5’

P7-i7-Read2-N(0-6)-

caggtgcagctgcaggaaagcggcggcggcctggtgcaggcgggcggcagcctgcgcctgagctgcgcggcgagcggcWMTattTYTxxxxxxxxxxxxatgggctggtatcgccaggcgccgggcaaagaacgcgaaYTTgttgccRSTattRVTxxxggtRSTANTaccWATtatgcggatagcgtgaaaggccgctttaccattagccgcgataacgcgaaaaacaccgtgtatctgcagatgaacagcctgaaaccggaagataccgcggtgtattattgcgcgGYTxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxYWTxxxtattggggccagggcacccaggtgaccgtgagca

-N(0-6)-Read1-P5

3’

N(0-6) means:

Either no base or N or NN or NNN or NNNN or NNNNN or NNNNNN

The result is a staggered sequencing run:

I suggest finding ‘caggtgcagctgcaggaaag’ in RD2 as a landmark to start analyzing/counting from there.

And similarly, ‘tgctcacggtcacctgggtg’ in RD1.

CDR1

CDR2

CDR3