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Erratum: Prevalence and Spectrum of Germline *BRCA1* and *BRCA2* Variants of Uncertain Significance in Breast/Ovarian Cancer: Mysterious Signals From the Genome

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Keywords: *BRCA1*, *BRCA2*, breast cancer, genetic testing, ovarian cancer, variants of uncertain significance (VUS)

An Erratum on:

Prevalence and Spectrum of Germline BRCA1 and BRCA2 Variants of Uncertain Significance in Breast/Ovarian Cancer: Mysterious Signals From the Genome
By Fanale D, Fiorino A, Incorvaia L, Dimino A, Filorizzo C, Bono M, Cancelliere D, Calò V, Brando C, Corsini LR, Sciacchitano R, Magrin L, Pivetti A, Pedone E, Madonia G, Cucinella A, Badalamenti G, Russo A and Bazan V (2021). Front. Oncol. 11:682445. doi: 10.3389/fonc.2021.682445

Due to a production error, there was a mistake in **Table 2** as published. Some *BRCA1* variants were incorrectly listed. The correct **Table 2** appears below. The publisher apologizes for this mistake.

The original version of this article has been updated.

TABLE 2 | *BRCA1* gene variants of unclear significance harbored by patients with breast and ovarian cancers.

BRCA1 VUS

Nucleotide change HGVS nomenclature	Amino acid change	Type of VUS	ClinVar classification	ENIGMA/ VarSome	PolyPhen-2/ SIFT	HCI Prior/ Align-GVGD[a]	BC patients	OC patients	ExAC/ GnomAD[b]	pCR
c.3367G>T	p.Asp1123Tyr	MISSENSE	CIP	NYR/VUS	Light/ Damaging	0.02/C0	2	\	0.00002/ 0.00001	OCCR
c.889A>C	p.Met297Leu	MISSENSE	CIP	NYR/VUS	Light/ Tolerated	0.02/C0	1	\	\	\
c.2417C>G	p.Ala806Gly	\	NF	No data	Light/-	0.02/C0	1	\	\	OCCR
c.81-12dupC	\	IVS	NF	No data	\	\	1	\	\	\
c.301+6T>C	\	IVS	VUS	NYR/VUS	\	0.34/\	1	\	0.00002/ 0.00001	BCCR1
c.4063_4065delAAT	p.Asn1355del	In-frame DEL	CIP	NYR/VUS	\	\	1	\	\	\
c.4460A>G	p.Lys1487Arg	MISSENSE	VUS	NYR/VUS	Light/ Tolerated-Damaging	0.02/C0	1	\	\	BCCR2
c.1881C>G	p.Val627=	synonymous	CIP	NYR/LBV	\	0.02/\	1	1	-/0.00003	OCCR
c.2447A>G*	p.His816Arg	MISSENSE	CIP	NYR/VUS	Light/ Tolerated	0.02/C0	1	\	0.00001/ 0.00002	OCCR
c.3952A>G	p.Ile1318Val	MISSENSE	VUS	NYR/VUS	Light/ Tolerated	0.02/C0	1	\	\	OCCR
c.742A>C	p.Thr248Pro	MISSENSE	CIP	NYR/VUS	Light/ Tolerated	0.02/C0	1	\	\	\
c.4185+8_4185+8delG	\	IVS	NF	NF/VUS	\	\	1	\	\	\
c.4054G>A	p.Glu1352Lys	MISSENSE	VUS	NYR/VUS	Light/ Damaging	0.02/C0	1	\	0.00004/ 0.00002	OCCR
c.4739C>T	p.Ser1580Phe	MISSENSE	VUS	NYR/VUS	Light/ Damaging	0.02/C15	1	\	\	BCCR2
c.4009G>C	p.Asp1337His	MISSENSE	VUS	NYR/VUS	Light/ Tolerated	0.02/C0	1	\	\	OCCR
c.2218G>C	p.Val740Leu	MISSENSE	VUS	NYR/VUS	Light/ Tolerated	0.02/C0	1	\	\	OCCR
c.4096+3A>G	\	IVS	VUS	VUS/LPV	\	0.97/\	1	1	\	\
c.4963T>G	p.Ser1655Ala	MISSENSE	Not provided	NYR/LPV	Light/ Damaging	0.03/C0	\	3	\	\
c.4543G>A	p.Gly1515Arg	\	NF	NF/VUS	Light/ Tolerated	0.02/C0	\	1	\	BCCR2
c.1007C>T	p.Thr336Ile	\	NF	NF/VUS	Light/ Damaging	0.02/C0	\	1	\	\
c.1705A>G	p.Asn569Asp	MISSENSE	VUS	NYR/VUS	Light/ Tolerated	0.02/C0	\	1	\	OCCR

**This BRCA1 variant is simultaneously present together with the BRCA2 VUS c.8262T>G (reported in Table 3) in one of probands with BC. Novel variants are reported in bold.*

[a]The Align-GVGD program predicts where the variants in BRCA1 and BRCA2 genes fall in a spectrum ranging from enriched deleterious to enriched neutral. The prediction classes form a spectrum (C0, C15, C25, C35, C45, C55, C65) with C65 most likely to interfere with protein function and C0 least likely. The HCI Prior database, based on Align-GVGD scores, defines four classes of probability of pathogenicity: C0 = 0.03; C15-C25 = 0.29; C35-C55 = 0.66; C65 = 0.81.

[b]The Exome Aggregation Consortium (ExAC) and Genome Aggregation Database (gnomAD) aggregate both exome and genome sequencing data from a wide variety of large-scale sequencing projects, by providing values of allelic frequency.

BC, breast cancer; BCCR, breast cancer cluster region; CIP, conflicting interpretations of pathogenicity; DEL, deletion; HGVS, Human Genome Variant Society; IVS, intronic variants; LBV, likely benign variant; LPV, likely pathogenic variant; NF, not found; NYR, not yet reviewed; OC, ovarian cancer; OCCR, ovarian cancer cluster region; pCR, putative cluster region (defined by Rebbeck et al.); VUS, variant of uncertain significance.