**Table S1** BAC clones covering the *Ghd7* regions in *Oryza* species.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| 　 | Genome type | Clone Address | Insert Size (bp) | Total Length Sequenced |
| *O. glaberrima* | AA | OG\_BBa01D19a | 141,474 | 514,555b |
| OG\_BBa67O20a | 294,849 |
| OG\_BBa89K05 | 150,094 |
| *O. rufipogon* | AA | OR\_CBa03A17a | 139,663 | 419,405 |
| OR\_CBa11E20a | 115,539 |
| OR\_CBa34O09 | 168,978 |
| OR\_CBa47B10 | 131,985 |
| OR\_CBa24P03 | 133,611 |
| *O. glumaepatula* | AA | OG\_EBa09A20 | 177,017 | 439,498 |
| OG\_EBa68C15a | 227,891 |
| OG\_EBa63B05a | 27,818 |
| OG\_EBa106O14 | 120,434 |
| OG\_EBa162O14 | 145,660 |
| *O. nivara* | AA | OR\_BBa95E20a | 192,302 | 346,186 |
| OR\_BBa128I03 | 202,433 |
| OR\_BBa33E21 | 187,941 |
| *O. punctata* | BB | OP\_Ba20P16a | 188,211 | 665,912 |
| OP\_Ba04C12a | 182,354 |
| OP\_Ba14G24a | 173,660 |
| OP\_Ba13G18a | 193,805 |
| OP\_Ba18C07 | 133,105 |
| OP\_Ba13B20 | 172,610 |
| OP\_Ba68H01 | 196,294 |
| *O. officinalis* | CC | OO\_Ba113G01a | 258,843 | 440,945 |
| OO\_Ba47F06 a | 273,447 |
| OO\_Ba46E10 | 244,799 |
| *O. australiensis* | EE | OA\_CBa34D10 | 228,105 | 744,605 |
| OA\_CBa165D12 | 127,850 |
| OA\_CBa178E24 | 144,140 |
| OA\_CBa07H08 | 252,608 |
| OA\_CBa167D03 | 124,530 |
| OA\_CBa130A18 | 181,472 |
| *O. brachyantha* | FF | OB\_Ba09F13 a | 197,437 | 284,909 b |
| Total | 　 | 　 | 5,830,959 | 3,856,015 |

aSequenced by Illumina Genome Analyzer sequencing technology. The other BACs were sequenced by Roche/454GenomeSequencer FLX Instrument.

bObtained from unpublished whole genome data.