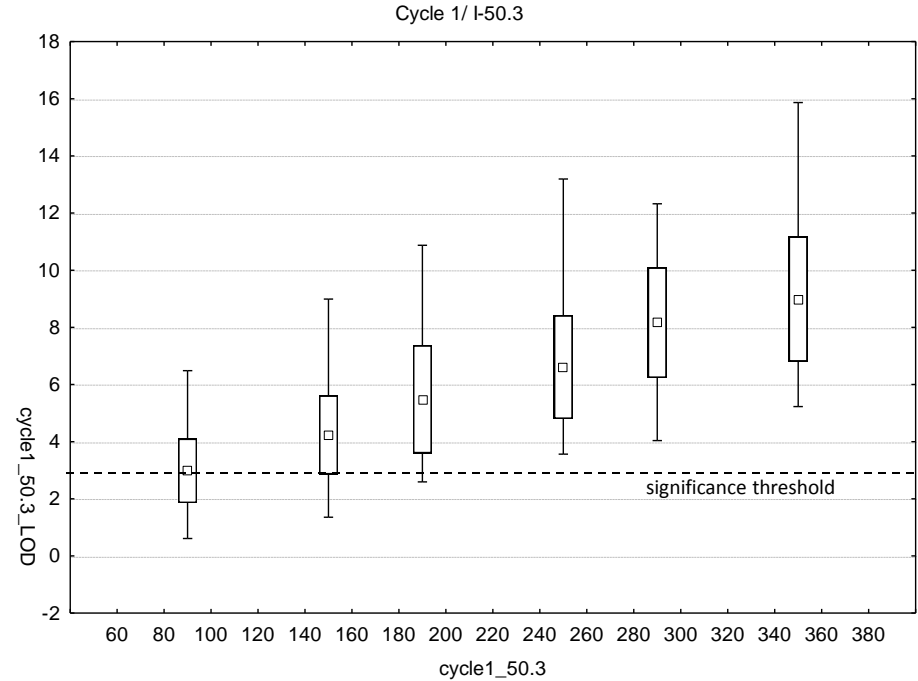
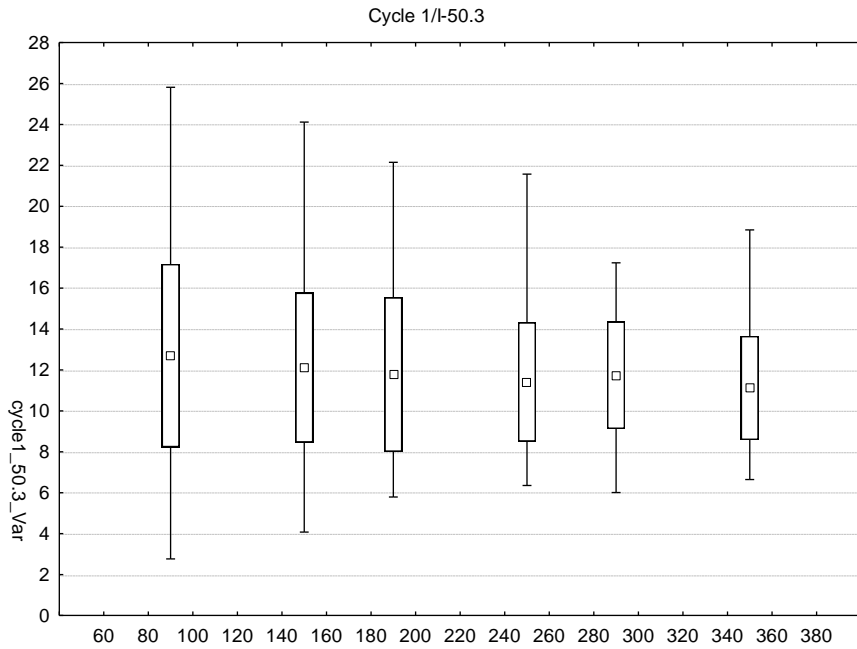


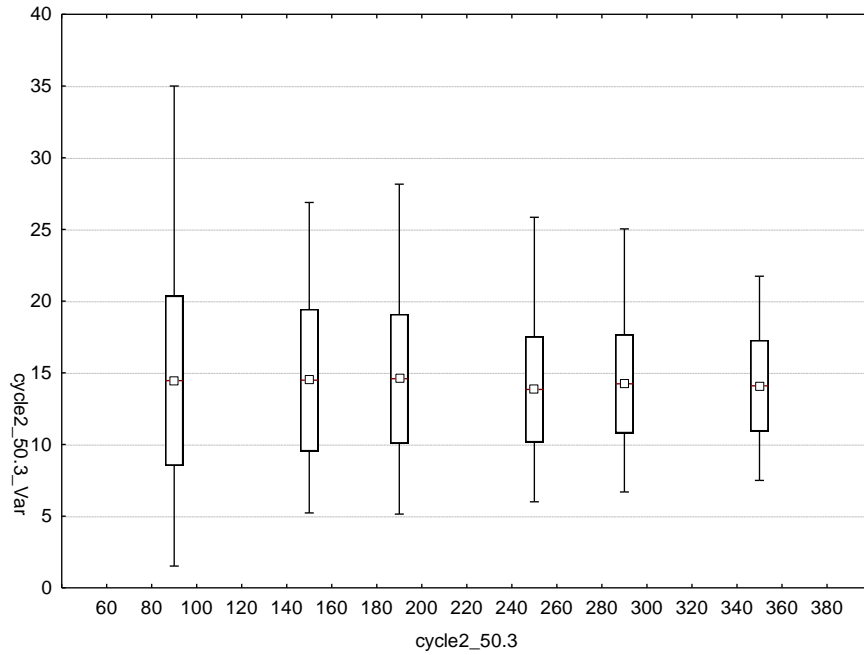
**SOM Figure 1: Effect of sample size on estimation of explained phenotypic variance (Beavis effect) for cycle time 1-4, headnod 1-4, latency and fix-nod.** For all traits the explained phenotypic variance (left panel) and LOD scores (right panel) is shown as a function of sample size based on a bootstrap analysis (1000 bootstraps/sample size). Boxplots show means/SD/min-max. In a significant number of permutations, QTL would go undetected because they fall below the genome wide detection limit of 1% if the number of individuals in a mapping population is lower than 200 (for most traits the 0.01 significance threshold is around LOD 2.7, dashed line in the second panel). As predicted, the variance in the estimation of a QTL effect becomes smaller as sample size goes up (left panel). A significant QTL in our studies should always be detected if the mapping population is larger than 250 individuals (all LOD scores are above the detection threshold). For each trait the location of the QTL under consideration is given as chromosome and position, i.e. Cycle 1 / 1\_50.3 means that the analysis was focused on the cycle 1 QTL at position 50.3 (see table 2).

# Cycle 1 / I\_50.3

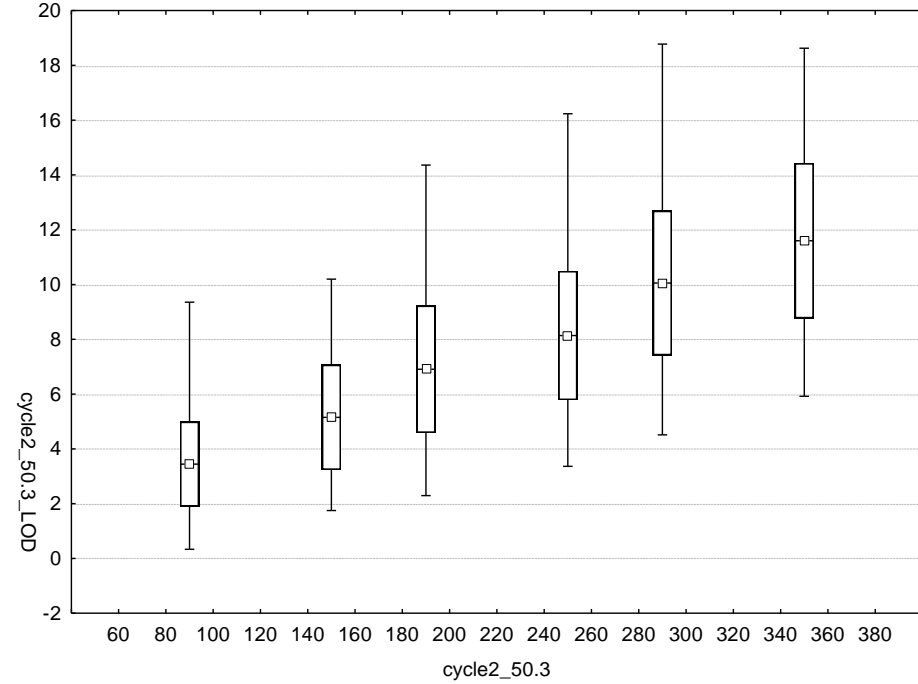


\*Mean, Mean±SD (Box); Min-Max (Whiskers)

# Cycle 2 1\_50.3

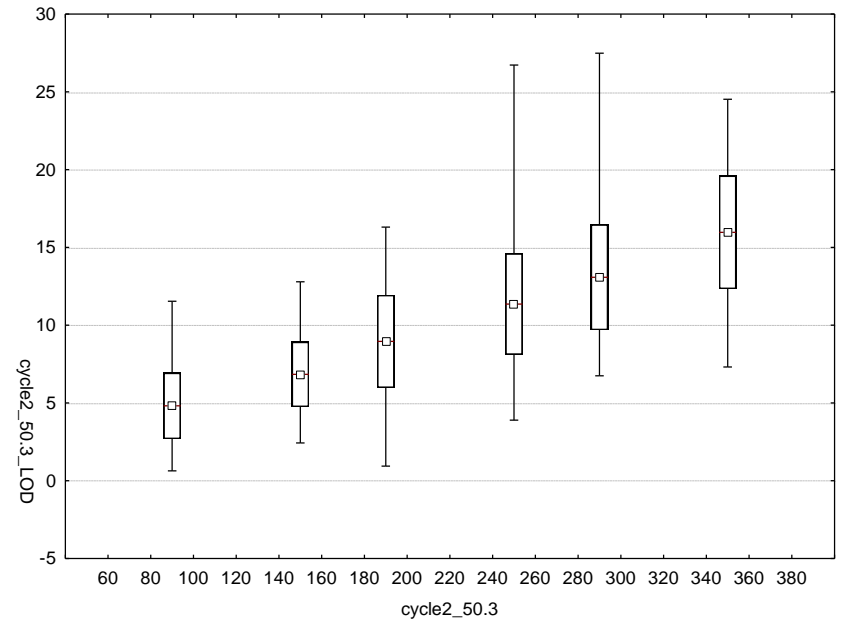
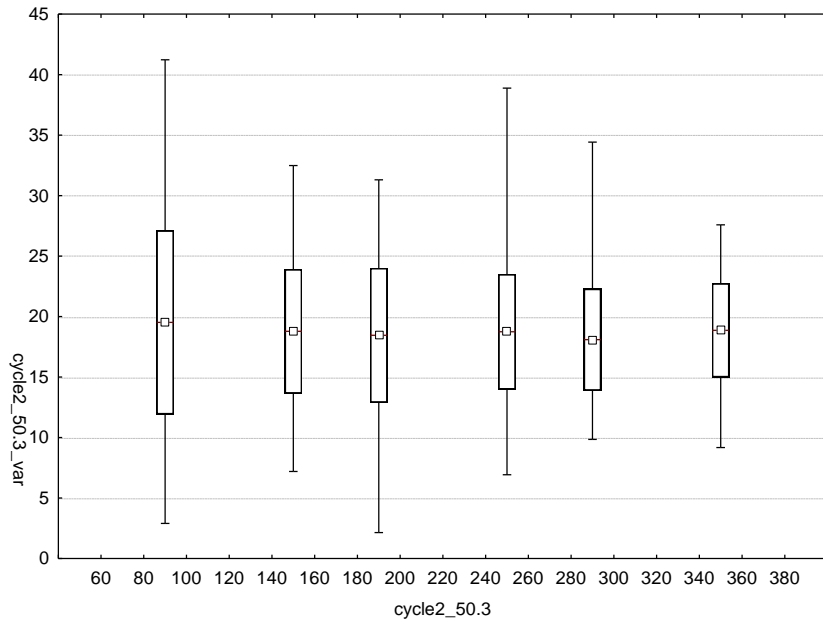


Variance explained

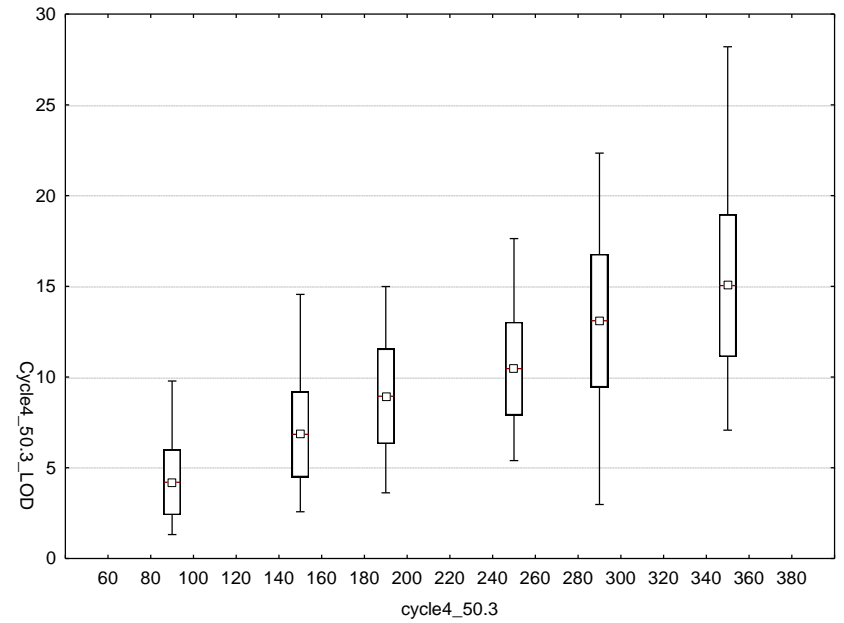
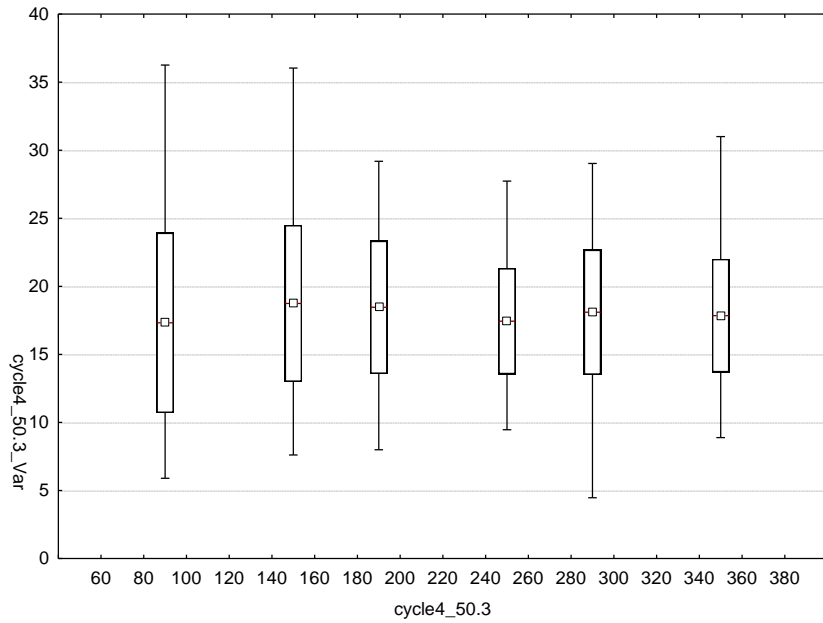


LOD scores

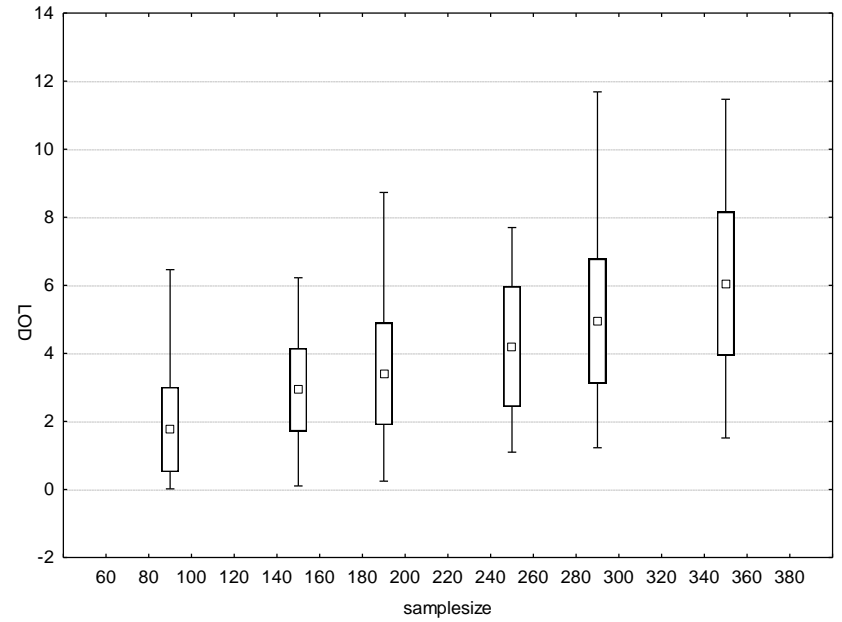
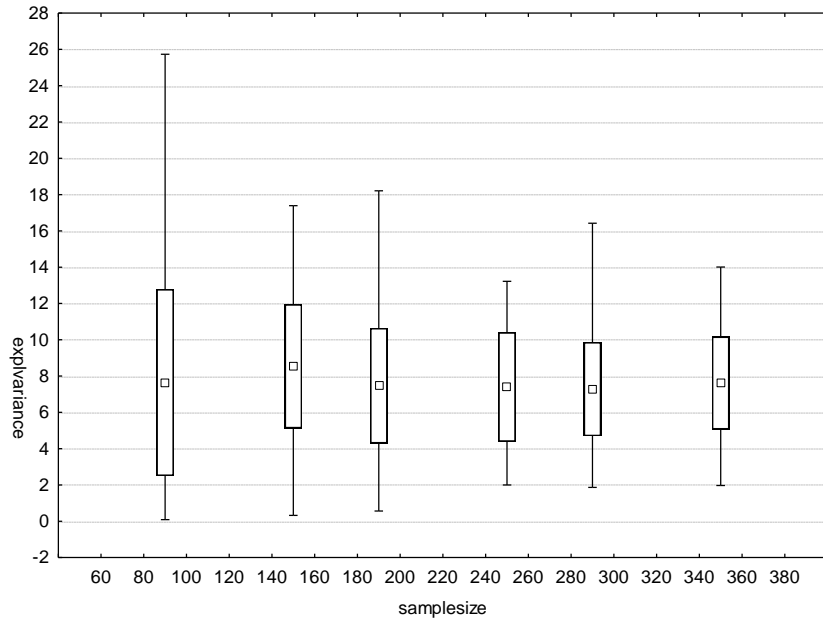
# Cycle 3 1\_50.3



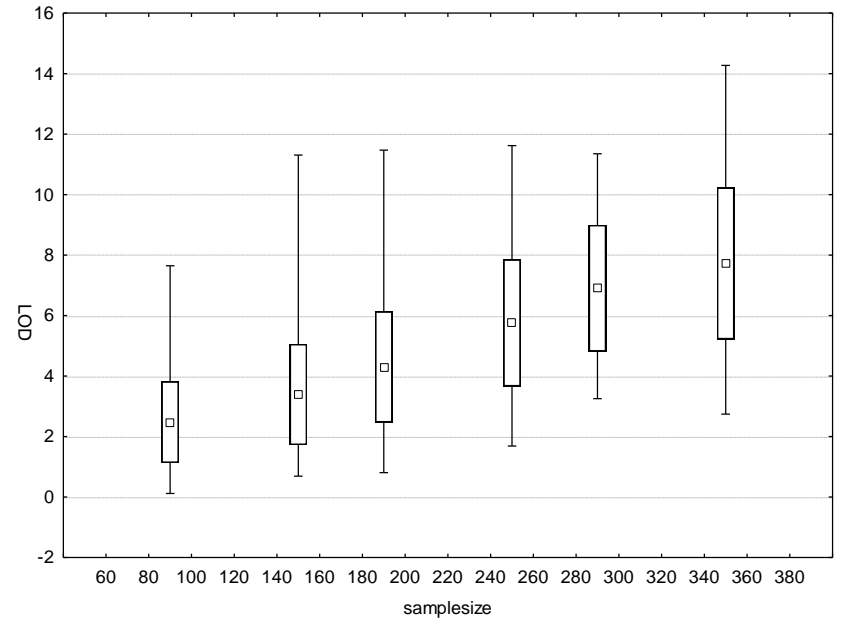
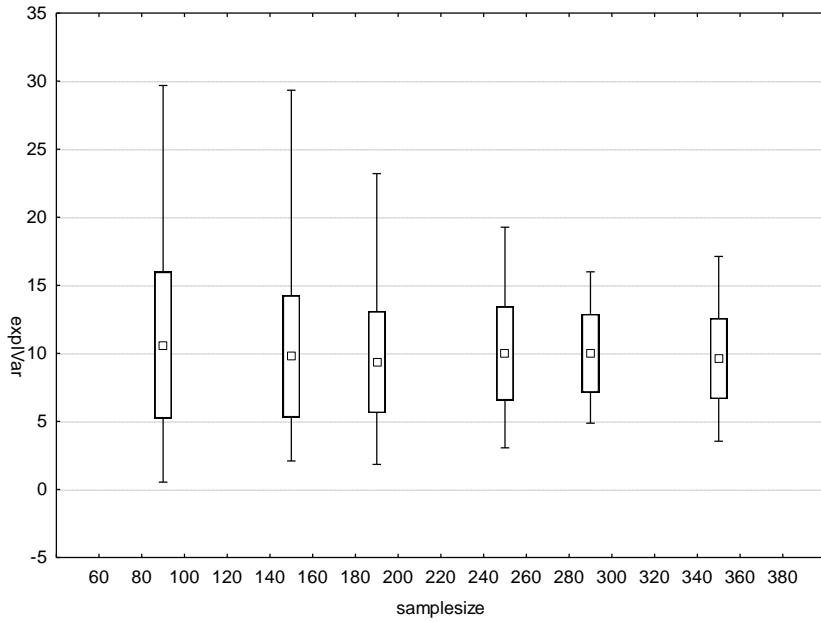
# Cycle 4 1\_50.3



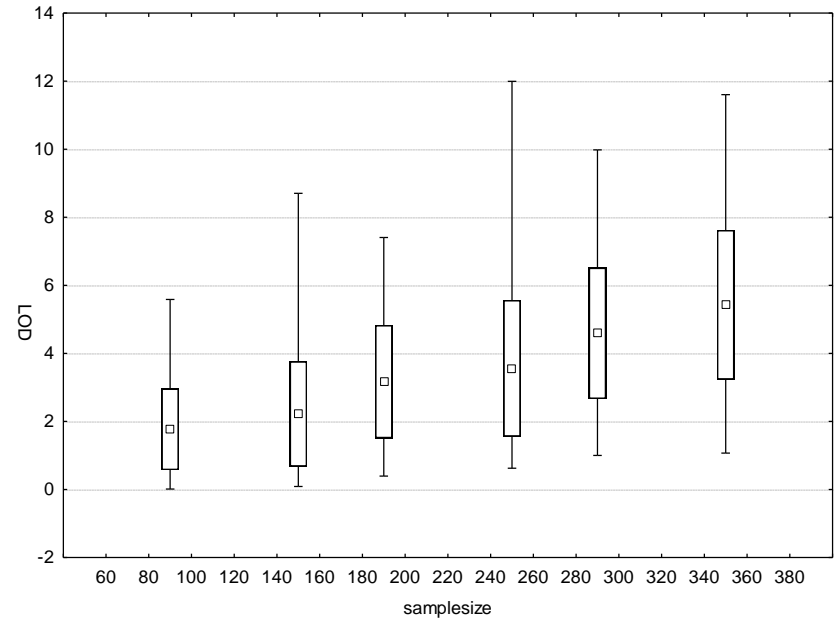
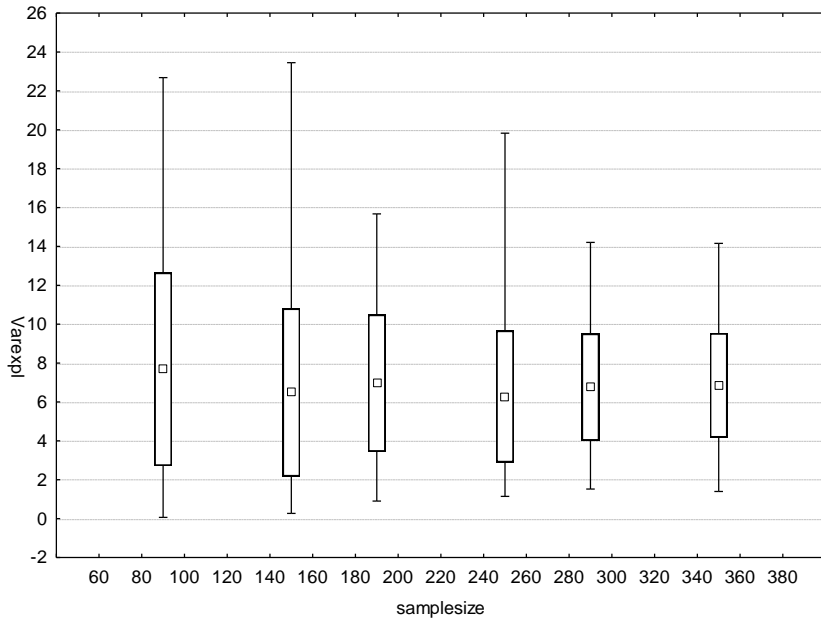
# Headnod 1-III-66.3



# Headnod 2 - III-66.3

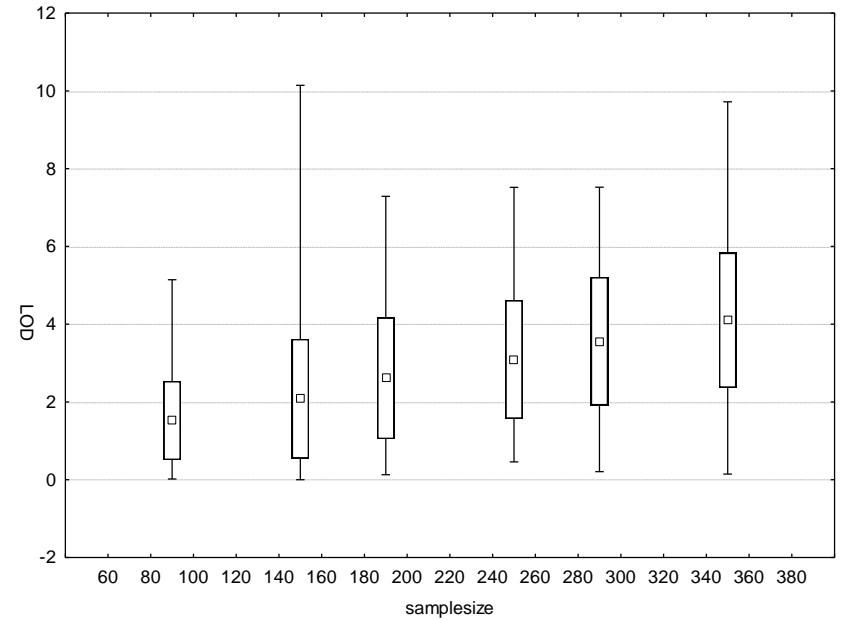
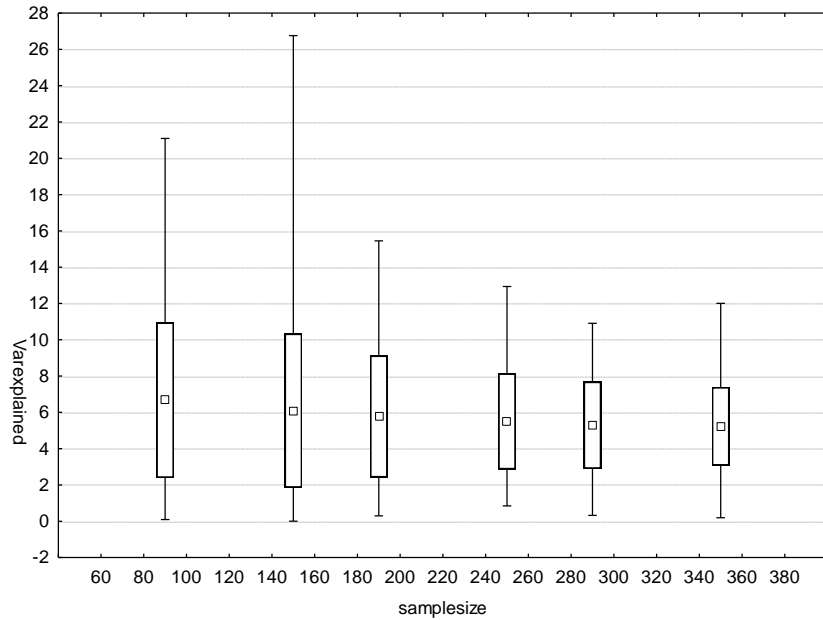


# Headnod 3 – III-66.3

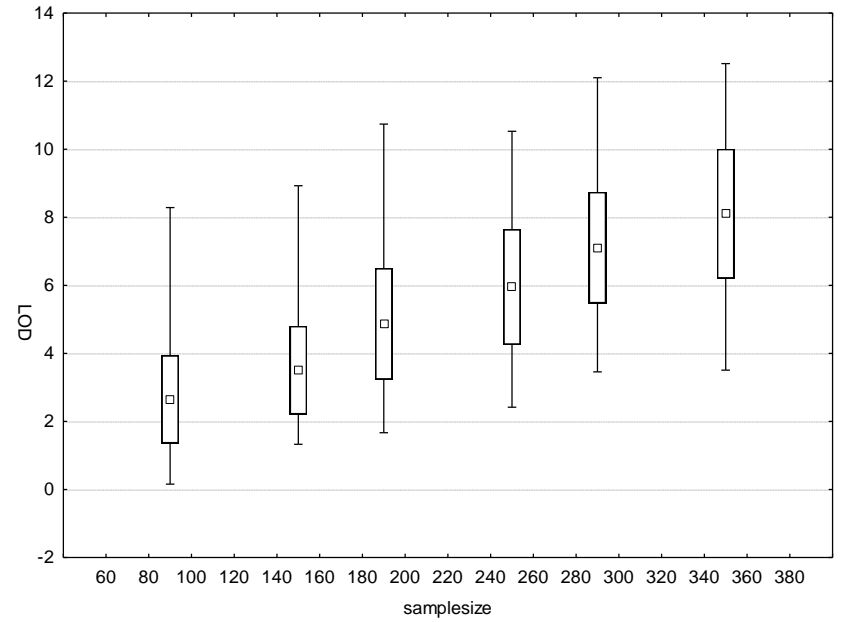
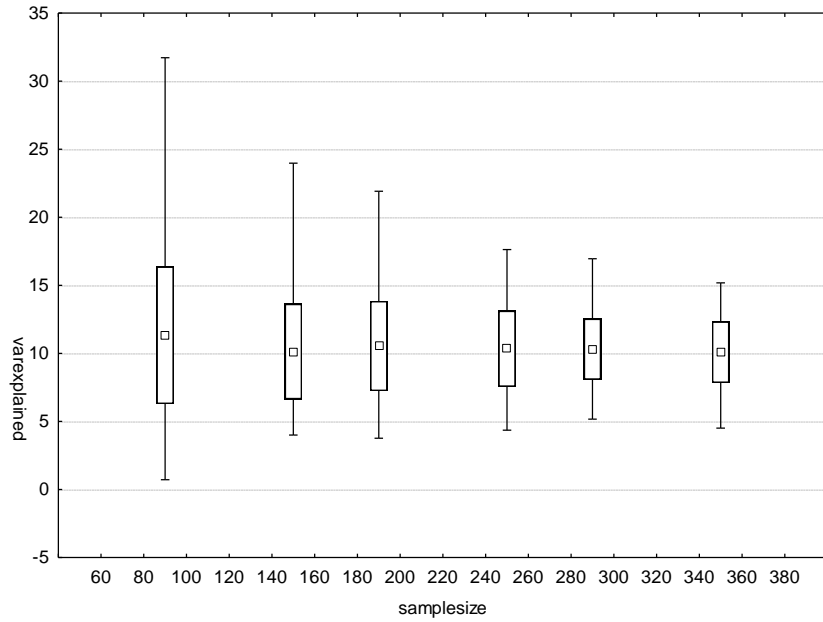




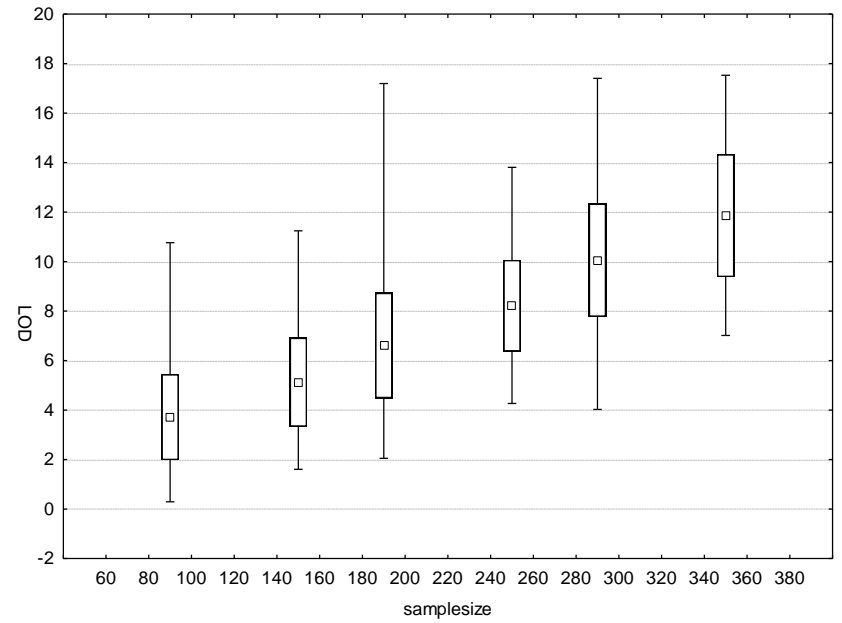
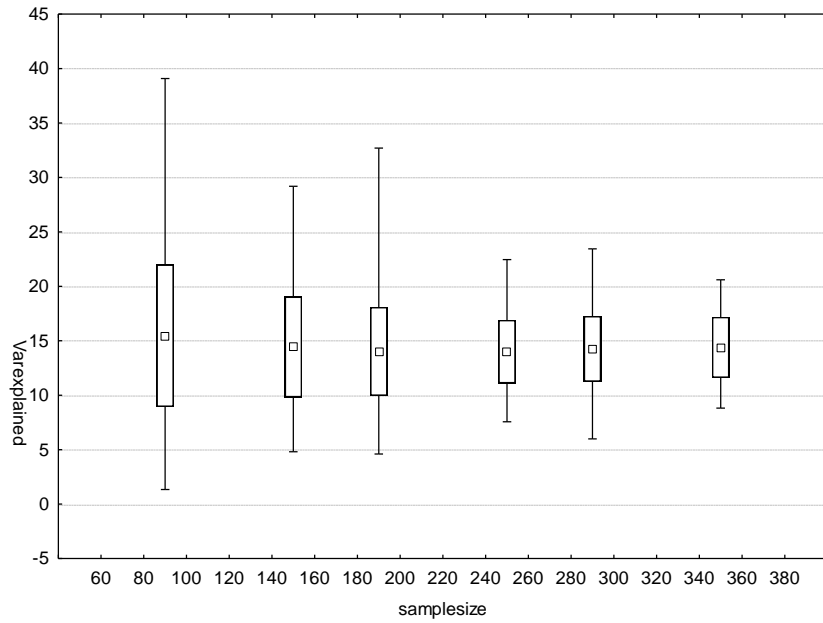
# Headnod 4 – III-66.3



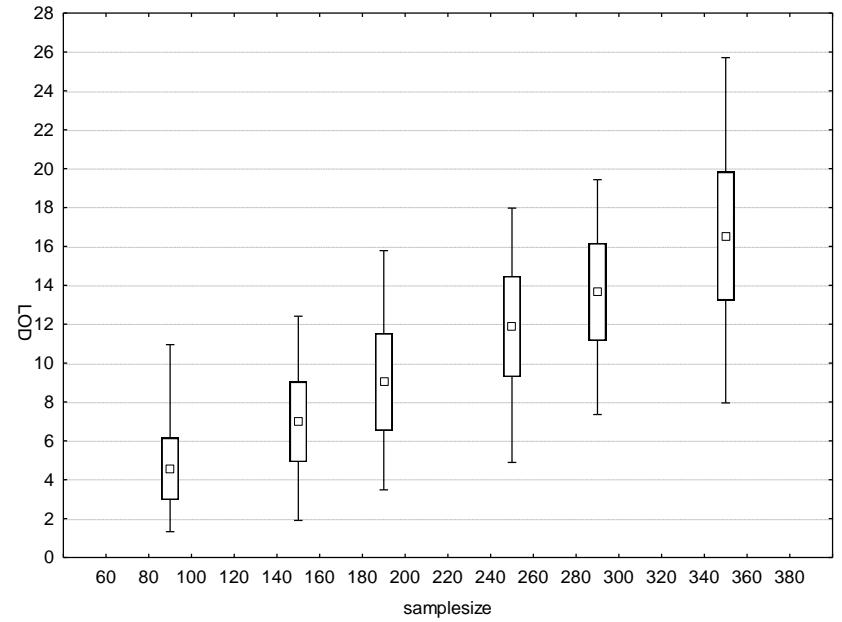
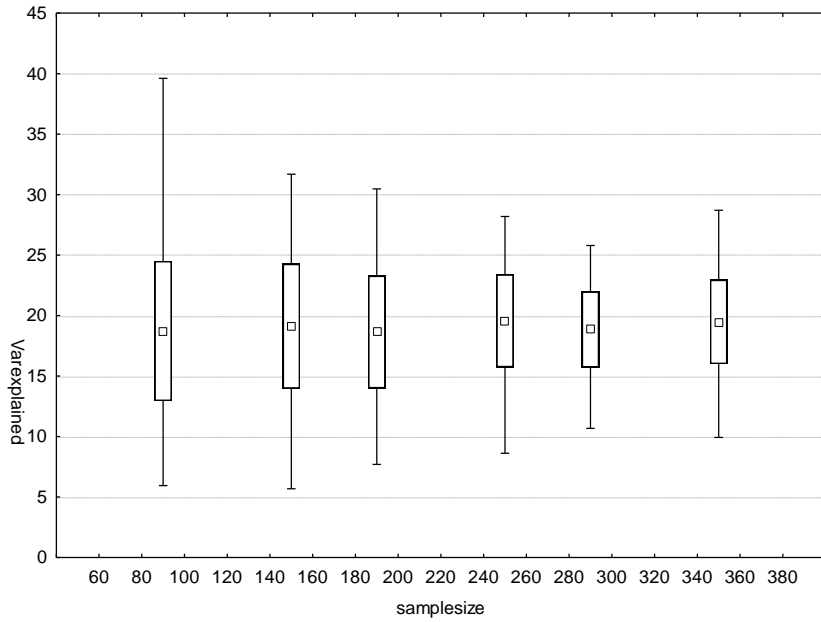
# Cycle 1 – V-55



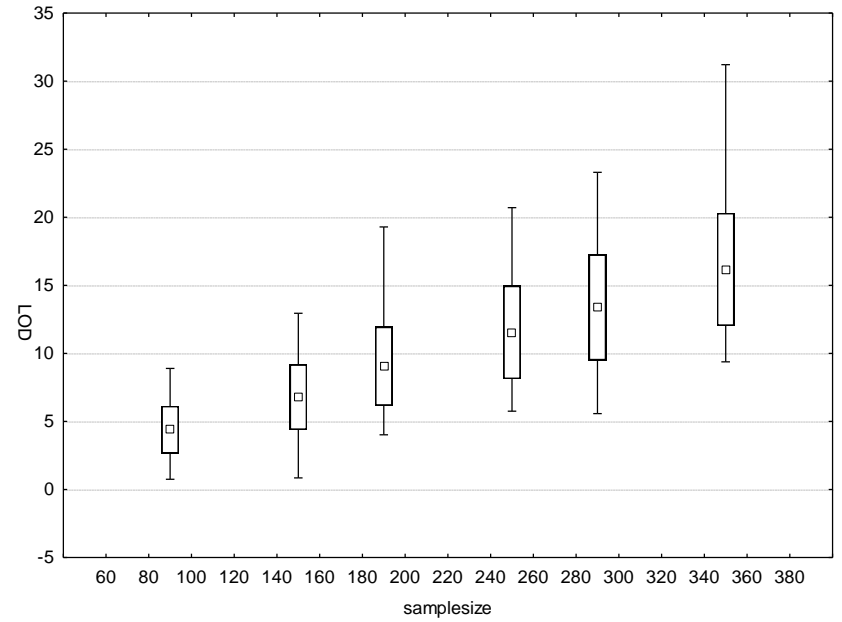
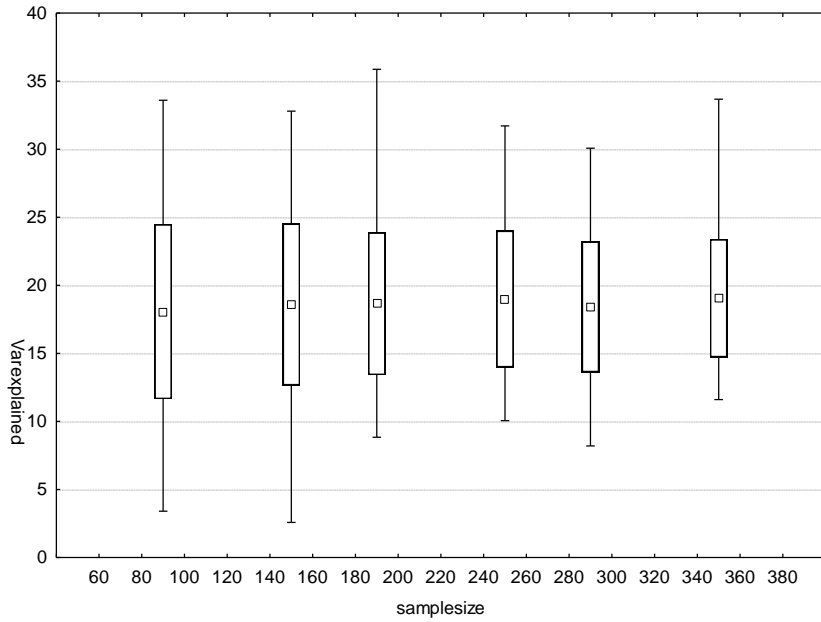
# Cycle 2 – V-55



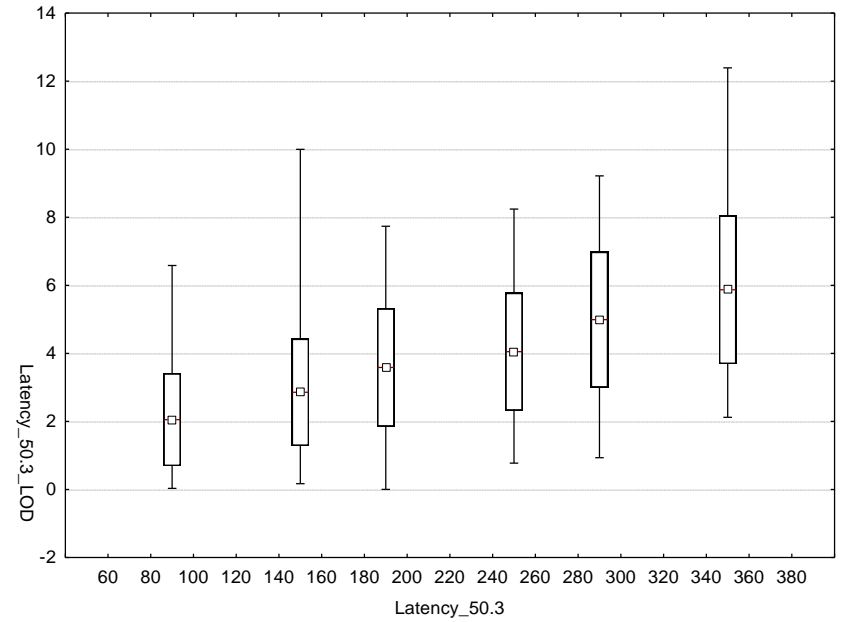
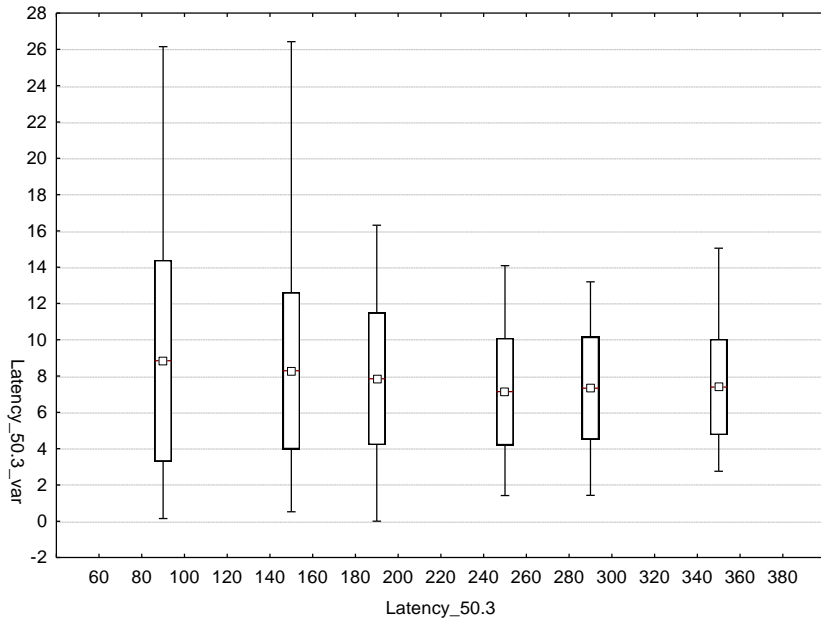
# Cycle 3 – V-55



# Cycle 4 – V-55



# Latency 1\_50.3



# Fix-Nod 1-37.1

