CORRECTION

Correction to: The value of single-molecule real-time technology in the diagnosis of rare thalassemia variants and analysis of phenotype–genotype correlation

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In the original Table 1 of this article, the names of seventh and eighth columns were misplaced to each other. The name of seventh column should be "Detection range of conventional technology", while the name of eighth column should be "Detection range of SMRT". The corrected table is shown below. The conclusions of the paper are not affected.

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Table 1. Thalassemia variants identified by SMRT and conventional technology

Common name	HGVS name	Clinical significance	Allele frequency[a]	Occurrence[a]	*n* (%)	Detection range of conventional technology	Detection range of SMRT	Verification method	Reference
$-\alpha^{4.2}$	N/A1	Pathogenic	None	Chinese East Asian Indian	130 (26.80)	YES	YES	Gap-PCR/MLPA	[2]
-α3.7	NG_000006.1: g.34164_37967del3804	Pathogenic	None	African, Far East, Indian, Mediterranean	95 (19.59)	YES	YES	Gap-PCR/MLPA	[2]
$--^{SEA}$	NG_000006.1: g.26264_45564del19301	Pathogenic	None	East Asian	94 (19.38)	YES	YES	Gap-PCR/MLPA	[2]
$--^{THAI}$	NC_000016.10: g.149863_183312del	Pathogenic	None	Thai	2 (0.41)	YES	YES	Gap-PCR/MLPA	[2]
$-\alpha^{2.4}$	N/A1	Pathogenic	None	Chinese	1 (0.21)	NO	YES	Gap-PCR/MLPA	[8]
HS-40 deletion	NC_000016.10:g. (47217_113592)_ (113687_143639)del	Pathogenic	None	Chinese	2 (0.41)	YES	NO	MLPA	[9]
HBG1-HBG2	N/A1	Uncertain-Significance	None	Chinese	1 (0.21)	YES	NO	MLPA	This study
Hkαα	N/A1	Uncertain-Significance	None	Chinese	6 (1.24)	NO	YES	Gap-PCR	[12]
$\alpha\alpha\alpha^{anti-4.2}$	N/A1	Uncertain-Significance	None	Chinese	2 (0.41)	NO	YES	Gap-PCR	[10, 11]
$\alpha\alpha\alpha^{anti-3.7}$	N/A1	Uncertain-Significance	None	Chinese	2 (0.41)	NO	YES	Gap-PCR	[10, 11]
CD142(TAA>CAA)	*HBA2:c.427T>C*	Pathogenic	14/248854, GnomAD_exome	Arabian Cambodian Chinese Greek Indian Indonesian Laotian Malasian Sicilian Vietnamese	18 (3.71)	YES	YES	RDB/Sanger	[2]
CD125(CTG>CCG)	*HBA2:c.377T>C*	Pathogenic	1/136864, GnomAD	Chinese	3 (0.62)	YES	YES	RDB/Sanger	[2]
CD122(CAC>CAG)	*HBA2:c.369C>G*	Uncertain-Significance	19/116218, ExAC	Chinese Laotian	2 (0.41)	YES	YES	RDB/Sanger	[2]
CD11(AAG>CAG)	HBA1:c.34A>C	Uncertain-Significance	19/116218, ExAC	Chinese	1 (0.21)	NO	YES	Sanger	[13]
CD16(AAG>AAC)	*HBA1:c.51G>C*	Uncertain-Significance	None	Chinese Pakistani	1 (0.21)	NO	YES	Sanger	[14]
CD27(AAG>AAT)	*HBA1*:c.84G>T	Uncertain-Significance	None	Chinese	2 (0.41)	NO	YES	Sanger	[15]
CD6(GAC>TAC)	*HBA1*:c.19G>T	Uncertain-Significance	None	Vietnamese	1 (0.21)	NO	YES	Sanger	[16]

Table 1. continued

Common name	HGVS name	Clinical significance	Allele frequency[a]	Occurrence[a]	*n* (%)	Detection range of conventional technology	Detection range of SMRT	Verification method	Reference
CD18(GGC>CGC)	*HBA1*:c.55G>C	Uncertain-Significance	2/138328, GnomAD	Chinese Indian Saudi Arabian	4 (0.82)	NO	YES	Sanger	[17]
Init CD(ATG>A-G)	*HBA2*:c.2delT	Pathogenic	None	Vietnamese	1 (0.21)	NO	YES	Sanger	[18]
Init CD(ATG>ACG)	*HBA2*:c.2T>C	Pathogenic	0/654, ALFA	Italian	1 (0.21)	NO	YES	Sanger	[19]
CD17(GTC>TTC)	*HBA2*:c.52G>T	Uncertain-Significance	None	Chinese	1 (0.21)	NO	YES	Sanger	[20]
CD30(GAG>CAG)	*HBA2*:c.91G>C	Uncertain-Significance	1/264690, TOPMED	Chinese	3 (0.62)	NO	YES	Sanger	[21]
-22 C>T	*HBA2*:c.-59C>T	Pathogenic-Likely-Pathogenic	None	Nedlands	1 (0.21)	NO	YES	Sanger	[22]
CD85(GAC>AAC)	*HBA2:c.256G>A*	Uncertain-Significance	None	English	1 (0.21)	NO	YES	Sanger	[23]
CD41/42(-TTCT)	*HBB*:c.126_129delCTTT	Pathogenic	7/140174, GnomAD	Chinese 41.84% English 4.35% Indonesian 1.69% Japanese 5.99% Korean 4.17% Malaysian 26.32% Pakistani 6.7% Punjabi 13.22% Singapore 37.59% Taiwanese 30.63% Thai 37.24%	22 (4.54)	YES	YES	RDB/Sanger	[2]
CD17(AAG>TAG)	*HBB*:c.52A>T	Pathogenic	3/140268, GnomAD	Chinese 14.1% Indonesian 1.69% Japanese 0.32% Korean 16.67% Malaysian 5.26% Singapore 9.02% Taiwanese 8.13% Thai 18.56%	15 (3.09)	YES	YES	RDB/Sanger	[2]
-28(A>G)	*HBB*:c.-78A>G	Pathogenic-Likely-Pathogenic	1/140226, GnomAD	Chinese 12.31% Japanese 0.32% Malaysian 6.43% Taiwanese 9.38% Thai 6.83%	10 (2.06)	YES	YES	RDB/Sanger	[2]
CD26(GAG>AAG)	*HBB*:c.79G>A	Pathogenic	9/140272, GnomAD	Thai 0.12%	5 (1.03)	YES	YES	RDB/Sanger	[2]
CD71/72(+A)	*HBB*:c.216_217insA	Pathogenic	2/251430, GnomAD_exome	Chinese East Asian	3 (0.62)	YES	YES	RDB/Sanger	[2]

Table 1. continued

Common name	HGVS name	Clinical significance	Allele frequency[a]	Occurrence[a]	*n* (%)	Detection range of conventional technology	Detection range of SMRT	Verification method	Reference
IVS-II-654(C>T)	*HBB*:c.316-197C>T	Pathogenic	7/140170, GnomAD	Chinese 21.37% Indonesian 11.86% Japanese 11.99% Malaysian 10.53% Russian 1.52% Singapore 25.56% Taiwanese 46.25% Thai 5.13%	2 (0.41)	YES	YES	RDB/Sanger	[2]
CD14/15(+G)	HBB:c.45dupG	Pathogenic	1/251224, GnomAD_exome	Chinese Thai 0.12%	1 (0.21)	YES	YES	RDB/Sanger	[2]
-29(A>G)	*HBB*:c.-79A>G	Pathogenic	127/140260, GnomAD	Algerian 3.8% Black 59.38% Chinese 2.37% Malaysian 0.58% Taiwanese 0.63%	1 (0.21)	YES	YES	RDB/Sanger	[2]
CD27/28(+C)	*HBB*:c.84_85insC	Pathogenic	1/264690, TOPMED	Chinese 0.59% Singapore 0.75% Taiwanese 2.5% Thai 0.24%	1 (0.21)	YES	YES	RDB/Sanger	[2]
IVS-I-5(G>C)	*HBB*:c.92+5G>C	Pathogenic	1/140258, GnomAD	Frequent in Asian Indian, UAE, and East Asian populations	1 (0.21)	YES	YES	RDB/Sanger	[2]
-50(G>A)	*HBB*:c.-100G>A	Uncertain-Significance	2/140260, GnomAD	Chinese	1 (0.21)	NO	YES	Sanger	[24]
-86 (C>G)	*HBB*:c.-136C>G	Pathogenic	0/78698, GnomAD	Lebanese, Thai 0.24%	1 (0.21)	NO	YES	Sanger	[25]
IVS-II-5(G>C)	*HBB*:c.315+5G>C	Pathogenic	1/140204, GnomAD	Chinese 0.15%	10 (2.06)	NO	YES	Sanger	[26]
CD126 (GTG>GGG)	*HBB*:c.380T>G	Pathogenic	1/140228, GnomAD	German Italian Thai	1 (0.21)	NO	YES	Sanger	[27]
-31(A>C)	*HBB*:c.-81A>C	Pathogenic	1/264690, TOPMED	Italian Chinese	1 (0.21)	NO	YES	Sanger	[22]
CD30 (A>G)	*HBB*:c.91A>G	Likely-Pathogenic	None	Sephardic Jewish	5 (1.03)	NO	YES	Sanger	[28]
CD56 (GGC>GAC)	*HBB*:c.170G>A	Likely-Benign	5/251448, GnomAD_exome	Found in Thai, Indonesian, Black, and Chinese families	5 (1.03)	NO	YES	Sanger	[29]
CD 64 (GGC>AGC)	*HBB*:c.193G>A	Likely-Benign	None	Chinese	1 (0.21)	NO	YES	Sanger	[30]

Table 1. continued

Common name	HGVS name	Clinical significance	Allele frequency[a]	Occurrence[a]	*n* (%)	Detection range of conventional technology	Detection range of SMRT	Verification method	Reference
CD77 (CAC>TAC)	*HBB*:c.232C>T	Likely-Benign	1/251428, GnomAD_exom	Caucasian Indonesian Japanese Swedish	1 (0.21)	NO	YES	Sanger	[31]
-198A>G	*HBB*:c.-248A>G	Uncertain-Significance	None	This study	3 (0.62)	NO	YES	Sanger	This study
CD113(GTG>GAG)	*HBB*:c.341T>A	Pathogenic	2/140270, GnomAD	American Chinese	14 (2.89)	NO	YES	Sanger	[32]
CD143(CAC>CGC)	*HBB*:c.431A>G	Likely-Pathogenic	1/251362, GnomAD_exome	American Italian	1 (0.21)	NO	YES	Sanger	[33]
IVS- II-806 (G>C)	*HBB*:c.316-45G>C	Benign-Likely-Benign	34/140174, GnomAD	Chinese	3 (0.62)	NO	YES	Sanger	This study
IVS- II-672 (A>C)	*HBB*:c.316-179A>C	Benign-Likely-Benign	None	Chinese	1 (0.21)	NO	YES	Sanger	This study
IVS -II-308 (-A)	*HBB*:c.315+308delA	Benign-Likely-Benign	None	Chinese	1 (0.21)	NO	YES	Sanger	This study
Total					485 (100)				

Gap-PCR Gap- polymerase chain reaction, *MLPA* multiple ligation probe amplification technology, *RDB* reverse dot blot.
[a]Data come from HbVar (https://globin.bx.psu.edu/hbvar/hbvar.html), genomAD (https://gnomad.broadinstitute.org/) and dbSNP (https://www.ncbi.nlm.nih.gov/snp/).