Yow et al., Genome Sequence of *Monilinia vaccinii-corymbosi* Sheds Light on Mummy Berry Disease Infection of Blueberry and Mating Type

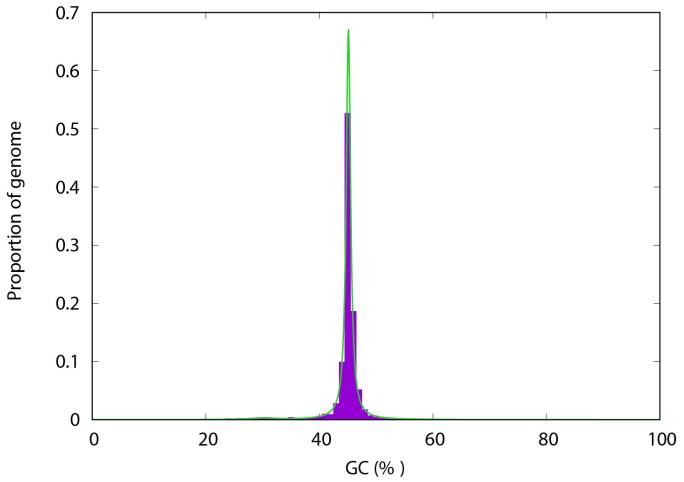


FIGURE S1. Percent GC distribution across the *Monilinia vaccinii-corymbosi* genome. Genomic binned regions are defined by OcculterCut v1.1 using default parameters.

Yow et al., Genome Sequence of *Monilinia vaccinii-corymbosi* Sheds Light on Mummy Berry Disease Infection of Blueberry and Mating Type

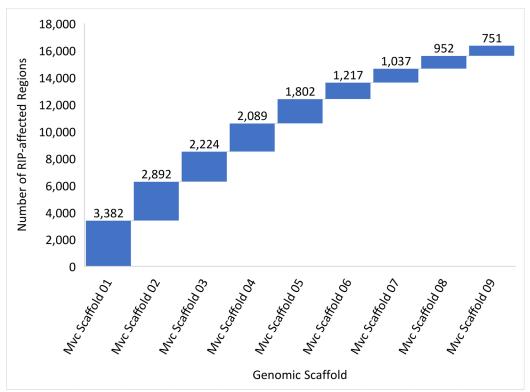


FIGURE S2. Distribution of Repeat-Induced Point mutation (RIP)-affected regions across the *Monilinia vaccinii-corymbosi* genome.

Yow et al., Genome Sequence of *Monilinia vaccinii-corymbosi* Sheds Light on Mummy Berry Disease Infection of Blueberry and Mating Type

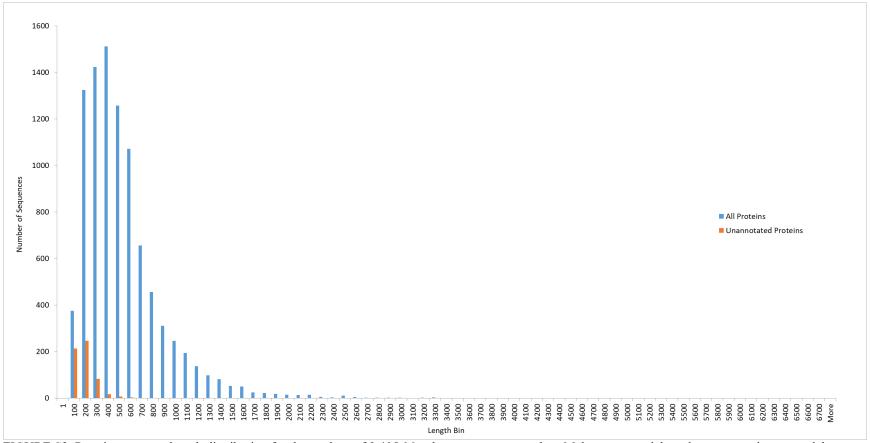


FIGURE S3. Protein sequence length distribution for the total set of 9,405 *Monilinia vaccinii-corymbosi* Maker gene models and unannotated gene models. Sequence lengths are divided into bins of 100 amino acids.

Yow et al., Genome Sequence of *Monilinia vaccinii-corymbosi* Sheds Light on Mummy Berry Disease Infection of Blueberry and Mating Type

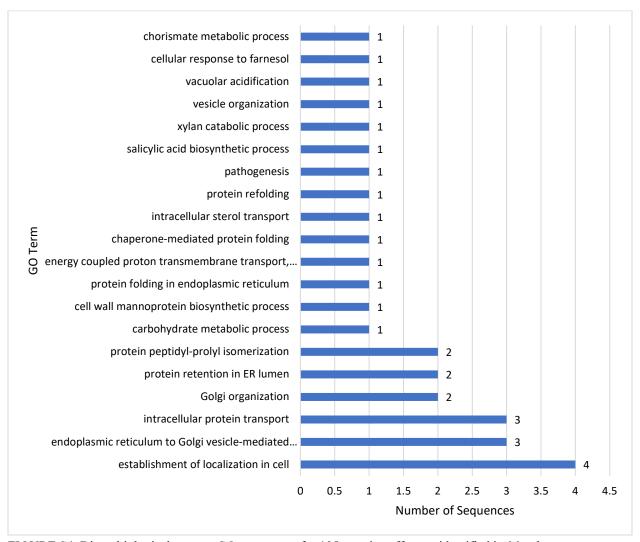


FIGURE S4. Direct biological process GO term count for 105 putative effectors identified in *Monilinia vaccinii-corymbosi* by EffectorP.

Yow et al., Genome Sequence of *Monilinia vaccinii-corymbosi* Sheds Light on Mummy Berry Disease Infection of Blueberry and Mating Type

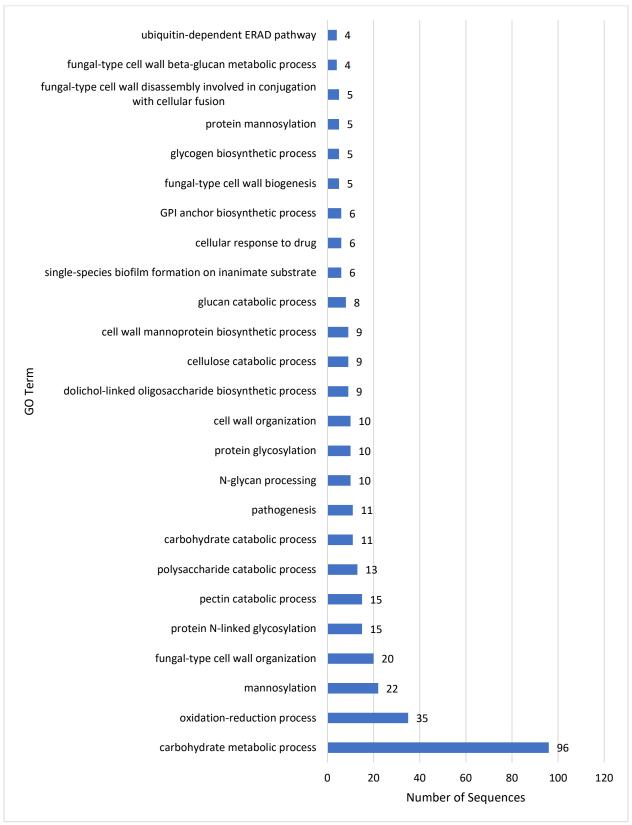


FIGURE S5. Direct biological process GO term count for 366 putative CAZymes identified in *Monilinia vaccinii-corymbosi* by dbCAN2. Only the first 25 GO terms are shown.

Yow et al., Genome Sequence of *Monilinia vaccinii-corymbosi* Sheds Light on Mummy Berry Disease Infection of Blueberry and Mating Type

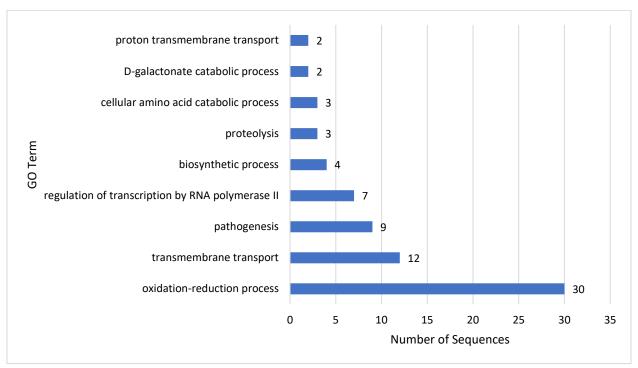


FIGURE S6. Direct biological process GO term count for 90 SM biosynthesis-related genes identified in *Monilinia vaccinii-corymbosi* by SMURF. Only GO terms with >1 sequence are shown.

Yow et al., Genome Sequence of *Monilinia vaccinii-corymbosi* Sheds Light on Mummy Berry Disease Infection of Blueberry and Mating Type

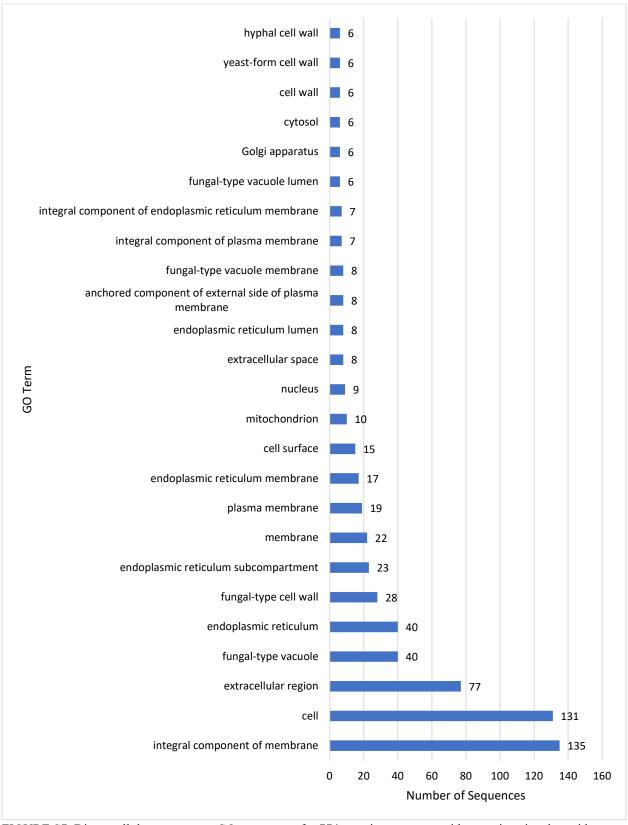


FIGURE S7. Direct cellular component GO term count for 774 protein sequences with secretion signal peptides identified in *Monilinia vaccinii-corymbosi* by SignalP. Only the first 25 GO terms are shown.

Yow et al., Genome Sequence of *Monilinia vaccinii-corymbosi* Sheds Light on Mummy Berry Disease Infection of Blueberry and Mating Type

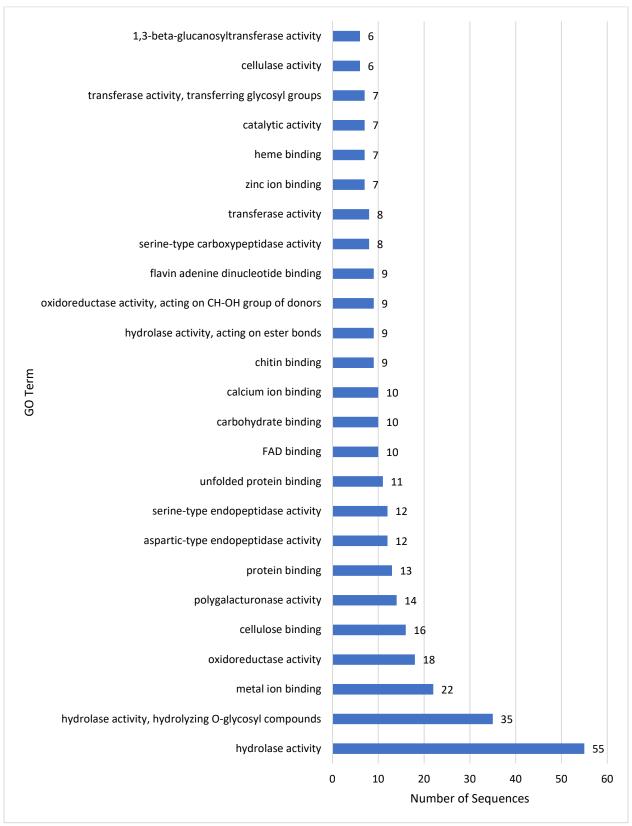


FIGURE S8. Direct molecular function GO term count for 774 protein sequences with secretion signal peptides identified in *Monilinia vaccinii-corymbosi* by SignalP. Only the first 25 GO terms are shown.

Yow et al., Genome Sequence of *Monilinia vaccinii-corymbosi* Sheds Light on Mummy Berry Disease Infection of Blueberry and Mating Type

Ss	ATACCCTTATGAGAGATACCA-ATGTCAGAAGAACTGTCTCTGAGTACCTTGCTCTTGTA	5
Sm	ATACCCTTATGAGAGATACCA-ATGTCAGAAGAACTGTCTCTGAGTACCTTGCTCTTGTA	5
St	ATACCCTTATGAGAGACGCTA-ATGTCAAGAGAACCGTCTCTGAATTTCTTGTTCTTGTA	5
Mvc-1	ACACTCTCATGAGAGATGCTG-GTGTCAAGAGAACTGTTGCCGAATTCCTCTTTGTTGCA	5
Mvc-2	ATACCATCATGCAAAGTCCTCGTGAAAAGGGAAACTGTTGCTGAATTCCTCTTCGTAGCA	6
	• ** * ** * * * * * * * * * * * * * * *	*
Ss	TGTCCTTACATTGGTATCCTTGCTGTTAATGATTATCTTACCGATCTCAATTGGATA	1
Sm	TGTCCTTATATTGGTATCCTTGCTGTTAATGATTATCTTACCGATCTCAATTGGATA	1
St	TGTCCTTATGTTGGTATCCTTGCTGTTAA <mark>TGATTACCTTGTCAATCTCAATTGGACA</mark>	1
√lvc-1	TGCCCATACATTGGTATAATCTCAATTAGCAATTATCTTTCTGATCTAAACTGG <mark>ACA</mark>	1
√vc-2	TGTTCATACATTATTAGTATAATCTCAATTAACAATTACTTTTCTAACTTAAACTAA <mark>ACA</mark>	1
	** * * * ** ** * * * * * * * * * * * * *	
Ss	TTCGAAACAAATGAAGAAGGGATTGTTTTGTCTTCGTCAAACTTCTCCATCAGATATCCGT	1
Sm	TTCGAAACAAATGAAGAAGGGATTGTCTGTCTTCGTCAAACTTCTCCATCAGATATCCGT	1
St	$\tt CTCGAAACAAATGAAGAAGGGATTGTCTGTCTTCGTCAAACTTTTCCACCAGATATCCGT$	1
VI∨c-1	TTTGAAACCAATGAAAAAAGTACTGTTTGTCTTCGTCAAGTTTCTTTACCAGATATAACC	1 -
∕lvc-2	TTTGAAACCAATGAAAAAAGTACTGTTTGTCTTCGTCAAGTTTCTTTACCAGATATAACC * **** **** ** * * * * * * * * * * *	1
Ss		
Sm	TCGTTTCCAGCACATATCGCTAGAACTACCTTGACAGATTTGGACGTTATCACTTTCTGT	
St	TTGTTTCCAGCACATATCGCTAGAACTACCTTGACAGATTTGGATGTTATCACTTTCTGT TCATTTTCAGCACACACGCTAGCACTACCTTAACAGATTTGGACATCACTACACTTTCTGT	_
√vc-1	TTATTTTCAGCACACATCATCGCTAGCACTACCTTAACAGATTTGGACATCATCATCTTTTGT	
	TITI I I I I I I I I I I I I I I I I I	_
	ТТАТТТА АСА АСАТАТТСССА СА АСТА АСТО В СТО В СТ	_
Mvc-2	TTATTTACACAACATATTGCCAGAACTAACTTGACAGATTTGGACATCATCAACTTTTGT * *** * *** ** ** ** *** *** *** ***	
∕lvc-2	* *** * *** ** ** ** ** *** *** *** * *	
Mvc-2 Ss	* *** * *** ** ** ** ** *** *** *** **	
Mvc-2 Ss Sm	* *** * *** ** ** ** ** *** *** *** * *	
	* *** * *** ** ** ** ** *** *** *** **	

FIGURE S9. Multiple sequence alignment of repeat sequences (highlighted) and flanking sequences (not highlighted) present in *MAT* loci of *Sclerotinia* spp. and *Monilinia vaccinii-corymbosi* (*Mvc*). Asterisks indicate nucleotide positions that are identical in all six sequences. Ss: *Sclerotinia sclerotiorum* 250 bp inverted repeat sequence and flanking sequences from the first copy in the Inv- allele (GenBank: JQ815883.1); Sm: *S. minor* 256 bp repeat sequence and flanking sequences from the first copy in the Inv- allele (GenBank: KC894719.1); St: *S. trifoliorum* 146 bp repeat from the single copy present in the S-type idiomorph (GenBank: KU726097.1); Mvc-1: 115 bp direct repeat and flanking sequences from the *tfMAT1-1-1* copy; Mvc-2: 115 bp direct repeat and flanking sequences from the *tfMAT1-2-10* copy.