|  |  |  |  |
| --- | --- | --- | --- |
| Restriction types | Site number | Length of fragments | Representive stain |
| SAG1-A | 1 | 334, 56 | I |
| SAG1-B | 1 | 293, 97 | II/III |
| SAG1-C\* | 2 | 237, 97, 56 | MAS |
| SAG1-D\* | 2 | 230, 101, 59 | ARI |
| alt. SAG2-A | 4 | 343, 161, 33, (6, 3) | I |
| alt. SAG2-B | 5 | 343, 112, 49, 33, (6, 3) | II |
| alt. SAG2-C | 3 | 376, 161, (6, 3) | III |
| SAG3-A | 2 | 100, 64 (62) | I |
| SAG3-B | 0 | 226 | II |
| SAG3-C | 1 | 162, 64 | III |
| BTUB-A | 2 | 220, 118, 73 | I |
| BTUB-B | 2 | 191, 127, 93 | II |
| BTUB-C | 3 | 127, 118, 93, 73 | III |
| GRA6-A | 1 | 258, 86 | I |
| GRA6-B | 1 | 183, 161 | II |
| GRA6-C | 2 | 161, 97 (86) | III |
| c22-8-A | 4 | 175, 160, 113, 54, (19) | I |
| c22-8-B | 2 | 229, 160, 132 | II |
| c22-8-C | 2 | 248, 160, 113 | III |
| c22-8-D | 3 | 175, 160, 113, 73 | MAS |
| c29-2-A | 3 | 307, 50 (45, 41) | I |
| c29-2-B | 3 | 183, 165, 53 (45) | II |
| c29-2-C | 2 | 348, 50 (45) | III |
| L358-A | 5 | 281, 44, (34, 27, 27, 4) | I |
| L358-B | 5 | 201, 114, 44, (27, 27, 4) | II |
| L358-C | 6 | 167, 114, 44, (34, 27, 27, 4) | III |
| PK1-A | 4 | 380, 263, 125, 100, (35) | I |
| PK1-B | 6 | 241,215,139,125, 100, 48, (35) | II |
| PK1-C | 5 | 380, 215, 125, 100, 48, (35) | III |
| PK1-D | 7 | 353, 125, 108 (107), 100, 48, (35, 27) | TgCatBr5 |
| PK1-E | 6 | 315\*\*, 215, 125, 100, 48, (35, 27) | TgCtCo5 |
| Apico-A | 6 | 318, 107(103), 69, (17, 14, 12) | I |
| Apico-B | 7 | 167,150, 107(103), 69, (17, 14, 12) | II |
| Apico-C | 5 | 317, 117, 107, 69, (17, 12) | III |
| \*Minor changes in length are not able to be distinguished. | | | |
| \*\*A deletion in the PK1 results in 315 bp rather than 353 bp. | | | |
| () Bands in brackets indicated they are likely to be undetectable or merge with bands of similar molecular size. | | | |

**Table S1.** Predicted fragment lengths after restriction enzyme digestion based on sequences from ToxoDB and PCR sequencing.