

Names for RH (ISBT 004) Blood Group Alleles

General description: The Rh blood group system consists of 54 antigens carried on two proteins (RhD and RhCE) each consisting of 417 amino acids. Combinations (hybrids) between the two genes are not uncommon. The proteins consist of 12 membrane-spanning domains.

Gene name: *RHD*
 Number of exons: 10
 Initiation codon: Beginning of exon 1
 Stop codon: middle of exon 10
 NCBI RefSeq: NG_007494 (gene)
 NM_016124 (mRNA)
 Entrez Gene ID: 6007
 Preferred: *RHD*01*

Common category or name Phenotype(s)	Allele name	Nucleotide change	Exon(s)	Amino Acid(s)	Allele Name Detail	Comments Reported as:
D RH:1	<i>RHD*01</i>					
Normal D antigen	<i>RHD*01.01</i>	c.48G>C	1	p.Trp16Cys	<i>RHD*48C</i>	DUC-3
DII	<i>RHD*02</i> <i>RHD*DII</i>	c.1061C>A	7	p.Ala354Asp	<i>RHD*1061A</i>	
DIIIa RH:54 (DAK+)	<i>RHD*03.01</i> <i>RHD*DIIIa</i>	c.186G>T; c.410C>T; c.455A>C; c.602C>G; c.667T>G; c.819G>A	2,3,4,5,6	p.Leu62Phe p.Ala137Val p.Asn152Thr p.Thr201Arg p.Phe223Val silent	<i>RHD*186T,410T,455C,602G,667G</i>	Also reported as DIIIa type 5 (obsolete) Original DIIIa report missed 186G>T, 410C>T, and 819G>A
DIIIb Caucasian RH:54 (DAK+) RH:—12 (G—)	<i>RHD*03.02</i> <i>RHD*DIIIb</i>	c.150T>C; c.178A>C; c.201G>A; c.203G>A; c.307T>C	2	Silent p.Ile60Leu Silent p.Ser68Asn p.Ser103Pro	<i>RHD*D-CE(2)-D</i>	
DIIIc	<i>RHD*03.03</i> <i>RHD*DIIIc</i>	c.361T>A; c.380T>C; c.383A>G; c.455A>C	3	p.Leu121Met p.Val127Ala p.Asp128Gly p.Asn152Thr	<i>RHD*D-CE(3)-D</i>	
DIII type 4	<i>RHD*03.04</i> <i>RHD*DIII.04</i>	c.186G>T; c.410C>T; c.455A>C	2, 3	p.Leu62Phe p.Ala137Val p.Asn152Thr	<i>RHD*186T,410T,455C</i>	
Not tested	<i>RHD*03.04.02</i> <i>RHD*DIII.04.02</i>	c.186G>T; c.307T>C; c.410C>T; c.455A>C	2,3	p.Leu62Phe p.Ser103Pro p.Ala137Val p.Asn152Thr	<i>RHD*186T,307C,410T,455C</i>	<i>In trans</i> to DAR1

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DIII type 6	RHD*03.06 RHD*DIII.06	c.410C>T; c.455A>C; c.602C>G; c.667T>G; c.819G>A	3,4,5,6	p.Ala137Val p.Asn152Thr p.Thr201Arg p.Phe223Val silent	RHD*410T,455C,602G,667G	
DIII type 7 (likely the historically defined DIIIb)	RHD*03.07 RHD*DIII.07	c.150T>C; c.178A>C; c.201G>A; c.203G>A; c.307T>C; c.410C>T; c.455A>C c.602C>G c.667T>G	2,3,4,5	Silent p.Ile60Leu Silent p.Ser68Asn p.Ser103Pro p.Ala137Val p.Asn152Thr p.Thr201Arg p.Phe223Val	RHD*D-CE(2)-410T,455C,602G,667G-D	
DIII type 8	RHD*03.08 RHD*DIII.08	c.410C>T; c.455A>C	3	p.Ala137Val p.Asn152Thr	RHD*410T,455C	
DIVa RH30+ (Goa+)	RHD*04.01 RHD*DIVa	c.186G>T; c.410C>T; c.455A>C; c.1048G>C	2,3,7	p.Leu62Phe p.Ala137Val p.Asn152Thr p.Asp350His	RHD*186T,410T,455C,1048C	Often with RHCE*ceTI
DIVa type 2 obsolete						original DIVa report missed 410C>T change
DIVa-like or DIVa type 3	RHD*04.01.02	c.186G>T; c.410C>T; c.455A>C; c.667T>G; c.1048G>C	2,3,7	p.Leu62Phe p.Ala137Val p.Asn152Thr p.Phe223Val p.Asp350His	RHD*186T,410T,455C,667G,1048C	Was found with RHCE*ceTI

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DIV type 3	RHD*04.03 RHD* DIV.3	c.916G>A; c.932A>G; c.941G>T; c.968C>A; c.974G>T; c.979A>G; c.985G>C; c.986G>A; c.989A>C; c.992A>T; c.1025T>C; c.1048G>C; c.1053C>T; c.1057G>T; c.1059A>G; c.1060G>A; c.1061C>A; c.1063 G>T; c.1170 T>C; c.1193 A>T	6,7,8,9	p.Val306Ile p.Tyr311Cys p.Gly314Val p.Pro323His p.Ser325Ile p.Ile327Val p.Gly329His p.Gly329His p.Tyr330Ser p.Asn331Ile p.Ile343Thr p.Asp350His Silent p.Gly353Trp p.Gly353Trp p.Ala354Asn p.Ala354Asn Silent Silent p.Glu398Val	<i>RHD*D-CE(6-9)-D</i>	
DIV type 4	RHD*04.04 RHD*DIV.4	c.1048G>C, c.1053C>T; c.1057G>T; c.1059A>G; c.1060G>A; c.1061C>A	7	p.Asp350His Silent p.Gly353Trp p.Gly353Trp p.Ala354Asn p.Ala354Asn	<i>RHD*1048C,1057T,1059G,1060A,1061A</i>	
DIV type 5	RHD*04.05 RHD*DIV.5	c.941G>T; c.968C>A; c.974G>T; c.979A>G; c.985G>C; c.986G>A; c.989A>C; c.992A>T; c.1025T>C; c.1048G>C; c.1053C>T; c.1057G>T c.1059A>G; c.1060G>A; c.1061C>A; c.1063G>T; c.1170T>C; c.1193A>T	7,8,9	p.Gly314Val p.Pro323His p.Ser325Ile p.Ile327Val p.Gly329His p.Gly329His p.Tyr330Ser p.Asn331Ile p.Ile342Thr p.Asp350His Silent p.Gly353Trp p.Gly353Trp p.Ala354Asn p.Ala354Asn Silent Silent p.Glu398Val	<i>RHD*D-CE(7-9)-D</i>	

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DIVb	RHD*04.06 RHD*DIVb	c.1048G>C; c.1053C>T; c.1057G>T; c.1059A>G; c.1060G>A; c.1061C>A; c.1170T>C; c.1193A>T	7,8,9	p.Asp350His Silent p.Gly353Trp p.Gly353Trp p.Ala354Asn p.Ala354Asn Silent p.Glu398Val	RHD*D-1048C, 1057T, 1059G, 1060A, 1061A -CE(8- 9)-D	
DV type 1	RHD*05.01 RHD*DV.1	c.667T>G; c.697G>C	5	p.Phe223Val p.Glu233Gln	RHD*667G, 697C	Kou FK
DV type 2	RHD*05.02 RHD*DV.2	c.667T>G; c.697G>C; c.712G>A; c.733G>C; c.744C>T; c.787G>A; c.800A>T	5	p.Phe223Val p.Glu233Gln p.Val238Met p.Val245Leu Silent p.Gly263Arg, p.Lys267Met	RHD*D-CE(5)-D	Hus
DV type 3	RHD*05.03 RHD*DV.3	c.667T>G; c.676G>C; c.697G>C; c.712G>A	5	p.Phe223Val p.Ala226Pro p.Glu233Gln p.Val238Met	RHD*667G, 676C, 697C, 712A	Also known as DBSO
DV Type 4 RH:23 (D ^{w+})	RHD*05.04 RHD*DV.4	c.697G>C	5	p.Glu233Gln	RHD*697C	SM
DV type 5 RH:-23 (D ^{w-})	RHD*05.05 RHD*DV.5	c.697G>A	5	p.Glu233Lys	RHD*697A	DHK, DYO
DV type 6	RHD*05.06 RHD*DV.6	c.667T>G; c.697G>C; c.712G>A	5	p.Phe223Val p.Glu233Gln p.Val238Met	RHD*667G, 697C, 712 A	Jpn
DV type 7	RHD*05.07 RHD*DV.7	c.667T>G; c.697G>C; c.712G>A; c.733G>C; c.744C>T; c.787G>A	5	p.Phe223Val p.Glu233Gln p.Val238Met p.Val245Leu p.Gly263Arg silent p.Gly263Arg	RHD*667G, 697C, 712 A, 733C, 787A	DAL
DV type 8	RHD*05.08 RHD*DV.8	c.667T>G; c.697G>C; c.712G>A; c.733G>C; c.744C>T	5	p.Phe223Val p.Glu233Gln p.Val238Met p.Val245Leu silent		TT
DV type 9	RHD*05.09 RHD*DV.9	c.697G>C; c.712G>A	5	p.Glu233Gln p.Val238Met	RHD*697C, 712A	TO

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DV type 10	<i>RHD*05.10</i> <i>RHD*DV.10</i>	c.667T>G; c.697G>C; c.712G>A; c.733G>C; c.744C>T; c.787G>A; c.800A>T; c.916G>A; c.932A>G	5,6	p.Phe223Val p.Glu233Gln p.Val238Met p.Val245Leu Silent p.Gly263Arg p.Lys267Met p.Val306Ile p.Tyr311Cys	<i>RHD*D-CE-(5-6)-D</i>	
DVI type 1 RH:-52 (BARC-)	<i>RHD*06.01</i> <i>RHD*DVI.1</i>	c.505A>C; c.509T>G; c.514A>T; c.544T>A; c.577G>A; c.594A>T; c.602C>G; c.667T>G; c.676G>C; c.697G>C; c.712G>A; c.733G>C; c.744C>T; c.787G>A; c.800A>T	4,5	p.Met169Leu p.Met170Arg p.Ile172Phe p.Ser182Thr p.Glu193Lys p.Lys198Asn p.Thr201Arg p.Phe223Val p.Ala226Pro p.Glu233Gln p.Val238Met p.Val245Leu Silent p.Gly263Arg p.Lys267Met	<i>RHD*D-CE(4-5)-D</i>	linked to <i>RHCE*cE</i>
DVI type 2 RH:52 (BARC+)	<i>RHD*06.02</i> <i>RHD*DVI.2</i>	c.505A>C; c.509T>G; c.514A>T; c.544T>A; c.577G>A; c.594A>T; c.602C>G; c.667T>G; c.697G>C; c.712G>A; c.733G>C; c.744C>T; c.787G>A; c.800A>T; c.916G>A; c.932A>G	4,5,6	p.Met169Leu p.Met170Arg p.Ile172Phe p.Ser182Thr p.Glu193Lys p.Lys198Asn p.Thr201Arg p.Phe223Val p.Glu233Gln p.Val238Met p.Val245Leu Silent p.Gly263Arg p.Lys267Met p.Val306Ile p.Tyr311Cys	<i>RHD*D-CE(4-6)-D</i>	linked to <i>RHCE*Ce</i>

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DVI type 3 RH:52 BARC+	RHD*06.03.01 RHD*DVI.3	c.361T>A; c.380T>C; c.383A>G; c.455A>C; c.505A>C; c.509T>G; c.514A>T; c.544T>A; c.577G>A; c.594A>T; c.602C>G; c.667T>G; c.697G>C; c.712G>A; c.733G>C; c.744C>T; c.787G>A; c.800A>T; c.916G>A; c.932A>G	3,4,5,6	p.Leu121Met p.Val127Ala p.Asp128Gly p.Asn152Thr p.Met169Leu p.Met170Arg p.Ile172Phe p.Ser182Thr p.Glu193Lys p.Lys198Asn p.Thr201Arg p.Phe223Val p.Glu233Gln p.Val238Met p.Val254Leu Silent p.Gly263Arg p.Lys267Met p.Val306Ile p.Tyr311Cys	RHD*D-CE(3-6)-D	linked to RHCE*Ce
DVI type 3.2 BARC not tested	RHD*06.03.02 RHD*DVI.03.02	As above and c.1195G>A	3, 4, 5, 6, 9	As above and p.Ala399Thr	RHD*D-CE(3-6)-D 1195A	
DVI type 4 RH:52 (BARC+)	RHD*06.04 RHD*DVI.4	c.361T>A; c.380T>C; c.383A>G; c.455A>C; c.505A>C; c.509T>G; c.514A>T; c.544T>A; c.577G>A; c.594A>T; c.602C>G; c.667T>G; c.697G>C; c.712G>A; c.733G>C; c.744C>T; c.787G>A; c.800A>T	3,4,5	p.Leu121Met p.Val127Ala p.Asp128Gly p.Asn152Thr p.Met169Leu p.Met170Arg p.Ile172Phe p.Ser182Thr p.Glu193Lys p.Lys198Asn p.Thr201Arg p.Phe223Val p.Glu233Gln p.Val238Met p.Val245Leu Silent p.Gly263Arg p.Lys267Met	RHD*D-CE(3-5)-D	linked to RHCE*Ce
DVII RH:40 (Tar+)	RHD*07.01 RHD*DVII.1	c.329T>C	2	p.Leu110Pro	RHD*329C	
DVII type 2	RHD*07.02 RHD*DVII.2	c.307T>C; c.329T>C	2	p.Ser103Pro p.Leu110Pro	RHD*307C,329C	

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DFV	RHD*08.01 RHD*DFV	c.667T>G	5	p.Phe223Val	RHD*667G	
DAR(T203A)	RHD*09.01 RHD*DAR	c.602C>G; c.607A>G; c.667T>G; c.744C>T; c.957G>A; c.1025T>C	4	p.Thr201Arg p.Thr203Ala p.Phe223Val silent silent p.Ile342Thr	RHD*602G,607G,667G,744T,957A,1025C	
DAR1 (weak D 4.2)	RHD*09.01.00 RHD*DAR1.00	c.602C>G; c.667T>G; c.1025T>C	4,5,7	p.Thr201Arg p.Phe223Val p.Ile342Thr	RHD*602G,667G,1025C	
DAR1.1 (weak D 4.2.1)	RHD*09.01.01 RHD*DAR1.01	c.602C>G; c.667T>G; c.957G>A; c.1025T>C	4,5,7	p.Thr201Arg p.Phe223Val Silent p.Ile342Thr	RHD*602G,667G,1025C	
DAR1.2 (weak D 4.2.2)	RHD*09.01.02 RHD*DAR1.02	c.602C>G; c.667T>G; c.744C>T; c.957G>A; c.1025T>C	4,5,7	p.Thr201Arg p.Phe223Val Silent Silent p.Ile342Thr	RHD*602G,667G,1025C	
DAR1.3 (weak D 4.2.3)	RHD*09.01.03 RHD*DAR1.03	c.602C>G; c.667T>G; c.744C>T; c.1025T>C	4,5,7	p.Thr201Arg p.Phe223Val Silent p.Ile342Thr	RHD*602G,667G,1025C	
DAR2 (DARE)	RHD*09.02.00 RHD*DAR2.00	c.602C>G; c.667T>G; c.697G>C; c.957G>A; c.1025 T>C	4,5,7	p.Thr201Arg p.Phe223Val p.Glu233Gln Silent p.Ile342Thr	RHD*602G,667G,697C,1025C	Reported as DAR-E
DAR2.1	RHD*09.02.01 RHD*DAR2.01	c.602C>G; c.667T>G; c.697G>C; c.744C>T; c.957G>A; c.1025 T>C	4,5,7	p.Thr201Arg p.Phe223Val p.Glu233Gln Silent Silent p.Ile342Thr	RHD*602G, 557G, 697C, 744T, 957A	
DAR3 (weak partial D 4.0.1)	RHD*09.03 RHD*DAR3	c.602C>G; c.667T>G	4, 5	p.Thr201Arg p.Phe223Val	RHD*602G,667G	
DAR3.1 (weak partial D 4.0)	RHD*09.03.01 RHD*DAR3.01	c.602C>G; c.667T>G; c.819G>A	4, 5, 6	p.Thr201Arg p.Phe223Val silent	RHD*602G,667G	

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DAR4 (weak D 4.1)	RHD*09.04 RHD*DAR4	c.48G>C; c.602C>G; c.667T>G; c.819G>A	1,4,5,6	p.Trp16Cys p.Thr201Arg p.Phe223Val silent	<i>RHD*48C,602G,667G</i>	
DAR5 (weak D 4.3 or Del)	RHD*09.05 RHD*DAR5	c.602C>G; c.667T>G; c.819G>A; c.872C>G	4,5,6	p.Thr201Arg p.Phe223Val Silent p.Pro291Arg	<i>RHD*602G,667G,872G</i>	
DAR6 Or DAR(CE2:V50V-S68N)	RHD*09.06 RHD*DAR6 Or RHD*09.06 RHD*DAR(CE2:V50V-S68N)	c.150T>C; c.178A>C; c.201G>A; c.203G>A; c.602C>G; c.667T>G; c.1025T>C	2, 4, 5, 7	Silent p.Ile60Leu Silent p.Ser68Asn p.Thr201Arg p.Phe223Val p.Ile342Thr	<i>RHD*150C, 178C, 201A, 203A, 602G, 667G, 1025C</i>	
DAU0	RHD*10.00 RHD*DAU0	c.1136C>T	8	p.Thr379Met	<i>RHD*1136T</i>	
DAU0.01	RHD*10.00.01 RHD*DAU0.01	c.1136C>T; c.579G>A	8 4	p.Thr379Met silent	<i>RHD*1136T,579A</i>	
DAU0.02	RHD*10.00.02 RHD*DAU0.02	c.1136C>T; c.150T>C	8 2	p.Thr370Met Silent(commo n)	<i>RHD*1136T,150C</i>	
DAU1	RHD*10.01 RHD*DAU1	c.689G>T; c.1136C>T	5,8	p.Ser230Ile p.Thr379Met	<i>RHD*689T,1136T</i>	
DAU2	RHD*10.02 RHD*DAU2	c.209G>A; c.998G>A; c.1136C>T	2,7,8	p.Arg70Gln p.Ser333Asn p.Thr379Met	<i>RHD*209A,998A,1136T</i>	
DAU3	RHD*10.03 RHD*DAU3	c.835G>A; c.1136C>T	6, 8	p.Val279Met p.Thr379Met	<i>RHD*835A,1136T</i>	
DAU4	RHD*10.04 RHD*DAU4	c.697G>A; c.1136C>T	5, 8	p.Glu233Lys p.Thr379Met	<i>RHD*697A,1136T</i>	
DAU5	RHD*10.05 RHD*DAU5	c.667T>G; c.697G>C; c.1136C>T	5, 8	p.Phe223Val p.Glu233Gln p.Thr379Met	<i>RHD*667G,697C,1136T</i>	
DAU5.1	RHD*10.05.01 RHD*DAU5.01	c.667T>G; c.697G>C; c.1122C>T; c.1136C>T	5, 8	p.Phe223Val p.Glu233Gln silent p.Thr379Met	<i>RHD*667G, 697C, 1122T, 1136T</i>	
DAU6	RHD*10.06 RHD*DAU6	c.998G>A; c.1136C>T	7, 8	p.Ser333Asn p.Thr379Met	<i>RHD*998A,1136T</i>	
DAU7	RHD*10.07 RHD*DAU7	c.835G>A; c.998G>A; c.1136C>T;	6,7,8	p.Val279Met p.Ser333Asn p.Thr379Met	<i>RHD*835A,998A,1136T</i>	

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DAU8	RHD*10.08 RHD*DAU8	c.340C>T; c.579G>A; c.1136C>T	3, 4, 8	p.Arg114Trp silent p.Thr379Met	RHD*340T, 579A, 1136T	
DAU9	RHD*10.09 RHD*DAU9	c.535T>C; c.1136C>T	4, 8	p.Phe179Leu p.Thr379Met	RHD*535C, 1136T	
DAU10	RHD*10.10 RHD*DAU10	c.579G>A; c.739G>C; c.1136C>T	4, 5, 8	Silent p.Val247Leu p.Thr379Met	RHD*579A, 739C, 1136T	
DAU11	RHD*10.11 RHD*DAU11	c.254C>T; c.835G>A; c.1136C>T	2, 6, 8	p.Ala85Val p.Val279Met p.Thr379Met	RHD*254T, 835A, 1136T	
DAU12	RHD*10.12 RHD*DAU12	c.542T>C; c.1136C>T	4, 8	p.Leu181Pro p.Thr379Met	RHD*542C, 1136T	
DAU13	RHD*10.13 RHD*DAU13	c.48G>C c.1136C>T	1, 8	p.Trp16Cys p.Thr379Met	RHD*48C, 1136T	
DAU14	RHD*10.14 RHD*DAU14	c.201G>A; c.203G>A; c.1136C>T	2, 8	Silent p.Ser68Asn p.Thr379Met	RHD*201A, 203A, 1136T	
RHD(M1V,T379M) Or DAU15	RHD*10.15 RHD*DAU15 Or RHD10.15	c.1A>G; c.1136C>T	1, 8	p.Met1Val p.Thr379Met	RHD*1G, 1136T	
weak partial 11 or Del	RHD*11 RHD*weak partial 11	c.885G>T	6	p.Met295Ile	RHD*885T	allo-anti-D reported Del phenotype when with RHCE*Ce
DOL1 RH:54(DAK+)	RHD*12.01 RHD*DOL1	c.509T>C; c.667T>G	4,5	p.Met170Th, p.Phe223Val	RHD*509C,667G	
DOL2 RH:54(DAK+)	RHD*12.02 RHD*DOL2	c.509T>C; c.667T>G; c.1132C>G	4,5,8	p.Met170Thr p.Phe223Val p.Leu378Val	RHD*509C,667G, 1132G	
DOL3	RHD*12.03 RHD*DOL3	c.410C>T; c.509T>C; c.667T>G	3,4,5	p.Ala137Val p.Met170Thr p.Phe223Val	RHD*410T,509C,667G	
DBS1	RHD*13.01 RHD*DBS1	c.667T>G; c.676G>C; c.697G>C; c.712G>A; c.733G>C; c.744 C>T; c.787G>A; c.800 A>T	5	p.Phe223Val p.Ala226Pro p.Glu233Gln p.Val238Met p.Val245Leu Silent p.Gly263Arg p.Lys267Met	RHD*D-cE(5)-D	

Common category or name Phenotype(s)	Allele name	Nucleotide change	Exon(s)	Amino Acid(s)	Allele Name Detail	Comments Reported as:
DBS2	RHD*13.02 RHD*DBS2	c.667T>G; c.676G>C; c.697G>C	5	p.Phe223Val p.Ala226Pro p.Glu233Gln	RHD*667G,676C,697C	
DBT1	RHD*14.01 RHD*DBT1	c.667T>G; c.697G>C; c.712 G>A; c.733G>C; c.744C>T; c.787G>A; c.800A>T; c.916G>A; c.932A>G; c.941G>T; c.968C>A; c.974G>T; c.979A>G; c.985 G>C; c.986 G>A; c.989 A>C; c.992 A>T; c.1025T>C; c.1048G>C; c.1053C>T; c.1057G>T; c.1059A>G; c.1060G>A; c.1061C>A	5,6.7	p.Phe223Val p.Glu233Gln p.Val238Met p.Val254Leu Silent p.Gly263Arg p.Lys267Met p.Val306Ile p.Tyr311Cys p.Gly314Val p.Pro323His p.Ser325Ile p.Ile327Val p.Gly329His p.Gly329His p.Tyr330Ser p.Asn331Ile p.Ile342Thr p.Asp350His Silent p.Gly353Trp p.Gly353Trp p.Ala354Asn p.Ala354Asn	RHD*D-CE(5-7)-D	

Common category or name Phenotype(s)	Allele name	Nucleotide change	Exon(s)	Amino Acid(s)	Allele Name Detail	Comments Reported as:
DBT2	RHD*14.02 RHD*DBT2	c.667T>G; c.697G>C; c.712G>A; c.733G>C; c.744C>T; c.787G>A; c.800A>T; c.916G>A; c.932A>G; c.941G>T; c.968C>A; c.974G>T; c.979A>G; c.985G>C; c.986G>A; c.989A>C; c.992A>T; c.1025T>C; c.1048G>C; c.1053C>T; c.1057G>T; c.1059A>G; c.1060G>A; c.1061C>A; c.1170T>C; c.1193 A>T	5,6,7,8, 9	p.Phe223Val p.Glu233Gln p.Val238Met p.Val245Leu Silent p.Gly263Arg p.Lys267Met p.Val306Ile p.Tyr311Cys p.Gly314Val p.Pro323His p.Ser325Ile p.Ile327Val p.Gly329His p.Gly329His p.Tyr330Ser p.Asn331Ile p.Ile342Thr p.Asp350His Silent p.Gly353Trp p.Gly353Trp p.Ala354Asn p.Ala354Asn Silent p.Glu398Val	<i>RHD*D-CE(5-9)-D</i>	
Weak partial Type 15	RHD*15 RHD*weak partial 15	c.845G>A	6	p.Gly282Asp	<i>RHD*845A</i>	allo anti-D reported
DCS1	RHD*16.01 RHD*DCS1	c.667T>G; c.676G>C	5	p.Phe223Val p.Ala226Pro	<i>RHD*667T,676C</i>	
DCS2	RHD*16.02 RHD*DCS2	c.676G>C	5	p.Ala226Pro	<i>RHD*676C</i>	
DCS-3	RHD*16.02 RHD*DCS3	c.667T>G; c.676G>C; c.697G>C	5	p.Phe223Val p.Ala226Pro p.Glu233Gln	<i>RHD*667G,676C,697C</i>	linked to <i>RHCE*cE</i>
DFR1	RHD*17.01 RHD*DFR1	c.505A>C; c.509T>G; c.514A>T	4	p.Met169Leu p.Met170Arg p.Ile172Phe	<i>RHD*505C,509G,514T</i>	

Common category or name Phenotype(s)	Allele name	Nucleotide change	Exon(s)	Amino Acid(s)	Allele Name Detail	Comments Reported as:
DFR2	RHD*17.02 RHD*DFR2	c.505A>C; c.509T>G; c.514A>T; c.544T>A; c.577G>A; c.594A>T; c.602C>G	4	p.Met169Leu p.Met170Arg p.Ile172Phe p.Ser182Thr p.Glu193Lys p.Lys198Asn p.Thr201Arg	<i>RHD*D-CE(4)-D</i>	
DFR3	RHD*17.03 RHD*DFR3	c.505A>C; c.509T>G; c.514A>T; c.539G>C	4	p.Met169Leu p.Met170Arg p.Ile172Phe p.Gly180Ala	<i>RHD*505C,509G,514T,539C</i>	
DFR4	RHD*17.04 RHD*DFR4	c.505A>C; c.509T>G	4	p.Met169Leu p.Met170Arg	<i>RHD*505C,509G</i>	
DFR5	RHD*17.05 RHD*DFR5	c.361 T>A; c.380 T>C; c.383 A>G; c.455 A>C; c.505 A>C; c.509 T>G; c.514 A>T; c.544 T>A; c.577 G>A; c.594 A>T; c.602 C>G	3,4	p.Leu121Met p.Val127Ala p.Asp128Gly p.Asn152Thr p.Met169Leu p.Met170Arg p.Ile172Phe p.Ser182Thr p.Glu193Lys p.Lys198Asn p.Thr201Arg	<i>RHD*D-CE(3-4)-D</i>	
DFW	RHD*18 RHD*DFW	c.497A>C	4	p.His166Pro	<i>RHD*497C</i>	
DHMi	RHD*19 RHD*DHMi	c.848C>T	6	p.Thr283Ile	<i>RHD*848T</i>	
DHO	RHD*20 RHD*DHO	c.704A>C	5	p.Lys235Thr	<i>RHD*704C</i>	
Weak partial Type 21	RHD*21 RHD*weak partial D 21	c.938C>T	6	p.Pro313Leu	<i>RHD*938T</i>	allo-anti-D reported
DHR	RHD*22 RHD*DHR	c.686G>A	5	p.Arg229Lys	<i>RHD*686A</i>	
DMH	RHD*23 RHD*DMH	c.161T>C	2	p.Leu54Pro	<i>RHD*161C</i>	
DNAK	RHD*24 RHD*DNAK	c.1070G>A	7	p.Gly357Asp	<i>RHD*1070A</i>	
DNB	RHD*25 RHD*DNB	c.1063G>A	7	p.Gly355Ser	<i>RHD*1063A</i>	
DNU	RHD*26 RHD*DNU	c.1057G>A	7	p.Gly353Arg	<i>RHD*1057A</i>	

Common category or name Phenotype(s)	Allele name	Nucleotide change	Exon(s)	Amino Acid(s)	Allele Name Detail	Comments Reported as:
DDE	RHD*27 RHD*DDE	c.120T>A	1	p.Asp40Glu	<i>RHD*120A</i>	
DFL	RHD*28 RHD*DFL	c.494A>G	4	p.Tyr165Cys	<i>RHD*494G</i>	
DYU (DQC)	RHD*29 RHD*DYU	c.700A>T	5	p.Arg234Trp	<i>RHD*700T</i>	
DTO	RHD*30 RHD*DTO	c.667T>G; c.674C>T	5	p.Phe223Val p.Ser225Phe	<i>RHD*667G,674T</i>	
DVL1	RHD*31 RHD*DVL1	c.684_686 del GAG	5	p.Arg229del	<i>RHD*684_686delGAG</i>	
DVL2	RHD*32 RHD*DVL2	c.705_707 del GAA	5	p.Lys235del	<i>RHD*705_707delGAA</i>	
DWI (DWLLE)	RHD*33 RHD*DWI	c.1073T>C	7	p.Met358Thr	<i>RHD*1073C</i>	
DIM (DIlleM)	RHD*34 RHD*DIM	c.854G>A	6	p.Cys285Tyr	<i>RHD*854A</i>	
DMA	RHD*35 RHD*DMA	c.621G>C	4	p.Leu207Phe	<i>RHD*621C</i>	
DLO	RHD*36 RHD*DLO	c.851C>T	6	p.Ser284Leu	<i>RHD*851T</i>	
DUC2	RHD*37 RHD*DUC2	c.733G>C	5	p.Val245Leu	<i>RHD*733C</i>	
DNT	RHD*38 RHD*DNT	c.455A>C	3	p.Asn152Thr	<i>RHD*455C</i>	
<i>RHD(S103P)</i> RH:—12 (G—)	RHD*39	c.307T>C	2	p.Ser103Pro	<i>RHD*307C</i>	
D-SPM	RHD*40 RHD*D-SPM	c.186G>T; c.410C>T; c.455A>C; c.509T>C; c.667T>G	2,3,4,5	p.Leu62Phe p.Ala137Val p.Asn152Thr p.Met170Thr p.Phe223Val	<i>RHD*186T,410T,455C ,509C,667G</i>	

Common category or name Phenotype(s)	Allele name	Nucleotide change	Exon(s)	Amino Acid(s)	Allele Name Detail	Comments Reported as:
DBU	RHD*41 RHD*DBU	c.667T>G; c.676G>C; c.697G>C; c.712G>A; c.733G>C; c.744C>T; c.787G>A; c.800A>T; c.916G>A; c.932A>G; c.941G>T; c.968C>A; c.974G>T; c.979A>G; c.985G>C; c.986G>A; c.989A>C; c.992A>T; c.1025T>C c.1048G>C c.1053C>T c.1057G>T; c.1059A>G; c.1060G>A; c.1061C>A	5,6,7	p.Phe223Val p.Ala226Pro p.Glu233Gln p.Val238Met p.Val245Leu silent p.Gly263Arg p.Lys267Met p.Val306Ile p.Tyr311Cys p.Gly314Val p.Pro323His p.Ser325Ile p.Ile327Val p.Gly329His p.Gly329His p.Tyr330Ser p.Asn331Ile p.Ile342Thr p.Asp350His silent p.Gly353Trp p.gly353Trp p.Ala354Asn p.Ala354Asn		
DCC	RHD*42 RHD*DCC	c.677 C>A	5	p.Ala226Asp	<i>RHD*677A</i>	
DDN	RHD*43 RHD*DDN	c.490G>A	4	p.Asp164Asn	<i>RHD*490A</i>	
DHQ	RHD*44 RHD*DHQ	c.513C>A	4	p.His171Gln	<i>RHD*513A</i>	
DKK	RHD*45 RHD*DKK	c.150T>C; c.178A>C; c.201G>A; c.203G>A; c.307T>C; c.361T>A; c.380T>C; c.383A>G; c.455A>C	2,3	Silent p.Ile60Leu silent p.Ser68Asn p.Ser103Pro p.Leu121Met p.Val127Ala p.Asp128Gly p.Asn152Thr	<i>RHD*D-CE(2-3)-D</i>	

Common category or name Phenotype(s)	Allele name	Nucleotide change	Exon(s)	Amino Acid(s)	Allele Name Detail	Comments Reported as:
DLX	RHD*46 RHD*DLX	c.667T>G; c.712G>A; c.733G>C; c.744C>T; c.787G>A; c.800A>T; c.916G>A; c.932A>G	5,6	p.Phe223Val p.Val238Met p.Val245Leu silent p.Gly263Arg p.Lys267Met p.Val306Ile p.Tyr311Cys	RHD*D(F223V)- CE(5:712-6)-D	
DMI	RHD*47 RHD* DMI	c.510G>A	4	p.Met170Ile	RHD*510A	
DMI-1.1	RHD*47.01 RHD*DMI-1.1	c.510G>T	4	p.Met170Ile	RHD*510T	
DNS	RHD*48 RHD*DNS	c.485A>G	3	p.Asn162Ser	RHD*485G	
DWN	RHD*49 RHD*DWN	c.1053C>T; c.1057G>G; c.1059A>G; c.1060G>A; c.1061C>A	7	Silent p.Gly353Trp p.Gly353Trp p.Ala354Asn p.Ala354Asn	RHD*1053T, 1057G, 1059G, 1060A, 1061A	
<i>RHD(A354T)</i>	RHD*50	c.1060G>A	7	p.Ala354Thr	RHD*1060A	
<i>RHD(del44L)</i>	RHD*51	c.130_132 delCTC	1	p.Leu44del	RHD*130_132 delCTC	
<i>RHD(F223S)</i>	RHD*52	c.668T>C	5	p.Phe223Ser	RHD*668C	
<i>RHD(IVS2-2delA)</i>	RHD*53	c.336-2delA	Intron 2	Splice site change	RHD*336-2delA	
<i>RHD(IVS4-2A>C)</i>	RHD*54	c.635-2A>C	Intron 4	Splice site change	RHD*635-2A>C	
<i>RHD(L81P)</i>	RHD*55	c.242T>C	2	p.Leu81Pro	RHD*242C	
DBA	RHD*56 RHD*DBA	c.680T>C	5	p.Leu227Pro	RHD*680C	
weak partial type 57	RHD*57 RHD*weak partial 57	c.640C>T	5	p.Leu214Phe	RHD*640T	

Common category or name Phenotype(s)	Allele name	Nucleotide change	Exon(s)	Amino Acid(s)	Allele Name Detail	Comments Reported as:
<i>RHD</i> *D-CE(7)-D	<i>RHD</i>*58	c.941G>T; c.968C>A; c.974G>T; c.979A>G; c.985G>C; c.986G>A; c.989A>C; c.992A>T; c.1025T>C; c.1048G>C; c.1053C>T; c.1057G>T; c.1059A>G; c.1060G>A; c.1061C>A	7	p.Gly314Val p.Pro323His p.Ser325Ile p.Ile327Val p.Gly329His p.Gly329His p.Tyr330Ser p.Asn331Ile p.Ile342Thr p.Asp350His silent p.Gly353Trp p.Gly353Trp p.Ala354Asn p.Ala354Asn	<i>RHD</i> *D-CE(7)-D	
<i>RHD</i> (F175L)	<i>RHD</i>*59	c.525C>T	4	p.Phe175Leu	<i>RHD</i> *525T	
weak Partial D	<i>RHD</i>*60	c.178A>C; c.689G>T	2,5	p.Ile60Leu p.Ser230Ile	<i>RHD</i> *178C,689T	
weak Partial D	<i>RHD</i>*61	c.492C>A	4	p.Asp164Glu	<i>RHD</i> *492A	
DNT(V270G)	<i>RHD</i>*62	c.455A>C; c.809T>G	3,6	p.Asn152Thr p.Val270Gly	<i>RHD</i> *455C,809G	