



AlloSeq Assign Motifs



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Stem Cell Transplant Recipient

CareDx Technical Support

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TEC747-S_AlloSeq Assign 1.0_Motifs version 2.0 Effective 02 Oct 23



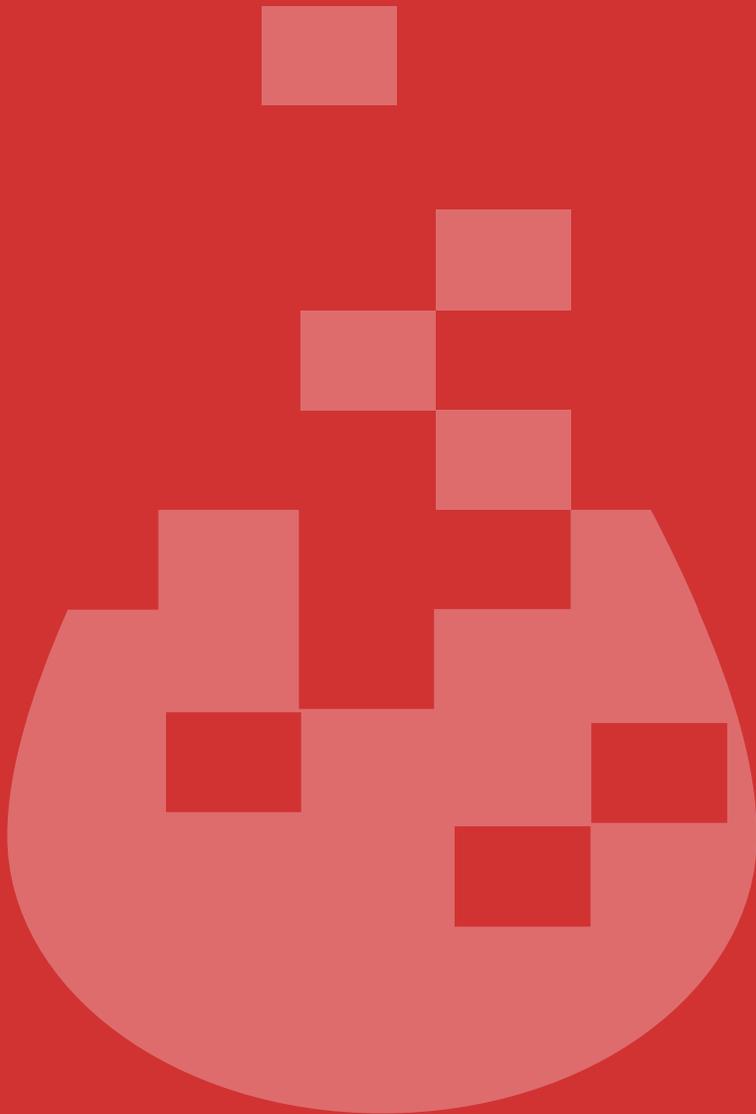
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 - MICB98 Met/Ile

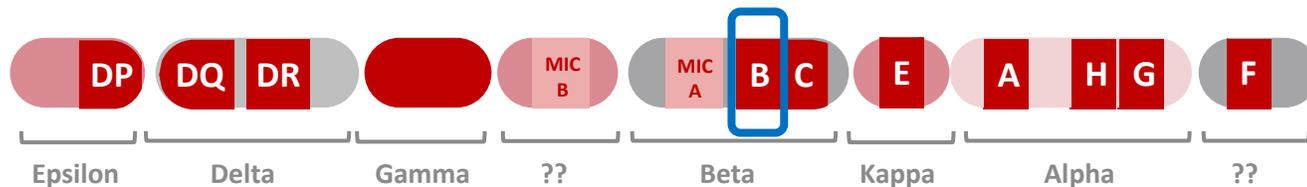
Overview

Reporting of sequence motifs from AlloSeq Assign enables efficient means of identifying potentially problematic donor/patient mismatches. The sequence motifs reported by AlloSeq Assign have been included as they are of clinical significance in patient outcomes. Review of the motifs may aid in selecting a donor that will reduce the risk of rejection or GVHD in the patient.

Motif	Clinical Significance
HLA-B rs1050458C>T	This SNP located in exon 1 of HLA-B has been implicated in significantly higher risk of severe GVHD when it is mismatched. For donor patient pairs that are HLA-B genotype mismatched, selecting a donor that is matched at this marker reduces this risk.
HLA-G rs1610696C>G	Reports suggest elevated HLA-G expression is associated with reduced allograft rejection. Patient G + Donor C = reduced risk of rejection. Patient C + Donor C = best outcome.
HLA-DPB1 rs9277534A>G	This SNP is associated with level of DPB1 expression. The rs9277534-A allele is associated with low DPB1 expression, whereas the rs9277534-G allele is associated with high DPB1 expression. Among recipients of HLA-DPB1-mismatched transplants from donors with the low-expression allele, recipients with the high-expression allele had a high risk of GVHD. For donor patient pairs that are DPB1 mismatched, this marker can be used to select a DPB1-mismatched donors who generate a permissive DPB1 mismatch against low-expression patient DPB1 alleles.
MICA rs1051792G>A	This marker has been implicated in a higher risk of GVHD when it is mismatched. Donor + patient mismatched at rs1051792 = increased risk. Donor + patient matched at rs1051792 = reduced risk.
MICB98 Met/Ile	This marker has been implicated in a higher risk of GVHD when it is mismatched. Donor + Patient matched at HLA&MICA but mismatched at MICB98 = increased risk of GVHD, and higher rate of relapse. Donor + Patient matched at HLA&MICA AND matched at MICB98 = decreased risk of GVHD.



HLA-B rs1050458C>T



HLA-B rs1050458C>T

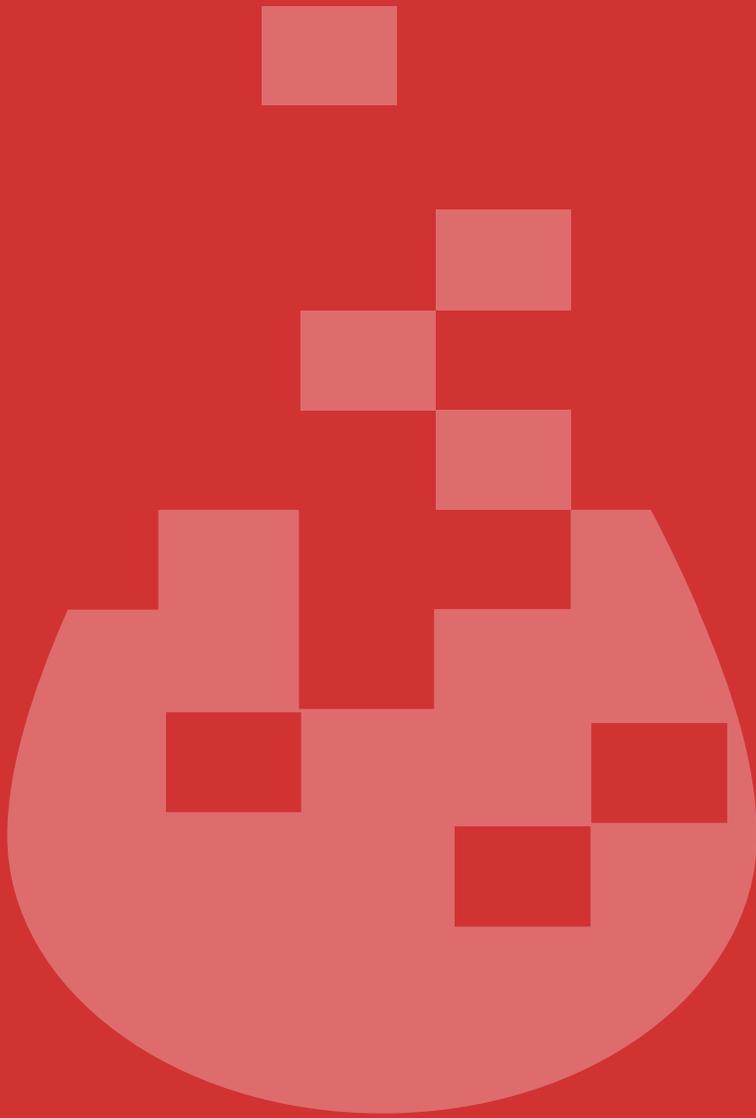
Motif ID:	rs1050458C>T	Locus:	HLA-B	Implemented (Ref. Version #):	3.41
Supporting Publication:	Petersdorf EW, Carrington M, O'hUigin C, Bengtsson M, De Santis D, Dubois V, Gooley T, Horowitz M, Hsu K, Madrigal JA, Maiers MJ, Malkki M, McKallor C, Morishima Y, Oudshoorn M, Spellman SR, Villard J, Stevenson P; International Histocompatibility Working Group in Hematopoietic Cell Transplantation. Role of HLA-B exon 1 in graft-versus-host disease after unrelated haemopoietic cell transplantation: a retrospective cohort study. <i>Lancet Haematol.</i> 2020 Jan;7(1):e50-e60.				
Impact of polymorphism:	<p>The mature HLA Class I molecule that is expressed on the cell surface is encoded by exons 2–7. Exon 1 of Class I genes encodes a separate leader peptide, which is not a structural moiety of the mature Class I molecule, but can be bound and presented by Class I, notably HLA-E. HLA-A and HLA-C leader sequences are largely invariant and encode methionine at the –21 position. A sequence dimorphism (rs1050458) in exon 1 of HLA-B gives rise to leader peptides containing methionine (Met; M) or threonine (Thr; T), which differentially influence natural killer and T-cell alloresponses. <i>Severe GVHD was significantly higher with HLA-B leader mismatching compared to leader matching, and when the shared HLA-B allotype had an M leader compared with a T leader.</i> The preferred HLA-B-mismatched donor is leader-matched and shares a T leader allotype.</p> <p>This mutation is common among HLA-B*07, 08, 14, 38, 39, 42, 48, 67, 73 and 81 allele groups.</p>				

Motif ID:	rs1050458C>T	Locus:	HLA-B	Implemented (Ref. Version #):	3.41
Example Display:	<div style="border: 1px solid red; padding: 5px;"> <p style="color: red; font-weight: bold; margin: 0;">Homozygous C</p> </div>				

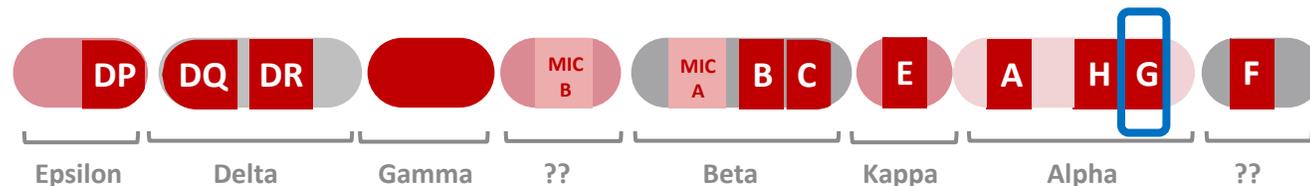
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Example Display:	<h3>Heterozygous C/T</h3> <div style="border: 1px solid red; padding: 5px;"> <p>Assign1 x</p> <p>5' UTR E Intr Exon 2 Intron 2 Exon 3 Intron 3 Exon 4 Int Exo Intron 5 Int 3' UTR</p> <p>IMGT/B 3.41.0.0 2020-07-13 ... 821.....831.....841.....851.....861.....871.....881.... 154UCLA949 B - Allele Pair Size: 43654</p> <p>Base 853 ACTCARARTCTCCTCAGACCCRAGATGCKGGTCAYGGCCCGAACCTCCTCCTGCTGCTCTSGGSR Start: 1, 5' UTR 1</p> <p>cDNA 4.2, Exon 1 11 C A 2 1 R Stop: 4653, 3' UTR 1121</p> <table border="1"> <thead> <tr> <th>Allele</th> <th>Allele 1</th> <th>Allele 2</th> <th>CORE</th> <th>EXONS</th> <th>N-C</th> <th>PHASE1</th> <th>PHASE2</th> <th>Differences</th> </tr> </thead> <tbody> <tr> <td>154UCLA945</td> <td>.....G.....A.....T.....T.....C..C.</td> <td></td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>154UCLA946</td> <td>.....A.....G.....G.....C.....G..G.</td> <td>B*14:02:01:01 B*35:01:01:05</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> <td>Intron 2</td> </tr> <tr> <td>154UCLA947</td> <td>ACTCAGARTCTCCTCAGACGCCRAGATGCKGGTCAYGGCCCGAACCTCCTCCTGCTGCTCTSGGSR</td> <td>B*14:02:01:01 B*35:01:01:42</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> <td>Exon 2</td> </tr> <tr> <td>154UCLA948</td> <td></td> <td>B*14:02:03 B*35:01:64</td> <td>0</td> <td>0</td> <td>0</td> <td>1</td> <td>1</td> <td>Exon 2</td> </tr> <tr> <td>A</td> <td>G A T T C C</td> <td>B*14:02:13 B*35:01:46</td> <td>0</td> <td>0</td> <td>0</td> <td>1</td> <td>1</td> <td>Exon 2</td> </tr> <tr> <td>154UCLA949* B</td> <td>A G G C</td> <td>B*14:02:17 B*35:01:17</td> <td>0</td> <td>0</td> <td>0</td> <td>1</td> <td>1</td> <td>Exon 3</td> </tr> <tr> <td>C</td> <td></td> <td>B*14:11 B*35:54</td> <td>0</td> <td>0</td> <td>0</td> <td>1</td> <td>1</td> <td>Exon 2</td> </tr> <tr> <td>DPA1</td> <td></td> <td>B*14:18 B*35:29:01</td> <td>0</td> <td>0</td> <td>0</td> <td>1</td> <td>1</td> <td>Exon 2</td> </tr> <tr> <td>DPB1</td> <td></td> <td>B*14:22 B*35:484</td> <td>0</td> <td>0</td> <td>0</td> <td>1</td> <td>1</td> <td>Exon 3</td> </tr> <tr> <td>DQA1</td> <td></td> <td>B*14:62 B*35:24:01</td> <td>0</td> <td>0</td> <td>0</td> <td>1</td> <td>1</td> <td>Exon 3</td> </tr> <tr> <td>DQB1</td> <td></td> <td>B*14:27 B*35:93</td> <td>0</td> <td>0</td> <td>0</td> <td>2</td> <td>2</td> <td>Exon 3</td> </tr> <tr> <td>DRB1G03</td> <td>500</td> <td>B*14:02:01:01 B*35:01:01:01</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>DRB3</td> <td></td> <td>B*14:02:01:01 B*35:01:01:03</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>E</td> <td></td> <td>B*14:02:01:01 B*35:01:01:07</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>F</td> <td></td> <td>B*14:02:01:01 B*35:01:01:08</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>G</td> <td></td> <td>B*14:02:01:01 B*35:01:01:09</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>H</td> <td></td> <td>B*14:02:01:01 B*35:01:01:10</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICA</td> <td><< HLA. 37-5929</td> <td>B*14:02:01:01 B*35:01:01:11</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB</td> <td></td> <td>B*14:02:01:01 B*35:01:01:12</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>154UCLA950</td> <td></td> <td>B*14:02:01:01 B*35:01:01:15</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>155UCLA951</td> <td></td> <td>B*14:02:01:01 B*35:01:01:17</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>155UCLA952</td> <td></td> <td>B*14:02:01:01 B*35:01:01:20</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>155UCLA953</td> <td></td> <td>B*14:02:01:01 B*35:01:01:23</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>155UCLA954</td> <td></td> <td>B*14:02:01:01 B*35:01:01:24</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> </tbody> </table> <p>Read Depth: 500</p> <p>HLA. 37-5929</p> <p>154UCLA949</p> <p>ACCEPT 853 Apply SIGN OFF</p> <p>Full Gene Master</p> </div>					Allele	Allele 1	Allele 2	CORE	EXONS	N-C	PHASE1	PHASE2	Differences	154UCLA945G.....A.....T.....T.....C..C.		0	0	0	0	0		154UCLA946A.....G.....G.....C.....G..G.	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Example Display:	<p>Summary Table Report:</p> <p>Motifs.</p> <table border="1"> <thead> <tr> <th></th> <th>IMGT/F</th> <th>IMGT/G</th> <th>IMGT/H</th> <th>IMGT/A</th> <th>IMGT/E</th> <th>IMGT/C</th> <th>IMGT/B</th> <th>IMGT/MICA</th> <th>IMGT/MICB</th> </tr> </thead> <tbody> <tr> <td>154UCLA945</td> <td></td> <td>rs1610696:</td> <td></td> <td></td> <td></td> <td></td> <td>Bw6, rs1050458:CC</td> <td>129Met, 129\ 98Ile</td> <td></td> </tr> <tr> <td>154UCLA946</td> <td></td> <td>rs1610696:**</td> <td></td> <td></td> <td></td> <td>Bw6</td> <td>Bw6, rs1050458:TT</td> <td>129Val</td> <td>98Met</td> </tr> <tr> <td>154UCLA947</td> <td></td> <td>rs1610696:GC</td> <td></td> <td></td> <td></td> <td>Bw6</td> <td>Bw6, rs1050458:TT</td> <td>129Val</td> <td>98Met, 98Ile</td> </tr> <tr> <td>154UCLA948</td> <td></td> <td>rs1610696:**</td> <td></td> <td>Bw4</td> <td></td> <td>Bw6</td> <td>Bw4, Bw6, rs1050458:CC</td> <td>129Val</td> <td>98Ile</td> </tr> <tr> <td>154UCLA949</td> <td></td> <td>rs1610696:</td> <td></td> <td>Bw4</td> <td></td> <td>Bw6</td> <td>Bw6, rs1050458:TC</td> <td>129Met</td> <td>98Ile</td> </tr> </tbody> </table> <p>Genotyping Report:</p> <p>Reference: IMGT/B 3.41.0.0 2020-07-13</p> <p>Summary</p> <p>The allele pairs listed below are compatible with the consensus sequence.</p> <table border="1"> <tr> <td>B*14:02:01:01</td> <td>B*35:01:01:05</td> <td></td> </tr> <tr> <td>B*14:02:01:01</td> <td>B*35:01:01:42</td> <td>Intron 2</td> </tr> </table> <p>Motifs: Bw6, rs1050458:TC Heterozygous</p>						IMGT/F	IMGT/G	IMGT/H	IMGT/A	IMGT/E	IMGT/C	IMGT/B	IMGT/MICA	IMGT/MICB	154UCLA945		rs1610696:					Bw6, rs1050458:CC	129Met, 129\ 98Ile		154UCLA946		rs1610696:**				Bw6	Bw6, rs1050458:TT	129Val	98Met	154UCLA947		rs1610696:GC				Bw6	Bw6, rs1050458:TT	129Val	98Met, 98Ile	154UCLA948		rs1610696:**		Bw4		Bw6	Bw4, Bw6, rs1050458:CC	129Val	98Ile	154UCLA949		rs1610696:		Bw4		Bw6	Bw6, rs1050458:TC	129Met	98Ile	B*14:02:01:01	B*35:01:01:05		B*14:02:01:01	B*35:01:01:42	Intron 2
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154UCLA949		rs1610696:		Bw4		Bw6	Bw6, rs1050458:TC	129Met	98Ile																																																														
B*14:02:01:01	B*35:01:01:05																																																																						
B*14:02:01:01	B*35:01:01:42	Intron 2																																																																					

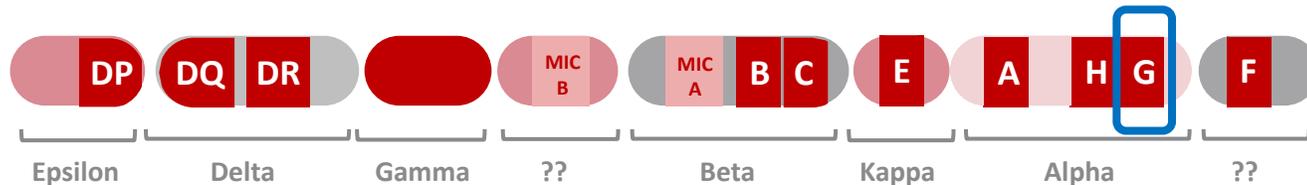


HLA-G rs1610696C>G



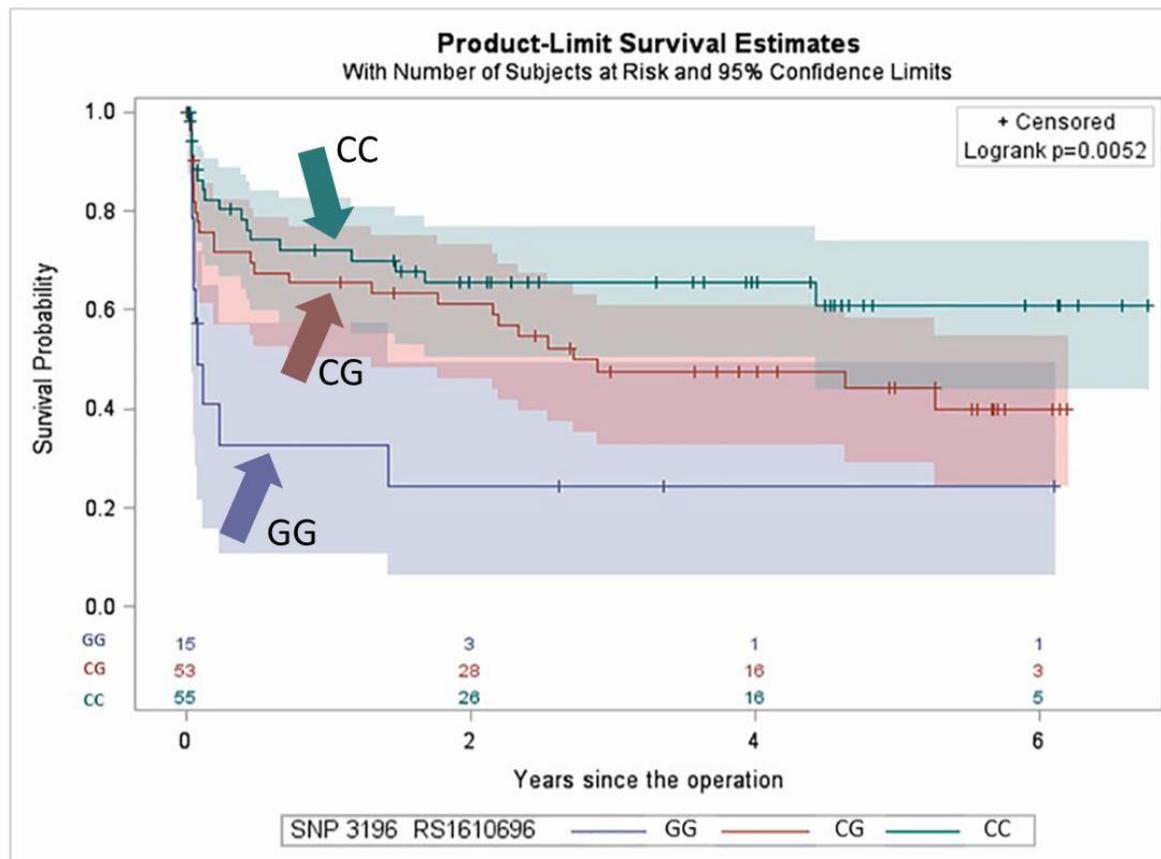
HLA-G rs1610696C>G

Motif ID:	rs1610696C>G	Locus:	HLA-G	Implemented (Ref. Version #):	3.41
Supporting Publication:	Adamson MB, Di Giovanni B, Ribeiro RVP, Yu F, Lazarte J, Rao V, Delgado DH. HLA-G +3196 polymorphism as a risk factor for cell mediated rejection following heart transplant. <i>Hum Immunol.</i> 2020 Apr;81(4):134-140.				
Impact of polymorphism:	<p>Human leukocyte antigen-G (HLA-G) is an immune checkpoint which dampens the immune response. Reports suggest elevated HLA-G expression is associated with reduced allograft rejection. The +3196C/G polymorphism is located within the 3'UTR of the HLA-G gene, 3196 base pairs downstream of the initiation sequence. The 3'UTR, specifically exon 8, is a vital component for HLA-G transcriptional regulation. The current study identified the +3196 G allele as a risk factor for cell mediated rejection (CMR). Compared to the minor GG genotype, CG had a 47.2% reduction in CMR risk while CC had a 66.9% reduction.</p> <p>Note: Equivalent to c.*287C>G (using standard HGVS nomenclature, which means 287 bp downstream of the T in the TGA stop codon). Currently this position is not included in IMGT /Unknown.</p>				

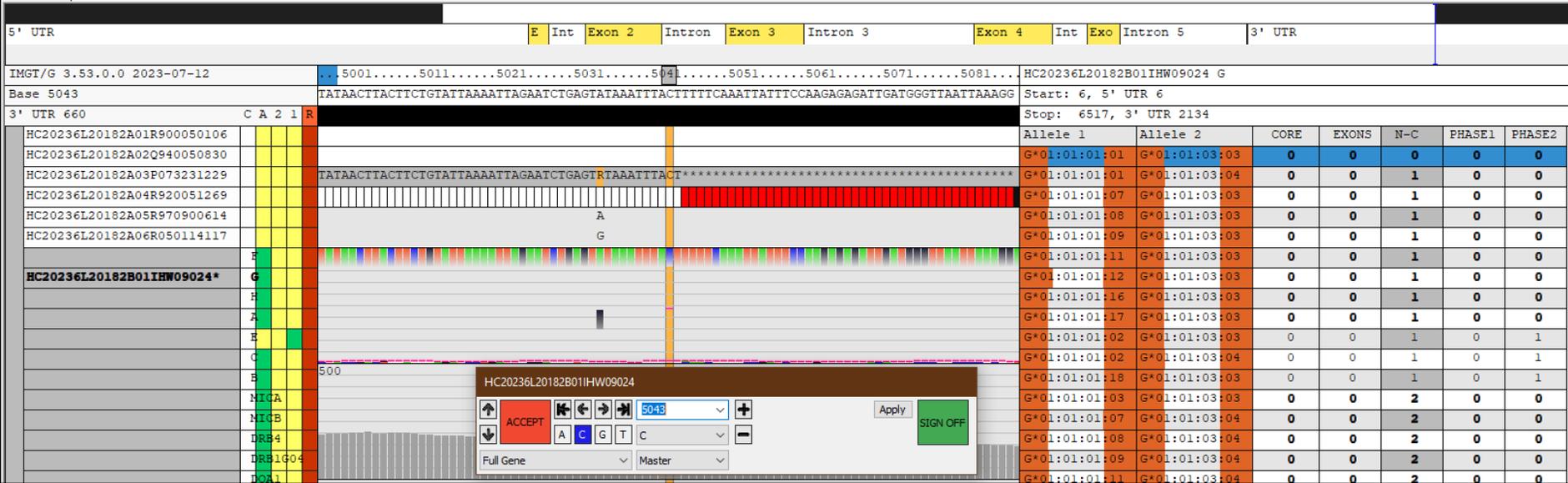


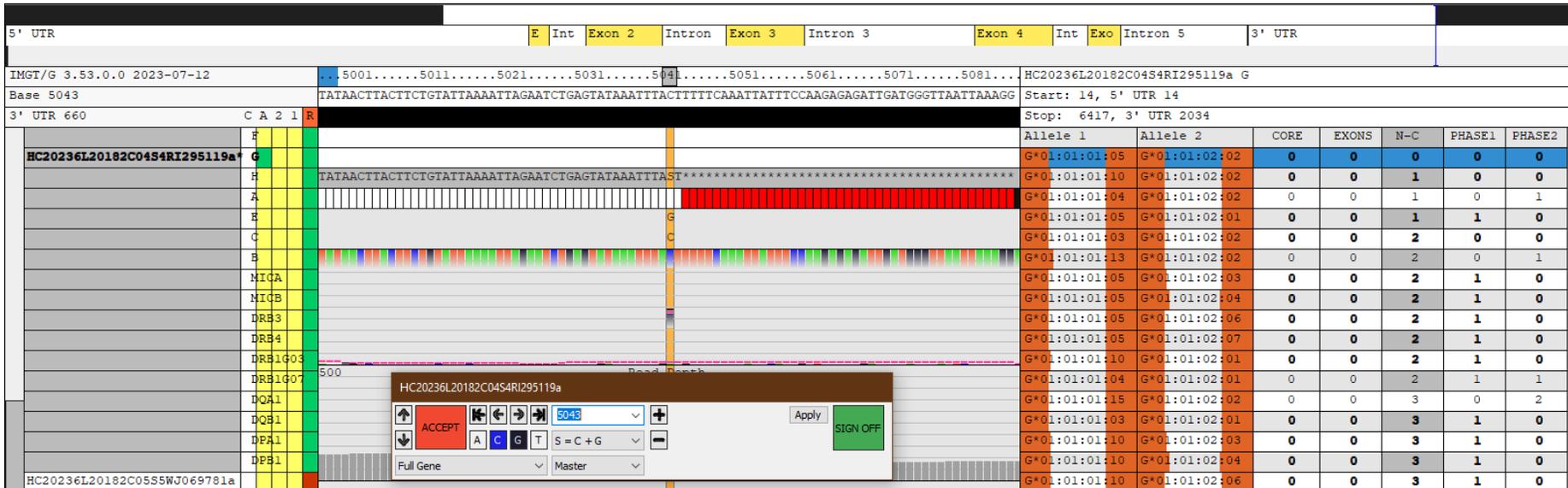
HLA-G rs1610696C>G

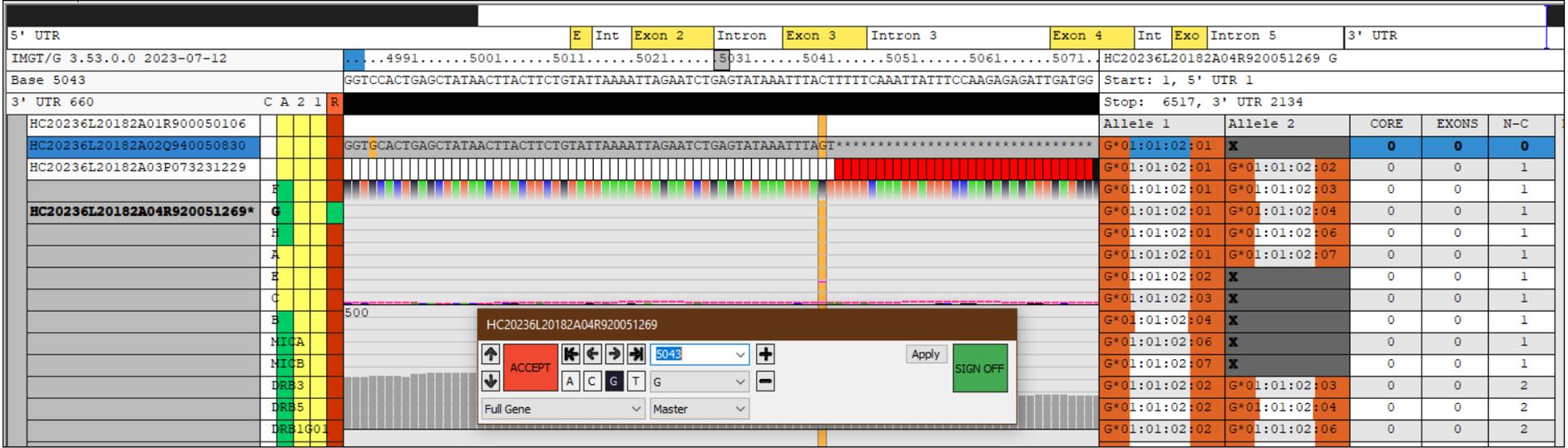
The freedom from cell mediated rejection (CMR) stratified by each +3196C/G genotype. Highest risk was observed in the group homozygous for the G risk allele, whereas the lowest risk was observed with the presence of the C allele. Risk of CMR increased proportionally with an increase in the number of risk allele G ($p = 0.0052$).



Adamson. et al. *Hum Immunol.* 2020 Apr;81(4):134-140

Motif ID:	rs1610696C>G	Locus:	HLA-G	Implemented (Ref. Version #):	3.41																																																																																																																														
Example Display:	<p>Homozygous C</p>  <table border="1"> <thead> <tr> <th>Allele 1</th> <th>Allele 2</th> <th>CORE</th> <th>EXONS</th> <th>N-C</th> <th>PHASE1</th> <th>PHASE2</th> </tr> </thead> <tbody> <tr> <td>G*01:01:01:01</td> <td>G*01:01:03:03</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:01</td> <td>G*01:01:03:04</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:07</td> <td>G*01:01:03:03</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:08</td> <td>G*01:01:03:03</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:09</td> <td>G*01:01:03:03</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:11</td> <td>G*01:01:03:03</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:12</td> <td>G*01:01:03:03</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:16</td> <td>G*01:01:03:03</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:17</td> <td>G*01:01:03:03</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:02</td> <td>G*01:01:03:03</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:01:02</td> <td>G*01:01:03:04</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:01:18</td> <td>G*01:01:03:03</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:01:03</td> <td>G*01:01:03:03</td> <td>0</td> <td>0</td> <td>2</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:07</td> <td>G*01:01:03:04</td> <td>0</td> <td>0</td> <td>2</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:08</td> <td>G*01:01:03:04</td> <td>0</td> <td>0</td> <td>2</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:09</td> <td>G*01:01:03:04</td> <td>0</td> <td>0</td> <td>2</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:11</td> <td>G*01:01:03:04</td> <td>0</td> <td>0</td> <td>2</td> <td>0</td> <td>0</td> </tr> </tbody> </table>					Allele 1	Allele 2	CORE	EXONS	N-C	PHASE1	PHASE2	G*01:01:01:01	G*01:01:03:03	0	0	0	0	0	G*01:01:01:01	G*01:01:03:04	0	0	1	0	0	G*01:01:01:07	G*01:01:03:03	0	0	1	0	0	G*01:01:01:08	G*01:01:03:03	0	0	1	0	0	G*01:01:01:09	G*01:01:03:03	0	0	1	0	0	G*01:01:01:11	G*01:01:03:03	0	0	1	0	0	G*01:01:01:12	G*01:01:03:03	0	0	1	0	0	G*01:01:01:16	G*01:01:03:03	0	0	1	0	0	G*01:01:01:17	G*01:01:03:03	0	0	1	0	0	G*01:01:01:02	G*01:01:03:03	0	0	1	0	1	G*01:01:01:02	G*01:01:03:04	0	0	1	0	1	G*01:01:01:18	G*01:01:03:03	0	0	1	0	1	G*01:01:01:03	G*01:01:03:03	0	0	2	0	0	G*01:01:01:07	G*01:01:03:04	0	0	2	0	0	G*01:01:01:08	G*01:01:03:04	0	0	2	0	0	G*01:01:01:09	G*01:01:03:04	0	0	2	0	0	G*01:01:01:11	G*01:01:03:04	0	0	2	0	0
Allele 1	Allele 2	CORE	EXONS	N-C	PHASE1	PHASE2																																																																																																																													
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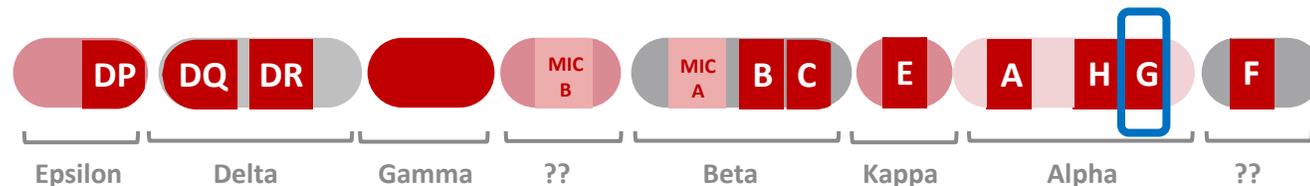
Motif ID:	rs1610696C>G	Locus:	HLA-G	Implemented (Ref. Version #):	3.41																																																																																																																														
Example Display:	Heterozygous C/G																																																																																																																																		
 <table border="1" data-bbox="1809 635 2458 1063"> <thead> <tr> <th>Allele 1</th> <th>Allele 2</th> <th>CORE</th> <th>EXONS</th> <th>N-C</th> <th>PHASE1</th> <th>PHASE2</th> </tr> </thead> <tbody> <tr> <td>G*01:01:01:05</td> <td>G*01:01:02:02</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:10</td> <td>G*01:01:02:02</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:04</td> <td>G*01:01:02:02</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:01:05</td> <td>G*01:01:02:01</td> <td>0</td> <td>0</td> <td>1</td> <td>1</td> <td>0</td> </tr> <tr> <td>G*01:01:01:03</td> <td>G*01:01:02:02</td> <td>0</td> <td>0</td> <td>2</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:13</td> <td>G*01:01:02:02</td> <td>0</td> <td>0</td> <td>2</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:01:05</td> <td>G*01:01:02:03</td> <td>0</td> <td>0</td> <td>2</td> <td>1</td> <td>0</td> </tr> <tr> <td>G*01:01:01:05</td> <td>G*01:01:02:04</td> <td>0</td> <td>0</td> <td>2</td> <td>1</td> <td>0</td> </tr> <tr> <td>G*01:01:01:05</td> <td>G*01:01:02:06</td> <td>0</td> <td>0</td> <td>2</td> <td>1</td> <td>0</td> </tr> <tr> <td>G*01:01:01:05</td> <td>G*01:01:02:07</td> <td>0</td> <td>0</td> <td>2</td> <td>1</td> <td>0</td> </tr> <tr> <td>G*01:01:01:10</td> <td>G*01:01:02:01</td> <td>0</td> <td>0</td> <td>2</td> <td>1</td> <td>0</td> </tr> <tr> <td>G*01:01:01:04</td> <td>G*01:01:02:01</td> <td>0</td> <td>0</td> <td>2</td> <td>1</td> <td>1</td> </tr> <tr> <td>G*01:01:01:15</td> <td>G*01:01:02:02</td> <td>0</td> <td>0</td> <td>3</td> <td>0</td> <td>2</td> </tr> <tr> <td>G*01:01:01:03</td> <td>G*01:01:02:01</td> <td>0</td> <td>0</td> <td>3</td> <td>1</td> <td>0</td> </tr> <tr> <td>G*01:01:01:10</td> <td>G*01:01:02:03</td> <td>0</td> <td>0</td> <td>3</td> <td>1</td> <td>0</td> </tr> <tr> <td>G*01:01:01:10</td> <td>G*01:01:02:04</td> <td>0</td> <td>0</td> <td>3</td> <td>1</td> <td>0</td> </tr> <tr> <td>G*01:01:01:10</td> <td>G*01:01:02:06</td> <td>0</td> <td>0</td> <td>3</td> <td>1</td> <td>0</td> </tr> </tbody> </table>						Allele 1	Allele 2	CORE	EXONS	N-C	PHASE1	PHASE2	G*01:01:01:05	G*01:01:02:02	0	0	0	0	0	G*01:01:01:10	G*01:01:02:02	0	0	1	0	0	G*01:01:01:04	G*01:01:02:02	0	0	1	0	1	G*01:01:01:05	G*01:01:02:01	0	0	1	1	0	G*01:01:01:03	G*01:01:02:02	0	0	2	0	0	G*01:01:01:13	G*01:01:02:02	0	0	2	0	1	G*01:01:01:05	G*01:01:02:03	0	0	2	1	0	G*01:01:01:05	G*01:01:02:04	0	0	2	1	0	G*01:01:01:05	G*01:01:02:06	0	0	2	1	0	G*01:01:01:05	G*01:01:02:07	0	0	2	1	0	G*01:01:01:10	G*01:01:02:01	0	0	2	1	0	G*01:01:01:04	G*01:01:02:01	0	0	2	1	1	G*01:01:01:15	G*01:01:02:02	0	0	3	0	2	G*01:01:01:03	G*01:01:02:01	0	0	3	1	0	G*01:01:01:10	G*01:01:02:03	0	0	3	1	0	G*01:01:01:10	G*01:01:02:04	0	0	3	1	0	G*01:01:01:10	G*01:01:02:06	0	0	3	1	0
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Motif ID:	rs1610696C>G	Locus:	HLA-G	Implemented (Ref. Version #):	3.41
Example Display:	<p>Homozygous G</p> 				

Motif ID:	rs1610696C>G	Locus:	HLA-G	Implemented (Ref. Version #):	3.41																																																																																																																																																																																				
Example Display:	Summary Table Report: <table border="1"> <thead> <tr> <th>Motifs.</th> <th>IMGT/F</th> <th>IMGT/G</th> <th>IMGT/H</th> <th>IMGT/A</th> <th>IMGT/E</th> <th>IMGT/C</th> <th>IMGT/B</th> <th>IMGT/MICA</th> <th>IMGT/MICB</th> <th>IMGT/DRB3</th> <th>IMGT/DRB4</th> <th>IMGT/DRB5</th> <th>IMGT/DRB1</th> <th>IMGT/DQA1</th> <th>IMGT/DQB1</th> <th>IMGT/DPA1</th> <th>IMGT/DPB1</th> </tr> </thead> <tbody> <tr> <td>HC20237L20182A01R900050106</td> <td></td> <td>rs1610696:CC</td> <td></td> <td>Bw4</td> <td></td> <td>Bw6</td> <td>Bw6, rs1050: 129Val</td> <td></td> <td>98Ile</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>rs9277534:GG</td> </tr> <tr> <td>HC20237L20182A02Q940050830</td> <td></td> <td>rs1610696:CC</td> <td></td> <td></td> <td></td> <td>Bw6</td> <td>Bw4, rs1050: 129Met, 129⁹ 98Ile</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>rs9277534:GA</td> </tr> <tr> <td>HC20237L20182A03P073231229</td> <td></td> <td>rs1610696:CG</td> <td></td> <td></td> <td></td> <td>Bw6</td> <td>Bw4, Bw6, rs129Val</td> <td></td> <td>98Ile</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>rs9277534:GA</td> </tr> <tr> <td>HC20237L20182A04R920051269</td> <td></td> <td>rs1610696:GG</td> <td></td> <td></td> <td></td> <td>Bw6</td> <td>Bw6, rs1050: 129Val</td> <td></td> <td>98Met, 98Ile</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>rs9277534:AA</td> </tr> <tr> <td>HC20237L20182A05R970900614</td> <td></td> <td>rs1610696:CG</td> <td></td> <td></td> <td></td> <td>Bw6</td> <td>Bw4, Bw6, rs129Val</td> <td></td> <td>98Met, 98Ile</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>rs9277534:GG</td> </tr> <tr> <td>HC20237L20182A06R050114117</td> <td></td> <td>rs1610696:CG</td> <td></td> <td></td> <td></td> <td>Bw6</td> <td>Bw4, Bw6, rs129Val</td> <td></td> <td>98Ile</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>rs9277534:GA</td> </tr> <tr> <td>HC20237L20182B01HW09024</td> <td></td> <td>rs1610696:CC</td> <td></td> <td></td> <td></td> <td>Bw6</td> <td>Bw6, rs1050: 129Met, 129⁹ 98Ile</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>rs9277534:GG</td> </tr> <tr> <td>HC20237L20182B02HW09050</td> <td></td> <td>rs1610696:CC</td> <td></td> <td></td> <td></td> <td>Bw6</td> <td>Bw4, rs1050: 129Val</td> <td></td> <td>98Ile</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>rs9277534:AA</td> </tr> <tr> <td>HC20237L20182B03HW09058</td> <td></td> <td>rs1610696:CC</td> <td></td> <td></td> <td></td> <td>Bw6</td> <td>Bw6, rs1050: 129Met</td> <td></td> <td>98Ile</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>rs9277534:GG</td> </tr> </tbody> </table>					Motifs.	IMGT/F	IMGT/G	IMGT/H	IMGT/A	IMGT/E	IMGT/C	IMGT/B	IMGT/MICA	IMGT/MICB	IMGT/DRB3	IMGT/DRB4	IMGT/DRB5	IMGT/DRB1	IMGT/DQA1	IMGT/DQB1	IMGT/DPA1	IMGT/DPB1	HC20237L20182A01R900050106		rs1610696:CC		Bw4		Bw6	Bw6, rs1050: 129Val		98Ile								rs9277534:GG	HC20237L20182A02Q940050830		rs1610696:CC				Bw6	Bw4, rs1050: 129Met, 129 ⁹ 98Ile										rs9277534:GA	HC20237L20182A03P073231229		rs1610696:CG				Bw6	Bw4, Bw6, rs129Val		98Ile								rs9277534:GA	HC20237L20182A04R920051269		rs1610696:GG				Bw6	Bw6, rs1050: 129Val		98Met, 98Ile								rs9277534:AA	HC20237L20182A05R970900614		rs1610696:CG				Bw6	Bw4, Bw6, rs129Val		98Met, 98Ile								rs9277534:GG	HC20237L20182A06R050114117		rs1610696:CG				Bw6	Bw4, Bw6, rs129Val		98Ile								rs9277534:GA	HC20237L20182B01HW09024		rs1610696:CC				Bw6	Bw6, rs1050: 129Met, 129 ⁹ 98Ile										rs9277534:GG	HC20237L20182B02HW09050		rs1610696:CC				Bw6	Bw4, rs1050: 129Val		98Ile								rs9277534:AA	HC20237L20182B03HW09058		rs1610696:CC				Bw6	Bw6, rs1050: 129Met		98Ile								rs9277534:GG
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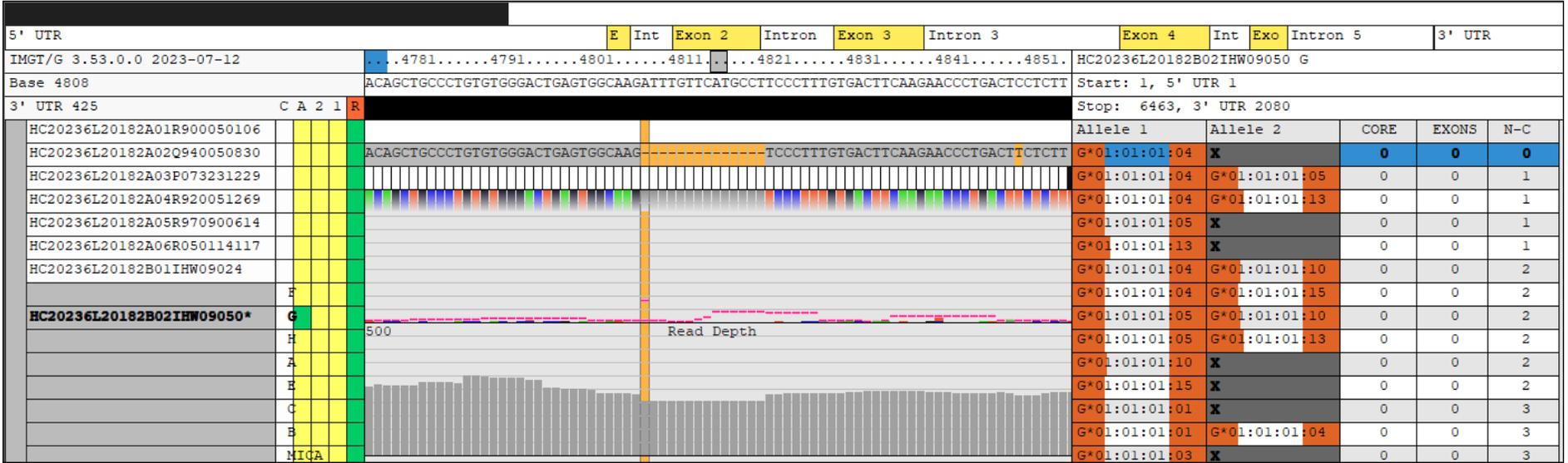


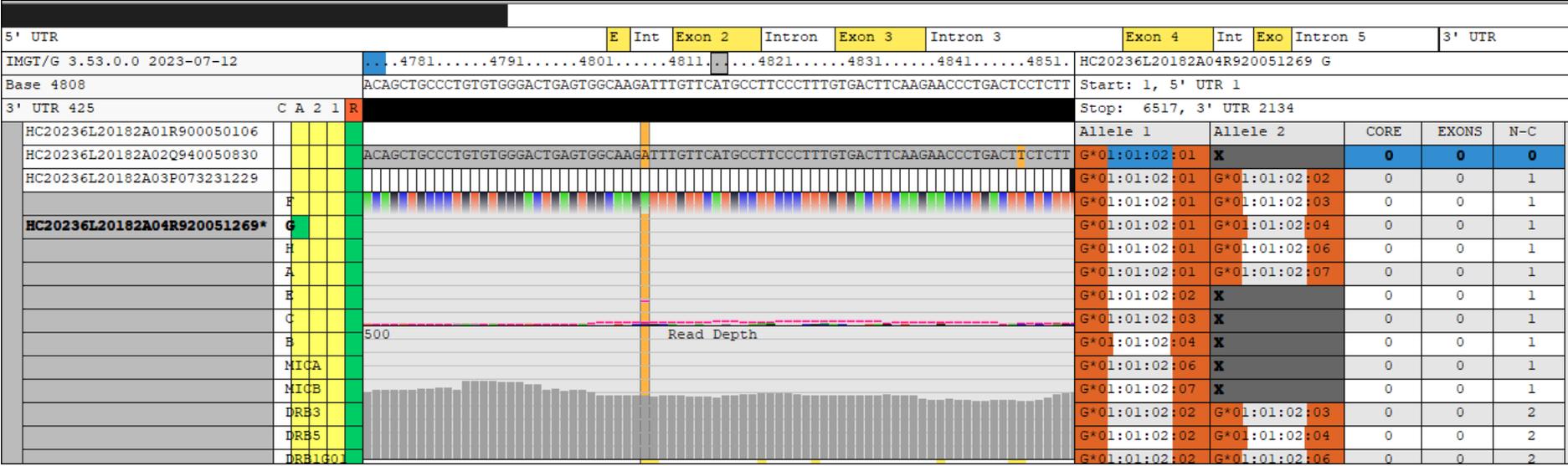
HLA-G rs371194629 3'UTR 14bp indel

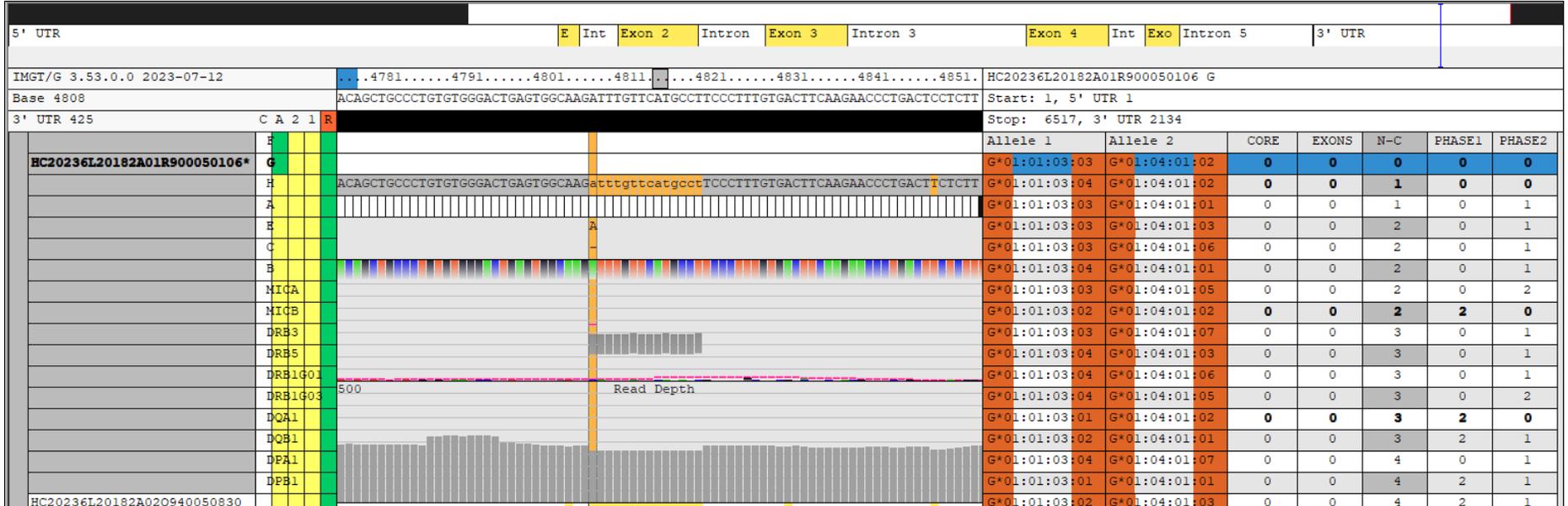


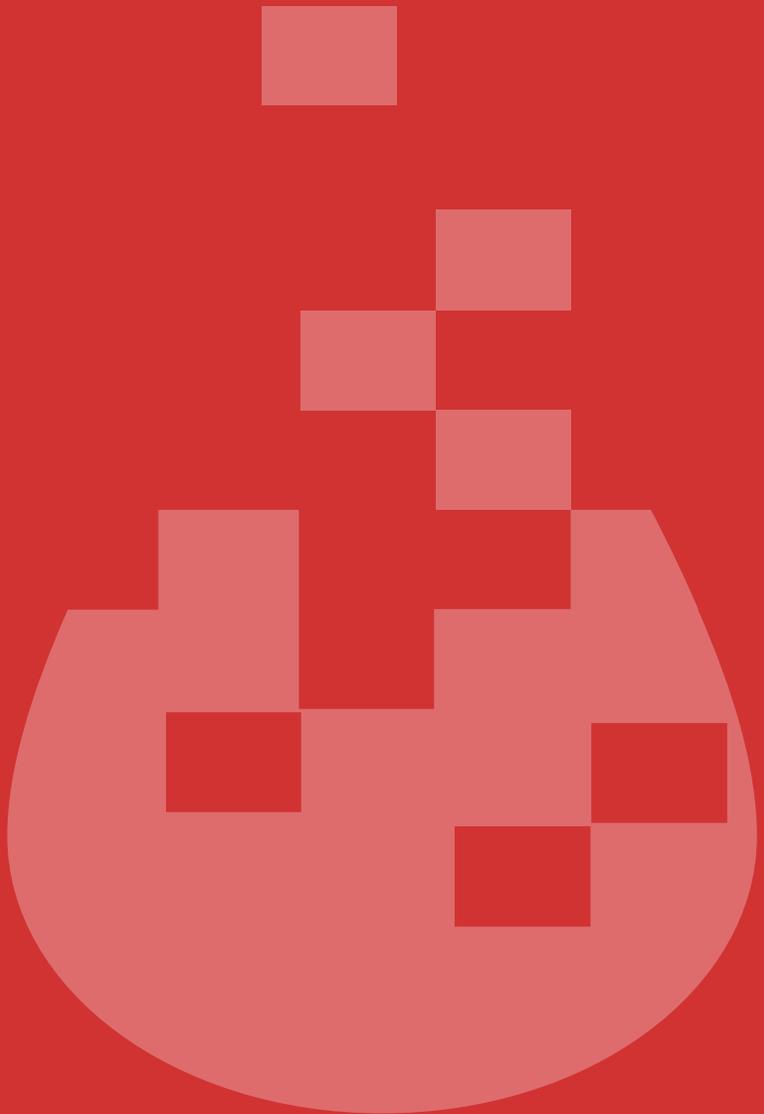
HLA-G rs371194629 3'UTR 14bp indel

Motif ID:	rs371194629	Locus:	HLA-G	Implemented (Ref. Version #):	3.53
Supporting Publication:	<p>La Nasa, G. The human leucocyte antigen-G 14-basepair polymorphism correlates with graft-versus-host disease in unrelated bone marrow transplantation for thalassaemia. BJH. 2007 May.</p> <p>Chen, D.P. The association between genetic variants at 3'-UTR and 5'-URR of HLA-G gene and the clinical outcomes of patients with leukemia receiving hematopoietic stem cell transplantation. Frontiers Immunol. 2023 Feb.</p> <p>Boukouaci, W. Association of HLA-G low expressor genotype with severe acute graft-versus-host disease after sibling bone marrow transplantation. Frontiers Immunol. 2011 Dec.</p> <p>Zhan-Kui Jin. Impact of HLA-G 14-bp polymorphism on acute rejection and cytomegalovirus infection in kidney transplant recipients from north-western China. Transplant Immunology. 2012 Jun.</p>				
Impact of polymorphism:	<ul style="list-style-type: none"> • Studies have demonstrated that patients with low expression of HLA-G have an increased risk of severe aGVHD after HSCT • The 14bp indel in the 3'UTR of HLA-G has been shown in multiple studies to have an association with the risk of a HCST patient developing GVHD. • The 14bp insertion genotype is associated with low expression of HLA-G • DEL allele provides a higher stability of the mRNA, associated with a high expression of HLA-G • Patients with the 14bp insertion have increased risk of GVHD • Likely donors indel status doesn't have any effect on the patients GVHD risk • Some studies have confirmed that high levels of soluble HLA-G (sHLA-G) are correlated with better acceptance of the allograft. 				

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Example Display:	<p>Homozygous del</p>  <table border="1"> <thead> <tr> <th>Allele 1</th> <th>Allele 2</th> <th>CORE</th> <th>EXONS</th> <th>N-C</th> </tr> </thead> <tbody> <tr> <td>G*01:01:01:04</td> <td>X</td> <td>0</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:01:04</td> <td>G*01:01:01:05</td> <td>0</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:01:04</td> <td>G*01:01:01:13</td> <td>0</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:01:05</td> <td>X</td> <td>0</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:01:13</td> <td>X</td> <td>0</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:01:04</td> <td>G*01:01:01:10</td> <td>0</td> <td>0</td> <td>2</td> </tr> <tr> <td>G*01:01:01:04</td> <td>G*01:01:01:15</td> <td>0</td> <td>0</td> <td>2</td> </tr> <tr> <td>G*01:01:01:05</td> <td>G*01:01:01:10</td> <td>0</td> <td>0</td> <td>2</td> </tr> <tr> <td>G*01:01:01:05</td> <td>G*01:01:01:13</td> <td>0</td> <td>0</td> <td>2</td> </tr> <tr> <td>G*01:01:01:10</td> <td>X</td> <td>0</td> <td>0</td> <td>2</td> </tr> <tr> <td>G*01:01:01:15</td> <td>X</td> <td>0</td> <td>0</td> <td>2</td> </tr> <tr> <td>G*01:01:01:01</td> <td>X</td> <td>0</td> <td>0</td> <td>3</td> </tr> <tr> <td>G*01:01:01:01</td> <td>G*01:01:01:04</td> <td>0</td> <td>0</td> <td>3</td> </tr> <tr> <td>G*01:01:01:03</td> <td>X</td> <td>0</td> <td>0</td> <td>3</td> </tr> </tbody> </table>					Allele 1	Allele 2	CORE	EXONS	N-C	G*01:01:01:04	X	0	0	0	G*01:01:01:04	G*01:01:01:05	0	0	1	G*01:01:01:04	G*01:01:01:13	0	0	1	G*01:01:01:05	X	0	0	1	G*01:01:01:13	X	0	0	1	G*01:01:01:04	G*01:01:01:10	0	0	2	G*01:01:01:04	G*01:01:01:15	0	0	2	G*01:01:01:05	G*01:01:01:10	0	0	2	G*01:01:01:05	G*01:01:01:13	0	0	2	G*01:01:01:10	X	0	0	2	G*01:01:01:15	X	0	0	2	G*01:01:01:01	X	0	0	3	G*01:01:01:01	G*01:01:01:04	0	0	3	G*01:01:01:03	X	0	0	3
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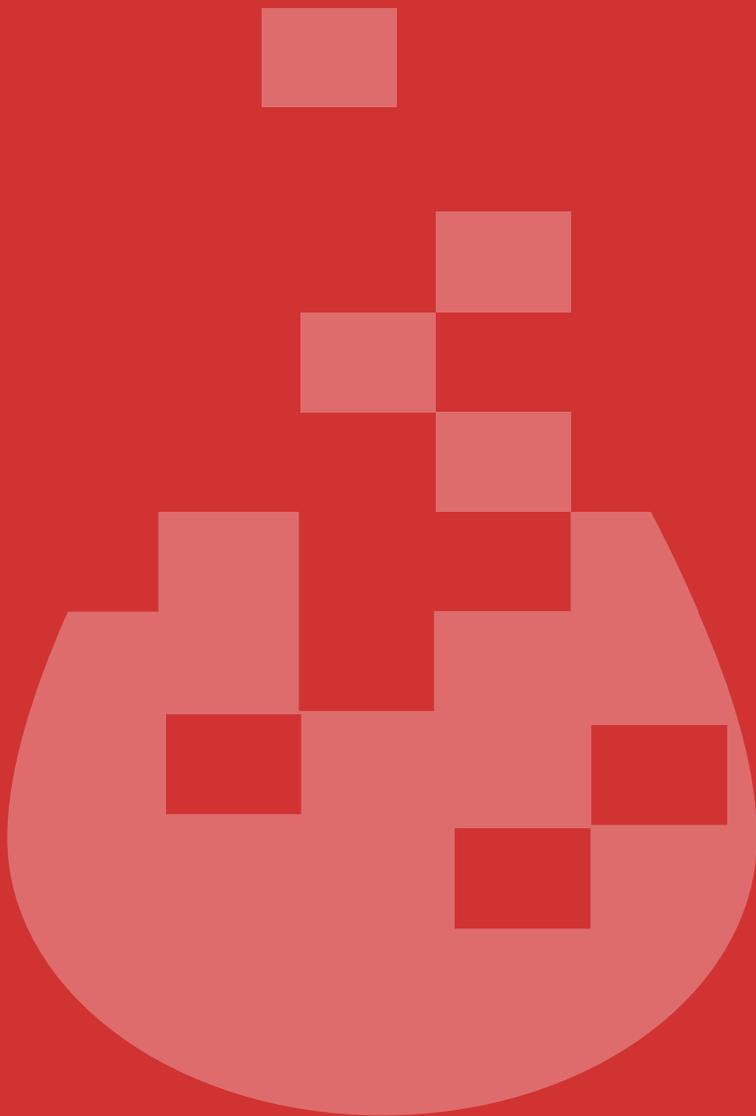
Motif ID:	rs371194629	Locus:	HLA-G	Implemented (Ref. Version #):	3.53
Example Display:	<p>Homozygous ins</p> 				

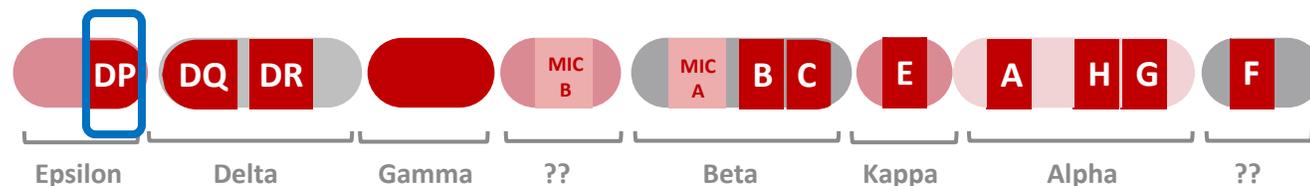
Motif ID:	rs371194629	Locus:	HLA-G	Implemented (Ref. Version #):	3.53																																																																																																																														
Example Display:	Heterozygous																																																																																																																																		
 <p>The visualization shows a genomic track for the HLA-G locus. At the top, a gene model indicates the structure: 5' UTR, Exon 2, Intron 3, Exon 3, Intron 3, Exon 4, Intron 5, and 3' UTR. Below this, a sequence alignment shows the reference sequence (IMGT/G 3.53.0.0) and the observed sequence (HC20236L20182A01R900050106 G). The main part of the track displays read depth for various polymorphisms. The polymorphisms listed on the left include MICA, MICA, DRB3, DRB5, DRB1G01, DRB1G03, DQA1, DQB1, DPA1, and DPB1. The read depth is shown as a bar chart, with a vertical line indicating the position of the variant. The right side of the track provides a table of allele frequencies and phase information for each polymorphism.</p> <table border="1"> <thead> <tr> <th>Allele 1</th> <th>Allele 2</th> <th>CORE</th> <th>EXONS</th> <th>N-C</th> <th>PHASE1</th> <th>PHASE2</th> </tr> </thead> <tbody> <tr> <td>G*01:01:03:03</td> <td>G*01:04:01:02</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:03:04</td> <td>G*01:04:01:02</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> </tr> <tr> <td>G*01:01:03:03</td> <td>G*01:04:01:01</td> <td>0</td> <td>0</td> <td>1</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:03:03</td> <td>G*01:04:01:03</td> <td>0</td> <td>0</td> <td>2</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:03:03</td> <td>G*01:04:01:06</td> <td>0</td> <td>0</td> <td>2</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:03:04</td> <td>G*01:04:01:01</td> <td>0</td> <td>0</td> <td>2</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:03:03</td> <td>G*01:04:01:05</td> <td>0</td> <td>0</td> <td>2</td> <td>0</td> <td>2</td> </tr> <tr> <td>G*01:01:03:02</td> <td>G*01:04:01:02</td> <td>0</td> <td>0</td> <td>2</td> <td>2</td> <td>0</td> </tr> <tr> <td>G*01:01:03:03</td> <td>G*01:04:01:07</td> <td>0</td> <td>0</td> <td>3</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:03:04</td> <td>G*01:04:01:03</td> <td>0</td> <td>0</td> <td>3</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:03:04</td> <td>G*01:04:01:06</td> <td>0</td> <td>0</td> <td>3</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:03:04</td> <td>G*01:04:01:05</td> <td>0</td> <td>0</td> <td>3</td> <td>0</td> <td>2</td> </tr> <tr> <td>G*01:01:03:01</td> <td>G*01:04:01:02</td> <td>0</td> <td>0</td> <td>3</td> <td>2</td> <td>0</td> </tr> <tr> <td>G*01:01:03:02</td> <td>G*01:04:01:01</td> <td>0</td> <td>0</td> <td>3</td> <td>2</td> <td>1</td> </tr> <tr> <td>G*01:01:03:04</td> <td>G*01:04:01:07</td> <td>0</td> <td>0</td> <td>4</td> <td>0</td> <td>1</td> </tr> <tr> <td>G*01:01:03:01</td> <td>G*01:04:01:01</td> <td>0</td> <td>0</td> <td>4</td> <td>2</td> <td>1</td> </tr> <tr> <td>G*01:01:03:02</td> <td>G*01:04:01:03</td> <td>0</td> <td>0</td> <td>4</td> <td>2</td> <td>1</td> </tr> </tbody> </table>						Allele 1	Allele 2	CORE	EXONS	N-C	PHASE1	PHASE2	G*01:01:03:03	G*01:04:01:02	0	0	0	0	0	G*01:01:03:04	G*01:04:01:02	0	0	1	0	0	G*01:01:03:03	G*01:04:01:01	0	0	1	0	1	G*01:01:03:03	G*01:04:01:03	0	0	2	0	1	G*01:01:03:03	G*01:04:01:06	0	0	2	0	1	G*01:01:03:04	G*01:04:01:01	0	0	2	0	1	G*01:01:03:03	G*01:04:01:05	0	0	2	0	2	G*01:01:03:02	G*01:04:01:02	0	0	2	2	0	G*01:01:03:03	G*01:04:01:07	0	0	3	0	1	G*01:01:03:04	G*01:04:01:03	0	0	3	0	1	G*01:01:03:04	G*01:04:01:06	0	0	3	0	1	G*01:01:03:04	G*01:04:01:05	0	0	3	0	2	G*01:01:03:01	G*01:04:01:02	0	0	3	2	0	G*01:01:03:02	G*01:04:01:01	0	0	3	2	1	G*01:01:03:04	G*01:04:01:07	0	0	4	0	1	G*01:01:03:01	G*01:04:01:01	0	0	4	2	1	G*01:01:03:02	G*01:04:01:03	0	0	4	2	1
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HLA Class II Motifs

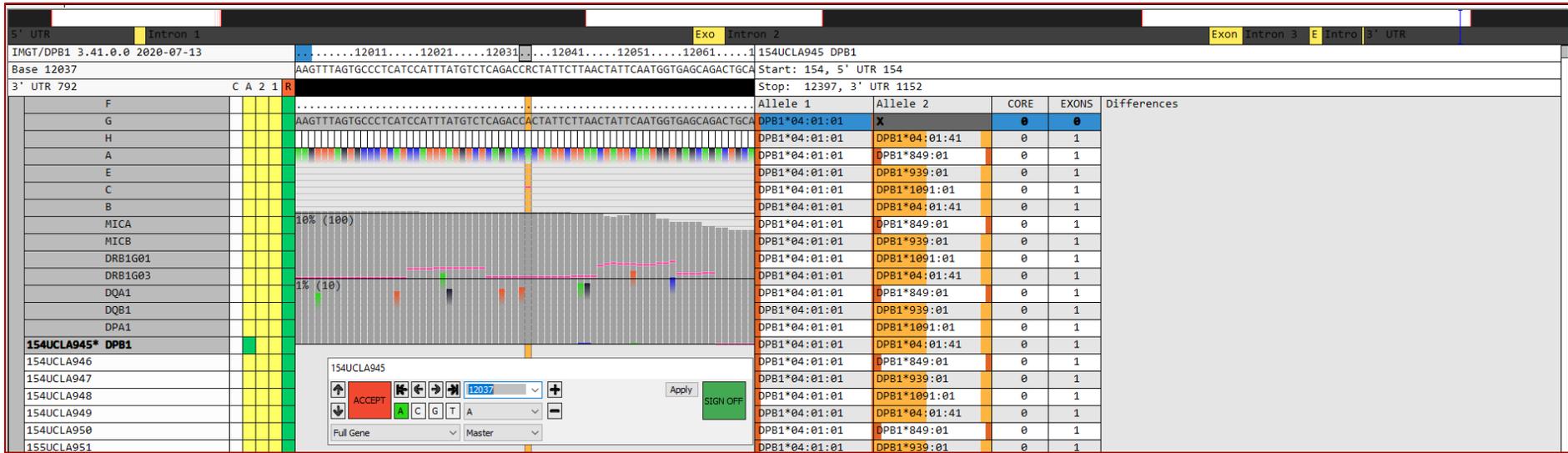
HLA-DPB1 rs9277534A>G

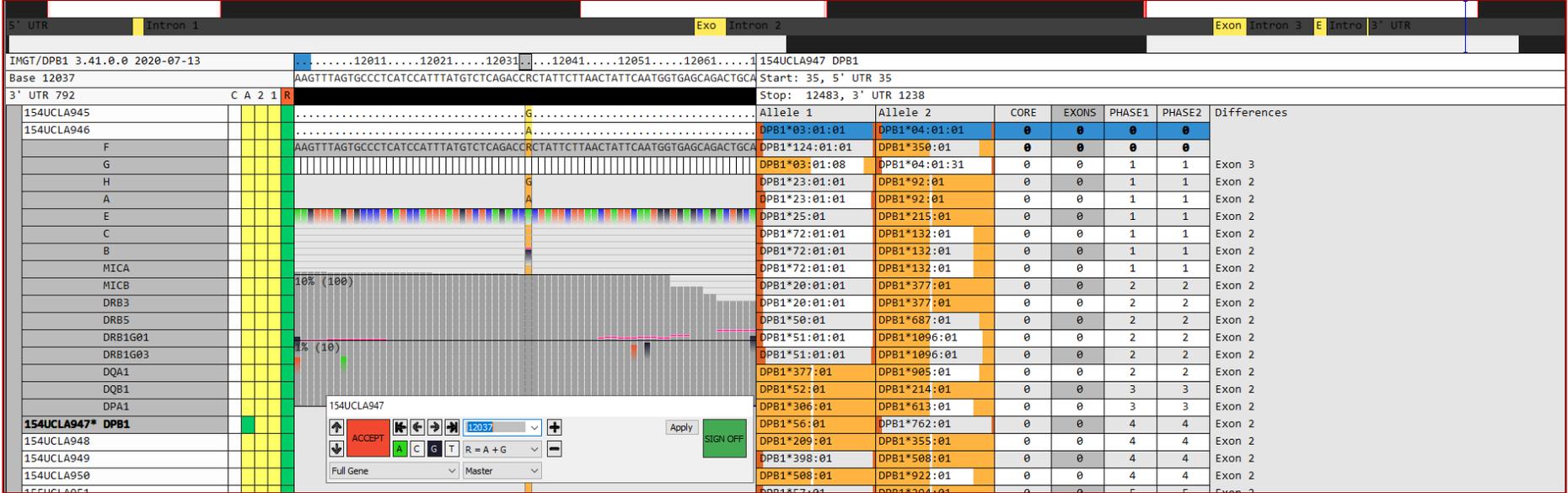


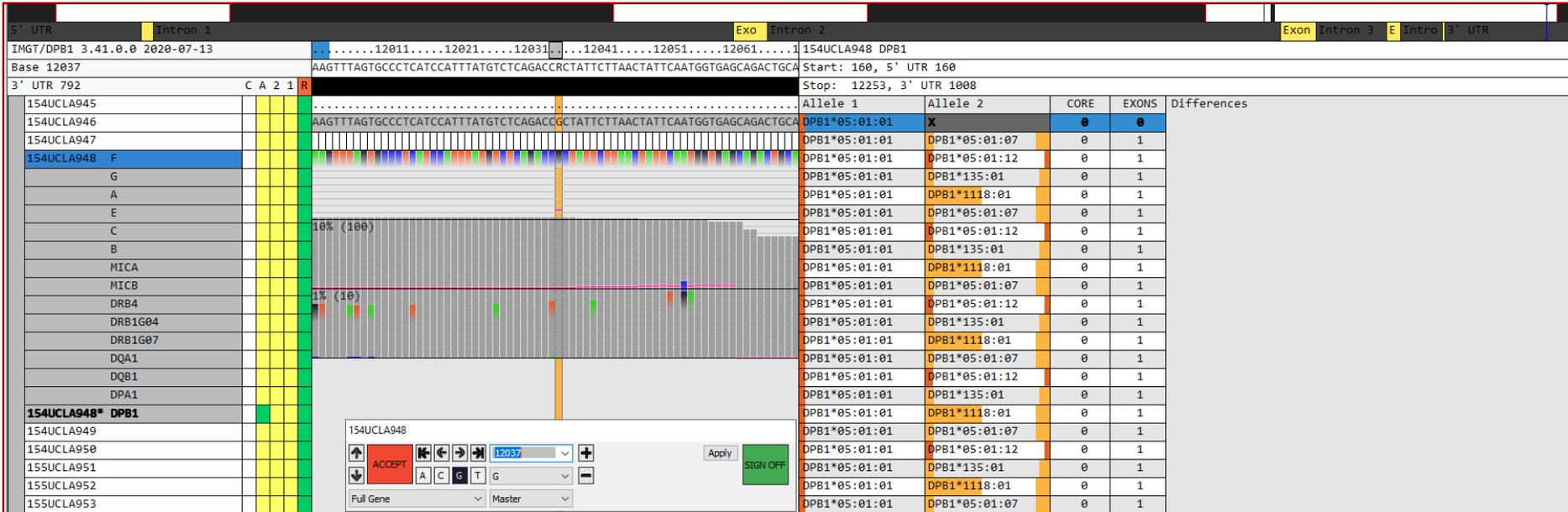


HLA-DPB1 rs9277534A>G

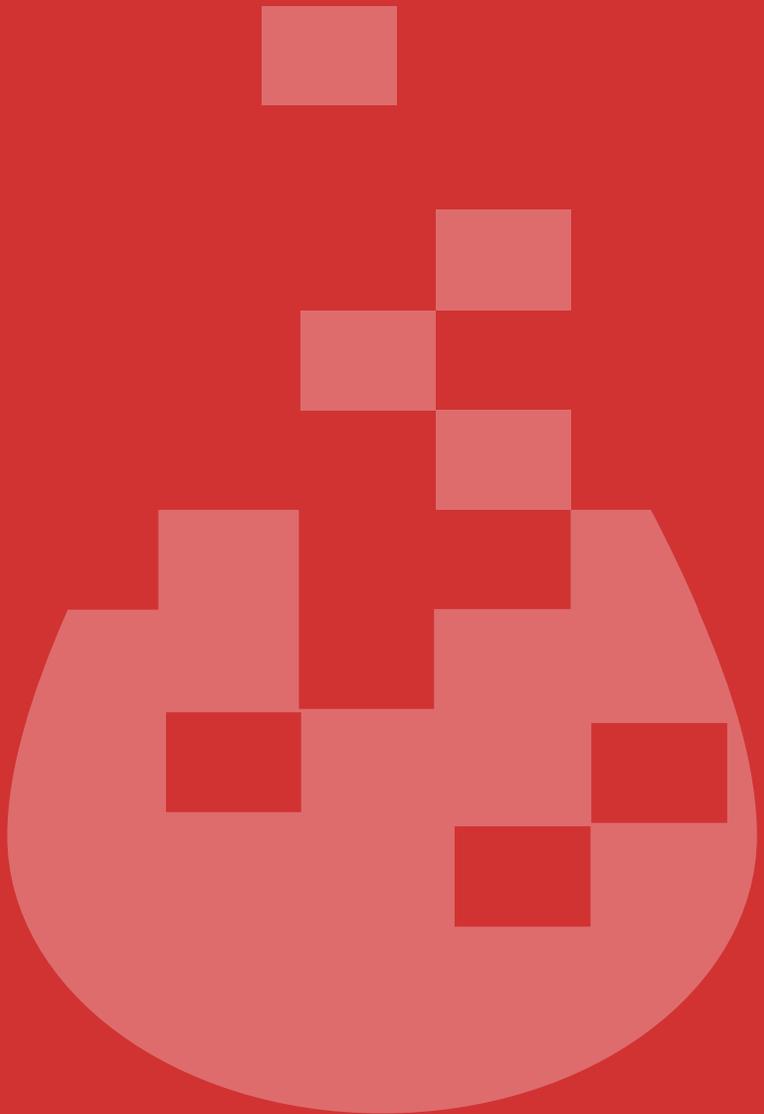
Motif ID:	rs9277534A>G	Locus:	HLA-DPB1	Implemented (Ref. Version #):	3.37.0
Supporting Publication:	<ul style="list-style-type: none"> • Petersdorf EW, Malkki M, O'hUigin C, Carrington M, Gooley T, Haagenson MD, Horowitz MM, Spellman SR, Wang T, Stevenson P. High HLA-DP Expression and Graft-versus-Host Disease. <i>N Engl J Med.</i> 2015 Aug 13;373(7):599-609 • Schöne B, Bergmann S, Lang K, Wagner I, Schmidt AH, Petersdorf EW, Lange V. Predicting an HLA-DPB1 expression marker based on standard DPB1 genotyping: Linkage analysis of over 32,000 samples. <i>Hum Immunol.</i> 2018 Jan;79(1):20-27. 				
Impact of polymorphism:	<p>HLA-DPB1 expression is associated with the rs9277534 A/G polymorphism located in the 3'UTR of the HLA-DPB1 gene. The rs9277534-A allele is associated with low DPB1 expression, whereas the rs9277534-G allele is associated with high DPB1 expression. Among recipients of HLA-DPB1-mismatched transplants from donors with the low-expression allele, recipients with the high-expression allele had a high risk of GVHD. When DPB1-matched donors are not available, this expression marker can be used to prospectively identify DPB1-mismatched donors who generate a permissive DPB1 mismatch against low-expression patient DPB1 alleles.</p>				

Motif ID:	rs9277534A>G	Locus:	HLA-DPB1	Implemented (Ref. Version #):	3.37.0
Example Display:	Homozygous A				
					

Motif ID:	rs9277534A>G	Locus:	HLA-DPB1	Implemented (Ref. Version #):	3.37.0																																																																																																																																																										
Example Display:	<h3 style="color: red; margin: 0;">Heterozygous A/G</h3>  <p>The screenshot displays the HLA-DPB1 gene structure with exons and introns. A sequence alignment shows the reference sequence (154UCLA947) and the variant (154UCLA946) with a red 'A' at position 12037. A table below lists various alleles and their differences from the reference. The variant rs9277534A>G is highlighted in red in the table.</p> <table border="1" style="font-size: small; border-collapse: collapse;"> <thead> <tr> <th>Allele 1</th> <th>Allele 2</th> <th>CORE</th> <th>EXONS</th> <th>PHASE1</th> <th>PHASE2</th> <th>Differences</th> </tr> </thead> <tbody> <tr> <td>DPB1*03:01:01</td> <td>DPB1*04:01:01</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>DPB1*124:01:01</td> <td>DPB1*350:01</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>DPB1*03:01:08</td> <td>DPB1*04:01:31</td> <td>0</td> <td>0</td> <td>1</td> <td>1</td> <td>Exon 3</td> </tr> <tr> <td>DPB1*23:01:01</td> <td>DPB1*92:01</td> <td>0</td> <td>0</td> <td>1</td> <td>1</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*23:01:01</td> <td>DPB1*92:01</td> <td>0</td> <td>0</td> <td>1</td> <td>1</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*25:01</td> <td>DPB1*215:01</td> <td>0</td> <td>0</td> <td>1</td> <td>1</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*72:01:01</td> <td>DPB1*132:01</td> <td>0</td> <td>0</td> <td>1</td> <td>1</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*72:01:01</td> <td>DPB1*132:01</td> <td>0</td> <td>0</td> <td>1</td> <td>1</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*72:01:01</td> <td>DPB1*132:01</td> <td>0</td> <td>0</td> <td>1</td> <td>1</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*20:01:01</td> <td>DPB1*377:01</td> <td>0</td> <td>0</td> <td>2</td> <td>2</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*20:01:01</td> <td>DPB1*377:01</td> <td>0</td> <td>0</td> <td>2</td> <td>2</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*50:01</td> <td>DPB1*687:01</td> <td>0</td> <td>0</td> <td>2</td> <td>2</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*51:01:01</td> <td>DPB1*1096:01</td> <td>0</td> <td>0</td> <td>2</td> <td>2</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*51:01:01</td> <td>DPB1*1096:01</td> <td>0</td> <td>0</td> <td>2</td> <td>2</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*377:01</td> <td>DPB1*905:01</td> <td>0</td> <td>0</td> <td>2</td> <td>2</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*52:01</td> <td>DPB1*214:01</td> <td>0</td> <td>0</td> <td>3</td> <td>3</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*306:01</td> <td>DPB1*613:01</td> <td>0</td> <td>0</td> <td>3</td> <td>3</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*56:01</td> <td>DPB1*762:01</td> <td>0</td> <td>0</td> <td>4</td> <td>4</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*209:01</td> <td>DPB1*355:01</td> <td>0</td> <td>0</td> <td>4</td> <td>4</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*398:01</td> <td>DPB1*508:01</td> <td>0</td> <td>0</td> <td>4</td> <td>4</td> <td>Exon 2</td> </tr> <tr> <td>DPB1*508:01</td> <td>DPB1*922:01</td> <td>0</td> <td>0</td> <td>4</td> <td>4</td> <td>Exon 2</td> </tr> </tbody> </table>					Allele 1	Allele 2	CORE	EXONS	PHASE1	PHASE2	Differences	DPB1*03:01:01	DPB1*04:01:01	0	0	0	0		DPB1*124:01:01	DPB1*350:01	0	0	0	0		DPB1*03:01:08	DPB1*04:01:31	0	0	1	1	Exon 3	DPB1*23:01:01	DPB1*92:01	0	0	1	1	Exon 2	DPB1*23:01:01	DPB1*92:01	0	0	1	1	Exon 2	DPB1*25:01	DPB1*215:01	0	0	1	1	Exon 2	DPB1*72:01:01	DPB1*132:01	0	0	1	1	Exon 2	DPB1*72:01:01	DPB1*132:01	0	0	1	1	Exon 2	DPB1*72:01:01	DPB1*132:01	0	0	1	1	Exon 2	DPB1*20:01:01	DPB1*377:01	0	0	2	2	Exon 2	DPB1*20:01:01	DPB1*377:01	0	0	2	2	Exon 2	DPB1*50:01	DPB1*687:01	0	0	2	2	Exon 2	DPB1*51:01:01	DPB1*1096:01	0	0	2	2	Exon 2	DPB1*51:01:01	DPB1*1096:01	0	0	2	2	Exon 2	DPB1*377:01	DPB1*905:01	0	0	2	2	Exon 2	DPB1*52:01	DPB1*214:01	0	0	3	3	Exon 2	DPB1*306:01	DPB1*613:01	0	0	3	3	Exon 2	DPB1*56:01	DPB1*762:01	0	0	4	4	Exon 2	DPB1*209:01	DPB1*355:01	0	0	4	4	Exon 2	DPB1*398:01	DPB1*508:01	0	0	4	4	Exon 2	DPB1*508:01	DPB1*922:01	0	0	4	4	Exon 2
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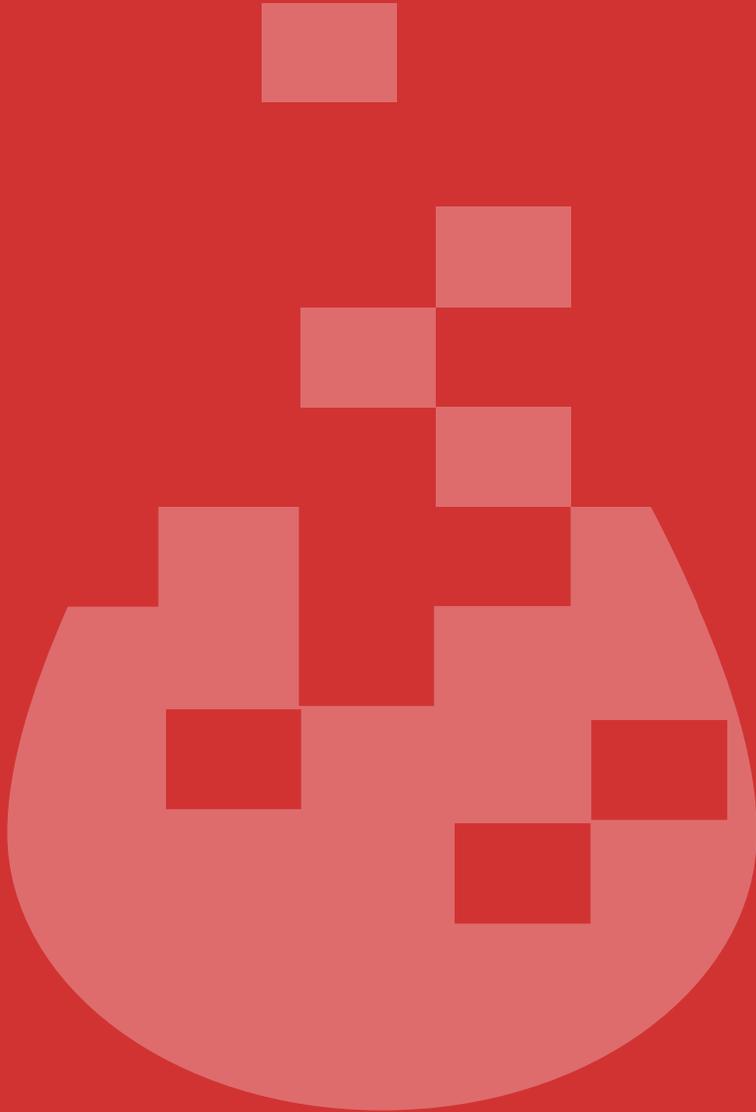
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Example Display:	Homozygous G				
					

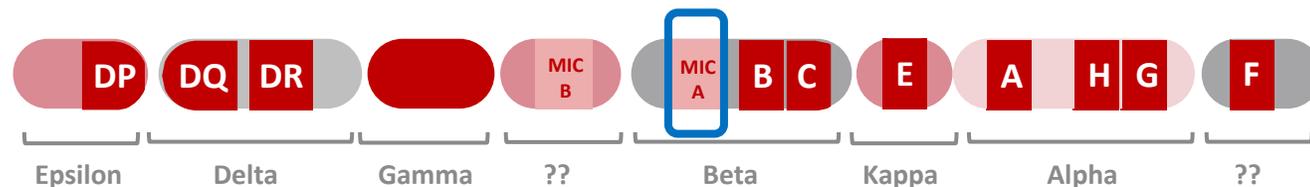
Motif ID:	rs9277534A>G	Locus:	HLA-DPB1	Implemented (Ref. Version #):	3.37.0																																
Example Display:	<p>Summary Table Report:</p> <table border="1"> <thead> <tr> <th colspan="3">Motifs.</th> </tr> </thead> <tbody> <tr> <td>154UCLA945</td> <td>IMGT/DPB1 rs9277534:AA</td> <td>Homozygous A</td> </tr> <tr> <td>154UCLA946</td> <td>rs9277534:GG</td> <td>Homozygous G</td> </tr> <tr> <td>154UCLA947</td> <td>rs9277534:GA</td> <td>Heterozygous A/G</td> </tr> </tbody> </table> <p>Genotyping Report:</p> <table border="1"> <thead> <tr> <th>Sample:</th> <th>Reference:</th> <th>Summary</th> </tr> </thead> <tbody> <tr> <td>154UCLA945</td> <td>IMGT/DPB1 3.41.0.0 2020-07-13</td> <td> <p>The allele pairs listed below are compatible with the consensus sequence.</p> <table border="1"> <tr> <td>DPB1*04:01:01</td> <td>X</td> </tr> </table> <p>Motifs: rs9277534:AA Homozygous A</p> </td> </tr> <tr> <td>154UCLA947</td> <td></td> <td> <p>The allele pairs listed below are compatible with the consensus sequence.</p> <table border="1"> <tr> <td>DPB1*03:01:01</td> <td>DPB1*04:01:01</td> </tr> <tr> <td>DPB1*124:01:01</td> <td>DPB1*350:01</td> </tr> </table> <p>Motifs: rs9277534:GA Heterozygous A/G</p> </td> </tr> <tr> <td>154UCLA948</td> <td></td> <td> <p>The allele pairs listed below are compatible with the consensus sequence.</p> <table border="1"> <tr> <td>DPB1*05:01:01</td> <td>X</td> </tr> </table> <p>Motifs: rs9277534:GG Homozygous G</p> </td> </tr> </tbody> </table>					Motifs.			154UCLA945	IMGT/DPB1 rs9277534:AA	Homozygous A	154UCLA946	rs9277534:GG	Homozygous G	154UCLA947	rs9277534:GA	Heterozygous A/G	Sample:	Reference:	Summary	154UCLA945	IMGT/DPB1 3.41.0.0 2020-07-13	<p>The allele pairs listed below are compatible with the consensus sequence.</p> <table border="1"> <tr> <td>DPB1*04:01:01</td> <td>X</td> </tr> </table> <p>Motifs: rs9277534:AA Homozygous A</p>	DPB1*04:01:01	X	154UCLA947		<p>The allele pairs listed below are compatible with the consensus sequence.</p> <table border="1"> <tr> <td>DPB1*03:01:01</td> <td>DPB1*04:01:01</td> </tr> <tr> <td>DPB1*124:01:01</td> <td>DPB1*350:01</td> </tr> </table> <p>Motifs: rs9277534:GA Heterozygous A/G</p>	DPB1*03:01:01	DPB1*04:01:01	DPB1*124:01:01	DPB1*350:01	154UCLA948		<p>The allele pairs listed below are compatible with the consensus sequence.</p> <table border="1"> <tr> <td>DPB1*05:01:01</td> <td>X</td> </tr> </table> <p>Motifs: rs9277534:GG Homozygous G</p>	DPB1*05:01:01	X
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Additional MHC Motifs

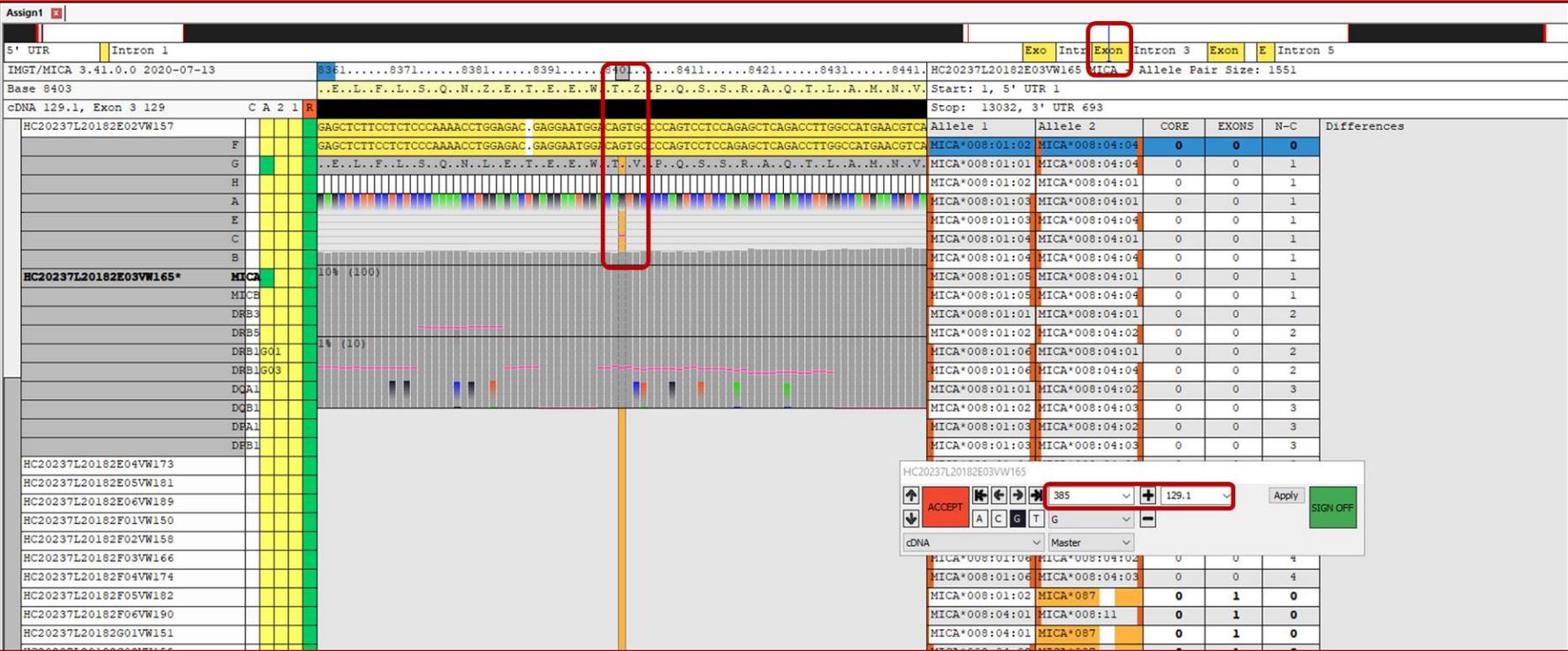
MICA rs1051792G>A; MICA-129Val/Met





MICA rs1051792G>A; MICA-129Val/Met

Motif ID:	rs1051792G>A; MICA-129Val/Met	Locus:	MICA	Implemented (Ref. Version #):	3.37.0.1
Supporting Publication:	<ul style="list-style-type: none"> Isernhagen A, Malzahn D, Bickeböller H, Dressel R. Impact of the MICA-129Met/Val Dimorphism on NKG2D-Mediated Biological Functions and Disease Risks. <i>Front Immunol.</i> 2016 Dec 12;7:588 Fuerst D, Neuchel C, Niederwieser D, Bunjes D, Gramatzki M, Wagner E, Wulf G, Glass B, Pfreundschuh M, Einsele H, Arnold R, Stuhler G, Schaefer-Eckart K, Freitag S, Casper J, Kaufmann M, Wattad M, Hertenstein B, Klein S, Ringhoffer M, Mytilineos D, Tsamadou C, Mueller C, Schrezenmeier H, Mytilineos J. Matching for the MICA-129 polymorphism is beneficial in unrelated hematopoietic stem cell transplantation. <i>Blood.</i> 2016 Dec 29;128(26):3169-3176. 				
Impact of polymorphism:	<p>The MICA-129Val/Met dimorphism, caused by SNP rs1051792 at nucleotide position 454 (G>A) of the MICA gene causes a valine (Val) to methionine (Met) exchange at position 129 of the MICA protein, separating MICA into isoforms that bind NKG2D with high (Met) and low affinities (Val).</p> <p>Adverse overall survival and worse outcome for disease-free survival was observed in the 10/10 match group if MICA-129 was mismatched (10/10, hazard ratio, 1.77). Higher rates of acute GVHD were seen in MICA-129 mismatched cases.</p> <p>Exon 3, Position 8403 in AlloSeq Assign</p>				

Motif ID:	rs1051792G>A; MICA-129Val/Met	Locus:	MICA	Implemented (Ref. Version #):	3.37.0.1																																																																																																												
Example Display:	<p style="color: red; font-weight: bold;">Homozygous G - 129Val/Val</p>  <p>The screenshot displays the following components:</p> <ul style="list-style-type: none"> Genomic Track: Shows sequence alignment for MICA. A red box highlights a G allele at position 129. The track includes labels for 5' UTR, Intron 1, Exon, Intron 3, Exon, and Intron 5. Allele Pair Table: <table border="1"> <thead> <tr> <th>Allele 1</th> <th>Allele 2</th> <th>CORE</th> <th>EXONS</th> <th>N-C</th> <th>Differences</th> </tr> </thead> <tbody> <tr> <td>MICA*008:01:02</td> <td>MICA*008:04:04</td> <td>0</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICA*008:01:01</td> <td>MICA*008:04:04</td> <td>0</td> <td>0</td> <td>1</td> <td></td> </tr> <tr> <td>MICA*008:01:02</td> <td>MICA*008:04:01</td> <td>0</td> <td>0</td> <td>1</td> <td></td> </tr> <tr> <td>MICA*008:01:03</td> <td>MICA*008:04:01</td> <td>0</td> <td>0</td> <td>1</td> <td></td> </tr> <tr> <td>MICA*008:01:03</td> <td>MICA*008:04:04</td> <td>0</td> <td>0</td> <td>1</td> <td></td> </tr> <tr> <td>MICA*008:01:04</td> <td>MICA*008:04:01</td> <td>0</td> <td>0</td> <td>1</td> <td></td> </tr> <tr> <td>MICA*008:01:04</td> <td>MICA*008:04:04</td> <td>0</td> <td>0</td> <td>1</td> <td></td> </tr> <tr> <td>MICA*008:01:05</td> <td>MICA*008:04:01</td> <td>0</td> <td>0</td> <td>1</td> <td></td> </tr> <tr> <td>MICA*008:01:05</td> <td>MICA*008:04:04</td> <td>0</td> <td>0</td> <td>1</td> <td></td> </tr> <tr> <td>MICA*008:01:01</td> <td>MICA*008:04:01</td> <td>0</td> <td>0</td> <td>2</td> <td></td> </tr> <tr> <td>MICA*008:01:02</td> <td>MICA*008:04:02</td> <td>0</td> <td>0</td> <td>2</td> <td></td> </tr> <tr> <td>MICA*008:01:06</td> <td>MICA*008:04:01</td> <td>0</td> <td>0</td> <td>2</td> <td></td> </tr> <tr> <td>MICA*008:01:06</td> <td>MICA*008:04:04</td> <td>0</td> <td>0</td> <td>2</td> <td></td> </tr> <tr> <td>MICA*008:01:01</td> <td>MICA*008:04:02</td> <td>0</td> <td>0</td> <td>3</td> <td></td> </tr> <tr> <td>MICA*008:01:02</td> <td>MICA*008:04:03</td> <td>0</td> <td>0</td> <td>3</td> <td></td> </tr> <tr> <td>MICA*008:01:03</td> <td>MICA*008:04:02</td> <td>0</td> <td>0</td> <td>3</td> <td></td> </tr> <tr> <td>MICA*008:01:03</td> <td>MICA*008:04:03</td> <td>0</td> <td>0</td> <td>3</td> <td></td> </tr> </tbody> </table> Control Panel: Shows 'ACCEPT' and 'SIGN OFF' buttons. A dropdown menu is set to 'G' and '129.1'. 					Allele 1	Allele 2	CORE	EXONS	N-C	Differences	MICA*008:01:02	MICA*008:04:04	0	0	0		MICA*008:01:01	MICA*008:04:04	0	0	1		MICA*008:01:02	MICA*008:04:01	0	0	1		MICA*008:01:03	MICA*008:04:01	0	0	1		MICA*008:01:03	MICA*008:04:04	0	0	1		MICA*008:01:04	MICA*008:04:01	0	0	1		MICA*008:01:04	MICA*008:04:04	0	0	1		MICA*008:01:05	MICA*008:04:01	0	0	1		MICA*008:01:05	MICA*008:04:04	0	0	1		MICA*008:01:01	MICA*008:04:01	0	0	2		MICA*008:01:02	MICA*008:04:02	0	0	2		MICA*008:01:06	MICA*008:04:01	0	0	2		MICA*008:01:06	MICA*008:04:04	0	0	2		MICA*008:01:01	MICA*008:04:02	0	0	3		MICA*008:01:02	MICA*008:04:03	0	0	3		MICA*008:01:03	MICA*008:04:02	0	0	3		MICA*008:01:03	MICA*008:04:03	0	0	3	
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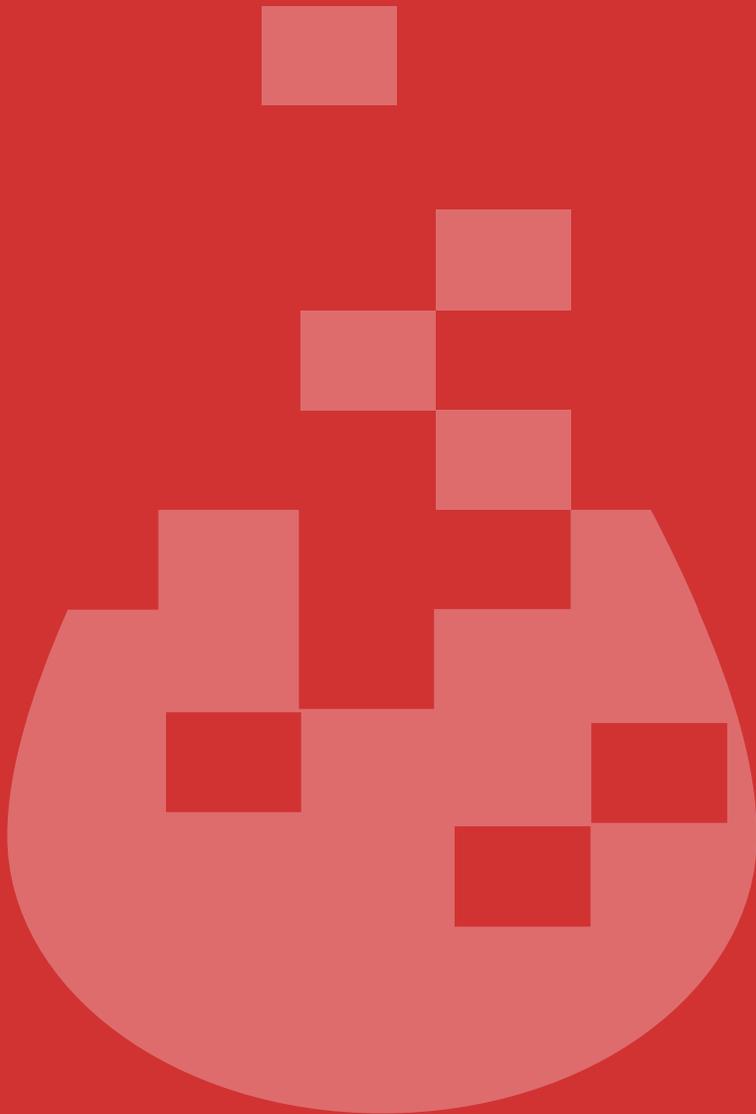
Motif ID:	rs1051792G>A; MICA-129Val/Met	Locus:	MICA	Implemented (Ref. Version #):	3.37.0.1
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Example Display: **Heterozygous G/A- 129Met/Val**

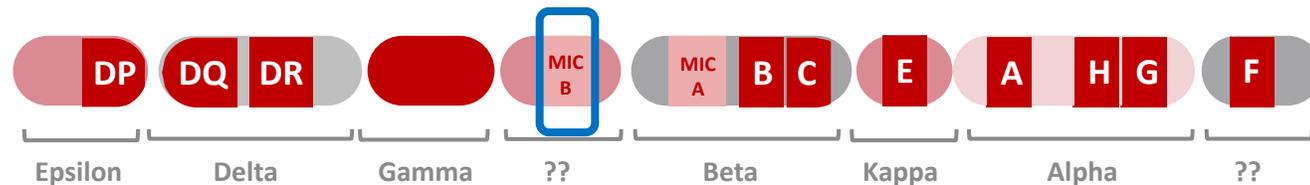
The screenshot displays the MICA gene structure with exons and introns. The sequence alignment shows a heterozygous G/A variant at position 129. The variant call table below the alignment shows the following data:

Allele 1	Allele 2	CORE	EXONS	N-C	PHASE1	PHASE2	Difference
MICA*007:01:01	MICA*008:01:01	0	0	0	0	0	
MICA*007:01:02	MICA*008:01:01	0	0	0	0	0	Intron 5
MICA*007:01:03	MICA*008:01:01	0	0	0	0	0	Intron 1
MICA*007:01:04	MICA*008:01:01	0	0	0	0	0	Intron 1
MICA*007:01:01	MICA*008:01:02	0	0	1	0	1	
MICA*007:01:02	MICA*008:01:02	0	0	1	0	1	
MICA*007:01:03	MICA*008:01:02	0	0	1	0	1	
MICA*007:01:04	MICA*008:01:02	0	0	1	0	1	
MICA*007:01:01	MICA*008:01:03	0	0	2	0	1	
MICA*007:01:02	MICA*008:01:03	0	0	2	0	1	
MICA*007:01:03	MICA*008:01:03	0	0	2	0	1	
MICA*007:01:04	MICA*008:01:03	0	0	2	0	1	
MICA*007:01:01	MICA*008:01:04	0	0	2	0	1	
MICA*007:01:02	MICA*008:01:04	0	0	2	0	1	
MICA*007:01:03	MICA*008:01:04	0	0	2	0	1	
MICA*007:01:04	MICA*008:01:04	0	0	2	0	1	

Motif ID:	rs1051792G>A; MICA-129Val/Met	Locus:	MICA	Implemented (Ref. Version #):	3.37.0.1																																																																																																																																																						
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IMGT/F	IMGT/G	IMGT/H	IMGT/A	IMGT/E	IMGT/C	IMGT/B	IMGT/MICA		HC20237L20182A01R900050106		rs1610696:CC		Bw4		Bw6	Bw6, rs1050-129Val		Homozygous G	HC20237L20182A02Q940050830		rs1610696:CC				Bw6	Bw4, rs1050-129Met, 129Val		Heterozygous G/A	HC20237L20182A03P073231229		rs1610696:CG				Bw6	Bw4, Bw6, rs129Val			HC20237L20182A04R920051269		rs1610696:GG				Bw6	Bw6, rs1050-129Val			HC20237L20182A05R970900614		rs1610696:CG				Bw6	Bw4, Bw6, rs129Val			HC20237L20182A06R050114117		rs1610696:CG				Bw6	Bw4, Bw6, rs129Val			HC20237L20182B01IHW09024		rs1610696:CC				Bw6	Bw6, rs1050-129Met, 129Val			HC20237L20182B02IHW09050		rs1610696:CC				Bw6	Bw4, rs1050-129Val			HC20237L20182B03IHW09058		rs1610696:CC				Bw6	Bw6, rs1050-129Met		Homozygous A	Sample:	Summary	HC20237L20182B04IHW09074		The allele pairs listed below are compatible with the consensus sequence.		MICA*008:04:02	MICA*027:01:01	MICA*008:04:02	MICA*027:01:02	Intron 1		Motifs: 129Val Homozygous G		Sample:	Summary	HC20237L20182C04S4RI295119a		The allele pairs listed below are compatible with the consensus sequence.		MICA*002:01:03	MICA*008:04:02	MICA*002:01:04	MICA*008:04:02	MICA*002:01:07	MICA*008:04:02	MICA*002:01:08	MICA*008:04:02	Intron 1		Motifs: 129Met, 129Val Heterozygous G/A		Sample:	Summary	HC20237L20182C06S6UI976259a		The allele pairs listed below are compatible with the consensus sequence.		MICA*011:01:01	MICA*018:01:01	MICA*011:01:01	MICA*018:01:03	MICA*011:01:06	MICA*018:01:01	MICA*011:01:06	MICA*018:01:03	Intron 1		Motifs: 129Met Homozygous A	
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HC20237L20182A06R050114117		rs1610696:CG				Bw6	Bw4, Bw6, rs129Val																																																																																																																																																				
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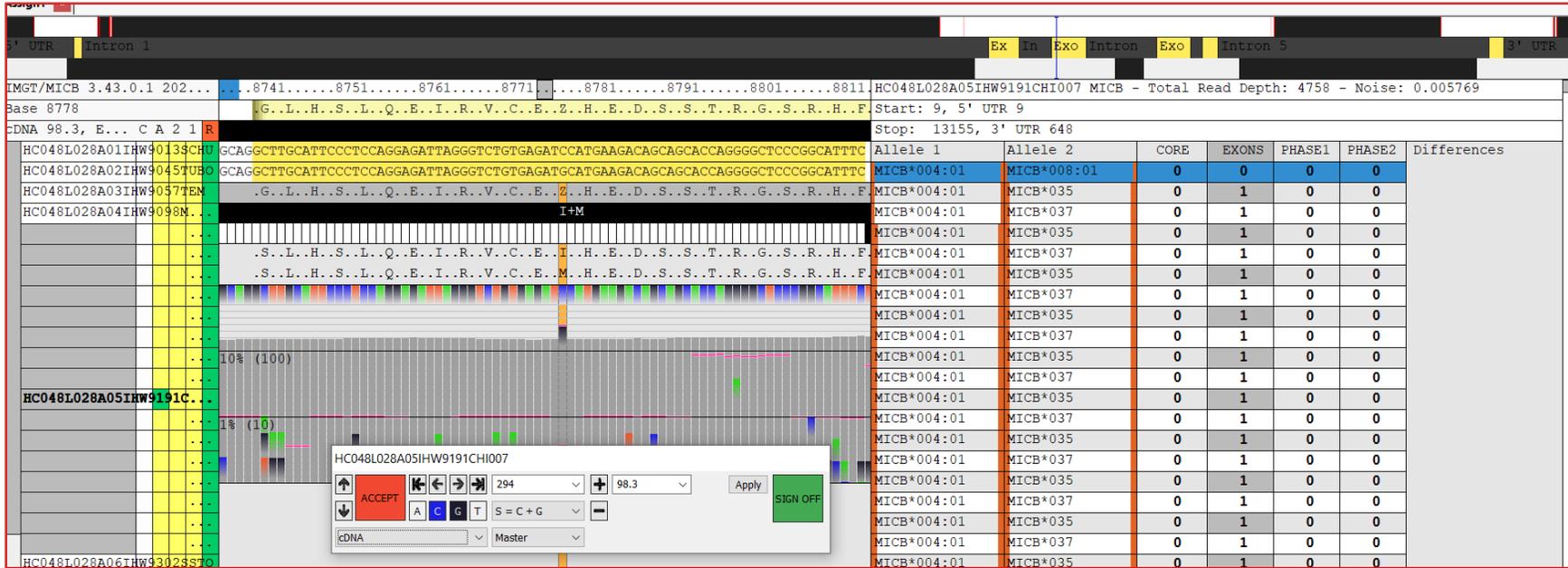
MICB98 Met/Ile, rs3134900



MICB98 Met/Ile, rs3134900

Motif ID:	MICB98 Met/Ile	Locus:	MICB	Implemented (Ref. Version #):	3.37.0.1
Supporting Publication:	<p>Carapito R, Aouadi I, Pichot A, Spinnhirny P, Morlon A, Kotova I, Macquin C, Rolli V, Cesbron A, Gagne K, Oudshoorn M, van der Holt B, Labalette M, Spierings E, Picard C, Loiseau P, Tamouza R, Toubert A, Parissiadis A, Dubois V, Paillard C, Maumy-Bertrand M, Bertrand F, von dem Borne PA, Kuball JHE, Michallet M, Lioure B, Peffault de Latour R, Blaise D, Cornelissen JJ, Yakoub-Agha I, Claas F, Moreau P, Charron D, Mohty M, Morishima Y, Socié G, Bahram S. Compatibility at amino acid position 98 of MICB reduces the incidence of graft-versus-host disease in conjunction with the CMV status. <i>Bone Marrow Transplant.</i> 2020 Jul;55(7):1367-1378.</p> <p>Kanya Klumkrathok. Allelic MHC Class I Chain Related B (MICB) Molecules Affect the Binding to the Human Cytomegalovirus (HCMV) Unique Long 16 (UL16) Protein: Implications for Immune Surveillance. <i>Journal of Microbiology.</i> 2013</p>				
Impact of polymorphism:	<p>The isoleucine (Ile) to methionine (Met) substitution in MICB amino acid position 98 is a key polymorphic residue involved in UL16 binding. A MICB98 mismatched but otherwise fully HLA and MICA matched donor increases risk of both acute and chronic GvHD development. MICB98 mismatches showed a GvHD-independent association with a higher incidence of CMV infection/reactivation. In addition, MICB98 mismatches were associated with a higher rate of relapse. The variation Ile > Met is exclusively present in MICB*008. Mismatch occurs in approximately 6% of transplantations.</p>				

Motif ID:	MICB98 Met/Ile	Locus:	MICB	Implemented (Ref. Version #):	3.37.0.1																																																																																																																														
Example Display:	<h2 style="color: red;">Homozygous C Ile/Ile</h2> <table border="1" style="margin-top: 10px;"> <thead> <tr> <th>Allele 1</th> <th>Allele 2</th> <th>CORE</th> <th>EXONS</th> <th>PHASE1</th> <th>PHASE2</th> <th>Differences</th> </tr> </thead> <tbody> <tr> <td>MICB*002:01</td> <td>MICB*005:06</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*005:06</td> <td>MICB*036</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*005:06</td> <td>MICB*036</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*005:06</td> <td>MICB*036</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*002:01</td> <td>MICB*005:02</td> <td>1</td> <td>0</td> <td>--</td> <td>--</td> <td></td> </tr> <tr> <td>MICB*002:01</td> <td>MICB*005:02</td> <td>1</td> <td>0</td> <td>--</td> <td>--</td> <td></td> </tr> <tr> <td>MICB*002:01</td> <td>MICB*005:02</td> <td>1</td> <td>0</td> <td>--</td> <td>--</td> <td></td> </tr> <tr> <td>MICB*002:01</td> <td>MICB*005:02</td> <td>1</td> <td>0</td> <td>--</td> <td>--</td> <td></td> </tr> <tr> <td>MICB*002:01</td> <td>MICB*005:02</td> <td>1</td> <td>0</td> <td>--</td> <td>--</td> <td></td> </tr> <tr> <td>MICB*002:01</td> <td>MICB*005:02</td> <td>1</td> <td>0</td> <td>--</td> <td>--</td> <td></td> </tr> <tr> <td>MICB*002:01</td> <td>MICB*005:02</td> <td>1</td> <td>0</td> <td>--</td> <td>--</td> <td></td> </tr> <tr> <td>MICB*002:01</td> <td>MICB*005:02</td> <td>1</td> <td>0</td> <td>--</td> <td>--</td> <td></td> </tr> <tr> <td>MICB*002:01</td> <td>MICB*005:02</td> <td>1</td> <td>0</td> <td>--</td> <td>--</td> <td></td> </tr> <tr> <td>MICB*002:01</td> <td>MICB*005:02</td> <td>1</td> <td>0</td> <td>--</td> <td>--</td> <td></td> </tr> <tr> <td>MICB*002:01</td> <td>MICB*005:02</td> <td>1</td> <td>0</td> <td>--</td> <td>--</td> <td></td> </tr> <tr> <td>MICB*002:01</td> <td>MICB*005:02</td> <td>1</td> <td>0</td> <td>--</td> <td>--</td> <td></td> </tr> <tr> <td>MICB*002:01</td> <td>MICB*005:02</td> <td>1</td> <td>0</td> <td>--</td> <td>--</td> <td></td> </tr> </tbody> </table>					Allele 1	Allele 2	CORE	EXONS	PHASE1	PHASE2	Differences	MICB*002:01	MICB*005:06	0	0	0	0		MICB*005:06	MICB*036	0	1	0	0		MICB*005:06	MICB*036	0	1	0	0		MICB*005:06	MICB*036	0	1	0	0		MICB*002:01	MICB*005:02	1	0	--	--		MICB*002:01	MICB*005:02	1	0	--	--		MICB*002:01	MICB*005:02	1	0	--	--		MICB*002:01	MICB*005:02	1	0	--	--		MICB*002:01	MICB*005:02	1	0	--	--		MICB*002:01	MICB*005:02	1	0	--	--		MICB*002:01	MICB*005:02	1	0	--	--		MICB*002:01	MICB*005:02	1	0	--	--		MICB*002:01	MICB*005:02	1	0	--	--		MICB*002:01	MICB*005:02	1	0	--	--		MICB*002:01	MICB*005:02	1	0	--	--		MICB*002:01	MICB*005:02	1	0	--	--		MICB*002:01	MICB*005:02	1	0	--	--	
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Example Display:	<p>Heterozygous C/G Ile/Met</p>  <table border="1" data-bbox="1587 621 2186 1096"> <thead> <tr> <th>Allele 1</th> <th>Allele 2</th> <th>CORE</th> <th>EXONS</th> <th>PHASE1</th> <th>PHASE2</th> <th>Differences</th> </tr> </thead> <tbody> <tr> <td>MICB*004:01</td> <td>MICB*008:01</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*004:01</td> <td>MICB*035</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*004:01</td> <td>MICB*037</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*004:01</td> <td>MICB*035</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*004:01</td> <td>MICB*037</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*004:01</td> <td>MICB*035</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*004:01</td> <td>MICB*037</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*004:01</td> <td>MICB*035</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*004:01</td> <td>MICB*037</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*004:01</td> <td>MICB*035</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*004:01</td> <td>MICB*037</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*004:01</td> <td>MICB*035</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*004:01</td> <td>MICB*037</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*004:01</td> <td>MICB*035</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*004:01</td> <td>MICB*037</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> <tr> <td>MICB*004:01</td> <td>MICB*035</td> <td>0</td> <td>1</td> <td>0</td> <td>0</td> <td></td> </tr> </tbody> </table>					Allele 1	Allele 2	CORE	EXONS	PHASE1	PHASE2	Differences	MICB*004:01	MICB*008:01	0	0	0	0		MICB*004:01	MICB*035	0	1	0	0		MICB*004:01	MICB*037	0	1	0	0		MICB*004:01	MICB*035	0	1	0	0		MICB*004:01	MICB*037	0	1	0	0		MICB*004:01	MICB*035	0	1	0	0		MICB*004:01	MICB*037	0	1	0	0		MICB*004:01	MICB*035	0	1	0	0		MICB*004:01	MICB*037	0	1	0	0		MICB*004:01	MICB*035	0	1	0	0		MICB*004:01	MICB*037	0	1	0	0		MICB*004:01	MICB*035	0	1	0	0		MICB*004:01	MICB*037	0	1	0	0		MICB*004:01	MICB*035	0	1	0	0		MICB*004:01	MICB*037	0	1	0	0		MICB*004:01	MICB*035	0	1	0	0	
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Motif ID:	MICB98 Met/Ile	Locus:	MICB	Implemented (Ref. Version #):	3.37.0.1																																				
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Revision History

Version	Date	Modification	Reference/Justification
1.0	17-Jan-22	Drafted by J.Edwards and E.Carr. Issued by L. Langley 14 Jun 22	N/A
2.0	02-Oct-23	J.Edwards added header slides for each motif. Added rs# to MICB Met/Ile motif slide. Added slides for new motif HLA-G rs371194629 3'UTR 14bp indel. Updated the location of HLA-G rs1610696C>G motif. A. Bereza-Jarocinska updated the disclaimer on first slide	N/A