Genotypes of patients with combined factor V and VIII deficiency

Gene	Mutation	Location	Type	Genotype	Origin	comments	Reference
LMAN1	Met1Thr*	Exon 1	Initiation codon	Hom	Italy		1,2,3,4,5
LMAN1	nt 23 del G	Exon 1	Frameshift	Hom	Iran		2
LMAN1	nt 31 del G	Exon 1	Frameshift	Hom	Algeria		2
LMAN1	nt 89 ins G*	Exon 1	Frameshift	Hom	Middle Eastern Jewish	Founder effect	1,2,5,6,7
LMAN1	nt 89 ins G*	Exon 1	Frameshift	Hom	Iran		2
LMAN1	nt 89 ins G* nt 912 ins A*	Exon 1 Exon 8	Frameshift Frameshift	Comp het	Iran		2
LMAN1	Trp67Ser	Exon 1	Missense	Hom	Japan		8
LMAN1	Gly114stop	Exon 2	Nonsense	Hom	India		9
LMAN1	nt 422 del C Undefined	Exon 3	Frameshift	Comp het	Japan		1
LMAN1	IVS4+17 del T Arg202stop*	Exon 4 Exon 5	Frameshift Missense	Comp het	Turkey		10
LMAN1	Arg202stop*	Exon 5	Nonsense	Hom	Japan		1,11
LMAN1	Arg202stop*	Exon 5	Nonsense	Hom	Iran		2
LMAN1	Arg202stop*	Exon 5	Nonsense	Hom	Tunis		12
LMAN1	IVS5+1G>T	Intron 5	Splicing	Hom	Italy		2
LMAN1	nt 720 del 16bp	Exon 6	Frameshift	Hom	Venezuela		1
LMAN1	nt 781 del T	Exon 7	Frameshift	Hom	Austria		3
LMAN1	nt 795 del C	Exon 7	Frameshift	Hom	Turkey		5
LMAN1	nt 813 del 72 bp	Exon 7	Frameshift	Hom	India		13
LMAN1	nt 822 G>A*	Exon 7	Splicing	Hom	Iran		2
LMAN1	IVS7+1 G>A	Intron 7	Splicing	Hom	Belgium		3
LMAN1	IVS7+33 ins GGTT Undefined	Intron 7	Splicing	Comp het	USA	Skipping exon 8	3

LMAN1	IVS7-1 G>C Arg456stop*	Intron 7 Exon 11	Splicing Nonsense	Comp het	Thailand		14
LMAN1	nt 841 del A	Exon 8	Frameshift	Hom	Poland		3
LMAN1	Lys302stop*	Exon 8	Nonsense	Hom	Pakistan		2
LMAN1	Lys302stop*	Exon 8	Nonsense	Hom	France		1
LMAN1	nt 912 ins A*	Exon 8	Frameshift	Hom	Iran		2
LMAN1	nt 912 ins A* Arg456stop*	Exon 8 Exon 11	Frameshift Missense	Com het	China		15
LMAN1	Gln317stop Arg456stop*	Exon 8 Exon 11	Nonsense Nonsense	Comp het	China		16
LMAN1	Glu321stop	Exon 9	Nonsense	Hom	Iraq		3
LMAN1	nt 1109 del TC	Exon 9	Frameshift	Hom	USA		1
LMAN 1	Gln380stop nt 1271 del G	Exon 9 Exon 11	Nonsense Splicing	Comp het	Lebanon		17
LMAN1	IVS9+2 T>G	Intron 9	Splicing	Hom	Iran		2
LMAN1	IVS9+2 T>C*	Intron 9	Splicing	Hom	Tunisian Jewish	Founder effect	1,5,6,7,18
LMAN1	nt 1208 ins T	Exon 10	Frameshift	Hom	Italy		2
LMAN1	nt 1214 del 5 bp	Exon 10	Frameshift	Hom	Iran		2
LMAN1	nt 1356 del C	Exon 11	Frameshift	Hom	Iraq		5
LMAN1	Arg456stop*	Exon 11	Nonsense	Hom	China		2
LMAN1	Arg456stop*	Exon 11	Nonsense	Hom	Pakistan		2
LMAM1	Cys475Arg Undefined	Exon 12	Missense	Comp het	Argentina	Italian origin	3
LMAN1	nt 1524 del A	Exon 13	Frameshift	Hom	USA (Armenian)		1
MCFD2	IVS1-1 G>C	Intron 1	Splicing	Hom	Iran		3
MCFD2	IVS2+5 G>A*	Intron 2	Splicing	Hom	Undefined, Italy, India, Serbia,	Different haplotypes Common in India	3,5,9,13,19
MCFD2	IVS3+1 G>A*	Intron 3	Splicing	Hom			19

MCFD2	nt 103 del C	Exon 2	Frameshift	Hom			19
MCFD2	nt 210 del 35 bp	Exon 3	Frameshift	Hom	India	Additional unrelated homozygote	13
MCFD2	D81Y	Exon 3	Missense	Hom	Saudi Arabia	Expression	5
MCFD2	D81H D81H and V100D	Exon 3	Missense	Com het	Tunis		12,20
MCFD2	nt 249 del T	Exon 3	Frameshift	Hom			19
MCFD2	nt 263 del 8 bp	Exon 3	Frameshift	Hom			19
MCFD2	Asp89Ala	Exon 3	Missense	Hom		Expression	3,5
MCFD2	Asp122Val	Exon 4	Missense	Hom	India	Expression	5,13
MCFD2	nt 375 ins GA	Exon 4	Frame shift	Hom	Afro Caribbean		5
MCFD2	Asp129Glu	Exon 4	Missense	Hom		Expression	5,19
MCFD2	Tyr135Asn	Exon 4	Missense	Hom	Poland		21
MCFD2	Ile136Thr*	Exon 4	Missense	Hom	Undefined, Kosovo		3,19
MCFD2	8.4 kb deletion Ser144stop	Promoter and exon 1 Exon 4	Big deletion Nonsense	Comp het	South America	Expression	22

Nucleotide numbers of *LMAN1* are based on the Genebank file X716661 using the A (nt 22) of the ATG initiation methionine as +1.
Nucleotide numbers of *MCFD2* are based on the Genebank file NM_139279 using the A (nt 90) of the ATG initiation methionine as +1.
*A mutation that was identified in more than 1 family.

Mutations causing combined Factor V and VIII deficiency according to their types

LMAN1				MCFD2			
Missense	Nonsense	Splice	Deletion/Insertion	Missense	Nonsense	Splice	Deletion/Insertion
M1T*	G114X	IVS5+1 G>T	nt 23 del G	D81Y	S144X	IVS1-1 G>C	nt 103 del C
W67S	R202X*	nt 822 G>A	nt 31 del G	D81H		IVS2+5 G>A*	nt 210 del 35 bp
C475R	K302X*	IVS7+1 G>A	nt 89 ins G*	V100D		IVS3+1 G>A*	nt 249 del T
	Q317X	IVS7+33 ins GGTT	nt 422 del C	D89A		IVS4+17 del T	nt 263 del 8bp
	E321X	IVS7-1G>C	nt 720 del 16bp	D122V			nt 375 ins GA
	Q380X	IVS9+2 T>G	nt 781 del T	D129E			8.4 Kb deletion
	R456X*	IVS9+2 T>C*	nt795 del C	Y135N			
			nt 813 del 72bp	I136T*			
			nt 841 del A				
			nt 912 ins A*				
			nt 1109 del TC				
			nt 1208 ins T				
			nt 1214 del 5 bp				
			nt1271 del G				
			nt 1356 del C				
			nt 1524 del A				

* Mutations that were identified in more than one family

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