

[Additional file 2: Supplementary Figures](#)

Genomic dissection of maternal, additive and non-additive genetic effects for growth and carcass traits in Nile tilapia

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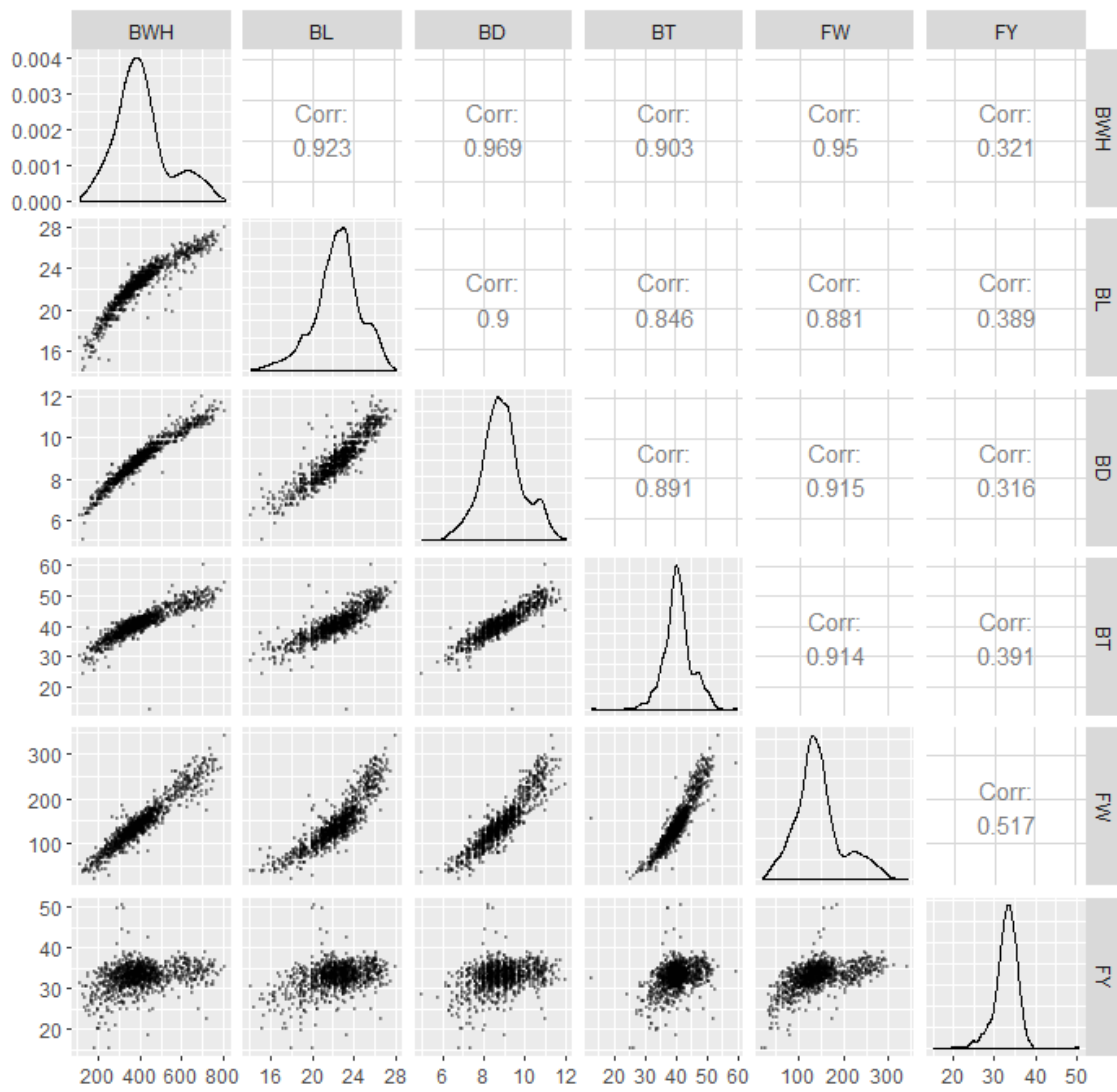


Figure S1: Scatterplots, histograms and the phenotypic correlations for the 6 traits studied.

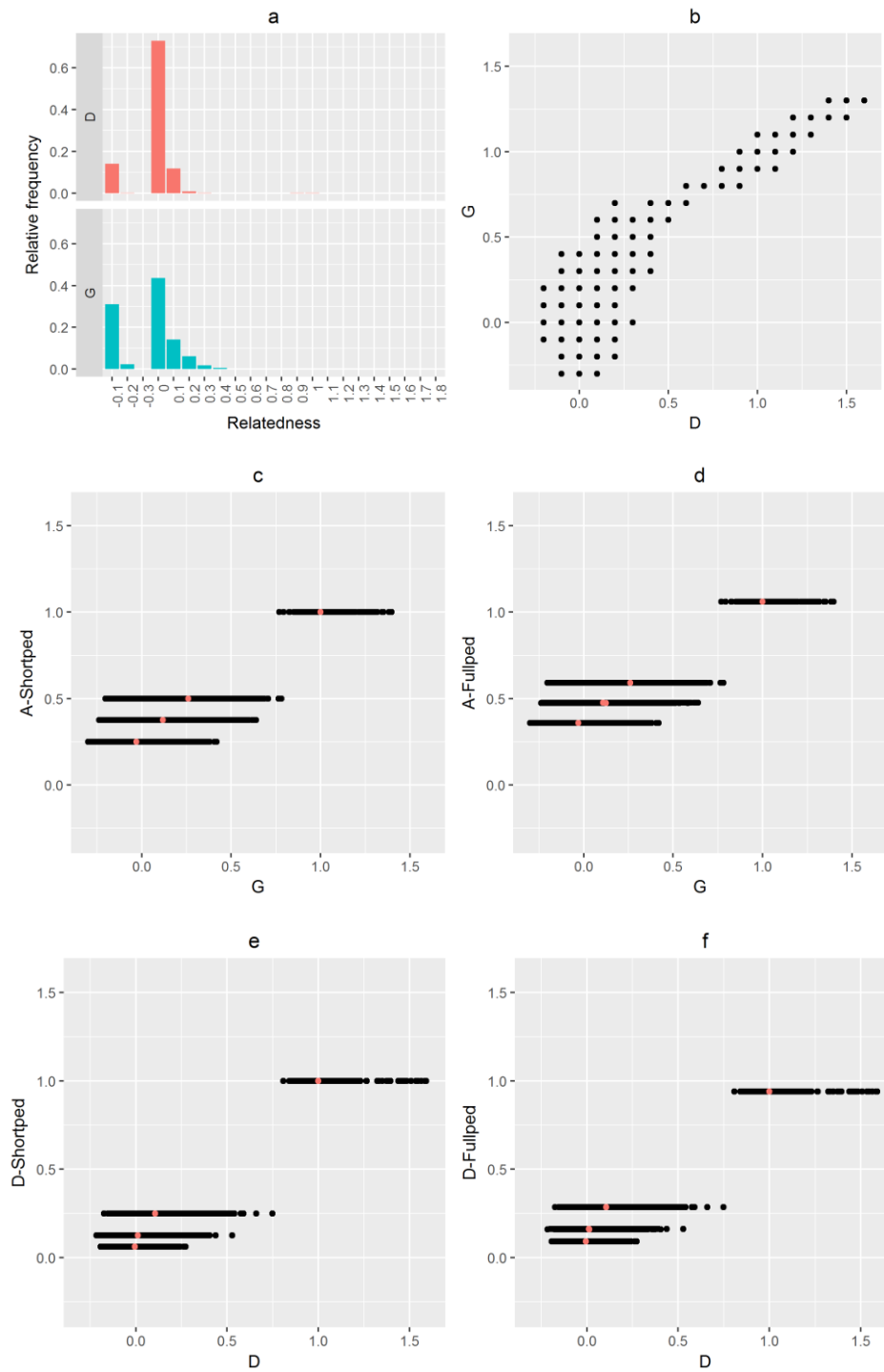


Figure S2: Scatterplots for different additive and dominance relationships. **a)** Relative frequency plots for genomic relationships (G_{NOIA}) and dominance relationships using genomic information (D_{NOIA}). **b)** Scatterplot of G_{NOIA} with D_{NOIA} (correlation = 0.47). **c)** Scatterplot of G_{NOIA} with the pedigree relationships using 3 generations of pedigree (A-Shortped) (correlation = 0.72). **d)** Scatterplot of G_{NOIA} with the pedigree relationships using 20 generations of pedigree (A-Fullped) (correlation = 0.72). **e)** Scatterplot of D_{NOIA} with the dominance relationships using 3 generations of pedigree (D-Shortped) (correlation = 0.65). **f)** Scatterplot of D_{NOIA} with the dominance relationships using 20 generations of pedigree (D-Fullped) (correlation = 0.62). Mean values of G_{NOIA} and D_{NOIA} are shown as orange dots in the respective plots.

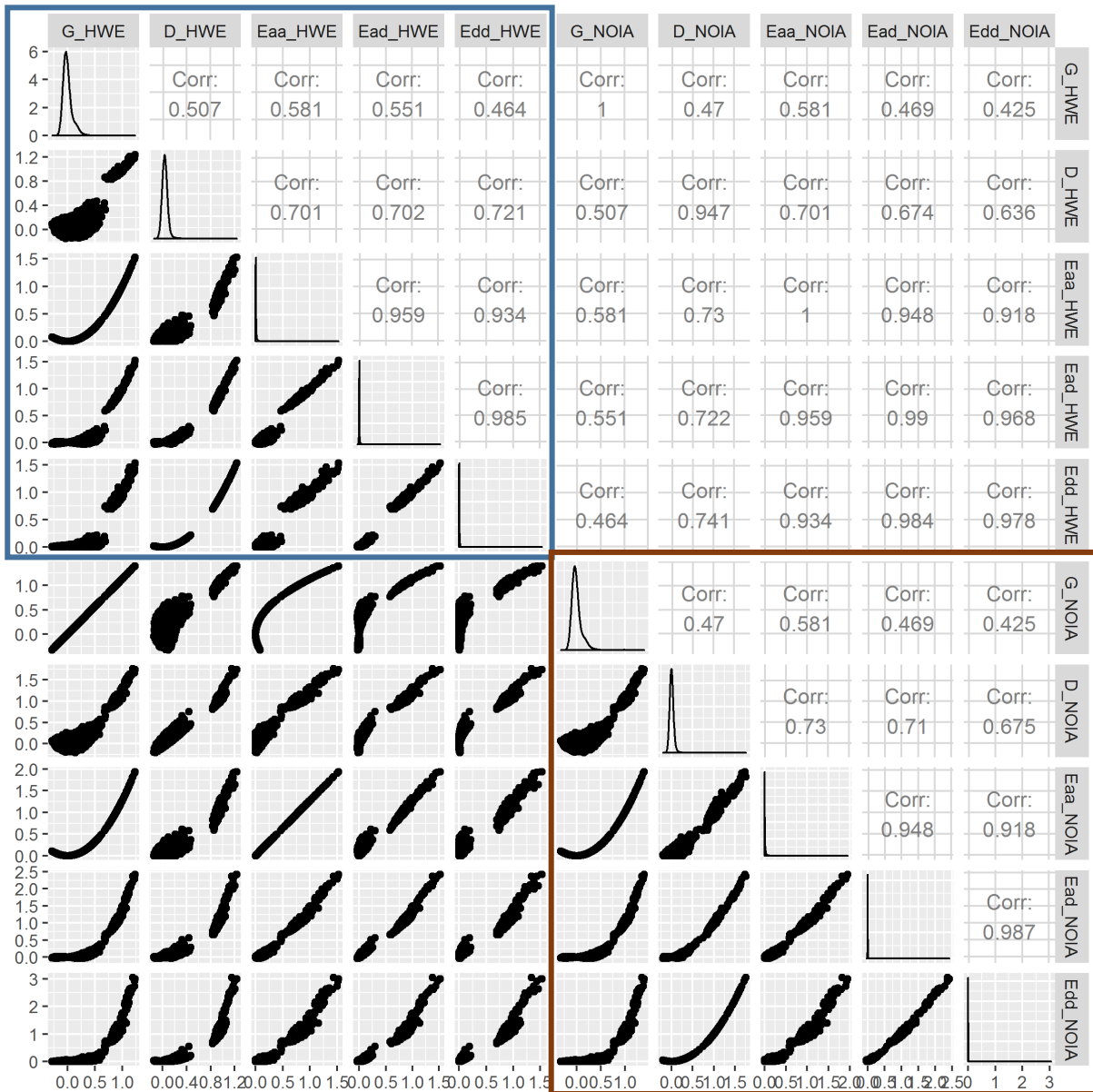


Figure S3: Scatterplots for different additive, dominance and epistasis relationships using NOIA (inside brown box) and HWE approaches (inside blue box).

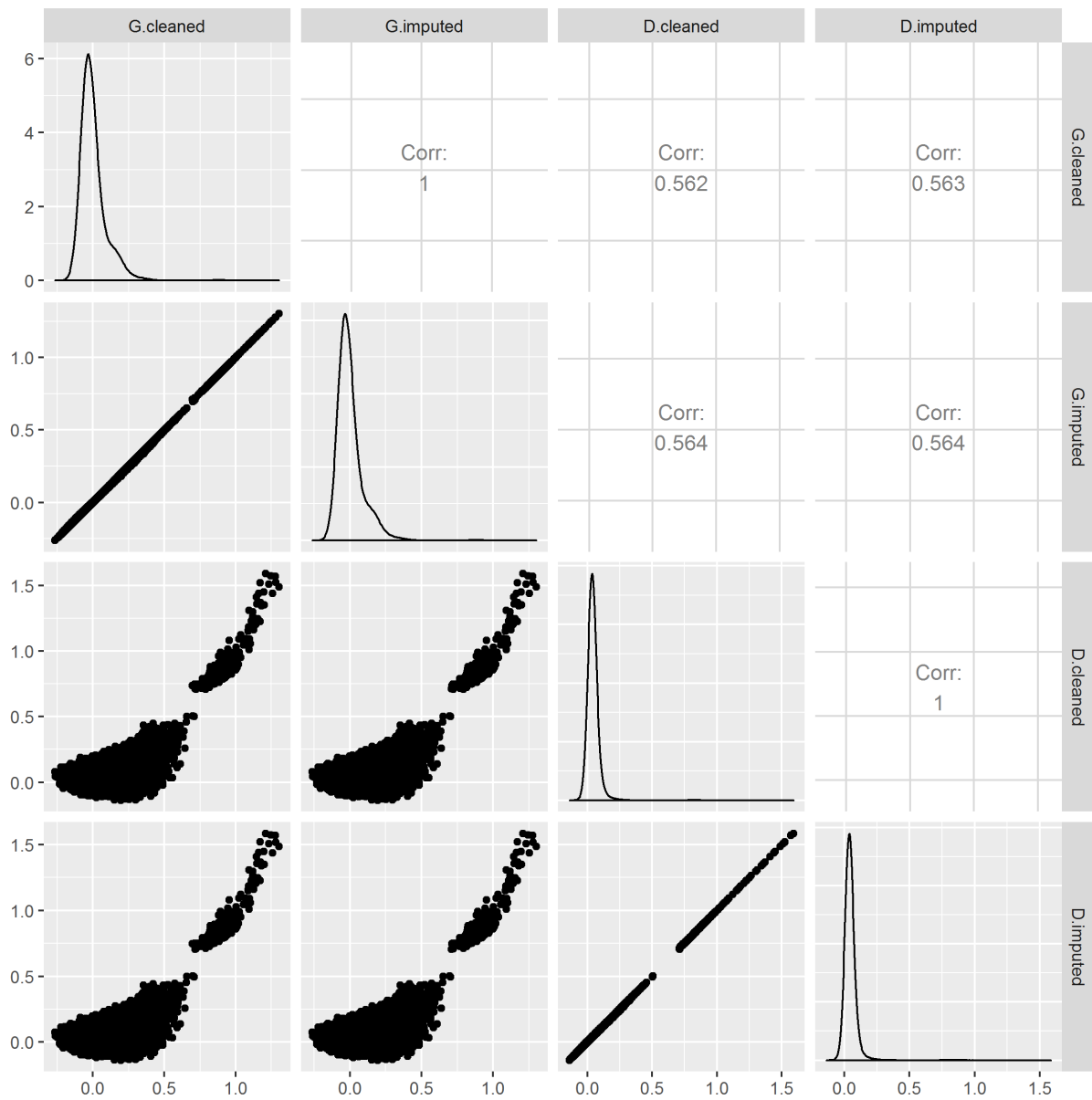


Figure S4: Scatterplot and correlation of the additive and dominance relationships using imputed ('G.imputed' and 'D.imputed' respectively) and without imputed genotypes, i.e. with some missing genotypes ('G.cleaned' and 'D.cleaned' respectively).

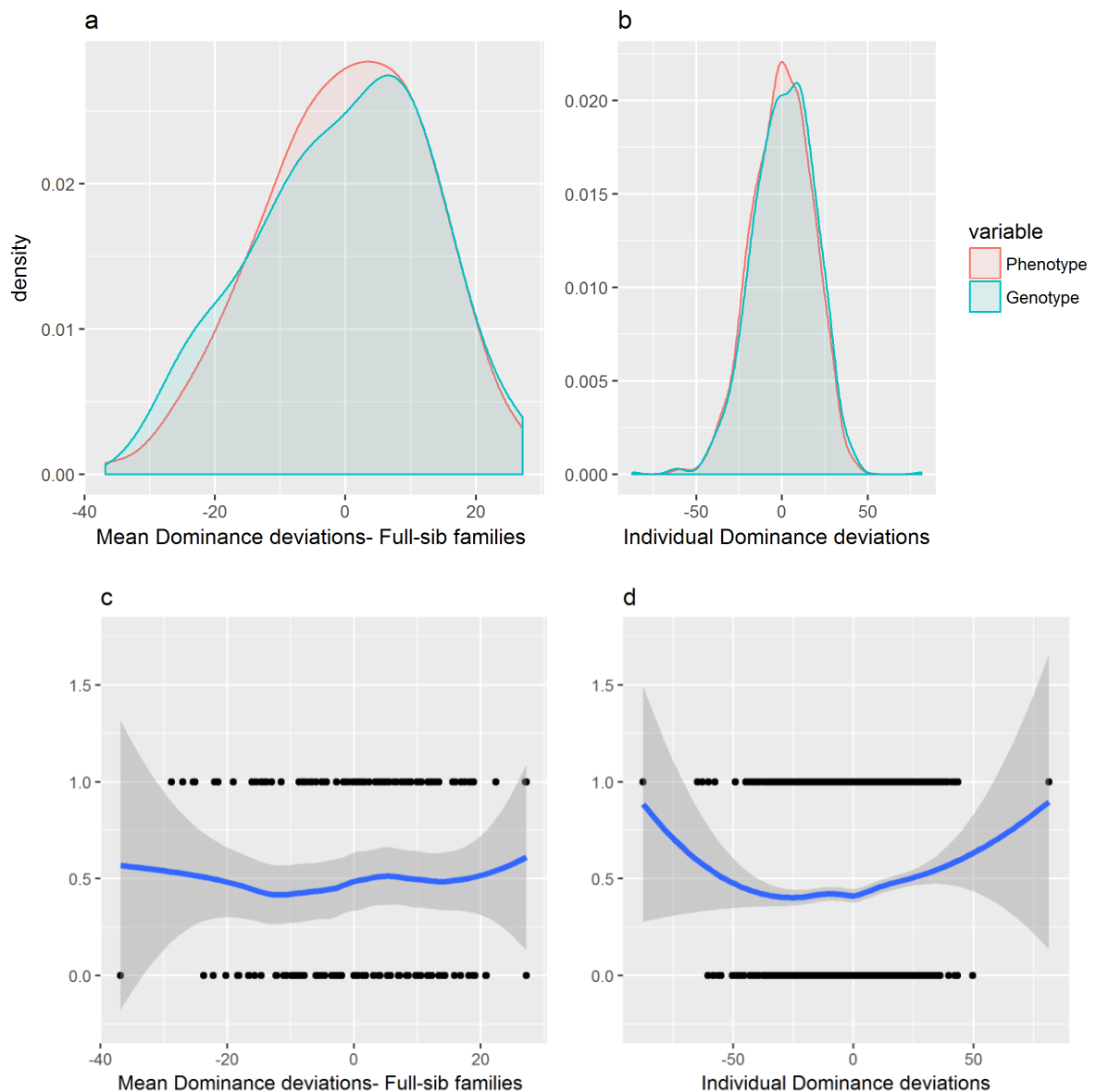


Figure S5: Density plots, scatterplot and LOESS regression between the selected and non-selected individuals. **a)** and **b)** are density plots showing the dominance deviations for BWH between the 2524 animals having phenotypes, and the subset of 1119 genotyped individuals included in this study. **c)** and **d)** are scatterplots showing LOESS regressions. In **c)** the 74 full-sib families represented in this study are coded as 1, and the remaining 81 families are coded as 0 and are plotted against the mean family dominance deviation. In **d)** the 1119 individuals included in this study were coded as 1 and the remainder were coded as 0 and are plotted against individual dominance deviations. The dominance deviations were obtained from the ADM model given in [1].

Literature cited

1. Joshi R, Woolliams JA, Meuwissen THE, Gjøen HM. Maternal, dominance and additive genetic effects in Nile tilapia; influence on growth, fillet yield and body size traits. *Heredity* (Edinb). 2018;120:452-62.