

Figs. S5A and S5B. Lichens with atranorin and usnic acid BGCs (A) Phyletic distribution of PKS8 family (*aka.* MPAS) and PKS23 (Atr1) family that is responsible for biosynthesis of usnic acid and atranorin, respectively. Black squares indicate the presence of indicated PKS families, and a grey square for *Lobaria pulmonaria* indicates a partial PKS8 gene. Note that *Cladonia rangiferina*, *Evernia prunastri*, and *Parmelia sp.* KoLRI021559 possess both PKS8 and PKS23 BGCs. **(B)** HPLC profiles of acetone extracts of *C. rangiferina* (upper panel) and *Parmelia sp.* KoLRI021559 (lower panel). Lichen substances are identified by comparison their retention time and UV spectra to the lichen substance database. Note that *C. rangiferina* and *Parmelia sp.* produce atranorin as a cortical substance and a 3MOA-derived depsidone as a medullary substance (fumarprotocetraric acid for *C. rangiferina*; salazinic acid for *Parmelia sp.*), lacking usnic acid.

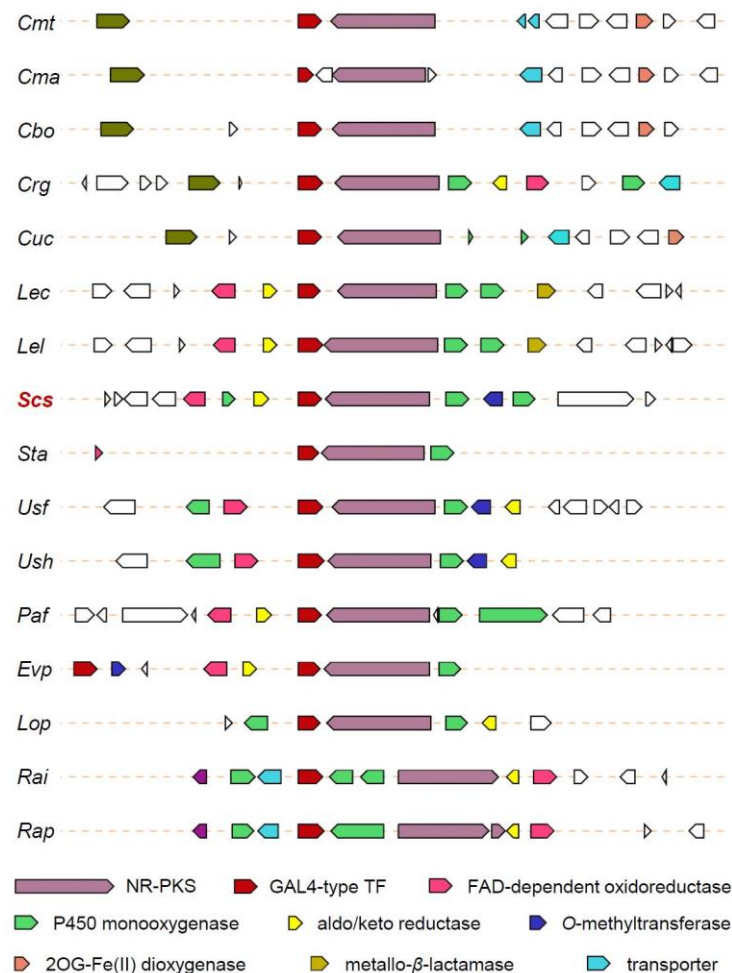
C

Fig. S5C. Detection of conserved PKS1 BGCs in lichens. Sixteen BGCs including a PKS1 homolog are identified from 1,527 BGCs detected in the 30 genomes, using the CORASON analysis pipeline. A GAL4-type transcription factor and the PKS1 BGC in *C. rangiferina* (*Crg*) are used as the query gene and as the query gene cluster, respectively. Lichen species with a homologous PKS1 BGC are labelled with their abbreviated names, as in Figure 1. Note that *Sclerophora sanguinea* (*Scs*, labelled in red) that belongs to Coniocybomycetes possesses a homologous PKS1 BGC. Genes related to secondary metabolism are color-coded, based on their predicted function. NR-PKS, non-reducing type I PKS; TF, transcription factor.

D

	NR-PKS groups										Sum
	I	II	III	IV	V	VI	VII	VIII	IX	NC	
<i>C. borealis</i>	1	4	1	3	2	4	1	2	2	1	21
<i>C. grayi</i>	3	3	0	1	0	0	0	0	2	1	10
<i>C. macilenta</i>	2	3	2	3	2	2	1	2	2	0	19
<i>C. metacorallifera</i>	2	3	1	3	1	2	1	2	2	0	17
<i>C. rangiferina</i>	3	3	1	1	1	1	0	1	3	1	15
<i>C. uncialis</i>	1	3	1	0	2	2	1	2	2	2	16
<i>S. alpinum</i>	2	1	0	0	0	1	0	1	3	0	8
<i>A. fumigatus</i>	0	0	1	0	3	1	1	1	0	0	7
<i>A. nidulans</i>	1	0	1	1	3	3	6	0	0	0	15
<i>A. niger</i>	0	1	1	0	2	1	3	0	0	1	9
<i>A. terreus</i>	0	1	0	1	1	2	3	0	0	0	8

Fig. S5D. NR-PKS diversity in *Cladonia* and *Aspergillus* species. NR-PKSs in the six *Cladonia* spp., *Stereocaulon alpinum* and four *Aspergillus* spp. are categorized by the nine phylogenetic groups (Groups I–IX). The information on NR-PKSs in the four *Aspergillus* spp. are retrieved from Romsdahl and Wang 2019. The PKS16 family is considered to belong to the Group I, although the PKS16 formed a monophyletic clade sister to the Group I (also see Fig. 5). NC, not categorized.