



Antibiotic Treatment Drives the Diversification of the Human Gut Resistome

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CORRIGENDUM

Corrigendum to “Antibiotic Treatment Drives the Diversification of the Human Gut Resistome” [Genomics Proteomics Bioinformatics 17 (1) (2019) 39–51]

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The editors regret there was an error in “Shotgun metagenome library construction and sequencing” section. “The raw sequences can be found in BGID (CRA000815)” should be corrected to “The raw metagenome sequencing data have been deposited in the Genome Sequence Archive at Beijing Institute of Genomics, Chinese Academy of Sciences (GSA: CRA000815), and are publicly accessible at <https://bigd.big.ac.cn/gsa/>”. The correct section is shown below. The editors would like to apologize for any inconvenience caused.

Shotgun metagenome library construction and sequencing

Culture-independent fecal extracts from treated subject samples Day 0, Day 2, Day 5, Day 12, Day 19, Day 26, Day 33, and Day 97 and control subject samples Day 0, Day 2, Day 19, and Day 97 were used to build shotgun metagenomic

libraries using the Nextera XT kit with the standard protocol. The HiSeq 1500 was used for 100 bp PE sequencing in the CGS of The University of Hong Kong and the average throughput for each sample was 10.5 Gbp. The raw metagenome sequencing data have been deposited in the Genome Sequence Archive at Beijing Institute of Genomics, Chinese Academy of Sciences (GSA: CRA000815), and are publicly accessible at <https://bigd.big.ac.cn/gsa/>.