Functional profiling of the rumen microbiota in dairy calves fed copper and grape-pomace dietary supplementations

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step	Phred3	Phred19
multiple_extract_barcodes	16787720	16787720
multiple_join_paired_ends	8393698	8393698
multiple_split_library	8206524	5620806
closed_otupicking	4164028	4089545
filter_otus	4141362	4058283

S3 Table: Number of 16S rRNA gene sequences retained after successive steps of the bioinformatics processing and filtering: comparison between two quality filtering thresholds (Phred¿3, default in the Qiime pipeline; Phred¿19, threshold used in this study).