



**Fig S4. Performance of different GBLUP models in a three way cross. A:** All F2 are predicted using F0. **B:** 20% of F2 is predicted using F0 and rest of F2. **C:** 20% of F2 is predicted using F0, F1 and rest of F2. The following models are shown: QTN, GRM computed with all QTNs; SEQ, all SNPs; 60KI, Illumina's 60k array; 700KA, Affymetrix; 50KR, 50k random SNPs; 500KR, 500k random SNPs; MAF01, 1M SNPs with MAF < 0.01; MAF10, 1M SNPs with MAF > 0.1; 2MAF, the model uses MAF01 and MAF10. A neutral architecture was simulated and GBLUP was employed for prediction. The cross involved (LW x DU) x MS. Values reported are squared correlation between true and predicted genetic values. Dots correspond to each of the ten replicates, horizontal bars represent the mean.