SUPPLEMENTARY DATA

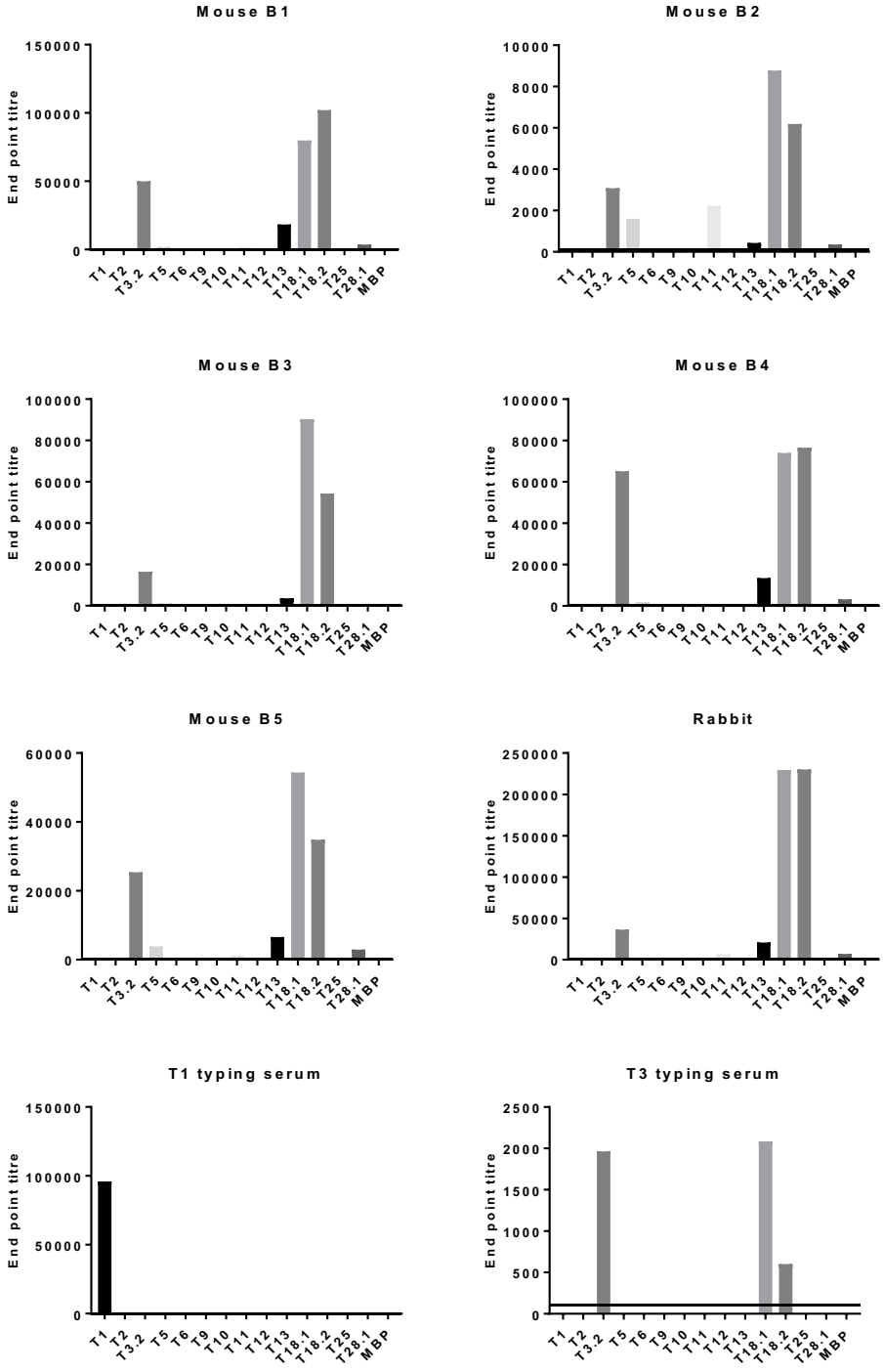

FIG S1: Endpoint titers of the anti-T-antigen sera to the T-antigen panel measured by ELISA. The endpoint titer was defined as the highest serum dilution above the control (absorbance of pre-immune rabbit serum +3 times the standard deviation).

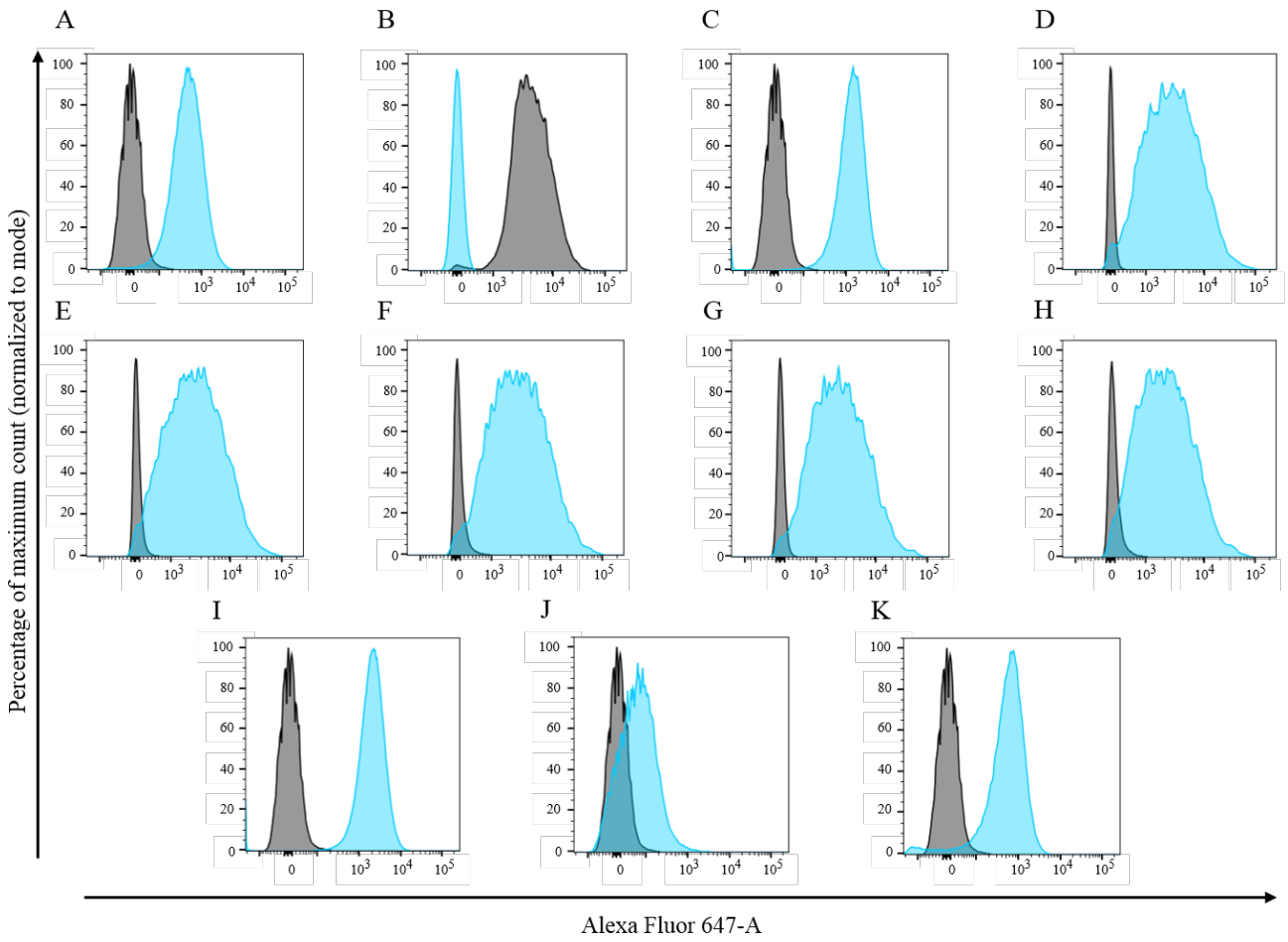

FIG S2: Binding of animal sera and affinity purified antibodies to the full T1 (black) and T18.1 (blue) pili expressed on the surface of *L. lactis* measured by flow cytometry. (A) T18.1 immunized rabbit (B) T1 typing serum (C) T3 typing serum (D) B1 mouse (E) B2 mouse (F) B3 mouse (G) B4 mouse (H) B5 mouse (I) T18.1 immunized rabbit serum passed over T18.1-coupled resin (J) T18.1 immunized rabbit serum passed over T3.2-coupled resin and (K) T18.1 immunized rabbit serum passed over T13-coupled resin.

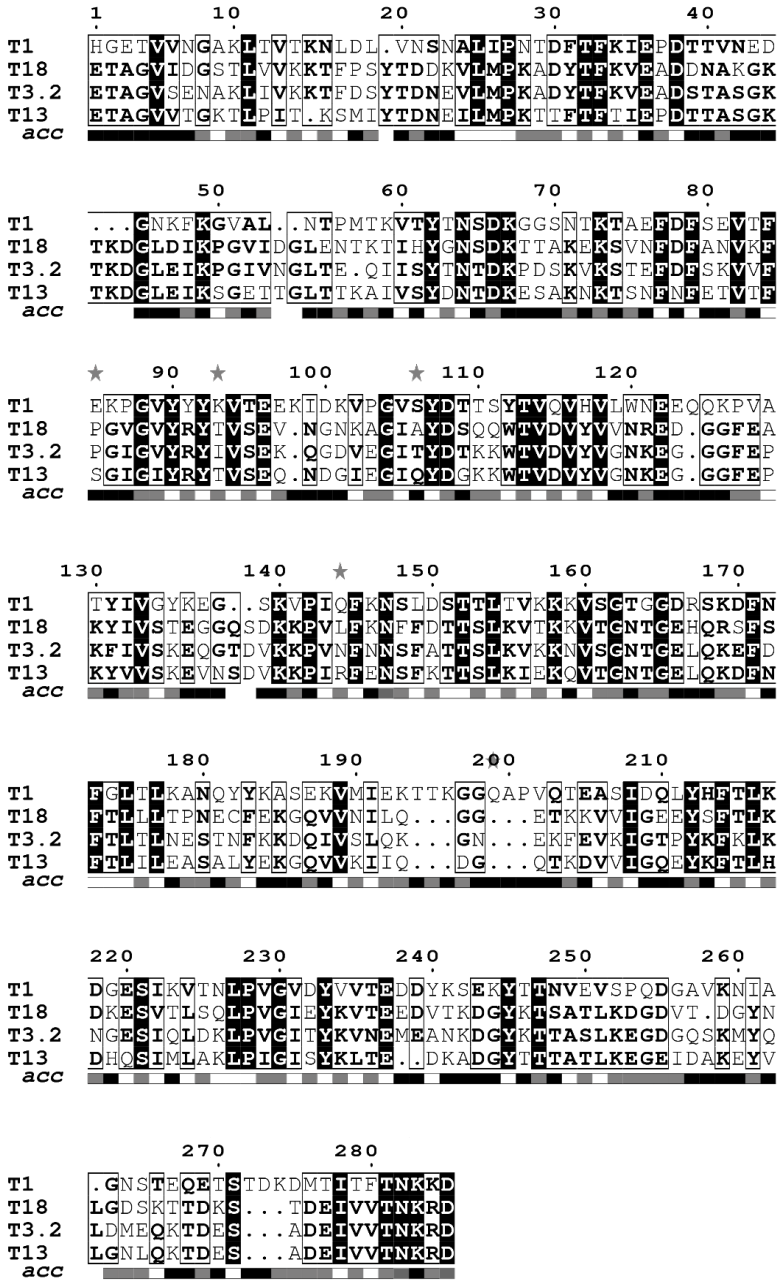

FIG. S3 Amino acid sequence alignment of T1, T3.2, T18.1 and T18.2. The sequences in the alignment represent the mature recombinant T-antigens used in this study. The residues are numbered according to the sequence of T1 and solvent accessibility (acc), predicted from the structure of T1, is shown as a bar below the sequences. Darker shading indicates more accessible residues.

TABLE S1. Construct details for the T-antigens used in this study.

Tee type	Strain No.	NCBI accession	*emm* type	Cloned sequence	Vector	PCR PRIMERS	Structure PDB accession
18.1	MGAS8232	NP_606439.1	*emm*18	ETAGVIDGSTLVVKKTFPSYTDDKVLMPKADYTFKVEADDNAKGKT KDGLDIKPGVIDGLENTKTIHYGNSDKTTAKEKSVNFDFANVKFPG VGVYRYTVSEVNGNKAGIAYDSQQWTVDVYVVNREDGGFEAKYIVS TEGGQSDKKPVLFKNFFDTTSLKVTKKVTGNTGEHQRSFSFTLLLT PNECFEKGQVVNILQGGETKKVVIGEEYSFTLKDKESVTLSQLPVG IEYKVTEEDVTKDGYKTSATLKDGDVTDGYNLGDSKTTDKSTDEIV VTNKRD	pProEX Hta and pProEX Hta-AviTag	TEE18FWD: GTATTTTCAGGGCGCC GAGACAGCAGGAGTGATTGATGGTTCA TEE18REV: GACTGCAGGCTCTAGA*TT*AGTCACGCT TATTTGTGACAACGATTTCGTC	6NOA This study
13	GAS131465	KJ816975	*emm*53	ETAGVVTGKTLPITKSMIYTDNEILMPKTTFTFTIEPDTTASGKTK DGLEIKSGETTGLTTKAIVSYDNTDKESAKNKTSNFNFETVTFSGI GIYRYTVSEQNDGIEGIQYDGKKWTVDVYVGNKEGGGFEPKYVVSK EVNSDVKKPIRFENSFKTTSLKIEKQVTGNTGELQKDFNFTLILEA SALYEKGQVVKIIQDGQTKDVVIGQEYKFTLHDHQSIMLAKLPIGI SYKLTEDKADGYTTTATLKEGEIDAKEYVLGNLQKTDESADEIVVT NKRD	MBP-pProEX Hta	M53_222FWD: AAAGGCGCCGAGACGGCAGGGGTTGTA AC M53_222REV: AAAGAATTCTTAGTCACGCTTATTTGT GACAACG	6BBT This study
3.2	GAS13637	KJ816984	*emm*65	ETAGVSENAKLIVKKTFDSYTDNEVLMPKADYTFKVEADSTASGKT KDGLEIKPGIVNGLTEQIISYTNTDKPDSKVKSTEFDFSKVVFPGI GVYRYIVSEKQGDVEGITYDTKKWTVDVYVGNKEGGGFEPKFIVSK EQGTDVKKPVNFNNSFATTSLKVKKNVSGNTGELQKEFDFTLTLNE STNFKKDQIVSLQKGNEKFEVKIGTPYKFKLKNGESIQLDKLPVGI TYKVNEMEANKDGYKTTASLKEGDGQSKMYQLDMEQKTDESADEIV VTNKRD	MBP-pProEX Hta	M65104FWD: AAAGGCGCCGAGACGGCAGGAGTGTCC G M65_104REV: AAAGAATTCTTAGTCACGCTTATTTGT GACAACG	6BBW This study
1	SF370	NP_268517.1	emm1	ATTVHGETVVNGAKLTVTKNLDLVNSNALIPNTDFTFKIEPDTTVN EDGNKFKGVALNTPMTKVTYTNSDKGGSNTKTAEFDFSEVTFEKPG VYYYKVTEEKIDKVPGVSYDTTSYTVQVHVLWNEEQQKPVATYIVG YKEGSKVPIQFKNSLDSTTLTVKKKVSGTGGDRSKDFNFGLTLKAN QYYKASEKVMIEKTTKGGQAPVQTEASIDQLYHFTLKDGESIKVTN LPVGVDYVVTEDDYKSEKYTTNVEVSPQDGAVKNIAGNSTEQETST DKDMTITFTNKKFE	pGEX-3c	TEE1FWD: CGGGATCCGCTACAACAGTTCACGG TEE1REV: CGGAATTCTTATTCAAAGACTTTTTTA TTTG	3B2M *Kang et al. 2007* (1)
2	MGAS10270	ABF33174.1	emm2	EDTRVPSQTQPDKTTVNIYKLQGADFSKQPEGIKNENGEPIDITKL KDTFGTAVTYLPGVKFKYYKVKNYSTSDDVLKSIKTVEQADSKTDL LDVAGAKETEATDQSGKVSIDLPSNDKVKYLFVESSNQDTVNKVVG YTAVPFILHLPVSNSNGKGYYDEVNVYPKNTTVNEPKVDKDVTKLG KDDDTYQIGDKITWFLKSTVPSNIKTLDKFGFTDTLNKGLSFIGDK TQTVTKVQFGTTVLSPDTDYTVEILDSKLTVSLTSAGIEKVSGLVA SKQLITEAEKLYKAEDNTDEAAFLSVEVNAKLNADAVMGSRIENDV ELDYGHESDIYKSKVPTNEVPEVHTGGARFEKVDATNQTDKLQDAE FGLYSNIEATETVKWTEELLKANEAAINAGKFKESNTTVGTPIIFK SASDGSFEIKGLRYGDDSTNTRSDGTVGTAEKTGKTTYYIKELVAP KGYVVSQDIVQFDVTYSSYYKDPTKVTLGTEAGDAAPTSVKNNKRP SIPNTGG	pProEX Htb	TEE2FWD: CGGGATCCGAGGACACCAGAGTGCCTT CTC TEE2REV: CGAAGCTTTTAACCACCAGTATTAGGG ATTGAAGG	-

5	GAS10514	KJ816997	emm82	ETAGVVTGKSLQVTKTMTYDDEEVLMPETAFTFTIEPDMTASGKEG DLDIKNGIVEGLDKQVTVKYKNTDKTSQKTKIAQFDFSKVKFPAIG VYRYMVSEKNDKKDGIRYDDKKWTVDVYVGNKANNEEGFEVLYIVS KEGTSSTKKPIEFTNSIKTTSLKIEKQITGNAGDRKKSFNFTLTLQ PSEYYKTGSVVKIEQDGSKKDVTIGTPYKFTLGHGKSVMLSKLPIG INYYLSEDEANKDGYTTTATLKEQGKEKSSDFTLSTQNQKTDESAD EIVVTNKRD	pProEX Hta	TEE5FWD: AAAGGATCCTGAGACGGCAGGAGTTGT AAC TEE5REV: AAAGAATTCTTAGTCACGCTTATTTGT GACAACGAT	Modelled
6	MGAS10394	ABF33174.1	emm2	KDDTAQLKITNIEGGPTVTLYKIGEGVYNTNGDSFINFKYAEGVSL TETGPTSQEITTIANGINTGKIKPFSTENVSISNGTATYNARGASV YIALLTGATDGRTYNPILLAASYNGEGNLVTKNIDSKSNYLYGQTS VAKSSLPSITKKVTGTIDDVNKKTTSLGSVLSYSLTFELPSYTKEA VNKTVYVSDNMSEGLTFNFNSLTVEWKGKMANITEDGSVMVENTKI GIAKEVNNGFNLSFIYDSLESISPNISYKAVVNNKAIVGEEGNPNK AEFFYSNNPTKGNTYDNLDKKPDKGNGITSKEDSKIVYTYQIAFRK VDSVSKTPLIGAIFGVYDTSNKLIDIVTTNKNGYAISTQVSSGKYK IKELKAPKGYSLNTETYEITANWVTATVKTSANSKSTTYTSDKNKA TDNSEQVGWLKNGIFYSIDSRPTGNDVKEAYIESTKALTDGTTFSK SNEGSGTVLLETDIPNTKL	pProEX Htb	TEE6FWD: CGGGATCCTTATCAAAAGATGATACTG CACAAC TEE6REV: CGAAGCTTTTATCCACCTGTCGAAGGT AATTCACC	4POD *Young et al., 2014* (2)
9	GAS11262	KJ816988	emm74	EGGVSTGSILNVKKTFSSYNDIEVLMPNATFTFKIQADTVKNGEKD KKSGLDIKTGIMGEGLVDQIVTYTNDSKPVDKEKNVNFDFSKVEFP NVGIYRYKVSEEKGNVAGVRYDDKTWTVDVYVVSENGNFIPKYIIS TTTENDKKPIVFDNEFTTTSLIVKKQVLGNSGDKTEGFDFTLLLKE NSLFEKGKQVSLIKITSDQKEEKVKVTIGEKYDFKLKDGEQVKLDK LPIGINYQVNEKDANTNGYTTTAAILEGNGTSQPYTLDSLKETDLS IDTITVTNKRD	pProEX Hta	TEE9FWD: AAAGGATCCAGAAGGTGGAGTGAGTAC TGG TEE9REV: AAAGAATTCTTAGTCACGCTTATTTGT GACTGTAAT	-
10	emm89_198	KJ817015.1	emm89	ETAGVVSSGQLTIKKSITNFNDDTLLMPKATFTFDVKPVDVTGEEK DTASGLKIQKGIAGVASQTIQYDNTDKPTNKEKAVNFDFSTVTFPN VGVYRYEVSEQAGDVKGITYDSKKWTVDVYVVNENNKFTPKYIVSK ETTDSSKKPIVFNNELKTTSLTIKKEVTGNSGDKTSDFTFTLLLKE NTQFETGQKVKATKKKSGAEEETVEVTIGKQYTFTLKDSEELILDK LPIGITYQVDETDKNKEQYETSAKMTEDSKEAQGYTLNDLKTTDET ADTITVTNKRN	pET101/D-TOPO	TEE10TOPOF2: CACCATGGAGACGGCAGGGGTTG TEE10TOPOR: GTTTCTCTTATTGGTAACAGTGAT	Modelled
11	GAS05151	KJ817016	emm89	EVNYVKSGVIDGAKLEIHKTIKNYDDDKVLMPNVIFKFNIKPDDSV VAGKKEEKSGLDIKPGIVDGLETSKEVSYTNSDKPNSKDKYTYFDF SQVKFTNVGIYRYVVEEVQDTVSGIHYDSQKWYIDVYVVEGDNGFV PKYIVSSKTLETKEPVLFSNSFDTTSLVVKKEVTGNTGDKTKNFKF QLLLKENAYFSAGQKVSVTITSEKASEVTTATIGQPLIFELKHNEQ LKLDKLPVGITYQIDETSKNSDSYTTTATIQEGEQSQNSYVLNSDK ETDKSPDIITVTNKRD	pProEX Hta	TEE11FWD: AAAGGCGCCGAAGTAAATTATGTAAAA TC TEE11REV: AAAGAATTCTTAGTCACGCTTATTTGT GACTG	Modelled
12	GAS12303	KJ816951	emm12	ETAGVVSSGQLTIKKSITNFNDDTLLMPKTDYTFSVNPDSAATGTE SNLPIKPGIAVNNQDIKVSYSNTDKTSGKEKQVVVDFMKVTFPSVG IYRYVVTENKGTAEGVTYDDTKWLVDVYVGNNEKGGLEPKYIVSKK GDSATKEPIQFNNSFETTSLKIEKEVTGNTGDHKKAFNFTLTLQPN EYYEASSVVKIEENGQTKDVKIGEAYKFTLNDSQSVILSKLPVGIN YKVEEAEANQGGYTTTATLKDGEKLSTYNLGQEHKTDKTADEIVVT NNRD	pProEX Hta	TEE12FWD: AAAGGATCCTGAGACGGCAGGGGTTGT TAG TEE12REV: AAAGAATTCTTAGTCACGGTTATTTGT GACAACGAT	Modelled

18.2	NZ131 Spy49_0114	ACI60465	emm49	ETAGVIDGSTLVVKKTFPSYTDDNVLMPKADYSFKVEADDNAKGKT KDGLDIKPGVIDGLENTKTIRYSNSDKITAKEKSVNFEFANVKFPG VGVYRYTVAEVNGNKAGITYDSQQWTVDVYVVNKEGGGFEVKYIVS TEVGQSEKKPVLFKNSFDTTSLKIEKQVTGNTGEHQRLFSFTLLLT PNECFEKGQVVNFLQGGETKKVVIGEEYSFTLKDKESVTLSQIPVG IEYKLTEEDVTKDGYKTSATLKDGEQSSTYELGKDHKTDKSADEIV VTNKRDTQVPT	pProEX Hta	M49FWD: AAAGGCGCCGAGACAGCAGGAGTGATT GATG M49REV: AAAGAATTCTTAAGTTGGAACTTGAGT GTCACGC	Modelled
25	LN144	EU725507	emm75	IPSSTVRAETLQDRTQKTIPEATEVVITKLQADDYNDDVKPNGKAN ENGLPINNLGELGRNVKPLSDVTFVAYKIPEGIAEEKVKELKTKQT VVDVENYLNAQNLKIEKTVLTKTDGNGQTTFTVQKSSYGKYFVVED MTATGTPETISKAYAVPFTLELPISASDGTGYLTKVNIYPKNVTSS LPKPGKDVKELGLNHSSYNIGERFSWFLKGTVPKNMLDYEKYSFTD TLDSQLDFISVKSVKYGSQILEKNNDYTFSEPTAQNRTLKVELTEA GIKKVAGLYPDRQEVLDTEIEAIKENTDQKPFLEVEFETNINSTVI LGKPVTNEVKIEFDNKPDKIAKPVTTPPSDNPEVHTGGKRFVKVAA GNDATKLGGAEFDLLTEANQPINWTAELIRANNKSEYIVGTPQEGQ PVKLKSDTDGSFEIKGLAYAIDAEATGAGVKYKLKETKAPAGYVIP EAPIEFAVNQTSYNKTPTTIDVDKADAEPQKVENNKRPE	pProEX Hta	TEE25FWD: AAAGGATCCAATACCAAGTAGTACGGT AAGGG TEE25REV: AAAGAATTCTTATTCAGGACGTTTGTT GTTTTCTAC	-
28.2	GAS11209	KJ817028	emm91	ETAGVTNGAQLTIKKTIANYNDSEVLMPKAIFTFEVKPDNSVTGVE KTVDGLTIKAGIAEGLVKTGNVEYSNTDKVENKDKTTTFDFSTVKF PEVGVYRYTVSETDSKVSGIKYDTKTWIVDVYVVNDGNGGFKAQYI VSKEKGQNDKKPVVFENSFKTTSLKVEKQVTGNTGELKKDFNFTLT INPNDNFVAGQVIKLEKGGIKADVKIGEPYKFALKNGEKVTLSKLP VGITYSIIEDDAGKDGYKTTAILKDGEQSSTYELGKNQKTDESADE IVVTNNRE	pProEX Hta	TEE28.1FWD: AAAGGATCCTGAGACGGCAGGGGTAAC TAA TEE28.1REV: AAAGAATTCTTATTCACGGTTATTTGT GACAACGAT	Modelled

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