ONLINE DATA SUPPLEMENT

ABCA3 Mutations Associated with Pediatric Interstitial Lung Disease

Janine E. Bullard, Susan E. Wert, Jeffrey A. Whitsett, Michael Dean, and Lawrence M. Nogee

Detailed information about enrollment into the ongoing study designed to detect defects in surfactant metabolism, including ABCA3, is available through contact with Dr. Lawrence Nogee. Email: lnogee@jhmi.edu. Clinical testing for SP-B gene (*SFTPB*) and SP-C *(SFTPC)* mutations is available through the DNA Diagnostics lab at Johns Hopkins Hospital, http.//wwwhopkinsmedicine.org/dnadiagnostic.

Table E1: *ABCA3* Gene Primers

ABCA3 Exon	Forward Primer Sequence (5'→ 3')	Reverse Primer Sequence (3'→ 5')	Genomic Position	Product Size (bp)	Anneal Temp (°C)
4, 5	CCCACTCTGCGTGTTTCTATTG	CAGCTGCTTCGCACATCCTG	2988-3620	633	60
6	AAGCCCTAGAGGATTTGCC	TGAGGGAACAGAAAGGAGC	4896-5397	502	60
7	TAGGACAGGGACCACTCAG	GACTGTCACTAGTCAACAGCC	5676-6071	396	60
8	GGGTCCTGAGCTGAAGTCAC	CCAAGCCTTTGGACATGG	9571- 10030	460	60
9,10	GTCACGTCTCACAGCCATG	GTTATTTCCATGCAGATGG	11361- 12323	963	60
9		GACTCTCTCTGAAGTCTCTG	11978	618	60
10	TGTCCAACTCCTCTCGGTG		12027	296	60
11	CGTGAGGTGTGCAGTGTC	GTGCTCTCGAAGGTTACTG	20623-21140	517	62
12	TTATGCTAAATGCACATTGACC	ACAGGGCAGGGTTCTGTGTG	25033-25695	663	58
13, 14	TTGTTGCTTTGCTCGTCAC	GCGCTGAGATGGTGTTAAAG	29325- 30190	866	60
13		GCC GTG CTG GTA AGT CTT C	29575	251	60
14	GAT GGT GAC GCT AGG CTT G		29882	309	60
15, 16, 17	GGTCCTCAGAGGAAATTAGG	TGAAGGTAGCAGCCATTCC	30839-32222	1394	60
15		TAGCTCCTCGGAAGACTG	31170	362	60
16	TGCATCTCCCCAGCTACG		31447	226	58
18	AGAACCACACCATAACCATC	TGCCTCTGAGCACAAAGC	33370-33971	602	60
19	ACAGGTGTGAGGCACTGTG	AAGTCCTCTGCAGCACGG	37135- 37395	261	64
20	TCAGGAGTTCCAGATCAGC	GCTTACATGAGGCGTTTGG	39624- 40114	491	60
21	TCAACGCTCTGGGAGTCTC	AACTCTGGCTGCAGGACTGG	41007- 41513	507	60
22	TGCCCAGGTGTCACCTCTTC	TGGGAGGGCAGACACAATGC	42461-42891	431	62
23, 24	TCATAACCGAGAACCCGAC	GGCTGGTGAGCATGAACTG	43758-44826	1069	60
23		GGT AAA GGC TGA GGG TGC A	44206	449	60
24	TCC GGG TGC AAG GGG ATG		44269	558	60
25, 26	ACACAGCACGGATAAGGC	TACAGTGGGAGACCATCTGG	44941-46425	1484	60
25		CAGGCCACTCAGACGCAG	45290	350	60
26	CTGTGACCTACTGG CTTC		45973	318	60
27, 28	CTGAGATTGGGACGAGAAG	ATTACCTTGTCTCGCTGTC	47838-48610	773	60
29, 30	ACACACTGGCAGGAACCAC	ATGCTGATGGGTCTCCTGG	50226- 51277	1052	64
29		GACATCTCTCACTGCTGGCTT	50738	513	64
30	CTCTTCACTAGGGCTGTTCTG		50894	384	64
31, 32	TGTCTGCACAAGCCTTTG	AAGAGCCTGCAGTCACCAC	51354-51974	621	64
33	ATTGCCAGAGGACTCCCAGGTC	GGAGAGAGAGGATGTAAGATG	52596- 52879	284	58