Names for MNS (ISBT 002) Blood Group Alleles

Intro

General description: The MNS blood group system consists of 48 antigens carried on glycophorin A (GPA), glycophorin B (GPB) or on hybrids of these glycophorins. These proteins are single pass type I membrane glycoproteins that are heavily O-glycosylated. GPA carries an N-glycan. GPA consists of 150 amino acids, GPB of 72 amino acids and both have a leader sequence of 19 amino acids that is cleaved from the membrane bound protein. The hybrid proteins vary in length based on their composition but also have a 19 amino acid leader sequence. GPA is encoded by *GYPA*, GPB by *GYPB*. A third gene in this family, *GYPE*, normally does not encode detectable protein at the red cell surface but the gene has been shown to be involved in some gene rearrangements that encode cell-surface borne hybrid proteins. As described above, the proteins are encoded by *GYPA* or *GYPB*, or MNS if analysis is to predict a blood group antigen.

	GYPA	*GYPB*	*GYPE*
Gene name:			
Number of exons:	7	5 plus 1 pseudoexon	4 plus 2 pseudoexons
Initiation codon:	Exon 2	Exon 2	Exon 2
Stop codon:	Exon 7	Exon 6‡	Exon 6‡
Entrez Gene ID:	2993	2994	2996
LRG sequences:			
(genomic)	NG_007470.3	NG_007483.2	NG_009173.1
(transcript)	NM_002099.5	NM_002100.5	NM_002102.3

‡ Exon numbering accounts for the presence of pseudoexons in *GYPB* and *GYPE*. Thus, *GYPB* pseudoexon 3 corresponds to the *GYPA* exon 3 sequence. This *GYPB* pseudoexon is involved in many gene rearrangements encoding hybrid glycophorins in this blood group system. Similarly, *GYPE* pseudoexons 3 and 4 correspond to *GYPA* exon 3 and 4 sequences. These *GYPE* pseudoexons are involved in gene rearrangements encoding hybrids.

Ref. allele (*GYPA*): *GYPA*01*
Acceptable: *GYPA*M* or *M* if inferred by hemagglutination

Ref. allele (*GYPB*): *GYPB*04*
Acceptable: *GYPB*s* or *s* if inferred by hemagglutination

Commentary regarding naming of unexpressed *GYPA* and *GYPB* alleles. Causal polymorphism for GPA (MNS28, En^a) negativity and GPB (MNS5, U) negativity is heterogenous. In both cases either gene mutations, or alternatively (almost) full gene deletions may be observed. We therefore chose to use *GYPA*01N*, or *02N* to name unexpressed *GYPA* alleles with genomic sequences present. For (almost) full *GYPA* gene deletions we choose *GYPA*28N*. With respect to GPB, *GYPB*03N* and *GYPB*04N* alleles are considered to present (unexpressed) alleles, whereas *GYPB*05N* alleles represent (almost) full gene deletions.

Table 1. MNS alleles with single nucleotide polymorphisms that generate blood group antigens.
A. *GYPA* : Reference allele *MNS*01* encodes M, Ena, ENKT, ENEP, ENEH, ENAV, ENDA, ENEV.
Note: In most cases, the nucleotide changes also can occur on an N allele; these nucleotide changes are not given.

Phenotype	Allele name	Nucleotide change	EI	Pred. amino acid change	(Reference No.) PMID	Accession number	rs number	Comment
MNS:1 or M+	*GYPA*01* or *GYPA*M*					NG_007470.3 AJ309841.1 AY297544.1 LC495309.1		
MNS:2 or N+	*GYPA*02* or *GYPA*N*	c.59C>T c.71G>A c.72T>G	2	p.Ser20Leu p.Gly24Glu	PMID: 3456608	AC107023.5 AY297543.1 LC495311.1	rs7682260 rs7687256 rs7658293	BAC DNA
MNS:1,-2,8† or M^c+	*GYPA*08* or *GYP*Mc*	c.71G>A c.72T>G	2	p.Gly24Glu	PMID: 6166001		rs7687256 rs7658293	Most anti-M but only few anti-N react with Mc+ RBCs.
MNS:7,9,–40 or Vw+	*GYPA*09* or *GYPA*Vw*	c.140C>T	3	p.Thr47Met	PMID: 6697986	M81826.1 MT361771.1	rs144802902	
MNS:7,9,–40 or Vw+	*GYPA*09.02* *or GYPA*Vw.02*	*c.59C>T* *c.71G>A* *c.72T>G* *c.140C>T*	3	p.Thr47Met	PMID: 6697986	MT361770.1	rs144802902	formerly partially known as *GYPA*Vw.01* and vice versa
MNS:−1,−2,11,32 or M^g+DANE+	*GYPA*11* or *GYPA*Mg*	c.68C>A	2	p.Thr23Asn	PMID: 6166001		rs753693249	
MNS:12 or Vr+	*GYPA*12* or *GYPA*Vr*	c.197C>A	3	p.Ser66Tyr	PMID: 10729812	AY950613.1	rs56077914	
MNS:14 or Mt(a+)	*GYPA*14* or *GYPA*Mta*	c.230C>T	3	p.Thr77Ile	PMID: 10729812	AY950614.1	rs56172553	
MNS:16 or Ri(a+)	*GYPA*16* or *GYPA*Ria*	c.226G>A	3	p.Glu76Lys	Abstract (5)	AY950615.1	rs774808285	

Phenotype	Allele name	Nucleotide change	EI	Pred. amino acid change	(Reference No.) PMID	Accession number	rs number	Comment
MNS:18 or Ny(a+)	*GYPA*18* or *GYP*Nya*	c.138T>A	3	p.Asp46Glu	PMID: 10827258		rs754762997	
MNS:7,19,–40 or Hut+	*GYPA*19* or *GYPA*Hut*	c.140C>A	3	p.Thr47Lys	PMID: 6697986		rs144802902	
MNS:31 or Or+	*GYPA*31* or *GYPA*Or*	c.148C>T	3	p.Arg50Trp	Abstract (7)	KR710187.1	rs375241297	
MNS:37 or ERIK+	*GYPA*37* or *GYPA*ERIK*	c.232G>A	4	p.Gly78Arg	PMID: 7690638 Abstract (9)	U00177.1	rs1800582	See also *GYP*EBH* in hybrid table
MNS:38 or Os(a+)	*GYPA*38* or *GYPA*Osa*	c.217C>T	3	p.Pro73Ser	PMID: 10827258		rs753301274	
MNS:–39,41 or HAG+	*GYPA*41* or *GYPA*HAG*	c.250G>C	4	p.Ala84Pro	PMID: 10354388		rs755106250	
MNS:–42,43 or MARS+	*GYPA*43* or *GYPA*MARS*	c.244C>A	4	p.Gln82Lys	Abstract (11)		rs1204136459	
MNS:–45 or ENEV-	*GYPA*–45*	c.242T>G	4	p.Val81Gly	Abstract (12)		rs778091564	
MNS:46 or MNTD+	*GYPA*46* or *GYPA*MNTD*	c.107C>G	2	p.Thr36Arg	Abstract (13)		rs1731125550	
MNS:47 or SARA+	*GYPA*47* or *GYPA*SARA*	c.240G>T	4	p.Arg80Ser	PMID: 25523184 Abstract (5)	KF973190.1	rs771906843	
MNS:50 or SUMI+	*GYPA*50* or *GYPA*SUMI*	c.91A>C	2	p.Thr31Pro	PMID: 32358867 PMID: 1421409	LC495310.1 AH002821.2		
GYPA Weak								
MNS:w1 or M+^{w}	*GYPA*01W.01*	c.305G>A	5	p.Gly102Asp	Abstract (74)		rs574776481	

Table 2. MNS alleles with single nucleotide polymorphisms that generate blood group antigens.
B. *GYPB*: Reference allele *GYPB*04* encodes 'N', s, JENU, and U antigens.
Note: Expression of the U antigen involves GPB and another protein, probably RhAG. The amino-terminal of GPB, ^{20}LSTTE^{24}, is responsible for 'N' (MNS30).

Phenotype	Allele name	Nucleotide change	EI	Pred. amino acid change	(Reference No.) PMID	Accession number	rs number	Comment
MNS:4 or s+	*GYPB*04* or *GYPB*s*					NG_007483.2	Abstract (7)	
MNS:3 or S+	*GYPB*03* *or GYPB*S*	c.143C>T	4	p.Thr48Met	PMID: 3477806 Abstract (9)	LN880516.1	rs7683365	See also *GYP*EBH* in hybrid table
MNS:21or M^{v}+	*GYPB*21* *or GYPB*Mv*	c.65C>G	2	p.Thr22Ser	PMID: 11239234	not available	rs199937833	
MNS:23 or s^{D}+	*GYPB*23* or *GYPB*sD*	c.173C>G	4	p.Pro58Arg	PMID: 11239234 PMID: 36062546	OK345035	rs374811215	
MNS:24 or Mit+	*GYPB*24* *or GYPB*Mit*	c.161G>A	4	p.Arg54His	PMID: 11239234 Abstract (11)	not available	rs370332485	GPB.Mit affects expression of S abstract(19) and s antigens abstract(20)
MNS:3 (S+ partial)	*GYPB*03.02*	c.143C>T c.166A>T	4	p.Thr48Met p.Thr56Ser	PMID: 30523644	LC333395	rs7683365 rs1374399511	
MNS:w3 or S+^{w}	*GYPB*03.03*	c.56C>T c.143C>T	2 4	p.Ala19Val p.Thr48Met	PMID: 30927367	MK288019	rs371480888 rs7683365	
MNS:3 (S+ partial)	*GYPB*03.04*	c.130A>T c.143C>T	2 4	p.Thr44Ser p.Thr48Met	Abstract (23)		rs752857317 rs7683365	
MNS:w3 or S+^{w}	*GYPB*03.05*	c.137–6T>G c.143C>T	i3 4	Alternative splicing p.Thr48Met	Abstract (24)		rs190746696 rs7683365	
MNS:3 or S+	*GYPB*03.06*	c.143C>T c.270+3G>A	4 i5	p.Thr48Met	Abstract (25)		rs7683365 rs189650740	
MNS:3 or S+	*GYPB*03.07*	c.143C>T c.145G>A	4 4	p.Thr48Met p.Gly49Arg	Abstract (26)		rs7683365 rs1275078171	
MNS:4 (s+ partial)	*GYPB*04.02*	c.164T>G	4	p.Phe55Cys	Abstract (27)		rs751780610	
MNS:w4,w5 or s+^{w}, U+^{w}	*GYPB*04.03*	c.234C>T	5	p.Ile78=	Abstract (28), (29)		rs372113714	

Phenotype	Allele name	Nucleotide change	EI	Pred. amino acid change	(Reference No.) PMID	Accession number	rs number	Comment
MNS:4,5 (s+, U+) altered GPB	*GYPB*04.04*	c.260G>A	5	p.Arg87Gln	Abstract (30)		rs112711627	
MNS:4 or s+	*GYPB*04.05*	c.144G>A	4	p.Thr48=	Abstract (31)		rs369684356	
MNS:4,5 (s+, U+) altered U/GPB	*GYPB*04.06*	c.251G>C	5	p.Ser84Thr	Abstract (32)		rs1132783	
MNS:4 or s+	*GYPB*04.07*	c.160C>T	4	p.Arg54Cys	Not yet available	OR247747	rs757106926	
MNS:4,6 or s+, He+	*GYPB*06.01*	c.59T>G c.60A>G c.67A>T c.71A>G c.72G>T	2	p.Leu20Trp p.Thr23Ser p.Glu24Gly	PMID: 6723663 PMID: 14641872	not available	rs189622883 rs185195348 rs189456867 rs775580417 rs772460739	
MNS:3,6 or S+, He+	*GYPB*06.02*	c.59T>G c.60A>G c.67A>T c.71A>G c.72G>T c.143C>T	2 4	p.Leu20Trp p.Thr23Ser p.Glu24Gly p.Thr48Met	PMID: 6723663 PMID: 14641872	not available	rs189622883 rs185195348 rs189456867 rs775580417 rs772460739 rs7683365	
MNS:–3,w5 or S–U+^{var}	*GYPB*03N.01* *or GYPB*NY*	c.143C>T c.208G>T c.230C>T c.251C>G	4 5	p.Thr48Met p.Val70Leu p.Thr77Met p.Thr84Ser Alternative splicing	PMID: 14641872		rs7683365 rs147719799 rs79492560	
MNS:–3,w5 or S–U+^{var}	*GYPB*03N.02* or *GYP*He(NY)*	c.59T>G c.60A>G c.67A>T c.71A> c.72G>T c.143C> c.208G>T c.230C>T c.251C>G	2 4 5	p.Leu20Trp p.Thr23Ser p.Glu24Gly p.Thr48Metp.Val70Leu p.Thr77Met Alternative splicing	PMID: 14641872		rs189622883 rs185195348 rs189456867 rs775580417 rs772460739 rs7683365 rs147719799 rs79492560	

Phenotype	Allele name	Nucleotide change	EI	Pred. amino acid change	(Reference No.) PMID	Accession number	rs number	Comment
MNS:–3,w5 or S–U+^{var}	*GYPB*03N.03* or *GYPB*P2*	143C>T c.270+5G>T	4 i5	p.Thr48Met Alternative splicing	PMID: 14641872	U05254 U05255	rs7683365 rs139511876	
MNS:–3,w5 or S–U+^{var}	*GYPB*03N.04* or *GYP*He(P2)*	c.59T>G c.60A>G c.67A>T c.71A>G c.72G>T c.143C>T c.270+5G>T	2 4 i5	p.Leu20Trp p.Thr23Ser p.Glu24Gly p.Thr48Met Alternative splicing	PMID: 14641872 PMID: 8144668	U05254 U05255	rs189622883 rs185195348 rs189456867 rs775580417 rs772460739 rs7683365 rs139511876	
MNS:–3,w5 or S–U+^{var}	*GYPB*03N.05*	c.59T>G c.60A>G c.67A>T c.71A>G c.72G>T c.87T>C c.96T>C c.102A>G c.143C>T c.230C>T c.270+5G>T	2 4 5 i5	p.Leu20Trp p.Thr23Ser p.Glu24Gly p.Thr29= p.Ser32= p.Ser34= p.Thr48Met p.Thr77Met Alternative splicing	PMID: 33733475	MK208314	rs189622883 rs185195348 rs189456867 rs775580417 rs772460739 rs184895867 rs181496233 rs138856510 rs7683365 rs79492560 rs139511876	
MNS:–3,w5 or S–U+^{var}	*GYPB*03N.06*	c.143C>T c.208G>T c.230C>T c.270+5G>T	4 5 i5	p.Thr48Met p.Val70Leu p.Thr77Met Alternative splicing	Abstract (29)		rs7683365 rs147719799 rs79492560 rs139511876	
MNS:–3,w5 or S–U+^{var}	*GYPB*03N.07*	c.137–8C>T c.143C>T c.270+5G>T	i3 4 i5	p.Thr48Met Alternative splicing	Abstract (37)		rs183176514 rs7683365 rs139511876	

Phenotype	Allele name	Nucleotide change	EI	Pred. amino acid change	(Reference No.) PMID	Accession number	rs number	Comment
MNS:–3,–5	*GYPB*03N.08*	c.143C>T c.218G>A	4 5	p.Thr48Met p.Gly73Asp	Abstract: (26)		rs7683365 rs762860304	*GYPB*03* c.218G>A was described as, "We identified a G145A(Gly49Arg) mutation in the *GYPB*03* primer binding-site and two donors with a presumably new *GYPB*03* null-allele with a G218A(Gly73Asp) substitution (1Ss, 2ss)."
MNS:–4,w5 or s–U+^{var}	*GYPB*04N.01*	c.270+5G>A	i5	Alternative splicing	Abstract: (38)		rs139511876	
MNS:–4,–5 or s–U–	*GYPB*04N.02*	c.37+4_8delAGTGA	i1	Alternative splicing	PMID: 35441363 PMID: 2823938	OK631534	rs139511876	*GYPB* c.37+4_8delAGTGA was described as U-negative in the articles.
MNS:–4,w5 or s–U+^{var}	*GYPB*04N.03*	c.227G>A	5	p.Gly76Glu Alternative splicing	Abstract (30)		rs112711627	
MNS:–4,–5 or s–U–	*GYPB*04N.04*	*c.17_26delTCTTTGTATT*	1	p.Ile6Asnfs*7	Abstract (24)			*GYPB* c.17_26del was described as s-negative in the abstract
MNS:–3,–4,–5 or S–s–U–	*GYPB*04N.05*	*GYPB* Exon 4 deletion		GPB absent	Abstract (72)			
MNS:–4, or s–	*GYPB*04N.06*	*GYPB* transcript 83bp insertion c.37_38insN *GYPB* Exon 4 deletion		p.Val15Ter	Abstract (73)			cDNA analysis study showed 83 base pair insertion at the 3'-end of exon 1
	*GYPB*04N.07*							removed
	*GYPB*04N.08*							removed
MNS:–4 or S-s-U-	*GYPB*04N.09*	c.248dupA	i5	p.Tyr83*	PMID: 37021677	OP783352		

Phenotype	Allele name	Nucleotide change	E I	Pred. amino acid change	(Reference No.) PMID	Accession number	rs number	Comment
Table 3. MNS alleles created by gene rearrangement events within the *GYP* gene family. Parent allele is *GYPA*.								
GYP(A-B-A) and *GYP(A-E-A)* hybrid series								
MNS:15 or St(a+)	*GYP*101.01 or GYP*Zan*	*GYPA*: del exon 3		GPA: p.Asp46_Thr77del	PMID: 8444872	L07103 L07251 L07253		GYP(A1-2-BΨ3-A4-7) Trypsin-resistant M antigen
MNS:15 or St(a+)	*GYP*101.02 or GYP*EBH*	*GYPA*: c.232G>A *GYPA*: del exon 3		GPA: p.Asp46_Thr77del	PMID: 7690638 Abstract (9)	n.a.		Nucleotide change at 232 destabilises normal splicing. St^a is encoded by a *GYPA* transcript that lacks exon 3. Full-length transcript encodes ERIK (MNS37; see table 1).
MNS:15 or St(a+)	*GYP*101.03 or GYP*Mar*	*GYPA* del exon 3		GPA: p.Asp46_Thr77del	PMID: 10862083	AF239850		*GYP(A1-2-EΨ3-A4-7)* Trypsin-resistant M antigen
MNS:6,15 or He+,St(a+)	*GYP*101.04 or GYP*Cal*	*GYPA*: c.59C>G *GYPA: c.60A>G* *GYPA: c.67A>T* *GYPA: del exon 3*		GPA: p.Ser20Trp GPA: p.Thr23Ser GPA: p.Asp46_Thr77del	PMID: 8193374			*GYP(A1-2-BΨ3-A4-7)*

Phenotype	Allele name	Nucleotide change	E I	Pred. amino acid change	(Reference No.) PMID	Accession number	rs number	Comment
GYP(A-B) hybrid series								
MNS:−3,4,20,34 or S−s+, Hil+, MINY+	*GYP*201.01 or GYP*Hil*	*GYP(A1-232–B233-366)*		*GP(A1-77-B78-123)*	PMID: 2792104 PMID: 2015404	LN880513.1		*GYP(A1-3-B4-6)*
MNS:3,−4,32, 33,34 or S+s−, TSEN+, MINY+	*GYP*202.01 or GYP*JL*	*GYP(A1-232–B233-366)* c.239C>T		GP(A1-77-B78-123) p.Thr80Met	PMID: 2015404			*GYP(A1-3-B4-6)*
MNS:−1,2,−3, −4,−5,36 or M−N+S−s−U−, SAT+	*GYP*203.01 or GYP*SAT*	*GYP(A1-271–B272-369)* c.59C>T c.71G>A c.72T>G		GYPA(1-90-B91-123) p.Ser20Leu p.Gly24Glu	PMID: 7718894			breakpoint in intron 4 not defined Previously *GYP*TK*
GYP(A-B-A) hybrid series								
	*GYP*Vw*			Numbers have not been assigned to these alleles in this series and they are included in table1. It has been proposed that they are derived from hybrid genes but the crossover points have not been determined experimentally.				
	*GYP*Hut*							
	*GYP*Mc*							
	*GYP*Mg*							
MNS:10,32 or Mur+, DANE+	*GYP*301.01* or *GYP*Dane*	*GYP(A1-159–BΨ160-175–A176-447)* c.160G>C c.165-167delCAC c.170C>A c.172G>C c.173A>T c.177C>A c.191T>A		GP(A1-52-B53-58-A59-149) p.52-TYPAHTANEV-61 p.Ile64Asn	PMID: 1421409	M87285	rs759961576 rs779902540 rs748831665 rs772722765 rs769622582 rs45480892 rs754816038	Also expresses Mur antigen. Not known if the allele encodes ENDA as person homozygous for *GYP*301.01* has not been found.

Phenotype	Allele name	Nucleotide change	EI	Pred. amino acid change	(Reference No.) PMID	Accession number	rs number	Comment
MNS:10,32,–44 or Mur+, DANE+, ENDA–	*GYP*301.02* or *GYP*Dane*	*GYP(A1-159–BΨ160-175–A176-447)* ; c.160G>C c.165-167delCAC c.170C>A c.172G>C c.173A>T c.177C>A		GP(A1-52-B53-58-A59-149) p.52-TYPAHTANEV-61	PMID: 18764826		rs759961576 rs779902540 rs748831665 rs772722765 rs769622582 rs45480892	Also expresses Mur antigen; does not express ENDA.
MNS:26,27 or Hop+,Nob+	*GYP*302.01* or *GYP*Joh*	*GYP(A1-202–BΨ203–A204-450)* c.203G>C		GPA(1-67)-B(68)-GPA(69-150) p.Arg68Thr	PMID: 2590469		rs45518635	Gene conversion in exon 3 replaces *GYPA* nucleotide 203 with the corresponding nucleotide from *GYPBΨ3*. This is the minimum but the breakpoint is not defined.
MNS:–26,27,−29 or Hop–,Nob+, ENKT−	*GYP*302.02* or *GYP*Nob*	*GYP(A1-202–BΨ203-212–A213-450)* c.203G>C c.212A>C		GPA(1-67)-B(68-72)-GPA(73-150) p.Arg68Thr p.Tyr71Ser	PMID: 2439339		rs45518635 rs45495595	Gene conversion in exon 3 replaces *GYPA* nucleotides (203-212) with corresponding nucleotides from *GYPBΨ3*. This is the minimum but the breakpoint is not defined.
MNS:20, –34 or Hil+, MINY–	*GYP*303* or *GYP*KI*	*GYP(A1-238–B239-242–A243-450)* c.239G>C c.242T>G		GPA(1-79)-B(80-81)-GPA(82-150) p.Arg80Thr p.Val81Gly	Abstract (51)		rs775395980 rs778091564	Gene conversion in exon 4 replaces *GYPA* nucleotides (239-242) with corresponding nucleotides from *GYPB*. This is the minimum but the breakpoint is not defined.
MNS:15 or St(a+)	*GYP*304*	*GYP(A1-177-BΨ178-232-A233-450)* Exon 3 is an ABΨ3 hybrid with inactive splice site		GP(A1-45)-(A-78-150)	Abstract (52)			GYP(A-BΨ-A) This abstract also reports Sta+ GYPA with 3' of Exon 3 deleted and a GP(E-A) – parent gene of Exon 1 not defined

Phenotype	Allele name	Nucleotide change	EI	Pred. amino acid change	(Reference No.) PMID	Accession number	rs number	Comment
Table 4. MNS alleles created by gene rearrangement events within the *GYP* gene family Parent allele is *GYPB*.								
GYP(B-A) hybrid series								
MNS:15 or St(a+)	*GYP*401.01* or *GYP*Sch(type A)*	GYP(B1-136-A137-354)		GPB(1-46)-A(47-118)	PMID: 2015404	M71243.1		Reciprocal product is *GYP.Hil*
MNS:15 or St(a+)	*GYP*401.02* or *GYP*Sch(type B)*	GYP(B1-136-A137-354)		GPB(1-46)-A(47-118)	PMID: 2015404	M71244.1		Reciprocal product is *GYP.Hil*
MNS:15 or St(a+)	*GYP*401.03* or *GYP*Sch(type C)*	GYP(B1-136-A137-354)		GPB(1-46)-A(47-118)	PMID: 2015404	AH006935.2		Reciprocal product is *GYP.Hil*
MNS:15 or St(a+)	*GYP*401.04* or *GYP*Sch(type D)*	GYP(B1-136-A137-354)		GPB(1-46)-A(47-118)	PMID: 2015404	GQ365679.1		Reciprocal product is *GYP.Hil*
MNS:15 or St(a+)	*GYP*401.05* or *GYP*Sch(type E)*	GYP(B1-136-A137-354)		GPB(1-46)-A(47-118)	PMID: 2015404	text DNA PMID: 24858913		Reciprocal product is *GYP.Hil*
MNS:15 or St(a+)	*GYP*401.06* or *GYP*Sch(type F)*	GYP(B1-136-A137-354)		GPB(1-46)-A(47-118)	PMID: 2015404	text DNA PMID: 24858913		Reciprocal product is *GYP.Hil*
MNS:15 or St(a+)	*GYP*401.07* or *GYP*Sch(type G)*	GYP(B1-136-A137-354)		GPB(1-46)-A(47-118)	PMID: 27072601	LN880514		Reciprocal product is *GYP.Hil*
MNS:15 or St(a+)	*GYP*401.08* or *GYP*Sch(type H)*	GYP(B1-136-A137-354)		GPB(1-46)-A(47-118)	PMID: 27072601	LN880515		Reciprocal product is *GYP.Hil*

Phenotype	Allele name	Nucleotide change	E I	Pred. amino acid change	(Reference No.) PMID	Accession number	rs number	Comment
MNS:15 or St(a+)	*GYP*401.09* or *GYP*Sch(type I)*	GYP(B1-136-A137-354)		GPB(1-46)-A(47-118)	PMID: 32394466	text DNA PMID: 32394466		Reciprocal product is *GYP.Hil*
MNS:15 or St(a+)	*GYP*401.10* or *GYP*Sch(type J)*	GYP(B1-136-A137-354)		GPB(1-46)-A(47-118)	PMID: 32394466	text DNA PMID: 32394466		Reciprocal product is *GYP.Hil*
MNS:–3,4,25 or S−s+,Dantu+	*GYP*402* or *GYP*Dantu*	GYP(B1-175-A176-354)		GPB(1-58)-A(59-118)	PMID: 3305497			Reciprocal product is *GYP.Tk*
MNS:7,–9,10,-20, –26,–34,35,48	*GYP*403 or GYP*MOT*			GPB (20–45)-GPΨB (46–70)-GPA (71–149) Exon 3 GPB(46-DKHKRDTYPAHTANEV SEISVTTVSPPE-68) GPA(71-EET-73)	PMID: 34369596	LC565490		Amino acid sequence for Exon 3 is similar to *GYP*Kip*
GYP(B-A-B) hybrid series								
MNS:–3,4,7,10, 20,34,35 or S–s+, Mi(a+), Mur+, Hil+, MINY+, MUT+	*GYP*501 or GYP*Mur*	*GYP(B1-136-Bψ137-199-A200-229-B230-366)*		GP(B1-66-A67-76-B77-122) †GPB^{s} ins 46-76 DKHKRDTYPAHTANEV SEISVRTVYPPEEET	PMID: 2016325	AF090739		Novel sequence derived from composite exon; *GYPB* 5' pseudoexon 3 + *GYPA* 3' exon 3
MNS:3,–4,7,10, 26,33,34,35 or S+s–,Mi(a+), Mur+,Hop+, TSEN+,MINY+, MUT+	*GYP*502 or GYP*Hop*	*GYP(B1-136-Bψ137-208-A209-229-B230-366)* c.236C>T		GP(B1-69-A70-76-B77-122) †GPB^{S} ins 46-76 DKHKRDTYPAHTANEV SEISVTTVYPPEEET; p.Thr79Met	PMID: 10827259 PMID: 27435823	KR815995		Novel sequence derived from composite exon; *GYPB* 5' pseudoexon 3 + *GYPA* 3' exon 3

Phenotype	Allele name	Nucleotide change	E I	Pred. amino acid change	(Reference No.) PMID	Accession number	rs number	Comment
MNS:–3,4,7,10,20, 2634,35 or S–s+, Mi(a+), Mur+, Hil+, MINY+, MUT+,	*GYP*503 or GYP*Bun*	*GYP(B1-136-Bψ137-208-A209-229-B230-366)*		GP(B1-69-A70-76-B77-122) †GPB^{s} ins 46-76 DKHKRDTYPAHTANEV SEISVTTVYPPEEET	PMID: 2016325	M60710		Novel sequence derived from composite exon; *GYPB* 5' pseudoexon 3 + *GYPA* 3' exon 3
MNS:–3,4,7, 20,34,35 or S–s+, Mi(a+), Hil+, MINY+, MUT+	*GYP*504 or GYP*HF*	*GYP(B1-136-Bψ137-159-A160-232-B233-369)*		GP(B1-53-A54-77-B78-123) †GPB^{s} ins 46-77 DKHKRDTYAATPRAHE VSEISVRTVYPPEEET	PMID: 1737789	M81079		Novel sequence derived from composite exon; *GYPB* 5' pseudoexon 3 + *GYPA* 3' exon 3
MNS:–3,–4,–5,6 or S–s–U–He+	*GYP*505 or GYP*He(GL)*	*GYP(B1-12-A13-78-B79-168)* *GYP(B1-69-A70-136-B137-234)*		GP(B1-4-A5-26-B27-59) p.Leu20Trp p.Thr23Ser p.Glu24Gly	PMID: 9207475			
MNS:–3,4,10,20,3 4,35,48 or s+ Mur+ MUT+, MINY+, Hil+, Kipp+	*GYP*506 or GYP*KIP*	*GYP(B1-136-Bψ137-218-A219-229-B230-366)*		GP(B1-45-ψB46-73-A74-76-B^{s}77-122) †GPB^{s} ins 46-76 DKHKRDTYPAHTANEV SEISVTTVSPPEEET	PMID: 26718482	KF501485		The amino acid sequence encoded by the hybrid *ΨB-A* Exon 3 of *GYP*Kip* and *GYP*MOT* is identical.
MNS:4,24 or s+ partial, Mit+	*GYP*507*	*GYP(B1-154)-(A155-174)-(B175-273)*		GP(B1-51)-(A52-58)-(B59-91)	PMID: 36349463	OP263737		GYP*B(1-Ψ3)-BA(4)-B(5-6). GPB amino acid sequence 52VHRFTVP58 was replaced by the GPA sequence 52AHHFSEP58.
MNS:–3,–4	*GYP*508 or GYP*NGU*	*GYP(B1-136)-A(137-271)-B(272-369)*		GP(B1-45)-(A46-90)-GPB(91-123)	PMID: 26247620	KP406622		*GYP*B(1-2)-A(3-4)-B(5-6)*
MNS:–3,–4,5	*GYP*509*	*GYP(B1-135)-(A136-174)-(B175-273)*		GP(B1-45)-(A46-58)-(B59-91)	Abstract (63)			*GYP*B(1-Ψ3)-A(4)-B(5-6)*

Phenotype	Allele name	Nucleotide change	E I	Pred. amino acid change	(Reference No.) PMID	Accession number	rs number	Comment
GYP(B-E-B) hybrid series								
MNS:–3,–4	*GYP*601 or GYP*Man*	*GYP(B1-234)*		GPB(1-78)	PMID: 25740598	KP052854		*GYP*B(1-Ψ3)-EΨ4-B(5-6)*
MNS:–3,–4	*GYP*602 or GYP*Dia*	*GYP(B1-234)*		GPB(1-78)	PMID: 25740598	KP052856		*GYP*B(1-Ψ3)-EΨ4-B(5-6)*
MNS:–3,–4	*GYP*604*	*GYP(B1-37-E38-136-B137-234)*		GPB(1-12)-GPE(13-45)-G	PMID: 32314425	LC505672 LC505673		*GYP*B(1)-E(2-Ψ3-Ψ4)-B(5-6)* Gene structure maybe similar to *GYP*Ros* (*GYP*603*) reported by Willemetz et al. PMID: 25740598

†The insertion interrupts the JENU antigen on GPB

Table 5. MNS alleles with genetic variants encoding a null phenotype								
GYP Deletion hybrids								
MNS:–1,–2,–3, –4,–5 or M^kM–N–S–s–U−	*GYP*01N*	Del *GYPA* exons 2-7 *GYPB* exons 1-5		GPA andGPB absent	PMID: 9269716			
MNS:–1,–2,−28 or M–N– En(a–)	*GYPA*28N.01*	Del *GYPA* exons 2-7 *GYPB* exon 1		GPA absent	PMID: 3197721 PMID: 9269716			*En(Fin)*

Phenotype	Allele name	Nucleotide change	EI	Pred. amino acid change	(Reference No.) PMID	Accession number	rs number	Comment
GYPA Null alleles								
MNS:–1,−28 or M–N– En(a–)	*GYPA*01N.02*	c.295delG (Exon 5)		GPA absentp.Val99Ter	PMID: 36102166	OL860988		
MNS:–1,–2−28 or M–N– En(a–)	*GYPA*01N.03*	*GYPA:* c.314dupG (Exon 5)		GPA absentp.Thr106Asnfs	Abstract (69)	MG874776	rs1442690784	*En(IND)* Reported as c.314_315insG
MNS:–1,–2−28 or M–N– En(a–)	*GYPA*02N.01*	c.357+1G>T (Intron 5)		GPA absent	Abstract (70)		rs1236260993	
GYPB Null alleles								
MNS:–3,–4,–5 or S–s–U–	*GYPB*05N.01*	Whole *GYPB* deletion		GPB absentDel 110kb	PMID: 32884505	MN005664		
MNS:–3,–4,–5 or S–s–U–	*GYPB*05N.02*	Whole *GYPB* deletion		GPB absentDel 103kb	PMID: 32884505	MN005663		
MNS:–3,–4,–5 or S–s–U–	*GYPB*05N.03*	Del *GYPB* Exon 2-6		GPB absentDel 19kb	PMID: 32884505	MN005662		
MNS:–3,–4,–5 or S–s–U–	*GYPB*05N.04*	Del *GYPB* exons 2-5 *GYPE* exon 1		GPB absent	PMID: 2823938 PMID: 9269716 PMID: 2024643			

References

PMID 3456608 Siebert PD, Fukuda M: Isolation and characterization of human glycophorin A cDNA clones by a synthetic oligonucleotide approach: nucleotide sequence and mRNA structure. *Proc Natl Acad Sci U S A* 1986; 83: 1665-9.

PMID 6166001 Furthmayr H, Metaxas MN, Metaxas-Bühler M: Mg and Mc: mutations within the amino-terminal region of glycophorin A. *Proc Natl Acad Sci U S A* 1981; 78: 631-5.

PMID 6697986 Dahr W, Newman RA, Contreras M, Kordowicz M, Teesdale P, Beyreuther K*, et al.* : Structures of Miltenberger class I and II specific major human erythrocyte membrane sialoglycoproteins. *European journal of biochemistry* 1984; 138: 259-65.

PMID 10729812 Storry JR, Coghlan G, Poole J, Figueroa D, Reid ME: The MNS blood group antigens, Vr (MNS12) and Mt(a) (MNS14), each arise from an amino acid substitution on glycophorin A. *Vox Sang* 2000; 78: 52-6.

Abstract 5 Storry JR, Reid ME: A point mutation in GYPA exon 3 encodes the low incidence antigen, MNS16 [Abstract P025]. *Vox Sang* 2000; 78.

PMID 10827258 Daniels GL, Bruce LJ, Mawby WJ, Green CA, Petty A, Okubo Y*, et al.* : The low-frequency MNS blood group antigens Nya (MNS18) and Osa (MNS38) are associated with GPA amino acid substitutions. *Transfusion* 2000; 40: 555-9.

Abstract 7 Tsuneyama H, Uchikawa M, Matsubara M, Onodcra T, Yokota T, Nakajima K*, et al.* : Molecular basis of Or in the MNS blood group system [Abstract 1446]. *Vox Sang* 1998; 74 (Suppl 1).

PMID 7690638 Daniels GL, Green CA, Poole J, Jerne D, Smart E, Wilcox D*, et al.* : ERIK, a low-frequency red cell antigen of the MNS blood group system associated with Sta. *Transfusion Medicine* 1993; 3: 129-35.

Abstract 9 Huang CH, Blumenfeld, Reid M, Daniels G: Molecular analysis of human glycophorin ERIK gene whose transcript processing results in two low frequency antigens ERIK and STa [Abstract S182]. *Transfusion* 1992; 32 Suppl: 48S.

PMID 10354388 Poole J, Banks J, Bruce LJ, Ring SM, Levene C, Stern H*, et al.* : Glycophorin A mutation Ala65 --> Pro gives rise to a novel pair of MNS alleles ENEP (MNS39) and HAG (MNS41) and altered Wrb expression: direct evidence for GPA/band 3 interaction necessary for normal Wrb expression. *Transfus Med* 1999; 9: 167-74.

Abstract 11 Jarolim P, Moulds JM, Moulds JJ, Rubin HL, Dahr W: MARS and AVIS blood group antigens: polymorphism of glycophorin A affects band 3 - glycophorin A interaction [Abstract]. *Blood* 1996; 88: 182a.

Abstract 12 Lomas-Francis C, Hu Z, Hue-Roye K, Velliquette RW, Reid ME, Allen JL*, et al.* : Novel single nucleotide change in GYPA in a person who made an alloantibody to a new high prevalence MNS antigen called ENEV [Abstract S68-040B]. *Transfusion* 2006; 46: 25A.

Abstract 13 Uchikawa M, Tsuneyama H, Ogasawara K, Suzuki Y, Yabe R, Enomoto T*, et al.* : Molecular basis for a novel low-frequency antigen in the MNS blood group system, TD [Abstract P-253]. *Vox Sang* 2006; 91: 133.

PMID 25523184 McBean RS, Hyland CA, Hendry JL, Shabani-Rad MT, Flower RL: SARA: a "new" low-frequency MNS antigen (MNS47) provides further evidence of the extreme diversity of the MNS blood group system. *Transfusion* 2015; 55: 1451-6.

PMID 32358867 Ito S, Kaito S, Miyazaki T, Kikuchi G, Isa K, Tsuneyama H*, et al.* : A new antigen SUMI carried on glycophorin A encoded by the *GYPA*M* with c.91A>C (p.Thr31Pro) belongs to the MNS blood group system. *Transfusion* 2020; 60: 1287-93.

PMID 3477806 Siebert PD, Fukuda M: Molecular cloning of a human glycophorin B cDNA: nucleotide sequence and genomic relationship to glycophorin A. *Proc Natl Acad Sci U S A* 1987; 84: 6735-9.

PMID 11239234 Storry JR, Reid ME, MacLennan S, Lubenko A, Nortman P: The low-incidence MNS antigens M(v), s(D), and Mit arise from single amino acid substitutions on GPB. *Transfusion* 2001; 41: 269-75.

PMID 36062546 Lopez GH, Emthip M, Suwanwootichai P, Millard GM, Wilson B, Onpuns S*, et al.* : Hemolytic disease of the fetus and newborn caused by anti-s(D) antibody in a GP.Mur/Mur Thai mother and review of the prevalence of s(D) in Thai blood donors. *Transfusion* 2022; 62(10): 2137-42.

Abstract 19 Lomas-Francis C, Louzon M, Vege S, Harris S, Hess J, Hu ZG*, et al.* : The S antigen encoded by *GYPB*Mit* is a partial antigen: first report of alloanti-S in a person with S+ Mit+ RBCs. *Vox Sang* 2016; 111 (Suppl 1): 68 [Abstract 5B-S35-02].

Abstract 20 Moulds JM, Noumsi GT, Hendrix J, McCaskill D: Evidence that microarray genotyping is an accurate predictor of a blood group phenotype. *Transfusion* 2013; 53 Suppl 2 [Abstract S73-030L]: 47A.

PMID 30523644 Suzuki Y, Isa K, Ogasawara K, Kikuchi Y, Yabe R, Tsuno N-H*, et al.* : A novel c.166A>T (p.Thr56Ser) mutation in GYPB*S accounting for unusual S antigen expression. *Vox Sang* 2019; 114: 171-3.

PMID 30927367 Cote J, Cen S, Fennell K, Pambrun C, Branch DR, Ochoa-Garay G: A GYPB variant encoding an altered leader peptide leads to a weak S phenotype. *Transfusion* 2019; 59: 2461-2.

Abstract 23 Aeschlimann J, Lomas-Francis C, Vege S, Sidhu M, DePalma H, Westhoff CM: Discordance between historical type, DNA prediction, and serologic reagents reveals new GYPB*S variant allele. *Transfusion* 2019; 59 Suppl 3 [P-IM-27]: 125A.

Abstract 24 Aeschlimann J, Vege S, Israel B, Cusick R, Lomas-Francis C, Westhoff CM: Two novel GYPB alleles discovered by investigation of discordant testing results. *Transfusion* 2020; 60 Suppl 5 [OA2-AM20-19]: 12A.

Abstract 25 Westhoff CM, Vege S, Copeland T, Baker E, Velliquette R, Lomas-Francis C: A new Glycophorin B allele, GYPB (IVS5+3G>A), in trans to GYPB (IVS5+5G>T) is associated with discrepant prediction of S and U antigens status. *Vox Sang* 2012; 103 Suppl 1 [P-457]: 212.

Abstract 26 Meyer S, Vollmert C, Trost N, Gottschalk J, Ries J, Marcovic A*, et al.* : MALDI-TOF MS for MNS typing – high pheno/genotype concordance in 5743 Swiss. *Vox Sang* 2015; 109 Suppl 1 [Abstract P-564]: 279.

Abstract 27 Engstrom C, Caesar A, Meyer S, Portmann C, Trost N, Schwind P*, et al.* : A new GYPB*04(164T>G, Phe55Cys) allele with a phenotypic partial character of small s [Abstract P02-12]. *Transfus Med Hemother* 2016; 43: 40.

Abstract 28 Slayten JK, Halverson GR, Yassai MB, Bedel B, Denomme GA: A suspected Uvar blood donor homozygous for a novel s (MNS4) allele. *Transfusion* 2015; 55 Suppl 3 [Abstract SP234]: 147A.

Abstract 29 Yin L, Yassai MB, Bensing K, Udani R, Denomme GA: Comparative genomic hybridization array analysis of blood group gene chromosomal alterations. *Transfusion* 2016; 56 Suppl 4: 151A.

Abstract 30 Aeschlimann J, Lomas-Francis C, Lerma F, Li C, Burgos A, Smith A*, et al.* : Investigation of U/GPB antibodies in two patients uncovers three novel *GYPB* alleles. *Transfusion* 2018; 58 Suppl 2 [IGT13-ST4-24]: 43A.

Abstract 31 Smith A, Keller J, Keller MA: Rare Glycophorin B gene variant discovered through discrepancy between little s serologic and molecular results. *Transfusion* 2020; 60 Suppl 5 [P-IG-34]: 157A.

Abstract 32 Lomas-Francis C, Vege S, Shakarian G, Burgos A, Lerma F, Boyd P*, et al.* : GYPB 251G>C change (Ser84Thr) in Glycophorin B is associated with an U-like allo antibody. *Vox Sang* 2017; 112 Suppl 1 [Abstract 4B-S22-06]: 55.

PMID 6723663 Dahr W, Kordowicz M, Judd WJ, Moulds J, Beyreuther K, Krüger J: Structural analysis of the Ss sialoglycoprotein specific for Henshaw blood group from human erythrocyte membranes. *European journal of biochemistry* 1984; 141: 51-5.

PMID 14641872 Storry JR, Reid ME, Fetics S, Huang CH: Mutations in GYPB exon 5 drive the S–s–U+(var) phenotype in persons of African descent: implications for transfusion. *Transfusion* 2003; 43: 1738-47.

PMID 8144668 Huang CH, Reid ME, Blumenfeld OO: Remodeling of the transmembrane segment in human glycophorin by aberrant RNA splicing. *J Biol Chem* 1994; 269: 10804-12.

PMID 33733475 Lapadat R, Anani WQ, Bensing KM, Aeschlimann J, Vege S, Lomas-Francis C*, et al.* : A pair of S-silencing single nucleotide variants cis-linked on GYPB. *Transfusion* 2021; 61: E34-E6.

Abstract 37 Arnaud L, Saison C, Nataf J, Vrignaud C, Peyrard T: A recurrent GYPB mutation (c.137-8C>T) found in so-called P2 alleles induces a genotyping error for *GYPB*S*. *Vox Sang* 2013; 105 Suppl 1 [Abstract P-494]: 233.

Abstract 38 Yazer MH, Gabert K, Bolen N, Sood C, Ochoa G: A new variant at position IVS5+5 of GYPB*s associated with an s-phenotype. *Transfusion* 2015; 55 Suppl 3 [Abstract SP233]: 147A.

PMID 35441363 Thonier VL, Floch A, Babinet J, Pirenne F, Vege S, Tournamille C*, et al.* : First report of a null allele on a GYPB*s background: GYPB*s(37 + 4_8delAGTGA). *Transfusion* 2022; 62: E24-E6.

Abstract 40 Tournamille C, Willemetz A, Vrignaud C, Muralitharan V, Babinet J, Landre C*, et al.* : A novel deletion mechanism in GYPB abolishes red blood cell expression of the U antigen in a proband of African descent. *Vox Sang* 2017; 112 Suppl 1 [Abstract P-533]: 231.

Abstract 41 Keller MA, Smith A, Lindquist MR, Bewley SL, Zawacki K, Dixon D, Chou MCH (2022). Rare GYPB intronic single nucleotide variant associated with allele dropout and little s typing discrepancies. Transfusion, 62(Suppl 2 [Abstract P-IG-38]), 143A. doi:https://doi.org/10.1111/trf.17058

PMID 8444872 Huang CH, Reid ME, Blumenfeld OO: Exon skipping caused by DNA recombination that introduces a defective donor splice site into the human glycophorin A gene. *J Biol Chem* 1993; 268: 4945-52.

PMID 10862083 Huang C-H, Chen Y, Blumenfeld OO: A novel Sta glycophorin produced via gene conversion of pseudoexon III from glycophorin E to glycophorin A gene. *Human Mutat* 2000; 15: 533-40.

Abstract 43 Huang CH, Lomas C, Daniels G, Blumenfeld OO: Glycophorin He(Sta) of the human red blood cell membrane is encoded by a complex hybrid gene resulting from two recombinational events. *Blood* 1994; 83: 3369-76.

PMID 10862083 Vignal A, Rahuel C, el Maliki B, London J, le van Kim C, Blanchard D*, et al.* : Molecular analysis of glycophorin A and B gene structure and expression in homozygous Miltenberger class V (Mi. V) human erythrocytes. *European journal of biochemistry* 1989; 184: 337-44.

PMID 2015404 Huang CH, Blumenfeld OO: Identification of recombination events resulting in three hybrid genes encoding human MiV, MiV(J.L.), and Sta glycophorins. *Blood* 1991; 77: 1813-20.

PMID 7718894 Huang CH, Reid ME, Okubo Y, Daniels GL, Blumenfeld OO: Glycophorin SAT of the human erythrocyte membrane is specified by a hybrid gene reciprocal to glycophorin Dantu gene. *Blood* 1995; 85: 2222-7.

PMID 1421409 Huang CH, Skov F, Daniels G, Tippett P, Blumenfeld OO: Molecular analysis of human glycophorin MiIX gene shows a silent segment transfer and untemplated mutation resulting from gene conversion via sequence repeats. *Blood* 1992; 80: 2379-87.

PMID 18764826 Velliquette RW, Palacajornsuk P, Hue-Roye K, Lindgren S, Ilstrup S, Green C*, et al.* : Novel GYP(A-B-A) hybrid gene in a DANE+ person who made an antibody to a high-prevalence MNS antigen. *Transfusion* 2008; 48: 2618-23.

PMID 2590469 Dahr W, Vengelen-Tyler V, Dybkjaer E, Beyreuther K: Structural analysis of glycophorin A from Miltenberger class VIII erythrocytes. *Biol Chem Hoppe Seyler* 1989; 370: 855-9.

PMID 2439339 Dahr W, Beyreuther K, Moulds JJ: Structural analysis of the major human erythrocyte membrane sialoglycoprotein from Miltenberger class VII cells. *European journal of biochemistry* 1987; 166: 27-30.

Abstract 51 Poole J, Bruce LJ, Tanner MJA, Pisacka M: Novel molecular basis for the Hil (MNS20) antigen. *Transfusion* 1998; 38 (Suppl). 103S [Abstract].

Abstract 52 Watanabe-Okochi N, Tsuneyama H, Isa K, Sasaki K, Suzuki Y, Yabe R*, et al.* : Novel splice site mutations creating the Sta antigen [Abstract P-545]. *Vox Sang* 2018; 113: 249.

PMID 3305497 Blumenfeld OO, Smith AJ, Moulds JJ: Membrane glycophorins of Dantu blood group erythrocytes. *J Biol Chem* 1987; 262: 11864-70.

PMID 34369596 Oda A, Suzuki Y, Isa K, Ogasawara K, Yabe R, Kimura T*, et al.* : GP.MOT: A novel glycophorin variant identified in a Japanese blood donor. *Transfusion* 2021; 61: 2825-9.

PMID 2016325 Huang CH, Blumenfeld OO: Molecular genetics of human erythrocyte MiIII and MiVI glycophorins. Use of a pseudoexon in construction of two delta-alpha-delta hybrid genes resulting in antigenic diversification. *J Biol Chem* 1991; 266: 7248-55.

PMID 10827259 Storry JR, Poole J, Condon J, Reid ME: Identification of a novel hybrid glycophorin gene encoding GP.Hop. *Transfusion* 2000; 40: 560-5.

PMID 27435823 Wei L, Lopez GH, Ji Y, Condon JA, Irwin DL, Luo G*, et al.* : Genotyping for Glycophorin GYP(B-A-B) Hybrid Genes Using a Single Nucleotide Polymorphism-Based Algorithm by Matrix-Assisted Laser Desorption/Ionisation, Time-of-Flight Mass Spectrometry. *Mol Biotechnol* 2016; 58: 665-71.

PMID 1737789 Huang CH, Kikuchi M, McCreary J, Blumenfeld OO: Gene conversion confined to a direct repeat of the acceptor splice site generates allelic diversity at human glycophorin (GYP) locus. *J Biol Chem* 1992; 267: 3336-42.

PMID 9207475 Huang CH, Blumenfeld OO, Reid ME, Chen Y, Daniels GL, Smart E: Alternative splicing of a novel glycophorin allele GPHe(GL) generates two protein isoforms in the human erythrocyte membrane. *Blood* 1997; 90: 391-7.

PMID 26718482 Lopez GH, Wei L, Ji Y, Condon JA, Luo G, Hyland CA*, et al.* : GYP*Kip, a novel GYP(B-A-B) hybrid allele, encoding the MNS48 (KIPP) antigen. *Transfusion* 2016; 56: 539-41.

PMID 36349463 Storry JR, Lammers C, Olsson ML, Robb JS: A novel GYP(B-A-B) hybrid in a blood donor identified by a phenotyping discrepancy with different anti-s reagents. Transfusion 2022; https://doi.org/10.1111/trf.17181.

PMID 26247620 Willemetz A, Nataf J, Peyrard T, Arnaud L: A novel GYPB-A-B hybrid gene responsible for Ss and MN typing discrepancies. *Transfusion* 2015.

Abstract 63 Lomas-Francis C, Vege S, Fuertes J, Burgos A, Tahiri T, Blackman M*, et al.* : Molecular investigation of uncommon S–s–U+ phenotypes reveal novel silencing alleles. *Transfusion* 2022; 62: 139A-40A.

PMID 25740598 Willemetz A, Nataf J, Thonier V, Peyrard T, Arnaud L: Gene conversion events between GYPB and GYPE abolish expression of the S and s blood group antigens. *Vox Sang* 2015; 108: 410-6.

PMID 32314425 Tsuneyama H, Isa K, Watanabe-Okochi N, Ogasawara K, Uchikawa M, Satake M: An unusual variant glycophorin expressing protease-resistant M antigen encoded by the GYPB-E(2-4)-B hybrid gene. *Vox Sang* 2020; 115: 579-85.

PMID 9269716 Blumenfeld OO, Huang CH: Molecular genetics of glycophorin MNS variants. *Transfus Clin Biol* 1997; 4: 357-65.

PMID 3197721 Rahuel C, London J, Vignal A, Cherif-Zahar B, Colin Y, Siebert P*, et al.* : Alteration of the genes for glycophorin A and B in glycophorin-A-deficient individuals. *European journal of biochemistry* 1988; 177: 605-14.

PMID 36102166 Suwanwootichai P, Lopez GH, Emthip M, Wilson B, Millard GM, Onpuns S*, et al.* : Fatal haemolytic transfusion reaction due to anti-Ena and identification of a novel GYPA c.295delG variant in a Thai family. *Vox Sang* 2022; 117: 1327-31.

Abstract 69 Lindholm PF, Drouillard JS, Hartman K, Vege S, Lomas-Francis C, Westhoff CM*, et al.* : En(IND), a single nucleotide insertion GYPA variant causing absence of Glycophorin A. *Transfusion* 2018; 58 Suppl 2 [Abstract IGT34]: 175A

Abstract 70 Lomas-Francis C, Gillen B, Cai C, Vege S, Fuertes J, Fugate A*, et al.* : Antibody to a high prevalence antigen made in response to pregnancy reveals a novel GYPA*N (357 + 1T) null allele in trans to GYP*Hil. *Vox Sang* 2022; 117, Suppl 1 [Abstract P-223].

PMID 32884505 Gassner C, Denomme GA, Portmann C, Bensing KM, Mattle-Greminger MP, Meyer S*, et al.* : Two Prevalent approximately 100-kb GYPB Deletions Causative of the GPB-Deficient Blood Group MNS Phenotype S–s–U– in Black Africans. *Transfus Med Hemother* 2020; 47: 326-36.

Abstract 72 Crowley JA, Colvin CJ, Horn T, Keller MA: Unexpected HEA Beadchip findings point to unusual variant GYPB alleles. *Transfusion* 2014; 54 Suppl 2 [Abstract S72-030L): 46A.

Abstract 73 Smith A, Keller J, Horn T, Troughton MC, Keller MA: Patient with U typing discrepancy associated with aberrant Glycophorin B mRNA transcript. *Transfusion* 2020; 60 Suppl 5 [P-IG-32]: 156A.

PMID 2823938 Huang CH, Johe K, Moulds JJ, Siebert PD, Fukuda M, Blumenfeld OO: Delta glycophorin (glycophorin B) gene deletion in two individuals homozygous for the S–s–U– blood group phenotype. *Blood* 1987; 70: 1830-5.

PMID 37021677 Tie Costa, Stef M, Santos LH et al.: A novel homozygous nonsense mutation in *GYPB* causes S-s-U-phenotype. Transfusion 2023 Jun;63(6):E36-E37. doi:10.1111/trf.17321. 2023 Apr 6.

Abstract 74 Miyazaki T, Isa K, Suzuki Y, Toyoda C, Kurita R, Ogasawara K, et al. A missense single nucleotide variant, c.305G>A (p. Gly102Asp), in the GYPA*01 gene disrupts the dimerization motif of glycophorin A, resulting in a weakened M phenotype. Vox Sang 2023;118 (Suppl. 1) 6-379

Track of changes

			from	to
1	**Version**		**v5.6 31-JUL-2023**	**v5.7 30-SEP-2023**
2	Author	created	Genghis Lopez, Catherine	Genghis Lopez, Catherine Hyland, September 2023
3	Reviewer	reviewed	Jill Storry, July 2023	Christoph Gassner, September 2023
4	Reference	changed	PMID: 37021677	Full reference text updated: PMID: 37021677, Transfusion 2023 Jun;63(6): E36-E37. doi: 10.1111/trf.17321. 2023 Apr 6.
5	Allele	added		*GYPB*04.07*
6	Allele	added		Headline *'GYPA Weak'*
7	Allele	added		*GYPA*01W.01*
8	Reference	added		Abstract (74)
9	**End Version**		**v5.6 31-JUL-2023**	**v5.7 30-SEP-2023**

Track of changes

			from	to
1	**Version**		**v5.5 31-MAR-2023**	**v5.6 31-JUL-2023**
2	Author	created	Genghis Lopez, March 2023	Genghis Lopez, Catherine Hyland, July 2023
3	Reviewer	reviewed	Jill Storry, Margaret Keller, March 2023	Jill Storry, July 2023
4	Allele	added		*GYPB*04N.09*
5	Reference	changed		Abstract (74) to PMID: 37021677
6	**End Version**		**v5.5 31-MAR-2023**	**v5.6 31-JUL-2023**

Track of changes

			from	to
1	**Version**		**v5.4 31-DEC-2022**	**v5.5 31-MAR-2023**
2	Author	created	Genghis Lopez, December 2022	Catherine Hyland, Genghis Lopez, March 2023
3	Reviewer	reviewed	Jill Storry, December 2022	Jill Storry, Margaret Keller, March 2023
4	Reference	added		Abstract 41
5	Allele	removed		*GYPB*04N.07* removed, is partially no Null-allele
6	Allele	removed		*GYPB*04N.08* removed, is partially no Null-allele
7	**End Version**		**to v5.4 31-DEC-2022**	**v5.5 31-MAR-2023**

Track of changes

			from	to
1	**Version**		**v4.1 170119**	**v5.4 31-DEC-2022**
2	Author	created	n.a., v4.1 170119	Genghis Lopez, December 2022
3	Reviewer	reviewed	n.a.	Jill Storry, December 2022
4	General		Last word version published on ISBT website	First Excel map version. Spread-sheets "Intro", "Allele Table", "References", and "Versioning" created.
5	Accesssion nrs.	added	n.a.	added all accesssion numbers
6	Rs-numbers	added	n.a.	added all rs-numbers
7	References	added	n.a.	added all references on tabsheet "References" until PMID 2823938
8	Allele	added	n.a.	*GYPA*09.02 or GYPA*Vw.02*
9	Allele	added	n.a.	*GYPA*50* or *GYPA*SUMI*
10	Allele	added	n.a.	*GYPB*03.02*
11	Allele	added	n.a.	*GYPB*03.03*
12	Allele	added	n.a.	*GYPB*03.04*
13	Allele	added	n.a.	*GYPB*03.05*
14	Allele	added	n.a.	*GYPB*03.06*
15	Allele	added	n.a.	*GYPB*03.07*
16	Allele	added	n.a.	*GYPB*04.02*
17	Allele	added	n.a.	*GYPB*04.03*
18	Allele	added	n.a.	*GYPB*04.04*
19	Allele	added	n.a.	*GYPB*04.05*
21	Allele	added	n.a.	*GYPB*04.06*
22	Allele	added	n.a.	*GYPB*03N.05*
23	Allele	added	n.a.	*GYPB*03N.06*
24	Allele	added	n.a.	*GYPB*03N.07*
25	Allele	added	n.a.	*GYPB*03N.08*
26	Allele	added	n.a.	*GYPB*04N.02*
27	Allele	added	n.a.	*GYPB*04N.03*
28	Allele	added	n.a.	*GYPB*04N.04*
29	Allele	added	n.a.	*GYPB*04N.05*

1	**Version**		**v4.1 170119**	**v5.4 31-DEC-2022**
30	Allele	added	n.a.	*GYPB*04N.06*
31	Allele	added	n.a.	*GYPB*04N.07*
32	Allele	added	n.a.	*GYPB*04N.08*
33	Allele	added	n.a.	*GYP*401.01* or *GYP*Sch(type A)*
34	Allele	added	n.a.	*GYP*401.02* or *GYP*Sch(type B)*
35	Allele	added	n.a.	*GYP*401.03* or *GYP*Sch(type C)*
36	Allele	added	n.a.	*GYP*401.04* or *GYP*Sch(type D)*
37	Allele	added	n.a.	*GYP*401.05* or *GYP*Sch(type E)*
38	Allele	added	n.a.	*GYP*401.06* or *GYP*Sch(type F)*
39	Allele	added	n.a.	*GYP*401.07* or *GYP*Sch(type G)*
40	Allele	added	n.a.	*GYP*401.08* or *GYP*Sch(type H)*
41	Allele	added	n.a.	*GYP*401.09* or *GYP*Sch(type I)*
42	Allele	added	n.a.	*GYP*401.10* or *GYP*Sch(type J)*
43	Allele	added	n.a.	*GYP*403 or GYP*MOT*
44	Allele	added	n.a.	*GYP*507*
45	Allele	added	n.a.	*GYP*508 or GYP*NGU*
46	Allele	added	n.a.	*GYP*509*
47	Allele	added	n.a.	*GYP*601 or GYP*Man*
48	Allele	added	n.a.	*GYP*602 or GYP*Dia*
49	Allele	added	n.a.	*GYP*603 or GYP*Ros*
50	Allele	added	n.a.	*GYP*604*
51	Allele	added	n.a.	*GYPA*01N.02*
52	Allele	added	n.a.	*GYPA*01N.03*
53	Allele	added	n.a.	*GYPA*02N.01*
54	Allele	added	n.a.	*GYPB*05N.01*
55	Allele	added	n.a.	*GYPB*05N.02*
56	Allele	added	n.a.	*GYPB*05N.03*
57	Allele	added	n.a.	*GYPB*05N.04*
58	Allele	renamed	*GYPA*01N*	*GYPA*28N.01*
59	**End Version**		**v4.1 170119**	**v5.4 31-DEC-2022**