MAGeCK Comparison Report

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Contents

I	Summary	_
2	Comparison results of fxn 2 vs rest neg.	2
3	Comparison results of fxn 2 vs rest pos.	6

1 Summary

The statistics of comparisons is as indicated in the following table.

	Comparison	Genes	Selection	FDR1%	FDR5%	FDR25%
1	fxn_2_vs_rest neg.	19280	negative	0	0	0
2	fxn_2_vs_rest pos.	19280	positive	0	0	3

Table 1: Summary of comparisons

The meanings of the columns are as follows.

- Comparison: The label for comparisons;
- **Genes**: The number of genes in the library;
- **Selection**: The direction of selection, either positive selection or negative selection;
- **FDR1%**: The number of genes with FDR < 1%;
- FDR5%: The number of genes with FDR < 5%;
- FDR25%: The number of genes with FDR < 25%;

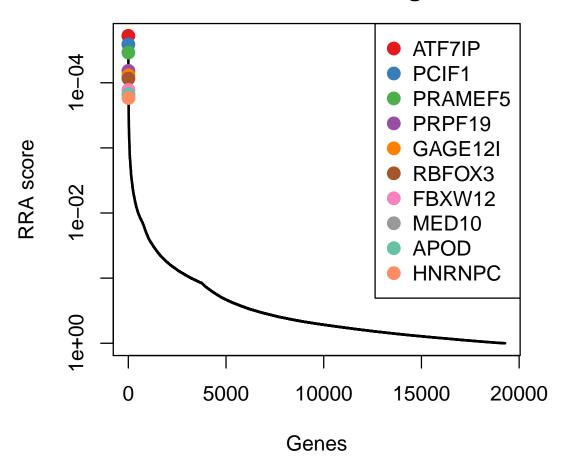
The following figures show:

- Individual sgRNA read counts of selected genes in selected samples;
- The distribution of RRA scores and p values of all genes; and
- The RRA scores and p values of selected genes.

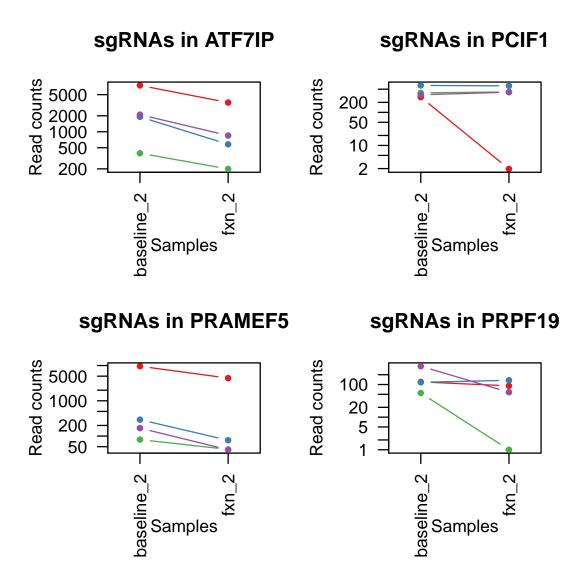
2 Comparison results of fxn 2 vs rest neg.

The following figure shows the distribution of RRA score in the comparison fxn 2 vs rest neg., and the RRA scores of 10 genes.

Distribution of RRA scores in fxn_2_vs_rest neg.

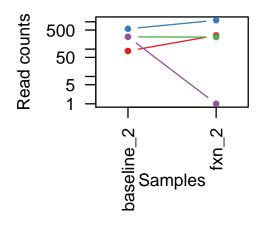


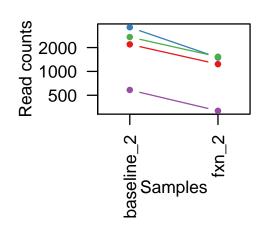
The following figures show the distribution of sgRNA read counts (normalized) of selected genes in selected samples.



sgRNAs in GAGE12I

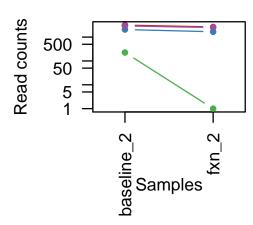
sgRNAs in RBFOX3

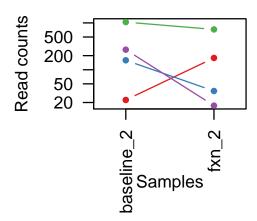




sgRNAs in FBXW12

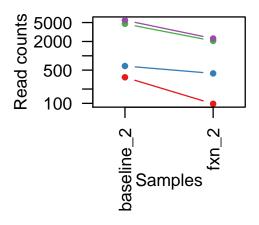
sgRNAs in MED10

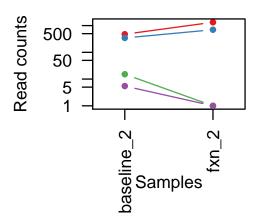




sgRNAs in APOD

sgRNAs in HNRNPC

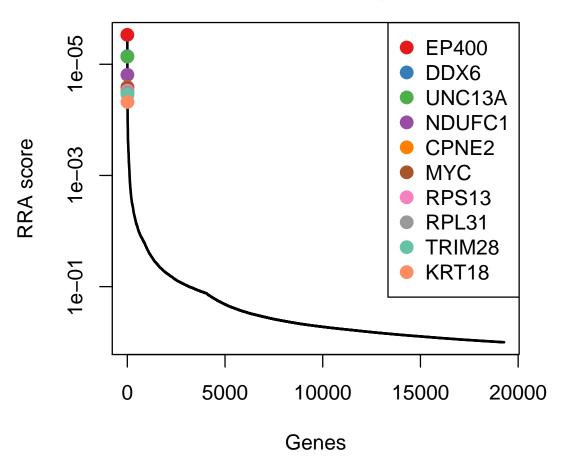




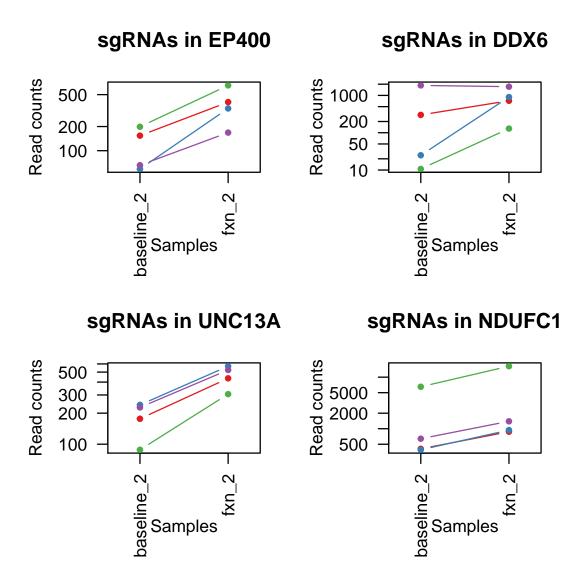
3 Comparison results of fxn 2 vs rest pos.

The following figure shows the distribution of RRA score in the comparison fxn 2 vs rest pos., and the RRA scores of 10 genes.

Distribution of RRA scores in fxn_2_vs_rest pos.

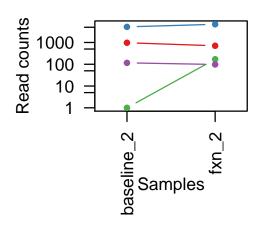


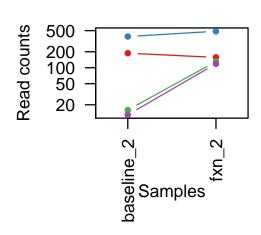
The following figures show the distribution of sgRNA read counts (normalized) of selected genes in selected samples.



sgRNAs in CPNE2

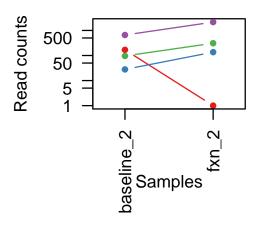
sgRNAs in MYC

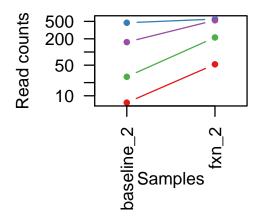




sgRNAs in RPS13

sgRNAs in RPL31





sgRNAs in TRIM28

sgRNAs in KRT18

