

Table S1 All possible 52 nucleotide string combinations descriptive of known pairwise MICA allele combinations according to IMGT/HLA release v3.7.0.

String ^{1,2,3}	Combination 1		Combination 2		Additional Typing Needed to Resolve Ambiguity
	MICA Allele 1	MICA Allele 2	MICA Allele 1	MICA Allele 2	
GTNCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055			Exon 5
GTNCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*002:02			
GNNCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*002:03			
GTNCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*002:04			
GTTNNTNCTNNCNNTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*004			
GTTNNTNCTNNGCCTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACN	MICA*001	MICA*005			Please see footnote 3
GTTNNTNCTNNGNNTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*006			
GTTCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*007:01/MICA*026	MICA*018:02	MICA*040	Insufficient data available
GTTCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*007:02	MICA*018:01	MICA*040	Insufficient data available
GTTCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*007:03			
GTTCNTGCTAGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*007:04			
GTTNNTNCTNNGCCTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*008:01:01/MICA*008:01:02/MICA*008:04/MICA*027/MICA*048			Exons 1 and 5 and intron 1
GTTNNTNCTNNGCCTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*008:02			
GTTNNTNCTNNGCCTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*008:03			
GTTNNTNCTNNGCCTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*009:01/MICA*049			Exon 6
GTTNNTNCTNNGCCTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*009:02			
NTTNNTNCTNNGCCTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*010:01/MICA*010:02			Exon 5
GTNCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGANG	MICA*001	MICA*011			
GTTATGCTAGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*012:01			
GTTATGCTAGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGANGGACG	MICA*001	MICA*012:02			
GTTATGCTAGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*012:03			
GTNCNTGCTNGCCCTTCGNNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACN	MICA*001	MICA*013			Please see footnote 3
GTNCNTGCTNNGCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACN	MICA*001	MICA*014			Please see footnote 3
GTNCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACN	MICA*001	MICA*015			
GTTNNTNCTNNGCCTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*016			
GTNCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACN	MICA*001	MICA*017			
GTTATGCTAGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*018:01			
GTTATGCTAGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*018:02			
GTTNNTNCTNNGCCTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*019			
GTNCNTGCTNNGCCTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*022			
GTTNNTNCTNNGCCTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*024			
NTTNNTNCTNNGCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*025			
GTTNNTNCTNNGCCTTCGNNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*028			
GTTCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*029			
GTNCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGANG	MICA*001	MICA*030			
GTTNNTNCTNNGCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*031			
GTTNNTNCTNNGCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*032			
GTTNNTNCTNNGCCTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*033			
GTNCNTGCTNGCCCTTCGTNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*034			
GTNCNTGCTNGCCCTTCGTNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*035			
GTNCNTGCTNNGCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*036			
GTTCNTGCTNGCCCTTCGTNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*037			
GTTCNTGCTNGCCCTTCGTNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*038			
GTTCNTGCTNGCCCTTCGTNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*039			
GTTCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*040			
GTNCNNGCTNNGCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*041			
GTTNNTNCTNNGCCTTCGTNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*042			
GTTCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*043			
GTNCNTNCTNNCNNTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*044			
GTTCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*045			
GTNCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*046			
GTNCNNGCTNNGCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGANG	MICA*001	MICA*047			
GTNCNTGCTNGCCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*050			
GTTNNTNCTNNGCCTTCGTNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*001	MICA*051			
GTNCNTGCTNGCCCTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*018:02	MICA*031		Insufficient data available
GTNCNTGCTNGCCCTTCGNNTGCGCTTGCCCNANNCNGGGCCAGAGGGACG	MICA*001	MICA*053			

GTNCGTGCTGGCCNTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGNGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*043			Exon 5
GTGCGTGTGNCNNTTCGNCTNCGCTTGCCCNNNANNCNGGGCCAGAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*044			Exon 5
GTNCGTGCTGGCCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCNAGAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*045			Exon 5
GTGCGTGCTGGCCCTTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*046			Exon 5
GTGCGNGCTGGCCCTTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGANG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*047	MICA*030	MICA*041	Exon 5
GTGCGTGCTGGCCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*050			Exon 5
GTNNGTNCGTGCCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*051			Exon 5
GTGCGTGCTGGCCNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*053			Exon 5
NTNNGTNCGTGGCNNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*054			Exon 5
GTNNGTNCGTGGCNNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*056			Exon 5
GTNNGTNCGTGGCNNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*057			Exon 5
GTNNGTNCGTGGCNNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*058			Exon 5
GTNCGNGCTGGCCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCNAGAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*059	MICA*041	MICA*045	Exon 5
GTNCGTGTGNCCTTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGNACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*060			Exon 5
GTNCGTGTGNCCTTTCGTCTGCGCTTGCCCTTGATCGGGGCCANAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*061			Exon 5
NTNNGTNCGTGGCNNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGNACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*062			Exon 5
GTNNGTNCGTGGCNNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*063N			Exon 5
GTNNGTNCGTGGCNNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*064N			Exon 5
NTNNGTNCGTGGCNNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*065			Exon 5
NTNNGTNCGTGGCNNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*066			Exon 5
GTNNGTNCGTGGCNNTTCGNCTGCGCTTGCCCNNNANNCNGGGCCAGAGGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*067			Exon 5
GNGCGTGCTGGCCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACG	MICA*002:02	MICA*002:03			
GTGCGTGCTGGCCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACG	MICA*002:02	MICA*002:04			
GTNNGTNCGTGGCNNTTCGNCTNCGCTTGCCCNNNANNCNGGGCCAGAGGGACG	MICA*002:02	MICA*004			
GTNNGTNCGTGGCCCTTTCGNCTGCGCTTGCCNCTNANNCNGGGCCNAGAGGGACN	MICA*002:02	MICA*005			
GTNNGTNCGTGGCNNTTCGNCTNCGCTTGCCCNNNANNCNGGGCCAGAGGGACG	MICA*002:02	MICA*006			Please see footnote 3
GTNCGTGCTGGCCCTTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:02	MICA*007:01/MICA*026			Exon 5
GTNCGTGCTGGCCCTTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:02	MICA*007:03			
GTNCGTGCTNCGCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACG	MICA*002:02	MICA*007:04			
GTNNGTNCGTGGCNNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:02	MICA*008:01:01/MICA*008:01:02/MICA*008:04/MICA*027/MICA*048	MICA*051	MICA*053	Insufficient data available
GTNNGTNCGTGGCCNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:02	MICA*008:02			
GTNNGTNCGTGGCCNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:02	MICA*008:03			
GTNNGTNCGTGGCNNTTCGNCTNCGCTTGCCCNNNANNCNGGGCCAGAGGGACG	MICA*002:02	MICA*009:01/MICA*049			Exon 6
GTNNGTNCGTGGCNNTTCGNCTNCGCTTGCCCNNNANNCNGGGCCAGAGGGACG	MICA*002:02	MICA*009:02			
NTNNGTNCGTGGCNNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:02	MICA*010:01/MICA*010:02			Exon 5
GTGCGTGCTGGCCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGANG	MICA*002:02	MICA*011			
GTNCGTGTGNCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACG	MICA*002:02	MICA*012:01			
GTNCGTGTGNCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACG	MICA*002:02	MICA*012:02			
GTNCGTGTGNCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACG	MICA*002:02	MICA*012:03			
GTGCGTGCTGGCCNTTCGNCTGCGCTTGCCNCTTGATCGGGGCCNAGAGGGACN	MICA*002:02	MICA*013			Please see footnote 3
GTGCGTGCTGGCCNTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACN	MICA*002:02	MICA*014			Please see footnote 3
GTGCGTGCTGGCCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACN	MICA*002:02	MICA*015			
GTNNGTNCGTGGCNNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:02	MICA*016			
GTGCGTGCTGGCCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACN	MICA*002:02	MICA*017			
GTNCGTGTGNCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACG	MICA*002:02	MICA*018:02			
GTNNGTNCGTGGCNNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:02	MICA*019	MICA*022	MICA*051	Insufficient data available
GTGCGTGCTGGCCNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:02	MICA*022			
GTNNGTNCGTGGCCNTTCGNCTGCGCTTGCCCNNNANNCNGGGCCAGAGGGACG	MICA*002:02	MICA*024			
NTNNGTNCGTGGCCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACG	MICA*002:02	MICA*025			
GTNNGTNCGTGGCCNTTCGNCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACG	MICA*002:02	MICA*028			
GTNCGTGCTGGCCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACG	MICA*002:02	MICA*029			
GTGCGTGCTGGCCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGANG	MICA*002:02	MICA*030			
GTNNGTNCGTGGCCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACG	MICA*002:02	MICA*031			
GTNNGTNCGTGGCNNTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACG	MICA*002:02	MICA*032			
GTNNGTNCGTGGCCNTTCGNCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:02	MICA*033			
GTGCGTGCTGGCCCTTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACG	MICA*002:02	MICA*034			
GTGCGTGCTGGCCCTTTCGTCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:02	MICA*035			
GTGCGTGCTGGCCNTTCGTCTGCGCTTGCCNCTTGATCGGGGCCAGAGGGACG	MICA*002:02	MICA*036			
GTNCGTGCTGGCCCTTTCGTCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:02	MICA*037	MICA*007:01/MICA*026	MICA*035	Insufficient data available

GNNNGTNCNTGNCNTNTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:03	MICA*032
GNNNGTNCNTGNCNNTTCGNCNGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:03	MICA*033
GNGCGTGCTGGCCCTTTCGCTCTGCGCTTGCCCNNNANNCNGGGCCAGAGGGACG	MICA*002:03	MICA*034
GNGCGTGCTGGCCCTTTCGCTCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:03	MICA*035
GNGCGTGCTGGCCNNTTCGCTCTGCGNTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:03	MICA*036
GNNCGTGCTGGCCCTTTCGCTCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:03	MICA*037
GNNCGTGCTGGCCCTTTCGCTCTGCGCTTGCCCNNNANNCNGGGCCAGAGGGACG	MICA*002:03	MICA*038
GNNCGTGCTGGCCCTTTCGCTCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:03	MICA*039
GNNCGTGCTGGCCCTTTCGNTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:03	MICA*040
GNGCGNGCTGGCCCTTTCGCTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:03	MICA*041
GNNNGTNCNTGGCCCTTTCGCTCTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:03	MICA*042
GNNCGTGCTGGCCNTTCGCTCTGCGCTTGCCCTTGATCGGGGCCAGAGNGACG	MICA*002:03	MICA*043
GNGCGTNCNTGNCNNTTCGNTGCGCTTGCCCNNNANNCNGGGCCAGAGGGACG	MICA*002:03	MICA*044
GNNCGTGCTGGCCCTTTCGCTCTGCGCTTGCCCTTGATCGGGGCCNAGAGGGACG	MICA*002:03	MICA*045
GNGCGTGCTGGCCCTTTCGCTCTGCGCTTGCCCTTGNTCGGGGCCAGAGGGACG	MICA*002:03	MICA*046
GNGCGNGCTGGCCCTTTCGCTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGANG	MICA*002:03	MICA*047
GNGCGTGCTGGCCCTTTCGCTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:03	MICA*050
GNNNGTNCNTGGCCCTTTCGCTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:03	MICA*051
GNGCGTGCTGGCCNTTCGNTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:03	MICA*053
GNNNGTNCNTGGCCNNTTCGNTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:03	MICA*054
GNNNGTNCNTGGCCNNTTCGNTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:03	MICA*056
GNNNGTNCNTGGCCNNTTCGNTGCGCTTGCCCNNNANNNNGGGCCAGAGGGACG	MICA*002:03	MICA*057
GNNNGTNCNTGGCCNNTTCGNTGCGCTTGCCCNNNANNNNGGGCCNAGAGGNACG	MICA*002:03	MICA*058
GNNCGNGCTGGCCCTTTCGCTCTGCGCTTGCCCTTGATCGGGGCCNAGAGGGACG	MICA*002:03	MICA*059
GNNCNTGCTNGCCNTTCGCTCTGCGCTTGCCCTTGATCGGGGCCAGAGGNACG	MICA*002:03	MICA*060
GNNCNTGCTNGCCNTTCGCTCTGCGCTTGCCCTTGATCGGGGCCANAGAGGACG	MICA*002:03	MICA*061
NNNNGTNCNTGGCCNNTTCGNTGCGCTTGCCCNNNANNNNGGGCCNAGAGGNACG	MICA*002:03	MICA*062
GNNNGTNCNTGGCCNNTTCGNTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:03	MICA*063N
GNNNGTNCNTGGCCNNTTCGNTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:03	MICA*064N
NNNNGTNCNTGGCCNNTTCGNTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:03	MICA*065
NNNNGTNCNTGGCCNNTTCGNTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:03	MICA*066
GNNNGTNCNTGNCNNTTCGNTGCGCTTGCCCNNNANNCNGGGCCAGAGGGACG	MICA*002:03	MICA*067
GTNNGTNCNTGNCNNTTCNNTGCGCTTGCCCNNNANNCNGGGCCAGAGGGACG	MICA*002:04	MICA*004
GTNNGTNCNTGCGCTTTCNNTGCGCTTGCCCTTNANNCNGGGCCNAGAGGGACN	MICA*002:04	MICA*005
GTNNGTNCNTGNNNTTCNNTGCGCTTGCCCNNNANNCNGGGCCAGAGGGACG	MICA*002:04	MICA*006
GTNCGTGCTGGCCCTTTCNTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:04	MICA*007:01/MICA*026
GTNCGTGCTGGCCCTTTCNTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:04	MICA*007:02
GTNCGTGCTGGCCCTTTCNTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:04	MICA*007:03
GTNCGTGCTGGCCCTTTCNTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:04	MICA*007:04
GTNNGTNCNTGGCCNNTTCNNTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:04	MICA*008:01:01/MICA*008:01:02/MICA*008:04/MICA*027/MICA*048
GTNNGTNCNTGGCCNNTTCNNTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:04	MICA*008:02
GTNNGTNCNTGGCCNNTTCNNTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:04	MICA*008:03
GTNNGTNCNTGGCCNNTTCNNTGCGCTTGCCCNNNANNCNGGGCCAGAGGGACG	MICA*002:04	MICA*009:01/MICA*049
GTNNGTNCNTGGCCNNTTCNNTGCGCTTGCCCNNNANNCNGGGCCAGAGGGACG	MICA*002:04	MICA*009:02
NTNNGTNCNTGGCCNNTTCNNTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:04	MICA*010:01/MICA*010:02
GTGCGTGCTGGCCCTTTCNTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGANG	MICA*002:04	MICA*011
GTNCGTGCTGCGCTTTCNTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:04	MICA*012:01
GTNCGTGCTGCGCTTTCNTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:04	MICA*012:02
GTNCGTGCTGCGCTTTCNTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:04	MICA*012:03
GTGCGTGCTGGCCNNTTCNNTGCGCTTGCCCTTGATCGGGGCCNAGAGGGACN	MICA*002:04	MICA*013
GTGCGTGCTGNCNNTTCNNTGNGCTTGCCCTTGATCGGGGCCAGAGGGACN	MICA*002:04	MICA*014
GTGCGTGCTGGCCCTTTCNTCTGNGCTTGCCCTTGATCGGGGCCAGAGGGACN	MICA*002:04	MICA*015
GTNNGTNCNTGGCCNNTTCNNTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:04	MICA*016
GTGCGTGCTGGCCCTTTCNTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACN	MICA*002:04	MICA*017
GTNCGTGCTGGCCCTTTCNTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:04	MICA*018:01
GTNCGTGCTGGCCCTTTCNTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*002:04	MICA*018:02
GTNNGTNCNTGGCCNNTTCNNTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:04	MICA*019
GTGCGTGCTGGCCNNTTCNNTGCGCTTGCCCNNNANNNNGGGCCNAGAGGGACG	MICA*002:04	MICA*022
GTNNGTNCNTGGCCNNTTCNNTGCGCTTGCCCNNNANNCNGGGCCAGAGGGACG	MICA*002:04	MICA*024

Please see footnote 3

Exon 5

Exons 1 and 5 and intron 1

Exon 6

Exon 5

Please see footnote 3

Please see footnote 3

GTNCGTGCTGNCNNTTTCGTCTGNGCTTGCCCTTGATCGGGGCCAGAGGGACN	MICA*007:02	MICA*014			
GTNCGTGCTGGCCCTTTCGTCTGNGCTTGCCCTTGATCGGGGCCAGAGGGACN	MICA*007:02	MICA*015			Please see footnote 3
GTTNNGTCTGGCCNNTTCGNCTGCGCTTGCCCNNNANNNNGGCCNAGAGGGACG	MICA*007:02	MICA*016			
GTNCGTGCTGGCCCTTTCGTCTGCGCTNGCCCTTGATCGGGGCCAGAGGGACN	MICA*007:02	MICA*017			
GTTNCGTCTGNGCCCTTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*007:02	MICA*018:01			
GTTNNGTCTGGCCNNTTCGNCTGCGCTTGCCCNNNANNNNGGCCNAGAGGGACG	MICA*007:02	MICA*019			
GTNCGTGCTGGCCNNTTCGNCTGCGCTTGCCCNNNANNNNGGCCNAGAGGGACG	MICA*007:02	MICA*022			
GTTNNGTCTGGCCNNTTCGNCTGCGCTTGCCCNNNANNNNGGCCNAGAGGGACG	MICA*007:02	MICA*024			
NTTNGTCTGGCCCTTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*007:02	MICA*025	MICA*028	MICA*038	Insufficient data available
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GTNCGTGCTGGCCCTTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGANG	MICA*007:02	MICA*030			
GTTNNGTCTGGCCCTTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*007:02	MICA*031			
GTTNNGTCTGNCNNTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*007:02	MICA*032			
GTTNNGTCTGGCCNNTTCGNCTGCGCTTGCCCNNNANNNNGGCCNAGAGGGACG	MICA*007:02	MICA*033			
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GTNCGTGCTGGCCNNTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*007:02	MICA*036			
GTTCTGTCTGGCCCTTTCGTCTGCGCTTGCCCNNNANNNNGGCCNAGAGGGACG	MICA*007:02	MICA*037			
GTTCTGTCTGGCCCTTTCGTCTGCGCTTGCCCNNNANNNNGGCCNAGAGGGACG	MICA*007:02	MICA*038			
GTTCTGTCTGGCCCTTTCGTCTGCGCTTGCCCNNNANNNNGGCCNAGAGGGACG	MICA*007:02	MICA*039			
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GTTCTGTCTGGCCCTTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*007:02	MICA*043			
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NTTNGTCTGGCCNNTTCGNCTGCGCTTGCCCNNNANNNNGGCCNAGAGGGACG	MICA*007:02	MICA*065			
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GTTNNGTCTGNCNNTTCGNCTGCGCTTGCCCNNNANNNNGGCCNAGAGGGACG	MICA*007:02	MICA*067			
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GTTNNGTCTGGCCNNTTCGNCTGCGCTTGCCCNNNANNNNGGCCNAGAGGGACG	MICA*007:03	MICA*008:01:01/MICA*008:01:02/MICA*008:04/MICA*027/MICA*048			Exons 1 and 5 and intron 1
GTTNNGTCTGGCCNNTTCGNCTGCGCTTGCCCNNNANNNNGGCCNAGAGGGACG	MICA*007:03	MICA*008:02			
GTTNNGTCTGGCCNNTTCGNCTGCGCTTGCCCNNNANNNNGGCCNAGAGGGACG	MICA*007:03	MICA*008:03			
GTTNNGTCTGGCCNNTTCGNCTGCGCTTGCCCNNNANNNNGGCCNAGAGGGACG	MICA*007:03	MICA*009:02			
NTTNGTCTGGCCNNTTCGNCTGCGCTTGCCCNNNANNNNGGCCNAGAGGGACG	MICA*007:03	MICA*010:01/MICA*010:02			Exon 5
GTNCGTGCTGGCCCTTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGANG	MICA*007:03	MICA*011			
GTTNCGTCTGNGCCCTTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*012:01			
GTTNCGTCTGNGCCCTTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*012:02			
GTTNCTGNCNNGCCCTTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*012:03			
GTNCGTGCTGGCCNNTTCGNCTGCGCTTGCCCTTGATCGGGGCCNAGAGGGACN	MICA*007:03	MICA*013			Please see footnote 3
GTNCGTGCTGNCNNTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACN	MICA*007:03	MICA*014			Please see footnote 3
GTNCGTGCTGGCCCTTTCGTCTGCGCTTGCCCTTGATCGGGGCCAGAGGGACN	MICA*007:03	MICA*015			
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GTNTNGTCTGGCCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*019	
GTNCGTGCTGGCCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*022	
GTTTNGTCTGGCCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*024	
NTTNGTCTGGCCCTTCGTCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*025	
GTTTNGTCTGGCCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*028	
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GTTTNGTCTGGCCCTTCGTCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*031	
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GTTTNGTCTGGCCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*033	
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GTTTNGTCTGGCCCTTCGTCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*043	
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GTNCGTGCTGGCCCTTCGTCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*046	
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GTTTNGTCTGGCCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*057	
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NTTNGTCTGGCCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*062	
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GTTTNGTCTGGCCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*064N	
NTTNGTCTGGCCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*065	
NTTNGTCTGGCCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*066	
GTTTNGTCTGNCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:03	MICA*067	
GTTTNGTCTGNCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:04	MICA*008:01:01/MICA*008:01:02/MICA*008:04/MICA*027/MICA*048	Exons 1 and 5 and intron 1
GTTTNGTCTGNCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:04	MICA*008:02	
GTTTNGTCTGNCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:04	MICA*008:03	
GTTTNGTCTGNCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:04	MICA*009:01/MICA*049	Exon 6
GTTTNGTCTGNCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:04	MICA*009:02	
NTTNGTCTGNCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:04	MICA*010:01/MICA*010:02	Exon 5
GTNCGTGCTNGCCCTTCGTCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:04	MICA*011	
GTTTNGTCTAGCCCTTCGTCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:04	MICA*012:01	
GTTTNGTCTAGCCCTTCGTCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:04	MICA*012:02	
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GTTTNGTCTGNCNNTTCGNCTGCNCTTGATCGGGGCCAGAGGGACG	MICA*007:04	MICA*016	
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GTNNGTACTGGCCNTTCGNCTGCGCTTGCCCCCAACTCGGGNCGGAGGGACG	MICA*008:02	MICA*035	MICA*042	MICA*053 Insufficient data available
GTNNGTACTGGCCNTTCGNCTGCGNTTGCCCNANNNNGGGNCNGAGGGACG	MICA*008:02	MICA*036		
GTTNGTACTGGCCNTTCGNCTGCGCTTGCCCCCAACTCGGGNCGGAGGGACG	MICA*008:02	MICA*037		
GTNNGTACTGGCCNTTCGNCTGCGCTTGCCCCCAACNCGGGNCNGAGGGACG	MICA*008:02	MICA*038		
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GTTTGACTGGCCNTTCGCTTCNCTTGCCNCCAACNCGGGNCNGAGGGACG	MICA*008:03	MICA*009:02		
NTTTGACTGGCCNTTCGCTGCGCTTGCCNCCAACTCGGGNCGGAGGGACG	MICA*008:03	MICA*010:01/MICA*010:02		Exon 5
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GTNNGTACTGNCCTTCGNCTGNGCTTGCCCNANNNNGGGNCNGAGGGACN	MICA*008:03	MICA*014		Please see footnote 3
GTNNGTACTGGCCNTTCGNCTGNGCTTGCCCNANNNNGGGNCNGAGGGACN	MICA*008:03	MICA*015		
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GTTTGACTGGCCNTTCGCCNCGCTTGCCNCCAACTCGGGNCGGAGGGACG	MICA*008:03	MICA*033		
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Please see footnote 3
Please see footnote 3

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MICA*045 MICA*047 Insufficient data available

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GTTNNTNCTGNCNNTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGGACG	MICA*057	MICA*061
NTTTGACTGGCTCTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGNACG	MICA*057	MICA*062
GTTTGACTGGCNCCTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGGACG	MICA*057	MICA*063N
GTTTGACTGGCNCCTTCGCCTGCGCTTGCCCCAACTCGNGCCNAGAGGACG	MICA*057	MICA*064N
NTTTGACTGGCTCTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGGACG	MICA*057	MICA*065
NTTTGACTGGCTCTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGGACG	MICA*057	MICA*066
GTTTGACTGNCCTTCGCCTGCGCTTGCCCCAAACNCGGGCCNAGAGGACG	MICA*057	MICA*067
GTTNNGNCTGGCNCCTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGNACG	MICA*058	MICA*059
GTTNNTNCTGNCNNTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGGACG	MICA*058	MICA*060
GTTNNTNCTGNCNNTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGNACG	MICA*058	MICA*061
NTTTGACTGGCNCCTTCGCCTGCGCTTGCCCCAACTCGGGCCGGAGGACG	MICA*058	MICA*062
GTTTGACTGGCNCCTTCGCCTGCGCTTGCCCCAACTCGGGCCGGAGGNACG	MICA*058	MICA*063N
GTTTGACTGGCNCCTTCGCCTGCGCTTGCCCCAACTCGNGCCGGAGGNACG	MICA*058	MICA*064N
NTTTGACTGGCNCCTTCGCCTGCGCTTGCCCCAACTCGGGCCGGAGGNACG	MICA*058	MICA*065
NTTTGACTGGCNCCTTCGCCTGCGCTTGCCCCAACTCGGGCCGGNNGNACG	MICA*058	MICA*066
GTTTGACTGNCNCTTCGCCTGCGCTTGCCCCAAACNCGGGCCNAGAGNACG	MICA*058	MICA*067
GTTCCNNGCTGNCCTNTGCTGCGCTTGCGCTTGATCGGGCCNAGAGGNACG	MICA*059	MICA*060
GTTCCNNGCTGNCCTNTGCTGCGCTTGCGCTTGATCGGGCCNANAGGACG	MICA*059	MICA*061
NTTNGNCTGGCNCCTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGNACG	MICA*059	MICA*062
GTTNNGNCTGGCNCCTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGGACG	MICA*059	MICA*063N
GTTNNGNCTGGCNCCTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGGACG	MICA*059	MICA*064N
NTTNGNCTGGCNCCTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGGACG	MICA*059	MICA*065
NTTNGNCTGGCNCCTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGGACG	MICA*059	MICA*066
GTTNNGNCTGNCNNTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGGACG	MICA*059	MICA*067
GTTTCATGCTAGCCTATGCTGCGCTTGCCCCAACTCGGGCCNAGAGNACG	MICA*060	MICA*061
NTTNTNCTGNCNNTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGGACG	MICA*060	MICA*062
GTTNNTNCTGNCNNTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGNACG	MICA*060	MICA*063N
GTTNNTNCTGNCNNTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGNACG	MICA*060	MICA*064N
NTTNTNCTGNCNNTTCGCCTGCGCTTGCCCCAACTCGGGCCNAGAGNACG	MICA*060	MICA*065

NTTNNCTNCTNGCNCNNTCGNCTGCGCTTGCCCNANNNNGGGCCNGGAGGACG	MICA*060	MICA*066	
GTTNNCTNCTNCCNNTCGNCTGCGCTTGCCCNANNNNGGGCCAGAGGACG	MICA*060	MICA*067	
NTTNNCTNCTNGCNCNNTCGNCTGCGCTTGCCCNANNNNGGGCCNAGAGGACG	MICA*061	MICA*062	
GTTNNCTNCTNGCNCNNTCGNCTGCGCTTGCCCNANNNNGGGCCNAGAGGACG	MICA*061	MICA*063N	
GTTNNCTNCTNGCNCNNTCGNCTGCGCTTGCCCNANNNNGGGCCNAGAGGACG	MICA*061	MICA*064N	
NTTNNCTNCTNGCNCNNTCGNCTGCGCTTGCCCNANNNNGGGCCNAGAGGACG	MICA*061	MICA*065	
NTTNNCTNCTNGCNCNNTCGNCTGCGCTTGCCCNANNNNGGGCCNAGAGGACG	MICA*061	MICA*066	
GTTNNCTNCTNCCNNTCGNCTGCGCTTGCCCNANNNNGGGCCANAGAGGACG	MICA*062	MICA*067	
NTTGTANTGGCNCCTTGCCTGCGCTTGCCCCAACTCGGGCCGAGGACG	MICA*062	MICA*063N	
NTTGTACTGGCNCCTTGCCTGCGCTTGCCCCAACTCGGGCCGAGGACG	MICA*062	MICA*064N	
CTTTGTACTGGCTCTTGCCTGCGCTTGCCCCAACTCGGGCCGAGGACG	MICA*062	MICA*065	
CTTTGTACTGGCTCTTGCCTGCGCTTGCCCCAACTCGGGCCGAGGACG	MICA*062	MICA*066	
NTTGTACTGNCTCTTGCCTNCGCNTGCCCCAACTCGGGCCGAGGACG	MICA*062	MICA*067	
GTTGTANTGGCCCTTGCCTGCGCTTGCCCCAACTCGGGCCGAGGACG	MICA*063N	MICA*064N	
NTTGTANTGGCNCCTTGCCTGCGCTTGCCCCAACTCGGGCCGAGGACG	MICA*063N	MICA*065	
NTTGTANTGGCNCCTTGCCTGCGCTTGCCCCAACTCGGGCCGAGGACG	MICA*063N	MICA*066	
GTTGTANTGNCNCTTGCCTNCGCNTGCCCCAACTCGGGCCGAGGACG	MICA*063N	MICA*067	
NTTGTACTGGCNCCTTGCCTGCGCTTGCCCCAACTCGGGCCGAGGACG	MICA*064N	MICA*065	
NTTGTACTGGCNCCTTGCCTGCGCTTGCCCCAACTCGGGCCGAGGACG	MICA*064N	MICA*066	
GTTGTACTGNCNCTTGCCTNCGCNTGCCCCAACTCGGGCCGAGGACG	MICA*064N	MICA*067	
GTTGATGCTAGCCTTTGCTGCGCTTGCCCCAACTCGGGCCGAGGACG	MICA*065	MICA*066	
NTTGTACTGNCNCTTGCCTNCGCNTGCCCCAACTCGGGCCGAGGACG	MICA*065	MICA*067	
NTTGTACTGNCTCTTGCCTNCGCNTGCCCCAACTCGGGCCGAGGACG	MICA*066	MICA*067	
GTTGATGCTAGCCTTTGCTGCGCTTGCCCCAACTCGGGCCGAGGACG	MICA*001	MICA*001	
GTGCGTGTGGCCTTTGCTGCGCTTGCCCTTGATCGGGCCAGAGGACG	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	MICA*002:01/MICA*020/MICA*023/MICA*052/MICA*055	Exon 5
GTGCGTGTGGCCTTTGCTGCGCTTGCCCTTGATCGGGCCAGAGGACG	MICA*002:02	MICA*002:02	
GCGCGTGTGGCCTTTGCTGCGCTTGCCCTTGATCGGGCCAGAGGACG	MICA*002:03	MICA*002:03	
GTGCGTGTGGCCTTTGCTGCGCTTGCCCTTGATCGGGCCAGAGGACG	MICA*002:04	MICA*002:04	
GTTTGTACTGCCCTTTGCTGCGCTTGCCCCAACTCGGGCCAGAGGACG	MICA*004	MICA*004	
GTTTGTACTGGCCTTTGCTGCGCTTGCCCTCAACCCGGCCAGAGGAC*	MICA*005	MICA*005	Please see footnote 3
GTTTGTACTGGCTTTGCTGCGCTTGCCCCAACTCGGGCCAGAGGACG	MICA*006	MICA*006	
GTTGCTGTGGCCTTTGCTGCGCTTGCTTGATCGGGCCAGAGGACG	MICA*007:01/MICA*026	MICA*007:01/MICA*026	Exon 5
GTTGCTGTGGCCTTTGCTGCGCTTGCCCTTGATCGGGCCAGAGGACG	MICA*007:02	MICA*007:02	
GTTGCTGTGGCCTTTGCTGCTGCACTTGCTTGATCGGGCCAGAGGACG	MICA*007:03	MICA*007:03	
GTTGCTGTAGCCTTTGCTGCGCTTGCCCTTGATCGGGCCAGAGGACG	MICA*007:04	MICA*007:04	
GTTTGTACTGGCCTTTGCTGCGCTTGCCCCAACTCGGGCCAGAGGACG	MICA*008:01:01/MICA*008:01:02/MICA*008:04/MICA*027/MICA*048	MICA*008:01:01/MICA*008:01:02/MICA*008:04/MICA*027/MICA*048	Exons 1 and 5 and intron 1
GTTTGTACTGGCCTTTGCTGCGCTTGCCCCAACTCGGGCCAGAGGACG	MICA*008:02	MICA*008:02	
GTTTGTACTGGCCTTTGCTGCGCTTGCCCAACTCGGGCCAGAGGACG	MICA*008:03	MICA*008:03	
GTTTGTACTGGCTTTGCTGCGCTTGCCCCAACTCGGGCCAGAGGACG	MICA*009:01/MICA*049	MICA*009:01/MICA*049	Exon 6
GTTTGTACTGGCTTTGCTGCGCTTGCCCCAACTCGGGCCAGAGGACG	MICA*009:02	MICA*009:02	
CTTTGTACTGGCTTTGCTGCGCTTGCCCCAACTCGGGCCAGAGGACG	MICA*010:01/MICA*010:02	MICA*010:01/MICA*010:02	Exon 5
GTGCGTGTGGCCTTTGCTGCGCTTGCCCTTGATCGGGCCAGAGGACG	MICA*011	MICA*011	
GTTGATGCTAGCCTATCGCTGCGCTTGCCCTTGATCGGGCCAGAGGACG	MICA*012:01	MICA*012:01	
GTTGATGCTAGCCTATCGCTGCGCTTGCCCTTGATCGGGCCAGAGGACG	MICA*012:02	MICA*012:02	
GTTGATGCTAGCCTATCGCTGCGCTTGCCCTTGATCGGGCCAGAGGACG	MICA*012:03	MICA*012:03	
GTGCGTGTGGCCTTTGCTGCGCTTGCCCTTGATCGGGCCAGAGGAC*	MICA*013	MICA*013	Please see footnote 3
GTGCGTGTGGCCTTTGCTGCGCTTGCCCTTGATCGGGCCAGAGGAC*	MICA*014	MICA*014	Please see footnote 3
GTTGCTGTGGCCTTTGCTGCGCTTGCCCTTGATCGGGCCAGAGGAC.	MICA*015	MICA*015	
GTTTGTACTGGCTTTGCTGCGCTTGCCCCAACTCGGGCCAGAGGACG	MICA*016	MICA*016	
GTGCGTGTGGCCTTTGCTGCGCTTGCCCTTGATCGGGCCAGAGGACG	MICA*017	MICA*017	
GTTGATGCTAGCCTTTGCTGCGCTTGCCCTTGATCGGGCCAGAGGACG	MICA*018:01	MICA*018:01	
GTTGATGCTAGCCTTTGCTGCGCTTGCTTGATCGGGCCAGAGGACG	MICA*018:02	MICA*018:02	
GTTTGTACTGGCTTTGCTGCGCTTGCCCCAACTCGGGCCAGAGGACG	MICA*019	MICA*019	
GTGCGTGTGGCTTTGCTGCGCTTGCCCCAACTCGGGCCAGAGGACG	MICA*022	MICA*022	
GTTTGTACTGGCCTTTGCTGCGCTTGCCCCAACTCGGGCCAGAGGACG	MICA*024	MICA*024	
CTTTGTACTGGCCTTTGCTGCGCTTGCCCTTGATCGGGCCAGAGGACG	MICA*025	MICA*025	
GTTTGTACTGGCCTTTGCTGCGCTTGCCCTTGATCGGGCCAGAGGACG	MICA*028	MICA*028	
GTTGCTGTGGCCTTTGCTGCGCTTGCCCTTGATCGGGCCAGAGGACG	MICA*029	MICA*029	
GTGCGTGTGGCCTTTGCTGCGCTTGCCCTTGATCGGGCCAGAGGACG	MICA*030	MICA*030	

GTTTGTACTGGCCTTCGTTTGC	GCTTGC	CCTGCC	CTTGATCGGGGCCAGAGGGACG	MICA*031	MICA*031
GTTTGTACTGCCTTATCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*032	MICA*032	
GTTTGTACTGGCTCTTCGCCA	GCCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*033	MICA*033	
GTGCGTGTGGCCTTCCTGCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*034	MICA*034	
GTGCGTGTGGCCTTTCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*035	MICA*035	
GTGCGTGTGGCCTTTCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*036	MICA*036	
GTTCTGTGTGGCCTTTCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*037	MICA*037	
GTTCTGTGTGGCCTTTCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*038	MICA*038	
GTTCTGTGTGGCCTTTCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*039	MICA*039	
GTTCTGTGTGGCCTTTCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*040	MICA*040	
GTGCGGGCTGGCCTTTCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*041	MICA*041	
GTTTGTACTGGCCTTTCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*042	MICA*042	
GTTCTGTGTGGCCTTTCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*043	MICA*043	
GTGCGTACTGCCTTTCGCCTC	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*044	MICA*044	
GTTCTGTGTGGCCTTTCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*045	MICA*045	
GTGCGTGTGGCCTTTCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*046	MICA*046	
GTGCGGGCTGGCCTTTCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*047	MICA*047	
GTGCGTGTGGCCTTTCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*050	MICA*050	
GTTTGTACTGGCCTTTCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*051	MICA*051	
GTGCGTGTGGCCTTTCGCCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*053	MICA*053	
CTTTGTACTGGCTCTTCGCCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*054	MICA*054	
GTTTGTACTGGCTCTTCGCCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*056	MICA*056	
GTTTGTACTGGCTCTTCGCCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*057	MICA*057	
GTTTGTACTGGCCTTTCGCCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*058	MICA*058	
GTTCTGGCTGGCCTTTCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*059	MICA*059	
GTTCTAGCTAGCCTATCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*060	MICA*060	
GTTCTAGCTAGCCTATCGTCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*061	MICA*061	
CTTTGTACTGGCTCTTCGCCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*062	MICA*062	
GTTTGATTGGCCCTTCGCCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*063N	MICA*063N	
GTTTGTACTGGCCCTTCGCCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*064N	MICA*064N	
CTTTGTACTGGCTCTTCGCCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*065	MICA*065	
CTTTGTACTGGCTCTTCGCCTG	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*066	MICA*066	
GTTTGTACTGCCTTTCGCCTC	CGCTTG	CCTTGATCGGGGCCAGAGGGACG	MICA*067	MICA*067	

¹N refers to heterozygosity at that position.

Polymorphic positions in the 52 nucleotide string are listed as sense strand for exon 2 (nucleotides 1-10), antisense strand for exon 3 (nucleotides 11-28) and sense strand for exon 4 (nucleotides 29-52) in 5'-3' direction.

²cDNA position 536 in exon 3 can encode A, C or T (in antisense strand). There are no ambiguous combinations involving this position; however, the program will provide all possible combinations as if it were ambiguous. A sample heterozygous for MICA*012:01, MIC*043 will have an A/C at this position. A sample heterozygous for MICA*018:01, MICA*043 will have T/C at this position.

³MICA*005, MICA*013 and MICA*014 have insufficient data for the cDNA position 892 in exon 4. In the string, this 52nd position displays as * or N when these alleles are present. If the string is truncated to 51 nucleotides by excluding nucleotide 52, the combinations listed above do not change and the only additional ambiguities are the combination of MICA*022, MIC*028 or MICA*013, MICA*057.

Table S2 Further characterization of exon 5 for groups of alleles with identical sequences in exons 2, 3, and 4 (adapted from Zou et al., reference 1). Sequencing of exon 5 in the reverse direction provides information on the number of GTC repeats and four polymorphic positions shown below that can be used to delineate some of the ambiguous allele combinations.

Group ¹	Alleles	STR type ²	Exon 5 polymorphic position ³			
			981	982	985	1017
1	MICA*002:01	A9	G	C	A	C
	MICA*020	A10	G	C	A	C
	MICA*023	A5.1	A	C	G	*
	MICA*052	A9	G	T	A	C
	MICA*055	A8	G	C	A	*
2	MICA*008:01:01	A5.1	A	C	G	C
	MICA*008:01:02	A5.1	A	C	G	C
	MICA*008:04	A5.1	A	C	G	C
	MICA*027	A5	A	C	G	C
	MICA*048	A5	A	C	G	A
3	MICA*007:01	A4	A	C	G	C
	MICA*026	A6	A	C	G	C
4	MICA*009:01	A6	A	C	G	C
	MICA*049	A6	A	C	G	C
5	MICA*010:01	A5	A	C	G	C
	MICA*010:02	A5	A	C	G	C

¹ Group 2 alleles MICA*008:01:01 and MICA*008:01:02 differ in intron 1.

MICA*008:04 differs from MICA*008:01:01 and MICA*008:01:02 in exon 1 at cDNA nucleotide position 21.

Group 4 alleles MICA*009:01 and MICA*049 differ in exon 6 at cDNA nucleotide position 1067.

Group 5 alleles MICA*010:01 and MICA*010:02 differ in exon 5 at cDNA nucleotide position 933; this position can be read with the help of Supplementary Table 3.

²Short tandem repeat (STR) type named according to Mizuki et al. (2).

³Numbered according to IMGT/HLA database v.3.7.0 (<http://www.ebi.ac.uk/imgt/hla/>).

Nucleotides for exon 5 positions are shown for antisense strand.

* Unknown sequence.

References

1. Zou Y, Han M, Wang Z, Stastny P. MICA allele-level typing by sequence-based typing with computerized assignment of polymorphic sites and short tandem repeats within the transmembrane region. *Hum Immunol* 2006; 67:145-51.
2. Mizuki N, Ota M, Kimura M, et al. Triplet repeat polymorphism in the transmembrane region of the MICA gene: a strong association of six GCT repetitions with Behçet disease. *Proc Natl Acad Sci USA* 1997; 94: 1298-303.

22	A6/A10	A G C A G C A G C A G C A G C A G C A G C A A/G C A G C A G A/C A A/G C A A/T C/G A/G A/G A/C A/T G A/T A/C A/T
23	A7/A8	A G C A G C A G C A G C A G C A G C A G C A G C A A/G C A A/G C A G A/C A A/G A/C A A/T C/G A/G A/T A/G G/T A/G A/T C/T G/T
24	A7/A9	A G C A G C A G C A G C A G C A G C A G C A G C A A/G C A G C A A/G A/C A A/G C A G/T A/G A/G A A/C A/T G/T G/T C/G A/T
25	A7/A10	A G C A G C A G C A G C A G C A G C A G C A G C A A/G C A G C A G A/C A A C A G/T C/G A/G A/G A A/T A/G C/T A/C T
26	A8/A9	A G C A G C A G C A G C A G C A G C A G C A G C A G C A A/G C A A/G C A G A/C A A/G A/C A A/T C/G A/G A/T A/G G/T A/G A/T
27	A8/A10	A G C A G C A G C A G C A G C A G C A G C A G C A G C A A/G C A G C A A/G A/C A A/G C A G/T A/G A/G A A/C A/T G/T G/T
28	A9/A10	A G C A G C A G C A G C A G C A G C A G C A G C A G C A A/G C A A/G C A G A/C A A/G A/C A A/T C/G A/G A/T A/G G/T A/G A/T C/T G/T
29	MICA*010:02 A5/A4	A G C A G C A G C A G C A G C A A/G C A A/G C A G A/C A A/G A/C A A/T C/G G A/T A/G G/T A/G A/T C/T G/T
30	MICA*010:02 A5/A5.1	A G C A G C A G C A/G A/G C/G A/C A/G C/G A/C A A/C A/C A/G C/G A/C A/G A/G A A A/C C/G A/T G/T G A/G A A/T G/T G/T C/T C/T
31	MICA*010:02 A5/A6	A G C A G C A G C A G C A G C A G C A A/G C A A/G C A G A/C A A/G A/C A/G A/T C/G A/G A/T A/G G/T A/G A/T C/T G/T
32	MICA*010:02 A5/A7	A G C A G C A G C A G C A G C A G C A A/G C A G C A A/G A/C A A/G C A/G G/T A/G A/G A A/C A/T G/T G/T C/G A/T
33	MICA*010:02 A5/A8	A G C A G C A G C A G C A G C A G C A A/G C A G C A G A/C A A C A/G G/T C/G A/G A/G A A/T A/G C/T A/C T
34	MICA*010:02 A5/A9	A G C A G C A G C A G C A G C A G C A A/G C A G C A G A/C A A/G C A/G A/T C/G A/G A/G A/C A/T G A/T A/C A/T
35	MICA*010:02 A5/A10	A G C A G C A G C A G C A G C A G C A A/G C A G C A G A/C A A/G C A/G G/T C/G A/G A A/C A/T G C/T A/C G/T

¹ All nucleotides are shown on antisense strand in the 5'-3' direction.

In addition to the STR repeat, the MICA*010:02 allele has a polymorphic position at cDNA nucleotide position 933 which can be determined by the unique patterns (pattern numbers 29-35).