

Table 2: List of *FLNC* variants retained in the cohort of cardiomyopathy patients –DCM, Dilated, HCM, Hypertrophic, RCM, Restrictive and LVNC, Left ventricle non-compaction cardiomyopathy. Columns indicate variant coordinates (genomic, cDNA, and protein levels), GnomAD frequency and allele count, conclusion of prediction sites for pathogenicity of missense variants. Finally, if variants were already published and their ACMG classification.

	Patient	Variant Type	Protein Domain	Exon	Position g.	Position c.	Position p.	GnomAD frequency	GnomAD allele count	GVGD	SIFT	Polyphen	CADD	Conservation	Publication	If YES (ref)	Lab cohort, already found	Conclusion
DCM	1	Fs	ABD	4	g.128477463del	c.711del	p.Glu238Argfs*14	/	/	NA	NA	NA	NA	NA	NO	NA	NO	Classe 4
	2	Fs	ABD	1	g.128470710del	c.19del	p.Tyr7Thrfs*51	/	/	NA	NA	NA	NA	NA	NO	NA	NO	Classe 4
	3	Splice	ABD	2	g.128475629G>T	c.601+1G>T	/	/	/	NA	NA	NA	NA	NA	YES	Ref23	NO	Classe 5
	4	STOP	ROD1	18	g.128483604C>G	c.2784C>G	p.Tyr928*	/	/	NA	NA	NA	NA	NA	NO	NA	NO	Classe 4
	5	Fs	ROD1	21	g.128485111dup	c.3592dup	p.Val1198Glyfs*64	/	/	NA	NA	NA	NA	NA	NO	NA	NO	Classe 4
	6	Fs	ROD1	13	g.128481541_128481547dup	c.2041-2047 dup	p.Ile683Argfs*9	/	/	NA	NA	NA	NA	NA	NO	NA	NO	Classe 4
	7	Splice	ROD1	9	g.128480076G>A	c.1412-1G>A	/	4.10-6	1/ 248519	NA	NA	NA	NA	NA	NO	NA	NO	Classe 4
	8	STOP	ROD2	46	g.128497255C>T	c.7645C>T	p.Gln2549*	/	/	NA	NA	NA	NA	NA	NO	NA	NO	Classe 4
	9	Fs	ROD2	42	g.128494949_128494950del	c.7118_7119del	p.Tyr2373Cysfs*7	/	/	NA	NA	NA	NA	NA	NO	NA	NO	Classe 4
	10	STOP	ROD2	46	g.128497275T>A	c.7665T>A	p.Cys2555*	/	/	NA	NA	NA	NA	NA	NO	NA	NO	Classe 4
HCM	11	MS	ROD1	24	g.128486942G>T	c.4271G>T	p.Gly1424Val	/	/	Deleterious (C65)	Deleterious	Probably damaging (0.988)	32	Highly conserved	NO	NA	NO	Classe 4
	12	MS	ROD1	28	g.128488980C>T	c.4871C>T	p.Ser1624Leu	3.10-5	1/31361	Deleterious (C65)	Deleterious	Possibly damaging (0.884)	31	Highly conserved	YES	Ref.3	NO	Classe 5
	13	MS	ROD1	21	g.128485100C>T	c.3581C>T	p.Ser1194Leu	4.10-6	1/ 249329	Deleterious (C65)	Deleterious	Benin (0.08)	22.9	Highly conserved	NO	NA	NO	Classe 3 VUS Favor pathogenic
	14	MS	ROD2	41	g.128494634G>A	c.6895G>A	p.Gly2299Ser	/	/	Deleterious (C55)	Deleterious	Probably damaging (1.0)	29.7	Highly conserved	NO	NA	NO	Classe 3 VUS Favor pathogenic
	15	MS	ROD2	45	g.128496898G>A	c.7484G>A	p.Arg2495His	2.10-5	6/280872	Class C0	Deleterious	Benin (0.13)	26.8	Highly conserved	NO	NA	NO	Classe 4
	16	MS	ROD2	42	g.128494907T>C	c.7076T>C	p.Ile2359Thr	/	/	Deleterious (C65)	Deleterious	Possibly damaging (0.89)	27	Highly conserved	NO	NA	NO	Classe 3 VUS Favor pathogenic
	17	MS	ROD2	43	g.128495367A>C	c.7250A>C	p.Gln2417Pro	/	/	Deleterious (C65)	Deleterious	Probably damaging (0.95)	28.4	Highly conserved	NO	NA	NO	Classe 3 VUS Favor pathogenic

	18	MS	ROD2	37	g.128492909G>A	c.6032G>A	p.Gly2011Glu	/	/	Deleterious (C65)	Deleterious	Probably damaging (1.0)	27.2	Highly conserved	NO	NA	NO	Classe 3 VUS Favor pathogenic
	19	MS	ROD2	43	g.128495345C>T	c.7228C>T	p.Arg2410Cys	2.10-5	6/249466	Deleterious (C65)	Deleterious	Benin (0.02)	23.2	Highly conserved	NO	NA	NO	Classe 3 VUS Favor pathogenic
	20	MS	ROD2	41	g.128494691C>T	c.6952C>T	p.Arg2318Trp	/	/	Deleterious (C65)	Deleterious	Probably damaging (0.99)	25.2	Highly conserved	YES	Ref19	NO	Classe 4
	21	MS	ROD2	42	g.128494954G>C	c.7123G>C	p.Val2375Leu	/	/	Deleterious (C25)	Deleterious	Probably damaging (0.46)	23.1	Highly conserved	YES	Ref19	NO	Classe 4
	22	MS	ROD2	39	g.128493826G>A	c.6419G>A	p.Arg2140Gln	2.10-5	5/249332	Deleterious (C35)	Deleterious	Probably damaging (0.99)	33	Highly conserved	YES	Ref19,20	NO	Classe 5
	23	MS	ROD2	37	g.128492992G>A	c.6115G>A	p.Gly2039Arg	7.10-6	2/280702	Deleterious (C65)	Deleterious	Probably damaging (1.0)	33	Highly conserved	YES	Ref.20	NO	Classe 4
RCM	24	MS	ROD2	41	g.128494628G>A	c.6889G>A	p.Val2297Met	4.10-6	1/236862	Deleterious (C15)	Deleterious	Probably damaging (0.99)	28.6	Highly conserved	YES	Ref 24	NO	Classe 5
	25	MS	ROD2	41	g.128494632C>T	c.6893C>T	p.Pro2298Leu	/	/	Deleterious (C65)	Deleterious	Probably damaging (0.95)	29.5	Highly conserved	YES	Ref 25	NO	Classe 5
	26	Inframe dup	ROD2	35	g.128491676_128491681dup	c.5836-5841dup	p.Ile1946_Thr1947dup	/	/	/	/	/	/	NA	NO	NA	NO	Classe 4
	27	Inframe del	D	47	g.128498208_128498216del	c.7927_7935del	p.Pro2643_Leu2645del	/	/	/	/	/	/	NA	NO	NA	NO	Classe 4
LVNC	28-LO	MS	ROD1	30	g.128489430T>C	c.4997T>C	p.Ile1666Thr	/	/	Deleterious (C65)	Deleterious	Probably damaging (0.46)	26.6	Highly conserved	NO	NA	NO	Classe 3 VUS Favor pathogenic

GnomAD frequency or allele count: / mean that this variation is not reference in GnomAD, NA : not applicable