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TABLE S1. Summary statistics of PacBio genomic library Sequel and RSII runs.

<b>Name</b>	<b>Total Bases (Gb)</b>	<b>Number of Subreads</b>	<b>Total Length of Subreads (bp)</b>	<b>Average Subread Length (bp)</b>
NCSU Sequel SMRT 1	2.3	598,771	2,266,251,245	4,135
NCSU Sequel SMRT 2	2.2	559,740	2,180,250,324	4,419
NCSU Sequel SMRT 3	2.6	683,036	2,570,244,405	4,355
NCSU Sequel SMRT 4	2.8	863,469	2,786,669,336	3,513
UF RSII SMRT 1	1.4	194,830	1,455,041,026	7,539
UF RSII SMRT 2	1.1	152,785	1,082,248,013	7,160
<b>Total</b>	12.4	3,052,631	12,340,704,349	-

TABLE S2. Summary statistics of Hi-C library Illumina NextSeq500 run.

<b>Name</b>	<b>Total Bases (bp)</b>	<b>Number of Reads</b>	<b>Total Bases After Trimming (bp)</b>	<b>Number of Reads After Trimming</b>
Mvc-RL1 Hi-C	26,005,669,980	172,222,980	22,837,383,723	172,200,538

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TABLE S3. Contig makeup for *Monilinia vaccinii-corymbosi* HGAP4\_59 Assembly.

Contig Name	Contig Length (bp)	Sequence Content
MvcIV1-Contig1	5,195,418	Nuclear
MvcIV1-Contig2	4,062,641	Nuclear
MvcIV1-Contig3	3,929,668	Nuclear
MvcIV1-Contig4	3,635,407	Nuclear
MvcIV1-Contig5	3,356,619	Nuclear
MvcIV1-Contig6	2,573,042	Nuclear
MvcIV1-Contig7	2,240,868	Nuclear
MvcIV1-Contig8	1,745,410	Nuclear
MvcIV1-Contig9	1,415,376	Nuclear
MvcIV1-Contig10	1,312,492	Nuclear
MvcIV1-Contig11	540,959	Nuclear
MvcIV1-Contig12	122,821	mitochondrial
MvcIV1-Contig13	57,143	rDNA repeat
MvcIV1-Contig14	51,741	mitochondrial
MvcIV1-Contig15	50,784	rDNA repeat
MvcIV1-Contig16	50,106	rDNA repeat
MvcIV1-Contig17	35,562	mitochondrial
MvcIV1-Contig18	32,565	mitochondrial
MvcIV1-Contig19	29,674	mitochondrial
MvcIV1-Contig20	28,469	mitochondrial
MvcIV1-Contig21	27,795	mitochondrial
MvcIV1-Contig22	27,483	mitochondrial
MvcIV1-Contig23	24,953	mitochondrial
MvcIV1-Contig24	24,029	mitochondrial
MvcIV1-Contig25	23,915	mitochondrial
MvcIV1-Contig26	22,919	rDNA repeat
MvcIV1-Contig27	22,452	mitochondrial
MvcIV1-Contig28	22,343	mitochondrial
MvcIV1-Contig29	20,839	mitochondrial
MvcIV1-Contig30	20,549	mitochondrial
MvcIV1-Contig31	20,034	mitochondrial
MvcIV1-Contig32	18,380	mitochondrial
MvcIV1-Contig33	16,447	mitochondrial
MvcIV1-Contig34	15,865	mitochondrial
MvcIV1-Contig35	15,716	mitochondrial
MvcIV1-Contig36	15,655	mitochondrial
MvcIV1-Contig37	15,341	mitochondrial
MvcIV1-Contig38	13,399	rDNA repeat
MvcIV1-Contig39	13,335	mitochondrial

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Contig Name	Contig Length (bp)	Sequence Content
MvcIV1-Contig40	12,349	mitochondrial
MvcIV1-Contig41	11,873	rDNA repeat
MvcIV1-Contig42	11,537	rDNA repeat
MvcIV1-Contig43	10,999	mitochondrial
MvcIV1-Contig44	10,688	nuclear*
MvcIV1-Contig45	10,569	mitochondrial
MvcIV1-Contig46	9,163	mitochondrial
MvcIV1-Contig47	8,857	mitochondrial
MvcIV1-Contig48	8,756	rDNA repeat
MvcIV1-Contig49	7,481	mitochondrial
MvcIV1-Contig50	6,982	mitochondrial
MvcIV1-Contig51	6,698	mitochondrial
MvcIV1-Contig52	6,272	mitochondrial
MvcIV1-Contig53	6,238	mitochondrial
MvcIV1-Contig54	4,703	mitochondrial
MvcIV1-Contig55	4,209	mitochondrial
MvcIV1-Contig56	4,096	mitochondrial
MvcIV1-Contig57	4,035	mitochondrial
MvcIV1-Contig58	3,536	mitochondrial
MvcIV1-Contig59	1,353	mitochondrial

Asterisk (\*) denote a small nuclear contig encoding a retrotransposon and low complexity sequences.

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TABLE S4. Statistics for centromeric regions of *Monilinia vaccinii-corymbosi* (Mvc) nuclear genome scaffolds.

Scaffold ID	Scaffold Length	Estimated Centromere Length	GC Content (%)	Number of Genes	Number of Genes Per Kb	Tandem Repeats
Mvc_scaffold_01	6,208,549	32,000	33.8	5	0.16	47
Mvc_scaffold_02	5,195,418	38,000	23.5	3	0.08	93
Mvc_scaffold_03	4,062,641	30,000	24.3	6	0.20	106
Mvc_scaffold_04	3,929,668	30,000	25.9	6	0.20	59
Mvc_scaffold_05	3,356,619	35,000	23.0	5	0.14	87
Mvc_scaffold_06	2,240,868	38,000	22.7	4	0.11	101
Mvc_scaffold_07*	1,853,551	50,000	44.5	17	0.34	20
Mvc_scaffold_08	1,745,410	29,000	17.7	5	0.17	32
Mvc_scaffold_09	1,415,376	41,000	23.8	4	0.10	66

\*Scaffold 07 does not appear to have an actual centromere.

TABLE S5. Results for Repeat-Induced Point (RIP) di-nucleotide mutation analysis of *Monilinia vaccinii-corymbosi* genomic repeats. Alignment-based RIP mutation analysis was performed using the degenerate consensus model of RIPCAL v2.0.

Repeat Class	CA → TA	CC → TC	CG → TG	CT → TT	CA → TA	CC → TC	CG → TG	CT → TT
					CN → TN	CN → TN	CN → TN	CN → TN
Copia	735	204	182.67	586.17	0.43	0.12	0.11	0.34
MuDR	122.5	104.75	9	354.5	0.21	0.18	0.02	0.60
rRNA	1173.92	2109.58	1644.33	1571.08	0.18	0.32	0.25	0.24
Gypsy	8249.92	1548.03	2727.75	10320	0.36	0.07	0.12	0.45
EnSpm-CACTA	18	3	40.5	36	0.18	0.03	0.42	0.37
Tad1	179.25	58.33	104.5	181.67	0.34	0.11	0.20	0.35
Mariner	80	26.5	25.5	89.5	0.36	0.12	0.12	0.40
Harbinger	19.75	45.5	4.5	111	0.11	0.25	0.02	0.61

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TABLE S6. Fisher's Exact Test results for GO cellular component term enrichment of putative effectors identified by EffectorP in *Monilinia vaccinii-corymbosi* (*Mvc*). The EffectorP subset was compared to the entire set of *Mvc* predicted gene models.

Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:0110165	cellular anatomical entity	CELLULAR_COMPONENT	1.53E-14
[UNDER]	GO:0005622	intracellular	CELLULAR_COMPONENT	4.45E-12
[UNDER]	GO:0043229	intracellular organelle	CELLULAR_COMPONENT	2.63E-09
[UNDER]	GO:0043226	organelle	CELLULAR_COMPONENT	2.63E-09
[UNDER]	GO:0043227	membrane-bounded organelle	CELLULAR_COMPONENT	5.18E-08
[UNDER]	GO:0043231	intracellular membrane-bounded organelle	CELLULAR_COMPONENT	1.32E-07
[UNDER]	GO:0032991	protein-containing complex	CELLULAR_COMPONENT	8.95E-07
[UNDER]	GO:0005634	nucleus	CELLULAR_COMPONENT	1.49E-06
[UNDER]	GO:0005737	cytoplasm	CELLULAR_COMPONENT	1.58E-06
[UNDER]	GO:0043228	non-membrane-bounded organelle	CELLULAR_COMPONENT	2.52E-04
[UNDER]	GO:0043232	intracellular non-membrane-bounded organelle	CELLULAR_COMPONENT	2.52E-04

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TABLE S7. Distribution of the *Monilinia vaccinii-corymbosi* CAZyome predicted by dbCAN2.

Enzyme Class	Family	Number of Sequences
Glycoside hydrolases (GH)	GH1	3
	GH2	2
	GH3	9
	GH5	14
	GH6	1
	GH7	3
	GH10	2
	GH11	2
	GH12	3
	GH13	9
	GH15	3
	GH16	18
	GH17	6
	GH18	10
	GH20	1
	GH26	1
	GH27	3
	GH28	16
	GH31	4
	GH32	1
	GH35	3
	GH36	1
	GH37	1
	GH38	1
	GH43	6
	GH45	2
	GH47	7
	GH51	2

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Enzyme Class	Family	Number of Sequences
	GH53	2
	GH54	1
	GH55	3
	GH63	1
	GH64	2
	GH65	2
	GH71	3
	GH72	5
	GH76	9
	GH78	3
	GH79	2
	GH81	1
	GH89	1
	GH92	5
	GH93	1
	GH95	1
	GH105	2
	GH106	1
	GH114	1
	GH115	1
	GH125	3
	GH127	2
	GH128	4
	GH131	2
	GH132	2
	GH135	2
	GH145	1
	GH152	1
	Total	198
Glycosyltransferases (GT)	GT1	5

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Enzyme Class	Family	Number of Sequences
	GT2	17
	GT3	1
	GT4	4
	GT8	5
	GT15	4
	GT17	2
	GT20	3
	GT21	1
	GT22	4
	GT24	1
	GT25	3
	GT31	4
	GT32	4
	GT33	1
	GT34	2
	GT35	1
	GT39	3
	GT41	2
	GT48	1
	GT50	1
	GT57	2
	GT58	1
	GT59	1
	GT62	3
	GT66	1
	GT69	3
	GT71	5
	GT76	1
	GT90	3
	Total	89



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Enzyme Class	Family	Number of Sequences
Polysaccharide Lyases (PL)	PL1	4
	PL7	1
	Total	5
Carbohydrate esterases (CE)	CE4	3
	CE5	3
	CE8	4
	CE9	2
	CE12	3
	CE16	6
	Total	21
Auxiliary Activities (AA)	AA1	8
	AA3	22
	AA4	1
	AA5	4
	AA6	1
	AA7	2
	AA9	7
	AA11	2
	AA16	1
	Total	48
Carbohydrate-binding module (CBM)	CBM1	1
	CBM18	6
	CBM20	2
	CBM21	1
	CBM24	1
	CBM42	1
	CBM43	1
	CBM48	1
	Total	14

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TABLE S8. Fisher's Exact Test results for GO biological process term enrichment of CAZymes identified by dbCAN2 in *Monilinia vaccinii-corymbosi* (*Mvc*). The dbCAN2 subset was compared to the entire set of *Mvc* predicted gene models.

Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:0034641	cellular nitrogen compound metabolic process	BIOLOGICAL_PROCESS	4.06E-34
[UNDER]	GO:0006725	cellular aromatic compound metabolic process	BIOLOGICAL_PROCESS	2.11E-30
[UNDER]	GO:0046483	heterocycle metabolic process	BIOLOGICAL_PROCESS	2.11E-30
[UNDER]	GO:0006139	nucleobase-containing compound metabolic process	BIOLOGICAL_PROCESS	6.76E-30
[UNDER]	GO:1901360	organic cyclic compound metabolic process	BIOLOGICAL_PROCESS	3.48E-28
[UNDER]	GO:0090304	nucleic acid metabolic process	BIOLOGICAL_PROCESS	8.56E-27
[UNDER]	GO:0010467	gene expression	BIOLOGICAL_PROCESS	1.21E-25
[UNDER]	GO:0044271	cellular nitrogen compound biosynthetic process	BIOLOGICAL_PROCESS	5.16E-22
[UNDER]	GO:0016070	RNA metabolic process	BIOLOGICAL_PROCESS	7.27E-22
[UNDER]	GO:0065007	biological regulation	BIOLOGICAL_PROCESS	1.05E-20
[UNDER]	GO:0050789	regulation of biological process	BIOLOGICAL_PROCESS	2.74E-18
[UNDER]	GO:0050794	regulation of cellular process	BIOLOGICAL_PROCESS	1.90E-17
[UNDER]	GO:0019438	aromatic compound biosynthetic process	BIOLOGICAL_PROCESS	2.81E-16
[UNDER]	GO:0051179	localization	BIOLOGICAL_PROCESS	1.26E-15
[UNDER]	GO:0018130	heterocycle biosynthetic process	BIOLOGICAL_PROCESS	3.15E-15
[UNDER]	GO:1901362	organic cyclic compound biosynthetic process	BIOLOGICAL_PROCESS	4.38E-15
[UNDER]	GO:0034654	nucleobase-containing compound biosynthetic process	BIOLOGICAL_PROCESS	6.30E-15
[UNDER]	GO:0006996	organelle organization	BIOLOGICAL_PROCESS	2.20E-14
[UNDER]	GO:0019222	regulation of metabolic process	BIOLOGICAL_PROCESS	3.04E-14
[UNDER]	GO:0060255	regulation of macromolecule metabolic process	BIOLOGICAL_PROCESS	3.79E-14
[UNDER]	GO:0051234	establishment of localization	BIOLOGICAL_PROCESS	6.65E-14
[UNDER]	GO:0080090	regulation of primary metabolic process	BIOLOGICAL_PROCESS	1.35E-13
[UNDER]	GO:0051171	regulation of nitrogen compound metabolic process	BIOLOGICAL_PROCESS	3.19E-13
[UNDER]	GO:0006810	transport	BIOLOGICAL_PROCESS	3.56E-13
[UNDER]	GO:0031323	regulation of cellular metabolic process	BIOLOGICAL_PROCESS	5.66E-13
[UNDER]	GO:0010468	regulation of gene expression	BIOLOGICAL_PROCESS	7.25E-13
[UNDER]	GO:0031326	regulation of cellular biosynthetic process	BIOLOGICAL_PROCESS	1.68E-12
[UNDER]	GO:0009889	regulation of biosynthetic process	BIOLOGICAL_PROCESS	1.68E-12

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Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:2000112	regulation of cellular macromolecule biosynthetic process	BIOLOGICAL_PROCESS	9.26E-12
[UNDER]	GO:0010556	regulation of macromolecule biosynthetic process	BIOLOGICAL_PROCESS	9.26E-12
[UNDER]	GO:0019219	regulation of nucleobase-containing compound metabolic process	BIOLOGICAL_PROCESS	2.14E-11
[UNDER]	GO:0032774	RNA biosynthetic process	BIOLOGICAL_PROCESS	3.27E-11
[UNDER]	GO:0097659	nucleic acid-templated transcription	BIOLOGICAL_PROCESS	4.98E-11
[UNDER]	GO:0006351	transcription, DNA-templated	BIOLOGICAL_PROCESS	4.98E-11
[UNDER]	GO:0051252	regulation of RNA metabolic process	BIOLOGICAL_PROCESS	2.48E-10
[UNDER]	GO:1903506	regulation of nucleic acid-templated transcription	BIOLOGICAL_PROCESS	1.26E-09
[UNDER]	GO:2001141	regulation of RNA biosynthetic process	BIOLOGICAL_PROCESS	1.26E-09
[UNDER]	GO:0043933	protein-containing complex subunit organization	BIOLOGICAL_PROCESS	1.37E-09
[UNDER]	GO:0006355	regulation of transcription, DNA-templated	BIOLOGICAL_PROCESS	1.98E-09
[UNDER]	GO:0048522	positive regulation of cellular process	BIOLOGICAL_PROCESS	1.37E-08
[UNDER]	GO:0071702	organic substance transport	BIOLOGICAL_PROCESS	1.66E-08
[UNDER]	GO:0006396	RNA processing	BIOLOGICAL_PROCESS	3.34E-08
[UNDER]	GO:0006366	transcription by RNA polymerase II	BIOLOGICAL_PROCESS	3.44E-08
[UNDER]	GO:0051641	cellular localization	BIOLOGICAL_PROCESS	3.85E-08
[UNDER]	GO:0048518	positive regulation of biological process	BIOLOGICAL_PROCESS	4.39E-08
[UNDER]	GO:0065003	protein-containing complex assembly	BIOLOGICAL_PROCESS	4.92E-08
[UNDER]	GO:0006807	nitrogen compound metabolic process	BIOLOGICAL_PROCESS	1.31E-07
[UNDER]	GO:0048519	negative regulation of biological process	BIOLOGICAL_PROCESS	1.40E-07
[UNDER]	GO:0034622	cellular protein-containing complex assembly	BIOLOGICAL_PROCESS	1.68E-07
[UNDER]	GO:0006357	regulation of transcription by RNA polymerase II	BIOLOGICAL_PROCESS	1.72E-07
[UNDER]	GO:0033036	macromolecule localization	BIOLOGICAL_PROCESS	1.74E-07
[UNDER]	GO:0051276	chromosome organization	BIOLOGICAL_PROCESS	2.13E-07
[UNDER]	GO:0031325	positive regulation of cellular metabolic process	BIOLOGICAL_PROCESS	3.61E-07
[UNDER]	GO:0009893	positive regulation of metabolic process	BIOLOGICAL_PROCESS	3.91E-07
[UNDER]	GO:0070727	cellular macromolecule localization	BIOLOGICAL_PROCESS	7.43E-07
[UNDER]	GO:0006259	DNA metabolic process	BIOLOGICAL_PROCESS	8.05E-07
[UNDER]	GO:0046907	intracellular transport	BIOLOGICAL_PROCESS	9.63E-07
[UNDER]	GO:0034613	cellular protein localization	BIOLOGICAL_PROCESS	1.08E-06

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Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:0071705	nitrogen compound transport	BIOLOGICAL_PROCESS	1.09E-06
[UNDER]	GO:0051173	positive regulation of nitrogen compound metabolic process	BIOLOGICAL_PROCESS	1.18E-06
[UNDER]	GO:0008104	protein localization	BIOLOGICAL_PROCESS	1.56E-06
[UNDER]	GO:0006518	peptide metabolic process	BIOLOGICAL_PROCESS	1.74E-06
[UNDER]	GO:0034660	ncRNA metabolic process	BIOLOGICAL_PROCESS	1.78E-06
[UNDER]	GO:0010604	positive regulation of macromolecule metabolic process	BIOLOGICAL_PROCESS	1.78E-06
[UNDER]	GO:0055085	transmembrane transport	BIOLOGICAL_PROCESS	2.23E-06
[UNDER]	GO:0048523	negative regulation of cellular process	BIOLOGICAL_PROCESS	4.17E-06
[UNDER]	GO:0016310	phosphorylation	BIOLOGICAL_PROCESS	5.52E-06
[UNDER]	GO:0043043	peptide biosynthetic process	BIOLOGICAL_PROCESS	5.52E-06
[UNDER]	GO:0022613	ribonucleoprotein complex biogenesis	BIOLOGICAL_PROCESS	5.59E-06
[UNDER]	GO:0043604	amide biosynthetic process	BIOLOGICAL_PROCESS	6.67E-06
[UNDER]	GO:0006412	translation	BIOLOGICAL_PROCESS	1.26E-05
[UNDER]	GO:0065009	regulation of molecular function	BIOLOGICAL_PROCESS	1.81E-05
[UNDER]	GO:0010629	negative regulation of gene expression	BIOLOGICAL_PROCESS	1.81E-05
[UNDER]	GO:0051128	regulation of cellular component organization	BIOLOGICAL_PROCESS	2.18E-05
[UNDER]	GO:0042886	amide transport	BIOLOGICAL_PROCESS	4.15E-05
[UNDER]	GO:0043603	cellular amide metabolic process	BIOLOGICAL_PROCESS	4.40E-05
[UNDER]	GO:0009892	negative regulation of metabolic process	BIOLOGICAL_PROCESS	5.62E-05
[UNDER]	GO:0045184	establishment of protein localization	BIOLOGICAL_PROCESS	5.90E-05
[UNDER]	GO:0015833	peptide transport	BIOLOGICAL_PROCESS	5.90E-05
[UNDER]	GO:0006886	intracellular protein transport	BIOLOGICAL_PROCESS	8.02E-05
[UNDER]	GO:0033043	regulation of organelle organization	BIOLOGICAL_PROCESS	8.54E-05
[UNDER]	GO:0034470	ncRNA processing	BIOLOGICAL_PROCESS	8.67E-05
[UNDER]	GO:0051649	establishment of localization in cell	BIOLOGICAL_PROCESS	1.11E-04
[UNDER]	GO:0015031	protein transport	BIOLOGICAL_PROCESS	1.13E-04
[UNDER]	GO:0031328	positive regulation of cellular biosynthetic process	BIOLOGICAL_PROCESS	1.18E-04
[UNDER]	GO:0009891	positive regulation of biosynthetic process	BIOLOGICAL_PROCESS	1.18E-04
[UNDER]	GO:0010605	negative regulation of macromolecule metabolic process	BIOLOGICAL_PROCESS	1.57E-04
[UNDER]	GO:0051726	regulation of cell cycle	BIOLOGICAL_PROCESS	1.78E-04

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Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:0031327	negative regulation of cellular biosynthetic process	BIOLOGICAL_PROCESS	1.85E-04
[UNDER]	GO:0009890	negative regulation of biosynthetic process	BIOLOGICAL_PROCESS	1.85E-04
[UNDER]	GO:0050896	response to stimulus	BIOLOGICAL_PROCESS	2.07E-04
[UNDER]	GO:0044281	small molecule metabolic process	BIOLOGICAL_PROCESS	2.07E-04
[UNDER]	GO:0065008	regulation of biological quality	BIOLOGICAL_PROCESS	2.09E-04
[UNDER]	GO:0042254	ribosome biogenesis	BIOLOGICAL_PROCESS	2.64E-04
[UNDER]	GO:0016192	vesicle-mediated transport	BIOLOGICAL_PROCESS	2.73E-04
[UNDER]	GO:0022607	cellular component assembly	BIOLOGICAL_PROCESS	2.80E-04
[UNDER]	GO:0006796	phosphate-containing compound metabolic process	BIOLOGICAL_PROCESS	2.85E-04
[UNDER]	GO:0043436	oxoacid metabolic process	BIOLOGICAL_PROCESS	3.16E-04
[UNDER]	GO:0006082	organic acid metabolic process	BIOLOGICAL_PROCESS	3.29E-04
[UNDER]	GO:0050790	regulation of catalytic activity	BIOLOGICAL_PROCESS	3.70E-04
[UNDER]	GO:2000113	negative regulation of cellular macromolecule biosynthetic process	BIOLOGICAL_PROCESS	3.70E-04
[UNDER]	GO:0016071	mRNA metabolic process	BIOLOGICAL_PROCESS	3.70E-04
[UNDER]	GO:0045935	positive regulation of nucleobase-containing compound metabolic process	BIOLOGICAL_PROCESS	3.70E-04
[UNDER]	GO:0045934	negative regulation of nucleobase-containing compound metabolic process	BIOLOGICAL_PROCESS	3.70E-04
[UNDER]	GO:0010557	positive regulation of macromolecule biosynthetic process	BIOLOGICAL_PROCESS	3.74E-04
[UNDER]	GO:0010558	negative regulation of macromolecule biosynthetic process	BIOLOGICAL_PROCESS	3.79E-04
[UNDER]	GO:0006793	phosphorus metabolic process	BIOLOGICAL_PROCESS	5.20E-04
[UNDER]	GO:0035556	intracellular signal transduction	BIOLOGICAL_PROCESS	5.24E-04
[UNDER]	GO:0048285	organelle fission	BIOLOGICAL_PROCESS	5.35E-04
[UNDER]	GO:0010628	positive regulation of gene expression	BIOLOGICAL_PROCESS	5.69E-04
[UNDER]	GO:0019752	carboxylic acid metabolic process	BIOLOGICAL_PROCESS	6.33E-04
[UNDER]	GO:0000280	nuclear division	BIOLOGICAL_PROCESS	7.94E-04
[UNDER]	GO:0006281	DNA repair	BIOLOGICAL_PROCESS	7.94E-04
[UNDER]	GO:0033365	protein localization to organelle	BIOLOGICAL_PROCESS	8.39E-04
[UNDER]	GO:0051253	negative regulation of RNA metabolic process	BIOLOGICAL_PROCESS	0.001108048
[UNDER]	GO:0010564	regulation of cell cycle process	BIOLOGICAL_PROCESS	0.001108048
[UNDER]	GO:0051254	positive regulation of RNA metabolic process	BIOLOGICAL_PROCESS	0.001138644
[UNDER]	GO:0031324	negative regulation of cellular metabolic process	BIOLOGICAL_PROCESS	0.001300044

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Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:1903507	negative regulation of nucleic acid-templated transcription	BIOLOGICAL_PROCESS	0.001607891
[UNDER]	GO:1903508	positive regulation of nucleic acid-templated transcription	BIOLOGICAL_PROCESS	0.001607891
[UNDER]	GO:1902679	negative regulation of RNA biosynthetic process	BIOLOGICAL_PROCESS	0.001607891
[UNDER]	GO:1902680	positive regulation of RNA biosynthetic process	BIOLOGICAL_PROCESS	0.001607891
[UNDER]	GO:0045892	negative regulation of transcription, DNA-templated	BIOLOGICAL_PROCESS	0.001607891
[UNDER]	GO:0006974	cellular response to DNA damage stimulus	BIOLOGICAL_PROCESS	0.00163032
[UNDER]	GO:0051716	cellular response to stimulus	BIOLOGICAL_PROCESS	0.001811095
[UNDER]	GO:0072594	establishment of protein localization to organelle	BIOLOGICAL_PROCESS	0.002214484
[UNDER]	GO:0045893	positive regulation of transcription, DNA-templated	BIOLOGICAL_PROCESS	0.002214484
[UNDER]	GO:0016072	rRNA metabolic process	BIOLOGICAL_PROCESS	0.002315881
[UNDER]	GO:0051172	negative regulation of nitrogen compound metabolic process	BIOLOGICAL_PROCESS	0.002418381
[UNDER]	GO:0006325	chromatin organization	BIOLOGICAL_PROCESS	0.003109595
[UNDER]	GO:0006811	ion transport	BIOLOGICAL_PROCESS	0.003312314
[UNDER]	GO:0006468	protein phosphorylation	BIOLOGICAL_PROCESS	0.003367796
[UNDER]	GO:0044283	small molecule biosynthetic process	BIOLOGICAL_PROCESS	0.003367796
[UNDER]	GO:0007059	chromosome segregation	BIOLOGICAL_PROCESS	0.004713985
[UNDER]	GO:0006364	rRNA processing	BIOLOGICAL_PROCESS	0.004713985
[UNDER]	GO:0051246	regulation of protein metabolic process	BIOLOGICAL_PROCESS	0.004765366
[UNDER]	GO:0044770	cell cycle phase transition	BIOLOGICAL_PROCESS	0.006824561
[UNDER]	GO:0045944	positive regulation of transcription by RNA polymerase II	BIOLOGICAL_PROCESS	0.006824561
[UNDER]	GO:0032268	regulation of cellular protein metabolic process	BIOLOGICAL_PROCESS	0.006824561
[UNDER]	GO:0070647	protein modification by small protein conjugation or removal	BIOLOGICAL_PROCESS	0.006824561
[UNDER]	GO:0023052	signaling	BIOLOGICAL_PROCESS	0.007115669
[UNDER]	GO:0007346	regulation of mitotic cell cycle	BIOLOGICAL_PROCESS	0.007401468
[UNDER]	GO:0006397	mRNA processing	BIOLOGICAL_PROCESS	0.00992434
[UNDER]	GO:0090305	nucleic acid phosphodiester bond hydrolysis	BIOLOGICAL_PROCESS	0.00992434
[UNDER]	GO:0044093	positive regulation of molecular function	BIOLOGICAL_PROCESS	0.00992434
[UNDER]	GO:0140014	mitotic nuclear division	BIOLOGICAL_PROCESS	0.00992434
[OVER]	GO:0005975	carbohydrate metabolic process	BIOLOGICAL_PROCESS	1.00E-175
[OVER]	GO:0005976	polysaccharide metabolic process	BIOLOGICAL_PROCESS	9.43E-94

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Tags	GO ID	GO Name	GO Category	FDR
[OVER]	GO:0000272	polysaccharide catabolic process	BIOLOGICAL_PROCESS	2.16E-68
[OVER]	GO:0016052	carbohydrate catabolic process	BIOLOGICAL_PROCESS	9.13E-68
[OVER]	GO:0044264	cellular polysaccharide metabolic process	BIOLOGICAL_PROCESS	1.23E-60
[OVER]	GO:0044262	cellular carbohydrate metabolic process	BIOLOGICAL_PROCESS	1.89E-50
[OVER]	GO:0071554	cell wall organization or biogenesis	BIOLOGICAL_PROCESS	7.21E-44
[OVER]	GO:0044036	cell wall macromolecule metabolic process	BIOLOGICAL_PROCESS	1.19E-43
[OVER]	GO:0070085	glycosylation	BIOLOGICAL_PROCESS	1.62E-39
[OVER]	GO:0044042	glucan metabolic process	BIOLOGICAL_PROCESS	3.37E-37
[OVER]	GO:0009100	glycoprotein metabolic process	BIOLOGICAL_PROCESS	3.74E-36
[OVER]	GO:0010383	cell wall polysaccharide metabolic process	BIOLOGICAL_PROCESS	4.11E-34
[OVER]	GO:0006073	cellular glucan metabolic process	BIOLOGICAL_PROCESS	1.15E-33
[OVER]	GO:0097502	mannosylation	BIOLOGICAL_PROCESS	1.21E-32
[OVER]	GO:0009101	glycoprotein biosynthetic process	BIOLOGICAL_PROCESS	7.64E-29
[OVER]	GO:0043413	macromolecule glycosylation	BIOLOGICAL_PROCESS	2.95E-28
[OVER]	GO:0006486	protein glycosylation	BIOLOGICAL_PROCESS	2.95E-28
[OVER]	GO:1901135	carbohydrate derivative metabolic process	BIOLOGICAL_PROCESS	9.81E-28
[OVER]	GO:0009251	glucan catabolic process	BIOLOGICAL_PROCESS	8.56E-27
[OVER]	GO:0045229	external encapsulating structure organization	BIOLOGICAL_PROCESS	1.89E-25
[OVER]	GO:0008152	metabolic process	BIOLOGICAL_PROCESS	2.01E-25
[OVER]	GO:0071555	cell wall organization	BIOLOGICAL_PROCESS	1.14E-24
[OVER]	GO:0051273	beta-glucan metabolic process	BIOLOGICAL_PROCESS	3.58E-23
[OVER]	GO:0044247	cellular polysaccharide catabolic process	BIOLOGICAL_PROCESS	8.34E-23
[OVER]	GO:0044275	cellular carbohydrate catabolic process	BIOLOGICAL_PROCESS	4.12E-22
[OVER]	GO:0044238	primary metabolic process	BIOLOGICAL_PROCESS	8.40E-22
[OVER]	GO:0042546	cell wall biogenesis	BIOLOGICAL_PROCESS	8.48E-22
[OVER]	GO:1901575	organic substance catabolic process	BIOLOGICAL_PROCESS	1.22E-21
[OVER]	GO:0044038	cell wall macromolecule biosynthetic process	BIOLOGICAL_PROCESS	1.64E-21
[OVER]	GO:0070589	cellular component macromolecule biosynthetic process	BIOLOGICAL_PROCESS	1.64E-21
[OVER]	GO:0006487	protein N-linked glycosylation	BIOLOGICAL_PROCESS	1.82E-21
[OVER]	GO:0071852	fungal-type cell wall organization or biogenesis	BIOLOGICAL_PROCESS	1.26E-20



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Tags	GO ID	GO Name	GO Category	FDR
[OVER]	GO:1901137	carbohydrate derivative biosynthetic process	BIOLOGICAL_PROCESS	2.60E-20
[OVER]	GO:0071704	organic substance metabolic process	BIOLOGICAL_PROCESS	1.21E-19
[OVER]	GO:0034637	cellular carbohydrate biosynthetic process	BIOLOGICAL_PROCESS	3.52E-19
[OVER]	GO:0009057	macromolecule catabolic process	BIOLOGICAL_PROCESS	5.12E-19
[OVER]	GO:0033692	cellular polysaccharide biosynthetic process	BIOLOGICAL_PROCESS	1.01E-18
[OVER]	GO:0010393	galacturonan metabolic process	BIOLOGICAL_PROCESS	1.28E-18
[OVER]	GO:0045488	pectin metabolic process	BIOLOGICAL_PROCESS	1.28E-18
[OVER]	GO:0045490	pectin catabolic process	BIOLOGICAL_PROCESS	1.28E-18
[OVER]	GO:0000271	polysaccharide biosynthetic process	BIOLOGICAL_PROCESS	2.89E-18
[OVER]	GO:0009056	catabolic process	BIOLOGICAL_PROCESS	1.66E-17
[OVER]	GO:0071966	fungus-type cell wall polysaccharide metabolic process	BIOLOGICAL_PROCESS	3.30E-15
[OVER]	GO:0031505	fungus-type cell wall organization	BIOLOGICAL_PROCESS	3.88E-15
[OVER]	GO:0016051	carbohydrate biosynthetic process	BIOLOGICAL_PROCESS	4.33E-14
[OVER]	GO:0051275	beta-glucan catabolic process	BIOLOGICAL_PROCESS	3.53E-13
[OVER]	GO:0070592	cell wall polysaccharide biosynthetic process	BIOLOGICAL_PROCESS	1.36E-12
[OVER]	GO:0070879	fungus-type cell wall beta-glucan metabolic process	BIOLOGICAL_PROCESS	5.34E-12
[OVER]	GO:0042737	drug catabolic process	BIOLOGICAL_PROCESS	6.34E-11
[OVER]	GO:0009250	glucan biosynthetic process	BIOLOGICAL_PROCESS	7.88E-11
[OVER]	GO:0030243	cellulose metabolic process	BIOLOGICAL_PROCESS	1.57E-10
[OVER]	GO:0030245	cellulose catabolic process	BIOLOGICAL_PROCESS	1.57E-10
[OVER]	GO:0044347	cell wall polysaccharide catabolic process	BIOLOGICAL_PROCESS	1.57E-10
[OVER]	GO:0006491	N-glycan processing	BIOLOGICAL_PROCESS	1.58E-10
[OVER]	GO:0034406	cell wall beta-glucan metabolic process	BIOLOGICAL_PROCESS	1.86E-10
[OVER]	GO:0009311	oligosaccharide metabolic process	BIOLOGICAL_PROCESS	2.14E-10
[OVER]	GO:1901071	glucosamine-containing compound metabolic process	BIOLOGICAL_PROCESS	3.86E-10
[OVER]	GO:0016998	cell wall macromolecule catabolic process	BIOLOGICAL_PROCESS	7.67E-10
[OVER]	GO:0006490	oligosaccharide-lipid intermediate biosynthetic process	BIOLOGICAL_PROCESS	1.37E-09
[OVER]	GO:0006030	chitin metabolic process	BIOLOGICAL_PROCESS	2.47E-09
[OVER]	GO:0035268	protein mannosylation	BIOLOGICAL_PROCESS	2.76E-09
[OVER]	GO:0006040	amino sugar metabolic process	BIOLOGICAL_PROCESS	4.97E-09



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Tags	GO ID	GO Name	GO Category	FDR
[OVER]	GO:0009272	fungus-type cell wall biogenesis	BIOLOGICAL_PROCESS	7.32E-09
[OVER]	GO:0031506	cell wall glycoprotein biosynthetic process	BIOLOGICAL_PROCESS	8.19E-09
[OVER]	GO:0000032	cell wall mannoprotein biosynthetic process	BIOLOGICAL_PROCESS	8.19E-09
[OVER]	GO:0006057	mannoprotein biosynthetic process	BIOLOGICAL_PROCESS	8.19E-09
[OVER]	GO:0006056	mannoprotein metabolic process	BIOLOGICAL_PROCESS	8.19E-09
[OVER]	GO:0044277	cell wall disassembly	BIOLOGICAL_PROCESS	8.81E-09
[OVER]	GO:0071853	fungus-type cell wall disassembly	BIOLOGICAL_PROCESS	8.81E-09
[OVER]	GO:0006022	aminoglycan metabolic process	BIOLOGICAL_PROCESS	1.60E-08
[OVER]	GO:0006488	dolichol-linked oligosaccharide biosynthetic process	BIOLOGICAL_PROCESS	2.08E-08
[OVER]	GO:1901136	carbohydrate derivative catabolic process	BIOLOGICAL_PROCESS	7.00E-08
[OVER]	GO:0010412	mannan metabolic process	BIOLOGICAL_PROCESS	1.94E-07
[OVER]	GO:0006037	cell wall chitin metabolic process	BIOLOGICAL_PROCESS	1.98E-07
[OVER]	GO:0070880	fungus-type cell wall beta-glucan biosynthetic process	BIOLOGICAL_PROCESS	3.02E-07
[OVER]	GO:0051274	beta-glucan biosynthetic process	BIOLOGICAL_PROCESS	7.45E-07
[OVER]	GO:0005984	disaccharide metabolic process	BIOLOGICAL_PROCESS	1.13E-06
[OVER]	GO:0010410	hemicellulose metabolic process	BIOLOGICAL_PROCESS	1.18E-06
[OVER]	GO:0051278	fungus-type cell wall polysaccharide biosynthetic process	BIOLOGICAL_PROCESS	1.83E-06
[OVER]	GO:0009313	oligosaccharide catabolic process	BIOLOGICAL_PROCESS	1.86E-06
[OVER]	GO:0034410	cell wall beta-glucan biosynthetic process	BIOLOGICAL_PROCESS	4.17E-06
[OVER]	GO:0070871	cell wall organization involved in conjugation with cellular fusion	BIOLOGICAL_PROCESS	4.17E-06
[OVER]	GO:1904541	fungus-type cell wall disassembly involved in conjugation with cellular fusion	BIOLOGICAL_PROCESS	4.17E-06
[OVER]	GO:0006493	protein O-linked glycosylation	BIOLOGICAL_PROCESS	8.31E-06
[OVER]	GO:0044248	cellular catabolic process	BIOLOGICAL_PROCESS	1.02E-05
[OVER]	GO:0006074	(1->3)-beta-D-glucan metabolic process	BIOLOGICAL_PROCESS	1.57E-05
[OVER]	GO:1901072	glucosamine-containing compound catabolic process	BIOLOGICAL_PROCESS	2.70E-05
[OVER]	GO:0046348	amino sugar catabolic process	BIOLOGICAL_PROCESS	2.70E-05
[OVER]	GO:0046352	disaccharide catabolic process	BIOLOGICAL_PROCESS	2.70E-05
[OVER]	GO:0006664	glycolipid metabolic process	BIOLOGICAL_PROCESS	4.50E-05
[OVER]	GO:1903509	liposaccharide metabolic process	BIOLOGICAL_PROCESS	4.50E-05

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Tags	GO ID	GO Name	GO Category	FDR
[OVER]	GO:0071970	fungus-type cell wall (1->3)-beta-D-glucan biosynthetic process	BIOLOGICAL_PROCESS	7.14E-05
[OVER]	GO:0071969	fungus-type cell wall (1->3)-beta-D-glucan metabolic process	BIOLOGICAL_PROCESS	7.14E-05
[OVER]	GO:0090605	submerged biofilm formation	BIOLOGICAL_PROCESS	8.54E-05
[OVER]	GO:0009269	response to desiccation	BIOLOGICAL_PROCESS	8.67E-05
[OVER]	GO:0046354	mannan biosynthetic process	BIOLOGICAL_PROCESS	8.67E-05
[OVER]	GO:0042631	cellular response to water deprivation	BIOLOGICAL_PROCESS	8.67E-05
[OVER]	GO:0071465	cellular response to desiccation	BIOLOGICAL_PROCESS	8.67E-05
[OVER]	GO:0071462	cellular response to water stimulus	BIOLOGICAL_PROCESS	8.67E-05
[OVER]	GO:0009415	response to water	BIOLOGICAL_PROCESS	8.67E-05
[OVER]	GO:0009414	response to water deprivation	BIOLOGICAL_PROCESS	8.67E-05
[OVER]	GO:0005977	glycogen metabolic process	BIOLOGICAL_PROCESS	1.12E-04
[OVER]	GO:0042710	biofilm formation	BIOLOGICAL_PROCESS	1.54E-04
[OVER]	GO:0017144	drug metabolic process	BIOLOGICAL_PROCESS	2.14E-04
[OVER]	GO:0005991	trehalose metabolic process	BIOLOGICAL_PROCESS	2.73E-04
[OVER]	GO:0006112	energy reserve metabolic process	BIOLOGICAL_PROCESS	2.73E-04
[OVER]	GO:0042545	cell wall modification	BIOLOGICAL_PROCESS	3.70E-04
[OVER]	GO:0045493	xylan catabolic process	BIOLOGICAL_PROCESS	3.70E-04
[OVER]	GO:0045491	xylan metabolic process	BIOLOGICAL_PROCESS	3.70E-04
[OVER]	GO:0006026	aminoglycan catabolic process	BIOLOGICAL_PROCESS	3.70E-04
[OVER]	GO:0006032	chitin catabolic process	BIOLOGICAL_PROCESS	3.70E-04
[OVER]	GO:0009247	glycolipid biosynthetic process	BIOLOGICAL_PROCESS	4.61E-04
[OVER]	GO:0090609	single-species submerged biofilm formation	BIOLOGICAL_PROCESS	5.92E-04
[OVER]	GO:0044010	single-species biofilm formation	BIOLOGICAL_PROCESS	0.001037668
[OVER]	GO:0006687	glycosphingolipid metabolic process	BIOLOGICAL_PROCESS	0.001618843
[OVER]	GO:0034411	cell wall (1->3)-beta-D-glucan biosynthetic process	BIOLOGICAL_PROCESS	0.001618843
[OVER]	GO:0034407	cell wall (1->3)-beta-D-glucan metabolic process	BIOLOGICAL_PROCESS	0.001618843
[OVER]	GO:0006075	(1->3)-beta-D-glucan biosynthetic process	BIOLOGICAL_PROCESS	0.001618843
[OVER]	GO:0030259	lipid glycosylation	BIOLOGICAL_PROCESS	0.001639325
[OVER]	GO:0016137	glycoside metabolic process	BIOLOGICAL_PROCESS	0.001639325
[OVER]	GO:0016139	glycoside catabolic process	BIOLOGICAL_PROCESS	0.001639325

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Tags	GO ID	GO Name	GO Category	FDR
[OVER]	GO:0000918	division septum site selection	BIOLOGICAL_PROCESS	0.001639325
[OVER]	GO:0046379	extracellular polysaccharide metabolic process	BIOLOGICAL_PROCESS	0.001639325
[OVER]	GO:0031221	arabinan metabolic process	BIOLOGICAL_PROCESS	0.001639325
[OVER]	GO:0036503	ERAD pathway	BIOLOGICAL_PROCESS	0.001930135
[OVER]	GO:0035269	protein O-linked mannosylation	BIOLOGICAL_PROCESS	0.001980602
[OVER]	GO:0071712	ER-associated misfolded protein catabolic process	BIOLOGICAL_PROCESS	0.001980602
[OVER]	GO:0005980	glycogen catabolic process	BIOLOGICAL_PROCESS	0.001980602
[OVER]	GO:0018196	peptidyl-asparagine modification	BIOLOGICAL_PROCESS	0.001980602
[OVER]	GO:0018279	protein N-linked glycosylation via asparagine	BIOLOGICAL_PROCESS	0.001980602
[OVER]	GO:0044011	single-species biofilm formation on inanimate substrate	BIOLOGICAL_PROCESS	0.002214484
[OVER]	GO:0051703	intraspecies interaction between organisms	BIOLOGICAL_PROCESS	0.002214484
[OVER]	GO:0005978	glycogen biosynthetic process	BIOLOGICAL_PROCESS	0.002328269
[OVER]	GO:0006643	membrane lipid metabolic process	BIOLOGICAL_PROCESS	0.003367796
[OVER]	GO:0022610	biological adhesion	BIOLOGICAL_PROCESS	0.003911006
[OVER]	GO:0031589	cell-substrate adhesion	BIOLOGICAL_PROCESS	0.004895195
[OVER]	GO:0046373	L-arabinose metabolic process	BIOLOGICAL_PROCESS	0.005831702
[OVER]	GO:0070413	trehalose metabolism in response to stress	BIOLOGICAL_PROCESS	0.005831702
[OVER]	GO:0043170	macromolecule metabolic process	BIOLOGICAL_PROCESS	0.008357138
[OVER]	GO:0044419	interspecies interaction between organisms	BIOLOGICAL_PROCESS	0.009268417
[OVER]	GO:0046467	membrane lipid biosynthetic process	BIOLOGICAL_PROCESS	0.009660083
[OVER]	GO:0043934	sporulation	BIOLOGICAL_PROCESS	0.00992434

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TABLE S9. Secondary metabolite biosynthesis backbone genes identified in *Monilinia vaccinii-corymbosi* by SMURF.

Backbone Gene ID	Gene Description	Chromosome	Cluster	SMURF Backbone Gene
ASPCAL07647	polyketide synthase, putative	2	None	PKS-Like
BCON_0348g00080	putative nonribosomal peptide synthase -like protein	4	1	NRPS
BELL_0182g00140	NRPS-like enzyme	1	2	NRPS-Like
BGAL_0051g00170	BcPKS16, polyketide synthase	9	3	PKS
BHYA_0070g00460	putative hc-toxin synthetase protein	2	4	NRPS-Like
BO71DRAFT_436033	polyketide synthase	7	5	PKS
BP6252_13184	non-ribosomal peptide synthetase	8	6	NRPS
BPOR_0045g00020	nonribosomal peptide synthase SidD	1	7	NRPS
BTUL_0024g00210	nonribosomal peptide synthetase	4	None	NRPS
BTUL_0098g00380	BcPKS12, polyketide synthase	2	8	PKS
BTUL_0198g00060	3-oxoacyl-[acyl-carrier-protein] synthase	1	None	PKS-Like
BcDW1_3470	nonribosomal peptide synthetase	1	None	NRPS
BcDW1_4610	putative hybrid pks-nrps protein	3	13	PKS
Bcpks8	BcPKS8, polyketide synthase	4	9	PKS
MAA_01626	polyketide synthase 3	1	None	HYBRID
PEX2_074870	Acyl transferase/acyl hydrolase/lysophospholipase	7	10	PKS
S40285_06294	Reducing polyketide synthase	6	11	PKS
SS1G_02020	putative alpha-1,2-mannosidase family protein	4	12	NRPS-Like
SS1G_09240	putative polyketide synthase protein	3	13	PKS
SS1G_13322	polyketide synthase	6	None	PKS
TCE0_044f16394	putative polyketide synthase	1	14	PKS
perA	peramine synthetase	1	15	NRPS-Like
sscle_08g064270	NRPS-like enzyme	7	None	NRPS-Like

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TABLE S10. Secondary metabolite biosynthesis clusters identified in *Monilinia vaccinii-corymbosi* by SMURF.

Gene ID*	Gene Positions	Chromosome	Gene Order	Domain Score	Gene Description
<b>Cluster:1</b>					
BCON_0348g00040	-3	4	668	1	putative cytochrome p450 oxidoreductase protein
BCON_0348g00050	-2	4	667	1	hypothetical protein DID88_003153
SBOR_3743	-1	4	666	1	hypothetical protein EYC84_000427
BCON_0348g00080	0	4	665	0	putative nonribosomal peptide synthase-like protein
SBOR_3701	1	4	664	0	thiamin pyrophosphokinase-related protein
BCIN_12g04840	2	4	663	0	predicted protein
BCIN_12g04850	3	4	662	0	putative integral membrane channel protein
BPOR_0275g00110	4	4	661	0	putative bifunctional pyrimidine biosynthesis protein
BofuT4P0000074001	5	4	660	1	putative mfs multidrug transporter protein
BPAE_0050g00100	6	4	659	0	hypothetical protein EYC84_000432
BPOR_0019g00140	7	4	658	1	putative maltose permease protein
BGAL_0396g00020	8	4	657	1	putative salicylate protein
<b>Cluster:2</b>					
BofuT4_P012380.1	-2	1	57	1	Zn(II)2Cys6 transcription factor
BTUL_0046g00590	-1	1	56	0	Zn(II)2Cys6 transcription factor
BELL_0182g00140	0	1	55	0	NRPS-like enzyme
BofuT4_P012420.1	1	1	54	1	putative mfs transporter protein
<b>Cluster:3</b>					
BcDW1_10428	-1	9	275	1	putative polyketide synthase protein
BGAL_0051g00170	0	9	274	0	BcPKS16, polyketide synthase
BHYA_0044g00180	1	9	273	0	hypothetical protein SBOR_8148
BPOR_0073g00150	2	9	272	1	cytochrome P450 monooxygenase
<b>Cluster:4</b>					
BGAL_0140g00060	-3	2	929	1	putative mfs transporter protein
SS1G_10565	-2	2	928	1	alcohol dehydrogenase
BCIN_04g01380	-1	2	927	0	putative pyrroline-5-carboxylate reductase protein
BHYA_0070g00460	0	2	926	0	putative hc-toxin synthetase protein
<b>Cluster:5</b>					

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Gene ID*	Gene Positions	Chromosome	Gene Order	Domain Score	Gene Description
CJF30_00009638	-3	7	363	1	hexose transporter
SS1G_11401	-2	7	362	1	short-chain dehydrogenase, putative
BO94DRAFT_532539	-1	7	361	0	alpha beta hydrolase fold-3 domain containing protein
BO71DRAFT_436033	0	7	360	0	polyketide synthase
M426DRAFT_109244	1	7	359	0	L-amino acid amidase
ANO14919_102910	2	7	358	0	hypothetical protein ANO14919_102910
DM02DRAFT_478682	3	7	357	0	hypothetical protein M434DRAFT_282681
VM1G_04709	4	7	356	1	Choline transport protein
<b>Cluster:6</b>					
SBOR_8377	-2	8	63	1	MFS transporter, SIT family, siderophore-iron:H <sup>+</sup> symporter
SS1G_11626	-1	8	62	0	putative inositol 5-phosphatase protein
BP6252_13184	0	8	61	0	non-ribosomal peptide synthetase
DID88_003025	1	8	60	0	hypothetical protein EYC84_007856
SBOR_8381	2	8	59	1	putative ABC bile acid transporter
<b>Cluster:7</b>					
BPOR_0045g00020	0	1	295	0	nonribosomal peptide synthase SidD
BELL_0279g00030	1	1	294	1	ABC multidrug transporter SitT
<b>Cluster:8</b>					
smr1	-1	2	546	1	transcription factor
BTUL_0098g00380	0	2	545	0	BcPKS12, polyketide synthase
<b>Cluster:9</b>					
sscle_01g004380	-5	4	329	1	hypothetical protein sscle_01g004380
BofuT4_P118950.1	-4	4	328	0	putative glycoside hydrolase family 25 protein
DID88_005849	-3	4	327	0	putative gtp-binding protein gtr1 protein
BCIN_07g02900	-2	4	326	1	putative abc transporter protein
SS1G_01999	-1	4	325	0	putative ef-hand calcium-binding domain protein
Bcpks8	0	4	324	1	BcPKS8, polyketide synthase
BOTNAR_0001g00750	1	4	323	0	NADPH dehydrogenase
SBOR_5242	2	4	322	0	hypothetical protein EYC80_004819
BOTNAR_0100g00210	3	4	321	1	aromatic amino acid aminotransferase

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Gene ID*	Gene Positions	Chromosome	Gene Order	Domain Score	Gene Description
<b>Cluster:10</b>					
SBOR_1121	-3	7	241	1	MFS multidrug transporter
BOTCAL_0018g00270	-2	7	240	0	peptidyl-tRNA hydrolase PTH2
BOTNAR_0199g00210	-1	7	239	0	hypothetical protein EYC84_001176
PEX2_074870	0	7	238	0	Acyl transferase/acyl hydrolase/lysophospholipase
<b>Cluster:11</b>					
DL768_004486	-9	6	446	1	Flavine halogenase
DID88_004562	-8	6	445	1	FAD-linked oxidoreductase
NEUTE2DRAFT_98132	-7	6	444	1	FAD-linked oxidoreductase
DL771_009216	-6	6	443	0	NAD(P)-binding protein
GE21DRAFT_2377	-5	6	442	1	2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase
SMU2925	-4	6	441	1	FAD/NAD(P)-binding domain-containing protein
PFICI_14519	-3	6	440	1	NAD(P)-binding protein
BCR38DRAFT_519830	-2	6	439	0	Bifunctional epoxide hydrolase
M419DRAFT_85683	-1	6	438	1	short-chain dehydrogenase/reductase
S40285_06294	0	6	437	1	Reducing polyketide synthase
<b>Cluster:12</b>					
BGAL_0104g00200	-5	4	338	1	putative polyamine acetyltransferase protein
BPOR_0027g00120	-4	4	337	0	putative aspartyl protease protein
BcDW1_3400	-3	4	336	0	putative ribosomal rna-processing protein 8 protein
BTUL_0318g00060	-2	4	335	1	putative c6 finger domain-containing protein
BofuT4P90000024001	-1	4	334	0	putative alpha-1,2-mannosidase family protein
SS1G_02020	0	4	333	0	putative alpha-1,2-mannosidase family protein
<b>Cluster:13</b>					
BPOR_0121g00040	-6	3	221	1	Cytochrome P450 monooxygenase BOA3
BOTNAR_0328g00100	-5	3	220	1	cytochrome P450 protein
BCON_0375g00080	-4	3	219	0	putative alcohol dehydrogenase protein
BcDW1_4610	-3	3	218	1	putative hybrid pks-nrps protein
SS1G_09238	-2	3	217	0	putative cytochrome p450 monooxygenase protein
BCON_0375g00050	-1	3	216	1	FAD-dependent monooxygenase BOA8

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Gene ID*	Gene Positions	Chromosome	Gene Order	Domain Score	Gene Description
SS1G_09240	0	3	215	1	putative polyketide synthase protein
CJF31_00004990	1	3	214	0	Probable thioesterase BOA10
BcDW1_4606	2	3	213	1	putative trichothecene 3-o-acetyltransferase protein
<b>Cluster:14</b>					
BCIN_05g03610	-3	1	1104	1	ABC transporter
BofuT4_P041370.1	-2	1	1103	1	N-acetyltransferase 9
BP6252_10650	-1	1	1102	0	Adaptor protein-like protein complex AP-2
TCE0_044f16394	0	1	1101	0	putative polyketide synthase
<b>Cluster:15</b>					
CC77DRAFT_23848	-2	1	831	1	Aminotriazole resistance
DL769_002837	-1	1	830	1	hypothetical protein DL769_002837
perA	0	1	829	0	peramine synthetase
MAC_04541	1	1	828	0	branched-chain-amino-acid aminotransferase
MAN_01724	2	1	827	0	methyltransferase MppJ
XA68_14724	3	1	826	0	Glycine amidinotransferase, mitochondrial
LEL_07888	4	1	825	1	cytochrome p450

\*Highest scoring match from BLASTp



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TABLE S11. Secondary metabolites identified in *Monilinia vaccinii-corymbosi* (*Mvc*) and the corresponding Maker gene model IDs.

Secondary Metabolite	Mvc Gene IDs
PKS	MvcIVH1_09511; MvcIVH1_08510; MvcIVH1_02794; MvcIVH1_03991; MvcIVH1_05498; MvcIVH1_08328; MvcIVH1_07942; MvcIVH1_03988; MvcIVH1_07322; MvcIVH1_01583
PKS-like	MvcIVH1_02022; MvcIVH1_01524
NRPS	MvcIVH1_05953; MvcIVH1_08639; MvcIVH1_00410; MvcIVH1_05756; MvcIVH1_00581
NRPS-like	MvcIVH1_00086; MvcIVH1_03357; MvcIVH1_05513; MvcIVH1_01187; MvcIVH1_08279
PKS-NRPS Hybrid	MvcIVH1_00044

TABLE S12. Fisher's Exact Test results for GO biological process term enrichment of secondary metabolite biosynthesis clusters identified by SMURF in *Monilinia vaccinii-corymbosi* (*Mvc*). The SMURF subset was compared to the entire set of *Mvc* predicted gene models.

Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:0071840	cellular component organization or biogenesis	BIOLOGICAL_PROCESS	0.006057944
[UNDER]	GO:0016043	cellular component organization	BIOLOGICAL_PROCESS	0.007482038
[OVER]	GO:0055114	oxidation-reduction process	BIOLOGICAL_PROCESS	1.00E-08
[OVER]	GO:0009405	pathogenesis	BIOLOGICAL_PROCESS	4.47E-04
[OVER]	GO:0044419	interspecies interaction between organisms	BIOLOGICAL_PROCESS	0.001973408

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TABLE S13. Fisher's Exact Test results for GO biological process term enrichment of signal peptide sequences identified by SignalP in *Monilinia vaccinii-corymbosi* (*Mvc*). The SignalP subset was compared to the entire set of *Mvc* predicted gene models.

Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:0034641	cellular nitrogen compound metabolic process	BIOLOGICAL_PROCESS	4.78E-52
[UNDER]	GO:0046483	heterocycle metabolic process	BIOLOGICAL_PROCESS	6.74E-49
[UNDER]	GO:1901360	organic cyclic compound metabolic process	BIOLOGICAL_PROCESS	2.66E-48
[UNDER]	GO:0006139	nucleobase-containing compound metabolic process	BIOLOGICAL_PROCESS	7.36E-48
[UNDER]	GO:0010467	gene expression	BIOLOGICAL_PROCESS	1.95E-46
[UNDER]	GO:0006725	cellular aromatic compound metabolic process	BIOLOGICAL_PROCESS	3.85E-46
[UNDER]	GO:0090304	nucleic acid metabolic process	BIOLOGICAL_PROCESS	9.01E-44
[UNDER]	GO:0044271	cellular nitrogen compound biosynthetic process	BIOLOGICAL_PROCESS	3.69E-39
[UNDER]	GO:0016070	RNA metabolic process	BIOLOGICAL_PROCESS	8.46E-38
[UNDER]	GO:0009058	biosynthetic process	BIOLOGICAL_PROCESS	2.82E-33
[UNDER]	GO:0044249	cellular biosynthetic process	BIOLOGICAL_PROCESS	3.58E-32
[UNDER]	GO:0050789	regulation of biological process	BIOLOGICAL_PROCESS	1.09E-31
[UNDER]	GO:1901576	organic substance biosynthetic process	BIOLOGICAL_PROCESS	1.89E-31
[UNDER]	GO:0019222	regulation of metabolic process	BIOLOGICAL_PROCESS	2.22E-31
[UNDER]	GO:0065007	biological regulation	BIOLOGICAL_PROCESS	4.48E-31
[UNDER]	GO:0018130	heterocycle biosynthetic process	BIOLOGICAL_PROCESS	9.10E-31
[UNDER]	GO:0009987	cellular process	BIOLOGICAL_PROCESS	2.82E-30
[UNDER]	GO:0019438	aromatic compound biosynthetic process	BIOLOGICAL_PROCESS	4.85E-30
[UNDER]	GO:0050794	regulation of cellular process	BIOLOGICAL_PROCESS	4.96E-30
[UNDER]	GO:0060255	regulation of macromolecule metabolic process	BIOLOGICAL_PROCESS	5.76E-30
[UNDER]	GO:1901362	organic cyclic compound biosynthetic process	BIOLOGICAL_PROCESS	7.76E-30
[UNDER]	GO:0080090	regulation of primary metabolic process	BIOLOGICAL_PROCESS	1.10E-29
[UNDER]	GO:0031323	regulation of cellular metabolic process	BIOLOGICAL_PROCESS	1.29E-29
[UNDER]	GO:0034654	nucleobase-containing compound biosynthetic process	BIOLOGICAL_PROCESS	1.38E-29
[UNDER]	GO:0051171	regulation of nitrogen compound metabolic process	BIOLOGICAL_PROCESS	9.38E-29
[UNDER]	GO:0031326	regulation of cellular biosynthetic process	BIOLOGICAL_PROCESS	1.97E-28
[UNDER]	GO:0009889	regulation of biosynthetic process	BIOLOGICAL_PROCESS	1.97E-28
[UNDER]	GO:0010556	regulation of macromolecule biosynthetic process	BIOLOGICAL_PROCESS	6.93E-27

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Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:2000112	regulation of cellular macromolecule biosynthetic process	BIOLOGICAL_PROCESS	1.07E-26
[UNDER]	GO:0010468	regulation of gene expression	BIOLOGICAL_PROCESS	2.36E-26
[UNDER]	GO:0044237	cellular metabolic process	BIOLOGICAL_PROCESS	2.47E-26
[UNDER]	GO:0032774	RNA biosynthetic process	BIOLOGICAL_PROCESS	1.51E-25
[UNDER]	GO:0097659	nucleic acid-templated transcription	BIOLOGICAL_PROCESS	3.75E-25
[UNDER]	GO:0006807	nitrogen compound metabolic process	BIOLOGICAL_PROCESS	4.62E-25
[UNDER]	GO:0006351	transcription, DNA-templated	BIOLOGICAL_PROCESS	5.86E-25
[UNDER]	GO:0006996	organelle organization	BIOLOGICAL_PROCESS	8.98E-25
[UNDER]	GO:0019219	regulation of nucleobase-containing compound metabolic process	BIOLOGICAL_PROCESS	1.67E-24
[UNDER]	GO:0009059	macromolecule biosynthetic process	BIOLOGICAL_PROCESS	3.38E-23
[UNDER]	GO:0034645	cellular macromolecule biosynthetic process	BIOLOGICAL_PROCESS	4.98E-23
[UNDER]	GO:0051252	regulation of RNA metabolic process	BIOLOGICAL_PROCESS	4.68E-22
[UNDER]	GO:1903506	regulation of nucleic acid-templated transcription	BIOLOGICAL_PROCESS	5.54E-22
[UNDER]	GO:2001141	regulation of RNA biosynthetic process	BIOLOGICAL_PROCESS	5.54E-22
[UNDER]	GO:0006355	regulation of transcription, DNA-templated	BIOLOGICAL_PROCESS	8.78E-22
[UNDER]	GO:0051276	chromosome organization	BIOLOGICAL_PROCESS	3.10E-20
[UNDER]	GO:0022607	cellular component assembly	BIOLOGICAL_PROCESS	2.16E-19
[UNDER]	GO:0051179	localization	BIOLOGICAL_PROCESS	6.22E-19
[UNDER]	GO:0051234	establishment of localization	BIOLOGICAL_PROCESS	5.06E-17
[UNDER]	GO:0043933	protein-containing complex subunit organization	BIOLOGICAL_PROCESS	1.35E-16
[UNDER]	GO:0006366	transcription by RNA polymerase II	BIOLOGICAL_PROCESS	4.30E-16
[UNDER]	GO:0006810	transport	BIOLOGICAL_PROCESS	8.64E-16
[UNDER]	GO:0044260	cellular macromolecule metabolic process	BIOLOGICAL_PROCESS	1.62E-15
[UNDER]	GO:0016043	cellular component organization	BIOLOGICAL_PROCESS	3.23E-15
[UNDER]	GO:0071840	cellular component organization or biogenesis	BIOLOGICAL_PROCESS	4.70E-15
[UNDER]	GO:0006357	regulation of transcription by RNA polymerase II	BIOLOGICAL_PROCESS	1.15E-14
[UNDER]	GO:0034622	cellular protein-containing complex assembly	BIOLOGICAL_PROCESS	1.75E-14
[UNDER]	GO:0048519	negative regulation of biological process	BIOLOGICAL_PROCESS	1.83E-14
[UNDER]	GO:0048522	positive regulation of cellular process	BIOLOGICAL_PROCESS	4.22E-14
[UNDER]	GO:0007049	cell cycle	BIOLOGICAL_PROCESS	9.11E-14

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Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:0034660	ncRNA metabolic process	BIOLOGICAL_PROCESS	1.00E-13
[UNDER]	GO:0048518	positive regulation of biological process	BIOLOGICAL_PROCESS	1.29E-13
[UNDER]	GO:0006396	RNA processing	BIOLOGICAL_PROCESS	1.84E-13
[UNDER]	GO:0065003	protein-containing complex assembly	BIOLOGICAL_PROCESS	2.62E-13
[UNDER]	GO:0048523	negative regulation of cellular process	BIOLOGICAL_PROCESS	4.82E-13
[UNDER]	GO:0051128	regulation of cellular component organization	BIOLOGICAL_PROCESS	9.27E-13
[UNDER]	GO:0009893	positive regulation of metabolic process	BIOLOGICAL_PROCESS	9.64E-13
[UNDER]	GO:0044085	cellular component biogenesis	BIOLOGICAL_PROCESS	1.12E-12
[UNDER]	GO:0031325	positive regulation of cellular metabolic process	BIOLOGICAL_PROCESS	1.39E-12
[UNDER]	GO:0022402	cell cycle process	BIOLOGICAL_PROCESS	3.79E-12
[UNDER]	GO:0006412	translation	BIOLOGICAL_PROCESS	8.80E-12
[UNDER]	GO:0000278	mitotic cell cycle	BIOLOGICAL_PROCESS	1.02E-11
[UNDER]	GO:0051173	positive regulation of nitrogen compound metabolic process	BIOLOGICAL_PROCESS	2.26E-11
[UNDER]	GO:0033043	regulation of organelle organization	BIOLOGICAL_PROCESS	2.51E-11
[UNDER]	GO:0010604	positive regulation of macromolecule metabolic process	BIOLOGICAL_PROCESS	3.37E-11
[UNDER]	GO:1903047	mitotic cell cycle process	BIOLOGICAL_PROCESS	4.74E-11
[UNDER]	GO:0006259	DNA metabolic process	BIOLOGICAL_PROCESS	5.99E-11
[UNDER]	GO:0050896	response to stimulus	BIOLOGICAL_PROCESS	7.20E-11
[UNDER]	GO:0051726	regulation of cell cycle	BIOLOGICAL_PROCESS	8.31E-11
[UNDER]	GO:0031327	negative regulation of cellular biosynthetic process	BIOLOGICAL_PROCESS	8.61E-11
[UNDER]	GO:0009890	negative regulation of biosynthetic process	BIOLOGICAL_PROCESS	8.61E-11
[UNDER]	GO:0009892	negative regulation of metabolic process	BIOLOGICAL_PROCESS	9.79E-11
[UNDER]	GO:0043604	amide biosynthetic process	BIOLOGICAL_PROCESS	1.42E-10
[UNDER]	GO:0071702	organic substance transport	BIOLOGICAL_PROCESS	2.02E-10
[UNDER]	GO:0016310	phosphorylation	BIOLOGICAL_PROCESS	3.18E-10
[UNDER]	GO:0022613	ribonucleoprotein complex biogenesis	BIOLOGICAL_PROCESS	3.18E-10
[UNDER]	GO:2000113	negative regulation of cellular macromolecule biosynthetic process	BIOLOGICAL_PROCESS	4.04E-10
[UNDER]	GO:0045934	negative regulation of nucleobase-containing compound metabolic process	BIOLOGICAL_PROCESS	4.04E-10
[UNDER]	GO:0033036	macromolecule localization	BIOLOGICAL_PROCESS	4.05E-10
[UNDER]	GO:0010558	negative regulation of macromolecule biosynthetic process	BIOLOGICAL_PROCESS	4.06E-10

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Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:0006325	chromatin organization	BIOLOGICAL_PROCESS	4.33E-10
[UNDER]	GO:0034470	ncRNA processing	BIOLOGICAL_PROCESS	4.35E-10
[UNDER]	GO:0010629	negative regulation of gene expression	BIOLOGICAL_PROCESS	4.90E-10
[UNDER]	GO:0010605	negative regulation of macromolecule metabolic process	BIOLOGICAL_PROCESS	8.86E-10
[UNDER]	GO:0031324	negative regulation of cellular metabolic process	BIOLOGICAL_PROCESS	9.37E-10
[UNDER]	GO:0044267	cellular protein metabolic process	BIOLOGICAL_PROCESS	9.37E-10
[UNDER]	GO:0031328	positive regulation of cellular biosynthetic process	BIOLOGICAL_PROCESS	1.33E-09
[UNDER]	GO:0071705	nitrogen compound transport	BIOLOGICAL_PROCESS	1.33E-09
[UNDER]	GO:0009891	positive regulation of biosynthetic process	BIOLOGICAL_PROCESS	1.33E-09
[UNDER]	GO:0006974	cellular response to DNA damage stimulus	BIOLOGICAL_PROCESS	1.38E-09
[UNDER]	GO:0008104	protein localization	BIOLOGICAL_PROCESS	1.67E-09
[UNDER]	GO:0051641	cellular localization	BIOLOGICAL_PROCESS	1.74E-09
[UNDER]	GO:1901566	organonitrogen compound biosynthetic process	BIOLOGICAL_PROCESS	4.28E-09
[UNDER]	GO:0051172	negative regulation of nitrogen compound metabolic process	BIOLOGICAL_PROCESS	4.33E-09
[UNDER]	GO:0042254	ribosome biogenesis	BIOLOGICAL_PROCESS	4.38E-09
[UNDER]	GO:0043412	macromolecule modification	BIOLOGICAL_PROCESS	5.72E-09
[UNDER]	GO:0010557	positive regulation of macromolecule biosynthetic process	BIOLOGICAL_PROCESS	9.68E-09
[UNDER]	GO:0051253	negative regulation of RNA metabolic process	BIOLOGICAL_PROCESS	9.90E-09
[UNDER]	GO:0010564	regulation of cell cycle process	BIOLOGICAL_PROCESS	9.90E-09
[UNDER]	GO:0070727	cellular macromolecule localization	BIOLOGICAL_PROCESS	1.23E-08
[UNDER]	GO:0006518	peptide metabolic process	BIOLOGICAL_PROCESS	1.70E-08
[UNDER]	GO:0045892	negative regulation of transcription, DNA-templated	BIOLOGICAL_PROCESS	2.12E-08
[UNDER]	GO:0010628	positive regulation of gene expression	BIOLOGICAL_PROCESS	2.14E-08
[UNDER]	GO:1903507	negative regulation of nucleic acid-templated transcription	BIOLOGICAL_PROCESS	2.20E-08
[UNDER]	GO:1902679	negative regulation of RNA biosynthetic process	BIOLOGICAL_PROCESS	2.20E-08
[UNDER]	GO:0043043	peptide biosynthetic process	BIOLOGICAL_PROCESS	2.37E-08
[UNDER]	GO:0051716	cellular response to stimulus	BIOLOGICAL_PROCESS	2.55E-08
[UNDER]	GO:0042886	amide transport	BIOLOGICAL_PROCESS	2.56E-08
[UNDER]	GO:0034613	cellular protein localization	BIOLOGICAL_PROCESS	3.24E-08
[UNDER]	GO:0006281	DNA repair	BIOLOGICAL_PROCESS	4.47E-08

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Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:0015833	peptide transport	BIOLOGICAL_PROCESS	4.97E-08
[UNDER]	GO:0044281	small molecule metabolic process	BIOLOGICAL_PROCESS	5.27E-08
[UNDER]	GO:0006796	phosphate-containing compound metabolic process	BIOLOGICAL_PROCESS	7.01E-08
[UNDER]	GO:0045184	establishment of protein localization	BIOLOGICAL_PROCESS	7.25E-08
[UNDER]	GO:0045935	positive regulation of nucleobase-containing compound metabolic process	BIOLOGICAL_PROCESS	1.43E-07
[UNDER]	GO:0046907	intracellular transport	BIOLOGICAL_PROCESS	1.46E-07
[UNDER]	GO:0015031	protein transport	BIOLOGICAL_PROCESS	1.94E-07
[UNDER]	GO:0051246	regulation of protein metabolic process	BIOLOGICAL_PROCESS	1.96E-07
[UNDER]	GO:0007059	chromosome segregation	BIOLOGICAL_PROCESS	2.21E-07
[UNDER]	GO:0007346	regulation of mitotic cell cycle	BIOLOGICAL_PROCESS	2.21E-07
[UNDER]	GO:0055085	transmembrane transport	BIOLOGICAL_PROCESS	2.22E-07
[UNDER]	GO:0043603	cellular amide metabolic process	BIOLOGICAL_PROCESS	2.38E-07
[UNDER]	GO:0048285	organelle fission	BIOLOGICAL_PROCESS	3.03E-07
[UNDER]	GO:0006793	phosphorus metabolic process	BIOLOGICAL_PROCESS	3.07E-07
[UNDER]	GO:0032268	regulation of cellular protein metabolic process	BIOLOGICAL_PROCESS	4.05E-07
[UNDER]	GO:0016072	rRNA metabolic process	BIOLOGICAL_PROCESS	4.41E-07
[UNDER]	GO:1903508	positive regulation of nucleic acid-templated transcription	BIOLOGICAL_PROCESS	4.53E-07
[UNDER]	GO:1902680	positive regulation of RNA biosynthetic process	BIOLOGICAL_PROCESS	4.66E-07
[UNDER]	GO:0044770	cell cycle phase transition	BIOLOGICAL_PROCESS	4.76E-07
[UNDER]	GO:0000280	nuclear division	BIOLOGICAL_PROCESS	6.41E-07
[UNDER]	GO:0045893	positive regulation of transcription, DNA-templated	BIOLOGICAL_PROCESS	6.41E-07
[UNDER]	GO:0044772	mitotic cell cycle phase transition	BIOLOGICAL_PROCESS	7.25E-07
[UNDER]	GO:0098813	nuclear chromosome segregation	BIOLOGICAL_PROCESS	7.52E-07
[UNDER]	GO:0006464	cellular protein modification process	BIOLOGICAL_PROCESS	9.86E-07
[UNDER]	GO:0036211	protein modification process	BIOLOGICAL_PROCESS	9.86E-07
[UNDER]	GO:0140014	mitotic nuclear division	BIOLOGICAL_PROCESS	1.04E-06
[UNDER]	GO:0051254	positive regulation of RNA metabolic process	BIOLOGICAL_PROCESS	1.31E-06
[UNDER]	GO:0051649	establishment of localization in cell	BIOLOGICAL_PROCESS	2.52E-06
[UNDER]	GO:0000819	sister chromatid segregation	BIOLOGICAL_PROCESS	3.42E-06
[UNDER]	GO:0006886	intracellular protein transport	BIOLOGICAL_PROCESS	3.63E-06



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Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:0006364	rRNA processing	BIOLOGICAL_PROCESS	4.45E-06
[UNDER]	GO:0043170	macromolecule metabolic process	BIOLOGICAL_PROCESS	4.55E-06
[UNDER]	GO:0033044	regulation of chromosome organization	BIOLOGICAL_PROCESS	5.20E-06
[UNDER]	GO:0065009	regulation of molecular function	BIOLOGICAL_PROCESS	5.38E-06
[UNDER]	GO:0016071	mRNA metabolic process	BIOLOGICAL_PROCESS	6.92E-06
[UNDER]	GO:0019752	carboxylic acid metabolic process	BIOLOGICAL_PROCESS	7.37E-06
[UNDER]	GO:0006082	organic acid metabolic process	BIOLOGICAL_PROCESS	8.50E-06
[UNDER]	GO:0045944	positive regulation of transcription by RNA polymerase II	BIOLOGICAL_PROCESS	9.27E-06
[UNDER]	GO:0070647	protein modification by small protein conjugation or removal	BIOLOGICAL_PROCESS	9.35E-06
[UNDER]	GO:0043436	oxoacid metabolic process	BIOLOGICAL_PROCESS	1.16E-05
[UNDER]	GO:0006468	protein phosphorylation	BIOLOGICAL_PROCESS	1.23E-05
[UNDER]	GO:0071824	protein-DNA complex subunit organization	BIOLOGICAL_PROCESS	1.64E-05
[UNDER]	GO:1901987	regulation of cell cycle phase transition	BIOLOGICAL_PROCESS	1.68E-05
[UNDER]	GO:0000070	mitotic sister chromatid segregation	BIOLOGICAL_PROCESS	1.74E-05
[UNDER]	GO:1901990	regulation of mitotic cell cycle phase transition	BIOLOGICAL_PROCESS	2.57E-05
[UNDER]	GO:0051130	positive regulation of cellular component organization	BIOLOGICAL_PROCESS	2.93E-05
[UNDER]	GO:0051640	organelle localization	BIOLOGICAL_PROCESS	6.48E-05
[UNDER]	GO:0044283	small molecule biosynthetic process	BIOLOGICAL_PROCESS	6.55E-05
[UNDER]	GO:0002181	cytoplasmic translation	BIOLOGICAL_PROCESS	6.65E-05
[UNDER]	GO:0045786	negative regulation of cell cycle	BIOLOGICAL_PROCESS	7.96E-05
[UNDER]	GO:0006260	DNA replication	BIOLOGICAL_PROCESS	8.10E-05
[UNDER]	GO:0016458	gene silencing	BIOLOGICAL_PROCESS	8.32E-05
[UNDER]	GO:0006399	tRNA metabolic process	BIOLOGICAL_PROCESS	9.07E-05
[UNDER]	GO:0010638	positive regulation of organelle organization	BIOLOGICAL_PROCESS	1.17E-04
[UNDER]	GO:0040029	regulation of gene expression, epigenetic	BIOLOGICAL_PROCESS	1.18E-04
[UNDER]	GO:0007010	cytoskeleton organization	BIOLOGICAL_PROCESS	1.18E-04
[UNDER]	GO:0051783	regulation of nuclear division	BIOLOGICAL_PROCESS	1.18E-04
[UNDER]	GO:0006261	DNA-dependent DNA replication	BIOLOGICAL_PROCESS	1.72E-04
[UNDER]	GO:0097549	chromatin organization involved in negative regulation of transcription	BIOLOGICAL_PROCESS	1.73E-04
[UNDER]	GO:0045814	negative regulation of gene expression, epigenetic	BIOLOGICAL_PROCESS	1.73E-04

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Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:0006342	chromatin silencing	BIOLOGICAL_PROCESS	1.73E-04
[UNDER]	GO:0071103	DNA conformation change	BIOLOGICAL_PROCESS	1.82E-04
[UNDER]	GO:0006913	nucleocytoplasmic transport	BIOLOGICAL_PROCESS	1.82E-04
[UNDER]	GO:0051169	nuclear transport	BIOLOGICAL_PROCESS	1.82E-04
[UNDER]	GO:0034401	chromatin organization involved in regulation of transcription	BIOLOGICAL_PROCESS	1.82E-04
[UNDER]	GO:0032270	positive regulation of cellular protein metabolic process	BIOLOGICAL_PROCESS	1.96E-04
[UNDER]	GO:0031399	regulation of protein modification process	BIOLOGICAL_PROCESS	2.02E-04
[UNDER]	GO:0051247	positive regulation of protein metabolic process	BIOLOGICAL_PROCESS	2.02E-04
[UNDER]	GO:0006811	ion transport	BIOLOGICAL_PROCESS	2.42E-04
[UNDER]	GO:0065008	regulation of biological quality	BIOLOGICAL_PROCESS	2.44E-04
[UNDER]	GO:0016569	covalent chromatin modification	BIOLOGICAL_PROCESS	2.53E-04
[UNDER]	GO:0016570	histone modification	BIOLOGICAL_PROCESS	2.53E-04
[UNDER]	GO:1901564	organonitrogen compound metabolic process	BIOLOGICAL_PROCESS	2.60E-04
[UNDER]	GO:0051174	regulation of phosphorus metabolic process	BIOLOGICAL_PROCESS	2.67E-04
[UNDER]	GO:0019220	regulation of phosphate metabolic process	BIOLOGICAL_PROCESS	2.67E-04
[UNDER]	GO:0044087	regulation of cellular component biogenesis	BIOLOGICAL_PROCESS	2.71E-04
[UNDER]	GO:0070925	organelle assembly	BIOLOGICAL_PROCESS	2.76E-04
[UNDER]	GO:0051656	establishment of organelle localization	BIOLOGICAL_PROCESS	3.63E-04
[UNDER]	GO:0023052	signaling	BIOLOGICAL_PROCESS	3.68E-04
[UNDER]	GO:0045787	positive regulation of cell cycle	BIOLOGICAL_PROCESS	3.97E-04
[UNDER]	GO:0051188	cofactor biosynthetic process	BIOLOGICAL_PROCESS	4.01E-04
[UNDER]	GO:0035556	intracellular signal transduction	BIOLOGICAL_PROCESS	4.47E-04
[UNDER]	GO:0007005	mitochondrion organization	BIOLOGICAL_PROCESS	4.58E-04
[UNDER]	GO:0051186	cofactor metabolic process	BIOLOGICAL_PROCESS	7.44E-04
[UNDER]	GO:0090068	positive regulation of cell cycle process	BIOLOGICAL_PROCESS	7.94E-04
[UNDER]	GO:0051129	negative regulation of cellular component organization	BIOLOGICAL_PROCESS	7.94E-04
[UNDER]	GO:0006338	chromatin remodeling	BIOLOGICAL_PROCESS	8.00E-04
[UNDER]	GO:0008380	RNA splicing	BIOLOGICAL_PROCESS	8.63E-04
[UNDER]	GO:0016192	vesicle-mediated transport	BIOLOGICAL_PROCESS	8.69E-04
[UNDER]	GO:0016053	organic acid biosynthetic process	BIOLOGICAL_PROCESS	9.27E-04



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Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:0006397	mRNA processing	BIOLOGICAL_PROCESS	9.27E-04
[UNDER]	GO:0050790	regulation of catalytic activity	BIOLOGICAL_PROCESS	9.70E-04
[UNDER]	GO:0055086	nucleobase-containing small molecule metabolic process	BIOLOGICAL_PROCESS	0.001031009
[UNDER]	GO:0090407	organophosphate biosynthetic process	BIOLOGICAL_PROCESS	0.001055755
[UNDER]	GO:0006950	response to stress	BIOLOGICAL_PROCESS	0.001139747
[UNDER]	GO:0010608	posttranscriptional regulation of gene expression	BIOLOGICAL_PROCESS	0.001162732
[UNDER]	GO:0006403	RNA localization	BIOLOGICAL_PROCESS	0.001164836
[UNDER]	GO:0007088	regulation of mitotic nuclear division	BIOLOGICAL_PROCESS	0.001164836
[UNDER]	GO:0032446	protein modification by small protein conjugation	BIOLOGICAL_PROCESS	0.001176254
[UNDER]	GO:0000122	negative regulation of transcription by RNA polymerase II	BIOLOGICAL_PROCESS	0.001181645
[UNDER]	GO:0006310	DNA recombination	BIOLOGICAL_PROCESS	0.001193091
[UNDER]	GO:0031503	protein-containing complex localization	BIOLOGICAL_PROCESS	0.001210611
[UNDER]	GO:0010948	negative regulation of cell cycle process	BIOLOGICAL_PROCESS	0.001210611
[UNDER]	GO:0006753	nucleoside phosphate metabolic process	BIOLOGICAL_PROCESS	0.001277992
[UNDER]	GO:0071826	ribonucleoprotein complex subunit organization	BIOLOGICAL_PROCESS	0.001308012
[UNDER]	GO:0046394	carboxylic acid biosynthetic process	BIOLOGICAL_PROCESS	0.001311187
[UNDER]	GO:0044093	positive regulation of molecular function	BIOLOGICAL_PROCESS	0.001311187
[UNDER]	GO:0010639	negative regulation of organelle organization	BIOLOGICAL_PROCESS	0.001656722
[UNDER]	GO:0007017	microtubule-based process	BIOLOGICAL_PROCESS	0.001674978
[UNDER]	GO:0045930	negative regulation of mitotic cell cycle	BIOLOGICAL_PROCESS	0.001674978
[UNDER]	GO:0006302	double-strand break repair	BIOLOGICAL_PROCESS	0.001718766
[UNDER]	GO:0009117	nucleotide metabolic process	BIOLOGICAL_PROCESS	0.001743762
[UNDER]	GO:0065004	protein-DNA complex assembly	BIOLOGICAL_PROCESS	0.001751114
[UNDER]	GO:0006732	coenzyme metabolic process	BIOLOGICAL_PROCESS	0.001882239
[UNDER]	GO:0033554	cellular response to stress	BIOLOGICAL_PROCESS	0.002058571
[UNDER]	GO:0051321	meiotic cell cycle	BIOLOGICAL_PROCESS	0.002082944
[UNDER]	GO:0061024	membrane organization	BIOLOGICAL_PROCESS	0.002161774
[UNDER]	GO:0000398	mRNA splicing, via spliceosome	BIOLOGICAL_PROCESS	0.002326647
[UNDER]	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	BIOLOGICAL_PROCESS	0.002326647

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Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:0051983	regulation of chromosome segregation	BIOLOGICAL_PROCESS	0.002349103
[UNDER]	GO:0034248	regulation of cellular amide metabolic process	BIOLOGICAL_PROCESS	0.002349103
[UNDER]	GO:0000375	RNA splicing, via transesterification reactions	BIOLOGICAL_PROCESS	0.002367155
[UNDER]	GO:0007165	signal transduction	BIOLOGICAL_PROCESS	0.002448922
[UNDER]	GO:0051052	regulation of DNA metabolic process	BIOLOGICAL_PROCESS	0.002493835
[UNDER]	GO:0022618	ribonucleoprotein complex assembly	BIOLOGICAL_PROCESS	0.002613075
[UNDER]	GO:0007154	cell communication	BIOLOGICAL_PROCESS	0.002890453
[UNDER]	GO:0051301	cell division	BIOLOGICAL_PROCESS	0.002955666
[UNDER]	GO:2000241	regulation of reproductive process	BIOLOGICAL_PROCESS	0.003317581
[UNDER]	GO:0033365	protein localization to organelle	BIOLOGICAL_PROCESS	0.003440662
[UNDER]	GO:0045931	positive regulation of mitotic cell cycle	BIOLOGICAL_PROCESS	0.003442932
[UNDER]	GO:0006839	mitochondrial transport	BIOLOGICAL_PROCESS	0.003465396
[UNDER]	GO:0140053	mitochondrial gene expression	BIOLOGICAL_PROCESS	0.003633543
[UNDER]	GO:0072594	establishment of protein localization to organelle	BIOLOGICAL_PROCESS	0.003805352
[UNDER]	GO:0032502	developmental process	BIOLOGICAL_PROCESS	0.004352971
[UNDER]	GO:0016567	protein ubiquitination	BIOLOGICAL_PROCESS	0.004718217
[UNDER]	GO:0048583	regulation of response to stimulus	BIOLOGICAL_PROCESS	0.0047811
[UNDER]	GO:0006611	protein export from nucleus	BIOLOGICAL_PROCESS	0.005017265
[UNDER]	GO:0006520	cellular amino acid metabolic process	BIOLOGICAL_PROCESS	0.005074896
[UNDER]	GO:0017038	protein import	BIOLOGICAL_PROCESS	0.005113277
[UNDER]	GO:0050658	RNA transport	BIOLOGICAL_PROCESS	0.005113277
[UNDER]	GO:0033045	regulation of sister chromatid segregation	BIOLOGICAL_PROCESS	0.005113277
[UNDER]	GO:0051236	establishment of RNA localization	BIOLOGICAL_PROCESS	0.005113277
[UNDER]	GO:0050657	nucleic acid transport	BIOLOGICAL_PROCESS	0.005305836
[UNDER]	GO:0051168	nuclear export	BIOLOGICAL_PROCESS	0.005305836
[UNDER]	GO:0022414	reproductive process	BIOLOGICAL_PROCESS	0.005357661
[UNDER]	GO:0034220	ion transmembrane transport	BIOLOGICAL_PROCESS	0.005512929
[UNDER]	GO:0000003	reproduction	BIOLOGICAL_PROCESS	0.006326998
[UNDER]	GO:0032879	regulation of localization	BIOLOGICAL_PROCESS	0.006350132
[UNDER]	GO:0043085	positive regulation of catalytic activity	BIOLOGICAL_PROCESS	0.00652363

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Tags	GO ID	GO Name	GO Category	FDR
[UNDER]	GO:1901293	nucleoside phosphate biosynthetic process	BIOLOGICAL_PROCESS	0.006587748
[UNDER]	GO:0051304	chromosome separation	BIOLOGICAL_PROCESS	0.007186818
[UNDER]	GO:0006417	regulation of translation	BIOLOGICAL_PROCESS	0.007243282
[UNDER]	GO:0000226	microtubule cytoskeleton organization	BIOLOGICAL_PROCESS	0.007418803
[UNDER]	GO:0033047	regulation of mitotic sister chromatid segregation	BIOLOGICAL_PROCESS	0.007687769
[UNDER]	GO:0008152	metabolic process	BIOLOGICAL_PROCESS	0.008459925
[UNDER]	GO:0006820	anion transport	BIOLOGICAL_PROCESS	0.008928988
[UNDER]	GO:0009108	coenzyme biosynthetic process	BIOLOGICAL_PROCESS	0.009518281
[UNDER]	GO:0009165	nucleotide biosynthetic process	BIOLOGICAL_PROCESS	0.009841265
[OVER]	GO:0005975	carbohydrate metabolic process	BIOLOGICAL_PROCESS	2.02E-47
[OVER]	GO:0005976	polysaccharide metabolic process	BIOLOGICAL_PROCESS	1.12E-29
[OVER]	GO:0000272	polysaccharide catabolic process	BIOLOGICAL_PROCESS	4.50E-29
[OVER]	GO:0016052	carbohydrate catabolic process	BIOLOGICAL_PROCESS	1.43E-24
[OVER]	GO:0071554	cell wall organization or biogenesis	BIOLOGICAL_PROCESS	1.07E-17
[OVER]	GO:0044264	cellular polysaccharide metabolic process	BIOLOGICAL_PROCESS	5.21E-14
[OVER]	GO:0044036	cell wall macromolecule metabolic process	BIOLOGICAL_PROCESS	6.02E-12
[OVER]	GO:0010383	cell wall polysaccharide metabolic process	BIOLOGICAL_PROCESS	7.53E-12
[OVER]	GO:0051273	beta-glucan metabolic process	BIOLOGICAL_PROCESS	5.34E-10
[OVER]	GO:0044042	glucan metabolic process	BIOLOGICAL_PROCESS	1.27E-09
[OVER]	GO:0010393	galacturonan metabolic process	BIOLOGICAL_PROCESS	6.76E-09
[OVER]	GO:0045488	pectin metabolic process	BIOLOGICAL_PROCESS	6.76E-09
[OVER]	GO:0045490	pectin catabolic process	BIOLOGICAL_PROCESS	6.76E-09
[OVER]	GO:0006073	cellular glucan metabolic process	BIOLOGICAL_PROCESS	1.66E-08
[OVER]	GO:0071852	fungus-type cell wall organization or biogenesis	BIOLOGICAL_PROCESS	2.03E-08
[OVER]	GO:0071555	cell wall organization	BIOLOGICAL_PROCESS	2.33E-08
[OVER]	GO:0045229	external encapsulating structure organization	BIOLOGICAL_PROCESS	3.57E-08
[OVER]	GO:0071966	fungus-type cell wall polysaccharide metabolic process	BIOLOGICAL_PROCESS	6.02E-08
[OVER]	GO:0044262	cellular carbohydrate metabolic process	BIOLOGICAL_PROCESS	1.17E-07
[OVER]	GO:0034975	protein folding in endoplasmic reticulum	BIOLOGICAL_PROCESS	1.79E-07
[OVER]	GO:0044247	cellular polysaccharide catabolic process	BIOLOGICAL_PROCESS	3.46E-07

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Tags	GO ID	GO Name	GO Category	FDR
[OVER]	GO:0070879	fungus-type cell wall beta-glucan metabolic process	BIOLOGICAL_PROCESS	3.85E-07
[OVER]	GO:0009251	glucan catabolic process	BIOLOGICAL_PROCESS	1.97E-06
[OVER]	GO:0044347	cell wall polysaccharide catabolic process	BIOLOGICAL_PROCESS	3.13E-06
[OVER]	GO:0044275	cellular carbohydrate catabolic process	BIOLOGICAL_PROCESS	6.74E-06
[OVER]	GO:0034406	cell wall beta-glucan metabolic process	BIOLOGICAL_PROCESS	6.83E-06
[OVER]	GO:0016998	cell wall macromolecule catabolic process	BIOLOGICAL_PROCESS	9.87E-06
[OVER]	GO:0006508	proteolysis	BIOLOGICAL_PROCESS	1.65E-05
[OVER]	GO:0042546	cell wall biogenesis	BIOLOGICAL_PROCESS	2.27E-05
[OVER]	GO:1901575	organic substance catabolic process	BIOLOGICAL_PROCESS	5.01E-05
[OVER]	GO:0070880	fungus-type cell wall beta-glucan biosynthetic process	BIOLOGICAL_PROCESS	6.22E-05
[OVER]	GO:0010410	hemicellulose metabolic process	BIOLOGICAL_PROCESS	6.76E-05
[OVER]	GO:0009272	fungus-type cell wall biogenesis	BIOLOGICAL_PROCESS	7.60E-05
[OVER]	GO:0042737	drug catabolic process	BIOLOGICAL_PROCESS	1.68E-04
[OVER]	GO:0031505	fungus-type cell wall organization	BIOLOGICAL_PROCESS	1.68E-04
[OVER]	GO:0009057	macromolecule catabolic process	BIOLOGICAL_PROCESS	1.72E-04
[OVER]	GO:0009395	phospholipid catabolic process	BIOLOGICAL_PROCESS	4.01E-04
[OVER]	GO:0051275	beta-glucan catabolic process	BIOLOGICAL_PROCESS	4.01E-04
[OVER]	GO:0051274	beta-glucan biosynthetic process	BIOLOGICAL_PROCESS	4.10E-04
[OVER]	GO:0034410	cell wall beta-glucan biosynthetic process	BIOLOGICAL_PROCESS	7.28E-04
[OVER]	GO:0030243	cellulose metabolic process	BIOLOGICAL_PROCESS	0.001290578
[OVER]	GO:0030245	cellulose catabolic process	BIOLOGICAL_PROCESS	0.001290578
[OVER]	GO:0071970	fungus-type cell wall (1->3)-beta-D-glucan biosynthetic process	BIOLOGICAL_PROCESS	0.001742689
[OVER]	GO:0071969	fungus-type cell wall (1->3)-beta-D-glucan metabolic process	BIOLOGICAL_PROCESS	0.001742689
[OVER]	GO:0051278	fungus-type cell wall polysaccharide biosynthetic process	BIOLOGICAL_PROCESS	0.003718481
[OVER]	GO:0009100	glycoprotein metabolic process	BIOLOGICAL_PROCESS	0.004496616
[OVER]	GO:0009056	catabolic process	BIOLOGICAL_PROCESS	0.004520098
[OVER]	GO:0045493	xylan catabolic process	BIOLOGICAL_PROCESS	0.004867517
[OVER]	GO:0045491	xylan metabolic process	BIOLOGICAL_PROCESS	0.004867517
[OVER]	GO:0046938	phytochelatins biosynthetic process	BIOLOGICAL_PROCESS	0.004867517
[OVER]	GO:0046937	phytochelatins metabolic process	BIOLOGICAL_PROCESS	0.004867517

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Tags	GO ID	GO Name	GO Category	FDR
[OVER]	GO:0009250	glucan biosynthetic process	BIOLOGICAL_PROCESS	0.00801222

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TABLE S14. Mating type locus (*MAT*) genes for *Monilinia vaccinii-corymbosi* and closely related fungi *Botrytis cinerea*, *Monilinia fructicola*, *Monilinia fructigena*, *Monilinia laxa*, and *Sclerotinia sclerotiorum*.

Gene	Species	Strain	Gene Length (bp)	Number of Introns	CDS Length (bp)	Protein Length (aa)
MAT1-1-1	<i>S. trifoliorum</i>	G27	1,212	2	1,110	370
	<i>S. minor</i>	SM1	1,106	2	1,005	335
	<i>S. sclerotiorum</i>	1980	826	1	777	259
	<i>S. sclerotiorum</i>	44Ba1	1,106	2	1,005	335
	<i>S. sclerotiorum</i>	44Ba12	354	0	354	117
	<i>B. cinerea</i>	B05.10	1,161	2	1,062	354
	<i>M. laxa</i>	-	1,132	1	1,083	360
	<i>M. fructigena</i>	-	1,132	1	1,083	360
	<i>M. fructicola</i>	-	1,137	1	1,083	360
	<i>M. vaccinii-corymbosi</i>	RL1	727	1	678	225*
MAT1-1-5	<i>S. trifoliorum</i>	G27	1,306	3	1,131	377
	<i>S. minor</i>	SM1	1,303	3	1,131	377
	<i>S. sclerotiorum</i>	1980	1,303	3	1,131	377
	<i>S. sclerotiorum</i>	44Ba1	1,303	3	1,131	377
	<i>S. sclerotiorum</i>	44Ba12	1,303	3	1,131	377
	<i>B. cinerea</i>	B05.10	1,301	3	1,131	377
	<i>M. laxa</i>	-	1,304	3	1,131	376
	<i>M. fructigena</i>	-	1,304	3	1,131	376
	<i>M. fructicola</i>	-	1,304	3	1,131	376
	<i>M. vaccinii-corymbosi</i>	RL1	1,038	2	913	289
MAT1-2-1	<i>S. trifoliorum</i>	G22	1,210	2	1,098	366
	<i>S. minor</i>	SM1	1,289	2	1,185	395
	<i>S. sclerotiorum</i>	1980	1,289	2	1,185	395
	<i>S. sclerotiorum</i>	44Ba1	1,289	2	1,185	395
	<i>S. sclerotiorum</i>	44Ba12	1,289	2	1,185	395
	<i>B. cinerea</i>	T4	1,248	2	1,143	381
	<i>M. laxa</i>	-	1,176	2	1,065	354
	<i>M. fructigena</i>	-	1,176	2	1,065	354
	<i>M. fructicola</i>	-	1,176	2	1,065	354
	<i>M. vaccinii-corymbosi</i>	RL1	1,172	2	1,065	354
MAT1-2-10	<i>S. trifoliorum</i>	G22	925	1	879	293
	<i>S. minor</i>	SM1	941	2	843	281
	<i>S. sclerotiorum</i>	1980	944	2	846	282
	<i>S. sclerotiorum</i>	44Ba1	944	2	846	282
	<i>S. sclerotiorum</i>	44Ba12	944	2	846	282
	<i>B. cinerea</i>	T4	1,517	3	1,230	409
	<i>M. laxa</i>	-	957	2	861	286
	<i>M. fructigena</i>	-	957	2	861	286
	<i>M. fructicola</i>	-	957	2	861	286
	<i>M. vaccinii-corymbosi</i>	RL1	1,817	4	1,263	420*

\*The C-terminus of the *Mvc*-RL1 MAT1-1-1 protein is truncated, the truncated sequence is found fused to the C-terminus of the *Mvc* RL1 MAT1-2-10 protein.

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TABLE S15. *Monilinia vaccinii-corymbosi* sequences identified with GO terms for mating processes.

Description	Mvc Sequences
Mating type switching	MvcIVH1_00649; MvcIVH1_00885; MvcIVH1_02894; MvcIVH1_03419; MvcIVH1_04274; MvcIVH1_05665; MvcIVH1_06290; MvcIVH1_06331; MvcIVH1_07527; MvcIVH1_08737; MvcIVH1_08742
Gene conversion at mating-type locus	MvcIVH1_00330; MvcIVH1_00649; MvcIVH1_01179; MvcIVH1_01358; MvcIVH1_02195; MvcIVH1_02798; MvcIVH1_02824; MvcIVH1_05002; MvcIVH1_06283; MvcIVH1_06870
Pheromone signaling	MvcIVH1_01267; MvcIVH1_01531; MvcIVH1_01568; MvcIVH1_01613; MvcIVH1_02063; MvcIVH1_02418; MvcIVH1_02606; MvcIVH1_02851; MvcIVH1_03515; MvcIVH1_04596; MvcIVH1_06286; MvcIVH1_07646; MvcIVH1_07740; MvcIVH1_07741; MvcIVH1_07923; MvcIVH1_09031
Cellular fusion	MvcIVH1_00037; MvcIVH1_01267; MvcIVH1_01531; MvcIVH1_01568; MvcIVH1_01613; MvcIVH1_01840; MvcIVH1_01841; MvcIVH1_02063; MvcIVH1_02121; MvcIVH1_02418; MvcIVH1_02606; MvcIVH1_02648; MvcIVH1_02851; MvcIVH1_02944; MvcIVH1_03079; MvcIVH1_03515; MvcIVH1_04464; MvcIVH1_04596; MvcIVH1_05025; MvcIVH1_06000; MvcIVH1_06279; MvcIVH1_06286; MvcIVH1_06290; MvcIVH1_06656; MvcIVH1_07315; MvcIVH1_07646; MvcIVH1_07740; MvcIVH1_07741; MvcIVH1_09031; MvcIVH1_09361
Heterokaryon incompatibility	MvcIVH1_00069; MvcIVH1_01659; MvcIVH1_01678; MvcIVH1_01686; MvcIVH1_03598; MvcIVH1_04121; MvcIVH1_04503; MvcIVH1_04515; MvcIVH1_04874; MvcIVH1_05018; MvcIVH1_05021; MvcIVH1_05047; MvcIVH1_05066; MvcIVH1_05100; MvcIVH1_06116; MvcIVH1_06718; MvcIVH1_07263; MvcIVH1_08040; MvcIVH1_08203; MvcIVH1_08574