

## Baronciani L, Peake I, Schneppenheim R, et al. Genotypes of European and Iranian patients with type 3 von Willebrand disease enrolled in 3WINTERS-IPS. *Blood Adv.* 2021;5(15):2987-3001.

Page 2987: Author affiliation no. 28 (Flora Peyvandi) was incorrect. The affiliation should be the Department of Pathophysiology and Transplantation, Università degli Studi di Milano, Milan, Italy.

Page 2991: Figure 2 has the following corrections:

- The word "different" was misspelled in the top heading.
- The variant c.7729-7C>T should appear as c.7729 + 7C>T.
- The following variants were not clearly readable: p.S1699F, p.S2469P, and p.C2739Y.

<b>121 European patients</b> (101 different variants in 115 unrelated)	
Del Ex 1_52	Underlined: Splice Variants
Ins Ex 1_28	Italic: Missense Variants
Del Ex 1_5	Blue: Not Previously Reported
Del Ex 1_3 Del Ex 17 Del Ex 4_34	Red: Variants in Both Populations
Del Ex 4_5	<u>c.7887+2T&gt;A</u> c.7770+1G>T
Del Ex 6	c.7730-1G>C
p.W377* p.C372*	<u>с.7729+7С&gt;Т</u> р.N2546Y
p.R365* c.1051del c.2516del	p.Q2544*
p.R324* c.243-1G>C	p.R2535* c.7524_7525del
c.874+2T>C c.2435del p.R1659*	p.\$2505*
p.C275S c.2269_2270del c.4944del p.E2233K c.763 766del c.2157del p.M771V p.Y1542* p.R1853* p.C2212R	<b>p.Q2470*</b> p.S2469P
p.W222* c.2124_2125del c.3770_3771del c.4570del c.5455+2T>C p.C2184S	c.7360_7376dup c.8244_8252del
p.Q198* c.2071_2072delinsG p.C1227R p.R1779* p.S2079* c.533-2A>G c.1931 1945+5del p.C1190R c.5170+10C>T c.6188del	р. <b>R2434</b> * р.С2739Y с.7287+1G>C р.С2724Y
p.L150P c.1729+3A>C p.T1156M c.5170+1G>A c.6182del	p.C2394W <u>c.8155+6T&gt;C</u>
c.414_426del p.W553* c.3379+1G>A c.4470del p.A1716T p.Q1931* p.C2325S c.276del c.1534-3C>A p.W1120* c.3940del p.S1699F p.C1927R c.6917del	
p.Q77* p.C440* p.R924Q c.3839 3849del c.5085_5087del p.C2304Y	<u>c.7082-13G&gt;C</u> <u>c.8155+1G&gt;T</u>
SP p.R34* c.1239dup p.S918* p.V1279I-Q1311*-I1343V-V1360A-F1369Ip.C2283R	<u>с.7082-2А&gt;G</u> р.С2671Y
NH2 D1 D2 - D' D3 A1 A2 A3 D4 C1	С2 С3 С4 С5 С6 СК СООН
p.G74R p.G525E c.2310del c.2965dup p.P1266L-V1279I-Q1311* c.5981_5982insT	p.R2535* p.S2775P
c.311_312del c.1581del c.2310dup p.K968* p.Q1311* c.6227del c.6901 p.Q104* p.Q565* p.C792W c.3101_3103del p.R1336Q p.A1810E p.C2174G	+1G>T c.7618del p.V2540D
p.N166K p.E644* p.Q793* c.3222+2dup p.Q1346* p.R1853*	c.7674dup
c.533-3C>T c.1945+1G>T c.2393_2396dup c.4309del p.E216* c.2017_2018del c.2397_2400dup p.E1598*	
p.E216* c.2017_2018del c.2397_2400dup p.E1598* p.Q218* p.Q706* c.2430_2431delinsA p.R1659*	
p.C275S c.2186+2T>C p.C810* p.E1660*	
c.874+1G>A c.2282-2A>G c.2547-1G>C p.R854W c.3285_3307delinsTCC	
c.3379+2T>C	
c.3406_3407del c.3675-1G>A	
Del Ex 1_5 Del Ex 14_15	Del Ex 35 52
<b>110 Iranian patients</b> (58 different variants in 91 unrelated)	

The corrected Figure 2 is shown below.

Figure 2. Distribution of the 154 different unique variants identified in the 3WINTERS-IPS cohort. A schmatic representation of the pro-VWF polypeptide with the homologous repeated domain structure. Variants identified in the European population are reported at the top; those found in the Iranian population are reported at the bottom. The candidate missense mutations are reported in italics, and the potential splice site mutations are undefined. The 5 variants identified in both populations are reported in red. The variants not previously reported in the EAHAD, HGMD, or Ensembl databases are reported in blue.

Page 2996: In Table 3, the reference number in the "First reported" column for variant NM\_000552.3:c.3379 + 1G>A should be 80, not 81.

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