**Section 3.7: Supplementary Material**

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**Table 3.1S: Improved Annotation with piClusterBusteR**

|  |  |
| --- | --- |
| Species | Datasets |
| *Dr. melanogaster* | ♀ - SRR618933, SRR797070, SRR797071, SRR797172, SRR797179, SRR797182, SRR797187, SRR797193, SRR797195, SRR797196, SRR797197, SRR797198, SRR797199, SRR797200, SRR797203♂ - GSM280085 |
| *Ae. aegypti* | RNAlib17  |
| *An. gambiae* | SRR1927173 |
| *H. sapiens* | ♀ - SRR1755247,SRR1755248, SRR1755251, SRR1755252, SRR1755255, SRR1755256♂ - ERR328151, SRR835324, SRR835325, SRR950451 |
| *Ma. mulatta* | ♂ - SRR116839,  SRR553581, SRR606728 |
| *Ma. fascicularis* | ♀ - SRR1755241, SRR1755242♂ - SRR1755243, SRR1755244 |
| *C. jacchus* | ♂ - SRR606715, SRR1041905, SRR1041906, SRR1041907 |
| *Mu. musculus* | ♀ - SRR014234  ♂ - SRR014231, SRR014232, SRR014233, SRR014235, SRR772028, SRR772029, SRR772030, SRR772031, SRR772032, SRR772033, SRR772050, SRR772051, SRR772052, SRR772053, SRR772054, SRR772055 |
| *R. norvegicus* | ♂ - SRR035663 |
| *B. taurus* | ♀ - SRR1755229, SRR1755230♂ - SRR1755231, SRR1755232 |
| *S. scrofa* | ♀ - SRR066809, SRR1274763♂ - SRR066810, SRR1274764, SRR1654828 |
| *G. gallus* | ♂ - SRR772069 |
| *Da. rerio* | ♀ - SRR578904, SRR578905, SRR578906, SRR578913, SRR578914, SRR578915♂ - SRR578922, SRR578923 |

 **Table 3.2S: Description of Datasets**

|  |  |  |  |
| --- | --- | --- | --- |
| Species | Number of piRNA Clusters | Genome Size (Mb) | Total Read Count |
| *Dr. melanogaster* | 10 | 148 | 205,554,806 |
| *Ae. aegypti* | 210 | 1064 | 10,655,147 |
| *An. gambiae* | 30 | 236 | 22,370,627 |
| *H. sapiens* | 303 | 2996 | 29,968,314 |
| *Ma. fascicularis* | 213 | 2946 | 10,117,534 |
| *Mu. musculus* | 336 | 2689 | 269,297 |
| *B. taurus* | 42 | 2697 | 4,528,165 |
| *S. scrofa* | 48 | 2508 | 17,661,429 |
| *Da. rerio* | 166 | 1391 | 35,936,571 |

 **Table 3.3S: Ovary Genome Size and Read Count**

|  |  |  |  |
| --- | --- | --- | --- |
| Species | Number of piRNA Clusters | Genome Size (Mb) | Total Read Count |
| *H. sapiens* | 355 | 2996 | 50,251,433 |
| *Ma. mulatta* | 316 | 3097 | 41,304,681 |
| *Ma. fascicularis* | 467 | 2946 | 42,234,678 |
| *C. jacchus* | 441 | 2621 | 158,431,380 |
| *Mu. musculus* | 879 | 2689 | 454,610,320 |
| *R. norvegicus* | 231 | 2870 | 8,407,181 |
| *B. taurus* | 618 | 2697 | 55,482,891 |
| *G. gallus* | 166 | 1230 | 116,234,474 |
| *D. rerio* | 166 | 1391 | 47,798,654 |
| *S. scrofa* | 527 | 2508 | 37,221,910 |

 **Table 3.4S: Testis Genome Size and Read Count**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Pearson Correlation Test Relative to piRNA Cluster Calls** | **Tissue** | **T value** | **Pearson Correlation Value** | **P value** |
| Genome Size | Ovary | 1.8787 | 0.5789624 | 0.1024 |
|  | Testis | -1.3173 | -0.4457003 | 0.2292 |
| Number of Reads | Ovary | 1.7516 | 0.5520267  | 0.1233 |
|  | Testis | 2.936 | 0.7428724 | 0.02184 |

 **Table 3.5S: Correlations of piRNA Cluster Definition**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Species** | **Number of piRNA Clusters Called** | **Average piRNA Cluster Size (kb)** | **Total Nucleotides Occupied by piRNA Clusters** | **Genome Occupancy** | **% TE** | **% Gene** | **% Other** | **% Unannotated** |
| *Dr. melanogaster* | 10 | 11.4 | 113,593 | 0.07% | 78 | 4 | 0 | 18 |
| *Ae. aegypti* | 210 | 10 | 2,109,482 | 0.15% | 45 | 4 | 0 | 51 |
| *An. gambiae* | 30 | 8.9 | 268,084 | 0.10% | 35 | 3 | 9 | 53 |
| *H. sapiens* | 303 | 10 | 3,023,129 | 0.09% | 27 | 6 | 4 | 63 |
| *Ma. fascicularis* | 213 | 21.8 | 4,635,040 | 0.15% | 26 | 1 | 3 | 70 |
| *Mu. musculus* | 336 | 7.67 | 2,576,831 | 0.09% | 45 | 3 | 4 | 48 |
| *B. taurus* | 42 | 15.5 | 652,933 | 0.02% | 22 | 3 | 8 | 67 |
| *S. scrofa* | 48 | 17.8 | 856,408 | 0.03% | 20 | 4 | 7 | 69 |
| *Da. rerio* | 166 | 10.6 | 1,761,421 | 0.13% | 61 | 1 | 2 | 36 |

 **Table 3.6S: piRNA Cluster Contents - Ovary**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Species** | **Number of piRNA Clusters Called** | **Average piRNA Cluster Size (kb)** | **Total Nucleotides Occupied by piRNA Clusters** | **Genome Occupancy** | **% TE** | **% Gene** | **% Other** | **% Unannotated** |
|  |
| *H. sapiens* | 355 | 12.9 | 4578738 | 0.14 | 28 | 3 | 6 | 63 |
| *Ma. mulatta* | 300 | 11.2 | 3360121 | 0.12 | 32 | 3 | 4 | 61 |
| *Ma. fascicularis* | 213 | 12 | 5602830 | 0.15 | 29 | 2 | 4 | 65 |
| *C. jacchus* | 441 | 13.5 | 5959699 | 0.22 | 27 | 2 | 5 | 66 |
| *Mu. musculus* | 167 | 21.8 | 3642073 | 0.13 | 31 | 3 | 3 | 63 |
| *R. norvegicus* | 231 | 18 | 4146688 | 0.14 | 25 | 4 | 3 | 68 |
| *B. taurus* | 618 | 12 | 7434999 | 0.28 | 29 | 2 | 4 | 65 |
| *G. gallus* | 166 | 10.7 | 1772287 | 0.18 | 23 | 11 | 3 | 63 |
| *D. rerio* | 157 | 10.8 | 1691347 | 0.12 | 62 | 0 | 3 | 35 |
| S. scrofa | 527 | 43.2 | 6147214 | 0.24 | 30 | 5 | 0 | 65 |

 **Table 3.7S: piRNA Cluster Contents - Testis**

|  |  |  |  |
| --- | --- | --- | --- |
| **Species** | **Nucleotide Occupancy of Top 30 piRNA clusters** |  **Nucleotide Occupancy of All piRNA Cluster Calls** | **Percent Composition of Top 30 piRNA Clusters** |
| *Dr. melanogaster* | 113,593 | 113,593 | 100% |
| *Ae. aegypti* | 585,679 | 2,109,482 | 27.8% |
| *An. gambiae* | 268,084 | 268,084 | 100% |
| *H. sapiens* | 741,925 | 3,023,129 | 24.5% |
| *Ma. fascicularis* | 2,326,841 | 4,635,040 | 50.2% |
| *Mu. musculus* | 496,848 | 2,576,831 | 19.3% |
| *B. taurus* | 569,934 | 652,933 | 87.3% |
| *S. scrofa* | 722,238 | 856,408 | 84.3% |
| *Da. rerio* | 575,932 | 1,761,421 | 32.7% |

 **Table 3.8S: Nucleotide Occupancy of the Top 30 piRNA Clusters - Ovary**

|  |  |  |  |
| --- | --- | --- | --- |
| **Species** | **Nucleotide Occupancy of Top 30 piRNA clusters** |  **Nucleotide Occupancy of All piRNA Cluster Calls** | **Percent Composition of Top 30 piRNA Clusters** |
| *H. sapiens* | 1,054,062 | 4,578,738 | 23.0% |
| *Ma. mulatta* | 979,655 | 3,360,121 | 29.2% |
| *Ma. fascicularis* | 1,472,922 | 5,602,830 | 26.3% |
| *C. jacchus* | 1,609,193 | 5,959,699 | 27.0% |
| *Mu. musculus* | 1,570,168 | 3,642,073 | 43.1% |
| *R. norvegicus* | 1,719,232 | 4,146,688 | 41.5% |
| *B. taurus* | 1,496,074 | 7,434,999 | 20.1% |
| *G. gallus* | 505,336 | 1,772,287 | 28.5% |
| *D. rerio* | 622,435 | 1,691,347 | 36.8% |
| *S. scrofa* | 1,297,435 | 6,147,214 | 21.1% |

 **Table 3.9S: Nucleotide Occupancy of the Top 30 piRNA Clusters - Testis**

|  |  |  |  |
| --- | --- | --- | --- |
| **Species** | **piRNA Generation of Top 30 piRNA clusters** |  **piRNA Generation of All piRNA Cluster Calls** | **Percent piRNA Generation of Top 30 piRNA Clusters** |
| *Dr. melanogaster* | 27,422 | 27,422 | 100% |
| *Ae. aegypti* | 80,000 | 161,016 | 49.7% |
| *An. gambiae* | 124,402 | 124,402 | 100% |
| *H. sapiens* | 97,707 | 121,570 | 80.4% |
| *Ma. fascicularis* | 3,280 | 25,222 | 13.0% |
| *Mu. musculus* | 95,879 | 164,121 | 58.4% |
| *B. taurus* | 3,630 | 3,854 | 94.2% |
| *S. scrofa* | 792 | 1,176 | 67.3% |
| *Da. rerio* | 8,5872 | 175,856 | 48.8% |

 **Table 3.10S: piRNA Generation of the Top 30 piRNA Clusters - Ovary**

|  |  |  |  |
| --- | --- | --- | --- |
| **Species** | **piRNA Generation of Top 30 piRNA clusters** |  **piRNA Generation of All piRNA Cluster Calls** | **Percent piRNA Generation of Top 30 piRNA Clusters** |
| *H. sapiens* | 308061 | 383126 | 80.4% |
| *Ma. mulatta* | 414155 | 477018 | 86.8% |
| *Ma. fascicularis* | 411479 | 488199 | 84.3% |
| *C. jacchus* | 559813 | 631692 | 88.6% |
| *Mu. musculus* | 363370 | 476957 | 76.2% |
| *R. norvegicus* | 751565 | 876417 | 85.8% |
| *B. taurus* | 820381 | 903538 | 90.8% |
| *G. gallus* | 195819 | 362278 | 54.1% |
| *D. rerio* | 95038 | 178252 | 53.3% |
| *S. scrofa* | 578459 | 621844 | 93.0% |

 **Table 3.11S: piRNA Generation of the Top 30 piRNA Clusters - Testis**

Wilcoxon Rank Sum Test with Continuity Correction

Testis vs Ovary

W = 25, p-value = 0.08225

Testis vs Between Tissue

W = 1, p-value = 0.002165

Ovary vs Between Tissue

W = 7, p-value = 0.08874

**Table 3.12S: Degree of Agreement of piRNA Cluster Definition**