Table S1- Summary of processed 454-sequencing reads

**Nbases N1 Polymer2 NumSeqs**

Minimum: 243 0 3 1

2.5%-tile: 278 0 4 2867

25%-tile: 295 0 4 28668

Median: 307 0 5 57336

75%-tile: 315 0 5 86003

97.5%-tile: 325 0 6 111804

Maximum: 346 0 8 114670

Mean: 304.646 0 4.65

# of unique seqs: 44158

total # of seqs: 114670

1 N: Number of ambiguous bases in sequence reads

2 Polymer: length of homopolymer runs in sequence reads