MAGeCK Comparison Report

Wei Li

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1 Summary

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

Comparison	Genes	Selection	FDR1%	$\mathrm{FDR}5\%$	FDR10%
1 FXN High Gate vs Baseline	19280	positive	32	183	419
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Table 1: Number of genes detected as significantly enriched in FXN High samples

	Comparison	Genes	Selection	FDR1%	FDR5%	FDR10%
1	FXN High Gate vs Baseline	19280	positive	32	183	419

Table 2: Number of genes detected as significantly enriched in FXN High samples

	Comparison	Genes	Selection	FDR1%	FDR5%	FDR10%
1	FXN High Gate vs Baseline	19280	positive	32	183	419

Table 3: Number of genes detected as significantly enriched in FXN High samples

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%;

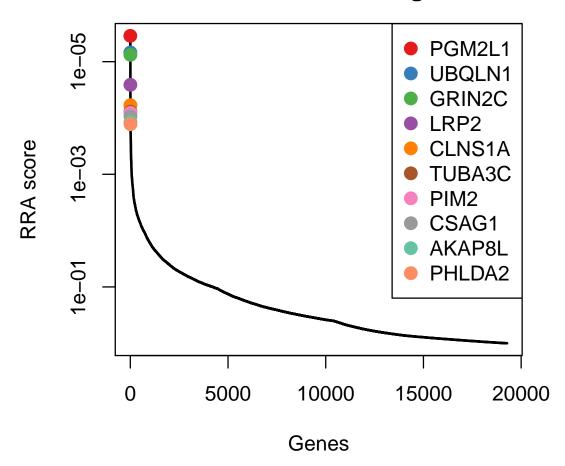
The following figures show:

- 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.

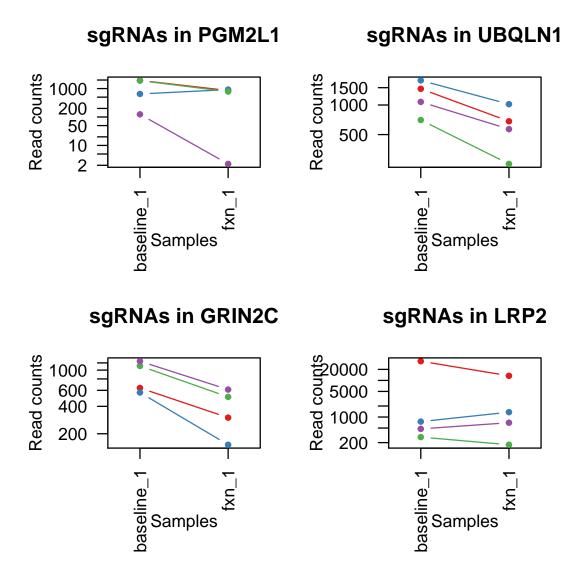
2 Comparison results of fxn 1 vs rest neg.

The following figure shows the distribution of RRA score in the comparison fxn 1 vs rest neg., and the RRA scores of 10 genes.

Distribution of RRA scores in fxn_1_vs_rest neg.

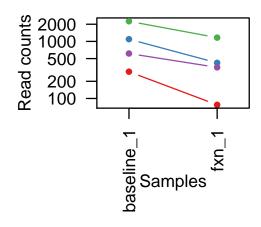


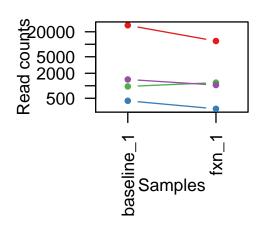
The following figures show the distribution of sgRNA read counts (normalized) of selected genes in selected samples.



sgRNAs in CLNS1A

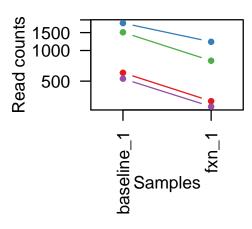
sgRNAs in TUBA3C

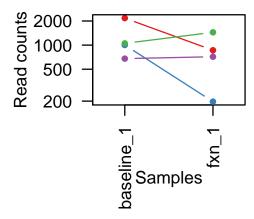




sgRNAs in PIM2

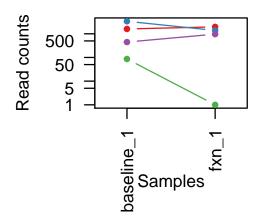
sgRNAs in CSAG1

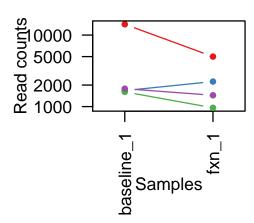




sgRNAs in AKAP8L

sgRNAs in PHLDA2

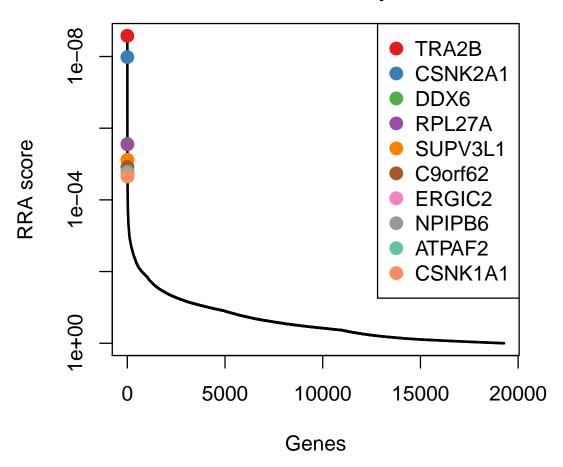




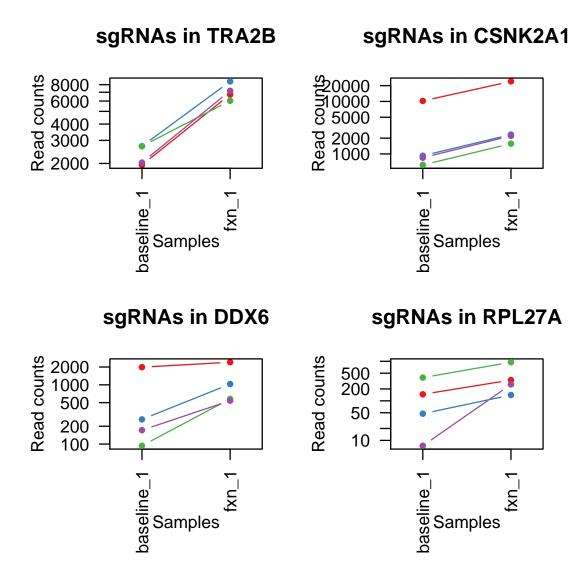
3 Comparison results of fxn 1 vs rest pos.

The following figure shows the distribution of RRA score in the comparison fxn 1 vs rest pos., and the RRA scores of 10 genes.

Distribution of RRA scores in fxn_1_vs_rest pos.

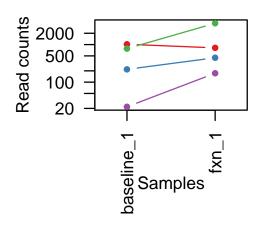


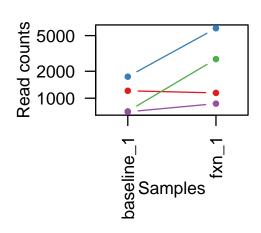
The following figures show the distribution of sgRNA read counts (normalized) of selected genes in selected samples.



sgRNAs in SUPV3L1

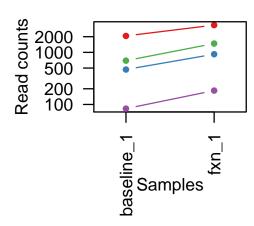
sgRNAs in C9orf62

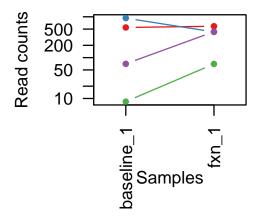




sgRNAs in ERGIC2

sgRNAs in NPIPB6





sgRNAs in ATPAF2

sgRNAs in CSNK1A1

