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Title: An integrated catalog of reference genes in the human gut microbiome**Author(s):** Li, JH (Li, Junhua); Jia, HJ (Jia, Huijue); Cai, XH (Cai, Xianghang); Zhong, HZ (Zhong, Huanzi); Feng, Q (Feng, Qiang); Sunagawa, S (Sunagawa, Shinichi); Arumugam, M (Arumugam, Manimozhiyan); Kultima, JR (Kultima, Jens Roat); Prifti, E (Prifti, Edi); Nielsen, T (Nielsen, Trine); Juncker, AS (Juncker, Agnieszka Sierakowska); Manichanh, C (Manichanh, Chaysavanh); Chen, B (Chen, Bing); Zhang, WW (Zhang, Wenwei); Levenez, F (Levenez, Florence); Wang, J (Wang, Juan); Xu, X (Xu, Xun); Xiao, L (Xiao, Liang); Liang, SS (Liang, Suisha); Zhang, DY (Zhang, Dongya); Zhang, ZX (Zhang, Zhaoxi); Chen, WN (Chen, Weineng); Zhao, HL (Zhao, Hailong); Al-Aama, JY (Al-Aama, Jumana Yousuf); Edris, S (Edris, Sherif); Yang, HM (Yang, Huanming); Wang, J (Wang, Jian); Hansen, T (Hansen, Torben); Nielsen, HB (Nielsen, Henrik Bjorn); Brunak, S (Brunak, Soren); Kristiansen, K (Kristiansen, Karsten); Guarner, F (Guarner, Francisco); Pedersen, O (Pedersen, Oluf); Dore, J (Dore, Joel); Ehrlich, SD (Ehrlich, S. Dusko); Bork, P (Bork, Peer); Wang, J (Wang, Jun)**Group Author(s):** MetaHIT Consortium**Source:** NATURE BIOTECHNOLOGY **Volume:** 32 **Issue:** 8 **Pages:** 834-841 **DOI:** 10.1038/nbt.2942 **Published:** AUG 2014**Times Cited in Web of Science Core Collection:** 190**Total Times Cited:** 196**Usage Count (Last 180 days):** 15**Usage Count (Since 2013):** 110**Cited Reference Count:** 53**Abstract:** Many analyses of the human gut microbiome depend on a catalog of reference genes. Existing catalogs for the human gut microbiome are based on samples from single cohorts or on reference genomes or protein sequences, which limits coverage of global microbiome diversity. Here we combined 249 newly sequenced samples of the Metagenomics of the Human Intestinal Tract (MetaHit) project with 1,018 previously sequenced samples to create a cohort from three continents that is at least threefold larger than cohorts used for previous gene catalogs. From this we established the integrated gene catalog (IGC) comprising 9,879,896 genes. The catalog includes close-to-complete sets of genes for most gut microbes, which are also of considerably higher quality than in previous catalogs. Analyses of a group of samples from Chinese and Danish individuals using the catalog revealed country-specific gut microbial signatures. This expanded catalog should facilitate quantitative characterization of metagenomic, metatranscriptomic and metaproteomic data from the gut microbiome to understand its variation across populations in human health and disease.**Accession Number:** WOS:000346455900045**PubMed ID:** 24997786**Language:** English**Document Type:** Article**KeyWords Plus:** EUKARYOTIC DIVERSITY; FECAL MICROBIOTA; POPULATION-SIZE; METAGENOME; SEQUENCES; GENOMES; TOOL; ALIGNMENT; IMPACT; TWINS**Addresses:** [Li, Junhua; Jia, Huijue; Cai, Xianghang; Zhong, Huanzi; Feng, Qiang; Arumugam, Manimozhiyan; Chen, Bing; Zhang, Wenwei; Wang, Juan; Xu, Xun; Xiao, Liang; Liang, Suisha; Zhang, Dongya; Zhang, Zhaoxi; Chen, Weineng; Zhao, Hailong; Yang, Huanming; Wang, Jian; Wang, Jun] BGI Shenzhen, Shenzhen, Peoples R China.

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