Names for H (ISBT 018) Blood Group Alleles

Intro

General description: The H blood group system consists of one antigen, H, that is carried on glycolipids and glycoproteins on the RBC membrane, where it is synthesised by the fucosyltransferase product of the *FUT1* gene; as well as on glycoproteins on epithelial cells and in body fluids, where it is synthesised by the fucosyltransferase product of the *FUT2* gene.
In group O individuals, H antigen is the terminal antigen however, in group A and B individuals, the H antigen serves as the precursor structure for A and B blood-group-specific glycosyltransferases.
Thus, group O people will test strongly H+ whereas groups A, B and AB will express very little H antigen. Mutations that negatively affect the α2FucT1 enzyme activity (encoded by FUT1) will result in reduced or absent H production (and a concomitant decrease in A and/or B antigens in individuals where those enzymes are encoded). Total absence of H, A and B antigens is called the Oh or Bombay phenotype. Weak expression is referred to as the paraBombay phenotype.
The enzymes α2FucT1and α2FucT2 are single pass type II membrane glycoproteins in the Golgi. The α2FucT1 protein consists of 365 amino acids and is encoded by FUT1 or H, if analysis is to predict a blood group antigen. The *FUT2* gene produces two transcripts; one of 343 amino acids and another more abundant form of 332 amino acids. The longer transcript encodes a protein with approximately one fourth the enzymatic activity and the shorter form is considered to be the active enzyme. Thus, the numbers given below are counted from the second initiating codon. The α2FucT2 protein is encoded by FUT2 or Se, if analysis is to predict a blood group antigen.

Gene name: *FUT1*
Number of exons: 4
Initiation codon: Beginning of exon 4
Stop codon: Within exon 4
Entrez Gene ID: 2523
LRG sequence: NG_007510.1 (genomic)
NM_000148.3 (transcript)
Reference allele: *FUT1*01* (shaded)
Acceptable: *H* if inferred by hemagglutination/inhibition

Gene name: *FUT2*
Number of exons: 2
Initiation codon: Beginning of exon 2
Stop codon: Within exon 2
Entrez Gene ID: 2524
LRG sequence: NG_007511.1 (genomic)
NM_000511.5 (transcript)
Reference allele: *FUT2*01* (shaded)
Acceptable: *Se* if inferred by hemagglutination/inhibition

Phenotype	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
H+	*FUT1*01*						
H+	*FUT1*01.02 (old: FUT1*02)*	c.35C>T	4	p.Ala12Val	PMID: 15476160 PMID: 16331565		rs2071699
Weak phenotypes†							
H+weak	*FUT1*01W.01*	c.293C>T	4	p.Thr98Met	PMID: 15847661	AY611628	rs1469074926
H+weak	*FUT1*01W.02*	c.328G>A	4	p.Ala110Thr	PMID: 15476160 PMID: 34487549	DQ092446 DQ321370	rs56342683
H+weak	*FUT1*01W.03*	c.349C>T	4	p.His117Tyr	PMID: 9745152		rs150074056
H+weak	*FUT1*01W.04*	c.442G>T	4	p.Asp148Tyr	PMID: 9226185	AB004862	rs150074056
H+weak	*FUT1*01W.05.01*	c.460T>C	4	p.Tyr154His	PMID: 9031499		rs757349699
H+weak	*FUT1*01W.05.02*	c.460T>C c.1042G>A	4	p.Tyr154His p.Glu348Lys	PMID: 9226185 PMID: 9031498	AB004863	rs757349699 rs764739319
H+weak	*FUT1*01W.07*	c.491T>A	4	p.Leu164His	PMID: 7912436		rs104894687
H+weak	*FUT1*01W.08*	c.522C>A	4	p.Phe174Leu	PMID: 12366770	AF455028	rs747696745
H+weak	*FUT1*01W.09*	c.658C>T	4	p.Arg220Cys	PMID: 9031499		rs574691621
H+weak	*FUT1*01W.10*	c.659G>A	4	p.Arg220His	PMID: 11045762		rs1229284545
H+weak	*FUT1*01W.11*	c.661C>T	4	p.Arg221Cys	(5), Abstract		rs1452890889
H+weak	*FUT1*01W.12*	c.682A>G	4	p.Met228Val	PMID: 16403295 PMID: 17163878 PMID: 21988368		
H+weak	*FUT1*01W.13*	c.689A>C	4	p.Gln230Pro	PMID: 17176328		rs1445220556
H+weak	*FUT1*01W.14*	c.721T>C	4	p.Tyr241His	PMID: 9226185	AB004861	rs765114567
H+weak	*FUT1*01W.15*	c.801G>C	4	p.Trp267Cys	(1), Abstract (2), Abstract		

Phenotype	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
H+weak	*FUT1*01W.16*	c.801G>T	4	p.Trp267Cys	(1), Abstract (2), Abstract		
H+weak	*FUT1*01W.17*	c.832G>A	4	p.Asp278Asn	(1), Abstract (2), Abstract		
H+weak	*FUT1*01W.18*	c.903_904insAAC	4	p.Asn301_His302insAsn	n.a.	n.a.	
H+weak	*FUT1*01W.19*	c.917C>T	4	p.Thr306Ile	PMID: 17176328		
H+weak	*FUT1*01W.20*	c.990delG	4	p.Pro331Glnfs*6	PMID: 9226185	AB004860	
H+weak	*FUT1*01W.21*	c.235G>C	4	p.Gly79Arg	PMID: 20533259 PMID: 21988368	FJ665616	rs1399735219
H+weak	*FUT1*01W.22*	c.991C>A	4	p.Pro331Thr	PMID: 19572973	FM162557	rs1381389919
H+weak	*FUT1*01W.23*	c.424C>T	4	p.Arg142Trp	(3), Abstract PMID: 34487549	HQ891007	rs772921327
H+weak	*FUT1*01W.24*	c.649G>T	4	p.Val217Phe	PMID: 21839020 PMID: 34967725	GQ336988 HM584610	rs541722036
H+weak	*FUT1*01W.25*	obsolete					rs1399735219
H+weak	*FUT1*01W.26*	c.545G>A	4	p.Arg182His		KF385398	rs1284994775
H+weak	*FUT1*01W.27*	c.958G>A	4	p.Gly320Arg	PMID: 27893357	KF581194	rs762020231
H+weak	*FUT1*01W.28*	c.896A>C	4	p.Gln299Pro	PMID: 25858679 PMID: 30186784	KJ804401.1	
H+weak	*FUT1*01W.29*	c.655G>C	4	p.Val219Leu	PMID: 25538540	JX078970	
H+weak	*FUT1*01W.30*	avoided					
H+weak	*FUT1*01W.31* *(old: FUT1*02W.01)*	c.35C>T c.269G>T	4 4	p.Ala12Val p.Gly90Val	PMID: 17176328		rs897829842
H+weak	*FUT1*01W.32* *(old: FUT1*02W.02)*	c.35C>T c.371T>G	4 4	p.Ala12Val p.Phe124Cys	n.a.	n.a.	rs529462057

Phenotype	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
H+weak	*FUT1*01W.33* *(old: FUT1*02W.03)*	c.35C>T c.682A>G	4 4	p.Ala12Val p.Met228Val	PMID: 20533259		
H+weak	*FUT1*01W.34* *(old: FUT1*02W.05)*	c.35C>T c.748C>T	4 4	p.Ala12Val p.Arg250Trp	PMID: 25538540	JX317627	
H+weak	*FUT1*01W.35*	c.424C>T	4	p.Arg142Try	(6), Abstract		
H+weak	*FUT1*01W.36*	c.755G>C	4	p.Arg253Pro	PMID: 30217757		
H+weak	*FUT1*01W.37*	c.803G>A	4	p.Cys268Tyr	PMID: 34693534	MW821348	
H+weak	*FUT1*01W.38*	c.814A>G	4	p.Ile272Val	PMID: 30217757		
H+weak	*FUT1*01W.39*	c.229C>T c.302C>T	4	p.Leu77Phe Ala101Val	PMID: 34792200	MN971576	
Null alleles							
H–	*FUT1*01N.01*	c.422G>A	4	p.Trp141Ter	PMID: 17176328		rs749165173
H–	*FUT1*01N.02*	c.461A>G	4	p.Tyr154Cys	PMID: 9122901		
H–	*FUT1*01N.03*	c.462C>A	4	p.Tyr154Ter	(4), Abstract		
H–	*FUT1*01N.04*	c.513G>C	4	p.Trp171Cys	PMID: 9122901		
H–	*FUT1*01N.05*	c.538C>T	4	p.Gln180Ter	PMID: 17176328		rs746629771
H– /H+w (‡)	*FUT1*01N.06*	c.551_552delAG	4	p.Glu184Valfs*85	PMID: 9031499		rs573412368
H–	*FUT1*01N.07*	c.586C>T	4	p.Gln196Ter	PMID: 15476160	DQ157279	
H–	*FUT1*01N.08*	c.695G>A	4	p.Trp232Ter	PMID: 9226185	AB004859	
H–	*FUT1*01N.09*	c.725T>G	4	p.Leu242Arg	PMID: 9299444 PMID: 9745152		rs28934588
H–	*FUT1*01N.10*	c.776T>A	4	p.Val259Glu	PMID: 9122901		
H–	*FUT1*01N.11*	c.785G>A c.786C>A	4	p.Ser262Lys	PMID: 11161242	AJ276886	

Phenotype	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
H–	*FUT1*01N.12*	c.826C>T	4	p.Gln276Ter	PMID: 7912436		rs104894688
H–	*FUT1*01N.13*	c.881_882delTT	4	p.Phe294Cysfs*40	PMID: 9031499		rs777455020
H–	*FUT1*01N.14*	c.944C>T	4	p.Ala315Val	PMID: 9122901		
H–	*FUT1*01N.15*	c.948C>G	4	p.Tyr316Ter	PMID: 7912436		rs104894686
H–	*FUT1*01N.16 (old: FUT1*02W.04)*	c.980A>C	4	p.Asn327Thr	PMID: 15487706 PMID: 23560544 PMID: 9031499		rs777291875
H–	*FUT1*01N.17*	c.1047G>C	4	p.Trp349Cys	PMID: 9122901		rs1438752561
H–	*FUT1*01N.18*	c.684G>A	4	p.Met228Ile	n.a.		
H–	*FUT1*01N.19*	c.694T>C	4	p.Trp232Arg	n.a.		
H–	*FUT1*01N.20*	c.768delC	4	p.Val257Phefs*23	PMID: 34967725	KM514482	
H–	*FUT1*01N.21*	c.13_19dup	4	p.Arg7Glnfs*63	n.a.		rs150995632
H–	*FUT1*01N.22*	c.791_792insG	4	p.Met265Hisfs*5		MG987419	
H–	*FUT1*01N.23*	c.710delG	4	p.Gly237Alafs*43		MH298872	rs1486913817
H–	*FUT1*01N.24*	c.454delG	4	p.Glu152Argfs*6		MH298873	rs1409390706
H–	*FUT1*01N.25*	c.288T>A	4	p.Tyr96Ter		MH298874	
H–	*FUT1*01N.26 (old: FUT1*02N.01)*	c.35C>T c.423G>A	4 4	p.Ala12Val p.Trp141Ter	PMID: 21839020	HQ699894	rs2071699
H–	*FUT1*01N.27*	c.49T>C	4	p.Val17Arg	PMID: 29441582	KX644898	
H–	*FUT1*01N.28*	c.361G>A	4	p.Ala121Thr	PMID: 34539321	MN938362	
H–	*FUT1*01N.29*	c.366-398del33	4	p.Val123Glu fsX355	PMID:17922418		
H–	*FUT1*01N.30*	c.392T>C	4	p.Leu131Pro	PMID: 26926997		
H–	*FUT1*01N.31*	c.508dupT	4	p. 170 fsX268	PMID: 33175455	KM255205	

Phenotype	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
H–	*FUT1*01N.32*	c.668-670delACT	4	p.Tyr224del	PMID: 26926997 PMID: 30988570		
H–	*FUT1*01N.33*	c.749-765delGGGC ACGGCACGAAGCC	4		PMID: 34799859	MT078122	
H–	*FUT1*01N.34*	c.787A>C	4	p.Asn263His	PMID: 33175455	KM255206	
H–	*FUT1*01N.35*	c.985insG c.961G>A	4 4	p.319Glyfs334 p.Asp321Asn	PMID: 28026021	KT989645	
H–	*FUT1*01N.36*	c.1051G>T	4	p.Gly351Cys	PMID: 30988570		
H–	*FUT1*01N.37*	c.35C>T c.980A>C	4 4	p.Ala12Val p.Asn327Thr	PMID: 15487706 PMID: 23560544 PMID: 9031499		rs777291875
‡ PMID: 32110200: Adsorption-elution studies with the patient's RBCs revealed positive reactions with anti-B, confirming a weak B phenotype. Flow cytometric analysis using fluorochrome-conjugated anti-H (BRIC198) detected minimal amounts of H antigens on the patient's RBCs withhomozygous c.515_516delAG of FUT1.							
Null phenotypes – Gene deletions							
H–	*FUT1*0N.01*	Coding region deletion (5443-bp length of deletion including the 1098-bp coding sequence of FUT1 gene)	-	p.0	PMID: 26926997		
† Note that H expression will be masked if a functional A or B allele is also inherited. Also, that H antigen may be weakly detectable on RBCs where FUT*01N homozygosity occurs, due to the adsorption of soluble H antigen synthesized by FUT2.							
Phenotype (saliva) †	**Allele name**	**Nucleotide change**	**Exon Intron**	**Predicted amino acid change**	**(Reference No.) PMID**	**Accession number**	**rs number**
H+	*FUT2*01*						
H+	*FUT2*01.02 (old: FUT2*02)*	c.4G>A	2	p.Ala2Thr	PMID: 18422843		rs532291838

Phenotype	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
H+	*FUT2*01.03.01 (old: FUT2*03.01)*	c.40A>G	2	p.Ile14Val	PMID: 9760207		rs1800021
H+	*FUT2*01.03.02 (old: FUT2*03.02)*	c.40A>G c.113C>T	2	p.Ile14Val p.Ala38Val	PMID: 9760207		rs1800021 rs114018037
H+	*FUT2*01.03.03 (old: FUT2*03.03)*	c.40A>G c.481G>A	2	p.Ile14Val p.Asp161Asn			rs1800021 rs1800025
H+	*FUT2*01.04 (old: FUT2*04)*	c.379C>T	2	p.Arg127Cys	PMID: 9760207		rs1800022
H+	*FUT2*01.05 (old: FUT2*05)*	c.400G>A	2	p.Val134Ile	PMID: 10980544 PMID: 1456946		rs370886251
H+	*FUT2*01.06 (old: FUT2*06)*	c.481G>A	2	p.Asp161Asn	PMID: 9760207		rs1800025
H+	*FUT2*01.07 (old: FUT2*07)*	c.665G>A	2	p.Arg222His	PMID: 18422843		rs776245547
H+	*FUT2*01.08 (old: FUT2*08)*	c.685G>A	2	p.Val229Met	PMID: 10980544		rs375360260
H+	*FUT2*01.09 (old: FUT2*09)*	c.716G>A	2	p.Arg239Gln	PMID: 15476160	DQ321371	rs369911091
H+	*FUT2*01.10 (old: FUT2*10)*	c.747_748insGTG	2	p.249_250insVal	PMID: 17655580		
H+	*FUT2*01.11*	c.98A>G c.101T>G	2 2	p.Gln33Arg p.Ile34Arg	PMID: 34487549	MW309872	
Weak phenotypes							
H+w	*FUT2*01W.01*	c.278C>T	2	p.Ala93Val			rs149356814
H+w	*FUT2*01W.02.01*	c.385A>T	2	p.Ile129Phe			rs1047781
H+w	*FUT2*01W.02.02*	c.385A>T c.617T>G	2 2	p.Ile129Phe p.Val206Gly			rs1047781

Phenotype	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
H+w	*FUT2*01W.02.03*	c.385A>T c.841G>A	2 2	p.Ile129Phe p.Gly281Arg			rs1047781 rs548111243
H+w	*FUT2*01W.03*	c.853G>A	2	p.Ala285Thr			rs79097987
H+w	*FUT2*01W.04*	c.617T>C	4	p.Val206Ala	PMID: 34487549	MW661069	
Null phenotypes – Nucleotide polymorphisms							
H–	*FUT2*01N.01*	c.244G>A c.385A>T	2	p.Ala82Thr p.Ile129Phe			rs112722916 rs1047781
H–	*FUT2*01N.02*	c.428G>A c.739A>G (after termination?)	2 2	p.Trp143Ter p.Gly247Ser (after termination?)	PMID: 7876235	U17894	rs601338
H–	*FUT2*01N.03*	c.569G>A	2	p.Arg190His	PMID: 18422843		rs572832908
H–	*FUT2*01N.04*	c.571C>T	2	p.Arg191Ter	PMID: 8755920 PMID: 10550557 PMID: 8928486 PMID: 8670215 PMID: 11606829		rs1800028
H–	*FUT2*01N.05*	c.628C>T	2	p.Arg210Ter	PMID: 8755920		rs1800029
H–	*FUT2*01N.06*	c.658C>T	2	p.Arg220Ter	PMID: 10319583 PMID: 34487549		rs144566043
H–	*FUT2*01N.07*	c.664C>T	2	p.Arg222Cys	PMID: 14569463		rs768236330
H–	*FUT2*01N.08*	c.685_686delGT	2	p.Val229Glyfs*4	PMID: 10085528 PMID: 1160682		
H–	*FUT2*01N.09*	c.688_690delGTC	2	p.Val230del	PMID: 10550557		
H–	*FUT2*01N.10*	c.400G>A c.760G>A	2 2	p.Val134Ile p.Asp254Asn	PMID: 14569463		rs370886251 rs907232085
H–	*FUT2*01N.11*	c.778delC	2	p.Pro260Leufs*16	PMID: 9760207		

Phenotype	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
H–	*FUT2*01N.12*	c.849G>A	2	p.Trp283Ter	PMID: 10550557 PMID: 8670215 PMID: 11606829		rs1800030
H–	*FUT2*01N.13*	c.868 G>A	2	p.Gly290Arg	PMID: 14569463		rs144269088
H–	*FUT2*01N.14*	c.950C>T	2	p.Pro317Leu	PMID: 18422843		rs200626231
H–	*FUT2*01N.15*	c.302C>T	2	p.Pro101Leu	PMID: 10533829		rs200157007
H–	*FUT2*01N.16*	c.960A>G (wrong position?)	2	p.Gly247Ser (wrong position?)			rs485186
H–	*FUT2*01N.17*	c.412G>A	2	p.Gly138Ser	PMID: 19572973	FM180558	rs200543547
H–	*FUT2*01N.18*	c.818C>A	2	p.Thr273Asn	PMID: 22188519		rs371279676
Null phenotypes – Gene deletions							
H–	*FUT2*0N.01*	Gene deletion		p.0			
H–	*FUT2*0N.01*	Coding region deleted		p.0	PMID: 9299444 PMID: 9745152 PMID: 10982186		
H–	*FUT2*0N.03*	Fusion gene 1 between *FUT2* and *Sec1*		-	PMID: 8755920 PMID: 18067503	D82933	
H–	*FUT2*0N.04*	Fusion gene 2 between *FUT2* and *Sec1*		-			
H–	*FUT2*0N.05*	Deletion of *FUT2*			PMID: 26926997		

† Saliva phenotype is shown here to represent secreted H antigen in all body fluids

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Track of changes

			from	to
1	**Version**		**v5.2 18th April 2019**	**v6.0 30-JUN-2022**
2	Author	created	Franz Wagner, April 2019	Franz Wagner, Yanli Ji, June 2022
3	Reviewer	reviewed	n.a.	Franz Wagner, C. Gassner, June 2022
4	General		Word version	First Excel map version. Spread-sheets "Intro", "Allele Table", "References", and "Versioning" created.
5	References	moved		Moved reference's texts to tab-sheet 'References'
6	References	numbering		renumbered Abstract (47) to (5)
7	Comment			General comment by Franz Wagner: Since most *FUT1* alleles are found in trans to a functional *FUT2* and usually, no expression studies are done, it is extremely difficult to discriminate between *FUT1*01W* and *FUT1*01N*. Obviously, the new alleles were assigned in an "optimistic" fashion, i.e. if no data showing a residual activity are present, the allele was assigned to the *FUT*01N* series although the inactivity of the allele isn't proven. Some of the old *FUT1*01W* alleles were assigned in a "pessimistic" way, i.e. if no data showing residual activity is absent and the mutation did not destroy protein expression, the allele was assigned to the *FUT1*01W* series although data showing residual activity are lacking. This change might lead to inconsistencies in the future, but admittedly I have no better solution (as you know, I would have supported a single series for weak or non-functional alleles, but such solution is not in line with the ISBT approach).
8	Allele	changed	*FUT1*02*	changed to *FUT1*01.02*
9	Allele	changed	*FUT1*02W.01*	changed to *FUT1*01W.31*
10	Allele	changed	*FUT1*02W.02*	changed to *FUT1*01W.32*
11	Allele	changed	*FUT1*02W.03*	changed to *FUT1*01W.33*

Track of changes

			from	to
1	**Version**		**v5.2 18th April 2019**	**v6.0 30-JUN-2022**
12	Allele	changed	*FUT1*02W.04*	changed to *FUT1*01W.34*
13	Allele	changed	*FUT1*02W.05*	changed to *FUT1*01W.35*
14	Allele	changed	*FUT1*02N.01*	changed to *FUT1*01N.26*
15	Allele	changed	*FUT2*02*	changed to *FUT2*01.02*
16	Allele	changed	*FUT2*03.01*	changed to *FUT2*01.03.01*
17	Allele	changed	*FUT2*03.02*	changed to *FUT2*01.03.02*
18	Allele	changed	*FUT2*03.03*	changed to *FUT2*01.03.03*
19	Allele	changed	*FUT2*04*	changed to *FUT2*01.04*
20	Allele	changed	*FUT2*05*	changed to *FUT2*01.05*
21	Allele	changed	*FUT2*06*	changed to *FUT2*01.06*
22	Allele	changed	*FUT2*07*	changed to *FUT2*01.07*
23	Allele	changed	*FUT2*08*	changed to *FUT2*01.08*
24	Allele	changed	*FUT2*09*	changed to *FUT2*01.09*
25	Allele	changed	*FUT2*10*	changed to *FUT2*01.10*
26	Allele	PMIDs added		PMIDs added
27	References	added		added authors
28	Allele	removed	*FUT1*01W.25*	obsolete now (provisionally)
29	Allele	avoided		The allele name *FUT1*01W.30* is avoided because of the use of this name in a publication, although this allele had not yet been officially ratified by the ISBT WP.
30	Allele	added		*FUT1*01W.31*
31	Allele	added		*FUT1*01W.32*
32	Allele	added		*FUT1*01W.33*
33	Allele	added		*FUT1*01W.34*
34	Allele	added		*FUT1*01W.35*
35	Allele	added		*FUT1*01W.36*
36	Allele	added		*FUT1*01W.37*
37	Allele	added		*FUT1*01W.38*
38	Allele	added		*FUT1*01W.39* (provisionally)
39	Allele	changed		*FUT1*01N.06* added Phenotype H+w and footnote
40	Allele	changed		*FUT1*01N.16* added c.35C>T, PMID 9031499
41	Allele	changed		*FUT1*01N.20* added PMID 34967725

Track of changes

			from	to
1	**Version**		**v5.2 18th April 2019**	**v6.0 30-JUN-2022**
42	Allele	changed		*FUT1*01N.24*
43	Allele	changed		*FUT1*01N.25*
44	Allele	changed	*FUT1*02N.01*	*FUT1*01N.26* added c.35C>T and rs2071699
45	Allele	added		*FUT1*01N.27* (provisionally)
46	Allele	added		*FUT1*01N.28*
47	Allele	added		*FUT1*01N.29*
48	Allele	added		*FUT1*01N.30*
49	Allele	added		*FUT1*01N.31*
50	Allele	added		*FUT1*01N.32*
51	Allele	added		*FUT1*01N.33*
52	Allele	added		*FUT1*01N.34*
53	Allele	added		*FUT1*01N.35*
54	Allele	added		*FUT1*01N.36*
55	Allele	added		*FUT1*01N.37*
56	Allele	added		*FUT1*0N.01*
57	Allele	changed	*FUT2*02*	*FUT2*01.02*
58	Allele	changed	*FUT2*03.01*	*FUT2*01.03.01*
59	Allele	changed	*FUT2*03.02*	*FUT2*01.03.02*
60	Allele	changed	*FUT2*03.03*	*FUT2*01.03.03*
61	Allele	changed	*FUT2*04*	*FUT2*01.04*
62	Allele	changed	*FUT2*05*	*FUT2*01.05*
63	Allele	changed	*FUT2*06*	*FUT2*01.06*
64	Allele	changed	*FUT2*07*	*FUT2*01.07*
65	Allele	changed	*FUT2*08*	*FUT2*01.08*
66	Allele	changed	*FUT2*09*	*FUT2*01.09*
67	Allele	changed	*FUT2*10*	*FUT2*01.10*
68	Allele	added		*FUT2*01.11*
69	Allele	added		*FUT2*01W.04*
70	Allele	changed		*FUT2*01N.04* added PMID 11606829
71	Allele	added		*FUT2*0N.05*
72	Allele	changed	*FUT1*02W.01*	*FUT1*01W.31*

Track of changes

			from	to
1	**Version**		**v5.2 18th April 2019**	**v6.0 30-JUN-2022**
73	Allele	changed	*FUT1*02W.02*	*FUT1*01W.32*
74	Allele	changed	*FUT1*02W.03*	*FUT1*01W.33*
75	Allele	changed	*FUT1*02W.04*	deleted, is now *FUT1*01N.16*
76	Allele	changed	*FUT1*02W.05*	*FUT1*01W.34*
77	Allele	changed		added rs-numbers
78	**End Version**		**v5.2 18th April 2019**	**v6.0 30-JUN-2022**

ack of changes		**from**	**to**
Version		**v5.1 170221**	**v5.2 18th April 2019**
Author	created	Franz Wagner, February 2017	Franz Wagner, April 2019
Reviewer	reviewed	n.a.	n.a.
General		Word version	Word version
Allele Table	allele added		*FUT1*01N.21*
Allele Table	allele added		*FUT1*01N.22*
Allele Table	allele added		*FUT1*01N.23*
Allele Table	allele added		*FUT1*01N.24*
End Version		**v5.1 170221**	**v5.2 18th April 2019**