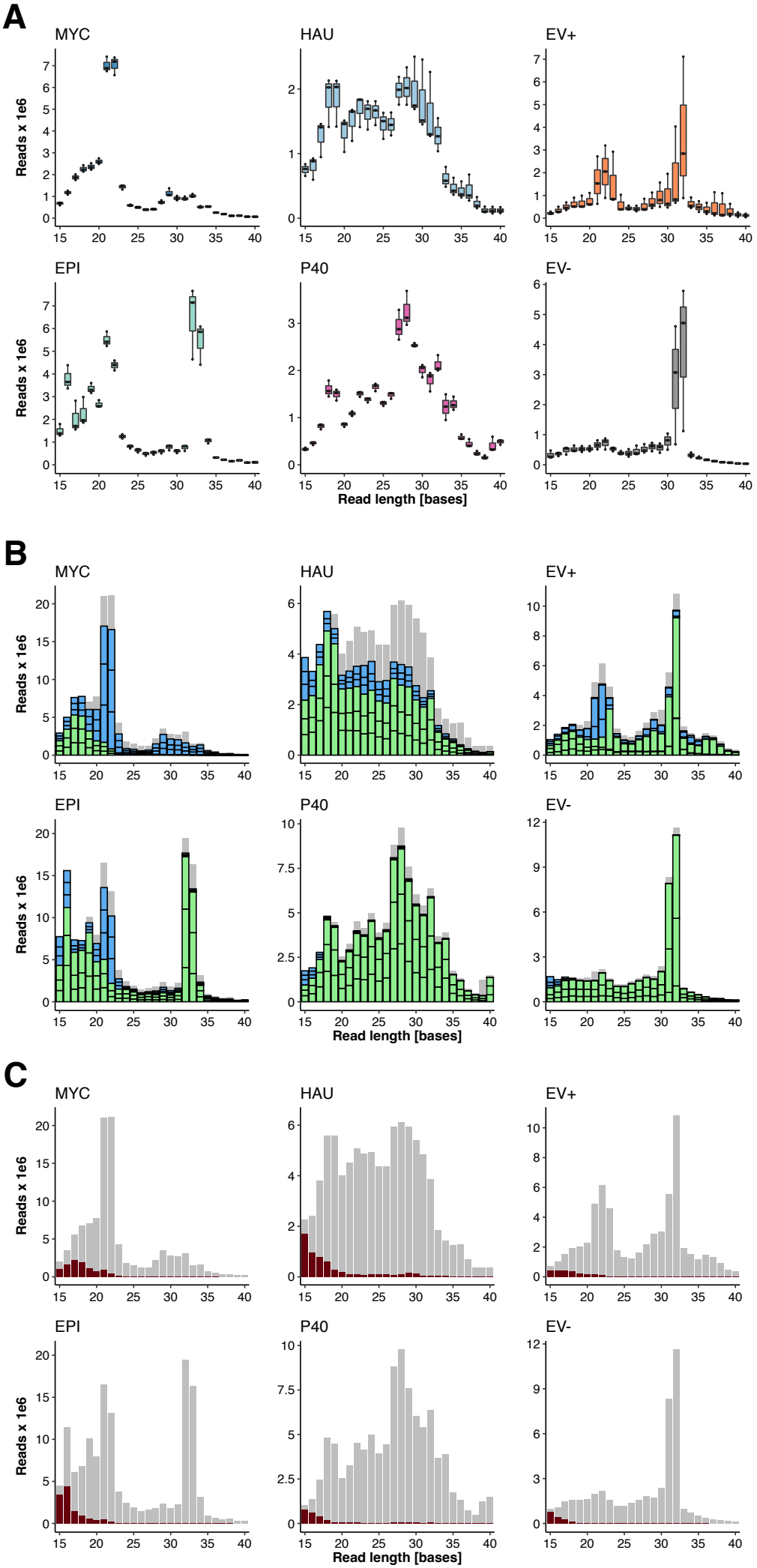
A
MYC
HAU
EV+
EPI
P40
EV-
Reads x 1e6
Read length [bases]
B
MYC
HAU
EV+
EPI
P40
EV-
Reads x 1e6
Read length [bases]
C
MYC
HAU
EV+
EPI
P40
EV-
Reads x 1e6
Read length [bases]

Supplementary Figure 1. Each sample type exhibits a distinctive sRNA read size distribution. (**A**) We determined the sRNA read counts for read lengths between 15 and 40 bases and plotted the read length (x-axis) against the respective number of reads (y-axis). Three replicates were analyzed for each of our six sample types: Epiphytic fungal mycelium (MYC), infected epidermis without mycelium (EPI), fungal haustoria (HAU), microsomes of the epidermis without haustoria (P40), apoplastic extracellular vesicles (EV+), and apoplastic extracellular vesicles of non-infected control plants (EV-). (**B**) We mapped sRNA sequencing reads of 15 and 40 bases long to the reference genomes of *H. vulgare* IBSCv2 (Mascher *et al.* 2017) and *B. hordei* DH14 (Frantzeskakis *et al.* 2018). The stacked bar graph shows the read counts (y-axis) for the respective read size (x-axis) from the three replicates. Green, reads mapping to the *H. vulgare* genome; blue, reads mapping to the *B. hordei* DH14 genome; grey, reads that did not map to either of the two genomes. (**C**) We also identified all reads that mapped to both reference genomes for 15- to 40-bases long reads. Grey indicates the total number of reads for each read length, red indicates reads with ambiguous mapping to both genomes.