



СЕРБАЛАБ

ЦЕНТР ГЕНОМНЫХ ТЕХНОЛОГИЙ

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ОТЧЕТ О ПРОВЕДЕНИИ МОЛЕКУЛЯРНО-ГЕНЕТИЧЕСКОГО ИСЛЕДОВАНИЯ BR1826

СЕКВЕНИРОВАНИЕ ЛОКУСОВ HLA ВЫСОКОГО РАЗРЕШЕНИЯ МЕТОДОМ NGS

ФИО ПАЦИЕНТА:	
ПОЛ:	
ДАТА РОЖДЕНИЯ ПАЦИЕНТА:	
МАТЕРИАЛ ДЛЯ АНАЛИЗА	Венозная кровь
ЛАБОРАТОРНЫЙ НОМЕР:	
НАПРАВЛЯЮЩЕЕ УЧРЕЖДЕНИЕ:	
ДАТА ВЫДАЧИ:	

НАИМЕНОВАНИЕ ИССЛЕДОВАНИЯ:

Типирование генов главного комплекса гистосовместимости I класса (HLA-A, HLA-B, HLA-C) и II класса (HLA-DRB1, HLA-DQB1).

РЕЗУЛЬТАТЫ МОЛЕКУЛЯРНО-ГЕНЕТИЧЕСКОГО ИСЛЕДОВАНИЯ:

Методом секвенирования нового поколения (NGS) с помощью технологии секвенирования NGSgo («GenDx», Нидерланды) на аппарате «MiSeq» («Illumina», США) было проведено исследование первичной последовательности генов главного комплекса гистосовместимости (HLA-A, HLA-B, HLA-C, HLA-DRB1, HLA-DQB1):

Ген	Аллель 1	Аллель 2
HLA-A	02:01:01	24:314
HLA-B	18:01:01	35:03:01
HLA-C	04:01:01	12:03:01:01
HLA-DRB1	04:02:01	11:04:01
HLA-DQB1	03:01P	03:02

РЕКОМЕНДАЦИИ:

- консультация врача-генетика по результатам исследования

Ген. директор ООО «Сербалаб», к.б.н.:

Асеев М. В.

Sample: BR1826

Optimized typing result

	Allele 1	Allele 2	Serol. 1	Serol. 2	CWD 1	CWD 2	Review status
HLA-A	02:01:01	24:314	A2	A24	C	No	Accepted (1 st rev.)
HLA-B	18:01:01	35:03:01	B18	B35	No	C	Accepted (1 st rev.)
HLA-C	04:01:01	12:03:01:01	Cw4	?	C	C	Accepted (1 st rev.)
DRB1	04:02:01	11:04:01	DR4	DR11	C	C	Accepted (1 st rev.)
DQB1	03:01P	03:02	DQ7	DQ8	No	C	Accepted (1 st rev.)

Genotype ambiguities

Typing result P group

HLA-A	02:01P	24:26P	A2	A24	C	No	Accepted (1 st rev.)
HLA-B	18:01P	35:03P	B18	B35	No	C	Accepted (1 st rev.)
HLA-C	04:01P	12:03P	Cw4	?	C	C	Accepted (1 st rev.)
DRB1	04:02P	11:04P	DR4	DR11	C	C	Accepted (1 st rev.)
DQB1	03:01P	03:02P	DQ7	DQ8	No	C	Accepted (1 st rev.)

Genotype ambiguities

Typing result

HLA-A	02:01:01:01	24:314	A2	A24	C	No	Accepted (1 st rev.)
HLA-B	18:01:01:02	35:03:01:01	B18	B35	No	C	Accepted (1 st rev.)
HLA-C	04:01:01:01	12:03:01:01	Cw4	?	C	C	Accepted (1 st rev.)
DRB1	04:02:01	11:04:01	DR4	DR11	C	C	Accepted (1 st rev.)
DQB1	03:01:01:02	03:02:01:01	DQ7	DQ8	No	C	Accepted (1 st rev.)

Genotype ambiguities

Allele ambiguities

Major fields

Serol. CWD

3rd field

Serol. CWD

4th field

Serol. CWD

DQB1*03:01:01:02
: DQB1*03:297

DQ3 No

DQB1*03:02:01:01
: DQB1*03:02:26

DQ8 No

A*02:01:01:01		
: A*02:01:01:16	A2	No
: A*02:01:01:31	A2	No
: A*02:01:01:50	A2	No
B*18:01:01:02		
: B*18:01:01:05	B18	No
: B*18:01:01:17	B18	No
: B*18:01:01:20	B18	No
B*35:03:01:01		
: B*35:03:01:03	B35	No
C*04:01:01:01		
: C*04:01:01:10	Cw4	No
: C*04:01:01:11	Cw4	No
: C*04:01:01:14	Cw4	No
DQB1*03:01:01:02		
: DQB1*03:01:01:03	DQ7	No
: DQB1*03:01:01:09	DQ7	No
: DQB1*03:01:01:16	DQ7	No
: DQB1*03:01:01:18	DQ7	No
DQB1*03:02:01:01		
: DQB1*03:02:01:02	DQ8	No
: DQB1*03:02:01:08	DQ8	No

Typing result G group

HLA-A	02:01:01G	24:26:01G	A2	A24	C	No	Accepted (1 st rev.)
HLA-B	18:01:01G	35:03:01G	B18	B35	No	C	Accepted (1 st rev.)
HLA-C	04:01:01G	12:03:01G	Cw4	?	C	C	Accepted (1 st rev.)
DRB1	04:02:01G	11:04:01G	DR4	DR11	C	C	Accepted (1 st rev.)
DQB1	03:01:01G	03:02:01G	DQ7	DQ8	No	C	Accepted (1 st rev.)

Genotype ambiguities

Libraries used

IMGT 3.37.0

Sample: BR1826

Locus: HLA-A

Optimized typing result

Allele 1	Allele 2	Serol. 1	Serol. 2	CWD 1	CWD 2	Review status
A*02:01:01	A*24:314			C	No	Accepted (1 st rev.)

Typing result

A*02:01:01:01	A*24:314	A2	A24	C	No	Accepted (1 st rev.)
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Allele ambiguities 4th field

Allele	Serol.	CWD
A*02:01:01:01		
: A*02:01:01:16	A2	No
: A*02:01:01:31	A2	No
: A*02:01:01:50	A2	No

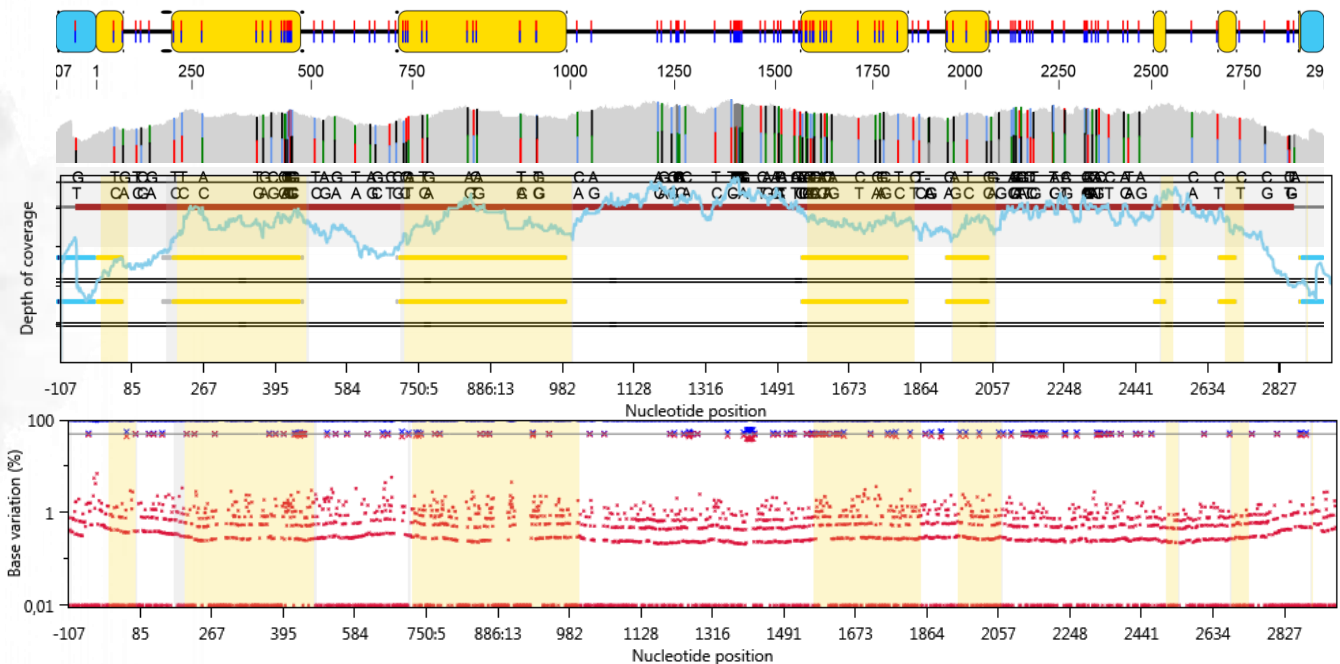
Typing result P group

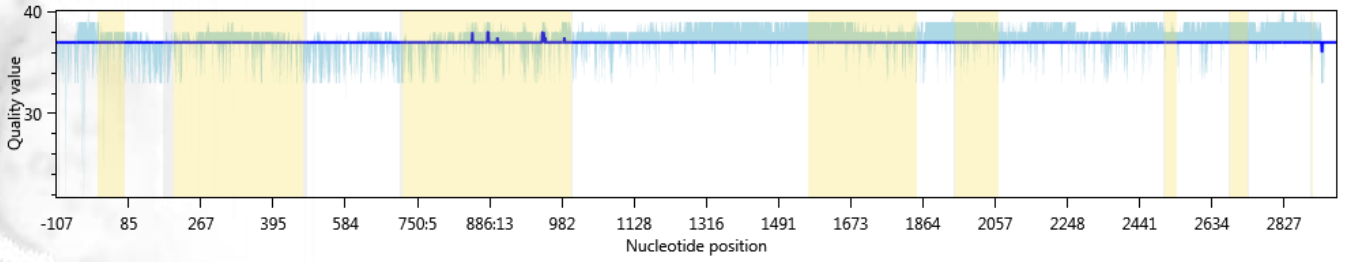
A*02:01P	A*24:26P	A2	A24	C	No	Accepted (1 st rev.)
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Typing result G group

A*02:01:01G	A*24:26:01G			C	No	Accepted (1 st rev.)
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Visualization





Analysis

Date: 07 July 2022
 Library: IMGT 3.37.0
 Software: NGSengine 2.15.0.15000

Sample: BR1826

Locus: HLA-B

Optimized typing result

Allele 1	Allele 2	Serol. 1	Serol. 2	CWD 1	CWD 2	Review status
B*18:01:01	B*35:03:01			No	C	Accepted (1 st rev.)

Typing result

B*18:01:01:02	B*35:03:01:01	B18	B35	No	C	Accepted (1 st rev.)
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Allele ambiguities 4th field

	Serol.	CWD
B*18:01:01:02		
: B*18:01:01:05	B18	No
: B*18:01:01:17	B18	No
: B*18:01:01:20	B18	No
B*35:03:01:01		
: B*35:03:01:03	B35	No

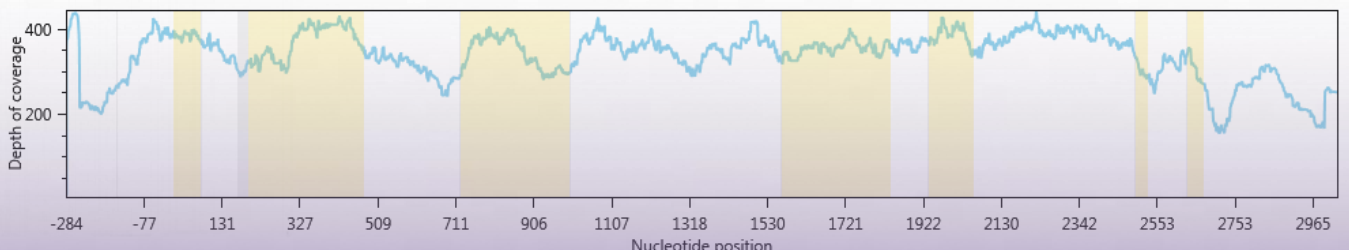
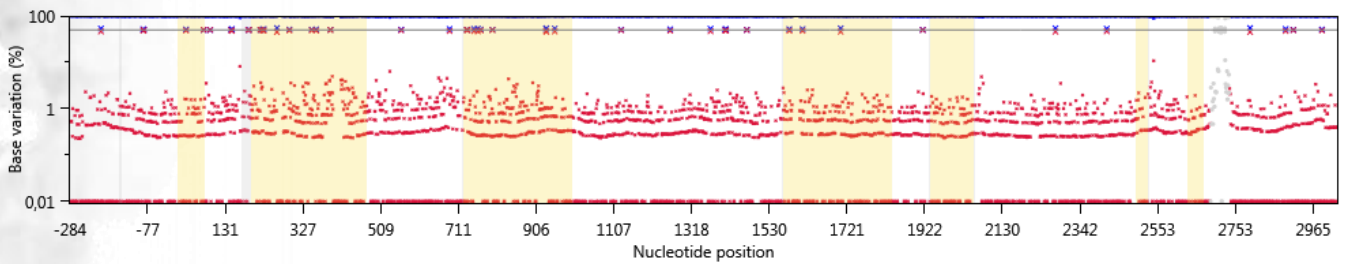
Typing result P group

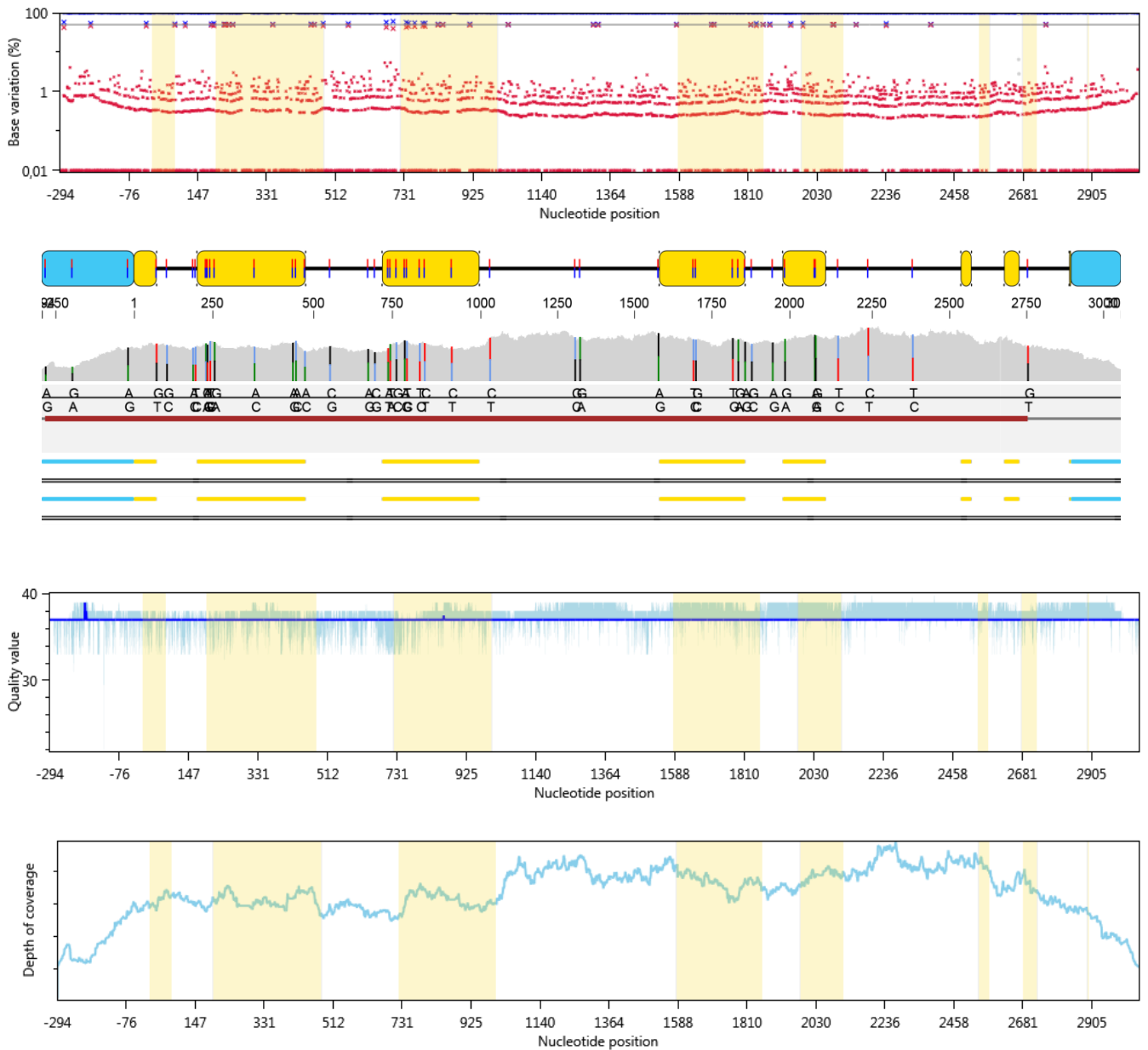
B*18:01P	B*35:03P	B18	B35	No	C	Accepted (1 st rev.)
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Typing result G group

B*18:01:01G	B*35:03:01G			No	C	Accepted (1 st rev.)
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Visualization





Analysis

Date: 07 July 2022
 Library: IMGT 3.37.0
 Software: NGSengine 2.15.0.15000

Sample: BR1826

Locus: DRB1

Optimized typing result

Allele 1	Allele 2	Serol. 1	Serol. 2	CWD 1	CWD 2	Review status
DRB1*04:02:01	DRB1*11:04:01			C	C	Accepted (1 st rev.)

Typing result

DRB1*04:02:01	DRB1*11:04:01	DR4	DR11	C	C	Accepted (1 st rev.)
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Typing result P group

DRB1*04:02P	DRB1*11:04P	DR4	DR11	C	C	Accepted (1 st rev.)
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Typing result G group

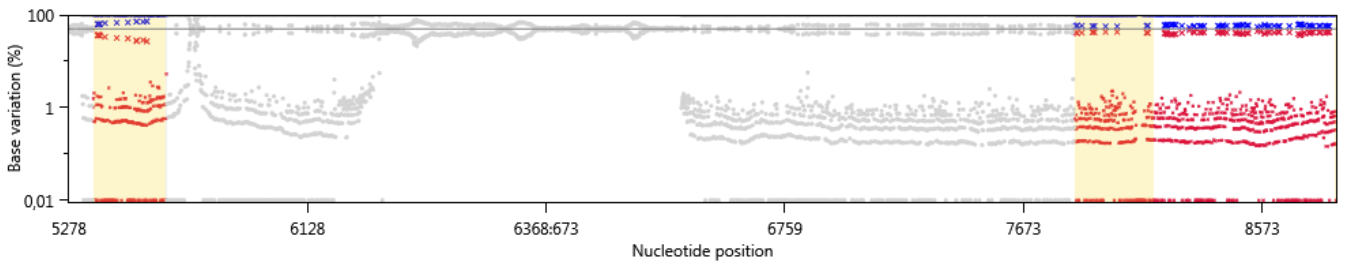
DRB1*04:02:01G

DRB1*11:04:01G

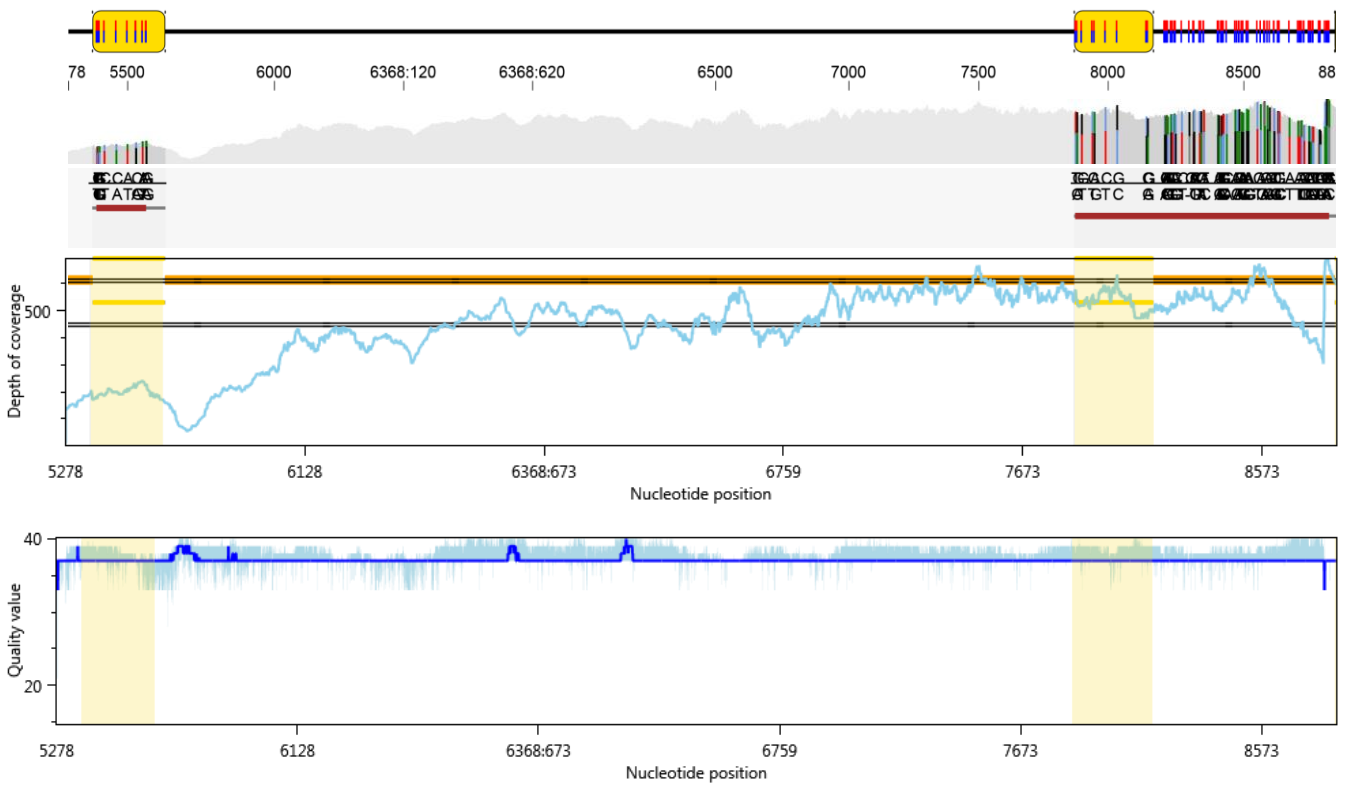
C

C

Accepted (1st rev.)



Visualization



Analysis

Date: 07 July 2022
 Library: IMGT 3.37.0
 Software: NGSengine 2.15.0.15000

Sample: BR1826

Locus: DQB1

Optimized typing result

Allele 1	Allele 2	Serol. 1	Serol. 2	CWD 1	CWD 2	Review status
DQB1*03:01P	DQB1*03:02			No	C	Accepted (1 st rev.)

Typing result

DQB1*03:01:01:02	DQB1*03:02:01:01	DQ7	DQ8	No	C	Accepted (1 st rev.)
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Allele ambiguities

Major fields	Serol.	CWD	3rd field	Serol.	CWD	4th field	Serol.	CWD
DQB1*03:01:01:02 : DQB1*03:297	DQ3	No				DQB1*03:01:01:02 : DQB1*03:01:01:03	DQ7	No

				: DQB1*03:01:01:09	DQ7	No
				: DQB1*03:01:01:16	DQ7	No
				: DQB1*03:01:01:18	DQ7	No
	DQB1*03:02:01:01			DQB1*03:02:01:01		
	: DQB1*03:02:26	DQ8	No	: DQB1*03:02:01:02	DQ8	No
				: DQB1*03:02:01:08	DQ8	No

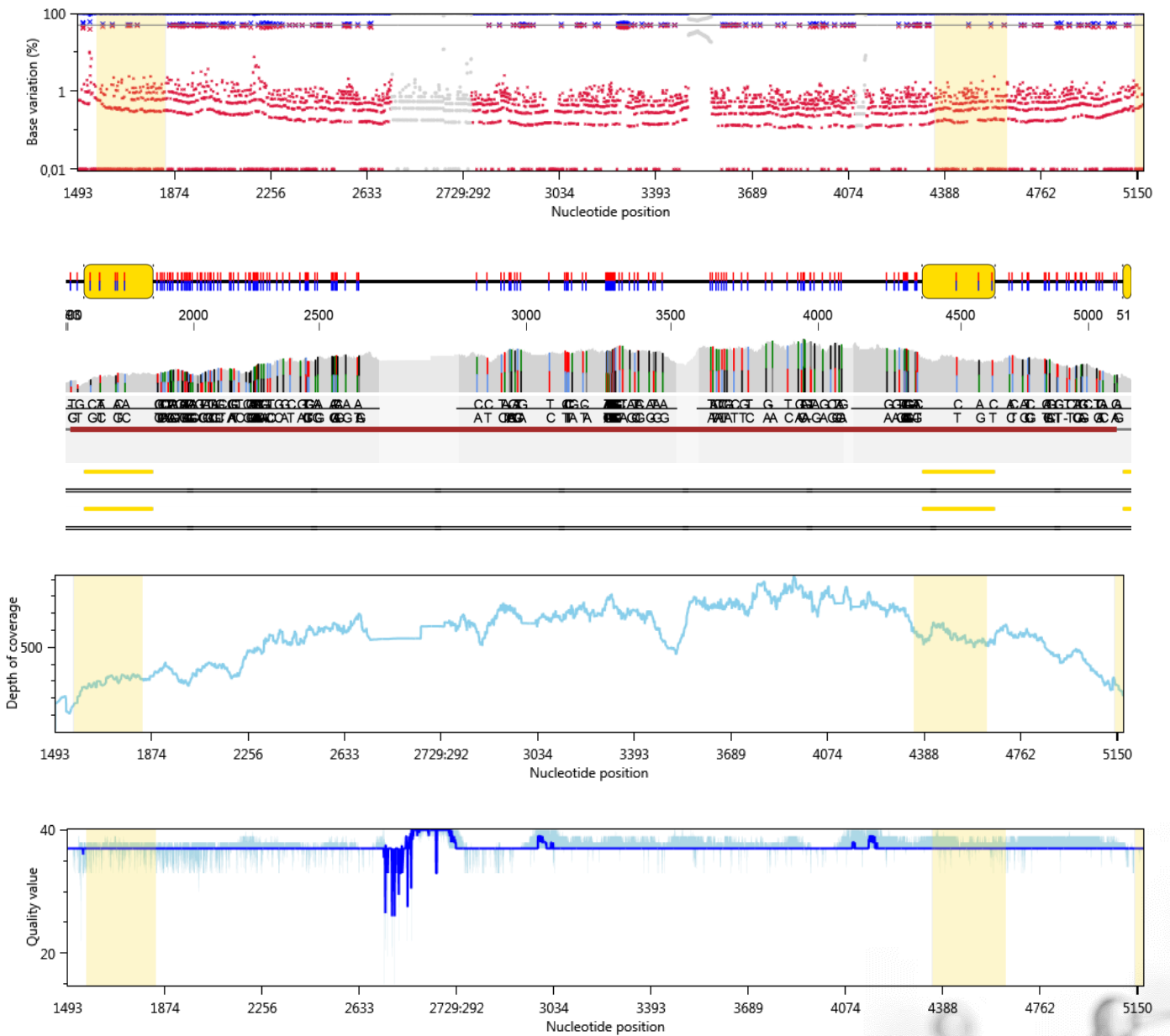
Typing result P group

DQB1*03:01P DQB1*03:02P DQ7 DQ8 No C Accepted (1st rev.)

Typing result G group

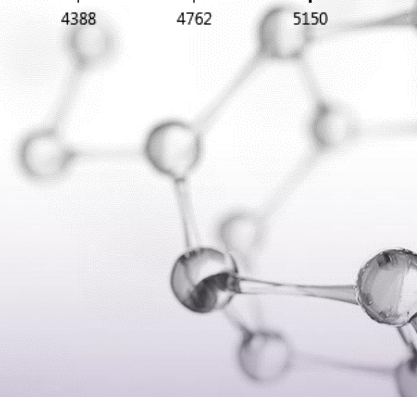
DQB1*03:01:01G DQB1*03:02:01G No C Accepted (1st rev.)

Visualization



Analysis

Date: 07 July 2022
 Library: IMGT 3.37.0
 Software: NGSengine 2.15.0.15000



Sample details

Reads

Total number of reads: 4234144
 Mappability: 47173 of 50000 reads used
 Software: NGSengine 2.15.0.15000

Locus	Number of reads	Reads Perc.
HLA-A	6953	14%
HLA-B	7226	15%
HLA-C	7058	15%
DRB1	12178	25%
DQB1	13758	28%
	1629	4%
HLA-B, HLA-C	302	1%
DRB1, DQB1	191	1%
HLA-B, DQB1	98	1%
HLA-C, DQB1	96	1%
HLA-A, DRB1	93	1%
HLA-C, DRB1	89	1%
HLA-A, DQB1	77	1%
HLA-B, DRB1	74	1%
HLA-A, HLA-B, HLA-C	54	1%
HLA-A, HLA-C	45	1%
HLA-A, HLA-B	32	1%
HLA-B, HLA-C, DRB1	17	1%
HLA-B, HLA-C, DQB1	10	1%
HLA-A, HLA-B, HLA-C, DRB1	7	1%
HLA-A, HLA-B, HLA-C, DQB1	6	1%
HLA-A, HLA-C, DRB1	5	1%
HLA-A, HLA-B, DRB1	1	1%
HLA-A, HLA-C, DQB1	1	1%

Analysis settings

Locus	Amplicon	Analysis Region	Ignore Regions	Phasing algorithm	Read depth threshold	Allele ratio threshold	Quality trimming
HLA-A	NGSgo-AmpX	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-B	NGSgo-AmpX	Amplicon	Default	Cluster	20	20	20, 70, 10
HLA-C	NGSgo-AmpX	Amplicon	Default	Cluster	20	20	20, 70, 10
DRB1	NGSgo-AmpX	Amplicon	Default	Classic	20	20	20, 70, 10
DQB1	NGSgo-AmpX	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	14	Yes
HLA-B	14	Yes
HLA-C	14	Yes
DRB1	14	Yes
DQB1	14	Yes

Optimized typing resolution flow

4-field → 3-field → 2-field → P-group

