**TABLES**

Table S1. The nucleotide sequence and base pair of 36 cowpea simple sequence repeat (SSR) markers screened for amplification across eighty African yam bean (AYB) DNA.

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| primer | Sequence(5'-3') | Base pair |
| VuUGM01 | F: AACAAGATGTGGCATGCTGA |  |
|  | R: TGAAAACGGAAAAGGGATCA | 155 |
| CLM0899 | F: CTCCTTTGTTGGGTTTGAG |  |
|  | R: TCTTTCATTACCATTGCTGAC | 155 |
| VuUGM100 | F: TCTCCACATCTCAACCCTCA |  |
|  | R: CACCAATGGCTACAACCACA | 181 |
| VuUGM48 | F: ACCTACTCACGAATATCCACAG |  |
|  | R: CACCGATAATCTCCAAAACA | 184 |
| CLM0858.1 | F: GGAAGAGATGGAGAGAGAGG |  |
|  | R: CTGGGCTGGTTGTTCACT | 186 |
| VuUGM16 | F: GGACATTTCCGGATGTCAAC |  |
|  | R: CTTTGCCATTCACTTTCACG | 188 |
| VuUGM92 | F: AAACAACAGGGAATTTGCAG |  |
|  | R: ATTTGCTCTGAATGCTCCTC | 195 |
| CLM0850 | F: CACACACAACACAAATACCTC |  |
|  | R:CTCAAGGGAGAGAAAGGG | 204 |
| CLM0938 | F: ATCATCGTGTCAAATACCAAG |  |
|  | R: TAGAAGAGCAACAGCAGCA | 209 |
| VuUGM36 | F: TGTGCCAAAAGGAAAAGACA |  |
|  | R: GGGATGGTATGTTCCTCACG | 217 |
| VuUGM25 | F: AGGGATGAGTTCCTTCAACG |  |
|  | R: AAGAAAGTGGTGAGGGCACAG | 222 |
| VuUGM63 | F: TTCTGCCTTCACGCTATTTC |  |
|  | R: TGGCTTTCTTTAGCAGCAGT | 226 |
| VuUGM72 | F: GTGCATGCAGGTAATGTGGT |  |
|  | R: TGGAGTTATGTGACGGGAGA | 229 |
| VuUGM80 | F: GTGTTGATTACAAGTGTCAACGTG |  |
|  | R: CTTAATCCCCCACCTCTGCT | 231 |
| CLM1012 | F: AAGCTCGGAGGTTTGAATTT |  |
|  | R: TTCTCAATGGTTATTCGGAACT | 274 |
| CLM0936 | F: ACCCAATCAAACACACACTC |  |
|  | R: GTAGCCAGAGAAGGAGAAGG | 294 |
| CLM0904 | F: AGAAAGAGAAAGCACATCACA |  |
|  | R: CGAAAGTGGAAGGTAAGAGAG | 322 |

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| primer | Sequence(5'-3') | Base pair |
| CLM1245 | F: GAATCCCTGACCCAATTAACAA |  |
|  | R: ATAAGGTGCATTGTCTTGTCCC | 326 |
| CLM0905 | F:CATAGCCACAGTTTGAGCC |  |
|  | R: GTTCACAGAATCATAAGGCAA | 356 |
| CLM0672 | F:TTTCCTCTGTCTCACTTCTT |  |
|  | R: TCTCTCATTCAAACAAACACA | 399 |
| VM31 | F: CGCTCTTCGTTGATGGTTATG |  |
|  | R: GTCTTCTAGAGGGTGTGATGGTA | 200 |
| VM74 | F: CTGCTACACCTTCCATCATTC |  |
|  | R: CCTTTGCTGTGTGGTGGTTT | 135 |
| VM37 | F: TGTCCGCGTTCTATAAAT |  |
|  | R: CGAGGATGAAGTAACAGA | 289 |
| VM51 | F: CATTGCCACTGGTTTCACTTA |  |
|  | R: GAGGCTCAGCATTTTGTTTCTAT | 256 |
| VM54 | F: CACACACACACATAGATATAG |  |
|  | R: TCCATCACTGATCACCTGTT | 179 |
| VM40 | F: TATTACGAGAGGCTATTT |  |
|  | R: CTCTAACACCTCAAGTTA | 200 |
| VM71 | F: TCGTGGCAGAGAATCAAAGACAC |  |
|  | R: TGGGTGGAGGCAAAAACAAAAC | 225 |
| VM9 | F:ACCGCACCCGATTTA |  |
|  | R:ATCAGCAGACAGGCA | 271 |
| VM39 | F:GATGGTTGTAATGGG |  |
|  | R:AAAAGGATGAAATTAGGA | 212 |
| VM94 | F:TCGAACTTTGGCTTGAGG |  |
|  | R:TGTCGTTTTGTCCCCCATTA | 253 |
| VM53 | F:GAGTTCCGTTCGTTGTGAGTAGAG |  |
|  | R:ACAGAGGAGGAAAAGGAAGTATGC | 288 |
| VM57 | F:GGAAGGGGTAGAGGAAAAGTGAA |  |
|  | R:TGATGATGATGGGTGAATGAGTTG | 325 |
| VM70 | F:AAAATCGGGGAAGGAAACC |  |
|  | R:GAAGGCAAAATACATGGCGTCAC | 186 |
| Bmd17 | F:GTTAGATCCCGCCCAATAGTC |  |
|  | R:AGATAGGAAGGGCGTGGTTT | 98 |
| Bmd2 | F:AGCGACAGCAAGAGAACC |  |
|  | R:CAACAAACGGTGATTGACCA | 106 |
| VM30 | F:CTCTTTCGCGTTCCACACTT |  |
|  | R:GCATCGCAATGGGTTGTGGTCTGTG | 150 |