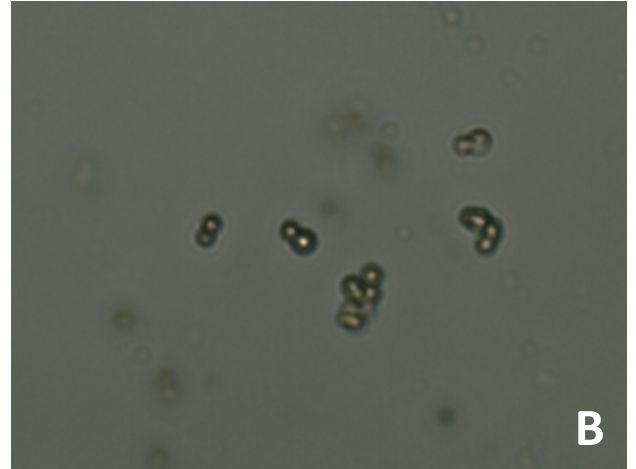
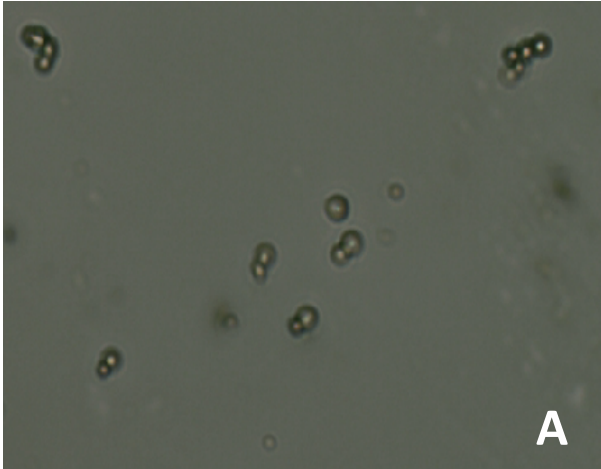


# Fig. S1

Range 1: 1 to 613 [Graphics](#) ▼ Next Match ▲ Previous Match

NW Score	Identities	Gaps	Strand
1197	610/614(99%)	2/614(0%)	Plus/Plus
Query 1	ATATCAAAAA-GCGGAGGAAAAGAAACCAACCGGGATTGCCTTAGTAAACGGCGAGTGA		57
Sbjct 1	GCATATCAAAAAAGCGGAGGAAAAGAAACCAACCGGGATTGCCTTAGTAAACGGCGAGTGA		60
Query 58	AGCGGC AAAAGCTCAAATTTGAAATCTGGTACCTTCGGTGCCCGAGTTGTAATTTGGAGA		117
Sbjct 61	AGCGGC AAAAGCTCAAATTTGAAATCTGGTACCTTCGGTGCCCGAGTTGTAATTTGGAGA		120
Query 118	GGGCAACTTTGGGGCCGTTCCCTTGCTATGTTCCCTTGGAAACAGGACGTCATAGAGGGTGA		177
Sbjct 121	GGGCAACTTTGGGGCCGTTCCCTTGCTATGTTCCCTTGGAAACAGGACGTCATAGAGGGTGA		180
Query 178	GAATCCCGTGTGGCGAGGAGTGC GGTTCTTTGTAAAAGTGCCTTCGAAGAGTCGAGTTGTT		237
Sbjct 181	GAATCCCGTGTGGCGAGGAGTGC GGTTCTTTGTAAAAGTGCCTTCGAAGAGTCGAGTTGTT		240
Query 238	TGGGAATGCAGCTCTAAGTGGGTGGTAAATTCATCTAAAGCTAAATATTGGCGAGAGAC		297
Sbjct 241	TGGGAATGCAGCTCTAAGTGGGTGGTAAATTCATCTAAAGCTAAATATTGGCGAGAGAC		300
Query 298	CGATAGCGAACAAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAA		357
Sbjct 301	CGATAGCGAACAAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAA		360
Query 358	GTACGTGAAATTGTTGAAAGGGAAGGGCATTGATCAGACATGGTGT TTTGTGCCCTCTG		417
Sbjct 361	GTACGTGAAATTGTTGAAAGGGAAGGGCATTGATCAGACATGGTGT TTTGTGCCCTCTG		420
Query 418	CTCCTTGTGGGTAGGGGAATCTCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGA		477
Sbjct 421	CTCCTTGTGGGTAGGGGAATCTCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGA		480
Query 478	TAAATCCATAGGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCAG		537
Sbjct 481	TAAATCCATAGGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCAG		540
Query 538	CTGGGACTGAGGACTGCGACGTAAGTCAAGGATGCTGGCATAATGGTTATATGCCGCCCG		597
Sbjct 541	CTGGGACTGAGGACTGCGACGTAAGTCAAGGATGCTGGCATAATGGTTATATGCCGCCCG		600
Query 598	TCTTGAAACACGGG 611		
Sbjct 601	TCTTGAAACACGG 613		

**Fig. S2**



# Fig. S3

