Lactococcus garvieae ATCC 49156

Lactococcus garvieae UNIUD074

Lactococcus garvieae 21881

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Lactococcus lactis subsp. cremoris SK11

Lactococcus lactis subsp. cremoris NZ9000

Lactococcus lactis subsp. cremoris MG1363

Lactococcus lactis subsp. lactis KF147

Lactococcus lactis subsp. lactis CV56

Lactococcus lactis subsp. lactis IL1403

Streptococcus pneumoniae TIGR4

Streptococcus thermophilus CNRZ1066

Streptococcus pyogenes MGAS315

Streptococcus agalactiae 2603V/R

Enterococcus faecalis V583

Supplementary Figure 1. Miyauchi et al.
### Supplementary Table 1

Sequences of the four possible adhesins specific to *L. garvieae* 21881

| Contig         | Sequence                                                                 |
|---------------|--------------------------------------------------------------------------|
| >contig00042 complement(5326..8865) 1179aa (PF06458) | MESKNYKILKSVLVCGAAIMSMTTINALADETEPLQNFTQQMDSMDTEASNFLRSYGL            |
|               | R NGTVAGSKVSVRTSSGFTVQNPKENVESFTANWITDTSKIKLTVNSAFYVNTPIEFSF            |
|               | KIKQPLAKGEELIPLNITGTFNSSSSYTYEGNTQNNGTNYTSQDGFSYNYDNKTGN               |
|               | LKVKA LDDRGLTDLTSL LLNNWIPVPLRENPMPLKGGVAGNYGA KSGATVKVKGD             |
|               | KETSETLTNTADIFTTTTLQAYNDFIGKGAETYTTQKTASSSTNLF LNFPLINQLKKGKT          |
|               | K N L L D E S M H N Y E V K V N A K F K N E E D I F K G L S I E T I P I G S S S S S G A P I A I Q N A V T D Y K |  |
|               | PEFKSVIKNASYDKEKQIFSFDSLNSKND TWDQALGADLLLQNEAYGSSNGKEARRA AW IT D Y K |  |
|               | AMANGNVDQNTFTSSY YPVNSVSPVPVNNFSLK DVTVTNLSKAKTTNH NIVDPV K A G        |
|               | NGD TTKA AVQQL QM DSEGNGP I GELQTPSY YSGDAYTVPPVI KGYRLLNVNPQSLIDKL    |
|               | GITN VDQQQKF DS S N I G I N Y V V Y E Y V K EVPLTYS VIDD TGETLEEHQDLATGALNQ |  |
|               | ANI K E N Q D K L KAL Q E SY K GKYL GNI ENGLP VPT DEKGY NVT LH LS DA HK A V ID G K S |  |
|               | K T I T Q TVHYQAG N ET PEDNVQTL TLTFSK I QTID SVQAVLSEEAPV WSEO Q TTA K V T T |  |
|               | P QI K Dy EADQ A VVEGSTNF DNSKKTVDSTPYKSLAPLTYIV DDTDKTLEKEVFDMAG        |
|               | TVGE EVNT S D NQ E K LKL Q L K L I K SY TD GY LLGN SE N ADL P PK DNTGY IT TL HF T HAT EQ V |  |
|               | VDGET K KVQTQIHYQAG N ET PEDDVQVL TLTFSK I QTID NVTH RV LAE AKP FWPEQST |  |
|               | RAVDSPTL K DYA A D K E S V P S MN YN D SE D V VLEVNYSSTAPITYSVID DTAG T KLED K |  |
|               | DFVMSHVL EP IN TSENQ DKL KSI A K SY TD GYLVGNIEEELPVPGD TKGYDVVFHLTHG |  |
|               | TSEKVIDDESKVTQ KIQY K G A G ATPE IDIQKFVF STSLTQTIDDDVTDGVSVSTSGPTWS |  |
|               | DNQHS K AVK T PE I DGYSS D I D T V K S YDHEAK DKTIT SYVE PV PPVKEV KKVKNILP |  |
|               | QTGTEAE IGL AFTG A ALV L IA G Y V KSKL R K ES K N D D |  |
| >contig00042 complement(39668..43489) 1273aa (PF05738) | MKKQH KI R Q L T K L E K KL SHFSMRKSGKR WITRSAIVLALAGGTGLIAVINPSLSTVA |  |
|               | YALTLP PGNTQ I G S I NAPQVIQTSNNFSTMQ PLFSLTG I QPEYIVGD TDQDGTGGKPV |  |
|               | AWNSSTTYAGTA IS NSLV NGA NGLSY D T I HYMG ISDGFQDNDF N YVSKG QEI N K N |  |
|               | I GT AYN V KTG KNVPI GMA VK IN DAT Y Y D SST S S P RNVF GDG FR LL VGAR N NGGT IL GY |  |
|               | MVSMDG IPNS GSGQG N EGGGGGG SGGDA IG AASG I P E S VRGT IS LD MDTRQNL PASTIM |  |
|               | AMKVSD IDAGQSAQLSNGALGYIVSKPTNLELRD NI LTAK GNDTV VGD SANL N ANSY IAL |  |
|               | YNGS STA LN F V D T NQGQG SI IQA VFNG LG STS PH SQ S L G Y IE ID K TQY KGK DL PNNL |  |
DFQDISFDVLDSTGKKVDTLKLDSSGKSVKSKGLPPGKYTLHETSGKWSSTGQTVPDF
VEVKAGDTTTAKPKNTAVTGETIITIKSGVESGDAMWNENYTELGTTFKLTSKTDGKYTA
VIGKESNGEWKTTKVDLPGLTYTIEETKASPFGTNTFEKKEVTLASYKDQHTEIVFGETK
TNQEVKGENTLKSDNGETGTDQNGKGVLTAKAYFHDGDGSTGSSPHKGDVPVKWSEKPA
PKLAGEVVHSAIIGGNPVSYGDNVIEIDDESLSIALGLNLPAGKYKVREVDAGEGYVT
DTEHKFEIQKDDKTNIVTPESSESSKEQLIKAKITLDKMVTLPDSQGSYNGIEFTAEP
MEGTVDAPVKFVTGPNTGDYASQELAYDGKVSETKGVGEYVDPKPYIHMETDTE
KDILTISASYEDFSKPSKRTFSLKDSSTSNPNGETGVGEVTPEVPTISLSTIHFNDN
PTPEKVPISIDIEKANDKIPPEGNHDKDNDINGENDRDTPDTELEVESGKSTAIKFRFT
NNGETAHLKVSDDKTIEEGGISIKDPWFFNEKGLSTNKDGEVTGKLLQLQPDEFVT
GEGLPESDGLHDEGSVSGVWESTGKEVGDDEWKGKPEEVPISIDIEKADSKAPEA
GEGNHDKPPNANGENDHDTEartaKELENEKATEIFFFKTNNGETLHLKIVDTJIAKG
NVKNIKLTYKEKPLKVRKDLTDDDGKLLVLNPGETIEGTKYGLAAGDIVGDNVTVD
GVGHSVGWGGDDNDWYGKVTPKTEQPPNNFNTSLPKTMKAQITIALIAAVIVVIVA
GGLTFYYRKNMK

>contig00026 complement(51658..52068) 136aa (PF06458)
VTFTRQVSTDVTGEKTYGWSADQSFAAVTPSPVIKGYTPDQAEGQATVSVDGDSDLDF
VIYTKDAPTPVNPSPQTTPAKPVQAQQAAATNFVDQRLPQTGETDQHMTLSGLLLLAM
SSVGLFLGMKTRQRKE

>contig00049 complement(2350..3180) 276aa
MKKTALGLLILVTISVQASADSINGYQTLDATSNTAIGKNGLIWHNDGFTWADDSE
NGFIAPDKPEAPIAKPTKPESTAKPIVPHKVLPEQKIPTKLLTVTDDNPGEVNPQ
HIEQLTPNPNVGALDAPQHEIAPKPIQNIPEPAVVLTEKPKINKSSSTVRIIE
PKKLDNSVTHYIIPSDTEQUEIKAINTDHTVATLTPKTEQVAVLTLGTMKSSPTRYQAK
GTPATGDEDRTMTYVVGLMSVSIVGAAVLALALQRNS

* The LPxTG-type motifs are highlighted in blue.