

(A)

5'-variable region

SAR0438	ATGGGAAA	TAAAAA	GTTTGC	ATGTA	CAAAAG	TCTT	GCTTTT	TAATAG	TGTTG	TAGCAG	GTTC	GGCAA	...AAGT	GATAA	: 83	
SAB0389	ATGGGATA	TAAAAA	GGATGG	ATGTA	CAAAAG	TCTT	TATTTT	TAATAG	TGTTG	TAGCAG	GTTC	GGAAA	...AGATA	TG.....A	: 83	
SAU0397	ATGGGATA	TAAAAA	AGCTTGC	ATGTA	CAAAAG	TCTT	TATTTT	GGGCAT	TTTAT	TAATAG	TTTAT	GATATG	TCACG	CAATG	CTG	: 95	
SAA0419	ATCGAGTA	TAAAAA	AAATTC	CTTGT	ATGTA	CAAAAG	TCTT	TAATCA	TTTAT	TGTTGG	GTTC	GGAATAT	GAAAC	AGAAAA	AGAGG	: 100	
SAC0486	ATGGGATA	TAAAAA	AAATTC	CTTGT	ATGTA	CAAAAG	TCTT	TAATCA	TTTAT	TGTTGG	GTTC	GGAATAT	GAAAC	AGAAAA	AGAGG	: 100	
SAO0405	ATGGAGTA	TAAAAA	AAATTC	CTTGT	ATGTA	CAAAAG	TCTT	TAATCA	TTTAT	TGTTGG	GTTC	GGAATAT	GAAAC	AGAAAA	AGAGG	: 100	
SAM0397	ATGGGATA	TAAAAA	GGTTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TAGCAG	GTTC	GGCAA	...AAGT	GATAA	: 83	
SAB0390p	ATGGGATA	TAAAAA	GGTTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TAGCAG	GTTC	GGTAA	...AAGT	GATAA	: 83	
SAR0440p	ATGGGACA	TAAAAA	AGCTTGC	ATGTA	CAAAAG	TCTT	TATTTT	GAGCAT	TTTAT	TAATAG	TTTAT	GATATG	TCACG	CAATG	CTG	: 95	
SAU0402	ATGGGTAT	TAAAAA	GACCTG	TATG	TACAA	AGTTA	TGGT	TATG	AGTCT	TTTAT	TAATAG	TTTAT	GATATG	TCACG	CAATG	: 98	
SAM0399	ATGGAAAT	TAAAAA	GGCTTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TAGCAG	GTTC	GATAGT	CAAGCG	AT	..ACTG	: 98	
SAC0396p	ATGGAGTA	TAAAAA	AAATTC	CTTGT	ATGTA	CAAAAG	TCTT	TAATCA	TTTAT	TGTTGG	GTTC	GGAATAT	GAAAC	AGAAAA	AGAGG	: 99	
SAU0396	ATCGGATA	TAAAAA	GACCTT	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TAGCAG	GTTC	GGCAA	...GGTA	TG.....A	: 88	
SAA0410	ATGGGATA	TAAAAA	GGTTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TAGCAG	GTTC	GGCAA	...GGTA	TG.....A	: 88	
SAR0439	ATGGGATA	TAAAAA	GGTTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TAGCAG	GTTC	GGCAA	...GGTA	TG.....A	: 88	
SAU0403	ATGGGATA	TAAAAA	GAGTTC	TAC	TACAA	AAATG	TGTTG	TATG	AGTCT	TTTAT	TAATAG	TTTAT	GATATG	TCACG	CAATG	: 100	
SAR0443	ATGGATA	TAAAAA	GAGTTC	TAC	TACAA	AAATG	TGTTG	TATG	AGTCT	TTTAT	TAATAG	TTTAT	GATATG	TCACG	CAATG	: 100	
SAA0417	ATGGGATA	TAAAAA	GAAATTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TGTTGG	GTTC	GGAATAT	GAAAC	AGAAAA	AGAGG	: 100	
SAC0484	ATGGGATA	TAAAAA	GAAATTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TGTTGG	GTTC	GGAATAT	GAAAC	AGAAAA	AGAGG	: 100	
SAO0402	ATGGGATA	TAAAAA	GGTTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TGTTGG	GTTC	GGCAA	...AGTA	TG.....A	: 94	
SAM0401	ATGGAGTA	TAAAAA	AAATTC	CTTGT	ATGTA	CAAAAG	TCTT	TAATCA	TTTAT	TGTTGG	GTTC	GGAATAT	GAAAC	AGAAAA	AGAGG	: 100	
SAU0405	ATCGAGTA	TAAAAA	AAATTC	CTTGT	ATGTA	CAAAAG	TCTT	TAATCA	TTTAT	TGTTGG	GTTC	GGAATAT	GAAAC	AGAAAA	AGAGG	: 100	
SAA0413	ATGGGTAT	TAAAAA	GACCTG	TATG	TACAA	AGTTA	TGGT	TATG	AGTCT	TTTAT	TAATAG	TTTAT	GATATG	TCACG	CAATG	: 97	
SAU0400	ATGAGGGA	TCAAAAA	GAGTTC	AGTAT	GTA	CAAAAG	TCTT	GATATG	TCACG	CAATG	TTTAT	TAATAG	TTTAT	GATATG	TCACG	: 88	
SAA0411	ATCGGATA	TAAAAA	AGCTTGC	ATGTA	CAAAAG	TCTT	TATTTT	GAGCAT	TTTAT	TAATAG	TTTAT	GATATG	TCACG	CAATG	CTG	: 100	
SAR0442	ATGGGATA	TAAAAA	GGATTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TAGCAG	GTTC	GGTGGT	...GGTA	TG.....A	: 88	
SAB0393	ATGAATAA	TTTAGG	CAATG	CGCGT	GTG	TAA	AGGTC	CATCGG	TCTT	TAATCA	TTTAT	TAGT	TCACG	CAATG	CTG	: 88	
SAM0398	ATCGGATA	TAAAAA	GGATTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TAGCAG	GTTC	GGTGGT	...GGTA	TG.....A	: 88	
SAA0414	ATGAAGTC	TAAAAA	GGATTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TAGCAG	GTTC	GATGGT	...GATA	TG.....A	: 88	
SAC0481	ATGGGATA	TAAAAA	GGTTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TAGCAG	GTTC	GGCAA	...GGTA	TG.....A	: 88	
SAU0398	ATGGGATA	TAAAAA	GGTTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TAGCAG	GTTC	GGC	...AAAA	GATG.....A	: 89	
SAB0392	ATGGGATA	TAAAAA	AGGTTGC	ATG	TAA	AGCCG	TGTA	GATTT	TAATAG	TTTAT	TAGCAG	GTTC	GGT	...GGT	GATG.....A	: 89
SAU0399p	ATGAATAA	TTTAGG	CAATG	CGCGT	GTG	TAA	AGGTC	CATCGG	TCTT	TAATCA	TTTAT	TAGT	TCACG	CAATG	CTG	: 88	
SAU0404	ATCAAGTC	TAAAAA	GGATTC	GCATG	TA	CAAAAG	TCTT	TAATCA	TTTAT	TGCAAC	ATCT	CGT	...AGT	...AAT	...AAG	: 86	
SAR0444	ATGAAGTC	TAAAAA	GGATTC	GCATG	TA	CAAAAG	TCTT	TAATCA	TTTAT	TGCAAC	ATCT	CGT	...AGT	...AAT	...AAG	: 86	
SAO0404	ATGAAGTC	TAAAAA	GGATTC	GCATG	TA	CAAAAG	TCTT	TAATCA	TTTAT	TGCAAC	ATCT	CGT	...AGT	...AAT	...AAG	: 86	
SAC0485	ATGAAGTC	TAAAAA	GGATTC	GCATG	TA	CAAAAG	TCTT	TAATCA	TTTAT	TGCAAC	ATCT	CGT	...AGT	...AAT	...AAG	: 86	
SAA0418	ATGAAGTC	TAAAAA	GGATTC	GCATG	TA	CAAAAG	TCTT	TAATCA	TTTAT	TGCAAC	ATCT	CGT	...AGT	...AAT	...AAG	: 86	
SAA0416	ATGAAGTC	TAAAAA	GGATTC	GCATG	TA	CAAAAG	TCTT	TAATCA	TTTAT	TGCAAC	ATCT	CGT	...AGT	...AAT	...AAG	: 86	
SAC0483	ATGAAGTC	TAAAAA	GGATTC	GCATG	TA	CAAAAG	TCTT	TAATCA	TTTAT	TGCAAC	ATCT	CGT	...AGT	...AAT	...AAG	: 86	
SAB0395	ATGAAGTC	TAAAAA	GGATTC	GCATG	TA	CAAAAG	TCTT	TAATCA	TTTAT	TGCAAC	ATCT	CGT	...AGT	...AAT	...AAG	: 86	
SAM0400	ATGGGATA	TAAAAA	GAGTTC	TAC	TACAA	AAATG	TGTTG	TATG	AGTCT	TTTAT	TAATAG	TTTAT	GATATG	TCACG	CAATG	: 100	
SAA0415	ATGGAATA	TAAAAA	GGCTTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TGTTGG	GTTC	GATAGT	CAAGCG	AT	..ACTG	: 100	
SAC0482	ATGGAATA	TAAAAA	GGCTTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TGTTGG	GTTC	GATAGT	CAAGCG	AT	..ACTG	: 100	
SAB0394	ATGAGATA	TAAAAA	GAGTTC	TAC	TACAA	AAATG	TGTTG	TATG	AGTCT	TTTAT	TAATAG	TTTAT	GATATG	TCACG	CAATG	: 100	
SAU0401	ATCGGATA	TAAAAA	GGTTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TAGCAG	GTTC	GGTAA	...AAGT	GATAA	: 90	
SAA0412p	ATGTGGT	CAAAAA	GAAATTC	GCATG	TA	CAAAAG	TCTT	TAATAG	TTTAT	TAGCAG	GTTC	GATAGT	CAAGCG	AT	..GCAG	: 98	
SAR0445	ATGGGATA	TAAAAA	AAATTC	CTTGT	ATGTA	CAAAAG	TCTT	TAATCA	TTTAT	TGTTGG	GTTC	GGAATAT	GAAAC	AGAAAA	AGAGG	: 100	

Predicted signal peptide

Cys

5'-variable region

Central conserved region

SAR0438	AACAAAAGAA	GATTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 176
SAB0389	AATAAAAGAA	TATTC	CAAAAGAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 176	
SAU0397	AGCAAAGAA	GATTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 188
SAA0419	AACAAACGAATAAAACA	GATTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 200
SAC0486	AACAAACGAATAAAACA	GATTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 200
SAO0405	AACAAACGAATAAAACA	GATTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 200
SAM0397	AACAAAAGAA	GATTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 176
SAB0390p	AACAAAAGAA	GATTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 176
SAR0440p	AGCAAAGAA	GATTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 188
SAU0402	AAAAGA	AGTTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 188
SAM0399	AAAAGA	AGTTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 188
SAC0396p	AACAAACGAATAAAACA	GATTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 199
SAU0396	AAGAA	AGTTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 176
SAA0410	AAGAA	AGTTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 176
SAR0439	AAGAA	AGTTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 176
SAU0403	AAGAA	AGTTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 188
SAR0443	AAGAA	AGTTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 188
SAA0417	AACAAACAAATAAAACA	GATTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 200
SAC0484	AACAAACAAATAAAACA	GATTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 200
SAO0402	A.....	TTCAA	AGGAAGAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 176	
SAM0401	AACAAACGAATAAAACA	GATTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 200
SAU0405	CAAAATCAAAATAAAACA	GATTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 200
SAA0413	CAAA	AGAA	CACT	CGAAAGAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 188
SAU0400	AAGAA	GATTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 176
SAA0411	AAGAA	GATTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 188
SAR0442	CTGGA	GATTC	CAAAAGAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 176	
SAB0393	CTGAA	GATTC	CAAAAGAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 176	
SAM0398	CTGGA	GATTC	CAAAAGAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 176	
SAA0414	CTGGA	GATTC	CAAAAGAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 176	
SAC0481	AAGAA	GATTC	CAAAAGAA	GAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 176
SAU0398	A.....	AGTTC	CAAAAGAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 176	
SAB0392	T.....	GG.....	AGTTC	CAAAAGAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 176	
SAU0399p	T.....	GG.....	AGTTC	CAAAAGAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 175	
SAU0404	T.....	GG.....	AGTTC	CAAAAGAA	CAAAAT	TAAAAAG	AGCTTT	GCGAAA	CA	TAGATAT	GTA	TCAA	TAAGAA	CTC	GAG	CACT	TATAT	G	: 173	
SAR0444	T.....	GG.....	AGTTC	CAAAAGAA	CAAAAT	T														

3'-variable region

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SAR0438  GATGAAGATA..GCTAA.....:783
SAB0389  GATGAAGATA..GCTAA.....:783
SAU0397  GATGAAGATA..GCTAA.....:795
SAA0419  GAAGGTGAGAATGTTGAGTAG.....:813
SAC0486  GAAGGTGAGAATGTTGAGTAG.....:813
SAO0405  GAAGGTGAGAATGTTGAGTAG.....:813
SAM0397  GATGGAGTTA..GCTAA.....:783
SAB0390P GATGAAAATA..GCTAA.....:782
SAR0440P GATGGAGG.A..GCTAAAGTTTATTAG:803
SAU0402  CACAGT..AATTAG.....:792
SAM0399  CATAGT..AATTAG.....:792
SAB0396P AAAAGGTGGAATAATGACTAA.....:812
SAU0396  AAAAAA..TAG.....:774
SAA0410  AAAAAA..TAG.....:774
SAR0439  AAAAAA..TAG.....:774
SAU0403  AAAGTGGATGAAGATGATGAATGA...:801
SAR0443  AAAGTGAATGAAGATGATGAATGA...:801
SAA0417  AAAGTAGATGAAGATGATGAATGA...:813
SAC0484  AAAGTAGATGAAGATGATGAATGA...:813
SAO0402  AAAGTAGATGAAGATGATGAATGA...:789
SAM0401  AAAGTGGATGAAGATGAAAAGATAA...:813
SAU0405  AAAGTGGATGAAGATGAAAAGATAA...:813
SAA0413  AAAACTAATAAAGATGATGAATAA...:801
SAU0400  AAAAAA..TAAAGATGATGAATGA...:786
SAA0411  AAAAAAAATAAAGATGATGAATGA...:801
SAR0442  AAAAAA..TAG.....:771
SAB0393  AAAAAA..TAG.....:771
SAM0398  AAAAAA..TAG.....:771
SAA0414  AAAAAA..TAG.....:771
SAC0481  AAAAAA..TAG.....:771
SAU0398  GAGAACTATTAG.....:786
SAB0392  GAGGACTATTAA.....:786
SAU0399P GACTAA.....:779
SAU0404  GAGGATAAATAA.....:783
SAR0444  GAGGATAAATAATAATTACTAA.....:795
SAO0404  GAGGATAAATAA.....:786
SAC0485  GAGGATAAATAA.....:786
SAA0418  GAGGATAAATAA.....:786
SAA0416  GAGGATAAATAA.....:777
SAC0483  GAGGATAAATAA.....:777
SAB0395  GTGGATAAATAA.....:777
SAM0400  GAGGATAAATAA.....:798
SAA0415  AAGTAA.....:792
SAC0482  AAGTAA.....:792
SAB0394  AAGTAA.....:792
SAU0401  .AACAAAATGA.....:783
SAA0412P .AACAAAATAA.....:797
SAR0445  GAGGAGACTATAATGAGTAA.....:819

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(B)

5'-variable region

Central conserved region

3'-variable region

SAR0438	MGNI	SFA	YISILL	IVVVAG	CGKS	...	DKTKE	...	DSKEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	DE	: 90	
SAB0389	MGYL	RIG	YISIFI	IVMVAG	CGKD	...	NEIKE	...	YSKET	QIKNSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	GV	: 90	
SAU0397	MGYL	KLA	FISVIT	GIFIFI	CGDSS	...	DTAEKAE	...	DSKEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	GE	: 94	
SAO0405	MEYL	KIA	YMSVLL	IIFIGG	CGNMKD	...	EQQKEEQ	TNKT	DSKEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	GV	: 98	
SAC0486	MEYL	KIA	YMSVLL	IIFIGG	CGNMKD	...	EQQKEEQ	TNKT	DSKEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	GV	: 98	
SAA0419	MEYL	KIA	YMSVLL	IIFIGG	CGNMKD	...	EQQKEEQ	TNKT	DSKEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	GV	: 98	
SAM0397	MGYL	GFA	YISILL	IVFIAG	CGKS	...	DKTKE	...	DSKEA	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	GE	: 90	
SAU0402	MGYL	RLV	YIVIMV	SVFIIG	CDKSS	...	DTAENPKE	...	GSKEA	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGE	: 94	
SAM0399	MEYL	RLA	FISVIT	TIFIMG	CDSSD	...	TAENPKE	...	GSKEA	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	GE	: 94	
SAU0396	MRYL	RLSWY	ISILL	IVVIAG	CGKGN	...	ET	...	KEGS	KEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	GE	: 90
SAA0410	MGYL	RFA	YISVMI	IFAIAG	CGKGN	...	ET	...	KEGS	KEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	GE	: 90
SAR0439	MGYL	RFA	YISVMI	IFAIAG	CGKGN	...	ET	...	KEGS	KEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	GE	: 90
SAM0398	MGYL	RIG	CISLLI	VIFVTS	CGGNKI	...	ET	...	TG	SKET	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	GE	: 90
SAR0442	MGYL	RIG	CISLLI	VIFVTS	CGGNKI	...	ET	...	TG	SKET	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	GE	: 90
SAA0414	MKSI	RIG	CISLLI	SIFVTS	CDGDNKI	...	ET	...	TG	SKET	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	GE	: 90
SAB0393	MNFR	QCAL	CIGTSV	ILLVGS	CSGVFD	...	ET	...	PE	SKET	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	GE	: 90
SAC0481	MGYL	RFA	YISVMI	IFAIAG	CGKGN	...	ET	...	KE	DSKEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	GE	: 90
SAU0403	MGYF	RVV	YIIVMV	SVFIIG	CNKSS	...	DTSEKP	...	KE	SKET	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 94
SAR0443	MRYL	RVV	YIIVMV	SVFIIG	CNKSS	...	DTSEKP	...	KE	SKET	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 94
SAO0402	MGYL	RFA	YISVMI	IFAIAG	CGKGN	...	ET	...	KE	DSKEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 90
SAA0417	MGYI	RMA	YMSVFL	IIFIVG	CRNMK	...	DEQKKEEQ	TNKT	DSKEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 98	
SAC0484	MGYI	RMA	YMSVFL	IIFIVG	CRNMK	...	DEQKKEEQ	TNKT	DSKEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 98	
SAM0401	MEYL	KIA	YMSVLL	IIFIGG	CGNMK	...	DEQKKEEQ	TNKT	DSKEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 98	
SAU0405	MEYL	KIA	YMSVLL	IIFIGG	CGNMK	...	DEQKKEEQ	TNKT	DSKEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 98	
SAA0413	MGYL	RLV	YIVIMV	SVFIIG	CDKSS	...	DTAENKS	...	KE	SKET	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 94
SAU0400	MRS	RVV	YISIMV	SIFITG	CG	...	KNEL	...	KE	DAKEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 90
SAA0411	MRYL	KLAWF	SIVIT	GIFIFI	CGDSS	...	DTGKA	...	KE	SKET	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 94
SAU0398	MGYS	RFA	YISVMI	IFAIAG	CGK	...	SDTKE	...	GS	KEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 90
SAB0392	MGYL	KVGM	CISLLI	VIFVTS	CGG	...	GNKITG	...	DS	KET	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 90
SAA0415	MEYL	RLA	LISVIT	TIFIMG	CDSSD	...	TAENPKE	...	GS	KEA	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 94
SAC0482	MEYL	RLA	LISVIT	TIFIMG	CDSSD	...	TAENPKE	...	GS	KEA	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 94
SAB0394	MRYL	RVV	YRIVMV	SVFIIG	CDKSS	...	DTSEKPE	...	DS	KEA	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 94
SAO0404	MKSI	RIG	CISLLI	IIFVTS	CD	...	GNKIIG	...	DS	KEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 90
SAA0418	MKSI	RIG	CISLLI	IIFVTS	CD	...	GNKIIG	...	DS	KEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 90
SAC0485	MKSI	RIG	CISLLI	IIFVTS	CD	...	GNKIIG	...	DS	KEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 90
SAU0404	MKSI	RIG	CISLLI	IIFVTS	C	...	GNKITG	...	DS	KEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 89
SAR0444	MKSI	RIG	CISLLI	IIFVTS	CD	...	GNKITG	...	DS	KEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 90
SAA0416	MKCF	QK	YIFILL	IVLMAG	CE	...	SNKITG	...	DS	KET	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 87
SAC0483	MKCF	QK	YIFILL	IVLMAG	CE	...	SNKITG	...	DS	KET	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 87
SAB0395	MKCF	QK	YIFILL	IVLMAG	CE	...	SNKITG	...	DS	KET	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 87
SAM0400	MGYF	RVV	YIIVMV	SVFIIG	CDKSS	...	DTSEKSKG	...	DS	KEA	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 94
SAU0401	MGYS	RFA	YISILL	IVMVAG	CG	...	KDETKE	...	DS	KEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 90
SAR0445	MEYL	KIA	YMSVLL	IIFIGG	CGNM	...	KDEQKKEEQ	TNKT	DS	KEE	QIKKSF	AKTLD	MYPI	IKNLED	LYDKE	GYR	DGE	FFKK	GDKGT	WTL	LLTS	FSKSN	KP	QGG	: 98

Predicted signal peptide Cys

3'-variable region

SAR0438	IDDE	GMVL	YLN	RNTKKA	TGY	FVN	KIYDDIS	..	KNQNE	KKYR	VELK	NKIVL	DNVE	EKLKQK	IEN	FFFS	QYADF	FD	KNY	QD	GSITT	NENI	PS	YEA	: 188
SAB0389	IDDE	GMVL	YLN	RNTKKA	TGY	FVN	KIYDDIS	..	KNQNE	KKYR	VELK	NKIVL	DNVE	EKLKQK	IEN	FFFS	QYADF	FD	KNY	QD	GSITT	NENI	PS	YEA	: 188
SAU0397	IDDE	GMVL	YLN	RNTKKA	TGY	FVN	KIYDDIS	..	KNQNE	KKYR	VELK	NKIVL	DNVE	EKLKQK	IEN	FFFS	QYADF	FD	KNY	QD	GSITT	NENI	PS	YEA	: 192
SAO0405	LDDE	GMVL	YLN	RNTKKA	TGY	FVN	KVYDDIS	..	KNHNE	KKYR	VELK	NKIVL	DNVE	EKLKQK	IEN	FFFS	QYADF	FD	KNY	QD	GNITT	NENI	PS	YEA	: 196
SAC0486	LDDE	GMVL	YLN	RNTKKA	TGY	FVN	KVYDDIS	..	KNHNE	KKYR	VELK	NKIVL	DNVE	EKLKQK	IEN	FFFS	QYADF	FD	KNY	QD	GNITT	NENI	PS	YEA	: 196
SAA0419	LDDE	GMVL	YLN	RNTKKA	TGY	FVN	KIYDDIS	..	KNHNE	KKYR	VELK	NKIVL	DNVE	EKLKQK	IEN	FFFS	QYADF	FD	KNY	QD	GSITT	NENI	PS	YEA	: 196
SAM0397	IDDE	GMVL	FLN	RNIKKA	TGY	YTS	KVHDEFN	..	EKEHQ	KKYR	VELK	NKIVL	DNVE	EKLKQK	IEN	FFFS	QYADF	FD	KNY	QD	GNISS	ADN	PS	YEA	: 188
SAU0402	MNSE	GMVL	HFN	RNTR	TAKGH	FV	TTFYRNG	..	KLARE	KKYR	VELK	NKIVL	DNVE	EKLKQK	IEN	FFFS	QYADF	FD	KNY	QD	GNISS	ADN	PS	YEA	: 192
SAM0399	MDS	GMVL	NLDRN	RNTKKA	TGY	FVN	KIYDDIS	..	KNHNE	KKYR	VELK	NKIVL	DNVE	EKLKQK	IEN	FFFS	QYADF	FD	KNY	QD	GNISS	ADN	PS	YEA	: 192
SAU0396	LDDE	GMVL	NLDRN	RNTKKA	TAKGH	FV	TTFYRNG	..	KLARE	KKYR	VELK	NKIVL	DNVE	EKLKQK	IEN	FFFS	QYADF	FD	KNY	QD	GNISS	ADN	PS	YEA	: 187
SAA0410	LDDE	GMVL	NLDRN	RNTKKA	TAKGH	FV	TTFYRNG	..	KLARE	KKYR	VELK	NKIVL	DNVE	EKLKQK	IEN	FFFS	QYADF	FD	KNY	QD	GNISS	ADN	PS	YEA	: 187
SAR0439	LDDE	GMVL	NLDRN	RNTKKA	TAKGH	FV	TTFYRNG	..	KLARE	KKYR	VELK	NKIVL	DNVE</												

3'-variable region

SAR0438 YKLNNSDENVKKLRDIYPIITKKAAPILKLLHIDGDIKGSVGYKKEIYKFSKVKDQETTLRDYLN.FGSEDEDS...:260
 SAB0389 YKLNNSDTNVKCLRDIYPIITKKAAILKLLHIDGDIKGSVGYKKEIYKFSKVKDQETTLRDYLN.FGSEDEDS...:260
 SAU0397 YKLNNSDTNVKCLRDIYPIITKKAAPILKLLHIDGDIKGSVGYKKEIYKFSKVKDQETTLRDYLN.FGSEDEDS...:264
 SAO0405 YKMNNSDKNVKCLRREIYPIITNNSPILKLLYIDGDIKGSVGYKKEIYKFSKDKGQETTLRDYLN.FGSEGENVE...:270
 SAC0486 YKMNNSDKNVKCLRREIYPIITNNSPILKLLYIDGDIKGSVGYKKEIYKFSKDKGQETTLRDYLN.FGSEGENVE...:270
 SAA0419 YKMNNSDKNVKCLRREIYPIITNNSPILKLLYIDGDIKGSVGYKKEIYKFSKDKGQETTLRDYLN.FGSEGENVE...:270
 SAM0397 YQISNTDKNVKCLRREIYPIITKKSPIVILKLLHIDGDIKGSVGYKKEIYKFSKVKDEETAVRDFVN.FGSDGVS...:260
 SAU0402 YKRNNSDGNVKCLRREIYPIITKQSPILKLLHIDGDIKGSVGYKQIEYTFSSKEKDETFMSDFLN.FGSHSK...:263
 SAM0399 YKRNNSDGNVKCLRREIYPIITKQSPILKLLHIDGDIKGSVGYKQIEYTFSSKEKDETFMSDFLN.FGSHSN...:263
 SAU0396 YKMSNKDEIVKELRSRWNISFEKSPILKMHIDGDLKGSVGYRKLIEDFSKRENSKLSVIEFLS.YKAKK...:257
 SAA0410 YKMSNKDEIVKELRSRWNISFEKSPILKMHIDGDLKGSVGYRKLIEDFSKRENSKLSVIEFLS.YKAKK...:257
 SAR0439 FKMSNKDENVKQLRSRWNISFEKSPILKMHIDGDLKGSVGYRKLIEDFSKRENSKLSVIEFLS.YKAKK...:257
 SAM0398 YKMSNKDENVKQLRSRWNIPDKAPVILKMHIDGDLKGSVGYRKLIEDFSK.EDRDISVIDYLS.YKAKK...:256
 SAR0442 YKMSNKDENVKQLRSRWNIPDKAPVILKMHIDGDLKGSVGYRKLIEDFSK.EDRDISVIDYLS.YKAKK...:256
 SAA0414 YKMSNKDENVKQLRSRWNIPDKAPVILKMHIDGDLKGSVGYRKLIEDFSK.EGRDISVIDYLS.YKAKK...:256
 SAB0393 YKMSNKDENVKQLRSRWNIPDKAPVILKMHIDGDLKGSVGYRKLIEDFSK.EDRDISVIDYLS.YKAKK...:256
 SAC0481 YKMSNKDENVKQLRSRWNIPDKAPVILKMHIDGDLKGSVGYRKLIEDFSK.EGRDISVIDYLS.YKAKK...:256
 SAU0403 FKMSNKDENVKQLRSRWNIPDKAPVILKMHIDGDLKGSVGYRKLIEDFSKGEKSDLSVIDSLN.FQAKVDEDEDE:266
 SAR0443 FKMSNKDENVKQLRSRWNIPDKAPVILKMHIDGDLKGSVGYRKLIEDFSKGEKSDLSVIDSLN.FQAKVNEDDE:266
 SAO0402 FKMSNKDENVKQLRSRWNIPDKAPVILKMHIDGDLKGSVGYRKLIEDFSKGEKSDLSVIDSLN.FQAKVDEDEDE:262
 SAA0417 FKMSNKDENVKQLRSRWNIPDKAPVILKMHIDGDLKGSVGYRKLIEDFSKGEKSDLSVIDSLN.FQAKVDEDEDE:270
 SAC0484 FKMSNKDENVKQLRSRWNIPDKAPVILKMHIDGDLKGSVGYRKLIEDFSKGEKSDLSVIDSLN.FQAKVDEDEDE:270
 SAM0401 FKMSNKDENVKQLRSRWNIPDKAPVILKMHIDGDLKGSVGYRKLIEDFSKGEKSDLSVIDSLN.FQAKVDEDEDE:270
 SAU0405 YKMSNKDENVKQLRSRWNIPDKSPVILKMHIDGDLKGSVGYRKLIEDFSKRENSHLSVIDSLD.YQAKVDEDEDE:270
 SAA0413 YKMSNKDENVKQLRSRWNIPDKSPVILKMHIDGDLKGSVGYRKLIEDFSKRENSHLSVIDSLD.YQAKTNKDDDE:266
 SAU0400 FKMSNKDENVKQLRSRWNIPDKAPVILKMHIDGDLKGSVGYRKLIEDFSKEENSELSIVDSLN.FQAK.NKDDDE:261
 SAA0411 FKMSNKDENVKQLRSRWNIPDKAPVILKMHIDGDLKGSVGYRKLIEDFSKEENSELSIVDSLN.FQAKKNKDDDE:266
 SAU0398 YQLKNSDYNVQQLRKRWDISFEKAPKLLKKTGDLKGSVGYKKEIYKFTFVENQENIYFTDSIY.FNSEDK...:261
 SAB0392 FQLSNDYVQQLRKRWDISFEKAPKLLKKTGDLKGSVGYKKEIYKFTFVENQENIYFTDSIY.FTSEDEY...:261
 SAA0415 YQLHNSDYNVQQLRKRWDISFKETPKLLKGGGDLKNSVGYKKEIYKFTFVERKGENIYFNDSVE.FIISK...:263
 SAC0482 YQLHNSDYNVQQLRKRWDISFKETPKLLKGGGDLKNSVGYKKEIYKFTFVERKGENIYFNDSVE.FIISK...:263
 SAO0394 YQLHNSDYNVQQLRKRWDISFEKAPKLLKGGGDLKNSVGYKKEIYKFTFVERKGENIYFNDSVE.FIISK...:263
 SAO0404 YQLKNSDYNVQQLRKRWNIPQKAPKLLKGSGLKGSVGYKKEIYKFTFIENKKEENIYFTDSIY.FNSEDK...:261
 SAA0418 YQLKNSDYNVQQLRKRWNIPQKAPKLLKGSGLKGSVGYKKEIYKFTFIENKKEENIYFTDSIY.FNSEDK...:261
 SAC0485 YQLKNSDYNVQQLRKRWNIPQKAPKLLKGSGLKGSVGYKKEIYKFTFIENKKEENIYFTDSIY.FNSEDK...:261
 SAU0404 YQLKNSDYNVQQLRKRWNIPQKAPKLLKGSGLKGSVGYKKEIYKFTFIENKKEENIYFTDSVY.FNSEDK...:260
 SAR0444 YQLKNSDYNVQQLRKRWNIPQKAPKLLKGSGLKGSVGYKKEIYKFTFIENKKEENIYFTDSVY.FNSEDK...:264
 SAA0416 YQLKNSDYNVQQLRKRWNIPQKAPKLLKGSGLKGSVGYKKEIYKFTFIENKKEENIYFTDSIN.FNSEDK...:258
 SAC0483 YQLKNSDYNVQQLRKRWNIPQKAPKLLKGSGLKGSVGYKKEIYKFTFIENKKEENIYFTDSIN.FNSEDK...:258
 SAB0395 YQLKNSDYNVQQLRKRWNIPQKAPKLLKGSGLKGSVGYKKEIYKFTFIENKKEENIYFTDSIY.FNSEDK...:258
 SAM0400 YQLKNSDYNVQQLRKRWNIPQKAPKLLKGSGLKGSVGYKKEIYKFTFIENKKEENIYFTDSVY.FNSEDK...:265
 SAU0401 YKMKRNDNRNIQQLKRRFNLIKSKTPRLFLFKGSGDIKGSVGYKKEIYKFTFVSRKKEAFMLTALSSFQVTK...:260
 SAR0445 YKINDDDNINIKQLKRNRFNIKSNKNPRLFLFKGSGDIKGSVGYKKEIYKFTFVSRKKEESVSCIDISIE.FKSEGDYNE...:272