

**Table S5.**

**Sequence of main families of *B.coagulans* satellites**

Family name	Consensus Sequence
1_52_139	GTgAAGgAAGgcCnTCnTTTTTcCncGCTTcCTTAACGTAGACGcgCTCTAT
2_52_35	TTTTGTCCTTTTgACaGcTTCAAAAnGACATTTcGgGCCCgGATgCAgCntG
8_52_18	TGTCCTTCATaagggtGATGAAaGACAAAACaCnGGcCgggaAAcGgCgAAt
360_52_1	TTTTGTC <b>TTTTGA</b> ACCGTTGT <b>AAAAGACA</b> GTTcGgTGGAAAGCTGGAACGC

We have used the consensus sequence of the main satellite families previously determined [15] from the genome sequence of seven strains of *B.coagulans*. We have also used a unique satellite (360\_52\_1), which is only present in the 2-6 strain studied by Qin et al. [11]. Note that part of the consensus sequence of this satellite (shown in red) is identical with the consensus sequence of the 2\_52\_35 family.