In order to fully specify the likelihood function in equation 3 , we need to calculate $p\left(A_{i} \mid Y_{1 i}, Y_{2 i}\right)$
and $p\left(Y_{1 i}, Y_{2 i} \mid \vec{X}_{i}, \vec{Z}_{i}\right)$. According the null model, the primary and secondary traits in the general population follow a multivariate normal distribution. Therefore, $p\left(Y_{1 i}, Y_{2 i} \mid \vec{X}_{i}, \vec{Z}_{i}\right)$ satisfies

$$
\binom{Y_{1 i}}{Y_{2 i}} \sim \operatorname{MVN}\left(\binom{\beta_{10}+\sum_{s} \beta_{1 s} X_{i}^{s}+\sum_{j_{1}} \alpha_{1 j_{1}} Z_{i j_{1}}}{\beta_{20}+\sum_{j_{2}} \alpha_{2 j_{2}} Z_{j_{2}}},\left[\begin{array}{cc}
\sigma_{1}^{2} & \rho \sigma_{1} \sigma_{2} \\
\rho \sigma_{1} \sigma_{2} & \sigma_{2}^{2}
\end{array}\right]\right)
$$

When selected samples are used, it is assumed that the sampling proportions from each extreme tail are known. For a selective sampling study that collects $N^{H}$ individuals from the upper extreme (i.e. with primary trait $Y_{1 i} \geq y^{H}$ ) and $N^{L}$ individuals from the lower extreme (i.e. with primary trait $\left.Y_{1 i} \leq y^{L}\right)$, the probability $p\left(A_{i} \mid Y_{1 i}, Y_{2 i}\right)$ in the likelihood satisfies

$$
p\left(A_{i} \mid Y_{1 i}, Y_{2 i}\right) \propto \begin{cases}N^{H} / \operatorname{Pr}\left(Y_{1 i} \geq y^{H}\right) & \text { if } Y_{1 i} \geq y^{H} \\ N^{L} / \operatorname{Pr}\left(Y_{1 i} \leq y^{H}\right) & \text { if } Y_{1 i} \leq y^{L}\end{cases}
$$

The model is also applicable to random population based studies, where each individual has equal probability of being sampled. In this case, the sampling probability is proportional to a constant, regardless of the primary and secondary trait values, i.e. $p\left(A_{i} \mid Y_{1 i}, Y_{2 i}\right) \propto C$.

In order to obtain interchangeable residuals under the null hypothesis, the likelihood model needs to be re-parameterized. Specifically, we use $\tau_{1}=\sigma_{1}, \tau_{2}=\left(1-\rho^{2}\right) \sigma_{2}, \beta_{2 \gamma_{1}}=\sigma_{2} \rho / \sigma_{1}$. The Jacobian for the transformation is given by
$\partial\left(\tau_{1}, \tau_{2}, \beta_{2 \mathfrak{r}_{1}}\right) / \partial\left(\sigma_{1}, \sigma_{2}, \rho\right)=\left(\begin{array}{ccc}1 & 0 & 0 \\ 0 & 1-\rho^{2} & -2 \rho \sigma_{2} \\ -\rho \sigma_{2} / \sigma_{1}^{2} & \rho / \sigma_{1} & \sigma_{2} / \sigma_{1}\end{array}\right)$. The determinant of
$\partial\left(\tau_{1}, \tau_{2}, \beta_{2 r_{1}}\right) / \partial\left(\sigma_{1}, \sigma_{2}, \rho\right)$ is always positive and non-zero, i.e.
$\operatorname{det}\left(\partial\left(\tau_{1}, \tau_{2}, \beta_{2 r_{1}}\right) / \partial\left(\sigma_{1}, \sigma_{2}, \rho\right)\right)=1+\rho^{2} \sigma_{2} / \sigma_{1}>0$ Therefore, the transformation is one-to-one and non-degenerate. After the re-parameterization, an equivalent mean model can be fitted,

$$
\left\{\begin{array}{c}
\mu\left(Y_{1 i}\right)=\beta_{10}+\sum_{s} \beta_{1 s} X_{s}+\sum_{j_{1}} \alpha_{1 j_{1}} Z_{j_{1}} \\
\mu\left(Y_{2 i}\right)=\beta_{20}+\beta_{2 r_{i}}\left(Y_{1 i}-\mu\left(Y_{1 i}\right)\right)+\sum_{j_{2}} \alpha_{2 j_{2}} Z_{j_{2}}
\end{array}\right.
$$

The residuals $e_{1 i}=Y_{1 i}-\mu\left(Y_{1 i}\right)$ and $e_{2 i}=Y_{2 i}-\mu\left(Y_{2 i}\right)$ from the model are interchangeable under the null hypothesis.

