

1 **Mutational signatures in countries affected by SARS-CoV-2: Implications in host-**
2 **pathogen interactome**

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9 **Keywords:** Signature Amino Acid Mutations, Mutational Hotspots, Antigenic drift, COVID-
10 19, SARS-CoV-2

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15 Running Title: Signature mutations in SARS-CoV-2.

16

17 **Abstract**

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19 We are in the midst of the third severe coronavirus outbreak caused by SARS-CoV-2 with
20 unprecedented health and socio-economic consequences due to the COVID-19. Globally, the
21 major thrust of scientific efforts has shifted to the design of potent vaccine and anti-viral
22 candidates. Earlier genome analyses have shown global dominance of some mutations
23 purportedly indicative of similar infectivity and transmissibility of SARS-CoV-2 worldwide.
24 Using high-quality large dataset of 25k whole-genome sequences, we show emergence of new
25 cluster of mutations as result of geographic evolution of SARS-CoV-2 in local population
26 ($\geq 10\%$) of different nations. Using statistical analysis, we observe that these mutations have
27 either significantly co-occurred in globally dominant strains or have shown mutual exclusivity
28 in other cases. These mutations potentially modulate structural stability of proteins, some of
29 which forms part of SARS-CoV-2-human interactome. The high confidence druggable host
30 proteins are also up-regulated during SARS-CoV-2 infection. Mutations occurring in potential
31 hot-spot regions within likely T-cell and B-cell epitopes or in proteins as part of host-viral
32 interactome, could hamper vaccine or drug efficacy in local population. Overall, our study
33 provides comprehensive view of emerging geo-clonal mutations which would aid researchers
34 to understand and develop effective countermeasures in the current crisis.

35

36 **Significance**

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38 Our comparative analysis of globally dominant mutations and region-specific mutations in 25k
39 SARS-CoV-2 genomes elucidates its geo-clonal evolution. We observe locally dominant
40 mutations (co-occurring or mutually exclusive) in nations with contrasting COVID-19
41 mortalities per million of population) besides globally dominant ones namely, P314L (ORF1b)
42 and D164G (S) type. We also see exclusive dominant mutations such as in Brazil (I33T in
43 ORF6 and I292T in N protein), England (G251V in ORF3a), India (T2016K and L3606F in
44 ORF1a) and in Spain (L84S in ORF8). The emergence of these local mutations in ORFs within
45 SARS-CoV-2 genome could have interventional implications and also points towards their
46 potential in modulating infectivity of SARS-CoV-2 in regional population.

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50 **Introduction**

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52 The rapid spread of SARS-CoV-2 has created an unprecedented global crisis. The evolving
53 SARS-CoV-2 viral variants have shown dominance (present in >50% genomes) of some
54 mutations indicating their concurrent emergence worldwide. However, co-dominance of
55 geographically distinct mutations may hamper global vaccine development and
56 pharmacological interventions. The genome organization of the 29kb SARS-CoV-2 (1)
57 involves 12 Open Reading Frames (ORF) encoding for ORF1a and 1b, surface glycoprotein -
58 Spike (S), ORF3a, envelope (E), membrane (M), ORF6, ORF7a and 7b, ORF8, nucleocapsid
59 (N) proteins and ORF10 (2,3). Our earlier phylogenetic analysis of >250 SARS-CoV-2 isolates
60 showed clustering of clinical samples in multiple clades derived from the molecular divergence
61 in ORF1ab/1b, S and ORF8 proteins (4). Subsequent analysis of isolates sequenced in India
62 showed higher mutational frequency in ORF1a from Indian samples (n=25) compared to global
63 isolates (n=3932) (5). This prompted us to look for similar dominant mutations, concurrent or
64 unique, present both globally and unique to nations with higher COVID-19 incidence namely
65 Brazil, India, Italy, Spain, UK and USA and compare it to countries where incidence was low,
66 Australia, Germany, Republic of Congo and Saudi Arabia. Here, we provide a comprehensive
67 report on the evolution of local clusters of mutations explored in a large dataset of >25k
68 genomes (whole genome sequences) from multiple geographical locations around the globe
69 and their co-occurrence or exclusivity with common global mutations. We further ascertained
70 effects of these mutations on the structural stability in the corresponding proteins, some of
71 which interact with host proteins, which were shown to be upregulated in patients with severe
72 COVID-19 symptoms. Identification of such mutations may further aid researchers in
73 developing broad spectrum vaccines or understanding variability in drug efficacy.

74

75 **Methods**

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77 High quality, full length whole genome sequences of clinical isolates of SARS-CoV-2 were
78 downloaded from Global Initiative on Sharing All Influenza Data (Table 1) (GISAID;
79 <https://www.gisaid.org>) (23). Glimmer was used for gene prediction (ORFs), and ORF
80 sequences with Ns were masked out and were not considered for protein translation (24).
81 Throughout, site numbering and genome structure are given using Wuhan-Hu-1
82 (NC_045512.2) as reference genome (https://www.ncbi.nlm.nih.gov/nuccore/NC_045512).

83 MAFFT was used for ORF alignment and mutations were computed using BioInception's in-
84 house pipeline based on R (<https://cran.r-project.org/>) and Python. Alignment regions with
85 >25% gaps against the reference genome were ruled out for amino acid mutational changes.
86 The change or mutation ratio for an ORF alignment is computed by the presence of a mutation
87 divided by total number of sequences in the alignment. This ratio is changed into a percentage.
88 Analysis of co-occurring or exclusive mutations (number of times two mutation occur together
89 in a clinical genome) across various ORFs was defined in terms of log-odds ratio (with p-value
90 and standard error) where a positive ratio indicates co-occurring mutations and negative value
91 denotes an exclusive mutation in the significant part of population using statsmodel
92 (Supplementary Data Sheet 1) (25). Structural effects of mutations on protein conformation,
93 flexibility and stability were predicted using DynaMut (26). The structural models were
94 retrieved from i-tasser COVID-19 database (27).

95

96 **Results**

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98 **Mutations occurring globally in $\geq 25\%$ of the population**

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100 Here, we report recurrent occurrence of (i) global and (ii) local (region specific) non-
101 synonymous mutations present in >25K SARS-CoV-2 clinical isolates (Table 1). To achieve
102 better signal-to-noise ratio, we have used a double layered protocol to identify statistically
103 significant signature mutations. In general, recurrent or dominant mutations occurring in $\geq 10\%$
104 of the functional genome (ORFs), compared to Wuhan_HU-1 (NC_045512), were classified
105 into mutually exclusive or co-occurring (mutations which also have the propensity to exist
106 together with another mutation). These were defined using log-odds ratio (LOR) where a
107 positive or negative log-odds value represents co-occurring and mutually exclusive mutations,
108 respectively. Vibrational entropy changes were predicted for both wild type and mutant
109 proteins for evaluating the impact of mutations on conformation, flexibility and stability of
110 proteins. The SARS-CoV-2 proteome can be classified into ORF1a, ORF1b (or ORF1ab joint),
111 S, E, ORF7a, ORF7b, N, ORF8 and ORF 10. ORF1a and ORF1b code for polyproteins which
112 are further cleaved to non-structural proteins (nsp), necessary for infection and replication of
113 virus. Our analysis revealed high propensity mutations present in the ORF1a and 1b, S, ORF3a,
114 ORF6, ORF8 and N proteins of SARS-CoV-2 (Figure 1, Supplementary Table 1). Our findings
115 agree with earlier reports on global co-occurrence of P314L (70.97%) and D614G (71.57%)
116 mutations in ORF1b (corresponding to P323L in nsp12) and S proteins, respectively.

117 Subsequently, high occurrence of mutation Q57H (25.54%) in ORF3a protein, R203K
118 (24.34%) and G204R (24.29%) in N protein (Supplementary Table 1) was globally reported.
119 They were also found to be widely accumulated in North American and European populations
120 (6).

121

122 **A comparative study between region specific mutations and globally dominant mutations**

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124 By capturing the most prominent mutations present in samples (through application of a coarse
125 data filter for mutations present in >25% of samples), our hierarchical (ward based) clustering
126 analysis of regional isolates placed European nations (except Spain and Scotland) and Brazil
127 into one cluster and Australia, India, Saudi Arabia, Scotland, Spain, USA, and DRC into
128 another cluster (Figure 2). Brazil and India, however, do not cluster with the rest of populations
129 and seem to possess distinct signature mutations, indicating early signs of genetic drift. In
130 isolates obtained from populations with the incidence of over a hundred mortalities per million
131 e.g. Italy, England, Wales, we observed positive log-odds ratio amongst mutations P314L-
132 D614G (LOR: 10.75, p-value 0.0) and R203K-G204R (LOR: 14.39, p-value 4.089e-146).
133 Interestingly Germany and Italy (with contrasting mortalities per million of population) (7)
134 show similar mutation signatures in their genomes. However, in relatively high viral burden
135 populations such as in Spain, we observed mutually exclusive presence of L84S (ORF8)
136 mutation along with globally occurring mutations P314L (ORF1b) and D614G (S) (Figure 1).
137 Whereas in the USA, T265I (ORF1a) and Q57H (ORF3a) were highly concurrent with P314L-
138 D614G mutations. The globally dominant P314L, D614G and Q57H were predicted to be
139 stabilizing mutations for nsp12, S and ORF3a proteins, respectively (Table 2). Similarly, other
140 mutations were predicted to confer mild stabilization or destabilization effects on respective
141 proteins ($\Delta\Delta G$ -0.64 to 0.46 kcal.mol⁻¹) (Table 2).

142

143 Specific (present only in the particular region within the cut-off limit) mutations - L3606F
144 (corresponding to L37F in nsp6) (30.96%) and T2016K (corresponding to T1198K in nsp3)
145 (26.61%) both in ORF1a, A88V (corresponding to A97V in nsp6) (25.67%) in ORF1b and
146 P13L (31.24%) in Nucleoprotein (N protein) were present in Indian isolates and did not co-
147 occur with P314L, D614G type (Supplementary Table 1, Supplementary Data Sheet 1). The
148 outlier Indian samples could be attributed to these mutations which can account for an entirely
149 separate Indian clade. Though the L3606F mutation also occurs in \leq 25% of isolates from
150 Australia, DRC, England and Wales, the P13L, T2016K mutant strains seem to have newly co-

151 evolved with L3606F variants in later stages of transmission in India. Brazil, another outlier,
152 has two distinct mutations I33T (52.53%) in ORF6 and I292T (59.6%) in N protein which were
153 absent in other nations. These co-occurred with P314L and D614G unlike the Indian exclusive
154 mutations L3606F, T2016K and P13L which did not co-occur. The Brazilian exclusive
155 mutations I33T and I292T co-occurred with P314L, D614G, R203K and G204R. It is also
156 worth noting that within the N protein, the Indian and Brazilian isolates show different country
157 specific mutations - P13L and I292T mutations, respectively. Stability analysis on these
158 mutations predicted induction of significant and contrasting conformational changes in N
159 protein. The P13L mutation was predicted to induce high stabilization ($\Delta\Delta G$ 2.25 kcal.mol⁻¹)
160 owing to hydrophobic interactions of mutated Leu with Ala152 (Supplementary Figure 1). On
161 the contrary, the I292T (exclusive in Brazil) was predicted to destabilize N protein ($\Delta\Delta G$ -1.99
162 kcal.mol⁻¹). The destabilization was observed due to changes in weak H-bond interactions in
163 the vicinity of T292 (Supplementary Figure 2).

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165 **Mutations occurring in more than 10% of population**

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167 While prominent mutations (by applying a coarse data filter for mutations present in >25% of
168 samples) yielded specific mutations in isolates from India, Brazil, USA and Spain, further
169 reducing the cut-off to $\geq 10\%$ showed additional country specific signature mutations in
170 different ORFs (Figure 3). Geographically defined genomic evolution is expected. In United
171 Kingdom, country specific mutations were observed in England, Wales, Northern Ireland and
172 Scotland. Mutations in England (G251V in ORF3a), Wales (G392D, A876T in ORF1a; S193I
173 in N protein), Scotland (S194L in N protein) and Northern Ireland (P2144L and T3579I in
174 ORF1a) displayed mutual exclusivity (negative LOR) with P314L, D614G and R203K, G204R
175 mutations. Interestingly in England, the G251V mutation was highly concurrent with L3606F
176 mutation of nsp6. Contrarily in Wales, the G392D, A876T and S193I mutations (which have
177 high propensity to co-occur together, showed mutual exclusivity with the L3606F mutation
178 (Supplementary Data Sheet 1). The P2144L and T3579I mutations showed a high propensity
179 to co-occur in Northern Ireland population. Distribution of co-occurring and exclusive
180 mutations in United Kingdom clearly shows G392D, A876T, S193I for Wales and P2144L,
181 T3579I as specific for Northern Ireland, distinct from England.

182

183 Antigenic drift is believed to occur due to immune pressure resulting in selection of viruses
184 that can escape, hence exploring mutations will aid towards vaccine design and development

185 (8). Virus circulating in humans undergo antigenic drift, thus necessitating periodic updates to
186 the virus strains contained in the seasonal vaccine to maintain a good match with circulating
187 viruses (9) (10). In general, variations in the virus can lead to reduced efficacy and narrow
188 protection from most vaccinations. The mutating strains might weaken the memory B cells that
189 have the capacity to generate and improve antibody response to new infection. A correlation
190 of the occurrence of hotspot mutations within potential T cell and B cell epitopes revealed that
191 F3071Y and L3606F (ORF1a) are within the epitope regions predicted for both CD4+ and
192 CD8+ T cell activity (11). The R203K and G204R from N protein have a strong propensity for
193 B cell epitopes.

194

195 **Discussion**

196

197 The viral mutation rates (12) are important for understanding the tractability of using variable
198 regions as vaccine candidates and how virus populations will respond to the application of a
199 mutagen (13). Bioinformatics and computational biology can assist in the discovery of
200 conserved epitopes through sequence variability analysis (14). This is particularly relevant
201 when dealing with virus capable of evading the immune system due to their high mutation
202 rates. These approaches, combined with experimental evolution and deeper mechanistic
203 studies, will aid in the understanding of whether mutation rates are likely to change in the
204 future. While our observations on geographical distribution of mutations could indicate
205 significant public health outcomes, these also raises fundamental questions on the likely basis
206 for emergence of such mutations as a function of geography. A number of factors such as
207 differences in the microbiome population in a given region, drug pressure, and host genetics
208 could be attributed. In separate studies on various human infecting viruses, it has been shown
209 that commensal microbiome can prime the viral infections in hosts (15). The ongoing long and
210 short term evolutions in the microbiome may further add complexity to our understanding of
211 host shaped viral adaptations (16). Drug selection pressures can also work at regional and sub-
212 regional levels (17,18). Analysis of mutation rates are equally crucial in terms of protein-
213 protein interactions within coronavirus ORFeome and host-pathogen interaction interface. In
214 SARS-CoV, nsp2, nsp8 (both part of ORF1ab) and ORF9b were shown to interact with other
215 viral proteins (19). For instance, nsp8 (part of ORF1ab) showed prominent interactions with
216 replicase proteins including nsp2, nsp5, nsp6, nsp7, nsp9, nsp12, nsp13 and nsp14 (all part of
217 ORF1ab), indicating crucial role of intra-viral protein-protein interactions in replication
218 machinery. The mutations in ORFs could be equally crucial in terms of host-viral interactome.

219 Shen Bo *et. al.* (20) classified severity of COVID-19 on the basis of differential expression of
220 93 serum proteins and 204 metabolite signatures, highlighting immune and metabolic
221 dysregulation in COVID-19 patients.

222

223 Another study by Gordon *et. al.* (21) identified physical interactions of host (human) proteins
224 with SARS-CoV-2. Protein-protein interactome (PPI) analysis yielded 332 high confidence
225 druggable human proteins which are involved in protein trafficking, transcription-translation
226 and ubiquitination regulation. We observed three common proteins in these studies (20,21)
227 which are both high confidence druggable targets and dysregulated between healthy and severe
228 COVID-19 symptoms. Two of these proteins; CD antigen CD155 and gamma-Glu-X
229 carboxypeptidase were shown to interact with ORF8, while the other glycoprotein GP36b with
230 nsp7. These proteins are involved in immune regulation and other metabolic processes (22).
231 These studies present likely evidence that mutations in these ORFs interacting druggable host
232 proteins could perturb host-pathogen interactome, host immune responses or modulate
233 therapeutic efficacy of anti-viral agents. The conspicuous distribution of co-occurring or
234 exclusive mutations in the non-structural proteins; ORF1ab, ORF3a, ORF8 and N proteins of
235 SARS-CoV-2 could be indicative of one or more of the following: a) Perturbations within
236 SARS-CoV-2 proteome; b) Human-SARS-CoV-2 interactome or, c) Alteration of
237 pharmacological profile of either known, or newly designed anti-viral candidates.

238

239 The current work highlights specific mutations in the functional genome of SARS-CoV-2
240 occurring worldwide and evolution of SARS-CoV-2 across different regions. While earlier
241 reports have suggested the dominance of P314L and D614G subtype, we show additional
242 dominance of other exclusive mutations in various countries like India, England Spain, and
243 Brazil (Figure 1, 2). While the exact role of such mutations in conferring disease phenotype
244 still needs to be deciphered, the proposed structural-mutation correlations for some of these
245 mutations point toward their role in governing functional genome pathogenicity of SAR-CoV-
246 2. The mutually dependent or exclusive role of these crucial mutations in global isolates is
247 indicative of clonal geo-distribution, which may affect infectivity of SARS-CoV-2 in localized
248 population. The identification of potential signature mutations in the evolving SARS-CoV-2
249 genome will aid the development of vaccines, drugs and diagnostics.

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251

252 Author Contributions

253 SEH and SAR designed this research; SAR, JS and HS performed research; SEH, SAR, JS and
254 HS analysed data; and JS, SAR and HS wrote the paper. The authors declare no competing
255 interest.

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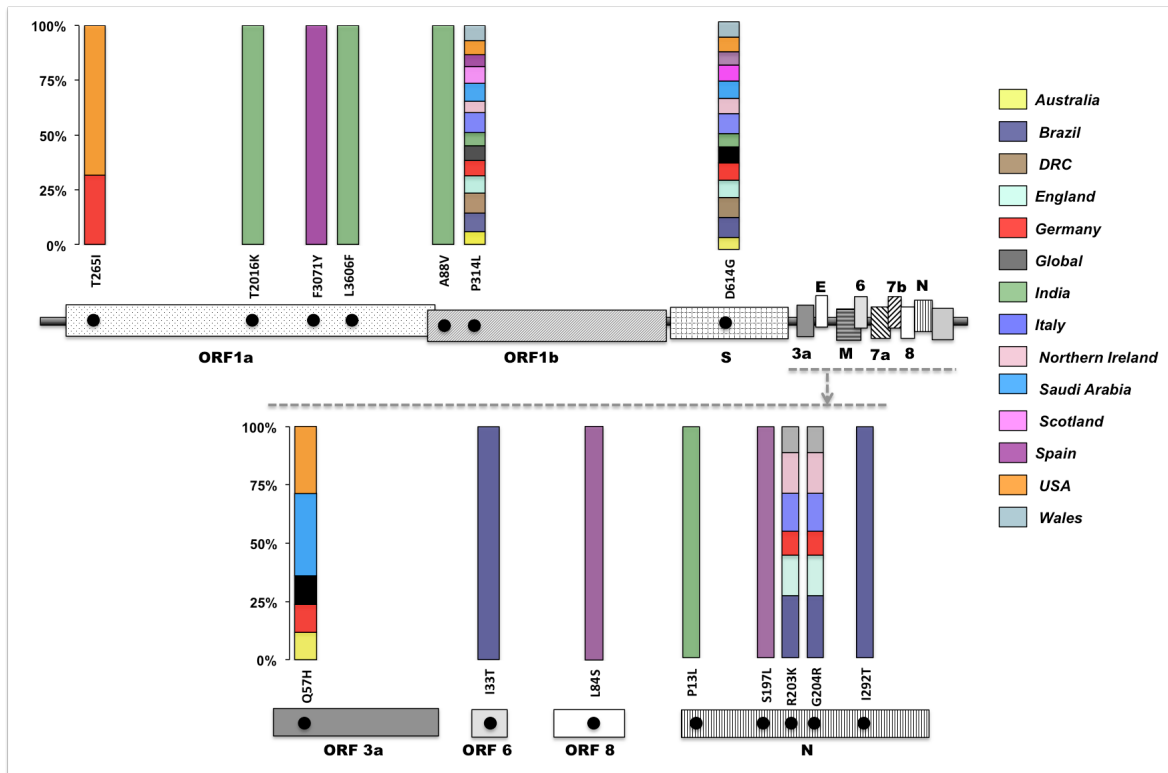
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355 **Figure 1**

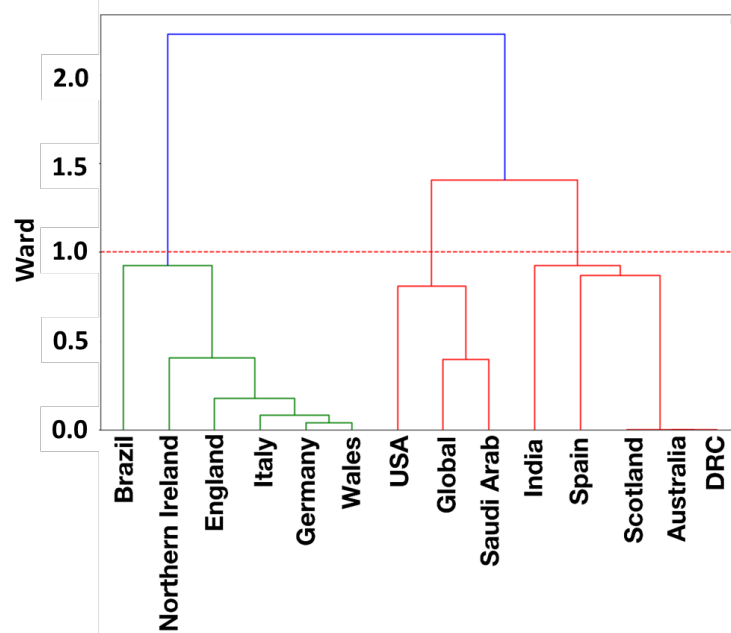
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359 **Figure 1. Mutation analysis of ORF's predicted for 25K SARS-CoV-2 genomes.** Position
 360 of mutations present in $\geq 25\%$ of genome samples in different ORF's along with stacked percent
 361 occupancy of these mutations. Single stacked occupancy highlights mutations specifically
 362 observed in samples from respective nations. e.g. T2016K, L3606F (ORF1a) and P13L in N
 363 protein are specifically observed in the Indian Isolates while F3071Y (ORF1a) and L84S
 364 (ORF8) are observed in Spain.



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367 **Figure 2.** Hierarchical (Ward) Clustering of regional isolates based on propensity (present in
368 $\geq 25\%$ of samples) of mutations to co-occur or be mutually exclusive. Two major groups can
369 be observed based on co-occurring and mutually exclusive mutations. India and Brazil
370 segregate from both groups owing to some country specific mutations.

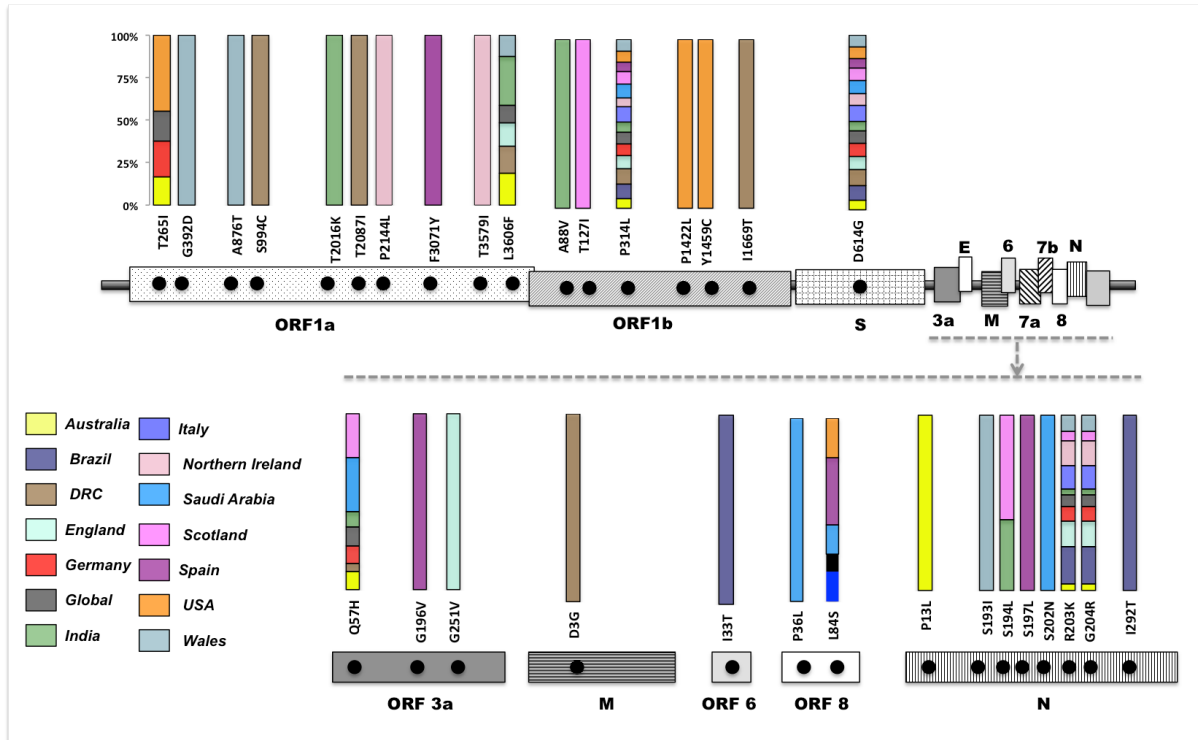
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Figure 3. Position of mutations present in $\geq 10\%$ (including the $>25\%$ mutations as depicted in Figure 1a) of genome samples in different ORFs along with stacked percent occupancy of these mutations. Single stacked occupancy highlights mutations specifically observed in samples from respective nations.

383

384 **Table 1:** Distribution of ORFs (amino acid sequences) in SARS-CoV-2 genomes used in this
385 study. The start and end positions for respective ORFs were taken on the basis of gene
386 coordinates of reference genome NC_045512.

ORF	Start	End	Number of Sequences
1a	266	13468	22650
1b	13468	21555	19827
S	21563	25384	21757
3a	25393	26220	25066
E	26245	26472	25329
M	26523	27191	25211
6	27202	27387	25356
7a	27394	27759	24792
7b	27756	27887	24977
8	27894	28259	25297
N	28274	29533	24937
10	29558	29674	25154

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388

389 **Table 2: Predictions on effect of mutations on protein stability and flexibility.** Positive and
 390 negative $\Delta\Delta G$ indicate an overall stabilization or destabilization effect of mutation on tertiary
 391 architecture, respectively. $\Delta\Delta G_{\text{vib}}$ (ENCoM) indicates vibrational entropy energy between wild
 392 type and mutant and dictates effects of mutation on protein flexibility. Positive and negative
 393 $\Delta\Delta G_{\text{vib}}$ indicate increase and decrease in molecule flexibility, respectively.

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ORF	Mutation	$\Delta\Delta G$ kcal.mol⁻¹	$\Delta\Delta G_{\text{vib}}$ (ENCoM) kcal.mol⁻¹.K⁻¹	Mutation Effect
1a	T265I	0.09	0.02	Stabilizing
	T2016K	-0.64	0.43	Destabilizing
	L3606F	0.35	-0.18	Stabilizing
1b	P314L	0.46	-0.32	Stabilizing
3a	Q57H	0.07	-0.40	Stabilizing
S	D614G	0.25	0.20	Stabilizing
6	I33T	-0.04	0.58	Destabilizing
8	L84S	-0.345	0.03	Destabilising
N	P13L	2.25	-1.16	Stabilizing
	S197L	0.382	0.05	Stabilizing
	R203K	-0.25	0.47	Destabilizing
	G204R	0.23	-1.19	Stabilizing
	I292T	-1.99	0.77	Destabilizing

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