SUPPLEMENTAL MATERIALS

Supplemental Tables

Table S1. Candidate variants tested for association with CMV reactivation and disease

Table S2. Quality control of candidate variant genotyping and imputation (Excel file)

Table S3. Association of candidate variants with CMV reactivation in the discovery cohort (Excel file)

Table S4. Association of candidate variants with high-level CMV reactivation in the discovery cohort (Excel file)

Table S5. Association of candidate variants with CMV disease in the discovery cohort (Excel file)

Table S6. Association of donor and recipient variants with CMV reactivation and disease from GWAS analysis (Excel file)

Table S7. Quality Control of discovery variants that met criteria for GWAS replication testing (Excel file)

Table S8. GWAS associations with p-values $<1 \times 10^{-6}$ in the combined discovery and replication cohorts (Excel file)

Table S9. GWAS Quality Control of variants in Table S8 (Excel file)

Supplemental Figure

Figure S1. Manhattan plots showing recipient and donor SNP associations with CMV reactivation and disease in the combined discovery and replication cohorts

Footnotes for Tables S1-S9 (Excel files)

Abbreviations: AIDS, acquired immunodeficiency syndrome; Chr, chromosome; CMV, cytomegalovirus; HCT, hematopoietic cell transplantation; HIV, Human Immunodeficiency virus; HR, hazard ratio; HWE, Hardy-Weinberg equilibrium; LB, lower boundary of the 95% confidence interval; MAF, minor allele frequency; SNP, single nucleotide polymorphism; SOT, solid organ transplantation; Type, genotyped (G) or imputed (I); UB, upper boundary of the 95% confidence interval.

Where beta is listed as "ND" In Tables S3, S4 and S6, a model could not be fit due to lack of observations (i.e., the recessive model with no ‘aa’ genotypes). Where beta is listed as "NC", a model could be fit but failed to converge due to lack of events, meaning HR = 0 but no valid s.e. or confidence interval.

Table S1. Candidate SNPs and associated phenotypes

			Phenotypes					
Chr	Gene	SNP/Indel	HSCT	SOT	Congenital/ Pediatric CMV	HIV/ AIDS	Other	References
1	*IL10*	rs1800893	x					[1]
1	*IL10*	rs1800896	x	x		x	x	[1–4]
1	*IL10*	rs1800871	x				x	[1,4]
1	*IL10*	rs1800872					x	[4]
1	*IL10*	rs3024492	x					[1]
1	*IL10*	rs1878672	x					[1]
1	*IKBKE*	rs1953090					x	[5]
1	*MTHFR*	rs1801133					x	[6]
2	*IL1B*	rs16944			x			[7]
2	*IL1B*	rs1143634			x		x	[8,9]
2	*PDCD1*	rs11568821		x				[10,11]
2	*IL1A*	rs1800587			x		x	[8,9]
2	*STAT4*	rs7574865	x					[12]
2	*SLC11A1*	rs17235409				x		[2]
2	*CD28*	rs3116496	x					[13]
2	*CTLA-4*	rs4553808	x	x				[11,13,14]
2	*CTLA-4*	rs231775		x				[14]
2	*CTLA-4*	rs3087243	x	x				[14,15]
2	*CTLA-4*	rs5742909		x				[14]
2	*CTLA-4*	rs11571317		x				[14]
2	*CTLA-4*	rs16840252		x				[14]
2	*ITGAV*	rs3795865					x	[5]
3	*CCR5*	rs1800023	x				x	[1,16,17]
3	*CCR5*	rs2734648	x					[1]
3	*CCR5*	rs17141079	x					[1]
3	*CCR5*	rs1799988				x		[18]
3	*CCR2*	rs1799864				x		[18]
3	*TLR9*	rs187084			x			[19]
3	*TLR9*	rs352139			x			[19]
3	*TLR9*	rs352140	x		x		x	[19–25]
3	*TLR9*	rs5743836	x	x				[26,27]
3	*TLR9*	rs5743849					x	[5]
3	*PTX3*	rs2305619	x					[28]
3	*PTX3*	rs3816527	x					[28]
4	*TLR1*	rs5743572					x	[29]
4	*TLR2*	rs1898830			x			[22,30,31]
4	*TLR2*	rs5743708		x	x		x	[20,26,32–36]
4	*TLR2*	rs121917864					x	[37]
4	*TLR2*	rs3804100			x			[22,31]
4	*TLR3*	rs3775291			x		x	[36,38,39]
4	*TLR3*	rs3775292					x	[5]
4	*TLR3*	rs3775296			x			[39]
4	*TLR10*	rs4513579					x	[29]
4	*IL2*	rs2069762					x	[40]
4	*IL2*	rs2069763					x	[40]

4	*NFKB1*	rs28362491		x					41
5	*IL7R*	rs6897932	x						42
5	*IL12B*	rs3212227		x	x	x			2,9,10,43,44
5	*IL4*	rs2243248					x		40
5	*IL4*	rs2243250					x		40
5	*IL4*	rs2070874					x		40
5	*microRNA*	rs2910164		x					45
6	*TNF*	rs1799964			x				30
6	*TNF*	rs1800629			x	x	x		9,46,47
6	*HLA-C*	rs2308557	x						48
6	*HLA-C*	rs17408553	x						48
6	*HLA-C*	rs9264942					x		49
6	*HLA-E*	rs1264457					x		50
6	*HLA-G*	rs1063320		x					51
6	*MICA*	rs2596538		x					52
6	*MICA*	rs1051792		x					53
6	*MICB*	rs2523651					x		54
6	*IL17A*	rs8193036	x						55
6	*HLA-G*	rs13675/rs1704/rs371194629		x	x		x		56–59
7	*LANCL2*	rs1568821		x					60
7	*NOD1*	rs2284358					x		29
7	*NOD1*	rs2970500					x		29
7	*NOD1*	rs10267377					x		29
7	*IL6*	rs1800795			x		x		8
7	*ABCB1*	rs1128503		x					61
7	*ABCB1*	rs2032582		x					61
7	*ABCB1*	rs1045642		x					61
7	*CYP3A5*	rs776746		x					62
8	*LY96*	rs6472812					x		29
8	*DEFB1*	rs1799946			x				63
8	*DEFB1*	rs1800972			x				63
8	*DEFB1*	rs11362			x				63
8	*SDC2*	rs1042381	x						64
9	*TLR4*	rs4986790		x	x		x		22,24,36,37,65
9	*TLR4*	rs4986791		x	x				22,24,36,65
9	*FCN2*	rs7851696		x					66
10	*MBL2*	rs11003125			x				22
10	*MBL2*	rs7096206			x				22,65,67
10	*MBL2*	rs1800450			x				22,65,67,68
10	*MBL2*	rs5030737		x					65,66,68
10	*MBL2*	rs1800451		x					65,66,68
10	*MAPK8*	rs17010454					x		5
10	*CXCL12*	rs1801157				x			18
11	*IL10R1*	rs3135932					x		69,70
11	*IL10R1*	rs2229113					x		69,70
11	*IL10R1*	rs2229114				x			70
11	*IL10R1*	rs2228055				x			70
11	*IL10R1*	rs4252279				x			70
11	*IL10R1*	rs4252314				x			70
11	*IL10R1*	rs4252286				x			70

12	*INFG*	rs2430561	x	x					71–73
12	*IRAK4*	rs1838341						x	5
12	*VDR*	rs2228570		x					74
12	*VDR*	rs1544410		x					75
12	*VDR*	rs731236		x					75
12	*KLRK1*	rs2255336			x				76
12	*microRNA*	rs11614913		x					45
14	*IGHG1*	rs1071803		x				x	77–79
17	*CCL2*	rs13900	x		x				1,7
17	*CCL2*	rs1024611	x		x				1,7
17	*CCL8*	rs3138035		x					80
19	*IFNL4*	rs12979860	x	x					26,81–84
19	*IFNL4*	rs368234815	x	x		x			83,85,86
19	*IFNL4*	rs8099917		x					87
19	*LILRB1*	rs10423364		x					88
19	*LILRB1*	rs1061680				x			2
19	*DC-SIGN*	rs735240	x	x					26,64
19	*DC-SIGN*	rs2287886	x						64
19	*TGFβ1*	rs1800470						x	40
19	*TGFβ1*	rs1800471						x	40
20	*microRNA*	rs3746444		x					45
22	*PPARA*	rs4253728		x					89
22	*EP300*	rs20551						x	90
X	*FOXP3*	rs3761548	x						91
X	*TLR7*	rs179009						x	5,36
X	*TLR7*	rs179008						x	5,36
X	*TLR7*	rs179018						x	5,36
X	*TLR7*	rs179013						x	5,36
X	*TLR8*	rs3764880	x						64
X	*TLR8*	rs3747414	x						64

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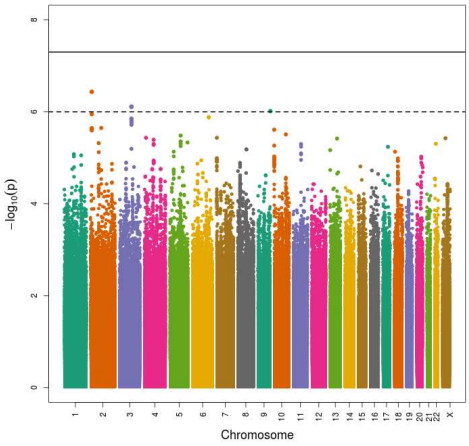
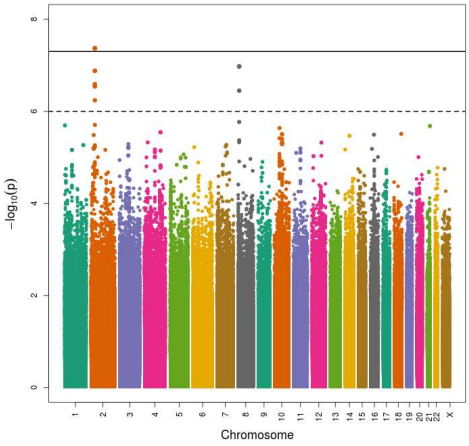
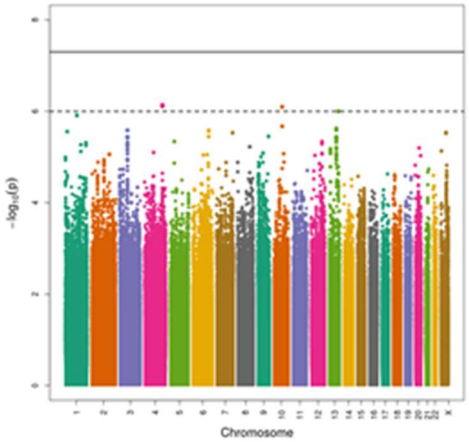
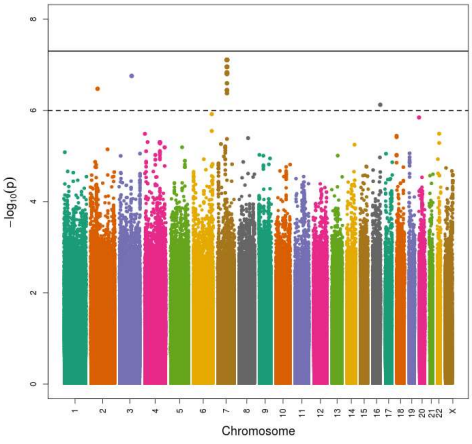
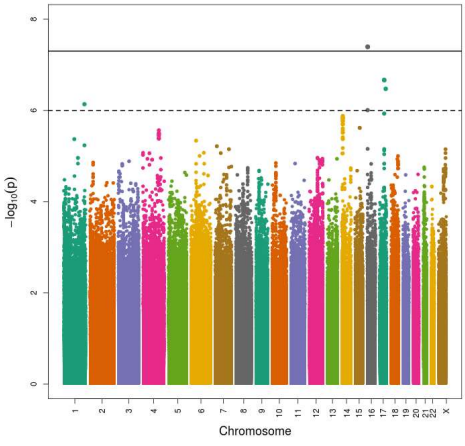
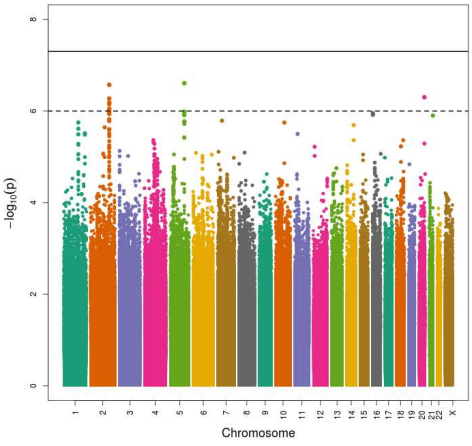
	Recipient	Donor
Reactivation		
High-Level Reactivation		
Disease		

Figure S1. Manhattan plots show recipient and donor SNP associations with CMV reactivation and disease in the combined discovery and replication cohorts. Each panel shows the $-\log_{10}$(p-value) for post-QC variants with MAF > 1% for autosomes and chromosome X. The results in each panel represent ~8.7×10^6 variants. The solid line shows genome-wide significance (5×10^{-8}). The dotted line shows the threshold used to select variants for replication (1×10^{-6}). Vertically aligned associations reflect variants that are strongly correlated by linkage disequilibrium. Recipient genomic inflation values were 1.009 for CMV reactivation, 1.009 for high-level reactivation, and 1.008 for CMV disease, and donor genomic inflation values were 1.004 for CMV reactivation, 1.005 for high-level reactivation, and 1.017 for CMV disease.