



**Supplementary figure 4.** Sashimi plots of **(A)** the NRPS-like melanin biosynthase *melA* and **(B)** the tyrosinase *tyrP* describing the strand-specific alignment coverage of the read sequences of *A. terreus* MUCL38669 over the corresponding genomic regions of NIH2624 Supercontig\_1.4. The curved splice junctions represent the number of spliced reads indicating an intron at that specific location. The RNA to be sequenced was extracted from the set of samples where butyrolactone I had been added at 120 hours post inoculation. The samples were collected at 24, 48, 96, 120, 144 and 216 hours post inoculation and the extracted RNA was pooled prior to sequencing.