

Table S2. Overview of the different scenarios used for genomic prediction (GP), brief description, mathematical description, validation scheme, sample size (N_i) and composition of the training set.

| Scenario | | Description | Math. | Validation scheme [†] | Sample size (N_i) and TS composition |
|------------|---|---|---|--------------------------------|---|
| sL | one-library | GP within a single library | $L_i \rightarrow L_i$ | LOOCV | a) $N_i = 50$ b) $N_i = 20, \dots, 90$ |
| LwL | Library-with-library | GP trained on a single library to predict another library | $L_i \rightarrow L_{i*}$ | SV | a) $N_i = 50$ b) $N_i = 90$ |
| cLi | Library-with-combined-libraries-inclusive | GP combining libraries for the TS, including the library used as PS | $\bigcup_{i \in I} L_i \rightarrow L_i$ | LOOCV | $50 \times 4 = 200$ $I = \{\text{GB, SF, SM, WA}\}$ |
| cLe | Library-with-combined-libraries-exclusive | GP combining libraries for the TS, excluding the library used as PS | $\bigcup_{i \in I \setminus \{i'\}} L_i \rightarrow L_{i*}$ | SV | a) $50 \times 3 = 150$ $I = \{\text{GB, SF, SM, WA}\}$ b) $19 \times 5 = 95$, $I = \{\text{GB, SF, SM, WA, CG, RT}\}$ |

[†] LOOCV = leave-one-out cross-validation; SV = simple validation