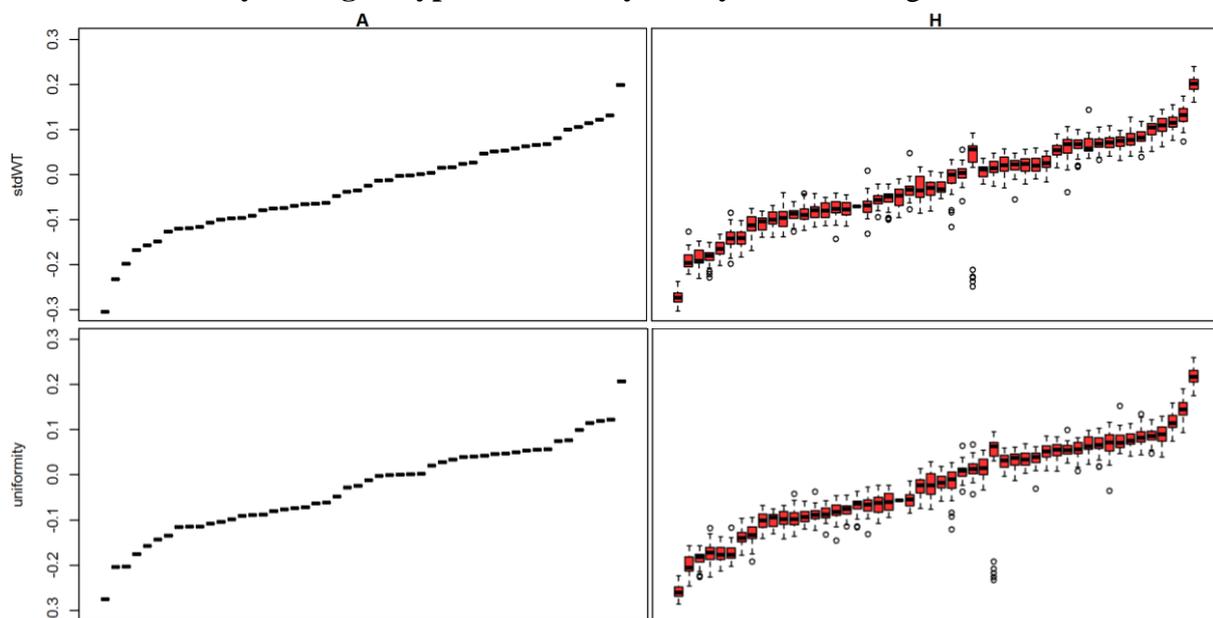


# Additional file 1

## Estimated breeding values for standardized body weight (stdWT) and its uniformity from genotype animals based on sire-dam DHGLM

The use of **H** with sire-dam DHGLM resulted in higher variation of within-family GEBVs for stdWT and its uniformity, compared to within family EBVs (Figure. S1). However, the animal DHGLM resulted in considerably higher variation of within-family EBVs and GEBVs for stdWT and its uniformity, compared to sire-dam DHGLM (see Figure. 2).

**Figure S1** Boxplot of estimated breeding values of standardized body weight (stdWT) and its uniformity from genotyped animals by family. The breeding values were estimated



using sire-dam double hierarchical generalized linear model. The green boxplots are estimated breeding values (EBVs) using **A** matrix while the red boxplots are genomic estimated breeding values (GEBVs) using **H** matrix. The x-axis is the family identification.