Detailed Materials and Methods

Subject selection and sample collection. The study subjects were recruited among the subjects of a larger study in which Swedish students from the universities in Umeå, Stockholm and Gothenburg travelling for international exchange studies as part of their university education were invited to participate from April 2010 through January 2014. The study protocol included responding to questionnaire data and self-submission of fecal specimens before and after travel. Each study subject submitted a fecal swab specimen (Copan Venturi Transystem®, Copan diagnostics Inc. USA) for bacterial culture and a fecal specimen in a half filled 101*16,5mm plastic collection tube (Faeces tube, Sarstedt, Nümbrecht, Germany) for metagenomic analysis. For the present study, only healthcare students (medical, nursing and dentistry) travelling to the Indian peninsula or to Central Africa and having submitted a full set of fecal specimens qualified for inclusion. None of the subjects included were allowed to have taken antibiotics within six months prior to sampling. The inclusion was consecutive with a target of 15-20 study subjects travelling to each of the two destinations.

Fecal specimens for metagenomics were sent to the lab in the collection tubes, and stored at -20°C upon arrival. DNA extraction was performed using the QIAamp® DNA Stool Mini Kit (QIAGEN) according to the manufacturer's protocol. DNA concentrations were measured using a Qubit instrument, and samples were stored at -20°C before sequencing. Paired-end sequencing libraries (2x100 bp) were prepared using the TrueSeq DNA Kit for multiplexing. Sequencing was done at Science for Life Laboratories (Stockholm, Sweden) using Illumina HiSeq2000 technology. The study was approved by the regional ethical review board in Umeå, Sweden (2011-357-32M).

Culturing of ESBL-producing bacteria. Screening for ESBL producing bacteria was done using swab culture on chromogenic media (crohmID ESBL, bioMérieux SA, Marcy-l´Etoile France). All positive isolates were analyzed through culture-based methods according to EUCAST guidelines (http://www.eucast.org). The definition of ESBL producing Enterobacteriaceae by Giske *et al.* (1) was used. Antibiotic susceptibility testing (including cefotaxime, ceftazidime, piperacillin/tazobactam and meropenem) was done by disc diffusion (Oxoid Ltd./Thermo Fisher Scientific, Cambridge, United Kingdom) on Mueller-Hinton (MH) agar (Oxoid Ltd.). E-tests® (bioMérieux) were used to test for the presence of $ESBL_A$ phenotype (detecting the presence of CTX-M, SHV and TEM enzymes) with cefotaxime/cefotaxime + clavulanic acid and ceftazidime/ceftazidime + clavulanic acid as well as cefepime/cefepime+ clavulanic acid if warranted. If applicable, phenotypic detection of AMPc type beta-lactamases with cloxacillin inhibitable ESBL enzymes (cefotetan/cefotetan + cloxacillin) was performed. Since not all carbapenemase-producers show reduced susceptibility to carbapenems, particularly not OXA-48/OXA-181 producers that do not yield an ESBL (2, 3), all post-travel samples of this study (before screening on chromogenic media) were tested by disc diffusion for susceptibility to meropenem (10µg), piperacillin/tazobactam (30µg/6µg) and ceftazidim (10µg) on MH agar (Thermo Scientific) containing 7,5mg/L vancomycin, a modified zone diameter cut-off (≥16 mm) for piperacillin-tazobactam was used (4). Resistant Enterobacteriaceae isolates were further tested with temocillin (30 µg, Rosco Diagnostica, Taastrup, Denmark) and our test scheme contained additional analysis by the CT-103 XL microarray (Check-Points Health B.V., Wageningen, The Netherlands) of isolates with reduced sensitivity to temocillin. Phenotypic species identification of ESBL positive Enterobacteriaceae isolates was done using an API® identification system (API-20E, bioMérieux). Species identification of non-Enterobacteriaceae isolates growing on the chromogenic media was performed with MALDI-TOF-MS using a Bruker Daltonics Microflex

LT mass spectrometer and the MALDI-Biotyper 3.0 software (Bruker Daltonik GmbH, Bremen, Germany).

DNA from ESBL-producing strains was extracted using QIAamp® DNA Mini Kit (QIAGEN) according to the manufacturer's protocol. DNA concentrations were measured using a Qubit instrument, and samples were stored at -20°C before sequencing. The samples were sequenced using the Illumina MiSeq instrument (FOI, Umeå), producing 299,202 – 1,575,161 (average 760,896) 250 bp paired-end reads per sample for each library.

Sequence pre-processing and quality filtering. FASTQ sequences from both genomes and metagenomes were trimmed with respect to adapters and low-quality nucleotide stretches using TrimGalore! version 0.2.8, www.bioinformatics.babraham.ac.uk/projects/trim_galore/ with parameter settings "-stringency 6 -q 28". Host sequences were subsequently removed from the metagenomic data by aligning the trimmed sequences to the hg19 human genome reference assembly using Bowtie2 v. 2.0.2 (5) with parameters "-p 8 -un-conc-gz *OUTFILE*" and discarding those reads that had a valid alignment to it. Trimmed and filtered sequences were used as input for all further analysis, including resistance gene mapping, reference-genome mapping, and *de novo* assembly. Sequence data have been submitted to the European Nucleotide Archive under project accession number PRJEB7369 (http://www.ebi.ac.uk/ena/data/view/PRJEB7369).

Analysis of genomes from isolates. Filtered and trimmed sequences from the isolated ESBL-producing *Escherichia coli* genomes were assembled using the SPAdes assembler (version 2.5.1) with the additional parameter "-m 32" (6). Resistance genes were identified by matching the assembled

contigs against the Resqu database version 1.1 www.1928diagnostics.com/resdb containing 3,019 non-redundant protein sequences corresponding to 325 resistance gene families using blastx (7). See Table S5 for the complete list of genes in Resqu. Only matches longer than 100 bp and with 90% identity or higher were kept. Identified beta-lactam resistance genes were further characterized by BLAST against the entire NCBI protein database, to determine if variants were known or novel.

rRNA analysis and resistance gene mapping. Quality filtered read pairs were scanned with Metaxa2 version 2.0 (8) to extract bacterial 16S rRNA (SSU) sequences (additional option "--align none"). In each library, the 16S counts for different genera, families and phyla were normalized to the total number of 16S counts in that library, yielding relative abundances for each organism group. Enterotypes (9) were determined using Principal Component Analysis (PCA) to mainly be driven by the abundances of the *Prevotella* and *Bacteroides* genera, and therefore we defined enterotypes by the ratio of reads mapping to *Prevotella* 16S rRNA sequences and reads mapping to *Bacteroides* 16S rRNA. If the ratio was above one or below one in both the before and after samples from the same individual, the enterotypes was deemed unchanged by travel in that individual. Quality filtered reads were mapped against the Resqu antibiotic resistance gene database using Vmatch (http://vmatch.de), allowing two mismatched amino acids per translated read to account for sequencing errors but retain stringency with regards to finding the sought target genes (options "-showdesc 60 -dnavsprot 11 -l 20 -h 2"), and thus avoiding inflation by false positive matches (10). The number of matches to each resistance gene was counted and normalized to the length of the respective gene to avoid bias due to differential length of the resistance genes. The length-normalized numbers were then used for deriving an approximation of the number of resistance genes per 16S rRNA sequence identified by Metaxa2 (see above). The length-normalized numbers were divided by the length of the 16S gene.

De novo **metagenomic assembly.** *De novo* assembly of the sequences from each sample was performed using Ray Méta (11) on 512 cores of a Cray XE6 system at the PDC Center for High Performance Computing at the Royal Institute of Technology in Stockholm. The k-mer length parameter k was set to 49 based on trials using a range of values in Ray and Velvet (12) assemblies.

Annotation of assemblies. Prodigal (13) version 2.60 with parameters "-c -m -p meta" was used to identify open reading frames in assembled contigs and translate those into amino acid sequences. These were subsequently mapped using blastp (in NCBI Blast (7) version 2.2.28+) to the Resqu resistance gene database in order to identify contigs containing sequences resembling known resistance genes. Networks of co-localized resistance genes were generated in Cytoscape version 3.0 (14). Contigs were additionally mapped to a reference collection of gastrointestinal microbial genomes to discern taxonomic origin (see below).

Mapping to reference genomes and contigs. Quality-filtered reads and assembled contigs were mapped against the Human Microbiome Project (HMP) gastrointestinal_tract reference genome collection (http://downloads.hmpdacc.org/data/reference_genomes/body_sites/Gastrointestinal_tract.nuc.fsa) using Burrows-Wheeler Aligner, bwa (15), version 0.7.5a with the "mem" subcommand. Reads from all libraries were also mapped back to the total collection of contigs from all samples using Bowtie2 (v. 2.0.2) to estimate their abundance in different libraries.

Statistical testing. Resistance gene copies per bacterial 16S rRNA counts were log-transformed by adding a number corresponding to the smallest relative abundance for any detected gene across all samples, and significant changes of average abundances between before and after samples were assessed using paired Student's t-tests. Wilcoxon signed-rank test was used as a complement to find genes with changed median abundance. All p-values were corrected for multiple testing using a Benjamini-Hochberg False Discovery Rate (FDR) and genes with an FDR <0.05 were considered significant (16). The same procedure was adapted for resistance gene categories. Changes in normalized log-transformed relative abundances of taxonomic groups were similarly tested using paired Student's t-tests and tests with an FDR of <0.05 were considered significant. Contigs with significantly different abundance between the groups of travelers returning from the Indian peninsula and Africa were identified using the Limma package (17). Correlations between resistance gene abundances and other factors (gender, age, length of visit, time between return from trip and sample delivery, health care work, sickness during travel, diarrhea, malaria prophylaxis and ESBL culturing results) were assessed using linear regression in the R statistical program (http://www.r-project.org). The p-values for each coefficient were corrected for multiple testing and tests with an FDR <0.05 were considered significant.

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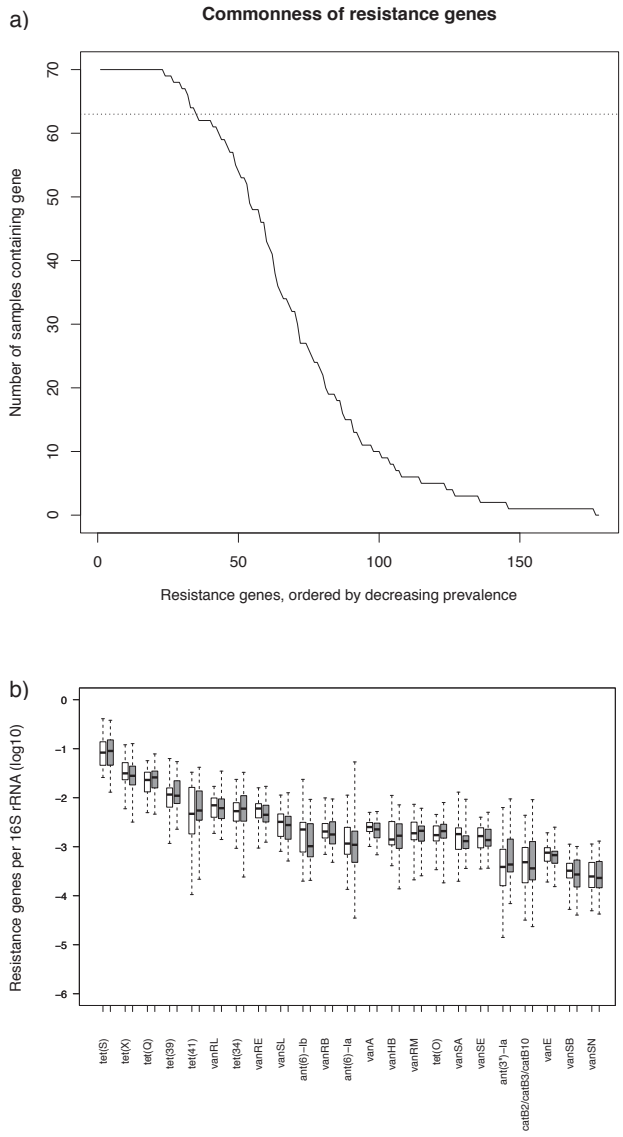

Figure S1. The core resistome of the cohort. a) The number of samples containing a certain resistance gene. b) Abundance of the resistance genes detected in all samples (log 10 scale).

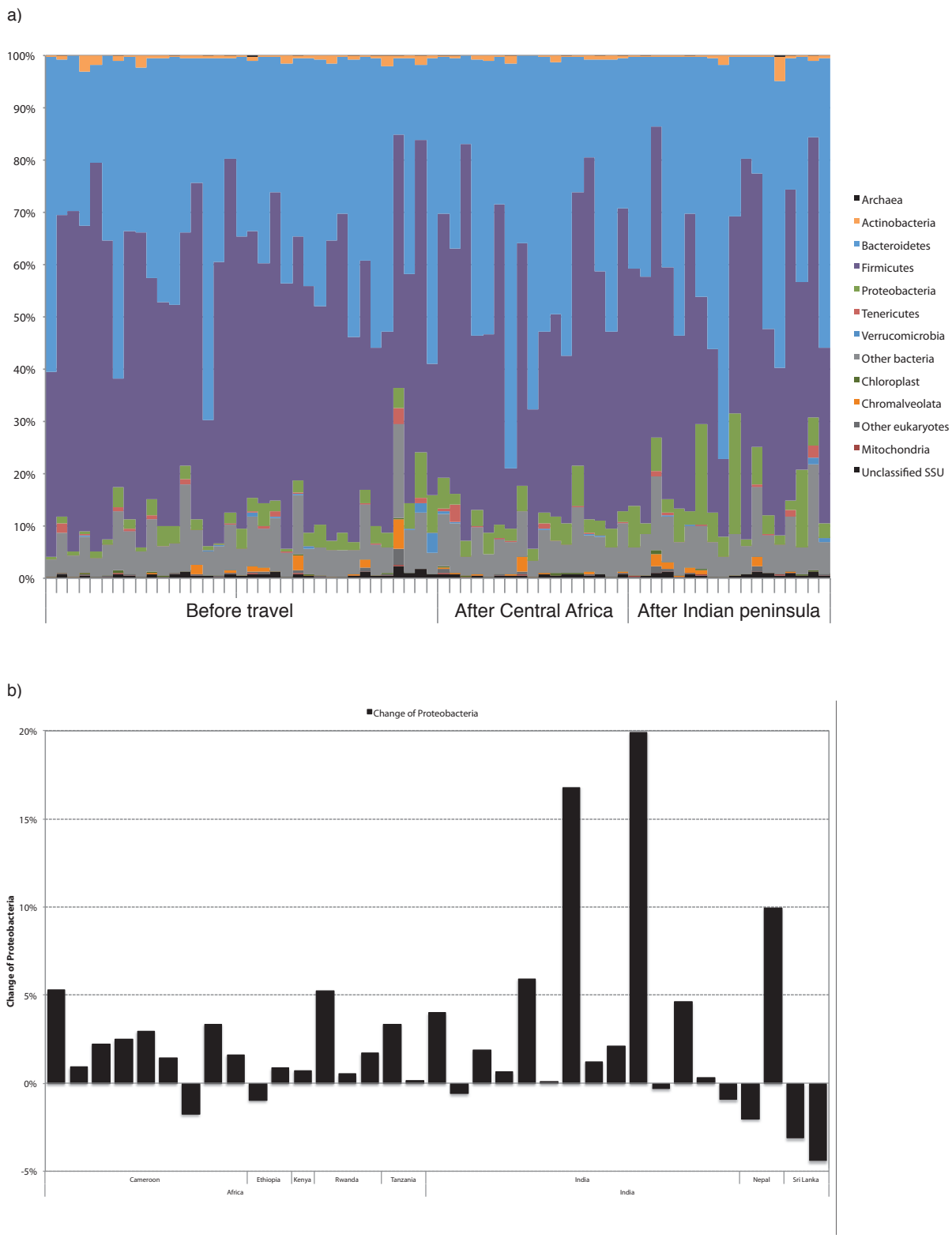

Figure S2. a) Taxonomic composition at the phylum level. b) Changes of the relative abundance of Proteobacteria, measured as proteobacterial 16S rRNA sequences per total 16S rRNA sequences, before and after travel.

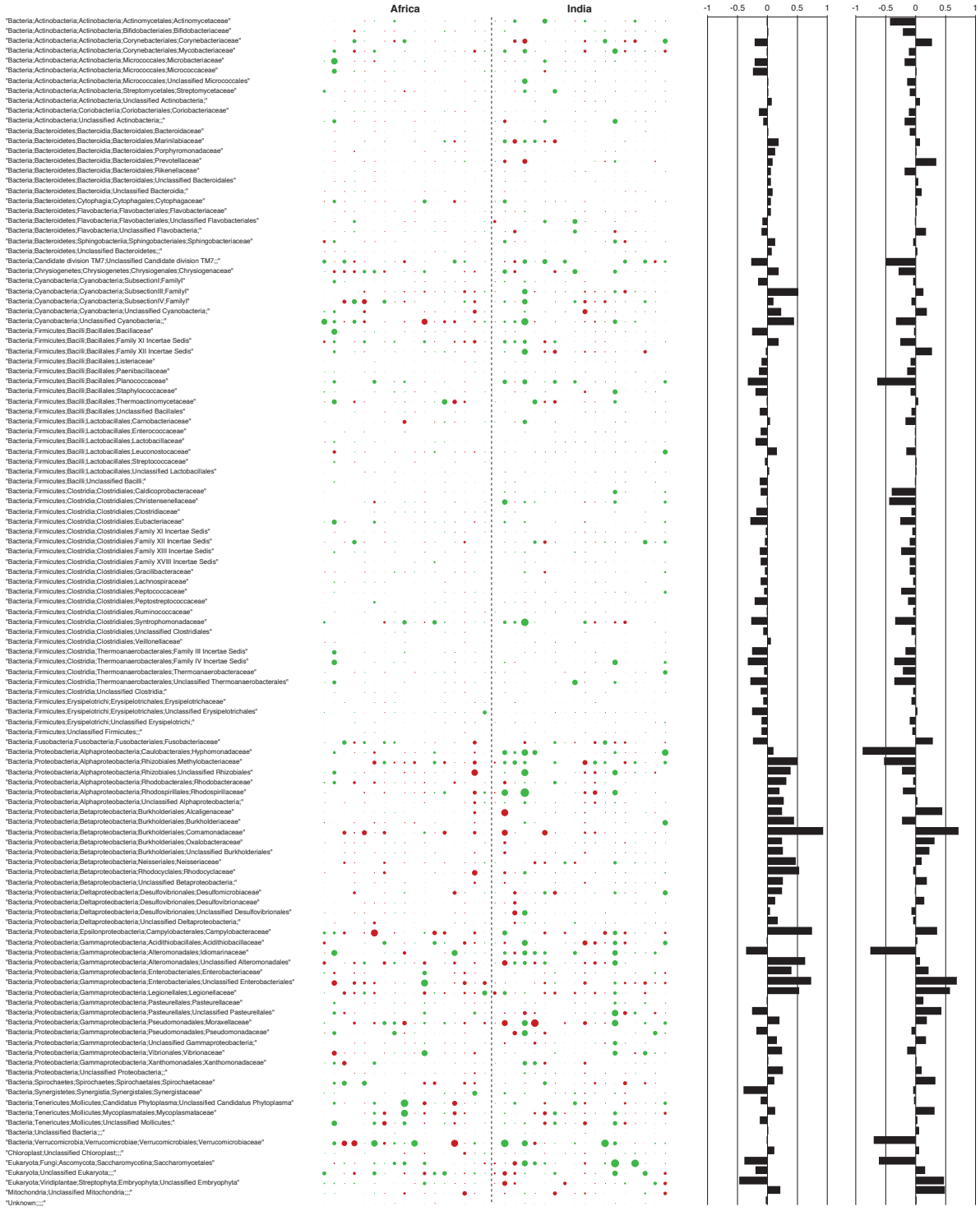

Figure S3. Changes of the most abundant taxonomic families, for each individual. The diameter of each dot represents the magnitude of change in that individual (log 10 scale). Green color indicates decreases and red color indicates increases. To the right, the mean fold changes across all individuals traveling to central Africa (left) and the Indian peninsula (right) are shown (log 10 scale).

Figure S4. Changes of the most abundant genera, for each individual. The diameter of each dot represents the magnitude of change in that individual (log 10 scale). Green color indicates decreases and red color indicates increases.

Table S1. Study subject and travel characteristics

Region	Destination	Field of study	Days before departure	Length of stay	Days after return	Sex	Age	Patient work in hospital	Travellers diarrhoea		Sought medical care		Anti-malarial prophylaxis	
									Fell ill	Days ill	Outpatient	Admitted	Atovaquone-Proguanil	Mefloquine
Central Africa	Cameroon	Medical	76	49	16	Female	23							x
	Cameroon	Medical	3	29	39	Male	25	x	x	3				x
	Cameroon	Medical	3	30	38	Male	28	x	x	2				x
	Cameroon	Medical	69	49	31	Female	23		x	N/A				x
	Cameroon	Medical	19	34	18	Female	24	x					x	x
	Cameroon	Medical	0	37	35	Female	25		x	3				x
	Cameroon	Medical	41	34	16	Female	25	x	x	6				x
	Cameroon	Medical	25	34	18	Female	28	x	x	4				x
	Cameroon	Medical	11	33	13	Male	25	x	x	1				x
	Ethiopia	Medical	0	150	11	Female	28	x	x	4				x
	Ethiopia	Dentistry	16	32	51	Female	24		x	6	x		x	
	Kenya	Medical	3	19	61	Female	28						x	
	Tanzania	Medical	0	31	21	Female	24	x	x	12			x	
	Tanzania	Nursing	18	47	32	Male	25	x						x
	Rwanda	Medical	2	22	25	Female	25	x	x	15			x	
	Rwanda	Medical	2	22	73	Female	25	x	x	1			x	
	Rwanda	Medical	2	21	41	Female	26						x	
			Range 0-76	Range 19-150	Range 11-73	76% female	Range 23-28	65%	71%	Range 1-15	6%	0%	41%	65%
			Median 3	Median 33	Median 31	(13/17)	Median 25	(11/17)	(12/17)	Median 4	(1/17)	0	(7/17)	(11/17)
	India	Medical	2	36	5	Male	24	x	x	5				
	India	Medical	15	33	21	Female	26	x					x	
Indian peninsula	India	Medical	10	29	19	Female	25	x	x	2			x	
	India	Medical	23	29	44	Female	25	x	x	3				
	India	Medical	4	98	25	Male	23		x	1				
	India	Medical	1	38	2	Female	29	x	x	5			x	
	India	Medical	0	119	22	Female	23	x	x	7			x	
	India	Medical	77	106	20	Female	23	x	x	5				
	India	Medical	10	40	120	Female	22		x	1		x		x
	India	Medical	0	105	19	Female	23		x	2	x			x
	India	Medical	16	32	20	Male	24	x	x	5	x			
	India	Medical	1	43	25	Female	27		x	1				
	India	Midwife	7	58	32	Female	28	x						
	India	Medical	4	53	12	Male	26							
	Sri Lanka	Medical	7	23	47	Female	34						x	x
	Sri Lanka	Medical	9	24	25	Female	24	x						x
	Nepal	Medical	4	14	4	Male	28	x						
	Nepal	Medical	4	14	4	Female	29	x	x	11				
			Range 0-77	Range 14-119	Range 2-120	72% female	Range 23-34	67%	67%	Range 1-7	11%	6%	28%	22%
			Median 6	Median 37	Median 21	(13/18)	Median 25	(12/18)	(12/18)	Median 4	(2/18)	(1/18)	(5/18)	(4/18)

Table S2. Details of the individual sequencing libraries

Location data		SSU sequences identified by Metaxa2						Library sizes				
Before or after	Destination	Archaea	Bacteria	Chloroplast	Eukaryota	Mitochondria	Unknown	Raw library size (reads)	Raw library size (Gbp)	Quality-filtered size	Low quality reads	Bacterial 16S per million reads
Before	Cameroon	0	220,291	22	157	9	433	125,907,692	25.18	116,985,641	8,922,051	1,883.06
Before	Cameroon	23	121,442	47	141	97	929	78,430,878	15.69	70,967,328	7,463,550	1,711.24
Before	Cameroon	0	182,229	16	24	23	506	110,624,462	22.12	102,862,162	7,762,300	1,771.58
Before	Cameroon	0	203,600	157	703	38	1,010	138,278,024	27.66	129,038,382	9,239,642	1,577.83
Before	Cameroon	0	189,107	40	97	20	265	97,108,136	19.42	84,768,485	12,339,651	2,230.86
Before	Cameroon	0	208,475	231	394	45	585	105,488,039	21.10	96,338,305	9,149,734	2,163.99
Before	Cameroon	15	217,277	1,113	515	38	1,947	94,583,689	18.92	86,709,535	7,874,154	2,505.80
Before	Cameroon	0	112,218	8	217	4	578	57,708,298	11.54	55,274,739	2,433,559	2,030.19
Before	Cameroon	0	199,666	54	141	20	429	93,610,789	18.72	80,289,041	13,321,748	2,486.84
Before	Ethiopia	0	198,146	394	513	22	1,480	114,623,643	22.92	107,097,525	7,526,118	1,850.15
Before	Ethiopia	0	208,188	355	1	2	576	96,158,167	19.23	94,094,185	2,063,982	2,212.55
Before	Kenya	17	222,448	44	71	36	1,858	152,444,626	30.49	143,428,931	9,015,695	1,550.93
Before	Tanzania	0	184,030	19	433	4	596	94,496,474	18.90	91,204,324	3,292,150	2,017.78
Before	Tanzania	84	363,035	88	2,734	80	2,848	186,020,932	37.20	178,004,607	8,016,325	2,039.47
Before	Rwanda	0	136,406	177	9	1	1,635	79,870,933	15.97	73,992,049	5,878,884	1,843.52
Before	Rwanda	0	111,466	21	2,103	184	496	58,683,097	11.74	56,688,930	1,994,167	1,966.27
Before	Rwanda	2	248,514	1	12	0	1,140	116,336,923	23.27	112,218,587	4,118,336	2,214.55
Before	India	0	164,203	74	100	16	1,907	94,168,067	18.83	86,725,925	7,442,142	1,893.36
Before	India	0	213,993	83	6	1	530	125,452,729	25.09	120,493,836	4,958,893	1,775.97
Before	India	9	123,055	166	4,387	151	1,116	81,137,887	16.23	77,796,173	3,341,714	1,581.76
Before	India	0	219,475	6	7	4	529	105,390,115	21.08	99,898,565	5,491,550	2,196.98
Before	India	12	108,377	1	192	7	487	68,826,005	13.77	65,736,512	3,089,493	1,648.66
Before	India	0	187,490	159	4,177	97	2,485	126,672,111	25.33	117,356,765	9,315,346	1,597.61
Before	India	16	215,319	56	197	24	1,051	114,873,991	22.97	110,841,646	4,032,345	1,942.58
Before	India	0	191,903	37	157	41	744	108,862,964	21.77	100,505,030	8,357,934	1,909.39
Before	India	224	152,457	140	2,199	143	1,277	89,041,296	17.81	84,176,188	4,865,108	1,811.17
Before	India	0	180,204	335	2,298	72	1,200	104,860,302	20.97	97,572,943	7,287,359	1,846.86
Before	India	0	144,228	36	269	68	554	119,776,667	23.96	111,456,534	8,320,133	1,294.03
Before	India	0	154,785	32	334	67	410	108,484,366	21.70	102,117,614	6,366,752	1,515.75
Before	India	0	164,743	8	29	13	499	108,191,129	21.64	98,753,669	9,437,460	1,668.22
Before	India	1	200,324	114	821	52	913	120,944,486	24.19	111,299,634	9,644,852	1,799.86
Before	Sri Lanka	146	137,803	214	13	4	2,439	101,623,663	20.32	97,424,636	4,199,027	1,414.46
Before	Sri Lanka	0	196,377	24	109	0	1,423	180,821,242	36.16	168,578,941	12,242,301	1,164.90
Before	Nepal	11	100,230	198	9,846	251	2,677	81,153,547	16.23	75,267,243	5,886,304	1,331.65
Before	Nepal	0	141,454	18	8	0	1,292	97,563,912	19.51	91,026,911	6,537,001	1,553.98
After	Cameroon	5	112,023	169	1,382	239	857	68,589,271	13.72	64,867,085	3,722,186	1,726.96
After	Cameroon	2	160,097	70	275	32	1,169	92,482,953	18.50	85,135,965	7,346,988	1,880.49
After	Cameroon	0	149,056	21	15	12	513	95,181,317	19.04	80,837,880	14,343,437	1,843.89

After	Cameroon	0	182,566	71	719	46	760	108,827,882	21.77	94,736,141	14,091,741	1,927.10
After	Cameroon	0	157,990	10	5	2	310	112,558,957	22.51	105,987,973	6,570,984	1,490.64
After	Cameroon	0	185,416	27	557	62	914	113,933,461	22.79	105,653,830	8,279,631	1,754.94
After	Cameroon	6	215,167	312	376	24	1,047	74,880,136	14.98	71,943,878	2,936,258	2,990.76
After	Cameroon	0	206,543	372	6,979	630	1,179	127,104,270	25.42	119,741,546	7,362,724	1,724.91
After	Cameroon	0	264,177	7	24	15	558	138,551,617	27.71	124,497,835	14,053,782	2,121.94
After	Ethiopia	0	258,280	45	218	20	2,127	148,483,688	29.70	139,510,543	8,973,145	1,851.33
After	Ethiopia	0	54,397	294	42	2	287	82,739,446	16.55	40,538,343	42,201,103	1,341.87
After	Kenya	20	168,496	10	191	18	1,348	118,039,879	23.61	110,534,095	7,505,784	1,524.38
After	Tanzania	0	264,522	59	86	80	690	132,236,558	26.45	127,715,066	4,521,492	2,071.19
After	Tanzania	8	100,527	160	420	30	798	463,791,736	92.76	54,987,641	408,804,095	1,828.17
After	Rwanda	0	243,606	352	1	2	1,885	137,856,261	27.57	127,235,892	10,620,369	1,914.60
After	Rwanda	0	204,169	31	1,718	243	865	98,323,380	19.66	92,301,898	6,021,482	2,211.97
After	Rwanda	14	169,981	102	111	20	1,267	108,508,604	21.70	103,146,520	5,362,084	1,647.96
After	India	0	308,378	152	5,518	131	3,696	172,298,973	34.46	164,171,030	8,127,943	1,878.39
After	India	0	213,865	46	244	30	600	95,916,677	19.18	92,069,410	3,847,267	2,322.87
After	India	1	271,377	35	3,645	226	1,820	145,856,676	29.17	139,769,906	6,086,770	1,941.60
After	India	0	156,408	4	5	7	598	80,858,580	16.17	77,801,453	3,057,127	2,010.35
After	India	0	186,891	13	79	7	1,271	103,809,366	20.76	95,299,798	8,509,568	1,961.08
After	India	0	196,638	143	5,629	140	2,428	119,333,838	23.87	111,437,652	7,896,186	1,764.56
After	India	0	142,048	37	26	6	1,494	79,961,086	15.99	74,749,858	5,211,228	1,900.31
After	India	0	191,360	16	324	277	585	114,439,546	22.89	80,387,488	34,052,058	2,380.47
After	India	6	123,942	42	66	47	621	78,223,579	15.64	75,053,057	3,170,522	1,651.39
After	India	0	208,535	1,555	8,091	178	2,001	103,437,332	20.69	94,520,827	8,916,505	2,206.23
After	India	0	228,654	191	2,104	466	1,308	109,989,613	22.00	102,842,328	7,147,285	2,223.35
After	India	0	131,170	6	1	10	158	70,806,355	14.16	68,666,720	2,139,635	1,910.24
After	India	0	96,110	2	28	3	91	77,982,751	15.60	75,870,339	2,112,412	1,266.77
After	India	197	137,542	47	105	81	838	101,742,471	20.35	89,404,424	12,338,047	1,538.42
After	Sri Lanka	35	163,143	301	5	6	2,155	101,637,724	20.33	97,729,754	3,907,970	1,669.33
After	Sri Lanka	0	108,658	53	32	7	663	85,438,843	17.09	81,634,162	3,804,681	1,331.04
After	Nepal	35	221,127	157	137	24	2,394	136,599,459	27.32	125,704,413	10,895,046	1,759.10
After	Nepal	0	93,541	22	21	3	567	58,982,996	11.80	51,705,957	7,277,039	1,809.10

Table S3. Details of the individual assemblies

Before or after	Destination	Total # contigs	Shortest contig	Longest contig	N95	N90	N75	N50	N10	N5	N1	Assembled nts
Before	Cameroon	304 651	195	677 010	216	244	381	1 283	87 295	147 428	292 113	210 271 561
Before	Cameroon	289 552	195	546 930	224	265	530	3 269	101 634	163 629	356 927	256 764 347
Before	Cameroon	164 747	195	625 381	230	283	643	5 068	171 600	308 581	514 102	164 872 534
Before	Cameroon	390 000	195	686 235	222	261	522	3 271	113 228	183 464	375 787	343 151 870
Before	Cameroon	191 344	195	370 704	226	269	536	3 277	57 992	108 955	254 203	170 403 312
Before	Cameroon	228 523	195	638 635	233	288	623	3 591	158 619	243 926	449 335	223 269 782
Before	Cameroon	265 143	195	1 034 084	217	246	430	2 341	107 808	200 425	492 323	206 539 384
Before	Cameroon	231 178	195	669 622	218	249	441	3 444	176 773	302 750	642 811	189 106 799
Before	Cameroon	299 556	195	655 059	218	248	411	1 433	57 330	100 317	262 481	216 976 116
Before	Ethiopia	306 967	195	668 934	217	246	405	2 211	80 270	124 213	238 150	232 142 538
Before	Ethiopia/Tanzania	190 514	195	604 614	230	281	708	9 984	171 187	267 131	447 984	201 897 907
Before	India	330 010	195	385 183	215	242	392	1 636	71 205	108 714	228 895	237 587 577
Before	India	262 964	195	488 691	231	283	620	4 685	98 571	161 137	341 682	258 126 988
Before	India	287 142	195	986 116	224	265	532	3 806	130 615	204 703	583 765	257 518 591
Before	India	266 170	195	582 541	234	291	656	3 912	106 229	172 750	358 026	266 117 369
Before	India	155 183	195	504 951	226	272	641	7 872	141 847	213 096	376 269	155 381 630
Before	India	340 166	195	464 391	223	261	476	2 813	104 351	172 932	342 811	284 893 519
Before	India	413 096	195	454 123	218	248	403	1 608	48 086	76 576	167 784	300 624 285
Before	India	361 379	195	535 133	222	260	484	1 963	60 889	129 469	279 214	292 379 866
Before	India	397 200	195	677 891	216	245	405	1 917	95 269	172 543	406 452	296 105 864
Before	India	229 038	195	507 494	227	273	628	6 633	133 055	200 205	379 706	227 208 920
Before	India	302 561	195	965 767	222	261	508	3 410	130 021	213 801	532 790	264 268 324
Before	India	254 168	195	729 054	224	263	504	4 148	137 391	267 364	558 894	224 169 639
Before	India	222 760	195	621 989	226	270	569	5 361	94 452	153 369	269 142	211 284 201
Before	India	214 464	195	713 702	231	291	930	10 879	153 916	232 553	508 999	249 223 292
Before	Kenya	288 175	195	437 960	229	275	523	2 282	56 298	92 246	202 721	248 796 045
Before	Nepal	260 331	195	493 197	218	249	461	2 749	81 670	146 445	296 184	211 898 098
Before	Nepal	253 939	195	702 833	230	278	541	1 901	122 755	217 426	469 921	219 176 966
Before	Rwanda	311 754	195	671 695	221	258	475	2 251	98 890	172 649	439 517	255 303 877
Before	Rwanda	240 070	195	598 027	224	268	600	5 651	164 097	251 201	416 165	229 539 441
Before	Rwanda	213 409	195	492 677	226	272	571	3 827	113 534	176 648	322 873	198 407 892
Before	Sri Lanka	352 299	195	513 082	217	247	443	3 771	130 651	217 326	328 968	287 802 763
Before	Sri Lanka	279 440	195	510 083	219	252	433	2 263	112 230	184 183	318 329	219 114 320
Before	Tanzania	221 587	195	569 499	225	270	601	4 174	125 839	197 692	392 952	209 928 190
Before	Tanzania	498 701	195	651 252	225	267	573	4 895	130 625	212 559	440 061	467 567 394
After	Cameroon	331 815	195	897 544	213	238	365	1 573	96 012	172 543	537 897	230 334 376
After	Cameroon	309 539	195	613 299	223	264	572	3 581	87 485	182 943	428 177	282 115 397
After	Cameroon	191 927	195	732 150	228	274	540	3 792	119 241	207 116	514 103	176 059 046
After	Cameroon	249 133	195	608 332	226	272	659	5 390	129 139	207 085	351 196	247 443 758
After	Cameroon	213 274	195	399 154	230	281	612	5 149	97 946	152 721	263 805	209 240 511
After	Cameroon	314 147	195	439 564	223	262	511	4 172	113 880	168 629	315 367	279 775 935
After	Cameroon	229 635	195	332 816	214	240	364	1 014	54 238	99 511	258 488	146 515 231
After	Cameroon	274 199	195	688 444	232	287	654	5 161	137 449	199 168	367 281	276 903 801
After	Cameroon	266 749	195	286 774	218	248	389	1 242	59 703	92 568	163 277	185 286 948
After	Ethiopia	334 544	195	579 978	221	257	492	3 594	98 551	158 997	340 604	286 716 551
After	Ethiopia/Tanzania	180 052	195	495 159	228	279	748	6 353	93 364	164 364	329 429	189 244 376
After	India	436 912	195	563 327	223	263	492	2 086	60 689	112 311	308 042	359 645 939
After	India	228 290	195	486 138	220	254	488	4 435	98 396	148 571	309 960	197 923 213
After	India	431 768	195	904 314	221	257	478	2 649	99 197	161 050	273 685	357 765 144
After	India	250 089	195	794 891	223	262	506	2 772	78 880	141 563	396 728	214 270 817
After	India	148 844	195	483 374	221	259	536	6 177	106 200	154 208	298 932	136 952 506
After	India	413 206	195	760 545	219	252	428	2 745	129 487	227 350	456 826	326 437 095
After	India	341 997	195	415 561	216	243	379	1 231	70 373	115 857	242 323	232 956 968
After	India	320 809	195	503 646	215	241	387	1 661	51 532	103 795	353 767	229 116 244
After	India	250 556	195	699 691	225	268	590	5 687	153 869	222 728	351 652	241 108 483
After	India	322 569	195	570 839	220	256	490	3 345	129 444	197 224	388 893	274 434 535
After	India	337 596	195	673 239	217	247	416	1 850	90 690	186 516	358 771	253 746 415
After	India	155 554	195	770 438	222	259	546	12 724	242 592	378 677	584 961	149 716 621
After	India	140 237	195	612 196	226	268	605	4 932	147 838	247 257	392 477	134 407 172
After	India	223 694	195	824 065	233	293	820	5 610	126 591	193 238	360 886	244 595 882
After	Kenya	310 097	195	437 308	225	266	511	3 104	83 528	132 932	264 280	270 965 973
After	Nepal	422 252	195	534 823	220	253	437	2 044	78 001	145 043	294 830	328 796 930
After	Nepal	147 876	195	457 251	225	269	596	5 059	174 335	248 738	336 821	141 570 833
After	Rwanda	297 772	195	547 706	228	277	675	4 186	87 908	138 804	265 422	294 926 042
After	Rwanda	340 397	195	787 724	223	262	524	3 908	131 238	258 685	482 710	302 997 331
After	Rwanda	317 585	195	494 034	226	271	581	3 545	87 449	152 162	360 214	294 945 290
After	Sri Lanka	352 695	195	761 388	221	257	501	2 758	101 602	177 221	427 820	299 962 627
After	Sri Lanka	256 500	195	479 240	219	252	428	2 232	144 832	210 048	343 761	200 290 810
After	Tanzania	344 686	195	748 015	221	257	458	2 797	108 158	175 157	391 576	283 408 098
After	Tanzania	306 968	195	476 472	221	256	477	2 413	76 165	146 086	281 032	251 076 482

	Total # contigs	Shortest contig	Longest contig	N95	N90	N75	N50	N10	N5	N1	Assembled nts
Mean	283 031	195	604 200	223	263	526	3 779	109 603	181 132	366 919	243 135 351
Stdev	76 910	0	154 939	5	14	109	2 184	36 440	55 674	101 821	58 987 174
Min	140 237	195	286 774	213	238	364	1 014	48 086	76 576	163 277	134 407 172
Max	498 701	195	1 034 084	234	293	930	12 724	242 592	378 677	642 811	467 567 394

	Total # contigs										Assembled nts
Total, all libraries	19 812 144	195	1 034 084								17 019 474 581

Table S4. Beta-lactam resistance genes found in the genomes of ESBL-producing *E. coli*

Individual	CTX-M	OXA-1	SHV	TEM
103	x	x	x	
107	x	x		x
120	x	x		
139	x	x		x
147	x			x
154	x	x		x
155	x			
170	x			x
176	x	x	x	x
177	x			x
183	x			x
184	x	x		x
211[a]	x	x		x

[a] Individual 211 had ESBL-producing *E. coli* before travel, but not after.

Table S5. Resistance genes included in the Resqu database

Gene family	Classification	Resistance
ACC	Ambler class C	Beta-lactam
CTX-M	Ambler class A	Beta-lactam
CAR	Ambler class A	Beta-lactam
OXA-63	Ambler class D	Beta-lactam
OXA-62	Ambler class D	Beta-lactam
PER	Ambler class A	Beta-lactam
OXA-60	Ambler class D	Beta-lactam
ACT	Ambler class C	Beta-lactam
SME	Ambler class A	Beta-lactam
MIR	Ambler class C	Beta-lactam
GES	Ambler class A	Beta-lactam
TEM	Ambler class A	Beta-lactam
CMY1	Ambler class C	Beta-lactam
OXA-55	Ambler class D	Beta-lactam
NDM	Ambler class B	Beta-lactam
OXA-50	Ambler class D	Beta-lactam
OXA-51	Ambler class D	Beta-lactam
CMY2	Ambler class C	Beta-lactam
OXA-10	Ambler class D	Beta-lactam
FOX	Ambler class C	Beta-lactam
OXA-58	Ambler class D	Beta-lactam
OXA-48	Ambler class D	Beta-lactam
SHV	Ambler class A	Beta-lactam
OXA-1	Ambler class D	Beta-lactam
OXA-2	Ambler class D	Beta-lactam
KPC	Ambler class A	Beta-lactam
VEB	Ambler class A	Beta-lactam
DHA	Ambler class C	Beta-lactam
IND	Ambler class B	Beta-lactam
MOX	Ambler class C	Beta-lactam
IMP	Ambler class B	Beta-lactam
CFE	Ambler class C	Beta-lactam
CAR (RTG)	Ambler class A	Beta-lactam
VIM	Ambler class B	Beta-lactam
OXA-23	Ambler class D	Beta-lactam
OXA-20	Ambler class D	Beta-lactam
OXA-24	Ambler class D	Beta-lactam
LAT	Ambler class C	Beta-lactam
aac(6')-Ig	acetyltransferase	Aminoglycoside
aac(6')-If	acetyltransferase	Aminoglycoside
aac(6')-Ia	acetyltransferase	Aminoglycoside
aac(6')-Ic	acetyltransferase	Aminoglycoside
aac(6')-Ib	acetyltransferase	Aminoglycoside
aac(6')-Im	acetyltransferase	Aminoglycoside
aac(6')-Il	acetyltransferase	Aminoglycoside
aph(6)-Ia	phosphotransferase	Aminoglycoside
ant(6)-Ib	nucleotidyltransferase	Aminoglycoside
aac(6')-Ii	acetyltransferase	Aminoglycoside
aph(6)-Ib	phosphotransferase	Aminoglycoside

aac(6')-Ik	acetyltransferase	Aminoglycoside
aac(6')-Ij	acetyltransferase	Aminoglycoside
ant(9)-Ib	nucleotidyltransferase	Aminoglycoside
ant(6)-Ia	nucleotidyltransferase	Aminoglycoside
aac(6')-Ir	acetyltransferase	Aminoglycoside
aac(6')-IIa	acetyltransferase	Aminoglycoside
aac(6')-29a/29b	acetyltransferase	Aminoglycoside
aac(6')-IIc	acetyltransferase	Aminoglycoside
aac(3)-Ie	acetyltransferase	Aminoglycoside
aac(3)-Ib	acetyltransferase	Aminoglycoside
aac(3)-Ic	acetyltransferase	Aminoglycoside
aac(3)-Ia	acetyltransferase	Aminoglycoside
aac(2')-Ia	acetyltransferase	Aminoglycoside
ant(3'')-Ia	nucleotidyltransferase	Aminoglycoside
aac(2')-Ic	acetyltransferase	Aminoglycoside
aac(6')-IIb	acetyltransferase	Aminoglycoside
aph(3')-Vc	phosphotransferase	Aminoglycoside
aac(6')-32	acetyltransferase	Aminoglycoside
aac(3)-VIa	acetyltransferase	Aminoglycoside
aph(3')-Vb	phosphotransferase	Aminoglycoside
aac(6')-Iai	acetyltransferase	Aminoglycoside
aph(3')-VIIa	phosphotransferase	Aminoglycoside
aac(3)-IXa	acetyltransferase	Aminoglycoside
aph(4)-Ia	phosphotransferase	Aminoglycoside
aph(3')-VIa	phosphotransferase	Aminoglycoside
aph(4)-Ib	phosphotransferase	Aminoglycoside
aac(3)-IIIb/IIIc	acetyltransferase	Aminoglycoside
aph(3'')-Ic	phosphotransferase	Aminoglycoside
aac(6')-sk	acetyltransferase	Aminoglycoside
ant(4')-Ia	nucleotidyltransferase	Aminoglycoside
aph(6)-Id	phosphotransferase	Aminoglycoside
aac(6')-Iae	acetyltransferase	Aminoglycoside
aac(6')-Iad	acetyltransferase	Aminoglycoside
aph(3')-IIa	phosphotransferase	Aminoglycoside
aac(3)-IVa	acetyltransferase	Aminoglycoside
aph(6)-Ic	phosphotransferase	Aminoglycoside
aph(3')-Va	phosphotransferase	Aminoglycoside
ant(4')-IIa	nucleotidyltransferase	Aminoglycoside
aph(3')-IIb	phosphotransferase	Aminoglycoside
ant(4')-IIb	nucleotidyltransferase	Aminoglycoside
aph(9)-Ia	phosphotransferase	Aminoglycoside
aac(3)-IIb	acetyltransferase	Aminoglycoside
aac(2')-Ib	acetyltransferase	Aminoglycoside
aac(6')-Iy/z/aa	acetyltransferase	Aminoglycoside
aph(3'')-Ib	phosphotransferase	Aminoglycoside
aph(3')-IVa	phosphotransferase	Aminoglycoside
aac(3)-IIa/IIc	acetyltransferase	Aminoglycoside
aac(2')-Id	acetyltransferase	Aminoglycoside
aac(3)-VIIIa	acetyltransferase	Aminoglycoside
aac(6')-Ip/q/af	acetyltransferase	Aminoglycoside
aac(3)-VIIa	acetyltransferase	Aminoglycoside
aph(3'')-Ia	phosphotransferase	Aminoglycoside

ant(9)-Ia	nucleotidyltransferase	Aminoglycoside
aph(3')-IIIa	phosphotransferase	Aminoglycoside
aac(3)-Xa	acetyltransferase	Aminoglycoside
aph(9)-Ib	phosphotransferase	Aminoglycoside
aac(6')-Iid	acetyltransferase	Aminoglycoside
aac(6')-Iih	acetyltransferase	Aminoglycoside
aph(2'')-Ie/IVa	phosphotransferase	Aminoglycoside
aac(3)-IIIa	acetyltransferase	Aminoglycoside
aph(2'')-IIIa	phosphotransferase	Aminoglycoside
aph(3')-Ib	phosphotransferase	Aminoglycoside
aph(2'')-IIa	phosphotransferase	Aminoglycoside
aph(3')-Ia	phosphotransferase	Aminoglycoside
aac(6')-33/I30	acetyltransferase	Aminoglycoside
aac(6')-Ih/Is/It/Iu/Iv/Iw/Ix	acetyltransferase	Aminoglycoside
ant(2'')-Ia	nucleotidyltransferase	Aminoglycoside
qnrC	pentapeptide repeat protein class C	Quinolone
qnrB	pentapeptide repeat protein class B	Quinolone
qnrA	pentapeptide repeat protein class A	Quinolone
qnrS	pentapeptide repeat protein class S	Quinolone
qnrD	pentapeptide repeat protein class D	Quinolone
smr/qac/ebr	efflux pump	Multidrug
qacAB	efflux pump	Multidrug
nhsA	methyltransferase	Thiostrepton
tsnRA	methyltransferase	Thiostrepton
tsnRB	methyltransferase	Thiostrepton
catA1	acetyltransferase	Amphenicol
catA2	acetyltransferase	Amphenicol
catA3	acetyltransferase	Amphenicol
catA4	acetyltransferase	Amphenicol
catA5	acetyltransferase	Amphenicol
catA6	acetyltransferase	Amphenicol
catA7/catA8	acetyltransferase	Amphenicol
catA9	acetyltransferase	Amphenicol
catA10	acetyltransferase	Amphenicol
catA11	acetyltransferase	Amphenicol
catA12	acetyltransferase	Amphenicol
catA13	acetyltransferase	Amphenicol
catA15	acetyltransferase	Amphenicol
catA16	acetyltransferase	Amphenicol
catB1	acetyltransferase	Amphenicol
catB2/catB3/catB10	acetyltransferase	Amphenicol
catB7	acetyltransferase	Amphenicol
catB9	acetyltransferase	Amphenicol
cmlA	efflux pump	Amphenicol
cml-II	efflux pump	Amphenicol
floR	efflux pump	Amphenicol
fexA	efflux pump	Amphenicol
cml-III	efflux pump	Amphenicol
cmlv	efflux pump	Amphenicol
cmrA	efflux pump	Amphenicol
cmr-II	efflux pump	Amphenicol
pexA	efflux pump	Amphenicol

erm(A)	methylase	Macrolide
erm(B)	methylase	Macrolide
erm(C)	methylase	Macrolide
erm(D)	methylase	Macrolide
erm(E)	methylase	Macrolide
erm(F)	methylase	Macrolide
erm(G)	methylase	Macrolide
erm(H)	methylase	Macrolide
erm(N)	methylase	Macrolide
erm(O)	methylase	Macrolide
erm(Q)	methylase	Macrolide
erm(R)	methylase	Macrolide
erm(S)	methylase	Macrolide
erm(T)	methylase	Macrolide
erm(U)	methylase	Macrolide
erm(V)	methylase	Macrolide
erm(W)	methylase	Macrolide
erm(X)	methylase	Macrolide
erm(Y)	methylase	Macrolide
erm(Z)	methylase	Macrolide
erm(30)	methylase	Macrolide
erm(31)	methylase	Macrolide
erm(32)	methylase	Macrolide
erm(33)	methylase	Macrolide
erm(34)	methylase	Macrolide
erm(35)	methylase	Macrolide
erm(36)	methylase	Macrolide
erm(41)	methylase	Macrolide
erm(42)	methylase	Macrolide
cfr	methylase	Macrolide
msr(A)	efflux pump	Macrolide
vga(A)	efflux pump	Macrolide
vga(B)	efflux pump	Macrolide
vga(C)	efflux pump	Macrolide
ere(A)/ere(C)	esterase	Macrolide
ere(B)	esterase	Macrolide
vgb(A)	lyase	Macrolide
vgb(B)	lyase	Macrolide
lnu(A)	transferase	Macrolide
lnu(B)	transferase	Macrolide
lnu(C)	transferase	Macrolide
lnu(D)	transferase	Macrolide
lnu(F)	transferase	Macrolide
vat(A)	transferase	Macrolide
vat(B)	transferase	Macrolide
vat(C)	transferase	Macrolide
vat(D)	transferase	Macrolide
vat(E)	transferase	Macrolide
vat(F)	transferase	Macrolide
vat(G)	transferase	Macrolide
mph(A)	phosphorylase	Macrolide
mph(B)	phosphorylase	Macrolide

mph(C)	phosphorylase	Macrolide
mph(E)	phosphorylase	Macrolide
cmr	NA	Macrolide
mdt(A)	efflux pump	Macrolide
qepA	efflux pump	quinolone
sul1	dihydropteroate synthetase inhibitor	sulfonamide
sul2	dihydropteroate synthetase inhibitor	sulfonamide
sul3	dihydropteroate synthetase inhibitor	sulfonamide
otr(A)		Tetracycline
tetB(P)		Tetracycline
tet(M)		Tetracycline
tet(O)		Tetracycline
tet(Q)		Tetracycline
tet(S)		Tetracycline
tet(T)		Tetracycline
tet(W)		Tetracycline
tet(32)		Tetracycline
tet(36)		Tetracycline
tet(44)		Tetracycline
otr(B)	efflux pump	Tetracycline
otr(C)	efflux pump	Tetracycline
tcr	efflux pump	Tetracycline
tet(A)	efflux pump	Tetracycline
tetA(P)	efflux pump	Tetracycline
tet(B)	efflux pump	Tetracycline
tet(C)	efflux pump	Tetracycline
tet(D)	efflux pump	Tetracycline
tet(E)	efflux pump	Tetracycline
tet(G)	efflux pump	Tetracycline
tet(H)	efflux pump	Tetracycline
tet(J)	efflux pump	Tetracycline
tet(K)	efflux pump	Tetracycline
tet(L)	efflux pump	Tetracycline
tet(V)	efflux pump	Tetracycline
tet(Y)	efflux pump	Tetracycline
tet(Z)	efflux pump	Tetracycline
tet(30)	efflux pump	Tetracycline
tet(31)	efflux pump	Tetracycline
tet(33)	efflux pump	Tetracycline
tet(39)	efflux pump	Tetracycline
tet(40)	efflux pump	Tetracycline
tet(41)	efflux pump	Tetracycline
tet(42)	efflux pump	Tetracycline
tet(43)	efflux pump	Tetracycline
tet(X)		Tetracycline
tet(34)		Tetracycline
tet(37)		Tetracycline
tet(U)		Tetracycline
dfrA1/dfrA15	dihydrofolate reductase	Sufonamide
dfrA3	dihydrofolate reductase	Sufonamide
dfrA5/dfrA14/dfrA25/dfrA30	dihydrofolate reductase	Sufonamide
dfrA6/dfrA31	dihydrofolate reductase	Sufonamide

dfrA7/dfrA17/dfrA32	dihydrofolate reductase	Sufonamide
dfrA8	dihydrofolate reductase	Sufonamide
dfrA9	dihydrofolate reductase	Sufonamide
dfrA10	dihydrofolate reductase	Sufonamide
dfrA12/dfrA13/dfrA21/dfrA22/dfrA33	dihydrofolate reductase	Sufonamide
dfrA16	dihydrofolate reductase	Sufonamide
dfrA18	dihydrofolate reductase	Sufonamide
dfrA20	dihydrofolate reductase	Sufonamide
dfrA23	dihydrofolate reductase	Sufonamide
dfrA24	dihydrofolate reductase	Sufonamide
dfrA26	dihydrofolate reductase	Sufonamide
dfrA27/dfrA28	dihydrofolate reductase	Sufonamide
dfrB1/dfrB5/dfrB6/dfrB8	dihydrofolate reductase	Sufonamide
dfrB2/drfB3/dfrB7	dihydrofolate reductase	Sufonamide
dfrB4	dihydrofolate reductase	Sufonamide
dfrC	dihydrofolate reductase	Sufonamide
dfrD	dihydrofolate reductase	Sufonamide
dfrG	dihydrofolate reductase	Sufonamide
dfrK	dihydrofolate reductase	Sufonamide
vanA	ligase of type A	Glycopeptide
vanRA	transcriptional regulator of type A	Glycopeptide
vanSA	histidine protein kinase of type A	Glycopeptide
vanHA	dehydrogenase of type A	Glycopeptide
vanXA	dipeptidase of type A	Glycopeptide
vanYA	carboxypeptidase of type A	Glycopeptide
vanZA	teicoplanin resistance protein of type A	Glycopeptide
vanB	ligase of type B	Glycopeptide
vanXB	dipeptidase of type B	Glycopeptide
vanHB	dehydrogenase of type B	Glycopeptide
vanWB	glycopeptide resistance gene of type B	Glycopeptide
vanYB	carboxypeptidase of type B	Glycopeptide
vanSB	transcriptional regulator of type B	Glycopeptide
vanRB	histidine protein kinase of type B	Glycopeptide
vanD	ligase of type D	Glycopeptide
vanXD	dipeptidase of type D	Glycopeptide
vanHD	dehydrogenase of type D	Glycopeptide
vanYD	carboxypeptidase of type D	Glycopeptide
vanSD	transcriptional regulator of type D	Glycopeptide
vanRD	histidine protein kinase of type D	Glycopeptide
vanG	ligase of type D	Glycopeptide
vanXYG	dipeptidase/carboxypeptidase of type G	Glycopeptide
vanWG	glycopeptide resistance gene of type G	Glycopeptide
vanYG	carboxypeptidase of type G	Glycopeptide
vanSG	transcriptional regulator of type G	Glycopeptide
vanRG	histidine protein kinase of type G	Glycopeptide
vanTG	serine racemase of type G	Glycopeptide
vanE	ligase of type E	Glycopeptide
vanXYE	dipeptidase/carboxypeptidase of type E	Glycopeptide
vanTE	serine racemase of type E	Glycopeptide
vanRE	transcriptional regulator of type E	Glycopeptide
vanSE	histidine protein kinase of type E	Glycopeptide
vanL	ligase of type type L	Glycopeptide

vanXYL	dipeptidase/carboxypeptidase of type L	Glycopeptide
vanTmL	serine racemase of type L	Glycopeptide
vanTrL	serine racemase of type L	Glycopeptide
vanRL	transcriptional regulator of type L	Glycopeptide
vanSL	histidine protein kinase of type L	Glycopeptide
vanM	ligase of type M	Glycopeptide
vanXM	dipeptidase of type M	Glycopeptide
vanHM	dehydrogenase of type M	Glycopeptide
vanYM	carboxypeptidase of type M	Glycopeptide
vanSM	histidine protein kinase of type M	Glycopeptide
vanRM	transcriptional regulator of type M	Glycopeptide
vanN	ligase of type N	Glycopeptide
vanXYN	dipeptidase/carboxypeptidase of type N	Glycopeptide
vanTN	serine racemase of type N	Glycopeptide
vanRN	transcriptional regulator of type N	Glycopeptide
vanSN	histidine protein kinase of type N	Glycopeptide
intI9	Integron-associated integrase (class 9)	
intI8	Integron-associated integrase (class 8)	
intI7	Integron-associated integrase (class 7)	
intI6	Integron-associated integrase (class 6)	
intI1	Integron-associated integrase (class 1)	
intI3	Integron-associated integrase (class 3)	
intI2	Integron-associated integrase (class 2)	
intI10	Integron-associated integrase (class 10)	
ISCR8	ISCR transposase	
ISCR3	ISCR transposase	
ISCR4	ISCR transposase	
ISCR5	ISCR transposase	
ISCR14	ISCR transposase	
ISCR7	ISCR transposase	
ISCR1	ISCR transposase	
ISCR2	ISCR transposase	
ISCR6	ISCR transposase	

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