

101.704-48/12 – including *Taq* polymerase  
101.704-48u/12u – without *Taq* polymerase

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“Instructions for Use” (IFU)

Lot No.: **5R0**

Lot-specific information

**Olerup SSP® DQ-DR SSP Combi Tray**

<b>Product number:</b>	101.704-48/12 – including <i>Taq</i> pol. 101.704-48u/12u – without <i>Taq</i> pol.
<b>Lot number:</b>	5R0
<b>Expiry date:</b>	2026-12-01
<b>Number of tests:</b>	48 tests – Product No. 101.704-48/48u 12 tests – Product No. 101.704-12/12u
<b>Number of wells per test:</b>	46 + 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. 5R0.**

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

**CHANGES COMPARED TO THE PREVIOUS OLERUP SSP®  
DQ-DR SSP COMBI TRAY LOT (7N1)**

The product documentation has been updated for new alleles of IMGT 3.50.0.

The DQ low primer set, specificity and interpretation tables have been updated for the HLA-DQB1 alleles described since the previous *Olerup SSP®* DQ-DR Combi Tray lot was made (**Lot No. 7N1**).

The **DQ low resolution** primer set is unchanged compared to the previous lot.

The DR low primer set, specificity and interpretation tables have been updated for the HLA-DRB1 alleles described since the previous *Olerup SSP®* DQ-DR Combi Tray lot was made (**Lot No. 7N1**).

The primers of the wells detailed below have been exchanged, added or modified compared to the previous lot (**Lot No. 7N1**).

Well	5'-primer	3'-primer	rationale
16	Added, removed		5'-primer added for the DRB1*01:131N and DRB1*01:134 alleles. Excess 5'-primer removed.
33	-	Exchanged	3'-primer exchanged for reducing tendency for primer oligomer formation.
46	-	Added	3'-primer added for DRB5*02:33 allele.



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Well **47** 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

### DQ-DR SSP Combi Tray

#### CONTENT

The primer set contains 5'- and 3'-primers for grouping the DQB1 alleles in to the serological groups DQ2 to DQ9.

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.

*Please note that DQB1 amplifications usually are somewhat less pronounced than e.g. DRB and DQA1 amplifications even when using the same DNA preparation and exactly the same experimental procedures.*

#### PLATE LAYOUT

Each test consists of 47 PCR reactions in a 48 well cut PCR plate. Well 48 is empty.

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	32
33	34	35	36	37	38	39	40
41	42	43	44	45	46	NC	empty

The 48 well cut PCR plate is marked with ‘DQ-DR’.

Well No. 1 is marked with the Lot No. ‘5R0’ in silver/gray ink.

Wells 1 to 15 – DQ low resolution primers.

Wells 16 to 46 – DR low resolution primers.

Well 47 – Negative Control (NC).

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 48 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 the DQB1 alleles will be amplified by the 15 wells of the DQ low resolution primer set, **wells 1 to 15**. Thus, the interpretation of DQ low resolution typings is not influenced by the DQB2 and DQB3 genes.



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Only HLA-DRB alleles will be amplified by the 31 wells of the DR low resolution primer set, **wells 16 to 46**. Thus, the interpretation of DR low resolution typings is not influenced by other HLA class II genes.

## UNIQUELY IDENTIFIED ALLELES

All the DQB1 alleles, i.e. **DQB1\*02:01 to 02:206N**, **DQB1\*03:01 to 03:500**, **DQB1\*04:01 to 04:94**, **DQB1\*05:01 to 05:310**, and **DQB1\*06:01 to 06:448**, recognized by the HLA Nomenclature Committee in October 2022<sup>1,2</sup> will be amplified by the primers in the DQ low resolution SSP primer set, **wells 1 to 15**. The DQB1 alleles will be grouped into their corresponding serological specificities<sup>3,4</sup>, i.e.:

DQ5(1) =	DQB1*05:01:01-05:05
DQ6(1) =	DQB1*06:01:01-06:44
DQ2 =	DQB1*02:01:01-02:05
DQ3 =	DQB1*03:06, 03:10, 03:14
DQ7(3) =	DQB1*03:01:01-03:01:06, 03:04, 03:09, 03:13, 03:16, 03:19
DQ8(3) =	DQB1*03:02:01-03:02:05, 03:05:01-03:05:04, 03:07-03:08, 03:11, 03:18
DQ9(3) =	DQB1*03:03:02:01-03:03:04, 03:12, 03:15, 03:17, 03:20
DQ4 =	DQB1*04:01-04:02

<sup>1</sup>DQB1 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 serological split of the DQB1\*05:05 to 05:310 alleles, the DQB1\*06:33 to 06:448 alleles, the DQB1\*02:08-02:206N alleles, the DQB1\*03:20-03:500 alleles and the DQB1\*04:02-04:94 alleles is not known. In this table we have used the expert-assigned serological grouping in Tissue Antigens (2009) 73:95-170, and also inferred the serological grouping from the naming of the sequence-defined allele.

<sup>4</sup>The DQB1 alleles will be grouped into their corresponding serological specificities, except that the following alleles give rise to identical amplification patterns. These alleles can be separated by the respective high resolution SSP primer sets.

### Alleles

DQB1\*05:01:01:01-05:01:15, 05:01:17-05:02:26, 05:03:01:01-05:03:23, 05:03:26-05:03:30, 05:05:01-05:43:02, 05:45-05:51, 05:53, 05:55-05:59, 05:61-05:71, 05:73-05:76, 05:78-05:81, 05:84-05:97, 05:99-05:104, 05:106-05:113, 05:115, 05:117-05:127, 05:129-05:131, 05:133-05:145, 05:147-05:174, 05:177-05:206N, 05:208N-05:217, 05:219-05:243, 05:245-05:257, 05:259-05:261, 05:263-05:299, 05:301-05:303, 05:305-05:310, DQB1\*06:325

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** and **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>3,4</sup>.



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<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 serological split of all DRB1 alleles is not known. In this table we use the expert-assigned serological grouping in Tissue Antigens (2009) 73:95-170 and the serological grouping of the sequence-defined allele.

<sup>4</sup>The DRB1 alleles will be grouped into their corresponding serological specificities, except that the following alleles give rise to identical amplification patterns. These alleles can be separated by the respective high resolution SSP primer sets.

**Alleles**

DRB1\*03:126, DRB1\*13:193

DRB1\*08:31, DRB1\*11:05

DRB1\*11:293, DRB1\*13:45

DRB1\*12:57, DRB3\*02:111



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Lot-specific information  
**SPECIFICITY TABLE**

**DQ low resolution primer set**

**Specificities and sizes of the PCR products of the 15 primer mixes of the DQ low resolution primer set**

Primer Mix	Size of spec. PCR product <sup>1</sup>	Size of control band <sup>2</sup>	DQ serology <sup>3</sup>	Amplified DQB1 alleles <sup>4</sup>
1	135 bp, 230 bp	<b>515 bp</b>	5	*05:01:01:01-05:01:15, 05:01:17-05:03:24, 05:03:26-05:59, 05:61-05:81, 05:84-05:97, 05:99-05:115, 05:117-05:174, 05:176-05:217, 05:219-05:257, 05:259-05:310, 06:325, 06:389
2 <sup>7</sup>	135 bp, 185 bp, 220 bp, 270 bp	<b>515 bp</b>	1, 5, 6	*02:03:02, 03:23:01-03:23:02, 03:217, 03:259, 03:355, 04:10, 05:176, 06:01:01:01-06:155, 06:157-06:161, 06:163-06:168, 06:170-06:219, 06:221-06:324, 06:326-06:382, 06:384-06:398, 06:400-06:448
3	210 bp	430 bp	2	*02:01:01:01-02:01:09, 02:01:11-02:01:13, 02:01:15-02:206N
4	130 bp, 220 bp	<b>515 bp</b>	3, 7	*03:01:01:01-03:01:01:12, 03:01:01:14-03:01:56, 03:04:01:01-03:04:04, 03:09-03:10:03, 03:13-03:14:02, 03:16, 03:19:01:01-03:19:06, 03:21-03:22:02, 03:24, 03:27-03:29, 03:35-03:36, 03:42, 03:44, 03:46-03:60, 03:69, 03:71, 03:73, 03:75-03:77, 03:80, 03:82-03:84N, 03:92-03:94, 03:101-03:103, 03:108-03:109, 03:114-03:116, 03:118N-03:122, 03:127-03:131, 03:133-03:135, 03:138-03:140, 03:142-03:144, 03:147-03:148, 03:150, 03:152, 03:154, 03:157-03:160, 03:162-03:167, 03:169-03:173, 03:180, 03:182-03:183, 03:186-03:188, 03:191-03:198:02, 03:201-03:202, 03:206-03:208, 03:216, 03:218-03:219, 03:231-03:232, 03:235-03:236, 03:241-03:243, 03:246, 03:252-03:257, 03:260, 03:264, 03:266-03:268, 03:271, 03:275-03:276N, 03:281, 03:284-03:286, 03:288, 03:290-03:294, 03:297, 03:302-03:303N, 03:305-03:307, 03:309:01-03:309:02, 03:311-03:312, 03:317:01-03:318, 03:326-03:331, 03:335, 03:338N, 03:340N-03:342, 03:347, 03:350, 03:353-03:355, 03:358N, 03:360-03:361, 03:366, 03:370, 03:372-03:373, 03:376N-03:378, 03:380-03:381, 03:385N, 03:387, 03:389-03:391, 03:394, 03:396, 03:399N-03:401, 03:404, 03:407N-03:408, 03:417-03:421, 03:423-03:428, 03:430-03:432, 03:434-03:436, 03:438-03:439, 03:443, 03:448-03:449, 03:451, 03:454-03:455, 03:458, 03:460, 03:465, 03:467-03:470, 03:472-03:476, 03:480Q, 03:482-03:483, 03:485-03:486, 03:488N, 03:491-03:492, 03:496-03:497, 03:499N, 06:209
5 <sup>6</sup>	130 bp, 220 bp	<b>515 bp</b>	6, 8	*03:02:01:01-03:02:36, 03:05:01-03:05:05, 03:07-03:08, 03:11, 03:18, 03:32, 03:37, 03:45:01-03:45:02,



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				03:61, 03:63-03:64, 03:66N-03:68, 03:70, 03:85, 03:104, 03:106-03:107, 03:125, 03:132, 03:146, 03:153, 03:161, 03:174-03:175, 03:178-03:179, 03:181, 03:184-03:185, 03:189-03:190, 03:199, 03:203-03:205, 03:210-03:211, 03:213N-03:215, 03:220-03:221, 03:223-03:224, 03:226, 03:228-03:229, 03:233, 03:237N, 03:240, 03:245, 03:247, 03:250-03:251, 03:261-03:263:01:02, 03:265, 03:269N, 03:273-03:274, 03:277-03:279, 03:287, 03:289, 03:295-03:296, 03:298-03:301, 03:310N, 03:315, 03:320-03:324, 03:333-03:334N, 03:339N, 03:343-03:346, 03:348-03:349, 03:352, 03:362, 03:364, 03:367-03:369, 03:371, 03:379, 03:383, 03:386, 03:388, 03:392, 03:403N, 03:409-03:410, 03:412, 03:415-03:416, 03:422N, 03:429, 03:433, 03:437, 03:440N-03:442, 03:444, 03:446-03:447, 03:450, 03:452, 03:456-03:457, 03:459, 03:462-03:464, 03:466, 03:471, 03:479, 03:481, 03:484, 03:490, 03:493, 03:495, 03:498, 03:500, 04:75, 06:29, 06:123, 06:139, 06:337
6 <sup>6</sup>	135 bp	515 bp	2, 3, 9	*02:77, 02:180, 03:03:02:01-03:03:25, 03:03:27-03:03:29, 03:06, 03:12, 03:15, 03:20, 03:23:03, 03:25:01-03:26, 03:30-03:31, 03:33-03:34, 03:38:01-03:41, 03:43, 03:65, 03:74, 03:79, 03:86-03:91Q, 03:95N-03:99Q, 03:104-03:105, 03:111-03:113, 03:117, 03:123-03:124, 03:126, 03:136-03:137, 03:141, 03:145, 03:149, 03:155-03:156, 03:168, 03:176-03:177, 03:200, 03:209, 03:212, 03:222, 03:227, 03:230, 03:234, 03:238-03:239, 03:248-03:249, 03:258, 03:270, 03:280, 03:282N-03:283, 03:304, 03:313, 03:316, 03:319, 03:332, 03:336-03:337, 03:351, 03:356N-03:357N, 03:359, 03:363, 03:365, 03:374-03:375N, 03:382, 03:384, 03:393, 03:395, 03:397-03:398, 03:402, 03:405-03:406, 03:411N, 03:414, 03:445, 03:453, 03:461, 03:477-03:478, 03:487, 03:489, 03:494, 04:03:01-04:03:03, 06:02:43, 06:03:10, 06:03:33, 06:51:01, 06:66, 06:96:01, 06:118:04, 06:168, 06:172, 06:322:01-06:322:02, 06:377
7 <sup>5,6</sup>	80 bp	515 bp	3, 7, 8, 9	*03:01:01:01-03:01:01:12, 03:01:01:14-03:01:06, 03:01:07 <sup>w</sup> , 03:01:08-03:02:05, 03:02:07-03:02:17, 03:02:19-03:02:29, 03:02:31-03:05:05, 03:07, 03:08 <sup>w</sup> , 03:09-03:12, 03:13 <sup>w</sup> , 03:14:01-03:24, 03:26-03:57, 03:58 <sup>w</sup> , 03:59-03:64, 03:65 <sup>w</sup> , 03:66N-03:106, 03:107 <sup>w</sup> , 03:108-03:124, 03:126-03:136, 03:137 <sup>w</sup> , 03:138-03:146, 03:148-03:193, 03:194 <sup>w</sup> , 03:195-03:227, 03:229-03:231, 03:232 <sup>w</sup> , 03:233-03:261, 03:262 <sup>w</sup> , 03:263:01:01-03:282N, 03:283 <sup>w</sup> , 03:284-03:324, 03:326-03:410, 03:412-03:417, 03:419-03:448, 03:450-03:500
8 <sup>6</sup>	135 bp, 160 bp, 185 bp, 210 bp	430 bp	4	*03:132, 04:01:01:01-04:02:01:01, 04:02:01:04-04:03:02, 04:04-04:94



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Lot No.	Fragment 1	Fragment 2	Number of Wells	Well IDs
9	225 bp	430 bp	4	*04:01:01:01-04:02:01:01, 04:02:01:04-04:02:18, 04:02:20-04:03:03, 04:06-04:21, 04:22 <sup>w</sup> , 04:23, 04:24 <sup>w</sup> , 04:25N-04:32, 04:34-04:37, 04:38 <sup>w</sup> , 04:39-04:48, 04:50-04:94
10	185 bp, 215 bp	430 bp	5	*05:01:01:01-05:02:26, 05:03:01:01-05:03:23, 05:03:25-05:03:30, 05:05:01-05:43:02, 05:45-05:51, 05:53, 05:55-05:71, 05:73-05:76, 05:78-05:104, 05:106-05:113, 05:115-05:127, 05:129-05:131, 05:133-05:145, 05:147-05:175, 05:177-05:206N, 05:208N-05:243, 05:245-05:261, 05:263-05:299, 05:301-05:303, 05:305-05:310, 06:156, 06:162, 06:169, 06:325
11	185 bp	430 bp	8, 9	*03:03:11, 03:05:01, 03:05:03, 03:05:05, 03:17:01, 03:61, 03:72, 03:100, 03:181, 03:250, 03:346
12 <sup>6</sup>	185 bp	430 bp	3, 7, 8, 9	*03:01:01:01-03:01:01:12, 03:01:01:14-03:01:01:48, 03:01:03-03:01:07, 03:01:09-03:02:02:02, 03:02:04-03:02:12, 03:02:14-03:03:02:10, 03:03:04-03:03:15, 03:03:17-03:04:04, 03:05:03-03:05:04, 03:06-03:17:01, 03:18-03:19:06, 03:21-03:22:02, 03:23:02-03:36, 03:38:01, 03:39-03:60, 03:62-03:71, 03:74, 03:76-03:98, 03:101-03:103, 03:106-03:108, 03:110-03:111, 03:113-03:117, 03:119-03:131, 03:133-03:153, 03:155, 03:157-03:161, 03:163-03:180, 03:182, 03:184-03:188, 03:190-03:203, 03:205-03:222, 03:224-03:225, 03:227-03:232, 03:234-03:236, 03:239-03:249, 03:251, 03:253-03:257, 03:259-03:261, 03:263:01:01-03:290, 03:292-03:324, 03:326-03:334N, 03:337-03:345, 03:347-03:350, 03:353, 03:355-03:370, 03:372-03:390, 03:392-03:442, 03:444-03:500, 04:01:03, 04:02:16, 04:03:03
13	185 bp	<b>515 bp</b>	6	*04:10, 06:02:01:01-06:02:42, 06:02:44-06:02:59, 06:14:01-06:16, 06:19:01-06:20, 06:23-06:24, 06:33, 06:37, 06:46-06:50, 06:51:02, 06:68, 06:70-06:84:01:02, 06:95, 06:96:02-06:97, 06:107, 06:109, 06:111-06:117, 06:122, 06:124-06:127, 06:136-06:138, 06:146:01-06:147, 06:150-06:152, 06:156, 06:159, 06:161-06:163, 06:166, 06:173-06:175, 06:178-06:179N, 06:182-06:183, 06:188, 06:192, 06:197-06:198, 06:200-06:201, 06:208:01-06:208:02, 06:211, 06:213, 06:215-06:216N, 06:219, 06:224-06:228, 06:232, 06:235-06:237, 06:240, 06:242, 06:249, 06:255-06:256, 06:262, 06:264, 06:270:02-06:271, 06:273, 06:284, 06:286, 06:289-06:290, 06:293-06:298, 06:300, 06:304N, 06:306N, 06:308N, 06:311, 06:314-06:315, 06:317N, 06:322:03, 06:324, 06:326, 06:333, 06:335, 06:338, 06:341N, 06:344, 06:347, 06:354-06:357, 06:363-06:364, 06:366, 06:370, 06:372, 06:374, 06:376, 06:379N-06:380, 06:383N-06:384, 06:386, 06:388, 06:390, 06:395, 06:397N, 06:401-06:402, 06:404-06:406, 06:409, 06:411-06:413, 06:416Q, 06:422N, 06:430-06:431, 06:436-06:438, 06:445-06:448
14	185 bp	430 bp	1, 5, 6	*06:02:01:01-06:02:12, 06:02:14-06:03:10, 06:03:12-06:03:46, 06:05:02 <sup>?</sup> -06:06 <sup>?</sup> , 06:08:01-06:08:03, 06:10-06:11:04, 06:13:01-06:14:03, 06:16,



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15	135 bp	430 bp	3, 5, 6, 9	*03:10:01-03:10:02:02, 03:12, 03:14:01-03:14:02, 03:70, 03:179, 03:183, 03:195, 03:474, 06:01:01:01-06:01:06, 06:01:08-06:01:31, 06:01:33-06:01:34, 06:06 <sup>?</sup> , 06:43, 06:54N-06:58, 06:98, 06:99:02-06:105, 06:108, 06:120, 06:132, 06:140, 06:153:01-06:153:02, 06:157, 06:167-06:168, 06:177, 06:181, 06:194, 06:205, 06:209, 06:214, 06:229, 06:239, 06:243, 06:245-06:247, 06:251, 06:257-06:258, 06:260, 06:263, 06:268, 06:274, 06:277, 06:285, 06:302, 06:305, 06:307, 06:309-06:310, 06:312, 06:321, 06:323, 06:330N, 06:342, 06:359, 06:377, 06:382, 06:415, 06:418-06:419, 06:421, 06:427, 06:435

<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 DQ 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.

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.



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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. In the presence of a specific amplification the intensity of the control band often decreases.

<sup>3</sup>The serological reactivity of all DQ alleles is not known. In this table we use the expert-assigned serological grouping in Tissue Antigens (2009) 73:95-170 and the serological grouping of the sequence-defined allele. The DQB1\*03:10 allele has been assigned type DQ7 by NMDP.

<sup>4</sup>For several DQB1 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 5, 6, 7, 8 and 12 may give a lower yield of HLA-specific PCR products than the other DQ low resolution primer mixes.

<sup>7</sup>Primer mix 2 has a tendency of giving rise to primer oligomer formation.

Abbreviations

‘w’, may be weakly amplified.

‘?’, nucleotide sequence information not available for the primer matching sequence.



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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</sup>
<b>16</b> <sup>11,13</sup>	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>17</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>18</b> <sup>11,13</sup>	200 bp, 230 bp	430 bp	2, 15	*15:01:01:01-15:211, 16:66
<b>19</b> <sup>13</sup>	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>20</b> <sup>5,8</sup>	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>21</b> <sup>5,8</sup>	75 bp, 205 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,



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<b>22<sup>5</sup></b>	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
<b>23<sup>5</sup></b>	100 bp, 175 bp	430 bp	3, 4	*04:01:01:01-04:05:11, 04:05:13-04:353
<b>24<sup>13</sup></b>	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>
<b>25<sup>5</sup></b>	85 bp, 120 bp, 215 bp, 250 bp	<b>515 bp</b>	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
<b>26<sup>5,9,14</sup></b>	85 bp, 100 bp, 135 bp, 165 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>
<b>27<sup>5,13</sup></b>	70 bp, 155 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
<b>28<sup>5</sup></b>	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
<b>29<sup>5</sup></b>	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
<b>30<sup>9</sup></b>	215 bp, 235 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,



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<b>42<sup>13</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>43<sup>9,11</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,



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For *In Vitro* Diagnostic Use

MA123 v02 SSP PI Template

Date: January 2023, Rev. No: 00

101.704-48/12 – including *Taq* polymerase  
101.704-48u/12u – without *Taq* polymerase

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Lot No.: **5R0**

Lot-specific information

Well	Allele	Size (bp)	Well	Allele	Size (bp)
				14:194-14:195N, 14:198, 14:200, 14:209, 14:212, 14:242, <b>DRB3*02:27, DRB3*02:58</b>	
<b>44</b> <sup>5,8,9,13,15</sup>	80 bp, 110 bp, 170 bp, 240 bp	<b>515 bp</b>	12, 52	*12:05, 12:15, 12:57, 14:141, <b>DRB3*01:01:02:01-01:110, DRB3*02:01-02:130, DRB3*02:132-02:185, DRB3*03:01:01:01-03:21, DRB3*03:23-03:60</b>	
<b>45</b> <sup>7,10</sup>	130 bp, 210 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>46</b> <sup>6</sup>	175 bp, 220 bp	430 bp	51	<b>DRB5*01:01:01:01-01:129, DRB5*02:02:01-02:36</b>	
<b>47</b> <sup>16</sup>	-	-	-	<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.

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.

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 16 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. In the presence of a specific amplification the intensity of the control band often decreases.

<sup>3</sup>The serological split of all DRB1 alleles is not known. In this table we use the expert-assigned serological grouping in Tissue Antigens (2009) 73:95-170 and the serological grouping of the sequence-defined allele.

<sup>4</sup>For several DRB1 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 fragments shorter than 125 base pairs have a lower intensity and are less sharp than longer PCR bands.

<sup>6</sup>DRB5\*01:08:01N-01:08:02N is amplified by the primer pairs in well 39 in addition to primer mix 46.

<sup>7</sup>The DRB4\*01:03:01:02N allele is amplified by the primer pairs in primer mixes 33 and 45, whereas the DRB4\*02:01N and DRB4\*03:01N null alleles are only amplified by the primer pairs in primer mix 45.

<sup>8</sup>Due to sharing of sequence motifs in codon 38 and 47, DRB3\*01:14 will also be amplified in primer mixes 20, 21 and 32 and DRB3\*01:23 and DRB3\*02:32 in mix 20, in addition to primer mix 44.

<sup>9</sup>Due to sharing of sequence motifs, DRB3\*01:42 is amplified by the primer pairs in primer mix 26, DRB3\*02:27 is amplified by the primer pairs in primer mix 30 and the DRB3\*02:27 and DRB3\*02:58 alleles are amplified in primer mix 43, in addition to primer mix 44.

<sup>10</sup>Due to sharing of sequence motifs, DRB4\*01:31 is amplified by the primer pairs in primer mix 35 in addition to primer mix 45.

<sup>11</sup>Primer mixes 16, 18, 31, 34, 37 and 43 may have a tendency of giving rise to primer oligomer formation.



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<sup>12</sup>Primer mix 34 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>13</sup>Primer mixes 16, 18, 19, 24, 27, 37, 41, 42 and 44 may have a tendency of unspecific amplification.

<sup>14</sup>Primer mix 26 may give a lower yield of HLA-specific PCR products than the other DR low resolution primer mixes.

<sup>15</sup>In primer mix 44 the specific PCR product of 240 base pairs may be difficult to distinguish from the internal control band.

<sup>16</sup>Primer mix 47 contains a negative control, which will amplify the majority of the 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-specific information

### DQ LOW PRIMER SPECIFICATION

Well No.	1	2	3	4	5	6	7	8	9	10	11	12
Length of spec.	135	135	210	130	130	135	80	135	225	185	185	185
PCR product	230	185 220		220	220			160 185		215		
		270						210				
Length of int.	515	515	430	515	515	515	515	430	430	430	430	430
pos. control <sup>1</sup>												
5'-primer(s) <sup>2</sup>	26(173) 5'-ggg 3'	9(122) 5'-gCT 3'	28(178) 5'-TgC 3'	26(173) 5'-TTA 3'	28(179) 5'-gAC 3'	26(173) 5'-TCT 3'	72(312) 5'-Cgg 3'	21(159) 5'-ACC 3'	9(122) 5'-gTT 3'	30(184) 5'-gAC 3'	21(159) 5'-ACC 3'	38(210) 5'-gCA 3'
	26(173) 5'-ggA 3'	25(169) 5'-TgT 3'	30(184) 5'-gAg 3'		28(179) 5'-gAC 3'			23(164) 5'-gCT 3'				
	26(173) 5'-ggg 3'	26(172) 5'-ATC 3'	30(185) 5'-AAG 3'		28(179) 5'-gAC 3'			38(210) 5'-gCg 3'				
	26(173) 5'-gTg 3'	26(173) 5'-TTA 3'	30(185) 5'-AAA 3'									
		26(173) 5'-TCT 3'										
		30(184) 5'-gAT 3'										
3'-primer(s) <sup>3</sup>	57(266) 5'-CAA 3'	57(266) 5'-CAA 3'	86(353) 5'-gCT 3'	55(260) 5'-gCg 3'	57(266) 5'-Cgg 3'	57(266) 5'-CgT 3'	86(353) 5'-gCT 3'	70(304) 5'-CTC 3'	70(304) 5'-CTC 3'	77(327) 5'-ACT 3'	70(304) 5'-CCT 3'	86(353) 5'-gCT 3'
	87(356) 5'-ggT 3'	57(266) 5'-CAT 3'		86(353) 5'-gCT 3'	57(266) 5'-CAg 3'	57(266) 5'-CgT 3'	89(361) 5'-CgT 3'	77(327) 5'-ACg 3'		87(356) 5'-ggT 3'		87(357) 5'-CgT 3'
	87(356) 5'-ggT 3'	86(353) 5'-ACg 3'		86(354) 5'-AgT 3'	57(266) 5'-Cgg 3'					87(356) 5'-ggA 3'		
	89(361) 5'-CCT 3'	86(353) 5'-ACC 3'			87(356) 5'-ggg 3'							
		86(354) 5'-AAT 3'										
Well No.	1	2	3	4	5	6	7	8	9	10	11	12

Well No.	13	14	15
Length of spec.	185	185	135
PCR product			
Length of int.	515	430	430
pos. control <sup>1</sup>			
5'-primer(s) <sup>2</sup>	9(122) 5'-gTT 3'	38(209) 5'-CgC 3'	13(134) 5'-ggC 3'
3'-primer(s) <sup>3</sup>	57(266) 5'-CAT 3'	86(353) 5'-ACg 3'	45(230) 5'-CCC 3'
	58(270) 5'-TCC 3'		
Well No.	13	14	15

<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.



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Lot-specific information

## DR LOW PRIMER SPECIFICATION

Well No.	16	17	18	19	20	21	22	23	24	25	26	27
Length of spec.	210	200	200	210	120	75	85	100	200	85	85	70
PCR product	235		230		225	205	210	175	240		215	135
										250	165	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'-gCg <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.	28	29	30	31	32	33	34	35	36	37	38	39
Length of spec.	100	90	215	195	175	75	110	110	170	75	135	170
PCR product	175	110	235	215		100	145	150		175	195	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>									



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

101.704-48/12 – including *Taq* polymerase  
101.704-48u/12u – without *Taq* polymerase

Visit [www.caredx.com](http://www.caredx.com) for  
“Instructions for Use” (IFU)

Lot No.: 5R0

Lot-specific information

Well No.	40	41	42	43	44	45	46
Length of spec.	150	145	145	140	80	130	175
PCR product			210	170	110	210	220
			235		170		
					240		
Length of int. i. control <sup>1</sup>	430	430	515	515	515	430	430
Primer(s) <sup>2</sup>	34(189) 5'-CAg 3'	13(125) 5'-gTC 3'	13(125) 5'-gTC 3'	28(171) 5'-gAg 3'	10(116) 5'-gCT 3'	28(170) 5'-gAT 3'	9(112) 5'-TgC 3'
	34(189) 5'-CAg 3'		37(197) 5'-gTT 3'	37(196) 5'-AgA 3'	10(116) 5'-gCT 3'	28(170) 5'-gAg 3'	13(125) 5'-gTA 3'
			114(429) 5'-CTg 3'		11(119) 5'-gCT 3'	105(401) 5'-AAA 3'	
					38(199) 5'-TCC 3'		
Primer(s) <sup>3</sup>	71(298) 5'-CTC 3'	47(227) 5'-ggA 3'	70(296) 5'-TCC 3'	70(295) 5'-CTg 3'	51(239) 5'-CCC 3'	81(328) 5'-gTA 3'	57(256) 5'-gTC 3'
		48(229) 5'-CCA 3'	74(307) 5'-CAg 3'	71(298) 5'-CTT 3'	60(266) 5'-Agg 3'	87(346) 5'-CTC 3'	57(256) 5'-gCT 3'
			181(630) 5'-CTT 3'		77(317) 5'-AAT 3'	87(346) 5'-CTT 3'	57(258) 5'-gCg 3'
						135(490) 5'-gCT 3'	57(258) 5'-gCT 3'
							58(260) 5'-CCT 3'
							70(296) 5'-TgT 3'
Well No.	40	41	42	43	44	45	46

<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 16 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.



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For *In Vitro* Diagnostic Use

MA123 v02 SSP PI Template

Date: January 2023, Rev. No: 00

101.704-48/12 – including *Taq* polymerase  
101.704-48u/12u – without *Taq* polymerase

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Lot No.: **5R0**

Lot-specific information

CELL LINE VALIDATION SHEET																			
DQ low resolution primer set <sup>2</sup>																			
					Well														
					1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
					202020301	202246302	202241103	202241104	202241105	202241106	202020307	202241108	202020309	202020310	202020311	202020312	202246313	202020314	202020315
				Prod. No.:															
	IHCW cell line <sup>1</sup>		DQB1																
1	9001	SA	*05:01		+	-	-	-	-	-	-	-	-	+	-	-	-	-	-
2	9280	LK707	*06:01 *02:02		-	+	+	-	-	-	-	-	-	-	-	-	-	-	+
3	9011	E4181324	*06:01		-	+	-	-	-	-	-	-	-	-	-	-	-	-	+
4	9275	GU373	*02:01		-	-	+	-	-	-	-	-	-	-	-	-	-	-	-
5	9009	KAS011	*05:02		+	-	-	-	-	-	-	-	-	+	-	-	-	-	-
6	9353	SM	*03:02 *06:01		-	+	-	-	+	-	+	-	-	-	-	+	-	-	+
7	9020	QBL	*02:01		-	-	+	-	-	-	-	-	-	-	-	-	-	-	-
8	9025	DEU	*03:01		-	-	-	+	-	-	+	-	-	-	-	+	-	-	-
9	9026	YAR	*03:02		-	-	-	-	+	-	+	-	-	-	-	+	-	-	-
10	9107	LKT3	*04:01		-	-	-	-	-	-	-	+	+	-	-	-	-	-	-
11	9051	PITOUT	*02:02		-	-	+	-	-	-	-	-	-	-	-	-	-	-	-
12	9052	DBB	*03:03		-	-	-	-	-	+	+	-	-	-	-	+	-	-	-
13	9004	JESTHOM	*05:01		+	-	-	-	-	-	-	-	-	+	-	-	-	-	-
14	9071	OLGA	*04:02		-	-	-	-	-	-	-	+	+	-	-	-	-	-	-
15	9075	DKB	*03:03		-	-	-	-	-	+	+	-	-	-	-	+	-	-	-
16	9037	SWEIG007	*03:01		-	-	-	+	-	-	+	-	-	-	-	+	-	-	-
17	9282	CTM 3953540	*02:01 *06:03		-	+	+	-	-	-	-	-	-	-	-	-	-	+	-
18	9257	32367	*06:02 *02:02		-	+	+	-	-	-	-	-	-	-	-	-	+	+	-
19	9038	BM16	*03:01		-	-	-	+	-	-	+	-	-	-	-	+	-	-	-
20	9059	SLE005	*06:04		-	+	-	-	-	-	-	-	-	-	-	-	-	-	-
21	9064	AMALA	*03:01		-	-	-	+	-	-	+	-	-	-	-	+	-	-	-
22	9056	KOSE	*05:03 *06:04		+	+	-	-	-	-	-	-	-	+	-	-	-	-	-
23	9124	IHL	*05:03 *06:01		+	+	-	-	-	-	-	-	-	+	-	-	-	-	+
24	9035	JBUSH	*03:01		-	-	-	+	-	-	+	-	-	-	-	+	-	-	-
25	9049	IBW9	*02:02		-	-	+	-	-	-	-	-	-	-	-	-	-	-	-
26	9285	WT49	*02:01		-	-	+	-	-	-	-	-	-	-	-	-	-	-	-
27	9191	CH1007	*04:01 *05:01		+	-	-	-	-	-	-	+	+	+	-	-	-	-	-
28	9320	BEL5GB	*02:02 *03:01		-	-	+	+	-	-	+	-	-	-	-	+	-	-	-
29	9050	MOU	*02:02		-	-	+	-	-	-	-	-	-	-	-	-	-	-	-
30	9021	RSH	*04:02		-	-	-	-	-	-	-	+	+	-	-	-	-	-	-
31	9019	DUCAF	*02:01		-	-	+	-	-	-	-	-	-	-	-	-	-	-	-
32	9297	HAG	*03:01		-	-	-	+	-	-	+	-	-	-	-	+	-	-	-
33	9098	MT14B	*03:02		-	-	-	-	+	-	+	-	-	-	-	+	-	-	-
34	9104	DHIF	*03:01		-	-	-	+	-	-	+	-	-	-	-	+	-	-	-
35	9302	SSTO	*03:05		-	-	-	-	+	-	+	-	-	-	+	-	-	-	-
36	9024	KT17	*03:02		-	-	-	-	+	-	+	-	-	-	-	+	-	-	-
37	9065	HHKB	*06:03		-	+	-	-	-	-	-	-	-	-	-	-	-	+	-
38	9099	LZL	*03:01		-	-	-	+	-	-	+	-	-	-	-	+	-	-	-
39	9315	CML	*02:01 *03:01		-	-	+	+	-	-	+	-	-	-	-	+	-	-	-
40	9134	WHONP199	*02:02 *03:03		-	-	+	-	-	+	+	-	-	-	-	+	-	-	-
41	9055	H0301	*06:09		-	+	-	-	-	-	-	-	-	-	-	-	-	-	-
42	9066	TAB089	*06:01		-	+	-	-	-	-	-	-	-	-	-	-	-	-	+
43	9076	T7526	*03:03		-	-	-	-	-	+	+	-	-	-	-	+	-	-	-
44	9057	TEM	*05:03		+	-	-	-	-	-	-	-	-	+	-	-	-	-	-
45	9239	SHJO	*02:02		-	-	+	-	-	-	-	-	-	-	-	-	-	-	-
46	9013	SCHU	*06:02		-	+	-	-	-	-	-	-	-	-	-	-	+	+	-
47	9045	TUBO	*03:01		-	-	-	+	-	-	+	-	-	-	-	+	-	-	-
48	9303	TER-ND	*05:01		+	-	-	-	-	-	-	-	-	+	-	-	-	-	-



0197

101.704-48/12 – including *Taq* polymerase  
101.704-48u/12u – without *Taq* polymerase

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Lot No.: **5R0**

Lot-specific information

<b>CELL LINE VALIDATION SHEET</b>																			
<b>DR low resolution primer set<sup>2</sup></b>																			
			Prod. No.:	Well															
				16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
				202243801	202128502	202128503	202128504	202128505	202128506	202128507	202128508	202137109	202128510	202241011	202134312	202128513	202128514	202128515	202128516
	<b>IHWC cell line<sup>1</sup></b>	<b>DRB1</b>																	
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		-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-



**0197**



101.704-48/12 – including *Taq* polymerase  
101.704-48u/12u – without *Taq* polymerase

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Lot No.: **5R0**

Lot-specific information

CELL LINE VALIDATION SHEET																			
DR low resolution primer set <sup>2</sup>																			
				Well															
				32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	
				Prod. No.:	202137117	202128518	202128519	202128520	202137121	202137122	202137123	202137124	202137125	202137126	202137127	202137128	202128529	202128530	202243831
	IHCW 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		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-



0197

101.704-48/12 – including *Taq* polymerase  
 101.704-48u/12u – without *Taq* polymerase

Visit [www.caredx.com](http://www.caredx.com) for  
 “Instructions for Use” (IFU)

Lot No.: **5R0**

**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 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 5'-primer and one or more 3'-primers in primer solutions 2, 26, 30, 33 and 42 were tested by separately adding one 5'-primer or 3'-primer.

One or more 3'-primers in primer solutions 6, 10, 16 to 18, 20, 24, 35 and 37 and were tested by separately adding additional 5'-primers.

One 5'-primer in primer solutions 19, 21, 27, 31 and 43 was tested by separately adding additional 3'-primers. In primer solutions 1, 2, 4, 5, 12, 13, 16 to 21, 24, 28, 30, 32, 36, 37, 41, 45 and 46 one or more 3'-primers were not possible to be tested, and in primer solutions 1 to 3, 5, 18, 19, 23 to 25, 28 to 31, 34 to 37, 42 and 45 one or more 5'-primers were not possible to be tested.



**0197**

101.704-48/12 – including *Taq* polymerase  
 101.704-48u/12u – without *Taq* polymerase

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 “Instructions for Use” (IFU)

Lot No.: **5R0**

Lot-specific information

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For *In Vitro* Diagnostic Use

MA123 v02 SSP PI Template

Date: January 2023, Rev. No: 00