

Supplementary Table 1. Sequencing results.

Sample ID	Virus_name	Sample Type [#]	Raw valid reads	On-target reads (%)	Genome coverage	Depth	Mean Depth*
2	Mexico/CDMX-INNER_01	NPS	13,949,246	12,406 (0.09)	99.17	30	30
5	Mexico/CDMX-INNER_02	NPS	26,958,293	28,208 (0.10)	98.56	69	70
6	Mexico/CDMX-INNER_03	NPS	11,143,321	3,970 (0.04)	84.25	9	11
7	Mexico/CDMX-INNER_04	NPS	10,372,811	21,080 (0.20)	99.82	51	51
8	Mexico/CDMX-INNER_05	NPS	2,274,643	11,648 (0.51)	99.73	28	28
13	Mexico/Chihuahua-IMSS_01	NPS	12,785,238	7,331 (0.06)	90.98	18	20
16	Mexico/Chiapas-InDRE_02	OPS	4,322,780	1,739 (0.04)	83.06	4	8
17	Mexico/EdoMex-InDRE_03	NAS	8,173,886	85,170 (1.04)	99.90	200	200
19	Mexico/Queretaro-InDRE_04	OPS	9,394,551	60,545 (0.64)	99.91	145	145
22	Mexico/Puebla-InDRE_05	OPS	5,030,534	39,210 (0.78)	99.90	93	93
24	Mexico/CDMX-InDRE_06	OPS	3,890,600	109,000 (2.81)	99.92	256	256
27	Mexico/CDMX-INCMNSZ_01	NPS	14,770,367	79,364 (0.54)	99.88	164	164
28	Mexico/CDMX-INCMNSZ_02	NPS	2,898,415	21,985 (0.76)	99.90	53	53
30	Mexico/CDMX-INCMNSZ_03	NPS	3,956,195	23,550 (0.60)	99.91	57	57
31	Mexico/CDMX-INCMNSZ_04	NPS	4,581,562	97,388 (2.13)	99.92	228	228
32	Mexico/CDMX-INCMNSZ_05	NPS	2,648,330	7,813 (0.30)	99.34	19	19
33	Mexico/CDMX-InDRE_01	NPS	2,662,304	1,000,109 (37.57)	100.00	3983	3983

[#] Abbreviation: NPS=nasopharyngeal swab, OP= oropharyngeal swab, NAS=nasopharyngeal aspirate

* In relationship to the ratio of unambiguous bases to the reference sequence length (using at least 5 unique reads and 90% agreement during base calling)

Supplementary Table 2. Clustering patterns for the Mexican samples within the reduced and large-scale WG and individual ORF ML trees.

reduced -WG ¹	large-scale WG ¹	large-scale Orf1a ¹	large-scale Orf1b ¹	large-scale S ¹
IE1-bs 78 22_Mexico/Puebla-IndRE_05/2020 EPI_ISL_424672 Mexico_Puebla 31 M EH_Spain_France 3_11_2020 Portugal/PT0024/2020 EPI_ISL_418009 PRT_Portugal Age_29 Sex_F D0_NA EH_NA 3_15_2020 Basal-bs 96: Spain/Madrid_H11_40/2020 EPI_ISL_417967 ESP_Madrid Age_44 Sex_F D0_NA EH_NA 3_12_2020	IE1-bs 6 YES	IE1-bs 0 NO	IE1-bs 0 YES	IE1-bs 0 NO-POLYTOMY
IE2-bs 8 32_Mexico/CDMX-INCMNSZ_05/2020 EPI_ISL_426365 Mexico_CDMX 70 F EH_Vail_USA 3_12_2020 Australia/VIC254/2020 EPI_ISL_419949 AUS_Victoria Age_67 Sex_M D0_NA EH_NA 2020_03_21 Basal-bs 0: Australia/VIC164/2020 EPI_ISL_419861 AUS_Victoria Age_37 Sex_NA D0_NA EH_NA 2020_03_18	IE2-bs 27 YES	IE2-bs 0 NO	IE2-bs 0 NO	IE2-bs 0 NO
IE3-bs 0 5_Mexico/CDMX-INER_02/2020 EPI_ISL_424348 Mexico_CDMX 55 F EH_Spain_France 3_13_2020 Spain/Madrid_H12_1905/2020 EPI_ISL_421175 ESP_Madrid Age_25 Sex_F D0_NA EH_NA 2020_03_29 Basal-bs: None	IE3-bs 0 YES	IE3-bs 0 NO	IE3-bs 0 YES-POLYTOMY	IE3-bs 0 NO
IE4-bs 56 2_Mexico/CDMX-INER_01/2020 EPI_ISL_424345 Mexico_CDMX 42 M EH_Spain 3_12_2020 Hungary/2/2020 EPI_ISL_418183 HUN_Baranya Age_26 Sex_F D0_H EH_NA 2020_03_17 Basal-bs 0: None	IE4-bs 61 NO	IE4-bs 0 NO	IE4-bs 0 NO-POLYTOMY	IE4-bs 0 NO
IE5-bs 68 Wales/PHWC_25551/2020 EPI_ISL_421004 GBR_Wales Age_73 Sex_M D0_NA EH_NA 2020_03_23 16_Mexico/Chiapas-IndRE_02/2020 EPI_ISL_424666 Mexico_Chiapas 18 F EH_Italy 2_29_2020 Basal-bs 0: None	IE5-bs 19 YES	IE5-bs 0 NO	IE5-bs 0 NO	IE5-bs 0 NO-POLYTOMY
IE6-bs 0 33_Mexico/CDMX-INRE_01/2020 EPI_ISL_412972 Mexico_CDMX 35 M EH_Italy 2_27_2020 Basal-bs 1: England/20122119502/2020 EPI_ISL_418681 GBR_England Age_31 Sex_F D0_NA EH_NA 2020_03_17	IE6-bs 1 NO	IE6-bs 0 NO-POLYTOMY	IE6-bs 0 NO-POLYTOMY	IE6-bs 0 NO-POLYTOMY
IE7-bs 84 6_Mexico/CDMX-INER_03/2020 EPI_ISL_424625 Mexico_CDMX 29 M EH_Spain 3_13_2020 England/20108034006/2020 EPI_ISL_417258 GBR_England Age_74 Sex_F D0_NA EH_NA 2020_03_06	IE7-bs 67 YES	IE7-bs 0 YES	IE7-bs 27 YES	IE7-bs 0 NO
IE8-bs 42 Italy/TE4959/2020 EPI_ISL_418259 ITA_Abruzzo Age_76 Sex_M D0_NA EH_NA 2020_03_14 13_Mexico/Chihuahua-IMSS_01/2020 EPI_ISL_424731 Mexico_Chihuahua 21 M EH_UK_France_USA 3_13_2020 Basal-bs 0: None	IE8-bs 18 YES	IE8-bs 0 NO	IE8-bs 0 NO-POLYTOMY	IE8-bs 0 NO-POLYTOMY
IE9-bs 91 7_Mexico/CDMX-INER_04/2020 EPI_ISL_424626 Mexico_CDMX 25 F EH_Egypt_Barcelona_Spain 3_15_2020 England/SHEF_C0707/2020 EPI_ISL_420270 GBR_England Age_73 Sex_F D0_NA EH_NA 2020_03_22 Basal-bs: None	IE9-bs 79 YES	IE9-bs 0 YES	IE9-bs 0 NO-POLYTOMY	IE9-bs 0 NO
IE10-bs 99 Australia/VIC110/2020 EPI_ISL_419716 AUS_Victoria Age_62 Sex_F D0_NA EH_NA 2020_03_18 24_Mexico/CDMX-INRE_06/2020 EPI_ISL_424673 Mexico_CDMX 63 F EH_Denver_USA 3_12_2020	IE10-bs 0 NO	IE10-bs 2 YES	IE10-bs 0 YES-POLYTOMY	IE10-bs 0 YES-POLYTOMY
LT11-bs 100 CLUSTER 31_Mexico/CDMX-INCMNSZ_04/2020 EPI_ISL_426364 Mexico_CDMX 70 M EH_Vail_USA 3_12_2020 8_Mexico/CDMX-INER_05/2020 EPI_ISL_424627 Mexico_CDMX 38 M EH_None 3_15_2020 27_Mexico/CDMX-INCMNSZ_01/2020 EPI_ISL_426361 Mexico_CDMX 32 M EH_None 3_12_2020 30_Mexico/CDMX-INCMNSZ_03/2020 EPI_ISL_426363 Mexico_CDMX 38 M EH_None 3_12_2020 Basal-bs: None	IE11-bs 98 CLUSTER YES	C11.1-bs 0 BROKEN CLUSTER	C11.1-bs 0 BROKEN CLUSTER	IE11-bs 89 CLUSTER YES
IE12-bs 2 28_Mexico/CDMX-INCMNSZ_02/2020 EPI_ISL_426362 Mexico_CDMX 71 M EH_Vail_USA_Germany 3_10_2020 Basal-bs 0: Spain/CastillaLeon201372/2020 EPI_ISL_418249 ESP_Castilla_y_Leon Age_25 Sex_F D0_NA EH_NA 2020_03_03	IE12-bs 0 YES	IE12-bs 0 YES	IE12-bs 0 YES-POLYTOMY	IE12-bs 0 NO
IE13-bs 87 Chile/Talca_2/2020 EPI_ISL_414578 CHL_Talca Age_33 Sex_F D0_NA EH_NA 2020_03_04 Chile/Talca_1/2020 EPI_ISL_414577 CHL_Talca Age_33 Sex_M D0_R EH_Asia_Europe 2020_03_02 17_Mexico/EdoMex-IndRE_03/2020 EPI_ISL_424667 Mexico_Edomex 71 M EH_Italy 3_4_2020 Basal-bs 2: 19_Mexico/Queretaro-IndRE_04/2020 EPI_ISL_424670 Mexico_Queretaro 43 M EH_Spain_Holand_USA 13_10_2020	IE13-bs 0 YES	IE13-bs 0 YES	IE13-bs 33 YES	IE13-bs 0 NO
	NO-POLYTOMY-BROKEN CLUSTER WITH 19	NO-POLYTOMY-BROKEN CLUSTER WITH 19	NO-POLYTOMY-BROKEN CLUSTER WITH 19	NO

¹Consistency for clustering patterns observed within >2 trees and/or bootstrap support values >50 are indicated in red. YES/NO indicates conserved clustering patterns.

Supplementary Table 5. Amino acid changes within the Mexican samples compared to the reference strain Wuhan-Hu-1.

	Genomic region in WG concatenated ORF a1n ¹ site/aa change compared to MN908947																														
	Orf1a (1-4405)							Orf1b (4406-7000)										Orf3 (8505-8779)				Orf7a (8780-8900)		Orf8 (8901-9021)	N (9022-9440)						
	224	889	892	1649	2193	2244	3071	3606	4619	5190	5207	5696	5732	5769	6068	6103	7058	7582	7623	7739	8208	8268	8571	8700	8771	8817	8885	8984	9224	9225	
MN908947	T	L	P	A	S	I	F	L	P	E	N	S	P	Y	P	A	H	T	D	S	D	D	K	G	P	G	A	L	R	G	
7_Mexico/CDMX-INER_04	.	.	L	.	T	.	.	.	L	.	.	L	G
22_Mexico/Puebla-IN-DRE_05	L	.	.	L	G	V	
2_Mexico/CDMX-INER_01	X	.	.	.	L	G	
32_Mexico/CDMX-INCMNSZ_05	L	G	
5_Mexico/CDMX-INER_02	L	G	
6_Mexico/CDMX-INER_03	.	X	X	L	X	X	.	.	L	.	D	.	.	.	X	G	.	.	X	.	E	A	X	X	.	X	
13_Mexico/Chiuhua-IMSS_01	.	F	.	.	X	F	X	.	L	A	.	.	.	G	C	.	.	E	.	.	.	X	.	.	K	
33_Mexico/CDMX-IN-DRE_01	L	G	K	
16_Mexico/Chiapas-IN-DRE_02	X	X	.	.	X	K	X	.	.	X	X	.	.	.	X	.	X	.	X	X	.	K	
27_Mexico/CDMX-INCMNSZ_01	L	C	.	.	Y	S	
30_Mexico/CDMX-INCMNSZ_03	L	C	.	.	Y	S	
31_Mexico/CDMX-INCMNSZ_04	L	C	.	.	Y	S	
8_Mexico/CDMX-INER_05	L	C	.	.	Y	S	
24_Mexico/CDMX-IN-DRE_06	I	F	L	C	S	
28_Mexico/CDMX-INCMNSZ_02	Y	S	
19_Mexico/Queretaro-IN-DRE_04	S	
17_Mexico/EdoMex-IN-DRE_03	S	
Frequency ³	T99	L99	P99	A99	S99	I99	F98 Y2	L83 F15	L58 P42	E99	N99	S99	P87 L12	Y86 C13	P99	A99	H99	T99	Y58 D41	S99	D99	D99	K99	G98 V2	P99	G99	A99	L82 S18	R83 K16	G83 R16	
Non-conservative amino-acid change ²	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
Changes observed ²	#	■	■	■	NS	§	WS NS	WS	WS	WS	WS	WS	WS	WS	WS	WS	WS	WS	WS	WS	NS	§	§	§	‡	WS	WS	WS	WS		
Lineage defining mutations ²								A2a (P314L)											A2/G (D614G)									B/S (L84S)			
Evidence for positive selection ⁴																															

¹ General lineage defining mutations are shown in blue and orange, as defined in <https://nextstrain.org/ncov/global> and in GISAID preliminary analysis summary update 2020-04-08 1500UTC. No changes observed in M CDS (8283-8504).

² Non-conservative amino-acid changes shown in red

³ Cluster defining homoplasic mutation of the Mexican sequences are shown in black.

⁴ Widespread mutations are indicated under WS. Mutations also in Nexstrain are marked as NS. Unique changes to the Mexican sequences representing singletons are shown in gray.

■ Shared with USA/WA_UW153/2020|EPI_ISL_416691|2020_03_13

■ Shared with England/SHEF_C0707/2020|EPI_ISL_420270|2020_03_22

§ Shared with 45 sequences, mostly from Spain.

† Shared with 5 sequences from Australia, Portugal, Spain and USA.

‡ Shared with Portugal/PT0024/2020|EPI_ISL_418009|2020_03_15

* USA/WA_UW304/2020|EPI_ISL_418872|2020_03_23

³ Frequency of a given aa in percentage observed in the a1n. Only changes present in > 1% of the sequences in the a1n are shown.

⁴ Sites with a dN/dS >1 are shown in green, as compared to the list of sites determined under diverse dN/dS models described in <http://covid19.datamonkey.org/2020/04/01/covid19-analysis/>