



GUIDE-Seq Results

CCR5 knockout experiment

Generated 04/11/2017

Summary

Condition	Organism	Cell Type	Genome	Nuclease	Sequencer	Number of Samples
CD34-MYC-10nm	Human	U2OS	hg19	Cas9 (VRER variant)	MiSeq	1
CD34-MYC-20nm	Human	U2OS	hg19	Cas9 (VRER variant)	MiSeq	1

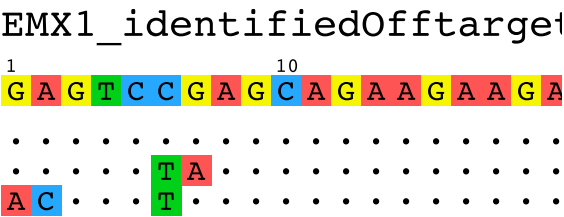
Read Mapping Statistics

Sample	Condition	Total Reads	High Quality Mapped Reads	Number of On-target Reads	Number of Off-target Reads
EMX1-10nm	CD34-MYC-10nm	4868	768	489	193
EMX1-20nm	CD34-MYC-20nm	4868	768	489	193

Sample 1: EMX1-10nm

Cleavage ID	Location	Targeting Status	GUIDE-Seq Reads	Closest Gene	Distance to Closest Gene	Relationship with Closest Gene	Regulatory Region?
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Figure

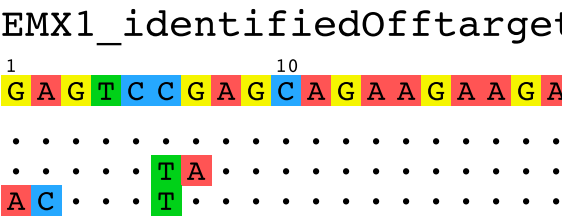


Sequences of off-targets detected by GUIDE-Seq. The full target sequence is displayed in the first row. Each subsequent row indicates a cleaved site detected by GUIDE-Seq. Consensus is represented by a black dot, while nucleotide mismatches are represented by colored squared with the mismatched base. GUIDE-Seq read counts for each cleavage event are listed on the right of each row.

Sample 2: EMX1-20nm

Cleavage ID	Location	Targeting Status	GUIDE-Seq Reads	Closest Gene	Distance to Closest Gene	Relationship with Closest Gene	Regulatory Region?
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Figure



Sequences of off-targets detected by GUIDE-Seq. The full target sequence is displayed in the first row. Each subsequent row indicates a cleaved site detected by GUIDE-Seq. Consensus is represented by a black dot, while nucleotide mismatches are represented by colored squared with the mismatched base. GUIDE-Seq read counts for each cleavage event are listed on the right of each row.

Footnotes

Footnotes about where reference data came from goes here