

## 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	<b>RHD*03.06</b> <b>RHD*DIII.06</b>	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	<b>RHD*410T,455C,602G,667G</b>	
DIII type 7 (likely the historically defined DIIIb)	<b>RHD*03.07</b> <b>RHD*DIII.07</b>	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	<b>RHD*D-CE(2)-410T,455C,602G,667G-D</b>	
DIII type 8	<b>RHD*03.08</b> <b>RHD*DIII.08</b>	c.410C>T; c.455A>C	3	p.Ala137Val; p.Asn152Thr	<b>RHD*410T,455C</b>	
DIII type 9	<b>RHD*03.09</b> <b>RHD*DIII.09</b>	c.186G>T c.410C>T c.455A>C c.667T>G	2,3,4,5	p.Leu62Phe; p.Ala137Val; p.Asn152Thr; p.Phe223Val	<b>RHD*186T,410T,455C,667G</b>	
DIVa RH30+ (Goa+)	<b>RHD*04.01</b> <b>RHD*DIVa</b>	c.186G>T; c.410C>T; c.455A>C; c.1048G>C	2,3,7	p.Leu62Phe; p.Ala137Val; p.Asn152Thr; p.Asp350His	<b>RHD*186T,410T,455C,1048C</b>	Often with <b>RHCE*ceTI</b>
DIVa type 2 obsolete						original DIVa report missed 410C>T change
DIVa-like or DIVa type 3	<b>RHD*04.01.02</b>	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	<b>RHD*186T,410T,455C,667G,1048C</b>	Was found with <b>RHCE*ceTI</b>

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DIV type 3	<b>RHD*04.03</b> <b>RHD* DIV.3</b>	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	<b>RHD*04.04</b> <b>RHD*DIV.4</b>	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	<b>RHD*04.05</b> <b>RHD*DIV.5</b>	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	<b>RHD*04.06</b> <b>RHD*DIVb</b>	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	<b>RHD*D-1048C,</b> <b>1057T, 1059G,</b> <b>1060A, 1061A -CE(8-</b> <b>9)-D</b>	
DV type 1	<b>RHD*05.01</b> <b>RHD*DV.1</b>	c.667T>G; c.697G>C	5	p.Phe223Val; p.Glu233Gln	<b>RHD*667G, 697C</b>	Kou FK
DV type 2	<b>RHD*05.02</b> <b>RHD*DV.2</b>	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	<b>RHD*D-CE(5)-D</b>	Hus
DV type 3	<b>RHD*05.03</b> <b>RHD*DV.3</b>	c.667T>G; c.676G>C; c.697G>C; c.712G>A	5	p.Phe223Val; p.Ala226Pro; p.Glu233Gln; p.Val238Met	<b>RHD*667G, 676C,</b> <b>697C, 712A</b>	Also known as <b>DBSO</b>
DV Type 4 RH:23 (D <sup>w+</sup> )	<b>RHD*05.04</b> <b>RHD*DV.4</b>	c.697G>C	5	p.Glu233Gln	<b>RHD*697C</b>	SM
DV type 5 RH:-23 (D <sup>w-</sup> )	<b>RHD*05.05</b> <b>RHD*DV.5</b>	c.697G>A	5	p.Glu233Lys	<b>RHD*697A</b>	DHK, DYO
DV type 6	<b>RHD*05.06</b> <b>RHD*DV.6</b>	c.667T>G; c.697G>C; c.712G>A	5	p.Phe223Val; p.Glu233Gln; p.Val238Met	<b>RHD*667G, 697C, 712</b> <b>A</b>	Jpn
DV type 7	<b>RHD*05.07</b> <b>RHD*DV.7</b>	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	<b>RHD*667G, 697C, 712</b> <b>A, 733C, 787A</b>	DAL
DV type 8	<b>RHD*05.08</b> <b>RHD*DV.8</b>	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	<b>RHD*05.09</b> <b>RHD*DV.9</b>	c.697G>C; c.712G>A	5	p.Glu233Gln; p.Val238Met	<b>RHD*697C, 712A</b>	TO

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DV type 10	<b><i>RHD*05.10</i></b> <b><i>RHD*DV.10</i></b>	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-)	<b><i>RHD*06.01</i></b> <b><i>RHD*DVI.1</i></b>	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+)	<b><i>RHD*06.02</i></b> <b><i>RHD*DVI.2</i></b>	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+	<b>RHD*06.03.01</b> <b>RHD*DVI.3</b>	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	<b>RHD*D-CE(3-6)-D</b>	linked to <i>RHCE*Ce</i>
<b>DVI type 3.2</b> <b>BARC not tested</b>	<b>RHD*06.03.02</b> <b>RHD*DVI.03.02</b>	As above <b>and</b> c.1195G>A	3, 4, 5, 6, 9	As above <b>and</b> p.Ala399Thr	<b>RHD*D-CE(3-6)-D</b> <b>1195A</b>	
DVI type 4 RH:52 (BARC+)	<b>RHD*06.04</b> <b>RHD*DVI.4</b>	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	<b>RHD*D-CE(3-5)-D</b>	linked to <i>RHCE*Ce</i>
DVII RH:40 (Tar+)	<b>RHD*07.01</b> <b>RHD*DVII.1</b>	c.329T>C	2	p.Leu110Pro	<b>RHD*329C</b>	
DVII type 2	<b>RHD*07.02</b> <b>RHD*DVII.2</b>	c.307T>C; c.329T>C	2	p.Ser103Pro; p.Leu110Pro	<b>RHD*307C,329C</b>	

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

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DAR4 (weak D 4.1)	<b>RHD*09.04</b> <b>RHD*DAR4</b>	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)	<b>RHD*09.05</b> <b>RHD*DAR5</b>	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)	<b>RHD*09.06</b> <b>RHD*DAR6</b> Or <b>RHD*09.06</b> <b>RHD*DAR(CE2:V50V-S68N)</b>	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	<b>RHD*10.00</b> <b>RHD*DAU0</b>	c.1136C>T	8	p.Thr379Met	<i>RHD*1136T</i>	
DAU0.01	<b>RHD*10.00.01</b> <b>RHD*DAU0.01</b>	c.1136C>T; c.579G>A	8 4	p.Thr379Met silent	<i>RHD*1136T,579A</i>	
DAU0.02	<b>RHD*10.00.02</b> <b>RHD*DAU0.02</b>	c.1136C>T; c.150T>C	8 2	p.Thr370Met Silent(common)	<i>RHD*1136T,150C</i>	
DAU1	<b>RHD*10.01</b> <b>RHD*DAU1</b>	c.689G>T; c.1136C>T	5,8	p.Ser230Ile; p.Thr379Met	<i>RHD*689T,1136T</i>	
DAU2	<b>RHD*10.02</b> <b>RHD*DAU2</b>	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	<b>RHD*10.03</b> <b>RHD*DAU3</b>	c.835G>A; c.1136C>T	6, 8	p.Val279Met; p.Thr379Met	<i>RHD*835A,1136T</i>	
DAU4	<b>RHD*10.04</b> <b>RHD*DAU4</b>	c.697G>A; c.1136C>T	5, 8	p.Glu233Lys; p.Thr379Met	<i>RHD*697A,1136T</i>	
DAU5	<b>RHD*10.05</b> <b>RHD*DAU5</b>	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	<b>RHD*10.05.01</b> <b>RHD*DAU5.01</b>	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	<b>RHD*10.06</b> <b>RHD*DAU6</b>	c.998G>A; c.1136C>T	7, 8	p.Ser333Asn; p.Thr379Met	<i>RHD*998A,1136T</i>	
DAU7	<b>RHD*10.07</b> <b>RHD*DAU7</b>	c.835G>A; c.998G>A; c.1136C>T;	6,7,8	p.Val279Met; p.Ser333Asn; p.Thr379Met	<i>RHD*835A,998A,1136T</i>	



Common category or name Phenotype(s)	Allele name	Nucleotide change	Exon(s)	Amino Acid(s)	Allele Name Detail	Comments Reported as:
DAU8	<b>RHD*10.08</b> <b>RHD*DAU8</b>	c.340C>T; c.579G>A; c.1136C>T	3, 4, 8	p.Arg114Trp; silent; p.Thr379Met	<b>RHD*340T, 579A, 1136T</b>	
DAU9	<b>RHD*10.09</b> <b>RHD*DAU9</b>	c.535T>C; c.1136C>T	4, 8	p.Phe179Leu; p.Thr379Met	<b>RHD*535C, 1136T</b>	
DAU10	<b>RHD*10.10</b> <b>RHD*DAU10</b>	c.579G>A; c.739G>C; c.1136C>T	4, 5, 8	silent; p.Val247Leu; p.Thr379Met	<b>RHD*579A, 739C, 1136T</b>	
DAU11	<b>RHD*10.11</b> <b>RHD*DAU11</b>	c.254C>T; c.835G>A; c.1136C>T	2, 6, 8	p.Ala85Val; p.Val279Met; p.Thr379Met	<b>RHD*254T, 835A, 1136T</b>	
DAU12	<b>RHD*10.12</b> <b>RHD*DAU12</b>	c.542T>C; c.1136C>T	4, 8	p.Leu181Pro; p.Thr379Met	<b>RHD*542C, 1136T</b>	
DAU13	<b>RHD*10.13</b> <b>RHD*DAU13</b>	c.48G>C c.1136C>T	1, 8	p.Trp16Cys; p.Thr379Met	<b>RHD*48C, 1136T</b>	
DAU14	<b>RHD*10.14</b> <b>RHD*DAU14</b>	c.201G>A; c.203G>A; c.1136C>T	2, 8	silent; p.Ser68Asn; p.Thr379Met	<b>RHD*201A, 203A, 1136T</b>	
RHD(M1V,T379M ) Or DAU15	<b>RHD*10.15</b> <b>RHD*DAU15</b> Or <b>RHD10.15</b>	c.1A>G; c.1136C>T	1, 8	p.Met1Val; p.Thr379Met	<b>RHD*1G, 1136T</b>	
weak partial 11 or Del	<b>RHD*11</b> <b>RHD*weak</b> <b>partial 11</b>	c.885G>T	6	p.Met295Ile	<b>RHD*885T</b>	allo-anti-D reported Del phenotype when with <b>RHCE*Ce</b>
DOL1 RH:54(DAK+)	<b>RHD*12.01</b> <b>RHD*DOL1</b>	c.509T>C; c.667T>G	4,5	p.Met170Thr; p.Phe223Val	<b>RHD*509C,667G</b>	
DOL2 RH:54(DAK+)	<b>RHD*12.02</b> <b>RHD*DOL2</b>	c.509T>C; c.667T>G; c.1132C>G	4,5,8	p.Met170Thr; p.Phe223Val; p.Leu378Val	<b>RHD*509C,667G, 1132G</b>	
DOL3	<b>RHD*12.03</b> <b>RHD*DOL3</b>	c.410C>T; c.509T>C; c.667T>G	3,4,5	p.Ala137Val; p.Met170Thr; p.Phe223Val	<b>RHD*410T,509C,667G</b>	
DOL4	<b>RHD*12.04</b> <b>RHD*DOL4</b>	c.410C>T c.455A>C c.509T>C c.667T>G	3,4,5	p.Ala137Val; p.Asn152Thr; p.Met170Thr; p.Phe223Val	<b>RHD*410T, 455C, 509C, 667G</b>	

Common category or name Phenotype(s)	Allele name	Nucleotide change	Exon(s)	Amino Acid(s)	Allele Name Detail	Comments Reported as:
DBS1	<b>RHD*13.01</b> <b>RHD*DBS1</b>	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	<i>RHD*D-cE(5)-D</i>	
DBS2	<b>RHD*13.02</b> <b>RHD*DBS2</b>	c.667T>G; c.676G>C; c.697G>C	5	p.Phe223Val; p.Ala226Pro; p.Glu233Gln	<i>RHD*667G,676C,697C</i>	
DBT1	<b>RHD*14.01</b> <b>RHD*DBT1</b>	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	<i>RHD*D-CE(5-7)-D</i>	

Common category or name Phenotype(s)	Allele name	Nucleotide change	Exon(s)	Amino Acid(s)	Allele Name Detail	Comments Reported as:
DBT2	<b>RHD*14.02</b> <b>RHD*DBT2</b>	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	<b>RHD*15</b> <b>RHD*weak</b> <b>partial 15</b>	c.845G>A	6	p.Gly282Asp	<i>RHD*845A</i>	allo anti-D reported
DCS1	<b>RHD*16.01</b> <b>RHD*DCS1</b>	c.667T>G; c.676G>C	5	p.Phe223Val; p.Ala226Pro	<i>RHD*667T,676C</i>	
DCS2	<b>RHD*16.02</b> <b>RHD*DCS2</b>	c.676G>C	5	p.Ala226Pro	<i>RHD*676C</i>	
DCS-3	<b>RHD*16.02</b> <b>RHD*DCS3</b>	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	<b>RHD*17.01</b> <b>RHD*DFR1</b>	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	<b>RHD*17.02</b> <b>RHD*DFR2</b>	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	<b>RHD*17.03</b> <b>RHD*DFR3</b>	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	<b>RHD*17.04</b> <b>RHD*DFR4</b>	c.505A>C; c.509T>G	4	p.Met169Leu; p.Met170Arg	<i>RHD*505C,509G</i>	
DFR5	<b>RHD*17.05</b> <b>RHD*DFR5</b>	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	<b>RHD*18</b> <b>RHD*DFW</b>	c.497A>C	4	p.His166Pro	<i>RHD*497C</i>	
DHMi	<b>RHD*19</b> <b>RHD*DHMi</b>	c.848C>T	6	p.Thr283Ile	<i>RHD*848T</i>	
DHO	<b>RHD*20</b> <b>RHD*DHO</b>	c.704A>C	5	p.Lys235Thr	<i>RHD*704C</i>	
Weak partial Type 21	<b>RHD*21</b> <b>RHD*weak partial D 21</b>	c.938C>T	6	p.Pro313Leu	<i>RHD*938T</i>	allo-anti-D reported
DHR	<b>RHD*22</b> <b>RHD*DHR</b>	c.686G>A	5	p.Arg229Lys	<i>RHD*686A</i>	
DMH	<b>RHD*23</b> <b>RHD*DMH</b>	c.161T>C	2	p.Leu54Pro	<i>RHD*161C</i>	
DNAK	<b>RHD*24</b> <b>RHD*DNAK</b>	c.1070G>A	7	p.Gly357Asp	<i>RHD*1070A</i>	
DNB	<b>RHD*25</b> <b>RHD*DNB</b>	c.1063G>A	7	p.Gly355Ser	<i>RHD*1063A</i>	
DNU	<b>RHD*26</b> <b>RHD*DNU</b>	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	<b>RHD*27</b> <b>RHD*DDE</b>	c.120T>A	1	p.Asp40Glu	<i>RHD*120A</i>	
DFL	<b>RHD*28</b> <b>RHD*DFL</b>	c.494A>G	4	p.Tyr165Cys	<i>RHD*494G</i>	
DYU (DQC)	<b>RHD*29</b> <b>RHD*DYU</b>	c.700A>T	5	p.Arg234Trp	<i>RHD*700T</i>	
DTO	<b>RHD*30</b> <b>RHD*DTO</b>	c.667T>G; c.674C>T	5	p.Phe223Val; p.Ser225Phe	<i>RHD*667G,674T</i>	
DVL1	<b>RHD*31</b> <b>RHD*DVL1</b>	c.684_686 del GAG	5	p.Arg229del	<i>RHD*684_686delGAG</i>	
DVL2	<b>RHD*32</b> <b>RHD*DVL2</b>	c.705_707 del GAA	5	p.Lys235del	<i>RHD*705_707delGAA</i>	
DWI (DWLLE)	<b>RHD*33</b> <b>RHD*DWI</b>	c.1073T>C	7	p.Met358Thr	<i>RHD*1073C</i>	
DIM (DIlleM)	<b>RHD*34</b> <b>RHD*DIM</b>	c.854G>A	6	p.Cys285Tyr	<i>RHD*854A</i>	
DMA	<b>RHD*35</b> <b>RHD*DMA</b>	c.621G>C	4	p.Leu207Phe	<i>RHD*621C</i>	
DLO	<b>RHD*36</b> <b>RHD*DLO</b>	c.851C>T	6	p.Ser284Leu	<i>RHD*851T</i>	
DUC2	<b>RHD*37</b> <b>RHD*DUC2</b>	c.733G>C	5	p.Val245Leu	<i>RHD*733C</i>	
DNT	<b>RHD*38</b> <b>RHD*DNT</b>	c.455A>C	3	p.Asn152Thr	<i>RHD*455C</i>	
<i>RHD(S103P)</i> RH:—12 (G—)	<b>RHD*39</b>	c.307T>C	2	p.Ser103Pro	<i>RHD*307C</i>	
D-SPM	<b>RHD*40</b> <b>RHD*D-SPM</b>	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	<b>RHD*41</b> <b>RHD*DBU</b>	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	<b>RHD*42</b> <b>RHD*DCC</b>	c.677 C>A	5	p.Ala226Asp	<i>RHD*677A</i>	
DDN	<b>RHD*43</b> <b>RHD*DDN</b>	c.490G>A	4	p.Asp164Asn	<i>RHD*490A</i>	
DHQ	<b>RHD*44</b> <b>RHD*DHQ</b>	c.513C>A	4	p.His171Gln	<i>RHD*513A</i>	
DKK	<b>RHD*45</b> <b>RHD*DKK</b>	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	<b>RHD*46</b> <b>RHD*DLX</b>	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	<b>RHD*D(F223V)-CE(5:712-6)-D</b>	
DMI	<b>RHD*47</b> <b>RHD* DMI</b>	c.510G>A	4	p.Met170Ile	<b>RHD*510A</b>	
DMI-1.1	<b>RHD*47.01</b> <b>RHD*DMI-1.1</b>	c.510G>T	4	p.Met170Ile	<b>RHD*510T</b>	
DNS	<b>RHD*48</b> <b>RHD*DNS</b>	c.485A>G	3	p.Asn162Ser	<b>RHD*485G</b>	
DWN	<b>RHD*49</b> <b>RHD*DWN</b>	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	<b>RHD*1053T, 1057G, 1059G, 1060A, 1061A</b>	
<i>RHD(A354T)</i>	<b>RHD*50</b>	c.1060G>A	7	p.Ala354Thr	<b>RHD*1060A</b>	
<i>RHD(del44L)</i>	<b>RHD*51</b>	c.130_132 delCTC	1	p.Leu44del	<b>RHD*130_132 delCTC</b>	
<i>RHD(F223S)</i>	<b>RHD*52</b>	c.668T>C	5	p.Phe223Ser	<b>RHD*668C</b>	
<i>RHD(IVS2-2delA)</i>	<b>RHD*53</b>	c.336-2delA	Intron 2	Splice site change	<b>RHD*336-2delA</b>	
<i>RHD(IVS4-2A&gt;C)</i>	<b>RHD*54</b>	c.635-2A>C	Intron 4	Splice site change	<b>RHD*635-2A&gt;C</b>	
<i>RHD(L81P)</i>	<b>RHD*55</b>	c.242T>C	2	p.Leu81Pro	<b>RHD*242C</b>	
DBA	<b>RHD*56</b> <b>RHD*DBA</b>	c.680T>C	5	p.Leu227Pro	<b>RHD*680C</b>	
weak partial type 57	<b>RHD*57</b> <b>RHD*weak partial 57</b>	c.640C>T	5	p.Leu214Phe	<b>RHD*640T</b>	

Common category or name Phenotype(s)	Allele name	Nucleotide change	Exon(s)	Amino Acid(s)	Allele Name Detail	Comments Reported as:
<i>RHD*D-CE(7)-D</i>	<b><i>RHD*58</i></b>	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*D-CE(7)-D</i>	
<i>RHD(F175L)</i>	<b><i>RHD*59</i></b>	c.525C>T	4	p.Phe175Leu	<i>RHD*525T</i>	
weak Partial D	<b><i>RHD*60</i></b>	c.178A>C; c.689G>T	2,5	p.Ile60Leu; p.Ser230Ile	<i>RHD*178C,689T</i>	
weak Partial D	<b><i>RHD*61</i></b>	c.492C>A	4	p.Asp164Glu	<i>RHD*492A</i>	
DNT(V270G)	<b><i>RHD*62</i></b>	c.455A>C; c.809T>G	3,6	p.Asn152Thr; p.Val270Gly	<i>RHD*455C,809G</i>	