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Supplementary Data
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Angiopoietin-like protein 3 (ANGPTL3) deficiency and familial combined hypolipidemia

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ANGPTL3 (1p31.3)

Angptl3 gene (GenBank-NCBI accession no.): NG_028169.1, GI 325053740, ENSG00000132855
Angptl3 mRNA (GenBank-NCBI accession no.): NM_014495.3, GI 452408443, ENST00000371129
ANGPTL3 protein (GenBank-NCBI accession no.): NP_055310.1, GI 7656888, ENSP00000360170, UniPro Q9Y5C1, signal peptide 1-16

Supplementary Table 1 **ANGPTL3 loss of function (LOF) variants**

Exon	cDNA[†]	Type	Pro-protein[†]	Mature protein	Ref.
1	c.50-51 CC > GA	deletion/insertion	p.(Ser17*)	p.(Ser1*)	2, 3, 4, 10
1	c.55delA	frameshift	p.(Ile19Leufs*22)	p.(Ile3Leufs*22)	5
1	c.124G > A	missense	p.(Asp42Asn)	p.(Asp26Asn)	9
1	c.177delC	frameshift	p.(Phe60Leufs*40)	p.(Phe44Leufs*40)	9
1	c.188A > C	missense	p.(Lys63Thr)	p.(Lys47Thr)	1
1	c.247delT	frameshift	p.(Tyr83Metfs*17)	p.(Tyr67Metfs*17)	2
1	c.249T > A	nonsense	p.(Tyr83*)	p.(Tyr67*)	9
1	c.272A > G	missense	p.(Glu91Gly)	p.(Glu75Gly)	1
1	c.280G > T	nonsense	p.(Glu94*)	p.(Glu78*)	8
1	c.286_288delGAA	deletion	p.(Glu96del)	p.(Glu80del)	3, 4
1	c.361_365delAACTC	frameshift	p.(Asn121Lysfs*3)	p.(Asn105Lysfs*3)	4, 9, 10
1	c.362_363insCTCAT	frameshift	p.(Lys123Serfs*8)	p.(Lys107Serfs*8)	4
1	c.363_364delCT	frameshift	p.(Ser122Lysfs*3)	p.(Ser106Lysfs*3)	3
1	c.363_367delCTCAA	frameshift	p.(Asn121Lysfs*3)	p.(Asn105Lysfs*3)	6
1	c.364_367delTCAA	frameshift	p.(Ser122Asnfs*6)	p.(Ser106Asnfs*6)	1, 2
1	c.385G > T	nonsense	p.(Glu129*)	p.(Glu113*)	2, 4
1	c.439_442delAACT	frameshift	p.(Asn147*)	p.(Asn131*)	2, 4, 5, 9, 10
1	c.490C > T	missense	p.(Leu164Phe)	p.(Leu148Phe)	1

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Supplementary Table 1 **ANGPTL3 loss of function (LOF) variants** (continued)

Exon	cDNA†	Type	Pro-protein†	Mature protein	Ref.
IVS1	c.495 + 6T > C	splice-site *	?	?	9, 10
2	c.518A > G	missense	p.(Asn173Ser)	p.(Asn157Ser)	1
2	c.558T > A	nonsense	p.(Tyr186*)	p.(Tyr170*)	9
2	c.572delA	frameshift	p.(Gln191Hisfs*6)	p.(Gln175Hisfs*6)	10
2	c.574C > T	nonsense	p.(Gln192*)	p.(Gln176*)	9
2	c.575delA	frameshift	p.(Gln192Argfs*5)	p.(Gln176Argfs*5)	1, 2, 9
3	c.643delT	frameshift	p.(Ser215Leufs*17)	p.(Ser199Leufs*17)	9
3	c.694delA	frameshift	p.(Asn232Metfs*3)	p.(Asn216Metfs*3)	9, 10
IVS3	c.721 + 2T > C	splice-site*	?	?	10
IVS4	c.835-1G > C	splice-site*	?	?	9
5	c.862C > T	nonsense	p.(Arg288*)	p.(Arg272*)	9
5	c.862_864delCGA	deletion	p.(Arg288del)	p.(Arg272del)	1
5	c.863G > A	missense	p.(Arg288Gln)	p.(Arg272Gln)	1
5	c.874T > C	missense	p.(Ser292Pro)	p.(Ser276Pro)	1
5	c.918delT	frameshift	p.(Phe306Leufs*12)	p.(Phe290Leufs*12)	9
IVS5	c.931 + 2dupT	splice-site*	?	?	10
6	c.1031A > C	missense	p.(Tyr344Ser)	p.(Tyr328Ser)	7
6	c.1041T > G	nonsense	p.(Tyr347*)	p.(Tyr331*)	9
6	c.1123G > A	missense	p.(Glu375Lys)	p.(Glu359Lys)	1
6	c.1147A > T	missense	p.(Thr383Ser)	p.(Thr367Ser)	9
6	c.1167delA	frameshift	p.(Gly390Aspfs*24)	p.(Gly374Aspfs*24)	2
6	c.1190delG	frameshift	p.(Gly397Valfs*17)	p.(Gly381Valfs*17)	10
6	c.1198delG	frameshift	?	?	9
IVS6	c.1198 + 1G > T	spice-site	p.(Gly400Valfs*5)	p.(Gly384Valfs*5)	1, 5
7	c.1211G > A	nonsense	p.(Trp404*)	p.(Trp388*)	9, 10
7	c.1250A > G	missense	p.(Tyr417Cys)	p.(Tyr401Cys)	1
7	c.1263delG	frameshift	p.(Ala422Glnfs*23)	p.(Ala406Glnfs*23)	9
7	c.1329dupT	frameshift	p.(Ile444Tyrfs*17)	p.(Ile428Tyrfs*17)	9, 10
7	c.1330_1333delATAA	frameshift	p.(Ile444Asnfs*6)	p.(Ile428Asnfs*6)	9
7	c.1333_1334insT	frameshift	p.(Lys445Ilefs*16)	p.(Lys429Ilefs*16)	1, 2
7	c.1360_1361delAC	frameshift	p.(Thr454Argfs*6)	p.(Thr438Argfs*6)	9
7	c.1378G > T	nonsense	p.(Glu460*)	p.(Glu444*)	9

Note: † The *ANGPTL3* gene variants were reported according to the Human Genome Variation Society version 15.11, 2016 (http://varnomen.hgvs.org/recommendations/DNA/); ANGPTL3 protein sequence variants according to (http://varnomen.hgvs.org/recommendations/protein/). * From "in silico" analysis: "splice-site broken"

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