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Supplementary Table SV **Carrying status of the *RYR2* and *PLXNB2* variants identified by whole exome sequencing in unexplained recurrent miscarriage tissues.**

Gene name	Case ID	Variant	cDNA change	AAChange	Variant ID	Nhet.	ExAC	gnomAD	SIFT	PPH2	LRT	MutationTaster	CADD	GER
RYR2	79,42	chr1:237765380	c.A4652G	p.N1551S	rs185237690	2/113	0.0045	0.0036	T	P	D	D	23.9	5.53
	.	chr1:237538041	c.409C>T	p.R137W	rs761916230	0/113	1.32E−04	5.58E−05	D	D	D	D	35	5.09
PLXNB2	66,93,113	chr22:50726459	c.G1388A	p.R463Q	rs192965378	3/113	0.0138	0.0107	D	P	N	D	24.1	2.98
	.	chr22:50716877	c.4719C>A	p.D1573E		0/113			T	P	D	D	24.2	1.17

AA, amino acid; B, Benign; D, deleterious; Nhet, number with heterozygous variant; P, possibly damaging; T, tolerated.