

**Supplementary Table 4. COMBREX [4] functional annotations of new genes predicted from TM7a metagenomic assembly.**

<b>Gene ID</b>	<b>Annotation</b>	<b>Best BLAST hit</b>
7_7	Redoxin domain protein( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_0054(e-value: 9e-87)
16_1	ribonuclease H( <i>Polynucleobacter necessarius</i> subsp. asymbioticus QLW-P1DMWA-1)	rnhA(e-value: 1e-18)
25_1	ATP synthase F1, epsilon subunit( <i>Desulfovibrio desulfuricans</i> subsp. <i>desulfuricans</i> str. ATCC 27774)	Ddes_2189(e-value: 5e-09)
38_0	hypothetical protein( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_2039(e-value: 7e-52)
61_1	Lipoprotein spr( <i>Cronobacter turicensis</i> )	spr(e-value: 4e-23)
68_1	hypothetical protein( <i>Cronobacter turicensis</i> )	Ctu_37530(e-value: 4e-88)
71_1	transfer protein( <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> AD011)	BLA_0430(e-value: 9e-19)
72_0	putative ATP-dependent Clp protease, proteolytic subunit( <i>Streptococcus suis</i> 05ZYH33)	SSU05_1551(e-value: 7e-16)
73_3	peptide chain release factor-like protein( <i>Bacteroides fragilis</i> NCTC 9343)	prfH(e-value: 6e-06)
88_0	polar amino acid ABC transporter ATP-binding protein( <i>Synechococcus</i> sp. JA-3-3Ab)	CYA_0228(e-value: 1e-33)
111_1	oxidoreductase( <i>Rhodococcus erythropolis</i> PR4)	RER_50690(e-value: 1e-10)
118_1	Na <sup>+</sup> transporting oxaloacetate decarboxylase beta chain( <i>Streptococcus pyogenes</i> MGAS10750)	MGAS10750_Spy1053(e-value: 9e-31)
121_0	homoserine dehydrogenase( <i>Thermomicrobium roseum</i> DSM 5159)	trd_0367(e-value: 2e-41)
152_0	SNO glutamine amidotransferase( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_1507(e-value: 5e-86)
156_0	MATE efflux family protein DinF, truncated( <i>Streptococcus thermophilus</i> CNRZ1066)	str0947(e-value: 1e-29)
207_1	hypothetical protein( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_0616(e-value: 9e-57)
243_1	uracil-DNA glycosylase( <i>Clostridium difficile</i> R20291)	ung(e-value: 3e-61) LC705_01296(e-value: 6e-21)
255_0	predicted ORF( <i>Lactobacillus rhamnosus</i> Lc 705)	GWCH70_0296(e-value: 3e-47)
273_0	binding-protein-dependent transport systems inner membrane component( <i>Geobacillus</i> sp. WCH70)	Lebu_1637(e-value: 7e-102)
309_0	hypothetical protein( <i>Leptotrichia buccalis</i> C-1013-b)	
313_0	UDP-N-acetylglucosamine 1-carboxyvinyltransferase( <i>Clostridium thermocellum</i> ATCC 27405)	Cthe_0973(e-value: 3e-10)
318_0	cell division protein FtsI/penicillin-binding protein 2( <i>Dictyoglomus thermophilum</i> H-6-12)	DICTH_0339(e-value: 3e-11)
328_1	transcriptional regulator, MarR family( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_0428(e-value: 8e-71)
355_0	GTP-binding protein TypA/BipA( <i>Streptococcus pyogenes</i> MGAS2096)	MGAS2096_Spy1275(e-value: 7e-17)
356_0	hypothetical protein( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_0216(e-value: 6e-83)
366_0	hypothetical protein( <i>Pelotomaculum thermopropionicum</i> SI)	PTH_1502(e-value: 5e-07)
372_1	FtsW/RodA/SpoVE family peptidoglycan biosynthesis protein( <i>Desulfotomaculum reducens</i> MI-1)	Dred_0313(e-value: 4e-17)
376_0	glycosyltransferase( <i>Clostridium thermocellum</i> ATCC 27405)	Cthe_0209(e-value: 5e-22)
386_2	phage SPO1 DNA polymerase-related protein( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_1116(e-value: 1e-76)
421_2	UTP--glucose-1-phosphate uridylyltransferase protein( <i>Nitrosomonas europaea</i> ATCC 19718)	galU1(e-value: 6e-19)

421_5	DNA polymerase III, subunit alpha (dnaE)-like protein( <i>Clostridium perfringens</i> SM101)	CPR_0339(e-value: 2e-91)
441_1	chloride channel protein( <i>Streptococcus equi</i> subsp. zooepidemicus MGCS10565)	Sez_0752(e-value: 4e-07)
467_0	polysaccharide deacetylase family protein( <i>Streptococcus pyogenes</i> MGAS2096)	MGAS2096_Spy1182(e-value: 4e-35)
471_2	tRNA-dihydrouridine synthase( <i>Acinetobacter baumannii</i> ACICU)	ACICU_00749(e-value: 1e-16)
484_1	protein of unknown function DUF74( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_1999(e-value: 2e-51)
496_0	hypothetical protein( <i>Caldicellulosiruptor saccharolyticus</i> DSM 8903)	Csac_2063(e-value: 4e-08)
497_0	polar amino acid ABC transporter, inner membrane subunit( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_1162(e-value: 4e-115)
510_1	general secretion pathway protein F( <i>Methylococcus capsulatus</i> str. Bath)	xpsF(e-value: 1e-40)
522_2	GTP-binding protein TypA( <i>Rickettsia bellii</i> RML369-C)	RBE_0285(e-value: 6e-37)
528_0	protein of unknown function DUF1275( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_0162(e-value: 1e-98)
555_1	hypothetical protein( <i>Cellvibrio japonicus</i> Ueda107)	CJA_2591(e-value: 2e-15)
558_1	putative protease HtpX( <i>Tropheryma whipplei</i> str. Twist)	TWT013(e-value: 3e-82)
574_0	hypothetical protein( <i>Methylacidiphilum infernorum</i> V4)	Minf_1845(e-value: 6e-10)
574_1	Holliday junction DNA helicase RuvB( <i>Vibrio vulnificus</i> CMCP6)	VV1_2161(e-value: 3e-25)
594_0	glycosyl transferase, group 1( <i>Acidithiobacillus ferrooxidans</i> ATCC 53993)	Lferr_0086(e-value: 3e-08)
603_0	glutamine amidotransferase class-I( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_1909(e-value: 6e-97)
604_0	hypothetical protein( <i>Roseiflexus</i> sp. RS-1)	RoseRS_3685(e-value: 1e-10)
634_0	metalloendopeptidase( <i>Bifidobacterium animalis</i> subsp. lactis AD011)	BLA_1066(e-value: 3e-06)
636_1	transcriptional regulator( <i>Bacillus clausii</i> KSM-K16)	ABC3138(e-value: 1e-25)
646_0	similar to hemolysin-like( <i>Bacillus licheniformis</i> ATCC 14580)	yrkA2(e-value: 2e-15)
666_1	putative cytoplasmic protein( <i>Geobacillus thermodenitrificans</i> NG80-2)	GTNG_3408(e-value: 6e-16)
669_0	phosphotransacetylase( <i>Helicobacter pylori</i> HPAG1)	HPAG1_0885(e-value: 2e-32)
681_0	hypothetical protein( <i>Staphylococcus carnosus</i> subsp. carnosus TM300)	Sca_1875(e-value: 7e-18)
681_1	EmrB/QacA family drug resistance transporter( <i>Bacillus cereus</i> ATCC 10987)	BCE_2916(e-value: 3e-45)
699_1	trans-sulfuration enzyme family protein( <i>Chlorobium tepidum</i> TLS)	CT0703(e-value: 1e-10)
712_0	phosphoglucomutase( <i>Deinococcus radiodurans</i> R1)	pgm(e-value: 2e-07)
712_1	penicillin-binding protein 1A( <i>Staphylococcus aureus</i> RF122)	SAB1588(e-value: 3e-22)
717_1	Glycoside hydrolase family 57( <i>Thermotoga neapolitana</i> DSM 4359)	CTN_1055(e-value: 2e-32)
728_0	PEBP family protein( <i>Geobacter uraniireducens</i> Rf4)	Gura_1648(e-value: 5e-27)
734_2	putative nitrogen regulatory IIA protein (enzyme IIA-ntr) (phosphotransferase enzyme II, A component)( <i>Candidatus</i> Protochlamydia amoebophila UWE25)	ptsN(e-value: 2e-06)
748_9	RNA polymerase sigma-G factor( <i>Clostridium tetani</i> E88)	CTC01128(e-value: 3e-07)
755_1	mannose-1-phosphate guanylyltransferase( <i>Rickettsia bellii</i> RML369-C)	RBE_0245(e-value: 7e-08)
793_0	single-strand binding protein( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_0211(e-value: 4e-54)
802_0	Tyrosyl-tRNA synthetase ( <i>Geobacillus stearothermophilus</i> )	tyrS(e-value: 6e-64)

814_2	elongation factor Ts( <i>Thermus thermophilus</i> HB27)	tsf(e-value: 2e-42)
814_4	30S ribosomal protein S2( <i>Acinetobacter baumannii</i> ATCC 17978)	A1S_2323(e-value: 1e-16)
828_0	narrowly conserved hypothetical protein( <i>Bifidobacterium longum</i> subsp. <i>infantis</i> ATCC 15697)	Blon_1036(e-value: 1e-17)
831_0	ribonuclease P protein component( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_2305(e-value: 2e-45)
836_4	holliday junction DNA helicase motor protein( <i>Haemophilus parasuis</i> SH0165)	ruvA(e-value: 3e-13)
843_0	Rossmann fold nucleotide-binding protein involved in DNA uptake( <i>Streptococcus suis</i> 05ZYH33)	SSU05_0987(e-value: 8e-16)
851_0	transcriptional regulator( <i>Streptococcus suis</i> 05ZYH33)	SSU05_2193(e-value: 2e-23) P9515_05771(e-value: 8e-08)
851_1	Signal peptidase I( <i>Prochlorococcus marinus</i> str. MIT 9515) truncated resolvase( <i>Staphylococcus aureus</i> subsp. <i>aureus</i> Mu50)	truncated-res(e-value: 2e-13)
852_0	hypothetical protein( <i>Leifsonia xyli</i> subsp. <i>xyli</i> str. CTCB07)	Lxx01200(e-value: 4e-74)
855_0	ribosomal protein L31( <i>Catenulispora acidiphila</i> DSM 44928)	Caci_4370(e-value: 8e-23)
861_1	ammonium transporter( <i>Renibacterium salmoninarum</i> ATCC 33209)	RSaI33209_1070(e-value: 2e-08)
867_0	OmpA/MotB domain protein( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_1720(e-value: 8e-23)
903_1	excinuclease ABC subunit A( <i>Erythrobacter litoralis</i> HTCC2594)	ELI_07895(e-value: 8e-06)
905_0	H <sup>+</sup> -transporting two-sector ATPase E subunit( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_0755(e-value: 8e-86)
941_0	Spo0B-associated GTP-binding protein( <i>Lysinibacillus sphaericus</i> C3-41)	Bsph_3946(e-value: 5e-50)
945_0	cytidine deaminase( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_0864(e-value: 4e-64)
954_0	Probable deoxyribose-phosphate aldolase( <i>Thermococcus sibiricus</i> MM 739)	TSIB_1148(e-value: 1e-53)
964_0	hemolysin activator protein precursor( <i>Fusobacterium nucleatum</i> subsp. <i>nucleatum</i> ATCC 25586)	FN0293(e-value: 8e-10)
980_0	Putative AAA+ superfamily ATPase( <i>Bifidobacterium longum</i> DJO10A)	BLD_0142(e-value: 9e-19)
1072_0	hypothetical protein( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_1795(e-value: 1e-44)
1090_1	uroporphyrinogen III synthase (hemD)( <i>Methanocaldococcus jannaschii</i> DSM 2661)	MJ0994(e-value: 1e-13)
1092_2	uroporphyrinogen-III C-methyltransferase( <i>Lysinibacillus sphaericus</i> C3-41)	Bsph_3433(e-value: 2e-15)
1092_3	hypothetical protein( <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> MGCS10565)	Sez_1955(e-value: 9e-09)
1095_0	hypothetical protein( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_1783(e-value: 4e-45)
1138_2	branched-chain amino acid transport protein( <i>Bacillus cereus</i> E33L)	aziC(e-value: 1e-13)
1141_0	hypothetical protein( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_1940(e-value: 7e-65)
1187_4	PTS system, mannose-specific IIAB component( <i>Streptococcus pyogenes</i> MGAS2096)	MGAS2096_Spy1506(e-value: 2e-33)
1285_1	riboflavin kinase( <i>Bacillus cereus</i> 03BB102)	BCA_2148(e-value: 5e-17)
1306_0	NUDIX hydrolase( <i>Pyrobaculum arsenaticum</i> DSM 13514)	Pars_2356(e-value: 5e-08)
1319_0	heat shock protein Hsp20( <i>Sulfurihydrogenibium</i> sp. YO3AOP1)	SYO3AOP1_1159(e-value: 5e-13)
1323_8	phosphoribosyltransferase( <i>Candidatus Solibacter usitatus</i> Ellin6076)	Acid_3419(e-value: 1e-12)
1323_9	ribosomal protein L33( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_1899(e-value: 2e-21)
1365_3	Dihydrolipoyllysine-residue succinyltransferase( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_0543(e-value: 3e-140)
1426_1		

1468_2	putative metal dependent phosphohydrolase( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_1403(e-value: 1e-49)
1473_5	hypothetical protein( <i>Listeria monocytogenes</i> EGD-e)	Imo2078(e-value: 7e-21)
1531_0	50S ribosomal protein I14( <i>Heliobacterium modesticaldum</i> lce1)	rplN(e-value: 2e-43)
1561_4	TfoX domain protein( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_1291(e-value: 3e-52)
1604_0	phosphoribosyl-ATP pyrophosphatase( <i>Lactobacillus fermentum</i> IFO 3956)	hisE(e-value: 3e-25)
1616_0	30S ribosomal protein S8( <i>Pelobacter propionicus</i> DSM 2379)	rpsH(e-value: 3e-26)
1619_1	hypothetical protein( <i>Staphylococcus saprophyticus</i> subsp. <i>saprophyticus</i> ATCC 15305)	SSP0469(e-value: 1e-07)
1634_0	ABC type periplasmic choline/glycine/betaine binding protein( <i>Yersinia pestis</i> Nepal516)	YPN_2780(e-value: 8e-08)
1640_1	ribosomal protein L15( <i>Coprothermobacter proteolyticus</i> DSM 5265)	rplO(e-value: 1e-19)
1646_0	hypothetical protein( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_1518(e-value: 5e-113)
1674_0	MarR family transcriptional regulator( <i>Streptococcus agalactiae</i> A909)	SAK_1868(e-value: 9e-39)
1685_0	hypothetical protein( <i>Macrococcus caseolyticus</i> JCSC5402)	MCCL_1596(e-value: 9e-24)
1695_0	hypothetical protein( <i>Yersinia pestis</i> Nepal516)	YPN_2781(e-value: 5e-11)
1707_0	sodium-glutamate/aspartate symporter( <i>Bacillus halodurans</i> C-125)	BH3227(e-value: 5e-10)
1710_1	membrane protein of unknown function( <i>Delftia acidovorans</i> SPH-1)	Daci_0859(e-value: 2e-08)
1713_1	50S ribosomal protein L5( <i>Psychrobacter</i> sp. PRwf-1)	rplE(e-value: 6e-44)
1717_2	mannose-1-phosphate guanylyltransferase, putative( <i>Clostridium novyi</i> NT)	NT01CX_0602(e-value: 3e-12)
1718_0	NUDIX hydrolase( <i>Novosphingobium aromaticivorans</i> DSM 12444)	Saro_2655(e-value: 3e-06)
1728_0	hypothetical protein( <i>Bacillus cereus</i> ATCC 10987)	BCE_4466(e-value: 1e-13)
1729_0	hypothetical protein( <i>Actinobacillus pleuropneumoniae</i> serovar 7 str. AP76)	APP7_0688(e-value: 1e-15)
1735_0	50S ribosomal protein L6( <i>Bradyrhizobium</i> sp. BTAi1)	rplF(e-value: 8e-40)
1736_0	phenazine biosynthesis protein PhzF family( <i>Akkermansia muciniphila</i> ATCC BAA-835)	Amuc_0023(e-value: 8e-81)
1740_0	hypothetical protein( <i>Methanosphaera stadtmanae</i> DSM 3091)	Msp_0734(e-value: 2e-20)
1754_1	Protein of unknown function DUF214( <i>Brucella abortus</i> S19)	BAbS19_I15750(e-value: 3e-22)
1754_3	putative ABC transporter, ATP-binding protein( <i>Streptococcus mutans</i> UA159)	SMU.863(e-value: 8e-68)
1760_0	ribosome-binding factor A( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_1316(e-value: 3e-58)
1766_1	hypothetical protein( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_1144(e-value: 1e-39)
1769_1	30S ribosomal protein S10( <i>Lactobacillus reuteri</i> JCM 1112)	LAR_1395(e-value: 1e-31)
1773_0	lipid A biosynthesis acyltransferase( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_0285(e-value: 1e-143)
1776_2	UDP-N-acetylmuramate--L-alanine ligase( <i>Burkholderia cenocepacia</i> MC0-3)	murC(e-value: 5e-44)
1777_1	malate dehydrogenase( <i>Lactobacillus rhamnosus</i> GG)	LGG_02876(e-value: 2e-27)
1778_1	hypothetical protein( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_0532(e-value: 1e-36)
1780_0	D-tyrosyl-tRNA(Tyr) deacylase( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_0701(e-value: 2e-55)
1783_1	hypothetical protein( <i>Chlamydophila pneumoniae</i> J138)	CPj0340(e-value: 2e-09)
1784_1	hypothetical protein( <i>Porphyromonas gingivalis</i> ATCC 33277)	PGN_0382(e-value: 5e-21)
1788_1	small GTP-binding protein( <i>Leptotrichia buccalis</i> C-1013-b)	Lebu_1928(e-value: 1e-85)

1798_0	Type IV pili nucleotide-binding protein( <i>Francisella tularensis</i> subsp. holarctica)	FTL_1770(e-value: 2e-53)
1800_1	ParA family ATPase( <i>Symbiobacterium thermophilum</i> IAM 14863)	STH3333(e-value: 2e-76)
1801_0	single-stranded-DNA-specific exonuclease( <i>Streptococcus pyogenes</i> MGAS9429)	MGAS9429_Spy0784(e-value: 5e-43)
1804_1	recombinase( <i>Fusobacterium nucleatum</i> subsp. polymorphum ATCC 10953)	FNP_pFN3g09(e-value: 2e-26)
1805_1	hypothetical protein( <i>Flavobacterium psychrophilum</i> JIP02/86)	FP0837(e-value: 3e-35)
1811_1	ribosomal protein S9( <i>Petrotoga mobilis</i> SJ95)	Pmob_0800(e-value: 2e-31)
1812_0	ribonucleotide-diphosphate reductase subunit beta( <i>Candidatus Liberibacter asiaticus</i> str. psy62)	CLIBASIA_00075(e-value: 4e-16)
1813_0	phosphotransferase system IIC component, glucose/maltose/N-acetylglucosamine-specific( <i>Streptococcus suis</i> 98HAH33)	SSU98_1936(e-value: 2e-68)
1814_0	dihydrolipoamide dehydrogenase( <i>Desulfotomaculum reducens</i> MI-1)	Dred_2832(e-value: 5e-36)
1821_11	hypothetical protein( <i>Clostridium kluveri</i> NBRC 12016)	CKR_1146(e-value: 5e-09)
1828_4	phage protein( <i>Flavobacterium psychrophilum</i> JIP02/86)	FP2178(e-value: 1e-12)
1829_0	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase( <i>Lysinibacillus sphaericus</i> C3-41)	Bsph_2979(e-value: 9e-65)
1833_0	rRNA methylase( <i>Micrococcus luteus</i> NCTC 2665)	Mlut_02030(e-value: 1e-54)
1842_0	ABC-type polysaccharide/polyol phosphate transport system, ATPase component( <i>Streptococcus suis</i> 98HAH33)	SSU98_1301(e-value: 9e-86)
1842_1	ABC-type polysaccharide/polyol phosphate export system, permease component( <i>Streptococcus suis</i> 98HAH33)	SSU98_1302(e-value: 9e-66)
1843_0	FoID bifunctional protein( <i>Thermodesulfovibrio yellowstonii</i> DSM 11347)	THEYE_A0674(e-value: 1e-33)
1844_0	CTP synthase( <i>Mycoplasma mycoides</i> subsp. <i>mycoides</i> SC str. PG1)	pyrG(e-value: 3e-40)
1844_1	large conductance mechanosensitive channel protein( <i>Dyadobacter fermentans</i> DSM 18053)	Dfer_3491(e-value: 4e-06)
1845_1	chaperonin Hsp40(uncultured methanogenic archaeon RC-1)	dnaJ(e-value: 7e-51)
1850_1	hypothetical protein( <i>Thermobifida fusca</i> YX)	Tfu_0647(e-value: 4e-24)
1850_2	hypothetical protein( <i>Corynebacterium aurimucosum</i> ATCC 700975)	cauri_2344(e-value: 1e-24) Chy400_2582(e-value: 3e-48)
1853_1	ribosomal protein S4( <i>Chloroflexus</i> sp. Y-400-fl)	rplQ(e-value: 4e-28)
1853_4	ribosomal protein L17( <i>Nautilia profundicola</i> AmH)	Lebu_0669(e-value: 8e-71)
1889_2	ybaK/ebcC protein( <i>Leptotrichia buccalis</i> C-1013-b)	
1968_2	ABC transporter, permease; probable glutamine ABC transporter, permease( <i>Bacillus cereus</i> Q1)	glnP(e-value: 1e-17)
2054_1	glycosyl transferase, group 1( <i>Acaryochloris marina</i> MBIC11017)	AM1_2714(e-value: 7e-13)
2133_1	protein of unknown function DUF45( <i>Prosthecochloris aestuarii</i> DSM 271)	Paes_0312(e-value: 1e-09)