

Table S19. A putative polyketide biosynthesis cluster that is partly conserved in *S. macrospora* and *Phaeosphaeria nodorum*.

locus_tag	closest homolog in <i>P. nodorum</i>	predicted Pfam domains (see also Table S6)	Best BLASTP hit in non-redundant database (NCBI)	e-value
SMAC_01188	SNOG_02561	PKS	ref XP_001273596.1 polyketide synthase, putative [<i>Aspergillus clavatus</i> NRRL 1]	0.0
SMAC_01189	SNOG_05064		ref XP_002148606.1 conserved hypothetical protein [<i>Penicillium marneffei</i> ATCC 18224]	2e-71
SMAC_01190	SNOG_09915	prenyltransferase	ref XP_001800201.1 hypothetical protein SNOG_09915 [<i>Phaeosphaeria nodorum</i> SN15]	e-142
SMAC_01191	SNOG_09921	short chain dehydrogenase	ref XP_001258624.1 short chain dehydrogenase (AtsC), putative [<i>Neosartorya fischeri</i>]	e-119
SMAC_01192	SNOG_08188	aldehyde reductase	gb EEY20659.1 aldehyde reductase [<i>Verticillium albo-atrum</i> VaMs.102]	e-141
SMAC_01193	SNOG_09917		ref XP_001800203.1 hypothetical protein SNOG_09917 [<i>Phaeosphaeria nodorum</i> SN15]	4e-55
SMAC_01194	SNOG_09918	FAD binding domain	ref XP_001800204.1 hypothetical protein SNOG_09918 [<i>Phaeosphaeria nodorum</i> SN15]	e-178
SMAC_01195	SNOG_09916	Cytochrome P450	ref XP_001800202.1 hypothetical protein SNOG_09916 [<i>Phaeosphaeria nodorum</i> SN15]	0.0
SMAC_01196	SNOG_09914	phenylalanine ammonia lyase	ref XP_001800200.1 hypothetical protein SNOG_09914 [<i>Phaeosphaeria nodorum</i> SN15]	e-163
SMAC_01197	SNOG_09920	FAD binding domain	gb EEY20661.1 FAD binding domain-containing protein [<i>Verticillium albo-atrum</i> VaMs.102]	0.0
SMAC_01198	SNOG_07866	PKS/NRPS hybrid, pseudogene	ref XP_001274946.1 polyketide synthase, putative [<i>Aspergillus clavatus</i> NRRL 1]	0.0
SMAC_01201	SNOG_11395	Zn cluster transcription factor	ref XP_001274942.1 hypothetical protein ACLA_055640 [<i>Aspergillus clavatus</i> NRRL 1]	6e-37