

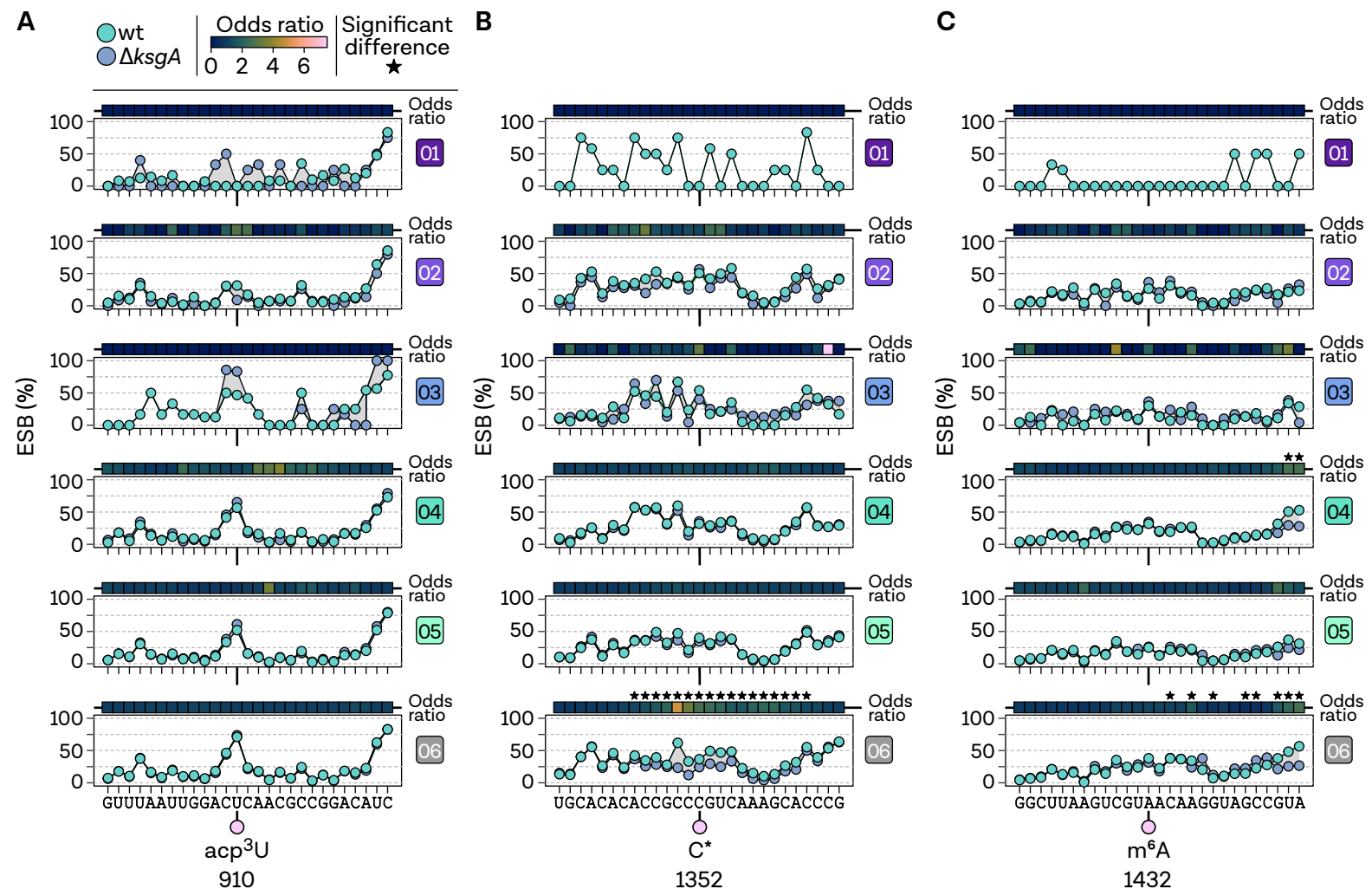


Fig. S18 | Direct RNA base modification analysis of 16S rRNA base modifications in *H. volcanii*.

A, Mean ESB values (of two biological replicates each) calculated for wild-type (green) and $\Delta ksgA$ reads (purple) grouped according to the categories used during the rRNA processing stage analysis are shown as connected points. Panel on top of each diagram shows a heatmap coloured by the mean odds ratio calculated using Eligos2 for all pairwise comparisons for each class. Positions that show significant different error profiles (multiple testing corrected (Benjamini-Hochberg) adjusted p value < 0.01 in all four test/control pairwise comparisons) are highlighted by a star. Profiles are shown for acp³U modification at position 910, **B**, unknown C* modification at position 1352 and **C**, m⁶A at position 1432.