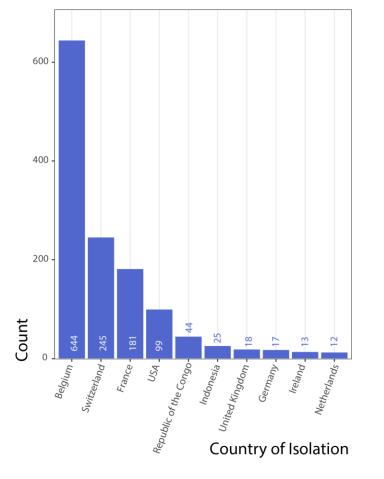
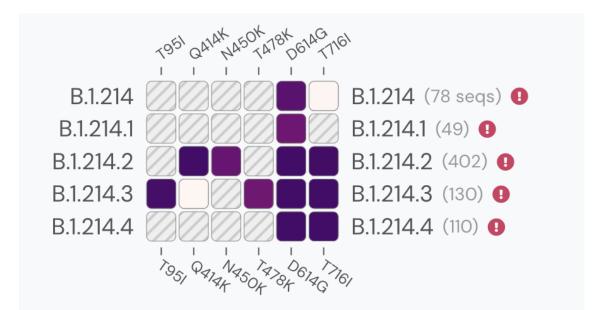
## **Supplemental Figures**

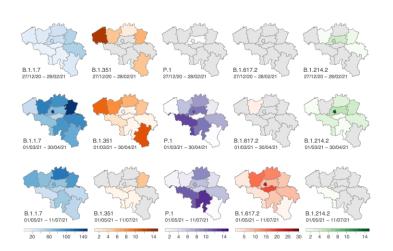


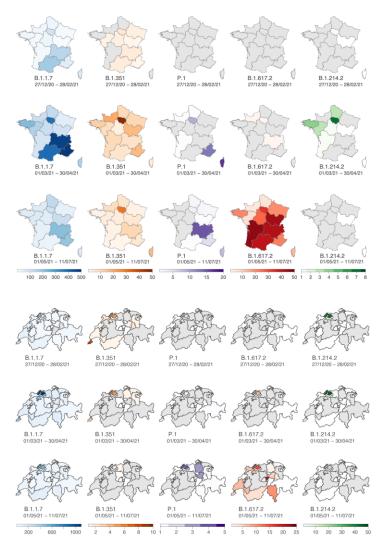
Country	# Sequences		
Belgium	644		
Switzerland	245		
France	181		
USA	99		
Republic of the Congo	44		
Indonesia	25		
United Kingdom	18		
Germany	17		
Ireland	13		
Netherlands	12		
Portugal	11		
Liechtenstein	10		
Angola	6		
Rwanda	6		
India	3		
Democratic Republic of the Congo	2		
Gabon	2		
Australia	1		
Finland	1		
Togo	1		

**Supp. Figure 1. Sequenced cases of B.1.214.2 per country.** Number of sequences are shown by country. The ten countries with the most B.1.214.2 sequences are shown in the bar plot on the left. The table on the right shows the total number of countries and number of sequences of the variant submitted to GISAID. This does not include travel-history additions.

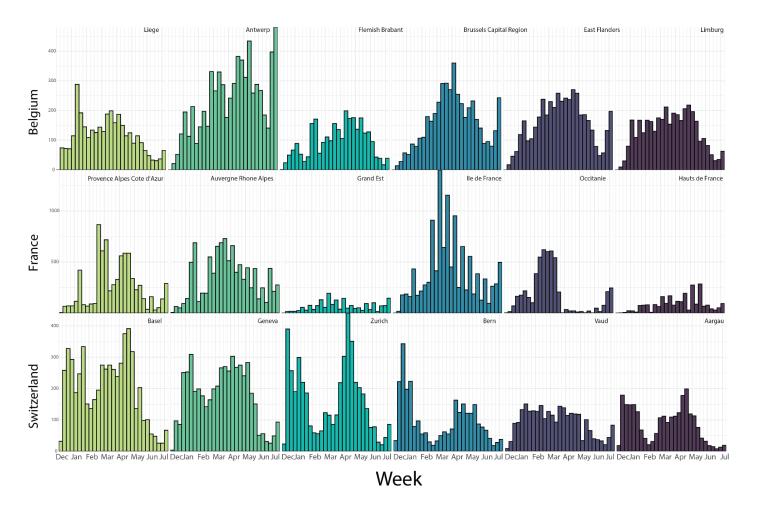


**Supp. Figure 2. Spike protein mutational prevalence across B.1.214 descending lineages.** This figure was taken from outbreak.info





Supp. Fig. 3: Incidence values of each VOC in Belgian Provinces (cases/ $10^6$  people), French regions (cases/ $10^5$  people) grouped into three successive time periods: 27/12/2021 - 28/02/2021, 01/03/2021 - 30/04/2021, 01/05/2021 - 11/07/2021. Incidence values are calculated by the number of sequences deposited on GISAID for that region divided by the population of that region/province/canton (2021). Brussels in Belgium, Ile-de-France in France and Basel canton (here merged with Basel-Lanschaft and Basel-Stadt for presentation) in Switzerland show the highest incidence of B.1.214.2. The variant quickly dies off in the last period as B.1.617.2 begins expanding. B.1.214.2 has relatively low incidence values outside of the Basel, Brussels, and Ile-de-France regions.



**Supp Figure 4. Number of Sequenced Cases of SARS-CoV-2 in Belgium, France, and Switzerland.** Each country is represented by the sequence totals per week by the six regions with the greatest number of sequences. Sequences submitted to GISAID were grouped by French region, Belgian Province, and Swiss Canton. In Switzerland, Basel is the combination of Basel-Stadt and Basel-Landschaft.

## **Supplemental Tables**

**Supp. Table 1. Travel-history associate with B.1.214.2 sequences.** These travel histories were collected from GISAID metadata and from contacting country sequencing laboratories. Travel days are the suspected number of days an individual was in the country of travel before the sample date.

Name	Location	Sampling Date	Travel History	Travel Days	Prior Mean	Prior Stdev
hCoV-19/Belgium/rega-						
1632/2021 EPI_ISL_890291 2021-		03/01/202				
01-03	Belgium	1	Republic of the Congo	NA	10	3

hCoV-19/Belgium/rega- 1638/2021 EPI_ISL_890294 2021- 01-03	Belgium	03/01/202	Republic of the Congo	NA	10	3
hCoV-19/Belgium/ULG- 11260/2021 EPI_ISL_833185 202 1-01-07	Belgium	07/01/202	Republic of the Congo	3	NA	NA
hCoV-19/Belgium/rega- 1778/2021 EPI_ISL_894200 2021- 01-08	Belgium	08/01/202 1	Spain	NA	10	3
hCoV-19/Belgium/rega- 1784/2021 EPI_ISL_894201 2021- 01-08	Belgium	08/01/202 1	Spain	NA	10	3
hCoV-19/Belgium/rega- 1865/2021 EPI_ISL_912424 2021- 01-12	Belgium	12/01/202 1	Democratic Republic of the Congo	NA	10	3
hCoV-19/Belgium/ULG- 12537/2021 EPI_ISL_1123370 20 21-01-19	Belgium	19/01/202 1	Democratic Republic of theCongo	0	NA	NA
hCoV-19/Belgium/Jessa_55-2105- 001118/2021 EPI_ISL_1128129 2 021-02-04	Belgium	04/02/202	France	12	NA	NA
hCoV-19/Belgium/rega- 5194/2021 EPI_ISL_1382699 202 1-03-02	Belgium	02/03/202	France	NA	10	3
hCoV-19/Belgium/WHT- UMONS- CV2100704647/2021 EPI_ISL_15 24721 2021-03-09	Belgium	09/03/202 1	France	38	10	3
hCoV-19/Angola/CERI-KRISP- K014923/2021 EPI_ISL_2493007  2021-04-17	Angola	17/04/202 1	Guinea-Bissau	NA	10	3
hCoV-19/Angola/CERI-KRISP- K014924/2021 EPI_ISL_2492994  2021-04-17	Angola	18/04/202 1	Chile	NA	10	3
hCoV-19/Belgium/rega- 8462/2021 EPI_ISL_2833326 202 1-04-27	Belgium	27/04/202 1	Germany	NA	10	3
hCoV-19/France/NOR- IPP11606/2021 EPI_ISL_2259092  2021-04-30	France	30/04/202 1	Nigeria	NA	10	3

**Supp. Table 2. First country introductions and country transitions up to the root.** First country introductions from the MCC tree are shown here with subtrees larger than or greater to 15 tips. If country introductions are smaller than 15 tips, the two introductions with the largest subtree per country are shown. Country jumps are not nodes, but rather they indicate country change.

	Country Jump	Country Jump	Country Jump	Final Country	Tips	Date	Node Date	95% Low	95% High
Root				RC	1360	10/06/2020	2020.443	2020.164	2020.681
Branch 1			RC	France	827	22/08/2020	2020.646	2020.490	2020.777
Branch 1	RC	RC	France	Switzerland	247	03/11/2020	2020.845	2020.791	2020.888
Branch 1	RC	RC	France	Belgium	59	13/11/2020	2020.868	2020.793	2020.933
Branch 1	RC	RC	France	Belgium	225	28/11/2020	2020.911	2020.853	2020.976
Branch 2			RC	Belgium	18	29/11/2020	2020.913	2020.994	2020.831
Branch 2			RC	Belgium	219	03/12/2020	2020.922	2020.987	2020.854
Branch 1	RC	France	Belgium	Indonesia	25	03/12/2020	2020.929	2020.838	2021.005
Branch 1		RC	France	UK	86	09/12/2020	2020.940	2020.885	2020.984
Branch 1		RC	France	RC	7	16/12/2020	2020.958	2020.880	2021.024
Branch 2			RC	UK	23	16/12/2020	2020.959	2020.915	2020.992
Branch 2			RC	France	20	26/12/2020	2020.986	2020.917	2021.045

Branch 1	RC	France	Switzerland	Portugal	6	28/12/2020	2020.992	2020.944	2021.030
Branch 1	RC	France	Belgium	Ireland	8	29/12/2020	2020.994	2020.943	2021.028
Branch 2			RC	Germany	8	03/01/2021	2021.005	2020.914	2021.076
Branch 2			RC	Belgium	118	05/01/2021	2021.010	2021.010	2021.008
Branch 1	RC	France	UK	USA	80	06/01/2021	2021.014	2020.961	2021.058
Branch 2			RC	Belgium	41	12/01/2021	2021.031	2021.035	2020.997
Branch 2		RC	Belgium	France	20	02/02/2021	2021.088	2021.042	2021.133
Branch 2		RC	Belgium	Netherlands	4	15/02/2021	2021.124	2021.094	2021.145
Branch 2		RC	Belgium	Germany	10	17/02/2021	2021.130	2021.099	2021.161
Branch 1		RC	France	Ireland	3	25/02/2021	2021.149	2021.108	2021.178
Branch 1		RC	France	Portugal	4	01/04/2021	2021.248	2021.228	2021.265
Branch 2		RC	Belgium	Netherlands	3	29/05/2021	2021.406	2021.371	2021.428

Supp. Table 3: Overlap between upregulated genes in B.1.214.2 infected nursing home residents and Gamma/Delta/Mu-infected nursing home residents with mild/moderate vs. fatal outcome

Gene Set	Num. of genes	Gene Symbol
B.1.214 up PCR+ up	12	CXCL10, SERPING1, CCL5, FYN, GZMB, TAP1, BST2, LAG3, CIITA, LILRB1, CCL2, IFIT2
B.1.214 up Fatal up	11	IFI35, TP53, NOS2, UBE2L3, CDKN1A, ILF3, IL6ST, ATG5, CCL7, CTNNB1, PSMC2
PCR+ up		PRF1, ZAP70, CTLA4_all, C1S, C1R, CARD9, EB13, KLRC3, PDCD1, CXCL11, CD2, IRF8, LAIR1

В.1.214 ир	FKBP5, LGALS3, IFI16, CLEC7A, TOLLIP, LAMP3, CD45R0, TNFSF10, TNFSF13B, CEACAM1, MUC1, ARG2, LEF1, GBP1, CUL9, STAT2, IDO1, IFNAR2, CD46, IRF5, MALT1, ITGAE, TMEM173, CTSS, TNF, MX1, TRAF4, PSMB8, C1QBP, RAF1, CX3CL1, IKZF2, MYD88, IFITM1, HLA-DRB1, CASP2, CXCL9, ITGB1, IRF3, CD40, CD59, CXCL13, PPBP, CFH, HLA-DMB, CLEC5A, MRC1, KIT, IRAK2, CFB, PSMB5, CXCL1, JAK2, CHUK, IL10, TBK1, CASP1, STAT3, ATG7, MAPK1, CCL20, MCL1, RELA, PSMB7, SOCS1, IL13RA1, CCND3, STAT1, IFIH1, CFD, SMAD3, IFNAR1, RUNX1, IKBKAP, TRAF5, TCF4, B2M, PSMD7, IRAK3, TAP2, NFKB1, CD58, CD164, AHR, DUSP4, CASP3, PSMB9, NOTCH2, FAS, C3, ITGA4
Fatal up	TRAF2, XCL1, KCNJ2, ITGAM, IFNG, CD79B, IL17F, C14orf166, TNFAIP6, C8G, IL26, BID, C4A/B, IFNA1/13, LILRA4, CR2, IFNB1, TNFSF15, TLR2, CCL16, TIGIT, TGFB1, RAG2, EOMES, CCL3, BCAP31, CD19, ABL1, B3GAT1, PDGFB, CCR1, ITGA2B, NCAM1, THY1, PTPN22, IL6R, CDH5, CCR5, CD99, TLR1, CTSG, IL28A, LILRA5, IL17B, CD80, IL22, RORC, ICAM5, CD1A, KIR3DL2, ARG1, STAT5A, CCL19, C6, PTGER4, KIR3DL3, SRC, FCAR, NT5E, C9, PLA2G2A, CD79A, CSF2, CCRL2, AIRE, CCL13, KLRC1