**Supplementary text describing WES filtering strategy**

Starting with 126,642 variants spanning 16,843 genes, variants were kept with call quality at least 20.0, with read depth at least 5.0, with allele fraction at least 25.0, with genotype quality at least 25.0, outside top 5.0% most exonically variable 100base windows in healthy public genomes, outside top 1.0% most exonically variable genes in healthy public genomes. Excluded variants that are observed with an allele frequency greater than or equal to 1.0% of the genomes in the 1000 genomes projec, greater than or equal to 1.0% of the NHLBI ESP exomes, greater than or equal to 1.0% of the ExAC Frequency, or greater than or equal to 1.0% of the gnomAD Frequency. Kept variants that are experimentally observed to be associated with a phenotype: Pathogenic, Possibly Pathogenic, disease-associated according to HGMD or CLINVAR, or variants that are Frameshift, in-frame indel, stop codon change, or missense unless predicted to be innocuous by SIFT or Polyphen-2, or variants that disrupt splice site up to 2.0 bases into intron. Finally, ariants that are predicted deleterious by having CADD score > 20 were kept.

Additional filtering strategy included keeping variants within the criteria described above that are known or predicted to affect various viral processes or antiviral responses broadly, including:

ADAR1 , AIM2, AMFR, APOBEC3G, ATF2, ATM, BST2 , BTK, CASP1, CASP10 , CASP8 , CD74, CHUK , CIITA , CXCL10 , CXCL11 , CXCL9 , DDX41 , DDX58, DDX60 , DHX36, DHX58 , DHX9 , DNA viruses deactivation (inactivation of DNA virus), DNA viruses inhibition (inhibition of DNA virus) (affected genes: APOBEC3G, BST2, CAV1, CAV3, IFNB1, IFNG, IL6, NCOR1, SLC10A1, SP100, TNF, TRIM5), DOCK2, DOCK8 , GATA2 , GBP1, GBP2, HPSE, IFI16, IFI6, IFIH1, IFIT1, IFIT2 , IFIT3, IFITM1 , IFITM2, IFITM3, IFNA1 , IFNA10 , IFNA13 , IFNA14, IFNA16, IFNA17 , IFNA2, IFNA21, IFNA4, IFNA5, IFNA6, IFNA7 , IFNA8, IFNAR1, IFNAR2, IFNB1 , IFNG , IFNGR1 , IFNGR2, IFNL1 , IFNL2 , IFNL3 , IFNL4, IFNLR1, IKBKB, IKBKE, IKBKG, IL10RB , IL1RN , IRAK1, IRAK2 , IRAK4, IRF1, IRF3, IRF5, IRF7, IRF8, IRF9, ISG15, ISG2,IFNA4, JAK1 , JAK2, JAK3 , MAP3K14 , MAVS, MB21D1, MRE11, MX1, MX2, MYD88, NAMPT, NFKB2, NFKBIA, NHEJ1, NLRP12, NLRP2, NLRP3, NOD2, OAS1, OAS2, OAS3, OASL, PRKRA, RBBP6, PGM3, EIF2AK2, PKLR, POLR3A, POLR3B, POLR3C, POLR3D, POLR3E, POLR3F, POLR3G, POLR3GL, POLR3H, POLR3K, PRKDC, PYCARD, RELA, RHBDF2, RIPK1, RIPK3, RNASEH2A, RNASEH2B, RNASEH2C, RNASEL, RNF135, RTP4, SAMHD1, STAT1, STAT2, STAT3, STAT4, STAT5A, STAT5B, TANK , TBK1 , TICAM1 , TICAM2, TIRAP , TLR2, TLR3, TLR4 , TLR7, TLR8, TLR9, TMEM173, TRAF3, TRAF6, TREX1, PML, TRIM21, TRIM22, TRIM25, TRIM32, TRIM5, TYK2, UNC93B1, VPS45, VZV replication (replication of human herpesvirus 3) (affected genes: BCL2L11), XIAP, XRCC5, XRCC6 , ZBP1, ZDHHC1, encephalomeningitides (meningoencephalitis) (affected genes: APP, IFNG), infection by DNA virus (affected genes: ACTA1, ACTA2, ACTB, ACTC1, ACTG1, ACTG2, ADA, ADAR, ADCY10, ADK, AKT1S1, AKT2, ANXA1, APAF1, APOE, APP, ATM, C2, C3, C4A/C4B, C5, CAV1, CCL2, CCL3, CCL3L3, CCL4, CCL5, CD209, CD274, CD40, CD40LG, CD46, CD70, CD79A, CD79B, CDC42, CH25H, CHRNA10, CISH, CLIP1, CRP, CSF1, CSF2RA, CSF2RB, CSF3R, CTBP1, CXADR, CXCL1, CXCL10, CXCL8, CXCL9, CXCR2, CYP1A2, CYP3A4, CYP3A43, CYP3A5, CYP3A7, CYP3A7-CYP3A51P, DCTN1, DEFB1, DEFB103A/DEFB103B, DNM1, DNM1L, DNM2, DNM3, EGFR, EIF2AK2, EIF2AK4, EPS15, F10, F2, F2R, F3, F7, F9, FASLG, FCGR1A, FCGR1B, FCGR2A, FCGR2B, FCGR2C, FCGR3A/FCGR3B, FGF4, FGFR1, FGFR2, FGFR3, FGFR4, FKBP1A, FLT3LG, FRS2, GAB1, GNB1L, GOT1, GOT1L1, GOT2, GPT, GPT2, GRB2, GRIN3A, HMGCR, HRAS, HS3ST1, HTR2A, IFNA1/IFNA13, IFNA10, IFNA14, IFNA16, IFNA17, IFNA2, IFNA21, IFNA4, IFNA5, IFNA6, IFNA7, IFNA8, IFNAR1, IFNAR2, IFNB1, IFNGR1, IFNL2, IFNL3, IFNLR1, IGF2R, IL10, IL10RB, IL15, IL17A, IL17RA, IL18, IL1RN, IL23A, IL23R, IL2RA, IL2RB, IL2RG, IL3RA, IL6, ILF3, IMPDH1, IMPDH2, IRAK4, IRF1, IRF3, IRS1, IRS2, ITGB1, ITK, KL, KLB, LGALS1, LTA, LTB, MAGT1, MAPRE1, MAVS, MCAM, MLST8, MR1, MTOR, MX1, MYD88, NECTIN1, NFKBIZ, NLRX1, NOS2, NR3C1, OPRD1, OPRK1, OPRM1, PAK1, PDCD1, PDGFA, PDGFB, PI3, PIK3C2A, PIK3C2B, PIK3C2G, PIK3C3, PIK3CA, PIK3CB, PIK3CD, PIK3CG, PIK3R1, PIK3R2, PIK3R3, PIK3R4, PIK3R5, PIK3R6, PLCG2, POLA1, POLB, POLD1, POLG, PPP3CA, PPP3CB, PPP3CC, PRF1, PRKCA, PRKCB, PRKCD, PRKCE, PRKCG, PRKCH, PRKCI, PRKCQ, PRKCZ, PRKD1, PRKD3, PRKRA, PRNP, PTGS1, PTGS2, PTPN11, RAB5A, RAB5B, RAB5C, RAC1, RARA, RASSF1, RPTOR, RXRA, SAMD9, SLC10A1, SLC22A11, SLC22A12, SLC22A6, SLC22A8, SLC6A2, SLC6A4, ST3GAL5, ST6GAL1, STAT1, STAT6, TBK1, TGFB1, TICAM1, TIMP1, TK1, TK2, TLR2, TLR3, TLR7, TLR9, TMEM2, TNF, TNFRSF10B, TNFRSF14, TNFRSF4, TNFSF10, TNFSF11, TNFSF12, TNFSF12-TNFSF13, TNFSF13, TNFSF13B, TNFSF14, TNFSF15, TNFSF18, TNFSF4, TNFSF8, TNFSF9, TP73, TRAF3, TRIM21, TRPV1, TYK2, TYMS, UNC93B1, VIP), infection by VZV (infection by human herpesvirus 3) (affected genes: IGF2R), meningitides (inflammation of meninges) (affected genes: ANXA1, APP, CASP1, CD40LG, CD47, CD70, CST3, CTSB, CYP51A1, DHFR, EGFR, ERBB2, F5, F8, FASLG, FCGR2B, FN1, GABRA1, GABRA3, GABRA4, GABRA5, GABRA6, GABRB1, GABRB2, GABRB3, GABRE, GABRG1, GABRG2, GABRG3, GABRP, IFNG, IL18, IL1B, IL1R1, IRAK4, LTA, LTB, MC2R, NFKB1, NFKB2, NLRP3, NOD1, NOD2, NR3C1, POLA1, POLB, POLD1, POLG, PYCARD, REL, RELA, RELB, SCN1A, SCN1B, SCN5A, SERPINE1, SLC6A4, TIRAP, TLR1, TLR2, TLR4, TLR9, TNF, TNFRSF1A, TNFRSF1B, TNFSF10, TNFSF11, TNFSF12, TNFSF12-TNFSF13, TNFSF13, TNFSF13B, TNFSF14, TNFSF15, TNFSF18, TNFSF4, TNFSF8, TNFSF9, TOB1, TYMS).