**TABLE S1 |** Sequence data from the CPS metagenome

|  |  |
| --- | --- |
| **Parameter** | **Value** |
| Total sequence bp count | 3,303,312,400 |
| Artificial duplicate reads sequence count | 3,690,631 |
| Post QC bp count | 2,927,826,500 |
| Sequence length | 100 ± 0 bp |
| GC percent | 56.14 ± 14 % |
| Predicted protein features | 26,127,903 |
| Predicted rRNA features | 311,695 |
| Identified protein features | 4,424,138 |
| Identified rRNA features | 12,533 |
| Identified functional categories | 2,855,527 |