

101.101-48/12 – including *Taq* polymerase  
101.101-48u/12u – without *Taq* polymerase

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“Instructions for Use” (IFU)

Lot No.: **5R8**

Lot-specific information

## **Olerup SSP<sup>®</sup> DR low resolution**

<b>Product number:</b>	101.101-48/12 – including <i>Taq</i> pol. 101.101-48u/12u – without <i>Taq</i> pol.
<b>Lot number:</b>	5R8
<b>Expiry date:</b>	2027-01-01
<b>Number of tests:</b>	48 tests – Product No. 101.101-48/48u 12 tests – Product No. 101.101-12/12u
<b>Number of wells per test:</b>	31 + 1
<b>Storage - pre-aliquoted primers:</b>	dark, between -15°C and -25°C
- PCR Master Mix:	between -15°C and -25°C
- Adhesive PCR seals	RT

### **This Product Description is only valid for Lot No. 5R8.**

Complete product documentation consists of generic Instructions for Use (IFU), lot specific Product Insert, Worksheet and Certificate.

### **CHANGES COMPARED TO THE PREVIOUS OLERUP SSP<sup>®</sup> DR LOW RESOLUTION LOT (7N0)**

The DR low resolution primer set, specificity and interpretation tables have been updated for the HLA-DRB1 alleles described since the previous *Olerup SSP<sup>®</sup>* DR low resolution lot was made (**Lot No. 7N0**). The kit design is based on IMGT/HLA database 3.50.0.

The primers of the wells detailed below have been exchanged, added or modified compared to the previous lot.

<b>Well</b>	<b>5'-primer</b>	<b>3'-primer</b>	<b>rationale</b>
1	Added, removed		5'-primer added for the DRB1*01:131N and DRB1*01:134 alleles. Excess 5'-primer removed.
29	-	Added	3'-primer added for the DRB3*02:131 alleles.
31	-	Added	3'-primer added for DRB5*02:33 allele.



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Well **32** contains Negative Control primer pairs, that will amplify the majority of the Olerup SSP<sup>®</sup> HLA Class I, DRB, DQB1, DPB1 and DQA1 amplicons as well as all the amplicons generated by the control primer pairs matching the human growth hormone gene.

HLA-specific PCR product sizes range from 75 to 200 base pairs.  
The PCR product generated by the positive control primer pair is 200 base pairs.

Length of PCR product	105	200	105	80	75	80	85
<b>5'-primer<sup>1</sup></b>	<b>164</b>	<b>340</b>	<b>440</b>	<b>45</b>	<b>45</b>	<b>43</b>	<b>36</b>
	5'-CAC <sup>3'</sup>	5'-Agg <sup>3'</sup>	5'-TTA <sup>3'</sup>	5'-Tgg <sup>3'</sup>	5'-Tgg <sup>3'</sup>	5'-Tgg <sup>3'</sup>	5'-TAC <sup>3'</sup>
							<b>36</b>
							5'-TAT <sup>3'</sup>
<b>3'-primer<sup>2</sup></b>	<b>231</b>	<b>2<sup>nd</sup> I</b>	<b>507</b>	<b>59</b>	<b>58</b>	<b>57</b>	<b>47</b>
	5'-TgC <sup>3'</sup>	5'-AAA <sup>3'</sup>	5'-TTg <sup>3'</sup>	5'-CTC <sup>3'</sup>	5'-ggC <sup>3'</sup>	5'-CTC <sup>3'</sup>	5'-ACA <sup>3'</sup>
							<b>48</b>
							5'-gCA <sup>3'</sup>
							<b>48</b>
							5'-gCC <sup>3'</sup>
							<b>52</b>
							5'-TgT <sup>3'</sup>
<b>A*</b>	<b>+</b>	<b>+</b>	<b>+</b>				
<b>B*</b>	<b>+</b>	<b>+</b>	<b>+</b>				
<b>C*</b>	<b>+</b>	<b>+</b>	<b>+</b>				
<b>DRB1</b>				<b>+</b>	<b>+</b>		
<b>DRB3</b>				<b>+</b>	<b>+</b>		
<b>DRB5</b>				<b>+</b>			
<b>DQB1</b>					<b>+</b>		
<b>DPB1</b>						<b>+</b>	
<b>DQA1</b>							<b>+</b>

<sup>1</sup>The nucleotide position for HLA class I genes and the codon for HLA class II genes, in the 2<sup>nd</sup> or 3<sup>rd</sup> exon, matching the specificity-determining 3'-end of the primer is given. Nucleotide and codon numbering as on the [www.ebi.ac.uk/imgt/hla](http://www.ebi.ac.uk/imgt/hla) web site. The sequence of the 3 terminal nucleotides of the primer is given.

<sup>2</sup>The nucleotide position for HLA class I genes and the codon for HLA class II genes, in the 2<sup>nd</sup> or 3<sup>rd</sup> exon or the 2<sup>nd</sup> intron, matching the specificity-determining 3'-end of the primer is given in the anti-sense direction. Nucleotide and codon numbering as on the [www.ebi.ac.uk/imgt/hla](http://www.ebi.ac.uk/imgt/hla) web site. The sequence of the 3 terminal nucleotides of the primer is given.



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## PRODUCT DESCRIPTION

### DR low resolution

#### CONTENT

The primer set contains 5'- and 3'-primers for grouping the DRB1\*01:01 to DRB1\*10:45 alleles into the corresponding serological groups DR1 to DR18 as well as primer pairs for recognizing the DRB3, DRB4 and DRB5 groups of alleles.

#### PLATE LAYOUT

Each test consists of 32 PCR reactions in a 32 well cut PCR plate.

**Note:** This lot was manufactured using white plastic trays.

1	2	3	4	5	6	7	8
9	10	11	12	13	14	15	16
17	18	19	20	21	22	23	24
25	26	27	28	29	30	31	NC

The 32 well cut PCR plate is marked with ‘DR low’ in silver/gray ink.

Well No. 1 is marked with the Lot No. ‘5R8’.

Wells 1 to 31 – DR low resolution primers.

Well 32 – Negative Control.

A faint row of numbers is seen between wells 1 and 2 or wells 7 and 8 of the PCR trays. These stem from the manufacture of the trays, and should be disregarded.

The PCR plates are covered with a PCR-compatible foil.

**Please note:** When removing each 32 well PCR plate, make sure that the remaining plates stay covered. Use a scalpel or a similar instrument to carefully cut the foil between the plates.

#### INTERPRETATION

Only HLA-DRB alleles will be amplified by the 31 wells of the DR low resolution primer set, **wells 1 to 31**. Thus, the interpretation of DR low resolution typings is not influenced by other HLA class II genes.

#### UNIQUELY IDENTIFIED ALLELES

All the HLA-DRB1, -DRB3, -DRB4 and -DRB5 alleles, i.e. **DRB1\*01:01 to DRB1\*10:45, DRB3\*01:01 to DRB3\*03:60, DRB4\*01:01 to DRB4\*03:01N, DRB5\*01:01 to DRB5\*02:36**, recognized by the HLA Nomenclature Committee in October 2022<sup>1,2</sup> will be amplified by the primers in the DR low resolution SSP kit. The HLA-DRB alleles will be grouped into their corresponding serological specificities<sup>3</sup>.

<sup>1</sup>DRB alleles listed on the IMGT/HLA web page 2022-October-12, release 3.50.0, [www.ebi.ac.uk/imgt/hla](http://www.ebi.ac.uk/imgt/hla).

<sup>2</sup>Alleles that have been deleted from or renamed in the official WHO HLA Nomenclature up to and including the last IMGT/HLA database release can be retrieved from web page <http://hla.alleles.org/alleles/deleted.html>.

<sup>3</sup>The following alleles give rise to identical amplification patterns with the DR low resolution primer set. These alleles can be separated by the respective high-resolution primer sets.

#### Alleles

DRB1\*03:126, DRB1\*13:193  
DRB1\*08:31, DRB1\*11:05

#### Alleles

DRB1\*11:293, DRB1\*13:45  
DRB1\*12:57, DRB3\*02:111



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Lot-specific information  
**SPECIFICITY TABLE**

**DR low resolution primer set**

**Specificities and sizes of the PCR products of the 31+1 primer mixes of the DR low resolution primer set**

Primer Mix	Size of spec. PCR product <sup>1</sup>	Size of control band <sup>2</sup>	DR serology <sup>3</sup>	Amplified HLA-DRB alleles <sup>4,6</sup>
<b>1<sup>6,8</sup></b>	210 bp, 235 bp, 260 bp	<b>515 bp</b>	1	*01:01:01:01-01:02:13, 01:04-01:38, 01:40N-01:98, 01:100-01:101, 01:103-01:111, 01:113-01:126, 01:128-01:139
<b>2</b>	200 bp	430 bp	1, 103	*01:03:01:01-01:03:05, 01:39N, 01:42, 01:61, 01:89, 01:99, 01:102, 01:112, 01:127
<b>3<sup>6,8</sup></b>	200 bp, 230 bp	430 bp	2, 15	*15:01:01:01-15:211, 16:66
<b>4<sup>12</sup></b>	210 bp	430 bp	11, 16	*11:30, 11:288, 12:57, 16:01:01:01-16:05:02, 16:07-16:73, <b>DRB3*02:111</b>
<b>5<sup>5,11</sup></b>	120 bp, 225 bp	<b>515 bp</b>	3, 11, 13, 17, 18	*03:01:01:01-03:11:01, 03:11:03-03:125, 03:127-03:203, 11:07:01-11:07:02, 11:27:02-11:27:03, 11:84:02-11:84:03, 11:103:01-11:103:02, 11:105, 11:107, 11:124:02-11:125, 11:136, 11:173, 13:33:01, 13:61:02, 13:94:01, 13:96:01, 14:38:02, 14:104, 14:111, 14:171, 15:25, 15:37:01, 15:100, 15:104:01
<b>6<sup>5,11</sup></b>	75 bp, 200 bp, 220 bp	430 bp	3, 6, 11, 13, 14, 17	*03:01:01:01-03:01:23, 03:01:25-03:01:41, 03:04:01-03:06, 03:08-03:11:01, 03:11:03-03:16, 03:18-03:20, 03:22-03:23, 03:25:01-03:26, 03:28, 03:30-03:31, 03:33-03:34, 03:36-03:37, 03:43-03:48, 03:50-03:52:02, 03:54-03:68N, 03:70-03:73, 03:75-03:86, 03:89, 03:91-03:93, 03:95-03:96, 03:98-03:100:02, 03:104, 03:106-03:114, 03:116-03:118, 03:121-03:130, 03:132-03:149, 03:151-03:153, 03:156N-03:166, 03:168-03:170, 03:172, 03:174N-03:175, 03:177, 03:180-03:184, 03:186-03:187, 03:189N, 03:191-03:203, 08:40, 08:92, 11:02:01:01-11:03:04, 11:11:01, 11:11:03, 11:14:01:01-11:14:02, 11:16:01:01-11:16:01:02, 11:20-11:21, 11:36, 11:40-11:41, 11:48, 11:59, 11:63:01-11:63:02, 11:65:01-11:65:02, 11:68, 11:70, 11:73, 11:76, 11:79-11:80, 11:83, 11:85-11:87, 11:93, 11:118:01-11:118:02, 11:122, 11:124:01-11:124:02, 11:127, 11:131-11:132, 11:135, 11:138-11:139, 11:142, 11:151, 11:153, 11:161, 11:168, 11:171, 11:176, 11:182, 11:184, 11:213, 11:229, 11:231, 11:233, 11:237, 11:241-11:242, 11:251, 11:256, 11:260, 11:270, 11:276, 11:290, 11:293, 11:301N, 12:73, 13:01:01:01-13:02:01:14, 13:02:02 <sup>?</sup> , 13:02:03-13:04, 13:08, 13:10, 13:15-13:17, 13:19-13:20:01:03, 13:22:01:01-13:24:01:03, 13:27:01-13:29:01:02, 13:31-13:41, 13:43, 13:45, 13:48, 13:51-13:54, 13:57, 13:59, 13:61:01-13:61:02, 13:63-13:66:02, 13:68-13:76, 13:78-13:81, 13:83-13:85, 13:87-13:99, 13:101-13:102, 13:104-13:107, 13:109, 13:110 <sup>?</sup> , 13:111-13:117:01:02, 13:120-13:131, 13:133, 13:135, 13:137N-13:145, 13:147-13:149, 13:151-13:153, 13:155, 13:159, 13:162, 13:165-13:166, 13:167 <sup>?</sup> , 13:168, 13:170-13:180,



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7 <sup>5</sup>	85 bp, 210 bp	430 bp	3, 6, 11, 13, 14, 1403, 18	*03:02:01:01-03:03, 03:27, 03:29, 03:38, 03:53, 03:74, 03:88, 03:90, 03:102-03:103, 03:115, 03:119, 03:126, 03:131, 03:154, 03:167, 03:176-03:177, 03:179, 11:13:01 <sup>w</sup> -11:13:02 <sup>w</sup> , 11:26, 11:34, 11:267, 13:15, 13:19, 13:26:01-13:26:02, 13:44, 13:53, 13:57, 13:85-13:86, 13:104, 13:193, 13:198, 13:206, 13:235, 14:02:01:01-14:03:02, 14:06:01-14:06:06, 14:09, 14:12:01-14:13, 14:17-14:21, 14:24, 14:27:01-14:27:02, 14:29-14:30, 14:32:01 <sup>w</sup> -14:32:02 <sup>w</sup> , 14:33, 14:40-14:41, 14:47-14:49, 14:51, 14:63, 14:65 <sup>w</sup> , 14:67, 14:77-14:78, 14:80-14:81, 14:83, 14:85, 14:89, 14:94, 14:98, 14:102, 14:106, 14:108-14:109, 14:115, 14:119, 14:121, 14:135, 14:146, 14:154, 14:156, 14:159-14:160, 14:165, 14:170, 14:174, 14:176-14:177, 14:179, 14:181, 14:183, 14:194-14:195N, 14:198, 14:200, 14:209, 14:212, 14:218, 14:221-14:223, 14:226, 14:239, 14:242
8 <sup>5</sup>	100 bp, 175 bp	430 bp	3, 4	*04:01:01:01-04:05:11, 04:05:13-04:353
9 <sup>8,12,13</sup>	200 bp, 240 bp	430 bp	1, 7	*01:13, 03:54, 07:01:01:01-07:01:01:02, 07:01:01:04-07:01:30, 07:03-07:141, 08:101, 11:177, 13:92, 15:24, <b>DRB3*01:99, DRB3*02:87, DRB4*01:66</b>
10 <sup>5</sup>	85 bp, 120 bp, 215 bp, 250 bp	515 bp	7, 8, 14	*07:06, 08:01:01:01-08:01:02, 08:01:04-08:19, 08:21-08:30:03, 08:32-08:56, 08:58-08:66, 08:68:01-08:79, 08:81-08:97, 08:99-08:117, 11:67, 11:193:01-11:193:02, 12:16:01-12:16:03, 12:22, 12:39:01-12:39:02, 13:171:01, 13:197, 14:15, 14:68:01-14:68:02, 14:93
11 <sup>5,12,14</sup>	85 bp, 100 bp, 135 bp, 160 bp, 190 bp	430 bp	3, 9, 11	*03:08, 03:65, 03:140, 09:01:02:01-09:52N, 11:07:01-11:07:02, 11:103:01-11:103:02, 11:105, 11:107, 11:125, 11:173, <b>DRB3*01:42, DRB5*02:31, DRB5*02:34</b>
12 <sup>5,6</sup>	70 bp, 175 bp	430 bp	10, 11, 13	*03:76, 03:125, 03:174N, 10:01:01:01, 10:01:01:03-10:45, 11:59, 11:80, 11:83, 11:87, 11:135, 11:142, 11:182, 13:27:01-13:27:02, 13:41, 13:71, 13:129, 13:176, 13:277, 13:326, 14:179
13 <sup>5</sup>	100 bp, 175 bp	430 bp	3, 8, 11, 13, 14	*03:08, 03:65, 03:140, 08:31, 08:41, 08:63, 08:75, 11:01:01:01, 11:01:01:03-11:11:01, 11:11:03-11:70, 11:72-11:263, 11:265-11:292, 11:294N-11:307
14 <sup>5</sup>	90 bp, 110 bp	430 bp	12, 14	*08:32, 08:53, 08:87, 12:01:01:01-12:56, 12:58-12:100, 14:52
15 <sup>12</sup>	220 bp	430 bp	6, 8, 11, 13, 14, 1403	*03:76, 03:125, 03:174N, 08:20-08:21, 11:01:01:01, 11:01:01:03-11:01:27, 11:01:28 <sup>?</sup> , 11:01:29-11:04:22, 11:06:01-11:06:03, 11:08:01-11:11:01, 11:11:03-11:12:03, 11:14:01:01-11:16:01:02, 11:18-11:21, 11:23:01-11:25, 11:27:01-11:33, 11:35-11:51, 11:54:01-11:54:02, 11:56-11:66:02, 11:68, 11:70, 11:72-11:81, 11:83-11:88, 11:90-11:97, 11:99-11:102:02, 11:106, 11:108-11:124:02,



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Lot-specific information

<b>27<sup>8</sup></b>	145 bp, 210 bp, 235 bp	<b>515 bp</b>	4, 6, 8, 11, 13, 14, 1403, 1404	*03:157, 08:09:01-08:09:02, 08:20-08:21, 08:35, 11:03:04, 11:04:17, 11:13:01-11:13:02, 11:17, 11:23:01-11:23:02, 11:25, 11:45, 11:52, 11:55, 11:64, 11:89, 11:119, 11:149, 11:159, 11:202, 11:264, 11:266, 11:283, 13:01:27, 13:02:21, 13:08, 13:13, 13:18, 13:47, 13:55, 13:119, 13:144, 13:146, 13:154, 13:156, 13:158:01-13:158:02, 13:164, 13:232, 13:286, 13:331, 14:01:01-14:01:05, 14:02:02 <sup>?</sup> -14:02:03 <sup>?</sup> , 14:02:06 <sup>?</sup> , 14:03:01-14:05:05, 14:07:01-14:08, 14:10:01:01- 14:12:02, 14:14-14:16, 14:18, 14:22 <sup>?</sup> , 14:23:01:01-14:23:04, 14:25:01 <sup>?</sup> -14:25:02 <sup>?</sup> , 14:26-14:28, 14:29 <sup>?</sup> -14:30 <sup>?</sup> , 14:31- 14:32:02, 14:32:03 <sup>?</sup> -14:33 <sup>?</sup> , 14:34-14:36, 14:37 <sup>?</sup> , 14:38:01- 14:40, 14:41 <sup>?</sup> , 14:42-14:45, 14:48 <sup>?</sup> -14:49 <sup>?</sup> , 14:50:01-14:50:02, 14:51 <sup>?</sup> -14:52 <sup>?</sup> , 14:54:01:01-14:65, 14:67-14:68:02, 14:69 <sup>?</sup> , 14:70-14:72, 14:73 <sup>?</sup> -14:74 <sup>?</sup> , 14:75, 14:76 <sup>?</sup> , 14:77-14:78, 14:79 <sup>?</sup> -14:80 <sup>?</sup> , 14:81-14:82, 14:83 <sup>?</sup> , 14:84-14:93, 14:94 <sup>?</sup> , 14:95-14:97, 14:98 <sup>?</sup> , 14:99-14:103, 14:104 <sup>?</sup> -14:109 <sup>?</sup> , 14:110- 14:118, 14:119 <sup>?</sup> , 14:120, 14:121 <sup>?</sup> , 14:122-14:127:02, 14:128 <sup>?</sup> , 14:129-14:145, 14:146 <sup>?</sup> , 14:147-14:158, 14:159 <sup>?</sup> , 14:160- 14:164, 14:165 <sup>?</sup> , 14:166N-14:169, 14:170 <sup>?</sup> , 14:171-14:175, 14:176 <sup>?</sup> , 14:178, 14:179 <sup>?</sup> , 14:180-14:182, 14:183 <sup>?</sup> , 14:184- 14:193, 14:196-14:197N, 14:199, 14:201-14:202, 14:203 <sup>?</sup> , 14:204-14:208, 14:210Q-14:211, 14:213-14:220, 14:222N- 14:225, 14:227-14:241, 14:243-14:247
<b>28<sup>6,12</sup></b>	140 bp, 170 bp	<b>515 bp</b>	6, 13, 14	*03:76, 03:126, 03:174N, 03:177, 04:211, 04:230, 12:66 <sup>w</sup> , 13:10, 13:85-13:86, 13:120, 13:170, 13:176, 13:178, 13:193, 13:196, 13:216, 14:02:01:01-14:02:09, 14:06:01-14:06:06, 14:09, 14:13, 14:17, 14:19-14:21, 14:29-14:30, 14:33, 14:41, 14:46-14:49, 14:51-14:52, 14:80, 14:83, 14:94, 14:106, 14:108-14:109, 14:121, 14:159, 14:165, 14:170, 14:176- 14:177, 14:179, 14:183, 14:194-14:195N, 14:198, 14:200, 14:209, 14:212, 14:242, <b>DRB3*02:27, DRB3*02:58</b>
<b>29<sup>5,11,12,15</sup></b>	80 bp, 110 bp, 160 bp, 190 bp, 240 bp	<b>515 bp</b>	52	*12:05, 12:15, 12:57, 14:141, <b>DRB3*01:01:02:01-01:110, DRB3*02:01-02:185, DRB3*03:01:01:01-03:21, DRB3*03:23-03:60</b>
<b>30<sup>9,13</sup></b>	130 bp, 215 bp	430 bp	53	*01:139, 10:19, 14:217, 15:141, <b>DRB4*01:01:01:01, DRB4*01:01:01:03-01:164, DRB4*02:01N, DRB4*03:01N</b>
<b>31<sup>10, 14</sup></b>	175 bp, 220 bp	430 bp	51	<b>DRB5*01:01:01:01-01:129, DRB5*02:02:01-02:36</b>
<b>32<sup>16</sup></b>	-	-		<b>Negative control</b>

<sup>1</sup>Alleles are assigned by the presence of specific PCR product(s). However, the sizes of the specific PCR products may be helpful in the interpretation of DR low resolution SSP subtypings.

When the primers in a primer mix can give rise to HLA-specific PCR products of more than one length this is indicated if the size difference is more than 20 base pairs. Size differences of 20 base pairs or less are not given. For high resolution SSP kits, the alleles listed are specified according to amplicon length.

Nonspecific amplifications, i.e. a ladder or a smear of bands, may sometimes be seen. GC-rich primers have a higher tendency of giving rise to nonspecific amplifications than other primers, e.g. the primers in wells 3, 18, 19 and 20.

PCR fragments longer than the control bands may sometimes be observed. Such bands should be disregarded and do not influence the interpretation of the SSP typings.

PCR fragments migrating faster than the control bands, but slower than a 400 bp fragment may be seen in some gel read-outs. Such bands can be disregarded and do not influence the interpretation of the SSP typings.



**0197**

For *In Vitro* Diagnostic Use

MA123 v02 SSP PI Template

Date: January 2023, Rev. No: 00

**101.101-48/12 – including *Taq* polymerase**  
**101.101-48u/12u – without *Taq* polymerase**

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**Lot No.: 5R8**

**Lot-specific information**

Some primers may give rise to primer oligomer artifacts. Sometimes this phenomenon is an inherent feature of the primer pair(s) of a primer mix. More often it is due to other factors such as too low amount of DNA in the PCR reactions, taking too long time in setting up the PCR reactions, working at elevated room temperature or using thermal cyclers that are not pre-heated.

<sup>2</sup>The internal positive control primer pairs amplify segments of the human growth hormone gene. The internal positive control bands are 430 or 515 base pairs respectively, well distribution as outlined in the table. Well number 1 contains the longer, 515 bp, internal positive control band. The well distribution of the internal controls can help in orientation of the kit on gel photo, as well as allow for kit identification. In the presence of a specific amplification the intensity of the control band often decreases.

<sup>3</sup>The serological reactivity of all DRB alleles is not known. In this table we use the information in the HLA Dictionary 2004 on the [www.ebi.ac.uk/imgt/hla](http://www.ebi.ac.uk/imgt/hla) web site and the expert-assigned serological grouping in Tissue Antigens (2009) 73:95-170.

<sup>4</sup>For several DRB alleles 1<sup>st</sup> and/or 3<sup>rd</sup> exon(s) and beyond, as well as intron nucleotide sequences, are not available. In these instances it is not known whether some of the primers of the SSP sets are completely matched with the target sequences or not. Assumption is made that unknown sequences in these regions are conserved within allelic groups.

<sup>5</sup>HLA-specific PCR products shorter than 125 base pairs have a lower intensity and are less sharp than longer PCR products.

<sup>6</sup>Primer mixes 1, 3, 12, 16, 19 and 28 have a tendency to giving rise to primer oligomer formation.

<sup>7</sup>Primer mix 19 has a tendency of primer oligomer formation and also has an intense primer cloud due to the high number of primers present in the primer mix.

<sup>8</sup>Primer mixes 1, 3, 9 and 27 may have tendencies of unspecific amplifications.

<sup>9</sup>The DRB4\*01:03:01:02N, DRB4\*01:03:01:13N and DRB4\*01:14N alleles are amplified by the primer pairs in primer mixes 18 and 30, whereas the DRB4\*02:01N and DRB4\*03:01N null alleles are only amplified by the primer pairs in primer mix 30.

<sup>10</sup>The DRB5\*01:08:01N-01:08:02N and DRB5\*02:26N alleles are amplified by the primer pairs in primer mix 24 in addition to primer mix 31.

<sup>11</sup>Due to sharing of sequence motifs in codon 38 and 47, DRB3\*01:14 will also be amplified in primer mixes 5, 6 and 17 and the DRB3\*01:23 and DRB3\*02:32 alleles are amplified in mix 5, in addition to primer mix 29.

<sup>12</sup>Due to sharing of sequence motifs, some DRB3 alleles are amplified by primer mixes 4, 9, 11, 15, 16, 20, 25 and 28 in addition to primer mix 29.

<sup>13</sup>Due to sharing of sequence motifs, some DRB4 alleles are amplified by primer mixes 9 and 20 in addition to primer mix 30.

<sup>14</sup>Due to sharing of sequence motifs, some DRB5 alleles are amplified by primer mix 11 in addition to primer mix 31.

<sup>15</sup>In primer mix 29, the specific PCR product of 240 base pairs may be difficult to distinguish from the internal control band.

<sup>16</sup>Primer mix 32 contains a negative control, which will amplify the majority of HLA amplicons as well as the amplicons generated by the control primer pairs matching the human growth hormone gene. HLA-specific PCR product sizes range from 75 to 200 base pairs and the PCR product generated by the HGH positive control primer pair is 200 base pairs.

Abbreviations

w: might be weakly amplified.

?: nucleotide sequence information not available for the primer matching sequence.



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Lot No.: 5R8

Lot-specific information

### PRIMER SPECIFICATION

Well No.	1	2	3	4	5	6	7	8	9	10	11	12
Length of spec.	210	200	200	210	120	75	85	100	200	85	85	70
PCR product	235		230		225	200	210	175	240	120	100	175
	260					220				215	135	
										250	160	
											190	
Length of int.	515	430	430	430	515	430	430	430	430	515	430	430
pos. control <sup>1</sup>												
5'-primer(s) <sup>2</sup>	11(119) 5'-gCT <sup>3'</sup>	14(129) 5'-gAA <sup>3'</sup>	12(121) 5'-CTg <sup>3'</sup>	11(119) 5'-gCT <sup>3'</sup>	13(125) 5'-gTC <sup>3'</sup>	12(122) 5'-TAC <sup>3'</sup>	13(125) 5'-gTC <sup>3'</sup>	13(124) 5'-AAC <sup>3'</sup>	11(118) 5'-AgA <sup>3'</sup>	16(133) 5'-gTT <sup>3'</sup>	26(165) 5'-TAT <sup>3'</sup>	26(164) 5'-gTA <sup>3'</sup>
		14(129) 5'-gAA <sup>3'</sup>	13(126) 5'-Agg <sup>3'</sup>	13(126) 5'-Agg <sup>3'</sup>	47(227) 5'-gTT <sup>3'</sup>	13(125) 5'-gTC <sup>3'</sup>		13(125) 5'-ATA <sup>3'</sup>	14(127) 5'-ATA <sup>3'</sup>	16(133) 5'-gTT <sup>3'</sup>	37(196) 5'-AgA <sup>3'</sup>	31(178) 5'-gCg <sup>3'</sup>
			13(126) 5'-AAg <sup>3'</sup>	13(126) 5'-AAg <sup>3'</sup>		16(133) 5'-gTT <sup>3'</sup>		13(125) 5'-gTC <sup>3'</sup>	14(127) 5'-ATA <sup>3'</sup>	16(133) 5'-gCT <sup>3'</sup>	58(261) 5'-gAg <sup>3'</sup>	
			13(126) 5'-AgA <sup>3'</sup>							14(127) 5'-gTA <sup>3'</sup>	60(265) 5'-AgT <sup>3'</sup>	
									25(161) 5'-gCA <sup>3'</sup>			
3'-primer(s) <sup>3</sup>	67(286) 5'-gAg <sup>3'</sup>	67(286) 5'-gAT <sup>3'</sup>	67(286) 5'-gAT <sup>3'</sup>	67(286) 5'-gAA <sup>3'</sup>	73(305) 5'-ggC <sup>3'</sup>	26(164) 5'-ggT <sup>3'</sup>	28(171) 5'-CTC <sup>3'</sup>	33(184) 5'-gTg <sup>3'</sup>	78(319) 5'-CAC <sup>3'</sup>	74(307) 5'-CAg <sup>3'</sup>	57(257) 5'-CgA <sup>3'</sup>	38(200) 5'-gCg <sup>3'</sup>
	67(286) 5'-gAg <sup>3'</sup>	67(286) 5'-gAA <sup>3'</sup>	67(286) 5'-gAT <sup>3'</sup>	67(286) 5'-gAg <sup>3'</sup>	73(305) 5'-ggC <sup>3'</sup>	67(286) 5'-gAT <sup>3'</sup>	70(295) 5'-CTg <sup>3'</sup>	58(260) 5'-Cgg <sup>3'</sup>	78(319) 5'-gTA <sup>3'</sup>	86(344) 5'-CAC <sup>3'</sup>	73(305) 5'-ggC <sup>3'</sup>	72(303) 5'-gCA <sup>3'</sup>
	67(286) 5'-gAT <sup>3'</sup>	67(286) 5'-gAA <sup>3'</sup>	67(286) 5'-gAT <sup>3'</sup>	67(286) 5'-gAg <sup>3'</sup>	73(305) 5'-ggC <sup>3'</sup>	71(299) 5'-gCT <sup>3'</sup>			78(319) 5'-CAA <sup>3'</sup>		78(319) 5'-CAC <sup>3'</sup>	74(307) 5'-CgC <sup>3'</sup>
	70(297) 5'-CTg <sup>3'</sup>		70(295) 5'-CTg <sup>3'</sup>	70(296) 5'-TgT <sup>3'</sup>	73(305) 5'-ggC <sup>3'</sup>				78(319) 5'-CgC <sup>3'</sup>			
	71(299) 5'-gCg <sup>3'</sup>		70(295) 5'-Tg <sup>3'</sup>	72(302) 5'-Cgg <sup>3'</sup>	73(306) 5'-Tgg <sup>3'</sup>							
	73(305) 5'-ggC <sup>3'</sup>		70(296) 5'-TCC <sup>3'</sup>		74(308) 5'-CCC <sup>3'</sup>							
	77(317) 5'-AgT <sup>3'</sup>		71(299) 5'-gCg <sup>3'</sup>		75(310) 5'-CAA <sup>3'</sup>							
	86(344) 5'-CCA <sup>3'</sup>		71(299) 5'-gCT <sup>3'</sup>		77(317) 5'-AgT <sup>3'</sup>							
			72(301) 5'-Cg <sup>3'</sup>									
			73(305) 5'-ggC <sup>3'</sup>									
			77(317) 5'-AgT <sup>3'</sup>									
Well No.	1	2	3	4	5	6	7	8	9	10	11	12



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For *In Vitro* Diagnostic Use

MA123 v02 SSP PI Template

Date: January 2023, Rev. No: 00

101.101-48/12 – including *Taq* polymerase  
101.101-48u/12u – without *Taq* polymerase

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Lot No.: **5R8**

Lot-specific information

Well No.	13	14	15	16	17	18	19	20	21	22	23	24
Length of spec.	100	90	220	195	175	75	110	110	170	75	135	170
PCR product	175	110		225		100	145	150		175		195
						140	170	180		265		
						170		220				
Length of int.	430	430	430	430	430	430	430	430	430	515	430	430
pos. control <sup>1</sup>												
5'-primer(s) <sup>2</sup>	13(125) 5'-gTC <sup>3'</sup>	13(124) 5'-Cgg <sup>3'</sup>	10(116) 5'-gCT <sup>3'</sup>	10(116) 5'-gCT <sup>3'</sup>	13(125) 5'-gTC <sup>3'</sup>	5(101) 5'-CAA <sup>3'</sup>	26(164) 5'-gTA <sup>3'</sup>	13(125) 5'-gTC <sup>3'</sup>	13(125) 5'-ggg <sup>3'</sup>	12(122) 5'-TAg <sup>3'</sup>	16(133) 5'-gTT <sup>3'</sup>	13(125) 5'-gTC <sup>3'</sup>
	16(133) 5'-gTC <sup>3'</sup>	16(133) 5'-gTT <sup>3'</sup>	12(122) 5'-TAT <sup>3'</sup>	12(122) 5'-TAT <sup>3'</sup>		37(197) 5'-gTT <sup>3'</sup>	34(189) 5'-CAg <sup>3'</sup>	34(189) 5'-CAg <sup>3'</sup>	16(133) 5'-gCT <sup>3'</sup>	74(308) 5'-CCT <sup>3'</sup>		108(409) 5'-AgA <sup>3'</sup>
	38(200) 5'-CgT <sup>3'</sup>		13(125) 5'-gTC <sup>3'</sup>	12(123) 5'-ACA <sup>3'</sup>		37(197) 5'-gTA <sup>3'</sup>	34(189) 5'-CAg <sup>3'</sup>	37(196) 5'-AgC <sup>3'</sup>	16(133) 5'-gTT <sup>3'</sup>			
				13(125) 5'-gTC <sup>3'</sup>			34(189) 5'-CCg <sup>3'</sup>		16(133) 5'-gTT <sup>3'</sup>			
				13(125) 5'-gTg <sup>3'</sup>								
				16(133) 5'-gTC <sup>3'</sup>								
				16(133) 5'-gTT <sup>3'</sup>								
3'-primer(s) <sup>3</sup>	58(260) 5'-CCT <sup>3'</sup>	28(171) 5'-CTC <sup>3'</sup>	70(295) 5'-gTC <sup>3'</sup>	67(286) 5'-gAA <sup>3'</sup>	57(257) 5'-CAT <sup>3'</sup>	48(230) 5'-CCT <sup>3'</sup>	57(257) 5'-CAg <sup>3'</sup>	57(257) 5'-CAg <sup>3'</sup>	57(256) 5'-gCT <sup>3'</sup>	57(256) 5'-gCT <sup>3'</sup>	47(227) 5'-ggA <sup>3'</sup>	57(256) 5'-gCT <sup>3'</sup>
	58(260) 5'-CCT <sup>3'</sup>	30(175) 5'-gTg <sup>3'</sup>	71(299) 5'-gCT <sup>3'</sup>	71(298) 5'-CTC <sup>3'</sup>	58(260) 5'-Cgg <sup>3'</sup>	57(257) 5'-CAg <sup>3'</sup>	70(295) 5'-CTg <sup>3'</sup>	60(265) 5'-gTg <sup>3'</sup>	57(257) 5'-CAT <sup>3'</sup>	86(344) 5'-CCA <sup>3'</sup>		160(565) 5'-CAT <sup>3'</sup>
	58(260) 5'-CCT <sup>3'</sup>	38(199) 5'-CAg <sup>3'</sup>	71(299) 5'-ACT <sup>3'</sup>	71(298) 5'-CgC <sup>3'</sup>	58(260) 5'-CAg <sup>3'</sup>	71(298) 5'-CgC <sup>3'</sup>	70(296) 5'-TCC <sup>3'</sup>	70(296) 5'-TCC <sup>3'</sup>	57(257) 5'-CAT <sup>3'</sup>	86(344) 5'-CAA <sup>3'</sup>		
	58(261) 5'-TCT <sup>3'</sup>		74(307) 5'-CgT <sup>3'</sup>					74(307) 5'-CAg <sup>3'</sup>				
			78(319) 5'-CAC <sup>3'</sup>									
Well No.	13	14	15	16	17	18	19	20	21	22	23	24

Well No.	25	26	27	28	29	30	31
Length of spec.	150	145	145	140	80	130	175
PCR product			210	170	110	215	220
			235		160		
					190		
					240		
Length of int.	430	430	515	515	515	430	430
pos. control <sup>1</sup>							
5'-primer(s) <sup>2</sup>	34(189) 5'-CAg <sup>3'</sup>	13(125) 5'-gTC <sup>3'</sup>	13(125) 5'-gTC <sup>3'</sup>	28(171) 5'-gAg <sup>3'</sup>	10(116) 5'-gCT <sup>3'</sup>	28(170) 5'-gAT <sup>3'</sup>	9(112) 5'-TgC <sup>3'</sup>
	34(189) 5'-CAg <sup>3'</sup>		37(197) 5'-gTT <sup>3'</sup>	37(196) 5'-AgA <sup>3'</sup>	10(116) 5'-gCT <sup>3'</sup>	28(170) 5'-gAg <sup>3'</sup>	13(125) 5'-gTA <sup>3'</sup>
			114(429) 5'-CTg <sup>3'</sup>		11(119) 5'-gCT <sup>3'</sup>	105(401) 5'-AAA <sup>3'</sup>	
					38(199) 5'-TCC <sup>3'</sup>		
3'-primer(s) <sup>3</sup>	71(298) 5'-CTC <sup>3'</sup>	47(227) 5'-ggA <sup>3'</sup>	70(296) 5'-TCC <sup>3'</sup>	70(295) 5'-CTg <sup>3'</sup>	51(239) 5'-CCC <sup>3'</sup>	81(328) 5'-gTA <sup>3'</sup>	57(256) 5'-gTC <sup>3'</sup>
		48(229) 5'-CCA <sup>3'</sup>	74(307) 5'-CAg <sup>3'</sup>	71(298) 5'-CTT <sup>3'</sup>	57(256) 5'-gCT <sup>3'</sup>	87(346) 5'-CTC <sup>3'</sup>	57(256) 5'-gCT <sup>3'</sup>
			181(630) 5'-CTT <sup>3'</sup>		60(266) 5'-Agg <sup>3'</sup>	87(346) 5'-CTT <sup>3'</sup>	57(258) 5'-gCg <sup>3'</sup>
					77(317) 5'-AAT <sup>3'</sup>	135(490) 5'-gCT <sup>3'</sup>	57(258) 5'-gCT <sup>3'</sup>
							58(260) 5'-CCT <sup>3'</sup>
							70(296) 5'-TgT <sup>3'</sup>
Well No.	25	26	27	28	29	30	31



0197

For *In Vitro* Diagnostic Use  
MA123 v02 SSP PI Template  
Date: January 2023, Rev. No: 00

101.101-48/12 – including *Taq* polymerase  
101.101-48u/12u – without *Taq* polymerase

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Lot No.: **5R8**

#### Lot-specific information

<sup>1</sup>The internal positive control primer pairs amplify segments of the human growth hormone gene. The internal positive control bands are 430 or 515 base pairs respectively, well distribution as outlined in the table. Well number 1 contains the longer, 515 bp, internal positive control band. The well distribution of the internal controls can help in orientation of the kit on gel photo, as well as allow for kit identification. In the presence of a specific amplification the intensity of the control band often decreases.

<sup>2</sup>The nucleotide position matching the specificity-determining 3'-end of the primer is given. Nucleotide numbering as on the [www.ebi.ac.uk/imgt/hla](http://www.ebi.ac.uk/imgt/hla) web site. The sequence of the 3 terminal nucleotides of the primer is given.

<sup>3</sup>The nucleotide position matching the specificity-determining 3'-end of the primer is given in the anti-sense direction. Nucleotide numbering as on the [www.ebi.ac.uk/imgt/hla](http://www.ebi.ac.uk/imgt/hla) web site. The sequence of the 3 terminal nucleotides of the primer is given.



0197

For *In Vitro* Diagnostic Use  
MA123 v02 SSP PI Template  
Date: January 2023, Rev. No: 00

101.101-48/12 – including *Taq* polymerase  
101.101-48u/12u – without *Taq* polymerase

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Lot No.: **5R8**

Lot-specific information

CELL LINE VALIDATION SHEET																				
DR low resolution primer set <sup>3</sup>																				
				Well <sup>2</sup>																
				1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	
				Prod. No.:	202243801	202243802	202243803	202243804	202243805	202243806	202243807	202243808	202137109	202243810	202243811	202134312	202243813	202243814	202243815	202243816
IHC cell line <sup>1</sup>		DRB1																		
1	9001 SA	*01:01		+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2	9280 LK707	*15:02	*04:05	-	-	+	-	-	-	-	-	+	-	-	-	-	-	-	-	-
3	9011 E4181324	*15:02		-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4	9275 GU373	*03:01		-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	-
5	9009 KAS011	*16:01		-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-
6	9353 SM	*04:07	*08:03	-	-	-	-	-	-	-	-	+	-	+	-	-	-	-	-	-
7	9020 QBL	*03:01		-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	-
8	9025 DEU	*04:01		-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-
9	9026 YAR	*04:02		-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-
10	9107 LKT3	*04:05		-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-
11	9051 PITOUT	*07:01		-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-
12	9052 DBB	*07:01		-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-
13	9004 JESTHOM	*01:01		+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
14	9071 OLGA	*08:02		-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	+
15	9075 DKB	*09:01		-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-
16	9037 SWEIG007	*11:01		-	-	-	-	-	-	-	-	-	-	-	-	+	-	+	+	+
17	9282 CTM3953540	*03:01	*13:01	-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	+	+
18	9257 32367	*09:01	*11:01	-	-	-	-	-	-	-	-	-	-	+	-	+	-	+	+	+
19	9038 BM16	*12:01		-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
20	9059 SLE005	*13:02		-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	+	+
21	9064 AMALA	*14:02		-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-
22	9056 KOSE	*13:02	*14:54	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	+	+
23	9124 IHL	*08:03	*14:14	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-
24	9035 JBUSH	*11:01		-	-	-	-	-	-	-	-	-	-	-	-	+	-	+	+	+
25	9049 IBW9	*07:01		-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-
26	9285 WT49	*03:01		-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	-
27	9191 CH1007	*04:05	*10:01	-	-	-	-	-	-	-	-	+	-	+	-	+	-	-	-	-
28	9320 BEL5GB	*04:16	*07:01	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	-
29	9050 MOU	*07:01		-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-
30	9021 RSH	*03:02		-	-	-	-	+	-	+	-	-	-	-	-	-	-	-	-	-
31	9019 DUCAF	*03:01		-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	-
32	9297 HAG	*13:03		-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	+	-
33	9098 MT14B	*04:04		-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-
34	9104 DHIF	*11:01		-	-	-	-	-	-	-	-	-	-	-	-	+	-	+	+	+
35	9302 SSTO	*04:03		-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-
36	9024 KT17	*04:03	*04:06	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-
37	9065 HHKB	*13:01		-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	+	+
38	9099 LZL	*14:02		-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-
39	9315 CML	*03:01	*04:01	-	-	-	-	+	+	-	+	-	-	-	-	-	-	-	-	-
40	9134 WHONP199	*07:01	*09:01	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	-	-
41	9055 H0301	*13:02		-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	+	+
42	9066 TAB089	*08:03		-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-
43	9076 T7526	*09:01		-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-
44	9057 TEM	*14:01		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
45	9239 SHJO	*07:01		-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-
46	9013 SCHU	*15:01		-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-
47	9045 TUBO	*11:04	*12:01	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+
48	9303 TER-ND	*01:03		-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-



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101.101-48/12 – including *Taq* polymerase  
101.101-48u/12u – without *Taq* polymerase

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Lot No.: **5R8**

Lot-specific information

CELL LINE VALIDATION SHEET																			
DR low resolution primer set <sup>3</sup>																			
			Prod. No.:	Well <sup>2</sup>															
				17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	
	IHWC cell line <sup>1</sup>	DRB1		202137117	202243818	202243819	202243820	202137121	202137122	202137123	202137124	202137125	202137126	202137127	202137128	202247129	202243830	202243831	
1	9001 SA	*01:01		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2	9280 LK707	*15:02	*04:05	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+
3	9011 E4181324	*15:02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
4	9275 GU373	*03:01		+	-	-	-	-	-	-	-	-	+	-	-	+	-	-	-
5	9009 KAS011	*16:01		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
6	9353 SM	*04:07	*08:03	-	-	-	-	+	-	-	-	-	-	-	-	-	-	+	-
7	9020 QBL	*03:01		+	-	-	-	-	-	-	-	-	+	-	-	+	-	-	-
8	9025 DEU	*04:01		-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
9	9026 YAR	*04:02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
10	9107 LKT3	*04:05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
11	9051 PITOUT	*07:01		-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
12	9052 DBB	*07:01		-	+	-	-	-	-	-	-	-	-	-	-	-	-	+	-
13	9004 JESTHOM	*01:01		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
14	9071 OLGA	*08:02		-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-
15	9075 DKB	*09:01		-	-	+	-	-	-	-	-	-	-	-	-	-	-	+	-
16	9037 SWEIG007	*11:01		-	-	-	-	-	-	-	-	-	+	-	-	+	-	-	-
17	9282 CTM3953540	*03:01	*13:01	+	-	-	-	-	-	-	-	+	+	-	-	+	-	-	-
18	9257 32367	*09:01	*11:01	-	-	+	-	-	-	-	-	-	+	-	-	+	+	-	-
19	9038 BM16	*12:01		-	-	-	-	-	-	+	-	-	-	-	-	+	-	-	-
20	9059 SLE005	*13:02		+	-	-	-	-	-	-	-	+	+	-	-	+	-	-	-
21	9064 AMALA	*14:02		+	-	+	-	-	-	-	-	-	-	-	+	+	-	-	-
22	9056 KOSE	*13:02	*14:54	+	+	+	+	-	-	-	-	+	+	+	-	+	-	-	-
23	9124 IHL	*08:03	*14:14	+	-	+	+	+	-	-	-	-	-	+	-	+	-	-	-
24	9035 JBUSH	*11:01		-	-	-	-	-	-	-	-	-	+	-	-	+	-	-	-
25	9049 IBW9	*07:01		-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
26	9285 WT49	*03:01		+	-	-	-	-	-	-	-	-	+	-	-	+	-	-	-
27	9191 CH1007	*04:05	*10:01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
28	9320 BEL5GB	*04:16	*07:01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
29	9050 MOU	*07:01		-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
30	9021 RSH	*03:02		+	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
31	9019 DUCAF	*03:01		+	-	-	-	-	-	-	-	-	+	-	-	+	-	-	-
32	9297 HAG	*13:03		+	-	-	-	-	-	-	+	-	-	-	-	+	-	-	-
33	9098 MT14B	*04:04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
34	9104 DHIF	*11:01		-	-	-	-	-	-	-	-	-	+	-	-	+	-	-	-
35	9302 SSTO	*04:03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
36	9024 KT17	*04:03	*04:06	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
37	9065 HHKB	*13:01		+	-	-	-	-	-	-	-	+	+	-	-	+	-	-	-
38	9099 LZL	*14:02		+	-	+	-	-	-	-	-	-	-	-	+	+	-	-	-
39	9315 CML	*03:01	*04:01	+	-	-	-	-	-	-	-	-	+	-	-	+	+	-	-
40	9134 WHONP199	*07:01	*09:01	-	-	+	-	-	-	-	-	-	-	-	-	-	-	+	-
41	9055 H0301	*13:02		+	-	-	-	-	-	-	-	+	+	-	-	+	-	-	-
42	9066 TAB089	*08:03		-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-
43	9076 T7526	*09:01		-	-	+	-	-	-	-	-	-	-	-	-	-	-	+	-
44	9057 TEM	*14:01		-	+	+	+	-	-	-	-	-	-	+	-	+	-	-	-
45	9239 SHJO	*07:01		-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
46	9013 SCHU	*15:01		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
47	9045 TUBO	*11:04	*12:01	-	-	-	-	-	-	+	-	-	+	-	-	+	-	-	-
48	9303 TER-ND	*01:03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-



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For *In Vitro* Diagnostic Use  
MA123 v02 SSP PI Template  
Date: January 2023, Rev. No: 00



101.101-48/12 – including *Taq* polymerase  
101.101-48u/12u – without *Taq* polymerase

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“Instructions for Use” (IFU)

Lot No.: **5R8**

**Lot-specific information**

<sup>1</sup>The provided cell line HLA specificities are retrieved from the <http://www.ihwg.org/hla> web site. The specificity of an individual cell line may thus be subject to change.

<sup>2</sup>The DRB4\*01:03:01:02N allele is amplified by primer mix 18 in the 9052 (DBB) cell line.

<sup>3</sup>The specificity of each primer solution in the kit has been tested against 48 well characterized cell line DNAs and where applicable, additional cell line DNAs.

One or more 5'- and 3'-primers in primer solutions 11, 15, 18 and 27 were tested by separately adding one 3'-primer and one 5'-primer respectively.

One or more 5'-primers in primer solutions 4, 6, 12, 16 and 28 were tested by separately adding one 3'-primer. Additional 3'-primers in primer solutions 1 to 3, 5, 9, 20, 22, 29 and 31 were tested by separately adding one, two, four or five 5'-primers.

In primer solutions 3, 4, 8 to 10, 13 to 16, 19 to 22, 27 and 30 one or more of the 5'-primers were not possible to test. In primer solutions 1 to 6, 9, 13, 15, 17, 21, 22, 26, 30 and 31 one or more of the 3'-primers were not possible to test.



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For *In Vitro* Diagnostic Use

MA123 v02 SSP PI Template

Date: January 2023, Rev. No: 00

101.101-48/12 – including *Taq* polymerase  
101.101-48u/12u – without *Taq* polymerase

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Lot No.: **5R8**

Lot-specific information

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