

Journal name: Applied Microbiology and Biotechnology

Manuscript Title: Coaggregated *E. faecalis* with *F. nucleatum* regulated environmental stress responses and inflammatory effects

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Fig. S1. The TEM of coaggregate (A) or coculture (B) Ef and Fnp. The yellow arrows indicate intergeneric coaggregation of long rod-shaped Fnp and spherical Ef. The Ef and Fnp was scattered in the coculture state.

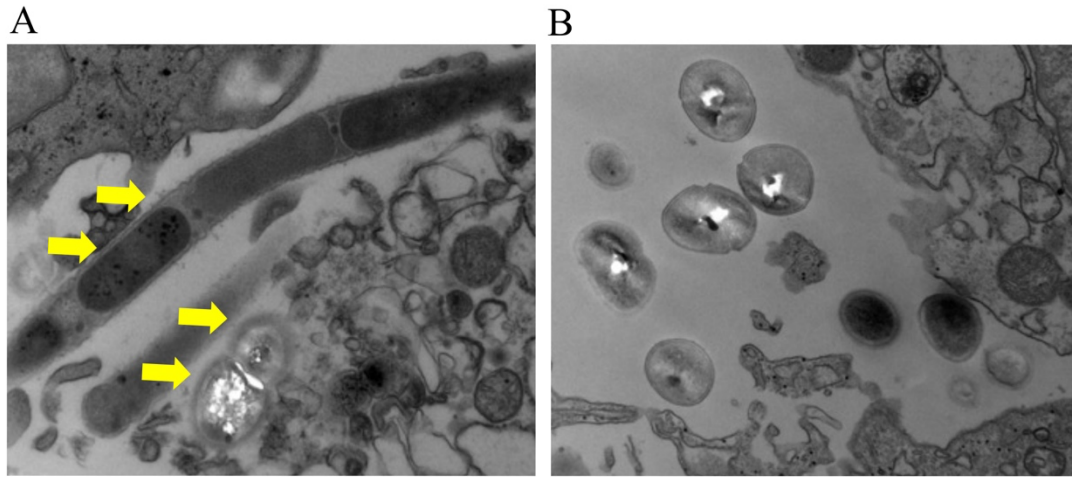


Fig.S2. Validation of RNA-Seq results by RT-qPCR. The levels of selected genes in dual-species coaggregates versus monoculture Ef (A) or Fnp (B) were assessed by RT-qPCR via normalized to 16S rRNA. Graphs show the mean $\pm$ S.D. of three independent assays. There were strong correlations between the RNA-seq and RT-qPCR in each species (Pearson's correlation coefficients were 0.97 for Ef and 0.96 for Fnp, $P < 0.05$).

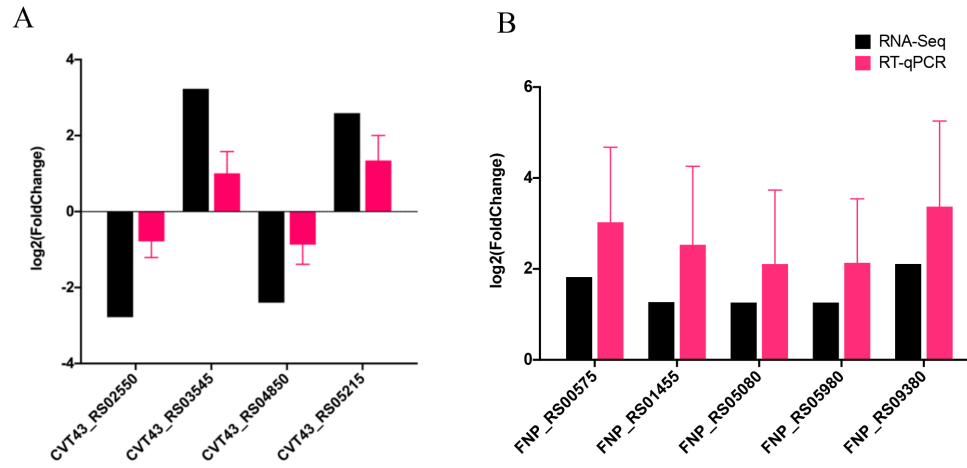


Table S1. Primers used for RT-qPCR.

Gene ID ^a	Prime sequence (5'-3')	Product length (bp)
Ef-16S rRNA	F: CCGAGTGCTTGCACTCAATTGG R: CTCTTATGCCATGCGGCATAAAC	137
CVT43_RS02550 (<i>arcC</i>)	F: CACAAACCGCTGCAAAATCC R: AACGGCACGACATCTTCTGG	142
CVT43_RS03545 (<i>msmX</i>)	F: AAACGGGTGGAAAATGCTGC R: AGACTTTGGCATCACGGACA	130
CVT43_RS04850 (<i>ulaC</i>)	F: GCAAGAGGCGATTTCAGGAAAG R: CCTCTGATGAATGTGGCATGG	149
CVT43_RS05215 (<i>ireB</i>)	F: ACCCGGCTTACATTCTCGT R: TCGATTCCGTGGTTCGCTA	112
Fnp-16S rRNA	F: AGCTATGGTATCAACTGGAATGTCT R: TCATAGGCAATCTTAGCTCCTACA	140
FNP_RS05980 (<i>lptF</i>)	F: AGCTATGGTATCAACTGGAATGTCT R: TCATAGGCAATCTTAGCTCCTACA	156
FNP_RS01455 (K08974)	F: CCTGGAGTTTCTGGTGGAACAT R: AATTCCTGTTCTGCTCCAAGT	153
FNP_RS00575 (<i>murI</i>)	F: CTGTTTTTGATGCTGGACTTGGT R: TGTTTTTGCACCATAAGGGAAGC	119
FNP_RS05080 (<i>mutS2</i>)	F: ACTACTCACTTTGACTCTGTTGTTG R: AGCATCTTTTGGCACTTCTGTTT	183
FNP_RS09380 (<i>aroE</i>)	F: GATGAGGCAAAGGGGATAGGT R: TATACACACTGGCACTTGCTCC	175

^a‘CVT43’ numbers refer to Ef genes, whereas ‘FNP’ numbers indicate Fnp genes. F, forward primer; R, reverse primer.

Table S2. Ef genes that were significantly regulated by coaggregation with Fnp.

Gene ID	gene	Predicted function	log2 (Ef-fnp/Ef)
CVT43_RS03545	<i>msmX,msmK, malK,sugC, ggtA,msiK</i>	multiple sugar transport system ATP-binding protein	3.23
CVT43_RS09730	<i>ppsR</i>	[pyruvate, water dikinase]-phosphate phosphotransferase	2.32
CVT43_RS05095	<i>scrK</i>	fructokinase [EC:2.7.1.4]	2.32
CVT43_RS08305	<i>pgl</i>	6-phosphogluconolactonase [EC:3.1.1.31]	2.08
CVT43_RS08540	<i>cggR</i>	central glycolytic genes regulator	1.99
CVT43_RS01950	<i>nagB</i>	glucosamine-6-phosphate deaminase [EC:3.5.99.6]	1.83
CVT43_RS10395	<i>bglG</i>	beta-glucoside operon transcriptional antiterminator	1.54
CVT43_RS01750	<i>kduI</i>	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase [EC:5.3.1.17]	1.51
CVT43_RS04850	<i>ulaC</i>	PTS system, ascorbate-specific IIA component [EC:2.7.1.194]	-2.40
CVT43_RS09810	<i>scrA</i>	PTS system, sucrose-specific IIB component [EC:2.7.1.211]	-1.72
CVT43_RS09815	<i>murQ</i>	N-acetylmuramic acid 6-phosphate etherase [EC:4.2.1.126]	-1.67
CVT43_RS02760	<i>cspA</i>	cold shock protein (beta-ribbon, CspA family)	2.14
CVT43_RS13305	<i>ctsR</i>	transcriptional regulator of stress and heat shock response	2.04
CVT43_RS09415	<i>clpB</i>	ATP-dependent Clp protease ATP-binding subunit ClpB	1.89
CVT43_RS13300	<i>clpC</i>	ATP-dependent Clp protease ATP-binding subunit ClpC	1.83
CVT43_RS06910	<i>perR</i>	Fur family transcriptional regulator, peroxide stress response regulator	1.59
CVT43_RS01510	<i>doc</i>	death on curing protein	1.50
CVT43_RS03260	<i>dnaB</i>	replication initiation and membrane attachment protein	2.86
CVT43_RS05220	<i>ruvX</i>	putative holliday junction resolvase [EC:3.1]	2.69
CVT43_RS03265	<i>dnaI</i>	primosomal protein DnaI	2.42
CVT43_RS06880	<i>lexA</i>	repressor LexA [EC:3.4.21.88]	2.41
CVT43_RS01035	<i>mfd</i>	transcription-repair coupling factor (superfamily II helicase) [EC:3.6.4]	1.70
CVT43_RS06735	<i>hupB</i>	DNA-binding protein HU-beta	-1.75
CVT43_RS08355	<i>glpK</i>	glycerol kinase [EC:2.7.1.30]	2.60
CVT43_RS08350	E1.1.3.21	alpha-glycerophosphate oxidase [EC:1.1.3.21]	2.37
CVT43_RS08345	<i>glpF</i>	glycerol uptake facilitator protein	2.30
CVT43_RS07015	<i>clsA_B</i>	cardiolipin synthase A/B [EC:2.7.8]	1.71
CVT43_RS06110	<i>gldA</i>	glycerol dehydrogenase [EC:1.1.1.6]	-2.11
CVT43_RS05215	<i>ireB</i>	iron responsive element binding protein	2.59
CVT43_RS10955	<i>lsa</i>	lincosamide and streptogramin A transport	2.03

		system ATP-binding/permease protein	
CVT43_RS09775	<i>padR</i>	PadR family transcriptional regulator, regulatory protein PadR	1.69
CVT43_RS06395	<i>msrA</i>	macrolide transport system ATP- binding/permease protein	-2.33
CVT43_RS08405	ATP2C	Ca ²⁺ -transporting ATPase [EC:3.6.3.8]	1.86
CVT43_RS03185	<i>opuA</i>	osmoprotectant transport system ATP- binding protein	1.85
CVT43_RS08820	<i>mntA</i>	manganese/zinc transport system ATP- binding protein [EC:3.6.3.35]	1.66
CVT43_RS12005	<i>allP</i>	allantoin permease	-2.29
CVT43_RS12520	ABC-2.P	ABC-2 type transport system permease protein	-2.20
CVT43_RS03750	<i>psiE</i>	protein PsiE	2.25
CVT43_RS09545	<i>rseP</i>	regulator of sigma E protease [EC:3.4.24]	1.82
CVT43_RS09930	<i>ftsW</i>	cell division protein FtsW	1.66
CVT43_RS12245	<i>srtA</i>	sortase A [EC:3.4.22.70]	1.83
CVT43_RS11590	<i>ppiB</i>	peptidyl-prolyl cis-trans isomerase B (cyclophilin B) [EC:5.2.1.8]	1.90
CVT43_RS06905	<i>cysK</i>	cysteine synthase [EC:2.5.1.47]	1.81
CVT43_RS02550	<i>arcC</i>	carbamate kinase [EC:2.7.2.2]	-2.78
CVT43_RS05290	ABC.SP.P1	putative spermidine/putrescine transport system permease protein	-2.58
CVT43_RS02540	<i>gadC</i>	glutamate:GABA antiporter	-2.52
CVT43_RS05300	ABC.SP.A	putative spermidine/putrescine transport system ATP-binding protein	-2.37
CVT43_RS02025	<i>tyrS</i>	tyrosyl-tRNA synthetase [EC:6.1.1.1]	-1.65
CVT43_RS02880	ABC.PA.S	polar amino acid transport system substrate-binding protein	-1.65
CVT43_RS03255	<i>nrdR</i>	transcriptional repressor NrdR	3.00
CVT43_RS09420	K15977	putative oxidoreductase	3.43
CVT43_RS11165	<i>tmk</i>	dTMP kinase [EC:2.7.4.9]	2.19
CVT43_RS07850	<i>purM</i>	phosphoribosylformylglycinamide cyclo- ligase [EC:6.3.3.1]	-2.79
CVT43_RS11880	E3.1.3.1	alkaline phosphatase [EC:3.1.3.1]	-1.88
CVT43_RS09170	<i>tadA</i>	tRNA(adenine34) deaminase [EC:3.5.4.33]	-1.47
CVT43_RS02640	<i>bapA</i>	large repetitive protein	-2.23
CVT43_RS05900	<i>ftsK</i>	DNA segregation ATPase FtsK/SpoIIIE, S- DNA-T family	-1.99
CVT43_RS02140	<i>glcR</i>	DeoR family transcriptional regulator, carbon catabolite repression regulator	-1.63

Table S3. Fnp genes that were significantly regulated by coaggregation with Ef.

Gene ID	gene	Predicted function	log2 (Ef-fnp/Ef)
FNP_RS03635	<i>ppa</i>	inorganic pyrophosphatase [EC:3.6.1.1]	3.31
FNP_RS09050	<i>rnmV</i>	ribonuclease M5 [EC:3.1.26.8]	2.51
FNP_RS02885	<i>rluB</i>	23S rRNA pseudouridine2605 synthase [EC:5.4.99.22]	2.24
FNP_RS09695	<i>pilD</i>	leader peptidase (prepilin peptidase) / N- methyltransferase [EC:3.4.23.43 2.1.1]	2.20
FNP_RS02455	<i>bioC</i>	malonyl-CoA O-methyltransferase [EC:2.1.1.197]	2.12
FNP_RS05330	<i>rsmC</i>	1 16S rRNA (guanine1207-N2)- methyltransferase [EC:2.1.1.172]	2.10
FNP_RS03450	<i>hsdS</i>	type I restriction enzyme, S subunit [EC:3.1.21.3]	2.08
FNP_RS04550	K07027	glycosyltransferase 2 family protein	2.03
FNP_RS08120	<i>ksgA</i>	16S rRNA (adenine1518-N6/adenine1519- N6)-dimethyltransferase [EC:2.1.1.182]	1.85
FNP_RS05955	<i>rluC</i>	23S rRNA pseudouridine955/2504/2580 synthase [EC:5.4.99.24]	1.85
FNP_RS08360	<i>folA</i>	dihydrofolate reductase [EC:1.5.1.3]	1.72
FNP_RS08820	<i>rng, cafA</i>	ribonuclease G [EC:3.1.26]	1.68
FNP_RS11175	<i>ppaC</i>	manganese-dependent inorganic pyrophosphatase [EC:3.6.1.1]	1.66
FNP_RS07675	<i>atpI</i>	ATP synthase protein I	1.55
FNP_RS04530	<i>neuA</i>	N-acylneuraminate cytidyltransferase [EC:2.7.7.43]	1.54
FNP_RS09480	<i>nadA</i>	quinolinate synthase [EC:2.5.1.72]	1.53
FNP_RS10470	<i>coaE</i>	dephospho-CoA kinase [EC:2.7.1.24]	1.51
FNP_RS03200	<i>rsuA</i>	16S rRNA pseudouridine516 synthase [EC:5.4.99.19]	1.41
FNP_RS06550	<i>nadD</i>	nicotinate-nucleotide adenylyltransferase [EC:2.7.7.18]	1.39
FNP_RS10765	<i>ispD</i>	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase [EC:2.7.7.60]	1.35
FNP_RS04285	<i>gidB</i>	16S rRNA (guanine527-N7)- methyltransferase [EC:2.1.1.170]	1.32
FNP_RS05885	<i>nrnA</i>	bifunctional oligoribonuclease and PAP phosphatase NrnA [EC:3.1.3.7 3.1.13.3]	1.28
FNP_RS06935	<i>rsmE</i>	16S rRNA (uracil1498-N3)- methyltransferase [EC:2.1.1.193]	1.26
FNP_RS04875	<i>kdtA</i>	3-deoxy-D-manno-octulosonic-acid transferase [EC:2.4.99.12 2.4.99.13 2.4.99.14 2.4.99.15]	1.19
FNP_RS08245	<i>ppnK</i>	NAD ⁺ kinase [EC:2.7.1.23]	1.19
FNP_RS07160	<i>nagD</i>	NagD protein	1.18
FNP_RS08365	<i>thyA</i>	thymidylate synthase [EC:2.1.1.45]	1.18
FNP_RS09510	<i>rnpA</i>	ribonuclease P protein component [EC:3.1.26.5]	1.17
FNP_RS02645	<i>kdsB</i>	3-deoxy-manno-octulosonate cytidyltransferase (CMP-KDO synthetase)	1.14

[EC:2.7.7.38]			
FNP_RS08115	<i>hprT</i>	hypoxanthine phosphoribosyltransferase [EC:2.4.2.8]	1.14
FNP_RS10675	<i>truA</i>	tRNA pseudouridine38-40 synthase [EC:5.4.99.12]	1.12
FNP_RS03025	<i>dinG</i>	ATP-dependent DNA helicase DinG [EC:3.6.4.12]	1.11
FNP_RS07485	<i>tmk</i>	dTMP kinase [EC:2.7.4.9]	1.10
FNP_RS02460	<i>bioG</i>	pimeloyl-[acyl-carrier protein] methyl ester esterase [EC:3.1.1.85]	1.09
FNP_RS02860	<i>coaX</i>	type III pantothenate kinase [EC:2.7.1.33]	1.08
FNP_RS07515	<i>rsmD</i>	16S rRNA (guanine966-N2)- methyltransferase [EC:2.1.1.171]	1.07
FNP_RS07510	<i>xseB</i>	exodeoxyribonuclease VII small subunit [EC:3.1.11.6]	1.06
FNP_RS05415	<i>relA</i>	GTP pyrophosphokinase [EC:2.7.6.5]	1.06
FNP_RS08350	<i>cca</i>	tRNA nucleotidyltransferase (CCA-adding enzyme) [EC:2.7.7.72 3.1.3.- 3.1.4]	1.06
FNP_RS10775	K11145	ribonuclease III family protein [EC:3.1.26]	1.05
FNP_RS05345	E2.4.2.21	nicotinate-nucleotide-- dimethylbenzimidazole phosphoribosyltransferase [EC:2.4.2.21]	1.03
FNP_RS07520	<i>queA</i>	S-adenosylmethionine:tRNA ribosyltransferase-isomerase [EC:2.4.99.17]	1.03
FNP_RS11755	<i>parA</i>	chromosome partitioning protein	1.00
FNP_RS02290	<i>ribH</i>	6,7-dimethyl-8-ribityllumazine synthase [EC:2.5.1.78]	-1.06
FNP_RS03000	<i>nudF</i>	ADP-ribose pyrophosphatase [EC:3.6.1.13]	-1.05
FNP_RS05215	<i>thiN</i>	thiamine pyrophosphokinase [EC:2.7.6.2]	2.42
FNP_RS08265	E5.2.1.8	peptidylprolyl isomerase [EC:5.2.1.8]	2.29
FNP_RS06470	<i>pepE</i>	dipeptidase E [EC:3.4.13.21]	2.15
FNP_RS09380	<i>aroE</i>	shikimate dehydrogenase [EC:1.1.1.25]	2.11
FNP_RS02595	<i>aroK</i>	shikimate kinase [EC:2.7.1.71]	1.99
FNP_RS05705	<i>purC</i>	phosphoribosylaminoimidazole- succinocarboxamide synthase [EC:6.3.2.6]	1.91
FNP_RS02315	<i>cysE</i>	serine O-acetyltransferase [EC:2.3.1.30]	1.87
FNP_RS05455	<i>aroA</i>	3-phosphoshikimate 1- carboxyvinyltransferase [EC:2.5.1.19]	1.86
FNP_RS00575	<i>murI</i>	epidermal growth factor receptor substrate 15	1.82
FNP_RS02880	<i>scpB</i>	segregation and condensation protein B	1.62
FNP_RS03245	<i>scpA</i>	segregation and condensation protein A	1.55
FNP_RS05395	<i>thrB2</i>	homoserine kinase type II [EC:2.7.1.39]	1.54
FNP_RS05735	<i>leuS</i>	leucyl-tRNA synthetase [EC:6.1.1.4]	1.52
FNP_RS00620	<i>patB</i>	cystathione beta-lyase [EC:4.4.1.8]	1.45
FNP_RS05430	<i>tsaD</i>	N6-L-threonylcarbamoyladenine synthase [EC:2.3.1.234]	1.41
FNP_RS05090	<i>kamE</i>	beta-lysine 5,6-aminomutase beta subunit [EC:5.4.3.3]	1.41

FNP_RS05095	<i>lysE</i>	L-lysine exporter family protein LysE/ArgO	1.39
FNP_RS05060	<i>kce</i>	3-keto-5-aminoheptanoate cleavage enzyme [EC:2.3.1.247]	1.34
FNP_RS07650	<i>rimI</i>	[ribosomal protein S18]-alanine N- acetyltransferase [EC:2.3.1.266]	1.33
FNP_RS07470	<i>ppiD</i>	peptidyl-prolyl cis-trans isomerase D [EC:5.2.1.8]	1.31
FNP_RS02910	<i>ansA</i>	L-asparaginase [EC:3.5.1.1]	1.31
FNP_RS05770	E3.4.11	aminopeptidase [EC:3.4.11]	1.27
FNP_RS07525	<i>hemK</i>	release factor glutamine methyltransferase [EC:2.1.1.297]	1.25
FNP_RS06930	<i>mtaB</i>	threonylcarbamoyladenosine tRNA methylthiotransferase MtaB [EC:2.8.4.5]	1.23
FNP_RS05680	<i>purD</i>	phosphoribosylamine---glycine ligase [EC:6.3.4.13]	1.20
FNP_RS05690	<i>purN</i>	phosphoribosylglycinamide formyltransferase 1 [EC:2.1.2.2]	1.18
FNP_RS11095	<i>barA</i>	two-component system, NarL family, sensor histidine kinase BarA [EC:2.7.13.3]	1.18
FNP_RS05065	<i>kdd</i>	L-erythro-3,5-diaminoheptanoate dehydrogenase [EC:1.4.1.11]	1.15
FNP_RS05435	<i>tsaE</i>	tRNA threonylcarbamoyladenosine biosynthesis protein TsaE	1.15
FNP_RS06685	<i>gloB</i>	hydroxyacylglutathione hydrolase [EC:3.1.2.6]	1.12
FNP_RS03070	<i>thrC</i>	threonine synthase [EC:4.2.3.1]	1.11
FNP_RS03230	<i>coaBC</i>	phosphopantothenoylcysteine decarboxylase / phosphopantothenate---cysteine ligase [EC:4.1.1.36 6.3.2.5]	1.09
FNP_RS04170	<i>thiH</i>	2-iminoacetate synthase [EC:4.1.99.19]	1.08
FNP_RS10235	<i>tilS</i>	tRNA(Ile)-lysine synthase [EC:6.3.4.19]	1.07
FNP_RS05085	<i>kamD</i>	beta-lysine 5,6-aminomutase alpha subunit [EC:5.4.3.3]	1.05
FNP_RS05650	<i>cobD</i>	threonine-phosphate decarboxylase [EC:4.1.1.81]	1.02
FNP_RS12260	TC.AGCS	alanine or glycine:cation symporter, AGCS family	-10.44
FNP_RS00020	<i>livG</i>	branched-chain amino acid transport system ATP-binding protein	-1.89
FNP_RS00015	<i>livM</i>	branched-chain amino acid transport system permease protein	-1.82
FNP_RS00025	<i>livF</i>	branched-chain amino acid transport system ATP-binding protein	-1.78
FNP_RS03685	<i>putP</i>	sodium/proline symporter	-1.58
FNP_RS00010	<i>livH</i>	branched-chain amino acid transport system permease protein	-1.30
FNP_RS03495	E4.3.1.15	diaminopropionate ammonia-lyase [EC:4.3.1.15]	-1.27
FNP_RS08955	<i>eutB</i>	ethanolamine ammonia-lyase large subunit [EC:4.3.1.7]	-1.21
FNP_RS01560	<i>rlmH</i>	23S rRNA (pseudouridine1915-N3)- methyltransferase [EC:2.1.1.177]	2.55

FNP_RS05380	<i>hola</i>	DNA polymerase III subunit delta [EC:2.7.7.7]	2.50
FNP_RS10785	<i>holB</i>	DNA polymerase III subunit delta' [EC:2.7.7.7]	2.43
FNP_RS09630	<i>relE</i>	mRNA interferase RelE/StbE	2.39
FNP_RS12030	K07496	putative transposase	2.01
FNP_RS08480	<i>fnr</i>	CRP/FNR family transcriptional regulator, anaerobic regulatory protein	1.99
FNP_RS01500	<i>rpoE</i>	RNA polymerase sigma-70 factor, ECF subfamily	1.73
FNP_RS06855	<i>dinB</i>	DNA polymerase IV [EC:2.7.7.7]	1.71
FNP_RS03505	<i>rpoN</i>	RNA polymerase sigma-54 factor	1.51
FNP_RS12445	K07485	transposase	1.47
FNP_RS10620	<i>miaA</i>	tRNA dimethylallyltransferase [EC:2.5.1.75]	1.37
FNP_RS06330	<i>rapZ</i>	RNase adapter protein RapZ	1.36
FNP_RS07660	<i>cmoA</i>	tRNA (cmo5U34)-methyltransferase [EC:2.1.1]	1.36
FNP_RS10990	<i>sigH</i>	RNA polymerase sporulation-specific sigma factor	1.29
FNP_RS09490	<i>mnmE</i>	tRNA modification GTPase [EC:3.6.]	1.27
FNP_RS07795	<i>dtd</i>	D-aminoacyl-tRNA deacylase [EC:3.1.1.96]	1.21
FNP_RS06905	<i>yhbY</i>	RNA-binding protein	1.15
FNP_RS02360	<i>spoU</i>	RNA methyltransferase, TrmH family	1.14
FNP_RS10940	<i>fixB</i>	electron transfer flavoprotein alpha subunit	1.03
FNP_RS10245	K07082	UPF0755 protein	1.03
FNP_RS09755	ABC.X4.S	putative ABC transport system substrate- binding protein	4.83
FNP_RS09760	ABC.X4.P	putative ABC transport system permease protein	3.61
FNP_RS09765	ABC.X4.A	putative ABC transport system ATP-binding protein	2.70
FNP_RS10575	EPS15	epidermal growth factor receptor substrate 15	2.19
FNP_RS07870	<i>corA</i>	magnesium transporter	2.03
FNP_RS06430	<i>oppF</i>	oligopeptide transport system ATP-binding protein	1.86
FNP_RS02380	<i>crcB</i>	fluoride exporter	1.84
FNP_RS06435	ABC.PE.A	peptide/nickel transport system ATP-binding protein	1.75
FNP_RS00830	<i>lolD</i>	ribonuclease G [EC:3.1.26]	1.65
FNP_RS06570	<i>phnC</i>	phosphonate transport system ATP-binding protein [EC:3.6.3.28]	1.50
FNP_RS12035	<i>smpB</i>	SsrA-binding protein	1.46
FNP_RS08040	ABC.FEV.A	iron complex transport system ATP-binding protein [EC:3.6.3.34]	1.45
FNP_RS07430	<i>exbD</i>	biopolymer transport protein ExbD	1.34
FNP_RS01535	<i>cutC</i>	copper homeostasis protein	1.32
FNP_RS10060	<i>opuC</i>	osmoprotectant transport system substrate- binding protein	1.32

FNP_RS00750	ABCB-BAC	ATP-binding cassette, subfamily B, bacterial	1.30
FNP_RS09725	<i>gspD</i>	general secretion pathway protein D	1.29
FNP_RS10090	<i>ecfA1</i>	energy-coupling factor transport system ATP-binding protein [EC:3.6.3]	1.19
FNP_RS07615	<i>afuB</i>	iron(III) transport system permease protein	1.07
FNP_RS03840	<i>znuA</i>	zinc transport system substrate-binding protein	1.03
FNP_RS11950	<i>phnE</i>	phosphonate transport system permease protein	1.02
FNP_RS03270	<i>secF</i>	preprotein translocase subunit SecF	1.02
FNP_RS07440	ABC.PE.S	peptide/nickel transport system substrate- binding protein	1.01
FNP_RS03400	ABC.X4.S	putative ABC transport system substrate- binding protein	-1.65
FNP_RS00960	<i>trbC</i>	type IV secretion system protein TrbC	-1.53
FNP_RS08490	<i>mgtC</i>	putative Mg ²⁺ transporter-C (MgtC) family protein	-1.36
FNP_RS08345	<i>copZ</i>	copper chaperone	-1.20
FNP_RS01925	ABCB-BAC	ATP-binding cassette, subfamily B, bacterial	-1.13
FNP_RS07780	<i>nhaC</i>	Na ⁺ :H ⁺ antiporter, NhaC family	-1.03
FNP_RS11870	<i>dinJ</i>	DNA-damage-inducible protein J	3.35
FNP_RS02255	<i>recO</i>	DNA repair protein RecO (recombination protein O)	3.10
FNP_RS06745	<i>cas2</i>	CRISPR-associated protein Cas2	2.39
FNP_RS01235	<i>dnaN</i>	DNA polymerase III subunit beta [EC:2.7.7.7]	2.35
FNP_RS05080	<i>mutS2</i>	DNA mismatch repair protein MutS2	2.02
FNP_RS07640	<i>recJ</i>	single-stranded-DNA-specific exonuclease [EC:3.1]	1.67
FNP_RS00505	<i>recR</i>	recombination protein RecR	1.63
FNP_RS01285	<i>uvrD</i>	DNA helicase II / ATP-dependent DNA helicase PcrA [EC:3.6.4.12]	1.54
FNP_RS05340	<i>radC</i>	DNA repair protein RadC	1.54
FNP_RS10520	<i>dam</i>	DNA adenine methylase [EC:2.1.1.72]	1.49
FNP_RS06755	<i>cas4</i>	CRISPR-associated exonuclease Cas4 [EC:3.1.12.1]	1.44
FNP_RS09530	<i>recF</i>	DNA replication and repair protein RecF	1.34
FNP_RS06750	<i>casI</i>	CRISP-associated protein CasI	1.33
FNP_RS06335	<i>uvrC</i>	excinuclease ABC subunit C	1.31
FNP_RS03280	<i>ruvX</i>	putative holliday junction resolvase [EC:3.1]	1.24
FNP_RS00635	K03653	N-glycosylase/DNA lyase [EC:3.2.2.- 4.2.99.18]	1.23
FNP_RS08235	<i>xerD</i>	integrase/recombinase XerD	1.21
FNP_RS08225	<i>recG</i>	ATP-dependent DNA helicase RecG [EC:3.6.4.12]	1.20
FNP_RS06765	<i>cas5t</i>	CRISPR-associated protein Cas5t	1.10
FNP_RS01295	<i>sbcC</i> ,	DNA repair protein SbcC/Rad50	1.07
FNP_RS03300	<i>mutS</i>	DNA mismatch repair protein MutS	1.05
FNP_RS04680	RP-L23	large subunit ribosomal protein L23	2.40

FNP_RS07290	RP-L17	large subunit ribosomal protein L17	1.63
FNP_RS03015	<i>ybeY</i>	probable rRNA maturation factor	1.12
FNP_RS04640	RP-S18	small subunit ribosomal protein S18	1.06
FNP_RS03370	<i>rsgA</i>	ribosome biogenesis GTPase / thiamine phosphate phosphatase [EC:3.6.1.-3.1.3.100]	1.01
FNP_RS04535	<i>wecB</i>	UDP-N-acetylglucosamine 2-epimerase (non-hydrolysing) [EC:5.1.3.14]	1.70
FNP_RS04450	<i>galM</i>	aldose 1-epimerase [EC:5.1.3.3]	1.49
FNP_RS11910	<i>citE</i>	citrate lyase subunit beta / citryl-CoA lyase [EC:4.1.3.34]	-1.08
FNP_RS06555	<i>nagA</i>	N-acetylglucosamine-6-phosphate deacetylase [EC:3.5.1.25]	-1.01
FNP_RS05400	<i>clsA_B</i>	cardiolipin synthase A/B [EC:2.7.8]	1.65
FNP_RS04995	<i>ybgC</i>	acyl-CoA thioester hydrolase [EC:3.1.2]	1.24
FNP_RS01475	<i>lip</i>	triacylglycerol lipase [EC:3.1.1.3]	1.22
FNP_RS07415	E2.7.7.41,	phosphatidate cytidyltransferase [EC:2.7.7.41]	1.21
FNP_RS07410	<i>pgsA</i>	CDP-diacylglycerol---glycerol-3-phosphate 3-phosphatidyltransferase [EC:2.7.8.5]	1.10
FNP_RS08840	<i>acpP</i>	acyl carrier protein	1.04
FNP_RS07865	<i>glpP</i>	glycerol uptake operon antiterminator	1.00
FNP_RS11025	<i>glpF</i>	glycerol uptake facilitator protein	-1.15
FNP_RS07075	<i>waaL</i>	O-antigen ligase [EC:2.4.1]	2.00
FNP_RS07085	<i>waaY</i>	heptose II phosphotransferase [EC:2.7.1]	1.99
FNP_RS07125	<i>licD</i>	lipopolysaccharide cholinephosphotransferase [EC:2.7.8]	1.79
FNP_RS05980	<i>lptF</i>	lipopolysaccharide export system permease protein	1.26
FNP_RS00755	<i>lpxB</i>	lipid-A-disaccharide synthase [EC:2.4.1.182]	1.08
FNP_RS05910	<i>lpxL</i>	Kdo2-lipid IVA lauroyltransferase [EC:2.3.1.241]	1.05
FNP_RS09460	<i>yafQ</i>	mRNA interferase YafQ [EC:3.1]	3.47
FNP_RS10665	<i>yefM</i>	antitoxin YefM	2.34
FNP_RS11925	<i>abiQ</i>	protein AbiQ	2.09
FNP_RS11850	<i>yoeB</i>	toxin YoeB [EC:3.1]	1.77
FNP_RS04600	<i>higA-1</i>	antitoxin HigA-1	1.70
FNP_RS04435	<i>yggT</i>	YggT family protein	1.70
FNP_RS09880	<i>perR</i>	Fur family transcriptional regulator, peroxide stress response regulator	1.16
FNP_RS01260	<i>cspA</i>	cold shock protein (beta-ribbon, CspA family)	1.06
FNP_RS06560	<i>tabA</i>	biofilm protein TabA	1.39
FNP_RS01455	K08974	putative membrane protein	1.27
FNP_RS05985	<i>cypA</i>	membrane protein required for colicin V production	1.07
FNP_RS02870	<i>maf</i>	septum formation protein	1.06
FNP_RS05515	<i>cobK-cbiJ</i>	precorrin-6A/cobalt-precorin-6A reductase	2.54

[EC:1.3.1.54 1.3.1.106]			
FNP_RS01220	<i>met8</i>	precorrin-2 dehydrogenase / sirohydrochlorin ferrochelatase [EC:1.3.1.76 4.99.1.4]	1.83
FNP_RS07200	<i>cblK</i>	sirohydrochlorin cobaltochelatase [EC:4.99.1.3]	1.39
FNP_RS05285	<i>mtfS</i>	5-formyltetrahydrofolate cyclo-ligase [EC:6.3.3.2]	1.31
FNP_RS05900	<i>folC</i>	dihydrofolate synthase / folylpolyglutamate synthase [EC:6.3.2.12 6.3.2.17]	1.09
FNP_RS05780	<i>bioD</i>	dethiobiotin synthetase [EC:6.3.3.3]	1.98
FNP_RS06030	<i>nirA</i>	ferredoxin-nitrite reductase [EC:1.7.7.1]	1.74
FNP_RS07990	E2.1.1.104	caffeoyl-CoA O-methyltransferase [EC:2.1.1.104]	1.35
FNP_RS07500	<i>uppS</i>	undecaprenyl diphosphate synthase [EC:2.5.1.31]	1.02
FNP_RS02815	<i>chuW</i>	anaerobillin synthase [EC:2.1.1.342]	1.02
FNP_RS02000	<i>ftsQ</i>	cell division protein FtsQ	2.16
FNP_RS08710	<i>minE</i>	cell division topological specificity factor	2.09
FNP_RS05265	<i>splB</i>	spore photoproduct lyase [EC:4.1.99.14]	1.68
FNP_RS05880	<i>sepF</i>	cell division inhibitor SepF	1.01
FNP_RS00790	<i>yesN</i>	two-component system, response regulator YesN	1.78
FNP_RS08965	<i>pdtaS</i>	two-component system, sensor histidine kinase PdtaS [EC:2.7.13.3]	1.70
FNP_RS08470	K02477	two-component system, LytTR family, response regulator	1.36
FNP_RS07475	K02481	two-component system, NtrC family, response regulator	1.22
FNP_RS11990	E4.2.1.46	dTDP-glucose 4,6-dehydratase [EC:4.2.1.46]	1.89
FNP_RS01900	<i>amiABC</i>	N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]	1.17
FNP_RS10860	<i>yfiH</i>	polyphenol oxidase [EC:1.10.3]	1.09
FNP_RS02030	<i>mraY</i>	phospho-N-acetylmuramoyl-pentapeptide- transferase [EC:2.7.8.13]	-1.02
FNP_RS01545	<i>cidA</i>	holin-like protein	1.72
FNP_RS04970	<i>bax</i>	Bax protein	1.43
FNP_RS02265	<i>mreC</i>	rod shape-determining protein MreC	1.41
FNP_RS09010	<i>lspA</i>	signal peptidase II [EC:3.4.23.36]	1.57
FNP_RS05015	<i>thiJ</i>	protein deglycase [EC:3.5.1.124]	1.31