Table S1 – Barcode selection points

Feature Description	Number of Features in BMB171 Genome
Intergenic Regions > 500 bp	294
with convergently transcribed flanking genes	22
with consistent assembly and annotation between BMB171 and T03a001	4
with no repetitive structure	3

Table S2 – Primer sequences and concentrations used

Primer Name	Sequence	Final Concentration Used per Reaction
Common Tag Forward	5’-GGGGTAATGGTAATACGGATAGAT-3’	80nM
Common Tag Reverse	5’-TCATAGTATGTAAAGCGTCGGC-3’	20nM
Specific Tag1 Forward	5’-GGTAGAGCCACAAACAGC-3’	60nM
Specific Tag1 Reverse	5’-TCCAAAAAGAAAAGACACCT-3’	60nM
Specific Tag2 Forward	5’-GGTACAAGCAACGATCTCCAGAAT-3’	80nM
Specific Tag2 Reverse	5’-TGAAGGTTAATTAGCGCATTTGAA-3’	40nM
Target 1 Forward	5’-TGCGAAAGAAGAAGAATGGC-3’	78.5nM
Target 1 Reverse	5’-AGAACCAGAGGATGTATTACC-3’	83nM