

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**

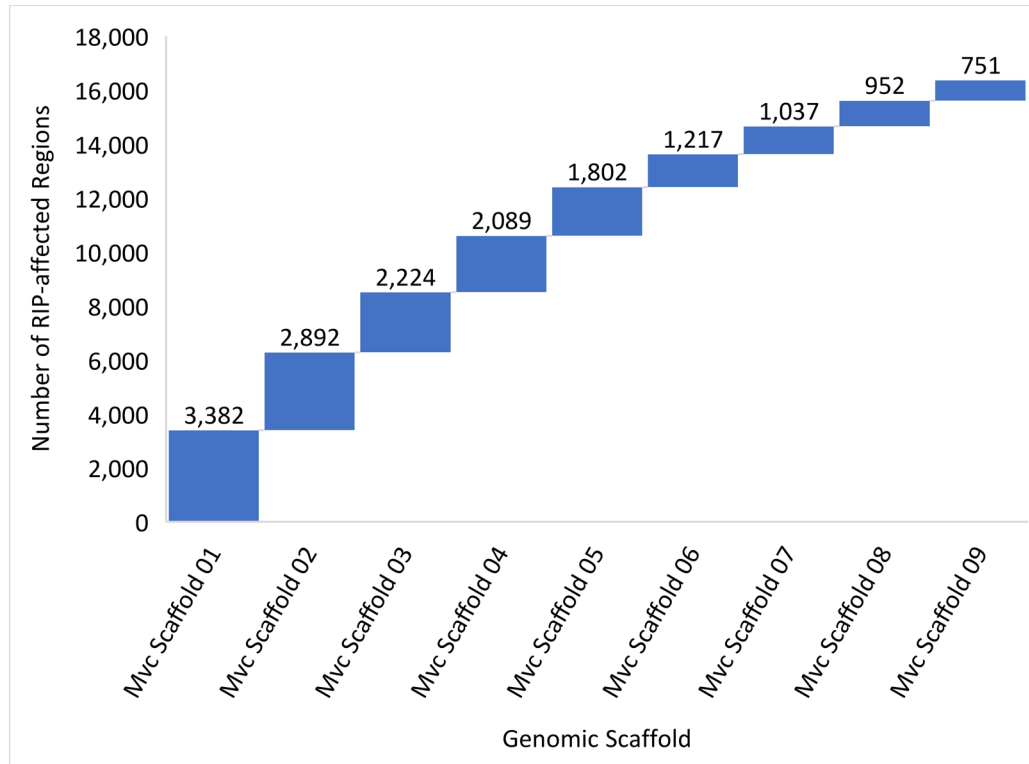


FIGURE S2. Distribution of Repeat-Induced Point mutation (RIP)-affected regions across the *Monilinia vaccinii-corymbosi* genome.

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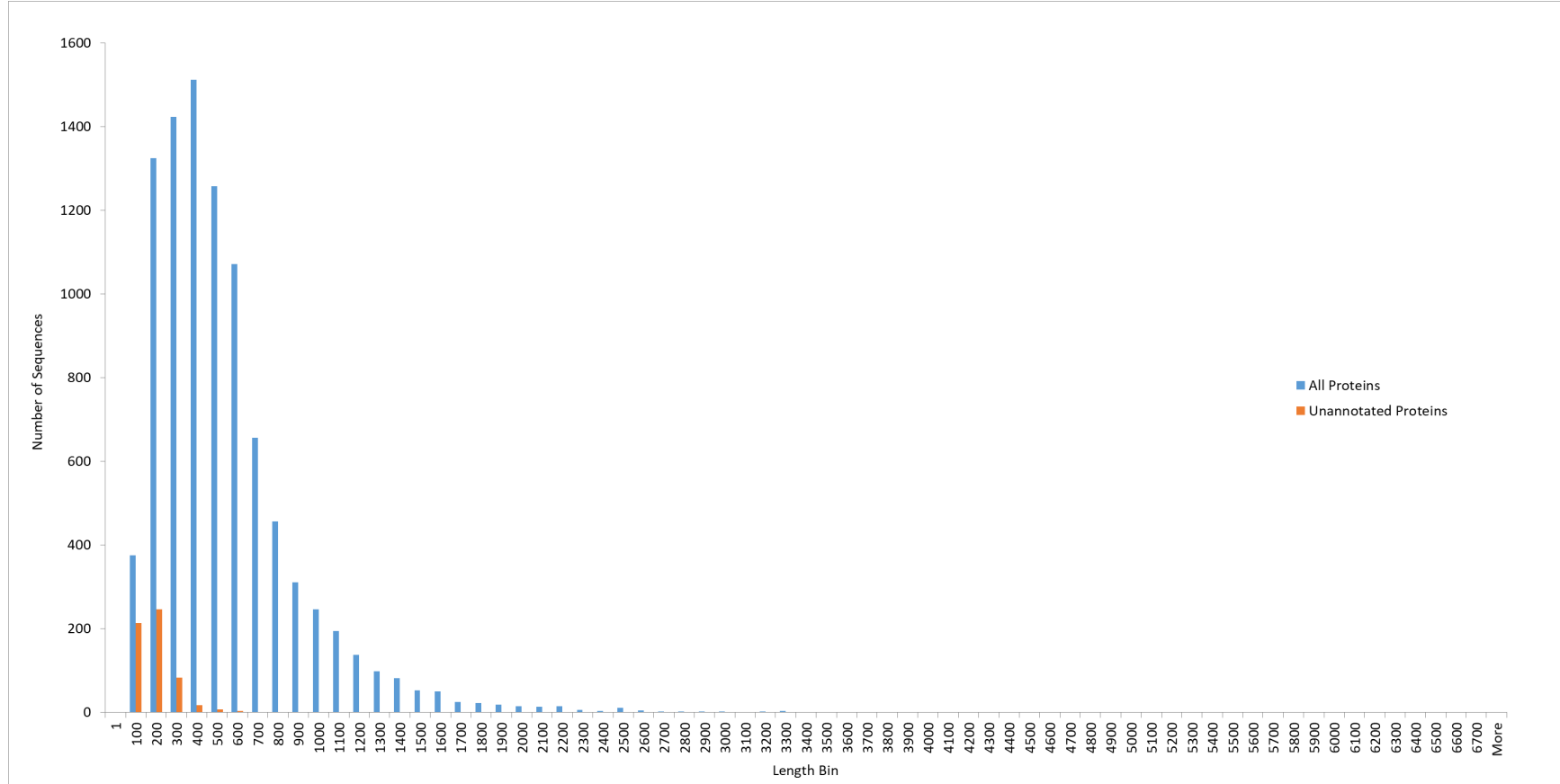


FIGURE S3. Protein sequence length distribution for the total set of 9,405 *Monilinia vaccinii-corymbosi* Maker gene models and unannotated gene models. Sequence lengths are divided into bins of 100 amino acids.

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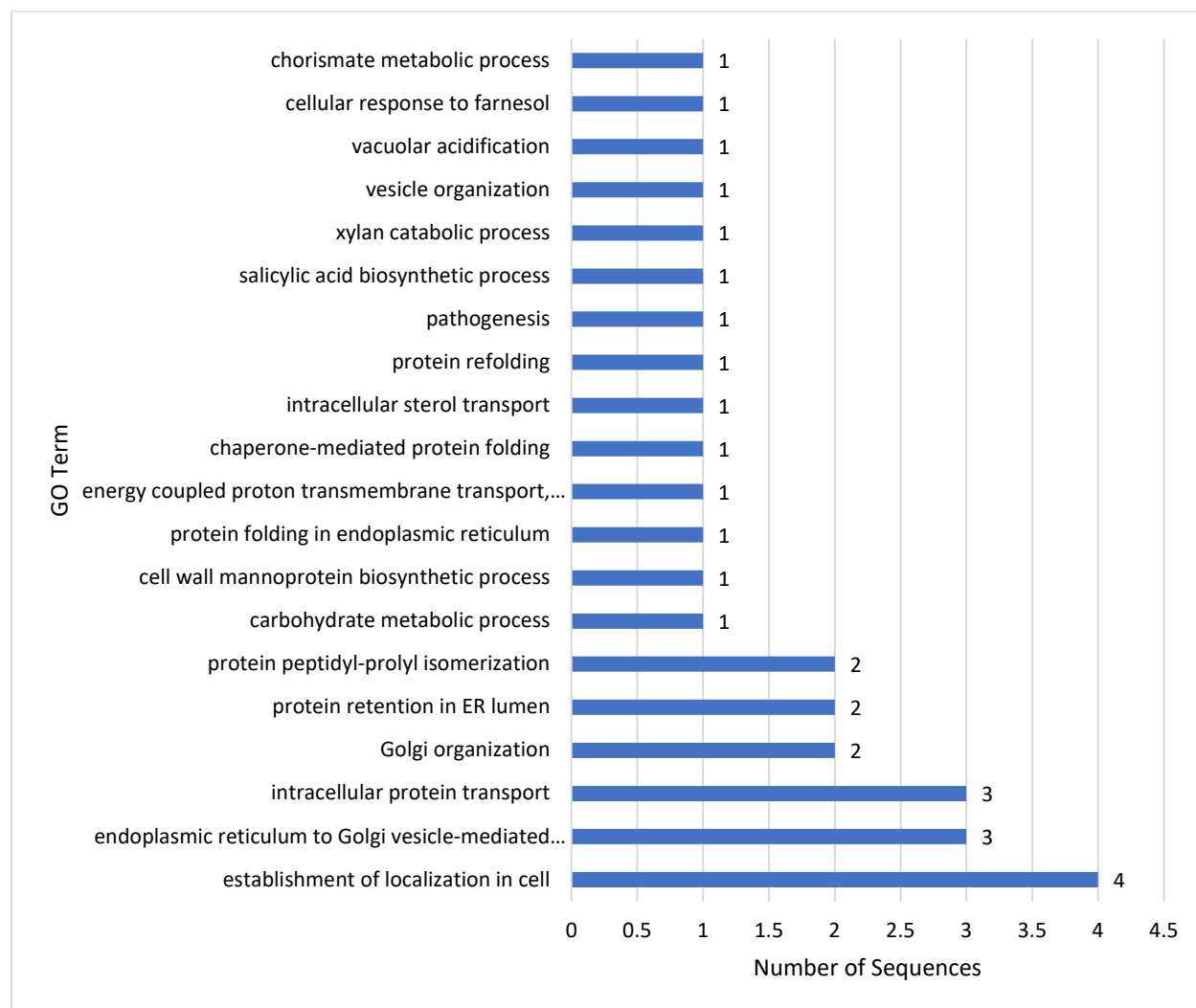


FIGURE S4. Direct biological process GO term count for 105 putative effectors identified in *Monilinia vaccinii-corymbosi* by EffectorP.

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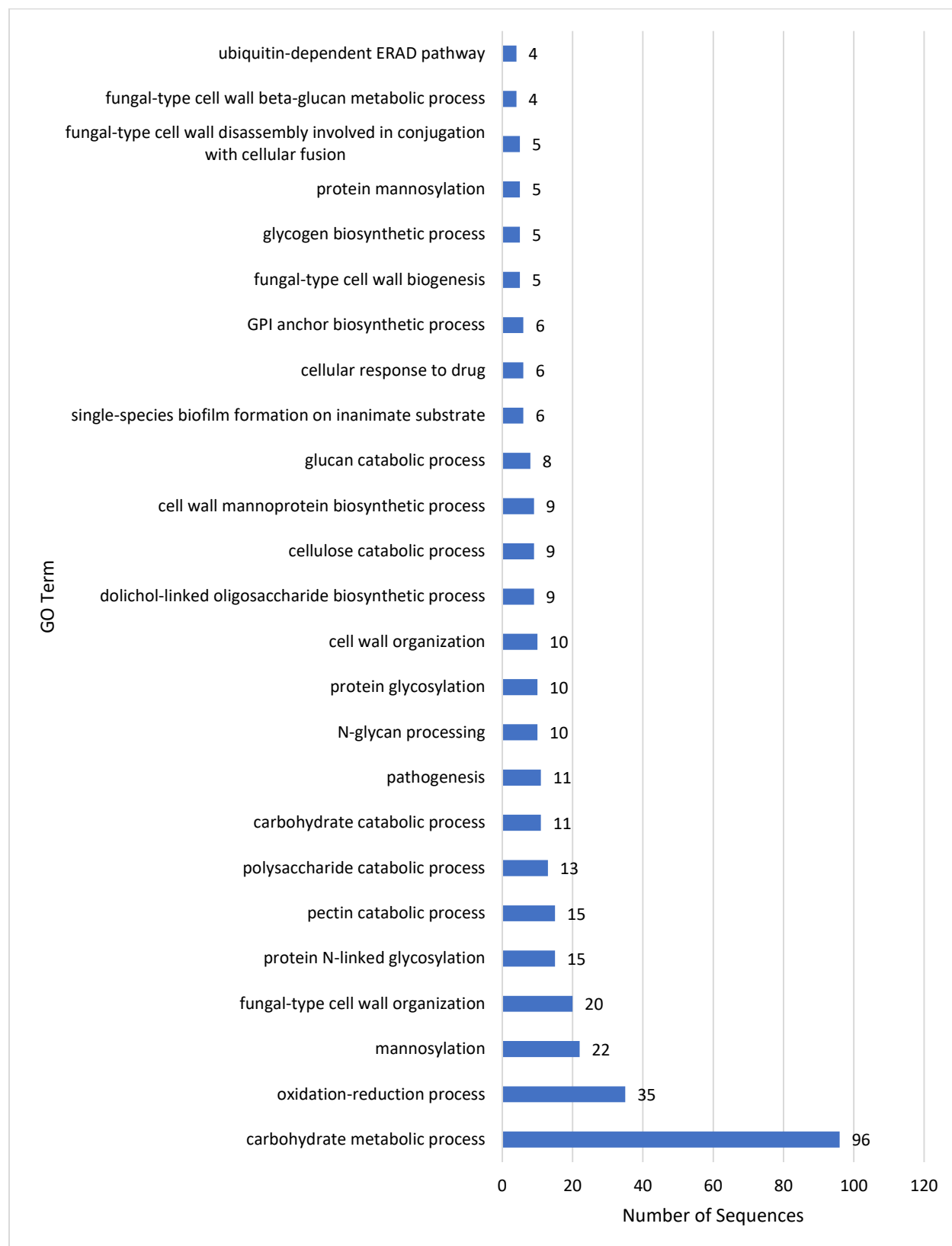


FIGURE S5. Direct biological process GO term count for 366 putative CAZymes identified in *Monilinia vaccinii-corymbosi* by dbCAN2. Only the first 25 GO terms are shown.

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

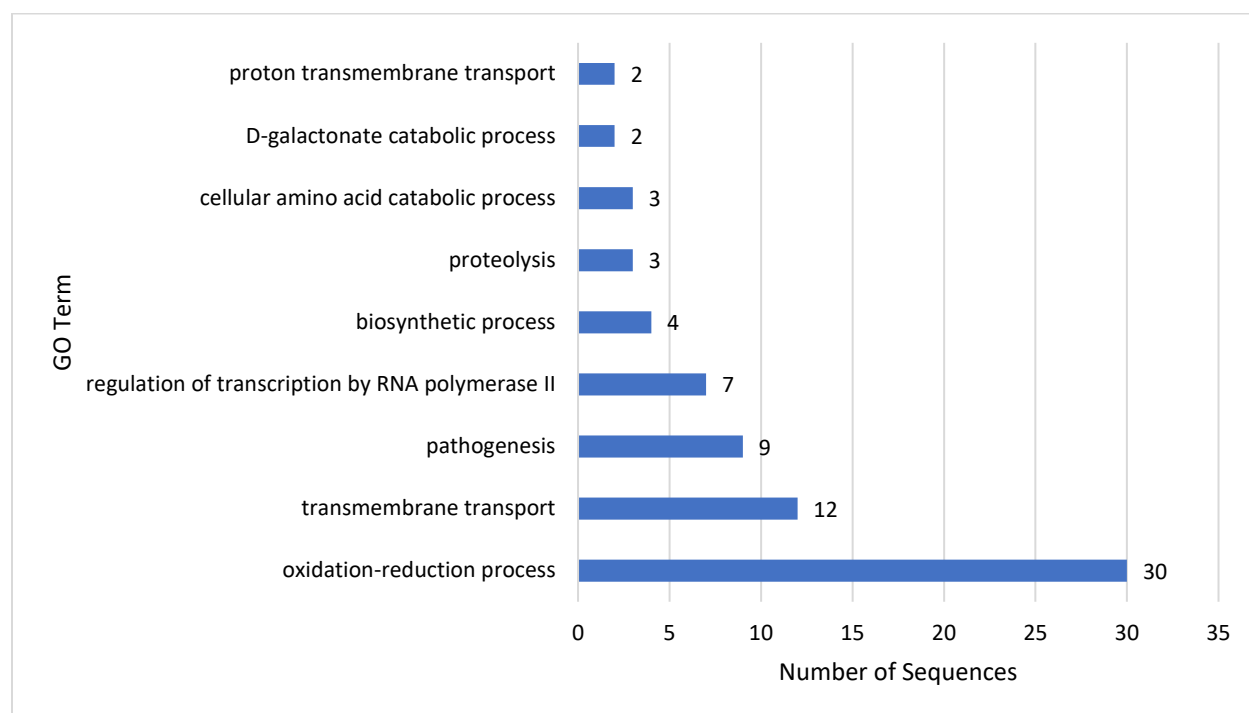


FIGURE S6. Direct biological process GO term count for 90 SM biosynthesis-related genes identified in *Monilinia vaccinii-corymbosi* by SMURF. Only GO terms with >1 sequence are shown.

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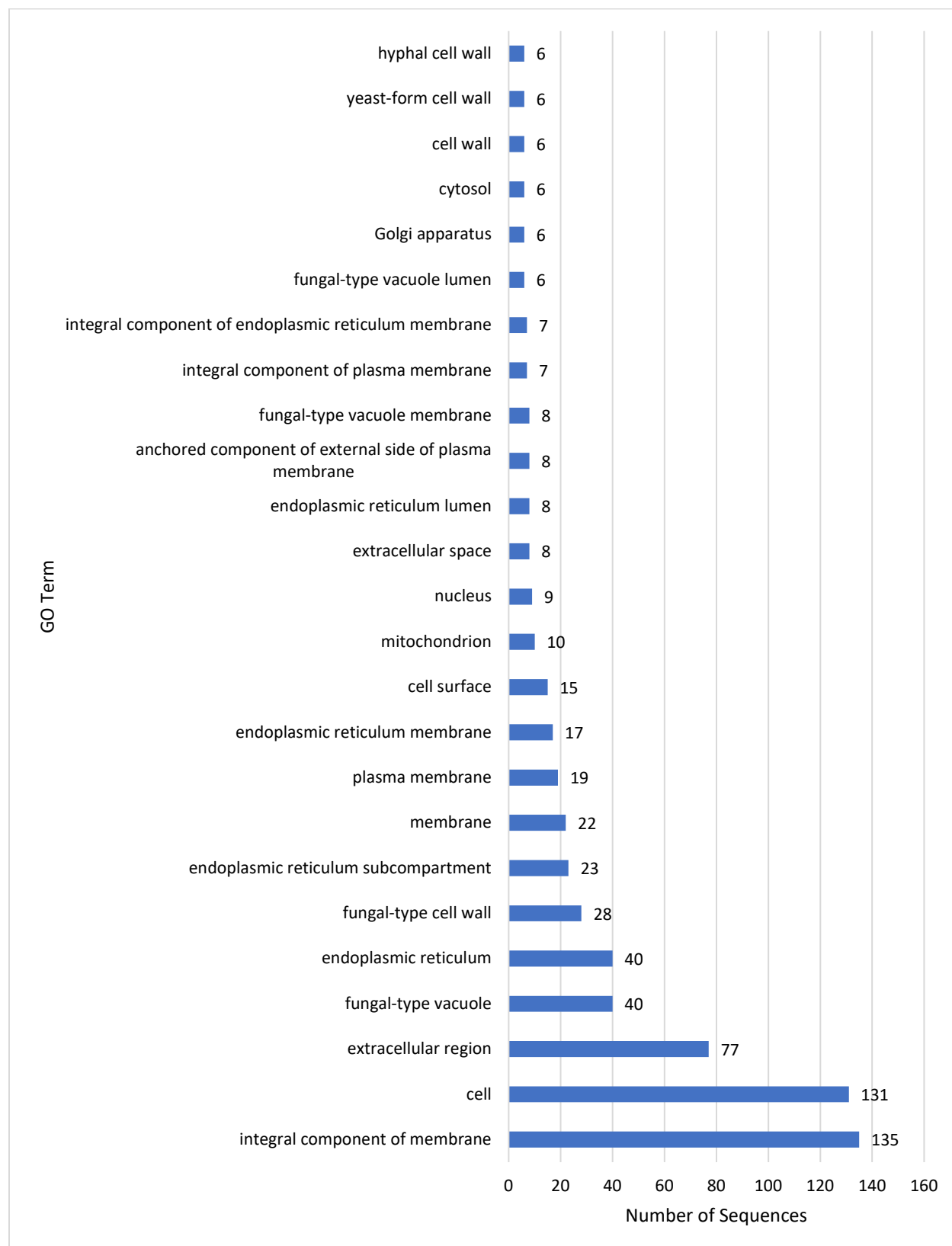


FIGURE S7. Direct cellular component GO term count for 774 protein sequences with secretion signal peptides identified in *Monilinia vaccinii-corymbosi* by SignalP. Only the first 25 GO terms are shown.

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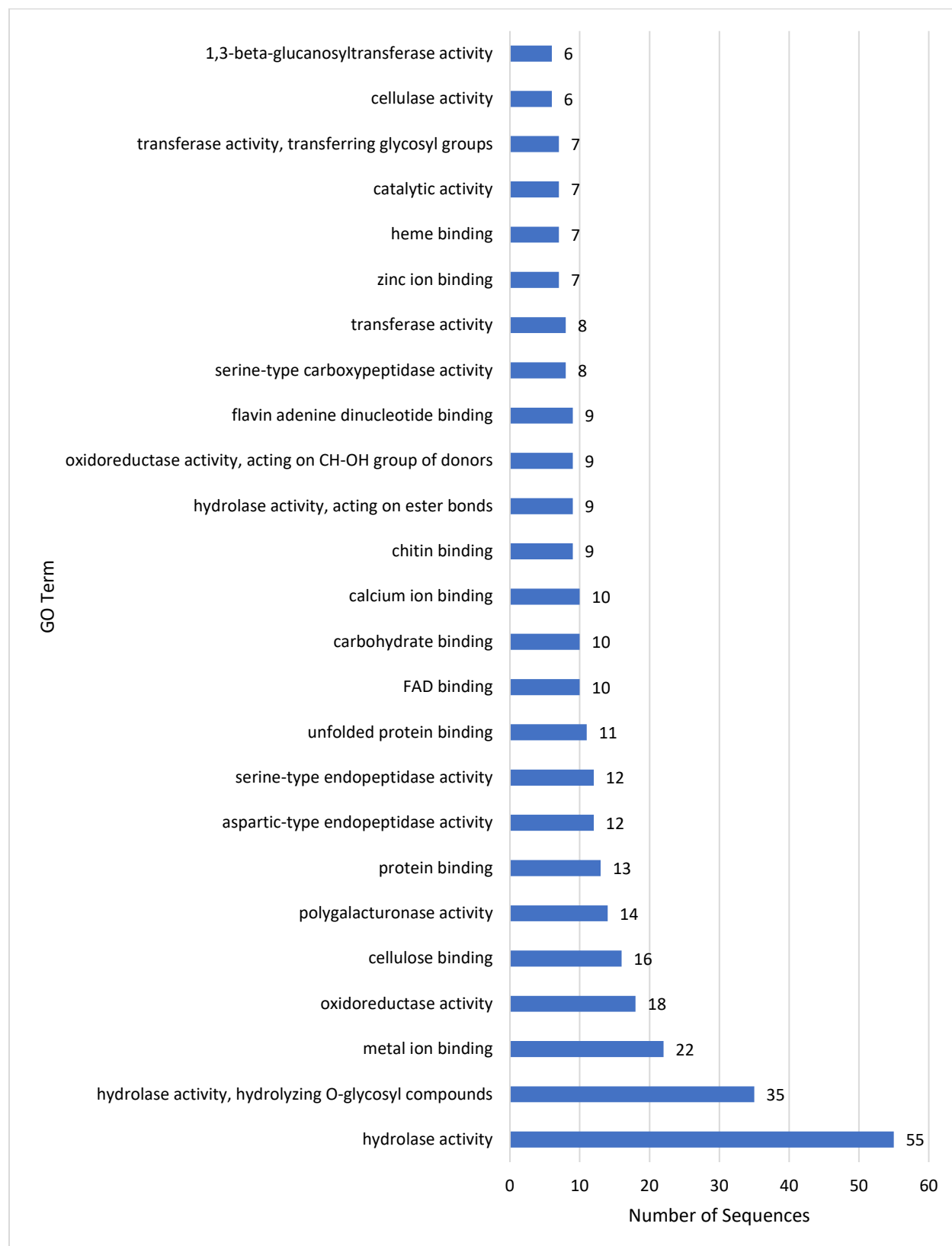


FIGURE S8. Direct molecular function GO term count for 774 protein sequences with secretion signal peptides identified in *Monilinia vaccinii-corymbosi* by SignalP. Only the first 25 GO terms are shown.



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

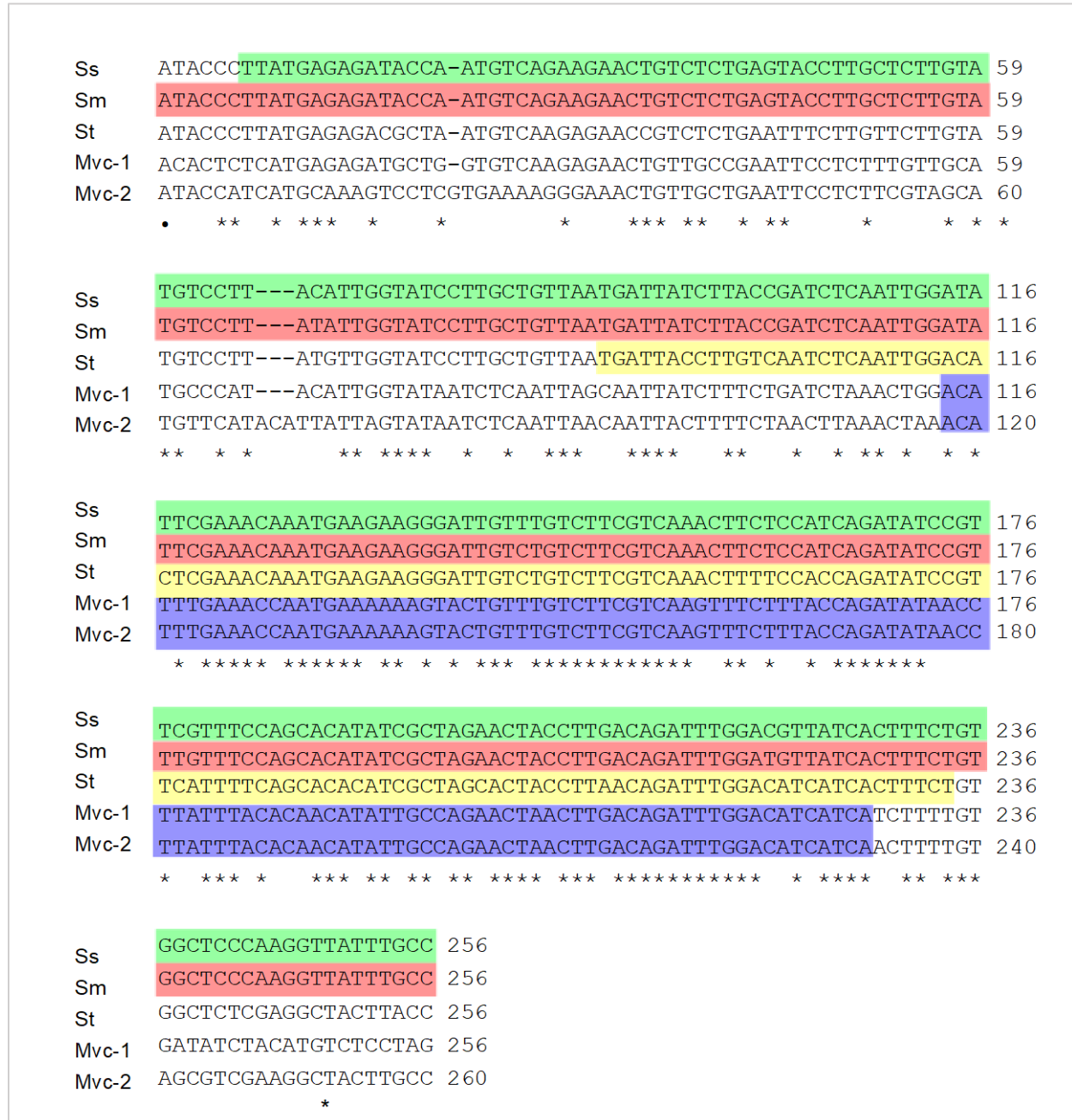


FIGURE S9. Multiple sequence alignment of repeat sequences (highlighted) and flanking sequences (not highlighted) present in *MAT* loci of *Sclerotinia* spp. and *Monilinia vaccinii-corymbosi* (Mvc). Asterisks indicate nucleotide positions that are identical in all six sequences. Ss: *Sclerotinia sclerotiorum* 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.