# Additional file 2

## List of Figures

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**Table S1: Overview of sequenced samples included in the study**
Abbreviations: NL: the Netherlands; LF: Large fowl; NB: neo-bantam; B: true bantam

| Breed name | No. individual | Management | Origin |
|---|---|---|---|
| Assendelft Fowl | 3 | LF | NL |
| Assendelft Fowl Bantam | 2 | NB | NL |
| Barnevelder | 4 | LF | NL |
| Barnevelder Bantam | 3 | NB | NL |
| Brabanter | 3 | LF | NL |
| Brabanter Bantam | 3 | NB | NL |
| Breda Fowl | 3 | LF | NL |
| Breda Fowl Bantam | 3 | NB | NL |
| Chaam Fowl | 2 | LF | NL |
| Creeper | 2 | LF | NL |
| Drenthe Fowl | 1 | LF | NL |
| Drenthe Fowl Bantam | 1 | NB | NL |
| Drenthe Fowl Bolstaat | 2 | LF | NL |
| Dutch Bantam | 3 | B | NL |
| Dutch Booted Bantam | 1 | B | NL |
| Dutch Fowl | 4 | LF | NL |
| Dutch Fowl Bantam | 2 | NB | NL |
| Dutch Owl Bearded | 3 | LF | NL |
| Dutch Owl Bearded Bantam | 3 | NB | NL |
| Dutch Polish Bearded | 2 | LF | NL |
| Dutch Polish Bearded Bantam | 2 | NB | NL |
| Dutch Polish non Bearded | 2 | LF | NL |
| Dutch Polish non Bearded Bantam | 2 | NB | NL |
| Eikenburger Bantam | 2 | B | NL |
| Frisian Fowl | 4 | LF | NL |
| Frisian Fowl Bantam | 2 | NB | NL |
| Gallugs sonneratii | 1 | LF | ? |
| Gallus gallus | 1 | LF | ? |
| Gallus lafayetii | 1 | LF | ? |
| Gallus varius | 1 | LF | ? |
| Groninger Mew | 4 | LF | NL |
| Groninger Mew Bantam | 4 | NB | NL |
| Java | 1 | B | NL |
| Kraienkoppe | 3 | LF | NL |
| Kraienkoppe Fowl Bantam | 3 | NB | NL |
| Lakenvelder | 3 | LF | NL |
| Lakenvelder Bantam | 3 | NB | NL |
| North Holland Blue | 1 | LF | NL |
| North Holland Blue Bantam | 1 | NB | NL |
| Schijndelaar | 1 | LF | NL |
| Schijndelaar Bantam | 1 | NB | NL |
| Welsummer | 4 | LF | NL |
| Welsummer bantam | 4 | NB | NL |

**Table S2: Summary of variants and indels kept after variant calling and post-filtering**
The fifth column shows the average number of variants in bins of 10 Kb, the sixth column the total number of transitions, the seventh the total number of transversion, and the last column the average transition to transvertion ratio

| Chrom | # records | # SNPs | # Indels | Var/10 Kb | Ts | Tv | Ts/Tv |
|---|---|---|---|---|---|---|---|
| 1 | 3877122 | 3551646 | 257622 | 19.76 | 2445981 | 1066838 | 2.29 |
| 2 | 2956232 | 2704405 | 200314 | 19.76 | 1862453 | 813223 | 2.29 |
| 3 | 2198459 | 2006472 | 153563 | 19.75 | 1390239 | 593274 | 2.34 |
| 4 | 1788716 | 1628925 | 128255 | 19.59 | 1130606 | 478874 | 2.36 |
| 5 | 1188298 | 1082810 | 84449 | 19.86 | 758333 | 311177 | 2.44 |
| 6 | 793498 | 728334 | 51273 | 22.69 | 504249 | 216418 | 2.33 |
| 7 | 748910 | 684870 | 51251 | 20.27 | 481039 | 196259 | 2.45 |
| 8 | 562037 | 514773 | 38119 | 18.75 | 364158 | 144468 | 2.52 |
| 9 | 513764 | 471603 | 33553 | 21.77 | 333464 | 132935 | 2.51 |
| 10 | 413767 | 379651 | 27350 | 20.75 | 271128 | 104380 | 2.60 |
| 11 | 359527 | 328316 | 25389 | 17.78 | 233449 | 91080 | 2.56 |
| 12 | 425025 | 389956 | 28005 | 21.31 | 278949 | 106399 | 2.62 |
| 13 | 369740 | 340674 | 22678 | 20.65 | 242232 | 94321 | 2.57 |
| 14 | 317877 | 291637 | 20488 | 20.37 | 210130 | 77715 | 2.70 |
| 15 | 238505 | 219014 | 15522 | 18.67 | 158287 | 57784 | 2.74 |
| 16 | 13984 | 13067 | 547 | 21.18 | 8661 | 4225 | 2.05 |
| 17 | 211597 | 195634 | 12466 | 20.22 | 142572 | 50581 | 2.82 |
| 18 | 224726 | 207088 | 13551 | 20.31 | 149000 | 55790 | 2.67 |
| 19 | 192302 | 177608 | 11523 | 19.26 | 129562 | 46006 | 2.82 |
| 20 | 281958 | 260172 | 17095 | 19.99 | 187485 | 69555 | 2.70 |
| 21 | 140593 | 129769 | 8432 | 20.49 | 94308 | 33809 | 2.79 |
| 22 | 67960 | 62277 | 4300 | 14.36 | 44396 | 16811 | 2.64 |
| 23 | 122947 | 113664 | 7112 | 21.23 | 83003 | 28835 | 2.88 |
| 24 | 133926 | 124455 | 7314 | 21.32 | 91619 | 31403 | 2.92 |
| 25 | 51268 | 46927 | 3196 | 17.61 | 33596 | 12340 | 2.72 |
| 26 | 115278 | 106660 | 6569 | 21.66 | 78615 | 26572 | 2.96 |
| 27 | 125699 | 115853 | 6943 | 22.24 | 79455 | 34491 | 2.30 |
| 28 | 107433 | 98251 | 6999 | 21.57 | 71153 | 25427 | 2.80 |
| 30 | 316 | 247 | 57 | 10.53 | 167 | 73 | 2.29 |
| 31 | 718 | 687 | 7 | 14.36 | 407 | 272 | 1.50 |
| 32 | 1327 | 1164 | 126 | 16.58 | 889 | 243 | 3.66 |
| 33 | 32602 | 29107 | 2735 | 19.75 | 20883 | 7532 | 2.77 |
| **Total** | **18576111** | **17005716** | **1246803** | **19.96** | **11880468** | **4929110** | **2.58** |

### Table S3: Functional annotation of variants

The table reports for each functional class the total number of variants with most severe consequences identified in the 59 highly covered samples for which the ancestral and derived state of a variant was inferred

| **Consequences of variant** | **Total number** |
|---|---|
| Splice donor | 846 |
| Splice acceptor | 658 |
| Stop gained | 536 |
| Frameshift | 1469 |
| Stop lost | 123 |
| Start lost | 270 |
| Inframe insertion | 528 |
| Inframe deletion | 558 |
| Protein altering variant | 41 |
| Missense variant | 66599 |
| Splice region | 33569 |
| Synonymous variant | 154855 |
| Stop retained | 77 |
| Mature miRNA | 266 |
| 5'UTR | 24091 |
| 3'UTR | 128003 |
| Intron variant | 8831024 |
| Non coding transcript | 1 |
| Upstream gene | 1269188 |
| Downstream gene | 927319 |
| Intergenic | 7800108 |
| **Sum (LoF)** | 4988 |
| **Sum(protein-coding)** | 226442 |
| **Sum (all)** | 19240129 |

### Table S4: SIFT classification

The table reports the total number of missense variants classified by SIFT as deleterious and tolerated

| **SIFT** | **Total number** |
|---|---|
| deleterious - low confidence | 4519 |
| tolerated - low confidence | 10205 |
| deleterious | 12266 |
| tolerated | 61202 |

**Table S5: Overview of samples used in SMC++**

The table reports the individuals used to infer past effective population size and demographic history. Management is the group the sample belongs to and coverage is the average genome-wide coverage calculated after mapping. The percentage of missing sites was calculated on the filtered vcf files. Abbreviations: LF, large fowl; NB, neo-bantam; B, true bantam

| Sample ID | Breed name | Management | Coverage | Fraction missing sites |
|---|---|---|---|---|
| ADIV00007 | Groninger Mew | LF | 15.398 | 4.175 |
| ADIV00010 | Groninger Mew | LF | 12.451 | 6.634 |
| ADIV00022 | Groninger Mew | LF | 15.962 | 4.125 |
| ADIV00025 | Groninger Mew Bantam | NB | 14.655 | 4.237 |
| ADIV00031 | Groninger Mew Bantam | NB | 16.425 | 4.091 |
| ADIV00040 | Groninger Mew Bantam | NB | 14.613 | 4.251 |
| ADIV00048 | Lakenvelder | LF | 15.699 | 4.113 |
| ADIV00050 | Lakenvelder | LF | 14.139 | 4.254 |
| ADIV00052 | Lakenvelder | LF | 15.685 | 4.150 |
| ADIV00055 | Lakenvelder Bantam | NB | 14.032 | 4.213 |
| ADIV00056 | Lakenvelder Bantam | NB | 16.571 | 4.035 |
| ADIV00058 | Lakenvelder Bantam | NB | 18.061 | 4.031 |
| ADIV00095 | Frisian Fowl | LF | 17.250 | 4.017 |
| ADIV00097 | Frisian Fowl | LF | 16.211 | 4.109 |
| ADIV00100 | Frisian Fowl | LF | 15.770 | 4.071 |
| ADIV00127 | Dutch Fowl Bantam | NB | 15.415 | 4.200 |
| ADIV00128 | Dutch Fowl Bantam | NB | 18.426 | 4.051 |
| ADIV00130 | Dutch Polish Bearded | LF | 15.802 | 4.067 |
| ADIV00131 | Dutch Polish Bearded | LF | 15.842 | 4.129 |
| ADIV00147 | Dutch Owl Bearded | LF | 17.091 | 4.040 |
| ADIV00151 | Dutch Owl Bearded | LF | 17.136 | 4.030 |
| ADIV00165 | Dutch Owl Bearded Bantam | NB | 18.361 | 3.986 |
| ADIV00170 | Dutch Owl Bearded Bantam | NB | 15.869 | 5.252 |
| ADIV00189 | Dutch Polish non Bearded Bantam | NB | 33.530 | 3.934 |
| ADIV00190 | Dutch Polish non Bearded Bantam | NB | 16.136 | 4.051 |
| ADIV00203 | Kraienkoppe | LF | 17.009 | 4.048 |
| ADIV00209 | Kraienkoppe | LF | 16.479 | 4.079 |
| ADIV00317 | Barnevelder | LF | 24.184 | 3.967 |
| ADIV00322 | Barnevelder | LF | 28.533 | 3.983 |
| ADIV00334 | Barnevelder | LF | 16.423 | 4.155 |
| ADIV00346 | Barnevelder Bantam | NB | 16.031 | 4.317 |
| ADIV00348 | Barnevelder Bantam | NB | 17.455 | 4.119 |
| ADIV00351 | Welsummer | LF | 11.247 | 8.099 |
| ADIV00352 | Welsummer | LF | 12.222 | 4.451 |
| ADIV00356 | Welsummer | LF | 15.606 | 4.203 |
| ADIV00384 | Breda Fowl | LF | 16.303 | 4.128 |
| ADIV00389 | Breda Fowl | LF | 19.623 | 4.206 |
| ADIV00406 | Chaam Fowl | LF | 25.303 | 3.892 |
| ADIV00408 | Chaam Fowl | LF | 13.620 | 4.230 |

**Figure S1: Principal Component Analysis (PCA)**. The principal component analysis was performed on 95 samples from 39 traditional Dutch chicken breeds. Samples belonging to the same management group are here shown with the same color and shape. Abbreviations: LF, large fowls; NB, neo-bantams; B, true bantams

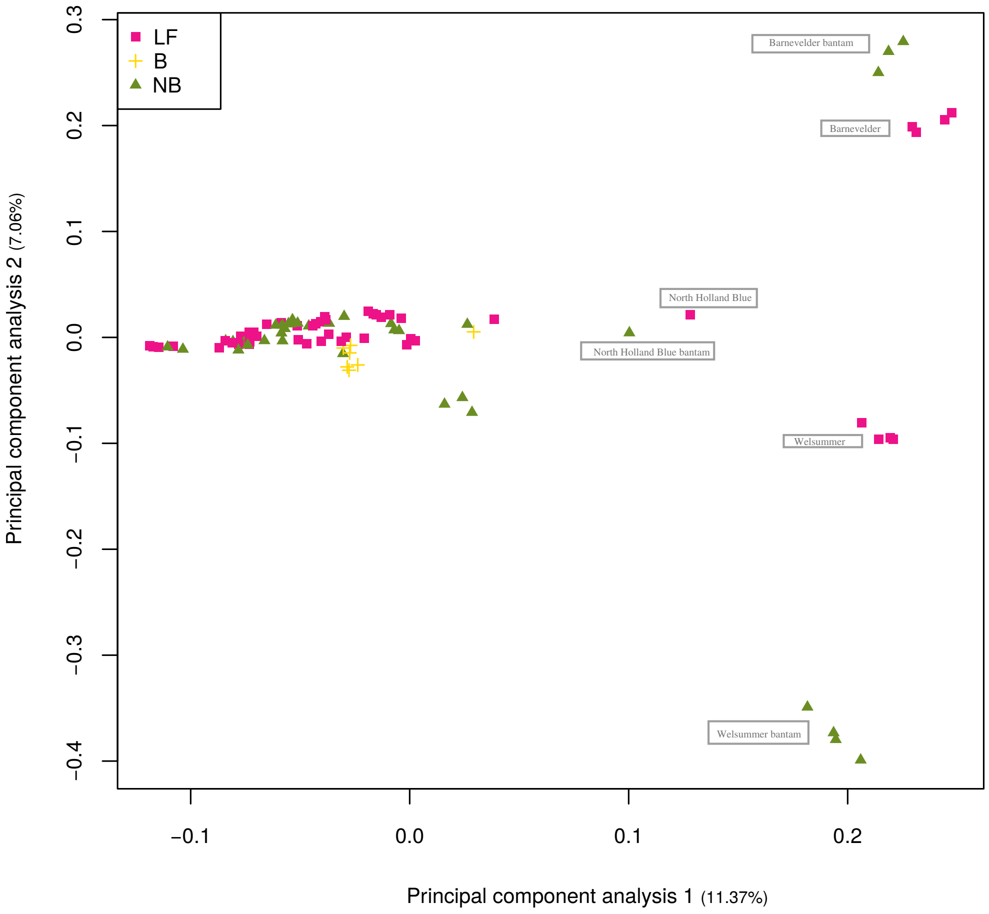
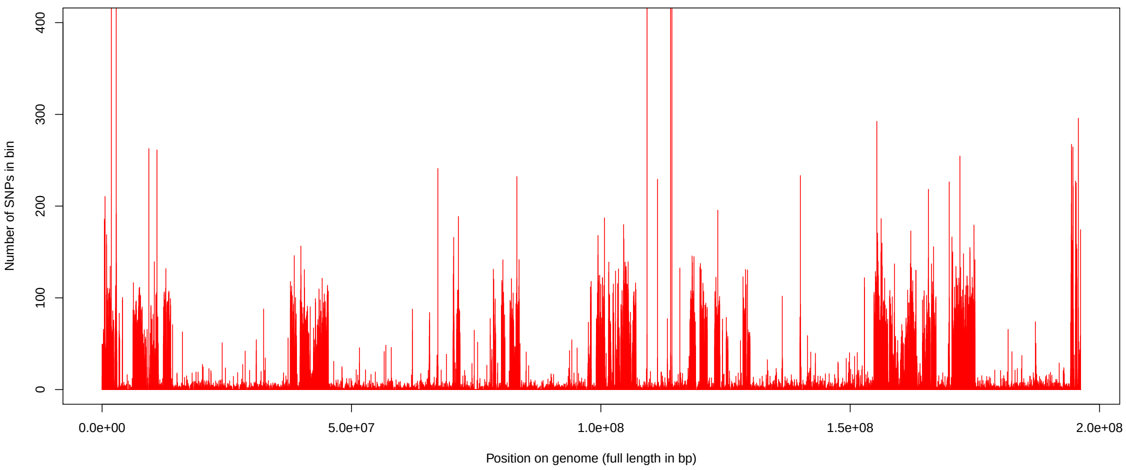
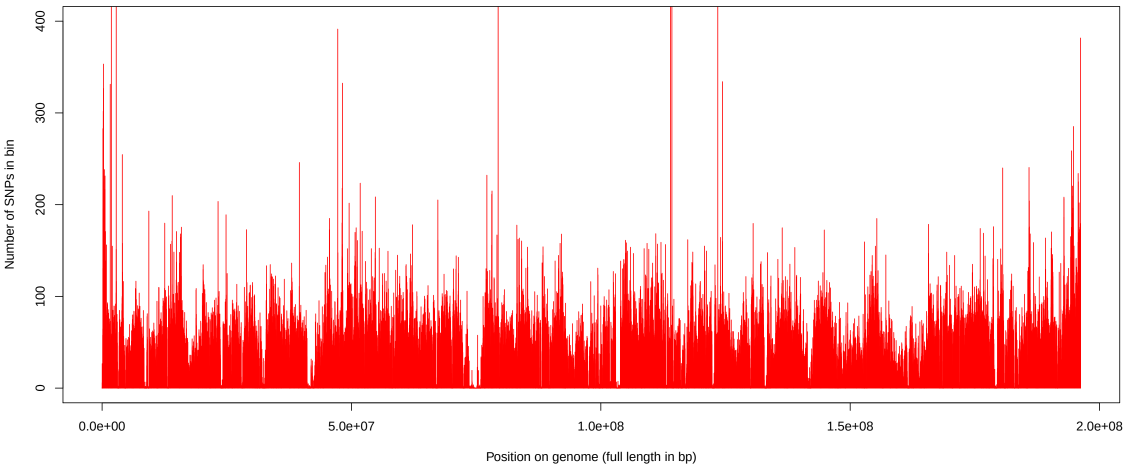


**Figure S2: Heterozygosity along chromosome 1.** Heterozygosity is shown for **(a)** an Eikenburger bantam and **(b)** a Drenthe fowl bolstaat individual. The x-axis shows the position in base pairs (bps) along chromosome 1 and the y-axis displays the corrected number of heterozygous SNPs counted in non-overlapping windows of 10 Kb



**(a)**



**(b)**

**Figure S3: Estimates of past effective population size.** Changes in effective population size are shown for (**A**) large fowl and (**B**) neo-bantam breeds. The x-axis shows the years back in time and the y-axis the estimated effective population size, $N_e$. Abbreviations: Barnev, Barnevelder; BarnevB, Barnevelder bantam; BreFw, Breda fowl; ChamFw, Chaam fowl; DFwB, Dutch fowl bantam; DOwBd, Dutch owl bearded; DOwBdB, Dutch owl bearded bantam; DPBd, Dutch Polish bearded; DPnBdB, Dutch Polish non bearded bantam; FriFw, Frisian fowl; GrMw, Groninger mew; GrMwB, Groninger mew bantam; KraiK, Kraienkoppe; LakVe, Lakenvelder; LakVeB, Lakenvelder bantam; Welsum, Welsummer; WelsumB, Welsummer bantam

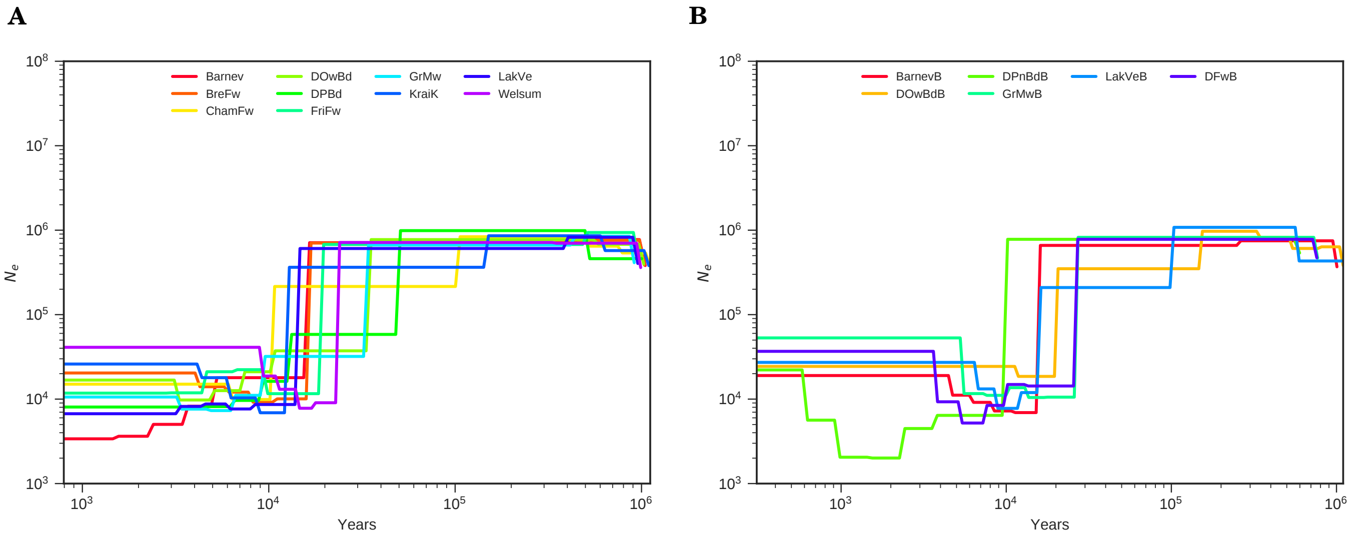
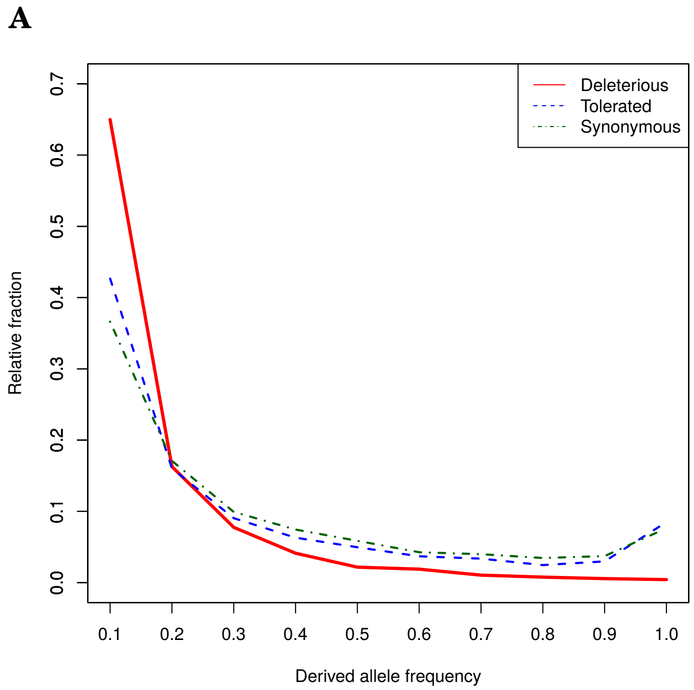


**Figure S4: Derived allele frequency of large fowl and neo-bantam breeds**. **A.** Derived allele frequency of large fowl breeds ($n$=35). **B.** Derived allele frequency of neo-bantam breeds ($n$=22). Derived allele frequency was inferred for synonymous, missense deleterious (SIFT $< 0.05$) and missense tolerated (SIFT $\geq 0.05$) mutations



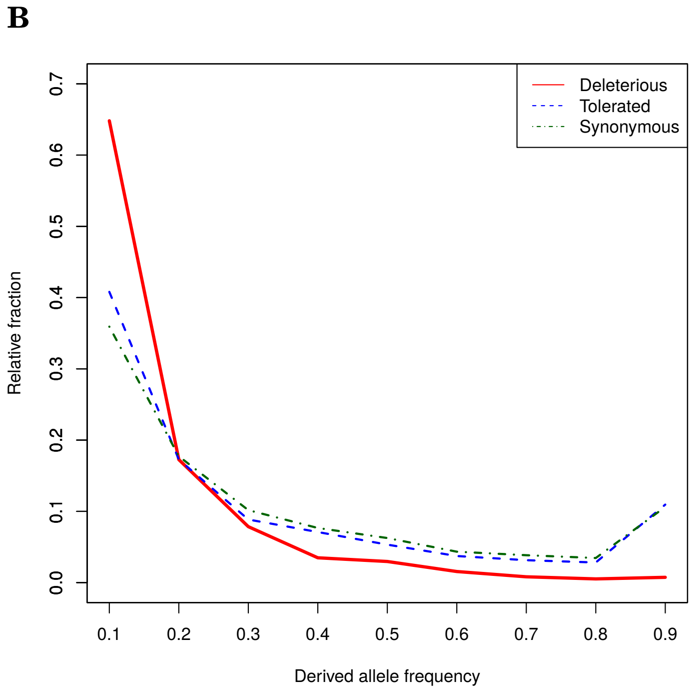


**Figure S5: Distribution of the number of heterozygous and homozygous genotypes per individual**. **A.** Total number of putatively neutral heterozygous genotypes. **B.** Total number of putatively neutral homozygous derived genotypes. **C.** Total number of putatively deleterious heterozygous genotypes. **D.** Total number of putatively deleterious homozygous derived genotypes. Traditional breeds are here grouped based on their management into large fowls (LF), neo-bantam (NB), and true bantam (B)

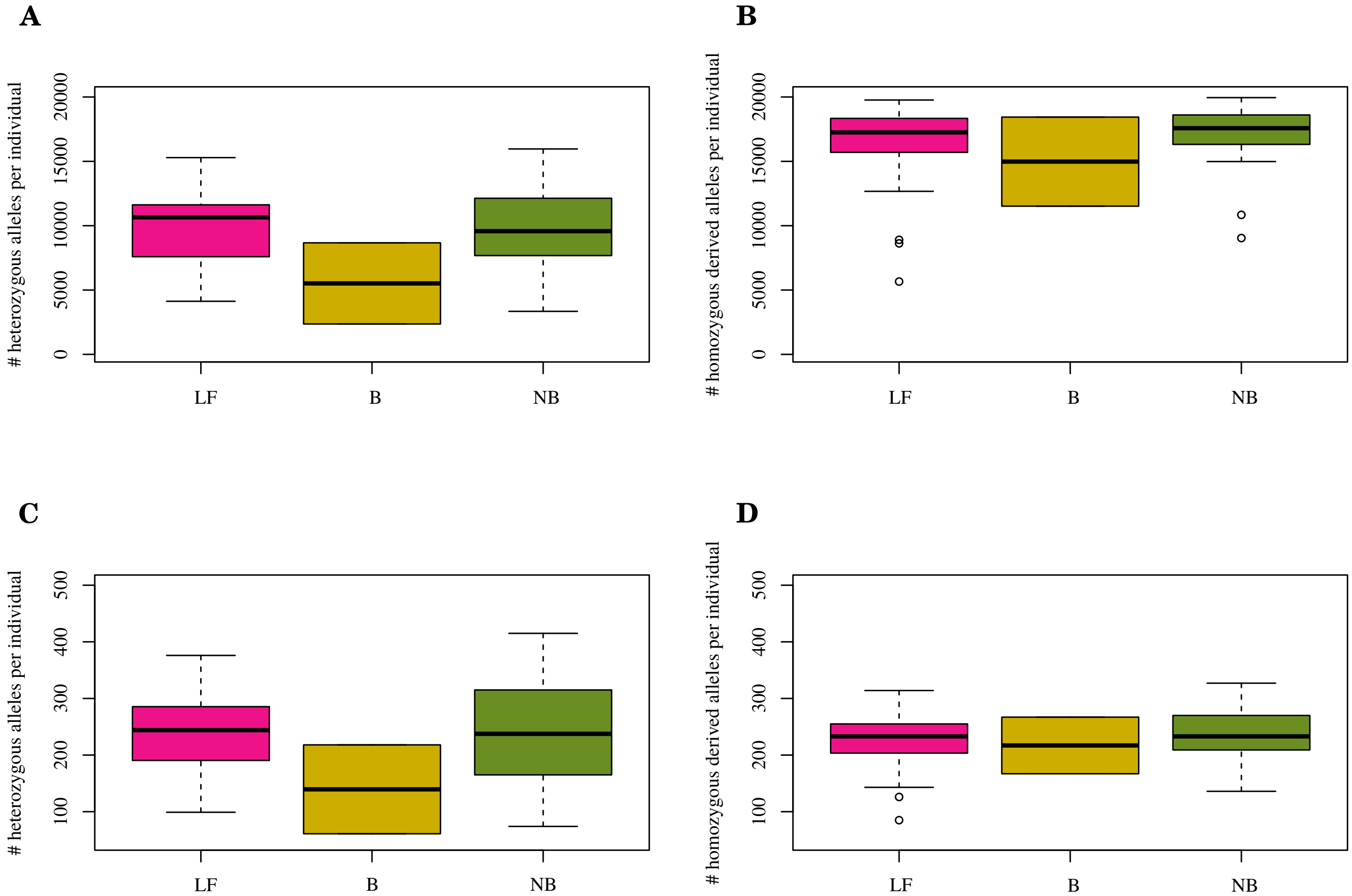


**Figure S6: Number of nondamaging and damaging homozygous derived sites inside and outside ROHs**. **A.** Number of nondamaging homozygotes. **B.** Number of damaging homozygotes. Green points represent the number of nondamaging (A) and damaging (B) homozygotes outside ROHs