**Supplementary Table 8.** Summary of genome scan results. Genome scan methods are labelled as follows: SweeD, CLR; hapFLK, FLK; *nSL*: NSL. The second and third columns [field (CLR ∩ NSL ∩ FLK)] correspond to the intersection of the 5% quantile windows across all three genome scan methods in SL and Vv1. The fourth and fifth columns [field (CLR ∩ NSL) ∪ (CLR ∩ FLK) ∪ (NSL ∩ FLK)] correspond to the union of the three possible intersections of the 5% quantile windows between all pairs of genome scan methods. This approach allows us to select genomic windows supported by at least two methods. The first number of each cell corresponds to the number of windows passing the significance threshold; the number in brackets corresponds to the number of genes contained in these windows. The total may not reflect the sum of gene numbers in the top 5% for two or three scores since a gene can be distributed in two adjacent windows.

|  |  |  |  |
| --- | --- | --- | --- |
| Chromosome | (CLR ∩ NSL ∩ FLK) | (CLR ∩ NSL) ∪ (CLR ∩ FLK) ∪ (NSL ∩ FLK) | Total |
| Sl | Vv1 | Sl | Vv1 | Sl | Vv1 |
| BCIN01 |  |  | 4 (15) | 7 (28) | 4 (15) | 7 (28) |
| BCIN02 | 1 (5) |  | 7 (26) | 5 (14) | 8 (30) | 5 (14) |
| BCIN03 | 1 (2) | 1 (6) | 4 (15) | 8 (28) | 5 (16) | 9 (33) |
| BCIN04 |  | 1 (5) | 1 (2) | 8 (27) | 1 (2) | 9 (32) |
| BCIN05 | 1 (5) |  | 5 (14) | 1 (4) | 6 (19) | 1 (4) |
| BCIN06 |  |  | 3 (10) | 3 (7) | 3 (10) | 3 (7) |
| BCIN07 | 1 (3) |  | 1 (4) | 7 (25) | 2 (7) | 7 (25) |
| BCIN08 |  |  | 1 (1) | 1 (1) | 1 (1) | 1 (1) |
| BCIN09 |  |  |  | 3 (10) |  | 3 (10) |
| BCIN10 |  |  |  | 2 (4) |  | 2 (4) |
| BCIN11 |  |  | 1 (0) | 3 (5) | 1 (0) | 3 (5) |
| BCIN12 |  |  | 2 (7) |  | 2 (7) |  |
| BCIN13 |  |  |  |  |  |  |
| BCIN14 |  |  | 5 (8) | 2 (1) | 5 (8) | 2 (1) |
| BCIN15 |  | 2 (7) | 7 (24) | 3 (11) | 7 (24) | 5 (17) |
| BCIN16 |  | 1 (3) | 4 (11) | 1 (4) | 7 (24) | 4 (11) |
| Total | 4 (15) | 5 (21) | 48(142) | 54(169) | 48 (140) | 59 (188) |