

**Supplemental Table 1.** Prediction estimates of genetic variants of vitamin D mechanistic pathways for serum 25-hydroxyvitamin D in the HKU-TRS derivation cohort

Pathway mechanistic relevance/loci of interest	SNP	R <sup>2</sup> (%)	F-statistic	p value
Vitamin D biosynthesis				
CYP27B1	<i>rs4646536</i>	0.1	2.6	0.11
CYP27B1	<i>rs10877012</i>	0	1.7	0.19
NADSYN1/DHCR7	<i>rs3829251</i>	0.1	2	0.15
NADSYN1/DHCR7	<i>rs1790349</i>	0.1	3.8	0.05
Vitamin D activation				
CYP2R1	<i>rs2060793</i> <sup>#</sup>	0.1	4.1	0.044*
CYP2R1	<i>rs1993116</i>	0.1	3.9	0.049*
Vitamin D-binding protein				
GC	<i>rs2282679</i>	1.4	56.5	<0.001*
GC	<i>rs4588</i> <sup>#</sup>	1.4	57.3	<0.001*
GC	<i>rs1155563</i>	0.5	21.5	<0.001*
GC	<i>rs7041</i> <sup>#</sup>	0.5	17.7	<0.001*
Vitamin D receptor				
VDR	<i>rs1544410</i>	0	0.6	0.43
VDR	<i>rs10735810</i> <sup>†</sup>	0	0.6	0.45
Genetic risk score (GRS) <sup>‡</sup>	<i>rs2060793 + rs4588 + rs7041</i>	1.3	50.5	<0.001*

<sup>#</sup>Constituent genetic polymorphisms for genetic risk score. <sup>†</sup>Merged into *rs2228570*. <sup>‡</sup>GRS construction based on multi-loci inclusion of genetic variants with the greatest resultant F-Statistic and absence of linkage disequilibrium of constituent variants (refer to Supplemental Table 2).