Supplementary Table 1. All mutations in the SARS-CoV-2 genome from mildly and severely affected COVID-19 patients

Gene/genomic region	Nucleotide variation	Amino acid variation	Number of mutations	
			Mild (n=46)	Severe (n=56)
5´ UTR	22A>T	N/A	0	2
	25T>C	N/A	0	1
	25T>G	N/A	0	1
	40C>A	N/A	0	1
	41T>C	N/A	0	1
	204G>T	N/A	1	0
	219G>T	N/A	0	1
	222C>T	N/A	0	2
	241C>T	N/A	21	48
ORF1ab	313C>T	---	6	0
	490T>A	D75E (Leader prot)	0	1
	710C>T	L149F (Leader prot)	0	1
	884C>T	R207C (nsp2)	1	0
	1059C>T	T265I (nsp2)	4	2
	1348C>T	---	1	0
	1397G>A	V378I (nsp2)	2	0
	1440G>A	G392D (nsp2)	0	1
	1457C>T	R398C (nsp2)	0	1
	1541C>T	R426C (nsp2)	1	0
	1594C>T	---	0	1
	2113C>T	---	1	1
	2306C>T	L681F (nsp2)	0	1
	2388C>T	T708I (nsp2)	1	0
	2480A>G	I739V (nsp2)	1	0
	2550A>G	D762G (nsp2)	3	0
	2558C>T	P765S (nsp2)	2	0
	2836C>T	---	0	3
	2891G>A	A876T (nsp3)	0	1
	3037C>T	---	21	36
	3039A>G	Y925C (nsp3)	1	0
	3177C>T	P971L (nsp3)	0	1
	3270T>C	I1002T (nsp3)	0	1
	3371G>T	D1036Y (nsp3)	1	0
	3455T>C	Y1064H (nsp3)	0	1
	3602C>T	H1113Y (nsp3)	0	1
	3634C>T	---	1	2
	3874C>T	---	1	0
	4002C>T	T1246I (nsp3)	0	2
	4011T>C	L1249P (nsp3)	0	1

	4582C>T	---	0	1
	4679C>T	P1472S (nsp3)	3	0
	5230G>T	K1655N (nsp3)	1	0
	5700C>A	A1812D (nsp3)	7	0
	5784C>T	T1840I (nsp3)	1	0
	6040C>T	---	0	1
	6190C>T	---	1	0
	6310C>A	S2015R (nsp3)	2	0
	6312C>A	T2016K (nsp3)	4	0
	6507A>G	N2081S (nsp3)	1	0
	7164C>T	T2300I (nsp3)	1	0
	7765C>T	---	1	1
	7823C>T	H2520Y (nsp3)	1	0
	8653G>T	M2796I (nsp4)	1	0
	8782C>T	---	12	3
	8950C>T	---	0	1
	9166C>T	---	1	0
	9477T>A	F3071Y (nsp4)	1	0
	9628T>C	---	1	0
	9656A>G	M3131V (nsp4)	1	0
	9880T>C	---	3	0
	9993A>T	N3243I (nsp4)	0	1
	10097G>A	G3278S (3C-like proteinase)	0	2
	10771T>C	---	1	0
	11083G>T	L3606F (nsp6)	13	1
	11093G>A	A3610T (nsp6)	0	1
	11109C>T	A3615V (nsp6)	0	1
	11398T>C	---	1	0
	11457T>C	I3731T (nsp6)	0	2
	11518C>T	---	1	0
	11563C>T	---	1	0
	11822A>G	I3853V (nsp6)	0	1
	11842G>T	Q3859H (nsp6)	0	1
	12049C>T	---	0	1
	12312C>T	A4016V (nsp8)	1	0
	12439C>A	---	1	0
	12478G>A	M4071I (nsp8)	0	1
	12521G>A	G4086S (nsp8)	1	0
	12541A>G	---	1	0
	12781C>T	---	1	0
	13536C>T	---	0	2
	13542T>C	---	1	0
	13639G>A	D4459N (RdRp)	1	0
	13730C>T	A4489V (RdRp)	4	0

	13860C>T	---	0	1
	14195C>A	T4644N (RdRp)	0	1
	14230C>T	P4656S (RdRp)	1	0
	14407C>T	P4715S (RdRp)	0	1
	14408C>T	P4715L (RdRp)	21	46
	14636C>T	A4791V (RdRp)	0	1
	14805C>T	---	5	2
	15246A>G	---	0	1
	15324C>T	---	1	5
	15380G>T	S5039I (RdRp)	1	0
	15603C>T	---	1	0
	15857C>T	T5198I (RdRp)	3	0
	15957G>T	---	0	5
	16078G>A	V5272I (RdRp)	0	1
	16166A>G	N5301S (RdRp)	0	1
	17247T>C	---	2	2
	17440C>T	P5726S (helicase)	3	0
	17690C>T	S5809L (helicase)	1	1
	17694T>C	---	0	1
	17747C>T	P5828L (helicase)	2	2
	17808G>T	K5848N (helicase)	1	0
	17858A>G	Y5865C (helicase)	2	2
	18052A>G	T5930A (3-to-5 exonuclease)	1	0
	18060C>T	---	2	2
	18457C>T	P6065S (3-to-5 exonuclease)	0	2
	18736T>C	F6158L (3-to-5 exonuclease)	0	1
	18877C>T	---	1	11
	19101G>T	Q354H (3-to-5 exonuclease)	0	1
	19524C>T	---	2	0
	19816G>T	V6518L (endoRNAse)	1	0
	20081C>T	S6606F (endoRNAse)	3	0
	20134G>T	V6624L (endoRNAse)	1	0
	20268A>G	---	3	8
	20719C>T	---	0	1
	20773G>T	G6837C (2-O-ribose methyl..)	1	0
	21452G>T	G7063V (2-O-ribose methyl..)	1	0

S (Spike)	21627C>T	T22I	1	0
	21707C>T	H49Y	0	1
	21805C>T	---	0	1
	21976T>C	---	0	1
	22081G>T	Q173H	0	1
	22155A>G	D198G	0	2
	22444C>T	---	0	4
	22450C>T	---	0	1
	22468G>T	---	8	0
	22521T>G	V320G	0	1
	22991A>G	S477G	0	1
	23282G>T	D574Y	0	1
	23311G>T	E583D	0	1
	23403A>G	D614G	21	48
	23422C>T	---	0	1
	23426G>T	V622F	0	1
	23593G>T	Q677H	1	0
	23731C>T	---	0	2
	23815T>C	---	3	0
	23929C>T	---	4	0
	23952T>G	F797C	1	0
	24034C>T	---	0	1
	24040G>T	---	0	1
	24197G>T	A879S	0	5
	24501T>C	I980T	0	1
	24621C>T	A1020V	0	1
	24642C>T	T1027I	0	1
	24694A>T	---	0	1
	25019G>T	D1153Y	0	1
	25098T>A	I1179N	1	0
ORF3a	25483G>A	A31T	1	0
	25563G>T	Q57H	5	15
	25596A>G	---	1	0
	25721C>T	A110V	1	0
	25979G>T	G196V	1	0
	26144G>T	G251V	4	2
E (Envelop)	26265A>T	E7D	0	1
	26338G>T	A32X	1	0
	26351_26356del CGCTTC	A36G, L37_R38del	3	0
M (Membrane)	26530A>G	D3G	0	2
	26607C>T	L29F	0	1
	26642C>T	---	1	0
	26729T>C	---	0	1
	26735C>T	---	0	9

	26750C>T	---	0	2
	26779G>T	C86F	1	0
	27046C>T	T175M	1	2
	27093T>A	S191T	0	1
ORF7a	27415G>T	A8S	0	1
ORF7b	27770A>T	---	0	1
	27855C>T	---	0	1
	27861G>T	D36Y	0	1
ORF8	27964C>T	S24L	2	0
	28045C>T	A51V	0	1
	28077G>C	V62L	0	1
	28144T>C	L84S	12	3
	28194C>T	R101C	0	1
	28253C>T	---	1	0
N (Nucleocapsid)	28311C>T	P13L	4	0
	28329G>A	G19E	0	1
	28362G>T	G30V	1	0
	28395G>C	R41P	0	1
	28512C>T	P80L	1	0
	28657C>T	---	1	0
	28688T>C	---	2	0
	28690G>T	L139F	0	1
	28765A>G	---	0	1
	28795A>G	---	1	0
	28854C>T	S194L	0	5
	28863C>T	S197L	1	0
	28878G>A	S202N	8	0
	28881G>A, 28882G>A	R203K	9	14
	28883G>C	G204R	9	13
	28896C>G	A208G	0	1
	29236C>T	---	0	2
	29291G>A	D340N	0	1
	29315G>C	D348H	0	1
	29421C>T	P383L	1	0
	29451C>T	T393I	0	1
ORF10	29647A>G	---	0	1
3´ UTR	29700A>G	N/A	0	1
	29705G>T	N/A	3	0
	29711G>T	N/A	0	1
	29734G>C	N/A	0	3
	29737G>T	N/A	0	1
	29742G>A	N/A	8	0
	29742G>T	N/A	2	0
	29743C>T	N/A	0	1

	29747G>C	N/A	0	1
	29759G>T	N/A	0	1
	29821T>C	N/A	1	0
	29827A>T	N/A	16	0
	29829T>A	N/A	1	0
	29830G>T	N/A	20	0
	29848T>A	N/A	0	1
	29850A>T	N/A	0	1
	29857C>T	N/A	0	1
	29858T>C	N/A	0	1
	29862G>A	N/A	0	1
	29862G>C	N/A	0	1
	29863A>T	N/A	1	0
	29867T>A	N/A	1	0
	29868G>C	N/A	0	1
	29871A>G	N/A	0	1

All mutations in mildly affected and severely affected groups are included in this Table. UTR, un-translated region, ORF, open reading frame; N/A, not applicable; nsp, non-structural protein; RdRp, RNA-dependent RNA polymerase; ---, silent mutation; Mild, mildly affected group; Severe, severely affected group.