# Read Structure

Below is the complete read structure with primer locations / sequences labeled.

```
                          5'-ACACAAGCAGTGGTATCAACGCAGAGTGAATGGG-> (Custom Read 1 Primer (oPCf40))
5'-AATGATACGGCGACCACCGAGATCTACACAAGCAGTGGTATCAACGCAGAGTG-> (Final Amplification Primer i5 side (oPCf39))
                                |template switch oligo oPCf42|
5'-AATGATACGGCGACCACCGAGATCTACACAAGCAGTGGTATCAACGCAGAGTGAATGGG#NNNNNNNACTCCGACAAGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTACTCGATCTCGTATGCCGTCTTCTGCTTG-3'
3'-TTACTATGCCGCTGGTGGCTCTAGATGTGTTCGTCACCATAGTTGCGTCTCACTTACCC#NNNNNNNTGAGGCTGTTCTAGCCTTCTCGTGTGCAGACTTGAGGTCAGTGTAATGAGCTAGAGCATACGGCAGAAGACGAAC-5'
                                                    insert^|------#barcode#----RT Primer--------|            ########<-(i7 barcode)
                                (Final Amplification Primer i7 side (oPCf161)) <-TCTAGCCTTCTCGTGTGCAGACTTGAGGTCAGTGTAATGAGCTAGAGCATACGGCAGAAGACGAAC-5'
                                                                                <-TCTAGCCTTCTCGTGTGCAGACTTGAGGTCAGTG-5' (Illumina Read 2 Primer)
```

`read.is_reverse == False` only left-side reads for all fragments, thus all `read.template_length > 0` . Of these, `read.is_read1 == True` is the forward strand and `read.is_read2 == True` is the reverse strand.

For right-side reads (where `read.is_reverse == True`), if `read.is_read1 == True` then the read maps to the reverse strand.