

Additional File 3: Example of a grape EST contig matched by multiple MPSS signatures.

Contig ID: CTG1027770

Annotation: putative transcription factor BTF3-like mRNA

#	Signature	Abundance	Strand	Position
1	GATCTCCTCAAACAAAG	6	+	316
2	GATCTTGTTGCTGGGCA	1367	+	480
3	GATCCACTAACAAACCCA	8	-	319

MPSS signatures identified within the sense-strand sequence of CTG1027770. Uppercase text indicates the predicted ORF; lowercase indicates the predicted UTRs. Sense signatures are highlighted in blue. The position of the most abundant signature (#2) is consistent with the most-3' *DpnII* site, which is the position predicted to be measured by MPSS. Other signatures may result from signatures resulting from other transcripts, alternative polyadenylation or incomplete digestion during the construction of the cDNA library.

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gggggaagctctctcaatcactgctatccacccaaaccctagctctaaccctacccaagATGAATAGGGAGAAGCTTA
TGAAGATGGCTGGTGCAGTTCGCACCGGTGAAAGGGTAGCATGAGAAGAAAGAAGAAGGCTGTTTACAAAACAACCA
CAACTGATGACAAAAGGCTTCAAAGCACCCATAAGAGAATAGGAGTCAATGCCATACCTGCTATTGAGGAGGTCAACA
TCTTTAAAGATGATGTGGTTATTCAGTTTTTTAAACCCCAAAGTTCAAGCCTCTATAGCCGCAAACACTTGGGTTGTTA
GTGGATCTCCTCAAACAAAGAAATTGCAGGACATTCTTCCCTGGAATTATCAACCAGTTGGGACCAGATAACTTGGACA
ACCTGAGGAAGCTGGCTGAGCAGTTCCAGAAGCAGGCACCTGGTGCAGCAGCAGCCCAAGACGATGATGATG
ATGAGGTCCCCGATCTTGTGCTGGGCAGACCTTTGAAGCTGCAGCAGAAGAGGGTCACACTGCTtgagagagttttt
agaggggttttgtgccattacttataatttccaattgagagttttatcctttatcttctgtttaaccaagtgtttcatttta
tgctctccttgtgacaccatactagacagttgtatgctcctgctgaagactttactatcttccaaatgcctgatttg
gtgttgtctagttaccttaaaagcattttctcagaccatccaattccttttactttcatggttttgcctttatcagag
gaattcattttctccct
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