

Table 2 Alignment view using combination of NCBI GenBank and RDP database showing the close homologs of the sample 'N'

ID	Alignment results	Sequence description
<u>SampleN</u>	0.97	Studied sample
<u>AM779000</u>	0.99	<i>Bacillus thuringiensis</i> strain SBS-BT4
<u>AM778997</u>	0.98	<i>Bacillus thuringiensis</i> strain CMBL-BT4
<u>AY138279</u>	0.99	<i>Bacillus cereus</i> strain 2000031513
<u>AY138383</u>	1.00	<i>Bacillus anthracis</i> strain 2000031664
<u>AY138358</u>	1.00	<i>Bacillus anthracis</i> strain AMES
<u>AY853168</u>	0.99	<i>Bacillus sp.</i> 4
<u>AM747228</u>	0.98	<i>Bacillus mycoides</i> strain SDA NFMO448
<u>DQ521606</u>	0.99	<i>Bacillus cereus</i> strain DBM
<u>AJ577292</u>	1.00	<i>Bacillus cereus</i> strain B 204
<u>AY741718</u>	0.99	<i>Bacillus thuringiensis</i>