

## AlloSeq Assign Motifs

CareDx Technical Support



Margot Duane Stem Cell Transplant Recipient

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TEC747-S\_AlloSeq Assign 1.0\_Motifs version 1.0 Effective 14 Jun 22



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### **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	<b>Reports suggest elevated HLA-G expression is associated with reduced allograft rejection</b> . 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. <b>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.</b> 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/lle	<b>This marker has been implicated in a higher risk of GVHD when it is mismatched.</b> 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 Class I Motifs







#### 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, MJ, Malkki M, McKallor C, Morishima Y, O Working Group in Hematopoietic Cell Trar <b>haemopoietic cell transplantation: a retr</b>	Bengtsson M, De Sant udshoorn M, Spellmar nsplantation. <b>Role of H</b> ospective cohort study	is D, Dubois V, Go n SR, Villard J, Ste <b>ILA-B exon 1 in g</b> y. <i>Lancet Haemat</i>	Gooley T, Horowitz M, Hsu K, Madrigal JA, Maie evenson P; International Histocompatibility graft-versus-host disease after unrelated atol. 2020 Jan;7(1):e50-e60.						
Impact of polymorphism:	The mature HLA Class I molecule that is encodes a separate leader peptide, whic presented by Class I, notably HLA-E. HLA –21 position. A sequence dimorphism (r (Met; M) or threonine (Thr; T), which dif <i>significantly higher with HLA-B leader n</i> <i>had an M leader compared with a T lea</i> leader allotype. This mutation is common among HLA-B*	expressed on the cell ch is not a structural r A-A and HLA-C leader s1050458) in exon 1 o ferentially influence r <i>nismatching compare</i> <i>der.</i> The preferred HL	surface is encod noiety of the ma sequences are la of HLA-B gives ris natural killer and ed to leader mat A-B-mismatched	ed by exons 2–7. Exon 1 of C ture Class I molecule, but car rgely invariant and encode m te to leader peptides containing T-cell alloresponses. <b>Severe</b> <b>ching, and when the shared</b> I donor is leader-matched an 81 allele groups.	lass I genes to be bound and tethionine at the ing methionine <b>GVHD was</b> <b>HLA-B allotype</b> d shares a T					



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Motif ID:	rs1050458C>T		Locus:	HLA-B	Implem (Ref. Ve	nente ersion	d (#):		3	.41	
Example Display:	Homozygous C										
	Assign1										
	5' UTR	E Intr Exon 2 Intro	n 2 Exon 3 Intron 3	Exon 4 Int Exo	Intron 5	Int	3' UTR				
	IMGT/B 3.41.0.0 2020-07-13		41	881 154UCLA945 B -	Allele Pair Siz	e: 26218					
	Base 853	ACTCARARTCTCCTCAGACRCCRA	G <mark>ATGCKGGTCAYGGCRCCCCGAACCSTCCT<mark>CCT</mark>GCT(</mark>	GCTCTSGGSR Start: 9, 5' U	IR 9						
	A		G.	Stop. 4055, 5	Allele 2	CORE	EXONS	N-C	PHASE1	PHASE2	Differences
	154UCLA945* B			CC. B*35:01:01:05	B*50:01:01:01	0	0	0	0	0	
	С	ACTCAGAATCTCCTCAGACGCCGAG	GATGCGGGTCACGGCCCCCGAACCGTCCTCCTGCT	GCTCTSGGSG <mark>B*</mark> 35:01:01:42	B*50:01:01:01	0	0	0	0	0	Intron 2
	DPA1			B*35:280	B*50:13	0	0	0	1	1	Exon 2
	DPB1		G	G G B*35:10	B*50:15	0	0	0	2	2	Exon 2, 3' U
	DQA1		A	C C <mark>B*35:01:01:0</mark> 1	B*50:01:01:01	0	0	1	0	0	
	DQB1			B*35:01:01:03	B*50:01:01:01	0	0	1	0	0	
	DRB1G01			B*35:01:01:05	B*50:01:01:03	0	0	1	0	0	
	DRB1G03			B*35:01:01:05	B*50:01:01:04	0	0	1	0	0	
	E			B 35:01:01:05	B*50:01:01:05	0	0	1	0	0	
	r C	500	Read Depth	B*35:01:01:05	B*50:01:01:00	0	0	1	0	0	
	н		· ·	B*35.01.01.07	B*50:01:01:01	0	0	1	0	0	
	MTCA			B*35:01:01:09	B*50:01:01:01	0	0	1	0	0	
	MICB			B*35:01:01:10	B*50:01:01:01	0	0	1	0	0	
	154UCLA946			B*35:01:01:11	B*50:01:01:01	0	0	1	0	0	
	154UCLA947			B*35:01:01:12	B*50:01:01:01	0	0	1	0	0	
	154UCLA948			B*35:01:01:1 <mark>3</mark>	B*50:01:01:01	0	0	1	0	0	
	154UCLA949	154UCLA945		B*35:01:01:15	B*50:01:01:01	0	0	1	0	0	
	154UCLA950	↑ ★ ★ ★ ★ ★ ★	853 ~ 🕂 Apply	B*35:01:01:17	B*50:01:01:01	0	0	1	0	0	
	155UCLA951		c ~ -	B*35:01:01:20	B*50:01:01:01	0	0	1	0	0	
	155UCLA952		Matter	B*35:01:01:23	B*50:01:01:01	0	0	1	0	0	
	155UCLA953	Fuil Gene		B*35:01:01:24	B*50:01:01:01	0	0	1	0	0	



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Motif ID:	rs1050458C>T		Locus:	HLA-B	Implem (Ref. Vei	enteo rsion	d #):		3.4	11	
Example Display:	Heterozygous C/T	eterozygous C/T									
	Assign1 ×	gn1 🔀									
	5' UTR	E Intr Exon 2 Intro	n 2 <mark>Exon 3</mark> Intron 3	Exon 4 Int Exo	Intron 5	Int	3' UTR				
	TMCT /P 2 41 0 0 2020 07 12	021 021 02	11 0 <b>E1</b> 061 071	001 154UCT 2040 P	Allolo Pair Sir	12654					
	Base 853	ACTCARARTCTCCTCAGACRCCRAG	ATGCKGGTCAYGGCRCCCCGAACCSTCCTCCTGCT	GCTCTSGGSR Start: 1, 5' U	TR 1	.e. 43034					
	CDNA 4.2, Exon 1 11 C A 2 1			Stop: 4653, 3	' UTR 1121						
	154UCLA945	<mark>G</mark> <mark>A</mark>	<mark>T</mark> <mark>T</mark>	<mark>C</mark> Allele 1	Allele 2	CORE	EXONS	N-C	PHASE1	PHASE2	Differences
	154UCLA946		<mark>G</mark> <mark>C</mark>	<mark>G</mark> G. <mark>B*</mark> 14:02:01:01	B*35:01:01:05	0	0	0	0	0	
	154UCLA947	ACTCAGARTCTCCTCAGACGCCRAC	GATGCKGGTCA <mark>Y</mark> GGCGCCCCGAACCGTCCTCCTGCT	rgctctsggsg <mark>b*14:02:01:01</mark>	B*35:01:01:42	0	0	0	0	0	Intron 2
	154UCLA948			B*14:02:03	B*35:01:64	0	0	0	1	1	Exon 2
		G A		C = C = B*14:02:13	B*35:01:46	0	0	0	1	1	Exon 2
	C.	A G		B*14:11	B*35:54	0	0	0	1	1	Exon 2
	DPA1			B*14:18	B*35:29:01	0	0	0	1	1	Exon 2
	DPB1	<b>.</b>		B*14:22	B*35:484	0	0	0	1	1	Exon 3
	DQA1			B*14:62	B*35:24:01	0	0	0	1	1	Exon 3
	DQB1			B*1 <mark>4:27</mark>	B*35:93	0	0	0	2	2	Exon 3
	DRB1G03	500	Read Depth	B*14:02:01:01	B*35:01:01:01	0	0	1	0	0	
	DRB3			B*14:02:01:01	B*35:01:01:03	0	0	1	0	0	_
	E			B*14:02:01:01	B*35:01:01:07	0	0	1	0	0	-
	F'			B*14:02:01:01	B*35:01:01:08	0	0	1	0	0	-
	н		TGCCGGTCAAGGCGCCCCGAACCGTCCTCCTGCC	CGCTCTCGGCGB*14.02.01.01	B*35.01.01.09	0	0	1	0	0	-
	MICA	<< HLA.37-5929		B*14:02:01:01	B*35:01:01:11	0	0	1	0	0	-
	MICB	154UCLA949		B*14:02:01:01	B*35:01:01:12	0	0	1	0	0	-
	154UCLA950		853 ~ 🕂 Apply	B*14:02:01:01	B*35:01:01:15	0	0	1	0	0	
	155UCLA951		Y = C + T V	SIGN OFF B*14:02:01:01	B*35:01:01:17	0	0	1	0	0	]
	155UCLA952			B*14:02:01:01	B*35:01:01:20	0	0	1	0	0	
	155UCLA953		Master V	B*14:02:01:01	B*35:01:01:23	0	0	1	0	0	_
	L155UCT 2054			₽*14.02.01.01	D*25-01-01-04			1			



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Motif ID:	rs1050458C>T		Locus:	HLA-B	Impleme (Ref. Ver	ented sion #):		3.41
Example Display:	Homozygous T							
	Assign1	1	1 1					
	5' UTR	E Intr Exon 2 Intron	2 Exon 3 Intron 3	Exon 4 Int Exo	intron 5	Int 3' UTR		
	IMGT/B 3.41.0.0 2020-07-13		1	881 154UCLA946 B -	Allele Pair Size:	44282		
	Base 853	ACTCARARTCTCCTCAGACRCCRAG	ATGCKGGTCAYGGCRCCCCGAACCSTCCTCCTGCTG	CTCTSGGSR Start: 1, 5' UI	R 1			
	CDNA 4.2, Exon 1 11 C A 2 1	R		Stop: 4653, 3	UTR 1121	CODE	NGDi	66
	154UCLA945			CTCTCCCCCC Pk08.01.01.01	Allele 2	CORE EXONS	N-C D1	IIerences
	154UCLA946* B	ACICAGAGICICCICAGACGCCGAG		B*08:01:01:01	▲ B*08:01:01:02	0 0	1	
	C			B*08:01:01:01	B*08:01:01:03	0 0	1	
	DPA1			B*08:01:01:01	B*08:01:01:0	0 0	1	
	DPB1			B*08:01:01:01	B*08:01:01:0 <mark>7</mark>	0 0	1	
	DQA1			B*08:01:01:01	B*08:01:01:09	0 0	1	
	DQB1	E 00	Dood Dooth	B*08:01:01:01	B*08:01:01: <mark>10</mark>	0 0	1	
	DRB1G03	500	Read Depth	B*08:01:01:01	B*08:01:01:11	0 0	1	
	DRB3			B*08:01:01:01	B*08:01:01:13	0 0	1	
	E			B*08:01:01:01	B*08:01:01:14	0 0	1	
	G			B*08:01:01:01	B*08.01.01.10	0 0	1	
	н	ACTCAGAATCCCCTCAGACGCCGAG	ATGC <mark>G</mark> GGTCA <mark>C</mark> GGCGCCCCGAACCGTCCTCCTGCTG	GCTCTGGGGGGG	B*08:01:01:18	0 0	1	
	MICA	< HLA.37-3561		B*08:01:01:01	B*08:01:01:19	0 0	1	
	MICB	G	ATGCTGG <mark>A</mark> CA <mark>A</mark> GGCGCCCCGAACCGTCCTCCTGCTG	GCTCTCGGCGB*08:01:01:01	B*08:01:01:20	0 0	1	
	154UCLA947	<< HLA.37-4069		B*08:01:01:01	B*08:01:01: <mark>21</mark>	0 0	1	
	154UCLA948	TCAAAATCTCCTCAGACGCCGAG.	ATGC <mark>G</mark> GGTCACGGCGCCCCGAACCGTCCTCCTGCTG	GCTCTCGGGAB*08:01:01:01	B* <mark>08:01:01:</mark> 22	0 0	1	
	154UCLA949	<< HLA.37 0047		B*08:01:01:01	B*08:01:01: <mark>23</mark>	0 0	1	
	154UCLA950	154UCLA946		B*08:01:01:01	B*08:01:01: <mark>25</mark>	0 0	1	
	155UCLA951	★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★	853 ~ 🕂 Apply	B*08:01:01:01	B*08:01:01:26	0 0	1	
	155UCLA952		T ~ -	B*08:01:01:01	B*08:01:01:27	0 0	1	
	155UCLA953	Eull Gene	Master V	B*08:01:01:01	B*08:01:01:30	0 0	1	
	1550CLA954			B×08:01:01:01	B*08:01:01:31	0 0	1	
	155UCLA955			B*08:01:01:01	B*08:01:01:33	0 0	1	
	I 11220/CITAA220			Br08:01:01:01	8^08:01:01:34			



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Motif ID:	rs1050458C>T		Locu	s:		HLA-B	Implemented (Ref. Version #):	3.41
Example Display:	Summary Table Report:         Motifs.         Motifs.         154UCLA945       IMGT/F       IMGT/G       IMGT/H         154UCLA946       rs1610696:**         154UCLA947       rs1610696:GC         154UCLA948       rs1610696:**         154UCLA949       rs1610696:**         154UCLA949       rs1610696:**         154UCLA949       rs1610696:         Reference:       IMGT/B 3.41.0.0 2020-07-13         Summary       The allele pairs listed below are compatible with the	IMGT/A IMGT/E Bw4 Bw4 e consensus sequence.	IMGT/C Bw6 Bw6 Bw6 Bw6	IMGT/B Bw6, rs1050458:CC Bw6, rs1050458:TT Bw6, rs1050458:TT Bw4, Bw6, rs1050458:CC Bw6, rs1050458:TC	IMGT/h 129Me 129Val 129Val 129Val	MICA IMGT/MICB t, 129\ 98lle 98Met 98Met, 98lle 98lle t 98lle	(Ref. Version #):	
	B*14:02:01:01         B*35:01:01:05           B*14:02:01:01         B*35:01:01:42           Intron 2           Motifs: Bw6, rs1050458:TC	IS						







#### 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, mediated rejection following heart trans	Yu F, Lazarte J, Rao V, plant. Hum Immunol.	Delgado DH. <b>HLA</b> 2020 Apr;81(4):13	H. <b>HLA-G +3196 polymorphism as a risk factor</b> ( 81(4):134-140.					
Impact of polymorphism:	Human leukocyte antigen-G (HLA-G) is a elevated HLA-G expression is associated 3'UTR of the HLA-G gene, 3196 base pai component for HLA-G transcriptional re- mediated rejection (CMR). Compared to 66.9% reduction. Note: Equivalent to c.*287C>G (using sta stop codon). Currently this position is not included in	in immune checkpoin with reduced allogra rs downstream of the gulation. The current the minor GG genoty andard HGVS nomeno IMGT /Unknown.	t which dampens ft rejection. The initiation seque study identified ype, CG had a 47 clature, which me	s the immune response. Report +3196C/G polymorphism is l nce. The 3'UTR, specifically e the +3196 G allele as a risk fa .2% reduction in CMR risk wh eans 287 bp downstream of t	orts suggest ocated within the exon 8, is a vital actor for cell nile CC had a the T in the TGA				





#### 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



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Motif ID:	rs1610696C>G		Locus:	HLA-G	Implemente (Ref. Version	d #):	3.41
Example Display:	Homozygous C						
	5' UTR		E Int Exon 2 Intron Exon 3 Intro	n 3 Exon 4 I	Int Exo Intron 5 3'	UTR	
	IMGT/G 3.41.0.0 2020-07-13 Base 5029 3' UTR 645 C A		5021503150415051 GTATAAATTTACTTTTTCAAATTATTTCCAAGAGAGAATTGA	50615071 HC20237I TGGGTTAATTAAAGGAGAAG Start: 1 Stop: 6	20182A01R900050106 G - Alle 1, 5' UTR 1 5362, 3' UTR 1978	le Pair Size: 580	
	F HC20237L20182A01R900050106* G	TTCTCTATTAAATTACAATCTCA		Allele J G*01:01:	Allele 2         COR           :03:03         G*01:04:01:02         0           :03:04         G*01:04:01:02         0	E EXONS N-C	PHASE1 PHASE2 I
	A E			G*01:01: G*01:01: G*01:01:	03:03 G*01:04:01:01 0 03:03 G*01:04:01:01 0 03:03 G*01:04:01:03 0	0 2 0 3	0 2 0 2
	HC20237L20182A01R900050106 B MICA			G*01:01: G*01:01: G*01:01:	:03:02         G*01:04:01:01         0           :03:04         G*01:04:01:02         0           :03:04         G*01:04:01:03         0	0 3 0 4	2 1 0 2
	MICE DRB3 DRB5	10% (100)		G*01:01: G*01:01: G*01:01:	:03:01         G*01:04:01:02         0           :03:02         G*01:04:01:01         0           :03:01         G*01:04:01:01         0	0 4 0 4 0 5	2 1 2 2 2 2
	DRB1G0 DRB1G0 DCA1	1		G*01:01: G*01:01: G*01:01:	:03:02 G*01:04:01:03 0 :03:01 G*01:04:01:03 0 :03:03 G*01:23 0	0 5 0 6 1 2	2 2 2 2 0 2
	DCB1 DFA1 DFB1			G*01:01: G*01:01: G*01:01:	:03:04 G*01:23 0 :03:02 G*01:23 0 :03:01 G*01:23 0	1 3 1 4 1 5	0 2 2 2 2 2
	HC20237L20182A02Q940050830 HC20237L20182A03P073231229 HC20237L20182A03P073231229			HC20237L20182A	01R900050106	Apply	
	HC20237L20182A05R970900614 HC20237L20182A06R050114117 HC20237L20182B01IHW09024			Full Gene	C G T C ✓ ■ ✓ Master ✓ :03:01 G*01:11 1		
	HC20237L20182B02IHW09050 HC20237L20182B03IHW09058 HC20237L20182B03IHW09058			G*01:01: G*01:01: G*01:01:	:03:02 G*01:01:08 1 :03:02 G*01:04:01:04Q 1 :03:02 G*01:04:03 1	3 31 0 4 0 4	 
	HC20237L20182B05IHW09085			G*01:01:	:03:02 G*01:04:04 1	0 4	



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Motif ID:	rs1610696C>G	Lo	cus:	HLA-G	Impleme (Ref. Vers	nted ion #	ŧ):		3.	41
Example Display:	Assign1									
	5' UTR IMGT/G 3.41.0.0 2020-07-13 Base 5029 TICTGTAT 3' UTR 645 C A 2 1 R	E Int	Exon 2 Intron Exon 3 Intron 5031	.50615071 HC20237L GGGTTAATTAAAGGAGAAG Start: 1 Stop: 6	nt Exo Intron 5 20182A03P073231229 G , 5' UTR 1 503, 3' UTR 2119	- Allele	Pair Siz	e: 1580		
	HC20237L20182A01R900050106 HC20237L20182A020940050830			Allele 1 G*01:01:	Allele 2 01:04 G*01:01:02:02	CORE	EXONS	N-C	PHASE1	PHASE2
	F TTCTGTAT	TAAAATTAGAATCTGAGTATAAAT	TTTA <mark>S</mark> T************************************	**************************************	01:05 G*01:01:02:02 01:13 G*01:01:02:02	0	0	1	0	0
	H A		C G	G*01:01: G*01:01:	01:04 G*01:01:02:01 01:10 G*01:01:02:02	0	0	1 2	0	1
				G*01:01: G*01:01: G*01:01:	01:04 G*01:01:02:03 01:04 G*01:01:02:04 01:05 G*01:01:02:01	0	0	2 2 2 2	0	1
	MICA 10% (100 MICB 10% (100	)		G*0 <mark>1:01: G*0</mark> 1:01:	01:13 G*01:01:02:01 01:03 G*01:01:02:02	0	0	2 3	0	1
	DRB4			G*01:01: G*01:01:	01:05 G*01:01:02:03 01:05 G*01:01:02:04	0	0	3	0	1
	DRB1601 1% (10) DRB1607 1% (10) DQA1	=		G*01:01:  G*01:01: G*01:01:	01:10 G*01:01:02:01 01:13 G*01:01:02:03 01:13 G*01:01:02:04	0	0	3	0	1
	DQB1 DEAL			G*01:01:	01:01 G*01:01:02:02	0	0	3	1	<b>0</b>
	DFB1 HC20237L20182A04R920051269 HC20237L20182A05R970900614				<ul> <li>← → →</li> <li>5029 ~</li> <li>C G T S = C + G ~</li> </ul>	+		Apply	GN OFF	1 1 0
	HC20237L20182A06R050114117 HC20237L20182B01IHW09024 HC20237L20182B02IHW09050			Full Gene	<pre></pre>	0	0	4	1	0
	HC20237L20182B03IHW09058 HC20237L20182B03IHW09074			G*01:01: G*01:01: G*01:01:	01:12 G*01:01:02:02 01:01 G*01:01:02:02	0 0	0 0	<b>4</b> 4	1	0



■AlloSeq<sup>™</sup>Assign<sup>®</sup>

Motif ID:	rs1610696C>G		Locus:	HLA-G		Implemer (Ref. Vers	nted ion #	<i>‡</i> ):		3.41
Example Display:	Homozygous G									
· · · ·	Assign1 🗙									
	5' UTR	1	E Int Exon 2 Intron Exon 3 I	Intron 3 Ex	on 4 Int	Exo Intron 5	3' UTR	R .		
	IMGT/G 3.41.0.0 2020-07-13		011502150315041	50515061	5 HC20237L201	.82F06VW190 G - A11	ele Pair	Size: 10	69	
	Base 5029	AACTTACTTCTGTATTAAAATTAGA	ATCTGAGTATAAATTTACTTTTTCAAATTATTTCCA	AGAGAGATTGATGGGTTAATTAA	A Start: 1, 5	UTR 1				
	3' UTR 645 C A 2 .				Stop: 6503	3, 3' UTR 2119	COPE	EVONS	N-C I	lifferences
	HC20237L20182E03VW165				G*01:01:02	01 G*01:06:01:01	0	0	1	JILIELENGES
	HC20237L20182E04VW173	AACTTACTTCTGTATTAAAATTAGA	ATCTGAGTATAAATTTAGT****************	*****	* G*01:01:02	01 G*01:06:01:02	0	0	2	
	HC20237L20182E05VW181				G*01:01:02	02 G*01:06:01:01	0	0	2	
	HC20237L20182E06VW189				G*01:01:02	03 G*01:06:01:01	0	0	2	
	HC20237L20182F01VW150				G*01:01:02	04 G*01:06:01:01	0	0	2	
	HC20237L20182F02VW158				G*01:01:02	02 G*01:06:01:02	0	0	3	
	HC20237L20182F03VW166				G*01:01:02	03 G*01:06:01:02	0	0	3	
	HC20237L20182F04VW174	10% (100)			G*01:01:02	04 G*01:06:01:02	0	0	3	
	HC20237L20182F05VW182				G*01:06:01	01 G*01:24	0	1	1	
	F				G*01:06:01:	02 G*01:24	0	1	2	
	HC20237L20182F06VW190* G	1% (10)			G*01:01:22	01 G*01:06:01:01	0	1	3	
	Н	<b></b>		<sup></sup>	G*01:01:22	01 G*01:06:01:02	0	1	4	
	A				G*01:01:22		0	1	5	
	E				G*01:01:22	02 G*01:06:01:02	0	1	6	
	В				G*01:01:22	03 G*01:06:01:02	0	1	6	
	MICA	<b>-</b>			G*01:01:02	01 G*01:01:02:01	1	0	1	
	MICB			lue:		(100				
	DRB4			HC	023/L20182F06VW		-			
	DRB1G01			1	ACCEPT	<b>7 7</b> 5029 ~	+		Apply	NOFF
	DRB1 <mark>G0</mark> 7			*	A C	G T G 🗸 🗸	-			
	DQA1			Ful	Gene	$\sim$ Master $\sim$				
	DCB1				G*01:01:02:	01 G*01:01:22:02	1	1	5	
	DFA1				G*01:01:02:	01 G*01:01:22:03	1	1	5	
	DFB1				G*01:01:02:	01 G*01:09	1	0	0	
	HC20237L20182G01VW151				G*01:01:02:	01 G*01:24	1	1	1	



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Motif ID:	rs1610696C>G	Locus:	HLA-G	Implemented (Ref. Version #):	3.41
Example Display:	Summary Table Report: Motifs.				
	IMGT/F         IMGT/G         IMGT/A         IMGT/A           HC20237L20182A01R900050106         rs1610696:CC         Bw4           HC20237L20182A02Q940050830         rs1610696:CC         Bw4           HC20237L20182A03P073231229         rs1610696:CG         Heterozygou           HC20237L20182A04R920051269         rs1610696:CG         Homozygou           HC20237L20182A05R970900614         rs1610696:CG         Homozygou           HC20237L20182A06R050114117         rs1610696:CG         Homozygou           HC20237L20182B01IHW09024         rs1610696:CC         Homozygou           HC20237L20182B01IHW09050         rs1610696:CC         Homozygou	IMGT/E         IMGT/C         IMGT/B         IMGT/MIC           Bw6         Bw6, rs1050/ 129Val         Bw6, rs1050/ 129Val           Bw6         Bw4, rs1050/ 129Met, 1           JS         Bw6         Bw4, Bw6, rs 129Val           S G         Bw6         Bw4, sr1050/ 129Val           Bw6         Bw4, Bw6, rs 129Val           Bw6         Bw6, rs1050/ 129Met, 1           Bw6         Bw6, rs1050/ 129Val	CA IMGT/MICB IMGT/DRB3 IMGT/D 98lle 129' 98lle 98lle 98Met, 98lle 98Met, 98lle 98lle 129' 98lle 98lle	DRB4 IMGT/DRB5 IMGT/DRB1 IMGT/DQA1 IMGT/DQB	1 IMGT/DPA1 IMGT/DPB1 rs9277534:GG rs9277534:GA rs9277534:GA rs9277534:GA rs9277534:GG rs9277534:GG rs9277534:GG rs9277534:GG
	HC20237L20182B03IHW09058 rs1610696:CC	Bw6 Bw6, rs1050-129Met	98lle		rs9277534:GG
	Reference: IMGT/G 3.41.0.0 2020-07-13	Reference: IMGT/G 3.41.0.0 2020-0	07-13	Reference: IMGT/G 3.41.0.0 2020-07-13	
	Summary	Summary		Summary	
	G*01:01:01:05 G*01:01:03:03	G*01:01:01:04 G*01:01:02:02	with the consensus sequence.	G*01:01:02:01 G*01:01:22:01	le consensus sequence.
	Motifs: rs1610696:CC Homozygous C	Motifs: rs1610696:CG Heterozygou	ıs C/G	Motifs: rs1610696:GG Homozygous G	





## HLA Class II Motifs







#### HLA-DPB1 rs9277534A>G

Motif ID:	rs9277534A>G	Locus:	HLA-DPB1	Implemented (Ref. Version #):	3.37.0					
Supporting Publication:	<ul> <li>Petersdorf EW, Malkki M, O'hUigin C, Ca P. High HLA-DP Expression and Graft-ve</li> <li>Schöne B, Bergmann S, Lang K, Wagner I based on standard DPB1 genotyping: Li</li> </ul>	rrington M, Gooley T, I <b>rsus-Host Disease</b> . <i>N E</i> I, Schmidt AH, Petersdo <b>nkage analysis of over</b>	Haagenson MD, H Engl J Med. 2015 Forf EW, Lange V. <b>F</b> S 32,000 samples	, Horowitz MM, Spellman SR, Wang T, Stevenso 5 Aug 13;373(7):599-609 /. <b>Predicting an HLA-DPB1 expression marker</b> es. Hum Immunol. 2018 Jan;79(1):20-27.						
Impact of polymorphism:	HLA-DPB1 expression is associated with rs9277534-A allele is associated with low expression. Among recipients of HLA-DP with the high-expression allele had a hig marker can be used to prospectively ide low-expression patient DPB1 alleles.	the rs9277534 A/G po w DPB1 expression, w B1-mismatched trans gh risk of GVHD. Wher ntify DPB1-mismatche	A/G polymorphism located in the 3'UTR of the HLA-DPB1 gene. The ion, whereas the rs9277534-G allele is associated with high DPB1 d transplants from donors with the low-expression allele, recipient . When DPB1-matched donors are not available, this expression matched donors who generate a permissive DPB1 mismatch again							



■AlloSeq<sup>™</sup>Assign<sup>®</sup>

Motif ID:	rs9277534A>G	Locus:	HLA-DPB1	Implemented (Ref. Version #):	3.37.0
Example Display:	S' UTR       Intron 1         IMOT/DPB1 3.41.0.0 2020-07-13       Imot/DPB1 3.41.0.0 2020-07-13         Base 12037       AAGTITAGTGCCCTCATCCATTTATGTCTCAG         3' UTR 792       C A 2 1 R         G       AAGTITAGTGCCCTCATCCATTTATGTCTCAG         H       Imot/DPB1 3.41.0.0 2020-07-13         Base 12037       AAGTITAGTGCCCTCATCCATTTATGTCTCAG         3' UTR 792       C A 2 1 R         G       AAGTITAGTGCCCTCATCCATTTATGTCTCAG         H       Imot/DPB1 1         A       Imot/DPB1 1         A       Imot/DPB1 1         DRB1G03       Imot/DPB1 1         DPB1       Imot/DPB1 1         IS4UCLA945       IpB1         IS4UCLA946       Imot/DPB1 1         IS4UCLA948       Imot/DPB1 1	Exo         Intron 2           3311204112051120611         154UCL           SACCACTATICITAACTATICAATGGTGAGCAGACTGCA         Start:           Stop:	A945 DPB1 154, 5' UTR 154 12397, 3' UTR 154 12397, 3' UTR 152 1 Allele 2 4:01:01 DPB1*04;01:41 4:01:01 DPB1*04;01;01 4:01:01 DPB1*	CORE       EXONS         0       1	70 3' UTR
	ISAUCLA950 ISSUCLA951 ISSUCLA951 ISSUCLA951	VPB1*0	4:01:01 DP81*039:01 4:01:01 DP81*039:01 4:01:01 DP81*939:01		



■AlloSeq<sup>™</sup>Assign<sup>®</sup>

Example Display:       Heterozygous A/G         VIII 7000       VIIII 7000       VIII 7000       VIII 7	Motif ID:	rs9277534A>G		Locus:	HLA-DPB1	Implemented (Ref. Version #):	3.37.0
C 00       MAX	Example Display:	Heterozygous A/G	ì				
St. Ultra         Loco							
Intr/OPDP13.441.0.0 2020-07-13       I.20011201120112011201120112011201120112011201		5' UTR Intron 1		Exo Intron 2		Exon Intron 3 E I	ntro 3' UTR
Two://post 3.41.0.0 2020-07.13       0							
Base 12837       C A 2 1 R       Startt asy, 5 Utr 35         3* UTR 792       C A 2 1 R       Startt asy, 5 Utr 35         154ULLA945       I I I I I I I I I I I I I I I I I I I		IMGT/DPB1 3.41.0.0 2020-07-13		)31 <mark>1204112051120611</mark> 154UCL	A947 DPB1		
Support 12/68/5       Support 12/68/5       Support 12/68/5       OCRE       EXXVIS       PHASE1       PHASE2       Differences         154/UCLA96       Image: Support 12/68/5       Image: Support 1		Base 12037	AAGTTTAGTGCCCTCATCCATTTATGTCTCAG	ACCRCTATTCTTAACTATTCAATGGTGAGCAGACTGCA Start:	35, 5' UTR 35		
154UCLA946       1		154UCL 0945		G Allele	1 Allele 2	CORE EXONS PHASE1 PHASE2 Differences	
F       I       I       And ITAGISCECCOTECATITAGISTECADACCECATITAGISTECADACCEC       P21*24:81:81       P21*23:81:81       P21*04:81:31       0       0       1       1         G		154UCLA946		A DPB1*0	3:01:01 DPB1*04:01:01		
6       0       0       0       0       0       1       1       Exon 3         H       0       0       0       0       1       1       Exon 2         A       0       0       0       1       1       Exon 2         E       0       0       0       1       1       Exon 2         B       0       0       0       1       1       Exon 2         P01*23:01:01       0001*23:01:0       0001*23:01:0       0       0       1       1       Exon 2         B       0       0       0       1       1       Exon 2       2       Exon 2         N1CA       0       0       0       0       0       1       1       Exon 2         N1CB       0       0       0       0       0       1       1       Exon 2         DR85       0       0       0       0       2       2       Exon 2         DR85       0       0       0       0       2       2       Exon 2         D041       0       0       0       0       2       2       Exon 2         D051000       0<		F	AAGTTTAGTGCCCTCATCCATTTATGTCTCAG	ACCRCTATTCTTAACTATTCAATGGTGAGCAGACTGCA DPB1*1	24:01:01 DPB1*350:01	0 0 0 0	
H       I		G		DPB1*0	3:01:08 DPB1*04:01:31	0 0 1 1 Exon 3	
A       A       B       A       A       B       B       B       C       A       A       B       B       A       C       A       A       A       B       B       A       A       A       B       B       A       A       A       B       B       A       A       A       B		Н		G DPB1*2	3:01:01 DPB1*92:01	0 0 1 1 Exon 2	
F       C       I       F		A		A DPB1*2	3:01:01 DPB1*92:01	0 0 1 1 Exon 2	
C       B       C       B       C       B       C		E		DPB1*2	5:01 DPB1*215:01	0 0 1 1 Exon 2	
B       NICA       Image: Constraint of the second		C		DPB1*7	2:01:01 DPB1*132:01	0 0 1 1 Exon 2	
Internet       Image: Ima		B		DPB1*7	2:01:01 DPB1*132:01	0 0 1 1 Exon 2	
Index       Index <td< td=""><th></th><td>MICA</td><td>10% (100)</td><td>DPDI*7</td><td>0-01-01 DPB1*132.01</td><td>0 0 1 1 EX012</td><td></td></td<>		MICA	10% (100)	DPDI*7	0-01-01 DPB1*132.01	0 0 1 1 EX012	
DRB5       DRB1601		DRB3		DPB1*2	0:01:01 DPB1*377:01	0 0 2 2 Exon 2	
DRB1601       I </td <th></th> <td>DRB5</td> <td></td> <td>DPB1*5</td> <td>0:01 DPB1*687:01</td> <td>0 0 2 2 Exon 2</td> <td></td>		DRB5		DPB1*5	0:01 DPB1*687:01	0 0 2 2 Exon 2	
DRB1603       13       14         DQA1       1         DQB1       0         DQB1       0         DQB1       0         DPA1       0         154UCLA947*       DPB1         DPB1       0         DPB1*50:01       <		DRB1G01		DPB1*5	1:01:01 DPB1*1096:01	0 0 2 2 Exon 2	
DQA1       DQA       Description       Descr		DRB1G03	1% (10)	DPB1*5	1:01:01 DPB1*1096:01	0 0 2 2 Exon 2	
DQB1       OQB       Family CLA947*       DPB1       DPB1       DPB1*26       OPB1*26       O       A       A       Exon 2         154UCLA947*       DPB1       Image: Company and		DQA1		DPB1*3	77:01 DPB1*905:01	0 0 2 2 Exon 2	
DPA1       DPA1       DPA1       DPA1       DPA1       DPA1       DPA1       DPB1*68:01       DPB1*613:01       0       0       3       3       Exon 2         154UCLA947*       DPB1       Image: Control of the term of term		DQB1		DPB1*5	2:01 DPB1*214:01	0 0 3 3 Exon 2	
154UCLA947* DP81       Image: Constraint of the state of		DPA1	154UCLA947	DPB1*3	06:01 DPB1*613:01	0 0 3 3 Exon 2	
154UCLA948     Image: Constraint of the second		154UCLA947* DPB1		Apply CICH OF	6:01 DPB1*762:01	0 0 4 4 Exon 2	
		154UCLA948	ACCEPT A C G T R = A + G		09:01 DPB1*355:01	0 0 4 4 Exon 2	
		15400LA949	Full Gene V Master	V DPB1*5	98:01 DPB1*508:01		
					7.01 0001322.01		



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Motif ID:	rs9277534A>G	Locus:	HLA-DPB1	Implemented (Ref. Version #):	3.37.0
Example Display:	Structure       Intron 1         TMGT/DPB1 3.41.0.0 2020-07-13		n 2         154UCLA948 DPB1         Start: 166, 5' UTR 160         Stop: 12253, 3' UTR 1008         Allele 1       Allele 2         DPB1*05:01:01       DPB1*05:01:         DPB1*05:01:01       DPB1*118:00         DPB1*05:01:01       DPB1*118:01         DPB1*05:01:01	CORE       EXONS       Differences         0       0       1         12       0       1         12       0       1         12       0       1         12       0       1         12       0       1         12       0       1         12       0       1         12       0       1         14       0       1         15       0       1         16       0       1         17       0       1         18       0       1         19       1       1         10       1       1         11       0       1         12       0       1         11       0       1         12       0       1         13       0       1         14       0       1         15       0       1         16       1       1         17       0       1         18       1       1         19       1       1         10	



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Motif ID:	rs9277534A>G	Locus:	HLA-DPB1	Implemented (Ref. Version #):	3.37.0
Example Display:	Summary Table Report: Motifs. 154UCLA945 154UCLA946 154UCLA946 154UCLA947 rs9277534:GG Homozygous G Heterozygous A/G Genotyping Report:				
	Sample:       154UCLA945         Reference:       IMGT/DPB1 3.41.0.0 2020-07-13         Summary	Sample: 154UCLA947 Summary The allele pairs listed below are compatible with DPB1*03:01:01 DPB1*04:01:01 DPB1*124:01:01 DPB1*350:01 Motifs: rs9277534:GA Heterozygous A	n the consensus sequence.	Sample:       154UCLA948         Summary       The allele pairs listed below are compatible with the DPB1*05:01:01         Motifs:       rs9277534:GG	e consensus sequence.





# Additional MHC Motifs







#### MICA rs1051792G>A; MICA-129Val/Met

Motif ID:	rs1051792G>A; MICA- 129Val/Met	Locus:	cus:MICAImplemented (Ref. Version #):3.37.0.1								
Supporting Publication:	<ul> <li>Isernhagen A, Malzahn D, Bickeböller H, Biological Functions and Disease Risks.</li> <li>Fuerst D, Neuchel C, Niederwieser D, Bu Stuhler G, Schaefer-Eckart K, Freitag S, C Tsamadou C, Mueller C, Schrezenmeier I hematopoietic stem cell transplantation</li> </ul>	Dressel R. <b>Impact of t</b> Front Immunol. 2016 I njes D, Gramatzki M, N Casper J, Kaufmann M, H, Mytilineos J. <b>Match</b> n. <i>Blood.</i> 2016 Dec 29;	he MICA-129Me Dec 12;7:588 Wagner E, Wulf G Wattad M, Herte ing for the MICA 128(26):3169-31	t <b>/Val Dimorphism on NKG2D-</b> , Glass B, Pfreundschuh M, Eir Instein B, Klein S, Ringhoffer M - <b>129 polymorphism is benefic</b> 76.	<b>Mediated</b> nsele H, Arnold R, 1, Mytilineos D, <b>:ial in unrelated</b>						
Impact of polymorphism:	The MICA-129Val/Met dimorphism, cau valine (Val) to methionine (Met) exchang NKG2D with high (Met) and low affinitie Adverse overall survival and worse outco was mismatched (10/10, hazard ratio, 1. Exon 3, Position 8403 in AlloSeq Assign	sed by SNP rs1051792 ge at position 129 of t s (Val). ome for disease-free s .77). Higher rates of a	2 at nucleotide p the MICA protein survival was obse cute GVHD were	osition 454 (G>A) of the MIC a, separating MICA into isofor erved in the 10/10 match gro seen in MICA-129 mismatch	A gene causes a rms that bind oup if MICA-129 ed cases.						



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Motif ID:	rs1051792G>A; MI 129Val/Met	CA-	Locus:	MICA	Impleme (Ref. Ver	ented rsion #):	3.37.0.1
Example Display:	Homozygous G - 12	29Val/Val					
	Assignt I 5' UTR Intron 1 IMGT/MICA 3.41.0.0 2020-07-13 Base 8403	33€183718381 ELFLSQNZE	.8391	E 84318441. HC20237L20182E 2TLAMNV. Start: 1, 5' U	xo Intr <mark>Exon</mark> Intron 3 03VW165 XICA Allele P TR 1	Exon E Intron 5 Pair Size: 1551	
	HC20237L20182E02VW157         F           G         G           HC20237L20182E02VW157         F           G         G           H         A           E         C           B         HC20237L20182E03VW165*           HC20237L20182E03VW165*         MICCR           DR33         DR85           DR33         DR85           DR31G01         DR31G03           DC31         DR31           DR31         DR31           DR31         DR31           HC20237L20182E04VW173         DR31           HC20237L20182E05VW181         HC20237L20182F02VW150           HC20237L20182F01VW150         HC20237L20182F02VW150           HC20237L20182F02VW150         HC20237L20182F02VW150           HC20237L20182F02VW150         HC20237L20182F02VW150	GAGCTCTTCCTCTCCCAAAACCTGGAGAC GAGCTCTTCCTCTCCCAAAACCTGGAGAC E.L.F.F.L.S.Q.N.L.E' 	. CAGGANTGE: GAGGANTGE: CAGTCC CCAGTCCTCCAGAGCTCA GAGGANTGE: CAGTCC CCCAGTCCTCCAGAGCTCA T. F. F. W. T. V. P. Q. S. S. S. R. A. (	ACCTTGGCCATGAAGGTCA Allele 1     SACCTTGGCCATGAAGGTCA Allele 1     SACCTTGGCCATGAAGGTCA MICA*008:01:02     UICA*008:01:03     MICA*008:01:03     MICA*008:01:03	Allele 2         CORE           MICA*008:04:04         0           HICA*008:04:04         0           MICA*008:04:04         0           MICA*008:04:04         0           MICA*008:04:01         0           MICA*008:04:04         0           MICA*008:04:01         0           MICA*008:04:04         0           MICA*008:04:04         0           MICA*008:04:01         0           MICA*008:04:02         0           MICA*008:04:02         0           MICA*008:04:02         0           MICA*008:04:03         0           Master         •           MICA*0008:04:03         0           MICA*0008:04:03         0	EXONS N-C Differences	



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Motif ID:	rs1051792G>A; MI 129Val/Met	ICA-	Locus:	MICA	Implem (Ref. Ve	ented rsion #)	:	3.37.0.1
Example Display:	Assignt I	- 129Met/Val	8391	Exo	Intr Exon Intron 3	Exon E Intr	on 5	
	Base \$403           cDNA 129.1, Exon 3 129         C A 2           HC20237L20182E03VW165         HC20237L20182E03VW165           HC20237L20182E03VW165         HC20237L20182E03VW165           HC20237L20182E03VW181         HC20237L20182E03VW189           HC20237L20182E03VW185         HC20237L20182F03VW186           HC20237L20182F03VW166         HC20237L20182F03VW166           HC20237L20182F03VW166         HC20237L20182F03VW166           HC20237L20182F03VW181         HC20237L20182G02VW151           HC20237L20182G02VW151         HC20237L20182G02VW151           HC20237L20182G02VW151         HC20237L20182G02VW151           HC20237L20182G02VW151         HC20237L20182G02VW151           HC20237L20182G02VW151         HC20237L20182G02VW151           HC20237L20182G02VW151         HC20237L20182G02VW153           HC20237L20182G02VW151         HC20237L20182G02VW153           HC20237L20182G02VW151         HC20237L20182G02VW157           HC20237L20182G02VW153         HC20237L20182G02VW154           HC20237L20182G02VW154         HC20237L20182G02VW155           HC20237L20182G02VW154         HC20237L20182G02VW154	EL.FL.S.Q.N.Z.E.T         B         GAGCTCTTCCTCTCCCAAAACCTGGAGAC.         GAGCTCTTCCTCCCCAAAACCTGGAGAC.        E.L.F.L.S.Q.N.L.E.T        E.L.F.T.L.S.Q.N.L.E.T        E.L.F.T.L.S.Q.N.L.E.T        E.L.F.T.T.S.Q.T        E.T.F.T.T.S.Q.T        E.T.T.F.T.T.S.Q.T        E.T.T.F.T.T.S.Q.T        E.T.T.F.T.T.S.Q.T        E.T.T.T.F.T.T.T.S.Q.T        E.T.T.T.T.T.T	EEW. TZ. PQ.S.S.R.A.Q.T.L. BAGGAATGGA AATGC CCAGTCCTCCAGAGCTCAGACCTGGG SAGGAATGGA AGTGC CCCAGTCCTCCAGAGCTCAGACCTGGG EEW. T.,Z.P.Q.S.S.S.R.A.Q.T.L. EEW. T.,W.P.Q.S.S.S.R.A.Q.T.L. EE.W. T.,V.P.Q.S.S.S.R.A.Q.T.L.	A. M. N. V.       Start: 1, 5' UTR         Stop:       13017, 3' U         CATGAACGTCA       Allele         A. M. N. V.       MICA*007:01:01         MICA*007:01:01       MIC         A. M. N. V.       MICA*007:01:01         MICA*007:01:01       MIC         MICA*007:01:02       MIC         MICA*007:01:01       MIC         MICA*007:01:01       MIC         MICA*007:01:01       MIC         MICA*007:01:01       MIC         MICA*007:01:02       MIC         MICA*007:01:01       MIC         MICA*007:01:02       MIC         MICA*007:01:02       MIC         MICA*007:01:03       MIC         MICA*007:01:03	1 TTR 678 TTR 678 Tele 2 CORE TX 008:01:01 O CA*008:01:01 O CA*008:01:02 O CA*008:01:02 O CA*008:01:02 O CA*008:01:02 O CA*008:01:03 O CA*008:01:04 C CA*008:01:04 C CA*008:01:04 C CA*008:01:04 C CA*008:01:04 C C CA*008:01:04 C C CA*008:01:04 C C CA*008:01:04 C C C CA*008:01:04 C C C C C C C C C C C C C C C C C C C	EXONS N-C 0 0 0 0 0 1 0 1 0 1 0 1 0 1 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0 2	PHASE1         PHASE1           0         0           0         0           0         1	2 Difference Intron 5 Intron 1 Intron 1
	HC20237L20182G04VW175* HTCA MTCE DRB3 DRB3 DRB4			dNA VICA*007:01:02 HI HICA*007:01:03 HI HICA*007:01:04 HI HICA*007:01:04 HI	Aaster V LA*UUS:DI:UG U CA*008:01:06 0 CA*008:01:06 0	0 3 0 3 0 3	0 1 0 1 0 1	



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Motif ID:	rs1051792G>A; MICA 129Val/Met	<b>\</b> -	Locus:	MICA	Impler (Ref. V	nent ersio	ed n #)	:		3.3	37.0.1
Example Display:	Homozygous A – 129	Met/Met									
	Assign1										
	5' UTR Intron 1				Exo Intr Exon	Intron 3	Exon	E Intror	1 5		
	IMGT/MICA 3.41.0.0 2020-07-13	836183718381	8391	184318441. HC20237L2	182F06VW190 MICA -	Allele Pa	ir Size:	685			
	Base 8403	ELFLSQNZE	TEEW. TZ .PQSSR.A	QTLAMNV. Start: 1,	5' UTR 1						
	CDNA 129.1, Exon 3 129 C A 2 1 R	2		Stop: 13	32, 3' UTR 693	0000	PHONE		DUD OD 1	DUDODO	D
	HC20237L20182E02VW157	GAGCTCTTCCTCTCCCAAAACCTGGAG	AC.GAGGAATGGA AATG CCCAGTCCTCCAGAGCT	CAGACCTTGGCCATGAACGTCA Allele 1	Allele 2	CORE	EXONS	N-C	PHASE1	PHASE2	Differences
	HC20237L20182E04VW173	ELFLSQNLE		QTLAMNV. MICA*007:	1:02 MICA*017	0	0	0	0	0	Intron 5
	HC20237L20182E05VW181			MICA*007:	1:03 MICA*017	0	0	0	0	0	Intron 1
	HC20237L20182E06VW189	ELFLSQNLE	TEEW. T <mark>.</mark> .M .PQSSRA	QTLAMNV. MICA*007:0	1:04 MICA*017	0	0	0	0	0	Intron 1
	HC20237L20182F01VW150	ELFLSQNLE	TEEW. T <mark>.</mark> .M .PQSSRA	QTLAMNV. MICA*002:	2 MICA*084	0	0	0	1	1	
	HC20237L20182F02VW158			MICA*007:	1:01 MICA*095	0	1	0	0	0	
	HC20237L20182F03VW166			MICA*007:	1:02 MICA*095	0	1	0	0	0	
	HC20237L20182F04VW174			MICA*007:	1:03 MICA*095	0	1	0	0	0	
	HC20237L20182F05VW182	108 (100)		MICA*007:	01:04 MICA*095	0	1	0	0	0	
	F			MICA*017	MICA*100	0	1	0	0	0	
	G			MICA*017	MICA*026	0	1	0	1	0	
	A	-		MICA+026	MICA+095	0	1	0	1	0	
	E E	1% (10)		MICA*093	1.01 MICA*084	1	4	5			
	c	<b></b>		MICA*002:0	1:02 MICA*084	1	3	4			
	B			MICA*002:0	1:03 MICA*084	1	3	3			
	HC20237L20182F06VW190* MICA				4/100						
	МІСВ	GAGCICITCCICICCCAAAACCIGGAG	ACTGAGGAATGGACAGTGCCCCAGTCCTCCAGAGCT	CAGACCITGGCCATGAAC HC2023/L20182F06V							
	DRB4	GAGCTETTECTETCEAAAACCTGGAG	ACT AGGAATGGACAGTGCCCCAGTCCTCCAGAGCT		385 ~	129.1	~	Apply			
	DRB1 <mark>G01</mark>	HIA 33-1273	ACT CABGARIGGACAGI GCCCCAGI CCI CCAGAGCI		G T A 🗸	-		Ī			
	DRB1 <mark>G0</mark> 7	GAGCTCTTCCTCTCCCAAAACCTGGAG	ACTCAGGAATGGACAGTGCCCCAG	cDNA .	Master V						
	DQA1	<< HLA.32-1911		MICA*002:	1:09 MICA*084	1	3	3			
	DQB1	GAGCTCTTCCTCTCCCAAAACCTGGAG	ACT <mark>C</mark> AGGAATGGACA <mark>G</mark> TGCCCCAG	MICA*002:0	2 MICA*017	1	0	0			
	DEA1	<< HLA.33-3549		MICA*002:0	2 MICA*095	1	0	0			
	ndal			MTC3*007+	1.01 MTC3*068.01.0	1 1	0	1			



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Motif ID:	rs1051792G>A; MICA- 129Val/Met	Locus:	MICA	Implemented (Ref. Version #):	3.37.0.1
Example Display:	Summary Table Report:           Motifs.           MGT/F         IMGT/F         IMGT/F	ST/E         IMGT/C         IMGT/B         IMGT/MICA           Bw6         Bw6, rs1050² 129Val         Bw6         Bw6, rs1050² 129Val           Bw6         Bw4, rs1050² 129Val         Bw6         Bw6, rs129Val           Bw6         Bw6, rs1050² 129Val         Bw6         Bw6, rs1050² 129Val           Bw6         Bw6, rs1050² 129Val         Bw6         Bw4, Bw6, rs 129Val           Bw6         Bw4, Bw6, rs 129Val         Bw6         Bw4, rs1050² 129Val           Bw6         Bw6, rs 1050² 129Val         Bw6         Bw6, rs1050² 129Val	Homozygous G Heterozygous G/A		
	HC20237L20182B03IHW09058       rs1610696:CC         Genotyping Report:         Sample:       HC20237L20182B04IHW09074         Summary       The allele pairs listed below are compatible with the consensus sequer         MICA*008:04:02       MICA*027:01:01         MICA*008:04:02       MICA*027:01:02         Intron 1       Motifs: 129Val	Bw6         Bw6, rs1050/ 129Met           Sample:         HC20237L201820           Summary         The allele pairs listed below are com           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           MICA*002:01:08         MICA*008:04:02           MICA*1002:01:08         MICA*008:04:02           Motifs:         129Met, 129Val	patible with the consensus sequence Intron 1 Intron 1 Jintron 1 Drygous G/A	Sample:         HC20237L20182C06S6UI9762           Summary         The allele pairs listed below are compatible with the micA*011:01:01           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           MICA*011:01:06         MICA*018:01:03           Motifs: 129Met         HOMOZYBOUS	t <mark>59a</mark> he consensus sequence.







#### MICB98 Met/Ile

Motif ID:	MICB98 Met/Ile	IICB98 Met/Ile     Locus:     MICB     Implemented (Ref. Version #):     3.37								
Supporting Publication:	Carapito R, Aouadi I, Pichot A, Spinnhirny Holt B, Labalette M, Spierings E, Picard C, M, Bertrand F, von dem Borne PA, Kuball Claas F, Moreau P, Charron D, Mohty M, N <b>reduces the incidence of graft-versus-ho</b> Jul;55(7):1367-1378.	P, Morlon A, Kotova I, Loiseau P, Tamouza R, JHE, Michallet M, Liou Aorishima Y, Socié G, B <b>st disease in conjuncti</b>	Macquin C, Rolli Toubert A, Pariss re B, Peffault de L ahram S. <b>Compa</b> <b>on with the CMV</b>	V, Cesbron A, Gagne K, Oudsh siadis A, Dubois V, Paillard C, N atour R, Blaise D, Cornelissen tibility at amino acid position status. Bone Marrow Transpl	oorn M, van der 1aumy-Bertrand JJ, Yakoub-Agha I, <b>98 of MICB</b> ant. 2020					
Impact of polymorphism:	The isoleucine (IIe) to methionine (Met) in UL16 binding. A MICB98 mismatched chronic GvHD development. MICB98 mi infection/reactivation. In addition, MICE The variation IIe > Met is exclusively pre	substitution in MICB but otherwise fully H smatches showed a G 398 mismatches were sent in MICB*008. M	amino acid posit LA and MICA ma wHD-independer associated with ismatch occurs ir	tion 98 is a key polymorphic r tched donor increases risk of nt association with a higher in a higher rate of relapse. n approximately 6% of transp	esidue involved both acute and ncidence of CMV lantations.					



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Motif ID:	MICB98 Met/Ile	Locus:	МІСВ	Imple (Ref.	emen Versi	ited on #)	:	3.37.0.1
Example Display:	Homozygous C Ile/Ile							
	5' UTR Intron 1		Ex	In <mark>Exo</mark> Intron	Exo	Intron 5		3' 0'
	IMGT/MICB 3.43.0.1 202	3771 <mark></mark> 878187918801 CE.Z.H.E.D.S.S.T.R.G.S.R.	8811.HC048L028B05IHW92 HF.Start: 12, 5' UTR	39SHJO MICB - To 12 ITR 648	otal Read	Depth: 50	)68 - Noise: (	0.006356
	HC048L028A02THW9045TUR0 GCAGGCTTGCATTCCCTCCAGGAGATTAGGGTCTC	TGAGATCCATGAAGACAGCACCAGGGGCTCCCGGCA	TTTC Allele 1 A	llele 2	CORE	EXONS PH	ASE1 PHASE2	Differences
	HC048L028A03IHW9057TEN GCAGGCTTGCATTCCCTCCAGGAGATTAGGGTCTC	TGAGATCCATGAAGACAGCAGCACCAGGGGCTCCCGGCA	TTTC MICB*002:01 M	ICB*005:06	0	0	0 0	
	HC048L028A04IHW9098M	.CEIHEDSSTRGSR	HF.MICB*005:06 M	ICB*036	0	1	0 0	
	HC048L028A05IHW9191C		MICB*005:06 M	ICB*036	0	1	0 0	
	HC048L028A06IHW9302\$STO .SLHSLQEIRV	.CE <mark>I</mark> HEDSSTRGSR	HF.MICB*005:06 M	ICB*036	0	1	0 0	
	HC048L028B01IHW9019DSLHSLQEIRV	.CE <mark>I</mark> HEDSSTRGSR	HF. <mark>MICB*002:01</mark> M	ICB*005:02	1	0		
	HC048L028B02IHW90491BW9		MICB*002:01 M	ICB*005:02	1	0		
	HC048L028B03IHW9065HHKB		MICB*002:01 M	ICB*005:02	1	0		
	HC048L028B04IHW9099IZI		MICB*002:01 M	ICB*005:02	1	0		
	··· 10% (100)		MICB*002:01 M	ICB*005:02	1	0		
			MICB*002:01 M	ICB*005:02	1	0		
			MICB*002:01 M	ICB*005:02	1	0		
			MICB*002:01 M	ICB*005:02	1	0		
			MICB*002:01 M	ICB*005:02	1	0		
			MICB*002:01 M	ICB*005:02	1	0		
	HC048L028B05IHW9239SHJO		MICB*002:01 M	ICB*005:02	1	0		
	HC048L028B05IHW9239S ♠ ♠ ♠ ♦ ₱ 294	✓	MICB*002:01 M	ICB*005:02	1	0		
		✓ ■ SIGN OFF	MICB*002:01 M	ICB*005:02	1	0		
			MICB*002:01 M	ICB*005:02	1	0		
	CDNA V Mast	ei	MTCB*002.01 M	ICB*005-02	1	0		



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Motif ID:	MICB98 Met/	'lle		Locus:	МІСВ		Impler (Ref. V	nented ersion a	<b>#)</b> :	3.37.0.1
Example Display:	Heterozygous	s C/G II	e/Met							
	5' UTR Intron 1 IMGT/MICB 3.43.0.1 202	. <mark></mark> .8741	875187618771		8811 HC048L028A05	EX IN Exo IHW9191CHI007	Intron Exo MICB - Total P	Intron 5 Read Depth: 4	58 - Noise: 0	3' UTR
	Base 8778	.GLH	ISLQEIRVCE	ZHEDSSTRGS.	RHF.Start: 9, 5'	UTR 9				
	CDNA 98.3, E C A 2 1	R			Stop: 13155	, 3' UTR 648	2000 D	BUONG DUA		
	HC048L028A011HW9013SCH	GCAGGCTTGCA1	TCCCTCCAGGAGATTAGGGTCTGTGAG	ATCCATGAAGACAGCAGCACCAGGGGCTCCCC	GCATTTC Allele 1	Allele 2	CORE	EXONS PHA:	E1 PHASE2 I	lfferences
	HC048L028A02IAW904510B	GCAGGCTTGCAT	TCCCTCCAGGAGATTAGGGTCTGTGAG	ATGCATGAAGACAGCAGCACCAGGGGGCTCCCC	R H E MICB*004:01	MICB*008.0			0	
	HC048L028A04THW9098N	.0		T+M	MICB*004:01	MICB*037	0	1	0	
					MICB*004:01	MICB*035	0	1	0	
		SLH	HSLQEIRVCE	<mark>I</mark> HEDSSTRGS.	RHF.MICB*004:01	MICB*037	0	1	0	
		SLH	ISL.QEIRVCE		RHF.MICB*004:01	MICB*035	0	1	0	
					MICB*004:01	MICB*037	0	1 (	0	
	· · ·				MICB*004:01	MICB*035	0	1	0	
					MICB*004:01	MICB*037	0	1 (	0	
	· · ·	10% (100)		<u>, , , , , , , , , , , , , , , , , , , </u>	MICB*004:01	MICB*035	0	1	0	
	• •	•			MICB*004:01	MICB*037	0	1 (	0	
	HC048L028A05IHW9191C.	•			MICB*004:01	MICB*035	0	1	0	
		1% (10)			MICB*004:01	MICB*037	0	1	0	
					MICB*004:01	MICB*035	0	1	0	
	· · ·		HC048L028A05IHW9191CHI007		MICB*004:01	MICB*037	0	1	0	
	· · ·		▲ ★ ★ ★ ★ ★ 294	✓	MICB*004:01	MICB*035	0	1	0	
	· · ·	•	ACCEPT A C G T $S = C + G$	V -	MICB*004:01	MICB*037	0	1	0	
	<u> </u>	•			MICB*004:01	MICB*035	0	1	0	
		-	Master		MICB*004:01	MICB*037	0	1	0	
	HC048L028A06IHW9302sst				MICB*004:01	MICB*035	0	1	0	



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Motif ID:	MICB98 Met/Ile	Locus:	МІСВ	Implemente (Ref. Version	d #):	3.37.0.1				
Example Display:	Homozygous G Met/Met									
	IMGT/MICE 3.43.0.1 2021-01-18	.1 2021-01-188/518/618/618/718/9188018801881HC048L028C051HW928SWT49 MICB - TOTAL REAG DEPTN: 5394 - NG								
	Base 8//8 .LHSL.Q.	.L.H.S.L.Q.E.I.R.V.C.E.Z.H.E.D.S.S.T.R.G.S.R.H. Start: 52, 5' UTR 52								
						Differenc				
	HC048L028C01NTC L H S L O E T B V C E M H E D S S T B G S E				0 0					
	HC048L028C02IHW9050MOU		MICB*0	08:01 MICB*035	0 1					
	HC048L028C03IHW9066TAB089		MICB*0	08:01 MICB*037	0 1	_				
	HC048L028C04IHW9104DHIF		MICB*0	08:01 MICB*035	0 1					
	HC048L028C05IHW9285WT49 F		MICB*0	08:01 MICB*037	0 1					
	G 10% (100)		MICB*0	08:01 MICB*035	0 1					
	Н		MICB*0	08:01 MICB*037	0 1					
			MICB*0	08:01 MICB*035	0 1					
	E 1% (10)		MICB*0	08:01 MICB*037	0 1					
		╡ <b>║</b> ╎╎╎ <b>║</b> ╎╎ <b>║</b> ╎╎╎ <sub>───</sub> ╼╼╼╴╎╎	MICB*0	08:01 MICB*035	0 1					
	B	TCCAGGAGATTAGGGTCTGTGAGATCCATGAAGACAGCACCACGAGGCACCCCGG	MICB*0	08:01 MICB*037	0 1					
	TGCATTCCCTCCAGG		AGAGGCTCCCGGCATT	08:01 MICB*035	0 1					
	HC048L028C05IHW9285WT49*		MICB*0	08:01 MICB*037	0 1					
		TTAGGGTCTGTGAGATCCATGAAGACAGCAGCAC	MICB*0	08:01 MICB*035	0 1					
			MICB*0	08:01 MICB*037	0 1					
	TGCATTCCCTCCAGGA	gattagggtctgtgagat <mark>c</mark> catgaagacagcagcacca	AGAGGCTCCCGGCATT	08:01 MICB*035	0 1					
		9285WT49	MICB*0	08:01 MICB*037	0 1					
			GGCATT MICB*0	08:01 MICB*037	0 1					
	HC048L028C06IHW9315CML		SIGN OFF	08:01 MICB*035	0 1					
	HC048L028D01IHW9024KT17	G T G ~	MICB*0	08:01 MICB*037	0 1					
	HC048L028D02IHW9055H0301 CDNA	✓ Master ✓	MICB*0	08:01 MICB*035	0 1					
	HC048L028D03IHW9076T7526 TGCATTCCCTCCAGGA	GATTAGGGTCTGTGAGAT <mark>C</mark> CATGAAGACAGCAGCACCA	MICB*0	08:01 MICB*037	0 1					



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Motif ID:	MICB98 Met/Ile	Locus:	МІСВ	Implemented (Ref. Version #):	3.37.0.1
Example Display:	Summary Table Report:         Motifs.       IMGT/MICB         HC048L028C05IHW9285WT49       98Met         HC048L028C06IHW9315CML       98Met, 98IIe         HC048L028D01IHW9024KT17       98IIe         HC048L028D02IHW9055H0301       98IIe         HC048L028D03IHW9076T7526       98IIe         HC048L028D03IHW9076T7526       98IIe         HC048L028D04IHW9134WHONP199       98IIe         HC048L028D05IHW9297HAG       98IIe         HC048L028D06IHW9320BEL5GB       98IIe	s G is C/G s C			
	Sample:       HC048L028A02IHW9045TUBO         Summary       The allele pairs listed below are compatible with the consensus sequence.         MICB*002:01       MICB*005:02         Motifs: 98lle       HOMOZYGOUS C	Sample:       HC048L028A05IHW919         Summary       The allele pairs listed below are compatible w         MICB*004:01       MICB*008:01         Motifs: 98Met, 98lle       Heterozygou	tcHi007 with the consensus sequence. s C/G	Sample:       HC048L028C05IHW9285WT49         Summary       The allele pairs listed below are compatible with the comparison of the second secon	onsensus sequence.



