**Supplementary Figures for**


# Genic introgression from an invasive exotic fungal forest pathogen increases the establishment potential of a sibling native pathogen

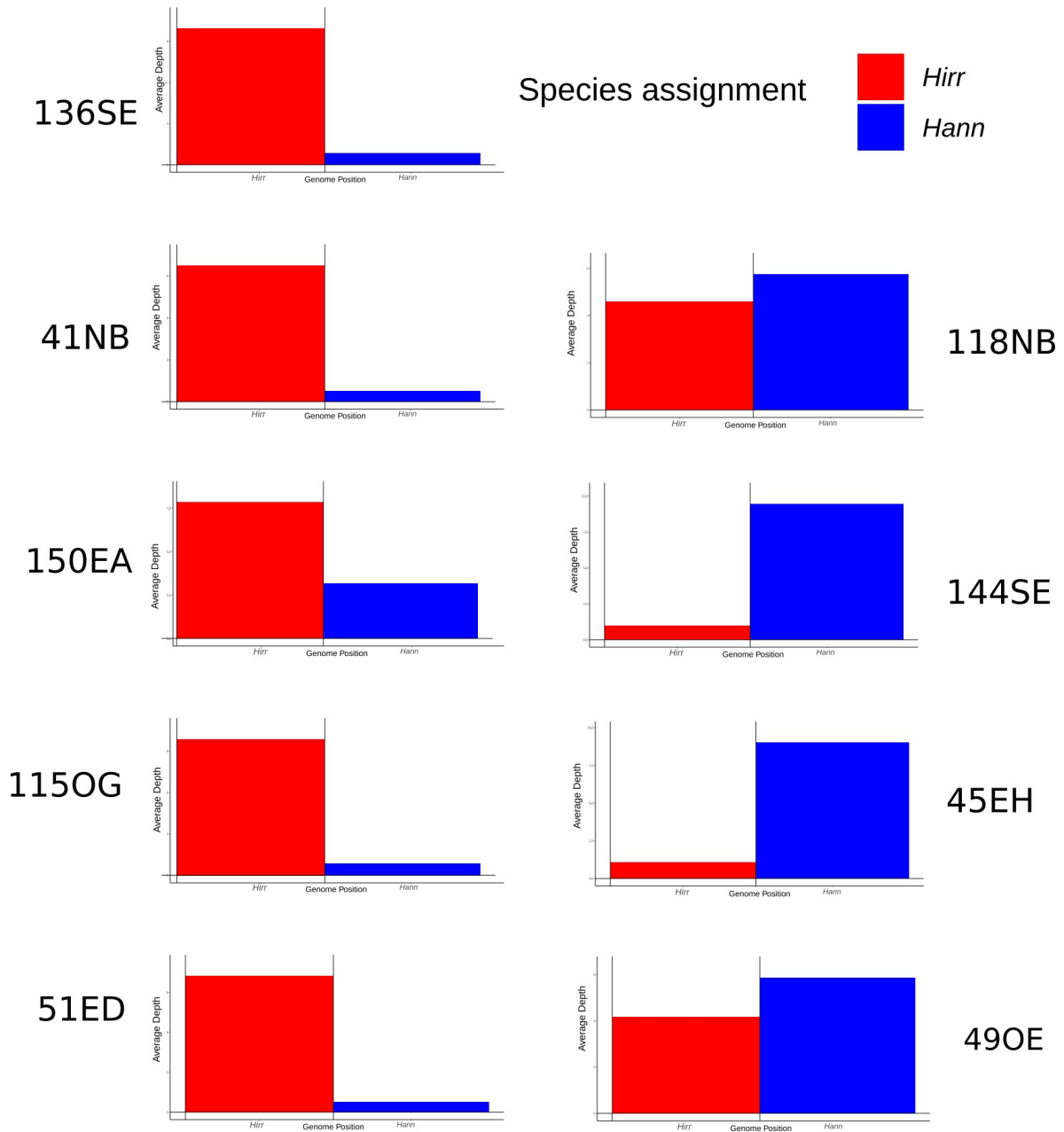Fabiano Sillo, Matteo Garbelotto, Luana Giordano, Paolo Gonthier

**Figure S1.** Barplots showing different percentage of parental genome contribution to the hybrid genome, as inferred by *sppIDer* analysis.
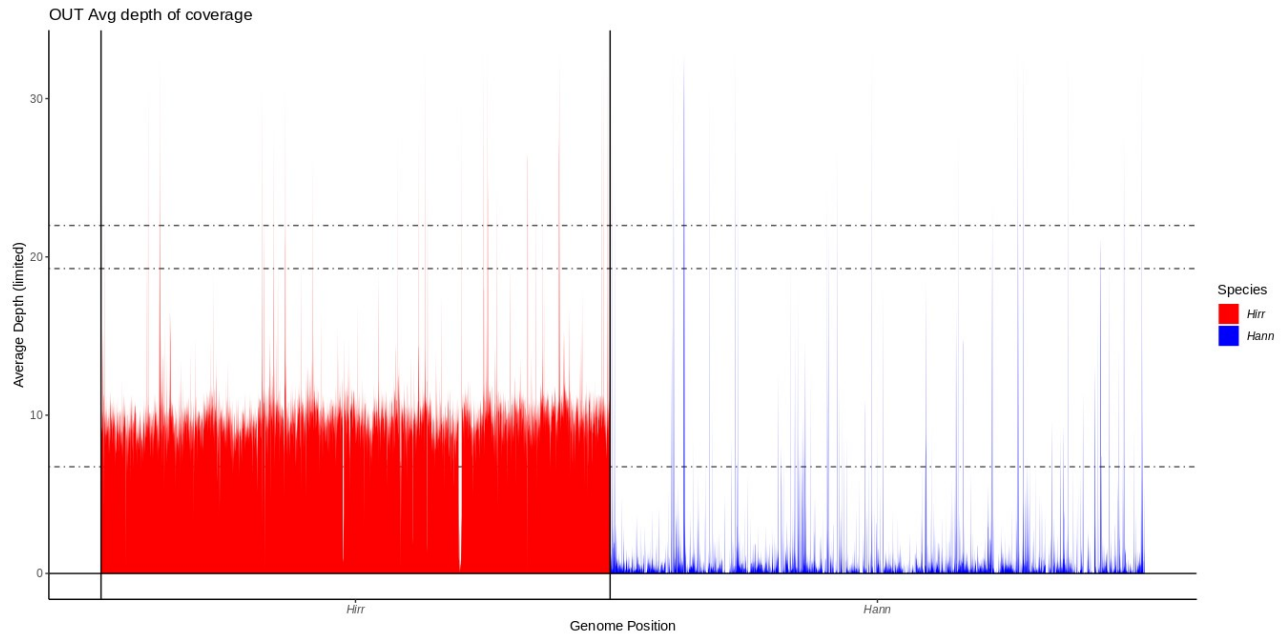
**Fig. S2.** Whole genome alignment through sppIDer of genotype 136SE. Average depth coverage of reads after the alignment with the two parental species along the two parental genomes.
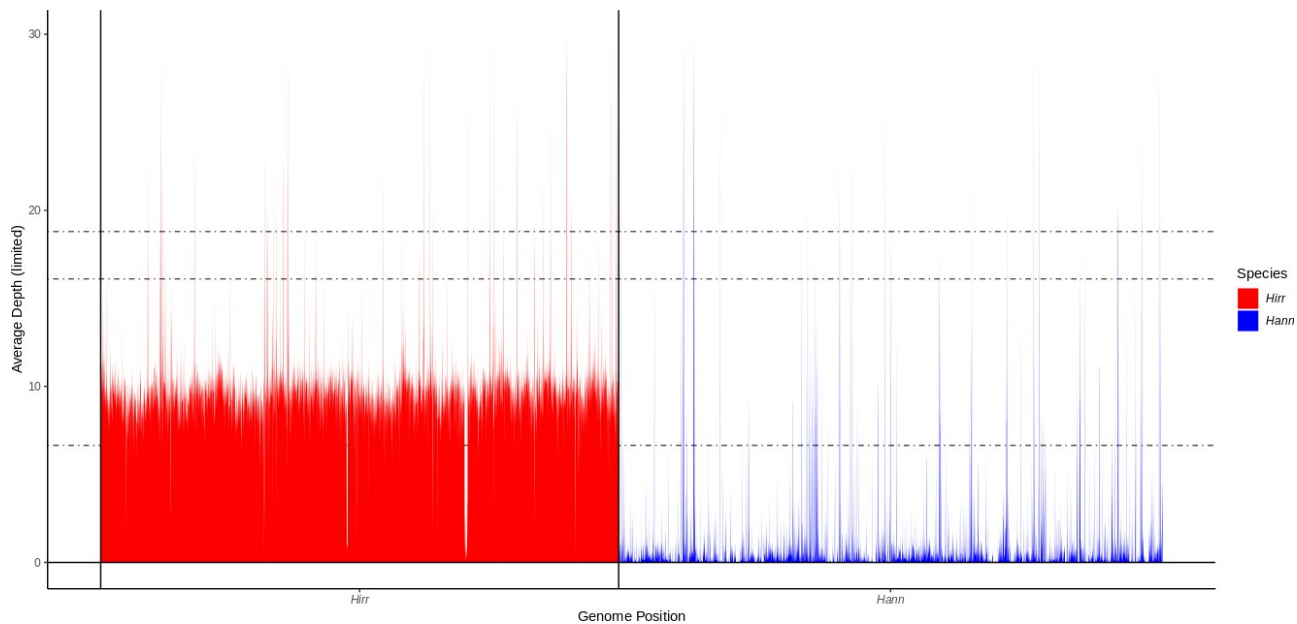
**Fig. S3.** Whole genome alignment through sppIDer of genotype 41NB. Average depth coverage of reads after the alignment with the two parental species along the two parental genomes.
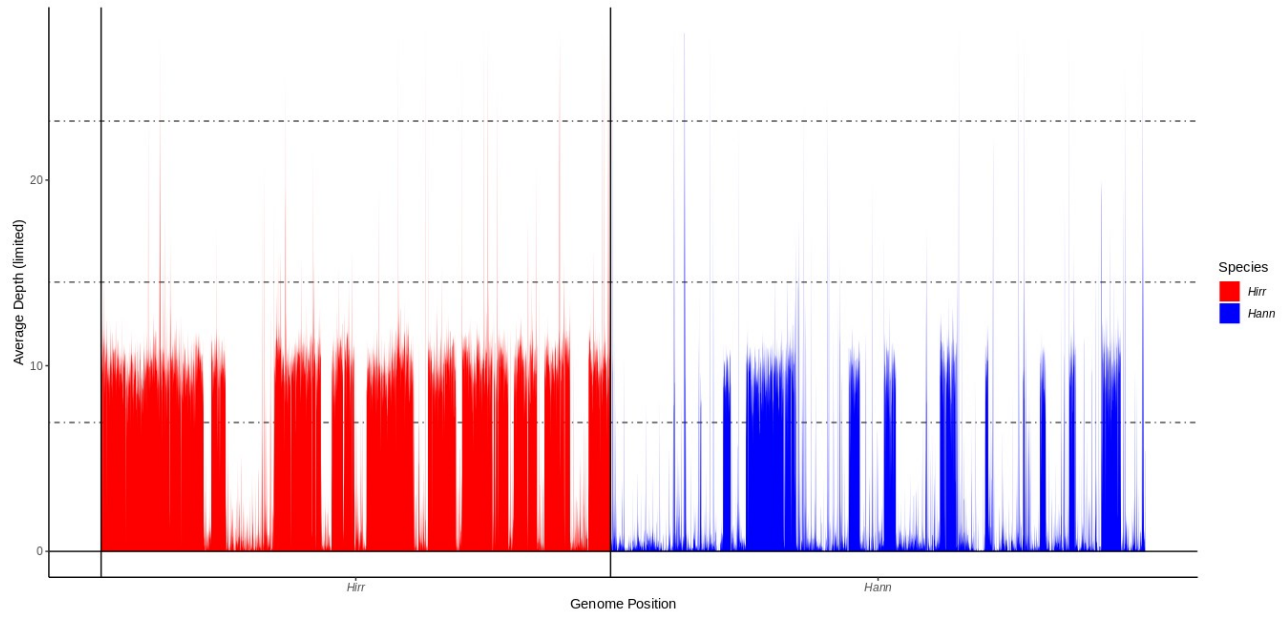
**Fig. S4.** Whole genome alignment through sppIDer of genotype 150EA. Average depth coverage of reads after the alignment with the two parental species along the two parental genomes.
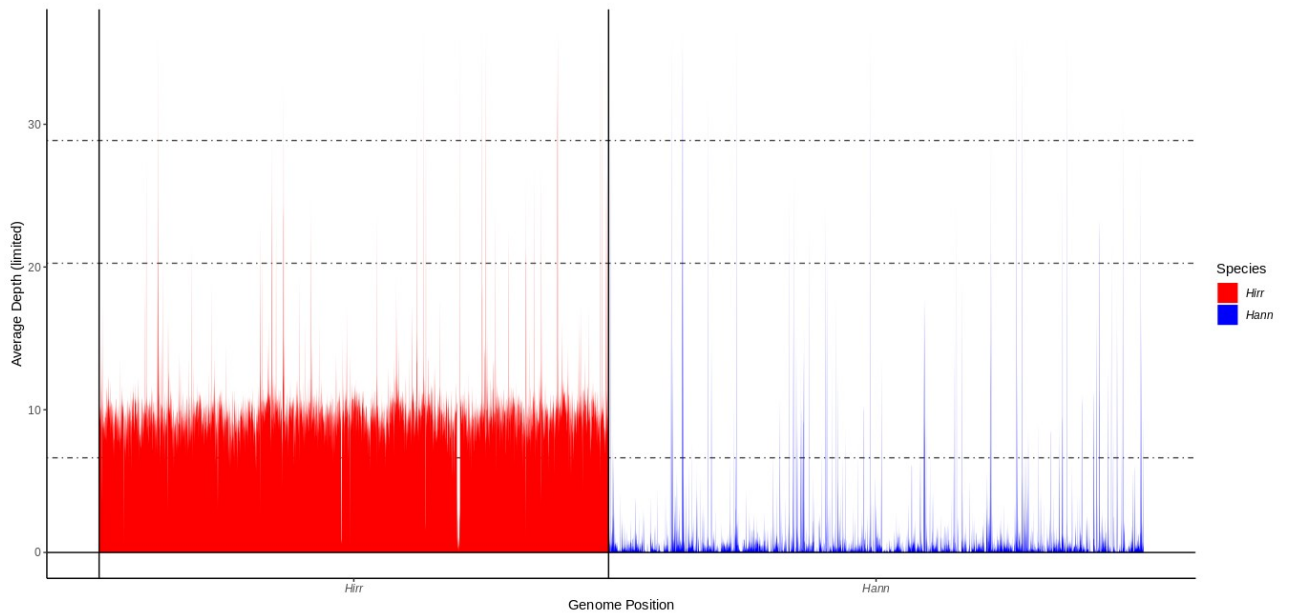
**Fig. S5.** Whole genome alignment through sppIDer of genotype 115OG. Average depth coverage of reads after the alignment with the two parental species along the two parental genomes.
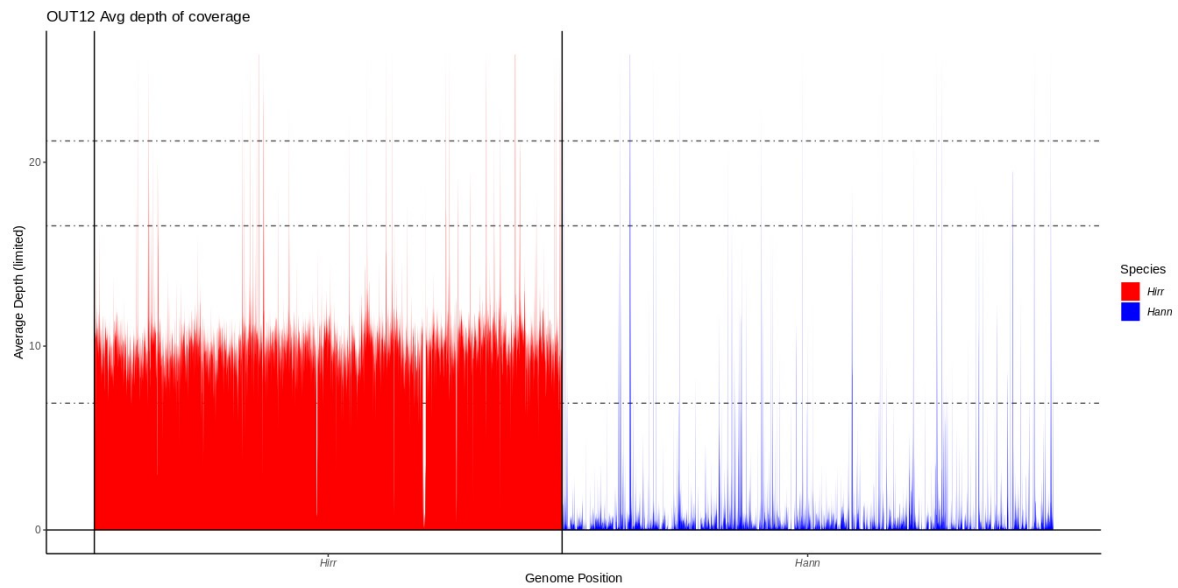
**Fig. S6.** Whole genome alignment through sppIDer of genotype 51ED. Average depth coverage of reads after the alignment with the two parental species along the two parental genomes.
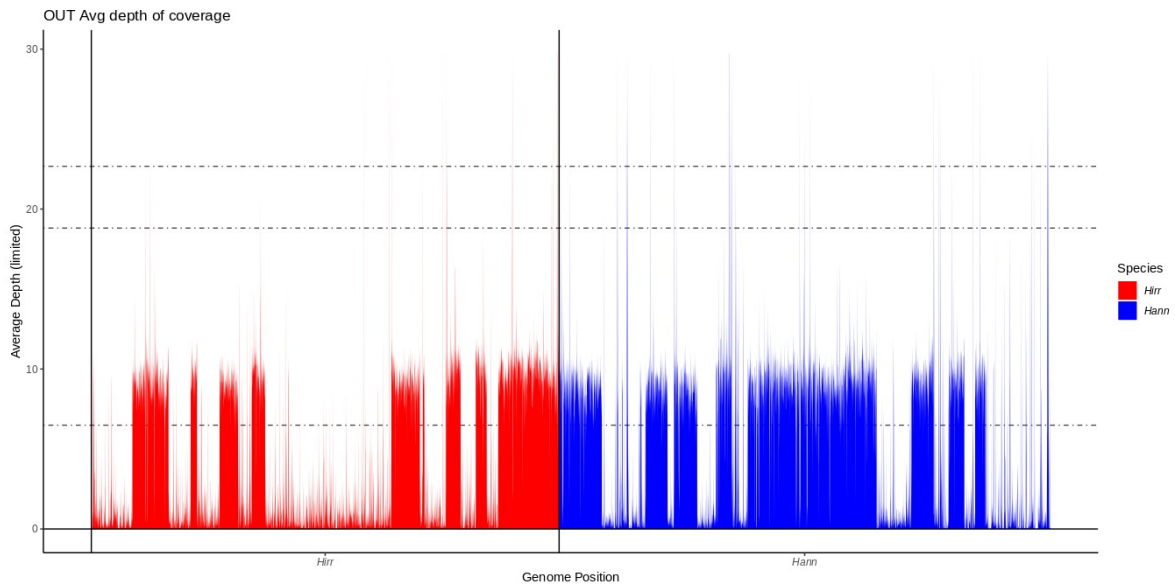
**Fig. S7.** Whole genome alignment through sppIDer of genotype 118NB. Average depth coverage of reads after the alignment with the two parental species along the two parental genomes.
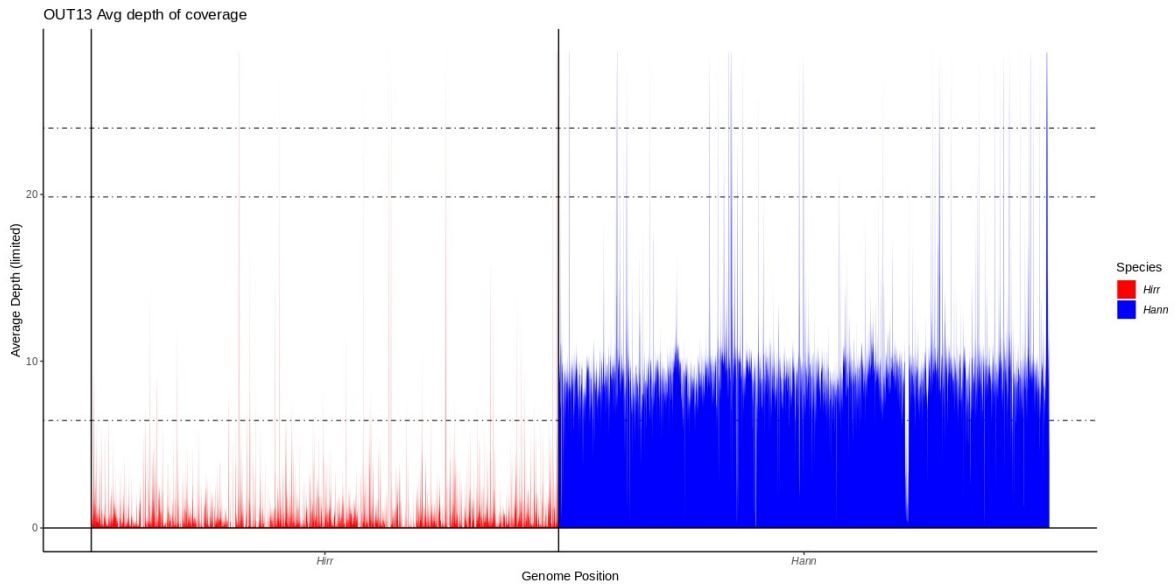
**Fig. S8.** Whole genome alignment through sppIDer of genotype 144SE. Average depth coverage of reads after the alignment with the two parental species along the two parental genomes.
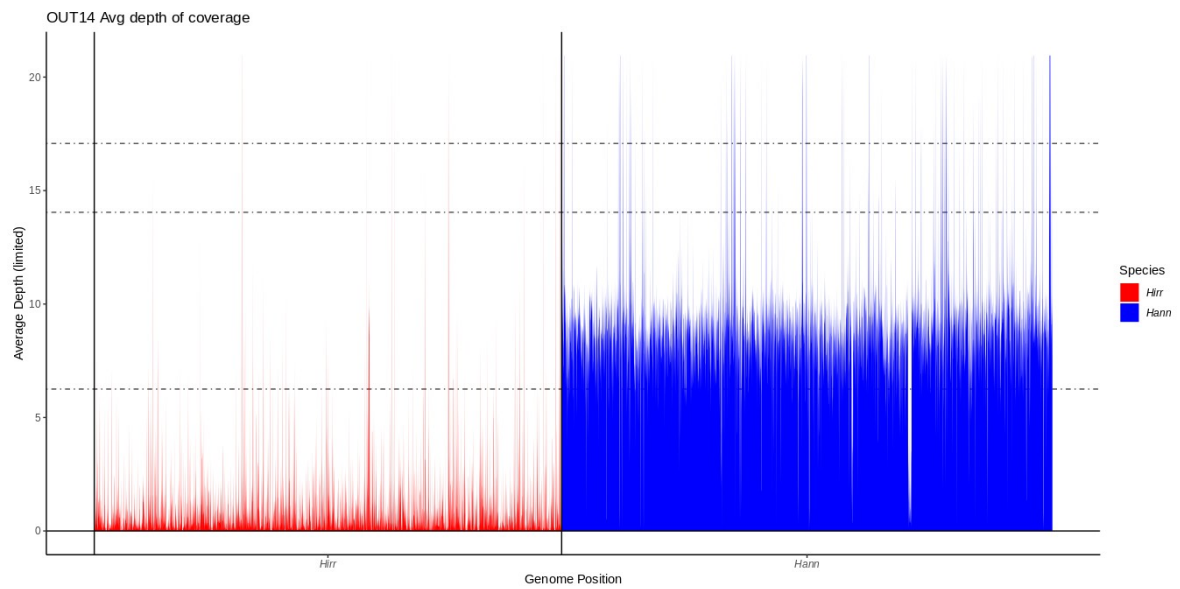
**Fig. S9.** Whole genome alignment through sppIDer of genotype 45EH. Average depth coverage of reads after the alignment with the two parental species along the two parental genomes.
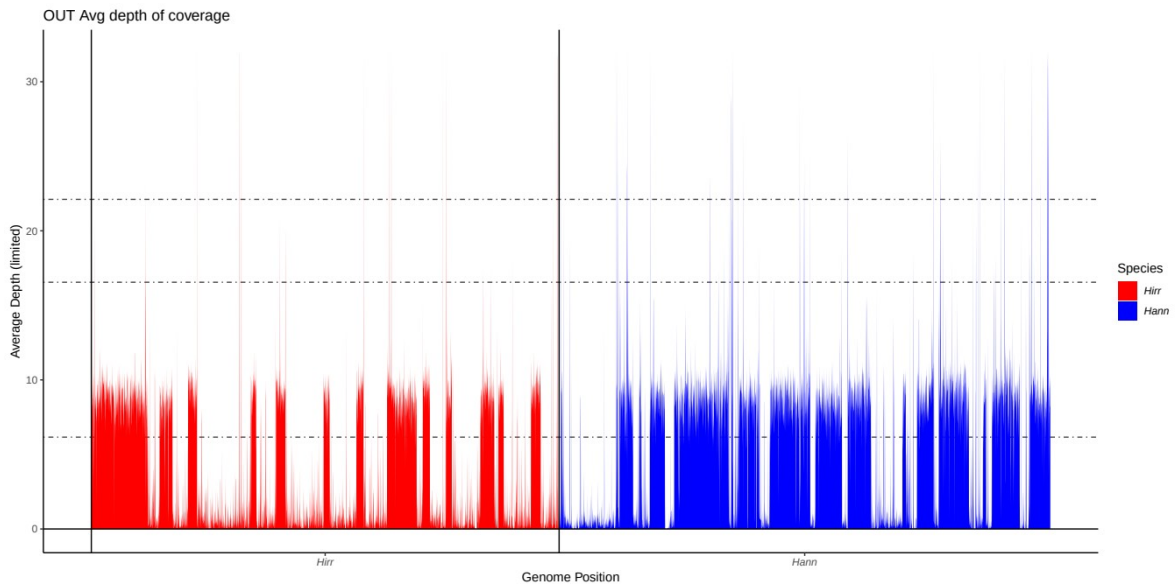
**Fig. S10.** Whole genome alignment through sppIDer of genotype 49OE. Average depth coverage of reads after the alignment with the two parental species along the two parental genomes.
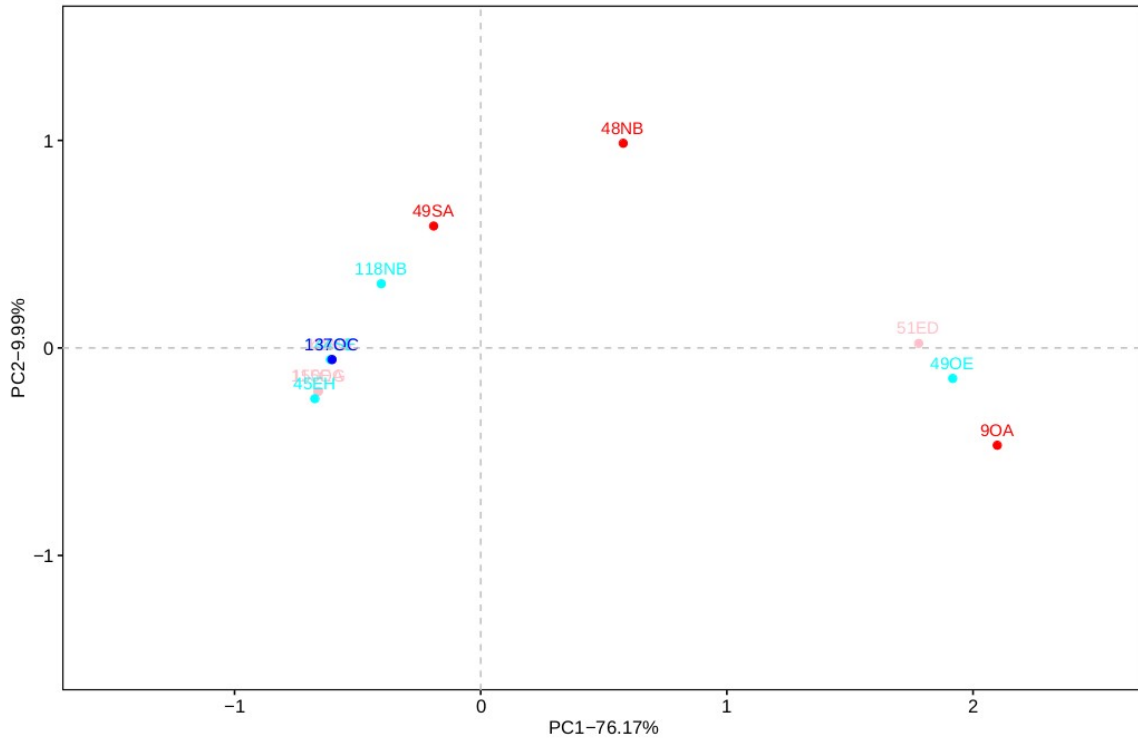
**Fig. S11.** Results of PCoA on phenotypic data obtained from the virulence assay. Red and blue dots represent pure *H. irregulare* and *H. annosum* genotypes, respectively. Pink and cyan dots represents hybrid genotypes assigned as *H. irregulare* and *H. annosum*, respectively.