

Table S3 The comparison between HFSs and consensus sequences of IME09 genome.

Sequences	Calculated results
HFSs (calculated from raw reads)	360049 (s)
Genome length	166499 (bp)
Consensus sequences (extracted by degenerate motif finder)	25227 (forward: 12556, reverse: 12671)
Matched	19215 (forward: 11031, reverse: 8184)