**Table 5** Summary of homology search of the DArTseq markers of integrated map against the MPOB *pisifera* genome assembly P5

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Linkage group | TM | Chromosomes | Scaffold | No-hit | Single-hit |
| 1 | 200 | 168 | 17 | 15 | 171 |
| 2 | 277 | 187 | 73 | 17 | 241 |
| 3 | 189 | 149 | 24 | 16 | 157 |
| 4A | 76 | 33 | 32 | 11 | 62 |
| 4B | 66 | 57 | 3 | 6 | 58 |
| 5 | 131 | 99 | 21 | 11 | 117 |
| 6 | 154 | 105 | 38 | 11 | 134 |
| 7 | 97 | 68 | 25 | 4 | 88 |
| 8 | 112 | 92 | 11 | 9 | 92 |
| 9 | 96 | 72 | 22 | 2 | 86 |
| 10 | 95 | 71 | 18 | 6 | 82 |
| 11 | 147 | 103 | 34 | 10 | 128 |
| 12 | 88 | 55 | 24 | 9 | 70 |
| 13 | 114 | 68 | 37 | 9 | 97 |
| 14 | 80 | 62 | 8 | 10 | 63 |
| 15 | 91 | 70 | 16 | 5 | 80 |
| 16 | 17 | 14 | 2 | 1 | 13 |
| Total | **2030** | **1473** | **405** | **152** | **1739** |
| Mean | 119.47 | 86.65 | 23.82 | 8.94 | 102.29 |
| Min | 17 | 14 | 2 | 1 | 13 |
| Max | 277 | 187 | 73 | 17 | 241 |

TM = Total number of DArTseq markers for each linkage group

Chromosomes = Number of DArTseq markers aligned to 16 chromosomes of MPOB *pisifera* genome assembly *P5*

Scaffolds = Number of DArTseq markers aligned to small unanchored scaffolds

No-hit = Number of DArTseq markers with no hit

Single-hit = Number of DArTseq markers with only a single hit with no sub-alignment score