CaRpools Report - CRISPR Screen Analysis

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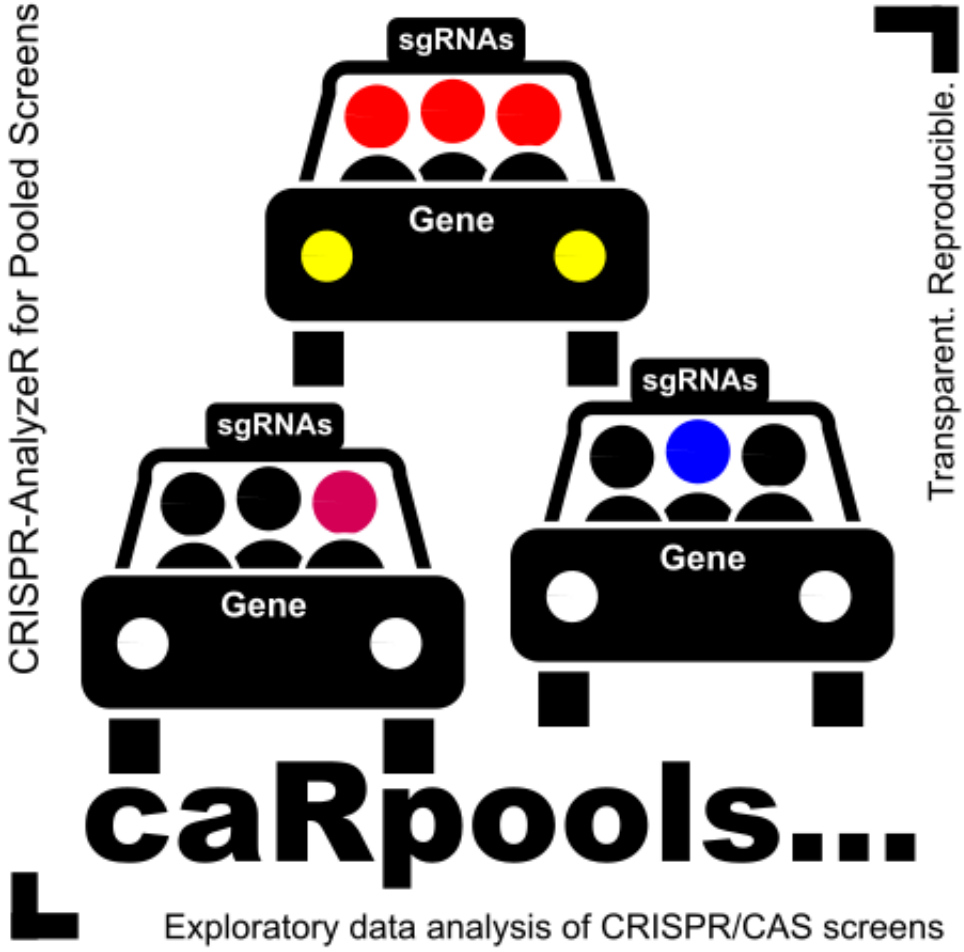

CRISPR-AnalyzeR for Pooled Screens
sgRNAs
Gene
sgRNAs
Gene
sgRNAs
Gene
Transparent. Reproducible.
caRpools...
Exploratory data analysis of CRISPR/CAS screens

Screen

Screen	Information
Screen ID	not apllicable
Screening Date	See puplication: Genome-scale CRISPR-Cas9 knockout screening in human cells. http://www.
Organism	Homo sapiens
Cell Line	A375 cells; www.sciencemag.org/cgi/content/full/science.1247005/DC1.
Drug	www.sciencemag.org/cgi/content/full/science.1247005/DC1.2uM PLX4032
Control	www.sciencemag.org/cgi/content/full/science.1247005/DC1. DMSO
Number of Target	18,080; whole genome library;
Designs per Gene	average of 3-4 sgRNAs per gene; library size was 64,751 sgRNAs
Library	GECKO library; 64,751 unique sgRNA stargeting 18,080 coding genes with an average of 3-4 s
Library Reference File	shalem_lib
NGS	www.sciencemag.org/cgi/content/full/science.1247005/DC1

MIACCS
The MIACCS-file can be found at

./

MIACCS.xls

Description
See puplication: Genome-scale CRISPR-Cas9 knockout screening in human cells. http://www.ncbi.nlm.nih.gov/pubmed/24336571. "…By applying the GeCKO library to A375 cells (which are homozygous for the BRAF V600E mutation), we identified several genes whose loss resulted in resistance to PLX…"

Load Data

Load Files

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

DMSO1
shalem_raw_DMSO1.txt

	DesignID	Readcount
20543	FBXO42_2	15
53677	SRPR_3	69
27909	ISM2_0	169
11836	CHRND_2	35
63431	ZNF324_2	122
18657	ERO1LB_2	50
18639	ERMN_5	291
13616	CRIPT_0	36
63687	ZNF454_1	77
40335	PAX4_3	50

DMSO2
shalem_raw_DMSO2.txt

	DesignID	Readcount
20543	FBXO42_2	100
53677	SRPR_3	75
27909	ISM2_0	192
11836	CHRND_2	66
63431	ZNF324_2	160
18657	ERO1LB_2	104
18639	ERMN_5	477
13616	CRIPT_0	89
63687	ZNF454_1	144
40335	PAX4_3	88

PLX1
shalem_raw_PLX1.txt

	DesignID	Readcount
20543	FBXO42_2	36
53677	SRPR_3	23
27909	ISM2_0	103
11836	CHRND_2	37
63431	ZNF324_2	109
18657	ERO1LB_2	8
18639	ERMN_5	73
13616	CRIPT_0	334
63687	ZNF454_1	23
40335	PAX4_3	26

PLX2
shalem_raw_PLX2.txt

	DesignID	Readcount
20543	FBXO42_2	36
53677	SRPR_3	9
27909	ISM2_0	143
11836	CHRND_2	24
63431	ZNF324_2	161
18657	ERO1LB_2	4
18639	ERMN_5	101
13616	CRIPT_0	552
63687	ZNF454_1	26
40335	PAX4_3	27

Stats

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

General

General stats can be found in
PLX_resistance_YTAR-STATS.xls.
The following read count statistics were calculated for the single datasets.

Readcount	DMSO1	DMSO2	PLX1	PLX2
Mean	177	235	265	308
Median	126	168	70	81
SD	190	249	7284	8452
Min	0	0	0	0
Max	5238	6187	1373768	1630220
# sgRNA not present	205	151	453	741

Missing sgRNAs in Datasets

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

./

PLX_resistance_YTAR_DROPOUT.xls

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

DMSO1: 205 missing sgRNAs

DMSO2: 151 missing sgRNAs

PLX1: 453 missing sgRNAs

PLX2: 741 missing sgRNAs

All Stats

In depth dataset read count stats can be found in

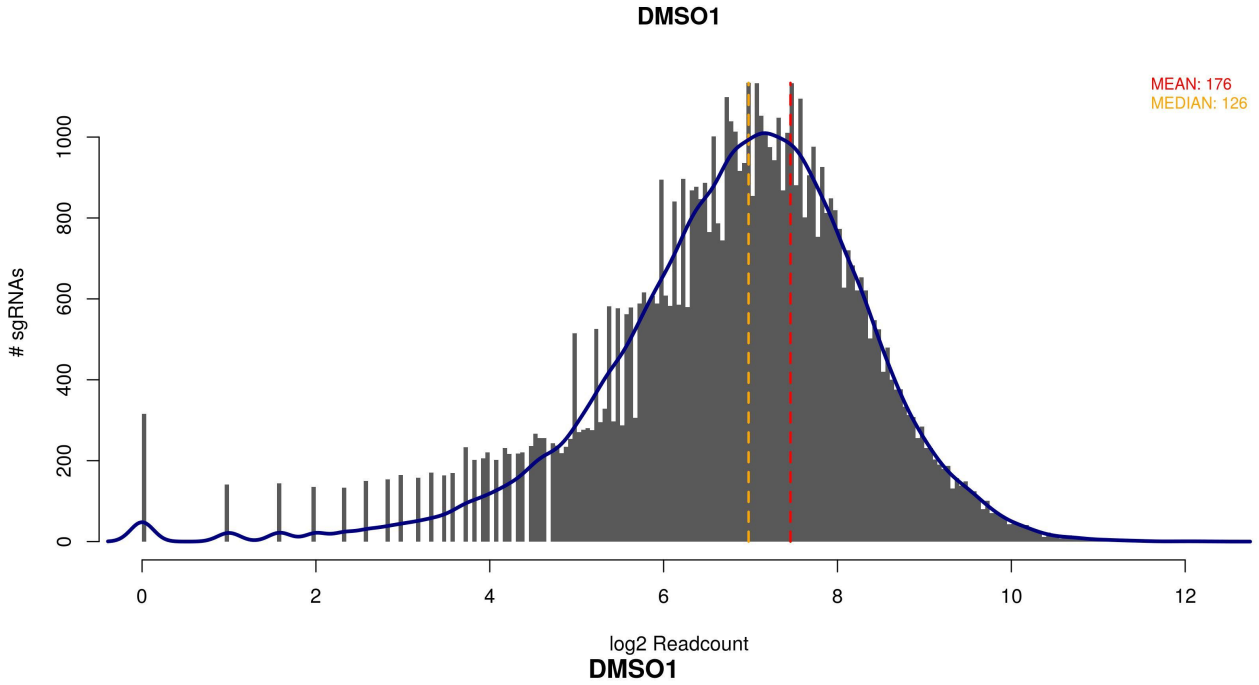
./

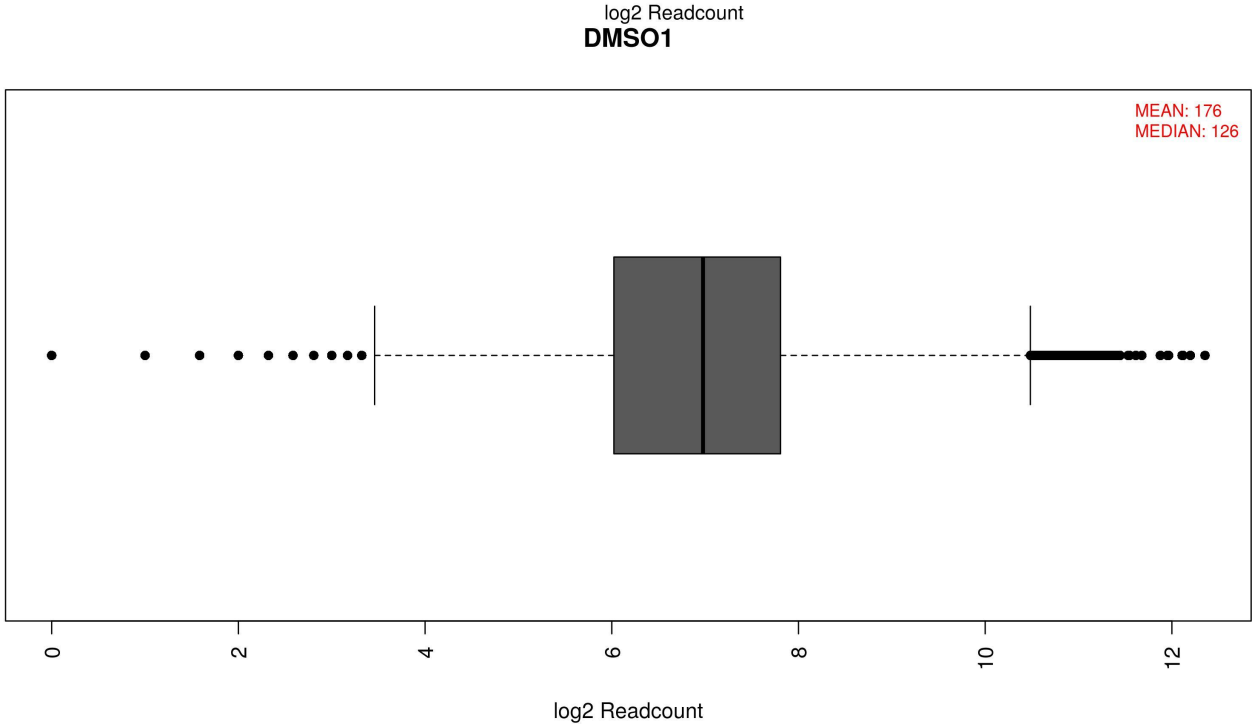
PLX_resistance_YTAR-STATS.xls

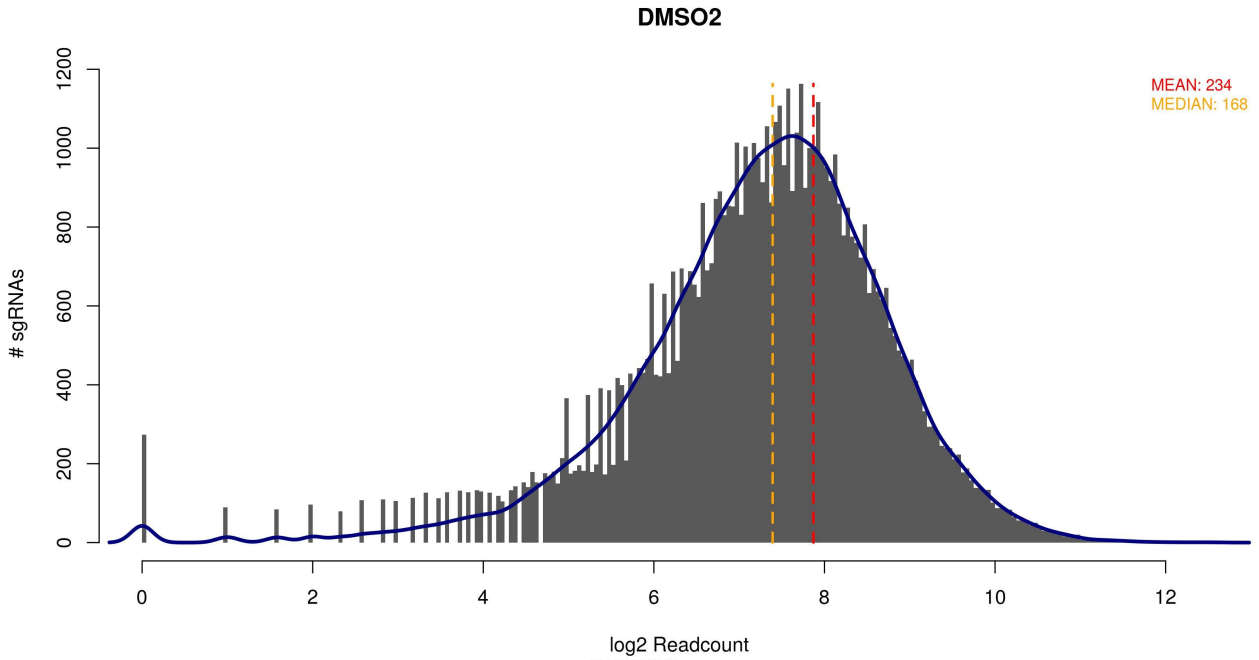
Quality Control

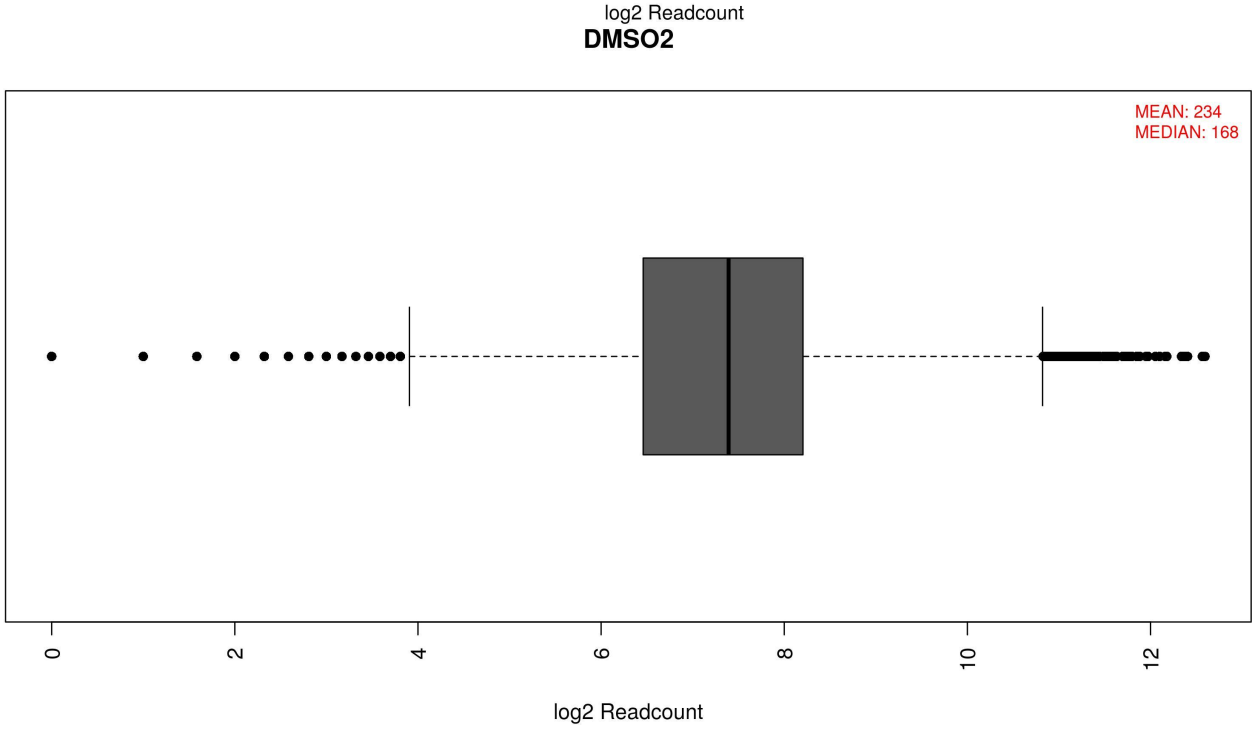
Read Distribution

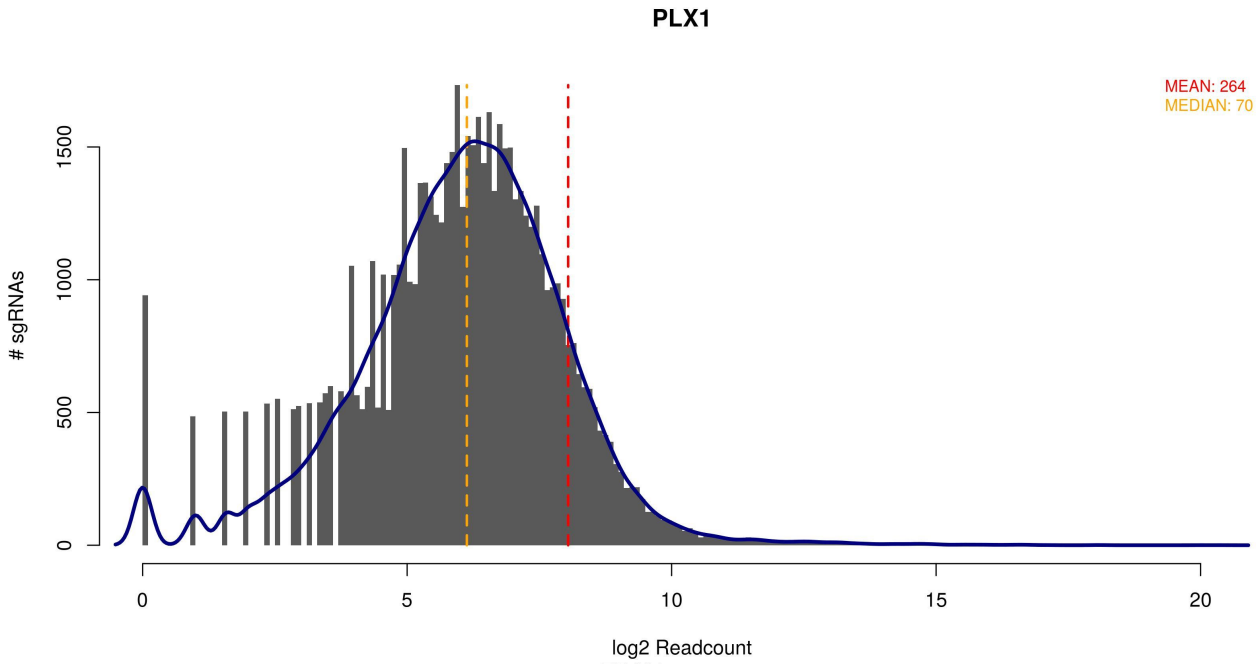
These plots show how the read count of the sgRNAs for each dataset is distributed. Depending on the treatment stringency, e.g. in resistance or dropout screens, the data can show asymmetry. However, the major population should be more or less normally distributed.

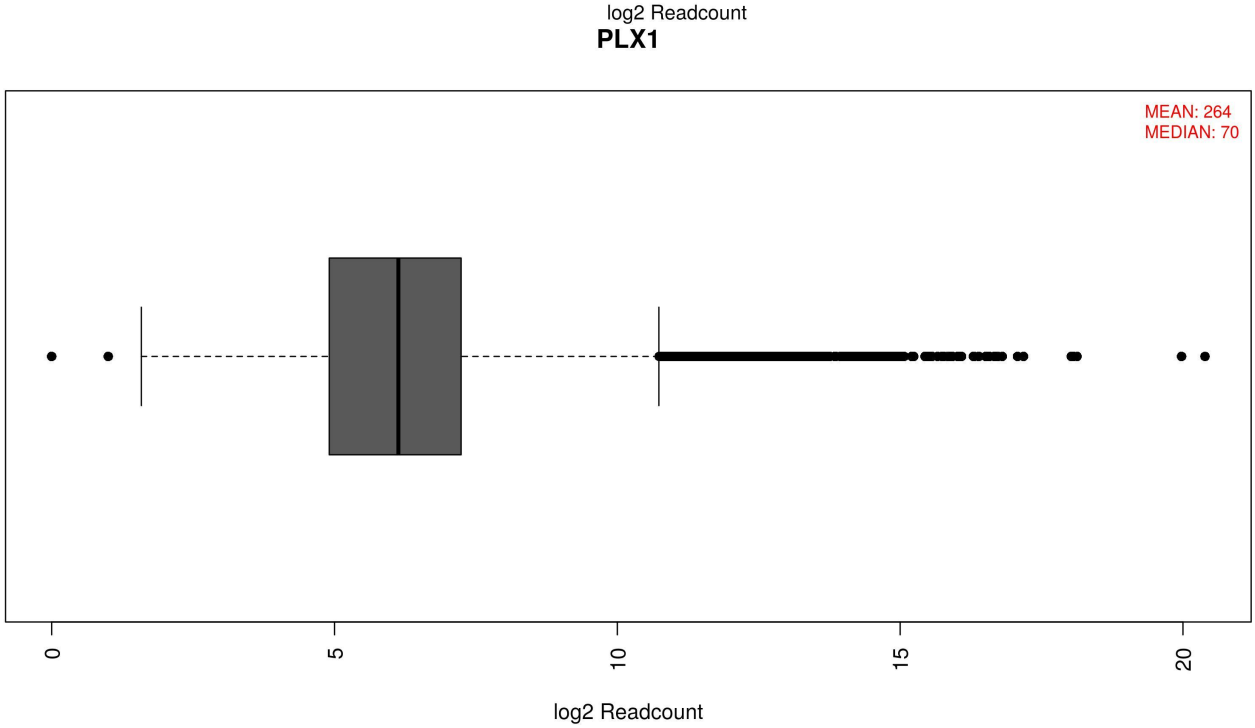


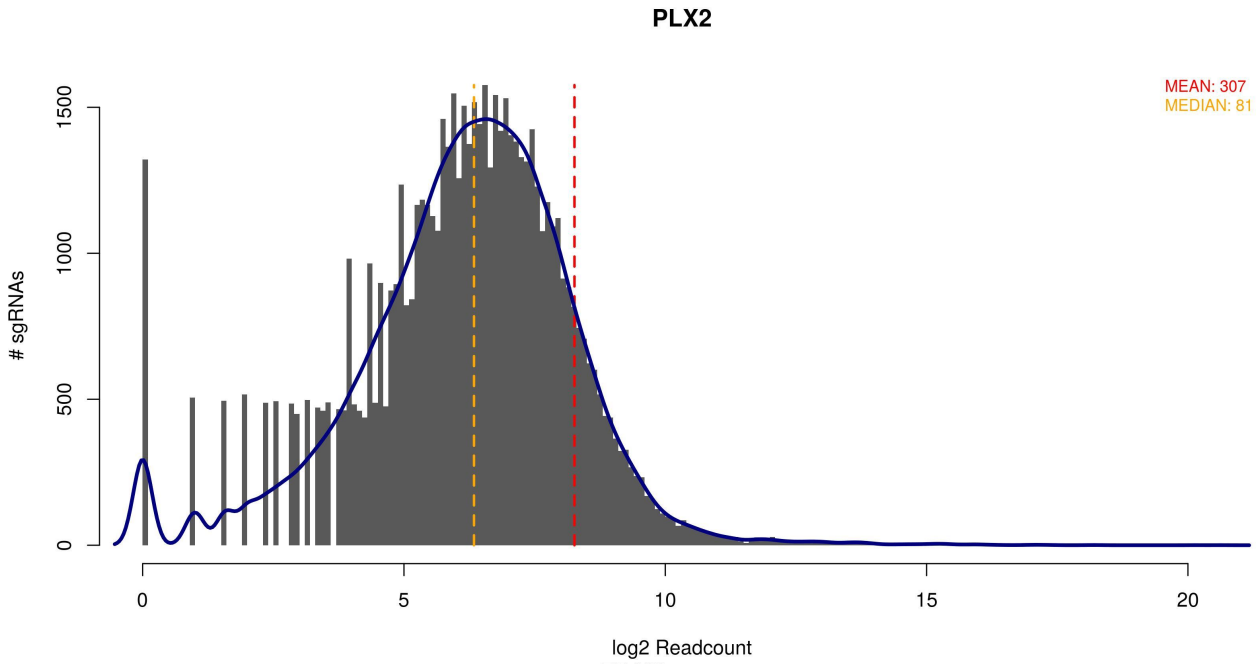


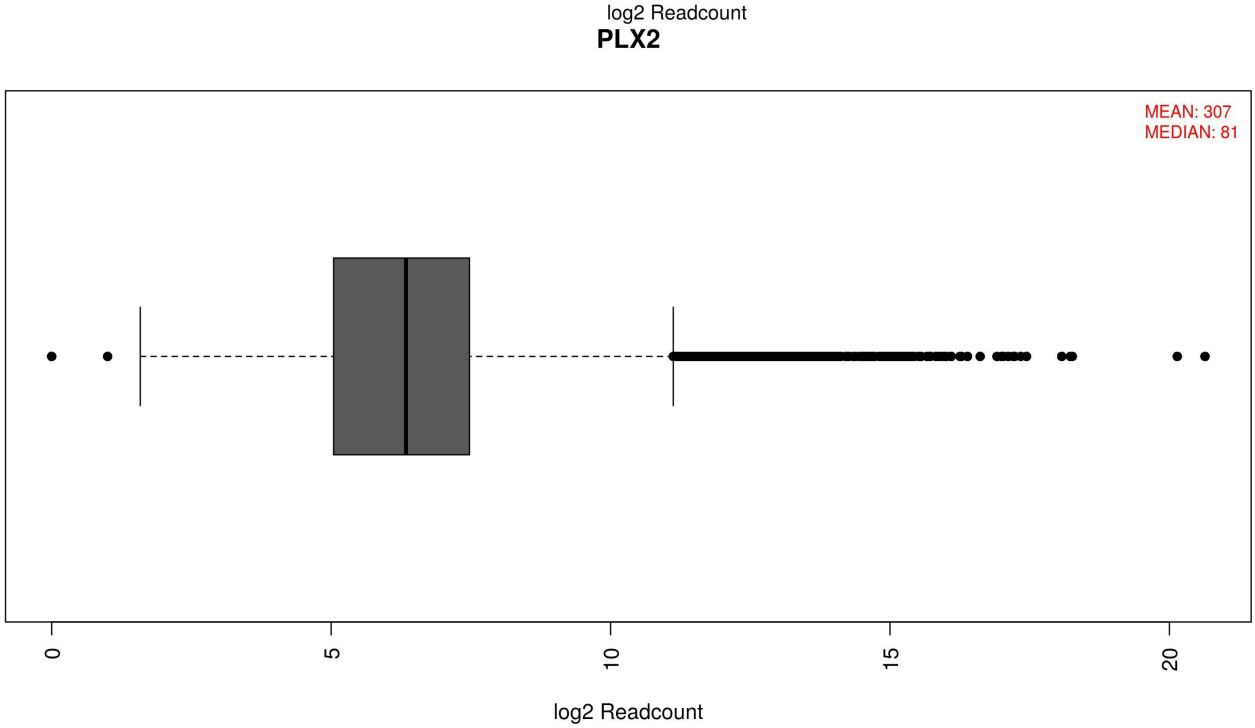

DMSO2
MEAN: 234
MEDIAN: 168
sgRNAs
0
200
400
600
800
1000
1200
0
2
4
6
8
10
12
log2 Readcount


DMSO2
MEAN: 234
MEDIAN: 168
0
2
4
6
8
10
12
log2 Readcount


PLX1
MEAN: 264
MEDIAN: 70
sgRNAs
0
500
1000
1500
0
5
10
15
20
log2 Readcount

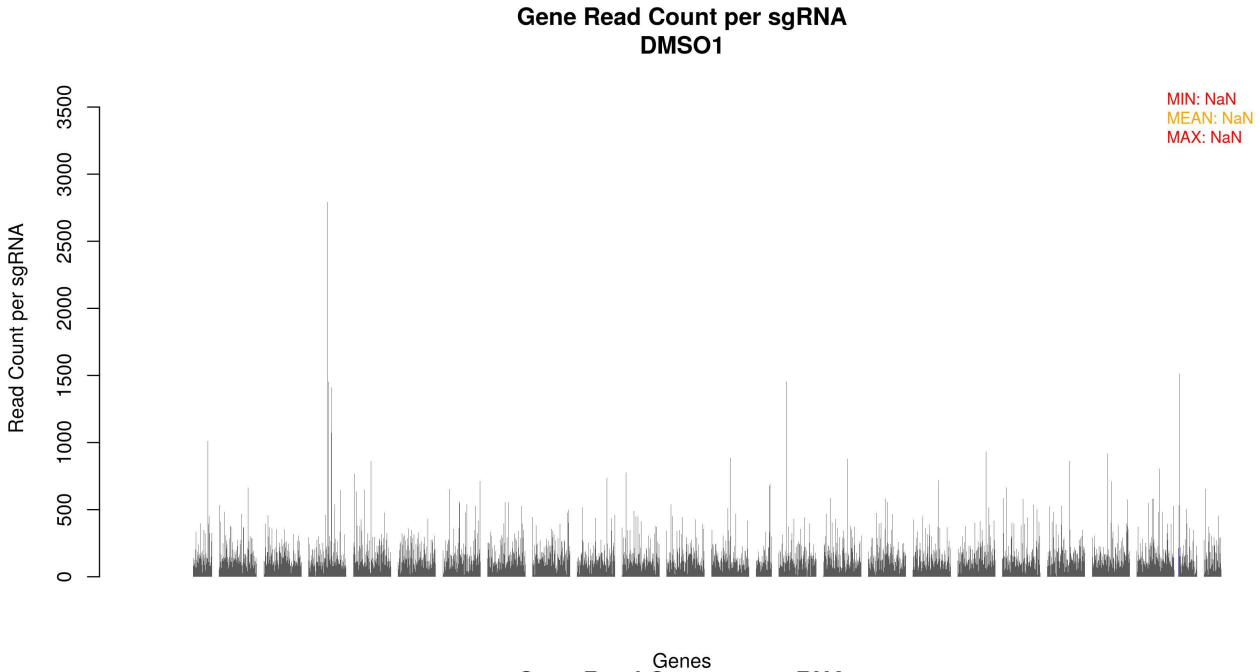

PLX1
MEAN: 264
MEDIAN: 70
0
5
10
15
20
log2 Readcount

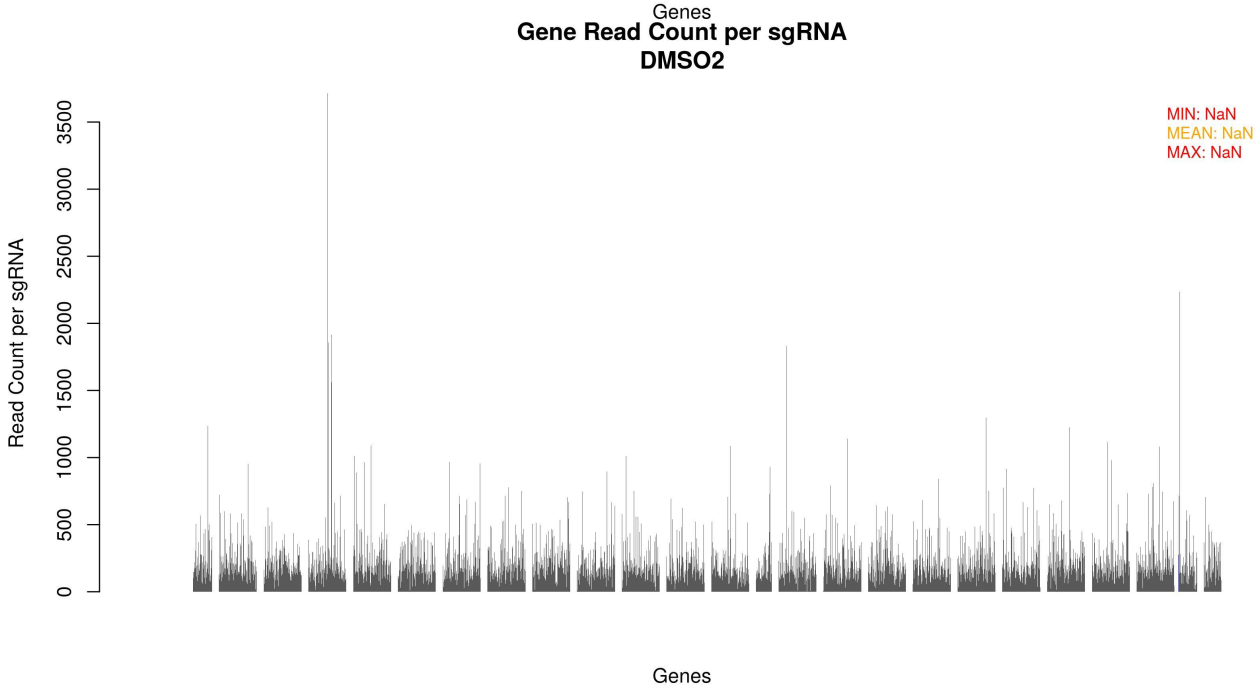

PLX2
MEAN: 307
MEDIAN: 81
sgRNAs
0
500
1000
1500
0
5
10
15
20
log2 Readcount

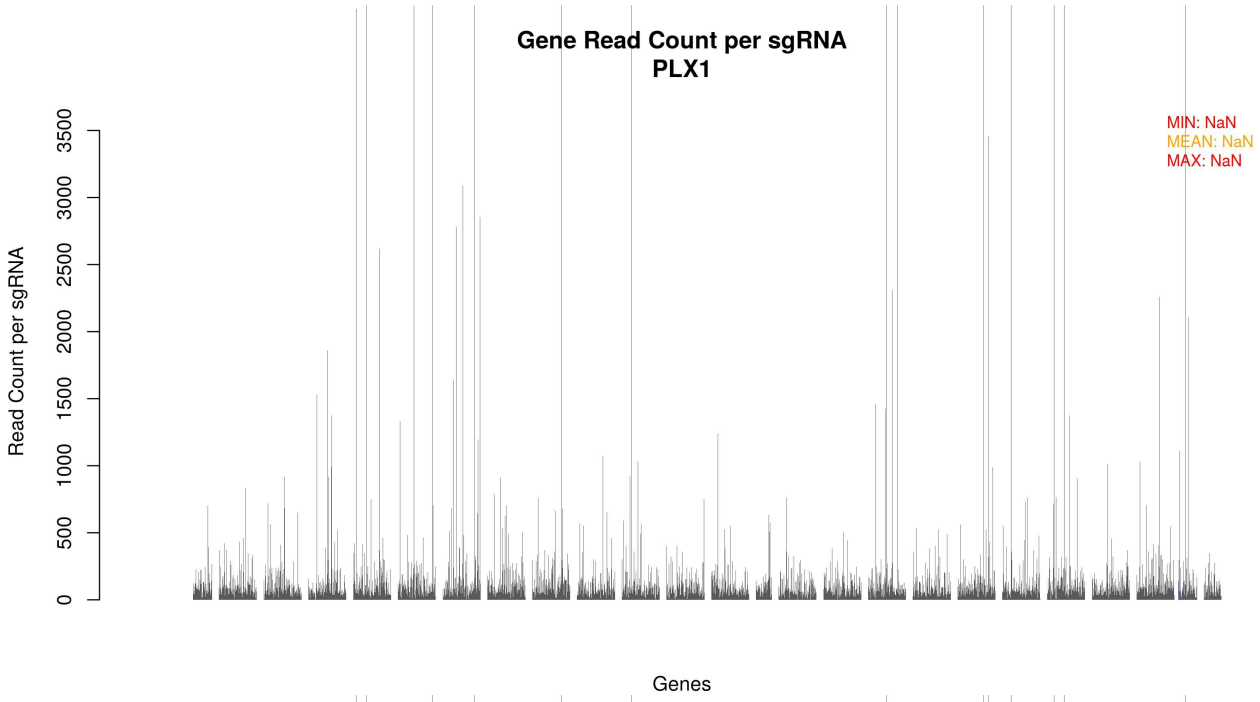

PLX2
MEAN: 307
MEDIAN: 81
0
5
10
15
20
log2 Readcount

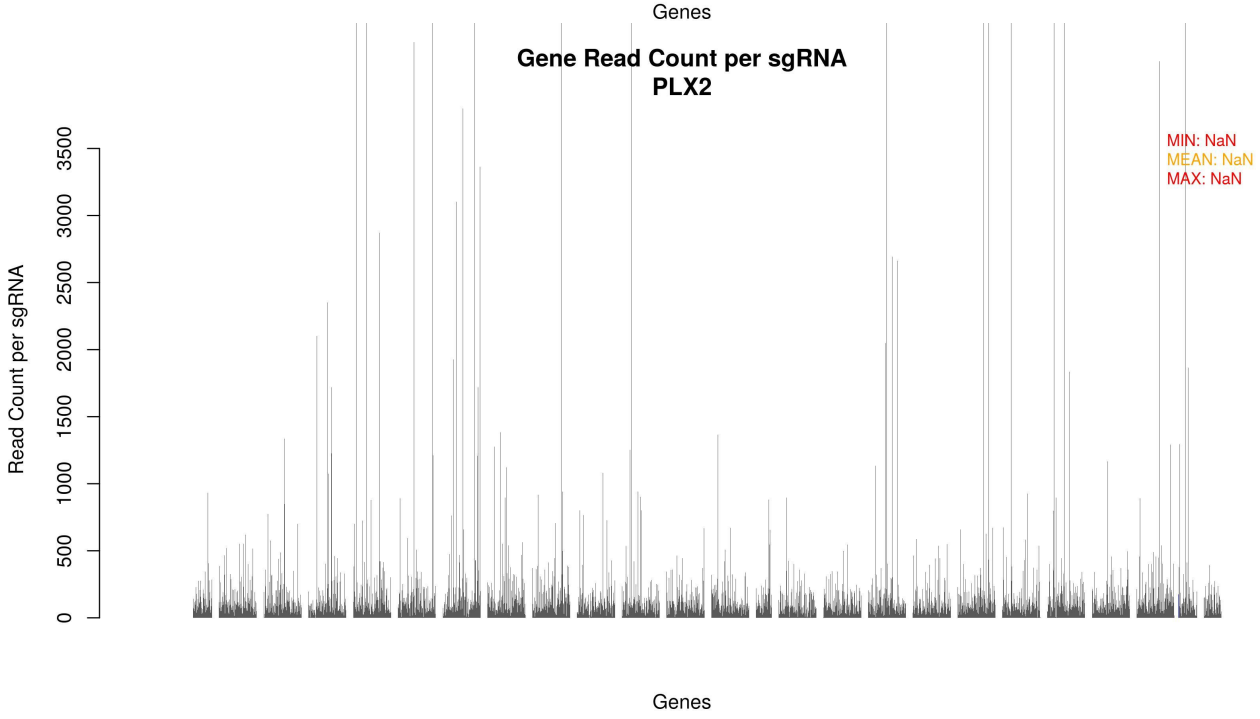
Read Depth

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.



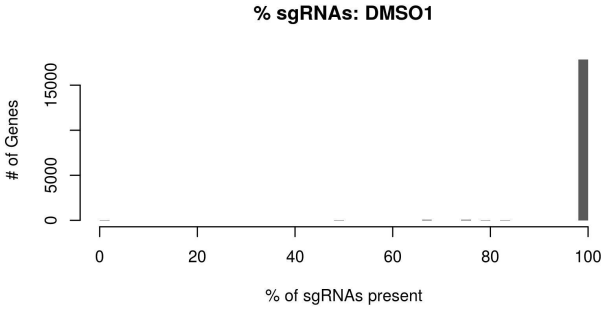


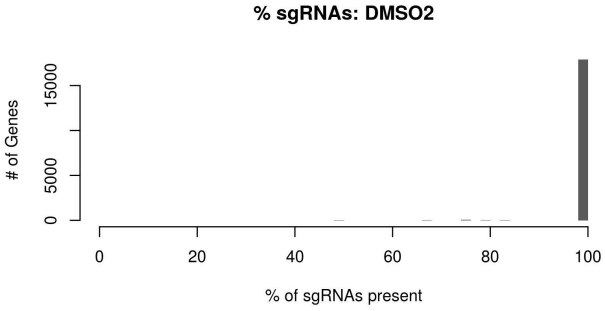

Gene Read Count per sgRNA
PLX1
MIN: NaN
MEAN: NaN
MAX: NaN
Read Count per sgRNA
0
500
1000
1500
2000
2500
3000
3500
Genes

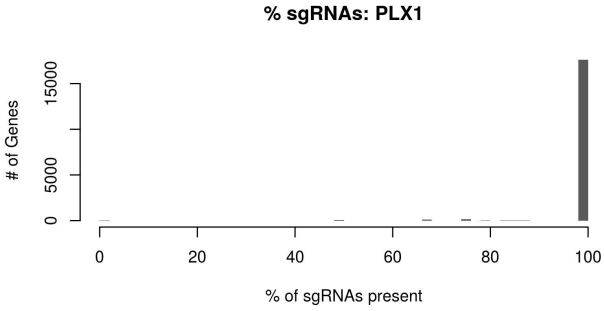

Gene Read Count per sgRNA
PLX2
MIN: NaN
MEAN: NaN
MAX: NaN
Read Count per sgRNA
0
500
1000
1500
2000
2500
3000
3500
Genes

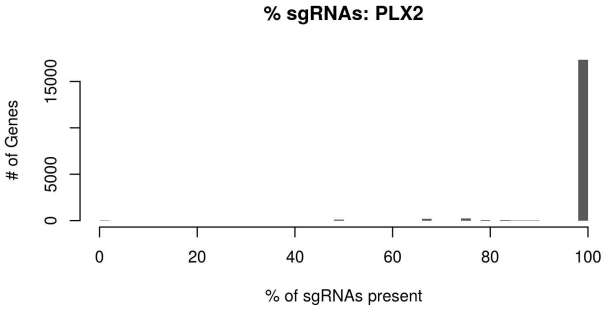
Designs per Gene

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.







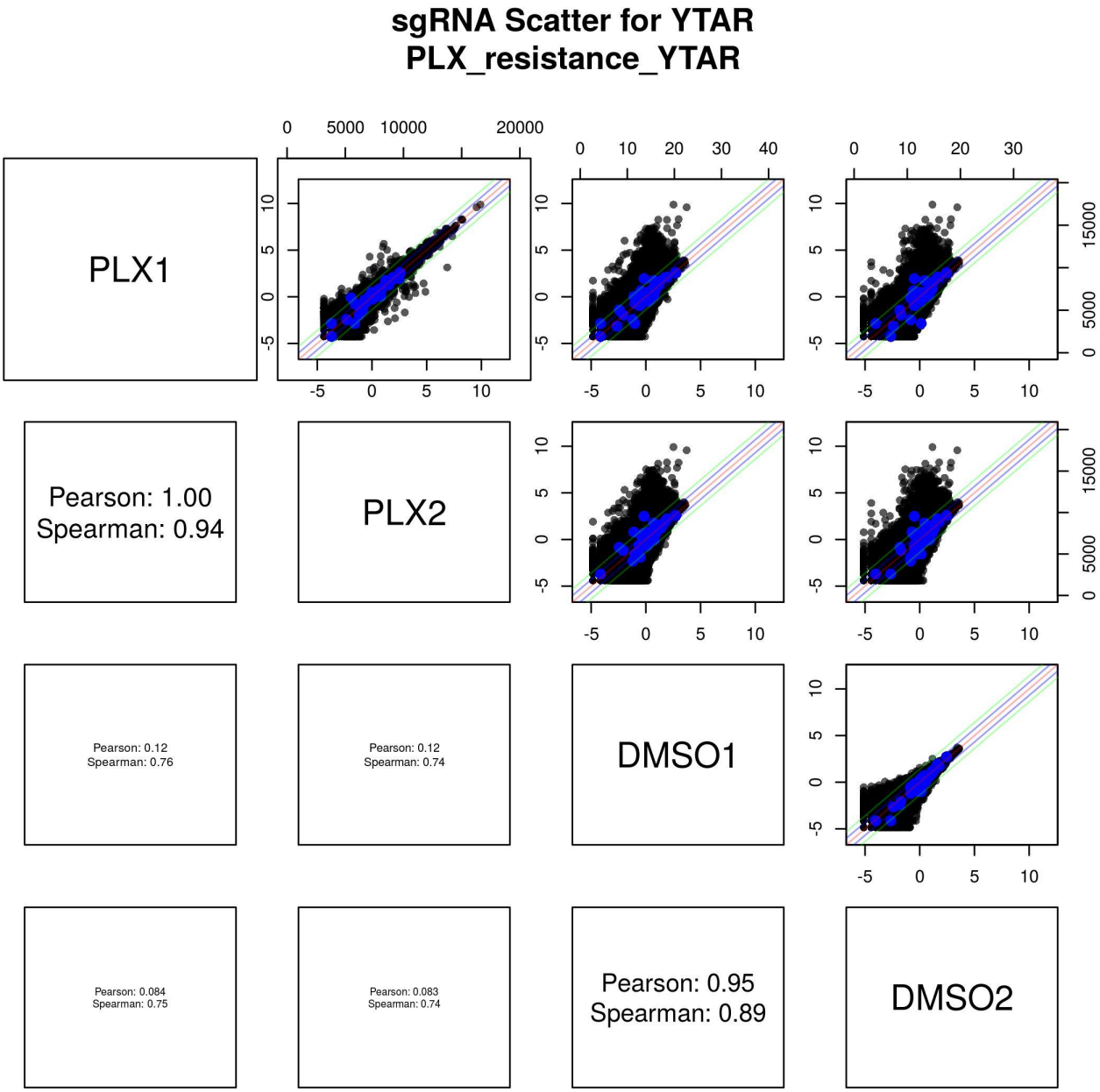


Controls

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.

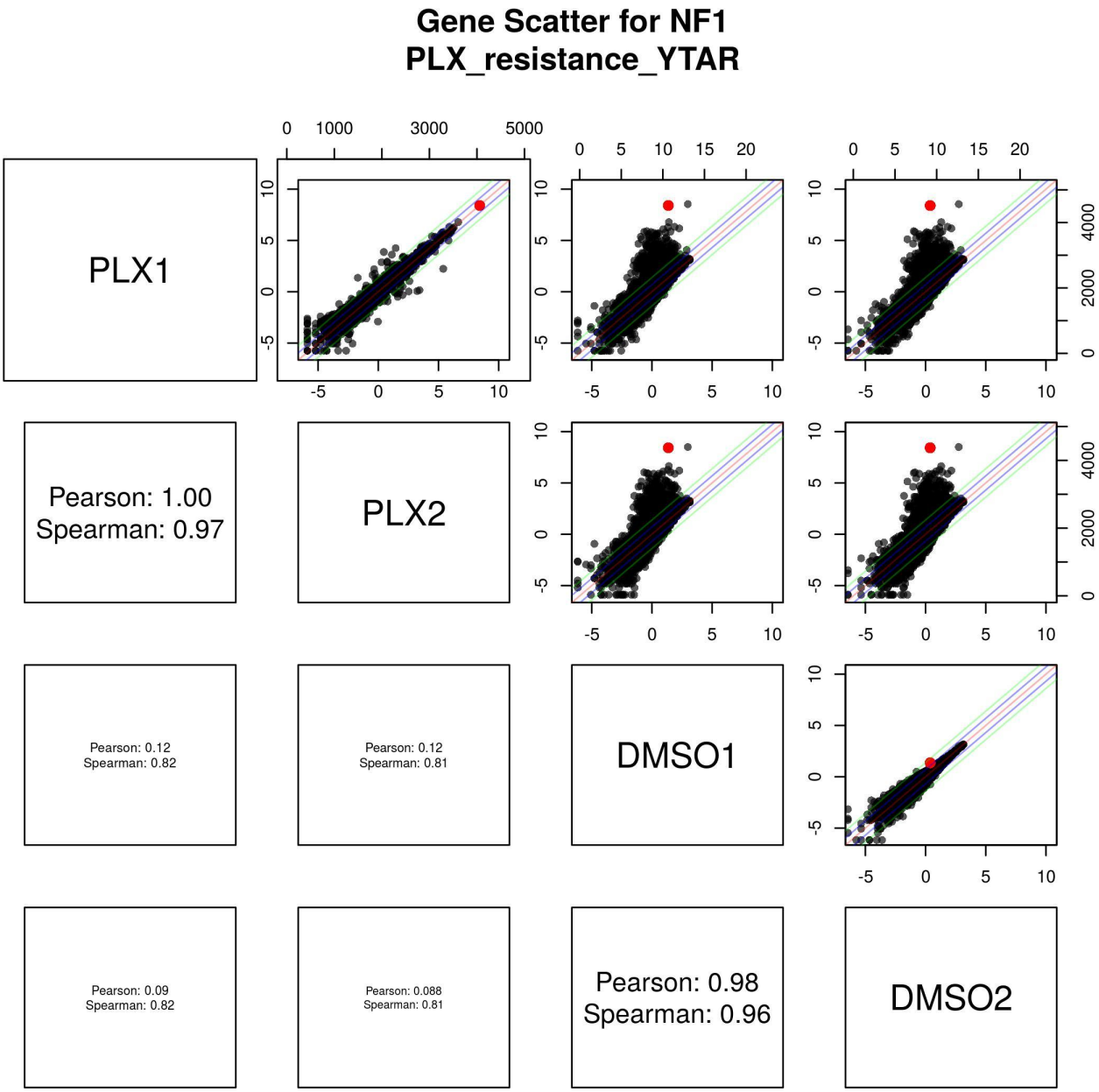
Non-targeting control: YTAR



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: NF1



Hit Analysis

Hit analsysis 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 **PLX_resistance_YTAR_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.

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 perfomed, which includes the estimation of size-factors, the variance stabilization using a parametric fit and a Wald-Test for differnece 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.

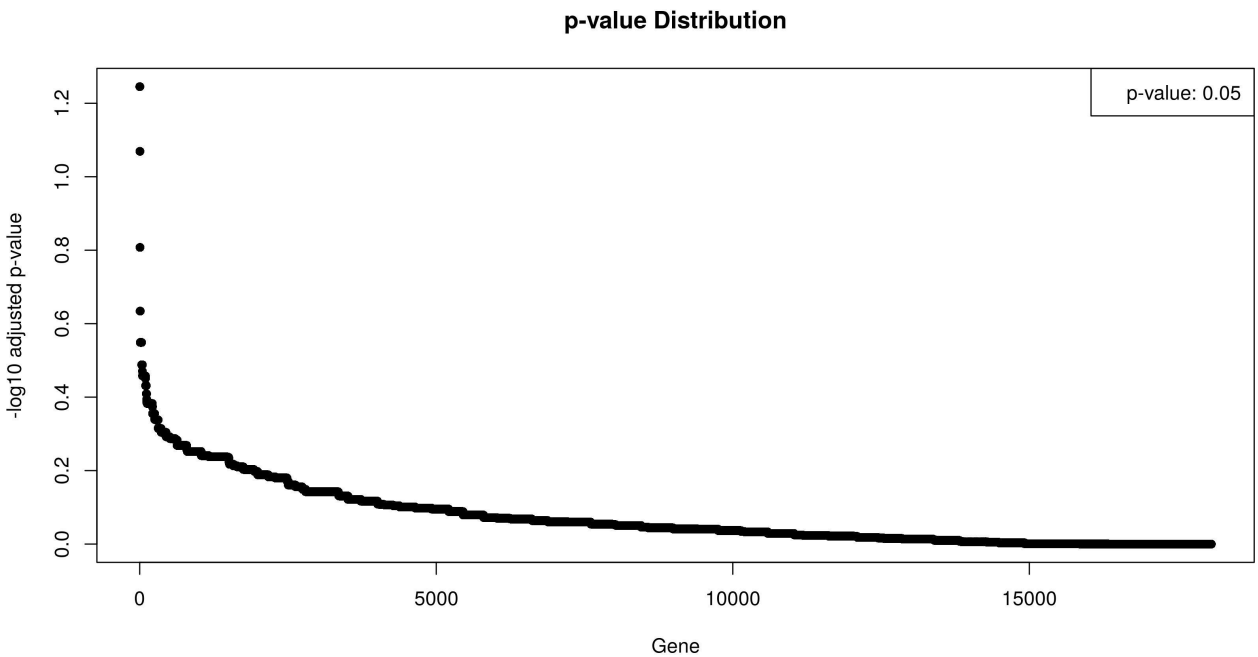
Wilcox

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

```
## Warning in wilcox.test.default(x$foldchange, control.test, alternative =
## "t"): cannot compute exact p-value with ties
```

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**:

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

According to the value set, the **top 1 % enriched genes** were:

	untreated	treated	foldchange	p.value
DPH2	2.120040	10.579733	4.836299	0.0568540
MED12	2.196429	333.928020	140.250758	0.0568540
NF2	17.723710	5600.207959	282.156150	0.0568540
MED15	2.573909	18.281526	7.879254	0.0852810
CDH13	4.663029	18.428586	4.145714	0.1557131
BCL2L12	3.142857	15.589506	4.514373	0.2321539
TADA2B	1.784391	36.783745	22.076309	0.2321539
UBE2E1	3.083829	6.667328	2.061185	0.2321539
ALG3	3.448165	55.795040	20.877160	0.2824934

	untreated	treated	foldchange	p.value
BRD9	1.801162	3.374843	1.997933	0.2824934
C11orf49	4.651290	923.135450	271.166253	0.2824934
CBFB	3.188244	9.830556	2.654298	0.2824934
CCDC101	1.568783	24.333862	13.654340	0.2824934
EED	1.913194	8.506944	5.253757	0.2824934
GEN1	2.409226	5.854519	2.682740	0.2824934
INA	1.881696	5.346010	3.120969	0.2824934
KANK2	2.765377	5.945569	2.192512	0.2824934
PPT1	5.094643	23.835291	5.783105	0.2824934
SMARCB1	2.316799	15.337360	5.974984	0.2824934
TAF6L	1.574405	10.834539	6.900748	0.2824934
TAOK1	6.520172	59.869459	7.184299	0.2824934
ZEB2	1.908400	3.853792	1.965446	0.2824934
ZNF592	2.587302	8.018056	3.321205	0.2824934
GADD45GIP1	1.277034	7.408466	6.245312	0.3250154
KCTD10	1.903770	9.005467	4.658951	0.3250154
MED19	1.789931	12.293408	6.257286	0.3250154
MLN	4.115741	15.752557	3.825117	0.3250154
NCOR2	5.849950	30.664352	4.650794	0.3250154
NFASC	4.526124	9.049971	1.873397	0.3250154
PTPN12	2.892857	13.971993	3.244100	0.3250154
NSUN4	1.920511	3.414550	1.741347	0.3383934
ATRNL1	1.807292	3.734039	1.958436	0.3482308
BBX	2.682540	8.556526	3.461374	0.3482308
CCDC93	1.652183	2.729806	1.589946	0.3482308
CREBBP	2.623512	6.395855	2.189726	0.3482308
DMD	3.400595	5.377416	1.492319	0.3482308
ECHDC1	2.159524	5.673580	2.464979	0.3482308
MOB3B	1.917659	24.193298	9.378349	0.3482308
MRPL53	1.472553	2.617431	1.782182	0.3482308
NDUFAF5	2.070106	55.308348	24.355703	0.3482308
NF1	6.084325	10061.043871	1160.268665	0.3482308
NOD2	1.824653	3.365630	1.949013	0.3482308
PCSK7	2.180060	4.144246	2.018127	0.3482308
PDCD10	2.856746	12.708078	4.643489	0.3482308
PGD	1.217262	4.529071	3.592575	0.3482308
PLXNC1	2.466766	4.885295	2.175860	0.3482308
PVRL3	3.938988	7.127513	1.781622	0.3482308
SGSM3	1.627728	3.353858	2.018485	0.3482308
SMG7	2.985119	6.053153	2.020321	0.3482308
TADA1	2.123512	73.144996	32.534616	0.3482308
TAF5L	2.537698	47.634171	19.722343	0.3482308
TCEB2	2.118552	5.572310	2.371996	0.3482308
TFAP2C	1.709722	2.882152	1.781195	0.3482308
WDR20	4.016245	8.034799	1.972264	0.3482308
ZBTB7A	2.172123	5.058598	2.215978	0.3482308
ZC3H18	1.765873	5.069165	2.880495	0.3482308
DLGAP1	7.643353	31.840947	3.054943	0.3540851
ARNTL2	5.441220	9.926918	1.720210	0.3703194
GIT2	7.910218	24.175132	2.622841	0.3703194
MRPL11	2.332837	4.055666	1.704495	0.3703194
PCLO	2.811756	5.160207	1.849886	0.3703194

	untreated	treated	foldchange	p.value
RCOR2	1.940476	6.448633	2.969147	0.3703194
SPACA1	1.396329	2.603086	1.873872	0.3703194
SWSAP1	2.094990	3.765190	1.824269	0.3703194
ATXN7	1.951786	3.206878	1.677881	0.3898331
GGCT	2.971478	15.729200	7.851503	0.3898331
RALB	2.232804	3.464550	1.520687	0.3898331
RP11-428C6.1	2.908565	4.723854	1.636602	0.3898331
ATP5A1	2.962963	6.762111	2.125558	0.4038307
CRYGN	1.716270	4.314491	2.572967	0.4038307
GLIPR1L2	3.252315	6.885949	2.150704	0.4038307
AHCYL2	3.789848	15.546811	4.422040	0.4116144
CHST3	1.963294	4.480754	2.096077	0.4116144
METTL17	2.234127	3.983311	1.806474	0.4116144
PUS3	1.944940	3.220172	1.624057	0.4116144
ZMAT3	3.747222	6.779189	1.798236	0.4133059
AIF1L	5.896164	42.850588	9.328672	0.4143370
ANO6	4.097966	8.502072	1.981076	0.4143370
ARHGAP17	4.082341	7.688250	1.730379	0.4143370
ARHGAP35	2.005952	4.115785	2.072749	0.4143370
ATP6V1G2	3.741468	5.905556	1.610697	0.4143370
ATXN2L	4.990575	51.496164	9.845926	0.4143370
BCLAF1	2.372355	4.379100	1.883589	0.4143370
CARD9	2.921627	5.060538	1.730455	0.4143370
CNGA3	3.754564	6.709488	1.830280	0.4143370
CUX1	4.263228	8.008348	1.882106	0.4143370
DAPL1	1.680060	2.481636	1.471161	0.4143370
ELMOD1	2.345734	43.594709	16.871501	0.4143370
EML1	4.243304	22.706129	6.436590	0.4143370
ERCC1	4.404762	26.958245	5.041993	0.4143370
FGGY	4.271991	30.541564	5.367850	0.4143370
FOXJ3	4.335648	8.789682	1.993117	0.4143370
GPR123	2.952381	136.400838	46.519519	0.4143370
HIPK3	2.787698	6.279483	2.437901	0.4143370
ILF2	2.027778	3.249559	1.597128	0.4143370
INTU	2.878224	4.936221	1.692449	0.4143370
KLK10	2.026538	3.428792	1.614077	0.4143370
LGALS4	1.938244	91.087125	50.964243	0.4143370
LITAF	2.954117	28.888183	6.622317	0.4143370
MED23	1.893353	15.014021	7.441797	0.4143370
NDUFA8	1.994709	7.203439	3.553555	0.4143370
NR2F2	2.460813	3.454909	1.398617	0.4143370
PCIF1	1.708003	4.164462	2.470157	0.4143370
PDE1A	4.040923	6.653219	1.567178	0.4143370
PIK3C2B	2.199405	3.372046	1.495730	0.4143370
PLEKHB2	5.596627	8.405026	1.475464	0.4143370
PPP1R14D	5.121528	52.004453	9.862483	0.4143370
PYCARD	2.277579	3.716279	1.573662	0.4143370
RAB20	2.294643	3.739264	1.581401	0.4143370
RASGEF1A	2.281002	3.606636	1.696675	0.4143370
SLIT1	1.987434	4.166343	2.122004	0.4143370
STAMBP	2.365410	4.306496	1.853552	0.4143370
TADA3	2.316964	40.585979	15.814414	0.4143370

	untreated	treated	foldchange	p.value
TMED3	2.394511	9.474780	4.155596	0.4143370
TP53	5.955605	28.592394	4.024534	0.4143370
TREML2	1.793403	2.906107	1.595621	0.4143370
TSPAN1	1.443204	3.617284	2.467628	0.4143370
VEZT	1.820437	3.433135	1.790730	0.4143370
YAE1D1	1.759425	3.168144	1.875361	0.4143370
ZNF444	2.544312	4.952293	2.029086	0.4143370
AEBP2	4.399140	32.865814	5.845296	0.4411848
AHR	2.589286	6.432892	2.181087	0.4411848
AP4M1	1.888889	3.738918	2.177984	0.4411848
BPIFB1	2.518188	6.834744	2.595146	0.4411848
C14orf101	4.548859	7.058135	1.520976	0.4411848
CDK8	3.048942	5.956320	1.973529	0.4411848
DEFB121	2.113426	4.198413	2.083843	0.4411848
KIAA0319	3.810516	41.806908	9.802939	0.4411848
PDP1	2.446759	4.789153	1.950808	0.4411848
PFKFB3	3.278770	26.797002	9.662872	0.4411848
PHLPP1	2.303075	3.505445	1.518564	0.4411848
RAB37	3.367063	5.681393	1.603665	0.4411848
STAP1	2.269511	4.417460	1.888470	0.4411848
SUFU	4.053571	11.969606	3.051712	0.4411848
TBX10	2.427249	7.525044	3.615302	0.4411848
TRAPPC6A	2.527282	4.208929	1.619800	0.4411848
TRHR	2.187500	4.165763	2.015753	0.4411848
ZFHX3	2.403026	3.942593	1.671852	0.4411848
APOA4	2.463790	3.457099	1.410094	0.4580261
BMPR2	2.020238	37.544815	13.397275	0.4580261
DENND4A	3.039683	5.217416	1.667841	0.4580261
IRF1	3.238095	5.967460	2.198970	0.4580261
KAT6B	3.337798	6.976036	2.359493	0.4580261
MYO1A	2.258929	3.301764	1.457496	0.4580261
SLC39A2	3.871528	6.934458	1.702887	0.4580261
SOLH	2.911210	5.240785	1.837174	0.4580261
TCF15	1.734871	2.616843	1.475793	0.4580261
TRPC3	2.696429	5.190675	2.236406	0.4580261
CCNT2	3.248347	6.327866	1.876496	0.4590367
CELF2	10.587302	27.595767	2.807322	0.4590367
COPS3	3.042328	5.235538	1.748229	0.4590367
CRAMP1L	1.861359	3.279034	1.740928	0.4590367
CUL3	3.176091	397.578072	141.390553	0.4590367
CXorf66	2.429233	4.939447	2.077458	0.4590367
F3	2.699653	5.186817	1.937112	0.4590367
FOPNL	1.545139	3.167041	2.037454	0.4590367
FXC1	1.879464	5.100309	2.716241	0.4590367
GMEB1	3.563740	15.849669	4.863730	0.4590367
HPN	1.888393	3.122950	1.658631	0.4590367
LRFN2	1.826720	3.069547	1.669298	0.4590367
MFSD9	2.336310	11.599162	4.911456	0.4590367
MUM1	1.669973	3.099206	1.744174	0.4590367
NFS1	2.202381	4.397472	2.151274	0.4590367
RERE	1.619489	2.598932	1.614150	0.4590367
STAU2	8.443948	16.541865	2.078775	0.4590367

	untreated	treated	foldchange	p.value
TOX3	6.158234	16.304321	2.647971	0.4590367
ABCB5	2.242504	4.544807	2.233002	0.4843050
ARMC5	2.116567	2.956437	1.384507	0.4843050
C10orf67	1.994048	4.152734	2.019367	0.4843050
C2orf42	1.692791	2.880041	1.706400	0.4843050
C9orf174	3.188244	18.531437	5.027686	0.4843050
CCL22	1.900132	3.722399	1.995765	0.4843050
FAM50A	2.034722	4.803233	2.386395	0.4843050
FAR2	2.150050	3.656019	1.702705	0.4843050
GBP4	2.486772	4.209259	1.709364	0.4843050
GIMAP6	3.701885	6.033510	1.580487	0.4843050
PLIN3	2.069444	23.675617	8.199217	0.4843050
PRSS36	4.039434	23.220635	4.492484	0.4843050
TDRD3	2.538690	8.901534	3.084914	0.4843050
TMEM150C	2.256614	4.569812	1.985664	0.4843050
TRIP12	2.215443	7.078733	3.506237	0.4843050

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 1 % depleted genes** were:

	untreated	treated	foldchange	p.value
NLGN3	2.879819	2.142089	0.7352105	0.2321539
FAM177A1	2.898148	1.737478	0.6124113	0.2824934
GRB2	2.440807	1.558083	0.6390447	0.2824934
LCLAT1	2.995833	1.964409	0.6642309	0.2824934
MAPKAPK2	3.498347	2.007025	0.5763186	0.2824934
MCL1	1.846561	1.172134	0.6382256	0.2824934
MTUS1	2.725595	2.072496	0.7862343	0.2824934
PARD6B	2.309028	1.555622	0.6739080	0.2824934
SNAPC5	2.542659	1.618122	0.6582114	0.2824934
CAMKK1	3.522817	2.289727	0.6730894	0.3250154
DIDO1	2.085152	1.529541	0.7582531	0.3250154
FOXA2	3.212632	1.876308	0.6176658	0.3250154
MS4A6E	2.255622	1.486596	0.6552375	0.3250154
OR10J5	2.381283	1.520723	0.6394277	0.3250154
TRAPPC2L	2.708995	1.697707	0.6258884	0.3250154
ADCY9	2.228671	1.643585	0.7327168	0.3482308
AIM2	2.117808	1.484656	0.7121475	0.3482308
ARTN	3.068122	2.402690	0.7761098	0.3482308
BRAP	2.398810	1.738713	0.7266457	0.3482308
C17orf107	2.065724	1.356504	0.6772231	0.3482308
CCL11	2.554563	1.677572	0.6621828	0.3482308
CD59	2.206680	1.280276	0.6087704	0.3482308
CLCA2	2.422421	1.786490	0.7456578	0.3482308
CMKLR1	4.087798	2.547487	0.6221055	0.3482308
CTNND2	2.037698	1.601940	0.7857976	0.3482308
ITFG3	2.538690	1.771825	0.7128494	0.3482308
LMO4	2.126736	1.545591	0.7217479	0.3482308
MPRIP	2.608135	1.770282	0.6813676	0.3482308
OR10H1	2.391369	1.496076	0.6218753	0.3482308
OR4K14	2.393849	1.439771	0.6003596	0.3482308
PLCB1	3.469577	2.331335	0.6710336	0.3482308
RNF144B	2.832589	2.028792	0.7245255	0.3482308
RXFP4	1.908730	1.245944	0.6575082	0.3482308
SLC15A3	2.353919	1.705027	0.7257203	0.3482308
SLC38A2	1.832341	1.178513	0.6506747	0.3482308
SOCS4	2.655754	1.524515	0.5726512	0.3482308
SPOCK2	2.119756	1.665659	0.7848339	0.3482308
TEX15	2.218254	1.291138	0.5838225	0.3482308
TRIM35	1.814484	1.309171	0.7200388	0.3482308
TRIM37	2.832837	1.704762	0.6006432	0.3482308
SLC38A9	2.664848	2.035170	0.7836074	0.3540851
CD34	4.272321	3.021473	0.6957148	0.3703194
CYB5D1	3.014385	2.182099	0.7261382	0.3703194
FAM13C	2.784722	2.063316	0.7562907	0.3703194
HSPG2	1.745536	1.229453	0.7202754	0.3703194
PGM2L1	2.296379	1.498611	0.6881227	0.3703194

	untreated	treated	foldchange	p.value
TMPRSS11D	2.029365	1.492240	0.7454555	0.3703194
CXCL13	2.218056	1.689259	0.7575810	0.3898331
KLHL3	2.187610	1.757652	0.8124882	0.4116144
AJAP1	2.458829	1.698765	0.7162002	0.4143370
APTX	3.109127	2.345062	0.7469262	0.4143370
BCAN	2.598214	1.939118	0.7622114	0.4143370
C11orf31	1.969246	1.378366	0.7051117	0.4143370
C8orf86	2.098876	1.453909	0.7000031	0.4143370
CCL27	2.027282	1.537257	0.7560890	0.4143370
CDH26	2.210884	1.756916	0.8022330	0.4143370
CLN8	2.118304	1.539131	0.7352807	0.4143370
CNTF	2.340030	1.786199	0.7529417	0.4143370
CRK	2.186756	1.404497	0.6800822	0.4143370
CYP4B1	4.080357	3.109436	0.7494695	0.4143370
DEFB115	2.617808	1.949008	0.7303159	0.4143370
EGFR	4.712798	3.643342	0.7304477	0.4143370
FOXN2	1.708829	1.294488	0.7574740	0.4143370
HOXB1	2.367312	1.679343	0.7410638	0.4143370
IL7R	2.087103	1.636914	0.7837755	0.4143370
IRF2BP2	2.371362	1.730159	0.7229853	0.4143370
KIF24	2.292989	1.550529	0.6886258	0.4143370
KIR3DL1	2.105903	1.442350	0.7145519	0.4143370
KLF5	1.824074	1.183833	0.6721219	0.4143370
KLHL20	1.961310	1.446759	0.7435023	0.4143370
KLK6	2.147487	1.681482	0.7962917	0.4143370
LDHAL6A	2.023313	1.521605	0.7497634	0.4143370
LZTS2	2.150298	1.533554	0.7270898	0.4143370
MON1B	2.003472	1.530864	0.7603646	0.4143370
MPL	2.217427	1.713125	0.7926459	0.4143370
NOTCH1	2.274306	1.701168	0.7454615	0.4143370
ODF4	1.720238	1.223574	0.7132337	0.4143370
OTX2	2.256944	1.622112	0.7068665	0.4143370
PABPC1L	3.145585	2.343452	0.7206638	0.4143370
PINK1	1.858466	1.254292	0.6801128	0.4143370
PIP	1.811508	1.303197	0.7395919	0.4143370
PRH2	2.090609	1.488125	0.7146225	0.4143370
RCBTB1	2.633267	1.888066	0.7193528	0.4143370
SLC23A2	2.830026	1.946002	0.6987517	0.4143370
SLC9A8	3.245370	2.129365	0.6621171	0.4143370
SMO	2.817956	2.014947	0.7369311	0.4143370
SPERT	1.982639	1.481085	0.7515236	0.4143370
SS18L1	1.649306	1.266468	0.7699145	0.4143370
TATDN2	1.762235	1.416402	0.7996974	0.4143370
TMEM74B	2.221726	1.423942	0.6790950	0.4143370
TNKS	2.248264	1.611949	0.7206747	0.4143370
TRHDE	2.794974	2.016020	0.7213398	0.4143370
FAM20B	1.912103	1.441499	0.7493453	0.4225178
MFSD10	2.107738	1.616296	0.7630598	0.4225178
PGM2	1.693056	1.296914	0.7789334	0.4225178
ABLIM1	2.181672	1.667196	0.8037563	0.4411848
BTNL9	2.076389	1.554541	0.7566479	0.4411848
CCK	1.933929	1.527160	0.7836098	0.4411848

	untreated	treated	foldchange	p.value
DUOX2	1.793320	1.292210	0.7194201	0.4411848
FOXN1	2.390129	1.833818	0.7755715	0.4411848
HTR6	2.080357	1.556989	0.7537370	0.4411848
LEMD3	1.833003	1.330276	0.7266073	0.4411848
LHCGR	1.850860	1.294150	0.7146059	0.4411848
MTTP	1.889286	1.476155	0.7799474	0.4411848
OSM	2.326885	1.733333	0.7603690	0.4411848
PAK7	2.345569	1.673457	0.7189852	0.4411848
PAX9	1.857143	1.352352	0.7241294	0.4411848
PI16	2.600942	1.779762	0.7217873	0.4411848
PNLIP	1.741071	1.353527	0.7657528	0.4411848
RP11-268F1.2	2.276786	1.619996	0.7356895	0.4411848
SDC1	2.338128	1.824691	0.7861975	0.4411848
TRIM15	1.854663	1.398413	0.7537953	0.4411848
USP25	2.001653	1.430188	0.7225383	0.4411848
GBA	2.120866	1.648868	0.7952591	0.4564804
CHRNA10	1.998760	1.458047	0.7464540	0.4580261
FAM53C	1.838046	1.404167	0.7685247	0.4580261
GADD45G	1.881944	1.418408	0.7616873	0.4580261
LRRC72	2.135913	1.613514	0.7623268	0.4580261
MAP2K5	5.152034	4.020084	0.7777109	0.4580261
ABCD1	2.295635	1.599206	0.6957299	0.4590367
AC092031.1	3.168320	2.152587	0.7095697	0.4590367
ACOT9	2.757937	1.803307	0.6450009	0.4590367
BCL9L	1.554812	1.192174	0.7700172	0.4590367
BLCAP	2.153770	1.431129	0.6664013	0.4590367
BTC	1.637566	1.217607	0.7441095	0.4590367
C17orf85	1.804563	1.170503	0.6487265	0.4590367
C3orf52	2.526124	1.766902	0.7167881	0.4590367
CDK3	1.790013	1.302146	0.7325845	0.4590367
CHST12	3.094246	2.024559	0.6565392	0.4590367
CNKSR3	1.888889	1.326720	0.7121213	0.4590367
EVI2B	2.668155	1.748280	0.6542351	0.4590367
FOXL1	2.024306	1.301235	0.6501139	0.4590367
GABRA5	2.044974	1.512816	0.7418863	0.4590367
IQGAP3	2.434028	1.584921	0.6509930	0.4590367
OR2A14	3.631944	2.272266	0.6100092	0.4590367
OR9Q1	1.966766	1.292769	0.6561547	0.4590367
PAPSS2	3.145833	2.291534	0.7354990	0.4590367
RHOG	1.812500	1.189153	0.6591632	0.4590367
RNF152	2.669643	1.673280	0.6308585	0.4590367
RP4-788L13.1	2.545304	1.855482	0.7545022	0.4590367
SLC17A9	2.242063	1.596531	0.7260072	0.4590367
SLC2A14	2.028770	1.278792	0.6416184	0.4590367
SLC7A6	1.905423	1.413698	0.7442515	0.4590367
SLC9C2	2.025794	1.302690	0.6407898	0.4590367
VWA5A	3.269841	2.530313	0.7805670	0.4590367
APPL2	3.639087	2.902681	0.7775627	0.4830951
ABCA13	2.763558	2.006379	0.7297957	0.4843050
AP1S3	2.452877	1.777227	0.7392493	0.4843050
APOBR	2.077877	1.632385	0.7922095	0.4843050
C10orf113	4.149802	3.466402	0.8175245	0.4843050

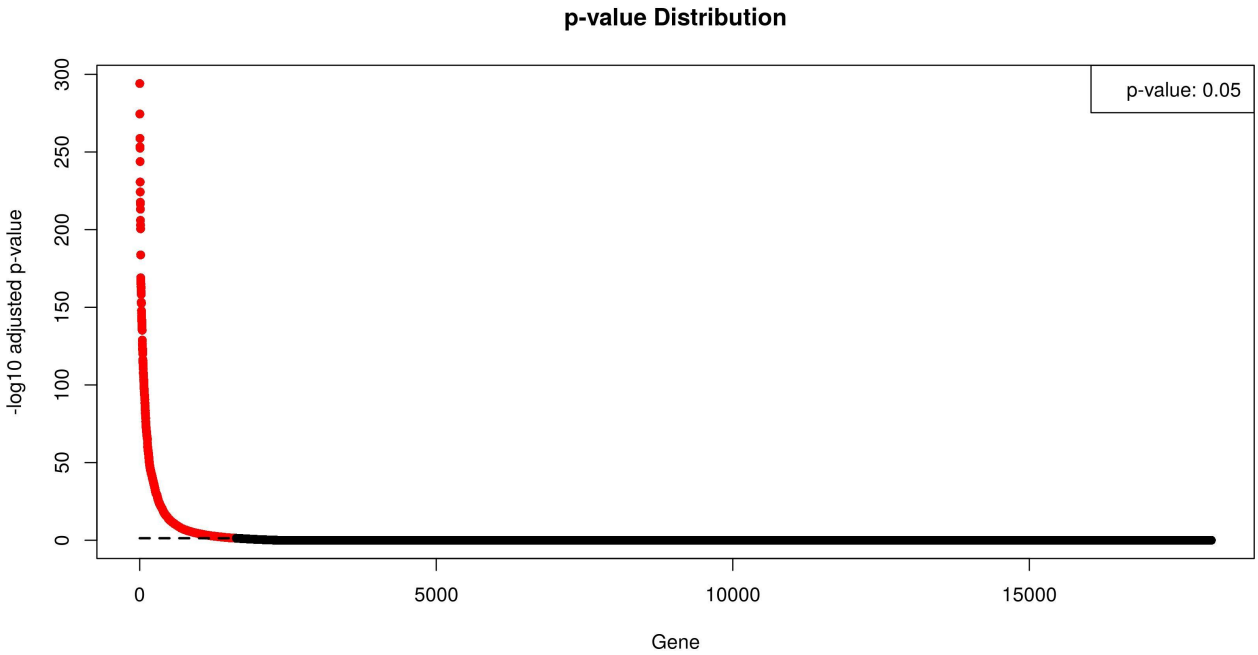
	untreated	treated	foldchange	p.value
C17orf108	2.622024	1.970459	0.7471473	0.4843050
CHCHD6	1.924273	1.459553	0.7570980	0.4843050
CMIP	3.227348	2.328292	0.7607998	0.4843050
CNTLN	3.098876	2.268078	0.7204119	0.4843050
CPNE1	4.188492	3.209436	0.7600976	0.4843050
CST11	2.383929	1.753821	0.7272850	0.4843050
ESRRG	3.515873	2.525626	0.7529049	0.4843050
FAM170A	1.756151	1.382928	0.7966269	0.4843050
KCNV2	1.769180	1.271399	0.7260672	0.4843050
KLHL29	2.320271	1.753042	0.7850142	0.4843050
KLK11	3.339534	2.572156	0.7717199	0.4843050
LPP	1.953373	1.565021	0.7969617	0.4843050
LRRC16B	1.969246	1.280952	0.6853646	0.4843050
LY6G6F	2.964534	2.330423	0.7871450	0.4843050
MYH2	1.810847	1.273810	0.7249218	0.4843050
NBEA	1.530919	1.238492	0.8188343	0.4843050
PAX4	2.165675	1.586993	0.7598224	0.4843050
PHIP	2.020172	1.432599	0.7154862	0.4843050
PTK6	1.904266	1.407981	0.7557106	0.4843050
RARG	4.812500	3.604968	0.7379456	0.4843050
RASL10B	2.649802	2.076720	0.7796177	0.4843050
SBK1	2.339947	1.612316	0.7096947	0.4843050
SFRP2	2.179167	1.644145	0.7706646	0.4843050
SPESP1	2.323082	1.746149	0.7471323	0.4843050
SYNPO	2.912037	2.402851	0.7926169	0.4843050
TIRAP	2.394097	1.675397	0.7415696	0.4843050
VMAC	1.969907	1.428395	0.7381905	0.4843050
ZNF786	2.511574	1.817137	0.7431733	0.4843050
APBA2	2.676339	1.988801	0.7683820	0.4963201
BARX2	1.951885	1.493254	0.7642956	0.4963201
BATF	1.638227	1.231452	0.7569498	0.4963201

DESeq2

All analysis data can be found in the **PLX_resistance_YTAR_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
ACTA2	9.338286	0.2526421	0.0000000	1
GNA14	8.069706	0.2259080	0.0000000	1
C1orf27	7.366291	0.2123102	0.0000000	2
SNCG	7.902688	0.2277764	0.0000000	1
CLDN10	7.350818	0.2140744	0.0000000	2
NF2	7.936644	0.2315726	0.0000000	3
C11orf49	7.559413	0.2243719	0.0000000	1
ZP1	8.565882	0.2613221	0.0000000	0
NLGN1	7.376830	0.2281904	0.0000000	2
HGS	6.991316	0.2194959	0.0000000	1
CUL3	7.104205	0.2235502	0.0000000	2
CPAMD8	7.338817	0.2327893	0.0000000	1
PHC2	7.106705	0.2292402	0.0000000	1
RNH1	6.808820	0.2212518	0.0000000	1
STT3A	9.064755	0.2963053	0.0000000	1

	log2FoldChange	lfcSE	padj	sgRNA
KRT31	6.762881	0.2308151	0.0000000	1
MAP2K6	6.307783	0.2242981	0.0000000	0
ZSCAN1	6.731427	0.2402109	0.0000000	1
MIER3	6.202215	0.2219922	0.0000000	1
SERPINB6	6.466586	0.2324437	0.0000000	0
P4HB	6.897199	0.2481859	0.0000000	1
LBX1	7.759880	0.2808092	0.0000000	1
PRAM1	6.235969	0.2261683	0.0000000	1
MYO1E	8.547978	0.3121458	0.0000000	0
EHMT2	5.701878	0.2093030	0.0000000	1
MED12	7.560338	0.2776105	0.0000000	0
YTARVE19	6.328500	0.2360511	0.0000000	1
LGALS4	6.193239	0.2316681	0.0000000	1
MIA	6.588108	0.2502594	0.0000000	1
CEMP1	7.992845	0.3037934	0.0000000	0
ITFG1	6.251511	0.2386738	0.0000000	0
CACNB2	5.634675	0.2166708	0.0000000	1
GPR123	5.754574	0.2223640	0.0000000	0
TGFB3	6.081914	0.2355533	0.0000000	1
MNT	5.531416	0.2147847	0.0000000	1
EN2	7.105250	0.2764822	0.0000000	0
DMRT3	7.080885	0.2766271	0.0000000	0
NF1	9.724947	0.3812358	0.0000000	0
EPS8L1	6.076266	0.2387123	0.0000000	0
ANGEL1	5.485403	0.2165289	0.0000000	0
ZNF181	6.846511	0.2714563	0.0000000	0
SIGLEC9	5.850854	0.2321164	0.0000000	1
IL17REL	6.443761	0.2616995	0.0000000	1
KHK	5.506337	0.2237913	0.0000000	1
H2BFM	5.733252	0.2350696	0.0000000	0
GGT5	5.371806	0.2209324	0.0000000	1
ALDH16A1	5.405175	0.2243221	0.0000000	0
KCMF1	5.970485	0.2478522	0.0000000	0
DUS1L	5.234072	0.2181175	0.0000000	0
MARCH9	5.365378	0.2240985	0.0000000	0
KCTD7	5.313948	0.2227077	0.0000000	1
KIF13A	5.072697	0.2132921	0.0000000	1
ORC4	5.796772	0.2474226	0.0000000	1
NDUFAF5	5.310484	0.2271320	0.0000000	1
SLC37A3	5.611549	0.2412926	0.0000000	0
ZDHHC15	4.910957	0.2118107	0.0000000	1
ATG13	5.098733	0.2215154	0.0000000	0
SLC26A11	5.201130	0.2261180	0.0000000	0
TSHZ2	5.265230	0.2289415	0.0000000	1
CLC	5.981083	0.2620030	0.0000000	0
NPHS1	5.044634	0.2233433	0.0000000	0
TADA2B	5.158877	0.2290938	0.0000000	0
TSHZ1	6.530483	0.2913705	0.0000000	0
GTF3C6	5.355434	0.2391990	0.0000000	0
LSM4	5.558865	0.2485285	0.0000000	0
ZSWIM1	7.742572	0.3473327	0.0000000	0
GTF2E1	5.099043	0.2305588	0.0000000	1

	log2FoldChange	lfcSE	padj	sgRNA
ZFP82	5.758315	0.2604507	0.0000000	0
CCDC101	5.011924	0.2281743	0.0000000	0
EDIL3	4.701848	0.2150116	0.0000000	0
STK11	5.642961	0.2603659	0.0000000	1
C7orf44	4.982733	0.2303733	0.0000000	0
BMPR2	4.827518	0.2233804	0.0000000	2
SPECC1	5.935965	0.2758859	0.0000000	0
GLIS2	4.705422	0.2188324	0.0000000	0
FAM8A1	5.577840	0.2613678	0.0000000	0
PAPOLG	4.599119	0.2156004	0.0000000	0
RBAK	5.075482	0.2382819	0.0000000	0
FTO	5.159386	0.2426730	0.0000000	0
PLA2R1	6.062036	0.2873962	0.0000000	2
HBG1	6.128551	0.2908350	0.0000000	0
JMJD4	5.044956	0.2395965	0.0000000	0
PRR23B	6.153843	0.2924475	0.0000000	0
TAF5L	4.597939	0.2200371	0.0000000	0
PRLH	4.384423	0.2109276	0.0000000	0
TADA3	4.585672	0.2210488	0.0000000	0
ASIC1	5.546473	0.2675085	0.0000000	0
OXR1	4.308680	0.2101521	0.0000000	1
XRCC4	5.633933	0.2749364	0.0000000	0
OLA1	4.854227	0.2392028	0.0000000	0
CEBPZ	5.455162	0.2712529	0.0000000	0
SLC22A23	4.454831	0.2225487	0.0000000	0
WDR74	5.117015	0.2562150	0.0000000	0
NLRP14	4.318274	0.2164592	0.0000000	0
RPH3A	4.218168	0.2134338	0.0000000	1
CUBN	5.289401	0.2694670	0.0000000	1
ALG3	4.180852	0.2131998	0.0000000	0
ELMOD1	4.633026	0.2375055	0.0000000	0
SGIP1	5.790750	0.2969479	0.0000000	0
TADA1	5.531092	0.2844749	0.0000000	0
RP5-862P8.2	6.783811	0.3505102	0.0000000	0
TMEM194A	4.196772	0.2197127	0.0000000	0
TRA2A	5.833496	0.3071586	0.0000000	0
TNFRSF17	5.975815	0.3155635	0.0000000	0
LEO1	4.971464	0.2633555	0.0000000	0
STK25	4.883451	0.2600373	0.0000000	0
SLC3A1	5.072492	0.2711645	0.0000000	0
TTC4	4.360258	0.2340794	0.0000000	0
TCP1	6.245183	0.3355812	0.0000000	0
EXPH5	4.679216	0.2524584	0.0000000	0
PDC	3.913700	0.2114457	0.0000000	0
PECR	7.066847	0.3826771	0.0000000	0
SPATA4	4.083636	0.2214210	0.0000000	0
OR6T1	4.742546	0.2589093	0.0000000	0
GSTA4	4.960515	0.2708118	0.0000000	0
AICDA	4.738962	0.2597619	0.0000000	0
CTSS	4.190558	0.2302146	0.0000000	0
STATH	3.971793	0.2193582	0.0000000	0
DOK2	4.236346	0.2348882	0.0000000	0

	log2FoldChange	lfcSE	padj	sgRNA
VSIG8	4.341556	0.2409319	0.0000000	0
NAT16	4.703002	0.2612772	0.0000000	0
LGALS13	3.871039	0.2157214	0.0000000	0
TNP1	3.864242	0.2158701	0.0000000	0
FAM129C	3.893236	0.2179035	0.0000000	0
EFNA5	3.904110	0.2190591	0.0000000	0
TRPV4	3.978101	0.2234071	0.0000000	0
FAM198A	4.127573	0.2322948	0.0000000	0
ADH1B	5.193003	0.2924105	0.0000000	0
ZCCHC24	4.136986	0.2339212	0.0000000	0
DDX54	6.278706	0.3551529	0.0000000	0
ANKRD39	3.920981	0.2258696	0.0000000	0
PLIN3	4.080239	0.2351741	0.0000000	1
CKAP5	3.893229	0.2285014	0.0000000	0
EPHA6	3.691534	0.2167774	0.0000000	0
SMARCE1	4.412301	0.2594900	0.0000000	0
TGFBR1	3.628380	0.2137654	0.0000000	0
OR4D9	4.516331	0.2662007	0.0000000	0
CRP	3.828385	0.2274688	0.0000000	0
DNAH14	3.862036	0.2296801	0.0000000	0
DEPDC5	4.387015	0.2609997	0.0000000	1
DPYSL5	3.812655	0.2280616	0.0000000	1
DRD4	4.808762	0.2884586	0.0000000	0
CARD16	4.278443	0.2574365	0.0000000	0
KAT7	4.215960	0.2544368	0.0000000	0
TAF6L	3.789237	0.2288556	0.0000000	0
PSG8	3.501229	0.2115590	0.0000000	0
HEMK1	3.576316	0.2162697	0.0000000	0
GPC6	3.707113	0.2252174	0.0000000	1
ABCC5	3.631643	0.2219177	0.0000000	0
GALNT9	3.529426	0.2157309	0.0000000	1
DYNC2H1	3.949518	0.2424754	0.0000000	0
C22orf43	3.613546	0.2218797	0.0000000	0
C6orf225	3.980879	0.2460784	0.0000000	0
TMEM171	3.686871	0.2281821	0.0000000	0
LITAF	3.543073	0.2202217	0.0000000	0
RRP36	3.542757	0.2214537	0.0000000	0
MS4A3	3.352942	0.2114071	0.0000000	1
IQSEC2	3.566842	0.2254991	0.0000000	1
TRMT2B	3.528124	0.2234424	0.0000000	0
GRIA1	3.361573	0.2133908	0.0000000	0
C7orf69	3.396034	0.2165563	0.0000000	0
C18orf32	4.042007	0.2590921	0.0000000	0
DSC1	3.372077	0.2171840	0.0000000	0
SUSD1	3.418729	0.2212476	0.0000000	1
OR2T33	3.605168	0.2343164	0.0000000	0
CASK	3.306026	0.2151936	0.0000000	0
CD8B	3.277309	0.2133374	0.0000000	0
NUGGC	3.504167	0.2282866	0.0000000	0
GFRA4	3.473893	0.2269155	0.0000000	0
HSD11B2	3.787430	0.2477479	0.0000000	0
GJA10	4.869288	0.3186474	0.0000000	0

	log2FoldChange	lfcSE	padj	sgRNA
APOBEC3C	3.926731	0.2574783	0.0000000	0
HMBS	3.203951	0.2111360	0.0000000	0
RFPL3	3.904716	0.2575942	0.0000000	0
HPRT1	4.254211	0.2816501	0.0000000	0
CYP2S1	5.434194	0.3599385	0.0000000	1
PPP1R14D	3.342205	0.2217278	0.0000000	1
LILRA2	3.292533	0.2202113	0.0000000	0
CACFD1	3.231289	0.2161260	0.0000000	0
ATXN2L	3.368761	0.2253310	0.0000000	0
KIAA0319	3.548164	0.2373354	0.0000000	0
ENDOD1	4.166475	0.2797797	0.0000000	0
TBC1D2	4.395156	0.2953056	0.0000000	0
CRNN	3.385241	0.2276444	0.0000000	0
NPPC	3.726096	0.2506002	0.0000000	0
MED19	3.528518	0.2377055	0.0000000	0
LAMP2	3.225746	0.2180217	0.0000000	0
ARAP2	3.249326	0.2202607	0.0000000	0
FAM168A	3.535475	0.2396782	0.0000000	1
S100B	3.877599	0.2648632	0.0000000	0
PSG6	3.953233	0.2705878	0.0000000	1
AGR2	3.629592	0.2486791	0.0000000	0
SH3YL1	3.338735	0.2291589	0.0000000	1
MOV10	3.834535	0.2634908	0.0000000	0
CCNC	3.055699	0.2099933	0.0000000	0
FBXL3	3.275436	0.2251166	0.0000000	0
TAAR1	3.363097	0.2317197	0.0000000	0
TAOK1	3.138359	0.2164000	0.0000000	0
BTF3L4	3.878493	0.2679471	0.0000000	0
HRAS	3.397918	0.2348820	0.0000000	0
PGD	3.681974	0.2545284	0.0000000	0
MOB3B	4.234701	0.2933756	0.0000000	1
ATP5B	4.281956	0.2969084	0.0000000	0
PSMD5	3.137787	0.2179978	0.0000000	1
FGF10	3.606056	0.2506380	0.0000000	1
ATP2A1	3.229826	0.2248054	0.0000000	0
COTL1	4.531563	0.3161069	0.0000000	1
YY2	3.564016	0.2497516	0.0000000	0
GFPT1	3.141059	0.2210468	0.0000000	0
ACN9	3.137431	0.2208652	0.0000000	2
KCTD19	3.922903	0.2781596	0.0000000	0
HOMER2	3.302905	0.2342271	0.0000000	0
POLR3D	3.889248	0.2762348	0.0000000	0
ADRA2B	3.379256	0.2401422	0.0000000	0
AQP2	3.213635	0.2287247	0.0000000	0
CAND1	3.881321	0.2763031	0.0000000	1
C5orf24	3.154849	0.2254627	0.0000000	0
CHCHD7	3.058663	0.2188671	0.0000000	1
DPP4	4.248329	0.3041673	0.0000000	0
RXFP2	2.975345	0.2131206	0.0000000	0
PRRT4	3.034682	0.2181475	0.0000000	0
GADD45GIP1	4.108552	0.2963254	0.0000000	1
MED15	3.167509	0.2285489	0.0000000	0

	log2FoldChange	lfcSE	padj	sgRNA
AEBP2	2.959211	0.2135404	0.0000000	1
PET112	3.348845	0.2423211	0.0000000	0
ZDHHC23	3.186817	0.2315484	0.0000000	0
TYSND1	3.500037	0.2547000	0.0000000	1
MED12L	3.378385	0.2458869	0.0000000	0
RGS8	3.070463	0.2239165	0.0000000	0
CD320	4.296445	0.3145466	0.0000000	0
PRSS12	4.577598	0.3361416	0.0000000	1
PATE1	3.492728	0.2566695	0.0000000	1
IP6K2	3.337445	0.2453393	0.0000000	2
DRD3	2.858017	0.2105328	0.0000000	0
VASH2	3.240706	0.2390707	0.0000000	0
UGT2A1	3.471829	0.2565948	0.0000000	0
PLOD3	3.269233	0.2428526	0.0000000	0
KCNQ5	3.445893	0.2565756	0.0000000	0
TMEM217	3.113187	0.2318559	0.0000000	0
C8orf33	3.272465	0.2442361	0.0000000	0
ETV3	2.949900	0.2202461	0.0000000	2
GLCCI1	3.433612	0.2564650	0.0000000	0
SPRED1	2.881014	0.2152267	0.0000000	0
RARS2	3.408508	0.2566105	0.0000000	0
IL9	3.669389	0.2769411	0.0000000	0
ETV5	3.800295	0.2876792	0.0000000	1
ARID1A	3.242295	0.2456831	0.0000000	0
EMD	2.988307	0.2272348	0.0000000	0
CYP24A1	2.904255	0.2210849	0.0000000	1
C10orf99	3.195180	0.2433664	0.0000000	0
OR9K2	3.170776	0.2423015	0.0000000	0
RUSC1	3.003821	0.2303867	0.0000000	0
HIBCH	2.767328	0.2123278	0.0000000	0
FUT5	3.700965	0.2840829	0.0000000	0
DNMT3A	3.384676	0.2605049	0.0000000	1
ABCB9	3.498442	0.2701812	0.0000000	1
SHBG	3.413726	0.2637874	0.0000000	0
SLC5A10	3.446850	0.2663844	0.0000000	0
HOOK3	4.174127	0.3235205	0.0000000	0
CA7	2.728486	0.2120874	0.0000000	0
FNDC3A	4.443346	0.3480707	0.0000000	1
PTGER4	4.020931	0.3153906	0.0000000	0
LRRC1	3.051211	0.2396762	0.0000000	1
ZNF800	2.886245	0.2278633	0.0000000	1
ERP27	2.784077	0.2200894	0.0000000	0
AIF1L	2.822204	0.2233707	0.0000000	1
PCMTD1	2.939444	0.2338677	0.0000000	0
GGCT	2.642568	0.2110605	0.0000000	1
CAMKV	2.829909	0.2262235	0.0000000	1
ERBB2IP	2.602530	0.2083252	0.0000000	0
AGTPBP1	3.040637	0.2436094	0.0000000	0
CISD1	2.721539	0.2191589	0.0000000	0
MFSD9	2.720002	0.2194456	0.0000000	0
HECW1	3.446675	0.2790110	0.0000000	0
FAIM3	2.628326	0.2128563	0.0000000	2

	log2FoldChange	lfcSE	padj	sgRNA
KCTD10	2.866037	0.2323020	0.0000000	0
FAN1	2.607943	0.2113866	0.0000000	0
MYCN	2.793798	0.2266270	0.0000000	0
FGGY	2.888693	0.2343718	0.0000000	0
RBP7	2.987414	0.2424268	0.0000000	0
SMARCB1	3.132458	0.2542986	0.0000000	0
NCDN	4.275136	0.3474931	0.0000000	0
TCHH	2.765478	0.2249907	0.0000000	1
SPP2	2.627741	0.2138907	0.0000000	1
ACP1	2.962517	0.2411864	0.0000000	0
F8	3.746050	0.3051912	0.0000000	1
DNAJC10	2.919622	0.2380264	0.0000000	0
UBR2	3.933313	0.3209395	0.0000000	0
CBLN1	2.643532	0.2167789	0.0000000	1
HEG1	2.817722	0.2311315	0.0000000	0
DPH2	2.816845	0.2318548	0.0000000	0
HAUS8	2.955979	0.2435027	0.0000000	0
OTUD7A	2.610888	0.2156370	0.0000000	0
CYYR1	3.492103	0.2885405	0.0000000	0
TRPC4AP	2.817138	0.2336796	0.0000000	0
EBF4	2.724346	0.2267707	0.0000000	1
EED	2.761251	0.2315113	0.0000000	0
MED23	3.578684	0.3002504	0.0000000	0
ZNF732	3.224148	0.2709493	0.0000000	0
DDX60L	3.306494	0.2782261	0.0000000	1
FAM96A	3.281986	0.2764427	0.0000000	0
MYL7	2.776594	0.2342792	0.0000000	0
TRPM4	3.424801	0.2904998	0.0000000	0
NNAT	3.396674	0.2885909	0.0000000	0
NRXN3	2.459022	0.2099881	0.0000000	0
KIAA1210	2.698769	0.2307868	0.0000000	0
PTPN12	2.518705	0.2156696	0.0000000	0
IRX6	3.037491	0.2604864	0.0000000	0
APOBEC3F	2.589847	0.2224600	0.0000000	1
UBA1	4.507578	0.3887466	0.0000000	0
ASPA	2.709257	0.2342045	0.0000000	1
SND1	3.109932	0.2692010	0.0000000	0
SLC30A1	2.901848	0.2517423	0.0000000	1
AGR3	2.718090	0.2358406	0.0000000	0
CCDC160	3.302488	0.2871392	0.0000000	0
TPT1	2.826021	0.2465898	0.0000000	0
PDCD10	2.404865	0.2104470	0.0000000	0
TMEM30B	3.203213	0.2810073	0.0000000	0
GDE1	2.891682	0.2540970	0.0000000	0
ABHD14A	3.898116	0.3432318	0.0000000	0
WDR3	3.124453	0.2753613	0.0000000	0
PPIE	2.464091	0.2176901	0.0000000	0
NCOR2	2.363069	0.2088124	0.0000000	1
CAMTA1	3.061452	0.2712554	0.0000000	0
KRTAP13-1	2.916517	0.2584980	0.0000000	0
DARS	2.581097	0.2297028	0.0000000	0
VTN	2.766484	0.2463736	0.0000000	0

	log2FoldChange	lfcSE	padj	sgRNA
CALN1	2.487449	0.2216435	0.0000000	1
CHST7	2.521202	0.2247385	0.0000000	0
ENGASE	3.515070	0.3139191	0.0000000	0
TWF2	2.610041	0.2334280	0.0000000	1
C9orf174	2.714538	0.2429755	0.0000000	0
RGS12	2.370904	0.2127629	0.0000000	0
ILK	2.633606	0.2384786	0.0000000	0
CD200	2.351215	0.2132540	0.0000000	3
BTNL3	2.809336	0.2554415	0.0000000	1
GSS	2.470973	0.2247911	0.0000000	0
HIST1H2BC	2.918442	0.2655543	0.0000000	0
SH2D4A	3.001038	0.2736160	0.0000000	0
PRSS36	2.592556	0.2365163	0.0000000	0
FAM53A	2.365954	0.2160039	0.0000000	0
RNF157	2.683208	0.2450272	0.0000000	0
SPATA18	3.438685	0.3148666	0.0000000	0
NT5E	2.473568	0.2268891	0.0000000	0
IL2RA	2.954320	0.2714646	0.0000000	1
PRR11	2.770618	0.2546620	0.0000000	0
OR7D2	2.392626	0.2203087	0.0000000	0
C8orf48	2.546156	0.2348693	0.0000000	1
ZNF195	2.904527	0.2685675	0.0000000	0
PPP4R2	2.424247	0.2242701	0.0000000	0
SEC63	3.201706	0.2965531	0.0000000	0
SEPT8	2.314211	0.2145099	0.0000000	1
KAT5	2.357926	0.2189250	0.0000000	0
MBD2	3.196893	0.2970201	0.0000000	0
MED16	2.927941	0.2725776	0.0000000	0
CSH2	3.341381	0.3119827	0.0000000	0
CCDC132	2.354462	0.2200150	0.0000000	0
NADSYN1	3.709669	0.3466902	0.0000000	0
RUFY1	2.394220	0.2238980	0.0000000	1
EIF4G2	2.263291	0.2125431	0.0000000	1
RASGEF1C	2.679275	0.2516299	0.0000000	0
KIAA0368	2.589651	0.2438253	0.0000000	0
TMED3	2.346334	0.2209371	0.0000000	0
EML1	2.472773	0.2328696	0.0000000	1
SORBS2	2.225874	0.2101229	0.0000000	0
LUM	2.385439	0.2253337	0.0000000	1
CAT	4.700354	0.4445507	0.0000000	0
C17orf77	2.588165	0.2453426	0.0000000	0
UBE2B	2.695521	0.2558665	0.0000000	0
TP53	2.229420	0.2117057	0.0000000	1
C20orf43	2.610071	0.2483761	0.0000000	1
SMUG1	3.343481	0.3185400	0.0000000	1
ALDH3A1	2.218072	0.2114177	0.0000000	0
ZNF711	3.330890	0.3183743	0.0000000	0
ABCF1	2.400457	0.2295058	0.0000000	1
SETDB1	2.207055	0.2112965	0.0000000	1
GIMAP1	2.581082	0.2474501	0.0000000	0
FAM21C	2.534099	0.2432503	0.0000000	0
ZNF354C	3.434725	0.3306199	0.0000000	0

	log2FoldChange	lfcSE	padj	sgRNA
MGAT4C	2.618975	0.2523632	0.0000000	0
PVRL1	2.245391	0.2164115	0.0000000	1
CCT8	2.653445	0.2558296	0.0000000	0
TNC	2.247834	0.2177941	0.0000000	0
DBX2	2.906909	0.2822724	0.0000000	0
KEAP1	2.276680	0.2220184	0.0000000	0
PRSS42	2.919346	0.2851654	0.0000000	0
FAM161A	2.603308	0.2547301	0.0000000	0
RAB11FIP2	2.301754	0.2253029	0.0000000	0
NDUFA8	2.373174	0.2324173	0.0000000	0
NFKBIA	2.212022	0.2166494	0.0000000	0
RPL3L	2.361370	0.2319869	0.0000000	0
NECAB3	2.315386	0.2283059	0.0000000	0
CDC37	2.437561	0.2407718	0.0000000	0
ERCC1	2.632278	0.2605680	0.0000000	0
SPOPL	2.250155	0.2230023	0.0000000	0
LCOR	2.442268	0.2420815	0.0000000	0
CSAD	2.461458	0.2442205	0.0000000	0
PODN	2.425691	0.2408484	0.0000000	0
C1orf49	2.392445	0.2401283	0.0000000	1
DPH5	2.623860	0.2636260	0.0000000	0
SCGB2A2	2.464940	0.2478321	0.0000000	0
AUTS2	2.160132	0.2173436	0.0000000	0
BAAT	2.612181	0.2629798	0.0000000	0
BDKRB1	3.985699	0.4012578	0.0000000	0
FTSJ1	2.754301	0.2775749	0.0000000	0
GREB1L	2.454698	0.2485730	0.0000000	0
NXT2	2.470917	0.2505216	0.0000000	1
OR51T1	2.441779	0.2478019	0.0000000	0
MAGI2	2.477301	0.2524725	0.0000000	0
PFKFB3	3.106574	0.3167244	0.0000000	0
ZNF679	2.123629	0.2168073	0.0000000	0
CDHR1	2.199059	0.2246986	0.0000000	0
FLAD1	2.434688	0.2492689	0.0000000	0
DPP8	2.125906	0.2176734	0.0000000	0
IRX5	2.176231	0.2228492	0.0000000	0
MRPL12	2.781995	0.2857189	0.0000000	0
SLC25A15	2.133584	0.2191293	0.0000000	1
CXCR2	2.471150	0.2542992	0.0000000	0
BCL2L12	2.480141	0.2555979	0.0000000	1
RCOR2	2.270366	0.2340436	0.0000000	0
TSPAN1	2.293357	0.2365580	0.0000000	0
ASCC2	2.455108	0.2536963	0.0000000	0
GRIA3	2.527490	0.2616315	0.0000000	0
ZC3H18	2.155601	0.2235297	0.0000000	0
APOA1	2.522305	0.2624172	0.0000000	0
TLN2	2.326207	0.2429592	0.0000000	0
PAICS	2.819438	0.2950498	0.0000000	0
GMEB1	2.267416	0.2373986	0.0000000	0
C7orf71	2.156738	0.2262461	0.0000000	0
RBM46	2.096042	0.2199128	0.0000000	1
PLAGL1	2.333073	0.2449343	0.0000000	0

	log2FoldChange	lfcSE	padj	sgRNA
PRPS2	2.161269	0.2278953	0.0000000	0
TP53BP1	2.212316	0.2335458	0.0000000	0
ATP2C1	1.992447	0.2106809	0.0000000	0
BCO2	2.177323	0.2303139	0.0000000	3
C16orf78	2.332516	0.2470383	0.0000000	0
RBM15B	2.410281	0.2556148	0.0000000	0
WFDC2	3.315891	0.3519165	0.0000000	0
SHH	2.185156	0.2319955	0.0000000	0
DLX4	2.438042	0.2588488	0.0000000	1
ANPEP	2.117472	0.2248708	0.0000000	1
USP11	3.481178	0.3700718	0.0000000	1
EIF3D	2.256929	0.2399630	0.0000000	0
AGT	2.501425	0.2661330	0.0000000	0
UGT3A2	2.071621	0.2205583	0.0000000	0
PRICKLE3	2.517452	0.2683715	0.0000000	1
REEP4	2.624436	0.2798627	0.0000000	0
TBC1D19	2.237401	0.2387098	0.0000000	0
PHF2	2.586293	0.2762400	0.0000000	0
MEF2B	2.020957	0.2160741	0.0000000	0
PCMT1	2.261885	0.2428547	0.0000000	0
ZNF423	2.388762	0.2565964	0.0000000	0
INTS12	2.134080	0.2297557	0.0000000	1
DNAJC24	2.155451	0.2322990	0.0000000	0
OR12D2	2.399539	0.2587747	0.0000000	0
C22orf13	2.894764	0.3124391	0.0000000	2
KRT15	2.267023	0.2447499	0.0000000	0
FAM160A2	2.284547	0.2467056	0.0000000	0
GLTPD1	2.102812	0.2279960	0.0000000	0
SLC26A7	2.382525	0.2583505	0.0000000	0
SYT5	2.033886	0.2206957	0.0000000	1
MIEN1	2.503399	0.2718114	0.0000000	0
PLCL1	3.167883	0.3452432	0.0000000	0
ARHGEF16	2.560597	0.2791486	0.0000000	1
CCR1	2.382407	0.2597853	0.0000000	0
COLEC12	2.387056	0.2604703	0.0000000	1
RNF7	1.960798	0.2140341	0.0000000	0
DLGAP1	1.971590	0.2158328	0.0000000	0
SLC15A4	2.845937	0.3117525	0.0000000	0
GPR133	2.205255	0.2416722	0.0000000	0
TRIP12	2.070429	0.2272333	0.0000000	2
BRMS1L	2.142087	0.2368632	0.0000000	0
LYPD5	2.005456	0.2224360	0.0000000	0
GAB2	2.048004	0.2273522	0.0000000	1
FAT1	2.803026	0.3118817	0.0000000	0
RCAN3	2.061533	0.2293958	0.0000000	1
BRSK1	2.440292	0.2718524	0.0000000	0
SPRYD3	2.715451	0.3029831	0.0000000	1
LRRC70	2.284263	0.2552054	0.0000000	0
OR13C2	2.580240	0.2893010	0.0000000	0
SCAMP4	2.237891	0.2514238	0.0000000	0
CPE	2.688936	0.3032543	0.0000000	0
GPR143	2.176259	0.2454871	0.0000000	0

	log2FoldChange	lfcSE	padj	sgRNA
SLC41A3	2.119922	0.2399229	0.0000000	0
RIF1	1.925917	0.2179892	0.0000000	0
RUFY2	2.350811	0.2660881	0.0000000	0
NPM3	2.002320	0.2267964	0.0000000	0
NAT9	2.234453	0.2533418	0.0000000	1
CDH23	1.931383	0.2191206	0.0000000	0
TM9SF4	2.432010	0.2763619	0.0000000	0
SLC35A1	1.889879	0.2147936	0.0000000	1
PYROXD1	2.624206	0.2984609	0.0000000	0
CYB5R1	2.245994	0.2554705	0.0000000	2
MYOG	2.403906	0.2735839	0.0000000	0
LILRB3	2.247558	0.2558842	0.0000000	0
AGPAT1	2.353382	0.2679763	0.0000000	0
LYNX1	2.092841	0.2390972	0.0000000	0
PPT1	2.204445	0.2520095	0.0000000	3
FUT2	2.368810	0.2709170	0.0000000	0
SEPHS1	3.193126	0.3655161	0.0000000	0
SDSL	2.281094	0.2611656	0.0000000	0
PLSCR2	2.104690	0.2411171	0.0000000	0
GUCY1B3	1.900905	0.2180932	0.0000000	1
RTP3	2.012807	0.2310043	0.0000000	1
KIAA1524	1.921593	0.2206177	0.0000000	1
RCBTB2	2.175028	0.2508200	0.0000000	0
SWT1	1.950903	0.2250872	0.0000000	0
VANGL1	1.923850	0.2224068	0.0000000	0
RDH11	2.112326	0.2442556	0.0000000	0
VIT	2.399204	0.2777474	0.0000000	0
GLRA4	1.997889	0.2318603	0.0000000	0
TRIM23	2.523532	0.2928815	0.0000000	0
IPP	1.824731	0.2122291	0.0000000	1
KCTD9	3.385372	0.3945905	0.0000000	1
MSRA	2.540471	0.2961207	0.0000000	0
FAM13B	2.598297	0.3034930	0.0000000	0
VPS39	2.200659	0.2579686	0.0000000	0
MLN	1.989615	0.2334625	0.0000000	0
ROBO3	3.411090	0.4005117	0.0000000	0
NCEH1	1.981189	0.2329216	0.0000000	1
NCL	2.072411	0.2437600	0.0000000	0
TMCO3	2.291124	0.2695605	0.0000000	1
ATP6V0A1	1.827492	0.2151800	0.0000000	0
NHP2	2.215204	0.2610445	0.0000000	0
PLK1	2.155666	0.2546439	0.0000000	0
CLEC2B	1.923793	0.2273162	0.0000000	0
DHTKD1	1.941967	0.2295253	0.0000000	0
C17orf57	1.842486	0.2179134	0.0000000	0
CCRL1	2.301822	0.2723708	0.0000000	1
CEP135	2.365226	0.2807505	0.0000000	0
THAP10	2.309204	0.2745274	0.0000000	0
PMFBP1	1.864437	0.2220165	0.0000000	0
EDC4	1.947027	0.2320466	0.0000000	0
CRIPT	2.253613	0.2686027	0.0000000	0
COQ6	1.949261	0.2323795	0.0000000	0

	log2FoldChange	lfcSE	padj	sgRNA
CEND1	2.398676	0.2868221	0.0000000	0
CDKN2B	3.022313	0.3617089	0.0000000	1
PGBD1	2.136903	0.2562906	0.0000000	0
CCDC50	1.845470	0.2218631	0.0000000	0
GNB2	1.983582	0.2385930	0.0000000	0
SPTBN1	1.777926	0.2138747	0.0000000	0
SEC31A	1.737612	0.2092069	0.0000000	2
CDH13	1.993257	0.2399915	0.0000000	2
DMXL1	3.623871	0.4375723	0.0000000	0
NOC3L	1.974483	0.2384687	0.0000000	0
CD4	2.313051	0.2795555	0.0000000	0
RND1	1.934936	0.2340181	0.0000000	0
TCEB2	1.793087	0.2168834	0.0000000	1
RPL7A	2.122944	0.2568040	0.0000000	0
HEBP1	1.863331	0.2254182	0.0000000	1
OR2T2	2.428984	0.2955155	0.0000000	0
CDKN2C	1.800099	0.2191693	0.0000000	1
SCLY	2.030206	0.2473084	0.0000000	1
SORBS1	1.828948	0.2229786	0.0000000	0
REXO2	1.883205	0.2296110	0.0000000	0
KCNK16	1.827065	0.2228928	0.0000000	0
ADIPOQ	1.748745	0.2134470	0.0000000	0
SCPEP1	1.890885	0.2310061	0.0000000	0
SPINK14	1.804635	0.2206355	0.0000000	0
TLR2	1.772984	0.2169559	0.0000000	0
TXNDC17	2.065055	0.2527422	0.0000000	1
IKZF5	2.105409	0.2578288	0.0000000	0
FES	1.898623	0.2325681	0.0000000	1
THBS1	2.210612	0.2711123	0.0000000	0
PPP1R12C	1.987747	0.2440285	0.0000000	0
BSPRY	2.650766	0.3254914	0.0000000	0
MMS19	1.837530	0.2256681	0.0000000	0
PAIP2B	1.768994	0.2172513	0.0000000	1
GPX4	2.497528	0.3070302	0.0000000	0
BCL2L11	1.720773	0.2120060	0.0000000	2
SYT6	1.725784	0.2130720	0.0000000	0
RLN3	2.057235	0.2540636	0.0000000	0
RUNDC3A	1.870389	0.2311005	0.0000000	0
EP300	1.934195	0.2393595	0.0000000	0
ID3	2.071362	0.2563700	0.0000000	0
SGCE	1.962554	0.2429695	0.0000000	0
OR4E2	1.851798	0.2295506	0.0000000	0
LRRTM2	1.908352	0.2368943	0.0000000	0
OR52J3	2.162812	0.2686583	0.0000000	0
DTX1	1.857408	0.2312623	0.0000000	0
ECHDC1	1.770782	0.2205746	0.0000000	1
SHMT1	2.384016	0.2994668	0.0000000	0
ZMIZ2	1.999431	0.2513106	0.0000000	0
OBFC1	1.874659	0.2356764	0.0000000	0
LGI3	2.020335	0.2540817	0.0000000	0
ZNF208	2.341808	0.2946849	0.0000000	0
ICAM5	2.125500	0.2675440	0.0000000	0

	log2FoldChange	lfcSE	padj	sgRNA
TONSL	1.959514	0.2468013	0.0000000	0
SPP1	1.856617	0.2341169	0.0000000	0
METTL5	1.931589	0.2437645	0.0000000	0
BBX	1.912262	0.2414593	0.0000000	0
GTF3A	2.179957	0.2752840	0.0000000	0
ZNF250	1.706959	0.2161502	0.0000000	0
CASQ1	2.010602	0.2546330	0.0000000	0
MATN4	2.026896	0.2571327	0.0000000	0
MAP1LC3A	2.181195	0.2768766	0.0000000	0
TAT	1.850980	0.2349872	0.0000000	0
PERP	1.986878	0.2522461	0.0000000	0
OR5P2	1.695199	0.2152305	0.0000000	0
CASQ2	1.940411	0.2476755	0.0000000	0
NDUFA7	2.564926	0.3275298	0.0000000	0
TAS2R5	2.346555	0.2997013	0.0000000	0
TM6SF2	1.996311	0.2550769	0.0000000	0
NAPRT1	1.751716	0.2239292	0.0000000	0
ZNF79	1.708782	0.2188948	0.0000000	0
ZNF645	1.702606	0.2182941	0.0000000	0
TBC1D4	2.140664	0.2749090	0.0000000	0
IL12A	1.841470	0.2368272	0.0000000	1
KCNH2	2.173421	0.2797435	0.0000000	1
FGF2	1.800352	0.2318595	0.0000000	0
PKD2	1.836161	0.2366309	0.0000000	0
RHOD	1.905638	0.2456558	0.0000000	0
BTBD10	1.751704	0.2258322	0.0000000	1
TBC1D8	1.674602	0.2165029	0.0000000	0
PNPLA4	1.852291	0.2394789	0.0000000	1
PRKCE	1.779700	0.2301479	0.0000000	1
TBX10	1.932084	0.2499264	0.0000000	0
FLG2	1.997596	0.2585481	0.0000000	0
UNC79	1.654797	0.2143544	0.0000000	0
SCN3A	1.626926	0.2114280	0.0000000	0
FBXW10	1.776437	0.2310210	0.0000000	0
LSM14A	1.720984	0.2241427	0.0000000	0
KIAA1024L	1.976366	0.2575598	0.0000000	0
SH2B3	1.711993	0.2234610	0.0000000	0
FLG	1.881176	0.2456158	0.0000000	2
SUFU	1.614294	0.2112921	0.0000000	0
URB1	2.401123	0.3143934	0.0000000	0
TICAM1	1.668629	0.2185924	0.0000000	0
BEND2	1.885910	0.2471224	0.0000000	0
BUD13	1.679057	0.2200681	0.0000000	0
SBSN	2.026961	0.2658545	0.0000000	0
RORB	1.931238	0.2542201	0.0000000	0
RPRD2	1.746226	0.2299121	0.0000000	1
ZFP30	1.846350	0.2435124	0.0000000	0
NDUFS8	1.853839	0.2447638	0.0000000	0
CRYGN	1.940692	0.2565693	0.0000000	1
C7orf26	2.085218	0.2762253	0.0000000	0
LRIG1	1.674751	0.2221313	0.0000000	1
LAMA1	2.144854	0.2845176	0.0000000	0

	log2FoldChange	lfcSE	padj	sgRNA
CYP2F1	1.632505	0.2165643	0.0000000	0
AHCYL2	2.091461	0.2775587	0.0000000	2
RPS4X	2.009609	0.2668344	0.0000000	0
MVD	1.875645	0.2491083	0.0000000	0
ICT1	1.760307	0.2340596	0.0000000	0
ATP6AP1L	2.163818	0.2879123	0.0000000	0
PCIF1	1.899399	0.2532597	0.0000000	1
MYO9B	1.935103	0.2584712	0.0000000	1
ZCCHC3	2.515257	0.3361042	0.0000000	0
NRD1	1.609026	0.2153131	0.0000000	1
ATAT1	1.730749	0.2317602	0.0000000	0
KCNE1	1.679115	0.2251761	0.0000000	0
DENND1B	1.740900	0.2338197	0.0000000	2
PLA2G4D	2.238824	0.3009754	0.0000000	0
PKIG	1.838435	0.2481025	0.0000000	1
BPIFB1	1.700792	0.2298392	0.0000000	0
PLCG1	1.678403	0.2270915	0.0000000	1
CCDC127	1.753972	0.2374497	0.0000000	0
GPR115	2.475624	0.3353763	0.0000000	0
DRG1	2.070689	0.2807540	0.0000000	0
RAB27A	1.934247	0.2622604	0.0000000	0
GPLD1	2.539325	0.3443545	0.0000000	0
ARL17A	2.976530	0.4036697	0.0000000	0
ARHGEF7	1.767141	0.2399960	0.0000000	1
C19orf77	2.639143	0.3585002	0.0000000	0
SPACA1	1.765571	0.2398603	0.0000000	2
GTF2H3	2.155900	0.2931157	0.0000000	0
GLT6D1	1.704841	0.2317981	0.0000000	0
TXNDC16	2.389051	0.3253014	0.0000000	0
APOL6	1.802314	0.2456767	0.0000000	0
HDAC6	1.898705	0.2590812	0.0000000	0
CDC123	1.873207	0.2556898	0.0000000	0
ZNF280D	1.778715	0.2431447	0.0000000	0
ATF3	1.833984	0.2509399	0.0000000	0
ORC5	1.749009	0.2399661	0.0000000	0
ZNF592	1.880116	0.2582455	0.0000000	0
FAM50A	1.639543	0.2252532	0.0000000	0
FASTKD1	1.603800	0.2203800	0.0000000	1
FAM47E	1.739342	0.2397991	0.0000000	1
ZBTB7A	1.560819	0.2159512	0.0000000	0
UBE2L6	1.535815	0.2125489	0.0000000	0
ANLN	1.856763	0.2578332	0.0000000	1
FAM19A4	1.573227	0.2190662	0.0000000	0
ASB7	1.778168	0.2476384	0.0000000	1
GNAS	1.532712	0.2136918	0.0000000	1
TMEM184C	1.681689	0.2351264	0.0000000	0
GTPBP5	1.642011	0.2296883	0.0000000	1
SLC25A37	1.546366	0.2163484	0.0000000	0
KRTAP12-4	1.912613	0.2676667	0.0000000	0
CCDC96	2.000803	0.2801365	0.0000000	0
INA	2.013823	0.2823600	0.0000000	0
ELK1	1.645959	0.2310990	0.0000000	1

	log2FoldChange	lfcSE	padj	sgRNA
CTC-360G5.1	1.563956	0.2200285	0.0000000	0
NAT1	1.616563	0.2275305	0.0000000	0
RAB43	1.763050	0.2484682	0.0000000	0
ESRRA	1.685150	0.2376627	0.0000000	0
WBP4	1.579875	0.2228576	0.0000000	1
MYO1H	1.743339	0.2461077	0.0000000	0
KATNA1	1.695293	0.2396223	0.0000000	0
PLSCR1	2.199568	0.3112518	0.0000000	0
S100A1	1.937042	0.2742645	0.0000000	0
CHCHD1	2.030284	0.2876709	0.0000000	0
ZBTB7B	1.490935	0.2112555	0.0000000	2
MCCC2	1.550409	0.2197252	0.0000000	1
EPB41L5	2.013691	0.2856520	0.0000000	0
CDKN3	1.586407	0.2257255	0.0000000	2
DENND2C	1.565390	0.2227735	0.0000000	1
USE1	2.075791	0.2954242	0.0000000	0
SKA2	2.084416	0.2967654	0.0000000	0
FXC1	1.939373	0.2761265	0.0000000	0
CUL5	1.663112	0.2368464	0.0000000	0
HIST1H3H	1.815873	0.2588018	0.0000000	0
WEE2	1.862474	0.2654671	0.0000000	0
C16orf74	2.553975	0.3640462	0.0000000	0
MED24	1.658054	0.2369229	0.0000000	0
MRPS12	1.626425	0.2324845	0.0000000	0
AGBL3	1.552218	0.2220414	0.0000000	0
LSMD1	1.558880	0.2230508	0.0000000	0
HIST3H2A	2.052256	0.2940856	0.0000001	0
ABCC12	1.787475	0.2562613	0.0000001	1
TIAF1	1.623688	0.2330602	0.0000001	0
UPK1A	1.637156	0.2357227	0.0000001	0
YIPF1	1.934288	0.2786592	0.0000001	0
HDGF	1.506042	0.2169793	0.0000001	0
RP11-24B21.1	1.844781	0.2658736	0.0000001	0
PRODH	2.324910	0.3355020	0.0000001	0
PRDX3	1.987974	0.2874760	0.0000001	0
LAX1	1.748908	0.2531554	0.0000001	0
CHIT1	2.047690	0.2964207	0.0000001	0
CBFB	1.755825	0.2543193	0.0000001	1
PSG3	2.335240	0.3401619	0.0000001	0
MBTD1	1.580516	0.2305948	0.0000001	1
METTL7B	1.691958	0.2469827	0.0000001	0
ZNF12	1.559661	0.2277475	0.0000001	0
ARID3C	1.908173	0.2788078	0.0000001	1
PTPRR	1.445979	0.2113447	0.0000001	0
GPR179	1.613303	0.2358014	0.0000001	0
KRT2	1.604192	0.2345105	0.0000001	0
CCT6B	1.495166	0.2187158	0.0000001	0
AMELX	1.553404	0.2272664	0.0000001	1
MAP3K4	1.763264	0.2581662	0.0000001	0
U2AF1	1.550023	0.2269943	0.0000001	0
NR0B2	1.617926	0.2372979	0.0000002	0
ELOVL1	1.918636	0.2814246	0.0000002	0

	log2FoldChange	lfcSE	padj	sgRNA
UBE2M	2.234248	0.3278412	0.0000002	1
KLHL8	1.471989	0.2160308	0.0000002	2
IGF1R	1.549247	0.2275419	0.0000002	0
ARHGAP27	1.973604	0.2900234	0.0000002	1
GIT2	1.513499	0.2227273	0.0000002	1
MRPL53	1.539934	0.2272113	0.0000002	0
RNF13	1.620569	0.2393518	0.0000002	1
PAQR4	1.560017	0.2304396	0.0000002	1
SUMF2	1.580507	0.2334815	0.0000002	1
KRTAP6-2	1.925079	0.2845251	0.0000002	0
DNAJC7	1.619118	0.2393148	0.0000002	1
SKIV2L2	1.591768	0.2353756	0.0000002	1
SLC30A6	1.454005	0.2150166	0.0000002	0
C5orf45	1.682940	0.2489030	0.0000002	0
CTU2	2.166840	0.3204826	0.0000002	0
CHST3	1.608727	0.2381639	0.0000002	0
AMOTL2	1.523546	0.2263175	0.0000003	0
SCO2	1.820936	0.2706850	0.0000003	0
APOA2	1.879905	0.2797355	0.0000003	1
F13B	1.656021	0.2464569	0.0000003	1
BNIP3L	2.054538	0.3057825	0.0000003	0
OR52E2	2.271421	0.3383194	0.0000003	1
TAF8	1.850180	0.2757777	0.0000003	1
ZNF326	1.575097	0.2357345	0.0000004	0
RRNAD1	1.666280	0.2496606	0.0000004	0
AGMO	1.474076	0.2210079	0.0000004	0
KRTAP4-2	2.065634	0.3099327	0.0000005	0
OR10G9	1.533533	0.2301025	0.0000005	1
GRIN2D	1.521679	0.2288297	0.0000005	0
TDP1	1.773904	0.2667756	0.0000005	0
CD248	2.309283	0.3473299	0.0000005	0
GTF2A1	1.737866	0.2617466	0.0000005	0
C16orf88	1.485297	0.2238394	0.0000006	0
GGT7	1.756420	0.2647424	0.0000006	0
TTC8	1.613369	0.2437704	0.0000006	0
KIAA0922	1.449865	0.2190664	0.0000006	0
GLI3	1.496576	0.2262714	0.0000006	0
SORT1	1.555405	0.2352080	0.0000007	1
CDKAL1	1.807942	0.2736336	0.0000007	0
PDE8A	1.571198	0.2378135	0.0000007	1
PELI1	1.445801	0.2197525	0.0000008	0
COL4A6	1.937030	0.2945305	0.0000008	0
SPRY2	1.578201	0.2401562	0.0000009	1
C21orf91	1.776978	0.2706149	0.0000009	0
BRCA1	1.613869	0.2457994	0.0000009	0
AEN	1.776663	0.2706674	0.0000009	0
RAB40AL	1.466613	0.2234503	0.0000009	0
CABP5	1.728892	0.2635964	0.0000009	1
PODXL2	1.603288	0.2448860	0.0000010	0
CNFN	1.418510	0.2166966	0.0000010	0
CYSLTR1	1.566293	0.2392842	0.0000010	0
HMGN3	1.708978	0.2610974	0.0000010	0

	log2FoldChange	lfcSE	padj	sgRNA
KRT18	1.722136	0.2631277	0.0000010	0
CAPZA1	1.858754	0.2842258	0.0000011	0
C1orf74	1.511600	0.2312054	0.0000011	0
ATRNL1	1.523214	0.2330644	0.0000011	1
SNX1	1.395870	0.2137906	0.0000011	0
RER1	1.571439	0.2406826	0.0000011	0
OR8A1	1.658167	0.2541532	0.0000012	0
OR4F5	1.600425	0.2455847	0.0000012	0
SCN9A	1.577271	0.2420489	0.0000012	0
UBE2N	1.663687	0.2554963	0.0000013	0
MMP8	1.478334	0.2270324	0.0000013	0
GPR12	1.803236	0.2770176	0.0000013	0
KLHL17	1.506590	0.2317048	0.0000014	1
SGSM3	1.650969	0.2539885	0.0000014	2
CRADD	1.486814	0.2287788	0.0000014	0
MFSD5	1.736095	0.2672367	0.0000014	0
MAPRE2	1.498493	0.2309675	0.0000015	0
TMEM127	1.395033	0.2150972	0.0000015	0
CCDC64B	1.856652	0.2866224	0.0000016	0
GNB2L1	1.981332	0.3065694	0.0000018	0
KRR1	1.676510	0.2597729	0.0000019	0
OR6C68	1.768466	0.2742895	0.0000020	0
OR10J1	1.540339	0.2390532	0.0000020	0
AP5Z1	1.712203	0.2657573	0.0000020	1
ZDHHC17	1.774283	0.2755680	0.0000021	0
SLC35A2	1.396758	0.2169436	0.0000021	0
UBAP2L	1.691890	0.2630320	0.0000022	0
ZNF571	1.569788	0.2441772	0.0000022	0
CRB3	1.676581	0.2608336	0.0000022	0
SLIT1	1.449520	0.2256871	0.0000023	0
IST1	1.557220	0.2425013	0.0000023	0
WDR13	1.680891	0.2628470	0.0000028	1
KCTD18	1.735661	0.2721567	0.0000031	0
ZSCAN4	1.830649	0.2871184	0.0000031	0
ZEB2	1.420748	0.2230460	0.0000033	1
CCDC172	1.452962	0.2281442	0.0000033	1
CSE1L	1.368404	0.2149511	0.0000033	1
PAQR8	1.477064	0.2323385	0.0000035	1
CREBBP	1.494127	0.2350660	0.0000036	1
DHRS13	1.652392	0.2600275	0.0000036	0
ST6GALNAC2	1.754308	0.2763889	0.0000038	0
SCML1	1.553587	0.2449089	0.0000039	2
IL20RB	1.427015	0.2250959	0.0000040	0
PDE10A	1.522619	0.2402129	0.0000040	0
SATL1	1.460913	0.2306622	0.0000041	0
GPR151	2.123915	0.3358392	0.0000044	0
SIGLEC5	2.134605	0.3376145	0.0000044	0
GGA2	1.429675	0.2265040	0.0000047	0
DR1	1.615107	0.2562244	0.0000050	0
GNE	1.397365	0.2220422	0.0000053	1
GEN1	1.540025	0.2447828	0.0000054	0
ADAMTS8	1.639312	0.2606521	0.0000055	0

	log2FoldChange	lfcSE	padj	sgRNA
CD68	1.546628	0.2460401	0.0000056	0
RFX4	1.369761	0.2179863	0.0000057	0
ROM1	1.681362	0.2677890	0.0000059	0
PTP4A2	1.529292	0.2437306	0.0000060	0
ORAI1	1.513132	0.2411585	0.0000060	0
FAM205A	1.673938	0.2679736	0.0000072	0
DYNC1LI2	1.583835	0.2537205	0.0000074	0
ANKRD55	1.418171	0.2273560	0.0000076	0
TBC1D29	1.651349	0.2650074	0.0000079	0
KRTAP5-2	1.397221	0.2242342	0.0000080	0
KCNC4	2.613380	0.4194965	0.0000080	0
TRIM4	1.547647	0.2484281	0.0000080	0
MAP3K5	2.008184	0.3226603	0.0000083	0
TCF7	1.605318	0.2579577	0.0000084	0
CMC1	1.465332	0.2355096	0.0000084	0
DEDD2	1.750846	0.2820832	0.0000093	0
UTS2R	1.606032	0.2589066	0.0000095	0
NSMAF	1.360574	0.2196741	0.0000101	0
TATDN3	1.357347	0.2194553	0.0000106	0
COX19	1.413706	0.2288669	0.0000112	0
DUSP5	1.571824	0.2548840	0.0000120	0
STK33	1.521523	0.2467591	0.0000120	1
SUMF1	1.341407	0.2177488	0.0000125	0
BIRC8	1.895518	0.3077525	0.0000125	0
TIGD3	1.622167	0.2634249	0.0000126	0
ATPAF1	2.188447	0.3555398	0.0000129	0
ZNF783	1.760930	0.2863720	0.0000134	0
ORMDL3	1.653320	0.2689253	0.0000135	0
FAM40A	1.597240	0.2598346	0.0000135	0
FRMD6	1.292472	0.2103239	0.0000137	0
TNFRSF21	1.391642	0.2265096	0.0000138	0
SRM	1.575089	0.2565644	0.0000142	0
SOSTDC1	1.369080	0.2231323	0.0000145	1
SLC25A26	1.402913	0.2288622	0.0000151	1
ALDH1L1	1.283174	0.2094242	0.0000153	0
NUP107	1.506469	0.2461443	0.0000160	0
FAM83E	1.564013	0.2557038	0.0000164	0
FOPNL	1.720215	0.2815423	0.0000171	2
NDUFB10	1.601499	0.2621979	0.0000173	0
CD19	1.439904	0.2359750	0.0000180	1
ZC3H3	1.362008	0.2234539	0.0000187	1
BRD9	1.340585	0.2202123	0.0000196	0
SLC25A33	1.607824	0.2642748	0.0000201	0
TSPYL2	1.453462	0.2391763	0.0000210	0
TOX3	1.342516	0.2209335	0.0000210	0
ZNF705B	1.573909	0.2591260	0.0000214	0
MAFF	1.675589	0.2759676	0.0000217	0
FANCD2	1.297043	0.2138616	0.0000226	1
TXNIP	1.733886	0.2859775	0.0000229	1
EPC2	1.327183	0.2191522	0.0000239	0
NBEAL2	1.566872	0.2588143	0.0000242	1
BAX	1.305193	0.2157326	0.0000248	0

	log2FoldChange	lfcSE	padj	sgRNA
OR13C5	1.629105	0.2692775	0.0000248	0
QSOX1	1.445486	0.2389575	0.0000249	1
EHF	1.464430	0.2421287	0.0000251	0
PCNXL2	1.375129	0.2273995	0.0000252	1
PRRX1	1.368747	0.2267926	0.0000272	0
MPLKIP	2.089526	0.3471142	0.0000299	0
SNAPIN	1.683624	0.2797272	0.0000301	1
UBE2L3	1.292243	0.2147317	0.0000302	1
PHC3	1.285340	0.2137410	0.0000310	0
CDC42BPA	1.385934	0.2305506	0.0000314	1
HIF1A	1.336675	0.2223782	0.0000316	2
YBEY	1.538800	0.2560335	0.0000317	0
GFAP	1.336861	0.2225489	0.0000323	1
CEBPB	1.464788	0.2441549	0.0000339	1
IRS4	1.692964	0.2825239	0.0000354	0
CEBPA	2.112772	0.3527678	0.0000361	0
PPP1R14C	1.645813	0.2748464	0.0000363	0
LCN2	2.357862	0.3938073	0.0000365	0
NOLC1	1.489421	0.2489327	0.0000374	0
OR5B12	1.397487	0.2336917	0.0000381	0
ACP6	1.353260	0.2265352	0.0000396	0
KIRREL	1.342842	0.2249636	0.0000408	1
TYMS	1.449209	0.2429022	0.0000415	1
PGK1	1.837092	0.3079189	0.0000415	0
CASP2	1.319526	0.2213333	0.0000426	1
HAUS1	2.076735	0.3483536	0.0000427	0
SLFN5	1.312204	0.2203892	0.0000447	0
KIAA1147	1.492824	0.2508256	0.0000453	0
PRPF8	1.415709	0.2378877	0.0000455	1
SFXN3	1.523358	0.2562265	0.0000471	0
SCCPDH	1.358713	0.2285412	0.0000472	0
PTPLAD2	1.314163	0.2210787	0.0000474	0
AMT	1.469137	0.2474563	0.0000496	3
TTLL9	1.351458	0.2278110	0.0000510	1
AP4M1	1.388652	0.2346985	0.0000560	1
UTRN	1.288124	0.2179212	0.0000581	0
ZNF627	1.408678	0.2384192	0.0000590	0
CELF2	1.251029	0.2118200	0.0000598	0
UTS2D	1.505255	0.2548708	0.0000598	1
TECRL	1.380565	0.2339076	0.0000612	1
CAMK2N2	1.298104	0.2199800	0.0000616	0
SEC22A	1.566974	0.2659870	0.0000654	0
NEIL3	1.530533	0.2598190	0.0000656	0
SELRC1	1.583196	0.2688960	0.0000668	1
DEFB121	1.296868	0.2202755	0.0000669	0
CD151	1.821242	0.3093578	0.0000670	0
MPST	1.305316	0.2220171	0.0000703	0
HIST1H2BM	2.154579	0.3670809	0.0000745	0
TMEM150C	1.282169	0.2185125	0.0000753	0
TSPAN14	1.371683	0.2340855	0.0000790	0
LAMTOR1	1.405628	0.2407030	0.0000892	0
PRKCA	1.658254	0.2845750	0.0000961	0

	log2FoldChange	lfcSE	padj	sgRNA
NLRX1	1.300903	0.2233705	0.0000979	0
DHFRL1	1.336155	0.2295046	0.0000991	0
TDO2	1.501798	0.2580114	0.0000999	2
SCD	1.569927	0.2699410	0.0001028	0
SRSF11	1.799760	0.3096486	0.0001050	0
CFHR5	1.590190	0.2736455	0.0001057	0
TOP1	1.447645	0.2491189	0.0001058	0
PAK2	1.303835	0.2245006	0.0001079	0
EPSTI1	1.266652	0.2182604	0.0001107	0
PDCD11	1.452387	0.2510294	0.0001229	0
KRTAP19-3	1.670263	0.2887729	0.0001242	1
NDUFB2	1.688407	0.2920689	0.0001266	0
OR9G1	1.352772	0.2341034	0.0001283	0
NDUFA4L2	1.610037	0.2787071	0.0001296	0
OR10G2	1.739170	0.3013726	0.0001343	0
FMN2	1.555909	0.2696255	0.0001344	0
CCDC142	1.500261	0.2599837	0.0001345	2
ALKBH6	1.428839	0.2476683	0.0001356	0
RAB10	1.709960	0.2973266	0.0001509	0
EXOC7	1.395682	0.2429251	0.0001561	0
RAB33B	1.421194	0.2476658	0.0001627	0
KANK2	1.262468	0.2200057	0.0001627	2
KRT5	2.299349	0.4009473	0.0001661	0
ZRANB3	1.466671	0.2557610	0.0001663	0
GPA33	1.344438	0.2344543	0.0001665	0
HIST1H2BO	1.339350	0.2341419	0.0001809	0
ASH2L	1.308333	0.2288430	0.0001842	0
C8orf40	1.398654	0.2448301	0.0001890	0
TWIST1	1.527702	0.2674559	0.0001899	0
SLC25A45	1.376669	0.2410520	0.0001909	0
STRADB	1.234844	0.2162279	0.0001911	1
ZMYND19	1.441372	0.2524308	0.0001921	0
PDS5B	1.579547	0.2766692	0.0001930	0
OXCT1	1.291782	0.2263054	0.0001941	1
MUM1	1.408815	0.2468619	0.0001956	2
MBIP	1.241766	0.2176529	0.0001974	1
DDAH1	1.610125	0.2823514	0.0002006	0
CXCR1	2.136876	0.3748843	0.0002035	1
RUFY3	1.249001	0.2197137	0.0002227	1
YAE1D1	1.287136	0.2265808	0.0002279	0
OR8H2	1.615230	0.2845939	0.0002348	1
HES5	1.252561	0.2207876	0.0002382	0
BACE2	1.210579	0.2135797	0.0002454	0
VAC14	1.361917	0.2403066	0.0002462	1
HINFP	1.240085	0.2190769	0.0002564	0
SST	1.251736	0.2213575	0.0002650	0
ABCB5	1.284436	0.2271701	0.0002661	1
LINGO1	1.652416	0.2923113	0.0002678	0
MUSK	1.778785	0.3146665	0.0002678	0
SLITRK2	1.353306	0.2396834	0.0002785	0
CNTN2	1.428426	0.2530121	0.0002793	0
PAK1	1.239126	0.2195101	0.0002805	1

	log2FoldChange	lfcSE	padj	sgRNA
ZW10	2.063589	0.3659978	0.0002916	0
KRTAP16-1	1.630010	0.2895727	0.0003076	0
KRTAP1-5	1.343931	0.2388434	0.0003115	0
COG5	1.383606	0.2462381	0.0003259	0
TMEM60	1.324477	0.2357336	0.0003267	1
UBE2E1	1.221648	0.2175489	0.0003325	1
ALPPL2	1.386632	0.2471164	0.0003407	0
KCNIP1	1.283832	0.2292304	0.0003623	0
RIMBP3	1.903031	0.3403409	0.0003817	0
DERL2	1.378444	0.2469340	0.0004027	0
CXorf66	1.238736	0.2220319	0.0004099	1
PCDHB1	1.467915	0.2631840	0.0004136	0
NES	1.388909	0.2493325	0.0004306	0
BCORL1	1.447302	0.2602203	0.0004525	0
RAE1	1.809616	0.3257873	0.0004716	0
PCNP	1.784683	0.3214729	0.0004798	0
MBD3L1	1.305287	0.2353433	0.0004944	0
SIX3	1.326463	0.2392108	0.0004976	0
DNAH5	1.419519	0.2560137	0.0004989	0
PTGDS	1.527970	0.2758086	0.0005125	0
ITGA8	1.317082	0.2377547	0.0005134	0
R3HDML	1.237692	0.2236303	0.0005286	1
PLXNC1	1.185440	0.2143882	0.0005442	2
MTHFD1	1.510525	0.2732318	0.0005474	0
SLC22A12	1.456384	0.2634934	0.0005510	1
GS1-211B7.1	1.759886	0.3186371	0.0005638	1
HKDC1	1.378220	0.2495354	0.0005638	1
IGSF5	1.343857	0.2434051	0.0005705	0
OPALIN	1.314316	0.2381731	0.0005795	0
NAA25	1.492692	0.2705661	0.0005840	0
AIP	1.341938	0.2434667	0.0006013	2
CCL22	1.356700	0.2463482	0.0006170	1
THY1	1.258855	0.2286193	0.0006201	0
DPF3	1.231538	0.2237050	0.0006242	1
MYCT1	1.229884	0.2237747	0.0006571	1
RAB27B	1.229102	0.2237121	0.0006644	0
CCT8L2	1.281574	0.2333093	0.0006685	0
LARP7	1.301803	0.2375222	0.0007164	1
RAB2B	1.239278	0.2261549	0.0007203	2
EIF2AK3	1.207158	0.2203675	0.0007278	0
GIMAP8	1.285537	0.2346823	0.0007284	1
MRPL41	1.777487	0.3245682	0.0007338	1
AGPAT2	1.179719	0.2155216	0.0007449	1
BOLA1	1.433579	0.2619198	0.0007467	0
CDKN1B	1.379865	0.2521093	0.0007469	0
ZBTB48	1.476865	0.2701587	0.0007753	0
COX7B2	1.981140	0.3625811	0.0007870	0
NDUFA12	1.393471	0.2554260	0.0008256	0
DENND5B	1.373555	0.2521845	0.0008677	1
CAGE1	1.237491	0.2276179	0.0009174	0
NSUN4	1.171472	0.2156123	0.0009352	2
ZNF677	1.541114	0.2837577	0.0009465	0

	log2FoldChange	lfcSE	padj	sgRNA
ATP5O	1.463163	0.2695743	0.0009647	0
SNAP29	1.314257	0.2424008	0.0009966	0

According to the value set, the **top 1 % enriched genes** were:

	log2FoldChange	lfcSE	padj	sgRNA
ACTA2	9.338286	0.2526421	0	1
GNA14	8.069706	0.2259080	0	1
C1orf27	7.366291	0.2123102	0	2
SNCG	7.902688	0.2277764	0	1
CLDN10	7.350818	0.2140744	0	2
NF2	7.936644	0.2315726	0	3
C11orf49	7.559413	0.2243719	0	1
ZP1	8.565882	0.2613221	0	0
NLGN1	7.376830	0.2281904	0	2
HGS	6.991316	0.2194959	0	1
CUL3	7.104205	0.2235502	0	2
CPAMD8	7.338817	0.2327893	0	1
PHC2	7.106705	0.2292402	0	1
RNH1	6.808820	0.2212518	0	1
STT3A	9.064755	0.2963053	0	1
KRT31	6.762881	0.2308151	0	1
MAP2K6	6.307783	0.2242981	0	0
ZSCAN1	6.731427	0.2402109	0	1
MIER3	6.202215	0.2219922	0	1
SERPINB6	6.466586	0.2324437	0	0
P4HB	6.897199	0.2481859	0	1
LBX1	7.759880	0.2808092	0	1
PRAM1	6.235969	0.2261683	0	1
MYO1E	8.547978	0.3121458	0	0
EHMT2	5.701878	0.2093030	0	1
MED12	7.560338	0.2776105	0	0
YTARVE19	6.328500	0.2360511	0	1
LGALS4	6.193239	0.2316681	0	1
MIA	6.588108	0.2502594	0	1
CEMP1	7.992845	0.3037934	0	0
ITFG1	6.251511	0.2386738	0	0
CACNB2	5.634675	0.2166708	0	1
GPR123	5.754574	0.2223640	0	0
TGFB3	6.081914	0.2355533	0	1
MNT	5.531416	0.2147847	0	1
EN2	7.105250	0.2764822	0	0
DMRT3	7.080885	0.2766271	0	0
NF1	9.724947	0.3812358	0	0
EPS8L1	6.076266	0.2387123	0	0
ANGEL1	5.485403	0.2165289	0	0
ZNF181	6.846511	0.2714563	0	0
SIGLEC9	5.850854	0.2321164	0	1
IL17REL	6.443761	0.2616995	0	1
KHK	5.506337	0.2237913	0	1
H2BFM	5.733252	0.2350696	0	0

	log2FoldChange	lfcSE	padj	sgRNA
GGT5	5.371806	0.2209324	0	1
ALDH16A1	5.405175	0.2243221	0	0
KCMF1	5.970485	0.2478522	0	0
DUS1L	5.234072	0.2181175	0	0
MARCH9	5.365378	0.2240985	0	0
KCTD7	5.313948	0.2227077	0	1
KIF13A	5.072697	0.2132921	0	1
ORC4	5.796772	0.2474226	0	1
NDUFAF5	5.310484	0.2271320	0	1
SLC37A3	5.611549	0.2412926	0	0
ZDHHC15	4.910957	0.2118107	0	1
ATG13	5.098733	0.2215154	0	0
SLC26A11	5.201130	0.2261180	0	0
TSHZ2	5.265230	0.2289415	0	1
CLC	5.981083	0.2620030	0	0
NPHS1	5.044634	0.2233433	0	0
TADA2B	5.158877	0.2290938	0	0
TSHZ1	6.530483	0.2913705	0	0
GTF3C6	5.355434	0.2391990	0	0
LSM4	5.558865	0.2485285	0	0
ZSWIM1	7.742572	0.3473327	0	0
GTF2E1	5.099043	0.2305588	0	1
ZFP82	5.758315	0.2604507	0	0
CCDC101	5.011924	0.2281743	0	0
EDIL3	4.701848	0.2150116	0	0
STK11	5.642961	0.2603659	0	1
C7orf44	4.982733	0.2303733	0	0
BMPR2	4.827518	0.2233804	0	2
SPECC1	5.935965	0.2758859	0	0
GLIS2	4.705422	0.2188324	0	0
FAM8A1	5.577840	0.2613678	0	0
PAPOLG	4.599119	0.2156004	0	0
RBAK	5.075482	0.2382819	0	0
FTO	5.159386	0.2426730	0	0
PLA2R1	6.062036	0.2873962	0	2
HBG1	6.128551	0.2908350	0	0
JMJD4	5.044956	0.2395965	0	0
PRR23B	6.153843	0.2924475	0	0
TAF5L	4.597939	0.2200371	0	0
PRLH	4.384423	0.2109276	0	0
TADA3	4.585672	0.2210488	0	0
ASIC1	5.546473	0.2675085	0	0
OXR1	4.308680	0.2101521	0	1
XRCC4	5.633933	0.2749364	0	0
OLA1	4.854227	0.2392028	0	0
CEBPZ	5.455162	0.2712529	0	0
SLC22A23	4.454831	0.2225487	0	0
WDR74	5.117015	0.2562150	0	0
NLRP14	4.318274	0.2164592	0	0
RPH3A	4.218168	0.2134338	0	1
CUBN	5.289401	0.2694670	0	1
ALG3	4.180852	0.2131998	0	0

	log2FoldChange	lfcSE	padj	sgRNA
ELMOD1	4.633026	0.2375055	0	0
SGIP1	5.790750	0.2969479	0	0
TADA1	5.531092	0.2844749	0	0
RP5-862P8.2	6.783811	0.3505102	0	0
TMEM194A	4.196772	0.2197127	0	0
TRA2A	5.833496	0.3071586	0	0
TNFRSF17	5.975815	0.3155635	0	0
LEO1	4.971464	0.2633555	0	0
STK25	4.883451	0.2600373	0	0
SLC3A1	5.072492	0.2711645	0	0
TTC4	4.360258	0.2340794	0	0
TCP1	6.245183	0.3355812	0	0
EXPH5	4.679216	0.2524584	0	0
PDC	3.913700	0.2114457	0	0
PECR	7.066847	0.3826771	0	0
SPATA4	4.083636	0.2214210	0	0
OR6T1	4.742546	0.2589093	0	0
GSTA4	4.960515	0.2708118	0	0
AICDA	4.738962	0.2597619	0	0
CTSS	4.190558	0.2302146	0	0
STATH	3.971793	0.2193582	0	0
DOK2	4.236346	0.2348882	0	0
VSIG8	4.341556	0.2409319	0	0
NAT16	4.703002	0.2612772	0	0
LGALS13	3.871039	0.2157214	0	0
TNP1	3.864242	0.2158701	0	0
FAM129C	3.893236	0.2179035	0	0
EFNA5	3.904110	0.2190591	0	0
TRPV4	3.978101	0.2234071	0	0
FAM198A	4.127573	0.2322948	0	0
ADH1B	5.193003	0.2924105	0	0
ZCCHC24	4.136986	0.2339212	0	0
DDX54	6.278706	0.3551529	0	0
ANKRD39	3.920981	0.2258696	0	0
PLIN3	4.080239	0.2351741	0	1
CKAP5	3.893229	0.2285014	0	0
EPHA6	3.691534	0.2167774	0	0
SMARCE1	4.412301	0.2594900	0	0
TGFBR1	3.628380	0.2137654	0	0
OR4D9	4.516331	0.2662007	0	0
CRP	3.828385	0.2274688	0	0
DNAH14	3.862036	0.2296801	0	0
DEPDC5	4.387015	0.2609997	0	1
DPYSL5	3.812655	0.2280616	0	1
DRD4	4.808762	0.2884586	0	0
CARD16	4.278443	0.2574365	0	0
KAT7	4.215960	0.2544368	0	0
TAF6L	3.789237	0.2288556	0	0
PSG8	3.501229	0.2115590	0	0
HEMK1	3.576316	0.2162697	0	0
GPC6	3.707113	0.2252174	0	1
ABCC5	3.631643	0.2219177	0	0

	log2FoldChange	lfcSE	padj	sgRNA
GALNT9	3.529426	0.2157309	0	1
DYNC2H1	3.949518	0.2424754	0	0
C22orf43	3.613546	0.2218797	0	0
C6orf225	3.980879	0.2460784	0	0
TMEM171	3.686871	0.2281821	0	0
LITAF	3.543073	0.2202217	0	0
RRP36	3.542757	0.2214537	0	0
MS4A3	3.352942	0.2114071	0	1
IQSEC2	3.566842	0.2254991	0	1
TRMT2B	3.528124	0.2234424	0	0
GRIA1	3.361573	0.2133908	0	0
C7orf69	3.396034	0.2165563	0	0
C18orf32	4.042007	0.2590921	0	0
DSC1	3.372077	0.2171840	0	0
SUSD1	3.418729	0.2212476	0	1
OR2T33	3.605168	0.2343164	0	0
CASK	3.306026	0.2151936	0	0
CD8B	3.277309	0.2133374	0	0
NUGGC	3.504167	0.2282866	0	0
GFRA4	3.473893	0.2269155	0	0
HSD11B2	3.787430	0.2477479	0	0
GJA10	4.869288	0.3186474	0	0
APOBEC3C	3.926731	0.2574783	0	0
HMBS	3.203951	0.2111360	0	0
RFPL3	3.904716	0.2575942	0	0
HPRT1	4.254211	0.2816501	0	0
CYP2S1	5.434194	0.3599385	0	1
PPP1R14D	3.342205	0.2217278	0	1
LILRA2	3.292533	0.2202113	0	0
CACFD1	3.231289	0.2161260	0	0
ATXN2L	3.368761	0.2253310	0	0
KIAA0319	3.548164	0.2373354	0	0

Depleted

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

	log2FoldChange	lfcSE	padj	sgRNA
MCL1	-2.367552	0.2785976	0.0000000	3
CD59	-2.197555	0.2667494	0.0000000	1
KLF5	-2.233800	0.2780824	0.0000000	2
KRTAP19-2	-3.512249	0.4599180	0.0000000	0
SLC38A2	-2.281088	0.2998086	0.0000000	1
PGAM4	-2.697786	0.3599118	0.0000000	1
C17orf85	-2.287259	0.3113941	0.0000000	2
RBMXL2	-2.507745	0.3451416	0.0000000	0
SOCS4	-1.778028	0.2473351	0.0000000	1
DEFB4A	-2.086804	0.2916660	0.0000000	0
NUDCD2	-2.290182	0.3202051	0.0000000	1
HSPG2	-1.814812	0.2553551	0.0000000	2
FOXL1	-1.867338	0.2682983	0.0000001	1
SEC23A	-2.024705	0.2923542	0.0000001	2
FIBIN	-2.549163	0.3712380	0.0000001	0
LYRM7	-1.631277	0.2377052	0.0000001	1
ANP32D	-2.391336	0.3489899	0.0000001	1
TMPRSS5	-2.097455	0.3080975	0.0000002	0
KRTAP23-1	-1.824401	0.2696100	0.0000002	1
SLC9C2	-1.858599	0.2749747	0.0000002	0
TGM3	-1.955641	0.2907600	0.0000003	0
RCVRN	-1.637771	0.2468474	0.0000006	2
FOXC2	-2.206823	0.3333684	0.0000006	2
TEX15	-2.116707	0.3209011	0.0000007	2
CRK	-1.673947	0.2544888	0.0000008	2
TLK2	-2.675877	0.4074812	0.0000009	1
EHBP1L1	-2.201658	0.3382077	0.0000013	0
FAM177A1	-1.499628	0.2322435	0.0000018	2
TMEM200A	-1.625976	0.2518120	0.0000018	1
FAM75A1	-2.512400	0.3893089	0.0000019	1
FAM110A	-1.740362	0.2698495	0.0000019	1
PTPN11	-1.768828	0.2748387	0.0000021	0
FAM217B	-2.004023	0.3114018	0.0000021	0
LHCGR	-1.648545	0.2565906	0.0000023	1
RAB6C	-1.982739	0.3098345	0.0000027	0
OR8H1	-2.446257	0.3832302	0.0000030	0
FSIP1	-1.860283	0.2915173	0.0000030	0
KDELC1	-1.767968	0.2771400	0.0000031	0
SLN	-3.003845	0.4716293	0.0000033	1
CYP8B1	-1.808227	0.2840500	0.0000033	0
LAMB1	-1.566723	0.2499054	0.0000062	2
ZNF813	-1.795330	0.2866565	0.0000065	1
PRMT6	-1.970435	0.3150689	0.0000069	1
OR4K14	-1.756642	0.2813338	0.0000073	2
LRRC16B	-1.859578	0.2980013	0.0000075	2
GRB2	-1.501196	0.2411530	0.0000083	1
ATXN2	-1.915381	0.3095859	0.0000105	1
SNAPC5	-1.456175	0.2371391	0.0000141	1
PINK1	-1.840153	0.2996929	0.0000141	0

	log2FoldChange	lfcSE	padj	sgRNA
OR10J5	-1.533944	0.2502641	0.0000151	2
BTC	-1.655922	0.2713381	0.0000179	1
KCNV2	-1.621483	0.2657051	0.0000179	1
OR6C76	-1.680265	0.2753387	0.0000179	0
UBE2F	-2.193820	0.3596728	0.0000182	1
PLAC1	-1.940939	0.3185333	0.0000189	1
GSC	-1.571987	0.2580820	0.0000192	1
EPS8	-1.687669	0.2784329	0.0000231	2
CNKSR3	-1.567618	0.2596181	0.0000267	1
H3F3C	-1.991880	0.3299365	0.0000268	0
PGM2L1	-1.506033	0.2501653	0.0000298	3
VKORC1L1	-1.669570	0.2777111	0.0000314	1
RGS9	-1.525028	0.2563599	0.0000461	1
MKL1	-2.056752	0.3458524	0.0000467	1
TRIM37	-1.507002	0.2534436	0.0000469	2
BHLHB9	-2.135820	0.3592118	0.0000470	0
ARL1	-1.466138	0.2472243	0.0000516	1
NSF	-2.070661	0.3492835	0.0000522	1
MT1A	-1.820725	0.3093032	0.0000673	1
OR4S1	-1.769293	0.3012113	0.0000726	1
TOR4A	-1.485235	0.2531322	0.0000755	0
ZNF674	-1.725911	0.2942934	0.0000768	1
CDK3	-1.512899	0.2580864	0.0000780	0
GPR110	-1.394404	0.2389593	0.0000915	2
OR9Q1	-1.805528	0.3097693	0.0000953	1
MYH2	-1.659531	0.2847225	0.0000953	1
HIST1H2BG	-1.572305	0.2701674	0.0001004	1
NBPF10	-1.552028	0.2666876	0.0001005	1
MERTK	-1.539628	0.2656502	0.0001159	1
AIM2	-1.346730	0.2325529	0.0001191	0
RXFP4	-1.931841	0.3338325	0.0001221	1
SLC2A14	-1.946722	0.3367654	0.0001267	2
KIR3DL1	-1.450283	0.2513759	0.0001354	1
NXPE2	-1.385774	0.2411576	0.0001552	1
PCDHB3	-1.841751	0.3209581	0.0001627	1
DUOX2	-1.550426	0.2702036	0.0001630	0
NXT1	-1.797669	0.3141069	0.0001779	1
LACRT	-1.499197	0.2620544	0.0001802	0
NABP2	-1.420937	0.2485868	0.0001854	1
PAFAH1B1	-1.695848	0.2974800	0.0002027	1
MAPKAPK2	-1.438692	0.2543210	0.0002616	1
ZHX2	-2.062148	0.3656013	0.0002880	1
KLF14	-2.313356	0.4108694	0.0003052	0
TAB2	-1.703363	0.3026261	0.0003083	0
PARD6B	-1.371168	0.2437675	0.0003150	2
ODF4	-1.756969	0.3126439	0.0003246	0
SNAPC2	-1.612890	0.2870307	0.0003255	0
GCGR	-1.543798	0.2747600	0.0003264	1
OR52B4	-1.565622	0.2793037	0.0003523	0
SEC16B	-1.402564	0.2512738	0.0004036	1
NOC2L	-1.859613	0.3332298	0.0004065	1
PHIP	-1.373837	0.2462037	0.0004076	2

	log2FoldChange	lfcSE	padj	sgRNA
RPL26L1	-1.539219	0.2763967	0.0004346	1
SPANXC	-1.537697	0.2762774	0.0004424	1
SLAIN2	-1.349295	0.2429672	0.0004748	0
MC5R	-2.301024	0.4149502	0.0004972	1
DPP7	-1.510674	0.2728927	0.0005249	0
SERGEF	-1.760013	0.3182086	0.0005393	0
CCR10	-1.999267	0.3623263	0.0005809	1
FAM47A	-1.561653	0.2837174	0.0006274	1
RPL21	-1.917157	0.3485635	0.0006421	1
MTM1	-1.598905	0.2911528	0.0006738	1
FAM103A1	-2.158646	0.3933522	0.0006884	0
C1orf21	-1.468003	0.2675882	0.0006953	1
FZD5	-2.052564	0.3745452	0.0007188	0
BLCAP	-1.535003	0.2804163	0.0007440	1
TUBGCP3	-1.977722	0.3638194	0.0009209	1
PIP	-1.528514	0.2811893	0.0009214	1
LCLAT1	-1.199626	0.2210937	0.0009744	2

According to the value set, the **top 1 % depleted genes** were:

	log2FoldChange	lfcSE	padj	sgRNA
MCL1	-2.367552	0.2785976	0.0000000	3
CD59	-2.197555	0.2667494	0.0000000	1
KLF5	-2.233800	0.2780824	0.0000000	2
KRTAP19-2	-3.512249	0.4599180	0.0000000	0
SLC38A2	-2.281088	0.2998086	0.0000000	1
PGAM4	-2.697786	0.3599118	0.0000000	1
C17orf85	-2.287259	0.3113941	0.0000000	2
RBMXL2	-2.507745	0.3451416	0.0000000	0
SOCS4	-1.778028	0.2473351	0.0000000	1
DEFB4A	-2.086804	0.2916660	0.0000000	0
NUDCD2	-2.290182	0.3202051	0.0000000	1
HSPG2	-1.814812	0.2553551	0.0000000	2
FOXL1	-1.867338	0.2682983	0.0000001	1
SEC23A	-2.024705	0.2923542	0.0000001	2
FIBIN	-2.549163	0.3712380	0.0000001	0
LYRM7	-1.631277	0.2377052	0.0000001	1
ANP32D	-2.391336	0.3489899	0.0000001	1
TMPRSS5	-2.097455	0.3080975	0.0000002	0
KRTAP23-1	-1.824401	0.2696100	0.0000002	1
SLC9C2	-1.858599	0.2749747	0.0000002	0
TGM3	-1.955641	0.2907600	0.0000003	0
RCVRN	-1.637771	0.2468474	0.0000006	2
FOXC2	-2.206823	0.3333684	0.0000006	2
TEX15	-2.116707	0.3209011	0.0000007	2
CRK	-1.673947	0.2544888	0.0000008	2
TLK2	-2.675877	0.4074812	0.0000009	1
EHBP1L1	-2.201658	0.3382077	0.0000013	0
FAM177A1	-1.499628	0.2322435	0.0000018	2
TMEM200A	-1.625976	0.2518120	0.0000018	1
FAM75A1	-2.512400	0.3893089	0.0000019	1

	log2FoldChange	lfcSE	padj	sgRNA
FAM110A	-1.740362	0.2698495	0.0000019	1
PTPN11	-1.768828	0.2748387	0.0000021	0
FAM217B	-2.004023	0.3114018	0.0000021	0
LHCGR	-1.648545	0.2565906	0.0000023	1
RAB6C	-1.982739	0.3098345	0.0000027	0
OR8H1	-2.446257	0.3832302	0.0000030	0
FSIP1	-1.860283	0.2915173	0.0000030	0
KDELC1	-1.767968	0.2771400	0.0000031	0
SLN	-3.003845	0.4716293	0.0000033	1
CYP8B1	-1.808227	0.2840500	0.0000033	0
LAMB1	-1.566723	0.2499054	0.0000062	2
ZNF813	-1.795330	0.2866565	0.0000065	1
PRMT6	-1.970435	0.3150689	0.0000069	1
OR4K14	-1.756642	0.2813338	0.0000073	2
LRRC16B	-1.859578	0.2980013	0.0000075	2
GRB2	-1.501196	0.2411530	0.0000083	1
ATXN2	-1.915381	0.3095859	0.0000105	1
SNAPC5	-1.456175	0.2371391	0.0000141	1
PINK1	-1.840153	0.2996929	0.0000141	0
OR10J5	-1.533944	0.2502641	0.0000151	2
BTC	-1.655922	0.2713381	0.0000179	1
KCNV2	-1.621483	0.2657051	0.0000179	1
OR6C76	-1.680265	0.2753387	0.0000179	0
UBE2F	-2.193820	0.3596728	0.0000182	1
PLAC1	-1.940939	0.3185333	0.0000189	1
GSC	-1.571987	0.2580820	0.0000192	1
EPS8	-1.687669	0.2784329	0.0000231	2
CNKSR3	-1.567618	0.2596181	0.0000267	1
H3F3C	-1.991880	0.3299365	0.0000268	0
PGM2L1	-1.506033	0.2501653	0.0000298	3
VKORC1L1	-1.669570	0.2777111	0.0000314	1
RGS9	-1.525028	0.2563599	0.0000461	1
MKL1	-2.056752	0.3458524	0.0000467	1
TRIM37	-1.507002	0.2534436	0.0000469	2
BHLHB9	-2.135820	0.3592118	0.0000470	0
ARL1	-1.466138	0.2472243	0.0000516	1
NSF	-2.070661	0.3492835	0.0000522	1
MT1A	-1.820725	0.3093032	0.0000673	1
OR4S1	-1.769293	0.3012113	0.0000726	1
TOR4A	-1.485235	0.2531322	0.0000755	0
ZNF674	-1.725911	0.2942934	0.0000768	1
CDK3	-1.512899	0.2580864	0.0000780	0
GPR110	-1.394404	0.2389593	0.0000915	2
OR9Q1	-1.805528	0.3097693	0.0000953	1
MYH2	-1.659531	0.2847225	0.0000953	1
HIST1H2BG	-1.572305	0.2701674	0.0001004	1
NBPF10	-1.552028	0.2666876	0.0001005	1
MERTK	-1.539628	0.2656502	0.0001159	1
AIM2	-1.346730	0.2325529	0.0001191	0
RXFP4	-1.931841	0.3338325	0.0001221	1
SLC2A14	-1.946722	0.3367654	0.0001267	2
KIR3DL1	-1.450283	0.2513759	0.0001354	1

	log2FoldChange	lfcSE	padj	sgRNA
NXPE2	-1.385774	0.2411576	0.0001552	1
PCDHB3	-1.841751	0.3209581	0.0001627	1
DUOX2	-1.550426	0.2702036	0.0001630	0
NXT1	-1.797669	0.3141069	0.0001779	1
LACRT	-1.499197	0.2620544	0.0001802	0
NABP2	-1.420937	0.2485868	0.0001854	1
PAFAH1B1	-1.695848	0.2974800	0.0002027	1
MAPKAPK2	-1.438692	0.2543210	0.0002616	1
ZHX2	-2.062148	0.3656013	0.0002880	1
KLF14	-2.313356	0.4108694	0.0003052	0
TAB2	-1.703363	0.3026261	0.0003083	0
PARD6B	-1.371168	0.2437675	0.0003150	2
ODF4	-1.756969	0.3126439	0.0003246	0
SNAPC2	-1.612890	0.2870307	0.0003255	0
GCGR	-1.543798	0.2747600	0.0003264	1
OR52B4	-1.565622	0.2793037	0.0003523	0
SEC16B	-1.402564	0.2512738	0.0004036	1
NOC2L	-1.859613	0.3332298	0.0004065	1
PHIP	-1.373837	0.2462037	0.0004076	2
RPL26L1	-1.539219	0.2763967	0.0004346	1
SPANXC	-1.537697	0.2762774	0.0004424	1
SLAIN2	-1.349295	0.2429672	0.0004748	0
MC5R	-2.301024	0.4149502	0.0004972	1
DPP7	-1.510674	0.2728927	0.0005249	0
SERGEF	-1.760013	0.3182086	0.0005393	0
CCR10	-1.999267	0.3623263	0.0005809	1
FAM47A	-1.561653	0.2837174	0.0006274	1
RPL21	-1.917157	0.3485635	0.0006421	1
MTM1	-1.598905	0.2911528	0.0006738	1
FAM103A1	-2.158646	0.3933522	0.0006884	0
C1orf21	-1.468003	0.2675882	0.0006953	1
FZD5	-2.052564	0.3745452	0.0007188	0
BLCAP	-1.535003	0.2804163	0.0007440	1
TUBGCP3	-1.977722	0.3638194	0.0009209	1
PIP	-1.528514	0.2811893	0.0009214	1
LCLAT1	-1.199626	0.2210937	0.0009744	2
KLHL11	-1.414060	0.2608941	0.0010066	0
C11orf31	-1.473023	0.2723072	0.0010681	1
SBK1	-1.273508	0.2355112	0.0010800	1
FAM166A	-1.394460	0.2580867	0.0011063	0
BCL9L	-1.627635	0.3013602	0.0011193	2
KRTAP26-1	-1.576267	0.2921445	0.0011538	0
MYH3	-1.439216	0.2668248	0.0011642	1
OR1E1	-1.452441	0.2693020	0.0011675	1
RPS10	-1.836254	0.3405691	0.0011780	0
MAP2K4	-1.428817	0.2651411	0.0011967	1
SPRR4	-1.473573	0.2736501	0.0012234	0
FBXL8	-1.501494	0.2794847	0.0013111	1
HORMAD1	-1.735543	0.3234385	0.0013587	1
OR5D18	-1.556001	0.2900297	0.0013658	0
VMAC	-1.314699	0.2451258	0.0013779	0
PFDN4	-2.293292	0.4277880	0.0013974	0

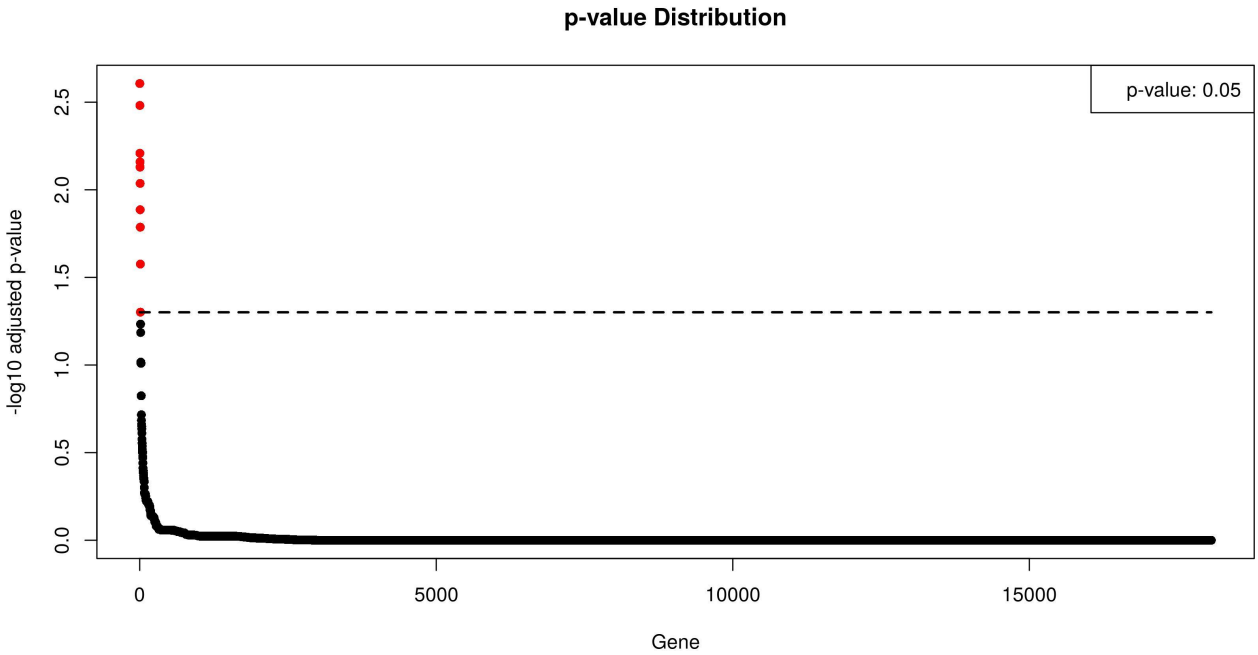
	log2FoldChange	lfcSE	padj	sgRNA
ZNF230	-1.368112	0.2555275	0.0014503	1
C12orf4	-1.291726	0.2417883	0.0015465	1
BPIFA2	-1.672122	0.3131202	0.0015652	1
FAM160A1	-1.382727	0.2590807	0.0015924	0
TRAPPC2L	-1.417492	0.2665045	0.0017599	2
FOXA2	-1.454712	0.2738310	0.0018222	2
GPRIN3	-1.892912	0.3563669	0.0018297	0
C17orf107	-1.662524	0.3131386	0.0018545	2
NBEA	-1.294696	0.2439115	0.0018663	0
GSDMC	-1.365911	0.2573671	0.0018745	0
ENTPD4	-1.282037	0.2415782	0.0018777	1
KRT82	-1.485660	0.2806459	0.0020179	0
TRIM35	-1.509529	0.2854885	0.0020870	1
C1orf9	-1.635180	0.3093589	0.0021077	1
DBH	-1.247718	0.2362344	0.0021540	1
MS4A6E	-1.482809	0.2810286	0.0022171	0
FAM22G	-1.493495	0.2832202	0.0022546	0
TEC	-1.353499	0.2569857	0.0023344	1
GLIPR1	-1.302262	0.2477452	0.0024694	0
FOXN2	-1.391987	0.2648924	0.0024900	0
CTGF	-1.380226	0.2629985	0.0025842	1
LACTB2	-1.312916	0.2504512	0.0026665	1
PSPC1	-1.293152	0.2468542	0.0027196	1
CST2	-1.486568	0.2837979	0.0027253	1
KRTAP4-6	-1.695665	0.3237215	0.0027264	0
RNPS1	-1.680299	0.3208158	0.0027330	0
RRP7A	-1.891515	0.3613148	0.0027694	0
C1orf229	-1.548990	0.2960214	0.0028052	0
C22orf29	-1.455449	0.2781652	0.0028108	0
TSC22D2	-1.435928	0.2744768	0.0028229	1
PGM2	-1.351479	0.2584609	0.0028620	1
KRTAP4-3	-1.807338	0.3461845	0.0029915	0
LIMD2	-1.463809	0.2805418	0.0030391	0
C8orf86	-1.400962	0.2686319	0.0030819	1
ZBTB39	-1.950501	0.3745730	0.0032154	0
RRM1	-1.596906	0.3067607	0.0032423	0
UBTD1	-1.459089	0.2812277	0.0035600	0
MPRIP	-1.207913	0.2328608	0.0035790	1
GATA1	-1.238033	0.2387943	0.0036322	1
RCCD1	-1.253364	0.2419869	0.0037310	1
OR1D5	-1.804547	0.3496494	0.0041159	2
CNNM1	-1.462817	0.2836297	0.0041940	1
OR4K17	-2.585651	0.5028595	0.0045565	0
PLK2	-1.307834	0.2545147	0.0046381	0
OR2A5	-2.099904	0.4098501	0.0050197	0
CETP	-1.566556	0.3057975	0.0050390	0
EIF3A	-1.656646	0.3236755	0.0051634	1

MAGeCK

All analysis data for MAGeCK can be found in the **PLX_resistance_YTAR_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
MED12	0.002475	1	1	18069	0	4
NF2	0.002475	2	1	18068	0	4
CUL3	0.003300	3	1	15040	0	5
DPH2	0.006188	4	1	18067	0	6
TADA2B	0.006931	5	1	18066	0	3
MED15	0.007426	6	1	18065	0	4
CCDC101	0.009194	7	1	18064	0	3
NF1	0.012995	8	1	18063	0	2
CDH13	0.016337	9	1	18062	0	6
CLDN10	0.016337	10	1	17061	0	3
TADA1	0.026553	11	1	17936	0	4
CCNC	0.049917	12	1	6704	2	3

According to the value set, the **top 1 % enriched genes** were:

	pos	rank.pos	neg	rank.neg	sgrna.neg.good	sgrna.pos.good
MED12	0.002475	1	1.000000	18069	0	4
NF2	0.002475	2	1.000000	18068	0	4
CUL3	0.003300	3	1.000000	15040	0	5
DPH2	0.006188	4	1.000000	18067	0	6
TADA2B	0.006931	5	1.000000	18066	0	3
MED15	0.007426	6	1.000000	18065	0	4
CCDC101	0.009194	7	1.000000	18064	0	3
NF1	0.012995	8	1.000000	18063	0	2
CDH13	0.016337	9	1.000000	18062	0	6
CLDN10	0.016337	10	1.000000	17061	0	3
TADA1	0.026553	11	1.000000	17936	0	4
CCNC	0.049917	12	1.000000	6704	2	3
ZNF592	0.058416	13	1.000000	18061	0	4
PPT1	0.058416	14	1.000000	18060	0	5
PGD	0.058416	15	1.000000	18059	0	3
ALG3	0.065285	16	1.000000	17963	0	4
ZEB2	0.096287	17	1.000000	18008	0	5
ABCB5	0.096287	18	1.000000	12727	1	6
PDCD10	0.096287	19	1.000000	17908	0	4
MLN	0.096287	20	1.000000	18058	0	3
BCL2L12	0.097885	21	1.000000	18057	0	4
SPECC1	0.097885	22	0.981701	2692	3	3
UBE2E1	0.149798	23	1.000000	18056	0	6
CBFB	0.149798	24	1.000000	18055	0	4
GADD45GIP1	0.149798	25	1.000000	18023	0	4
TAF6L	0.149798	26	1.000000	18054	0	3
RNF7	0.149798	27	1.000000	9325	1	4
C11orf49	0.192185	28	1.000000	18044	0	4
SMARCB1	0.207067	29	1.000000	18053	0	3
KANK2	0.218872	30	1.000000	18052	0	4
ACTA2	0.218872	31	0.940662	1067	1	1
NFASC	0.218872	32	1.000000	17795	0	5
KCTD10	0.218872	33	1.000000	18051	0	3
TAF5L	0.223791	34	1.000000	18050	0	2
BRD9	0.230976	35	1.000000	18024	0	6
PTPN12	0.244637	36	1.000000	17984	0	5
MED19	0.264915	37	1.000000	18049	0	4
SMG7	0.264915	38	1.000000	18048	0	4
EED	0.264915	39	1.000000	18007	0	4
BBX	0.278797	40	1.000000	18047	0	3
INA	0.278797	41	1.000000	18046	0	4
NRD1	0.279939	42	0.981701	2468	1	5
TAOK1	0.290928	43	1.000000	18043	0	3
ATXN2L	0.304343	44	1.000000	18045	0	2
MYO1E	0.310781	45	1.000000	10966	0	1
GNAS	0.315149	46	1.000000	9520	1	4
P4HB	0.315149	47	1.000000	6342	1	2
STT3A	0.315149	48	1.000000	17479	0	3
BIN1	0.315149	49	1.000000	6260	1	5
CCM2	0.315149	50	1.000000	8556	1	4
ZP1	0.334013	51	1.000000	6621	1	1
MFSD9	0.337871	52	1.000000	18042	0	2

	pos	rank.pos	neg	rank.neg	sgrna.neg.good	sgrna.pos.good
TSPAN1	0.362395	53	1.000000	17790	0	3
NPPC	0.362395	54	1.000000	8000	1	4
PLXNC1	0.386934	55	1.000000	18041	0	4
CEMP1	0.386934	56	1.000000	16528	0	2
ZC3H18	0.400990	57	1.000000	18040	0	3
ARID1A	0.400990	58	0.981701	2815	1	3
NCOR2	0.400990	59	1.000000	18030	0	4
FRMD6	0.400990	60	1.000000	12342	1	4
AHCYL2	0.400990	61	1.000000	17407	0	5
ATRNL1	0.414165	62	1.000000	18039	0	4
MED23	0.428256	63	1.000000	18037	0	2
SWSAP1	0.428256	64	1.000000	18036	0	4
ZDHHC15	0.428256	65	1.000000	10296	1	2
AMT	0.435419	66	0.944944	1210	1	6
SNCG	0.437491	67	1.000000	13382	0	2
TADA3	0.445616	68	1.000000	18035	0	2
GLIPR1L2	0.445616	69	1.000000	18034	0	3
GEN1	0.449937	70	1.000000	18033	0	4
SGSM3	0.449937	71	1.000000	18032	0	4
ELMOD1	0.451114	72	1.000000	18031	0	2
TRIP12	0.460264	73	1.000000	14214	1	5
ZBTB7A	0.460264	74	1.000000	18003	0	4
GPR123	0.460264	75	1.000000	18029	0	2
PET117	0.463588	76	1.000000	18028	0	3
SEC31A	0.501157	77	1.000000	11337	1	4
NOD2	0.536200	78	1.000000	18027	0	4
GIT2	0.536200	79	1.000000	17922	0	4
SPNS1	0.536200	80	0.940662	917	1	3
ATP5A1	0.542050	81	1.000000	18026	0	3
DMD	0.542050	82	1.000000	18038	0	7
TOX3	0.542050	83	1.000000	18025	0	2
LGALS4	0.542050	84	1.000000	17610	0	3
NLGN1	0.542050	85	0.961212	1837	3	2
PUS3	0.545116	86	1.000000	18022	0	4
MOB3B	0.545116	87	1.000000	18021	0	3
PLA2R1	0.545116	88	1.000000	17008	0	3
RP11-428C6.1	0.545116	89	1.000000	17890	0	5
LBX1	0.545116	90	1.000000	11525	0	1
CUX1	0.545116	91	1.000000	18020	0	3
C1orf27	0.545116	92	1.000000	8845	1	2
NDUFAF5	0.545116	93	1.000000	18019	0	3
PVRL3	0.545116	94	1.000000	18018	0	4
EHMT2	0.545116	95	1.000000	16703	0	1
CD320	0.545116	96	1.000000	14293	0	3
PRKCE	0.545116	97	1.000000	15620	0	3
CELF2	0.553900	98	1.000000	18017	0	2
FOXJ3	0.557406	99	1.000000	18016	0	3
FPGT	0.558720	100	1.000000	13093	0	3
ZSWIM1	0.558720	101	1.000000	17369	0	2
EN2	0.576636	102	1.000000	8892	1	2
PDC	0.588631	103	1.000000	11025	1	3
CCDC93	0.588631	104	1.000000	18015	0	5

	pos	rank.pos	neg	rank.neg	sgrna.neg.good	sgrna.pos.good
BCLAF1	0.588631	105	1.000000	18014	0	3
KDM5C	0.588631	106	1.000000	17499	0	3
ARHGAP35	0.588631	107	1.000000	18013	0	3
CPAMD8	0.588631	108	1.000000	11454	0	1
TCP1	0.588631	109	1.000000	8018	1	2
WDR20	0.588631	110	1.000000	17886	0	7
ARNTL2	0.588631	111	1.000000	18012	0	4
TFAP2C	0.588631	112	1.000000	18011	0	5
SPOPL	0.588631	113	1.000000	7955	1	2
NRXN3	0.588631	114	1.000000	15875	0	4
TNFRSF17	0.600911	115	1.000000	12099	0	3
GNA14	0.600911	116	1.000000	17104	0	2
PECR	0.600911	117	1.000000	12627	0	1
EBF4	0.600911	118	0.973010	2146	1	3
TXNDC17	0.600911	119	1.000000	17073	0	3
KLHL8	0.600911	120	1.000000	13934	1	5
PTGS1	0.600911	121	1.000000	18010	0	3
TXN2	0.600911	122	1.000000	18009	0	3
NSUN4	0.600911	123	1.000000	17986	0	6
YTARVE19	0.600911	124	1.000000	15589	0	3
EP300	0.600911	125	1.000000	7653	1	3
ZNF679	0.600911	126	1.000000	5573	2	2
PHC2	0.600911	127	0.981701	2441	3	2
MIA	0.600911	128	1.000000	11627	1	1
PCSK7	0.600911	129	1.000000	18006	0	4
ZNF444	0.600911	130	1.000000	18005	0	3
CTSB	0.600911	131	1.000000	13202	0	3
MAP1LC3A	0.600911	132	1.000000	15483	0	2
STK25	0.600911	133	1.000000	15212	0	4
TP53	0.600911	134	1.000000	17830	0	3
HGS	0.600911	135	1.000000	16850	0	2
SPACA1	0.600911	136	1.000000	18004	0	4
DMRT3	0.600911	137	1.000000	12036	0	2
FGGY	0.600911	138	1.000000	17983	0	3
CHCHD1	0.612211	139	1.000000	15057	0	3
MRPL53	0.612211	140	1.000000	17954	0	5
TCEB2	0.612211	141	1.000000	18002	0	4
TSHZ1	0.612781	142	1.000000	12175	0	1
ECHDC1	0.616012	143	1.000000	17888	0	4
TREML2	0.616012	144	1.000000	18001	0	4
SIGLEC9	0.616012	145	0.940662	935	2	1
CCT8	0.621789	146	1.000000	18000	0	2
PRODH	0.621789	147	1.000000	16550	0	2
INTU	0.621789	148	1.000000	17999	0	4
DAPL1	0.621789	149	1.000000	17998	0	4
CRYGN	0.621789	150	1.000000	17997	0	3
KEAP1	0.621789	151	1.000000	15301	0	3
ASIC1	0.621789	152	1.000000	12821	1	5
FAM19A4	0.621789	153	1.000000	5663	1	3
MED16	0.623473	154	1.000000	15685	0	3
NDUFA8	0.631713	155	1.000000	17877	0	3
CREBBP	0.631713	156	1.000000	17996	0	4

	pos	rank.pos	neg	rank.neg	sgrna.neg.good	sgrna.pos.good
RCOR2	0.631713	157	1.000000	17995	0	4
SERPINB6	0.631713	158	1.000000	12646	0	2
R3HDML	0.631713	159	1.000000	14901	0	3
TRPC4AP	0.631713	160	1.000000	16580	0	2
PCIF1	0.631713	161	1.000000	17994	0	3
LITAF	0.631713	162	1.000000	17799	0	3
ZMAT3	0.631713	163	1.000000	17905	0	4
MUM1	0.631713	164	1.000000	17993	0	3
ILF2	0.631713	165	1.000000	17992	0	4
IL17REL	0.633219	166	1.000000	17021	0	2
KLK10	0.633219	167	1.000000	17989	0	4
RNH1	0.640706	168	0.995377	5398	1	2
PPP1R14D	0.647636	169	1.000000	17720	0	3
CLEC2B	0.651281	170	1.000000	9243	1	2
ZSCAN1	0.656389	171	1.000000	8561	1	1
DDX54	0.668345	172	1.000000	15558	0	2
PRR23B	0.668345	173	1.000000	17988	0	1
EML1	0.668345	174	1.000000	17903	0	4
HEBP1	0.669109	175	1.000000	13937	0	3
EPHB2	0.673352	176	1.000000	14646	0	3
PCLO	0.676372	177	1.000000	17987	0	4
SH3GLB1	0.679503	178	1.000000	17305	0	3
KLHL5	0.679503	179	1.000000	17752	0	3
SRM	0.679503	180	1.000000	17870	0	4
ITFG1	0.679503	181	1.000000	5917	1	1

Depleted

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

	pos	rank.pos	neg	rank.neg	sgrna.neg.good	sgrna.pos.good
RREB1	0.999967	5256	0.014851	1	3	1

According to the value set, the **top 1 % depleted genes** were:

	pos	rank.pos	neg	rank.neg	sgrna.neg.good	sgrna.pos.good
RREB1	0.999967	5256	0.014851	1	3	1
CMIP	0.999967	10878	0.438614	2	5	1
LCLAT1	0.999967	18005	0.438614	3	4	0
CDKN1C	0.999967	17411	0.438614	4	2	0
NLGN3	0.999967	18069	0.438614	5	7	0
CAMKK1	0.999967	17949	0.508801	6	3	0
NLRP1	0.999967	13426	0.508801	7	3	1
FGFR1	0.999967	12192	0.508801	8	1	0
MAPKAPK2	0.999967	18068	0.508801	9	3	0
MCL1	0.999967	18066	0.605611	10	3	0
CD59	0.999967	18018	0.605611	11	3	0
LYRM7	0.999967	15805	0.605611	12	2	0
LTF	0.999967	10958	0.605611	13	2	2
PLCB1	0.999967	18065	0.605611	14	3	0
GRB2	0.999967	18064	0.605611	15	3	0
ARL1	0.999967	14292	0.655391	16	2	0
MLF1	0.999967	6191	0.655391	17	2	2
CMKLR1	0.999967	18063	0.655391	18	2	0
C22orf31	0.999967	15682	0.658214	19	1	0
CRK	0.999967	17534	0.658214	20	3	0
PGM2L1	0.999967	17754	0.658214	21	3	0
EEF1E1	0.999967	12168	0.658214	22	2	0
STRADA	0.999967	7228	0.658214	23	3	1
CPNE6	0.999967	6842	0.658214	24	3	1
TEX15	0.999967	18060	0.658214	25	2	0
PTPN13	0.999967	7171	0.658214	26	3	1
RNF144B	0.999967	18059	0.658214	27	4	0
TAF1B	0.999967	6261	0.658214	28	2	2
KLHL3	0.999967	17976	0.658214	29	7	0
CREB3L4	0.999967	14816	0.658214	30	3	1
SNAPC5	0.999967	18058	0.658214	31	4	0
RAI14	0.999967	9260	0.658214	32	4	1
MPRIP	0.999967	18057	0.658214	33	3	0
TRIM37	0.999967	18056	0.658214	34	2	0
PARD6B	0.999967	18055	0.658214	35	4	0
FAM177A1	0.999967	18054	0.658214	36	3	0
APTX	0.999967	18053	0.658214	37	4	0
DLG1	0.999967	16828	0.658214	38	1	0
KCNJ13	0.999967	16888	0.658214	39	3	0
PAIP1	0.999967	12899	0.658214	40	2	1
LZTS2	0.999967	17700	0.658214	41	3	0
OR4K14	0.999967	18052	0.658214	42	2	0

	pos	rank.pos	neg	rank.neg	sgrna.neg.good	sgrna.pos.good
NPC1L1	0.999967	3299	0.658214	43	2	1
OR2A14	0.999967	18051	0.658214	44	2	0
ACVR1B	0.996896	2785	0.658214	45	2	2
C2orf72	0.999967	13730	0.658214	46	2	0
ADCY9	0.999967	18050	0.658214	47	4	0
CCL11	0.999967	18049	0.658214	48	3	0
SOCS4	0.999967	18048	0.658214	49	2	0
TRAPPC2L	0.999967	18023	0.677525	50	3	0
KIR3DL1	0.999967	17483	0.699742	51	3	0
CD34	0.999967	17954	0.699742	52	3	0
RXFP4	0.999967	18046	0.699742	53	3	0
EMR3	0.999967	15093	0.699742	54	2	0
TMEM74B	0.999967	17710	0.699742	55	3	0
BCAN	0.999967	16854	0.699742	56	4	0
ATF6B	0.999967	16874	0.699742	57	1	0
FOXA2	0.999967	17999	0.699742	58	3	0
PEMT	0.999967	6916	0.699742	59	2	1
GPRC6A	0.999967	5143	0.699742	60	3	1
ITFG3	0.999967	18045	0.699742	61	4	0
BRAP	0.999967	18044	0.699742	62	4	0
RCVRN	0.999967	15730	0.699742	63	3	0
C17orf98	0.999967	16825	0.699742	64	2	0
AIM2	0.999967	18043	0.699742	65	4	0
MITF	0.999967	15960	0.699742	66	2	1
MAP2K5	0.999967	18042	0.699742	67	4	0
MNT	0.773599	251	0.699742	68	2	2
SPOCK2	0.999967	18062	0.699742	69	6	0
CLCN5	0.999967	5149	0.721726	70	5	1
SLURP1	0.999967	13517	0.721726	71	1	1
RP4-788L13.1	0.999967	17680	0.743056	72	4	0
C17orf107	0.999967	17988	0.745409	73	3	0
H2AFY	0.999967	6568	0.745409	74	2	1
USP25	0.999967	18041	0.745409	75	3	0
ANP32E	0.999967	6238	0.745409	76	3	1
PAM	0.999967	9179	0.745409	77	1	1
PHGDH	0.999967	9202	0.745409	78	4	1
PKP4	0.999967	11121	0.745409	79	1	1
TMEM8A	0.999967	13763	0.745409	80	1	0
OR10H1	0.999967	18040	0.745409	81	2	0
DIDO1	0.999967	18047	0.745409	82	5	0
SLC38A2	0.999967	18039	0.745409	83	3	0
ZNF321P	0.987716	2456	0.745409	84	1	2
ACHE	0.999967	13183	0.745409	85	2	1
ESAM	0.999967	16037	0.745409	86	2	0
MTUS1	0.999967	18067	0.745409	87	5	0
PINK1	0.999967	18036	0.745409	88	3	0
CHRNA10	0.999967	18035	0.745409	89	4	0
C20orf202	0.999967	16883	0.745409	90	1	0
GPR110	0.999967	17001	0.745409	91	2	0
ABHD12	0.999967	6949	0.745409	92	2	1
AGXT	0.999967	17052	0.745409	93	4	0
SLC15A3	0.999967	18034	0.745409	94	4	0

	pos	rank.pos	neg	rank.neg	sgrna.neg.good	sgrna.pos.good
CNTF	0.999967	18033	0.745409	95	4	0
CLDN18	0.999967	10493	0.745409	96	4	2
RARA	0.999967	7158	0.745409	97	3	2
COL2A1	0.999967	5351	0.745409	98	4	2
NTM	0.999967	6826	0.745409	99	2	2
SLC2A14	0.999967	18032	0.745409	100	2	0
PLCG2	0.999967	4817	0.745409	101	1	1
C7orf49	0.999967	11065	0.745409	102	1	1
MYOM1	0.999967	5624	0.745409	103	3	1
PNKD	0.999967	5595	0.745409	104	3	3
OR10J5	0.999967	18004	0.745409	105	3	0
MS4A6E	0.999967	18019	0.745409	106	3	0
RAET1E	0.999967	5362	0.745409	107	1	2
LEMD3	0.999967	18030	0.745409	108	3	0
CDK20	0.947277	1348	0.745409	109	2	3
TRIM35	0.999967	18029	0.745409	110	4	0
OXTR	0.999967	7696	0.745409	111	2	2
ADPRH	0.976674	2126	0.745409	112	3	2
NR2C1	0.999967	17099	0.745409	113	2	0
TNPO2	0.999967	6565	0.745409	114	2	1
MON1B	0.999967	18028	0.745409	115	4	0
PSEN1	0.994266	2640	0.745409	116	2	1
NOTCH1	0.999967	18027	0.745409	117	4	0
MYOF	0.999967	14047	0.756178	118	2	0
PKP2	0.999967	18026	0.756178	119	2	0
ODF4	0.999967	18025	0.758559	120	3	0
C14orf182	0.999967	14697	0.758559	121	2	0
FAM180A	0.999967	15821	0.758559	122	3	0
SLC12A2	0.999967	16190	0.758559	123	1	0
RTN1	0.999967	8025	0.758559	124	3	3
DEFB115	0.999967	17381	0.758559	125	3	0
CPNE1	0.999967	18021	0.758559	126	3	0
SEMA4A	0.999967	17431	0.758559	127	2	0
TRIM28	0.999967	12089	0.758559	128	2	1
TRHDE	0.999967	18020	0.758559	129	3	0
ISOC2	0.999967	6584	0.758559	130	2	1
MYBPC3	0.999967	5407	0.758559	131	3	1
FKBP7	0.999967	7471	0.783598	132	3	2
ACD	0.999967	15705	0.783598	133	3	0
LRRC16B	0.999967	17484	0.783598	134	2	0
KLF5	0.999967	17968	0.783598	135	3	0
DMXL2	0.999967	11108	0.783598	136	2	1
SF3B4	0.985678	2401	0.810400	137	1	2
OR5L1	0.999967	9316	0.810841	138	1	1
LHCGR	0.999967	18017	0.814566	139	3	0
EXT2	0.999967	5075	0.814566	140	2	2
NOS2	0.999967	9892	0.814566	141	2	1
CDK4	0.999967	13890	0.814566	142	3	0
EVI2B	0.999967	18015	0.824947	143	2	0
CIDEC	0.999967	17529	0.824947	144	2	0
EIF4G1	0.999967	14223	0.824947	145	1	1
CCL27	0.999967	18014	0.824947	146	4	0

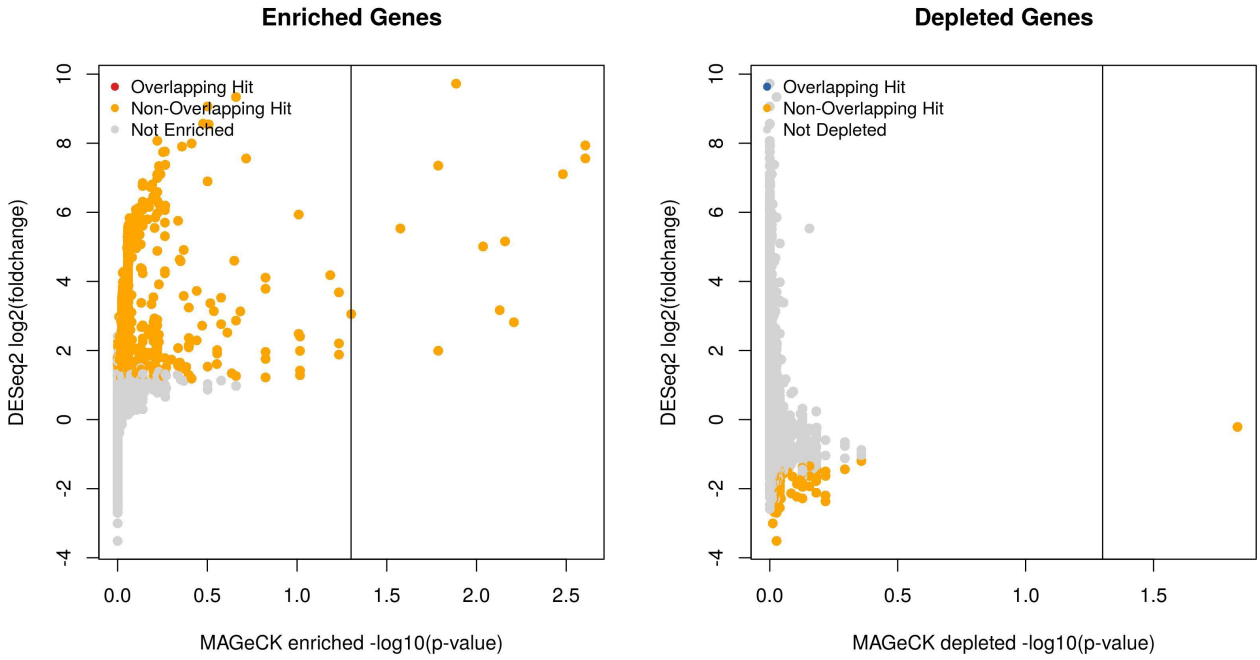
	pos	rank.pos	neg	rank.neg	sgrna.neg.good	sgrna.pos.good
NKX6-1	0.999967	16424	0.824947	147	4	0
LDHAL6A	0.999967	18013	0.824947	148	4	0
ENTPD4	0.999967	13297	0.824947	149	3	1
BHLHB9	0.999967	17499	0.824947	150	2	0
TMEM25	0.999967	12937	0.824947	151	3	1
AKR1C4	0.999967	18012	0.824947	152	2	0
MTTP	0.999967	17942	0.824947	153	4	0
SLC7A2	0.999967	13096	0.824947	154	2	0
RAD51AP2	0.999967	3634	0.824947	155	5	1
JMJD6	0.999967	3210	0.824947	156	1	3
APOBR	0.999967	18011	0.824947	157	4	0
ADAM28	0.999967	17274	0.824947	158	1	0
HDAC7	0.999967	13796	0.833509	159	1	0
BICD1	0.999967	3722	0.833509	160	2	2
PARP1	0.999967	4403	0.836511	161	2	1
C16orf53	0.999967	15434	0.838131	162	2	0
IQGAP3	0.999967	18010	0.840286	163	2	0
EGFR	0.999967	18009	0.840286	164	4	0
PI4KA	0.996896	2872	0.854561	165	2	1
DPP7	0.999967	14037	0.854561	166	1	0
CRYL1	0.999967	10805	0.854561	167	2	1
ZNF157	0.999967	5206	0.854561	168	3	1
TOR4A	0.999967	18008	0.854561	169	2	0
PLA2G2A	0.999967	5939	0.857767	170	2	2
PRH2	0.999967	18006	0.857767	171	3	0
IL31RA	0.999967	5366	0.866650	172	5	4
FXYD2	0.999967	6640	0.866650	173	2	1
ZSCAN2	0.985678	2419	0.866650	174	1	3
PQBP1	0.999967	8229	0.866789	175	3	1
HS2ST1	0.999967	16758	0.868239	176	2	0
SLC9A8	0.999967	17730	0.868239	177	2	0
CHST12	0.999967	18000	0.883274	178	2	0
EIF2C1	0.999967	12615	0.883663	179	4	1
RNF152	0.999967	17998	0.883663	180	2	0
MR1	0.999967	16501	0.883663	181	1	0

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.



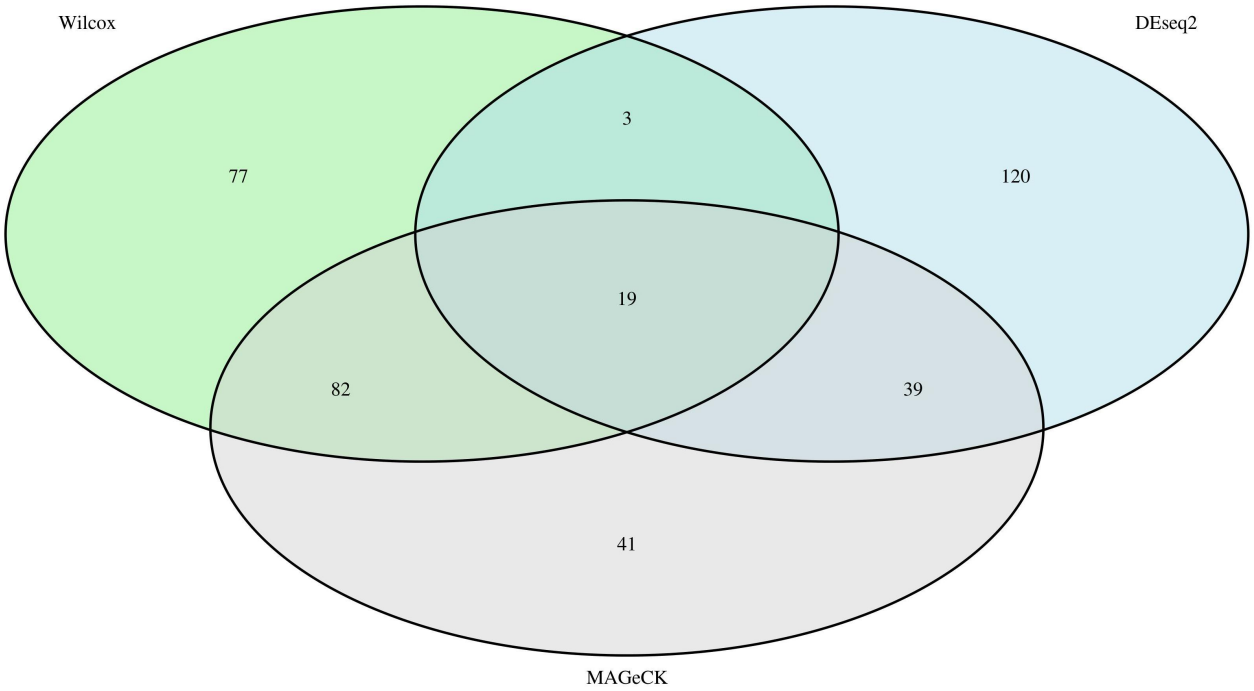
Overlaps in Enrichment Analysis

ATTENTION
No overlapping enriched genes were found between all three methods.

Therefore, the overlap from the 1 % of genes within all methods is used for plotting possible gene 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 enriched hits**, the overlap of enriched hits per analysis method is displayed as follows:



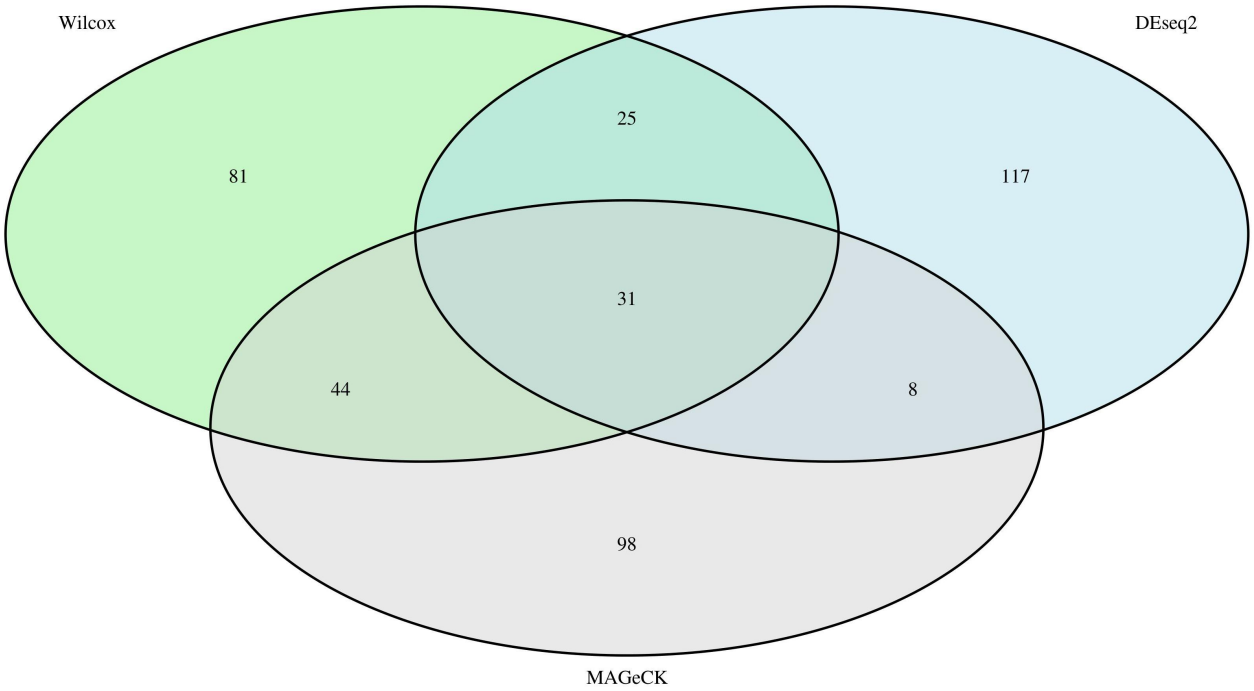
Overlaps in Depletion Analysis

ATTENTION
No overlapping depleted genes were found between all three methods.

Therefore, the overlap from the 1 % of genes within all methods is used for plotting possible hit candidates.

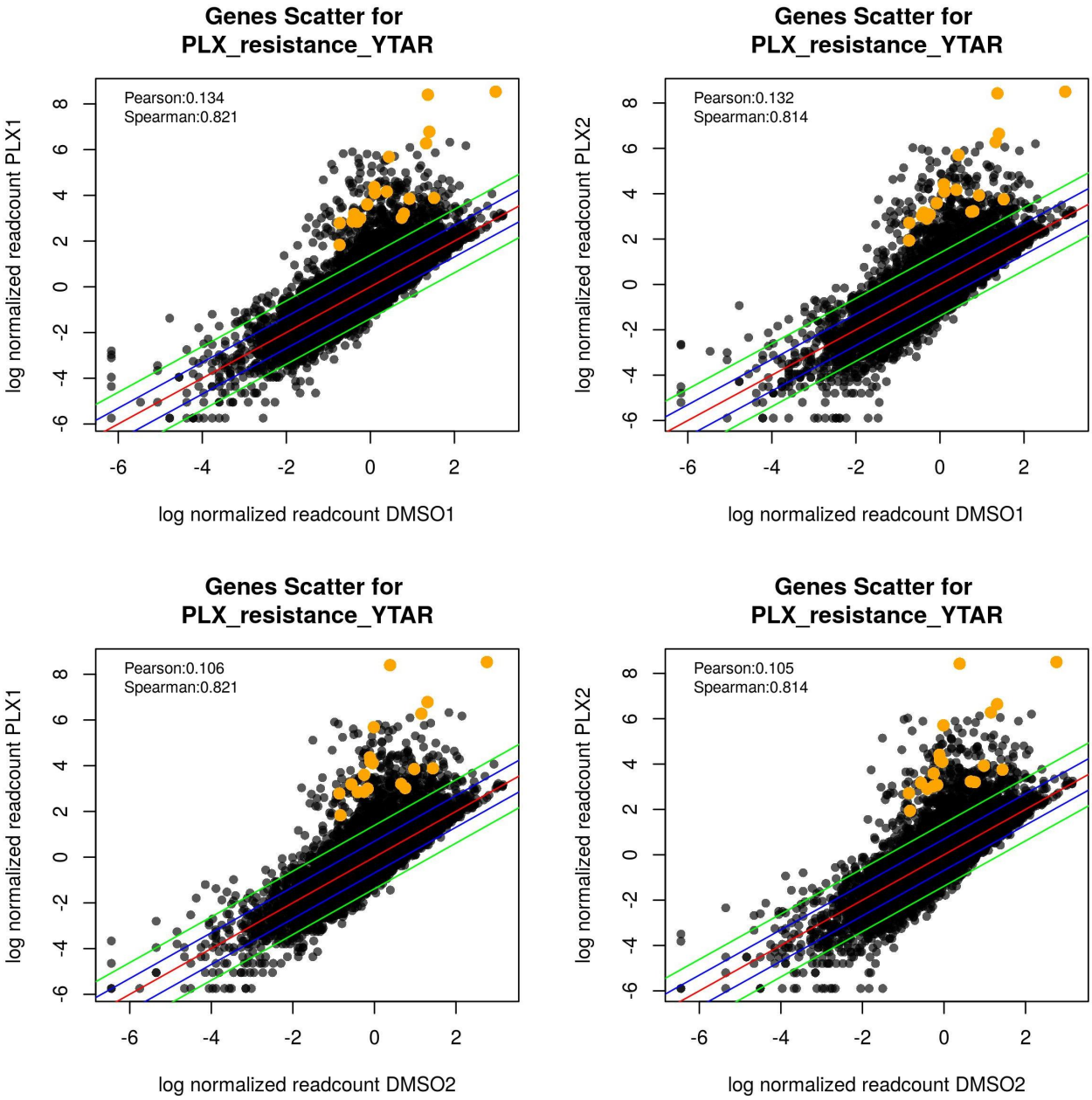
We strongly advise you to have a closer look at the individual outputs of the analysis methods and to carefully look at the following candidate genes.

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



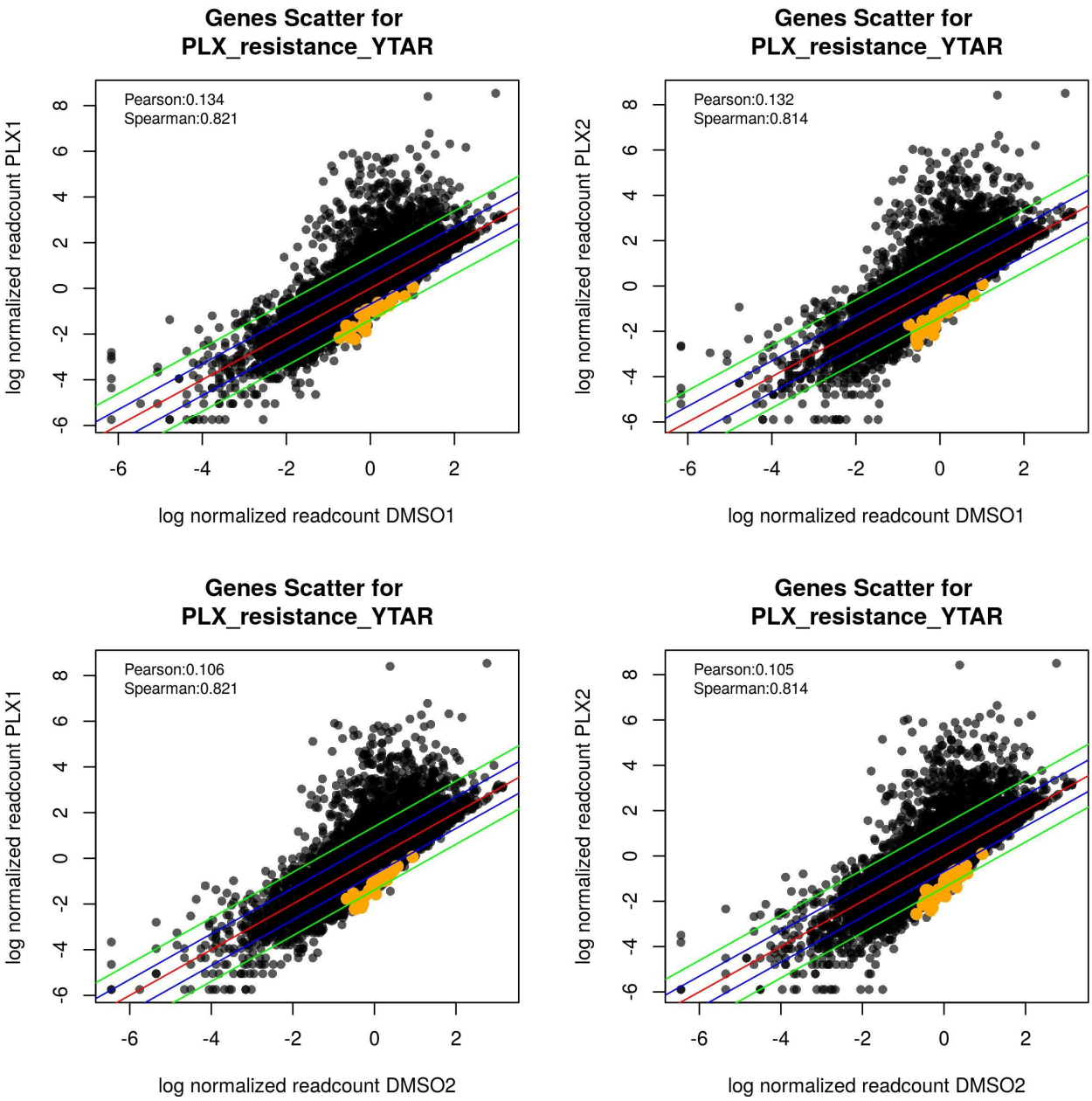
Enriched Overlapping Hit Candidates

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



Depleted Overlapping Hit Candidates

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


Genes Scatter for
PLX_resistance_YTAR
Pearson:0.134
Spearman:0.821
log normalized readcount PLX1
log normalized readcount DMSO1
Genes Scatter for
PLX_resistance_YTAR
Pearson:0.132
Spearman:0.814
log normalized readcount PLX2
log normalized readcount DMSO1
Genes Scatter for
PLX_resistance_YTAR
Pearson:0.106
Spearman:0.821
log normalized readcount PLX1
log normalized readcount DMSO2
Genes Scatter for
PLX_resistance_YTAR
Pearson:0.105
Spearman:0.814
log normalized readcount PLX2
log normalized readcount DMSO2

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 *signficantly* 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 1 % of top enriched and the top 1 % 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

MED12

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

ENSEMBL ID (links to Ensembl) ENSG00000184634

HGNC SYMBOL (links to GeneCards) MED12

GENE DESCRIPTION
mediator complex subunit 12 [Source:HGNC Symbol;Acc:HGNC:11957]

GO TERM
protein complex

MIM GENE DESCRIPTION
MEDIATOR COMPLEX SUBUNIT 12; MED12;;MEDIATOR OF RNA POLYMERASE II TRANSCRIPTION, SUBUNIT 12, S. CEREVISIAE,HOMOLOG OF;;TRINUCLEOTIDE REPEAT-CONTAINING GENE 11; TNRC11;;THYROID HORMONE RECEPTOR-ASSOCIATED PROTEIN, 230-KD SUBUNIT; TRAP230;;HUMAN OPPOS /…/IRED GENE; HOPA;;KIAA0192

ENSEMBL PROTEIN ID
ENSP00000333125

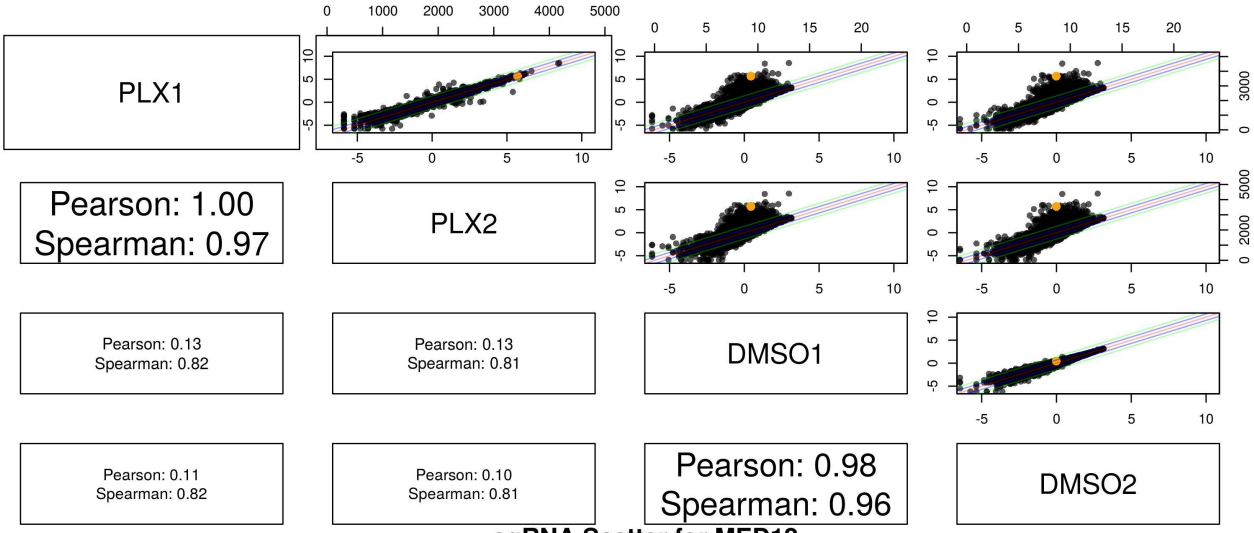
PROTEIN FAMILY DESCRIPTION
MEDIATOR OF RNA POLYMERASE II TRANSCRIPTION SUBUNIT 12 MEDIATOR COMPLEX SUBUNIT 12 TRINUCLEOTIDE REPEAT CONTAINING GENE 11

Wilcox p-value: 0.05685401

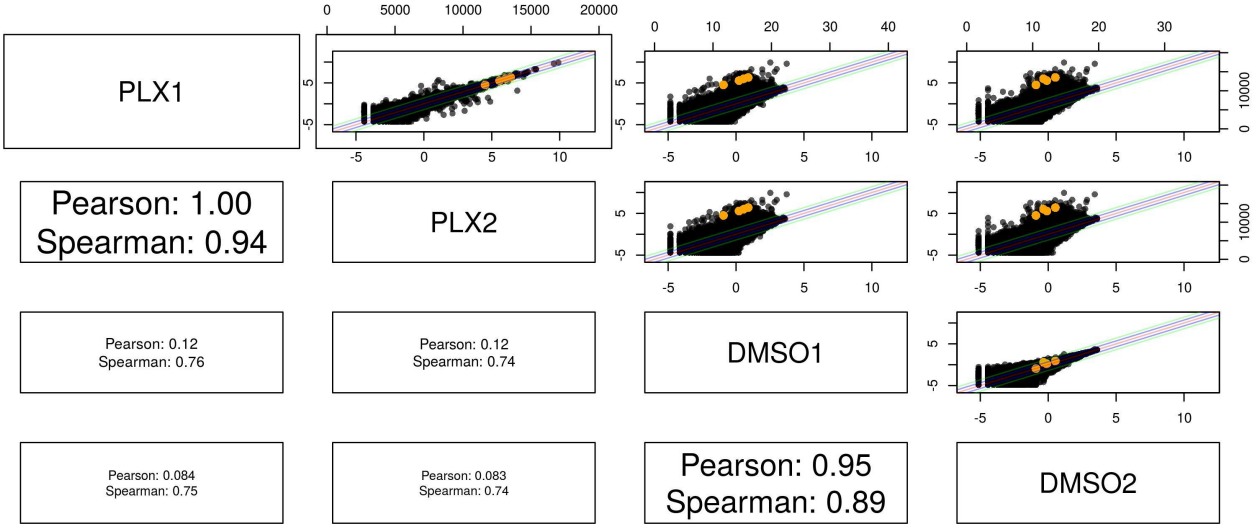
DESeq2 p-value: 4.687767e-159

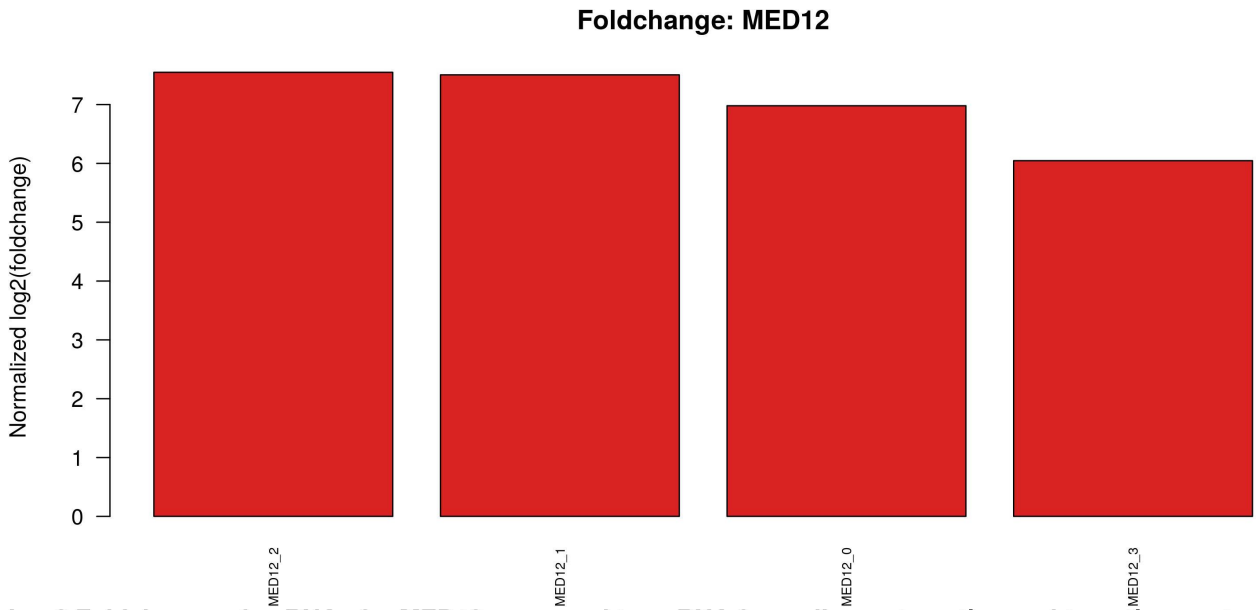
MAGeCK p-value: 0.002475

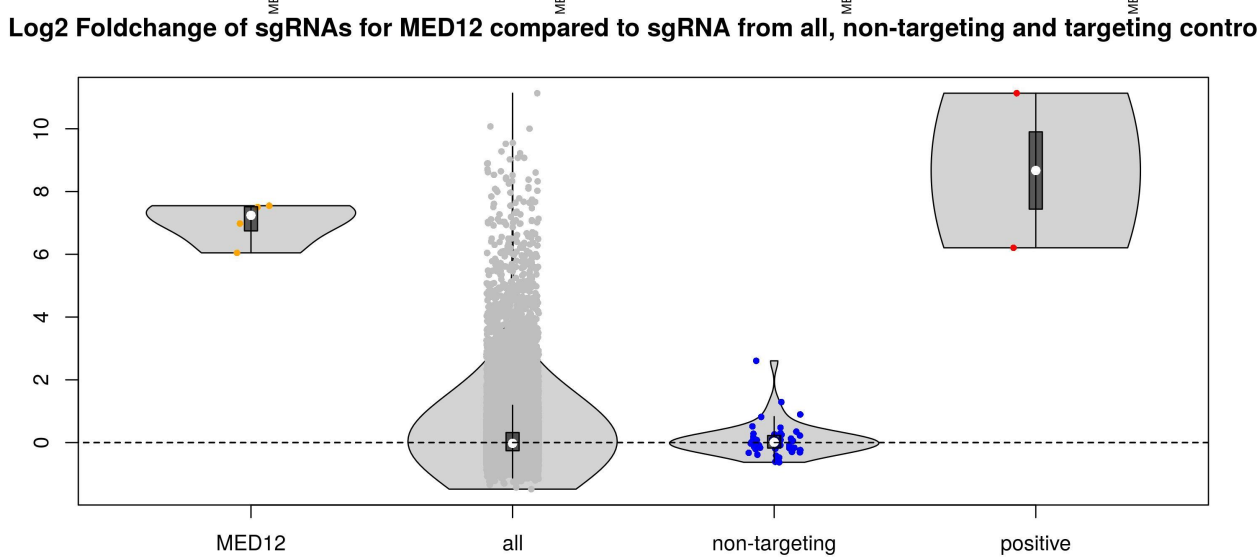
Gene Scatter for MED12
PLX_resistance_YTAR



sgRNA Scatter for MED12
PLX_resistance_YTAR




Foldchange: MED12
Normalized log2(foldchange)
0
1
2
3
4
5
6
7
MED12_2
MED12_1
MED12_0
MED12_3


Log2 Foldchange of sgRNAs for MED12 compared to sgRNA from all, non-targeting and targeting contro
0
2
4
6
8
10
MED12
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
3	MED12_2	MED12	none	7.548066
2	MED12_1	MED12	none	7.504600
1	MED12_0	MED12	none	6.979513
4	MED12_3	MED12	none	6.045672

NF2

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

ENSEMBL ID (links to Ensembl) LRG_511

HGNC SYMBOL (links to GeneCards) NF2

GENE DESCRIPTION
neurofibromin 2 (merlin) [Source:HGNC Symbol;Acc:HGNC:7773]

GO TERM

MIM GENE DESCRIPTION
NEUROFIBROMIN 2; NF2;;MERLIN;;SCHWANNOMIN; SCH

ENSEMBL PROTEIN ID
LRG_511p2

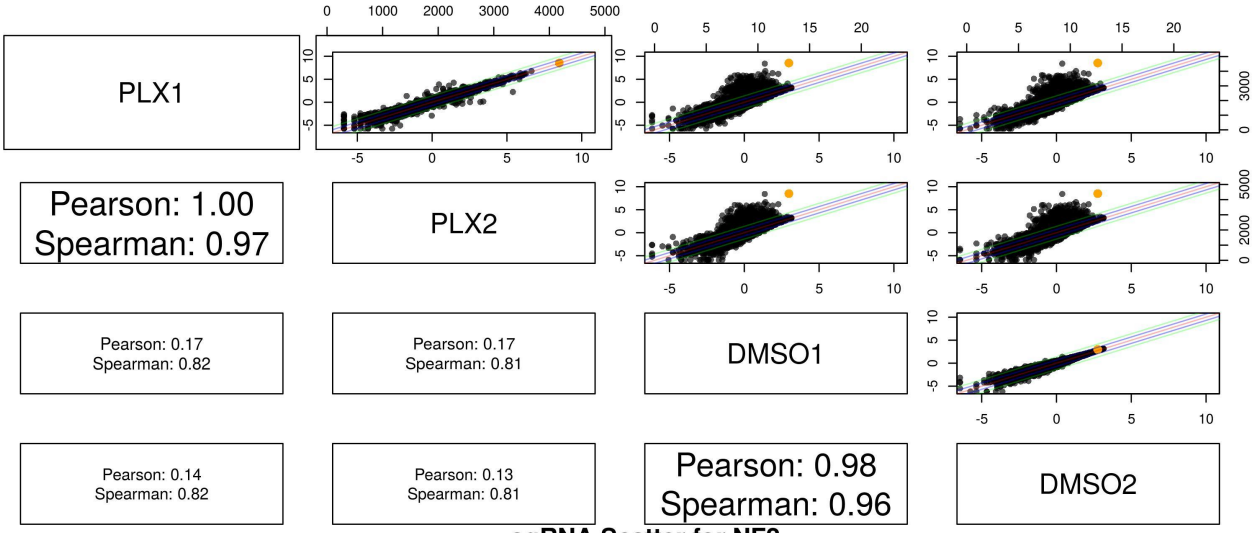
PROTEIN FAMILY DESCRIPTION
MERLIN MOESIN EZRIN RADIXIN NEUROFIBROMIN 2 SCHWANNOMIN

Wilcox p-value: 0.05685401

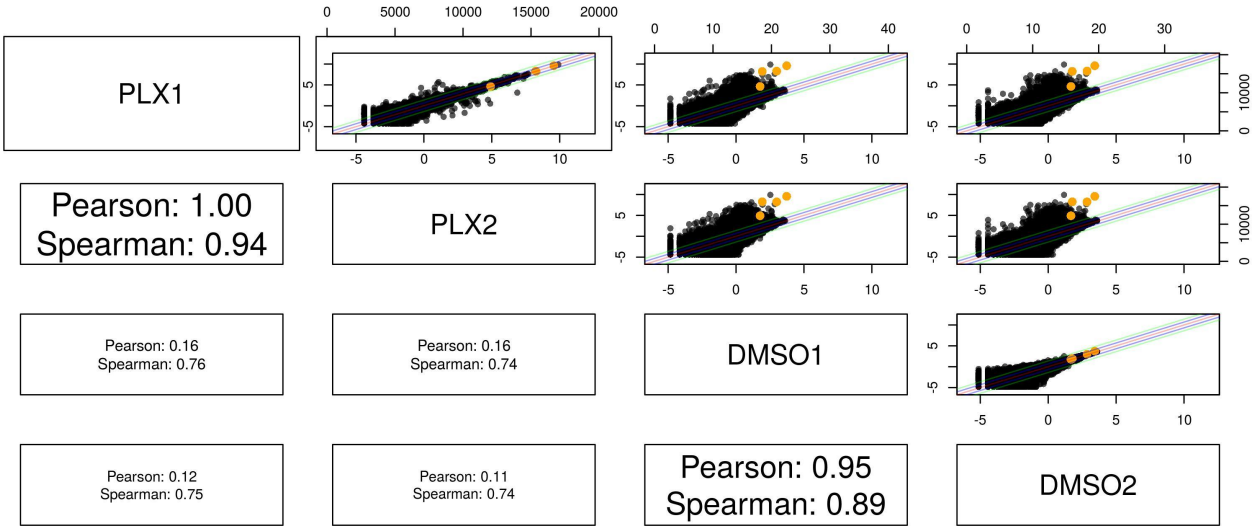
DESeq2 p-value: 3.603367e-253

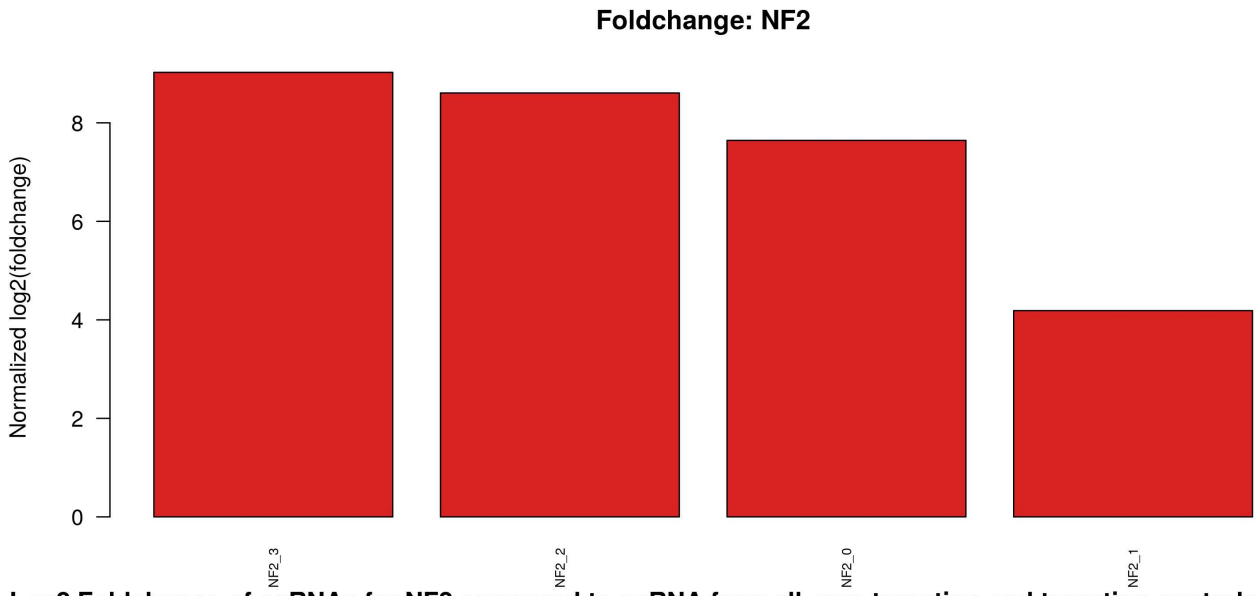
MAGeCK p-value: 0.002475

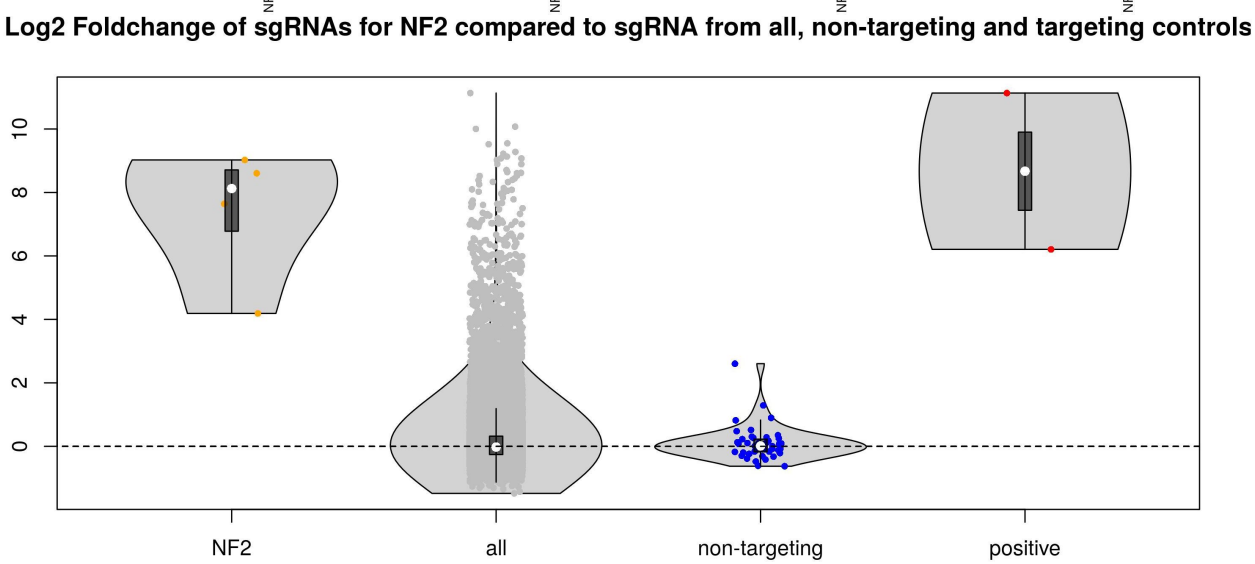
Gene Scatter for NF2
PLX_resistance_YTAR



sgRNA Scatter for NF2
PLX_resistance_YTAR




Foldchange: NF2
Normalized log2(foldchange)
0
2
4
6
8
NF2_3
NF2_2
NF2_0
NF2_1


Log2 Foldchange of sgRNAs for NF2 compared to sgRNA from all, non-targeting and targeting controls
0
2
4
6
8
10
NF2
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
4	NF2_3	NF2	none	9.024719
3	NF2_2	NF2	none	8.606060
1	NF2_0	NF2	none	7.643126
2	NF2_1	NF2	none	4.187524

CUL3

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

ENSEMBL ID (links to Ensembl) ENSG00000036257

HGNC SYMBOL (links to GeneCards) CUL3

GENE DESCRIPTION
cullin 3 [Source:HGNC Symbol;Acc:HGNC:2553]

GO TERM
enzyme binding

MIM GENE DESCRIPTION
CULLIN 3; CUL3

ENSEMBL PROTEIN ID
ENSP00000477851

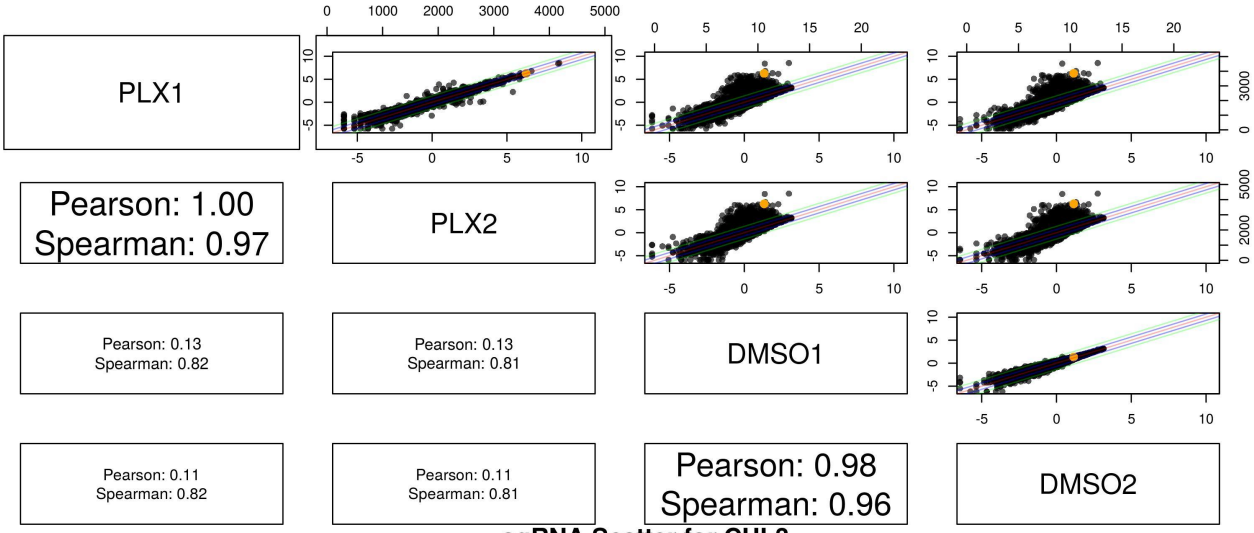
PROTEIN FAMILY DESCRIPTION
CULLIN 3 CUL 3

Wilcox p-value: 0.4590367

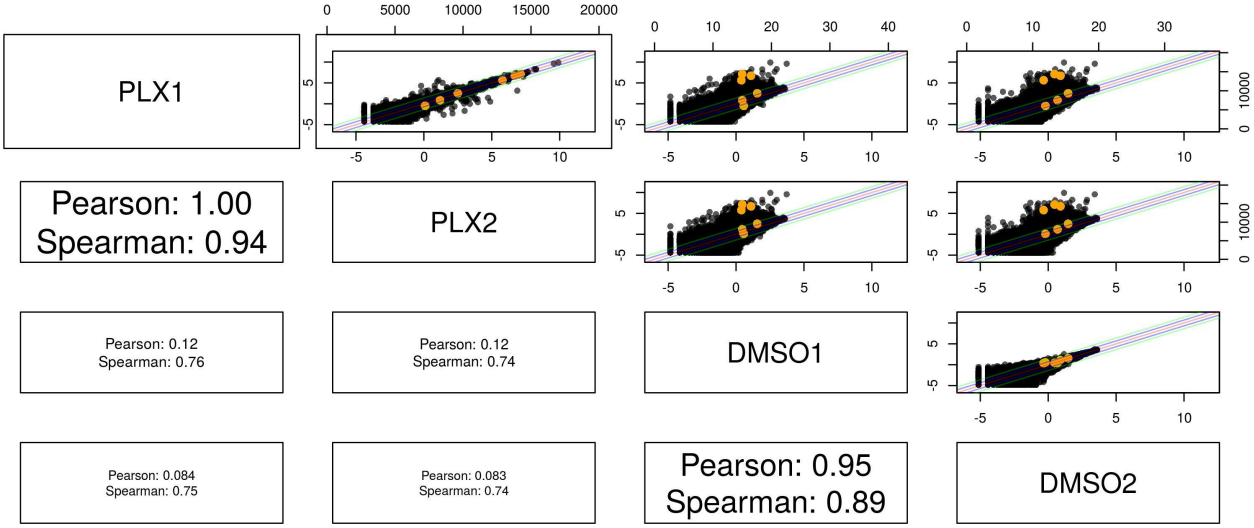
DESeq2 p-value: 2.279754e-217

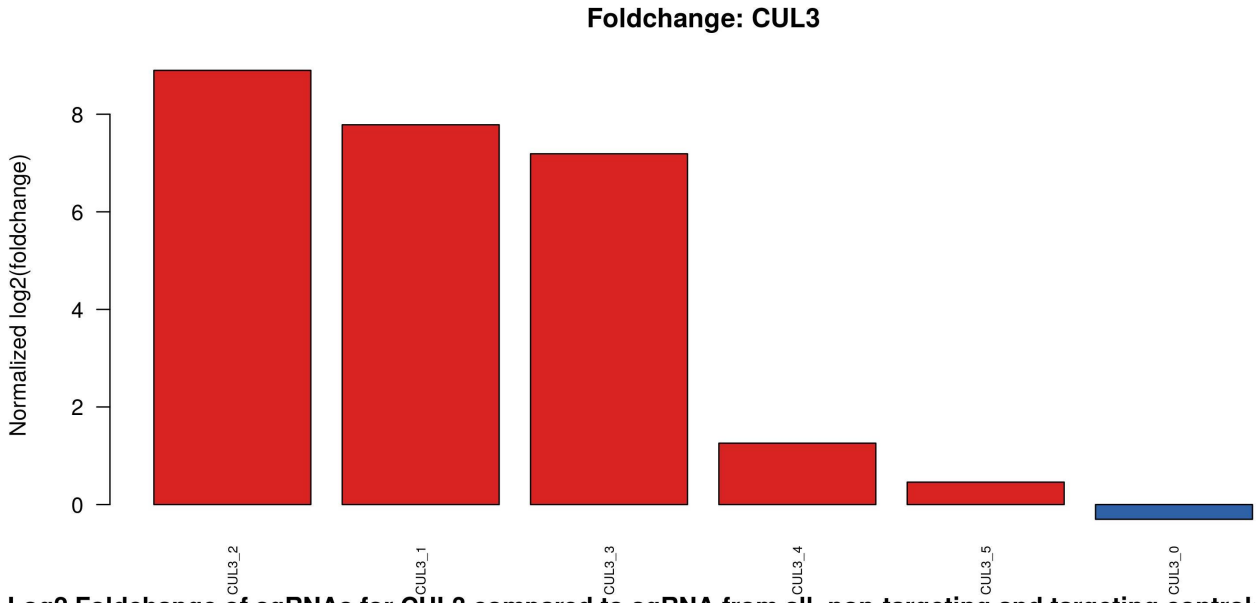
MAGeCK p-value: 0.0033

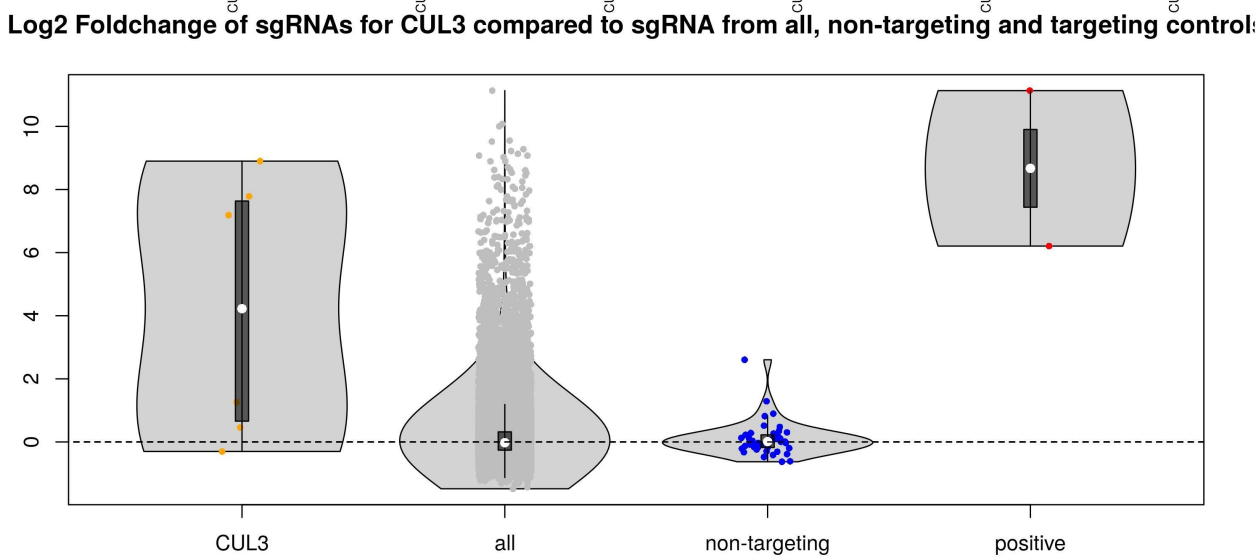
Gene Scatter for CUL3
PLX_resistance_YTAR



sgRNA Scatter for CUL3
PLX_resistance_YTAR




Foldchange: CUL3
Normalized log2(foldchange)
0
2
4
6
8
CUL3_2
CUL3_1
CUL3_3
CUL3_4
CUL3_5
CUL3_0


Log2 Foldchange of sgRNAs for CUL3 compared to sgRNA from all, non-targeting and targeting control
0
2
4
6
8
10
CUL3
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
3	CUL3_2	CUL3	none	8.8991604
2	CUL3_1	CUL3	none	7.7836768
4	CUL3_3	CUL3	none	7.1895962
5	CUL3_4	CUL3	none	1.2579963
6	CUL3_5	CUL3	none	0.4594545
1	CUL3_0	CUL3	none	-0.3019172

TADA2B

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

ENSEMBL ID (links to Ensembl) ENSG00000173011

HGNC SYMBOL (links to GeneCards) TADA2B

GENE DESCRIPTION
transcriptional adaptor 2B [Source:HGNC Symbol;Acc:HGNC:30781]

GO TERM

MIM GENE DESCRIPTION
TRANSCRIPTIONAL ADAPTOR 2B; TADA2B;;ADA2, YEAST, HOMOLOG OF, BETA; ADA2B;;ADA2-BETA

ENSEMBL PROTEIN ID
ENSP00000425731

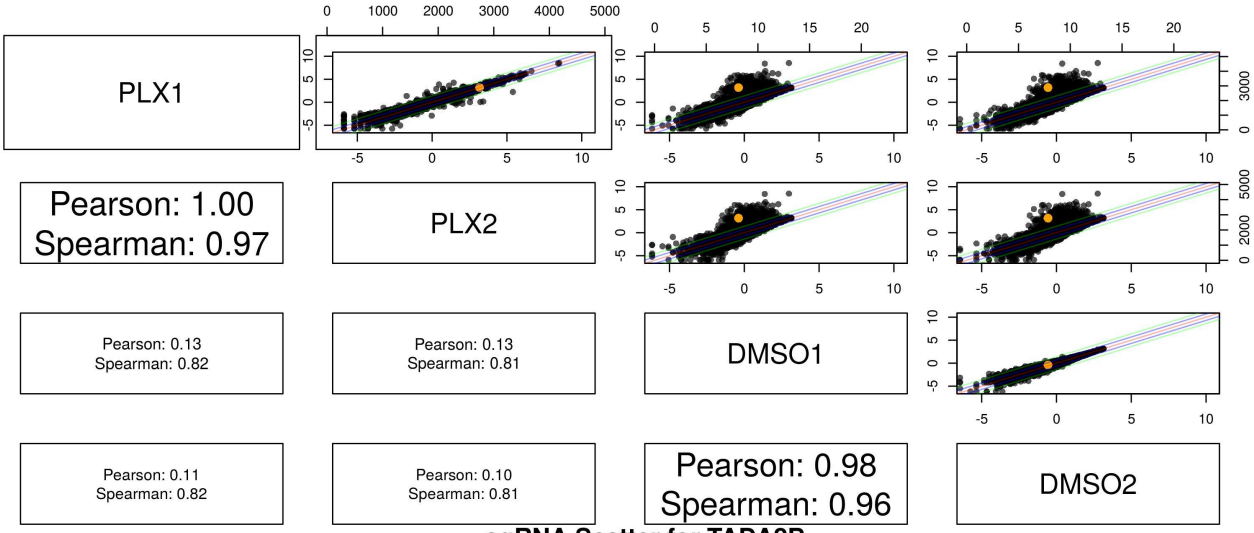
PROTEIN FAMILY DESCRIPTION
TRANSCRIPTIONAL ADAPTER 2 BETA

Wilcox p-value: 0.2321539

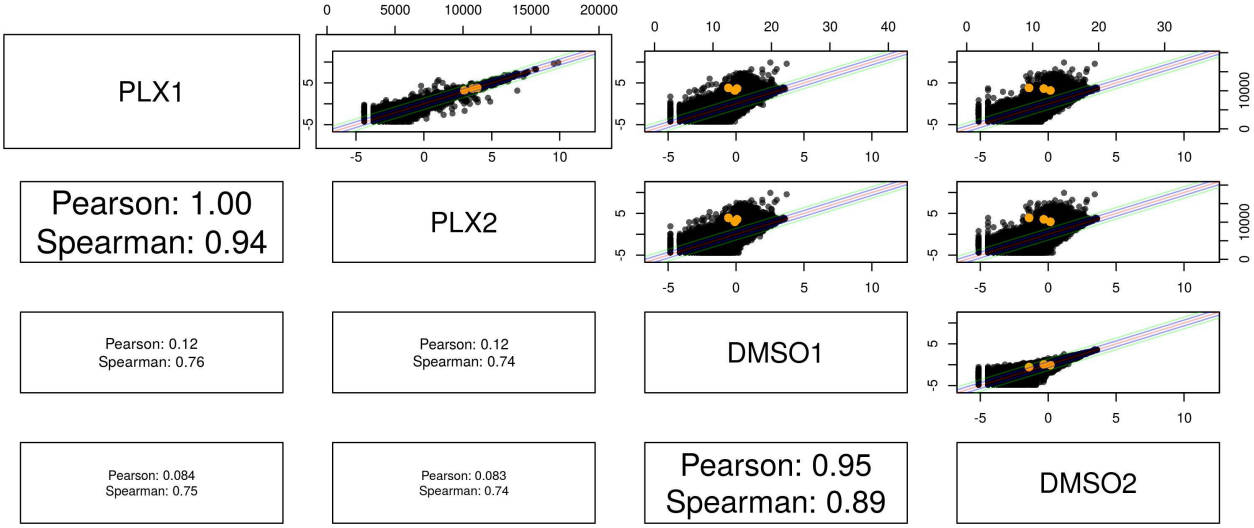
DESeq2 p-value: 4.911321e-108

MAGeCK p-value: 0.006931

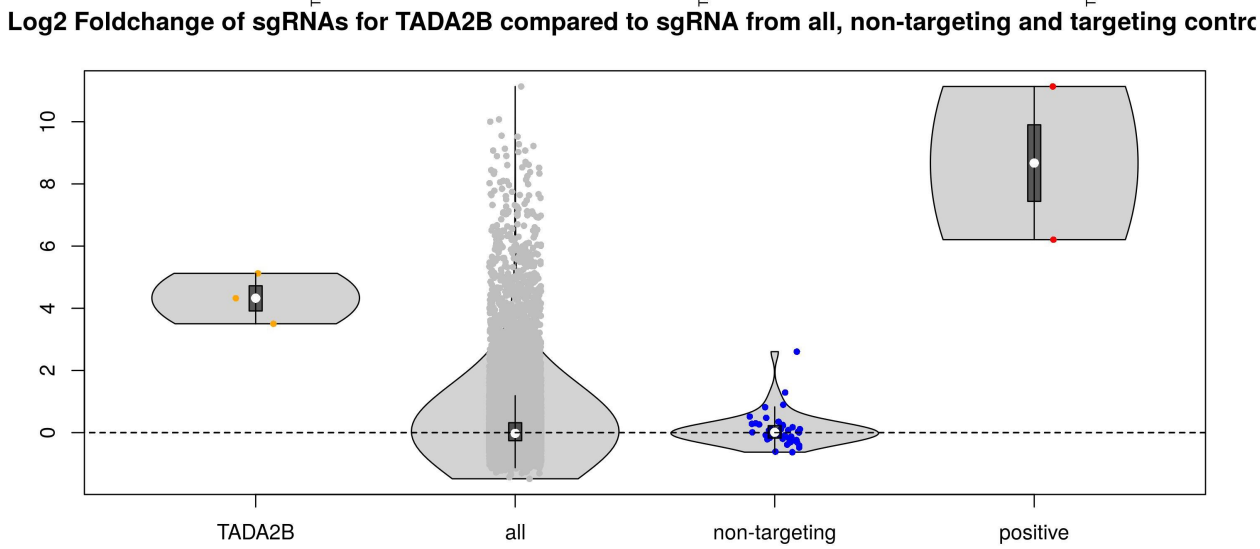
Gene Scatter for TADA2B
PLX_resistance_YTAR



sgRNA Scatter for TADA2B
PLX_resistance_YTAR



Foldchange: TADA2B
Normalized log2(foldchange)
0
1
2
3
4
5
TADA2B_0
TADA2B_1
TADA2B_2


Log2 Foldchange of sgRNAs for TADA2B compared to sgRNA from all, non-targeting and targeting contrc
0
2
4
6
8
10
TADA2B
all
non-targeting
positive

designs	genes	sequence	log2Foldchange
TADA2B_0	TADA2B	none	5.123137
TADA2B_1	TADA2B	none	4.325271
TADA2B_2	TADA2B	none	3.502245

CCDC101

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

ENSEMBL ID (links to Ensembl) ENSG00000176476

HGNC SYMBOL (links to GeneCards) CCDC101

GENE DESCRIPTION
coiled-coil domain containing 101 [Source:HGNC Symbol;Acc:HGNC:25156]

GO TERM

MIM GENE DESCRIPTION
COILED-COIL DOMAIN-CONTAINING PROTEIN 101; CCDC101;;STAF36

ENSEMBL PROTEIN ID
ENSP00000454730

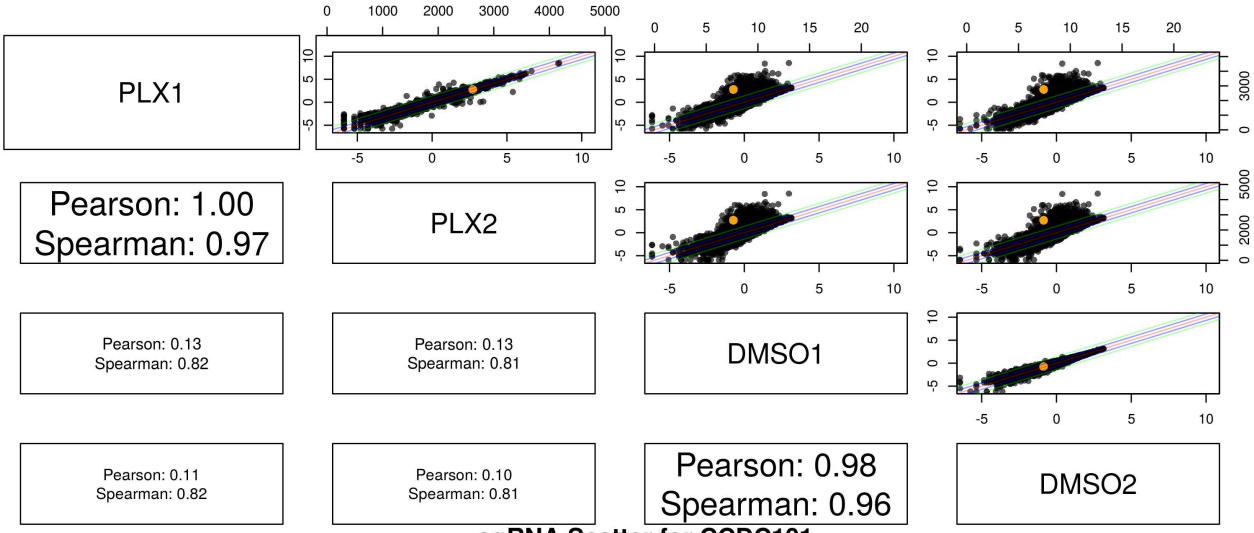
PROTEIN FAMILY DESCRIPTION
SAGA ASSOCIATED FACTOR 29 HOMOLOG COILED COIL DOMAIN CONTAINING 101

Wilcox p-value: 0.2824934

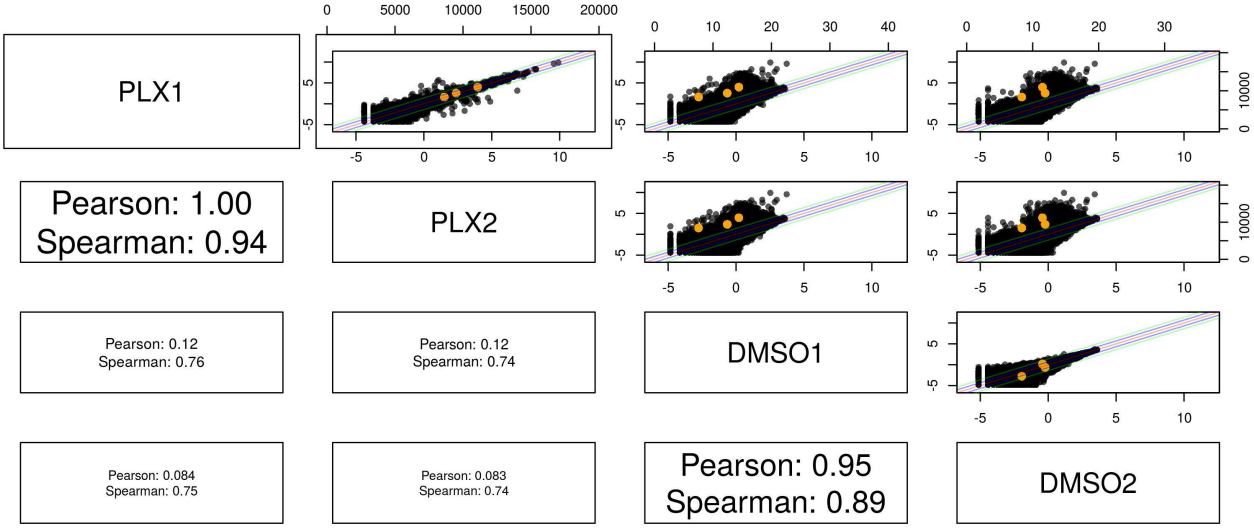
DESeq2 p-value: 1.112529e-102

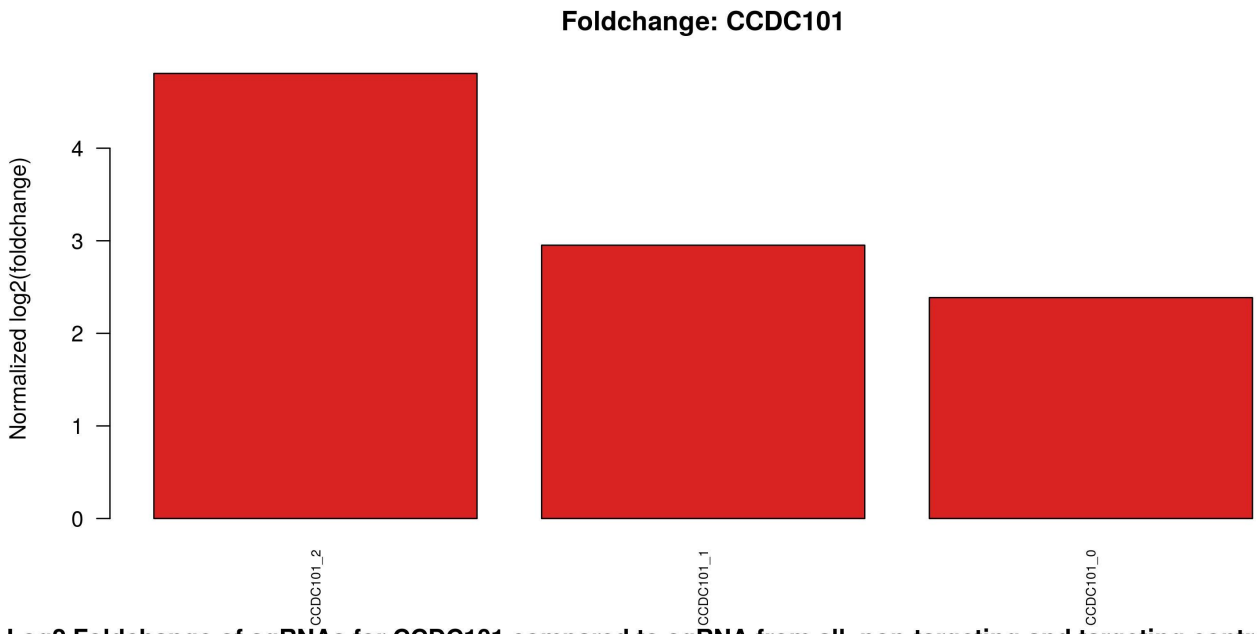
MAGeCK p-value: 0.009194

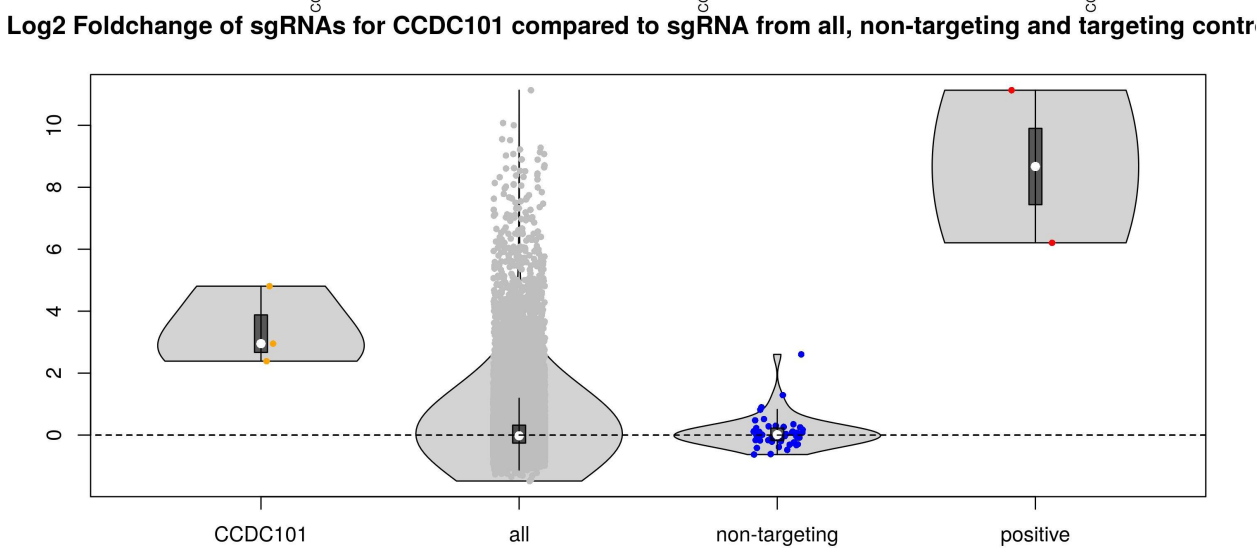
Gene Scatter for CCDC101
PLX_resistance_YTAR



sgRNA Scatter for CCDC101
PLX_resistance_YTAR




Foldchange: CCDC101
Normalized log2(foldchange)
0
1
2
3
4
CCDC101_2
CCDC101_1
CCDC101_0


Log2 Foldchange of sgRNAs for CCDC101 compared to sgRNA from all, non-targeting and targeting contr
0
2
4
6
8
10
CCDC101
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
3	CCDC101_2	CCDC101	none	4.807198
2	CCDC101_1	CCDC101	none	2.952140
1	CCDC101_0	CCDC101	none	2.386010

NF1

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

ENSEMBL ID (links to Ensembl) LRG_214

HGNC SYMBOL (links to GeneCards) NF1

GENE DESCRIPTION
neurofibromin 1 [Source:HGNC Symbol;Acc:HGNC:7765]

GO TERM

MIM GENE DESCRIPTION
NEUROFIBROMIN 1; NF1;;NEUROFIBROMIN

ENSEMBL PROTEIN ID
LRG_214p2

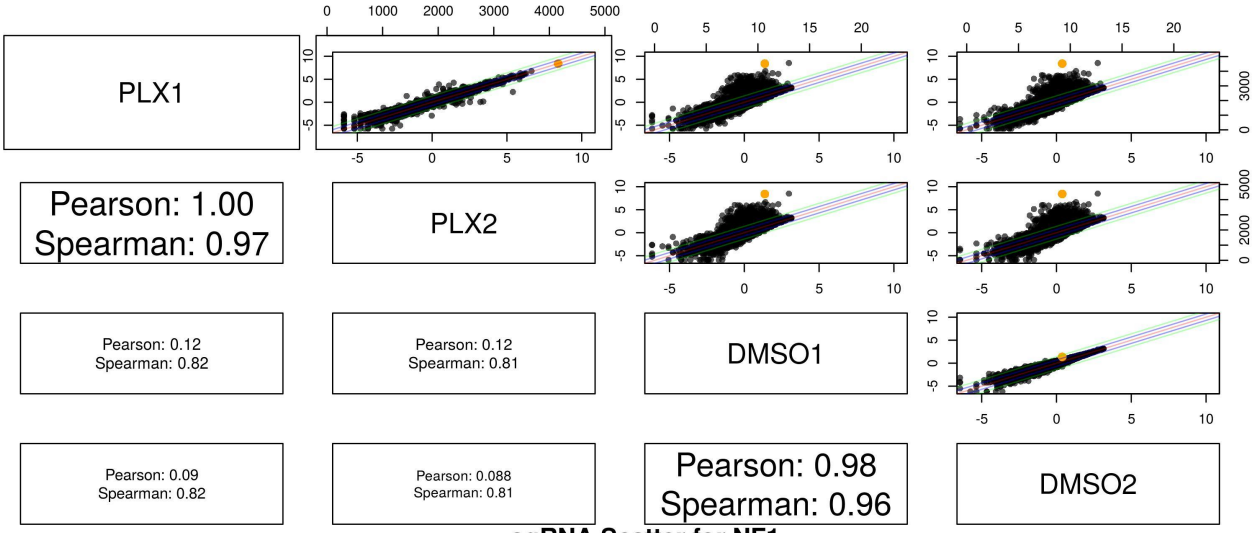
PROTEIN FAMILY DESCRIPTION
NEUROFIBROMIN NEUROFIBROMATOSIS RELATED NF 1

Wilcox p-value: 0.3482308

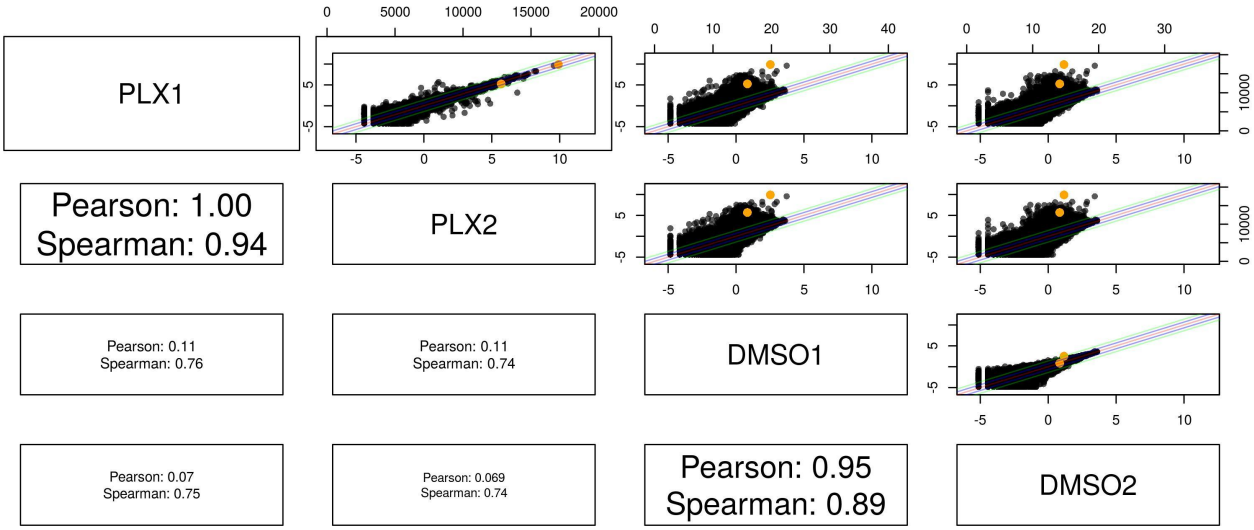
DESeq2 p-value: 2.824132e-139

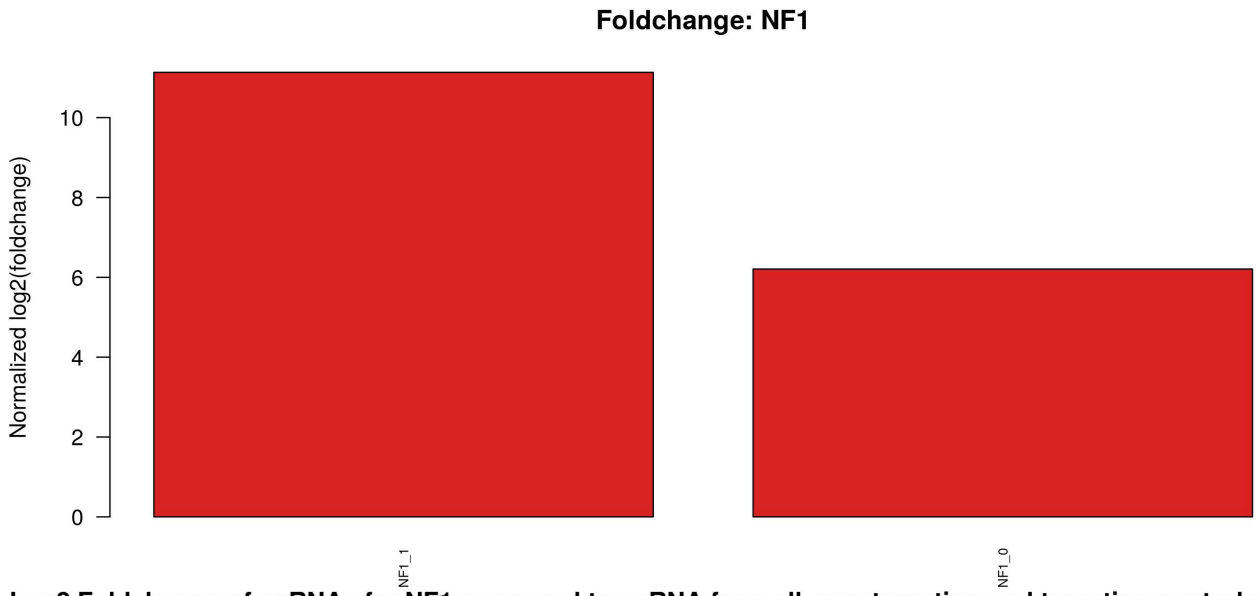
MAGeCK p-value: 0.012995

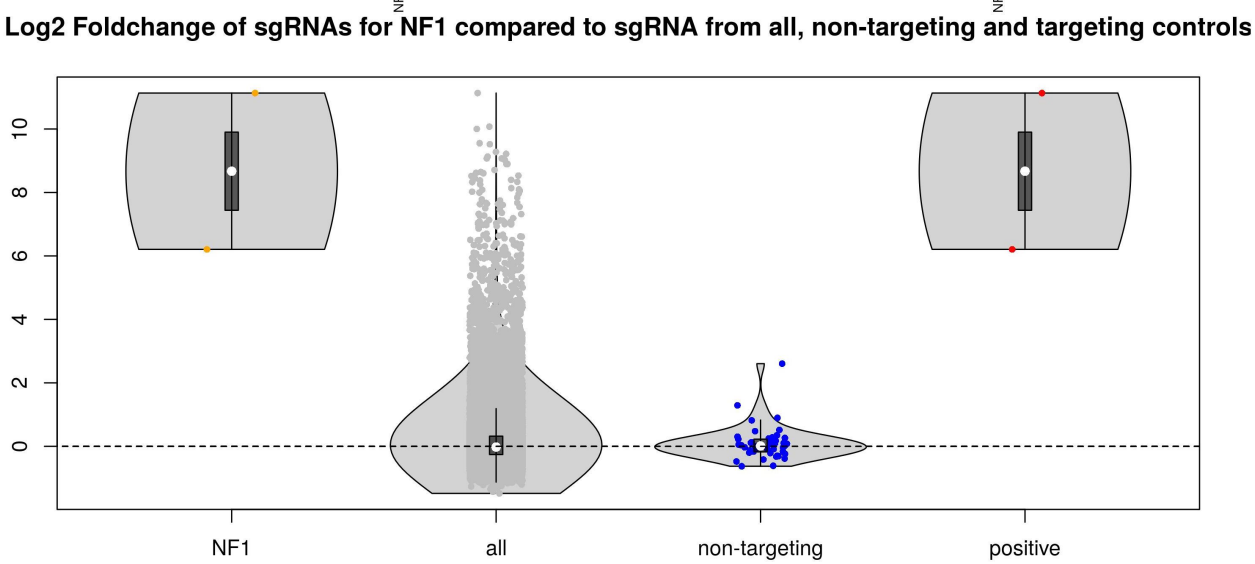
Gene Scatter for NF1
PLX_resistance_YTAR



sgRNA Scatter for NF1
PLX_resistance_YTAR




Foldchange: NF1
Normalized log2(foldchange)
0
2
4
6
8
10
NF1_1
NF1_0


Log2 Foldchange of sgRNAs for NF1 compared to sgRNA from all, non-targeting and targeting controls
0
2
4
6
8
10
NF1
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
2	NF1_1	NF1	none	11.133567
1	NF1_0	NF1	none	6.207027

TADA1

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

ENSEMBL ID (links to Ensembl) ENSG00000152382

HGNC SYMBOL (links to GeneCards) TADA1

GENE DESCRIPTION
transcriptional adaptor 1 [Source:HGNC Symbol;Acc:HGNC:30631]

GO TERM
protein binding

MIM GENE DESCRIPTION
TRANSCRIPTIONAL ADAPTOR 1-LIKE; TADA1L;;HFI1/ADA1, YEAST, HOMOLOG OF;;SPT3-ASSOCIATED FACTOR 42; STAF42

ENSEMBL PROTEIN ID
ENSP00000356848

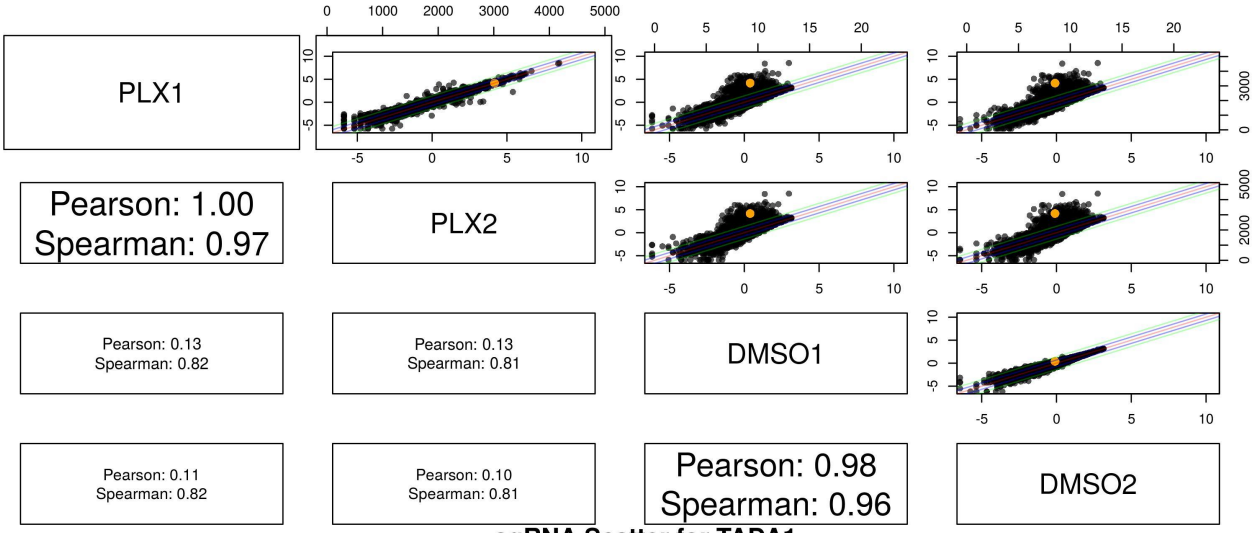
PROTEIN FAMILY DESCRIPTION
TRANSCRIPTIONAL ADAPTER 1 TRANSCRIPTIONAL ADAPTER 1

Wilcox p-value: 0.3482308

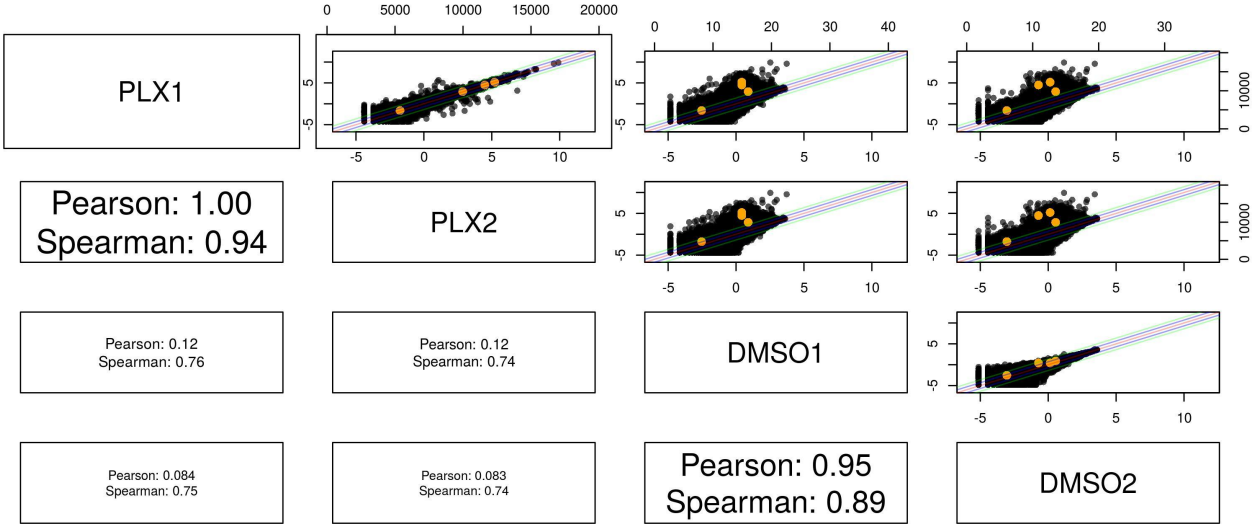
DESeq2 p-value: 5.983366e-80

MAGeCK p-value: 0.026553

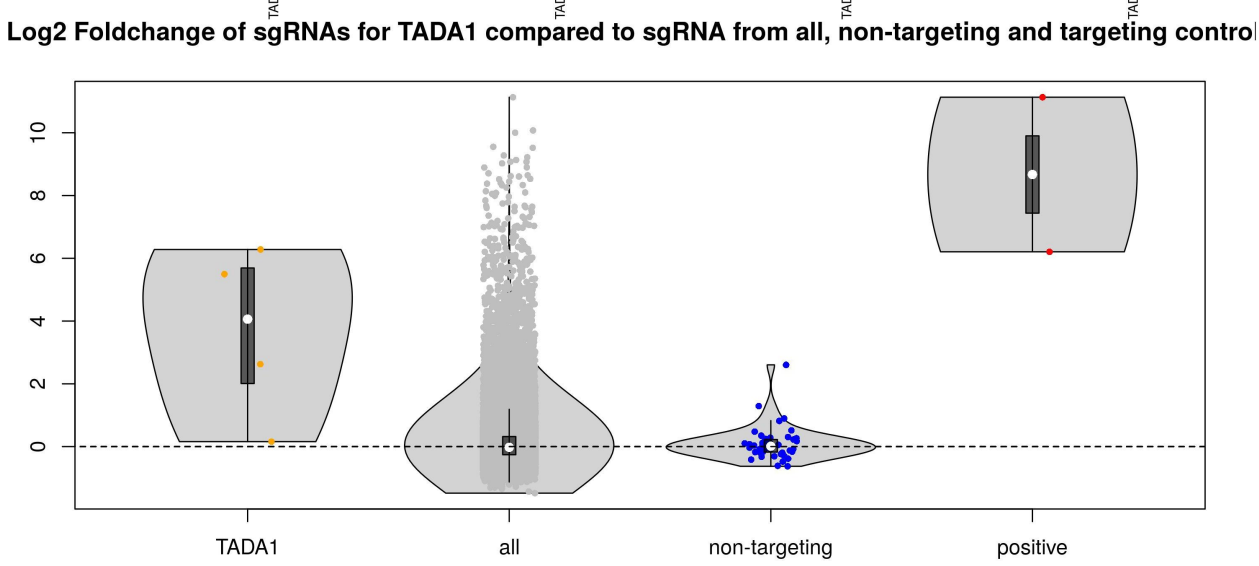
Gene Scatter for TADA1
PLX_resistance_YTAR



sgRNA Scatter for TADA1
PLX_resistance_YTAR



Foldchange: TADA1
Normalized log2(foldchange)
0
1
2
3
4
5
6
TADA1_1
TADA1_0
TADA1_3
TADA1_2


Log2 Foldchange of sgRNAs for TADA1 compared to sgRNA from all, non-targeting and targeting control
0
2
4
6
8
10
TADA1
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
2	TADA1_1	TADA1	none	6.2805825
1	TADA1_0	TADA1	none	5.4952689
4	TADA1_3	TADA1	none	2.6267542
3	TADA1_2	TADA1	none	0.1578053

ALG3

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

ENSEMBL ID (links to Ensembl) ENSG00000214160

HGNC SYMBOL (links to GeneCards) ALG3

GENE DESCRIPTION
ALG3, alpha-1,3- mannosyltransferase [Source:HGNC Symbol;Acc:HGNC:23056]

GO TERM

MIM GENE DESCRIPTION
ALG3, S. CEREVISIAE, HOMOLOG OF; ALG3;;NOT56-LIKE PROTEIN; NOT56L

ENSEMBL PROTEIN ID
ENSP00000407011

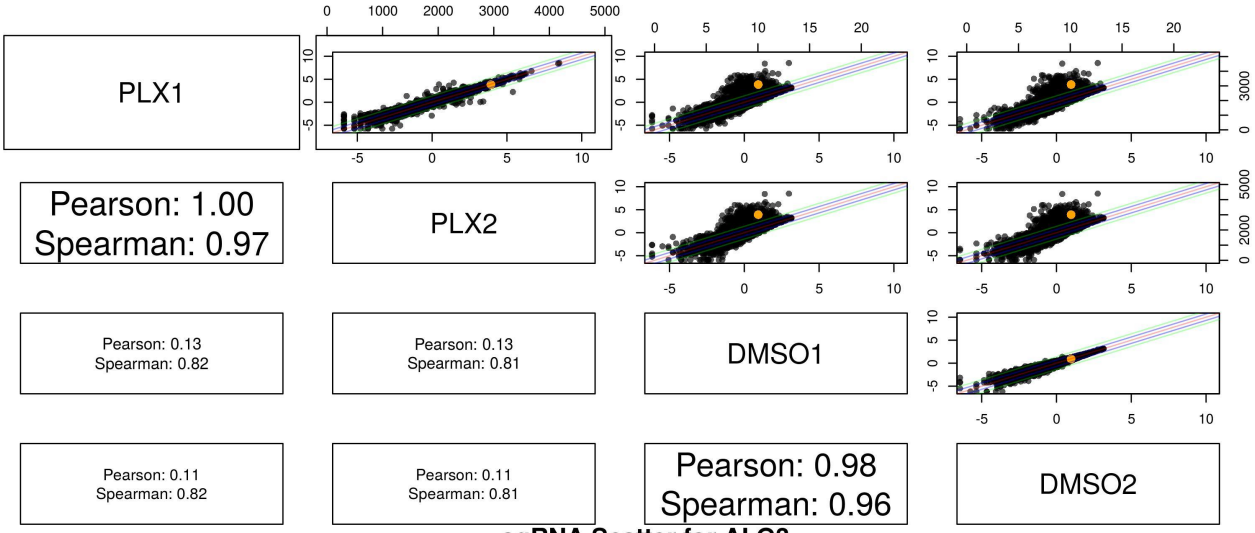
PROTEIN FAMILY DESCRIPTION
UNKNOWN

Wilcox p-value: 0.2824934

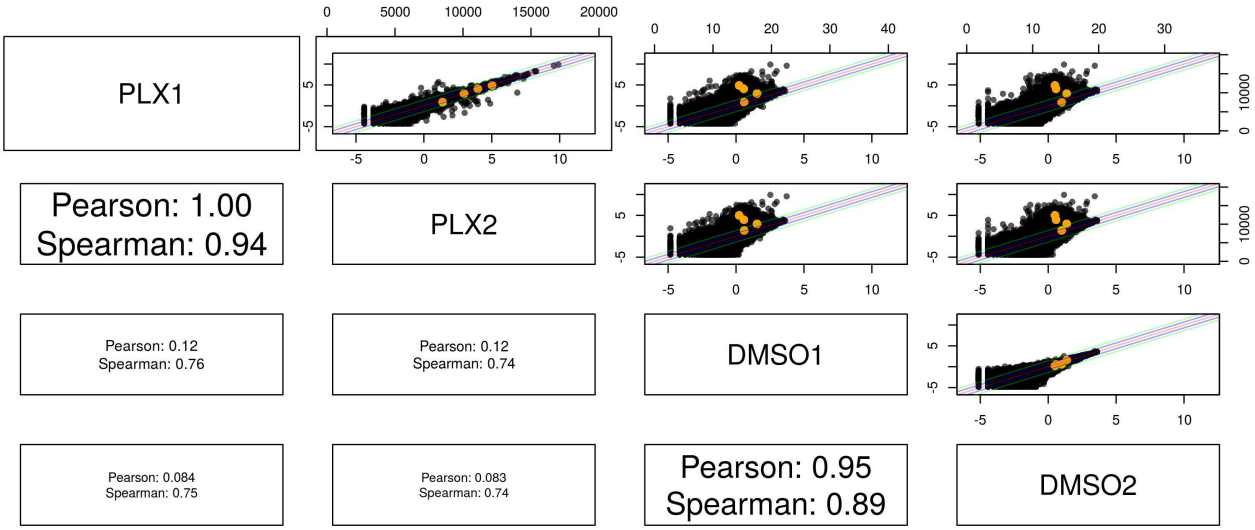
DESeq2 p-value: 2.282362e-81

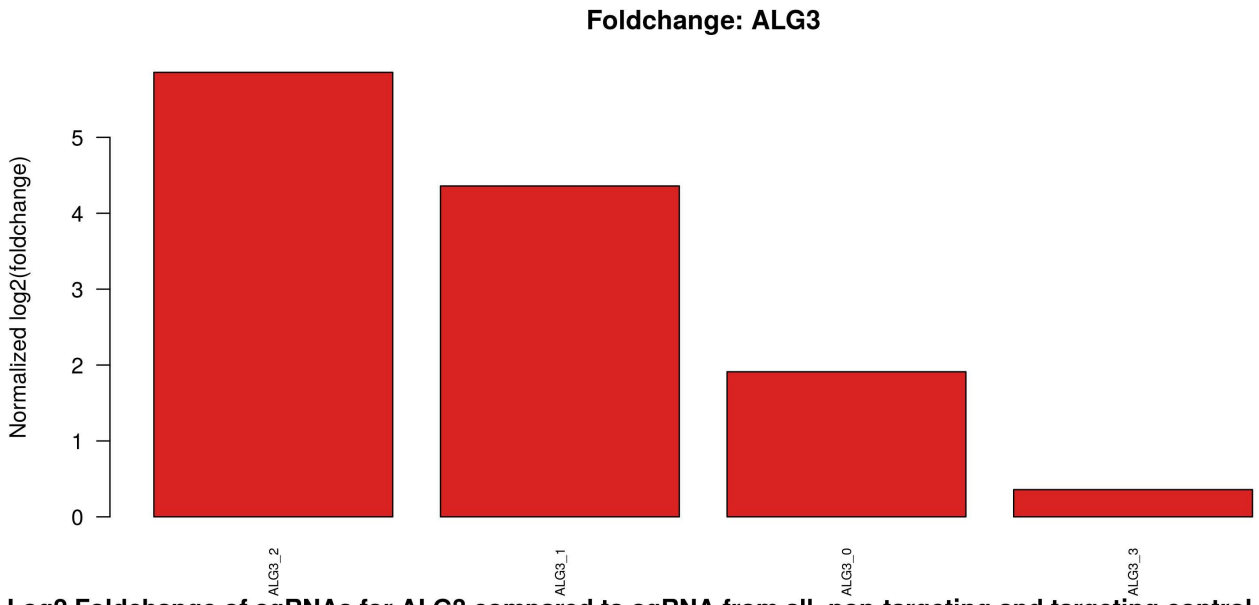
MAGeCK p-value: 0.065285

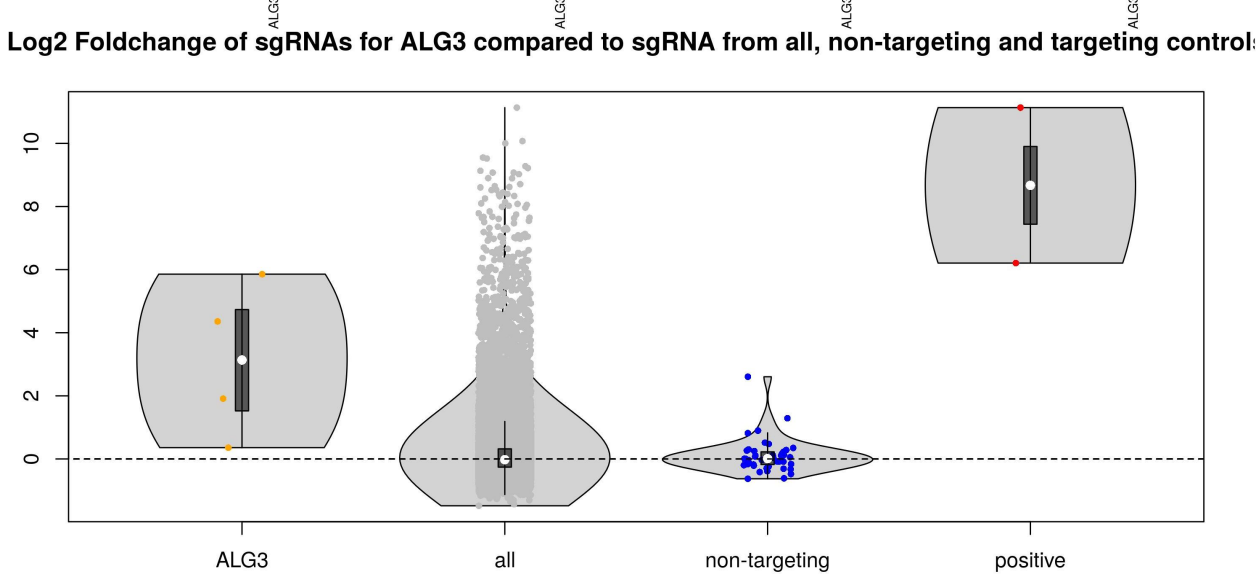
Gene Scatter for ALG3
PLX_resistance_YTAR



sgRNA Scatter for ALG3
PLX_resistance_YTAR




Foldchange: ALG3
Normalized log2(foldchange)
0
1
2
3
4
5
ALG3_2
ALG3_1
ALG3_0
ALG3_3


Log2 Foldchange of sgRNAs for ALG3 compared to sgRNA from all, non-targeting and targeting control
0
2
4
6
8
10
ALG3
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
3	ALG3_2	ALG3	none	5.8564292
2	ALG3_1	ALG3	none	4.3594225
1	ALG3_0	ALG3	none	1.9115355
4	ALG3_3	ALG3	none	0.3587384

TAF6L

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

ENSEMBL ID (links to Ensembl) ENSG00000162227

HGNC SYMBOL (links to GeneCards) TAF6L

GENE DESCRIPTION
TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa [Source:HGNC Symbol;Acc:HGNC:17305]

GO TERM
molecular_function

MIM GENE DESCRIPTION
TAF6-LIKE RNA POLYMERASE II; TAF6L;;PCAF-ASSOCIATED FACTOR 65 ALPHA; PAF65A;;PCAF-ASSOCIATED FACTOR, 65-KD

ENSEMBL PROTEIN ID
ENSP00000434662

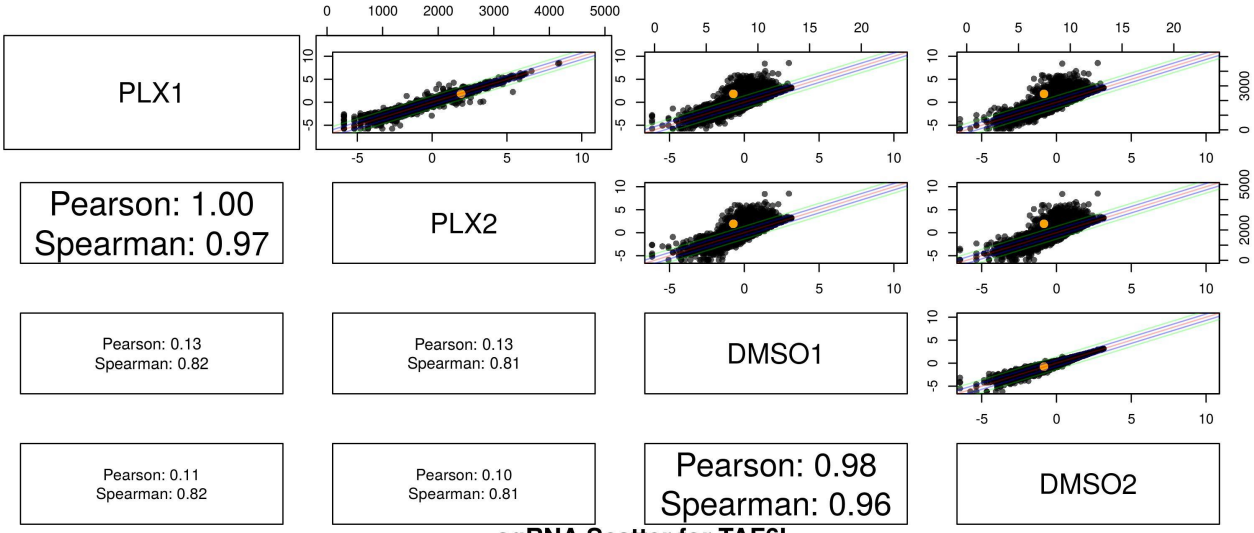
PROTEIN FAMILY DESCRIPTION
TAF6 RNA POLYMERASE II P300/CBP ASSOCIATED FACTOR ASSOCIATED FACTOR 65 KDA SUBUNIT 6L PCAF ASSOCIATED FACTOR 65 ALPHA PAF65 ALPHA

Wilcox p-value: 0.2824934

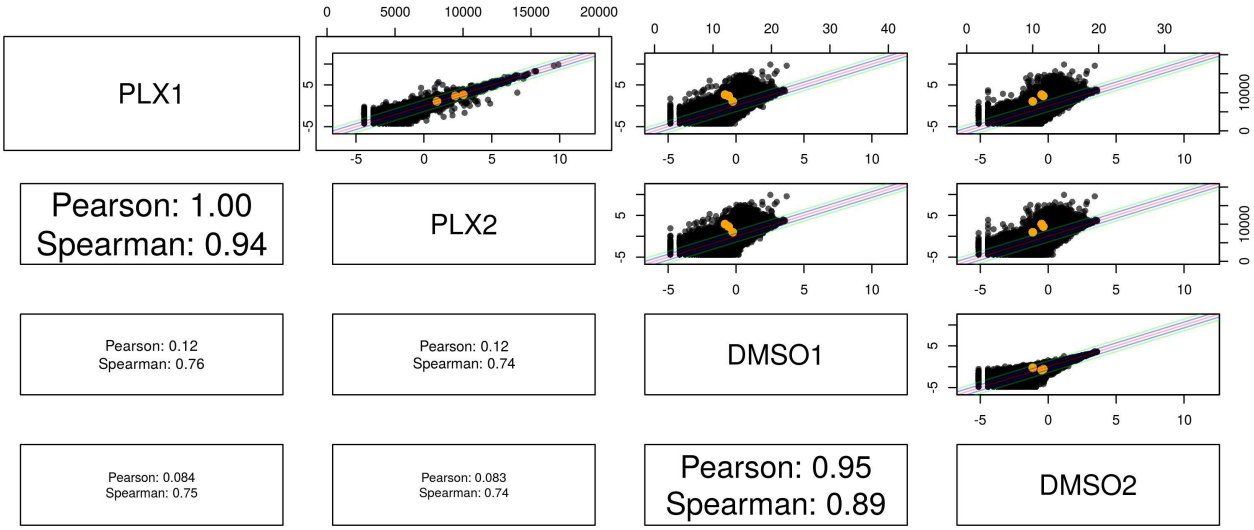
DESeq2 p-value: 2.540754e-57

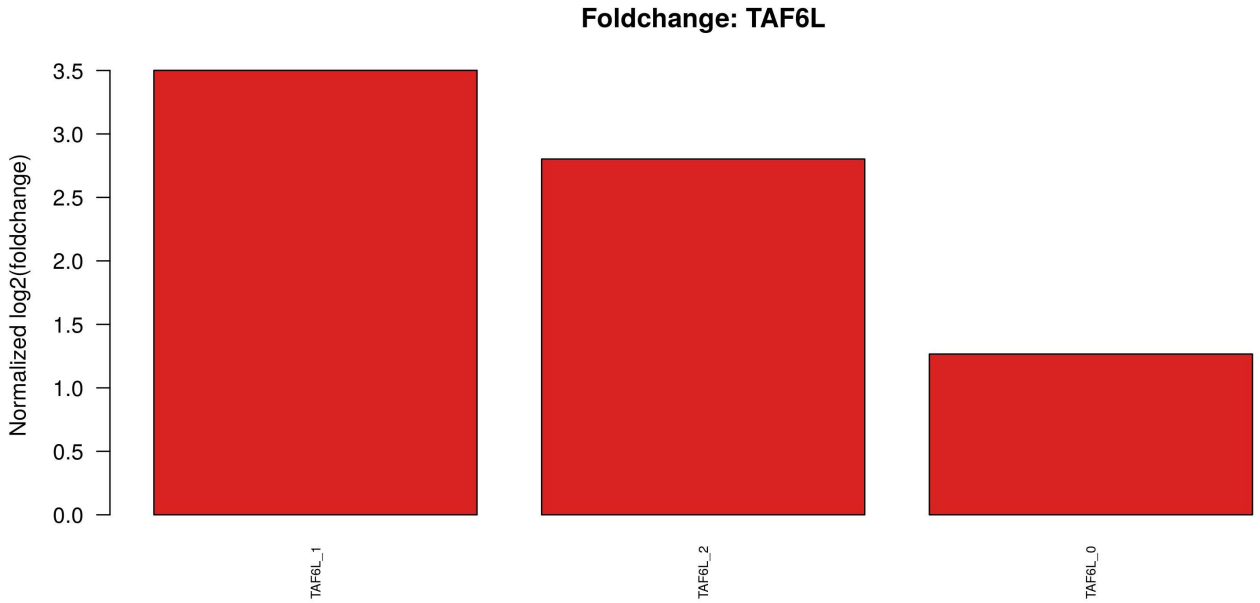
MAGeCK p-value: 0.149798

Gene Scatter for TAF6L
PLX_resistance_YTAR

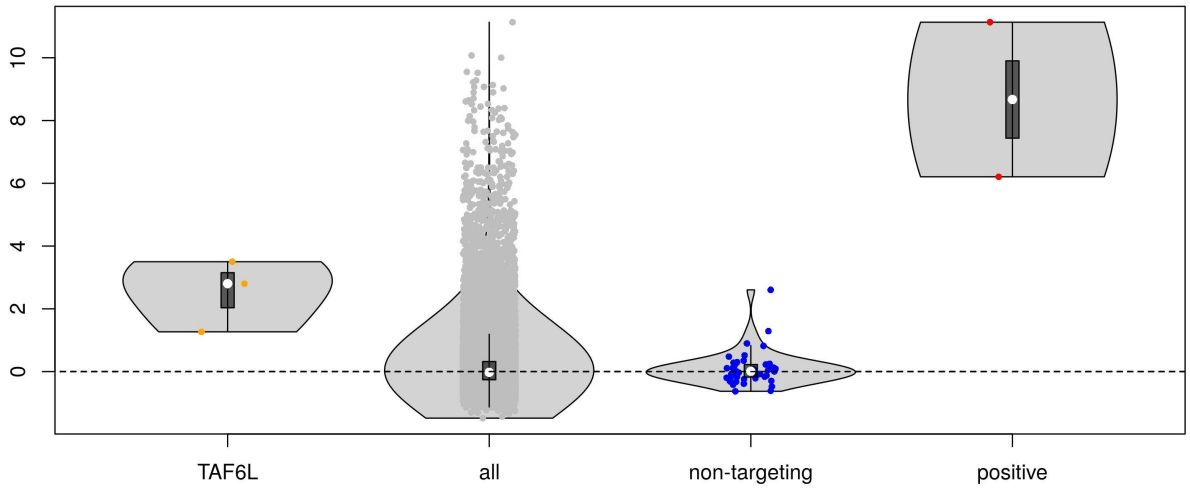


sgRNA Scatter for TAF6L
PLX_resistance_YTAR





Log2 Foldchange of sgRNAs for TAF6L compared to sgRNA from all, non-targeting and targeting control



	designs	genes	sequence	log2Foldchange
2	TAF6L_1	TAF6L	none	3.500858
3	TAF6L_2	TAF6L	none	2.802450
1	TAF6L_0	TAF6L	none	1.266374

C11orf49

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

ENSEMBL ID (links to Ensembl) ENSG00000149179

HGNC SYMBOL (links to GeneCards) C11orf49

GENE DESCRIPTION
chromosome 11 open reading frame 49 [Source:HGNC Symbol;Acc:HGNC:28720]

GO TERM
organelle

MIM GENE DESCRIPTION

ENSEMBL PROTEIN ID
ENSP00000433707

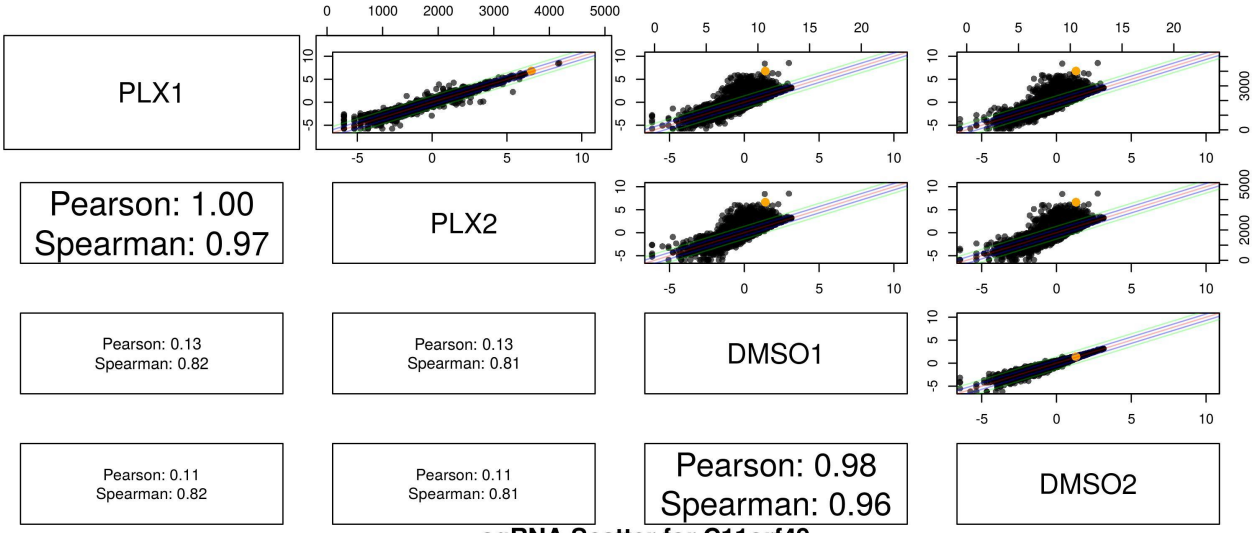
PROTEIN FAMILY DESCRIPTION
UNKNOWN

Wilcox p-value: 0.2824934

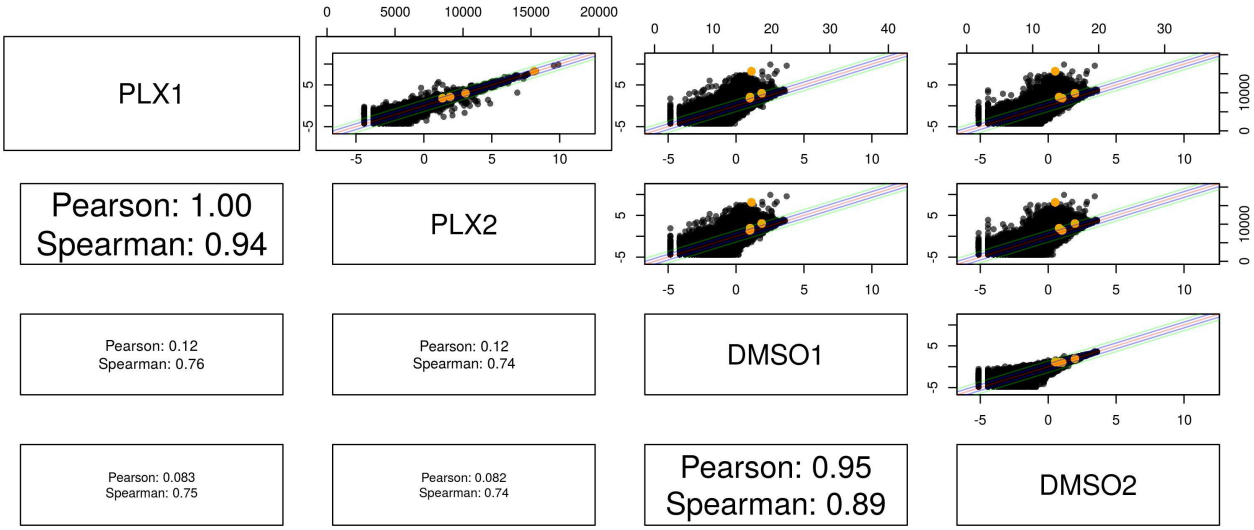
DESeq2 p-value: 1.393389e-244

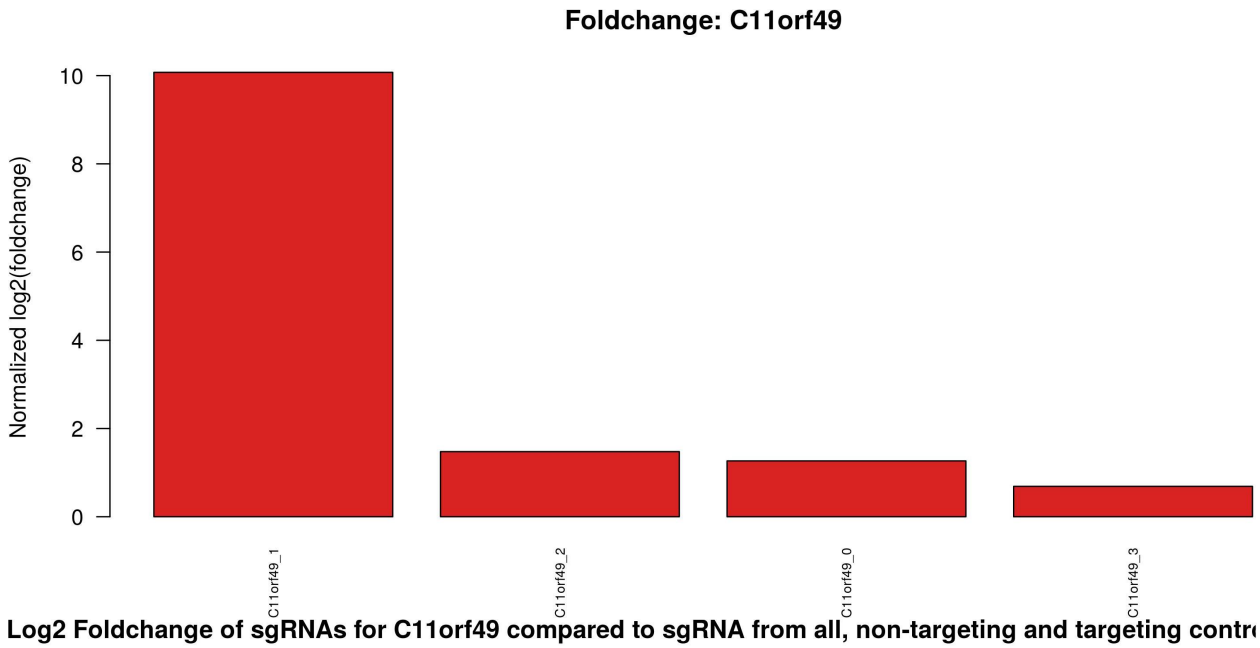
MAGeCK p-value: 0.192185

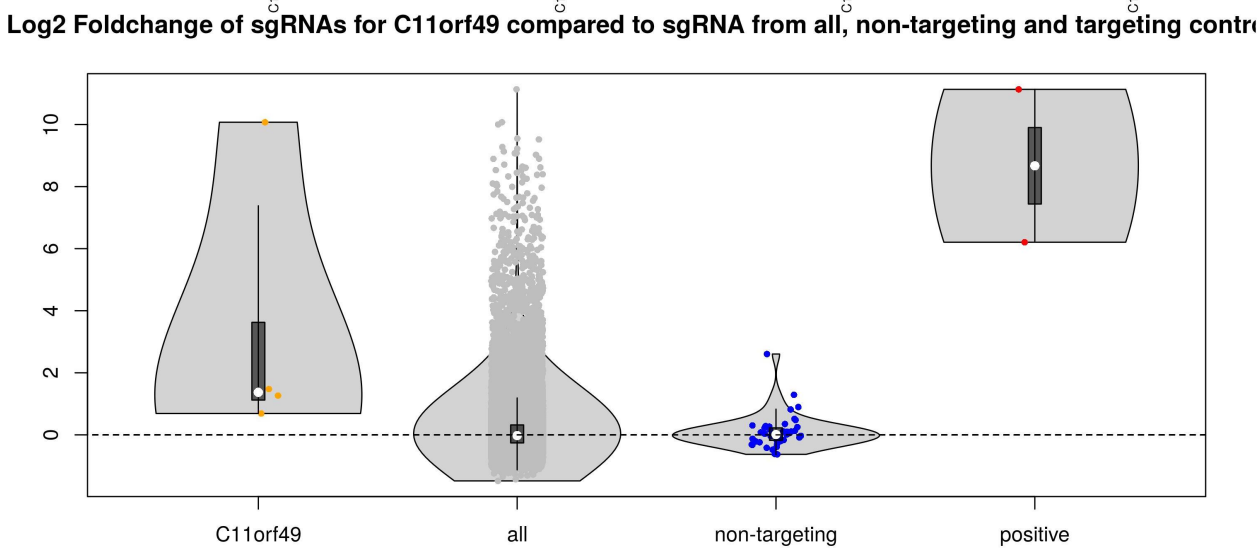
Gene Scatter for C11orf49
PLX_resistance_YTAR



sgRNA Scatter for C11orf49
PLX_resistance_YTAR




Foldchange: C11orf49
Normalized log2(foldchange)
10
8
6
4
2
0
C11orf49_1
C11orf49_2
C11orf49_0
C11orf49_3


Log2 Foldchange of sgRNAs for C11orf49 compared to sgRNA from all, non-targeting and targeting contr
10
8
6
4
2
0
C11orf49
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
2	C11orf49_1	C11orf49	none	10.0739627
3	C11orf49_2	C11orf49	none	1.4762504
1	C11orf49_0	C11orf49	none	1.2655638
4	C11orf49_3	C11orf49	none	0.6889849

TAF5L

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

ENSEMBL ID (links to Ensembl) ENSG00000135801

HGNC SYMBOL (links to GeneCards) TAF5L

GENE DESCRIPTION
TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa [Source:HGNC Symbol;Acc:HGNC:17304]

GO TERM
protein binding

MIM GENE DESCRIPTION

ENSEMBL PROTEIN ID
ENSP00000258281

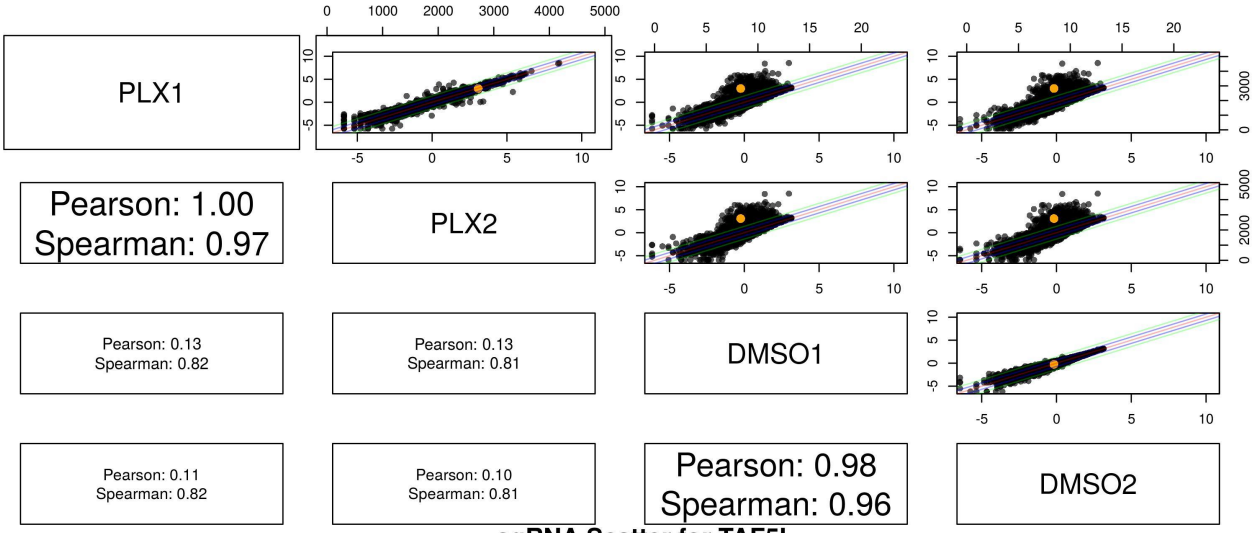
PROTEIN FAMILY DESCRIPTION
TRANSCRIPTION INITIATION FACTOR TFIID SUBUNIT 5 TRANSCRIPTION INITIATION FACTOR TFIID KDA SUBUNIT

Wilcox p-value: 0.3482308

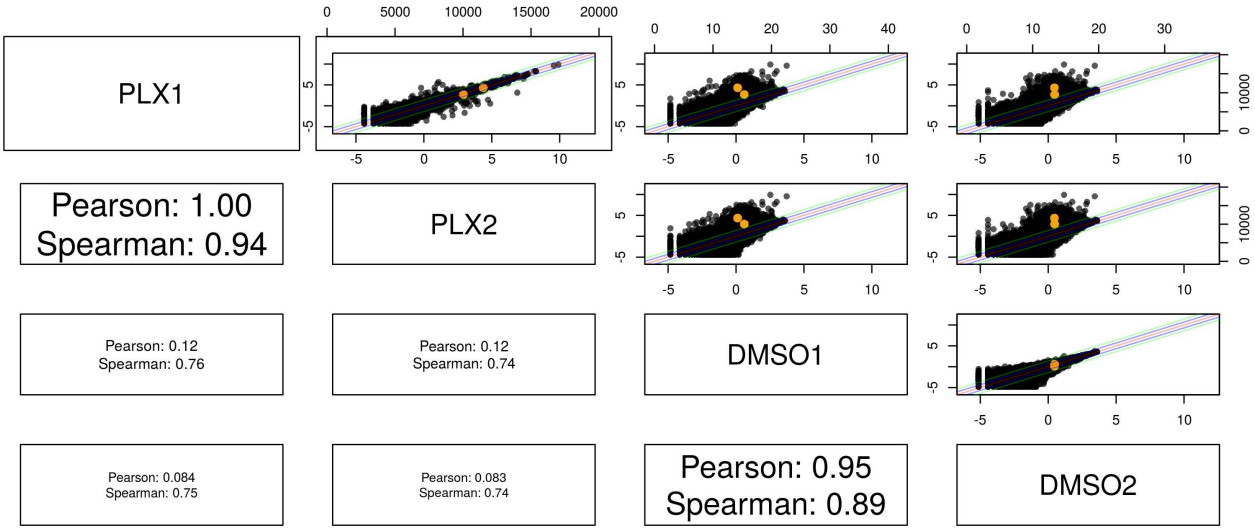
DESeq2 p-value: 1.042939e-92

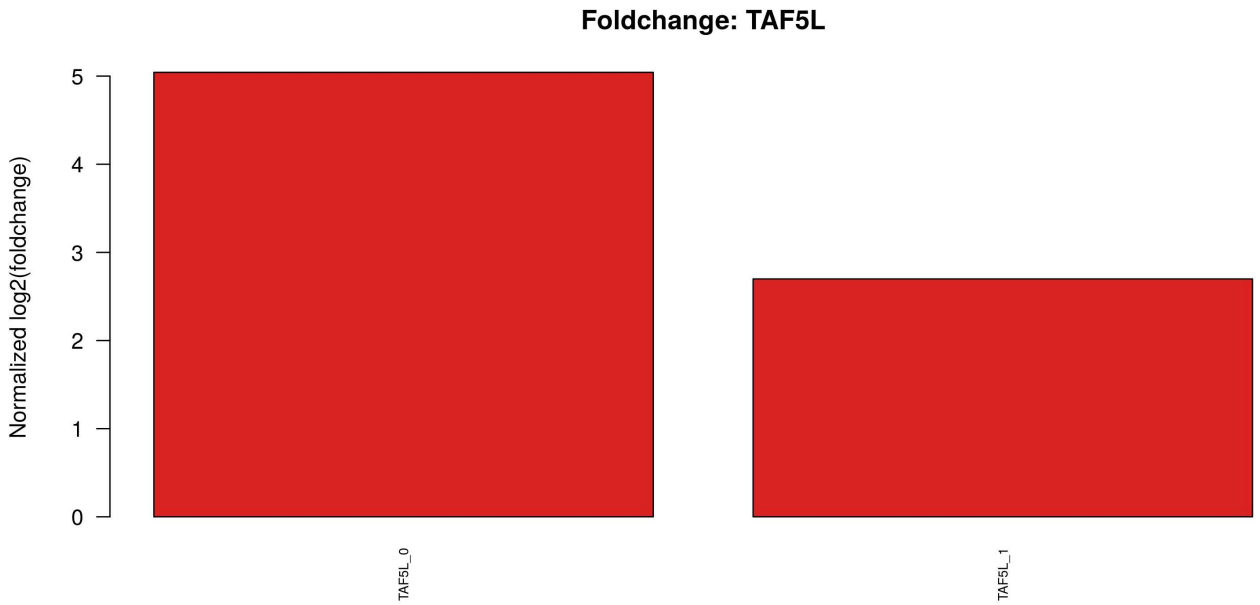
MAGeCK p-value: 0.223791

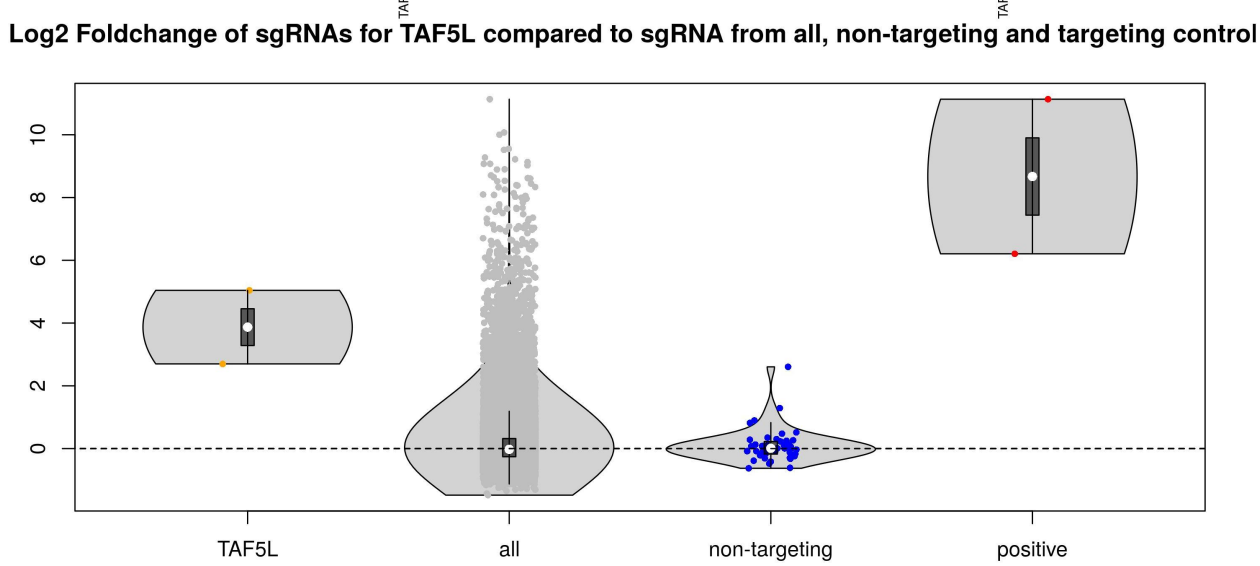
Gene Scatter for TAF5L
PLX_resistance_YTAR



sgRNA Scatter for TAF5L
PLX_resistance_YTAR




Foldchange: TAF5L
Normalized log2(foldchange)
0
1
2
3
4
5
TAF5L_0
TAF5L_1


Log2 Foldchange of sgRNAs for TAF5L compared to sgRNA from all, non-targeting and targeting control
0
2
4
6
8
10
TAF5L
all
non-targeting
positive

designs	genes	sequence	log2Foldchange
TAF5L_0	TAF5L	none	5.042354
TAF5L_1	TAF5L	none	2.698512

ATXN2L

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

ENSEMBL ID (links to Ensembl) ENSG00000168488

HGNC SYMBOL (links to GeneCards) ATXN2L

GENE DESCRIPTION
ataxin 2-like [Source:HGNC Symbol;Acc:HGNC:31326]

GO TERM

MIM GENE DESCRIPTION
ATAXIN 2-LIKE; ATXN2L

ENSEMBL PROTEIN ID
ENSP00000455560

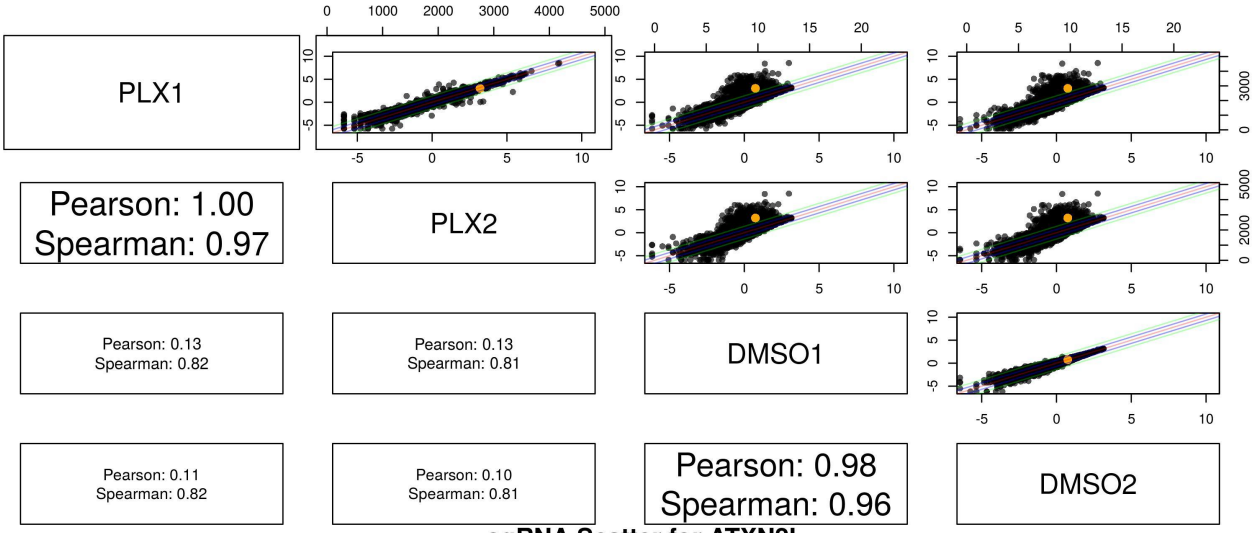
PROTEIN FAMILY DESCRIPTION
UNKNOWN

Wilcox p-value: 0.414337

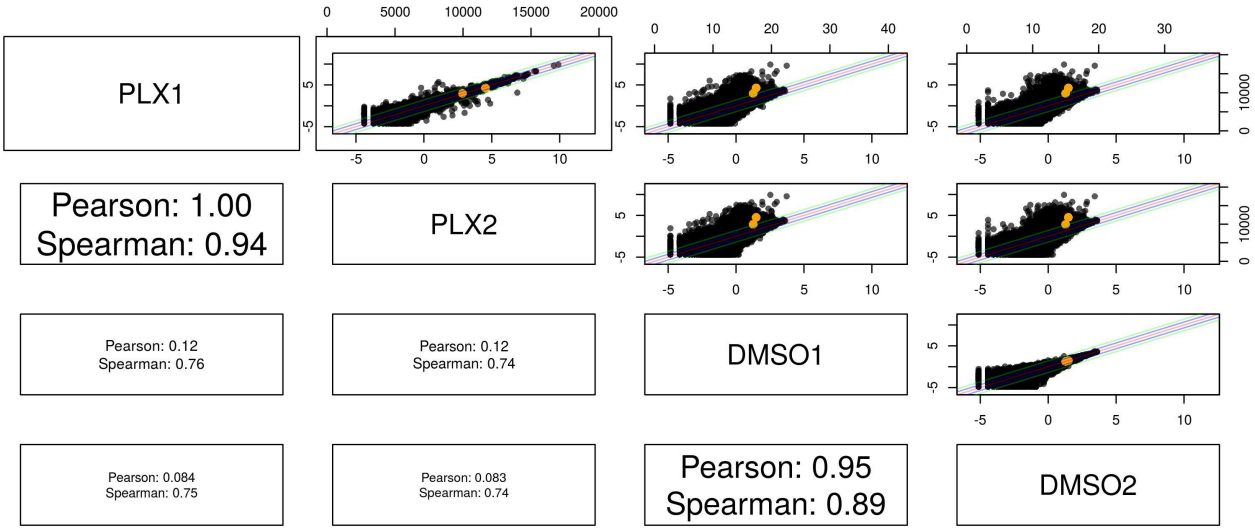
DESeq2 p-value: 2.774703e-46

MAGeCK p-value: 0.304343

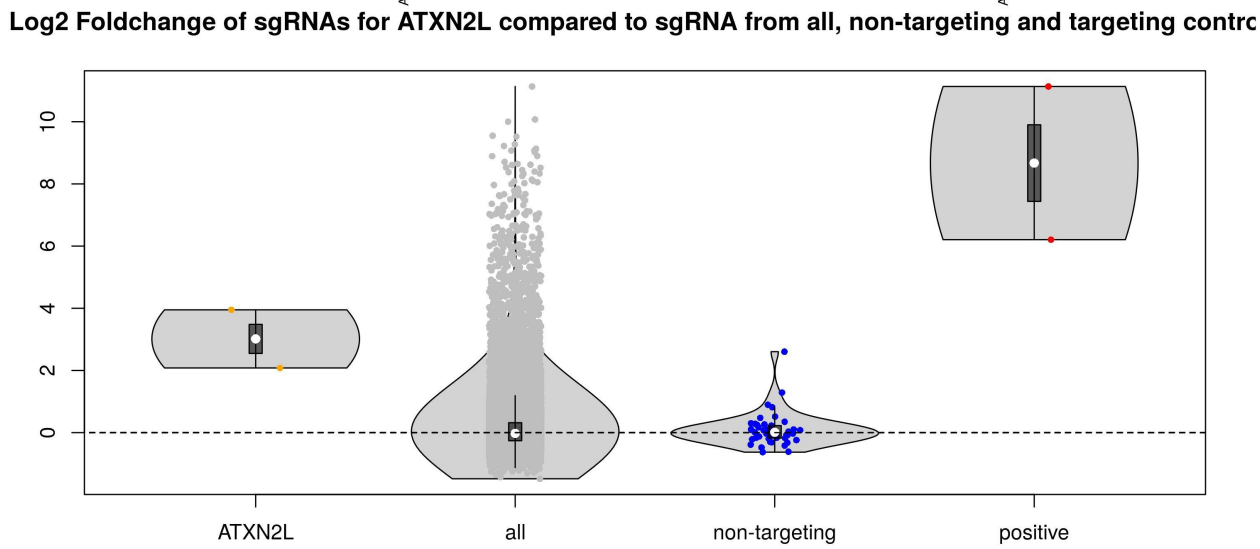
Gene Scatter for ATXN2L
PLX_resistance_YTAR



sgRNA Scatter for ATXN2L
PLX_resistance_YTAR



Foldchange: ATXN2L
Normalized log2(foldchange)
0
1
2
3
ATXN2L_0
ATXN2L_1


Log2 Foldchange of sgRNAs for ATXN2L compared to sgRNA from all, non-targeting and targeting contrc
0
2
4
6
8
10
ATXN2L
all
non-targeting
positive

designs	genes	sequence	log2Foldchange
ATXN2L_0	ATXN2L	none	3.950610
ATXN2L_1	ATXN2L	none	2.080772

TADA3

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

ENSEMBL ID (links to Ensembl) ENSG00000171148

HGNC SYMBOL (links to GeneCards) TADA3

GENE DESCRIPTION
transcriptional adaptor 3 [Source:HGNC Symbol;Acc:HGNC:19422]

GO TERM

MIM GENE DESCRIPTION
TRANSCRIPTIONAL ADAPTOR 3; TADA3;;TRANSCRIPTIONAL ADAPTOR 3-LIKE; TADA3L;;ADA3, YEAST, HOMOLOG OF; ADA3

ENSEMBL PROTEIN ID
ENSP00000395073

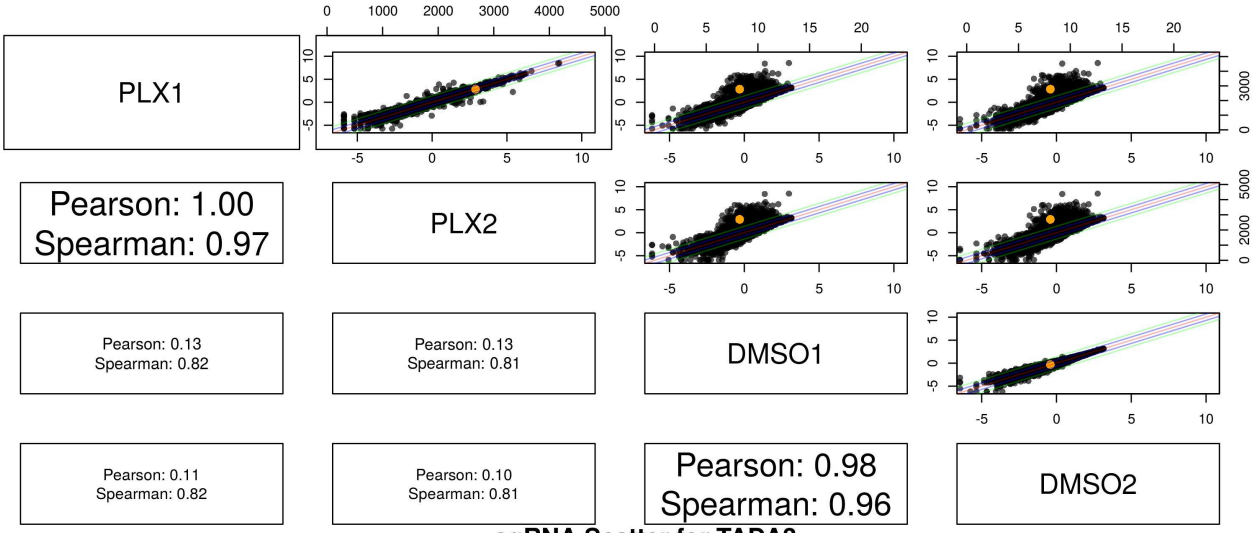
PROTEIN FAMILY DESCRIPTION
TRANSCRIPTIONAL ADAPTER 3 ADA3 HOMOLOG TRANSCRIPTIONAL ADAPTER 3 ADA3

Wilcox p-value: 0.414337

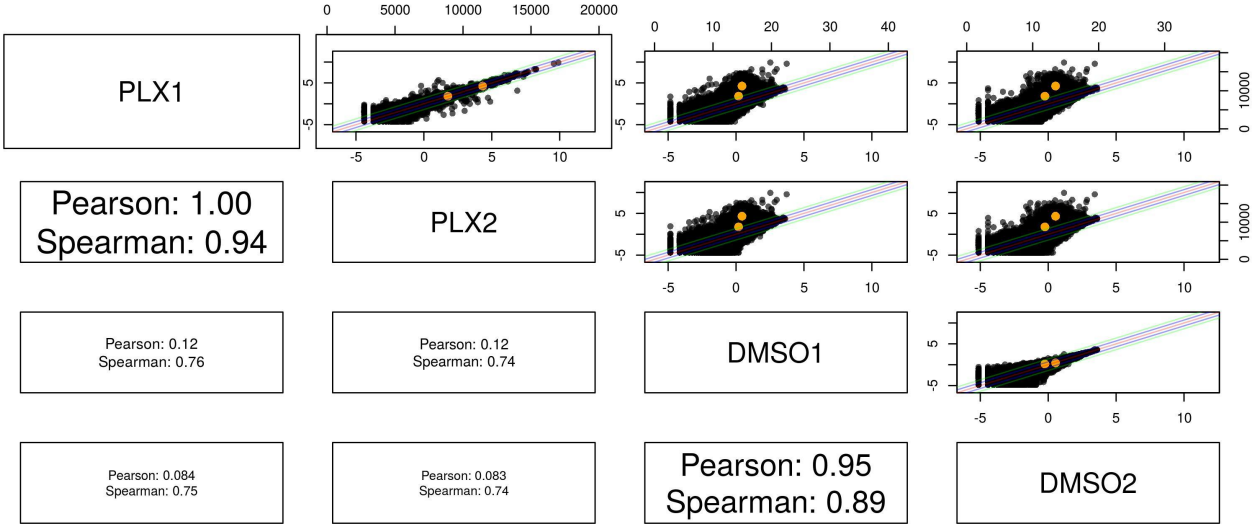
DESeq2 p-value: 2.442865e-91

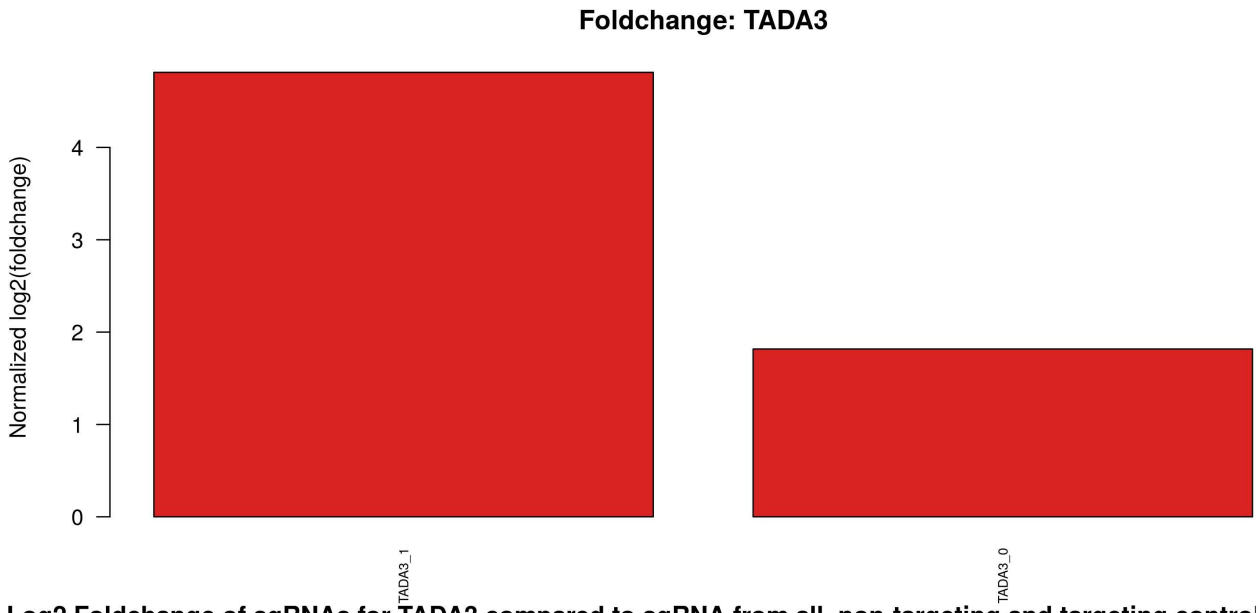
MAGeCK p-value: 0.445616

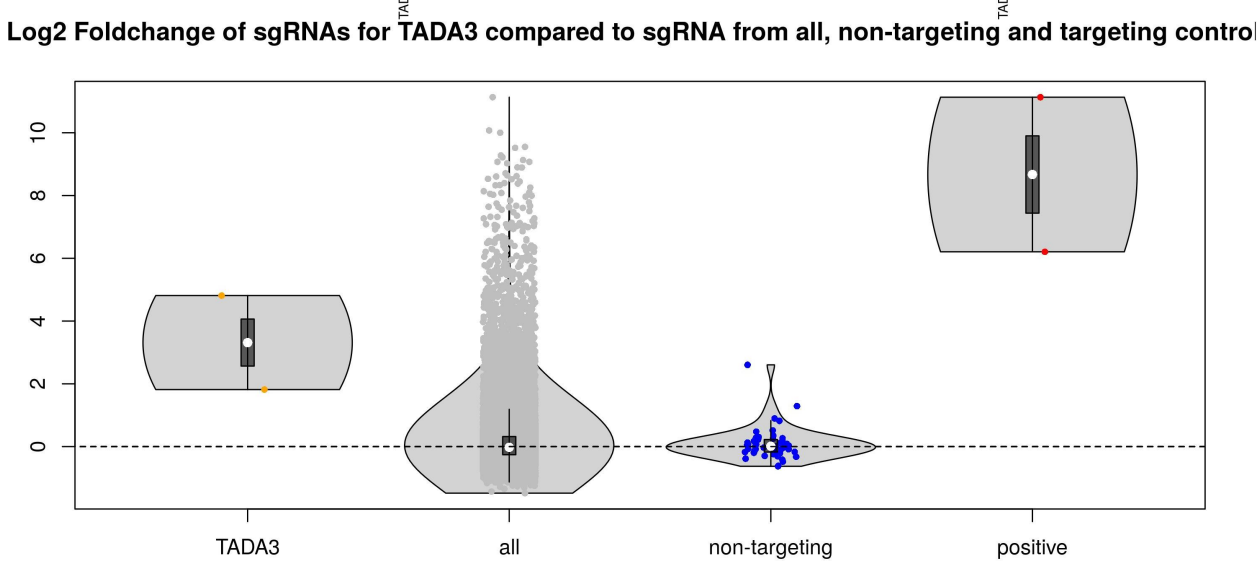
Gene Scatter for TADA3
PLX_resistance_YTAR



sgRNA Scatter for TADA3
PLX_resistance_YTAR




Foldchange: TADA3
Normalized log2(foldchange)
0
1
2
3
4
TADA3_1
TADA3_0


Log2 Foldchange of sgRNAs for TADA3 compared to sgRNA from all, non-targeting and targeting control
0
2
4
6
8
10
TADA3
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
2	TADA3_1	TADA3	none	4.812771
1	TADA3_0	TADA3	none	1.817020

ELMOD1

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

ENSEMBL ID (links to Ensembl) ENSG00000110675

HGNC SYMBOL (links to GeneCards) ELMOD1

GENE DESCRIPTION
ELMO/CED-12 domain containing 1 [Source:HGNC Symbol;Acc:HGNC:25334]

GO TERM
enzyme regulator activity

MIM GENE DESCRIPTION
ELMO/CED12 DOMAIN-CONTAINING PROTEIN 1; ELMOD1

ENSEMBL PROTEIN ID
ENSP00000412257

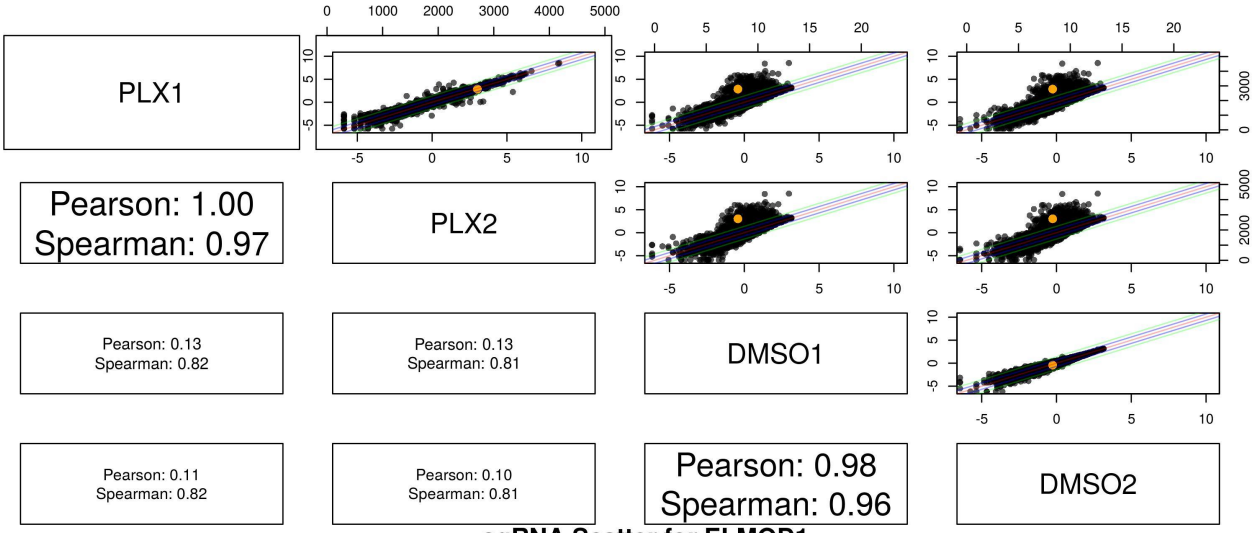
PROTEIN FAMILY DESCRIPTION
ELMO DOMAIN CONTAINING

Wilcox p-value: 0.414337

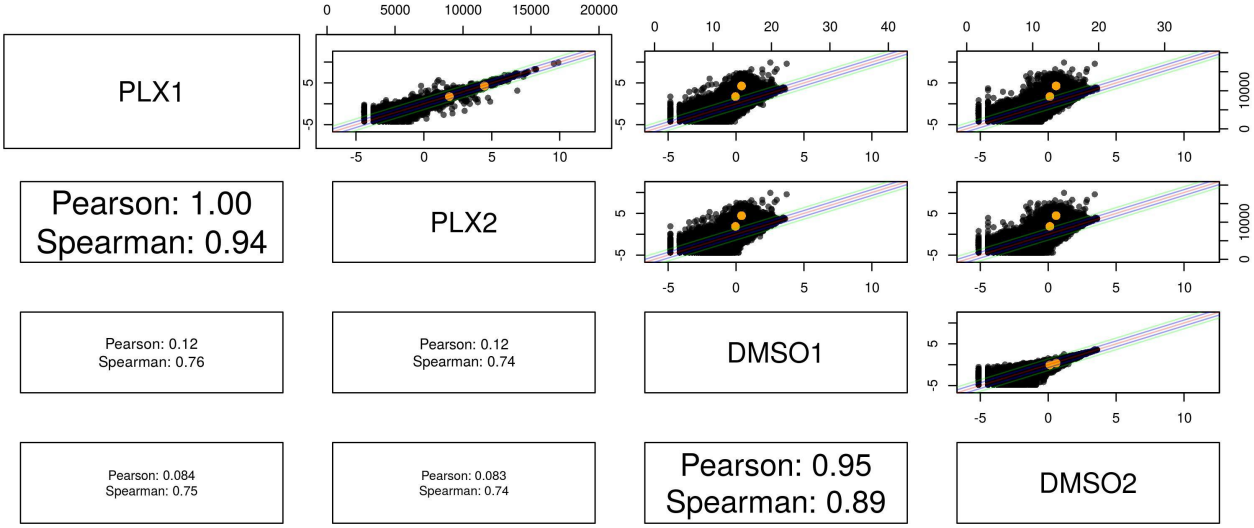
DESeq2 p-value: 1.719877e-80

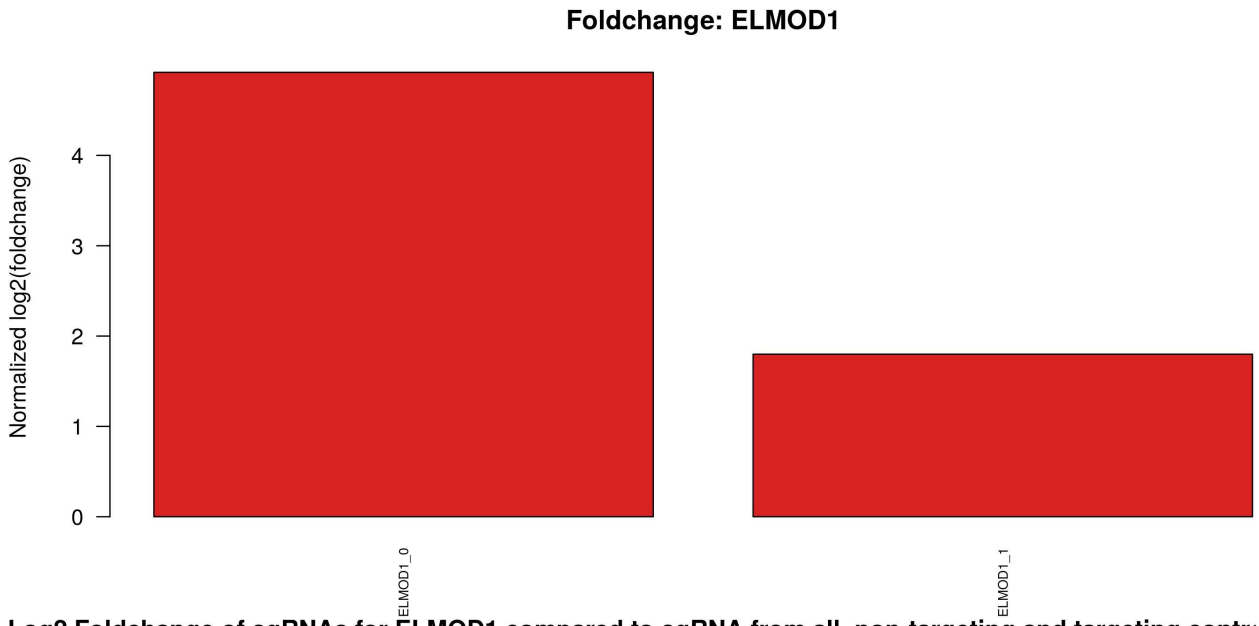
MAGeCK p-value: 0.451114

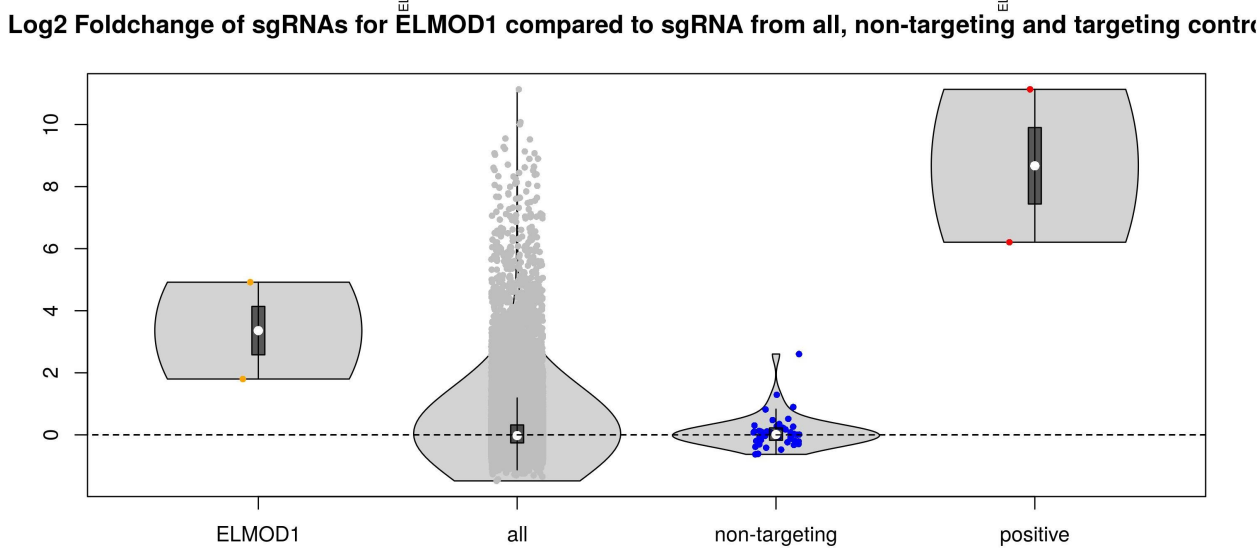
Gene Scatter for ELMOD1
PLX_resistance_YTAR



sgRNA Scatter for ELMOD1
PLX_resistance_YTAR




Foldchange: ELMOD1
Normalized log2(foldchange)
0
1
2
3
4
ELMOD1_0
ELMOD1_1


Log2 Foldchange of sgRNAs for ELMOD1 compared to sgRNA from all, non-targeting and targeting contr
0
2
4
6
8
10
ELMOD1
all
non-targeting
positive

designs	genes	sequence	log2Foldchange
ELMOD1_0	ELMOD1	none	4.919463
ELMOD1_1	ELMOD1	none	1.799261

GPR123

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

ENSEMBL ID (links to Ensembl) NA

HGNC SYMBOL (links to GeneCards) GPR123

GENE DESCRIPTION
NA

GO TERM
NA

MIM GENE DESCRIPTION
NA

ENSEMBL PROTEIN ID
NA

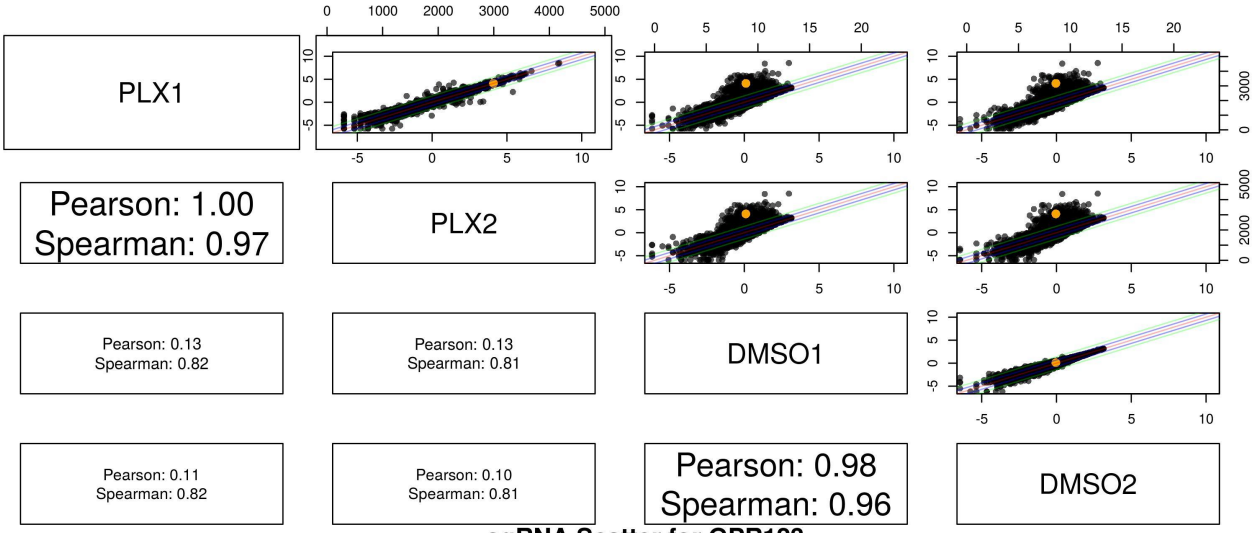
PROTEIN FAMILY DESCRIPTION
NA

Wilcox p-value: 0.414337

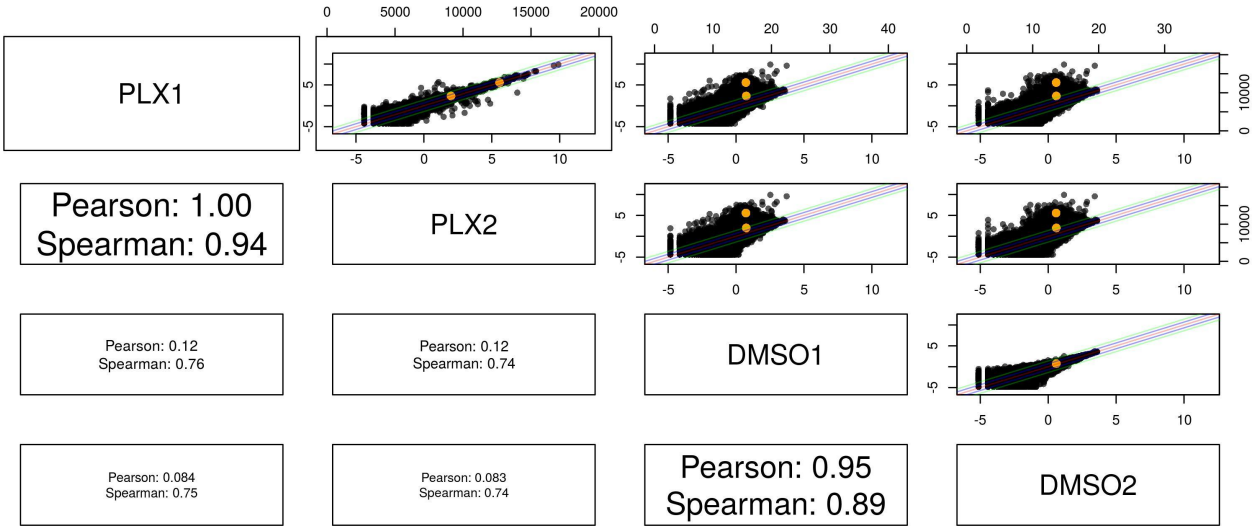
DESeq2 p-value: 2.066922e-143

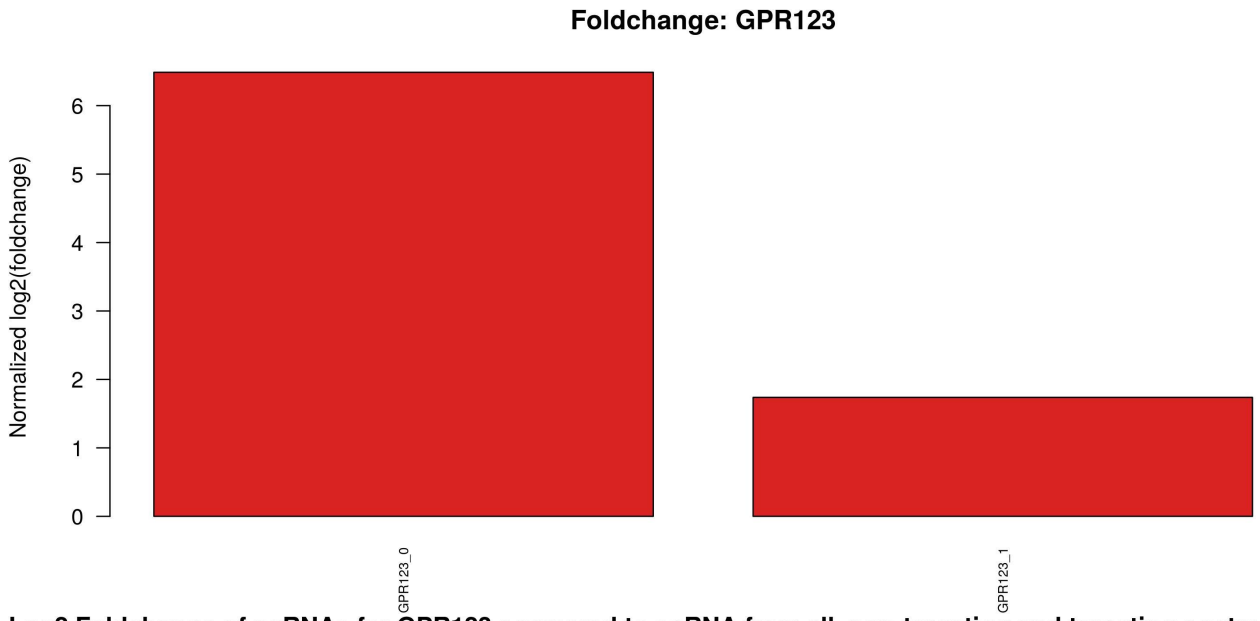
MAGeCK p-value: 0.460264

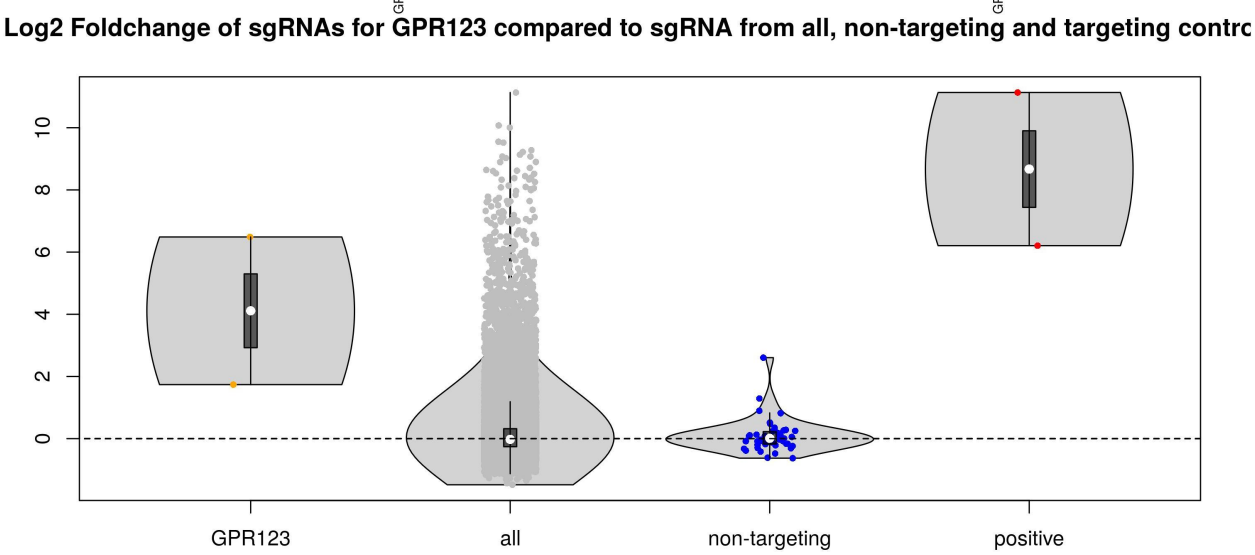
Gene Scatter for GPR123
PLX_resistance_YTAR



sgRNA Scatter for GPR123
PLX_resistance_YTAR




Foldchange: GPR123
Normalized log2(foldchange)
0
1
2
3
4
5
6
GPR123_0
GPR123_1


Log2 Foldchange of sgRNAs for GPR123 compared to sgRNA from all, non-targeting and targeting contrc
0
2
4
6
8
10
GPR123
all
non-targeting
positive

designs	genes	sequence	log2Foldchange
GPR123_0	GPR123	none	6.487091
GPR123_1	GPR123	none	1.737966

LGALS4

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

ENSEMBL ID (links to Ensembl) ENSG00000171747

HGNC SYMBOL (links to GeneCards) LGALS4

GENE DESCRIPTION
lectin, galactoside-binding, soluble, 4 [Source:HGNC Symbol;Acc:HGNC:6565]

GO TERM
molecular_function

MIM GENE DESCRIPTION
LECTIN, GALACTOSIDE-BINDING, SOLUBLE, 4; LGALS4;;GALECTIN 4; GAL4

ENSEMBL PROTEIN ID
ENSP00000472990

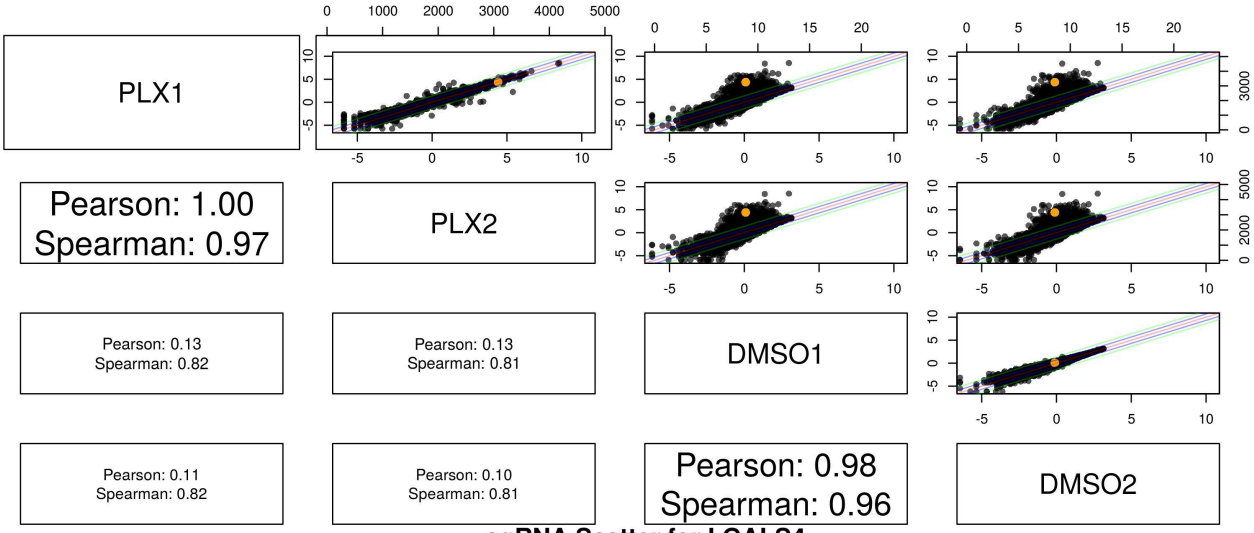
PROTEIN FAMILY DESCRIPTION
UNKNOWN

Wilcox p-value: 0.414337

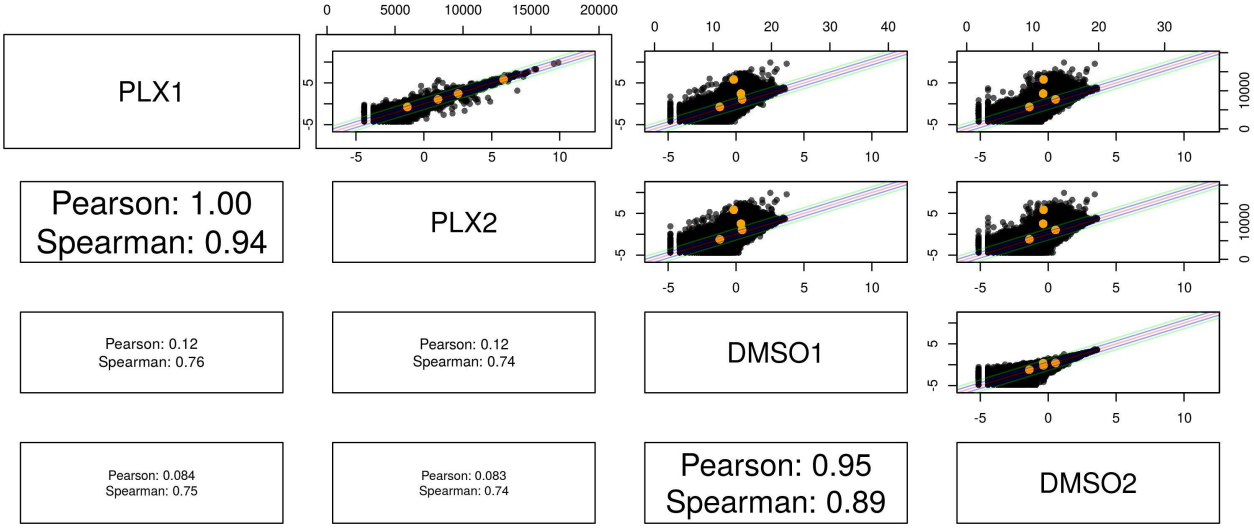
DESeq2 p-value: 3.490284e-153

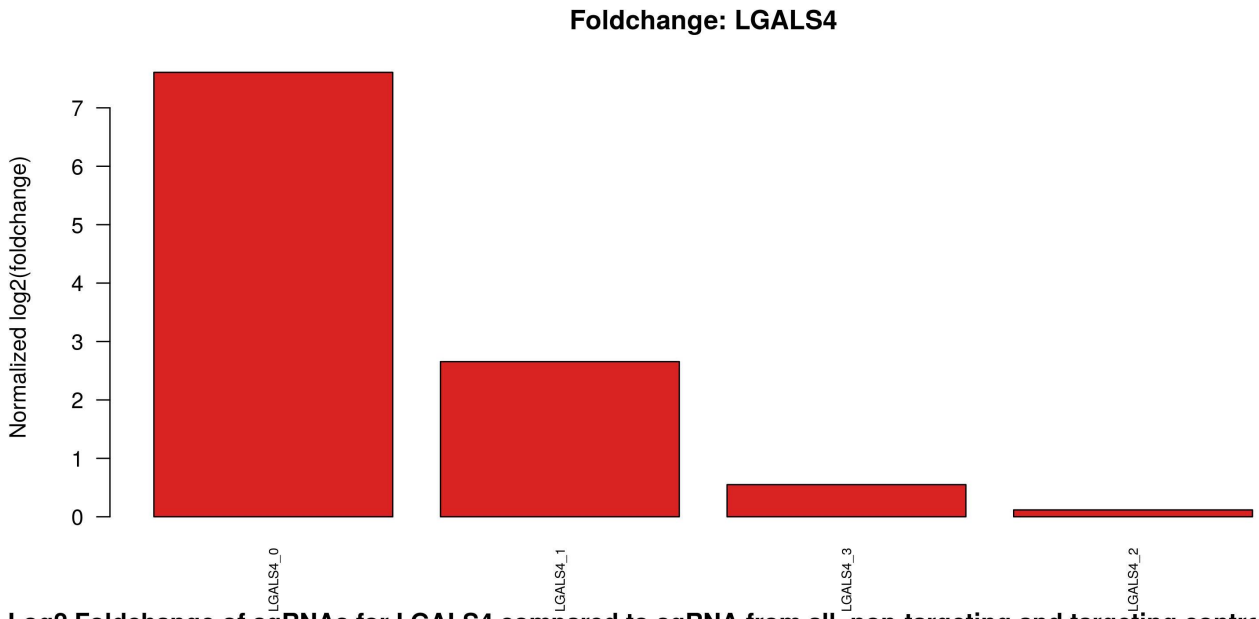
MAGeCK p-value: 0.54205

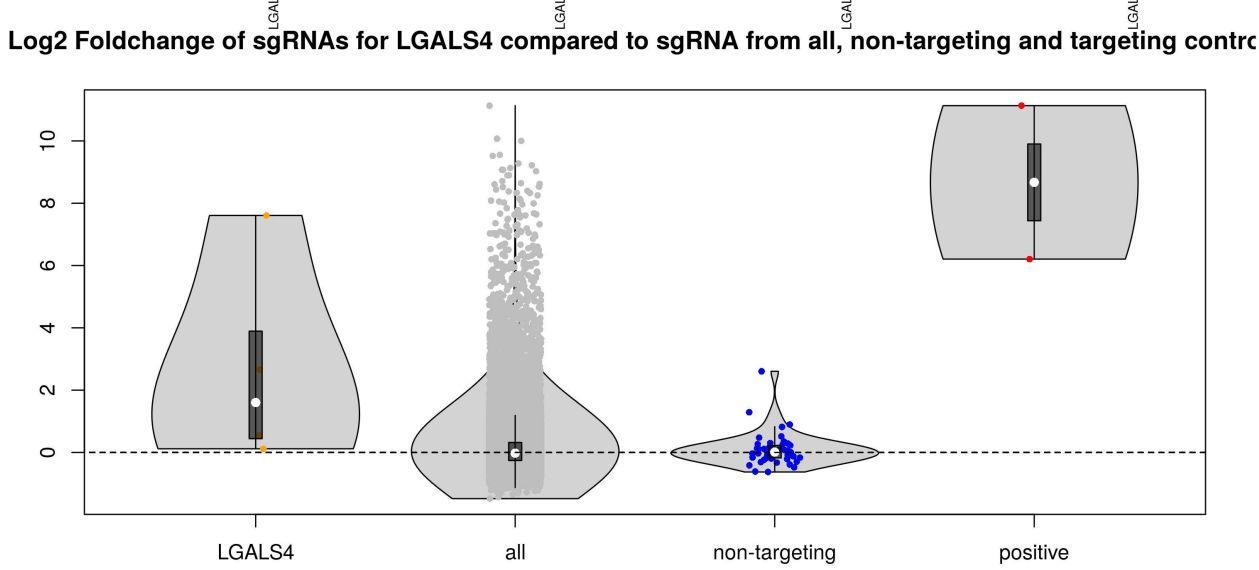
Gene Scatter for LGALS4
PLX_resistance_YTAR



sgRNA Scatter for LGALS4
PLX_resistance_YTAR




Foldchange: LGALS4
Normalized log2(foldchange)
0
1
2
3
4
5
6
7
LGALS4_0
LGALS4_1
LGALS4_3
LGALS4_2


Log2 Foldchange of sgRNAs for LGALS4 compared to sgRNA from all, non-targeting and targeting contro
0
2
4
6
8
10
LGALS4
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
1	LGALS4_0	LGALS4	none	7.6073844
2	LGALS4_1	LGALS4	none	2.6555475
4	LGALS4_3	LGALS4	none	0.5500078
3	LGALS4_2	LGALS4	none	0.1173055

NDUFAF5

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

ENSEMBL ID (links to Ensembl) ENSG00000101247

HGNC SYMBOL (links to GeneCards) NDUFAF5

GENE DESCRIPTION
NADH dehydrogenase (ubiquinone) complex I, assembly factor 5 [Source:HGNC Symbol;Acc:HGNC:15899]

GO TERM
organelle

MIM GENE DESCRIPTION
NADH DEHYDROGENASE (UBIQUINONE) COMPLEX I, ASSEMBLY FACTOR 5; NDUFAF5;;CHROMOSOME 20 OPEN READING FRAME 7; C20ORF7

ENSEMBL PROTEIN ID
ENSP00000420497

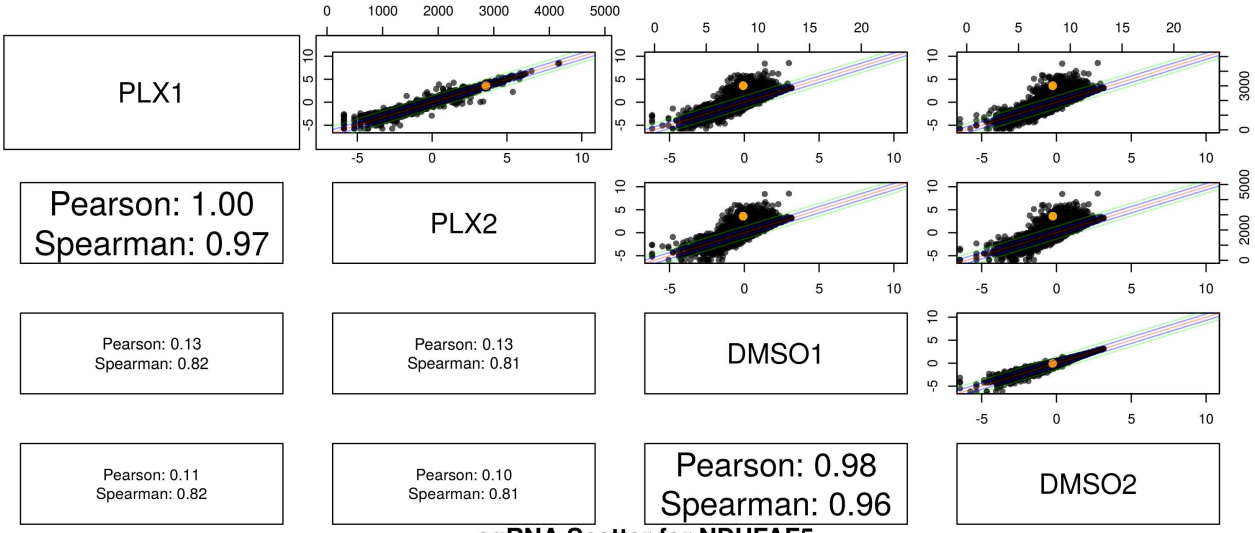
PROTEIN FAMILY DESCRIPTION
NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX ASSEMBLY FACTOR 5 PRECURSOR PROBABLE METHYLTRANSFERASE MITOCHONDRIAL EC_2.1.1.-

Wilcox p-value: 0.3482308

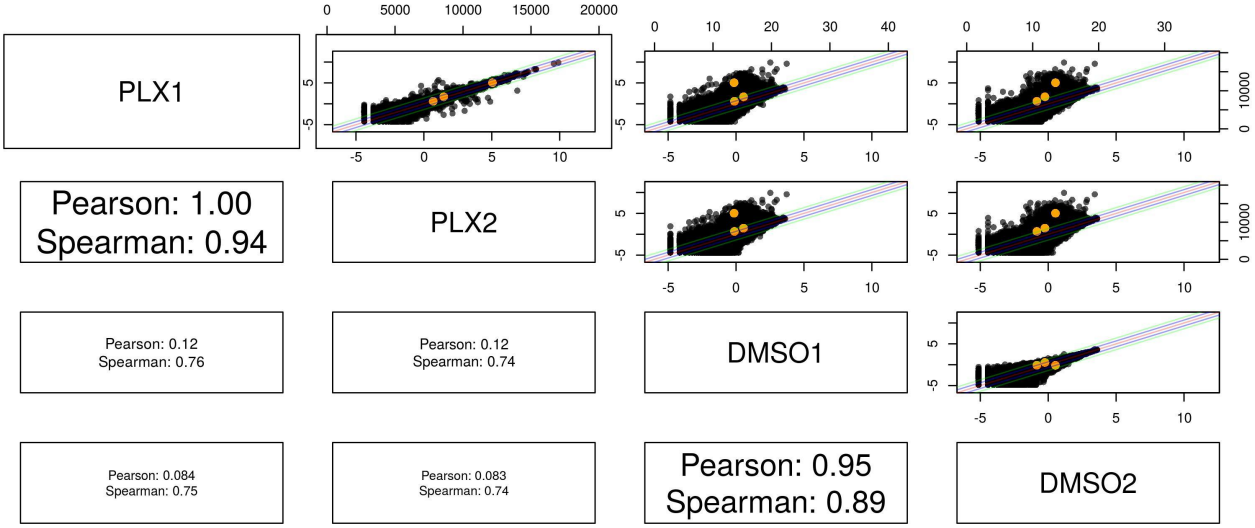
DESeq2 p-value: 1.212808e-116

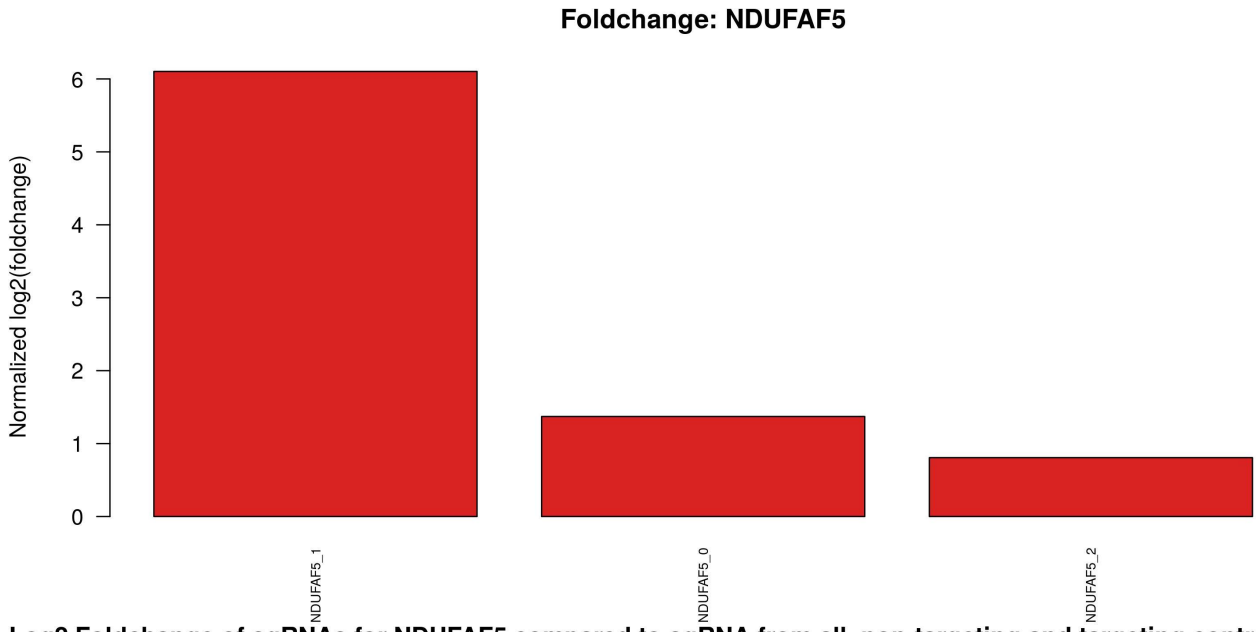
MAGeCK p-value: 0.545116

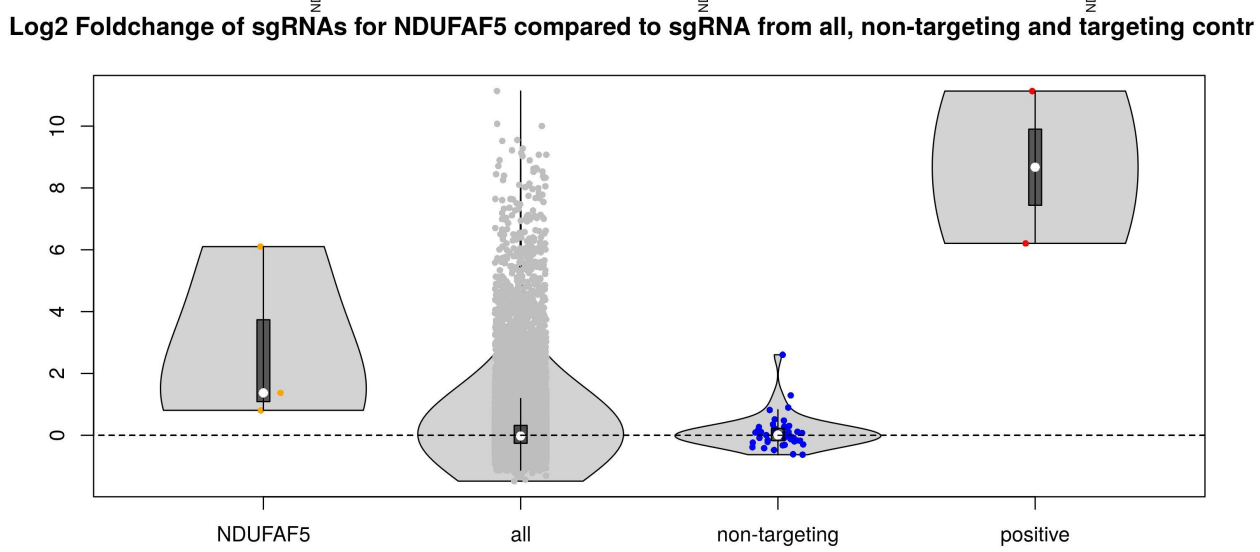
Gene Scatter for NDUFAF5
PLX_resistance_YTAR



sgRNA Scatter for NDUFAF5
PLX_resistance_YTAR




Foldchange: NDUFAF5
Normalized log2(foldchange)
0
1
2
3
4
5
6
NDUFAF5_1
NDUFAF5_0
NDUFAF5_2


Log2 Foldchange of sgRNAs for NDUFAF5 compared to sgRNA from all, non-targeting and targeting contr
0
2
4
6
8
10
NDUFAF5
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
2	NDUFAF5_1	NDUFAF5	none	6.1028520
1	NDUFAF5_0	NDUFAF5	none	1.3717246
3	NDUFAF5_2	NDUFAF5	none	0.8074178

LITAF

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

ENSEMBL ID (links to Ensembl) LRG_253

HGNC SYMBOL (links to GeneCards) LITAF

GENE DESCRIPTION
lipopolysaccharide-induced TNF factor [Source:HGNC Symbol;Acc:HGNC:16841]

GO TERM

MIM GENE DESCRIPTION
LIPOPOLYSACCHARIDE-INDUCED TUMOR NECROSIS FACTOR-ALPHA FACTOR; LITAF;;LPS-INDUCED TNF-ALPHA FACTOR;;SMALL INTEGRAL MEMBRANE PROTEIN OF LYSOSOME/LATE ENDOSOME; SIMPLE

ENSEMBL PROTEIN ID
LRG_253p1

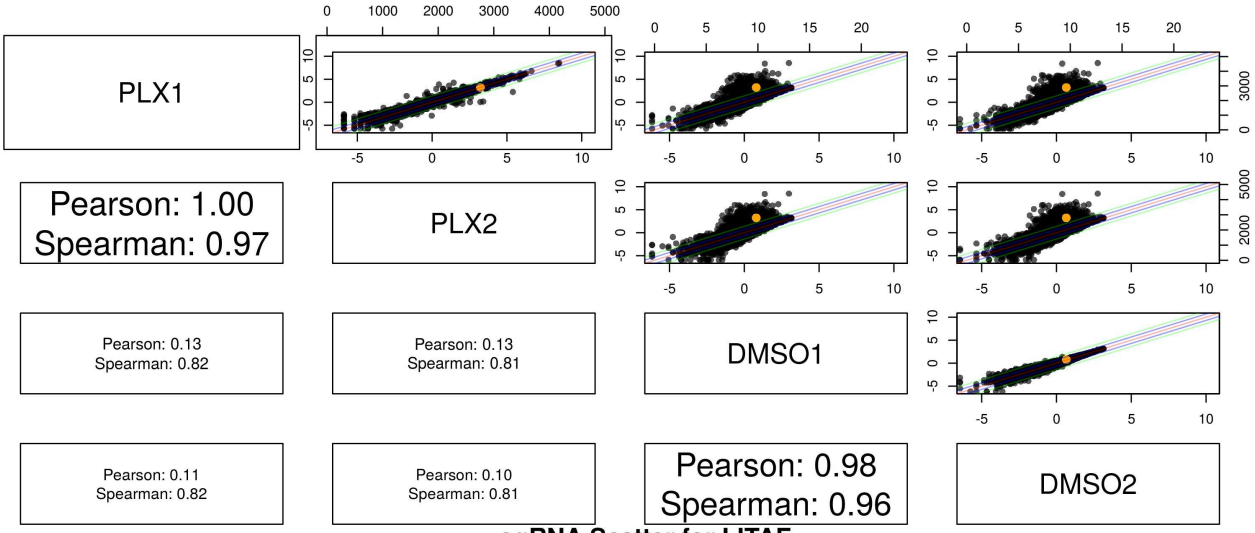
PROTEIN FAMILY DESCRIPTION
LIPOPOLYSACCHARIDE INDUCED TUMOR NECROSIS FACTOR ALPHA FACTOR LPS INDUCED TNF ALPHA FACTOR SMALL INTEGRAL MEMBRANE OF LYSOSOME/LATE ENDOSOME

Wilcox p-value: 0.414337

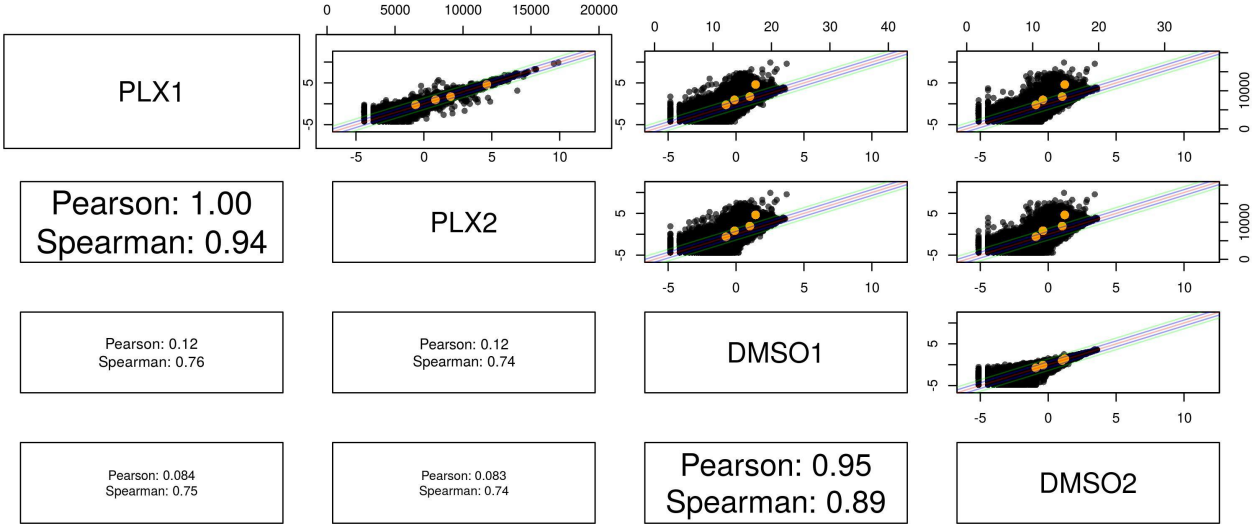
DESeq2 p-value: 5.488504e-54

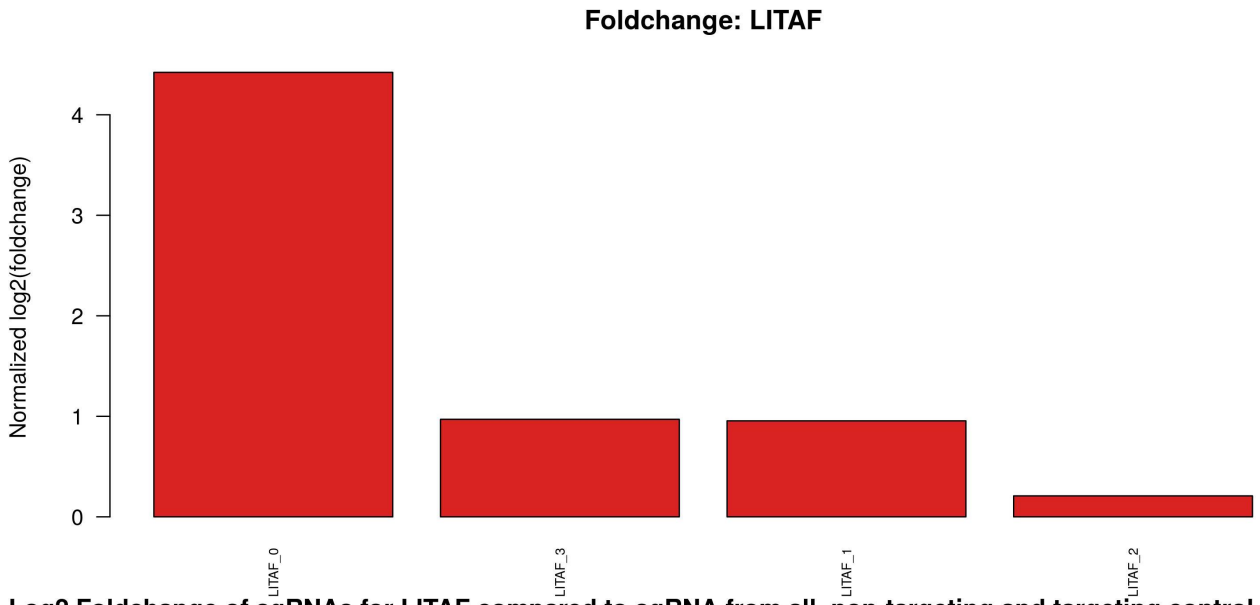
MAGeCK p-value: 0.631713

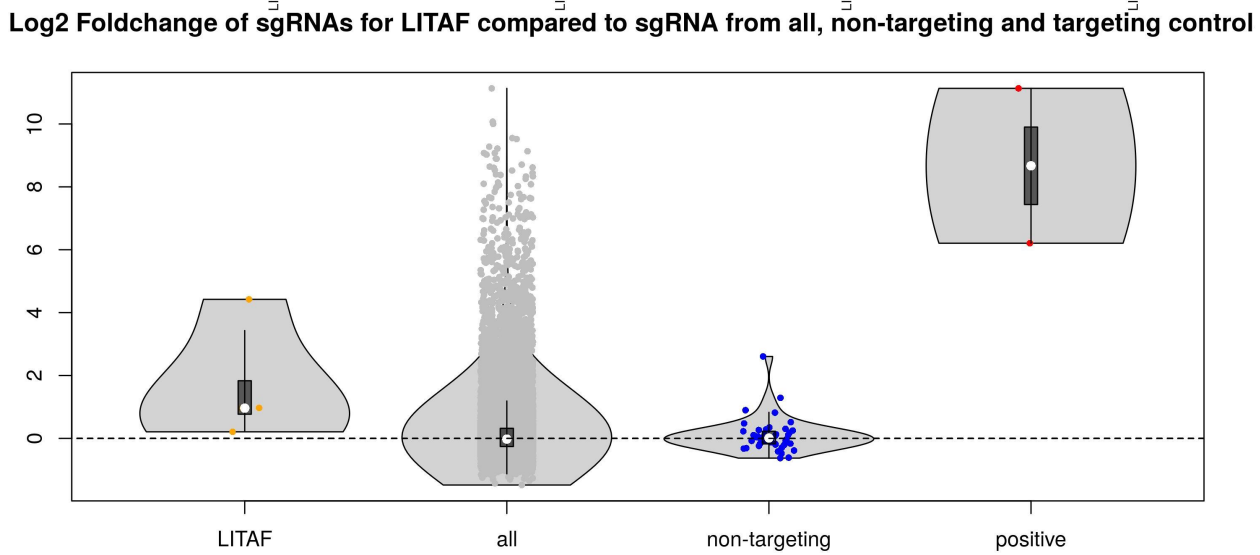
Gene Scatter for LITAF
PLX_resistance_YTAR



sgRNA Scatter for LITAF
PLX_resistance_YTAR




Foldchange: LITAF
Normalized log2(foldchange)
0
1
2
3
4
LITAF_0
LITAF_3
LITAF_1
LITAF_2


Log2 Foldchange of sgRNAs for LITAF compared to sgRNA from all, non-targeting and targeting control
0
2
4
6
8
10
LITAF
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
1	LITAF_0	LITAF	none	4.4219492
4	LITAF_3	LITAF	none	0.9703791
2	LITAF_1	LITAF	none	0.9550420
3	LITAF_2	LITAF	none	0.2085102

PPP1R14D

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

ENSEMBL ID (links to Ensembl) ENSG00000166143

HGNC SYMBOL (links to GeneCards) PPP1R14D

GENE DESCRIPTION
protein phosphatase 1, regulatory (inhibitor) subunit 14D [Source:HGNC Symbol;Acc:HGNC:14953]

GO TERM
regulation of protein dephosphorylation

MIM GENE DESCRIPTION
PROTEIN PHOSPHATASE 1, REGULATORY SUBUNIT 14D; PPP1R14D;;GUT AND BRAIN PHOSPHATASE INHIBITOR 1; GBPI1

ENSEMBL PROTEIN ID
ENSP00000398342

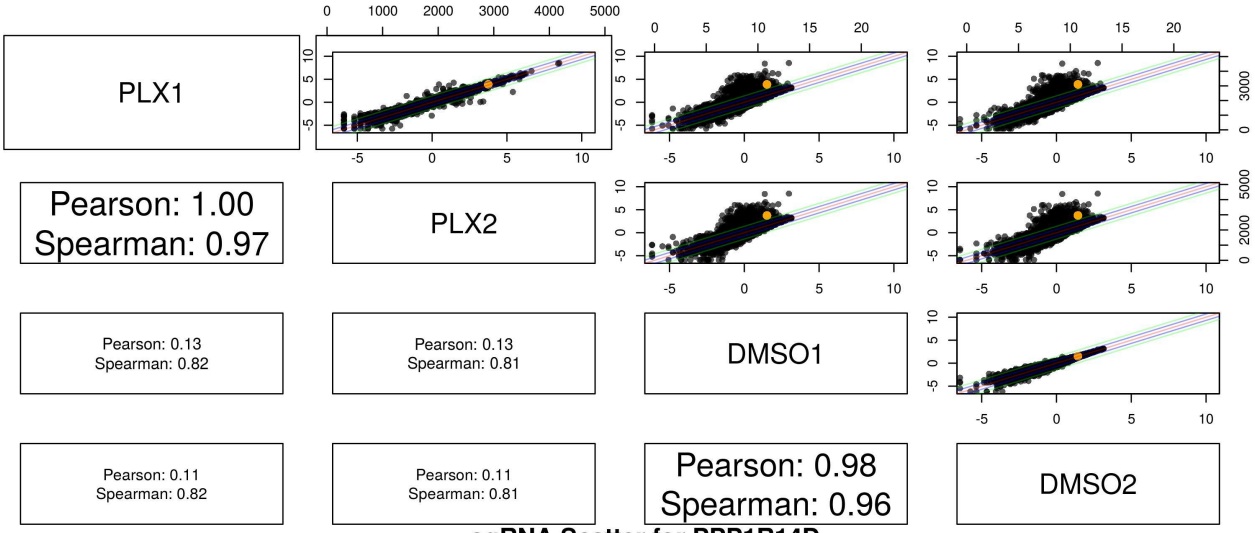
PROTEIN FAMILY DESCRIPTION
PHOSPHATASE 1 REGULATORY SUBUNIT 14D {ECO: |EMBL: 1} FRAGMENT

Wilcox p-value: 0.414337

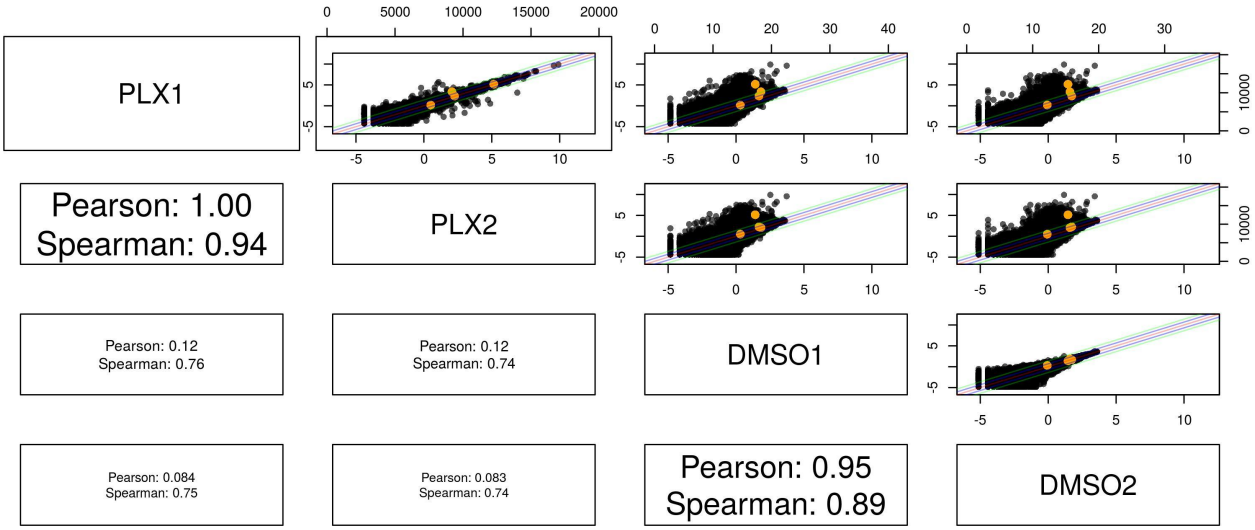
DESeq2 p-value: 4.331764e-47

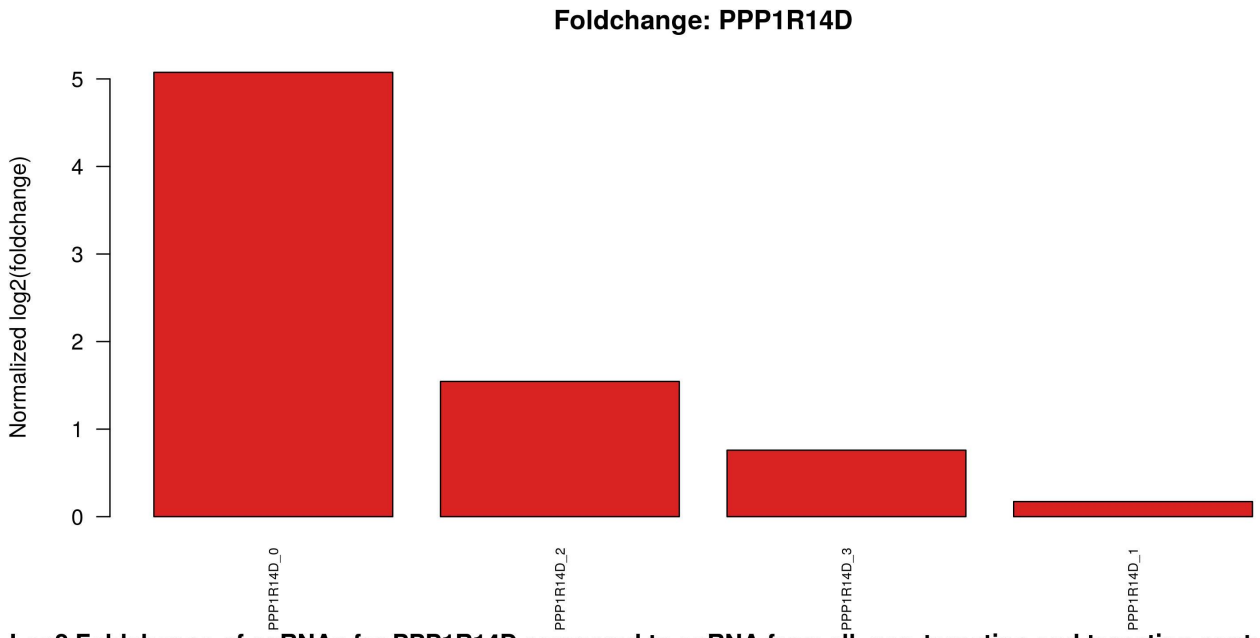
MAGeCK p-value: 0.647636

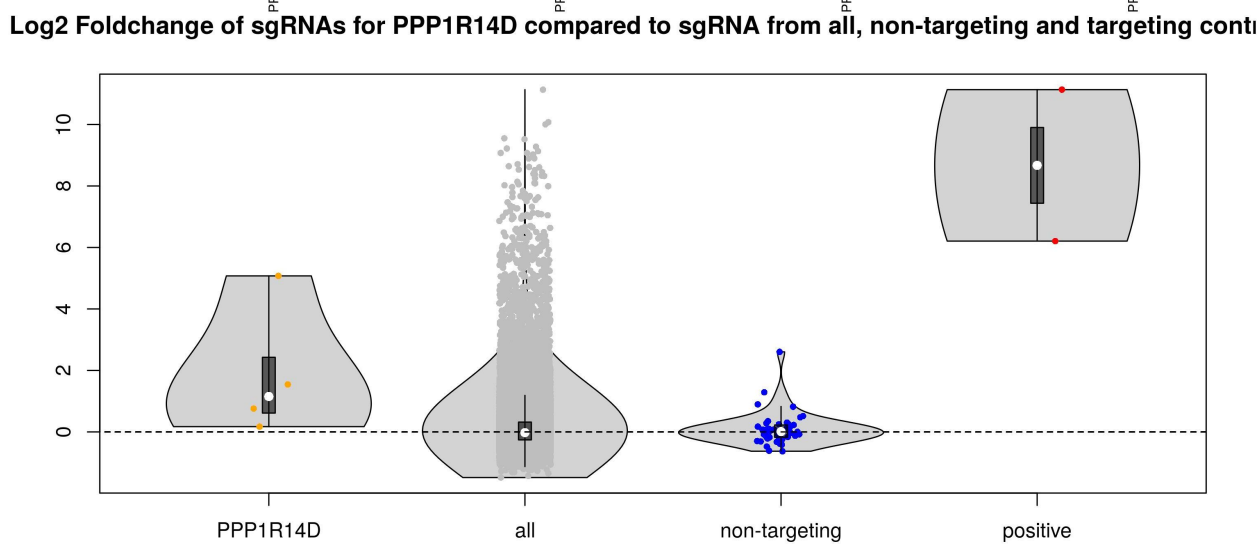
Gene Scatter for PPP1R14D
PLX_resistance_YTAR



sgRNA Scatter for PPP1R14D
PLX_resistance_YTAR




Foldchange: PPP1R14D
Normalized log2(foldchange)
0
1
2
3
4
5
PPP1R14D_0
PPP1R14D_2
PPP1R14D_3
PPP1R14D_1


Log2 Foldchange of sgRNAs for PPP1R14D compared to sgRNA from all, non-targeting and targeting contr
0
2
4
6
8
10
PPP1R14D
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
1	PPP1R14D_0	PPP1R14D	none	5.0752227
3	PPP1R14D_2	PPP1R14D	none	1.5446290
4	PPP1R14D_3	PPP1R14D	none	0.7595385
2	PPP1R14D_1	PPP1R14D	none	0.1724054

Depleted

LCLAT1

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

ENSEMBL ID (links to Ensembl) ENSG00000172954

HGNC SYMBOL (links to GeneCards) LCLAT1

GENE DESCRIPTION
lysocardiolipin acyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:26756]

GO TERM
molecular_function

MIM GENE DESCRIPTION

ENSEMBL PROTEIN ID
ENSP00000419444

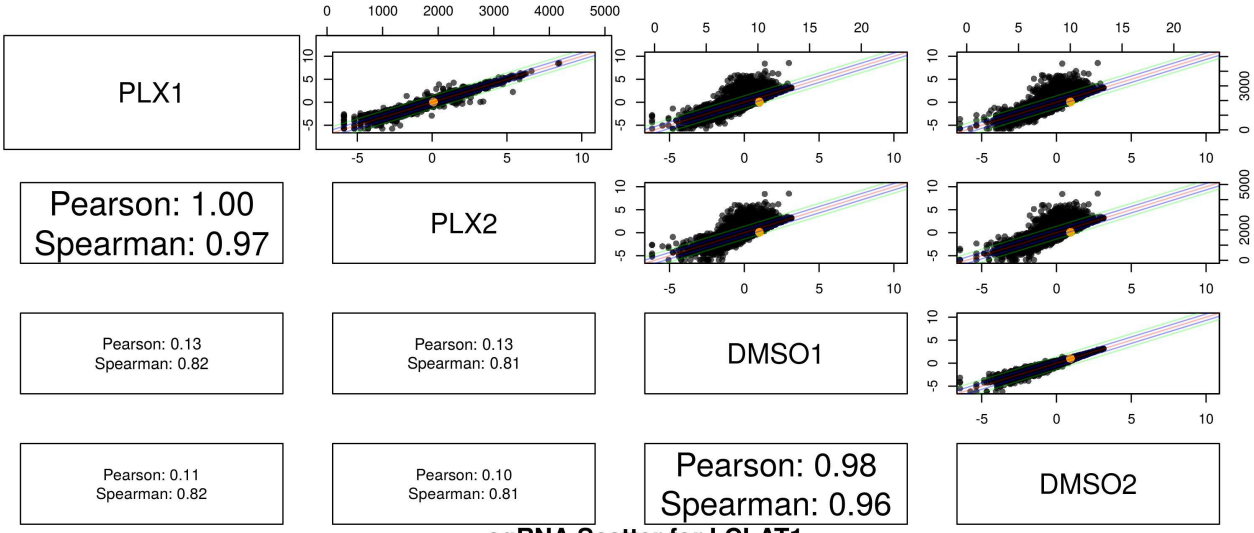
PROTEIN FAMILY DESCRIPTION
LYSOCARDIOLIPIN ACYLTRANSFERASE 1 EC_2.3.1.- EC_2.3.1.51 ACYL COA:LYSOCARDIOLIPIN ACYLTRANSFERASE 1

Wilcox p-value: 0.2824934

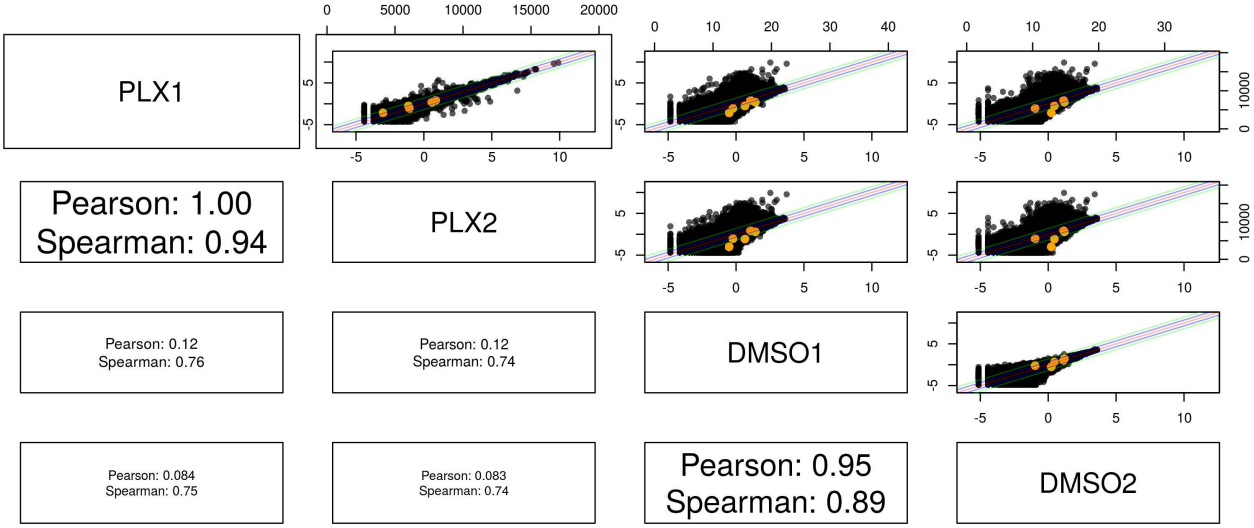
DESeq2 p-value: 0.000974428

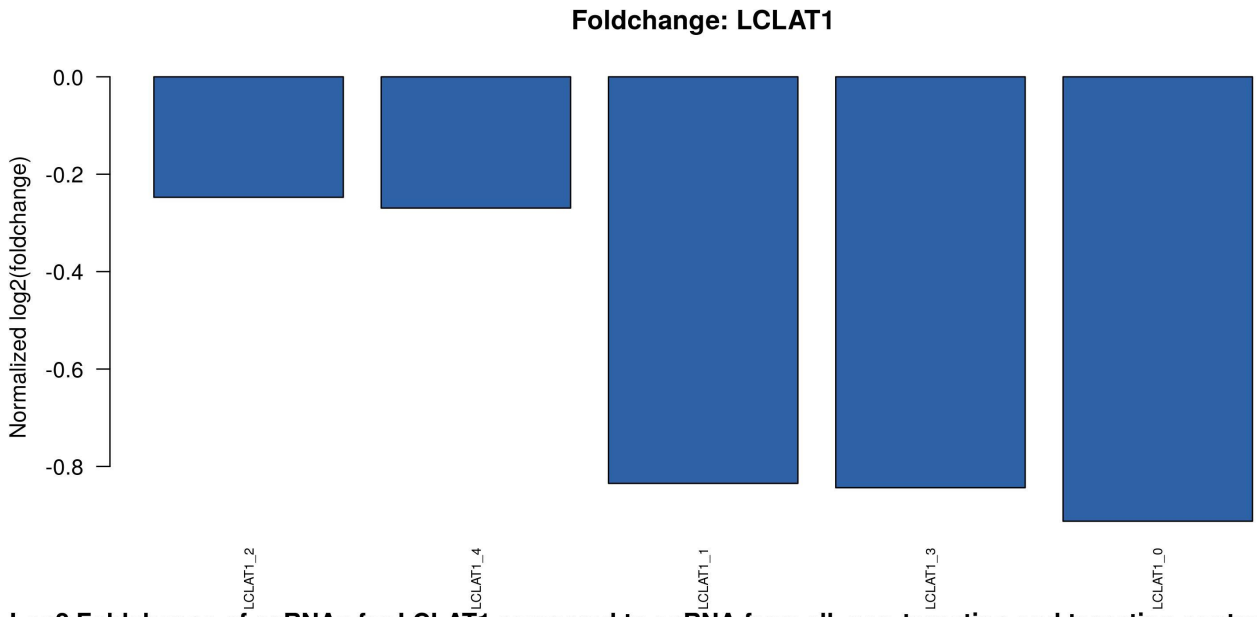
MAGeCK p-value: 0.438614

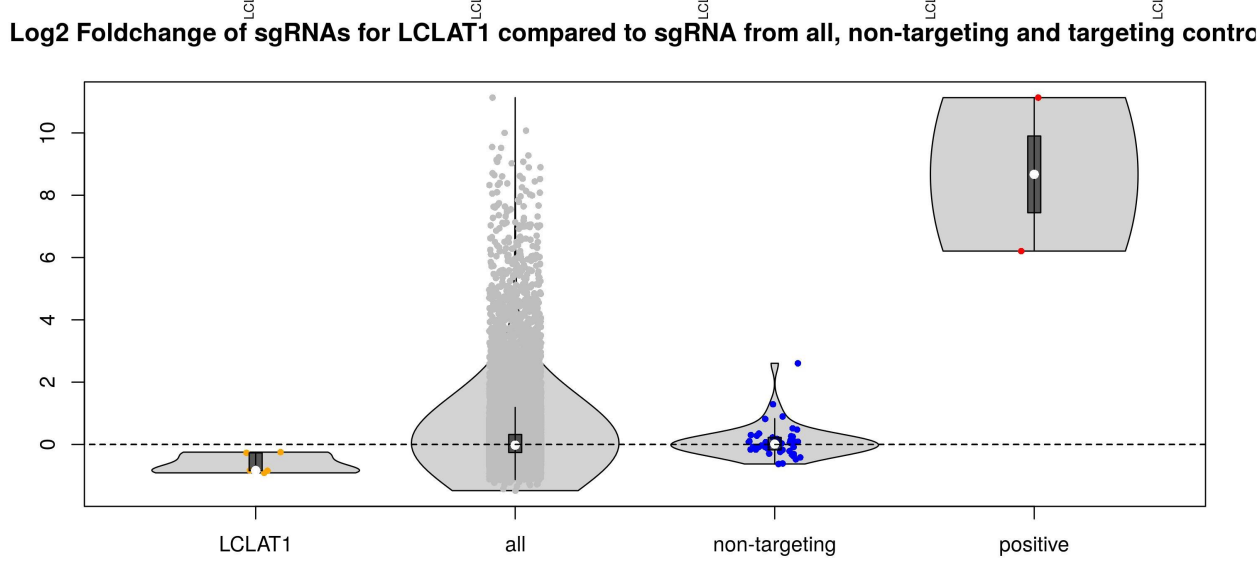
Gene Scatter for LCLAT1
PLX_resistance_YTAR



sgRNA Scatter for LCLAT1
PLX_resistance_YTAR




Foldchange: LCLAT1
Normalized log2(foldchange)
0.0
-0.2
-0.4
-0.6
-0.8
LCLAT1_2
LCLAT1_4
LCLAT1_1
LCLAT1_3
LCLAT1_0


Log2 Foldchange of sgRNAs for LCLAT1 compared to sgRNA from all, non-targeting and targeting contro
0
2
4
6
8
10
LCLAT1
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
3	LCLAT1_2	LCLAT1	none	-0.2474417
5	LCLAT1_4	LCLAT1	none	-0.2695119
2	LCLAT1_1	LCLAT1	none	-0.8347951
4	LCLAT1_3	LCLAT1	none	-0.8436744
1	LCLAT1_0	LCLAT1	none	-0.9124548

MAPKAPK2

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

ENSEMBL ID (links to Ensembl) ENSG00000162889

HGNC SYMBOL (links to GeneCards) MAPKAPK2

GENE DESCRIPTION
mitogen-activated protein kinase-activated protein kinase 2 [Source:HGNC Symbol;Acc:HGNC:6887]

GO TERM
inner ear development

MIM GENE DESCRIPTION
MITOGEN-ACTIVATED PROTEIN KINASE-ACTIVATED PROTEIN KINASE 2; MAPKAPK2;;MAPKAP KINASE 2;;MK2

ENSEMBL PROTEIN ID
ENSP00000356070

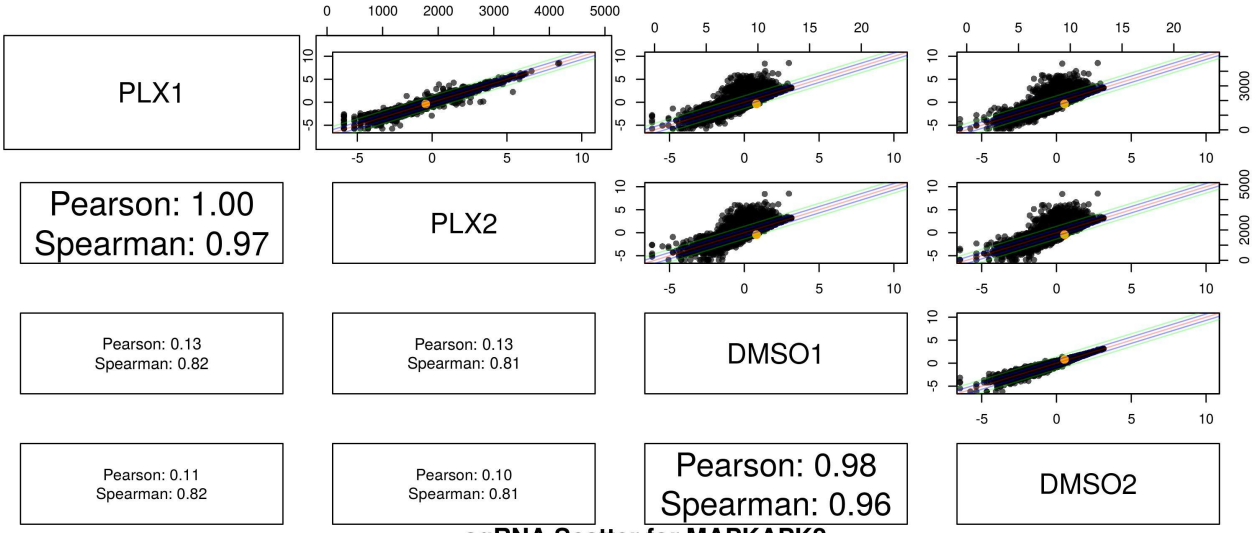
PROTEIN FAMILY DESCRIPTION
MAP KINASE ACTIVATED KINASE 2 MAPK ACTIVATED KINASE 2 MAPKAP KINASE 2 MAPKAP K2 MAPKAPK 2 MK 2 MK2 EC_2.7.11.1

Wilcox p-value: 0.2824934

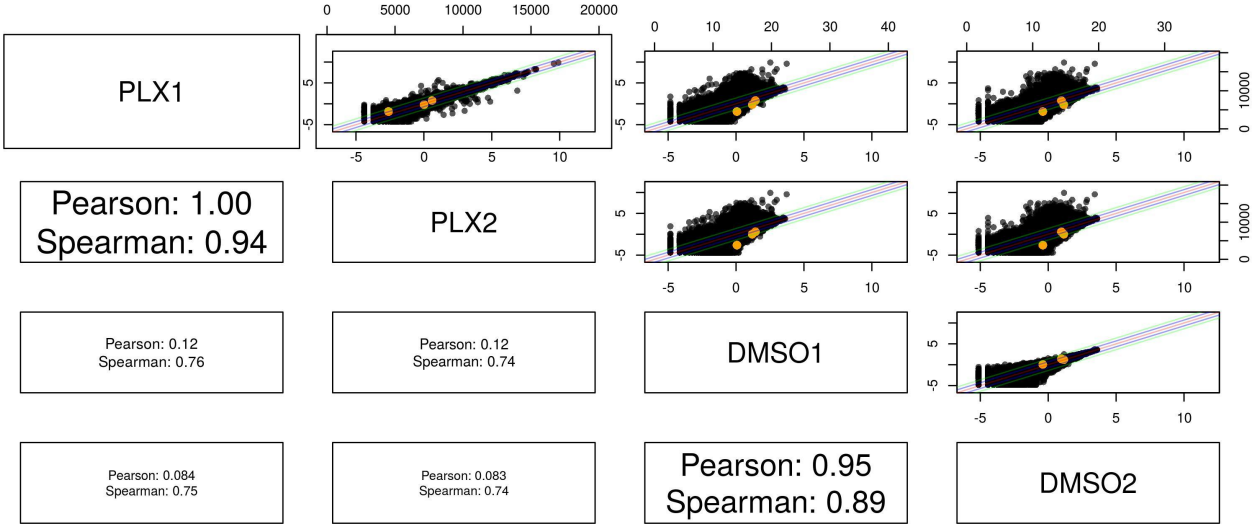
DESeq2 p-value: 0.0002616353

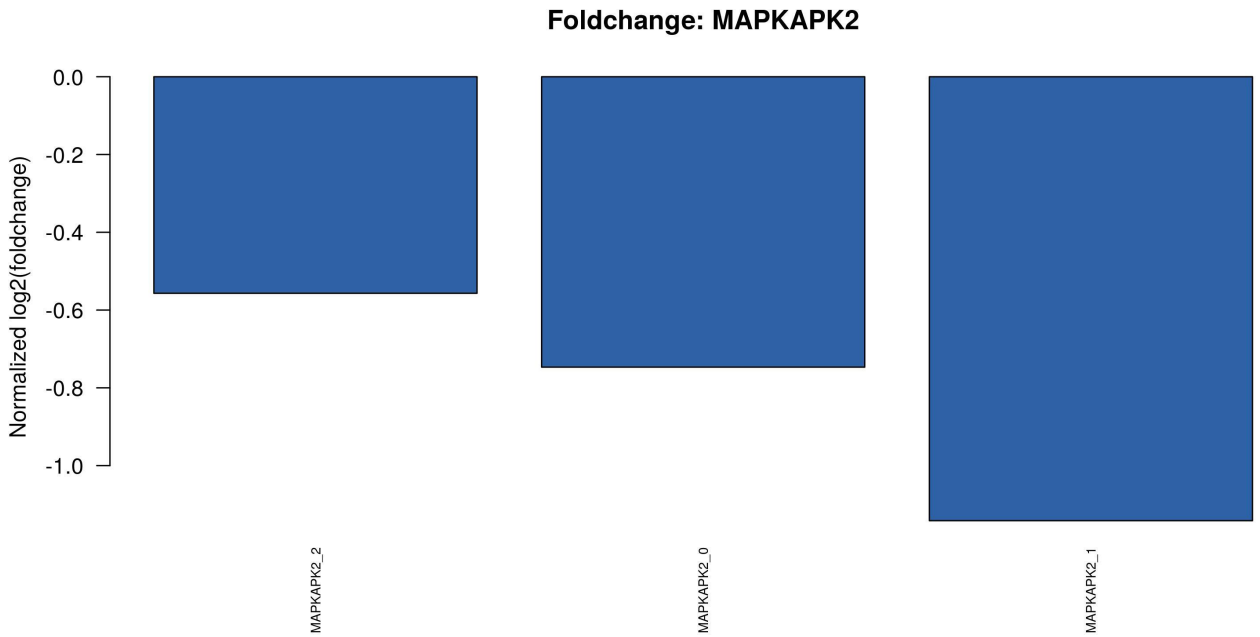
MAGeCK p-value: 0.508801

Gene Scatter for MAPKAPK2
PLX_resistance_YTAR

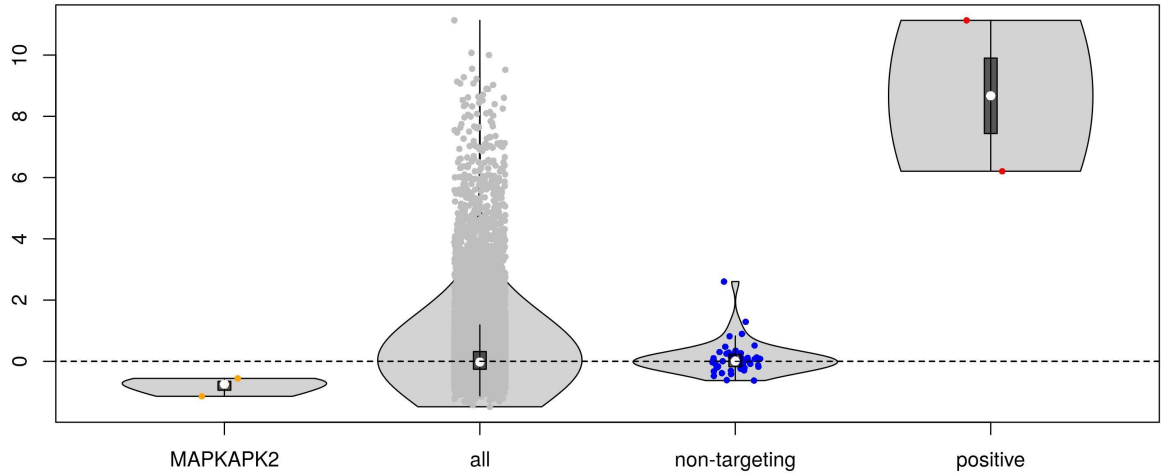


sgRNA Scatter for MAPKAPK2
PLX_resistance_YTAR





Log2 Foldchange of sgRNAs for MAPKAPK2 compared to sgRNA from all, non-targeting and targeting cont



	designs	genes	sequence	log2Foldchange
3	MAPKAPK2_2	MAPKAPK2	none	-0.5569056
1	MAPKAPK2_0	MAPKAPK2	none	-0.7467680
2	MAPKAPK2_1	MAPKAPK2	none	-1.1415886

MCL1

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

ENSEMBL ID (links to Ensembl) ENSG00000143384

HGNC SYMBOL (links to GeneCards) MCL1

GENE DESCRIPTION
myeloid cell leukemia 1 [Source:HGNC Symbol;Acc:HGNC:6943]

GO TERM
biological_process

MIM GENE DESCRIPTION
MYELOID CELL LEUKEMIA SEQUENCE 1; MCL1MYELOID CELL LEUKEMIA 1, LONG ISOFORM, INCLUDED; MCL1L, INCLUDED;;MYELOID CELL LEUKEMIA 1, SHORT ISOFORM, INCLUDED; MCL1S, INCLUDED

ENSEMBL PROTEIN ID
ENSP00000477624

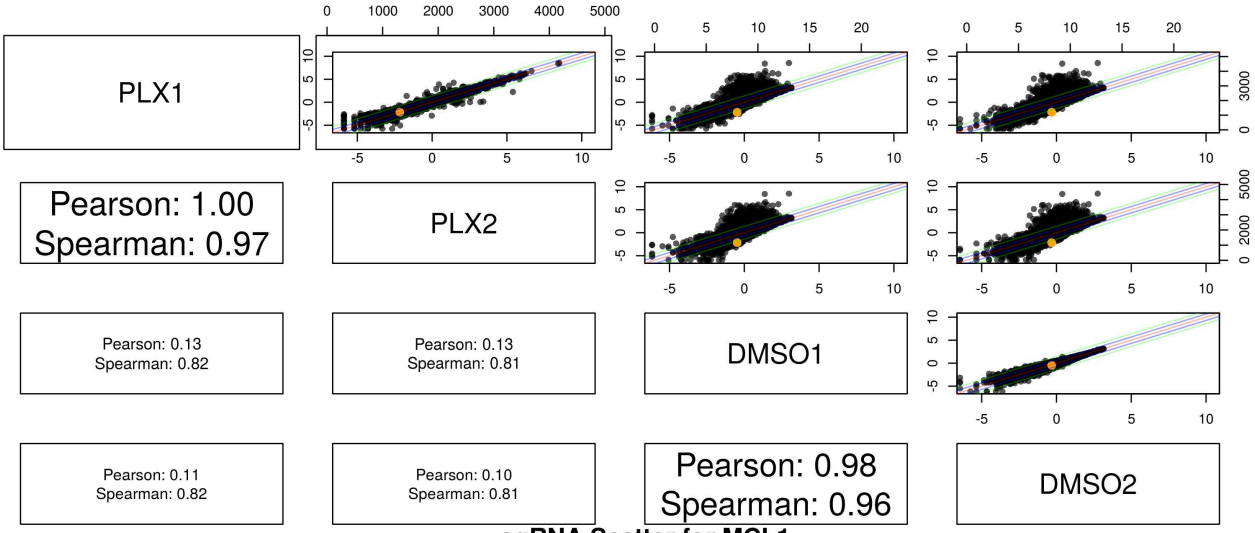
PROTEIN FAMILY DESCRIPTION
INDUCED MYELOID LEUKEMIA CELL DIFFERENTIATION MCL 1

Wilcox p-value: 0.2824934

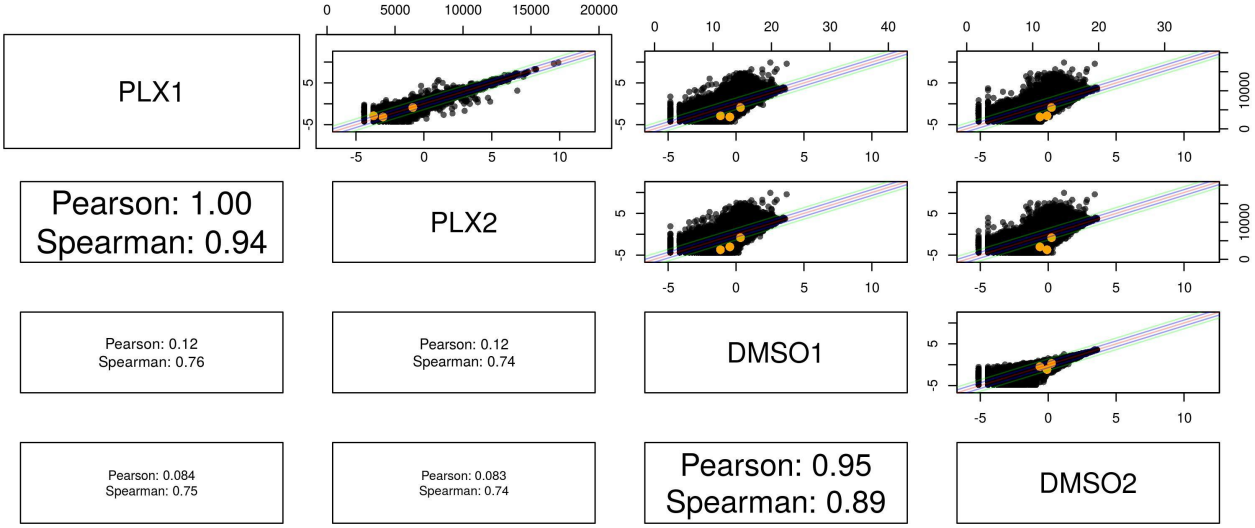
DESeq2 p-value: 3.381479e-13

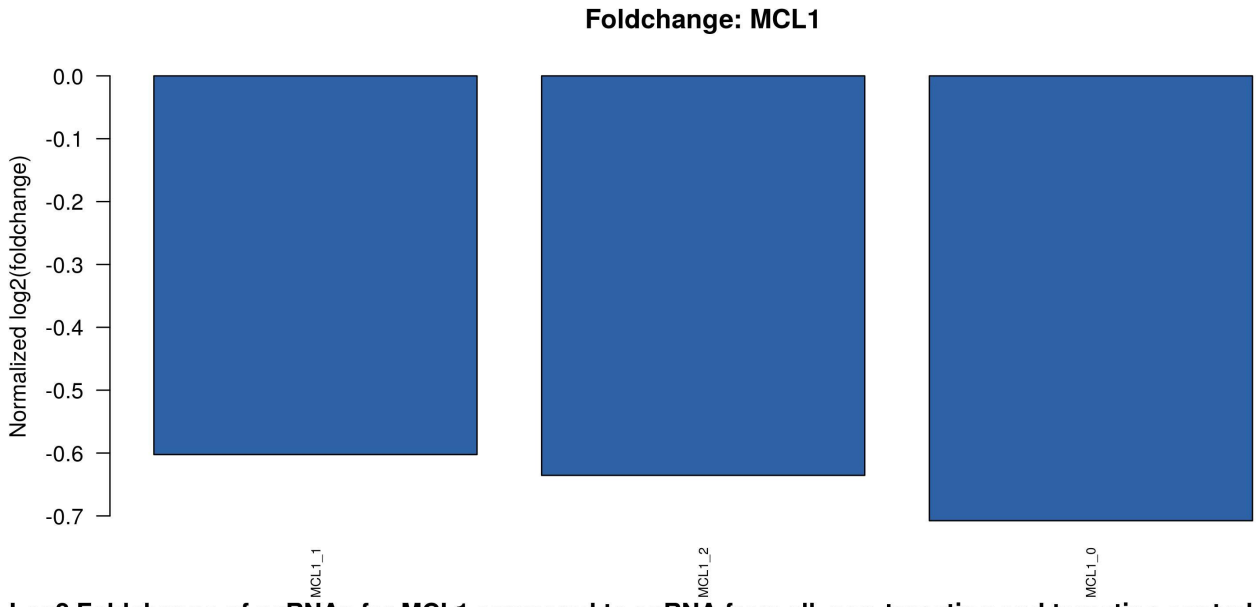
MAGeCK p-value: 0.605611

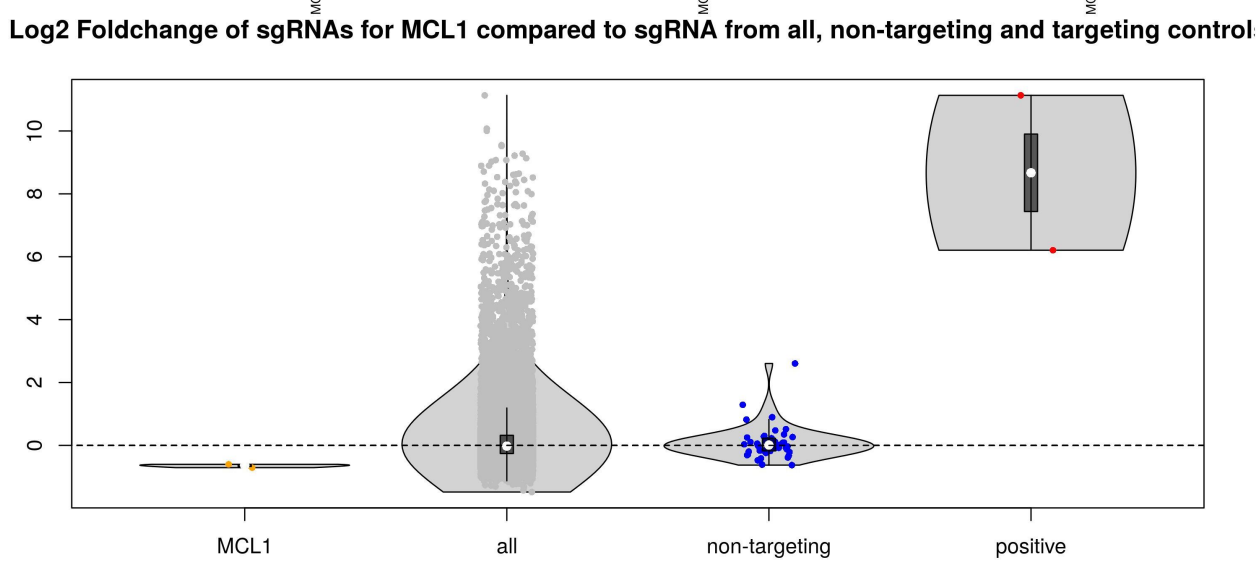
Gene Scatter for MCL1
PLX_resistance_YTAR



sgRNA Scatter for MCL1
PLX_resistance_YTAR




Foldchange: MCL1
Normalized log2(foldchange)
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
-0.6
-0.7
MCL1_1
MCL1_2
MCL1_0


Log2 Foldchange of sgRNAs for MCL1 compared to sgRNA from all, non-targeting and targeting control
0
2
4
6
8
10
MCL1
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
2	MCL1_1	MCL1	none	-0.6024294
3	MCL1_2	MCL1	none	-0.6355211
1	MCL1_0	MCL1	none	-0.7076312

CD59

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

ENSEMBL ID (links to Ensembl) LRG_41

HGNC SYMBOL (links to GeneCards) CD59

GENE DESCRIPTION
CD59 molecule, complement regulatory protein [Source:HGNC Symbol;Acc:HGNC:1689]

GO TERM

MIM GENE DESCRIPTION

ENSEMBL PROTEIN ID
LRG_41p1

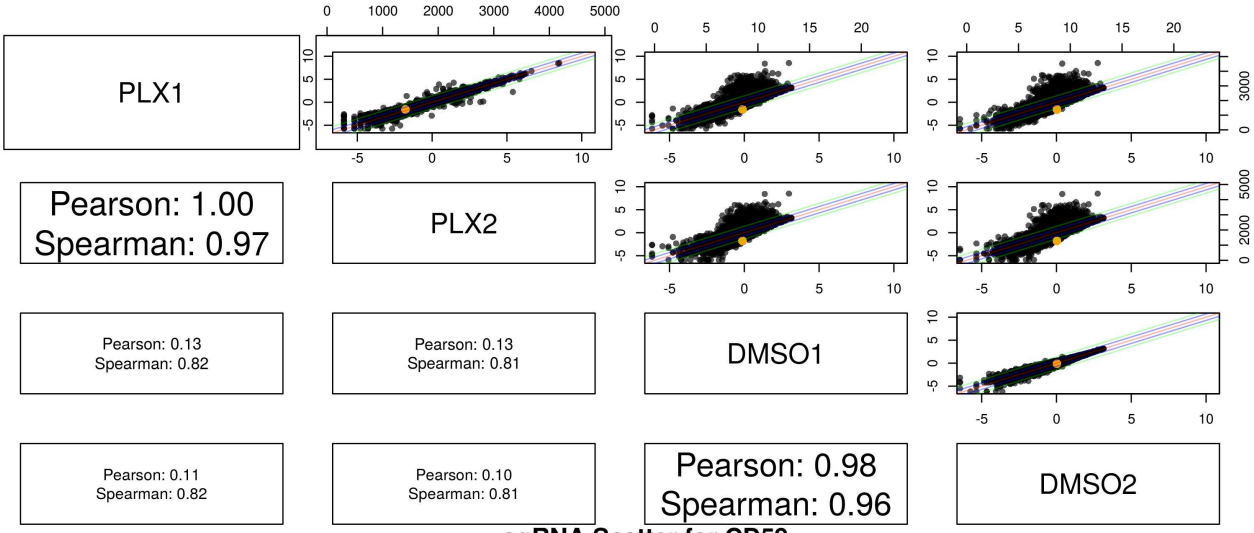
PROTEIN FAMILY DESCRIPTION
CD59 GLYCOPROTEIN PRECURSOR MAC INHIBITORY MAC IP MEMBRANE ATTACK COMPLEX INHIBITION FACTOR MACIF PROTECTIN CD59 ANTIGEN

Wilcox p-value: 0.3482308

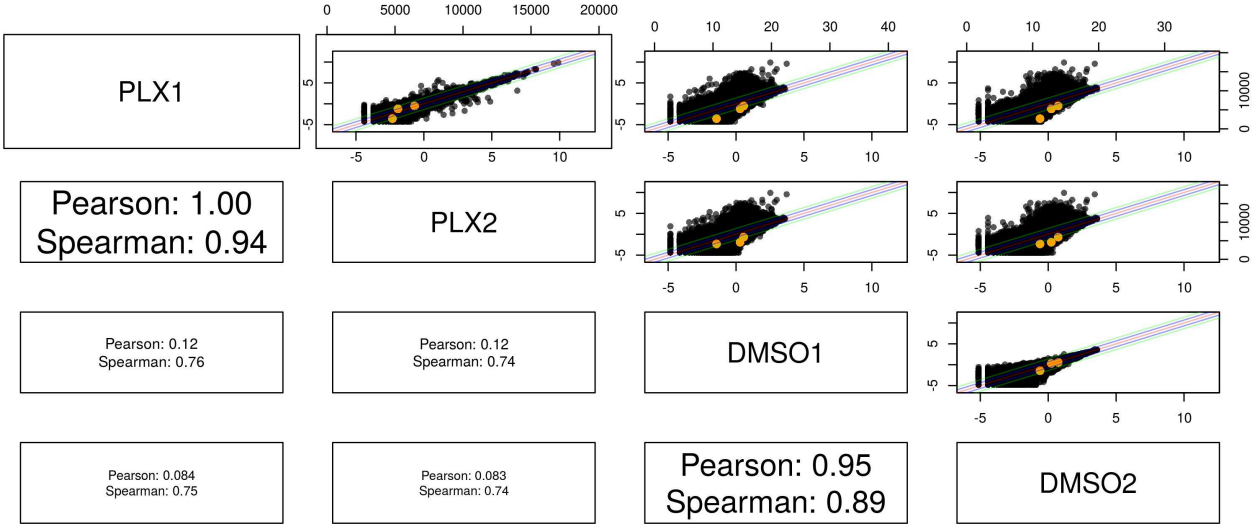
DESeq2 p-value: 3.06058e-12

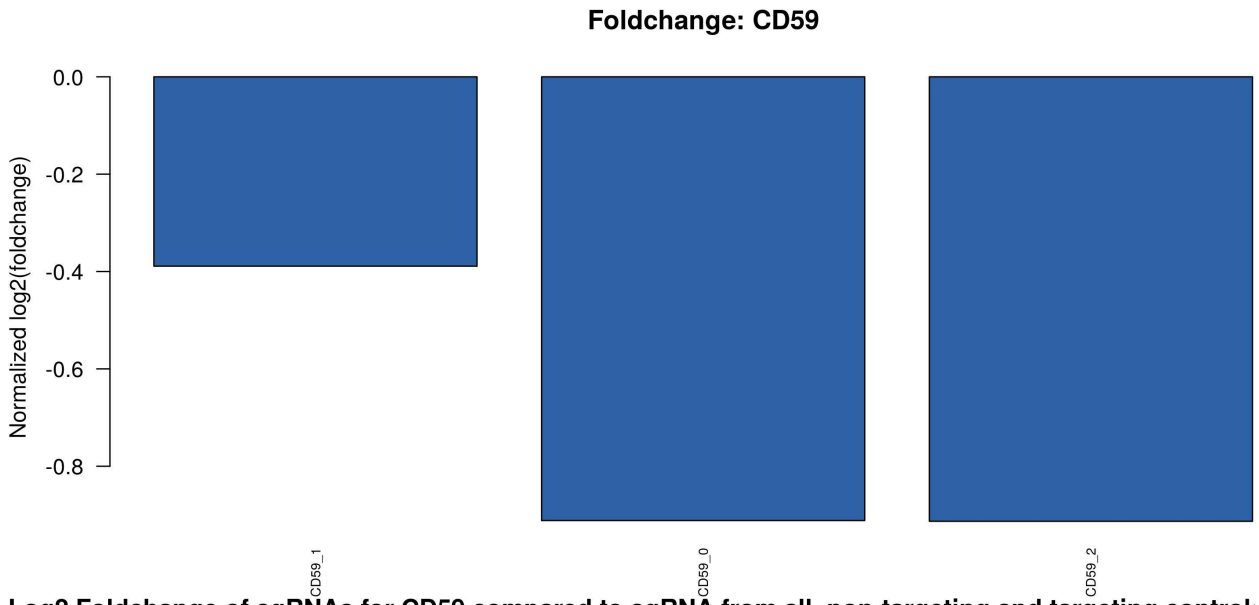
MAGeCK p-value: 0.605611

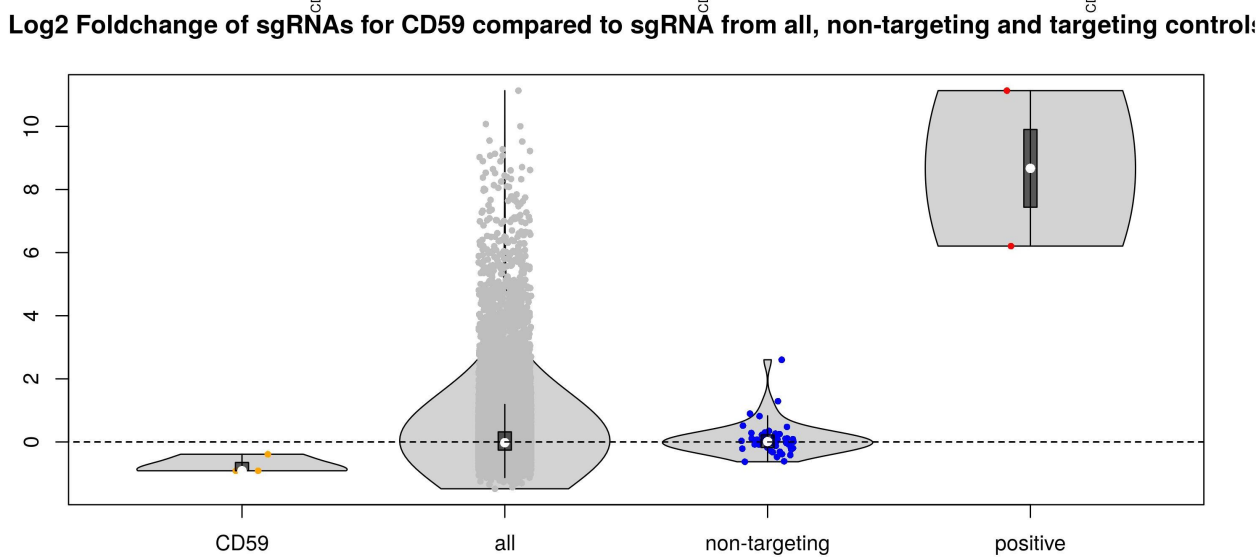
Gene Scatter for CD59
PLX_resistance_YTAR



sgRNA Scatter for CD59
PLX_resistance_YTAR




Foldchange: CD59
Normalized log2(foldchange)
0.0
-0.2
-0.4
-0.6
-0.8
CD59_1
CD59_0
CD59_2


Log2 Foldchange of sgRNAs for CD59 compared to sgRNA from all, non-targeting and targeting controls
0
2
4
6
8
10
CD59
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
2	CD59_1	CD59	none	-0.3889988
1	CD59_0	CD59	none	-0.9115600
3	CD59_2	CD59	none	-0.9131028

GRB2

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

ENSEMBL ID (links to Ensembl) ENSG00000177885

HGNC SYMBOL (links to GeneCards) GRB2

GENE DESCRIPTION
growth factor receptor-bound protein 2 [Source:HGNC Symbol;Acc:HGNC:4566]

GO TERM
protein binding, bridging

MIM GENE DESCRIPTION
GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2; GRB2;;ASH PROTEIN;;ABUNDANT SRC HOMOLOGY

ENSEMBL PROTEIN ID
ENSP00000317360

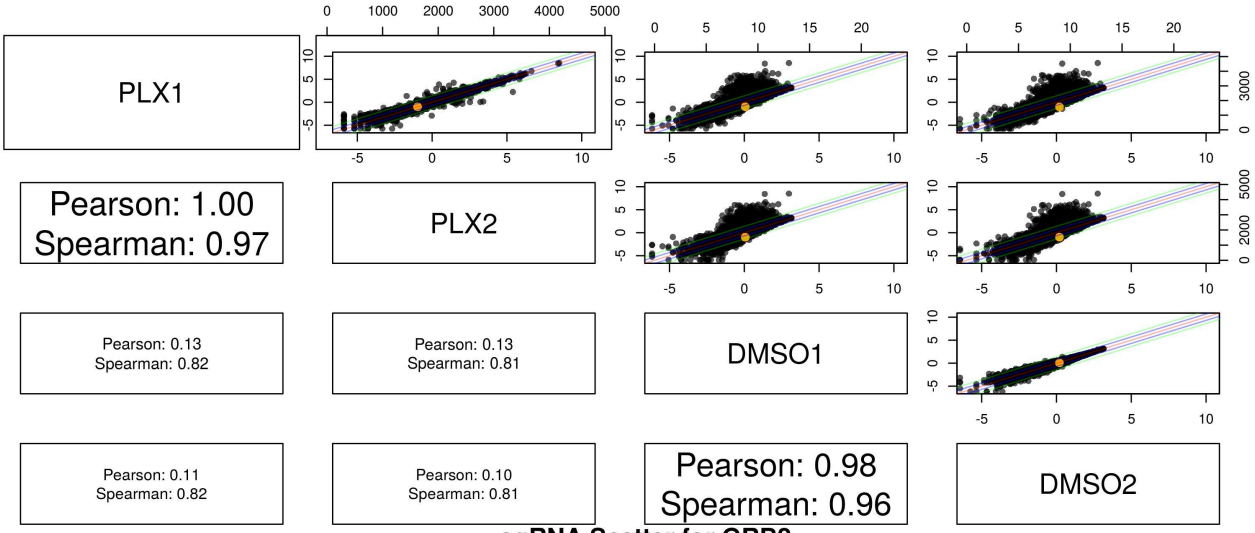
PROTEIN FAMILY DESCRIPTION
GROWTH FACTOR RECEPTOR BOUND 2 ADAPTER GRB2 SH2/SH3 ADAPTER GRB2

Wilcox p-value: 0.2824934

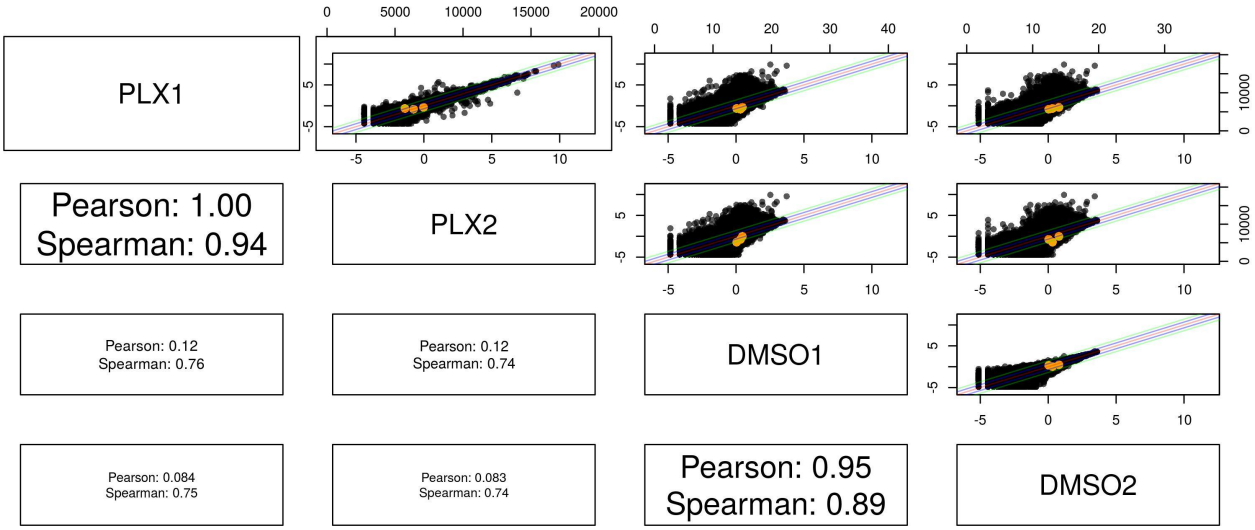
DESeq2 p-value: 8.261854e-06

MAGeCK p-value: 0.605611

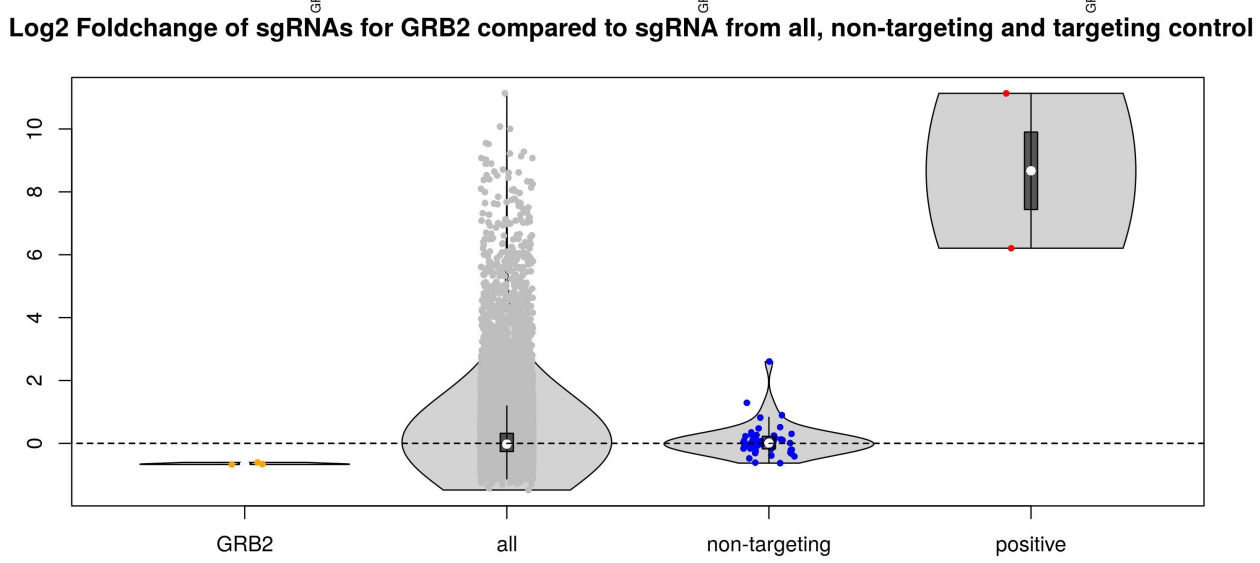
Gene Scatter for GRB2
PLX_resistance_YTAR



sgRNA Scatter for GRB2
PLX_resistance_YTAR



Foldchange: GRB2
Normalized log2(foldchange)
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
-0.6
GRB2_2
GRB2_1
GRB2_0


Log2 Foldchange of sgRNAs for GRB2 compared to sgRNA from all, non-targeting and targeting control
0
2
4
6
8
10
GRB2
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
3	GRB2_2	GRB2	none	-0.6054808
2	GRB2_1	GRB2	none	-0.6632137
1	GRB2_0	GRB2	none	-0.6702181

CRK

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

ENSEMBL ID (links to Ensembl) ENSG00000167193

HGNC SYMBOL (links to GeneCards) CRK

GENE DESCRIPTION
v-crk avian sarcoma virus CT10 oncogene homolog [Source:HGNC Symbol;Acc:HGNC:2362]

GO TERM

MIM GENE DESCRIPTION
V-CRK AVIAN SARCOMA VIRUS CT10 ONCOGENE HOMOLOG; CRK;;ONCOGENE CRK;;CRKII

ENSEMBL PROTEIN ID
ENSP00000459505

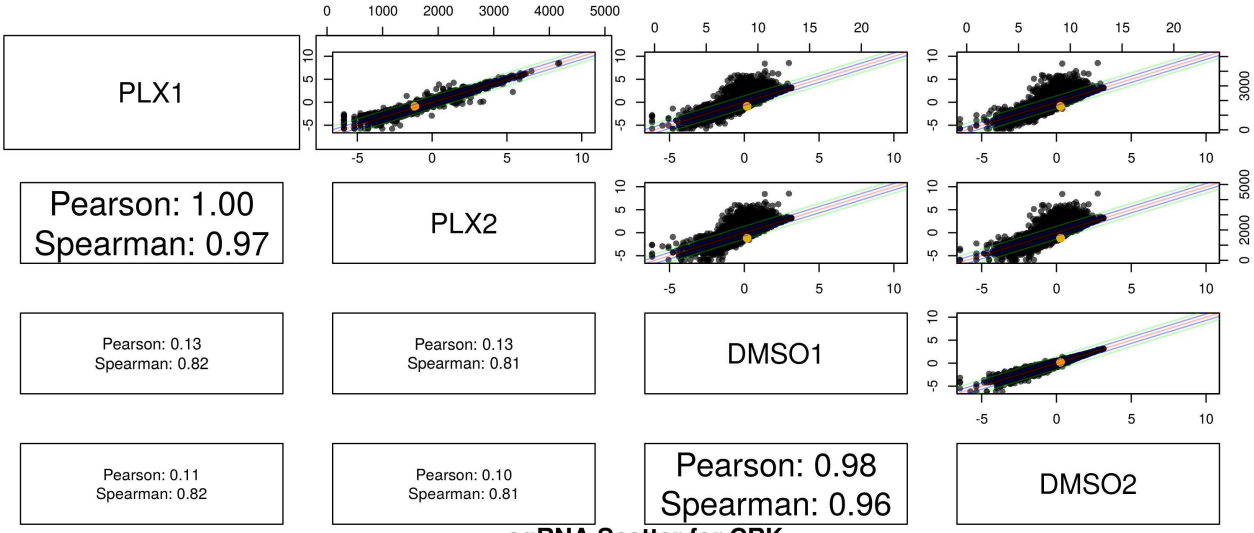
PROTEIN FAMILY DESCRIPTION
ADAPTER MOLECULE CRK PROTO ONCOGENE C CRK P38

Wilcox p-value: 0.414337

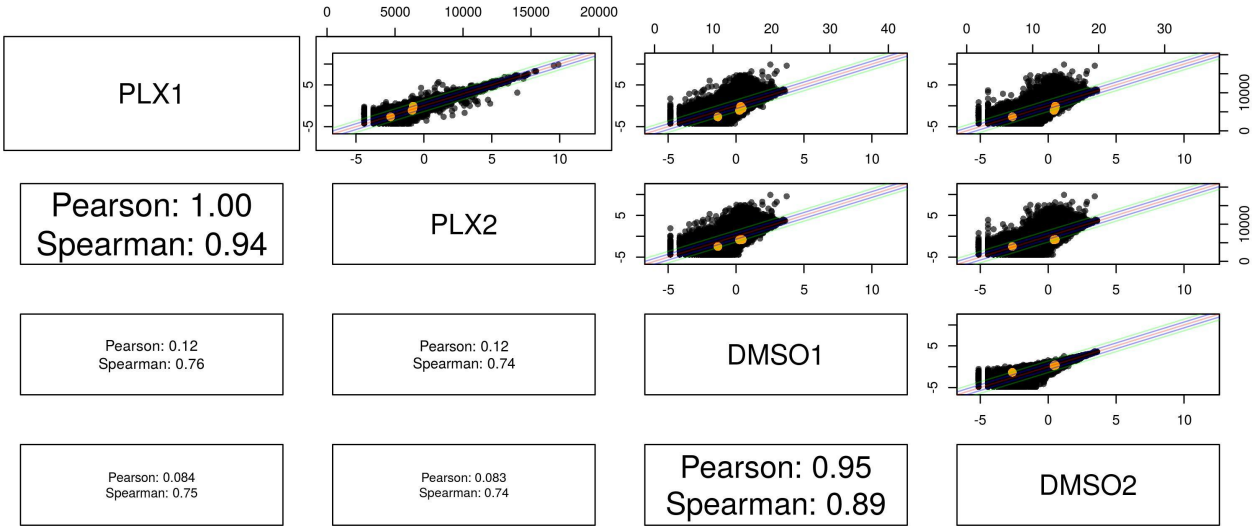
DESeq2 p-value: 8.247924e-07

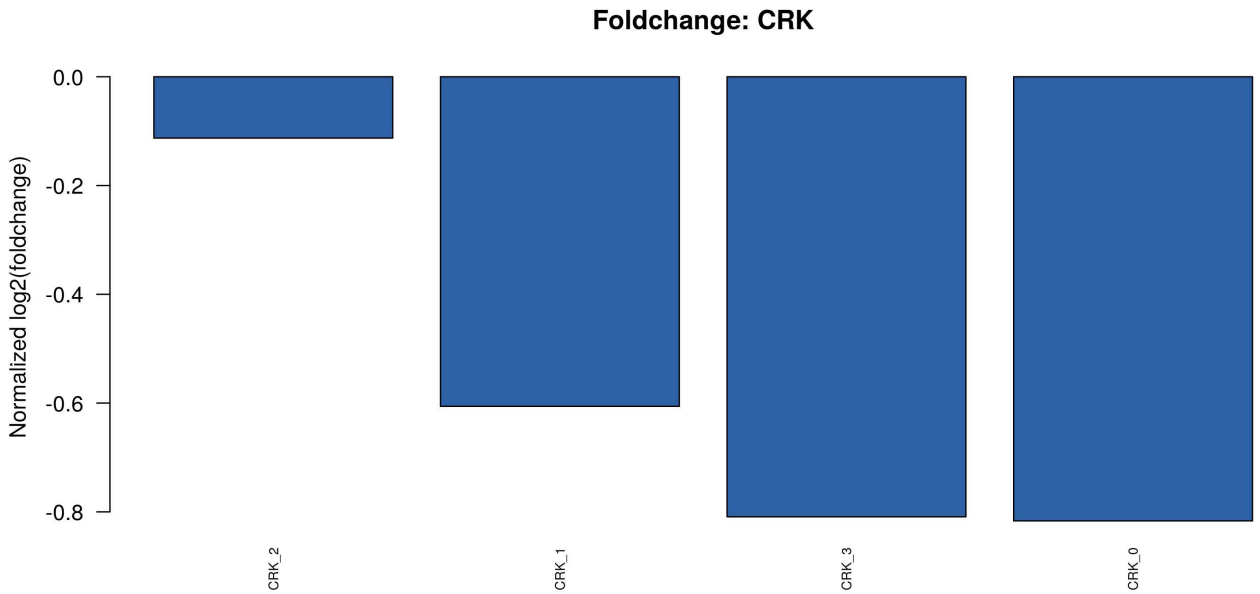
MAGeCK p-value: 0.658214

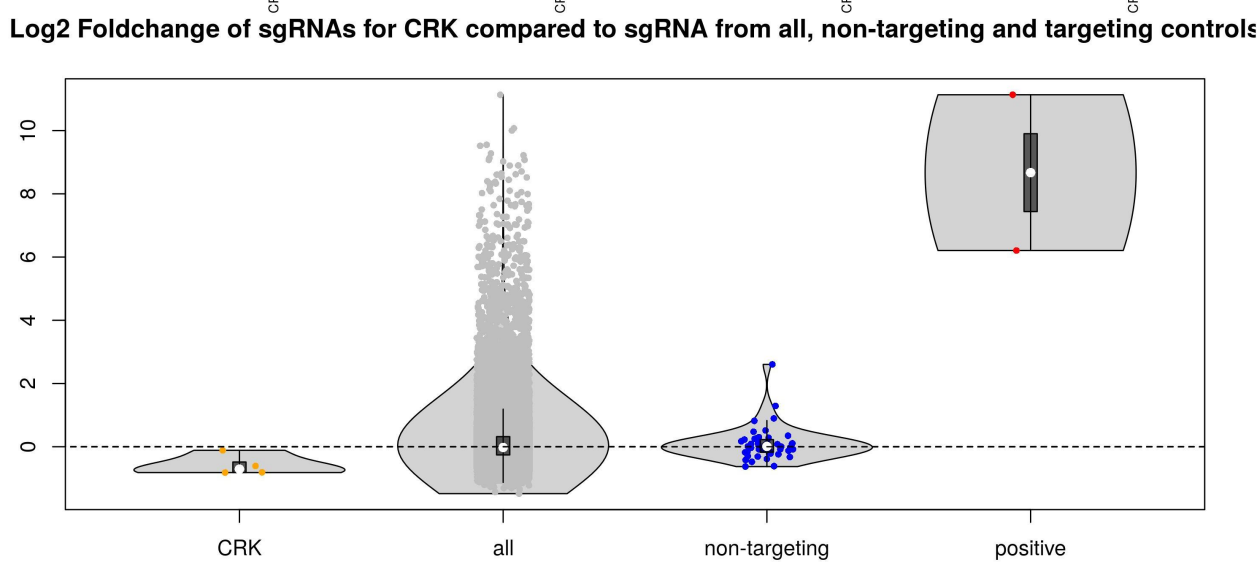
Gene Scatter for CRK
PLX_resistance_YTAR



sgRNA Scatter for CRK
PLX_resistance_YTAR




Foldchange: CRK
Normalized log2(foldchange)
0.0
-0.2
-0.4
-0.6
-0.8
CRK_2
CRK_1
CRK_3
CRK_0


Log2 Foldchange of sgRNAs for CRK compared to sgRNA from all, non-targeting and targeting controls
0
2
4
6
8
10
CRK
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
3	CRK_2	CRK	none	-0.1127990
2	CRK_1	CRK	none	-0.6059945
4	CRK_3	CRK	none	-0.8091261
1	CRK_0	CRK	none	-0.8165685

PGM2L1

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

ENSEMBL ID (links to Ensembl) ENSG00000165434

HGNC SYMBOL (links to GeneCards) PGM2L1

GENE DESCRIPTION
phosphoglucomutase 2-like 1 [Source:HGNC Symbol;Acc:HGNC:20898]

GO TERM
organic substance metabolic process

MIM GENE DESCRIPTION
PHOSPHOGLUCOMUTASE 2-LIKE 1; PGM2L1

ENSEMBL PROTEIN ID
ENSP00000298198

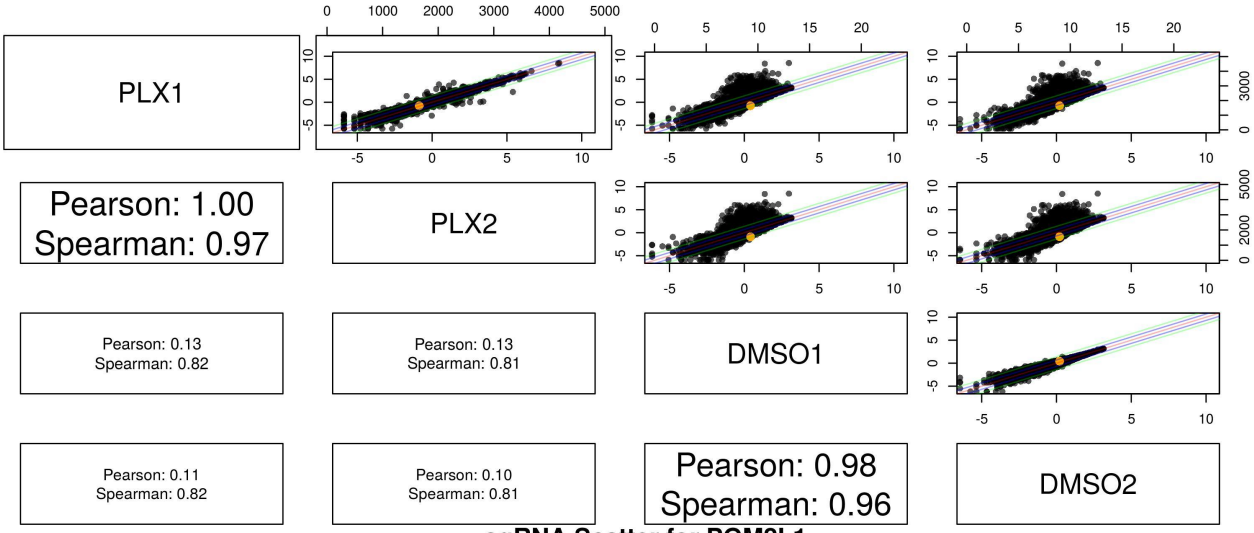
PROTEIN FAMILY DESCRIPTION
PHOSPHOGLUCOMUTASE

Wilcox p-value: 0.3703194

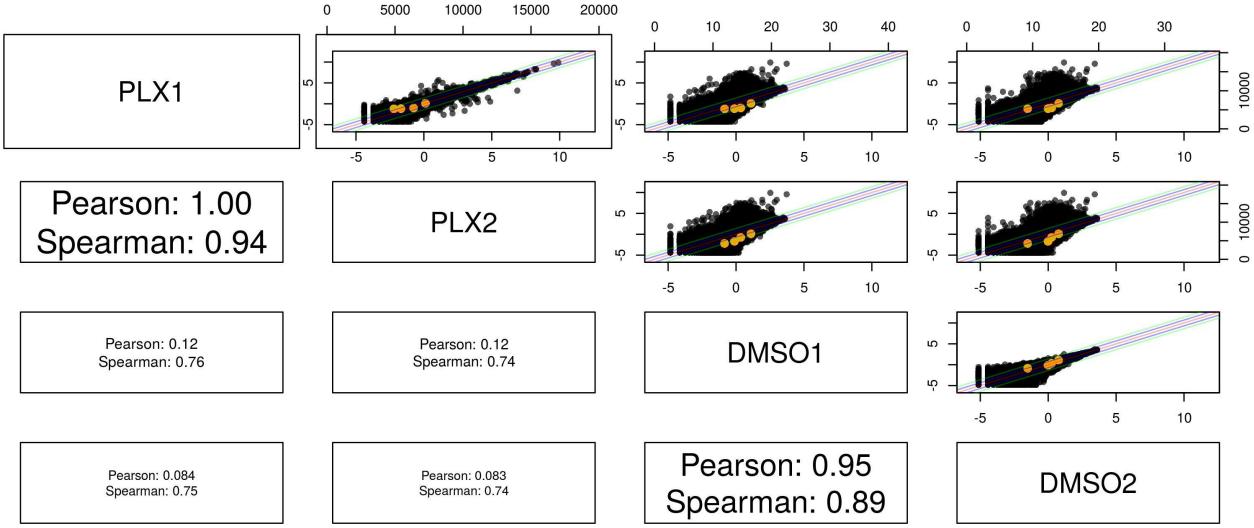
DESeq2 p-value: 2.980762e-05

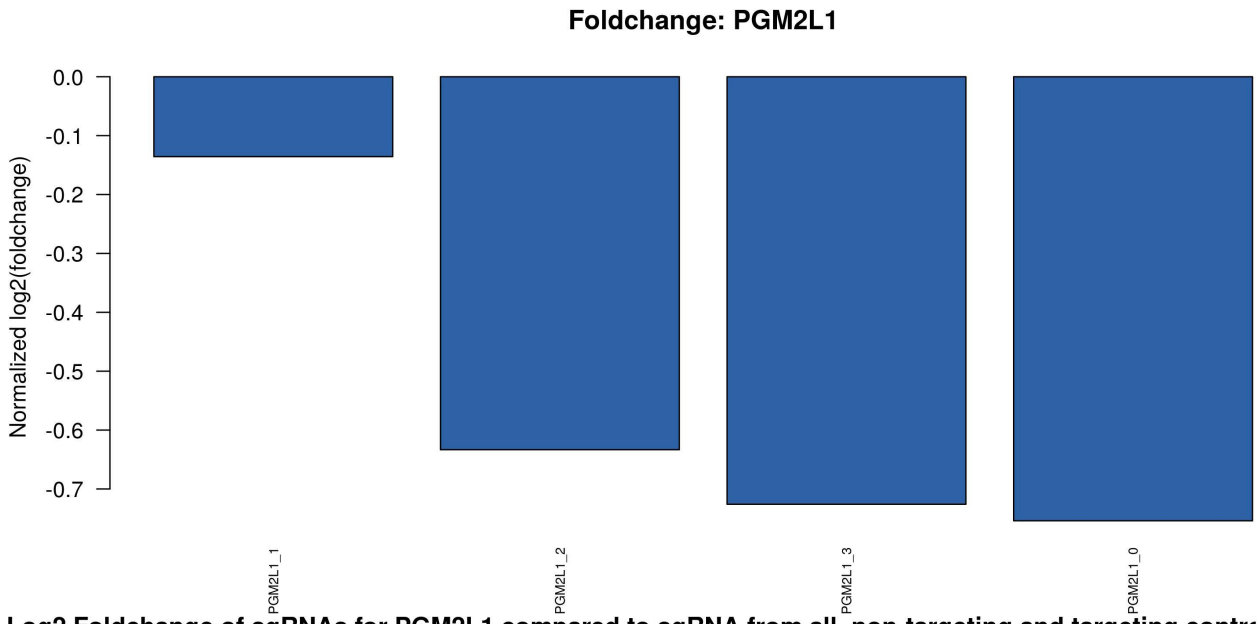
MAGeCK p-value: 0.658214

Gene Scatter for PGM2L1
PLX_resistance_YTAR

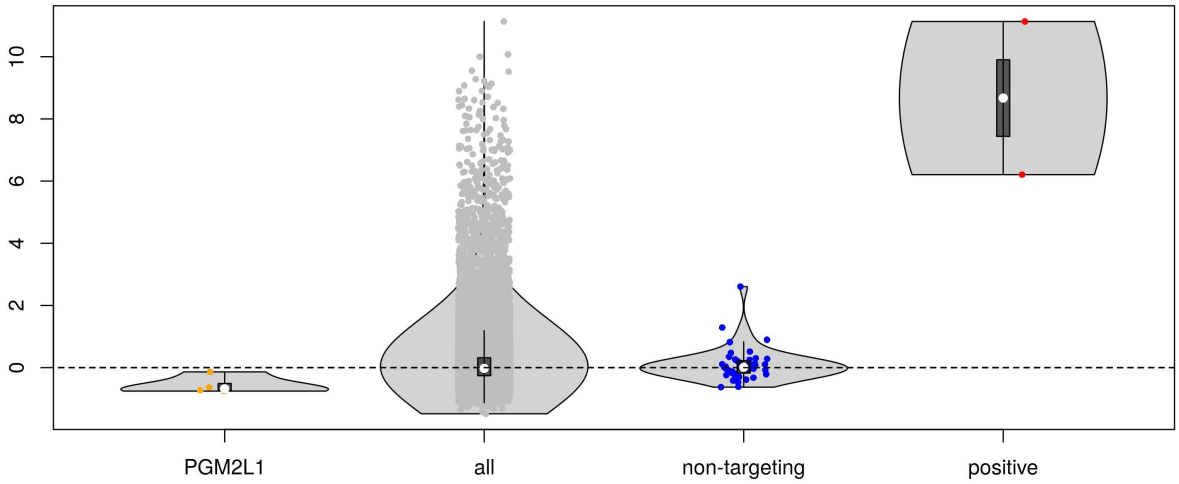


sgRNA Scatter for PGM2L1
PLX_resistance_YTAR





Log2 Foldchange of sgRNAs for PGM2L1 compared to sgRNA from all, non-targeting and targeting contro



	designs	genes	sequence	log2Foldchange
2	PGM2L1_1	PGM2L1	none	-0.1356460
3	PGM2L1_2	PGM2L1	none	-0.6333121
4	PGM2L1_3	PGM2L1	none	-0.7259958
1	PGM2L1_0	PGM2L1	none	-0.7540066

TEX15

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

ENSEMBL ID (links to Ensembl) ENSG00000133863

HGNC SYMBOL (links to GeneCards) TEX15

GENE DESCRIPTION
testis expressed 15 [Source:HGNC Symbol;Acc:HGNC:11738]

GO TERM
protein localization to chromosome

MIM GENE DESCRIPTION
TESTIS-EXPRESSED GENE 15; TEX15

ENSEMBL PROTEIN ID
ENSP00000256246

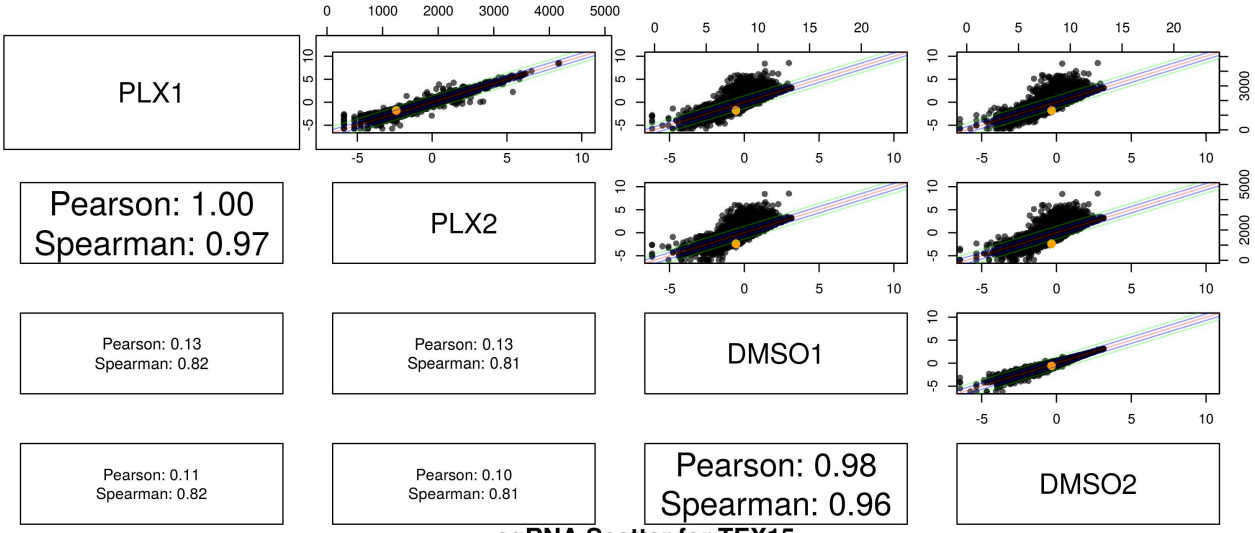
PROTEIN FAMILY DESCRIPTION
TESTIS EXPRESSED SEQUENCE 15 CANCER/TESTIS ANTIGEN 42 CT42

Wilcox p-value: 0.3482308

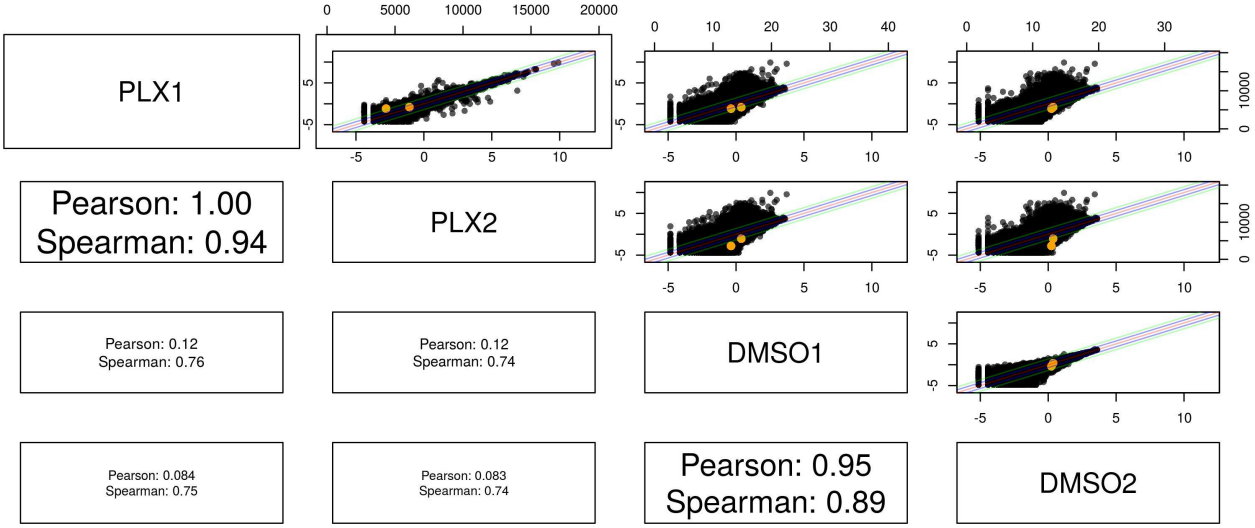
DESeq2 p-value: 7.285174e-07

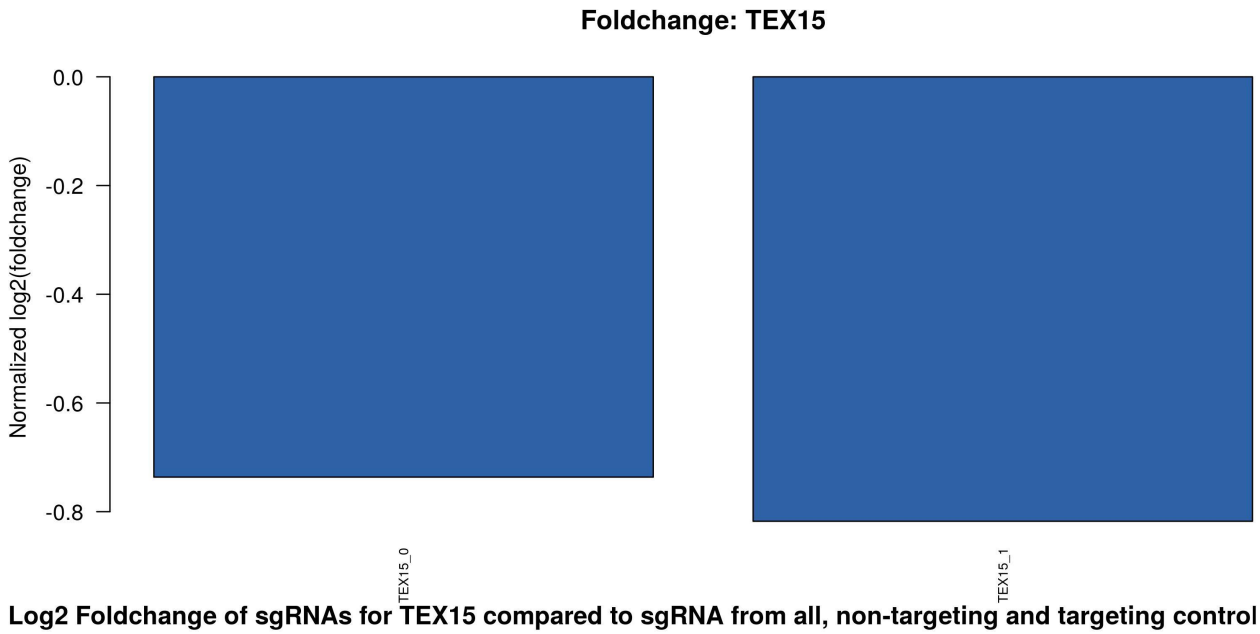
MAGeCK p-value: 0.658214

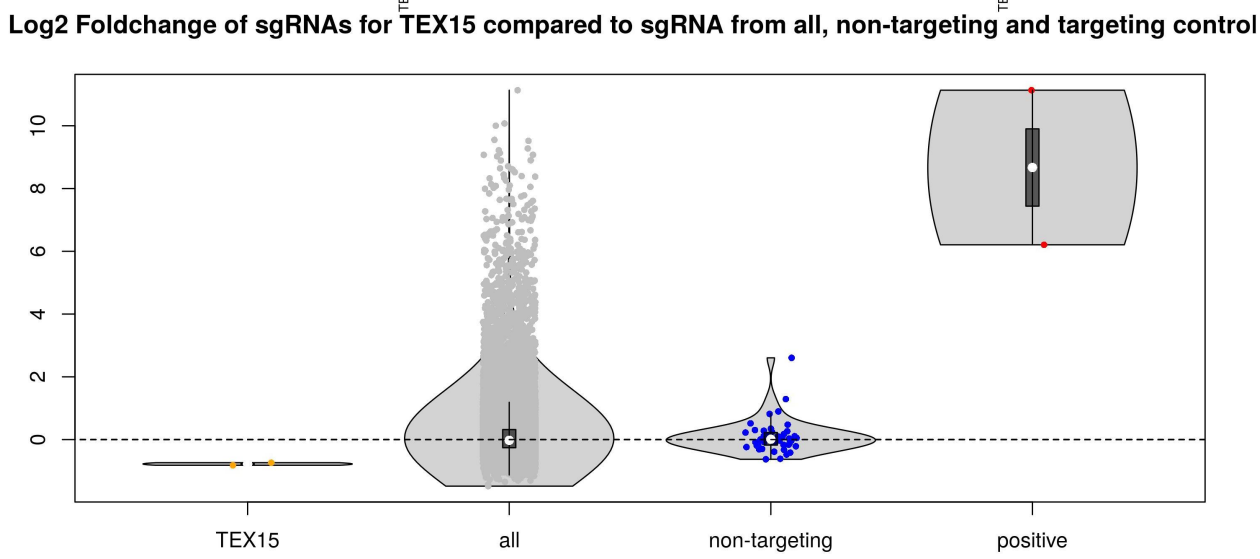
Gene Scatter for TEX15
PLX_resistance_YTAR



sgRNA Scatter for TEX15
PLX_resistance_YTAR




Foldchange: TEX15
Normalized log2(foldchange)
0.0
-0.2
-0.4
-0.6
-0.8
TEX15_0
TEX15_1


Log2 Foldchange of sgRNAs for TEX15 compared to sgRNA from all, non-targeting and targeting control
0
2
4
6
8
10
TEX15
all
non-targeting
positive

designs	genes	sequence	log2Foldchange
TEX15_0	TEX15	none	-0.7363497
TEX15_1	TEX15	none	-0.8175903

SNAPC5

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

ENSEMBL ID (links to Ensembl) ENSG00000174446

HGNC SYMBOL (links to GeneCards) SNAPC5

GENE DESCRIPTION
small nuclear RNA activating complex, polypeptide 5, 19kDa [Source:HGNC Symbol;Acc:HGNC:15484]

GO TERM
transcription initiation from RNA polymerase III promoter

MIM GENE DESCRIPTION
SMALL NUCLEAR RNA-ACTIVATING PROTEIN COMPLEX, POLYPEPTIDE 5; SNAPC5;;SMALL NUCLEAR RNA-ACTIVATING PROTEIN COMPLEX, 19-KD SUBUNIT; SNAP19

ENSEMBL PROTEIN ID
ENSP00000456716

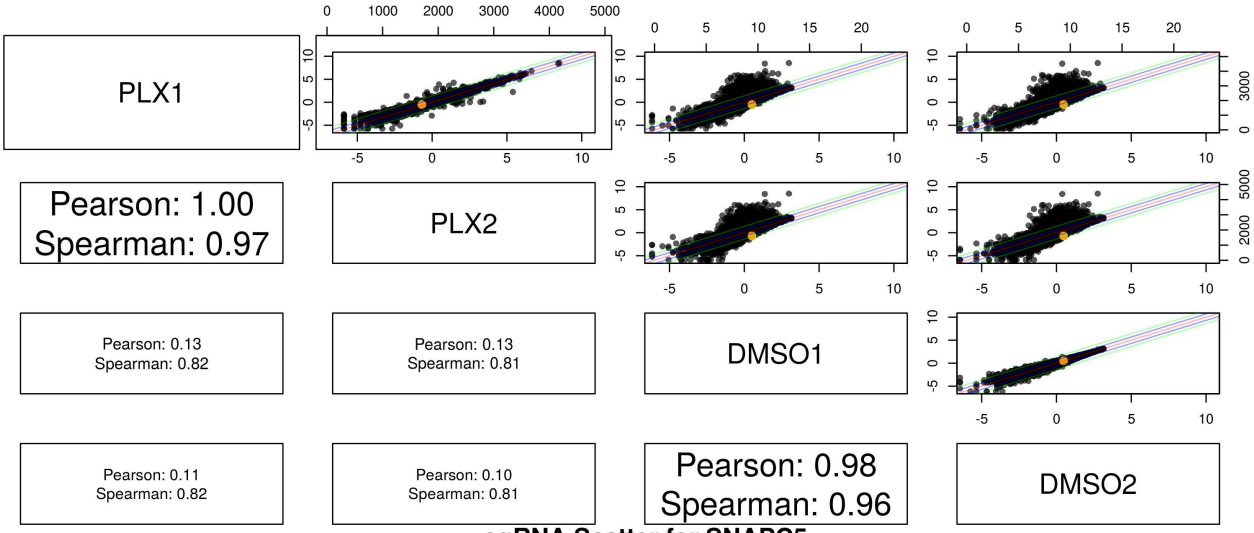
PROTEIN FAMILY DESCRIPTION
UNKNOWN

Wilcox p-value: 0.2824934

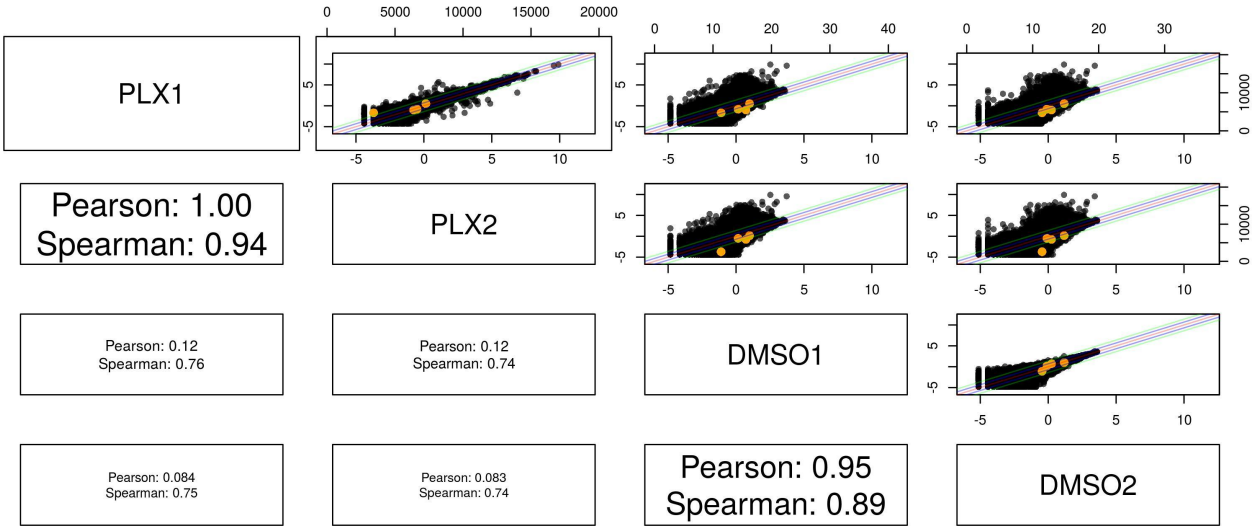
DESeq2 p-value: 1.40947e-05

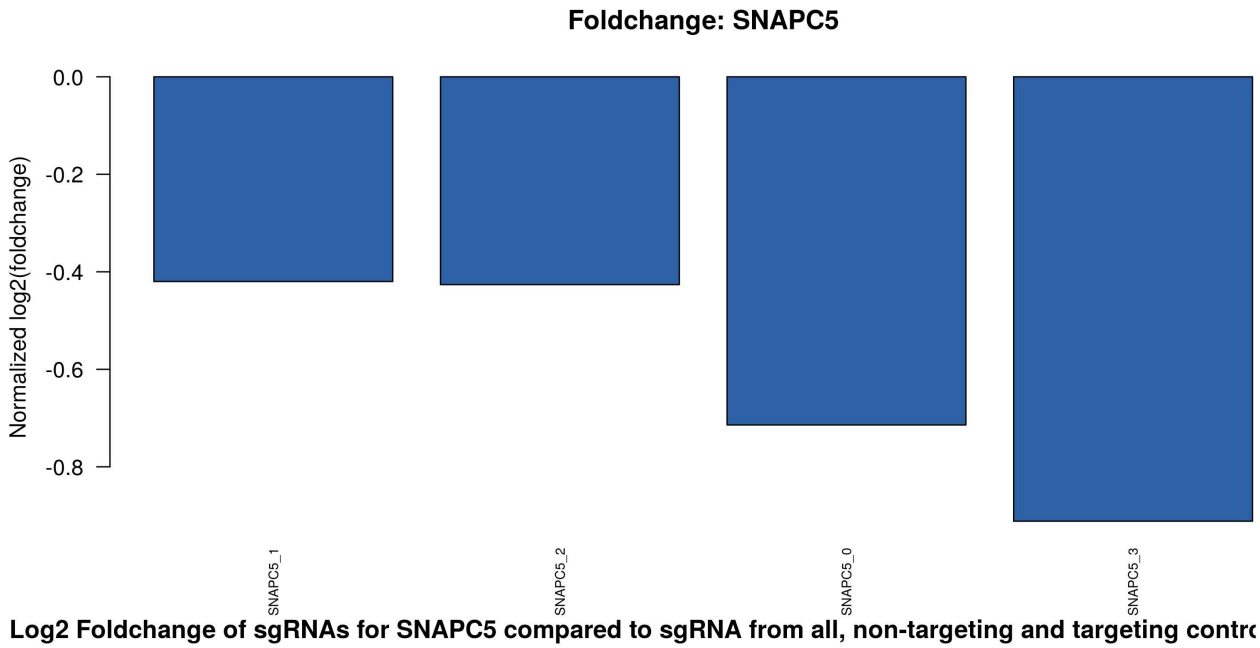
MAGeCK p-value: 0.658214

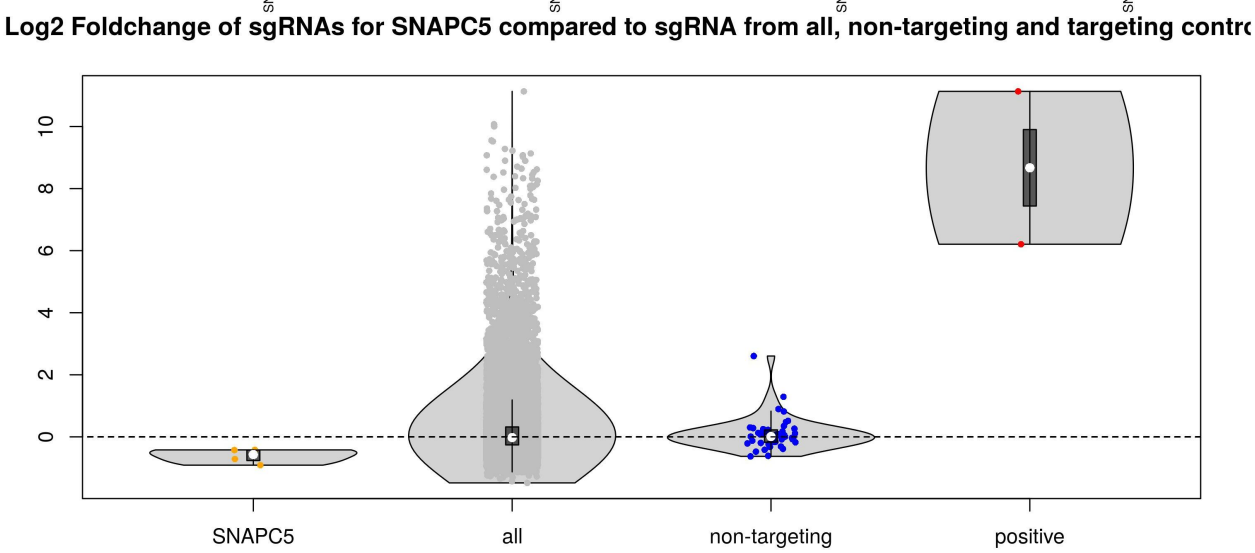
Gene Scatter for SNAPC5
PLX_resistance_YTAR



sgRNA Scatter for SNAPC5
PLX_resistance_YTAR




Foldchange: SNAPC5
Normalized log2(foldchange)
0.0
-0.2
-0.4
-0.6
-0.8
SNAPC5_1
SNAPC5_2
SNAPC5_0
SNAPC5_3


Log2 Foldchange of sgRNAs for SNAPC5 compared to sgRNA from all, non-targeting and targeting contro
0
2
4
6
8
10
SNAPC5
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
2	SNAPC5_1	SNAPC5	none	-0.4198767
3	SNAPC5_2	SNAPC5	none	-0.4262674
1	SNAPC5_0	SNAPC5	none	-0.7141705
4	SNAPC5_3	SNAPC5	none	-0.9115410

MPRIP

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

ENSEMBL ID (links to Ensembl) ENSG00000133030

HGNC SYMBOL (links to GeneCards) MPRIP

GENE DESCRIPTION
myosin phosphatase Rho interacting protein [Source:HGNC Symbol;Acc:HGNC:30321]

GO TERM

MIM GENE DESCRIPTION
MYOSIN PHOSPHATASE RHO-INTERACTING PROTEIN; MPRIP;;MRIP;;KIAA0864;;p116 RHO-INTERACTING PROTEIN; p116RIP;;RIP3

ENSEMBL PROTEIN ID
ENSP00000463367

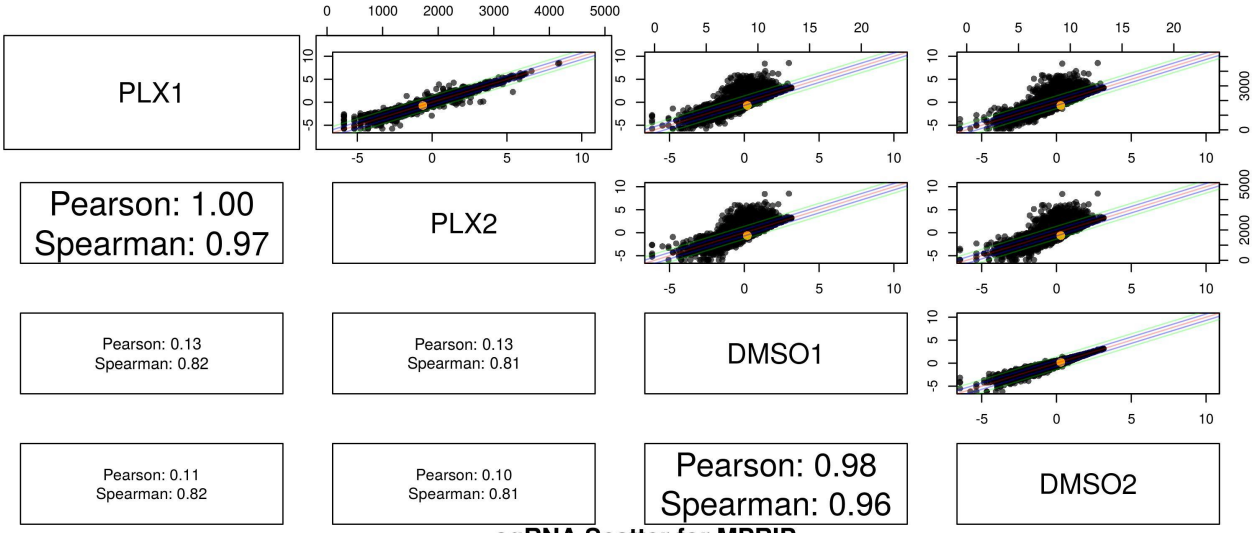
PROTEIN FAMILY DESCRIPTION
UNKNOWN

Wilcox p-value: 0.3482308

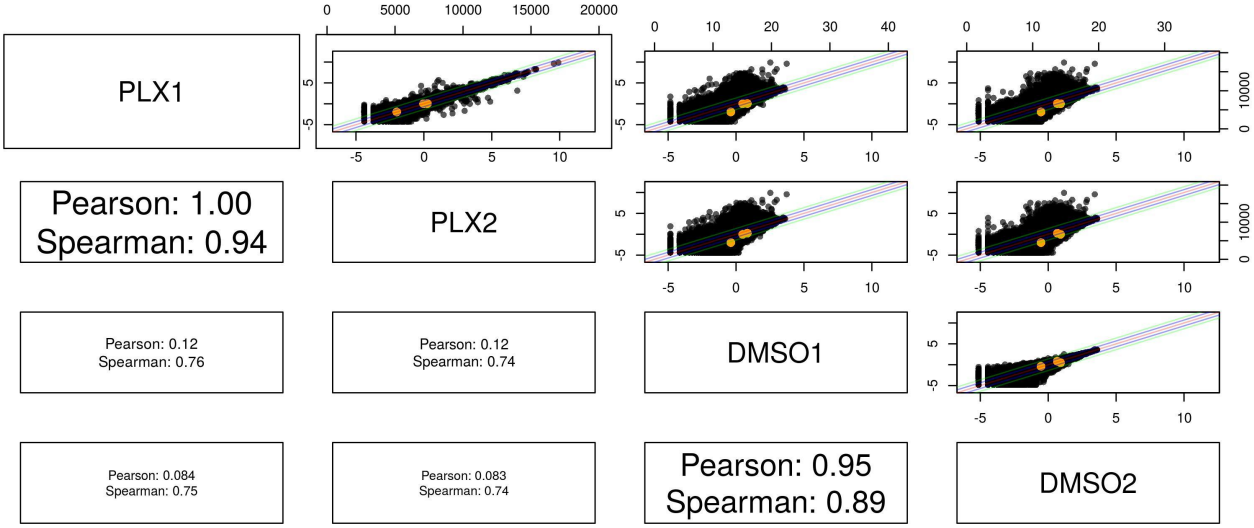
DESeq2 p-value: 0.003579026

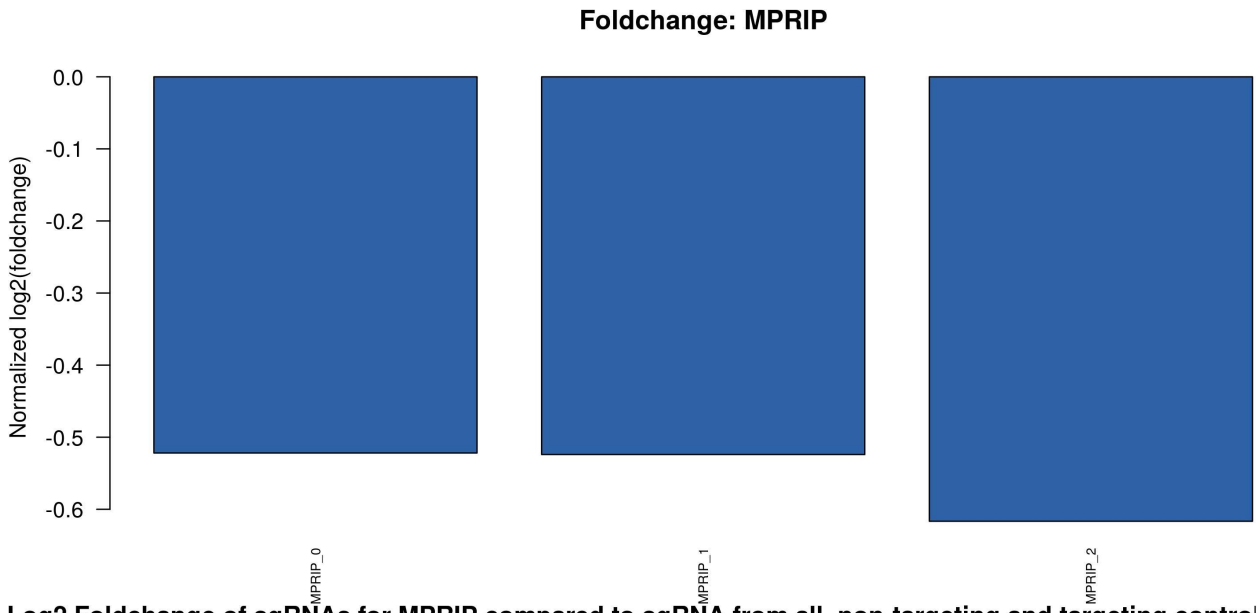
MAGeCK p-value: 0.658214

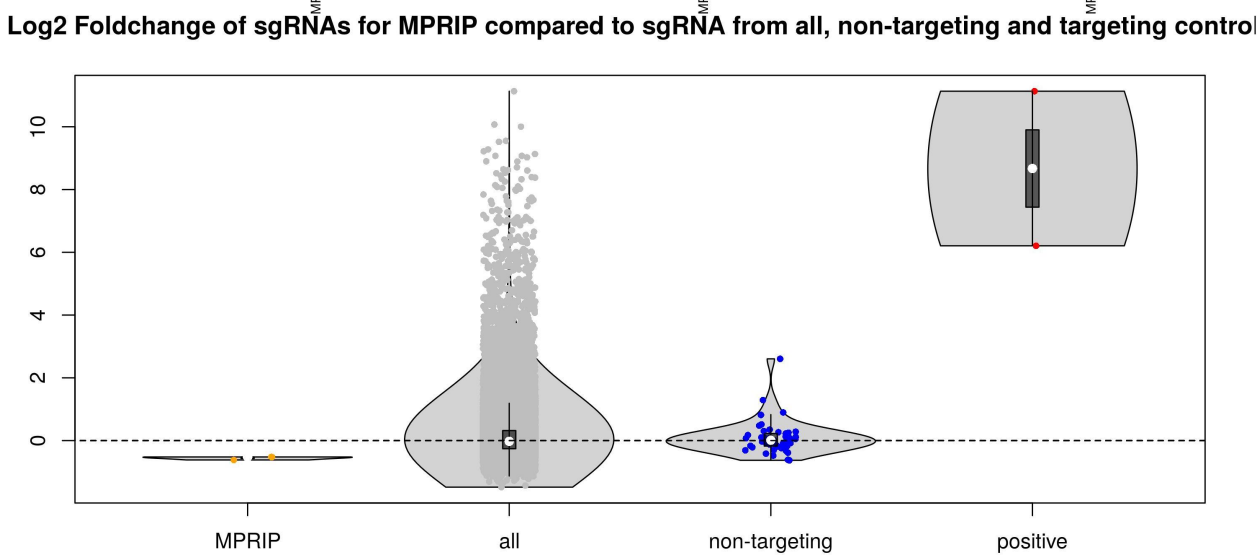
Gene Scatter for MPRIP
PLX_resistance_YTAR



sgRNA Scatter for MPRIP
PLX_resistance_YTAR




Foldchange: MPRIP
Normalized log2(foldchange)
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
-0.6
MPRIP_0
MPRIP_1
MPRIP_2


Log2 Foldchange of sgRNAs for MPRIP compared to sgRNA from all, non-targeting and targeting control
0
2
4
6
8
10
MPRIP
all
non-targeting
positive

designs	genes	sequence	log2Foldchange
MPRIP_0	MPRIP	none	-0.5219103
MPRIP_1	MPRIP	none	-0.5239888
MPRIP_2	MPRIP	none	-0.6165972

TRIM37

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

ENSEMBL ID (links to Ensembl) ENSG00000108395

HGNC SYMBOL (links to GeneCards) TRIM37

GENE DESCRIPTION
tripartite motif containing 37 [Source:HGNC Symbol;Acc:HGNC:7523]

GO TERM
ion binding

MIM GENE DESCRIPTION

ENSEMBL PROTEIN ID
ENSP00000485901

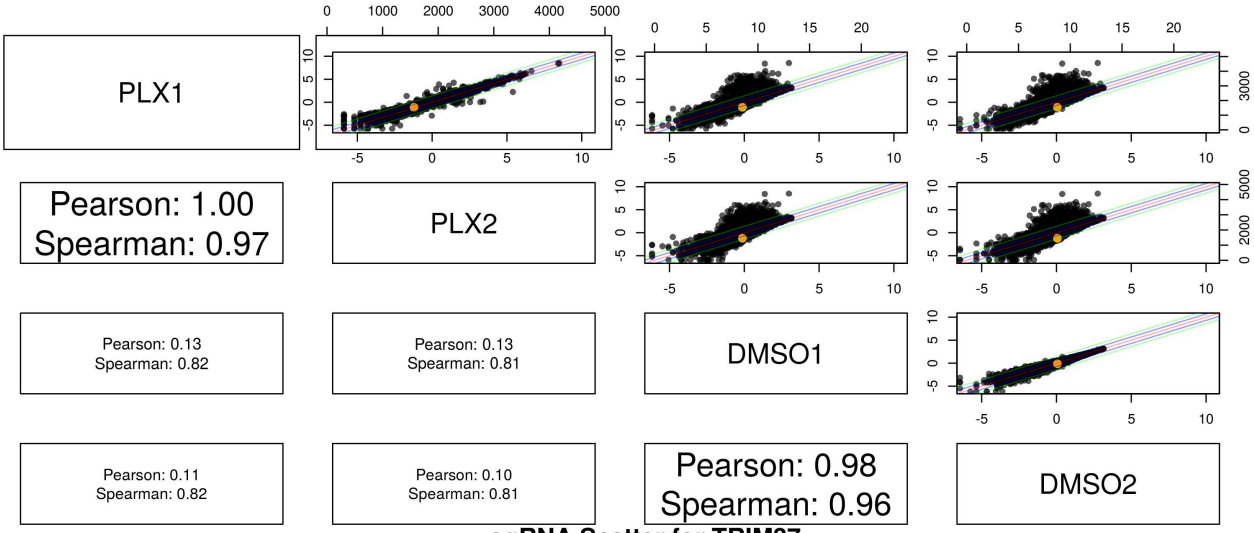
PROTEIN FAMILY DESCRIPTION
UNKNOWN

Wilcox p-value: 0.3482308

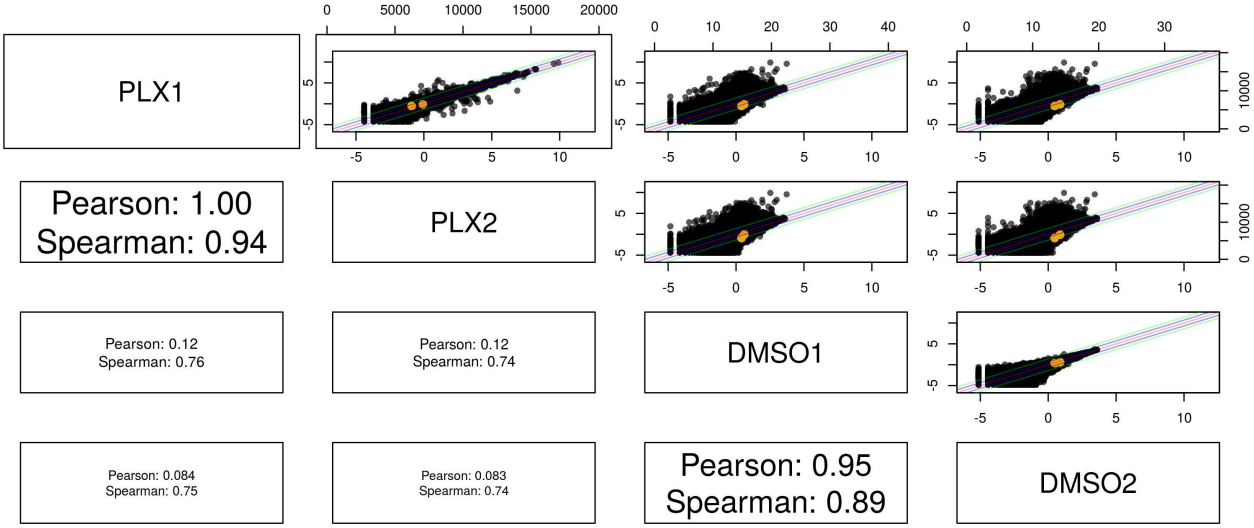
DESeq2 p-value: 4.689671e-05

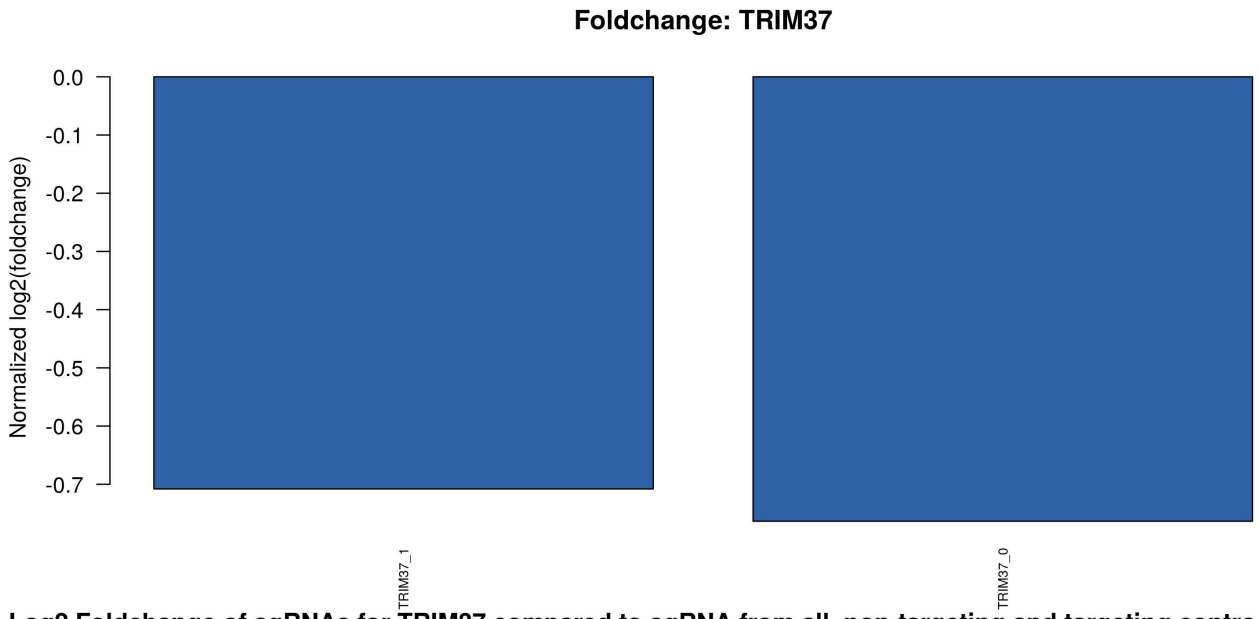
MAGeCK p-value: 0.658214

Gene Scatter for TRIM37
PLX_resistance_YTAR

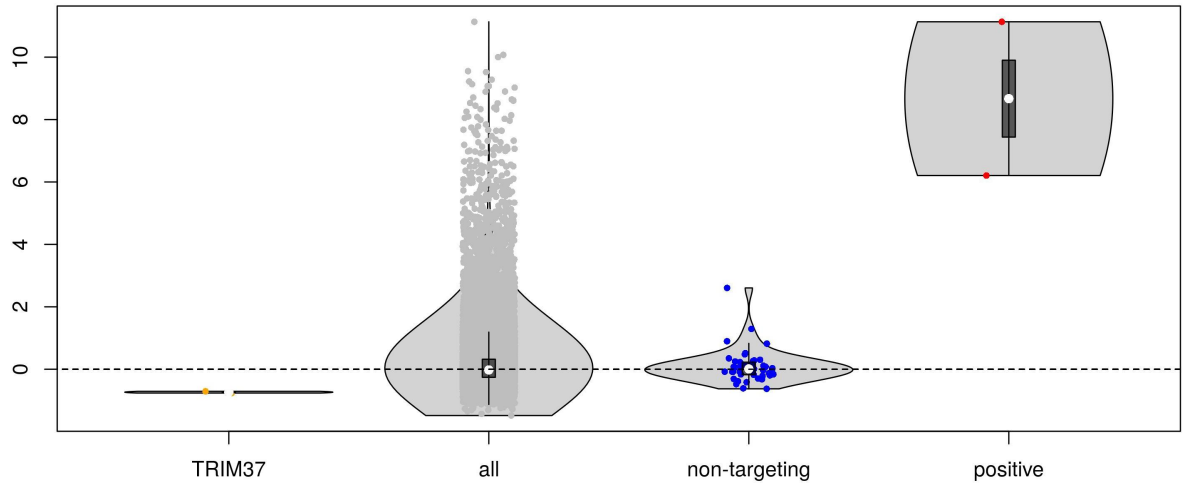


sgRNA Scatter for TRIM37
PLX_resistance_YTAR





Log2 Foldchange of sgRNAs for TRIM37 compared to sgRNA from all, non-targeting and targeting contro



	designs	genes	sequence	log2Foldchange
2	TRIM37_1	TRIM37	none	-0.7079378
1	TRIM37_0	TRIM37	none	-0.7634355

PARD6B

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

ENSEMBL ID (links to Ensembl) ENSG00000124171

HGNC SYMBOL (links to GeneCards) PARD6B

GENE DESCRIPTION
par-6 family cell polarity regulator beta [Source:HGNC Symbol;Acc:HGNC:16245]

GO TERM
molecular_function

MIM GENE DESCRIPTION
PARTITIONING-DEFECTIVE PROTEIN 6, C. ELEGANS, HOMOLOG OF, BETA; PARD6B;;PAR6-BETA

ENSEMBL PROTEIN ID
ENSP00000379354

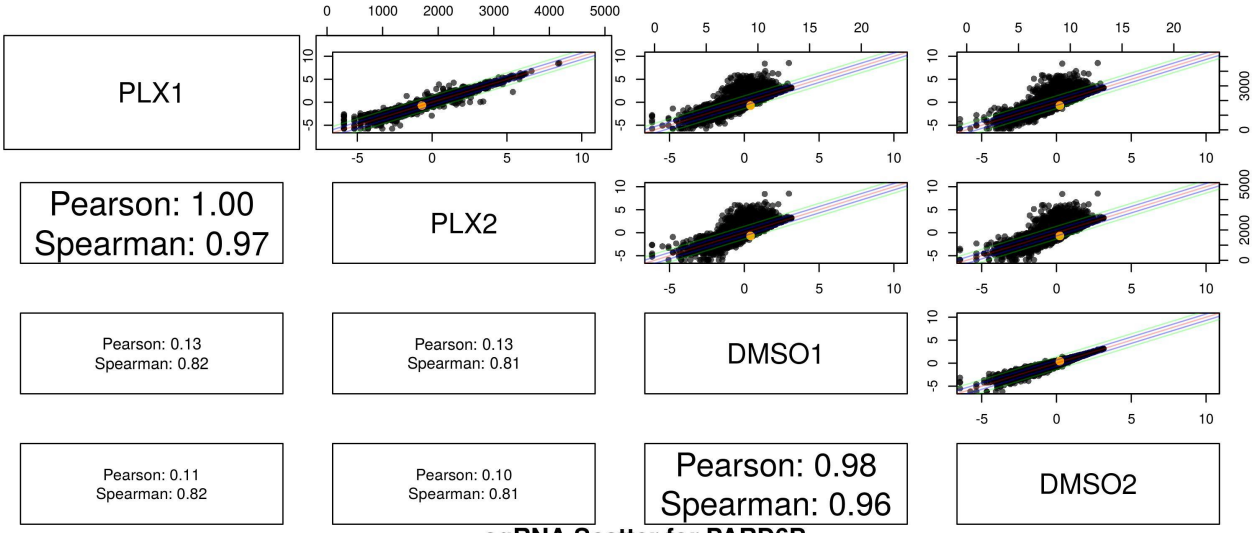
PROTEIN FAMILY DESCRIPTION
PARTITIONING DEFECTIVE 6 HOMOLOG PAR 6

Wilcox p-value: 0.2824934

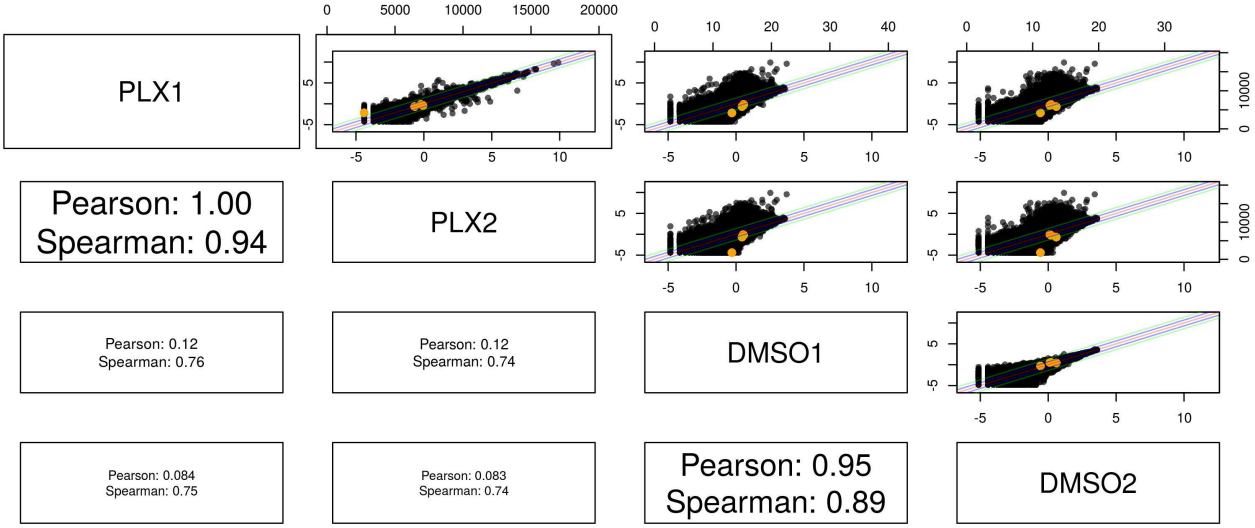
DESeq2 p-value: 0.0003149896

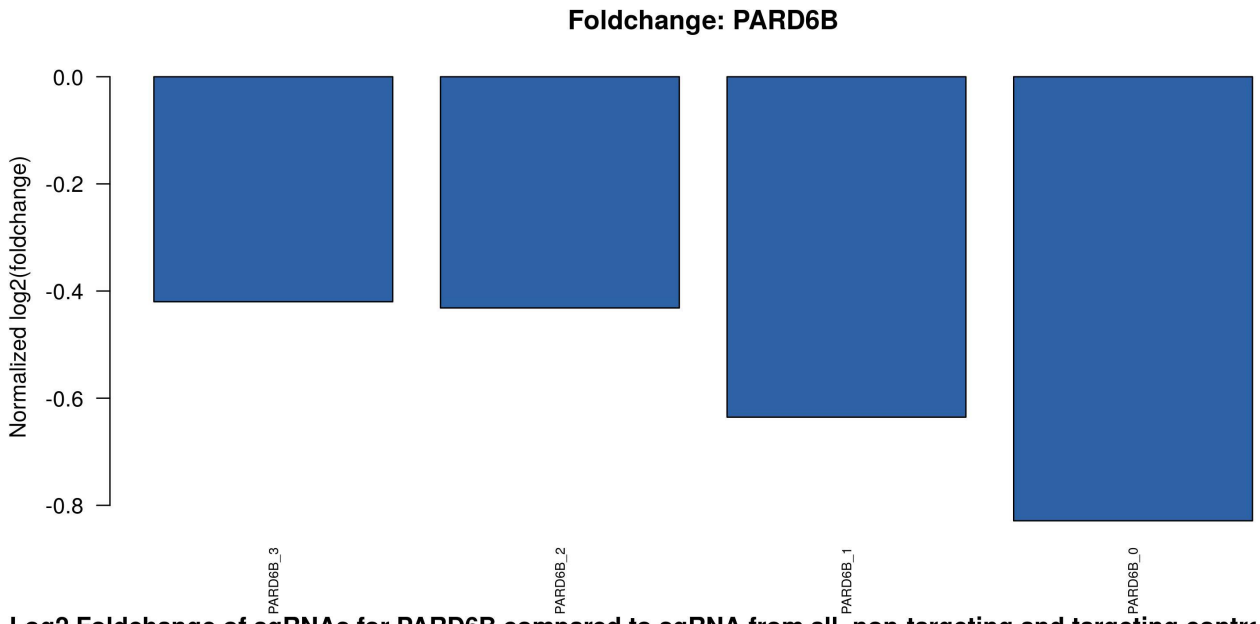
MAGeCK p-value: 0.658214

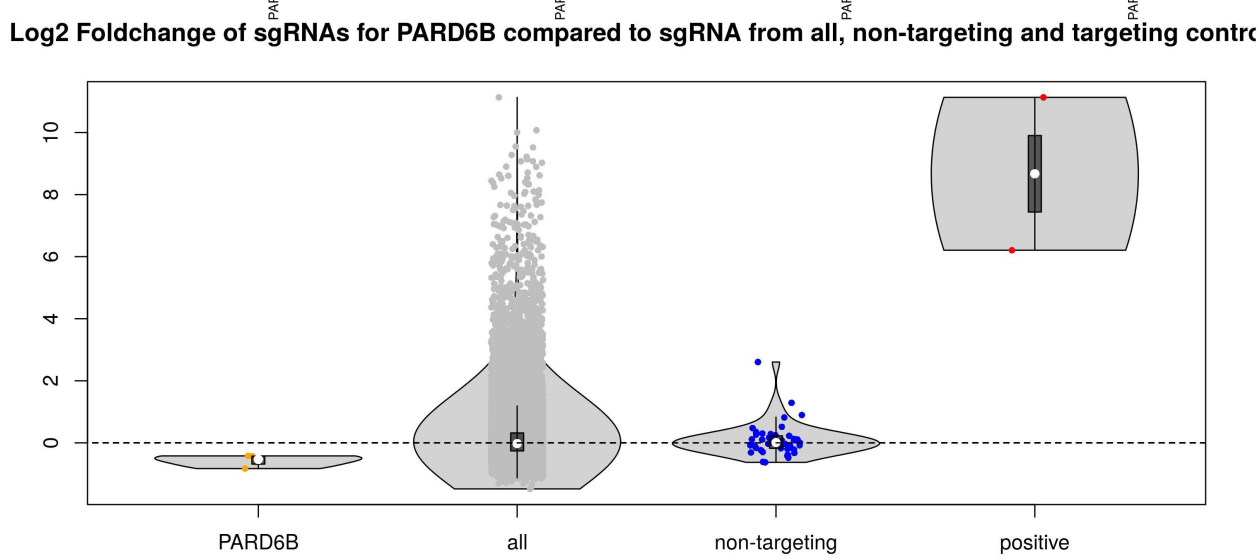
Gene Scatter for PARD6B
PLX_resistance_YTAR



sgRNA Scatter for PARD6B
PLX_resistance_YTAR




Foldchange: PARD6B
Normalized log2(foldchange)
0.0
-0.2
-0.4
-0.6
-0.8
PARD6B_3
PARD6B_2
PARD6B_1
PARD6B_0


Log2 Foldchange of sgRNAs for PARD6B compared to sgRNA from all, non-targeting and targeting contro
0
2
4
6
8
10
PARD6B
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
4	PARD6B_3	PARD6B	none	-0.4199545
3	PARD6B_2	PARD6B	none	-0.4315560
2	PARD6B_1	PARD6B	none	-0.6354565
1	PARD6B_0	PARD6B	none	-0.8288319

FAM177A1

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

ENSEMBL ID (links to Ensembl) ENSG00000151327

HGNC SYMBOL (links to GeneCards) FAM177A1

GENE DESCRIPTION
family with sequence similarity 177, member A1 [Source:HGNC Symbol;Acc:HGNC:19829]

GO TERM

MIM GENE DESCRIPTION

ENSEMBL PROTEIN ID
ENSP00000379734

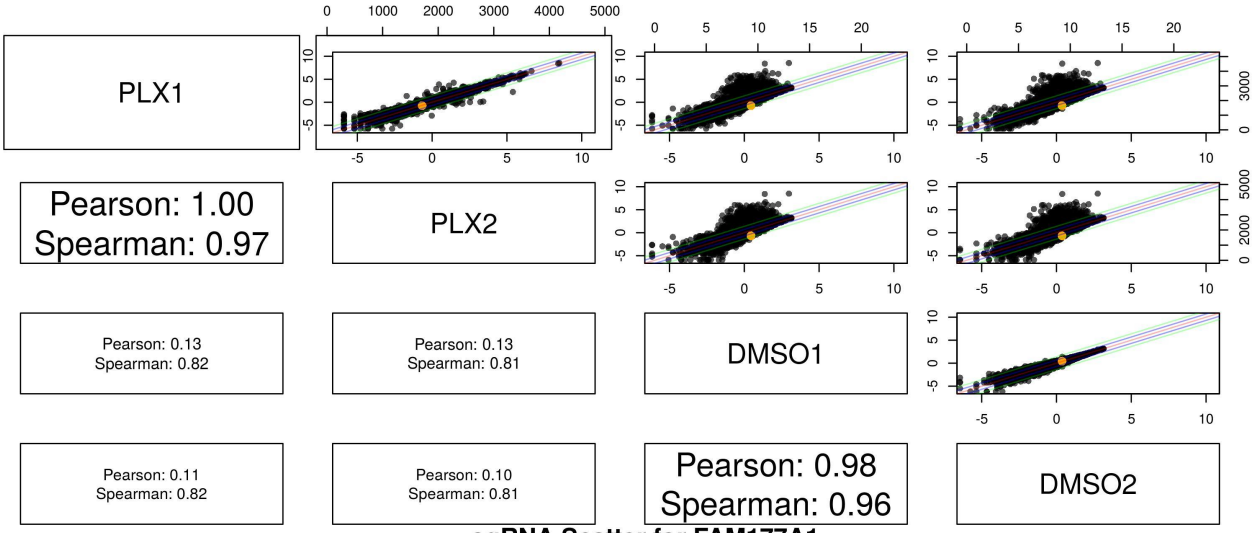
PROTEIN FAMILY DESCRIPTION
UNKNOWN

Wilcox p-value: 0.2824934

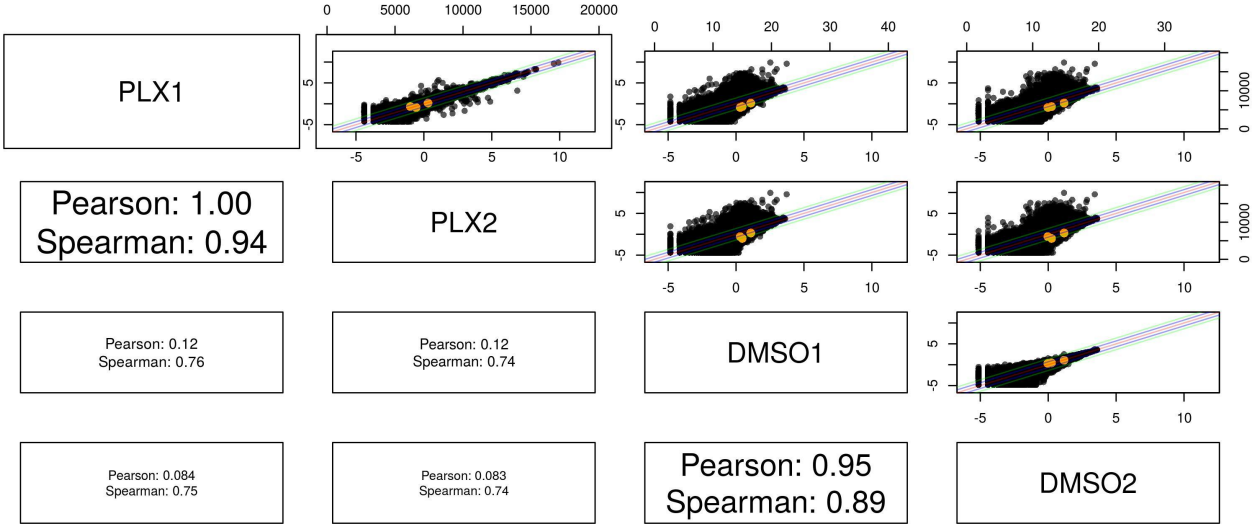
DESeq2 p-value: 1.838162e-06

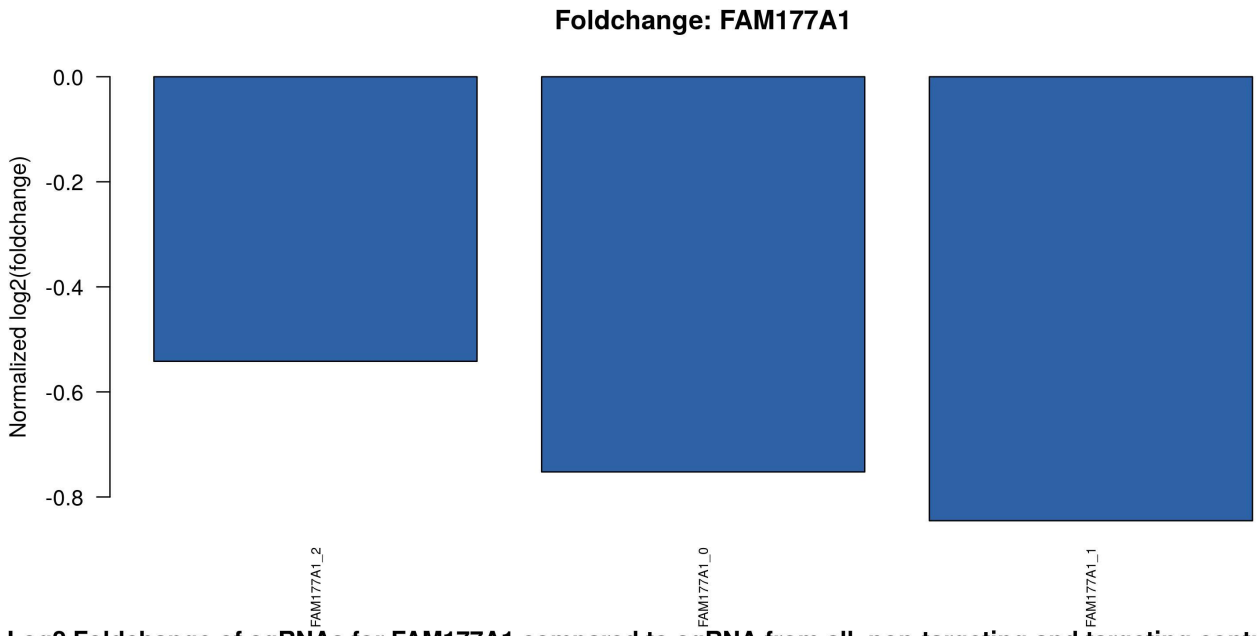
MAGeCK p-value: 0.658214

Gene Scatter for FAM177A1
PLX_resistance_YTAR

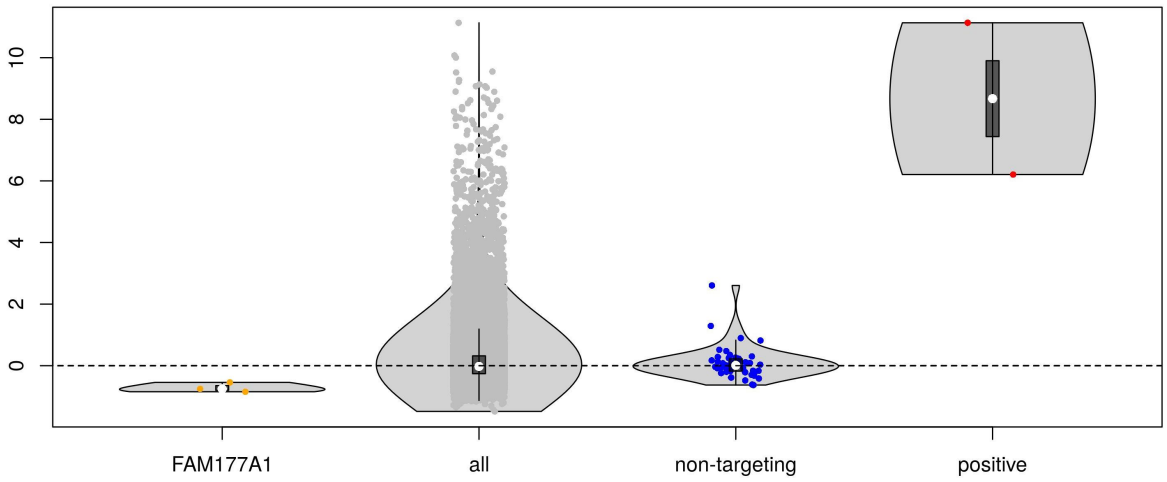


sgRNA Scatter for FAM177A1
PLX_resistance_YTAR





Log2 Foldchange of sgRNAs for FAM177A1 compared to sgRNA from all, non-targeting and targeting contr



	designs	genes	sequence	log2Foldchange
3	FAM177A1_2	FAM177A1	none	-0.5417464
1	FAM177A1_0	FAM177A1	none	-0.7522978
2	FAM177A1_1	FAM177A1	none	-0.8451891

OR4K14

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

ENSEMBL ID (links to Ensembl) ENSG00000169484

HGNC SYMBOL (links to GeneCards) OR4K14

GENE DESCRIPTION
olfactory receptor, family 4, subfamily K, member 14 [Source:HGNC Symbol;Acc:HGNC:15352]

GO TERM
detection of chemical stimulus involved in sensory perception of smell

MIM GENE DESCRIPTION

ENSEMBL PROTEIN ID
ENSP00000305011

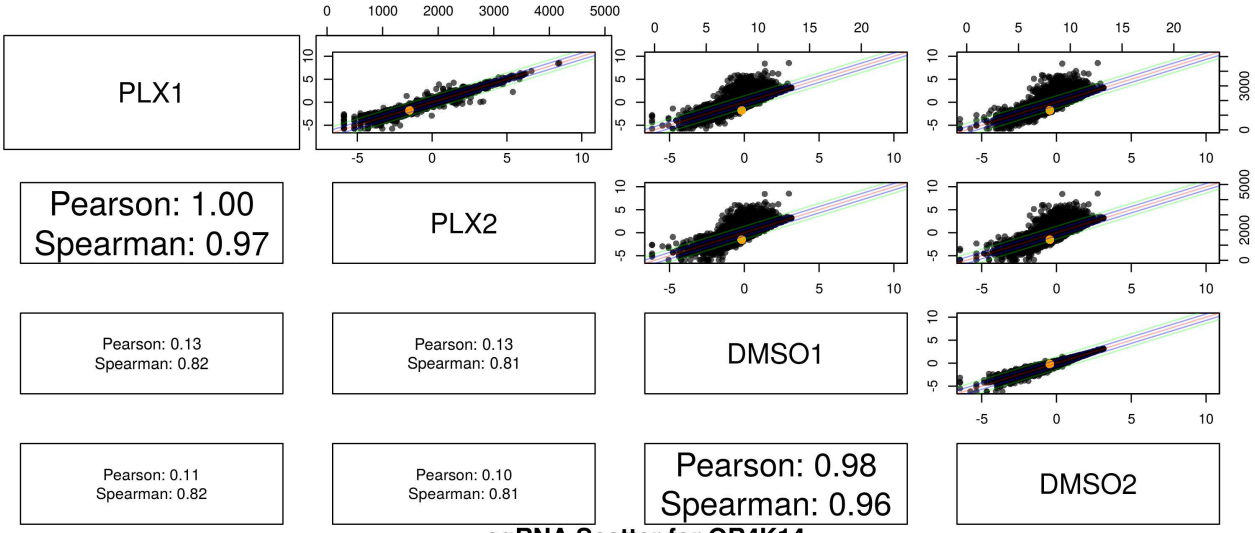
PROTEIN FAMILY DESCRIPTION
OLFACTORY RECEPTOR OLFACTORY RECEPTOR OR14

Wilcox p-value: 0.3482308

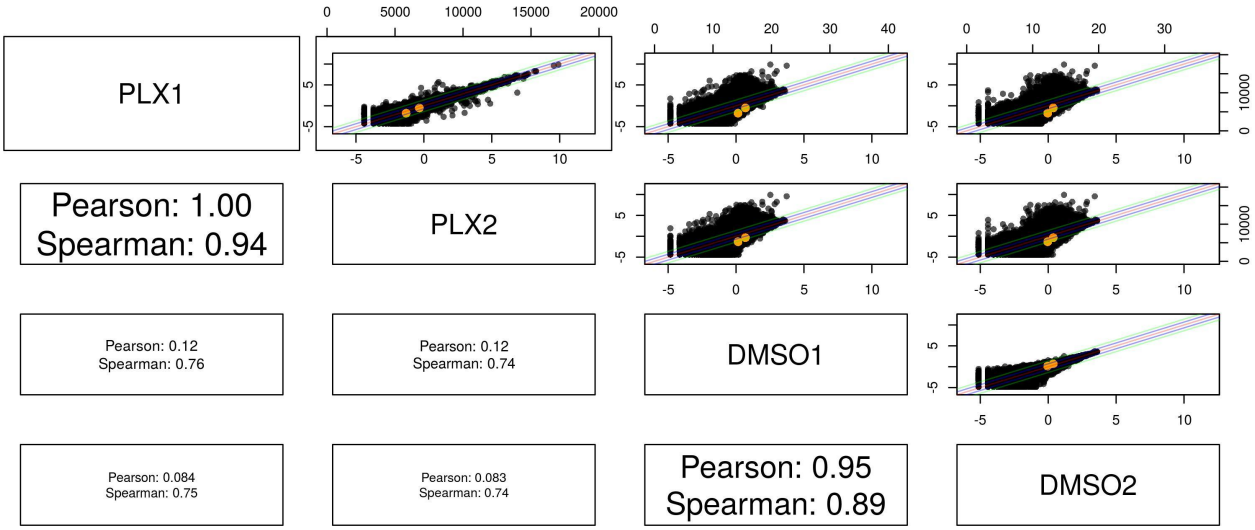
DESeq2 p-value: 7.325623e-06

MAGeCK p-value: 0.658214

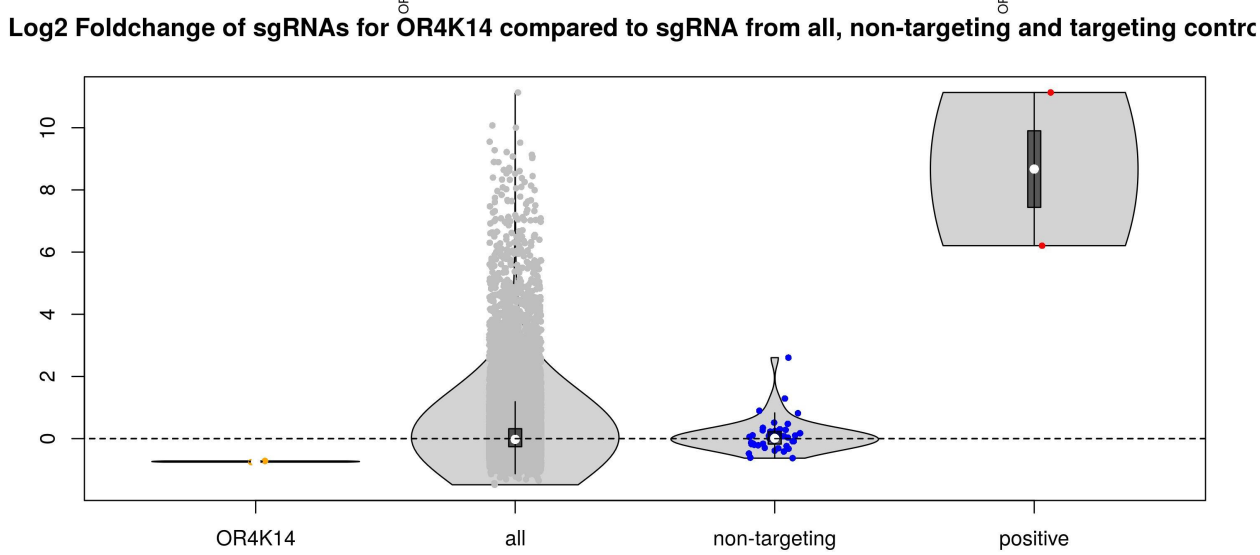
Gene Scatter for OR4K14
PLX_resistance_YTAR



sgRNA Scatter for OR4K14
PLX_resistance_YTAR



Foldchange: OR4K14
Normalized log2(foldchange)
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
-0.6
-0.7
OR4K14_1
OR4K14_0


Log2 Foldchange of sgRNAs for OR4K14 compared to sgRNA from all, non-targeting and targeting contrc
0
2
4
6
8
10
OR4K14
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
2	OR4K14_1	OR4K14	none	-0.7174209
1	OR4K14_0	OR4K14	none	-0.7550264

SOCS4

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

ENSEMBL ID (links to Ensembl) ENSG00000180008

HGNC SYMBOL (links to GeneCards) SOCS4

GENE DESCRIPTION
suppressor of cytokine signaling 4 [Source:HGNC Symbol;Acc:HGNC:19392]

GO TERM
negative regulation of JAK-STAT cascade

MIM GENE DESCRIPTION

ENSEMBL PROTEIN ID
ENSP00000341327

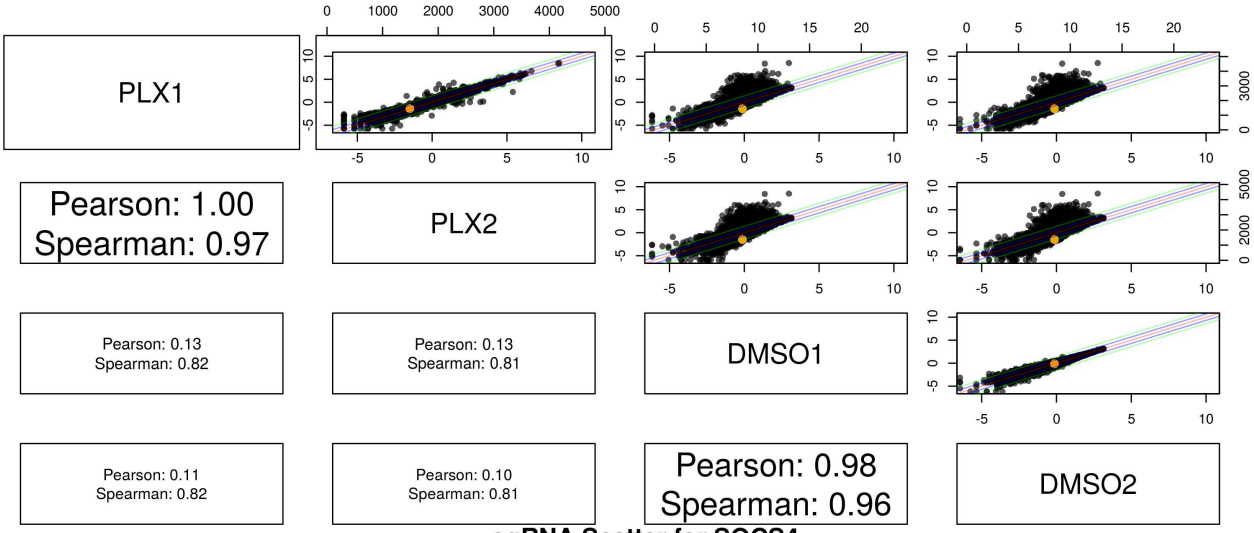
PROTEIN FAMILY DESCRIPTION
SUPPRESSOR OF CYTOKINE SIGNALING SOCS

Wilcox p-value: 0.3482308

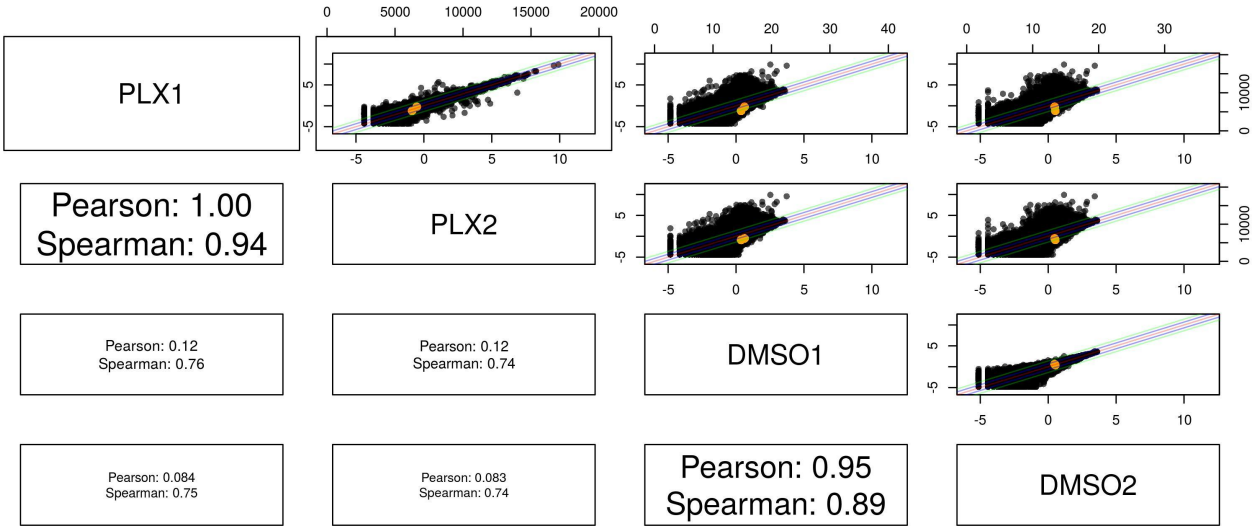
DESeq2 p-value: 1.136514e-08

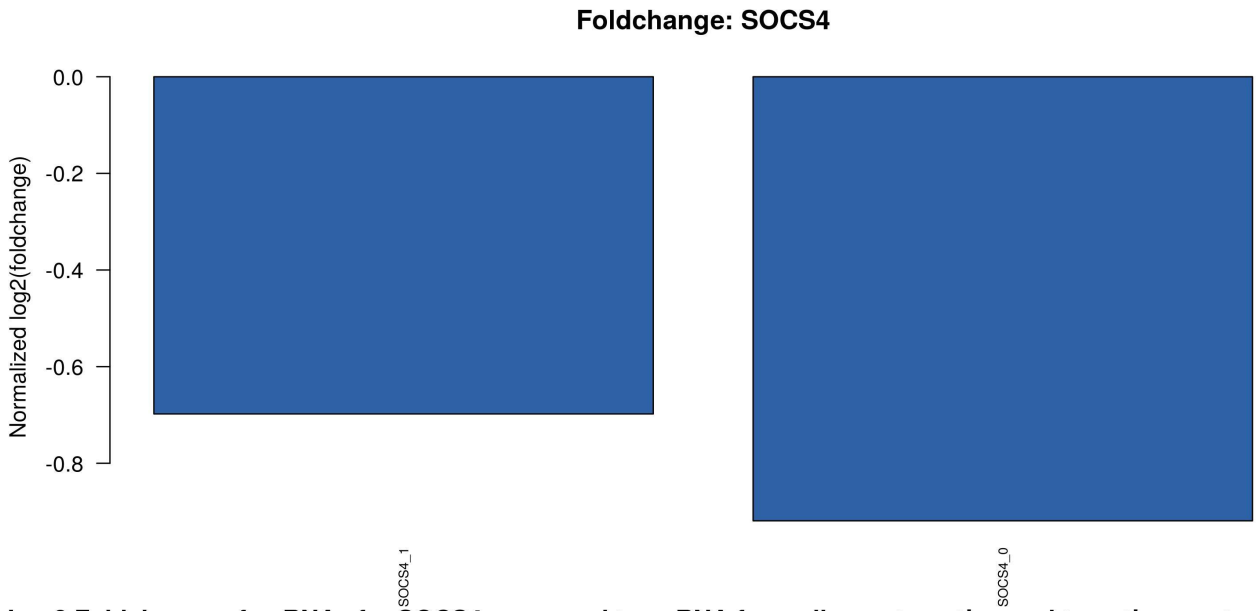
MAGeCK p-value: 0.658214

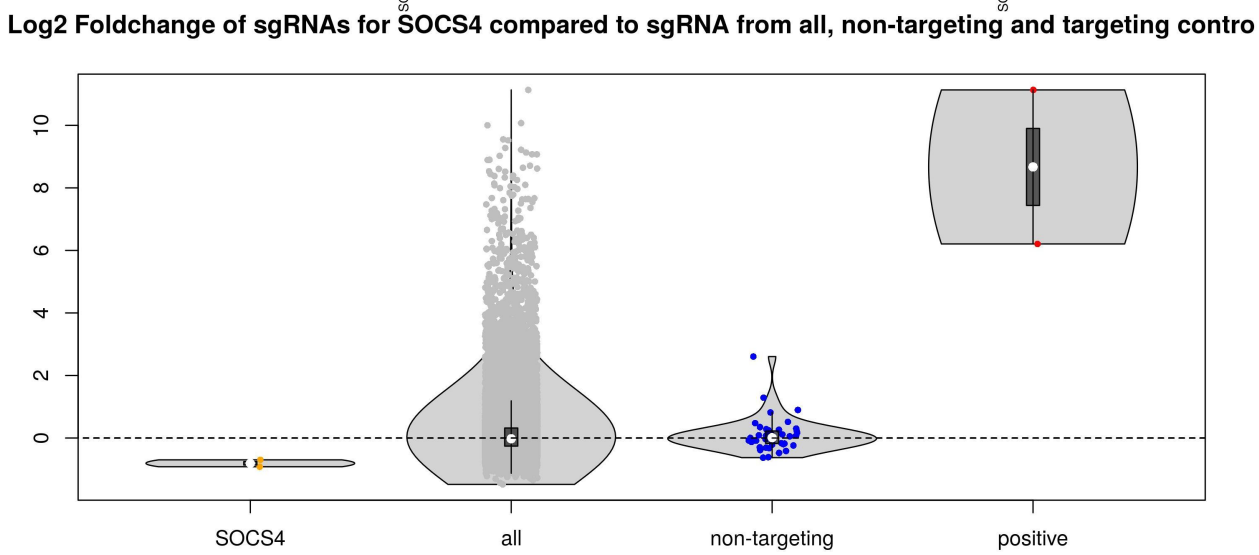
Gene Scatter for SOCS4
PLX_resistance_YTAR



sgRNA Scatter for SOCS4
PLX_resistance_YTAR




Foldchange: SOCS4
Normalized log2(foldchange)
0.0
-0.2
-0.4
-0.6
-0.8
SOCS4_1
SOCS4_0


Log2 Foldchange of sgRNAs for SOCS4 compared to sgRNA from all, non-targeting and targeting contro
0
2
4
6
8
10
SOCS4
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
2	SOCS4_1	SOCS4	none	-0.6979173
1	SOCS4_0	SOCS4	none	-0.9190944

TRAPPC2L

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

ENSEMBL ID (links to Ensembl) ENSG00000167515

HGNC SYMBOL (links to GeneCards) TRAPPC2L

GENE DESCRIPTION
trafficking protein particle complex 2-like [Source:HGNC Symbol;Acc:HGNC:30887]

GO TERM
vesicle-mediated transport

MIM GENE DESCRIPTION
TRAFFICKING PROTEIN PARTICLE COMPLEX 2-LIKE; TRAPPC2L

ENSEMBL PROTEIN ID
ENSP00000487584

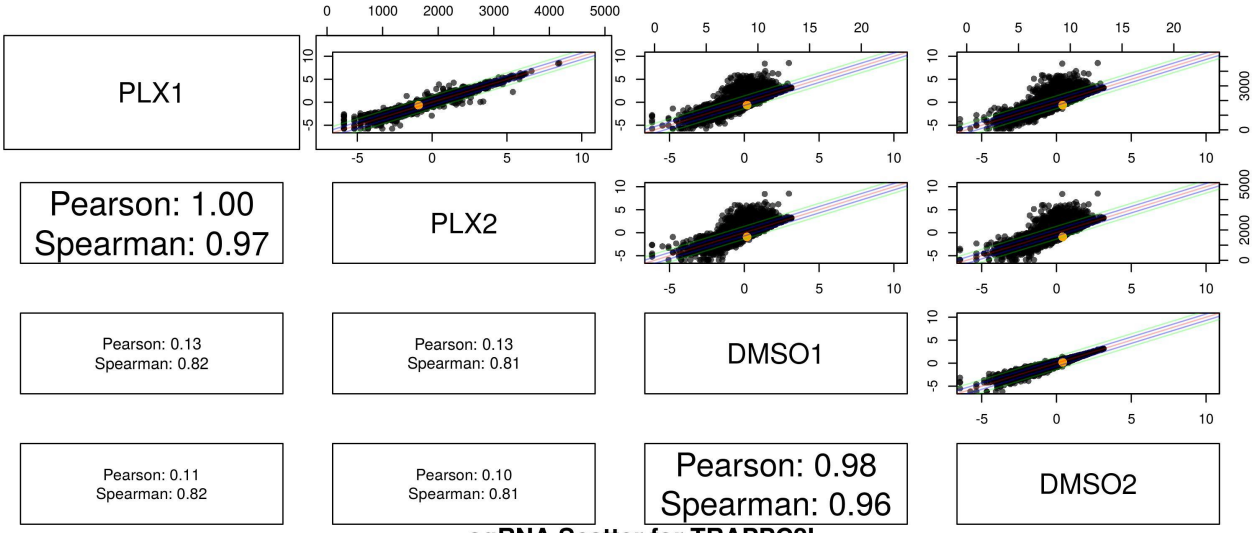
PROTEIN FAMILY DESCRIPTION
UNKNOWN

Wilcox p-value: 0.3250154

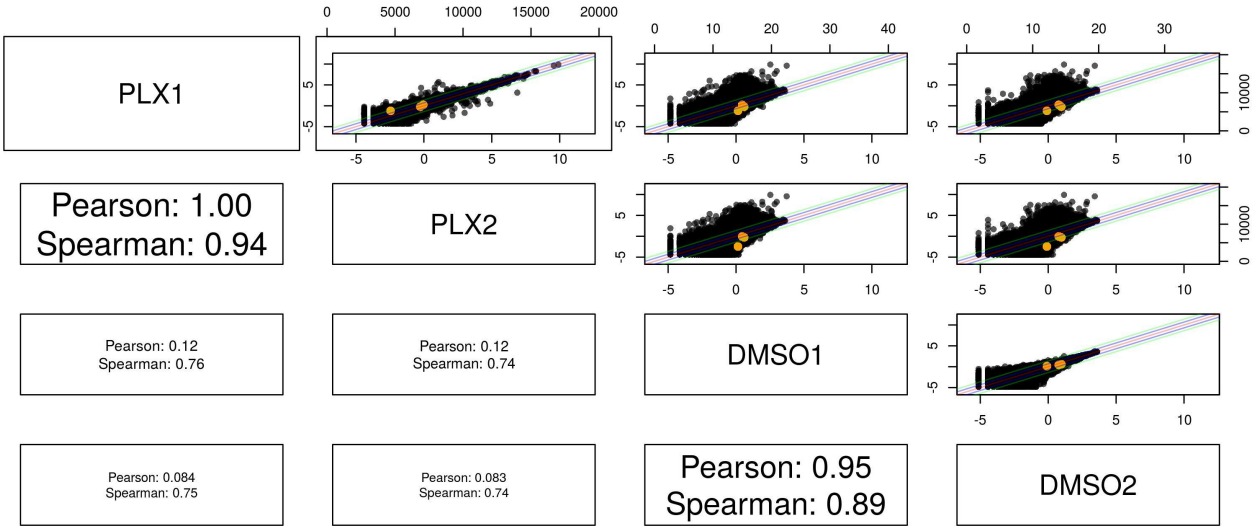
DESeq2 p-value: 0.001759867

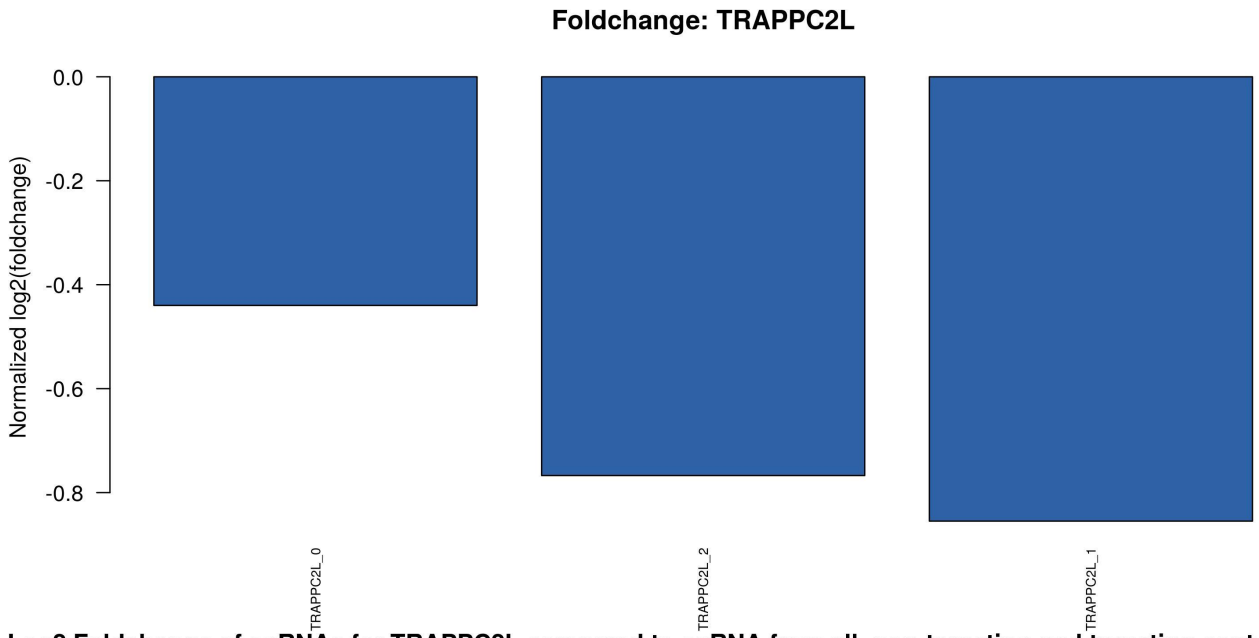
MAGeCK p-value: 0.677525

Gene Scatter for TRAPPC2L
PLX_resistance_YTAR

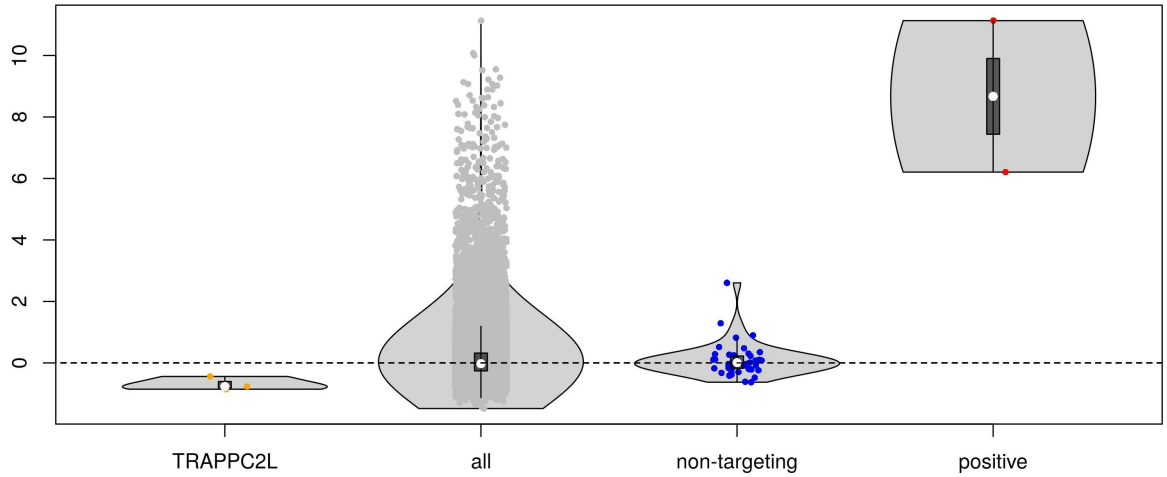


sgRNA Scatter for TRAPPC2L
PLX_resistance_YTAR





Log2 Foldchange of sgRNAs for TRAPPC2L compared to sgRNA from all, non-targeting and targeting cont



	designs	genes	sequence	log2Foldchange
1	TRAPPC2L_0	TRAPPC2L	none	-0.4399130
3	TRAPPC2L_2	TRAPPC2L	none	-0.7671676
2	TRAPPC2L_1	TRAPPC2L	none	-0.8548672

KIR3DL1

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

ENSEMBL ID (links to Ensembl) ENSG00000274948

HGNC SYMBOL (links to GeneCards) KIR3DL1

GENE DESCRIPTION
killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1 [Source:HGNC Symbol;Acc:HGNC:6338]

GO TERM

MIM GENE DESCRIPTION
KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR, THREE DOMAINS, LONG CYTOPLASMICTAIL, 1; KIR3DL1;;NK-ASSOCIATED TRANSCRIPT 3; NKAT3;;NKB1;;AMB11;;CD158E1KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR, THREE DOMAINS, SHORT CYTOPLASMICTAIL, 1, INCLUDED; KIR3DS1, I /…/D;;NK-ASSOCIATED TRANSCRIPT 10, INCLUDED; NKAT10, INCLUDED;;CD158E2, INCLUDED;;NK-ASSOCIATED TRANSCRIPT 3delIg1, INCLUDED; NKAT3delIg1, INCLUDED

ENSEMBL PROTEIN ID
ENSP00000483877

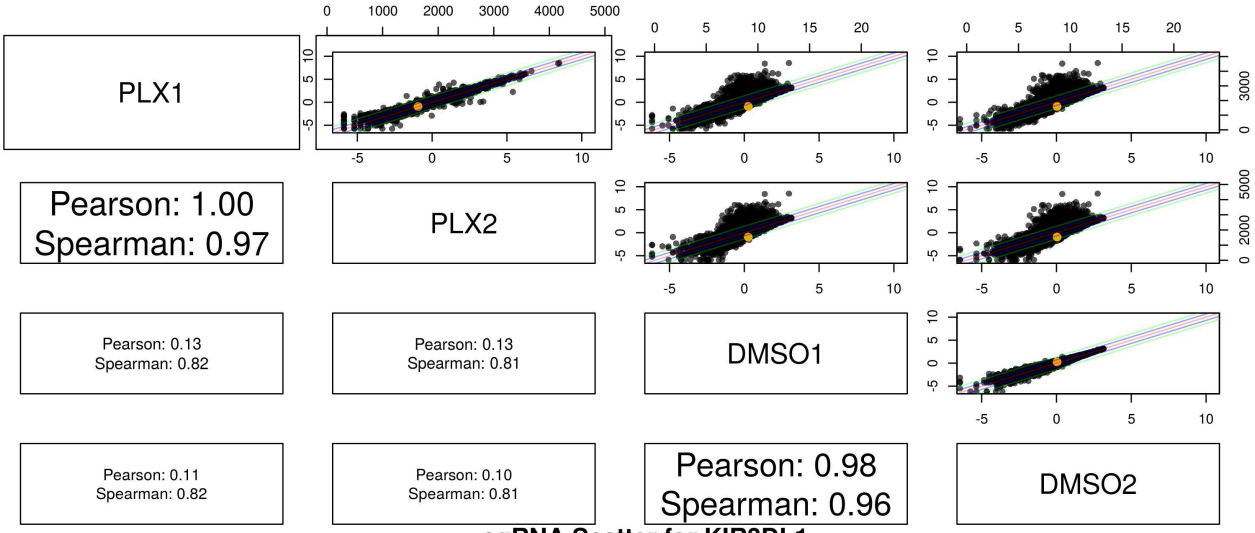
PROTEIN FAMILY DESCRIPTION
KILLER CELL IMMUNOGLOBULIN RECEPTOR PRECURSOR CD158 ANTIGEN FAMILY MEMBER MHC CLASS I NK CELL RECEPTOR NATURAL KILLER ASSOCIATED TRANSCRIPT NKAT ANTIGEN

Wilcox p-value: 0.414337

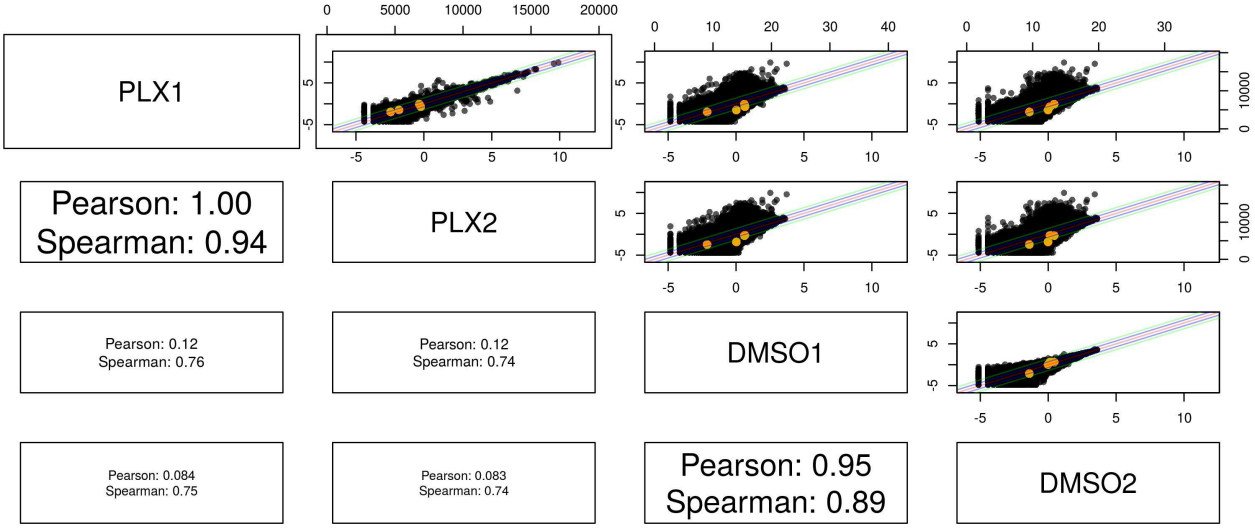
DESeq2 p-value: 0.0001354185

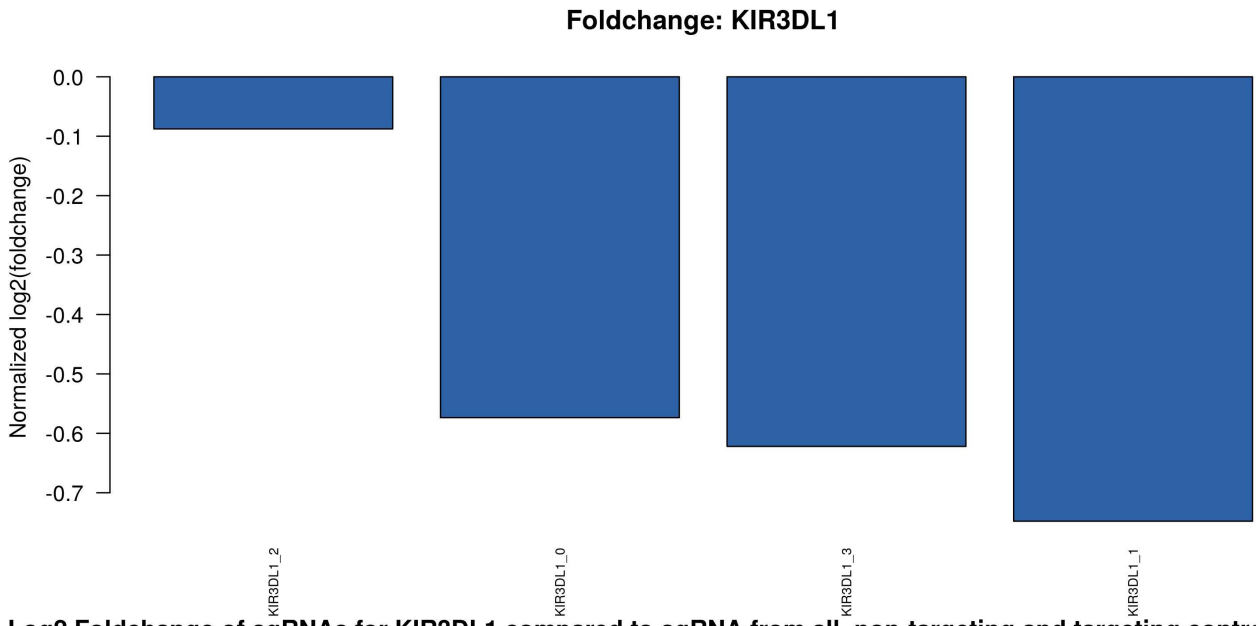
MAGeCK p-value: 0.699742

Gene Scatter for KIR3DL1
PLX_resistance_YTAR

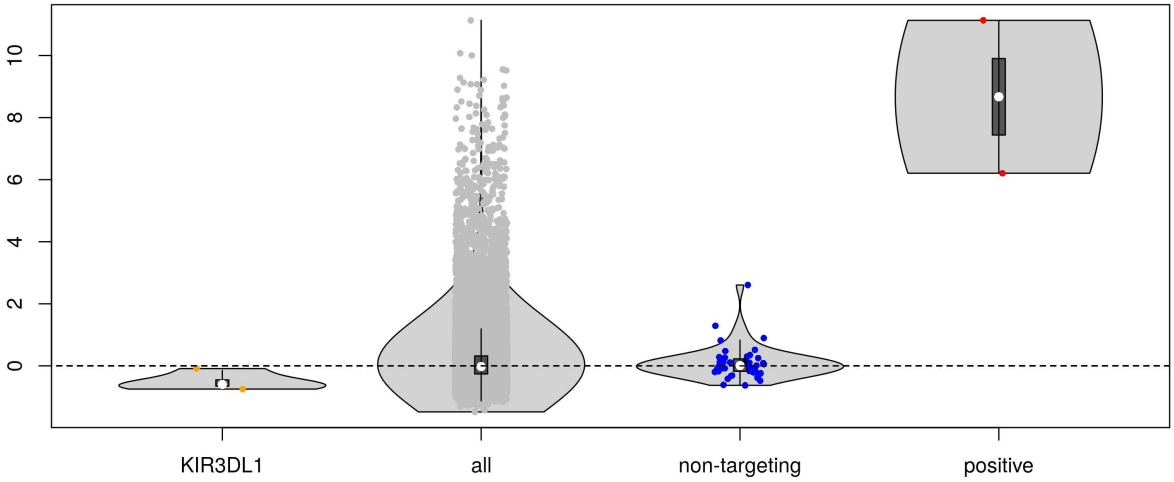


sgRNA Scatter for KIR3DL1
PLX_resistance_YTAR





Log2 Foldchange of sgRNAs for KIR3DL1 compared to sgRNA from all, non-targeting and targeting contro



	designs	genes	sequence	log2Foldchange
3	KIR3DL1_2	KIR3DL1	none	-0.0877314
1	KIR3DL1_0	KIR3DL1	none	-0.5735986
4	KIR3DL1_3	KIR3DL1	none	-0.6219910
2	KIR3DL1_1	KIR3DL1	none	-0.7478411

RXFP4

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

ENSEMBL ID (links to Ensembl) ENSG00000173080

HGNC SYMBOL (links to GeneCards) RXFP4

GENE DESCRIPTION
relaxin/insulin-like family peptide receptor 4 [Source:HGNC Symbol;Acc:HGNC:14666]

GO TERM
G-protein coupled receptor signaling pathway

MIM GENE DESCRIPTION
RELAXIN 3 RECEPTOR 2; RLN3R2;;RLN3 RECEPTOR 2;;G PROTEIN-COUPLED RECEPTOR 100; GPR100;;G PROTEIN-COUPLED RECEPTOR 142; GPCR142

ENSEMBL PROTEIN ID
ENSP00000357301

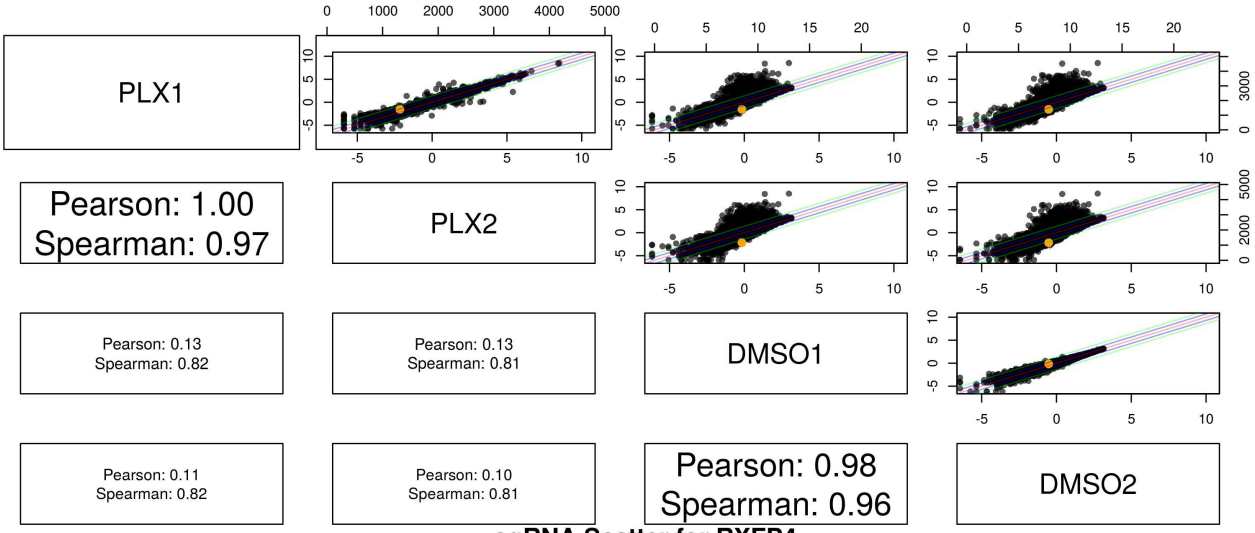
PROTEIN FAMILY DESCRIPTION
RELAXIN 3 RECEPTOR 2 RLN3 RECEPTOR 2 G COUPLED RECEPTOR 100 INSULIN PEPTIDE INSL5 RECEPTOR RELAXIN FAMILY PEPTIDE RECEPTOR 4

Wilcox p-value: 0.3482308

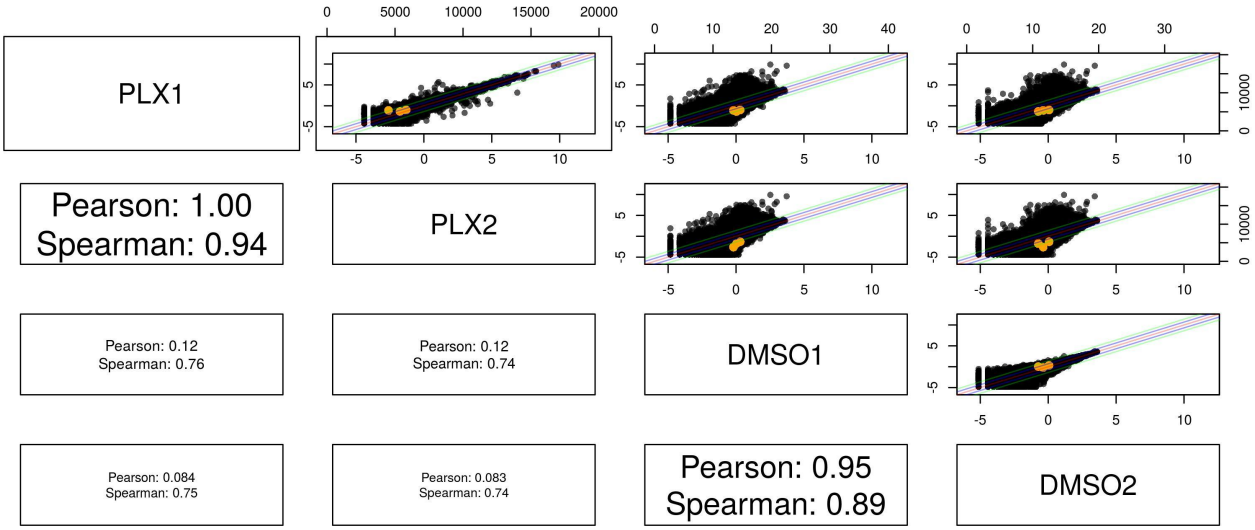
DESeq2 p-value: 0.0001221307

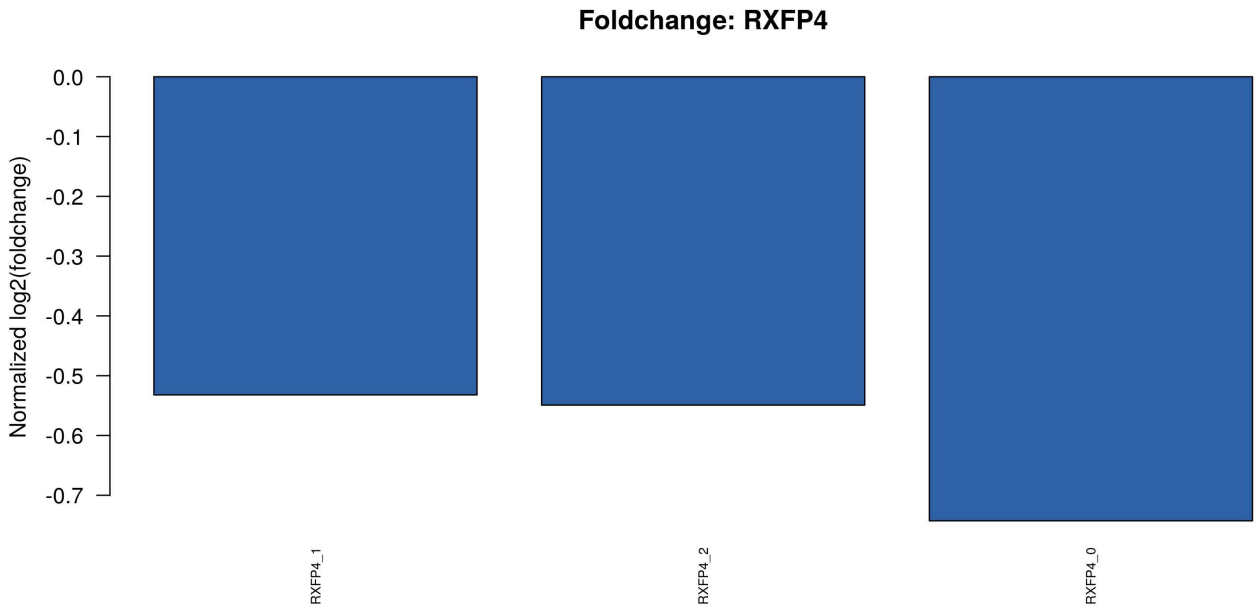
MAGeCK p-value: 0.699742

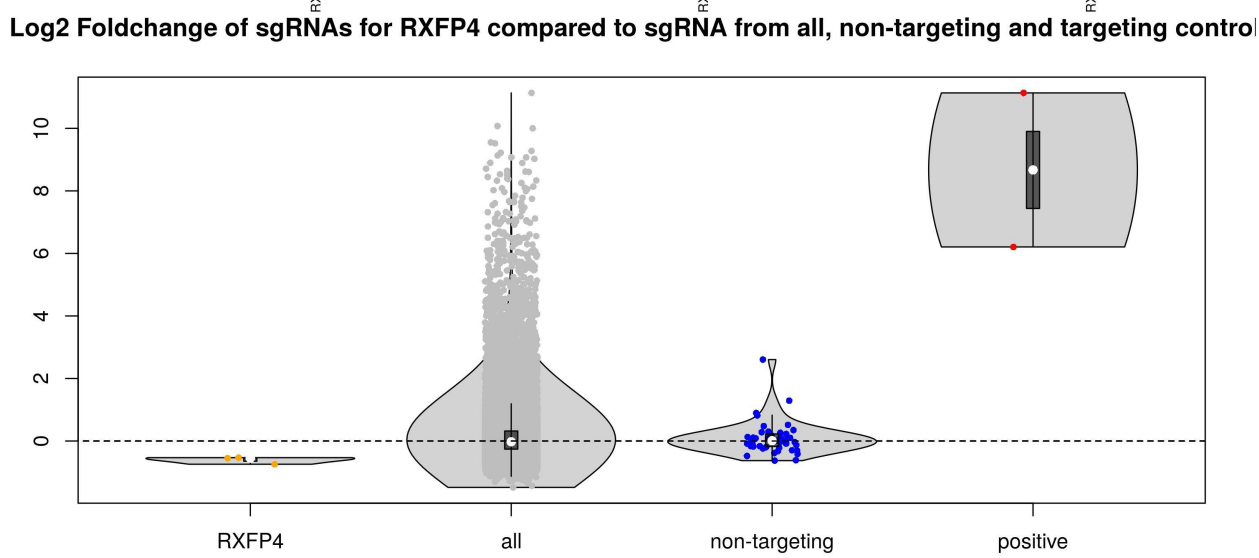
Gene Scatter for RXFP4
PLX_resistance_YTAR



sgRNA Scatter for RXFP4
PLX_resistance_YTAR




Foldchange: RXFP4
Normalized log2(foldchange)
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
-0.6
-0.7
RXFP4_1
RXFP4_2
RXFP4_0


Log2 Foldchange of sgRNAs for RXFP4 compared to sgRNA from all, non-targeting and targeting control
0
2
4
6
8
10
RXFP4
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
2	RXFP4_1	RXFP4	none	-0.5321227
3	RXFP4_2	RXFP4	none	-0.5492592
1	RXFP4_0	RXFP4	none	-0.7427063

FOXA2

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

ENSEMBL ID (links to Ensembl) ENSG00000125798

HGNC SYMBOL (links to GeneCards) FOXA2

GENE DESCRIPTION
forkhead box A2 [Source:HGNC Symbol;Acc:HGNC:5022]

GO TERM
regulation of transcription, DNA-templated

MIM GENE DESCRIPTION
FORKHEAD BOX A2; FOXA2;;HEPATOCYTE NUCLEAR FACTOR 3-BETA; HNF3B

ENSEMBL PROTEIN ID
ENSP00000366319

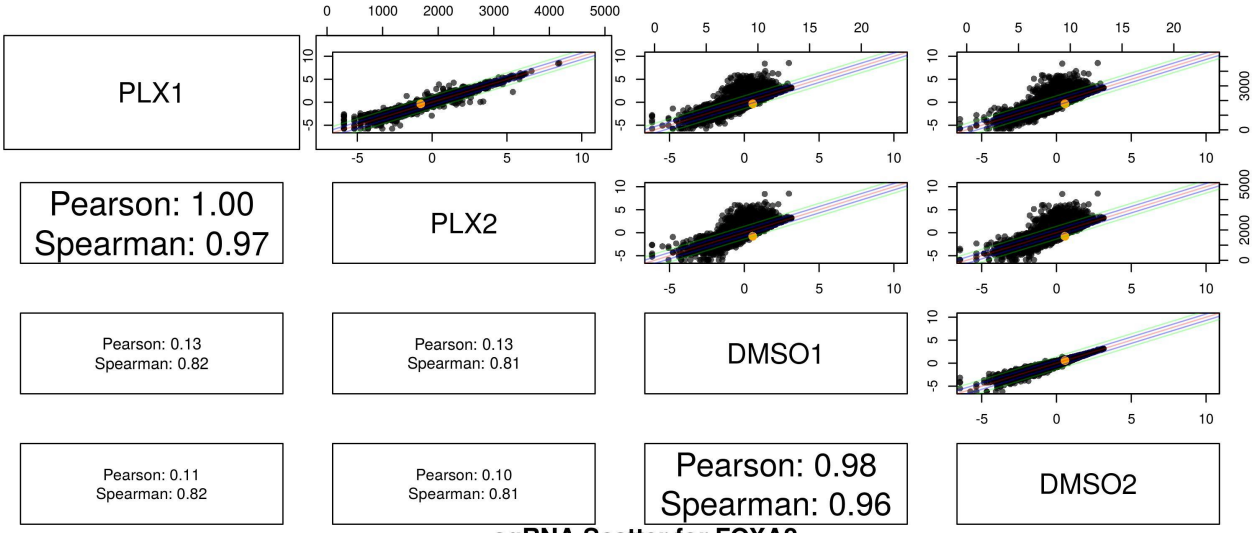
PROTEIN FAMILY DESCRIPTION
HEPATOCYTE NUCLEAR FACTOR 3 HNF 3 HNF FORKHEAD BOX

Wilcox p-value: 0.3250154

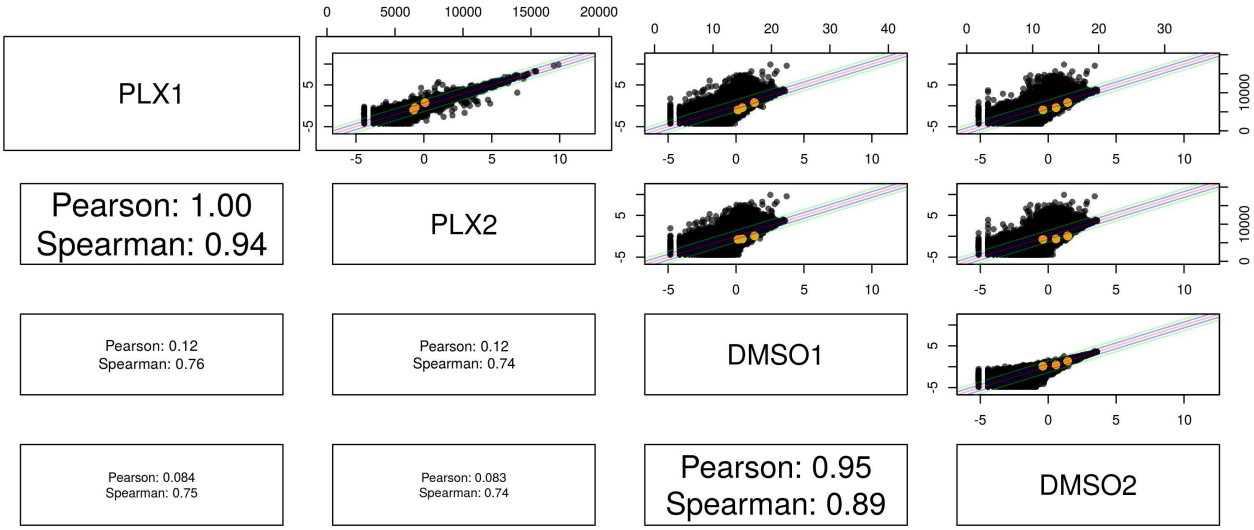
DESeq2 p-value: 0.00182224

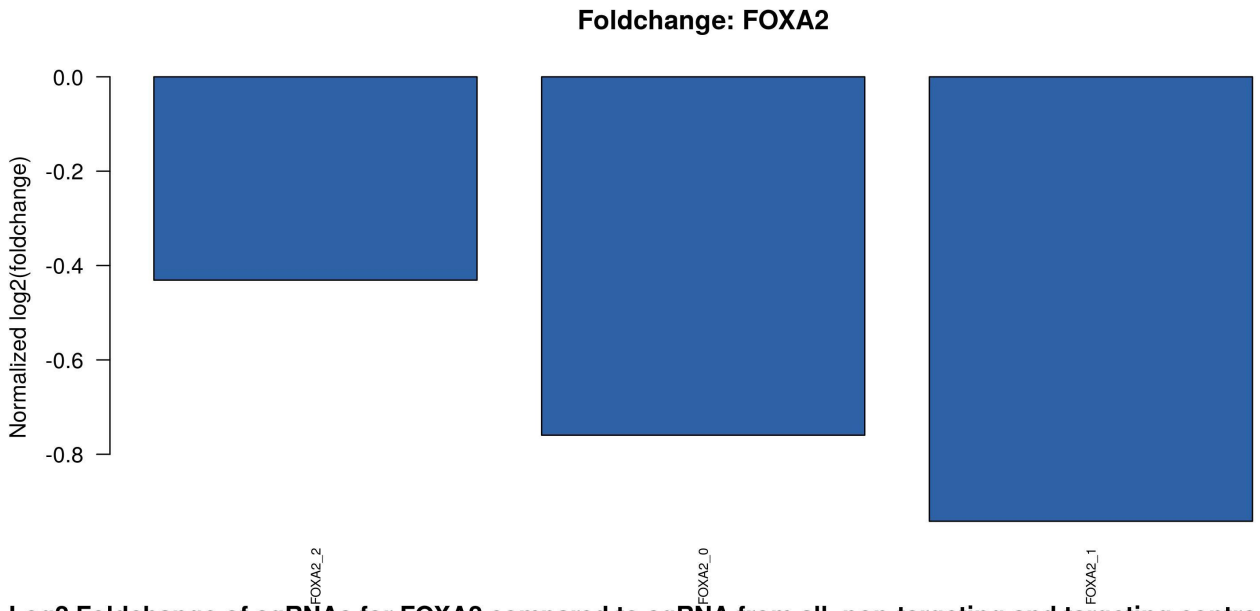
MAGeCK p-value: 0.699742

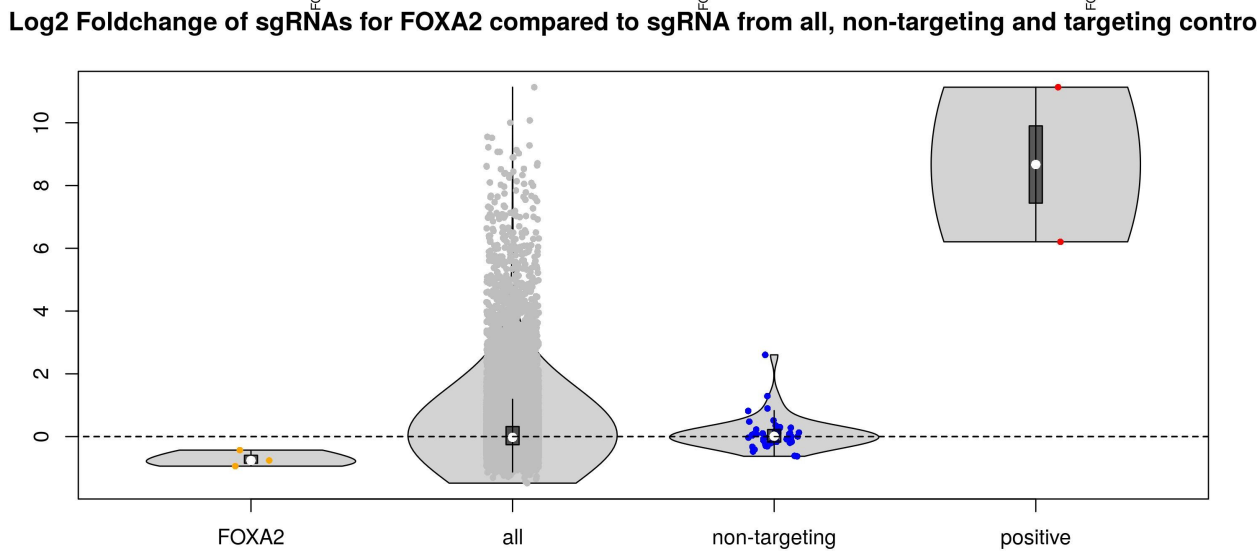
Gene Scatter for FOXA2
PLX_resistance_YTAR



sgRNA Scatter for FOXA2
PLX_resistance_YTAR




Foldchange: FOXA2
Normalized log2(foldchange)
0.0
-0.2
-0.4
-0.6
-0.8
FOXA2_2
FOXA2_0
FOXA2_1


Log2 Foldchange of sgRNAs for FOXA2 compared to sgRNA from all, non-targeting and targeting contro
0
2
4
6
8
10
FOXA2
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
3	FOXA2_2	FOXA2	none	-0.4309276
1	FOXA2_0	FOXA2	none	-0.7595566
2	FOXA2_1	FOXA2	none	-0.9419333

AIM2

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

ENSEMBL ID (links to Ensembl) ENSG00000163568

HGNC SYMBOL (links to GeneCards) AIM2

GENE DESCRIPTION
absent in melanoma 2 [Source:HGNC Symbol;Acc:HGNC:357]

GO TERM

MIM GENE DESCRIPTION
ABSENT IN MELANOMA 2; AIM2

ENSEMBL PROTEIN ID
ENSP00000483485

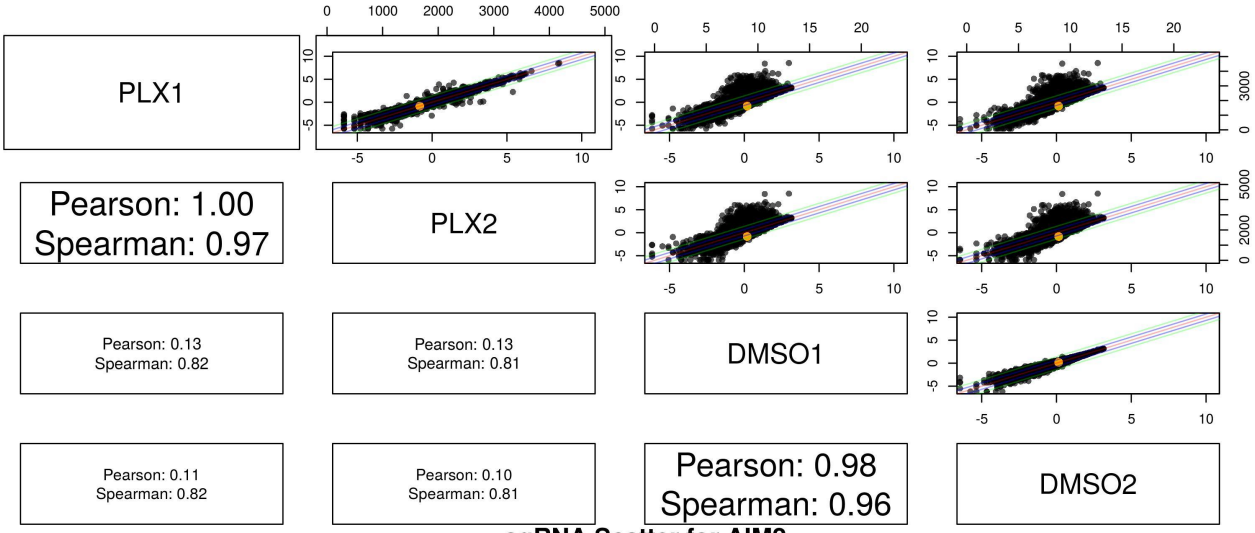
PROTEIN FAMILY DESCRIPTION
INTERFERON INDUCIBLE AIM2

Wilcox p-value: 0.3482308

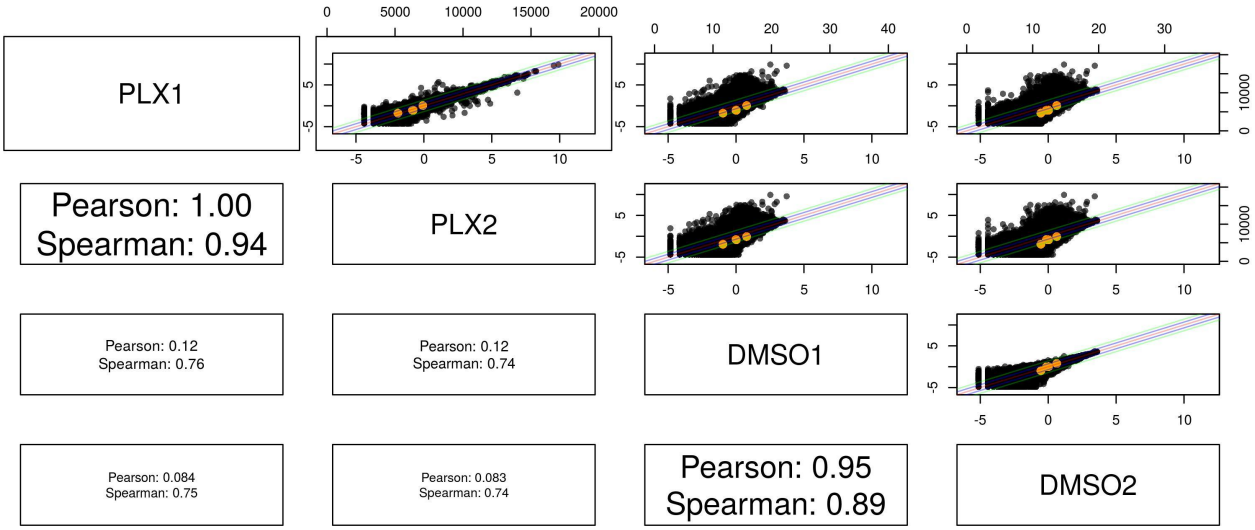
DESeq2 p-value: 0.0001191128

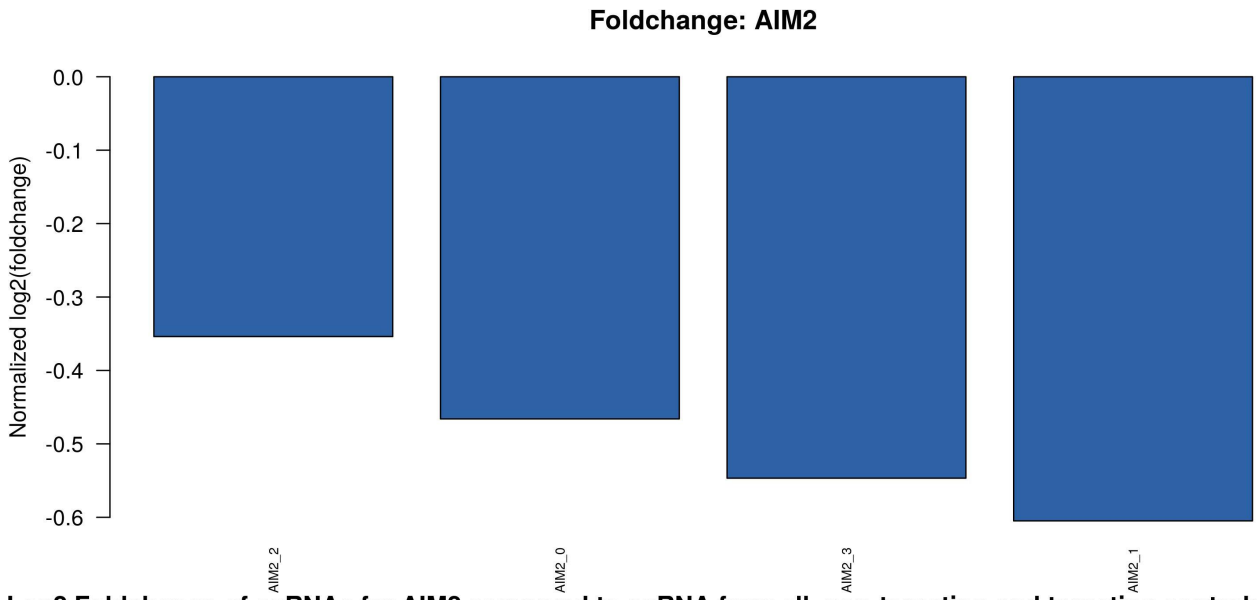
MAGeCK p-value: 0.699742

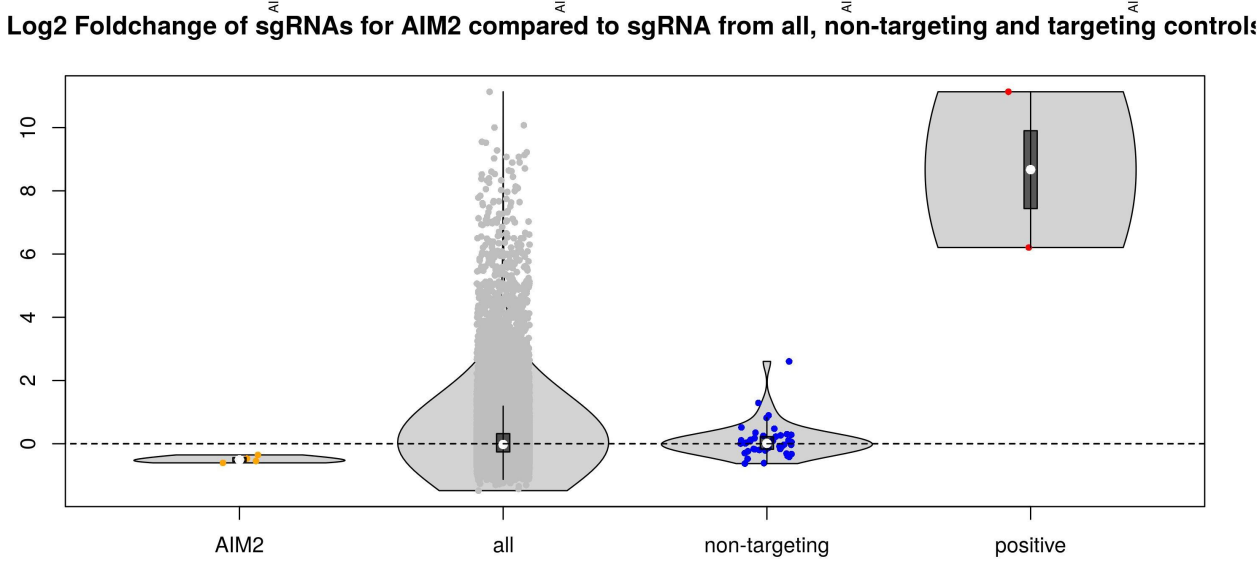
Gene Scatter for AIM2
PLX_resistance_YTAR



sgRNA Scatter for AIM2
PLX_resistance_YTAR




Foldchange: AIM2
Normalized log2(foldchange)
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
-0.6
AIM2_2
AIM2_0
AIM2_3
AIM2_1


Log2 Foldchange of sgRNAs for AIM2 compared to sgRNA from all, non-targeting and targeting controls
0
2
4
6
8
10
AIM2
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
3	AIM2_2	AIM2	none	-0.3538229
1	AIM2_0	AIM2	none	-0.4659934
4	AIM2_3	AIM2	none	-0.5467287
2	AIM2_1	AIM2	none	-0.6048516

C17orf107

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

ENSEMBL ID (links to Ensembl) ENSG00000205710

HGNC SYMBOL (links to GeneCards) C17orf107

GENE DESCRIPTION
chromosome 17 open reading frame 107 [Source:HGNC Symbol;Acc:HGNC:37238]

GO TERM

MIM GENE DESCRIPTION

ENSEMBL PROTEIN ID
ENSP00000429241

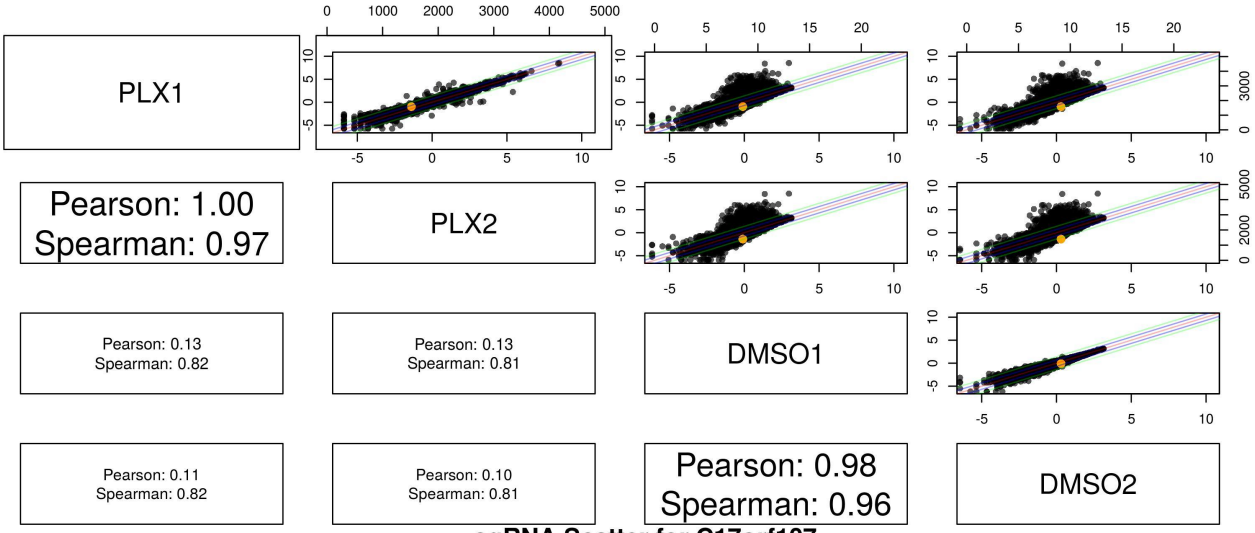
PROTEIN FAMILY DESCRIPTION
UNCHARACTERIZED

Wilcox p-value: 0.3482308

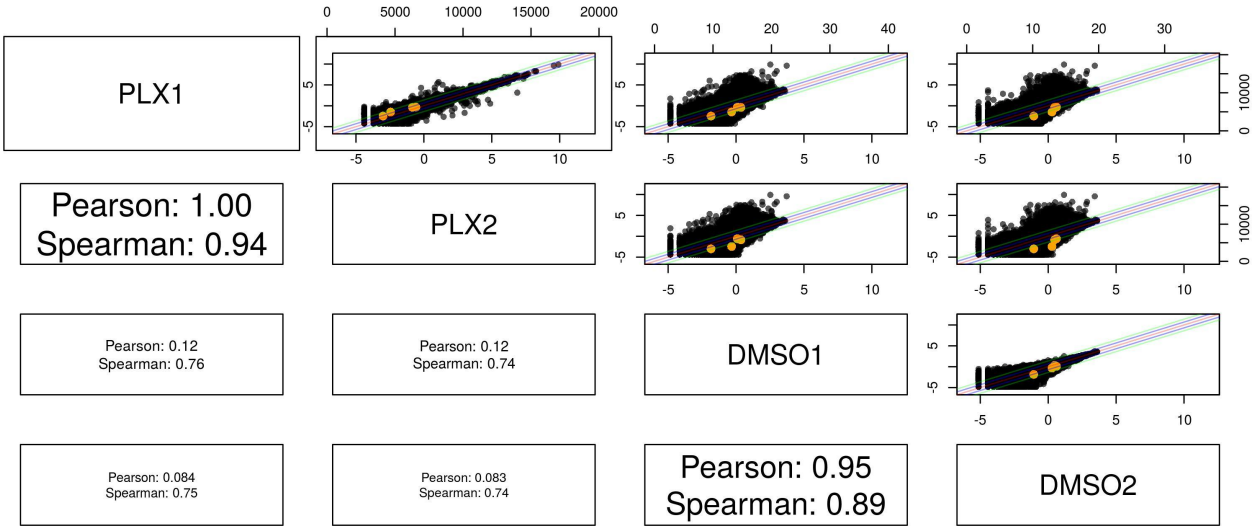
DESeq2 p-value: 0.001854469

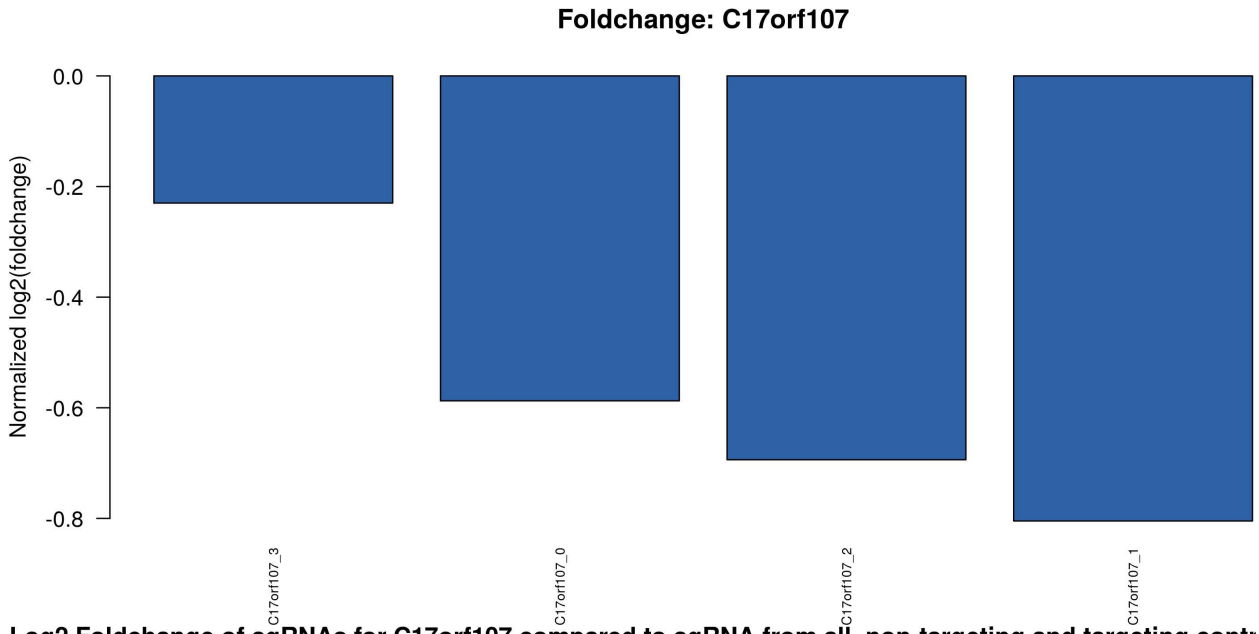
MAGeCK p-value: 0.745409

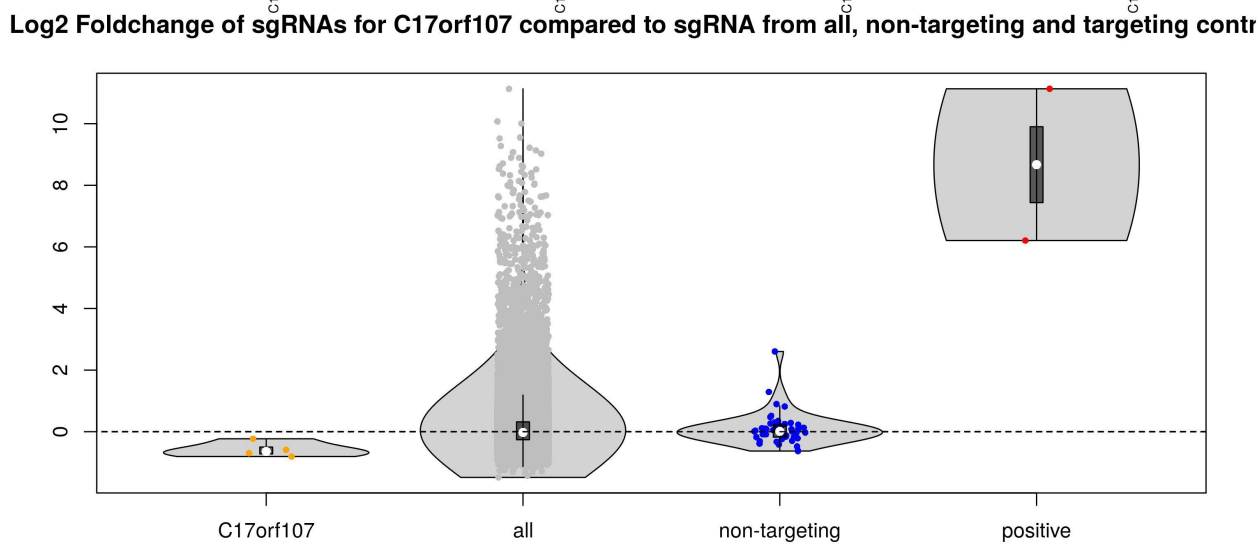
Gene Scatter for C17orf107
PLX_resistance_YTAR



sgRNA Scatter for C17orf107
PLX_resistance_YTAR




Foldchange: C17orf107
Normalized log2(foldchange)
0.0
-0.2
-0.4
-0.6
-0.8
C17orf107_3
C17orf107_0
C17orf107_2
C17orf107_1


Log2 Foldchange of sgRNAs for C17orf107 compared to sgRNA from all, non-targeting and targeting contr
0
2
4
6
8
10
C17orf107
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
4	C17orf107_3	C17orf107	none	-0.2299147
1	C17orf107_0	C17orf107	none	-0.5874010
3	C17orf107_2	C17orf107	none	-0.6939340
2	C17orf107_1	C17orf107	none	-0.8046517

SLC38A2

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

ENSEMBL ID (links to Ensembl) ENSG00000134294

HGNC SYMBOL (links to GeneCards) SLC38A2

GENE DESCRIPTION
solute carrier family 38, member 2 [Source:HGNC Symbol;Acc:HGNC:13448]

GO TERM
cell

MIM GENE DESCRIPTION
SOLUTE CARRIER FAMILY 38 (AMINO ACID TRANSPORTER), MEMBER 2; SLC38A2;;AMINO ACID TRANSPORTER A2; ATA2;;SODIUM-DEPENDENT NEUTRAL AMINO ACID TRANSPORTER 2; SNAT2

ENSEMBL PROTEIN ID
ENSP00000482873

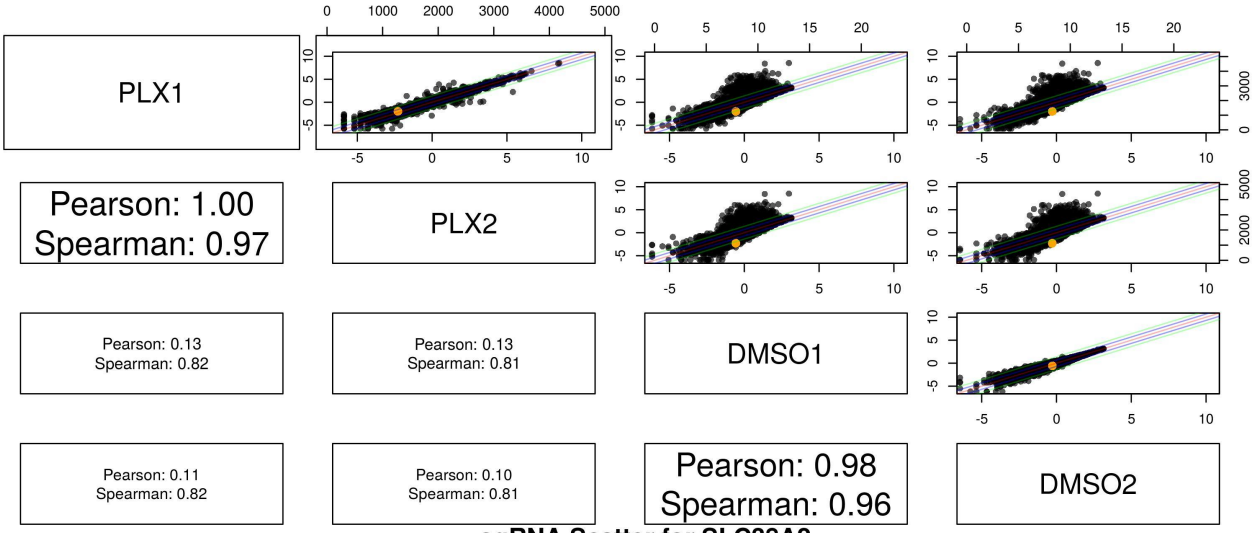
PROTEIN FAMILY DESCRIPTION
SODIUM COUPLED NEUTRAL AMINO ACID TRANSPORTER AMINO ACID TRANSPORTER SOLUTE CARRIER FAMILY 38 MEMBER SYSTEM A AMINO ACID TRANSPORTER 1 SYSTEM N AMINO ACID TRANSPORTER

Wilcox p-value: 0.3482308

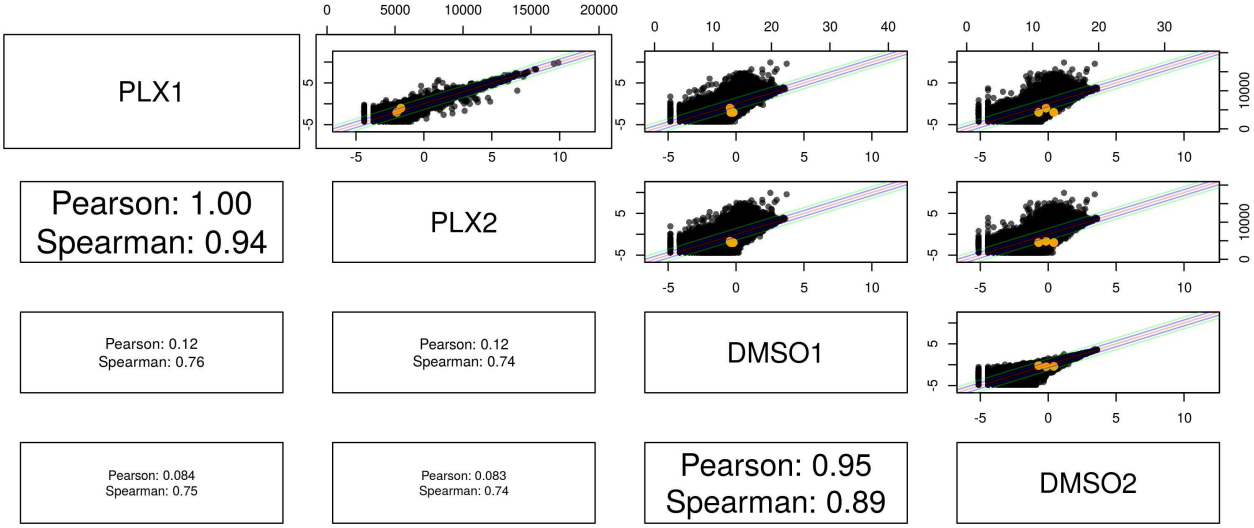
DESeq2 p-value: 4.835071e-10

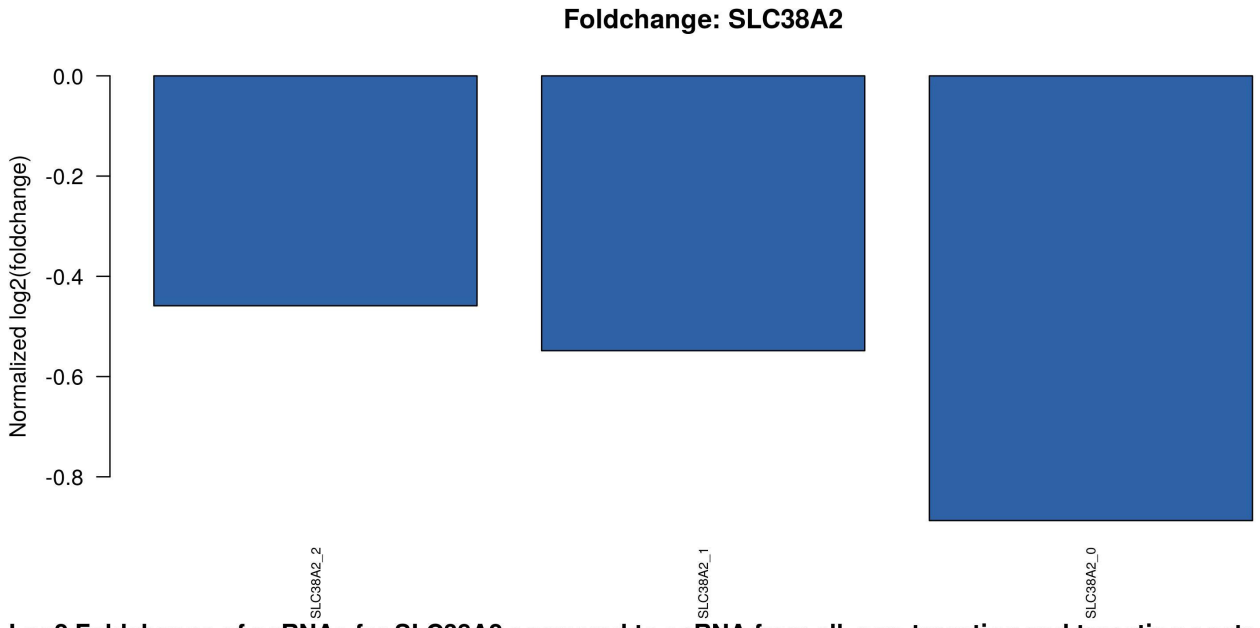
MAGeCK p-value: 0.745409

Gene Scatter for SLC38A2
PLX_resistance_YTAR

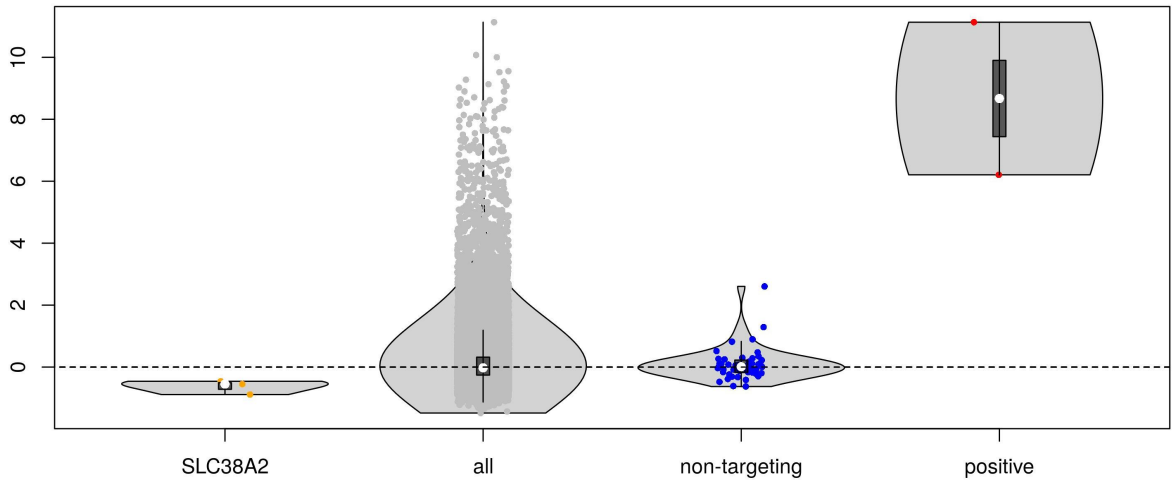


sgRNA Scatter for SLC38A2
PLX_resistance_YTAR





Log2 Foldchange of sgRNAs for SLC38A2 compared to sgRNA from all, non-targeting and targeting contr



	designs	genes	sequence	log2Foldchange
3	SLC38A2_2	SLC38A2	none	-0.4587491
2	SLC38A2_1	SLC38A2	none	-0.5483761
1	SLC38A2_0	SLC38A2	none	-0.8873187

PINK1

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

ENSEMBL ID (links to Ensembl) ENSG00000158828

HGNC SYMBOL (links to GeneCards) PINK1

GENE DESCRIPTION
PTEN induced putative kinase 1 [Source:HGNC Symbol;Acc:HGNC:14581]

GO TERM
negative regulation of hypoxia-induced intrinsic apoptotic signaling pathway

MIM GENE DESCRIPTION
PTEN-INDUCED PUTATIVE KINASE 1; PINK1

ENSEMBL PROTEIN ID
ENSP00000364204

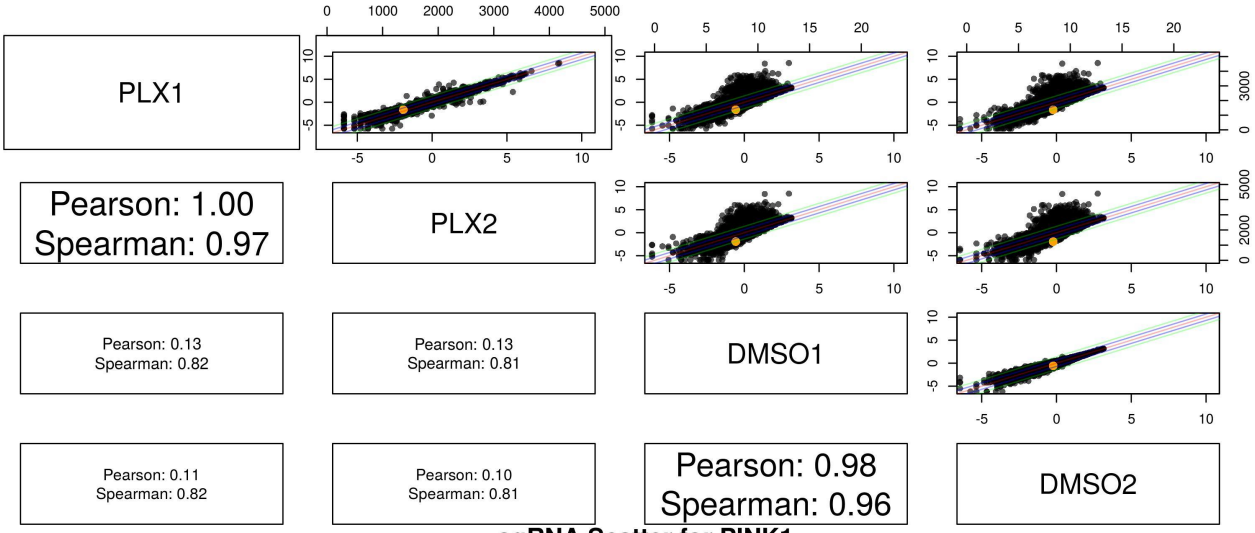
PROTEIN FAMILY DESCRIPTION
SERINE/THREONINE KINASE MITOCHONDRIAL PRECURSOR EC_2.7.11.1 PTEN INDUCED KINASE 1

Wilcox p-value: 0.414337

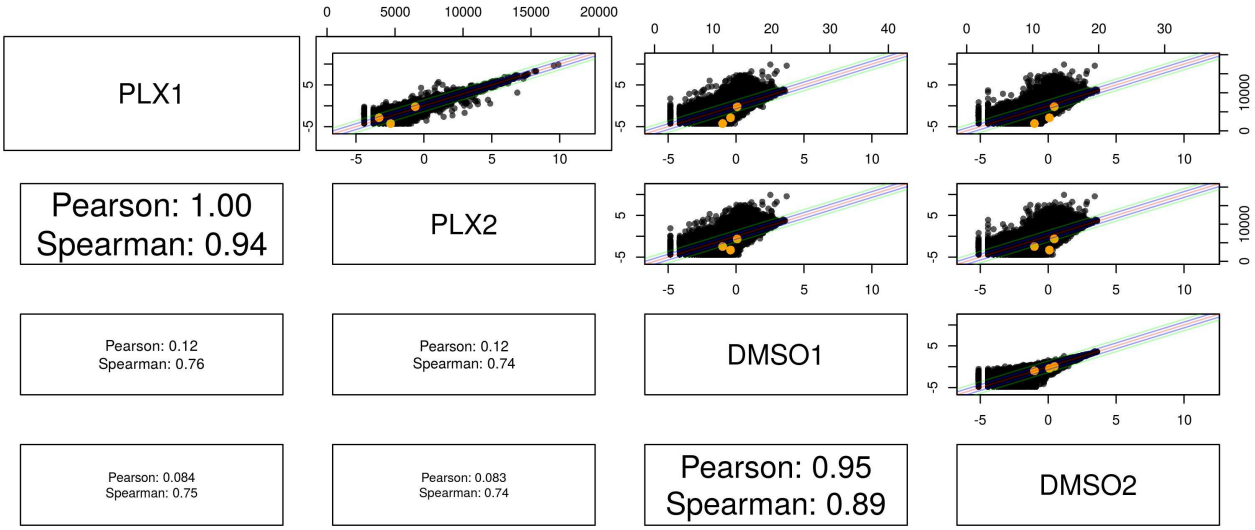
DESeq2 p-value: 1.41351e-05

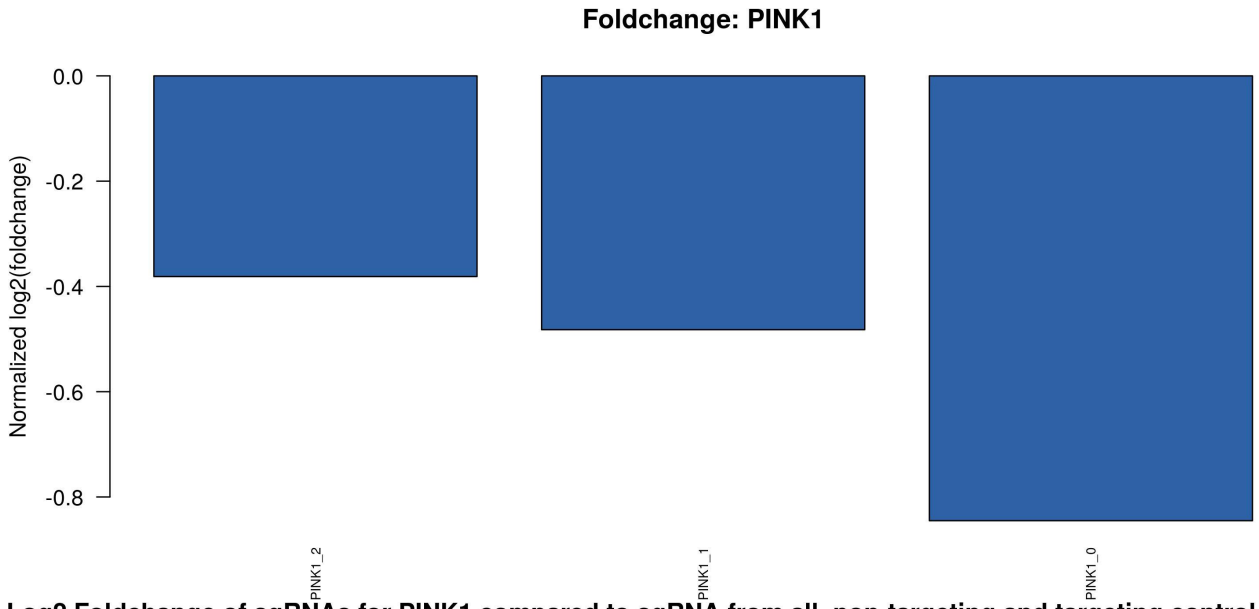
MAGeCK p-value: 0.745409

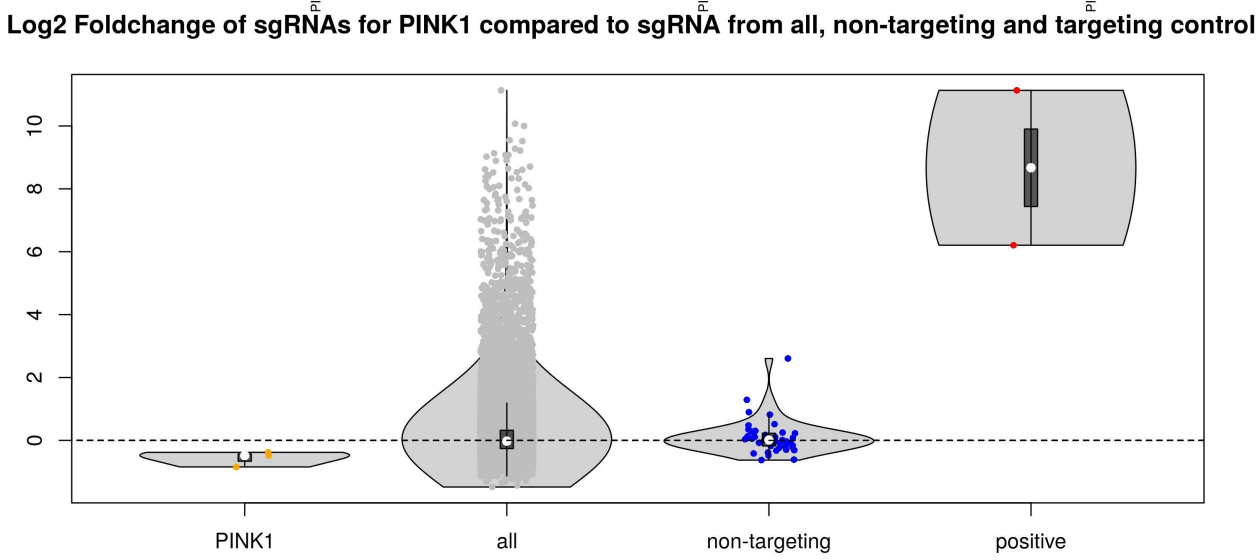
Gene Scatter for PINK1
PLX_resistance_YTAR



sgRNA Scatter for PINK1
PLX_resistance_YTAR




Foldchange: PINK1
Normalized log2(foldchange)
0.0
-0.2
-0.4
-0.6
-0.8
PINK1_2
PINK1_1
PINK1_0


Log2 Foldchange of sgRNAs for PINK1 compared to sgRNA from all, non-targeting and targeting control
0
2
4
6
8
10
PINK1
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
3	PINK1_2	PINK1	none	-0.3812529
2	PINK1_1	PINK1	none	-0.4821957
1	PINK1_0	PINK1	none	-0.8450779

SLC2A14

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

ENSEMBL ID (links to Ensembl) ENSG00000173262

HGNC SYMBOL (links to GeneCards) SLC2A14

GENE DESCRIPTION
solute carrier family 2 (facilitated glucose transporter), member 14 [Source:HGNC Symbol;Acc:HGNC:18301]

GO TERM
substrate-specific transmembrane transporter activity

MIM GENE DESCRIPTION
SOLUTE CARRIER FAMILY 2 (FACILITATED GLUCOSE TRANSPORTER), MEMBER14; SLC2A14;;GLUCOSE TRANSPORTER 14; GLUT14

ENSEMBL PROTEIN ID
ENSP00000482927

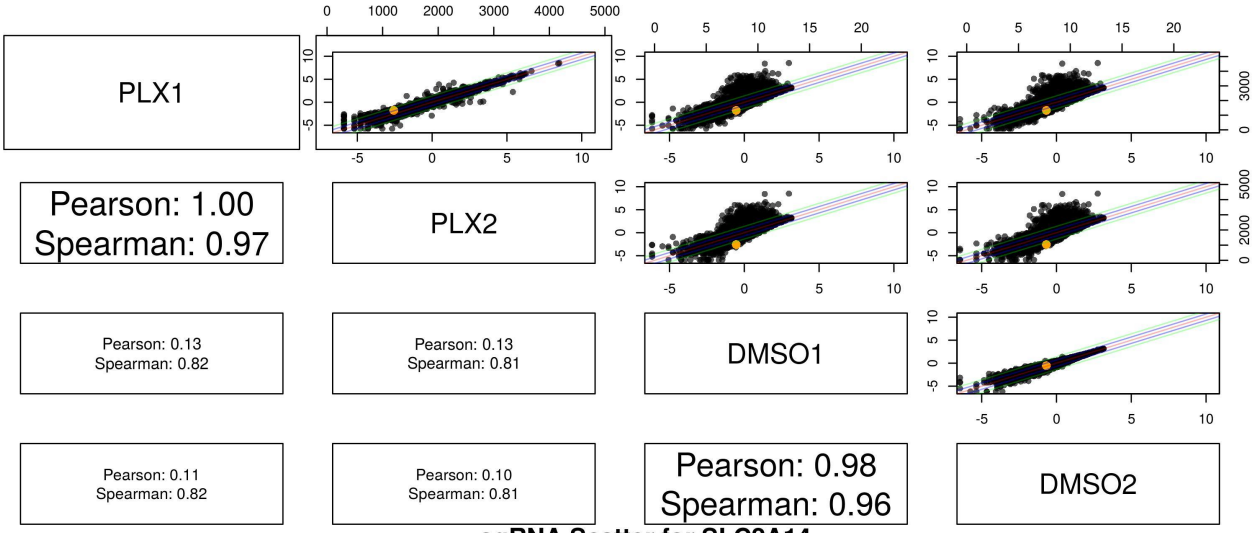
PROTEIN FAMILY DESCRIPTION
SOLUTE CARRIER FAMILY 2 FACILITATED GLUCOSE TRANSPORTER MEMBER GLUCOSE TRANSPORTER TYPE GLUT

Wilcox p-value: 0.4590367

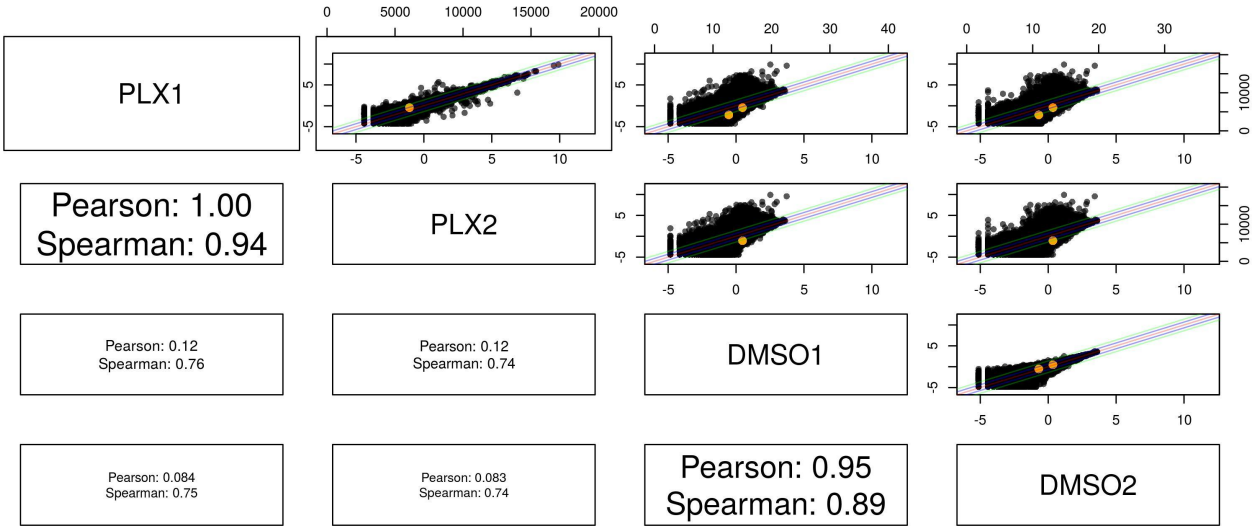
DESeq2 p-value: 0.0001266966

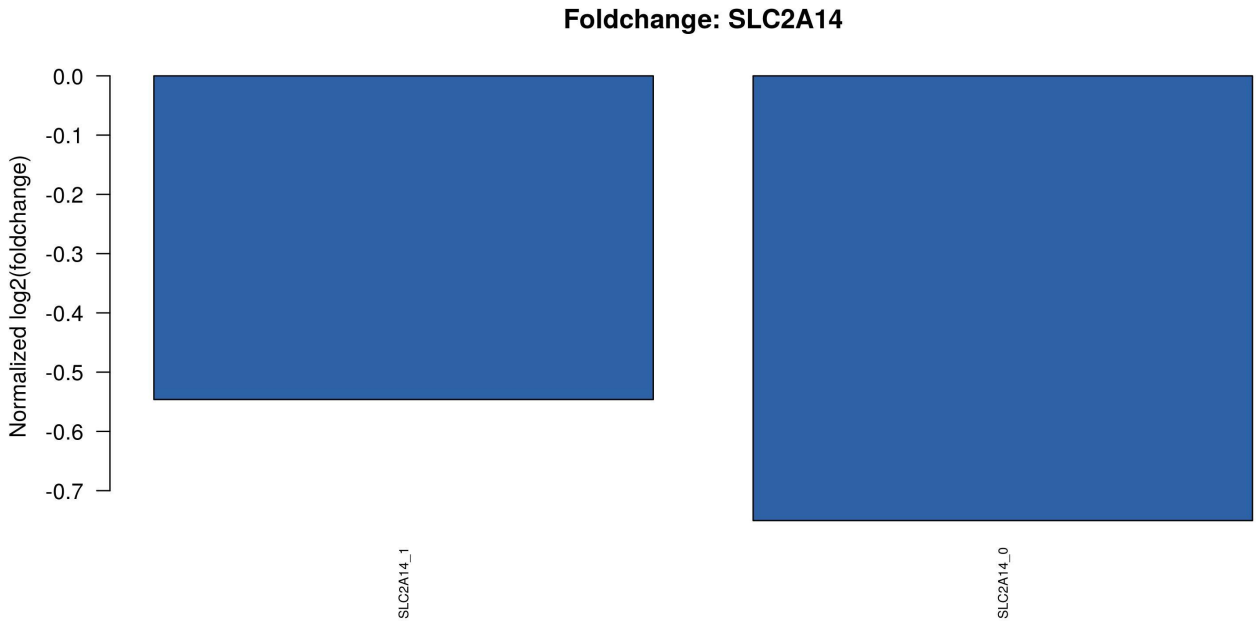
MAGeCK p-value: 0.745409

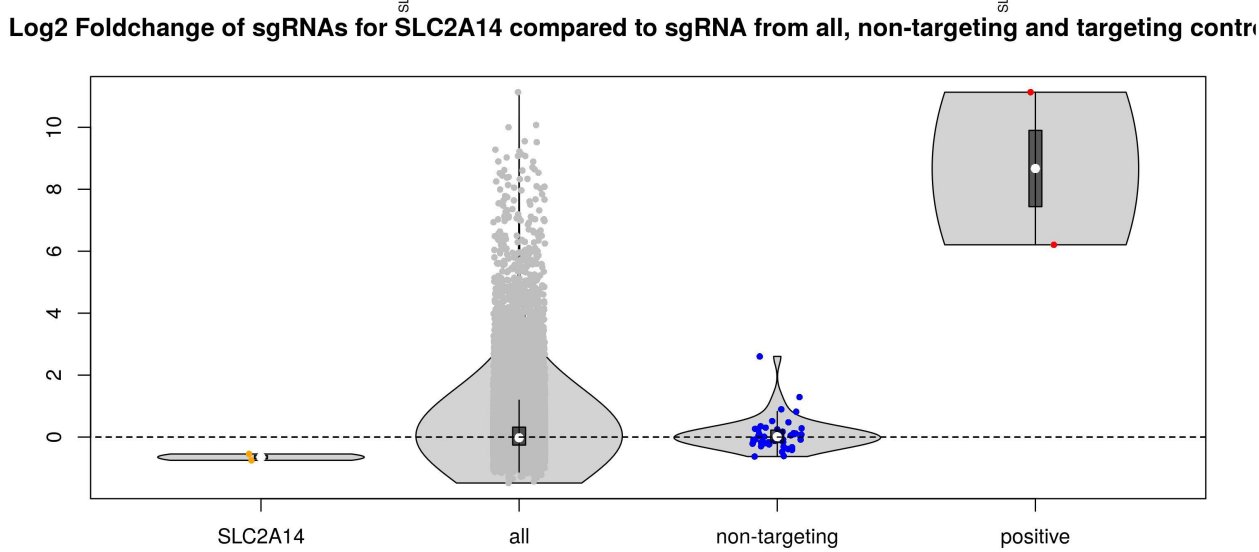
Gene Scatter for SLC2A14
PLX_resistance_YTAR



sgRNA Scatter for SLC2A14
PLX_resistance_YTAR




Foldchange: SLC2A14
Normalized log2(foldchange)
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
-0.6
-0.7
SLC2A14_1
SLC2A14_0


Log2 Foldchange of sgRNAs for SLC2A14 compared to sgRNA from all, non-targeting and targeting contr
0
2
4
6
8
10
SLC2A14
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
2	SLC2A14_1	SLC2A14	none	-0.5461761
1	SLC2A14_0	SLC2A14	none	-0.7504819

OR10J5

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

ENSEMBL ID (links to Ensembl) ENSG00000184155

HGNC SYMBOL (links to GeneCards) OR10J5

GENE DESCRIPTION
olfactory receptor, family 10, subfamily J, member 5 [Source:HGNC Symbol;Acc:HGNC:14993]

GO TERM
neurological system process

MIM GENE DESCRIPTION

ENSEMBL PROTEIN ID
ENSP00000334441

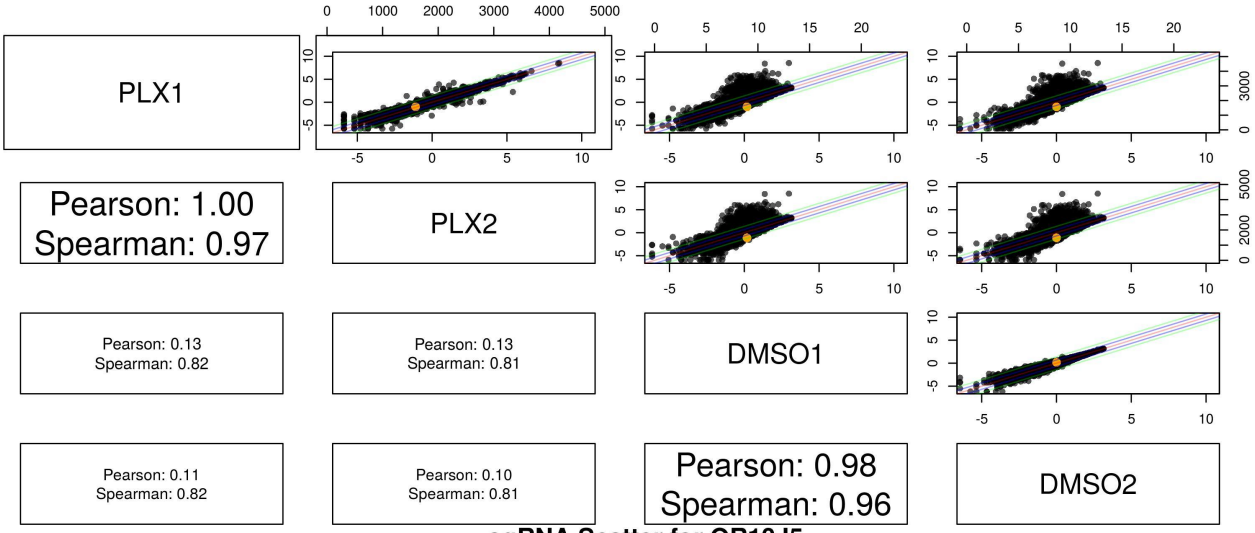
PROTEIN FAMILY DESCRIPTION
OLFACTORY RECEPTOR OLFACTORY RECEPTOR OR1

Wilcox p-value: 0.3250154

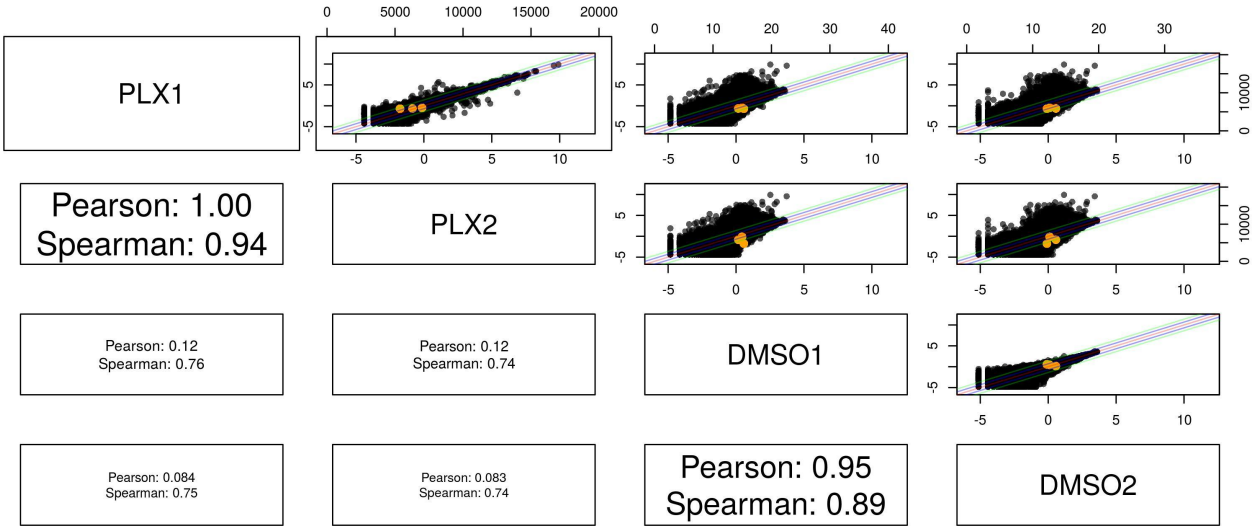
DESeq2 p-value: 1.512796e-05

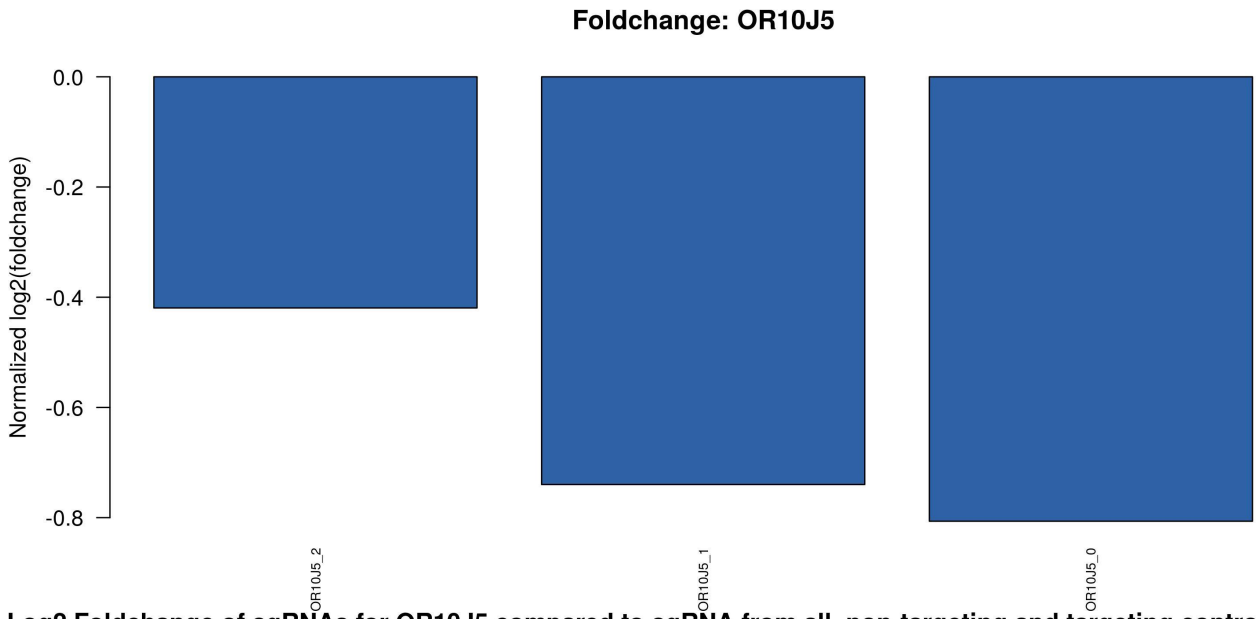
MAGeCK p-value: 0.745409

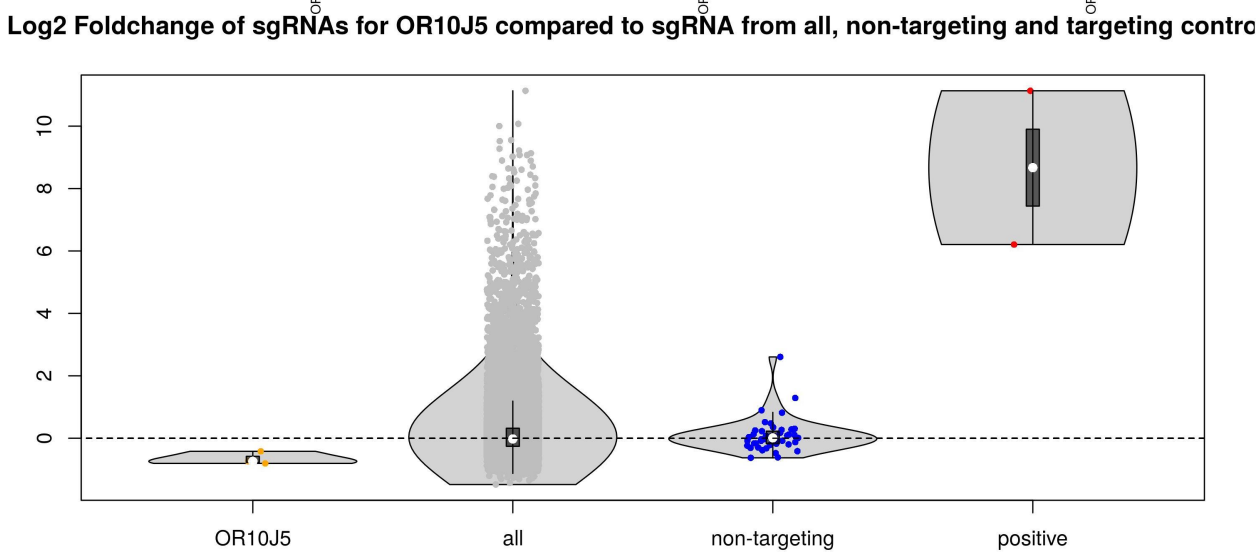
Gene Scatter for OR10J5
PLX_resistance_YTAR



sgRNA Scatter for OR10J5
PLX_resistance_YTAR




Foldchange: OR10J5
Normalized log2(foldchange)
0.0
-0.2
-0.4
-0.6
-0.8
OR10J5_2
OR10J5_1
OR10J5_0


Log2 Foldchange of sgRNAs for OR10J5 compared to sgRNA from all, non-targeting and targeting contro
0
2
4
6
8
10
OR10J5
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
3	OR10J5_2	OR10J5	none	-0.4194360
2	OR10J5_1	OR10J5	none	-0.7398846
1	OR10J5_0	OR10J5	none	-0.8064707

MS4A6E

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

ENSEMBL ID (links to Ensembl) ENSG00000166926

HGNC SYMBOL (links to GeneCards) MS4A6E

GENE DESCRIPTION
membrane-spanning 4-domains, subfamily A, member 6E [Source:HGNC Symbol;Acc:HGNC:14285]

GO TERM

MIM GENE DESCRIPTION
MEMBRANE-SPANNING 4-DOMAINS, SUBFAMILY A, MEMBER 6E; MS4A6E

ENSEMBL PROTEIN ID
ENSP00000436675

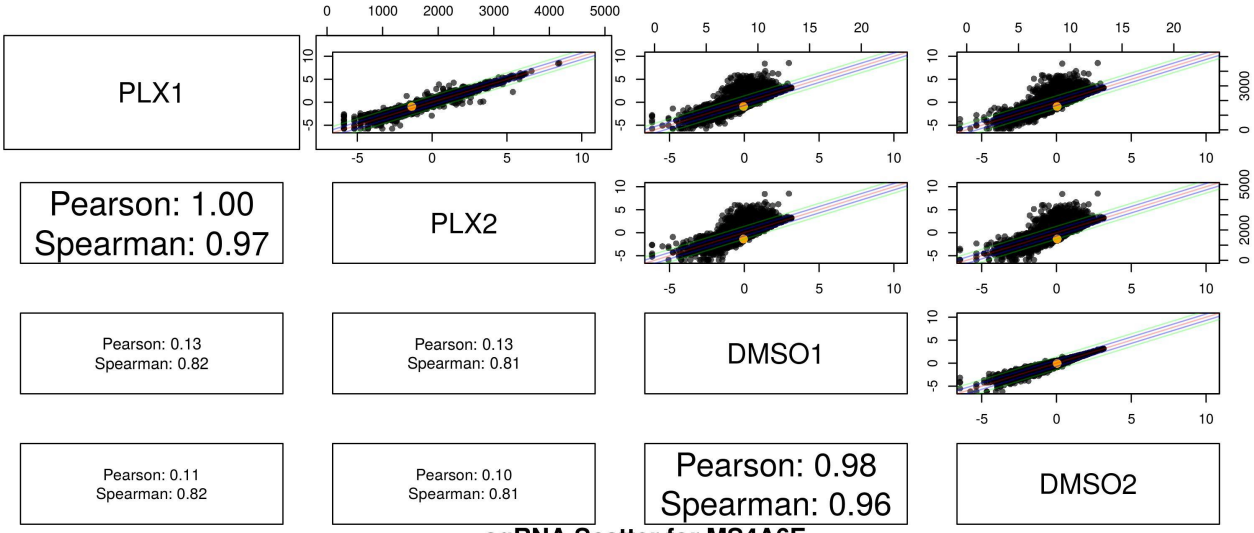
PROTEIN FAMILY DESCRIPTION
UNKNOWN

Wilcox p-value: 0.3250154

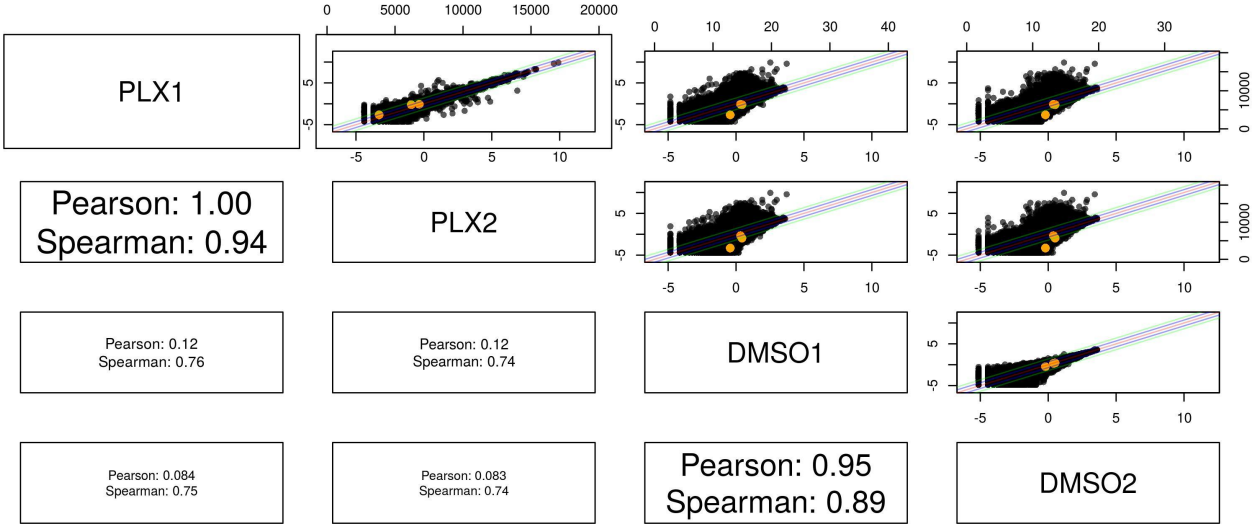
DESeq2 p-value: 0.002217052

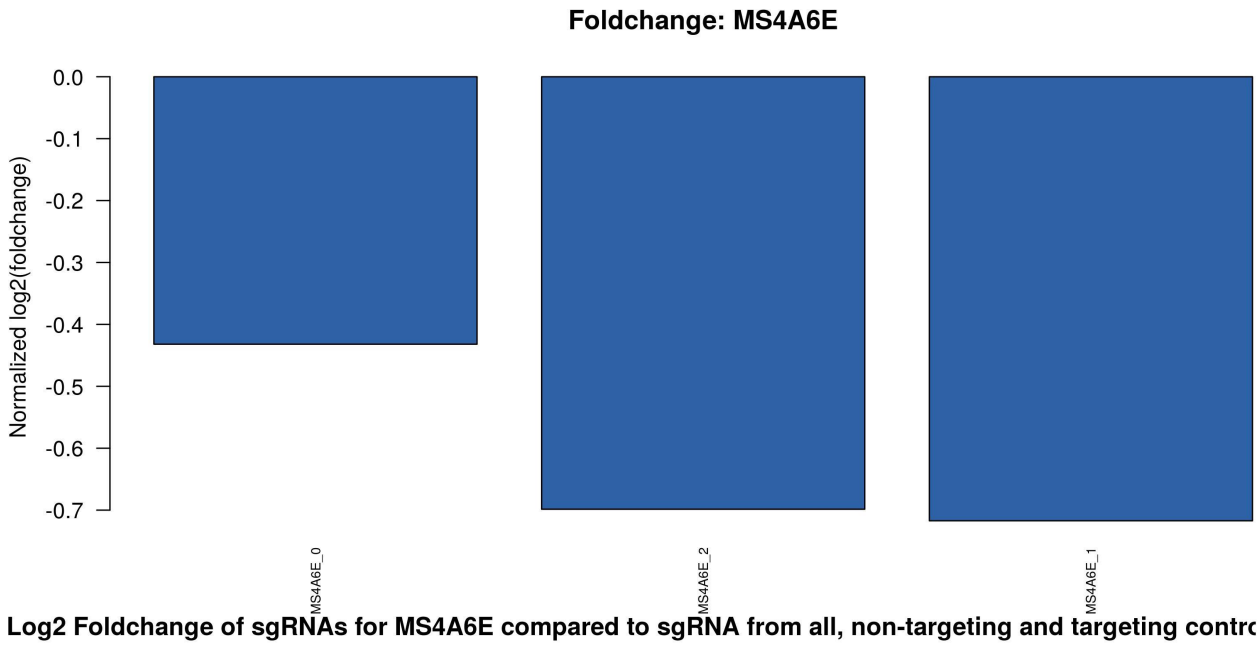
MAGeCK p-value: 0.745409

Gene Scatter for MS4A6E
PLX_resistance_YTAR

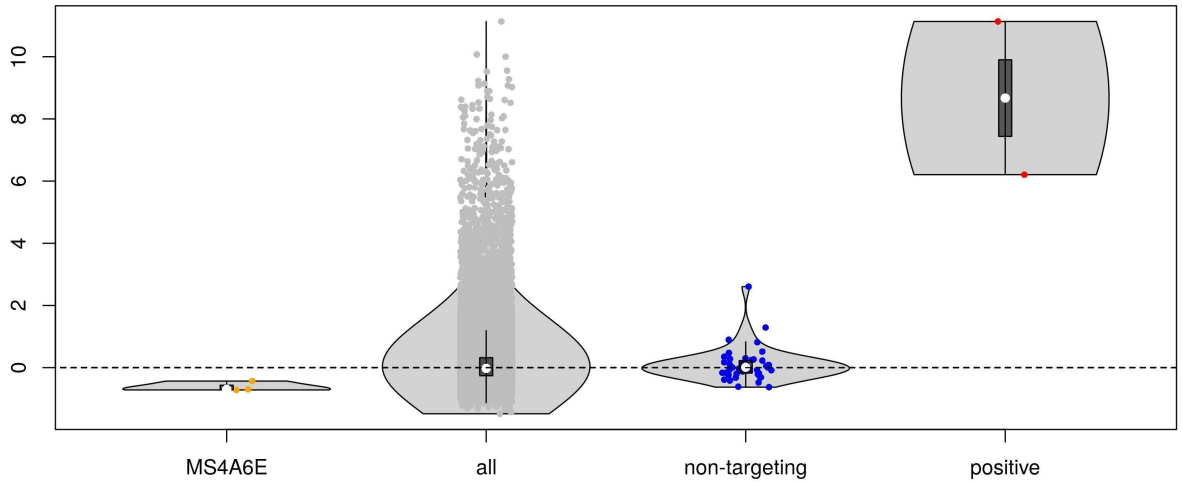


sgRNA Scatter for MS4A6E
PLX_resistance_YTAR





Log2 Foldchange of sgRNAs for MS4A6E compared to sgRNA from all, non-targeting and targeting contro



	designs	genes	sequence	log2Foldchange
1	MS4A6E_0	MS4A6E	none	-0.4319936
3	MS4A6E_2	MS4A6E	none	-0.6985418
2	MS4A6E_1	MS4A6E	none	-0.7171905

TRIM35

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

ENSEMBL ID (links to Ensembl) ENSG00000104228

HGNC SYMBOL (links to GeneCards) TRIM35

GENE DESCRIPTION
tripartite motif containing 35 [Source:HGNC Symbol;Acc:HGNC:16285]

GO TERM
metal ion binding

MIM GENE DESCRIPTION

ENSEMBL PROTEIN ID
ENSP00000428770

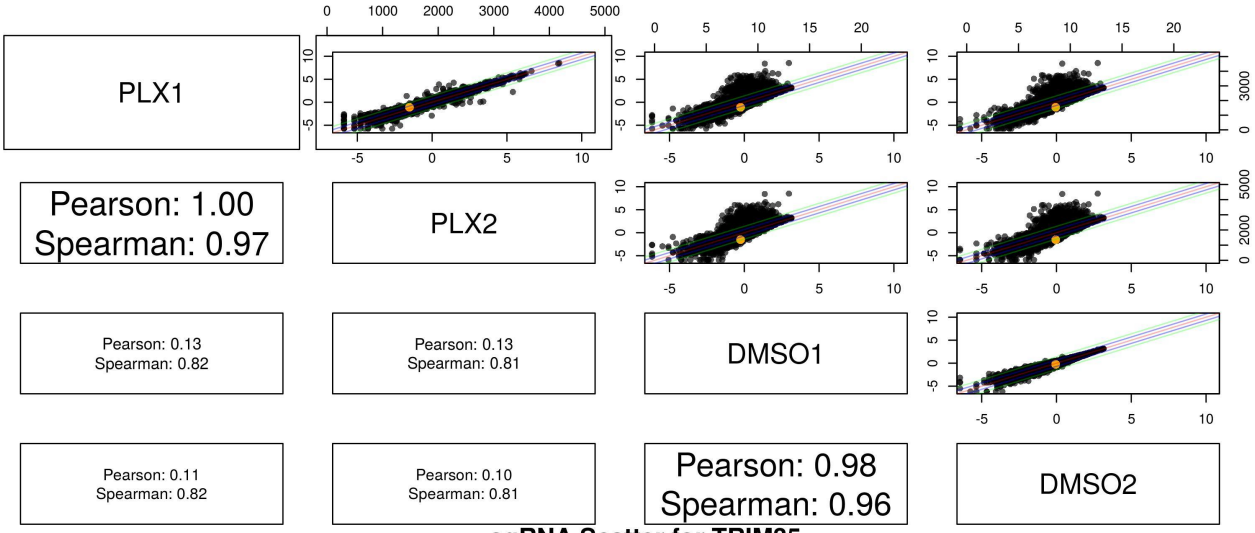
PROTEIN FAMILY DESCRIPTION
TRIPARTITE MOTIF CONTAINING 35 HEMOPOIETIC LINEAGE SWITCH 5

Wilcox p-value: 0.3482308

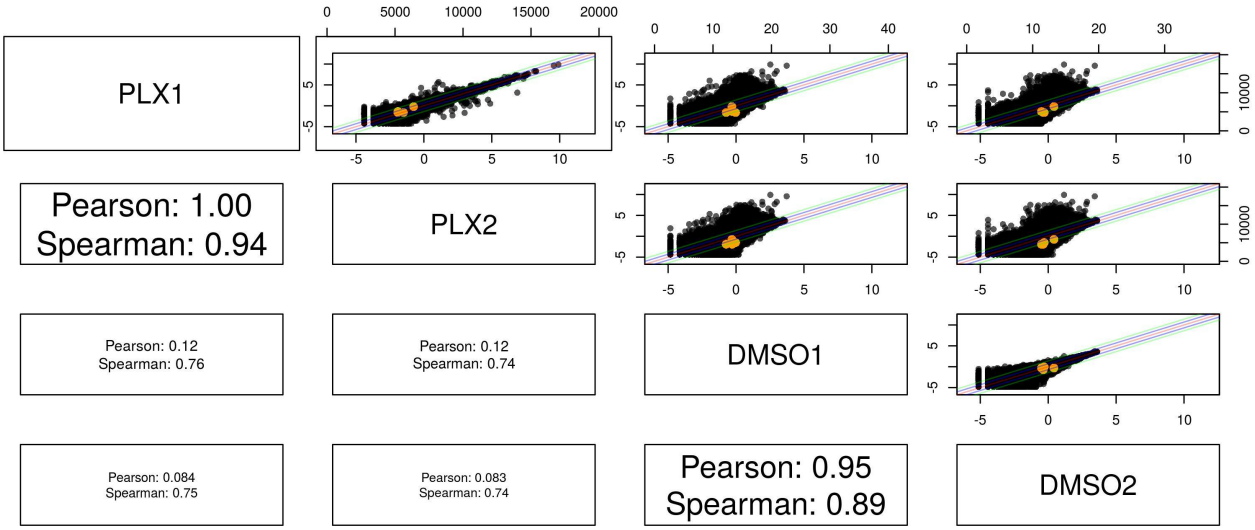
DESeq2 p-value: 0.00208696

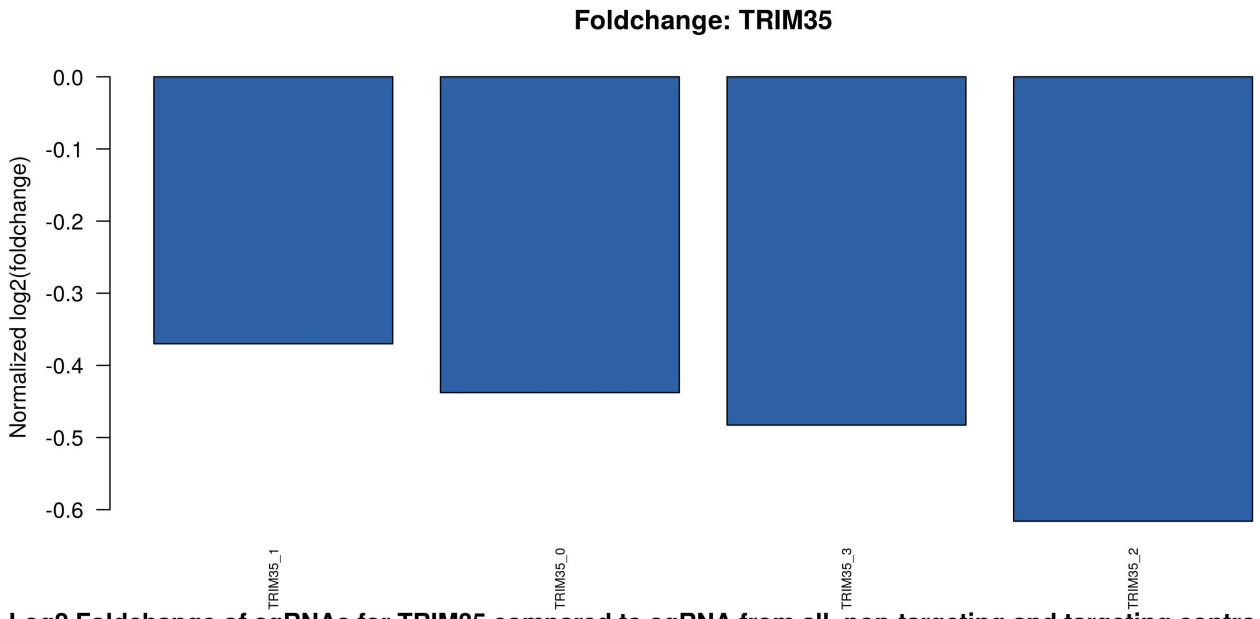
MAGeCK p-value: 0.745409

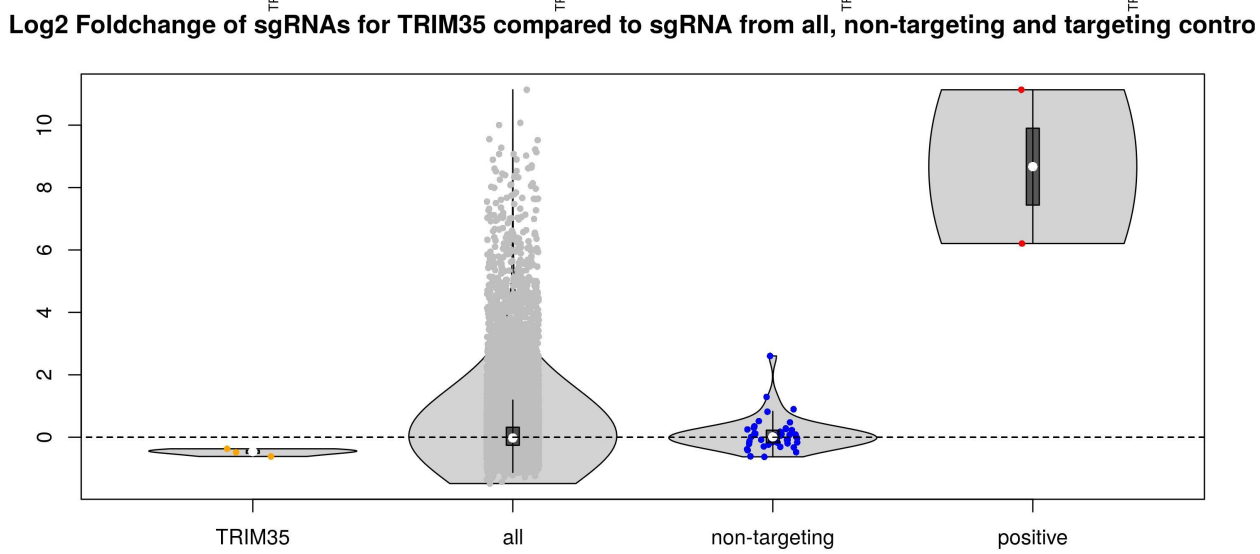
Gene Scatter for TRIM35
PLX_resistance_YTAR



sgRNA Scatter for TRIM35
PLX_resistance_YTAR




Foldchange: TRIM35
Normalized log2(foldchange)
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
-0.6
TRIM35_1
TRIM35_0
TRIM35_3
TRIM35_2


Log2 Foldchange of sgRNAs for TRIM35 compared to sgRNA from all, non-targeting and targeting contro
0
2
4
6
8
10
TRIM35
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
2	TRIM35_1	TRIM35	none	-0.3700350
1	TRIM35_0	TRIM35	none	-0.4377554
4	TRIM35_3	TRIM35	none	-0.4827268
3	TRIM35_2	TRIM35	none	-0.6159827

ODF4

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

ENSEMBL ID (links to Ensembl) ENSG00000184650

HGNC SYMBOL (links to GeneCards) ODF4

GENE DESCRIPTION
outer dense fiber of sperm tails 4 [Source:HGNC Symbol;Acc:HGNC:19056]

GO TERM

MIM GENE DESCRIPTION
OUTER DENSE FIBER OF SPERM TAILS 4; ODF4;;OPPO1

ENSEMBL PROTEIN ID
ENSP00000461942

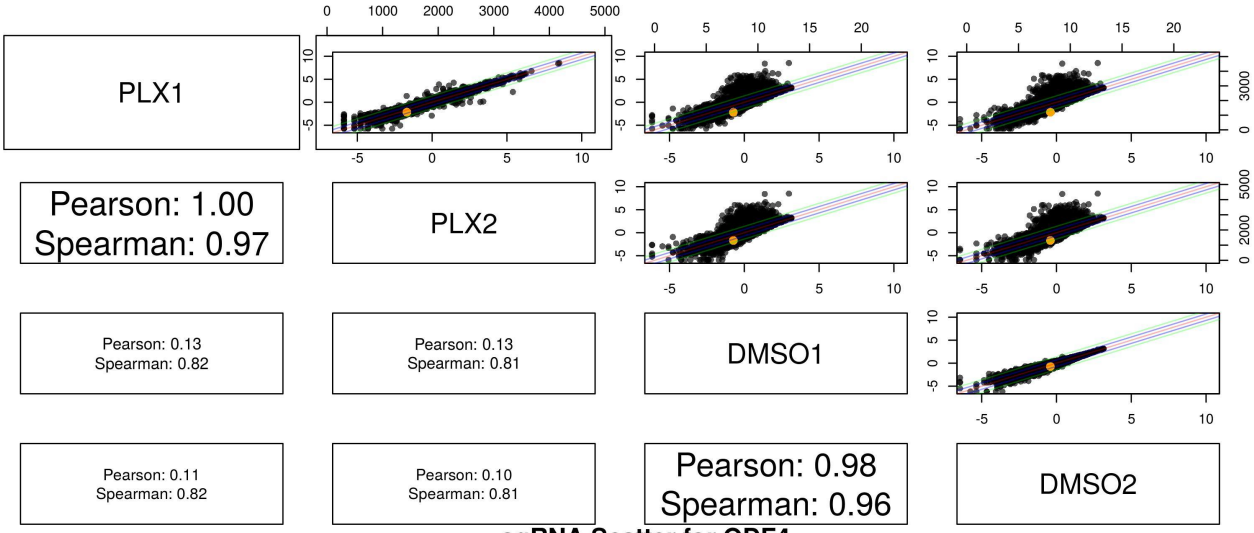
PROTEIN FAMILY DESCRIPTION
OUTER DENSE FIBER 4 OUTER DENSE FIBER OF SPERM TAILS 4 TESTIS SPECIFIC OPPO 1

Wilcox p-value: 0.414337

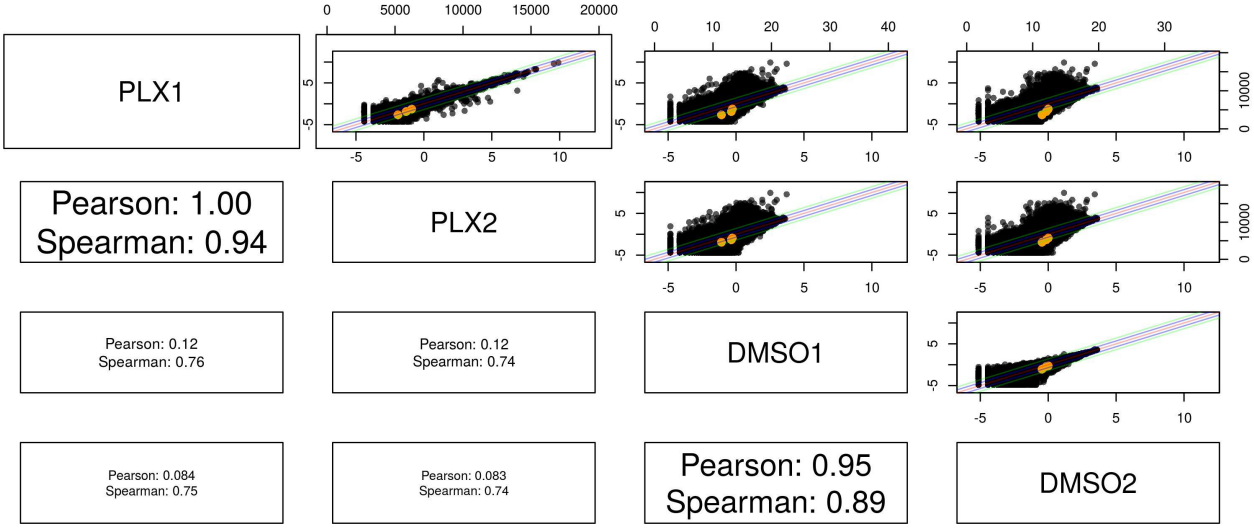
DESeq2 p-value: 0.0003245726

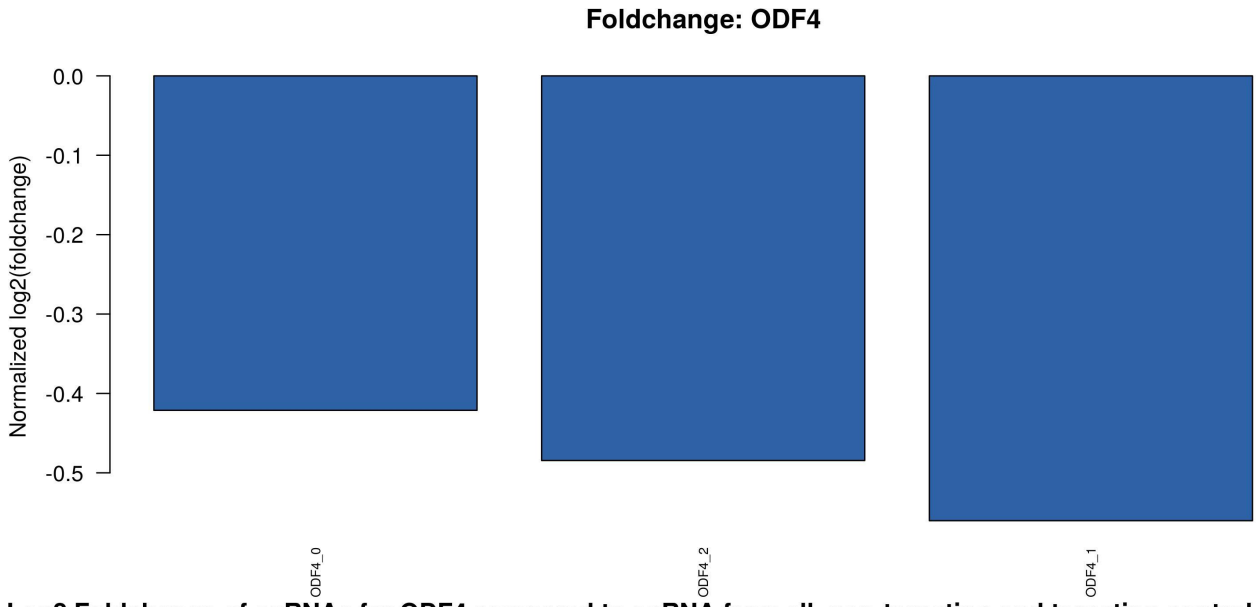
MAGeCK p-value: 0.758559

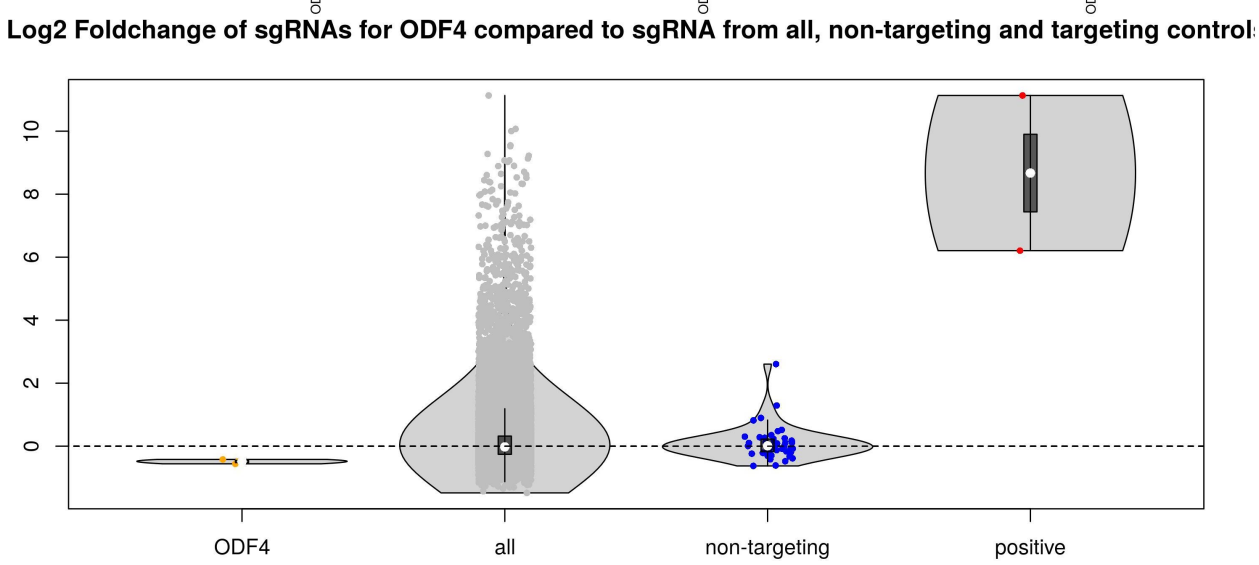
Gene Scatter for ODF4
PLX_resistance_YTAR



sgRNA Scatter for ODF4
PLX_resistance_YTAR




Foldchange: ODF4
Normalized log2(foldchange)
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
ODF4_0
ODF4_2
ODF4_1


Log2 Foldchange of sgRNAs for ODF4 compared to sgRNA from all, non-targeting and targeting controls
0
2
4
6
8
10
ODF4
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
1	ODF4_0	ODF4	none	-0.4212574
3	ODF4_2	ODF4	none	-0.4844648
2	ODF4_1	ODF4	none	-0.5602905

LRRC16B

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

ENSEMBL ID (links to Ensembl) ENSG00000186648

HGNC SYMBOL (links to GeneCards) LRRC16B

GENE DESCRIPTION
leucine rich repeat containing 16B [Source:HGNC Symbol;Acc:HGNC:20272]

GO TERM
cell

MIM GENE DESCRIPTION
LEUCINE-RICH REPEAT-CONTAINING PROTEIN 16B; LRRC16B

ENSEMBL PROTEIN ID
ENSP00000340467

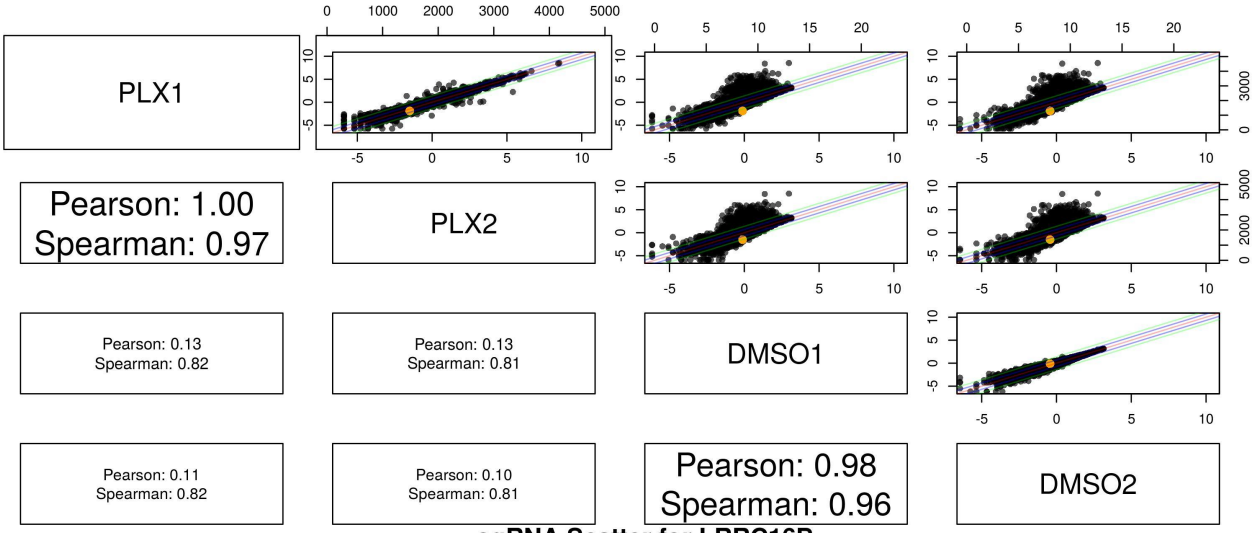
PROTEIN FAMILY DESCRIPTION
LEUCINE RICH REPEAT CONTAINING

Wilcox p-value: 0.484305

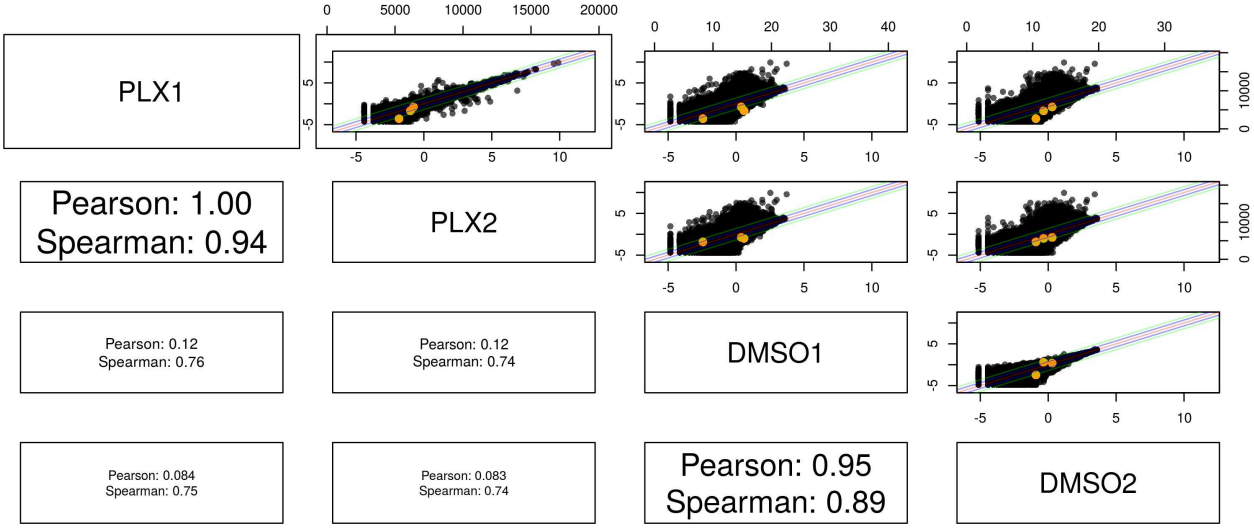
DESeq2 p-value: 7.505609e-06

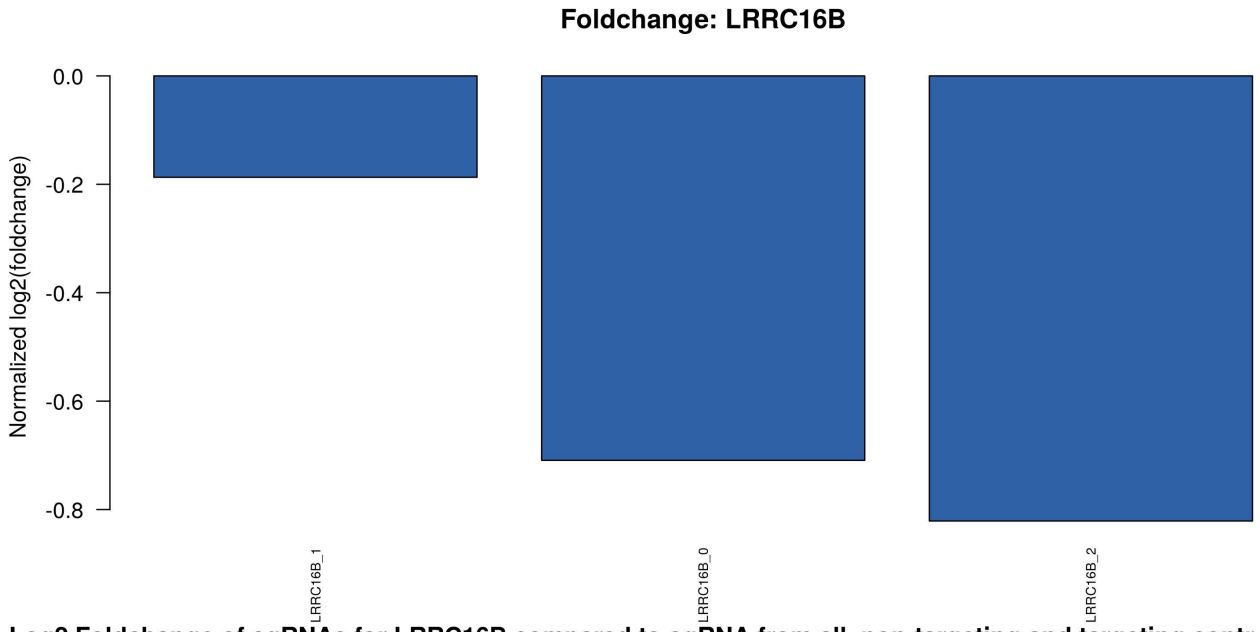
MAGeCK p-value: 0.783598

Gene Scatter for LRRC16B
PLX_resistance_YTAR

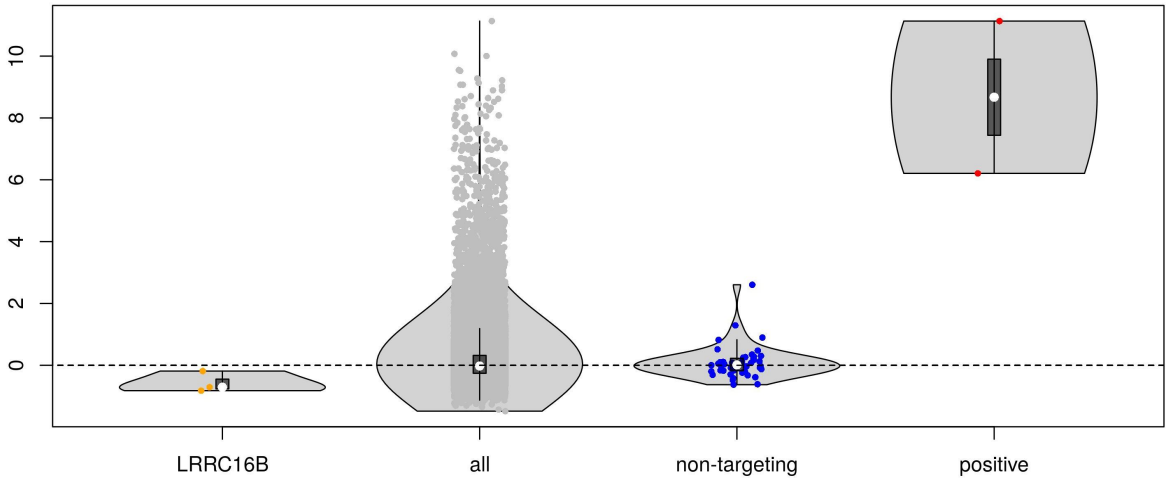


sgRNA Scatter for LRRC16B
PLX_resistance_YTAR





Log2 Foldchange of sgRNAs for LRRC16B compared to sgRNA from all, non-targeting and targeting contr



	designs	genes	sequence	log2Foldchange
2	LRRC16B_1	LRRC16B	none	-0.1870259
1	LRRC16B_0	LRRC16B	none	-0.7092057
3	LRRC16B_2	LRRC16B	none	-0.8210693

KLF5

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

ENSEMBL ID (links to Ensembl) ENSG00000102554

HGNC SYMBOL (links to GeneCards) KLF5

GENE DESCRIPTION
Kruppel-like factor 5 (intestinal) [Source:HGNC Symbol;Acc:HGNC:6349]

GO TERM
ion binding

MIM GENE DESCRIPTION
KRUPPEL-LIKE FACTOR 5; KLF5;;BASIC TRANSCRIPTION ELEMENT-BINDING PROTEIN 2; BTEB2

ENSEMBL PROTEIN ID
ENSP00000440407

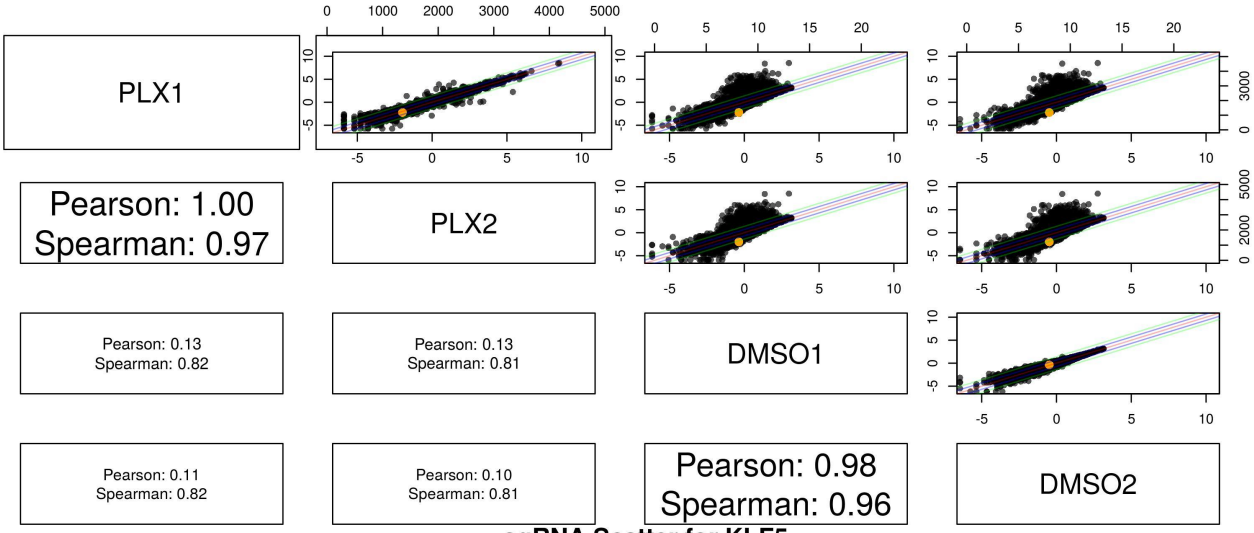
PROTEIN FAMILY DESCRIPTION
KRUEPPEL FACTOR 5 BASIC TRANSCRIPTION ELEMENT BINDING 2 BTE BINDING 2 INTESTINAL ENRICHED KRUEPPEL FACTOR TRANSCRIPTION FACTOR BTEB2

Wilcox p-value: 0.414337

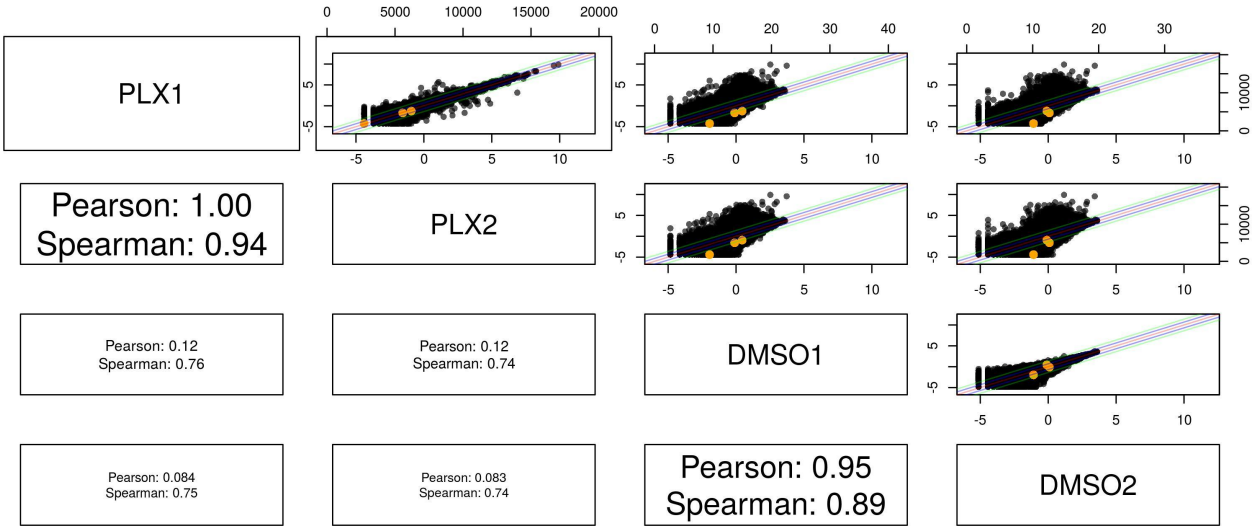
DESeq2 p-value: 1.665172e-11

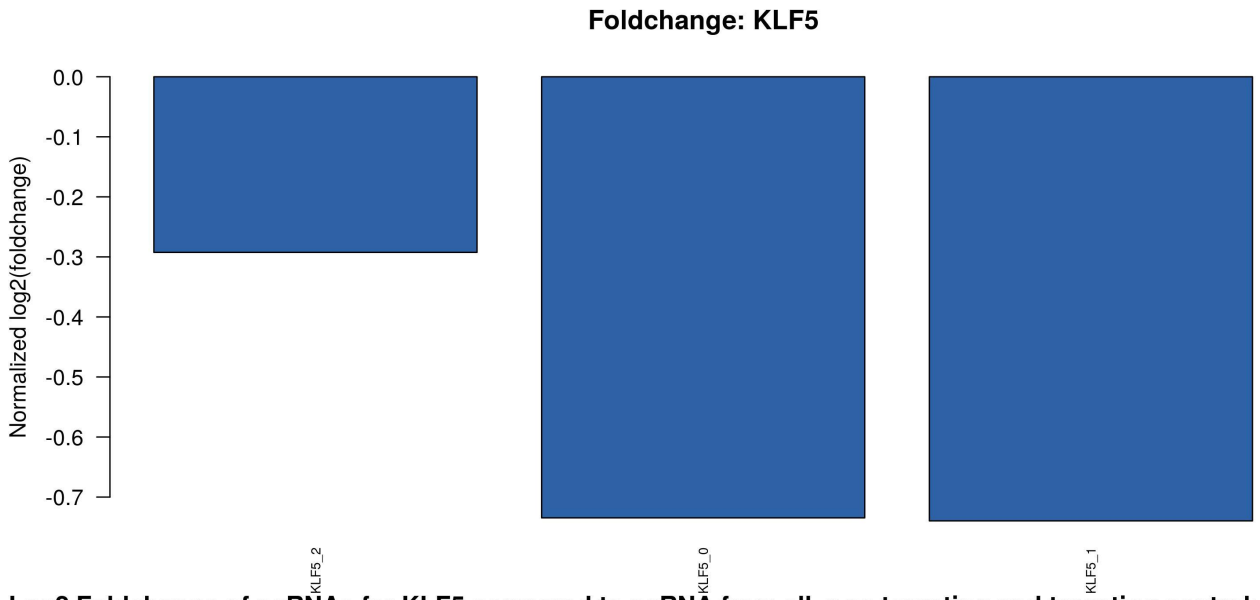
MAGeCK p-value: 0.783598

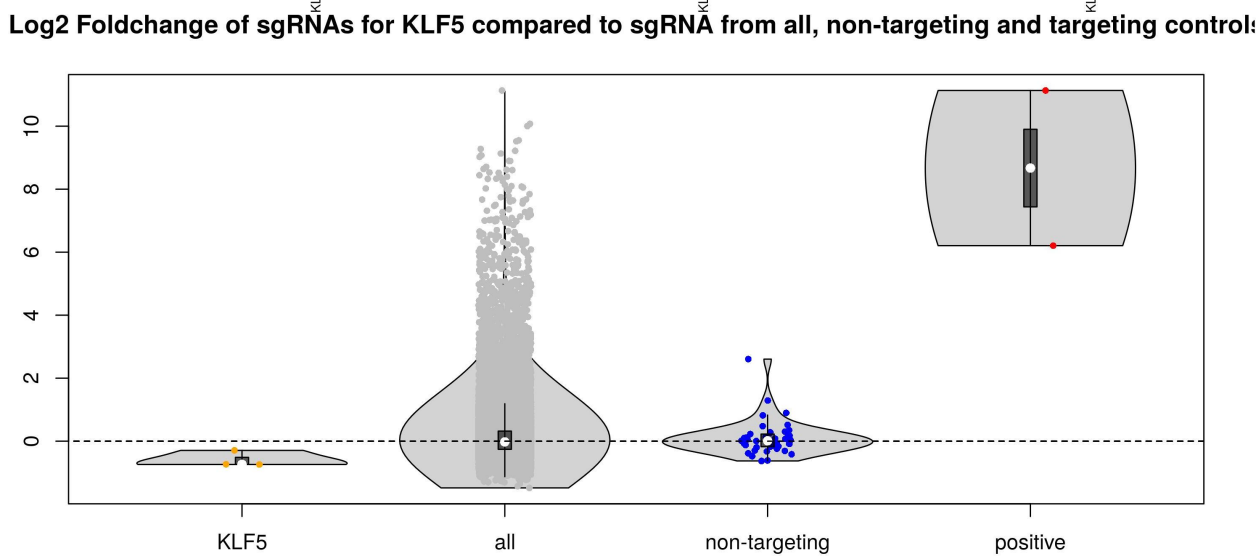
Gene Scatter for KLF5
PLX_resistance_YTAR



sgRNA Scatter for KLF5
PLX_resistance_YTAR




Foldchange: KLF5
Normalized log2(foldchange)
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
-0.6
-0.7
KLF5_2
KLF5_0
KLF5_1


Log2 Foldchange of sgRNAs for KLF5 compared to sgRNA from all, non-targeting and targeting controls
0
2
4
6
8
10
KLF5
all
non-targeting
positive

	designs	genes	sequence	log2Foldchange
3	KLF5_2	KLF5	none	-0.2925024
1	KLF5_0	KLF5	none	-0.7346004
2	KLF5_1	KLF5	none	-0.7396207

LHCGR

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

ENSEMBL ID (links to Ensembl) ENSG00000138039

HGNC SYMBOL (links to GeneCards) LHCGR

GENE DESCRIPTION
luteinizing hormone/choriogonadotropin receptor [Source:HGNC Symbol;Acc:HGNC:6585]

GO TERM
biological_process

MIM GENE DESCRIPTION
LUTEINIZING HORMONE/CHORIOGONADOTROPIN RECEPTOR; LHCGR;;LUTROPIN-CHORIOGONADOTROPIN RECEPTOR; LCGR;;LUTEINIZING HORMONE RECEPTOR; LHR;;GONADOTROPIN RECEPTOR

ENSEMBL PROTEIN ID
ENSP00000403748

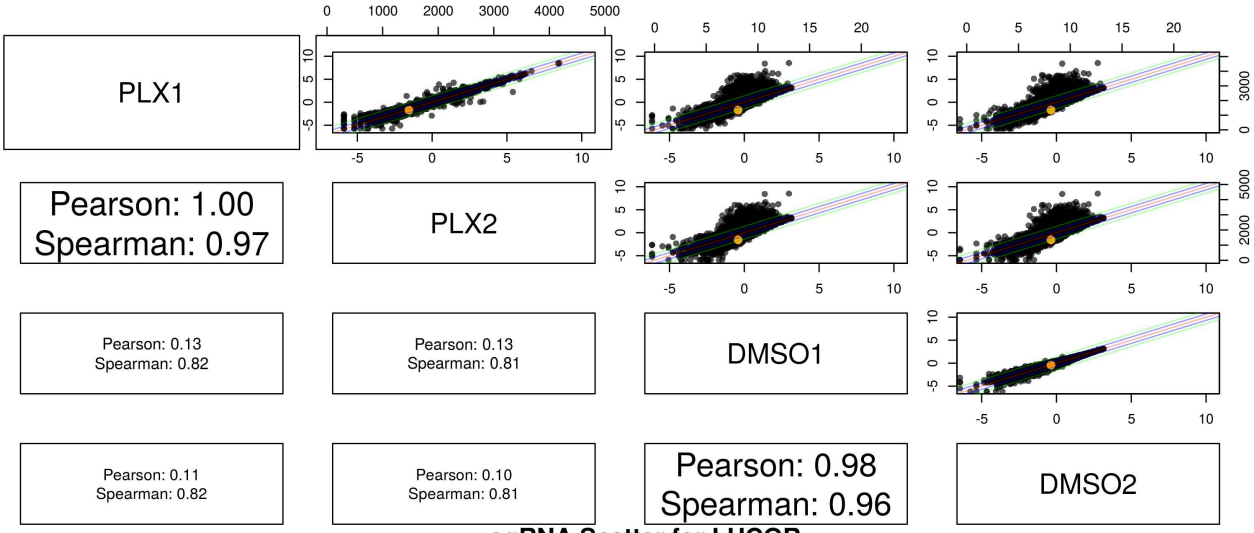
PROTEIN FAMILY DESCRIPTION
FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR FSH R FOLLITROPIN RECEPTOR

Wilcox p-value: 0.4411848

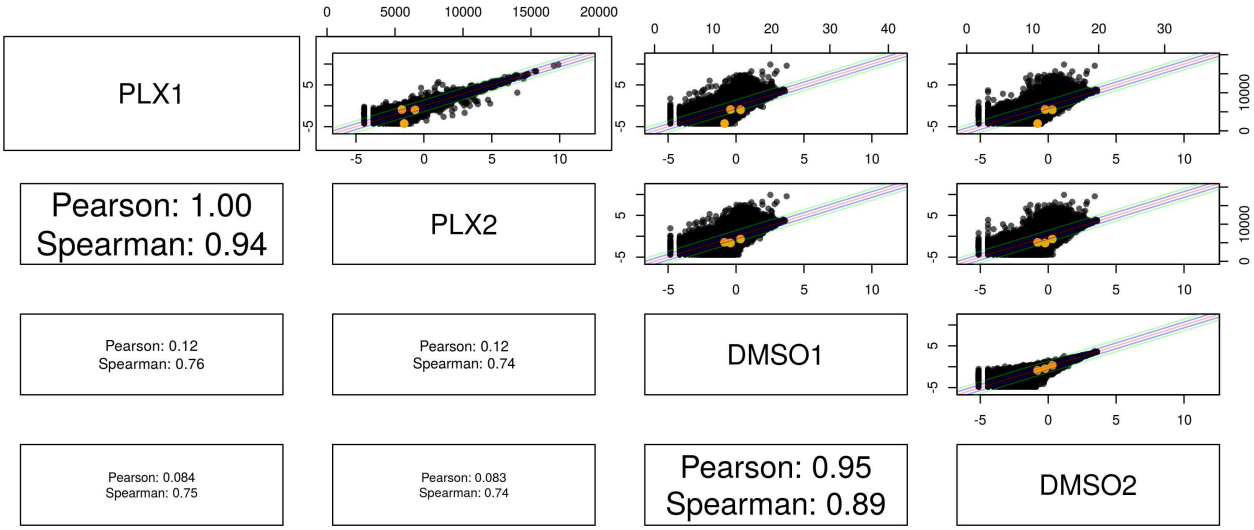
DESeq2 p-value: 2.272601e-06

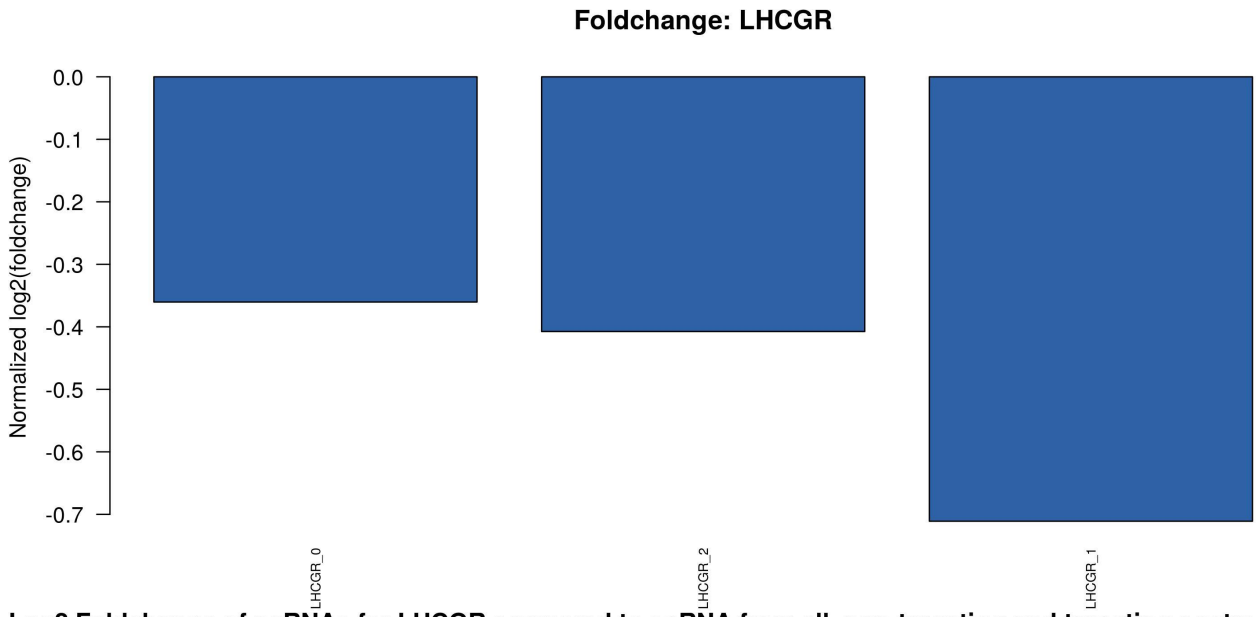
MAGeCK p-value: 0.814566

Gene Scatter for LHCGR
PLX_resistance_YTAR

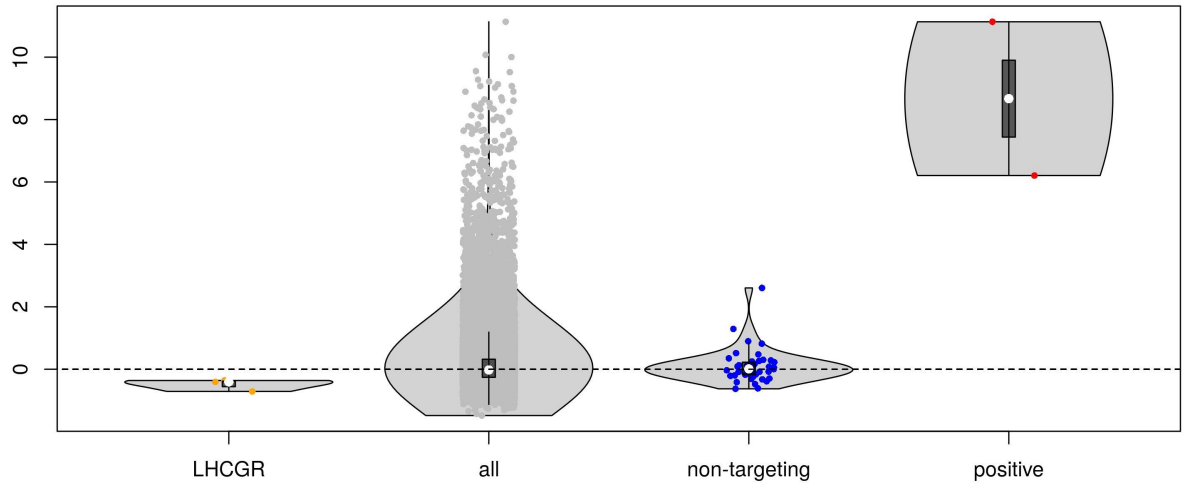


sgRNA Scatter for LHCGR
PLX_resistance_YTAR





Log2 Foldchange of sgRNAs for LHCGR compared to sgRNA from all, non-targeting and targeting contro



	designs	genes	sequence	log2Foldchange
1	LHCGR_0	LHCGR	none	-0.3603338
3	LHCGR_2	LHCGR	none	-0.4075043
2	LHCGR_1	LHCGR	none	-0.7109752

Compare Analysis

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

Enriched

List

Moreover, the **1 % top enriched hits** sorted according to **MAGeCK** are stored in **PLX_resistance_YTAR-COMPARE-HITS.xls** and are listed below:

	wilcox.log2fc	wilcox.pval	deseq.log2fc	deseq.pval	mageck.fdr	mageck.rank
MED12	7.1318648	0.0568540	7.5603379	0.0000000	0.002475	1
NF2	8.1403500	0.0568540	7.9366444	0.0000000	0.002475	2
CUL3	7.1435419	0.4590367	7.1042049	0.0000000	0.003300	3
DPH2	2.2739036	0.0568540	2.8168447	0.0000000	0.006188	4
TADA2B	4.4644271	0.2321539	5.1588768	0.0000000	0.006931	5
MED15	2.9780590	0.0852810	3.1675092	0.0000000	0.007426	6
CCDC101	3.7712876	0.2824934	5.0119241	0.0000000	0.009194	7
NF1	10.1802432	0.3482308	9.7249469	0.0000000	0.012995	8
CDH13	2.0516206	0.1557131	1.9932574	0.0000000	0.016337	9
CLDN10	6.8599241	0.4963201	7.3508178	0.0000000	0.016337	10
TADA1	5.0239036	0.3482308	5.5310923	0.0000000	0.026553	11
CCNC	2.4829278	0.8536632	3.0556990	0.0000000	0.049917	12
ZNF592	1.7317067	0.2824934	1.8801157	0.0000000	0.058416	13
PPT1	2.5318443	0.2824934	2.2044450	0.0000000	0.058416	14
PGD	1.8450184	0.3482308	3.6819744	0.0000000	0.058416	15
ALG3	4.3838536	0.2824934	4.1808517	0.0000000	0.065285	16
ZEB2	0.9748570	0.2824934	1.4207483	0.0000033	0.096287	17
ABCB5	1.1589844	0.4843050	1.2844358	0.0002661	0.096287	18
PDCD10	2.2152091	0.3482308	2.4048646	0.0000000	0.096287	19
MLN	1.9355038	0.3250154	1.9896149	0.0000000	0.096287	20
BCL2L12	2.1745257	0.2321539	2.4801408	0.0000000	0.097885	21
SPECC1	5.7989788	0.9851504	5.9359653	0.0000000	0.097885	22
UBE2E1	1.0434741	0.2321539	1.2216479	0.0003325	0.149798	23
CBFB	1.4083304	0.2824934	1.7558247	0.0000001	0.149798	24
GADD45GIP1	2.6427736	0.3250154	4.1085520	0.0000000	0.149798	25
TAF6L	2.7867527	0.2824934	3.7892372	0.0000000	0.149798	26
RNF7	1.7623460	0.5782483	1.9607982	0.0000000	0.149798	27
C11orf49	8.0830338	0.2824934	7.5594127	0.0000000	0.192185	28
SMARCB1	2.5789350	0.2824934	3.1324580	0.0000000	0.207067	29
KANK2	1.1325848	0.2824934	1.2624675	0.0001627	0.218872	30
ACTA2	8.4200881	0.9998213	9.3382862	0.0000000	0.218872	31
NFASC	0.9056567	0.3250154	0.9741500	0.1910206	0.218872	32
KCTD10	2.2200052	0.3250154	2.8660368	0.0000000	0.218872	33
TAF5L	4.3017590	0.3482308	4.5979391	0.0000000	0.223791	34
BRD9	0.9985081	0.2824934	1.3405851	0.0000196	0.230976	35
PTPN12	1.6978185	0.3250154	2.5187053	0.0000000	0.244637	36
MED19	2.6455370	0.3250154	3.5285179	0.0000000	0.264915	37
SMG7	1.0145843	0.3482308	1.1290770	0.0025204	0.264915	38
EED	2.3933495	0.2824934	2.7612506	0.0000000	0.264915	39
BBX	1.7913449	0.3482308	1.9122616	0.0000000	0.278797	40
INA	1.6419942	0.2824934	2.0138229	0.0000000	0.278797	41
NRD1	1.5767411	0.5162010	1.6090256	0.0000000	0.279939	42

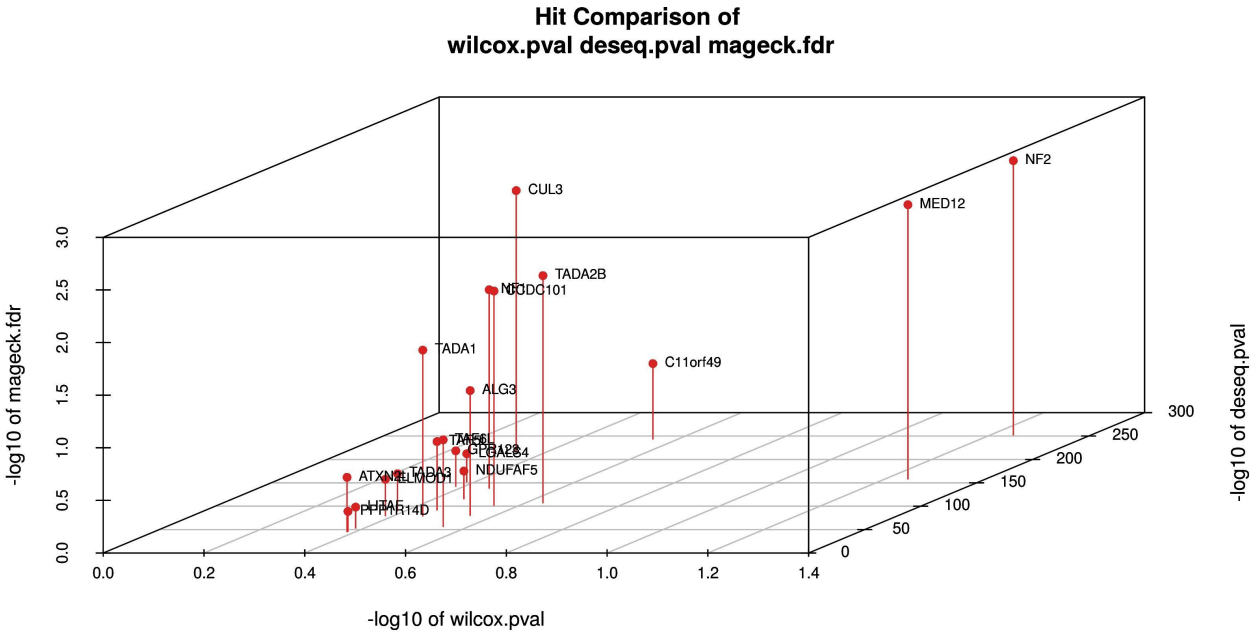
	wilcox.log2fc	wilcox.pval	deseq.log2fc	deseq.pval	mageck.fdr	mageck.rank
TAOK1	2.8448474	0.2824934	3.1383591	0.0000000	0.290928	43
ATXN2L	3.2995269	0.4143370	3.3687608	0.0000000	0.304343	44
MYO1E	8.0764183	0.9355996	8.5479780	0.0000000	0.310781	45
GNAS	1.2720449	0.5744013	1.5327123	0.0000000	0.315149	46
P4HB	6.1196206	0.8473385	6.8971987	0.0000000	0.315149	47
STT3A	7.9414200	0.5105479	9.0647551	0.0000000	0.315149	48
BIN1	0.9821178	0.5388553	1.0289756	0.1163987	0.315149	49
CCM2	0.9609132	0.5744013	0.8661121	1.0000000	0.315149	50
ZP1	7.5558757	0.9451159	8.5658821	0.0000000	0.334013	51
MFSD9	2.2961507	0.4590367	2.7200020	0.0000000	0.337871	52
TSPAN1	1.3031248	0.4143370	2.2933571	0.0000000	0.362395	53
NPPC	2.8751612	0.7555528	3.7260963	0.0000000	0.362395	54
PLXNC1	1.1215855	0.3482308	1.1854402	0.0005442	0.386934	55
CEMP1	8.0768989	0.6264892	7.9928450	0.0000000	0.386934	56
ZC3H18	1.5263169	0.3482308	2.1556010	0.0000000	0.400990	57
ARID1A	3.8077265	0.6904187	3.2422947	0.0000000	0.400990	58
NCOR2	2.2174772	0.3250154	2.3630687	0.0000000	0.400990	59
FRMD6	0.8656363	0.8632491	1.2924717	0.0000137	0.400990	60
AHCYL2	2.1447121	0.4116144	2.0914612	0.0000000	0.400990	61
ATRNL1	0.9697021	0.3482308	1.5232136	0.0000011	0.414165	62
MED23	2.8956511	0.4143370	3.5786840	0.0000000	0.428256	63
SWSAP1	0.8673184	0.3703194	1.1162389	0.0062058	0.428256	64
ZDHHC15	5.0720486	0.9586603	4.9109570	0.0000000	0.428256	65
AMT	1.7810369	0.5782483	1.4691365	0.0000496	0.435419	66
SNCG	7.6389025	0.8825171	7.9026880	0.0000000	0.437491	67
TADA3	3.9831682	0.4143370	4.5856724	0.0000000	0.445616	68
GLIPR1L2	1.1048093	0.4038307	1.1623009	0.0044526	0.445616	69
GEN1	1.4237074	0.2824934	1.5400247	0.0000054	0.449937	70
SGSM3	1.0132725	0.3482308	1.6509686	0.0000014	0.449937	71
ELMOD1	4.0765164	0.4143370	4.6330257	0.0000000	0.451114	72
TRIP12	1.8099235	0.4843050	2.0704290	0.0000000	0.460264	73
ZBTB7A	1.1479436	0.3482308	1.5608189	0.0000000	0.460264	74
GPR123	5.5397643	0.4143370	5.7545740	0.0000000	0.460264	75
PET117	0.5165252	0.5782483	1.2990229	1.0000000	0.463588	76
SEC31A	1.6084220	0.5782483	1.7376115	0.0000000	0.501157	77
NOD2	0.9627437	0.3482308	1.2713121	0.0920651	0.536200	78
GIT2	1.3911305	0.3703194	1.5134990	0.0000002	0.536200	79
SPNS1	0.9141725	0.7555528	0.9092236	0.4134223	0.536200	80
ATP5A1	1.0878416	0.4038307	1.3139800	0.0038656	0.542050	81
DMD	0.5775560	0.3482308	0.6588737	1.0000000	0.542050	82
TOX3	1.4048874	0.4590367	1.3425163	0.0000210	0.542050	83
LGALS4	5.6714135	0.4143370	6.1932388	0.0000000	0.542050	84
NLGN1	6.7041093	0.9978094	7.3768302	0.0000000	0.542050	85
PUS3	0.6996023	0.4116144	1.0096801	0.3117989	0.545116	86
MOB3B	3.2293339	0.3482308	4.2347014	0.0000000	0.545116	87
PLA2R1	6.9082593	0.5596412	6.0620364	0.0000000	0.545116	88
RP11-428C6.1	0.7107032	0.3898331	0.7562766	1.0000000	0.545116	89
LBX1	6.8665841	1.0000000	7.7598796	0.0000000	0.545116	90
CUX1	0.9123479	0.4143370	0.8905721	0.6639072	0.545116	91
C1orf27	6.5612745	0.9244268	7.3662907	0.0000000	0.545116	92
NDUFAF5	4.6061877	0.3482308	5.3104844	0.0000000	0.545116	93
PVRL3	0.8331912	0.3482308	0.8498282	0.9642836	0.545116	94

	wilcox.log2fc	wilcox.pval	deseq.log2fc	deseq.pval	mageck.fdr	mageck.rank
EHMT2	6.9434931	0.7640872	5.7018783	0.0000000	0.545116	95
CD320	3.3828486	0.9103523	4.2964448	0.0000000	0.545116	96
PRKCE	1.4436664	0.5782483	1.7796997	0.0000000	0.545116	97
CELF2	1.4891944	0.4590367	1.2510287	0.0000598	0.553900	98
FOXJ3	0.9950264	0.4143370	1.0043638	0.1647986	0.557406	99
FPGT	1.1828861	0.6264892	1.1501410	0.0012198	0.558720	100
ZSWIM1	7.1042742	0.5596412	7.7425715	0.0000000	0.558720	101
EN2	6.6303297	0.8698781	7.1052504	0.0000000	0.576636	102
PDC	2.9511410	0.9244268	3.9136999	0.0000000	0.588631	103
CCDC93	0.6689781	0.3482308	1.1741805	0.0366023	0.588631	104
BCLAF1	0.9134840	0.4143370	1.0711833	0.2341341	0.588631	105
KDM5C	0.9114096	0.4963201	0.8951188	0.5488183	0.588631	106
ARHGAP35	1.0515454	0.4143370	1.3855192	0.0024337	0.588631	107
CPAMD8	6.7519832	0.9623066	7.3388173	0.0000000	0.588631	108
TCP1	6.4212318	0.8708879	6.2451828	0.0000000	0.588631	109
WDR20	0.9798527	0.3482308	1.0019333	0.2929686	0.588631	110
ARNTL2	0.7825848	0.3703194	0.7940705	1.0000000	0.588631	111
TFAP2C	0.8328453	0.3482308	1.1660537	0.3405100	0.588631	112
SPOPL	1.6328638	0.8632491	2.2501551	0.0000000	0.588631	113
NRXN3	2.4517784	0.5782483	2.4590216	0.0000000	0.588631	114
TNFRSF17	5.7185882	0.6904187	5.9758146	0.0000000	0.600911	115
GNA14	6.6813786	0.5596412	8.0697056	0.0000000	0.600911	116
PECR	6.6549825	0.9188346	7.0668467	0.0000000	0.600911	117
EBF4	2.1242860	0.7980584	2.7243464	0.0000000	0.600911	118
TXNDC17	1.5038217	0.5162010	2.0650553	0.0000000	0.600911	119
KLHL8	1.0663091	0.5388553	1.4719886	0.0000002	0.600911	120
PTGS1	0.7783977	0.4963201	0.7783278	1.0000000	0.600911	121
TXN2	0.7390779	0.4843050	1.2764852	0.0043540	0.600911	122
NSUN4	0.8002034	0.3383934	1.1714721	0.0009352	0.600911	123
YTARVE19	5.9887715	0.6061429	6.3284999	0.0000000	0.600911	124
EP300	1.7647727	0.7396852	1.9341946	0.0000000	0.600911	125
ZNF679	1.4457987	0.9774343	2.1236290	0.0000000	0.600911	126
PHC2	6.2243666	0.9851504	7.1067054	0.0000000	0.600911	127
MIA	6.4076863	0.9918641	6.5881077	0.0000000	0.600911	128
PCSK7	1.0130171	0.3482308	1.1838160	0.0181779	0.600911	129
ZNF444	1.0208299	0.4143370	1.1310004	0.0269490	0.600911	130
CTSB	1.0476706	0.6476322	1.1936784	0.0098470	0.600911	131
MAP1LC3A	1.5201922	0.6904187	2.1811955	0.0000000	0.600911	132
STK25	4.6238868	0.5528104	4.8834514	0.0000000	0.600911	133
TP53	2.0088216	0.4143370	2.2294205	0.0000000	0.600911	134
HGS	6.2853884	0.5596412	6.9913159	0.0000000	0.600911	135
SPACA1	0.9060227	0.3703194	1.7655707	0.0000000	0.600911	136
DMRT3	6.3930054	0.9451159	7.0808846	0.0000000	0.600911	137
FGGY	2.4243443	0.4143370	2.8886930	0.0000000	0.600911	138
CHCHD1	1.0678024	0.5803657	2.0302838	0.0000000	0.612211	139
MRPL53	0.8336447	0.3482308	1.5399343	0.0000002	0.612211	140
TCEB2	1.2461019	0.3482308	1.7930868	0.0000000	0.612211	141
TSHZ1	6.3323897	0.9094708	6.5304834	0.0000000	0.612781	142
ECHDC1	1.3015752	0.3482308	1.7707819	0.0000000	0.616012	143
TREML2	0.6741177	0.4143370	1.0230684	1.0000000	0.616012	144
SIGLEC9	6.3376363	0.9094708	5.8508538	0.0000000	0.616012	145
CCT8	1.2758669	0.4963201	2.6534446	0.0000000	0.621789	146

	wilcox.log2fc	wilcox.pval	deseq.log2fc	deseq.pval	mageck.fdr	mageck.rank
PRODH	1.9849718	0.5782483	2.3249100	0.0000001	0.621789	147
INTU	0.7591127	0.4143370	0.8544688	1.0000000	0.621789	148
DAPL1	0.5569548	0.4143370	0.9060189	1.0000000	0.621789	149
CRYGN	1.3634327	0.4038307	1.9406922	0.0000000	0.621789	150
KEAP1	1.9507446	0.5803657	2.2766804	0.0000000	0.621789	151
ASIC1	4.8341262	0.5596412	5.5464726	0.0000000	0.621789	152
FAM19A4	1.3207395	0.8899415	1.5732269	0.0000000	0.621789	153
MED16	1.9676783	0.5162010	2.9279408	0.0000000	0.623473	154
NDUFA8	1.8292629	0.4143370	2.3731738	0.0000000	0.631713	155
CREBBP	1.1307501	0.3482308	1.4941274	0.0000036	0.631713	156
RCOR2	1.5700487	0.3703194	2.2703656	0.0000000	0.631713	157
SERPINB6	6.0807808	0.8156689	6.4665858	0.0000000	0.631713	158
R3HDML	0.8826519	0.5803657	1.2376917	0.0005286	0.631713	159
TRPC4AP	2.8937208	0.6264892	2.8171378	0.0000000	0.631713	160
PCIF1	1.3046027	0.4143370	1.8993986	0.0000000	0.631713	161
LITAF	2.7273361	0.4143370	3.5430730	0.0000000	0.631713	162
ZMAT3	0.8465825	0.4133059	0.8618116	1.0000000	0.631713	163
MUM1	0.8025441	0.4590367	1.4088148	0.0001956	0.631713	164
ILF2	0.6754800	0.4143370	0.9105561	1.0000000	0.631713	165
IL17REL	6.1011398	0.6343258	6.4437614	0.0000000	0.633219	166
KLK10	0.6907095	0.4143370	1.0208206	0.3114655	0.633219	167
RNH1	5.9023143	0.9025761	6.8088199	0.0000000	0.640706	168
PPP1R14D	3.3019509	0.4143370	3.3422050	0.0000000	0.647636	169
CLEC2B	1.4283533	0.8473385	1.9237935	0.0000000	0.651281	170
ZSCAN1	6.0394379	0.9451159	6.7314267	0.0000000	0.656389	171
DDX54	5.8625119	0.8708879	6.2787055	0.0000000	0.668345	172
PRR23B	5.7942059	0.5782483	6.1538429	0.0000000	0.668345	173
EML1	2.6862967	0.4143370	2.4727733	0.0000000	0.668345	174
HEBP1	1.7064349	0.6343258	1.8633310	0.0000000	0.669109	175
EPHB2	1.1881013	0.6343258	1.0067135	0.2273512	0.673352	176
PCLO	0.8874362	0.3703194	0.9715257	1.0000000	0.676372	177
SH3GLB1	0.8479677	0.5528104	1.0901897	0.1019766	0.679503	178
KLHL5	0.8879137	0.4963201	0.9386306	0.2656772	0.679503	179
SRM	0.7970524	0.5105479	1.5750894	0.0000142	0.679503	180
ITFG1	5.7904444	0.9586603	6.2515108	0.0000000	0.679503	181

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 **1 % top depleted hits** sorted according to ___MAGeCK_ are stored in **PLX__resistance__YTAR-COMPARE-HITS.xls** and are listed below:

	wilcox.log2fc	wilcox.pval	deseq.log2fc	deseq.pval	mageck.fdr	mageck.rank
RREB1	-0.0779626	0.7797476	-0.2133750	1.0000000	0.014851	1
CMIP	-0.3944112	0.4843050	-0.8926024	1.0000000	0.438614	2
LCLAT1	-0.5902432	0.2824934	-1.1996260	0.0009744	0.438614	3
CDKN1C	-0.4865222	0.5388553	-1.0305124	1.0000000	0.438614	4
NLGN3	-0.4437707	0.2321539	-0.8782767	1.0000000	0.438614	5
CAMKK1	-0.5711300	0.3250154	-1.1206700	0.0070598	0.508801	6
NLRP1	-0.4262068	0.5782483	-0.7618273	1.0000000	0.508801	7
FGFR1	-0.1978627	0.8698781	-0.6501169	1.0000000	0.508801	8
MAPKAPK2	-0.7950614	0.2824934	-1.4386920	0.0002616	0.508801	9
MCL1	-0.6478616	0.2824934	-2.3675521	0.0000000	0.605611	10
CD59	-0.7160300	0.3482308	-2.1975551	0.0000000	0.605611	11
LYRM7	-0.5277469	0.5782483	-1.6312766	0.0000001	0.605611	12
LTF	-0.0888792	0.9880323	-0.5931141	1.0000000	0.605611	13
PLCB1	-0.5755431	0.3482308	-1.0397677	0.3606889	0.605611	14
GRB2	-0.6460112	0.2824934	-1.5011962	0.0000083	0.605611	15
ARL1	-0.4834932	0.6560883	-1.4661376	0.0000516	0.655391	16
MLF1	-0.0820898	0.9657066	-0.2291285	1.0000000	0.655391	17
CMKLR1	-0.6847689	0.3482308	-1.1295218	0.6895293	0.655391	18
C22orf31	-0.3469461	0.6476322	-1.1544620	1.0000000	0.658214	19
CRK	-0.5562190	0.4143370	-1.6739468	0.0000008	0.658214	20
PGM2L1	-0.5392622	0.3703194	-1.5060331	0.0000298	0.658214	21
EEF1E1	-0.3023800	0.8545903	-1.0627084	1.0000000	0.658214	22
STRADA	-0.0115350	0.7203546	-0.3987152	1.0000000	0.658214	23
CPNE6	-0.0702685	0.6988636	-0.3162900	1.0000000	0.658214	24
TEX15	-0.7763982	0.3482308	-2.1167074	0.0000007	0.658214	25
PTPN13	-0.1558717	0.6988636	-0.2401480	1.0000000	0.658214	26
RNF144B	-0.4648915	0.3482308	-0.9804324	1.0000000	0.658214	27
TAF1B	NA	NA	-0.5573890	1.0000000	0.658214	28
KLHL3	-0.2995813	0.4116144	-0.8103540	1.0000000	0.658214	29
CREB3L4	-0.3027990	0.7203546	-0.5796807	1.0000000	0.658214	30
SNAPC5	-0.6033771	0.2824934	-1.4561749	0.0000141	0.658214	31
RAI14	-0.1837385	0.5744013	-0.4727405	1.0000000	0.658214	32
MPRIP	-0.5534947	0.3482308	-1.2079132	0.0035790	0.658214	33
TRIM37	-0.7354198	0.3482308	-1.5070015	0.0000469	0.658214	34
PARD6B	-0.5693765	0.2824934	-1.3711678	0.0003150	0.658214	35
FAM177A1	-0.7074271	0.2824934	-1.4996280	0.0000018	0.658214	36
APTX	-0.4209623	0.4143370	-0.8105814	1.0000000	0.658214	37
DLG1	-0.3217691	0.7096588	-1.0324623	0.0674813	0.658214	38
KCNJ13	-0.3154013	0.4963201	-0.7803889	1.0000000	0.658214	39
PAIP1	-0.1957826	0.8698781	-0.3823112	1.0000000	0.658214	40
LZTS2	-0.4597945	0.4143370	-1.2466321	0.0058442	0.658214	41
OR4K14	-0.7361011	0.3482308	-1.7566422	0.0000073	0.658214	42
NPC1L1	NA	NA	NA	NA	0.658214	43
OR2A14	-0.7130970	0.4590367	-1.1875791	0.0574498	0.658214	44
ACVR1B	NA	NA	NA	NA	0.658214	45
C2orf72	-0.4512472	0.7396852	-1.2627044	1.0000000	0.658214	46

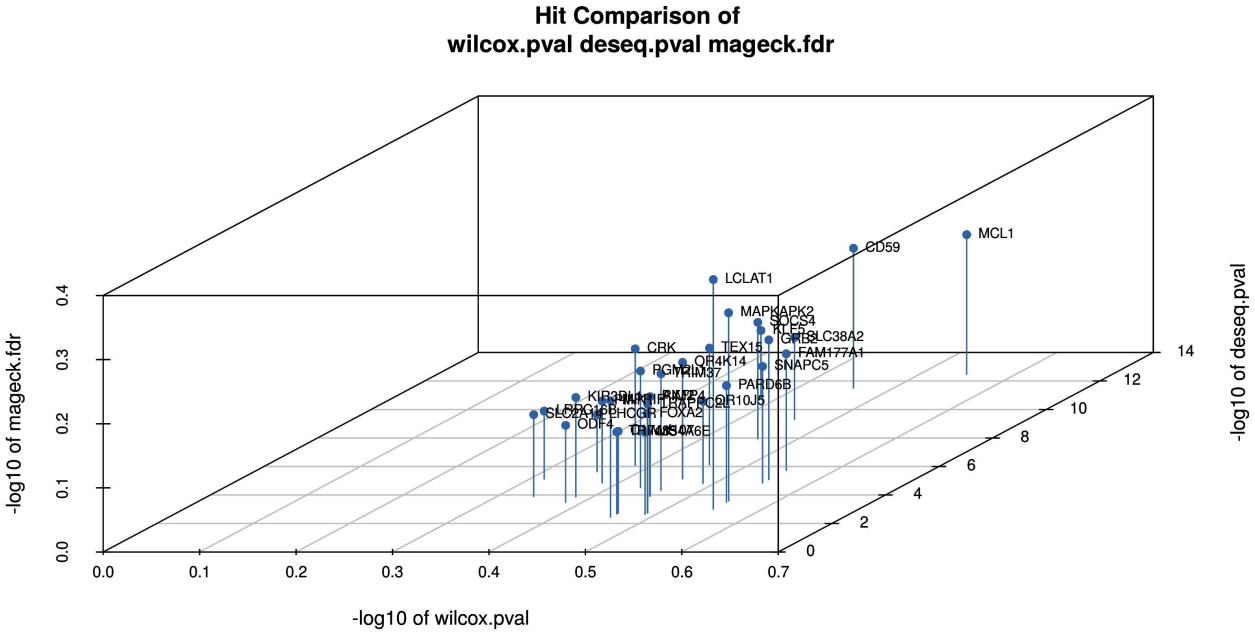
	wilcox.log2fc	wilcox.pval	deseq.log2fc	deseq.pval	mageck.fdr	mageck.rank
ADCY9	-0.4486723	0.3482308	-1.0619875	1.0000000	0.658214	47
CCL11	-0.5946985	0.3482308	-1.3268742	0.0084714	0.658214	48
SOCS4	-0.8042715	0.3482308	-1.7780278	0.0000000	0.658214	49
TRAPPC2L	-0.6760227	0.3250154	-1.4174921	0.0017599	0.677525	50
KIR3DL1	-0.4848893	0.4143370	-1.4502828	0.0001354	0.699742	51
CD34	-0.5234321	0.3703194	-0.8538334	1.0000000	0.699742	52
RXFP4	-0.6049191	0.3482308	-1.9318414	0.0001221	0.699742	53
EMR3	-0.2532180	0.7923545	-0.7965398	1.0000000	0.699742	54
TMEM74B	-0.5583146	0.4143370	-1.5669887	0.3351871	0.699742	55
BCAN	-0.3917369	0.4143370	-0.9239768	0.8243954	0.699742	56
ATF6B	-0.4228975	0.6264892	-0.9434614	0.3498826	0.699742	57
FOXA2	-0.6951017	0.3250154	-1.4547120	0.0018222	0.699742	58
PEMT	-0.1494014	0.8473385	-0.2568443	1.0000000	0.699742	59
GPRC6A	NA	NA	-0.2972763	1.0000000	0.699742	60
ITFG3	-0.4883307	0.3482308	-1.1445188	0.0145895	0.699742	61
BRAP	-0.4606760	0.3482308	-1.0682670	0.1577440	0.699742	62
RCVRN	-0.4614610	0.5206918	-1.6377712	0.0000006	0.699742	63
C17orf98	-0.5224439	0.5162010	-1.2394422	0.0092919	0.699742	64
AIM2	-0.4897521	0.3482308	-1.3467303	0.0001191	0.699742	65
MITF	-0.0791511	0.9513845	-0.2975880	1.0000000	0.699742	66
MAP2K5	-0.3626942	0.4580261	-0.6244749	1.0000000	0.699742	67
MNT	NA	NA	NA	NA	0.699742	68
SPOCK2	-0.3495407	0.3482308	-0.9119952	0.5335273	0.699742	69
CLCN5	NA	NA	-0.4278089	1.0000000	0.721726	70
SLURP1	-0.2345934	0.8507852	-0.7836693	1.0000000	0.721726	71
RP4-788L13.1	-0.4064030	0.4590367	-0.9968481	1.0000000	0.743056	72
C17orf107	-0.5622969	0.3482308	-1.6625242	0.0018545	0.745409	73
H2AFY	-0.0745387	0.8632491	-0.2940457	1.0000000	0.745409	74
USP25	-0.4688539	0.4411848	-1.3197347	0.5350962	0.745409	75
ANP32E	-0.0043433	0.6988636	-0.5451925	1.0000000	0.745409	76
PAM	-0.0101036	0.9998213	-0.1592633	1.0000000	0.745409	77
PHGDH	-0.2344180	0.5596412	-0.7044259	1.0000000	0.745409	78
PKP4	NA	NA	-0.3808332	1.0000000	0.745409	79
TMEM8A	-0.1435218	0.8990102	-0.8445560	1.0000000	0.745409	80
OR10H1	-0.6853027	0.3482308	-1.5748809	0.0112858	0.745409	81
DIDO1	-0.3992487	0.3250154	-1.1865714	0.0087435	0.745409	82
SLC38A2	-0.6199916	0.3482308	-2.2810878	0.0000000	0.745409	83
ZNF321P	NA	NA	NA	NA	0.745409	84
ACHE	-0.2585642	0.7980584	-0.4683442	1.0000000	0.745409	85
ESAM	-0.3357065	0.7203546	-0.9005926	1.0000000	0.745409	86
MTUS1	-0.3469689	0.2824934	-0.8445925	1.0000000	0.745409	87
PINK1	-0.5561540	0.4143370	-1.8401534	0.0000141	0.745409	88
CHRNA10	-0.4218748	0.4580261	-1.2065099	1.0000000	0.745409	89
C20orf202	-0.4304297	0.5782483	-1.1303367	0.0467981	0.745409	90
GPR110	-0.5429004	0.5162010	-1.3944036	0.0000915	0.745409	91
ABHD12	-0.0352017	0.8473385	-0.2680586	1.0000000	0.745409	92
AGXT	-0.3232496	0.5528104	-0.7199127	1.0000000	0.745409	93
SLC15A3	-0.4625144	0.3482308	-1.0927624	0.0246015	0.745409	94
CNTF	-0.4093899	0.4143370	-0.9122120	1.0000000	0.745409	95
CLDN18	-0.0653862	0.7980584	-0.4951141	1.0000000	0.745409	96
RARA	NA	NA	-0.0022500	1.0000000	0.745409	97
COL2A1	NA	NA	NA	NA	0.745409	98

	wilcox.log2fc	wilcox.pval	deseq.log2fc	deseq.pval	mageck.fdr	mageck.rank
NTM	-0.3127675	0.5782483	-0.1661917	1.0000000	0.745409	99
SLC2A14	-0.6402126	0.4590367	-1.9467218	0.0001267	0.745409	100
PLCG2	NA	NA	-0.2489201	1.0000000	0.745409	101
C7orf49	-0.0420971	0.9689335	-0.5057069	1.0000000	0.745409	102
MYOM1	NA	NA	-0.2674022	1.0000000	0.745409	103
PNKD	NA	NA	NA	NA	0.745409	104
OR10J5	-0.6451469	0.3250154	-1.5339437	0.0000151	0.745409	105
MS4A6E	-0.6099103	0.3250154	-1.4828093	0.0022171	0.745409	106
RAET1E	NA	NA	-0.0677461	1.0000000	0.745409	107
LEMD3	-0.4607523	0.4411848	-1.4453248	0.0137794	0.745409	108
CDK20	NA	NA	NA	NA	0.745409	109
TRIM35	-0.4738535	0.3482308	-1.5095286	0.0020870	0.745409	110
OXTR	-0.1142585	0.9451159	-0.6499380	1.0000000	0.745409	111
ADPRH	NA	NA	-0.1630749	1.0000000	0.745409	112
NR2C1	-0.4798164	0.5162010	-0.8897161	0.9860997	0.745409	113
TNPO2	NA	NA	-0.0716500	1.0000000	0.745409	114
MON1B	-0.3952367	0.4143370	-1.0681719	0.0897020	0.745409	115
PSEN1	NA	NA	-0.0422500	1.0000000	0.745409	116
NOTCH1	-0.4237942	0.4143370	-0.9999876	1.0000000	0.745409	117
MYOF	-0.4473711	0.6605586	-0.4957562	1.0000000	0.756178	118
PKP2	-0.5663109	0.5162010	-0.8675786	1.0000000	0.756178	119
ODF4	-0.4875531	0.4143370	-1.7569690	0.0003246	0.758559	120
C14orf182	-0.4431136	0.6476322	-1.1204927	0.3174939	0.758559	121
FAM180A	-0.4144487	0.5596412	-0.8120785	1.0000000	0.758559	122
SLC12A2	-0.4661378	0.6264892	-1.0503326	0.1428728	0.758559	123
RTN1	-0.0523799	0.8698781	-0.1107564	1.0000000	0.758559	124
DEFB115	-0.4534074	0.4143370	-0.9232729	1.0000000	0.758559	125
CPNE1	-0.3957434	0.4843050	-0.6932107	1.0000000	0.758559	126
SEMA4A	-0.4435417	0.5388553	-1.0695309	1.0000000	0.758559	127
TRIM28	-0.2408039	0.7980584	-1.0009774	1.0000000	0.758559	128
TRHDE	-0.4712491	0.4143370	-0.9772071	0.2572509	0.758559	129
ISOC2	-0.0462302	0.8632491	-0.2434941	1.0000000	0.758559	130
MYBPC3	NA	NA	NA	NA	0.758559	131
FKBP7	-0.0742875	0.8825171	-0.3326066	1.0000000	0.783598	132
ACD	-0.3988969	0.5744013	-1.0194740	0.2468865	0.783598	133
LRRC16B	-0.5450564	0.4843050	-1.8595775	0.0000075	0.783598	134
KLF5	-0.5732051	0.4143370	-2.2337999	0.0000000	0.783598	135
DMXL2	-0.2821937	0.7923545	-0.3367617	1.0000000	0.783598	136
SF3B4	NA	NA	NA	NA	0.810400	137
OR5L1	-0.2275709	0.9774343	-0.9777426	0.9267886	0.810841	138
LHCGR	-0.4847802	0.4411848	-1.6485454	0.0000023	0.814566	139
EXT2	NA	NA	-0.2190538	1.0000000	0.814566	140
NOS2	-0.1751269	0.7980584	-0.9267250	1.0000000	0.814566	141
CDK4	-0.4007079	0.6264892	-1.2039606	0.5429712	0.814566	142
EVI2B	-0.6121189	0.4590367	-1.2875349	0.0135254	0.824947	143
CIDEC	-0.4571104	0.4963201	-1.0960059	0.0356117	0.824947	144
EIF4G1	-0.0141263	1.0000000	-0.3173011	1.0000000	0.824947	145
CCL27	-0.4033720	0.4143370	-1.0854894	0.0679658	0.824947	146
NKX6-1	-0.2573385	0.5596412	-0.7487463	1.0000000	0.824947	147
LDHAL6A	-0.4154927	0.4143370	-1.1145835	0.1096112	0.824947	148
ENTPD4	-0.4066804	0.5803657	-1.2820373	0.0018777	0.824947	149
BHLHB9	-0.5795617	0.6122739	-2.1358201	0.0000470	0.824947	150

	wilcox.log2fc	wilcox.pval	deseq.log2fc	deseq.pval	mageck.fdr	mageck.rank
TMEM25	-0.2057605	0.6321930	-0.3216317	1.0000000	0.824947	151
AKR1C4	-0.5866673	0.5162010	-1.0126987	0.8131588	0.824947	152
MTTP	-0.3585512	0.4411848	-1.0413596	1.0000000	0.824947	153
SLC7A2	-0.3163531	0.7640872	-0.4899036	1.0000000	0.824947	154
RAD51AP2	NA	NA	NA	NA	0.824947	155
JMJD6	NA	NA	-0.0462149	1.0000000	0.824947	156
APOBR	-0.3360461	0.4843050	-0.9056700	1.0000000	0.824947	157
ADAM28	-0.3219334	0.6476322	-0.8332226	1.0000000	0.824947	158
HDAC7	-0.2241108	0.9025761	-0.4145384	1.0000000	0.833509	159
BICD1	NA	NA	NA	NA	0.833509	160
PARP1	NA	NA	-0.2318272	1.0000000	0.836511	161
C16orf53	-0.2080037	0.8156689	-0.7267125	1.0000000	0.838131	162
IQGAP3	-0.6192860	0.4590367	-1.4060101	0.0246770	0.840286	163
EGFR	-0.4531471	0.4143370	-0.6569809	1.0000000	0.840286	164
PI4KA	NA	NA	NA	NA	0.854561	165
DPP7	-0.4562920	0.7923545	-1.5106740	0.0005249	0.854561	166
CRYL1	-0.1373652	0.8825171	-0.2800191	1.0000000	0.854561	167
ZNF157	NA	NA	-0.1697390	1.0000000	0.854561	168
TOR4A	-0.5951510	0.5162010	-1.4852350	0.0000755	0.854561	169
PLA2G2A	NA	NA	-0.2883269	1.0000000	0.857767	170
PRH2	-0.4847467	0.4143370	-1.2860668	0.0419273	0.857767	171
IL31RA	-0.0597362	0.8825171	-0.3563761	1.0000000	0.866650	172
FXYD2	NA	NA	-0.5285095	1.0000000	0.866650	173
ZSCAN2	NA	NA	NA	NA	0.866650	174
PQBP1	-0.1212304	0.7203546	-0.5520700	1.0000000	0.866789	175
HS2ST1	-0.3150686	0.6264892	-0.6285406	1.0000000	0.868239	176
SLC9A8	-0.5948416	0.4143370	-1.1379792	0.0360587	0.868239	177
CHST12	-0.6070470	0.4590367	-1.1729116	0.0270571	0.883274	178
EIF2C1	-0.2876998	0.5782483	-0.8403656	1.0000000	0.883663	179
RNF152	-0.6646115	0.4590367	-1.3975569	0.3454002	0.883663	180
MR1	-0.5243273	0.5782483	-1.1130211	0.6110749	0.883663	181

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.

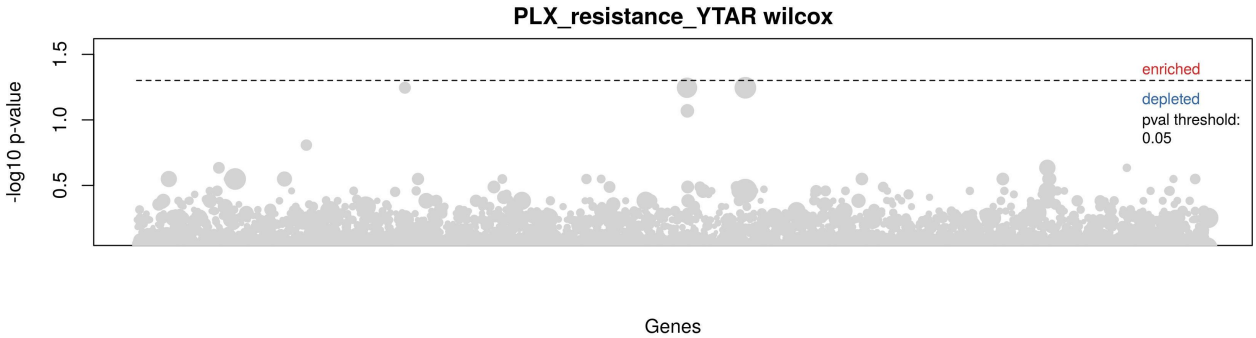


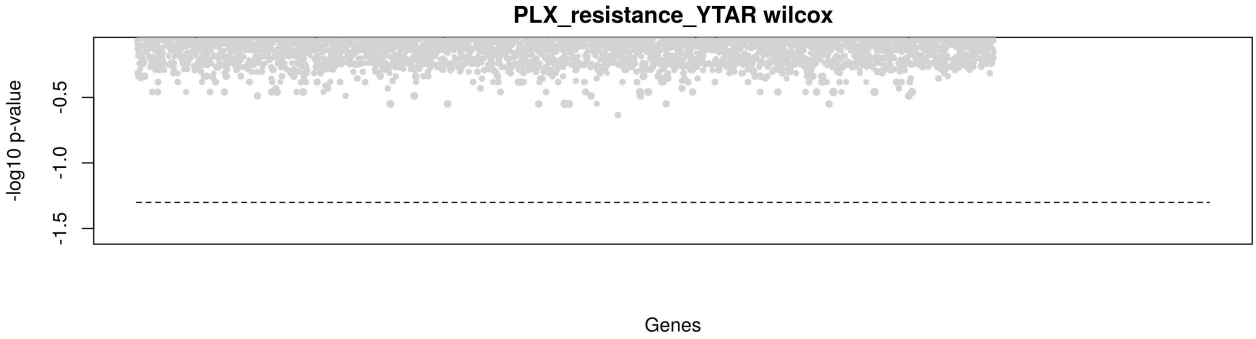
Visualize Analysis

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**.

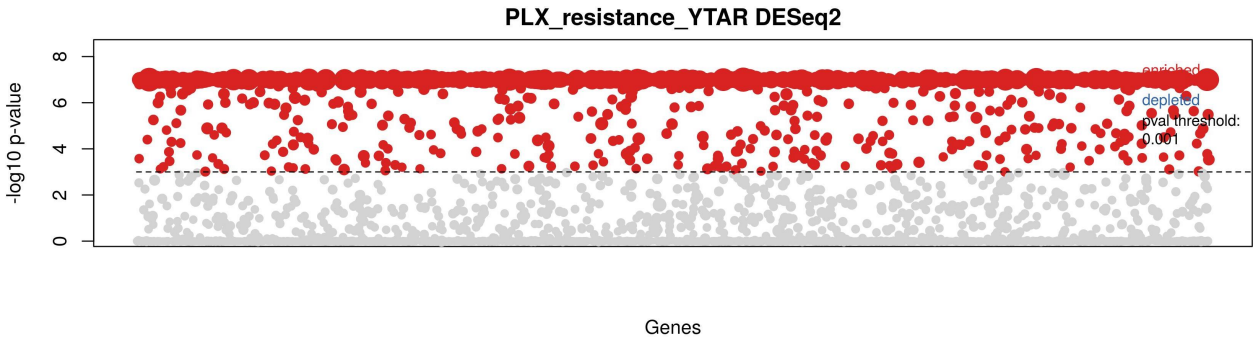
Moreover, the number of significant sgRNAs is presented for MAGeCK as well.

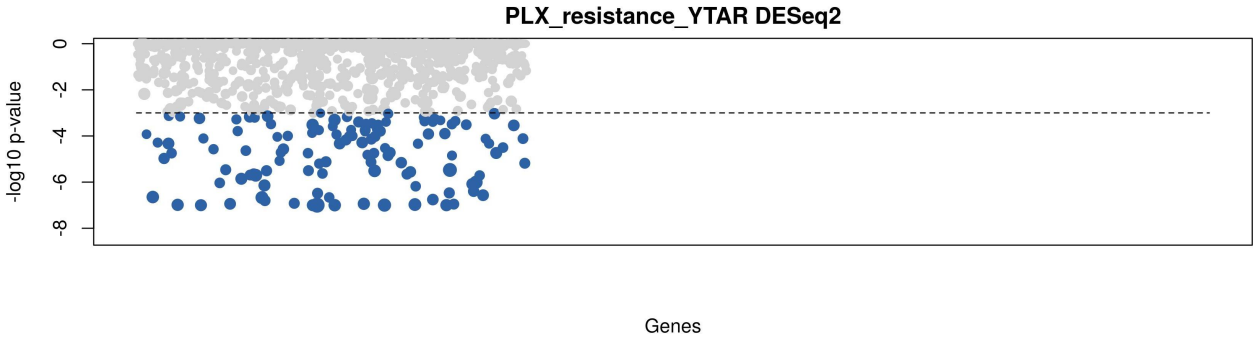
Wilcox



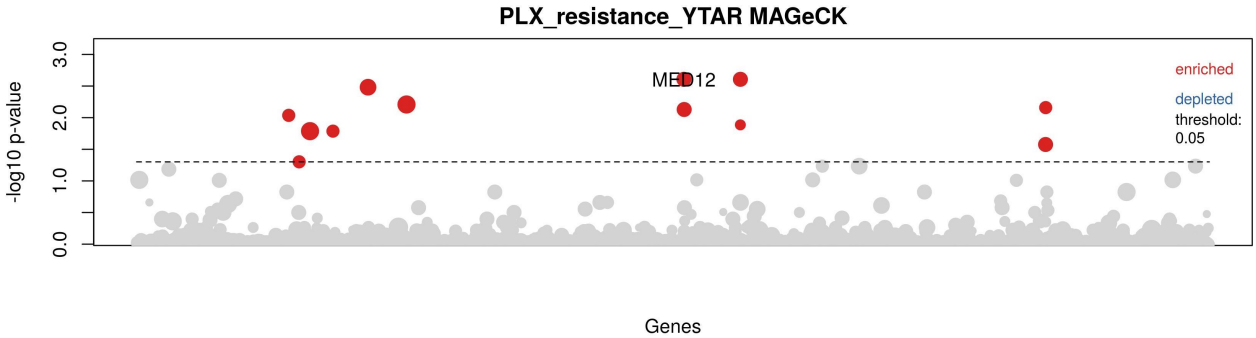


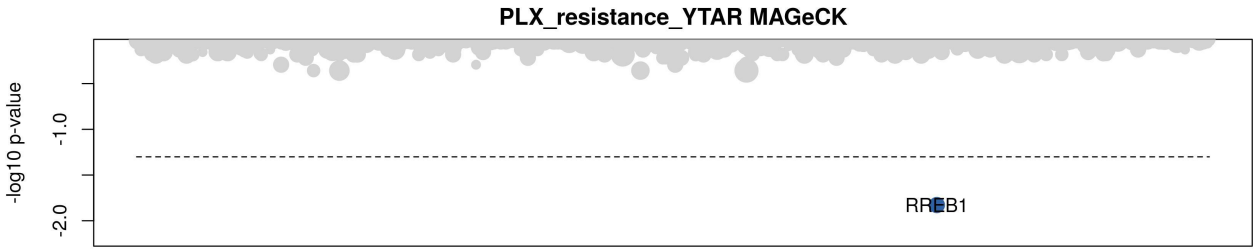
DESeq2

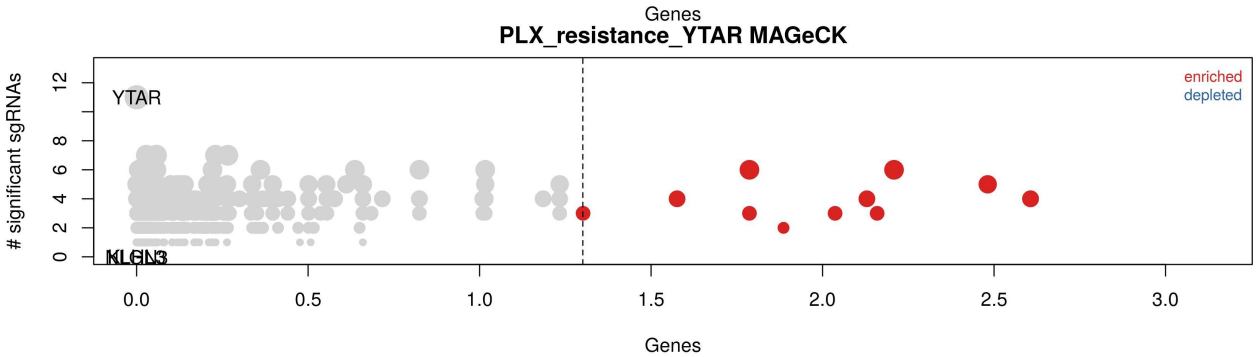

PLX_resistance_YTAR DESeq2
-log10 p-value
0
2
4
6
8
enriched
depleted
pval threshold:
0.001
Genes

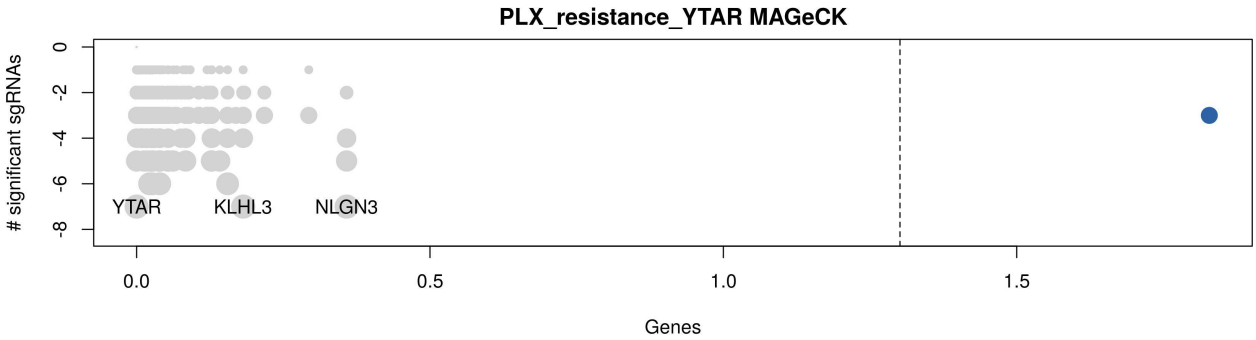

PLX_resistance_YTAR DESeq2
-log10 p-value
0
-2
-4
-6
-8
Genes

MAGeCK


PLX_resistance_YTAR MAGeCK
-log10 p-value
0.0
1.0
2.0
3.0
MED12
enriched
depleted
threshold:
0.05
Genes


PLX_resistance_YTAR MAGeCK
-log10 p-value
-1.0
-2.0
RREB1
Genes


PLX_resistance_YTAR MAGeCK
significant sgRNAs
0
2
4
6
8
12
YTAR
KLGN3
enriched
depleted
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Genes


PLX_resistance_YTAR MAGeCK
significant sgRNAs
0
-2
-4
-6
-8
YTAR
KLHL3
NLGN3
0.0
0.5
1.0
1.5
Genes

Final Gene Table

A final table with all information for each gene is stored in **./PLX_resistance_YTAR_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

- . *

** PLX_resistance_YTAR_ANNOTATION.xls **

Data Extraction, Mapping and Files

Dataset	.fastq file name	Description
Control #1	shalem_raw_DMSO1.txt	DMSO1
Control #2	shalem_raw_DMSO2.txt	DMSO2
Treatment #1	shalem_raw_PLX1.txt	PLX1
Treatment #2	shalem_raw_PLX2.txt	PLX2

The data is located in
.

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

All file-based output (e.g. tables) from MAGeCK is stored in:
/home/b110-ws01/CRISPR-Analyzer.

Parameter	Value
Reverse Complement Sequence	FALSE
Pattern of Data Extraction	ACC(.{20})GT{2,4}AGAGC
Maschine Identifier FASTq	@(M01100.+)
Create Bowtie2 Index?	FALSE
Bowtie2 Index File	shalem_lib
Reference .fasta File	shalem_lib
Bt2 Threads	4
Bt2 Sensitivity	NA
sgRNA Oligo Match	perfect