

## Supplementary Methods section S1 Text

## $Cov(GEBV_{I_{pr}})$ adjusted to account for the effect of first selection on $I_{v}$ :

From standard normal distribution theory, it follows that covariance between variables is affected by selection with truncation selection on trait y. For example, the genetic covariance between w and z after selection on y, i.e.,  $\sigma_{wz}^*$ , is:

$$\sigma_{wz}^* = \sigma_{wz} - k \frac{\sigma_{wy} \sigma_{zy}}{\sigma_v^2}, \dots (a)$$

where k=i(i-x), i is the selection intensity, and x is the standardized truncation point.

Then let an index at the second stage, which was adjusted to the first selection on  $I_y$  , be  $I_{prs}$  . Therefore,

$$var(I_{prs}) = var(I_{pr}) - k \frac{cov(I_{pr}, I_{y})cov(I_{y}, I_{pr})}{var(I_{y})}$$

$$= \operatorname{var}(I_{pr}) - k \frac{\operatorname{cov}(I_{pr}, I_{y}) \operatorname{cov}(I_{y}, I_{pr})}{\operatorname{var}(I_{y}) \operatorname{var}(I_{pr})} \operatorname{var}(I_{pr}) = \operatorname{var}(I_{pr}) (1 - r_{hy, Ipr}^{2} k),$$

where k is computed as the variance reduction coefficient during first selection on  $I_{_{V}}$ .

GEBVs for  $I_y$  and  $I_{pr}$  are assumed according to single-step genomic BLUP. When the traits are the same between the selection index and the aggregate genotype, selection index coefficients composed of GEBVs that are computed from MT-BLUP are the same as the economic weights of the aggregate genotype [7, 8, 18] Hence,

$$Cov_{ty,tyr} = \begin{bmatrix} a_1, a_2...a_m \end{bmatrix} Cov(GEBV_{I_y}, GEBV_{I_{pg}})_{m \times m} \begin{bmatrix} a_1 \\ a_2 \\ \vdots \\ a_m \end{bmatrix} = \begin{bmatrix} a_1 \\ a_2 \\ \vdots \\ a_m \end{bmatrix}$$

$$\begin{bmatrix} a_{1}a_{2} & \cdots & a_{m} \end{bmatrix} \begin{bmatrix} r_{GEBV1,bp}^{2}r_{GEBV1,bp}^{2}\sigma_{G_{1}}^{2} & r_{GEBV1,b}^{2}r_{GEBV2,bp}^{2}\sigma_{G_{12}} & \cdots & r_{GEBV1,b}^{2}r_{GEBVm,bp}^{2}\sigma_{G_{1n}} \\ & & & & & & & & & \\ r_{GEBV2,bp}^{2}\sigma_{G_{2}}^{2} & \cdots & r_{GEBV2,bp}^{2}\sigma_{G_{2m}}^{2} & \cdots & r_{GEBV2,bp}^{2}r_{GEBVm,bp}^{2}\sigma_{G_{2m}} \\ & & & & & & & & \\ & & & & & & & & \\ symmetry & & & & & & & & & \\ & & & & & & & & \\ symmetry & & & & & & & & \\ \end{bmatrix} \begin{bmatrix} a_{1} \\ a_{2} \\ \vdots \\ a_{m} \end{bmatrix} ....(b)$$

, and

$$\text{var}(I_{pr}) = \begin{bmatrix} a_1, a_2 ... a_m \end{bmatrix} \begin{bmatrix} r_{GEBV1, lpr}^2 \sigma_{G_1}^2 & r_{GEBV1, lpr}^2 r_{GEBV1, lpr}^2 r_{GEBV2, lpr}^2 \sigma_{G_{12}} & ... & r_{GEBV1, lpr}^2 r_{GEBVm, lpr}^2 \sigma_{G_{1m}} \\ & & & & & & & & & \\ r_{GEBV2, lpr}^2 \sigma_{G_2}^2 & ... & & & & & & \\ r_{GEBV2, lpr}^2 r_{GEBVm, lpr}^2 r_{GEBVm, lpr}^2 \sigma_{G_{2m}} \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \\ ... \\ ... \\ ... \\ ... \\ symmetry & ... & ... & & & & \\ r_{GEBVm, lpr}^2 \sigma_{G_m}^2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \\ ... \\ ... \\ ... \\ ... \\ a_m \end{bmatrix}$$

where  $a_i$  is a known economic value for the  $i^{th}$  trait. As a result,

$$r_{Iy,Ipr} = \frac{\text{cov}_{Iy,Ipr}}{\sqrt{\text{var}(I_y)\text{var}(I_{pr})}}.$$

Therefore, (co)variance (GEBV) in  $I_{prs}$  or  ${
m cov}(GEBV_{I_{prs}})$  which was adjusted to the effects due to first selection on  $I_y$ , can be computed from equation (a); that is,

$$Cov(\textit{GEBV}_{I_{pr}})_{m \sim m} = Cov(\textit{GEBV}_{I_{pr}})_{m \sim m} - \frac{k}{\text{var}(ly)}Cov(\textit{GEBV}_{I_{pr}}, \textit{GEBV}_{I_{pr}}) aa^{*}Cov(\textit{GEBV}_{I_{pr}}, \textit{GEBV}_{I_{pr}})$$

where  $GEBV_{I_{prs}}$  is an  $m\times 1$  vector of GEBVs in second-stage selection  $(I_{prs})$ .  $Cov(GEBV_{I_{pr}})_{m\times m}$  is as shown in equation (1) in main manuscript; a is an  $m\times 1$  vector of economic value for m traits in the aggregate genotype; and  $Cov(GEBV_{I_{pr}}, GEBV_{I_y})$  is as shown in equation (b).  $Cov(GEBV_{I_{pr}}, GEBV_{I_y})$  is the transpose of  $Cov(GEBV_{I_y}, GEBV_{I_{pr}})$ .

## Supplementary Methods section S2 Text

Variance of first selection index for SS and  $\mathrm{SD}(I_{y_{S,t}})$ , and that of second-stage selection index for SS  $(I_{prs_{SS,t}})$  and SD  $(I_{prs_{co.}})$ :

$$\operatorname{var}(I_{\gamma_{i,j}}) = \begin{bmatrix} a_i \\ a_2 \\ \vdots \\ a_m \end{bmatrix} \operatorname{cov}(GEBY_{b_{ij}}), \begin{bmatrix} a_i \\ a_2 \\ \vdots \\ a_m \end{bmatrix} = \begin{bmatrix} a_i a_2 \dots a_m \end{bmatrix} \begin{bmatrix} r_{GEW1,b_{ij}} r_{G_{ij}}^2 & r_{GEW1,b_{ij}} r_{GEW2,b_{ij}}^2 \sigma_{G_{ij,j}} & \cdots & r_{GEW1,b_{ij}}^2 r_{GEWm,b_{ij}} \sigma_{G_{ij,k}} \\ \vdots & \ddots & \ddots & \ddots & \vdots \\ r_{GEW1,b_{ij}} r_{GEW1,b_{ij}}^2 r_{GEW1,b_{ij}$$

..... (a

and, 
$$var(I_{prs_{SS_{s}}}) = [a_{1}, a_{2}, ...a_{m}] cov(GEBV_{Iprs_{SS}})_{t} \begin{bmatrix} a_{1} \\ a_{2} \\ . \\ . \\ a_{m} \end{bmatrix}$$

where  $Cov(GEBV_{Iprs_{SS}})_t$  is given by replacing  $I_y$  with  $I_{prs}$  in equation (a),  $r_{GEBVi,ly_{s,t}}^2$  is the reliability of GEBV in  $I_{y_{S,t}}$  for the  $i^{th}$  trait in the sire population of generation t,  $\sigma_{G_{l,s,t}}^2$  is the genetic variance for the  $i^{th}$  trait in the sire population of generation t, and  $\acute{o}_{G_{ij},S,t}$  is the genetic covariance for traits i and j in the sire population of generation t.

## Supplementary Methods section S3 Text

Variance of first selection index for  $DS(I_{y_{DS,I}})$  and  $DD(I_{y_{DD,I}})$ , and that of second-stage selection index for  $DS(I_{prs_{DS,I}})$ :



$$\operatorname{var}(I_{y_{DS_{J}}}) = [a_{1}, a_{2}, \dots a_{m}] \operatorname{Cov}(GEBV_{b_{DS}})_{t} \begin{bmatrix} a_{1} \\ a_{2} \\ \vdots \\ a_{m} \end{bmatrix} =$$

$$\left[ a_1, a_2, \dots a_m \right] \begin{bmatrix} r_{GEBV1, b_{TRS}}^2 \sigma_{G_{D,D}}^2 & r_{GEBV1, b_{TRS}}^2 r_{GEBV}^2 - b_{TRS} \sigma_{G_{D,D}}^2 & \dots & r_{GEBV1, b_{TRS}}^2 r_{GEBVm, b_{TRS}}^2 \sigma_{G_{Im,D,J}}^2 \\ \vdots & & & & & & & & & & & & & \\ I_{a_1} a_2 & \dots & & & & & & & & \\ I_{a_2} & \vdots & & & & & & & & \\ I_{a_3} & \vdots & & & & & & & \\ I_{a_3} & \vdots & & & & & & \\ I_{a_3} & \vdots & & & & & & \\ I_{a_3} & \vdots & & & & & & \\ I_{a_3} & \vdots & & & & & \\ I_{a_3} & \vdots & & & & & \\ I_{a_3} & \vdots & & & \\ I_{a_4} & \vdots & & & \\ I_{a_5} & \vdots & & \\ I_{a_5} & \vdots & & \\ I_{a_5} & \vdots & & & \\ I_{a_5} & \vdots & & & \\ I_{a_5} & \vdots & & \\ I_{a_5} & \vdots & & & \\$$

where  $r_{\textit{GEBVi},\textit{Iy}_{DS,\textit{J}}}^2$  is the reliability of GEBV in  $I_{\textit{y}_{DS,\textit{J}}}$  for the  $i^{th}$  trait in the dam population of generation t,  $\sigma_{G_{i,D,I}}^2$  is the genetic variance for the  $i^{th}$  trait in the dam population of generation t, and  $\sigma_{G_{i,j,D,t}}$  is the genetic covariance for traits i and j in the dam population of generation t. In addition,

$$\operatorname{var}(I_{prs_{DS_{J}}}) = \left[a_{1}, a_{2}, \dots a_{m}\right] \operatorname{Cov}(\operatorname{GEBV}_{lprs_{DS}})_{t} \begin{bmatrix} a_{1} \\ a_{2} \\ \vdots \\ a_{m} \end{bmatrix},$$

$$\text{var}(I_{y_{10,0}}) = \begin{bmatrix} a_1, a_2, \dots a_m \end{bmatrix} \begin{bmatrix} r_{GEBY1, b_{10,0}}^2 \sigma_{G_{1,D}}^2 & r_{GEBY1, b_{100}}^2 r_{GEBY1, b_{100}}^2 \sigma_{GEBY2, b_{100}}^2 \sigma_{G_{2,D,1}}^2 & \dots & r_{GEBY1, b_{100}}^2 r_{GEBYm, b_{20,0}}^2 \sigma_{G_{m,D,1}}^2 \\ \vdots & & & & & & & & \\ r_{GEBY2, b_{100}}^2 \sigma_{G_{2,D,1}}^2 & \dots & & & & & \\ r_{GEBY2, b_{20,0}}^2 \sigma_{G_{2,D,1}}^2 & \dots & & & & \\ \vdots & & & & & & & \\ symmetry & & & & & & & \\ r_{GEBYm, b_{20,0}}^2 \sigma_{G_{m,D,1}}^2 & \sigma_{m,D,1}^2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \\ \vdots \\ a_m \end{bmatrix}$$

where  $r_{GEBVi,Iy_{DD,j}}^2$  is the reliability of GEBV in  $I_{y_{DD,j}}$  for the  $i^{th}$  trait in the dam population of generation t.