



2019年HLAワークショップ

HLA Fusion4.3

MatchMakerマニュアル

株式会社ベリタス

2019年4月20日

MatchMakerとは

- Duquesnoyが作成したフリーソフト
 - 下記リンクよりダウンロード可能
<http://www.epitopes.net/index.html>
- HLA Fusion MatchMakerでは2つの解析が可能
 - Epitope Matching
PatientとDonorのタイピング結果を入力することMismatchの数を表示
 - Epitope Analysis
LABScreen Single Antigenデータをもとにエピトープ解析
- エピトープ解析を行うためには、ドナー、レシピエント共に4桁のタイピング情報が必要



データベースの設定

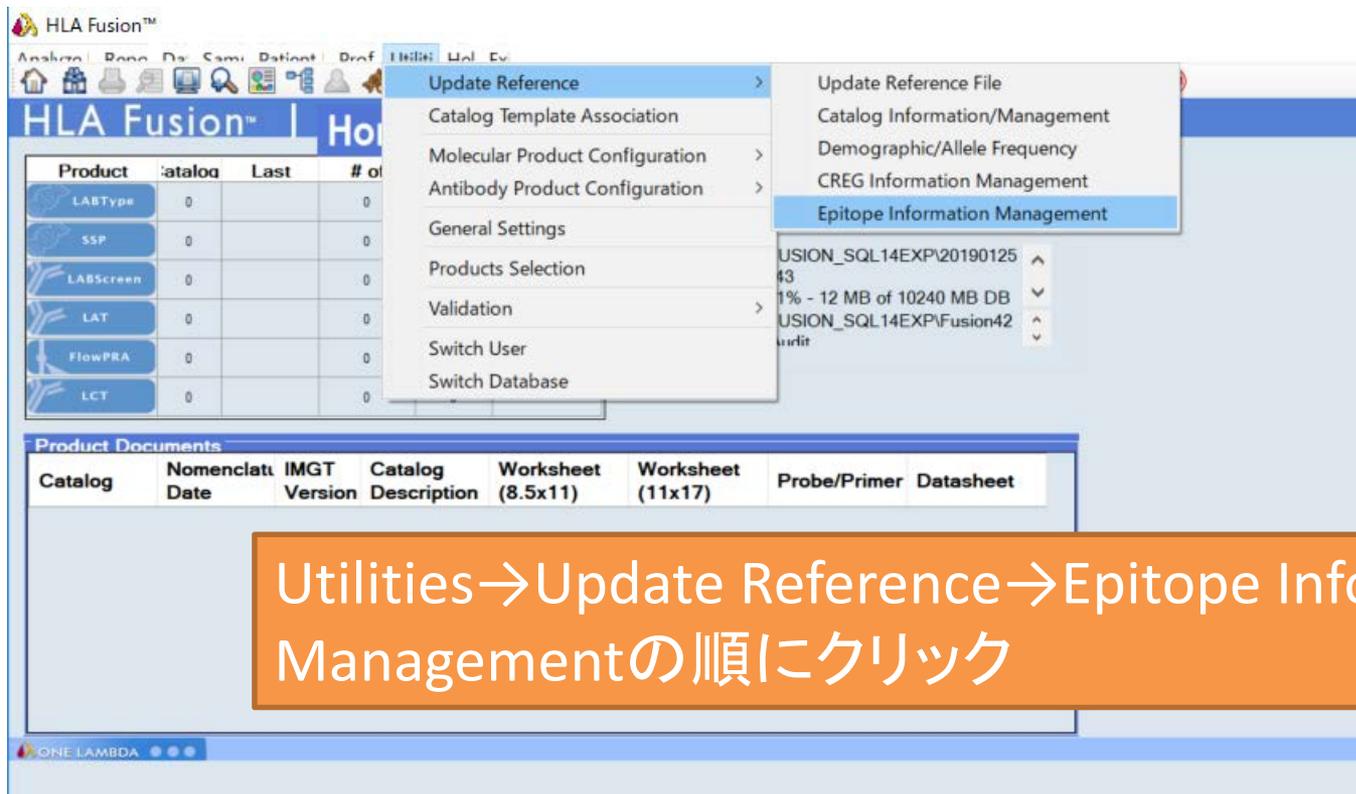
解析用ファイルとは

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	Class I												
2													
3	Class	Epitope Name	Sero Group	AA Position	Polymorphic Residues	Exposed	Antibody Reactivity	Frequency	Struct Epitope	Alleles			
4	I	1C		1	1C	Yes				C*01:02	C*02:02	C*02:10	C*05:01
5	I	16S		16	16S	Yes				C*02:02	C*02:10	C*04:03	C*02:03
6	I	17RS		14,17	R,S	Yes				A*30:01	A*30:02	A*01:02	A*01:20
7	I	17WR		14-17	14W17R(49E)	Yes				C*04:01	A*02:109	B*39:41	C*04:04
8	I	41T		41	41T	Yes	Confirmed			B*13:01	B*13:02	B*40:01	B*40:02
9	I	43RRM		43-44-45	43R44R45M	Yes				A*02:02	A*02:05	A*02:08	A*02:115
10	I	44KM ₃	44,45	(149,150,151,152)	(1K,M (A,V,H,A) (V)	Yes	Confirmed			A*01:01	A*36:01	A*01:02	A*01:03
11	I	44RM		44-45	44R45M	Yes				A*02:01	A*02:02	A*02:03	A*02:05
12	I	44RMA		44-45-46	44R45M46A	Yes	Confirmed			B*13:01	B*13:02	B*15:01	B*15:02
13	I	44RME		44-45-46	44R45M46E(67V)	Yes				A*02:01	A*02:02	A*02:03	A*02:05
14	I	44RT		44,45,46	R,T,E	Yes	Provisional			B*18:01	B*35:01	B*35:08	B*37:01
15	I	44RT+69TNT		44-45-46 + 69-70-71	44R45T46E + 69T70N71T	Yes	Provisional			R*18:01	R*18:02	R*18:03	R*18:04

- Duquesnoyのデータベースを参照にOne Lambdaが作成したエピトープ情報
 - Confirmed: 実験で証明されている
 - Provisional: 理論的に存在が予測されるが実験では証明されていない
 - Blank: unknown

解析用ファイルのインポート-1

解析用ファイル(Excelファイル)はClass1,Class2,MICAの3種類があります。



The screenshot shows the HLA Fusion™ software interface. The 'Utilities' menu is open, and the 'Update Reference' option is selected, which has opened a sub-menu. In this sub-menu, 'Epitope Information Management' is highlighted. Below the main menu, there is a 'Product Documents' table with columns for Catalog, Nomenclature, IMGT, Catalog Description, Worksheet (8.5x11), Worksheet (11x17), and Probe/Primer Datasheet. The table contains several rows with data for different product types like LABType, SSP, LABScreen, LAT, FlowPRA, and LCT.

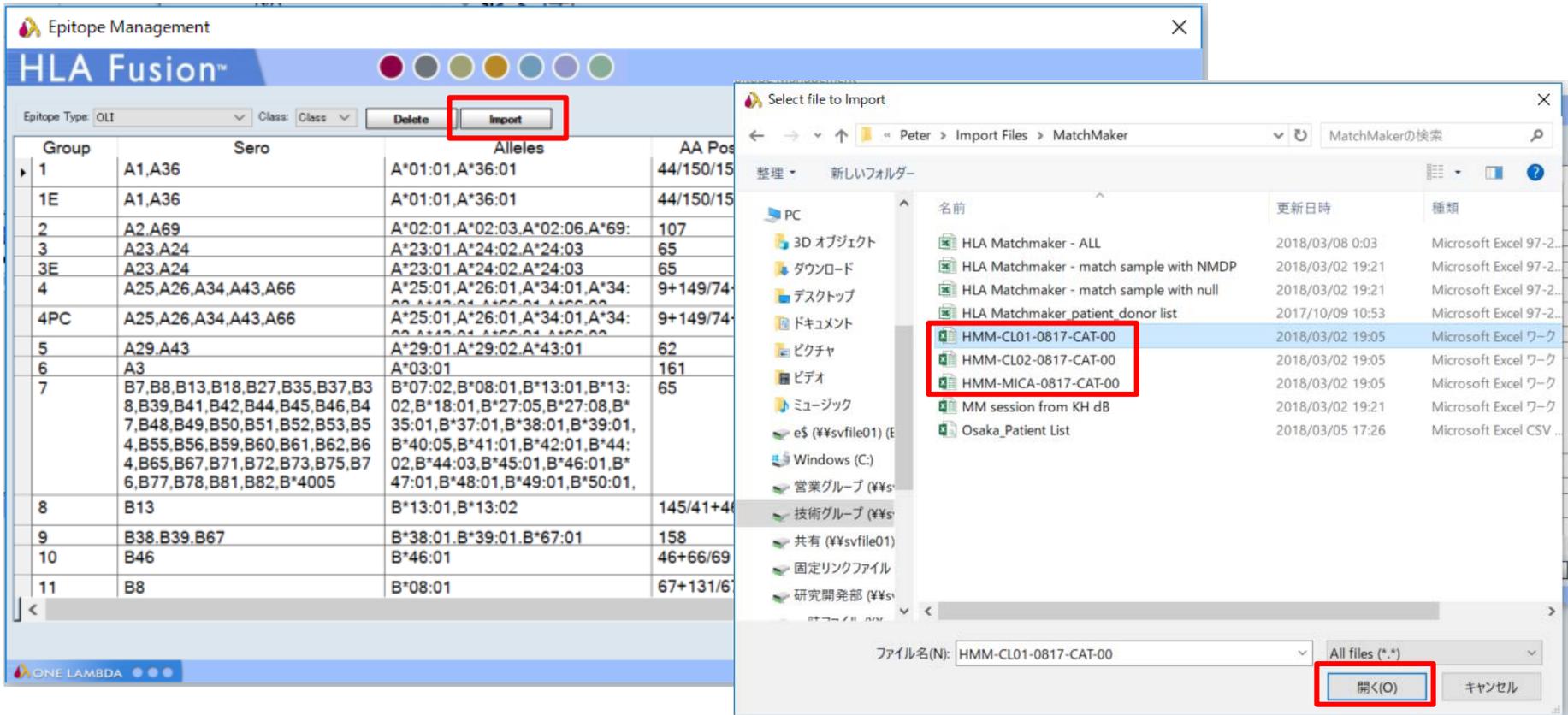
Product	atalog	Last	# of
LABType	0		0
SSP	0		0
LABScreen	0		0
LAT	0		0
FlowPRA	0		0
LCT	0		0

Product Documents

Catalog	Nomenclature	IMGT	Catalog	Worksheet	Worksheet	Probe/Primer	Datasheet
	Date	Version	Description	(8.5x11)	(11x17)		

Utilities → Update Reference → Epitope Information Managementの順にクリック

解析用ファイルのインポート-2

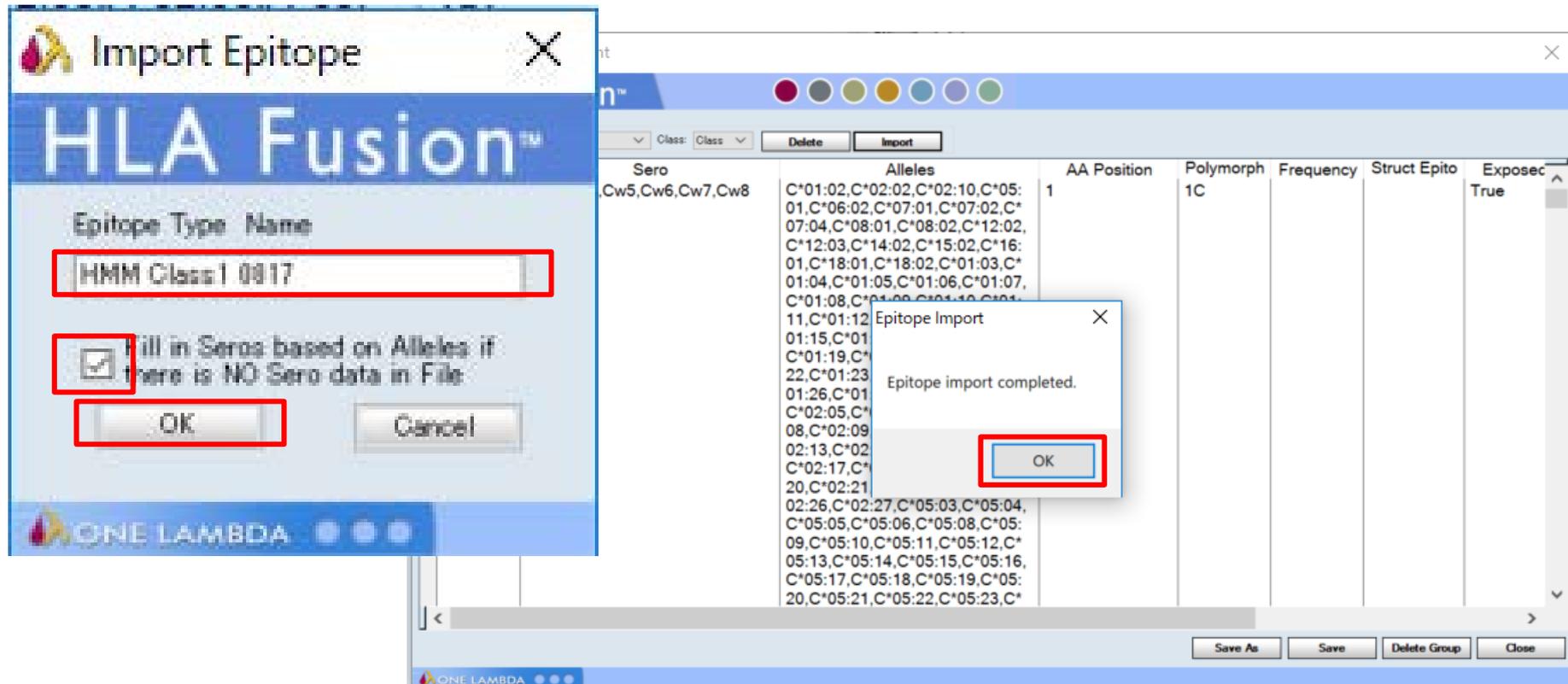


The screenshot shows the Epitepe Management HLA Fusion software interface. The 'Import' button is highlighted with a red box. A file selection dialog is open, showing a list of files. The file 'HMM-CL01-0817-CAT-00' is selected and highlighted with a red box. The '開く(O)' (Open) button is also highlighted with a red box.

Group	Sero	Alleles	AA Pos
1	A1,A36	A*01:01,A*36:01	44/150/15
1E	A1,A36	A*01:01,A*36:01	44/150/15
2	A2,A69	A*02:01,A*02:03,A*02:06,A*69:	107
3	A23,A24	A*23:01,A*24:02,A*24:03	65
3E	A23,A24	A*23:01,A*24:02,A*24:03	65
4	A25,A26,A34,A43,A66	A*25:01,A*26:01,A*34:01,A*34:	9+149/74
4PC	A25,A26,A34,A43,A66	A*25:01,A*26:01,A*34:01,A*34:	9+149/74
5	A29,A43	A*29:01,A*29:02,A*43:01	62
6	A3	A*03:01	161
7	B7,B8,B13,B18,B27,B35,B37,B38,B39,B41,B42,B44,B45,B46,B47,B48,B49,B50,B51,B52,B53,B54,B55,B56,B59,B60,B61,B62,B64,B65,B67,B71,B72,B73,B75,B76,B77,B78,B81,B82,B*4005	B*07:02,B*08:01,B*13:01,B*13:02,B*18:01,B*27:05,B*27:08,B*35:01,B*37:01,B*38:01,B*39:01,B*40:05,B*41:01,B*42:01,B*44:02,B*44:03,B*45:01,B*46:01,B*47:01,B*48:01,B*49:01,B*50:01,	65
8	B13	B*13:01,B*13:02	145/41+4
9	B38,B39,B67	B*38:01,B*39:01,B*67:01	158
10	B46	B*46:01	46+66/69
11	B8	B*08:01	67+131/6

Importをクリックし、ファイルを選択→開くをクリック
1度にインポートできるファイルは1つのみです。

解析用ファイルのインポート-3

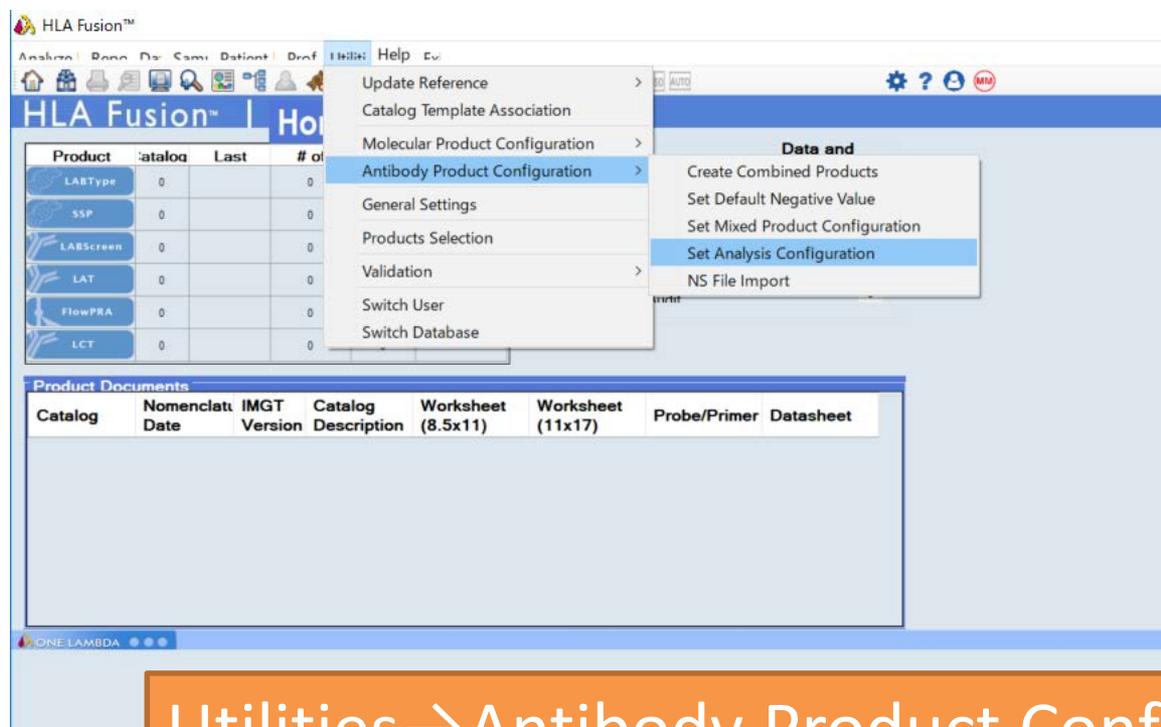


The screenshot shows the 'Import Epitope' dialog box in the HLA Fusion software. The dialog box has a title bar with the HLA Fusion logo and a close button. The main title is 'HLA Fusion™'. Below the title, there is a section for 'Epitope Type Name' with a text input field containing 'HMM Class I 0017'. Below this, there is a checkbox labeled 'Fill in Seros based on Alleles if there is NO Sero data in File', which is checked. At the bottom of the dialog box, there are 'OK' and 'Cancel' buttons. In the background, a table of HLA alleles is visible. The table has columns for 'Sero', 'Alleles', 'AA Position', 'Polymorph', 'Frequency', 'Struct Epito', and 'Exposec'. The 'Sero' column contains 'Cw5,Cw6,Cw7,Cw8'. The 'Alleles' column contains a list of HLA alleles such as 'C*01:02,C*02:02,C*02:10,C*05:01,C*06:02,C*07:01,C*07:02,C*07:04,C*08:01,C*08:02,C*12:02,C*12:03,C*14:02,C*15:02,C*16:01,C*18:01,C*18:02,C*01:03,C*01:04,C*01:05,C*01:06,C*01:07,C*01:08,C*01:09,C*01:10,C*01:11,C*01:12,C*01:15,C*01:19,C*01:22,C*01:23,C*01:26,C*01:27,C*02:05,C*02:08,C*02:09,C*02:13,C*02:17,C*02:20,C*02:21,C*02:26,C*02:27,C*05:03,C*05:04,C*05:05,C*05:06,C*05:08,C*05:09,C*05:10,C*05:11,C*05:12,C*05:13,C*05:14,C*05:15,C*05:16,C*05:17,C*05:18,C*05:19,C*05:20,C*05:21,C*05:22,C*05:23,C*05:24'. The 'AA Position' column contains the number '1'. The 'Polymorph' column contains '1C'. The 'Struct Epito' column is empty. The 'Exposec' column contains 'True'. At the bottom of the table, there are buttons for 'Save As', 'Save', 'Delete Group', and 'Close'. A small 'Epitope Import' dialog box is also visible, showing the message 'Epitope import completed.' and an 'OK' button.

Epitope Type Nameを入力し、にチェックを入れ、OKをクリック
Epitope Type Nameはcsvファイル名と同じで構いません。
インポート終了画面が表示されますのでOKをクリック

解析の設定-1

インポートした情報をLABScreen Single Antigenの解析の際に使用するための設定をします。



Utilities→Antibody Product Configuration→
Set Analysis Configurationの順にクリック

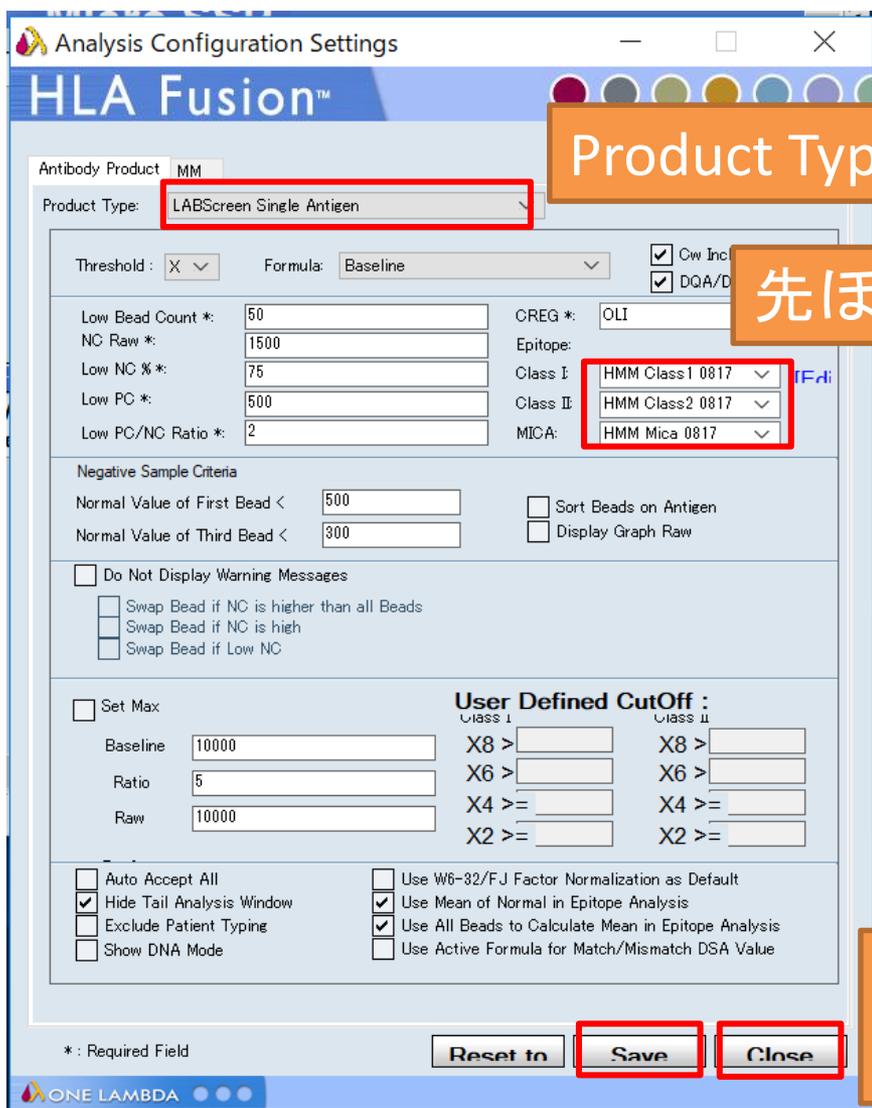
解析の設定-2

Product Type : LABScreen Single Antigenを選択

先ほどインポートしたファイルを選択

解析用ファイルの更新時は必ずスライドP5~10の操作を行い、最新の情報を使用して解析を行ってください。
更新情報は弊社のweb及びメールニュースにてご案内致します。

Save→Closeの順にクリックして終了です。



Analysis Configuration Settings

HLA Fusion™

Antibody Product: MM

Product Type: LABScreen Single Antigen

Threshold: X Formula: Baseline

Low Bead Count *: 50

NC Raw *: 1500

Low NC % *: 75

Low PC *: 500

Low PC/NC Ratio *: 2

OREG *: OLI

Epitope:

Class I: HMM Class1 0817

Class II: HMM Class2 0817

MICA: HMM Mica 0817

Negative Sample Criteria

Normal Value of First Bead < 500

Normal Value of Third Bead < 300

Do Not Display Warning Messages

Set Max

User Defined CutOff:

Baseline: 10000

Ratio: 5

Raw: 10000

Auto Accept All

Hide Tail Analysis Window

Exclude Patient Typing

Show DNA Mode

Use W6-32/FJ Factor Normalization as Default

Use Mean of Normal in Epitope Analysis

Use All Beads to Calculate Mean in Epitope Analysis

Use Active Formula for Match/Mismatch DSA Value

*: Required Field

Reset to Save Close

(参考) Patient情報インポート用ファイル

	A	B	C	D	E	F	G	AF	AG	AH	AI	AJ
1	PatientID	CategoryG	FamilyID	FirstName	MiddleName	LastName	Ssn	RhBloodT	PatientDo	Associate	Associated DonorIDs	HLA1
2	Patient 1			John		Cha			Patient		Donor 1,Donor 2,Donor 3,Donor 4,Donor 5	A*03:0
3	Patient 2			Michael		Maz			Patient		Donor 1,Donor 2,Donor 3,Donor 4,Donor 5	A*11:0
4	Donor 1			Peter		Brescia			Donor			A*34:0
5	Donor 2											A*23:1
6	Donor 3											A*29:0
7	Donor 4											A*03:0
8	Donor 5											A*01:0
9	Patient3			Veritas		demo1			Patient		Donor 1,Donor 2,Donor 3	A*11:0
10	Patient4			Veritas		demo2			Patient		Donor4	A*03:0

csvファイルを読み込むことでPatient情報をインポートすることができます。
ひな型がインストールCD内に入っています。



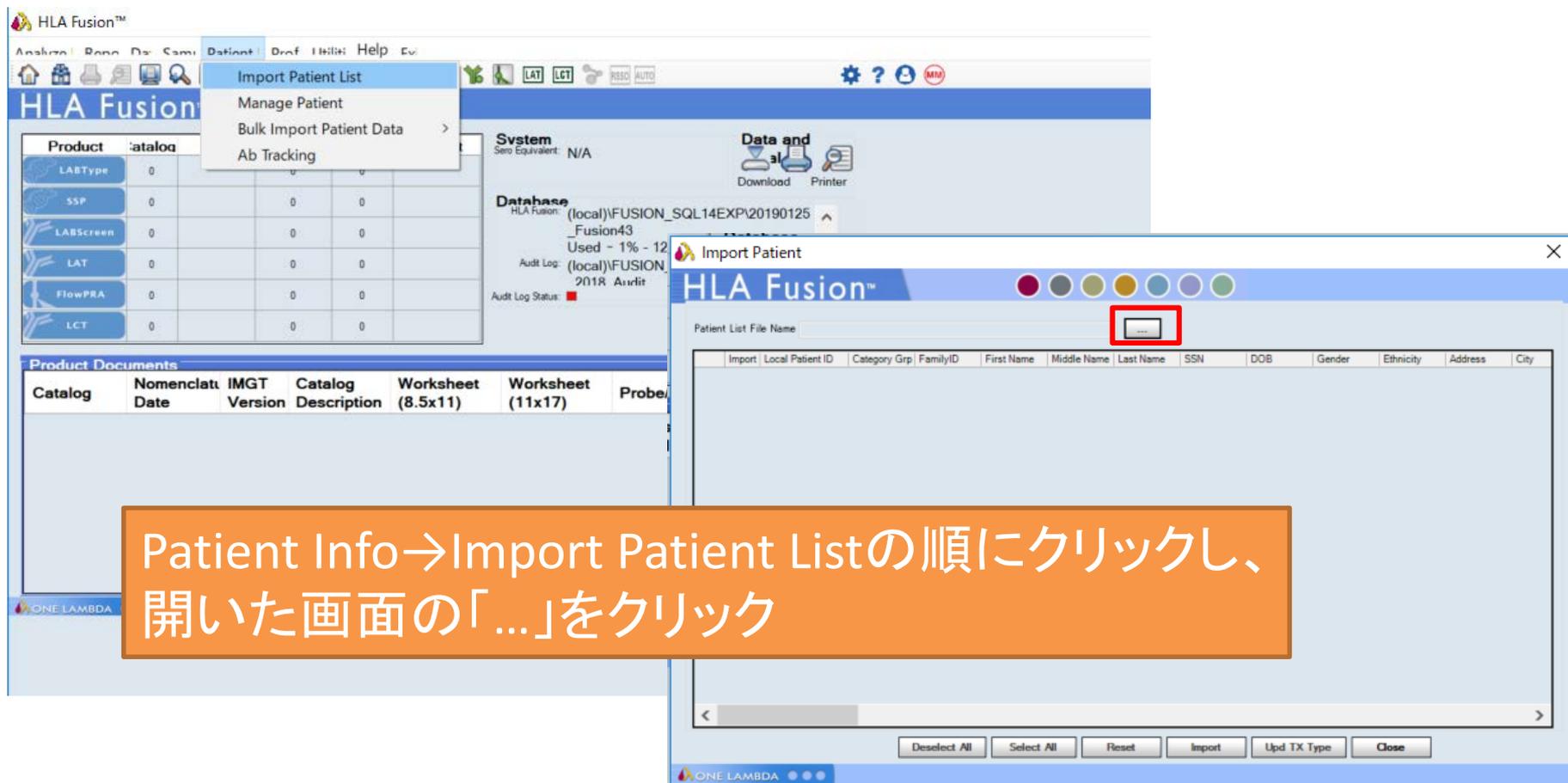
Import	Local Patient I	Category Grp	FamilyID	First Name	Middle Name	Last Name	SSN	DOB	Gender	Ethnicity	Address	City
<input checked="" type="checkbox"/>	Donor 1	Human	Brescia	Peter		Brescia						
<input checked="" type="checkbox"/>	Donor 2	Human	Govender	Ugene		Govender						
<input checked="" type="checkbox"/>	Donor 3	Human	Lopez	Harry		Lopez						
<input checked="" type="checkbox"/>	Donor 4	Human	Goldmann	Katja		Goldmann						
<input checked="" type="checkbox"/>	Donor 5	Human	Hsiao	Thomas		Hsiao						
<input checked="" type="checkbox"/>	Patient 1	Human	Cha	John		Cha						
<input checked="" type="checkbox"/>	Patient 2	Human	Maz	Michael		Maz						
<input checked="" type="checkbox"/>	Patient3	Human	demo1	Veritas		demo1						
<input checked="" type="checkbox"/>	Patient4	Human	demo2	Veritas		demo2						

HLA Fusionにインポートした画面

日本語不可です。半角英数字を使用してください。

AI列にDonor IDを入力することでPatient情報とDonor情報の紐づけができます。

(参考)Patient情報のインポート-1



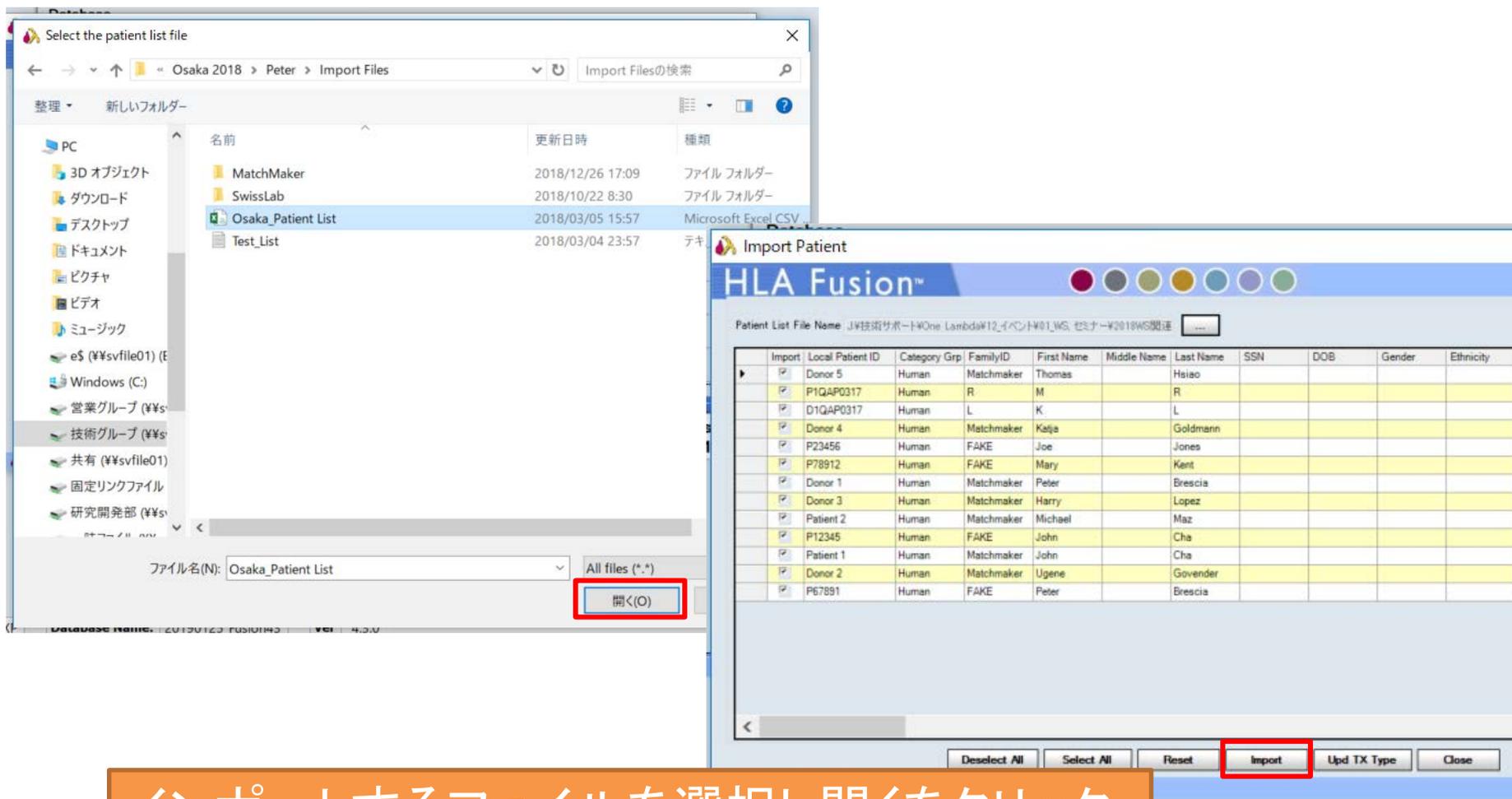
The screenshot shows the HLA Fusion software interface. The 'Patient' menu is open, highlighting 'Import Patient List'. Below it, the 'Import Patient' dialog box is displayed, showing a table with columns for patient information and a file selection button (indicated by a red box).

Import	Local Patient ID	Category Grp	FamilyID	First Name	Middle Name	Last Name	SSN	DOB	Gender	Ethnicity	Address	City
--------	------------------	--------------	----------	------------	-------------	-----------	-----	-----	--------	-----------	---------	------

Buttons at the bottom of the dialog: Deselect All, Select All, Reset, Import, Upd TX Type, Close.

Patient Info→Import Patient Listの順にクリックし、開いた画面の「...」をクリック

(参考)Patient情報のインポート-2



The image shows two overlapping windows. The left window is a file explorer titled "Select the patient list file" showing a directory structure with "Osaka_Patient List" selected. The right window is the "Import Patient" dialog in "HLA Fusion" software, displaying a table of patient data. Red boxes highlight the "開く(O)" button in the file explorer and the "Import" button in the software dialog.

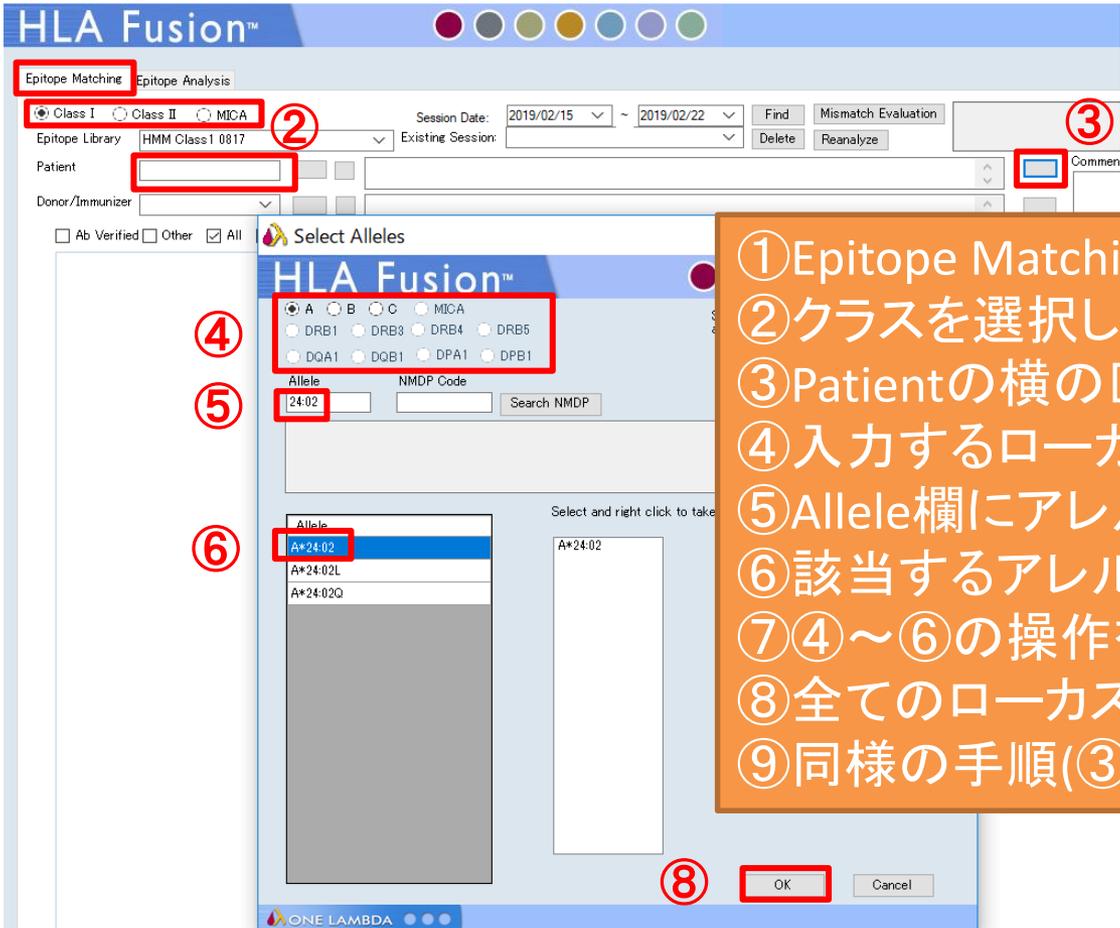
Import	Local Patient ID	Category Grp	FamilyID	First Name	Middle Name	Last Name	SSN	DOB	Gender	Ethnicity
<input type="checkbox"/>	Donor 5	Human	Matchmaker	Thomas		Hsiao				
<input type="checkbox"/>	P1QAP0317	Human	R	M		R				
<input type="checkbox"/>	D1QAP0317	Human	L	K		L				
<input type="checkbox"/>	Donor 4	Human	Matchmaker	Katja		Goldmann				
<input type="checkbox"/>	P23456	Human	FAKE	Joe		Jones				
<input type="checkbox"/>	P78912	Human	FAKE	Mary		Kent				
<input type="checkbox"/>	Donor 1	Human	Matchmaker	Peter		Brescia				
<input type="checkbox"/>	Donor 3	Human	Matchmaker	Harry		Lopez				
<input type="checkbox"/>	Patient 2	Human	Matchmaker	Michael		Maz				
<input type="checkbox"/>	P12345	Human	FAKE	John		Cha				
<input type="checkbox"/>	Patient 1	Human	Matchmaker	John		Cha				
<input type="checkbox"/>	Donor 2	Human	Matchmaker	Ugene		Govender				
<input type="checkbox"/>	P67891	Human	FAKE	Peter		Brescia				

インポートするファイルを選択し開くをクリック
Importをクリックして終了です

Epitope Matching

タイピング情報の入力

手入力する場合



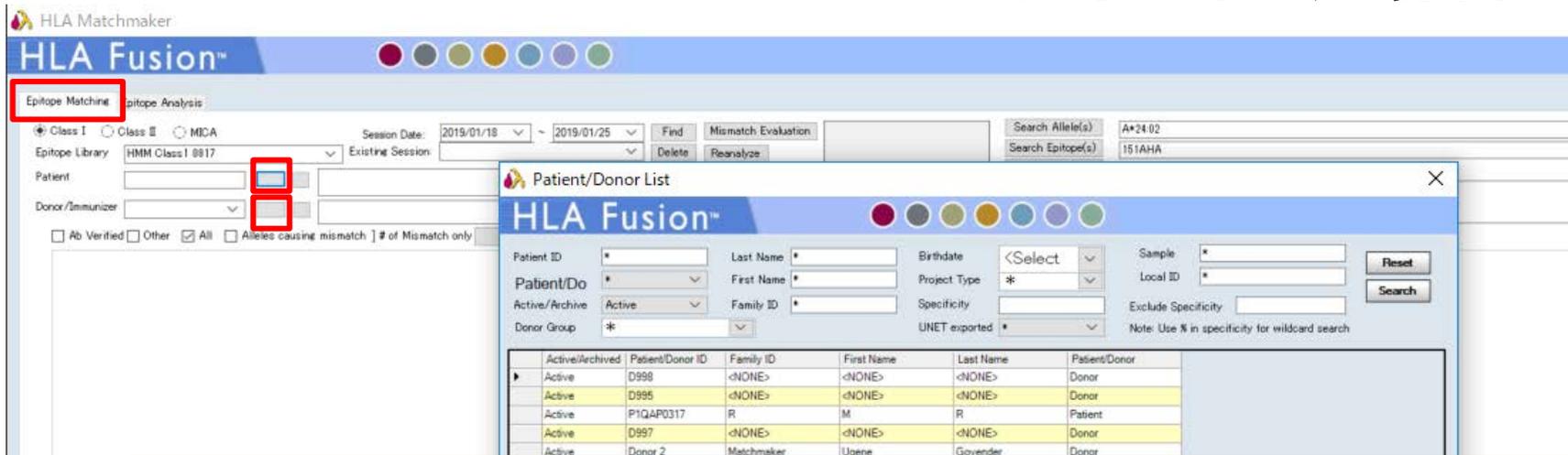
The screenshot shows the HLA Fusion software interface with the following elements highlighted by numbered callouts:

- ① Epitope Matching tab is selected.
- ② Class I radio button is selected.
- ③ A small square button next to the Patient field is clicked.
- ④ The A locus radio button is selected.
- ⑤ The allele 'A*24:02' is entered into the Allele field.
- ⑥ The 'A*24:02' entry in the list is double-clicked.
- ⑦ The process of selecting a locus and entering an allele is repeated.
- ⑧ The OK button is clicked after all loci are entered.

① Epitope Matchingタブを開く
② クラスを選択し、Patient名を入力
③ Patientの横の□(Select alleles)をクリック
④ 入力するローカスを選択
⑤ Allele欄にアレルを入力
⑥ 該当するアレルをダブルクリック
⑦ ④～⑥の操作を繰り返す
⑧ 全てのローカスの入力が終了後OKをクリック
⑨ 同様の手順(③～⑧)でDonor情報も入力

タイピング情報の入力

HLA Fusionのデータベースより呼び出す場合



The screenshot shows the HLA Fusion software interface. The 'Epitope Matching' tab is selected. In the 'Patient' field, a small square button is highlighted with a red box. A 'Patient/Donor List' dialog box is open, displaying a table of patient and donor information.

Active/Archived	Patient/Donor ID	Family ID	First Name	Last Name	Patient/Donor
Active	D998	<NONE>	<NONE>	<NONE>	Donor
Active	D995	<NONE>	<NONE>	<NONE>	Donor
Active	PIQAP0317	R	M	R	Patient
Active	D997	<NONE>	<NONE>	<NONE>	Donor
Active	Donor 2	Matchmaker	Ugene	Govender	Donor

MatchMakerを開き、Epitope Matchingタブを開く

Patientの横の□(Select a patient from database)をクリック

登録されている情報が一覧で表示されるので、該当する情報を選択しダブルクリックする

Donor情報の入力も同様

インポートするcsvファイル内でPatientとDonor情報を紐づけて入力しておくことで、Patientを選択することで自動でDonor情報も入ります

ミスマッチ数の解析

- Patient及びDonorのタイピング結果を入力後、Calculateをクリック→結果が表示される
- 必ずAb Verifiedを選択する

HLA Matchmaker

HLA Fusion™

Epitope Matching | Epitope Analysis

Class I Class II MICA Session Date: 2019/02/15 ~ 2019/02/22 Find Mismatch Evaluation Search Allele(s) A*24:02
 Epitope Library HMM Class I 0817 Existing Session: Delete Reanalyze Search Epitope(s) 151AHA
 Patient Patient1 A*03:01, A*31:01, B*07:02, B*40:01, C*03:04, C*07:02 Comment: List All Epitopes
 Donor/Immunizer Donor1 A*34:02, A*66:01, B*13:02, B*51:01, C*06:02, C*16:01

Ab Verified Other All Alleles causing mismatch] # of Mismatch only Reanalyze Calculate Reanalyze Import Export Save iCn3D Latest Version Session Name: MM_Match_20190222143804

Patient	Donor	A PatientE p	A DonorEp AbVerifie	A Mismatch AbVerifie	# Misma	B PatientE p	B DonorEp AbVerifie	B Mismatch AbVerifie	# Misma	C PatientE p	C DonorEp AbVerifie	C Mismatch AbVerifie	# Misma	ClassI # Misma
Patient1 A*03:01, A*31:01, B*07:02, B*40:01, C*03:04, C*07:02	Donor1 A*34:02, A*66:01, B*13:02, B*51:01, C*06:02, C*16:01	56R, 62QE+56G, 66NV, 79GT, 79GT, 138MI, 138MH+79G T, 144K, 144KR, 144KR+151 H, 150AAH, 161D, 253Q	62RR, 66NV, 79GT, 79GT+90D, 90D, 138MI, 138MH+79G T, 145RT, 149TAH, 163RW, 253Q	62RR, 79GT+90D, 145RT, 149TAH, 163R, 163RW	6	41T, 65QIA, 65QIA+76E SN, 69AA, 69AA+65QI , 69AA+76E, 69TNT, 69TNT+80 N, 70IAQ, 71TTS, 76ESN, 8...	41T, 44RMA, 44RT, 44RT+69T NT, 80I, 80I+69TNT, 80I 80I+90A, 80I+69TNT, 80TLR, 80I+90A, 82LR, 82LR+90A, 82LR+138T , 82LR+1...	44RMA, 44RT, 44RT+69T NT, 80I, 80I+69TNT, 80I 80I+90A, 80TLR, 82LR, 82LR+90A, 82LR+138T , 82LR+1...	16	21H, 65QKR+76 VS, 73AN, 76VRN, 80N, 90D, 80K, 80K+14R, 173K, 193PL3, 193PV, 219W, 253Q, 267QE	65QKR+76 VS, 73AN, 76VRN, 80K, 80K+14R, 80N, 90D, 193PV	73AN, 80K, 80K+14R	3	25

画面の見方

HLA Matchmaker

HLA Fusion™

Epitope Matching Epitope Analysis

Class I Class II MICA
 Epitope Library: HMM Class I 0817
 Patient: Patient1
 Donor/Immunizer: Donor1

Session Date: 2019/02/15 ~ 2019/02/22

Find Misr
 Existing Session: Delete Rea

A*03:01, A*31:01, B*07:02, B*40:01, C*03:04, C*07:02
 A*34:02, A*66:01, B*13:02, B*51:01, C*06:02, C*16:01

Ab Verified Other All Alleles causing mismatch] # of Mismatch only

Calculate Rerlar Import Export Save Latest Version Session Name: MM_Match_20190222143804

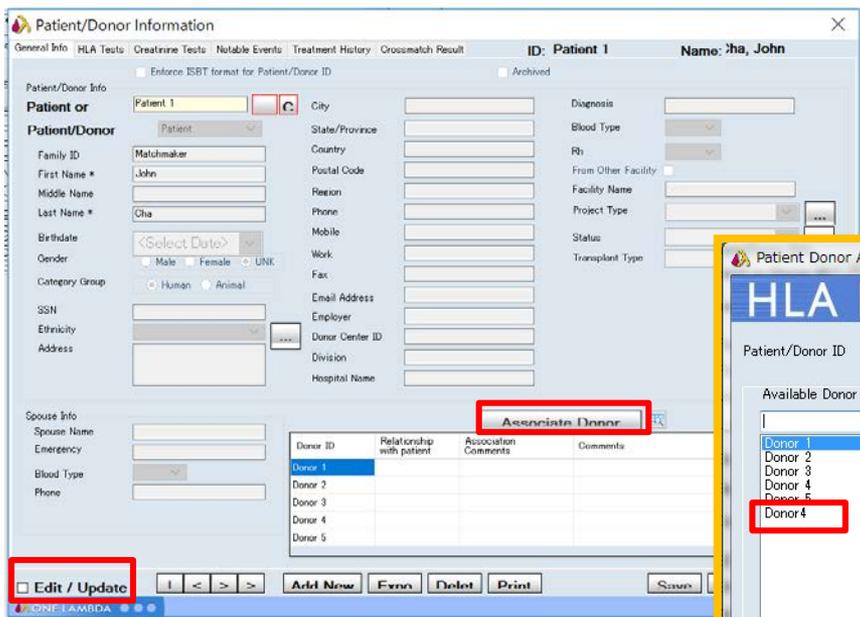
Patient	Donor	A PatientEp AbVerified	A DonorEp AbVerified	A Mismatch AbVerified	A # Mismatch	B PatientE	B DonorEp AbVerifie	B Mismatch AbVerifie	B # Misma	C PatientE	C DonorEp AbVerifie	C Mismatch AbVerifie	C # Misma	ClassI # Misma
Patient1	Donor1	56R, 62QE+56G, 66NV, 79GT, 138MI	62RR, 66NV, 79GT, 79GT+90D, 90D 138MI	62RR, 79GT+90D, 145RT, 149TAH	6	41T, 65QIA, 65QIA+76E, SN, 69AA, 69AA+65QI	41T, 44RMA, 44RT, 44RT+69T	44RMA, 44RT, 44RT+69T	16	21H, 65QKR+76, VS, 76VRN, 80N 90D	65QKR+76, VS, 73AN, 76VRN, 80K	73AN, 80K, 80K+14R	3	25

B及びCローカスの結果 (Aローカスと表示内容は同じです)

クラス I の MissMatch Epitope の合計

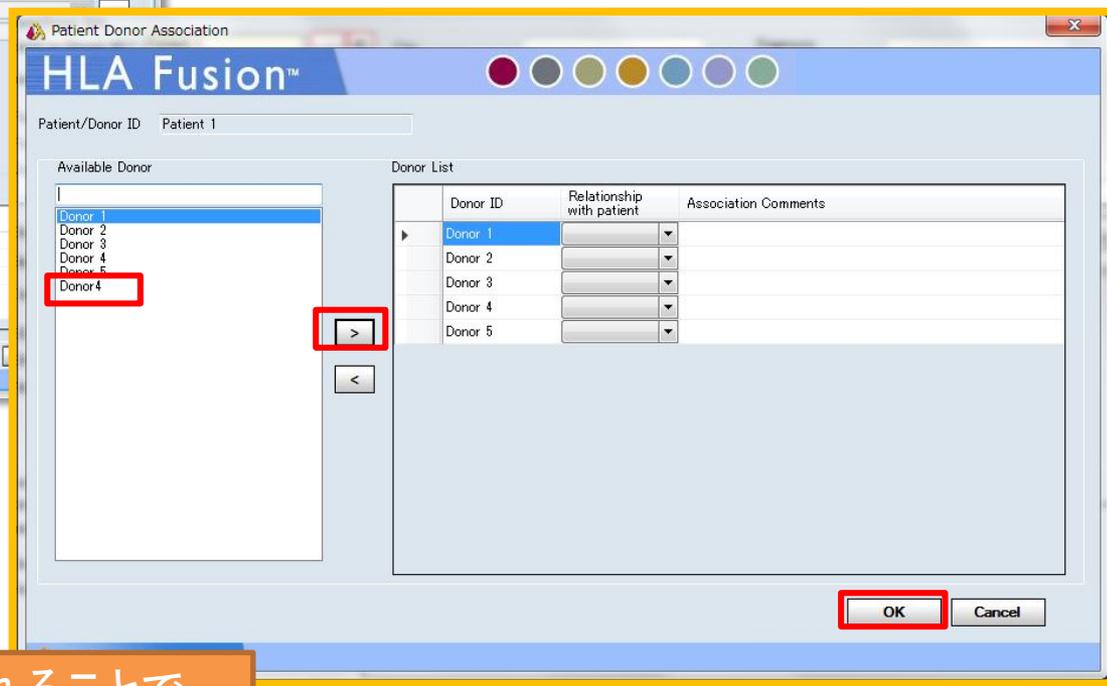
- Ab Verified: LABScreen Single Antigenで確認されたEpitope
 * 解析の際は「Ab Verified」にチェックを入れてください *
- Other: LABScreen Single Antigenで確認されていないEpitope
- All: Ab VerifiedとOtherの両方を表示
- Patient: PatientのHLAタイピング結果
- Donor: DonorのHLAタイピング結果
- A PatientEp AbVerified: 患者のAローカスのEpitope
- A DonorEp AbVerified: ドナーのAローカスのEpitope
- A Mismatch AbVerified: AローカスのMissMatch Epitope
- A# Mismatch AbVerified: AローカスのMissMatch Epitopeの数

Patient情報の編集



Patient/Donor Information form showing fields for Patient or Donor information, including Name, ID, Address, and Contact details. The 'Associate Donor' button is highlighted with a red box.

Donor ID	Relationship with patient	Association Comments	Comments
Donor 1			
Donor 2			
Donor 3			
Donor 4			
Donor 5			

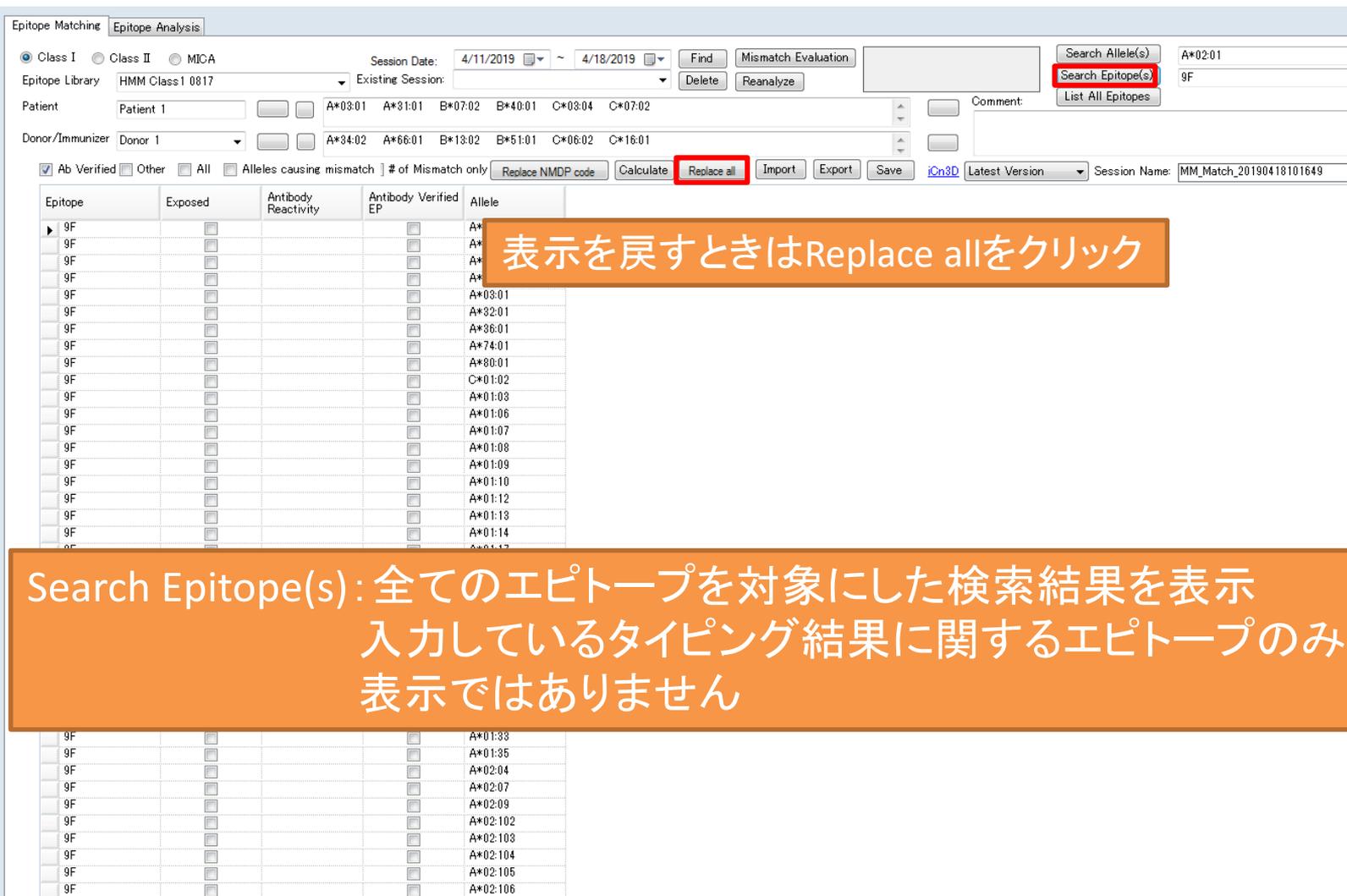


HLA Fusion Patient Donor Association dialog box. It shows a list of available donors and a table for associating donors with the patient. The 'Donor 4' in the Available Donor list and the right arrow button are highlighted with red boxes. The OK button is also highlighted with a red box.

Donor ID	Relationship with patient	Association Comments
Donor 1		
Donor 2		
Donor 3		
Donor 4		
Donor 5		

Edit/Updateにチェックを入れることで「Associate Donor IDs」からPatient情報とDonor情報の紐づけが可能

Search Epitope(s)



Epitope Matching Epitope Analysis

Class I Class II MICA Session Date: 4/11/2019 ~ 4/18/2019 Find Mismatch Evaluation Search Allele(s) A*02:01
Epitope Library: HMM Class1 0817 Existing Session: Delete Reanalyze Search Epitope(s) 9F
Patient: Patient 1 A*03:01 A*31:01 B*07:02 B*40:01 C*03:04 C*07:02 Comment: List All Epitopes
Donor/Immunizer: Donor 1 A*34:02 A*66:01 B*13:02 B*51:01 C*06:02 C*16:01
 Ab Verified Other All Alleles causing mismatch | # of Mismatch only Replace NMDP code Calculate **Replace all** Import Export Save iCn3D Latest Version Session Name: MM_Match_20190418101649

Epitope	Exposed	Antibody Reactivity	Antibody Verified EP	Allele
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*03:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*32:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*36:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*74:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*80:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	C*01:02
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:03
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:06
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:07
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:08
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:09
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:10
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:12
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:13
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:14
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:17
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:33
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:35
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:04
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:07
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:09
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:102
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:103
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:104
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:105
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:106

表示を戻すときはReplace allをクリック

Search Epitope(s): 全てのエピトープを対象にした検索結果を表示
入力しているタイピング結果に関するエピトープのみの表示ではありません

List All Epitopes

Epitope Matching Epitope Analysis

Class I Class II MICA

Session Date: 4/11/2019 ~ 4/18/2019 Find Mismatch Evaluation Search Allele(s) A*02:01

Epitope Library HMM Class1 0817 Existing Session: Delete Reanalyze Search Epitope(s) 9F

Patient Patient 1 A*03:01 A*31:01 B*07:02 B*40:01 C*03:04 C*07:02 Comment: List All Epitopes

Donor/Immunizer Donor 1 A*34:02 A*66:01 B*13:02 B*51:01 C*06:02 C*16:01

Ab Verified Other All Alleles causing mismatch # of Mismatch only Replace NMMP code Calculate **Replace all** Import Export Save iCn3D Latest Version Session Name: MM_Match_20190418101649

Epitope	Exposed	Antibody Reactivity	Antibody Verified EP	Allele
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:02
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:03
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*03:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*32:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*36:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*74:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*80:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	C*01:02
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:03
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:06
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:07
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:08
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:09
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:10
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:12
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:13
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:14
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:17
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:19
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:21
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:23
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:24
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:25
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:26
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:28
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:29
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:30
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:32
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:33
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:35
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:04
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:07
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:09
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:102
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:103
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:104
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:105
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:106

表示を戻すときはReplace allをクリック

List All Epitopes:
全てのエピトープを表示

Alleles causing mismatch

Epitope Matching Epitope Analysis

Class I Class II MICA Session Date: 4/11/2019 ~ 4/18/2019 Find Mismatch Evaluation Search Allele(s) A*02:01
 Epitope Library HMM Class I 0817 Existing Session: Delete Reanalyze Search Epitope(s) 9F
 Patient Patient 1 A*03:01,A*31:01,B*07:02,B*40:01,C*03:04,C*07:02 Comment: List All Epitopes
 Donor/Immunizer Donor 3 A*29:02,A*32:01,B*14:02,C*03:04,C*07:02

Ab Verified Other Alleles causing mismatch # of Mismatch **拡大図** Calculate Replace all Import Export Save iCn3D Latest Version Session Name: MM_Match_20190418101649

Patient	Donor	A PatientEp AbVerified	A DonorEp AbVerified	A Mismatch AbVerified	# Mis Abv.	B # Mismatch AbVerified	C PatientEp AbVerified	C DonorEp AbVerified	C Mismatch AbVerified	C # Mismatch AbVerified	ClassI # Mismatch AbVerified
Patient 1 A*03:01, A*31:01, B*07:02, B*40:01, C*03:04, C*07:02	Donor 1 A*34:02, A*66:01, B*13:02, B*51:01, C*06:02, C*16:01	56R, 62QE+56G, 66NV, 79GT, 138ML, 138MI+79GT, 144K, 144KR, 150AAH, 161D, 253Q	62RR, 66NV, 79GT, 79GT+90D, 90D, 138ML, 138MI+79GT, 145RT, 149TAH, 163R, 163RW, 253Q	62RR, 79GT+90D, 145RT, 149TAH, 163R, 163RW	6	16	21H, 65QKR+76VS, 76VRN, 80N, 90D, 163LW, 173K, 193PL3, 193PV, 219W, 253Q, 267QE	65QKR+76VS, 73AN, 76VRN, 80K, 80K+14R, 80N, 90D, 193PV	73AN, 80K, 80K+14R	3	25

Alleles contributing to the mismatch:
 A*34:02 (62RR, 79GT+90D, 145RT, 149TAH)
 A*66:01 (62RR, 79GT+90D, 145RT, 149TAH, 163R, 163RW)

Alleles contributing to the mismatch:
 A*34:02 (62RR, 79GT+90D, 145RT, 149TAH)
 A*66:01 (62RR, 79GT+90D, 145RT, 149TAH, 163R, 163RW)

Alleles causing mismatch:
 Mismatch Epitopeに起因するアレルが表示される

#of Mismatch only

Epitope Matching Epitope Analysis

Class I Class II MICA

Session Date: 4/11/2019 ~ 4/18/2019

Epitope Library: HMM Class1 0817

Patient: Patient 1

Donor/Immunizer: Donor 3

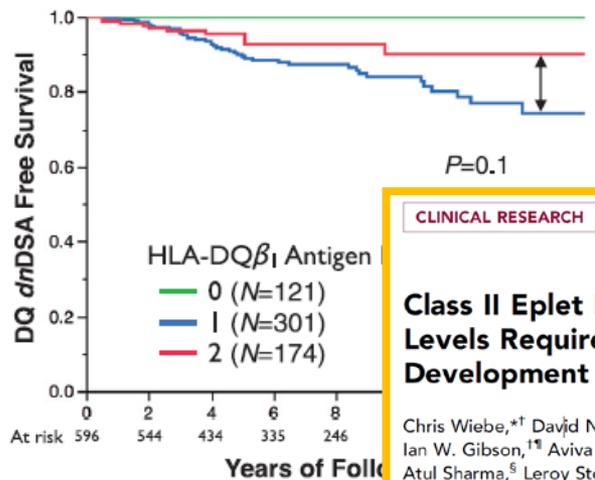
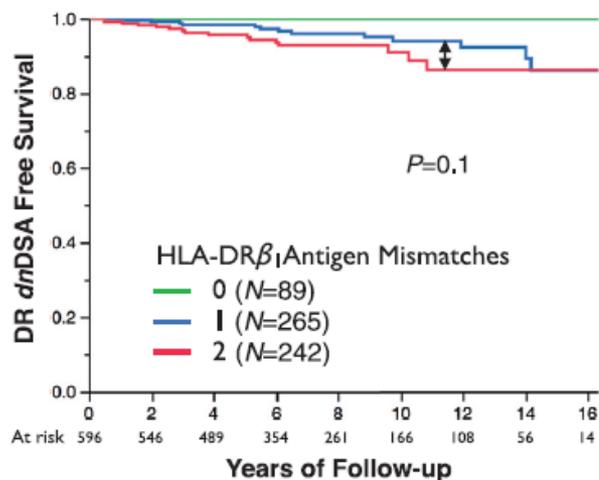
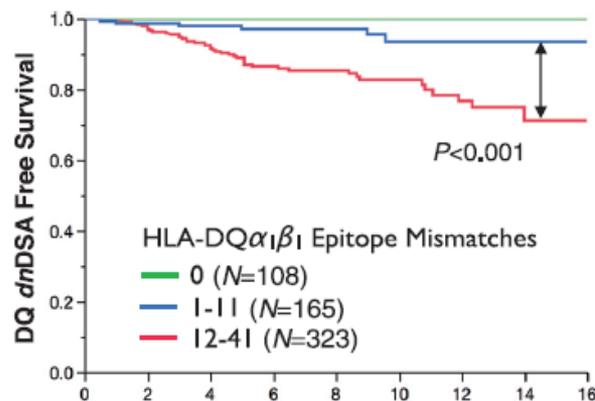
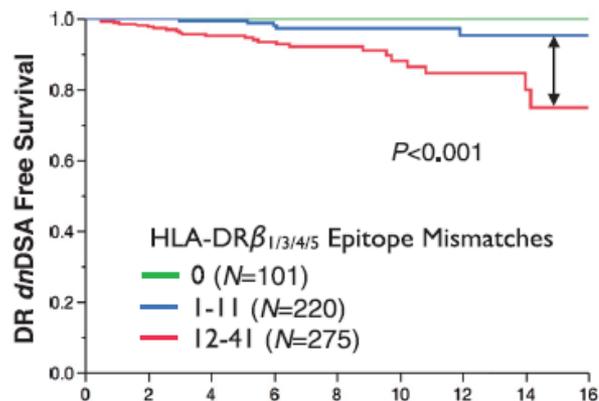
Ab Verified Other All Alleles causing mismatch # of Mismatch only

#of Mismatch only: Mismatchの数のみ表示

Patient	Donor	A # Mismatch AbVerified	B # Mismatch AbVerified	C # Mismatch AbVerified	ClassI # Mismatch AbVerified
Patient 1 A*03:01, A*31:01, B*07:02, B*40:01, C*03:04, C*07:02	Donor 1 A*34:02, A*66:01, B*13:02, B*51:01, C*06:02, C*16:01	6	16	3	25

表示を戻すには再度#of Mismatch onlyをクリック

論文の紹介



CLINICAL RESEARCH www.jasn.org

Class II Eplet Mismatch Modulates Tacrolimus Trough Levels Required to Prevent Donor-Specific Antibody Development

Chris Wiebe,^{*†} David N. Rush,^{*†} Thomas E. Nevins,[‡] Patricia E. Birk,[§] Tom Blydt-Hansen,^{||} Ian W. Gibson,^{1§} Aviva Goldberg,[§] Julie Ho,^{***} Martin Karpinski,^{*} Denise Pochinco,[†] Atul Sharma,[§] Leroy Storsley,^{*} Arthur J. Matas,^{††} and Peter W. Nickerson^{**†††}

Departments of ^{*}Medicine, [§]Pediatrics and Child Health, [‡]Pathology, and ^{**}Immunology, University of Manitoba, Winnipeg, Manitoba, Canada; ¹Diagnostic Services of Manitoba, Winnipeg, Manitoba, Canada; Departments of [†]Pediatrics and ^{††}Surgery, University of Minnesota, Minneapolis, Minnesota; and ^{||}Department of Pediatrics, University of British Columbia, Vancouver, British Columbia, Canada

Epitope Analysis

タイピング情報の入力

手入力する場合

① Epitope Analysisタブを開く

② Patientの横の□(Select alleles)をクリック

③ 入力するローカスを選択

④ Allele欄にアレルを入力

⑤ 該当するアレルをダブルクリック

⑥ ④～⑥の操作を繰り返す

⑦ 全てのローカスの入力が終了後OKをクリック

⑧ 同様の手順(②～⑦)でDonor情報も入力

Donor情報の入力
はここをクリック

Select Alleles

HI A Fusion™

A B C MICA
DRB1 DRB3 DRB4 DRB5
DOA1 DOB1 DPA1 DPB1

24

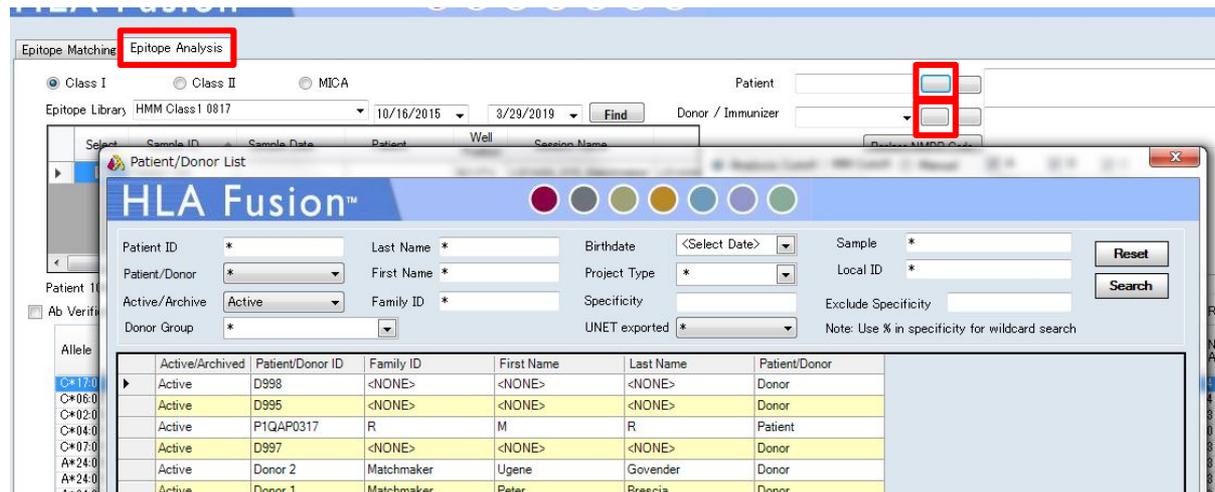
A*24:02

OK Cancel

Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	All
Cw12	091	C	262	120	11.69						25, 32, 205
B53, Bw4	068	B	223	116	12.65						7, 22, 23, 24
Cw7	089	C	277	97	10						25, 32, 37, 3
A1	003	A	100	0	3.32						1, 1E, 12, 13
A2	004	A	23	0	1.89						2, 13, 17, 17
A2	005	A	22	0	1.67						2, 13, 17, 17

タイピング情報の入力

HLA Fusionのデータベースより呼び出す場合



MatchMakerを開き、Epitope Analysisタブを開く
Patientの横の□(Select a patient)をクリック
登録されている情報が一覧で表示されるので、該当する情報を選択しダブルクリックする
Donor情報の入力も同様。



解析結果画面の表示-1

Ab Verified
 Other
 All
 # of Eplets Only
 Rxn Table
 iCn3D
 Latest Version

 Row Count: 99

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Verified	Imm Ab Verified	N. Imm Ab Verified	TP Ab Verified	N. TP Ab Verified
B*18:02	B18,Bw4	036	B	23747	23569	107.11	POS		2305	<input type="checkbox"/>	<input checked="" type="checkbox"/>	144QL	1	144QL	1		0
B*13:01	B13,Bw4	097	B	22791	22585	70.81	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>	144QL	1	144QL	1		0
A*02:06	A2	006	A	16955	16745	50.24	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>	43Q+62GER	6		0	43Q+62GER	6
A*02:01	A2	004	A	16536	16335	54.79	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>	43Q+62GER	6		0	43Q+62GER	6
A*02:03	A2	005	A	15562	15372	59.03	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>	43Q+62GER	5		0	43Q+62GER	5
A*68:02	A68	030	A	15154	14953	49.72	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>	127K, 144TKH	3		0	127K, 144TKH	3
A*69:01	A69	031	A	15105	14906	50.55	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>	107W, 127K	4		0	107W, 127K	4
A*68:01	A68	029	A	15035	14757	25.78	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>	127K, 144TKH	3		0	127K, 144TKH	3
A*24:03	A24	012	A	8964	8751	25.74	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>	65GK, 127K	3		0	65GK, 127K	3
A*24:02	A24	011	A	8645	8426	23.33	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>	65GK, 127K	3		0	65GK, 127K	3
A*23:01	A23	010	A	8287	8043	18.07	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>	65GK, 127K	2		0	65GK, 127K	2
A*66:02	A66	028	A	5848	5624	15.2	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>		0		0		0
A*66:01	A66	027	A	5322	5122	17.75	POS		2305	<input type="checkbox"/>	<input checked="" type="checkbox"/>		0		0		0
B*15:12	B76,Bw6	043	B	2520	2305	7.13	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>		0		0		0
B*58:01	B58,Bw4	074	B	1953	1730	5.11	NEG		2305	<input type="checkbox"/>	<input type="checkbox"/>		0		0		0
B*57:01	B57,Bw4	072	B	1876	1674	6.11	NEG		2305	<input type="checkbox"/>	<input type="checkbox"/>		0		0		0
B*73:01	B73,Bw6	077	B	1789	1608	7.71	NEG		2305	<input type="checkbox"/>	<input type="checkbox"/>		0		0		0

Self: Patientのアレルにチェックが付き(タイピング結果を入力している場合)

Imm: Donorのアレルにチェックが付き(タイピング結果を入力している場合)

Ab Verified: LABScreen Single Antigenで確認されたEpitope

N. Ab Verified: Ab VerifiedのEpitopeの数

Imm Ab Verified: ドナー由来と考えられるAb Verified

N. Imm Ab Verified: ドナー由来と考えられるAb VerifiedのEpitopeの数

TP Ab Verified: Third PartyのAb Verified

N. TP Ab Verified: Third PartyのAb Verifiedの数

解析結果画面の表示-2

Epitope Matching Epitope Analysis

Class I Class II MICA Patient Patient 1 A*03:01 A*31:01 B*07:02 B*40:01 C*03:04 C*07:02 Not in panel

Epitope Library HMM Class1 0817 4/ 3/2019 4/17/2019 Find Donor / Immunizer Donor 1 A*34:02 A*66:01 B*13:02 B*51:01 C*06:02 C*16:01

Select Sample ID Sample Date Patient Well Position Session Name

<input checked="" type="checkbox"/>	112			3 (C1)	05-25-17 SAC1_lot 7 Bordeaux P1
<input type="checkbox"/>	112			32 (H4)	05-25-17 SAC1_lot 7 Bordeaux P1

Analysis Cutoff MM Cutoff Manual A B C

Data Type Baseline Cutoff 2305 2305 2305

Mean of Self (m) 1116 1277 1370 703
SD 337 216 124 131
m+3SD 2128 1925 1742 1096

Positiveと判定されたEpitopeが全て表示

Ab Verified Other All # of Epitopes Only Rxn Table Can3D Latest Version Show Self Show Imm Show POS Reset Export Row Count: 99

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Verified	Imm Ab Verified	N. Imm Ab Verified	TP Ab Verified
B*13:02	B13.Bw4	036	B	23747	23569	107.11	POS		2305		<input checked="" type="checkbox"/>	144QL	1	144QL	1	
B*13:01	B13.Bw4	037	B	22791	22565	70.81	POS		2305		<input checked="" type="checkbox"/>	144QL	1	144QL	1	
A*02:06	A2	006	A	18955	16745	50.24	POS		2305		<input checked="" type="checkbox"/>	43Q+62GER, 6...	6		0	43Q+62GER, 6...
A*02:01	A2	004	A	15536	16335	54.79	POS		2305		<input checked="" type="checkbox"/>	43Q+62GER, 6...	6		0	43Q+62GER, 6...
A*02:03	A2	005	A	15562	15372	59.03	POS		2305		<input checked="" type="checkbox"/>	43Q+62GER, 6...	5		0	43Q+62GER, 6...
A*8:02	A68	030	A	15154	14953	49.72	POS		2305		<input checked="" type="checkbox"/>	127K, 144TKH, 14...	3		0	127K, 144TKH, 14...
A*69:01	A69	031	A	15105	14908	50.55	POS		2305		<input checked="" type="checkbox"/>	107W, 127K, 14...	4		0	107W, 127K, 14...
A*68:01	A68	029	A	15035	14757	25.78	POS		2305		<input checked="" type="checkbox"/>	127K, 144TKH, 14...	3		0	127K, 144TKH, 14...
A*24:03	A24	012	A	8964	8751	25.74	POS		2305		<input checked="" type="checkbox"/>	65GK, 127K, 14...	3		0	65GK, 127K, 14...
A*24:02	A24	011	A	8645	8426	23.33	POS		2305		<input checked="" type="checkbox"/>	65GK, 127K, 14...	3		0	65GK, 127K, 14...
A*23:01	A23	010	A	8287	8049	18.07	POS		2305		<input checked="" type="checkbox"/>	65GK, 127K, 14...	2		0	65GK, 127K, 14...
A*66:02	A66	028	A	5848	5624	16.2	POS		2305		<input checked="" type="checkbox"/>	65GK, 127K, 14...	2		0	65GK, 127K, 14...
A*66:01	A66	027	A	5322	5122	17.75	POS		2305		<input checked="" type="checkbox"/>		0		0	
B*15:12	B76.Bw6	043	B	2520	2305	7.13	POS		2305		<input checked="" type="checkbox"/>		0		0	
B*58:01	B58.Bw4	074	B	1953	1730	5.11	NEG		2305		<input type="checkbox"/>		0		0	
B*57:01	B57.Bw4	072	B	1876	1674	6.11	NEG		2305		<input type="checkbox"/>		0		0	
B*73:01	B73.Bw6	077	B	1789	1608	7.71	NEG		2305		<input type="checkbox"/>		0		0	
B*27:03	B27.Bw6	048	B	1792	1590	5.23	NEG		2305		<input type="checkbox"/>		0		0	
B*27:05	B27.Bw4	047	B	1720	1523	5.91	NEG		2305		<input type="checkbox"/>		0		0	
B*56:01	B56.Bw6	071	B	1711	1523	6.74	NEG		2305		<input type="checkbox"/>		0		0	

All positive epitopes (all locu 9): 11/14 Positive Alleles Covered.

Epitope	#	Locus	Residue
<input type="checkbox"/> 127K	9	A	127K
<input type="checkbox"/> 144TKH	6	A	142T143T144K145H
<input type="checkbox"/> 145KHA	5	A	144K145H149A
<input type="checkbox"/> 107W	4	A	107W
<input type="checkbox"/> 43Q+62GER	3	A	43Q + 62G6E65R
<input type="checkbox"/> 62GK2	3	A	62G6E65R66K (73T74H7...
<input type="checkbox"/> 65GK	3	A	E.E.G.K.A
<input type="checkbox"/> 144KR+127K	2	A	144K145T144K145R + 127K
<input type="checkbox"/> 144QL	2	B	144Q145L149A

Epitope Matching Epitope Analysis

Class I Class II MICA Patient Patient 1 A*03:01 A*31:01 B*07:02 B*40:01 C*03:04 C*07:02 Not in panel

Epitope Library HMM Class1 0817 4/ 3/2019 4/17/2019 Find Donor / Immunizer Donor 1 A*34:02 A*66:01 B*13:02 B*51:01 C*06:02 C*16:01

Select Sample ID Sample Date Patient Well Position Session Name

<input checked="" type="checkbox"/>	112			3 (C1)	05-25-17 SAC1_lot 7 Bordeaux P1
<input type="checkbox"/>	112			32 (H4)	05-25-17 SAC1_lot 7 Bordeaux P1

Analysis Cutoff MM Cutoff Manual A B C

Data Type Baseline Cutoff 2305 2305 2305

Mean of Self (m) 1116 1277 1370 703
SD 337 216 124 131
m+3SD 2128 1925 1742 1096

チェックを入れたEpitopeのみ表示

Ab Verified Other All # of Epitopes Only Rxn Table Can3D Latest Version Show Self Show Imm Show POS Reset Export Row Count: 3

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Verified	Imm Ab Verified	N. Imm Ab Verified	TP Ab Verified
A*02:06	A2	006	A	18955	16745	50.24	POS		2305		<input checked="" type="checkbox"/>	43Q+62GER, 6...	6		0	43Q+62GER, 6...
A*02:01	A2	004	A	15536	16335	54.79	POS		2305		<input checked="" type="checkbox"/>	43Q+62GER, 6...	6		0	43Q+62GER, 6...
A*02:03	A2	005	A	15562	15372	59.03	POS		2305		<input checked="" type="checkbox"/>	43Q+62GER, 6...	5		0	43Q+62GER, 6...

All positive epitopes (all locu 9): 3/14 Positive Alleles Covered.

Epitope	#	Locus	Residue
<input type="checkbox"/> 127K	9	A	127K
<input type="checkbox"/> 144TKH	6	A	142T143T144K145H
<input type="checkbox"/> 145KHA	5	A	144K145H149A
<input type="checkbox"/> 107W	4	A	107W
<input checked="" type="checkbox"/> 43Q+62GER	3	A	43Q + 62G6E65R
<input type="checkbox"/> 62GK2	3	A	62G6E65R66K (73T74H7...
<input type="checkbox"/> 65GK	3	A	E.E.G.K.A
<input type="checkbox"/> 144KR+127K	2	A	144K145T144K145R + 127K
<input type="checkbox"/> 144QL	2	B	144Q145L149A

Positive Alleles Covered

11/14 Positive Alleles Covered
 Positiveと判定されたアレルが14個
 14個のうち11個がEpitopeをシェアしている

All positive epitopes (all locu 9 : **11/14 Positive Alleles Covered.**

Epitope	#	Locus	Residue
<input type="checkbox"/> 127K	9	A	127K
<input type="checkbox"/> 144TKH	6	A	142T143T144K145H
<input type="checkbox"/> 145KHA	5	A	144K145H149A
<input type="checkbox"/> 107W	4	A	107W
<input type="checkbox"/> 43Q+62GER	3	A	43Q + 62G63E65R
<input type="checkbox"/> 62GK2	3	A	62G63E65R66K (73T74H)
<input type="checkbox"/> 65GK	3	A	E,E,G,K,A
<input type="checkbox"/> 144KR+127K	2	A	142I143T144K145R + 127K
<input type="checkbox"/> 144QL	2	B	144Q145L149A

拡大図

#	Locus	Residue
9	A	127K
6	A	142T143T144K145H
5	A	144K145H149A
4	A	107W
3	A	43Q + 62G63E65R
3	A	62G63E65R66K (73T74H)
3	A	E,E,G,K,A
2	A	142I143T144K145R + 127K
2	B	144Q145L149A

拡大図

Allele	Sero	Bead ID	Loc	Raw	Baseli	Ratio	Rxn	Miss EP Def	Cutoff	Self	Imm	Ab Verified
B*13:02	B13,Bw4	036	B	23747	23559	107.11	POS	<input type="checkbox"/>	2305	<input type="checkbox"/>	<input checked="" type="checkbox"/>	144QL
B*13:01	B13,Bw4	097	B	22791	22585	70.81	POS	<input type="checkbox"/>	2305	<input type="checkbox"/>	<input type="checkbox"/>	144QL
A*02:06	A2	006	A	16955	16745	50.24	POS	<input type="checkbox"/>	2305	<input type="checkbox"/>	<input type="checkbox"/>	43Q+62GER, 62GK2, 107W, 127K, 144TKH, 145KHA
A*02:01	A2	004	A	16536	16335	54.79	POS	<input type="checkbox"/>	2305	<input type="checkbox"/>	<input type="checkbox"/>	43Q+62GER, 62GK2, 107W, 127K, 144TKH, 145KHA
A*02:03	A2	005	A	15562	15372	59.03	POS	<input type="checkbox"/>	2305	<input type="checkbox"/>	<input type="checkbox"/>	43Q+62GER, 62GK2, 107W, 127K, 144TKH
A*68:02	A68	030	A	15154	14953	49.72	POS	<input type="checkbox"/>	2305	<input type="checkbox"/>	<input type="checkbox"/>	127K, 144TKH, 145KHA
A*69:01	A69	031	A	15105	14906	50.55	POS	<input type="checkbox"/>	2305	<input type="checkbox"/>	<input type="checkbox"/>	107W, 127K, 144TKH, 145KHA
A*68:01	A68	029	A	15035	14757	25.78	POS	<input type="checkbox"/>	2305	<input type="checkbox"/>	<input type="checkbox"/>	127K, 144TKH, 145KHA
A*24:03	A24	012	A	8964	8751	25.74	POS	<input type="checkbox"/>	2305	<input type="checkbox"/>	<input type="checkbox"/>	65GK, 127K, 144KR+127K
A*24:02	A24	011	A	8645	8426	23.33	POS	<input type="checkbox"/>	2305	<input type="checkbox"/>	<input type="checkbox"/>	65GK, 127K, 144KR+127K
A*23:01	A23	010	A	8287	8043	18.07	POS	<input type="checkbox"/>	2305	<input type="checkbox"/>	<input type="checkbox"/>	65GK, 127K
A*66:02	A66	028	A	5848	5624	15.2	POS	<input type="checkbox"/>	2305	<input type="checkbox"/>	<input type="checkbox"/>	
A*66:01	A66	027	A	5322	5122	17.75	POS	<input type="checkbox"/>	2305	<input type="checkbox"/>	<input type="checkbox"/>	
B*15:12	B76,Bw6	043	B	2520	2305	7.13	POS	<input type="checkbox"/>	2305	<input type="checkbox"/>	<input type="checkbox"/>	
B*58:01	B58,Bw4	074	B	1953	1730	5.11	NEG	<input type="checkbox"/>	2305	<input type="checkbox"/>	<input type="checkbox"/>	
B*57:01	B57,Bw4	072	B	1876	1674	6.11	NEG	<input type="checkbox"/>	2305	<input type="checkbox"/>	<input type="checkbox"/>	

Positive:14個

1	144QL	1		
1	144QL	1		
6		0	43C	
6		0	43C	
5		0	43C	
4		0	127	
3		0	107	
3		0	127	
3		0	65G	
3		0	65G	
2		0	65G	
0		0		
0		0		
0		0		
0		0		
0		0		
0		0		

11個がEpitopeをシェア

画面の表示

HLA Fusion™

Epitope Matching Epitope Analysis

Class I Class II MICA

Epitope Library: HMM Class I 0817 4/3/2019 4/17/2019 Find Donor / Immunizer: Donor 1

Select	Sample ID	Sample Date	Patient	Well Position	Session Name
<input checked="" type="checkbox"/>	112			3 (C1)	05-25-17 SAC1_lot 7 Bordeaux P1_
<input type="checkbox"/>	112			32 (H4)	05-25-17 SAC1_lot 7 Bordeaux P1

112 / 05-25-17 SAC1_lot 7 Bordeaux P1_adsorbout

Ab Verified Other All # of Epitopes Only Rxn Table iCn3D Latest Version

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff
A*02:06	A2	006	A	16955	16745	50.24	POS		2305
A*02:01	A2	004	A	16536	16335	54.79	POS		2305
A*02:03	A2	005	A	15562	15372	59.03	POS		2305
A*68:02	A68	030	A	15154	14953	49.72	POS		2305
A*69:01	A69	031	A	15105	14906	50.55	POS		2305
A*68:01	A68	029	A	15035	14757	25.78	POS		2305
A*24:03	A24	012	A	8964	8751	25.74	POS		2305

Find Allele Find Epit Find Pos Epit Find Cutoff 127K

Show Self Show Imm Show POS Reset Export

All positive epitopes (all loci): 9/14 Positive Alleles Cover

Epitope	#	Locus	Residue
<input checked="" type="checkbox"/> 127K	9	A	127K
<input type="checkbox"/> 144TKH	6	A	142T143T144K145H
<input type="checkbox"/> 145KHA	5	A	144K145H149A
<input checked="" type="checkbox"/> 107W	4	A	107W
<input type="checkbox"/> 49Q+62GER	3	A	49Q + 62G63E65R
<input type="checkbox"/> 62GK2	3	A	62G63E65R66K (73T74H)
<input type="checkbox"/> 65GK	3	A	E.E.G.K.A
<input type="checkbox"/> 144KR+127K	2	A	142I143T144K145R + 127
<input type="checkbox"/> 144QL	2	B	144Q145L149A

Row Count: 9

Statistics: 002) 19961.45 001) 161.72 C:123.432 14

Epitope Spec: B13 A2 A69 A68 A24 A23 A66

HLA Fusion™

HLA Matchmaker

Summary 112

A*02:01 A*02:03 A*02:06 Find Ag Sort Ag

5000 10000 15000

38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80

A B Bw C

10002 10001 10000 9999 9998 9997 9996 9995 9994 9993 9992 9991 9990 9989 9988 9987 9986 9985 9984 9983 9982 9981 9980 9979 9978 9977 9976 9975 9974 9973 9972 9971 9970 9969 9968 9967 9966 9965 9964 9963 9962 9961 9960 9959 9958 9957 9956 9955 9954 9953 9952 9951 9950 9949 9948 9947 9946 9945 9944 9943 9942 9941 9940 9939 9938 9937 9936 9935 9934 9933 9932 9931 9930 9929 9928 9927 9926 9925 9924 9923 9922 9921 9920 9919 9918 9917 9916 9915 9914 9913 9912 9911 9910 9909 9908 9907 9906 9905 9904 9903 9902 9901 9900 9899 9898 9897 9896 9895 9894 9893 9892 9891 9890 9889 9888 9887 9886 9885 9884 9883 9882 9881 9880 9879 9878 9877 9876 9875 9874 9873 9872 9871 9870 9869 9868 9867 9866 9865 9864 9863 9862 9861 9860 9859 9858 9857 9856 9855 9854 9853 9852 9851 9850 9849 9848 9847 9846 9845 9844 9843 9842 9841 9840 9839 9838 9837 9836 9835 9834 9833 9832 9831 9830 9829 9828 9827 9826 9825 9824 9823 9822 9821 9820 9819 9818 9817 9816 9815 9814 9813 9812 9811 9810 9809 9808 9807 9806 9805 9804 9803 9802 9801 9800 9799 9798 9797 9796 9795 9794 9793 9792 9791 9790 9789 9788 9787 9786 9785 9784 9783 9782 9781 9780 9779 9778 9777 9776 9775 9774 9773 9772 9771 9770 9769 9768 9767 9766 9765 9764 9763 9762 9761 9760 9759 9758 9757 9756 9755 9754 9753 9752 9751 9750 9749 9748 9747 9746 9745 9744 9743 9742 9741 9740 9739 9738 9737 9736 9735 9734 9733 9732 9731 9730 9729 9728 9727 9726 9725 9724 9723 9722 9721 9720 9719 9718 9717 9716 9715 9714 9713 9712 9711 9710 9709 9708 9707 9706 9705 9704 9703 9702 9701 9700 9699 9698 9697 9696 9695 9694 9693 9692 9691 9690 9689 9688 9687 9686 9685 9684 9683 9682 9681 9680 9679 9678 9677 9676 9675 9674 9673 9672 9671 9670 9669 9668 9667 9666 9665 9664 9663 9662 9661 9660 9659 9658 9657 9656 9655 9654 9653 9652 9651 9650 9649 9648 9647 9646 9645 9644 9643 9642 9641 9640 9639 9638 9637 9636 9635 9634 9633 9632 9631 9630 9629 9628 9627 9626 9625 9624 9623 9622 9621 9620 9619 9618 9617 9616 9615 9614 9613 9612 9611 9610 9609 9608 9607 9606 9605 9604 9603 9602 9601 9600 9599 9598 9597 9596 9595 9594 9593 9592 9591 9590 9589 9588 9587 9586 9585 9584 9583 9582 9581 9580 9579 9578 9577 9576 9575 9574 9573 9572 9571 9570 9569 9568 9567 9566 9565 9564 9563 9562 9561 9560 9559 9558 9557 9556 9555 9554 9553 9552 9551 9550 9549 9548 9547 9546 9545 9544 9543 9542 9541 9540 9539 9538 9537 9536 9535 9534 9533 9532 9531 9530 9529 9528 9527 9526 9525 9524 9523 9522 9521 9520 9519 9518 9517 9516 9515 9514 9513 9512 9511 9510 9509 9508 9507 9506 9505 9504 9503 9502 9501 9500 9499 9498 9497 9496 9495 9494 9493 9492 9491 9490 9489 9488 9487 9486 9485 9484 9483 9482 9481 9480 9479 9478 9477 9476 9475 9474 9473 9472 9471 9470 9469 9468 9467 9466 9465 9464 9463 9462 9461 9460 9459 9458 9457 9456 9455 9454 9453 9452 9451 9450 9449 9448 9447 9446 9445 9444 9443 9442 9441 9440 9439 9438 9437 9436 9435 9434 9433 9432 9431 9430 9429 9428 9427 9426 9425 9424 9423 9422 9421 9420 9419 9418 9417 9416 9415 9414 9413 9412 9411 9410 9409 9408 9407 9406 9405 9404 9403 9402 9401 9400 9399 9398 9397 9396 9395 9394 9393 9392 9391 9390 9389 9388 9387 9386 9385 9384 9383 9382 9381 9380 9379 9378 9377 9376 9375 9374 9373 9372 9371 9370 9369 9368 9367 9366 9365 9364 9363 9362 9361 9360 9359 9358 9357 9356 9355 9354 9353 9352 9351 9350 9349 9348 9347 9346 9345 9344 9343 9342 9341 9340 9339 9338 9337 9336 9335 9334 9333 9332 9331 9330 9329 9328 9327 9326 9325 9324 9323 9322 9321 9320 9319 9318 9317 9316 9315 9314 9313 9312 9311 9310 9309 9308 9307 9306 9305 9304 9303 9302 9301 9300 9299 9298 9297 9296 9295 9294 9293 9292 9291 9290 9289 9288 9287 9286 9285 9284 9283 9282 9281 9280 9279 9278 9277 9276 9275 9274 9273 9272 9271 9270 9269 9268 9267 9266 9265 9264 9263 9262 9261 9260 9259 9258 9257 9256 9255 9254 9253 9252 9251 9250 9249 9248 9247 9246 9245 9244 9243 9242 9241 9240 9239 9238 9237 9236 9235 9234 9233 9232 9231 9230 9229 9228 9227 9226 9225 9224 9223 9222 9221 9220 9219 9218 9217 9216 9215 9214 9213 9212 9211 9210 9209 9208 9207 9206 9205 9204 9203 9202 9201 9200 9199 9198 9197 9196 9195 9194 9193 9192 9191 9190 9189 9188 9187 9186 9185 9184 9183 9182 9181 9180 9179 9178 9177 9176 9175 9174 9173 9172 9171 9170 9169 9168 9167 9166 9165 9164 9163 9162 9161 9160 9159 9158 9157 9156 9155 9154 9153 9152 9151 9150 9149 9148 9147 9146 9145 9144 9143 9142 9141 9140 9139 9138 9137 9136 9135 9134 9133 9132 9131 9130 9129 9128 9127 9126 9125 9124 9123 9122 9121 9120 9119 9118 9117 9116 9115 9114 9113 9112 9111 9110 9109 9108 9107 9106 9105 9104 9103 9102 9101 9100 9099 9098 9097 9096 9095 9094 9093 9092 9091 9090 9089 9088 9087 9086 9085 9084 9083 9082 9081 9080 9079 9078 9077 9076 9075 9074 9073 9072 9071 9070 9069 9068 9067 9066 9065 9064 9063 9062 9061 9060 9059 9058 9057 9056 9055 9054 9053 9052 9051 9050 9049 9048 9047 9046 9045 9044 9043 9042 9041 9040 9039 9038 9037 9036 9035 9034 9033 9032 9031 9030 9029 9028 9027 9026 9025 9024 9023 9022 9021 9020 9019 9018 9017 9016 9015 9014 9013 9012 9011 9010 9009 9008 9007 9006 9005 9004 9003 9002 9001 9000 8999 8998 8997 8996 8995 8994 8993 8992 8991 8990 8989 8988 8987 8986 8985 8984 8983 8982 8981 8980 8979 8978 8977 8976 8975 8974 8973 8972 8971 8970 8969 8968 8967 8966 8965 8964 8963 8962 8961 8960 8959 8958 8957 8956 8955 8954 8953 8952 8951 8950 8949 8948 8947 8946 8945 8944 8943 8942 8941 8940 8939 8938 8937 8936 8935 8934 8933 8932 8931 8930 8929 8928 8927 8926 8925 8924 8923 8922 8921 8920 8919 8918 8917 8916 8915 8914 8913 8912 8911 8910 8909 8908 8907 8906 8905 8904 8903 8902 8901 8900 8899 8898 8897 8896 8895 8894 8893 8892 8891 8890 8889 8888 8887 8886 8885 8884 8883 8882 8881 8880 8879 8878 8877 8876 8875 8874 8873 8872 8871 8870 8869 8868 8867 8866 8865 8864 8863 8862 8861 8860 8859 8858 8857 8856 8855 8854 8853 8852 8851 8850 8849 8848 8847 8846 8845 8844 8843 8842 8841 8840 8839 8838 8837 8836 8835 8834 8833 8832 8831 8830 8829 8828 8827 8826 8825 8824 8823 8822 8821 8820 8819 8818 8817 8816 8815 8814 8813 8812 8811 8810 8809 8808 8807 8806 8805 8804 8803 8802 8801 8800 8799 8798 8797 8796 8795 8794 8793 8792 8791 8790 8789 8788 8787 8786 8785 8784 8783 8782 8781 8780 8779 8778 8777 8776 8775 8774 8773 8772 8771 8770 8769 8768 8767 8766 8765 8764 8763 8762 8761 8760 8759 8758 8757 8756 8755 8754 8753 8752 8751 8750 8749 8748 8747 8746 8745 8744 8743 8742 8741 8740 8739 8738 8737 8736 8735 8734 8733 8732 8731 8730 8729 8728 8727 8726 8725 8724 8723 8722 8721 8720 8719 8718 8717 8716 8715 8714 8713 8712 8711 8710 8709 8708 8707 8706 8705 8704 8703 8702 8701 8700 8699 8698 8697 8696 8695 8694 8693 8692 8691 8690 8689 8688 8687 8686 8685 8684 8683 8682 8681 8680 8679 8678 8677 8676 8675 8674 8673 8672 8671 8670 8669 8668 8667 8666 8665 8664 8663 8662 8661 8660 8659 8658 8657 8656 8655 8654 8653 8652 8651 8650 8649 8648 8647 8646 8645 8644 8643 8642 8641 8640 8639 8638 8637 8636 8635 8634 8633 8632 8631 8630 8629 8628 8627 8626 8625 8624 8623 8622 8621 8620 8619 8618 8617 8616 8615 8614 8613 8612 8611 8610 8609 8608 8607 8606 8605 8604 8603 8602 8601 8600 8599 8598 8597 8596 8595 8594 8593 8592 8591 8590 8589 8588 8587 8586 8585 8584 8583 8582 8581 8580 8579 8578 8577 8576 8575 8574 8573 8572 8571 8570 8569 8568 8567 8566 8565 8564 8563 8562 8561 8560 8559 8558 8557 8556 8555 8554 8553 8552 8551 8550 8549 8548 8547 8546 8545 8544 8543 8542 8541 8540 8539 8538 8537 8536 8535 8534 8533 8532 8531 8530 8529 8528 8527 8526 8525 8524 8523 8522 8521 8520 8519 8518 8517 8516 8515 8514 8513 8512 8511 8510 8509 8508 8507 8506 8505 8504 8503 8502 8501 8500 8499 8498 8497 8496 8495 8494 8493 8492 8491 8490 8489 8488 8487 8486 8485 8484 8483 8482 8481 8480 8479 8478 8477 8476 8475 8474 8473 8472 8471 8470 8469 8468 8467 8466 8465 8464 8463 8462 8461 8460 8459 8458 8457 8456 8455 8454 8453 8452 8451 8450 8449 8448 8447 8446 8445 8444 8443 8442 8441 8440 8439 8438 8437 8436 8435 8434 8433 8432 8431 8430 8429 8428 8427 8426 8425 8424 8423 8422 8421 8420 8419 8418 8417 8416 8415 8414 8413 8412 8411 8410 8409 8408 8407 8406 8405 8404 8403 8402 8401 8400 8399 8398 8397 8396 8395 8394 8393 8392 8391 8390 8389 8388 8387 8386 8385 8384 8383 8382 8381 8380 8379 8378 8377 8376 8375 8374 8373 8372 8371 8370 8369 8368 8367 8366 8365 8364 8363 8362 8361 8360 8359 8358 8357 8356 8355 8354 8353 8352 8351 8350 8349 8348 8347 8346 8345 8344 8343 8342 8341 8340 8339 8338 8337 8336 8335 8334 8333 8332 8331 8330 8329 8328 8327 8326 8325 8324 8323 8322 8321 8320 8319 8318 8317 8316 8315 8314 8313 8312 8311 8310 8309 8308 8307 8306 8305 8304 8303 8302 8301 8300 8299 8298 8297 8296 8295 8294 8293 8292 8291 8290 8289 8288 8287 8286 8285 8284 8283 8282 8281 8280 8279 8278 8277 8276 8275 8274 8273 8272 8271 8270 8269 8268 8267 8266 8265 8264 8263 8262 8261 8260 8259 8258 8257 8256 8255 8254 8253 8252 8251 8250 8249 8248 8247 8246 8245 8244 8243 8242 8241 8240 8239 8238 8237 8236 8235 8234 8233 8232 8231 8230 8229 8228 8227 8226 8225 8224 8223 8222 8221 8220 8219 8218 8217 8216 8215 8214 8213 8212 8211 8210 8209 8208 8207 8206 8205 8204 8203 8202 8201 8200 8199 8198 8197 8196 8195 8194 8193 8192 8191 8190 8189 8188 8187 8186 8185 8184 8183 8182 8181 8180 8179 8178 8177 8176 8175 8174 8173 8172 8171 8170 8169 8168 8167 8166 8165 8164 8163 8162 8161 8160 8159 8158 8157 8156 8155 8154 8153 8152 8151 8150 8149 8148 8147 8146 8145 8144 8143 8142 8141 8140 8139 8138 8137 8136 8135 8134 8133 8132 8131 8130 8129 8128 8127 8126 8125 8124 8123 8122 8121 8120 8119 8118 8117 8116 8115 8114 8113 8112 8111 8110 8109 8108 8107 8106 8105 8104 8103 8102 8101 8100 8099 8098 8097 8096 8095 8094 8093 8092 8091 8090 8089 8088 8087 8086 8085 8084 8083 8082 8081 8080 8079 8078 8077 8076 8075 8074 8073 8072 8071 8070 8069 8068 8067 8066 8065 8064 8063 8062 8061 8060 8059 8058 8057 8056 8055 8054 8053 8052 8051 8050 8049 8048 8047 8046 8045 8044 8043 8042 8041 8040 8039 8038 8037 8036 8035 8034 8033 8032 8031 8030 8029 8028 8027 8026 8025 8024 8023 8022 8021 8020 8019 8018 8017 8016 8015 8014 8013 8012 8011 8010 8009 8008 8007 8006 8005 8004 8003 8002 8001 8000 7999 7998 7997 7996 7995 7994 7993 7992 7991 7990 7989 7988 7987 7986 7985 7984 7983 7982 7981 7980 7979 7978 7977 7976 7975 7974 7973 7972 7971 7970 7969 796

Patient及びDonor情報の編集

The screenshot shows the 'Patient/Donor Information' window with the following details:

- General Info: ID: Patient 1, Name: Cha, John
- Enforce ISBT format for Patient/Donor ID: Archived:
- Patient/Donor Info: Patient or Donor ID: Patient 1, City: [empty], Diagnosis: [empty]
- Patient/Donor Flag: Patient
- Family ID: Matchmaker
- First Name: John, Middle Name: [empty], Last Name: Cha
- Birthdate: [empty], Gender: Male (selected), Female, UNK
- Category Group: Human (selected), Animal
- SSN: [empty], Ethnicity: [empty], Address: [empty]
- Spouse Info: Spouse Name: [empty], Emergency: [empty], Blood Type: [empty], Phone: [empty]
- Associate Donor IDs: [empty]
- Donor List Table:

Donor ID	Relationship with patient	Association Comments	Comments
Donor 1			
Donor 2			
Donor 3			

Patient情報、Donor情報の閲覧、編集ができる

The screenshot shows the HLA analysis results window with the following details:

- HLA Alleles: A*01:01L, A*24:02, B*07:06, B*27:01, C*01:02, C*05:01
- Not in panel: A*01:01L B*07:06 B*27:01
- Allele Selection Table:

Allele	A	B	C
0	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
0	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
0	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
- Buttons: Find Cutoff

LABScreen Single Antigenに含まれないアレルが表示される
この欄に表示されるアレルはEpitope解析に含まれません

Find Allele, Find Eplet

Find Allele
アレルを指定して検索

Reset
検索結果を解除

Find Eplet
Epitopeを指定して検索

Reset
検索結果を解除

Epitope Matching Epitope Analysis

Class I Class II MICA

Epitope Library HMM Class1 0817 10/16/2015 3/29/2019 Find

Patient Patient 1 A*03:01 A*31:01 B*07:02 B*40:01 C*03:04 C*07:02

Donor / Immunizer Donor 1 A*34:02 A*66:01 B*13:02 B*51:01 C*06:02 C*16:01

Analysis Cutoff MM Cutoff Manual A B C

Data Type Baseline Cutoff 2305 2305 2305

Mean of Self (m) 1116 1277 1370 703

SD 337 216 124 131

m+3SD 2128 1925 1742 1096

Find Allele Find Eplet Find Pos Eplet Find Cutoff A*01:01

Show Self Show Imm Show POS Reset Export

Allele	Sero	Bead ID	Locu	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab	N. Ab	All	N. All	Imm Ab	N. Imm Ab Ver
A*01:01	A1	003	A	817	597	2.19	NEG		2305								0

112 / 05-25-17 SAC1_lot 7 Bordeaux P1_adsorbout

Read LABScreen Analysis

Ab Verified Other All # of Eplets Only Rxn Table iCn3D Latest Version

Epitope Matching Epitope Analysis

Class I Class II MICA

Epitope Library HMM Class1 0817 10/21/2015 4/ 3/2019 Find

Patient Donor / Immunizer

Analysis Cutoff MM Cutoff Manual A B C

Data Type Baseline Cutoff 2305 2305 2305

Mean of Self (m)

SD

m+3SD

Find Allele Find Eplet Find Pos Eplet Find Cutoff 16S

Show Self Show Imm Show POS Reset Export

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Self	Cutoff	Imm	All	N. All	Imm All
C*02:02	Cw2	082	C	1823	1451	1.97	NEG			2305				0

112 / 05-25-17 SAC1_lot 7 Bordeaux P1_adsorbout

Read LABScreen Analysis

Ab Verified Other All # of Eplets Only Rxn Table iCn3D Latest Version

Find Pos Eplet

Epitope Matching Epitope Analysis

Class I Class II MICA

Epitope Library: HMM Class1 0817 10/21/2015 4/ 3/2019 **Find** Patient: Donor / Immunizer: **Replace NMDP Code**

Select	Sample ID	Sample Date	Patient	Well Position	Session Name
<input type="checkbox"/>	112			32 (H4)	05-25-17 SAC1_lot 7 Bordeaux P1
<input checked="" type="checkbox"/>	112			3 (C1)	05-25-17 SAC1_lot 7 Bordeaux P1

112 / 05-25-17 SAC1_lot 7 Bordeaux P1_adsorbout **Read LABScreen Analysis**

Ab Verified Other All # of Eplets Only Rxn Table iCn3D Latest Version

Analysis Cutoff: MM Cutoff Manual A B C

Data Type: Baseline Cutoff: 2305 2305 2305

Mean of Self (m): SD: m+3SD:

Find Allele **Find Eplet** **Find Pos Eplet** **Find Cutoff** 65GK

Show Self **Show Imm** **Show POS** **Reset** **Export** Row Count: 3

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Self	Cutoff	Imm	All	N. All	Imm All
A*24:03	A24	012	A	8864	8751	25.74	POS	<input type="checkbox"/>	<input type="checkbox"/>	2305	<input type="checkbox"/>	65GK, 66KAH, 127K, 144KR+127K, 151...	5	
A*24:02	A24	011	A	8645	8426	23.33	POS	<input type="checkbox"/>	<input type="checkbox"/>	2305	<input type="checkbox"/>	65GK, 66KAH, 127K, 144KR+127K, 151...	6	
A*23:01	A23	010	A	8287	8043	18.07	POS	<input type="checkbox"/>	<input type="checkbox"/>	2305	<input type="checkbox"/>	65GK, 66KAH, 127K, 163TG	4	

Find Pos Eplet

Positiveアレルの中からEpitopeを指定して検索

Show Self, Show Imm

Epitope Matching Epitope Analysis

Class I Class II MICA

Patient Patient 1 A*03:01 A*31:01 B*07:02 B*40:01 C*03:04 C*07:02

Epitope Library HMM Class1 0817 10/16/2015 3/29/2019 Find Donor / Immunizer Donor 1 A*34:02 A*66:01 B*13:02 B*51:01 C*06:02 C*16:01

Select	Sample ID	Sample Date	Patient	Well Position	Session Name
<input type="checkbox"/>	112			32 (H4)	05-25-17 SAC1_lot 7 Bordeaux P1
<input type="checkbox"/>	112			3 (C1)	05-25-17 SAC1_lot 7 Bordeaux P1

Analysis Cutoff MM Cutoff Manual A B C

Data Type Baseline Cutoff 2305 2305 2305

Mean of Self (m) 1116 1277 1370 703

SD 337 216 124 131

m+3SD 2128 1925 1742 1096

Find Allele Find Epitope Find Pos Epitope Find Cutoff

Show Self Show Imm Show POS Reset Export Row Count: 6

Allele	Sero	Bead ID	Locu	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Verified	All	N. All	Imm Ab Verified
B*07:02	B7.Bw6	034	B	1703	1494	5.1	NEG		2305	<input checked="" type="checkbox"/>	<input type="checkbox"/>		0		0	
A*31:01	A31	019	A	1747	1493	3.53	NEG		2305	<input checked="" type="checkbox"/>	<input type="checkbox"/>		0		0	
B*40:01	B60.Bw6	053	B	1443	1245	4.95	NEG		2305	<input checked="" type="checkbox"/>	<input type="checkbox"/>		0		0	
A*03:01	A3	007	A	1255	1061	4.5	NEG		2305	<input checked="" type="checkbox"/>	<input type="checkbox"/>		0		0	
C*07:02	Cw7	089	C	1173	834	1.46	NEG		2305	<input checked="" type="checkbox"/>	<input type="checkbox"/>		0		0	
C*03:04	Cw10	085	C	836	572	1.57	NEG		2305	<input checked="" type="checkbox"/>	<input type="checkbox"/>		0		0	

112 / 05-25-17 SAC1_lot 7 Bordeaux P1_adorsbort

Read LABScreen Analysis

Ab Verified Other All # of Epitopes Only Rxn Table iCh3D Latest Version

Show Self
Patientのタイプのみを表示

Epitope Matching Epitope Analysis

Class I Class II MICA

Patient Patient 1 A*03:01 A*31:01 B*07:02 B*40:01 C*03:04 C*07:02

Epitope Library HMM Class1 0817 10/16/2015 3/29/2019 Find Donor / Immunizer Donor 1 A*34:02 A*66:01 B*13:02 B*51:01 C*06:02 C*16:01

Select	Sample ID	Sample Date	Patient	Well Position	Session Name
<input type="checkbox"/>	112			32 (H4)	05-25-17 SAC1_lot 7 Bordeaux P1
<input type="checkbox"/>	112			3 (C1)	05-25-17 SAC1_lot 7 Bordeaux P1

Analysis Cutoff MM Cutoff Manual A B C

Data Type Baseline Cutoff 2305 2305 2305

Mean of Self (m) 1116 1277 1370 703

SD 337 216 124 131

m+3SD 2128 1925 1742 1096

Find Allele Find Epitope Find Pos Epitope Find Cutoff

Show Self **Show Imm Show POS Reset Export** Row Count: 6

Allele	Sero	Bead ID	Locu	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Verified	All	N. All	Imm Ab Verified
B*13:02	B13.Bw4	036	B	23747	23569	107.11	POS		2305	<input type="checkbox"/>	<input checked="" type="checkbox"/>		0		8	
A*66:01	A66	027	A	5322	5122	17.75	POS		2305	<input type="checkbox"/>	<input checked="" type="checkbox"/>		0		0	
C*16:01	Cw16	094	C	1490	1222	2.72	NEG		2305	<input type="checkbox"/>	<input checked="" type="checkbox"/>		0		0	
C*06:02	Cw6	088	C	1260	935	1.68	NEG		2305	<input type="checkbox"/>	<input checked="" type="checkbox"/>		0		0	
B*51:01	B51.Bw4	065	B	960	781	4.3	NEG		2305	<input type="checkbox"/>	<input checked="" type="checkbox"/>		0		0	
A*34:02	A34	024	A	895	662	2.14	NEG		2305	<input type="checkbox"/>	<input checked="" type="checkbox"/>		0		0	

112 / 05-25-17 SAC1_lot 7 Bordeaux P1_adorsbort

Read LABScreen Analysis

Ab Verified Other All # of Epitopes Only Rxn Table iCh3D Latest Version

Show Imm
Donorのタイプのみを表示

Show POS, Missing Ep Def

Epitope Matching Epitope Analysis

Class I Class II MICA Patient Patient 1 A*03:01 A*31:01 B*07:02 B*40:01 C*03:04 C*07:02

Epitope Library HMM Class1 0817 4/ 3/2019 4/17/2019 Find Donor / Immunizer Donor 1 A*34:02 A*66:01 B*13:02 B*51:01 C*06:02 C*16:01

Select Sar HMM Class1 0817 Patient Well Position Session Name

Analysis Cutoff MM Cutoff Manual A B C

Cutoff 2305 2305 2305

Ab (m) 1116 1277 1370 703

337 216 124 131

2128 1925 1742 1096

Find Pos Eplet Find Cutoff

112 / 05-2

Ab Verified Other All # of Eplets Only Rxn Table iCn3D Latest Version Show Self Show Imm Show POS Reset Export Row Count: 14

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Verified	Imm Ab Verified	N. Imm Ab Verified
B*13:02	B13,Bw4	036	B	23747	23569	107.11	POS		2305		<input checked="" type="checkbox"/>	144QL	1	144QL	1
B*13:01	B13,Bw4	097	B	22791	22585	70.81	POS		2305		<input type="checkbox"/>	144QL	1	144QL	1
A*02:06	A2	006	A	16955	16745	50.24	POS		2305		<input type="checkbox"/>	43Q+62GER, 6...	6		0
A*02:01	A2	004	A	16536	16335	54.79	POS		2305		<input type="checkbox"/>	43Q+62GER, 6...	6		0
A*02:03	A2	005	A	15562	15372	59.03	POS		2305		<input type="checkbox"/>	43Q+62GER, 6...	5		0
A*68:02	A68	030	A	15154	14953	49.72	POS		2305		<input type="checkbox"/>	127K, 144TKH...	3		0
A*69:01	A69	031	A	15105	14906	50.55	POS		2305		<input type="checkbox"/>	107W, 127K, 14...	4		0
A*68:01	A68	029	A	15035	14757	25.78	POS		2305		<input type="checkbox"/>	127K, 144TKH...	3		0
A*24:03	A24	012	A	8964	8751	25.74	POS		2305		<input type="checkbox"/>	65GK, 127K, 14...	3		0
A*24:02	A24	011	A	8645	8426	23.33	POS		2305		<input type="checkbox"/>	65GK, 127K, 14...	3		0
A*23:01	A23	010	A	8287	8043	18.07	POS		2305		<input type="checkbox"/>	65GK, 127K	2		0
A*66:02	A66	028	A	5048	5624	15.2	POS		2305		<input type="checkbox"/>		0		0
A*66:01	A66	027	A	5322	5122	17.75	POS		2305		<input checked="" type="checkbox"/>		0		0
B*15:12	B76,Bw6	043	B	2520	2305	7.13	POS		2305		<input type="checkbox"/>		0		0

Show POS
陽性と判定されたアレル情報のみを表示

Missing Ep Def
カタログに含まれるがEpitope Database
に含まれないアレルにチェックが入る
(カタログファイルとEpitope Databaseの
バージョンが異なる場合)

#of Eplets Only

Epitope Matching Epitope Analysis

Class I Class II MICA Patient: [] [] []

Epitope Library: HMM Class1 0817 10/21/2015 4/ 3/2019 Find Donor / Immunizer: [] []

Select	Sample ID	Sample Date	Patient	Well Position	Session Name
<input type="checkbox"/>	112				
<input checked="" type="checkbox"/>	112				

#of Eplets Only
Epletの数のみの表示となる

112 / 05-25-17 SAC1_lot 7 Bordeaux_P1Ladsorbout

Ab Verified Other All # of Eplets Only Rxn Table iCn3D Latest Version Show Self Show Imm Show POS Reset Export Row Count: 99

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	N. Ab Verif	N. Imm Ab Verif	N. TP Ab Verif
B*13:02	B13,Bw4	036	B	23747	23569	107.11	POS		2305			1		
B*13:01	B13,Bw4	097	B	22791	22585	70.81	POS		2305			1		
A*02:06	A2	006	A	16955	16745	50.24	POS		2305			6		
A*02:01	A2	004	A	16536	16395	54.79	POS		2305			6		
A*02:03	A2	005	A	15562	15372	59.03	POS		2305			5		
A*68:02	A68	030	A	15154	14953	49.72	POS		2305			3		
A*69:01	A69	031	A	15105	14906	50.55	POS		2305			4		

Epitope Matching Epitope Analysis

Class I Class II MICA Patient: [] [] []

Epitope Library: HMM Class1 0817 10/21/2015 4/ 3/2019 Find Donor / Immunizer: [] []

Select	Sample ID	Sample Date	Patient	Well Position	Session Name
<input type="checkbox"/>	112			32 (H4)	05-25-17 SAC1_lot 7 Bordeaux P1
<input checked="" type="checkbox"/>	112			3 (C1)	05-25-17 SAC1_lot 7 Bordeaux P1

112 / 05-25-17 SAC1_lot 7 Bordeaux_P1Ladsorbout

Ab Verified Other All # of Eplets Only Rxn Table iCn3D Latest Version Show Self Show Imm Show POS Reset Export Row Count: 99

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Verif	Imm Ab Verif
B*13:02	B13,Bw4	036	B	23747	23569	107.11	POS		2305			144QL	1	
B*13:01	B13,Bw4	097	B	22791	22585	70.81	POS		2305			144QL	1	
A*02:06	A2	006	A	16955	16745	50.24	POS		2305			43Q+62GER, 62GK2, 107W, 127K, 144TKH, 1...	6	
A*02:01	A2	004	A	16536	16395	54.79	POS		2305			43Q+62GER, 62GK2, 107W, 127K, 144TKH, 1...	6	
A*02:03	A2	005	A	15562	15372	59.03	POS		2305			43Q+62GER, 62GK2, 107W, 127K, 144TKH	5	
A*68:02	A68	030	A	15154	14953	49.72	POS		2305			127K, 144TKH, 145KHA	3	
A*69:01	A69	031	A	15105	14906	50.55	POS		2305			107W, 127K, 144TKH, 145KHA	4	
A*68:01	A68	029	A	15095	14757	25.78	POS		2305			127K, 144TKH, 145KHA	3	

Rxn Table-1



Epitope Matching Epitope Analysis

Class I Class II MICA

Patient Patient 1 A*03:01 A*31:01 B*07:02 B*40:01 C*03:04 C*07:02

Epitope Library HMM Class I 0817 2/17/2017 4/10/2019 Find Donor / Immunizer Donor 1 A*34:02 A*66:01 B*13:02 B*61:01 C*06:02 C*16:01

Select	Sample ID	Sample Date	Patient	Well Position	Session Name
<input type="checkbox"/>	112	Jan 15, 2019	112	32 (H4)	05-25-17 SAC1_lot 7 Bordeaux P1
<input type="checkbox"/>	112	Jan 15, 2019	112	3 (C1)	05-25-17 SAC1_lot 7 Bordeaux P1
<input checked="" type="checkbox"/>	112	Jan 15, 2019	112	3 (C1)	05-25-17 SAC1_lot 7 Bordeaux P1
<input type="checkbox"/>	171	Mar 05, 2019	112	78 (F10)	05-25-17 SAC1_lot 7 Bordeaux P1

Analysis Cutoff 1 MM Cutoff Manual A B C

Data Type Baseline Cutoff 2305 2305 2305

Mean of Self (m) 1116 1277 1370 703

SD 937 216 124 131

m+3SD 2128 1925 1742 1096

Find Allele Find Epit Find Pos Epit Find Cutoff

Read LABScreen Analysis

Ab Verified Other All # of Epitopes On Rxn Table On3D Latest Version Show Self Show Imm Show POS Reset Export Row Count: 99

Allele	Sero	Bead ID	Loc	Raw	Baseli	Ratio	Rxn	Miss EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Ve	Imm Ab Verit	N. Im Ab Ver	TP Ab Verit	N. TP Ab Verit
B*13:02	B13.Bw4	036	B	23747	23569	107.11	POS		2305			144QL	1	144QL	1		0
B*13:01	B13.Bw4	097	B	22791	22585	70.81	POS		2305			144QL	1	144QL	1		0
A*02:06	A2	006	A	16955	16745	50.24	POS		2305			430Q+62GER, 62GK2, 107W, 127K, 144TKH, 145KHA	6		0	430Q+62GER, 62GK2, 107W, 127K, 144TKH, 145KHA	6
A*02:01	A2	004	A	16936	16835	54.79	POS		2305			430Q+62GER, 62GK2, 107W, 127K, 144TKH, 145KHA	6		0	430Q+62GER, 62GK2, 107W, 127K, 144TKH, 145KHA	6
A*02:03	A2	005	A	16562	16372	59.03	POS		2305			430Q+62GER, 62GK2, 107W, 127K, 144TKH	5		0	430Q+62GER, 62GK2, 107W, 127K, 144TKH	5
A*68:02	A68	030	A	15154	14953	49.72	POS		2305			127K, 144TKH, 145KHA	3		0	127K, 144TKH, 145KHA	3
A*69:01	A69	031	A	15105	14906	50.55	POS		2305			107W, 127K, 144TKH, 145KHA	4		0	107W, 127K, 144TKH, 145KHA	4
A*68:01	A68	029	A	15035	14757	25.79	POS		2305			127K, 144TKH, 145KHA	3		0	127K, 144TKH, 145KHA	3
A*24:03	A24	012	A	8984	8751	25.74	POS		2305			65GK, 127K, 144KR+127K	3		0	65GK, 127K, 144KR+127K	3
A*24:02	A24	011	A	8645	8426	23.33	POS		2305			65GK, 127K, 144KR+127K	3		0	65GK, 127K, 144KR+127K	3
A*23:01	A23	010	A	8287	8043	18.07	POS		2305			65GK, 127K	2		0	65GK, 127K	2
A*66:02	A66	028	A	5848	5624	15.2	POS		2305				0		0		0
A*66:01	A66	027	A	5322	5122	17.75	POS		2305				0		0		0
B*15:12	B76.Bw6	043	B	2520	2305	7.13	POS		2305				0		0		0
B*58:01	B58.Bw4	074	B	1953	1730	5.11	NEG		2305				0		0		0
B*57:01	B57.Bw4	072	B	1876	1674	6.11	NEG		2305				0		0		0
B*73:01	B73.Bw6	077	B	1789	1608	7.71	NEG		2305				0		0		0

Allele Panel Pos MFI 127K 144TK 145KH 107W 430Q+6 62GK2 65GK 144KR 144QL

Allele	Panel	Pos	MFI	127K	144TK	145KH	107W	430Q+6	62GK2	65GK	144KR	144QL	62EE	82LR+	80I+90	82LR+	82LR+	166DG	82LR+	62GE	62RR	149TA	80TLR	145RT	44RM	82LR+	82LR	163LS	80I		
B*13:02			23569										75% 3/4	75% 3/4	60% 3/5	60% 3/5	60% 3/5	60% 3/5	50% 3/6	41% 5/12	37% 3/8	28% 2/7	28% 2/7	27% 3/11	22% 2/9	20% 5/24	20% 1/5	17% 3/17			
B*13:01			22585																												
A*02:06			16745	+	+	+	+	+	+																						
A*02:01			16835	+	+	+	+	+	+																						
A*02:03			16372	+	+	+	+	+	+																						
A*68:02			14953	+	+	+	+	+	+																						
A*69:01			14906	+	+	+	+	+	+																						
A*68:01			14757	+	+	+	+	+	+																						
A*24:03			8751							+	+																				
A*24:02			8426							+	+																				
A*23:01			8043																												
A*66:02			5624																												
A*66:01			5122																												
B*15:12			2305																												
B*58:01			1730																												
B*57:01			1674																												

112 / 05-25-17 SAC1_lot 7 Bordeaux P1_adsorbout

Read LABScreen Analysis

Find Allele Find Epit Find Pos Epit Find Cutoff

Row Count: 99

All positive epitopes (all locu 9): 11/14 Positive Alleles Covered.

Epitope	#	Locus	Residue
127K	9	A	127K
144TKH	6	A	142T143T144K145H
145KHA	5	A	144K145H149A
107W	4	A	107W
430Q+62GER	3	A	430Q + 62G68E65R
62GK2	3	A	62G68E65R66K (73T74H7...
65GK	3	A	E.E.G.K.A
144KR+127K	2	A	142I143T144K145R + 127K
144QL	2	B	144Q145L149A

Rxn Table-2

Allele	Panel	Pos	MFI	127K	144TK	145KH	107W	43Q+6	62GK2	65GK	144KR	144QL	62EE 75% 3/4	82LR+ 75% 3/4	80I+90 75% 3/4	82LF 60% 3/5
A*02:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	16335	+	+	+	+	+	+							
A*02:03	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	15372	+	+		+	+	+							
A*68:02	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	14953	+	+	+										
A*69:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	14906	+	+	+	+									
A*68:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	14757	+	+	+										
A*24:03	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	8751	+									/	/	/	/
A*24:02	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	8426	+									/	/	/	/
A*23:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	8043	+									/	/	/	/
A*66:02	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	5624													
A*66:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	5122													
B*15:12	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	2305													
B*58:01	<input checked="" type="checkbox"/>	<input type="checkbox"/>	1730													

ダブルクリックすると、
検索結果が表示される

112 / 05-25-17 SAC1_lot 7 Bordeaux P1_adsorbout_1

Read LABScreen Analysis Find Allele Find Epitope Find Pos Epitope Find Cutoff **62EE**

Ab Verified Other All # of Epitopes Only Rxn Table iCn3D Latest Version

Show Self Show Imm Show POS Reset Export

Allele	Sero	Bead ID	Loc	Raw	Baseli	Ratio	Rxn	Miss EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Ve	Imm Ab Verif	N. Im Ab Ver
A*24:03	A24	012	A	8964	8751	25.74	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>	65GK, 127K, 144KR+127K	3		0
A*24:02	A24	011	A	8645	8426	23.33	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>	65GK, 127K, 144KR+127K	3		0
A*23:01	A23	010	A	8287	8043	18.07	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>	65GK, 127K	2		0
A*80:01	A80	033	A	1045	801	2.28	NEG		2305	<input type="checkbox"/>	<input type="checkbox"/>		0		0

Rxn Table

+: Positive判定のアレルのみに含まれるEpitope (陽性と判定されたEpitopeのみが対象)

/: Negative判定のアレルにも含まれるEpitope

Positive判定のアレルにのみ「/」が表示される

例) 計4アレルのうち3アレルがPositive

All positive epitopes (all locu9: 11/14 Positive Alleles Covered.

Epitope	#	Locus	Residue
<input type="checkbox"/> 127K	9	A	127K
<input type="checkbox"/> 144TKH	6	A	142T143T144K145H
<input type="checkbox"/> 145KHA	5	A	144K145H149A
<input type="checkbox"/> 107W	4	A	107W
<input type="checkbox"/> 43Q+62GER	3	A	43Q + 62G63E65R
<input type="checkbox"/> 62GK2	3	A	62G63E65R66K (73T74H7...
<input type="checkbox"/> 65GK	3	A	E,E,G,K,A
<input type="checkbox"/> 144KR+127K	2	A	142I143T144K145R + 127K
<input type="checkbox"/> 144QL	2	B	144Q145L149A

カットオフ値 -Analysis Cutoff

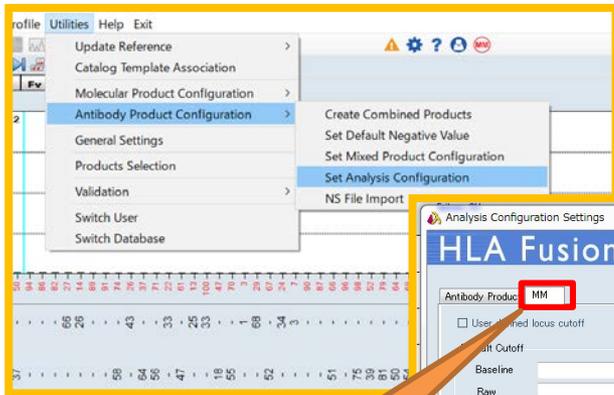
The screenshot displays the HLA Fusion software interface. On the left, a bar chart shows the distribution of scores for various HLA alleles. The main window shows the 'HLA Fusion' analysis results, including a table of HLA alleles and their corresponding scores. A red box highlights the 'Cutoff' value of 1863.94 in the 'Cutoff' column of the table. Another red box highlights the 'Analysis Cutoff' radio button in the 'Analysis Cutoff' section of the interface. A text box in the center of the image reads: 'HLA Fusionの解析画面で使用したカットオフ値を使用' (Use the cutoff value used in the HLA Fusion analysis screen).

Allele	Score	Pos	Self	Imm	All
C*17:01	1863.94	POS	1863		244, 5036C
C*06:02	11962	POS	1863		244, 5037C
C*02:02	11163	POS	1863		244, 5038C
C*04:01	10896	POS	1863		
C*07:02	10729	POS	1863		
A*24:03	10576	POS	1863		203, 407, 5
A*24:02	10453	POS	1863		203, 203PC
A*34:01	10225	POS	1863		5008C, 508
C*05:01	10196	POS	1863		40, 244
A*66:02	10171	POS	1863		5049PC, 50
C*18:02	9988	POS	1863		244, 5037C
C*12:03	8023	POS	1863		
B*08:01	7795	POS	1863		11, 5027C
A*68:01	7349	POS	1863		
A*68:02	6299	POS	1863		
A*43:01	6210	POS	1863		5, 5005C
C*01:02	6106	POS	1863		5032C
A*03:01	5715	POS	1863		
A*33:03	5320	POS	1863		
C*16:01	5290	POS	1863		5035C, 507
C*14:02	5109	POS	1863		
A*32:01	4931	POS	1863		
C*15:02	4598	POS	1863		244, 5034C
A*69:01	4519	POS	1863		5067E
A*33:01	3996	POS	1863		
C*03:04	3142	POS	1863		
C*03:02	3040	POS	1863		
C*03:03	2656	POS	1863		5080E
A*26:01	2420	POS	1863		5062E
A*34:02	2351	POS	1863		5009C

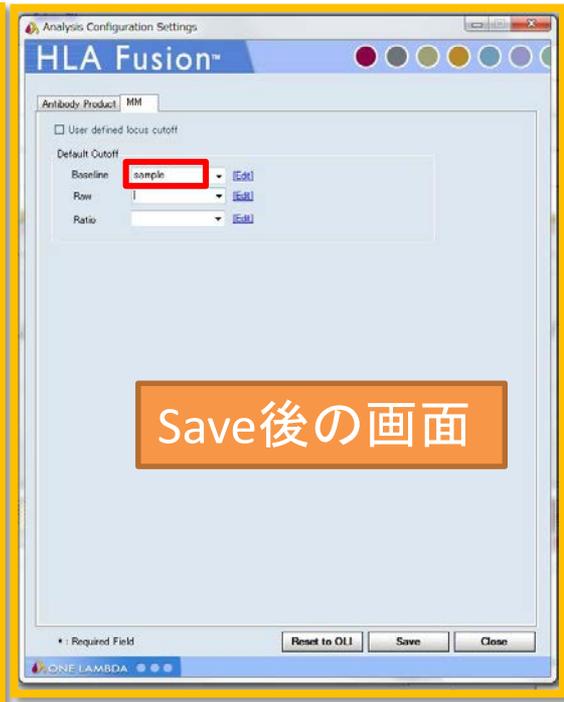
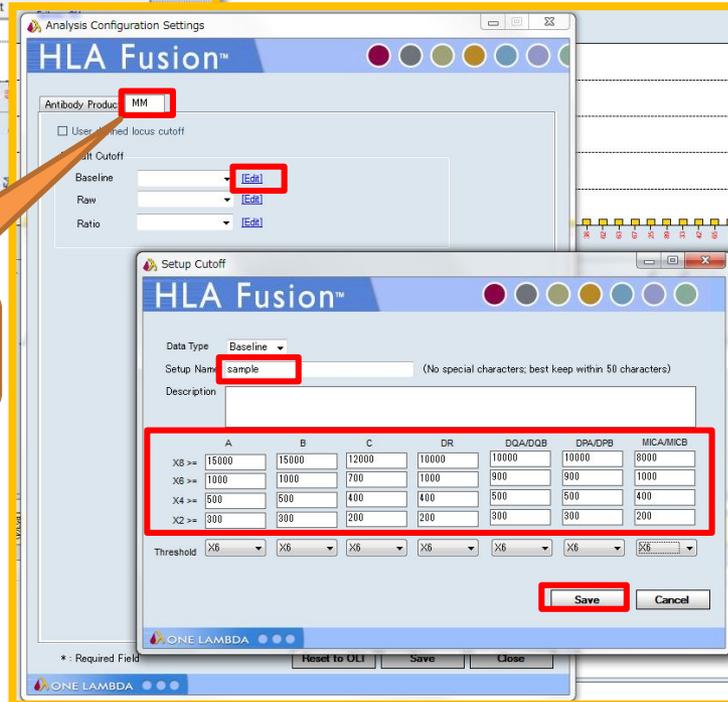
カットオフ値 -MM Cutoff-1

Utilities→Antibody Product Configuration→Set Analysis Configurationの順にクリック

MMタブを開き、Editをクリックする
各ローカスのカットオフ値を入力し、
Setup Nameに名前を入力しSave



注意
MMのタブです



Save後の画面

カットオフ値 -MM Cutoff-2

Epitope Matching Epitope Analysis

Class I Class II MICA

Epitope Library HMM Class1 0817 4/ 3/2019 4/17/2019 Find Donor / Immunizer Donor 1 A*03:01 A*31:01 B*07:02 B*40:01 C*03:04 C*07:02 A*34:02 A*66:01 B*13:02 B*51:01 C*06:02 C*16:01

Analysis Cutoff MM Cutoff Manual A B C

Data Type Baseline Cutoff 1000 1000 700

Mean of Self (m) 3542 3374 316 6936

SD 3734 2341 106 3794

m+3SD 14744 10397 634 18318

Find Allele Find Epitope Find Pos Epitope Find Cutoff

Ab Verified Other # of Epitopes Only Rxn Table Latest Version Row Count: 99

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Verified	Imm Ab Verified	N. Imm Ab Verified	TP Ab Verified
C*08:01									700							
A*66:01									1000							
A*11:01									1000							
A*29:02									1000							
B*46:01									1000							
A*29:01									1000							
A*74:01									1000							
A*11:02									1000							
B*51:02	B51,Bw4	066	B	1683	1587	11.86	POS		1000							
B*51:01	B51,Bw4	065	B	1478	1365	8.5	POS		1000							
A*02:03	A2	005	A	1467	1345	7.63	POS		1000							
B*53:01	B53,Bw4	068	B	1397	1246	5.63	POS		1000							
B*35:01	B35,Bw6	049	B	1279	1185	9.34	POS		1000							
B*15:16	B63,Bw4	046	B	1416	1139	2.88	POS		1000							
A*25:01	A25	013	A	1217	1118	8.29	POS		1000							
A*02:01	A2	004	A	1216	1102	6.96	POS		1000							
A*31:01	A31	020	A	1211	1033	4.04	POS		1000							
A*80:01	A80	033	A	1182	1000	3.95	POS		1000							
A*30:01	A30	018	A	1115	975	4.9	NEG		1000							
A*02:06	A2	006	A	1081	958	5.58	NEG		1000							
A*30:02	A30	019	A	1004	874	4.88	NEG		1000							
B*78:01	B78,Bw6	078	B	887	766	4.67	NEG		1000							
B*54:01	B54,Bw6	069	B	893	703	2.75	NEG		1000							
B*15:02	B75,Bw6	041	B	683	563	3.64	NEG		1000							
A*23:01	A23	010	A	656	548	3.99	NEG		1000							
B*39:01	B39,Bw6	052	B	614	525	4.8	NEG		1000							
B*38:01	B38,Bw4	051	B	572	485	4.6	NEG		1000							
B*15:10	B71,Bw6	043	B	543	437	3.37	NEG		1000							
B*15:11	B75,Bw6	098	B	566	430	2.59	NEG		1000							
B*07:02	B7,Bw6	034	B	600	423	2.01	NEG		1000							
B*81:01	B81,Bw6	079	B	541	412	2.64	NEG		1000							
B*15:13	B77,Bw4	045	B	430	339	3.27	NEG		1000							
B*49:01	B49,Bw4	060	B	344	269	3.39	NEG		1000							
B*40:02	B61,Bw6	054	B	390	253	1.77	NEG		1000							
B*18:01	B18,Bw6	047	B	375	250	1.89	NEG		1000							
B*27:08	B27,Bw6	048	B	346	248	2.37	NEG		1000							
B*50:01	B51,Bw4	064	B	330	230	2.11	NEG		1000							

手動で設定したカットオフ値のx6の値が反映される

カットオフ値 -Manual cutoff

Epitope Matching Epitope Analysis

Class I Class II MICA

Epitope Library HMM Class1 0817 4/ 3/2019 4/17/2019 Find

Patient Patient 1 A*03:01 A*31:01 B*07:02 B*40:01 C*03:04 C*07:02

Donor / Immunizer Donor 1 A*34:02 A*66:01 B*13:02 B*51:01 C*06:02 C*16:01

Analysis Cutoff MM Cutoff Manual A B C

Data Type Baseline Cutoff 1500 2000 500

Mean of Self (m) 3542 3374 316 6936

SD 3784 2341 106 3794

m+3SD 14744 10397 634 18318

Find Allele Find Epitope Find Pos Epitope Find Cutoff

Ab Verified Other All # of Epitopes Only Rxn Table iCR3D Latest Version Show Self Show Imm Show POS Reset Export Row Count: 99

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Verified	Imm Ab Verified	N. Imm Ab Verified	TP Ab Verified
C*08:01	Cw8	090	C	2522	2351	8.8										
A*66:01							POS		1500		<input checked="" type="checkbox"/>	177KT	1		0	177KT
A*11:01							POS		1500			151AHA	1		0	151AHA
A*29:02							POS		1500			62LQ	1		0	62LQ
B*46:01							POS		2000				0		0	
A*29:01							POS		1500			62LQ	1		0	62LQ
A*74:01							POS		1500				0		0	
A*11:02							POS		1500			151AHA	1		0	151AHA
B*51:02							NEG		2000				0		0	
B*51:01							NEG		2000		<input checked="" type="checkbox"/>		0		0	
A*02:03	A2	005	A	1467	1345	7.63	NEG		1500				0		0	
B*53:01	B53,Bw4	068	B	1397	1246	5.63	NEG		2000				0		0	
B*35:01	B35,Bw6	049	B	1279	1185	9.34	NEG		2000				0		0	
B*15:16	B63,Bw4	046	B	1416	1139	2.88	NEG		2000				0		0	
A*25:01	A25	013	A	1217	1118	8.29	NEG		1500				0		0	
A*02:01	A2	004	A	1216	1102	6.96	NEG		1500				0		0	
A*31:01	A31	020	A	1211	1033	4.04	NEG		1500		<input checked="" type="checkbox"/>		0		0	
A*80:01	A80	033	A	1182	1000	3.85	NEG		1500				0		0	
A*30:01	A30	018	A	1115	975	4.9	NEG		1500				0		0	
A*02:06	A2	006	A	1081	958	5.58	NEG		1500				0		0	
A*30:02	A30	019	A	1004	874	4.88	NEG		1500				0		0	
B*78:01	B78,Bw6	078	B	887	766	4.67	NEG		2000				0		0	
B*54:01	B54,Bw6	069	B	893	703	2.75	NEG		2000				0		0	
B*15:02	B75,Bw6	041	B	683	563	3.64	NEG		2000				0		0	
A*23:01	A23	010	A	656	548	3.99	NEG		1500				0		0	
B*39:01	B39,Bw6	052	B	614	525	4.8	NEG		2000				0		0	
B*38:01	B38,Bw4	051	B	572	485	4.6	NEG		2000				0		0	
B*15:10	B71,Bw6	043	B	543	437	3.37	NEG		2000				0		0	
B*15:11	B75,Bw6	098	B	566	430	2.59	NEG		2000				0		0	
B*07:02	B7,Bw6	034	B	600	423	2.01	NEG		2000		<input checked="" type="checkbox"/>		0		0	
B*81:01	B81,Bw6	079	B	541	412	2.64	NEG		2000				0		0	
B*15:13	B77,Bw4	045	B	430	339	3.27	NEG		2000				0		0	
B*49:01	B49,Bw4	060	B	344	269	3.39	NEG		2000				0		0	
B*40:02	B61,Bw6	054	B	390	253	1.77	NEG		2000				0		0	
B*18:01	B18,Bw6	047	B	375	250	1.89	NEG		2000				0		0	
B*27:08	B27,Bw6	048	B	346	248	2.37	NEG		2000				0		0	
B*50:01	B50,Bw6	064	B	339	229	2.01	NEG		2000				0		0	
B*40:01	B60,Bw6	050	B	240	210	1.57	NEG		2000				0		0	

MatchMaker上で手動で
カットオフ値の変更が可能

Find Cutoff

Patient 104 / LS1A04_010_Matchmaker

Read LABScreen Analysis Find Allele Find Eplet Find Pos Eplet **Find Cutoff** 127K

Ab Verified Other All # of Eplets Only Rxn Table [iCn3D](#) Latest Version

Eplet	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Verified
17:01	Cw17	095	C	13586	13347	32.55	POS		874			73AN, 80K, 80K...	3
06:02	Cw6	088	C	12173	11962	33.57	POS		874			73AN, 80K, 80K...	3
02:02	Cw2	082	C	11347	11163	36.55	POS		874			80K, 80K+14R	2
04:01	Cw4	086	C	11175	10896	22.58	POS		874			73AN, 80K	0
07:02	Cw7	089	C	10953	10729	28.18	POS		874			4KR+127K	1
24:03	A24	012	A	10697	10576	56.24	POS		874			4KR+127K	1
24:02	A24	011	A	10582	10453	51.77	POS		874			2RR, 145RT, 1...	3
34:01	A34	023	A	10552	10225	17.96	POS		874			2RR, 145RT, 1...	3
05:01	Cw5	087	C	10364	10196	37.04	POS		874			80K, 80K+14R...	4
66:02	A66	028	A	10360	10171	32.25	POS		874			2RR, 145RT, 1...	3
18:02	Cw18	096	C	9188	8988	26.74	POS		874			73AN, 80K, 80K...	3
12:03	Cw12	091	C	8209	8023	26.05	POS		874				0
08:01	B8,Bw6	035	B	7795	7668	38.67	POS		874				0
68:01	A68	029	A	7448	7349	50.85	POS		874			62RR, 144TKH...	3
68:02	A68	030	A	6442	6299	27.86	POS		874			62RR, 144TKH...	3

Find Cutoff
Positive判定とするための
カットオフ値が表示される

The cutoff should be below 548

Patient 104 / LS1A04_010_Matchmaker

Read LABScreen Analysis Find Allele Find Eplet Find Pos Eplet **Find Cutoff** 73AN

Ab Verified Other All # of Eplets Only Rxn Table [iCn3D](#) Latest Version

Row Count: 99

Eplet	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Verified	Imm Ab Verified
17:01	Cw17	095	C	13586	13347	32.55	POS		874			73AN, 80K, 80K...	3	73AN, 80K, 80K...
06:02	Cw6	088	C	12173	11962	33.57	POS		874		<input checked="" type="checkbox"/>	73AN, 80K, 80K...	3	73AN, 80K, 80K...
02:02	Cw2	082	C	11347	11163	36.55	POS		874			80K, 80K+14R	2	80K, 80K+14R
04:01	Cw4	086	C	11175	10896	22.58	POS		874			73AN, 80K	0	73AN, 80K
07:02	Cw7	089	C	10953	10729	28.18	POS		874				0	
24:03	A24	012	A	10697	10576	56.24	POS		874				0	
24:02	A24	011	A	10582	10453	51.77	POS		874				0	
34:01	A34	023	A	10552	10225	17.96	POS		874				0	
05:01	Cw5	087	C	10364	10196	37.04	POS		874				0	
66:02	A66	028	A	10360	10171	32.25	POS		874				0	
18:02	Cw18	096	C	9188	8988	26.74	POS		874				0	
12:03	Cw12	091	C	8209	8023	26.05	POS		874				0	
08:01	B8,Bw6	035	B	7795	7668	38.67	POS		874				0	
68:01	A68	029	A	7448	7349	50.85	POS		874				0	
68:02	A68	030	A	6442	6299	27.86	POS		874				0	
43:01	A43	026	A	6396	6210	20.31	POS		874			62LQ, 145RT, 1...	4	145RT, 149TA...
01:02	Cw1	081	C	6259	6106	24.96	POS		874			248M	1	
03:01	A3	007	A	5817	5715	38.08	POS		874		<input checked="" type="checkbox"/>		0	

The eplet is already positive. The cutoff is already below 8988

使用するデータの種類の選択

Epitope Matching Epitope Analysis

Class I Class II MICA

Epitope Library HMM Class1 0817 10/21/2015 4/ 3/2019 Find Donor / Immunizer

Analysis Cutoff MM Cutoff Manual A B C

Data Type **Baseline** Raw Baseline Ratio

Find Allele Find EpIet Find Pos EpIet Find Cutoff

Ab Verified Other All # of EpIets Only Rxn Table [iCn3D](#) Latest Version Row Count: 99

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	All	N. All	Imm All	N. Imm All
C*17:01	Cw17	095	C	13586	13347	32.55							32, 38, 41, 205, 222, 244, 5036C, 5037...		9
C*06:02	Cw6	088	C	12173	11962	33.57							32, 205, 232, 244, 5037C, 5038C, 5038...		7
C*02:02	Cw2	082	C	11347	11163	36.55							32, 205, 232, 244, 5038C, 5038...		6
C*04:01	Cw4	086	C	11175	10896	22.58									
C*07:02	Cw7	089	C	10953	10729	28.18									
A*24:03	A24	012	A	10697	10576	56.24									
A*24:02	A24	011	A	10582	10453	51.77									
A*34:01	A34	023	A	10552	10225	17.96									
C*05:01	Cw5	087	C	10364	10196	37.04									
A*66:02	A66	028	A	10360	10171	32.25									
C*18:02	Cw18	096	C	9188	8988	26.74									
C*12:03	Cw12	091	C	8209	8023	26.05									
B*08:01	B8,Bw6	035	B	7795	7668	38.67									
A*68:01	A68	029	A	7448	7349	50.85									
A*68:02	A68	030	A	6442	6299	27.86									
A*43:01	A43	026	A	6396	6210	20.31							4, 4PC, 5, 12, 15, 16, 27, 32, 38, 209, 2...		22
C*01:02	Cw1	081	C	6259	6106	24.96							25, 32, 205, 232, 246, 421, 5032C, 5075E		8
A*03:01	A3	007	A	5817	5715	38.08							6, 13, 32, 208, 210, 238, 242, 247, 248...		12
A*33:03	A33	100	A	5454	5320	25.44							32, 38, 213, 214, 214E, 215, 238, 242...		14
C*16:01	Cw16	094	C	5451	5290	20.38							32, 205, 232, 246, 421, 5035C, 5076E		7
C*14:02	Cw14	092	C	5328	5109	14.05							32, 205, 232, 246, 421, 5075E		6
A*32:01	A32	021	A	5048	4931	27.63							23, 24, 32, 33, 38, 204, 205, 212, 213, 2...		20
C*15:02	Cw15	093	C	4788	4598	14.84							32, 39, 205, 232, 244, 5034C		6
A*69:01	A69	031	A	4633	4519	26.31							2, 13, 18, 19, 19E, 32, 38, 210, 214, 21...		20
A*33:01	A33	022	A	4032	3896	18.39							32, 38, 213, 214, 214E, 215, 220, 238...		15
C*03:04	Cw10	085	C	3343	3142	9.75							25, 32, 39, 205, 245, 246, 421, 5075E...		9
C*03:02	Cw10	083	C	3194	3040	12.57							25, 32, 39, 205, 245, 246, 421, 5075E...		9
C*03:03	Cw9	084	C	2840	2656	9.12							25, 32, 39, 205, 245, 246, 421, 5075E...		10
A*26:01	A26	014	A	2564	2420	10.95							4, 4PC, 12, 15, 16, 27, 32, 38, 209, 211...		26
A*34:02	A34	024	A	2450	2351	16.5							4, 4PC, 16, 27, 32, 38, 211, 213, 214, 2...		23
C*08:01	Cw8	090	C	2522	2351	8.8							25, 32, 40, 205, 232, 246, 421, 5040C...		9
A*66:01	A66	027	A	2369	2242	11.71							4, 4PC, 12, 16, 27, 32, 38, 209, 211, 21...		22
A*11:01	A11	008	A	2267	2146	11.93							12, 13, 16, 32, 208, 209, 210, 238, 241...		17
A*29:02	A29	017	A	2286	2108	7.59							5, 15, 32, 38, 213, 238, 242, 247, 5004...		15
B*46:01	B46,Bw6	063	B	2265	2054	6.24							7, 10, 25, 32, 33, 43, 211, 221, 238, 234...		16
A*29:01	A29	015	A	2165	1993	7.5							5, 15, 32, 38, 213, 238, 242, 247, 5004...		16
A*74:01	A74	032	A	1976	1863	11.43							32, 33, 38, 204, 213, 238, 242, 5045PC...		13
A*11:02	A11	009	A	1833	1646	5.79							12, 13, 16, 30, 30E, 32, 208, 209, 210...		18
B*51:02	B51,Bw4	066	B	1683	1587	11.86							7, 22, 23, 24, 32, 33, 35, 212, 219, 220...		18

カットオフ値として使用する
データを選択可能
* Baselineを推奨します

Single&Supplement Combine data

Epitope Matching Epitope Analysis

Class I Class II MICA

Epitope Library HMM Class I 0817 10/21/2015 4/ 3/2019 Find Donor / Imm

Select	Sample ID	Sample Date	Patient	Well Position	Session Name
<input type="checkbox"/>	3001	Mar 01, 2019	3001	26(1,B4)	QCWS_LS1_20180416_123750
<input checked="" type="checkbox"/>	3001_tk	Mar 12, 2019	3001	12(1,D2)	QCWS30_SA1_010NC019_tk_2018
<input type="checkbox"/>	3001_tk	Mar 12, 2019	3001	14(1,F2)	QCWS30_Sup1_003NC019_tk_2018

3001_tk / QCWS30_SA1_010NC019_tk_20180510_20180510_130503

Ab Verified Other All # of Epitopes Only Rxn Table On3D Latest Version Combined

Read LABScreen Analysis

Find Allele Find Epitope Find Pos Epitope Find Cutoff

Show Self Show Imm Show POS Reset Export Row Count: 153

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Verified	Imm Ab Verified	N. Imm Ab Verified	TP Ab Verified
B*44:02	B44,Bw4	057	B	8496	8334	23.45	POS	<input type="checkbox"/>	1878	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	0		0	
C*15:02	Cw15	093	C	4325	4163	11.95	POS	<input type="checkbox"/>	1878	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	0		0	
C*16:02	Cw16	1057	C	5952	2194	1.11	POS	<input type="checkbox"/>	1878	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	0		0	
B*13:01	B13,Bw4	097	B	2310	2175	8.11	POS	<input type="checkbox"/>	1878	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	0		0	
C*03:02	Cw10	083	C	2025	1878	6.32	POS	<input type="checkbox"/>	1878	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	0		0	
B*15:13	B77,Bw4	045	B	1174	1073	6.2	NEG	<input type="checkbox"/>	1878	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	0		0	
C*03:04	Cw10	085	C	1185	1007	2.92	NEG	<input type="checkbox"/>	1878	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	0		0	
B*15:02	B75,Bw6	041	B	859	730	3.19	NE	<input type="checkbox"/>		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>				
B*44:03	B44,Bw4	058	B	462	324	1.59	NE	<input type="checkbox"/>		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>				
C*17:01	Cw17	095	C	477	298	1.17	NE	<input type="checkbox"/>		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>				
A*68:02	A68	030	A	493	269	0.92	NE	<input type="checkbox"/>		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>				
A*31:01	A31	020	A	381	237	1.23	NE	<input type="checkbox"/>		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>				
A*66:02	A66	028	A	344	207	1.18	NE	<input type="checkbox"/>		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>				
B*67:01	B67,Bw6	076	B	395	196	1.13	NE	<input type="checkbox"/>		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>				
A*30:02	A30	019	A	305	182	1.23	NE	<input type="checkbox"/>		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>				
A*34:01	A34	023	A	300	158	0.99	NE	<input type="checkbox"/>		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>				
B*07:14	B7,Bw6	1012	B	3978	157	0.46	NE	<input type="checkbox"/>		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>				
B*53:01	B53,Bw4	068	B	284	145	0.96	NE	<input type="checkbox"/>		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>				

Read LABScreen Analysis

解析画面でSAとSupplementをcombineした状態でMatchMakerを立ち上げ、クリックするとCombineしたデータを表示

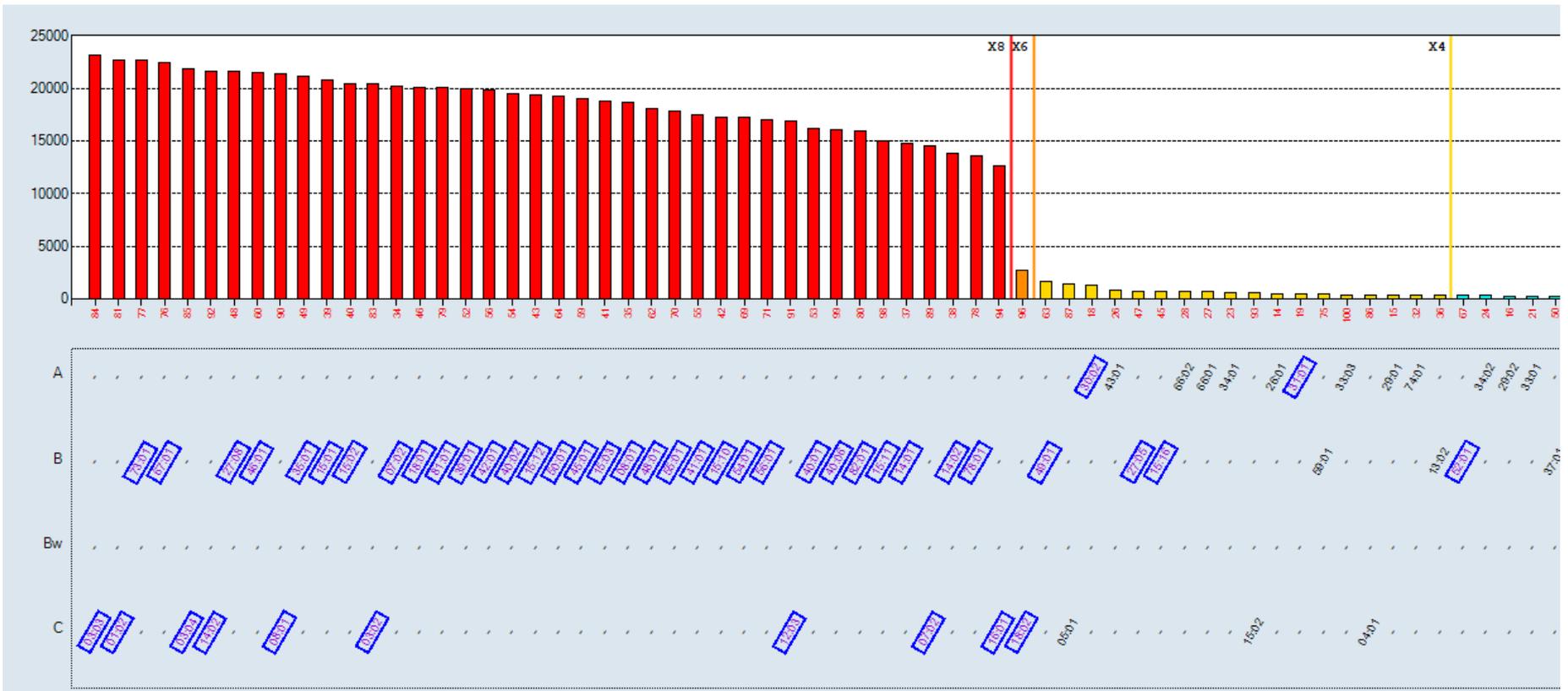
Summary 3001_tk

Send As Sort As Sort Locus List

BARBAR VERITAS Sample Date: 3/12/2019

Final Assignments

Case Study



Final Assignment

Bw6 (B73 B67 B27 B46 B35 B62 B75 B7 B18 B81 B39 B42 B61 B76 B50 B45 B72 B8 B48 B55 B41 B71 B54 B56 B60 B82 B64 B65 B78)

Cw1 Cw7 Cw8 Cw9 Cw10 Cw12 Cw14 Cw16 Cw18

Case Study



Ab Verified
 Other
 All
 # of Epitopes Only
 Rn Table
 Cn3D
 Latest Version

Row Count: 99

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rn	Missing EP Def	Outoff	Self	Imm	Ab Verified	N. Ab Verified	Imm Ab Verifie
C*03:03	Cw9	084	C	23992	23100	63.8	POS		2737			65QKR+76VS, 76VRI	80N, 73K	4
C*01:02	Cw1	081	C	22922	22683	52.2	POS		2737			65QKR+76VS, 76VRN	80N, 48M	4
B*73:01	B73,Bw6	077	B	22772	22632	131.85	POS		2737			76VRN, 80N		2
B*67:01	B67,Bw6	076	B	22610	22405	64.66	POS		2737			65QIA+76ESN, 70IAQ	76ES, 80N	4
C*03:04	Cw10	085	C	22087	21864	55.68	POS		2737			65QKR+76VS, 76VRN	80N, 73K	4
C*14:02	Cw14	092	C	21852	21654	66.49	POS		2737			65QKR+76VS, 76VRN	80N	3
B*27:08	B27,Bw6	048	B	21736	21565	85.36	POS		2737			65QIA+76ESN, 76ESN	80N	4
B*46:01	B46,Bw6	080	B	21726	21502	54.33	POS		2737			65QKR+76VS, 76VRN	80N	3
C*09:01	Cw9	090	C	21554	21347	60.91	POS		2737			65QKR+76VS, 76VRN	80N	3
B*35:01	B35,Bw6	049	B	21367	21194	81.5	POS		2737			69TNT+80N, 71TTS, 76ESN	80N	4
B*15:01	B82,Bw6	039	B	21011	20740	40.03	POS		2737			69TNT+80N, 71TTS, 76ESN	80N	4
B*15:02	B75,Bw6	040	B	20600	20440	91.41	POS		2737			69TNT+80N, 71TTS, 76ESN	80N	4
C*03:02	Cw10	083	C	20608	20421	68.69	POS		2737			65QKR+76VS, 76VRN, 80N	173K	4
B*07:02	B7,Bw6	034	B	20404	20236	82.07	POS		2737			65QIA+76ESN, 70IAQ, 76E	N, 80N, 100E	5
B*18:01	B18,Bw6	046	B	20321	20145	75.26	POS		2737			69TNT+80N, 71TTS, 76ESN	80N	4
B*13:01	B81,Bw6	079	B	20188	20037	99.6	POS		2737			65QIA+76ESN, 70IAQ, 76E	N, 80N, 13S+76ESN, 180E	6
B*39:01	B39,Bw6	052	B	20149	20021	140.26	POS		2737			69TNT+80N, 71TTS, 76ESN	80N	4
B*42:01	B42,Bw6	056	B	20014	19841	76.81	POS		2737			65QIA+76ESN, 70IAQ, 76E	N, 80N, 100E	5
B*40:02	B61,Bw6	054	B	19692	19532	86.49	POS		2737			69TNT+80N, 71TTS, 76ESN	80N	4
B*15:12	B76,Bw6	043	B	19580	19407	74.49	POS		2737			69TNT+80N, 71TTS, 76ESN	80N	4
B*50:01	B50,Bw6	064	B	19356	19207	98.31	POS		2737			69TNT+80N, 71TTS, 76ESN	80N	4
B*45:01	B45,Bw6	059	B	19270	19074	59.61	POS		2737			69TNT+80N, 71TTS, 76ESN	80N	4
B*15:03	B72,Bw6	041	B	18875	18742	121.9	POS		2737			69TNT+80N, 71TTS, 76ESN	80N	4
B*08:01	B8,Bw6	035	B	18850	18652	57.36	POS		2737			69TNT+80N, 71TTS, 76ESN	80N, 180E	5
B*48:01	B48,Bw6	062	B	18214	18028	61.43	POS		2737			69TNT+80N, 71TTS, 76ESN	80N, 14S+76ESN, 180E	6
B*55:01	B55,Bw6	070	B	18020	17881	104.5	POS		2737			65QIA+76ESN, 70IAQ, 76E	N, 80N	4
B*41:01	B41,Bw6	055	B	17657	17500	80.93	POS		2737			69TNT+80N, 71TTS, 76ESN	80N, 180E	5
B*15:10	B71,Bw6	042	B	17551	17270	31.71	POS		2737			69TNT+80N, 71TTS, 76ESN	80N	4
B*54:01	B54,Bw6	069	B	17395	17212	60.11	POS		2737			65QIA+76ESN, 70IAQ, 76E	N, 80N	4
B*56:01	B56,Bw6	071	B	17153	17007	90.79	POS		2737			65QIA+76ESN, 70IAQ, 76E	N, 80N	4
C*12:03	Cw12	091	C	17141	16840	28.37	POS		2737			65QKR+76VS, 76VRN, 80N		3
B*40:01	B60,Bw6	053	B	16386	16230	75.51	POS		2737			69TNT+80N, 71TTS, 76ESN	80N, 14S+76ESN, 180E	6
B*40:06	B61,Bw6	099	B	16302	16092	45.06	POS		2737			69TNT+80N, 71TTS, 76ESN	80N	4
B*02:01	B02,Bw6	080	B	16199	16002	53.81	POS		2737			65QIA+76ESN, 70IAQ, 76E	N, 80N	4
B*15:11	B75,Bw6	098	B	15286	15063	39.54	POS		2737			69TNT+80N, 71TTS, 76ESN	80N	4
B*14:01	B64,Bw6	037	B	15119	14765	20.22	POS		2737			69TNT+80N, 71TTS, 76ESN	80N	4
C*07:02	Cw7	089	C	14795	14488	24.82	POS		2737			65QKR+76VS, 76VRN, 80N	193PL3	4
B*14:02	B65,Bw6	038	B	14098	13779	21.53	POS		2737			69TNT+80N, 71TTS, 76ESN	80N	4

All positive epitopes (all locu) 18 40/41 Positive Alleles Cover

Epitope	#	Locus	Residue
80N	40	C	R,N,R,G
76ESN	29	B	76E77S79R80N
69TNT+80N	20	B	69T70N71T + 80N
71TTS	20	B	71T73T77S
76VRN	11	B,C	76V79R80N
65QKR+76VS	10	B,C	62R63E65Q66K67Y69R70...
65QIA+76ESN	9	B	65Q66I69A + 76E77S79R8...
70IAQ	8	B	IA,Q,A
180E	7	B	E
143S+76ESN	3	B	143S + 76E77S79R80N
173K	3	C	173K
248M	1	C	248M(6KX99C)
193PL3	1	C	P.L (A.E.P) (S)

「80N」が多くのアレルに含まれていることが分かる

iCn3D表示機能

AlleleまたはSeroをクリックすると立体構造を確認することができます
インターネットに接続しているPCでのみ使用できます

The screenshot shows the iCn3D software interface. At the top, there are tabs for 'Epitope Matching' and 'Epitope Analysis'. Below that, there are filters for 'Class I', 'Class II', and 'MICA'. A table lists various alleles with columns for 'Allele', 'Ser', 'Bead ID', 'Locus', 'Raw', 'Baseline', and 'Ratio'. A search panel on the right includes buttons for 'Search Allele(s)', 'Search Epitope(s)', and 'List All Epitopes'. A dropdown menu labeled 'Latest Version' is highlighted with a red box.

The screenshot shows the iCn3D 3D structure viewer. The main window displays a 3D model of the protein structure, labeled 'PDB ID 5E01: Crystal Structure Of Hla-b0702-r19'. The structure is rendered in blue and pink spheres. On the right side, there are 'Sequences and Annotations' panels for 'Protein SE01_A' and 'Protein SE01_B'. The 'Protein SE01_A' panel shows a sequence diagram with domains like 'MHC I' and 'IgC_MH...'. The 'Protein SE01_B' panel shows a sequence diagram with domains like 'IgC_beta2m'.

- Latest Version: 最新のwebsiteの閲覧
- Compatible Version: 機能が制限されたページの閲覧
- Safe Mode: 限られた機能のみでの閲覧