

CaRpools Report - CRISPR Screen Analysis

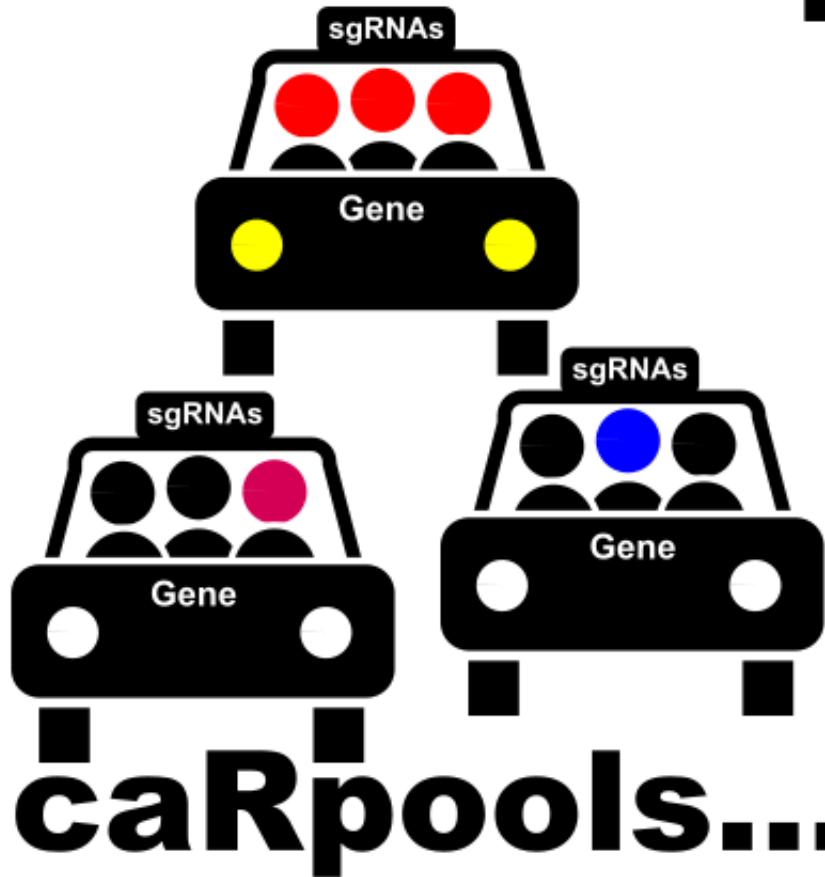
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FADD	51
PASK	55
Depleted	59
CDC42BPG	60
CHEK1	64
CSF1R	68
PRKACB	72
NRG3	76
MAPK7	80
BCL2L12	84
ITPKA	88
SGK2	92
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CRISPR-AnalyzeR for Pooled Screens



Transparent. Reproducible.

caRpools...

Exploratory data analysis of CRISPR/CAS screens

Screen

MIACCS

The MIACCS-file can be found at

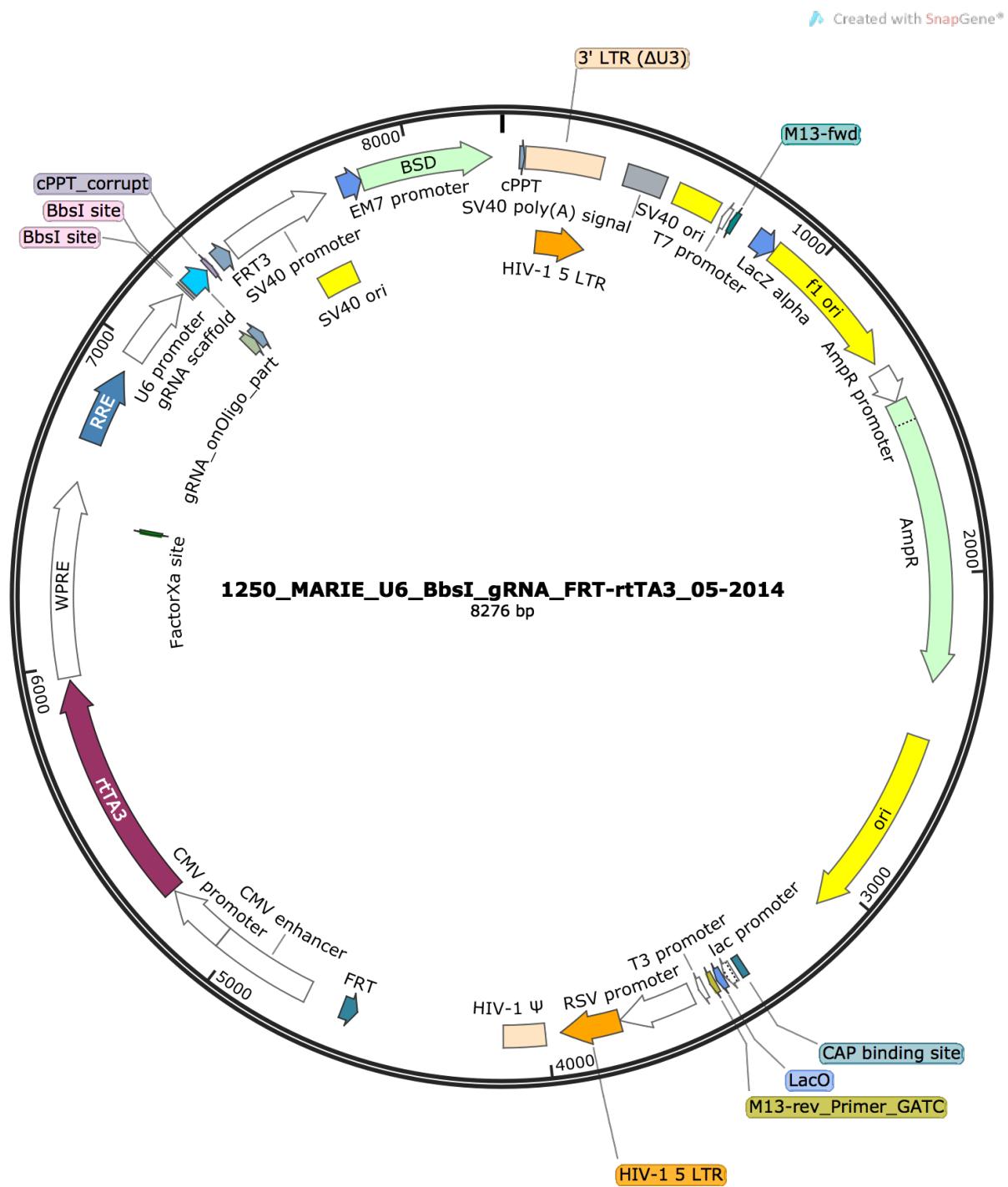
./data/

MIACCS.xls

Description

Apoptosis related genes/Kinome Library in HCT116 Cas9-GFP cells. TRAIL resistance screen.

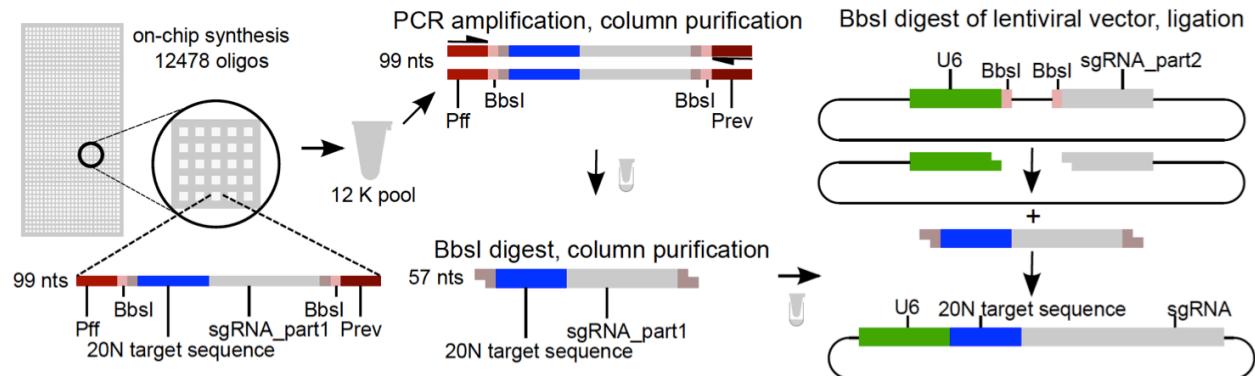
Plasmid Overview



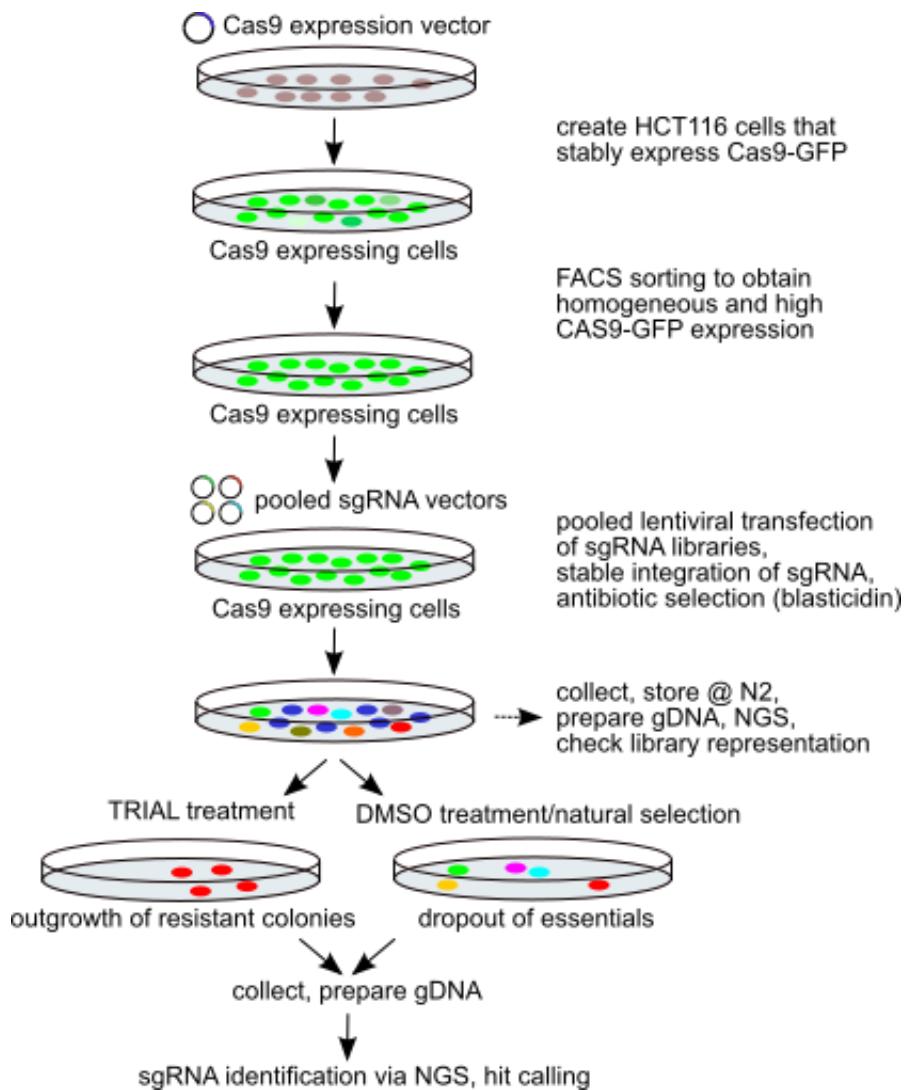
Plasmid Overview



Plasmid Overview



Experimental Setup



Load Data

A brief look into the data passed on to the analysis scripts:

Control #1

2180_CRISPR_KO3_Drug_DMSO1_extracted-designs.txt

	sgRNA	Count
7966	PFKP_107_10029	0
10444	STK31_111_0	109
6950	MYLK_1018_0	50
3544	DTYMK_10_4821	52
7340	NRBP1_14_0	277
5676	LYN_14_18832	39
8445	PKN1_113_33264	243
10245	SQSTM1_105_0	396
9653	ROR1_196_0	67
2067	CDC7_11_3559	29

Control #2

2277_CRISPR_KO3_Drug_DMSO2_extracted-designs.txt

	sgRNA	Count
7966	PFKP_107_10029	0
10444	STK31_111_0	121
6950	MYLK_1018_0	102
3544	DTYMK_10_4821	52
7340	NRBP1_14_0	272
5676	LYN_14_18832	84
8445	PKN1_113_33264	321
10245	SQSTM1_105_0	494
9653	ROR1_196_0	150
2067	CDC7_11_3559	51

TRAIL #1

2176_CRISPR_KO3_Drug_TRAIL1_extracted-designs.txt

	sgRNA	Count
7966	PFKP_107_10029	0
10444	STK31_111_0	139
6950	MYLK_1018_0	101
3544	DTYMK_10_4821	30
7340	NRBP1_14_0	18
5676	LYN_14_18832	44
8445	PKN1_113_33264	258
10245	SQSTM1_105_0	357
9653	ROR1_196_0	52
2067	CDC7_11_3559	74

TRAIL #2

2275_CRISPR_KO3_Drug_TRAIL2_extracted-designs.txt

	sgRNA	Count
7966	PFKP_107_10029	0
10444	STK31_111_0	134
6950	MYLK_1018_0	52
3544	DTYMK_10_4821	67
7340	NRBP1_14_0	75
5676	LYN_14_18832	8
8445	PKN1_113_33264	319
10245	SQSTM1_105_0	1028
9653	ROR1_196_0	40
2067	CDC7_11_3559	38

Stats

All file-based output (e.g. tables) is stored in:
./data.

General

General stats can be found in

TRAILscreen-STATS.xls.

The following read count statistics were calculated for the single datasets.

Readcount	Control #1	Control #2	TRAIL #1	TRAIL #2
Mean	79	108	109	109
Median	51	74	41	39
SD	90	115	244	260
Min	0	0	0	0
Max	1141	1304	6819	8257
# sgRNA not present	934	817	1563	1573

Missing sgRNAs in Datasets

Information of how many sgRNA per gene were not present in the mapped datasets is stored in:

./data/

TRAILscreen_DROPOUT.xls

In brief, the following number of sgRNAs had a *read count of 0* in the dataset:

Control #1: 934 missing sgRNAs

Control #2: 817 missing sgRNAs

TRAIL #1: 1563 missing sgRNAs

TRAIL #2: 1573 missing sgRNAs

All Stats

In depth dataset read count stats can be found in

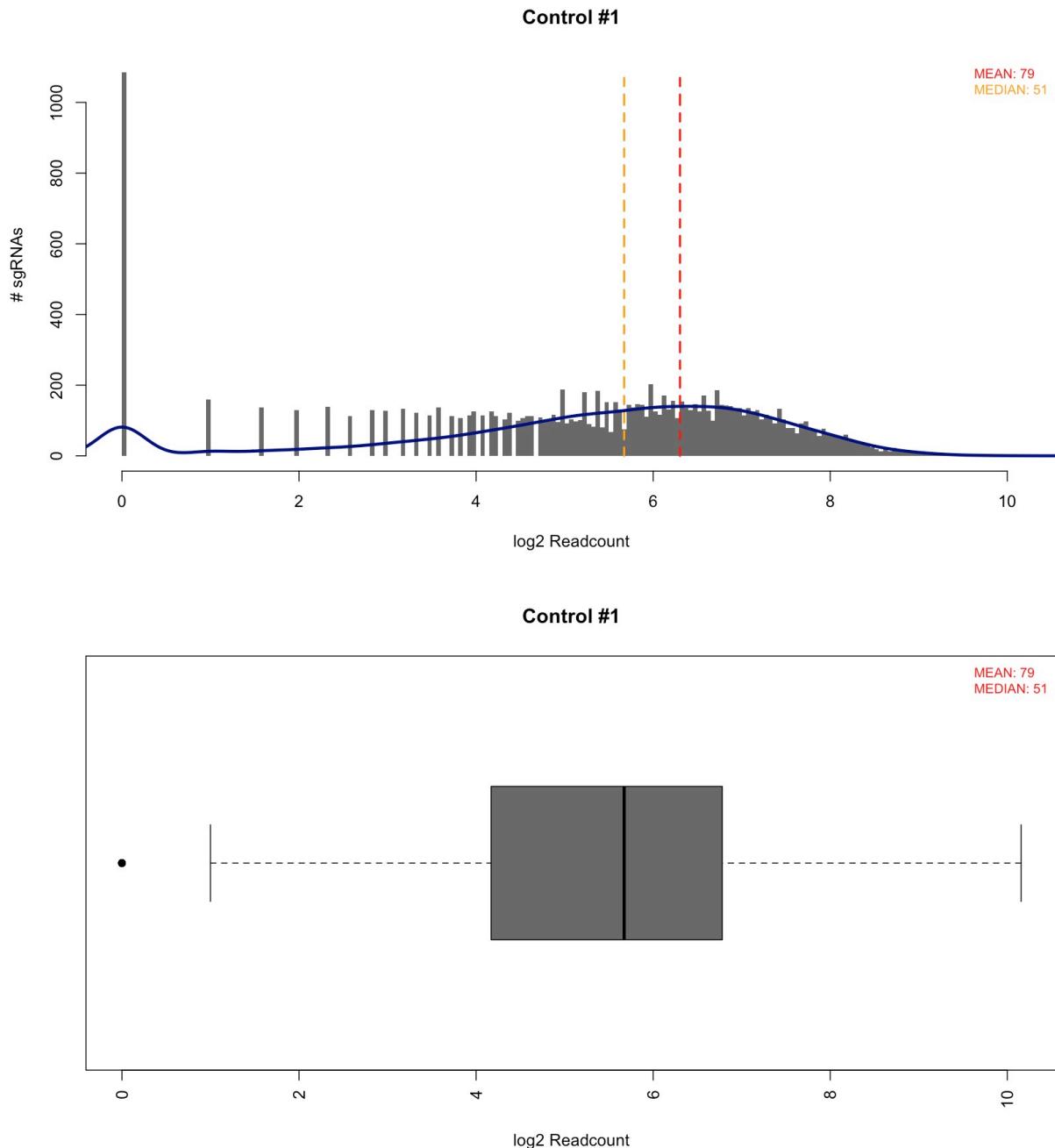
./data/

TRAILscreen-STATS.xls

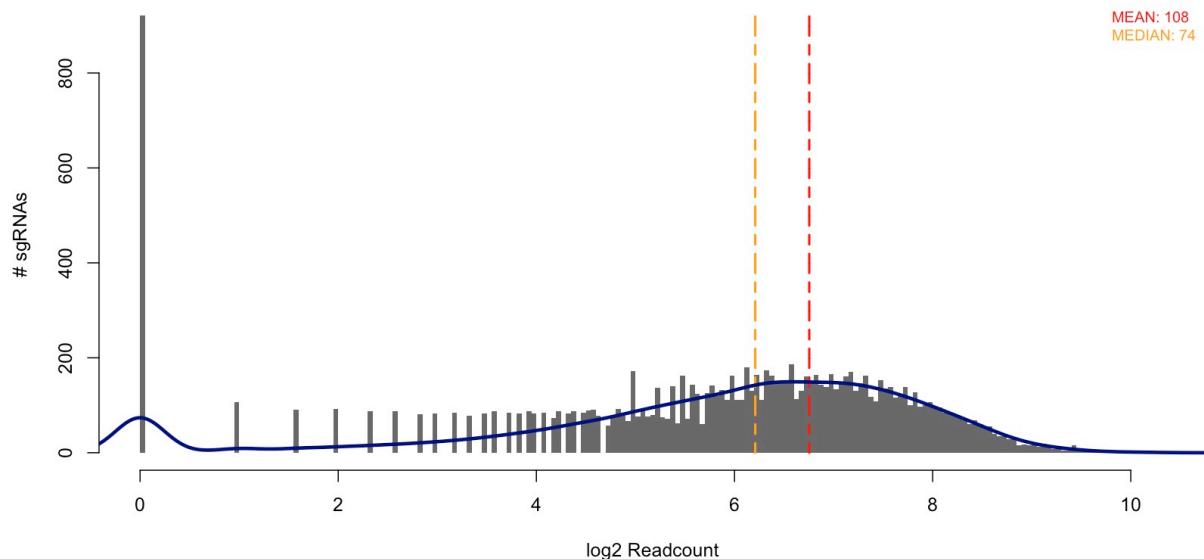
Quality Control

Read Distribution

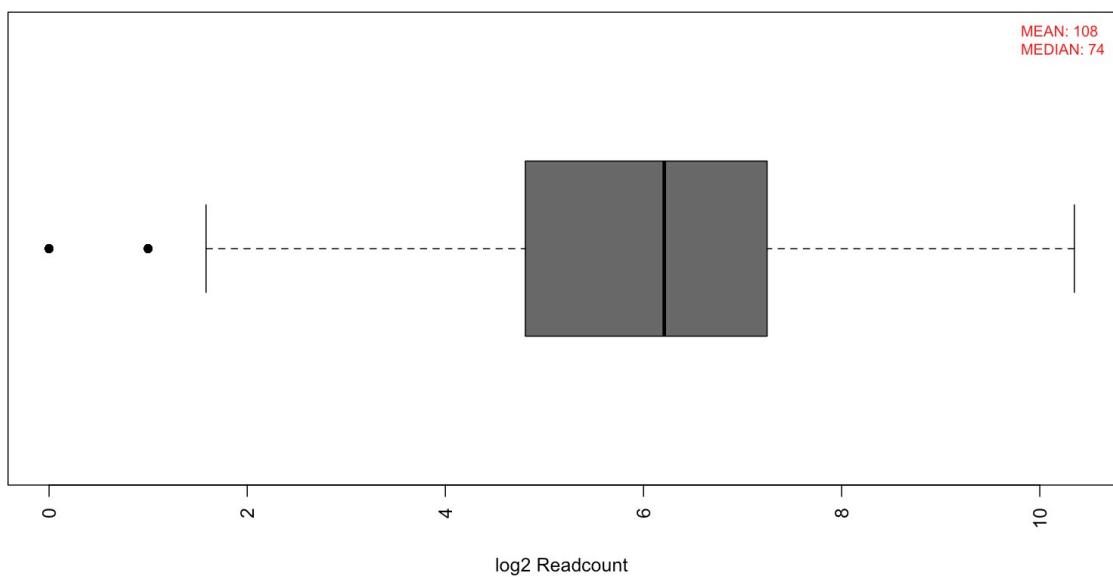
These plots show how the read count of the sgRNAs for each dataset is distributed. Depending on the treatment stringency, e.g. in resistance or dropout screens, the data can show asymmetry. However, the major population should be more or less normally distributed.



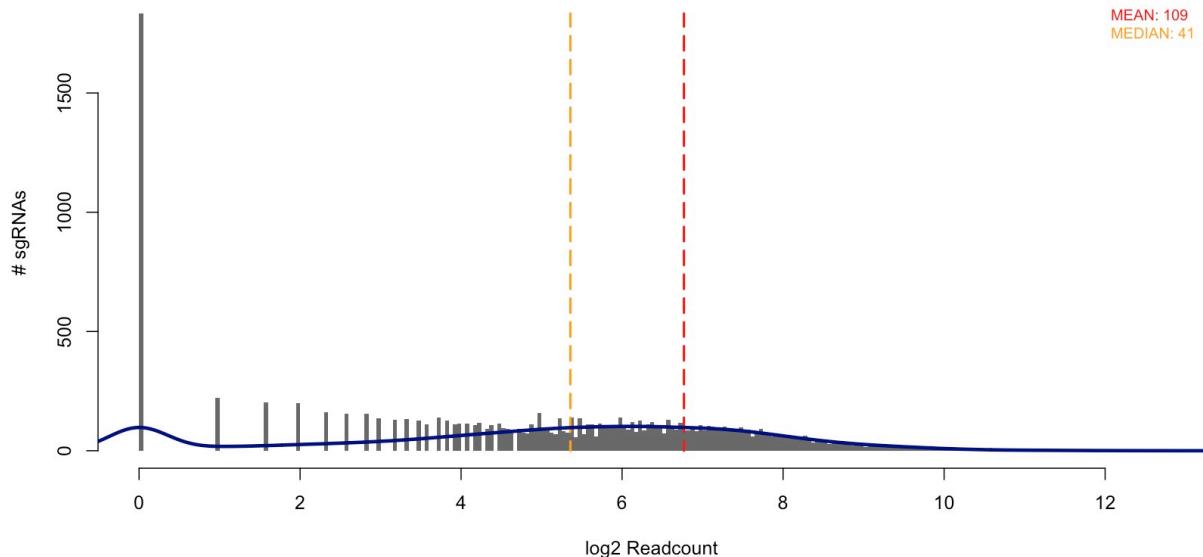
Control #2



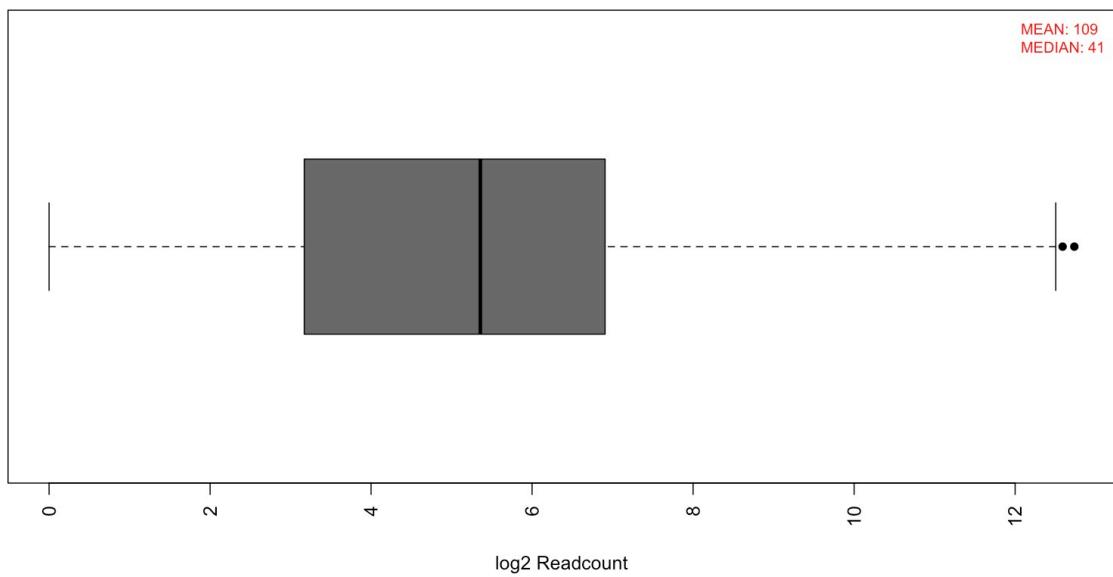
Control #2



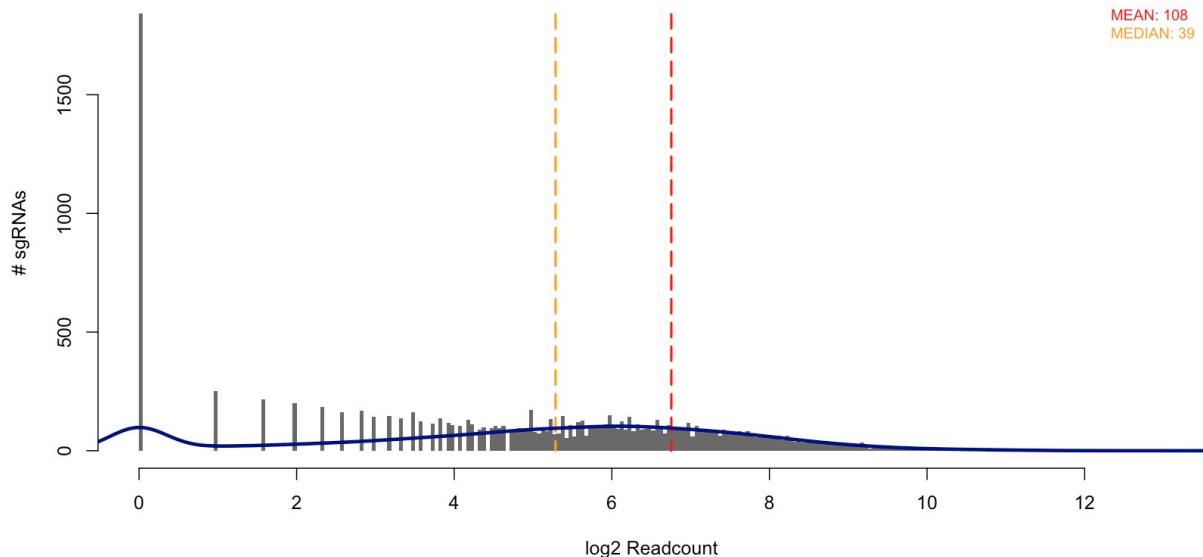
TRAIL #1



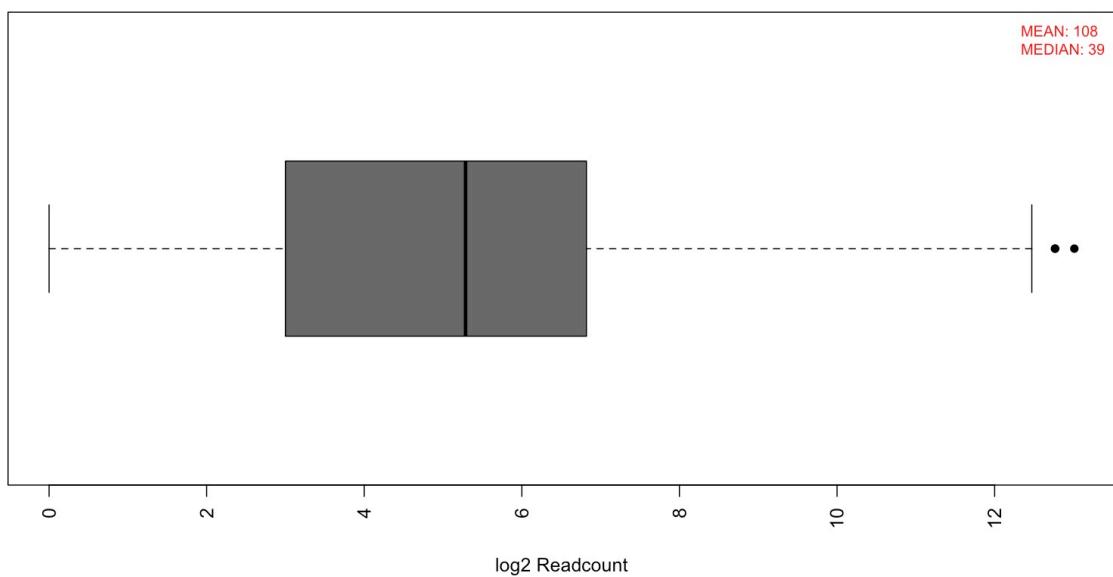
TRAIL #1



TRAIL #2



TRAIL #2

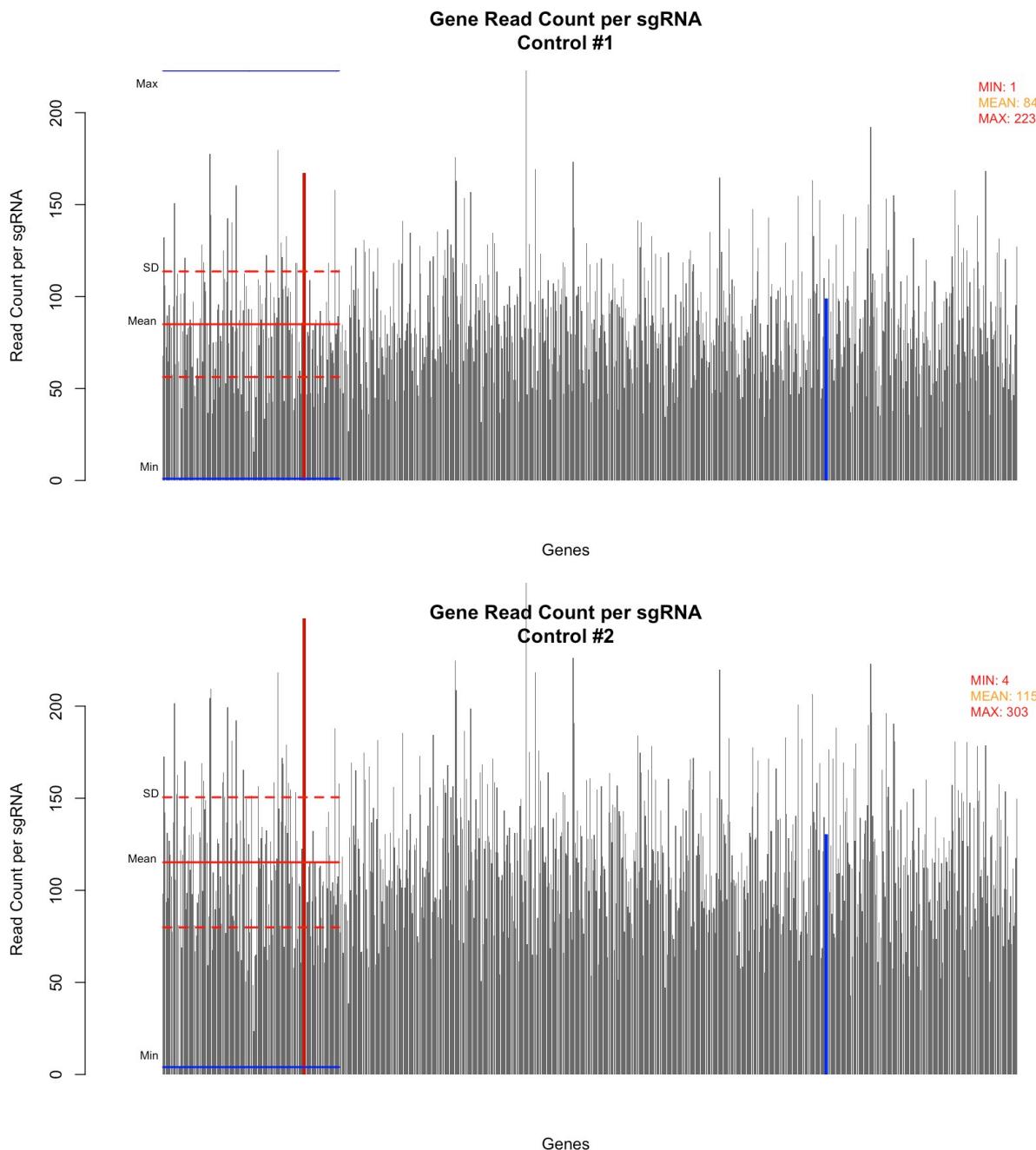


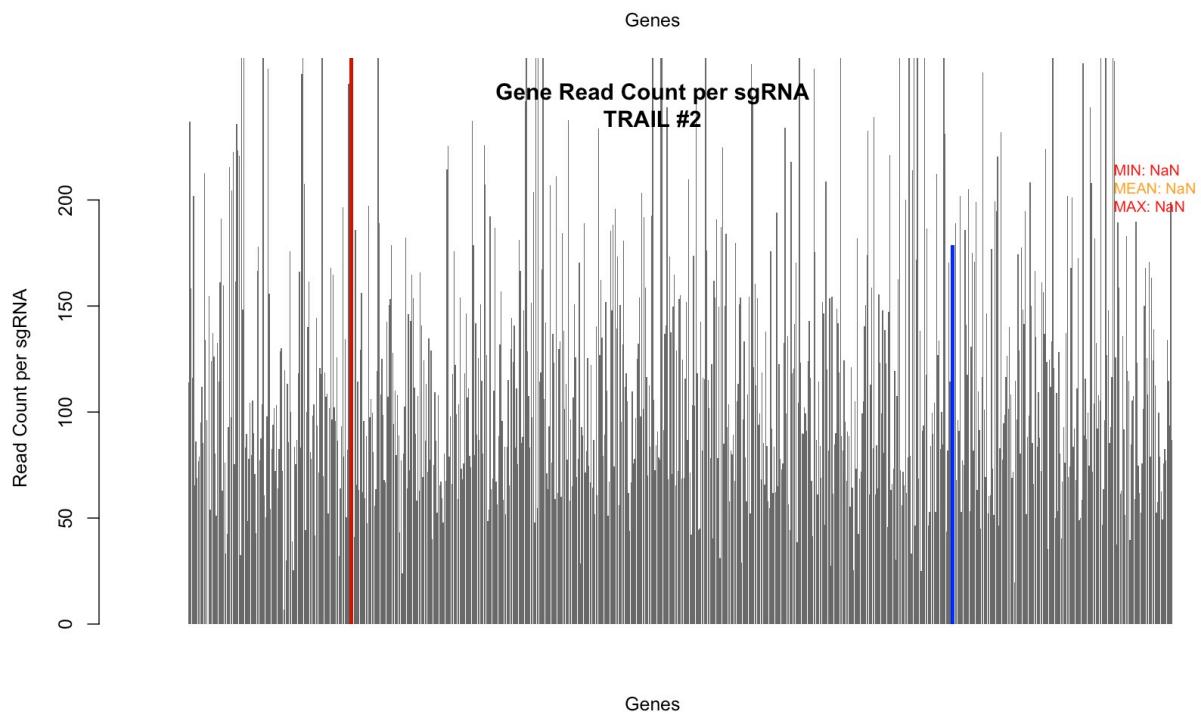
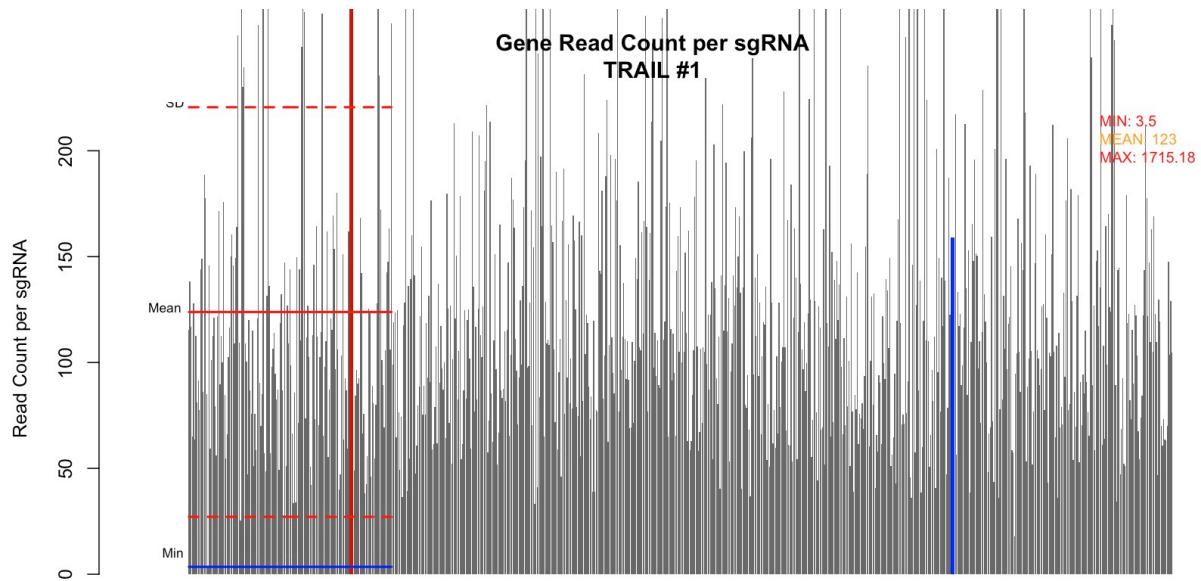
Read Depth

The following plot shows the read count for each gene normalized to the number of sgRNAs. Spikes indicate a higher read count per sgRNA for this particular gene.

One would expect no outstanding spikes within the untreated data samples, however spikes within the treated datasets indicate a read count enrichment for this particular gene.

If a non-targeting control has been set in the MIACCS file, this control is highlighted in **orange** color.

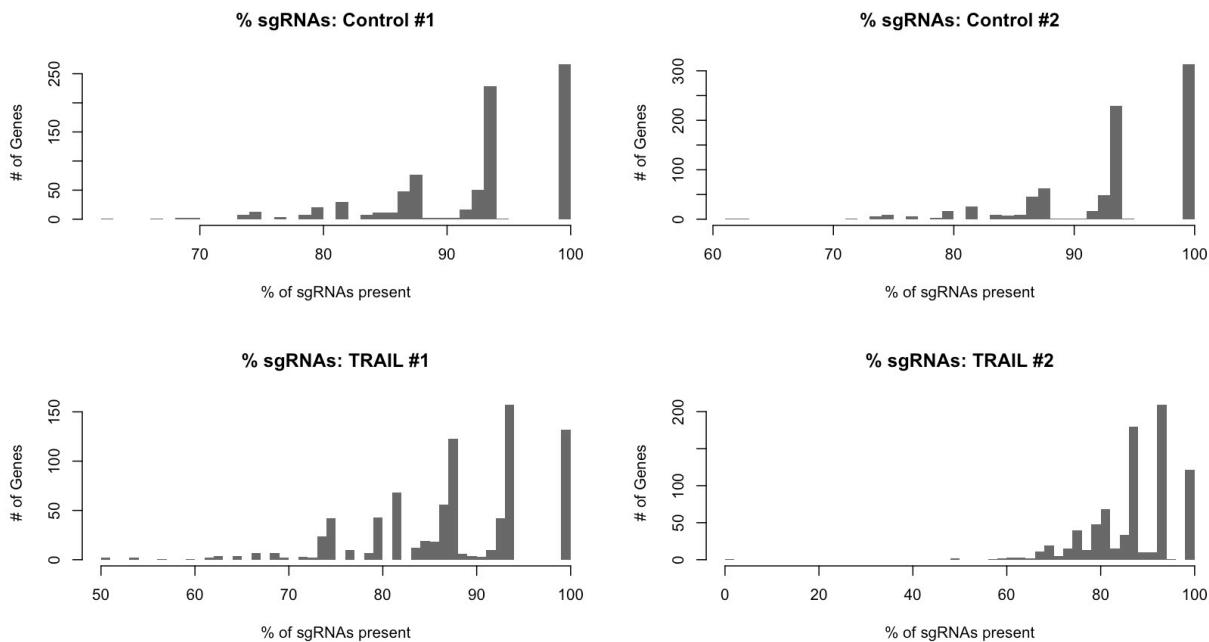




Designs per Gene

These plots provide an overview of the representation of sgRNAs per gene within your data.

Depending on the number of sgRNAs per gene in the library, one would expect a representation of more than 80 % of sgRNAs per gene in the untreated samples. Moreover, genes with a low percentage of present sgRNAs will also show a reduced readcount.



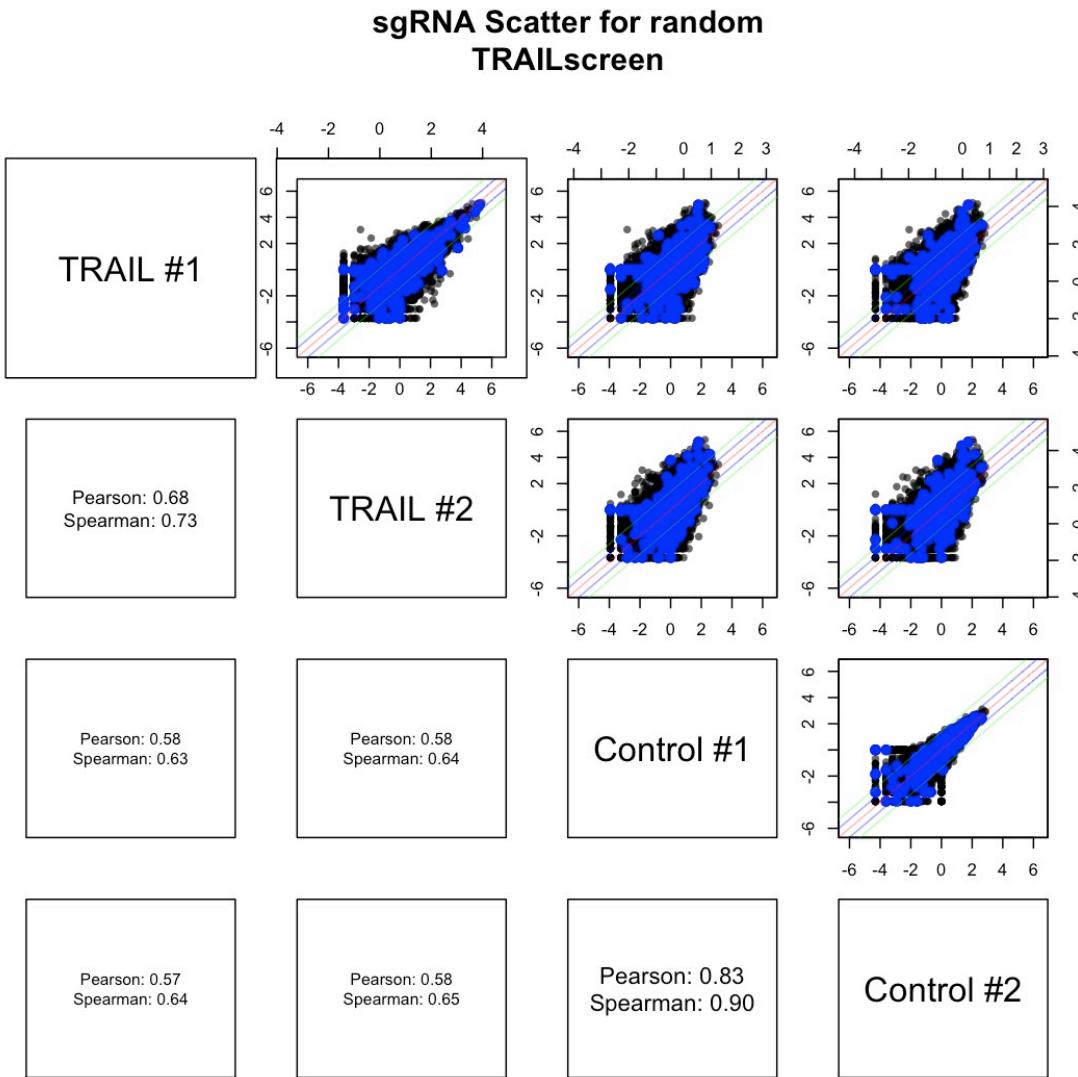
Controls

Non-Targeting

Non-targeting controls are sgRNAs that do either not target the genome at all (so called random or scramble sgRNAs) or target a gene that does not show a phenotype in the screen.

Therefore, the scatter for these, which are highlighted in **blue**, will be distributed within the main cloud of scatter points.

Non-targeting control: random

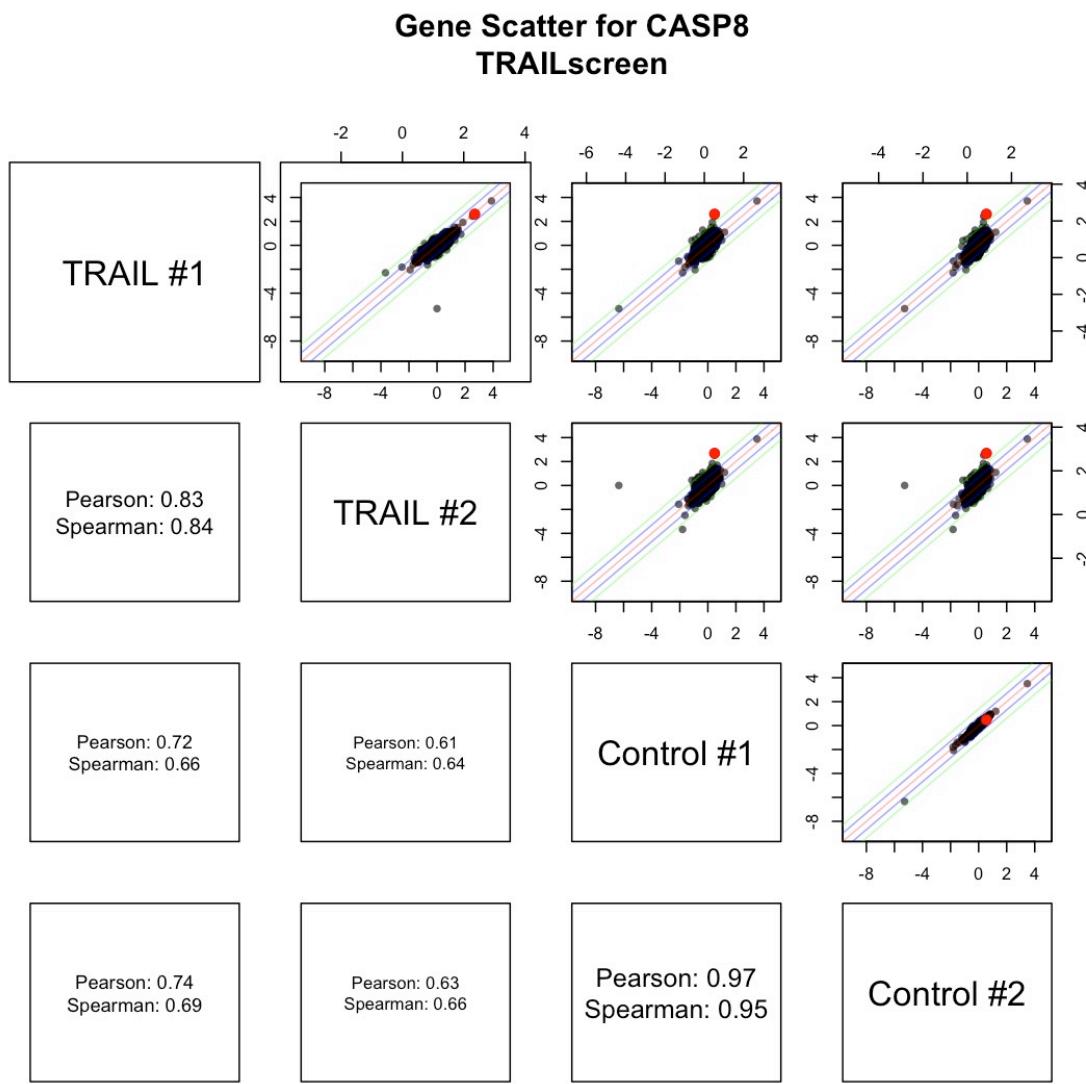


Positive Controls

SgRNAs targeting genes that will show a phenotype in the screening setup can be used as positive controls. These will show either an enrichment (in resistance screens) or a depletion (in dropout screens) in the treatment.

Within the scatter

Positive Control: CASP8



Hit Analysis

Hit analysis is performed using three different methods:

- Wilcox
- DESeq2
- MAGeCK

For each analysis method, separate plots will be created and analysis files will be written to **TRAILscreen_HIT-CALLING.xls**. See below for further information.

The following adjusted p-values are used to determine significance levels:

Method	p-value
Wilcox	0.05
DESeq2	0.001
MAGeCK	0.05

Wilcox

Within this approach, the read counts of all sgRNAs in one dataset are first normalized by the function set in the MIACCS file. By default, normalization is done by read count division with the dataset median.

Then, the fold change of each population of sgRNAs for a gene is tested against the population of either the non-targeting controls or randomly picked sgRNAs, as defined by the random picks option within the MIACCS file, using a two-sided Mann-Whitney test with FDR correction.

DESeq2

For the DESeq2 analysis implementation, the read counts of all sgRNAs for a given gene are first summed up to increase the available read count.

Then, DESeq2 analysis is performed, which includes the estimation of size-factors, the variance stabilization using a parametric fit and a Wald-Test for difference in log2 fold changes between the untreated and treated data.

More information about this can be found in *Love et al.*

[Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2](#)
Genome Biology 2014

MAGeCK

MAGeCK analysis uses a rank-based model to test for a change in abundance of sgRNAs after median normalization of the dataset.

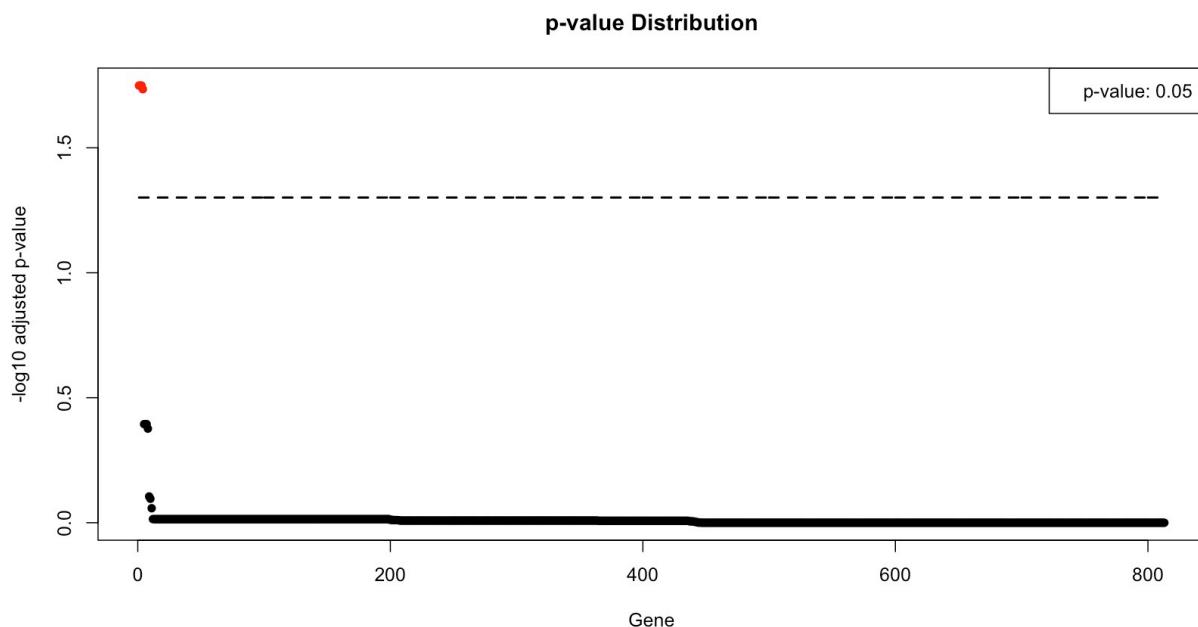
Further information can be found at the [MAGeCK Homepage](#).

Wilcox

All analysis data can be found in the **TRAILscreen_HIT-CALLING.xls** file.

P-Value Distribution

For all genes present in the data, the -log₁₀ corrected p-values are plotted to estimate how well the analysis method performed for this screen. A straight line of points with only small differences in the p-value indicates that the analysis method did not perform well. Genes that resulted in a p-value below the threshold set in the MIACCS file are highlighted in red color.



Enriched

The following genes showed enrichment in the treatment datasets with a **p-value smaller than 0.05**:

	untreated	treated	foldchange	p.value
BAX	3.747567	21.346353	5.542859	0.0178241
CASP8	4.037869	41.292318	7.151636	0.0178241
PASK	2.632026	7.833771	2.575938	0.0178241
FADD	3.765291	35.004169	7.126894	0.0184341

According to the value set, the **top 5 % enriched genes** were:

	untreated	treated	foldchange	p.value
BAX	3.747567	21.346353	5.542859	0.0178241
CASP8	4.037869	41.292318	7.151636	0.0178241
PASK	2.632026	7.833771	2.575938	0.0178241
FADD	3.765291	35.004169	7.126894	0.0184341
FN3K	2.394351	6.545106	2.767443	0.4030853

	untreated	treated	foldchange	p.value
SPA17	2.616958	5.136043	1.866767	0.4030853
CDK5RAP3	2.414025	4.678275	1.865306	0.4202992
TNFRSF11A	2.664088	6.650262	1.597737	0.7848917
IP6K3	2.313419	5.295556	2.520348	0.8019777
ABI1	2.999779	4.458453	1.463144	0.9671744
ADCK1	3.013987	5.668811	1.713397	0.9671744
AKAP6	2.124669	3.065627	1.367359	0.9671744
ALPK2	2.424144	4.293484	1.749312	0.9671744
AMHR2	2.206300	7.288762	2.761481	0.9671744
AURKA	2.668363	3.391432	1.368951	0.9671744
AVPR1B	2.980878	4.610329	1.469106	0.9671744
AXL	3.189164	6.108251	1.481180	0.9671744
BCL2L1	2.403153	4.073267	1.504323	0.9671744
BCL2L11	2.486840	2.879482	1.310120	0.9671744
BCL2L14	1.798592	2.359792	1.252899	0.9671744
BCL6B	2.150004	3.387478	1.557439	0.9671744
BID	1.984433	3.494241	1.451740	0.9671744
BIRC3	1.266241	1.677194	1.297998	0.9671744
BLK	2.414149	4.606897	1.694439	0.9671744
BMP2K	2.725432	7.364192	2.114134	0.9671744
BMPR1A	2.851042	11.049698	3.242482	0.9671744
BMPR1B	2.574995	6.898140	1.993310	0.9671744
BNIP2	1.795370	3.609330	1.824645	0.9671744
BNIP3	2.280309	2.488743	1.032476	0.9671744
CALM3	2.950194	8.018547	2.108928	0.9671744
CAMK1G	3.038230	3.284475	1.063666	0.9671744
CAMK4	3.120206	4.176575	1.298515	0.9671744
CAMKK2	3.096820	5.179529	1.571313	0.9671744
CARD14	2.505785	4.410819	1.693491	0.9671744
CASK	2.442766	3.036390	1.270888	0.9671744
CDC42BPA	1.765662	2.496069	1.478136	0.9671744
CDK1	2.480657	4.789994	1.816161	0.9671744
CDK10	2.357760	2.987199	1.135816	0.9671744
CDK17	2.000075	7.985030	2.652919	0.9671744
CDK8	2.849182	4.568695	1.020590	0.9671744
CINP	1.700964	2.942366	1.646489	0.9671744

Depleted

The following genes showed depletion in the treatment datasets with a **p-value smaller than 0.05**:

No genes showed significant depletion with a p-value lower than 0.05

According to the value set, the **top 5 % depleted genes** were:

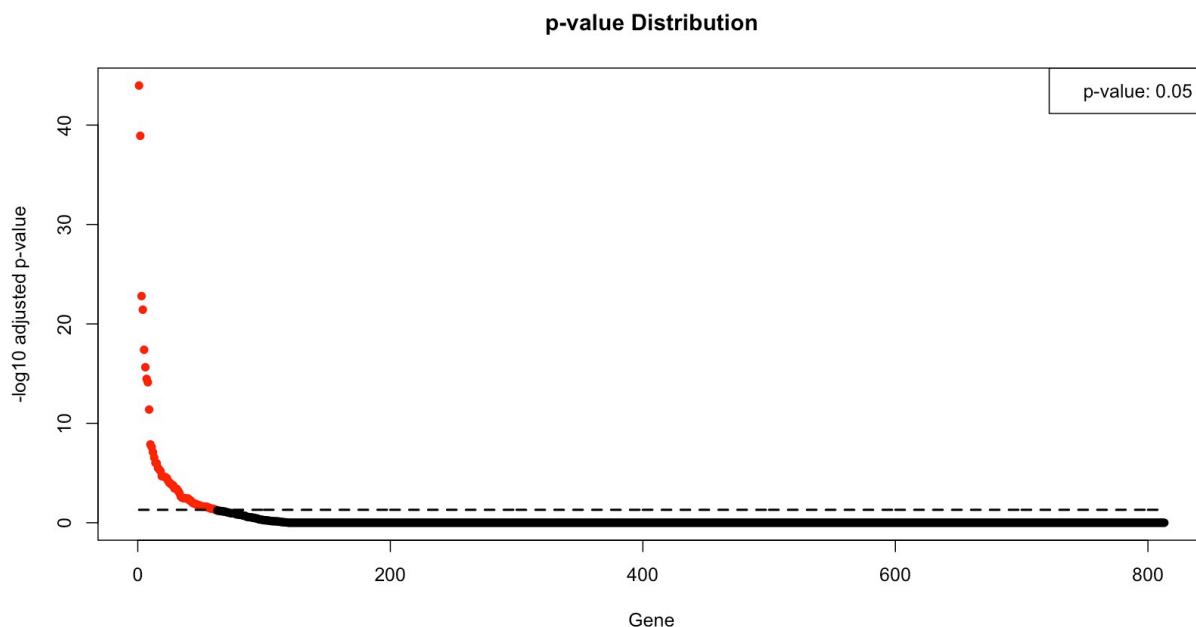
	untreated	treated	foldchange	p.value
MVD	2.437008	2.045153	0.8590363	0.4030853
CDC42BPG	2.457555	2.076689	0.8770324	0.8749233
AK1	2.354821	2.215271	0.9615239	0.9671744
ALPK3	1.759417	1.664550	0.9308875	0.9671744
AZU1	2.965272	2.961382	0.9237615	0.9671744
BBC3	2.429212	2.246981	0.9394726	0.9671744
BCL2L12	3.872529	3.402968	0.9480240	0.9671744
BCL3	2.893494	2.714992	0.9531555	0.9671744
BCL9	1.593733	1.361372	0.8862743	0.9671744
CAMK2G	2.710180	2.687168	0.9540536	0.9671744
CDKN1B	2.097322	1.966672	0.9655601	0.9671744
CHEK1	2.554584	2.300618	0.9370998	0.9671744
CSF1R	3.466243	3.247571	0.9083817	0.9671744
DFFA	2.417806	2.465291	0.9844160	0.9671744
DGCR14	3.287838	3.033271	0.9585501	0.9671744
DUSP2	2.424193	2.163852	0.9824662	0.9671744
DUSP6	2.394930	2.475443	0.9775693	0.9671744
FASTK	2.429278	2.201806	0.9555991	0.9671744
GMFB	2.359733	2.326454	0.9807980	0.9671744
GSK3A	1.900868	1.941428	0.9971515	0.9671744
ITPKA	2.607611	2.165611	0.9336513	0.9671744
MAPK3	2.309495	2.065603	0.9843943	0.9671744
MAPK7	2.961058	2.784324	0.9896817	0.9671744
MPP3	1.740669	1.618087	0.9367596	0.9671744
NEK8	2.423821	2.357821	0.9888161	0.9671744
NRG3	2.387979	2.226621	0.9159026	0.9671744
NTRK1	2.441251	2.275309	0.9450689	0.9671744
PAPSS2	2.400848	2.199667	0.9570816	0.9671744
PDK4	1.965118	1.889239	0.9622144	0.9671744
PFKFB2	1.875278	1.848614	0.9928155	0.9671744
PIK3R3	2.401635	2.197287	0.9221953	0.9671744
PKMYT1	3.075614	3.038899	0.9667207	0.9671744
PRKACB	2.211535	1.700751	0.8653760	0.9671744
PRKCE	2.877672	2.620680	0.9241182	0.9671744
PRKCQ	1.925311	1.762508	0.9351715	0.9671744
PTK6	3.124685	3.441370	0.9576040	0.9671744
RIPK1	3.451535	3.266084	0.9424100	0.9671744
RPS6KC1	2.023408	2.026696	0.9733447	0.9671744
SCYL3	2.114794	1.976152	0.9914523	0.9671744
SGK2	3.128786	2.851614	0.8730285	0.9671744
SHC1	4.391180	3.819887	0.9400818	0.9671744

DESeq2

All analysis data can be found in the **TRAILscreen_HIT-CALLING.xls** file.

P-Value Distribution

For all genes present in the data, the -log₁₀ corrected p-values are plotted to estimate how well the analysis method performed for this screen. A straight line of points with only small differences in the p-value indicates that the analysis method did not perform well. Genes that resulted in a p-value below the threshold set in the MIACCS file are highlighted in red color.



Enriched

The following genes showed enrichment in the treatment datasets with a **p-value smaller than 0.001**:

	log2FoldChange	lfcSE	padj	sgRNA
CASP8	2.8539899	0.1968984	0.0000000	2
FADD	2.7466780	0.2008926	0.0000000	4
BAX	2.0761255	0.1951457	0.0000000	2
RPS6KA5	2.0613922	0.1993450	0.0000000	5
CDK17	1.9749507	0.2098786	0.0000000	6
HRK	1.7832227	0.1986851	0.0000000	0
TP53	1.7263896	0.1990543	0.0000000	3
BMPR1A	1.6606699	0.1934715	0.0000000	2
AMHR2	1.5964273	0.2040561	0.0000000	3
PRKAR1A	1.3066797	0.1966018	0.0000000	2
PASK	1.3056495	0.2018553	0.0000001	2
PRKCH	1.2768183	0.2034549	0.0000003	4
PRKD3	1.2469315	0.2049320	0.0000009	4
PTPRR	1.1714789	0.1988912	0.0000031	2

	log2FoldChange	lfcSE	padj	sgRNA
FN3K	1.2257973	0.2101826	0.0000044	2
BMP2K	1.1356520	0.1969679	0.0000065	2
MDM2	1.1155550	0.2005697	0.0000212	3
PRKCZ	1.1267946	0.2027299	0.0000217	2
PAG1	1.2017977	0.2167288	0.0000233	3
BMPR1B	1.1476671	0.2081757	0.0000279	0
PRKY	1.1629272	0.2119197	0.0000322	1
MYC	1.0493447	0.1952001	0.0000603	4
DUSP4	1.0685262	0.2020427	0.0000972	5
CSNK2A2	1.3577535	0.2578919	0.0001106	2
LMTK3	1.0154113	0.1953558	0.0001587	3
MAP2K7	1.1032489	0.2128120	0.0001706	1
LATS1	1.2426869	0.2460336	0.0003452	1
CALM3	1.0844637	0.2148274	0.0003499	2
IP6K3	0.9775242	0.1947187	0.0004042	2
RIPK2	0.9771641	0.1981684	0.0006398	2

According to the value set, the **top 5 % enriched genes** were:

	log2FoldChange	lfcSE	padj	sgRNA
CASP8	2.8539899	0.1968984	0.0000000	2
FADD	2.7466780	0.2008926	0.0000000	4
BAX	2.0761255	0.1951457	0.0000000	2
RPS6KA5	2.0613922	0.1993450	0.0000000	5
CDK17	1.9749507	0.2098786	0.0000000	6
HRK	1.7832227	0.1986851	0.0000000	0
TP53	1.7263896	0.1990543	0.0000000	3
BMPR1A	1.6606699	0.1934715	0.0000000	2
AMHR2	1.5964273	0.2040561	0.0000000	3
PRKAR1A	1.3066797	0.1966018	0.0000000	2
PASK	1.3056495	0.2018553	0.0000001	2
PRKCH	1.2768183	0.2034549	0.0000003	4
PRKD3	1.2469315	0.2049320	0.0000009	4
PTPRR	1.1714789	0.1988912	0.0000031	2
FN3K	1.2257973	0.2101826	0.0000044	2
BMP2K	1.1356520	0.1969679	0.0000065	2
MDM2	1.1155550	0.2005697	0.0000212	3
PRKCZ	1.1267946	0.2027299	0.0000217	2
PAG1	1.2017977	0.2167288	0.0000233	3
BMPR1B	1.1476671	0.2081757	0.0000279	0
PRKY	1.1629272	0.2119197	0.0000322	1
MYC	1.0493447	0.1952001	0.0000603	4
DUSP4	1.0685262	0.2020427	0.0000972	5
CSNK2A2	1.3577535	0.2578919	0.0001106	2
LMTK3	1.0154113	0.1953558	0.0001587	3
MAP2K7	1.1032489	0.2128120	0.0001706	1
LATS1	1.2426869	0.2460336	0.0003452	1
CALM3	1.0844637	0.2148274	0.0003499	2
IP6K3	0.9775242	0.1947187	0.0004042	2
RIPK2	0.9771641	0.1981684	0.0006398	2
PRPS1	1.0154924	0.2099970	0.0010360	2

	log2FoldChange	lfcSE	padj	sgRNA
MAPK8IP2	0.9554903	0.2044514	0.0023104	2
CSNK2A1	0.9415114	0.2038046	0.0029940	5
PRKAG3	0.9230088	0.2009259	0.0033866	5
NEK11	0.9335366	0.2033509	0.0034314	3
TGFBR1	0.9607698	0.2096900	0.0035763	2
TNFRSF11B	0.9509991	0.2077597	0.0036486	0
MAPK13	0.9602742	0.2100303	0.0037378	3
MBIP	0.9025821	0.2012146	0.0056186	5
SEPHS1	0.8714230	0.1947709	0.0059241	1
TNFRSF11A	1.0021224	0.2284252	0.0088570	1

Depleted

The following genes showed depletion in the treatment datasets with a **p-value smaller than 0.001**:

	log2FoldChange	lfcSE	padj	sgRNA
SMG1	-1.429982	0.2123290	0.0e+00	7
PRKACB	-1.326844	0.2187738	1.1e-06	4

According to the value set, the **top 5 % depleted genes** were:

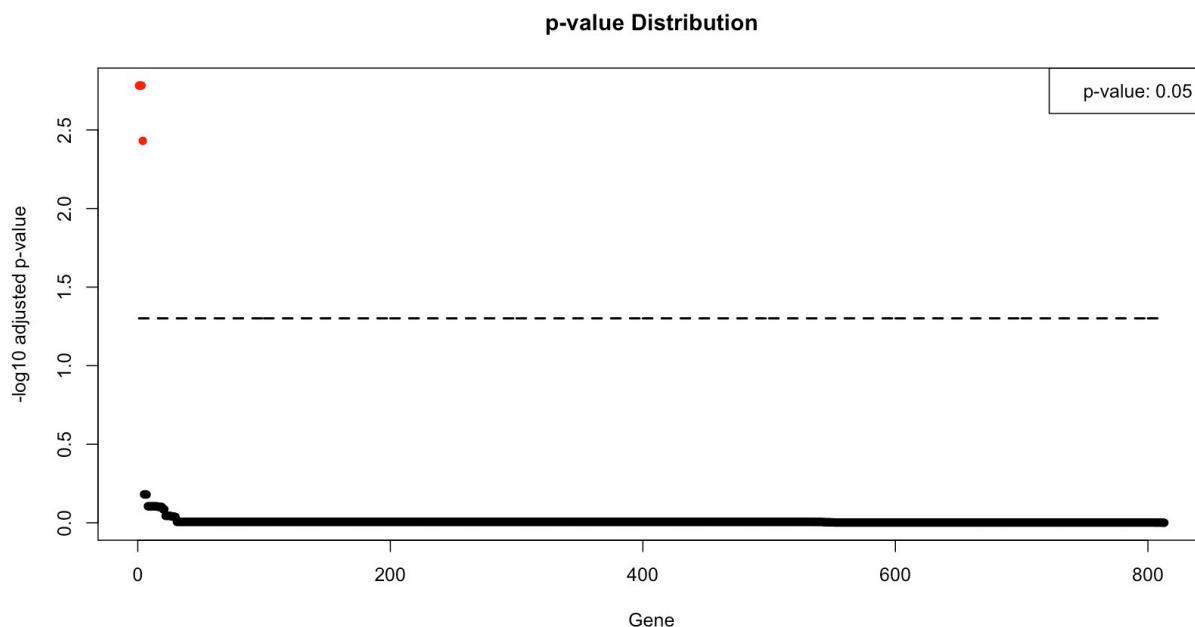
	log2FoldChange	lfcSE	padj	sgRNA
SMG1	-1.4299818	0.2123290	0.0000000	7
PRKACB	-1.3268439	0.2187738	0.0000011	4
DUSP2	-0.8839585	0.2036127	0.0109028	2
MAPK3	-0.8874385	0.2055074	0.0120925	4
MVD	-1.0079883	0.2337749	0.0124369	2
HK3	-0.8896877	0.2091965	0.0161867	2
BCL2L12	-0.8493349	0.2009970	0.0182295	0
ROCK1	-0.8921263	0.2144381	0.0241872	3
WIF1	-0.8396864	0.2018872	0.0242731	3
BBC3	-0.7995261	0.2002468	0.0491891	2
SGK2	-0.7987094	0.2001047	0.0493829	2
PRKCQ	-0.8650269	0.2190015	0.0587241	4
CDC42BPG	-0.9735155	0.2476437	0.0633304	1
NRG3	-0.7790845	0.1998423	0.0723033	3
MPP3	-0.8573709	0.2218129	0.0825529	4
CDKN1B	-0.7810259	0.2039736	0.0954487	2
MAPK7	-0.7443061	0.1956164	0.1051081	1
AK1	-0.7584758	0.1999155	0.1097052	2
CSF1R	-0.7419327	0.1957882	0.1115685	1
ITPKA	-0.9804692	0.2588762	0.1123445	1
CHEK1	-0.8384986	0.2227553	0.1231337	5
FASTK	-0.8297426	0.2226460	0.1427661	1
SHC1	-0.8360697	0.2249526	0.1483839	0
ALPK3	-0.7916102	0.2130996	0.1493037	2
SCYL3	-0.7831114	0.2119499	0.1613076	3
C9orf96	-0.7498465	0.2060267	0.1990927	0
PIK3R3	-0.8057038	0.2266208	0.2741052	3
DGKG	-0.7204221	0.2027228	0.2753605	5
PRKCE	-0.7937112	0.2241867	0.2892502	2
PRKG2	-0.8289301	0.2356366	0.3145684	7
MASTL	-0.7723763	0.2220390	0.3629619	4
BCL3	-0.7351915	0.2172953	0.5119468	1
LCK	-0.6660242	0.1988919	0.5781373	1
NTRK1	-0.7545015	0.2277952	0.6563060	0
NEK8	-0.6734080	0.2042739	0.6928860	3
TLR1	-0.7084222	0.2149545	0.6941480	2
PDK4	-0.7204333	0.2189604	0.7067081	5
TNFRSF4	-0.8135550	0.2473382	0.7082275	1
PIK3CB	-0.7376748	0.2258552	0.7653496	3
DGCR14	-0.7534509	0.2320389	0.8173098	5
PKMYT1	-0.6395897	0.1974689	0.8398297	0

MAGeCK

All analysis data for MAGeCK can be found in the **TRAILscreen_HIT-CALLING.xls** file.

P-Value Distribution

For all genes present in the data, the -log₁₀ corrected p-values are plotted to estimate how well the analysis method performed for this screen. A straight line of points with only small differences in the p-value indicates that the analysis method did not perform well. Genes that resulted in a p-value below the threshold set in the MIACCS file are highlighted in red color.



Enriched

The following genes showed enrichment in the treatment datasets with a p-value smaller than 0.05:

	pos	rank.pos	neg	rank.neg	sgrna.neg.good	sgrna.pos.good
CASP8	0.001650	1	0.994410	804	0	10
BAX	0.001650	2	0.994232	775	1	9
FADD	0.001650	3	0.994410	792	1	9
PASK	0.003713	4	0.994410	800	1	11

According to the value set, the **top 5 % enriched genes** were:

	pos	rank.pos	neg	rank.neg	sgrna.neg.good	sgrna.pos.good
CASP8	0.001650	1	0.994410	804	0	10
BAX	0.001650	2	0.994232	775	1	9
FADD	0.001650	3	0.994410	792	1	9
PASK	0.003713	4	0.994410	800	1	11
TYRO3	0.659241	5	0.981079	109	4	9

	pos	rank.pos	neg	rank.neg	sgrna.neg.good	sgrna.pos.good
AMHR2	0.659241	6	0.994410	796	1	5
FN3K	0.661245	7	0.994232	730	2	11
PRKY	0.785149	8	0.994232	479	4	8
CDK5RAP3	0.785149	9	0.994450	807	1	9
ROR2	0.785149	10	0.994232	734	3	7
BMPR1A	0.785149	11	0.994232	637	3	6
DGKI	0.785149	12	0.994232	609	4	5
IP6K3	0.785149	13	0.994232	678	2	10
SGK1	0.785149	14	0.994232	562	2	6
CSNK1A1	0.785149	15	0.993066	290	6	2
RPS6KA5	0.792340	16	0.994410	802	1	5
FGFR2	0.792340	17	0.994232	435	4	6
FER	0.792340	18	0.994232	707	2	8
GAK	0.792340	19	0.994232	527	2	7
MYC	0.819189	20	0.994232	740	2	8
NME7	0.819189	21	0.994232	359	3	9
MAP3K13	0.903465	22	0.993066	214	6	8
CDK17	0.903465	23	0.994232	533	1	6
UCK1	0.903465	24	0.994410	790	2	8
SPA17	0.903465	25	0.994232	781	2	9
STK32A	0.903465	26	0.994232	596	1	8
MVK	0.912769	27	0.994232	695	2	6
BIRC5	0.912769	28	0.993066	177	5	4
MAP2K7	0.912769	29	0.950888	62	7	7
TNFRSF8	0.919967	30	0.993066	225	4	6
RIPK2	0.987129	31	0.994232	524	3	7
MAP2K3	0.987129	32	0.993066	137	5	7
CDK9	0.987129	33	0.994232	493	3	5
DUSP10	0.987129	34	0.994232	633	1	8
LMTK3	0.987129	35	0.994232	673	2	4
TK2	0.987129	36	0.994232	602	3	9
NLK	0.987129	37	0.994232	663	2	8
PRKD2	0.987129	38	0.994232	444	5	7
PRPS1	0.987129	39	0.993066	247	4	6
SGK223	0.987129	40	0.993066	289	6	5
SRPK2	0.987129	41	0.994232	658	2	5

Depleted

The following genes showed depletion in the treatment datasets with a **p-value smaller than 0.05**:

No genes showed significant depletion with a p-value lower than 0.05

According to the value set, the **top 5 % depleted genes** were:

	pos	rank.pos	neg	rank.neg	sgrna.neg.good	sgrna.pos.good
TNFRSF13C	0.996031	555	0.701894	1	4	1
DYRK2	0.987129	373	0.701894	2	9	4
CDC42BPG	0.996304	803	0.701894	3	9	2
CHEK1	0.996304	777	0.701894	4	6	2
RAPGEF3	0.987129	78	0.701894	5	5	6
TNFRSF11A	0.987129	96	0.701894	6	9	1
CSF1R	0.996304	784	0.701894	7	8	1
PTK6	0.996304	743	0.701894	8	9	3
BMF	0.996304	585	0.701894	9	2	4
TESK2	0.987129	478	0.701894	10	6	4
NUAK2	0.987129	213	0.701894	11	3	5
AURKA	0.987129	219	0.701894	12	7	3
PRKACB	0.996304	769	0.701894	13	7	1
NRG3	0.996304	724	0.701894	14	8	3
TNFRSF13B	0.987129	344	0.701894	15	4	2
AZU1	0.996304	718	0.701894	16	6	3
WIF1	0.996304	799	0.701894	17	7	2
MAPK7	0.996304	678	0.701894	18	8	2
HK3	0.996304	650	0.701894	19	6	4
BCL2L12	0.996304	707	0.701894	20	6	2
TP53BP1	0.987129	395	0.701894	21	2	4
ITPKA	0.996304	795	0.701894	22	8	2
JAK3	0.987129	516	0.701894	23	8	3
CSNK1A1L	0.987129	451	0.736436	24	7	3
PAK7	0.987129	452	0.736436	25	7	5
MAP3K6	0.987129	350	0.790240	26	5	3
CAMK1G	0.996304	600	0.790240	27	6	3
PFKFB1	0.987129	340	0.790240	28	10	5
SGK2	0.996304	786	0.790240	29	6	1
PRKAA1	0.996304	697	0.790240	30	7	3
PKMYT1	0.996304	708	0.790240	31	9	3
TSSK3	0.996304	570	0.790240	32	6	3
NTRK3	0.987129	377	0.790240	33	7	3
FASTK	0.996304	703	0.790240	34	8	4
AK1	0.996304	757	0.790240	35	9	2
CLK3	0.996304	635	0.808760	36	9	3
MAPKAPK5	0.987129	514	0.808760	37	7	4
PTPRG	0.996304	624	0.808760	38	5	4
CDC42SE2	0.987129	517	0.808760	39	8	3
ACVRL1	0.996304	651	0.808760	40	6	4
PAPSS1	0.987129	527	0.808760	41	8	5

Hit Candidate Overview

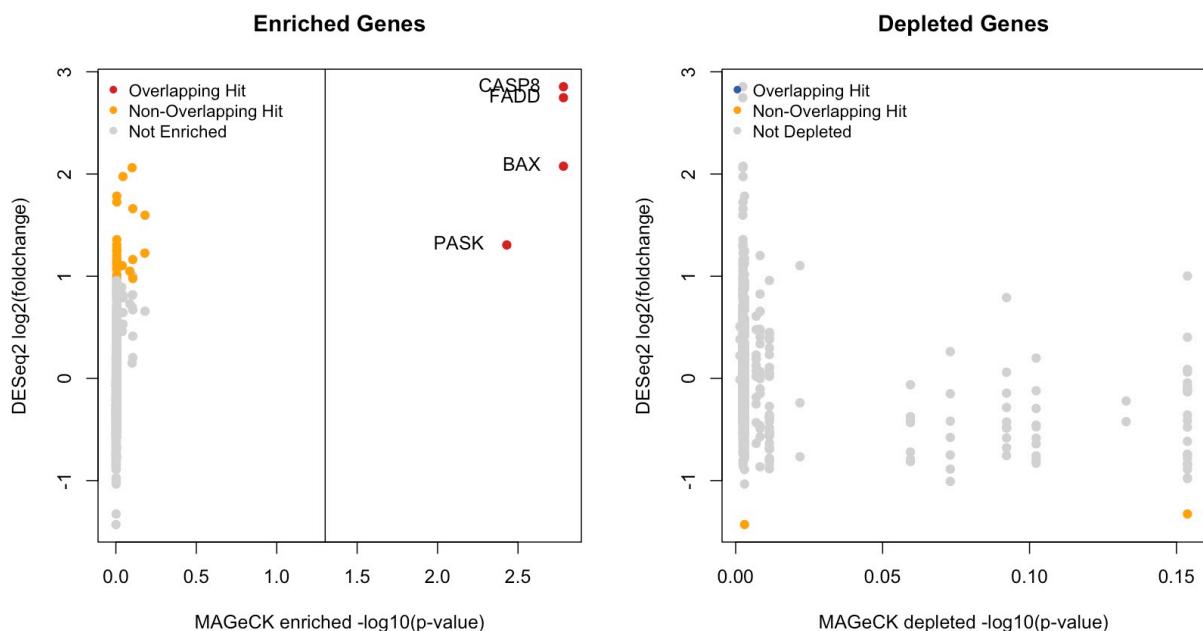
Overview

Genes which showed enrichment or depletion within the individual analysis methods are presented in the following section.

All genes that showed **significant enrichment** within Wilcox, DESeq2 and MAGeCK with the given p-value cutoffs are highlighted in **red** color.

All genes that showed **significant depletion** within Wilcox, DESeq2 and MAGeCK with the given p-value cutoffs are highlighted in **blue** color.

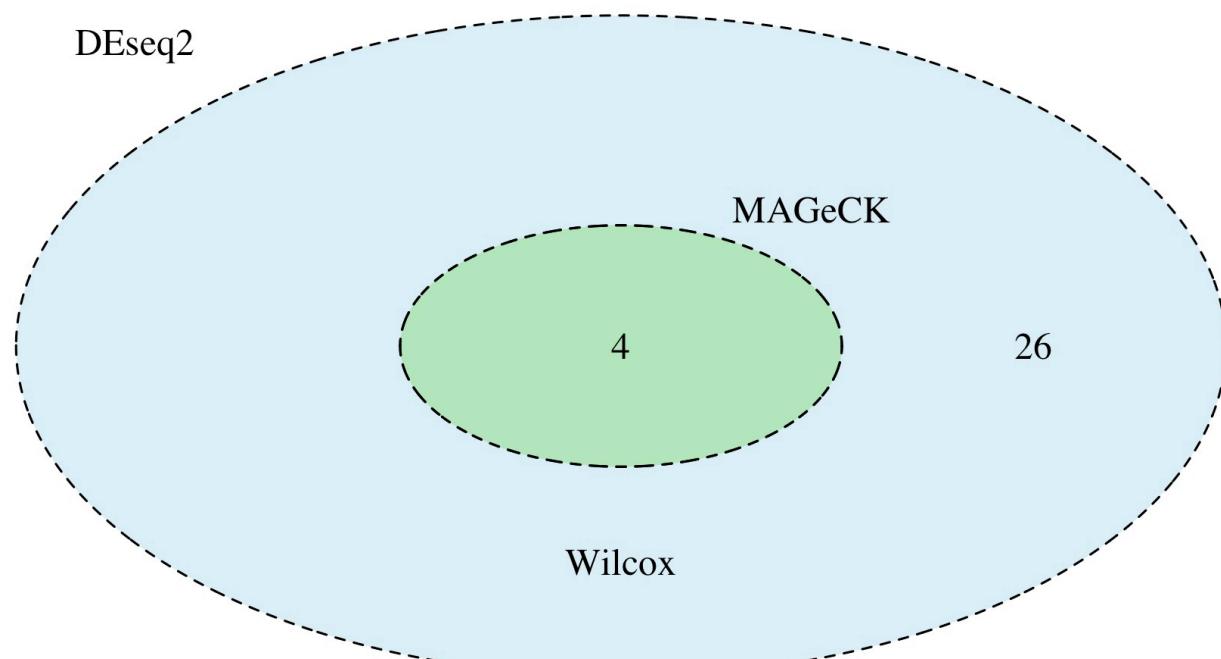
Moreover, all genes that showed up as *significantly* enriched or depleted in any of the analysis methods are highlighted in **orange** color. Genes that showed no significant effect are presented in grey or black color.



Overlaps in Enrichment Analysis

The following genes showed enrichment in all three analysis methods.

Within the **top enriched hits**, the overlap of enriched hits per analysis method is displayed as follows:



Overlaps in Depletion Analysis

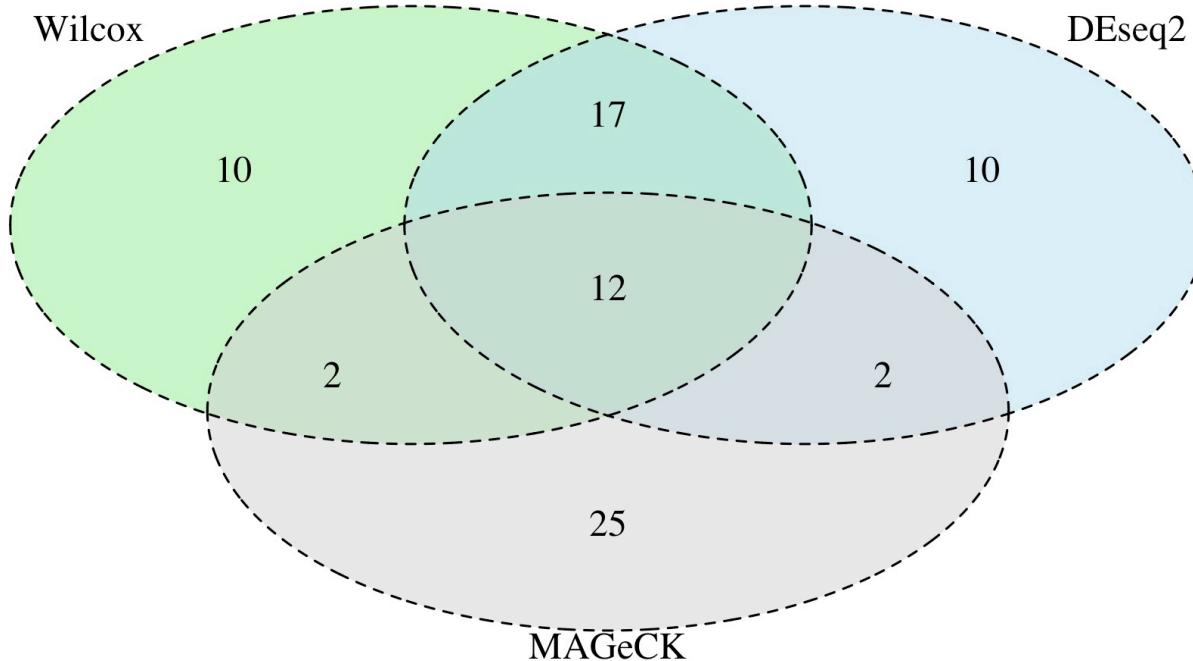
ATTENTION

No overlapping depleted genes were found between all three methods.

Therefore, the overlap from the 5 % of genes within all methods is used for plotting possible hit candidates.

We strongly advise you to have a closer look at the individual outputs of the analysis methods and to carefully look at the following candidate genes.

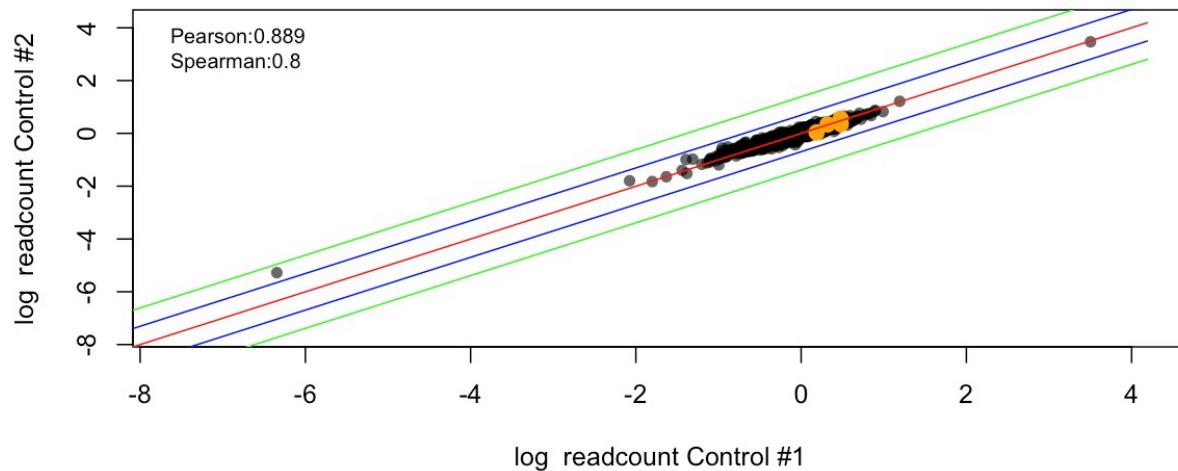
Within the **top depleted hits**, the overlap of depleted hits per analysis method is displayed as follows:



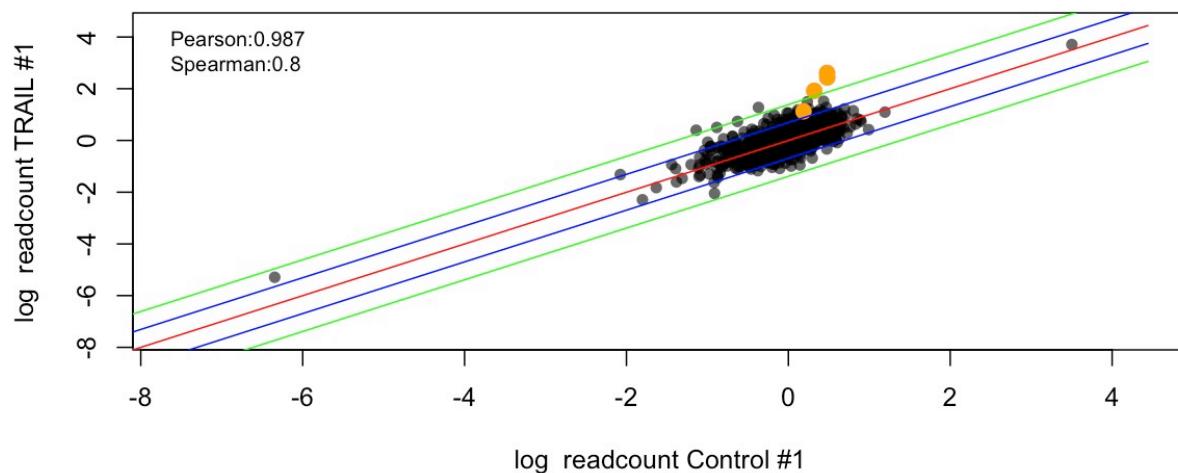
Enriched Overlapping Hit Candidates

All overlapping genes which showed enrichment are highlighted in **orange** color in the following plots.

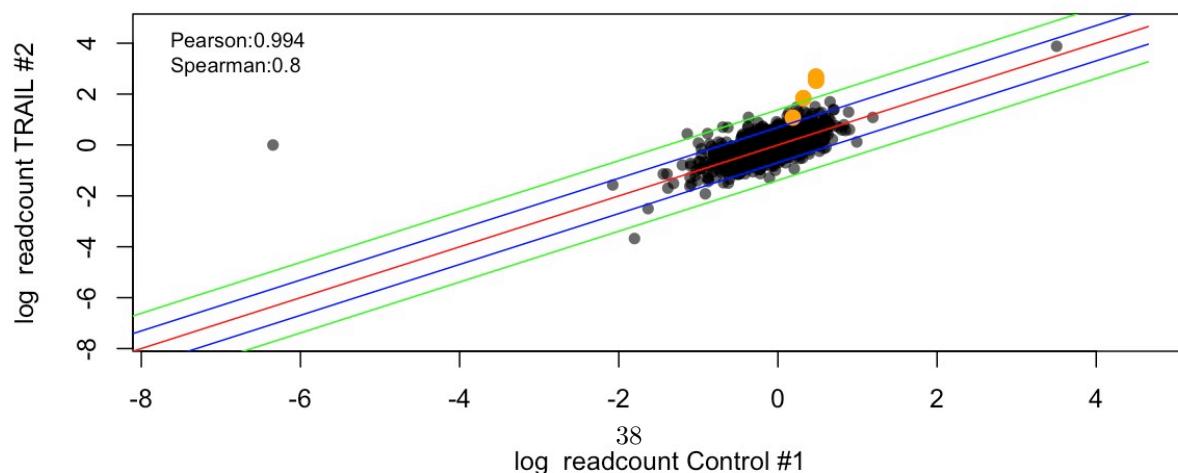
Gene Scatter Scatter for CASP8 BAX FADD PASK TRAILscreen



Gene Scatter Scatter for CASP8 BAX FADD PASK TRAILscreen



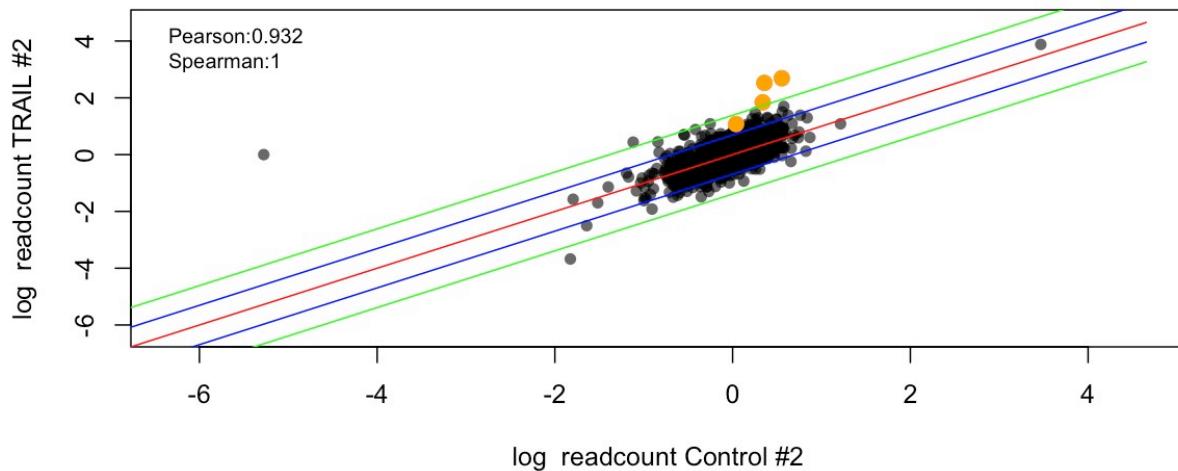
Gene Scatter Scatter for CASP8 BAX FADD PASK TRAILscreen



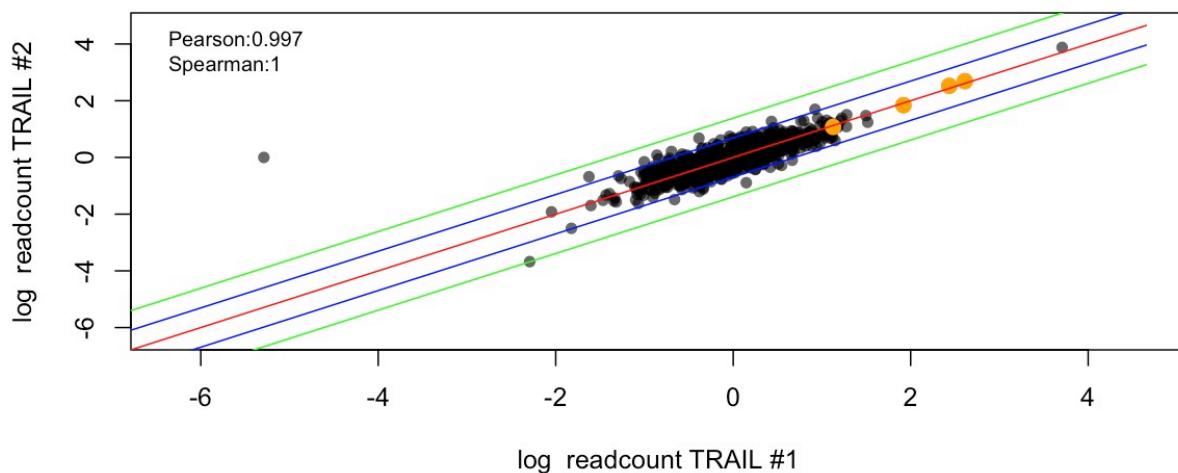
38

Gene Scatter Scatter for CASP8 BAX FADD PASK

Gene Scatter Scatter for CASP8 BAX FADD PASK TRAILscreen



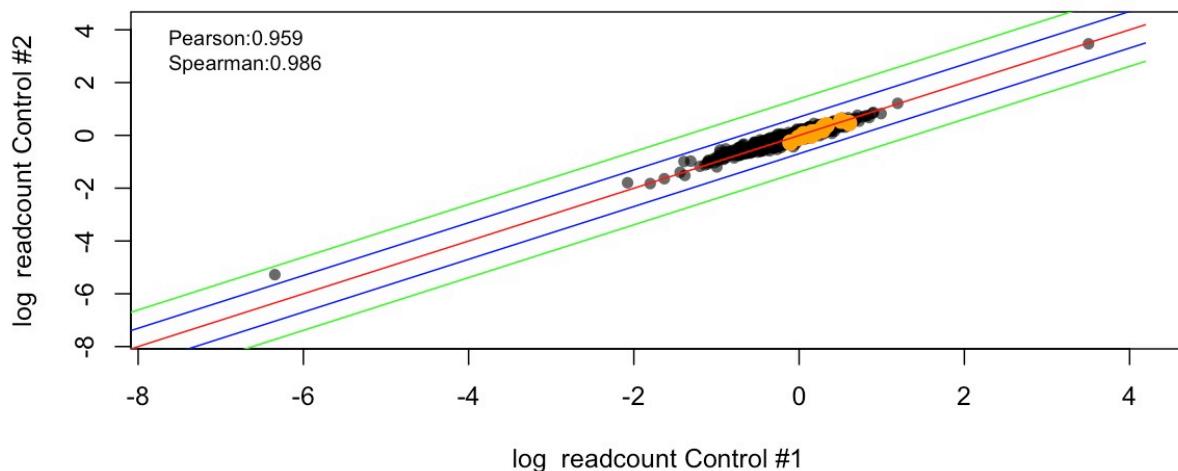
Gene Scatter Scatter for CASP8 BAX FADD PASK TRAILscreen



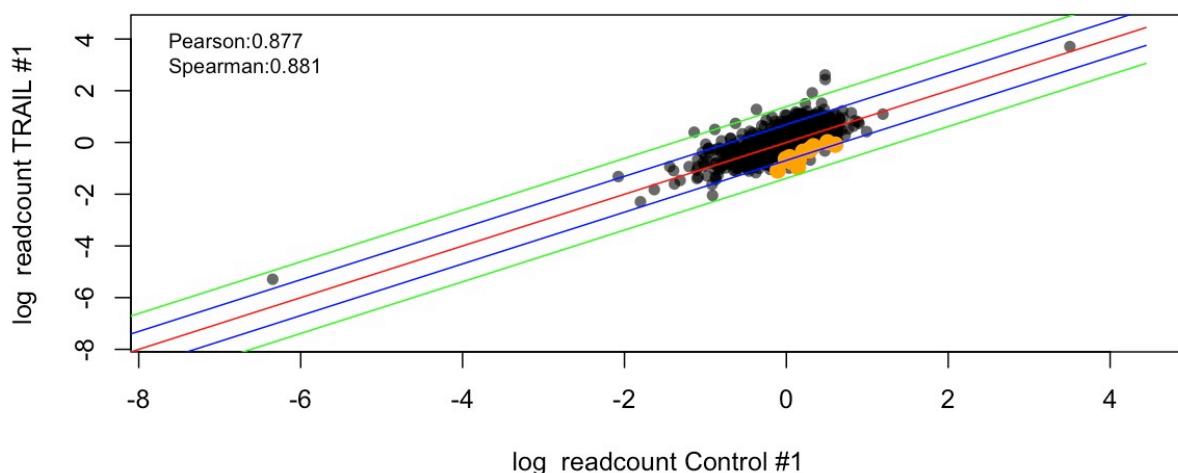
Depleted Overlapping Hit Candidates

All overlapping genes which showed depletion are highlighted in orange color in the following plots.

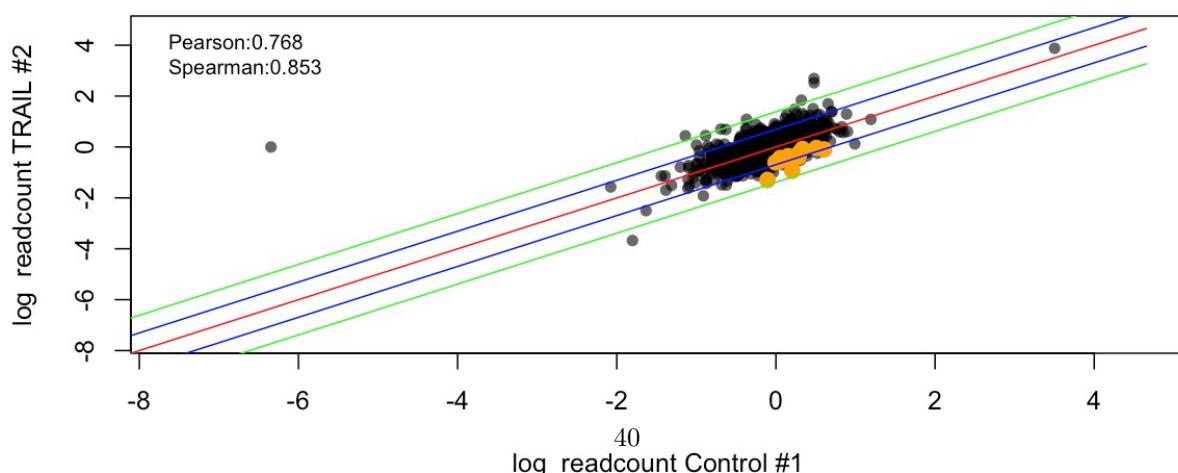
Scatter for CDC42BPG CHEK1 CSF1R PRKACB NRG3 MAPK7 BCL2L12 ITPKA SGK2 P
TRAILscreen



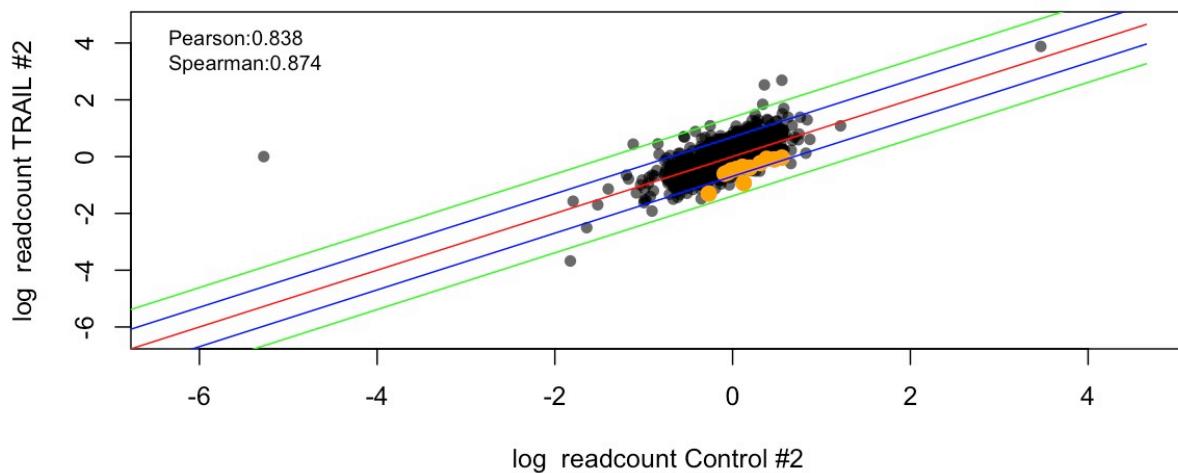
Scatter for CDC42BPG CHEK1 CSF1R PRKACB NRG3 MAPK7 BCL2L12 ITPKA SGK2 P
TRAILscreen



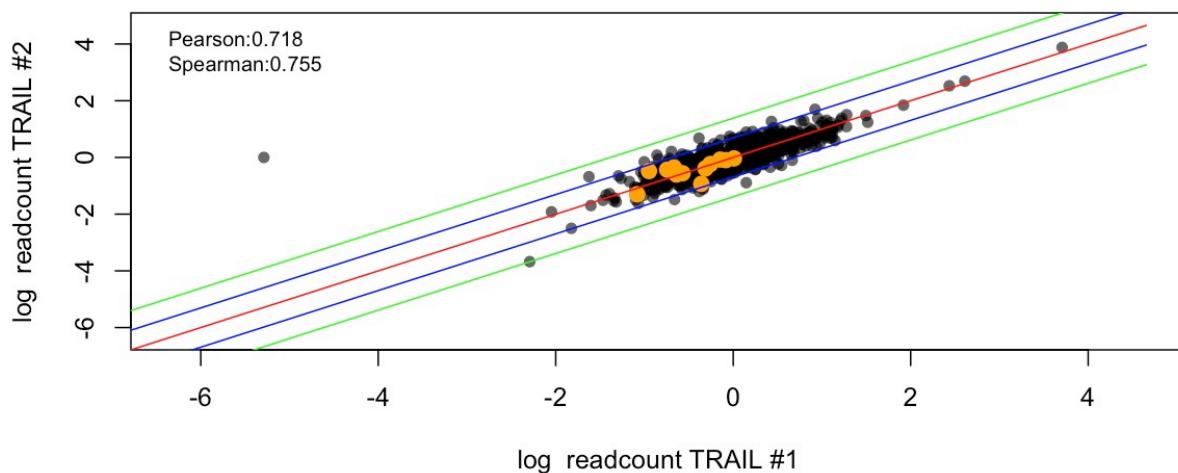
Scatter for CDC42BPG CHEK1 CSF1R PRKACB NRG3 MAPK7 BCL2L12 ITPKA SGK2 P
TRAILscreen



Scatter for CDC42BPG CHEK1 CSF1R PRKACB NRG3 MAPK7 BCL2L12 ITPKA SGK2 P
TRAILscreen



Scatter for CDC42BPG CHEK1 CSF1R PRKACB NRG3 MAPK7 BCL2L12 ITPKA SGK2 P
TRAILscreen



Hit Candidates

Scatterplots representing the gene read count as well as sgRNA read count for all overlapping hits are plotted in this section.

If there were *significantly* enriched or depleted genes that overlapped in all analysis methods, they will be presented here.

Therefore, the top overlapping hits of each Hit Analysis with a p-value below the thresholds for each analysis method are highlighted in orange within the scatter plots for all four samples.

In the case that no *significantly* enriched or depleted genes did overlap in all methods, those that overlapped within the 5 % of top enriched and the top 5 % depleted genes are used.

Therefore, the top overlapping hits of each Hit Analysis are highlighted in orange within the scatter plots for all four samples.

This allows a fast and easy view for single genes and its individual sgRNAs.

Moreover, individual sgRNA effects are plotted as well as the corresponding target sequence.

In this section, the following plots are **generated for each hit candidate**:

- Scatterplot with gene read count within all datasets
- Scatterplot with sgRNA read count within all datasets
- sgRNA log₂ fold changes
- sgRNA log₂ fold change distribution in comparison to all sgRNAs or given controls
- sgRNA target sequence list

The scatter plots show the median normalized, log read count of each genes/sgRNA. Moreover, the **blue lines indicate a read count foldchange of 2**, the **green lines indicate a read count foldchange of 4**.

Enriched

CASP8

In addition to the plots below, the following information has been retrieved via biomaRt:

ENSEMBL ID (links to Ensembl) [LRG_34](#)

HGNC SYMBOL (links to GeneCards) [CASP8](#)

GENE DESCRIPTION

caspase 8, apoptosis-related cysteine peptidase [Source:HGNC Symbol;Acc:HGNC:1509]

GO TERM

MIM GENE DESCRIPTION

CASPASE 8, APOPTOSIS-RELATED CYSTEINE PROTEASE; CASP8;;MORT1-ASSOCIATED CED3 HOMOLOG; MACH;;FADD-HOMOLOGOUS ICE/CED3-LIKE PROTEASE;;FADD-LIKE ICE; FLICE;;MCH5

ENSEMBL PROTEIN ID

LRG_34p2

PROTEIN FAMILY DESCRIPTION

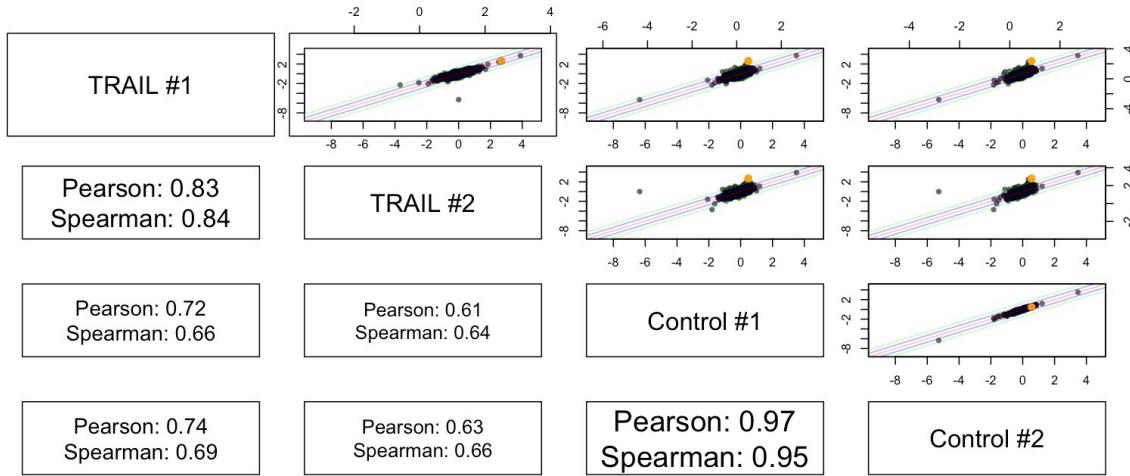
CASPASE PRECURSOR CASP APOPTOTIC PROTEASE MCH ICE APOPTOTIC PROTEASE [CONTAINS CASPASE SUBUNIT CASPASE SUBUNIT

Wilcox p-value: 0.01782408

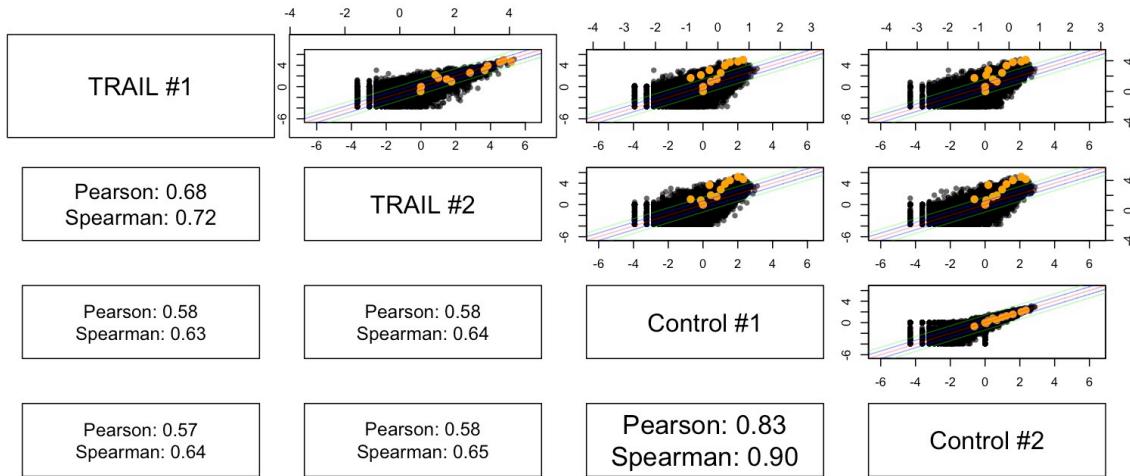
DESeq2 p-value: 1.063499e-44

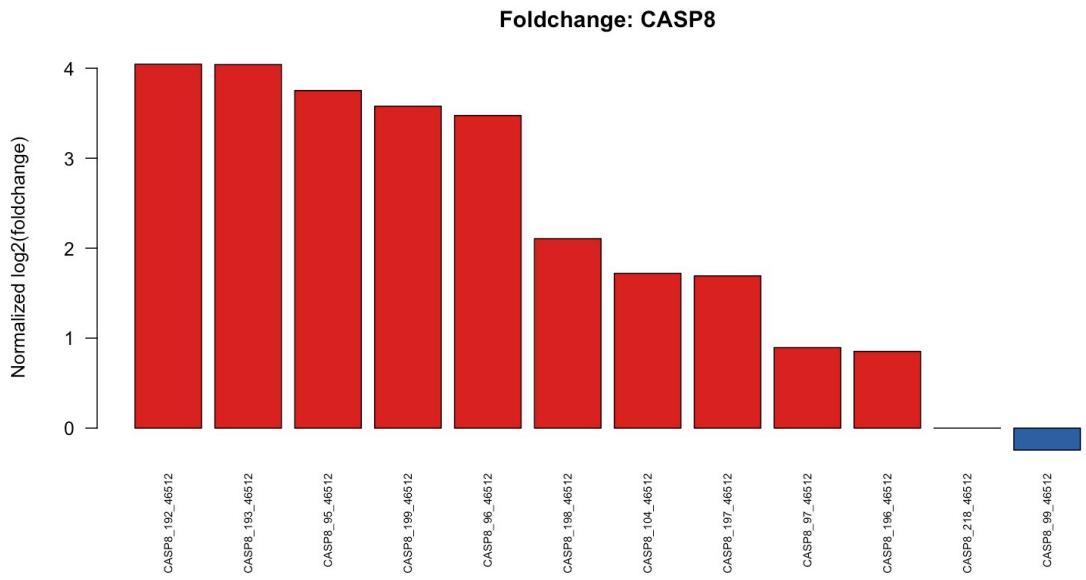
MAGeCK p-value: 0.00165

**Gene Scatter for CASP8
TRAILscreen**

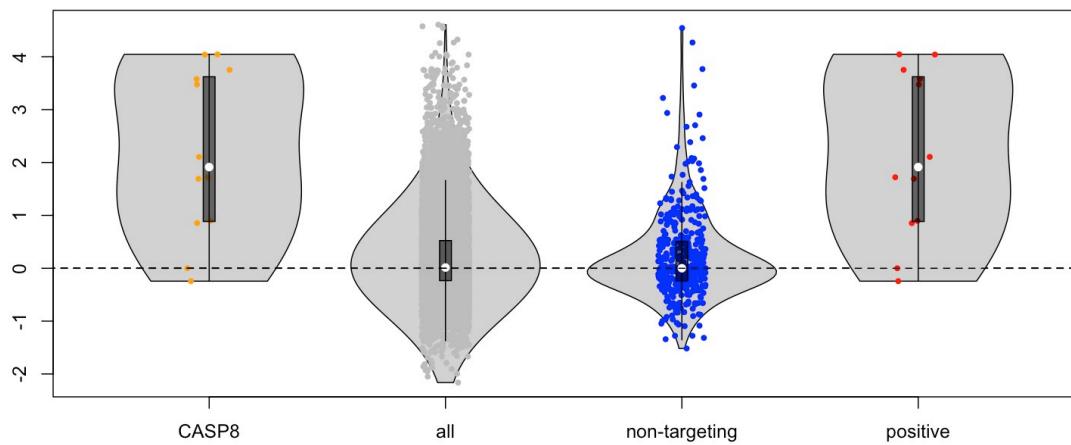


**sgRNA Scatter for CASP8
TRAILscreen**





Log2 Foldchange of sgRNAs for CASP8 compared to sgRNA from all, non-targeting and targeting control



	designs	genes	sequence	log2Foldchange
2	CASP8_192_46512	CASP8	gatgatgcccttgtctccat	4.0442283
3	CASP8_193_46512	CASP8	gagatgtcagctcatagatg	4.0404115
9	CASP8_95_46512	CASP8	ggagacaaggcatcatcta	3.7513973
7	CASP8_199_46512	CASP8	gacatcgctcttcaggctc	3.5778575
10	CASP8_96_46512	CASP8	ggcatcatctatggactga	3.4739444
6	CASP8_198_46512	CASP8	gcaaagtgactggatgtacc	2.1055251
1	CASP8_104_46512	CASP8	gcctgagagagcgatgtcct	1.7201422
5	CASP8_197_46512	CASP8	ggaaacacagtatttacag	1.6918053
11	CASP8_97_46512	CASP8	gagctgacatctcagttcac	0.8950126
4	CASP8_196_46512	CASP8	gcagaaagtgcgcctcatcc	0.8529520
8	CASP8_218_46512	CASP8	gaaggcataaaggcaaggttg	0.0000000
12	CASP8_99_46512	CASP8	ggagcaaccctatttagaaa	-0.2440090

BAX

In addition to the plots below, the following information has been retrieved via biomaRt:

ENSEMBL ID (links to Ensembl) [ENSG00000087088](#)

HGNC SYMBOL (links to GeneCards) [BAX](#)

GENE DESCRIPTION

BCL2-associated X protein [Source:HGNC Symbol;Acc:HGNC:959]

GO TERM

mitochondrial outer membrane

MIM GENE DESCRIPTION

BCL2-ASSOCIATED X PROTEIN; BAX

ENSEMBL PROTEIN ID

ENSP00000375744

PROTEIN FAMILY DESCRIPTION

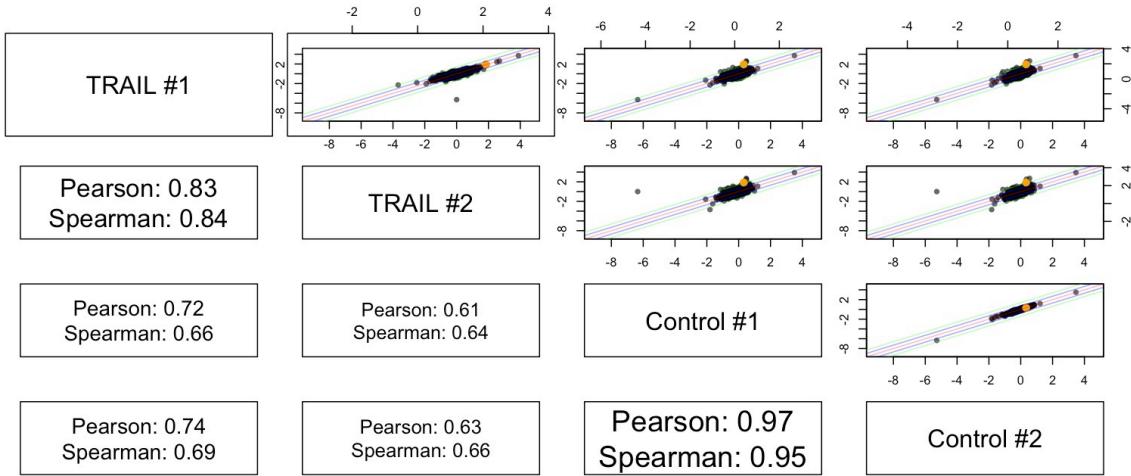
APOPTOSIS REGULATOR BAX

Wilcox p-value: 0.01782408

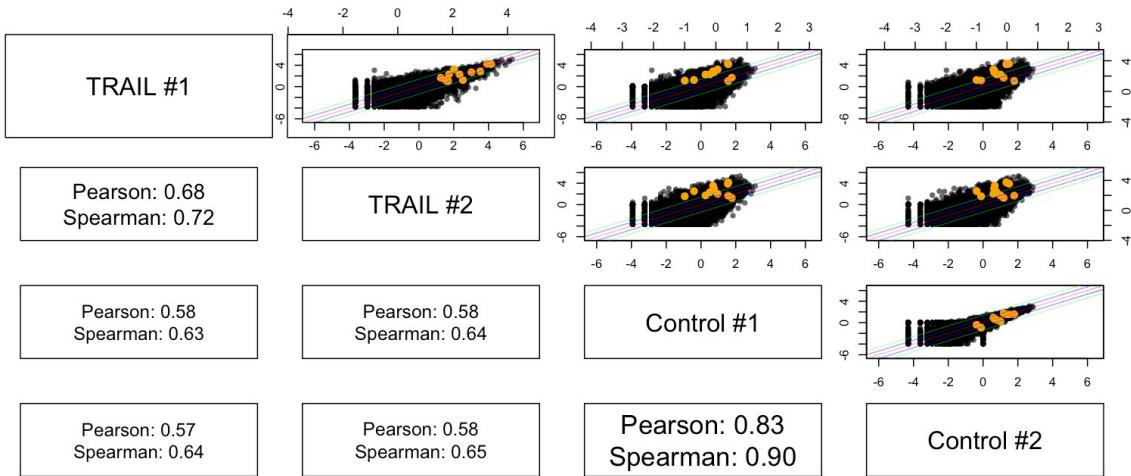
DESeq2 p-value: 1.593957e-23

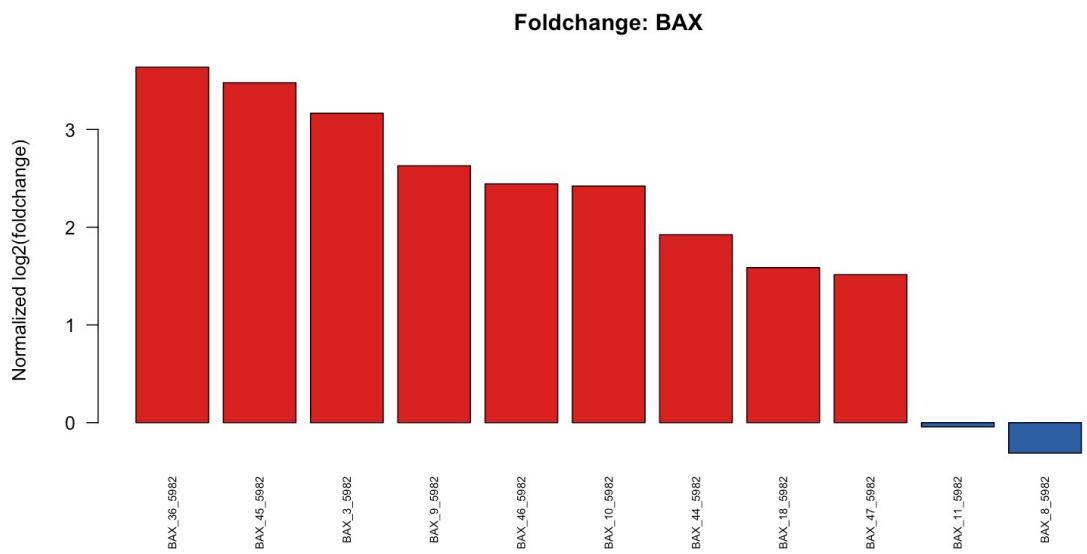
MAGECK p-value: 0.00165

**Gene Scatter for BAX
TRAILscreen**

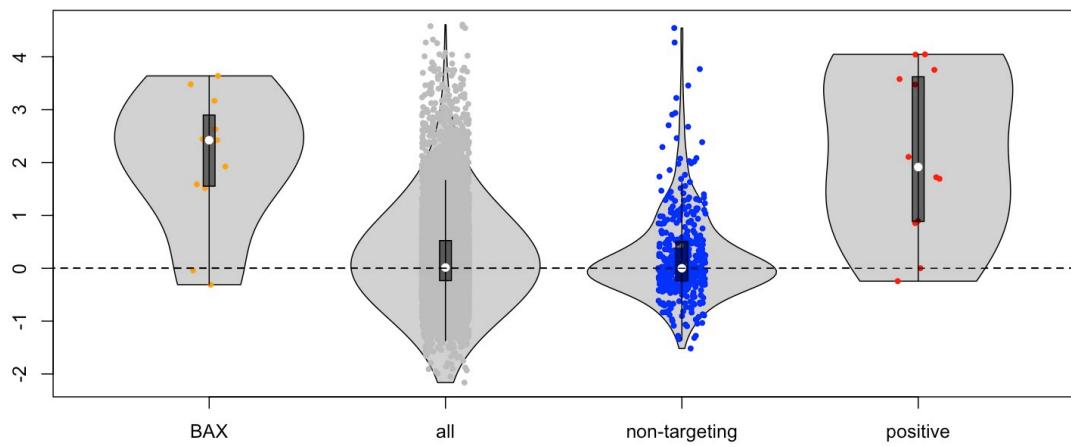


**sgRNA Scatter for BAX
TRAILscreen**





Log2 Foldchange of sgRNAs for BAX compared to sgRNA from all, non-targeting and targeting controls



	designs	genes	sequence	log2Foldchange
4	BAX_36_5982	BAX	gtccaatgtccagccatga	3.6370541
7	BAX_45_5982	BAX	gcgtcccaaagttaggagagg	3.4780185
5	BAX_3_5982	BAX	gaactgatcagaaccatcat	3.1659229
11	BAX_9_5982	BAX	gcagaccgtgaccatcttg	2.6287417
8	BAX_46_5982	BAX	gatggcacggtctgccacg	2.4434385
1	BAX_10_5982	BAX	gaccgtgaccatcttgtgg	2.4213382
6	BAX_44_5982	BAX	gaggaggccgtctggagac	1.9233456
3	BAX_18_5982	BAX	gggggtaataaacctcccttc	1.5871055
9	BAX_47_5982	BAX	gagcaactcccacaaaga	1.5148023
2	BAX_11_5982	BAX	gctgaggccccagctgcct	-0.0430781
10	BAX_8_5982	BAX	gacggcctctctactt	-0.3111825

FADD

In addition to the plots below, the following information has been retrieved via biomaRt:

ENSEMBL ID (links to Ensembl) [LRG_228](#)

HGNC SYMBOL (links to GeneCards) [FADD](#)

GENE DESCRIPTION

Fas (TNFRSF6)-associated via death domain [Source:HGNC Symbol;Acc:HGNC:3573]

GO TERM

MIM GENE DESCRIPTION

FAS-ASSOCIATED VIA DEATH DOMAIN; FADD;;FAS-ASSOCIATING PROTEIN WITH DEATH DOMAIN;;MORT1

ENSEMBL PROTEIN ID

LRG_228p1

PROTEIN FAMILY DESCRIPTION

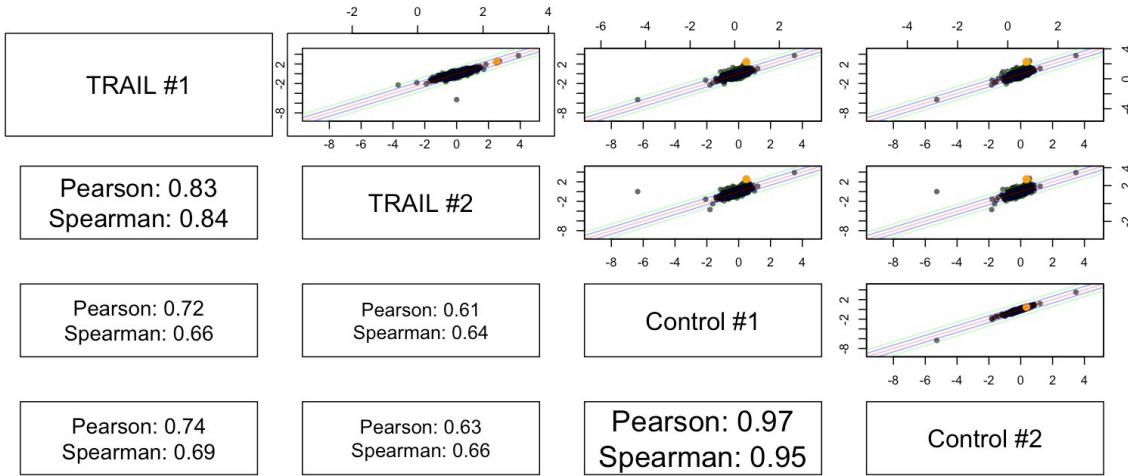
FAS ASSOCIATED DEATH DOMAIN FAS ASSOCIATING DEATH DOMAIN CONTAINING MEDIATOR OF RECEPTOR INDUCED TOXICITY FADD

Wilcox p-value: 0.01843405

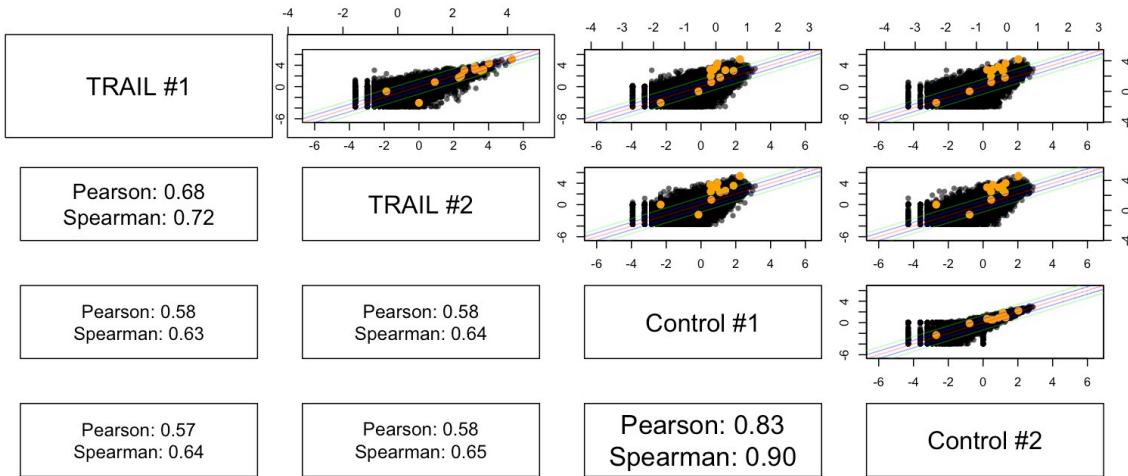
DESeq2 p-value: 1.205659e-39

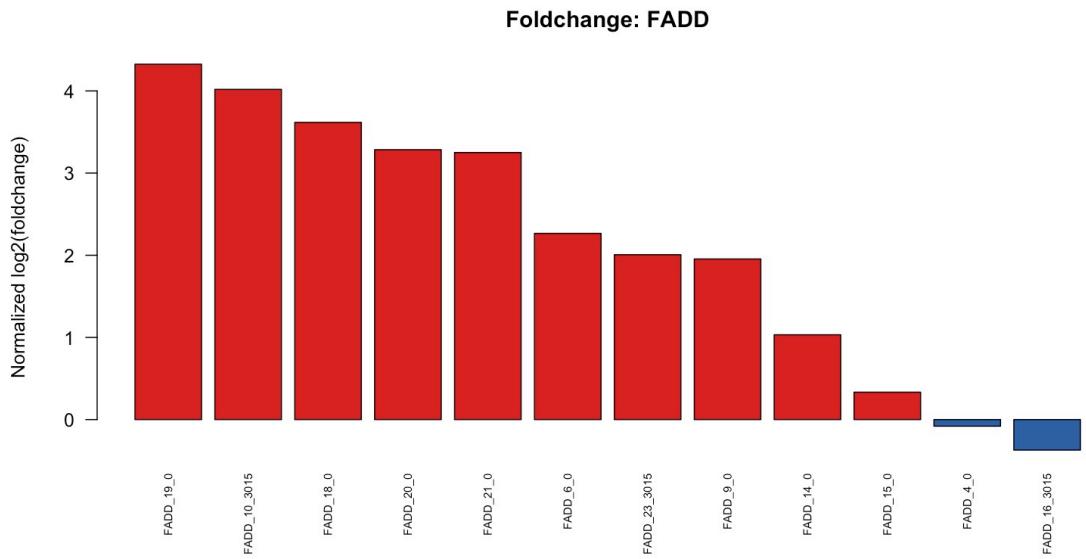
MAGECK p-value: 0.00165

**Gene Scatter for FADD
TRAILscreen**

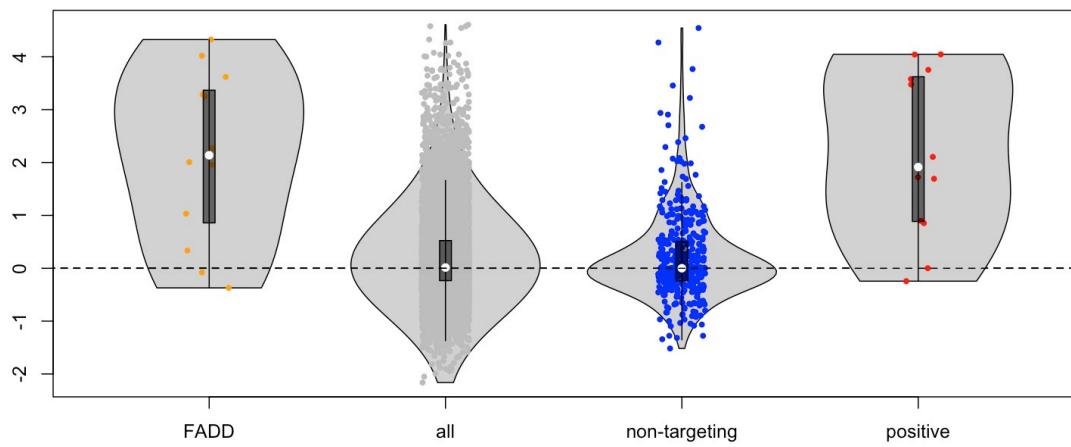


**sgRNA Scatter for FADD
TRAILscreen**





Log2 Foldchange of sgRNAs for FADD compared to sgRNA from all, non-targeting and targeting control



	designs	genes	sequence	log2Foldchange
6	FADD_19_0	FADD	gcagcatggagaagaggct	4.3250217
1	FADD_10_3015	FADD	gcaacctgacagagcgttg	4.0186830
5	FADD_18_0	FADD	gaggcataggaacttgagct	3.6167997
7	FADD_20_0	FADD	gctccagcagcatggagaag	3.2846277
8	FADD_21_0	FADD	gtcggtctgcgtccagcagca	3.2504992
11	FADD_6_0	FADD	gccgcttgcagaccccgcca	2.2663642
9	FADD_23_3015	FADD	gcacacgctgtcaggttgc	2.0061298
12	FADD_9_0	FADD	gtgtgtggaggcagaacgacc	1.9549099
2	FADD_14_0	FADD	gaaacggctggggcttcgt	1.0323283
3	FADD_15_0	FADD	gccgcttgcggccagcggccca	0.3338738
10	FADD_4_0	FADD	ggtgaaatccttggggcgt	-0.0800059
4	FADD_16_3015	FADD	gtcctcgatgtcgatct	-0.3712259

PASK

In addition to the plots below, the following information has been retrieved via biomaRt:

ENSEMBL ID (links to Ensembl) [ENSG00000115687](#)

HGNC SYMBOL (links to GeneCards) [PASK](#)

GENE DESCRIPTION

PAS domain containing serine/threonine kinase [Source:HGNC Symbol;Acc:HGNC:17270]

GO TERM

MIM GENE DESCRIPTION

PAS DOMAIN-CONTAINING SERINE/THREONINE KINASE; PASK;;PAS KINASE;;PASKIN;;KIAA0135

ENSEMBL PROTEIN ID

ENSP00000486149

PROTEIN FAMILY DESCRIPTION

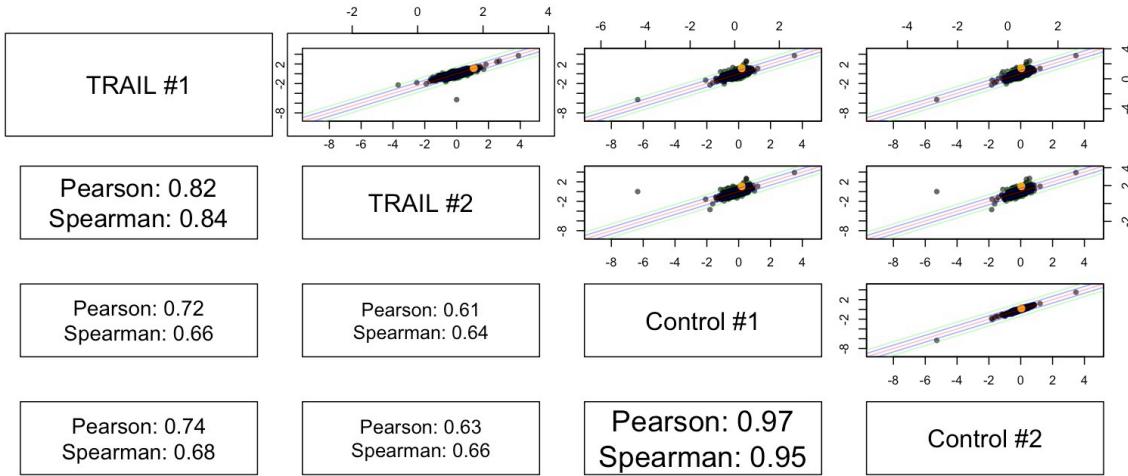
UNKNOWN

Wilcox p-value: 0.01782408

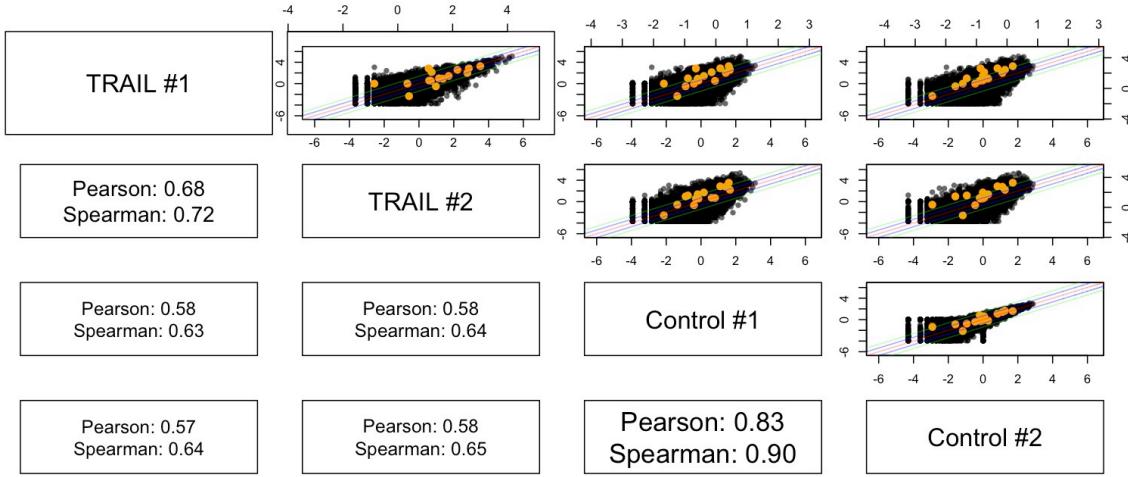
DESeq2 p-value: 7.9517e-08

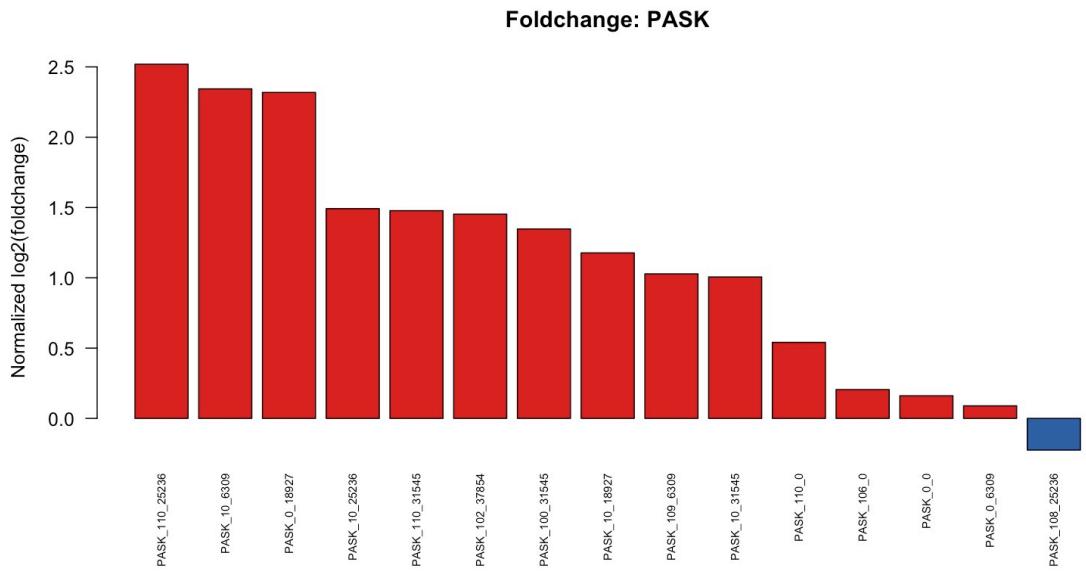
MAGECK p-value: 0.003713

**Gene Scatter for PASK
TRAILscreen**

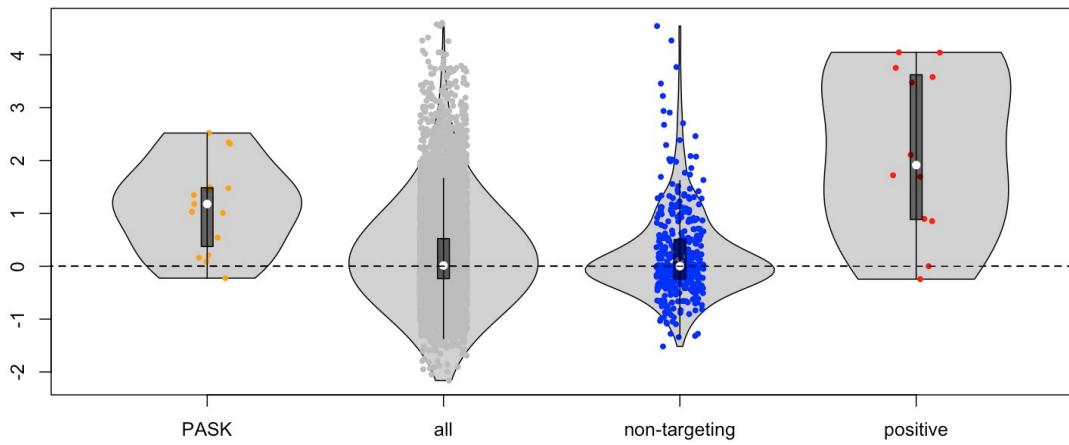


**sgRNA Scatter for PASK
TRAILscreen**





Log2 Foldchange of sgRNAs for PASK compared to sgRNA from all, non-targeting and targeting control



	designs	genes	sequence	log2Foldchange
14	PASK_110_25236	PASK	gaatgagcagattcggtta	2.5192130
12	PASK_10_6309	PASK	ggccacgttagccggcaagg	2.3438587
2	PASK_0_18927	PASK	gagcaccacacttcttccta	2.3183905
10	PASK_10_25236	PASK	gcaaggcacgacattaatcct	1.4918070
15	PASK_110_31545	PASK	gccagcacatcccaaaggta	1.4773762
5	PASK_102_37854	PASK	gatcagatctttatgcct	1.4529940
4	PASK_100_31545	PASK	gttctaacaacaaagcttg	1.3469513
9	PASK_10_18927	PASK	gccttggccaaggtaacac	1.1772435
8	PASK_109_6309	PASK	gaaataggcatggtgtgcgt	1.0279086
11	PASK_10_31545	PASK	gcgtgagctctggccaatc	1.0060151
13	PASK_110_0	PASK	gctgaccctgtcacctgtgag	0.5407919
6	PASK_106_0	PASK	gtatatgctcatctgagtga	0.2050875
1	PASK_0_0	PASK	ggatgctgagaaggcctacc	0.1610815
3	PASK_0_6309	PASK	gatgctctgtgccctggac	0.0893763
7	PASK_108_25236	PASK	gaaaggccaagacatcttcac	-0.2255927

Depleted

CDC42BPG

In addition to the plots below, the following information has been retrieved via biomaRt:

ENSEMBL ID (links to Ensembl) [ENSG00000171219](#)

HGNC SYMBOL (links to GeneCards) [CDC42BPG](#)

GENE DESCRIPTION

CDC42 binding protein kinase gamma (DMPK-like) [Source:HGNC Symbol;Acc:HGNC:29829]

GO TERM

cell leading edge

MIM GENE DESCRIPTION

CDC42-BINDING PROTEIN KINASE, GAMMA; CDC42BPG;;MYOTONIC DYSTROPHY KINASE-RELATED CDC42-BINDING KINASE, GAMMA; MRCKG;;MRCK-GAMMA

ENSEMBL PROTEIN ID

ENSP00000345133

PROTEIN FAMILY DESCRIPTION

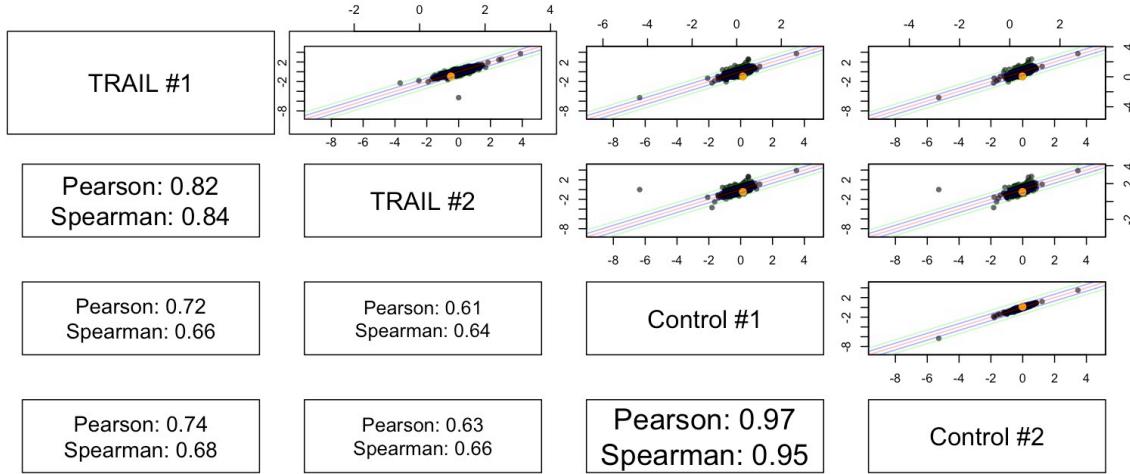
SERINE/THREONINE KINASE MRCK EC_2.7.11.1 CDC42 BINDING KINASE DMPK MYOTONIC DYSTROPHY KINASE RELATED CDC42 BINDING KINASE MRCK MYOTONIC DYSTROPHY KINASE

Wilcox p-value: 0.8749233

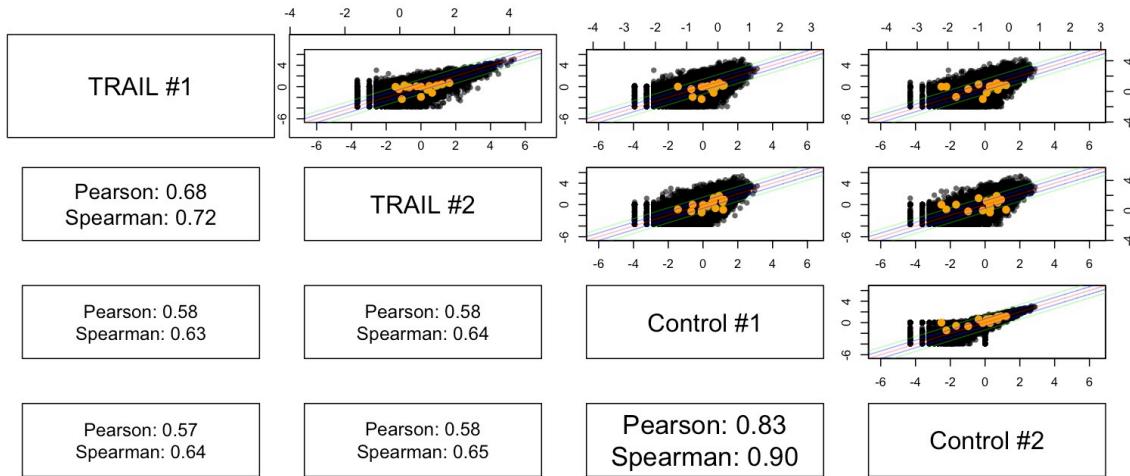
DESeq2 p-value: 0.06333045

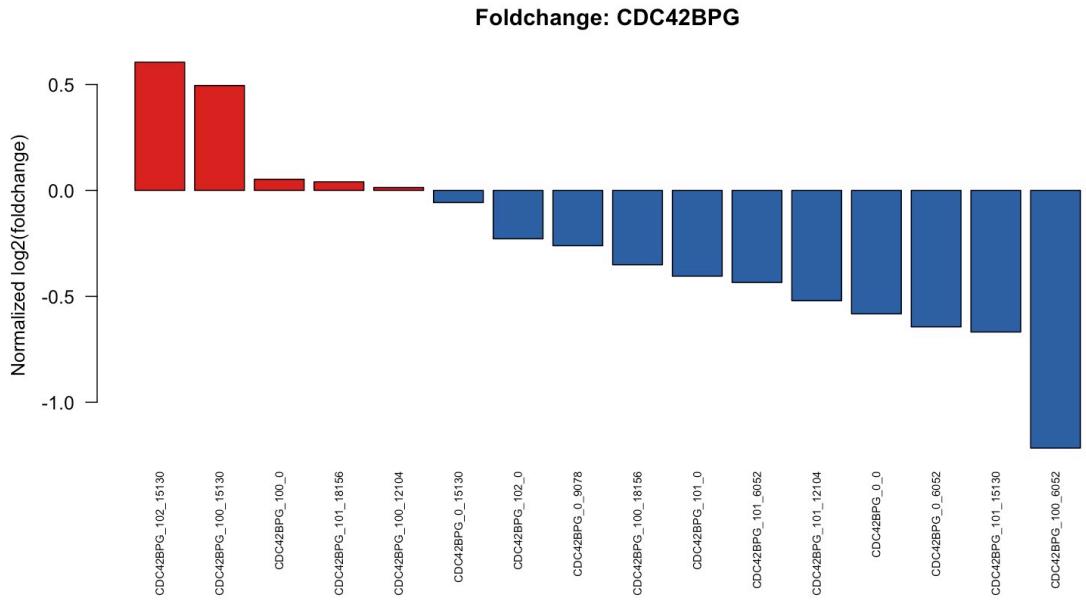
MAGECK p-value: 0.701894

**Gene Scatter for CDC42BPG
TRAILscreen**

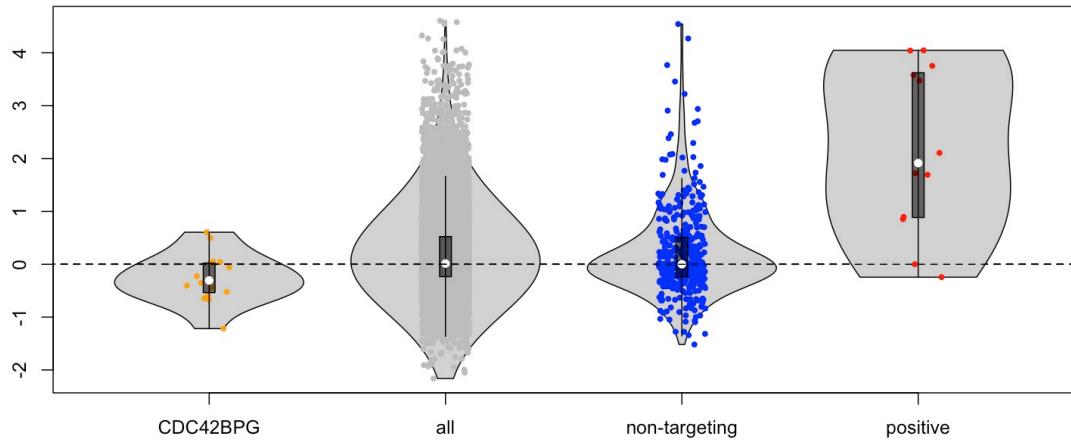


**sgRNA Scatter for CDC42BPG
TRAILscreen**





Log2 Foldchange of sgRNAs for CDC42BPG compared to sgRNA from all, non-targeting and targeting cont



	designs	genes	sequence	log2Foldchange
16	CDC42BPG_102_15130	CDC42BPG	ggaccgtctccgccccgagc	0.6054159
7	CDC42BPG_100_15130	CDC42BPG	ggacacccatccaactttgatg	0.4953713
5	CDC42BPG_100_0	CDC42BPG	ggggagggggtgcagtggcg	0.0525458
13	CDC42BPG_101_18156	CDC42BPG	ggtcaccgtgggtgaggcaga	0.0405820
6	CDC42BPG_100_12104	CDC42BPG	ggagctggagcagctacgga	0.0139267
2	CDC42BPG_0_15130	CDC42BPG	gttgctggcttgacatccc	-0.0573332
15	CDC42BPG_102_0	CDC42BPG	gagggagtcggagaacaaa	-0.2284839
4	CDC42BPG_0_9078	CDC42BPG	gttagaggctgttgtggcagt	-0.2611705
8	CDC42BPG_100_18156	CDC42BPG	gtgtgtgaggcagaggacac	-0.3513528
10	CDC42BPG_101_0	CDC42BPG	gaacaaagggtccttctct	-0.4051230
14	CDC42BPG_101_6052	CDC42BPG	gaggagctgccaccatcccg	-0.4346633
11	CDC42BPG_101_12104	CDC42BPG	gggttaccacccctccctccag	-0.5207291
1	CDC42BPG_0_0	CDC42BPG	ggccctaacagagggcatca	-0.5829203
3	CDC42BPG_0_6052	CDC42BPG	ggcccatcatttgagctgt	-0.6444921
12	CDC42BPG_101_15130	CDC42BPG	gctgggttatgtccacaggt	-0.6687819
9	CDC42BPG_100_6052	CDC42BPG	ggagctgccaccatcccgcg	-1.2168444

CHEK1

In addition to the plots below, the following information has been retrieved via biomaRt:

ENSEMBL ID (links to Ensembl) [ENSG00000149554](#)

HGNC SYMBOL (links to GeneCards) [CHEK1](#)

GENE DESCRIPTION

checkpoint kinase 1 [Source:HGNC Symbol;Acc:HGNC:1925]

GO TERM

replication fork

MIM GENE DESCRIPTION

CHECKPOINT, S. POMBE, HOMOLOG OF, 1; CHEK1;;CELL CYCLE CHECKPOINT KINASE; CHK1

ENSEMBL PROTEIN ID

ENSP00000388648

PROTEIN FAMILY DESCRIPTION

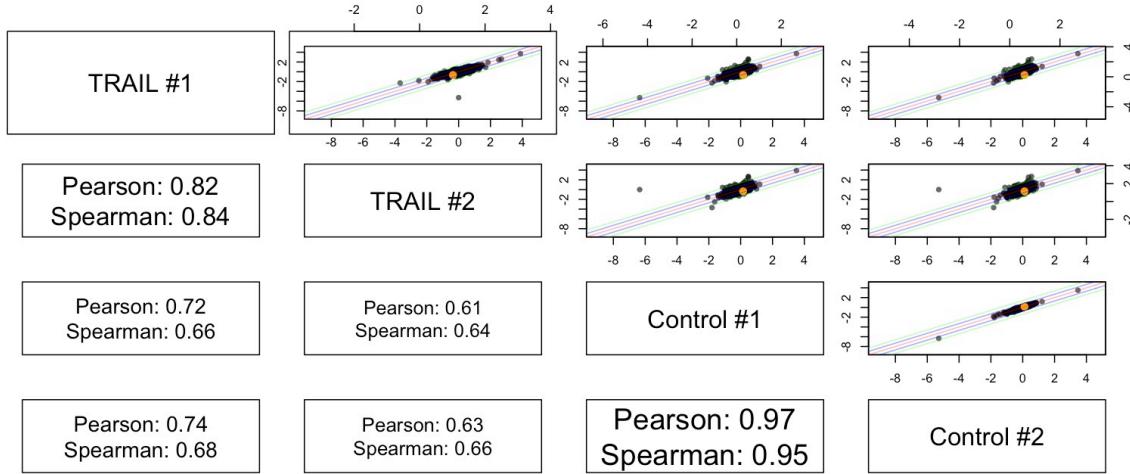
SERINE/THREONINE KINASE CHK1 EC_2.7.11.1 CHK1 CHECKPOINT HOMOLOG CHECKPOINT KINASE 1

Wilcox p-value: 0.9671744

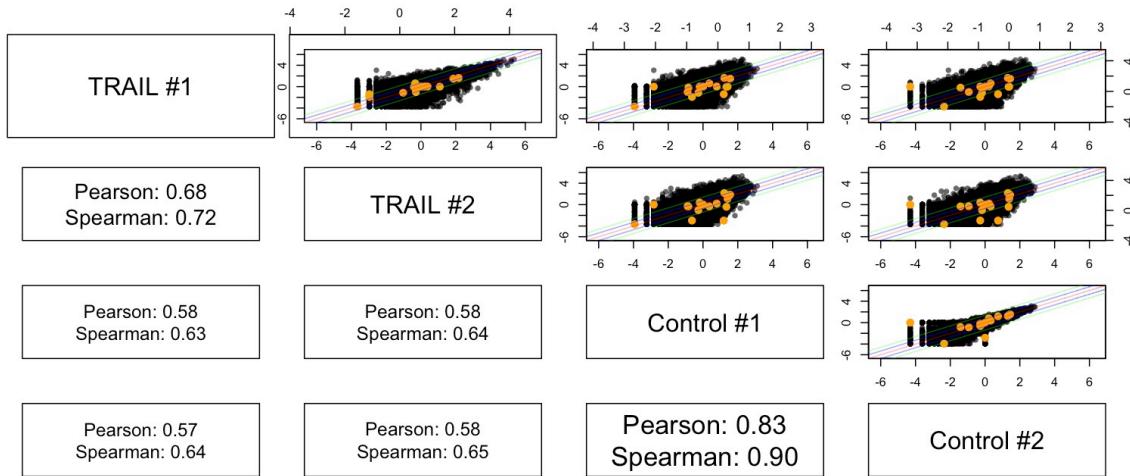
DESeq2 p-value: 0.1231337

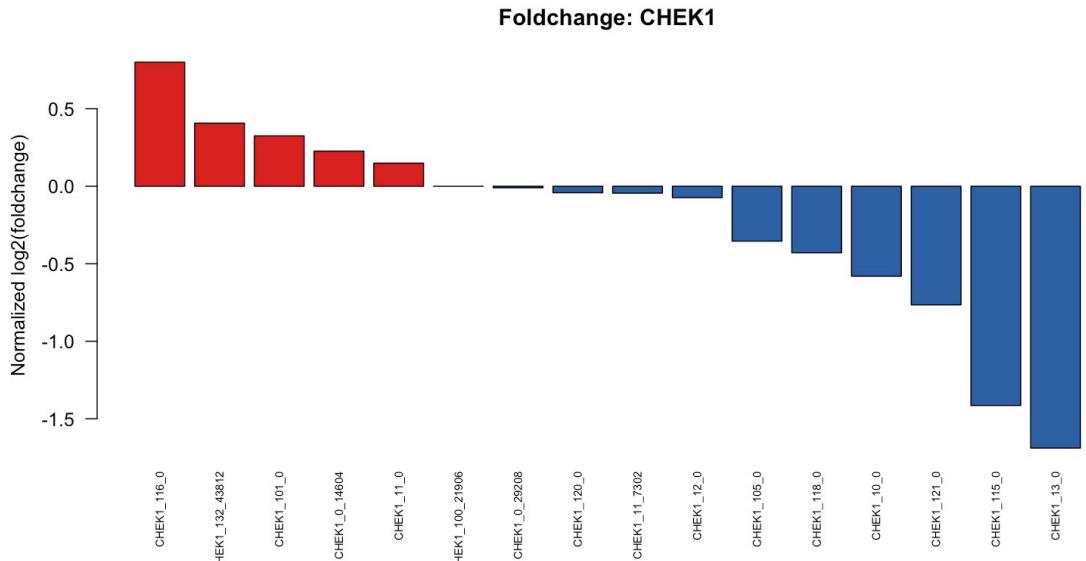
MAGECK p-value: 0.701894

Gene Scatter for CHEK1
TRAILscreen

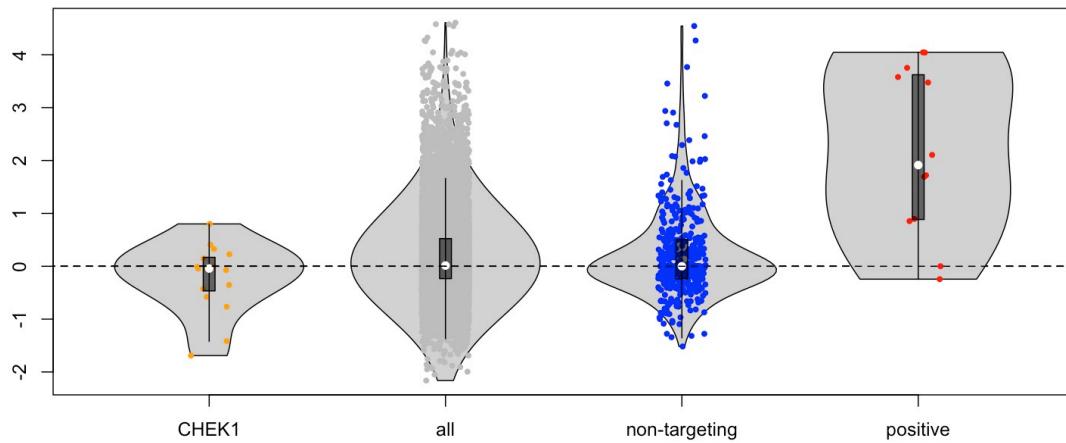


sgRNA Scatter for CHEK1
TRAILscreen





Log2 Foldchange of sgRNAs for CHEK1 compared to sgRNA from all, non-targeting and targeting control



	designs	genes	sequence	log2Foldchange
8	CHEK1_116_0	CHEK1	gatgttggcgctccggcca	0.8004400
15	CHEK1_132_43812	CHEK1	gaaatatgcctaggcatgg	0.4073559
4	CHEK1_101_0	CHEK1	gaccgcgctgcgttcagg	0.3253318
1	CHEK1_0_14604	CHEK1	gagccacaatgcctgccc	0.2268288
10	CHEK1_11_0	CHEK1	ggagctggttcacagaaaa	0.1493467
3	CHEK1_100_21906	CHEK1	gttgttgatatagtaaccta	0.0000000
2	CHEK1_0_29208	CHEK1	gtaaggcaaaacttggggaa	-0.0097152
12	CHEK1_120_0	CHEK1	gaatgtcgccggctccaaaa	-0.0418202
11	CHEK1_11_7302	CHEK1	ggatatacatacatgactttg	-0.0444676
14	CHEK1_12_0	CHEK1	gaggcagaattcaacacctt	-0.0732607
5	CHEK1_105_0	CHEK1	geccaggccctccaaggcctca	-0.3542135
9	CHEK1_118_0	CHEK1	gccccctccaaaagggtgacg	-0.4289122
6	CHEK1_10_0	CHEK1	gtaaaggcattttggagc	-0.5804622
13	CHEK1_121_0	CHEK1	gttttcccgccaaaacttg	-0.7653539
7	CHEK1_115_0	CHEK1	geccaggcgtcttgcagt	-1.4143340
16	CHEK1_13_0	CHEK1	gcaagagctgttaatttcg	-1.6893490

CSF1R

In addition to the plots below, the following information has been retrieved via biomarRt:

ENSEMBL ID (links to Ensembl) [ENSG00000182578](#)

HGNC SYMBOL (links to GeneCards) [CSF1R](#)

GENE DESCRIPTION

colony stimulating factor 1 receptor [Source:HGNC Symbol;Acc:HGNC:2433]

GO TERM

CSF1-CSF1R complex

MIM GENE DESCRIPTION

COLONY-STIMULATING FACTOR 1 RECEPTOR; CSF1R;;MCSFR;;ONCOGENE FMS; FMS;;c-FMS;;CD115 ANTIGEN; CD115;;V-FMS MCDONOUGH FELINE SARCOMA VIRAL ONCOGENE HOMOLOG, FORMERLY

ENSEMBL PROTEIN ID

ENSP00000445282

PROTEIN FAMILY DESCRIPTION

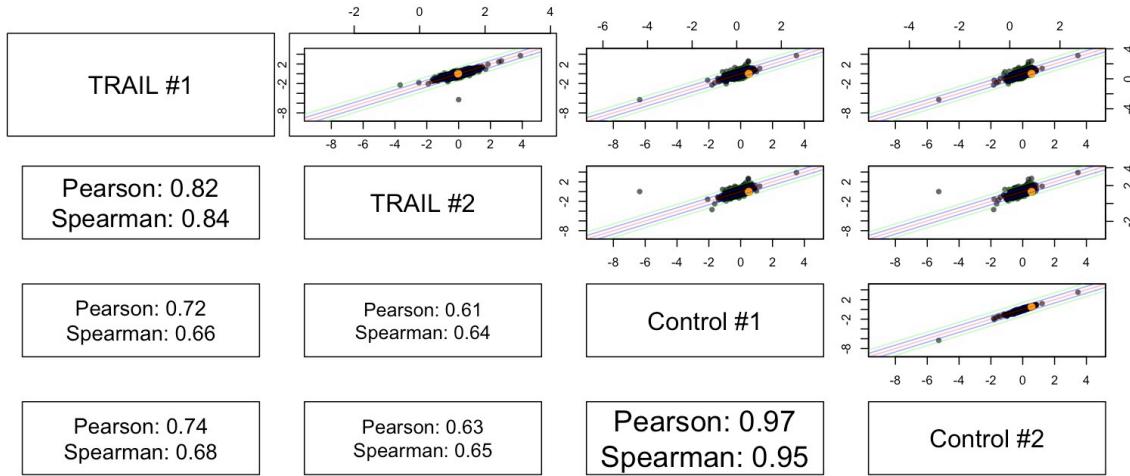
MAST/STEM CELL GROWTH FACTOR RECEPTOR KIT PRECURSOR SCFR EC_2.7.10.1 PROTO ONCOGENE C KIT TYROSINE KINASE KIT

Wilcox p-value: 0.9671744

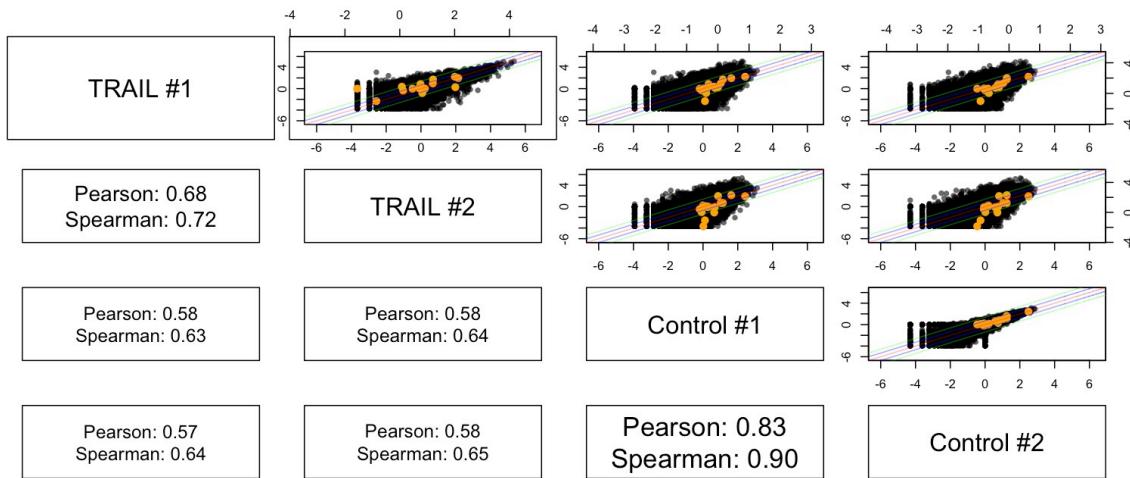
DESeq2 p-value: 0.1115685

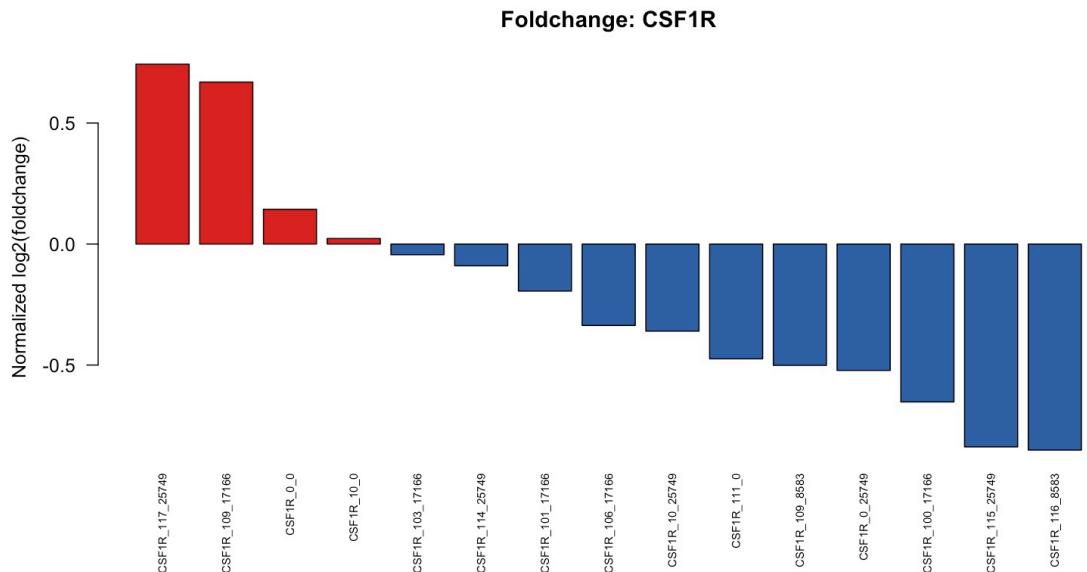
MAGECK p-value: 0.701894

**Gene Scatter for CSF1R
TRAILscreen**

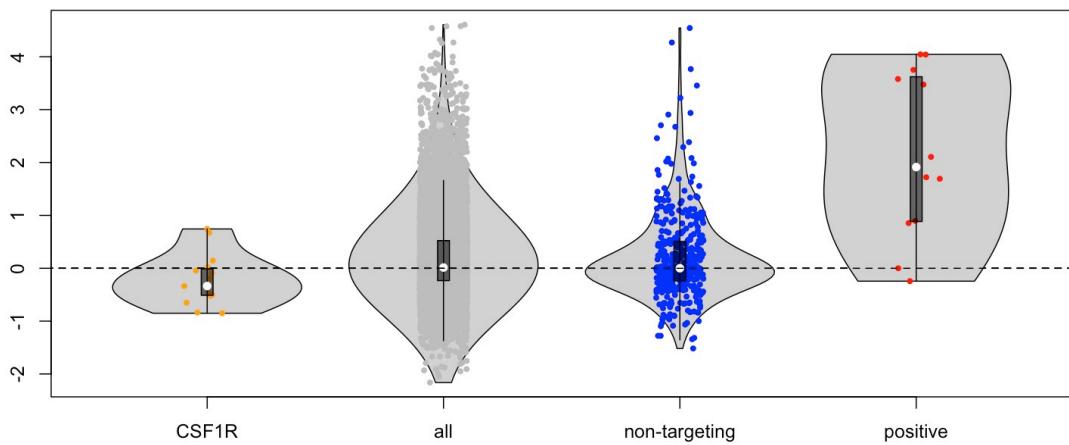


**sgRNA Scatter for CSF1R
TRAILscreen**





Log2 Foldchange of sgRNAs for CSF1R compared to sgRNA from all, non-targeting and targeting control



	designs	genes	sequence	log2Foldchange
15	CSF1R_117_25749	CSF1R	ggcctcggtgggaagtggc	0.7432286
7	CSF1R_109_17166	CSF1R	gtctgggcccattcagcaca	0.6694507
1	CSF1R_0_0	CSF1R	gtgtggccagccacatgccca	0.1437269
9	CSF1R_10_0	CSF1R	gataggacagaggatgccca	0.0229662
5	CSF1R_103_17166	CSF1R	ggcctgtcttaaagagacct	-0.0440560
12	CSF1R_114_25749	CSF1R	gctttaccatgccaagctg	-0.0897533
4	CSF1R_101_17166	CSF1R	gcttcaggcggggcagagag	-0.1942767
6	CSF1R_106_17166	CSF1R	gagggtgaaggtgtgcctgc	-0.3364257
10	CSF1R_10_25749	CSF1R	ggcagggtctagagttagagg	-0.3598989
11	CSF1R_111_0	CSF1R	gtgcagctcctgactattcc	-0.4741526
8	CSF1R_109_8583	CSF1R	gactcatgttggcatacagt	-0.5012091
2	CSF1R_0_25749	CSF1R	gggcactgcattgatagtcc	-0.5221593
3	CSF1R_100_17166	CSF1R	gccctggatgactgagacc	-0.6523193
13	CSF1R_115_25749	CSF1R	gccaagctgtggccaccage	-0.8383244
14	CSF1R_116_8583	CSF1R	gacatgcaggcgaccaccac	-0.8513914

PRKACB

In addition to the plots below, the following information has been retrieved via biomaRt:

ENSEMBL ID (links to Ensembl) [ENSG00000142875](#)

HGNC SYMBOL (links to GeneCards) [PRKACB](#)

GENE DESCRIPTION

protein kinase, cAMP-dependent, catalytic, beta [Source:HGNC Symbol;Acc:HGNC:9381]

GO TERM

transferase activity, transferring phosphorus-containing groups

MIM GENE DESCRIPTION

PROTEIN KINASE, cAMP-DEPENDENT, CATALYTIC, BETA; PRKACB

ENSEMBL PROTEIN ID

ENSP00000378314

PROTEIN FAMILY DESCRIPTION

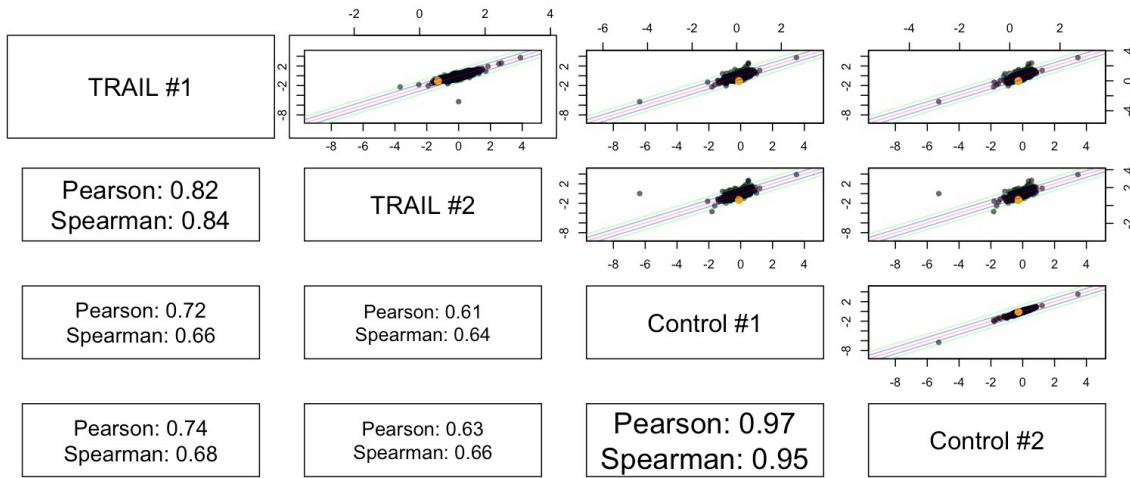
CAMP DEPENDENT KINASE CATALYTIC SUBUNIT PKA C EC_2.7.11.11

Wilcox p-value: 0.9671744

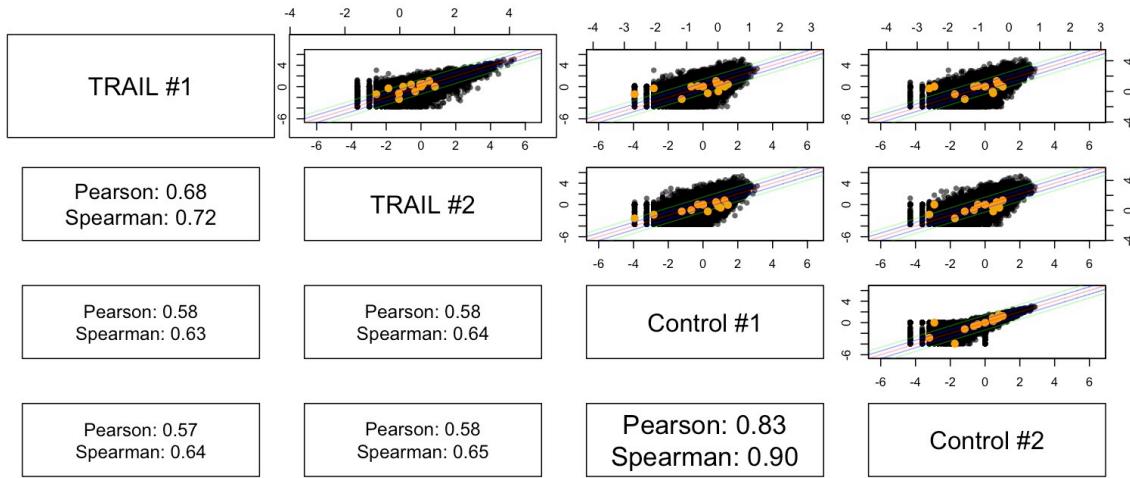
DESeq2 p-value: 1.054877e-06

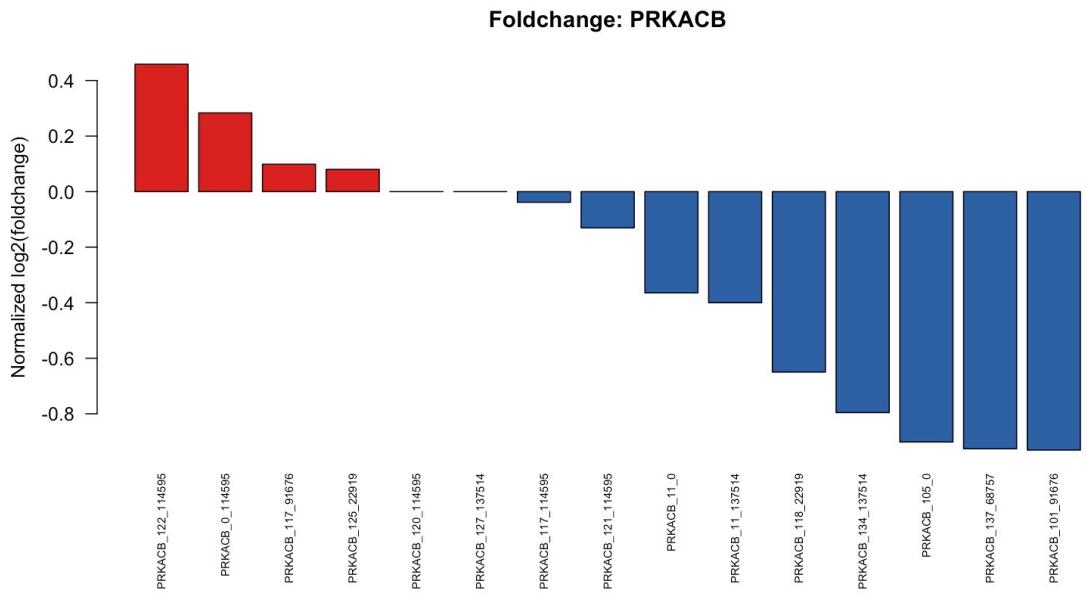
MAGECK p-value: 0.701894

Gene Scatter for PRKACB TRAILscreen

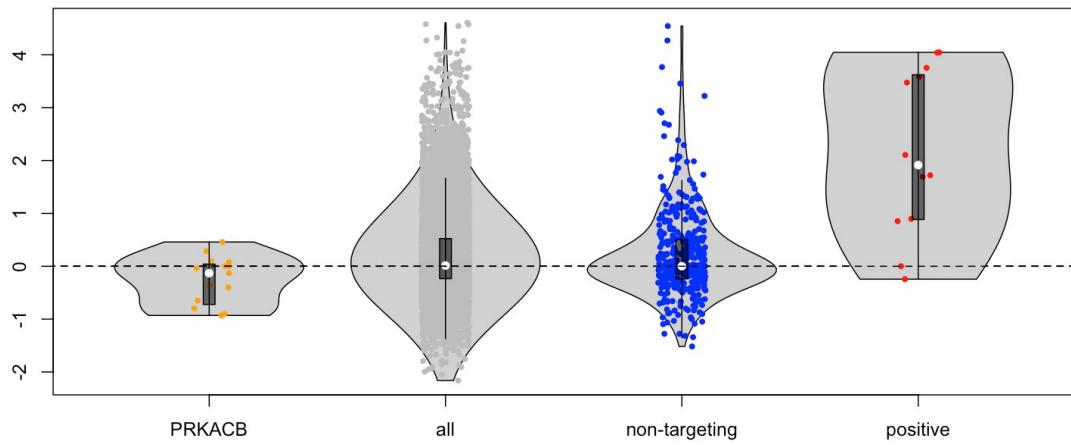


sgRNA Scatter for PRKACB TRAILscreen





Log2 Foldchange of sgRNAs for PRKACB compared to sgRNA from all, non-targeting and targeting controls



	designs	genes	sequence	log2Foldchange
11	PRKACB_122_114595	PRKACB	gataatttatatccacat	0.4588957
1	PRKACB_0_114595	PRKACB	gctacaataaggcagtggat	0.2836619
5	PRKACB_117_91676	PRKACB	gtgaaaacatttccccca	0.0988086
12	PRKACB_125_22919	PRKACB	gccaaatcatcttatatgtc	0.0802308
9	PRKACB_120_114595	PRKACB	gttcatatcaaaggctgc	0.0000000
13	PRKACB_127_137514	PRKACB	gtctgcaaggccaatttt	0.0000000
4	PRKACB_117_114595	PRKACB	ggttgtctgcaaagaatgg	-0.0384741
10	PRKACB_121_114595	PRKACB	gtcattttctaagggtgcc	-0.1305172
7	PRKACB_11_0	PRKACB	gacatgttagcactaaagt	-0.3644069
8	PRKACB_11_137514	PRKACB	gggagacatcctcaattcc	-0.4000529
6	PRKACB_118_22919	PRKACB	gcactactagcattgcatga	-0.6499614
14	PRKACB_134_137514	PRKACB	gtacacactgctgcttagtga	-0.7959443
3	PRKACB_105_0	PRKACB	gccggtgctaaggagttcgc	-0.9016024
15	PRKACB_137_68757	PRKACB	gtcaggagagtaatttacc	-0.9260958
2	PRKACB_101_91676	PRKACB	gttggatcattacagacagc	-0.9308058

NRG3

In addition to the plots below, the following information has been retrieved via biomaRt:

ENSEMBL ID (links to Ensembl) [ENSG00000185737](#)

HGNC SYMBOL (links to GeneCards) [NRG3](#)

GENE DESCRIPTION

neuregulin 3 [Source:HGNC Symbol;Acc:HGNC:7999]

GO TERM

embryo development

MIM GENE DESCRIPTION

NEUREGULIN 3; NRG3

ENSEMBL PROTEIN ID

ENSP00000441201

PROTEIN FAMILY DESCRIPTION

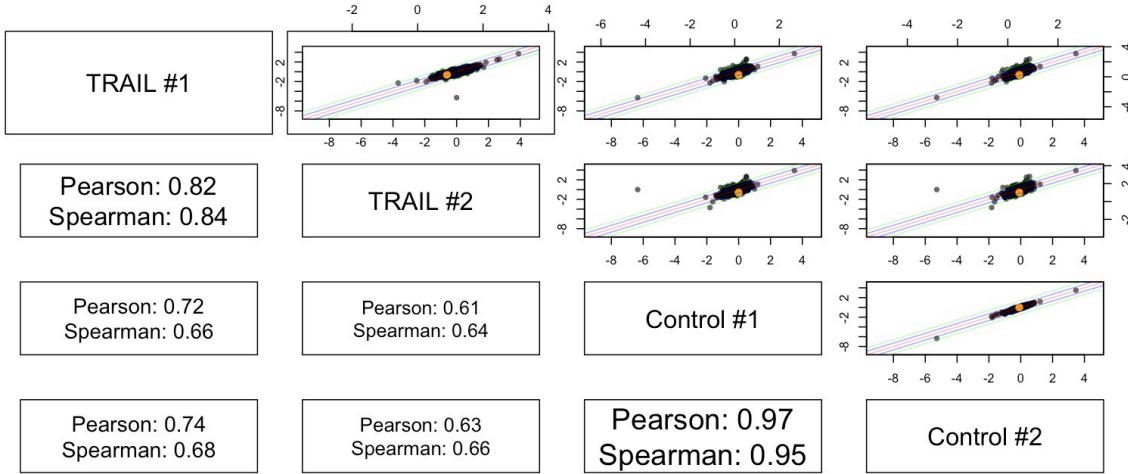
PRO NEUREGULIN 3 MEMBRANE BOUND PRECURSOR PRO NRG3 [CONTAINS NEUREGULIN 3
NRG 3]

Wilcox p-value: 0.9671744

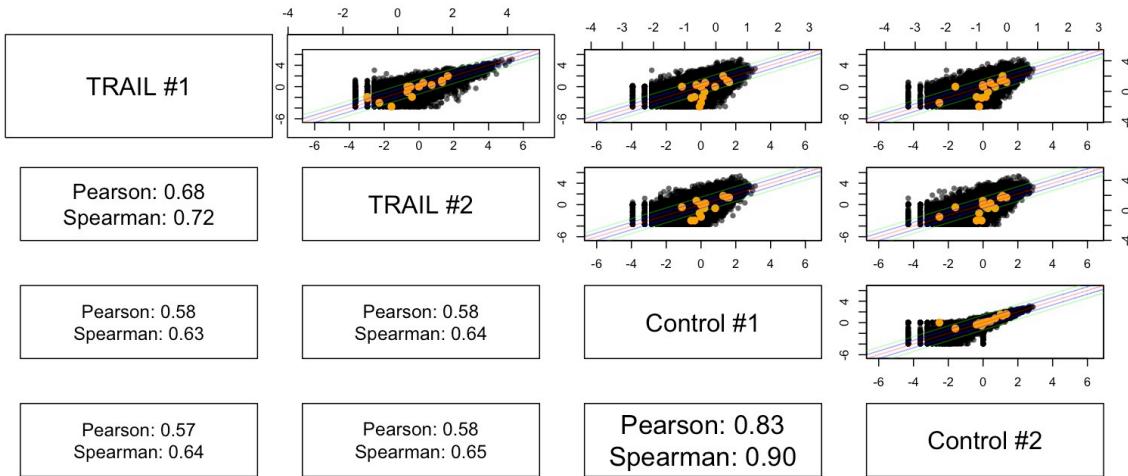
DESeq2 p-value: 0.0723033

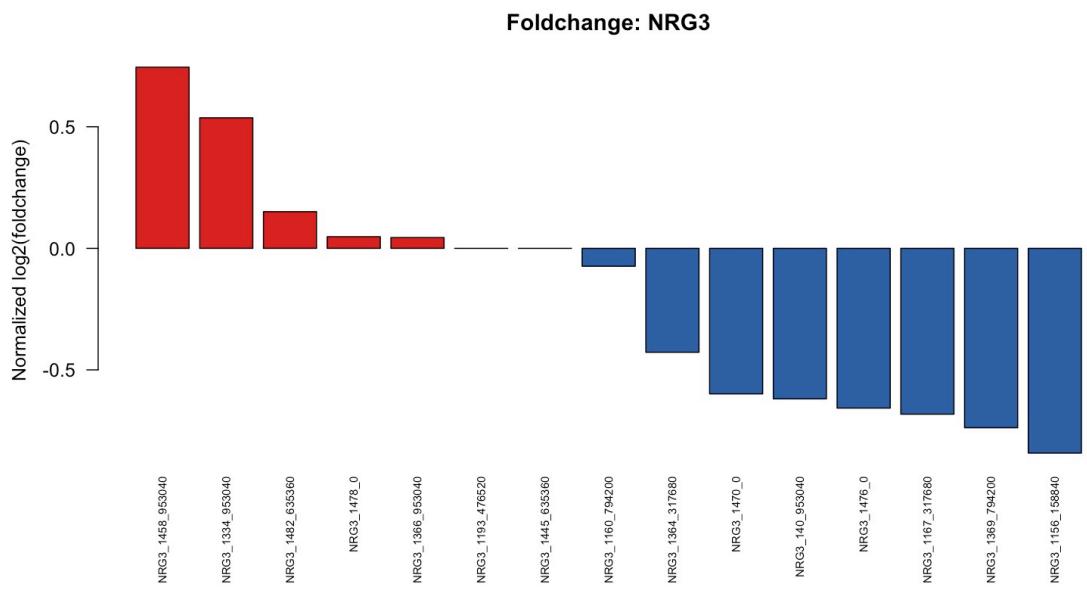
MAGECK p-value: 0.701894

Gene Scatter for NRG3
TRAILscreen

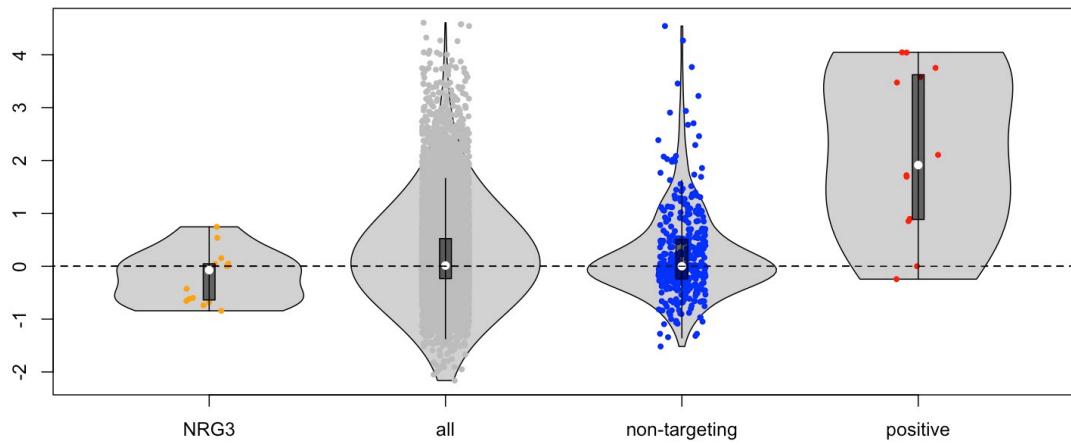


sgRNA Scatter for NRG3
TRAILscreen





Log2 Foldchange of sgRNAs for NRG3 compared to sgRNA from all, non-targeting and targeting control



	designs	genes	sequence	log2Foldchange
11	NRG3_1458_953040	NRG3	gagggccttgtccaaaattc	0.7452361
5	NRG3_1334_953040	NRG3	gcctcatatcgatgcatacat	0.5369936
15	NRG3_1482_635360	NRG3	gctgttcaaactccaaaga	0.1508644
14	NRG3_1478_0	NRG3	gctgccatatatgttaaatgaa	0.0479055
7	NRG3_1366_953040	NRG3	gtggcacttcagtcgtct	0.0444479
4	NRG3_1193_476520	NRG3	ggccagttgtctcaaaccc	0.0000000
10	NRG3_1445_635360	NRG3	gccataaacatgtttctct	0.0000000
2	NRG3_1160_794200	NRG3	gggctagtcctctaaccata	-0.0736764
6	NRG3_1364_317680	NRG3	gcgcctaaacccttactgg	-0.4276937
12	NRG3_1470_0	NRG3	gacctcagatggAACCGAA	-0.5988079
9	NRG3_140_953040	NRG3	gaatccctaggTCCCTATAACC	-0.6191415
13	NRG3_1476_0	NRG3	gcaggTTCCAGTCATGAC	-0.6572912
3	NRG3_1167_317680	NRG3	gaactcaacgttagaccatct	-0.6823694
8	NRG3_1369_794200	NRG3	gtctgtcacgtgtctcaact	-0.7381306
1	NRG3_1156_158840	NRG3	ggccagaatctcttagcactt	-0.8424093

MAPK7

In addition to the plots below, the following information has been retrieved via biomaRt:

ENSEMBL ID (links to Ensembl) [ENSG00000166484](#)

HGNC SYMBOL (links to GeneCards) [MAPK7](#)

GENE DESCRIPTION

mitogen-activated protein kinase 7 [Source:HGNC Symbol;Acc:HGNC:6880]

GO TERM

negative regulation of NFAT protein import into nucleus

MIM GENE DESCRIPTION

MITOGEN-ACTIVATED PROTEIN KINASE 7; MAPK7;;PROTEIN KINASE, MITOGEN-ACTIVATED, 7; PRKM7;;EXTRACELLULAR SIGNAL-REGULATED KINASE 5; ERK5

ENSEMBL PROTEIN ID

ENSP00000311005

PROTEIN FAMILY DESCRIPTION

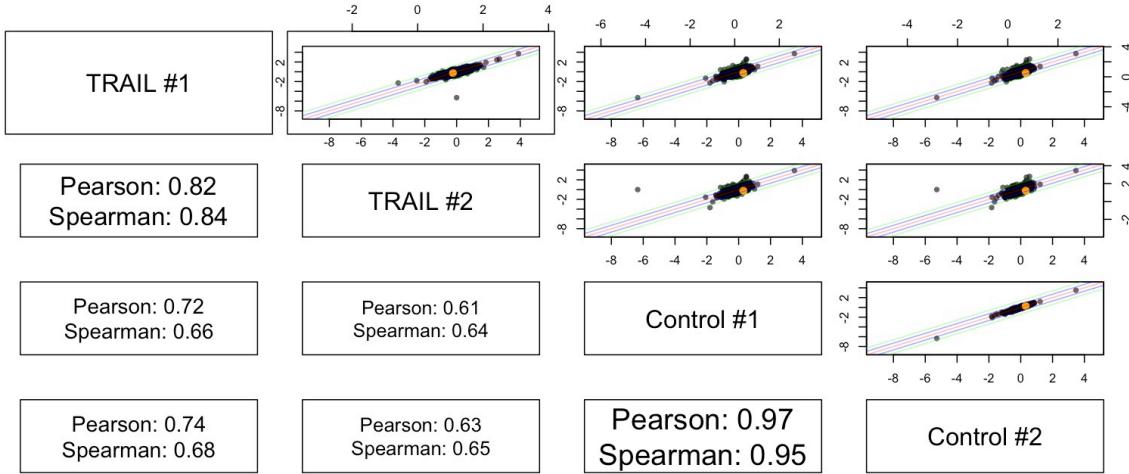
MITOGEN ACTIVATED KINASE 7 MAP KINASE 7 MAPK 7 EC_2.7.11.24 BIG MAP KINASE 1 BMK 1 EXTRACELLULAR SIGNAL REGULATED KINASE 5 ERK 5

Wilcox p-value: 0.9671744

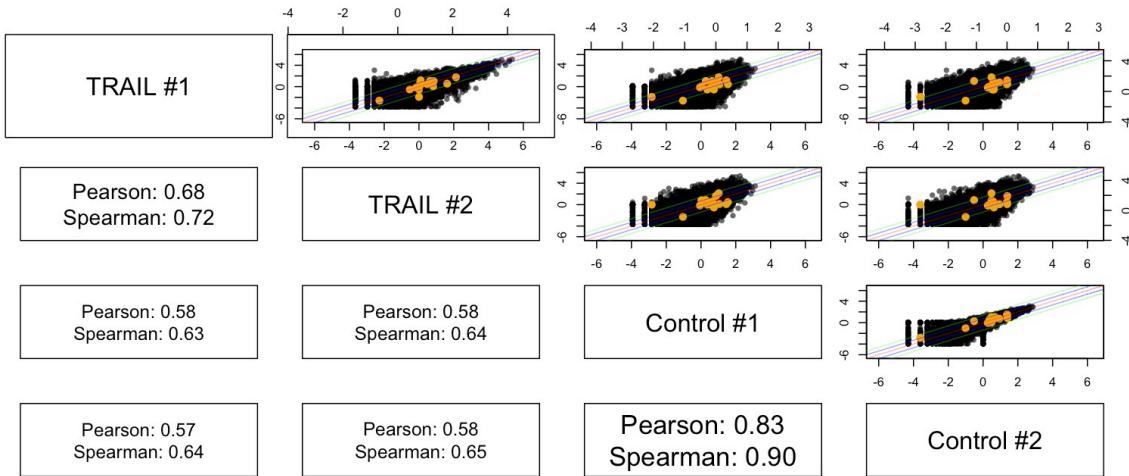
DESeq2 p-value: 0.1051081

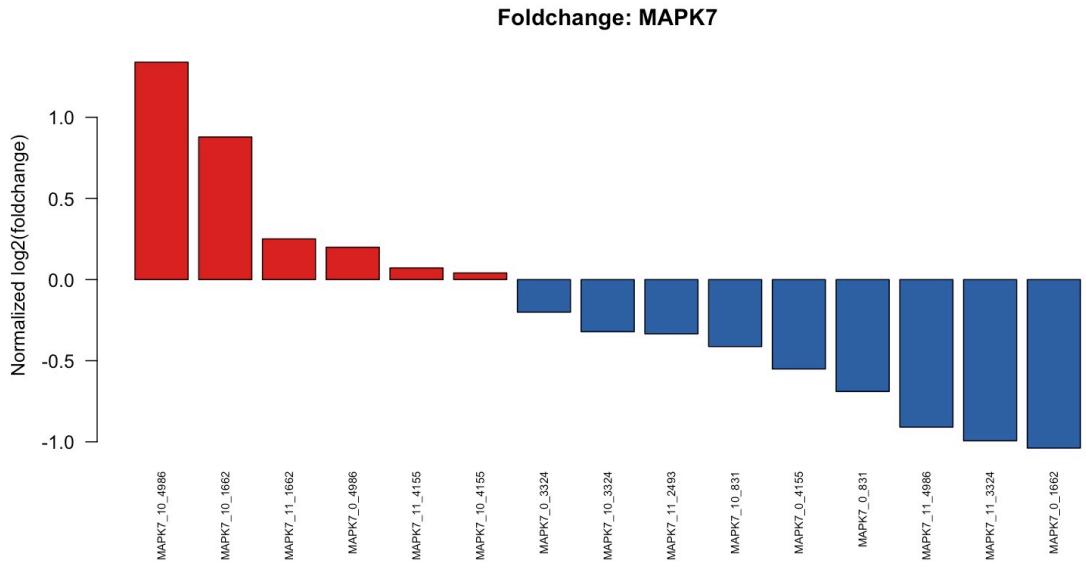
MAGECK p-value: 0.701894

**Gene Scatter for MAPK7
TRAILscreen**

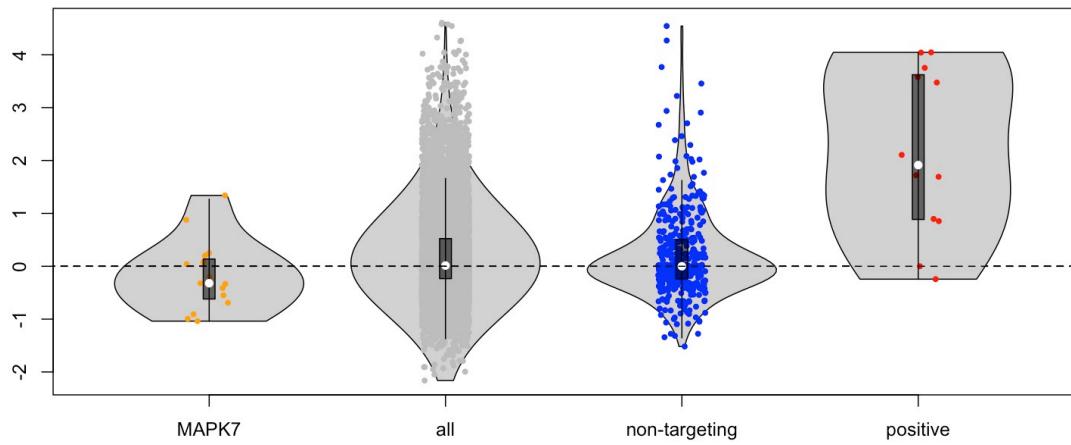


**sgRNA Scatter for MAPK7
TRAILscreen**





Log2 Foldchange of sgRNAs for MAPK7 compared to sgRNA from all, non-targeting and targeting control



	designs	genes	sequence	log2Foldchange
9	MAPK7_10_4986	MAPK7	ggactgtggggagaggttcc	1.3398243
6	MAPK7_10_1662	MAPK7	gatggccacctgctggcctg	0.8788394
11	MAPK7_11_1662	MAPK7	gtcaccacategaaaggcatt	0.2509378
4	MAPK7_0_4986	MAPK7	gtgttctcaggcacaccaaa	0.1995151
14	MAPK7_11_4155	MAPK7	ggccaaaggaaaatgggttc	0.0717681
8	MAPK7_10_4155	MAPK7	ggtctggccaaaggaaaat	0.0412438
2	MAPK7_0_3324	MAPK7	gcgcattaaggaggccattg	-0.2006852
7	MAPK7_10_3324	MAPK7	gggagacttggacttggaca	-0.3209398
12	MAPK7_11_2493	MAPK7	ggtgacttttgttatggctcg	-0.3341234
10	MAPK7_10_831	MAPK7	ggctcggttctctgaaactc	-0.4125705
3	MAPK7_0_4155	MAPK7	gttggAACGCTGGACTCGAA	-0.5507305
5	MAPK7_0_831	MAPK7	gcctaccCCTCCCCGACCC	-0.6895103
15	MAPK7_11_4986	MAPK7	gtgcaggAGACATGCACCTG	-0.9092088
13	MAPK7_11_3324	MAPK7	ggctctgAGCCTCGGAAGC	-0.9935284
1	MAPK7_0_1662	MAPK7	gccccgcaggggagttgtga	-1.0384330

BCL2L12

In addition to the plots below, the following information has been retrieved via biomaRt:

ENSEMBL ID (links to Ensembl) [ENSG00000126453](#)

HGNC SYMBOL (links to GeneCards) [BCL2L12](#)

GENE DESCRIPTION

BCL2-like 12 (proline rich) [Source:HGNC Symbol;Acc:HGNC:13787]

GO TERM

MIM GENE DESCRIPTION

BCL2-LIKE 12; BCL2L12

ENSEMBL PROTEIN ID

ENSP00000478415

PROTEIN FAMILY DESCRIPTION

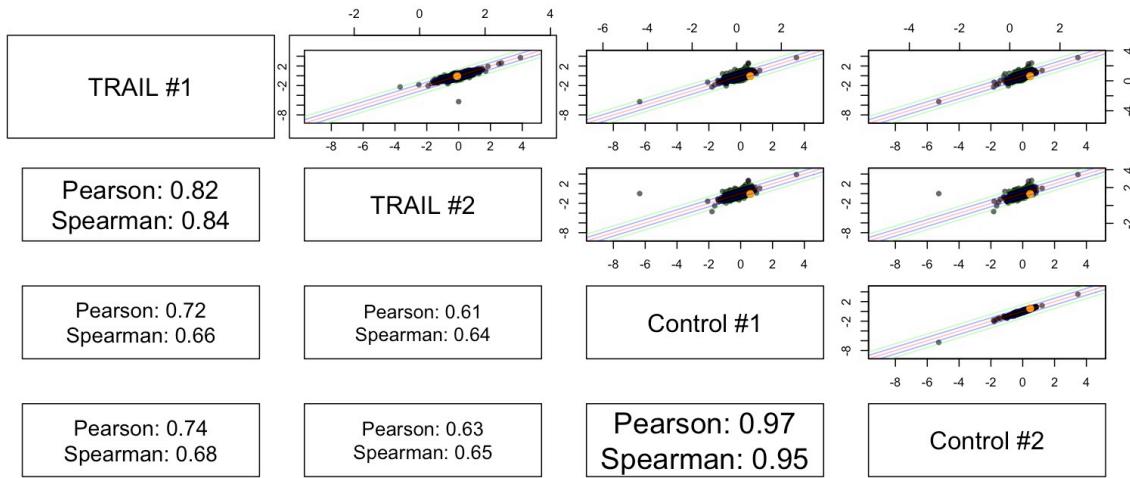
BCL 2 12 BCL2 L 12 BCL 2 RELATED PROLINE RICH

Wilcox p-value: 0.9671744

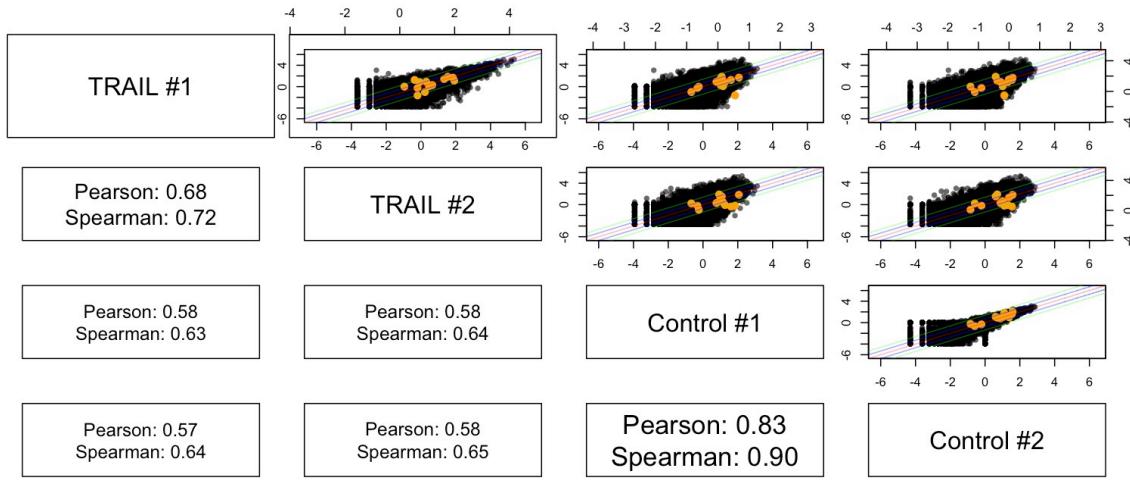
DESeq2 p-value: 0.01822949

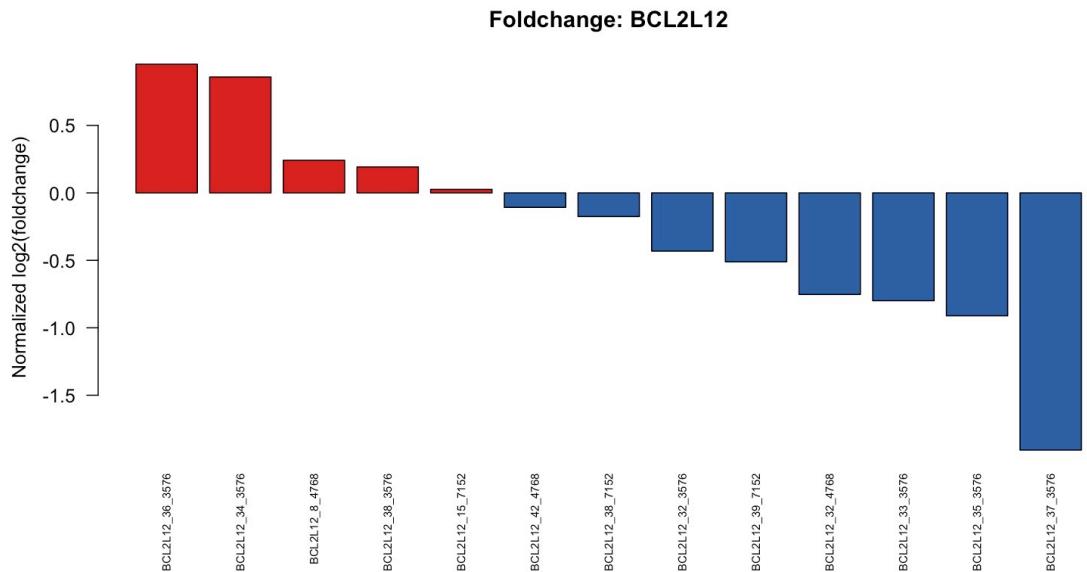
MAGECK p-value: 0.701894

Gene Scatter for BCL2L12
TRAILscreen

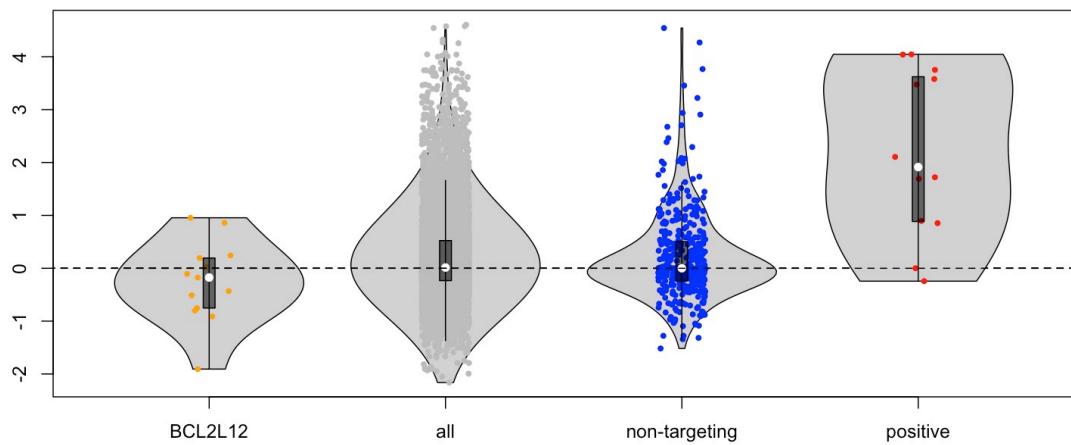


sgRNA Scatter for BCL2L12
TRAILscreen





Log2 Foldchange of sgRNAs for BCL2L12 compared to sgRNA from all, non-targeting and targeting controls



	designs	genes	sequence	log2Foldchange
7	BCL2L12_36_3576	BCL2L12	gaccagcttgcgtcgccagg	0.9538659
5	BCL2L12_34_3576	BCL2L12	ggggtcggaggccagctgtta	0.8589222
13	BCL2L12_8_4768	BCL2L12	ggcccgccctggccctagcca	0.2415422
9	BCL2L12_38_3576	BCL2L12	ggcggaccagcttgcgtgc	0.1920837
1	BCL2L12_15_7152	BCL2L12	gccactttcccttcagga	0.0261568
12	BCL2L12_42_4768	BCL2L12	gcttcacgctgagtccggcc	-0.1073999
10	BCL2L12_38_7152	BCL2L12	gcccttcgttggaaaggaaaag	-0.1755512
2	BCL2L12_32_3576	BCL2L12	ggccagctgttagggtgaaag	-0.4318455
11	BCL2L12_39_7152	BCL2L12	gccaggatgccctctggaa	-0.5109398
3	BCL2L12_32_4768	BCL2L12	gctccatggctagggccagg	-0.7531135
4	BCL2L12_33_3576	BCL2L12	gtccgaggccagctgttaggg	-0.7994554
6	BCL2L12_35_3576	BCL2L12	gctgcgcaggcggggtccg	-0.9113653
8	BCL2L12_37_3576	BCL2L12	gcggaccagcttgcgtcgca	-1.9067631

ITPKA

In addition to the plots below, the following information has been retrieved via biomaRt:

ENSEMBL ID (links to Ensembl) [ENSG00000137825](#)

HGNC SYMBOL (links to GeneCards) [ITPKA](#)

GENE DESCRIPTION

inositol-trisphosphate 3-kinase A [Source:HGNC Symbol;Acc:HGNC:6178]

GO TERM

positive regulation of dendritic spine morphogenesis

MIM GENE DESCRIPTION

INOSITOL 1,4,5-TRISPHOSPATE 3-KINASE A; ITPKA

ENSEMBL PROTEIN ID

ENSP00000260386

PROTEIN FAMILY DESCRIPTION

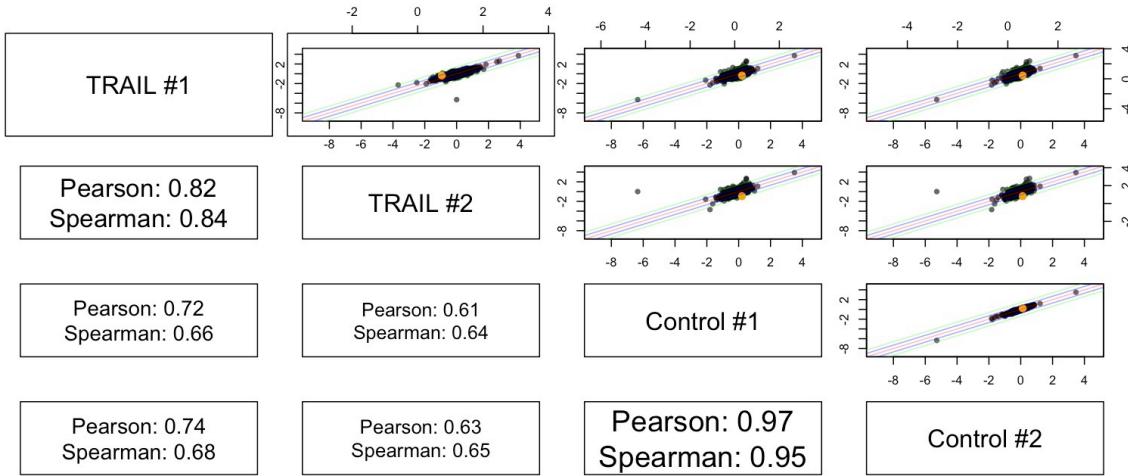
INOSITOL TRISPHOSPATE 3 KINASE EC_2.7.1.127 INOSITOL 1 4 5 TRISPHOSPATE 3 KINASE IP3 KINASE IP3K INSP 3 KINASE

Wilcox p-value: 0.9671744

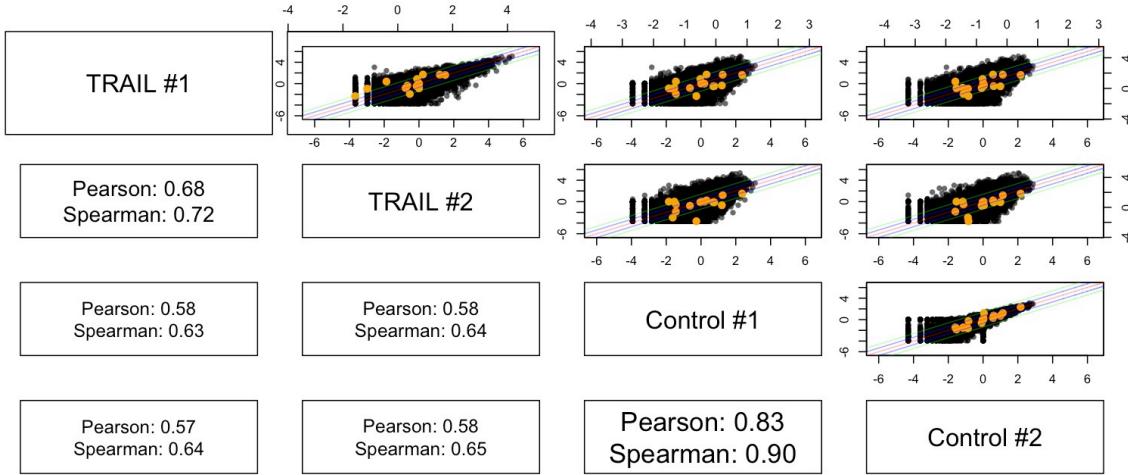
DESeq2 p-value: 0.1123445

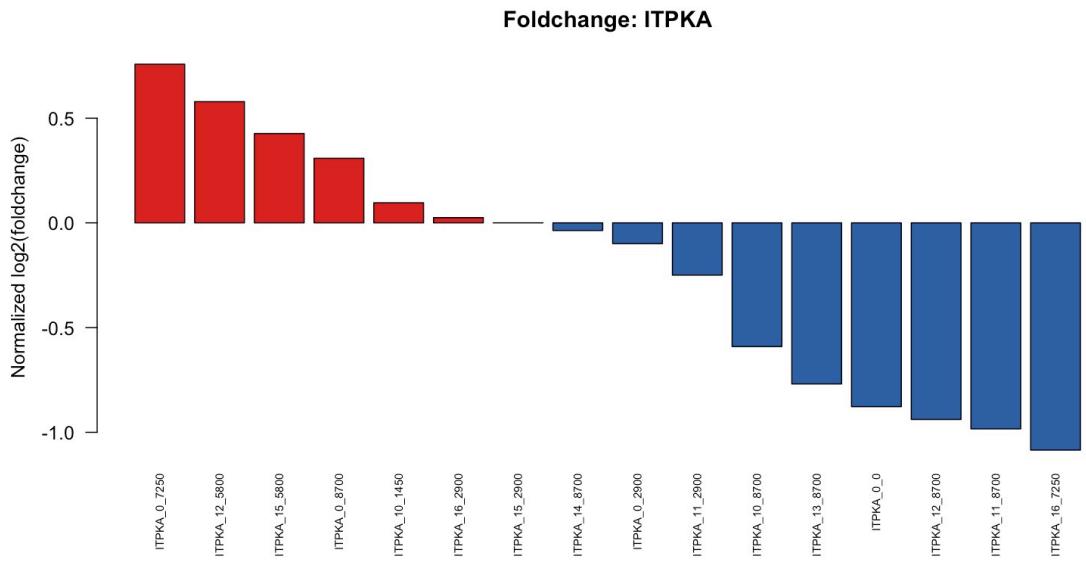
MAGECK p-value: 0.701894

**Gene Scatter for ITPKA
TRAILscreen**

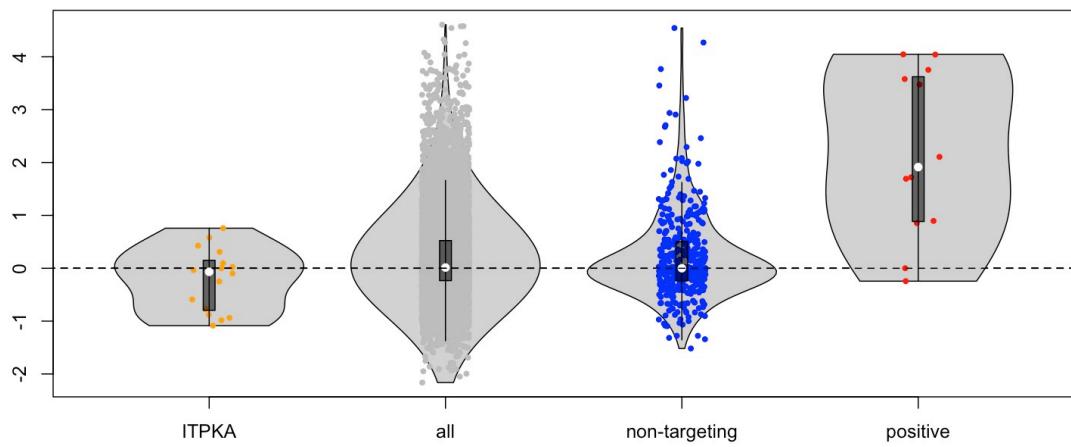


**sgRNA Scatter for ITPKA
TRAILscreen**





Log2 Foldchange of sgRNAs for ITPKA compared to sgRNA from all, non-targeting and targeting control



	designs	genes	sequence	log2Foldchange
3	ITPKA_0_7250	ITPKA	gctgatcctgaagcgctgct	0.7576987
9	ITPKA_12_5800	ITPKA	gtgtacttcagagaggacac	0.5788964
14	ITPKA_15_5800	ITPKA	gggatgctctcaagattagc	0.4267269
4	ITPKA_0_8700	ITPKA	gcgaggacggctatttgctg	0.3086007
5	ITPKA_10_1450	ITPKA	ggccaaatttagggctcccc	0.0961843
15	ITPKA_16_2900	ITPKA	gtgtcttcaaggctccgaa	0.0250445
13	ITPKA_15_2900	ITPKA	ggcatgagcaggtgtcttca	0.0000000
12	ITPKA_14_8700	ITPKA	ggaggctctgccctctccag	-0.0364790
2	ITPKA_0_2900	ITPKA	gaggatgttcaagcttctcc	-0.0990264
7	ITPKA_11_2900	ITPKA	ggctttcctaaccagccag	-0.2495652
6	ITPKA_10_8700	ITPKA	ggaccaggtgccagccacta	-0.5905395
11	ITPKA_13_8700	ITPKA	gggcaaaggcttcttcctc	-0.7691593
1	ITPKA_0_0	ITPKA	gcgaggacgtgggtcaggtta	-0.8777683
10	ITPKA_12_8700	ITPKA	gccagggtttgccaccc	-0.9386408
8	ITPKA_11_8700	ITPKA	gaccagggtgecagccactaa	-0.9836681
16	ITPKA_16_7250	ITPKA	ggacatgtacaagaaaatgc	-1.0849872

SGK2

In addition to the plots below, the following information has been retrieved via biomaRt:

ENSEMBL ID (links to Ensembl) [ENSG00000101049](#)

HGNC SYMBOL (links to GeneCards) [SGK2](#)

GENE DESCRIPTION

serum/glucocorticoid regulated kinase 2 [Source:HGNC Symbol;Acc:HGNC:13900]

GO TERM

positive regulation of transporter activity

MIM GENE DESCRIPTION

SERUM/GLUCOCORTICOID-REGULATED KINASE 2; SGK2

ENSEMBL PROTEIN ID

ENSP00000392795

PROTEIN FAMILY DESCRIPTION

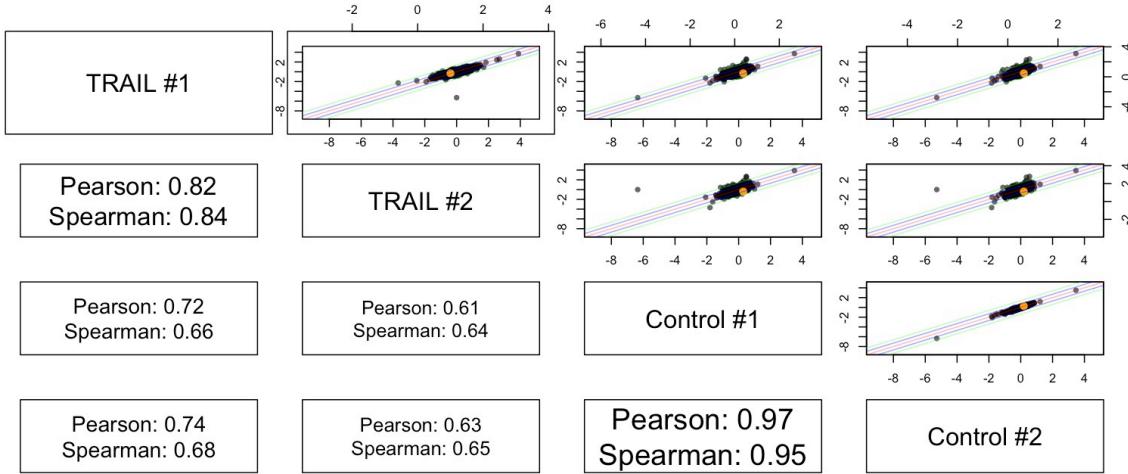
SERINE/THREONINE KINASE EC_2.7.11.1 SERUM/GLUCOCORTICOID REGULATED KINASE

Wilcox p-value: 0.9671744

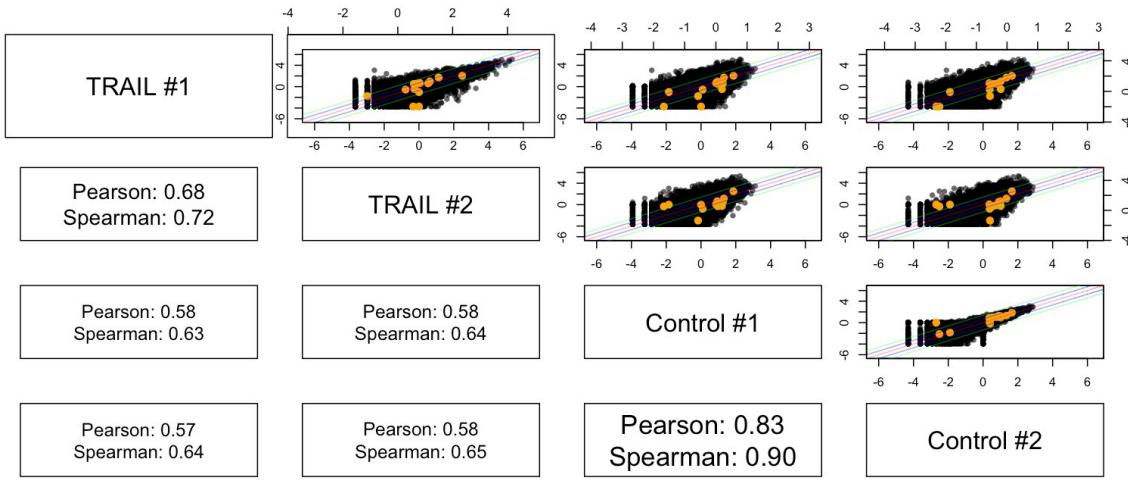
DESeq2 p-value: 0.04938286

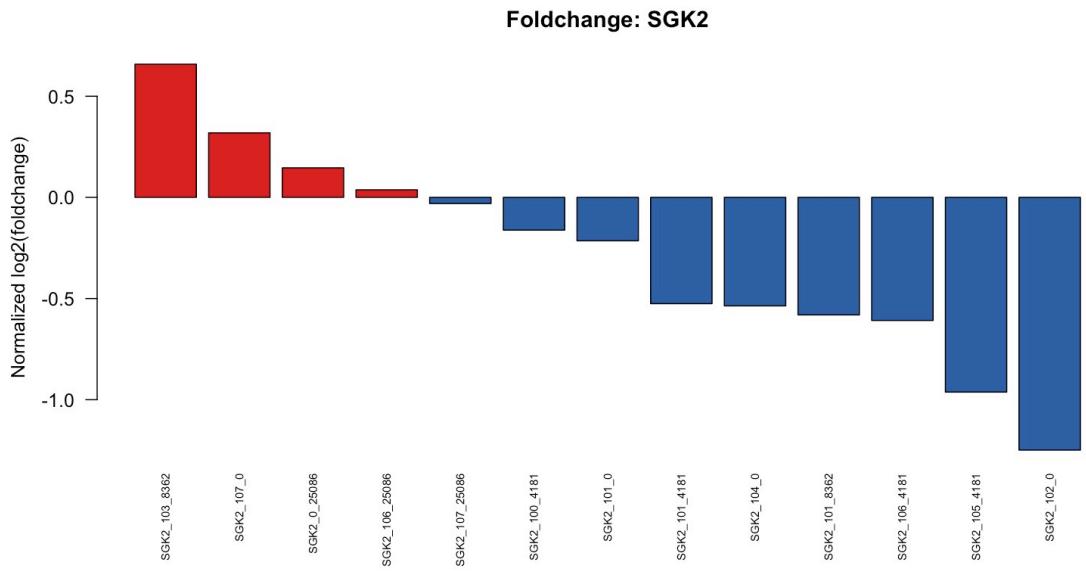
MAGECK p-value: 0.79024

Gene Scatter for SGK2
TRAILscreen

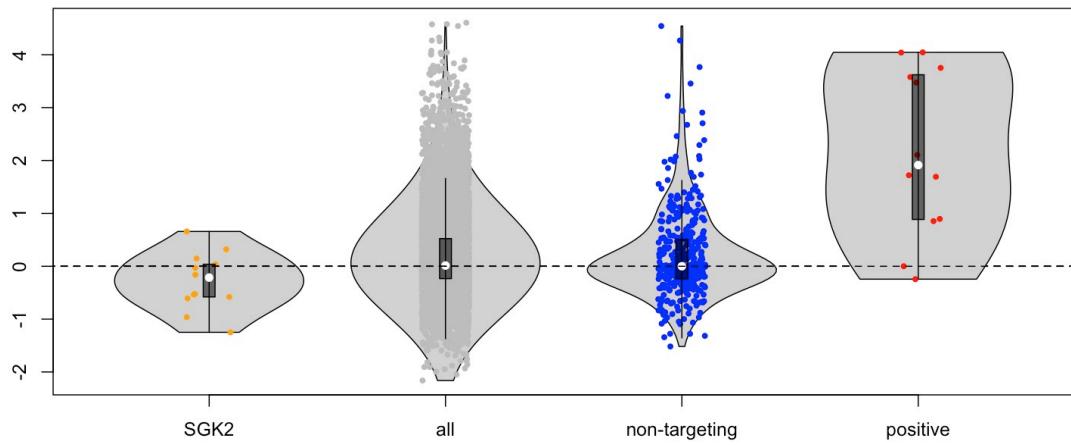


sgRNA Scatter for SGK2
TRAILscreen





Log2 Foldchange of sgRNAs for SGK2 compared to sgRNA from all, non-targeting and targeting control:



	designs	genes	sequence	log2Foldchange
7	SGK2_103_8362	SGK2	ggctccccatctgtataatg	0.6581153
12	SGK2_107_0	SGK2	gttttccactaacgtcatag	0.3187377
1	SGK2_0_25086	SGK2	gagtccaggactggcaggac	0.1458818
10	SGK2_106_25086	SGK2	ggtaacaagacttgaggaa	0.0372740
13	SGK2_107_25086	SGK2	gggtgaacaagaacttgaggaa	-0.0304471
2	SGK2_100_4181	SGK2	ggaacaccatctcacccctag	-0.1618814
3	SGK2_101_0	SGK2	gcctctcacctgaaaactcc	-0.2146417
4	SGK2_101_4181	SGK2	gactggagacttctgttccc	-0.5254519
8	SGK2_104_0	SGK2	gctaaaaccgctatagtcct	-0.5363070
5	SGK2_101_8362	SGK2	ggcttcaggaaaaccagcc	-0.5808980
11	SGK2_106_4181	SGK2	ggggctagctgtatgtcacg	-0.6085201
9	SGK2_105_4181	SGK2	ggggctagctgtatgtcacgc	-0.9623739
6	SGK2_102_0	SGK2	aatcctcagcactgagcac	-1.2491888

PKMYT1

In addition to the plots below, the following information has been retrieved via biomaRt:

ENSEMBL ID (links to Ensembl) [ENSG00000127564](#)

HGNC SYMBOL (links to GeneCards) [PKMYT1](#)

GENE DESCRIPTION

protein kinase, membrane associated tyrosine/threonine 1 [Source:HGNC Symbol;Acc:HGNC:29650]

GO TERM

MIM GENE DESCRIPTION

PROTEIN KINASE, MEMBRANE-ASSOCIATED TYROSINE/THREONINE, 1; PKMYT1;;CDC2-INHIBITORY KINASE, MEMBRANE-ASSOCIATED TYROSINE/THREONINE, 1;MYT1

ENSEMBL PROTEIN ID

ENSP00000461628

PROTEIN FAMILY DESCRIPTION

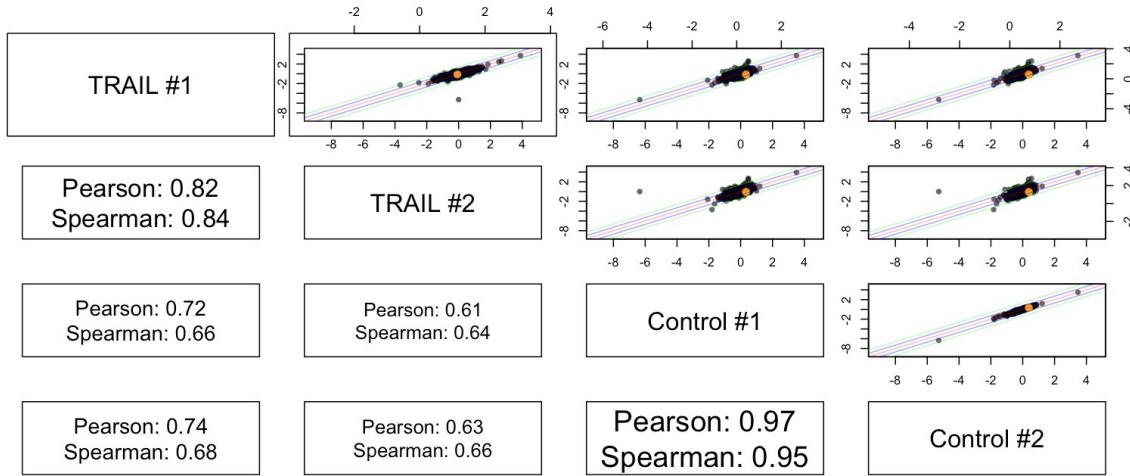
UNKNOWN

Wilcox p-value: 0.9671744

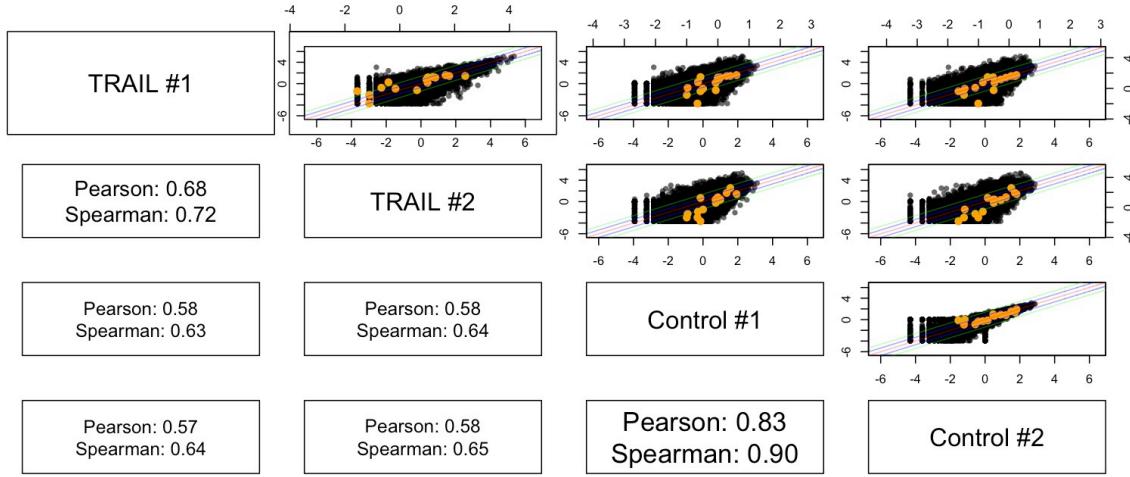
DESeq2 p-value: 0.8398297

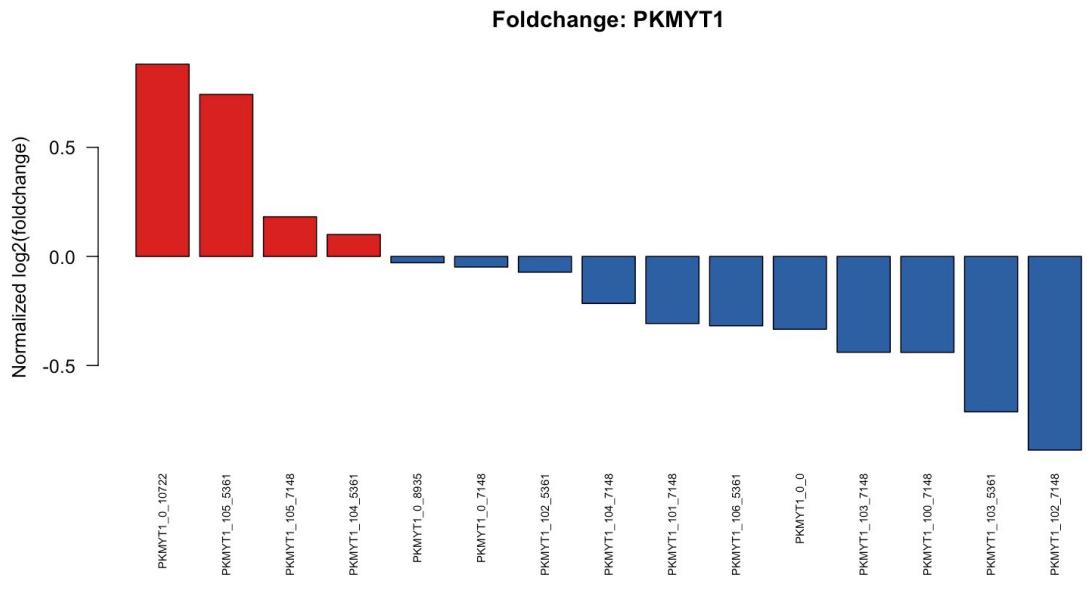
MAGECK p-value: 0.79024

Gene Scatter for PKMYT1
TRAILscreen

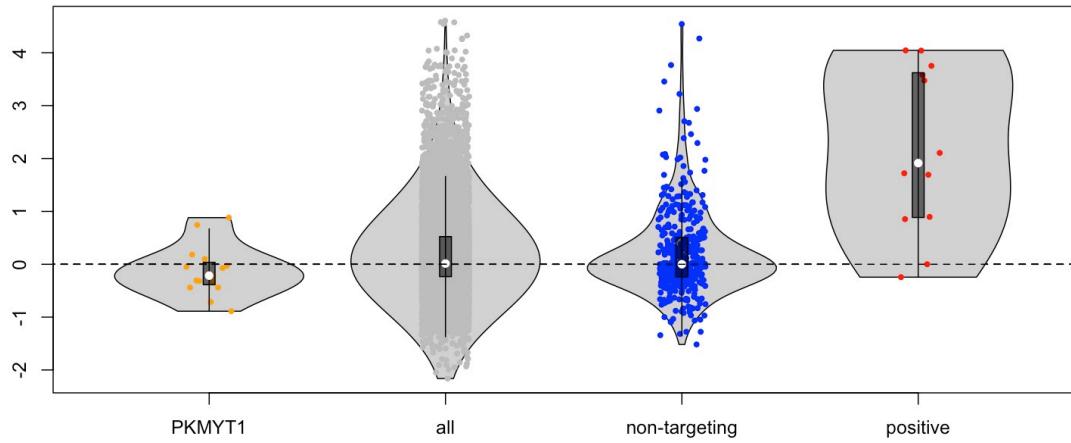


sgRNA Scatter for PKMYT1
TRAILscreen





Log2 Foldchange of sgRNAs for PKMYT1 compared to sgRNA from all, non-targeting and targeting controls



	designs	genes	sequence	log2Foldchange
2	PKMYT1_0_10722	PKMYT1	ggggtgacctccgcagcttc	0.8814200
13	PKMYT1_105_5361	PKMYT1	ggctggctcacccctgccagc	0.7427912
14	PKMYT1_105_7148	PKMYT1	gtgggtaccaccccttcc	0.1817254
11	PKMYT1_104_5361	PKMYT1	gccagctggctacagccccct	0.1005956
4	PKMYT1_0_8935	PKMYT1	ggtgccactcagagggtggcg	-0.0288452
3	PKMYT1_0_7148	PKMYT1	gctcaaaggcctgccagcctg	-0.0485978
7	PKMYT1_102_5361	PKMYT1	ggatgacgacagccttagggt	-0.0722303
12	PKMYT1_104_7148	PKMYT1	ggaggacggccggctatg	-0.2154798
6	PKMYT1_101_7148	PKMYT1	ggcccgcagaattggccgagg	-0.3074704
15	PKMYT1_106_5361	PKMYT1	ggcaggtaagctccgacag	-0.3181115
1	PKMYT1_0_0	PKMYT1	gccccggatgcacagtctga	-0.3338034
10	PKMYT1_103_7148	PKMYT1	gcgttccatgtcaccattcc	-0.4395002
5	PKMYT1_100_7148	PKMYT1	gcccccaagttggccgaggt	-0.4400416
9	PKMYT1_103_5361	PKMYT1	gggatgacgacagectaggg	-0.7124507
8	PKMYT1_102_7148	PKMYT1	gtcaccattccggggccca	-0.8879269

FASTK

In addition to the plots below, the following information has been retrieved via biomaRt:

ENSEMBL ID (links to Ensembl) [ENSG00000164896](#)

HGNC SYMBOL (links to GeneCards) [FASTK](#)

GENE DESCRIPTION

Fas-activated serine/threonine kinase [Source:HGNC Symbol;Acc:HGNC:24676]

GO TERM

protein phosphorylation

MIM GENE DESCRIPTION

FAS-ACTIVATED SERINE/THREONINE KINASE; FASTK;;FAST

ENSEMBL PROTEIN ID

ENSP00000444498

PROTEIN FAMILY DESCRIPTION

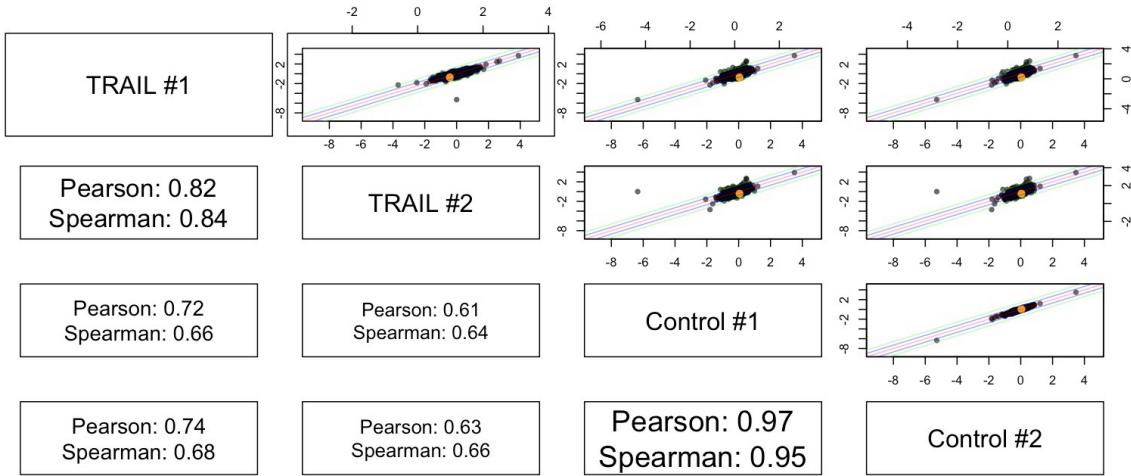
FAS ACTIVATED SERINE/THREONINE KINASE FAST KINASE EC_2.7.11.8

Wilcox p-value: 0.9671744

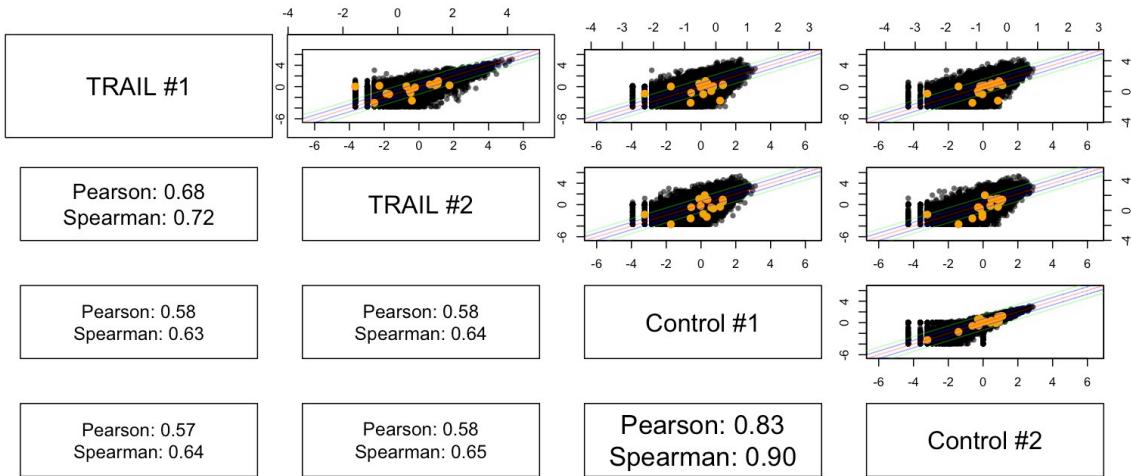
DESeq2 p-value: 0.1427661

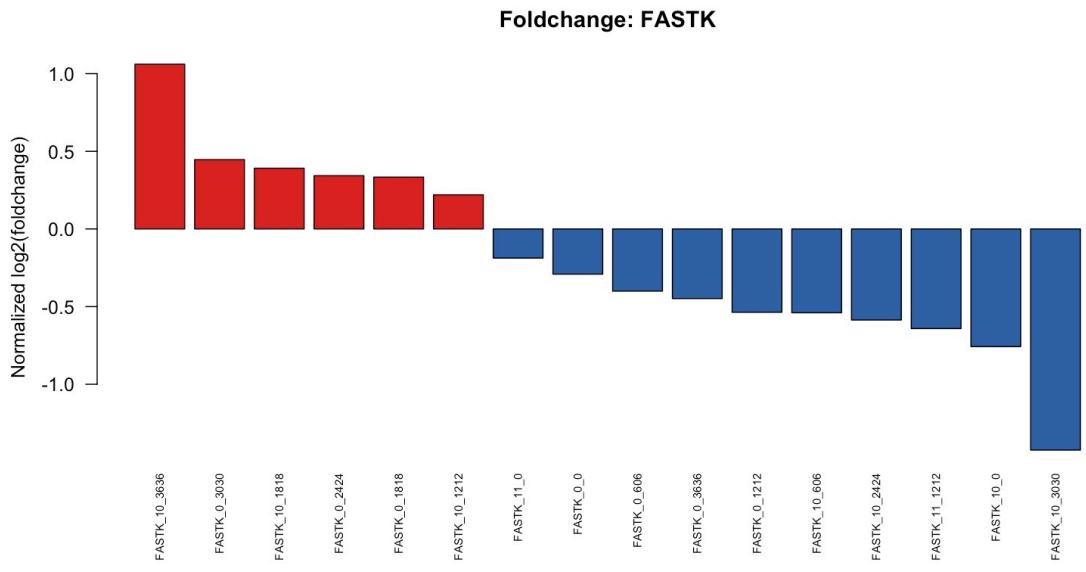
MAGECK p-value: 0.79024

**Gene Scatter for FASTK
TRAILscreen**

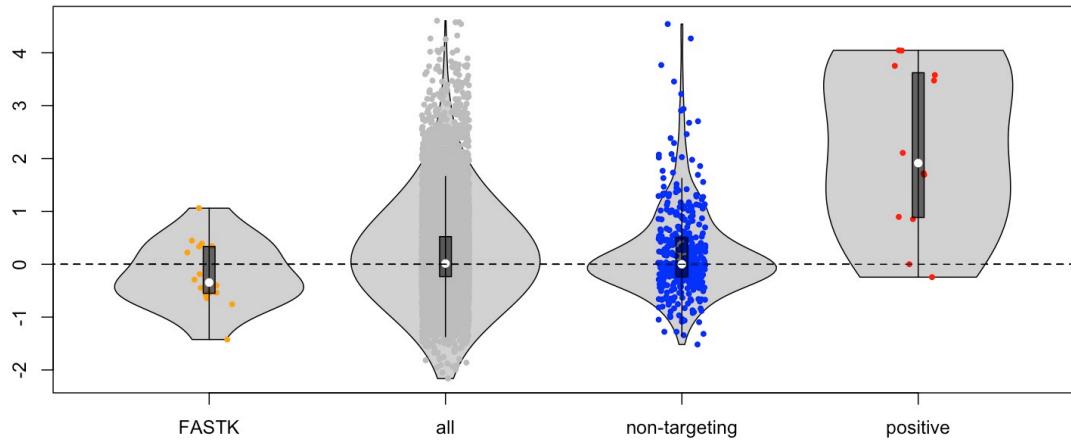


**sgRNA Scatter for FASTK
TRAILscreen**





Log2 Foldchange of sgRNAs for FASTK compared to sgRNA from all, non-targeting and targeting control



	designs	genes	sequence	log2Foldchange
13	FASTK_10_3636	FASTK	gccaatccgaaggcagctat	1.0609902
5	FASTK_0_3030	FASTK	gcactgggcctcctccaaac	0.4466181
10	FASTK_10_1818	FASTK	ggccaggagcaccatcaegt	0.3911856
4	FASTK_0_2424	FASTK	gagacatgtaaaagtatcatg	0.3431926
3	FASTK_0_1818	FASTK	ggtgtgtctgcgttcaggaaa	0.3339876
9	FASTK_10_1212	FASTK	gcatgctgtgcacaggaggt	0.2198671
15	FASTK_11_0	FASTK	gctggtagcccatcaggcct	-0.1872616
1	FASTK_0_0	FASTK	gggcctggagttctgcctc	-0.2910421
7	FASTK_0_606	FASTK	gtccttgcgtgactgaggagaa	-0.4000973
6	FASTK_0_3636	FASTK	gacggtgctgggttccatgc	-0.4481787
2	FASTK_0_1212	FASTK	gccaggatccctctaaggca	-0.5365657
14	FASTK_10_606	FASTK	gaggggtgcctgtgggagg	-0.5394610
11	FASTK_10_2424	FASTK	gagcaggagcaagcgttcct	-0.5862362
16	FASTK_11_1212	FASTK	ggaagcaggggtggcacccc	-0.6413484
8	FASTK_10_0	FASTK	gcaggagctggtagcccatc	-0.7574409
12	FASTK_10_3030	FASTK	gcgcgccaccactactcgg	-1.4239192

AK1

In addition to the plots below, the following information has been retrieved via biomaRt:

ENSEMBL ID (links to Ensembl) [ENSG00000106992](#)

HGNC SYMBOL (links to GeneCards) [AK1](#)

GENE DESCRIPTION

adenylate kinase 1 [Source:HGNC Symbol;Acc:HGNC:361]

GO TERM

MIM GENE DESCRIPTION

ADENYLYLATE KINASE 1; AK1;;ADENYLYLATE KINASE, SOLUBLE

ENSEMBL PROTEIN ID

ENSP00000448741

PROTEIN FAMILY DESCRIPTION

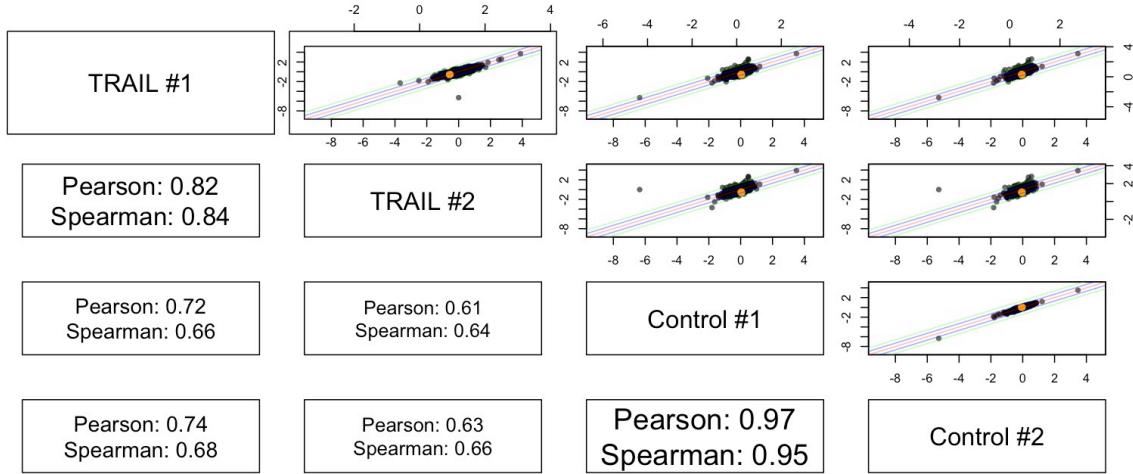
UNKNOWN

Wilcox p-value: 0.9671744

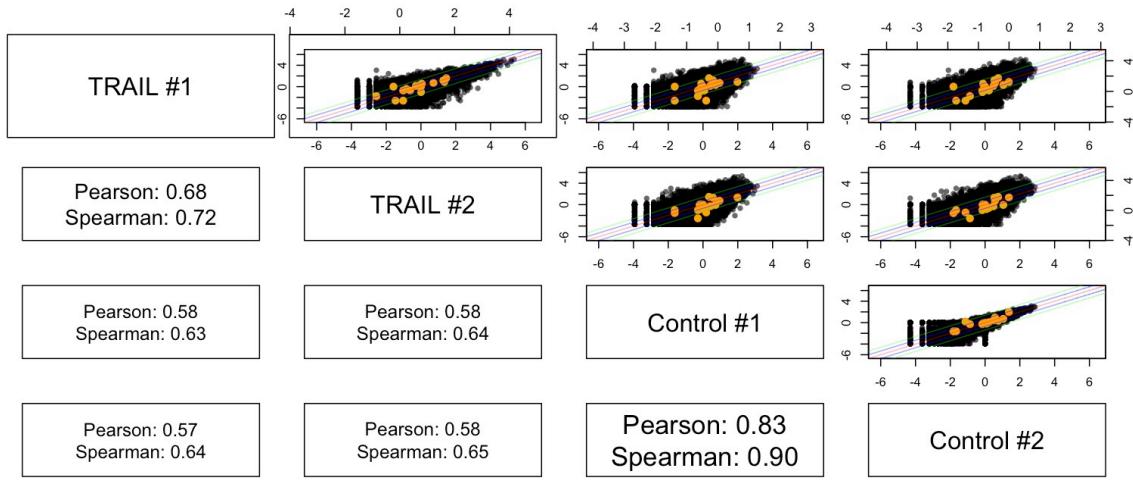
DESeq2 p-value: 0.1097052

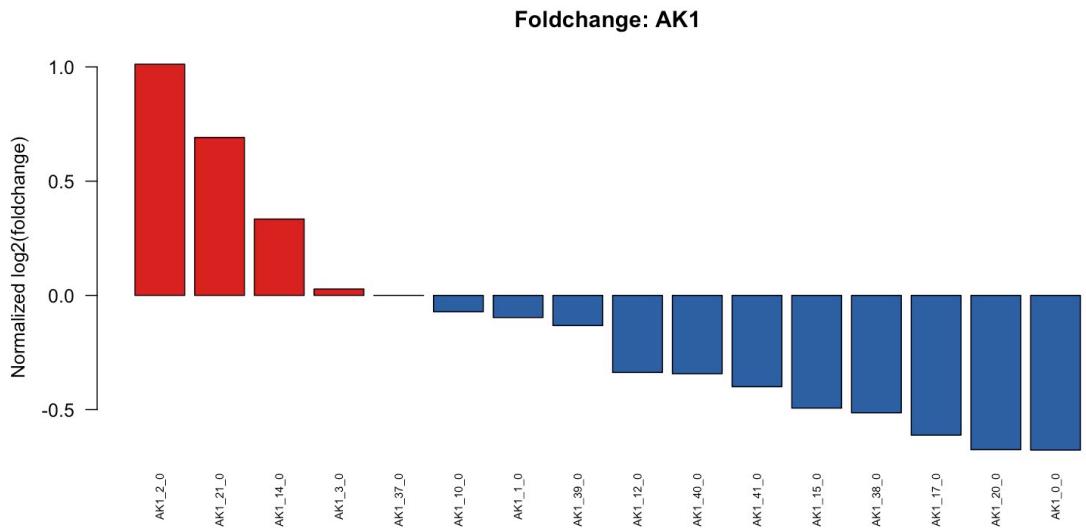
MAGECK p-value: 0.79024

Gene Scatter for AK1
TRAILscreen

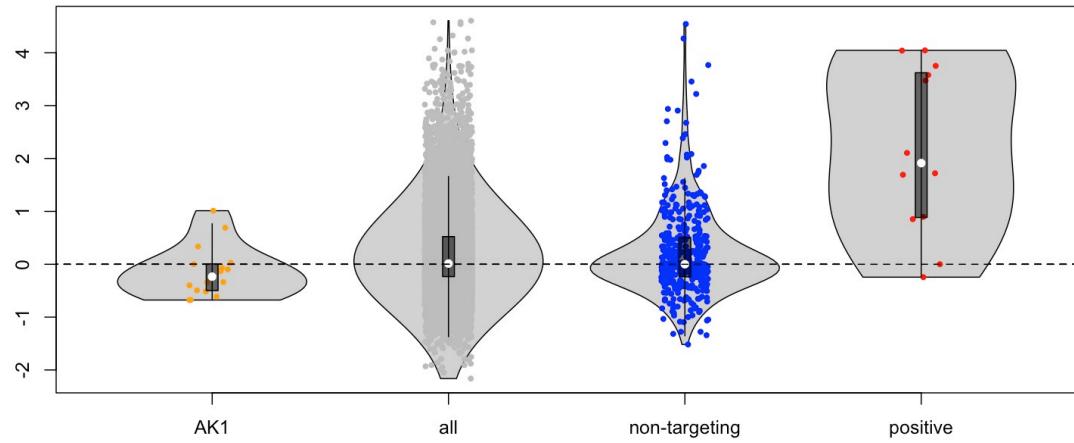


sgRNA Scatter for AK1
TRAILscreen





Log2 Foldchange of sgRNAs for AK1 compared to sgRNA from all, non-targeting and targeting controls



	designs	genes	sequence	log2Foldchange
10	AK1_2_0	AK1	ggaacatatgctcagagcga	1.0119537
9	AK1_21_0	AK1	gcttaaaggagccagctt	0.6911687
4	AK1_14_0	AK1	gaacggagggttgagggct	0.3342489
14	AK1_3_0	AK1	gaacatatgctcagagcgat	0.0280782
11	AK1_37_0	AK1	gtcaaaaaatgaaagcgcgc	0.0000000
2	AK1_10_0	AK1	gggccacaagaaggctct	-0.0714469
7	AK1_1_0	AK1	ggatttcattcggcaggcg	-0.0968484
13	AK1_39_0	AK1	gcaggaagggttctccccag	-0.1320204
3	AK1_12_0	AK1	gagggttgtggctggcaaagg	-0.3372427
15	AK1_40_0	AK1	ggttctcccaggggattc	-0.3427298
16	AK1_41_0	AK1	ggttctcccccaggggattct	-0.3996150
5	AK1_15_0	AK1	gttaggggctggggacttg	-0.4933369
12	AK1_38_0	AK1	gcgcaggaagggttctcccc	-0.5140515
6	AK1_17_0	AK1	gcacatgaatcaactccaac	-0.6116374
8	AK1_20_0	AK1	ggcttaaaggagccagct	-0.6754054
1	AK1_0_0	AK1	gtcagtccaggccccggca	-0.6771400

Compare Analysis

On the following pages, a comparison between the hit analysis methods is generated.

Enriched

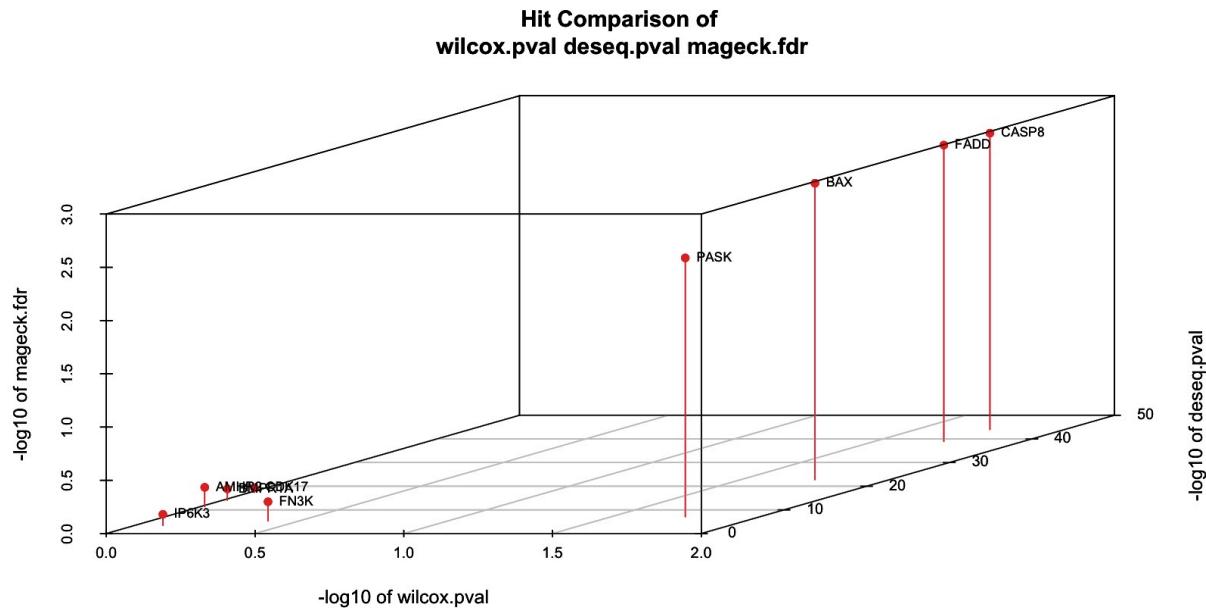
List

Moreover, the **5 % top enriched hits** sorted according to **MAGECK** are stored in **TRAILscreen-COMPARE-HITS.xls** and are listed below:

	wilcox.log2fc	wilcox.pval	deseq.log2fc	deseq.pval	mageck.fdr	mageck.rank
CASP8	2.8382733	0.0178241	2.8539899	0.0000000	0.001650	1
BAX	2.4706303	0.0178241	2.0761255	0.0000000	0.001650	2
FADD	2.8332735	0.0184341	2.7466780	0.0000000	0.001650	3
PASK	1.3650980	0.0178241	1.3056495	0.0000001	0.003713	4
TYRO3	1.0116807	0.9671744	0.6568340	1.0000000	0.659241	5
AMHR2	1.4654422	0.9671744	1.5964273	0.0000000	0.659241	6
FN3K	1.4685534	0.4030853	1.2257973	0.0000044	0.661245	7
PRKY	1.2424191	0.9671744	1.1629272	0.0000322	0.785149	8
CDK5RAP3	0.8994121	0.4202992	0.6707720	0.4964897	0.785149	9
ROR2	0.6903593	0.9671744	0.4127949	1.0000000	0.785149	10
BMPR1A	1.6970986	0.9671744	1.6606699	0.0000000	0.785149	11
DGKI	1.0784097	1.0000000	0.8176321	0.0921921	0.785149	12
IP6K3	1.3336231	0.8019777	0.9775242	0.0004042	0.785149	13
SGK1	1.0084174	0.9671744	1.0027240	0.0169285	0.785149	14
CSNK1A1	0.9112430	0.9802939	0.2043810	1.0000000	0.785149	15
RPS6KA5	1.0125970	0.9671744	2.0613922	0.0000000	0.792340	16
FGFR2	0.9059273	0.9802939	0.6981811	0.2598086	0.792340	17
FER	0.9117190	0.9671744	0.8130390	0.0356230	0.792340	18
GAK	0.5387169	0.9671744	0.1504273	1.0000000	0.792340	19
MYC	0.9824296	0.9671744	1.0493447	0.0000603	0.819189	20
NME7	1.0651572	0.9671744	0.7293105	1.0000000	0.819189	21
MAP3K13	0.8027186	0.9802939	0.7890949	0.1618026	0.903465	22
CDK17	1.4075806	0.9671744	1.9749507	0.0000000	0.903465	23
UCK1	0.9366588	0.9671744	0.8130611	0.0389347	0.903465	24
SPA17	0.9005421	0.4030853	0.6442567	0.7318362	0.903465	25
STK32A	0.7202280	0.9671744	0.5301267	1.0000000	0.903465	26
MVK	0.8969374	0.9671744	0.5232427	1.0000000	0.912769	27
BIRC5	1.0329737	1.0000000	0.4600186	1.0000000	0.912769	28
MAP2K7	1.4371620	1.0000000	1.1032489	0.0001706	0.912769	29
TNFRSF8	0.9060177	0.9820183	0.8932955	1.0000000	0.919967	30
RIPK2	1.0454989	0.9671744	0.9771641	0.0006398	0.987129	31
MAP2K3	0.6951014	1.0000000	0.5789501	1.0000000	0.987129	32
CDK9	1.0234281	0.9820183	0.6566444	1.0000000	0.987129	33
DUSP10	0.9243816	0.9671744	0.8461876	0.6000355	0.987129	34
LMTK3	1.4188888	1.0000000	1.0154113	0.0001587	0.987129	35
TK2	0.8383299	0.9671744	0.4435478	1.0000000	0.987129	36
NLK	0.8116484	0.9671744	0.7749996	1.0000000	0.987129	37
PRKD2	0.8994031	0.9671744	0.5585946	1.0000000	0.987129	38
PRPS1	1.2220187	0.9802939	1.0154924	0.0010360	0.987129	39
SGK223	0.7552550	1.0000000	0.5012950	1.0000000	0.987129	40
SRPK2	0.7442764	0.9671744	0.8655405	0.0257051	0.987129	41

3D Scatterplot

This plot shows you the p-value of overlapping enriched genes of all three methods. The best hits will show up in the upper right corner.



Depleted

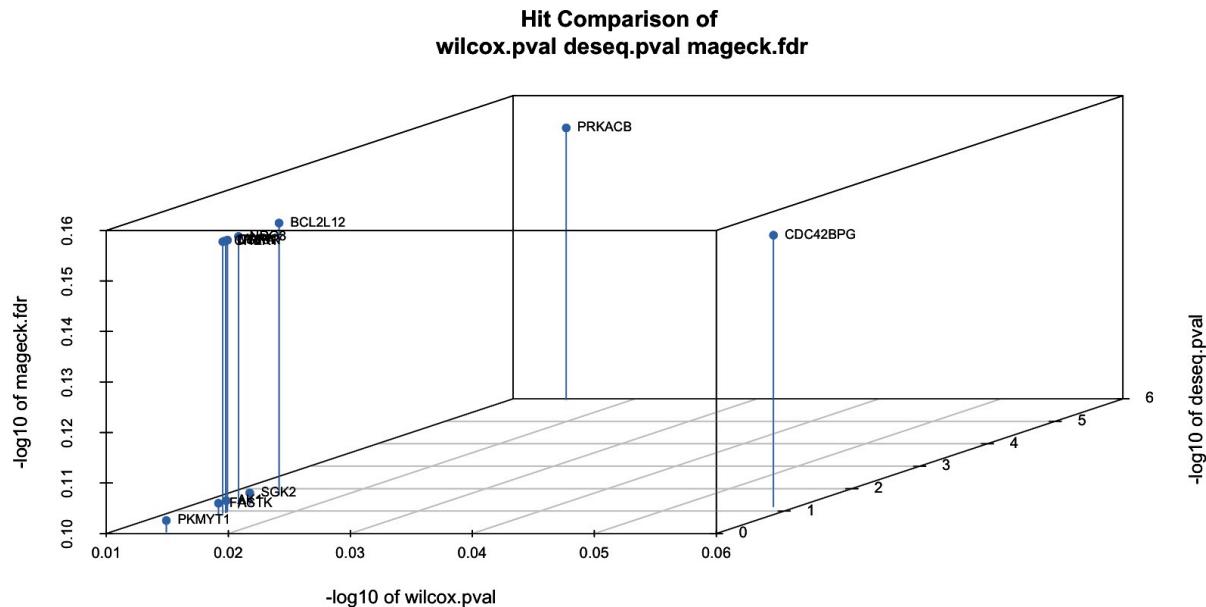
List

Moreover, the **5 % top depleted hits** sorted according to MAGECK are stored in **TRAILSscreen-COMPARE-HITS.xls** and are listed below:

	wilcox.log2fc	wilcox.pval	deseq.log2fc	deseq.pval	mageck.fdr	mageck.rank
TNFRSF13C	NA	NA	-0.0773572	1.0000000	0.701894	1
DYRK2	NA	NA	-0.1075289	1.0000000	0.701894	2
CDC42BPG	-0.1892980	0.8749233	-0.9735155	0.0633304	0.701894	3
CHEK1	-0.0937255	0.9671744	-0.8384986	0.1231337	0.701894	4
RAPGEF3	NA	NA	NA	NA	0.701894	5
TNFRSF11A	NA	NA	NA	NA	0.701894	6
CSF1R	-0.1386295	0.9671744	-0.7419327	0.1115685	0.701894	7
PTK6	-0.0624989	0.9671744	-0.4113096	1.0000000	0.701894	8
BMF	NA	NA	-0.3582229	1.0000000	0.701894	9
TESK2	NA	NA	-0.4762269	1.0000000	0.701894	10
NUAK2	NA	NA	NA	NA	0.701894	11
AURKA	NA	NA	-0.1312312	1.0000000	0.701894	12
PRKACB	-0.2086010	0.9671744	-1.3268439	0.0000011	0.701894	13
NRG3	-0.1267339	0.9671744	-0.7790845	0.0723033	0.701894	14
TNFRSF13B	NA	NA	-0.1269107	1.0000000	0.701894	15
AZU1	-0.1144076	0.9671744	-0.6156798	1.0000000	0.701894	16
WIF1	-0.0661615	0.9671744	-0.8396864	0.0242731	0.701894	17
MAPK7	-0.0149634	0.9671744	-0.7443061	0.1051081	0.701894	18
HK3	NA	NA	-0.8896877	0.0161867	0.701894	19
BCL2L12	-0.0770045	0.9671744	-0.8493349	0.0182295	0.701894	20
TP53BP1	NA	NA	-0.0432170	1.0000000	0.701894	21
ITPKA	-0.0990443	0.9671744	-0.9804692	0.1123445	0.701894	22
JAK3	NA	NA	NA	NA	0.701894	23
CSNK1A1L	NA	NA	-0.4230571	1.0000000	0.736436	24
PAK7	NA	NA	-0.2202468	1.0000000	0.736436	25
MAP3K6	NA	NA	NA	NA	0.790240	26
CAMK1G	NA	NA	-0.4575927	1.0000000	0.790240	27
PFKFB1	NA	NA	-0.2941408	1.0000000	0.790240	28
SGK2	-0.1958993	0.9671744	-0.7987094	0.0493829	0.790240	29
PRKAA1	NA	NA	-0.5851408	1.0000000	0.790240	30
PKMYT1	-0.0488289	0.9671744	-0.6395897	0.8398297	0.790240	31
TSSK3	NA	NA	-0.4741866	1.0000000	0.790240	32
NTRK3	NA	NA	-0.1207013	1.0000000	0.790240	33
FASTK	-0.0655226	0.9671744	-0.8297426	0.1427661	0.790240	34
AK1	-0.0566054	0.9671744	-0.7584758	0.1097052	0.790240	35
CLK3	NA	NA	-0.4754391	1.0000000	0.808760	36
MAPKAPK5	NA	NA	NA	NA	0.808760	37
PTPRG	NA	NA	-0.2841110	1.0000000	0.808760	38
CDC42SE2	NA	NA	-0.1443949	1.0000000	0.808760	39
ACVR1L	NA	NA	-0.4256669	1.0000000	0.808760	40
PAPSS1	NA	NA	-0.4826401	1.0000000	0.808760	41

3D Scatterplot

This plot shows you the p-value of overlapping depleted genes of all three methods. The best hits will show up in the upper right corner.



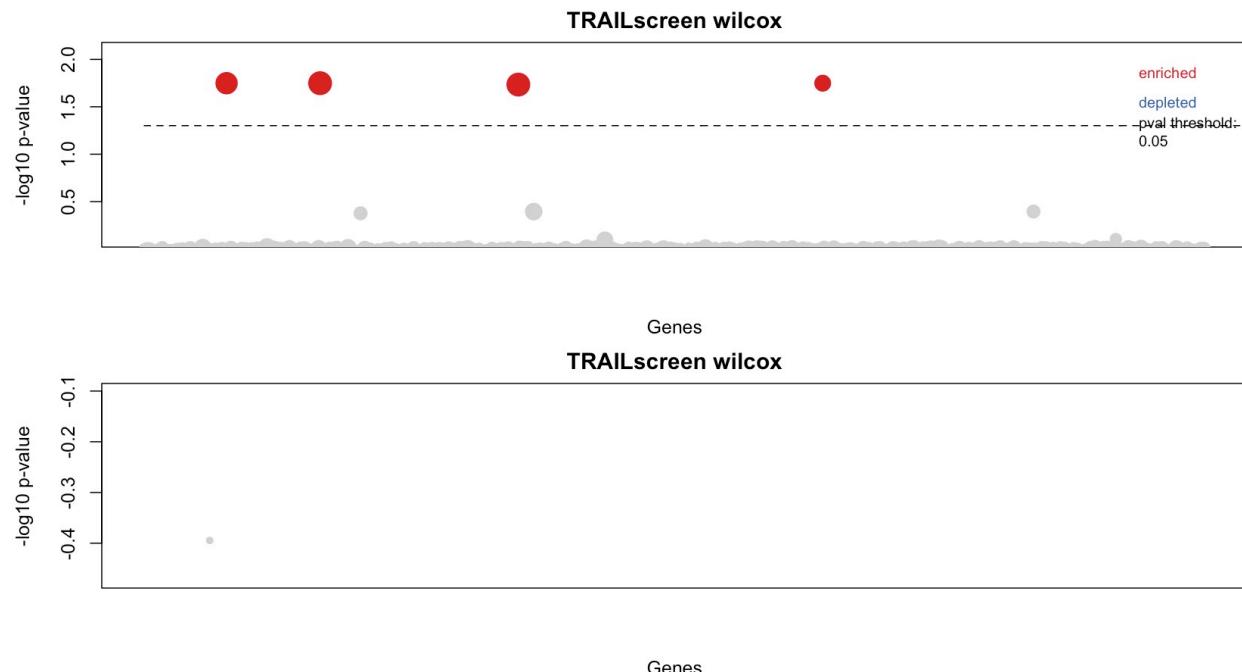
Visualize Analysis

The following pages present a visual representation of the p-value for single genes within all analysis methods. *Significantly* enriched genes, which had a corrected p-value below the threshold set for each method, are highlighted in **red**.

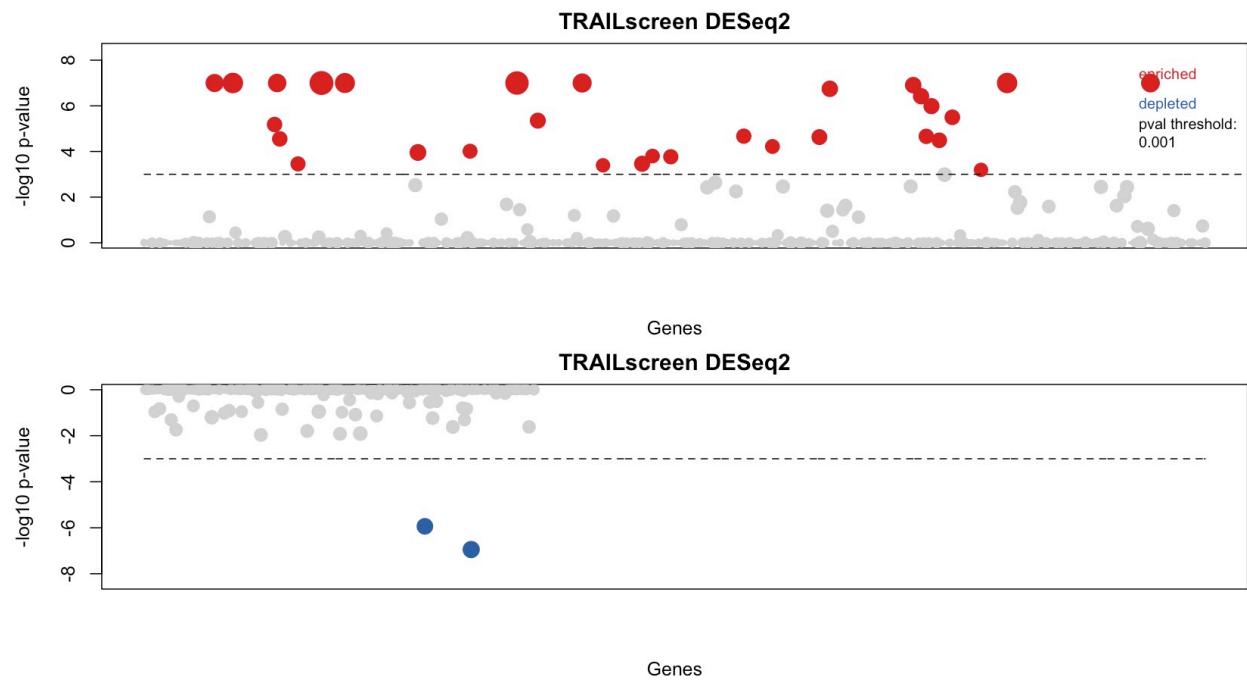
Significantly depleted genes, which had a corrected p-value below the threshold set for each method, are highlighted in **blue**.

Moreover, the number of significant sgRNAs is presented for MAGeCK as well.

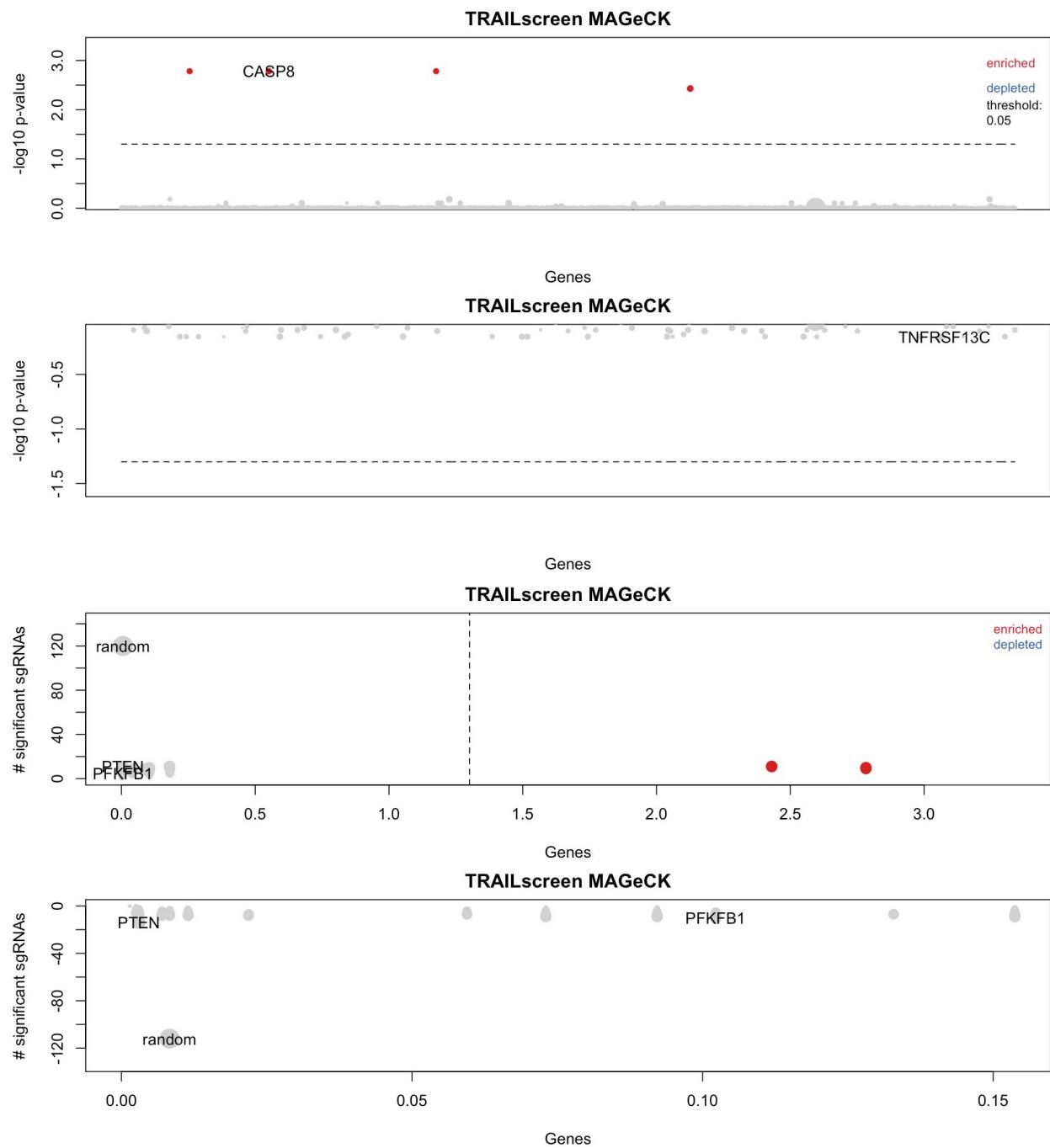
Wilcox



DESeq2



MAGeCK



Final Gene Table

A final table with all information for each gene is stored in
`./data/TRAILscreen_FINAL.xls`.

Annotate Hit Candidates

Hit candidates are annotated with additional information from **biomaRt**.

The following information is retrieved: **Database:** ensembl **Dataset:** hsapiens_gene_ensembl **Filters:** ensembl_gene_id description name_1006

The annotated list of all hit candidates is stored in

```
./data  
** TRAILscreen_ANNOTATION.xls **
```

Data Extraction, Mapping and Files

Dataset	.fastq file name	Description
Control #1	2180_CRISPR_KO3_Drug_DMSO1_extracted-designs.txt	Control #1
Control #2	2277_CRISPR_KO3_Drug_DMSO2_extracted-designs.txt	Control #2
Treatment #1	2176_CRISPR_KO3_Drug_TRAIL1_extracted-designs.txt	TRAIL #1
Treatment #2	2275_CRISPR_KO3_Drug_TRAIL2_extracted-designs.txt	TRAIL #2

The data is located in

./data

and the script files for data extraction and mapping are located in

./scripts.

All file-based output (e.g. tables) from MAGeCK is stored in:

/Users/janwinter/Documents/PhD/GitHub/caRpools.

Parameter	Value
Reverse Complement Sequence	FALSE
Pattern of Data Extraction	ACC(.{20})GT{2,4}AGAGC
Maschine Identifier FASTq	M01100
Create Bowtie2 Index?	FALSE
Reference .fasta File	pilot-screen-library
Bt2 Threads	4
Bt2 Sensitivity	very-sensitive-local
sgRNA Oligo Match	perfect