

**Appendix 1. Primer sequences used for Complement Factor H gene resequencing.**

Exon	Primer	Sequence (5'→3')	T <sub>m</sub> (°C)	size, bp	ref.
1	1F	TGGGAGTGCAGTGAGAATTG	66.1	330	2
	1R	TCCTGTGAAAAGCATCATTAGC	64.3		
2	2F	CCTGTGACTGTCTAGGCATTTT	66.4	385	2
	2R	GGCAATAGTGATATAATTCAGGCATA	64		
3	3F	TTCACCAATGCTGGGCAGGCT	69.6	852	1
	3R	AAGCAGGTGAAAGTCTTGATTTCT	66.9		
4	4F	AGTCCATGCACCAAGAAGGAGAGA	67.8	808	1
	4R	AGTCCACAGGCAACCTCCCT	68.8		
5	5F	TTTCTCCAATCTTATCCTGAG	64	356	2
	5R	TGCTGATATTCCTTAGAATGAACG	63.5		
6	6F	CCTGATGGAAACAACATTTCTG	65	450	2
	6R	TGAACTTTTCTGGCCCTGTT	65.7		
7	7F	TGTTCAATTTAATGCCATTTTG	62.4	417	2
	7R	TTTCGGCAACTTCGAAAAC	64.7		
8	8F	ACGCATCATGTGATCCACAAGACAT	67.1	976	1
	8R	AGAGCGTAGCCAGGATGGCAGG	69.4		
9	9F	GGGCCAAGAAAAGAGTTGTTCAAGC	67.7	883	1
	9R	ACTCCTTGTTGTGTCCACGTCCTT	68.7		
10	10F	TCTCAGCAAGCCTAACTCAGGGT	57.2	444	1
	10R	TGTCCCAGTGGAAGGGGGCA	59.7		
11	11F	TGAATGCTTATGGTTATCCAGGT	65.1	401	2
	11R	GCTTTGTTCTGCAGGTTTT	66.2		

12	12F	CTTAGAATGGGAAATACTCAGATTG	63.7	234	1
	12R	GGAAGGTAGGTGGCCCATAGGAA	68.6		
13	13F	TCTGATGCCCCCTCTGTATGACCCA	68.6	385	1
	13R	ACAGGCAATGGGAGCCCAAACA	68.9		
14	14F	ACTAGTGGCTGACAATGGAGGGAT	67.8	875	1
	14R	TGGGCCCAGCCATGTTCAAGT	69		
15	15F	TGGTCCACCTCCTGAACTCCT	68.4	453	1
	15R	AGCAACCACCCTGGAATCA	69.5		
16	16F	ATTCAGCGACAGAATACAGGGC	67.3	672	1
	16R	TGAGAAGCACTGGTCCTCCAACA	67.7		
17	17F	CTATGAGAATACAAGCCAAAAGTTC	64.1	448	2
	17R	TTGTTTACACGAAGCACAAGAGA	64.8		
18	18F	GGACCTAGGCACATTAATCAATCAC	66	941	1
	18R	GCGTTTGCTTCTCCCTCCACCA	69.6		
19	19F	ACATTCTTCCCACAATGCCCTTC	67.8	819	1
	19R	ATGAGTAGAGGCAGCTGTGCC	68.4		
20	20F	ACAGCATGTGGGAACTGCCACC	69.2	787	1
	20R	TGCATGTCACCATGCCCACT	69		
21	21F	CAAAATGAACACTAGGTGGAACC	65.6	380	2
	21R	CTGCTATACTCCCCAAAAT	65.1		
22	22F	AGTGCTGTGTTTGCCTTGCCT	68.6	308	1
	22R	ACAGAGATTTTTCCAGCCACGTGAA	66.8		
23	23F	TGTGTGTGTGTTTGTGGTGAGGACA	68.1	975	1
	23R	ACAGTGAGCCTCAGAAGCTGTGGA	68.5		

<sup>1</sup> Primers designed by us for this study.

<sup>2</sup> Abreera-Abeleda MA, et al. Variations in the complement regulatory genes factor H (CFH) and factor H related 5 (CFHR5) are associated with membranoproliferative glomerulonephritis type II (dense deposit disease) J Med Genet. 2006;43:582–589.

All primers are linked to M13 universal primers.

M13 forward GTTTTCCCAGTCACGAC or M13 Reverse AGGAAACAGCTATGACC