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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | | **Sample** | **Total** | **rRNA-filtered** | **BWA-Mapped** |  | **BWA-Others** |  | **Totally Mapped** | **Totally Used** | |  |  |  |  | Total | HISAT2\_mapped | HISAT2\_Unique |  |  | | N.4DAG.1 | 49,565,707 | 49,565,707 | 17,044,862 | 35,287,860 | 28,886,338 | 4,349,102 | 45,931,200 | 21,393,964 | |  |  | (100.00%) | (34.39%) | (71.19%) | (81.86%) | (15.06%) | (92.67%) | (46.58%) | | N.4DAG.2 | 42,976,826 | 42,976,826 | 17,103,499 | 31,220,523 | 20,964,092 | 3,143,385 | 38,067,591 | 20,246,884 | |  |  | (100.00%) | (39.80%) | (72.65%) | (67.15%) | (14.99%) | (88.58%) | (53.19%) | |

rRNA-filtered: the retained reads after the reads from rRNA were filtered.

BWA-Mapped: BWA-mapped read with MAPQ >= 20.

BWA\_Others: the read with MAPQ < 20 in BWA mapping. These reads were mapped again by HISAT2.

HISAT2\_Unique: HISAT2-mapped with the tag NH:i:1

Totally Mapped: sum of BWA-Mapped and HISAT2-mapped.

Totally Used: sum of BWA-Mapped and HISAT2\_Unique. These reads were used for subsequent analysis.