



Supplemental Material to:

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30322946	<i>Veillonella atypica</i> ACS-134-V-Col7a	KQYFVGLDITGNSVGVAVT	-N-----	TSYELL	-KFHSHKMGMSRL	-FEGESAV	TRRGF-RSMRRLLERKKRLRLKLEELFADAMAQV	-DPTFFIRLHESKYHYEDKTHGHSS	-KHLIFLDFEDYDQ	-DYTFE	-YPTIYHLR-KDL	
34762592	<i>Fusobacterium nucleatum</i> subsp. <i>vincentii</i> ATCC 49256	FDYVLFQFDIGTNSVGVAVT	-D-----	LDNVVL	-FKFKMKGMSRL	-FDSAKTAA	ERRVQ-RNSRRLLERKKRWRLLLEEIFSEIMKI	-DSMFFRRLKESLWLDKSNKSE	-KFTLFNDNDYKYD	-	-DFYKQ	-YPTIFHLRDELI
37430777	<i>Fillifactor aloccis</i> ATCC 35996	TRKYLVGLDVGTSVGVAVT	-D-----	SQINLC	-KFKHSHKMGMSRL	-FESANTAK	DRRLQ-RGNRRLLERKKQRDLQLQEIFSPEIKCI	-DPTFFIRLHESSLWLDKSNKSE	-KFTLFDYEDYDQ	-	-BYTKQ	-YPTIYHLRDELI
320529778	<i>Soiobacterium moorii</i> F0204	QONYVLGDDITGNSVGVAVT	-D-----	TDNVVL	-KFKHSHKMGMSRL	-FDESATAE	ERTTH-RGNRRLLERKKRWRLLLEQLFSEIKCI	-DPMFFIRLHESLNWDEKSKPS	-KFTLFDYEDYDQ	-	-DYTKKQ	-YPTIYHLRDELI
192520075	<i>Cocciococcus coccus</i> GD-7	KQYFVLGLDVGTSVGVAVT	-D-----	STYQVM	-KHGHKALGMSRL	-FESASTAE	ERRMF-RTARRLLDRNRWRVQLQEIFSEIKKI	-DQFFIRLHESKESKYPEDKRDACGNCEPL	-PYALFDNDNDYDQ	-	-NYHKQ	-YPTIYHLRDELI
42525843	<i>Treponea denticola</i> ATCC 35405	IKDYFLGLDVGTSVGVAVT	-D-----	TDYKLL	-KANRRLDGMSRL	-FETAETAE	VRLLH-RGARRRERKKRKLKLLQFSEIATQ	-DQFFIRLHESKESKYPEDKRDACGNCEPL	-ENTLFNDKDFPAK	-	-TYHKA	-YPTIYHLRDELI
304438954	<i>Peptinophilus duerdenii</i> ATCC BAA-1640	LKEYVILGLDVGTSVGVAVT	-D-----	ESYNIP	-KFKGKMGMSRL	-FDDAKTAE	ERTTQ-RGSRRLLERKKRINLQLDFATEISKV	-DPMFFIRLHESLNWDEKSKPS	-KFTLFDYEDYDQ	-	-DYHKKQ	-YPTIYHLRDELI
224544332	<i>Catenibacterium misotukai</i> DSM 15897	IVDYSIGLDDITGNSVGVAVT	-D-----	MNHLIM	-KHGHLGMSRL	-FSNAETAA	NRRAS-RSIRRYNRKRRERILLRAQLQDVLKKE	-DPTFFIRLEHSTFLDEEDKAKYLGTDYKYNLFDIFDFNDY	-	-	-TYHKQ	-YPTIYHLRDELI
34279809	<i>Streptococcus mitis</i> UA159	MGRVLGLDVGTSVGVAVT	-D-----	TDYVKDPARKMKVLQNTK	-SRHKLHLGMSRL	-FDSGNVTAE	DRLLK-RTARRRYRTRRRNLRLVQLQEIFSEIMKI	-DPMFFIRLHESSLWLDKSNKSE	-RHPIDFGNEEYD	-	-KYHEM	-YPTIYHLRDELI
310786728	<i>Streptococcus pyogenes</i> 5870	KYSLVGLDVGTSVGVAVT	-D-----	TDYKVA	-SRHKLHLGMSRL	-FDSGNVTAE	DRLLK-RTARRRYRTRRRNLRLVQLQEIFSEIMKI	-DPMFFIRLHESSLWLDKSNKSE	-RHPIDFGNEEYD	-	-KYHEM	-YPTIYHLRDELI
16018105	<i>Listeria innocua</i> Clijf11262	KQYFVLGLDVGTSVGVAVT	-D-----	TDYKVA	-KFKHSHKMGMSRL	-FDSGNVTAE	DRLLK-RTARRRYRTRRRNLRLVQLQEIFSEIMKI	-DPMFFIRLHESSLWLDKSNKSE	-RHPIDFGNEEYD	-	-KYHEM	-YPTIYHLRDELI
116628213	<i>Streptococcus thermophilus</i> LMD-9	TKPYSIGLDDITGNSVGVAVT	-D-----	TDNYVSKMVKLGNTSK	-KHKIKNKLGVLL	-FDSGITAE	GRLLK-RTARRRYRTRRRNLRLVQLQEIFSEIMKI	-DPMFFIRLHESSLWLDKSNKSE	-RHPIDFGNEEYD	-	-KYHEM	-YPTIYHLRDELI
323463801	<i>Staphylococcus pseudintermedius</i> E99	RKPYLGLDVGTSVGVAVT	-D-----	DKGFNVLL	-KYHKKDLGVLL	-FDGALTAQ	EREQF-RTSRRRNRKRIRKLLGLLQELLPALVQ	-NPNFY-OFQCFRLLKSNNDMDVF	-KNKLSLENDVSLF	-	-GYESKQ	-YPTIYHLRDELI
252684361	<i>Acidimicrococcus intestini</i> RY-CR-M95	GKMYVILGLDVGTSVGVAVT	-D-----	SVYHLL	-KFKGKMGMSRL	-FVAGNQA	ERSRF-RTSRRRNRKRIRKLLGLLQELLPALVQ	-NPNFY-OFQCFRLLKSNNDMDVF	-KNKLSLENDVSLF	-	-EYVSD	-YPTIYHLRDELI
320326020	<i>Olsenella uli</i> DSM 7084	TDEYVILGLDVGTSVGVAVT	-D-----	DKAGAIL	-KFKGKMGMSRL	-FDAQGTAA	GARIH-RSQRRYVRVRRVLDLQLSLQDVEVSKV	-DFFCFRLLKSNNDMDVF	-DYTWPIFNDSPFNEV	-	-DYTKKQ	-YPTIYHLRDELI
366983953	<i>Oenococcus oeni</i> DSM 17330	ARDYVGLDVGTSVGVAVT	-D-----	DMKVTAE	-RHSHKLHLGMSRL	-FDSVTAE	KRRTY-RTTRRRSLRHHVRLRLNDLDFAGPLTD	PGDFNEFLARLKYSVWHPDQSNQAHF	-GFFLVDFNEEYD	-	-KYHEM	-YPTIYHLRDELI
258190199	<i>Bifidobacterium bifidum</i> S17	VYRVLGLDVGTSVGVAVT	-D-----	DNVRLV	-RAKHLGLGMSRL	-FDDACTAE	SRMAH-RTTRRRSLRHHVRLRLNDLDFAGPLTD	PGDFNEFLARLKYSVWHPDQSNQAHF	-GFFLVDFNEEYD	-	-KYHEM	-YPTIYHLRDELI
259509199	<i>Lactobacillus rhamnosus</i> GJ	NQPYVGLDVGTSVGVAVT	-D-----	ANGSHL	-RLKGTATIGARR	-FRDQSA	DRRIS-RTTRRRSLRHHVRLRLNDLDFAGPLTD	PGDFNEFLARLKYSVWHPDQSNQAHF	-GFFLVDFNEEYD	-	-KYHEM	-YPTIYHLRDELI
300361537	<i>Lactobacillus gasseri</i> JV-003	KMEYVGLDVGTSVGVAVT	-D-----	FQNTLL	-MHGKATIGASHL	-FDAGNSAA	DRRAF-RTTRRRSLRHHVRLRLNDLDFAGPLTD	PGDFNEFLARLKYSVWHPDQSNQAHF	-GFFLVDFNEEYD	-	-KYHEM	-YPTIYHLRDELI
169823755	<i>Finegoldia magna</i> ATCC 29328	EKKYVILGLDVGTSVGVAVT	-D-----	EFYNL	-RAKGLDVGMSRL	-FEKADTAA	NTRIF-RSGRRNRKRIRKLLGLLQELLPALVQ	-NPNFY-OFQCFRLLKSNNDMDVF	-KNKLSLENDVSLF	-	-GYESKQ	-YPTIYHLRDELI
47958868	<i>Mycoplasma mobile</i> 163K	NKVVILGLDVGTSVGVAVT	-D-----	ISQKED	-NKFPILHGVLL	-FVTDGSD-DK	LNINTRFKK-QGRRNRRLTRKRDPIKYLIDN	-NIL-ELFEDPKPKLVLRNLEKY	-NPNFY-OFQCFRLLKSNNDMDVF	-	-EYVSD	-YPTIYHLRDELI
284931710	<i>Mycoplasma gallisepticum</i> str. F	KPEVTLGLDVGTSVGVAVT	-D-----	ETNI	-LHLLGMSRL	-FSQAQTA	DRRSF-RSIRRYNRKRRERILLRAQLQDVLKKE	-DPTFFIRLEHSTFLDEEDKAKYLGTDYKYNLFDIFDFNDY	-	-	-EYVSD	-YPTIYHLRDELI
363542550	<i>Mycoplasma ovipneumoniae</i> SC01	KNNITVGLDVGTSVGVAVT	-D-----	DS	-TTMGLDGTFRF	-FERETAN	ERRAF-RTTRRRSLRHHVRLRLNDLDFAGPLTD	PGDFNEFLARLKYSVWHPDQSNQAHF	-GFFLVDFNEEYD	-	-KYHEM	-YPTIYHLRDELI
394393286	<i>Bifidobacterium bifidum</i> S17	VYRVLGLDVGTSVGVAVT	-D-----	DNVRLV	-RAKHLGLGMSRL	-FDDACTAE	SRMAH-RTTRRRSLRHHVRLRLNDLDFAGPLTD	PGDFNEFLARLKYSVWHPDQSNQAHF	-GFFLVDFNEEYD	-	-KYHEM	-YPTIYHLRDELI
71894592	<i>Mycoplasma synoviae</i> 53	KEKIVLGLDVGTSVGVAVT	-D-----	NA	-ETKEVIDLGRV	-FSEPKAD	YBARK-RTTRRRSLRHHVRLRLNDLDFAGPLTD	PGDFNEFLARLKYSVWHPDQSNQAHF	-GFFLVDFNEEYD	-	-KYHEM	-YPTIYHLRDELI
28924075	<i>Eubacterium rectale</i> ATCC 33656	FMKYLLGLDVGTSVGVAVT	-D-----	DK	-ESTVEIAGSNI	-FPEASAAD-NQ	LRDM-RGAKNNRRKLRTRINDPIKLWENN	-	-K-STEVILKLVRAI	-	-EYVSD	-YPTIYHLRDELI
116627542	<i>Streptococcus thermophilus</i> LMD-9	MSDLVGLDVGTSVGVAVT	-D-----	NK	-VIGEIHKNSRI	-FPAQAEN-NL	VRTIN-QGRRLLARLKRHRVRLNRLKFEES	-	-GLIT	-	-DFTKSI	-NPNYQYLVKGL
315149830	<i>Enterococcus faecalis</i> TK0012	MYSIIGLDDITGNSVGVAVT	-D-----	RTGN	-VDLGRV	-FSAKNSK-NL	ERTIN-RGRRLLRKRTRNLKDKAKILA	-	-GLIT	-	-NPNYQYLVKGL	-NPNYQYLVKGL
315659848	<i>Staphylococcus lugdunensis</i> M23590	NQKFLGLDVGTSVGVAVT	-D-----	ETNI	-LHLLGMSRL	-FPEANVEN-NK	GRRSK-RSIRRYNRKRRERILLRAQLQDVLKKE	-DPTFFIRLEHSTFLDEEDKAKYLGTDYKYNLFDIFDFNDY	-	-	-SOPQ	-STNYPYLVKGL
160915782	<i>Eubacterium dolichum</i> DSM 3991	MGRVLGLDVGTSVGVAVT	-D-----	TDYVKDPARKMKVLQNTK	-SRHKLHLGMSRL	-FDSGNVTAE	DRLLK-RTARRRYRTRRRNLRLVQLQEIFSEIMKI	-DPMFFIRLHESSLWLDKSNKSE	-RHPIDFGNEEYD	-	-KYHEM	-YPTIYHLRDELI
339393381	<i>Lactobacillus coryniformis</i> subsp. <i>torquens</i> KCTC 3535	MGRVLGLDVGTSVGVAVT	-D-----	TDYVKDPARKMKVLQNTK	-SRHKLHLGMSRL	-FDSGNVTAE	DRLLK-RTARRRYRTRRRNLRLVQLQEIFSEIMKI	-DPMFFIRLHESSLWLDKSNKSE	-RHPIDFGNEEYD	-	-KYHEM	-YPTIYHLRDELI
10780384	<i>Lycobacterium minutus</i> DSM 2926	MYSIIGLDDITGNSVGVAVT	-D-----	NK	-VIGEIHKNSRI	-FPAQAEN-NL	VRTIN-QGRRLLARLKRHRVRLNRLKFEES	-	-GLIT	-	-NPNYQYLVKGL	-NPNYQYLVKGL
325677756	<i>Ruminococcus albus</i> 8	MYSIIGLDDITGNSVGVAVT	-D-----	RTGN	-VDLGRV	-FSAKNSK-NL	ERTIN-RGRRLLRKRTRNLKDKAKILA	-	-GLIT	-	-NPNYQYLVKGL	-NPNYQYLVKGL
187736489	<i>Akkermansia muciniphila</i> ATCC BAA-835	SRLTSFSSFDIGSISGVAI	-A-----	ASASHDD	-ADPSVCGGCTV	-FPKDDCAA	PKREY-RLLRNIRSRVRIERIGRLLVQA	-	-GLIT	-	-KETSQ	-HPAFFYLAELAL
117929158	<i>Acidothermus cellulolyticus</i> 11B	PVTRVGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
189440764	<i>Bifidobacterium longum</i> DJ010A	GKRYVIGLDDITGNSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
283451339	<i>Bifidobacterium dentium</i> Bd1	VYRVLGLDVGTSVGVAVT	-D-----	DNVRLV	-RAKHLGLGMSRL	-FDDACTAE	SRMAH-RTTRRRSLRHHVRLRLNDLDFAGPLTD	PGDFNEFLARLKYSVWHPDQSNQAHF	-GFFLVDFNEEYD	-	-KYHEM	-YPTIYHLRDELI
32632678	<i>Corynebacterium hirtchiae</i> NCTC 13129	DKPYVILGLDVGTSVGVAVT	-D-----	NDDGNV	-LPEIKIMVGRV	-FKASAGAA	DRKLS-RGQRNNHRVTRRMVRLKVAQG-KL	-	-ALPVPADLRKKN	-	-SSEGE	-TSAKRFLDGVV-LQNDYLVKGL
187520660	<i>Eluimicrobium minutum</i> Tel191	MKKVILGVDLIGTISGVAVT	-D-----	QGK	-VTRCLDMSVVM	-RNNPILYDEK-SG	SSQSIITRNL-KMRRLLERKKRRCVCAVPTG	-	-MLSY	-	-KPNND	-KNRWOLRAVDA
319957206	<i>Nitratifractor salinus</i> DSM 16511	SRPYSIGLDDITGNSVGVAVT	-A-----	ADPSVCGGCTV	-FPKDDCAA	-PKREY-RLLRNIRSRVRIERIGRLLVQA	-	-GLIT	-	-	-EDAVV	-RANPYELARKGL
325972003	<i>Sphaerochaeta globus</i> str. <i>Buddy</i>	MKKVILGVDLIGTISGVAVT	-D-----	QGK	-VTRCLDMSVVM	-RNNPILYDEK-SG	SSQSIITRNL-KMRRLLERKKRRCVCAVPTG	-	-MLSY	-	-KPNND	-KNRWOLRAVDA
261414553	<i>Fibrobacter succinogenes</i> subsp. <i>succinogenes</i> S85	MKRLLGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
60683389	<i>Bacteroides fragilis</i> NCTC 9343	MKRLLGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
256819408	<i>Capnocytophaga ochracea</i> DSM 7271	MKRLLGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
90425961	<i>Rhodospseudomonas palustris</i> B1S18	MKQVFLGDDITGNSVGVAVT	-D-----	ETNI	-LHLLGMSRL	-FPEANVEN-NK	GRRSK-RSIRRYNRKRRERILLRAQLQDVLKKE	-DPTFFIRLEHSTFLDEEDKAKYLGTDYKYNLFDIFDFNDY	-	-	-EYVSD	-YPTIYHLRDELI
373501184	<i>Prevotella nana</i> F0438	MKQVFLGDDITGNSVGVAVT	-D-----	ETNI	-LHLLGMSRL	-FPEANVEN-NK	GRRSK-RSIRRYNRKRRERILLRAQLQDVLKKE	-DPTFFIRLEHSTFLDEEDKAKYLGTDYKYNLFDIFDFNDY	-	-	-EYVSD	-YPTIYHLRDELI
294674019	<i>Prevotella ruminicola</i> 23	MKRLLGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
365959402	<i>Flavobacterium columnare</i> ATCC 49512	MKRLLGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
12879015	<i>Aminomonas paucivorans</i> DSM 12260	MKRLLGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
83591793	<i>Rhodospirillum rubrum</i> ATCC 11170	IEPVLGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
294086111	<i>Candidatus Puniceispirillum marinum</i> TMCC1322	MKRLLGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
121609211	<i>Verminephrobacter venetae</i> EFO1-2	AVYVFLGDDITGNSVGVAVT	-D-----	RIMEAR	-EPATILGMSRL	-FDRGMA	NS-EPAVLGRVVA-RAMRRDRRDLRKRKMHQVLQVH	-	-	-	-E-RLNYPQLRAGL	-E-RLNYPQLRAGL
344171927	<i>Ralstonia sisygyii</i> R24	MRLLGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
159042956	<i>Nitrososphaera shibae</i> DFU 12	VQYVFLSFLDITGNSVGVAVT	-D-----	NLDKQ	-KPRETRALGMSRL	-FSDGRDQ-DK	ASLAVARLRA-RQMRRRDRYVTRTRMGLMGLVAVT	-	-	-	-EVA	-VDYPYLRERAKT
288957741	<i>Azoaspirillum</i> sp- B510	SVLYRGLDVGTSVGVAVT	-HLE-----	KRGRDH	-EPVALGPGGVRI	-FPDGRDQ-SG	TSNAVARRA-RGAKRRDRYVTRTRMGLMGLVAVT	-	-	-	-EVA	-VDYPYLRERAKT
92109262	<i>Nitrobacter hamburgensis</i> X14	LRAYRGLDVGTSVGVAVT	-WLD-----	DHG	-QPEGLPGGVRI	-FPDGRDQ-SK	QSNAAAGRLA-RSARRDRYVTRTRMGLMGLVAVT	-	-	-	-EVA	-VDYPYLRERAKT
148255343	<i>Bradyrhizobium</i> sp. <i>BTAi1</i>	MKRLLGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
34557790	<i>Wolinella succinogenes</i> DSM 1740	MKRLLGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
220930482	<i>Clostridium cellulolyticum</i> H10	MKRLLGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
154250555	<i>Parvibaculum lavamentivorans</i> DS-1	MKRLLGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
257413184	<i>Roseburia intestinalis</i> LI-82	KMYVILGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
218767588	<i>Neisseria meningitidis</i> 22941	MNYDILGDDITGNSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
222109285	<i>Acidovorax eboursii</i> TSPY	MAQVFLGDDITGNSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
189485225	uncultured <i>Termite</i> group 1 bacterium phylotype Rad17	MKRLLGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
186264245	<i>Clostridium perfringens</i> D str. <i>JGS1721</i>	DINYVGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
220930482	<i>Clostridium cellulolyticum</i> H10	MKRLLGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
154250555	<i>Parvibaculum lavamentivorans</i> DS-1	MKRLLGLDVGTSVGVAVT	-D-----	EVSDEN	-SPVRLNLAQSVI	-HDGQVDE-RS	GASRLALRGMARRARLRFRARRLDLMLGSEL	-	-GWTPV-PQNTVSP	-	-VDVWLARKKLA	-VDVWLARKKLA
257413184	<i>Roseburia intestinalis</i> LI-82	KMYVILGLDVGTSVGVAVT										

303229466	<i>Veillonella atypica</i> ACS-134-V-Col7a	:- --MENGDDI----	RKLFVAVHHLLKYGKRNFLYEGA	-----	TFNSNAF--TFEDVLQALVNI TFNCFDTNSAISISINILMESGKTKSKAKAIERLVDVYTFVDEV
34762592	<i>Fusobacterium nucleatum</i> subsp. <i>vincentii</i> ATCC 49256	:- --KNPEKDI----	RLYLALHSIFPKRGHFL	-----	-----PEGQNLKEIKNFTLYNNLISFLIEDNGINKSIDKNDILEKELICDSGKGLKDKKFKGIFPN
374307738	<i>Fillofacter alocis</i> ATCC 35996	:- --EETKQDI----	RLYLALHSIIKTRGHFL	-----	-----LDGLQSAKQLRFLDITPFLSLQEQKNSVYLSLSEKQKDYFELKRNISIAKSERKVKLNLPFE
320529778	<i>Solobacterium moorii</i> G0204	:- --RNSFHHI----	RLVFLAHLHLKYRGHFI	-----	-----YINSANGOVYTSDEAVSDPEYLYNENDFEPINLENKKEFVNLKDLHLTKKEKIKSLKIKYDI
291520705	<i>Coprococcus catus</i> GD-7	:- --ETTEPDI----	RLVYLVLHMHMRGHFL	-----	-----LQSD--ISOIKFKFTFQLIQNIQDEELEWHLSLDDAAQFVEVHLKDRNLTRSTKSKLTKQ
42525843	<i>Treponema denticola</i> ATCC 35405	:- --ENKVKPPD----	RLLYLACHNI IKKRGHFL	-----	-----FGFDENSENQTFTIQALFEYLREDEWEDDANSQVKILKDSLSKNSKQSKRNKILGLKPK
304438954	<i>Pectoniphilus duerdenii</i> ATCC BAA-1640	:- --EDEGKDI----	RLLYLACHYLLKNGRHFIPEGQ	-----	-----KFDTKNSFDKSIDNLIKHLRDEYNIDLEFNNEIDLITTTTLMTKNKKELKNIVGDTKFLKAIIS
224543312	<i>Catenibacterium Mitsouaki</i> DSM 15897	:- --ESTEKADD----	RLLYLALHLIKYRGNFLEYEQ	-----	-----KFNMDASNIEEDKLSIDIFQPTSFNNIPEDEDEKNLELILEILKPLSKAKVDEVMTLIAPEKDYK
24379809	<i>Streptococcus kitaharae</i> DSM 17330	:- --DNPKEVDL----	RLVYLALAHIIKPRGHFLIE	-----	-----GRKDFTRNDVRFQFQFPLAVYDNTFENSS-----LQEQN-----VOVBEIITD-KIKSKAK
15765041	<i>Streptococcus pyogenes</i> 5370	:- --DSTKCADL----	RLVFLALAHIIKRGNFLEI	-----	-----GDLNFGNSGDKLFLTQLVCTNQNLFGP-----TRNSG-----VDKALVLA--RLSKRFR
16011805	<i>Gallibacterium anatum</i> DSM 11262	:- --NSSEKADL----	RLVFLALAHIIKRGNFLEI	-----	-----GALDTQNTVTSDEAVSDPEYLYNENDFEPINLENKKEFVNLKDLHLTKKEKIKSLKIKYDI
116628213	<i>Streptococcus thermophilus</i> LMD-9	:- --DSTKCADL----	RLVFLALAHIIKRGNFLEI	-----	-----GFNSKNNDIQKNFQDFLDYNAIFESDL-----SLENS-----KQEBEIKVD-KISKLEK
323463801	<i>Staphylococcus pseudintermedius</i> ED99	:- --LKEKDFPD----	ELLYMALYHLVYKRGHFLFD	-----	-----HLKIENLTNNDMHDVFEVLIETYENNNIKL-----NLDYEKT-KVIIEYIKDNTMTNDR
252648361	<i>Acidaminococcus intestini</i> RY-CR-M95	:- --ESSEKDDP----	RLVFLAVLHVLRHGHFLNEI	-----	-----VDKDNIGDVLSEFDAPYFPELAFLESDNG-----VSPWVCSKALQATLLS-RNSVNDK
302326020	<i>Olsonella uli</i> DSM 7084	:- --ETDEKADI----	RLVYLATHNIKVRHGNFLRE	-----	-----NNSKLSRSDANFAQAVKSLRLALNDCSEDEYCAWKGEDGDAIDEALINVLADGEKGRSDQ
369839953	<i>Oenococcus oeni</i> DSM 17330	:- --NDQPKHDL----	REVLATHHLVYKRGHFLIE	-----	-----GQVKAADFVHTFTADAIQRYVBSNNSDE-----NLLKGIDKLEKSAALTDKHSKSOR
312067728	<i>Bifidobacterium bifidum</i> S17	:- --EDDSQDDI----	REVLATHHMKYKRGNFLEI	-----	-----LSSNAFKEDLEKLLKRLTRVEMSESGQNSIDEGQDENKLVAPANQALALAKTRGSSSRVTR
259509199	<i>Lactobacillus rhamnosus</i> GG	:- --THTKADPD----	REIFLAHTHLIKSRGHFTPGA	-----	-----AKDNFTKVDLEIDIFFALTRVAQYVPDLEITFDLAKADDFKALLDQATPSTDTQKALVNLLSSE
300361537	<i>Lactobacillus thermophilus</i> JV-V03	:- --SEDKFDLD----	REYFLAHHIIVKYRGNFLYNTP	-----	-----VKDFEASKIDVKSLEKNELYELRDSFTVDESNLSALBIEKIRIDRCKVFKINKVKSIIHLLSLK
169823755	<i>Finexgoldia magna</i> ATCC 29328	:- --EETHGVDDI----	RYYFLAINQMKRHRGHFLIDQG	-----	-----ISHVTDKPKLEQLLINDLKLLEBELMESDIFEVLADVNEKRTDKNNKELIKQDFNKQEG
47458868	<i>Mycoplasma mobile</i> 163K	:- --NEKYKLDK----	SELVLYLFLYSLRGAFF	-----	-----DNPE-----
284931710	<i>Mycoplasma gallisepticum</i> str. F	:- --NAKIDP----	KALSWILHDVLYKNGHFYE	-----	-----
363542550	<i>Mycoplasma ovipneumoniae</i> SC01	:- --DSKIEK----	LDLWILHDLVLENGGFVVD	-----	-----
394303286	<i>Mycoplasma agalactiae</i> PG 14	:- --GGRLVQEP----	DELATWLHDLVLYKNGHFVDT	-----	-----
71894592	<i>Mycoplasma synoviae</i> 53	:- --KEEIKP----	SELVWILRDLVLYKNGGFVY	-----	-----KN-----
238924075	<i>Eubacterium rectale</i> ATCC 33656	:- --TEBITL----	DELVLYLVLKSRGHFI	-----	-----LEDALDDT-----
116627542	<i>Streptococcus thermophilus</i> LMD-9	:- --TDBLSN----	EELFIALKNMVKHGRGISY	-----	-----LDDAS-----
315149830	<i>Enterococcus faecalis</i> TX0012	:- --TEPLSR----	GEIYKVTLHLLKRGISY	-----	-----LDEV-----
315659848	<i>Staphylococcus lugdunensis</i> M23590	:- --SEALSK----	DELVIALHLIAKRRGIHK	-----	-----LDVIDS-----
160915782	<i>Eubacterium dolichum</i> DSM 3991	:- --NERLNG----	EELATLHLCKHGRGISY	-----	-----ETIIDEAK-----
336393381	<i>Lactobacillus coryniformis</i> subsp. <i>torquens</i> KCTC 3535	:- --DRRLTL----	SELVFLVYHFKHGRGFSD	-----	-----NRRKALMP-----
310780384	<i>Lytobacter polytocos</i> DSM 2926	:- --EAKISN----	KETAIQLLHLIAKRRGFKS	-----	-----FKRTDR-----
325677756	<i>Ruminococcus albus</i> 8	:- --SEKILP----	EETIACLIHCNRRGYK	-----	-----FYEYVVEDIED-----
187736489	<i>Akkermansia muciniphila</i> ATCC BAA-835	:- --KGHRTLAP----	IELHVLRWYAHNRGYDN	-----	-----NASWSNSL-----
117929158	<i>Acidothermus cellulolyticus</i> 11B	:- --EYVVDELTERR-----	RLLYGAVSHMARHRGNPWT	-----	-----IKDLKNLPOP-----
189440764	<i>Bifidobacterium longum</i> DJO10A	:- --TRYIETTELR-----	ESISIALRHMARHRGNRN	-----	-----PYQVDSLSIDNYP-----
283456135	<i>Bifidobacterium dentium</i> Bd1	:- --SSYIQDETTR-----	EVSAIARHIAHRGNRPYMS	-----	-----VESLFDVAP-----
38232678	<i>Corynebacterium urethrae</i> NCTC 13129	:- --NVTADKDEKRG-----	EKLSVALRHAHRRGNPFK	-----	-----VSSLYIPOP-----
187250660	<i>Elusimicrobium minutum</i> Bel191	:- --DERLSL-----	QLGQVLYHIAHGRGSSA	-----	-----LTFTEENSE-----
319957206	<i>Nitratifactor saluginis</i> DSM 16511	:- --KRPLSP-----	QELFALPAHMAKHRRGYK	-----	-----DLIYELLELGLNDRPEK-----
325972003	<i>Sphaerochaeta globus</i> str. Buddy	:- --NEQLTL-----	SELGYALYHIAHRRGSSS	-----	-----VTFIIDEK-----
261414553	<i>Fibrobacter succinogenes</i> subsp. <i>succinogenes</i> S85	:- --EKALSK-----	EELSWILLQFMKRRGYQ	-----	-----LRGEEEEEQTKKIEYLAQKVVEATD-----
60683389	<i>Bacteroides fragilis</i> NCTC 9343	:- --TEIISL-----	EFARVLLMINKRRGYKS	-----	-----SRKAGVEEGLIDGMDIARLYNNLTPGELCQLQLDAGKFLPDFYRSDL
256819408	<i>Capnocytophaga ochracea</i> DSM 7271	:- --TERIEK-----	EFARILLAINKRRGYKS	-----	-----SRKAKTEDEQAIDGMAIAKRLYDNLTPGQLSLQLLQKQKLLPDFYRSDL
90425961	<i>Rhodospseudomonas palustris</i> BisB18	:- --QRLLSN-----	EELAVLGHIAHRRGFS	-----	-----NARNAGANA-----
373501184	<i>Prevotella micans</i> F0438	:- --VQDFDPDQEPYKLGALYHIAHRRGPKS			-----SKGETIADQEK-----
294674019	<i>Prevotella ruminicola</i> 23	:- --TQKLLDSITQRFILGRALYHLNRRGFLS			-----NRRKATKES-----
365959402	<i>Flavobacterium columnare</i> ATCC 49512	:- --KQKVTL-----	FELGRALYHIAHRRGFLS	-----	-----NRID--QSAEVPFEEHNPQIQLNLEDDSSNLTNLEKEYIINLGIID-----
312879015	<i>Aminomonas paucivorans</i> DSM 12260	:- --DRPLSF-----	PEWVRLYHITKRRGFQS	-----	-----NRRNPVEDGQERS-----
83591793	<i>Rhodospirillum rubrum</i> ATCC 11170	:- --SRPLAP-----	DALWAALLHLAHRGFPS	-----	-----NRIDKREARAALKAKAPAKATAKATAPAKE-----
294086111	<i>Candidatus Puncicepirillum marinum</i> IMCC1322	:- --DEAIDP-----	YEMGRATFHIAHRGFKS	-----	-----NRRKSA-----
121608211	<i>Verminephrobacter eisenlaei</i> EF01-2	:- --HEALTP-----	GFARLFLHNRGPFKS	-----	-----NRKTDRK-----
344171927	<i>Ralstonia syzgii</i> R24	:- --DQALTL-----	PEFGRALFHLNRRGFQS	-----	-----NRKT-DRAT-----
159042956	<i>Dinoroseobacter shibae</i> DFL 12	:- --DEPLDL-----	PHLGRALFHLNRRGFQS	-----	-----NRKTRDG-----
288957741	<i>Azospirillum</i> sp- B510	:- --RERLPE-----	FEI GRALFHLNRRGFYK	-----	-----VRTATKP-----
92109262	<i>Nitrobacter hamburgensis</i> X14	:- --TDTLPA-----	HHVGRALFHLNRRGFQS	-----	-----NRKT-DSK-----
148255343	<i>Bradyrhizobium</i> sp- BTA11	:- --DEVLPD-----	HHVGRALFHLNRRGLFA	-----	-----NRAI-EQG-----
34557790	<i>Wolinella succinogenes</i> DSM 1740	:- --YRLKGG-----	DELARVLHIAHRRGYK	-----	-----IGDDEA-----
219561321	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> NCTC 11168	:- --NELLSK-----	QDFARVLHIAHRRGYD	-----	-----TKKS-D-----
791276265	<i>Helicobacter mustelae</i> 12198	:- --YRVLDK-----	EELARVLHIAHRRGYD	-----	-----ITYGVE-----
229113166	<i>Bacillus cereus</i> Rock1-15	:- --ERKLDN-----	REFARVLIHLVQRGFOT	-----	-----IRKSVE-----
222109285	<i>Acidovorax ebreus</i> TPSY	:- --DRLLTP-----	LEWAVLIHQCKRRGFHW	-----	-----TSKAEBAKADS-----
189485225	uncultured Termite group 1 bacterium phylotype RaD17	:- --DRKLTN-----	EQFVVVTLHLAKRRGYKS	-----	-----LRK-----
182624245	<i>Clostridium perfringens</i> D str. JGS1721	:- --DYKLSR-----	EWAKILINFCRRGFKS	-----	-----NRKNEAK-----
220930482	<i>Clostridium cellulolyticum</i> H10	:- --SRLKFP-----	EYLVQVLHTIKRRGFKS	-----	-----NRKE-DLS-----
154250555	<i>Parvibaculum lavamentivorans</i> DS-1	:- --EELSAA-----	YFGALYHLAQRHGFK	-----	-----RELESOTPD-----
257413184	<i>Roseburia intestinalis</i> LI-82	:- --DRKLPD-----	EELAQVLLHIAHRRGFS	-----	-----TRK-----AETRAK-----
218767588	<i>Neisseria meningitidis</i> Z2491	:- --DRKLPD-----	LEWSAVLHLLIKRRGYLS	-----	-----QRKNE-GETADK-----
15602992	<i>Pasteurella multocida</i> subsp. <i>multocida</i> str. Pm70	:- --EERLSA-----	IEWGAVLHLLIKRRGYLS	-----	-----KRKNE-SQTNK-----
319944583	<i>Sutterella wadswothensis</i> 3 1 45B	:- --KRGREALSGLLKRRGYSRPNADGEDLTPLENVNRADVFAAHPAFSTYFS-----EVRSLAEQWEEFTANIS-----NVEKFL-----GDPNIPA-----DKEF-----IEFAVAGLID-----			
254447899	<i>gamma proteobacterium</i> HTCC5015	:- --EPLKFPINGLLNRGYTYI-----SEEVDESMNVSPLPFSEMPDDYFN-----SSAPLLEQLAKLLSDKN-----KLVRFV-----AEGKIPS-----NKNEF-----KIL-LDTALDGKY-----			
54296138	<i>Legionella pneumophila</i> str. Paris	:- --ARETALCHYLNRRGYTYVTPD-LDEYIKDETLINLL--KELLP-----ESEHNIDW-----FLQAKM-----			
331001027	<i>Parasutterella excrementiformis</i> YIT 11859	:- --ENLRALSLSYLKRRGYARTAE-TDTSVLESLEDPVSSAPGFTAFNF--DSEPLNTOEARANSPE-----TKALM-----KELSOQ-----EADF-----KYL-ITKTSFPFYS-----			
34557932	<i>Wolinella succinogenes</i> DSM 1740	:- --LVDPEITRGLPNKRGYTAGF-LDEKSKDALESIDL--KEFLSEKIQSIDRSDYEDPILQIAS-----NAESFK-----DYKGF-----EAVFASHTSPNKLELDELKSEY-----			
118497352	<i>Francisella novicida</i> U112	:- --KDTPQASIFLNRRGSFSI-----TDGYSPEYLVNPEQVKAILMDIFDDYNGEDDLSYLKILATEQESKISEIYNKLMQKILEFKMLKCLTDIKDKVSTKTLKEITSVFELLADYLANYSELKTKQFSYTKQNLKELSYHDKYNIQDFEFKXKHAITINDRI-LDTLLDDDLIWN			
Motifs		:- --E-----R-----R_Nase_H_II-----			

#positions selected for tree reconstruction (272)

303229466 *Veillonella atypica* ACS-134-V-Col7a : ----DVSMED-----IIUD---ITIGFSGK---MLRQTLRNFQSQ---LN---DFTIK-K-LSKL---RYRD---WGRLSKLLGDGDDCK-----AGNGAPKTI-----

34762592 *Fusobacterium nucleatum* subsp. *vincentii* ATCC 49256 : ----YKIESK-----SILW---KCLYGDGDK---IFPKIKNYGDI---LN---KDEIK-K-INSF---KFPT---WGRLSKLLGTGIEFFNL---FTGECYSYVM-----

37430977 *Fillofactor* *alocis* ATCC 35896 : ----IQMLED-----TIKW---ITYVGNDRK---MLKRVIKAMYSQ---LP---EQMQK-I-TGF---QJSG---WGNFSKMPKLGISGDY---STGETFDLIT-----

320529778 *Soibacterium moorii* F024 : ----FTREIE---TIKJ---ILYVDPKDS---MLRWLKNNGY---LS---ENDVK-Y-LAKL---NYKE---WGRLSKTLTDITTYTNP---EDGRCASILDN-----

291520705 *Coprococcus catus* GD-7 : ----SQRAKEA-----VILN---VVLFGDDK---LLKQRLSKMYPN---LT---TQOLGK-ICSL---SYQG---WGRLSKTPLEEITVVPAP---GTGEVNIIMT-----

42525843 *Treponema denticola* ATCC 35405 : ----TKMLLEE---IIRWAT---IYDGEKGT---ILKTKIKAEGYKY---CS---DEQIKI-IINL---KFSG---WGRLSKRFLETVTSEMP---GFSEPV-----

304438954 *Peptoniophilus duerdenii* ATCC BAA-1640 : ----YKRIIEE---IKRL---IYLVYEDTK---VLKXKIKSAYNDK---FT---DDIKKI-IAAL---NYKD---WGRLSKRFELTGIEGVDK---TTGEGKSIIY-----

224543312 *Catenibacterium mitsuoaki* DSM 15897 : ----NFDLIEN---IIYV---LT-VEFDKK---IMKRRLKKYVA---LP---DDKVK-Q-ILKL---KYKD---WSRLSKLLDGIIVADNR---FGSSVTVLD-----

36798909 *Streptococcus mutans* DSM 1459 : ----NKILED---LIYV---LT-LFEDRE---MKRRLNRYSD---LL---TRQVVK-LERR---HYTG---WGRLSAEIILGRNKES---RKTILDYLDL-----

374309778 *Streptococcus pyogenes* S170 : ----NFDLED---NFDL---LT-LFEDRE---MIEELVQVLE---LP---MKVMNQ-LKRR---RYFD---WGRLSKINCRKGR---KTLTKLITKTRN-----

16901805 *Listeria innocua* Clpi11263 : ----NTRMLEN---NTRMEL---LT-LFEDRE---MIEELVQVLE---VF---DGVVK-Y-LQDQ---WGRLSAKLLMGRDKQS---HLTDLYLMDN-----

116628213 *Streptococcus thermophilus* LMD-9 : ----NEALIEE---IIHT---LT-LFEDRE---MIKQRLSKFEN---FL---DKSVLKK-LSRR---HYTG---WGRLSAKLINGRDKES---GNTILDYLDL-----

323463801 *Staphylococcus pseudintermedius* ED99 : ----KRAQEE---IIQW---IT-IFEDDK---ILVQLKKECEYP---EL---TSKQIQ-LKKL---NYSG---WGRLSKELLTHAYQ---GHSIIEHLH-----

352684361 *Acidaminococcus intestini* RY-CR-995 : ----TRDDVER---IVER---MT-YVSDTK---RVRLMANNYG---TL---TADVVKH-ISRLL---RKHD---FGRLSKMPFTLKGVKHKETGE---RASILDPMWN-----

302336020 *Olsenella* *ulii* DSM 7084 : ----DYTIMQ---IILW---ST-LFEDRD---ILKRIIEAYGGD---RL---TSEQIV-ICKK---RFTG---WGRLSKRLTDIKVNTDTG---RKSIIMDLREG-----

366983953 *Oenococcus oeni* DSM 17330 : ----NELLLEE---ITEL---QT-VEFDKK---VLRQLDQDLD---L---SDHNREK-LSRK---HYTG---WGRLSKLLTKLVONADKIDNQFTDVPFMQSIIDTLN-----

313068728 *Bifidobacterium bifidum* S17 : ----HRDLEK---IYEL---QT-VEFDKE---TLHRLQRLG---LS---BAQK-L-LVNT---HYTG---WGRLSKTLTKAGCECT---SDDFAPR---KHSIEI-----

259509199 *Lactobacillus rhamnosus* GG : ----KILDIEN---IYIM---ST-VEFDHT---IFETLKLAEW---LD---PWKINE-LSGI---RYRG---WQPSKRLLDGLKLGNG---HTVIG-----

300361537 *Lactobacillus gasseri* JV-V03 : ----YDKFER---IIEW---ST-IFEDEA---IYKDKLTKIW---LV---DROIDK-LSKI---RMOQ---WQLSKLLSQITDNNNG---QTI-----

169823755 *Finegoldia magna* ATCC 29328 : ----DVMVED---LIEK---ITIHTGNK---ILKKYIIEEYFD---LS---SSQIQ-IINL---KYKD---WGRLSKLLDGLKGTKK---ETE---KTDVIL-----

47458868 *Mycoplasma mobile* 163K : ----VLHIDA---I-SMI---LN-KFS---TIDDRIRILEGVEFFNSLK---TDQRIIRILEGVEFFNSLK---KDYKSSYEIAKLREFFSG---TSSLSFGAYYKIPNLI---SEGS---KNYSTI-----

284931710 *Mycoplasma gallisepticum* str. F : ----HLIYSNR---VDSANL---KE-FSDSNK---LPERILOQKQDGLKPLFQ---LYDKDK-ILAQ---TKDDEK-ILAQ---THSLSKAMLAITRMT---NL---DNEDDN-----

363542550 *Mycoplasma ovipneumoniae* SC01 : ----E-KSRGQ---DEVLYK---LT-KNPIFE---VLKIDREQLDFVKISIFSN---TKNFKK---IGNFSKALRFBFLPM---F---EONK-----

393932386 *Mycoplasma* *sp.* 14 : ----QKLSMNK---QSEL---QT-FKREEL---NENKLEKELFKLGNG---FKNINSE---THLSKAKAIRNIPCLR---L---DNEI-----

71894592 *Mycoplasma synoviae* 53 : ----NTEILYF---LDYVLAISYSSDKERNE---WFKLLKELYPKIKNNNLEIINVEDIPE---ITDQKFEFSPK---THLSREAFNHILPPLL---SMBEK-----

238924075 *Eubacterium rectale* ATCC 33656 : ----IGVI---MT-INTDKE---AMMAFQKSWID---LV---DDVQCLINMRKTNGALFNK---WQPSKIKINNMLPEMY---AQPKE---QMTLTL-----

116627542 *Streptococcus thermophilus* LMD-9 : ----RETLDK---LAVV---LT-LNTERE---GIQEALEH---FA---DGSFQKQVDELQVFRKANSIFGKWNHNSVKLMMELLPELY---ETSSE---QMTLTL-----

315149830 *Enterococcus faecalis* TK0012 : ----PTETDC---LAKV---LT-LNTERE---GIENLAFE---LP---ELSESVK-LLVLDRYKELSQISQTSWHRFSKTLHLLPELM---NAT---SEQLNT-----

315659848 *Staphylococcus lugdunensis* M23590 : ----NEVDLQ---TABI---LT-IYQKD---SISKLTLEDL---LL---NEEDKEN-IAQL---TGTY---THRLSKCIRLVLBEQW---YSSRN-----

160915782 *Eubacterium dolichum* DSM 3991 : ----DHFVDE---TABI---LT-KTKDIE---GRKKQISE---LS---SDLNSES-VHQLAGLTKFTA---YHSLSKALRIBNEEML---KTELN---QMSIT-----

393932386 *Lactobacillus* *corniformis* subsp. *torquens* KCTC 3535 : ----SRLGLR---TGTL---LT-PYSDRK---RRERFAPEM---LP---ABIE-K-LPLD---NFSK---FRLSLSKSMNIPFLE---MGQ---VYSAT-----

310780384 *Lysibacter polytrogus* DSM 2926 : ----DKSKLD---IIEI---LP-FYKSRK---ITRKNLAKLE---LD---REDFIL-LESE---FSGS---YAPLSKAKIRLIPLYE---KGL---SYNEK-----

325677756 *Ruminococcus albus* 8 : ----DNNVLR---IGIV---LS-OAQTPK---RREKALANIG---LD---DGLIN-E-LTKL---KLSG---TANVYSVQGSIEAFC---EGD---LVGQYQ-----

187736489 *Akkermansia muciniphila* ATCC BAA-835 : ----AANRLR---GKSVTPNYLLNL---LKSRSGESE---ALEKIEKESK---KE---ADYADTP-LPKK---YATG---RAPYARTVLKVVVEIL---DGE---DTPFA-----

117929158 *Acidothems cellulolyticus* 11B : ----LADNSI---LVAA---LADNSIAGE---EQUELVH---LD---DAEA-L-LEGL---ALPSG---RVAYSRLTSLGTRVMR---DDGV---DVHNR-----

189440764 *Bifidobacterium longum* DJ010A : ----SNEHSA---MIRL---LS-NTVID---KVEDVAYASAIIEIDGL---DAA---ITKLDSDVLPSSG---RAAYSVTLQKLTQML---TTDD---DLHEAR-----

256819408 *Bifidobacterium dentium* Bd1 : ----MYELLN---TYVID---VRREBDES---SAVAIDSL---L---GBEELTA-LDSV---DLSG---RAAYSQTLRQLTQRLM---NTDD---DLHEAR-----

393932386 *Corynebacterium* *theriacis* NCTC 13129 : ----TPEILR---TABI---LS-PREDIT---SIRNGLDGLDLDL---VV---BALMO---AAAGDFKPTR---AHSLSAKAIRNIPCLR---EGL---VISEK-----

187250660 *Elusimicrobium minutum* Bel191 : ----SEAQDS---PLYD---MM-SCPDEK---LITKLNENYH---LT---EERIDNA-FNEI---VLSGS---YAPLSKAKIRLIPLYE---NDL---SVTEAN-----

319957206 *Nitratifractor saluginis* DSM 16511 : ----ALQIFRE---LARI---LQ-SRKTPO---EALDRRLAMAKGG---ID---TDRE---LLEL-FMKNRS---TRELSHRMLLEALELFL---EGY---DEKVOQ-----

325972003 *Sphaerochaeta globus* str. *Buddy* : ----SEEQDD---FFSA---WT-NTPDK---LRSKYLKMLHL---LT---ENEVDA-LKTV---SLIGD---YGPIGKTATOLKMHLE---DGL---TYTEL-----

261414553 *Fibrobacter succinogenes* subsp. *succinogenes* S85 : ----SPELEMA---LWHI---LV-FYEDDK---ELETALHPAQKQ---WN---EKFAK-V-FSKA---KPKKD---YGSYSEKAIKLLSLMR---MGK---YNNQDN-----

60683389 *Bacteroides fragilis* NCTC 9343 : ----SNEELDN---OPYYKLWHL---LY-SFEGDNTPTGNRLQKMTLEYGF---EKELYAT-LANV---SPQDD---YGSLSAKAIHLLPHLK---EGN---RYDVAC-----

256819408 *Capnocytophaga* *chracea* DSM 7271 : ----QDYSQV---LWV---LV-SFEGDNTPTGNRLQKMTLEYGF---EKELYAT-LANV---SPQDD---YGSLSAKAIHLLPHLK---EGN---RYDVAC-----

393932386 *Rhodopseudomonas palustris* B18 : ----TPEILR---TABI---LS-PREDIT---SIRNGLDGLDLDL---VV---BALMO---AAAGDFKPTR---AHSLSAKAIRNIPCLR---EGL---VISEK-----

373501184 *Prevotella micans* F0438 : ----NEHIVSYTEED---IWHV---CV-NAEDPE---EVSNPARKALH---ND---ENIK-E-LVRL-TPSQG---YAMLSKAIKIRNINMLL---LGL---KYSDAVLLAKLPDVVPSVDLHAIETPEFLQEKLNQKQININSVLANKYS-----

294674019 *Prevotella ruminicola* 23 : ----RFQJND---WGVV---LV-FYDEDD---KLKEPAKDRLO---LD---DELAB-K-FSKI---SIPND---YAMLSKAIKIRNIPLYRD---YGL---IYSEAVFLANLVDIVPVHGWIKIE---MREAAENVI-----

365959402 *Flavobacterium columnare* ATCC 49512 : ----NTEKNEV---TKSVDDKDLWHL---LS-VATSDT---VLYDFAIEKLE---LE---PKNAK-A-FSKT---KLKDK---FASLSAAAIKILPYLK---QGL---LYSHAVFMANEIVDAIKWBDEEQKFQSKIVELVDNIYVEKSKLELIN-----

312879015 *Aminomonas paucivorans* DSM 12260 : ----RDLDLS---IADT---LT-FYKNEE---LILPRLESGL---LS---PENAR-A-LAPL---SFGS---THLSLSALGKLLPHLE---EGK---SYTOAR-----

83591793 *Rhodospirillum rubrum* ATCC 11170 : ----DRDRDR---VFSO---LWAARQRS---ALLALI GDPRPTR---VT---EDETAA-VADAIQIIVLPTG---RASLSAKAARAQAQA---PGI---GYDEAV-----

294806111 *Candidatus Punctispirillum marinum* TMCC1322 : ----DEBSQDS---PIIM---LQDDQKGD---EVRSLTQOYQ---LS---DDVADC-LDVR---LPGD---HGSLSKADIRLIPVLR---DQGL---IYDVAV-----

121608211 *Vermisphaera* *eiseniae* EF01-2 : ----SQAODE---IWMR---LV-SQSESG---ALIAWQJGT---VD---CVBAKAI-VNTRL---PDG---YRSLSKALRIPVLAQ---REVQ---TYDKAV-----

344171927 *Ralstonia snyderi* R24 : ----SLDQDR---LVCL---LD-DGNDNA---VLADALREHYG---IT---DAQID-T-LGLL---SFGDG---HWRGLRSALLRDLDALESGRDQQLPL---SYDKAV-----

159042956 *Dinoroseobacter shibae* DF1 12 : ----EVISR---IRR---VQ-SDAHEA---EALDNLTEAHD---LD---RAHAETAHAPL---PDG---YRGLGTATTRTLIYQLT---ADVV---TYDVAV-----

288957741 *Azoospirillum* *sp.* B510 : ----PLEEQDA---LVEL---LL-TEAPEE---RAIAALTARWA---LD---EAT---AAKLAGATLPDF---HGRYGRRAVARELLVPLERETRGDPPDGRV---RPRILEDVAV-----

92109262 *Nitrospirobacter hamburgensis* X14 : ----PPEIOIA---IVAR---LE-ETEDEN---ELTAWLEKECA---LD---DGAARV-VANT---TLPDF---HCRGLRAIKRVLPMQ---DGL---DDGVA-----

148255343 *Bradyrhizobium* *sp.* BTAi1 : ----SLDRQID---LPAV---LE-SALDEA---ATIASLGTHTS---LD---EAAQRA-LSAL---LPGD---YCRGLRAIKRVLPMQ---DGL---TYEAA-----

34557790 *Wolinella succinogenes* DSM 1740 : ----LGRHADE---ATKI---LT-YYKDEG---QKREELTKLP---LE---AEWV-R-LVKI---GSPD---FKLSLKAIRDILPAME---SGA---RYDEAV-----

21953121 *Campylobacter jejuni* subsp. *jejuni* NCTC 11168 : ----SQDLEE---IARD---IT-LIKDEI---KLKALKAYD---LN---QNDIQ-S-LSKL---EPFD---HNLISFKALRIPFLM---EGK---KYDEK-----

791276265 *Helicobacter mustelae* 12198 : ----DRKTDK---IANI---LG-ANKWDE---ALKELESIQ---LS---KEQITDKARL---NEFK---HINLSLEALVHLLPMLR---EGK---RYDGVQ-----

229113166 *Bacillus cereus* Rock1-15 : ----QKLLYDA---IAAA---ST-FFKNDI---EPRDYLRYVLDNNGKRSNIA---NKVFEK-VIAAVFELNFSK---VCHLSFKSLVKIPLHLE---KGL---DYKAI-----

222109285 *Acidovorax* *eburus* TPSY : ----DPTLQD---IATV---LS-YYKIDA---EVVQQLQLA---LP---EPAASIAVLEKI---SFPK---FSSLKALKALRIPVLMQ---SGL---RYDEAV-----

189485225 *uncultured* *Termite* group 1 bacterium phylotype RaD17 : ----NFDLDS---LVNI---IA-NLKDDE---S1KKFEQKLE---ID---EDIDV-LLNPF---EFKK---FINLSFKALRIPVLMQ---QOQ---KYITAS-----

182624245 *Clostridium* *perfringens* D str. JGS1721 : ----NRNLND---IAYV---LT-LGKTDI---E1EKQLRLE---VP---EELFES-LLDM---SFKN---FNNLSIYALEKILPFMK---EGY---QYNAC-----

220930482 *Clostridium cellulolyticum* H10 : ----NRESDN---LFCY---LT-YYKNDN---E1KDYQAN---L---LDYLLY-IAKL---PTFNK---FKHLSAMKRLIPFME---KGY---KYSDAC-----

154250555 *Parvibaculum lavamentivorans* DS-1 : ----ETPDKR---VILL---S-KDKD---AREAAANSF---VA---DFYITQALQKQLKLPFG---WEPYSFALALFALAE---KGE---RPSALV-----

257413184 *Roseburia intestinalis* L1-82 : ----VRLDFE---IGMI---LT-CYKNDI---S1RERLAKLG---LV---PIEMGL-LAYT---P-TK---PQHLSMAMNIPFLE---KGM---TYDKAV-----

218767588 *Neisseria meningitidis* 22491 : ----SFKLQDE---IGTA---FS-LYKTDI---DITRLKDR---IQ---PELLEL-LKHI---SFKD---FVQSLKALRIPVLMQ---QOK---RYDCAK-----

15602992 *Pasteurella multocida* subsp. *multocida* str. *Pm70* : ----KFDLDE---IGTA---FS-LYKTDI---DIQYLTN-K---VP---NSVINAL-LVSL---NFKD---F1ELSKSLRKLPLME---QOK---RYDQAC-----

319941583 *Sutterella wadswothensis* 3 1 45B : ----FGG---IYNAIYTAQVRENVNKLPRN---AQDKELL---T1RDRV---AETADFAIANGLS---DEQKRFANPFLAQFYTLIETEVEV---SGF---SATT1AVHLENARMT---IKDAVIN-----

254447899 *gamma* *proteobacterium* HTCC5015 : ----YLK-EYGLQO---LHLKAGKK---LDDKPLA---LLYKNS---GL1ASKI0EALNIE---PDEVRFASPSHLAQIPNIEGDV---AGF---NKTCTACTYENIWRMQEKEVSLTNQLLSE-----

54296138 *Legionella pneumophila* str. *Paris* : ----AFKIDYEEAL---NHEPE---SNNKALI---K1QTI---PDI1QAIQSHLGN---DSQALYHNPFLSGLYTLIETKR---DGF---HNHCVAVTENYRYSQKTEIDPELSY-----

331001027 *Parasutterella excrementiorum* YIT 11859 : ----YSEDYKFKV---TLKKEKTEKELSKFANV---KVLKW---SEVYPTKELRSL---VA---DEAQSEFNLSYLAQILNLETER---NGF---SVLSLAHLENARMT---MTDG-----

34557932 *Wolinella succinogenes* DSM 1740 : ----FTKDIIEEL---KDDPAELSKERAKL---RLTDVI---LNEWSQIINFDDI---DKHQRFNLSMAQLHTVITDPR---SGF---SNTCKACTAENRFPSTAFYNDTEGE-----

118497352 *Francisella novicida* U112 : ----LNHNINAR---NTKCKEKEIINLCKIE---GSEDEK---GNYKHGLAYELGLVLFGEFNEAKPE---PDKKIKFNISYFAIQIQAFAER---KGN---AANTCAVCSADNHRMQIKITEFVED-----

Motifs : -----

#positions selected for tree reconstruction (272) : -----

303229466	<i>Veillonella atypica</i> ACS-134-V-Col7a	----	I-----	-----ELMNRDYSNMLILGDQKFS-FMECI-EENAKLA-----	-----	-----QQQVNPDIIDEALSAPVAKRAVQALRIVDEVAHI-----	-----KKA-LP
34762592	<i>Fusobacterium nucleatum</i> subsp. <i>vincentii</i> ATCC 49256	----	-----	-----EALRRNTYNNLMELLSSKFT-LQESI-DNENKEMN-----	-----	-----EVSYRDLIELSEYSPSLKRAIQLTFLIYBEIKKI-----	-----TGR-VP
37430778	<i>Fillifactor aloocis</i> ATCC 35896	----	-----	-----AMWTDNMLIILSKFT-EMNIN-EDPNSKIV-----	-----	-----GKIDKITDITVKEFMSFENKRAVQTITQVABEIKVI-----	-----MGC-RP
32052878	<i>Solibacterium moorei</i> F0204	----	-----	-----MWNTRIMELIISNEKIQPKQKI-EYIKAEYI-----	-----	-----DEKQNLHELDMYSPARRSISWQLKIVDEIYDI-----	-----KKS-AP
291520705	<i>Coproccocus catus</i> GD-7	----	-----	-----LWQYTDNMLQLLSSRYG-FTNEV-EFNTLKK-----	-----	-----ETDLSYKTVDELVSFAVKRQIQTQLKVVKQLKIV-----	-----MGN-AP
42525843	<i>Treponema denticola</i> ATCC 35405	----	-----	-----NIITAMRRTQNNMELSSSEF-TFTENI-KKINSQFE-----	-----	-----DAEQKFSYDLGKPKLFLSPSVKMLQTLKLVKISHI-----	-----TQA-PP
304438954	<i>Peptoniphilus duerdenii</i> ATCC BAA-1640	----	-----	-----FMREYNLNMELMESHGT-FTEEV-EKLVPVEN-----	-----	-----RELCEYMEVDLIVLSPSVKMLQSLRVVDEIKRI-----	-----IGK-DP
224543312	<i>Catenibacterium mitsuokai</i> DSM 15897	----	-----	-----VLEMSRLNMLMEIINDRDLGVAQMI-EAETSCEP-----	-----	-----DGKFTYEVEERLAGSPALKRKIQWSLQIYVEITKV-----	-----MKC-RP
24379809	<i>Streptococcus kitaharae</i> DSM 17330	----	-----	-----GNSNRNFMOQLINDD-ALSFK-EBIAKAQV-----	-----	-----IGBTNMLNVVSDIAGSPFAIKKGIQLSGLVLDLVI-----	-----MGH-OP
151675041	<i>Streptococcus pyogenes</i> 5370	----	-----	-----GFANRNFMOQLINDD-SLTFK-EDIQGAKV-----	-----	-----SQQSSLMVWDLRSPVVKRGIQLSGLVLDLVI-----	-----MGR-KP
16801805	<i>Listeria innocua</i> Clpi11262	----	-----	-----MNRDNLNMLLINDS-MLSFK-ENYIKAEYI-----	-----	-----DEKQNLHELDMYSPARRSISWQLKIVDEIYDI-----	-----KKS-AP
116628213	<i>Streptococcus thermophilus</i> LMD-9	----	-----	-----GLSRRNFMOQLIHHDD-ALSFK-KKIQAQI-----	-----	-----IGD-EDKGNIEKVVSKLSPSAPKIKKGIQLSGLVLDLVI-----	-----MGR-KP
323463801	<i>Staphylococcus pseudintermedius</i> ED99	----	-----	-----SDENFMELIINDD-VYGFQ-NFIKEENQ-----	-----	-----V-QSNKIHQIDIANLTTSPALKKGIYRSTIKLVRITSI-----	-----FG-EP
352684361	<i>Acidaminococcus intestini</i> RCY-RM95	----	-----	-----TNDNLMLLIS-E-CYTF5-DEITKLQE-----	-----	-----AAYAKAQLSINDFLDSMYSINAVKRPYITLAVVDLIRKA-----	-----CGT-AP
302336020	<i>Olsenella uli</i> DSM 7084	----	-----	-----NPNNGQRSTVMFVMEVLRDE-DLGFQ-KAIDGLNR-----	-----	-----DYFRRHNLGMD-VNDLPGSPARRSIINQAVRIDEIASI-----	-----ARK-EP
366983953	<i>Oenococcus oeni</i> DSM 17330	----	-----	-----TKMNMELIINHAE-DDGFVR-AMIDKQNT-----	-----	-----TD-GDEQDYSVLIIDELAGPKEIKKGIQVGFRLIDDIITRA-----	-----VGY-AP
131028678	<i>Bifidobacterium bifidum</i> S17	----	-----	-----TMRAEDNMLMELITDQLGSDMVI-EENLGAE-----	-----	-----NGSSLMVWDLRSPVVKRGIQLSGLVLDLVI-----	-----MGR-KP
259509199	<i>Lactobacillus rhamnosus</i> GG	----	-----	-----EMLLSNNMLMQLIADDE-LKEMT-TLNQOKI-----	-----	-----RSTDIEDVINDAYTSPSNNKALQVLRIVDEIKHA-----	-----ANG-QP
300361537	<i>Lactobacillus gasseri</i> JV-V03	----	-----	-----IQQLWDSNNFMQIVNQSD-FKDAI-AVANONLL-----	-----	-----VNTSVEIILNAYTSPSNNKALQVLRIVDEIKHA-----	-----ASG-KV
169823755	<i>Finegoldia magna</i> ATCC 29328	----	-----	-----NFRNNSDNLMQIIGSQNYSFNEVI-DKLKRYKI-----	-----	-----PQELISYEVVENLYSPSVKMIQWVIRVTEITKV-----	-----MGY-DP
47458868	<i>Mycoplasma mobile</i> 163K	----	-----	-----SYEEKALQNKQN-----NF5HS-NLFKETW-----	-----	-----EDLSPASPTVKRSLRQTMMLLEKIFKY-----SEKNLEI	-----
284931710	<i>Mycoplasma gallisepticum</i> str. F	----	-----	-----QKNDRGNWFPAIKNFQPK-FIDIT-KKNNLSL-----	-----	-----KQNK-RYLDLDFRINDAALSLSQPAKILREATVFNALIQ-----FSEEDV	-----
363542550	<i>Mycoplasma ovipneumoniae</i> SC01	----	-----	-----NBYELKWKDEE-IRRWK-EBQSKLQ-----	-----	-----KTDKKTYLNAPRIPQDEIISFGPTNFFQDAVLVLAQIKK-----YSHENI1	-----
394303286	<i>Mycoplasma</i> sp. 14	----	-----	-----QWRLEAKNYDEE-IKSKI-EMSSLSMA-----	-----	-----KQDK-KYLINDNPLDKALRSPVVKRGIQLSGLVLDLVI-----	-----MGR-KP
71894592	<i>Mycoplasma synoviae</i> 53	----	-----	-----MYSELKHSNELKIRTEKA-ELAAQ-QN-----	-----	-----QKYLKMDPLKALVPLSFKTSVLQIKLIFNQILKN-----PGKVEI	-----
238924075	<i>Eubacterium reetale</i> ATCC 33656	----	-----	-----EMGVTKTGQVEFAG-----LKVI-PV-----	-----	-----DVSIEDIINFVVRSVRSISFKILNLAIVLK-----YK-AL	-----
116627542	<i>Streptococcus thermophilus</i> LMD-9	----	-----	-----RLGKQTKTSSNNK-----	-----	-----TKYIDEKLLTEIYNPVAKSVRQAIKIVNAIKE-----YG-DP	-----
315149830	<i>Enterococcus faecalis</i> TX0012	----	-----	-----LEQFQLKSDVRRKYSYEKLLPT-----	-----	-----KDLVLAIYNPTVNRVTSQAFKVLIDALLIK-----YQKQI	-----
315659848	<i>Staphylococcus lugdunensis</i> M23590	----	-----	-----QMLFTHLNIKPKKI-----NL7AA-NKIPKAMI-----	-----	-----DEFILSPVVKRFTTQQAINLNLKILEK-----YG-VP	-----
160915782	<i>Eubacterium dolichum</i> DSM 3991	----	-----	-----LPLGKQNNLEKSVG-----	-----	-----MKNIQADDTAALSLSQPAKILREATVFNALIQ-----YG-EF	-----
336393381	<i>Lactobacillus coryniformis</i> subsp. <i>corquens</i> KCTC 3535	----	-----	-----GWRLEAKNYDEE-IKSKI-EMSSLSMA-----	-----	-----DTRIEITNVPVRAVTKTITVILVIRK-----YK-RP	-----
310780384	<i>Lilyobacter polyotus</i> DSM 2926	----	-----	-----EKADYDYKNNGIKFKRGE-LLPVM-DK-----	-----	-----DLIANPVLRALISQTRKIVNAIIRK-----YQ-TB	-----
325677756	<i>Ruminococcus albus</i> 8	----	-----	-----EAKFNKEIPIDENAKPQ-KLPFP-KN-----	-----	-----EDDCEFFKNNVVRVSNETRKLINAIIIDK-----YK-AL	-----
187736489	<i>Akkermansia muciniphila</i> ATCC BAA-835	----	-----	-----RGEAHPDGLKAGDCLCYLLDDT-SSVNQHQK-----	-----	-----ERRLDTMNNLHVRHMLILDRLLKLDIQ-----FADGQK	-----
117929158	<i>Acidotherrum cellulolyticum</i> 11B	----	-----	-----KTFCGDDDNWRPPL-----	-----	-----PALHEATGHVDRNLALRFLSASATMR-----WG-PP	-----
189440764	<i>Bifidobacterium longum</i> DJO10A	----	-----	-----KTLFNVNDSWRPFA-----	-----	-----DPIGEPNDSVDRVLRKNNRVLNMCQQOR-----WG-NP	-----
283456135	<i>Bifidobacterium dentium</i> Bd1	----	-----	-----KAFVGVDDNNWPPV-----	-----	-----DAISVGVNPAVDRVLRKIVNRYLACQRK-----WR-NP	-----
38232679	<i>Corynebacterium jeikeium</i> NCTC 13129	----	-----	-----LQERHAFMELT-----	-----	-----LQERHAFMELT-----	-----
187250660	<i>Elusimicrobium minutum</i> Bel191	----	-----	-----EALKEGKLTKKEQAQIKD-RLPYV-GAVLQEST-----	-----	-----QKILAKGSPQPKDKGVKTPHTNMYEYLRVANPVHQITLNEKRLNVEIIDI-----LQK-RP	-----
319957206	<i>Nitratifactor saluginis</i> DSM 16511	----	-----R-----IL-----	-----GDFDRE-----DY5RY-PKSLRHHL-----	-----	-----LREGNLFKEEKNPINHAWKLSLAWALGLADLSDR-----YQ-PF	-----
325972003	<i>Sphaerochaeta globus</i> str. Buddy	----	-----	-----ERQMETQEPQLSVMGQQLLPPY-GQILTGST-----	-----	-----QALMGKYHSAFPEKRDSEGFPKPTNDSDEKGRIANPVHQITLNEKRLNVEIIDI-----LGA-KP	-----
261414553	<i>Fibrobacter succinogenes</i> subsp. <i>succinogenes</i> S85	----	-----IDKNTLDRIDKILINGEYDEKIS	-----	-----NRVRDANLNLDIS-----DFRGL-NKVLACYL-----	-----VYDRHSEAKDCTKNWSP-----EIDSYLKFKQHSRNPVEQVVTLETRVTDIWIQ-----EG-QI	-----
60683389	<i>Bacteroides fragilis</i> NCTC 9343	----	-----	-----VYGYRHSESSLT-----REBIA-NKVLKDL-----	-----	-----MLLKNLHNPPVVEKILNQMNVINIIDI-----YQ-KP	-----
256819408	<i>Capnocytophaga ochracea</i> DSM 7271	----	-----	-----EKAGYKSKLSLT-----TEELE-ARELKNII-----	-----	-----PLKKNALRNPPVVEKILNQMNVINIIDI-----YQ-KP	-----
90425961	<i>Rhodospseudomonas palustris</i> B1818	----	-----	-----ARVYDHAARLS-----	-----	-----VPLDQVSGVTRKLEALSQVFAVARE-----YQ-P1	-----
373501184	<i>Prevotella micans</i> F0438	----	-----	-----KLEENRPHDNQYQLGQDDEIDTIQIKSHIQAQLWQIGADEQTIKIPQAVRSKYQDFPKSYKRRFPVEP-KLGEVLAFLTEKFPNPKSQWRLVYHS-----	-----	-----QIAIYFPIVDNDR-----SKLRGMNIGAIXKNTVMRLVINTLRVGVQLLDD-----G-VIS-PDE	-----
294674019	<i>Prevotella ruminicola</i> 23	----	-----	-----DVMSYDKNNIDGI-TLEGCKYTKLERY-QVSDNKLKLYHS-----	-----	-----MLDYP-PRQPNDR-----GVFLQSGRSISVKNMAMHSLFRLKRVNMLKDK-----G-YIT-PD	-----
365959402	<i>Flavobacterium columnare</i> ATCC 49512	----	-----	-----GLLIYNTDEKGRKVVYSKEAESLFEADLRKLLVPFYKANIIEEHEQEIIQDFLPMDQLMQKQEFIKIQRLLDQIEAFLEGEENEGEIFCNH-TDKLKLHYPSDIEVFPKTIKDEWNEKVVLSPLTTSIKNPMAMKALHQLRVLNIIAN-----	-----	-----D-----QID-ED	-----
312879015	<i>Aminomonas paucivorans</i> DSM 12260	----	-----	-----ADAGYAAPDPRHP-----KLPLEE-----	-----	-----ADWRNVVFRALQTRVFNALVLR-----YQ-PP	-----
83591793	<i>Rhodospirillum rubrum</i> ATCC 11170	----	-----	-----TLALGLHSHRPQERLA-RLPYV-AAALDPDVG-----	-----	-----LDGDPVGPPEADDGAAEAAYGRINISVHIALNEKRIVNALH-----HG-P1	-----
294086111	<i>Candidatus Puncicepirillum marinum</i> IMCC1322	----	-----	-----KAPGLGEANLDPVAALSDKLDYV-GKALAGHV-----	-----	-----MGASQKFEDSDEKRYGTISNPTVTHIALNQVRAVNNLIRL-----HG-KP	-----
121608211	<i>Vermisphaera eiseneiae</i> EF01-2	----	-----	-----EHTLASTGEVQVQYAFKQDLPYV-GKALQERV-----	-----	-----AFQSGDADKHEEYCKIANTVTHIGLQVRYVNNLIR-----YQ-HP	-----
344171927	<i>Ralstonia syzgii</i> R24	----	-----V-----	-----AGVPAHTADLENGERD-ALPYV-CELLRWYV-----	-----	-----QDAPTAKNDAREFKPKIANTVTHIGLQVRYVNNLIR-----YQ-KP	-----
159042956	<i>Dinoroseobacter</i> sp. B12	----	-----	-----KACGWHSDHACTGFCBB-ALPYV-CEVLERHW-----	-----	-----IPGSHDDEDDITRGRITNPTVTHIGLQVRYVNNLIR-----YQ-KP	-----
288957741	<i>Azospirillum</i> sp. B510	----	-----	-----KLLRGGKHSDSPREGALLDALPYV-GAVLERHW-----	-----	-----AFTGNDPAPPEKRVGRVANPTVTHIALNQVRAVNNLIR-----HG-RP	-----
92109262	<i>Nitrobacter hamburgensis</i> X14	----	-----GAGYHI	-----	-----SAKRAGYDHAKLPTGSLGLRLPYV-GQWLQDAV-----	-----VGSQDARDKQEKYQVQFPNTVTHIGLQVRYVNNLIR-----YQ-PP	-----
148255343	<i>Bradyrhizobium</i> sp. BTA11	----	-----	-----SAQYVDHALLPGKLSPTGVLRYV-GQWLQNDV-----	-----	-----VGSDDERDNERNGRPLNPNTVTHIGLQVRYVNNLIR-----HG-PP	-----
34557790	<i>Wolinella succinogenes</i> DSM 1740	----	-----	-----LMLGVPKKEKSAIPLP-NK-----	-----	-----TDIDILNPVTRAFAPRQFRVANAIVLR-----YQ-AP	-----
219563121	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> NCTC 11168	----	-----N-----	-----EHLNKVAINDEKID-----FLDAP-NE-----	-----	-----TYDKDNPVTRAFAPRQFRVANAIVLR-----YQ-KV	-----
791276265	<i>Helicobacter mustelae</i> 12198	----	-----	-----EILQERGIKSPKQPKNRQ-LPLP-SELAK-----	-----	-----EESYFEDINPVTRAFAPRQFRVANAIVLR-----YQ-GF	-----
229113166	<i>Bacillus cereus</i> Rock1-15	----	-----	-----LQAGYVFRDEMKNRDKKL-FLV1-----	-----	-----QOETNPVVRHALQTRVFNALVLR-----YQ-SP	-----
222109285	<i>Acidovorax ebursus</i> TPSY	----	-----	-----AQIPEYGHHSQRTEPGAAKHLYLPPF-YEAQRKYA-----	-----	-----GKGDHIGSMQFRDDADIPRNPVRLRALQARVFNALVLR-----YQ-SP	-----
189485225	uncultured Termite group 1 bacterium phylotype RaD17	----	-----	-----TSAGYINKQGEIKN-----	-----	-----KLVPAKENVAVARAFAPRQFRVANAIVLR-----YQ-OF	-----
182624245	<i>Clostridium perfringens</i> D str. JGS1721	----	-----	-----EKAGYNFKAIYEGVTRK-KLPV1-E1-----	-----	-----DEIYNPVNRLAQAQTRVFNALVLR-----YQ-SP	-----
220930482	<i>Clostridium cellulolyticum</i> H10	----	-----	-----NMAELDFTGS5-----KLECK-NKLTV-----	-----	-----EPIENYVNPVTRAFAPRQFRVANAIVLR-----YQ-LP	-----
154250555	<i>Parvibaculum lavamentivorans</i> DS-1	----	-----	-----NGPDQRGRTNDFPRNQPTFEILKI-PSPAKSEE-----	-----	-----KERISQLRNPVTRAFAPRQFRVANAIVLR-----YQ-KP	-----
257413184	<i>Roseburia intestinalis</i> LI-82	----	-----	-----EBA-GYDFKADSKGTQK-LLTGE-NNYQT-----	-----	-----SAQCRRLPACVPRDFGFRICADIRNSWEVAKRILAEVKKVDVT-----NGT-VK	-----
218767588	<i>Neisseria meningitidis</i> 22491	----	-----	-----ARIYGDHY-GKKNTEKI-YLPI1-PA-----	-----	-----DEIRNPVRLRALQARVFNALVLR-----YQ-SP	-----
15602992	<i>Pasteurella multocida</i> subsp. <i>multocida</i> str. Pm70	----	-----	-----REIYGHY-GEANQKTSQ-LLPAL-PA-----	-----	-----QERNPVRLRALQARVFNALVLR-----YQ-SP	-----
319941583	<i>Sutterella wadsworthensis</i> 3 1 45B	----	-----	-----	-----	-----GETVRAAQSRLPAETARPFDGLVRLVRDQAWELAKRNVSDIQKVDF5-----NGI--VD	-----
254447899	gamma proteobacterium HTCC5015	----	-----	-----	-----	-----IHGERKVPKLSAMCTRLSADSTRPFDQMASIIEHIARKIAQKIAQINDVPK-----EFS--ID	-----
54296138	<i>Legionella pneumophila</i> str. Paris	----	-----	-----	-----	-----ASRLPADSVRPFQDGLARMQRILAYEAMAKWEQIEKHLPD-----NSS--LL	-----
331001027	<i>Parasutterella excrementiformis</i> YIT 11859	----	-----	-----	-----	-----SAQCRLPACVPRDFGFRICADIRNSWEVAKRILAEVKKVDVT-----NGT-VK	-----
34557932	<i>Wolinella succinogenes</i> DSM 1740	----	-----	-----	-----	-----FHKKATAQRLPQVDFGFRICADIRNSWEVAKRILAEVKKVDVT-----NGT-VK	-----
118497352	<i>Francisella novicida</i> U112	----	-----	-----	-----	-----NKDKILSAKAQRLLPAIPTRVDFGAVKMKMATLAKNIVDDMNKQVLSA-----KHQ--LH	-----

Motifs :
 #positions selected for tree reconstruction (272) :

303229466 Veillonella atypica ACS-134-V-Col7a : S--RIFVVARATNK--SEKKKDKSRQRLSDLSYAI--KDDVLSQGLQKDFEGALKSG-----L---ANYDDAALR-----SKKL-YYLYT---QMGK--CAY-TGNIIDLNLQMTDN---YDIDHYPKSL-TKD---DSFDN
34762592 Fusobacterium nucleatum subsp. vincentii ATCC 49256 : K--KVFIEMARGGDESMKMKIPARQEQKRLKYDSCG--NDIANFSDIKKEMNSLS-----KRL-LYYLY--QFGK--CMY-TGREILDRLQNDNT---YDIDHYPKSL-TKD---DSFDN
374307778 Filifactor alocis ATCC 35996 : K--KIFIEMARGG--KVKKTRKSRKAQLELYACE--EDCRLEKIEI-----DKDRDFNS-----MKL-FLYYT--QFGK--CMY-SGDEIDNLRIGNSK--WRDHIYPQSK-LKD---DSLND
320529778 Solibacterium moorei F0204 : K--KIFIEMAREKKSAMKKTETSRKDTLLELYKSCK--SQADPFYDRLEKFKLMSMS-----RLEK-----DKL-YYLYT--QMGK--SMY-TGRKIDKFLNKNKT---YDIDHYPKSL-LKD---DSLND
291520705 Coprococcus catus GD-7 : K--RVFVEMAREKQ--EKGSRDSRKKQLVLYRACK--NEERDWTIELM-----AQQSQDRLS-----DKL-FLYYI--QKGR--CMY-SGETITDLKMDNTK---YDIDHYPQSK-TMD---DSLNN
42525843 Treponema denticola ATCC 35405 : K--KIFIEMAKGAE--LEPARTKRLKLDQLYNNCK--NDADAFSSKIKDLSGKIE-----NEDRLSLK-----DKL-YYLYT--QLGK--CMY-CGKPIEIGHVFSTN---YDIDHYPQSK-LKD---DSLNS
304438954 Peptoniphilus duerdenii ATCC BAA-1640 : K--KIFIEMARAKE--AKNSKRSRKNLLLEFYKPKKAFINEIGBEERYNLLNEIN-----DNL-YYLYT--QLGR--CMY-SLEPIADLAKSNIN---YDIDHYPQSK-TMD---DSLNE
224544312 Catenibacterium mitouakai DSM 15897 : K--YIVIEFERSE--AKERTSKIKKLENYKDLDD--EQTKKEYKSVLEELKGFDTNK-----KISS-----DSL-FLYFT--QLGK--CMY-SGKLLDSDLSK---YDIDHYPQSL-VKD---DSFDN
324939809 Streptococcus mitans UA159 : E--RVYLEFARKTQ--PT-----NQGRNSO--QRLKGLTDSIKKFGSGILKEH-----PVENSQLOK-----DRL-FLYYL--QMGK--DMY-TGEELDIDLRSQ---YDIDHIPOAF-LKD---NSLND
157655941 Streptococcus pyogenes S170 : K--NIFVLEARDLQ--GQKQKRL--NMKRIKIRLEKLSQSLIKH-----KISKDLQK-----DRL-FLYYT--QMGK--DMY-TGEELDIDLRSQ---YDIDHIPOAF-LKD---NSLND
160180185 Listeria innocua Clp11262 : Q--KIVFEMAREKQ--TT-----GKGNKNSQ--PRYSLEKAIRKFGQILKEH-----PTDNQKLL-----DRL-FLYYT--QMGK--DMY-TGDDLDHNLGN--YDIDHYPQSK-LKD---DSLND
116628213 Streptococcus thermophilus LMD-9 : E--SIIVFEMAREQ--YT-----NOGKNSO--QRLKRLKSLKELGSKILKEN--I-----PAKLSKIDNNAJOK-----DRL-YYLYL--QMGK--DMY-TGDDLDLRLSN---YDIDHIPOAF-LKD---NSLND
323463801 Staphylococcus pseudintermedius ED99 : E--KIMIFATEDDQ--QK--GKQKSRK--QLW--DDNIKNNLKSVDYKQYI--IDVANNLNGEQLQK-----EKL-WLYLS--QMGK--CMY-SGQSIDLDLALLSNATKHYEVDHIFPSP-LKD---DSLND
352684361 Acidimicrococcus intestini RY-CR95 : K--RIFEMARETQ--SK--KKRSVTRR--EQIKNLVRSIRKDFQOV-DF-L--KILKENSQGLQSQ-----DAL-XYLFA--QLGR--DMY-TGSDILKLEHKDQS---FYNDHYPQSK-TMD---DSLND
302336202 Olsenella uli DSM 7084 : T--NIFVETRED--DP--RKGKRTK--RRYDAIKSALEKFKDDPSLV-----KELCEKARGMDK-----DRL-SLYFM--QRGK--CMY-SGRPIKEBLEHTGK---YEVDFIIPRSY-LKD---DSFDN
366983953 Oenococcus oeni DSM 17330 : K--RVYLEFARKTQ--E--ESHLTN--SRKQSTLLKKNAGSELVLTQ-----VSQVDAALQN-----DRL-YYLYL--QMGK--DMY-SGKIDNLELSTN---YDIDHIPOAF-LKD---NSLND
131026728 Bifidobacterium bifidum S17 : K--NIFVLEARDLQ--PGRTIRSRKRLQDLVRANLKLKFKGLADELN-----KISKDLQK-----DRL-FLYYT--QLGR--DMY-TGEELDIDLRSQ---YDIDHIPOAF-LKD---DSLND
259509199 Lactobacillus rhamnosus GG : S--MIFVETADTQK--TACKTQTSRQKQIOTVYANAQALIDSANRGELEKI-----ADKASPT-----DRL-YYLYM--QRGK--DIY-TGAPLNDIQSHG---YDIDHILPQSL-LKD---DSLND
300361537 Lactobacillus gasseri JV-003 : K--QIAIEFTRDAD--DKAKISQFRANKLKVYKELSNLASESTINRELERV-----AKDKQLK-----DKY-XYLYM--QLGR--DAY-TGFEINIDDLQK---YDIDHILPQSF-LKD---DSLNE
169823755 Finegoldia magna ATCC 29328 : D--KIFIEMAKSEE--EKKTITSRKNNLLDLYKAIKKDRDSQYKELLTGLN-----KLDDSDRLS-----RKL-YYLYT--QMGK--DMY-TGEIKDLDKLEFSTH---YKDHIPQSKMDD---S11NN
47458868 Mycoplasma mobile 163K : E--KIVVEVTRSSN--NKHERKKIEGINKYRK--EKYEBLKVVYDLP-----NLNTTLL-----KKL-WLLRQ--QGGY--DAY-SLRKIEANVINKPNW---YDIDHIVPRSI-SFD---DSFNS
284931710 Mycoplasma gallisepticum str. F : T--KVVIELARELS--EKELENTKNYKLIK--KNGDKISEGLKALGISEDEIK-----DILKSPAKL-----YKF-LWLLQ--QDHI--DPY-SLKEIAPDDIPTKTEK--FIDHIIPIYSI-SFD---DSSNS
363542550 Mycoplasma ovipneumoniae SC01 : D--AIIEVSPERNK--DKTITBIRK--KRNKK--GKGTKLEKILQINLNGKVKLS-----DLETPTKTL-----LDRL-RVYHQ--QDGI--DLY-TLKKINDLKLDDPNNA---YIEHIIPIYSI-SFD---NSQAN
394303286 Mycoplasma bialle S14 : D--KVVIELARELMT--QDQENDLAKIQAQK--SEKIKRERQAEHMLIGRQSPD-----DYLKELN-----DRL-FLYYL--QMGK--DMY-TGEELDIDLRSQ---YDIDHIPOAF-LKD---DSLND
71894592 Mycoplasma synoviae 53 : S--QVVIEMARELTKPMLKELLNNAITNSIKILKELK--DQTEKFDPTKXKPID-----KTPNSQVLR-----NKL-PLWFE--QDRK--DPY-TQLDKINRIDE---TRIDHVPYK-SAD---DSFNM
238924075 Eubacterium rectale ATCC 33656 : D--TIVIEMPDRDN--SEQKRRINDSQKLN--KEMEYI EKLAVTYGIKLSFS-----FDSQSKQS-----DRL-KLWNE--QDGI--CLY-SGKTIDNPNIDNNPOL---YDIDHIIPIYSI-SFD---DARNS
116627542 Streptococcus thermophilus LMD-9 : D--NIVIEMARETN--EDEKKAIQKIQKANK--DEKDAAMKAAQNGKALPHSVF-----HGKQLA-----TKI-LRWHQ--QGER--CLY-TGKTISHDLLNNSQK---FEVDHIIPIYSI-TFD---DSLAN
315149830 Enterococcus faecalis TK0012 : R--YITIEMPDRDN--EDEKRIKELHAKNS--QRKNSDSQYFMQKSGWSEKF-----QTI--EKKRFRF-----AKL-LYYE--QDGI--CMY-TGLPISEDLVSDS---YDIDHIIPIYSI-SLD---DSLNN
315659848 Staphylococcus lugdunensis M23590 : E--DIIEELARENN--SKDKQKFINEMQKNE--NTRKRIE IIGKYGN-----QAKRLV-----EKL-RLHDE--QBGK--CLY-SLESIPLEDLLNPNH---YEVDFIIPRSV-SFD---NSYHN
160915782 Eubacterium dolichum DSM 3991 : D--SIIVEMAREEN--SEEQKRIERKQKFFE--MRNKQVADIQDDR-----KINKAKLV-----EKL-VLYQE--QDGI--CMY-SGKIDNLELSTN---YDIDHIPIYSI-SFD---DSLTD
336393381 Lactobacillus coryniformis subsp. torquens KCTC 3535 : D--QVIELARELQK--RNFREKQIQKQKQK--QTNRIKARLTELGI-----PQQGKI-----IRY-KLHRE--QMGK--DPY-TGSDIPFERAISRQ---YEVDFIIPRSV-SFD---DSLND
310780384 Ilyobacter polytrogus DSM 2926 : H--KHVYEARDLA--KSYDDRQTIIEKANKRE--LENKTKRSEIPEGLK-----NVKGLL-----DRL-FLYYE--QDGI--CMY-SGKIDNLELSTN---YDIDHIPIYSI-SFD---DSYSN
325677756 Ruminococcus albus 8 : A--AVNIETADELN--KTFEDRAIDTKRNNDD--KENDRIKSIIEIKCDE-----VYARHLI-----EY-KLWEA--QBGK--CLY-SGETITKEDMLRDLKGL---FEVDHIIPIYSI-SLD---NTINN
187736489 Akkermansia muciniphila ATCC BAA-835 : DRISRVCVGEVKLT--TFSAMDKKIQRELTLRQ--KSHTDVNRKRLKLPK-----ALSNALI-----RKC-RIAMD--MWTV--CPF-TGATYGHLELN---LELHEIYPHF-RQS---NALLS
117929158 Acidothermus cellulolyticus 11B : Q--SIIVELARGAS--ESRERQAEAEARRAHR--KANDRIARLRSAGLS-----VRA-LLEL-----DRL-FLYYL--QMGK--DMY-CGAPISWEN---SLEDHIIPIYSI-SFD---NRHEN
189440764 Bifidobacterium longum DJ010A : V--SVNI EHVRSFP--SVAFARKDKREYKNN--EKRSIFRSLSLQRLADEQME-----KVRESDL-----RRL-ELQR--QNGO--CLY-CGRITFTF---CEMDHIVPKQGVST---NTRTN
283456135 Bifidobacterium dentium Bd1 : Q--SVOIEHVRSFP--SSVAKAKTEYRQGERA--RYRNDLRRLCQ--EGLN-----KIRSDI-----RRW-ESVQR--QNGT--CLY-CGSPITFTF---CEMDHIVPKQGVST---NTRTN
394303286 Mycoplasma bialle S14 : D--KVVIELARELMT--QDQENDLAKIQAQK--SEKIKRERQAEHMLIGRQSPD-----DYLKELN-----DRL-FLYYL--QMGK--DMY-TGEELDIDLRSQ---YDIDHIPOAF-LKD---DSLND
118250660 Eluimicrobium minutum bel191 : C--EIGLETAERLK--KSADRSKLSREQNDN--SNNRNIEYIYRPOQVLIIR-----R-----ENPNRYI-----LKF-ELIJE--QKSG--CPF-CGQGISPNIDNNG---ADIEHLPFIAE-SGD---NGRNN
319957206 Nitratifactor saluginis DSM 16511 : D--EILLETTRDAL--PEKRIEKIDKAMRRE--KALDKIIGKYKEF-----PSIDKRL-----ARKI-QLWER--QRGL--DLY-SGKVINLSQLDGS---ADIEHILPQSL-GGL---STDYD
325972003 Sphaerochaeta globus str. Buddy : Q--EITVELARELK--VGAEKREDIIKQTKQE--KEVALYKCYECPN-----NLDKRYI-----ERF-RLLED--QAFV--CPY-CLEHISVADIAAGR---ADVDFHFRDD-TAD---NSYGN
261414553 Fibrobacter succinogenes subsp. succinogenes S85 : D--EIHLELDGRLK--NPAKERRKMSENTLKN--NHLRIKAMLMFMPNPMGIE-----NVVAPY--NVSQDILRIYENALDNLTKDDKDFDFI---SKISKQAQPSKTDIIR--LYR-KLYKE--QKVR--SPY-TGKTIISFKLPTFA---YIEHIIPIYSI-YFD---DSFNS
60683389 Bacteroides fragilis NCTC 9343 : D--EIRVELARELK--KNAKERELTKSIQTT--KAHEEYKTLIQTEFGLT-----NPTSDI-----LRY-KLYKE--LESCGYK--TLY-SNTYISFKLPSKE---FIEHIIPOAF-LFD---DSFDN
256819408 Capnocytophaga ochracea DSM 7271 : D--EIRVELARELK--KNAQKREYMTQINKAK--LEHQKISELQKQKFI-----NPTSDI-----IRY-RLYQE--LEHNGYK--ELY-TMAPLARDMLKNG---YIEHIIPIYSI-SFD---DSFNS
90425561 Rhodopseudomonas palustris B1sB18 : D--YVHIELARLVG--KSAERKQKQIQDQKQ--VEKAKRERQAEHMLIGRQSPD-----DEL-----LRY-ELAKE--QMKF--CLY-SGDIADPAVANDTR---YEVDFIIPRSV-SFD---DSLND
373501184 Prevotella nana F0438 : T--RVVETARELN--DANTKWDALRYNRIAR--DENEKIKLILKLNPNFTNSISEQDIDKARYIFEQCQTFDFYTDKGVVYKMDI-----KYY-KLWLE--QGGQ--CLY-TGQITINDLTFNNA---FDMHIIPIYSI-SFD---NSDQK
294674019 Prevotella ruminicola 23 : D--KVHIEFTRDAD--DANKRWAIQTQWRENE--KERERCRIEKYIASPS-----DTDI-----LKY-QLWEE--QNHK--CLY-TGDEIRITDFILGNKPK---YDIEHIIPIYSA-GGD---STOKM
365959402 Flavobacterium columnare ATCC 49512 : T--RIHIEARELN--DANKRKGIQDFQENK--KFEBAEIKKILVLEECHD-----V---NPTDDI-----LRY-QLWLE--QKCK--EYEGGNISICDIIGSNPS---YDIEHIIPIYSI-SQD---NSQMN
312879015 Aminomonas paucivorans DSM 12260 : W--CIIHLEARELS--QPAKVRRIETEQAENE--KKQQAERFLDIVGT-----APGGDGL-----LMK-RLWRE--QGGF--CPY-CEEYLNPTLAEFG---AMDHIIPIYSI-SLD---NGWHN
83591793 Rhodospirillum rubrum ATCC 11170 : L--RLVMVETRELK--AGADERKRMIAEQARE--RENAEIDVELRKSDRWM-----ANARER-----QRV-RLAR--QNNL--CPY-TSPTIGHADLDGDA---YDIDHIIPIYSA-GGD---DSLND
294086111 Candidatus Puncicepirillum marinum TMCC1322 : D--EVVIEGRDLP--MAGDKRELERQKQKGR--AKNERARDMLKGLH-----IDSRER-----QKQ-QLWELQAKEP-VDRK--CPF-TGKMSISDLPDSK---YDIEHIIPIYSI-TLD---DSMAN
311608211 Verminephrobacter Eiseniae F01-2 : T--EVVIELARDLK--QSREKQKQOTQRBQADN--KRNIDIKRIAPILTSPE-----RVDRDI-----RKM-LWELANKIDADR--CPY-SGERISATMLLSGA---YEVDFIIPRSV-LKD---DSLND
344171927 Ralstonia syygii R24 : A--QIVVELARELK--AGLEEKRIKQQTANL--EENRIKRLQDAQV-----PDKNEM-----LML-RFEEELG--QGNGLGTPCIY--SGRQISLRMLPSMD---YVDHIIPIYSI-TLD---DSFAN
159042956 Dinoroseobacter shibae DFL1 12 : H--QIVVELARDLK--KSEEQKRAKIRIDTDT--EAKKRSKLELELEI-----ENGRNR-----MML-RWELNDNDMMARFR--CPY-TGTRISAMMFDGS---CVDHIIPIYSI-SLD---DSFPN
288957741 Azospirillum sp- B510 : E--EIVIELARDLK--RSAEDRRDKRQADNQ--KRNERRKRLLSLGE-----RPTPRNL-----LKL-RWEEQGVV--ENRR--CPY-SGETISMRMLLSQ---VIDHIIPIYSI-SLD---DSAN
92109262 Nitrobacter hamburgensis X14 : T--EISIEFTRDLK--LSEQQKAERQERQEN--DNKKAELAKLAFGR--PANPNL-----LKM-RLWELAHDP-LDRK--CVY-TGEQITIERLSDDE---VIDHIIPIYSI-TLD---DSAN
148255343 Bradyrhizobium sp- BTA11 : A--EITVELTRDLK--LSPRRLAEERQEAEN--RKNDKRTSLRLKGL-----PASPNNL-----LKL-RLWDE--QGVASBCPY--TGEAIGLERLSDDE---VIDHIIPIYSI-SFD---DSAN
34557790 Wolinella succinogenes DSM 1740 : D--RVHVELAREIN--TKGEIEDIKESQRKNE--KEREAADWIETSPQV-----PLTRKNI-----LKK-RLYIQ--QDGR--CAY-TGVEIIEKLEPDEGY---CEIDHIIPIYSI-SAD---DSFAN
219563121 Campylobacter jejuni subsp. jejuni NCTC 11168 : H--KIVIELAREVQ--KNSQRAKIEKQENY--KAKDALECEKGLG-----KINSKI-----LKL-RFKE--QRF--CAY-SGEKITIDQLQEK---LEIDHIIPIYSI-SFD---DSYMN
291276265 Helicobacter mustelae 12198 : H--YFHIEFTRDVC--KAKSARQMLEKINKNK--SENDASQLLEVLGL-----FNTYMMI-----LKC-RLWQK--QEY--CLY-SGEKITIDHLQDRA---LQIDHAPFLS-LKD---DSQSN
229113166 Bacillus cereus Rock1-15 : N--TIRFVANDLA--KTYQRKLESTLKKNR--AENKIKTKLLSMGII-----VYK-KLWEE--QSGI--CLY-TGROMLESLFKPGY---SIVNHIIPYK-SFD---DTHYN
222109285 Acidovorax ebreus TSPY : I--AVNIEMARDLS--RPLDERNKVKRAQEFER--DRNDARSEFERDFGY-----KPKAAF-----EKW-MLYRE--QLGQ--CAY-SQQLDQLRVLLDHHY---AQVDHALPYK-SYD---DSKNN
189485225 uncultured Termite group 1 bacterium phylotype RaD17 : D--QINIELATELK--NSKFDRSKIEBQKQKFQ--SQDKLIFEVQELRGM-----TPSSALF-----LKY-RLWRE--QDER--CVY-SGRKISFELDLTGF---YDIDHIIPIYSI-SMD---DSFPN
182624245 Clostridium perfringens D str. JGS1721 : V--RINIELARDLA--KMFDRKILIEKQKERN--ANLDKIRENLRELMDK-----EPTVVEV-----LKY-RLWQK--QRGE--CAY-TQSQPIERLRLSPGY---CEIDHIIPIYSI-SFD---DSLNS
220930482 Clostridium cellulolyticum H10 : Y--MVNIELAREAG--MTRQDRDNLKHEHNNR--KAREKISDLIRQNGR-----VSGSDI-----LKW-RLWED--QGGK--CAY-SGKPIPPCDLLNDSL---YDIDHIIPIYSI-SMD---DSYMN
154255055 Parvibaculum lavamentivorans DS-1 : D--RIIEVDRDVG--KSKREBEIQSIRME--KQKATBDILKNGIA-----NPSRDI-----EKW-LWKE--QGR--CPY-TQDIGNALPFRGR---YEVDFIIPRSV-LKD---NSPN
257413184 Roseburia intestinalis L1-82 : Q--AINIELAREMS--KTFEERRIKGMEKRO--KMNEDVKIQIQL-----GLKS-----LKY-RLWQK--QGI--CMY-SGKTIPELEKFKGY---DIDHIIPIYSI-TFD---DSFAN
116627588 Neisseria meningitidis 22491 : A--RIHIEAREVQ--KSFDRKEIEKRQENR--KREKAAAKFREYFPNFVGE-----PKSKDI-----LKL-RLYQE--QHGK--CLY-SGKINLGRMLEKGY---VEIDHALPFSR-TWD---DSFPN
150622992 Pasteurella multocida subsp. multocida str. Pm70 : A--RVHIEGRELG--KSFKERRIEIQQDENR--TKRESAVQKFKLFDSDFSSE-----PKSKDI-----LKF-RLYQE--QHGK--CLY-SGKINLGRMLEKGY---VEIDHALPFSR-TWD---DSFPN
319941583 Sutterella wadsworthensis 3 1 45B : V--SIFVEENKFFP--SASVADLK---K-----NKRVKDKM---LSEAELKLETRWLKN-----ERF-KKA--SRGT--CPY-TGDRLAGK---GEIDHIIPIYSI-KDARDIYVNAEPN
254447899 gamma proteobacterium HTCC5015 : I--PIIEENQFSP--TABLEIKRGRGS-----AKAKA-----KELGEKSKAGVSKT-----ERI-KTS--SEGI--CPY-TGAPLQGS---GEIDHIIPIYSL-TGRTKTVFNSAN
542961328 Legionella pneumophila str. Paris : I--PIVLEQNRFFP--EESFKIK-GSSS-----DRTLEG-----ALEKQNIQWEKRF-----ERI-INA--SMNI--CPY-KGASLDGQ---GEIDHIIPIYSL-SKKHFGVFNSEVN
331001027 Parasutterella excrementiformis YIT 11859 : I--PVAIEMSNFN--TASITLQYIQLK-----EQKLIKLEIQIQRNEQKWLKSE-----PTQDI-----ERI-INA--SMNI--CAY-TGRPLDQ---GEIDHIIPIYSL-TLKSYSYFNSEVN
34557932 Wolinella succinogenes DSM 1740 : V--PILEQNAFVE--EESLRKSTGSDN--RVINSKDRDKQKLAKAENADRDKDKD-----RRI-KAF--SSGI--CPY-CGDTITGQ---GEIDHIIPIYSL-TLKIYTVFNEGN
118497352 Francisella novicida U112 : I--PIITESNAFEP--EPALADVKGSKL-----DRRKK-----ALERISFENLKKDN-----KRI-KEF--AKGI--SAY-SGANLTGD---DFDGAKEELDHIIPRSH---KYYGTVNDREAN

Motifs : E { HNH * ** *
#positions selected for tree reconstruction (272) : *****


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303229466 Veillonella atypica ACS-134-V-Col7a : FRHNNTFI -----KV-----RSLNHHHAKDAVLIIVGNVYH-----EK--FTR-----NFRLLFFKNGANR-----TYNLAKPFIYNDVICT
34762592 Fusobacterium nucleatum subsp. vincentii ATCC 49256 : FRMFDFPI -----KV-----REINDTHHAKDAVLIIVGNVYH-----TK--FTE-----KPYRVLQKIKE-----NYDKMFIYNDI
347430778 Filifactor alocis ATCC 35896 : FRKKPLAYI -----KV-----RQVNDYHAKDAVLIIVGNVYH-----KK--FTS-----NPIQWKKNRDT-----NYSLNKVFBEHVTIN
320528778 Solibacterium moorii F0204 : FRNKDKKELP -----KV-----REINDLHHAKDAVLIIVGNVYH-----TK--FTE-----KPFNNIENE-----NYSLKKVVFQFV
291520705 Coprococcus catus GD-7 : FRQTYELL -----KV-----REMDLHHAKDAVLIIVGNVYH-----VK--FTK-----NAANFIRNNDGR-----SYNLKRMFFEDIERE
42525843 Treponema denticola ATCC 35405 : FRNKFDIV -----KV-----REINDPHHADAVLIIVGNVYH-----TK--FTN-----NPNWFIEKERNPKIAD-----TNYNYVFDYDVKRN
304438954 Peptoniphilus duerdenii ATCC BAA-1640 : FRQEFDII -----KV-----RTVNDLHHHADAVLIIVGNVYH-----TK--FTK-----NPLNF1KDKDNVR-----SYNLNMFYVDVVRG
224543312 Catenibacterium mitsuokai DSM 15897 : FRVKNHIY -----KV-----RQVNDYHHAHDVLIIVGGFMR-----NR--YFN-----MHSKAV-----YSEYKMFRRKNNQ
24739809 Streptococcus mitis UA159 : FRKDFELY -----KV-----REINDYHHAHDVLIIVAGKALL-----GV--YQC-----LEPEFVGYDPHFHGHE-----NKATAKFFSN1MMFFIK
313067738 Streptococcus pyogenes S170 : FRKDFELY -----KV-----REINDYHHAHDVLIIVAGKALL-----GV--YQC-----LEPEFVGYDPHFHGHE-----NKATAKFFSN1MMFFIK
16011805 Streptococcus innocuus Clp11263 : FRKDFELY -----KV-----RDVNDYHHAHDVLIIVAGVANTLL-----KV--YQC-----LEPEFVGYDPHFHGHE-----NKATAKFFSN1MMFFIK
116628213 Streptococcus thermophilus LMD-9 : FRKDFELY -----KV-----REINDPHHADAVLIIVAGKALL-----KV--YPK-----LEPEFVGYDPKYNFSE-----RKSATKFFSN1MMFFIK
323463801 Staphylococcus pseudintermedius ED99 : FRKKFDPI -----KV-----RQMDAHHAHDVLIIVAGVYHGAQ-----LA--YFN-----VDLF-----DFN--FKWEKV-----REKWKALGFNTKQSRLEF
352684361 Acidaminococcus intestini RYC-MR95 : FRHEPGLV -----KV-----RNINDLHHAKDAFLIIVGNTYH-----ER--F-----NRKRWFMVYVSVTKT-----NRKRWFMVYVSVTKT
302336020 Olsenella uli DSM 7084 : LREAAGLV -----KV-----REANDPHHADAFLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
369839953 Oenococcus oeni DSM 17330 : MRKYVDPI -----KV-----RDVNDYHHAHDVLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
310267738 Bifidobacterium S17 : MRKYVDPI -----KV-----RDVNDYHHAHDVLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
259509199 Lactobacillus rhamnosus G3 : LRKDFEFP -----KV-----RDVNDYHHAHDVLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
300361537 Lactobacillus gasseri JV-03 : LRKHLNLY -----KV-----RQVNDYHHAHDVLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
169823755 Finegoldia magna ATCC 29328 : LRKDMNTL -----KV-----RQVNDYHHAHDVLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
47458868 Mycoplasma mobile 163K : LRKQIAFV-GIKNNKTEREWRKPEGFK -----SI-----NSNDFLIEEKGKNDVKDVLKDRSPGHHAEDAVYFIIISQYFR-----SPKRIER-----LNVNRYKE-----YLDLLEKNNIKFK
284931710 Mycoplasma gallisepticum str. F : LRKNFDD-----SSYAK-----K-----DRDKN1IHAVDASIIISFNPTK-----TL--FNOL-----TQFADYKLFKN-----TDGSMKIDPKTGVV
363542550 Mycoplasma ovipneumoniae SC01 : FRKPVQKNGPNENLN-----NKPEKIE-----K-----NRENNHHADAIVAIIGKNNP-----QI--ANLLTA-----DNKTKRFLH-----DENYKNIIE--TQEL
394332386 Mycoplasma PG 14 : LRKDFEFP -----KV-----RQVNDYHHAHDVLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
71894592 Mycoplasma synoviae 53 : LRKSMWRK -----N-----QVVRFNPKWKKRDQFPFHAVDASIIIAIFSLKLTLYL-----NK--LRV-----EYDVFQVQREDC-----RVLNKTDEQVKKAD
238924075 Eubacterium rectale ATCC 33656 : MRCNLKL -----KV-----RQVNDYHHAHDVLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
116627542 Streptococcus thermophilus LMD-9 : LRKHGIE -----KV-----KTRDTHHHAHDVLIIVAGVYHGAQ-----WKK-----QKNTLVSYEDQ-----LIDLLETGELISDDEY
315149830 Enterococcus faecalis TX0012 : LRKKGAD -----KV-----KTRDTHHHAHDVLIIVAGVYHGAQ-----WKK-----QKNTLVSYEDQ-----LIDLLETGELISDDEY
315659848 Staphylococcus lugdunensis M23590 : LRKVKFK -----KV-----RHHYKHAHDVLIIVAGVYHGAQ-----WKK-----QKNTLVSYEDQ-----LIDLLETGELISDDEY
160915782 Eubacterium dolichum DSM 3991 : FRKINLK -----KV-----RQVNDYHHAHDVLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
394332386 Mycoplasma PG 14 : LRKDFEFP -----KV-----RQVNDYHHAHDVLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
310780384 Ilyobacter polytrophus DSM 2926 : LRARMLN -----KV-----RENDLHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
325677756 Ruminococcus albus 8 : FRWRV LN-----EK-----TWGRYDKA-ELKLLTYLHADAII IANCRPEVYVVLAGEKLLKLN-----MHQAKRIT1PEYEQSKKACIDNLKYLFRMDTRTEAKLLSGSGKTD
187736489 Akkermansia muciniphila ATCC BAA-835 : VRKAVDF -----KV-----FKELCPAADDPSGKILKENRSLTHLHLDACVGLIPIYIP-----AH-----LAD-----HNLRLVLMRRI-----HNLRLVLMRRI
117929158 Acidothermus cellulolyticus 11B : ARRWDLS -----IE-----FSRVAIFAQSTTKRLDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
189440764 Bifidobacterium longum DJ010A : ARRAAGIE -----QR-----IHF1GQQSKTRLDRRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
283456135 Bifidobacterium dentium Bd1 : ARKASGIE -----QR-----IHFAGEKTKELDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
394332386 Mycoplasma PG 14 : LRKDFEFP -----KV-----RQVNDYHHAHDVLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
187250660 Elusimicrobium minutum Bel191 : LRMAWGL -----GL-----MIPFAKQLITKEESEPNKDNVSNKIRLDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
319957206 Nitratifactor saluginis DSM 16511 : TRSLGK -----KV-----SRETFHHAHDVLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
325972003 Sphaerochaeta globus str. Buddy : LRKANWL -----GI-----DSSLGRHWSKDAITSPMKRRDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
261414553 Fibrobacter succinogenes subsp. succinogenes S85 : LRKDWGN -----SV-----LGHNTDQTPAKSRDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
60683389 Bacteroides fragilis NCTC 9343 : LRBDWGL -----DV-----MKELNWEKYLKALGVEYEDRDKGRKVTYINWTKRDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
256819408 Capnocytophaga ochracea DSM 7271 : LRKAWGL -----GL-----KQ-----DKRVEDDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
90425961 Rhodospirillum rubrum ATCC 34411 : LRKAWGL -----GL-----LGLGKRNDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
373501184 Prevotella micans F0438 : FRKILGL -----GI-----FRKIDRSLHSHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
294674019 Prevotella ruminicola 23 : FRKMGW -----ES-----FIDENWKKHYK--DKDRDKHTHTTDAITACMPKDYK-----DL--LAH-----AWRLEQDKKAAKVLIE-----QAKPKFTKEDIKI
365959402 Flavobacterium columnare ATCC 49512 : FRKMGW -----ES-----FIDENWKKHYK--DKDRDKHTHTTDAITACMPKDYK-----DL--LAH-----AWRLEQDKKAAKVLIE-----QAKPKFTKEDIKI
312879015 Aminomonas paucivorans DSM 12260 : LRKQWGL -----KV-----RKNGLDHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
83591793 Rhodospirillum rubrum ATCC 11170 : LRLAADIT -----INQ-----PGAPARDLLTPRDLALDDTAARFRLDGLTPPLAKAVEGAQRLAALGRSRVADAGLADLGLTLASLGGGKNRDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
294086111 Candidatus Puncicepstrillum marinum TMCC1322 : LRQFWGL -----SI-----LRGHNTDQTPAKSRDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
121608211 Verminephrobacter eisenaei EF01-2 : LRKQWGL -----KV-----LGLGKRNDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
344171927 Ralstonia syygii R24 : LRKAWGL -----RV-----LDGMEQGRVAVKRRDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
159042956 Dinoroseobacter shibae DFL12 : LRHWGL -----SL-----LSDAGRQVAKNRRDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
288957741 Azospirillum sp- B510 : LRHWGL -----AI-----LAEADGPPVPAETLDPSAPAKNRDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
92109262 Nitrobacter hamburgensis X14 : LRKQWGL -----DL-----LPSDNYAGVQDKAEFLASDDMEFSGVNKRDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
148255343 Bradyrhizobium sp- BTAi1 : LRATWGL -----DL-----LPGSDRA-AKSRKDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
34557790 Wolinella succinogenes DSM 1740 : LRQWGLE -----SK-----DRSSTHHAHDVLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
219563121 Campylobacter jejuni subsp. jejuni NCTC 11168 : LRHWGFS -----EK-----DRNHHLHHAHDVLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
791276265 Helicobacter mustelae 12198 : MRSPGQV -----EK-----NRDHLHHAHDVLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
229131366 Bacillus cereus Rock1-15 : LHSRWGN -----KN-----SREYLNHHAHDVLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
222109285 Acidovorax ebreus TPSY : LRARWGL -----KV-----RQDSDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
189485225 uncultured Termite group 1 bacterium phylotype RaD17 : LSYNWGMS -----KV-----REESYFHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
182624245 Clostridium perfringens D str. JGS1721 : LRSRWGL -----KV-----REDDGKHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
220930482 Clostridium cellulolyticum H10 : LRSRWGL -----KN-----REESDHLHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
154250555 Parvibaculum lavamentivorans DS-1 : LRKLWLN -----NT-----LADGGEKTRDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
257413184 Roseburia intestinalis LI-82 : LRKRWGL -----QK-----NRETDTHHAHDVLIIVAGVYHGAQ-----KR--HPS-----VYDNP1GLARIMEDYARMQ-----AREYKSHCLLQGTQVINS
218767588 Neisseria meningitidis Z2491 : LRQWGL -----KV-----RAENDRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
15602992 Pasteurella multocida subsp. multocida str. Pm70 : LRSRWGL -----KA-----RNNRHHADAIVAVDTQKAI-----NR--ISN-----ISYKELKNCKDVP1SEYHA-----LDETEYVFEEVRLT
319941583 Sutterella wadsworthensis 3 1 45B : IKNLANKI--REELQNWCTTNNRHLFQAQATNV-----SDAKNRLKLAQNQDFEK-----PDIQPIASHSIDALCSFVAGSAD-----AERDQNGFDYLDGKTVLQ-----LYPQCEVHILQAKQBEKSHFDVS-----ALFK
254447899 gamma proteobacterium HTCC5015 : AKI1ASKL--AEHL-----DKQRDYTLSAHQIDP-----WVSVKQRKMLASAEP1WAK-----KDPQPAASHVVDVCTFLALEAO-----PHTASRLKTIISSTFEEKTGWRSALIPDLKVDALDRPKYRKYNGT-----SLFK
54296138 Legionella pneumophila str. Paris : GRQIMFPL--STLA-----DSKQLQLEFSLKQITA-----EVSVDHREKLESLKQPKFLV-----SRQSFPSHAIADTLTMSIGLE-----FPQFQELDNSWF1NH-----LMPDEKVNPNRSKIKYKNPNISST-----PLFK
331001027 Parastutterella excrementiformis YIT 11859 : VRS1FSKV--RQLAAMTQCTQNELLIDASIVPA-----ADSSMRKFPALYEPFRK-----PKVQYASHSIDAMCIYLAACSDFPK-----PKVQFASHSIDAMCIYLAACSDFPK-----LFTQSCVQIANTPRFSDKNLST-----PIFK
34557932 Wolinella succinogenes DSM 1740 : AKI1QKLL--TKML-----PNRHLSEFLILADA-----TEVSELRQVYAKNPLLAK-----AEKQAFPSHHAIDAVAFYQKVPKDTGP-----NADEVKALAMDSDPNASNE-----LTKGLSTQKLEKMKKSGDYGKQKMFEPKQ-----SIFG
118497352 Francisella novicida U112 : AEVLNANI--YLRA--KKNLNTDKISFDYGIPTGNG-----RG1AEIRQLYEVKSDS1QAYAK-----GDKPOAYS1HLIDAMCFIAAEDHNDGSG-----LEIDKNYS1LPLKNTGVEV-----FTKD1FSQ1KIT1DNFSDK--KLWRK1EMLFNGHTQKTR

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Motifs : _R * * RNaseH_III }
#positions selected for tree reconstruction (272) : *****

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303229466 *Veillonella atypica* ACS-134-V-Col7a : NAQD-----GKAW--DVKTSMTVK-KM-----MANSNDR--VTRRLLEQ-----SGALADATI-----YKASVAAKADGAYIGMKTKYSVFD--VTKYGGMTKIKNAYSIIVOYTGKK---
34762592 *Fusobacterium nucleatum* subsp. *vincentii* ATCC 49256 : ----KNTV--KNMW--DKENSLIVKRM-----DKNTV--TRFPIKE-----KGLFNPNP-----IKGQTSNEIISIKPKLVDGDKNL--NKYGYYSLKAAYVIVVEHKNK--
374307738 *Fillifactor locis* ATCC 35896 : G-----EVTV--EKCTYHEDN-YY-----DGGLDRIRIKVERNDIL--IYEYAYCE-----KGFENATI-----QMKNGSYVSLKGLD--VKYGGYFSAMTSYFSLIF--
320528778 *Solibacterium moorii* F024 : ----DRII--FGAW--DAKSTPTIYIKY-----MARNPLI--IAPAYEV-----KGLDFYQI-----TIKPKNSGSKQIPKQGD--TKYGGYKNSLAPFAYE--YKAKAR--
291520705 *Coprococcus catus* GD-7 : G-----EIAW--KAGMKGSIYTKK-----VMQNNIL--VTRKAYEV-----KGLDFDQI-----MKKGQVPIKGNDRGLAD--IKYGGYKNAQTYFVMLSLDKGK--
42425843 *Treponema denticola* ATCC 35405 : N-----ITAW--EKGKTIITVK--DM-----LKNTPII--YTRGAACK--KGLDFNQTI-----MKGLGQPLKLEGGPFSN--ISKYGGYKNSYAAITYLIEYEK--
305443954 *Pectoniphilus duerdenii* ATCC BAA-1640 : S-----YTAW--IADDSGEVNAKTIK--K-----VKRELEGGNYR--FTRMSYIG--TGGLYQNLN-----MRKGGQIPQKENTKAG--IKYGGYKNSYAAITYLIEYEDGKAG--
224543312 *Catenibacterium mitsouaki* DSM 15897 : KRKKGDFVNSMNYVYEDGKLIWV--PDLINEKCK--FYKDYC--CTKLDQK-----KGFNLNIVY-----LSDNAHADRGVTKAVVPMNRSRSD--VHYGGYSGLOVTVLIEIQKKGK--
24379809 *Streptococcus mutans* DA159 : ----DDVR--TDKNGEIIW--KDEBHSINIKNVLSYQVNVK-----KVEEQ-----TGGFSKE-----SILPKNSDKSLIPKTKFYFD--NKYGGYDPSIIVYSLIVLADIEKQ--
15675044 *Streptococcus pyogenes* 1370 : --LANGE--TRRPLLETRNGE--EVMW--SEEDKILYK--VM-----DKGRDFATVYR--LSMPCQVYTK-----KTEVQ-----SILPFRKDKLARKVYV--NKYGGYDPSIIVYSLIVLADIEKQ--
160181805 *Listobacterium elii* 11262 : ----DRII--DENGE--ELW--DK--KYLK--VMYRQMVYK-----DKYVYK-----KGLDFYQI-----TIKPKNSGSKQIPKQGD--TKYGGYKNSLAPFAYE--YKAKAR--
116628213 *Streptococcus thermophilus* LMD-9 : --LADGR--VIERPLLEVNTEGSEVW--NKESDLATVRRVLSYQVNVK-----KVEEQ-----NHGLDRGKPKGLFN-----ANLSSKPKNSNENLVGAKAY--LD--PKYGGYAGISNSFTVVGTEIKG--
323463801 *Staphylococcus pseudintermedius* ED99 : : FPKKLEKM-----EVQGERL-----ISKILDMNHFKNYSR--K-----KLANI--PQGFYNG-----TAVSPKTAELKYSNKSIN--S-----EYVYKGL--TPYQTVVVALKSNYKGG--
352684361 *Acidaminococcus intestini* RCY-MR95 : --LFTHSIK-----NGNF--VAVNGEEDLGRVIMKLKQNTIHTFTRP-----SDFRK-----DIQPLKASTGLVPRKAG--LD--VYVYKGL--TPYQTVVVALKSNYKGG--
302336020 *Olsenella ulii* DSM 7084 : FLSGG--FDEBTEGEIFK--DDWDAKEVGEIRVNLNCRQCFISRMPPV-----EGDTR-----YGGYRWG-----ETIYSYKPKGHKHEIPLKQG--LD--PNLYGGYDLSLIVYLYEASDVSS--
366983953 *Oenococcus oeni* DSM 17330 : GFVVSGMRNAAPOKRLNPTGTEIPEENADWSI--ADDLVLKHMFRKTIIVTR-----RLKQD-----YKQYDES-----RYSPLVLDHAKSKASINFQK--KP--VLYGGYSGSAFAYALI--
110286728 *Bifidobacterium longum* S17 : : RQDQEQKRVNRTFG-----EVMW--SEEDKILYK--VM-----NYRKMV--VTQVGDQ-----FGALYDTR-----YAATDPRKGLLARKVYV--NKYGGYDPSIIVYSLIVLADIEKQ--
259509199 *Bifidobacterium rhamnosus* GJ : : HAKKNIKAKDGG--EIVW--DKERDIFELD--RE-----NYFKML--ITEHYVEF-----TADLFKQTI-----YAAKSKERGSGKQIPKQGDY--TYVGGYDPSIIVYLYEASDVSS--
300361537 *Lactobacillus zhangou* VJ-003 : : NEFI-----SQIFENKSNDSIISLETKKVV--FKDKDIIIEKHAYW--YKYMVLSR-----VTRFDQEM-----FMTIVVPRLSRDRSKSRNLISKMDP--PKYGGYDPSIIVYLYEASDVSS--
169823755 *Finegoldia magna* ATCC 29328 : G-----KVITPTEKGRKLIIVDTL-----NPKSVL--ISNEHSYK-----KGLDFENATI-----AGKKDYKKGKLIPLPKDRDLQD--VSKYGGYKNAQTYFVMLSLDKGK--
47458868 *Mycoplasma mobile* 163K : 47458868 *Mycoplasma mobile* 163K : : KASFP--DNFLINLALD--EL-----NEKLNQMR--FSRMVITK-----KNTQLFNETL-----YSKDYKQKNTIKKVEKLNLDNRDKI--KKIEFFEDDKLEKMLKHFNH--
284931710 *Mycoplasma gallisepticum* str. F : : TEVT--DENW--KQIRVNRQVS--E-----AKVIERKYQDSNIRKAR--YSRKLBNK-----TNSLFDNVTYSAKKVGEDQIKRKNLKTLDIHSAKENKNSKVRQVYKRLVNSLNL--NDKLADLPAEKDILMYRANPWVINA--
363542550 *Mycoplasma ovipneumoniae* SC01 : : KIKI--K--FEVDKIAKVE--DL-----K--IKIQEKYEAHKHTPAK--FSRKTPII-----LNGGLSDIITLYGFKYDEKDK--YFKIHKVIVT--SKNEKLYFENPFGKADGSEBYTLV--
394393286 *Mycoplasma pneumoniae* PG 14 : : KELK--KEW--TKIKNLEK--VM-----AKEIEEVLID--LDEYFV--FSRKNRQK-----TKGLNBTIETIGIATKTDGDTW-----TYGKESKILD--SKDYLFRKGLLARKVYV--NKYGGYDPSIIVYSLIVLADIEKQ--
71894592 *Mycoplasma synoviae* 53 : : : KDWKDHQNFILKRENAIEI-----KNVNLNVDPOQNV--YSRKNYK-----LANTQLFNETL-----YQVKEFENNFKYKLVNLSRDKLRFPLIL--EDLNESEBKNKNKNGSRRKLLA--
238924075 *Eubacterium rectale* ATCC 33656 : : DYLY--GCKW--AMINREVKA--K-----EKNV--MHYVMRQK-----SBRNCLNGT-----RGTEYDQYKQYIKMLDIRTEKQIVFA--KLFASFKKDSBRERLWYLN--
116627542 *Streptococcus thermophilus* LMD-9 : : KESVF--KAPY--QHVFDTLKSX--EF-----EDSIL--FSYQVDSK-----FNRKISDATT-----YATRQAKVGKKADETYVGLKIDDIYQDGYD--APMKIYKPKSFLMYRH--
315149830 *Enterococcus faecalis* TK0012 : : QVKN--QVKN--PNF--RE--QL-----KPVNLHPRKL--FSHQVDRK-----ANRKLSDATI-----YSVREKTEVTKLGGKQITDYTEYIGKIKDYD--DWEAFKPKQDKMLDKL--
315659848 *Staphylococcus lugdunensis* M23590 : : : EMFIIIPKQVQ--DI-----KDFRNF--YSHRVDDK-----PNRGLINDTL-----YSTRKDNSTYVQTIKDIYAKDN--TTLKQFDPKSPKFLYQH--
160915782 *Eubacterium dolichum* DSM 3991 : : YY-----DTRY--FAFIASLKA--I-----KVRK--FSHKIDTK-----PNRVADETI-----YSTRVLDGEEKVVKYKDYV--DPKFTLAEIILNAYQEKYALMALH--
160915782 *Eubacterium dolichum* DSM 3991 : : : AEAQRMDADLNKIFNFG--FLPW--LDFEKLRLYK--VM-----NPFVBMKSRSNYITPIELAKLFV--VRLANRQ-----LSCALHEFTF-----RSALKFDEKGLVLSRVSITLKNKGGV--ATGKGLRVD--EFCDFEKLRLYK--
310780384 *Ilyobacter polytropicus* DSM 2926 : : RP-----PMPW--SGDPLEKRLSEMPREFFYN--L--LSDKRYLQWYVE--GPIEKILVY--YSRMPRG-----VKGQAQHTI-----RKMKLSINQIYVS--KPLNSIKLXDLKMQGRDT--
325677756 *Ruminococcus albus* 8 : : PIIPLNDSSEVDLKNVIEQFW--K-----KDKDKKSCX--EL-----YRENASLYGDPKPKFASLSMPV--ISLKDPHG-----YRGTITGEEA-----IRVKEDIGKLIKLRKRSISEITA--SINISYTD--
187736489 *Akkermansia muciniphila* ATCC BAA-835 : : : PEKL--L--PQVRFVAN--QRHVIND--DGRMRLRD-----DGRMRLRD-----SASLKENIRLEQMEQRVGHV--ADMGGALLETMQRVLSV--
117929158 *Acidothermus cellulosilyticus* 11B : : TEEPQSPA--YRQW--KESCSGLGDLIS--S-----TAARDSIA--VAAPRLRL-----PTGALHEFTL-----RAFSEHTVGAWKGAELRRLE--PEVYAAFLATDPPGGFLKVPSP--
189440764 *Bifidobacterium longum* D010A : : : YES--LNDRIAV--MQSQRYVL-----LNDRIAV--MQSQRYVL-----HPLEKVPVLSGAMSADLIRRAST--PALWCAKLTLPDDEKGL--
283456135 *Bifidobacterium dentium* Bd1 : : KTR-----FKEW--DMDMNLDDLLD-----ALDSRIVPV--TRQRMSL-----GNSQAHAATI-----RMRKRVELFSPMDADLIRRAST--PALKYCALTR--LPEYSPKGL--
39232679 *Bifidobacterium denticolus* NCTC 13129 : : : RAA--WEP--QFMEKRLVYK--VM-----DLADRELV--MGLWV-----ARGKAEDATI-----KQREIIEBIRFEPKVE--KLMDLKEIPIKPIQVSPDRL--
178205660 *Eluimicrobium minutum* bel191 : : : LSKILLDPN--NIVW--ENIDADLESF--ES-----SVKTKANAF--ISVHSDS--DNGLRVKGTW-----YKIFSERGYTITTYKLSAKLITDPPQ--KTKPKDFLITALLKFKGRESMNEKI--
319597206 *Nitratifactor saluginis* DSM 16511 : : TLADYI--R9HMDTIRS--DEAF--RFMSKGEES--LF-----YRDMDTIRS--ISYVDDK-----PLSASSHGTV-----YSSRHVPTLRKILAEFDSLNVDIRKHTL--EEMFKRYDKIIBALHLRIGNT--
325972003 *Sphaerochaeta globus* str. Buddy : : : MIPY--PGYASPNLSFEA--K-----QRELFPRKILBFMDLHAF--VSMKTDND-----ANGALKDTV-----YSILGADTQGEDVFWVKKIKDI--GVIGDYVEVAISGRIT--
261414553 *Fibrobacter succinogenes* subsp. *succinogenes* S85 : : : IDGKEREVAKEF--LKPDL--DFSFSDSKNILEN-----IIVSFKQNRVINKTRKKG--FLHFDENGK--KTFIKQKGGDSWAKRILSHEDTI--FGENLNRKRVSNLNEAKVPERVNLKLRKLE--ELKNNLPPKAFAGNKLSDRQIWLDEKQ--
60683389 *Bacteroides fragilis* NCTC 9343 : : : A-----PMLD--REFRAEAKKHLE-----TLISIKAKNKVITGNKTRKKG--VMNKMOQT-----PGRQLHLETI-----YSGKQYLTKEEKNVNASFDMRKTGVSASAYRDLKRLYV--DNDNPKKAFAGNKLSDRQIWLDEKQ--
256819408 *Capnocytophaga ochracea* DSM 7271 : : : NGKNKRVFE--PIP--NFRQVAKKHLE-----IPISHKANNKVVTKNPKP--AGT--DRQQIITL-----PGRQLHLETI-----YSGKQYLTKEEKNVNASFDMRKTGVSASAYRDLKRLYV--DNDNPKKAFAGNKLSDRQIWLDEKQ--
394255961 *Rhodospudomonas palustris* B18b18 : : : DIF--HC-----RQFADRVRTVYGSST-----MQFI-----ARGKAEDATI-----KQREIIEBIRFEPKVE--KLMDLKEIPIKPIQVSPDRL--
373501184 *Prevotella micanis* F0438 : : : EKK-----DCRV--GRVNDLDF--E-----INENIIV--SHHTYQDA-----LTPAHRLEKR--GKIVGKHEHW--QDGLSBEIHK--ASYGAIQTFADKANGKYLKMDQQAQI--
294674019 *Prevotella ruminicola* 23 : : : PTF--DKPW--PSFVINDI--KH-----QDLELI--AHYAKND-----KFEKTKNLKRDK-----GRIIRDKFNGLKMQKSDTSNSLHN--DKFYGALIPKYSYVRYTNI--
365959402 *Flavobacterium columnare* ATCC 49512 : : : ETEILVSHFTPNVKKQ--SKSILKNRKKVYVKNL--EL-----PVNFKNIEGKDYFKLFPDSKI--LVKIPKK-----EKQDITFYEBEL-----KNYLVGEGKDYFKINTGTTFYKIPFNQDITRGLSLHQ--ETTYGALKLPDIETTKKPLTHDGGF--
312879015 *Aminomonas paucivorans* DSM 12260 : : : NGF-----SLPY--PAFRESVLARLPV-----TREIILLRDLQGGVYDEAFRNLRPVE--VSRAPSR-----LRGKAHMETL-----RSPKWKDPEGPRSHQ--RIPDLKLNLEKLEMMVKLR--
83591793 *Rhodospirillum rubrum* ATCC 11170 : : : TNF--EPPY--PTFRABVMQK-----WDHII--PSIRPAHR-----DQGLSHAATV--PGVNRNPARVLVORVPEKLFV--DANAKPLPAKIAIIDGFA--
294808611 *Candidatus Puncicepirillum marinum* TMCC1322 : : : GR-----IDPW--DGRFDEVKH-----IDAI--VSHRPRK-----SQCALINDTA--YGVHVAHAGSTVHRVP--GIREDG--RIRKPKAKSADI--
121608211 *Verminephrobacter eiseniae* EF01-2 : : : DM-----LLPW--PTYDABEVA-----URHTR--VSHRPHG-----FEGAMKKTATGHIRD-----YGVHVAHAGSTVHRVP--GIREDG--RIRKPKAKSADI--
344171927 *Ralstonia syygii* R24 : : : DM-----PTPW--PNFLDNRVA-----VAVCV--VSHKPDG-----PEGOLINDTA--YGVHVAHAGSTVHRVP--GIREDG--RIRKPKAKSADI--
159042956 *Dinoroseobacter shiba* DFU 12 : : : ARDT--PPPW--EGRDRLVRR-----LDRII--VSHRPHG-----RIDHAAKQRDRSTAGQLHQETA-----YSIVDDHVASRDLDS--LKPALDLEPGRSQVQ--
288957741 *Azospirillum* sp- B510 : : : RVLEGFK--EPWP--DGRFRELRR-----ARTIV--VSHRPHG-----IGGALKHETA--YGVDPPEEGFNLVV--RKPIDGLSKDEINSVR--
102109262 *Nitrobacter hamburgensis* X14 : : : VI-----LEKM--PTMRDDLKAA-----LEKMV--VSHKPDG-----IEGLHEDSA--YGVKPLDALTGLEEAGNLVY--RKAIESLSEKEDR--
148255343 *Bradyrhizobium* sp- BTA11 : : : L48255343 *Bradyrhizobium* sp- BTA11 : : : LLPW--PTFRIDLETR-----LKAML--VSHKPDG-----LQARLHEDTA--YGVHVAHAGSTVHRVP--GIREDG--RIRKPKAKSADI--
34557790 *Wolinella succinogenes* DSM 1740 : : : L-----AVPL--ANFRDAVEAETRI-----ENTETVKGVEVVKRLL--ISRFRAR-----VGGQAHEQTA-----KPYFRIKQVKNKWRPLAP--
220930482 *Cellulolyticum* H10 : : : F-----PEFP--SQRKVLK-----SLEW--PMSNKKIQES-----IQNII--FSHVSHK-----VTGELHQETV-----RTKEFY--YQAFGG-----
257413184 *Roseburia intestinalis* LI-82 : : : F-----PEPW--KFSFIELEARISP-----QVRDLIKLNLDSYLDVILHLKPVF--ISKPRPK-----VGAHKSTI-----RSLIGINEIKVTICITKRLPID--PNDNGPMDYKT--
218767588 *Neisseria meningitidis* 22941 : : : ARQH--PEPW--TFHAHLKARLFT-----DDLAAALREDMQRLGYSYTTEDLGRILTF--VSRAPQR-----SGGAVHKETI-----YAQPESLKQGGVIEKLLTSLK--QDFKLLNPENSDHVFPHR--
150262992 *Pasteurella multocida* subsp. *multocida* str. Pm70 : : : GEIISY--HEPEW--AYFRQVNVIRF--DNHDP-----VTLKEMLPDRQANHQVQPLF--VSRAPTR-----MSGQHMETI-----KSAKL--DQGVSLV--RIPQLKPLNEMLVN--KER--
319941583 *Sutterella wadsworthensis* 3 1 45B : : : GEIYAEQFLPFTLNE--KIWIQYE--TINAKGERGCAIEVSGKQPKLEMLLAPPFNK--PVGDLSAHTYRILKPKPAYEFLAKAAL-----QPLSABEKRLAAL--LNSIHFTQKTELRAKFSF--DSGK--
254447899 *gamma* proteobacterium HTCC5015 : : : DGIYARFRLILIDEN--GLMAGYD--IDNSLKAKGADVVESSLSPFLFK--GEEVGAQSLSDQERIDGRVLYMSIDKVKAFDYL-----QEVKGEKDLAAL--LNSIHFTQKTELRAKFSF--DSGK--
54296138 *Legionella pneumophila* str. Paris : : : DSIYARFIPVWVWGE--FPAIGS--EKDLFEK--PMSKELFTLKYSTNKPQSGSLQELQAKSKAWL-----YFPIKRLA--LFLHLYHFKIEVTPDPTVCHPINSRLRY-----TKES--ITVILKEPMLVLSFPESSKNVLLSFPKIALPAT--
331001027 *Parvibaculum lavamentivorans* DS-1 : : : : ETIYARFLDVISRG--EFIGYD--SMPFEKPNISIGKQDPSIISVLGALVAKAPSEKELTYRVKNAFELSKVAG-----SKFTABEDAKI--LEALHFTVQQAARVSD--LIKSK--DSIENHAKQKCKLKVVEYSK--EFPKSGSLIPAA--
34557932 *Wolinella succinogenes* DSM 1740 : : : ENAIGERYPLVIVQEG--GYIYQVATYKGELEKLVYTSKNDIAKLEIKNQDILSKENQYIKIFSNQTISELNSYNNMLVLRKEDIIVGLLEIVENCRYTKIKVDVFPKPYIETHYVYDFDWRPDEAMRY--LQENQK--TKSSK--DFVLIK--SLSNLYQDFK--
118497352 *Francisella novicida* U112 : : : DGIYAENYPLHLKHELENVKRGY--WNSKEIE--IFKGGVILQJLNLVLYKLVKDFKIPISIDIQISTLE-----ELRNLITPNNIAT-----AEYIYML--KTKLHEIENYNTALGVKKYKEMEFRLSLAY--RSERVK--IKSID--DVKQLDKD-----SNFJIKLTFPK--

#positions selected for tree reconstruction (272)


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303229466 Veillonella atypica ACS-134-V-Col7a : --RSTIGV-----KIHNLDFKII-NESITGLYSNEVTV-----
34762592 Fusobacterium nucleatum subsp. vincentii ATCC 49256 : EDTGRIRL-----GQSLGNKNEELLEESVTLGFVKIKL-----
374307738 Filifactor locis ATCC 35896 : -GSPVVK-----NTIGKSKILLV-NQSVTLGLYENRRRL-----
320528778 Solibacterium moorei F0204 : -AGVIVIP-----HFTKLSVFKVHQSTLGFPEKEMDLK-----
291520705 Coprococcus catus GD-7 : -AGILVMN-----NNITACKQISVINQSVPTGIYEKIDLKIL-----
42525843 Treponema denticola ATCC 35405 : -SGVAKIG-----NKISSLDNCILIQSITGFIFERIDLKLV-----
304438954 Peptoniphilus duerdenii ATCC BAA-1640 : -TGVVFP-----KKLNYKECKLI-NQSTLGLFENEVDLNL-----
224543312 Catenibacterium mitsukoi DSM 15897 : -----TKHNLNINIVFISQSPGTIYTKYKYL-----
24379809 Streptococcus kitaharae DSM 15159 : -----TSTTEILNATLHQSVTLGLYETRIDANLGGD-----
15675041 Streptococcus pyogenes SF70 : -----TSTKVELDATLHQSTLGLYETRIDLSQLGGD-----
16801805 Listeria innocua ClpI1263 : -----NMLKELNLSSTIYQSTLGLYETRIDLSQLGGD-----
116628213 Streptococcus thermophilus LMD-9 : -----TPSSLKDATLHQSVTLGLYETRIDLAKLGG-----
323463801 Staphylococcus pseudintermedius ED99 : -----TSISGLTKT--PKSLFKLAESRNL-----
352684361 Acidaminococcus intestini RYC-MR95 : -----SKKYSDRILVEQASGLFVSKSNLLEVL-----
302336020 Olsenella uli DSM 7084 : -----NPASFVLLDQSVTGMFERTRIGL-----
366983953 Oenococcus oeni DSM 17330 : -----TLADTDFPIQSVTGLFSTQKTVLAQLYQETK-----
310286728 Bifidobacterium bifidum S17 : -----FETVGLKRAKAKVNSKRNKRLPLSGASQP-----
259509199 Lactobacillus rhamnosus GG : -GLLQVGS-----GKLEKDTQIV-YQSPFGLFERPLADL-----
300361537 Lactobacillus gasseri JV-V03 : -LGFMQFS-----SGVLENSAKLIYQSTGLFERVKISDL-----
169823755 Finegoldia magna ATCC 29328 : -KP-----RITNLPDNTLYVYSITGIYEKIRIK-----
47458868 Mycoplasma mobile 163K : -----WKKV-NLTYMGEIFPK-----
284931710 Mycoplasma gallisepticum str. F : -FLMTLST-----ILNDYLLDAKDNDPLGLSKNRDEILNSKLGDKIVK-----
363542550 Mycoplasma ovipneumoniae SC01 : -VAPSTMP-----IPKEVPIHDB--LQNEYPVKIKHTDDKMLCTIK-----
394393286 Mycoplasma canis PG 14 : -LMPGLG-----KMTVGLQDIP--FKIK--KIFE-----
71894592 Mycoplasma synoviae 53 : -VSMK-----KTNPDDEYKILEHVPLGILNLAWTKLENNN-----
238924075 Eubacterium rectale ATCC 33656 : -----GLGKTKFIKY-RYDVLGNKYSCSEKFTSFC-----
116627542 Streptococcus thermophilus LMD-9 : -GQCKKG-----LGKSNISIVYK-RTDVLGNQHIKNEGDPKLDF-----
315149830 Enterococcus faecalis TX0012 : -NLNIAK-----YKGEKGLRKF-NTDLGKHKHLYEYKPKNIK-----
315659848 Staphylococcus lugdunensis M23590 : -----T-----IGKVNISEKL-TDVLGNVFTIYQTKPQLLFRKGN-----
160915782 Eubacterium dolichum DSM 3991 : -MRMPT-----ISKKIYPIKY-ATDVVGNLYVKRNTLKFEDF-----
336393381 Lactobacillus coryniformis subsp. torquens KCTC 3535 : -GLLGLFK-----GLGLLDFEKY-QVDVLGNVFKRQPLFVKRDE-----
310780384 Lycopobacter polytronus DSM 2926 : -MRI-----GKTKYKIKKY-QVDVLGNVFKRQPLFVKRDE-----
325677756 Ruminococcus albus 8 : -AVDLMG-----KVGQENNGKISGCEPLSLLEKKN-----
187736489 Akkermansia muciniphila ATCC BAA-835 : -NKTECNWREVDLISLLKQMKRYPYTYGTFP-----
117929158 Acidothermus cellulolyticus 11B : -KVLCHPLTVI-RRTALGQPRWRGRHLYSRRPWSADPWGGTP-----
189440764 Bifidobacterium longum DJ010A : -NTASKTAVRIV-RRNAPGEPRLSSAHHMPCSQWRHE-----
283456135 Bifidobacterium dentium Bd1 : -KGWVAV-----N-ILAKYHPVIRRNALGEPFRNTSNMGPVSRWDR-----
38232678 Corynebacterium hightheriae NCTC 13129 : -PWFJAV-----NRLSDGNVTVWRDLSLGRVIRNATVAFVFWVQ-----
187250660 Elusimicrobium minutum Bel191 : -QDSFTI-----NSMGQYNDREL-LSESQYIKVRSPLKNEKG-----
319957206 Nitratifactor salauginis DSM 16511 : -GIKAHL-----DLDGHVRSYEVFGLTPGSIWFKESSYGRVEDDPH-----
325972003 Sphaerochaeta globus str. Buddy : -DTSFTL-----TTIKNYDRKV-QLSAGLVRVSPLLVVKIEKDEVALCGE-----
261414553 Fibrobacter succinogenes subsp. succinogenes S85 : -DN-----KESIKDACVPV-ILDRLGNVIEFNGKRL-----
60683389 Bacteroides fragilis NCTC 9343 : -SSGLDTIVKV-RVNHIGQIVSVEY-----
256819408 Capnocytophaga ochracea DSM 7271 : -GLSLKDIVKY-RINHLGDIVSIGEY-----
90425961 Rhodopseudomonas palustris B1sB18 : -GLKTLASFKEP-TIDLRKRFIEFIEVRTWRGE--ACT-----
373501184 Prevotella micans F0438 : -PTAIRGKIKT-KPLMGKRRDFVRN-GNIEFKH-----
294674019 Prevotella ruminicola 23 : -RPLIVSYNPF-NALVQDLDFEINDLGEIRLLI-----
365959402 Flavobacterium columnare ATCC 49512 : --KINEN-----KPTRKMNNQF-TAFVGEIDFKVLPQKFKFI-----
312879015 Aminomonas paucivorans DSM 12260 : -TRKDLMSKY-QVDPLGEIRLVGSEKPPFVL-----
83591793 Rhodospirillum rubrum ATCC 11170 : -QSA-----EGIRKEKIRT-SC TALGRLLSKKAT-----
294086111 Candidatus Puncicepirillum marinum IMCC1322 : -SP-----GKLQASARKV-HISPTGLIREG-----
121608211 Verminephrobacter eiseniae EF01-2 : -DQLKRAKQV-TISPIRELDRPQFG-----
344171927 Ralstonia syyziji R24 : -KSP-----GALRDLGARRI-FVDLIGRVLDPGIKGD-----
159042956 Dinoroseobacter shibae DFL 12 : -GA-----RPAIASGIRRV-SVDEIGRLRDRGTRPI-----
288957741 Azospirillum sp- B510 : -DQLRARGARRV-RVDPLGRVIRVHAPGARVIGGDAGRTAMEPAEDI-----
92109262 Nitrobacter hamburgensis X14 : -LMASY-----NTLKLAAPV-RVDLGRVWRVMPN-----
148255343 Bradyrhizobium sp- BTA11 : -RWLFASF-----DKLEWNAELV-RIDTLGQPRWRKRGLETGSEDATRIGWTRPKWMP-----
34557790 Wolinella succinogenes DSM 1740 : -RKEFECQ-----GVKFLDKVYK-QIDPLGYEYVQKFKRLGTIPQMRSAKLWKK-----
219563121 Campylobacter jejuni subsp. jejuni NCTC 11168 : -GJMKLVFKY-----VSLALGVTKAEFRQREPK-----
291276265 Helicobacter mustelae 12198 : -MTRSC-----GIQGLVFKV-KLSVLGVELEHPRKQNIALKTTPKHV-----
229113166 Bacillus cereus Rock1-15 : -SLLARGI-----GKTNMLLEKY-QVDVLGRYKVGNEERQDKIQON-----
222109285 Acidovorax ebresus TFSY : -GVKTLSEKPY-NVDVLGRYILAPETRSGLA-----
189485225 uncultured Termite group 1 bacterium phylotype RaD17 : -GSRCLDFRKF-QVDVLGNVTEVHEKRMPIYTRKDKKH-----
182624245 Clostridium perfringens D str. JGS1721 : -LKVGVLEINKY-EVDVLGNVYKVKLGGN-----
220930482 Clostridium cellulolyticum H10 : -GVRTAISIEKY-NVDVLGNKSVKGEPRRGMKYNPSKSN-----
154250555 Parvibaculum lavamentivorans DS-1 : -NPIKDKAKV-SIDPIGRVRSND-----
257413184 Roseburia intestinalis L1-82 : -GIQSLDLEKC-QIDVIG-HVSVVRSKRRMGFS-----
218767588 Neisseria meningitidis Z2491 : -GVKTLSPQKY-QIDELGKEIRCPKRRKPPVR-----
15602992 Pasteurella multocida subsp. multocida str. Pm70 : -GVKTLSEKPY-QVDLGNKRCRQQRQPV-----
319941583 Sutterella wadsworthensis 3 1 45B : -LQQPR-----SEIFENVGNAKHIR-FWYIVVSNKMNESYNNVSKS-----
254447899 gamma proteobacterium HTCC5015 : -LIPPR-----SNLFLLETQKIT--FXYLANGANAIVKAYSLRRA-----
54296138 Legionella pneumophila str. Paris : -L-KPRD-----GKMKIVSTGKIVT--YFESDSTPQWITLYVTQLKQP-----
331001027 Parasutterella excrementihominis YIT 11859 : -LPKFREDNKH--GTFIEVLQPRVI--FNYIVGASLSKELFSEAKGERS-----
34557932 Wolinella succinogenes DSM 1740 : -KRMIFRAL--PEKEKGRKPKTT--ISFKESGPQDVLVFKIKVILQRLTDSGISN-----
118497352 Francisella novicida U112 : -MNHSLKRSY--PDKVLEILKQSTI--IEFESSGFNKTIKMLGKML--AGIYNETSNN-----

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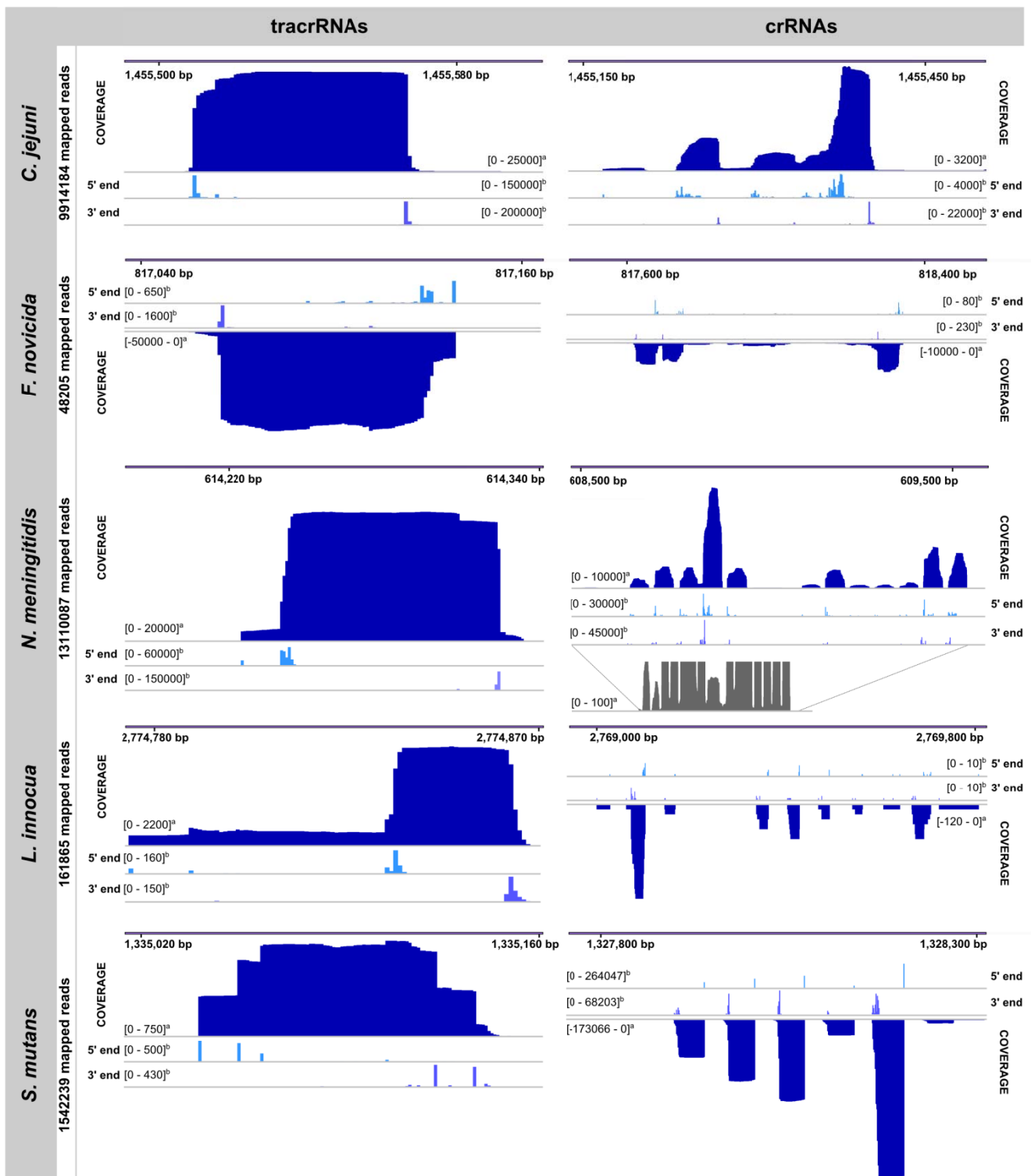
Motifs : _____G_____

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#positions selected for tree reconstruction (272) : _____

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Supplementary Figure 2. Expression of bacterial tracrRNA orthologues and crRNAs revealed by deep RNA sequencing. Expression profiles of tracrRNA orthologues and crRNAs of selected bacterial strains are represented along the corresponding genomes by blue bar charts (Images captured from the Integrative Genomics Viewer (IGV) tool). *Campylobacter jejuni* (GenBank: NC_002163), *Francisella novicida* (GenBank: NC_008601), *Neisseria meningitidis* (GenBank: NC_003116), *Listeria innocua* (GenBank: NC_003212) and *Streptococcus mutans* (GenBank: NC_004350). Genomic coordinates are given. ^aSequence coverage calculated using BEDTools-Version-2.15.0 (Scale given in reads per million). ^bDistribution of reads starting (5') and ending (3') at each nucleotide position are indicated (Scale given in numbers of reads). Upper panels correspond to transcripts from the positive strand and lower panels correspond to transcripts from the negative strand. The negative coverage values and peaks presented below the axes indicate transcription from the negative strand of the genome. Predominant 5'- and 3'-ends of the reads are plotted for all RNAs. Note that given the low quality of *L. innocua* cDNA library, the reads are shortened for crRNAs, and an accumulation of the reads at the 3' end of tracrRNA is observed, presumably due to RNA degradation.

Supplementary table 1. Bacterial species containing type II CRISPR-Cas loci characterized by the presence of the signature gene *cas9*.

Cluster ^a	Strains ^b	Cas9 GI	Length (aa)
1	<i>Enterococcus faecium</i> 1,231,408	257893735	1340
	<i>Enterococcus italicus</i> DSM 15952	315641599	1330
	<i>Listeria innocua</i> Clip11262	16801805	1334
	<i>Listeria monocytogenes</i> serotype 1-2a str. F6854	47097148	1334
	<i>Streptococcus agalactiae</i> 2603V-R	22537057	1370
	<i>Streptococcus agalactiae</i> A909	76788458	1370
	<i>Streptococcus agalactiae</i> NEM316	25010965	1377
	<i>Streptococcus anginosus</i> F0211	315223162	1345
	<i>Streptococcus bovis</i> ATCC 700338	306833855	1373
	<i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> GGS 124	251782637	1371
	<i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> MGCS10565	195978435	1348
	<i>Streptococcus equinus</i> ATCC 9812	320547102	1377
	<i>Streptococcus gallolyticus</i> subsp. <i>gallolyticus</i> ATCC BAA-2069	325978669	1370
	<i>Streptococcus gallolyticus</i> UCN34	288905639	1371
	<i>Streptococcus macacae</i> NCTC 11558	357636406	1338
	<i>Streptococcus mutans</i> NN2025	290580220	1345
	<i>Streptococcus mutans</i> UA159	24379809	1345
	<i>Streptococcus pseudoporcinus</i> SPIN 20026	313890160	1326
	<i>Streptococcus pyogenes</i> SF370	15675041	1368
	<i>Streptococcus pyogenes</i> MGAS10270	94990395	1368
	<i>Streptococcus pyogenes</i> MGAS10750	94994317	1371
	<i>Streptococcus pyogenes</i> MGAS2096	94992340	1368
	<i>Streptococcus pyogenes</i> MGAS315	21910213	1368
<i>Streptococcus pyogenes</i> MGAS5005	71910582	1368	
<i>Streptococcus pyogenes</i> MGAS6180	71903413	1368	
<i>Streptococcus pyogenes</i> MGAS9429	94988516	1368	
<i>Streptococcus pyogenes</i> NZ131	209559356	1368	
<i>Streptococcus pyogenes</i> SSI-1	28896088	1368	
<i>Streptococcus thermophilus</i> LMD-9	116628213	1388	
2	<i>Bacteroides coprophilus</i> DSM 18228	224026357	1509
	<i>Bacteroides dorei</i> DSM 17855	212694363	1504
	<i>Bacteroides</i> sp. 20 3	301311869	1517
	<i>Capnocytophaga gingivalis</i> ATCC 33624	228473057	1436
	<i>Fibrobacter succinogenes</i> subsp. <i>succinogenes</i> S85	261414553	1512
	<i>Flavobacterium columnare</i> ATCC 49512	365960762	1459
	<i>Fluviicola taffensis</i> DSM 16823	327405121	1458
	<i>Mucilagibacter paludis</i> DSM 18603	373954054	1473
	<i>Prevotella bivia</i> JCVIHMP010	282858617	1485
	<i>Prevotella buccae</i> ATCC 33574	315607525	1457
	<i>Prevotella melaninogenica</i> D18	288802595	1354
	<i>Prevotella veroralis</i> F0319	260592128	1496
	<i>Psychroflexus torquis</i> ATCC 700755	408489713	1052
	<i>Sphingobacterium spiritivorum</i> ATCC 33861	300771242	1426
	<i>Weeksella virosa</i> DSM 16922	325955459	1440
3	<i>Actinobacillus minor</i> NM305	240949037	1056
	<i>Actinobacillus pleuropneumoniae</i> serovar 10 str. D13039	307256472	1054
	<i>Actinobacillus succinogenes</i> 130Z	152978060	1062
	<i>Haemophilus parainfluenzae</i> T3T1	345430422	1052
	<i>Kingella kingae</i> ATCC 23330	333374624	1000
	<i>Neisseria bacilliformis</i> ATCC BAA-1200	329117879	1077
	<i>Neisseria cinerea</i> ATCC 14685	261378287	1082

Cluster ^a	Strains ^b	Cas9 GI	Length (aa)
3 (continued)	<i>Neisseria flavescens</i> SK114	241759613	1081
	<i>Neisseria lactamica</i> 020-06	313669044	1082
	<i>Neisseria meningitidis</i> 053442	161869390	1082
	<i>Neisseria meningitidis</i> alpha14	254804356	1082
	<i>Neisseria meningitidis</i> Z2491	218767588	1082
	<i>Pasteurella multocida</i> subsp. <i>multocida</i> str. Pm70	15602992	1056
	<i>Simonsiella muelleri</i> ATCC 29453	404379108	1065
4	<i>Lactobacillus farciminis</i> KCTC 3681	336394701	1126
	<i>Streptococcus gallolyticus</i> UCN34	288905632	1130
	<i>Streptococcus gordonii</i> str. Challis substr. CH1	157150687	1136
	<i>Streptococcus infantarius</i> subsp. <i>infantarius</i> ATCC BAA-102	171779984	1129
	<i>Streptococcus macedonicus</i> ACA-DC 198	374338350	1130
	<i>Streptococcus mitis</i> ATCC 6249	306829274	1134
	<i>Streptococcus pasteurianus</i> ATCC 43144	336064611	1130
	<i>Streptococcus suis</i> 89-1591	223932525	1122
	<i>Streptococcus suis</i> ST3	330833104	1122
	<i>Streptococcus thermophilus</i> CNRZ1066	55822627	1128
	<i>Streptococcus thermophilus</i> LMD-9	116627542	1121
	<i>Streptococcus thermophilus</i> LMG 18311	55820735	1122
	<i>Streptococcus vestibularis</i> ATCC 49124	322517104	1128
5	<i>Bacteroides cellulosilyticus</i> DSM 14838	224535832	1219
	<i>Bacteroides fragilis</i> NCTC 9343	60683389	1436
	<i>Bacteroidetes</i> oral taxon 274 str. F0058	298373376	1434
	<i>Capnocytophaga canimorsus</i> Cc5	340622236	1430
	<i>Capnocytophaga ochracea</i> DSM 7271	256819408	1426
	<i>Capnocytophaga sputigena</i> ATCC 33612	213962376	1426
	<i>Flavobacterium psychrophilum</i> JIP02-86	150025575	1354
	<i>Kordia algicida</i> OT-1	163754820	1391
	<i>Parabacteroides johnsonii</i> DSM 18315	218258638	1443
	<i>Parabacteroides</i> sp. D13	256840409	1424
	<i>Prevotella oralis</i> ATCC 33269	323344874	1391
<i>Zunongwangia profunda</i> SM-A87	295136244	1388	
6	<i>Lactobacillus brevis</i> subsp. <i>gravesensis</i> ATCC 27305	227509761	1377
	<i>Lactobacillus buchneri</i> ATCC 11577	227512703	1239
	<i>Lactobacillus buchneri</i> NRRL B-30929	331702228	1371
	<i>Lactobacillus fermentum</i> ATCC 14931	227514633	1381
	<i>Lactobacillus gasseri</i> JV-V03	300361537	1391
	<i>Lactobacillus jensenii</i> 269-3	238854567	1391
	<i>Lactobacillus johnsonii</i> DPC6026	385826041	1375
	<i>Lactobacillus ruminis</i> ATCC 25644	323340068	1375
	<i>Lactobacillus salivarius</i> UCC118	90961083	1149
	<i>Lactobacillus sanfranciscensis</i> TMW 1-1304	347534532	1331
<i>Pediococcus acidilactici</i> DSM 20284	304386254	1364	
7	<i>Gemella haemolysans</i> ATCC 10379	241889924	1392
	<i>Gemella moribillum</i> M424	317495358	1385
	<i>Megasphaera</i> sp. UPII 135-E	342218215	1352
	<i>Peptoniphilus</i> sp. oral taxon 386 str. F0131	299144352	1341
	<i>Veillonella atypica</i> ACS-134-V-Col7a	303229466	1398
	<i>Veillonella parvula</i> ATCC 17745	282849530	1398
8	<i>Actinomyces coleocanis</i> DSM 15436	227494853	1105
	<i>Corynebacterium accolens</i> ATCC 49726	306835141	1099
	<i>Corynebacterium diphtheriae</i> NCTC 13129	38232678	1084
	<i>Corynebacterium matruchotii</i> ATCC 14266	305681510	1089
	<i>Mobiluncus curtisii</i> subsp. <i>holmesii</i> ATCC 35242	315656340	1123

Cluster ^a	Strains ^b	Cas9 GI	Length (aa)
	<i>Mobiluncus mulieris</i> 28-1	269977848	1091
9	<i>Gluconacetobacter diazotrophicus</i> PAI 5	162147907	1050
	<i>Gluconacetobacter diazotrophicus</i> PAI 5	209542524	1003
	<i>Methylocystis</i> sp. ATCC 49242	323139312	1080
	<i>Methylosinus trichosporium</i> OB3b	296446027	1082
	<i>Rhodopseudomonas palustris</i> BisB18	90425961	1066
	<i>Rhodopseudomonas palustris</i> BisB5	91975509	1064
	10	<i>Acidovorax avenae</i> subsp. <i>avenae</i> ATCC 19860	326315085
<i>Alicyclophilus denitrificans</i> BC		319760940	1029
<i>Alicyclophilus denitrificans</i> K601		330822845	1029
<i>gamma proteobacterium</i> HdN1		304313029	1025
<i>Nitrosomonas</i> sp. AL212		325983496	1044
<i>Verminephrobacter eiseniae</i> EF01-2		121608211	1068
11		<i>Campylobacter jejuni</i> subsp. <i>doylei</i> 269-97	153952471
	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> 81116	157415744	984
	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> NCTC 11168	218563121	984
	<i>Helicobacter canadensis</i> MIT 98-5491	253828136	1007
	<i>Helicobacter cinaedi</i> CCUG 18818	313144862	1023
12	<i>Coriobacterium glomerans</i> PW2	328956315	1384
	<i>Eggerthella</i> sp. YY7918	339445983	1380
	<i>Gordonibacter pamelaeeae</i> 7-10-1-b	295106015	1371
	<i>Olsenella uli</i> DSM 7084	302336020	1399
13	<i>Lactobacillus casei</i> BL23	191639137	1361
	<i>Lactobacillus casei</i> str. Zhang	301067199	1361
	<i>Lactobacillus paracasei</i> subsp. <i>paracasei</i> 8700-2	239630053	1362
	<i>Lactobacillus rhamnosus</i> GG	258509199	1363
14	<i>Prevotella buccalis</i> ATCC 35310	282878504	1218
	<i>Prevotella ruminicola</i> 23	294674019	1204
	<i>Prevotella tanneriae</i> ATCC 51259	258648111	1234
	<i>Prevotella timonensis</i> CRIS 5C-B1	282880052	1218
15	<i>Bifidobacterium dentium</i> Bd1	283456135	1138
	<i>Bifidobacterium longum</i> DJO10A	189440764	1187
	<i>Gardnerella vaginalis</i> 5-1	298252606	1186
	<i>Scardovia inopinata</i> F0304	294790575	1178
16	<i>Anaerococcus tetradius</i> ATCC 35098	227501312	1361
	<i>Lactobacillus iners</i> LactinV 11V1-d	309803917	1369
	<i>Peptoniphilus duerdenii</i> ATCC BAA-1640	304438954	1364
17	<i>Coprococcus catus</i> GD-7	291520705	1338
	<i>Dorea longicatena</i> DSM 13814	153855454	1340
	<i>Ruminococcus lactaris</i> ATCC 29176	197301447	1341
18	<i>Phascolarctobacterium succinatutens</i> YIT 12067	323142435	1087
	<i>Roseburia intestinalis</i> L1-82	257413184	1140
	<i>Roseburia inulinivorans</i> DSM 16841	225377804	1152
19	<i>Dinoroseobacter shibae</i> DFL 12	159042956	1079
	<i>Maritimibacter alkaliphilus</i> HTCC2654	84685065	997
	<i>Sphingomonas</i> sp. S17	332188827	1090
20	<i>Flavobacterium branchiophilum</i> FL-15	347536497	1473
	<i>Flavobacterium columnare</i> ATCC 49512	365959402	1535
21	<i>Burkholderiales bacterium</i> 1 1 47	303257695	1428
	<i>Parasutterella excrementihominis</i> YIT 11859	331001027	1428
22	<i>Prevotella denticola</i> F0289	327314511	1218
	<i>Prevotella micans</i> F0438	373501184	1425
23	<i>Acidaminococcus intestini</i> RyC-MR95	352684361	1358
	<i>Acidaminococcus</i> sp. D21	227824983	1358

Cluster ^a	Strains ^b	Cas9 GI	Length (aa)
24	<i>Staphylococcus pseudintermedius</i> ED99	323463801	1334
	<i>Staphylococcus simulans</i> ACS-120-V-Sch1	410878248	1112
25	<i>Mycoplasma gallisepticum</i> str. F	284931710	1269
	<i>Mycoplasma gallisepticum</i> str. R-low	294660600	1270
26	<i>Elusimicrobium minutum</i> Pei191	187250660	1195
	uncultured Termite group 1 bacterium phylotype Rs-D17	189485059	1032
27	<i>Francisella tularensis</i> subsp. <i>tularensis</i> SCHU S4	56707712	1123
	<i>Francisella tularensis</i> subsp. <i>tularensis</i> WY96-3418	134302318	1125
28	<i>Clostridium spiroforme</i> DSM 1552	169349750	1116
	<i>Eubacterium dolichum</i> DSM 3991	160915782	1096
29	<i>Eubacterium rectale</i> ATCC 33656	238924075	1114
	<i>Eubacterium ventriosum</i> ATCC 27560	154482474	1107
30	<i>Staphylococcus aureus</i> M06/0171	403411236	1053
	<i>Staphylococcus lugdunensis</i> M23590	315659848	1054
31	<i>Francisella novicida</i> U112	118497352	1629
32	<i>Sutterella wadsworthensis</i> 3 1 45B	319941583	1422
33	<i>Bifidobacterium bifidum</i> S17	310286728	1420
34	<i>Wolinella succinogenes</i> DSM 1740	34557932	1409
35	<i>gamma proteobacterium</i> HTCC5015	254447899	1397
36	<i>Treponema denticola</i> ATCC 35405	42525843	1395
37	<i>Oenococcus kitaharae</i> DSM 17330	366983953	1389
38	<i>Fusobacterium nucleatum</i> subsp. <i>vincentii</i> ATCC 49256	34762592	1374
39	<i>Legionella pneumophila</i> str. Paris	54296138	1372
40	<i>Filifactor alocis</i> ATCC 35896	374307738	1365
41	<i>Finegoldia magna</i> ATCC 29328	169823755	1348
42	<i>Catenibacterium mitsuokai</i> DSM 15897	224543312	1329
43	<i>Solobacterium moorei</i> F0204	320528778	1327
44	<i>Mycoplasma synoviae</i> 53	71894592	1314
45	<i>Mycoplasma ovipneumoniae</i> SC01	363542550	1265
46	<i>Streptobacillus moniliformis</i> DSM 12112	269123826	1259
47	<i>Mycoplasma mobile</i> 163K	47458868	1236
48	<i>Mycoplasma canis</i> PG14	384393286	1233
49	<i>Sphaerochaeta globus</i> str. Buddy	325972003	1179
50	<i>Rhodospirillum rubrum</i> ATCC 11170	83591793	1173
51	<i>Azospirillum</i> sp. B510	288957741	1168
52	<i>Streptococcus sanguinis</i> VMC66	323351495	1167
53	<i>Nitrobacter hamburgensis</i> X14	92109262	1166
54	<i>Ruminococcus albus</i> 8	325677756	1156
55	<i>Enterococcus faecalis</i> TX0012	315149830	1150
56	<i>Acidothermus cellulolyticus</i> 11B	117929158	1138
57	<i>Nitratifractor salsuginis</i> DSM 16511	319957206	1132
58	<i>Acidovorax ebreus</i> TPSY	222109285	1131
59	<i>Lactobacillus coryniformis</i> subsp. <i>torquens</i> KCTC 3535	336393381	1119
60	<i>Akkermansia muciniphila</i> ATCC BAA-835	187736489	1101
61	<i>Ilyobacter polytropus</i> DSM 2926	310780384	1092
62	<i>Bacillus cereus</i> Rock1-15	229113166	1069
63	<i>Clostridium perfringens</i> D str. JGS1721	182624245	1065
64	<i>Bradyrhizobium</i> sp. BTAi1	148255343	1064
65	<i>Ralstonia syzygii</i> R24	344171927	1062
66	<i>Wolinella succinogenes</i> DSM 1740	34557790	1059
67	<i>Aminomonas paucivorans</i> DSM 12260	312879015	1052

Cluster ^a	Strains ^b	Cas9 GI	Length (aa)
68	<i>Parvibaculum lavamentivorans</i> DS-1	154250555	1037
69	<i>Candidatus Puniceispirillum marinum</i> IMCC1322	294086111	1035
70	uncultured Termite group 1 bacterium phylotype Rs-D17	189485225	1032
71	<i>Blastopirellula marina</i> DSM 3645	87307579	1027
72	<i>Helicobacter mustelae</i> 12198	291276265	1024
73	<i>Clostridium cellulolyticum</i> H10	220930482	1021
74	<i>Streptococcus downei</i> F0415	312866154	994
75	<i>Treponema vincentii</i> ATCC 35580	257456748	992
76	<i>Mycoplasma iowae</i> 695	350546886	933
77	<i>Listeria seeligeri</i> FSL N1-067	313631816	874
78	<i>Listeria ivanovii</i> FSL F6-596	315301624	849
	<i>Butyrivibrio fibrisolvens</i> 16-4	291518097	765
	<i>Coprococcus comes</i> ATCC 27758	226325213	686
	<i>Francisella tularensis</i> subsp. <i>holarctica</i> LVS	89256630	158
	<i>Francisella tularensis</i> subsp. <i>holarctica</i> LVS	89256631	393
	<i>Haemophilus pittmaniae</i> HK 85	343519679	650
	<i>Helicobacter hepaticus</i> ATCC 51449	32266975	131
	<i>Helicobacter pullorum</i> MIT 98-5489	242309214	702
	<i>Neisseria subflava</i> NJ9703	284799897	587
	<i>Nitrobacter hamburgensis</i> X14	92118334	641
	<i>Oribacterium sinus</i> F0268	227873236	653
	<i>Prevotella disiens</i> FB035-09AN	303237415	795
	<i>Pseudoramibacter alactolyticus</i> ATCC 23263	315926102	586
	<i>Treponema phagedenis</i> F0421	320536384	738
	uncultured Termite group 1 bacterium phylotype Rs-D17	189485058	166

^aSequences are grouped according to the BLASTclust clustering program. Only sequences longer than 800 amino acids were selected for the BLASTclust analysis (see Materials and Methods). ^bRepresentative strains harboring cas9 orthologue genes are listed; GI, GenInfo Identifier. Bold, representative sequences of each group chosen for the alignment and tree formation. Grey, discarded, incomplete Cas9 sequences (see Materials and Methods). Sequences that were not clustered are listed at the bottom of the table. They were considered as possible Cas9 sequences based on the presence of conserved motifs and/or other cas genes in their immediate vicinity. As incomplete, they were not selected for further analysis.

Supplementary Table 2. Predicted pre-crRNA repeat:tracrRNA anti-repeat base-pairing in selected bacterial species.

Strain ^a	CRISPR type II identifier ^b	pre-crRNA repeat:tracrRNA base-pairing ^c
<i>Francisella tularensis</i> subsp. <i>novicida</i> U112	NC_008601_1 ^d	GUUUCAGUUGCUGAAUUAUUUGGUAACUACU-GUUAG CAAAGUCAACAAUCUAAUAAACCAUAC-AUGAACACAA GUUUCAGUUGC-UGAAUUAUUUGGUAACUACUGUUAG • UAAUGUCU-CGUAAUUAAUAAACCAUGUAAAUUUAAA
<i>Wolinella succinogenes</i> DSM 1740	NC_005090_2 ^d	GCAACACUUUAUAGCAAUCCGCUUAGCCUG-UGAAAC CGUUGUGAAAUAUCGUUUAGGCAAGCUACGGAACUUU GCAACACUUUAUAGCAAUCCGCUUAGCCUGUGAAAC • • • • • CGUUGUGAGAUAUUUUAGGGUAGGUCGAAAUUGUUU
gamma proteobacterium HTCC5015	ND ^c	GUUUCAGAGCUUAUCCCAACAAACCA-ACAGCUGAAAC • AUAAGUCUUACGUAGGGUUGUAAGAUUAGU-GACUUUA GUUUCAGAGCUUAUCCCAACAAACCAACAGCUGAAAC CAAAGUCUCGAAUAGGUCGUUUUUGAGGGAAACAAUA
<i>Sutterella wadsworthensis</i> 3 1 45B	ND ^e	GCGAAGAUCAUACGCUACGAGCUAUAGCAGCUGAAAC • • • • UGUCUUUAGUAUUUGCGGUCGUAUACGAACCUUUG GCGAAGAUCAUACGCUACGAGCUAUAGCAGCUGAAAC • AAUCUCUAGUAUUUGCGAUACUCGAUAUCCUUUAGUGG
<i>Parasutterella excrementihominis</i> YIT 11859	ND	Not possible to analyze – too short contig
<i>Legionella pneumophila</i> str. Paris	NC_006368_1	CCAAUAAUCCCUCAUCUAAAAUCCA-ACCACUGAAAC AUUUAAUCUUUAGUAGAUUUUAAAGCUAUGG-GACUUUA
<i>Listeria innocua</i> Clip11262	NC_003212_2	GUUUUAG--AGCUAUGUUAUUUUGAAUGCUAACAAAAC • AAAUUGAACGAUACAAUAAAACUUAUGAUUGUUAUA
<i>Streptococcus thermophilus</i> LMD-9	NC_008532_5	GUUUUAG--AGCUGUGUUGUUUCGAAUGGUUCCAAAAC • AAAUUGAGCGACACAACAAAGCUUACCAAAGUUUGG
<i>Streptococcus mutans</i> UA159	NC_004350_1	GUUUUAG--AGCUGUGUUGUUUCGAAUGGUUCCAAAAC • AAAUUGAACGACACAACAAAGCUUACUAGGUUGUG
<i>Streptococcus pyogenes</i> SF370	NC_002737_1	GUUUUAG--AGCUAUGCUGUUUUGAAUGGUCCAAAAC • AAAUUGAACGAUACGACAAAACUUAACAAAGUUUGU
<i>Fusobacterium nucleatum</i> subsp. <i>vincentii</i> ATCC 49256	ND	GUUUGAGAGUAAUGUUAUUUAAAAUAGAUAUCAAAC • • • CAUAUACGAGGUAAAAUUAUGAAUUUAAUUUUUA
<i>Filifactor alocis</i> ATCC 35896	NC_016630_2	GUUUGAGAGUAGUGUAAUUUCAUAGUGAGUCAAC • • ACUUGG-CACAUACAUUAGAGUAUACCAUCAGUU-GA
<i>Peptoniphilus duerdenii</i> ATCC BAA-1640	ND	No significant anti-repeat found
<i>Treponema denticola</i> ATCC35405	NC_002967_1	GUUUGAG--AGUUGUGUAAUUUAGAUGGAUCUCAAAC • AACUUGAGCAACACAUUUAAUUUCAACCUAGAAUUUA

Supplementary table 3. tracrRNA orthologue and crRNA sequencing data.

sRNA	Strand	Size mature form	Region of interest		Reads	Coverage (%)	Sequence	5' end read number		3' end read number				
<i>C. jejuni</i> NCTC 11168 (NC_002163.1), total mapped reads: 9914184														
crRNA 4 spacers	→	crRNA1	36	1455167	1455202	781	0.0079	AGTTTTTAAAAAGAGCTTGGCGGTTGTTTTAGT CCCTTTT	1455162	A	1	1455198	T	5
									1455165	G	2	1455199	C	5
									1455166	C	3	1455200	C	16
									1455167	A	419	1455201	C	72
							1455168	G	19	1455202	T	385		
							1455169	T	7	1455203	T	82		
							1455170	T	75	1455204	T	30		
							1455171	T	24	1455205	T	112		
							1455172	T	9	1455206	T	5		
							1455173	T	11					
							1455174	A	4					
		crRNA2	38	1455231	1455268	2658	0.0268	CAAAGTTTCATTAGTTGAATTTAACTGTTTTA GTCCCTTTT	1455227	T	4	1455264	T	3
			29	1455240	1455268				1455228	T	1	1455265	C	14
									1455230	C	37	1455266	C	60
									1455231	C	206	1455267	C	240
									1455232	A	72	1455268	T	1364
									1455233	A	34	1455269	T	348
									1455234	A	59	1455270	T	29
									1455235	G	280	1455271	T	44
									1455236	T	168	1455272	T	15
									1455237	T	130	1455273	A	2
									1455238	T	36			
									1455239	C	259			
									1455240	A	317			
									1455241	T	148			
									1455242	T	298			
									1455243	A	157			
									1455244	G	40			
		crRNA3	35	1455300	1455334	4729	0.0477	AAGAATGAGGATGATGATATTTTACAGTTTTA GTCCCTTTT	1455292	T	16	1455329	G	21
									1455293	C	62	1455330	T	479
									1455294	T	5	1455331	C	23
									1455295	A	12	1455332	C	48
									1455296	C	23	1455333	C	179
									1455297	A	367	1455334	T	1226
									1455298	A	143	1455335	T	220
									1455299	G	563	1455336	T	54
									1455300	A	1014	1455337	T	49
									1455301	A	415	1455338	T	55
									1455302	T	242	1455339	A	1
									1455303	G	589			
									1455304	A	55			
									1455305	G	2			
		crRNA4	26	1455376	1455401	17404	0.1755	GTGTGCTAAAAAATGGACTTAAATGTTTTA GTCCCTTTT	1455360	T	6	1455398	C	63
									1455361	G	2	1455399	C	645
									1455362	A	9	1455400	T	9844
									1455363	G	261	1455401	T	1518
									1455364	T	51	1455402	T	481
									1455365	G	598	1455403	T	763
									1455366	T	77	1455404	T	578
									1455367	G	552	1455405	A	4
									1455368	C	579			
									1455369	T	901			
									1455370	A	816			
									1455371	A	227			
									1455372	A	262			
									1455373	A	1072			
									1455374	A	1269			
									1455375	A	1991			
									1455376	A	2204			
									1455377	A	1978			
									1455378	T	371			

sRNA	Strand	Size mature form	Region of interest		Reads	Coverage (%)	Sequence	5' end read number		3' end read number				
tracrRNA	→	tracrRNA1	65	1455502	1455566	833829	8.4105	AAGAAAATTAA AAGGGACTAAAATAAAGAGT TTGCGGGACTCTGCGGGTTACAATCCCCTAA AACCGCTTTT	1455496	T	1	1455565	G	12371
		tracrRNA2	58	1455509	1455566				1455497	A	31	1455566	C	713292
									1455498	A	27	1455567	T	74594
									1455499	G	24	1455568	T	10412
									1455500	A	19	1455569	T	9580
									1455501	A	232	1455570	T	426
									1455502	A	435	1455571	A	91
									1455503	T	369	1455572	A	97
									1455504	T	253	1455573	A	542
									1455505	T	85			
									1455506	A	65			
									1455507	A	193			
									1455508	A	33472			
									1455509	A	615001			
									1455510	A	131879			
							1455511	G	16444					
							1455512	G	9390					
							1455513	G	1053					
F. novicida U112 (NC_008601.1), total mapped reads: 48205														
crRNA 13 spacers	←	crRNA5	52	817556	817607	117	0.2427	ATAACTCGACCAATATTTGACAAAGTTTCAGT TGCTGAATTATTTGGTAAACCT	817612	T	10	817557	A	3
									817611	T	10	817556	C	55
									817607	A	53	817555	T	13
									817606	T	7	817553	C	12
												817552	T	1
		crRNA6	56	817627	817682	116	0.2406	GGCAGTTTTGTATGGTCATATAGGAGTGT CAGTTGCTGAATTATTTGGTAAACCT	817685	A	4	817629	A	4
									817682	G	23	817628	A	3
									817681	G	13	817627	C	53
									817679	A	2	817626	T	20
									817677	G	4			
		crRNA7	66	817699	817764	11	0.0228	AGCTATAGGGTTACCTATCTTTTGAGTGTGG CAAATAAGTTTCAGTTGCTGAATTATTTGGTA AACCT	817764	A	4	817699	A	2
									817763	G	1			
									817754	T	4			
							817745	T	2					
crRNA9	53	817845	817897	24	0.0498	ATGCTTTTAAACTACTGATATATACTTTCAG TTGCTGAATTATTTGGTAAACCT	817897	A	3	817845	C	7		
tracrRNA	←	tracrRNA1	74	817065	817138	2808	5.8251	GTACCAATAAATTAATGCTCTGTAAATCATT AAAGTATTTTGAACGGACCTCTGTTTGACACG TCTGAATAACTAAAAA	817140	A	2	817066	A	28
		tracrRNA2	64	817065	817128				817139	T	2	817065	C	1523
									817138	G	615	817064	T	440
									817136	A	9	817063	A	7
									817135	C	2	817062	A	10
									817134	C	37	817061	A	19
									817133	A	26	817060	A	14
									817132	A	7	817059	A	6
									817131	A	328	817058	G	5
									817130	T	355	817057	C	32
									817129	A	165	817055	A	10
									817128	A	484			
									817127	T	24			
									817126	T	55			
									817125	A	32			
							817124	A	19					
N. meningitidis Z2491 (NC_003116.1), total mapped reads: 13110087														
crRNA 16 spacers	→	crRNA1	48	608456	608503	1346	0.0103	TATCCATTCCCAGCCGGAATTAAGTTGTAGC TCCCTTTCATTTCCGAGT	608453	T	30	608500	T	25
									608454	G	105	608501	C	77
									608455	T	64	608502	G	175
									608456	A	259	608503	C	293
									608457	T	4	608504	A	78
									608458	C	21	608505	G	505
									608459	C	175	608507	T	1
									608460	A	118			
									608461	T	39			
		crRNA2	50	608520	608569	685	0.0052	GCCTTTTACAAGCTCGCTTTCCTTTGTTGAG CTCCCTTTCATTTCCGAGT	608517	T	5	608564	T	8
									608518	C	41	608565	T	16
									608519	T	7	608566	T	8
									608520	G	61	608567	C	31
							608521	C	21	608568	G	101		
							608522	C	44	608569	C	173		
							608523	T	21	608570	A	43		
							608524	T	31	608571	G	6		
							608525	T	17	608572	T	2		

sRNA	Strand	Size mature form	Region of interest	Reads	Coverage (%)	Sequence	5' end read number	3' end read number											
crRNA3	50	608586	608635	12402	0.0946	TAAAGGTTTCTGTGCGACCCGAATGTTGTAG CTCCCTTCTCATTTCGCAGT	608583	T	5	608631	T	75							
							608584	G	3	608632	T	114							
							608585	G	513	608633	C	414							
							608586	T	2243	608634	G	1510							
							608587	A	2091	608635	C	2219							
							608588	A	188	608636	A	297							
							608589	A	233	608637	G	52							
							608590	G	744	608638	T	8							
							608591	G	1152										
							crRNA4	49	608653	608701	26361	0.2011	TAACTTTGACCGTGTGCAATCCAGTTAGTTGT AGCTCCCTTCTCATTTCGCAGT	608646	T	7	608697	T	295
														608647	C	127	608698	T	569
														608648	T	203	608699	C	1167
608649	T	377	608700	G	4910														
608650	T	2751	608701	C	4968														
608651	A	477	608702	A	764														
608652	A	1334	608703	G	62														
608653	C	11694	608704	T	4														
608654	T	3665																	
608655	T	382																	
crRNA5	49	608719	608767	28747	0.2193	AACCCACTAAATTTTGCAARTGCGTTGTAGC TCCTTCTCATTTCGCAGT								608717	G	20	608764	T	426
														608718	C	1171	608765	C	1316
							608719	A	8128	608766	G	3040							
							608720	A	116	608767	C	6431							
							608721	C	59	608768	A	1049							
							608722	C	420	608769	G	102							
							608723	C	1089	608770	T	11							
							608724	A	557										
							crRNA6	50	608784	608833	121014	0.9231	TTTTTTGTACTGTTGTTTGAACGAGTTGTAG CTCCCTTCTCATTTCGCAGT	608781	G	42	608830	T	2295
														608782	C	630	608831	C	7060
														608783	C	10039	608832	G	13864
														608784	T	26026	608833	C	44472
608785	T	11430	608834	A	6853														
608786	T	8248	608835	G	802														
608787	T	3648	608836	T	69														
crRNA7	52	608848	608899	24611	0.1877	TTCGTTTCAGATAGCAACCGCAGTAGTGTGT AGCTCCCTTCTCATTTCGCAGT								608846	A	28	608896	T	369
														608847	A	631	608897	C	1114
														608848	T	11039	608898	G	3441
														608849	T	753	608899	C	9015
														608850	C	239	608900	A	1558
							608851	G	2205	608901	G	137							
							608852	T	1910	608902	T	8							
							608853	T	826										
							84	608916	608999	901	0.0069	ATATGACGGTGGGCAACTGGTACAGTTGTAG CTCCCTTCTCATTTCGCAGTGTACAATGCC GGATATGACGGTGGGCAACT	608913	C	6	608996	A	6	
													608914	G	3	608997	A	2	
													608915	G	2	608998	C	2	
													608916	A	266	608999	T	259	
608917	T	17	609000	G	171														
608918	A	96	609001	G	24														
608919	T	26	609004	T	16														
crRNA10	49	609049	609097	5027	0.0383	CTTTTGATGATTCAAGGTGCTTGTGTAGC TCCTTCTCATTTCGCAGT							609046	T	89	609094	T	81	
													609047	C	37	609095	C	218	
													609048	G	647	609096	G	845	
													609049	C	1614	609097	C	1237	
													609050	T	583	609098	A	219	
							609051	T	208	609099	G	36							
							609052	T	104	609101	G	7							
							609053	T	18										
							crRNA11	52	609112	609163	22711	0.1732	ATTTCGTGATGATGAACTCGAGCATGTTGT AGCTCCCTTCTCATTTCGCAGT	609109	A	58	609160	T	540
														609110	G	331	609161	C	1263
														609111	T	99	609162	G	2850
														609112	A	10627	609163	C	4882
609113	T	1234	609164	A	552														
609114	T	66	609165	G	52														
609115	C	191	609166	T	15														
609116	G	4906																	
609117	T	136																	
crRNA12	52	609178	609229	5067	0.0386	TAGCCAGTGTAAAACCGCACCCGCTTGTGT AGCTCCCTTCTCATTTCGCAGT								609175	G	4	609226	T	57
														609176	G	3	609227	C	189
														609177	G	42	609228	G	576
							609178	T	897	609229	C	1348							
							609179	A	72	609230	A	321							
							609180	G	584	609231	G	33							
							609181	C	154	609232	T	2							
							609182	C	314										
							609183	A	38										

sRNA	Strand	Size mature form	Region of interest	Reads	Coverage (%)	Sequence	5' end read number	3' end read number	
		crRNA13	51	609245	609295	4666	0.0356	ATAGAAATACATACGCCGAGTAATTAGTTGTA GCTCCCTTTCTCATTTCGCAGT	609243 A 6 609292 T 65 609244 A 62 609293 C 201 609245 A 1311 609294 G 475 609246 T 141 609295 C 1039 609247 A 116 609296 A 229 609248 G 44 609297 G 25 609298 T 1
		crRNA14	51	609311	609361	7147	0.0545	TTTTTGTAATTGTTCTGCCTTTTTAGTTGTA GCTCCCTTTCTCATTTCGCAGT	609308 T 12 609358 T 136 609309 T 22 609359 C 442 609310 C 207 609360 G 858 609311 T 1190 609361 C 2335 609312 T 774 609362 A 540 609313 T 577 609363 G 69 609314 T 195 609364 T 5 609315 T 37
		crRNA15	50	609378	609427	49818	0.3800	ACGGCGGAAACCATTGCCACAAACGTTGTAG CTCCCTTTCTCATTTCGCAGT	609375 C 319 609424 T 532 609376 C 7253 609425 C 1414 609377 C 7249 609426 G 2553 609378 A 19015 609427 C 7448 609379 C 547 609428 A 1854 609380 G 307 609429 G 210 609381 G 190 609430 T 10
		crRNA16	50	609444	609493	42398	0.3234	AATAATAACCCCAATACAGATGTTAAGTTGTA GCTCCCTTTCTCATTTCGCAGT	609441 A 8 609490 T 579 609442 A 548 609491 C 2197 609443 A 3686 609492 G 6466 609444 A 4638 609493 C 13217 609445 T 1428 609494 A 2438 609446 A 2861 609495 G 200 609447 A 1322 609496 T 12 609448 T 287
tracrRNA	→	tracrRNA1	163	614162	614324	208318	1.5890	TTGTCCTATTATATACAAATAGATTATTGAC TTATCATCTCACACCGCTAGAAATCCCAAAACA TATTGTCGCACCTGC GA AATGAGAACCGTTGCT ACAATAAGGCCCTCTGAAAAGATGTCCCGCAA CGCTCTGCCCTTAAAGCTTCTGCTTTAAGGG GCATCGTTTAT	614158 C 1 614319 G 311 614161 A 1 614320 G 109 614162 T 2 614321 G 258 614164 G 1 614322 G 150 614223 A 596 614323 C 41244 614224 C 39 614324 A 128531 614225 A 14761 614325 T 167 614226 T 169 614326 C 4197 614227 A 276 614327 G 36 614239 C 208 614328 T 122 614240 G 42037 614329 T 865 614241 A 39965 614330 T 1132 614242 A 22890 614331 A 1061 614243 A 51186 614332 T 2788 614244 T 17711 614333 T 3758 614245 G 4192 614334 T 77 614246 A 488 614335 C 18 614336 G 3 614337 G 3 614338 T 1
L. innocua Clip11262 (NC_003212.1), total mapped reads: 161865 (Note: low quality of the RNA library)									
crRNA 10 spacers	←	crRNA1	35	2769606	2769640	2	0.0012	GGTAACCTTGCCTAGGATAGTTTTAGAGCTAT GT	2769640 G 1 2769606 T 1
		crRNA2	22	2769540	2769561	2	0.0012	CATTATGTTTTAGAGCTATGT	2769561 C 1 2769540 T 1 2769560 A 1
		crRNA3	24	2769468	2769491	3	0.0019	GAGTTTTAGAGCTATGT ATTTG	2769491 G 3 2769468 G 1
		crRNA4	27	2769402	2769428	7	0.0043	TTATAGTTTTAGAGCTATGT ATTTG	2769428 T 5 2769407 A 1 2769427 T 2 2769406 T 1 2769405 T 1 2769403 T 1 2769402 G 1
		crRNA5	26	2769337	2769362	5	0.0031	TAAATGTTTTAGAGCTATGT ATTT	2769362 T 3 2769339 T 1 2769360 A 2 2769337 T 2
		crRNA8	23	2769142	2769164	2	0.0012	TACAAGTTTTAGAGCTATGT AT	2769164 T 1 2769143 A 1 2769163 A 1 2769142 T 1
		crRNA9	30	2769072	2769101	19	0.0117	TTTCATGTTGTTTTAGAGCTATGT ATTTG	2769101 T 6 2769079 T 4 2769100 T 1 2769078 T 1 2769099 C 4 2769075 T 2 2769098 A 3 2769073 T 3 2769097 T 3 2769072 G 6 2769096 G 2
		crRNA10	28	2769000	2769027	19	0.0117	GTTTTAGAGCTATGCTATTTCCGAATACT	2769027 G 1 2769000 T 1

sRNA	Strand	Size mature form	Region of interest		Reads	Coverage (%)	Sequence	5' end read number		3' end read number													
tracrRNA	→	tracrRNA1	90	2774774	2774863	367	0.2267	ATTGTTAGTATTCAAA AACATAGCAAGTTA	2774774	A	34	2774861	T	2									
		tracrRNA2	76	2774788	2774863			AAATAAGGCTTTGTCGGTTATCAACTTTTAAAT	2774783	A	1	2774862	T	47									
		tracrRNA3	68	2774796	2774863			TAAGTAGCGCTGTTTCGGCGCTTTT	2774786	C	1	2774863	T	150									
									2774787	A	1	2774864	T	67									
								2774788	A	22	2774865	T	30										
								2774794	C	1	2774866	G	15										
								2774795	A	1	2774867	T	6										
								2774796	T	5													
								2774797	A	2													
								2774799	C	5													
								2774801	A	1													
S. mutans UA159 (NC_004350.2), total mapped reads: 1542239																							
crRNA 5 spacers	←	crRNA1	38	1328162	1328199	267104	17.3192	GCCATTAAATTAATGGTGAGTTTTAGAGCTG T@TTGTTTCGA	1328201	A	8	1328166	G	18547									
									1328200	C	178	1328165	T	41345									
									1328199	G	264047	1328164	T	53386									
									1328198	C	191	1328163	G	9084									
									1328197	C	167	1328162	T	59197									
									1328196	A	117	1328161	T	28333									
												1328160	T	4240									
												1328159	C	18236									
												1328158	G	26742									
												1328157	A	5573									
			1328156	A	17																		
		crRNA2	36	1328098	1328133	26578	1.7233	GCTAGCGCAGTTAGTCTCTGTTTTAGAGCTG T@TTGTTTCGA	1328135	C	4	1328101	T	37									
									1328134	A	13	1328100	G	800									
									1328133	G	25656	1328099	T	6395									
									1328132	C	212	1328098	T	11256									
									1328131	T	25	1328097	G	301									
									1328130	A	62	1328096	T	1453									
									1328129	G	25	1328095	T	1755									
												1328094	T	447									
												1328093	C	1302									
												1328092	G	1996									
												1328091	A	670									
												1328090	A	5									
											crRNA3	34	1328034	1328067	138134	8.9567	TGTGTGTCATCATAGTTAGTTTTAGAGCTG T@TTGTTTCGA	1328069	G	4	1328036	G	2880
																		1328068	C	66	1328035	T	733
																		1328067	T	134361	1328034	G	68203
																		1328066	G	609	1328033	T	37212
																		1328065	T	321	1328032	T	24528
																					1328031	G	1003
																					1328030	T	889
			1328029	T	610																		
			1328028	T	124																		
			1328027	C	371																		
			1328026	G	546																		
			1328025	A	145																		
		crRNA4	35	1327967	1328001	104705	6.7892	CAATTAGACAATAGACAAACGTTTTAGAGCTG T@TTGTTTCGA										1328003	T	8	1327969	T	348
									1328002	T	36	1327968	G	8606									
									1328001	C	101017	1327967	T	59863									
									1328000	A	681	1327966	T	25845									
									1327999	A	216	1327965	G	756									
												1327964	T	3053									
												1327963	T	1433									
												1327962	T	1602									
												1327961	C	864									
												1327960	G	839									
												1327959	A	322									
											crRNA5	37	1327899	1327935	63999	4.1497	TTCGGACATGACTTGCCACAGTTTTAGAGCTG T@TTGTTTCGA	1327940	A	4	1327902	G	902
																		1327937	T	6	1327901	T	3296
																		1327936	A	17	1327900	T	12381
																		1327935	T	62587	1327899	G	19843
1327934	T	1029	1327898	T	2864																		
1327933	C	108	1327897	T	14180																		
1327932	G	19	1327896	T	2061																		
1327931	G	36	1327895	C	2079																		
			1327894	G	5259																		
			1327893	A	630																		

sRNA	Strand	Size mature form	Region of interest		Reads	Coverage (%)	Sequence	5' end read number		3' end read number				
tracrRNA	→	tracrRNA1	102	1335040	1335141	1299	0.0842	GTTGGAATCATTCGAAACAACAAGCAAGTTA AAATAAGGCAGTGATTTTAAATCCAGTCCGTA CACAACTTGAAAAAGTGCACCGATTCCGGTG CTTTTATTATT	1335038	G	1	1335140	T	13
		tracrRNA2	88	1335054	1335141				1335040	G	466	1335141	T	64
		tracrRNA3	80	1335062	1335141				1335041	T	6	1335142	T	29
									1335042	T	1	1335143	A	13
								1335051	T	4	1335144	T	6	
								1335053	G	3	1335145	T	13	
								1335054	A	415	1335146	T	1	
								1335055	A	2	1335149	T	1	
								1335057	C	1				
								1335058	A	1				
								1335062	C	186				
								1335063	A	15				

For the bacterial species studied, all tracrRNA orthologues and mature crRNAs retrieved by sequencing are listed, including coordinates (region of interest) and corresponding cDNA sequences (5' to 3').

The arrows represent the transcriptional direction (strand). Number of cDNA reads (calculated using SAMtools), coverage numbers (percentage of mapped reads) and predominant ends associated with each transcript are indicated.

Numbers of reads starting or stopping at each nucleotide position around the 5' and 3' ends of each transcript are displayed, the predominant ends are indicated in red in the sequence. The putative primary processing sites are indicated in dark blue (see Fig. 3). The sizes of each crRNA mature forms are indicated.

The number allocated to each crRNA species corresponds to the spacer sequence position in the pre-crRNA, according to the CRISPRdb. The number allocated to each tracrRNA species corresponds to different forms of the same transcript. Note that given the low quality of *L. innocua* cDNA library, values should be considered carefully.