

Table S3. Average error rates of replicated samples for iterating STACKS parameters of m (minimum number of raw reads required to form a stack) and M (distance allowed between two stacks). Standard errors are in parentheses.

Parameter	Locus error	Allele error	SNP error
Minimum number of raw reads required to form a stack (m)			
m3	0.052 (0.040)	0.019 (0.011)	0.019 (0.003)
m4	0.042 (0.035)	0.013 (0.009)	0.013 (0.003)
m5	0.036 (0.031)	0.009(0.008)	0.009 (0.002)
m6	0.034 (0.030)	0.008 (0.007)	0.008 (0.002)
m7	0.033 (0.030)	0.007 (0.007)	0.007 (0.002)
Distance allowed between two stacks (M)			
M1	0.053 (0.039)	0.021 (0.011)	0.021 (0.003)
M2	0.052 (0.040)	0.019 (0.010)	0.019 (0.003)
M3	0.052 (0.040)	0.018 (0.010)	0.018 (0.003)
M4	0.052 (0.040)	0.018 (0.010)	0.018 (0.003)
M5	0.053 (0.040)	0.018 (0.010)	0.018 (0.003)
M6	0.053 (0.040)	0.019 (0.010)	0.019 (0.003)
M7	0.053 (0.040)	0.019 (0.011)	0.019 (0.003)
M8	0.053 (0.040)	0.019 (0.011)	0.019 (0.003)