

Additional file 1. SAS codes (version 9.3) used to implement first stage of phenotypic analysis referred in Table 4.

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/*****
***** Appendix A*****
***** Some SAS code to fit the models of the first stage *****
*****referred in Table 4*****
*****/

**** Model 1. Baseline model -----;

proc mixed data=data1 ;
ods output FitStatistics=fits_M1 lsmeans= adjmeans_M1 covparms=cp_M1;
by year loc;
class year loc genotype tester trial rep block row column ;
model y1=genotype*tester/ddfm=residual solution ;
random int rep rep*block / sub=trial;
lsmeans genotype*tester /cov;
run;

**** Model 2. Baseline + row + column -----;

proc mixed data=data1;
ods output FitStatistics=fits_M2 lsmeans= adjmeans_M2 covparms=cp_M2;
by year loc;
class year loc genotype tester trial rep block row column ;
model y1=genotype*tester/ddfm=residual solution ;
random int rep rep*block / sub=trial;
random row / sub=trial*rep;
random column /sub=trial*rep;
lsmeans genotype*tester /cov;
run;

**** Model 3. Baseline ----- AR(1) ;

proc mixed data=data1;
ods output FitStatistics=fits_M3 lsmeans= adjmeans_M3 covparms=cp_M3;
by year loc;
class year loc genotype tester trial rep block row column plot ;
model y1=genotype*tester/ddfm=residual solution ;
random int rep rep*block / sub=trial;
repeated plot / sub=trial*rep*block type=AR(1);
lsmeans genotype*tester /cov;
parms 1 1 1 0.1 1 / lowerb= . , . , . , 1e-8 , . ;
run;

**** Model 4. Baseline ----- LV + nugget ;

proc mixed data=data1;
ods output FitStatistics=fits_M4 lsmeans= adjmeans_M4 covparms=cp_M4;
by year loc;
class year loc genotype tester trial rep block row column plot ;
model y1=genotype*tester/ddfm=residual solution ;
random int rep rep*block / sub=trial;
random plot / sub=trial*rep*block type=LIN(1) ldata=LV_matrix;
lsmeans genotype*tester /cov;
parms 1 1 1 0.1 1 / lowerb=. , . , . , 1e-8, . ;

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run;
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*** Model 5. Baseline ----- AR(1) x AR(1);
```

```
proc mixed data=data1;
ods output FitStatistics=fits_M5 lsmeans= adjmeans_M5 covparms=cp_M5;
by year loc;
class year loc genotype tester trial rep block row column plot ;
model y1=genotype*tester/ddfm=residual solution ;
random int rep rep*block / sub=trial;
repeated row*column / sub=trial*rep type=SP(POWA) (ro co);
lsmeans genotype*tester /cov;
parms 1 1 1 0.1 0.1 1 / lowerb= . , . , . , 1e-8 , 1e-8 , . ;
run;
```

```
*** Model 6. Baseline + row + column ----- AR(1) x AR(1);
```

```
proc mixed data=data1;
ods output FitStatistics=fits_M6 lsmeans= adjmeans_M6 covparms=cp_M6;
by year loc;
class year loc genotype tester trial rep block row column plot ;
model y1=genotype*tester/ddfm=residual solution ;
random int rep rep*block / sub=trial;
random row / sub=trial*rep;
random column/ sub=trial*rep;
repeated row*column / sub=trial*rep type=SP(POWA) (ro co); *ro and co are
numerical variables with row and column coordinates;
lsmeans genotype*tester /cov;
parms 1 1 1 1 1 0.1 0.1 1 / lowerb= . , . , . , . , . , 1e-8 , 1e-8 , . ;
run;
```

```
*** Model 7. Baseline ----- AR(1) + nugget ;
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```
proc mixed data=data1;
ods output FitStatistics=fits_M7 lsmeans= adjmeans_M7 covparms=cp_M7;
by year loc;
class year loc genotype tester trial rep block row column plot ;
model y1=genotype*tester/ddfm=residual solution ;
random int rep rep*block / sub=trial;
repeated plot / sub=trial*rep*block local type=AR(1);
lsmeans genotype*tester /cov;
parms (0 1) (1) (1) (1) (0.1) (1) / lowerb= . , . , . , . , 1e-8 , . ;
run;
```

```
*** Model 8. Baseline ----- AR(1) x AR(1) + nugget;
```

```
proc mixed data=data1;
ods output FitStatistics=fits_M8 lsmeans= adjmeans_M8 covparms=cp_M8;
by year loc;
class year loc genotype tester trial rep block row column plot ;
model y1=genotype*tester/ddfm=residual solution ;
random int rep rep*block / sub=trial;
random row / sub=trial*rep;
repeated row*column / sub=trial*rep local type=SP(POWA) (ro co); *ro and co
are numerical variables with row and column coordinates;
lsmeans genotype*tester /cov;
parms 1 1 1 1 0.1 0.1 1 / lowerb= . , . , . , . , 1e-8 , 1e-8 , . ;
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```
run;
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```
*** Model 9. Baseline + row + column ----- AR(1) x AR(1) + nugget;
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```
proc mixed data=data1;
ods output FitStatistics=fits_M8 lsmeans= adjmeans_M8 covparms=cp_M8;
by year loc;
class year loc genotype tester trial rep block row column plot ;
model y1=genotype*tester/ddfm=residual solution ;
random int rep rep*block / sub=trial;
random row / sub=trial*rep;
random column/ sub=trial*rep;
repeated row*column / sub=trial*rep local type=SP(POWA) (ro co); *ro and co
are numerical variables with row and column coordinates;
lsmeans genotype*tester /cov;
parms 1 1 1 1 1 1 0.1 0.1 1 / lowerb= . , . , . , . , . , 1e-8 , 1e-8 , .
;*hold=6,7;
run;
```