

Figure S5. ClustalW alignment of 16S rDNA sequences used for the phylogeny reconstruction. For the details on sequences' source see Table S1. The phylogenetic tree is presented in Figure 3.



KVJ4	GAGTAACGCGTGAGAATCTGCCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCCTTTAGG	GGTGAAAGATTAATTGCCTGA
KVJ2	GAGTAACGCGTGAGAATCTGCCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCCTTTAGG	GGTGAAAGATTAATTGCCTGA
KVSF4	GAGTAACGCGTGAGAATCTGCCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCCTTTAGG	GGTGAAAGATTAATTGCCTGA
SKS2	GAGTAACGCGTGAGAATCTGCCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCCTTTAGG	GGTGAAAGATTAATTGCCTGA
SKJF1	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTGA
SKS3	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTGA
SKJ6	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTGA
SKJ2	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTGA
SKS5	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTGA
SKS9	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTGA
KVJ18	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTGA
SKJ4	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTGA
SKSF1	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGGACAACAGTTGGAACGACTGCTAATACCGGATATGCCGAAA	GGTGAAAGGCTTGCTGCCTGA
KVSF7	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGCTTGCTGCCTGA
SKS8	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGCTTGCTGCCTGA
DQ185249	GAGTAACGCGTGAGAATCTGGCTTTAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCCGTAATTGGG	GGTGAAAGGTTAACTGCCTGA
DQ185255	GAGTAACGCGTGAGAATCTGGCTTTAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCCGTAATTGGG	GGTGAAAGGTTAACTGCCTGA
AY566855	GAGTAACGCGTGAGAATCTGGCTCTAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGTAG	GGTGAAAGGTTAACTGCCTAG
AM711545	GAGTAACGCGTGAGAATCTGGCTCTAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTAG
AM711536	GAGTAACGCGTGAGAATCTGGCTCTAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTAG
DQ185256	GAGTAACGCGTGAGAATCTGGCTCTAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTAG
DQ185245	GAGTAACGCGTGAGAATCTGGCTCTAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTAG
AM711527	GAGTAACGCGTGAGAATCTGGCTCTAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTAG
DQ185212	GAGTAACGCGTGAGAATCTGGCTCTAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTAG
AF062638	GAGTAACGCGTGAGAATCTGGCTCTAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTAG
HM623781	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGATTAATTGCCTGA
AM711540	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGATTAATTGCCTGA
DQ185254	GAGTAACGCGTGAGAATCTGCCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAAA	GGTGAAAGGTTAACTGCCTGA
DQ185251	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAAA	GGTGAAAGATTAATTGCCTGA
AM711535	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGATTAATTGCCTGA
AF027653	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTGA
DQ185244	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTGA
AM711531	GAGTAACGCGTGAGAATCTGCCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCCTTTAGG	GGTGAAAGATTAATTGCCTGA
AJ630449	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCCTTTAGG	GGTGAAAGATTAATTGCCTGA
AY328897	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTGA
AM230702	GAGTAACGCGTGAGAATCTAGCTTCAGGTCTGGGGACAACAGTTGGGAACGATGCTAATACCGGATGTGCCGAAA	GGTGAAAGGCTTGCTGCCTGA
EF568907	GAGTAACGCGTGAGAATCTAGCTTCAGGTCTGGGGACAACAGTTGGGAACGACTGCTAATACCGGATATGCCGAGA	GGTGAAAGGCTTGCTGCCTGA
AJ630458	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGGACAACAGTTGGGAACGACTGCTAATACCGGATATGCCGAGA	GGTGAAAGATTAATTGCCTGG
GQ443447	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGGACAACAGTTGGGAACGACTGCTAATACCGGATATGCCGAGA	GGTGAAAGATTAATTGCCTGG
AJ630457	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGCTTGCTGCCTGA
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AJ133161	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGCTTGCTGCCTGA
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DQ185209	GAGTAACGCGTGAGAATCTGGCTTTAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAAA	GGTGAAAGATTAATTGCCTGA
AY742451	GAGTAACGCGTGAGAATCTGGCTTCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGATTAATTGCCTGA
AF027655	GAGTAACGCGTGAGAATCTGGCTCTAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA	GGTGAAAGGTTAACTGCCTAG

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AY742449 GAGTAACGCGTGAGAATCTGGCTCTAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCGAGA --- GGTTGAAAGGTTAACTGCCTAG
EF174212 GAGTAACGCGTGAGAATCTGCCATCAGGTCTGGGACAACCACCTGGAACGGTGGCTAATACCGGATGTGCCCTTCGG --- GGTTGAAAGGTTAACTGCCTGT
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KVSF5 GAGTAACGCGTGAGAATCTGCCCTTAGGATGGGGACAACAGTTGGAACGACTGCTAAGACCCGATGTGCCGAGA --- GGTTGAAATATTTATAGCCTGA

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	310	320	330	340	350	360	370	380	390	400	
											
KVJ10	GACACGGCCCCAGACTCCTACGGGAGGAGCAGAGTGGGGAAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGGAAGGCTCTTTGGG										
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KVJ3	GACACGGCCCCAGACTCCTACGGGAGGAGCAGAGTGGGGAAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGGAAGGCTCTTTGGG										
SKS1	GACACGGCCCCAGACTCCTACGGGAGGAGCAGAGTGGGGAAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGGAAGGCTCTTTGGG										

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AJ630449 GCGTTATCCGGAATGATTGGGCGTAAAGCGTCCGCAGGTGGCTATGTAAGTCTGCTGTTAAAGAGTCTAGCTCAACTAGATAAGAGCAGTGGAAACTACA
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KVSF5 GCGTTATCCGGAATTTATTGGGCGTAAAGCGTCCGTAGGTGGTTTTATCAAGTCTGTTGTTAAAGAGTGGGGCTTAACCTCATAAAGGCAGTGGAAACTGAT

610 620 630 640 650 660 670 680 690 700
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KVJ10 TAGCTAGAGTACGTTTCGGGGCAGAGGGGAATTCCCTGGTGTTAGCGGTGAAATGCGTAGAGATCAGGAAGAACACCCAGTGGCGAAGGCGCTCTGCTAGGCCGT
KVJF8 TAGCTAGAGTACGTTTCGGGGCAGAGGGGAATTCCCTGGTGTTAGCGGTGAAATGCGTAGAGATCAGGAAGAACACCCAGTGGCGAAGGCGCTCTGCTAGGCCGT
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KVSF5 GGACTTGAGTGTGGTAGGGGGTAGAGGGAATTCCCAGTGTAGCGGTGAAATGCGTAGATATTTGGGAAGAACACCGGTGGCGAAGGCGCTCTACTGGACCTG

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 KVSF5 CACTGACACTGAGGGACGAAAGCTAGGGGAGCGAAGGGATTAGATACCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGCGTGGCTTGATCGACC

810 820 830 840 850 860 870 880 890 900
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SKJ1	CTCTAGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCTTACGCCTTTGGG	CTACACACGTACTACAATGCTCC								
KVJF4	CTCTAGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCTTACGCCTTTGGG	CTACACACGTACTACAATGCTCC								
KVS11	CTCTAGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCTTACGCCTTTGGG	CTACACACGTACTACAATGCTCC								
KVJ20	CTCTAGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCTTACGCCTTTGGG	CTACACACGTACTACAATGCTCC								
SKSF3	CTCTAGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCTTACGCCTTTGGG	CTACACACGTACTACAATGCTCC								
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KVJ4	CTCTAGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCTTACGCCTTTGGG	CTACACACGTACTACAATGCTCC								
KVJ2	CTCTAGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCTTACGCCTTTGGG	CTACACACGTACTACAATGCTCC								
KVSF4	CTCTAGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCTTACGCCTTTGGG	CTACACACGTACTACAATGCTCC								
SKS2	CTCTAGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCTTACGCCTTTGGG	CTACACACGTACTACAATGCTCC								
SKJF1	CTCTAGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCTTACGCCTTTGGG	CTACACACGTACTACAATGCTCC								
SKS3	CTCTAGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCTTACGCCTTTGGG	CTACACACGTACTACAATGCTCC								

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1210 1220 1230 1240 1250 1260 1270 1280 1290 1300

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 KVSF5 AG-ACAAATGGGAAGCTACACAGCGATGTGATGCGAAACTCAGAAACTGTGGCTCAGTTCAGATTGCAGGCTGCAACTCGCCTGCATGAAGGAGGAATCGC

	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400
										
KVJ10	TAGTAATTG	CAGGTG	CAGCATACTG	CAGTGAATTCG	TTCCCGGGC	CTTG	TACACACCGCCCGT	CACACCATGGAAGCT	GGTAGTG	CCCCGAAGTCATTACTC
KVJF8	TAGTAATTG	CAGGTG	CAGCATACTG	CAGTGAATTCG	TTCCCGGGC	CTTG	TACACACCGCCCGT	CACACCATGGAAGCT	GGTAGTG	CCCCGAAGTCATTACTC
KVJ3	TAGTAATTG	CAGGTG	CAGCATACTG	CAGTGAATTCG	TTCCCGGGC	CTTG	TACACACCGCCCGT	CACACCATGGAAGCT	GGTAGTG	CCCCGAAGTCATTACTC
SKS1	TAGTAATTG	CAGGTG	CAGCATACTG	CAGTGAATTCG	TTCCCGGGC	CTTG	TACACACCGCCCGT	CACACCATGGAAGCT	GGTAGTG	CCCCGAAGTCATTACTC
KVS1	TAGTAATTG	CAGGTG	CAGCATACTG	CAGTGAATTCG	TTCCCGGGC	CTTG	TACACACCGCCCGT	CACACCATGGAAGCT	GGTAGTG	CCCCGAAGTCATTACTC
SKJ1	TAGTAATTG	CAGGTG	CAGCATACTG	CAGTGAATTCG	TTCCCGGGC	CTTG	TACACACCGCCCGT	CACACCATGGAAGCT	GGTAGTG	CCCCGAAGTCATTACTC
KVJF4	TAGTAATTG	CAGGTG	CAGCATACTG	CAGTGAATTCG	TTCCCGGGC	CTTG	TACACACCGCCCGT	CACACCATGGAAGCT	GGTAGTG	CCCCGAAGTCATTACTC
KVS11	TAGTAATTG	CAGGTG	CAGCATACTG	CAGTGAATTCG	TTCCCGGGC	CTTG	TACACACCGCCCGT	CACACCATGGAAGCT	GGTAGTG	CCCCGAAGTCATTACTC
KVJ20	TAGTAATTG	CAGGTG	CAGCATACTG	CAGTGAATTCG	TTCCCGGGC	CTTG	TACACACCGCCCGT	CACACCATGGAAGCT	GGTAGTG	CCCCGAAGTCATTACTC
SKSF3	TAGTAATTG	CAGGTG	CAGCATACTG	CAGTGAATTCG	TTCCCGGGC	CTTG	TACACACCGCCCGT	CACACCATGGAAGCT	GGTAGTG	CCCCGAAGTCATTACTC

[illegible]

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 AF027655 TAGTAATTGCAGGTGAGCATACTGCAGTGAATTCGTTCCCGGGCCTTGTAACACACCGCCCGTCACACCATGGAAGCTGGTAGTGCCCGAAGTCATTACTC
 DQ185211 TAGTAATTGCAGGTGAGCATACTGCAGTGAATTCGTTCCCGGGCCTTGTAACACACCGCCCGTCACACCATGGAAGCTGGTAGTGCCCGAAGTCATTACTC
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	1410	1420	1430	1440	1450	1460	1470	1480	1490	1500
										
KVJ10	CAACCTTTTC	GGGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
KVJF8	CAACCTTTTC	GGGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
KVJ3	CAACCATTCG	TGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
SKS1	CAACCATTCG	TGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
KVS1	CAACCATTCG	TGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
SKJ1	CAACCATTCG	TGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
KVJF4	CAACCATTCG	TGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
KVS11	CAACCATTCG	TGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
KVJ20	CAACCTTTTC	GGGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
SKSF3	CAACCTTTTC	GGGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
SKSL1	CAACCTTTTC	GGGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
SKSL2	CAACCTTTTC	GGGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
KVJ4	CAACCATTCG	TGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
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KVSF4	CAACCATTCG	TGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
SKS2	CAACCTTTTC	GGGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
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KVJ18	CAACCATTCG	TGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
SKJ4	CAACCATTCG	TGGAGGAGGAT	GCCTAAGGC	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT
SKSF1	CAACCGTAAGGAG	-GGGG-ATGCCTAAGG	TAGGACTAGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT	
KVSF7	CAACCTTTTTT	GGA-GGGGATGCCTAAGG	TAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT	
SKS8	CAACTTTTT	CGAGAGGGGGATGCCTAAGG	CAGTGCTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGT	ACCGGAAGG	TGTGGCTGGATCACCTCCTT	
DQ185249	CAACCTTTTC	GGGGGGGAGGATGCCTAAGG	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGTAC	-----		
DQ185255	CAACCTTTTC	GGGGAGGAGGATGCCTAAGG	CAGGACTGGT	GACTGGGGT	GAAAGTCG	TAAACAAGG	TAGCCGTACCGGAAGG	-----		

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