

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

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“Instructions for Use” (IFU)

Lot No.: **1V2**

Lot-specific information

Olerup SSP[®] DQ-DR SSP Combi Tray

Product number:	101.704-48/12 – including <i>Taq</i> pol. 101.704-48u/12u – without <i>Taq</i> pol.
Lot number:	1V2
Expiry date:	2028-12-01
Number of tests:	48 tests – Product No. 101.704-48/48u 12 tests – Product No. 101.704-12/12u
Number of wells per test:	46 + 1
Storage - pre-aliquoted primers:	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. 1V2.

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 (2S9)**

The product documentation has been updated for new alleles of IMGT 3.58.0.

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. 2S9**).

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. 2S9**).

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

Well	5'-primer	3'-primer	rationale
21	Removed	-	5'-primer removed for decreased tendencies of primer oligomer formation.



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Well **47** contains Negative Control primer pairs, that will amplify the majority of the *Olerup* SSP[®] 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
5'-primer¹	164	340	440	45	45	43	36
	5'-CAC ^{3'}	5'-Agg ^{3'}	5'-TTA ^{3'}	5'-Tgg ^{3'}	5'-Tgg ^{3'}	5'-Tgg ^{3'}	5'-TAC ^{3'}
							36
							5'-TAT ^{3'}
3'-primer²	231	2nd I	507	59	58	57	47
	5'-TgC ^{3'}	5'-AAA ^{3'}	5'-TTg ^{3'}	5'-CTC ^{3'}	5'-ggC ^{3'}	5'-CTC ^{3'}	5'-ACA ^{3'}
							48
							5'-gCA ^{3'}
							48
							5'-gCC ^{3'}
							52
							5'-TgT ^{3'}
A*	+	+	+				
B*	+	+	+				
C*	+	+	+				
DRB1				+	+		
DRB3				+	+		
DRB5				+			
DQB1					+		
DPB1						+	
DQA1							+

¹The nucleotide position for HLA class I genes and the codon for HLA class II genes, in the 2nd or 3rd 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 web site. The sequence of the 3 terminal nucleotides of the primer is given.

²The nucleotide position for HLA class I genes and the codon for HLA class II genes, in the 2nd or 3rd exon or the 2nd 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 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*10:46 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. ‘1V2’ 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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Lot-specific information

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 02:238, DQB1*03:01 to 03:565, DQB1*04:01 to 04:104, DQB1*05:01 to 05:352, and DQB1*06:01 to 06:519**, recognized by the HLA Nomenclature Committee in October 2024^{1,2} 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^{3,4}, 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

¹DQB1 alleles listed on the IMGT/HLA web page 2024-October-09, release 3.58.0, www.ebi.ac.uk/imgt/hla.

²Alleles 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>.

³The serological split of the DQB1*05:05 to 05:352 alleles, the DQB1*06:33 to 06:519 alleles, the DQB1*02:08-02:238 alleles, the DQB1*03:20-03:565 alleles and the DQB1*04:02-04:104 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.

⁴The 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, 05:02:28-05:03:23, 05:03:26-05:03:37, 05:05:01-05:05:43:02, 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, 05:305-05:343, 05:345-05:349, 05:351-05:352, DQB1*06:325

DQB1*05:344, DQB1*06:01:07, 06:01:32, 06:01:35, 06:03:11, 06:04:01:01-06:05:01, 06:07:01-06:07:02, 06:09:01:01-06:09:13, 06:12, 06:17, 06:21-06:22:03, 06:25, 06:28, 06:34-06:36, 06:38-06:39, 06:42, 06:45, 06:52-06:53:02, 06:69:01-06:69:02, 06:85-06:86, 06:88:01:01-06:89, 06:92:02-06:94, 06:118:01-06:118:03, 06:119, 06:121, 06:129, 06:135, 06:142, 06:144N, 06:149, 06:155, 06:158N, 06:160, 06:164, 06:171, 06:180, 06:186, 06:189, 06:193N, 06:199, 06:202-06:204, 06:207, 06:210, 06:212, 06:217, 06:231, 06:241, 06:252N, 06:254, 06:261, 06:265-06:267, 06:275, 06:280-06:283, 06:287-06:288, 06:291-06:292, 06:299, 06:301, 06:303N, 06:313, 06:318, 06:320, 06:332, 06:339-06:340, 06:343, 06:348-06:349, 06:351, 06:353, 06:358, 06:361, 06:369, 06:375, 06:381, 06:385, 06:387, 06:398, 06:407, 06:414N, 06:420, 06:426, 06:429, 06:432, 06:434, 06:439Q, 06:441,



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06:444, 06:449, 06:452N, 06:458N, 06:465, 06:467, 06:473, 06:479, 06:484, 06:489-
06:490, 06:496, 06:498, 06:505-06:506, 06:508, 06:511, 06:519

All the HLA-DRB1, -DRB3, -DRB4 and -DRB5 alleles, i.e. **DRB1*01:01 to DRB1*10:46, DRB3*01:01 to DRB3*03:76, DRB4*01:01 to DRB4*03:01N and DRB5*01:01 to DRB5*02:39**, recognized by the HLA Nomenclature Committee in October 2024^{1,2,3} 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^{4,5}.

¹DRB alleles listed on the IMGT/HLA web page 2024-October-09, release 3.58.0, www.ebi.ac.uk/imgt/hla.

²Alleles 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>.

³The primers in this kit do not amplify the DRB1*04:382 and DRB5*01:131N alleles.

⁴The 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.

⁵The 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*03:218N, DRB1*13:176

DRB1*08:31, DRB1*11:05, 11:309

DRB1*08:129, DRB1*13:55

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 ¹	Size of control band ²	DQ serology ³	Amplified DQB1 alleles ⁴
1	135 bp, 230 bp	515 bp	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, 05:259-05:343, 05:345-05:352, 06:325, 06:389
2 ⁷	135 bp, 185 bp, 220 bp, 270 bp	515 bp	1, 5, 6	*02:03:02, 03:23:01-03:23:02, 03:217:01, 03:259, 03:355, 04:10, 05:176, 05:344, 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, 06:400-06:455, 06:457-06:519
3	210 bp	430 bp	2	*02:01:01:01-02:01:09, 02:01:11-02:01:13, 02:01:15-02:217, 02:219-02:233, 02:235-02:238
4	130 bp, 220 bp	515 bp	3, 7	*03:01:01:01-03:01:01:12, 03:01:01:14-03:01:68, 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, 03:360-03:361:02, 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, 03:488:01N-03:488:02N, 03:491-03:492, 03:496-03:497, 03:499N, 03:503, 03:506:01:01-03:506:01:02, 03:508, 03:513-03:514, 03:519-03:520, 03:522, 03:524, 03:526-03:531,



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				03:534, 03:537-03:539, 03:542N, 03:544, 03:546, 03:549-03:550, 03:552-03:553, 03:555-03:557, 03:562-03:565, 06:209, 06:475
5⁶	130 bp, 220 bp	515 bp	6, 8	*03:02:01:01-03:02:46, 03:05:01-03:05:05, 03:07-03:08, 03:11, 03:18, 03:32, 03:37, 03:45:01-03:45:02, 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, 03:500:01, 03:501-03:502, 03:504, 03:511-03:512, 03:515, 03:517, 03:525, 03:533, 03:535, 03:540-03:541N, 03:543, 03:547-03:548, 03:554, 03:558-03:559, 03:561, 04:75, 06:29, 06:123, 06:139, 06:337
6⁶	135 bp	515 bp	2, 3, 9	*02:77, 02:180:01-02:180:02, 03:03:02:01-03:03:25, 03:03:27-03:03:29, 03:03:31-03:03:34, 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, 03:217:02, 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, 03:382:01-03:382:02, 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, 03:505, 03:507, 03:509N-03:510, 03:516, 03:518, 03:521, 03:523, 03:532, 03:536, 03:545, 03:551N, 03:560N, 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^{5,6}	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 ^w , 03:01:08-03:01:58, 03:01:60-03:02:05, 03:02:07-03:02:17, 03:02:19-03:02:29, 03:02:31-03:05:05, 03:07, 03:08 ^w , 03:09-03:12, 03:13 ^w , 03:14:01-03:24, 03:26-03:57, 03:58 ^w , 03:59-03:64,



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				03:65 ^w , 03:66N-03:106, 03:107 ^w , 03:108-03:124, 03:126-03:136, 03:137 ^w , 03:138-03:146, 03:148-03:193, 03:194 ^w , 03:195-03:227, 03:229-03:231, 03:232 ^w , 03:233-03:261, 03:262 ^w , 03:263:01:01-03:282N, 03:283 ^w , 03:284-03:324, 03:326-03:410, 03:412-03:417, 03:419-03:448, 03:450-03:565
8⁶	135 bp, 160 bp, 185 bp, 210 bp	430 bp	4	*03:132, 04:01:01:01-04:02:01:01, 04:02:01:04-04:104
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 ^w , 04:23, 04:24 ^w , 04:25N-04:32, 04:34-04:37, 04:38 ^w , 04:39-04:48, 04:50-04:104
10	185 bp, 215 bp	430 bp	5	*05:01:01:01-05:02:26, 05:02:28-05:03:23, 05:03:25-05:03:37, 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, 05:305-05:343, 05:345-05:349, 05:351-05:352, 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
12⁶	185 bp	430 bp	3, 7, 8, 9	*03:01:01:01-03:01:01:12, 03:01:01:14-03:01:01:70, 03:01:03-03:01:07, 03:01:09-03:02:02:02, 03:02:04-03:02:12, 03:02:14-03:03:02:20Q, 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, 03:444-03:565, 04:01:03, 04:02:16, 04:03:03
13	185 bp	515 bp	6	*04:10, 06:02:01:01-06:02:42, 06:02:44-06:02:64, 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,



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14	185 bp	430 bp	1, 5, 6	*06:02:01:01-06:02:12, 06:02:14-06:03:10, 06:03:12-06:03:53, 06:05:02?-06:06?, 06:08:01:01-06:08:03, 06:10-06:11:04, 06:13:01-06:14:03, 06:16, 06:18:01-06:20, 06:23-06:24, 06:26N-06:27:02, 06:29-06:33, 06:37, 06:40-06:41:01:03, 06:44, 06:47-06:51:02, 06:59-06:65, 06:67-06:68, 06:70-06:78, 06:80-06:84:01:02, 06:87, 06:90-06:91, 06:95-06:97, 06:99:01-06:99:03, 06:106-06:107, 06:109-06:117, 06:122-06:128, 06:130-06:131, 06:133-06:134, 06:136-06:139, 06:141, 06:143, 06:145:01-06:145:02, 06:147-06:148, 06:150-06:152, 06:154, 06:156, 06:159, 06:161-06:163, 06:165-06:166, 06:169-06:170, 06:173-06:176, 06:178-06:179N, 06:182-06:185, 06:187-06:188, 06:190:01-06:192, 06:195-06:198, 06:200-06:201, 06:206:01-06:206:02, 06:208:01-06:208:02, 06:211, 06:213, 06:215-06:216N, 06:218-06:219, 06:221-06:228, 06:230, 06:232-06:234, 06:236-06:238, 06:240, 06:242, 06:244, 06:248-06:250, 06:253, 06:255-06:256, 06:259, 06:262, 06:264, 06:269-06:273, 06:276, 06:278-06:279, 06:284, 06:286, 06:289-06:290, 06:293-06:298, 06:300, 06:304N, 06:306N, 06:308N, 06:311, 06:314-06:317N, 06:319:01-06:319:02, 06:322:01-06:322:03, 06:324, 06:326-06:329, 06:331, 06:333-06:338, 06:341N, 06:344-06:347, 06:350, 06:352, 06:354-06:357, 06:360, 06:362-06:368, 06:370-06:374, 06:376, 06:378-06:380, 06:383N-06:384, 06:388-06:397N, 06:399-06:406, 06:408-06:413, 06:416:01:01Q-06:417, 06:422N-06:425, 06:428, 06:430-06:431, 06:433, 06:437-06:438, 06:440, 06:442-06:443, 06:445-06:448, 06:450, 06:453-06:457, 06:459-06:461, 06:468, 06:470, 06:474, 06:476-06:478, 06:480-06:481, 06:483, 06:485-06:488, 06:491N, 06:493-06:495, 06:497, 06:499-06:500, 06:502-06:504, 06:510, 06:512, 06:514-06:515, 06:517-06:518
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, 06:01:36, 06:06?, 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,



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¹Alleles 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.

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.

²The 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.

³The 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.

⁴For several DQB1 alleles 1st and/or 3rd 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.

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

⁶Primer 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.

⁷Primer 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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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 ¹	Size of control band ²	DR serology ³	Amplified HLA-DRB alleles ⁴
16 ^{11,13}	210 bp, 235 bp, 260 bp	515 bp	1	*01:01:01:01-01:02:14, 01:04:01-01:38, 01:40N-01:98, 01:100-01:101, 01:103-01:111, 01:113-01:126, 01:128-01:154
17	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
18 ^{11,13}	200 bp, 230 bp	430 bp	2, 15	*15:01:01:01-15:233, 16:66
19 ¹³	210 bp	430 bp	11, 16	*11:30, 11:288, 12:57, 16:01:01:01-16:05:02, 16:07-16:79, DRB3*02:111
20 ^{5,8}	120 bp, 225 bp	515 bp	3, 11, 13, 17, 18	*03:01:01:01-03:11:01, 03:11:03-03:125, 03:127-03:217, 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, 15:57:02, 15:100, 15:104:01
21 ^{5,8}	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, 03:106-03:110, 03:112-03:114, 03:116-03:118, 03:121-03:130, 03:132-03:149, 03:151-03:153, 03:156N-03:161, 03:163-03:166, 03:168-03:170, 03:172, 03:174N-03:175, 03:177, 03:180-03:184, 03:186-03:187, 03:189N, 03:191-03:205, 03:207-03:210, 03:214, 03:216-03:218N, 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, 11:85-11:87:02, 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, 11:319, 11:334-11:335, 11:338, 12:73, 13:01:01:01-13:02:01:14, 13:02:02 [?] , 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,



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22⁵	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, 03:206, 03:211-03:212, 03:215, 11:13:01 ^w -11:13:02 ^w , 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, 13:353, 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 ^w -14:32:02 ^w , 14:33, 14:40-14:41, 14:47-14:49, 14:51, 14:63, 14:65 ^w , 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, 14:242:01-14:242:02, 14:252, 14:261, 14:263
23⁵	100 bp, 175 bp	430 bp	3, 4	*04:01:01:01-04:05:11, 04:05:13-04:381, 04:383-04:389N, DRB3*02:190
24¹³	200 bp, 240 bp	430 bp	1, 7	*01:13, 03:54, 07:01:01:01-07:01:01:02, 07:01:01:04-07:01:34, 07:03-07:163N, 08:101, 11:177, 13:92, 15:24, DRB3*01:99, DRB3*02:87, DRB4*01:66
25⁵	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, 08:99-08:128, 08:130-08:131, 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
26^{5,9,14}	85 bp, 100 bp, 135 bp, 165 bp, 190 bp	430 bp	3, 9, 11	*03:08, 03:65, 03:140, 09:01:02:01-09:60, 11:07:01-11:07:02, 11:103:01-11:103:02, 11:105, 11:107, 11:125, 11:173, DRB3*01:42, DRB5*02:31, DRB5*02:34
27^{5,13}	70 bp, 155 bp	430 bp	10, 11, 13	*03:76, 03:125, 03:174N, 03:218N, 09:53, 10:01:01:01, 10:01:01:03-10:46, 11:59, 11:80, 11:83, 11:87:01-11:87:02, 11:135, 11:142, 11:182, 13:27:01-13:27:02, 13:41, 13:71, 13:129, 13:176, 13:277, 13:326, 13:355, 14:179



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28⁵	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-11:338
29⁵	90 bp, 110 bp	430 bp	12, 14	*08:32, 08:53, 08:87, 12:01:01:01-12:56, 12:58-12:113, 14:52
30⁹	215 bp, 235 bp	430 bp	6, 8, 11, 13, 14, 1403	*03:76, 03:125, 03:174N, 03:218N, 08:20-08:21, 08:129, 11:01:01:01, 11:01:01:03-11:01:27, 11:01:28 [?] , 11:01:29- 11:04:24, 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, 11:126-11:135, 11:137- 11:142, 11:144-11:158, 11:160-11:172, 11:174-11:192, 11:194:01-11:201, 11:203-11:208, 11:210-11:228, 11:230-11:260, 11:262-11:265, 11:268-11:269, 11:271- 11:282, 11:284-11:308, 11:310-11:338, 12:57, 13:01:01:01-13:02:01:14, 13:02:03-13:08, 13:10- 13:16:01:02, 13:18-13:43, 13:45-13:85, 13:87-13:115, 13:117:01:01-13:128, 13:130-13:145, 13:147-13:174, 13:176-13:182, 13:184-13:191, 13:194-13:205, 13:207- 13:209, 13:212-13:213, 13:215-13:221, 13:223-13:247, 13:249N-13:288, 13:290-13:298N, 13:300-13:313, 13:315-13:325, 13:327-13:330, 13:332-13:340, 13:342- 13:363, 14:03:01-14:03:02, 14:12:01-14:12:02, 14:16, 14:19, 14:21-14:22, 14:25:01-14:25:02, 14:27:01- 14:27:02, 14:40, 14:53, 14:63, 14:67, 14:69, 14:74, 14:77-14:78, 14:84-14:85, 14:98, 14:102, 14:105, 14:109, 14:115-14:116, 14:128, 14:135, 14:144, 14:156, 14:173-14:174, 14:181, 14:218, 14:222N-14:223, 14:235, 14:239, 14:252, DRB3*02:27, DRB3*02:111, DRB3*02:131, DRB3*02:160
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41¹³	145 bp 430 bp		3, 6, 11, 13, 14, 17	*03:01:01:01-03:01:22, 03:01:24-03:01:41, 03:04:01-03:05:03, 03:07:01:01-03:11:01, 03:11:03-03:16, 03:18-03:25:02, 03:28-03:30, 03:32-03:34, 03:36-03:37, 03:39-03:40, 03:43-03:52:02, 03:54-03:59, 03:61-03:68N, 03:70-03:73, 03:76-03:79, 03:81, 03:83-03:84, 03:86, 03:89, 03:91, 03:93-03:101, 03:104-03:110, 03:112-03:114, 03:116-03:121, 03:123-03:130, 03:132-03:137, 03:139-03:153, 03:156N-03:157, 03:159-03:161, 03:163-03:166, 03:168-03:172, 03:174N-03:175, 03:177-03:178, 03:180, 03:182-03:189N, 03:191-03:205, 03:207-03:210, 03:213-03:214, 03:216-03:218N, 11:01:01:01, 11:01:01:03-11:01:06, 11:01:08-11:01:27, 11:01:28?, 11:01:29-11:04:13, 11:04:15-11:04:24, 11:06:01-11:11:01, 11:11:03-11:16:01:02, 11:18-11:21, 11:23:01-11:29:02, 11:31-11:36, 11:38-11:40, 11:42:01-11:47, 11:49:01-11:49:02, 11:51, 11:53-11:55, 11:57-11:66:02, 11:68-11:70, 11:72-11:82, 11:84:01-11:87:02, 11:89-11:103:02, 11:105-11:106, 11:108-11:144, 11:146-11:148, 11:150-11:169N, 11:172-11:182, 11:185-11:188, 11:190-11:192, 11:194:01-11:199, 11:201-11:208, 11:210-11:228, 11:230-11:248Q, 11:250N-11:260, 11:262-11:263, 11:265-11:269, 11:271-11:272Q, 11:274-11:287N, 11:289-11:308, 11:310-11:331, 11:333-11:338, 13:01:01:01-13:01:08, 13:01:10-13:01:22, 13:01:24-13:02:22, 13:04-13:06, 13:09-13:11:02, 13:14:01-13:16:01:02, 13:18, 13:20:01:01-13:25, 13:27:01-13:31, 13:34, 13:39, 13:41-13:46, 13:50:01-13:52, 13:54, 13:56-13:57, 13:59, 13:61:01-13:64, 13:66:01-13:66:02, 13:68-13:69, 13:71, 13:73-13:75, 13:77-13:80, 13:82-13:83, 13:86-13:87, 13:91-13:93, 13:96:01-13:100, 13:102, 13:104-13:107, 13:109-13:114, 13:117:01:01-13:117:01:02, 13:119, 13:121, 13:123-13:132, 13:136-13:148, 13:150, 13:153-13:158:02, 13:162-13:163, 13:165-13:166, 13:168-13:173, 13:176, 13:178-13:179, 13:181, 13:184-13:187, 13:190, 13:192-13:193, 13:196-13:197, 13:199-13:213, 13:215, 13:217-13:218, 13:220-13:226, 13:229, 13:233-13:234, 13:236-13:245, 13:247, 13:249N-13:252N, 13:254-13:261, 13:263-13:294, 13:296-13:298N, 13:300-13:306, 13:308-13:315, 13:318, 13:320, 13:322N-13:328, 13:330-13:332, 13:335-13:341, 13:343-13:345, 13:348-13:352, 13:354-13:361, 13:363, 14:17, 14:21, 14:30, 14:33, 14:35, 14:42, 14:53, 14:64-14:65, 14:72, 14:95, 14:128, 14:132, 14:134, 14:179, 14:186-14:187, 14:208, 14:221, 14:263, 14:265
42¹³	145 bp, 210 bp, 235 bp	515 bp	4, 6, 8, 11, 13, 14, 1403, 1404	*03:157, 08:09:01-08:09:02, 08:20-08:21, 08:35, 08:129, 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,



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For *In Vitro* Diagnostic Use
MA123 v02 SSP PI Template
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101.704-48/12 – including *Taq* polymerase
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				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, 13:340, 14:01:01:01-14:01:05, 14:02:02 [?] -14:02:03 [?] , 14:02:06 [?] , 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 [?] , 14:23:01:01-14:23:04, 14:25:01 [?] -14:25:02 [?] , 14:26-14:28, 14:29 [?] -14:30 [?] , 14:31-14:32:02, 14:32:03 [?] -14:33 [?] , 14:34-14:36, 14:37 [?] , 14:38:01-14:40, 14:41 [?] , 14:42-14:45, 14:48 [?] -14:49 [?] , 14:50:01-14:50:02, 14:51 [?] -14:52 [?] , 14:54:01:01-14:65, 14:67-14:68:02, 14:69 [?] , 14:70-14:72, 14:73 [?] -14:74 [?] , 14:75, 14:76 [?] , 14:77-14:78, 14:79 [?] -14:80 [?] , 14:81-14:82, 14:83 [?] , 14:84-14:93, 14:94 [?] , 14:95-14:97, 14:98 [?] , 14:99-14:103, 14:104 [?] -14:109 [?] , 14:110-14:118, 14:119 [?] , 14:120, 14:121 [?] , 14:122-14:127:02, 14:128 [?] , 14:129-14:145, 14:146 [?] , 14:147-14:158, 14:159 [?] , 14:160-14:164, 14:165 [?] , 14:166N-14:169, 14:170 [?] , 14:171-14:175, 14:176 [?] , 14:178, 14:179 [?] , 14:180-14:182, 14:183 [?] , 14:184-14:193, 14:196-14:197N, 14:199, 14:201-14:202, 14:203 [?] , 14:204-14:208, 14:210Q-14:211, 14:213-14:220, 14:222N-14:225, 14:227-14:241, 14:243-14:249, 14:250 [?] , 14:251-14:256, 14:257 [?] , 14:258-14:260, 14:262 [?] , 14:264-14:269N
43^{9,11}	140 bp, 170 bp	515 bp	6, 13, 14	*03:76, 03:126, 03:174N, 03:177, 03:218N, 04:211, 04:230, 12:66 ^w , 13:10, 13:85-13:86, 13:120, 13:170, 13:176, 13:178, 13:193, 13:196, 13:216, 14:02:01:01-14:02:12, 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, 14:242:01-14:242:02, 14:261, 14:263, DRB3*02:27, DRB3*02:58
44^{5,8,9,13,15}	80 bp, 110 bp, 170 bp, 240 bp	515 bp	12, 52	*12:05, 12:15, 12:57, 14:141, 14:257, 14:262, DRB3*01:01:02:01-01:130, DRB3*02:01-02:212, DRB3*03:01:01:01-03:21, DRB3*03:23-03:76
45^{7,10}	130 bp, 210 bp	430 bp	53	*01:139, 03:211, 10:19, 14:217, 15:141, DRB4*01:01:01:01, DRB4*01:01:01:03-01:188, DRB4*02:01N, DRB4*03:01N
46⁶	175 bp, 220 bp	430 bp	51	DRB5*01:01:01:01-01:130, DRB5*01:132-01:142, DRB5*02:02:01-02:39
47^{11,16}	-	-	-	Negative Control

¹Alleles 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.



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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.

²The 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.

³The 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.

⁴For several DRB1 alleles 1st and/or 3rd 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.

⁵HLA-Specific PCR fragments shorter than 125 base pairs have a lower intensity and are less sharp than longer PCR bands.

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

⁷The 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.

⁸Due 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.

⁹Due 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.

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

¹¹Primer mixes 16, 18, 31, 34, 37, 43 and 47 may have a tendency of giving rise to primer oligomer formation.

¹²Primer 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.

¹³Primer mixes 16, 18, 19, 24, 27, 37, 41, 42 and 44 may have a tendency of unspecific amplification.

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

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

¹⁶Primer 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	185 220 270		220	220			160 185 210		215		
Length of int.	515	515	430	515	515	515	515	430	430	430	430	430
pos. control ¹												
5'-primer(s) ²	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'}	9(122) 5'-gTT ^{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'}			21(159) 5'-ACC ^{3'}				
	26(173) 5'-ggg ^{3'}	26(172) 5'-ATC ^{3'}	30(185) 5'-AAg ^{3'}		28(179) 5'-gAC ^{3'}			23(164) 5'-gCT ^{3'}				
	26(173) 5'-gTg ^{3'}	26(173) 5'-TTA ^{3'}	30(185) 5'-AAA ^{3'}					38(210) 5'-gCg ^{3'}				
		26(173) 5'-TCT ^{3'}										
		30(184) 5'-gAT ^{3'}										
3'-primer(s) ³	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 ¹			
5'-primer(s) ²	9(122) 5'-gTT ^{3'}	38(209) 5'-CgC ^{3'}	13(134) 5'-ggC ^{3'}
3'-primer(s) ³	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

¹The 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.

²The nucleotide position matching the specificity-determining 3'-end of the primer is given. Nucleotide numbering as on the www.ebi.ac.uk/imgt/hla web site. The sequence of the 3 terminal nucleotides of the primer is given.

³The 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 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. PCR product	210 235 260	200	200 230	210	120 225	75 205	85 210	100 175	200 240	85 215 250	85 100 165 190	70 155
Length of int. pos. control ¹	515	430	430	430	515	430	430	430	430	515	430	430
5'-primer(s) ²	11(119) 5'-gCT ³ 14(129) 5'-gAA ³ 13(126) 5'-AAg ³ 13(126) 5'-AAg ³ 13(126) 5'-AgA ³	14(129) 5'-gAA ³ 13(126) 5'-Agg ³ 13(126) 5'-AAg ³ 13(126) 5'-AgA ³	12(121) 5'-CTg ³ 13(126) 5'-Agg ³ 13(126) 5'-AAg ³ 13(126) 5'-AAg ³ 5'-AgA ³	11(119) 5'-gCT ³ 13(126) 5'-Agg ³ 13(126) 5'-AAg ³ 13(126) 5'-AAg ³ 5'-AgA ³	13(125) 5'-gTC ³ 47(227) 5'-gTT ³ 16(133) 5'-gTT ³	13(125) 5'-gTC ³ 16(133) 5'-gTT ³	13(125) 5'-gTC ³	13(124) 5'-AAC ³ 13(125) 5'-ATA ³ 13(125) 5'-gTC ³	11(118) 5'-AgA ³ 14(127) 5'-ATA ³ 14(127) 5'-ATA ³ 14(127) 5'-ATA ³ 25(161) 5'-gCA ³	16(133) 5'-gTT ³ 16(133) 5'-gTT ³ 16(133) 5'-gCT ³ 60(265) 5'-gTA ³ 5'-AgT ³	26(165) 5'-TAT ³ 37(196) 5'-AgA ³ 58(261) 5'-gAg ³	26(164) 5'-gTA ³ 31(178) 5'-gCg ³ 58(261) 5'-gAg ³
3'-primer(s) ³	67(286) 5'-gAg ³ 67(286) 5'-gAg ³ 67(286) 5'-gAT ³ 70(297) 5'-CTg ³ 71(299) 5'-gCg ³ 73(305) 5'-ggC ³ 77(317) 5'-AgT ³ 86(344) 5'-CCA ³	67(286) 5'-gAT ³ 67(286) 5'-gAA ³ 67(286) 5'-gAT ³ 70(297) 5'-CTg ³ 71(299) 5'-gCg ³ 73(305) 5'-ggC ³ 77(317) 5'-AgT ³ 86(344) 5'-CCA ³	67(286) 5'-gAT ³ 67(286) 5'-gAT ³ 70(295) 5'-CTg ³ 70(295) 5'-Tg ³ 70(296) 5'-TCC ³ 71(299) 5'-gCg ³ 71(299) 5'-gCT ³ 72(301) 5'-Cg ³ 73(305) 5'-ggC ³ 77(317) 5'-AgT ³	67(286) 5'-gAA ³ 67(286) 5'-gAg ³ 67(286) 5'-gAT ³ 70(296) 5'-TgT ³ 72(302) 5'-Cgg ³ 74(308) 5'-CCC ³ 75(310) 5'-CAA ³ 77(317) 5'-AgT ³	73(305) 5'-ggC ³ 67(286) 5'-gAT ³ 71(299) 5'-gCT ³ 73(305) 5'-ggC ³ 74(308) 5'-CCC ³ 75(310) 5'-CAA ³ 77(317) 5'-AgT ³	26(164) 5'-ggT ³ 70(295) 5'-CTg ³ 71(299) 5'-gCT ³	28(171) 5'-CTC ³ 70(295) 5'-CTg ³	33(184) 5'-gTg ³ 58(260) 5'-Cgg ³	78(319) 5'-CAC ³ 78(319) 5'-gTA ³ 78(319) 5'-CAA ³ 78(319) 5'-CgC ³	74(307) 5'-CAg ³ 86(344) 5'-CAC ³	57(257) 5'-CgA ³ 73(305) 5'-ggC ³ 78(319) 5'-gCA ³ 74(307) 5'-CgC ³	38(200) 5'-gCg ³ 72(303) 5'-gCA ³ 74(307) 5'-CgC ³
Well No.	16	17	18	19	20	21	22	23	24	25	26	27

Well No.	28	29	30	31	32	33	34	35	36	37	38	39
Length of spec. PCR product	100 175	90 110	215 235	195 215	175	75 100 140 170	110 145 180 220	110 150 180	170 265	75 175 265	135	170 195
Length of int. pos. control ¹	430	430	430	430	430	430	430	430	430	515	430	430
5'-primer(s) ²	13(125) 5'-gTC ³ 16(133) 5'-gTC ³ 38(200) 5'-CgT ³	13(124) 5'-Cgg ³ 16(133) 5'-gTT ³ 13(125) 5'-gTC ³	10(116) 5'-gCT ³ 12(122) 5'-TAT ³ 12(123) 5'-gTC ³	10(116) 5'-gCT ³ 12(122) 5'-TAT ³ 12(123) 5'-ACA ³ 13(125) 5'-gTC ³ 13(125) 5'-gTg ³ 16(133) 5'-gTC ³ 16(133) 5'-gTT ³	13(125) 5'-gTC ³ 37(197) 5'-gTT ³ 37(197) 5'-gTA ³ 34(189) 5'-CCg ³	5(101) 5'-CAA ³ 37(197) 5'-gTT ³ 34(189) 5'-gTA ³	26(164) 5'-gTA ³ 34(189) 5'-CAg ³ 34(189) 5'-CAg ³ 34(189) 5'-CCg ³	13(125) 5'-gTC ³ 34(189) 5'-CAg ³ 34(189) 5'-CAg ³ 37(196) 5'-AgC ³ 16(133) 5'-gTT ³	13(125) 5'-ggg ³ 16(133) 5'-gCT ³ 74(308) 5'-CCT ³ 16(133) 5'-gTT ³	12(122) 5'-TAG ³ 74(308) 5'-CCT ³ 16(133) 5'-gTT ³	16(133) 5'-gTT ³ 108(409) 5'-AgA ³	13(125) 5'-gTC ³ 108(409) 5'-AgA ³
3'-primer(s) ³	58(260) 5'-CCT ³ 58(260) 5'-CCT ³ 58(260) 5'-CCT ³ 58(261) 5'-TCT ³	28(171) 5'-CTC ³ 30(175) 5'-gTg ³ 38(199) 5'-CAg ³ 74(307) 5'-CgT ³ 78(319) 5'-CAC ³	70(295) 5'-gTC ³ 71(299) 5'-gCT ³ 71(299) 5'-ACT ³ 74(307) 5'-CgT ³ 78(319) 5'-CAC ³	67(286) 5'-gAA ³ 71(298) 5'-CTC ³ 71(298) 5'-CgC ³	57(257) 5'-CAT ³ 58(260) 5'-Cgg ³ 58(260) 5'-CAg ³	48(230) 5'-CCT ³ 57(257) 5'-CAg ³ 70(295) 5'-CTg ³ 71(298) 5'-CgC ³	57(257) 5'-CAg ³ 70(295) 5'-CTg ³ 70(296) 5'-TCC ³	57(257) 5'-CAg ³ 60(265) 5'-gTg ³ 70(296) 5'-TCC ³ 74(307) 5'-CAg ³	57(256) 5'-gCT ³ 57(257) 5'-CAT ³ 57(257) 5'-CAT ³	57(256) 5'-gCT ³ 86(344) 5'-CCA ³ 86(344) 5'-CAA ³	47(227) 5'-ggA ³	57(256) 5'-gCT ³ 160(565) 5'-CAT ³
Well No.	28	29	30	31	32	33	34	35	36	37	38	39



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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. pos. control ¹	430	430	515	515	515	430	430
5'-primer(s) ²	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'}		
3'-primer(s) ³	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'}	57(256) 5'-gCT ^{3'}	87(346) 5'-CTC ^{3'}	57(256) 5'-gCT ^{3'}
			181(630) 5'-CTT ^{3'}		60(266) 5'-Agg ^{3'}	87(346) 5'-CTT ^{3'}	57(258) 5'-gCg ^{3'}
					77(317) 5'-AAT ^{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

¹The 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.

²The nucleotide position matching the specificity-determining 3'-end of the primer is given. Nucleotide numbering as on the www.ebi.ac.uk/imgt/hla web site. The sequence of the 3 terminal nucleotides of the primer is given.

³The 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 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: December 2024, Rev. No: 00

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

Visit www.caredx.com for
“Instructions for Use” (IFU)

Lot No.: 1V2

Lot-specific information

CELL LINE VALIDATION SHEET																			
DQ low resolution primer set ²																			
				Well															
				1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
				Prod. No.:	202461101	202461102	202461103	202461104	202461105	202461106	202461107	202461108	202461109	202461110	202461111	202461112	202461113	202461114	202461115
				IHWC cell line ¹	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.: 1V2

Lot-specific information

CELL LINE VALIDATION SHEET																			
DR low resolution primer set ²																			
			Prod. No.:	Well															
				16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
				202461001	202461002	202461003	202461004	202461005	202461006	202461007	202461008	202461009	202461010	202461011	202461012	202461013	202461014	202461015	202461016
	IHWC cell line ¹	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
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Lot No.: 1V2

Lot-specific information

CELL LINE VALIDATION SHEET																			
DR low resolution primer set ²																			
				Well															
				32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	
				Prod. No.:	202461017	202461018	202461019	202461020	202461021	202461022	202461023	202461024	202461025	202461026	202461027	202461028	202461029	202461030	202461031
IHC cell line ¹			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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101.704-48/12 – including *Taq* polymerase
101.704-48u/12u – without *Taq* polymerase

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Lot No.: **1V2**

Lot-specific information

¹The 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.

The DRB4*01:03:01:02N allele is amplified by primer mix 33 in the 9052 (DBB) cell line.

²The 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, 37, 44 and 46 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.



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MA123 v02 SSP PI Template

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

Visit www.caredx.com for
 “Instructions for Use” (IFU)

Lot No.: **1V2**

Lot-specific information

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