Supplementary tables

Supplementary table 1 Altered microbial species in the first stage of RA.

Species	RAS1 (n=15)		HC (n=27)		p	q
	Mean	SEM	Mean	SEM		
Streptococcus sanguinis↑	8.48E-05	4.02E-05	1.52E-06	1.20E-06	5.37E-04	6.43E-02
Streptococcus mitis oralis pneumoniae↑	1.63E-04	5.73E-05	9.09E-06	4.72E-06	1.21E-03	6.43E-02
Bacteroides uniformis↓	9.98E-03	3.43E-03	7.83E-02	2.30E-02	1.36E-03	6.43E-02
Actinomyces graevenitzii↑	1.72E-05	7.22E-06	0.00E+00	0.00E+00	1.77E-03	6.43E-02
Streptococcus anginosus↑	8.26E-04	6.36E-04	0.00E+00	0.00E+00	1.77E-03	6.43E-02
Parabacteroides distasonis↓	1.18E-03	5.50E-04	4.97E-03	1.37E-03	1.95E-03	6.43E-02
Coprococcus comes↑	1.58E-03	6.26E-04	2.96E-04	8.87E-05	3.28E-03	7.92E-02
Streptococcus infantis↑†	6.18E-05	2.76E-05	5.93E-06	5.63E-06	3.43E-03	7.92E-02
Holdemania filiformis↑	3.45E-05	2.21E-05	3.23E-06	3.23E-06	3.60E-03	7.92E-02
Bacteroides ovatus↓†	1.22E-03	4.45E-04	1.60E-02	8.91E-03	4.21E-03	8.34E-02
Streptococcus cristatus↑	6.46E-06	3.15E-06	0.00E+00	0.00E+00	5.83E-03	9.62E-02
Streptococcus vestibularis↑	7.11E-05	4.24E-05	0.00E+00	0.00E+00	5.83E-03	9.62E-02
Streptococcus gordonii↑	5.69E-05	2.36E-05	1.81E-06	1.81E-06	7.49E-03	1.14E-01
Actinomyces odontolyticus↑	2.71E-05	1.75E-05	0.00E+00	0.00E+00	1.87E-02	1.95E-01
Atopobium parvulum↑†	1.58E-05	8.60E-06	0.00E+00	0.00E+00	1.87E-02	1.95E-01
Prevotella stercorea↑	3.84E-04	2.38E-04	0.00E+00	0.00E+00	1.87E-02	1.95E-01
Enterococcus faecium↑	4.24E-05	2.58E-05	0.00E+00	0.00E+00	1.87E-02	1.95E-01
Weissella confusa↑	6.79E-05	4.60E-05	0.00E+00	0.00E+00	1.87E-02	1.95E-01
Solobacterium moorei↑	6.03E-05	3.67E-05	0.00E+00	0.00E+00	1.87E-02	1.95E-01
Bacteroides cellulosilyticus↓	5.37E-04	3.89E-04	7.73E-03	4.77E-03	2.33E-02	2.16E-01
Parasutterella excrementihominis†	2.80E-04	2.62E-04	1.47E-03	6.70E-04	2.44E-02	2.16E-01
Granulicatella adiacens↑†	3.08E-05	1.94E-05	6.59E-07	6.59E-07	2.51E-02	2.16E-01
Turicibacter sanguinis↑†	8.02E-05	4.57E-05	1.11E-06	1.11E-06	2.51E-02	2.16E-01
Prevotella copri↑	1.46E-01	5.86E-02	1.04E-02	8.24E-03	3.46E-02	2.75E-01
Streptococcus parasanguinis↑	9.14E-04	5.85E-04	3.92E-05	2.56E-05	3.47E-02	2.75E-01
Dorea formicigenerans↑	8.21E-04	2.26E-04	3.85E-04	9.07E-05	3.81E-02	2.82E-01
Klebsiella pneumoniae↑	1.26E-02	1.02E-02	1.14E-03	8.56E-04	3.84E-02	2.82E-01
Coprobacter fastidiosus↓	8.14E-05	7.79E-05	2.14E-03	1.41E-03	4.10E-02	2.90E-01
Collinsella aerofaciens↑†	2.00E-03	9.48E-04	3.56E-04	1.73E-04	4.34E-02	2.96E-01

p values produced by Mann-Whitney-Wilcoxon test are displayed. q values are calculated using Benjamini and Hochberg corrections. Only results with p<0.05 are displayed here.

↑↓Species that are increased/decreased in RAS1 compared to HC.

†Species that are altered exclusively in RAS1, with p<0.05 only observed in comparisons between RAS1 and HC.

RAS1, individuals in the first stage of rheumatoid arthritis; HC, healthy controls; SEM, standard error of the mean.

Supplementary table 2 Altered microbial species in the second stage of RA.

Species	RAS2 (n=21)		HC (n=27)		p	q
	Mean	SEM	Mean	SEM		
Escherichia coli↑	5.59E-02	2.37E-02	4.74E-03	1.97E-03	1.27E-03	1.31E-01
Streptococcus anginosus↑	1.45E-04	7.82E-05	0.00E+00	0.00E+00	1.46E-03	1.31E-01
Clostridium nexile↑	8.02E-04	2.26E-04	5.64E-05	3.86E-05	1.89E-03	1.31E-01
Clostridium hathewayi↑	6.77E-04	5.60E-04	9.63E-07	6.71E-07	2.53E-03	1.31E-01
Bacteroides uniformis↓	1.81E-02	5.88E-03	7.83E-02	2.30E-02	5.35E-03	2.13E-01
Klebsiella pneumoniae↑	1.99E-02	1.80E-02	1.14E-03	8.56E-04	6.30E-03	2.13E-01
Bifidobacterium dentium↑	4.91E-04	2.37E-04	3.70E-05	3.70E-05	7.16E-03	2.13E-01
Blautia gnavus↑	5.71E-03	2.24E-03	1.22E-03	7.29E-04	8.76E-03	2.28E-01
Bacteroides salyersiae↓	5.63E-05	4.28E-05	2.21E-03	1.08E-03	1.23E-02	2.80E-01
Prevotella copri↑	8.60E-02	3.53E-02	1.04E-02	8.24E-03	1.35E-02	2.80E-01
Holdemania filiformis↑	1.15E-04	6.21E-05	3.23E-06	3.23E-06	1.62E-02	2.83E-01
Blautia torques↑	5.16E-03	1.48E-03	1.46E-03	3.78E-04	1.63E-02	2.83E-01
Clostridium clostridioforme↑†	3.94E-04	2.77E-04	1.12E-05	1.12E-05	1.95E-02	2.83E-01
Scardovia wiggsiae↑	1.35E-05	1.13E-05	0.00E+00	0.00E+00	2.04E-02	2.83E-01
Weissella confusa↑	3.25E-04	3.19E-04	0.00E+00	0.00E+00	2.04E-02	2.83E-01
Coprobacter fastidiosus↓	1.25E-04	7.51E-05	2.14E-03	1.41E-03	2.38E-02	3.09E-01
Bacteroides coprocola↓†	8.26E-03	4.20E-03	7.47E-02	2.01E-02	3.57E-02	3.67E-01
Streptococcus parasanguinis↑	4.92E-04	3.40E-04	3.92E-05	2.56E-05	3.63E-02	3.67E-01
Eubacterium ramulus↑	9.24E-04	5.07E-04	7.81E-05	2.84E-05	3.64E-02	3.67E-01
Parabacteroides johnsonii↓†	2.31E-06	2.31E-06	4.67E-04	2.35E-04	4.37E-02	3.67E-01
Paraprevotella clara↓	1.16E-03	6.88E-04	3.77E-03	1.72E-03	4.56E-02	3.67E-01
Akkermansia muciniphila↓	1.96E-03	1.66E-03	3.43E-03	1.33E-03	4.61E-02	3.67E-01
Actinomyces odontolyticus↑	1.03E-05	9.64E-06	0.00E+00	0.00E+00	4.76E-02	3.67E-01
Scardovia inopinata↑†	5.68E-06	3.95E-06	0.00E+00	0.00E+00	4.76E-02	3.67E-01
Porphyromonas somerae↑†	1.26E-05	9.64E-06	0.00E+00	0.00E+00	4.76E-02	3.67E-01
Lactobacillus salivarius↑	1.29E-04	1.12E-04	0.00E+00	0.00E+00	4.76E-02	3.67E-01
Streptococcus cristatus↑	1.66E-05	1.28E-05	0.00E+00	0.00E+00	4.76E-02	3.67E-01

p values produced by Mann-Whitney-Wilcoxon test are displayed. q values are calculated using Benjamini and Hochberg corrections. Only results with $p<0.05$ are displayed here.

↑↓Species that are increased/decreased in RAS2 compared to HC.

†Species that are altered exclusively in RAS2, with $p<0.05$ only observed in comparisons between RAS2 and HC.

RAS2, individuals in the second stage of rheumatoid arthritis; HC, healthy controls; SEM, standard error of the mean.

Supplementary table 3 Altered microbial species in the third stage of RA.

Species	**RAS3 (n=18)**		**HC (n=27)**		**p**	**q**
	Mean	**SEM**	**Mean**	**SEM**		
Lactobacillus salivarius↑	1.14E-03	8.44E-04	0.00E+00	0.00E+00	5.56E-04	5.45E-02
Streptococcus anginosus↑	1.81E-04	7.46E-05	0.00E+00	0.00E+00	5.56E-04	5.45E-02
Streptococcus parasanguinis↑	6.52E-04	2.07E-04	3.92E-05	2.56E-05	2.04E-03	1.33E-01
Bifidobacterium dentium↑	4.16E-04	2.47E-04	3.70E-05	3.70E-05	3.70E-03	1.39E-01
Parabacteroides distasonis	2.07E-03	9.12E-04	4.97E-03	1.37E-03	4.85E-03	1.39E-01
Dorea formicigenerans↑	1.74E-03	4.57E-04	3.85E-04	9.07E-05	4.85E-03	1.39E-01
Veillonella atypica↑	4.93E-04	2.15E-04	6.54E-05	3.46E-05	5.57E-03	1.39E-01
Clostridium hathewayi↑	3.46E-04	2.89E-04	9.63E-07	6.71E-07	5.92E-03	1.39E-01
Bacteroides uniformis↓	1.65E-02	6.81E-03	7.83E-02	2.30E-02	7.20E-03	1.39E-01
Escherichia coli↑	6.34E-02	2.08E-02	4.74E-03	1.97E-03	9.70E-03	1.39E-01
Klebsiella pneumoniae↑	7.06E-03	3.31E-03	1.14E-03	8.56E-04	1.09E-02	1.39E-01
Eubacterium ramulus↑	4.67E-04	1.48E-04	7.81E-05	2.84E-05	1.17E-02	1.39E-01
Actinomyces odontolyticus↑	2.69E-05	2.31E-05	0.00E+00	0.00E+00	1.21E-02	1.39E-01
Parascardovia denticolens↑†	1.25E-05	8.26E-06	0.00E+00	0.00E+00	1.21E-02	1.39E-01
Scardovia wiggsiae↑	6.48E-05	4.22E-05	0.00E+00	0.00E+00	1.21E-02	1.39E-01
Lactobacillus gasseri↑†	1.13E-04	6.15E-05	0.00E+00	0.00E+00	1.21E-02	1.39E-01
Weissella confusa↑	3.35E-05	2.35E-05	0.00E+00	0.00E+00	1.21E-02	1.39E-01
Ruminococcus 39BFAA↑	3.86E-03	1.36E-03	3.62E-04	2.07E-04	1.62E-02	1.73E-01
Blautia torques↑	4.26E-03	1.12E-03	1.46E-03	3.78E-04	1.70E-02	1.73E-01
Streptococcus gordonii↑	6.55E-05	2.88E-05	1.81E-06	1.81E-06	1.77E-02	1.73E-01
Clostridium nexile↑	1.06E-03	9.42E-04	5.64E-05	3.86E-05	1.88E-02	1.75E-01
Streptococcus pneumoniae↑	4.71E-05	1.69E-05	9.09E-06	4.72E-06	2.11E-02	1.86E-01
Holdemania filiformis↑	3.41E-05	1.64E-05	3.23E-06	3.23E-06	2.18E-02	1.86E-01
Veillonella parvula↑†	1.49E-03	6.11E-04	2.66E-04	8.53E-05	2.73E-02	2.17E-01
Enterococcus faecium↑	1.01E-03	9.96E-04	0.00E+00	0.00E+00	3.21E-02	2.17E-01
Lactobacillus crispatus↑†	4.82E-05	2.97E-05	0.00E+00	0.00E+00	3.21E-02	2.17E-01
Lactobacillus oris↑†	3.00E-05	1.84E-05	0.00E+00	0.00E+00	3.21E-02	2.17E-01
Streptococcus mutans↑†	3.72E-05	2.02E-05	0.00E+00	0.00E+00	3.21E-02	2.17E-01
Solobacterium moorei↑	1.57E-05	1.12E-05	0.00E+00	0.00E+00	3.21E-02	2.17E-01
Streptococcus salivarius↑	3.50E-03	1.51E-03	4.31E-04	1.64E-04	3.47E-02	2.23E-01
Paraprevotella clara↓	4.08E-04	1.75E-04	3.77E-03	1.72E-03	3.66E-02	2.23E-01
Dorea longicatena↑†	3.21E-03	1.61E-03	9.42E-04	3.77E-04	3.74E-02	2.23E-01
Enterobacter cloacae↑†	4.51E-03	3.67E-03	4.13E-03	3.98E-03	3.75E-02	2.23E-01
Parabacteroides merdae↓	3.07E-03	1.02E-03	7.83E-03	1.79E-03	4.67E-02	2.69E-01

p values produced by Mann-Whitney-Wilcoxon test are displayed. q values are calculated using Benjamini and Hochberg corrections. Only results with p<0.05 are displayed here.

↑↓Species that are increased/decreased in RAS3 compared to HC.

†Species that are altered exclusively in RAS3, with p<0.05 only observed in comparisons between RAS3 and HC.

RAS3, individuals in the third stage of rheumatoid arthritis; HC, healthy controls; SEM, standard error of the mean.

Supplementary table 4 Altered microbial species in the fourth stage of RA.

Species	**RAS4 (n=22)**		**HC (n=27)**		**p**	**q**
	Mean	**SEM**	**Mean**	**SEM**		
Actinomyces odontolyticus↑	2.46E-05	1.10E-05	0.00E+00	0.00E+00	7.88E-04	6.34E-02
Streptococcus anginosus↑	1.86E-04	1.36E-04	0.00E+00	0.00E+00	7.88E-04	6.34E-02
Bifidobacterium dentium↑	5.48E-04	3.90E-04	3.70E-05	3.70E-05	9.15E-04	6.34E-02
Veillonella atypica↑	3.71E-04	1.10E-04	6.54E-05	3.46E-05	1.25E-03	6.51E-02
Streptococcus sanguinis↑	4.20E-05	1.47E-05	1.52E-06	1.20E-06	1.60E-03	6.52E-02
Streptococcus vestibularis↑	6.59E-04	6.19E-04	0.00E+00	0.00E+00	1.90E-03	6.52E-02
Clostridium citroniae↑	8.92E-05	4.80E-05	4.85E-06	3.50E-06	2.29E-03	6.52E-02
Streptococcus parasanguinis↑	6.04E-04	3.99E-04	3.92E-05	2.56E-05	2.51E-03	6.52E-02
Clostridium hathewayi↑	2.00E-03	1.92E-03	9.63E-07	6.71E-07	2.96E-03	6.85E-02
Streptococcus gordonii↑	4.55E-05	2.40E-05	1.81E-06	1.81E-06	3.37E-03	7.01E-02
Bacteroides uniformis↓	3.06E-02	1.54E-02	7.83E-02	2.30E-02	5.71E-03	1.08E-01
Bacteroides cellulosilyticus↓	3.11E-04	2.67E-04	7.73E-03	4.77E-03	6.24E-03	1.08E-01
Parabacteroides distasonis↓	3.27E-03	1.94E-03	4.97E-03	1.37E-03	1.04E-02	1.54E-01
Enterococcus faecium↑	3.35E-03	2.82E-03	0.00E+00	0.00E+00	1.04E-02	1.54E-01
Akkermansia muciniphila↓	2.13E-03	1.66E-03	3.43E-03	1.33E-03	1.67E-02	1.96E-01
Ruminococcus 39BFAA↑	3.22E-03	1.13E-03	3.62E-04	2.07E-04	1.73E-02	1.96E-01
Eggerthella lenta↑†	1.11E-04	7.23E-05	1.56E-06	1.56E-06	1.82E-02	1.96E-01
Bacteroides salyersiae	7.13E-04	6.58E-04	2.21E-03	1.08E-03	1.93E-02	1.96E-01
Bacteroides faecis†	1.57E-04	1.02E-04	3.79E-03	1.47E-03	1.95E-02	1.96E-01
Streptococcus salivarius↑	7.74E-03	6.31E-03	4.31E-04	1.64E-04	2.15E-02	1.96E-01
Coprobacter fastidiosus↓	1.72E-04	1.23E-04	2.14E-03	1.41E-03	2.24E-02	1.96E-01
Bifidobacterium longum↑†	1.05E-02	5.10E-03	1.01E-03	3.23E-04	2.25E-02	1.96E-01
Actinomyces graevenitzii↑	1.70E-05	9.92E-06	0.00E+00	0.00E+00	2.35E-02	1.96E-01
Lactococcus garvieae↑†	7.46E-05	5.37E-05	0.00E+00	0.00E+00	2.35E-02	1.96E-01
Solobacterium moorei↑	1.88E-05	1.22E-05	0.00E+00	0.00E+00	2.35E-02	1.96E-01
Bacteroides caccae†	3.06E-03	1.03E-03	1.02E-02	3.41E-03	3.30E-02	2.64E-01
Parabacteroides merdae↓	4.55E-03	1.99E-03	7.83E-03	1.79E-03	3.85E-02	2.89E-01
Citrobacter freundii↑	1.70E-03	1.63E-03	1.74E-06	1.74E-06	3.89E-02	2.89E-01

p values produced by Mann-Whitney-Wilcoxon test are displayed. q values are calculated using Benjamini and Hochberg corrections. Only results with $p<0.05$ are displayed here.

↑↓Species that are increased/decreased in RAS4 compared to HC.

†Species that are altered exclusively in RAS4, with $p<0.05$ only observed in comparisons between RAS4 and HC.

RAS4, individuals in the fourth stage of rheumatoid arthritis; HC, healthy controls; SEM, standard error of the mean.

Supplementary table 5 Altered microbial species in OA.

Species	OA (n=19)		HC (n=27)		p	q
	Mean	SEM	Mean	SEM		
Coprococcus catus↑†	2.17E-03	7.19E-04	3.24E-04	1.43E-04	6.27E-05	1.22E-02
Blautia torques↑	8.49E-03	2.79E-03	1.46E-03	3.78E-04	3.72E-04	3.05E-02
Bacteroides cellulosilyticus↓	6.27E-05	6.01E-05	7.73E-03	4.77E-03	4.72E-04	3.05E-02
Enterococcus faecium↑	3.80E-04	1.81E-04	0.00E+00	0.00E+00	7.94E-04	3.85E-02
Coprococcus comes↑	1.39E-03	3.27E-04	2.96E-04	8.87E-05	1.85E-03	6.96E-02
Streptococcus anginosus↑	1.29E-04	5.94E-05	0.00E+00	0.00E+00	2.15E-03	6.96E-02
Holdemania filiformis↑	7.62E-05	3.72E-05	3.23E-06	3.23E-06	4.10E-03	1.14E-01
Blautia obeum↑†	2.91E-03	7.54E-04	1.26E-03	4.87E-04	4.77E-03	1.16E-01
Ruminococcus 39BFAA↑	4.97E-03	1.90E-03	3.62E-04	2.07E-04	8.68E-03	1.75E-01
Parabacteroides distasonis↓	3.03E-03	1.66E-03	4.97E-03	1.37E-03	9.01E-03	1.75E-01
Actinomyces odontolyticus↑	1.55E-05	8.27E-06	0.00E+00	0.00E+00	1.46E-02	1.90E-01
Lactobacillus salivarius↑	8.90E-04	4.79E-04	0.00E+00	0.00E+00	1.46E-02	1.90E-01
Streptococcus vestibularis↑	1.62E-03	1.58E-03	0.00E+00	0.00E+00	1.46E-02	1.90E-01
Solobacterium moorei↑	5.75E-06	3.90E-06	0.00E+00	0.00E+00	1.46E-02	1.90E-01
Bifidobacterium dentium↑	5.74E-05	2.29E-05	3.70E-05	3.70E-05	1.52E-02	1.90E-01
Clostridium citroniae↑	3.42E-05	1.68E-05	4.85E-06	3.50E-06	1.57E-02	1.90E-01
Prevotella copri↑	9.27E-02	3.36E-02	1.04E-02	8.24E-03	1.84E-02	2.10E-01
Streptococcus gordonii↑	6.14E-05	3.05E-05	1.81E-06	1.81E-06	2.22E-02	2.27E-01
Citrobacter freundii↑	4.04E-04	2.63E-04	1.74E-06	1.74E-06	2.22E-02	2.27E-01
Paraprevotella clara↓	6.19E-04	3.20E-04	3.77E-03	1.72E-03	2.66E-02	2.58E-01
Streptococcus parasanguinis↑	9.49E-04	4.41E-04	3.92E-05	2.56E-05	2.81E-02	2.60E-01
Blautia gnavus↑	4.17E-03	2.86E-03	1.22E-03	7.29E-04	3.24E-02	2.86E-01
Escherichia coli↑	8.35E-02	4.00E-02	4.74E-03	1.97E-03	3.58E-02	2.88E-01
Weissella confusa↑	1.07E-04	8.06E-05	0.00E+00	0.00E+00	3.71E-02	2.88E-01
Clostridium perfringens↑†	1.18E-04	7.26E-05	0.00E+00	0.00E+00	3.71E-02	2.88E-01
Dialister invisus↑†	2.22E-03	1.31E-03	8.17E-04	7.28E-04	4.10E-02	3.06E-01

p values produced by Mann-Whitney-Wilcoxon test are displayed. q values are calculated using Benjamini and Hochberg corrections. Only results with $p<0.05$ are displayed here.

↑↓Species that are increased/decreased in OA compared to HC.

†Species that are altered exclusively in OA, with $p<0.05$ only observed in comparisons between the OA and HC.

OA, individuals in the first stage of osteoarthritis; HC, healthy controls; SEM, standard error of the mean.

Supplementary table 6 Correlations of KEGG modules with rheumatoid factor and plasma cytokines.

	M00550		**M00879**		**M00545**	
	p ($p_{partial}$)	**q ($q_{partial}$)**	**p ($p_{partial}$)**	**q ($q_{partial}$)**	**p ($p_{partial}$)**	**q ($q_{partial}$)**
RF, IU/mL	0.217	0.547	0.00135**	0.0472*	0.00013***	0.0118*
	(0.480)	(0.773)	(0.00601**)	(0.0516*)	(0.00319**)	(0.0470*)
IL-1β, pg/mL	0.000544***	0.0370*	0.0126*	0.196	0.0000287***	0.00391*
	(0.00278**)	(0.0432*)	(0.0252*)	(0.294)	(0.000335***)	(0.0325*)
IL-4, pg/mL	0.00420**	0.0967*	0.243	0.55	0.00177**	0.0607*
	(0.0640)	(0.470)	(0.925)	(0.961)	(0.199)	(0.669)
IL-8, pg/mL	0.000745***	0.0707*	0.0201*	0.297	0.000246***	0.0669*
	(0.00400**)	(0.0851*)	(0.0337*)	(0.456)	(0.00347**)	(0.0751*)
IFN-γ, pg/mL	0.00313**	0.106	0.076	0.519	0.000392***	0.0356*
	(0.0366*)	(0.444)	(0.289)	(0.678)	(0.0325*)	(0.0946*)
IL-10, pg/mL	0.00155**	0.105	0.0162*	0.246	0.000041***	0.00557*
	(0.00642**)	(0.218)	(0.0330*)	(0.364)	(0.000373***)	(0.0464*)
IL-12p70, pg/mL	0.00347**	0.0931*	0.172	0.458	0.00261**	0.0888*
	(0.0490*)	(0.478)	(0.609)	(0.837)	(0.176)	(0.543)
IL-13, pg/mL	0.0858	0.421	0.0190*	0.215	0.0000163***	0.00441*
	(0.262)	(0.560)	(0.0139*)	(0.165)	(0.0000639***)	(0.0110*)
IL-17, pg/mL	0.104	0.421	0.829	0.915	0.777	0.895
	(0.600)	(0.820)	(0.493)	(0.810)	(0.111)	(0.451)
IL-2, pg/mL	0.000937***	0.0637*	0.0146*	0.233	0.000074***	0.0101*
	(0.00677**)	(0.0501*)	(0.0264*)	(0.362)	(0.00133**)	(0.0720*)
IL-6, pg/mL	0.00112**	0.0611*	0.125	0.467	0.00612**	0.151
	(0.0103*)	(0.0716*)	(0.358)	(0.738)	(0.204)	(0.587)
TNF-α, pg/mL	0.000659***	0.0504*	0.0318*	0.360	0.0000697***	0.00947*
	(0.00600**)	(0.0632*)	(0.0855)	(0.516)	(0.00182**)	(0.0876*)

*p<0.05 ($p_{partial}<0.05$), **p<0.01 ($p_{partial}<0.01$), ***p<0.001 ($p_{partial}<0.001$), Mann-Whitney-Wilcoxon test; *q<0.1 ($q_{partial}<0.1$), Benjamini and Hochberg corrections. Comparisons of SCCs were used for calculating p and q, while comparisons of partial SCCs with age and gender adjusted were used for calculating $p_{partial}$ and $q_{partial}$.

KEGG, Kyoto Encyclopedia of Genes and Genomes; RF, rheumatoid factor; IL, interleukin; TNF, tumour necrosis factor; IFN, Interferon; M00550, ascorbate degradation; M00879, arginine succinyltransferase pathway; M00545, trans-cinnamate degradation.

Supplementary table 7 The overlap of genera from gut metagenomic data and synovial fluid 16S data.

	Gut metagenome		**Synovial fluid 16S data**	
	Mean	**S.E.M.**	**Mean**	**S.E.M.**
Abiotrophia	6.45E-07	5.62E-07	5.46E-05	5.61E-06
Acidaminococcus	3.76E-05	2.32E-05	3.23E-06	8.82E-07
Acinetobacter	2.63E-06	2.54E-06	0.001319	0.00025738
Actinobacillus	1.22E-06	7.32E-07	0.00039202	7.36E-05
Actinomyces	4.10E-05	1.70E-05	0.00197494	0.0001988
Adlercreutzia	0.00094741	0.0003535	6.59E-06	1.23E-06
Aerococcus	7.06E-07	4.66E-07	2.93E-05	1.04E-05
Aggregatibacter	8.31E-06	5.13E-06	0.00108706	0.00014183
Akkermansia	0.00268821	0.00066918	0.00043613	0.00010519
Anaerococcus	8.54E-07	7.75E-07	1.58E-05	3.75E-06
Anaerostipes	0.00026032	6.53E-05	0.00034683	6.36E-05
Anaerotruncus	4.99E-05	1.80E-05	5.39E-06	2.67E-06
Atopobium	5.53E-06	2.23E-06	0.00042272	3.19E-05
Bacillus	6.64E-07	6.36E-07	1.84E-05	3.17E-06
Bacteroides	0.29013943	0.02109775	0.00840018	0.0013154
Bifidobacterium	0.01829813	0.0065187	0.00315388	0.00064278
Bilophila	0.00113221	0.0001444	0.00034651	6.52E-05
Blautia	0.01098432	0.001956	0.00526647	0.00099596
Brachybacterium	5.13E-08	5.13E-08	3.21E-05	5.29E-06
Brevundimonas	1.44E-07	1.44E-07	1.59E-06	4.31E-07
Bulleidia	6.85E-07	5.30E-07	0.00020587	1.40E-05
Burkholderia	1.36E-06	1.36E-06	3.73E-05	5.89E-06
Butyricimonas	7.75E-07	4.08E-07	1.29E-05	3.68E-06
Butyrivibrio	0.00666776	0.00289482	2.12E-05	2.49E-06
Campylobacter	6.30E-06	2.99E-06	0.00028281	5.46E-05
Catenibacterium	0.0002607	0.00013758	8.73E-06	2.88E-06
Caulobacter	8.14E-06	4.54E-06	4.71E-06	3.38E-06
Cetobacterium	4.80E-06	4.47E-06	7.04E-07	3.60E-07
Citrobacter	0.00078944	0.00046747	3.70E-05	3.02E-06
Clostridium	0.00343966	0.00085761	0.00035388	6.61E-05
Collinsella	0.00203712	0.00056893	0.00100336	0.00025988
Coprobacillus	0.00029756	0.00010014	8.17E-05	3.65E-05
Coprococcus	0.01041403	0.0024852	0.00244928	0.00040413
Corynebacterium	6.73E-06	4.83E-06	0.00059499	0.00010074
Deinococcus	6.97E-07	6.97E-07	4.93E-05	6.36E-06
Delftia	5.40E-08	5.40E-08	7.72E-05	9.51E-06
Desulfovibrio	0.00033105	0.00011009	0.00061664	0.00017221
Dialister	0.00190872	0.00069492	0.00139218	0.00023702
Dorea	0.00293626	0.00042856	0.0004349	5.84E-05

Eggerthella	0.00095208	0.00053581	6.71E-05	1.96E-05
Enterobacter	0.00249825	0.0010198	0.00426978	0.00017481
Enterococcus	0.00178069	0.00130997	0.00045165	0.0001509
Escherichia	0.05092025	0.0097853	5.49E-07	3.96E-07
Faecalibacterium	0.11490269	0.00978819	0.00025102	2.25E-05
Finegoldia	5.34E-06	4.89E-06	8.70E-06	1.76E-06
Fusobacterium	0.00147211	0.00122664	0.00252811	0.00027304
Gardnerella	2.31E-06	1.51E-06	1.48E-06	1.10E-06
Gemella	2.54E-05	1.42E-05	8.18E-05	6.69E-06
Granulicatella	2.74E-05	9.11E-06	0.00242879	0.00014535
Haemophilus	0.00230483	0.00049083	0.01195307	0.00111646
Holdemania	8.44E-05	2.01E-05	2.97E-05	7.72E-06
Klebsiella	0.00652499	0.00277918	7.14E-07	2.66E-07
Kocuria	6.89E-07	6.89E-07	7.25E-05	2.36E-05
Lactobacillus	0.00222834	0.0014829	0.00025986	3.40E-05
Lactococcus	3.20E-05	2.02E-05	1.07E-05	2.59E-06
Lautropia	7.20E-08	4.14E-08	0.00165815	0.00012318
Leptotrichia	9.00E-08	9.00E-08	0.00202201	0.00012525
Leuconostoc	3.13E-05	1.76E-05	3.41E-05	1.51E-05
Macrococcus	2.78E-06	2.78E-06	1.38E-06	3.84E-07
Megamonas	0.01585212	0.00474073	0.00037145	5.20E-05
Megasphaera	0.00093587	0.00037737	0.00054735	6.90E-05
Microcoleus	4.48E-07	4.48E-07	1.09E-06	1.09E-06
Mitsuokella	0.00139377	0.00092944	1.09E-06	3.51E-07
Morganella	6.11E-07	4.31E-07	3.08E-06	1.75E-06
Mycobacterium	1.45E-06	1.45E-06	3.06E-05	1.13E-05
Mycoplasma	4.85E-07	4.85E-07	1.96E-07	1.38E-07
Neisseria	1.12E-06	6.94E-07	0.02508268	0.00219087
Odoribacter	0.00362157	0.00058102	1.90E-05	2.53E-06
Oribacterium	1.65E-06	1.58E-06	0.00026302	1.99E-05
Oxalobacter	1.01E-05	6.04E-06	1.94E-06	6.16E-07
Parabacteroides	0.01438242	0.00176937	8.45E-05	1.22E-05
Paracoccus	7.80E-08	7.80E-08	8.29E-05	3.01E-05
Paraprevotella	0.00385868	0.00083775	2.84E-05	5.10E-06
Parvimonas	8.92E-06	6.01E-06	6.81E-05	5.29E-06
Peptoniphilus	3.14E-07	2.22E-07	1.91E-05	4.48E-06
Peptostreptococcus	2.23E-05	1.10E-05	7.40E-05	1.47E-05
Phascolarctobacterium	0.0048501	0.00152055	0.0064638	0.00108653
Porphyromonas	5.60E-05	3.65E-05	0.00725885	0.00051105
Prevotella	0.17470022	0.0238075	0.01687759	0.00100036
Propionibacterium	1.12E-05	1.03E-05	0.00076495	0.00015864
Proteus	8.41E-06	6.20E-06	5.44E-07	2.81E-07
Providencia	3.81E-07	3.81E-07	1.63E-06	6.24E-07

Pseudomonas	6.75E-06	3.10E-06	0.00115194	0.00016507
Pyramidobacter	5.20E-05	3.63E-05	4.35E-05	9.16E-06
Roseburia	0.02886248	0.0042608	0.00020924	5.07E-05
Rothia	6.59E-05	1.62E-05	0.00228264	0.00017808
Ruminococcus	0.02661598	0.00409609	0.00275781	0.00042481
Salmonella	0.00036895	0.00036895	1.88E-06	4.73E-07
Scardovia	2.02E-05	8.95E-06	1.04E-05	2.48E-06
Selenomonas	2.51E-05	1.96E-05	0.00057192	6.05E-05
Shuttleworthia	7.11E-07	4.44E-07	1.30E-05	1.39E-06
Staphylococcus	1.04E-05	6.94E-06	8.93E-05	7.56E-06
Stenotrophomonas	1.13E-06	1.13E-06	2.81E-05	4.76E-06
Streptococcus	0.0040409	0.00140639	0.01874711	0.00127545
Sutterella	0.00180087	0.0006182	0.00180496	0.00035735
Turicibacter	5.52E-05	2.04E-05	2.27E-05	4.44E-06
Veillonella	0.00345126	0.00078786	0.00672211	0.00040338
Weissella	0.00044631	0.00025918	5.45E-06	1.40E-06

The mean relative abundances and SEM of genera across all the samples from two datasets were calculated. SEM, standard error of the mean.

Supplementary table 8 16S rRNA gene sequencing of the isolated single colony from the joint synovial fluid of patients in the fourth stage of rheumatoid arthritis.

Sample	Sequences	Taxonomy
SF1, SF3, SF4, SF8, SF9	GCTGGCTCCTTACGGTTACCTCACGGACTTCGGGTGTTACCAGCTCTCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGACATTCTGATTCGCGATTACTAGCAACTCCAGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATAGGTTTTATAAGTTTTGCTCCACCTCACGGTCTTGCGTCTTATTGTACCTACCATTGTAGCACGTGTGTAGCCCTGGACATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCTGGTTACCCAGGCAGTCTCATTAGAGTGCTCAACTTAATGGTAGCAACTAATAACAAGGGTTGCGCTCGTTGCAGGACTTAACCTAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCTCCTTGCCCCGAAGGGCTTCACCTATCTCTAGGCTATGCAAGGGATGTCAAGTCCAGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCGCTGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTTAATCTTGCGACCGTACTCCCCAGGCGGATACTTATTGTGTTAACTGCGGCACAGGGGGAGTTGATACCCCCTACACCTAGTATCCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTACCCACGCTTTCGTGCCTCAGCGTCAGTTACAGTCCAGAAAGCCGCCTTCGCCACTGGTGTTCTTCCTAATCTCTACGCATTTCACCGCTACACTAGGAATTCCGCTTTCCTCTCCTGCACTCTAGATATCCAGTTTGGAATGCAGCCCCCAGGTTAAGCCCGGGGATTTCACATCCCACTTAAACATCCGCCTACGCACCCTTTACGCCCAGTAAATCCGGACAACGCTCGCCACCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGTGGCTTCCTCCTCTGGTACCGTCATTATCGTCCCAGAAAACAGGGCTTTACAATCCGAAGACCTTCATCACCCACGCGGCGTTGCTGCGTCAGGGTTTCCCCCATTGCGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAATGTGGCCGATCACCCTCTCAGGTCGGCTACGCATCGTTGCCTTGGTAAGCCGTTACCTTACCAACTAGCTAATGCGCCGCGGGTCCATCTCAAAGCAATAAATCTTTGATAAGAAAATCATGCGATTCTCTTATGTTATGCGGTATTAATCTTCCTTTCGGAAGGCTATCCCCCACTTTGAGGCAGGTTACCCACGTGTTACTCACCCGTCCGCCGCTAATCCACTTCCCGAAGGAAGCTTCATCGCTCGACTTGCATGTGTTAAGCACGCCGCCAGCGTTCGTCCTGAGCC	1. Clostridium sporogenes strain JCM 1416 (NR_113245.1); 2. Clostridium sporogenes strain McClung 2004 (NR_029231.1)
SF2, SF6, SF7	GGGGCCTGCGCAGCCTATACATGCAAGTCGAACGCTTTTTCTTTCACCGGAGCTTGCTCCACCGAAAGAAAAAGAGTGGCGAACGGGTGAGTAACACGTGGGTAACCTGCCCATCAGAAGGGGATAACACTTGGAAACAGGTGCTAATACCGTATAACACTATTTTCCGCATGGAAGAAAGTTGAAAGGCGCTTTTGCGTCACTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCCACGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGACGAAAGTCTGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAGAACAAGGATGAGAGTAGAACGTTCATCCCTTGACGGTATCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTCATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTGGAGGGTTTCCGCCCTTCAGTGCTGCAGCAAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCTTTGACCACTCTAGAGATAGAGCTTCCCCTTCGGGGGCAAAGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATTGTTAGTTGCCATCATTTAGTTGGGCACTCTAGCGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTGCTACAATGGGAAGTACAACGAGTTGCGAAGTCGCGAGGCTAAGCTAATCTCTTAAAGCTTCTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGCCGGAATCGCTAGTAATCGCGGATCAGCACGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGAGGTAACCTTTTGGAGCCAGCCGCCTAAGTGGAAAAGGAAGT	1. Enterococcus gallinarum strain NBRC 100675 (NR_113924.1); 2. Enterococcus gallinarum strain LMG 13129 (NR_104559.2)
SF5	GGGGCTGCGCGGCTACACTGCAGTCGAACGCTTCTTTCCTCCAGCTTGCTTGCTGTCTGACGAGTGGCGGATGGTGAGTAGTGTATGGGAAACTGCCCGATGGAAGGGGATACCTACTGGACACGGTAGCTAATACCGCATAACGTCTTGGACCATTATGGGGGACCTTCGGGCCTCTTGCCATCGGATGCGTGTCATGGGATTATGGACCCGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGATGGTCTGAATGATGACCAGCCATGCTGGGGCTATCACACCCACCAGACTCCAGCGGGAGGCAGCACTGGGGAATATGGCACGATGGGGGCAAGCCTGATGCAGCACTGCCGGGTGTATGAAGAAGGCCTTCTGGTTGAAAAGTGTTTTCAGCGAGGATGAAGGTGTTGTGGTTAATAACCAAGGAAATTGACGTTACTCGCTCCCCTGACACCGGCTAACTCCGTGCAACGGCCGCTACATACGGAGGGTGCAAGCGTTAATCGGAATTACTGCGCGTAAAGGACAATTGGGGGTCTGTCAAGTCGGATGTGAAATTCCCGGGGATACCTGGGAACTGCATCCGAAACTGGAGGGCTTTGTCTTGTGGAGGACGGTAGAATTCCAGGTGTAACGGTAATTTGCGGAGAGATCTGGAGGAATACCGATGGCGAAGGAGCCCCCCTGGACAAAGACTGACCCCTCAGGTGCTAACTCATGCTGAGCCCCAGGATTAGATACCCTGATAGTACACGCCGTACACGATGTCCACTTGCAGGTTGAGCACTTGAAGCGTGGCTACGGGAGCTAACGCGTTAGTCGACGACTGGAGAGTACCGCCGCGAGGGTAAAACTCAATGAATGACGGGGTCCATACAAGCGGCGGAGCATGTGTTACATTTCGATGCATCGCGTAGAATCTACCTACTCCTGACATCCCCATCAGGTTCTCAGAATTCCTTGGCGGCCTGCGGGAACTCCTATACAGTGCGGGACAGATTGACGAGGGTCCATGTGTGACTTAAGAGGCAGTCAGCCAACCCTGGAACTGAGACCTGTCAGACTCCTACGAGCAGCAGTGCGATCATCGCCATGACGACAGTCTGACTGCAGCCATGACGCGTGATTGCAGAGGCATCAGAGTTGTAAAGTACGTCATCGAGAGACGTGATCGTCGATTATTAGCAGCGTGCCACTGACGTACTCAGCAGAAGAAGCACCGGCTAACTACCGTGCCAGCAGCCGCGGTAATACGGAGGGGTGCAAGCGTGTAATCGGAATTATTGGGCGTAAAGCGACACGCAGGCGGTCTGTCAAGTCGGATGTGAAATCCCCCGGGCTCAACCGTGGGAGGGTGCATCTGAAACTGGCAGACTTAAAGTCTGATGGAGGAGAGATGGGAATTCCATGTGTAGCGGGTGAAAATGCGTAGATAATATGGAAGGAACACCAGTGGGCGAAGGGCGGGTCTCTTGGTACATAGACTGACGCTTCGGCTCGGAAAGCGTGGGGAAGCAAACACGGATTAGATACCCCTGTTATTCCCGCCCGTAACGGATGTCGACATGGAGTGTGGTGGGCCTTCACCTGTGGCTTCCGGAGCTAACGCATTAAGTCACTCCGCCTGGGGGAGTACGGCCGCAAGGTTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCACTCTTGACATCCAGAGACCTAGCAGAGATAGAGCTTTCCTTCGGGAACTCAAGGACAGGGTGGGCATGGCGGTTTCTCATCGTGTTGTGAAATGTTGTATTATGTCTCGCACCGAGAGCACCCCTTATCCTTAGTGCCATCATTCGGTCGGCAACTCAAAGGAGACTCCCAGGGCTAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGAGTAGGGCTCCACACGTGTTCCAATGGAAGATACAAAGAGAAGCAACCCCGGGAGTCCAAGCAATCTTCATAAGCTTCTTTCAATTCCGGATGCAGGTTGCAAATTGCCTTCATGAAGCTGGAAATCGTTAGTAATGGGGATCGCACGCCCCCGGTGAATAGTTTCCCGGCCTTTACCCCCCCCCCGTCACCACCGAGAATTGGAACCCAAGAAGTTGGGGAGGTAACCGTAAGGAGCCAGCTCCTAAGTGAACGTTGT	1. Citrobacter freundii strain LMG 3246 (NR_117752.1); 2. Citrobacter freundii strain JCM 1657 (NR_113340.1)

Supplementary table 9 QC metrics of metagenomic sequences.

Filename	Read count	base count	Q20 (%)	Q30 (%)	GC content (%)
HF16	45426814	6814022100	94.53	86.89	42.7
HF17	42464234	6369635100	96.79	91.31	44.75
HF18	41901214	6285182100	97.05	91.95	44.22
HF20	43980332	6597049800	94.36	86.63	45.49
HF21	44239462	6635919300	95.31	88.27	43.22
HF22	42648660	6397299000	96.68	91.15	45.89
HF25	41728154	6259223100	96.86	91.55	46.14
HF28	42442994	6366449100	97.02	91.77	43.74
HF31	48715360	7307304000	95.06	87.98	43.67
HF32	42228228	6334234200	95	87.81	46.25
HF33	43057824	6458673600	94.84	87.53	46.94
HF36	45431934	6814790100	97.71	93.31	44
HF37	45420844	6813126600	95.15	88.03	45.22
HF38	44381380	6657207000	94.3	86.56	45.06
HF39	41799946	6269991900	95.06	87.91	45.36
HF3	42678234	6401735100	95.19	88.11	44.44
HF41	46132006	6919800900	94.57	86.98	45.28
HF43	41788168	6268225200	94.44	86.81	48.96
HF44	45101768	6765265200	95.25	88.22	44.22
HF46	44819996	6722999400	95.03	87.8	45.08
HF49	42261648	6339247200	96.6	90.94	43.89
HF4	46476802	6971520300	94	85.75	45.38
HF51	41250820	6187623000	96.8	91.38	46.22
HF5	39758590	5963788500	94.5	86.82	42.44
HF7	49212934	7381940100	94.45	86.79	47.59
HF8	40649274	6097391100	94.66	87.15	44.74
HF9	42372194	6355829100	95.95	89.4	44.47
OAF33	44103910	6615586500	96.8	91.37	45.05
OAF39	41028814	6154322100	94.72	87.25	44.02
OAF40	42711768	6406765200	97.15	92.08	45.99
OAF41	41925700	6288855000	93.81	86.2	42.91
OAF43	41294354	6194153100	95.66	89.14	45.54
OAF44	39774718	5966207700	95.3	88.37	46.97
OAF45	40516468	6077470200	97	92.2	50.55
OAF46	42165434	6324815100	94.98	87.84	43.3
OAF49	43398242	6509736300	97.93	93.94	50.6
OAF53	45107442	6766116300	95.37	88.45	44.84
OAF54	43498328	6524749200	97.48	92.92	49.78
OAF63	44173628	6626044200	97.1	91.96	43.53
OAF66	42944028	6441604200	95.2	88.13	45.17
OAF68	45564888	6834733200	94.92	87.69	44.96
OAF69	45345760	6801864000	97.3	92.39	43.26

OAF70	41783728	6267559200	95.09	87.96	49.05
OAF74	40480268	6072040200	96.83	91.43	45.73
OAF77	43064918	6459737700	96.63	91.04	44.71
OAF79	40788874	6118331100	95.95	89.4	44.3
RAF101	43034368	6455155200	94.58	87.17	46.85
RAF102	43178154	6476723100	97.11	92.14	52.33
RAF104	41053400	6158010000	94.89	87.69	44.34
RAF106	44211600	6631740000	96.72	91.26	46.36
RAF107	45474716	6821207400	95.69	89.16	48.41
RAF111	41272668	6190900200	96.8	91.38	45.73
RAF112	44410128	6661519200	96.59	91.06	49.55
RAF113	41958710	6293806500	94.96	87.7	45.23
RAF116	41167720	6175158000	96.51	90.84	45.02
RAF117	40297500	6044625000	94.44	86.77	42.93
RAF118	41616114	6242417100	94.98	87.65	42.66
RAF120	46528830	6979324500	92.37	83.39	44.37
RAF122	42132620	6319893000	96.55	91.12	50.61
RAF123	43624680	6543702000	97.13	91.93	41.14
RAF124	44983948	6747592200	96.78	91.36	46.38
RAF125	40346302	6051945300	95.24	88.14	41.47
RAF126	42991048	6448657200	96.87	91.56	46.75
RAF127	40315134	6047270100	94.66	87.16	43.78
RAF128	44285618	6642842700	94.86	87.62	44.91
RAF129	40564390	6084658500	97.19	92.25	46.88
RAF131	41919100	6287865000	96.95	91.86	52.05
RAF132	41020208	6153031200	96.77	91.34	46.2
RAF135	40542788	6081418200	95.38	88.65	48.34
RAF137	43476654	6521498100	95.41	88.6	45.38
RAF138	43774724	6566208600	97.05	91.92	46.46
RAF139	41291580	6193737000	95.31	88.38	43.58
RAF140	45914110	6887116500	95.3	88.54	51.92
RAF141	47544378	7131656700	94.28	86.53	43.34
RAF142	45594532	6839179800	94.63	87.12	44.94
RAF143	42483748	6372562200	94.87	87.55	42.98
RAF146	47249506	7087425900	94.98	87.74	44.97
RAF147	40224094	6033614100	97.17	92.18	47.36
RAF149	45841894	6876284100	97.61	93.08	43.89
RAF150	40316734	6047510100	97.12	92.07	45.59
RAF151	45314032	6797104800	94.75	87.32	44.55
RAF153	40635770	6095365500	95.55	88.88	45.11
RAF158	40476348	6071452200	96.66	91.15	47.72
RAF159	40627908	6094186200	96.5	90.82	47.55
RAF160	42544754	6381713100	95.23	88.27	45.51
RAF161	41397638	6209645700	96.42	90.7	49.47

RAF166	41874280	6281142000	97.42	92.59	45.65
RAF167	41896240	6284436000	97.13	92.03	44.47
RAF170	43880640	6582096000	96.65	91.07	45.8
RAF174	43765520	6564828000	96.74	91.28	47.36
RAF177	42902240	6435336000	97.5	92.83	43.69
RAF179	41915000	6287250000	97.18	92.15	45.03
RAF180	44576348	6686452200	97.07	91.93	44.21
RAF184	44365800	6654870000	97.25	92.34	46.2
RAF185	43686968	6553045200	97.25	92.31	45.5
RAF186	44277220	6641583000	97.63	93.16	45.45
RAF187	40748474	6112271100	96.78	91.38	45.67
RAF25	43019142	6452871300	97.05	91.86	45.33
RAF44	43568814	6535322100	97.2	92.27	48.01
RAF58	41975628	6296344200	96.45	90.84	45.49
RAF61	42669114	6400367100	94.89	87.63	44.57
RAF63	40123452	6018517800	96.81	91.39	44.33
RAF66	44098600	6614790000	96.66	91.14	47.41
RAF68	44615320	6692298000	97.13	91.94	44.86
RAF70	43380268	6507040200	94.63	87.09	44.51
RAF71	44516994	6677549100	97.5	92.91	46.35
RAF74	41052480	6157872000	96.97	91.8	49.8
RAF75	44768028	6715204200	97.35	92.5	43.84
RAF77	42776628	6416494200	97.42	92.88	46.89
RAF78	40979382	6146907300	95	87.75	45.33
RAF79	43642800	6546420000	95.55	88.85	43.52
RAF80	45535296	6830294400	97.05	91.81	42.02
RAF81	46449788	6967468200	93.88	85.57	46.78
RAF84	43913220	6586983000	97.4	92.69	47.39
RAF86	41103940	6165591000	96.89	91.62	50.15
RAF87	42285100	6342765000	96.09	90.61	47.07
RAF88	47400690	7110103500	94.73	87.45	45.66
RAF89	40617160	6092574000	94.8	87.4	44.51
RAF90	47154162	7073124300	95.16	88.03	45.3
RAF92	40483234	6072485100	96.84	91.4	45.42
RAF95	42641890	6396283500	94.38	86.66	45.22
RAF96	44305868	6645880200	97.12	92.02	43.39

QC, quality control

Q20, percentages of bases whose correct base recognition rates are greater than 99% in total bases.

Q30, percentages of bases whose correct base recognition rates are greater than 99.9% in total bases.

GC content: (G & C base count) / (Total base count)