***Supplementary Material***

**Including phenotypic causal networks in genome-wide association studies using mixed effects structural equation models**

**Running Head:** Structural equation modeling for association studies

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**Figure 1**. Scatter plots of comparing MTM-GWAS effects with 1) total effects and 2) decomposition of total effects into direct and indirect effects from SEM-A75. All decomposed effects are from the common BM🡪BW causal path.



**Figure 2.** Scatter plots of comparing MTM-GWAS effects with 1) total effects and 2) decomposition of total effects into direct and indirect effects from SEM-G75. All decomposed effects are from the common BM🡪BW causal path.



**Figure 3**. Scatter plots of comparing MTM-GWAS effects with 1) total effects and 2) decomposition of total effects into direct and indirect effects from SEM-A85. All decomposed effects are from the common BM🡪BW causal path.



**Figure 4**. Scatter plots of comparing MTM-GWAS effects with 1) total effects and 2) decomposition of total effects into direct and indirect effects from SEM-A95. All decomposed effects are from the common BM🡪BW causal path.



**Figure S5**. Manhattan plots showing –log10 (corrected p-value) of overall, direct, and indirect SNP effects using a full recursive model based on A matrix (SEM-A75) for house-hen egg production (HHP) and the total effects from multiple-trait (MTM-A).The horizontal blue line represent the threshold for false discovery rate of 5%.