File S1

Running setups of imputation packages

magicImpute

The Mathematica command line of magicImpute is given by

```
magicImpute[inputfile, model, popdesign, options]
```

where `inputfile` specifies the input genotypic data. Here `model` is set to be `{"depModel", "jointModel"}` for the population types AI-RIL and MAGIC, so that `"depModel"` is used for parental imputation, and `"jointModel"` is used for offspring imputation. And it is set to be `"jointModel"` for the population types F2 and CP, so that `"jointModel"` is used for both parental imputation and offspring imputation. See the online manual for details.

`popdesign` specifies the breeding design information that is used to compute the process parameter values of the HMM. For the F2, it is set to be `{"Pairing","Selfing"}`. For the AI-RIL, it is set to be `{"RM1-NE-1000","RM1-NE",...,"RM1-NE","Selfing", ...,"Selfing"}` where `"RM1-NE"` is repeated for 5 times, and `"Selfing"` is repeated for 6 times. For the MAGIC, it is set to be `{"Pairing", "Pairing", "Pairing", "Selfing", ..., "Selfing"}` where `"Selfing"` is repeated for 4 times. For the CP, it is specified in terms of a pedigree file.

There are many options for magicImpute. The option `imputingTarget -> All` so that we by default impute both founder and offspring. The options `founderAllelicError -> 0.005` and `offspringAllelicError -> 0.005` specify ε_F and ε_O, respectively. The option `isFounderInbred -> True` specifies that the founders are inbred for the F2, the AI-RIL, and the MAGIC, and `isFounderInbred -> False` is used for the CP. The option `imputingThreshold -> 0.9` specifies P_{impute}, The option `detectingThreshold -> 0.9` specifies P_{detect}. The option `minPhredQualScore -> 30` specifies that the quality score $phred$ so that $\varepsilon = 10^{-phred/10}$. The option `priorFounderCallThreshold -> 0.99` specifies the prior genotype calling threshold P_{call} when the input parental data are allelic depths.

Beagle v4.1

The command line used for Bealge v4.1 is given by

```
java -jar beagle.21Jan17.6cc.jar ne=100
```

where the effective population size is fixed to be 100. In addition, The gt option is used to specify input offspring genotype data, and the ref option is used to specify the imputed phased founder genotypes as the reference panel. We run Beagle with and without the reference panel.

LB-Impute

The command line used for LB-Impute is given by

```
java -jar LB-Impute.jar  -method impute -readerr 0.001
     -genotypeerr 0.01 -recombdist 10000000 -window 7
     -parentimpute -offspringimpute
```

Here the $-readerr$ option specifies the sequencing error, and it is set to be 0.001 corresponding to the quality score 30. The $-genotypeerr$ option specifies the genotype error to be 0.01, corresponding to the depth-independence allelic error probability of 0.005 in magicImpute. The two founder names are specified by the $-parents$ option, and the input and output files are specified by the options $-f$ and $-o$, respectively.

mpimpute

The R command line used for mpimpute is given by

```
mpimpute(object,what="both",threshold=0.5,calls="discrete")
```

Here the $what$ option is set so that we impute both founders and offspring, and input genotypic data and pedigree information are specified by the $object$.

Supplementary figures

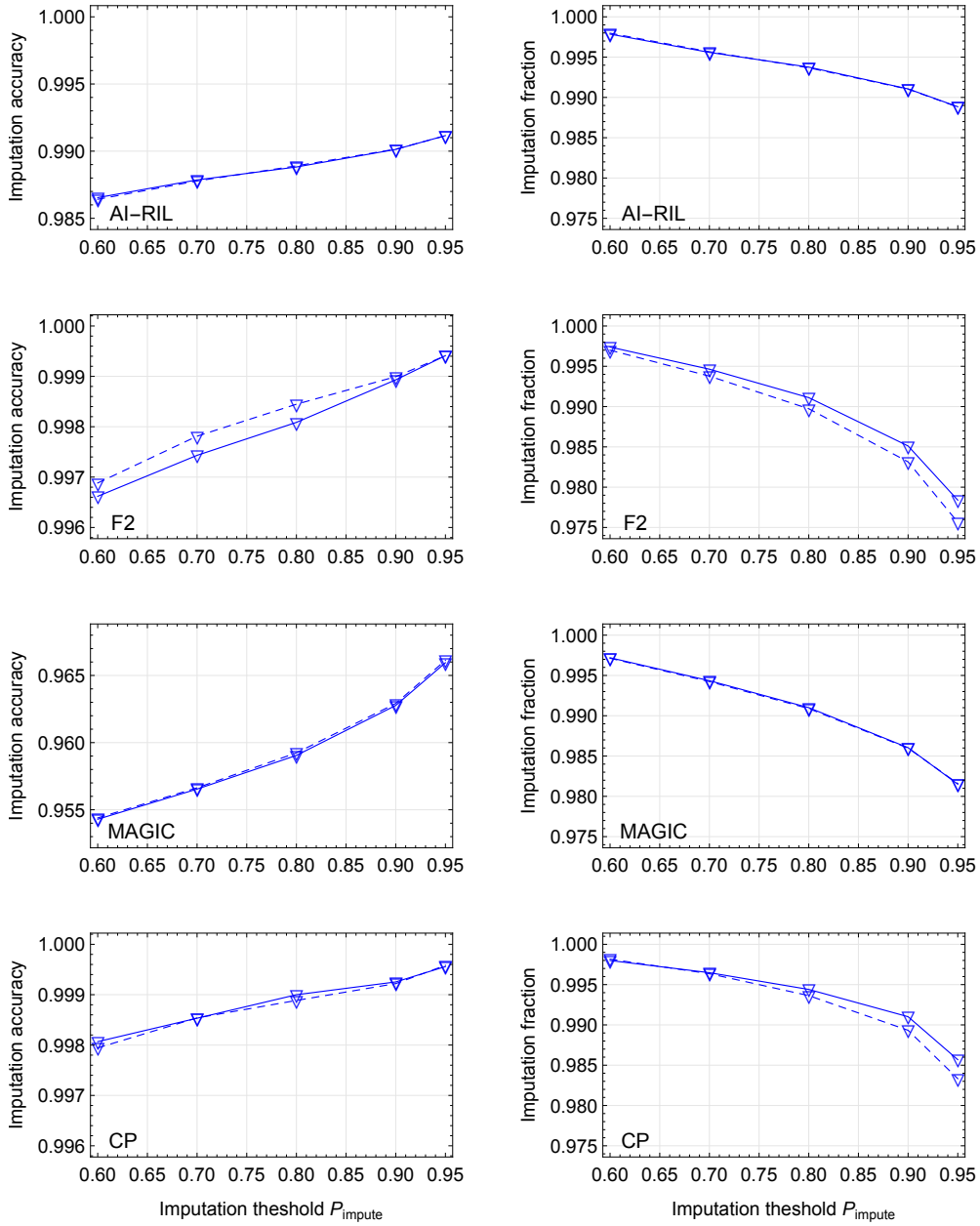

Figure S1: Sensitivity analysis of imputation threshold P_{impute} for the algorithm magicImpute. Panels from top to bottom denote the results for the AI-RIL, the F2, the MAGIC, and the CP, respectively. The solid and dashed lines denote the results corresponding to input parameter $\epsilon_O = 0.005$ and 0.05, respectively. The left and right panels denote the results for imputation accuracy and imputation fraction, respectively, which are obtained from the simulated datasets with the input data being called genotypes at read depth 0.85 and the first two founders' genotypes being not available.

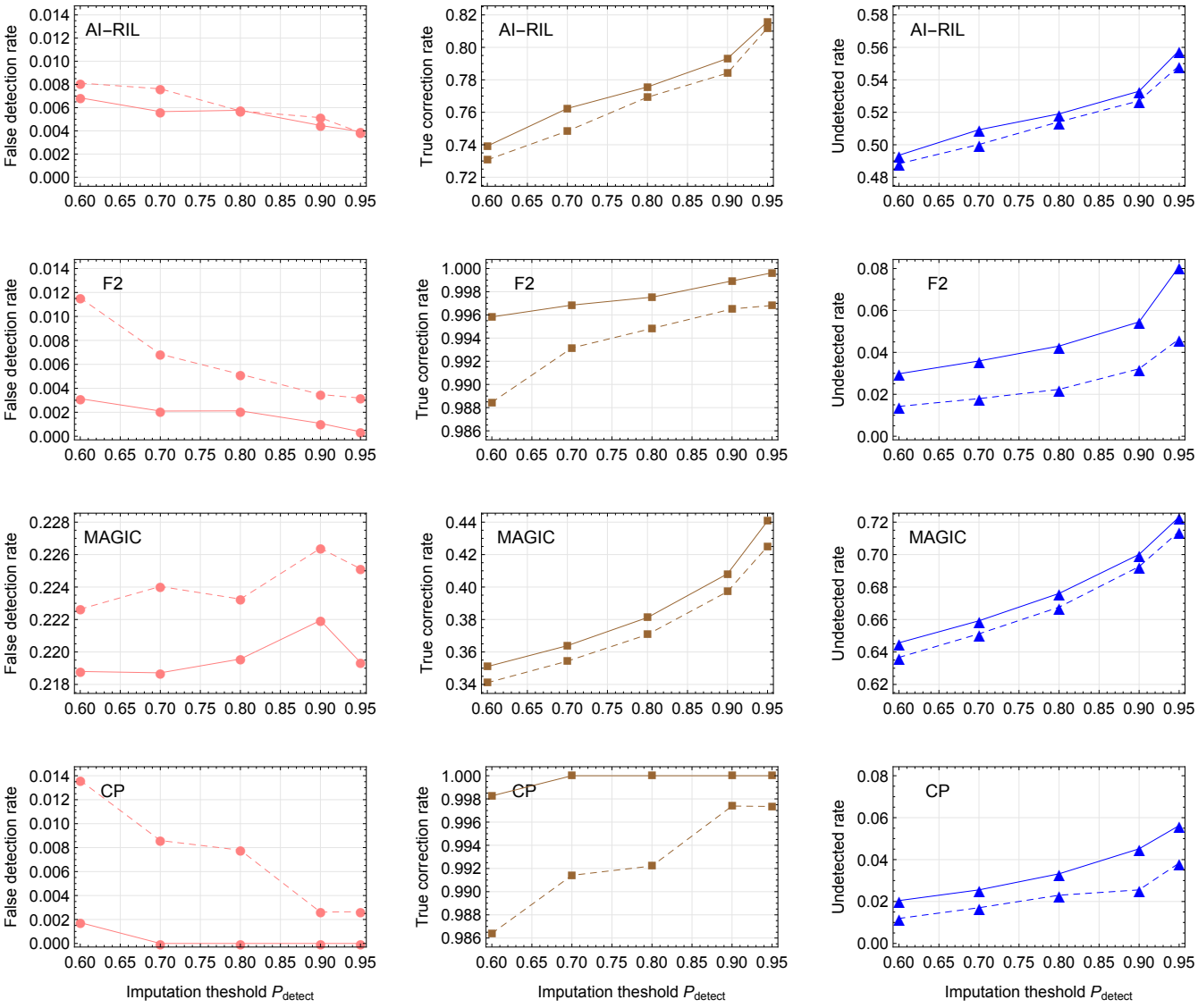

Figure S2: Sensitivity analysis of error detection threshold P_{detect} for the algorithm magicImpute. Panels from top to bottom denote the results for the AI-RIL, the F2, the MAGIC, and the CP, respectively. The solid and dashed lines denote the results corresponding to input parameter ϵ_O= 0.005 and 0.05, respectively. The left, middle and right panels denote false detection rate, true corretion rate, and undetected rate, respectively. For each simulated dataset with population size 200 and read depth 0.85, the results are obtained with the input data being called genotypes and the first two founders' genotypes being not available.

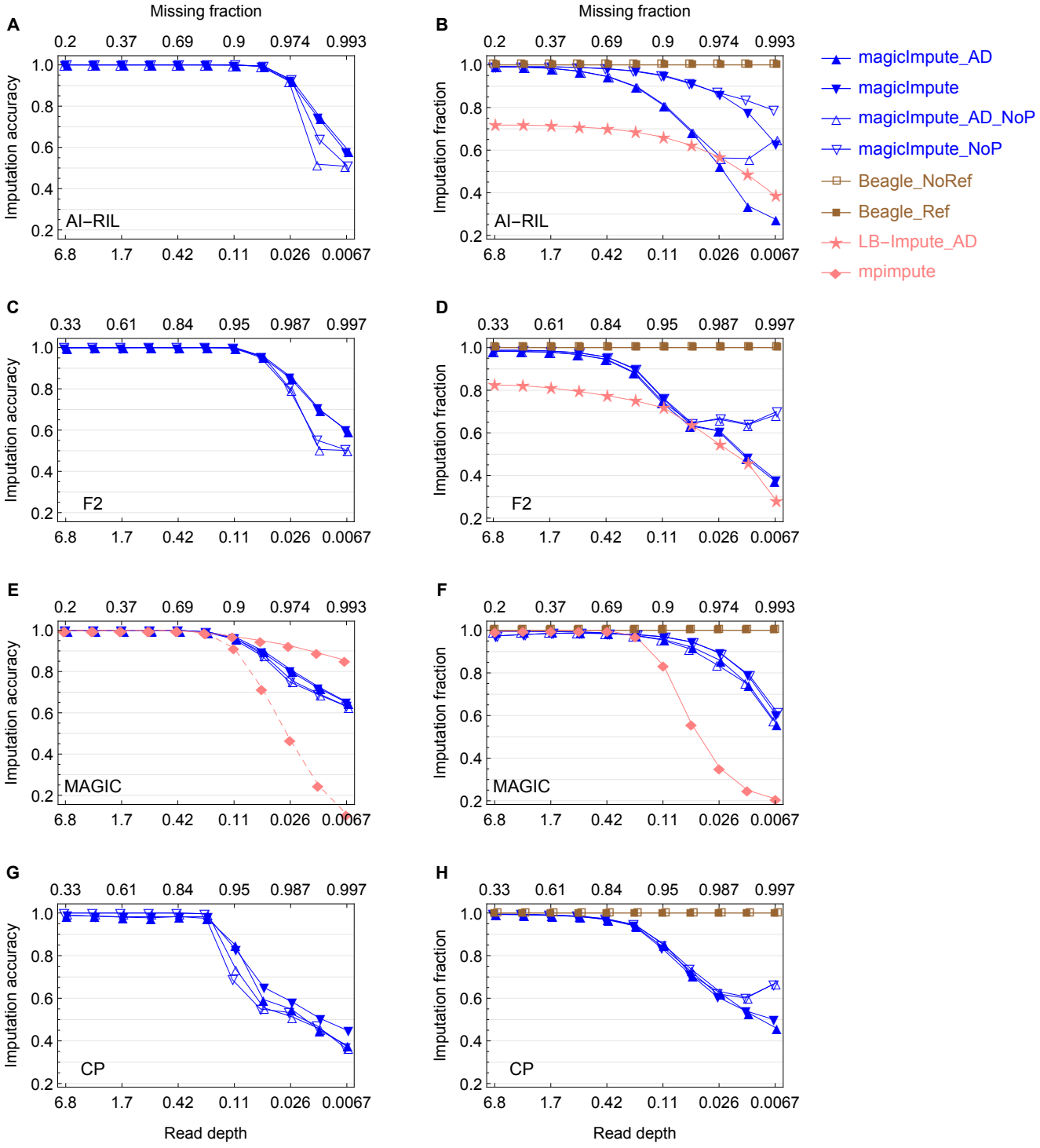

Figure S3: Simulation evaluation on the accuracy of imputing founder genotypes (left panels) and imputation fraction of offspring genotypes (right panels). Panels A&B, C&D, E&F, and G&H denote the results for the AI-RIL, the F2, the MAGIC, and the CP, respectively. The dashed lines in panel E denotes the mpimpute imputation fraction of founder genotypes. Beagle and LB-Impute do not impute founder genotypes, and magicImpute always imputes all the founder genotypes.

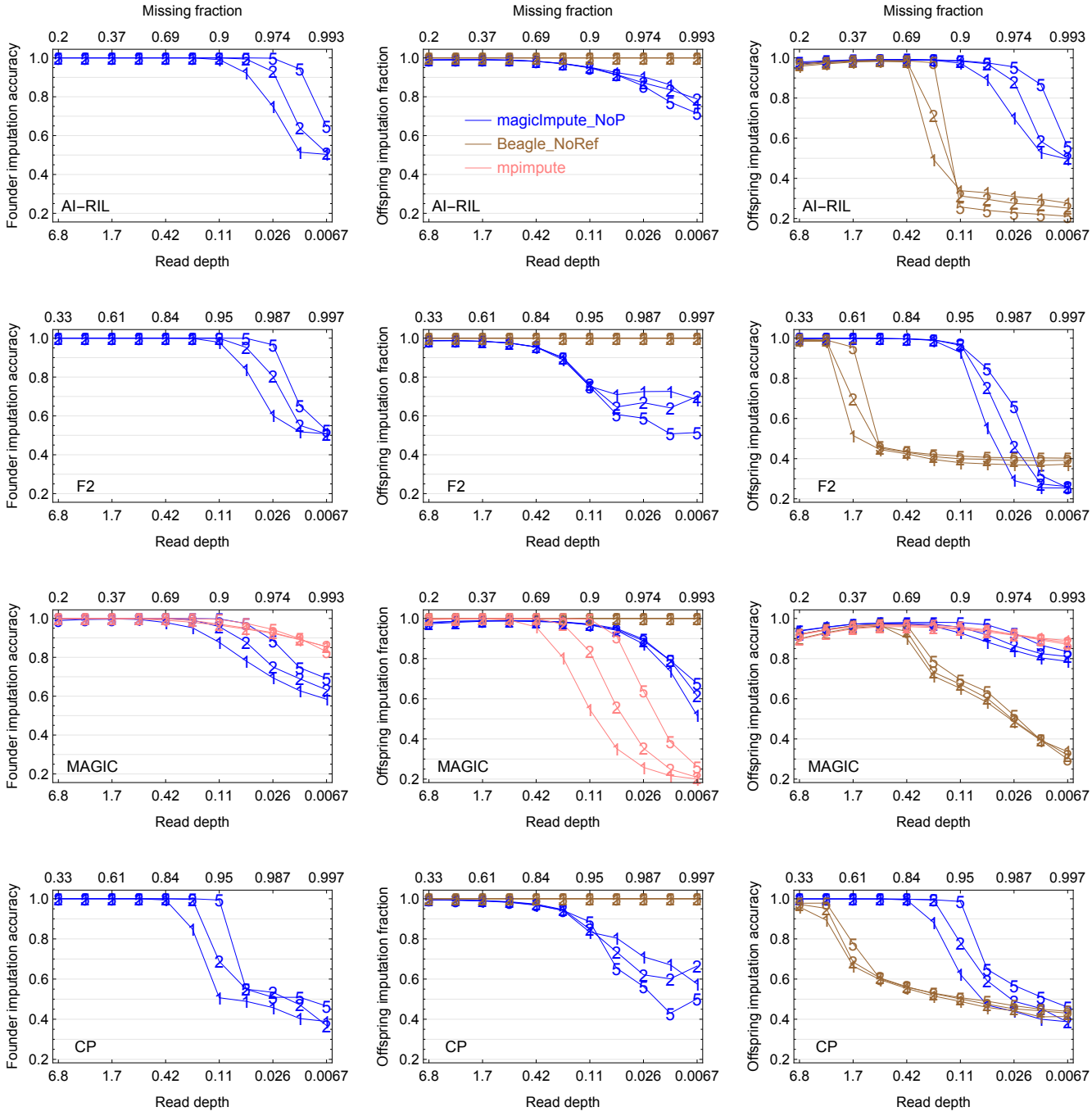

Figure S4: Dependencies of genotype imputation on population size. Panels from top to bottom denote the results for the AI-RIL, the F2, the MAGIC, and the CP, respectively. For magicImpute, the input data are called genotypes and the first two founders are missing; no reference panels for Beagle imputation. The plot markers "1", "2", and "5" denote population sizes 100, 200, and 500, respectively.

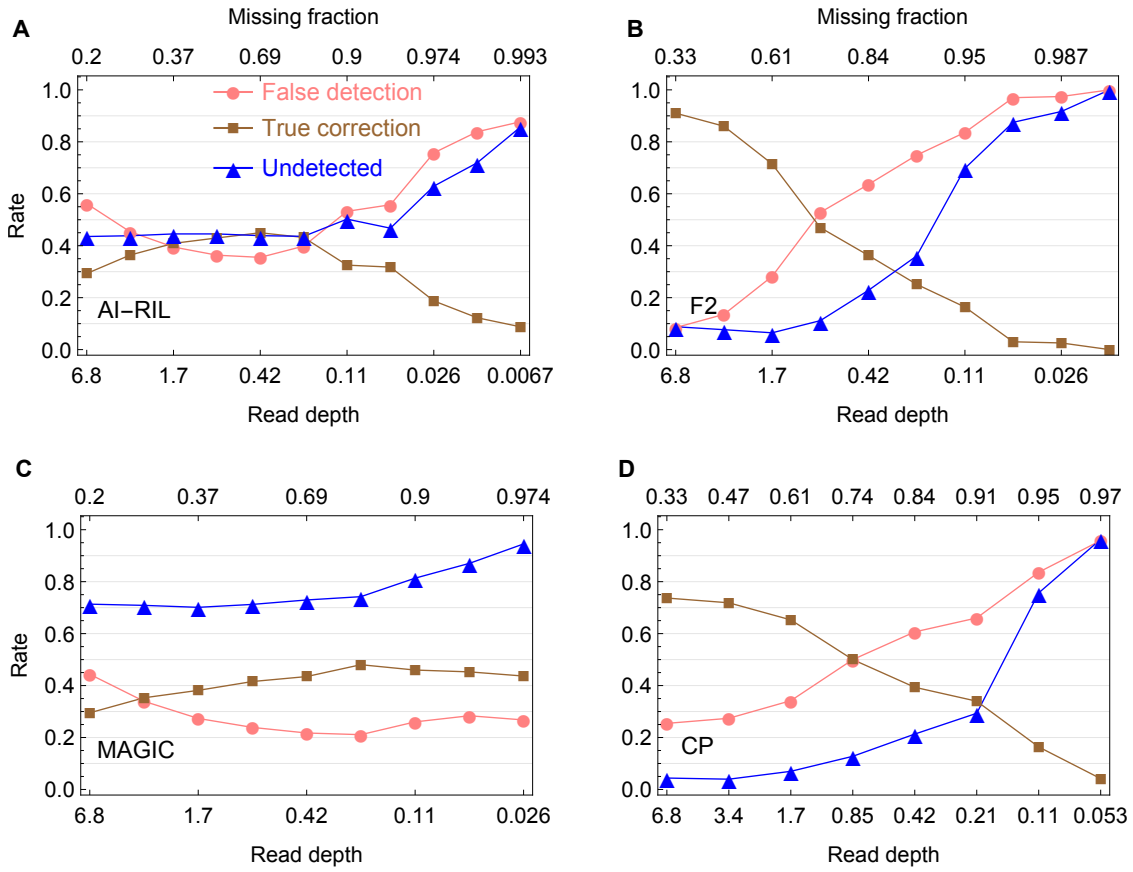

Figure S5: Similar to Figure 3 for the error detection by magicImpute but with the first two founders' genotypes being available.

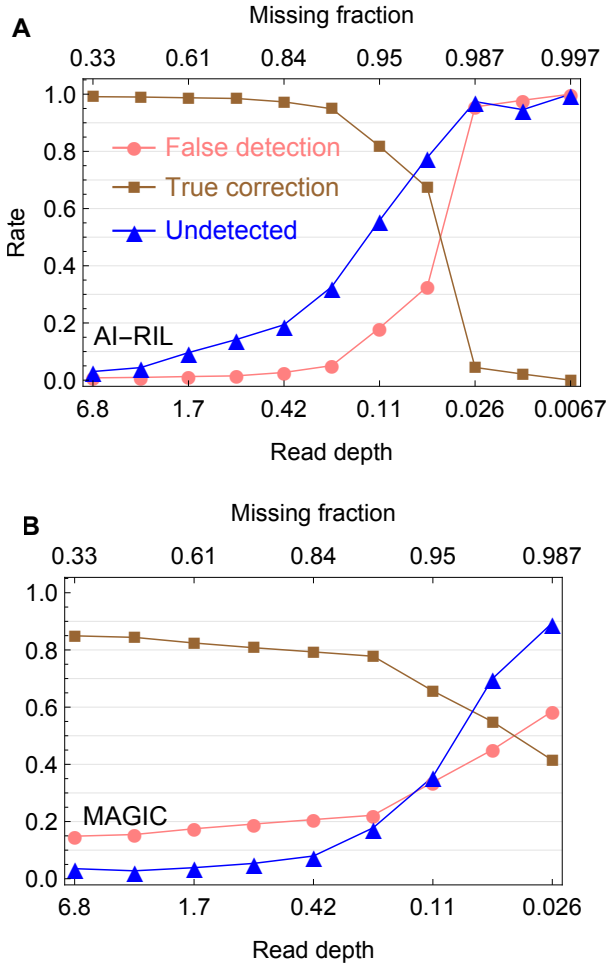

Figure S6: Similar to Figure 3 for the error detection by magicImpute but without assuming homozygosity for the almost homozygous populations AI-RIL (A) and MAGIC (B).

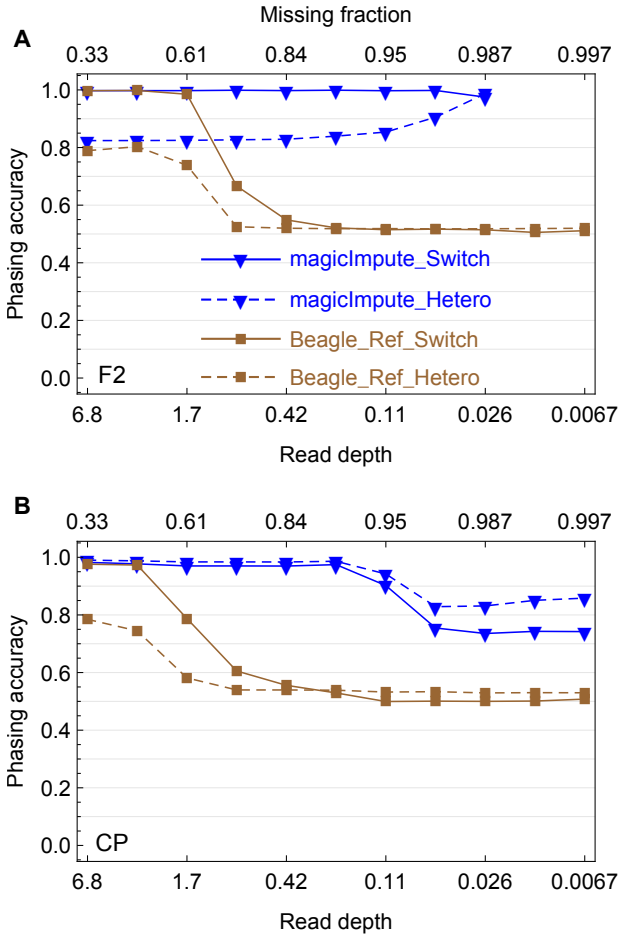

Figure S7: Similar to Figure 4 for the offspring phasing but for magicImpute with the first two founders' genotypes being available and for Beagle with the founder haplotypes (imputed by magicImpute) being the reference panels.

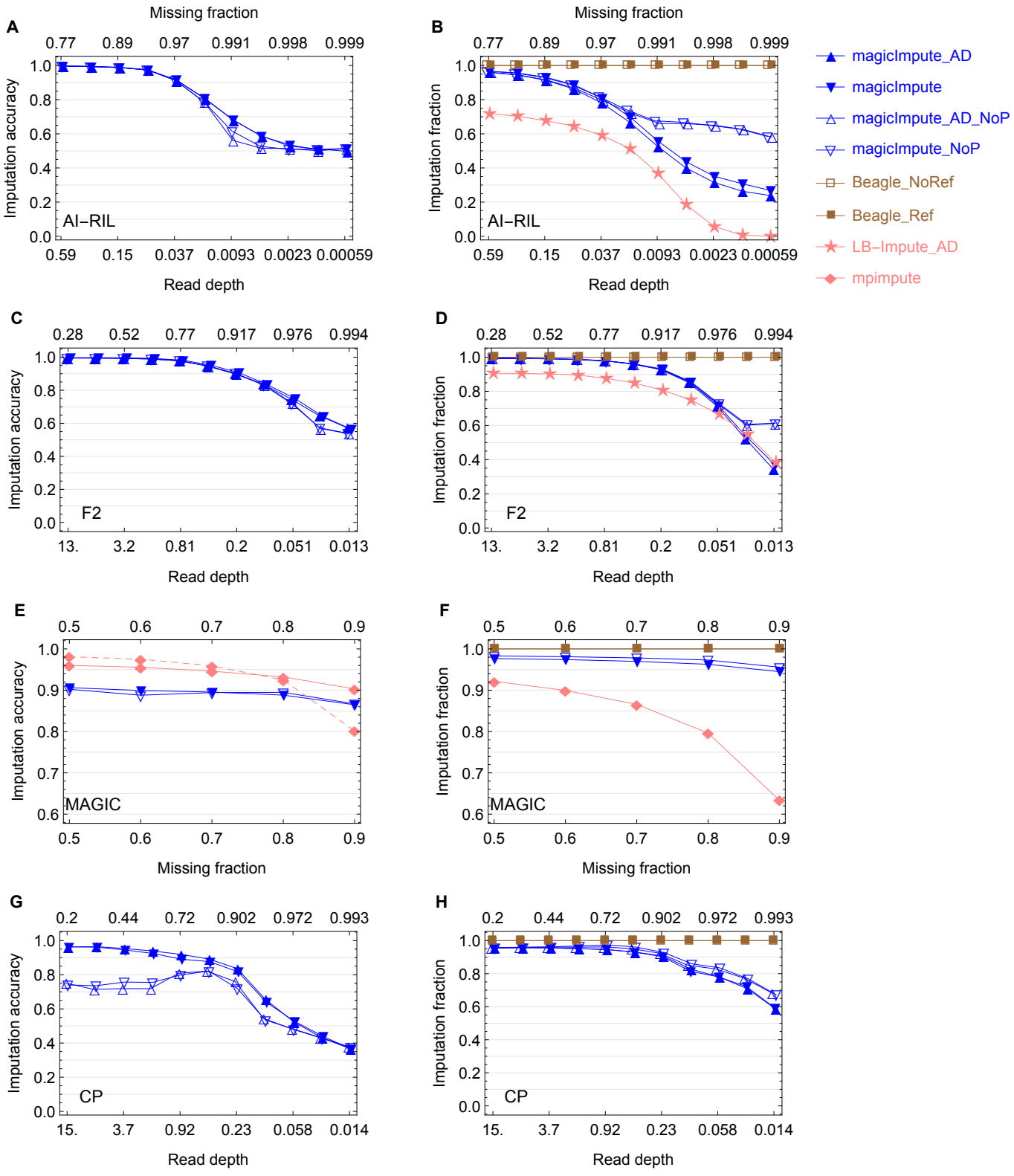

Figure S8: Evaluation on the accuracy of imputing founder genotypes and imputation fraction of offspring genotypes by real data. Panels A&B, C&D, E&F, and G&H denote the results for the AI-RIL, the F2, the MAGIC, and the CP, respectively. The dashed lines in panel E denotes the mpimpute imputation fraction of founder genotypes.