

e-Table 1. Variants of *CFTR* identified in 103 Chinese children (100 families) with CF presented to Beijing Children's Hospital

Case No.	Sex	Age at Dx, y	Sweat conductivity, mmol/L	Region	Nucleotide change (HGVS nomenclature)	Amino acid change	Type of mutation	Genotype	Familial targeted mutation study	
									Father	Mother
1 ^[4]	M	11.58	101	Ex 13	c.1699G>T	p.Asp567Tyr	Missense	Compound heterozygous	+/-	-/-
				Ex 24	c.3909C>G	p.Asn1303Lys	Missense		-/-	+/-
2 ^[4]	F	10.58	103	Ex 3	c.263T>G	p.Leu88X	Nonsense	Compound heterozygous	-/-	+/-
				In 13	c.1766+5G>T	-	Splicing		+/-	-/-
				3'UTR	c.*110C>G	-	Sequence variation		-/-	+/-
3 ^[4]	M	13.25	101	Ex 22	c.3700A>G	p.Ile1234Val	Missense	Compound heterozygous	+/-	-/-
				Ex 8	c.960dupA	p.Ser321IlefsX43	Frameshift		-/-	-/-
4 ^[4]	F	13.67	99	Ex 3	c.263T>G	p.Leu88X	Nonsense	Compound heterozygous	-/-	+/-
				Ex 18	c.2909G>A	p.Gly970Asp	Missense		+/-	-/-
5 ^[4]	M	7.17	106	Ex 4	c.326A>G	p.Tyr109Cys	Missense	Compound heterozygous	-/-	+/-
				Ex 8	c.1000C>T	p.Arg334Trp	Missense		+/-	-/-

				Ex 12	c.1666A>G	p.Ile556Val	Missense		+/+	-/-
6 ^[4]	F	10.67	127	Ex 6	c.595C>T	p.His199Tyr	Missense	Heterozygous	ND	ND
7 ^[4]	F	7.75	118	Ex 3	c.223C>T	p.Arg75X	Nonsense	Compound heterozygous	ND	ND
				Ex 4	c.326A>G	p.Tyr109Cys	Missense		ND	ND
8 ^[4]	F	7.33	118	Ex 8	c.1000C>T	p.Arg334Trp	Missense	Heterozygous	+/-	-/-
9 ^[4]	F	10.17	105	Ex 3	c.263T>G	p.Leu88X	Nonsense	Homozygous	+/-	+/-
10 ^[4]	F	11.08	96	Ex 12	c.1666A>G	p.Ile556Val	Missense	Heterozygous	ND	ND
11 ^[4]	M	8.25	115	Ex 4	c.293A>G	p.Gln98Arg	Missense	Compound heterozygous	-/-	+/-
				Ex 5	c.558C>G	p.Asn186Lys	Missense		+/-	-/-
12 ^[4]	F	4.17	101	Ex 4	c.326A>G	p.Tyr109Cys	Missense	Compound heterozygous	ND	ND
				Ex 14	c.2374C>T	p.Arg792X	Nonsense		ND	ND
13 ^[4]	M	3.67	99	Ex 12	c.1666A>G	p.Ile556Val	Missense	Homozygous	+/-	+/-
14 ^[4]	F	12.67	122	Ex 4	c.293A>G	p.Gln98Arg	Missense	Heterozygous	-/-	+/-
15 ^[4]	M	11.00	ND	Ex 6	c.648G>A	p.Trp216X	Nonsense	Homozygous	+/-	+/-
				In 14	c.2491-126T>C	-	Sequence variation		+/-	+/-
16 ^[4]	F	10.33	ND	Ex 20	c.3196C>T	p.Arg1066Cys	Missense	Homozygous	ND	ND

17 ^[4]	M	11.17	ND	Ex 4	c.413_415dupTA C	p.Leu138dup	In-frame insertion	Homozygous	ND	ND
18 ^[4]	F	3.42	ND	Ex 8	c.1075C>T	p.Gln359X	Nonsense	Compound heterozygous	ND	ND
				Ex 20	c.3307delA	p.Ile1103X	Nonsense		ND	ND
19 ^[4]	F	14.00	115	Ex 18	c.2909G>A	p.Gly970Asp	Missense	Homozygous	+/-	+/-
20 ^[6]	F	0.42	130	Ex 3	c.223C>T	p.Arg75X	Nonsense	Compound heterozygous	-/-	+/-
				Ex 18	c.2909G>A	p.Gly970Asp	Missense		+/-	-/-
21 ^[6]	F	2.16	134	Ex 11	c.1521_1523delC TT	p.Phe508del	In-frame deletion	Homozygous	+/-	+/-
22 ^[6]	F	8.25	122	Ex 8	c.1000C>T	p.Arg334Trp	Missense	Compound heterozygous	+/-	-/-
				Ex 13	c.1733T>C	p.Leu578Pro	Missense		-/-	+/-
23 ^[6]	M	0.75	134	Ex 3	c.264_268delAT ATT	p.Leu88PhefsX21	Frameshift	Compound heterozygous	-/-	+/-
				Ex 23	c.3860delG	p.Gly1287GlufsX 2	Frameshift		+/-	-/-
24 ^[6]	F	0.42	105	Ex 3	c.263T>G	p.Leu88X	Nonsense	Compound heterozygous	-/-	+/-
				Ex 18	c.2909G>A	p.Gly970Asp	Missense		+/-	-/-

25 ^[6]	M	0.67	93	In 8	c.1116+1G>A	–	Splicing	Compound heterozygous	+/-	-/-
				Ex 18	c.2909G>A	p.Gly970Asp	Missense		-/-	+/-
26 ^[6]	M	0.25	ND	Ex 18	c.2909G>A	p.Gly970Asp	Missense	Compound heterozygous	+/-	-/-
				Ex 23	c.3718-?_3873+? del	–	Large deletion		-/-	+/-
27 ^[6]	F	0.92	115	Ex 14	c.2236_2246delG AGGCGATACTi nsAAAAATC	p.Glu746LysfsX8	Frameshift	Compound heterozygous	-/-	+/-
				Ex 25	c.3635delT	p.Val1212AlafsX 16	Frameshift		+/-	-/-
28 ^[6]	M	6.67	125	In 9	c.1210-3C>G	–	Splicing	Compound heterozygous	+/-	-/-
				In 24	c.3964-7A>G	–	Splicing		-/-	+/-
29 ^[6]	M	0.75	125	Ex 19	c.3068T>G	p.Ile1023Arg	Missense	Compound heterozygous	+/-	-/-
				Ex 6	c.595C>T	p.His199Tyr	Missense		-/-	+/-
30-1	F	7.67	151	Ex 5	c.532G>A	p.Gly178Arg	Missense	Homozygous	+/-	+/-
30-2 ^[6]	F	0.50	ND	Ex 5	c.532G>A	p.Gly178Arg	Missense	Homozygous	+/-	+/-

31-1	M	9.33	102	In 5	c.579+1_579+2in sACAT	–	Splicing	Compound heterozygous	+/-	-/-
				In 13	c.1766+5G>T	–	Splicing		-/-	+/-
31-2 ^[6]	F	8.83	141	In 5	c.579+1_579+2in sACAT	–	Splicing	Compound heterozygous	+/-	-/-
				In 13	c.1766+5G>T	–	Splicing		-/-	+/-
32	F	1.08	125	Ex 11	c.1521_1523delC TT	p.Phe508del	In-frame deletion	Compound heterozygous	+/-	-/-
				Ex 11	c.1429_1437delC CTTCAGAG	p.Pro477_Glu479 del	In-frame deletion		-/-	+/-
33	M	7.33	125	Ex 20	c.3209G>C	p.Arg1070Pro	Missense	Compound	+/-	-/-
				Ex 14	c.2328dupA	p.Val777SerfsX2	Frameshift	heterozygous	-/-	+/-
34	F	9.00	104	Ex 4	c.293A>G	p.Gln98Arg	Missense	Compound	+/-	-/-
				Ex 19	c.3068T>G	p.Ile1023Arg	Missense	heterozygous	-/-	+/-
35	F	5.67	109	Ex 11	c.1572C>A	p.Cys524X	Nonsense	Compound	+/-	-/-
				Ex 1	c.3G>A	p.Met1Ile	Missense	heterozygous	-/-	+/-
36	F	10.67	127	Ex 6	c.595C>T	p.His199Tyr	Missense		+/-	-/-

				Ex 14	c.2058_2061delT T	p.Phe687X	Nonsense	Compound heterozygous	-/-	+/-
37	F	14.33	140	Ex 11	c.1409T>A	p.Val470Glu	Missense	Compound heterozygous	+/-	-/-
				In 9	c.1210-3C>G	-	Splicing		-/-	+/-
38	M	13.25	109	Ex 10	c.1347_1350delA GAA	p.Arg450AspfsX 18	Frameshift	Compound heterozygous	ND	ND
				Ex 18	c.2909G>A	p.Gly970Asp	Missense		Compound ND	ND
39	M	10.50	83	In 23	c.3874-4522A>G	-	Splicing	Compound	+/-	-/-
				Ex 18	c.2936A>C	p.Asp979Ala	Missense	Heterozygous	-/-	+/-
40	M	9.83	141	Ex 8	c.1000C>T	p.Arg334Trp	Missense	Compound heterozygous	-/-	+/-
				Ex 3	c.264_268delAT ATT	p.Leu88PhefsX21	Frameshift		+/-	-/-
41	F	5.58	67	Ex 6	c.650A>G	p.Glu217Gly	Missense	Compound heterozygous	-/-	+/-
				Ex 10	c.1231A>G	p.Lys411Glu	Missense		+/-	-/-
42	M	7.00	130	In 13	c.1766+5G>T	-	Splicing	Compound heterozygous	-/-	+/-
				Ex 22	c.3484C>T	p.Arg1162X	Nonsense		+/-	-/-

43	M	3.83	ND	Ex 6	c.595C>T	p.His199Tyr	Missense	Compound heterozygous	+/-	-/-
				Ex 14	c.2290C>T	p.Arg764X	Nonsense		-/-	+/-
44	M	14.42	64	In 22	c.3718-2477C>T	-	Sequence variation	Compound heterozygous	+/-	-/-
				Ex 17	c.2834C>T	p.Ser945Leu	Missense		-/-	+/-
				Ex 4	c.374T>C	p.Ile125Thr	Missense		-/-	+/-
45	M	8.50	163	Ex 11	c.1521_1523delC TT	p.Phe508del	In-frame deletion	Compound heterozygous	+/-	-/-
				Ex 4	c.293A>G	p.Gln98Arg	Missense		-/-	+/-
46	M	10.17	60	Ex 4	c.374T>C	p.Ile125Thr	Missense	Compound heterozygous	-/-	+/-
				Ex 14	c.2042A>T	p.Glu681Val	Missense		+/-	-/-
47	M	13.08	99	Ex 17	c.2834C>T	p.Ser945Leu	Missense	Homozygous	+/-	+/-
48	F	11.25	118	Ex 14	c.2036G>A	p.Trp679X	Nonsense	Compound heterozygous	+/-	-/-
				In 2	c.164+2T >C	-	Splicing		-/-	+/-
49	F	4.67	85	Ex 4	c.325T>G	p.Tyr109Asp	Missense	Compound heterozygous	-/-	+/-
				Ex 20	c.3196C>T	p.Arg1066Cys	Missense		+/-	-/-
50	M	9.08	96	Ex 4	c.350G>A-7T	p.Arg117His-7T	Missense		-/-	+/-

				Ex 14	c.2036G>A	p.Trp679X	Nonsense	Compound heterozygous	+/-	-/-
51	F	11.00	96	Ex 18	c.2909G>A	p.Gly970Asp	Missense	Compound heterozygous	+/-	-/-
				Ex 8	c.1000C>T	p.Arg334Trp	Missense		-/-	+/-
52	M	14.50	114	Ex 3	c.223C>T	p.Arg75X	Nonsense	Compound heterozygous	+/-	-/-
				Ex 4	c.293A>G	p.Gln98Arg	Missense		-/-	+/-
53	F	3.92	122	Ex 21	c.3387delT	p.Gly1130ValfsX 4	Frameshift	Compound heterozygous	+/-	-/-
				Ex 11	c.1409T>A	p.Val470Glu	Missense		-/-	+/-
54	F	8.58	125	Ex 12	c.1657C>T	p.Arg553X	Nonsense	Compound heterozygous	+/-	-/-
				Ex 14	c.1810A>C	p.Thr604Pro	Missense		-/-	+/-
55	M	10.67	108	Ex 18	c.2909G>A	p.Gly970Asp	Missense	Compound heterozygous	+/-	-/-
				Ex 20	c.3196C>A	p.Arg1066Ser	Missense		-/-	+/-
56	M	2.08	111	In 13	c.1766+2T>C	-	Splicing	Compound heterozygous	+/-	-/-
				In 21	c.3469-2A>T	-	Splicing		-/-	+/-
57	F	9.42	108	In 23	c.3874-4522A>G	-	Sequence variation	Compound heterozygous	+/-	-/-

				Ex 10	c.1368delT	p.Ala457LeufsX 12	Frameshift		-/-	+/-
58	F	8.75	136	Ex 11	c.1523_1534delT TGGTGTTCCT	p.Phe508_Ser511 del	In-frame deletion	Compound heterozygous	+/-	-/-
				Ex 11	c.1393-?_1584+? del	-	Large deletion		-/-	+/-
59	F	7.75	97	Ex 18	c.2977G>T	p.Asp993Tyr	Missense	Compound heterozygous	ND	ND
				Ex 10	c.1265C>T	p.Ser422Phe	Missense		ND	ND
				In 19	c.3140-26A>G	-	Missense		ND	ND
60	M	1.75	144	Ex 24	c.3908delA	p.Asn1303ThrfsX 25	Frameshift	Compound heterozygous	+/-	-/-
				Ex 18	c.2909G>A	p.Gly970Asp	Missense		-/-	+/-
61	F	4.17	ND	Ex 15	c.2551C>T	p.Arg851X	Nonsense	Compound heterozygous	-/-	+/-
				Ex 10	c.1219G>T	p.Glu407X	Nonsense		+/-	-/-
				Promoter	c.-152G>C	-	Sequence variation		-/-	+/-

62	M	16.83	ND	Ex 3	c.223C>T	p.Arg75X	Nonsense	Compound heterozygous	ND	ND
				Ex 18	c.2909G>A	p.Gly970Asp	Missense		ND	ND
63	F	13.75	ND	Ex 14	c.1810A>C	p.Thr604Pro	Missense	Compound heterozygous	ND	ND
				Ex 8	c.940G>T	p.Gly314Trp	Missense		ND	ND
				3'UTR	c.*133delT	–	Sequence variation		ND	ND
64	F	12.50	168	Ex 4	c.374T>C	p.Ile125Thr	Missense	Compound heterozygous	+/-	-/-
				Ex 11	c.1521_1523delC TT	p.Phe508del	In-frame deletion		-/-	+/-
65	F	1.67	89	Ex 13	c.1703T>A	p.Leu568X	Nonsense	Homozygous	+/-	+/-
66	M	4.00	ND	Ex 12	c.1657C>T	p.Arg553X	Nonsense	Homozygous	+/-	+/-
67	F	12.00	77	Ex 23	c.3841C>T	p.Gln1281X	Nonsense	Compound heterozygous	+/-	-/-
				Ex 4	c.298C>T	p.Leu100Phe	Missense		-/-	+/-
68	M	11.00	161	In 14	c.2491-2A>G	–	Missense	Compound heterozygous	-/-	-/-
				Ex 20	c.3196C>T	p.Arg1066Cys	Missense		-/-	+/-
69	F	6.33	85	Ex 22	c.3472C>T	p.Arg1158X	Nonsense		+/-	-/-

				Ex 2-3	c.54-?_273+?del	–	Large deletion	Compound heterozygous	-/-	+/-
70	F	3.25	101	Ex 6	c.607A>T	p.Ile203Phe	Missense	Compound heterozygous	+/-	-/-
				Ex 18-20	c.2909-?_3367+?del	–	Large deletion		-/-	+/-
71	F	13.25	122	Ex 20	c.3140-?_3367+?del	–	Large deletion	Compound heterozygous	-/-	+/-
				Ex 3	c.233dupT	p.Trp79LeufsX32	Frameshift		+/-	-/-
72	F	7.33	118	Ex 8	c.1000C>T	p.Arg334Trp	Missense	Compound heterozygous	+/-	-/-
				Ex 11	c.1393-?_1584+?del	–	Large deletion		-/-	+/-
73	F	15.33	149	Ex 4	c.293A>G	p.Gln98Arg	Missense	Compound heterozygous	+/-	-/-
				Ex 11	c.1521_1523delC TT	p.Phe508del	In-frame deletion		-/-	+/-
74	M	5.08	130	Ex 12	c.1657C>T	p.Arg553X	Nonsense	Compound heterozygous	+/-	-/-
				Ex 19	c.3068T>G	p.Ile1023Arg	Missense		-/-	+/-

75	F	8.58	146	Ex 3	c.222delG	p.Arg75AspfsX1 5	Frameshift	Compound heterozygous	+/-	-/-
				Ex 3	c.263T>G	p.Leu88X	Nonsense		-/-	+/-
76-1	M	7.75	130	Ex 18-20	c.2909-?_3367+? del	-	Large deletion	Compound heterozygous	+/-	-/-
				Ex 20	c.3196C>T	p.Arg1066Cys	Missense		-/-	+/-
76-2	F	5.58	120	Ex 18-20	c.2909-?_3367+? del	-	Large deletion	Compound heterozygous	+/-	-/-
				Ex 20	c.3196C>T	p.Arg1066Cys	Missense		-/-	+/-
77	F	4.50	60	Ex 4	c.298C>T	p.Leu100Phe	Missense	Compound heterozygous	-/-	+/-
				Ex 6	c.650A>G	p.Glu217Gly	Missense		+/-	-/-
78	F	12.92	119	Ex 22	c.3476C>T	p.Ser1159Phe	Missense	Compound heterozygous	+/-	-/-
				In 21	c.3469-12T>G	-	Splicing		-/-	+/-
79	M	2.75	134	Ex 22	c.3484C>T	p.Arg1162X	Nonsense	Compound heterozygous	+/-	-/-
				Ex 10	c.1369G>C	p.Ala457Pro	Missense		-/-	+/-
80	F	10.67	126	Ex 18-21	c.2909-?_3468+? del	-	Large deletion	Compound heterozygous	+/-	-/-

				Ex 18	c.2909G>A	p.Gly970Asp	Missense		-/-	+/-
81	F	10.58	127	Ex 3	c.223C>T	p.Arg75X	Nonsense	Compound	+/-	-/-
				Ex 18	c.2909G>A	p.Gly970Asp	Missense	heterozygous	-/-	+/-
82	M	6.00	144	In 13	c.1766+5G>T	-	Splicing	Homozygous	+/-	+/-
83	F	3.17	87	Ex 3	c.264_268delATA TT	p.Leu88PhefsX21	Frameshift	Compound	+/-	-/-
				In 22	c.3718-2477C>T	-	Sequence variation	heterozygous	-/-	+/-
84	F	0.50	ND	Ex 2-3	c.54-?_273+?del	-	Large deletion	Compound	+/-	-/-
				Ex 18	c.2909G>A	p.Gly970Asp	Missense	heterozygous	-/-	+/-
85	F	11.00	130	Ex 3	c.233dupT	p.Trp79LeufsX32	Frameshift	Compound	+/-	-/-
				Ex 14	c.2489dupA	p.Glu831GlyfsX 5	Frameshift	heterozygous	-/-	+/-
86	F	11.33	115	Ex 18	c.2909G>A	p.Gly970Asp	Missense	Compound	+/-	-/-
				Ex 18-20	c.2909-?_3367+? del	-	Large deletion	heterozygous	-/-	+/-

87	M	12.50	124	Ex 3	c.263T>G	p.Leu88X	Nonsense	Compound heterozygous	+/-	-/-
				Ex 11	c.1514delA	p.Asn505IlefsX2 2	Frameshift		-/-	+/-
88	F	5.67	95	Ex 4	c.374T>C	p.Ile125Thr	Missense	Compound heterozygous	+/-	-/-
				Ex 22	c.3659C>T	p.Thr1220Ile	Missense		-/-	+/-
89	M	4.83	152	Ex 10	c.1388G>A	p.Gly463Asp	Missense	Compound heterozygous	+/-	-/-
				In 16	c.2657+5G>A	-	Splicing		-/-	+/-
90	F	12.00	ND	Ex 18	c.2909G>A	p.Gly970Asp	Missense	Compound heterozygous	+/-	-/-
				Ex 20	c.233dupT	p.Trp79LeufsX32	Frameshift		-/-	+/-
91	F	5.42	ND	Ex 6	c.595C>T	p.His199Tyr	Missense	Compound heterozygous	+/-	-/-
				Ex 20	c.3176T>G	p.Leu1059X	Nonsense		-/-	+/-
92	F	3.17	ND	Ex 4	c.319_326delGC TTCCTA	p.Ala107X	Nonsense	Compound heterozygous	-/-	+/-
				Ex 11	c.1456G>T	p.Gly486X	Nonsense		+/-	-/-
93	F	7.58	112	Ex 14	c.2374C>T	p.Arg792X	Nonsense	Compound heterozygous	+/-	-/-
				Ex 4-11	c.274-?_1584+?d el	-	Large deletion		-/-	+/-

94	M	7.17	81	Ex 14	c.1772T>C	p.Val591Ala	Missense	Compound heterozygous	+/-	-/-
				Ex 4-11	c.274-?_1584+?del	-	Large deletion		-/-	+/-
95	M	0.50	ND	Ex 17	c.2812G>T	p.Val938Leu	Missense	Compound heterozygous	+/-	-/-
				Ex 18	c.2909G>A	p.Gly970Asp	Missense		-/-	+/-
96	F	3.75	ND	Ex 18	c.2909G>A	p.Gly970Asp	Missense	Compound heterozygous	+/-	-/-
				Ex 4	c.464C>G	p.Ala155Gly	Missense		-/-	+/-
97	M	0.58	ND	In 13	c.1766+2T>C	-	Splicing	Homozygous	+/-	+/-
98	F	6.00	ND	Ex 3	c.263T>G	p.Leu88X	Nonsense	Compound heterozygous	+/-	-/-
				In 13	c.1766+2T>C	-	Splicing		-/-	+/-
99	F	13.50	68	Ex 18	c.2909G>A	p.Gly970Asp	Missense	Compound heterozygous	+/-	-/-
				In 15	c.2619+2T>A	-	Splicing		-/-	+/-
100	M	0.42	103	Ex 8	c.1064C>G			Compound heterozygous	+/-	-/-
				In 9	c.1210-3C>G	-	Splicing		-/-	+/-

Novel variants are formatted in bold.

e-Table 2. Spectrum of *CFTR* variants detected in 202 Chinese patients with CF

No.	Region	Mutations	Amino acid change	Pathogenic significance	Reported/Novel	No. of alleles	Frequency, %
		(HGVS nomenclature)					
1 ^[4, 6, 10, 12, 16, 20, 24, 25, 27, 29, 36, 51]	Ex 18	c.2909G>A	p.Gly970Asp	CF-causing	Reported	47	12.11
2 ^[4, 6, 10, 32, 34, 40, 42, 43, 46-48, 50]	In 13	c.1766+5G>T	–	CF-causing	Reported (Chinese/Thai)	21	5.41

3 ^[9, 10, 12, 13, 34, 42, 45, 48]	Ex 12	c.1657C>T	p.Arg553X	CF-causing	Reported	14	3.61
4 ^[4, 10, 12]	Ex 4	c.293A>G	p.Gln98Arg	CF-causing	Reported	12	3.09
5 ^[6, 10, 42, 47, 48]	Ex 19	c.3068T>G	p.Ile1023Arg	Unknown	Reported (Chinese only)	11	2.84
6 ^[4, 6, 30, 37]	Ex 8	c.1000C>T	p.Arg334Trp	CF-causing	Reported	10	2.58
7 ^[4, 6, 20, 21]	Ex 3	c.263T>G	p.Leu88X	CF-causing	Reported	10	2.58
8 ^[4, 6, 10, 19, 27]	Ex 6	c.595C>T	p.His199Tyr	CF-causing	Reported	9	2.32

9 ^[4, 10, 26, 38]	Ex 20	c.3196C>T	p.Arg1066Cys	CF-causing	Reported	8	2.06
10 ^[6, 20]	Ex 11	c.1521_1523delCTT	p.Phe508del	CF-causing	Reported	7	1.80
11 ^[18, 31, 38]	Ex 6	c.650A>G	p.Glu217Gly	Unknown	Reported	6	1.55
12 ^[4, 12, 28]	3Ex 12	c.1666A>G	p.Ile556Val	Unknown	Reported	6	1.55
13 ^[4, 6]	Ex 3	c.223C>T	p.Arg75X	CF-causing	Reported	5	1.29
14 ^[33]	Ex 4	c.374T>C	p.Ile125Thr	Unknown	Reported	5	1.29
15 ^[6, 16]	In 9	c.1210-3C>G	–	Unknown	Reported (Chinese only)	4	1.03
16 ^[37]	Ex 11	c.1409T>A	p.Val470Glu	Unknown	Reported (Chinese only)	4	1.03
17 ^[17, 39]	Ex 14	c.2036G>A	p.Trp679X	Suspected	Reported	4	1.03
18 ^[38]	Ex 17	c.2834C>T	p.Ser945Leu	CF-causing	Reported	4	1.03

19 ^[12]	Ex 18-20	c.2909-?_3367+?del	–	Suspected	Reported	4	1.03
20 ^[27, 29, 38]	Ex 25	c.4056G>C	p.Gln1352His	Unknown	Reported	4	1.03
21 ^[10]	Ex 2-3	c.54-?_273+?del	–	Suspected	Reported	3	0.77
22	Ex 3	c.233dupT	p.Trp79LeufsX32	CF-causing	Reported	3	0.77
23 ^[6]	Ex 3	c.264_268delATATT	p.Leu88PhefsX21	Suspected	Reported	3	0.77
24 ^[4]	Ex 4	c.326A>G	p.Tyr109Cys	Unknown	Reported	3	0.77
25 ^[6, 24, 29]	In 8	c.1116+1G>A	–	CF-causing	Reported	3	0.77
26 ^[10, 20]	Ex 14	c.2125C>T	p.Arg709X	CF-causing	Reported	3	0.77
27 ^[4, 20]	Ex 14	c.2374C>T	p.Arg792X	CF-causing	Reported	3	0.77
28 ^[6, 10, 20]	Ex 22	c.3635delT	p.Val1212AlafsX1 6	Suspected	Reported (Chinese only)	3	0.77
29 ^[40]	Promoter	c.-152G>C	–	Unknown	Reported	2	0.52
30 ^[26]	Ex 1	c.3G>A	p.Met1Ile	Unknown	Reported	2	0.52

31 ^[12, 33]	Ex 2	c.95T>C	p.Leu32Pro	Unknown	Reported	2	0.52
32	Ex 4-11	c.274-?_1584+?del	–	Suspected	Reported	2	0.52
33	Ex 4	c.298C>T	p.Leu100Phe	Unknown	Novel	2	0.52
34 ^[51]	Ex 4	c.319_326delGCTTCCTA	p.Ala107X	Suspected	Reported	2	0.52
35 ^[10]	Ex 4	c.325T>G	p.Tyr109Asp	Unknown	Reported (Chinese only)	2	0.52
36 ^[36]	Ex 4	c.380T>G	p.Leu127X	Suspected	Reported	2	0.52
37 ^[4]	Ex 4	c.413_415dupTAC	p.Leu138dup	CF-causing	Reported	2	0.52
38 ^[6]	Ex 5	c.532G>A	p.Gly178Arg	CF-causing	Reported	2	0.52
39 ^[4, 12]	Ex 5	c.558C>G	p.Asn186Lys	Unknown	Reported (Chinese only)	2	0.52
40 ^[10]	Ex 6	c.607A>T	p.Ile203Phe	Unknown	Reported (Chinese only)	2	0.52
41 ^[4]	Ex 6	c.648G>A	p.Trp216X	Suspected	Reported (Chinese only)	2	0.52

42 ^[4,20]	Ex 8	c.960dupA	p.Ser321IlefsX43	Suspected	Reported (Chinese only)	2	0.52
43 ^[35]	Ex 10	c.1369G>C	p.Ala457Pro	Unknown	Reported	2	0.52
44 ^[10]	Ex 10	c.1388G>A	p.Gly463Asp	Unknown	Reported	2	0.52
45	Ex 11	c.1393-?_1584+?del	–	Suspected	Novel	2	0.52
46 ^[26]	Ex 11	c.1572C>A	p.Cys524X	CF-causing	Reported	2	0.52
47 ^[10,12]	In 12	c.1679+2T>C	–	Unknown	Reported	2	0.52
48	Ex 13	c.1703T>A	p.Leu568X	Suspected	Reported	2	0.52
49	Ex 14	c.1810A>C	p.Thr604Pro	Unknown	Novel	2	0.52
50 ^[46,43]	Ex 14	c.2083dupG	p.Glu695GlyfsX35	Suspected	Reported (Chinese only)	2	0.52
51 ^[19,25]	Ex 14	c.2290C>T	p.Arg764X	CF-causing	Reported	2	0.52
52 ^[4]	In 14	c.2491-126T>C	–	Unknown	Reported (Chinese only)	2	0.52

53 ^[10, 38]	Ex 15	c.2547C>A	p.Tyr849X	CF-causing	Reported	2	0.52
54 ^[38]	Ex 15	c.2551C>T	p.Arg851X	CF-causing	Reported	2	0.52
55 ^[10, 12]	In 16	c.2658-1G>C	–	CF-causing	Reported	2	0.52
56 ^[46, 43]	Ex 17	c.2684G>A	p.Ser895Asn	Unknown	Reported (Chinese only)	2	0.52
57 ^[29, 38]	Ex 19	c.3062C>T	p.Pro1021Leu	Unknown	Reported (Chinese only)	2	0.52
58 ^[48]	In 19	c.3140-26A>G	–	CF-causing	Reported	2	0.52
59 ^[23]	Ex 20	c.3140-454_c.3367+249del193ins 13	–	Suspected	Reported (Chinese only)	2	0.52
60 ^[10]	Ex 20	c.3196C>A	p.Arg1066Ser	Unknown	Reported	2	0.52
61	Ex 22	c.3484C>T	p.Arg1162X	CF-causing	Reported	2	0.52
62 ^[4, 20]	Ex 22	c.3700A>G	p.Ile1234Val	CF-causing	Reported	2	0.52

63	In 22	c.3717+10kbC>T	–	Unknown	Reported	2	0.52
64	In 22	c.3718-2477C>T	–	CF-causing	Reported	2	0.52
65	In 23	c.3874-4522A>G	–	Unknown	Reported	2	0.52
66 ^[36]	3'UTR	c.*133delT	–	Unknown	Reported	2	0.52
67 ^[44]	Ex 1	c.19G>T	p.Glu7X	Suspected	Reported (Chinese only)	1	0.26
68 ^[14]	Ex 2	c.54_164del30bp	–	Suspected	Reported (Chinese only)	1	0.26
69	In 2	c.164+2T>C	–	CF-causing	Reported	1	0.26
70 ^[18]	Ex 3	c.214G>A	p.Ala72Thr	Unknown	Reported	1	0.26
71	Ex 3	c.222delG	p.Arg75AspfsX16	Suspected	Novel	1	0.26
72 ^[22]	Ex 3	c.271G>A	p.Gly91Arg	CF-causing	Reported	1	0.26
73 ^[21]	Ex 4-6	c.274-?_743+?del	–	Suspected	Reported	1	0.26
74 ^[35]	Ex 4	c.320C>A	p.Ala107Asp	Unknown	Reported (Chinese only)	1	0.26
75	Ex 4	c.350G>A	p.Arg117His	CF-causing	Reported	1	0.26
76 ^[10]	Ex 4	c.405_406dupAC	p.Leu136HisfsX18	Suspected	Reported	1	0.26

77	Ex 4	c.464C>G	p.Ala155Gly	Unknown	Novel	1	0.26
78 ^[15]	Ex 5	c.567C>A	p.Asn189Lys	Unknown	Reported (Chinese only)	1	0.26
79 ^[6]	In 5	c.579+1_579+2insACAT	–	Unknown	Reported (Chinese only)	1	0.26
80 ^[30]	In 5	c.580-1G>T	–	CF-causing	Reported	1	0.26
81 ^[12]	Ex 7-11	c.744-?_1584+ ?del	–	Suspected	Reported (Chinese only)	1	0.26
82 ^[41]	Ex 7	c.753_754delAG	p.Arg251SerfsX6	Suspected	Reported (Chinese only)	1	0.26
83 ^[44]	Ex 7	c.860dupA	p.Asn287LysfsX21	Suspected	Reported (Chinese only)	1	0.26
84 ^[38]	Ex 7	c.861C>G	p.Asn287Lys	Unknown	Reported	1	0.26
85 ^[11]	Ex 7	c.865A>T	p.Arg289X	Suspected	Reported (Chinese only)	1	0.26
86 ^[48]	Ex 7	c.868C>T	p.Gln290X	CF-causing	Reported	1	0.26
87 ^[26]	In 7	c.870-1G>C	–	Unknown	Reported	1	0.26

88 ^[38]	Ex 8	c.884delT	p.Leu295ArgfsX8	Suspected	Reported (Chinese only)	1	0.26
89	Ex 8	c.940G>T	p.Gly314Trp	Unknown	Novel	1	0.26
90 ^[29]	Ex 8	c.1040G>A	p.Arg347His	CF-causing	Reported	1	0.26
91	Ex 8	c.1064C>G	p.Pro355Arg	Unknown	Novel	1	0.26
92 ^[4]	Ex 8	c.1075C>T	p.Gln359X	Suspected	Reported (Chinese only)	1	0.26
93 ^[27]	In 8	c.1117-1G>C	–	Unknown	Reported (Chinese only)	1	0.26
94	Ex 10	c.1219G>T	p.Glu407X	Suspected	Novel	1	0.26
95	Ex 10	c.1231A>G	p.Lys411Glu	Unknown	Reported	1	0.26
96^[41]	Ex 10	c.1240C>T	p.Gln414X	CF-causing	Reported	1	0.26
97	Ex 10	c.1265C>T	p.Ser422Phe	Unknown	Novel	1	0.26
98	Ex 10	c.1347_1350delAGAA	p.Arg450AspfsX1 8	Suspected	Novel	1	0.26
99 ^[38]	Ex 10	c.1352G>T	p.Gly451Val	Unknown	Reported	1	0.26
100	Ex 10	c.1368delT	p.Ala457LeufsX12	Suspected	Novel	1	0.26

101 ^[22]	Ex 10	c.1373G>A	p.Gly458Glu	Unknown	Reported (Chinese only)	1	0.26
102 ^[38]	In 10	c.1393-4C>A	–	Unknown	Reported (Chinese only)	1	0.26
103 ^[13]	Ex 11	c. 1423delC	p.Leu475TrpfsX52	Suspected	Reported (Chinese only)	1	0.26
104 ^[6]	Ex 11	c.1429_1437delCCTTCA GAG	p.Pro477_Glu479d el	Unknown	Reported (Chinese only)	1	0.26
105	Ex 11	c.1456G>T	p.Gly486X	Suspected	Reported	1	0.26
106	Ex 11	c.1514delA	p.Asn505IlefsX22	Suspected	Novel	1	0.26
107	Ex 11	c.1523_1534delTTGGTG TTTCCT	p.Phe508_Ser511d el	Suspected	Novel	1	0.26
108 ^[29]	Ex 11	c.1526G>C	p.Gly509Ala	Unknown	Reported (Chinese only)	1	0.26
109 ^[4]	Ex 13	c.1699G>T	p.Asp567Tyr	Unknown	Reported (Chinese only)	1	0.26
110 ^[10]	Ex 13	c.1716C>A	p.Asp572Glu	Unknown	Reported	1	0.26

					(Chinese only)		
111 ^[6]	Ex 13	c.1733T>C	p.Leu578Pro	Unknown	Reported (Chinese only)	1	0.26
112 ^[49]	In 13	c.1766+1G>T	–	CF-causing	Reported	1	0.26
113	In 13	c.1766+2T>C	–	Unknown	Reported	1	0.26
114	Ex 14	c.1772T>C	p.Val591Ala	Unknown	Novel	1	0.26
115 ^[20]	Ex 14	c.1997T>G	p.Leu666X	Suspected	Reported (Chinese only)	1	0.26
116	Ex 14	c.2042A>T	p.Glu681Val	Unknown	Novel	1	0.26
117 ^[38]	Ex 14	c.2052delA	p.Lys684AsnfsX38	CF-causing	Reported	1	0.26
118 ^[12]	Ex 14	c.2052dupA	p.Gln685ThrfsX4	CF-causing	Reported	1	0.26
119	Ex 14	c.2058_2061delTT	p.Phe687X	Suspected	Novel	1	0.26
120 ^[6]	Ex 14	c.2236_2246delGAGGCG ATACTinsAAAAATC	p.Glu746LysfsX8	Suspected	Reported (Chinese only)	1	0.26
121	Ex 14	c.2328dupA	p.Val777SerfsX2	Suspected	Novel	1	0.26
122 ^[10]	Ex 14	c.2353C>T	p.Arg785X	CF-causing	Reported	1	0.26
123	Ex 14	c.2475_2478dupCGAA	p.Glu827ArgfsX10	Suspected	Reported	1	0.26

					(Chinese only)		
124	Ex 14	c.2489dupA	p.Glu831GlyfsX5	Suspected	Novel	1	0.26
125	In 14	c.2491-2A>G	–	Unknown	Reported	1	0.26
126	In 15	c.2619+2T>A	–	Unknown	Reported	1	0.26
127	In 16	c.2657+5G>A	–	CF-causing	Reported	1	0.26
128 ^[32]	Ex 17	c.2805delA	p.Pro936HisfsX6	Suspected	Reported (Chinese only)	1	0.26
129	Ex 17	c.2812G>T	p.Val938Leu	Unknown	Reported	1	0.26
130 ^[20]	Ex 17	c.2907A>C	p.A969A	Unknown	Reported (Chinese only)	1	0.26
131	Ex 18-21	c.2909-?_3468+?del	–	Suspected	Novel	1	0.26
132	Ex 18	c.2936A>C	p.Asp979Ala	Unknown	Reported	1	0.26
133	Ex 18	c.2977G>T	p.Asp993Tyr	Unknown	Reported	1	0.26
134 ^[17]	In 18	c.2988+2T>C	–	Unknown	Reported (Chinese only)	1	0.26
135 ^[10]	Ex 19	c.2997_3000delAATT	p.Ile1000X	Suspected	Reported	1	0.26
136 ^[38]	Ex 19	c.3123dupA	p.Gln1042ThrfsX5	Suspected	Reported	1	0.26

137	Ex 20	c.3140-?_3367+?del	–	Suspected	Novel	1	0.26
138	Ex 20	c.3176T>G	p.Leu1059X	Suspected	Reported	1	0.26
139 ^[40]	Ex 20	c.3197G>A	p.Arg1066His	CF-causing	Reported	1	0.26
140	Ex 20	c.3209G>C	p.Arg1070Pro	Unknown	Reported	1	0.26
141 ^[4]	Ex 20	c.3307delA	p.Ile1103X	Suspected	Reported (Chinese only)	1	0.26
142	Ex 21	c.3387delT	p.Gly1130ValfsX4	Suspected	Reported	1	0.26
143 ^[18]	Ex 21	c.3406G>A	p.Ala1136Thr	Unknown	Reported	1	0.26
144	In 21	c.3469-12T>G	–	Unknown	Novel	1	0.26
145	In 21	c.3469-2A>T	–	Unknown	Novel	1	0.26
146	Ex 22	c.3472C>T	p.Arg1158X	CF-causing	Reported	1	0.26
147	Ex 22	c.3476C>T	p.Ser1159Phe	CF-causing	Reported	1	0.26
148 ^[11]	Ex 22	c.3653_3656dupAATA	p.Tyr1219X	Suspected	Reported (Chinese only)	1	0.26
149	Ex 22	c.3659C>T	p.Thr1220Ile	Unknown	Novel	1	0.26
150 ^[15]	Ex 22	c.3691delT	p.Ser1231ProfsX4	CF-causing	Reported	1	0.26
151 ^[6]	Ex 23	c.3718-?_3873+?del	–	Suspected	Reported	1	0.26

					(Chinese only)		
152	Ex 23	c.3841C>T	p.Gln1281X	Suspected	Reported	1	0.26
153 ^[6]	Ex 23	c.3860delG	p.Gly1287GlufsX2	Suspected	Reported (Chinese only)	1	0.26
154 ^[10]	Ex 24	c.3883_3886delATTT	p.Ile1295PhefsX32	CF-causing	Reported	1	0.26
155	Ex 24	c.3908delA	p.Asn1303ThrfsX2 5	CF-causing	Reported	1	0.26
156 ^[4]	Ex 24	c.3909C>G	p.Asn1303Lys	CF-causing	Reported	1	0.26
157 ^[6]	In 24	c.3964-7A>G	–	Unknown	Reported (Chinese only)	1	0.26
158 ^[4]	3'UTR	c.*110C>G	–	Unknown	Reported (Chinese only)	1	0.26

HGVS, Human Genome Variation Society.

Novel variants are formatted in bold.

e-Table 3. Demographic and clinical features of 24 Chinese CF patients with novel variants

Case No.	Sex	Age at Dx, y	Age of symptom onset, y	Weight at Dx, kg (centile)	Clinical presentation	Sputum pathogens	Fecal Sudan III stain	Sweat conductivity, mmol/L	Genotype	Distribution (Province)
33	M	7.33	7.00	18.0 (<3rd)	Bronchiectasis/Recurrent pneumonia/ABPA/Sinusitis/Steatorrhea/Liver disease/FTT/Finger clubbing	<i>P. aeruginosa/S. aureus</i>	+	125	c.2328dupA/c.3209G>C	Hebei
36	F	10.67	5.00	37.5 (50-75th)	Bronchiectasis/Recurrent pneumonia/Sinusitis/Liver disease/Diabetes/Finger clubbing	<i>H. influenzae/P. aeruginosa/S. aureus</i>	–	127	c.2058_2061delT T/c.595C>T	Shanxi

38	M	13.25	7.00	30.0 7 (<3 rd)	Bronchiectasis/Recurrent pneumonia/ABPA/Asthma/Hemoptysis/Sinusitis/Nasal polyps/FTT/Pancreatitis/Finger clubbing	<i>P. aeruginosa/S. aureus/A. fumigatus/A. niger</i>	+	109	c.1347_1350delA GAA/c.2909G>A	Zhejiang
46	M	10.17	7.00	27.0 (10th)	Bronchiectasis/ Asthma/Sinusitis	–	–	60	c.2042A>T/c.374 T>C	Yunnan
54	F	8.58	5.00	27.0 (25- 50th)	Bronchiectasis/Sinusitis/Nasal polyps	<i>P. aeruginosa</i>	–	125	c.1810A>C/c.165 7C>T	Shanghai
56	M	2.08	1.00	9.5 (<3 rd)	Bronchiectasis/Recurrent pneumonia/Sinusitis/Steatorrhea/FTT/Finger clubbing	<i>P. aeruginosa</i>	+	111	c.3469-2A>T/c.1766+2T >C	Henan
57	F	9.42	5.00	26.0 (10- 25th)	Bronchiectasis/Recurrent pneumonia/Sinusitis/Pancreatitis/Finger clubbing	<i>P. aeruginosa/A. fumigatus/A. flavus</i>	–	108	c.1368delT/c.387 4-4522A>G	Yunnan
58	F	8.75	2.00	19.0	Bronchiectasis/Recurrent	<i>P. aeruginosa/C.</i>	+	136	c.1393-?_1584+?	Henan

				(<3rd)	pneumonia/Sinusitis/Steatorrhea/Rectal prolapse/Liver disease/FTT/Finger clubbing	<i>Albicans</i>			del/c.1523_1534delTTGGTGTTTCCT	
59	F	7.75	0.75	21.0 (10-25th)	Bronchiectasis/Recurrent pneumonia/ABPA/Sinusitis/Finger clubbing	<i>P. aeruginosa/S. maltophilia</i>	-	97	c.1265C>T/c.2977G>T/c.3140-26A>G	Shandong
61	F	4.17	1.00	12.0 (<3rd)	Bronchiectasis/Recurrent pneumonia/Sinusitis/Meconium ileus/Steatorrhea/Rectal prolapse/Liver disease/FTT/Finger clubbing	<i>P. aeruginosa/S. aureus/C. lusitaniae</i>	+	ND	c.1219G>T/c.2551C>T/c.-152G>C	Zhejiang
63	F	13.75	5.00	29.0 (<3rd)	Bronchiectasis/Recurrent pneumonia/Sinusitis/Pancreatitis/Steatorrhea/FTT/Finger clubbing	<i>P. aeruginosa/A. flavus</i>	+	ND	c.1810A>C/c.940G>T/c.*133delT	Zhejiang

67	F	12.00	9.00	47.6 (75-90th)	Bronchiectasis/Sinusitis/ABPA/Wheeze	<i>P. aeruginosa/A. terreus</i>	–	77	c.298C>T/c.3841C>T	Anhui
71	F	13.25	8.00	35.0 (3rd-10th)	Bronchiectasis/Sinusitis/FTT/Finger clubbing	<i>P. aeruginosa/C. Albicans</i>	–	122	c.3140-?_3367+?del/c.233dupT	Shandong
72	F	7.33	1.00	19.0 (3rd-10th)	Bronchiectasis/Sinusitis/FTT	<i>K. pneumoniae/S. aureus</i>	–	118	c.1393-?_1584+?del/c.1000C>T	Shanxi
75	F	8.58	0.58	19.0 (<3rd)	Bronchiectasis/Recurrent pneumonia/ABPA/Sinusitis/Steatorrhea/Diabetes/FTT/Finger clubbing	<i>P. aeruginosa/A. fumigatus/C. Albicans</i>	+	146	c.222delG/c.263T>G	Jiangxi
77	F	4.50	4.00	19.0 (75th)	Atelectasis/Asthma/Sinusitis	–	–	60	c.298C>T/c.650A>G	Jiangsu
78	F	12.92	10.00	44.0 (50th)	Bronchiectasis/Hemoptysis/Sinusitis/Nasal polyps/Finger clubbing	<i>P. aeruginosa/M. abscessus/A. terreus/C. Albicans</i>	–	119	c.3469-12T>G/c.3476C>T	Liaoning

80	F	10.67	6.00	33.0 (25-50th)	Bronchiectasis/ABPA/Asthma/Sinusitis/Pancreatitis	<i>P. aeruginosa/S. aureus</i>	-	126	c.2909-?_3468+?del/c.2909G>A	Henan
85	F	11.00	10.00	30.5 (10-25th)	Bronchiectasis/Sinusitis/Appendicitis	<i>P. aeruginosa</i>	-	130	c.2489dupA/c.233dupT	Anhui
87	M	12.50	0.17	31.0 (3rd)	Bronchiectasis/Recurrent pneumonia/Sinusitis/Steatorrhea/Liver disease/FTT/Finger clubbing	<i>S. aureus/C. Albicans</i>	+	124	c.1514delA/c.263T>G	Sichuan
88	F	5.67	0.25	23.0 (90th)	Bronchiectasis/Asthma/Sinusitis	<i>S. pneumoniae/C. Albicans</i>	-	95	c.3659C>T/c.374T>C	Henan
94	M	7.17	6.00	19.0 (3rd)	Bronchiectasis/Sinusitis/FTT/Finger clubbing	<i>P. aeruginosa/C. Albicans</i>	-	ND	c.1772T>C/c.274-?_1584+?del)	Henan
96	F	3.75	3.00	13.0 (3rd-10th)	Bronchiectasis/ABPA/Sinusitis/FTT	-	-	ND	c.464C>G/c.2909G>A	Henan
102	M	0.42	0.08	8.0 (50th)	Pseudo-Bartter syndrome	-	-	103	c.1064C>G/c.1210-3C>G	Henan

Abbreviations: *A. fumigatus* = *Aspergillus fumigatus*; *A. flavus* = *Aspergillus flavus*; *A. niger* = *Aspergillus niger*; *A. terreus* = *Aspergillus terreus*; *C. Albicans* = *Candida Albicans*; *C. lusitaniae* = *Candida lusitaniae*; *H. influenzae* = *Haemophilus influenzae*; *K. pneumonia* = *Klebsiella pneumoniae*; *M. abscessus* = *Mycobacterium abscessus*; *MRSA* = *Methicillin-resistant Staphylococcus aureus*; *P. aeruginosa* = *Pseudomonas aeruginosa*; *S. aureus* = *Staphylococcus aureus*; *S. maltophilia* = *Stenotrophomonas maltophilia*; *S. pneumoniae* = *Streptococcus pneumoniae*; Dx = Diagnosis; FTT = Failure to thrive; ND = Not done; Y = Years.

Novel variants are formatted in bold.