



**Figure S6.** Sashimi plots of the transcription factors (A) *brlA* and (B) *abaA*, (C) the developmental regulatory protein *wetA* and (D) the alpha,alpha-trehalose-phosphate synthase 1, *tpsA* describing the strand-specific alignment coverage of the read sequences of *A. terreus* MUCL38669 over the corresponding genomic regions of NIH2624. The curved splice junctions represent the number of spliced reads indicating an intron at that specific location.