Supplemental information

A year of COVID-19 GWAS results from the GRASP portal reveals potential genetic risk factors

Florian Thibord, Melissa V. Chan, Ming-Huei Chen, and Andrew D. Johnson

Supplemental Figures

Figure S1: Quantile-Quantile Plots of the 4 GWAS including ALL ancestries and Population as controls for Covid-19 Susceptibility, Hospitalization, Severity and Death
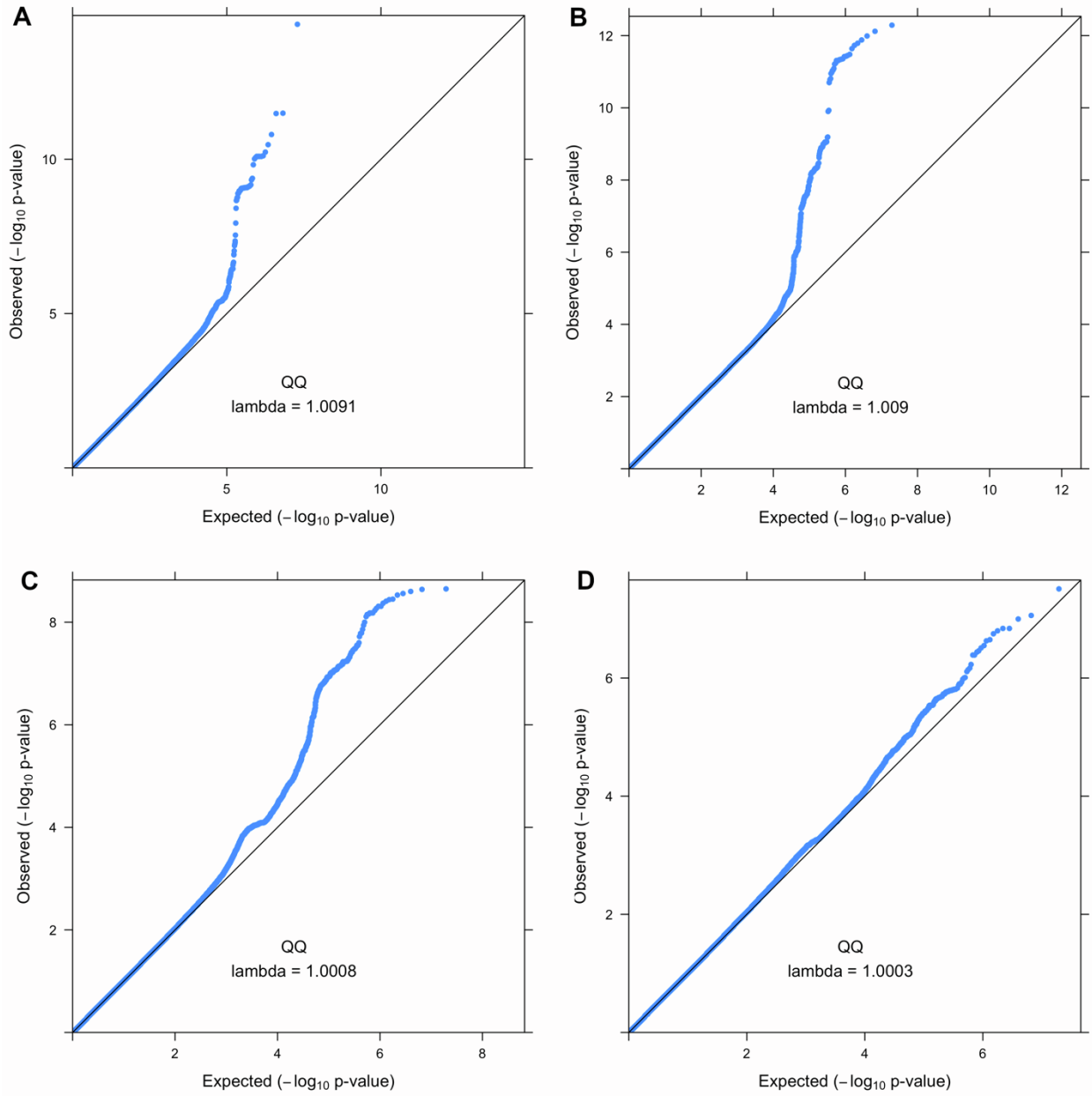
QQ-plots of ALL:Population GWAS for Covid-19 susceptibility (A), Hospitalization (B), Severity (C) and Death (D).

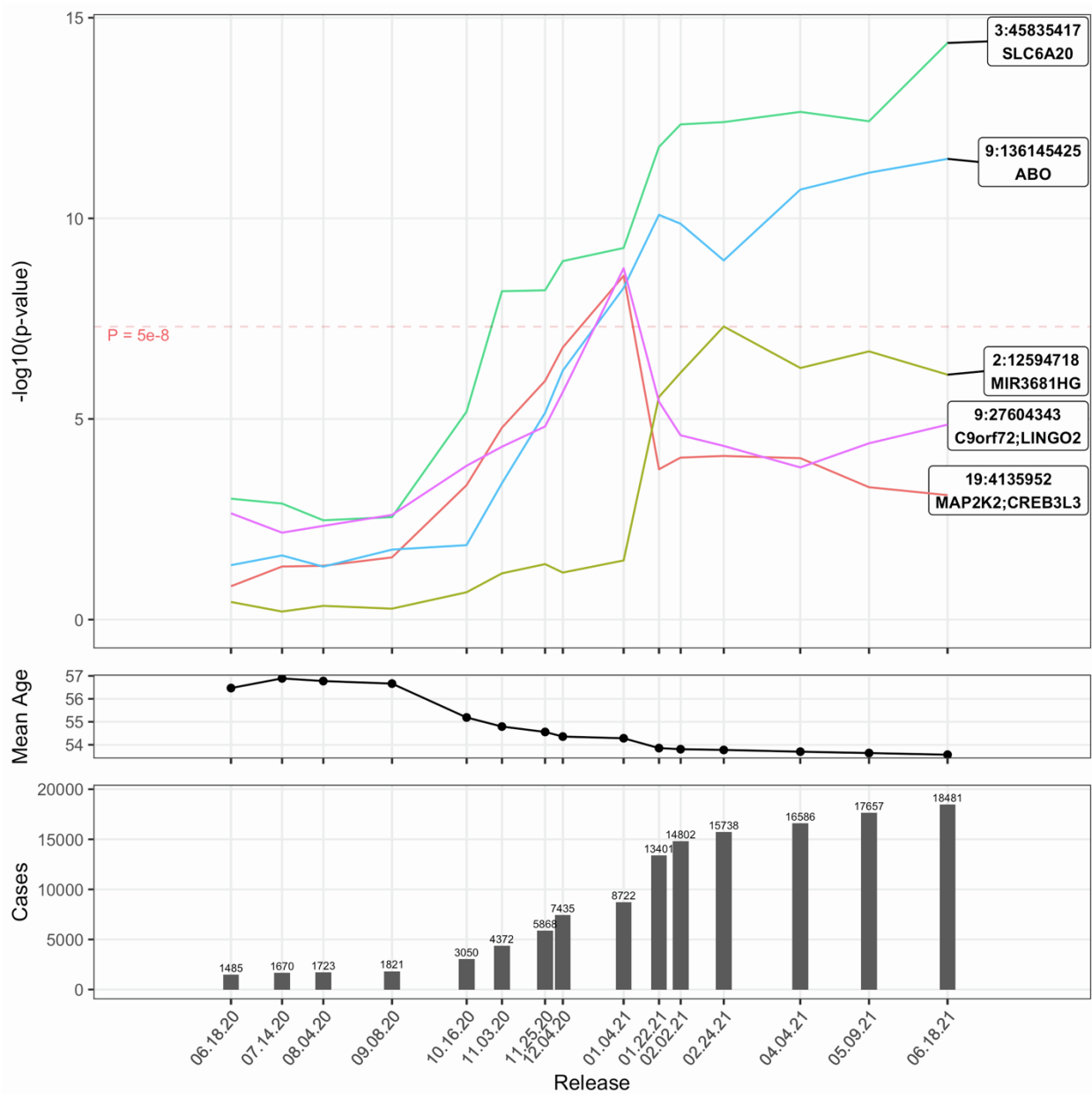Figure S2: Covid-19 Susceptibility in ALL:Pop
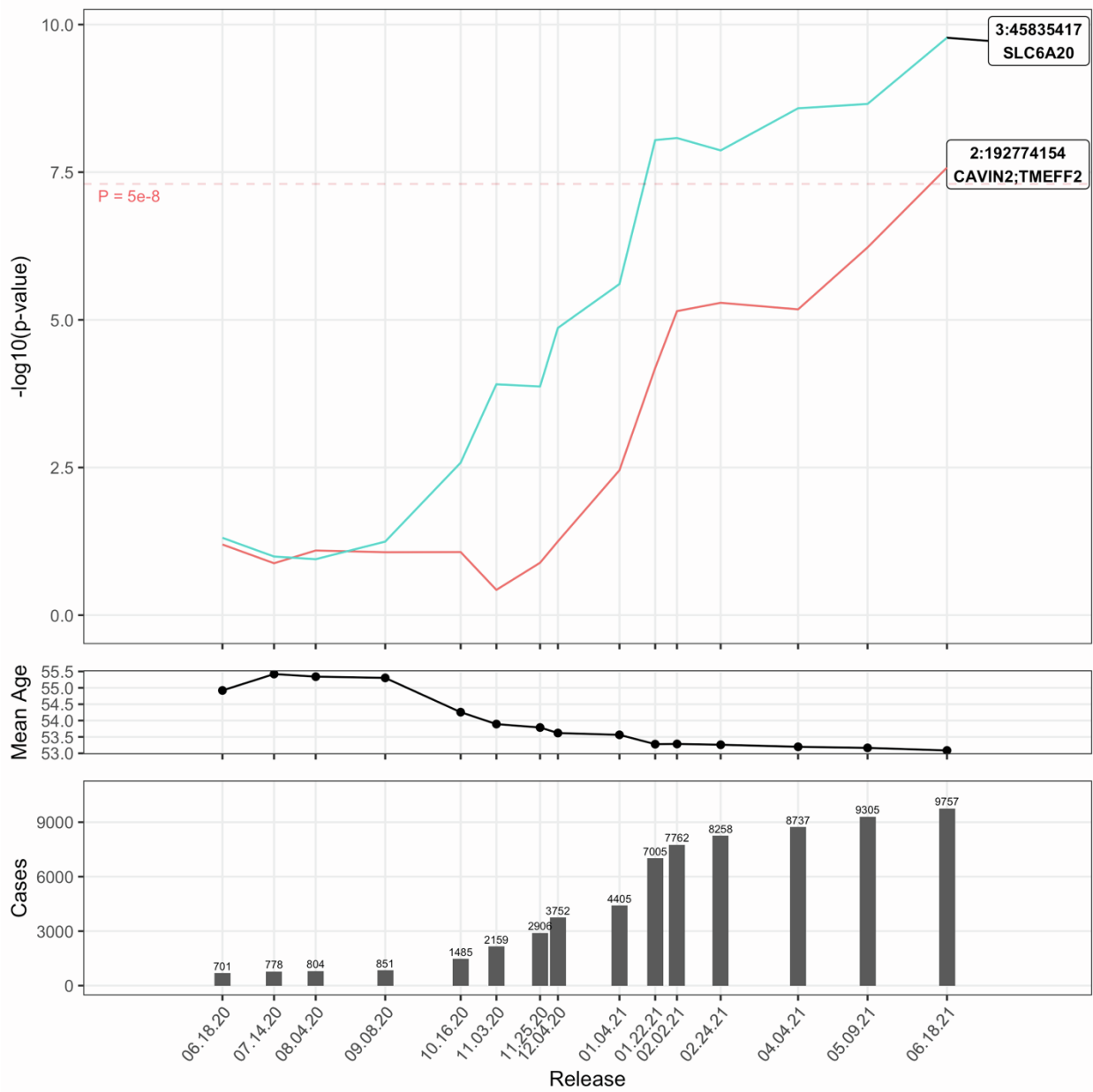
Figure S3: Covid-19 Susceptibility in ALL:Pop:F
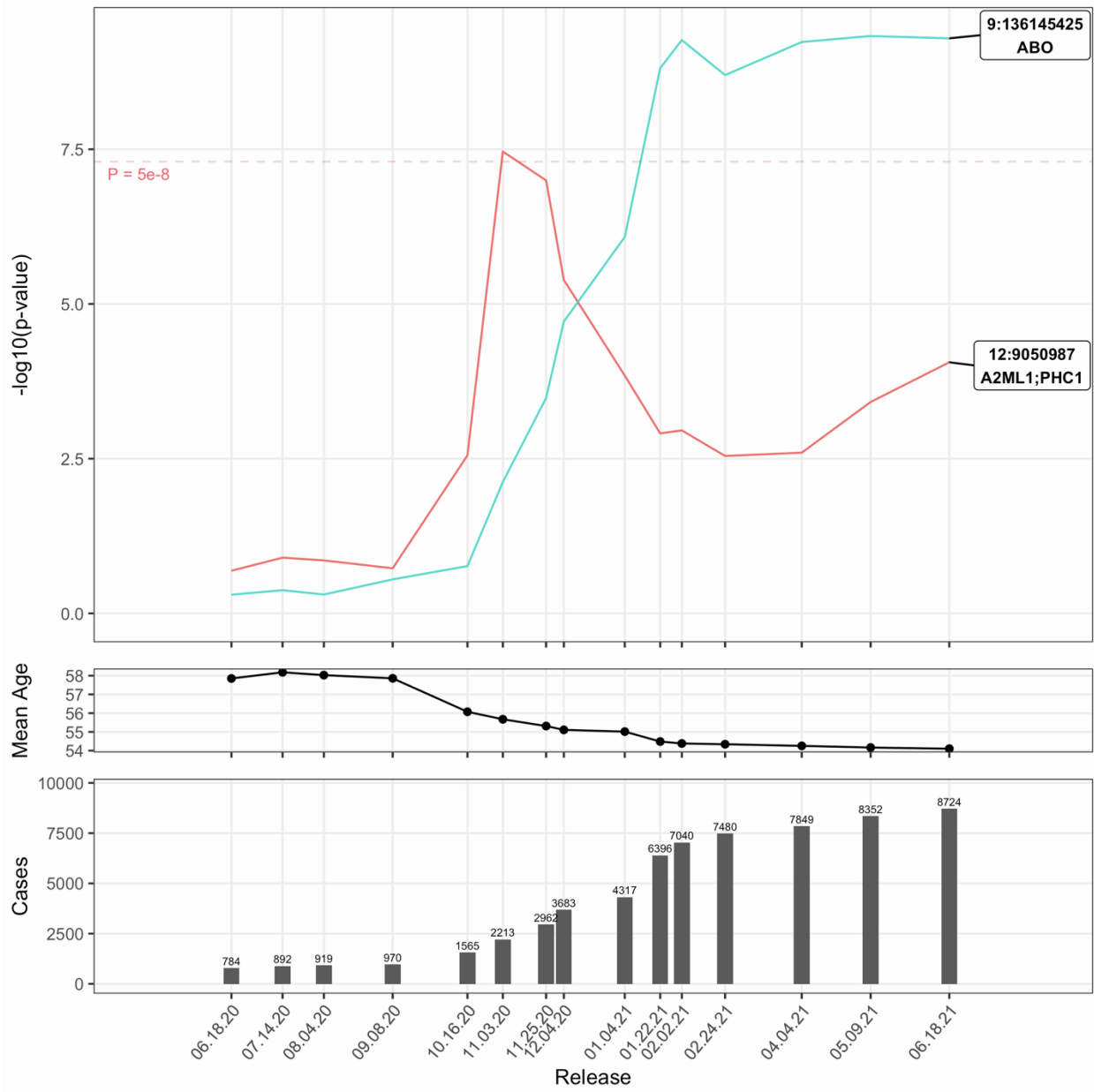
Figure S4: Covid-19 Susceptibility in ALL:Pop:M
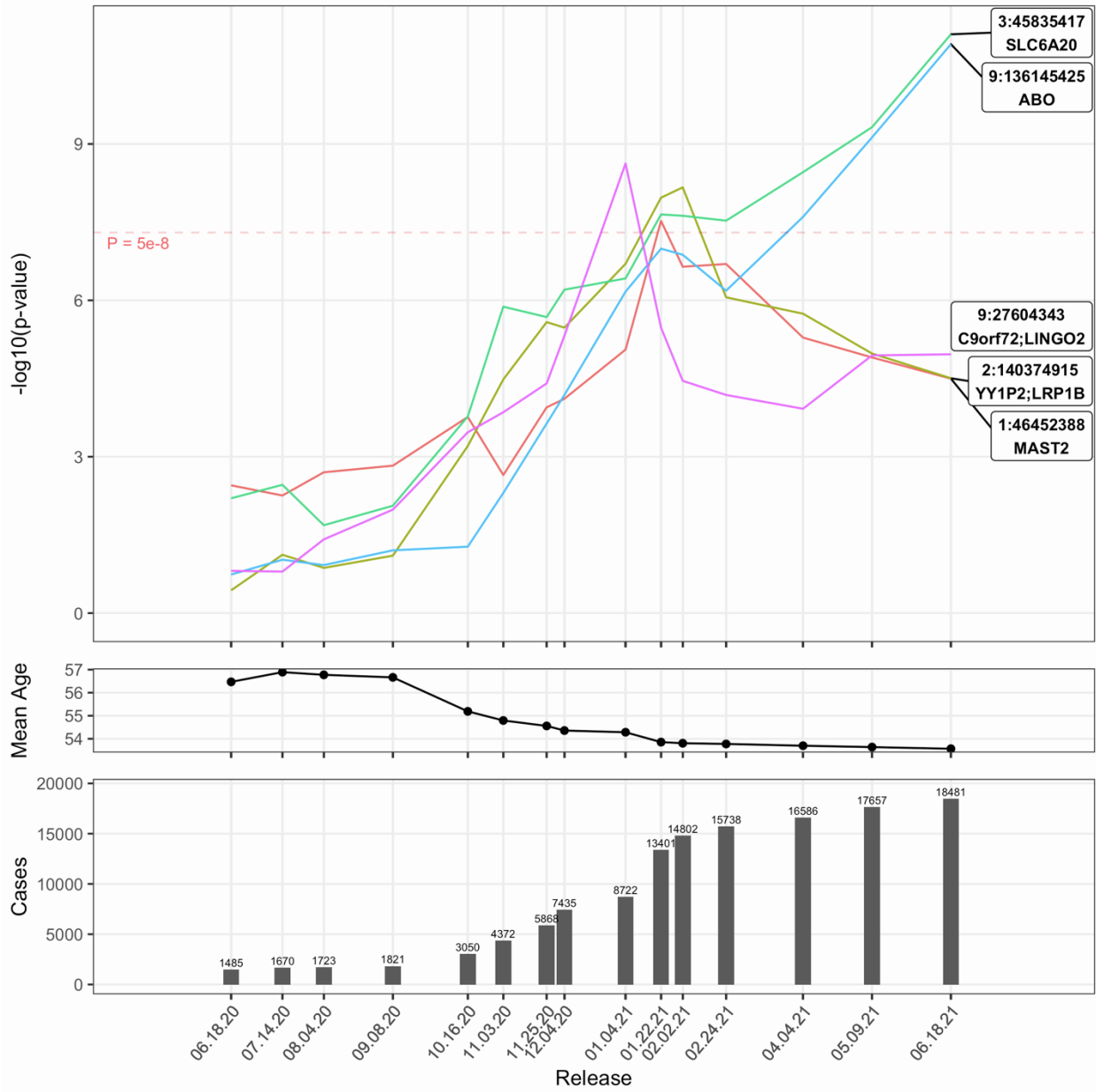
Figure S5: Covid-19 Susceptibility in ALL:Tested

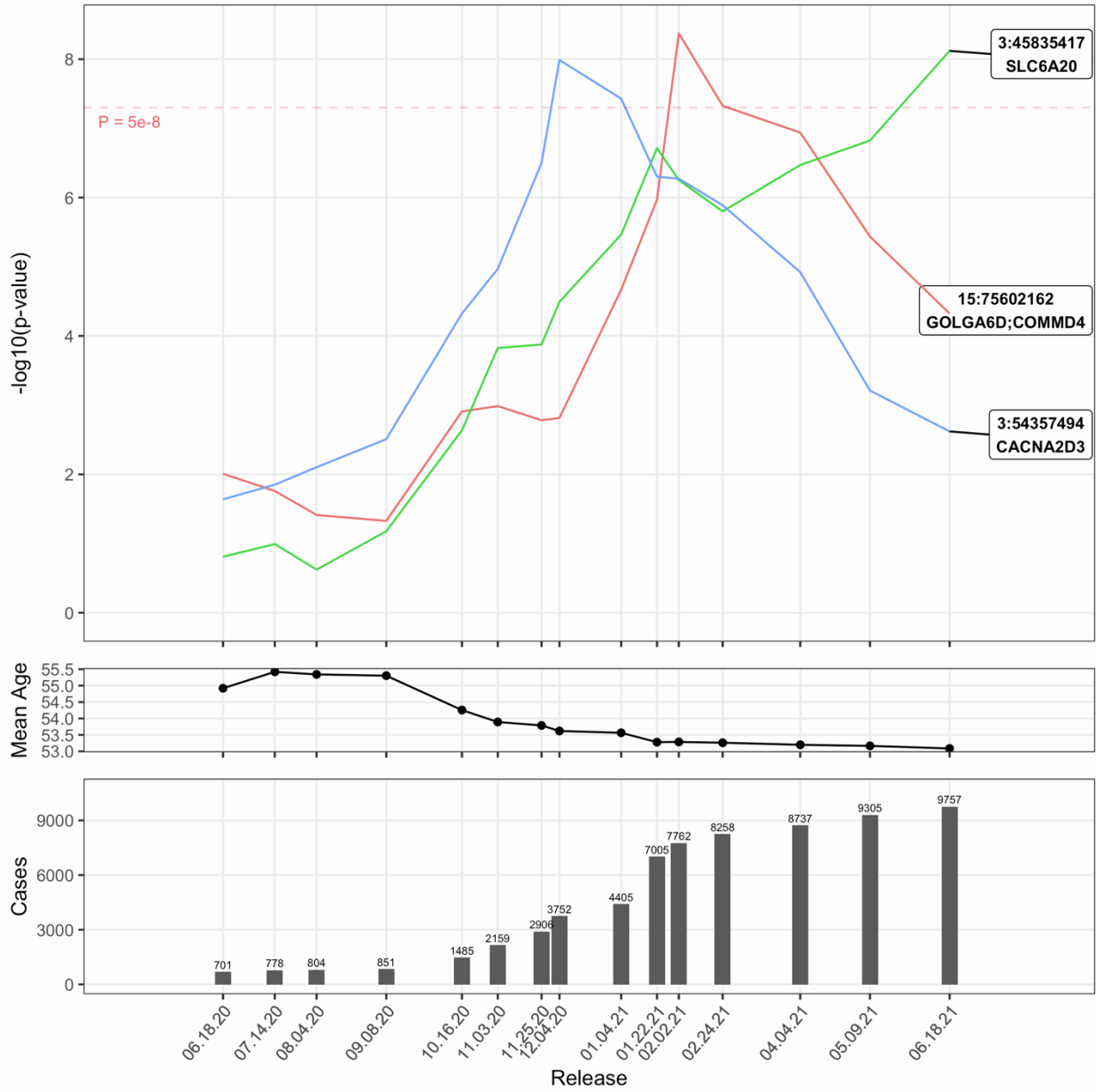Figure S6: Covid-19 Susceptibility in ALL:Tested:F

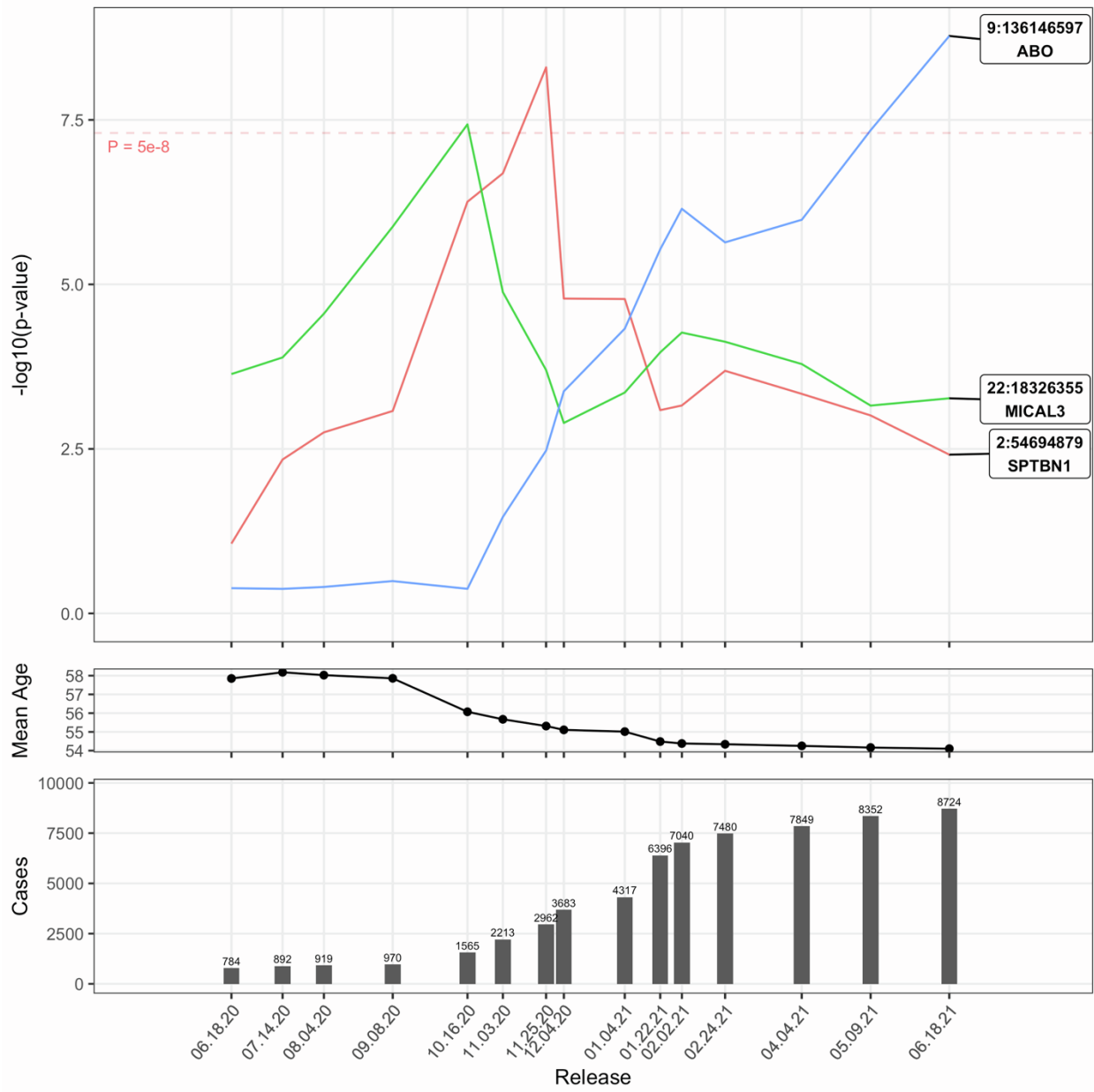Figure S7: Covid-19 Susceptibility in ALL:Tested:M

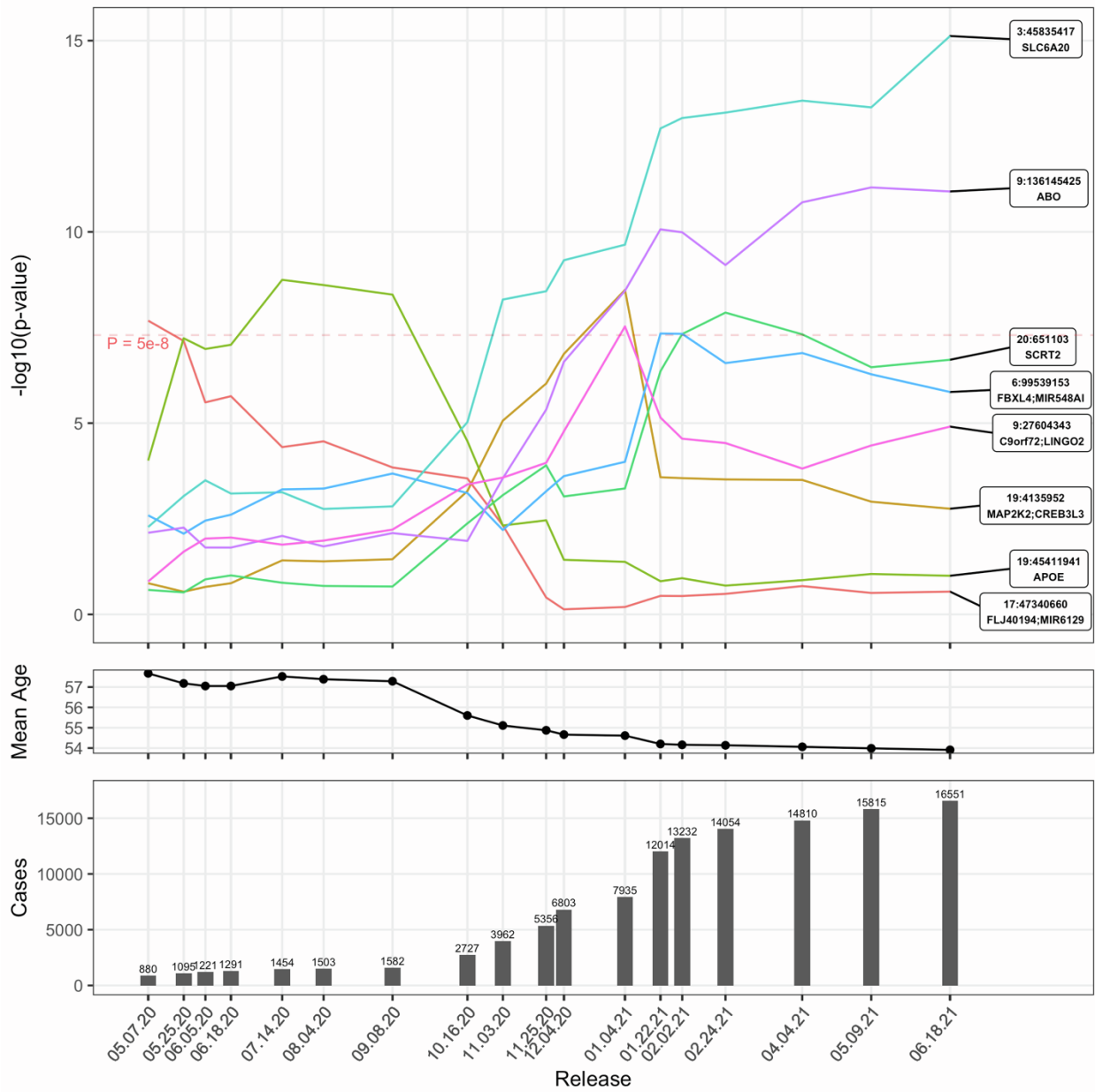Figure S8: Covid-19 Susceptibility in EUR:Pop
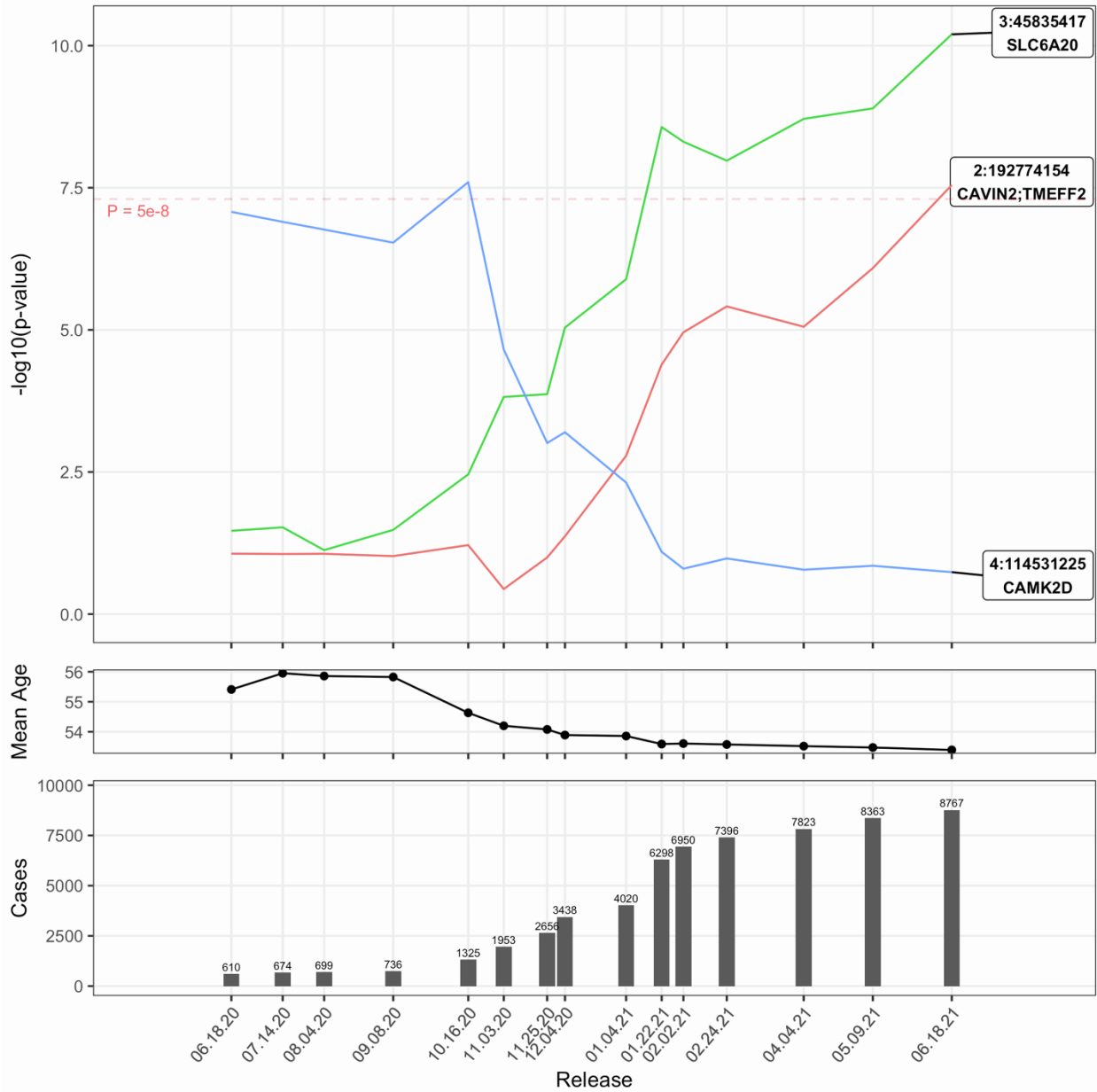
Figure S9: Covid-19 Susceptibility in EUR:Pop:F

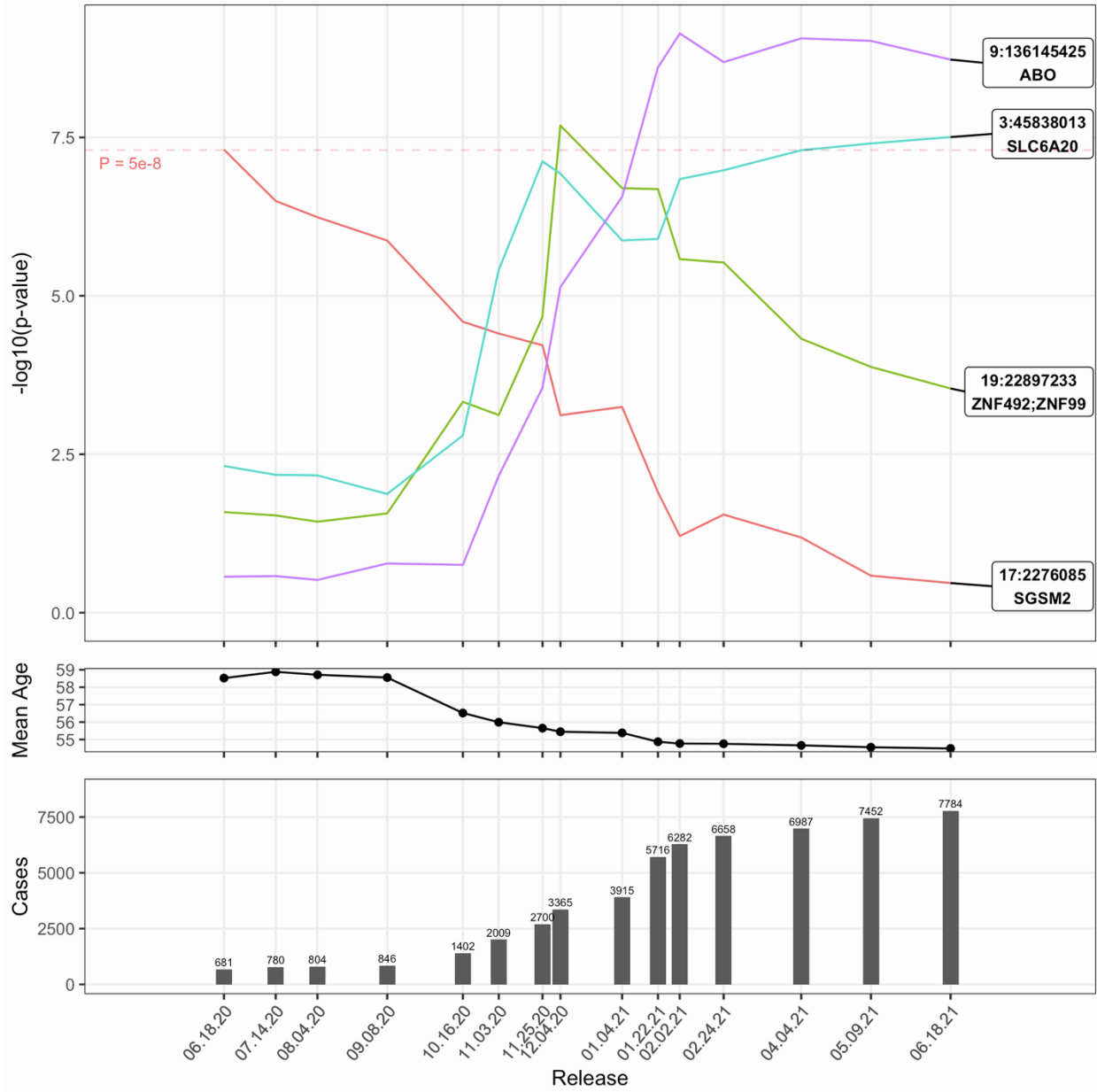Figure S10: Covid-19 Susceptibility in EUR:Pop:M

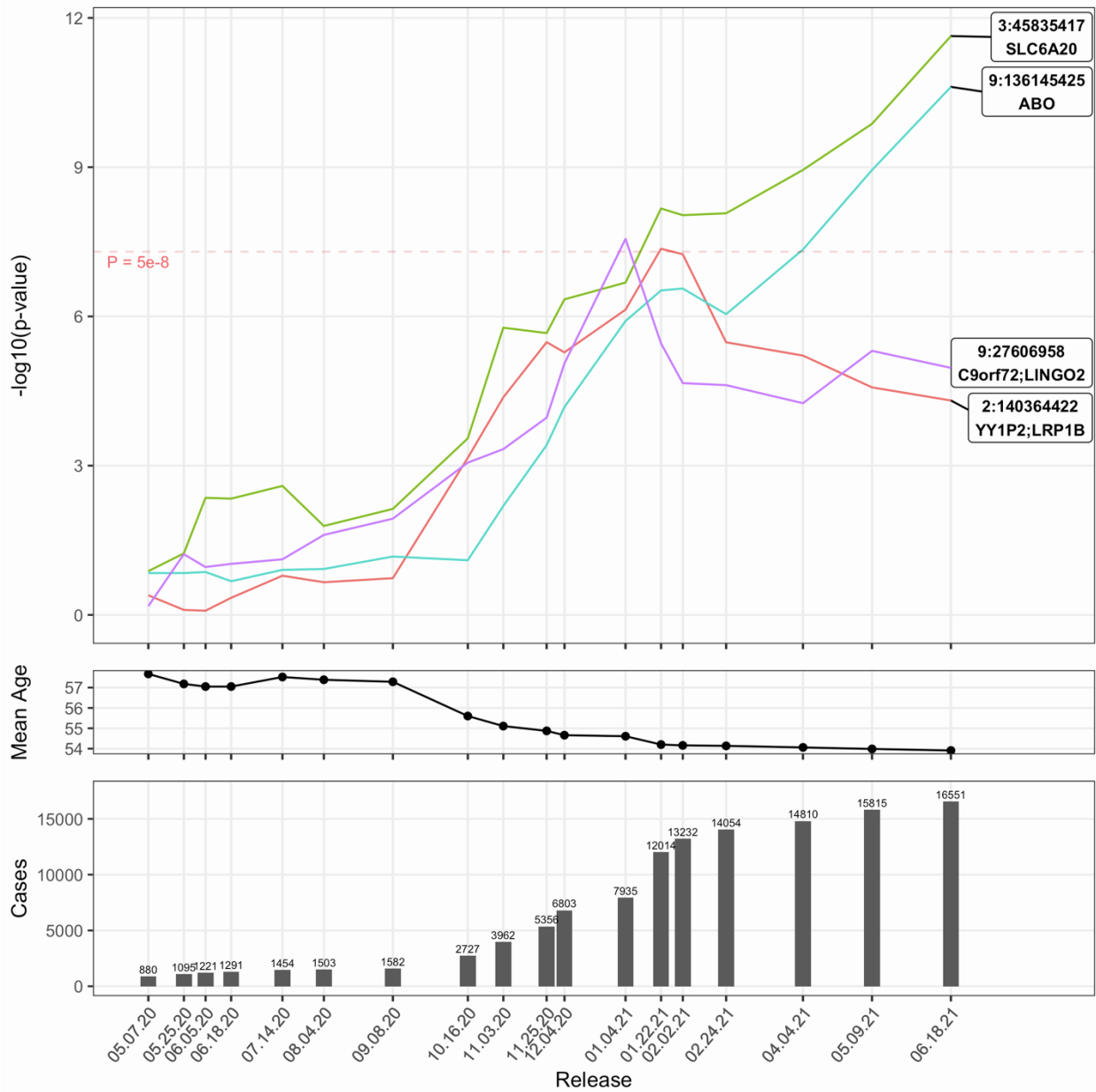Figure S11: Covid-19 Susceptibility in EUR:Tested

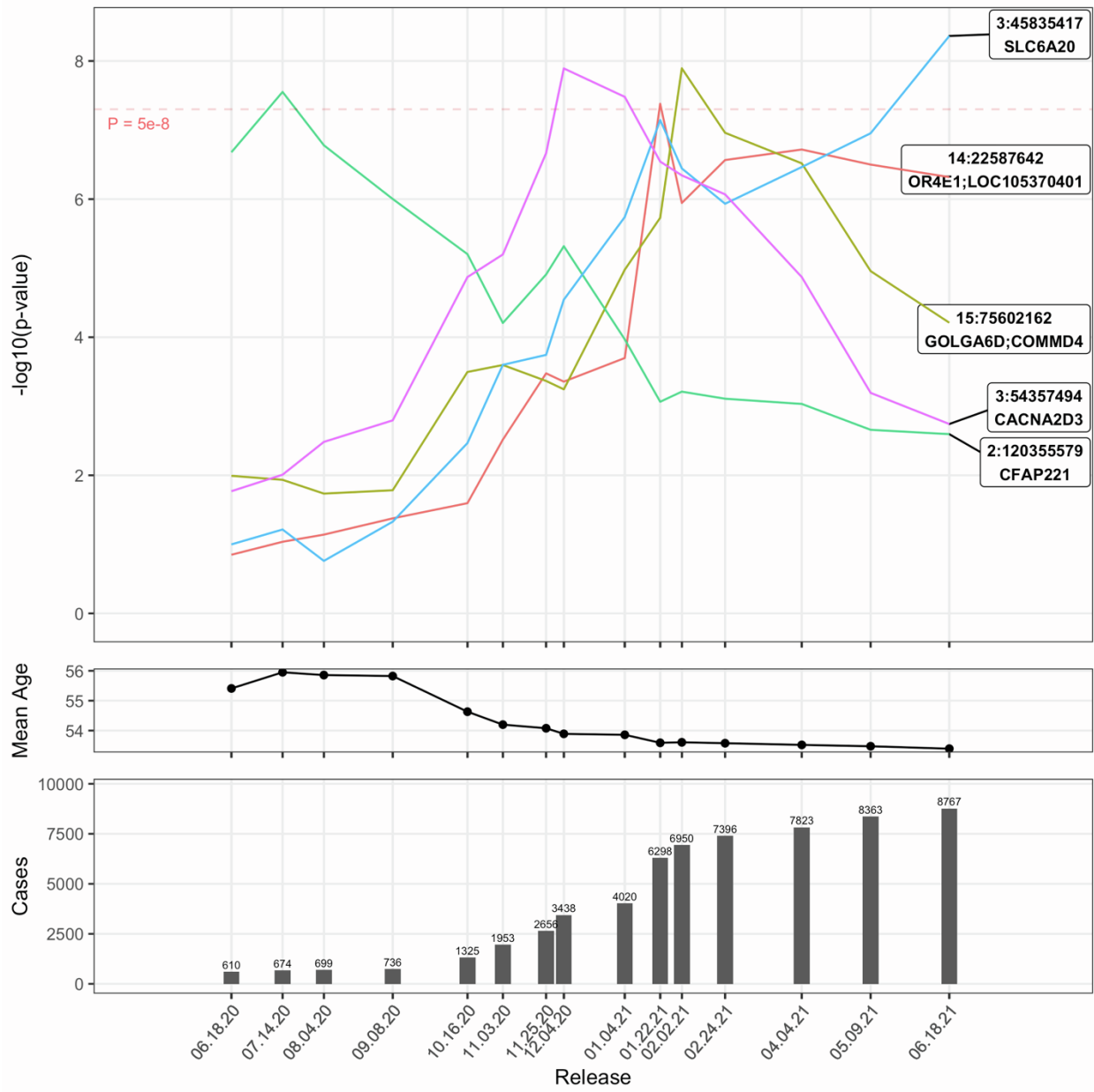Figure S12: Covid-19 Susceptibility in EUR:Tested:F

Figure S13: Covid-19 Susceptibility in EUR:Tested:M

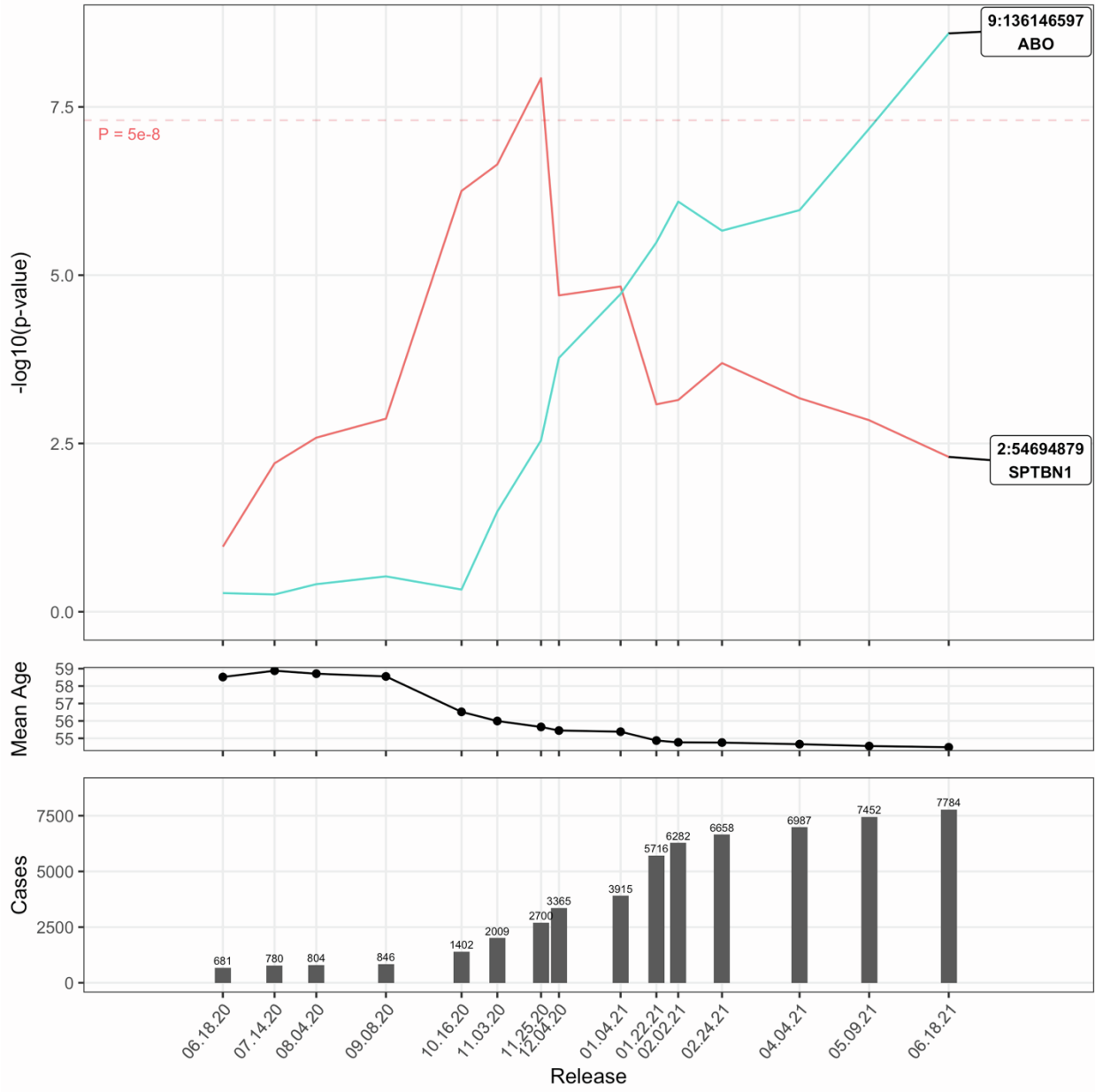Figure S14: Covid-19 Susceptibility in AFR:Pop

Figure S15: Covid-19 Susceptibility in AFR:Tested
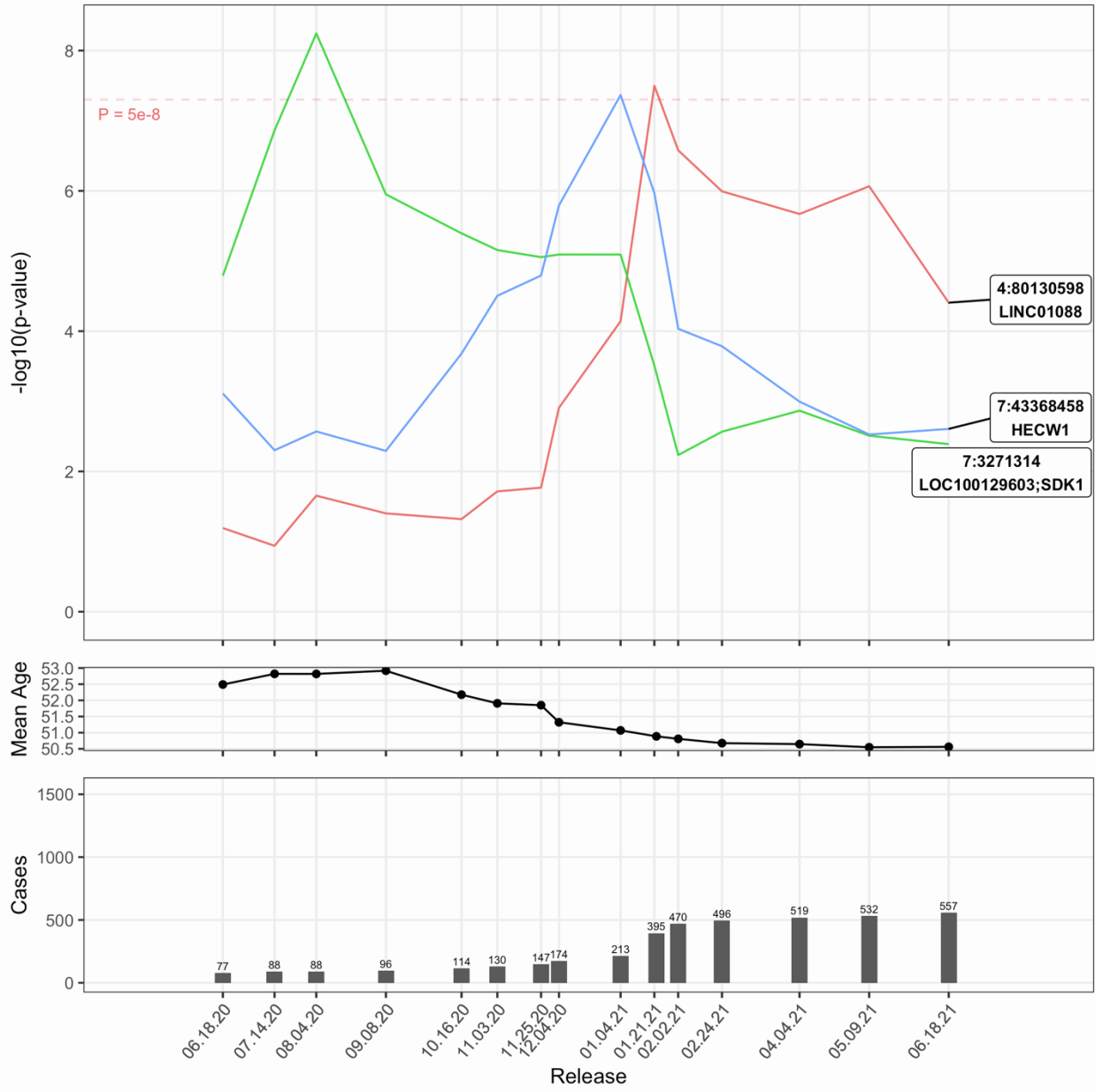
Figure S16: Covid-19 Susceptibility in SAS:Pop
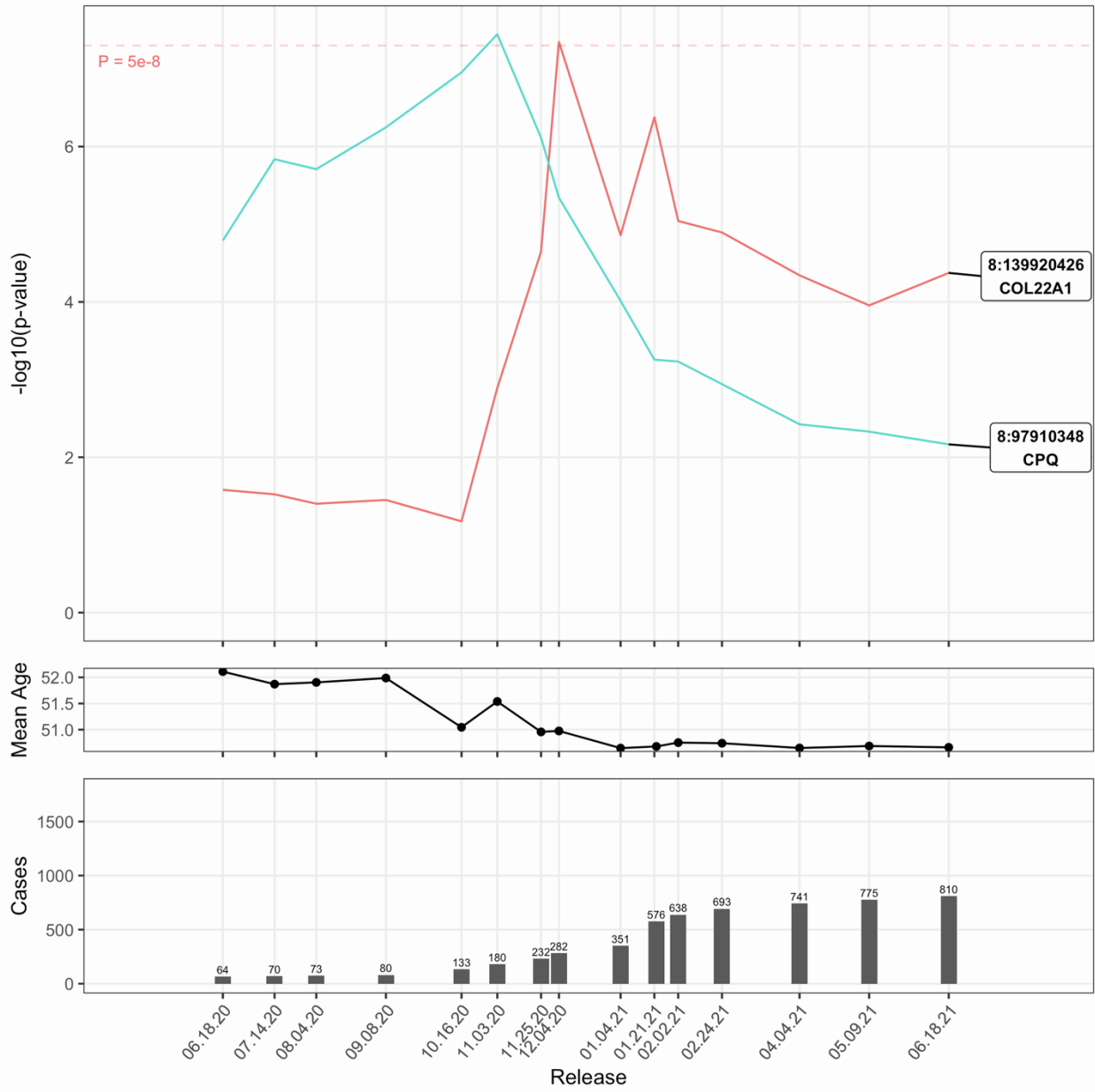
Figure S17: Covid-19 Susceptibility in SAS:Tested
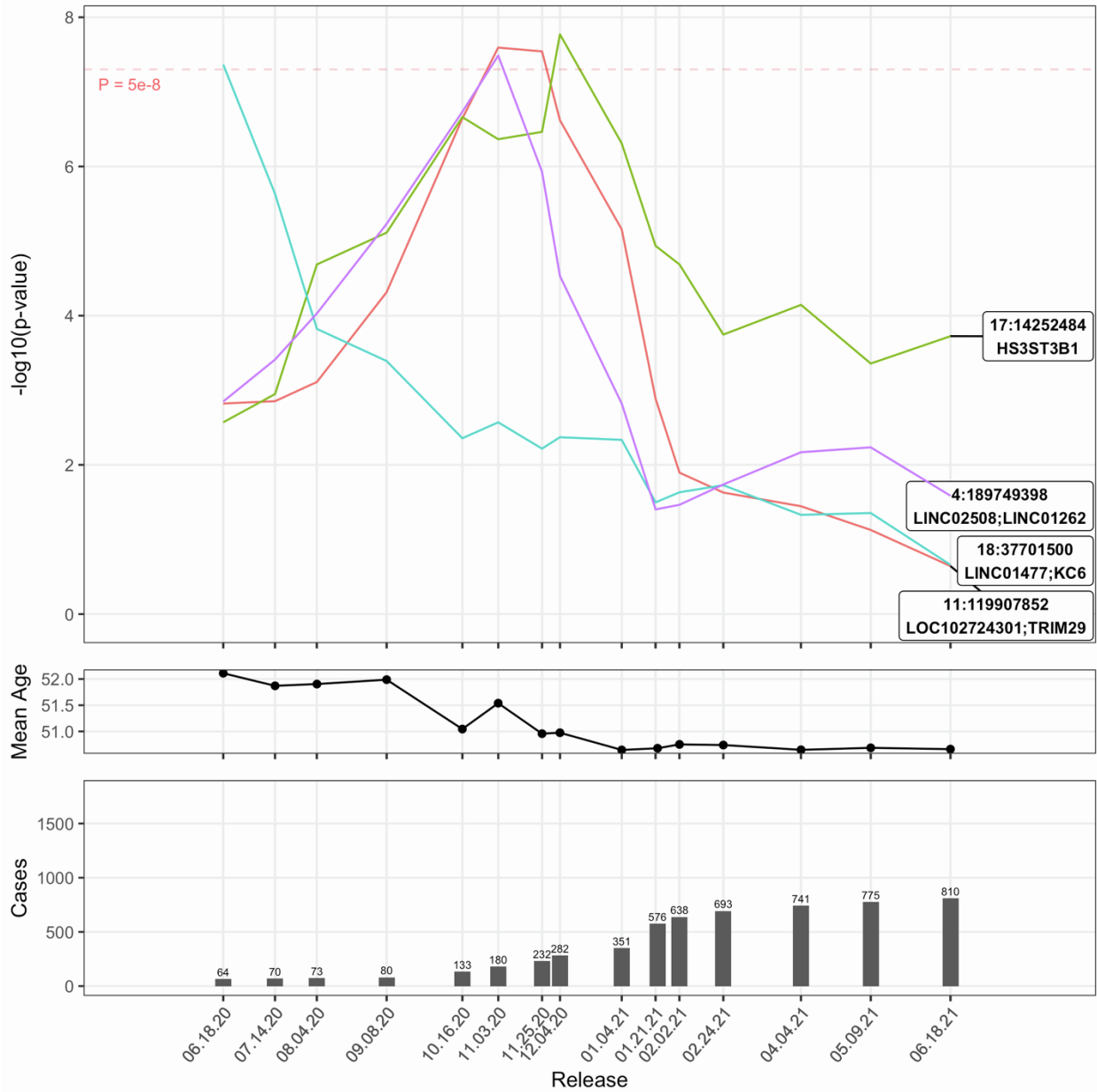
Figure S18: Covid-19 Susceptibility in OTHERS:Tested

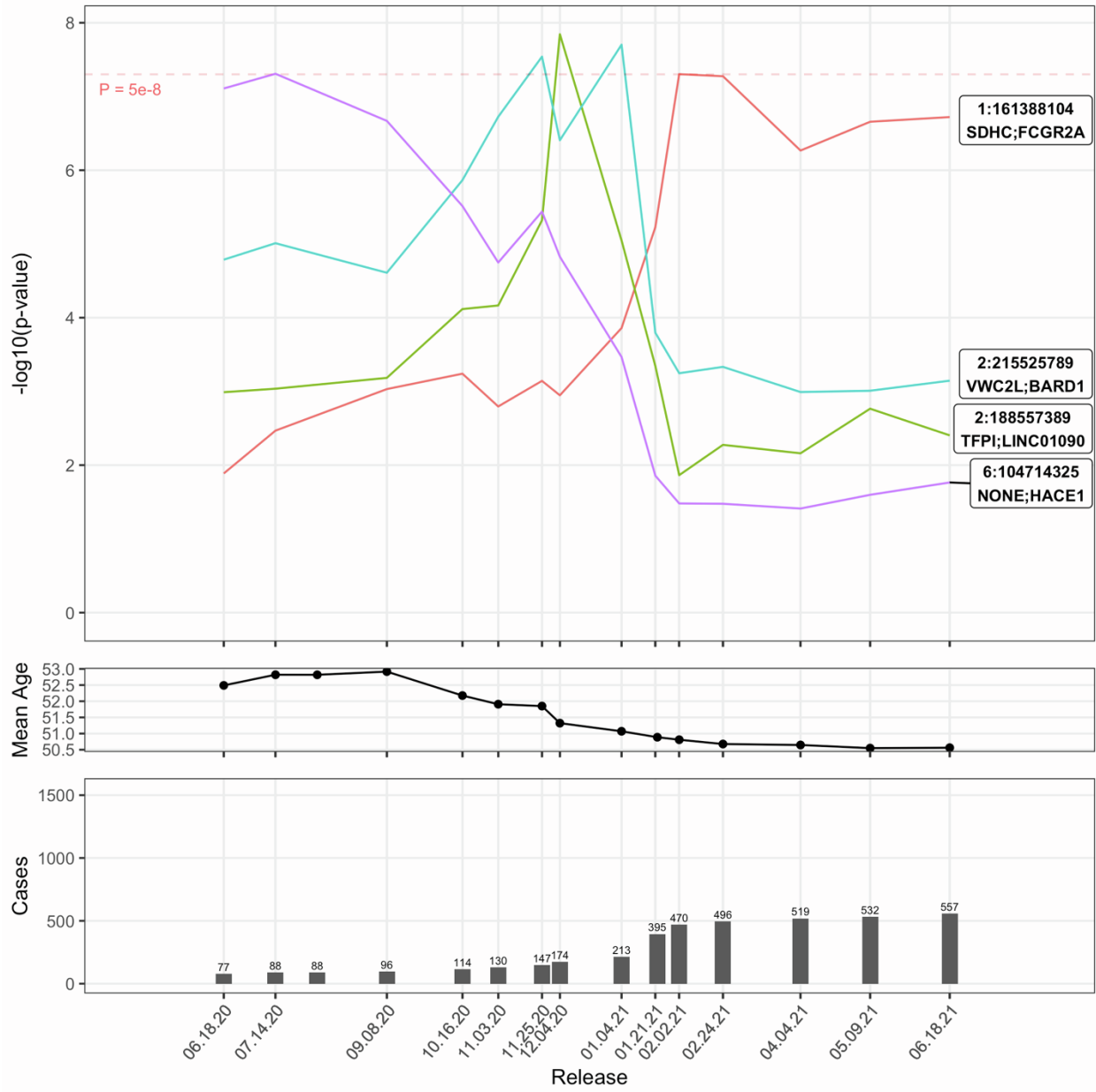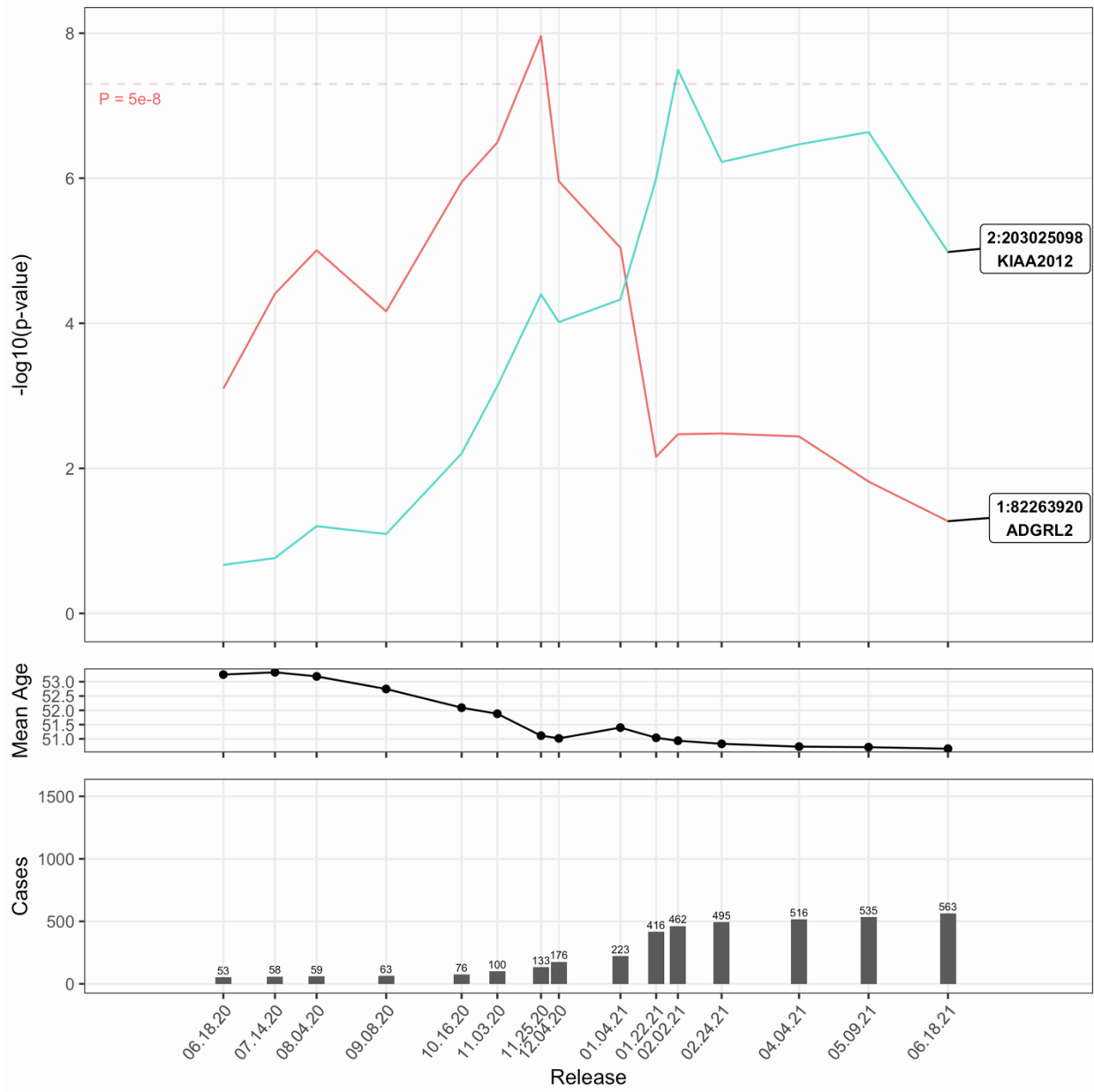# Figure S19: Covid-19 Susceptibility in nEUR:Pop

Figure S20: Covid-19 Hospitalization in ALL:Pop

Figure S21: Covid-19 Hospitalization in ALL:Pop:M

Figure S22: Covid-19 Hospitalization in ALL:Tested

Figure S23: Covid-19 Hospitalization in ALL:Tested:M
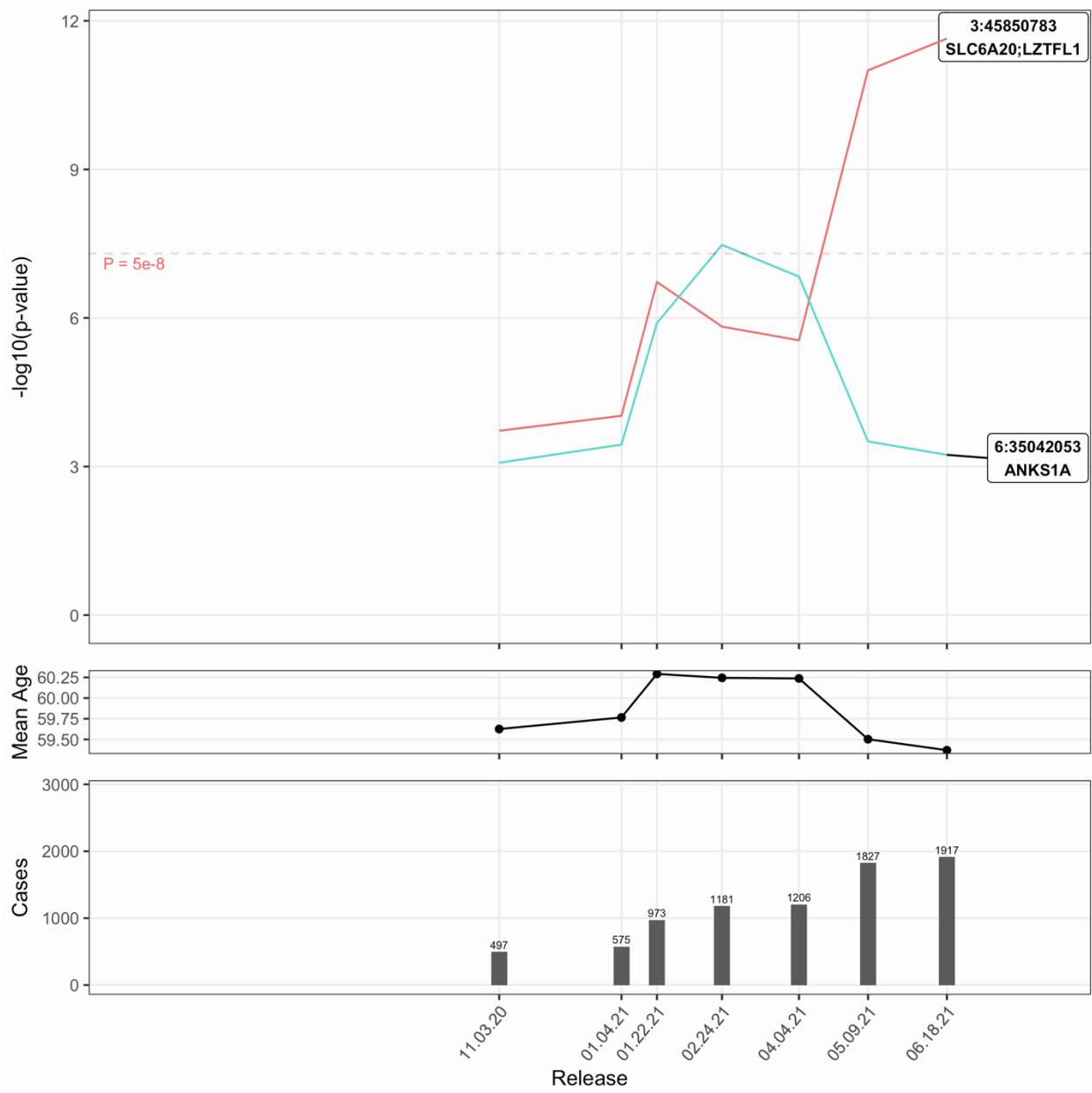
Figure S24: Covid-19 Hospitalization in ALL:Positive
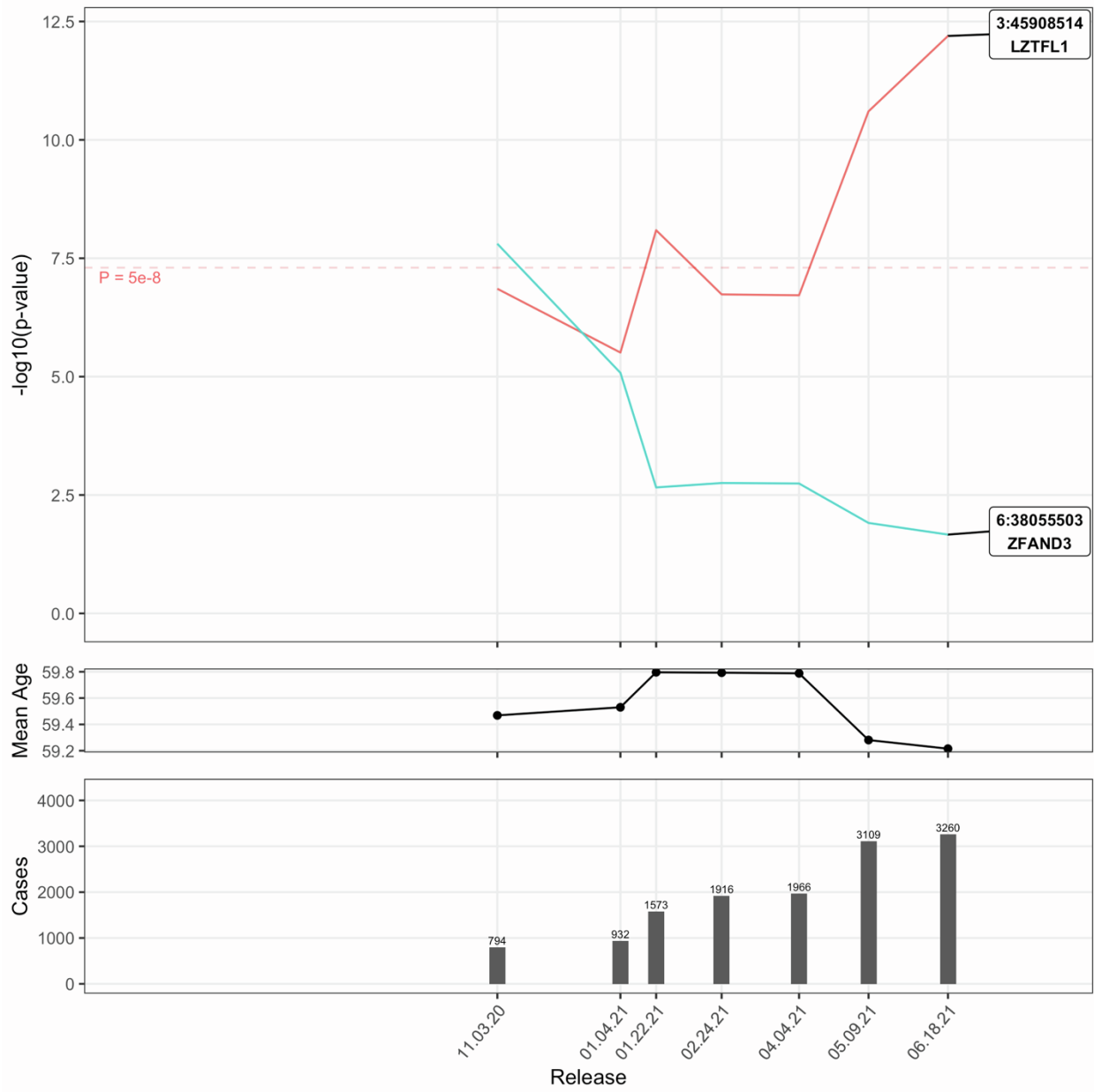
Figure S25: Covid-19 Hospitalization in ALL:Positive:M
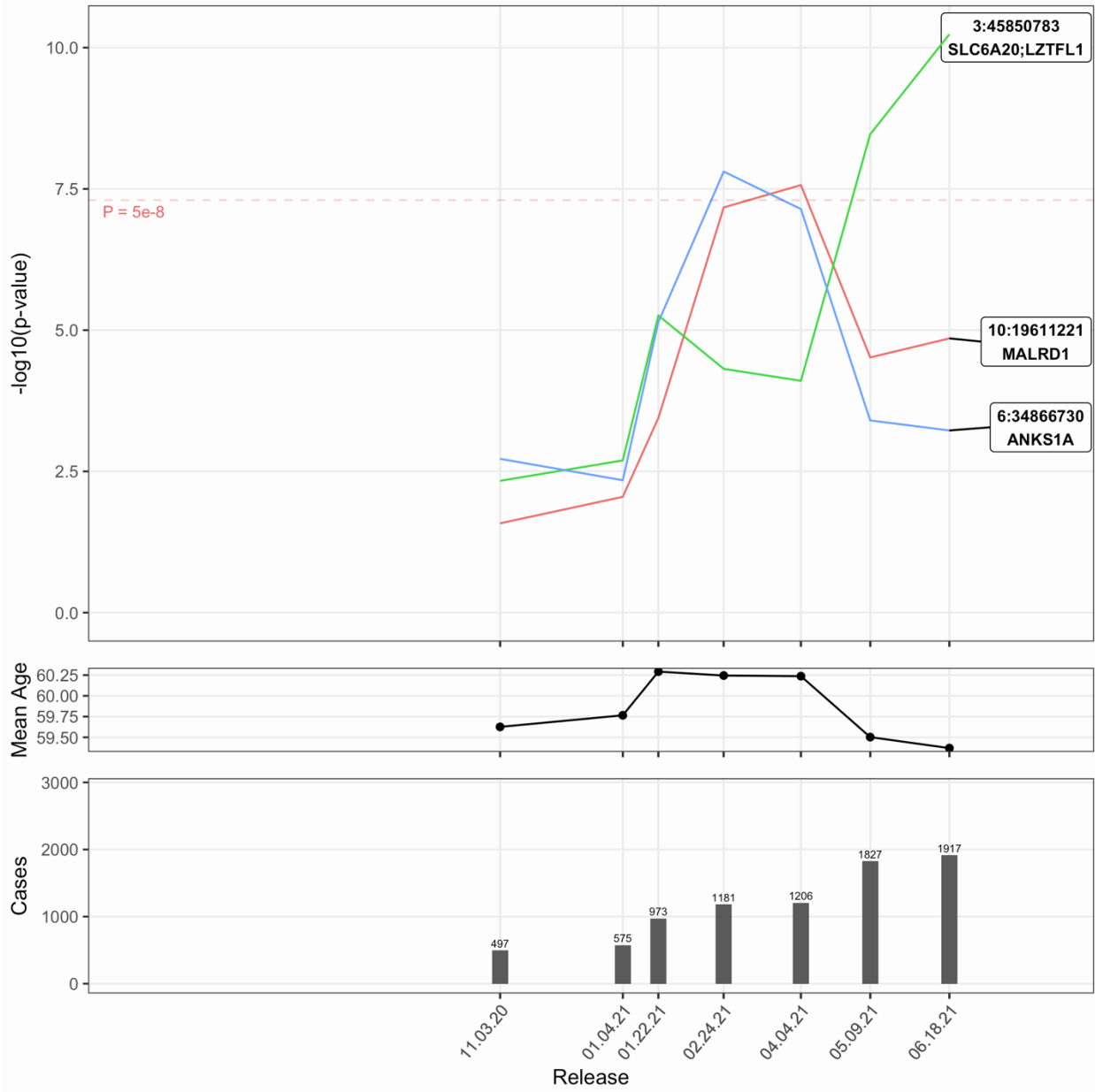
Figure S26: Covid-19 Hospitalization in EUR:Pop
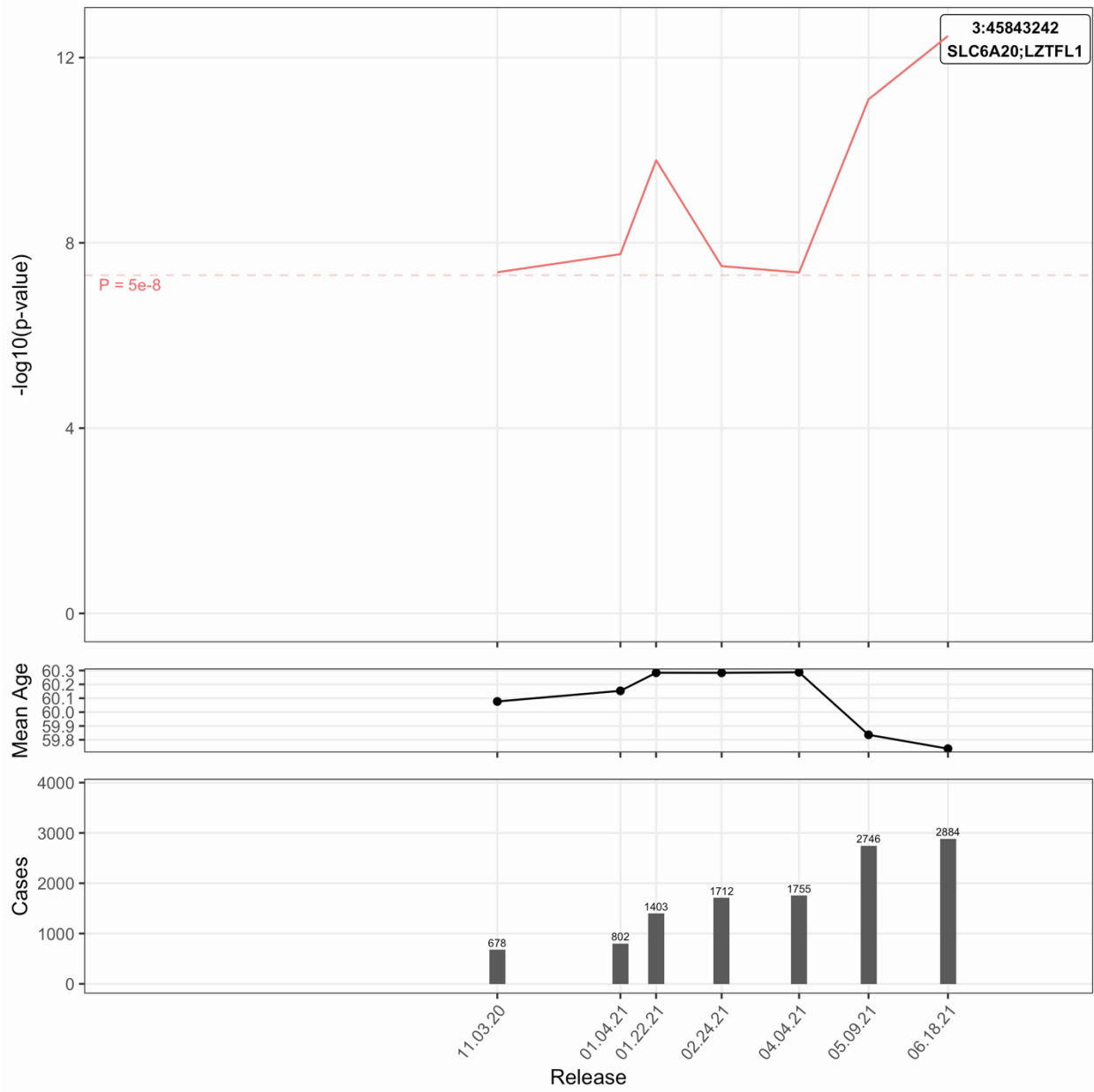
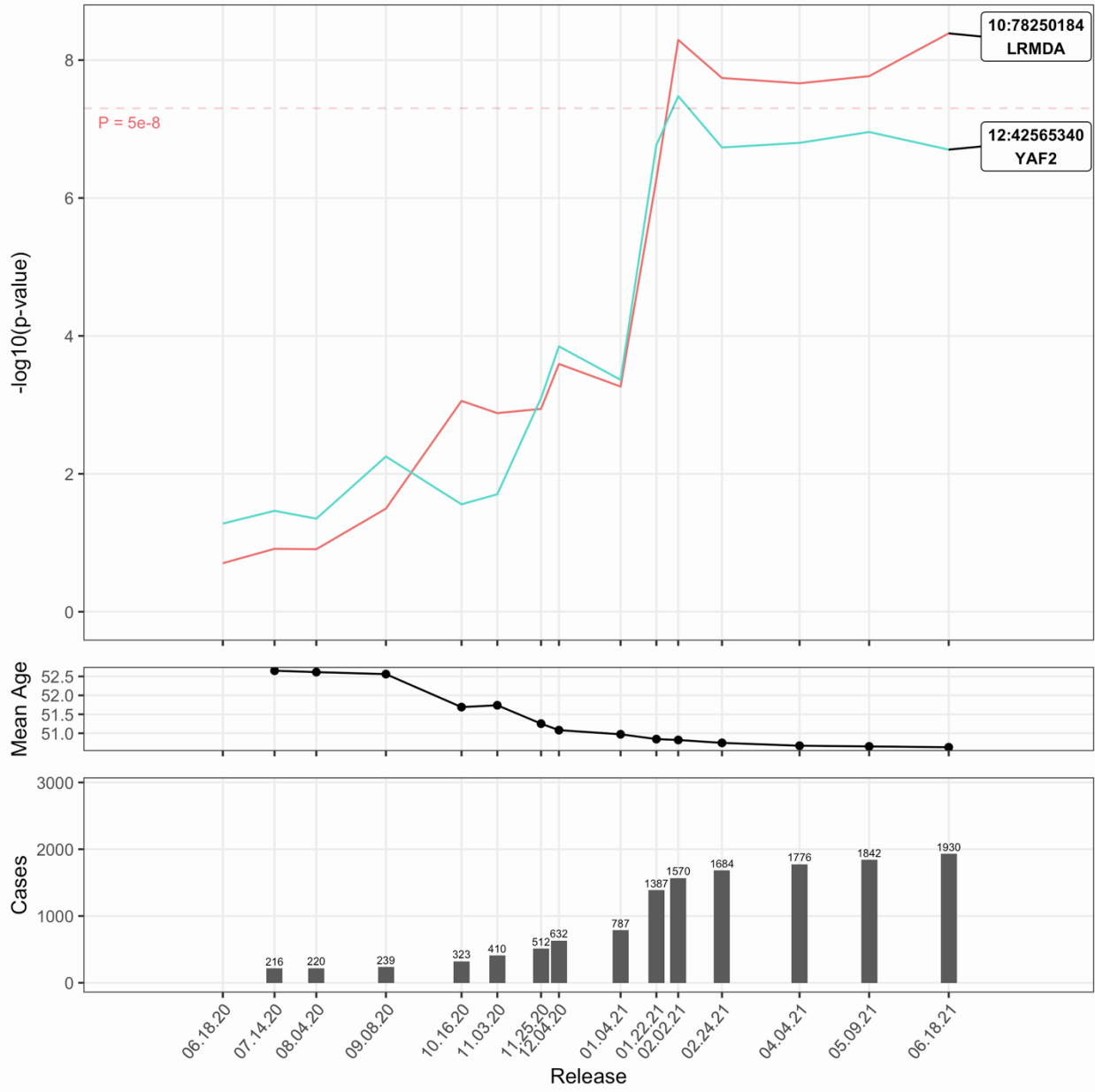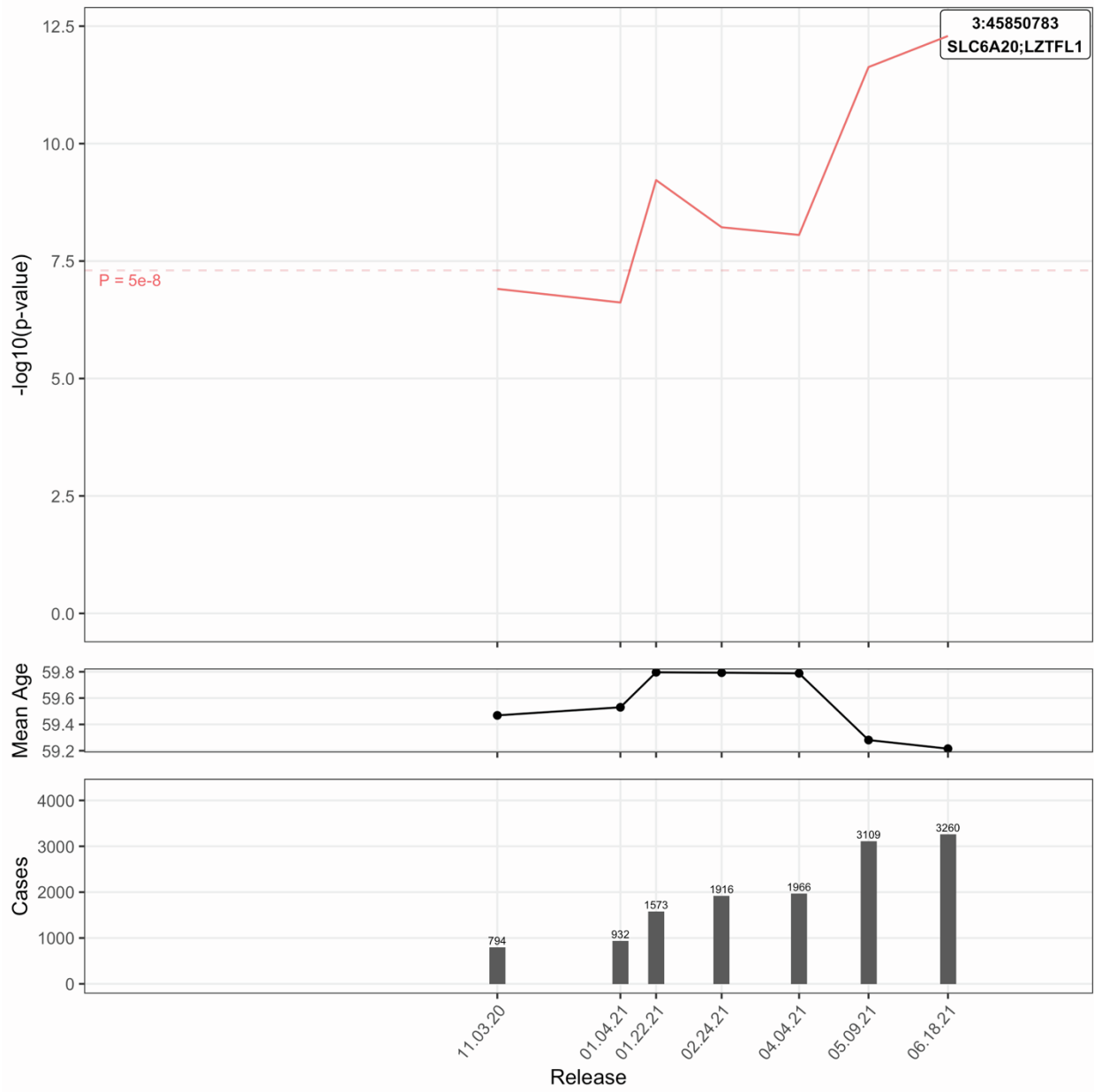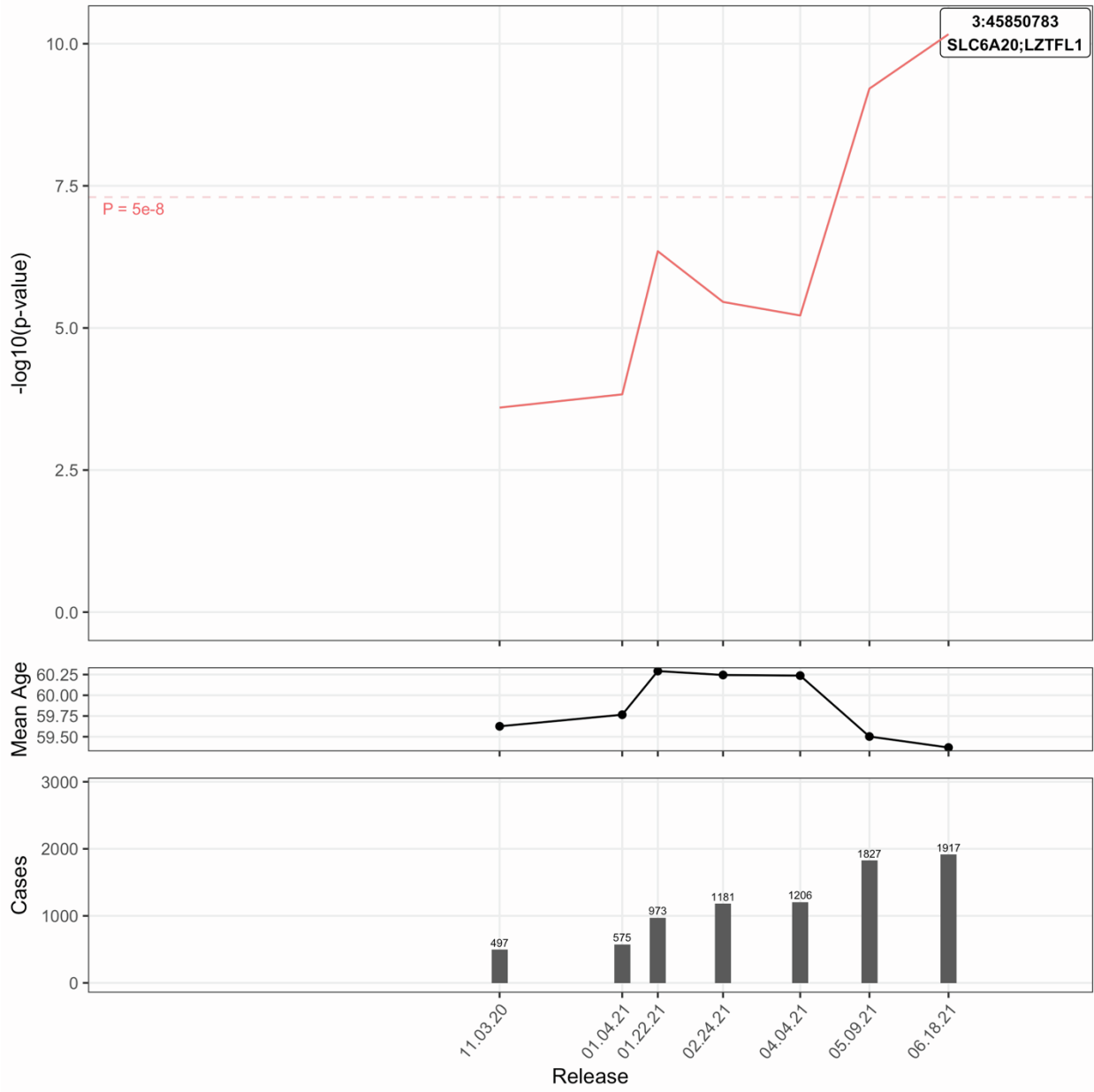Figure S27: Covid-19 Hospitalization in EUR:Pop:M
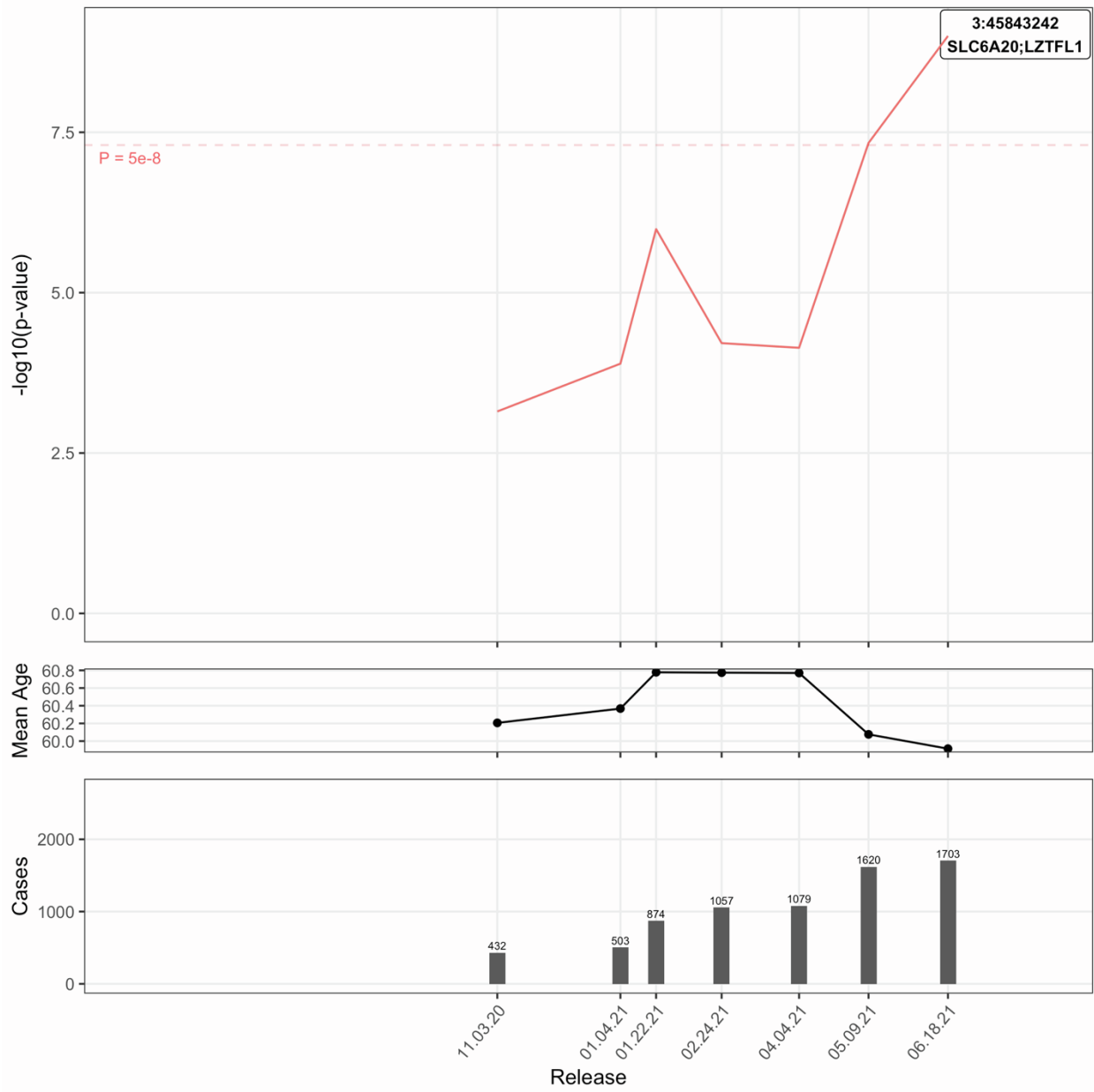
Figure S28: Covid-19 Hospitalization in EUR:Tested
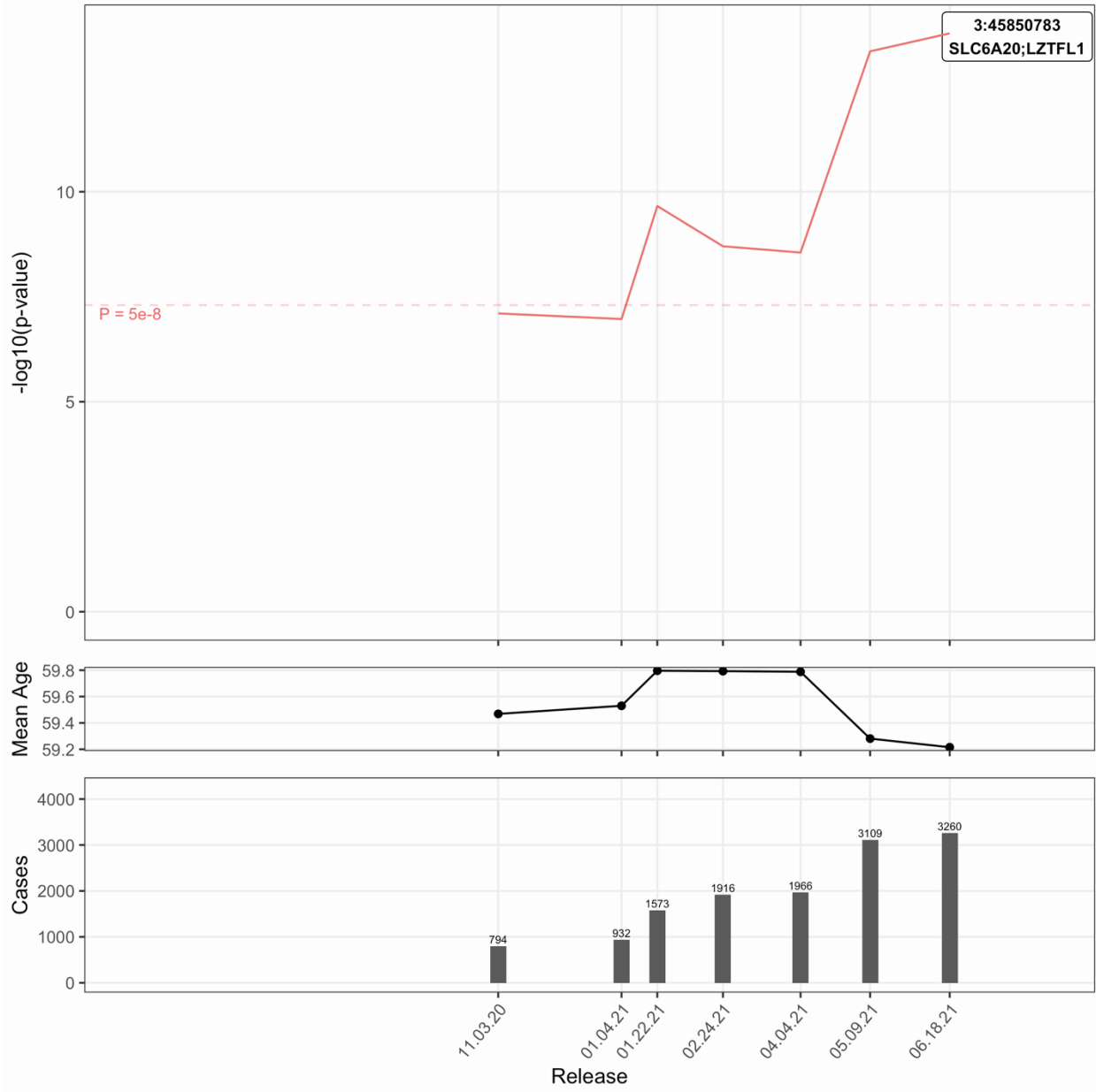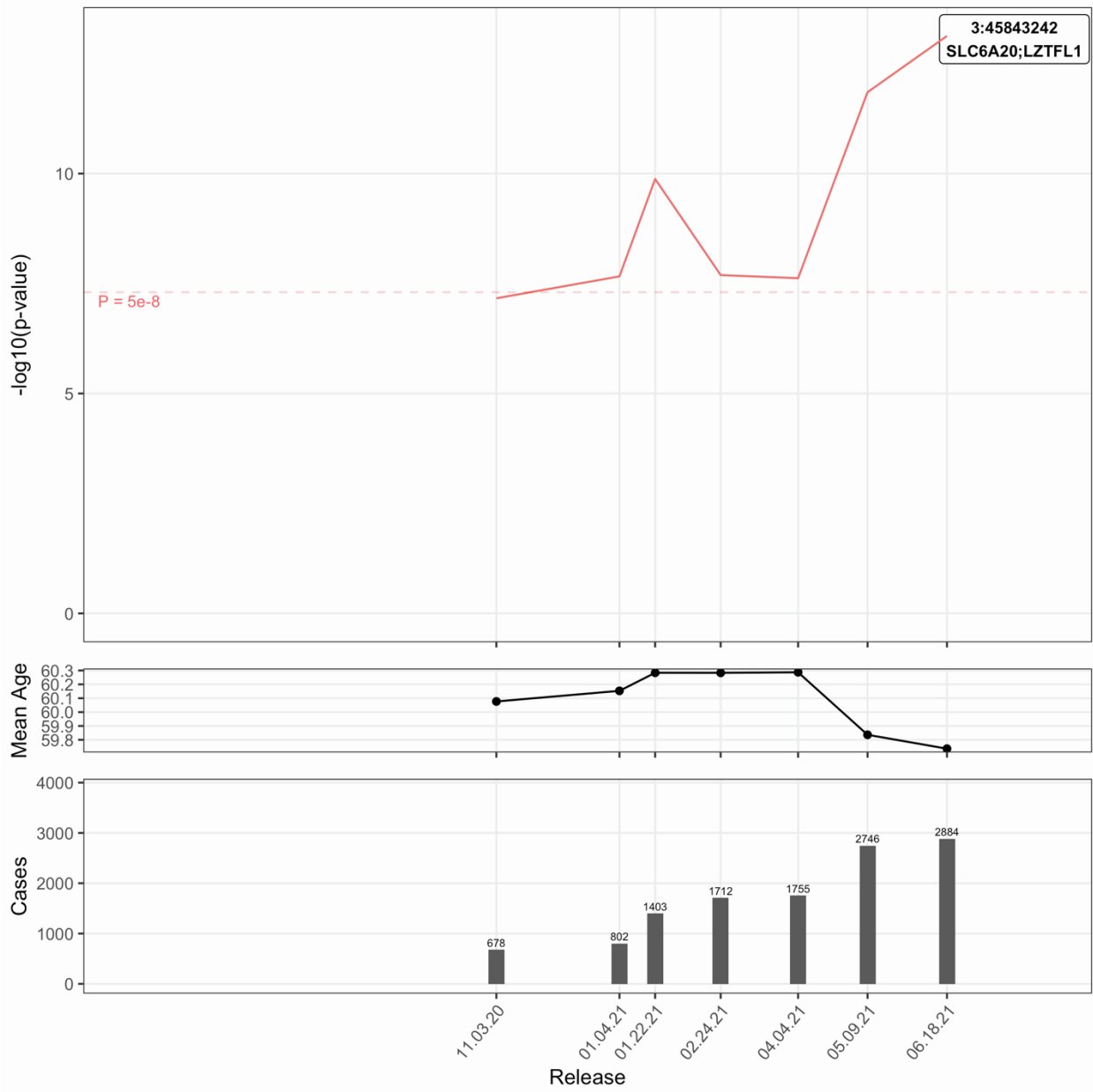
Figure S29: Covid-19 Hospitalization in EUR:Tested:M
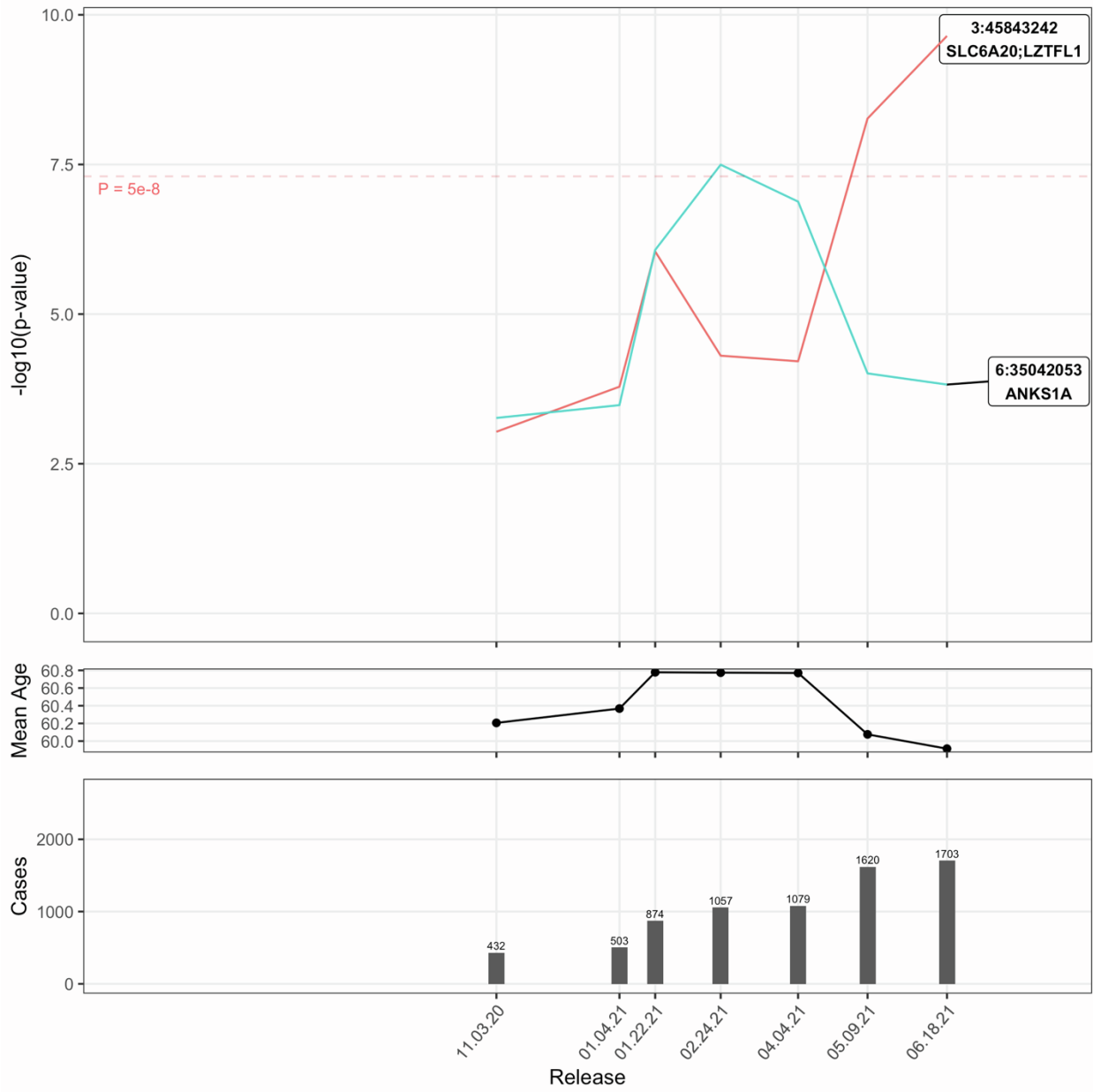
Figure S30: Covid-19 Hospitalization in EUR:Positive
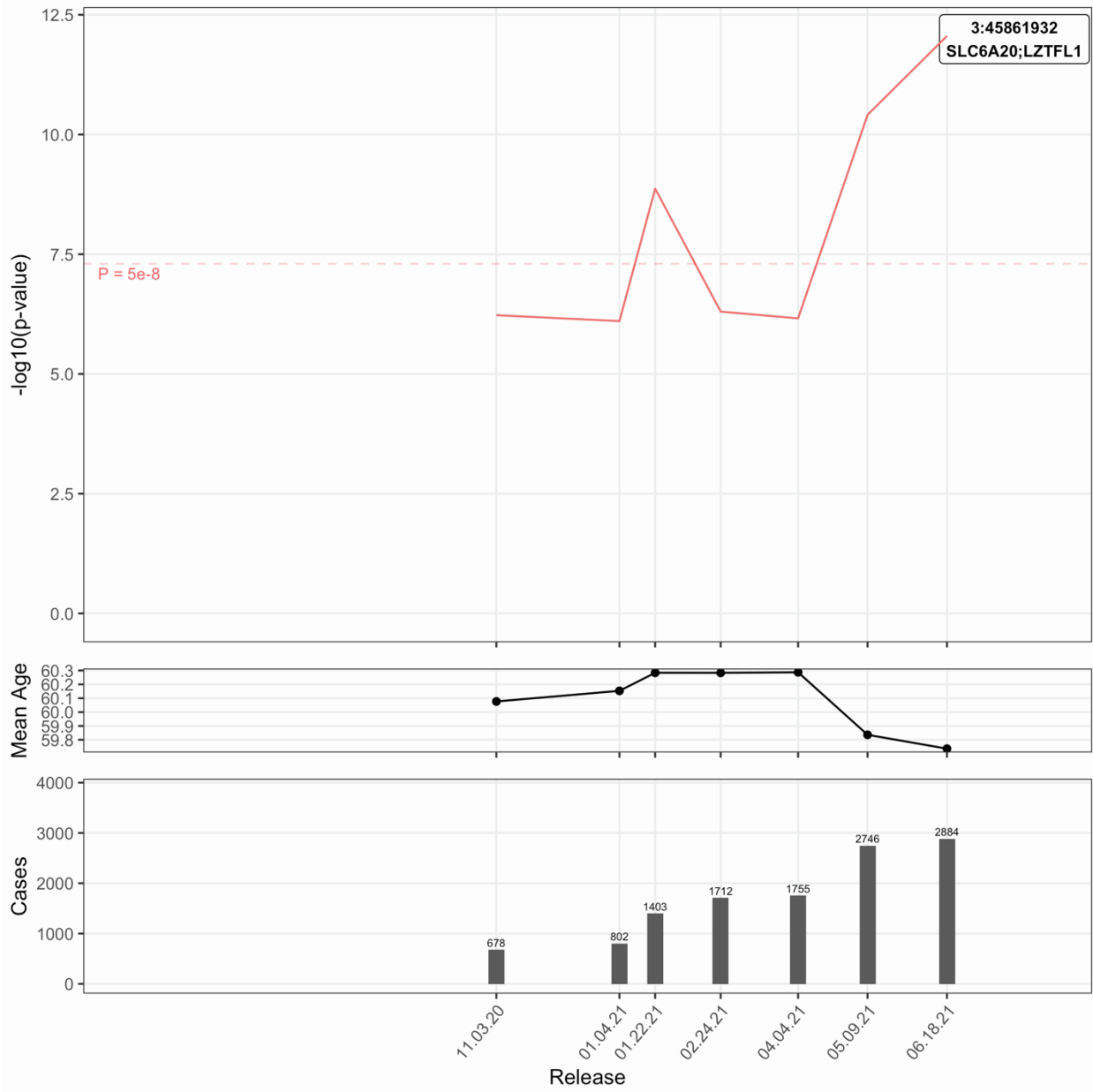
Figure S31: Covid-19 Hospitalization in EUR:Positive:F
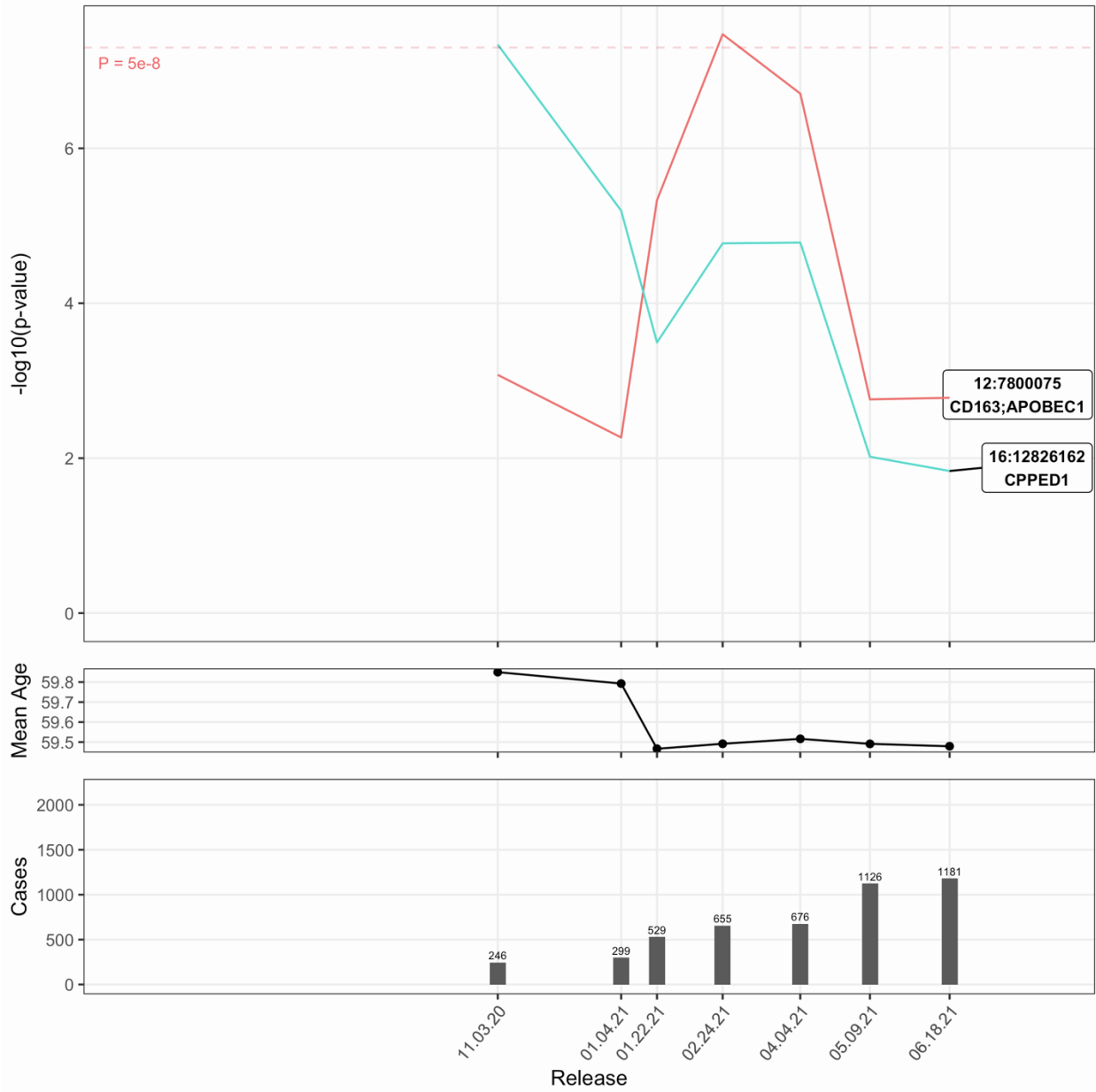
Figure S32: Covid-19 Hospitalization in EUR:Positive:M
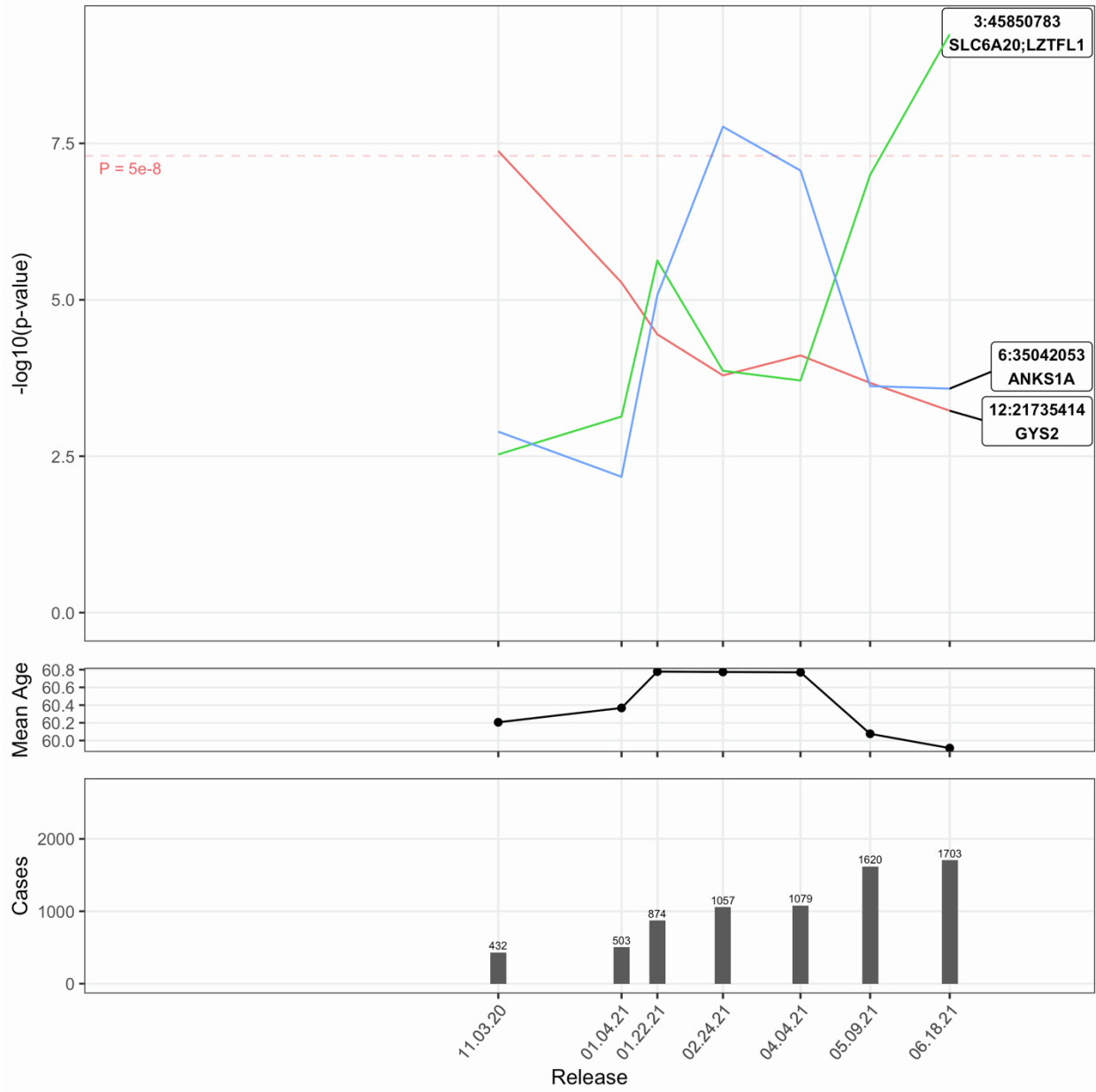
Figure S33: Severe Covid-19 in ALL:Pop
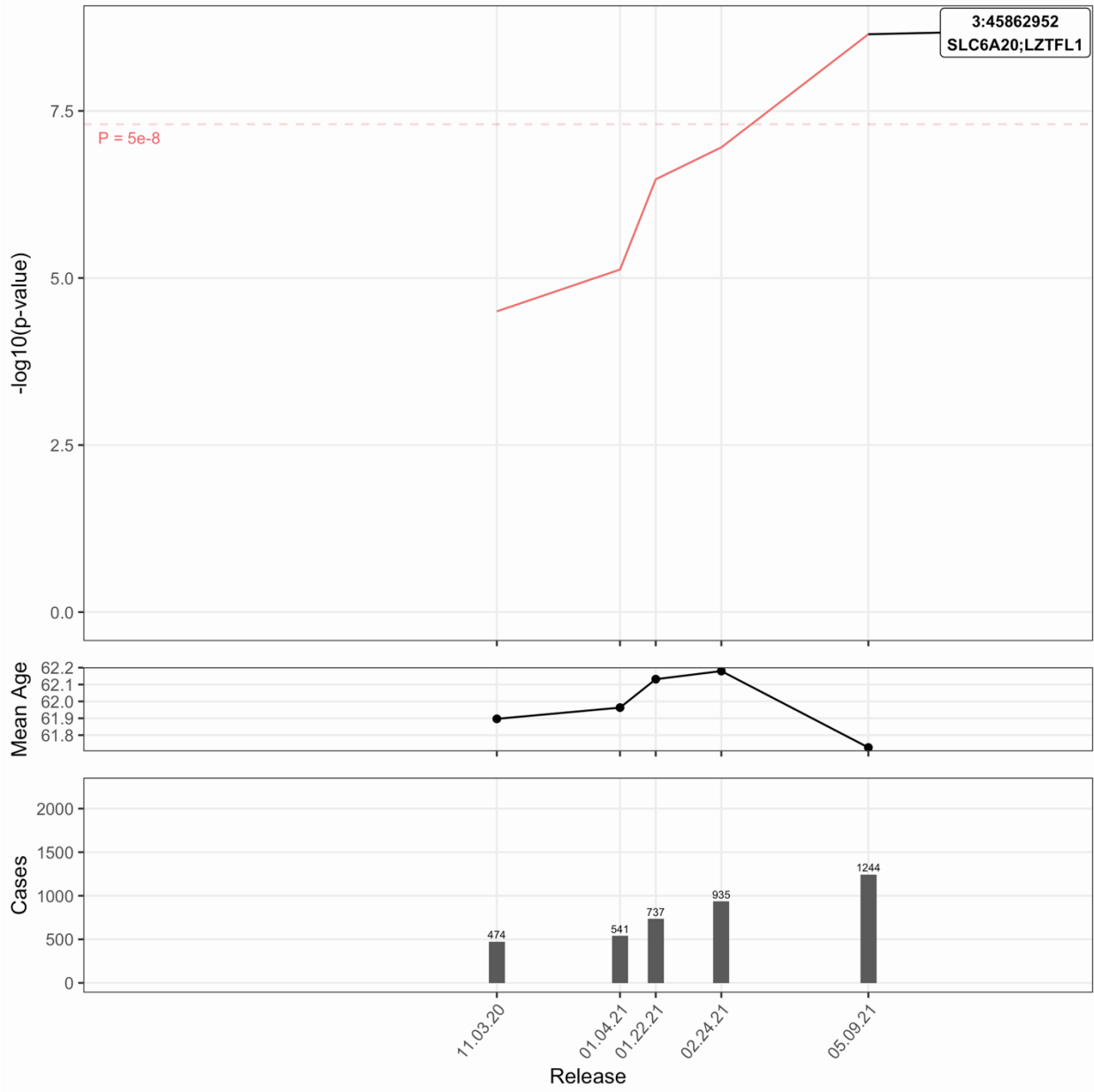
Figure S34: Severe Covid-19 in ALL:Pop:M
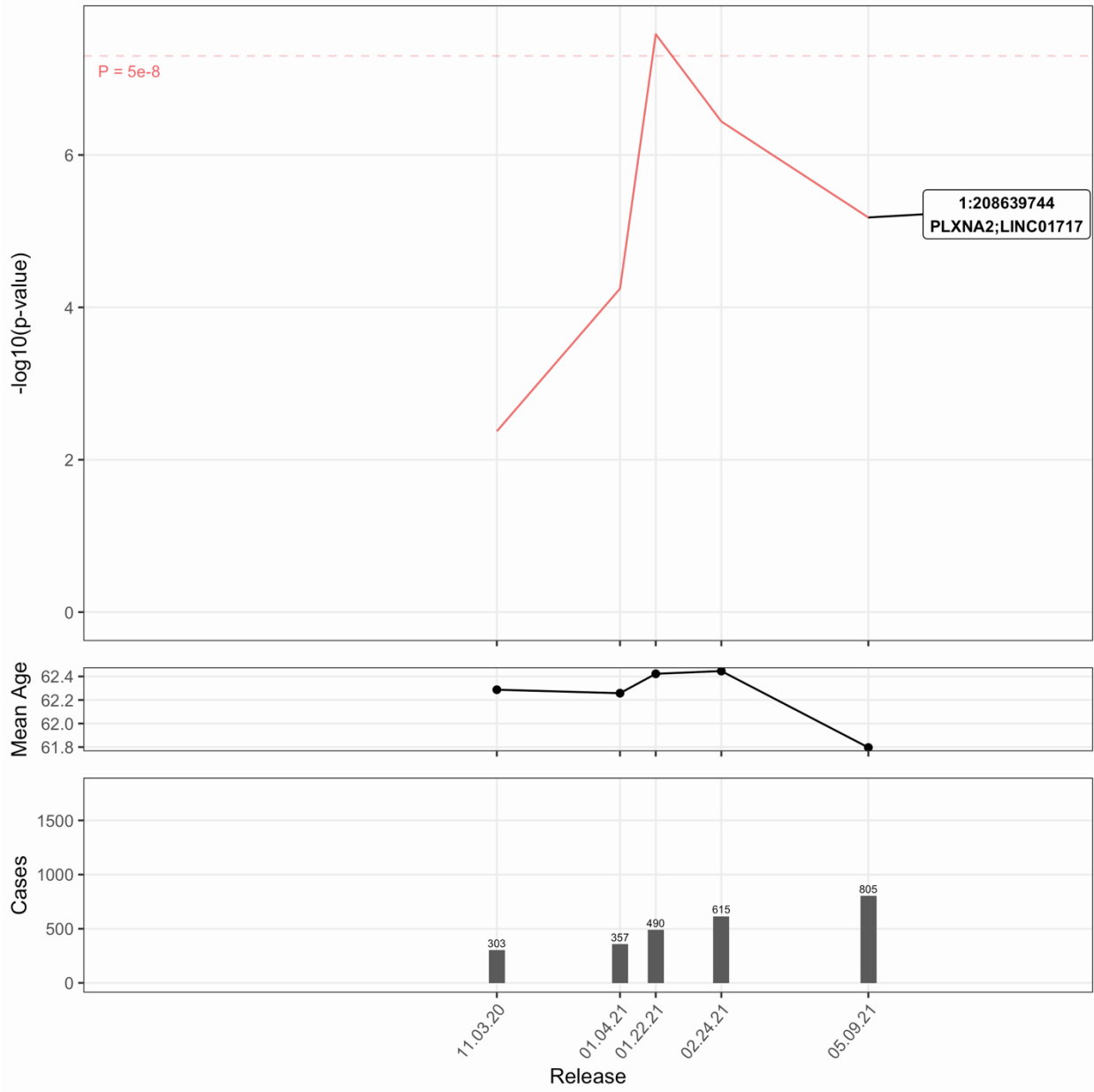
Figure S35: Severe Covid-19 in ALL:Tested
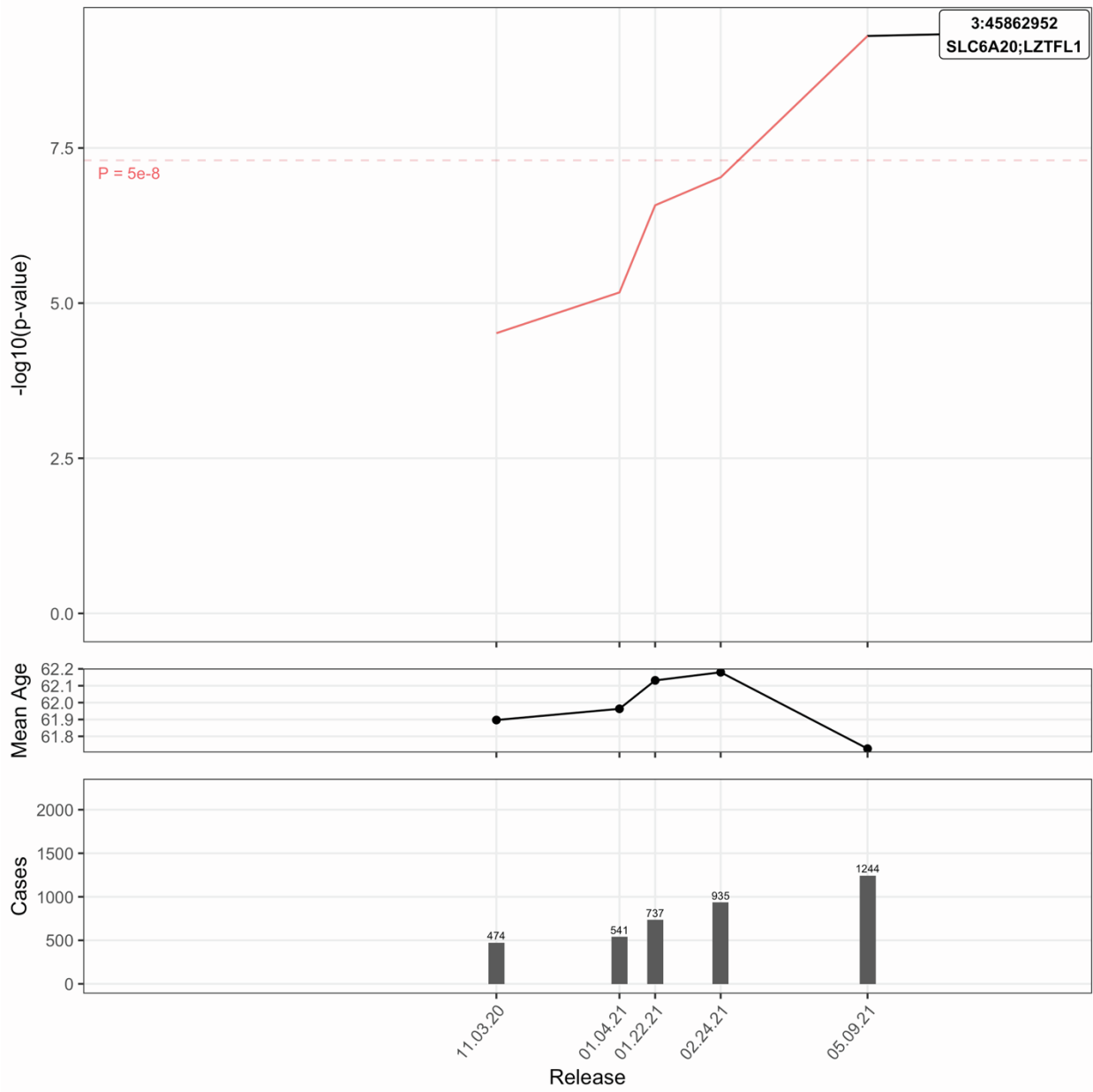
Figure S36: Severe Covid-19 in ALL:Tested:M
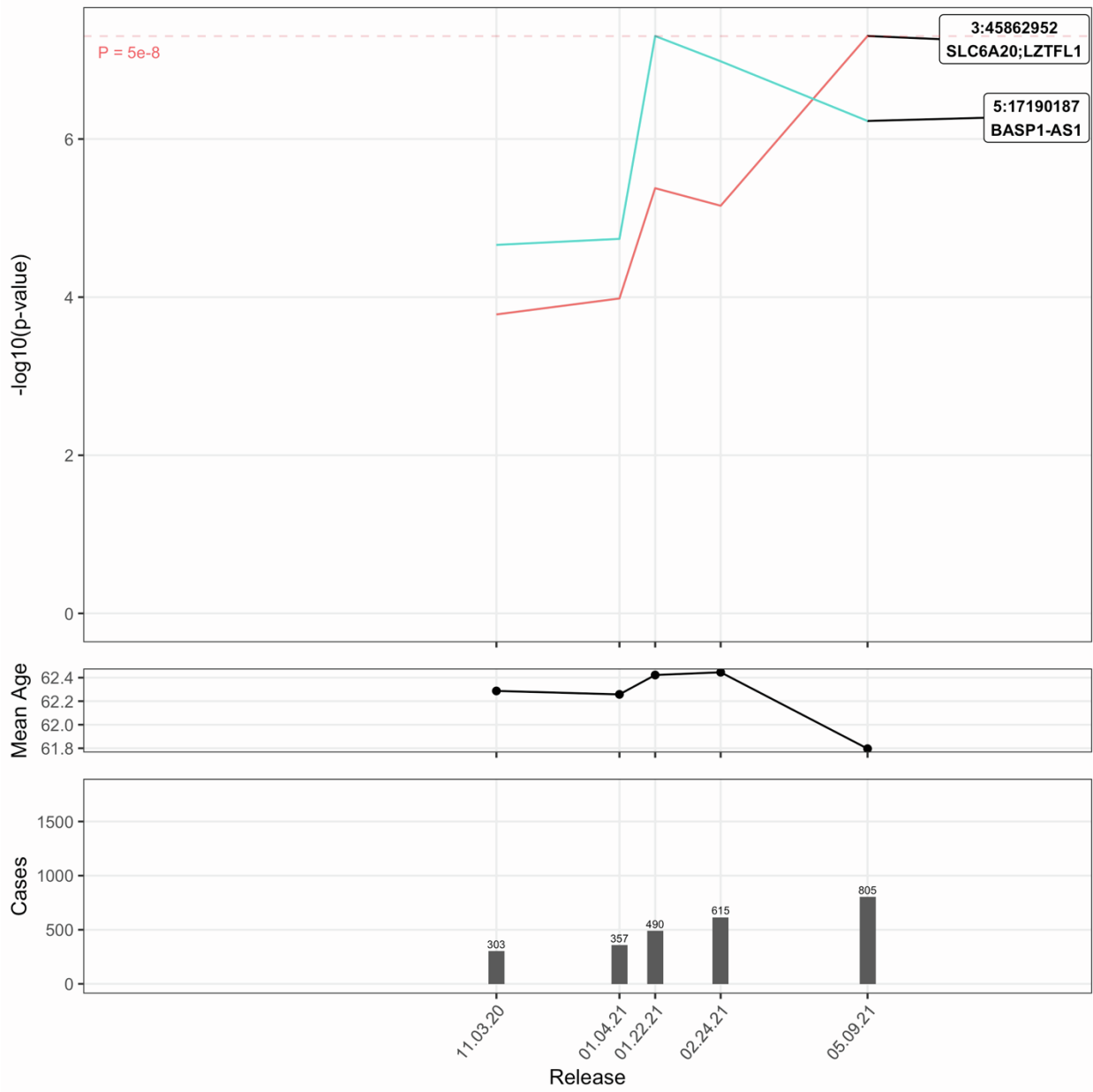
Figure S37: Severe Covid-19 in ALL:Positive
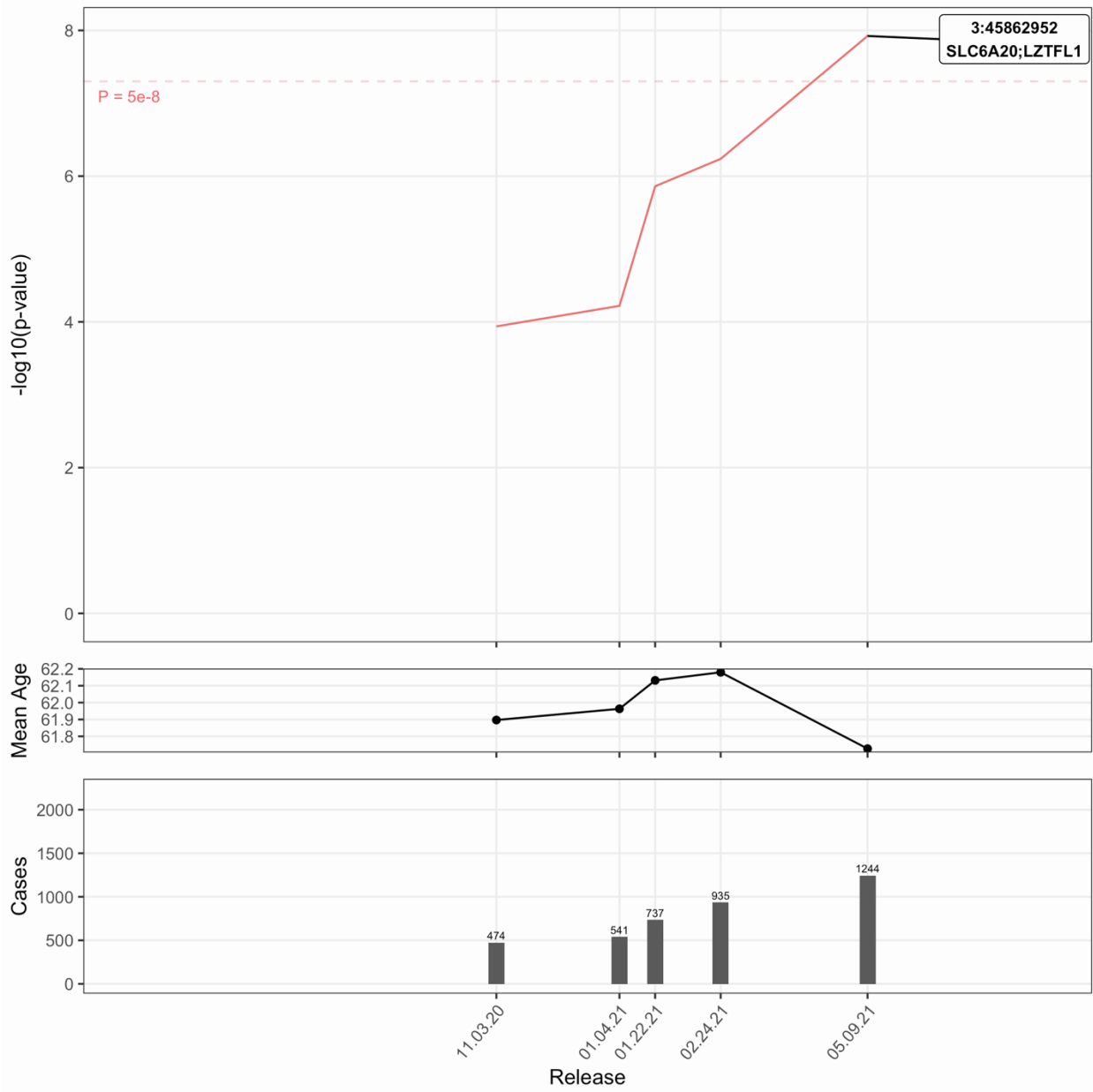
Figure S38: Severe Covid-19 in EUR:Pop
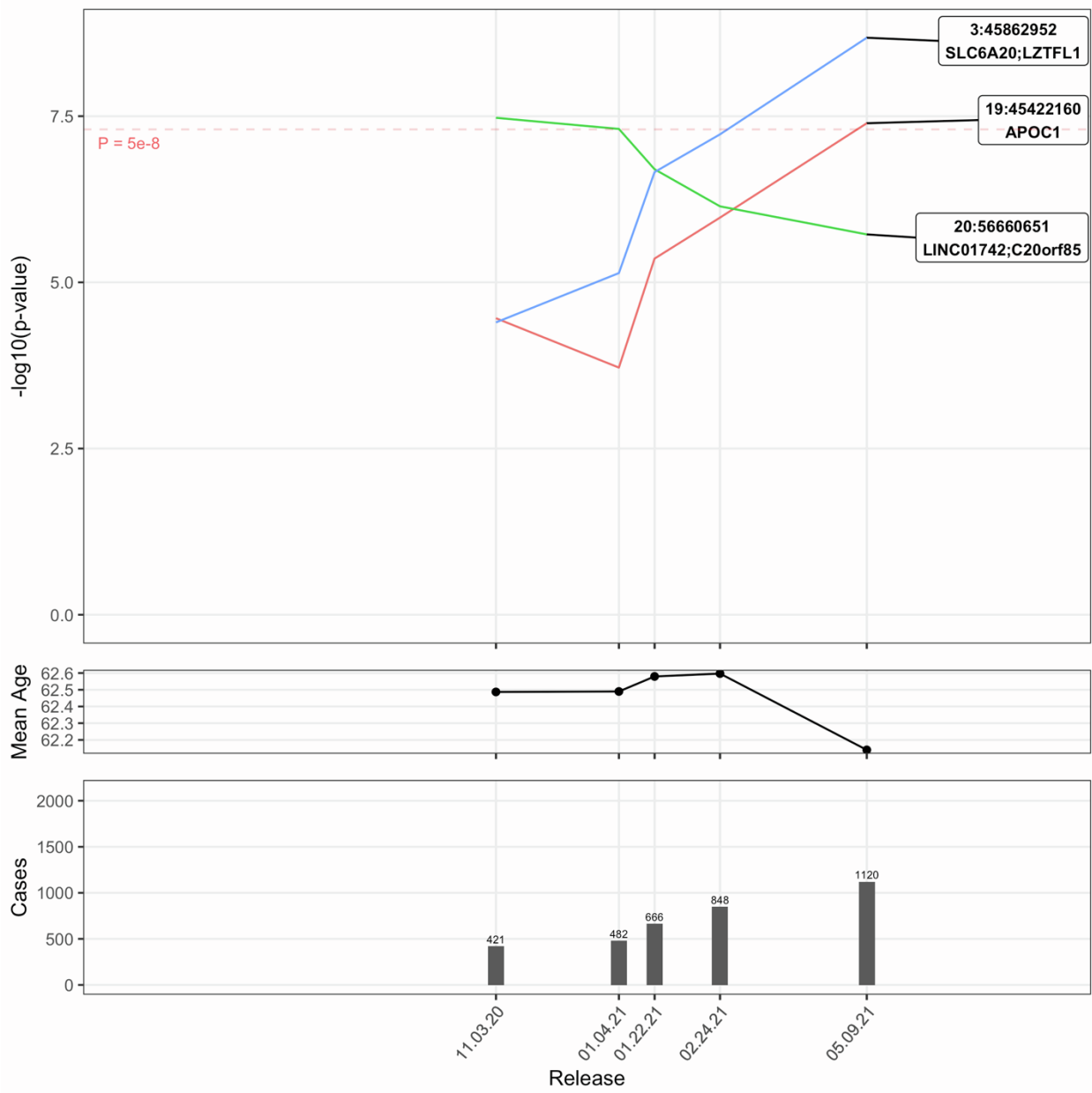
Figure S39: Severe Covid-19 in EUR:Pop:F
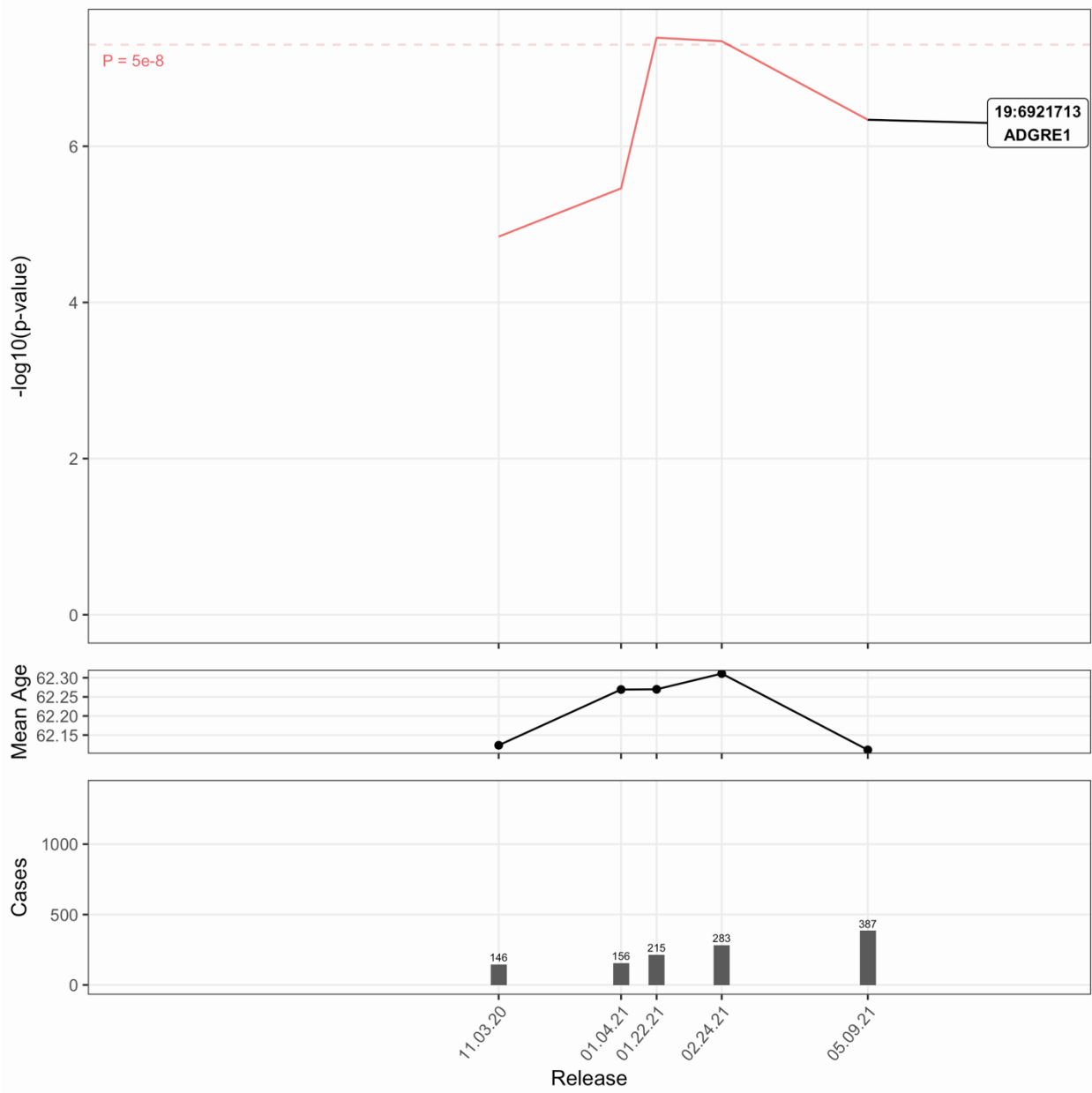
Figure S40: Severe Covid-19 in EUR:Tested
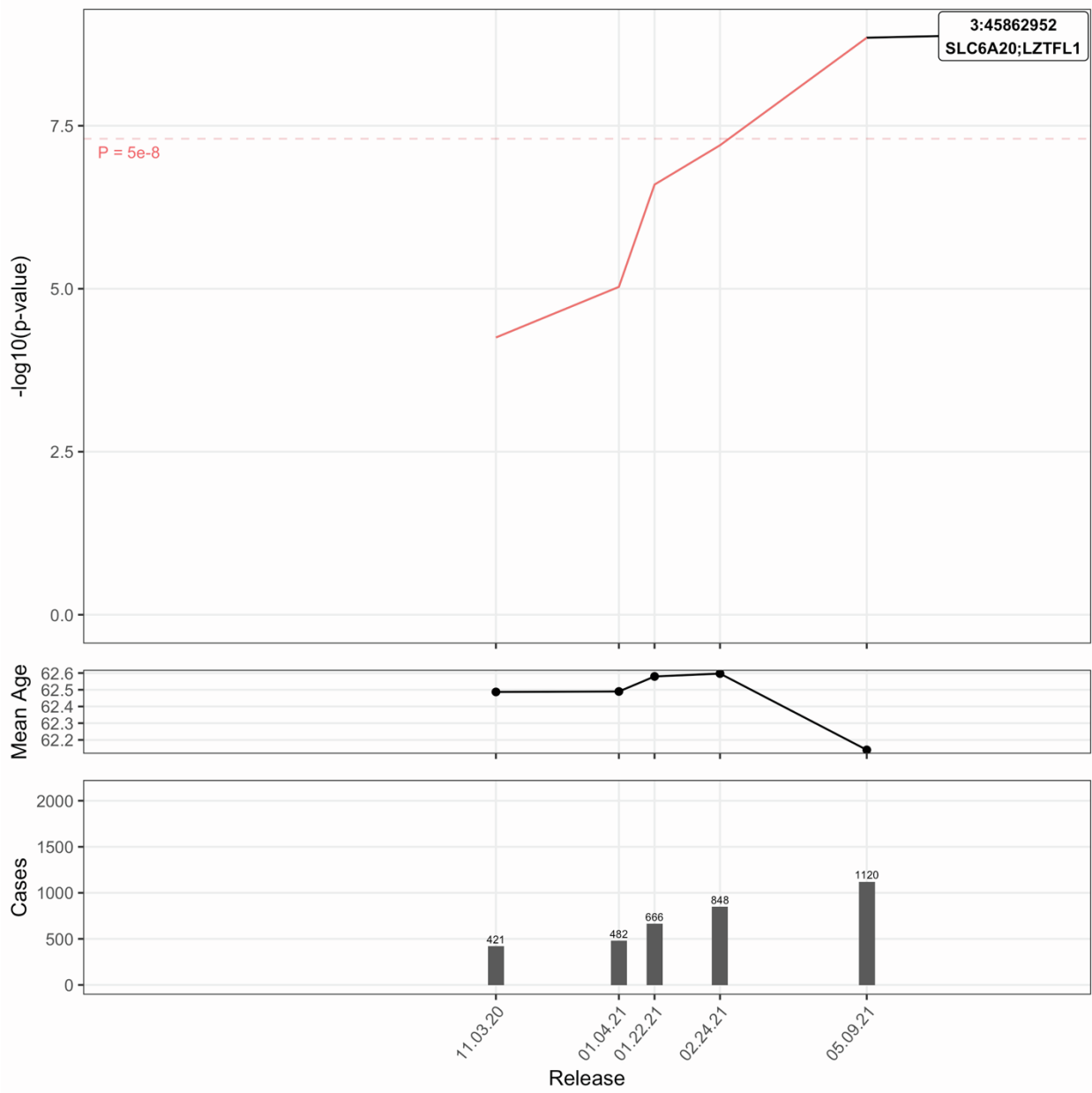
Figure S41: Severe Covid-19 in EUR:Tested:F
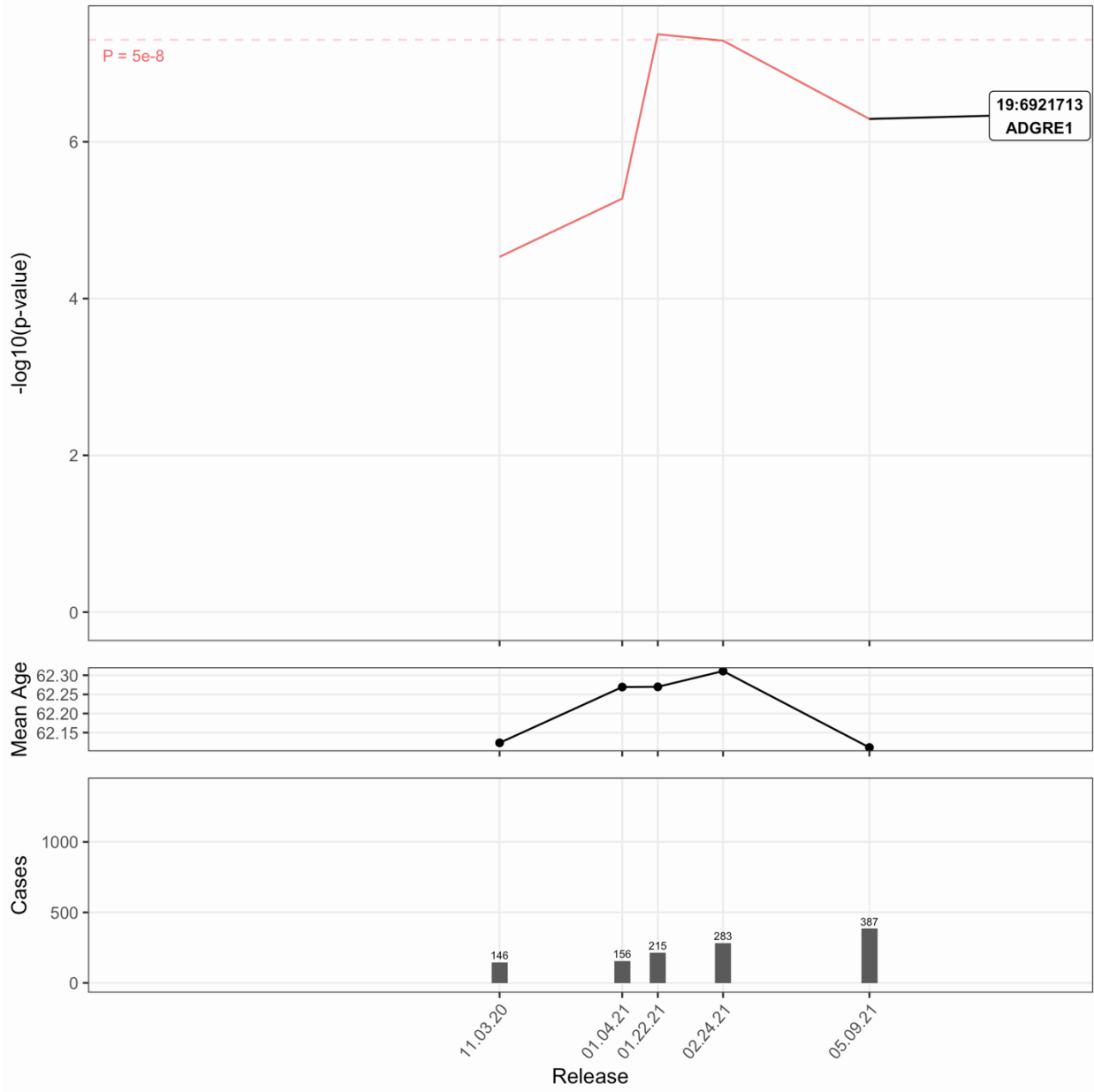
Figure S42: Severe Covid-19 in EUR:Positive
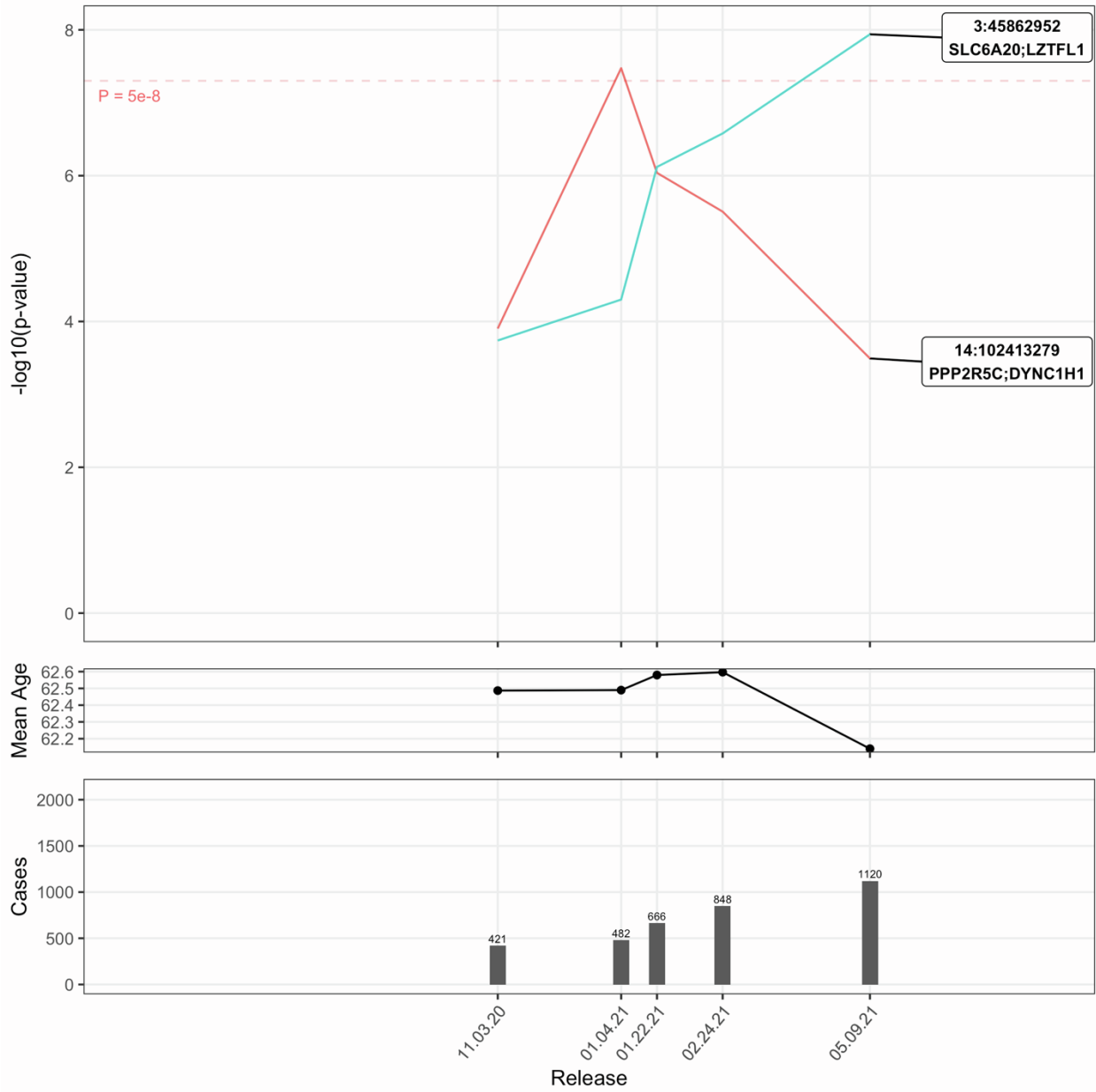
Figure S43: Severe Covid-19 in EUR:Positive:M
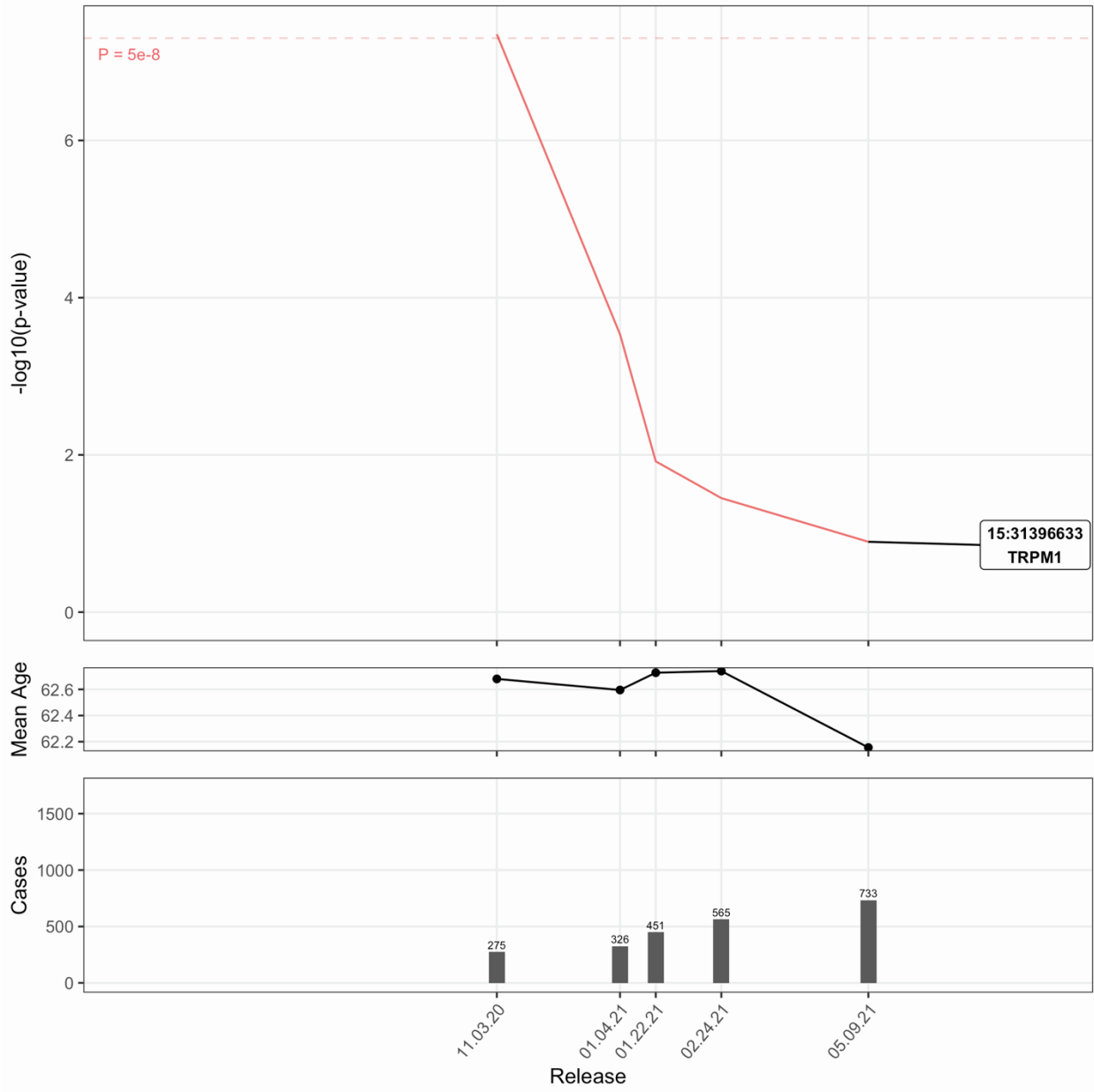
Figure S44: Covid-19 Death in ALL:Pop
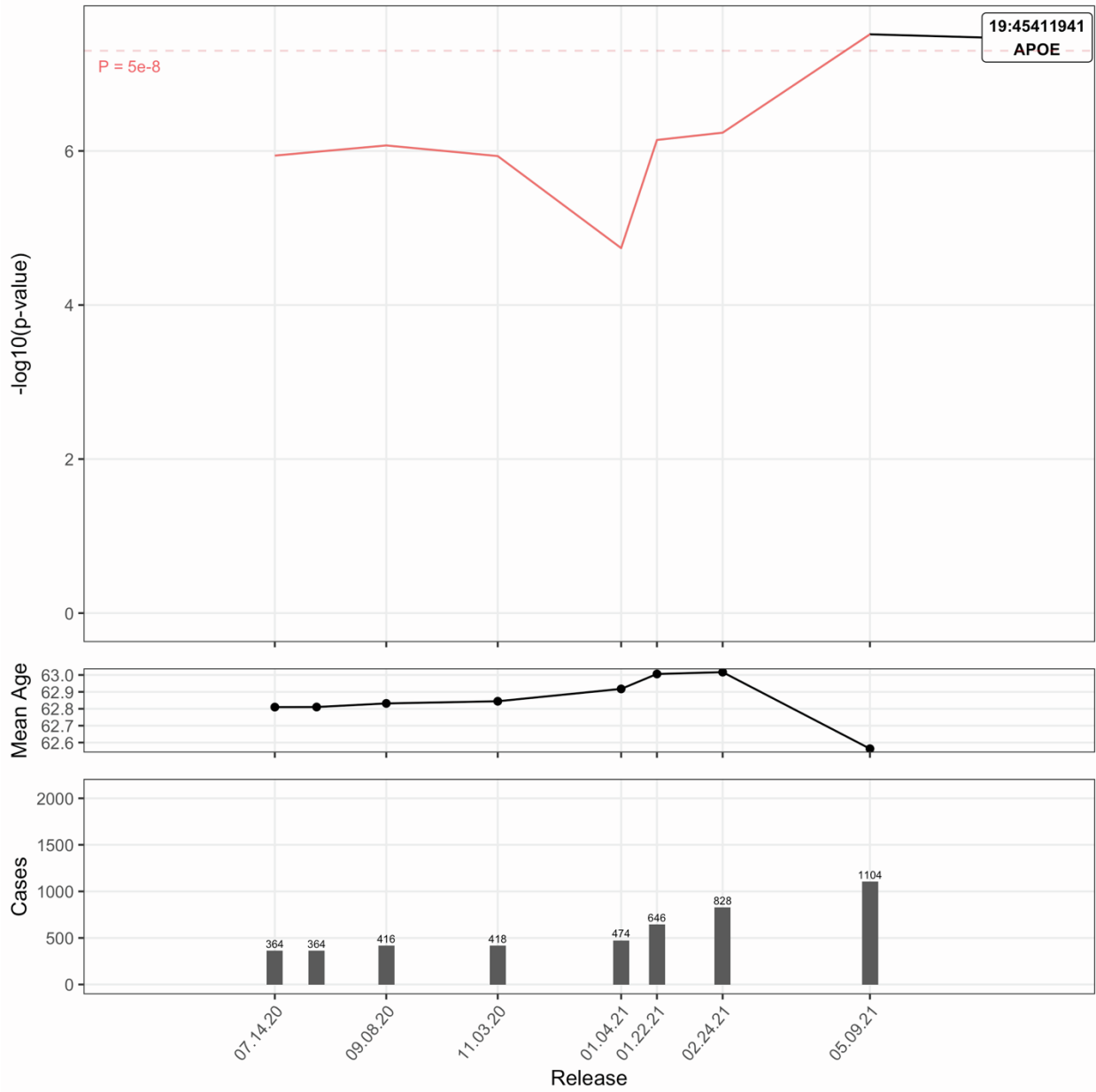
Figure S45: Covid-19 Death in ALL:Tested
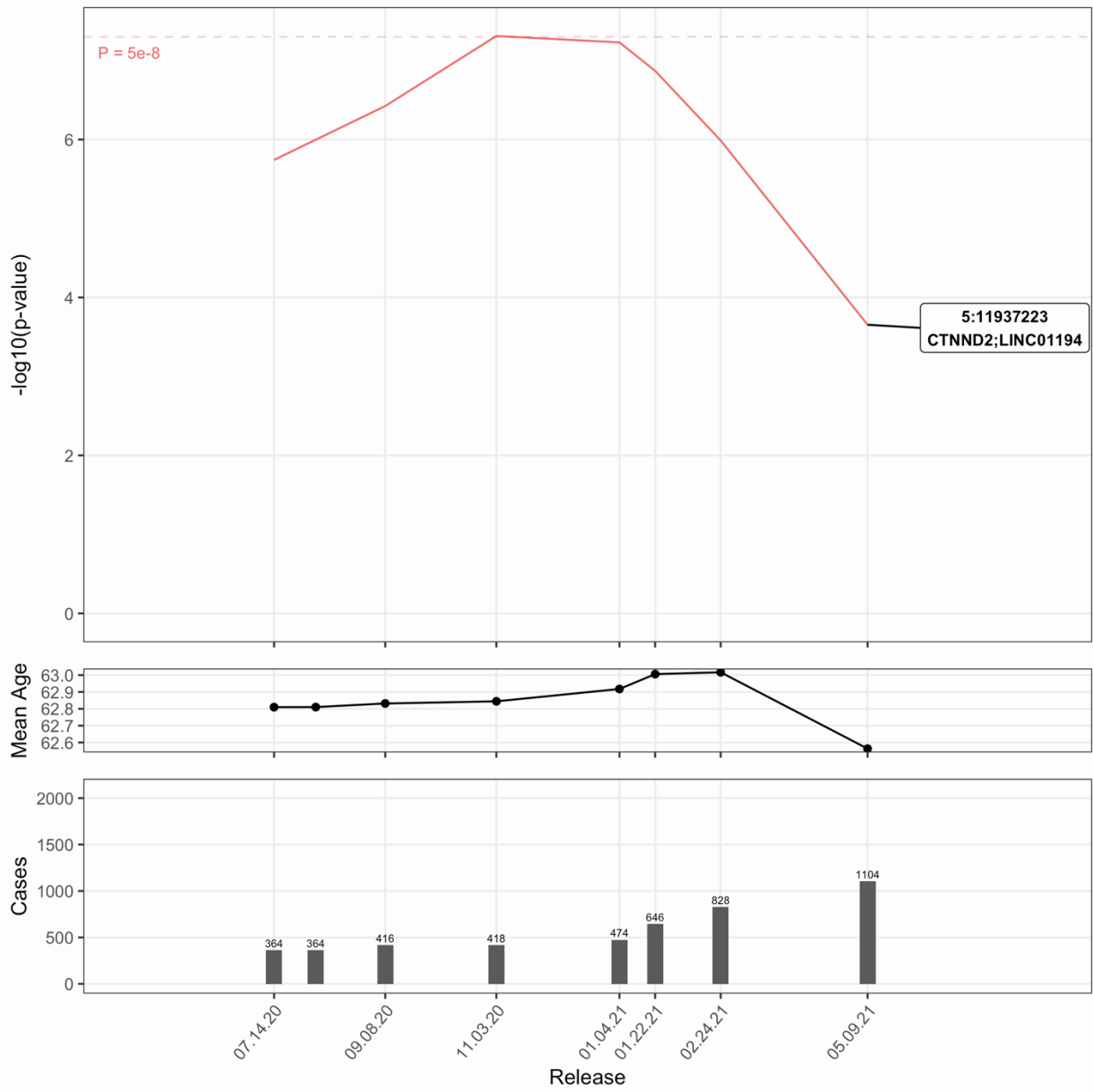
Figure S46: Covid-19 Death in EUR:Pop
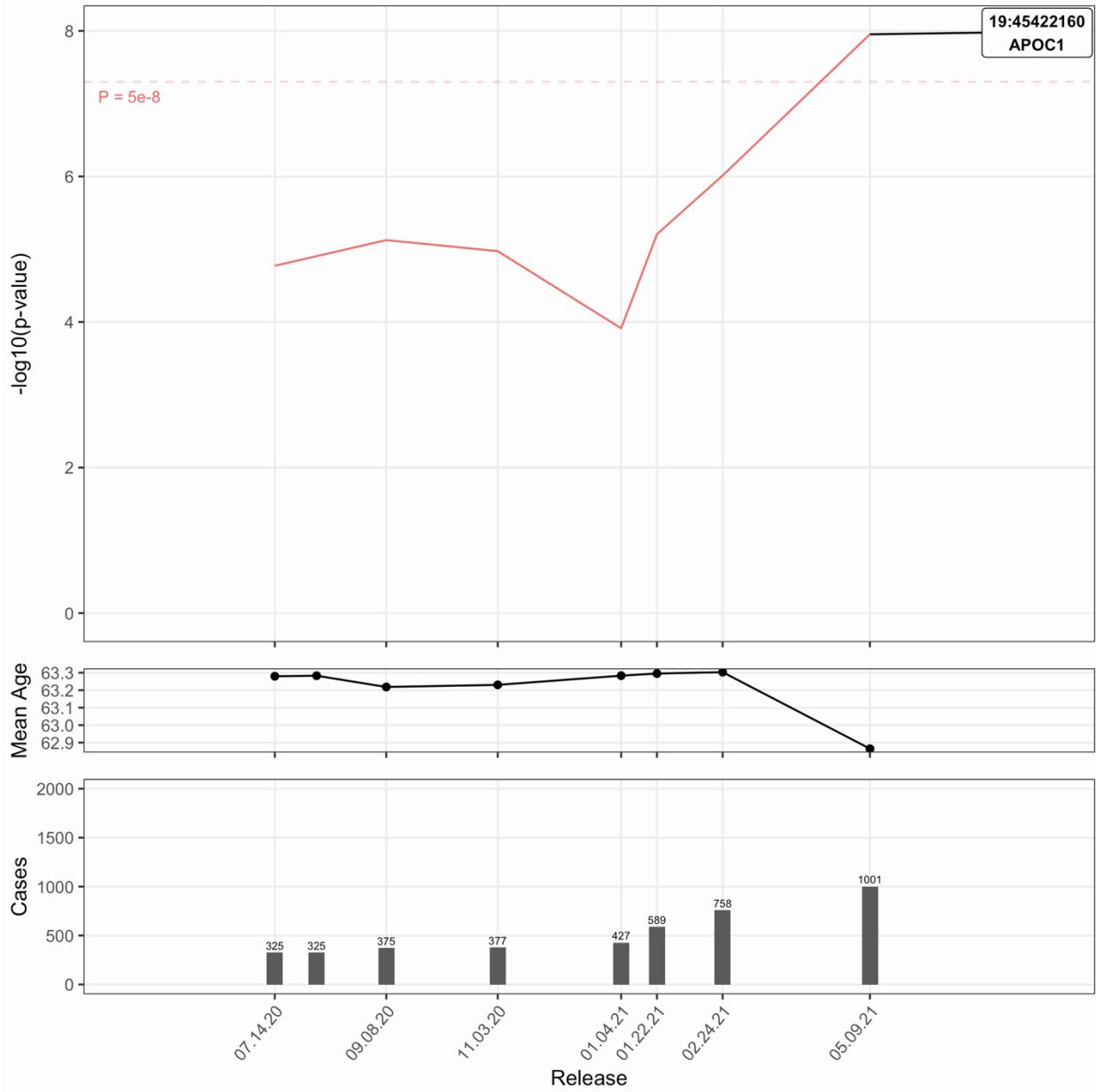
Figure S47: Covid-19 Death in EUR:Positive
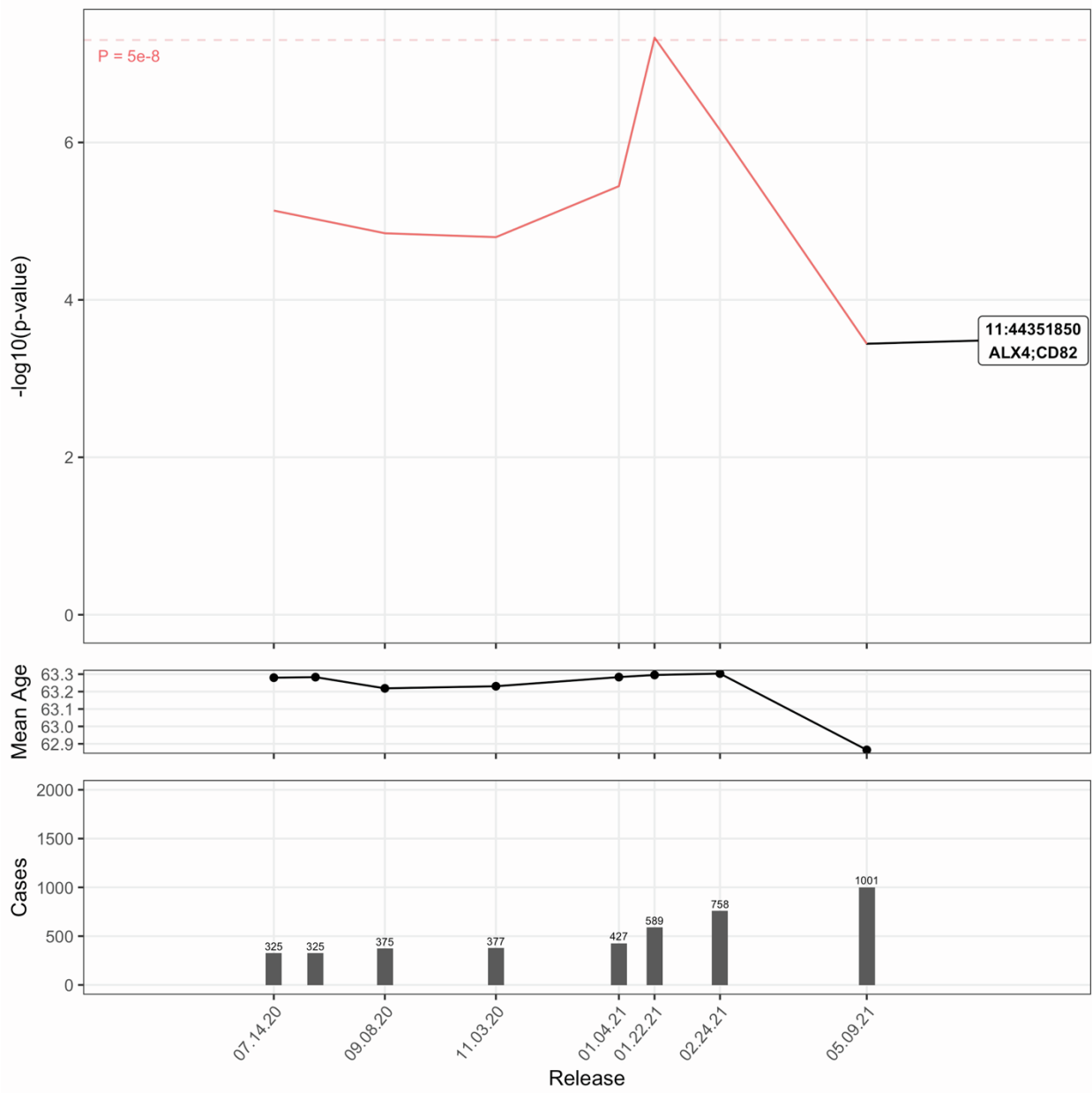
Figure S48: Comparison of genome-wide significant signals in analyses using Population and Tested controls
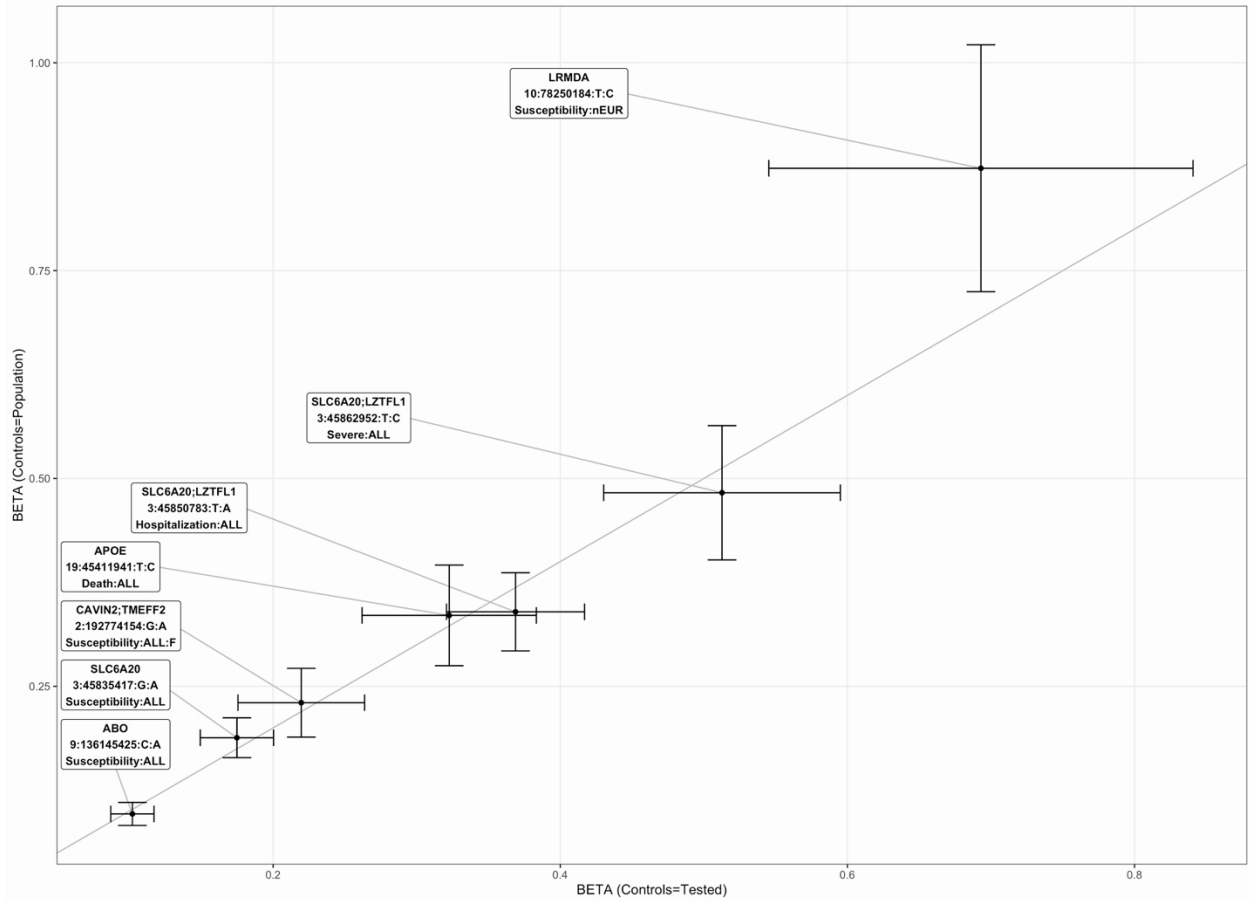
This figure presents the effect of each genome-wide significant signals and associated standard errors, when using the Population control set (on the Y-axis), or the Tested control set (on the X-axis).

Figure S49: Regional association plots of Covid-19 susceptibility and severity in Europeans (Population as controls), at the chr3p21.31 locus
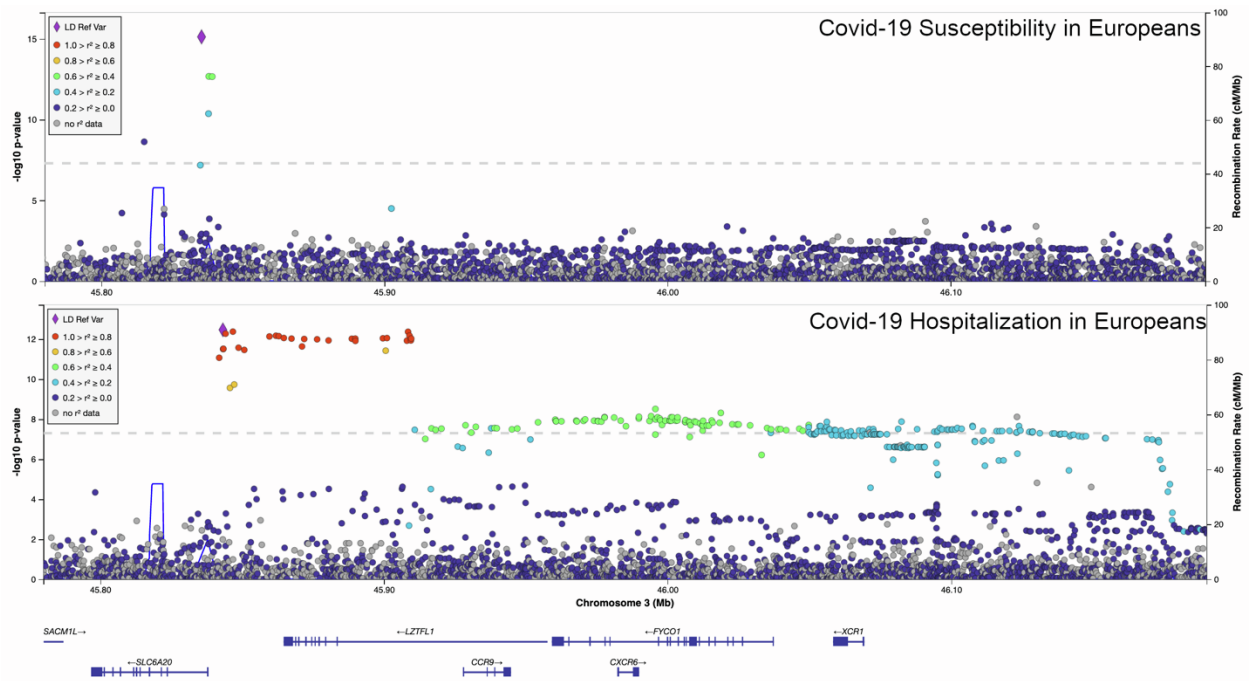
The top panel represent the Covid-19 susceptibility GWAS results in Europeans, at the chr3p21.31 locus, while the bottom panel represent the Covid-19 severity GWAS in Europeans at the same locus. The y-axis represents the -log10(P-value). The linkage disequilibrium between the lead SNP of both analyses (represented as a purple diamond) and each variant follows a color scheme presented on the left side of each panel.

Figure S50: Haplotype analysis of ABO blood groups, including the variant associated with Covid-19 susceptibility (from the LDlink tool LDhap)

|	RS Number	Position (GRCh37)	Allele Frequencies	O1	A1	A2	B	O2	B
				Haplotypes and corresponding blood groups:					
Variant tagging for O2 group :	rs41302905	chr9:136131316	C=0.971, T=0.029	C	C	C	C	T	C
Variant tagging for B group :	rs8176743	chr9:136131415	C=0.915, T=0.085	C	C	C	T	C	T
Variant tagging for A2 group :	rs1053878	chr9:136131651	G=0.901, A=0.099	G	G	A	G	G	G
Variant tagging for O1 group :	rs8176719	chr9:136132908	-=0.605, C=0.395	-	C	C	C	C	C
Variant tagging for A1 group :	rs2519093	chr9:136141870	C=0.815, T=0.185	C	T	C	C	C	C
Variant associated with Covid susceptibility :	rs9411378	chr9:136145425	C=0.701, A=0.299	C	A	A	C	C	A
			Haplotype Count	603	183	94	68	29	17
			Haplotype Frequency	0.5994	0.1819	0.0934	0.0676	0.0288	0.0169

The 5 SNPs tagging for the 5 most common blood groups, as well as the variant associated with Covid-19 susceptibility were included in this analysis. This analysis relies on the 1000 genome dataset. The resulting haplotypes, and corresponding blood groups (tagged by their associated variants) observed in this population are indicated on the right. The bottom part indicates the frequency of each haplotype observed. All A1 and A2 haplotypes contain the Covid-19 variant. Out of the 85 B haplotypes present in this population, 17 (20%) also contain the Covid-19 variant.

Figure S51: Evolution of the signals from Figure 1 (Susceptibility signals in EUR:Pop, from UKB) in Covid-19hgi C2 analyses
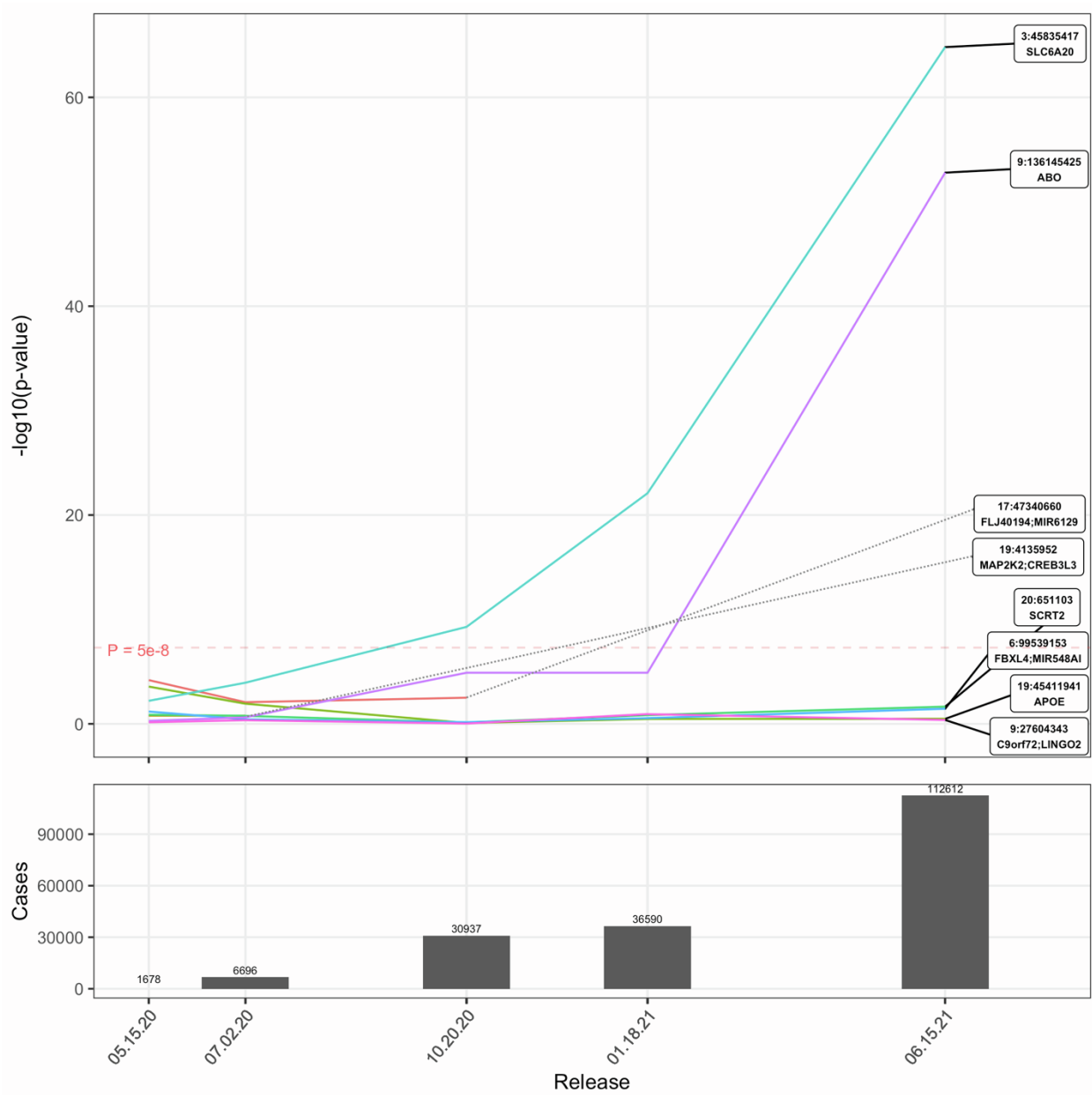
This figure represents the 8 signals from Figure 1 across the 5 C2 freezes from Covid-19hgi. 2 signals (19:4135952 and 17:47340660) were only available in the first 2 and first 3 freezes, respectively. The ABO signal was absent in freeze 5 (released on 01.18.21).