Supplemental Figures

Figure S1. Number of sequencing read pairs that match known microbial genomes are shown for the 25 most abundant genomes.

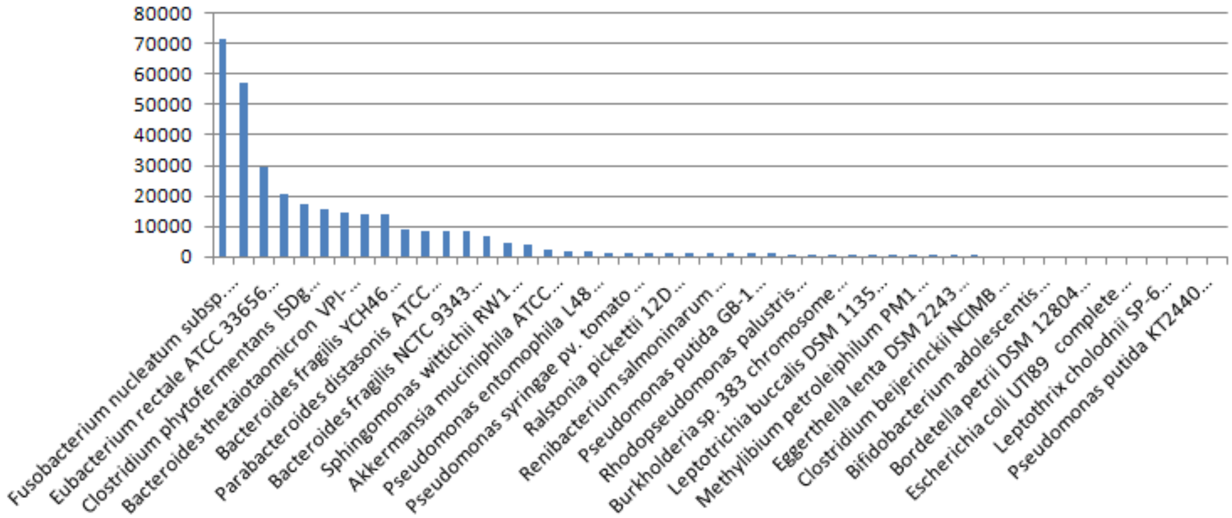
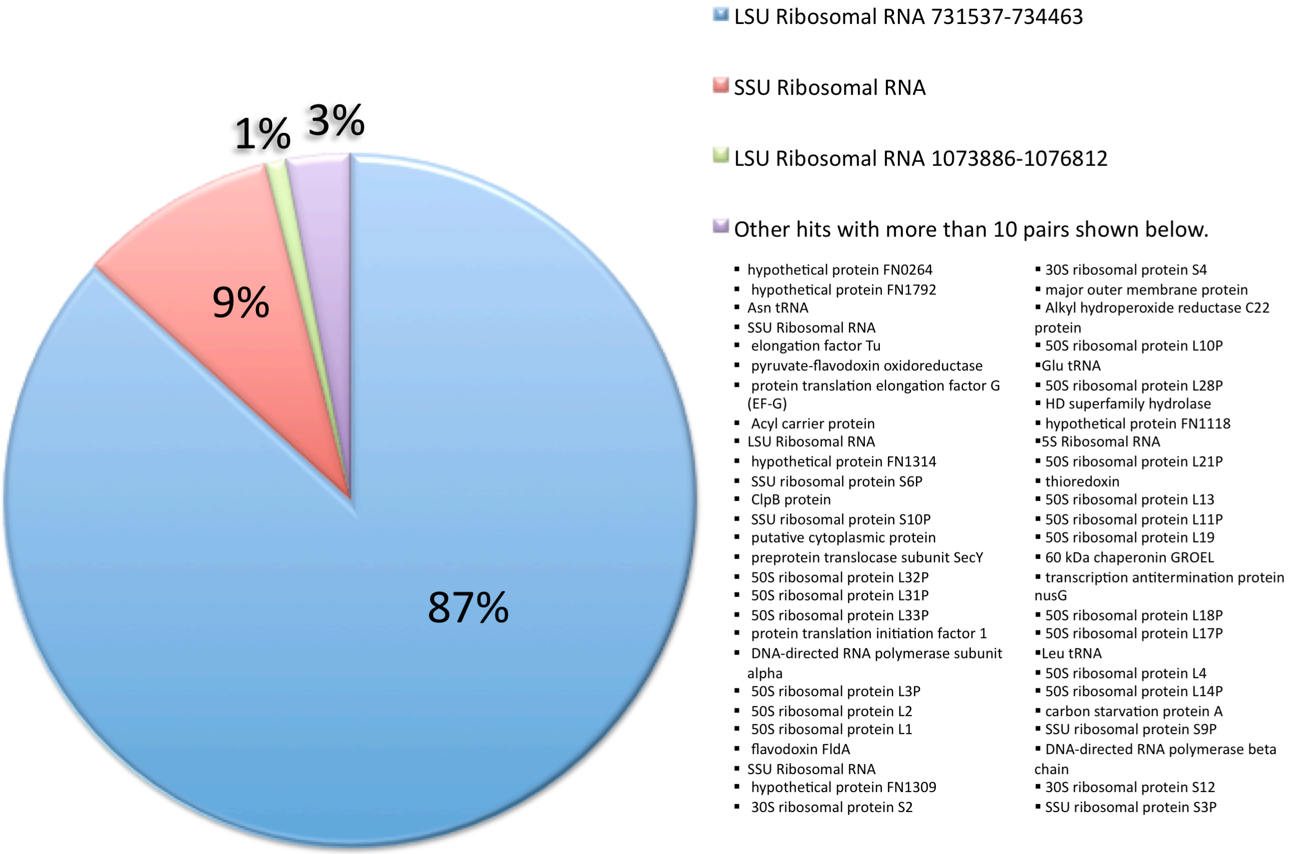
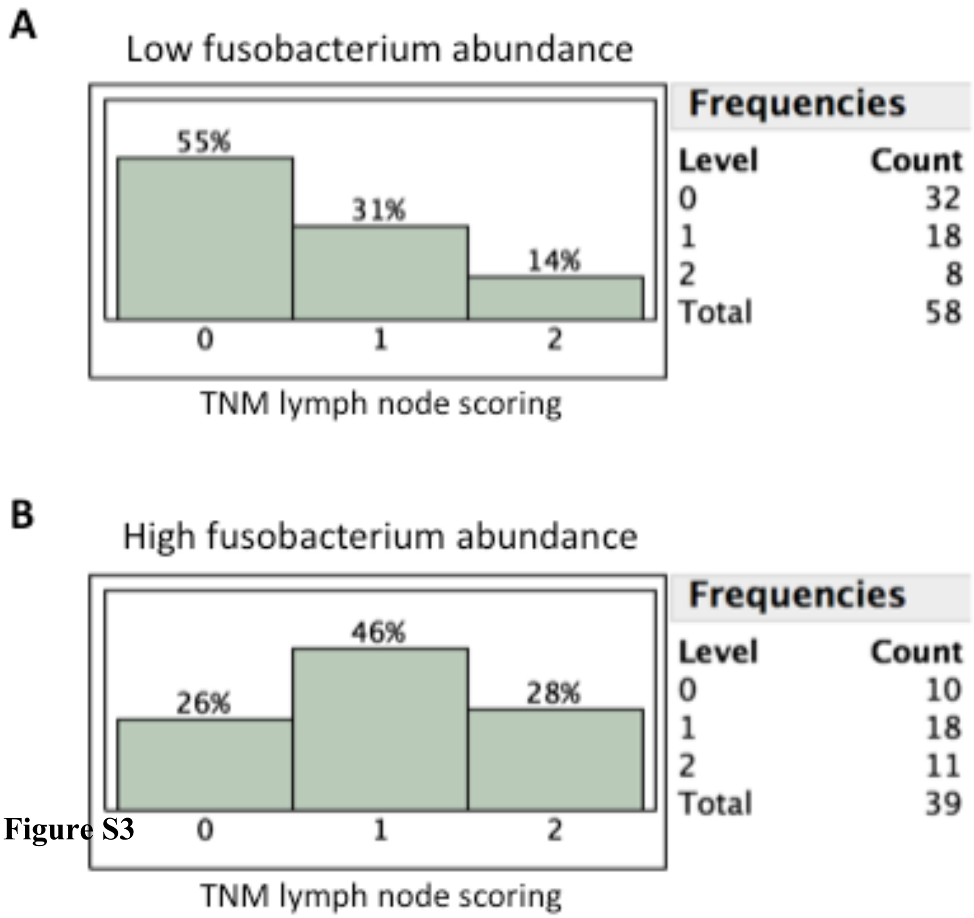


Figure S2. Distribution of hits from colorectal carcinoma RNA-Seq data to the annotated *F.nucleatum* subsp. nucleatum ATCC 25586 genome. The total number of read pair hits was 80,118.



- hypothetical protein FN0264
- hypothetical protein FN1792
- Asn tRNA
- SSU Ribosomal RNA
- elongation factor Tu
- pyruvate-flavodoxin oxidoreductase
- protein translation elongation factor G (EF-G)
- Acyl carrier protein
- LSU Ribosomal RNA
- hypothetical protein FN1314
- SSU ribosomal protein S6P
- ClpB protein
- SSU ribosomal protein S10P
- putative cytoplasmic protein
- preprotein translocase subunit SecY
- 50S ribosomal protein L32P
- 50S ribosomal protein L31P
- 50S ribosomal protein L33P
- protein translation initiation factor 1
- DNA-directed RNA polymerase subunit alpha
- 50S ribosomal protein L3P
- 50S ribosomal protein L2
- 50S ribosomal protein L1
- flavodoxin FldA
- SSU Ribosomal RNA
- hypothetical protein FN1309
- 30S ribosomal protein S2
- 30S ribosomal protein S4
- major outer membrane protein
- Alkyl hydroperoxide reductase C22 protein
- 50S ribosomal protein L10P
- Glu tRNA
- 50S ribosomal protein L28P
- HD superfamily hydrolase
- hypothetical protein FN1118
- 5S Ribosomal RNA
- 50S ribosomal protein L21P
- thioredoxin
- 50S ribosomal protein L13
- 50S ribosomal protein L11P
- 50S ribosomal protein L19
- 60 kDa chaperonin GROEL
- transcription antitermination protein nusG
- 50S ribosomal protein L18P
- 50S ribosomal protein L17P
- Leu tRNA
- 50S ribosomal protein L4
- 50S ribosomal protein L14P
- carbon starvation protein A
- SSU ribosomal protein S9P
- DNA-directed RNA polymerase beta chain
- 30S ribosomal protein S12
- SSU ribosomal protein S3P

Figure S3. Frequency of metastasis increases with higher *Fusobacterium* abundance in tumour biopsies. Patients with 5X or greater *Fusobacterium* in their tumour biopsies versus matched normal tissue were compared to those patients with less than 5X relative amounts of *Fusobacterium*. A significantly higher number of patients from the high *Fusobacterium* group (A) had more tumour spreading in their lymph nodes as measured by their surgical TNM scores than the low *Fusobacterium* group (B) (one-tailed Fisher's exact test p-value = 0.0035).



Frequencies

Level	Count
0	32
1	18
2	8
Total	58

Frequencies

Level	Count
0	10
1	18
2	11
Total	39

Figure S3

Supplemental Tables

Table S1. Host sequence subtraction RNA-seq data from eleven colorectal carcinoma and matched normal specimens.

	Control (mean +/- SD)	Tumour (mean +/- SD)
Raw read pairs	2,222,539 +/- 355,530	2,175,063 +/- 439,279
Filtered read pairs[1]	349,354 +/- 212,209	339,935 +/- 182,207
Read pairs matching bacterial or viral genomes[2]	17,154 +/- 22,837	15,681 +/- 29,568
Distinct bacterial or viral genome matches	546	544

1. Read pairs remaining after removal of low quality reads and reads matching human rRNA, transcriptome or genome reference sequences.

2. Unambiguous alignments where the best match for each mate pair is to the same accession.

Table S2. Gene content of gaps (segments from strain 3_1_36A2 accession that are missing from CC53).

Coordinates of unaligned region	***Unaligned region length***	***Protein id***	***CDS start coordinate***	***CDS end coordinate***	***Predicted product***
160980-162119	1139	EEU32070.1	161007	162053	predicted protein
163749-165149	1400	EEU32072.1	162670	163818	2-nitropropane dioxygenase
163749-165149	1400	EEU32073.1	163997	164458	N-acetylmuramoyl-L-alanine amidase
163749-165149	1400	EEU32074.1	164490	165128	conserved hypothetical protein
163749-165149	1400	EEU32075.1	166472	165135	conserved hypothetical protein
230196-237851	7655	EEU32133.1	230444	234547	CRISPR-associated protein
230196-237851	7655	EEU32134.1	234572	235450	CRISPR-associated protein cas1
230196-237851	7655	EEU32135.1	235440	235760	conserved hypothetical protein
230196-237851	7655	EEU32136.1	235757	236419	conserved hypothetical protein
230196-237851	7655	EEU32137.1	238229	237840	conserved hypothetical protein
413437-423361	9924	EEU32297.1	415519	413525	hemin receptor
413437-423361	9924	EEU32298.1	415901	416818	nickel ABC transporter
413437-423361	9924	EEU32299.1	416839	417642	nickel ABC transporter
413437-423361	9924	EEU32300.1	417655	418416	nickel import ATP-binding protein NikD
413437-423361	9924	EEU32301.1	418421	419113	nickel import ATP-binding protein NikE
413437-423361	9924	EEU32302.1	419110	420735	nickel import ATP-binding protein NikE
413437-423361	9924	EEU32303.1	421767	420790	transcriptional regulator AraC family
413437-423361	9924	EEU32304.1	421979	423325	MATE efflux family protein
800252-803854	3602	EEU32662.1	800383	798980	MATE efflux family protein
800252-803854	3602	EEU32663.1	801168	800395	phosphonate C-P lyase system protein PhnK
800252-803854	3602	EEU32664.1	802198	801161	transport system permease
800252-803854	3602	EEU32665.1	803435	802293	periplasmic binding protein
800252-803854	3602	EEU32666.1	803816	803643	predicted protein
804906-806958	2052	EEU32668.1	806372	805035	conserved hypothetical protein
804906-806958	2052	EEU32669.1	806844	806386	conserved hypothetical protein
854976-876729	21753	EEU32722.1	855099	855521	predicted protein
854976-876729	21753	EEU32723.1	855650	856117	predicted protein
854976-876729	21753	EEU32724.1	860232	856126	predicted protein
854976-876729	21753	EEU32725.1	862070	860229	predicted protein
854976-876729	21753	EEU32726.1	862942	862052	predicted protein

854976-876729	21753	EEU32727.1	864868	862955	predicted protein
854976-876729	21753	EEU32728.1	865392	864868	predicted protein
854976-876729	21753	EEU32729.1	865593	865405	conserved hypothetical protein
854976-876729	21753	EEU32730.1	866029	865598	conserved hypothetical protein
854976-876729	21753	EEU32731.1	866417	866037	conserved hypothetical protein
854976-876729	21753	EEU32732.1	866976	866473	predicted protein
854976-876729	21753	EEU32733.1	867481	866978	predicted protein
854976-876729	21753	EEU32734.1	868738	867494	predicted protein
854976-876729	21753	EEU32735.1	869642	868791	predicted protein
854976-876729	21753	EEU32736.1	870369	869653	predicted protein
854976-876729	21753	EEU32737.1	870587	870369	predicted protein
854976-876729	21753	EEU32738.1	872229	870577	predicted protein
854976-876729	21753	EEU32739.1	872706	872239	predicted protein
854976-876729	21753	EEU32740.1	874108	872717	predicted protein
854976-876729	21753	EEU32741.1	874781	874083	predicted protein
854976-876729	21753	EEU32742.1	875192	875425	predicted protein
854976-876729	21753	EEU32743.1	875441	875674	predicted protein
854976-876729	21753	EEU32744.1	875664	875915	predicted protein
854976-876729	21753	EEU32745.1	876091	875912	predicted protein
854976-876729	21753	EEU32746.1	876444	876091	predicted protein
854976-876729	21753	EEU32747.1	876724	876449	predicted protein
877026-882644	5618	EEU32748.1	877946	877146	replicative DNA helicase
877026-882644	5618	EEU32749.1	878688	877948	conserved hypothetical protein
877026-882644	5618	EEU32750.1	880025	879648	predicted protein
877026-882644	5618	EEU32751.1	880385	880164	predicted protein
877026-882644	5618	EEU32752.1	880941	880543	predicted protein
877026-882644	5618	EEU32753.1	881131	880952	predicted protein
877026-882644	5618	EEU32754.1	881328	881131	conserved hypothetical protein
877026-882644	5618	EEU32755.1	882003	881347	LexA repressor
877026-882644	5618	EEU32756.1	882166	882540	predicted protein
883266-886895	3629	EEU32757.1	883275	883967	conserved hypothetical protein
883266-886895	3629	EEU32758.1	883977	884489	gp157
883266-886895	3629	EEU32759.1	884500	885222	predicted protein

883266-886895	3629	EEU32760.1	885219	885518	conserved hypothetical protein
883266-886895	3629	EEU32761.1	885515	885745	phage protein
883266-886895	3629	EEU32762.1	885708	886172	phage protein
883266-886895	3629	EEU32763.1	886162	886734	conserved hypothetical protein
883266-886895	3629	EEU32764.1	886721	886873	predicted protein
887195-890120	2925	EEU32765.1	887406	887561	predicted protein
887195-890120	2925	EEU32766.1	887576	887806	predicted protein
887195-890120	2925	EEU32767.1	887775	888182	conserved hypothetical protein
887195-890120	2925	EEU32768.1	888187	888717	conserved hypothetical protein
887195-890120	2925	EEU32769.1	888731	888922	predicted protein
887195-890120	2925	EEU32770.1	888960	890027	DNA integration/recombination/invertion protein
965306-1019450	54144	EEU32841.1	966788	965571	DNA integration/recombination/invertion protein
965306-1019450	54144	EEU32842.1	967072	966854	predicted protein
965306-1019450	54144	EEU32843.1	967701	967090	predicted protein
965306-1019450	54144	EEU32844.1	968005	967811	predicted protein
965306-1019450	54144	EEU32845.1	968658	968203	predicted protein
965306-1019450	54144	EEU32846.1	968932	968690	predicted protein
965306-1019450	54144	EEU32847.1	969592	969347	conserved hypothetical protein
965306-1019450	54144	EEU32848.1	969875	969612	predicted protein
965306-1019450	54144	EEU32849.1	970173	969913	conserved hypothetical protein
965306-1019450	54144	EEU32850.1	970620	970282	conserved hypothetical protein
965306-1019450	54144	EEU32851.1	970875	970666	predicted protein
965306-1019450	54144	EEU32852.1	971132	970980	predicted protein
965306-1019450	54144	EEU32853.1	971450	971241	predicted protein
965306-1019450	54144	EEU32854.1	971649	971443	predicted protein
965306-1019450	54144	EEU32855.1	973026	972361	predicted protein
965306-1019450	54144	EEU32856.1	973736	973035	ATPase
965306-1019450	54144	EEU32857.1	973922	974233	predicted protein
965306-1019450	54144	EEU32858.1	974562	974254	predicted protein
965306-1019450	54144	EEU32859.1	975174	974566	lytic transglycosylase
965306-1019450	54144	EEU32860.1	977485	975188	predicted protein
965306-1019450	54144	EEU32861.1	978407	978042	predicted protein
965306-1019450	54144	EEU32862.1	978937	978455	conserved hypothetical protein

965306-1019450	54144	EEU32863.1	979139	978984	predicted protein
965306-1019450	54144	EEU32864.1	979795	979139	resolvase/recombinase
965306-1019450	54144	EEU32865.1	980528	979782	conserved hypothetical protein
965306-1019450	54144	EEU32866.1	980698	980540	predicted protein
965306-1019450	54144	EEU32867.1	981075	980707	resolvase/recombinase
965306-1019450	54144	EEU32868.1	981730	981062	conserved hypothetical protein
965306-1019450	54144	EEU32869.1	981903	981730	predicted protein
965306-1019450	54144	EEU32870.1	982381	982019	predicted protein
965306-1019450	54144	EEU32871.1	982653	982450	predicted protein
965306-1019450	54144	EEU32872.1	983480	982896	predicted protein
965306-1019450	54144	EEU32873.1	983895	983494	predicted protein
965306-1019450	54144	EEU32874.1	984215	983892	predicted protein
965306-1019450	54144	EEU32875.1	990789	984421	helicase
965306-1019450	54144	EEU32876.1	992550	990865	conserved hypothetical protein
965306-1019450	54144	EEU32877.1	993259	992810	predicted protein
965306-1019450	54144	EEU32878.1	993786	993256	predicted protein
965306-1019450	54144	EEU32879.1	996192	993802	type I topoisomease
965306-1019450	54144	EEU32880.1	996886	996269	predicted protein
965306-1019450	54144	EEU32881.1	997613	997140	predicted protein
965306-1019450	54144	EEU32882.1	998631	997690	predicted protein
965306-1019450	54144	EEU32883.1	999162	998644	conjugative transfer signal peptidase TraF
965306-1019450	54144	EEU32884.1	999454	999164	predicted protein
965306-1019450	54144	EEU32885.1	999851	999642	predicted protein
965306-1019450	54144	EEU32886.1	1000454	1000095	predicted protein
965306-1019450	54144	EEU32887.1	1000741	1000538	predicted protein
965306-1019450	54144	EEU32888.1	1001035	1000859	predicted protein
965306-1019450	54144	EEU32889.1	1001463	1001170	predicted protein
965306-1019450	54144	EEU32890.1	1002564	1001503	TrbL/VirB6 plasmid conjugal transfer protein
965306-1019450	54144	EEU32891.1	1003026	1002568	predicted protein
965306-1019450	54144	EEU32892.1	1003896	1003048	predicted protein
965306-1019450	54144	EEU32893.1	1006532	1004058	conjugal transfer protein TrbE
965306-1019450	54144	EEU32894.1	1006825	1006538	predicted protein
965306-1019450	54144	EEU32895.1	1007801	1006845	P-type conjugative transfer ATPase TrbB

965306-1019450	54144	EEU32896.1	1008154	1007801	predicted protein
965306-1019450	54144	EEU32897.1	1010223	1008154	TRAG protein
965306-1019450	54144	EEU32898.1	1010784	1010308	predicted protein
965306-1019450	54144	EEU32899.1	1012013	1010799	conjugation TrbI family protein
965306-1019450	54144	EEU32900.1	1012811	1012023	P-type conjugative transfer protein VirB9
965306-1019450	54144	EEU32901.1	1013518	1012823	conserved hypothetical protein
965306-1019450	54144	EEU32902.1	1013896	1013579	conjugal transfer protein TrbC
965306-1019450	54144	EEU32903.1	1014228	1013893	predicted protein
965306-1019450	54144	EEU32904.1	1015212	1014400	predicted protein
965306-1019450	54144	EEU32905.1	1015636	1015244	conserved hypothetical protein
965306-1019450	54144	EEU32906.1	1016055	1015723	conserved hypothetical protein
965306-1019450	54144	EEU32907.1	1016469	1016074	predicted protein
965306-1019450	54144	EEU32908.1	1016769	1016473	conserved hypothetical protein
965306-1019450	54144	EEU32909.1	1016991	1016851	conserved hypothetical protein
965306-1019450	54144	EEU32910.1	1017888	1017229	conserved hypothetical protein
965306-1019450	54144	EEU32911.1	1019162	1017885	predicted protein
1110825-1134389	23564	EEU32992.1	1111325	1110942	toxin secretion/phage lysis holin
1110825-1134389	23564	EEU32993.1	1111789	1111340	conserved hypothetical protein
1110825-1134389	23564	EEU32994.1	1112159	1111776	conserved hypothetical protein
1110825-1134389	23564	EEU32995.1	1112371	1112174	predicted protein
1110825-1134389	23564	EEU32996.1	1112940	1112431	conserved hypothetical protein
1110825-1134389	23564	EEU32997.1	1113824	1113054	conserved hypothetical protein
1110825-1134389	23564	EEU32998.1	1114533	1113811	conserved hypothetical protein
1110825-1134389	23564	EEU32999.1	1115187	1114537	conserved hypothetical protein
1110825-1134389	23564	EEU33000.1	1116244	1115180	baseplate J-like protein
1110825-1134389	23564	EEU33001.1	1116673	1116245	phage protein
1110825-1134389	23564	EEU33002.1	1117127	1116675	conserved hypothetical protein
1110825-1134389	23564	EEU33003.1	1118167	1117124	predicted protein
1110825-1134389	23564	EEU33004.1	1118618	1118172	conserved hypothetical protein
1110825-1134389	23564	EEU33005.1	1120539	1118632	phage protein
1110825-1134389	23564	EEU33006.1	1121062	1120601	predicted protein
1110825-1134389	23564	EEU33007.1	1121594	1121226	conserved hypothetical protein
1110825-1134389	23564	EEU33008.1	1122044	1121604	conserved hypothetical protein

1110825-1134389	23564	EEU33009.1	1123136	1122057	conserved hypothetical protein
1110825-1134389	23564	EEU33010.1	1123585	1123136	conserved hypothetical protein
1110825-1134389	23564	EEU33011.1	1123962	1123582	phage protein
1110825-1134389	23564	EEU33012.1	1124317	1123952	conserved hypothetical protein
1110825-1134389	23564	EEU33013.1	1124643	1124314	conserved hypothetical protein
1110825-1134389	23564	EEU33014.1	1124884	1124678	conserved hypothetical protein
1110825-1134389	23564	EEU33015.1	1126087	1124894	phage protein
1110825-1134389	23564	EEU33016.1	1126710	1126087	predicted protein
1110825-1134389	23564	EEU33017.1	1127074	1126856	conserved hypothetical protein
1110825-1134389	23564	EEU33018.1	1128740	1127058	phage protein
1110825-1134389	23564	EEU33020.1	1130040	1128724	terminase
1110825-1134389	23564	EEU33019.1	1130040	1128724	phage portal protein
1110825-1134389	23564	EEU33021.1	1131871	1131479	phage Terminase Small Subunit
1110825-1134389	23564	EEU33022.1	1132196	1131936	predicted protein
1110825-1134389	23564	EEU33023.1	1133038	1132538	predicted protein
1110825-1134389	23564	EEU33024.1	1133406	1133050	predicted protein
1110825-1134389	23564	EEU33025.1	1134145	1133408	phage antirepressor protein
1110825-1134389	23564	EEU33026.1	1134359	1134150	predicted protein
1134686-1141495	6809	EEU33027.1	1136021	1134807	replicative DNA helicase
1134686-1141495	6809	EEU33028.1	1136792	1136022	conserved hypothetical protein
1134686-1141495	6809	EEU33029.1	1137732	1137460	predicted protein
1134686-1141495	6809	EEU33030.1	1138145	1137930	predicted protein
1134686-1141495	6809	EEU33031.1	1138750	1138265	predicted protein
1134686-1141495	6809	EEU33032.1	1139046	1138882	predicted protein
1134686-1141495	6809	EEU33033.1	1139965	1139114	predicted protein
1134686-1141495	6809	EEU33034.1	1140391	1139975	conserved hypothetical protein
1134686-1141495	6809	EEU33035.1	1140823	1140404	predicted protein
1134686-1141495	6809	EEU33036.1	1141005	1141391	predicted protein
1142122-1145342	3220	EEU33037.1	1142129	1142821	conserved hypothetical protein
1142122-1145342	3220	EEU33038.1	1142831	1143343	predicted protein
1142122-1145342	3220	EEU33039.1	1143353	1143595	predicted protein
1142122-1145342	3220	EEU33040.1	1143607	1144329	predicted protein
1142122-1145342	3220	EEU33041.1	1144326	1144604	predicted protein

1142122-1145342	3220	EEU33042.1	1144729	1145166	conserved hypothetical protein
1142122-1145342	3220	EEU33043.1	1145169	1145321	predicted protein
1145607-1149818	4211	EEU33044.1	1145689	1145847	predicted protein
1145607-1149818	4211	EEU33045.1	1145834	1146547	conserved hypothetical protein
1145607-1149818	4211	EEU33046.1	1146612	1147022	predicted protein
1145607-1149818	4211	EEU33047.1	1147025	1147480	conserved hypothetical protein
1145607-1149818	4211	EEU33048.1	1147487	1147777	predicted protein
1145607-1149818	4211	EEU33049.1	1147777	1148307	conserved hypothetical protein
1145607-1149818	4211	EEU33050.1	1148298	1148429	predicted protein
1145607-1149818	4211	EEU33051.1	1148500	1148697	predicted protein
1145607-1149818	4211	EEU33052.1	1148672	1149727	phage integrase

Table S3. Annotation of CC53 contigs from *de novo* assembly of unaligned reads.

CC53 CONTIG (query)				**TOP BLAST MATCHES (subject)**					
Contig	**Size**	**No. of Reads**	**Coverage**	**Accession**	**Sequence identity (%)**	**Alignment start**	**Alignment end**	**Predicted gene product**	**Species**
96	2371	23500	876.63	ZP_06751356.1	89.8	2370	1	Outer membrane protein	*Fusobacterium* sp. 3_1_27
106	5747	65773	1016.8	ZP_00144646.1	99.6	39	1658	Oligopeptide-binding protein oppA	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
106	5747	65773	1016.8	ZP_00144647.1	99.4	1695	2702	Dipeptide transport system permease protein dppB	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
106	5747	65773	1016.8	ZP_00144648.1	100.0	2737	3531	Oligopeptide transport system permease protein oppC	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
106	5747	65773	1016.8	ZP_00144649.1	99.4	3543	4079	Oligopeptide transport ATP-binding protein oppD	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
106	5747	65773	1016.8	ZP_00144649.1	49.1	4322	4780	Oligopeptide transport ATP-binding protein oppD	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
116	518	1458	248.91	ZP_00144515.1	100.0	1	255	Hypothetical Membrane Spanning Protein	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
116	518	1458	248.91	ZP_05552202.1	100.0	276	518	Conserved hypothetical protein	*Fusobacterium* sp. 3_1_36A2
119	4031	37039	811.92	ZP_04574788.1	100.0	48	1598	Propionate CoA-transferase	*Fusobacterium* sp. 7_1
119	4031	37039	811.92	ZP_04574789.1	100.0	1677	3014	Propionate permease	*Fusobacterium* sp. 7_1
131	1521	6591	386.78	ZP_04571805.1	95.8	2	427	Hemolysin	*Fusobacterium* sp. 4_1_13
131	1521	6591	386.78	YP_003945856.1	82.6	458	733	Hemagglutination activity domain protein	Paenibacillus polymyxa SC2
131	1521	6591	386.78	ZP_04571802.1	90.9	1075	1305	Conserved hypothetical protein	*Fusobacterium* sp. 4_1_13
131	1521	6591	386.78	ZP_00144656.1	100.0	1337	1519	Hypothetical protein	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256

133	1344	6493	425.34	ZP_00144284.1	99.6	1343	3	Hemolysin	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
137	907	3104	306.18	ZP_05551287.1	100.0	485	3	Histidyl-tRNA synthetase	*Fusobacterium* sp. 3_1_36A2
137	907	3104	306.18	ZP_05442395.1	100.0	907	500	Recombination factor protein RarA	*Fusobacterium* sp. D11
138	1935	9406	441.42	ZP_00143333.1	99.4	1797	238	Hypothetical protein	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
138	1935	9406	441.42	ZP_05550632.1	97.9	1933	1793	Conserved hypothetical protein	*Fusobacterium* sp. 3_1_36A2
147	6018	36729	545.52	ZP_06750290.1	99.7	1685	693	ABC transporter iron chelate uptake transporter (FeCT) family	*Fusobacterium* sp. 3_1_27
147	6018	36729	545.52	ZP_06869931.1	99.4	2753	1704	Iron(III) dicitrate-binding protein	*Fusobacterium* nucleatum subsp. nucleatum ATCC 23726
147	6018	36729	545.52	ZP_05816109.1	98.9	4431	2779	Conserved hypothetical protein	*Fusobacterium* sp. 3_1_33
147	6018	36729	545.52	ZP_06750286.1	99.6	5210	4473	Nitrogenase iron protein	*Fusobacterium* sp. 3_1_27
147	6018	36729	545.52	NP_603209.1	99.2	6017	5295	Iron(III) dicitrate transport ATP-binding protein fecE	*Fusobacterium* nucleatum subsp. nucleatum ATCC 25586
151	1516	4712	280.53	ZP_04571805.1	99.4	1515	1	Hemolysin	*Fusobacterium* sp. 4_1_13
153	1072	3261	270.7	ZP_06749749.1	97.2	1072	2	Hemolysin	*Fusobacterium* sp. 3_1_27
154	2052	8508	365.31	ZP_04572815.1	99.8	1997	465	Dipeptide-binding protein	*Fusobacterium* sp. 4_1_13
157	2008	15927	706.84	ZP_05816112.1	100.0	1435	2007	Iron(III) dicitrate transport system permease fecD	*Fusobacterium* sp. 3_1_33
157	2008	15927	706.84	ZP_05816113.1	99.1	372	1340	Iron(III) dicitrate-binding protein	*Fusobacterium* sp. 3_1_33
161	2363	5320	201.38	ZP_04572103.1	99.6	1	1491	Conserved hypothetical protein	*Fusobacterium* sp. 4_1_13
161	2363	5320	201.38	ZP_00144407.1	100.0	1746	2363	Threonyl-tRNA synthetase	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256

164	1072	5821	482.41	ZP_00144406.1	100.0	517	20	Hypothetical protein	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
164	1072	5821	482.41	ZP_00144407.1	100.0	1072	551	Threonyl-tRNA synthetase	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
167	605	1915	268.06	ZP_06751328.1	100.0	475	248	Conserved hypothetical protein	*Fusobacterium* sp. 3_1_27
167	605	1915	268.06	ZP_04571297.1	100.0	79	216	Conserved hypothetical protein	*Fusobacterium* sp. 4_1_13
168	1032	2780	240.22	ZP_04971343.1	96.6	446	3	Short-chain alcohol dehydrogenase	*Fusobacterium* nucleatum subsp. polymorphum ATCC 10953
168	1032	2780	240.22	ZP_06750238.1	100.0	1030	614	Tetratricopeptide repeat family protein	*Fusobacterium* sp. 3_1_27
170	820	992	108.68	ZP_00143341.1	100.0	1	819	Hypothetical protein; Spore photoproduct lyase	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
177	550	2139	355.73	ZP_04571419.1	100.0	550	353	Outer membrane protein	*Fusobacterium* sp. 4_1_13
183	598	1195	166.51	ZP_02212678.1	85.2	244	2	Hypothetical protein CLOBAR_02295	Clostridium bartlettii DSM 16795
183	598	1195	166.51	ZP_04971346.1	96.3	406	567	Hypothetical protein FNP_1655	*Fusobacterium* nucleatum subsp. polymorphum ATCC 10953
184	1002	3195	282.52	ZP_04572112.1	100.0	1000	287	2-nitropropane dioxygenase	*Fusobacterium* sp. 4_1_13
185	736	4177	479.89	ZP_00143874.1	93.9	736	638	Hypothetical protein	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
186	922	1639	156.79	ZP_06750274.1	99.0	3	599	Conserved hypothetical protein	*Fusobacterium* sp. 3_1_27
186	922	1639	156.79	ZP_05442397.1	100.0	620	922	Hypothetical protein PrD11_11325	*Fusobacterium* sp. D11
194	1080	2883	241.44	ZP_06751048.1	100.0	935	3	Formimidoylglutamase	*Fusobacterium* sp. 3_1_27
196	2546	7657	269.47	ZP_04572326.1	99.6	1730	2545	Polysialic acid capsule expression protein kpsF	*Fusobacterium* sp. 4_1_13
200	1401	7817	508.57	ZP_06749764.1	95.0	545	72	Conserved hypothetical protein	*Fusobacterium* sp. 3_1_27

200	1401	7817	508.57	ZP_05631047.1	80.4	1017	559	Hypothetical protein FgonA2_04800	*Fusobacterium* gonidiaformans ATCC 25563
200	1401	7817	508.57	ZP_06749761.1	100.0	1399	1106	Hemolysin	*Fusobacterium* sp. 3_1_27
204	531	841	141.11	ZP_05440307.1	100.0	1	282	Uroporphyrinogen-III synthase	*Fusobacterium* sp. D11
212	529	755	120.99	ZP_00143146.1	98.9	528	1	Serine protease	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
218	906	2602	256.19	ZP_04572999.1	100.0	1	555	ATP-NAD kinase	*Fusobacterium* sp. 4_1_13
218	906	2602	256.19	ZP_06750251.1	100.0	537	905	DNA repair protein RecN	*Fusobacterium* sp. 3_1_27
224	1039	2609	222.98	ZP_00144496.1	98.3	1038	1	Outer membrane protein family	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
225	681	954	123.98	ZP_00144049.1	99.6	2	679	4-hydroxybutyrate:acetyl-CoA CoA transferase	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
232	734	1495	176.87	ZP_06750263.1	100.0	636	1	tRNA (guanine-N1)-methyltransferase	*Fusobacterium* sp. 3_1_27
235	517	504	87.56	ZP_04572837.1	100.0	180	515	Ribosomal-protein-alanine acetyltransferase	*Fusobacterium* sp. 4_1_13
237	882	1514	154.52	ZP_04574766.1	100.0	273	881	Methyltransferase	*Fusobacterium* sp. 7_1
246	1062	1254	100.11	ZP_05551301.1	100.0	123	680	Conserved hypothetical protein	*Fusobacterium* sp. 3_1_36A2
248	689	1443	193.6	ZP_00144645.1	100.0	434	670	Hypothetical protein	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
249	2756	5701	186.29	ZP_04571805.1	97.3	2	2755	Hemolysin	*Fusobacterium* sp. 4_1_13
250	581	688	104.33	ZP_06751292.1	99.5	3	569	Dipeptide-binding protein	*Fusobacterium* sp. 3_1_27
262	631	487	70.78	ZP_04574649.1	100.0	631	29	Membrane protein	*Fusobacterium* sp. 7_1
270	1010	2177	194.64	ZP_00143639.1	99.7	2	967	Aspartate aminotransferase	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
271	1143	1665	129.3	ZP_04574784.1	99.6	463	1143	Conserved hypothetical protein	*Fusobacterium* sp. 7_1

273	822	984	106.27	ZP_05550411.1	99.5	598	2	D-methionine ABC transporter, ATP-binding protein	*Fusobacterium* sp. 3_1_36A2
287	1047	2087	174.75	ZP_06524412.1	99.3	1001	180	Export ABC transporter	*Fusobacterium* sp. D11
294	1460	3081	189.01	ZP_04574771.1	100.0	2	652	Riboflavin kinase	*Fusobacterium* sp. 7_1
294	1460	3081	189.01	ZP_05814256.1	100.0	627	1301	Conserved hypothetical protein	*Fusobacterium* sp. 3_1_33
297	1359	1631	107.16	ZP_04572332.1	100.0	1044	151	Conserved hypothetical protein	*Fusobacterium* sp. 4_1_13
299	942	1989	192.42	ZP_06750860.1	99.4	3	941	Conserved hypothetical protein	*Fusobacterium* sp. 3_1_27
303	782	1239	141.49	ZP_04572817.1	98.9	3	782	Polysaccharide deacetylase	*Fusobacterium* sp. 4_1_13
305	839	2387	258.12	ZP_04970650.1	98.3	178	2	Possible DNA repair photolyase	*Fusobacterium* nucleatum subsp. polymorphum ATCC 10953
305	839	2387	258.12	ZP_00143340.1	100.0	475	206	Hypothetical protein	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
305	839	2387	258.12	ZP_00143339.1	100.0	749	471	Hypothetical protein	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
319	537	136	21.86	ZP_05816107.1	100.0	2	400	Iron(III) dicitrate transport system permease fecD	*Fusobacterium* sp. 3_1_33
334	667	616	81.93	ZP_04572103.1	100.0	1	666	Conserved hypothetical protein	*Fusobacterium* sp. 4_1_13
346	978	741	68.88	ZP_04572180.1	99.1	978	304	Filamentation induced by cAMP protein Fic	*Fusobacterium* sp. 4_1_13
352	1222	1250	88.31	ZP_06871387.1	100.0	3	395	Oxidoreductase	*Fusobacterium* nucleatum subsp. nucleatum ATCC 23726
352	1222	1250	88.31	ZP_04572329.1	100.0	768	466	Conserved hypothetical protein	*Fusobacterium* sp. 4_1_13
352	1222	1250	88.31	ZP_05550650.1	100.0	1220	810	Glycerol-3-phosphate dehydrogenase (NAD(+))	*Fusobacterium* sp. 3_1_36A2
367	1482	2576	154.43	ZP_04572735.1	100.0	2	526	Uracil-DNA glycosylase	*Fusobacterium* sp. 4_1_13
367	1482	2576	154.43	ZP_06750465.1	100.0	1482	667	Sensory Transduction Protein Kinase	*Fusobacterium* sp. 3_1_27

370	708	947	121.38	ZP_06749809.1	99.6	707	6	Methylaspartate mutase E subunit	*Fusobacterium* sp. 3_1_27
390	836	544	57.57	ZP_06748447.1	100.0	1	243	ATP synthase F1 beta subunit	*Fusobacterium* sp. 1_1_41FAA
390	836	544	57.57	ZP_00144388.1	100.0	256	552	ATP synthase epsilon chain sodium ion specific	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
395	610	469	68.64	ZP_04572312.1	100.0	610	293	Dihydrolipoamide acyltransferase	*Fusobacterium* sp. 4_1_13
434	628	548	78.94	ZP_06750801.1	98.6	3	626	NAD(FAD)-utilizing dehydrogenase	*Fusobacterium* sp. 3_1_27
460	590	728	108.91	ZP_05814379.1	100.0	580	2	Membrane protein	*Fusobacterium* sp. 3_1_33
480	957	1015	94.61	ZP_04572122.1	98.6	3	434	RNA polymerase sigma-54 factor rpoN	*Fusobacterium* sp. 4_1_13
480	957	1015	94.61	ZP_00144056.1	100.0	842	498	Bacterial/Archaeal Transporter family protein	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
499	501	321	55.66	ZP_06750657.1	100.0	3	368	branched-chain amino acid transport system II carrier protein	*Fusobacterium* sp. 3_1_27
510	605	636	93.46	ZP_04572207.1	99.0	599	3	Ribosomal large subunit pseudouridine synthase B	*Fusobacterium* sp. 4_1_13
514	710	267	33.69	ZP_00144400.1	98.0	2	295	Hypothetical protein	*Fusobacterium* nucleatum subsp. vincentii ATCC 49256
514	710	267	33.69	ZP_04572112.1	100.0	376	708	2-nitropropane dioxygenase	*Fusobacterium* sp. 4_1_13
617	630	96	14.17	ZP_04574788.1	100.0	2	628	Propionate CoA-transferase	*Fusobacterium* sp. 7_1
658	662	260	34.69	ZP_04572174.1	99.1	7	660	WD-repeat family protein	*Fusobacterium* sp. 4_1_13