

Genomic prediction for inbred and hybrid polysomic tetraploid potato offspring

Supplementary Figures

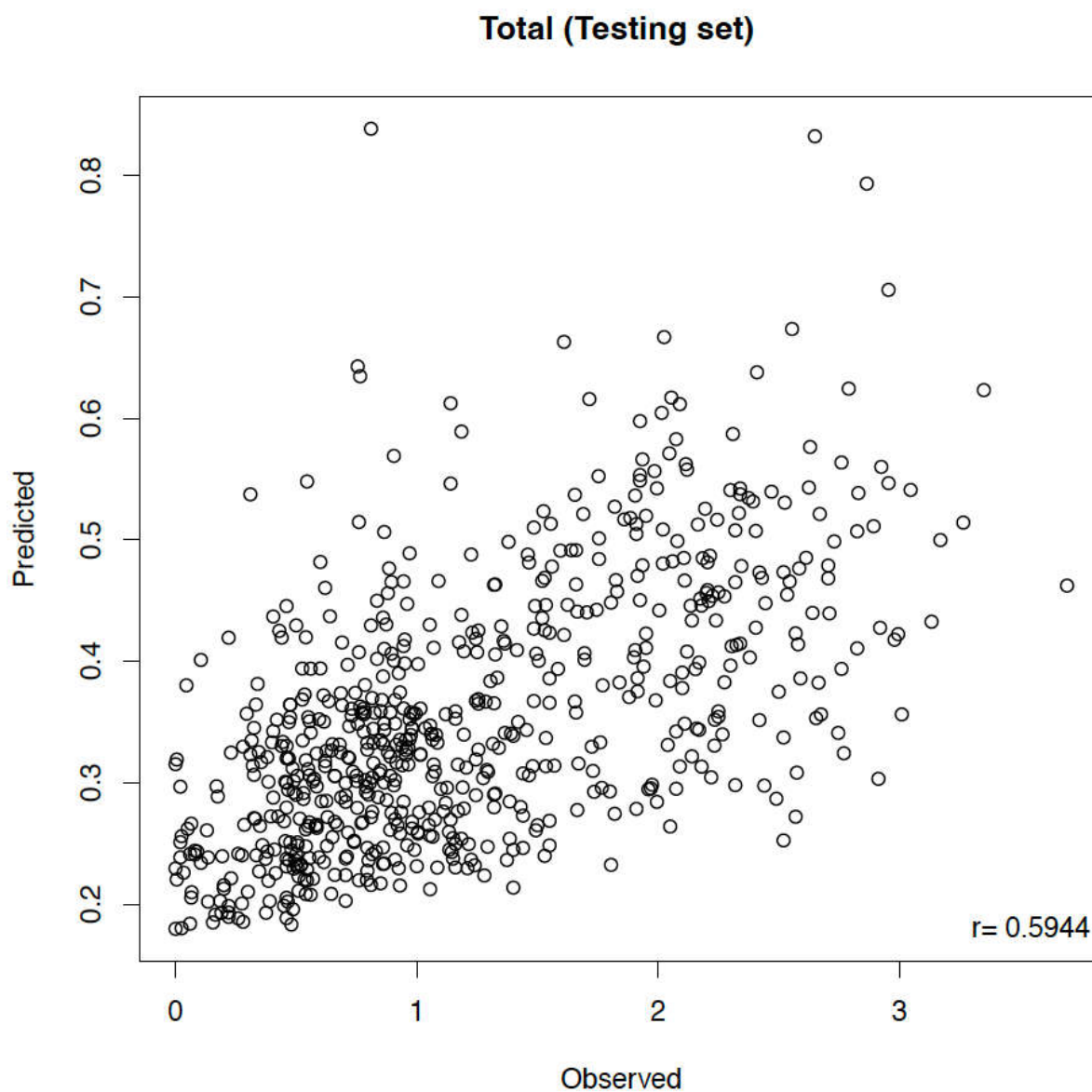


Figure S1. Genomic prediction of inbred and hybrid performance using Umeå 2021 as training population and Helgegården 2022 as breeding population. r: prediction ability

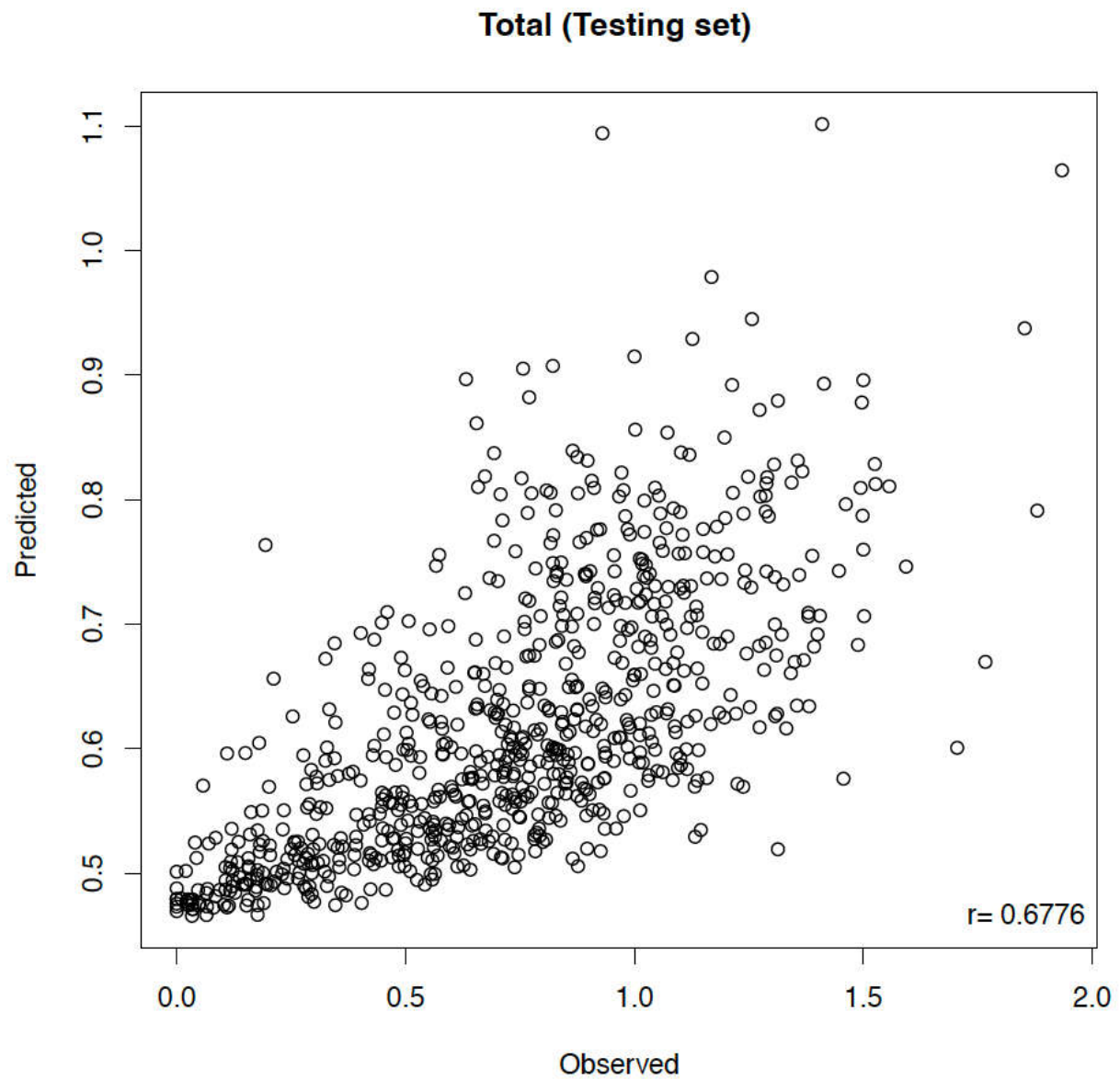


Figure S2. Genomic prediction of inbred and hybrid performance using Umeå 2021 as training population and Umeå 2022 as breeding population. r: prediction ability

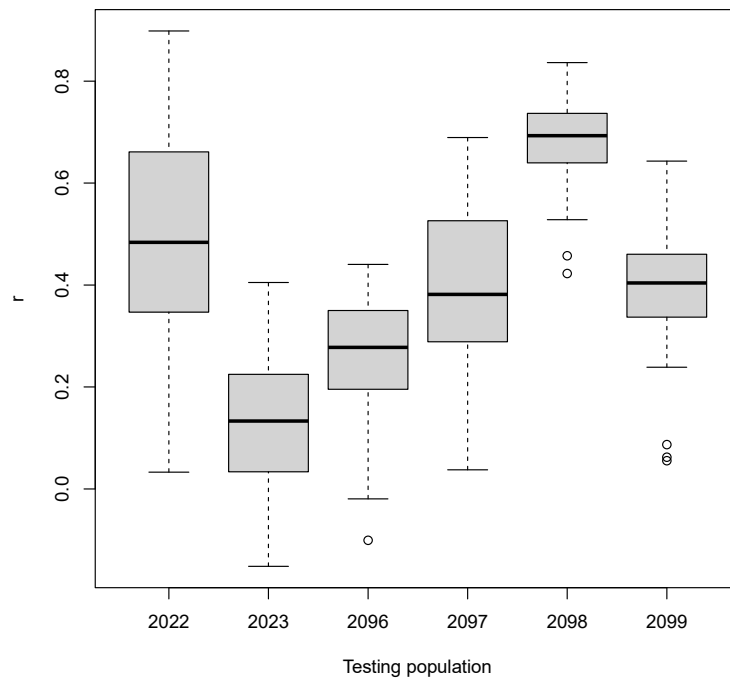


Figure S3. Distribution of correlations for prediction problem described in Table 2. 2022: Queen Anne \times Colleen, 2023: Queen Anne \times Melody, 2096: Colleen S_1 , 2097: Melody S_1 , 2098 Queen Anne S_1 , 2099: Rudolph S_1 . This plot provides a graphical statistical visualization summary of the distribution of the dataset. The BOX represents the range between the first quartile (Q1) and the third quartile (Q3), i.e., the interquartile range (IQR). The box is divided into two parts by a horizontal line, where the lower part corresponds to Q1 and the upper part to Q3. The WHISKERS extend from the BOX to indicate the data range outside IQR, and often 1.5 times the IQR. Individual data points beyond the WHISKERS are OUTLIERS, which are plotted individually. A vertical line inside the BOX represents the MEDIAN (Q2) of the dataset.

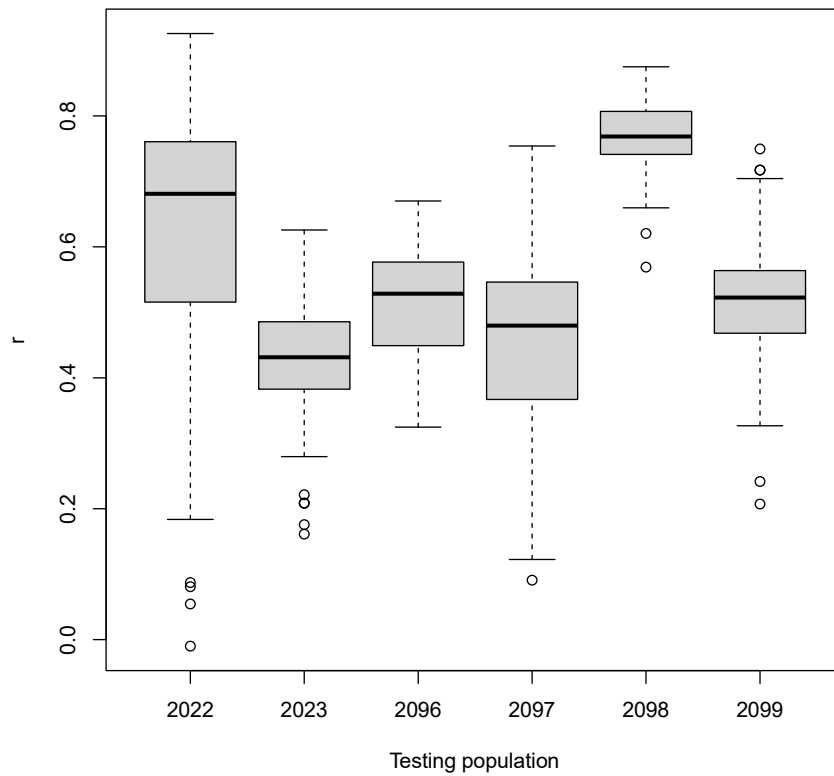


Figure S4. Distribution of correlations for prediction problem described in Table 3.

2022: Queen Anne \times Colleen, 2023: Queen Anne \times Melody, 2096: Colleen S_1 , 2097: Melody S_1 , 2098 Queen Anne S_1 , 2099: Rudolph S_1 . This plot provides a graphical statistical visualization summary of the distribution of the dataset. The BOX represents the range between the first quartile (Q1) and the third quartile (Q3), i.e., the interquartile range (IQR). The box is divided into two parts by a horizontal line, where the lower part corresponds to Q1 and the upper part to Q3. The WHISKERS extend from the BOX to indicate the data range outside IQR, and often 1.5 times the IQR. Individual data points beyond the WHISKERS are OUTLIERS, which are plotted individually. A vertical line inside the BOX represents the MEDIAN (Q2) of the dataset.

Rodomiño Ortiz is Chair Professor of Genetics and Plant Breeding at the Swedish Univ. Agricultural Sciences. He holds a PhD in Plant Breeding and Genetics from the Univ. Wisconsin-Madison and worked as a young researcher at UNALM (Perú) and Rutgers Univ. He was a scientist and director of various CGIAR Centers and held a Nordic professorship on plant genetic resources at the Royal Veterinary and Agricultural Univ. He has written over 400 journal articles and ca. 100 edited book chapters, with an h-index of 77 and 24094 citations [Google Scholar 2024.01.05]. The CGIAR awarded to IITA the 1994 King Baudouin Award to the plantain and banana improvement team, of which he was the leader. In 2012, Plant Breeding Reviews dedicated Vol. 36 to him. He was PI of the SLU/ICARDA research development project Adapting durum wheat varieties to the Senegal Basin for food security that won the 2017 Olam Prize for Innovation in Food Security. He received the Bertebos Prize 2022 for mastering the use of new molecular scientific methods for breeding crops of great importance for food supply in Africa, America, and Europe. Professor Ortiz was a member of the CGIAR Independent Science and Partnership Council (2015–2019) and the Commission on Sustainable Agriculture Intensification (2020–2021), international fellow of the Royal Swedish Academy of Agriculture and Forestry since 2019, member of the Royal Physiographic Society at Lund from 2021 onward and fellow of the African Academy of Sciences since 2021.