

**Sample: demultiplex.06896-3**

**Full typing result**

	Allele 1	Allele 2	CWD 1	CWD 2	Review status
HLA-A	01:01:01:01	26:01:01:01	C	C	Not reviewed
HLA-B	40:02:01:01	58:01:01:01	C	C	Not reviewed
HLA-C	02:02:02:01	03:02:02:01	C	WD	Not reviewed
DRB1	13:01:01:01	13:02:01:01	C	C	Not reviewed
DQB1	06:03:01:01	06:09:01:01	C	C	Not reviewed
DPB1	02:01:02:01	02:01:02:26	C	No	Not reviewed

**Genotype ambiguities**

**Allele ambiguities**

Major fields	CWD	3rd field	CWD	4th field	CWD
				A*01:01:01:01 : A*01:01:01:25	No
				B*40:02:01:01 : B*40:02:01:02 : B*40:02:01:03 : B*40:02:01:08	No No No
				B*58:01:01:01 : B*58:01:01:03	No
				C*03:02:02:01 : C*03:02:02:05	No
				DRB1*13:01:01:01 : DRB1*13:01:01:02 : DRB1*13:01:01:03	No No
				DRB1*13:02:01:01 : DRB1*13:02:01:03 : DRB1*13:02:01:04	No No
DQB1*06:09:01:01 : DQB1*06:281	No	DQB1*06:03:01:01 : DQB1*06:03:35	No	DQB1*06:03:01:01 : DQB1*06:03:01:02	No
				DPB1*02:01:02:01 : DPB1*02:01:02:04 : DPB1*02:01:02:05 : DPB1*02:01:02:07 : DPB1*02:01:02:15 : DPB1*02:01:02:17 <i>and 9 more</i>	No No No No No

**Libraries used**

IMGT 3.38.0

**Source files**

- demultiplex.06896-3.fastq

Sample: demultiplex.06896-3

Locus: HLA-A

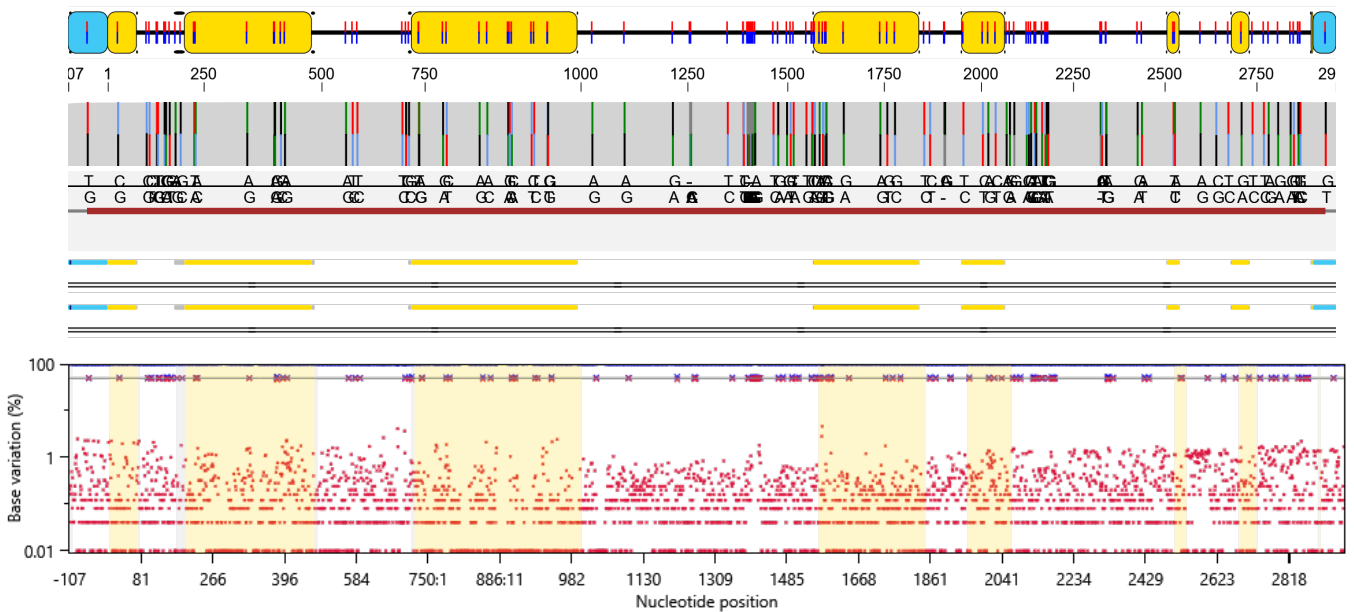
### Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
A*01:01:01:01	A*26:01:01:01	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

4th field	CWD
A*01:01:01:01	
: A*01:01:01:25	No

### Visualization



### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

Sample: demultiplex.06896-3

Locus: HLA-B

### Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
<b>B*40:02:01:01</b>	<b>B*58:01:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

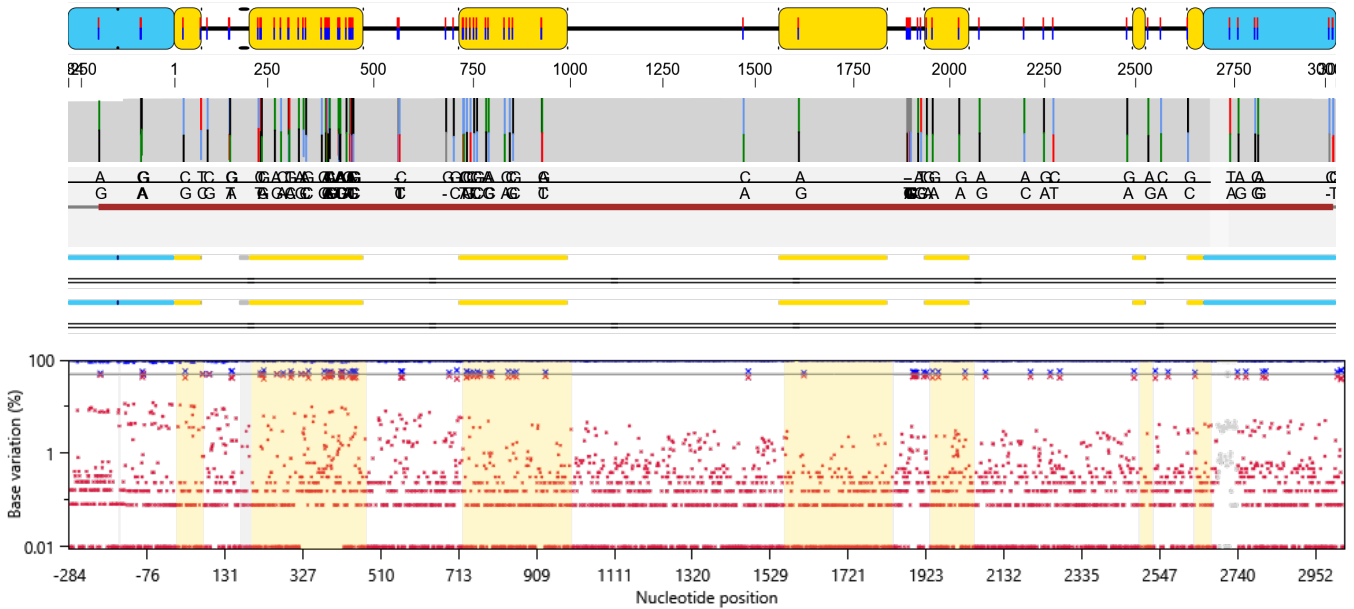
### Allele ambiguities

4th field CWD

B\*40:02:01:01  
: B\*40:02:01:02 No  
: B\*40:02:01:03 No  
: B\*40:02:01:08 No

B\*58:01:01:01  
: B\*58:01:01:03 No

### Visualization



### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

Sample: demultiplex.06896-3

Locus: HLA-C

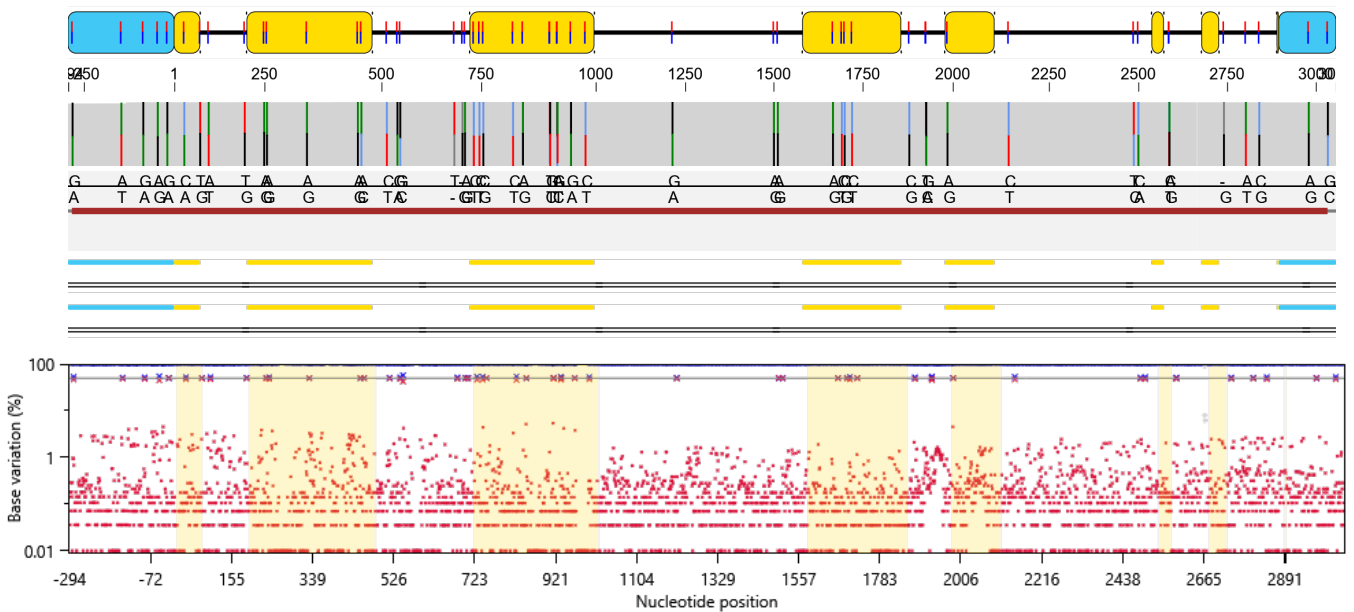
### Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
C*02:02:02:01	C*03:02:02:01	C	WD	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

4th field	CWD
C*03:02:02:01	
: C*03:02:02:05	No

### Visualization



### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

Sample: demultiplex.06896-3

Locus: DRB1

### Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
DRB1*13:01:01:01	DRB1*13:02:01:01	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

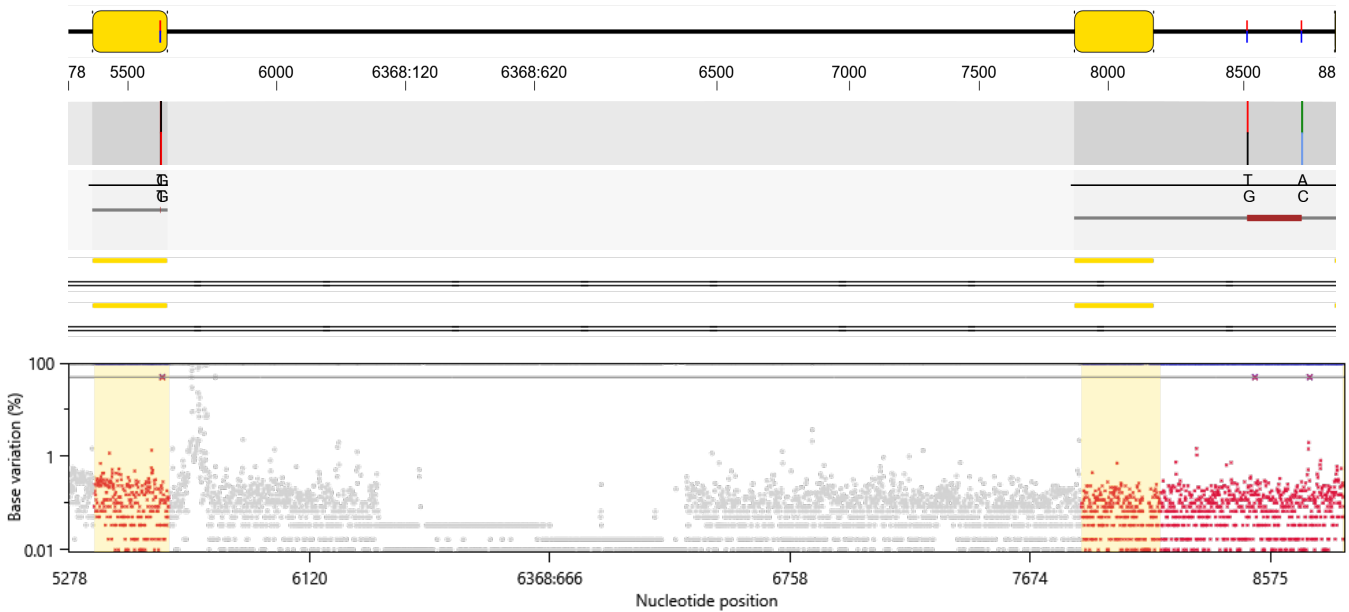
### Allele ambiguities

4th field CWD

DRB1\*13:01:01:01  
: DRB1\*13:01:01:02 No  
: DRB1\*13:01:01:03 No

DRB1\*13:02:01:01  
: DRB1\*13:02:01:03 No  
: DRB1\*13:02:01:04 No

### Visualization



### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

Sample: demultiplex.06896-3

Locus: DQB1

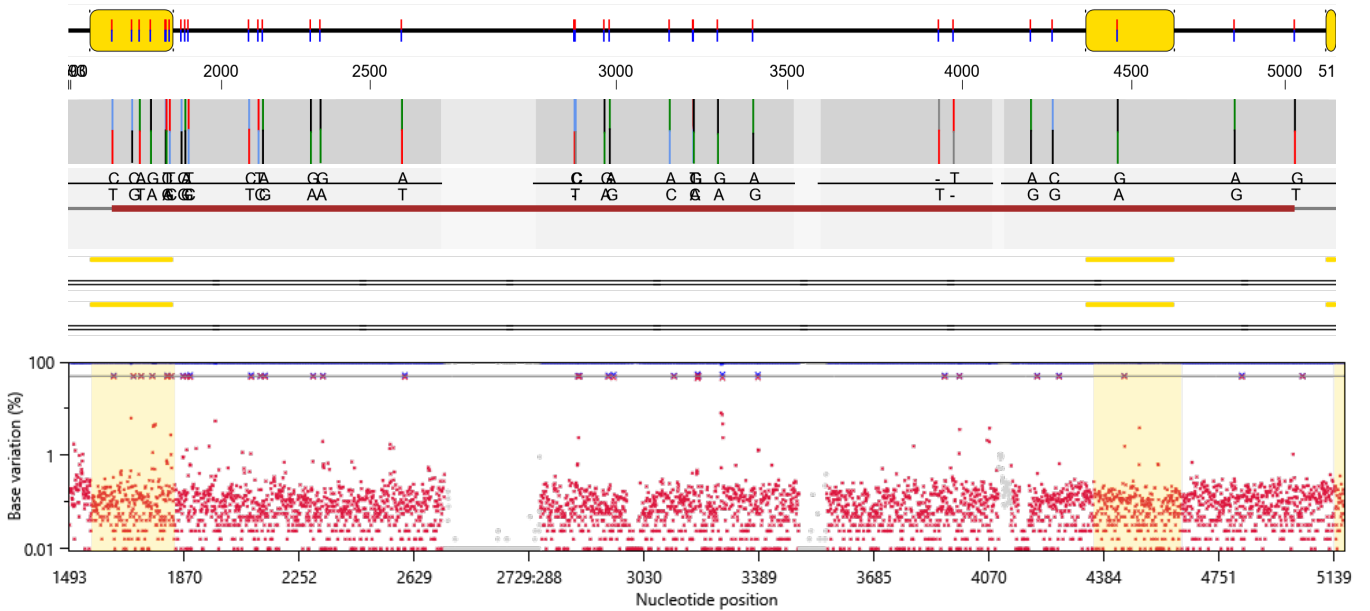
Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
DQB1*06:03:01:01	DQB1*06:09:01:01	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

Allele ambiguities

Major fields	CWD	3rd field	CWD	4th field	CWD
DQB1*06:09:01:01 : DQB1*06:281	No	DQB1*06:03:01:01 : DQB1*06:03:35	No	DQB1*06:03:01:01 : DQB1*06:03:01:02	No

Visualization



Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

Sample: demultiplex.06896-3

Locus: DPB1

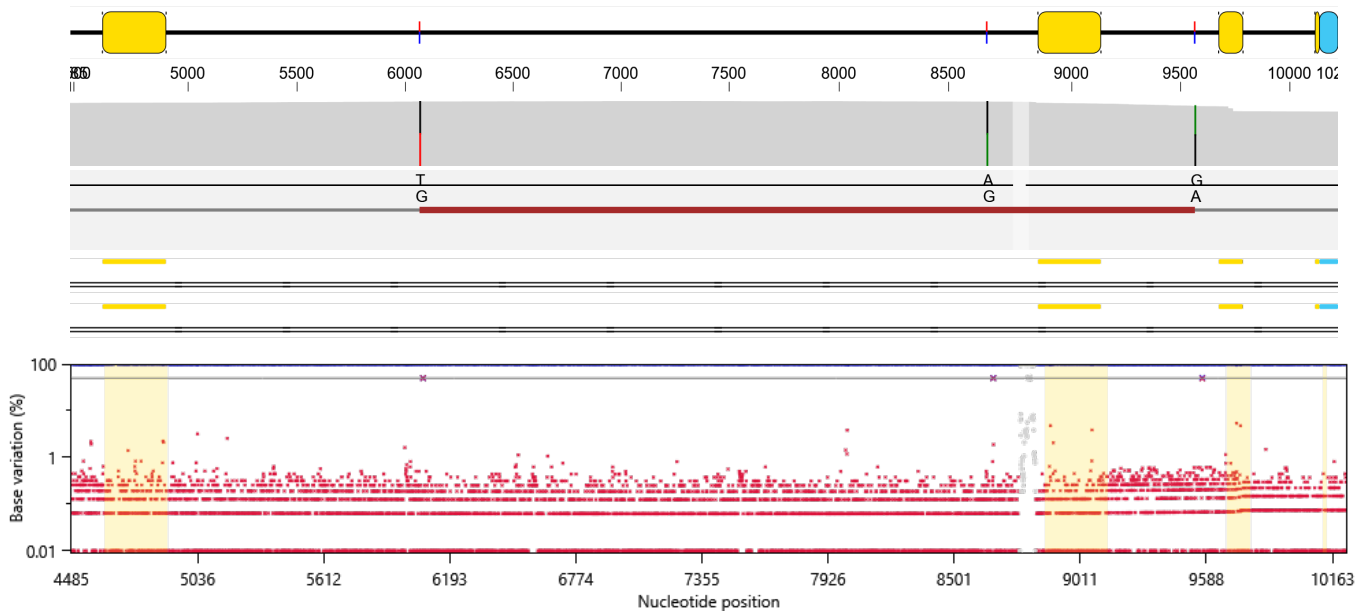
### Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
DPB1*02:01:02:01	DPB1*02:01:02:26	C	No	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

4th field	CWD
DPB1*02:01:02:01	
: DPB1*02:01:02:04	No
: DPB1*02:01:02:05	No
: DPB1*02:01:02:07	No
: DPB1*02:01:02:15	No
: DPB1*02:01:02:17	No
and 9 more	

### Visualization



### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

## Sample details

### Reads

Total number of reads: 26886  
Mappability: 26858 of 26886 reads used  
Software: NGSengine 2.18.0.17625

Locus	Number of reads	Reads Perc.
HLA-A	2512	9.4 %
HLA-B	1289	4.8 %
HLA-C	2864	10.7 %
DRB1	6048	22.5 %
DQB1	12525	46.6 %
DPB1	1620	6.1 %
	27	0.2 %
DRB1, DQB1	1	0.1 %

### Analysis settings

Locus	Amplicon	Analysis Region	Ignore Regions	Phasing algorithm	Read depth threshold	Allele ratio threshold	Quality trimming
HLA-A	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-B	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-C	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
DRB1	NGSgo-MX6-1	Amplicon	Default	Classic	20	15	20, 70, 10
DQB1	NGSgo-MX6-1	Amplicon	Default	Cluster	20	15	20, 70, 10
DPB1	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10

Quality trimming numbers: Absolute threshold, Relative threshold, Window size

### Analysis settings cont.

Locus	Noise threshold	CWD sorting applied
HLA-A	15	Yes
HLA-B	15	Yes
HLA-C	15	Yes
DRB1	10	Yes
DQB1	10	Yes
DPB1	10	Yes



**Sample: demultiplex.12878-HG001**

**Full typing result**

	Allele 1	Allele 2	CWD 1	CWD 2	Review status
HLA-A	01:01:01:01	11:01:01:01	C	C	Not reviewed
HLA-B	08:01:01:01	56:01:01:03	C	No	Not reviewed
HLA-C	01:02:01:01	07:01:01:01	C	C	Not reviewed
DRB1	01:01:01:01	03:01:01:01	C	C	Not reviewed
DQB1	02:01:01	05:01:01:02	C	No	Not reviewed
DPB1	04:01:01:01	14:01:01:01	C	C	Not reviewed

**Genotype ambiguities**

**Allele ambiguities**

Major fields	CWD	3rd field	CWD	4th field	CWD
				A*01:01:01:01 : A*01:01:01:25	No
				A*11:01:01:01 : A*11:01:01:13	No
				B*08:01:01:01 : B*08:01:01:16	No
				B*56:01:01:03 : B*56:01:01:04	No
				C*01:02:01:01 : C*01:02:01:05	No
				C*07:01:01:01 : C*07:01:01:15 : C*07:01:01:16 : C*07:01:01:69	No No No
DRB1*01:01:01:01 : DRB1*01:100	No	DRB1*01:01:01:01 : DRB1*01:01:32 : DRB1*01:01:33	No No	DRB1*01:01:01:01 : DRB1*01:01:01:02	No
DRB1*03:01:01:01 : DRB1*03:147	No			DRB1*03:01:01:01 : DRB1*03:01:01:02 : DRB1*03:01:01:03	No No
DQB1*02:01:01 : DQB1*02:109 : DQB1*02:148 : DQB1*02:163N	No No No			DQB1*05:01:01:02 : DQB1*05:01:01:03	No
				DPB1*04:01:01:01 : DPB1*04:01:01:02 : DPB1*04:01:01:04 : DPB1*04:01:01:05 : DPB1*04:01:01:06 : DPB1*04:01:01:14 <i>and 10 more</i>	No No No No No
				DPB1*14:01:01:01 : DPB1*14:01:01:02	No

**Libraries used**

IMGT 3.38.0

**Source files**

- demultiplex.12878-HG001.fastq

Sample: demultiplex.12878-HG001

Locus: HLA-A

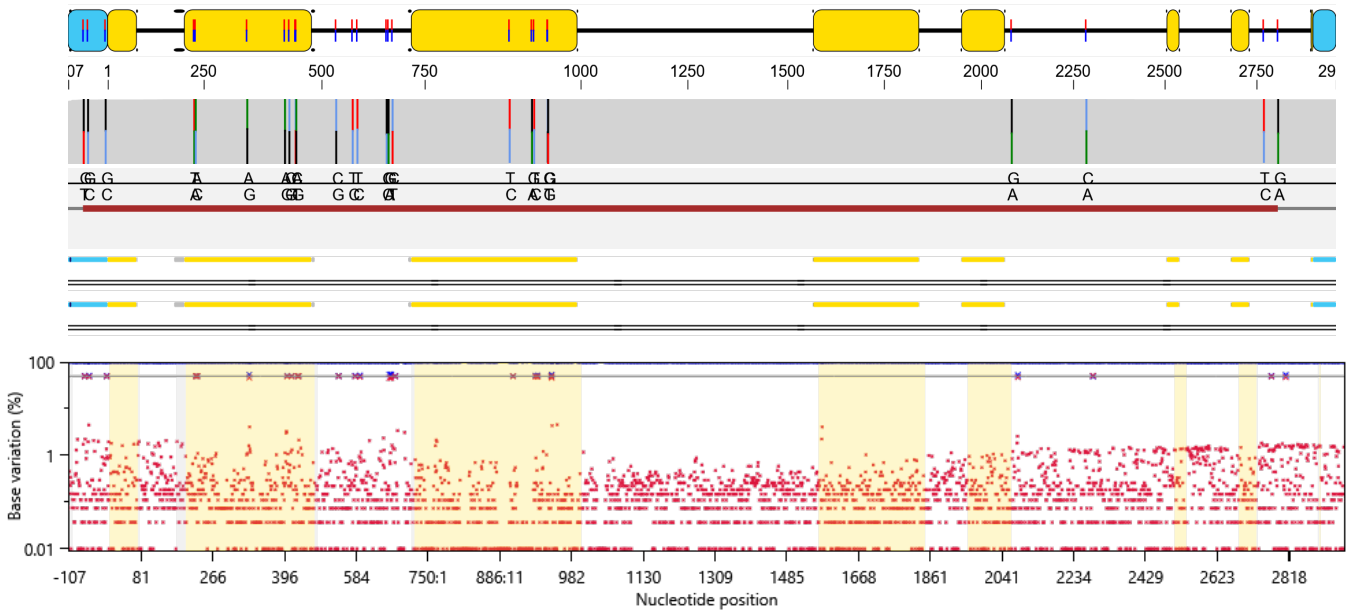
### Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
A*01:01:01:01	A*11:01:01:01	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

4th field	CWD
A*01:01:01:01 : A*01:01:01:25	No
A*11:01:01:01 : A*11:01:01:13	No

### Visualization



### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

Sample: demultiplex.12878-HG001

Locus: HLA-B

### Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
<b>B*08:01:01:01</b>	<b>B*56:01:01:03</b>	C	No	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

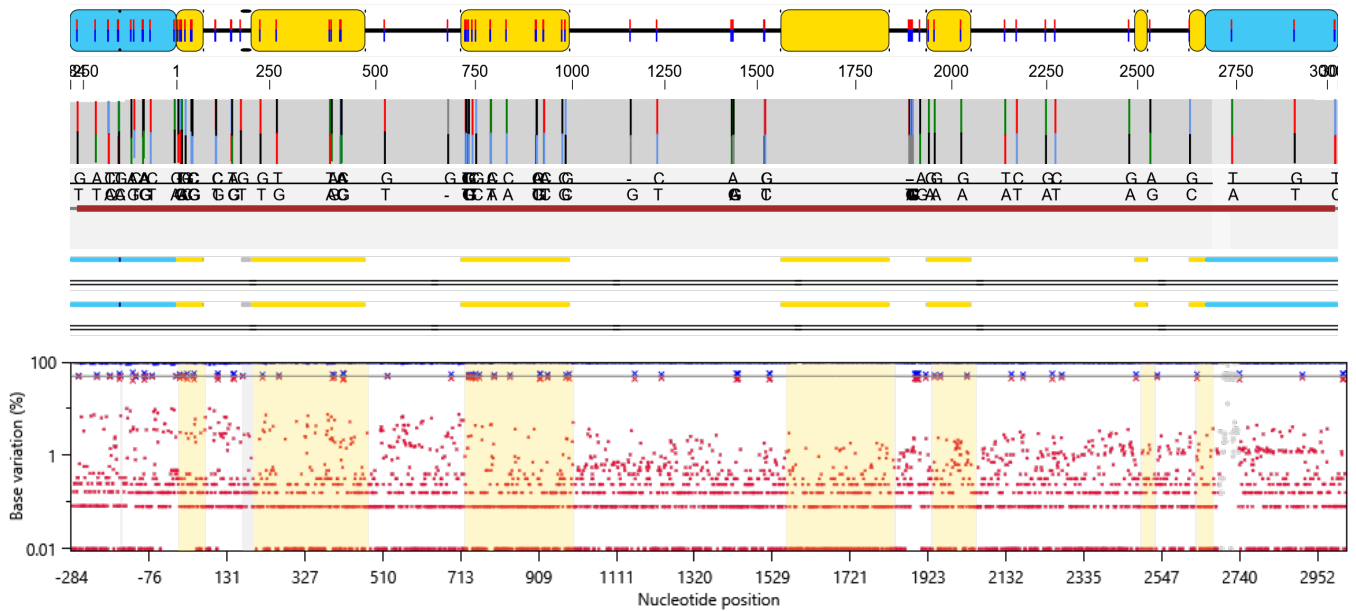
### Allele ambiguities

4th field CWD

B\*08:01:01:01  
: B\*08:01:01:16 No

B\*56:01:01:03  
: B\*56:01:01:04 No

### Visualization



### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

Sample: demultiplex.12878-HG001

Locus: HLA-C

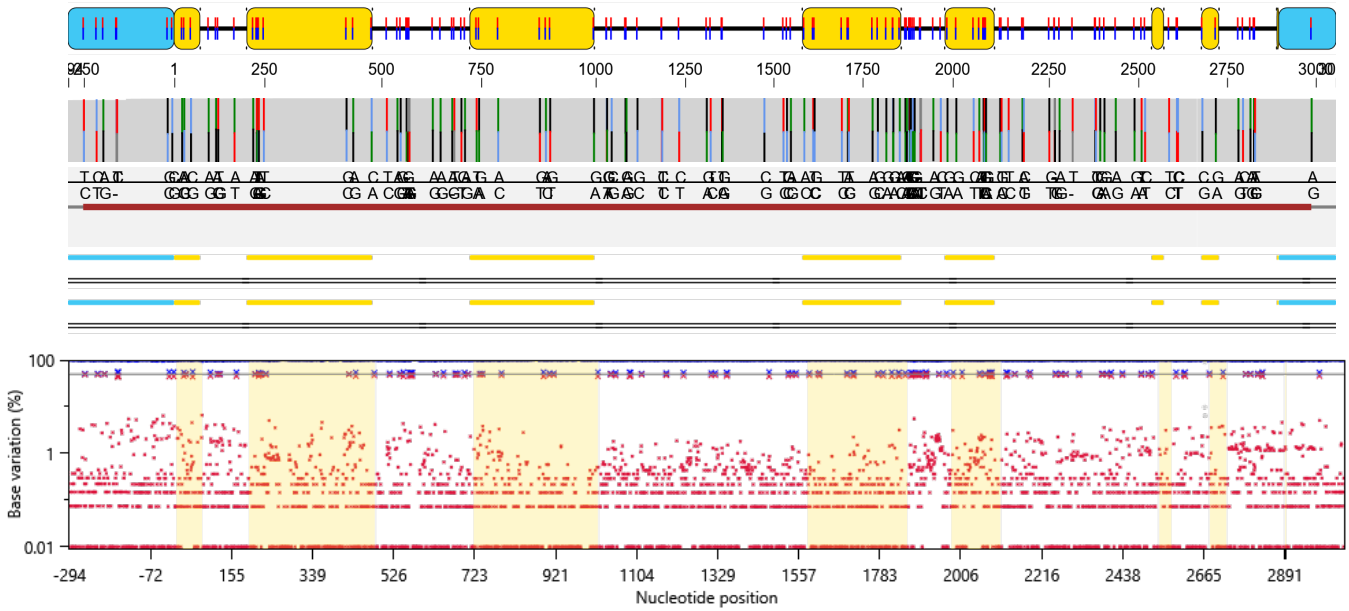
Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
C*01:02:01:01	C*07:01:01:01	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

Allele ambiguities

4th field	CWD
C*01:02:01:01	
: C*01:02:01:05	No
C*07:01:01:01	
: C*07:01:01:15	No
: C*07:01:01:16	No
: C*07:01:01:69	No

Visualization



Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

Sample: demultiplex.12878-HG001

Locus: DRB1

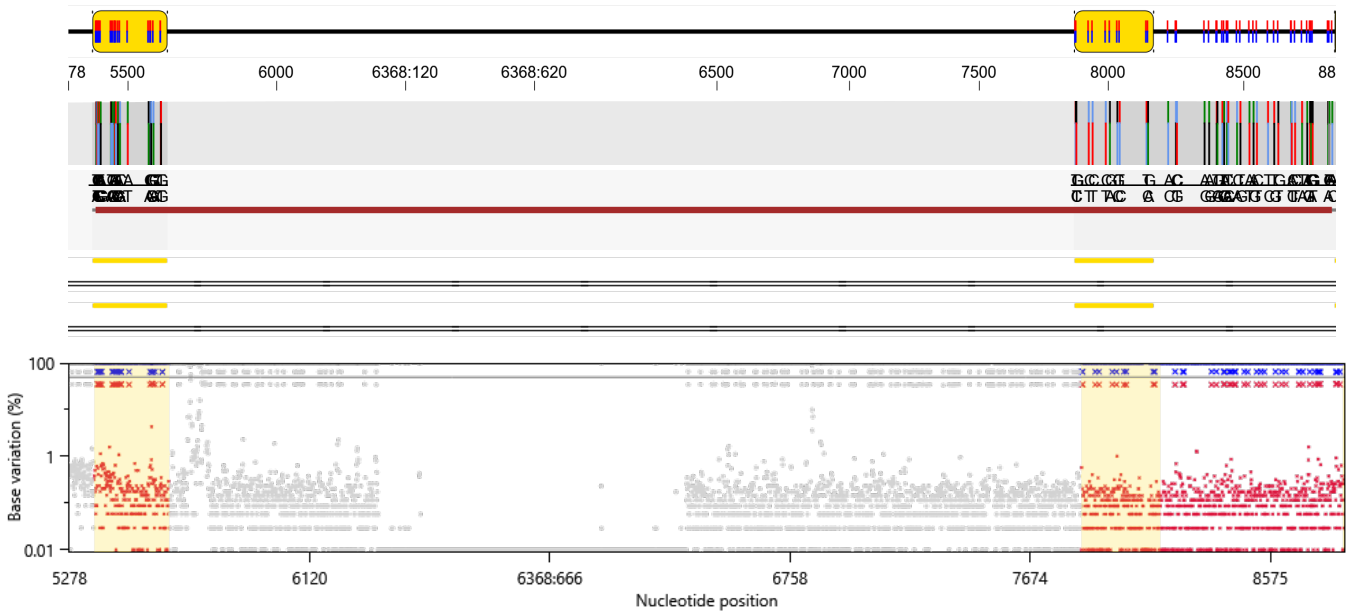
### Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
DRB1*01:01:01:01	DRB1*03:01:01:01	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

Major fields	CWD	3rd field	CWD	4th field	CWD
DRB1*01:01:01:01 : DRB1*01:100	No	DRB1*01:01:01:01 : DRB1*01:01:32 : DRB1*01:01:33	No No	DRB1*01:01:01:01 : DRB1*01:01:01:02	No
DRB1*03:01:01:01 : DRB1*03:147	No			DRB1*03:01:01:01 : DRB1*03:01:01:02 : DRB1*03:01:01:03	No No

### Visualization



### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

Sample: demultiplex.12878-HG001

Locus: DQB1

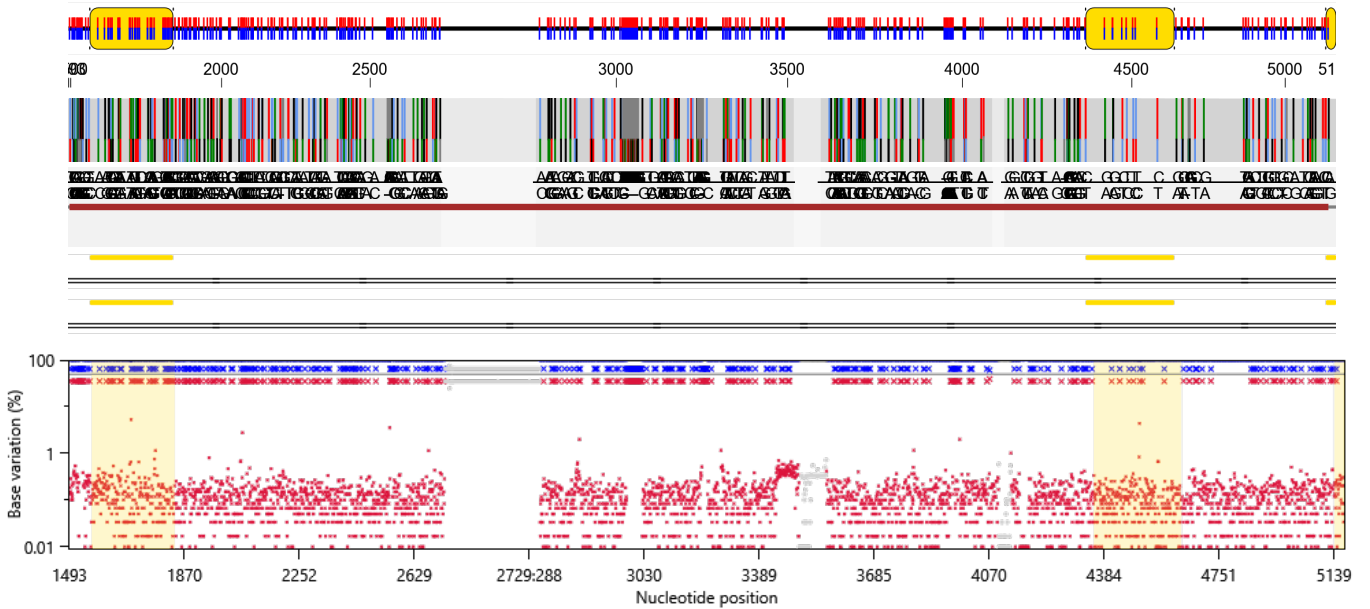
Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
DQB1*02:01:01	DQB1*05:01:01:02	C	No	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

Allele ambiguities

Major fields	CWD	4th field	CWD
DQB1*02:01:01	No		
: DQB1*02:109	No		
: DQB1*02:148	No		
: DQB1*02:163N	No		
		DQB1*05:01:01:02	
		: DQB1*05:01:01:03	No

Visualization



Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

Sample: demultiplex.12878-HG001

Locus: DPB1

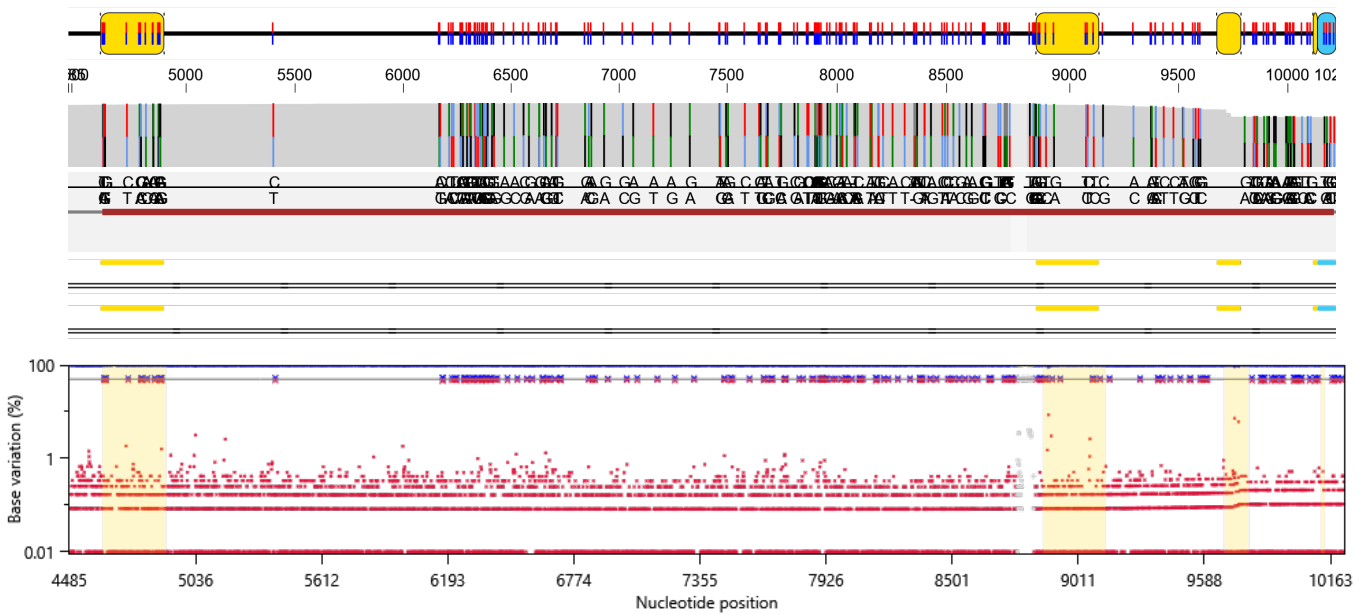
### Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
DPB1*04:01:01:01	DPB1*14:01:01:01	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

4th field	CWD
DPB1*04:01:01:01	No
: DPB1*04:01:01:02	No
: DPB1*04:01:01:04	No
: DPB1*04:01:01:05	No
: DPB1*04:01:01:06	No
: DPB1*04:01:01:14	No
and 10 more	
DPB1*14:01:01:01	No
: DPB1*14:01:01:02	No

### Visualization



### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

## Sample details

### Reads

Total number of reads: 16191  
Mappability: 16142 of 16191 reads used  
Software: NGSengine 2.18.0.17625

Locus	Number of reads	Reads Perc.
HLA-A	2730	16.9 %
HLA-B	1271	7.9 %
HLA-C	1395	8.7 %
DRB1	3503	21.7 %
DQB1	6010	37.2 %
DPB1	1233	7.7 %
	49	0.4 %

### Analysis settings

Locus	Amplicon	Analysis Region	Ignore Regions	Phasing algorithm	Read depth threshold	Allele ratio threshold	Quality trimming
HLA-A	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-B	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-C	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
DRB1	NGSgo-MX6-1	Amplicon	Default	Classic	20	15	20, 70, 10
DQB1	NGSgo-MX6-1	Amplicon	Default	Cluster	20	15	20, 70, 10
DPB1	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10

Quality trimming numbers: Absolute threshold, Relative threshold, Window size

### Analysis settings cont.

Locus	Noise threshold	CWD sorting applied
HLA-A	15	Yes
HLA-B	15	Yes
HLA-C	15	Yes
DRB1	10	Yes
DQB1	10	Yes
DPB1	10	Yes



**Sample: demultiplex.24143-HG004**

**Full typing result**

	<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>HLA-A</b>	<b>01:01:01:01</b>	<b>33:01:01:01</b>	C	C	Not reviewed
<b>HLA-B</b>	<b>14:02:01:01</b>	<b>35:08:01:01</b>	C	C	Not reviewed
<b>HLA-C</b>	<b>04:01:01:06</b>	<b>08:02:01:01</b>	No	C	Not reviewed
<b>DRB1</b>	<b>04:04:01</b>	<b>10:01:01:01</b>	C	C	Not reviewed
<b>DQB1</b>	<b>04:02:01:06</b>	<b>05:01:01:05</b>	No	No	Not reviewed
<b>DPB1</b>	<b>04:01:01:01</b>	<b>04:01:01:01</b>	C	C	Not reviewed

**Genotype ambiguities**

**Allele ambiguities**

<b>3rd field</b>	<b>CWD</b>	<b>4th field</b>	<b>CWD</b>
		A*01:01:01:01 : A*01:01:01:25	No
		C*08:02:01:01 : C*08:02:01:05	No
DRB1*10:01:01:01 : DRB1*10:01:12	No	DRB1*10:01:01:01 : DRB1*10:01:01:02 : DRB1*10:01:01:03	No No
DQB1*04:02:01:06 : DQB1*04:02:13	No	DQB1*04:02:01:06 : DQB1*04:02:01:08	No
		DPB1*04:01:01:01 : DPB1*04:01:01:02 : DPB1*04:01:01:04 : DPB1*04:01:01:05 : DPB1*04:01:01:06 : DPB1*04:01:01:14 <i>and 10 more</i>	No No No No No
		DPB1*04:01:01:01 : DPB1*04:01:01:02 : DPB1*04:01:01:04 : DPB1*04:01:01:05 : DPB1*04:01:01:06 : DPB1*04:01:01:14 <i>and 10 more</i>	No No No No No

**Libraries used**

IMGT 3.38.0

**Source files**

- demultiplex.24143-HG004.fastq

Sample: demultiplex.24143-HG004

Locus: HLA-A

### Full typing result

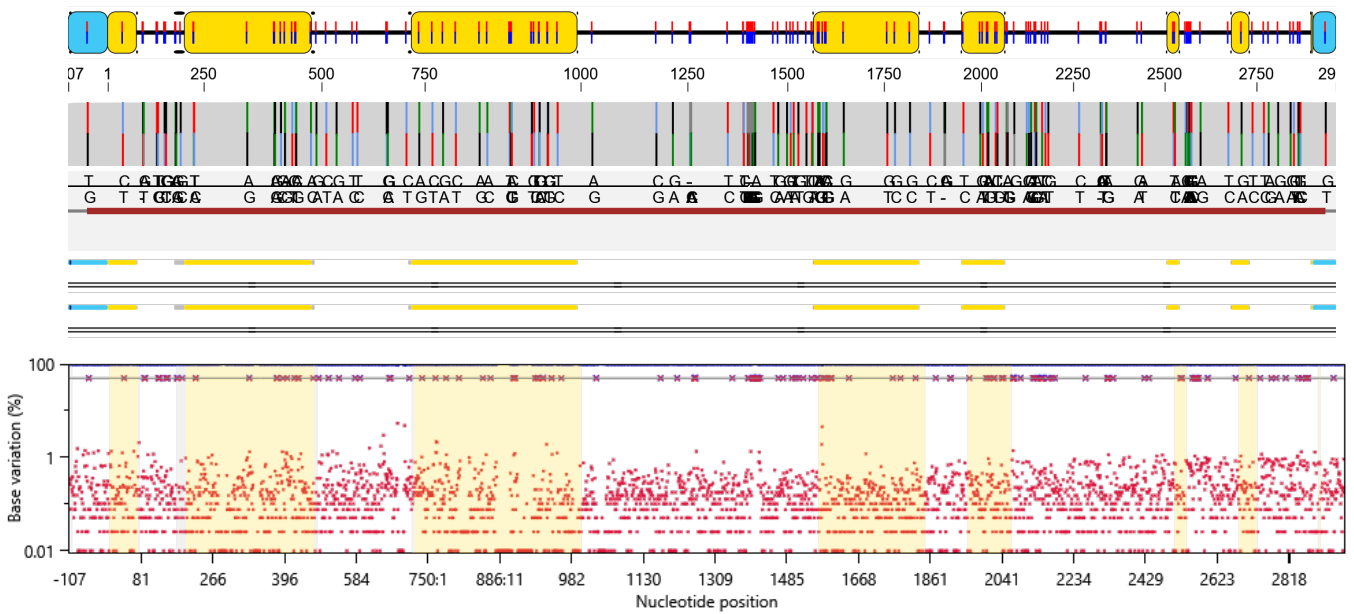
Allele 1	Allele 2	CWD 1	CWD 2	Review status
A*01:01:01:01	A*33:01:01:01	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

4th field CWD

A\*01:01:01:01  
: A\*01:01:01:25 No

### Visualization



### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

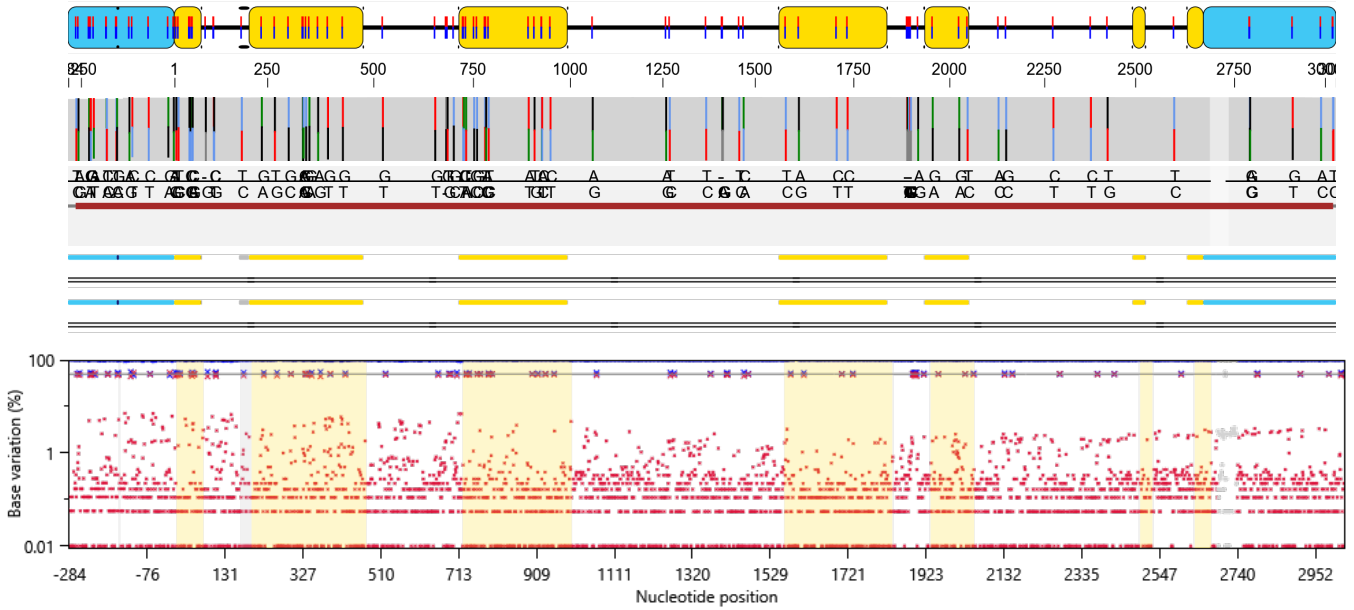
Sample: demultiplex.24143-HG004

Locus: HLA-B

### Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
<b>B*14:02:01:01</b>	<b>B*35:08:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Visualization



### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

Sample: demultiplex.24143-HG004

Locus: HLA-C

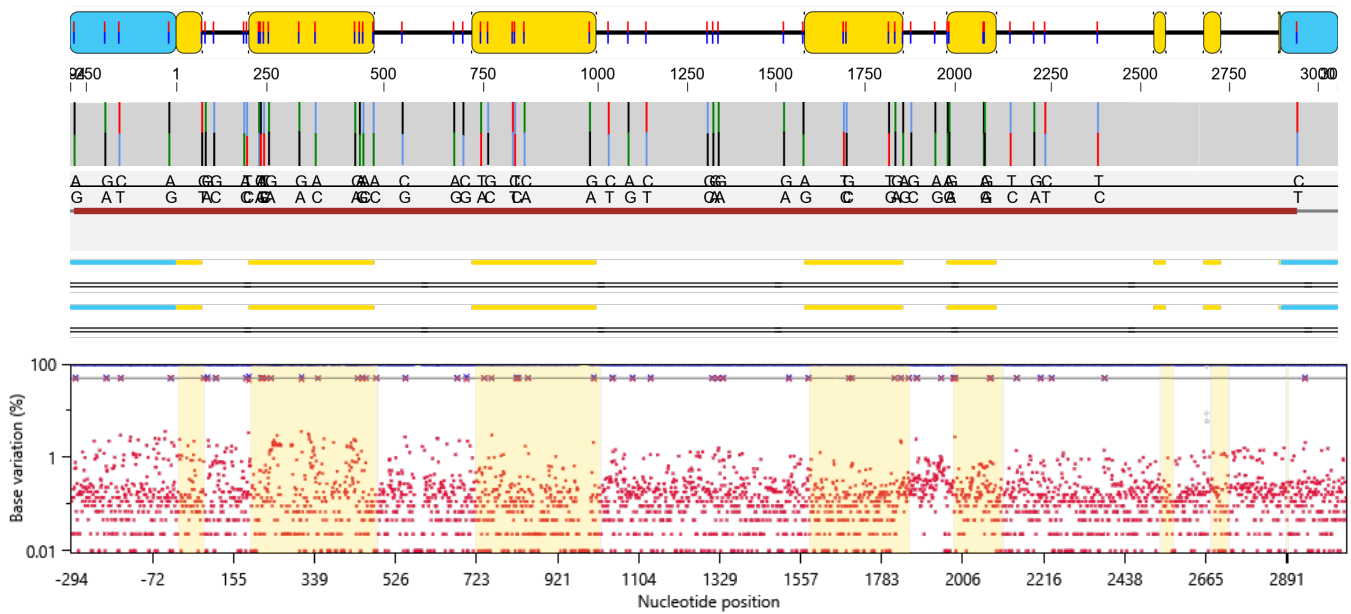
Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
C*04:01:01:06	C*08:02:01:01	No	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

Allele ambiguities

4th field	CWD
C*08:02:01:01	No
: C*08:02:01:05	No

Visualization



Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24143-HG004

**Locus:** DRB1

**Full typing result**

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>DRB1*04:04:01</b>	<b>DRB1*10:01:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 1	Intron mm: 0			

**Allele ambiguities**

<b>3rd field</b>	CWD	<b>4th field</b>	CWD
DRB1*10:01:01:01 : DRB1*10:01:12	No	DRB1*10:01:01:01 : DRB1*10:01:01:02 : DRB1*10:01:01:03	No No

**Visualization**

**Analysis**

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24143-HG004

**Locus:** DQB1

### Full typing result

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>DQB1*04:02:01:06</b>	<b>DQB1*05:01:01:05</b>	No	No	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

<b>3rd field</b>	CWD	<b>4th field</b>	CWD
DQB1*04:02:01:06 : DQB1*04:02:13	No	DQB1*04:02:01:06 : DQB1*04:02:01:08	No

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24143-HG004

**Locus:** DPB1

### Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
<b>DPB1*04:01:01:01</b>	<b>DPB1*04:01:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

#### 4th field

	CWD
DPB1*04:01:01:01	
: DPB1*04:01:01:02	No
: DPB1*04:01:01:04	No
: DPB1*04:01:01:05	No
: DPB1*04:01:01:06	No
: DPB1*04:01:01:14	No
<i>and 10 more</i>	

DPB1*04:01:01:01	
: DPB1*04:01:01:02	No
: DPB1*04:01:01:04	No
: DPB1*04:01:01:05	No
: DPB1*04:01:01:06	No
: DPB1*04:01:01:14	No
<i>and 10 more</i>	

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

## Sample details

### Reads

Total number of reads: 30460  
Mappability: 30403 of 30460 reads used  
Software: NGSengine 2.18.0.17625

Locus	Number of reads	Reads Perc.
HLA-A	4048	13.3 %
HLA-B	1824	6.0 %
HLA-C	4426	14.6 %
DRB1	6646	21.9 %
DQB1	10801	35.5 %
DPB1	2658	8.8 %
	57	0.2 %

### Analysis settings

Locus	Amplicon	Analysis Region	Ignore Regions	Phasing algorithm	Read depth threshold	Allele ratio threshold	Quality trimming
HLA-A	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-B	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-C	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
DRB1	NGSgo-MX6-1	Amplicon	Default	Classic	20	15	20, 70, 10
DQB1	NGSgo-MX6-1	Amplicon	Default	Cluster	20	15	20, 70, 10
DPB1	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10

Quality trimming numbers: Absolute threshold, Relative threshold, Window size

### Analysis settings cont.

Locus	Noise threshold	CWD sorting applied
HLA-A	15	Yes
HLA-B	15	Yes
HLA-C	15	Yes
DRB1	10	Yes
DQB1	10	Yes
DPB1	10	Yes



**Sample: demultiplex.24149-HG003**

**Full typing result**

	<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>HLA-A</b>	<b>26:01:01:01</b>	<b>30:01:01:01</b>	C	C	Not reviewed
<b>HLA-B</b>	<b>13:02:01:01</b>	<b>38:01:01:01</b>	C	C	Not reviewed
<b>HLA-C</b>	<b>06:02:01:01</b>	<b>12:03:01:01</b>	C	C	Not reviewed
<b>DRB1</b>	<b>04:02:01</b>	<b>07:01:01:01</b>	C	C	Not reviewed
<b>DQB1</b>	<b>02:02:01:01</b>	<b>03:02:01:01</b>	C	C	Not reviewed
<b>DPB1</b>	<b>04:01:01:03</b>	<b>04:02:01:02</b>	No	No	Not reviewed

**Genotype ambiguities**

**Allele ambiguities**

<b>Major fields</b>	<b>CWD</b>	<b>3rd field</b>	<b>CWD</b>	<b>4th field</b>	<b>CWD</b>
DRB1*07:01:01:01 : DRB1*07:79 : DRB1*07:93	No No			DRB1*07:01:01:01 : DRB1*07:01:01:02 : DRB1*07:01:01:03 : DRB1*07:01:01:04	No No No
DQB1*02:02:01:01 : DQB1*02:156	No	DQB1*02:02:01:01 : DQB1*02:02:09	No	DQB1*02:02:01:01 : DQB1*02:02:01:04	No
DQB1*03:02:01:01 : DQB1*03:289	No	DQB1*03:02:01:01 : DQB1*03:02:26	No	DQB1*03:02:01:01 : DQB1*03:02:01:02 : DQB1*03:02:01:08  DPB1*04:01:01:03 : DPB1*04:01:01:13 : DPB1*04:01:01:18  DPB1*04:02:01:02 : DPB1*04:02:01:05 : DPB1*04:02:01:10	No No No  No No No

**Libraries used**

IMGT 3.38.0

**Source files**

- demultiplex.24149-HG003.fastq

**Sample:** demultiplex.24149-HG003

**Locus:** HLA-A

### Full typing result

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>A*26:01:01:01</b>	<b>A*30:01:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24149-HG003

**Locus:** HLA-B

### Full typing result

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>B*13:02:01:01</b>	<b>B*38:01:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24149-HG003

**Locus:** HLA-C

**Full typing result**

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>C*06:02:01:01</b>	<b>C*12:03:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

**Visualization**

**Analysis**

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24149-HG003

**Locus:** DRB1

### Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
<b>DRB1*04:02:01</b>	<b>DRB1*07:01:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

Major fields	CWD	4th field	CWD
DRB1*07:01:01:01		DRB1*07:01:01:01	
: DRB1*07:79	No	: DRB1*07:01:01:02	No
: DRB1*07:93	No	: DRB1*07:01:01:03	No
		: DRB1*07:01:01:04	No

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24149-HG003

**Locus:** DQB1

**Full typing result**

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>DQB1*02:02:01:01</b>	<b>DQB1*03:02:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

**Allele ambiguities**

<b>Major fields</b>	CWD	<b>3rd field</b>	CWD	<b>4th field</b>	CWD
DQB1*02:02:01:01 : DQB1*02:156	No	DQB1*02:02:01:01 : DQB1*02:02:09	No	DQB1*02:02:01:01 : DQB1*02:02:01:04	No
DQB1*03:02:01:01 : DQB1*03:289	No	DQB1*03:02:01:01 : DQB1*03:02:26	No	DQB1*03:02:01:01 : DQB1*03:02:01:02 : DQB1*03:02:01:08	No No

**Visualization**

**Analysis**

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24149-HG003

**Locus:** DPB1

**Full typing result**

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>DPB1*04:01:01:03</b>	<b>DPB1*04:02:01:02</b>	No	No	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

**Allele ambiguities**

<b>4th field</b>	CWD
DPB1*04:01:01:03	
: DPB1*04:01:01:13	No
: DPB1*04:01:01:18	No
DPB1*04:02:01:02	
: DPB1*04:02:01:05	No
: DPB1*04:02:01:10	No

**Visualization**

**Analysis**

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

## Sample details

### Reads

Total number of reads: 24152  
Mappability: 24116 of 24152 reads used  
Software: NGSengine 2.18.0.17625

Locus	Number of reads	Reads Perc.
HLA-A	3208	13.3 %
HLA-B	1788	7.5 %
HLA-C	3494	14.5 %
DRB1	6340	26.3 %
DQB1	6437	26.7 %
DPB1	2849	11.8 %
	36	0.2 %

### Analysis settings

Locus	Amplicon	Analysis Region	Ignore Regions	Phasing algorithm	Read depth threshold	Allele ratio threshold	Quality trimming
HLA-A	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-B	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-C	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
DRB1	NGSgo-MX6-1	Amplicon	Default	Classic	20	15	20, 70, 10
DQB1	NGSgo-MX6-1	Amplicon	Default	Cluster	20	15	20, 70, 10
DPB1	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10

Quality trimming numbers: Absolute threshold, Relative threshold, Window size

### Analysis settings cont.

Locus	Noise threshold	CWD sorting applied
HLA-A	15	Yes
HLA-B	15	Yes
HLA-C	15	Yes
DRB1	10	Yes
DQB1	10	Yes
DPB1	10	Yes



**Sample: demultiplex.24385-HG002**

**Full typing result**

	Allele 1	Allele 2	CWD 1	CWD 2	Review status
HLA-A	01:01:01:01	26:01:01:01	C	C	Not reviewed
HLA-B	35:08:01:01	38:01:01:01	C	C	Not reviewed
HLA-C	04:01:01:06	12:03:01:01	No	C	Not reviewed
DRB1	04:02:01	10:01:01:01	C	C	Not reviewed
DQB1	03:02:01:01	05:01:01:05	C	No	Not reviewed
DPB1	04:01:01:01	04:01:01:03	C	No	Not reviewed

**Genotype ambiguities**

**Allele ambiguities**

Major fields	CWD	3rd field	CWD	4th field	CWD
				A*01:01:01:01 : A*01:01:01:25	No
		DRB1*10:01:01:01 : DRB1*10:01:12	No	DRB1*10:01:01:01 : DRB1*10:01:01:02 : DRB1*10:01:01:03	No No
DQB1*03:02:01:01 : DQB1*03:289	No	DQB1*03:02:01:01 : DQB1*03:02:26	No	DQB1*03:02:01:01 : DQB1*03:02:01:02 : DQB1*03:02:01:08	No No
				DPB1*04:01:01:01 : DPB1*04:01:01:02 : DPB1*04:01:01:04 : DPB1*04:01:01:05 : DPB1*04:01:01:06 : DPB1*04:01:01:14 <i>and 10 more</i>	No No No No No
				DPB1*04:01:01:03 : DPB1*04:01:01:13 : DPB1*04:01:01:18	No No

**Libraries used**

IMGT 3.38.0

**Source files**

- demultiplex.24385-HG002.fastq

**Sample:** demultiplex.24385-HG002

**Locus:** HLA-A

### Full typing result

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>A*01:01:01:01</b>	<b>A*26:01:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

#### 4th field

A\*01:01:01:01  
: A\*01:01:01:25

CWD

No

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24385-HG002

**Locus:** HLA-B

### Full typing result

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>B*35:08:01:01</b>	<b>B*38:01:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24385-HG002

**Locus:** HLA-C

### Full typing result

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>C*04:01:01:06</b>	<b>C*12:03:01:01</b>	No	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24385-HG002

**Locus:** DRB1

**Full typing result**

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>DRB1*04:02:01</b>	<b>DRB1*10:01:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

**Allele ambiguities**

<b>3rd field</b>	CWD	<b>4th field</b>	CWD
DRB1*10:01:01:01 : DRB1*10:01:12	No	DRB1*10:01:01:01 : DRB1*10:01:01:02 : DRB1*10:01:01:03	No No

**Visualization**

**Analysis**

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24385-HG002

**Locus:** DQB1

**Full typing result**

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>DQB1*03:02:01:01</b>	<b>DQB1*05:01:01:05</b>	C	No	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

**Allele ambiguities**

<b>Major fields</b>	CWD	<b>3rd field</b>	CWD	<b>4th field</b>	CWD
DQB1*03:02:01:01 : DQB1*03:289	No	DQB1*03:02:01:01 : DQB1*03:02:26	No	DQB1*03:02:01:01 : DQB1*03:02:01:02 : DQB1*03:02:01:08	No No

**Visualization**

**Analysis**

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24385-HG002

**Locus:** DPB1

### Full typing result

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>DPB1*04:01:01:01</b>	<b>DPB1*04:01:01:03</b>	C	No	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

#### 4th field

	CWD
DPB1*04:01:01:01	
: DPB1*04:01:01:02	No
: DPB1*04:01:01:04	No
: DPB1*04:01:01:05	No
: DPB1*04:01:01:06	No
: DPB1*04:01:01:14	No
<i>and 10 more</i>	
DPB1*04:01:01:03	
: DPB1*04:01:01:13	No
: DPB1*04:01:01:18	No

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

## Sample details

### Reads

Total number of reads: 26170  
Mappability: 26130 of 26170 reads used  
Software: NGSengine 2.18.0.17625

Locus	Number of reads	Reads Perc.
HLA-A	3107	11.9 %
HLA-B	1747	6.7 %
HLA-C	3276	12.6 %
DRB1	5994	23.0 %
DQB1	9429	36.1 %
DPB1	2577	9.9 %
	40	0.2 %

### Analysis settings

Locus	Amplicon	Analysis Region	Ignore Regions	Phasing algorithm	Read depth threshold	Allele ratio threshold	Quality trimming
HLA-A	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-B	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-C	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
DRB1	NGSgo-MX6-1	Amplicon	Default	Classic	20	15	20, 70, 10
DQB1	NGSgo-MX6-1	Amplicon	Default	Cluster	20	15	20, 70, 10
DPB1	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10

Quality trimming numbers: Absolute threshold, Relative threshold, Window size

### Analysis settings cont.

Locus	Noise threshold	CWD sorting applied
HLA-A	15	Yes
HLA-B	15	Yes
HLA-C	15	Yes
DRB1	10	Yes
DQB1	10	Yes
DPB1	10	Yes



**Sample: demultiplex.24631-HG005**

**Full typing result**

	Allele 1	Allele 2	CWD 1	CWD 2	Review status
HLA-A	24:02:01:01	24:02:01:01	C	C	Not reviewed
HLA-B	15:01:01:01	40:06:01:01	C	C	Not reviewed
HLA-C	04:01:01:01	08:01:01:01	C	C	Not reviewed
DRB1	04:05:01:01	09:01:02:01	C	C	Not reviewed
DQB1	03:03:02:02	04:01:01:01	No	C	Not reviewed
DPB1	05:01:01:01	135:01	C	No	Not reviewed

**Genotype ambiguities**

**Allele ambiguities**

Major fields	CWD	4th field	CWD
		A*24:02:01:01 : A*24:02:01:16	No
		A*24:02:01:01 : A*24:02:01:16	No
		C*04:01:01:01 : C*04:01:01:10 : C*04:01:01:11 : C*04:01:01:14 : C*04:01:01:75 : C*04:01:01:76	No No No No No
		DRB1*04:05:01:01 : DRB1*04:05:01:02 : DRB1*04:05:01:03 : DRB1*04:05:01:04	No No No
DRB1*09:01:02:01 : DRB1*09:21 : DRB1*09:31	No No	DRB1*09:01:02:01 : DRB1*09:01:02:02 : DRB1*09:01:02:03 : DRB1*09:01:02:04	No No No
		DQB1*03:03:02:02 : DQB1*03:03:02:03	No
		DPB1*05:01:01:01 : DPB1*05:01:01:02 : DPB1*05:01:01:05 : DPB1*05:01:01:07 : DPB1*05:01:01:08 : DPB1*05:01:01:09 <i>and 1 more</i>	No No No No No

**Libraries used**

IMGT 3.38.0

**Source files**

- demultiplex.24631-HG005.fastq

**Sample:** demultiplex.24631-HG005

**Locus:** HLA-A

### Full typing result

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>A*24:02:01:01</b>	<b>A*24:02:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

<b>4th field</b>	CWD
A*24:02:01:01 : A*24:02:01:16	No
A*24:02:01:01 : A*24:02:01:16	No

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24631-HG005

**Locus:** HLA-B

### Full typing result

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>B*15:01:01:01</b>	<b>B*40:06:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24631-HG005

**Locus:** HLA-C

### Full typing result

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>C*04:01:01:01</b>	<b>C*08:01:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

**4th field** CWD

C*04:01:01:01	
: C*04:01:01:10	No
: C*04:01:01:11	No
: C*04:01:01:14	No
: C*04:01:01:75	No
: C*04:01:01:76	No

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24631-HG005

**Locus:** DRB1

**Full typing result**

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>DRB1*04:05:01:01</b>	<b>DRB1*09:01:02:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

**Allele ambiguities**

<b>Major fields</b>	<b>CWD</b>	<b>4th field</b>	<b>CWD</b>
		DRB1*04:05:01:01	
		: DRB1*04:05:01:02	No
		: DRB1*04:05:01:03	No
		: DRB1*04:05:01:04	No
DRB1*09:01:02:01		DRB1*09:01:02:01	
: DRB1*09:21	No	: DRB1*09:01:02:02	No
: DRB1*09:31	No	: DRB1*09:01:02:03	No
		: DRB1*09:01:02:04	No

**Visualization**

**Analysis**

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24631-HG005

**Locus:** DQB1

### Full typing result

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>DQB1*03:03:02:02</b>	<b>DQB1*04:01:01:01</b>	No	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

#### 4th field

DQB1*03:03:02:02	CWD
: DQB1*03:03:02:03	No

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24631-HG005

**Locus:** DPB1

### Full typing result

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>DPB1*05:01:01:01</b>	<b>DPB1*135:01</b>	C	No	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

<b>4th field</b>	CWD
DPB1*05:01:01:01	
: DPB1*05:01:01:02	No
: DPB1*05:01:01:05	No
: DPB1*05:01:01:07	No
: DPB1*05:01:01:08	No
: DPB1*05:01:01:09	No
<i>and 1 more</i>	

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

## Sample details

### Reads

Total number of reads: 19482  
Mappability: 19434 of 19482 reads used  
Software: NGSengine 2.18.0.17625

Locus	Number of reads	Reads Perc.
HLA-A	3151	16.2 %
HLA-B	1266	6.5 %
HLA-C	1219	6.3 %
DRB1	5080	26.1 %
DQB1	5440	28.0 %
DPB1	3278	16.9 %
	47	0.3 %
HLA-B, HLA-C	1	0.1 %

### Analysis settings

Locus	Amplicon	Analysis Region	Ignore Regions	Phasing algorithm	Read depth threshold	Allele ratio threshold	Quality trimming
HLA-A	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-B	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-C	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
DRB1	NGSgo-MX6-1	Amplicon	Default	Classic	20	15	20, 70, 10
DQB1	NGSgo-MX6-1	Amplicon	Default	Cluster	20	15	20, 70, 10
DPB1	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10

Quality trimming numbers: Absolute threshold, Relative threshold, Window size

### Analysis settings cont.

Locus	Noise threshold	CWD sorting applied
HLA-A	15	Yes
HLA-B	15	Yes
HLA-C	15	Yes
DRB1	10	Yes
DQB1	10	Yes
DPB1	10	Yes



**Sample: demultiplex.24695-HG007**

**Full typing result**

	Allele 1	Allele 2	CWD 1	CWD 2	Review status
HLA-A	02:07:01:01	24:02:01:01	C	C	Not reviewed
HLA-B	40:06:01:01	46:01:01:01	C	C	Not reviewed
HLA-C	01:02:01:01	08:01:01:01	C	C	Not reviewed
DRB1	09:01:02:01	09:01:02:01	C	C	Not reviewed
DQB1	03:03:02:02	03:03:02:02	No	No	Not reviewed
DPB1	05:01:01:01	05:01:01:01	C	C	Not reviewed

**Genotype ambiguities**

**Allele ambiguities**

Major fields	CWD	4th field	CWD
		A*24:02:01:01 : A*24:02:01:16	No
		C*01:02:01:01 : C*01:02:01:05	No
DRB1*09:01:02:01 : DRB1*09:21 : DRB1*09:31	No No	DRB1*09:01:02:01 : DRB1*09:01:02:02 : DRB1*09:01:02:03 : DRB1*09:01:02:04	No No No
DRB1*09:01:02:01 : DRB1*09:21 : DRB1*09:31	No No	DRB1*09:01:02:01 : DRB1*09:01:02:02 : DRB1*09:01:02:03 : DRB1*09:01:02:04	No No No
		DQB1*03:03:02:02 : DQB1*03:03:02:03	No
		DQB1*03:03:02:02 : DQB1*03:03:02:03	No
		DPB1*05:01:01:01 : DPB1*05:01:01:02 : DPB1*05:01:01:05 : DPB1*05:01:01:07 : DPB1*05:01:01:08 : DPB1*05:01:01:09 <i>and 1 more</i>	No No No No No
		DPB1*05:01:01:01 : DPB1*05:01:01:02 : DPB1*05:01:01:05 : DPB1*05:01:01:07 : DPB1*05:01:01:08 : DPB1*05:01:01:09 <i>and 1 more</i>	No No No No

**Libraries used**

IMGT 3.38.0

**Source files**

- demultiplex.24695-HG007.fastq

**Sample:** demultiplex.24695-HG007

**Locus:** HLA-A

**Full typing result**

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>A*02:07:01:01</b>	<b>A*24:02:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

**Allele ambiguities**

<b>4th field</b>	CWD
A*24:02:01:01	
: A*24:02:01:16	No

**Visualization**

**Analysis**

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24695-HG007

**Locus:** HLA-B

### Full typing result

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>B*40:06:01:01</b>	<b>B*46:01:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24695-HG007

**Locus:** HLA-C

**Full typing result**

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>C*01:02:01:01</b>	<b>C*08:01:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

**Allele ambiguities**

<b>4th field</b>	CWD
C*01:02:01:01 : C*01:02:01:05	No

**Visualization**

**Analysis**

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24695-HG007

**Locus:** DRB1

**Full typing result**

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>DRB1*09:01:02:01</b>	<b>DRB1*09:01:02:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

**Allele ambiguities**

<b>Major fields</b>	<b>CWD</b>	<b>4th field</b>	<b>CWD</b>
DRB1*09:01:02:01		DRB1*09:01:02:01	
: DRB1*09:21	No	: DRB1*09:01:02:02	No
: DRB1*09:31	No	: DRB1*09:01:02:03	No
		: DRB1*09:01:02:04	No
DRB1*09:01:02:01		DRB1*09:01:02:01	
: DRB1*09:21	No	: DRB1*09:01:02:02	No
: DRB1*09:31	No	: DRB1*09:01:02:03	No
		: DRB1*09:01:02:04	No

**Visualization**

**Analysis**

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24695-HG007

**Locus:** DQB1

### Full typing result

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>DQB1*03:03:02:02</b>	<b>DQB1*03:03:02:02</b>	No	No	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

#### 4th field

DQB1*03:03:02:02	CWD
: DQB1*03:03:02:03	No

DQB1*03:03:02:02	No
: DQB1*03:03:02:03	No

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.24695-HG007

**Locus:** DPB1

### Full typing result

Allele 1	Allele 2	CWD 1	CWD 2	Review status
DPB1*05:01:01:01	DPB1*05:01:01:01	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

#### 4th field

	CWD
DPB1*05:01:01:01	
: DPB1*05:01:01:02	No
: DPB1*05:01:01:05	No
: DPB1*05:01:01:07	No
: DPB1*05:01:01:08	No
: DPB1*05:01:01:09	No

*and 1 more*

DPB1*05:01:01:01	
: DPB1*05:01:01:02	No
: DPB1*05:01:01:05	No
: DPB1*05:01:01:07	No
: DPB1*05:01:01:08	No
: DPB1*05:01:01:09	No

*and 1 more*

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

## Sample details

### Reads

Total number of reads: 25688  
Mappability: 25653 of 25688 reads used  
Software: NGSengine 2.18.0.17625

Locus	Number of reads	Reads Perc.
HLA-A	2770	10.8 %
HLA-B	1564	6.1 %
HLA-C	2485	9.7 %
DRB1	8117	31.6 %
DQB1	6499	25.3 %
DPB1	4218	16.5 %
	35	0.2 %

### Analysis settings

Locus	Amplicon	Analysis Region	Ignore Regions	Phasing algorithm	Read depth threshold	Allele ratio threshold	Quality trimming
HLA-A	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-B	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-C	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
DRB1	NGSgo-MX6-1	Amplicon	Default	Classic	20	15	20, 70, 10
DQB1	NGSgo-MX6-1	Amplicon	Default	Cluster	20	15	20, 70, 10
DPB1	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10

Quality trimming numbers: Absolute threshold, Relative threshold, Window size

### Analysis settings cont.

Locus	Noise threshold	CWD sorting applied
HLA-A	15	Yes
HLA-B	15	Yes
HLA-C	15	Yes
DRB1	10	Yes
DQB1	10	Yes
DPB1	10	Yes



**Sample: demultiplex.C1-218**

**Full typing result**

	Allele 1	Allele 2	CWD 1	CWD 2	Review status
HLA-A	02:01:01:01	66:02	C	C	Not reviewed
HLA-B	44:02:01:01	57:03:01:01	C	C	Not reviewed
HLA-C	05:01:01:02	06:02:01:01	WD	C	Not reviewed
DRB1	03:01:01:01	04:02:01	C	C	Not reviewed
DQB1	02:01:01	03:02:01:01	C	C	Not reviewed
DPB1	02:01:02:10	18:01:01:01	No	C	Not reviewed

**Genotype ambiguities**

**Allele ambiguities**

Major fields	CWD	3rd field	CWD	4th field	CWD
				A*02:01:01:01 : A*02:01:01:16 : A*02:01:01:31 : A*02:01:01:50	No No No
				B*44:02:01:01 : B*44:02:01:14 : B*44:02:01:20	No No
				C*05:01:01:02 : C*05:01:01:39	No
DRB1*03:01:01:01 : DRB1*03:147	No			DRB1*03:01:01:01 : DRB1*03:01:01:02 : DRB1*03:01:01:03	No No
DQB1*02:01:01 : DQB1*02:109 : DQB1*02:148 : DQB1*02:163N	No No No				
DQB1*03:02:01:01 : DQB1*03:289	No	DQB1*03:02:01:01 : DQB1*03:02:26	No	DQB1*03:02:01:01 : DQB1*03:02:01:02 : DQB1*03:02:01:08	No No
				DPB1*02:01:02:10 : DPB1*02:01:02:34	No
				DPB1*18:01:01:01 : DPB1*18:01:01:02 : DPB1*18:01:01:03 : DPB1*18:01:01:04	No No No

**Libraries used**

IMGT 3.38.0

**Source files**

- demultiplex.C1-218.fastq

**Sample:** demultiplex.C1-218

**Locus:** HLA-A

### Full typing result

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>A*02:01:01:01</b>	<b>A*66:02</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

<b>4th field</b>	CWD
A*02:01:01:01	
: A*02:01:01:16	No
: A*02:01:01:31	No
: A*02:01:01:50	No

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.C1-218

**Locus:** HLA-B

**Full typing result**

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>B*44:02:01:01</b>	<b>B*57:03:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

**Allele ambiguities**

<b>4th field</b>	CWD
B*44:02:01:01	
: B*44:02:01:14	No
: B*44:02:01:20	No

**Visualization**

**Analysis**

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.C1-218

**Locus:** HLA-C

**Full typing result**

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>C*05:01:01:02</b>	<b>C*06:02:01:01</b>	WD	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

**Allele ambiguities**

<b>4th field</b>	CWD
C*05:01:01:02 : C*05:01:01:39	No

**Visualization**

**Analysis**

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.C1-218

**Locus:** DRB1

**Full typing result**

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>DRB1*03:01:01:01</b>	<b>DRB1*04:02:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

**Allele ambiguities**

<b>Major fields</b>	<b>CWD</b>	<b>4th field</b>	<b>CWD</b>
DRB1*03:01:01:01		DRB1*03:01:01:01	
: DRB1*03:147	No	: DRB1*03:01:01:02	No
		: DRB1*03:01:01:03	No

**Visualization**

**Analysis**

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.C1-218

**Locus:** DQB1

**Full typing result**

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>DQB1*02:01:01</b>	<b>DQB1*03:02:01:01</b>	C	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

**Allele ambiguities**

<b>Major fields</b>	CWD	<b>3rd field</b>	CWD	<b>4th field</b>	CWD
DQB1*02:01:01					
: DQB1*02:109	No				
: DQB1*02:148	No				
: DQB1*02:163N	No				
DQB1*03:02:01:01		DQB1*03:02:01:01		DQB1*03:02:01:01	
: DQB1*03:289	No	: DQB1*03:02:26	No	: DQB1*03:02:01:02	No
				: DQB1*03:02:01:08	No

**Visualization**

**Analysis**

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

**Sample:** demultiplex.C1-218

**Locus:** DPB1

### Full typing result

<i>Allele 1</i>	<i>Allele 2</i>	<i>CWD 1</i>	<i>CWD 2</i>	<i>Review status</i>
<b>DPB1*02:01:02:10</b>	<b>DPB1*18:01:01:01</b>	No	C	Not reviewed
Core <sup>+</sup> mm: 0	Core <sup>+</sup> mm: 0			
Exon <sup>+</sup> mm: 0	Exon <sup>+</sup> mm: 0			
Intron mm: 0	Intron mm: 0			

### Allele ambiguities

<b>4th field</b>	CWD
DPB1*02:01:02:10 : DPB1*02:01:02:34	No
DPB1*18:01:01:01 : DPB1*18:01:01:02 : DPB1*18:01:01:03 : DPB1*18:01:01:04	No No No No

### Visualization

### Analysis

Date: 23 October 2020  
Library: IMGT 3.38.0  
Software: NGSengine 2.18.0.17625

## Sample details

### Reads

Total number of reads: 15388  
Mappability: 15358 of 15388 reads used  
Software: NGSengine 2.18.0.17625

Locus	Number of reads	Reads Perc.
HLA-A	3106	20.2 %
HLA-B	1414	9.2 %
HLA-C	2593	16.9 %
DRB1	2753	17.9 %
DQB1	4765	31.0 %
DPB1	727	4.8 %
	30	0.2 %

### Analysis settings

Locus	Amplicon	Analysis Region	Ignore Regions	Phasing algorithm	Read depth threshold	Allele ratio threshold	Quality trimming
HLA-A	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-B	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-C	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10
DRB1	NGSgo-MX6-1	Amplicon	Default	Classic	20	15	20, 70, 10
DQB1	NGSgo-MX6-1	Amplicon	Default	Cluster	20	15	20, 70, 10
DPB1	NGSgo-MX6-1	Amplicon	Default	Cluster	20	20	20, 70, 10

Quality trimming numbers: Absolute threshold, Relative threshold, Window size

### Analysis settings cont.

Locus	Noise threshold	CWD sorting applied
HLA-A	15	Yes
HLA-B	15	Yes
HLA-C	15	Yes
DRB1	10	Yes
DQB1	10	Yes
DPB1	10	Yes