**Supplementary Tables S1.** Description of moso bamboo clusters, with LTR copy numbers, length of LTR sequences and similarity ranges. The cluster sequences were used to generate IRAP amplicons to study the genetic diversity and population structure of different *Phyllostachys* species (Asian bamboo). The positions of the LTR primer are highlighted by underlined bold letters. A, B, C and D represent cluster name, LTR copy number, length of LTR sequences and similarity (%) (Ranges), respectively.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **A** | **LTR sequence (representative)** | **B** | **C** | **D** |
| Cluster 3 | ATCTCTATACGACTAGAGGCAATCATAGAGATGATTAAATTTCATTATGTTCATAATATTGGATAATATATTATCCTGTTCTTTGAATGAATCATTGGTTATGAAGATTAACAAATATGTGACTTGTTGGAGAAACTCTTAACTTATATGATGTCGTTCTAAATGAATCCCTGGTCGGATGTCGATGGTCGGAACACCAGTGACTCTATCGACCAACACGTGTATTGATTGACGACCATGTTTCACCGGTCATGGATATGGGGATATCGAATCAATAATGTGAACACATGTTAGAGAACATGGGGTTGGATTGACCCACCTTGAGAAACTATTGAGATTGTTATGATTCTATGTGTCGTTAGTTGGTCTCAAGCAATGATGATGTATAATCCTTAGACCTGAGATCAGCATGGTTTCCTACATGTGTAATAGCACTCTTAGGGGGTTTCCAATCGCTACTCGTAACTGGGTAGT**TATAAAGGTAGCTTTCGGGTAT**GCTATGAAACATGCTGAGGAATGTGACTAGTCGGATATGGGATTTGCCCCTCCTAACATAACAGGAGAGATGTCTCTGGGCCCCTCGTTGTGGTCGGATAAAGAAAGTGCATGGCCATGCCACTAGTGGTCAAAGTGTTCGACCACGTGAAGTTATCCGACACTCGATCGAGAAAGTATTGAACAGTCCATGGATGACACAACATCTCACCTGGAGTTCAACCAGACATCGTGAGGAAAAGGGAGAATACACGAGTAGGTCACTTAGTTCGATCAGTTACGGACTGGTTGTATGGAGATACGAGCTGATCGTAGACTGGTCGAACGTAATCACAGAGTGGTCGAAACCTGGTCGTAAGGAATTAGAAACTGGTTGTGACCAAATATGAACTAGTTGT | 121 | 115-893 | 90.60-100 |
| Cluster 4 | AACCCTACTCCTGTGTGTGTATGGTATTGAGTGTATACTGAACAATCAGGGGAAAAACTAAGACTATTACAGATAGTGCTTGTATTCCTGATGGCTCCATCCTCTCTCCCTTTCTCTAGTTGCCGCCTTTTATAGTTCGTGAAGGAGCAGCAGTTACTCCAGGTAAAGCGGCGCCTCATTATCTCCTGTAACGGGCGCATGTTGGTAGTGATTACCGGTGTATTAATTCCTCCA**CGTCGCTCAACAGCTATATACCAG**AGATAATGGGGTATTACGTGCCATTATTCTGTAGAATAACAGCGTATGATGACTGTTTGAATCCCTTAATCAATAAGACCCACTTGTCTGCAGGTTCATTTGATTATAAGGTGGTCGTGGCTGACCTAGTCGTAGAGGAATCTACGACTATGAGGTAGTCGTAGCAAGACTTACGACTATGGGATAGTCGTAGCATAACTTACGACTATGGGGGTGGTCGTAGAAGAACTTACGACCATCCATTTGGTTCTTCCTTCATAACATTAAGGGGTACACTCAGGGTTCACATGACGTCATATTTACCTATAATAAAAATTATAGATAAAAGGTAAAATGAGGATTATTATATCCTCGTCAATGACCGTGTC | 84 | 114-619 | 91.32-100 |
| Cluster 15 | AAATAGAGGAGATGTTAAGATATGCATACGGATTTAAATGTTGCTGATCCGTTGACTAAGCCTCTCACACAGCCAAAGCATGAGGCGTACACAAAGCTATCGGTATTAGATATCTTAATGATTGACTCTAGTACAAGTGGGAGACTATTGGAAATATGCCCTAGAGGCAATCATGGAGATGATTATATTTCATTATGTTTATAATATTGGATAATGTGTTATTATGTTCCTTGAATGAATCATCAGTTATGAAGATTAATAAGTATGTGACTTGTTGGTGAAACTCTTAACTTATATGATGTCATTCTAAATGTATCCCTGGTCGGATGTCAATGGTCGGAACACTATTGACTCTATCGACCAGCACATTGTATTGATTGATGACCATGTTTCACCGGTCATGGATATAGGGATATCGAATCAATAATGTGAACACATGTTAGAGAACATGGGGTTGGTTTGACCCATCTTGAGACACTATTGAGATTGTTATGATTCTATGTGTCGTTAGTTGGTCTCAAGCAATGATGATGTATAATCCTTAGACCTGAGATCAGCATGGTTTCCTACATGTGTAATAGCACTCTTAAGGGTTGCCAATCGCTACTCGTAACTGGGTAGTTATAAAGGTAGCTTTCGGGTATGCTATAAAACATGCAGAGAAATGTGACTGGTCGGATATGTGATTTGCCCCTCCTAACATAACAGGAGAGATGTCTCTGGACCCCTCGTTGTGGTCGGATAAAGTAAGTGCATGGTCATGCCACTAATGGTCGAAGTGTTTAACCACGTGAAGTTATCTGACACTCGATCGAGAAAGTATTGAACAGTCCATGGAAGACACAACATCTCACTTGGAGTTCAACCAGACATCGTGAG**GCAAAGGGAGAATACACGAG**TAGGTCACTTA | 76 | 132-911 | 90.49-100 |
| Cluster 22 | TAGATGATGAGGATCTAATAATCCTTATTTTATCTTTTATCTATAATTCTTATTATGGGTAAATATGATGTCATGTGGTCCCTACGTATACCCCTTATATTTACAAGGGAGAAGCCTACCAGGTGGTCGTAAGTTGTTCTACGACCACCCCCATAGTCGTAAGTCTTGCTACGACTACCTTATGGTCGTAAGTTCTTCTACGATCACTATCCAGTCGTAAGTTATTCTACGACTACCCCATGGTCGTAAGCTCTTCTACGACCAGGTCAGCTACGACCACCTTATGATCAATAAAATCTACAGATGAGTGGGCCCAATTGATTAAGGAATCCAAGCAGTCAACATACGTTGTTATTCTACGGAGTAATAGCACATAGTTACCCATTATCTCTGACAAATAACTGCCAGGCGGCATGAAGGAGTTAACACTTCGGTGATTACTGCAAACATGCGCCCGTTACAGGACATGATGAGGCGCCTCTTCACCTGGAGAAACGGCTACTCCTTCACGACTATATAAAGGCGG**TGATCAGAGAAGAAAGGGGA**GGCAATCGGAGAACACAGCAAGCAATCGGGAAGACAGGCACTATCTTCTGTAATAGTCTTAGTCTTTTCTCCCGATTGTACAAGATACACTCAATACCATACACACACAGGAGTAGGGTTGTTATTCTCCCCGGAGAAGGCCTGAACCTGTATAAAAATACC**CGTGTCAATCTCTCTGCGTG**ATTCCATTCTAGGAGACCCCCCGAATCAAACAATCTTTACGTAAGATCGGTTCTAAAACACCGATAGTTGGCTTTGCAACAAACCCTCATGGTAAGTTTC | 61 | 134-823 | 90.43-100 |
| Cluster 34 | CGGTTCTTGCATGTAATCTACCCATCGACATTGTGTCGGCGACTTCAAGTCGGCTCACGGTAGATTAGAAAGGATTTTCACCGTAGAAAACAATCTAGAAAGCGAATTTGCAGAATTGAAAGCGATCTAGAAAGAAGACGATTCAATCTACGAGTGTCGTTCATCGACAGTTACCTTTCGATCCGAGTAAAGTAGGCCTAGAAGTAGGCCGGAGTCGATCATGCTGATAACGTGTTGAGTAACCGTCACTGGTGAGTCCAGTCT**GAACGATTACCTCACAGACA**AGCGTAGAATCGCTTAGAACAAATCAAGAACACAAGAACAGAATAAGAGATTGAACACAGAGATATGAGGGGACTT**CGGGCTTCTCTTTATTGCTC**TTCAATAATGATCGATTACAATGAGGGGTCCCCTCTCCTTTATATAGACTACTGGAAACATGAGGTATCCAATTGGGCCAGGACTCCTGGTCATGGGCCCGGTTTCCTAACA | 43 | 163-487 | 90.28-100 |
| Cluster 37 | TGTCGGTGTTTTAGAACCGATCTTATGTAA**AGATTGTTTGATTCGGGGGG**TCTCCTAGAATGGAATCACGCAGAGAGATTGACACGGGTATTTTTATACAGGTTCAGGCCTTCTCCGGAGAGAATAACAACCCTACTCCTGTGTGTGTATGGTATTGAGTGTGTTTCGTACAATCTGGAGAAAAGACTAAGGCTATTACAAAAGATAGTATCTGACTGTCTTCCTGATTGCTTGTTGTCTCCTCCGATTGGATGTCCCCCTTTCCCTCTCTGACCGCTGCCTTTATATAGTCGTGAAGGAATAGCCGTTTTCCCCTGCTGAAGAGACACCTCATCAATTCCAGTAACAGGCGCACATTTGCAGTAATCATTGGGAT**GGTAACTCCTCCACGCCGC**TTGGCAGTTACTTGTCAGAGATAATGGGGTATTGCGTGTTATTATTTCGCATAATAACAGCGTATGTTGACTGCTTGGATTCCTTAATCAATTGGACTCACTCGCCTGTAGGTTTTATTGATCATAAAGTGGTCGTAGCTGACCTGGTCGTAGAAGAACTTACGACCATAAGGTAGTCGTAGCAAGACTTACGACTATGGGGTAGTCGTAGAATGACTTACGACTGGGTAGTGATCGTAGAAGAACTTACGACCATAAGGTAGTCGTAGCAAGACTTACGACTATGGGGGTGGTCGTAGAAGAACTTACGACCACCTGGTAGGCTTCTCCCTTGTAAATTTAAGGGGTATACCCAGGGACCACATGACATCACATTTACTCATAATAAGAATTATAGATAAAAGATAAAATGGGGATTATTAGATCCTCGTCATCTAGCC | 46 | 113-835 | 90.59-100 |
| Cluster 42 | CAGCAACCCTAAATGACCCATCTACAGTTCCTTTTATAGG**GCAACAACAAACCCTAAAAA**CCTTCTAGATGATTTACCCTAATGGGCTTCCGTTAGGGCCCAACATCAACGTAACACACATGCACGCAAATTAAAGCGCCGTCTTCATCGTCGATTGATCTAAACCGCTTCATCATGCATCGACCCGCGCCGCGGCTTAGTCAAAAGGTCACCAAGGCGGTATTTGGTAAAATTACCAAAATACCCCTTCTCGATCTTTTCCAAAAAACCGAGTCCATCTACGCGAAGCACTCGCCTGCTTCGCCACGTGTAGGTTGATCAACGGCTCCATGTCATCAAGTCTCTCCTGTCCGGATCCCACCGGCATCACTGAGCACTTGCAACGACTCCCGCGCCGCTTGATCCAACCAGTCGCACCGAACCGCCCGTCCGGTCATCTTGTCCATTCTGCGCCACGCTTGAGTCACTTGACCTCACCCGGCATCCATGATCGTTCTGGACCTCAGCTCTCCAAGCTTAGTCTCGATCCTCCTCGCCGTTGACCGTCATTGACCTACAAGCCACCTACACAACAATAGACAAGCAAACACGAATCTGGGAACAAGTTCTTCACAACTTGACCCACGTTAGTGAAAACATGCAATATGCAACACATATGCATTAACAAATATGGATATGACCTATCCCAAAATCAATTCACCACATATATCAACATTCAGCACAAAAGACGGTCAGACCGCCGCTGACCTGACAGATCTGAAACTTTGTCGAAAACACTTGAAACTTCAAACCAAAAGCAACATTGCCAATTGTTTCATCATCCTAAGATCATGGACATATCCCCATGATATCCACACTCTT | 41 | 190-830 | 91.41-100 |
| Cluster 54 | CCGTTGGATGTGTTAGGAAACTATGGGCCTGGCCTAGAAGCTGACCCATGTATCGGCTCCCCATCCCAAACCATAGCAGGGTTTGTAGTCTATAAATAGGGGGTGCTATTCATTGTAAGCGATTGATCGATTGATGAAGGAATAAAGAGAAGCAAGAAGCCCCCTATATCTCTGTGTTCAATCTATTAT**TCTGTTCTTATGTTCTTGC**ATTGTTCTAAGCGATTCTACGCTTGTCTACGAGGTAATCGTTCGGACTGGACTCGCCAGCGATGGTTACTCAACACATTATCAGCACGAT | 44 | 101-285 | 90.08-100 |
| Cluster 58 | CATACCGGGAGTGTCAATGTTGAGATGAAGTTTCTGAAAGGTTTTGTTATGATTGCTCAATCGCATACTTCTATATGGCGAGTCATGGCAGACATGATGAGTTAATCGTATCTTGTGGGTAAAGTGTACAACCTCTGCAGAGTGTTAAACAATCTATTCGAATAGCCGCGTCCGCGGTCATGAACATGCTTGGGGATTTCACACGAGGGGTAGATTTTCATAAAACTTGGGATGGGATAGCTGTGTGAGGTAACTTATGCAGCTATGTGAATAACTTATTTAGGACATGTGTCTTTGTGAAAACAACTGATAAAATTACTATTGTCTATTTGTTTTACTTGTGCTTTCAATCTATTATTCGTATTCAAATTGCAAATGTTGTATTTCTGCAAAAGAACCACAGAAGCCATTCCTTTGGAATAAGCCTGCATCTATAATTGCATCTCTGTGGTATGACTTGCTAGTACGGTGTGTACTCATGCTTGCTTTATTAAATCAAGCAGAAGTG**AAGGAATCGTCAGTCAACAA**GGTCTACTTCAAGGATCGTGGAGAACTAGGTCGCGCACCCCAGCCGATTGCCTGTGGGCATATGGATGGGCATCACTGAAGTCATTCTGTTTTGTTCCGCTGCAGCTTCATTGAGATATCTGCCTCTGAAGCATTAATTGTAAGCTTTGACCTTAAGGTCTTTACTCTGATGTTTATTATTATTTGCCTATTTATTAGTTATCTTTGTATATGGAAATGATATTTCACTGATGTTGCCACTGTGTGCACTAGCGTGATCCTGGACTAGTGCAGTATACACAGAGGGTCCAGAATTGCATATTTTGGGTCCCGACAGCTATGCCTCACCATGCAACCACATGTCTCCAGAATGGGGGCGTGGGACCTGGCCAATTAATTTGCAAAGTTCCACCGCGGTTATTCCACTTTGATGTGTGGGAGGTCTTCTATGGCCTATCGTCTTTTATAACCTATATTTTCCCCTAGCGTA | 35 | 103-997 | 90.88-100 |
| Cluster 59 | TTGACAGTAGAGATTACTTGGCTACGGTGGTTACTTGAGGATTTTGGTGTTTCTGTTACTACACCGACTCCTCTCT**TGTCAGACAGTACAGGTGCT**ATCAGTATTGCCTATGACCCTGTGAAGCATGAGCTCATAAAGCATATTGGTGTTGATGCTTCCTTCATGAGGTCTTGTGTGCATGATCAAGTGATTGCTCTTCAGTATGTGCTTTCAGAGCTTCAGATAGCGGATTTCTTCACGAAGGCCCAGACTCGAGCACAGCACGGCTTCTACCTCTCCAAACTCAGTGTTGTTGATCCACCACGAGTTTGAGGGGGGGGTGTTAGAGATATATGTATAGTGTGTTATTCCCCATTGTTATGAGGGGTTATTAGCATATTCACCGCATGTACTTTATGTATATATATTGGCCCATTGGCCTCATATTGAATACAAGCGCTATTCATAACAGGTCTGAGTTAGACTAGTGTCCTAGTCGTGTGCGTTGCGAGTTTTTAGGAGGGTTCATCAGATCGACCCCAGGTAGAGTAGCATGCGTGATGGCCTTACAAAGGTCAGGCATGGTATCCCTTAGACTTGTTATTTTCGTTTTGAGAAAAAAGTACAGAAAATGCCGTGGTGGGTTTGTGGCGCAAGGTGTGTGTGTTCGTGAGTTGAGATTGGTTCGTGAAATTTATCTAGAGAGAGTGAGAGCAAGATTGTTCTTGTGCAAGTTGAGAGCATCGTCGTTCTCAGATTGTG | 35 | 117-465 | 90.11-100 |
| Cluster 61 | AAATGAGGTAGGGCACACTAGAAGTCCATTTTGCGTGTTTCGTATTGATTGTCTTTCTGTGCCTCGATTTCGTAAAGTGGAGCTGTGGATACCGTCGTTCAGCCAAGTTTCACACTTGCTCGGAATTATTCCAAATGCACCTAGAA**ATGACATAGGGCACACCAGA**AGTCCATTTTGGGTGTTTGCGTTTATTTTCTTTCCGTGCCTCGATTTCGTAATGTGGAGCTCCGGGTACCCGTCGCTCTGCAAAGTTTTACACCTGCTCAGAATTATTCCAAATGCACCTAGAAATGACGTAGGGCACAGTAGAAGTCCATTATGGGTGTTTGGTTTTGATTTTATTTCCGTGCCTCGATTTCATAAATTGGAGCTCAGGGTACGCGTCGTTCTGGAAAGTTTCACACCGGCTCAGAAAGTTTCCAAATGCACCTAGAAATGAGGTAGGGCACACTAGAAGTCTATTATGAGAGTTTGATGTTCATTTTCTTTCCATGCCTCGATTTCATAAATTGGAGCTTAGGGTATGCGTCGTTCTGGAAAGTTTCACACCGGCTCGGAAGGATTCCAAATGCACCTAGAAATAAGGTAGGTCACACTAGAAGTCTATTTTGGGTGTTTCGTANNNNNNNNNNT | 46 | 103-633 | 90.78-100 |
| Cluster 62 | TGATGAACCCTAAGGTTCTATTTGTTGGCCCGATCTTTCGATGAGAACGATAAGTCCGGTAGGCGTCGCTCAACCCTCACGATCCTGGCTACAAACACGTAAGGCTCGCAACCACGCAATCGCTGAACTGATCGACTAGTCGTTATCAACCGTGCACGAATACCCGGTTGACCTGACCACGAAGGTCGATTCCTGCATACACCGAAGAAGCACGCAAGAACAAGATAATAAGCAATCTGAAATTGCAAATAGGACTGAAAGATTTAATTGAATTGGGATTCTGAATAAGGATCTTAATTGGGTGGTCTCGTCGACACACGCAAAAGATACAAGTTGCGACGAAGGCAAACTAAACTTAAACAAAATACAAGGAAAACTAAAGGGGTGCGGCCTCCT**TAAATAGGGAACGAGGAGCC**ACAAAACTAACGAACTAGCGAGGTGGTACTAACGGTCGTGGATTACTGTTTATGTGAACAGTACCGTGCCCTGGGTGGGCCGCCGGCAGATGAGCCAAGTTCAGTATGATTACAAAGCCCAGTTTGGCCCAAACAAGTGATATAACGCCTTCTTTTGATGATTGCGATCAGTCCGGAAGGAGTTTGGGGGTGAGGCTAGATCCGTTGGAAAGCGGACGAAATTATCTTTCCATCAAGTACTCGTGGACCTCCAACGGACGTCGTATGTGAAAGTTATGGGCGTTTGAAGTCAGTGCTGTCAGGCTGATTCCGGAGGCCGAACTGGATTCCAAAACGGGTCCCACTCAAACTGCTTGTTTGTCTTGGACCAAAAGTGACATGGTGCTGCACATATAGATATTCCATCATTAGGCAGCATCATATAGTTCATATAATATAAAGACACTCCTAAAAACGAGCTCACCTGATAAGTTAAGTGAAGCGTACGAGCTCTTGTACTTGGAATAGCAAGCATAGCAAATATGGTTGTATCCATAGGAGTCATGTCCTCATCATCCTC | 32 | 150-973 | 90.84-100 |
| Cluster 63 | GGGGCTAGATGACAAGGATCTAATAATCCTCATTTTATCTTTTATCTATAATTCTTATTATGGGTAAATATGATGTCATGTGGTCCCTTGGTATACCCCTTTATTTACAAGGGAGAAGCCTACCAAGTGATCGTAAGTTCTTCTACGACCACCCCCATAGTCGTAAGCCTTGCTACAACTACCTTATGGTCGTAATTTCTTCTACGACCACTATCCAGTCGTAAGTTATTCTACGACTACATCATAGTCATAAGCTCTTCTACGACCAGGTCAGCCACGACTACTTTATGATCAATAAAACCTACAGACGAGTGGGTCCAATTGATTAAGGAATCCAAGTAGTCAGCATACGCTATTACTATACGAAGTAATAGCACGTAATACCCCATTATCTCTGACAAGTAACTGCCAGGCGGCGTGAAAGGGTTACCACTCCGATGATTACTGCAAACATGCGCCCGTTACTGAATTTGATAAGGTGCCTCTTCACTAGGAGAAAACGGCTATTCCTTCACGACTATATAAAGGCAGCAATCAGAGAGGGAAAAGGGACGGATCGGAGGAGACAACAAGCAATCAGGAAGATAGTTAGACACTATCTTCTGTAATAGCCTTAGTCTTTTCTCCCAATTTTACGAAACACACTCAATACCATACACACACAGGAGTAGGGTTGTTATTCTCTCCGGAGAAGGCCTGAACTTGTATAAAAATACCCGTGTCAATCTCTTTGCGTGATTCCATTCTAGGAGA**CCCCCCGAATCAAACAATGTTT**ACGTAAGATCGGTTCTAAAACACCGATA | 32 | 186-799 | 90.82-100 |

**Supplementary Tables S3.** Description of total of the number of accessions commonly shared within each sub-population (PhSP1-PhSP4) of *Phyllostachys* species (Asian bamboo) by population structure, principal component (PCA), and hierarchical clustering analyses. The genetic diversity was assessed from the allele pattern produced by 16 inter-retrotransposon amplified polymorphism (IRAP) markers. Numbers on the table represent different Asian bamboo species as defined in the table 1.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sub-population** | **Population Structure** | **PCA** | **Hierarchical clustering** | **Consensual accessions among all three analyses** |
| PhSP1 | 1, 2, 3, 4, 5, 6, 16, 17, 18, 20, 21,22, 23. | 1, 2, 3, 4, 5, 6, 16, 17, 18, 20, 21, 22, 23 (Group 1) | 1, 15, 18, 20, 21, 22, 23 (PhC5) | 1, 18, 20, 21, 22,23. |
| PhSP2 | 19, 24, 25, 26, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 44. | 19, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 44 (Group 2) | 19, 24, 25, 26, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 44 (PhC1) | 19, 24, 25, 26, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 44. |
| PhSP3 | 14, 15, 27, 43, 45, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58. | 14, 15, 43, 45, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58 (Group 3) | 43, 45, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 58 (PhC2) and 27, 28 (PhC3)\*. | 43, 45, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 58. |
| PhSP4 | 7, 8, 9, 10, 11, 12, 13, 28, 46. | 7, 8, 9, 10, 11, 12, 13, 16, 17, 46 (Group 4) | 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, 17, 46, 57 (PhC4) | 7, 8, 9, 10, 11, 12, 13, 46. |

\*PhC2 and PhC3 got combined into one sub-population