Additional Figure 1. Multidimensional scaling plots. All studied breeds (**A**) were distinct genetic populations, presented by multidimensional scaling plots. There is no substructure in the Finnish Spitz (**D**) and Schipperke (**C**) cohorts. In Belgian Shepherd (**B**) and Beagle (**E**) cohorts, two subpopulations were identified, and represent breed lines.