

1 **Signatures of selection analyses reveal genomic differences among three heavy pig**
2 **breeds that constitute the genetic backbone of a dry-cured ham production system**

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12 **Supplementary data**

13 **All Excel tables are accessible through Zenodo link [10.5281/zenodo.11204407](https://doi.org/10.5281/zenodo.11204407).**

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15 **Supplementary Table S1.** ROH islands detected in the genome of Italian Duroc (ID),
16 Italian Landrace (IL) and Italian Large White (ILW) pig breeds. The table includes the
17 breed, chromosomes (SSC), positions of the signatures of selection regions identified at
18 the 99th and 99.5th percentile thresholds (start, end and length), as well as, for the 99.5th
19 regions, genes detected in NCBI (www.ncbi.nlm.nih.gov) and ENSEMBL
20 (www.ensembl.org) databases for Sscrofa11.1 genome version.

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22 **Supplementary Table S2.** iHS regions detected for the Italian Duroc (ID), Italian Landrace
23 (IL) and Italian Large White (ILW) pig breeds. The table includes the breed, chromosomes
24 (SSC), positions of the signatures of selection regions identified at the 99th and 99.5th

25 percentile thresholds (start, end and length), as well as, for the 99.5th regions, genes
26 detected in NCBI (www.ncbi.nlm.nih.gov) and ENSEMBL (www.ensembl.org) databases
27 for Sscrofa11.1 genome version.

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29 **Supplementary Table S3.** F_{ST} regions detected for the pairwise comparisons between pig
30 breeds. The table includes the breed pairwise comparison, chromosomes (SSC), positions
31 of the signatures of selection regions identified at the 99th and 99.5th percentile thresholds
32 (start, end and length), as well as, for the 99.5th regions, genes detected in NCBI
33 (www.ncbi.nlm.nih.gov) and ENSEMBL (www.ensembl.org) databases for Sscrofa11.1
34 genome version.

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36 **Supplementary Table S4.** XP-EHH regions detected for pairwise comparisons between
37 pig breeds. The table includes the breed pairwise comparison, chromosomes (SSC),
38 positions of the signatures of selection identified at the 99th and 99.5th percentile
39 thresholds (start, end and length), as well as, for the 99.5th regions, genes detected in
40 NCBI (www.ncbi.nlm.nih.gov) and ENSEMBL (www.ensembl.org) databases for
41 Sscrofa11.1 genome version.

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43 **Supplementary Table S5.** Overlapping between the signature of selection regions
44 detected in the three Italian pig breeds with signals detected in two previous studies
45 involving the same breeds.

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47 **Supplementary Table S6.** Overlapping between the signature of selection regions
48 detected in the three Italian pig breeds and the QTL detected by previous GWAS
49 investigations in Italian Duroc and Italian Large White.

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52 **Supplementary Table S7.** Complete enrichment tables for the different analyses of
53 signatures of selection analyses within pig breeds and across pig breeds.