

Veillonella(G)-seq98-		*	
Streptococcus(G)-seq49-		*	
Streptococcus(G)-seq4-		*	
Ruminococcaceae_UCG-004(G)-seq198-		*	
Ruminococcaceae_UCG-002(G)-seq538-		*	
Rothia mucilaginosa(S)-seq258-			*
Odoribacter splanchnicus(S)-seq206-		*	
Lachnospiraceae(F)-seq8-	*		
Lachnospiraceae(F)-seq271		*	
Lachnospiraceae(F)-seq17-		*	
Lachnoclostridium(G)-seq629-		*	
Lachnoclostridium(G)-seq319-		*	
Lachnoclostridium(G)-seq120-		*	
Lachnoclostridium(G)-seq104		*	
Haemophilus(G)-seq15-		*	
Granulicatella(G)-seq99-		*	
Erysipelatoclostridium ramosum(S)-seq92-	*		
Eggerthella lenta(S)-seq1080-		*	
Coprococcus_1(G)-seq212-		*	
Coprobacter fastidiosus(S)-seq275		*	
Bacteroides(G)-seq64-		*	
Bacteroides(G)-seq16-		*	
Bacteroides uniformis(S)-seq45		*	
Actinomyces odontolyticus(S)-seq448-		*	
	Fecal	Mucosal	Oral