Supplementary Figures

Figure S1. Direction of effects for causality model with rs6515375, mRNA expression of CST3, and FEV1 % predicted. Data are presented as described in Figure 2.

Figure S2. Direction of effects for causality model with rs769178, mRNA expression of NCR3, and FEV1 % predicted. Data are presented as described in Figure 2.
Figure S3. Direction of effects for causality model with rs2270859, mRNA expression of CSTA, and FEV1 % predicted. Data are presented as described in Figure 2.
Figure S4. Direction of effects for causality model with rs4550905, mRNA expression of PPARGC1A, and FEV1 % predicted. Data are presented as described in Figure 2.
Figure S5. Direction of effects for causality model with rs3803761, mRNA expression of FLCN, and FEV1 % predicted. Data are presented as described in Figure 2.
Figure S6. Direction of effects for causality model with rs1543438, mRNA expression of BCL2L1, and FEV1 % predicted. Data are presented as described in Figure 2.
Figure S7. Direction of effects for causality model with rs9880397, mRNA expression of CADM2, and FEV1 % predicted. Data are presented as described in Figure 2.
Figure S8. Direction of effects for causality model with rs2466183, mRNA expression of TNFRSF10B, and FEV1 % predicted. Data are presented as described in Figure 2.
Figure S9. Direction of effects for causality model with rs17754977, mRNA expression of GSTO2, and FEV1/FVC. Data are presented as described in Figure 2.
Figure S10. Direction of effects for causality model with rs9987135, mRNA expression of DEPDC6, and FEV1/FVC. Data are presented as described in Figure 2.
Figure S11. Direction of effects for causality model with rs10411704, mRNA expression of CD22, and FEV1/FVC. Data are presented as described in Figure 2.
Figure S12. Direction of effects for causality model with rs12179536, mRNA expression of MUC22, and FEV1/FVC. Data are presented as described in Figure 2.
Figure S13. Direction of effects for causality model with rs2287765, mRNA expression of SPINK5, and FEV1/FVC. Data are presented as described in Figure 2.
Figure S14. Causality genes in the Aryl Hydrocarbon Receptor Signaling pathway. Causality genes identified in this study are in red.
Figure S15. Causality genes in the Xenobiotic Metabolism Signaling pathway. Causality genes identified in this study are in red.

Figure S16. The glutathione metabolism pathway connecting the cyanoamino acid and the taurine/hypotaurine metabolism pathways.
Figure S17. Gene Ontology (GO) project functional categories enriched for causality genes
1. BH3 domain binding
2. phosphoserine phosphatase activity
3. MHC class 1 receptor activity
4. death domain binding
5. MDM2 binding
6. natural killer cell lectin-like receptor binding
7. aminoacyl-tRNA ligase activity
8. ligase activity, forming aminoacyl-tRNA and related compounds
9. ligase activity, forming carbon-oxygen bonds
10. gamma-glutamultransferase activity
11. BH domain binding