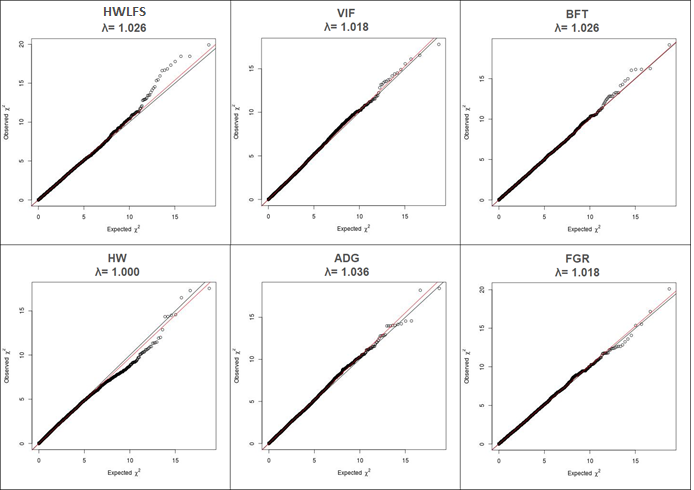
**Animal Journal**

**SUPPLEMENTARY MATERIAL**

**Genome wide association studies for seven production traits highlight genomic regions useful to dissect dry-cured ham quality and production traits in Duroc heavy pigs**

F. Bertolini,G. Schiavo, G. Galimberti, S. Bovo, M. D’Andrea,M. Gallo, L. Buttazzoni, M.F. Rothschild and L. Fontanesi



**Supplementary Figure S1** Q-Q plot calculated for each trait based on the P-value of the LMM analyses. The Q-Q plot and λ was calculated using the GenABEL software. Reference: Aulchenko YS, Ripke S, Isaacs A and van Duijn CM 2007. GenABEL: an R library for genome-wide association analysis. Bioinformatics 23, 1294-1296.

-HWLFS: ham weight loss at first salting

-VIF: visible intermuscular fat.

-BFT: backfat thickness.

-LC: lean cuts.

-HW: ham weight.

-ADG: average daily gain.

-FGR: feed:gain ratio

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Trait1 | SSC2 | Start | End | %Var | Confirmed by LMM |
| HWLFS | 2 | 15066021 | 15835538 | 1.22 | yes |
| HWLFS | 4 | 111011157 | 111985089 | 1.07 | yes |
| HWLFS | 6 | 151133883 | 151994661 | 3.05 | yes |
| HWLFS | 6 | 152000131 | 152878666 | 1.25 | yes |
| HWLFS | 7 | 93046623 | 93833065 | 2.02 | yes |
| HWLFS | 8 | 8020739 | 8831159 | 2.16 | yes |
| HWLFS | 12 | 18033035 | 18936672 | 3.73 | yes |
| VIF | 1 | 257046702 | 257928835 | 2.09 | yes |
| VIF | 1 | 270022511 | 270988558 | 2.02 | yes |
| VIF | 7 | 99138052 | 99997199 | 1.13 | - |
| VIF | 8 | 76008830 | 76967953 | 1 | yes |
| BFT | 1 | 2046775 | 2945015 | 1.86 | yes |
| BFT | 1 | 263022859 | 263779844 | 1.32 | yes |
| BFT | 6 | 145259351 | 145924094 | 1.37 | yes |
| BFT | 7 | 26002978 | 26976864 | 2.64 | yes |
| BFT | 9 | 111038153 | 111867248 | 1.43 | yes |
| LC | 10a | 44039931 | 44782433 | 2.74 | yes |
| LC | 18 | 10028924 | 10960969 | 1.89 | yes |
| LC | 18 | 45016156 | 45986389 | 1.07 | yes |
| LC | 18 | 48008832 | 48983680 | 2.03 | yes |
| HW | 10a | 44039931 | 44782433 | 2.33 | yes |
| HW | 11 | 75034203 | 75987785 | 1.85 | yes |
| HW | 12 | 7048858 | 7980955 | 1.31 | - |
| HW | 13 | 13035722 | 13969030 | 1.86 | yes |
| HW | 17 | 41036359 | 41992643 | 2.01 | yes |
| ADG | 2 | 96004482 | 96841354 | 1 | yes |
| ADG | 2 | 97221307 | 97953667 | 2.01 | - |
| ADG | 9 | 23096976 | 23975239 | 3.53 | yes |
| FGR | 16 | 20015065 | 20891745 | 1.24 | yes |
| FGR | 17 | 60015229 | 60981380 | 1.54 | yes |

1 HWLFS, ham weight loss at first salting; VIF, visible intermuscular fat; BFT, backfat thickness; LC, lean cuts; HW, ham weight; ADG, average daily gain; FGR, feed:gain ratio.

2 *Sus scrofa* chromosome.

**Supplementary Table S1** 1 Mb windows with percentage of the explained variance above or equal to 1% as result of Bayesian analyses for the 7 production traits. Windows that overlap at least one significant or suggestive single nucleotide polymorphism (SNP) derived from Linear Mixed Model (LMM) analysis are reported with “yes” in the “confirmed by LMM” column, while windows that do not overlap with any SNP will have the “-“ symbol in the “confirmed by LMM” column. Overlapping windows on chromosome 10 are reported with the “a” symbol in the chromosome (SSC) column.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Trait1 | SSC2 | SNP | Position | P value |
| HWLFS | 6 | ALGA0117611\* | 151867098 | 8.04E-06 |
| HWLFS | 8 | MARC0054934\* | 8757524 | 1.74E-05 |
| HWLFS | 8 | MARC0013261\* | 8771074 | 1.74E-05 |
| HWLFS | 12 | H3GA0033784\* | 18936672 | 2.47E-05 |
| HWLFS | 1 | DRGA0002473 | 263022859 | 3.15E-05 |
| HWLFS | 6 | MARC0021483\* | 152557005 | 4.06E-05 |
| HWLFS | 3 | H3GA0055945 | 19041757 | 4.45E-05 |
| HWLFS | 1 | ALGA0105013 | 262939016 | 4.57E-05 |
| HWLFS | 7 | ALGA0043776\* | 93276177 | 6.56E-05 |
| HWLFS | 1 | ALGA0006684 | 161853405 | 8.46E-05 |
| HWLFS | 1 | MARC0013872 | 161824864 | 9.01E-05 |
| HWLFS | 4 | ASGA0022210\* | 111821325 | 1.37E-04 |
| HWLFS | 1 | ASGA0004958 | 158260371 | 1.50E-04 |
| HWLFS | 7 | ASGA0035365\* | 93237554 | 1.72E-04 |
| HWLFS | 2 | MARC0063245\* | 15224720 | 2.01E-04 |
| HWLFS | 2 | MARC0099191\* | 15835538 | 2.40E-04 |
| HWLFS | 1 | ASGA0004963 | 158309021 | 2.46E-04 |
| HWLFS | 7 | ALGA0044119 | 100503197 | 2.49E-04 |
| HWLFS | 15 | H3GA0054084 | 31862002 | 2.95E-04 |
| HWLFS | 1 | INRA0004738 | 152100725 | 3.15E-04 |
| HWLFS | 12 | ASGA0053674 | 19181513 | 3.24E-04 |
| HWLFS | 6 | ALGA0124113\* | 152878666 | 3.28E-04 |
| HWLFS | 5 | ASGA0026057 | 66998856 | 3.38E-04 |
| HWLFS | 13 | ALGA0121680 | 146977 | 3.50E-04 |
| VIF | 1 | ASGA0008074\* | 270988558 | 2.47E-05 |
| VIF | 1 | ASGA0007129\* | 257101738 | 4.77E-05 |
| VIF | 6 | M1GA0008349 | 13923215 | 6.00E-05 |
| VIF | 1 | ASGA0008077\* | 270968825 | 8.01E-05 |
| VIF | 12 | DIAS0000407 | 22592702 | 1.13E-04 |
| VIF | 15 | MARC0013047 | 123697985 | 1.40E-04 |
| VIF | 7 | ASGA0031713 | 19919597 | 1.48E-04 |
| VIF | 14 | H3GA0043283 | 137171897 | 1.67E-04 |
| VIF | 8 | ALGA0112521 | 6212836 | 2.07E-04 |
| VIF | 8 | MARC0064781\* | 76967953 | 2.14E-04 |
| VIF | 6 | ASGA0029999 | 156110427 | 2.32E-04 |
| VIF | 7 | ALGA0037893 | 2662798 | 2.36E-04 |
| VIF | 6 | MARC0041561 | 16171435 | 2.54E-04 |
| VIF | 1 | DIAS0000076\* | 257210273 | 2.84E-04 |
| VIF | 1 | ASGA0007120\* | 257238787 | 2.84E-04 |
| VIF | 1 | INRA0007300 | 256776594 | 3.45E-04 |
| VIF | 13 | H3GA0055948 | 195708784 | 4.69E-04 |
| BFT | 7 | DRGA0007413\* | 26015939 | 1.19E-05 |
| BFT | 6 | ASGA0029653\* | 145259351 | 5.52E-05 |
| BFT | 9 | ASGA0044321\* | 111623821 | 5.83E-05 |
| BFT | 6 | H3GA0055786 | 146300263 | 5.86E-05 |
| BFT | 6 | ALGA0006224 | 147865580 | 6.19E-05 |
| BFT | 13 | ALGA0071902 | 125053681 | 1.08E-04 |
| BFT | 1 | ALGA0000289\* | 2887205 | 1.24E-04 |
| BFT | 4 | H3GA0012376 | 24186305 | 1.56E-04 |
| BFT | 1 | CASI0009856\* | 263049530 | 1.69E-04 |
| BFT | 9 | MARC0087389 | 112595728 | 2.70E-04 |
| BFT | 1 | ALGA0000120\* | 2272319 | 2.70E-04 |
| BFT | 16 | H3GA0046863 | 62204054 | 2.71E-04 |
| BFT | 1 | ALGA0000269\* | 2760415 | 2.94E-04 |
| BFT | 14 | H3GA0043283 | 137171897 | 3.39E-04 |
| BFT | 1 | H3GA0000320\* | 2785472 | 3.41E-04 |
| BFT | 1 | ALGA0000277\* | 2808072 | 3.41E-04 |
| BFT | 1 | ASGA0000364\* | 2831639 | 3.41E-04 |
| BFT | 7 | DRGA0007409 | 25901719 | 3.67E-04 |
| BFT | 14 | ASGA0067656 | 134977388 | 4.02E-04 |
| BFT | 2 | ALGA0013687 | 47326959 | 4.25E-04 |
| BFT | 6 | MARC0055650 | 168916590 | 4.69E-04 |
| LC | 18 | ASGA0080213\* | 48033491 | 2.91E-05 |
| LC | 18 | M1GA0023322\* | 48043433 | 2.91E-05 |
| LC | 18 | MARC0044039\* | 10555467 | 4.40E-05 |
| LC | 18 | ASGA0080217\* | 48067511 | 4.44E-05 |
| LC | 10 | ALGA0058903\* | 44743742 | 4.64E-05 |
| LC | 18 | ALGA0097688 | 26783189 | 1.59E-04 |
| LC | 8 | MARC0069337 | 74705127 | 1.71E-04 |
| LC | 8 | DIAS0001641 | 121231465 | 2.27E-04 |
| LC | 8 | MARC0003622 | 74560552 | 2.73E-04 |
| LC | 7 | H3GA0022882 | 108291529 | 2.99E-04 |
| LC | 1 | ASGA0002001 | 30148658 | 3.03E-04 |
| LC | 8 | ALGA0049450 | 120834247 | 3.12E-04 |
| LC | 10 | H3GA0030106 | 42729848 | 3.15E-04 |
| LC | 13 | ALGA0073973 | 203909045 | 3.81E-04 |
| LC | 13 | ASGA0056369 | 15386736 | 3.90E-04 |
| LC | 18 | ASGA0080089\* | 45727257 | 4.03E-04 |
| LC | 13 | ALGA0068433 | 15311477 | 4.21E-04 |
| LC | 8 | H3GA0024981 | 73962803 | 4.42E-04 |
| HW | 10 | ALGA0058903\* | 44743742 | 2.81E-05 |
| HW | 13 | ALGA0068184\* | 13388502 | 3.19E-05 |
| HW | 13 | MARC0069806\* | 13543085 | 4.89E-05 |
| HW | 17 | H3GA0049027\* | 41643251 | 1.35E-04 |
| HW | 11 | ASGA0052117\* | 75489668 | 1.40E-04 |
| HW | 17 | MARC0017435 | 6400877 | 1.51E-04 |
| HW | 13 | ALGA0068433 | 15311477 | 1.52E-04 |
| HW | 16 | H3GA0046545 | 41391450 | 3.33E-04 |
| ADG | 9 | ASGA0042095\* | 23333819 | 1.77E-05 |
| ADG | 9 | ALGA0051922\* | 23407515 | 1.98E-05 |
| ADG | 4 | ALGA0022712 | 7452366 | 1.36E-04 |
| ADG | 9 | DIAS0000868\* | 23147664 | 1.37E-04 |
| ADG | 17 | MARC0017435 | 6400877 | 1.63E-04 |
| ADG | 7 | ALGA0045559 | 120400325 | 1.69E-04 |
| ADG | 2 | ALGA0107007\* | 96469067 | 1.81E-04 |
| ADG | 2 | ASGA0010962\* | 96507329 | 1.81E-04 |
| ADG | 4 | MARC0047995 | 122002980 | 1.85E-04 |
| ADG | 6 | ALGA0034548 | 11881996 | 1.86E-04 |
| ADG | 9 | ALGA0051902\* | 23273419 | 1.86E-04 |
| ADG | 2 | H3GA0007211\* | 96652512 | 3.26E-04 |
| ADG | 4 | MARC0018660 | 6448473 | 3.39E-04 |
| ADG | 1 | MARC0013872 | 161824864 | 3.41E-04 |
| ADG | 2 | MARC0046666\* | 96622232 | 3.50E-04 |
| ADG | 2 | ALGA0014545\* | 96768653 | 3.50E-04 |
| ADG | 5 | ASGA0023920 | 6912871 | 4.08E-04 |
| ADG | 2 | MARC0015434 | 20157764 | 4.61E-04 |
| FGR | 14 | ALGA0074334 | 2575346 | 7.35E-06 |
| FGR | 16 | MARC0092324\* | 20220576 | 3.43E-05 |
| FGR | 17 | ALGA0096693\* | 60906867 | 8.14E-05 |
| FGR | 4 | MARC0047995 | 122002980 | 8.91E-05 |
| FGR | 1 | ASGA0002046 | 30816637 | 1.76E-04 |
| FGR | 6 | ALGA0034548 | 11881996 | 2.26E-04 |
| FGR | 1 | H3GA0001332 | 30782016 | 2.74E-04 |
| FGR | 17 | ALGA0096707 | 61039463 | 3.39E-04 |
| FGR | 17 | ASGA0078573 | 61837133 | 3.75E-04 |
| FGR | 17 | INRA0055080 | 61937591 | 3.75E-04 |
| FGR | 9 | ASGA0042095 | 23333819 | 3.85E-04 |
| FGR | 2 | MARC0015434 | 20157764 | 4.10E-04 |
| FGR | 17 | H3GA0050166\* | 60946245 | 4.32E-04 |
| FGR | 4 | ASGA0017873 | 7875059 | 4.34E-04 |
| FGR | 5 | ASGA0023920 | 6912871 | 4.39E-04 |
| FGR | 2 | ALGA0107007 | 96469067 | 4.82E-04 |
| FGR | 2 | ASGA0010962 | 96507329 | 4.82E-04 |

1 HWLFS, ham weight loss at first salting; VIF, visible intermuscular fat; BFT, back fat thickness; LC, lean cuts; HW, ham weight; ADG, average daily gain; FGR, feed:gain ratio.

2 *Sus scrofa* chromosome.

**Supplementary Table S2** LMM results for the seven production traits considered. SNPs with significant (P<5e05) or suggestive (P<5e04) associations are reported. SNPs that are contained in one of the 1Mb window Bayesian analyses are reported with the “\*” symbol next to the probe.

**See EXCEL file**

**Supplementary Table S3** Genes within identified windows from the Bayesian analyses for the seven analyzed traits. Single nucleotide polymorphisms (SNP) from Linear Mixed Model (LMM) were placed next to the closest genes and distance in kb is reported within brackets.