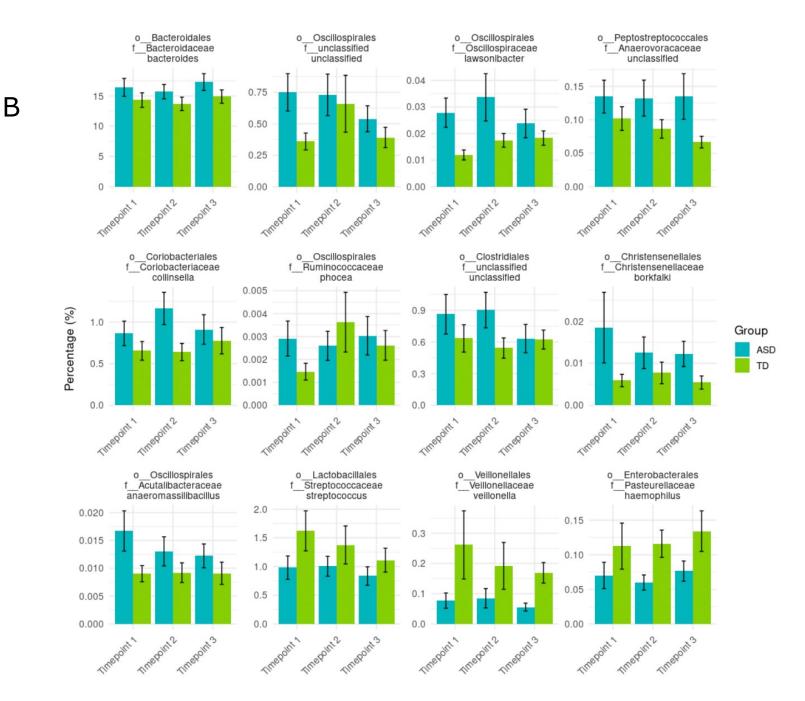
Order	Family	Genus	Enrichment	Method
Bacteroides	Bacteroidaceae	Bacteroides	ASD	DESEQ2
Oscillospirales	Unclassified	Unclassified	ASD	DESEQ2
Oscillospirales	Oscillospiraceae	Lawsonibacter	ASD	DESEQ2, Mtgseq
Peptostreptococcales	Anaerovoracaceae	Unclassified	ASD	DESEQ2, Mtgseq
Coriobacteriales	Coriobacteriaceae	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



Supplementary Figure 5: 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.