Table S7. Assessment of the Huagu11 genome assembly using 29399 EST sequences.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Dataset | Number | Total length(bp) | Bases covered by assembly (%) | with >90% sequence in one scaffold | | with >50% sequence in one scaffold | |
| Number | Percent | Number | Percent |
| >0bp | 29,399 | 16,633,380 | 97.37 | 27,628 | 93.98 | 28,553 | 97.12 |
| >200bp | 28,457 | 16,496,108 | 97.55 | 27,038 | 95.01 | 27,833 | 97.81 |
| >500bp | 19,441 | 12,850,583 | 97.86 | 18,636 | 95.86 | 19,096 | 98.23 |