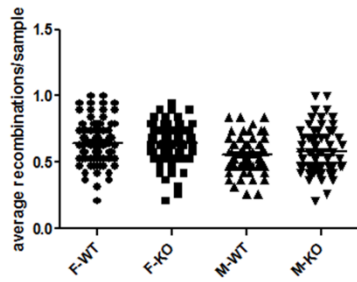
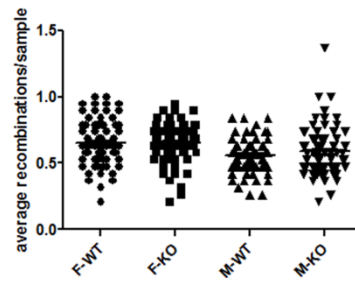


Figure S2.

Recombination frequency considering a conservative approach (no recombination in "no call" locations).



Recombination frequency considering a non-conservative approach (recombination in "no call" locations).



| ManWhitey Test | Fwt no rec | Fko no rec | Mwt no rec | Mko no rec |
|----------------|------------|------------|------------|------------|
| Fwt no rec     | na         | 0,6155     | 0,0007     | 0,0046     |
| Fko no rec     | na         | na         | < 0,0001   | 0,0008     |
| Mwt no rec     | na         | na         | na         | 0,8192     |
| Mko no rec     | na         | na         | na         | na         |

| ManWhitey Test | Fwt rec | Fko rec | Mwt rec  | Mko rec |
|----------------|---------|---------|----------|---------|
| Fwt rec        | na      | 0,6632  | 0,0004   | 0,0046  |
| Fko rec        | na      | na      | < 0,0001 | 0,0008  |
| Mwt rec        | na      | na      | na       | 0,7264  |
| Mko rec        | na      | na      | na       | na      |

**Figure S2** For the 17 SNP/sample pairs that passed the selection filters but had no detectable genotype signal, two extreme scenarios (recombination in all locations versus no recombination in all locations) were considered and overall recombination frequencies were calculated for the two extreme scenarios.