**Synthesized oligo sequences:**

File: /groups/gray/ars/MPRA/ForRory/SynthesizedTiles/Array3\_12k\_2014\_05\_12\_merged.fa

Description: Fasta file containing the sequences submitted for synthesis. Header contains a random unique identifier, species of origin, whether the sequence is endogenous or mutated, the genomic coordinated of the start of the tile, any binding motifs present.

Example:

>-249753741\_hs\_Endogenous\_chr1:6052584^WCGCGTYat-59^GATTGGYat-29^GATTGGYat14^YGCGGCKSat23

ACTGGCCGCTTCACTGaactccccagcagcctgtacgtttagtcctacccgggcCCGCCGCAggGATTGGCaccgcgagcgtttcgcgtcgggagctgaacccgagaGATTGGCaggcgccgggactgccgctgtcaGACGCGAccgcccaagaCACTGCGGCTCCTCA

Red = header

Green = Enhancer

Blue = PCR Adapters

**Plasmid Sequence:**

File: /groups/gray/ars/MPRA/ForRory/PlasmidSeqeunce/TN03vector

Description: The sequence of the viral vector with the enhancer sequence inserted. The first nucleotide is the first base of the primer used for sequencing. The enhancer element is shown as 142 Ns. Downstream of this region is constant 12bp restriction site and random 16bp barcode.

**Primer Sequences:**

File:/groups/gray/ars/MPRA/ForRory/SequencingPrimers

Description: Primers used to amplify the enhancer-BC pairs from the TN03 vector and append the p7 sequencing adapter.

**Mi-seq output files:**

Files: /groups/gray/ars/MPRA/ForRory/RawSequences/TN03\_S1\_L001\_R2\_001.fastq

/groups/gray/ars/MPRA/ForRory/RawSequences/TN03\_S1\_L001\_R1\_001.fastq

Description: Fasta files containing reads originating at the P7 (R1) or P5 (R2) primer. R1 sequences are the reverse complement of the paired R2 sequence.

Example:

@M00620:96:000000000-A8RLL:1:1101:11235:1377 1:N:0:1

CGAGGTTCGACGTCCCTCTAGAGGTACCTGAGGAGCCGCAGTGGCCAAGGAGGAAGTGAAGACTGGAGTCTGCGCCTGGTCCTCAGGAACCCGGGCGAAGGCTGAGAGCGTTGGAATGACAGGCCGTGCCTCCGGTGGGTGGGACTATAGGGTGACGTCATTCGGGCCATGTCCAGGCGCTCAGTGAAGCGGCCAG

+

Blue = 16bp random Barcode

Orange = KpnI and XbaI restriction sites

Green = enhancer

Black = PCR adapters from synthesized oligo