**Table 2,** thenumber of reads included in the analysis. Trimmed data required a perfect match for forward and reverse primers and barcodes and a quality score of 25 or greater.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **Location** | **Date (YBP)** | **Raw data** | **Trimmed data** | **Assigned data** | **Unique OTUs** |
| BE04 | Hinds Cave - USA | 8000 | 27478 | 45 | 45 | 25 |
| BE21 | Hinds Cave - USA | 8000 | 31113 | 47 | 34 | 10 |
| CA10 | Caserones – Chile | 1600 | 14640 | 3032 | 3028 | 50 |
| CA18 | Caserones – Chile | 1600 | 30695 | 6786 | 6784 | 42 |
| ZA04 | Rio Zape – Mexico | 1400 | 31222 | 6162 | 5668 | 197 |
| ZA23 | Rio Zape – Mexico | 1400 | 33252 | 6854 | 6735 | 249 |
| Hum | \* | Modern | \*\*\*\* | 2365 | 2226 | 118 |
| Pri | \*\* | Modern | \*\*\*\* | 1493 | 1181 | 173 |
| EX | \*\*\* | Modern | 47818 | 8218 | 7881 | 201 |

\* Pooled dataset from three modern humans (two from Gill 2006 and 399 sequences from one human sample retrieved from NCBI accession numbers GU939195.1 to GU939593.1)

\*\* Pooled dataset from one Bonobo (BNO), one Chimpanzee (Chimp), two Gorillas (GOR and GORSD), one Marmoset (ML) and one Orangutan (ORANG)

\*\*\* Negative contamination controls used during DNA extraction

\*\*\*\* Number of raw data reads was not provided for these previously published data