**Table S7: LD estimates in six model-based individual population groups and entire population as well as across eight chromosomes**

| Population groups | Global | | | | Linked | | | Unlinked | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | Number of marker-pairs used | [a]Number of significant marker-pairs in LD | [b]Significant LD (%) | Extent of LD ($r^2$) | Number of significant marker-pairs in LD | Significant LD (%) | Extent of LD ($r^2$) | Number of significant marker-pairs in LD | Significant LD (%) | Extent of LD ($r^2$) |
| **POP I** | 384117 | 949 | 2.47 | 0.25 | 179383 | 46.7 | 0.30 | 8182 | 2.13 | 0.22 |
| **POP II** | 384123 | 30768 | 80.1 | 0.20 | 337260 | 87.8 | 0.28 | 264661 | 68.9 | 0.18 |
| **POP III** | 384117 | 6876 | 1.79 | 0.27 | 158640 | 41.3 | 0.33 | 6261 | 1.63 | 0.25 |
| **POP IV** | 384108 | 14673 | 3.82 | 0.25 | 213948 | 55.7 | 0.27 | 13636 | 3.55 | 0.23 |
| **POP V** | 384122 | 6148 | 1.61 | 0.23 | 149423 | 38.9 | 0.28 | 5839 | 1.52 | 0.21 |
| **POP VI** | 384098 | 5531 | 1.44 | 0.19 | 128673 | 33.5 | 0.25 | 5070 | 1.32 | 0.17 |
| **Total population groups** | 384126 | 64572 | 16.81 | 0.22 | 163638 | 42.6 | 0.30 | 54277 | 14.13 | 0.20 |

| Chromosomes | Linked | | | |
|---|---|---|---|---|
| | Number of marker-pairs used | Number of significant marker-pairs in LD | Significant LD (%) | Extent of LD ($r^2$) |
| **CaChr01** | 5229 | 4983 | 95.3 | 0.26 |
| **CaChr02** | 4679 | 4464 | 95.4 | 0.28 |
| **CaChr03** | 7064 | 5658 | 80.1 | 0.31 |
| **CaChr04** | 5229 | 5198 | 99.4 | 0.28 |
| **CaChr05** | 7064 | 6054 | 85.7 | 0.30 |
| **CaChr06** | 6422 | 4373 | 68.1 | 0.27 |
| **CaChr07** | 5810 | 5595 | 96.3 | 0.40 |
| **CaChr08** | 4679 | 3977 | 85.0 | 0.29 |
| **Total chromosomes** | 5089 | 4361 | 85.6 | 0.31 |

[a]Percentage of microsatellite and SNP marker locus-pairs in significant ($P < 0.001$) LD

[b]Significant threshold ($P < 0.001$) at which pair-wise LD estimates is significant statistically