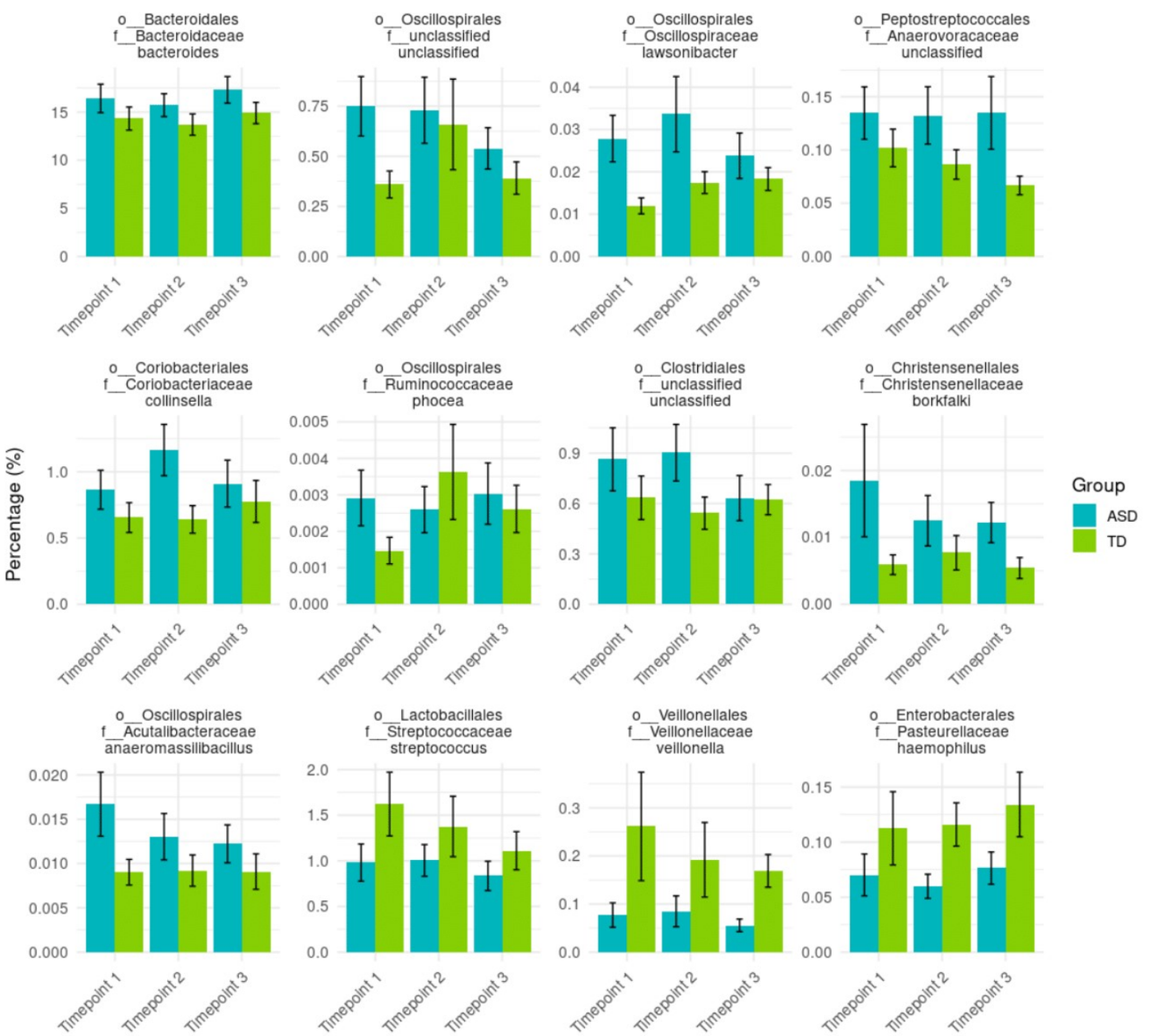
A

Order	Family	*Genus*	*Enrichment*	*Method*
Bacteroides	Bacteroidaceae	*Bacteroides*	ASD	DESEQ2
Oscillospirales	*Unclassified*	*Unclassified*	ASD	DESEQ2
Oscillospirales	*Oscillospiraceae*	*Lawsonibacter*	ASD	DESEQ2, Mtgseq
Peptostreptococcales	*Anaerovoracaceae*	*Unclassified*	ASD	DESEQ2, Mtgseq
Coriobacteriales	*Coriobacteriaceae*	*Collinsella*	ASD	Mtgseq
Oscillospirales	*Ruminococcaceae*	*Phocea*	ASD	Mtgseq
Clostridiales	*Unclassified*	*Unclassified*	ASD	DESEQ2
Christensenellales	*Christensenellaceae*	*Borkfalki*	ASD	Mtgseq
Oscillospirales	*Acutalibacteraceae*	*Anaeromassilibacillus*	ASD	Mtgseq
Lactobacillales	*Streptococcaceae*	*Streptococcus*	TD	Mtgseq
Veillonellales	*Veillonellaceae*	*Veillonella*	TD	DESEQ2, Mtgseq, ANCOM
Enterobacterales	*Pasteurellaceae*	*Haemophilus*	TD	Mtgseq, ANCOM

B



Supplementary Figure 4: Differentially abundant genera in ASD over 3 time points. ASV counts were aggregated by genus level annotation, ASVs that could not be assigned an annotation using the StrainSelect database were removed. Supp. 4A shows the taxonomic annotation of the genus, the phenotype the genus was enriched in, and the analysis method that identified it. Supp. 4B shows the relative percent of that genus in either group ASD or TD. MtgSeq refers to MetagenomeSeq.