



Fig. 13. Prevalence of HMO assimilation genes in *Bifidobacterium* genomes. The prevalence is indicated as the percent occurrence of each homolog gene in the genomes of *Bifidobacterium* species. The value in parenthesis indicates the number of the genomes examined. The occurrence of the homolog genes (identity ≥ 70 %; query coverage ≥ 60 %; e value $< 1 \times 10^{-50}$) was examined by tblastn analysis as described previously (ref. [105]). The data presented are an update of ref. [105] (Licensed under CC BY; <http://creativecommons.org/licenses/by/4.0/>).