PI: Shengdar Tsai

Project: A novel human T cell platform to define biological adverse effects of genome editing

Initiative: Biological Effects

Tsai Lab

Metadata file

Metadata table 1: this table includes the Lab\_sgRNA\_id, Protospacer (without PAM), Protospacer (PAM), Chr, Start, End, Strand, Protospacer length, Protospacer (PAM) length, Primer\_Forward, Primer\_Reverse. This table contains information for 110 sgRNA target sites across 13 loci in the human genome (hg38).

Metadata table 2: list of CHANGE-seq identified on- and off-target sites for the 110 sgRNA target sites from the Metadata table 1. This table includes the target site name, the off-target sequence, chr, start, end, strand and genomic coordinate from the identified off-target sites, as well as the number of mismatches to the intended target site. This table also includes the intended target site (on-target) sequence and CHANGE-seq read counts.

Metadata table 3: list of GUIDE-seq identified on- and off-target sites for a subset of sites listed in Metadata table 1 (59 sgRNA target sites). This table includes the target site name, the off-target sequence, chr, start, end, strand and genomic coordinate from the identified off-target sites, as well as the number of mismatches to the intended target site. This table also includes the intended target site (on-target) sequence, GUIDE-seq read counts and the number of GUIDE-seq runs performed for the respective target site (replicates).

Metadata table 4: list of primers used for targeted sequencing (standard target sequencing or rhAmpSeq), for validation of the off-target sites identified by CHANGE-seq and by GUIDE-seq in human primary T cells. This list includes primers used in a standard target sequencing approach, containing the target name based on the intended target site name, off-target genomic coordinate, strand, off-target sequence, CHANGE-seq reads, number of mismatches and classification according to CHANGE-seq enrichment, number of mismatches and the presence in the GUIDE-seq dataset. Forward and reverse primers are listed. Primers used in the rhAmpSeq method are listed according to the sgRNA target site.

Data file

Data table 1: this table includes the total number of sites identified by CHANGE-seq for each one of the 110 sgRNA target sites evaluated and described in the Metadata table 1 (sgRNA target sites). This table corresponds to Figure 2B of Lazzarotto et al., 2020.

Data table 2: this table includes the specificity ratio measured by CHANGE-seq for each one of the 110 sgRNA target sites evaluated and described in the Metadata table 1 (sgRNA target sites). This table corresponds to Figure 2C of Lazzarotto et al., 2020.

Data table 3: this table contains a list of on-target site targeted sequencing counts. This table corresponds to Figure 2D of Lazzarotto et al., 2020.

Data table 4: this table includes the total number of sites identified by GUIDE-seq for a subset of sites listed in Metadata table 1 (59 sgRNA target sites). This table corresponds to Figure 4A of Lazzarotto et al., 2020.

Data table 5: this table contains a list of off-target site targeted sequencing counts (standard targeted sequencing).

Data table 6: this table contains a list of off-target site targeted sequencing counts (rhAmpSeq).

Reference

Lazzarotto, C.R., Malinin, N.L., Li, Y. *et al.* CHANGE-seq reveals genetic and epigenetic effects on CRISPR–Cas9 genome-wide activity. *Nat Biotechnol* **38,**1317–1327 (2020). https://doi.org/10.1038/s41587-020-0555-7