT GTGTCGATGGCAATA;GGAGAGCCAACCCCT;GCTCCACAAGACCT;GAAGCAGTTGATAGA GATACGTTTGAGAAC;GTCGGACTTGACTGC;GTTACCCGCTTAACG;GTTGTAAAGAATGGA GCACTCTATGAGGAT;GAATATTACGACAAGTA;GAAGAAGTTACATCT;GTGCACTAGATCACAT GCGGATAAGAAAGGT;GACTTCGGACGAGGG;GGGAGCGCTCAAGACC;GTTGAGTACACAGTC GCAACTACACCAAGA;GATAATTACGGCAGC;GGGCAACCAGAAGCAT;GCTGCAACTAGGTCAC GCAACTACACCAAGA;GATAATTACGGCAGC;GGCAACCAGACGAT;GATGGGACCCACTAG GCAACTACACCAAGA;GATAATTACGGCAGC;GACACATCCGAGTA;GATGGGACCCACTGAC GTACACTACCCCAGTA;GTGGGTCATACAAGC;GACATGGCAGCTGAC GCACATTGTCGTGTA;GAGGAATACATCTAC;GCGATACTACCTGCTGTC	Most enriched perturbation 4 2 3 4 3 4 3 4 3 2 4	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057 0.887395 0.887395 0.837031 0.703285 0.575062	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.595315 0.53068 0.536189	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.27592 0.30997 0.416933 0.578395	FDR 0.025908 0.167939 0.264323 0.343743 0.535184 0.919732 0.885628 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Ptpn2 Socs3 Rnft28 Dgkz Olfr5 Cpt1a Entpd1	Number of perturbations 4 4 4 4 4 4 4 3 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 37;38;42;66 20;35;43;95 28;34;74 60;68;73;79 54;72;86;89	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAATA;GGAGAGCCACCCCT;GCTCCACAAGGACCT;GAAGCAGTTGATGAT GATACGTTTGAGAAC;GTCGGACCTGACCCCC;GCTCACCG;GTTGTAAAGAATGGA GCACTCTATGAGGAT;GACTTCGGACGAGGG;GTGAGCGTCAAGAC;GTTGAGAGAGCACTG GCGACTACAACAAGA;GATAATACGACGAGG;GTGAGCGTCAAGACC;GTTGAGAAGACACTC GCAACTACACCAAGA;GATAATACGGCAGC;GGCGAACCAGACGAT;GTCACAATGGTCACT GCAACTACCCAAGA;GATAATACGGCAGC;GGCGAACCAGACGAT;GTCACAATGGTCATC GCAACTTCTTCATC;GACCTCGGGTGCTATACAAGC;GACTGACAGTTGA GCACTTCTTTGATC;GAGGATAACTACTAC;GCATACCAGCGCACTGAC GCACTGTCGTGTA;GAGGATAACTACACCA;GCGATACCAGCGACTGACGGTTGA GCACATTGTCGTGA;GAGGATAACAACCAGCACAGCAGCTGATC;GACGTTGGACGAGTTGA GCACGTTGGTGTA;GAGCTATACAACCACAGCGACTGCAGTTGACACCTGTACAACCGAATC	Most enriched perturbation 4 3 4 3 4 3 2 4 3 2 4 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057 0.887395 0.837031 0.703285 0.575062 0.513187	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.595315 0.53068 0.536189 0.54987	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.27592 0.30997 0.416933 0.578395 0.691696	FDR 0.025908 0.167939 0.264323 0.343743 0.535184 0.919732 0.885628 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Entpd1 Tnfrsf9 Hours2	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 37;38;42;66 20;35;43;95 28;34;74 60;68;73;79 54;72;86;89 23;59;62;85	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAAT;A;GGAGACCCACCCCT;GCTCCACAAGACCT;GAAGCAGTTGATGAT GATACGTTTGAGAAC;GTCGGACTTGACTGC;GTTACCCGCTTAACG;GTTGTAAAGAATGGA GCACTCTATGAGGAT;GAATATTGAGAAAGTA;GAAGAAGTTACATCT;GTGCACTGGATCACATC GCGGATAAGAAAGT;GACTTCGGACGAGGG;GTGAGGCGTCAAGACC;GTTGAGTACACASTC GCAACTACACCAAGA;GATAATTACGGCAGC;GGGCAACCAGACGAT;GTCACAATGGTCATC GCAACTACCCAAGA;GATAATTACGGCGAC;GGGCAACCAGACGAT;GTCACAATGGTCATC GCAACTACCCAAGT;GTGGTGTGTG;GAGCAACTCGACGAGT;GACGACCACTGGA GTACACTACCCAGTA;GTGGGTCATACAAGC;GACAATGACCACTG GCACATTGTCGTGTA;GAGGAATACATCTAC;GCAACCTGTAACAGGTTGG GCACGTTGGAT;GAGCAATACATCTAC;GCAACCTGTAACAGGTTGG GCTGTGTGTGTGTG;GAGGAATACATCTAC;GCAACCTGTACTC;GCCACCTGTACAT GTTGGTGTGTGTGGCGCAGCACCTGCTG;GTGGATGAAGTCATC;GCCAGCCGACGGC GTTGGCCCCTCTACCCCGCCAGTACCTCTCT;GTGCATACCTACTC;GCCACCCGACGCGGCGACGAGCTGACCAGGT GTTGGCCCCCCTCTACCATCTCTC;GTGCATACCTACTC;GCCACCCGACGTGACGAGCTGACCAGGT GTTAACTACCCCGCCAGTACCTCTCT;GTGCATACCTACTC;GCCACCCGCCGCCAGGT GTTGGCCCCCACTCCCGCCACGTACCTCCTCCCCACCCCCCCC	Most enriched perturbation 4 3 4 3 4 3 4 3 2 4 4 2 4 2 3 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057 0.887395 0.837031 0.703285 0.575062 0.513187 0.505094	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.595315 0.53068 0.536189 0.54987 0.439632	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.27592 0.30997 0.416933 0.578395 0.691696 0.702429	FDR 0.025908 0.167939 0.264323 0.343743 0.535184 0.919732 0.886628 1 1 1 1
Lung Enriched Gene Symbol Pdod1 Adora2a Kdr Ptpn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Enrpd1 Tnfrsf9 Havcr2 Hr2	Number of perturbations 4 4 4 4 4 4 4 3 3 4 4 4 4 4 4 4 4	Ranks of perturbations 1:2:11:18 3:4:26:41 7:12:19:55 9:13:44:46 6:29:30:77 37:38:42:66 20:35:43:95 28:34:74 60:68:73:79 54:72:86:89 54:72:86:89 54:72:86:89 54:72:86:285 27:39:94:99	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAATA;GGAGAGCCAACCCCT;GCTCCACAAAGACCT;GAAGCAGTTGATGAT GATACGTTTGAGAAC;GTCGGACTGACTGC;GTTACCCGCTTAACG;GTTGTAAAGAATGGA GCACTCTATGAGGAT;GAATATTAGAGAAGTA;GAAGAAGTACACT;GTGCAGTGATCCATT GCGGATAAGAAAGT;GACTTCGGACGGGCGGAGGCGCTAAGCC;GTTGATACACAGTC GCAACTACACCAAGA;GATAATTACGGCAGG;GGGCGACAGCC;GTGAGTACACAGTC GCAACTACCCAAGA;GATAATTACGGCGGCGCAACAGC;GTGAGTACCACTG GCAACTACCCAGTA;GTGGGTCT;GAGCACAACG;GACTGAGCGCCACTGGA GCACATTGTCGTGA;GAGGCTATACAGC;GACTAGCAGCGTGACAGT GCACATGTCTGA;GAGGAATACATCTAC;GCATACGCGTATAGCAGCGTGGACGATC GCTGGATGTGGTA;GAGGCTATACAGC;GACTAGCGGCTGACAGC GTGCTCCTACCC;GCCAAGTACCTTC;GCGCATAGCTGCTGTATC;GACCAGCTGACACT GCTAAAGGGCGATCT;GTTACAACCTCTAC;GCTATGCGAACCC;GACTACGTGCTGACAGCT GCTAAAGGGCGATCT;GTTACACTCTATCTA;GTCTCCAAGAACCC;GACTACGTTCTGAGCAGCT	Most enriched perturbation 4 2 3 4 4 3 2 4 2 2 2 3 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.229057 0.887395 0.837031 0.703285 0.575062 0.513187 0.505094 0.502774	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.595315 0.53068 0.536189 0.54987 0.439632 0.438843 0.635182	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.27592 0.30997 0.416933 0.578395 0.691696 0.702429 0.717511	FDR 0.025908 0.167939 0.264323 0.343743 0.535184 0.919732 0.888628 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Ptpn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Enrpd1 Tnfrsf9 Havcr2 Hk2 Pfkab2	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12:19;55 9;13;44;46 6;29;30;77 37;38;42;66 0;48;73;79 54;72;86;89 23;59;62;45 27;39;94;99 61;71;92;97	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAATA;GCAAGACCACCCCT;GCTCCACAAAGACCT;GAAGCAGTTGATGAT GATACGTTTGAGAAC;GTCGGACCTGACCCCC;GCTCACACAGGCGCTGAACAGTGCACT GCACTCTATGAGAAC;GTCGGACCTGACGAGGGGTGAAGCGCTCAAGACC;GTTGAGAGACGACCCATT GCGAATAGAAAGA;GATATTGAGCAAGGG;GTGAGCGTCAAGACC;GTTGAGAGCACCACT GCAACTACACAAGA;GATAATTACGCCACC;GGGCAACCAGACCA;GTTGACAATGGTCACT GCAACTTCTTCATC;GACCTCGGCCACCAGGCG;GTGACGACCACACACCGCCACTGAC GTACACCAACCACCCAGTGGTTGT;GACCACTCCGGATGCACATGGCCACT GCAACTGTCGTGT;GAGCCACCAGGGG;GTGACGCACCACCGCCACCCAC GTCACCACCACCAGGCATCCCAGCGCACCAGCCACCCGCACCCCGCCACCCCGCCCCGCCCCGCCCCGCCCCGCCCCGCCCCGCCCGCCCGCCCC	Most enriched perturbation 4 2 3 4 4 3 4 3 2 4 2 2 3 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.229057 0.837039 0.703285 0.575062 0.575062 0.550594 0.505074 0.502774 0.682774	Average Score 2.43948 1.529918 1.224709 1.02761 0.807144 0.666794 0.53068 0.536189 0.53987 0.439632 0.439632 0.439635 0.6395183 0.605183 0.605183	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.27592 0.30997 0.416933 0.578395 0.691696 0.702429 0.717511 0.717511 0.754569	FDR 0.025908 0.167939 0.264323 0.343743 0.535184 0.919732 0.885628 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olf5 Cpt1a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;42;6;41 7;12;19;55 9;13;44;46 6;29;30;77 3;7;38;42;66 20;35;43;95 28;34;74 60;68;73;79 24;72;68;89 23;59;62;85 27;39;94;99 61;71;92;97 8;69;98;187	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAAT;GCAATACAGGGATAC;GCACCCCACAAGGACCT;GAAGCAGTTGATGAT GATACGTTTGAGAAC;GTCGGACTTGACGCCG;GTTGACAGCGGTGAGAGATGGA GCACTCTATGAGGAT;GCAATATTGAGAAAGTA;GAAGGAGCGTCAAGACC;GTTGATAAGAATGGA GCGGATAAGAAAGGT;GCACTTCGGACGAGGG;GTGAGGCGTCAAGACC;GTTGATAACACASTC GCAACTACACCAAG;QATAATTACGCCAGC;GGGCAACCAGACGAT;GTCACAATGGTCATC GCAAGTCTTTGATC;GAGCCAATCAGGG;GTGAGGCGTCAAGACC;GTTGATACACASTC GCAACTACCCAGGA;GTGATTATACGCCAC;GGGCAACCAGACGAT;GTCACAATGGTCATC GCAAGTCTTTGATC;GAGCCAATCAGCCACTGCAGT;GACGAGCACTGAC GTCACTACCCAGGA;GTGGGTCATACAAGC;GACATGGACGATC GCTTGGTGTGT;GAGGAATACATCTAC;GCAACCTGGTTGACGAGGTTGA GCTAGGCTACCC;GCCAGGACCACTGCCAGTGAGTGAATC GCTTGGATGTGTG;GAGCAATCACTCTCT;GTCCATACTACGTTGGACGAATC GCTAGGGCGCATC;GTLACCTCTACT;GTCCAAGACCC;GATCAGTTCGAGCA GGAGAGGCGGTCACT;GACACCACTCCAGCG;GATTCCCAAGACCA;GACTGCAGAGT GTACAACTCTTTG;GACCACCCCTTTACAGGAGCACAAGACC;GATCAGGTTGAACCAG GCAAAGGCGTCACAT;GAAGGCCACTCCACGC;GATCCTAAGTTCGAGCACAGGCGGCGAC	Most enriched perturbation 4 2 3 4 4 3 4 2 4 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 0.837031 0.703285 0.575062 0.513187 0.505094 0.502774 0.484154 0.455168	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.53068 0.536189 0.536189 0.536487 0.439632 0.439632 0.439632 0.4396414 0.447587	p-value 0.001295 0.016794 0.039648 0.068749 0.33796 0.27592 0.30997 0.416933 0.578395 0.691696 0.702429 0.717511 0.714511 0.734569 0.833449	FDR 0.025908 0.167939 0.264323 0.343743 0.919732 0.885628 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 Ilngr1	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2:11:18 3;4:26;41 7;12:19:55 9;13;44:46 6;29:30;77 37;38;42;66 20;35;43;95 28;34;74 60;68;73;79 54;72;86;89 23;59;62;85 27;39;94;99 61;71;192;97 8;69;81;87 16;65;83:102 15;45;76;88	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAAT;GCAATACAGGGATAC;GCACCCAAGGACCT;GAAGAGCTTGTCAAACT GATACGTTTGAGAAC;GTCGGACTTGACTGC;GTTGCACAGGCGTGTGACAATGGA GCACTCTATGAGGAT;GAATATTGAGAAAGTA;GAAGAAGTTACATCT;GTGCACTGATCCATT GCGGATAGAAAGGT;GAATATTGAGAAAGTA;GAAGGAAGCCGTCAAGACC;GTTGATAACAAATGGA GCAACTACACCAAGA;GATAATTACGGCAGG;GGGCAACCAGACGAT;GTCACAATGGTCATC GCAACTACCCAAGA;GATAATTACGGCAGC;GGGCAACCAGACGAT;GTCACAATGGTCATC GCAACTACCCACGA;GATAATTACGGCAGC;GGGCAACCAGACGAT;GTGCACAATGGTCATC GCAACTACCCCAGTA;GTGGGTCATACAAGC;GACCACTACCAGTGGAGCAAT GTGCACTACCCCAGTA;GTGGGTCATACCAGC;GACGACGACGGCTGGAGCAAT GCTTGGATGTGTG;GAGCAACTACCACC;GCTGACACGGTTGGACGAATC GCTTGGATGTGTGT;GCAGACACTCTCC;GTGACTACTTC;GACCAGGCTGACAGT GCTAAGGCGCGCACT;GAGCCAACTCCCCGGGGTGAAGCCAT;GATCCGGCGACAGG GCGAGATGCGCTCACT;GAGGCAATCACTCTCT;GTGCCAAGCCG;GATCAGTTCTGAGCA GGAGATGCGCTCACAT;GAGGCCATCCCCAGGCGTGAAGCCAT;GATCCGGGGGGGGCGGGGC	Most enriched perturbation 4 2 3 4 4 3 2 4 4 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.514539 1.229057 0.887395 0.837031 0.703285 0.575062 0.5513187 0.505094 0.502774 0.455168 0.455168	Average Score 2.43948 1.559918 1.02761 0.8067144 0.666794 0.595315 0.53068 0.596315 0.5396189 0.439632 0.438643 0.498414 0.447587 0.433002	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.27592 0.30997 0.416933 0.581959 0.717511 0.717511 0.717511 0.717511 0.717514	FDR 0.025908 0.167939 0.264323 0.343743 0.535184 0.919732 0.885628 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdod1 Adora2a Kdr Ptpn2 Socs3 Rnfr128 Dgkz Olfr5 Cpt1a Enripd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 Ingr1 Ilfr1	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 37;38;42;66 0;88;73;79 54;72;86;89 23;59;62;85 27;39;94;99 61;71;92;97 8;69;81;87 16;65;83;102 15;45;76;98	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAATA;GCAAGACGCCCC;GCTCCACAAAGACC;GAACAGTTGATGAT GATACGTTGAGAAC;GTCGGACCTGACCCC;GTTCACCAGGCGCTGAACGAGTGACAGT GCACTCTATGAGAAC;GTCGGACCTGACGAGGGGTGAGCGTCAAGACC;GTTGAGAGACGACGAG GCACTCTATGAGAAC;GCACTCGGACCAGGGGGTGAGCGTCAAGACC;GTTGAGAAGACGAC GCACTCTATGAGAA;GATATTAGGCAGC;GGGCAACCAGACCA;GTTGACAATGGTCACA GCAACTACCACAAGA;GATAATTACGCCAGC;GGGCAACCAGACCA;GTGACAATGGTCACA GCAACTTCTTTGATC;GAGCATGCGGTGCATACCAAGC;GACTGACAGTGG GCAACTGTCTTGATC;GAGGCATACTAC;GCGCATCCAGGTTGA GCACTTGTCGTGT;GAGGCATACTAC;GCGCATCCAGCTGCAGCTGGAC GTACACTACCCAGGGAATACCATCC;GTGCAACCGCGCAGCCACTGC GCTGGATGTCTGGT;GAGGCATACCAGC;GGGCTACACC;GGCCAGCGCAGCG	Most enriched perturbation 4 2 3 4 4 3 4 4 3 2 4 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.229057 0.887395 0.6375062 0.575062 0.513187 0.505094 0.502774 0.452168 0.455168 0.455168 0.455168	Average Score 2.43948 1.525918 1.224709 1.02761 0.807144 0.666794 0.5366189 0.5366189 0.54987 0.439632 0.438843 0.605183 0.498144 0.447587 0.433002 0.4338578	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.27592 0.30997 0.416933 0.578395 0.6891696 0.702429 0.717511 0.7754569 0.833449 0.833449 0.833449 0.833449	FDR 0.02590 0.167939 0.264323 0.343743 0.535184 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olir5 Cpt1a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 lingr1 lif11 Tnfrsf1a	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 3;738;42;66 20;35;43;95 28;34;74 60;68;73;79 54;72;86;89 23;59;62;85 27;39;94;99 61;71;92;97 8;69;81;87 17;64;84;91 22;47;70;96	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAAT;GGAGGACCACCCCT;GCTCCACAAGGCCT;GAGCAGTTGATGAT GATACGTTTGAGAAC;GTCGGACTTGACGCCCT;GTGCCACAAGGACC;GTTGATAAGAATGGA GCACTCTATGAGGAT;GAATATTGAGAAAGTA;GAAGGAAGTTACATCT;GTGCAGTGATACACATC GCGATAGAAAAGGT;GACTTCGGACGAGGG;GTGAGGCCTCAAGACC;GTTGATAACAACTG GCAACTACACCAAGA;GATAATTACGCAGG;GGCGACACAGACC;GTTGATACACACTC GCAACTACCCACGAGC;GTGAGTCGGACCGCACAGCCACTGCAGT;GTCACAATGGTCATC GCAACTACCCACGAGC;GTGGGTCATACAAGC;GACATGGACGAT GTCACTACCCAGTA;GTGGGTCATACAAGC;GACATGCAGGTTGGACGAAT GCCATGTGTGTG;GAGCATACTACCACCA;GTGGGTGAGGCACTGAC GTCGGTTGTGT;GAGGCATCCCAGCCA;GTGGGTGAGCCACTGCA GTCGGCGCTTGTC;GACGCTACCCAGCCA;GTGGGTGAGCGATC GCTTGGCGCTCTTACCC;GCCAACTCCCGTGTACTC;GCCACCCGTGACAG GCAGGGCGGCTTGTC;GACGCACCCGCGGATTCCCCAGGACCTGCACGG GGAGATGCGTCACAT;GAAGGCCACTCCACGGGATTCCCCGAGCAGTGCCCGGAG GGGGCGGCGTTTCT;GACCCCCTTTA;GAGGAGCAAGGTC;GTCCAGACCAGGCC GTAGCACACCCCCCGGCGTTGCCCCAGCGGATCCCCAGCAAGGATCCCGGGGGTTGCCCGGGACTGCCCGGGACTGCCCCGGGA GGGGCGGCGTTTCCTCCACCCCTTTA;GGAGGACAAGGCC;GTCCAGACCACGCGCG GTAGGACCCCCC;GGCGTATCCCCACCGCATCACCTGACCCAGGCCCCCGGGA GGGTGCCGGCTTTCCCAGCGCGTTCCCCAGCATAGCTCCGAGGACCCCCCGGGA GGTGCCGGGTTGTC;GAGTCCCACCGCTTACCCAGCATA;GTATCCCAATACCCCA	Most enriched perturbation 4 2 3 4 4 3 4 4 2 4 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057 0.887395 0.837031 0.703285 0.575062 0.513187 0.505074 0.502774 0.502774 0.48515168 0.455168 0.4455168 0.449544	Average Score 2.43948 1.559918 1.224709 1.02761 0.866794 0.536189 0.536189 0.536189 0.439632 0.439632 0.439632 0.439632 0.439638 0.4395183 0.4395183 0.4395183 0.4395183 0.439518 0.439	p-value 0.001295 0.016794 0.039648 0.068749 0.27592 0.30997 0.416933 0.578395 0.691696 0.702429 0.702429 0.717511 0.717511 0.774569 0.833449 0.833449 0.833449	FDR 0.025908 0.167939 0.264323 0.343743 0.343743 0.343743 0.343743 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Enripd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 Ifngr1 Il1r1 Tnfrsf1a Trigit	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 37;38;42;66 29;32;43;95 22;3;47;4 60;68;73;79 24;72;66;89 23;59;62;85 27;39;94;99 61;71;92;97 8;69;81;83;102 16;55;75;70;88 17;55;70;88 17;55;70;88 17;55;70;88 17;55;70;88 17;55;70;88 17;55;70;88 17;55;70;88 17;55;70;88 17;55;70;70;70;70;70;70;70;70;70;70;70;70;70;	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGCATGGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GATACGTTTGAGAAC;GTCGGACTTGACTGC;GTTCCACCAAGGCACT;GTAGCAGTTGATGAT GATACGTTTGAGAAC;GTCGGACTTGGACGCC;GTGACGCC;GTGAGTACACATG GCGGATAAGAAAGT;GCACTTCGGACGGCGGCGGCGCCACCACGC;GTTGACTACACAGTC GCAACTACACCAAGA;GATAATTACGGCAGC;GGGCAACCAGACGAT;GTCACAATGGTCATC GCAACTACCCAGTAGTTGGTGCTG;GAGCACCAGACGAT;GTCACAATGGTCACT GCAACTACCCAGTAGTTGGTGCTC;GAGCACCTGATC;GCGACCACTGAC GTACACTACCCAGTGGTGTCT;GAGCACATCCGAGTA;GATGGAGCACTG GCACGTTGTGTGTG;GAGGATACATCTAC;GCACTGTGACGAGTGG GCCACGTTGTGTGTG;GAGGATACATCTAC;GCACTGTGACGACTG GCTGGGTTGTGT;GAGGACTACCACAGCCA;GTGGAGGACTC;GCCAACCTGACAGT GCTTGGATGGTGGCGCCACTGAGCCACTGCGCGGCGACCAGGGCGCACGAGGCGCGACGGCGCGCGC	Most enriched perturbation 4 2 3 4 3 4 3 2 4 4 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057 0.837305 0.575062 0.575062 0.513187 0.505094 0.502774 0.455168 0.4455168 0.4455168 0.444543 0.444543	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.53068 0.536689 0.53068 0.53689 0.54987 0.439632 0.439842 0.433842 0.433002 0.4338578 0.439874 0.433002	p-value 0.0016794 0.039648 0.068749 0.333706 0.27592 0.30997 0.416933 0.578395 0.691696 0.702429 0.717511 0.774569 0.833449 0.833449 0.833449 0.863888 0.8666988 0.8666988	FDR 0.025908 0.167939 0.264323 0.343743 0.5335184 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0.912524 0.972727
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Ptpn2 Socs3 Rnf128 Dgkz Olfr5 Cp11a Enrpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 Ilingr1 Il1r1 Tnfrsf1a Tnfrsf1a Tnfrsf1a Tnfrsf1a	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12:19;55 9;13;44;46 6;29;30;77 37;38;42;66 0;88;73;79 54;72;86;89 23;59;62;85 27;39;94;99 61;71;92;97 8;69;81;87 16;65;83;102 15;45;76;98 17;74;48;49 12;24;77;108 25;57;80	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAATA;GCAAGACGCAGCCCCT;GCCCCAAAGACCT;GAAGCAGTTGATGAT GATACGTTGAGAAC;GTCGGACCTGACCCCT;GCTCCACAAAGACCT;GAAGCAGTTGATGAT GCGACTGTTGAGGAAC;GTCGGACCTGACCG;GTTGACGGCTCAAGCAGC;GTTGAGAAGACGC GCACTCTATGAGGAT;GACTTCGGACGAGGG;GTGAGCGTCAAGACC;GTTGAGAGCACAGAC GCACTCTTTGATC;GACTTCGGACGAGG;GTGAGCGTCAAGACC;GTTGAGAAGACCACAGC GCAACTCTTTGATC;GACTCGGGCACCAGGG;GTGAGCGTCAAGACC;GTTGAGACGACCACTGC GCAACTCTTTGATC;GAGCAGGGGATGACCACTCCGGAT;GTGCACAATGGTCATC GCAAGTCTTGGTG;GAGGCATACCAGC;GGGCACCAGACCGACTGCAGCTGAC GTACACTACCCAGGGAATACCTTCC;GACCATGCGGCACTGC GTTGGGTGCGGGAGGCATCACCAGC;GTGGATGAGCCCCTGACATC GCTGGATGTTGGTG;GAGGCATACACTCC;GTCGACCCGGCTGACATC GCTGGATGTCGTG;GAGGCATCACGC;GATCCCCGAGGCACCGGCGGGGCGG	Most enriched perturbation 4 2 3 4 4 3 2 4 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057 0.837031 0.703285 0.575062 0.575062 0.575062 0.575062 0.505094 0.502774 0.505094 0.502774 0.505168 0.484154 0.484154 0.4455168 0.444543 0.444543 0.444543 0.444543	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.595315 0.53068 0.53668 0.536189 0.54987 0.439632 0.439632 0.439632 0.439843 0.439632 0.4398444 0.447587 0.433002 0.438578 0.417592 0.405406	p-value 0.001295 0.016794 0.039648 0.068749 0.27592 0.30997 0.416933 0.578395 0.691696 0.702429 0.717511 0.717511 0.717514 0.833449 0.833449 0.833449 0.833449 0.833449 0.833449	FDR 0.025908 0.167939 0.264323 0.343743 0.343743 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0.912524 0.912524 0.912524
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 lingr1 li1r1 Tnfrsf1a Tigit Olfr8	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 3;7;38;42;66 20;35;43;95 28;34;74 60;68;73;79 54;72;86;89 23;59;62;85 27;39;94;99 61;77;19;297 8;69;94;187 16;65;83;102 15;45;76;98 40;63;78;108 22;47;70;96	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGGCTTGTCCAACT GTGTCGATGGCAAT;GCAATACGAGGCCCCGCCCCCCACAGGCCAAGCCCTGACACT GATACGTTTGACAGAC;GCGGGAGCCCCCGGCCCCAAGGCCTCAACGGTTGATAGAT GCGGATAGAAAAGGT;GACTTCGGCACGAGGCGTGCAAGCC;GTGAGTACACACTC GCAACTACACCAAGA;GATAATACGGCAGGC;GCAGCAGCCGCAAGACGC;GTGAGTACACACTC GCAACTACCCAAGA;GATAATACGCCGCCCCAAGCCGTCAAGCC;GTGAGTACACACTC GCAACTACCCACGAGCACTTCGGACGAGGC;GCACCAGACCA;GTGAGTACACACTC GCAACTACCCACGCCGTGCAGCC;GCGCCCCAAGCCGT;GTGACAAGGC;GCCCCAGGC GTACACTACCCAGG;GATAATACGCCGCCCCCAGCCGAT;GTCACAATGGTCACC GTACCTACCCAGGGATACACCC;GCGCCCCCGCCCCGGCCCCCGGC GTACACTACCCCGCGCAGCCC;GCGCCCCCGCGCCCCGGCCCCCGGC GTGCGCTCTGGTG;GAGGCCACCCGCCCCGCCCCGCCCCG	Most enriched perturbation 4 3 4 3 4 3 2 4 4 2 3 3 4 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057 0.837031 0.703285 0.575062 0.5513187 0.502774 0.502774 0.502774 0.455168 0.445548 0.445548 0.444543 0.444543 0.444543	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.53068 0.53068 0.53068 0.53068 0.54987 0.439832 0.438843 0.438843 0.438848 0.437582 0.438548 0.431592 0.438548 0.447558 0.438548 0.438548 0.4475598 0.4475588 0.4475598 0.447598 0.447598 0.447598056	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.30397 0.416933 0.578395 0.717511 0.717511 0.717511 0.734569 0.833449 0.833449 0.833449 0.833449 0.852972 0.866898 0.866898 0.977377	FDR 0.025908 0.167939 0.264323 0.343743 0.343743 0.888628 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0.912524 0.977377
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olfr5 Cp11a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 Ifngr1 Il1r1 Tnfrsf1a Tigit Olfr8	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 37;38;42;66 20;35;43;95 20;35;43;45 20;35;45;45 20;35;45;45 20;35;45 20;35;45;45 20;45;45;45 20;45;45;45 20;45;45;45;45;45;45;45;45;45;45;45;45;45;	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGGCTTGTCCAACT GTGTGCGATGGCAAT;GCAATACAGGGATAC;GCACCCCACAGGGCAAA;GCAGGCTTGATCAACT GATACGTTTGAGAAC;GTCGGACTTGACTGC;GTTACCCGCTTAACGGTTGTAAAGAATGGA GCACTCTATGAGGAT;GAATATTGAGAAAGTA;GAAGAAGTTACATCT;GTGCACTGACCACT GCGGATAGAAAAGT;GCACTTCGGACGGCGGCGGCGCCACCAGCCG;GTGCAGTACACACTC GCAACTACACCAAGA;GATAATTACGGCGCC;GGGCAACCAGACGAT;GTCACAATGGTCATC GCAACTACCCAAGA;GATAATTACGGCCGCC;GGGCAACCAGACGAT;GTCACAATGGTCATC GCAACTACCCAAGA;GATAATTACGGCCGCC;GGGCAACCAGACGAT;GTCACAATGGTCATC GCAAGTCTTGAT;GAGCAATCACTCTAC;GCAATCTGCAGTGAGAGCACTGG GTCACTACCCAGTAGTGGTGTCT;GAGCACATCCGCGAGTAGGCGGCCACCGAGC GTTGCTGTTGTGT;GAGGAATACATCTAC;GCAATCTGCTGTACATGGCGACAGT GCTAAGGCGCACAC;GAGCCACTCCAGCG;GAATCACTC;GCCAACCTGCACGT GCTAAGGGCGCACT;GTACACCTCTATCTA;GGCGTGAGCGATC;GTTCGGACGAATC GTTGGCGCTCACA;GAAGGCCATCCAGCG;GGATTCCCCGAGCAGCAGCGGCCACAGG GCGAGGGGGCGACAT;GATGCCCCACTCTACTCTACGTTCTAGACCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG	Most enriched perturbation 4 3 4 4 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057 0.887395 0.575062 0.575062 0.513187 0.505094 0.502774 0.455168 0.4455168 0.445543 0.445548 0.444543 0.444543 0.444543	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.530618 0.5366189 0.54987 0.439632 0.439843 0.605183 0.498144 0.447587 0.433002 0.438578 0.439878 0.417592 0.405406	p-value 0.001294 0.039648 0.068749 0.333796 0.27592 0.30997 0.416933 0.578395 0.691696 0.702429 0.717511 0.754569 0.833449 0.833449 0.833449 0.833449 0.836698 0.866698 0.866698	FDR 0.025908 0.167939 0.264323 0.343743 0.535184 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0.912524 0.912524 0.977377
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olfr5 Cp11a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 Ilngr1 Il1r1 Tnfrsf1a Tnfrsf1a Tnfrsf1a Tnfrsf1a Tnfrsf1a Tnfrsf1a Tnfrsf1a Tnfrsf1a Glfr8	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12:19;55 9;13;44;46 6;29;30;77 37;38;42;66 0;88;73;79 54;72;86;89 23;59;62;85 27;39;94;99 61;71;92;97 8;69;81;87 16;65;83;102 15;45;76;98 117;64;84;91 22;47;70;96 40;63;76;108 25;57;80 Ranks of perturbations	Perturbations SACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAAT;GCAATAGCAGGGATAC;GCACCCCAAGGCCAAGGCCTTGATCAAT GTGCGATGGCAATA;GCAGCGCGCGCGCGCACCAAGGCC;GTGAGCGCTGATCAGT GCGATGTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	Most enriched perturbation 4 2 3 4 4 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.52457 0.887395 0.575062 0.575062 0.505094 0.502774 0.455168 0.4455168 0.4455168 0.4455168 0.4455168 0.444543 0.444543 0.444543 0.444543 0.444543 0.444543	Average Score 2.43948 1.559918 1.0224709 1.02761 0.807144 0.666794 0.5905315 0.53068 0.53068 0.53068 0.53068 0.439632 0.439632 0.439632 0.439632 0.439632 0.4398578 0.417592 0.430578 0.417592 0.405406	p-value 0.001295 0.016794 0.039648 0.0687499 0.133796 0.30997 0.416933 0.578395 0.691696 0.717511 0.717511 0.717511 0.754569 0.833449 0.833449 0.833449 0.833449 0.833449 0.833449 0.833449 0.833449 0.833449	FDR 0.025908 0.167939 0.264323 0.343743 0.343743 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0.912524 0.912524 0.912524 0.912524
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 lingr1 li1r1 Tnfrsf1a Tigit Olfr8 Lung Depleted Gene Symbol Zap70	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 3;7;38;42;66 20;35;43;95 28;34;74 60;68;73;79 54;72;86;89 23;59;62;85 27;39;94;99 61;71;92;97 8;69;81;87 17;64;84;91 22;47;70;98 40;63;78;108 25;57;80 Ranks of perturbations 1;2;4;10	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGGCTTGTCCAACT GTGTCGATGGCAAT;GCAATAGGAGCCCCGCGCCCCAAGGCACA;GCAGCTTGATCAAT GATACGTTTGAGAAC;GCGGGAGCTGACGCGGTTAACGGCTGAAGACGTGAAGAAGGCG GCAGCTCTATGAGGAT;GCAGTTGGGCAGGGGGGGGGCGCCAAGACC;GTTGGTAACAATGGC GCAGCTCTTGATCGGGCGGCACCAGGGGGTGCAGGCGCTCAAGGC;GTTGACTACCACTGC GCAACTACCCAAG;GATAATACGGCGCCCCCAGGCGCTCAAGGC;GTTGACTACCACTGC GCAACTACCCACGCAGGGGTGCAGGGGGTGCAGCCCCCAGGCGAT;GTCACAATGGTCATC GCAACTACCCCCGTGACGCCGCCCCCAGGCGGTCAGCGGTGAAGCC;GTGGATGACCACTGC GCACTGCTGTGTGAGAGGAATACATCTCG;GCCACTCCGGCTGACGGTGGA GCACTGCTGTGTGAGAGGAATACATCTCG;GCCACTGCGGCTGACGGCGCGCGCGGGTGC GTCGGGTGTTGGT;GCGCGCACCCGCGCCCCGGCCCCGGCCCGG	Most enriched perturbation 4 2 3 4 4 3 4 2 2 4 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057 0.837031 0.703285 0.575062 0.5513187 0.502774 0.502774 0.502774 0.455168 0.455168 0.445544 0.445543 0.444543 0.444543 0.444543 Score Score 4.165577	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.53068 0.5366189 0.54987 0.439832 0.438843 0.438843 0.438848 0.437582 0.438848 0.4317592 0.438078 0.438046 Average Score 3.016835	p-value 0.001295 0.016794 0.039648 0.039769 0.133796 0.73792 0.416933 0.581596 0.702429 0.717511 0.717511 0.734569 0.833449 0.833449 0.833449 0.833449 0.852972 0.866988 0.866988 0.977377 p-value 4.63E-05	FDR 0.025908 0.167939 0.264323 0.343743 0.343743 0.343743 0.343743 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 Ifngr1 Il1r1 Il1r1 Tnfrsf1a Trigit Olfr8 Curg Depleted Gene Symbol Zap70 Cd28	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;42;6;41 7;12;19;55 9;13;44;46 6;29;30;77 37;38;42;66 20;35;43;95 22;34;74 60;68;73;79 24;72;86;89 23;59;62;85 27;39;94;99 61;71;92;87 8;59;62;85 27;39;94;99 61;71;92;87 8;59;62;85 27;39;94;99 61;71;92;87 8;59;62;85 27;39;94;99 61;71;92;87 8;59;62;85 27;39;94;99 61;71;92;87 8;59;62;85 27;39;94;99 61;71;92;87 8;59;62;85 27;39;94;99 61;71;92;87 8;59;62;85 27;39;94;99 17;64;84;91 22;47;70;96 40;63;77;80 25;57;80 Ranks of perturbations 1:2;4;10 5;7;23;29	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGGCTTGTCCAACT GTGTGCGATGGCAAT;GCAATACAGGGATAC;GCACCCCAAAGGCCT;GAAGCAGTTGATAGAT GATACGTTTGAGAAC;GTCGGACTTGACTGC;GTTACCCGCTTAACG;GTTGTAAAGAATGGA GCACTCTATGAGGAT;GCATTATGAGAAAGTA;GAAGGAGCGTCAAAGCC;GTTGATAACAATGGC GCAACTACACCAAGA;GATAATTACGGCAGG;GGGCGACCAGACCA	Most enriched perturbation 4 2 3 4 4 3 2 4 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.514539 1.229057 0.887395 0.837031 0.703285 0.575062 0.575062 0.513187 0.502774 0.455168 0.4455168 0.4455168 0.4455168 0.444543 0.444543 0.444543 0.4445548 0.444558 0.444558 0.444558 0.444558 0.444558 0.4455588 0.444558 0.445588 0.44588 0.445888 0.445888 0.445888 0.445888 0.4458888 0.4458888 0.44588888 0.44588888888888888888888888888888888888	Average Score 2.43948 1.559918 1.024709 1.02761 0.807144 0.666794 0.595315 0.53068 0.536189 0.54987 0.439832 0.438843 0.438843 0.438843 0.438878 0.438578 0.4398444 0.447587 0.433002 0.4395406 0.419546 0.417592 0.405406	p-value 0.001295 0.016794 0.039648 0.068749 0.3133796 0.3133796 0.30397 0.416933 0.578395 0.30997 0.416933 0.578395 0.717511 0.717511 0.717511 0.717511 0.733449 0.833449 0.8352972 0.8366498 0.866698 0.9677377 p-value 4.635-05 0.010502	FDR 0.025908 0.167939 0.264323 0.343743 0.535184 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0.912524 0.912524 0.912524 0.912524 0.912524 0.912524 0.912524 0.912524
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Ptpn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Enrpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 Ifngr1 Il1r1 Tnfrsf1a Tnfrsf1a Tnfrsf1a Colfr8 Lung Depleted Gene Symbol Zap70 Cd28 Diat	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;42;6;41 7;12;19;55 9;13;44;46 6;29;30;77 37;38;42;66 0;48;73;79 54;72;86;89 23;59;62;45 27;39;94;99 61;71;92;97 8;69;81;87 16;65;83;102 15;45;76;98 17;64;84;91 22;47;70;96 Ranks of perturbations 1;2;4;10 57;723;29 6;81;875	Perturbations GACACACGGCGCAAT;GCAATA;GCAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAAT;GCAATA;GCAGGCATCACGCCCT;GCACAGGCAAA;GCAGCTTGATGAT GATACGTTTGAGAAC;GTCGGACCTGACCCCC;GTTCACCAAGGCC;GTTGACAGTTGATAGAT GCGAATGTCTTGAGGAA;GACTTGAGCAGGG;GTGAGCGTCAAGACC;GTTGAGAGCACCTGATGAT GCGAATGTCTTGAGGA;GACTTCGGACGCAGGG;GTGAGCGTCAAGACC;GTTGAGAAGCC;GTGAGCGCACTCA GCACTTCTTGATC;GACTTCGGACGAGG;GTGAGCGTCAAGACC;GTTGAGACGCACTGC GCAACTACCACAAGA;GATATTACGCCGC;GGGCAACCAGACGA;GTGACCACTGC GCAACTACCACCAAGA;GATAATTACGCCGCAGC;GGGCAACCAGACGA;GATGACCACTGC GCAACTTCTTTGATC;GAGCATGCCCAGTGGGTCTAACAAGC;GACATGCAGCTGACCACGC GTACAACTACCCAGGGATACCTTCC;GACACTCGCGGTTGGACCACTGC GTACAACTACCCCAGGGATACCTCC;GTGCATCGCGCACCCGGC GCACGTTGTGTGTG;GAGGCATACACG;GATTCCCGAGGACCCGGCTGACACT GTTGGAGCGTCCTC;GTACAGCGCATCCCGGGATTCCCGAGGACCAGCGGA GGAGTGCGGCGTGTCT;GTTACAGCCACGCGACCCGGACTCCGGAGTGAGCC GTACAACTCTTTTG;TGTCACAGCGCACACG;GATTCCCGAGGACCAGCGGA GGAGGGGGGGGTGTCT;GTTACAGCGCACACGCGACCACGCGC GTACGAACTCTTTG;GTACCAGGGTACAC;GATCCTAACGCATACGCAGGCGA GGAGGGGGGGTGTCT;GTCAGCGGCAACCAGGGATACATTGTA;GACAGGCCACGCGC GTACGAACTCTTTG;GTACGAGGGTACAC;GATCCTAACGCATACGATTGCGAGCCAGCGGA GGAGGCGGGGTTGTC;GTCCGAGGCGTACAC;GATCCTACGCATACGCA GCAGCAAGGCCCCCA;GCGTATGCCTATAC;GATGGGATACATTGTA;GACTAGCCA GCAGCAAGGCCCCCA;GCGTATGCCTATAC;GATGGGATACATC;GACGGAGCCAAGCAGC GGTGCGGGCTGTCT;GTCAGGGGTACAC;GATGCAACAGCACGCAGCAGAGAGTCCCCGC GTACGAACTTGGTGCCTATCGAGGGATACATCG;GAGGCATCAACTTGTGGAGCCAGCGAA GCACCAAGGCCCCCA;GCGTATGCCTATACGATGGGATACACC;GAGGCATCAACGCA GCAGCAAGGCCCCCA;GCGTATGCCCTGTGGA;GATGGCATACACTGC;GAGGCCTACCAAGGC GTTCGGCCGTACCA;GGGAGCCCCTGTGGAGCGCCGATACAACTGC;GAGGCAGAACAGCCC GTTCGGCCGTACCA;GGGAGCCCCTGTGGAGCGCCGACAGCGCGTAACACTTACCTATC DEnturbations GTCTGGCGCGTACCA;GGAGGCCCTGTGGAGGCGCGACGAAGGCGCGTGACAC GCGGACAAGGCCACCA;GGCTTGCCAAGCGGCGCCGACGACGAGGCGGTGACAC GCGGCAGGAGGGGGGGCGCGTGCCAAGGGCTCTACAACGCGGGAGACACCCC GCGGCGGGGGGGGGGGGGACCCCTGGGAGGCCCTTACCAAGGCGGGGGGGG	Most enriched perturbation 4 2 3 4 4 3 4 2 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.514539 1.514539 0.837031 0.703285 0.637032 0.502774 0.502774 0.502774 0.502774 0.502774 0.484154 0.485168 0.485168 0.4455168 0.45516800000000000000000000000000000000000	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.595315 0.53068 0.54987 0.439832 0.438843 0.638183 0.643854 0.433852 0.438843 0.438542 0.447557 0.438542 0.447557 0.438542 0.447557 0.438542 0.447557 0.438542 0.447557 0.438542 0.447557 0.438542 0.4475577 0.4475577 0.4475577 0.44755777 0.44757777777777777777777777777777777777	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.07592 0.30997 0.416933 0.578395 0.691696 0.707511 0.717511 0.717511 0.754569 0.833449 0.833449 0.833449 0.833449 0.833449 0.8452972 0.866898 0.977377 p-value 4.632-05 0.010502 0.005702	FDR 0.025908 0.167939 0.264323 0.343743 0.3535184 0.913732 0.885628 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 lingr1 linr1 Tnfrsf1a Tigit Olfr8 Lung Depleted Gene Symbol Zap70 Cd28 Dlat Hk2	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 3;7;38;42;66 20;35;43;95 20;35;43;95 20;35;43;95 23;59;62;85 27;39;94;99 61;71;92;97 17;64;84;91 22;47;70;98 40;63;78;108 25;77;80 Ranks of perturbations 1;2;4;10 5;7;23;29 6;81;87;5 14;19;40;50 20;20;27;57	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGGCTTGTCCAACT GTGTCGATGGCAAT;GCAATACGAGGACCCCG;GCTCCACAAGGCCT;GAAGCAGTTGATGAT GATACGTTTGACGAAC;GCGGGAGCTGACCCCG;GTTCCCCACAAGGCC;GTGAGAGCAGCTGATGAT GATACGTTTGAGGAAC;GCGGGAGCTGGGCGGGCGCCACAGGC;GTTGAGAGCGCCCCT GCGGCTAGAQAAGGT;GACTTCGGCACGAGGG;GTGGCGCCCACAGGC;GTTGAGAAGTGCCACT GCGACTGCTTGACCAAGG;QATACTACGGCGCCCCAGGCCGCCACGAGCC;GTTGAGACAGTGC GCAACTACCCACAGG;QATAATACGGCGCCCCCAGGCCGCCACGAGCC;GTTGAGACGAGT GCAACTACCCACGCAGGGGTGTGCGGCCCCCCGCCACGCGGTGGAGCCCCTGAC GTACACCCACCGCCGCTACCGCGCCCCCGGCCCCCGGCCCCCGGC GTACCACCCCCGCCAGTGCCTCC;GCCACTGCGGTGAGCGGTGGAGCCCCTGAC GCTGGTGCTGTGGTGAGAGGGATACCATCTCC;GCCACCCGGTGGACCGGGTGCACCG GCACGGTTGTGTGAGAGGATACCATCTCC;GCCACCCGGTGCGCTGCACGG GCACGTTGTGGTGGCGCACCCCCCCGGCCACCGCGCCCCGGCCGG	Most enriched perturbation 4 2 3 4 4 3 4 2 2 4 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057 0.837031 0.703285 0.575062 0.513187 0.502774 0.502774 0.502774 0.502774 0.502774 0.455168 0.455168 0.455168 0.445548 0.445548 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.445517 2.315979 1.833905 1.369691 1.400000000000000000000000000000000000	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.6306189 0.5366189 0.5366189 0.549857 0.439832 0.438843 0.6498144 0.447587 0.433002 0.438678678 0.438678 0.438678 0.438678 0.438678 0.438678 0.438678 0.	p-value 0.0016794 0.039648 0.068749 0.333796 0.7592 0.30997 0.416933 0.578395 0.717511 0.717511 0.833449 0.833449 0.833449 0.833449 0.833449 0.852972 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.877377 p-value 4.63E-05 0.010502 0.032239 0.097062	FDR 0.025908 0.167939 0.264323 0.343743 0.343743 0.343743 0.343743 0.343743 0.343743 0.343743 0.343743 0.343743 0.343743 0.343743 0.343743 0.343743 0.343743 0.912524 0.912554 0.912554 0.912554 0.912554 0.912554 0.912554 0.915554 0.915556 0.915556 0.915566 0.915666 0.9156666 0.915666666666666666666666666666666666666
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 lifngr1 lifnr1 lifnr1 Tnfrsf1a Trigit Olfr8 Lung Depleted Gene Symbol Zap70 Cd28 Dlat Hk2 Cpt1a Entpd1	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;42;6;41 7;12;19;55 9;13;44;46 6;29;30;77 3;738;42;66 20;35;43;95 22;34;74 60;68;73;79 24;72;66;89 23;59;62;85 27;39;94;99 61;71;92;97 8;69;94;19 17;64;84;91 22;47;70;96 40;63;78;108 25;57;80 Ranks of perturbations 1;24;10 5;7;23;29 6;8;18;75 14;19;40;50 32;34;43;51 44;94;050 32;34;43;51 44;94;050 32;34;43;51	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGGCAAA;GCAGGCTTGTCCAACT GTGTGCGATGGCAAT;GCAATACAGGGATAC;GCACCCAAAGGACCT;GAAGCAGTTGATGAT GATACGTTTGAGAAC;GTGCGGACTTGACTGC;GTTACCCGCTTAACAGGGTTGAAAGATGGA GCACTCTATGAGGAT;GCATTATGAGAAAGTA;GAAGGAGCGTCAAAGCC;GTTGATAACACAGTC GCAGCTTATGAAGAAGGT;GCACACTTCGGACGAGGG;GTGAGGCGCTAACACGC;GTTGATAACACAGTC GCAACTACACCAAGA;GATAATTACGCCAG;GGGCACACAGACGAT;GTCACAATGGTCATC GCAACTACCCAAGA;GATAATTACGCCAGC;GGGCAACCAGACGAT;GTCACAATGGTCATC GCAACTACCCAAGA;GATAATTACGCCAGC;GGGCAACCAGACGAT;GTCACAATGGTCATC GCAACTCTCTGACCAGGAGTACATCTAC;GCAACCCCGTGAGTGAC GTCACTCACCCAGGA;GTGGGTCATACAAGC;GACAGTGACGGTGA GCACATTGTCGTGTA;GAGGAATACATCTAC;GCAACCTCGTGTAC;GCCACCCCTGACCT GTTGGTCTCTTGAC;GAGGCATCCCAGCG;GGGAGGCACTAGCAGGTGAA GCACATTGTCGTGTA;GAGGAATACATCTAC;GAGCATACTGCTGTACTACGACGAGT GCTAAAGGGCGATC;GTTACACCTGTTCT;GGCGATACGTACTG;GACGAATC GTTGGTGCTCTACCC;GCCAAGTACCTCTAC;GTGCTACGTACTG;GACCAAGCC GTACGCGCGCACA;GAGCCCCCCTCTAC;GTGCTACGTACTG;GACCAGGCC GTACGGTGCGGCACA;GAGGCCATCCAGCG;GATTCCCAGGACAT;GATCCGGAGTTGACC GTACGACACACCCCC;GCCGCGGTGTCCCCTCTAC;TCCTACATTCTAGGCCGACCCCCGGA GGGTGCCGGCGTTGCCT;GTCCTGACCACGTGCCTAACTTCC;GAGGACAT;GATCCCAGCGCA GCAACAACCCCCA;GCGTATGTCCTATAC;GAGCAATCGCAAGTCCCCGCG GTATGTGGAGCATA;GTCGCGGTATGTCCTAACCTGCTACTTGTGGAGCAACCCCCCA;GCCAGCACCAAGCCCCCACCCAGGCGTGCCTG;GAGCTACCAATGCCAAGCCCCCCA;GCCTACCCAAGCCCCCAAGCCCCCAAGCCCCCAACCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAACGCCACCCCAAGCCCCCAACGCCACCCCAAGCCCCCAACGCCACCCCAAGCCCCCAACGCCCCCAAGCGCATCCAACGCAAGCCCCCCAACGCCAACCCCCAAGCCCCCAAGCGCCTTCCCAACGCAACGCCACCCCAACCCCCAACGCCATCCAACCCCCAACCCCCAACCCCCAAGCCACCCCAAGCCACCCCAAGCCACCCCAAGCCACCCCAAGCCACCCCAAGCCACCCCAAGCCACCCCAAGCCACCCCAACCCCAAGCCACCCCAAGCCACCCCAAGCCATTCCAACCCAACCCCCAACCCCCAACCCCAACCCCCAAGCCATTCCAACCCAACCCCCAACCCCCAACCCCCAACCCCCAACCCC	Most enriched perturbation 4 2 3 4 4 3 2 4 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.514539 1.229057 0.887395 0.837031 0.505094 0.502774 0.505094 0.502774 0.455168 0.4455168 0.4455168 0.4455168 0.4455168 0.444543 0.444543 0.444543 0.444543 0.444543 0.444543 1.44565 1.356969 1.833905 1.336969 1.33529 1.33529	Average Score 2.43948 1.559918 1.024709 1.02761 0.807144 0.666794 0.595315 0.53068 0.536189 0.54987 0.439843 0.649787 0.4339632 0.438843 0.438843 0.438843 0.438843 0.438843 0.438843 0.438844 0.417592 0.405406 Average Score 3.016835 3.016835 0.91608 0.91608 0.916886 0.9166886 0.9166886 0.900000000000000000000000000000000000	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.7592 0.30997 0.416933 0.578395 0.691596 0.702429 0.833449 0.833449 0.833449 0.833449 0.8352972 0.866898 0.866898 0.977377 p-value 4.63E-05 0.010502 0.032339 0.097062 0.092762 0.093762 0.093762 0.093762 0.092762 0.092762 0.010512 0.092762 0.092762 0.010512 0.092762 0.0027777 0.002762 0.002762 0.0027777 0.00277777 0.002762 0.00277777 0.0027777 0.002762 0.00277777 0.00277777 0.0027777 0.0027777 0.00277777 0.0027777 0.0027777 0.0027777 0.00277777 0.0027777 0.0027777 0.0027777 0.0027777 0.00277777 0.0027777 0.00277777 0.002777 0.0027777 0.002777 0.002777 0.0027777 0.002777 0.002777 0.002777 0.002777 0.0027777 0.0027777 0.0027777 0.0027777 0.0027777 0.0027777 0.002777 0.0027777 0.002777 0.002777 0.0027777 0.002777 0.002777 0.00277777 0.002777777 0.00277777 0.00277777 0.002777777 0.002777777 0.0027777777777777777777777777777777777	FDR 0.025908 0.167939 0.264323 0.343743 0.535184 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0.912524 0.912524 0.912524 0.912524 0.912524 0.912524 0.912524 0.912524 0.9125541 0.485311 0.415267 0.485311 0.415267
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Ptpn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Enrpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 Ifngr1 Il1r1 Tnfrsf1a Tnfrsf1a Tnfrsf1a Tnfrsf1a Gene Symbol Zap70 Cd28 Dlat Hk2 Entpd1 Hk2 Frta	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11:18 3;42:641 7;12:19:55 9;13;44:46 6;29;30;77 37;38;42:66 0;48;73;79 54;72;86;89 23;59;62:45 27;39;94:99 61;71;92:97 8;69;81:87 16;65;83:102 15;45;76;98 Ranks of perturbations 1;2;410 5;7;23:29 Ranks of perturbations 1;2;411 5;7;23:29 8;81:87 14;19;40;50 2;2;39;67 12;2;2;39;67	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAAT;GCAATACGAGGACCCCCG;GCTCCACAAGGCAC;GCAGCAGTTGATGAT GATACGTTTGAGAAC;GTCGGACCTGACCCG;GTTCCCCAAAGGCC;GTGACAGCTGATGAT GCGAATGTCTGGGACGCGCGACCGGAGGGGGGGGGGGGG	Most enriched perturbation 4 2 3 4 4 3 4 2 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.514539 1.514539 0.837031 0.703285 0.637032 0.502774 0.502774 0.502774 0.502774 0.502774 0.484154 0.485168 0.485168 0.4455168 0.4556680000000000000000000000000000000000	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.595315 0.53068 0.54987 0.439832 0.438843 0.635183 0.438844 0.437892 0.438843 0.438844 0.447587 0.438878 0.417592 0.405406 Average Score 3.016835 1.519382 0.976689 0.766896 0.876496 0.867439	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.07592 0.30997 0.416933 0.578395 0.691696 0.717511 0.717511 0.745459 0.833449 0.833449 0.833449 0.833449 0.833449 0.833449 0.8452972 0.866898 0.977377 p-value 4.632-05 0.0103217 0.0103213 0.012339 0.97762 0.0103317 0.157391 0.228882 0.288845 0.28885	FDR 0.025908 0.167939 0.264323 0.343743 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 lingr1 li1r1 Tnfrsf1a Tigit Olfr8 Lung Depleted Gene Symbol Zap70 Cd28 Dlat Hk2 Cpt1a Entpd1 Hk2 Cpt1a Entpd1 Hk2 Cpt1a Entpd1 Hk2 Prkab2 Zap70 Cd28 Dlat Hk2 Cpt1a Entpd1 Hk2 Prkab2	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 3;7;38;42;66 20;35;43;95 20;35;43;95 20;35;43;95 23;59;62;85 27;39;94;99 61;71;92;97 17;64;84;91 22;47;70;96 40;63;78;108 25;57;80 Ranks of perturbations 1;2;4;10 5;7;23;29 6;81;87;51 4;19;40;50 23;39;57;12;17;72;34	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGGCTTGTCCAACT GTGTCGATGGCAAT;GCAATACAGGGATAC;GCACCCCAAGGGCAAA;GCAGGCTTGATCAAT GATACGTTGACAAC;GCGGAGCTGACCCCG;GTTCCCACAAGGCC;GTGACAGTGATGAT GATACGTTGAGAAC;GCGGGAGCTGAGCGGGCGGCACCAGAGCC;GTGAGACGCGCT GCGAGTGCTGACAAGA;GATAATAGGAGCGG;GTGAGCGCTCAAGAC;GTTGAGAAGTGCCACT GCGAGTGCTGGGGAGTCGGGCGGCGGCGGCGCACCAGACCGA;GTGACACAGGC GCAACTACCAACAAG;GATAATAGGCGCGCCCAAGCCGAT;GTCACAATGGTCACT GCGAGTGCTGTGA;GAGGCTGCAGCG;GTGAGCCGCCGCAGCGGT;GCACCAGGC GTACACCCACCAGGGGATACATCCTAC;GCACACTCCGAGTGAGCGCACTGAC GCACTTGTGGTGTGAGAGGAATACATCTCC;GCCAACCCGGTGACGCGGTGACCG GCACTTGTGGTGAGAGGAATACATCTCC;GCCAACCGCGCCGGCGGCGGCGCCACGGC GTACGACTACCCCGCGCAATACCACCCC;GCCACTGCGGTGGACGCACGGC GCTGCGCTCTCACC;GCCAATACCTCTC;GCCATACCTGCGGTGACCCGGCGGCGCCCGGC GTACAAACTCTTTG;GTCCCCGCCACCGCG;GATCCCCGAGGACCTGCACGGGG GGAGGGGCGCCCCCGCGCAGCCCCCCCGCCACCGCGATCCCGGAGGCGCACGCGG GTACAAACTCTTTG;GTCCCCCCCTTTA;GGAGGACAAGAC;GTTCCGAGACCCCGCG GTACAAACTCTTTG;GTCCGCGCGTACCCCCTAC;GACGAGCCACACACGCG GCAGCAAGGCCCCCCGGCTACCCCCCTAC;GACGACTACAATGCGCA GGAGCCGGGTTGTCC;GCCACGCGTACCCCCCTAC;GACGACCTACCAATGCCCGC GTACGACAAGCCCCCCGGCTGCTCCAAGCACGCATCAACCTCCCGAGCCAACACCCCCCCC	Most enriched perturbation 4 2 3 4 4 3 2 4 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.529057 0.837031 0.703285 0.575062 0.513187 0.502774 0.502774 0.502774 0.502774 0.502774 0.502774 0.485168 0.455168 0.455168 0.455168 0.445540 0.44543 0.444543 0.444543 0.444551 1.65571 1.33529 1.33529 1.33529 1.142071 1.33529	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.53068 0.53068 0.53068 0.53068 0.439832 0.438843 0.6498144 0.447587 0.433002 0.438678 0.43877878 0.438778 0.438778 0.438778 0.438778 0.4387787878 0.43877878 0.43	p-value 0.0016794 0.039648 0.068749 0.333796 0.7592 0.30997 0.416933 0.578395 0.717511 0.717511 0.717511 0.833449 0.833449 0.833449 0.833449 0.852972 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.86287377 p-value 4.63E-05 0.010502 0.032339 0.097062 0.157391 0.228082 0.297432	FDR 0.025908 0.167939 0.264323 0.343743 0.343743 0.343743 0.343743 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olifs Cpt1a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 lifngr1 liftr1 liftr1 Tnfrsf1a Trigit Olif8 Lung Depleted Gene Symbol Zap70 Cd28 Dlat Hk2 Cpt1a Entpd1 Havcr2 Prkab2 Lag3	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;42;6;41 7;12;19;55 9;13;44;46 6;29;30;77 3;738;42;66 20;35;43;95 22;34;74 60;68;73;79 24;72;66;89 23;59;62;85 27;39;94;99 61;71;92;87 8;69;94;99 17;64;84;91 22;47;70;96 40;63;78;108 25;57;80 Ranks of perturbations 1;2;41(0) 5;7;23;29 6;8;18;75 14;19;40;50 32;38;43;51 22;39;57;10 25;53;95;12 25;39;57 22;53;95;57 22;57;95;57 22;57;95;57 23;57 23;57;95;57 23;57;57 24;57;57 24;57;57 24;57;57 25;57;	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGGCAAA;GCAGGCTTGTCCAACT GTGTGCGATGGCAAT;GCAATACAGGGATAC;GCACCCAAAGGACCT;GAAGCAGTTGATAGAT GATACGTTTGAGAAC;GTCGGACTTGACTGC;GTTACCCGCTTAACG;GTTGTAAAGAATGGA GCACTCTATGAGGAT;GAATATTGAGAAAGTA;GAAGGAGCGTCAAAGCC;GTTGAGTACACAGTC GCAGCTTATGAAGAAGGT;GCACACTTCGGACGAGGG;GTGAGGCGCTAAAGCC;GTTGAGTACACAGTC GCAACTACACCAAGA;GATAATTACGGCCAC;GGGCAACCAGACGAT;GTCACAATGGTCATC GCAACTACCCAAGA;GATAATTACGGCCAC;GGCGAACCAGACGAT;GTCACAATGGTCATC GCAACTCTCGTCGACCAGTAGTAGCCAGCG;GGGCGACCAGACCA	Most enriched perturbation 4 3 4 4 3 2 4 2 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.514539 1.52905 0.837031 0.505094 0.502774 0.505094 0.502774 0.455168 0.455168 0.4455168 0.4455168 0.4455168 0.4455168 0.444543 0.445548 0.455688 0.455688 0.455688 0.455688 0.455688 0.4556888 0.4556888 0.455688888888888888888888888888888888888	Average Score 2.43948 1.559918 1.024709 1.02761 0.807144 0.666794 0.53068 0.536189 0.54987 0.439842 0.438843 0.438843 0.438843 0.438843 0.438843 0.438844 0.437587 0.433002 0.405406 0.417592 0.405406 0.417592 0.405406 0.419540 0.419540 0.417592 0.405406 0.53712 0.91608 0.637312 0.622855 0.6875412	p-value 0.001295 0.016794 0.039648 0.068749 0.333796 0.7592 0.30997 0.416933 0.578395 0.30997 0.717511 0.754569 0.833449 0.833449 0.833449 0.833449 0.833449 0.835492 p-value 4.63E-05 0.010502 0.032339 0.997062 0.03817 0.228082 0.228082 0.235792	FDR 0.025908 0.167939 0.264323 0.343743 0.535184 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Ptpn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Enrpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 Ifngr1 If1r1 Tnfrsf1a Tnfrsf1a Tnfrsf1a Tnfrsf1 Olfr8 Lung Depleted Gene Symbol Zap70 Cd28 Dlat Hk2 Cpt1a Enrpd1 Tigit Olfr8	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 37;38;42;66 0;68;73;79 5;4;72;86;89 23;59;62;45 27;39;94;99 61;71;92;97 8;69;81;87 16;65;83;102 15;45;76;80 Ranks of perturbations 1;2;4;10 5;7;23;29 6;8;18;75 14;19;40;50 22;39;57;80	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAAT;GCAATACAGGGATAC;GCACCCCAAAGGCAAA;GCAGCTTGATGAT GATACGTTTGAGAAC;GTCGGACCTGACCCC;GTTCACCAAGGCC;GTTGACAGTGCACTT GCGATGGCTTGAGAAC;GTCGGACCTGGCGACGCGGCACCAGAGCC;GTTGAGAGCGCACTGAC GCACTCTATGAGGA;GATATTACGCCAGC;GGGCAACCAGACCC;GTTGACAAGGCC GCAACTACACCAAGA;GATAATACGGCAGC;GGGCAACCAGACCC;GTTGACAATGGTCACT GCGAATGTCTTGATC;GACTTCGGACCAGGG;GTGAGGCTCAAGACC;GTTGACAATGGTCATC GCAACTACCCACGAGGATACTACGAGCC;GTGGACGACCAGAGCCACTGCAC GTACACTACCCAGGCATACTACCGCACC;GGGCACCAGACCAG	Most enriched perturbation 4 2 3 4 4 3 4 2 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.514539 1.514539 0.63703285 0.63703285 0.513187 0.502774 0.502774 0.502774 0.455168 0.455168 0.455168 0.445433 0.445433 0.445433 0.445518 Score 4.165571 2.315979 1.362991 1.335299 1.142071 0.989556 0.6861254 0.760537	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.595315 0.53068 0.54987 0.439832 0.438843 0.6365183 0.438844 0.438578 0.433802 0.438874 0.433878 0.4319446 0.438578 0.417592 0.405406 Xoreage Score 3.016835 1.581827 1.199382 0.976689 0.876392 0.622685 0.6765496	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.30997 0.416933 0.578395 0.775451 0.775451 0.7754519 0.833449 0.833449 0.832449 0.832449 0.852972 0.866898 0.977377 p-value 4.63E-05 0.012329 0.032339 0.097762 0.032339 0.09762 0.032337 0.228082 0.297432 0.297432 0.365349	FDR 0.025908 0.167939 0.264323 0.343743 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 lingr1 lif11 Tnfrsf1a Tigit Olfr8 Lung Depleted Gene Symbol Zap70 Cd28 Dlat Hk2 Cpt1a Entpd1 Hk2 Cpt1a Entpd1 Hk2 Zap70 Cd28 Dlat Hk2 Cpt1a Entpd1 Hk2 Zap70 Cd28 Dlat Hk2 Cpt1a Entpd1 Hk2 Zap70 Cd28 Dlat Hk2 Cpt1a Entpd1 Hk2 Cpt1a Entpd1 Hk2 Cpt1a Entpd1 Hk2 Cpt1a Entpd1 Tigit Dlat Hk2 Cpt1a Entpd1 Tigit Dlat Hk2 Cpt1a Entpd1 Hk2 Cpt1a Entpd1 Tigit Dlat Hk2 Cpt1a Entpd1 Tigit Hk2 Cpt1a Entpd1 Tigit Hk2 Cpt1a Entpd1 Tigit Hk2 Cpt1a Entpd1 Tigit Dlat Hk2 Cpt1a Entpd1 Tigit Hk2 Cpt1a Tigit Tigit Hk1 Hk2 Cpt1a Entpd1 Tif17 Tigit Tigit Hk1 Cd28 Dlat Hk2 Cpt1a Entpd1 Tif17 Tigit Tigit Hk1 Tif17 Tif18 Tigit Tigit Tigit Hk17 Tigit Tigit Hk2 Cpt13 Tigit Hk17 Tif18 Tigit Tigit Hk17 Tif18 Tigit	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 3;7;38;42;66 20;35;43;95 20;35;43;95 20;35;43;95 23;59;62;85 27;39;94;99 61;71;92;97 8;69;81;87 17;64;84;91 22;47;70;96 40;63;78;108 25;7;80 Ranks of perturbations 1;2;4;10 5;7;23;29 6;81;87;5 14;19;40;50 32;38;43;61 2;24;50;57 14;19;40;50 32;38;43;61 2;24;50;57 14;19;40;50 32;38;43;61 2;24;50;957 12;17;72;84 2;43;04;2;103 3;28;43;65 3;33;48;71 20;27;47;54	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGGCTTGTCCAACT GTGTCGATGGCAAT;GCAATAGGAGACCCCG;GCTCCACAAGGCCT;GAAGCAGTTGATGAT GATACGTTTGACAAC;GCGGGAGCTGACCCCG;GTCCACCAGGCGCTCAAGCG;GTGAGTACACTGC GCAGCTCTTGAGGAGAC;GCGGGAGCGGGGGGGGCGCCACAGCC;GTTGACTACCACTG GCGGATAGAAAGGG;GACTTCGGCGCGACGGG;GTGAGCGCCCACAGCC;GTTGACTACCACTGC GCAACTACCACACAG;GATAATACGGCGGC;GCAGCGCCCACAGCC;GTTGACTACCACTGC GCAACTACTCACCAAG;GATAATACGCGG;GGGCACCAGGCCGCACGAGCC;GTGAGTACCACTGC GCAACTACTCACCAAG;GATAATACGCCGC;GGGCGACCAGGCCGCTAACGGC;GTGACACTGCGC GTACACTACCCAGGGATACTACCACGC;GGGCGCCCCGGCCCCGGCCCCTGAC GCACTTGTGTGTGAGAGGAATACATCTCG;GCCACCGCGCGCTGACGGTTGAC GCACTTGTGTGTGAGAGGAATACATCTCG;GCCACCGCGCGCTGCACGGTGGACGCCCCTGAC GTGCGCTCTTGCC;GCCAATACCTCTC;GTGCATACGCGACTCCGGAGTGGAC GCACAGCTCCCGCGCATACCCACGCG;GATCCCCGAGGACCTGCACG GCACAGCGCCCCCGCCGCACTCCCGCGCATCCCGAGGACTACCTCTGCGCG GTACAAACTCTTTG;GTCCCCACCCTCTTA;GGAGGACAAGAC;GTCCGGAGTTGACC GTACAAACTCTTTG;GTCCCCCCCCTTAC;GAGGGCATACAATGCGGAGTGCCCGCG GTACAAACTCTTTG;GTCCCGCGCTCCCAC;GATCCTTCC;GAGACCTACCAATGCCCG GCACGCAGGCCCCCC;GGTACGTCCCTATC;GACGACAAGAT;GTCCGGAGCTGACAA GGATCCGTGCCCTG;GCGTTGTCCCAGCCGCATCACATGCGCA GGACCCCGGGTTGTCC;GCCACGCCCCCTAC;GAAGACCCCCCACGCAGA GGACCCCGGCGTTGCCCGGCTGCTCAAGCAGGCCCCACGCAGACGCA GGACCCCGGCGCTGTCCGACAACCGCGCACCCCTAC;GAAGGCCACGAACT GACCCATGGTTCCTC;GCCACGGCGCTCCTAACGCGCGGAGGCCTCCAACACC GTCGGCAGCCCCCC;GACTCCCTGTGAGGAGCCCCCCTACCGAAGGCCGCCCCCACCCA	Most enriched perturbation 4 2 3 4 4 3 4 2 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057 0.837031 0.703285 0.575062 0.513187 0.505094 0.5513187 0.502774 0.502774 0.502774 0.455168 0.455168 0.455168 0.445544 0.44543 0.444543 0.444543 0.444543 0.444551 1.33529 1.33529 1.33529 1.33529 1.33529 1.33529 1.33529 1.342057 0.769057 0.760537 0.769057 0.760537 0.769057	Average Score 2.43948 1.559918 1.559918 0.807144 0.666794 0.53068 0.53068 0.53068 0.53068 0.54987 0.439832 0.438843 0.438843 0.438843 0.438843 0.438843 0.438848 0.437592 0.438048 0.4317592 0.438578 0.458578 0.45858 0.458585 0.57858 0.45858 0.45858 0.458585 0.57858 0.458585 0.57858 0.458585 0.57858 0.458585 0.57858 0.458585 0.578585585	p-value 0.001295 0.016794 0.039648 0.068749 0.333766 0.77592 0.30397 0.416933 0.571592 0.30997 0.416933 0.5715611 0.717511 0.717511 0.733449 0.833449 0.833449 0.833449 0.852972 0.866898 0.866898 0.866898 0.866898 0.877377 p-value 4.63E-05 0.010502 0.032339 0.097062 0.157391 0.228082 0.297432 0.357992 0.337469	FDR 0.025908 0.167939 0.264323 0.343743 0.538184 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olf5 Cpt1a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 lingr1 linr1 linr1 Tnfrsf1a Trigit Olf78 Lung Depleted Gene Symbol Zap70 Cd28 Dlat Hk2 Cpt1a Entpd1 Havcr2 Prkab2 Lag3 Tigit Olf78	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;42;64:1 7;12;19;55 9;13;44;46 6;29;30;77 3;73;8;42;66 20;35;43;95 28;34;74 60;68;73;79 28;34;74 60;68;73;79 28;34;74 60;68;73;79 28;34;74 60;68;73;79 6;47;2;68;29 27;39;94;99 6;17;19;29 7;45;96;285 27;39;94;99 6;17;19;29 7;45;96;285 27;39;94;99 6;17;19;29 7;45;76;80 25;57;80 Ranks of perturbations 1;2;47;70;96 40;63;77;10 2;25;39;67 1;21;77;284 24;30;42;103 3;28;43;51 1;21;77;284 24;30;42;103 3;28;43;51 1;21;77;284 24;30;42;103 3;28;43;51 1;21;77;284 24;30;42;103 3;28;43;55 1;21;77;284 24;30;42;103 3;28;43;55 1;21;77;284 24;30;42;103 3;28;43;55 1;21;77;284	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGGCTTGTCCAACT GTGTGGCATA;GCAATAGGAGGCCACGCCCT;GCACCAAGGCCT;GAGCAGTTGATAGT GATACGTTTGAGAAC;GTCGGACTTGACTGC;GTTACCCGCTTAACG;GTTGTAAAGAATGGA GCACTCTATGAGGAT;GCATTATTACGCAGGG;GTGAGGCGTCAAGACC;GTTGATACACAGTC GCAGCTACACCAAGA;GATAATACGCGCGCCGCAGCAGCAGACCC;GTTGATACACAGTC GCAACTACCCAAGA;GATAATACGCCGCGCGCGCACCAGACGAT;GTCACAATGGTCATC GCAAGTCTTTGATC;GAGCAATACATCTAC;GCGCCCCTGTACC;GTGAGTACACAGTC GCTAGCTTGGTA;GAGGATACATCTAC;GCGCCCTGTATC;GCCACCTGTACC GTCGGCTTGTT;GTA;GAGGAATACATCTAC;GCGACCGGAGCAGCGAGCGCCCTGAC GTCGCTTGTGT;GCGCCAGCGCGCGCGCGCGCAGCCAGGCGCGCGCGCGCG	Most enriched perturbation 4 2 3 4 4 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.514539 1.529057 0.887395 0.837031 0.505094 0.502774 0.505094 0.502774 0.485168 0.455168 0.455168 0.4455168 0.4455168 0.444543 0.444545 0.445556 0.646544 0.645644 0.6866444 0.6866444 0.6866444 0.68664444444444444444444444444444444444	Average Score 2.43948 1.559918 1.022709 1.02761 0.807144 0.666794 0.53068 0.53068 0.53068 0.54987 0.439842 0.438843 0.438848 0.447587 0.4339632 0.438848 0.447587 0.433002 0.405406 0.417592 0.405406 0.4055400 0.4055400 0.405540000000000	p-value 0.001295 0.016794 0.039648 0.068749 0.333796 0.7592 0.30997 0.416933 0.578395 0.30997 0.416933 0.578395 0.374569 0.833449 0.833449 0.833449 0.833449 0.835492 0.866898 0.866898 0.866898 0.977377 p-value 4.63E-05 0.010502 0.032339 0.097062 0.010502 0.032339 0.097062 0.0157391 0.157391 0.157391 0.157391 0.228082 0.2357992 0.355792 0.3557469	FDR 0.025908 0.167939 0.264323 0.343743 0.538184 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Ptpn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Enrpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 Ilngr1 Il1r1 Tnfrsf1a Tnfrsf1a Tigit Olfr8 Lung Depleted Gene Symbol Zap70 Cd28 Dlat Hk2 Cpt1a Enrpd1 Tigit Olfr8	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 37;38;42;66 0;38;73;79 5;472;86;39 23;59;62;45 27;39;94;59 61;71;92;97 8;69;81;87 16;65;83;102 15;45;76;98 40;63;78;108 25;57;80 Ranks of perturbations 1;2;4;10 5;7;23;29 6;8;18;75 14;19;40;50 22;39;57;122 22;53;9;57 14;19;40;50 22;38;43;51 22;25;39;57 14;19;40;50 22;38;43;51 22;25;39;57 14;19;40;50 3;23;44;51 22;25;39;57 14;19;40;50 3;33;48;71 20;27;47;94 42;40;42;103 9;28;46;95	Perturbations GACACACGGCGCAAT;GCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAAT;GCAATAGCAGGGATAC;GCTCCACAAGGCCAAGCCGTTGATGAT GATACGTTTGAGAAC;GTCGGAACTGACCG;GTTCCCACAAGGCCCTTAACGATTGATAGAT GCGAATATGAGAAC;GTCGGACCTGACCAGGG;GTGACGGCTCAACGACC;GTTGACAAGGC GCACTCTATGAGAAC;GTCGGACCTGGCACGCAGGG;GTGACGGCTCAAGACC;GTTGACAATGGTCACT GCGAATGTCTTGATC;GACTTCGGACGCG;GGGCAACCAGACCA;GTGACACAGCC GTACAACAACAGC;GATATATGAGCAGC;GGGCAACCAGACCA;GTGACACAGGC GCAACTACACCAAGA;GATAATTACGGCAGC;GGGCCAACCAGACCA;GTGACACAGCCCACTGCA GCAACTACCACAGAC;GATACTACGGCACC;GGGCAACCAGACCA;GACTGCAGCTGAC GCACGTCTTGATC;GACGCAGCCACGAGCCA;GTGGACCAACCAGCCACTCCAGCG;GTCACACAGC GCACGTCTGGTTGTG;GACGCATACCACGCCA;GGGGATACACCCGC;GACCAGCGCACCAGC GCACGACCTCTTG;GTGCACACGCAC;GGATCCCCAGGCG;GATTCCCGAGACCCCGGCGGTTGCCCGGAGCGCGCGGGGTGCCGGGGTTGCC;GACCAGCGCACCGCG GTACAAACTCTTTG;GTCACCACGCG;GATCCCCAGCGGACCACGCGCGCACCCGCG GTACGAACCTCTTG;GTCGACACCGGATCCCTACGCAGCGCACGCGC GTACAACTCTTTG;GTCGCAGCGGCACACGGGCCACCAGCGA GGGTGCGGGGTTGTC;GTCGACACCGGTACCCCGCGGATTCCCGAGAGCCACGCGA GGGTGCGGGGTGTGT;GTTCGCAGACCCTTTA;GAGGCATACATTCG;GACGAGCACAGGC GGAGCGCGGTGCCG;GTACCCCAGCGGACACCGACCGACGAGCACACGCA GGGTGCGGGGTTGTC;GTCGACACCCCTTAC;GAGGCATACATCC;GAGAGCCACGCAGCAGA GGATCCCGTGCCTGT;GACTGCAGACCTCTACGAGCACGAGCACAGCAC	Most enriched perturbation 4 3 4 4 3 4 4 2 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.514539 1.514539 0.63703285 0.63703285 0.513187 0.502774 0.502774 0.502774 0.484154 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.445517 1.365991 1.365991 1.365991 1.365297 0.760537 0.77687 0.760537	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.595315 0.53068 0.54987 0.439832 0.438843 0.639632 0.438843 0.438843 0.438548 0.439874 0.438578 0.438578 0.438578 0.438578 0.438578 0.438578 0.438578 0.438578 0.438578 0.438578 0.438578 0.438578 0.438578 0.438578 0.438578 0.438578 0.438578 0.576846 0.676545 0.676546 0.677546 0.676546 0.677546 0.676546 0.677546 0.676546 0.677546 0.	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.30997 0.416933 0.578395 0.77542 0.30997 0.416933 0.775416 0.7754519 0.833449 0.833449 0.832449 0.832449 0.832449 0.832449 0.832449 0.832449 0.832449 0.832449 0.832449 0.832449 0.832449 0.832449 0.832449 0.832449 0.832449 0.832449 0.83249 0.977377 0.157391 0.228082 0.365348 0.377469 0.422669 0.4228799 0.42269 0.422819 0.42819 0.428819 0.4	FDR 0.025908 0.167939 0.264323 0.343743 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Enrbd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 lingr1 li1r1 Tnfrsf1a Tigit Olfr8 Lung Depleted Gene Symbol Zap70 Cd28 Dlat Hk2 Cpt1a Enrbd1 Tigit Dlat Hk2 Cpt1a Enrbd1 Hk2 Cpt1a Enrbd1 Hk2 Cpt1a Enrbd1 Cd28 Dlat Hk2 Cpt1a Enrbd1 Cd28 Dlat Hk2 Cpt1a Enrbd1 Hk2 Cpt1a Enrbd1 Cd28 Dlat Hk2 Cpt1a Enrbd1 Hk2 Cpt1a Cp	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;34;4;66 6;29;30;77 37;38;42;66 20;35;43;95 20;35;43;95 20;35;43;95 20;35;43;95 20;35;43;95 20;35;43;95 20;35;43;95 21;73;99;45;99 61;71;92;97 17;64;84;91 22;47;70;96 40;63;78;10 25;7;80 Ranks of perturbations 1;2;4;10 5;7;23;29 6;81;87;51 4;19;40;50 23;38;43;61 22;25;39;57 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;20;27;47;54 45;59;73;74 20;27;47;54 45;59;73;74 20;27;47;54 45;59;73;74 20;27;47;54 45;55;28 33;46;17 20;27;47;54 45;55;28 34;61;82;105 20;27;47;54 45;55;28 34;61;82;105 20;27;47;54 45;55;28 34;61;82;105 20;27;47;54 45;55;28 34;61;82;105 20;27;47;54 45;55;28 34;61;82;105 20;27;47;54 45;55;28 34;61;82;105 20;27;47;54 45;55;28 34;61;82;105 20;27;47;54 45;55;28 34;61;82;105 20;27;47;54 45;55;28 34;61;82;105 20;27;47;54 45;55;28 34;61;82;105 20;27;47;54 45;55;28 34;61;82;105 20;27;47;54 45;55;28 34;57;27;29 20;27;47;54 2	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAAT;GCAATAGGAGACCCGCGGCTCCACAAGGCCT;GAAGCAGTTGATGAT GATACGTTGAGAAC;GCGGAGCTTGGGACCGCGGGTCCACAAGGCC;GTGAGCAGTTGATGAT GCGGATAGAAAGGT;GACTTCGGACGAGGG;GTGGAGCTCAAGACC;GTTGAGAAGTGCACAT GCGGATAGAAAGGT;GACTTCGGACGAGGG;GTGAGCCTCAAGACC;GTTGACAATGGTCACT GCGAGTGCTTTGATC;GAGCCAGGG;GTGAGCCTCAAGGC;GTTGACAATGGTCACT GCGAGTGCTTTGATC;GACCCAGTGGTGTCT;GACCACTCCGAGT;GTACACATGGTCACT GCAAGTCTTTGTT;GTA,GAGGATAATACATCTAC;GCGATACGCGACTGACAGTTGGA GCACTTGTGGTGTGAGAGGAATACATCTAC;GCAACCCGCAGCAGCGGTTGACAGGGTGA GCACATTGTGGTGAGAGGAATACATCTAC;GCGATACGTGCGCGACCGCAGCAGC GTACACTACCCAGGGATAACATCTAC;GCATACGCGACTGCAGCGGTGACACG GCACGTTGGTGTGAGAGGAATACATCTAC;GCGATACGTGCGACTGCAGCGGTGACACG GCACGATGGTGTGAGAGGAATACATCTAC;GCACACGGCAGCAGCAGCGGTGACACG GCACGATGGTGTGAGAGGAATACATCTAC;GCGATACGTGCGACTGCCGGCTGACACG GCACGATGGGTGCACA;GAAGGACCACGCAGCACGCGATCCCGGAGGAGGACCCCCGCG GTACAAACTCTTTGGT;GCACCCCTCTTA;GGAGGACAAGAT;GTCCGGAGGTGACC GTACAAACTCTTTG;GTCCCCGCGTACCCCCCTAC;GACGAGTCCCGCGG GTACGACGCGGTTGTC;GCACGCGTACAC;GTTCCCAGACCCCCCCGACCAATACGCA GGAGCCGCGGTTGTCC;GCCACGCGTACCACCGCATACATTGCGGAGTTGACC GCAGCAAGGCCCCCC;GGTAGTCCCTCTATC;GACGGGCATACACTGCAGAGCCTACCAATACCCCC GTACGACAAGCCCCCC;GGCTATCCCTGGAGCATCCACGCAAGACT;GCTAACAATCCCCGC GTACGACAGCGCCCCC;GGCTGTGTGAGACAT;GATGGGGCTTACACC;GAAGGCCTACCAAGACT GACCCAGGGCGCCCCC;GCAGCTCCTGGAGGCCTCCAACCCCCTAC;GAAGGCCGACCACCACC GACCCAGGCGCCCCCC;GCATCCCCTGTGAG;GTCCTAACACCCTTC;GCAAGGCCGACCACC GACCCAGGCGCCCCCC;GCATCCCCTGTGAG;GTCCTACACCCCCTC;GCAAGGCCGTGCAACC GCCGCACAGCGCCCCCC;GCCTGTGGAGACGC;GTCCGACAACCCCTCCCGCGGTGTGTA GCGACAAGGCCCCCCC;GCCTGTGGAGGACT;GGTCCAACCCCCCCGCGCGTGTGT GCCACAGGCGCCCCCC;GCCCTGTGAGGACCC;GTCCAACACCCCCCCGCGGTGTGT GCCACAGCGGCCCCCCCGCGCTTGCAAGACCC;GTCCAACCCCCCCGCGGTGTGT GCCACAGCGCGCCCCCCGCGCACGACGGACGGTGCTCAACCACCCCCTCGCGCGGTGTGT GCCACAGCGCGCCGCCGCCGCACGACGAGACGGTGCTCCAACGCCGGGTGCTCT GCCACAGCGGGCCGCCCCCCCGCACCTACCATTGCT;GGCATGCCCCCCCCGCGTGTGTCT GCCACAGTGGCGCACCCACGCACGACGAGGCACGTGGTACGACCGCGGGGTGCTC GCCACAGGCGC	Most enriched perturbation 4 2 3 4 4 3 4 2 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057 0.837031 0.703285 0.575062 0.513187 0.505094 0.435148 0.455168 0.455168 0.455168 0.445544 0.44543 0.444543 0.444543 0.444543 0.444543 0.444551 1.33529 1.335529 1.3555555555555555555555555555555555555	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.53068 0.53068 0.53068 0.53068 0.54987 0.4339632 0.438843 0.6498144 0.447587 0.433878 0.447587 0.433878 0.447587 0.433878 0.447587 0.433678 0.438678 0.438678 0.438678 0.438678 0.438678 0.438678 0.438578 0.438678 0.438578 0.438578 0.438578 0.438578 0.438578 0.51288 0.766896 0.622685 0.676546 0.765895 0.576546 0.765895 0.512424 0.488047 0.48	p-value 0.0016794 0.039648 0.068749 0.033796 0.7592 0.30397 0.416933 0.581696 0.702429 0.717511 0.717511 0.833449 0.833449 0.833449 0.833449 0.852972 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.866898 0.877377 p-value 4.63E-05 0.010502 0.032339 0.097062 0.032339 0.097062 0.0323746 0.377469 0.22742 0.365348 0.377467 0.463983 0.467522 0.46752	FDR 0.025908 0.167939 0.264323 0.343743 0.343743 0.343743 0.343743 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olf5 Cpt1a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 lingr1 linr1 linr1 Tnfrsf1a Trigit Olf78 Lung Depleted Gene Symbol Zap70 Cd28 Dlat Hk2 Cpt1a Entpd1 Havcr2 Prkab2 Lag3 Tigit Olf78 Cd28 Dlat Hk2 Cpt1a Entpd1 Havcr2 Prkab2 Zag3 Tigit Il171 Havcr2 Prkab2 Lag3 Tigit Nirs Socs3 lingr1 Havcr2 Prkab2 Lag3 Tigit Il171 Havcr2 Prkab2 Cpt1a Entpd1 Havcr2 Prkab2 Cpt1a Entpd1 Havcr2 Prkab2 Cpt1a Entpd1 Havcr2 Prkab2 Cpt1a Entpd1 Havcr2 Prkab2 Cpt1a Entpd1 Havcr2 Prkab2 Cpt1a Entpd1 Havcr2 Prkab2 Cpt1a Entpd1 Havcr2 Dlat Havcr2 Prkab2 Cd28 Dlat Havcr2 Prkab2 Cpt1a Entpd1 Triff Havcr2 Prkab2 Cd28 Dlat Havcr2 Prkab2 Cpt1a Entpd1 Triff Havcr2 Prkab2 Cd28 Dlat Havcr2 Prkab2 Cpt1a Entpd1 Triff Havcr2 Prkab2 Cd28 Dlat Havcr2 Prkab2 Cpt1a Entpd1 Triff Havcr2 Prkab2 Cd28 Dlat Havcr2 Prkab2 Cd28 Dlat Havcr2 Prkab2 Cd28 Dlat Havcr2 Prkab2 Cpt1a Entpd1 Havcr2 Prkab2 Cd28 Dlat Havcr2 Prkab2 Cpt1a Entpd1 Havcr2 Prkab2 Cpt1a Entpd1 Havcr2 Prkab2 Cpt1a Entpd1 Havcr2 Prkab2 Cpt1a Entpd1 Havcr2 Prkab2 Cpt1a Entpd1 Havcr2 Prkab2 Co28 Dlat Havcr2 Prkab2 Co28 Dlat Havcr2 Prkab2 Co28 Dlat Havcr2 Prkab2 Co28 Dlat Havcr2 Prkab2 Co28 Dlat Havcr2 Prkab2 Co28 Dlat Havcr2 Prkab2 Triff Havcr2 Prkab2 Triff Havcr2 Prkab2 Triff Havcr2 Prkab2 Triff Havcr2 Prkab2 Triff Havcr2 Prkab2 Triff Havcr2 Prkab2 Triff Havcr2 Prkab2 Triff Havcr2 Prkab2 Triff Havcr2 Prkab2 Triff Havcr2 Prkab2 Triff Havcr2 Prkab2 Triff Havcr3 Havcr2 Prkab2 Triff Havcr2 Prkab2 Triff Havcr2 Prkab2 Havcr2 Prkab2 Havcr2 Havcr3 Havcr3 Havcr2 Havcr3 Ha	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;42;64:1 7;12;19;55 9;13;44;46 6;29;30;77 3;73;8;42;66 20;35;43;95 28;34;74 60;68;73;79 28;34;74 60;68;73;79 28;34;74 60;68;73;79 28;34;74 60;68;73;79 28;39;42;95 27;39;94;99 61;71;92;97 8;69;98;18;7 17;64;84;91 22;47;70;96 40;63;78;108 25;57;80	Perturbations GACACCACGGCGCAAT;GCAAT;GCACGGGCATA;GCACGCCCCAAGGCCAAC;GCAGGCGCAAT;GCAAT;GCAATGCAGGGCATA;GCACGCCCCT;GCCCCAAAGGCCTGAACGCTTGATGATGAT GATACGTTTGAGAAC;GTCGGACGCTGACGCCCTGCGCCACAAGGCC;GTTGGTACAACATGGC GCAACTCTCTGACGAGGCGCGCAGGGCGCGCACGCAGCCCGCTGACGCGCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCGCGCCACCACGCGGTGAGGCGCTGAAGCCCCCTGCCCCGCCACGCACG	Most enriched perturbation 4 2 3 4 4 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 0.1514539 1.514539 1.514539 1.52905 0.837031 0.505094 0.502774 0.505094 0.502774 0.484154 0.4455168 0.4455168 0.4455168 0.4455168 0.444543 0.4455168 0.645653 0.686644 0.652073 0.686644 0.652073 0.686644 0.645653 0.549161	Average Score 2.43948 1.559918 0.529018 0.807144 0.666794 0.53068 0.53068 0.53068 0.54987 0.439832 0.438843 0.438848 0.438548 0.437548 0.430548 0.430548 0.430548 0.430548 0.430548 0.430540 0.512424 0.4300540 0.512424 0.4300540 0.512424 0.4300540 0.512424 0.4300540 0.512424 0.4300540 0.512424 0.4300540 0.512424 0.4300540 0.512424 0.4300540 0.512424 0.4300540 0.512424 0.4300540 0.512424 0.4300540 0.512424 0.4300540 0.512424 0.4300540 0.512424 0.51244 0	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.7592 0.30997 0.416933 0.578395 0.30997 0.416933 0.578395 0.374569 0.833449 0.833449 0.833449 0.833449 0.833449 0.833449 0.866898 0.866898 0.977377 p-value 4.63E-05 0.010502 0.032339 0.976323 0.010502 0.032339 0.977432 0.357992 0.357992 0.357992 0.357992 0.3579432 0.3579432 0.357492 0.3579432 0.357492 0.3579432 0.3579432 0.3579432 0.3579432 0.357942 0.357952 0.	FDR 0.025908 0.167939 0.264323 0.343743 0.538184 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Ptpn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Enrpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 Ilngr1 Il1r1 Tnfrsf1a Tnfrsf1a Tnfrsf1a Gene Symbol Zap70 Cd28 Dlat Hk2 Cpt1a Enrpd1 Tnfrsf3 Jlat Hk2 Cpt1a Enrpd1 Tnfrsf3 Jlat Hk2 Cpt1a Enrpd1 Tnfrsf3 Socs3 Tnfrsf9 Socs3 Ilngr1 Il1r1 Havcr2 Kab2 Lag3 Dlat Hk2 Cpt1a Enrpd1 Tnfrsf3 Socs3 Ilngr1 Tnfrsf1a Dokr2	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 37;38;42;66 0;08;73;79 5;472;86;89 23;59;62;45 27;39;94;99 61;71;92;97 8;69;81;87 16;65;83;102 15;45;76;98 40;63;78;108 25;57;80 Ranks of perturbations 1;2;4;10 5;7;23;29 6;8;18;75 14;19;40;50 9;2;39;45;14 22;39;57;122;29 6;8;18;75 14;19;40;50 9;2;39;45;122;25;39;57 12;17;72;54 24;30;42;103 9;28;46;95 3;33;48;71 20;27;47;94 24;59;73;74 26;49;52;88 3;48;18;2;105 3;35;66;96	Perturbations GACACACGGCGCAAT;GCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAAT;GCAATA;GCAGGCCCCT;GCCACAAGGCCAAGCCGTTGATGAT GATACGTTTGAGAAC;GTCGGACCTGACCCCC;GCTCCACAAAGCC;GTTGAAAGAAGGCA GCACTCTATGAGAAC;GTCGGACCTGGACGAGGG;GTGAGCGTCAAGACC;GTTGACAAGGCA GCACTCTAGAGGA;GATATTACGGCCAGC;GGGCAACCAGACCC;GTTGACAAGGCACCACGCC GCAACTACACCAAGA;GATAATTACGGCCAC;GGGCAACCAGACCC;GTTGACAAGGCCACTGCA GCAACTACACCAAGA;GATAATTACGGCAGC;GGGCAACCAGACCA;GTGACACAGGCC GTACAACTACCCAGGGCTGACGCC;GGGCCAACCAGACCA;GTGGACCACCGACCCAGCGCACCACCGC GTACAACTACCCCAGTGGTTGTC;GACCATCCCGAGCGCATCCCGCGCAACCAGGCCACTGCA GCACTGTCGTGTG;GAGCGCAACCAGCCA;GGGGTACACCAGCCG;GATCCCGAGCGTGACACC GCTGGAGGCGTGCT;GTTACACGCCTATCC;GACCATCCGGCTGCACACCGGGTGCCGGGTTGCCC;GCCAACCCTGTACAC GCTGGAGGCGTGCT;GTTACACGCCTATCC;GGCCTACCACCCGGCGTGCCCGGCGGTTGCCCGGCGGTTGCCCGAGCGCACCGCGCGCG	Most enriched perturbation 4 2 3 4 4 3 4 2 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.514539 1.514539 0.63703285 0.63703285 0.513187 0.502774 0.502774 0.502774 0.484154 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.4455168 0.445517 1.365991 1.365297 1.3686941 1.33529 1.142071 0.686154 0.68653 0.645653 0.645653 0.6445653	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.595315 0.53068 0.54987 0.439832 0.438843 0.656183 0.438843 0.438843 0.431592 0.438843 0.431592 0.405406 Average Score 3.016835 1.581827 1.199352 0.91608 0.876496 0.876496 0.8765496 0.8765496 0.8765496 0.8765496 0.8765496 0.8765496 0.8765496 0.8765496 0.8765496 0.8765496 0.8765496 0.8765496 0.8765496 0.8765496 0.875539 0.611289 0.438647 0.47858 0.439546 0.478538 0.439546 0.478538 0.439546 0.478538 0.439546 0.478538	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.30997 0.416933 0.578395 0.77592 0.30997 0.416933 0.578395 0.377511 0.775459 0.833449 0.833449 0.832449 0.832449 0.832449 0.832449 0.832449 0.832449 0.832449 0.83249 0.977377 p-value 4.632-05 0.010502 0.032339 0.97762 0.365348 0.377469 0.422669 0.422689 0.422649 0.42383 0.476752 0.524705 0.524705 0.774659 0.4226459 0.426	FDR 0.025908 0.167939 0.264323 0.343743 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olfr5 Cpt1a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 lingr1 li1r1 Tnfrsf1a Tigit Olfr8 Lung Depleted Gene Symbol Zap70 Cd28 Dlat Hk2 Cpt1a Entpd1 Ravcr2 Hk2 Prkab2 Lag3 lingr1 li1r1 Tnfrsf1a Entpd1 Havcr2 Prkab2 Lag3 Dlat Hk2 Cpt1a Entpd1 Kap2 Cd28 Dlat Hk2 Cpt1a Entpd1 Ravcr2 Hk2 Dlat Hk2 Cpt1a Entpd1 Ravcr2 Rkab2 Lag3 Dlat Hk2 Cpt1a Entpd1 Tifrsf1a Dgkz Nors3 lingr1 Tnfrsf1a Dgkz Ptpn2	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;34;4;66 6;29;30;77 37;38;42;66 20;35;43;95 28;34;74 60;68;73;79 54;72;86;89 23;59;62;85 27;39;94;99 61;71;92;97 17;64;84;91 22;47;70;96 40;63;78;108 25;77;80 Ranks of perturbations 1;2;4;10 5;7;23;29 6;81;87;51 4;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 14;19;40;55 13;35;66;96 13;54;164;89 16;64;79;102	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGCAAA;GCAGCTTGTCCAACT GTGTCGATGGCAAT;GCAATACGAGGCCCCG;GCTCCACAAGGCCT;GAACACTTGATGAT GATACGTTGAGAAC;GCGGGAGCTTGGCACCCCG;GTTCCCCAAAGACC;GTTGACAAGTGGA GCACTCTTGAGAGAC;GCGGGAGCTGGAGCGCTCAAGACC;GTTGACAATGGTCACT GCGAGTGCTGCACAGAGGATACTTCGGACGAGGG;GTGGAGCCTCAAGACC;GTTGACAATGGTCACT GCAAGTCTTTGATC;GACCCAGTGGTGTCT;GACCACTCCGAGT;GTCACAATGGTCACT GCAAGTCTTTGTCT;GACACCCAGTGGGTGCTATCCAAGC;GCTGAAGCCGCTGAAGC GCAACTGCTGTGA;GAGGATAATACATCTAC;GCGACACGCAGCGACTGACGAGGTTGA GCAACTGCTGTGTA;GAGGCTATCCACACCC;GCACACTCCGAGTGAGCCACTGAC GTACACTACCCAAGGCTATCCACACCC;GCTACTGCGGTGAACCCAGCGC GTACACTACCCC;GCAAGTACCTTCT;GCGCAACCGCGCGGTGCACCG GCACGTTGTGTG;GAGGGCATACCACCCCC;GCACGCTGCACG GCACGTTGTGTG;GCCCCCCTTTAC;GAGGCGAACCAGGCC;GTCCCGAGCGCTGACACG GGAGGGGCGCCCCC;GCAAGTACCTTCT;GCCAACACC;GTCCGACGCAGCGAGC GTACAAACTCTTTG;GTCCCCCCCTTTA;GGAGGACAAGAT;GTCCGGAGTGACC GTACAAACTCTTTG;GTCCCCGCGTACCCCCACGCCATACATGCGGAGTTGACC GTACAAACTCTTTG;GTCCCCGCGTACCCCCTAC;GAGGACTACAATGCCGCG GTACGACGCCCCC;GCGTATGCCCCTCTTA;GGAGGGATACATCC;GAGACCTACCAATACCCC GCAGCAAGGCCCCCC;GGCTGTCCCAAGCATCCAGGGGATACACC;GTCCAAACCCCCCCC GTACGACAAGCCCCCC;GCGTATGCCCTCTTA;GGAGGGATACACC;GTACCAATGCCCGCC GTACGACAGCCCCCC;GCGTATGCCCTCTTAC;GAGGGGATACACC;GCAGACCTACCAAGA GGACCCGGGCTTCCCGCGGTTGTCCCAGCACGACGAAGACT;GCTACCAATGCCCCCC GACGCAAGGCCCCCC;GCGCTTGTGAGACATG;GTTCCAACACCCTTCC;GAAGGCCTACCAAGACT GACCCAGGCGCCCCCA;GGAGGTCCCCTGTGAG;GTCCTAACACCCTTCCGAGGCGTACAAC GCGCCAAGGCCCCCC;GCATCCCCTGTGAG;GTCCTAACACCCTTC;GAAGGCCGACCACCACCC GACCGGGCCACCCA;GCGACTCCCCTGTGAG;GTCCTAACACCCTTC;GCAAGACCCACCC GCCCGGAGCCCCCC;GCCTTGCGAGGACCC;GTCCGACAACCCCTTC;GCAAGGCCGTCCAACC GCCGCACAGCCGCCCCCCGCGCTTGCAAGGCCGTCCAACCCCCTCC;GCCGTTGTGAGCCACCA GCGCACAGGCCCCCCG;GCTTGCAAGACC;GTCCGACACCCCGCCGCTGTCCACCCTGCGGTTGTCT GCCAGCAGCCACCCAGCACCACGGACGACGGCTCCAACCCCCGTCCAAGCCCGGGTGTCT GCCAGCAGCAGCCCCCCGCGCTCAACCCCGGTCCAAGCCC;GTCGACGCCGGGTTGTCT GCCAGCAGCAGCCGCGCACCACCGACGACGTGCTGAACACCCGCGGGGTGTCT GCCAGCAGCAGCGCGCGCACCACCACGACGACGCAGGCGTACAACCGCGGGGGGGTCTCT GCCAGCAGGCGCT	Most enriched perturbation 4 3 4 3 4 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.229057 0.837031 0.703285 0.575062 0.513187 0.505094 0.435148 0.455168 0.455168 0.455168 0.445544 0.44543 0.444543 0.444543 0.444543 0.444543 0.444543 0.444551 1.33529 1.33529 1.33529 1.33529 1.33529 1.33529 1.33529 1.33529 1.33529 1.33529 1.33529 1.33529 1.33529 1.336951 0.6861254 0.6861254 0.652073 0.6484154 0.652073 0.6484154 0.652073 0.648154 0.484154 0.652073 0.648154 0.652073 0.648154 0.484154 0.652073 0.648154 0.652073 0.648154 0.652073 0.648154 0.648333 0.549161 0.484154 0.648154 0.65807 0.6	Average Score 2.43948 1.559918 1.224709 1.02761 0.807144 0.666794 0.53068 0.53068 0.53068 0.53068 0.54987 0.4339632 0.438843 0.649188 0.438843 0.438843 0.438848 0.437858 0.438848 0.447587 0.433002 0.438678 0.438678 0.438678 0.438678 0.438678 0.438678 0.438678 0.438678 0.438678 0.438678 0.438578 0.51288 0.766896 0.620865 0.676546 0.765895 0.676546 0.765895 0.613399 0.512424 0.49946 0.479351 0.4385167 0.429345 0.459346 0.459346 0.459345 0.459345 0.512424 0.459346 0.459346 0.459345 0.45945 0.4595456 0.4595456 0.4595456 0.4595456 0.4595456 0.4595456 0.4595456 0.4595456 0.4595456 0.4595456 0.4595456 0.4595456 0.4595456 0.4595456 0.4595456 0.4595456 0.45954566 0.459545666666666666666666666666666666666	p-value 0.001295 0.016794 0.039648 0.068749 0.333796 0.73792 0.416933 0.578395 0.30997 0.416933 0.571591 0.717511 0.717511 0.833449 0.833449 0.833449 0.833449 0.833449 0.833449 0.833449 0.833449 0.833449 0.833449 0.833449 0.83247 0.833449 0.833449 0.83247 0.833449 0.833449 0.83247 0.833449 0.833449 0.83247 0.833449 0.835472 0.835472 0.835472 0.365348 0.377469 0.422689 0.426898 0.426898 0.42	FDR 0.025908 0.167939 0.264323 0.343743 0.343743 0.343743 0.343743 0.343743 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Lung Enriched Gene Symbol Pdcd1 Adora2a Kdr Pipn2 Socs3 Rnf128 Dgkz Olif5 Cpt1a Entpd1 Tnfrsf9 Havcr2 Hk2 Prkab2 Lag3 lingr1 li1r1 Tnfrsf1a Tigit Olif8 Lung Depleted Gene Symbol Zap70 Cd28 Dlat Hk2 Cpt1a Entpd1 Hk2 Cpt1a Entpd1 Hk2 Cpt3 Ingr1 Lung Depleted Gene Symbol Zap70 Cd28 Dlat Hk2 Cpt1a Entpd1 Hk2 Cpt1a Entpd1 Hk2 Cpt3 Ingr1 Jirf Socs3 lingr1 Tnfrsf9 Socs3 lingr1 Tnfrsf1a Dgkz Pipn2 Olif8	Number of perturbations 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ranks of perturbations 1;2;11;18 3;4;26;41 7;12;19;55 9;13;44;46 6;29;30;77 3;738;42;66 20;35;43;95 28;34;74 60;68;73;79 6;06;87;379 6;472;86;89 23;59;62;85 27;39;94;99 61;71;92;97 8;69;84;87 17;64;84;91 22;47;70;96 40;63;78;108 25;57;80 Ranks of perturbations 1;2;4;10 5;7;23;29 6;8;18;75 14;19;40;50 32;38;43;51 14;19;40;50 32;38;43;51 12;24;70;96 42;57;80 22;57;80 23;34;35 14;19;40;50 32;33;43;71 20;27;72;44 24;30;42;105 3;33;48;71 20;27;74;94 45;69;73;74 20;37;74 2	Perturbations GACACACGGCGCAAT;GCAATACAGGGATAC;GCACCCCAAGGGCAAA;GCAGGCTTGTCCAACT GTGTCGATGGCAAT;GCAATATGGAGAGCCCCGCGCCCAAGGGCAAC,GCGGTTGTAAGAATGGA GCACTCTATGAGGAT;GCAATATGAGAAGTA;GAAGGAGCCTCAAGACC;GTTGGTACACATGGC GCAGCTTTGAGAAAGGT;GCACACTTCGGACGAGGG;GTGGAGCCGCTAAGACC;GTTGGATACACACGC GCAGCTCTATGAGGAT;GCATATTACGCCAC;GGGCACCAGACCGCTTCAGCACGCCCTGACG GCAACTACCCACGAG;GTTATACGCCAC;GGGCACCCAGACCGCTTCACAATGGTCATC GCAAGTCTTTGATC;GAGCATACTACCGCCG;GGCAACCAGACGAT;GTCACAATGGTCATC GCAAGTCTTTGATC;GAGCAATACATCTAC;GCGCACCCGCAGCGACCCAGGGC GTCACTCACCCAGGACTACCACGCC;GGCGAACCAGGCTGACGCCGTGACGC GTCACTTGCTGT;GCGCGCAGCACCCAGCGGGGGGGGGGG	Most enriched perturbation 4 2 3 4 4 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2	STARS Score 3.144481 2.132688 1.768209 1.514539 1.514539 1.229057 0.8837031 0.505094 0.502774 0.505094 0.502774 0.484154 0.455168 0.4455468 0.4455468 0.444543 0.44557 0.76057 0.76057 0.76057 0.76057 0.76057 0.747877 0.688644 0.652073 0.645653 0.549161 0.484154 0.434081	Average Score 2.43948 1.559918 0.50761 0.807144 0.666794 0.53068 0.53068 0.53068 0.54987 0.439832 0.438643 0.438643 0.438643 0.438643 0.438643 0.438648 0.437592 0.405406 0.405406 0.405406 0.405406 0.405406 0.405406 0.405406 0.405406 0.405406 0.405406 0.676686 0.6766896 0.6766896 0.6766896 0.6766896 0.6766896 0.6766895 0.6766896 0.6766895 0.6766896 0.6766895 0.676840 0.6766895 0.676840 0.473538 0.4435167 0.622685 0.4435167 0.429045 0.473538 0.435167 0.622646 0.4355167 0.622646 0.4355167 0.432045 0.435167 0.432045 0.435167 0.622646 0.4355167 0.622646 0.4355167 0.622646 0.4355167 0.622645 0.4355167 0.622646 0.4355167 0.622646 0.4355167 0.622646 0.4355167 0.622646 0.4355167 0.622645 0.435517 0.622645 0.435517 0.622645 0.435517 0.622645 0.435517 0.622645 0.435517 0.622645 0.435517 0.622645 0.435517 0.622645 0.435517 0.622645 0.435517 0.622645 0.435517 0.622645 0.435517 0.622645 0.435517 0.4355517 0.43555517 0.435517 0.435	p-value 0.001295 0.016794 0.039648 0.068749 0.133796 0.7592 0.30997 0.416933 0.578395 0.717511 0.754569 0.833449 0.833449 0.833449 0.833449 0.833449 0.833449 0.833449 0.835492 0.032339 0.977377 p-value 4.63E-05 0.010502 0.032339 0.032339 0.032339 0.032339 0.452972 0.032339 0.452972 0.157391 0.228082 0.032339 0.452972 0.357992 0.357992 0.357992 0.357492 0.357492 0.357492 0.357492 0.357492 0.357492 0.422689 0.422689 0.476752 0.624705 0.774609 0.777077 0.796669 0.9054	FDR 0.025908 0.167939 0.264323 0.343743 0.343743 0.343743 0.343743 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

Supplementary Ta	able 2: sgRNA and TIDE primer sequence	ces		
Gene Target	sgRNA	TIDE Primer Forward	TIDE Primer Reverse	
Pdcd1				
Pdcd1-1	GGTACCCTGGTCATTCACTT	CCCCACCTCTAGTTGCCTGTT	GGCATTTCACCTGTAAAACCCAC	
Pdcd1-2	ACAGCCCAAGTGAATGACCA	CACCTCTAGTTGCCTGTTCTCCC	GGGGTGGATTTTGAGCCCCA	
Pdcd1-3	GACACACGGCGCAATGACAG	GTACAGGCTCCTTCCTCACAGC	TCCATCCCTTAAAGGTAAATGGGCATC	
Batf				
Batf-1	AGAGATCAAACAGCTCACCG	ATAGACAGCAATCAGCAGTTGCC	AAGGGATCACGGGAGTAGCAT	
Batf-2	GTGGGTACTCACCAGGTGAA	AGGAGACCCAAGGGTGGGTA	TACATGCATGGGAGAGCGAAG	
Batf-3	TGTGAAGTACTTGAGCTCCT	ATAGACAGCAATCAGCAGTTGCC	AAGGGATCACGGGAGTAGCATC	
Ptpn2				
Ptpn2-1	GAATATGAGAAAGTATCGAA	GGGCACTGAGCAGCAAACTTTAT	GTGACTAGCTTTCATCTTTGCCTCTT	
Ptpn2-2	CTCACTTCCATTATACCACC	CTGGAAGGCTGGCTGTAGTGTT	CTAACCTCCTCAGGCACCAGTC	
Ly75				
Ly75-1	GTCACGAAACTCCATAATGG			
Ly75-2	GCTTGCTTGAGAAAACGTAA			
Ms4a1				
Ms4a1-1	GTCACGAAACTCCATAATGG			
Ms4a1-2	GCTTGCTTGAGAAAACGTAA			
Fcgr1				
Fcgr1-1	AGAGTACCATATAGCAAGGG			
Fcgr1-2	TGGGATGCTATAACTAGGCG			
Control	I		1	
Control-1	GCGAGGTATTCGGCTCCGCG			
Control-2	GCTTTCACGGAGGTTCGACG			

110 sgRNA Screen	]
Entpd1-1	GTGGATGAAGTCATCACTGAG
Entpd1-2	GAGCTATCACAGCCAAGATAG
Entpd1-3	GCCAACCTGTACATCTACAAG
Entpd1-4	GCTTGGATGTTGGTATCAGTT
Adora2a-1	GTGTCGATGGCAATAGCCAAG
Adora2a-2	GCTCCACAAAGACCTGCGGCG
Adora2a-3	GGAGAGCCAACCCCTACCAG
Adora2a-4	GAAGCAGTTGATGATGTGCAG
Kdr-1	GTTACCCGCTTAACGGTCCGT
Kdr-2	GATACGTTTGAGAACCTCACG
Kdr-3	GTTGTAAAGAATGGAGACACG
Kdr-4	GTCGGACTTGACTGCCCACTG
lfngr1-1	GTATGTGGAGCATAACCGGAG
lfngr1-2	GGTATTCCCAGCATACGACA
lfngr1-3	GTTCAGGGTGAAATACGAGGA
lfngr1-4	GTATACCAATACGCAAATACC
Tnfrsf1a-1	GAGTTGCAAGACATGTCGGAA
Tnfrsf1a-2	GAGACCTAGCAAGATAACCAG
Tnfrsf1a-3	GATGGGGATACATCCATCAG
Tnfrsf1a-4	GGATCCCGTGCCTGTCAAAG
ll1r1-1	GAGCATACAATTGTAGCCGTG
ll1r1-2	GCAGCAAGACCCCCATATCAG
ll1r1-3	GCGTATGTCCTATACGTTCCG
ll1r1-4	GACTGTGTTAGAGAATGACCC
Socs3-1	GTTGAGTACACAGTCGAAGCG
Socs3-2	GTGAGCGTCAAGACCCAGTCG
Socs3-3	GACTTCGGACGAGGGTTCCGT
Socs3-4	GCGGATAAGAAAGGTGCCCGC
Ptpn2-1	GAAGAAGTTACATCTTAACAC
Ptpn2-2	GAATATGAGAAAGTATCGAA
Ptpn2-3	GCACTCTATGAGGATAGTCAT
Ptpn2-4	GTGCAGTGATCCATTGCAGTG
Rnf128-1	GATAATTACGGCAGCAACCGT
Rnf128-2	GCAACTACACCAAGACTGAA
Rnf128-3	GTCACAATGGTCATCGAAGTA
Rnf128-4	GGGCAACCAGACGATACAGA
Cpt1a-1	GCACATTGTCGTGTACCACAG
Cpt1a-2	GCATACTGCTGTATCGTCGCA
Cpt1a-3	GAGGAATACATCTACCTGCG

Cpt1a-4	GACGTTGGACGAATCGGAACA
Hk2-1	GATTCCCGAGGACATCATGCG
Hk2-2	GGAGATGCGTCACATTGACA
ПКZ-3 Нk2-Л	
Dlat-1	GACTACCGCAACGGACCGCAG
Dlat-2	GCAGGCTCTCAAACCCAACAG
Dlat-3	GCGACAAGGCCACCATAGGTG
Dlat-4	GTTCAGAACCACACCTACCGG
Prkab2-1	GTTCAGACCAGCGGATAACGG
Prkab2-2	GIACAAACICIIIGICCCCG
Prkab2-3 Prkab2-4	
Lag3-1	GATCCTAACTTTCTACGAAG
Lag3-2	GAGAGAAGTCCCCGCGCTGG
Lag3-3	GTCAGCAGCGTACACTGTCAG
Lag3-4	GGGTGCGGGTTGTCTAGGCG
Havcr2-1	GTTACACTCTATCTACACCT
Haver2-2	
Haver2-4	GATCAGTTCTGAGCAACTCGT
Cd28-1	GTCGGCATTCGAGCGAAACTG
Cd28-2	GCTTGTGGTAGATAGCAACG
Cd28-3	GCAAGGGCGTGAACAGCGACG
Cd28-4	GTTCCTACAACCTTCTCGCAA
Tnfrsf9-1	GTGCATACGTACTTCGTCCA
Infrst9-2 Tofrst0_2	GUCAAGTACCTICTCCAGCAT
Thirsi9-3 Thfrsf9-4	GACCAGGCTGACAGTTATCAC
Zap70-1	GAAGCGAGAGAGAATCTCCTCG
Zap70-2	GTCGACAACCCCTACATCGTG
Zap70-3	GGAGATCCCTGTGAGCAATG
Zap70-4	GTCTGGCGCGTACCACTTCAG
Pdcd1-1	GCAATACAGGGATACCCACTA
Pdcd1-2 Pdcd1-3	
Pdcd1-4	GCAGCTTGTCCAACTGGTCGG
Dgkz-1	GACCCAGTGGTGTCTTACGA
Dgkz-2	GATGGAGCCACTGACCGGGT
Dgkz-3	GAGCACATCCGAGTAGTGGTG
Dgkz-4	GCAAGTCTTTGATCTGAGCCA
Tigit-1	GCCIAICAIACGIAICCIGGI
Tigit-2 Tigit-3	GTCTCTGACAATGAATGACA
Tigit-4	GAGCCATGGTTCCTCCAAGCG
Olfr5-1	GTGGGTCATACAAGCTATGAA
Olfr5-2	GACATGACAGGTTGAGTAATG
Olfr5-3	GTACACTACCCAGTACTCATG
Olfr8-1	GTACAAGATTCATTATGAGG
Olfr8-2	GAAGIACAIGGGIGIGIGCAG
BRDN0000737505	GAAAAAGTCCGCGATTACGTC
BRDN0000737693	GAAAACGGCTCGATCGGTGAT
BRDN0000737637	GAAAACGTAATTATACCGAGC
BRDN0000738185	GAAAATTGCACCTTCCCGGCC
BRDN0000737801	GAAACCCCCGCGCGGAGCGTC
BRDN0000737467	GAAACCTAGCGTAGATTCGGC
BRDN0000737848	
BRDN0000737434	GAAACTCCCGTGTCAACCGAT
BRDN0000738254	GAAAGACGTGCATTCAGCGAG
BRDN0000737777	GAACATGTTAAGTCGCGTTAT
BRDN0000737611	GAACCAGCATTTGACCGCGCT
BRDN0000737528	GAACCCCGGCTGTCATCGCCG
BRDN0000738228	
BRDN0000737483	
BRDN0000737872	GAACCTCGTCTCATGTACGAA
BRDN0000737516	GAACGCCCCGGATTTCGTTGA
BRDN0000737844	GAACGGCTGCGCCGCGGCAA
BRDN0000737412	GAACGGGCGCAATACCCTTTT
*BRDN = Broad GPP N	Non-targeting control sgRNAs