

Cystic Fibrosis 139-variant assay

The table below shows the *CFTR* gene variants included in the Illumina TruSight Cystic Fibrosis 139-Variant Assay – listed by genomic coordinate order. These variants are expected to account for 95.4% of cystic fibrosis-causing alleles in a broad-spectrum population and identify approximately 91% of couples at risk through the detection of both disease-causing alleles.

Bold text indicates that these variants are part of the variant set recommended by the American College of Medical Genetics for cystic fibrosis screening published in 2023. Variants listed at the end of the table in italics are conditionally reported. For each variant, the DNA nucleotide variant and the protein variant are given using HGVS nomenclature, followed by the legacy name.

c.1A>G p.(Met1Val) M1V	c.1329_1330insAGAT p.(Ile444Argfs*3) 1461ins4	c.2551C>T p.(Arg851*) R851X
c.54-5940_273+10250del21kb p.(Ser18Argfs*16) CFTRdele2,3	c.1364C>A p.(Ala455Glu) A455E	c.2583delT p.(Phe861Leufs*3) 2711delT
c.115C>T p.(Gln39*) Q39X	C.1393-1G>A p.(?) 1525-1G>A	c.2657+5G>A p.(?) 2789+5G>A
c.178G>T p.(Glu60*) E60X	c.1397C>A p.(Ser466*) S466X (C>A)	c.2668C>T p.(Gln890*) Q890X
c.200C>T p.(Pro67Leu) P67L	c.1397C>G p.(Ser466*) S466X (C>G)	c.2780T>C p.(Leu927Pro) L927P
c.223C>T p.(Arg75*) R75X	c.1400T>C p.(Leu467Pro) L467P	c.2834C>T p.(Ser945Leu) S945L
c.254G>A p.(Gly85Glu) G85E	c.1418delG p.(Gly473Glu fs*54) 1548delG	c.2875delG p.(Ala959His fs*9) 3007delG
c.262_263delTT p.(Leu88Ile fs*22) 394delTT	c.1466C>A p.(Ser489*) S489X	c.2908G>C p.(Gly970Arg) G970R

c.273+1G>A p.(?) 405+1G>A	c.1475C>T p.(Ser492Phe) S492F	c.2988G>A p.(?) 3120G>A
c.274-1G>A p.(?) 406-1G>A	c.1477C>T p.(Gln493*) Q493X	c.2988+1G>A p.(?) 3120+1G>A
c.274G>T p.(Glu92*) E92X	c.1519_1521delATC p.(Ile507del) I507del	c.2989-1G>A p.(?) 3121-1G>A
c.274G>A p.(Glu92Lys) E92K	c.1521_1523delCTT p.(Phe508del) F508del	c.3140-26A>G p.(?) 3272-26A>G
c.292C>T p.(Gln98*) Q98X	c.1545_1546delTA p.(Tyr515*) 1677delTA	c.3194T>C p.(Leu1065Pro) L1065P
c.325_327delTATinsG p.(Tyr109Glyfs*4) 457TAT>G	c.1558G>T p.(Val520Phe) V520F	c.3196C>T p.(Arg1066Cys) R1066C
c.328G>C p.(Asp110His) D110H	c.1573C>T p.(Gln525*) Q525X	c.3197G>A p.(Arg1066His) R1066H
c.349C>T p.(Arg117Cys) R117C	c.1585-8G>A p.(?) 1717-8G>A	c.3230T>C p.(Leu1077Pro) L1077P
c.350G>A p.(Arg117His) R117H	c.1585-1G>A p.(?) 1717-1G>A	c.3266G>A p.(Trp1089*) W1089X
c.366T>A p.(Tyr122*) Y122X	c.1624G>T p.(Gly542*) G542X	c.3276C>A p.(Tyr1092*) Y1092X (C>A)
c.442delA p.(Ile148Leufs*5) 574delA	c.1645A>C p.(Ser549Arg) S549R	C.3276C>G p.(Tyr1092*) Y1092X (C>G)
c.489+1G>T p.(?) 621+1G>T	c.1646G>A p.(Ser549Asn) S549N	c.3302T>A p.(Met1101Lys) M1101K
c.531delT p.(Ile177Metfs*12) 663delT	c.1647T>G p.(Ser549Arg) S549R	c.3310G>T p.(Glu1104*) E1104X
c.532G>A p.(Gly178Arg) G178R	c.1652G>A p.(Gly551Asp) G551D	c.3472C>T p.(Arg1158*) R1158X
c.579+1G>T p.(?) 711+1G>T	c.1654C>T p.(Gln552*) Q552X	c.3484C>T p.(Arg1162*) R1162X
c.579+3A>G p.(?) 711+3A>G	c.1657C>T p.(Arg553*) R553X	c.3528delC p.(Lys1177Serfs*15) 3659delC
c.579+5G>A p.(?) 711+5G>A	c.1675G>A p.(Ala559Thr) A559T	c.3587C>G p.(Ser1196*) S1196X
c.580-1G>T p.(?) 712-1G>T	c.1679G>C p.(Arg560Thr) R560T	c.3611G>A p.(Trp1204*) W1204X
c.595C>T p.(His199Tyr) H199Y	c.1679G>A p.(Arg560Lys) R560K	c.3612G>A p.(Trp1204*) W1204X
c.613C>T p.(Pro205Ser) P205S	c.1679+1.6kbA>G p.(?) 1811+1.6kbA>G	c.3659delC p.(Thr1220Lysfs*8) 3791delC
c.617T>G p.(Leu206Trp) L206W	c.1680-1G>A p.(?) 1812-1G>A	c.3717+12191C>T p.(?) 3849+10kbC>T
c.658C>T p.(Gln220*) Q220X	c.1753G>T p.(Glu585*) E585X	c.3731G>A p.(Gly1244Glu) G1244E
c.720_741delAGGGAGAATGATGATGAAGTAC p.(Gly241Glufs*13) 852del22	c.1766+1G>A p.(?) 1898+1G>A	c.3744delA p.(Lys1250Argfs*9) 3876delA
c.948delT p.(Phe316Leufs*12) 1078delT	c.1766+3A>G p.(?) 1898+3A>G	c.3752G>A p.(Ser1251Asn) S1251N
c.988G>T p.(p.Gly330*) G330X	c.2012delT p.(Ile671*) 2143delT	c.3773_3774insT p.(Leu1258Phefs*7) 3905insT

c.1000C>T p.(Arg334Trp) R334W	c.2051_2052delAAinsG p.(Lys684Serfs*38) 2183AA>G	c.3846G>A p.(Trp1282*) W1282X
c.1007T>A p.(Ile336Lys) I336K	c.2052delA p.(Lys684Asnfs*38) 2184delA	c.3873+1G>A p.(?) 4005+1G>A
c.1013C>T p.(Thr338Ile) T338I	c.2052_2053insA p.(Gln685Thrfs*4) 2184insA	c.3884_3885insT p.(Ser1297Phefs*5) 4016insT
c.1021T>C p.(Ser341Pro) S341P	c.2125C>T p.(Arg709*) R709X	c.3909C>G p.(Asn1303Lys) N1303K
c.1022_1023insTC p.(Phe342Hisfs*28) 1154insTC	c.2128A>T p.(Lys710*) K710X	c.3937C>T p.(Gln1313*) Q1313X
c.1040G>A p.(Arg347His) R347H	c.2175_2176insA p.(Glu726Argfs*4) 2307insA	c.4077_4080delTGTTinsAA p.(Val1360Thrfs*3) 4209TGTT>AA
c.1040G>C p.(Arg347Pro) R347P	c.2195T>G p.(Leu732*) L732X	c.3964-78_4242+577del) p.(?) CFTRdele22,23
c.1055G>A p(Arg352Gln) R352Q	c.2215delG p.(Val739Tyrfs*16) 2347delG	c.4251delA p.(Glu1418Argfs*14) 4382delA
c.1081delT p.(Trp361Glyfs*8) 1213delT	c.2290C>T p.(Arg764*) R764X	
c.1116+1G>A p.(?) 1248+1G>A	c.2453delT p.(Leu818Trpfs*3) 2585delT	
c.1127_1128insA p.(Gln378Alafs*4) 1259insA	c.2464G>T p.(Glu822*) E822X	<i>PolyTG/PolyT tract</i>
c.1202G>A p.(Trp401*) W401X	c.2490+1G>A p.(?) 2622+1G>A	<i>c.1516A>G p.(Ile506Val) I506V</i>
c.1203G>A p.(Trp401*) W401X	c.2491G>T p.(Glu831*) E831X	<i>c.1519A>G p.(Ile507Val) I507V</i>
c.1209+1G>A p.(?) 1341+1G>A	c.2537G>A p.(Trp846*) W846X	<i>c.1523T>G p.(Phe508Cys) F508C</i>

Further information about the clinical relevance/impact of these variants can be found at www.cftr2.org

Further information about the variants recommended by the ACMG can be found at <https://doi.org/10.1016/j.jim.2023.100867>

Further information about the nomenclature used for variant naming can be found at www.hgvs.org

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