**Folders**

READS – contains raw sequencing data from reads in fasta format

Quality\_score – contains the base quality values associated with the reads

Alignments – Alignments of the reads with the expected sequence and shown for all amplicons from all lines and for all generations (or rounds).

**Files**

Amplicon\_design – Shows design of amplicons with position and names of amplicons

Barcodes\_and\_primers – Barcode sequences for round (or generation) specific primers and amplicon specific primers as well as primer sequences

CONSTRUCTS – Expected sequence for each amplicon considering round or generation (denoted by GEN and a number) and amplicon specific barcode

READ\_files – Brief description of the read files in the READS folder

Line\_details – Details of the barcodes and the regions of the plate used for sequencing each of the ancestral strains and evolved lines

Microtiter\_Plate\_Regions – Details of the amplicons that were sequenced in each of the four regions of the microtiter plate

**Notations**

GEN – Generation or round number (1,2,3,4,8,12 etc.)

REG – Region of the microtiter plate from which the sequence comes from