



## GUIDE-Seq Results

### CCR5 knockout experiment

Generated 06/21/2017

#### 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                 |

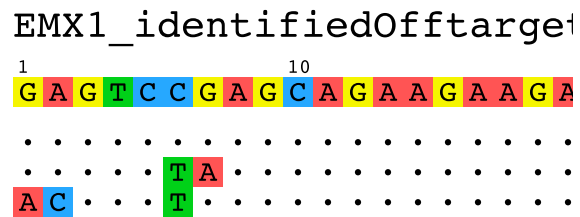
#### Read Mapping Statistics

| 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? |
|-------------------------|-------------------------|------------------|-----------------|--------------|--------------------------|--------------------------------|--------------------|
| chr2:73159981-73162004  | chr2:73159981-73162004  | On target        | TODO            | gene name    |                          |                                |                    |
| chr15:44108746-44110769 | chr15:44108746-44110769 | Off target       | TODO            | gene name    |                          |                                |                    |
| chr6:9117792-9119815    | chr6:9117792-9119815    | Off target       | TODO            | gene name    |                          |                                |                    |

### Figure

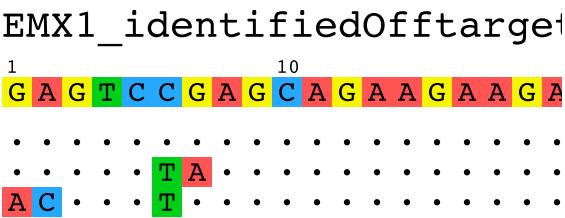


*Sequences of off-targets detected by GUIDE-Seq. The full target sequence is displayed in the first row. Each subsequent row indicates a cleaved site detected by GUIDE-Seq. Consensus is represented by a black dot, while nucleotide mismatches are represented by colored squares with the mismatched base. 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? |
|-------------------------|-------------------------|------------------|-----------------|--------------|--------------------------|--------------------------------|--------------------|
| chr2:73159981-73162004  | chr2:73159981-73162004  | On target        | TODO            | gene name    |                          |                                |                    |
| chr15:44108746-44110769 | chr15:44108746-44110769 | Off target       | TODO            | gene name    |                          |                                |                    |
| chr6:9117792-9119815    | chr6:9117792-9119815    | Off target       | TODO            | gene name    |                          |                                |                    |

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