

SUPPLEMENTARY TABLES

Please browse Full Text version to see the data of Supplementary Table 1.

Supplementary Table 1. Number of SNPs residing in regions common between the original GWAS-based networks. Genes with ‘long-lived’ phenotype are shown in bold.

Supplementary Table 2. Selected subnetworks centered around novel nodes with the highest degree in the extended Synthetic and DGRP GWAS-based networks.

| Novel node | Network | All other nodes in subnetwork | Degree | Total number of genes |
|------------|-----------|--|--------|-----------------------|
| 1220 | Synthetic | 244, 245, 255, 262, 270, 271, 272, 273, 275, 276, 277, 295, 302, 305, 334, 359, 799, 848, 920, 923 | 20 | 188 |
| 928 | Synthetic | 11, 233, 234, 238, 265, 343, 360, 361, 366, 370, 409, 456, 536, 531, 545 | 15 | 290 |
| 28 | DGRP | 27, 29, 30, 1063, 1124, 1152, 1179 | 7 | 114 |
| 2 | DGRP | 576, 655, 660, 670, 699, 736, 787, 1120, 1131, 1132, 1152, 1178, 1179, 1183 | 14 | 255 |

Please browse Full Text version to see the data of Supplementary Tables 3 and 4.

Supplementary Table 3. Nodes and interactions comprising each cluster of the extended Synthetic GWAS-based networks.

Supplementary Table 4. Nodes and interactions comprising each cluster of the extended DGRP GWAS-based networks.

Supplementary Table 5. List of nodes constituting selected clusters in the Synthetic GWAS-based network.

| Cluster | Nodes in cluster | Total number of | |
|---------|--|------------------|------------------|
| | | nodes in cluster | genes in cluster |
| 4 | 89, 90, 91, 92, 93, 94, 95, 97, 1319 | 9 | 92 |
| 5 | 124, 125, 126, 127, 128, 129, 130, 131, 711, 740, 929 | 11 | 229 |
| 11 | 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 578, 916, 930, 982, 1049, 1431, 1436 | 21 | 249 |
| 23 | 330, 331, 332, 333, 334, 335, 336, 337, 749 | 9 | 141 |
| 29 | 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 961, 1044, 1338 | 14 | 222 |
| 60 | 313, 385, 476, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 1218 | 14 | 174 |
| 67 | 502, 1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1386 | 11 | 150 |

Supplementary Table 6. List of nodes constituting selected clusters in the DGRP GWAS-based network.

| Cluster | Nodes in cluster | Total number of | |
|---------|---|------------------|------------------|
| | | nodes in cluster | genes in cluster |
| 4 | 53, 54, 55, 56, 57, 58, 59, 60, 61, 1078, 1079, 1338 | 12 | 125 |
| 18 | 523, 524, 525, 526, 527, 528, 529, 530, 531, 560, 1253 | 11 | 155 |
| 20 | 105, 478, 521, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 1227 | 14 | 256 |
| 26 | 321, 329, 412, 445, 499, 658, 659, 660, 661, 662, 663, 1324, 1367, 1418 | 14 | 223 |
| 28 | 330, 344, 366, 413, 669, 670, 671, 672, 673, 1419 | 10 | 177 |
| 34 | 318, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785 | 11 | 103 |
| 40 | 103, 426, 458, 983, 985, 986, 987, 988, 989, 990, 991, 992, 1210, 1336 | 14 | 156 |
| 44 | 361, 429, 448, 1089, 1090, 1091, 1092, 1093, 1094, 1095 | 10 | 156 |
| 49 | 63, 457, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155 | 11 | 142 |

Please browse Full Text version to see the data of Supplementary Table 7.

Supplementary Table 7. Genes sharing ‘long-lived’ and ‘short-lived’ phenotypes found in close proximity to mutated and non-mutated TAD border regions.

Supplementary Table 8. Top 30 long-range interacting regions for non-coding SNPs from the Synthetic GWAS dataset.

| Bin number | Non-coding SNP region | | Interacting region | | |
|------------|-----------------------|--------------------------------|---------------------------|---------------|------------------------|
| | Number of SNPs in bin | Highest recorded SNP's D-value | Strongest interacting bin | Distance (Kb) | Number of genes in bin |
| 2367 | 3 | 2.727 | 2362 | 50 | 2 |
| 3982 | 7 | 5.421 | 3987 | 50 | 16 |
| 5470 | 9 | 5.765 | 5465 | 50 | 13 |
| 2459 | 4 | 5.170 | 2463 | 40 | 6 |
| 4370 | 12 | 7.189 | 4366 | 40 | 10 |
| 4560 | 4 | 3.814 | 4566 | 40 | 10 |
| 5656 | 9 | 6.284 | 5660 | 40 | 16 |
| 11643 | 2 | 5.029 | 11647 | 40 | 6 |
| 1605 | 7 | 7.657 | 1608 | 30 | 9 |
| 2006 | 3 | 12.009 | 2003 | 30 | 7 |
| 2461 | 1 | 4.592 | 2464 | 30 | 6 |
| 3146 | 13 | 3.468 | 3149 | 30 | 13 |
| 3447 | 1 | 2.160 | 3444 | 30 | 10 |
| 4837 | 8 | 6.213 | 4840 | 30 | 15 |
| 5702 | 1 | 3.582 | 5705 | 30 | 8 |
| 6981 | 6 | 4.577 | 6978 | 30 | 4 |
| 7819 | 4 | 3.189 | 7816 | 30 | 6 |
| 7883 | 6 | 5.029 | 7886 | 30 | 11 |
| 7884 | 4 | 5.989 | 7887 | 30 | 12 |
| 8958 | 11 | 4.396 | 8995 | 30 | 11 |
| 155 | 14 | 7.658 | 153 | 20 | 6 |
| 229 | 7 | 7.550 | 227 | 20 | 10 |
| 324 | 3 | 5.987 | 326 | 20 | 15 |
| 556 | 11 | 6.606 | 554 | 20 | 10 |
| 592 | 1 | 2.066 | 590 | 20 | 12 |
| 945 | 6 | 4.168 | 943 | 20 | 10 |
| 994 | 5 | 5.459 | 996 | 20 | 3 |
| 1167 | 10 | 6.455 | 1165 | 20 | 13 |
| 1173 | 7 | 6.222 | 1171 | 20 | 10 |
| 1174 | 11 | 5.694 | 1176 | 20 | 9 |

Supplementary Table 9. Top 30 long-range interacting regions for non-coding SNPs from the DGRP GWAS dataset.

| Non-coding SNP region | | | Interacting region | | |
|-----------------------|-------------------|-----------------------------|---------------------------|---------------|----------------|
| Bin number | Number of SNPs in | Lowest recorded SNP P-value | Strongest interacting bin | Distance (Kb) | Number of SNPs |
| 2388 | 8 | 0.3858 | 2378 | 100 | 168 |
| 3644 | 26 | 0.1303 | 3637 | 70 | 190 |
| 2458 | 34 | 0.06431 | 2464 | 60 | 171 |
| 2367 | 53 | 0.05865 | 2362 | 50 | 74 |
| 2957 | 16 | 0.06397 | 2962 | 50 | 228 |
| 3982 | 256 | 0.007077 | 3987 | 50 | 205 |
| 5470 | 280 | 0.003503 | 5465 | 50 | 420 |
| 2457 | 28 | 0.08089 | 2453 | 40 | 81 |
| 2459 | 73 | 0.5731 | 2463 | 40 | 120 |
| 4370 | 297 | 0.008632 | 4366 | 40 | 192 |
| 4560 | 88 | 0.02264 | 4566 | 40 | 280 |
| 5656 | 222 | 0.002052 | 5660 | 40 | 307 |
| 11643 | 51 | 0.05711 | 11647 | 40 | 138 |
| 1605 | 95 | 0.0236 | 1608 | 30 | 230 |
| 2006 | 64 | 0.01037 | 2003 | 30 | 153 |
| 2124 | 14 | 0.0354 | 2121 | 30 | 22 |
| 2283 | 17 | 0.1617 | 2286 | 30 | 62 |
| 2372 | 68 | 0.01846 | 2375 | 30 | 128 |
| 2456 | 44 | 0.01432 | 2453 | 30 | 81 |
| 2461 | 32 | 0.04341 | 2464 | 30 | 171 |
| 3146 | 377 | 0.006937 | 3149 | 30 | 295 |
| 3447 | 44 | 0.13 | 3444 | 30 | 285 |
| 4837 | 181 | 0.007141 | 4840 | 30 | 359 |
| 5702 | 27 | 0.01703 | 5705 | 30 | 322 |
| 6981 | 87 | 0.00301 | 6978 | 30 | 83 |
| 7639 | 11 | 0.09939 | 7636 | 30 | 126 |
| 7819 | 238 | 0.001871 | 7816 | 30 | 203 |
| 7883 | 108 | 0.007967 | 7886 | 30 | 234 |
| 7884 | 120 | 0.006706 | 7887 | 30 | 255 |
| 8958 | 222 | 0.001062 | 8955 | 30 | 197 |

Please browse Full Text version to see the data of Supplementary Table 10.

Supplementary Table 10. Chromosome, start and end positions for each 80 Kb bin.