Genetic Mapping, Candidate Gene Identification and Marker Validation for Host Plant Resistance to the Race 4 of *Fusarium oxysporum* f. sp. *cubense* using *Musa acuminata* ssp. *malaccensis*

**Supplementary Data**

**Table S1**

**Table S2**

**Table S3.**

**Table S4.**

**Table S1.** ‘DH Pahang’ v4 gene models within the candidate region. Bold highlighted gene models were used as CAPS markers for mapping. Asterisk (\*) indicate the differentially expressed genes presented in **Figure 4**.

|  |  |  |
| --- | --- | --- |
| ‘DH-Pahang’ v4 | Chr3 position | Description |
| **Macma4\_03\_g31200.1 (Marker 28420)** | **41185133..41196344** | **F-box domain-containing protein** |
| Macma4\_03\_g31210.1 | 41206680..41207872 | Phytocyanin domain-containing protein |
| Macma4\_03\_g31220.1 | 41211260..41251694 | DNA-directed RNA polymerase I subunit 1 |
| Macma4\_03\_g31230.1 | 41253561..41255269 | SAE2 domain-containing protein |
| Macma4\_03\_g31240.1 | 41260568..41266884 | 60S ribosomal protein L6 |
| Macma4\_03\_g31250.1 | 41267214..41271887 | Protein kinase domain-containing protein |
| Macma4\_03\_g31260.1 | 41272437..41277100 | Phosphoenolpyruvate/phosphate translocator 1, chloroplastic |
| Macma4\_03\_g31270.1 | 41277244..41277947 | PMEI domain-containing protein |
| Macma4\_03\_g31280.1 | 41279040..41281384 | Conserved hypothetical protein |
| Macma4\_03\_g31290.1 | 41282123..41290354 | Farnesyl pyrophosphare synthase |
| Macma4\_03\_g31300.1 | 41295141..41296569 | Myb-related protein Hv33 |
| Macma4\_03\_g31310.1\* | 41300083..41303456 | LRRNT\_2 domain-containing protein |
| Macma4\_03\_g31320.1\* | 41385591..41449859 | LRR receptor-like serine/threonine-protein kinase GSO1 |
| Macma4\_03\_g31330.1 | 41320808..41323526 | Cysteine-rich receptor-like protein kinase 6 |
| Macma4\_03\_g31340.1 | 41312026..41315013 | LRRNT\_2 domain-containing protein |
| Macma4\_03\_g31350.1 | 41333081..41346645 | LRR receptor-like serine/threonine-protein kinase GSO1 |
| Macma4\_03\_g31360.1 | 41356337..41359555 | LRRNT\_2 domain-containing protein |
| Macma4\_03\_g31370.1 | 41351929..41352780 | Receptor-like protein EIX2 |
| Macma4\_03\_g31380.1\* | 41364558..41367455 | LRRNT\_2 domain-containing protein |
| Macma4\_03\_g31390.1 | 41369977..41396220 | Transcription factor MYB86 |
| Macma4\_03\_g31400.1 | 41373362..41377132 | LRRNT\_2 domain-containing protein |
| Macma4\_03\_g31410.1 | 41414485..41425094 | Receptor-like protein EIX2 |
| Macma4\_03\_g31420.1 | 41395720..41413012 | Conserved hypothetical protein |
| Macma4\_03\_g31430.1 | 41408283..41409167 | Cysteine-rich repeat secretory protein 38 |
| Macma4\_03\_g31440.1 | 41428541..41430963 | Hypothetical protein |
| Macma4\_03\_g31450.1 | 41431234..41435561 | Receptor-like protein EIX2 |
| Macma4\_03\_g31460.1\* | 41459414..41497257 | Receptor-like protein EIX2 |
| Macma4\_03\_g31470.1\* | 41517334..41520795 | Receptor-like protein EIX2 |
| Macma4\_03\_g31480.1 | 41472994..41475737 | Cysteine-rich receptor-like protein kinase 6 |
| Macma4\_03\_g31490.1 | 41489067..41490234 | Myb-related protein Hv33 |
| Macma4\_03\_g31500.1 | 41508341..41511598 | Receptor-like protein EIX2 |
| Macma4\_03\_g31510.1\* | 41524565..41527279 | Cysteine-rich receptor-like protein kinase 6 |
| Macma4\_03\_g31520.1 | 41544749..41548495 | Receptor-like protein EIX2 |
| Macma4\_03\_g31530.1 | 41532334..41535839 | Receptor-like protein EIX2 |
| Macma4\_03\_g31540.1 | 41566336..41569054 | Cysteine-rich receptor-like protein kinase 6 |
| Macma4\_03\_g31550.1 | 41555821..41593102 | Receptor-like protein EIX2 |
| Macma4\_03\_g31560.1 | 41595512..41595742 | Hypothetical protein |
| Macma4\_03\_g31570.1 | 41602983..41606582 | Receptor-like protein EIX2 |
| Macma4\_03\_g31580.1 | 41622231..41625464 | Receptor-like protein EIX2 |
| Macma4\_03\_g31590.1 | 41629507..41639565 | Receptor-like protein EIX2 |
| Macma4\_03\_g31600.1 | 41641838..41656824 | Hypothetical protein |
| Macma4\_03\_g31610.1 | 41645278..41648736 | Receptor-like protein EIX2 |
| Macma4\_03\_g31620.1 | 41652520..41655238 | Cysteine-rich receptor-like protein kinase 6 |
| Macma4\_03\_g31630.1 | 41658517..41661609 | Receptor-like protein EIX2 |
| Macma4\_03\_g31640.1 | 41671331..41674950 | Receptor-like protein EIX2 |
| Macma4\_03\_g31650.1 | 41677256..41678423 | Myb-related protein Hv33 |
| Macma4\_03\_g31660.1 | 41683972..41687720 | Receptor-like protein EIX2 |
| Macma4\_03\_g31670.1 | 41690735..41691128 | Hypothetical protein |
| **Macma4\_03\_g31680.1 (Marker 28820)** | **41695490..41699989** | **Bifunctional nuclease 2** |
| Macma4\_03\_g31690.1 | 41701523..41712616 | Phosphatidylinositol/phosphatidylcholine transfer protein SFH8 |
| Macma4\_03\_g31700.1 | 41715069..41719865 | Hypothetical protein |
| Macma4\_03\_g31710.1 | 41723662..41727708 | Mitogen-activated protein kinase kinase kinase 18 |
| Macma4\_03\_g31720.1 | 41726550..41729437 | Hypothetical protein |
| Macma4\_03\_g31730.1 | 41730302..41734414 | Zinc finger BED domain-containing protein RICESLEEPER 1 |
| Macma4\_03\_g31740.1 | 41734749..41737252 | Pentatricopeptide repeat-containing protein At4g04370 |
| Macma4\_03\_g31750.1 | 41738751..41742387 | Hypothetical protein |
| Macma4\_03\_g31760.1 | 41742883..41744394 | Hypothetical protein |
| Macma4\_03\_g31770.1 | 41746163..41747718 | Two-pore potassium channel 5 |
| Macma4\_03\_g31780.1 | 41751185..41752315 | Hypothetical protein |
| Macma4\_03\_g31790.1 | 41752658..41762344 | Glycosyltransferase BC10 |
| Macma4\_03\_g31800.1 | 41766079..41766204 | Hypothetical protein |
| Macma4\_03\_g31810.1 | 41772196..41775831 | Ubiquitin-conjugating enzyme E2 5A |
| Macma4\_03\_g31820.1 | 41776216..41779883 | Protein GAMETE EXPRESSED 3 |
| Macma4\_03\_g31830.1 | 41782445..41798498 | Conserved hypothetical protein |
| Macma4\_03\_g31840.1 | 41799341..41799785 | Hypothetical protein |
| Macma4\_03\_g31850.1 | 41800716..41803719 | Serine/threonine-protein kinase/endoribonuclease IRE1a |
| Macma4\_03\_g31860.1 | 41806710..41809547 | Serine/threonine-protein kinase/endoribonuclease IRE1 |
| Macma4\_03\_g31870.1 | 41805410..41806709 | Hypothetical protein |
| Macma4\_03\_g31880.1 | 41810853..41811823 | Conserved hypothetical protein |
| Macma4\_03\_g31890.1 | 41812631..41813493 | Conserved hypothetical protein |
| Macma4\_03\_g31900.1 | 41814473..41815783 | Hypothetical protein |
| Macma4\_03\_g31910.1 | 41815696..41816622 | Hypothetical protein |
| Macma4\_03\_g31920.1 | 41822154..41823333 | Hypothetical protein |
| Macma4\_03\_g31930.1 | 41824383..41832871 | Notchless protein |
| Macma4\_03\_g31940.1 | 41832872..41837859 | Conserved hypothetical protein |
| Macma4\_03\_g31950.1 | 41833882..41835411 | Palmitoyl-acyl carrier protein thioesterase, chloroplastic |
| Macma4\_03\_g31960.1 | 41839873..41845205 | Protein DETOXIFICATION 10 |
| Macma4\_03\_g31970.1 | 41847431..41852161 | Hypothetical protein |
| Macma4\_03\_g31980.1 | 41852762..41857256 | ATP synthase subunit beta, mitochondrial |
| Macma4\_03\_g31990.1 | 41861903..41862442 | Hypothetical protein |
| Macma4\_03\_g32000.1 | 41864457..41867377 | Ribose-5-phosphate isomerase 2 |
| Macma4\_03\_g32010.1 | 41871539..41879072 | Hypothetical protein |
| Macma4\_03\_g32020.1 | 41880517..41886745 | AUGMIN subunit 2 |
| Macma4\_03\_g32030.1 | 41890891..41893288 | IQ domain-containing protein IQM2 |
| Macma4\_03\_g32040.1 | 41893861..41895567 | Pentatricopeptide repeat-containing protein At4g39530 |
| Macma4\_03\_g32050.1\* | 41900067..41909547 | Conserved hypothetical protein |
| Macma4\_03\_g32060.1 | 41897661..41900656 | Conserved hypothetical protein |
| Macma4\_03\_g32070.1 | 41909935..41916078 | Conserved hypothetical protein |
| Macma4\_03\_g32080.1 | 41916897..41925044 | Conserved hypothetical protein |
| Macma4\_03\_g32090.1 | 41930452..41935037 | Conserved hypothetical protein |
| Macma4\_03\_g32100.1 | 41935101..41945359 | Protein NAR1 |
| Macma4\_03\_g32110.1 | 41947092..41948011 | Ethylene-responsive transcription factor 9 |
| Macma4\_03\_g32120.1 | 41949180..41971744 | Protein WRKY1 |
| Macma4\_03\_g32130.1 | 41972765..41975625 | Transcription factor bHLH92 |
| Macma4\_03\_g32140.1 | 41990262..41997002 | CRM-domain containing factor CFM3, chloroplastic/mitochondrial |
| Macma4\_03\_g32150.1 | 41997575..41998435 | PRA1 family protein B5 |
| Macma4\_03\_g32160.1 | 41998701..42010823 | Glutathione reductase, chloroplastic |
| Macma4\_03\_g32170.1 | 42012734..42015779 | Hypothetical protein |
| Macma4\_03\_g32180.1 | 42017982..42019326 | AP2/ERF and B3 domain-containing transcription repressor RAV2 |
| Macma4\_03\_g32190.1 | 42023042..42026327 | Conserved hypothetical protein |
| Macma4\_03\_g32200.1 | 42028072..42031234 | Receptor protein kinase-like protein ZAR1 |
| Macma4\_03\_g32210.1 | 42033960..42035510 | Glutamine amidotransferase GAT1\_2.1 |
| Macma4\_03\_g32220.1\* | 42035600..42038030 | *LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 2.1* |
| Macma4\_03\_g32230.1 | 42038571..42039543 | *LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.2* |
| Macma4\_03\_g32240.1 | 42043048..42045672 | *LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 2.1* |
| Macma4\_03\_g32250.1 | 42046320..42047515 | Hypothetical protein |
| Macma4\_03\_g32260.1 | 42048539..42049555 | *EAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.2* |
| Macma4\_03\_g32270.1 | 42052018..42058909 | *LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.3* |
| Macma4\_03\_g32280.1 | 42052949..42054869 | *LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.2* |
| Macma4\_03\_g32290.1 | 42059396..42062500 | Universal stress protein A-like protein |
| Macma4\_03\_g32300.1 | 42063437..42064515 | Hypothetical protein |
| Macma4\_03\_g32310.1 | 42065532..42066512 | Adenylate isopentenyltransferase |
| Macma4\_03\_g32320.1 | 42070221..42078056 | Caffeoylshikimate esterase |
| Macma4\_03\_g32330.1 | 42078115..42085871 | Hypothetical protein |
| Macma4\_03\_g32340.1 | 42088311..42089937 | LOB domain-containing protein 41 |
| Macma4\_03\_g32350.1 | 42089938..42092882 | Hypothetical protein |
| Macma4\_03\_g32360.1 | 42098922..42099597 | Ethylene-responsive transcription factor ERF070 |
| Macma4\_03\_g32370.1 | 42099885..42102752 | Beta-glucosidase 1 |
| Macma4\_03\_g32380.1 | 42105068..42106673 | Conserved hypothetical protein |
| Macma4\_03\_g32390.1 | 42110299..42112091 | Hypothetical protein |
| Macma4\_03\_g32400.1 | 42118206..42119901 | Receptor-like protein EIX2 |
| Macma4\_03\_g32410.1 | 42121987..42124957 | F-box/kelch-repeat protein At1g55270 |
| Macma4\_03\_g32420.1 | 42125460..42130238 | Peptidyl-tRNA hydrolase, mitochondrial |
| Macma4\_03\_g32430.1 | 42131732..42137853 | Eukaryotic translation initiation factor NCBP |
| **Macma4\_03\_g32440.1 (Marker 29590)** | **42138268..42142592** | **Pentatricopeptide repeat-containing protein At4g28010** |

**Table S2.** Enrichment of Gene Ontology (GO) terms detected in the candidate region using p and q cutoffs of 0.05 and 0.1, respectively. Using the GO tool at ‘<https://banana-genome-hub.southgreen.fr/content/go-enrichment>’ (accessed on 21 April 2023), 102 out of the 125 candidate gene models in DH-Pahang v4 (26,613 genes and 122,637 GO terms) are associated with at least 1 GO term. The gene models belonging to each GO term are listed, along with the gene ratio and the corresponding p-adj value. Asterisk (\*) indicate the differentially expressed genes presented in **Figure 4**.

|  |  |  |  |
| --- | --- | --- | --- |
| **Biological processes** | **Description** | **Gene Ratio** | **p-adj** |
| **GO:0042742** | **Defense response to bacterium** | **7/102** | **0.00043759** |
| Macma4\_03\_g31330.1 | Cysteine-rich receptor-like protein kinase 6 |  |  |
| Macma4\_03\_g31430.1 | Cysteine-rich repeat secretory protein 38 |  |  |
| Macma4\_03\_g31480.1 | Cysteine-rich receptor-like protein kinase 6 |  |  |
| Macma4\_03\_g31510.1\* | Cysteine-rich receptor-like protein kinase 6 |  |  |
| Macma4\_03\_g31540.1 | Cysteine-rich receptor-like protein kinase 6 |  |  |
| Macma4\_03\_g31620.1 | Cysteine-rich receptor-like protein kinase 6 |  |  |
| Macma4\_03\_g31850.1 | Serine/threonine-protein kinase/endoribonuclease IRE1a |  |  |
| **GO:0030968** | **Endoplasmic reticulum unfolded protein response** | **3/102** | **0.00192488** |
| Macma4\_03\_g31850.1 | Serine/threonine-protein kinase/endoribonuclease IRE1a |  |  |
| Macma4\_03\_g31860.1 | Serine/threonine-protein kinase/endoribonuclease IRE1 |  |  |
| Macma4\_03\_g32050.1\* | Conserved hypothetical protein |  |  |
| **GO:0050832** | **Defense response to fungus** | **5/102** | **0.03443587** |
| Macma4\_03\_g31370.1 | Receptor-like protein EIX2 |  |  |
| Macma4\_03\_g31410.1 | Receptor-like protein EIX2 |  |  |
| Macma4\_03\_g31450.1 | Receptor-like protein EIX2 |  |  |
| Macma4\_03\_g31590.1 | Receptor-like protein EIX2 |  |  |
| Macma4\_03\_g32400.1 | Receptor-like protein EIX2 |  |  |
| **GO:0071215** | **Cellular response to abscisic acid stimulus** | **2/102** | **0.04062588** |
| Macma4\_03\_g32230.1 | *LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.2* |  |  |
| Macma4\_03\_g32280.1 | *LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.2* |  |  |
| **Molecular function** | **Description** | **Gene Ratio** | **p-adj** |
| **GO:0030247** | **Polysaccharide binding** | **7/102** | **9.43E-06** |
| Macma4\_03\_g32220.1\* | *LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 2.1* |  |  |
| Macma4\_03\_g32230.1 | *LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.2* |  |  |
| Macma4\_03\_g32240.1 | *LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 2.1* |  |  |
| Macma4\_03\_g32250.1 | Hypothetical protein |  |  |
| Macma4\_03\_g32260.1 | *LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.2* |  |  |
| Macma4\_03\_g32270.1 | *LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.3* |  |  |
| Macma4\_03\_g32280.1 | *LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.2* |  |  |
| **GO:0004521** | **Endoribonuclease activity** | **3/102** | **0.00586628** |
| Macma4\_03\_g31850.1 | Serine/threonine-protein kinase/endoribonuclease IRE1a |  |  |
| Macma4\_03\_g31860.1 | Serine/threonine-protein kinase/endoribonuclease IRE1 |  |  |
| Macma4\_03\_g32050.1\* | Conserved hypothetical protein |  |  |

**Table S3.** Screening of the IITA germplasm collection (Uganda) using the A-genome specific marker A-29730 (**Table 2**). Genome subgroup and ploidy is indicated in brackets. F- and M-parent respectively indicate female and male parent used in the crossing. NARITA hybrids are EHABs named after the organizations involved in the collaborative development of these lines, namely the National Agricultural Research Organization (NARO) of Uganda and the International Institute of Tropical Agriculture (IITA). SH stands for selected hybrids developed by breeding program at the Honduran Agricultural Research Foundation, Honduras. A-29730 marker alleles were scored as per previous description (Table 2). A = marker allele for homozygous resistance, B = marker allele for homozygous susceptibility, H = heterozygous.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| sn | Genotype | Type | F-Parent | M-Parent | A-29730 |
| 1 | 1201K-1 (AAAA) | Matooke hybrid (Parental) | Nakawere (AAA) | Calcutta 4 (AA) | B |
| 2 | 1438K-1 (AAAA) | Matooke hybrid (Parental) | Entukura (AAA) | Calcutta 4 (AA) | H |
| 3 | 222K-1 (AAAA) | Matooke hybrid (Parental) | Nfuuka (AAA) | Calcutta 4 (AA) | B |
| 4 | 365K-1(AAAA) | Matooke hybrid (Parental) | Kabucuragye (AAA) | Calcutta 4 (AA) | B |
| 5 | 376K-7 (AAAA) | Matooke hybrid (Parental) | Nante (AAA) | Calcutta 4 (AA) | H |
| 6 | 401K-1 (AAAA) | Matooke hybrid (Parental) | Entukura (AAA) | Calcutta 4 (AA) | B |
| 7 | 660K-1 (AAAA) | Matooke hybrid (Parental) | Enzirabahima (AAA) | Calcutta 4 (AA) | B |
| 8 | NARITA 1 (AAA) | Maooke hybrid (NARITA) | 917K-2 (AAAA) | TMB2×9128-3 (AA) | H |
| 9 | NARITA 2 (AAA) | Maooke hybrid (NARITA) | 401K-1 (AAAA) | TMB2×9128-3 (AA) | B |
| 10 | NARITA 3 (AAA) | Maooke hybrid (NARITA) | 917K-2 (AAAA) | SH3362 (AA) | B |
| 11 | NARITA 4 (AAA) | Maooke hybrid (NARITA) | 660K-1 (AAAA) | TMB2×9128-3 (AA) | B |
| 12 | NARITA 5 (AAA) | Maooke hybrid (NARITA) | 917K-2 (AAAA) | SH3217 (AA) | H |
| 13 | NARITA 6 (AAA) | Maooke hybrid (NARITA) | 222K-1 (AAAA) | TMB2×9128-3 (AA) | H |
| 14 | NARITA 7 (AAA) | Maooke hybrid (NARITA) | 1201K-1 (AAAA) | SH3217 (AA) | H |
| 15 | NARITA 8 (AAA) | Maooke hybrid (NARITA) | 917K-2 (AAAA) | SH3217 (AA) | H |
| 16 | NARITA 9 (AAA) | Maooke hybrid (NARITA) | 917K-2 (AAAA) | SH3217 (AA) | H |
| 17 | NARITA 10 (AAA) | Maooke hybrid (NARITA) | 917K-2 (AAAA) | SH3217 (AA) | - |
| 18 | NARITA 11 (AAA) | Maooke hybrid (NARITA) | 1201K-1 (AAAA) | TMB2×9128-3 (AA) | B |
| 19 | NARITA 12 (AAA) | Maooke hybrid (NARITA) | 1201K-1 (AAAA) | TMB2×9128-3 (AA) | B |
| 20 | NARITA 13 (AAA) | Maooke hybrid (NARITA) | 1201K-1 (AAAA) | SH3362 (AA) | H |
| 21 | NARITA 14 (AAA) | Maooke hybrid (NARITA) | 917K-2 (AAAA) | TMB2×7197-2 (AA) | B |
| 22 | NARITA 15 (AAA) | Maooke hybrid (NARITA) | 660K-1 (AAAA) | TMB2×9128-3 (AA) | H |
| 23 | NARITA 16 (AAA) | Maooke hybrid (NARITA) | 917K-2 (AAAA) | SH3362 (AA) | H |
| 24 | NARITA 17 (AAA) | Maooke hybrid (NARITA) | 1438K-1 (AAAA) | TMB2×9719-7 (AA) | H |
| 25 | NARITA 18 (AAA) | Maooke hybrid (NARITA) | 365K-1 (AAAA) | 660K-1 (AAAA) | B |
| 26 | NARITA 19 (AAA) | Maooke hybrid (NARITA) | 1201K-1 (AAAA) | TMB2×8075-7 (AA) | H |
| 27 | NARITA 20 (AAA) | Maooke hybrid (NARITA) | Entukura (AAA) | 365K-1 (AAAA) | B |
| 28 | NARITA 21 (AAA) | Maooke hybrid (NARITA) | 1201K-1 (AAAA) | TMB2×7197-2 (AA) | B |
| 29 | NARITA 22 (AAA) | Maooke hybrid (NARITA) | 917K-2 (AAAA) | TMB2×9128-3 (AA) | H |
| 30 | NARITA 23 (AAA) | Maooke hybrid (NARITA) | Kazirakwe (AAA) | TMB2×7197-2 (AA) | H |
| 31 | NARITA 24 (AAA) | Maooke hybrid (NARITA) | Unknown | Unknown | B |
| 32 | NARITA 25 (AAA) | Maooke hybrid (NARITA) | Unknown | Unknown | H |
| 33 | NARITA 26 (AAA) | Maooke hybrid (NARITA) | Unknown | Unknown | B |
| 34 | 24948S-10 (AAA) | Matooke hybrid | 1438K-1 (AAAA) | 5610S-1 (AA) | H |
| 35 | 24948S-9 (AAA) | Matooke hybrid | 1438K-1 (AAAA) | 5610S-1 (AA) | H |
| 36 | 25356S-1 (AAA) | Matooke hybrid | Tereza (AAA) | TMB2×7197-2 (AA) | H |
| 37 | 25583S-2 (AAA) | Matooke hybrid | 1201K-1 (AAAA) | 5610S-1 (AA) | H |
| 38 | 25623S-11 (AAA) | Matooke hybrid | 8817S-1 (AA) | 917K-2 (AAAA) | H |
| 39 | 25909S-3 (AAA) | Matooke hybrid | 917K-2 (AAAA) | TMB2×7197-2 (AA) | H |
| 40 | 25974S-30 (AAA) | Matooke hybrid | 917K-2 (AAAA) | SH3362 (AA) | H |
| 41 | 25974S-31 (AAA) | Matooke hybrid | 917K-2 (AAAA) | SH3362 (AA) | H |
| 42 | 26260S-3 (AAA) | Matooke hybrid | 660K-1 (AAAA) | 5610S-1 (AA) | H |
| 43 | 26316S-7 (AAA) | Matooke hybrid | 1201K-1 (AAAA) | SH3362 (AA) | H |
| 44 | 26337S-37 (AAA) | Matooke hybrid | 1201K-1 (AAAA) | SH3217 (AA) | H |
| 45 | 26666S-1 (AAA) | Matooke hybrid | 917K-2 (AAAA) | SH3362 (AA) | B |
| 46 | 26815S-3 (AAA) | Matooke hybrid | 917K-2 (AAAA) | 5610S-1 (AA) | B |
| 47 | 27401S-1 (AAA) | Matooke hybrid | 917K-2 (AAAA) | Malaccensis\_250 (AA) | B |
| 48 | 27579S-1 (AAA) | Matooke hybrid | 1201K-1 (AAAA) | Malaccensis\_250 (AA) | B |
| 49 | 27825S-4 (AAA) | Matooke hybrid | 660K-1 (AAAA) | Malaccensis\_250 (AA) | B |
| 50 | 27873S-26 (AAA) | Matooke hybrid | 660K-1 (AAAA) | Malaccensis\_250 (AA) | B |
| 51 | 27873S-38 (AAA) | Matooke hybrid | 660K-1 (AAAA) | Malaccensis\_250 (AA) | B |
| 52 | 28033S-19 (AAA) | Matooke hybrid | 917K-2 (AAAA) | Malaccensis\_250 (AA) | H |
| 53 | 28033S-23 (AAA) | Matooke hybrid | 917K-2 (AAAA) | Malaccensis\_250 (AA) | B |
| 54 | 28060S-5 (AAA) | Matooke hybrid | 917K-2 (AAAA) | Malaccensis\_250 (AA) | B |
| 55 | 28060S-8 (AAA) | Matooke hybrid | 917K-2 (AAAA) | Malaccensis\_250 (AA) | B |
| 56 | 28257S-1 (AAA) | Matooke hybrid | 917K-2 (AAAA) | Malaccensis\_250 (AA) | H |
| 57 | 28434S-2 (AAA) | Matooke hybrid | 1201K-1 (AAAA) | 5610S-1 (AA) | B |
| 58 | 28465S-21 (AAA) | Matooke hybrid | 1201K-1 (AAAA) | Malaccensis\_250 (AA) | H |
| 59 | 28974S-11 (AAA) | Matooke hybrid | 1438K-1 (AAAA) | Malaccensis\_250 (AA) | H |
| 60 | 29114S-14 (AAA) | Matooke hybrid | 5610S-1 (AA) | Malaccensis\_250 (AA) | H |
| 61 | 29114S-24 (AAA) | Matooke hybrid | 5610S-1 (AA) | Malaccensis\_250 (AA) | H |
| 62 | 29275S-1 (AAAA) | Matooke hybrid (Parental) | Enzirabahima (AAA) | Malaccensis\_250 (AA) | B |
| 63 | 29275S-5 (AAAA) | Matooke hybrid (Parental) | Enzirabahima (AAA) | Malaccensis\_250 (AA) | B |
| 64 | 29364S-2 (AAAA) | Matooke hybrid (Parental) | Namwezi (AAA) | Cv. Rose (AA) | B |
| 65 | 29490S-1 (AAA) | Matooke hybrid | 917K-2 (AAAA) | 5610S-1 (AA) | H |
| 66 | 29561S-2 (AAA) | Matooke hybrid | 1201K-1 (AAAA) | Malaccensis\_250 (AA) | B |
| 67 | 29586S-4 (AAA) | Matooke hybrid | 1438K-1 (AAAA) | 5610S-1 (AA) | H |
| 68 | 29275S-4 (AAAA) | Matooke hybrid (Parental) | Enzirabahima (AAA) | Malaccensis\_250 (AA) | B |
| 69 | Zebrina (G.F.) (AA) | Diploid (Parental) | *Musa acuminata* ssp. *zebrina* | | B |
| 70 | TMB2×5265-1 (AA) | Diploid (Parental) | Tjau lagada (AA) | Calcutta 4 (AA) | B |
| 71 | 02145/1320 (AA) | Diploid (Parental) | Zebrina GF | Open pollination | B |
| 72 | 10969S-1 (AA) | Diploid (Parental) | 376K-7 (AAAA) | 5105-1 (AA) | B |

**Table S4.** IITA banksii collection from Ibadan, Nigeria, screened with the A-genome specific marker, A-29730. Marker alleles are described as per **Table S1**. aphylogenetic grouping refers to the clustering of these accessions in the UPGMA analysis described in [1].

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| sn | Accession name | ITC code | Phylogenetic groupinga | A-29730 |
| 1 | Galeo | ITC0259 | AA cv. IndonTriNG | B |
| 2 | Sowmuk | ITC0266 | AA cv. banksii sensu lato | B |
| 3 | NBA 14 | ITC0267 | AA cv. banksii sensu lato | B |
| 4 | Niyarma Yik | ITC0269 | AA cv. banksii sensu lato | B |
| 5 | Pitu | ITC0294 | AA cv. IndonTriNG | B |
| 6 | Beram | ITC0298 | AA cv. IndonTriNG | B |
| 7 | Guyod | ITC0299 | AA cv. IndonTriPh | B |
| 8 | UPLB | ITC0343 | AA cv. banksii sensu lato | B |
| 9 | Higa | ITC0428 | *M. acuminata* ssp. *banksii* | B |
| 10 | Banksii | ITC0453 | *M. acuminata* ssp. *banksii* | B |
| 11 | Waimara | ITC0600 | AA cv. banksii derivative | B |
| 12 | Hung Tu | ITC0601 | AA cv. IndonTriNG | B |
| 13 | Hawain 3 | ITC0602 | *M. acuminata* ssp. *banksii* | B |
| 14 | Somani | ITC0603 | AA cv. banksii sensu lato | B |
| 15 | Hybrid | ITC0606 | *M. acuminata* ssp. *banksii* | B |
| 16 | Mambee Thu | ITC0612 | AA cv. IndonTriNG | B |
| 17 | Hawain 3 | ITC0617 | *M. acuminata* ssp. *banksii* | B |
| 18 | Banksii | ITC0620 | *M. acuminata* ssp. *banksii* | B |
| 19 | Navaradam | ITC0770 | AA cv. banksii derivative | B |
| 20 | Mpiajhap | ITC0773 | AA cv. banksii derivative | B |
| 21 | Garunga | ITC0798 | AA cv. banksii derivative | B |
| 22 | Banksii | ITC0806 | *M. acuminata* ssp. *banksii* | B |
| 23 | Maleb | ITC0809 | AA cv. banksii sensu lato | B |
| 24 | Sihir | ITC0810 | AA cv. banksii derivative | B |
| 25 | Sepi | ITC0849 | AA cv. banksii sensu lato | B |
| 26 | Mala | ITC0869 | AA cv. IndonTriNG | B |
| 27 | Banksii | ITC0879 | *M. acuminata* ssp. *banksii* | B |
| 28 | Kwosriake | ITC0882 | AA cv. banksii sensu lato | B |
| 29 | Awondaeke | ITC0884 | AA cv. IndonTriNG | B |
| 30 | Banksii | ITC0885 | *M. acuminata* ssp. *banksii* | B |
| 31 | Wikago | ITC0888 | AA cv. banksii sensu lato | B |
| 32 | Pai ka | ITC0892 | AA cv. banksii sensu lato | B |
| 33 | Adina | ITC0893 | AA cv. banksii sensu lato | B |
| 34 | Tainga | ITC0894 | AA cv. banksii derivative | B |
| 35 | Fu Des | ITC0939 | AA cv. IndonTriNG | B |
| 36 | Kwaro | ITC0943 | AA cv. IndonTriNG | B |
| 37 | Tomolo | ITC1187 | AA cv. banksii sensu lato | B |
| 38 | Spiral | ITC1206 | AA cv. banksii derivative | B |
| 39 | Banksii | ITC1219 | *M. acuminata* ssp. *banksii* | B |
| 40 | Kokopo | ITC1243 | AA cv. IndonTriNG | B |
| 41 | Mapua | ITC1244 | AA cv. banksii sensu lato | B |
| 42 | SH3362 | n.a. | 2x hybrid parent | H |
| 43 | TMB2×8075-7 | n.a. | 2x hybrid parent | B |
| 44 | 30456-1 | n.a. | 3x BITA hybrid | B |
| 45 | 30456-2 | n.a. | 3x BITA hybrid | B |
| 46 | 30456-3 | n.a. | 4x BITA hybrid | B |

1. Christelová, P.; De Langhe, E.; Hřibová, E.; Čížková, J.; Sardos, J.; Hušáková, M.; Van den houwe, I.; Sutanto, A.; Kepler, A.K.; Swennen, R.; et al. Molecular and cytological characterization of the global Musa germplasm collection provides insights into the treasure of banana diversity. *Biodiversity and Conservation* **2017**, *26*, 801-824, doi:10.1007/s10531-016-1273-9.