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| Header | Description |
| Samples Sequenced | The total number of samples sequenced. |
| Average raw reads per sample | The average number of raw reads sequenced per sample. |
| Average reads post QC (Quality Control) | The average number of reads retained after various pre-processing and quality control steps. These steps include primer removal, read joining and quality filtering. |
| Average reads used for classification | The average number of reads retained after denoising and chimera removal steps. This will be the final number of reads that are used to make taxonomic classifications. |

Table 1. Description of the key headers found in the Summary Stats worksheet.

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| Header | Description |
| Sample ID | The Sample ID. |
| Raw Sequences | The number of raw reads. |
| Post Quality Filtering | The number of reads retained after basic quality filtering of the read data. |
| Final percentage of raw reads - Q1 | The final percentage of reads kept (compared to original raw reads) after undergoing the basic quality filtering. |
| Post Denoising | The number of reads retained after denoising and removing chimeras. This is the final number of reads per sample that will be used to make taxonomic classifications. |
| Final percentage of raw reads - Q2 | The final percentage of reads (compared to original raw reads) kept after undergoing the denoising an chimera removal steps. |
| Food Category | A metadata column, useful for identifying food categories that had a low number of a low number of reads used for classification, low number of raw reads etc. |

Table 2. Description of the key headers found in the Complete Stats worksheet.