



2020年 ユーザーワークショップ

LABScreenの解析と手技

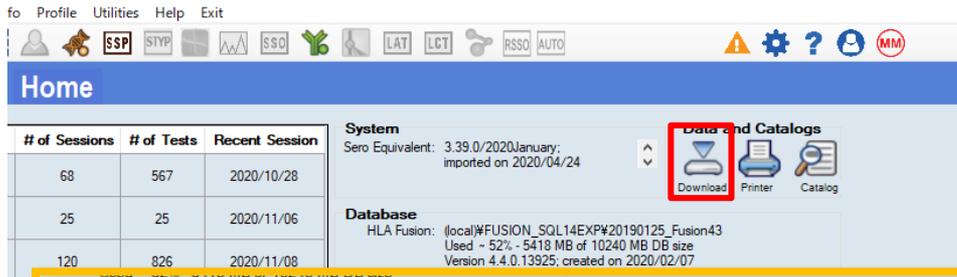
株式会社ベリタス

2020年11月25日

2020年11月28日

LABScreenの解析

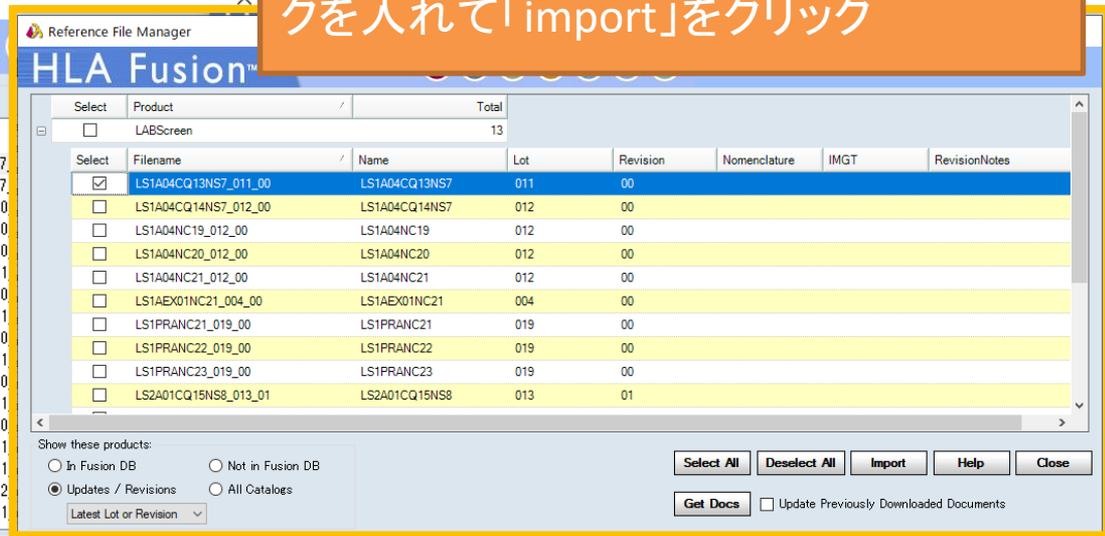
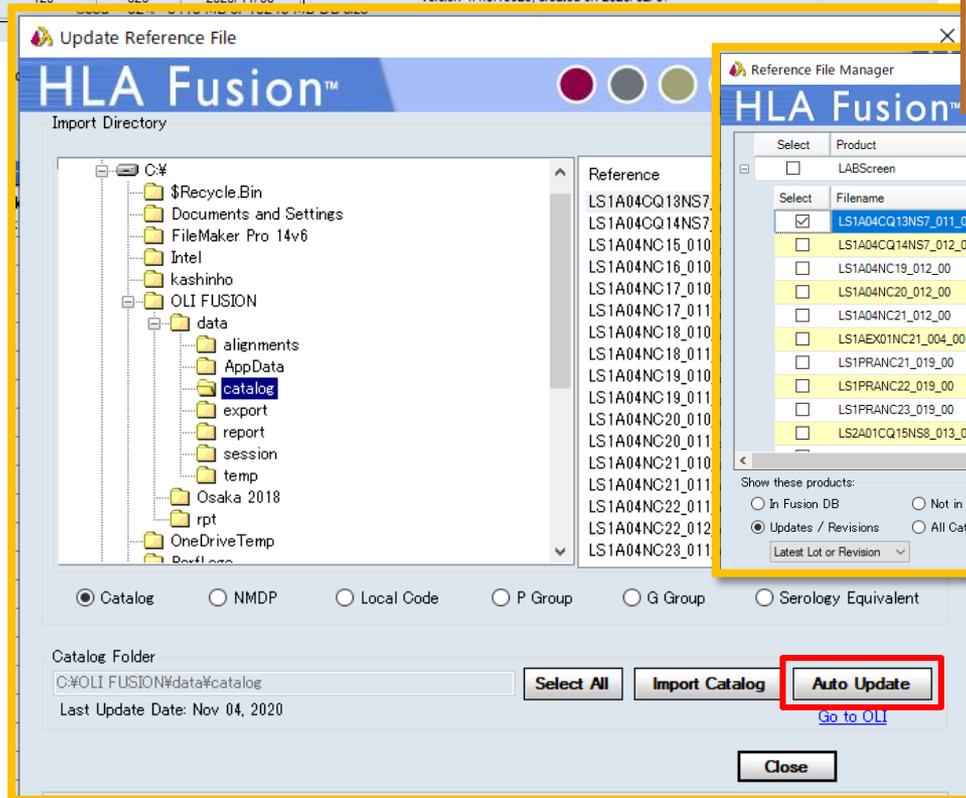
カタログファイルのインポート



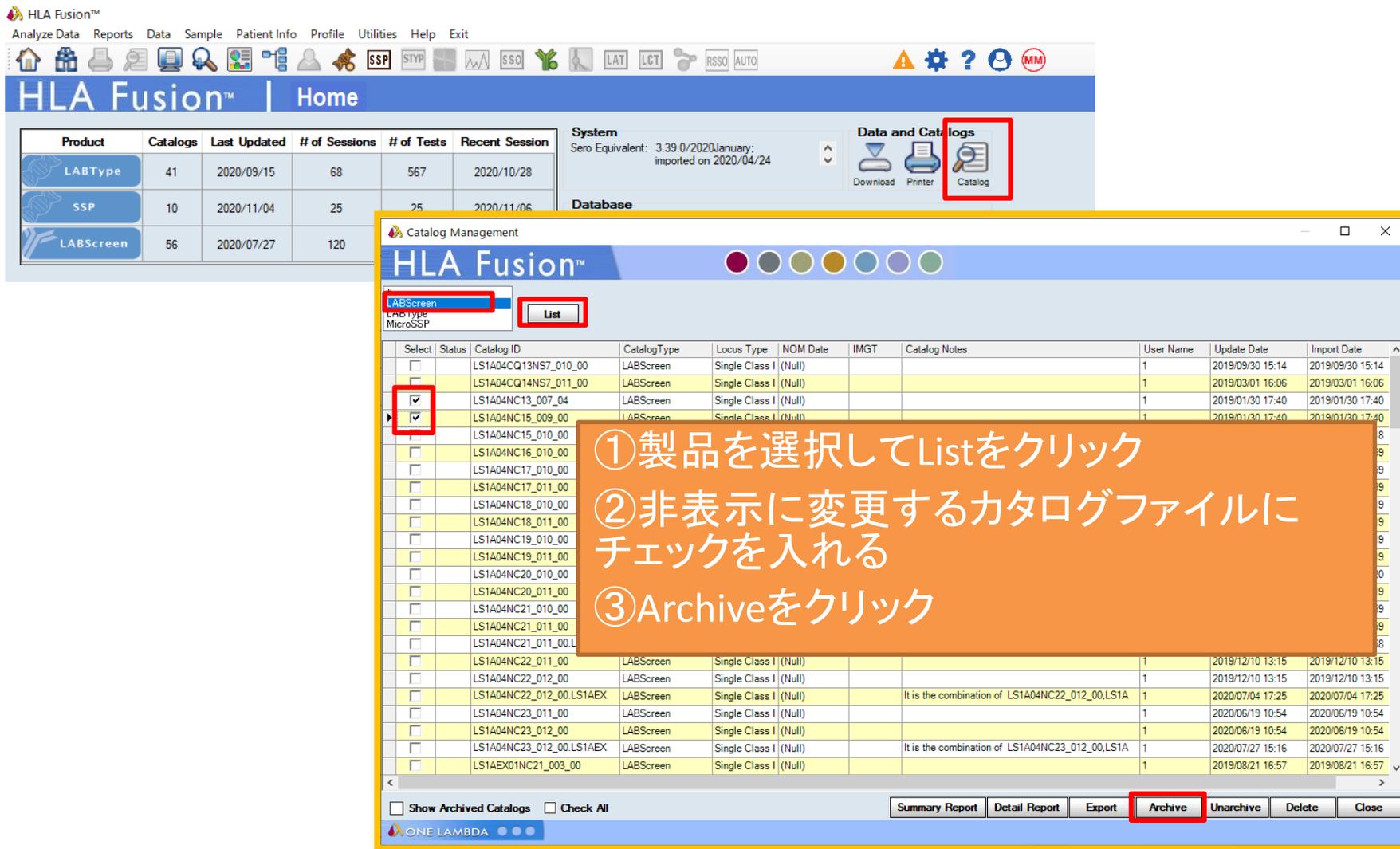
インターネットにつながっているPCのみ
Auto Update機能が使用できる

(One Lambda社のwebに自動的につながりインポートされる)

インポートするカタログファイルにチェックを入れて「import」をクリック



カタログファイルを非表示にする-1



The screenshot displays the HLA Fusion software interface. The main window shows a table of products and their associated catalogs. A secondary window, 'Catalog Management', is open, showing a list of catalog files. The 'List' button in the Catalog Management window is highlighted with a red box. The 'Archive' button in the bottom right of the Catalog Management window is also highlighted with a red box. An orange text box with three numbered steps is overlaid on the Catalog Management window.

HLA Fusion™ | Home

Product	Catalogs	Last Updated	# of Sessions	# of Tests	Recent Session
LABType	41	2020/09/15	68	567	2020/10/28
SSP	10	2020/11/04	25	25	2020/11/06
LABScreen	56	2020/07/27	120		

System
Sero Equivalent: 3.39.0/2020January; imported on 2020/04/24

Data and Catalogs
Download Printer Catalog

Catalog Management

LABScreen
List

Select	Status	Catalog ID	CatalogType	Locus Type	NOM Date	IMGT	Catalog Notes	User Name	Update Date	Import Date
<input type="checkbox"/>		LS1A04CQ13NS7_010_00	LABScreen	Single Class I	(Null)			1	2019/09/30 15:14	2019/09/30 15:14
<input type="checkbox"/>		LS1A04CQ14NS7_011_00	LABScreen	Single Class I	(Null)			1	2019/03/01 16:06	2019/03/01 16:06
<input checked="" type="checkbox"/>		LS1A04NC13_007_04	LABScreen	Single Class I	(Null)			1	2019/01/30 17:40	2019/01/30 17:40
<input checked="" type="checkbox"/>		LS1A04NC15_009_00	LABScreen	Single Class I	(Null)			1	2019/01/30 17:40	2019/01/30 17:40
<input type="checkbox"/>		LS1A04NC15_010_00								
<input type="checkbox"/>		LS1A04NC16_010_00								
<input type="checkbox"/>		LS1A04NC17_010_00								
<input type="checkbox"/>		LS1A04NC17_011_00								
<input type="checkbox"/>		LS1A04NC18_010_00								
<input type="checkbox"/>		LS1A04NC18_011_00								
<input type="checkbox"/>		LS1A04NC19_010_00								
<input type="checkbox"/>		LS1A04NC19_011_00								
<input type="checkbox"/>		LS1A04NC20_010_00								
<input type="checkbox"/>		LS1A04NC20_011_00								
<input type="checkbox"/>		LS1A04NC21_010_00								
<input type="checkbox"/>		LS1A04NC21_011_00								
<input type="checkbox"/>		LS1A04NC21_011_00.L								
<input type="checkbox"/>		LS1A04NC22_011_00	LABScreen	Single Class I	(Null)			1	2019/12/10 13:15	2019/12/10 13:15
<input type="checkbox"/>		LS1A04NC22_012_00	LABScreen	Single Class I	(Null)			1	2019/12/10 13:15	2019/12/10 13:15
<input type="checkbox"/>		LS1A04NC22_012_00.LS1AEX	LABScreen	Single Class I	(Null)		It is the combination of LS1A04NC22_012_00.LS1A	1	2020/07/04 17:25	2020/07/04 17:25
<input type="checkbox"/>		LS1A04NC23_011_00	LABScreen	Single Class I	(Null)			1	2020/06/19 10:54	2020/06/19 10:54
<input type="checkbox"/>		LS1A04NC23_012_00	LABScreen	Single Class I	(Null)			1	2020/06/19 10:54	2020/06/19 10:54
<input type="checkbox"/>		LS1A04NC23_012_00.LS1AEX	LABScreen	Single Class I	(Null)		It is the combination of LS1A04NC23_012_00.LS1A	1	2020/07/27 15:16	2020/07/27 15:16
<input type="checkbox"/>		LS1AEX01NC21_003_00	LABScreen	Single Class I	(Null)			1	2019/08/21 16:57	2019/08/21 16:57

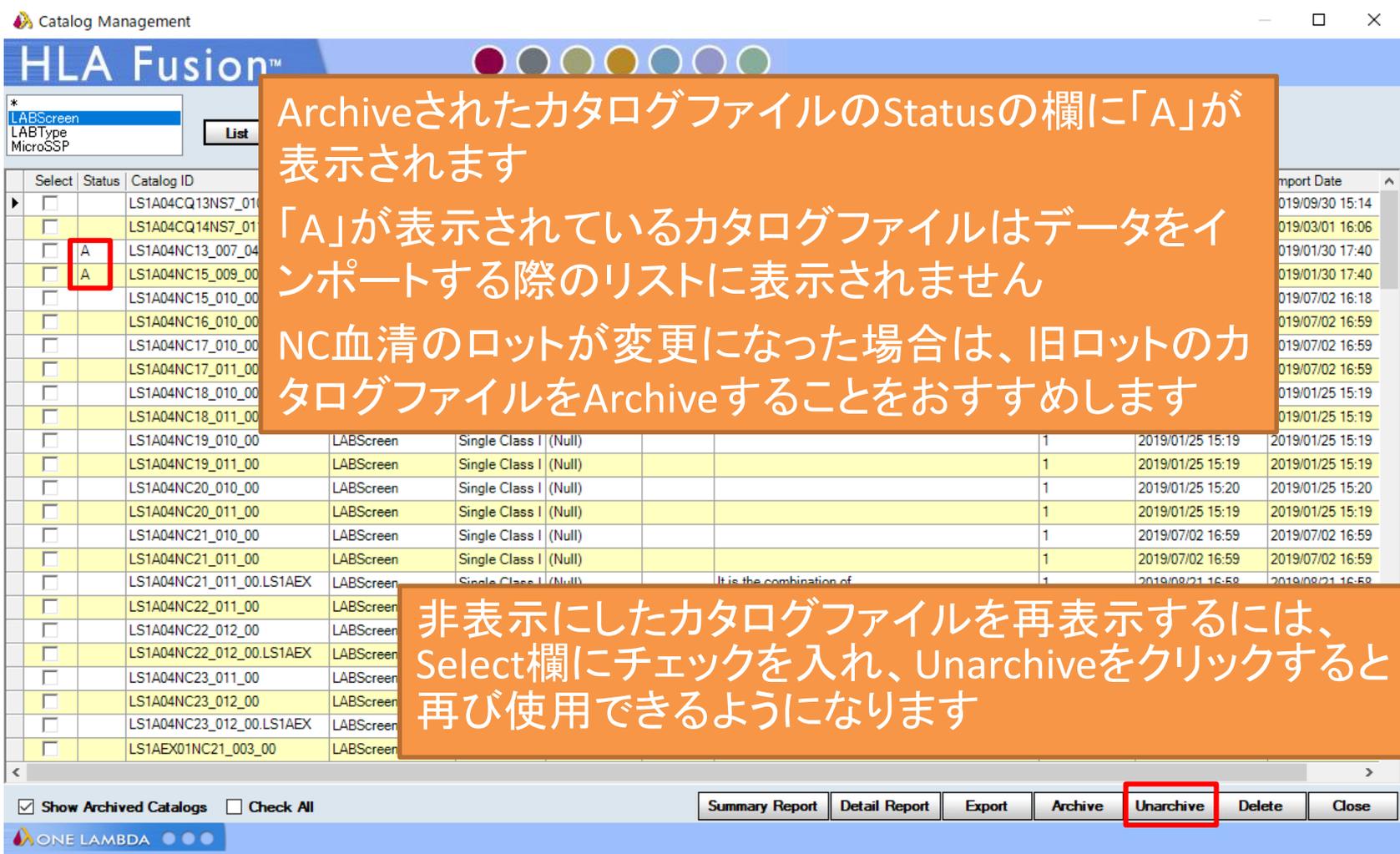
Show Archived Catalogs Check All

Summary Report Detail Report Export Archive Unarchive Delete Close

ONE LAMBDA

- ①製品を選択してListをクリック
- ②非表示に変更するカタログファイルにチェックを入れる
- ③Archiveをクリック

カタログファイルを非表示にする-2



ArchiveされたカタログファイルのStatusの欄に「A」が表示されます

「A」が表示されているカタログファイルはデータをインポートする際のリストに表示されません

NC血清のロットが変更になった場合は、旧ロットのカタログファイルをArchiveすることをおすすめします

非表示にしたカタログファイルを再表示するには、Select欄にチェックを入れ、Unarchiveをクリックすると再び使用できるようになります

Select	Status	Catalog ID	LABScreen	LABType	MicroSSP	Import Date		
<input type="checkbox"/>		LS1A04CQ13NS7_01				2019/09/30 15:14		
<input type="checkbox"/>		LS1A04CQ14NS7_01				2019/03/01 16:06		
<input type="checkbox"/>	A	LS1A04NC13_007_04				2019/01/30 17:40		
<input type="checkbox"/>	A	LS1A04NC15_009_00				2019/01/30 17:40		
<input type="checkbox"/>		LS1A04NC15_010_00				2019/07/02 16:18		
<input type="checkbox"/>		LS1A04NC16_010_00				2019/07/02 16:59		
<input type="checkbox"/>		LS1A04NC17_010_00				2019/07/02 16:59		
<input type="checkbox"/>		LS1A04NC17_011_00				2019/07/02 16:59		
<input type="checkbox"/>		LS1A04NC18_010_00				2019/01/25 15:19		
<input type="checkbox"/>		LS1A04NC18_011_00				2019/01/25 15:19		
<input type="checkbox"/>		LS1A04NC19_010_00	LABScreen	Single Class I	(Null)	1	2019/01/25 15:19	2019/01/25 15:19
<input type="checkbox"/>		LS1A04NC19_011_00	LABScreen	Single Class I	(Null)	1	2019/01/25 15:19	2019/01/25 15:19
<input type="checkbox"/>		LS1A04NC20_010_00	LABScreen	Single Class I	(Null)	1	2019/01/25 15:20	2019/01/25 15:20
<input type="checkbox"/>		LS1A04NC20_011_00	LABScreen	Single Class I	(Null)	1	2019/01/25 15:19	2019/01/25 15:19
<input type="checkbox"/>		LS1A04NC21_010_00	LABScreen	Single Class I	(Null)	1	2019/07/02 16:59	2019/07/02 16:59
<input type="checkbox"/>		LS1A04NC21_011_00	LABScreen	Single Class I	(Null)	1	2019/07/02 16:59	2019/07/02 16:59
<input type="checkbox"/>		LS1A04NC21_011_00.LS1AEX	LABScreen	Single Class I	(Null)	1	2019/08/21 16:58	2019/08/21 16:58
<input type="checkbox"/>		LS1A04NC22_011_00	LABScreen	Single Class I	(Null)	1	2019/08/21 16:58	2019/08/21 16:58
<input type="checkbox"/>		LS1A04NC22_012_00	LABScreen	Single Class I	(Null)	1	2019/08/21 16:58	2019/08/21 16:58
<input type="checkbox"/>		LS1A04NC22_012_00.LS1AEX	LABScreen	Single Class I	(Null)	1	2019/08/21 16:58	2019/08/21 16:58
<input type="checkbox"/>		LS1A04NC23_011_00	LABScreen	Single Class I	(Null)	1	2019/08/21 16:58	2019/08/21 16:58
<input type="checkbox"/>		LS1A04NC23_012_00	LABScreen	Single Class I	(Null)	1	2019/08/21 16:58	2019/08/21 16:58
<input type="checkbox"/>		LS1A04NC23_012_00.LS1AEX	LABScreen	Single Class I	(Null)	1	2019/08/21 16:58	2019/08/21 16:58
<input type="checkbox"/>		LS1AEX01NC21_003_00	LABScreen	Single Class I	(Null)	1	2019/08/21 16:58	2019/08/21 16:58

データのインポート

HLA Fusion™
Analyze Data Reports Data Sample Patient Info Profile Utilities Help Exit

LABScreen
 Include Imported
c:\OLI FUSION\data#session#LABScreen
CSV File Name
20190415sample2_20200624
20190519QCWS_SA2018_NC020_20190515_128530
20190720sample2_01190720_102137

Current
Luminex: FlexMAP 3D/xPONENT - 4.2.1513.0 / SN FM3DD14231002 Template: LS2A01018_LS30_42
Session ID: 20190519QCWS_SA2018_NC020_20190515_128530 Date: 2019/05/15 Samples: 7
File Path: c:\OLI FUSION\data#session#LABScreen#20190519QCWS_SA2018_NC020_20190515_128530.csv
Catalog ID: **LS2A01NC20_018_01** /met: -
Quantiplex Beads: (none) Apply FJ Factor

Set empty Patient ID Auto Analysis Secondary Ab: Apply to all

Check Control **Import** Delete Patient Close

Well	Sample	Sample Date	Sample Treatment	Sample Source	Dilution Factor	Secondary Ab	Luminex Min Bead Cnt	NS	Exist in DB	Patient ID	First Name	Last Name	Ethnicity	Patient/Donor
73(L,A)1	NC						100	<input checked="" type="checkbox"/>	N					
74(L,B)1	SH8101						100	<input type="checkbox"/>	N					
75(L,C)1	SH8102						100	<input type="checkbox"/>	N					
76(L,D)1	SH8103						100	<input type="checkbox"/>	N					
77(L,E)1	SH8104						100	<input type="checkbox"/>	N					
78(L,F)1	SH8105						100	<input type="checkbox"/>	N					
79(L,G)1	SH8106						100	<input type="checkbox"/>	N					

LABScreen Check NS
HLA Fusion™
Selected NS: NC Catalog: LS2A01NC20_018_01
Default NS: **01NSLS2A01NC20_018_01**

Selected NS Raw Count
NC 55 102
PC 10587 109

Column Graph Point Graph

Add Default NS Print Screen Close

ONE LAMBDA

Summary画面

Summary Report

Session: 20190515QCWS_SA2013_NC020_20190515_123530 Catalog: LS2A01NC20_013_01 Session Date: 2020/11/15 Luminex: xPONENT/FlexMAP 3D -

Min BeadCnt	NC	PC	PCNCRatio	Class II Donor PRA	SecondaryAb	Dilution Factor
100	55.68	10587.35	190.146			
100	40.69	9085.31	223.281			
100	32	12406.45	387.702			
100	546.38	16753.18	30.662			
100	31.15	9489.19	304.629			
100	26.5	8868.94	334.677			
100	57.04	10161.25	178.143			

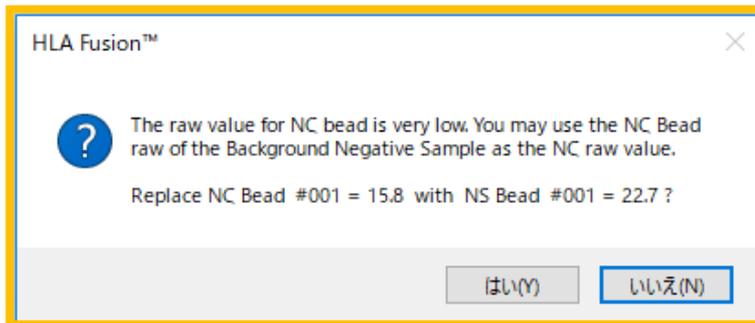
Field Chooser

- Analysis User
- Catalog
- Class I Suggested
- Class II %PRA / %SA
- Class II +/-
- Class II Donor PRA
- Class II Epitope
- Class II Final
- Class II Tail
- Confirm Date
- Confirm User
- Dilution Factor
- Edit
- Family
- First Name
- Last Name
- LocalID
- LocusType
- Min BeadCnt
- More Test
- NC
- New Antibody

確認項目

- Min Bead Cnt : 50以上
- NC : 1500以下
- PC : 500以上
- PC/NCRatio : 2以上

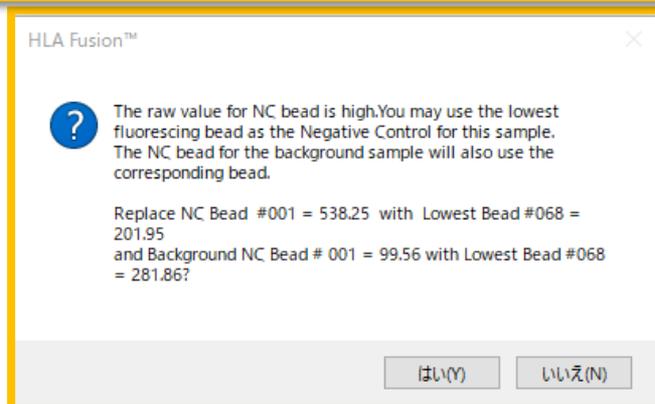
インポート時のメッセージ



検体のNCビーズが低いのでNC血清の数値と書き換えますか？

→「いいえ」を選択

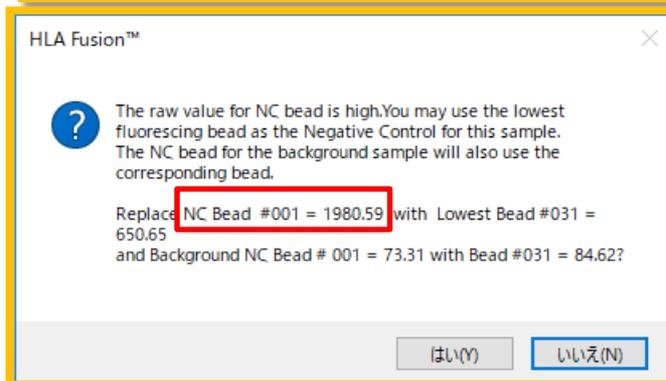
検体のNC値がNC血清の値より低い時に表示されます



検体のNCビーズの値が高いため、検体ビーズの中の一番低い値と置き換えますか？

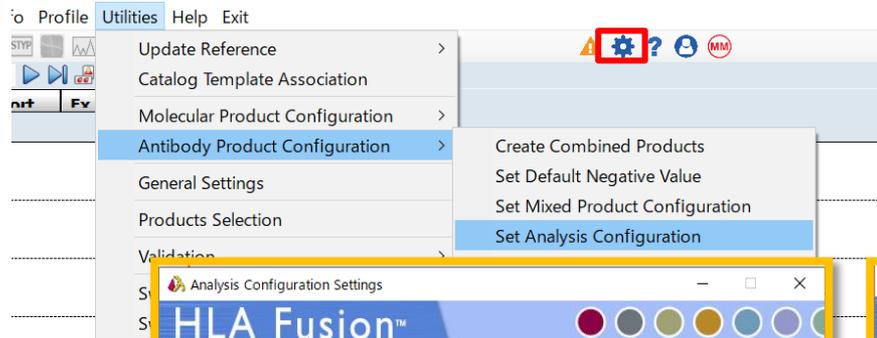
それに伴って、NC血清のNCビーズも変更しますか？

→「いいえ」を選択

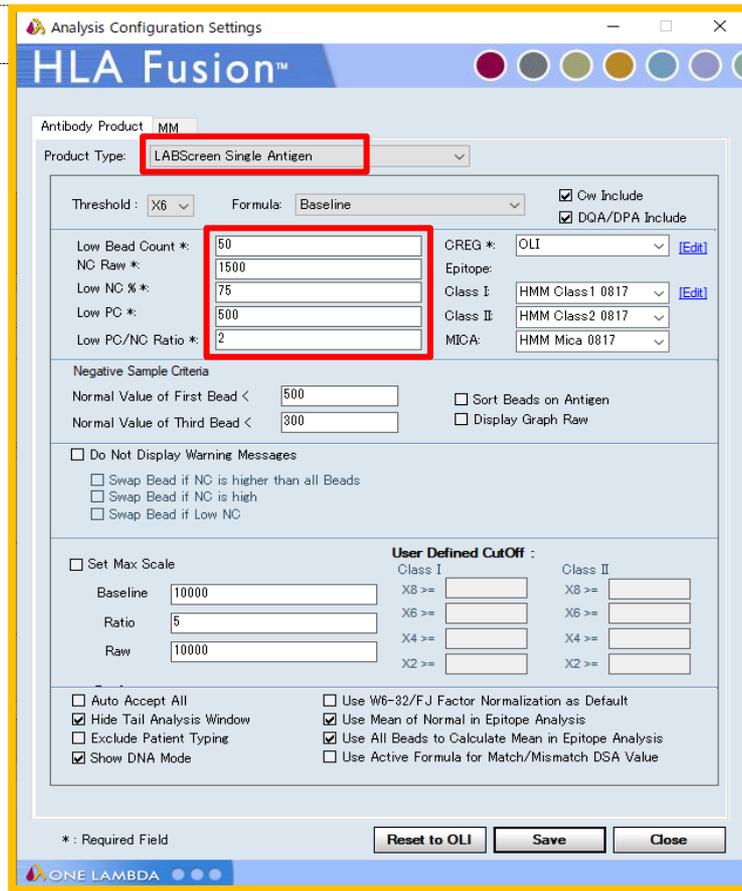
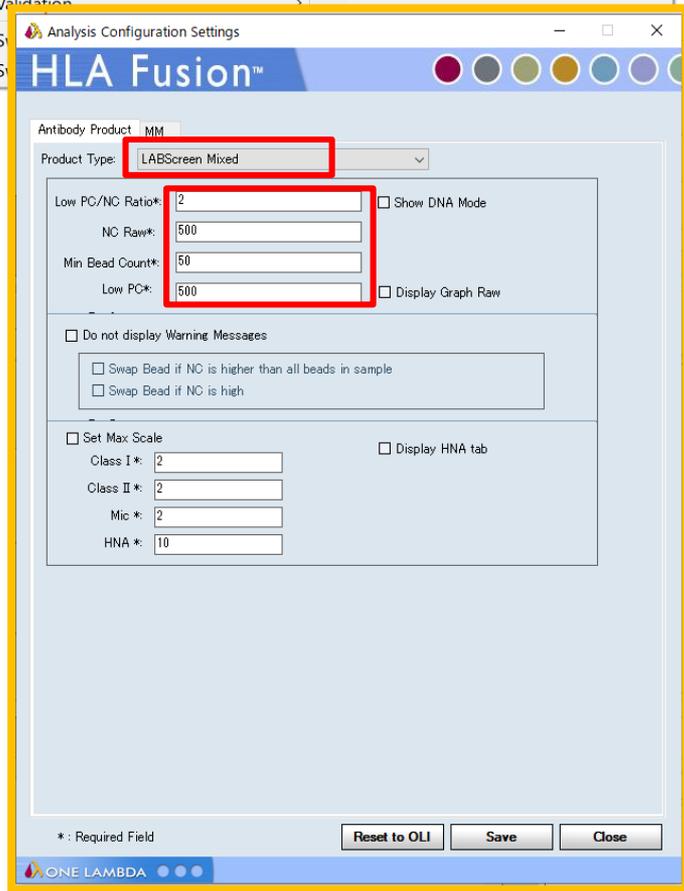


検体のNCビーズ値が1500を超えている場合は再検査をしてください

解析条件の設定



NC値やPC値などの再検査基準を変更することができます



カットオフ値の設定 -Single Antigen

Utilities Help Exit

- Update Reference
- Catalog Template Association
- Molecular Product Configuration
- Antibody Product Configuration
- General Settings
- Products Selection
- Validation
- Switch User
- Switch Database

1

1

Bar chart showing values for various loci: 24, 5, 29, 100, 30, 88, 91, 44, 34, 61, 87, 93, 90, 52, 86, 96, 94, 41, 74, 79, 82, 37, 12, 99, 8, 69, 25, 45, 63, 35, 81, 73, 92, 59, 50, 36, 3, 51, 46, 34, 2, 68, 33, 68, 24, 11, 36, 61, 54, 77, 46, 8, 57, 45, 37, 13, 38, 63, 67, 82, 76, 7, 47, 39, 75, 58, 81, 64, 61, 54, 77, 46, 8, 57, 45, 37, 13, 38, 63.

Analysis Configuration Settings

HLA Fusion™

Antibody Product: MM

Product Type: LABScreen Single Antigen

2

Threshold: X6 Formula: User CutOff (Baseline)

Low Bead Count *: 50

NC Raw *: 1500

Low NC % *: 75

Low PC *: 500

Low PC/NC Ratio *: 2

Formula options: User CutOff (Baseline), Baseline, Mixed Formula, Ratio Scoring, Raw Data, User CutOff (Raw Data), User CutOff (Ratio), Locus Specific CutOff (Baseline), Locus Specific CutOff (Raw Data), Locus Specific CutOff (Ratio)

Checkboxes: Ow Include, DQA/DPA Include

Negative Sample Criteria: Normal Value of First Bead < 500, Normal Value of Third Bead < 300

Do Not Display Warning Messages: Swap Bead if NC is higher than all Beads, Swap Bead if NC is high, Swap Bead if Low NC

Set Max Scale: Baseline 10000, Ratio 5, Raw 10000

User Defined CutOff:

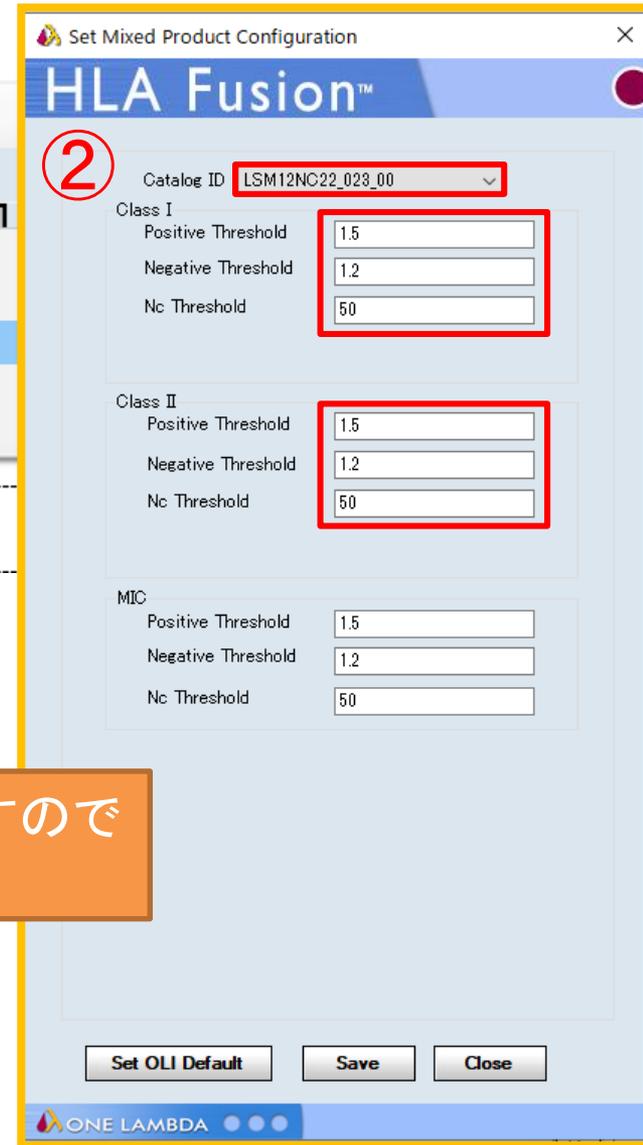
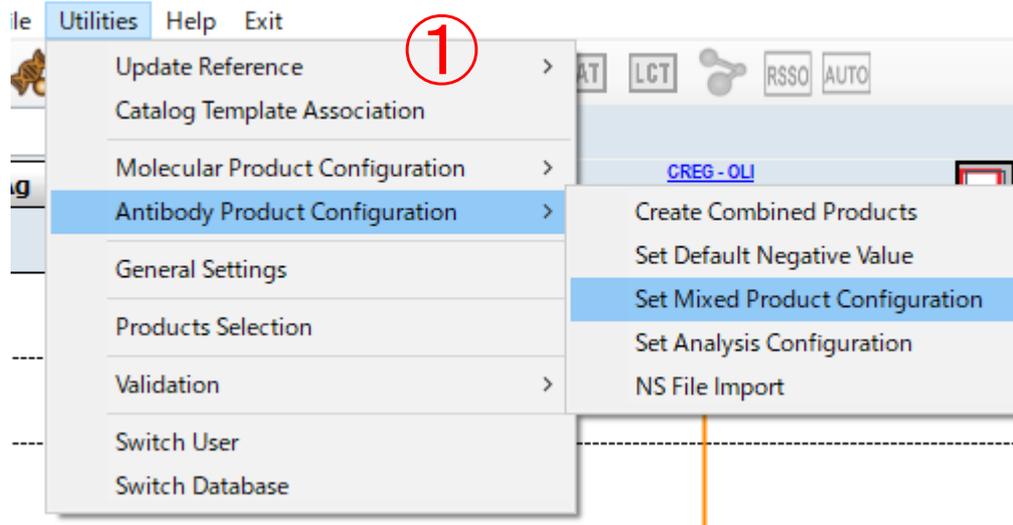
Class I		Class II	
X8 >=	3000	X8 >=	3000
X6 >=	1000	X6 >=	1000
X4 >=	500	X4 >=	500
X2 >=	300	X2 >=	300

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 OLI Save Close

カットオフ値の設定 -Mixed



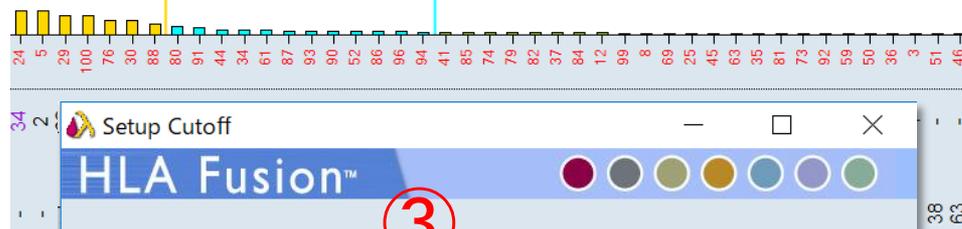
カタログファイルごとに設定が必要ですので
注意してください

ローカスごとのカットオフ値の設定-1

Utilities Help Exit

- Update Reference
- Catalog Template Association
- Molecular Product Configuration
- Antibody Product Configuration
- General Settings
- Products Selection
- Validation
- Switch User
- Switch Database

1



Analysis Configuration Settings

HLA Fusion™

Antibody Product: MM

Product Type: LABScreen Single Antigen

Threshold: X Formula: Locus Specific CutOff (Baseline)

Low Bead Count *: 50

NC Raw *: 1500

Low NC % *: 75

Low PC *: 500

Low PC/NC Ratio *: 2

Negative Sample Criteria

Normal Value of First Bead < 500

Normal Value of Third Bead < 300

Do Not Display Warning Messages

Swap Bead if NC is higher than all Beads

Swap Bead if NC is high

Swap Bead if Low NC

User Defined CutOff:

	Class I	Class II
Baseline	10000	X8 >
Ratio	5	X6 >
Raw	10000	X4 >=
		X2 >=

2

Setup Cutoff

HLA Fusion™

Data Type: aselin

Setup Name: sample

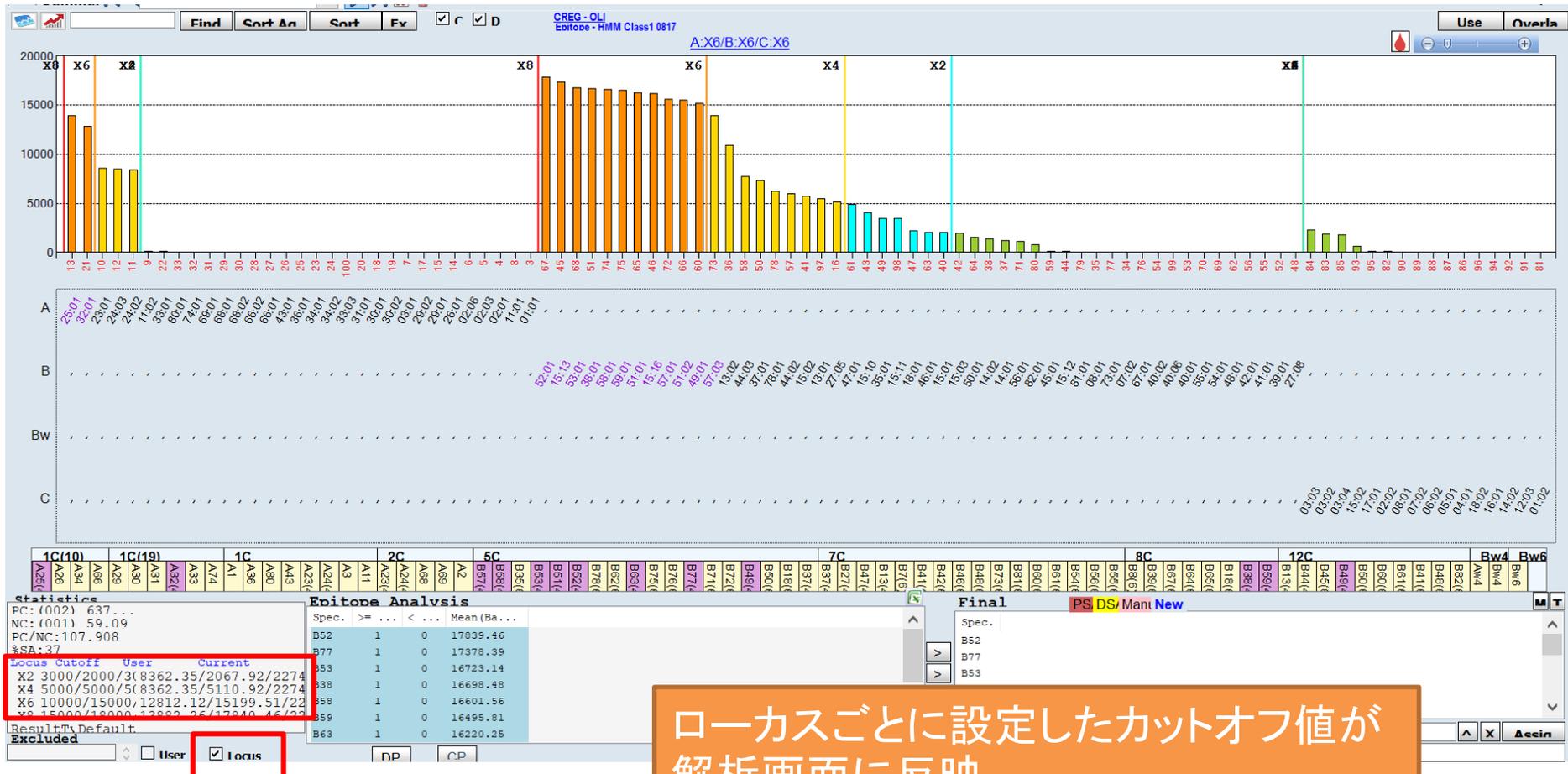
Description:

	A	B	C	DR	DQA/DQB	DPA/DPB	MICA/MICB
X8	15000	18000	13000	15000	10000	13000	15000
X6	10000	15000	8000	10000	8700	10000	10000
X4	00	5000	5000	5000	5000	5000	3000
X2	00	2000	3000	3000	2000	2000	2000

Threshold: X6 X6 X6 X6 X6 X6 X6

3

ローカスごとのカットオフ値の設定-2



ローカスごとに設定したカットオフ値が解析画面に反映

4桁表示への変更

Utilities Help Exit

- Update Reference
- Catalog Template Association
- Molecular Product Configuration
- Antibody Product Configuration
 - Create Combined Products
 - Set Default Negative Value
 - Set Mixed Product Configuration
 - Set Analysis Configuration
 - NS File Import
- General Settings
- Products Selection
- Validation
- Switch User
- Switch Database

Analysis Configuration Settings

HLA Fusion™

Antibody Product: MM

Product Type: LABScreen Single Antigen

Threshold: X Formula: Baseline Cw Include DQA/DPA Include

Low Bead Count *: 500 CREG *: OLI FcI

NC Raw *: 500 FcI

Low NC % *: FcI

Low PC % *: FcI

Low PC/NC % *: FcI

Negative Sample: Sort Beads on Antigen Display Graph Raw

Normal Value of First Bead < 500

Normal Value of Third Bead < 300

Do Not Display Warning Messages

- Swap Bead if NC is higher than all Beads
- Swap Bead if NC is high
- Swap Bead if Low NC

Set Max: **User Defined CutOff :**

Raw 10000 $\wedge 4 \leq$ $\wedge 4 \leq$
 $X 2 \geq$ $X 2 \geq$

- 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

CREG - OLI
Epitope - HMM Class1 0817

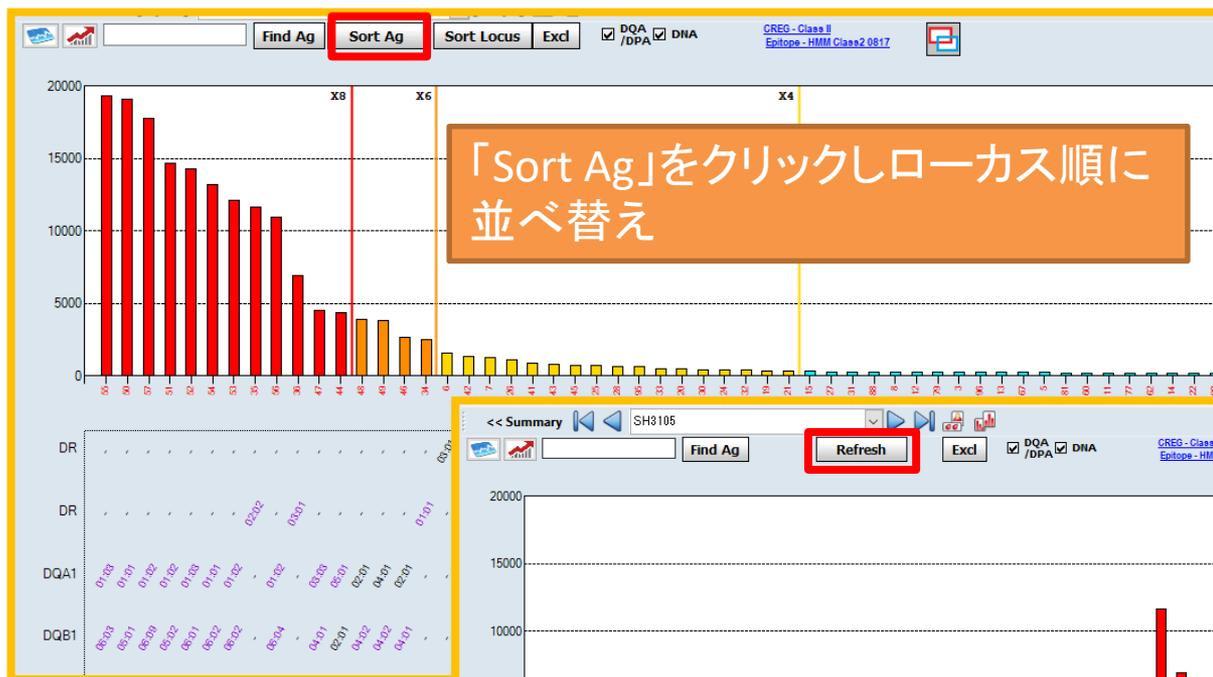
D

手動でその都度変更も可能

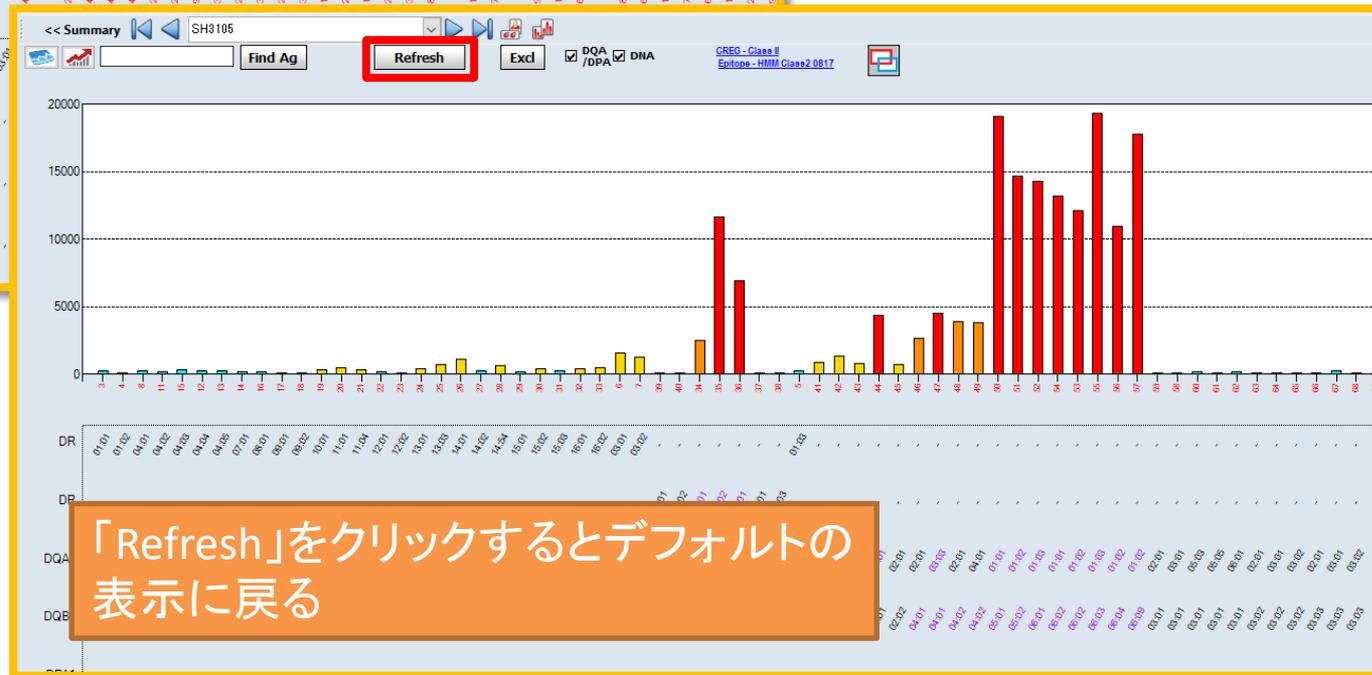
X8 X6 X2

11:02 33:01 43:01 80:01 01:01

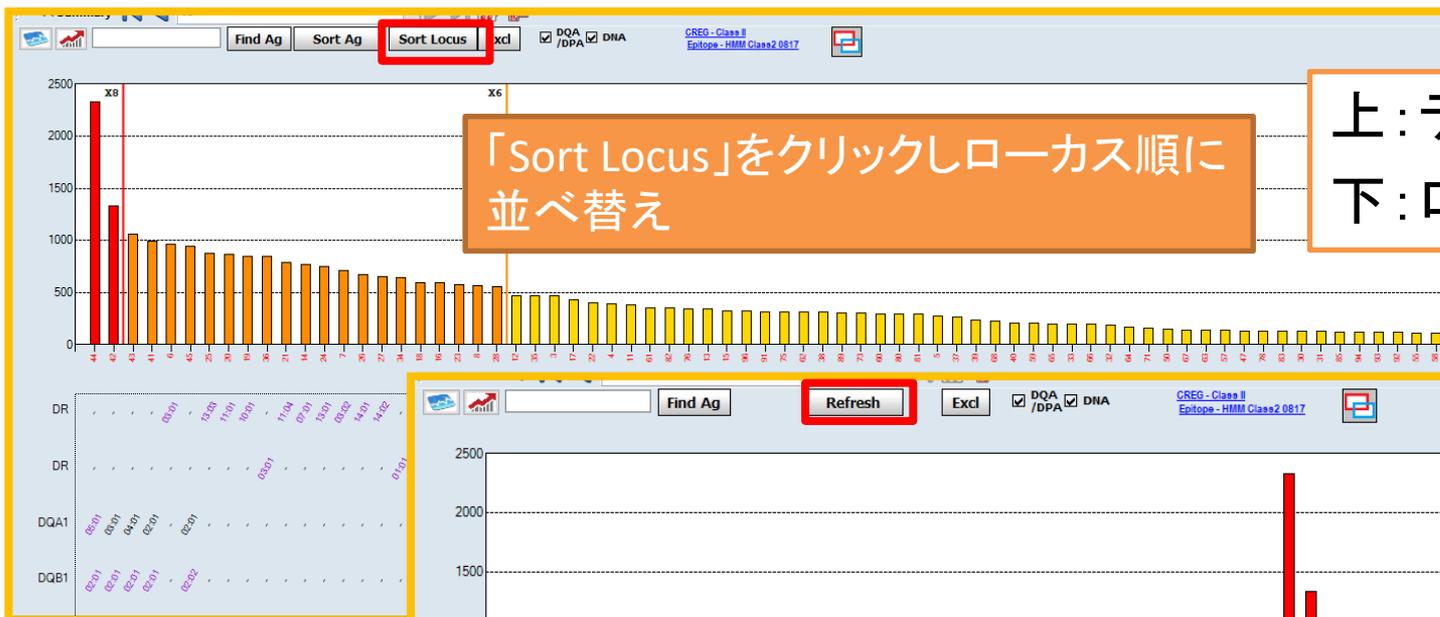
ローカス順に並べ替える-1



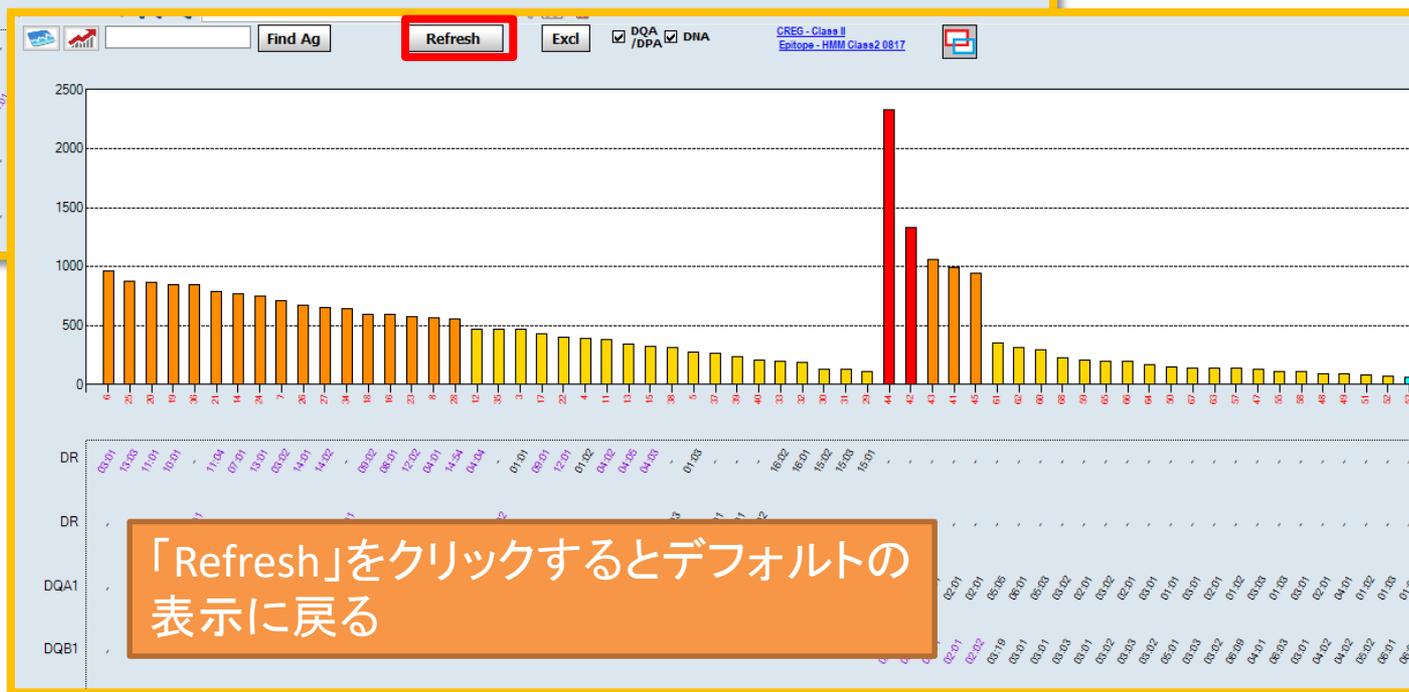
上: デフォルトの表示
下: ローカス順の表示



ローカス順に並べ替える-2



上: デフォルトの表示
下: ローカス順の表示



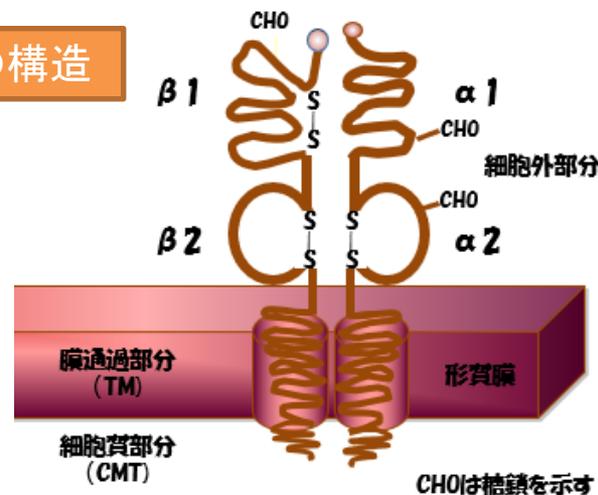
Single Antigen クラス2 解析のポイント

- DP及びDQのビーズには2種類のHLA抗原が貼りついている
- 判定する場合は、該当ビーズの反応が α 鎖と β 鎖のどちらによる反応であるかを判断することが必要

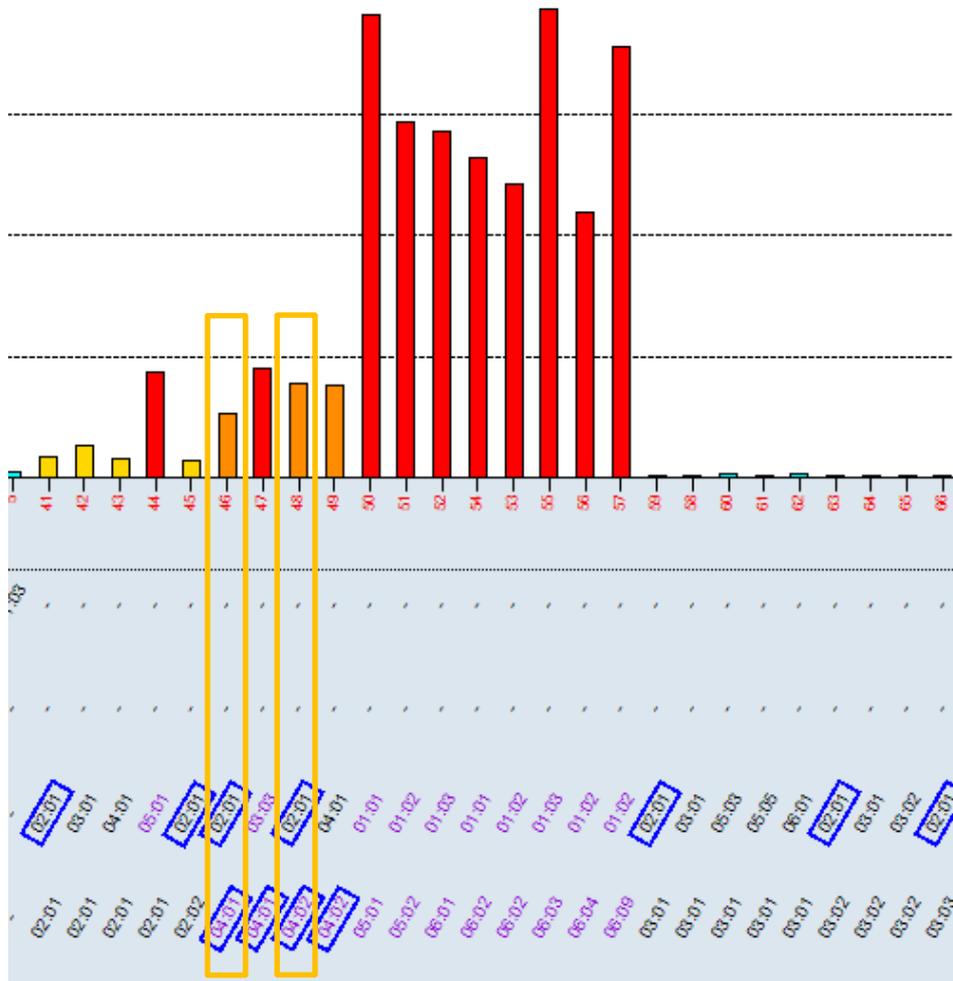
データシートの例

39	rDQ0201A0201	DQA1*02:01, DQB1*02:01	DQ2
40	rDQ0201A0301	DQA1*03:01, DQB1*02:01	DQ2
41	rDQ0201A0401	DQA1*04:01, DQB1*02:01	DQ2
42	C4987DQ0201	DQA1*05:01, DQB1*02:01	DQ2
43	rDQ0202A0201	DQA1*02:01, DQB1*02:02	DQ2
44	rDQ0401A0201	DQA1*02:01, DQB1*04:01	DQ4
45	C4107DQ0401	DQA1*03:03, DQB1*04:01	DQ4
46	rDQ0402A0201	DQA1*02:01, DQB1*04:02	DQ4
47	rDQ0402A0401	DQA1*04:01, DQB1*04:02	DQ4
48	C4905DQ0501	DQA1*01:01, DQB1*05:01	DQ5

Class 2の構造



Single Antigen クラス2の解析例-2



同じアレルが結合しているビーズが陽性と陰性が混在する場合

DQA1*02:01を例に説明します

DQA1*02:01が結合しているビーズが7個ありますが、陰性のビーズがあるのでDQA1*02:01は陰性です

46と48番ビーズはなぜ陽性なのか？

→ビーズ構成を確認します

ビーズ番号	DQA1	DQB1
46	02:01	04:01
48	02:01	04:02

DQB1*04:01は47番ビーズにも結合

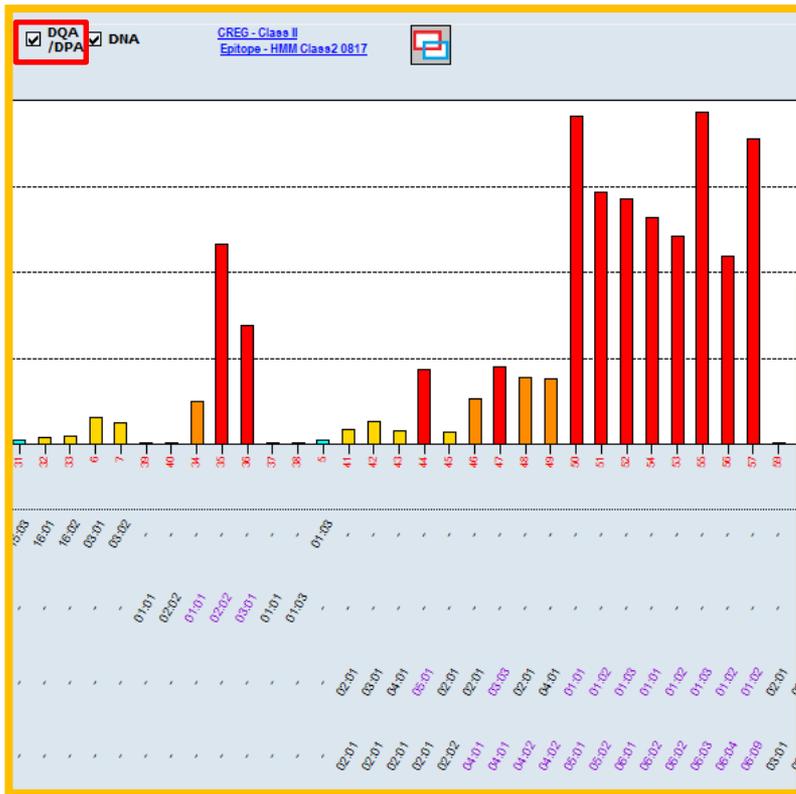
→47番は陽性= DQB1*04:01は陽性

DQB1*04:02は49番ビーズにも結合

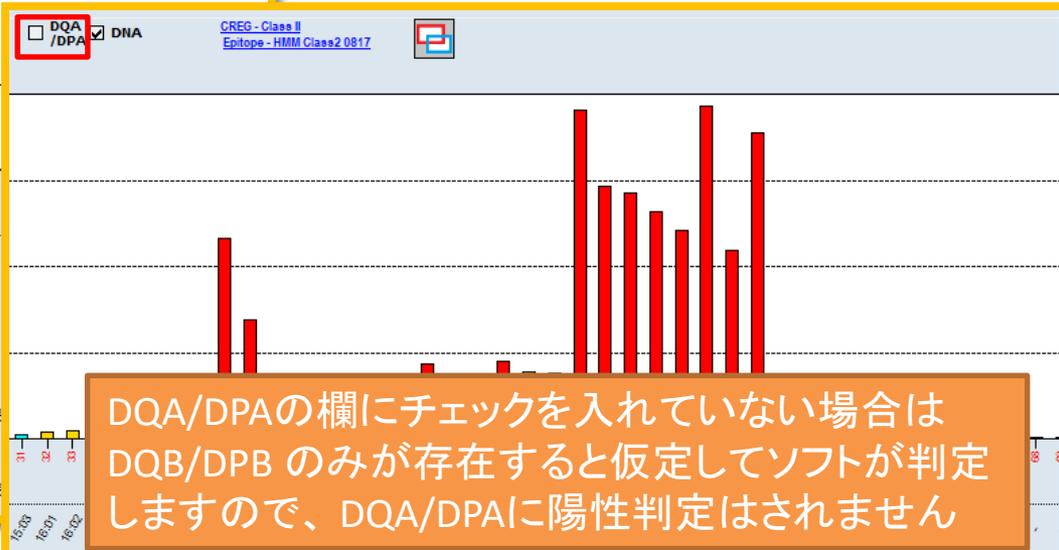
→49番は陽性= DQB1*04:02は陽性

上記より46と48番ビーズはDQB1抗体による陽性反応であるため、DQA1*02:01は陰性と判定ができます

Single Antigen クラス2の解析例-3

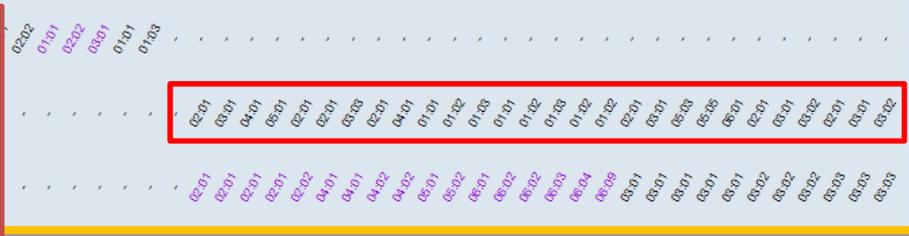


DQA/DPAの欄にチェックを入れた場合は、DQAの反応も考慮してソフトが自動判定を行います
ソフトが陽性と判定したアレルは紫色で表示されます

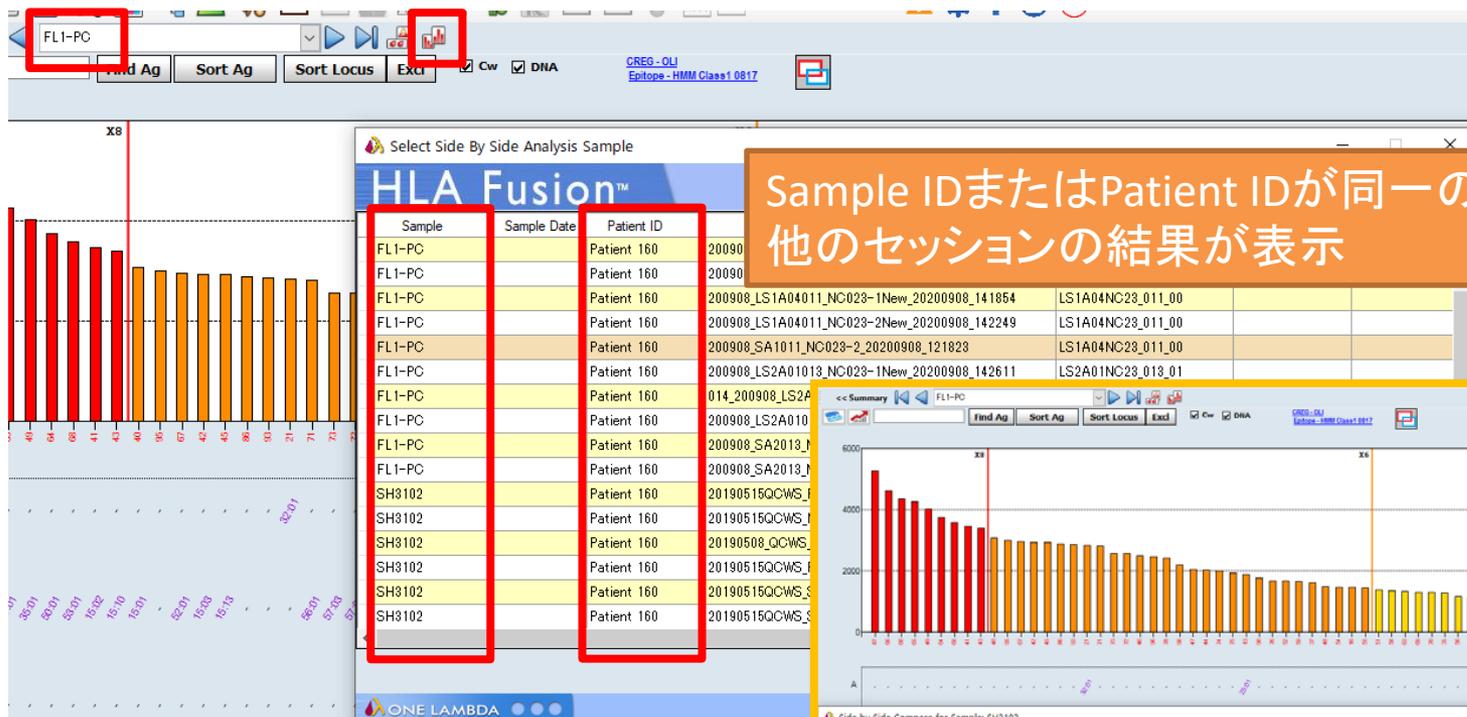


DQA/DPAの欄にチェックを入れていない場合はDQB/DPBのみが存在すると仮定してソフトが判定しますので、DQA/DPAに陽性判定はされません

*** 注意事項 ***
ソフトの自動判定の結果をそのまま採用せず、前ページで説明した手順に沿ってご自身で判定をお願い致します



同一患者の別のデータを並べて見る



The screenshot shows the HLA Fusion software interface. At the top, there are navigation buttons: 'Find Ag', 'Sort Ag', 'Sort Locus', and 'Excl'. Below these is a table titled 'Select Side By Side Analysis Sample' with columns for 'Sample', 'Sample Date', and 'Patient ID'. A red box highlights the 'Patient ID' column, which contains the value 'Patient 160' for all rows. Another red box highlights the 'Sample' column, which contains various sample IDs like 'FL1-PC' and 'SH3102'. To the right of the table is a bar chart with a y-axis labeled 'x8' and a red vertical line at position 43. Below the table is a blue bar with the text 'ONE LAMBDA'.

Sample	Sample Date	Patient ID
FL1-PC		Patient 160
SH3102		Patient 160

Sample IDまたはPatient IDが同一の他のセッションの結果が表示

ダブルクリックすると2つの結果を並べて表示可能



The screenshot shows a 'Side by Side Compare for Sample: SH3102' window. It features two bar charts side-by-side. The left chart has a y-axis labeled 'x8' and a red vertical line at position 43. The right chart has a y-axis labeled 'x4' and a red vertical line at position 43. The charts show a distribution of values across different loci. Below the charts is a blue bar with the text 'ONE LAMBDA'.

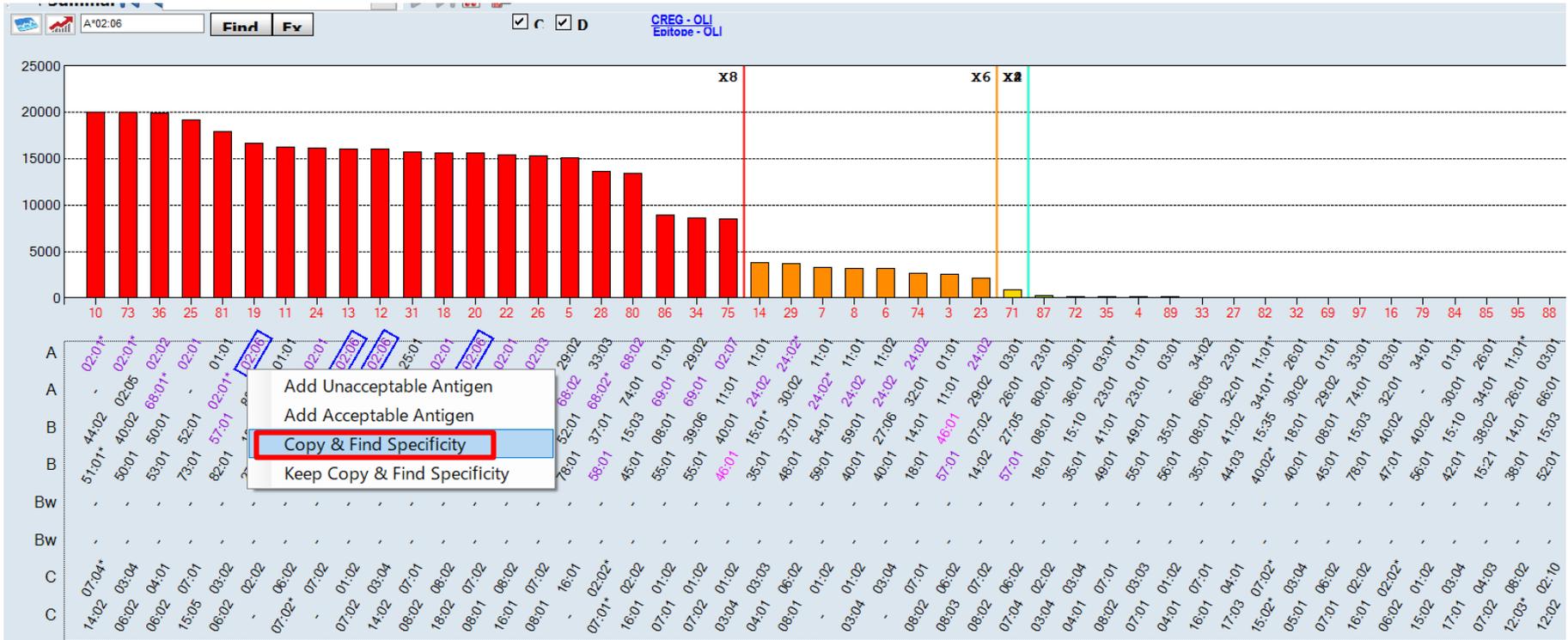
アレルの検索-1



2桁で入力し最後に「%」を入力して検索
→4桁での検索結果が表示される

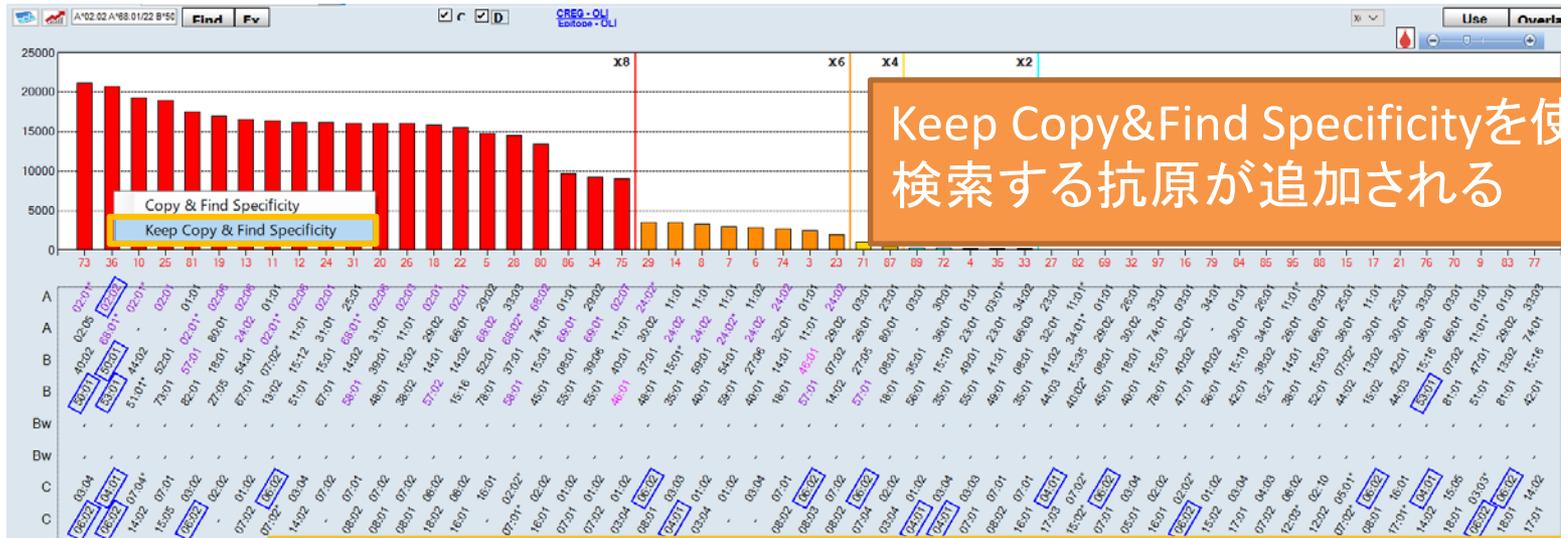
「%」は半角で入力してください

アレルの検索-3

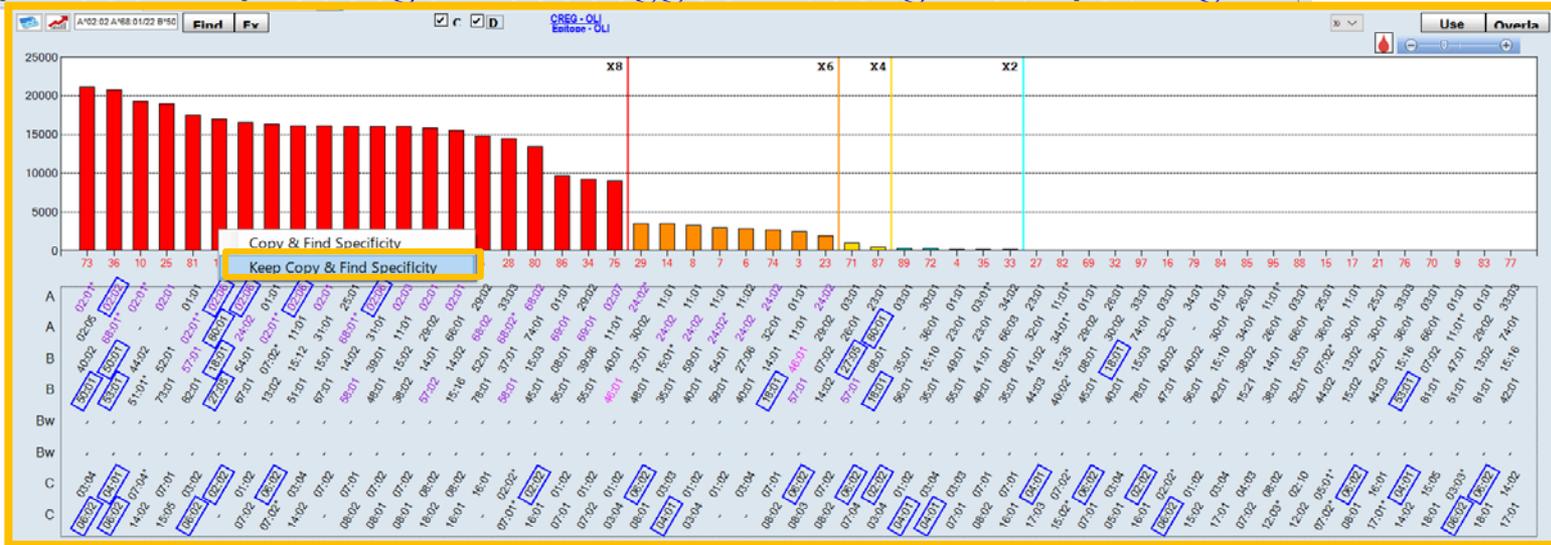


抗原名の上で右クリック→Copy&Find Specificity
選択した抗原を全て検索

アレルの検索-4

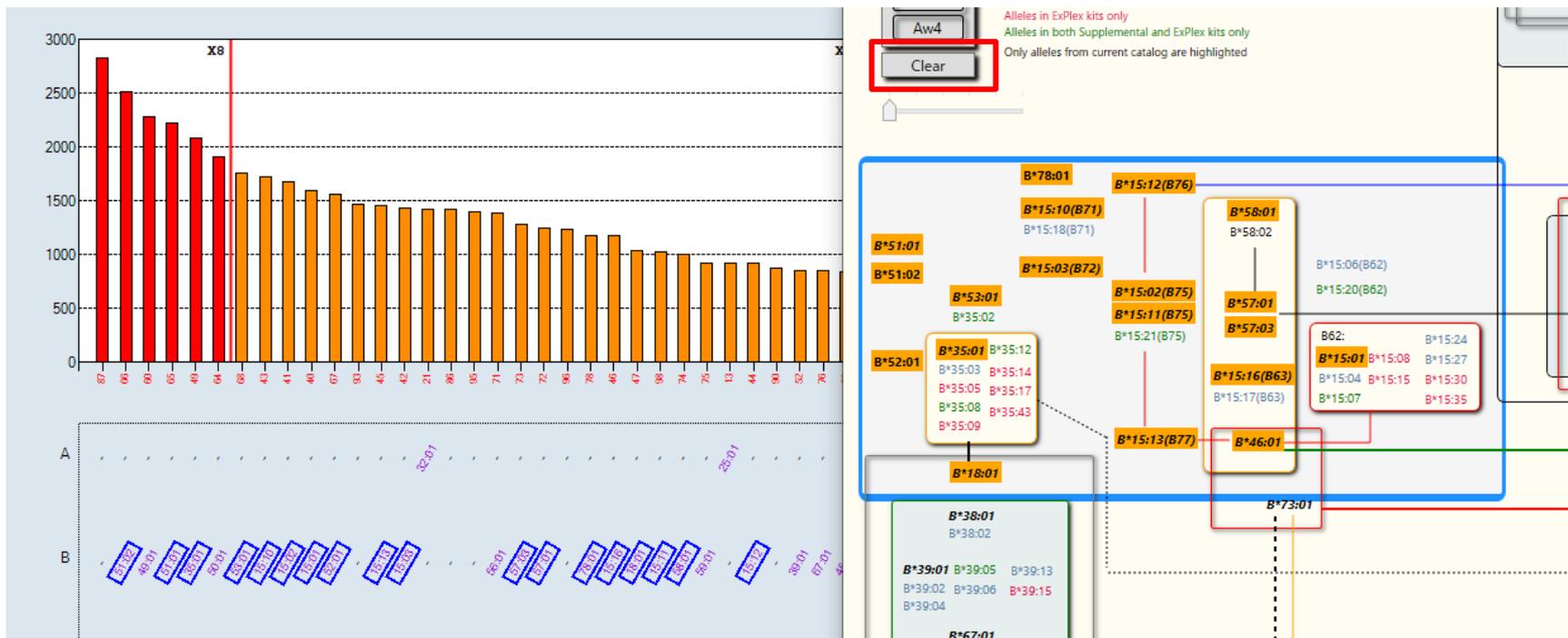


Keep Copy&Find Specificityを使用すると
検索する抗原が追加される



CREG Map -3

CREG Map上でグループを選択すると、選択したグループが青枠で表示され、製品に含まれるアレルはオレンジ色にハイライト
解析結果上では青枠で囲まれる
Clearをクリックするとハイライトは消える



解析結果の確定 - Final Assignment

Statistics
: (002) 8968.94
: (001) 26.5
/ NC: 334.677
v: 17
eff OLI Current
2 131.76 131.76
4 350.59 350.59
6 2480.59 2480.59
8 4338.21 4338.21
suitType: Modified
cluded Antigen

Spec.	>= X6	< X6	Mean (Ba...)
DQ5	2	0	16891.46
DQA1*01:03	2	0	16810.37
DQA1*01:01	2	0	16179.24
DQ6	6	0	14615.91
DQA1*01:02	4	0	13874.79
DR52	3	0	7024.46
DQA1*03:03	1	0	4532.36

Spec.	TP	FP	IN	FN	R	Inc.	Str.	Avg.
DQ5								
DQA1*01:03								
DQB1*06:04								

Final Assignment [PA] [DA] [Manual] [New]

Raw Data [Save>>] Confirm>

陽性と判定したアレルをFinal Assignment欄に入力

- Epitope Analysis Resultsよりダブルクリック
- グラフ内のアレルをダブルクリック(ピンクでハイライトされる)

削除する際は「×」をクリック

「Save」をクリックして保存

Epitopeの表示

DQA / DPA DNA
 GREG - Class II
 Epitope - HMM Class2 0817

Epitope
 All Ab Verified Other [iCn3D](#) Latest Version DNA Mode Assign epitope when it is double clicked

Group Name	AA Position	Polymorphic Residues											
70QRA	70QRA	70Q71R73A	DRB1*01:01	DRB1*01:02	DRB1*14:02	DRB1*04:04	DRB1*04:05	DRB1*04:03	DRB1*01:31	DRB1*01:32	DRB1*01:34		D
96Y2	96Y2	96Y98E120N(180L181T)	DRB1*04:01	DRB1*04:04	DRB1*04:05	DRB1*04:03	DRB1*04:02	DRB1*04:10	DRB1*04:06	DRB1*04:92	DRB1*04:34		D
13FEL	13FEL	13F14E26L	DRB1*01:01	DRB1*01:02	DRB1*10:01	DRB1*01:03	DRB1*01:28	DRB1*01:29	DRB1*01:30	DRB1*01:31	DRB1*01:32		D
96ES2	96ES2	96E98K120S(28E30C31)	DRB1*01:01	DRB1*01:02	DRB1*01:03	DRB1*01:04	DRB1*12:17	DRB1*01:13	DRB1*01:20				
57A	57A	57A58A60H	DRB1*14:01	DRB1*14:54	DRB1*14:120	DRB1*14:122	DRB1*14:124	DRB1*14:125	DRB1*14:16	DRB1*14:26	DRB1*14:28		D
111R	111R	111R	DPA1*02:01	DPA1*02:02									
74SR3	74SR3	71A75S77R(116I)(125S)	DQB1*05:01	DQB1*05:02	DQB1*05:03	DQB1*05:04	DQB1*05:05	DQB1*05:06	DQB1*05:07	DQB1*05:08	DQB1*05:09		D
55EA	55EA	55E56A57E	DPB1*05:01	DPB1*19:01	DPB1*47:01	DPB1*38:01	DPB1*36:01	DPB1*30:01	DPB1*24:01	DPB1*22:01	DPB1*21:01		D
31Q	31Q	31Q	DPA1*02:01	DPA1*02:02	DPA1*01:06	DPA1*02:04							
125SQ	125SQ	125S126Q	DQB1*05:01	DQB1*05:03	DQB1*05:07	DQB1*05:08	DQB1*05:10	DQB1*05:12	DQB1*05:15	DQB1*05:16			

青字：試薬に含まれるアレル

緑字：試薬に含まれないアレル

ピンクセル：Final Assignmentしたアレル

オレンジセル：Final Assignmentしたアレルと2桁レベルで同じアレル

4桁のアレルとしては試薬に含まれない

黄色セル：ドナーアレル(DSA)

赤色セル：患者アレル(自己抗体)

解析結果の確定 – EpitopeのAssignment

Epitope - HMM Class2 081

Epitope

All
 Ab Verified
 Other
 ICn3D
 Latest Version

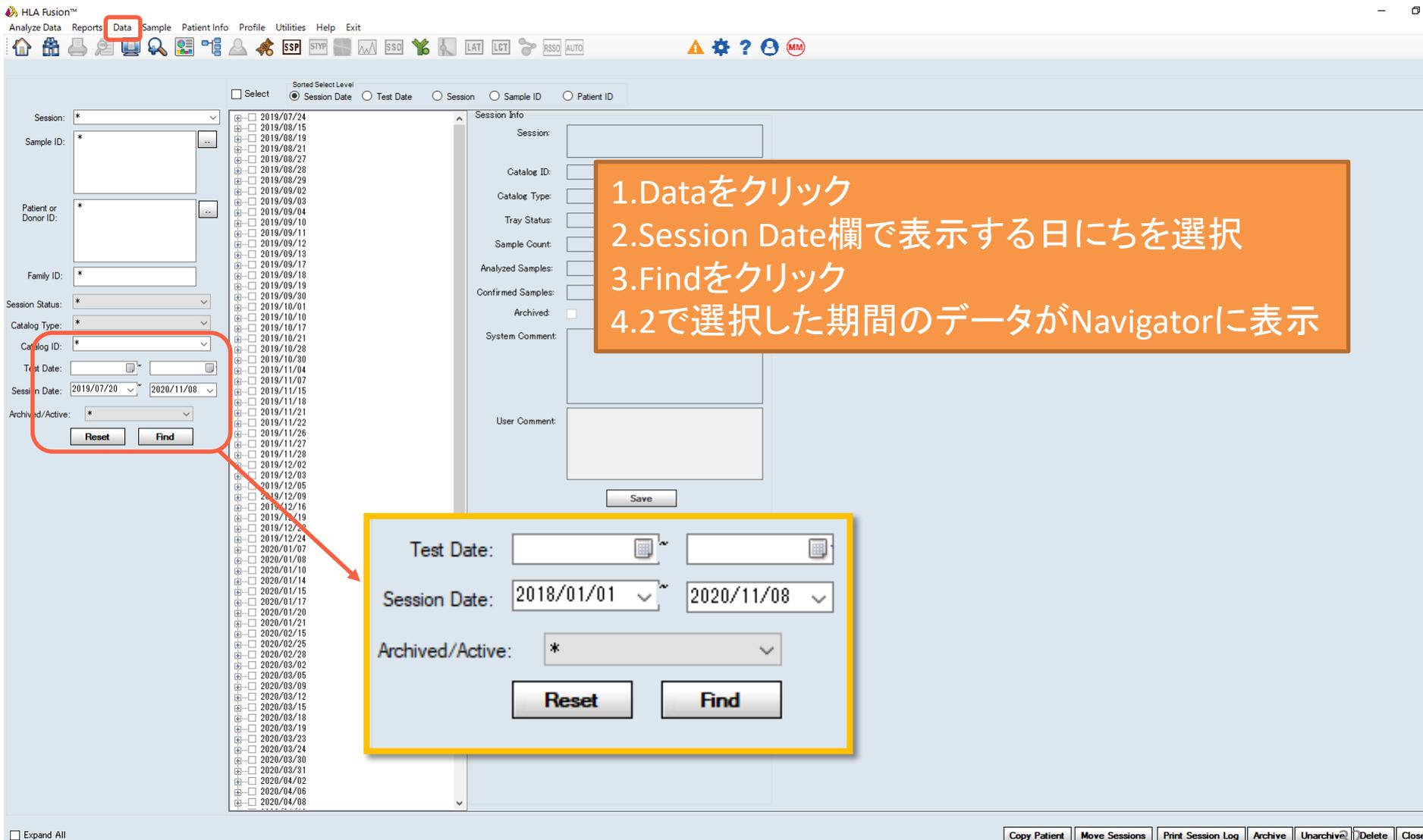
Group Name	AA Position	Polymorphic Residues												
52PR	52PR	52P55R	DQB1*06.03	DQB1*05.01	DQB1*06.09	DQB1*05.02	DQB1*06.01	DQB1*06.02	DQB1*06.04	DQB1*04.01	DQB1*04.02	DQB1*06.32	DQB1*06.31	DQB1*06.30
52PQ2	52PQ2	52P53Q55R56P(84E85V)	DQB1*06.03	DQB1*05.01	DQB1*06.09	DQB1*05.02	DQB1*06.01	DQB1*06.02	DQB1*06.04	DQB1*06.33	DQB1*06.32	DQB1*06.31	DQB1*06.30	DQB1*06.28
85VA	85VA	84E85V86A89G	DQB1*06.03	DQB1*05.01	DQB1*05.02	DQB1*06.01	DQB1*06.02	DQB1*06.23	DQB1*06.24	DQB1*06.27	DQB1*06.28	DQB1*06.29	DQB1*06.30	DQB1*06.31
125G	125G	125G	DQB1*06.03	DQB1*06.09	DQB1*06.01	DQB1*06.02	DQB1*06.04	DQB1*06.44	DQB1*06.43	DQB1*06.42	DQB1*06.41	DQB1*06.39	DQB1*06.36	DQB1*06.47
85VY	85VY	85V87Y89G	DQB1*05.01	DQB1*06.09	DQB1*05.02	DQB1*06.04	DQB1*06.12	DQB1*06.15	DQB1*06.17	DQB1*06.21	DQB1*06.22	DQB1*06.34	DQB1*06.07	DQB1*06.36
74SV2	74SV2	74S75V(26G)	DQB1*05.01	DQB1*05.02	DQB1*04.01	DQB1*04.02	DQB1*05.14	DQB1*05.13	DQB1*05.12	DQB1*05.11	DQB1*05.10	DQB1*05.09	DQB1*05.08	DQB1*05.07
30H	30	H	DQB1*06.03	DQB1*05.01	DQB1*05.02	DQB1*06.04	DQB1*05.08	DQB1*05.07	DQB1*05.06	DQB1*05.05	DQB1*05.03	DQB1*03.38	DRB3*03.02	DRB3*02.24
55RPD	55RPD	55R56P57D	DQB1*06.03	DQB1*05.02	DQB1*06.01	DQB1*06.02	DQB1*06.30	DQB1*06.31	DQB1*06.32	DQB1*06.33	DQB1*06.35	DQB1*06.37	DQB1*06.40	DQB1*06.42
67VG	67VG	66E67V70G	DQB1*06.03	DQB1*05.01	DQB1*05.02	DQB1*06.02	DQB1*06.17	DQB1*06.19	DQB1*06.20	DQB1*06.21	DQB1*06.23	DQB1*06.24	DQB1*06.28	DQB1*06.25
56PV	56PV	55R56P57V	DQB1*05.01	DQB1*06.09	DQB1*06.04	DQB1*06.39	DQB1*06.38	DQB1*06.36	DQB1*06.34	DQB1*06.27	DQB1*06.22	DQB1*06.21	DQB1*06.18	DQB1*06.11
52SK5	52SK5	52S53K55G56G(18F)(45)	DQA1*01.03	DQA1*01.01	DQA1*01.02	DQA1*01.04	DQA1*01.05	DQA1*01.06	DQA1*01.07	DQA1*01.08	DQA1*01.09	DQA1*01.10	DQA1*01.11	DQA1*01.12
9F	9F	9F	DQB1*06.02	DQB1*04.01	DQB1*04.02	DQB1*06.48	DQB1*06.47	DQB1*06.46	DQB1*06.37	DQB1*06.33	DQB1*06.29	DQB1*06.24	DQB1*06.23	DQB1*06.22
98Q	98Q	96H98Q120S	DRB3*02.02	DRB3*03.01	DRB3*01.01	DRB3*02.01	DRB3*03.03	DRB3*02.11	DRB3*02.10	DRB3*02.20	DRB3*02.28	DRB3*02.24		
87F	84,85,86,87,89	E,V,A,F,G	DQB1*06.03	DQB1*06.01	DQB1*06.02	DQB1*06.48	DQB1*06.47	DQB1*06.45	DQB1*06.44	DQB1*06.43	DQB1*06.41	DQB1*06.40	DQB1*06.37	DQB1*06.35
70GT	70GT	67V70G71T	DQB1*06.03	DQB1*06.02	DQB1*06.47	DQB1*06.46	DQB1*06.44	DQB1*06.41	DQB1*06.40	DQB1*06.33	DQB1*06.31	DQB1*06.29	DQB1*06.28	DQB1*06.23
70QQ	70QQ	70Q73G74Q	DRB3*02.02	DRB3*03.01	DRB3*01.07	DRB3*02.06	DRB3*02.07	DRB3*02.08	DRB3*02.26	DRB1*03.24	DRB1*03.11	DRB1*03.81	DRB3*02.09	DRB3*02.11
55RL3	55RL3	52P53L55R56L57D(66C)	DQB1*04.01	DQB1*04.02	DQB1*03.25	DQB1*04.03	DQB1*04.04	DQB1*04.05	DQB1*04.05	DQB1*04.07	DQB1*04.08			
86G2	86G2	84E85V86G87Y89G(13C)	DQB1*06.09	DQB1*06.04	DQB1*06.42	DQB1*06.39	DQB1*06.38	DQB1*06.36	DQB1*06.34	DQB1*06.25	DQB1*06.22	DQB1*06.21	DQB1*06.17	DQB1*06.15
41RA2	41RA2	40E41R45A(129Q130S)	DQA1*01.01	DQA1*01.02	DQA1*01.04	DQA1*01.05	DQA1*01.06	DQA1*01.07	DQA1*01.08	DQA1*01.09				
74SR3	74SR3	71A75S77R(116I)(125S)	DQB1*05.01	DQB1*05.02	DQB1*05.03	DQB1*05.04	DQB1*05.05	DQB1*05.06	DQB1*05.07	DQB1*05.08	DQB1*05.09	DQB1*05.10	DQB1*05.11	DQB1*05.12
41KA2	41KA2	40E41K45A(129H130A)	DQA1*01.03											
3P4	3P4	3P(9L)(37D)38V(67I)70R7	DQB1*06.01											
56PS	56	57	P	S	DQB1*05.02	DQB1*05.04	DQB1*05.05	DQB1*05.14	DQB1*06.10	DQB1*06.25				
51R2	51R2	51R(187E189S)	DRB3*02.02	DRB1*15.65	DRB3*02.24	DRB1*15.47	DRB3*01.07	DRB3*02.06	DRB3*02.08	DRB3*02.22	DRB1*13.131	DRB3*02.26	DRB1*14.96	DRB1*14.96
37FL2	37FL2	37F38L(183A)	DRB3*01.01	DRB3*01.12	DRB3*01.11	DRB3*01.10	DRB3*01.05	DRB3*01.04	DRB3*01.03	DRB3*01.02	DRB1*14.110	DRB1*12.15	DRB1*12.05	DRB1*03.42
23L	23L	23L	DQB1*04.01	DQB1*04.05	DQB1*04.06	DQB1*04.07	DQB1*04.08							
125SQ	125SQ	125S126Q	DQB1*05.01	DQB1*05.03	DQB1*05.07	DQB1*05.08	DQB1*05.10	DQB1*05.12	DQB1*05.15	DQB1*05.16				

Ab Assignment Epitope Assignment

52PR
52PQ2

陽性と判定したエピトープの記録も可能
Epitope名をダブルクリックする

Navigator表示の変更



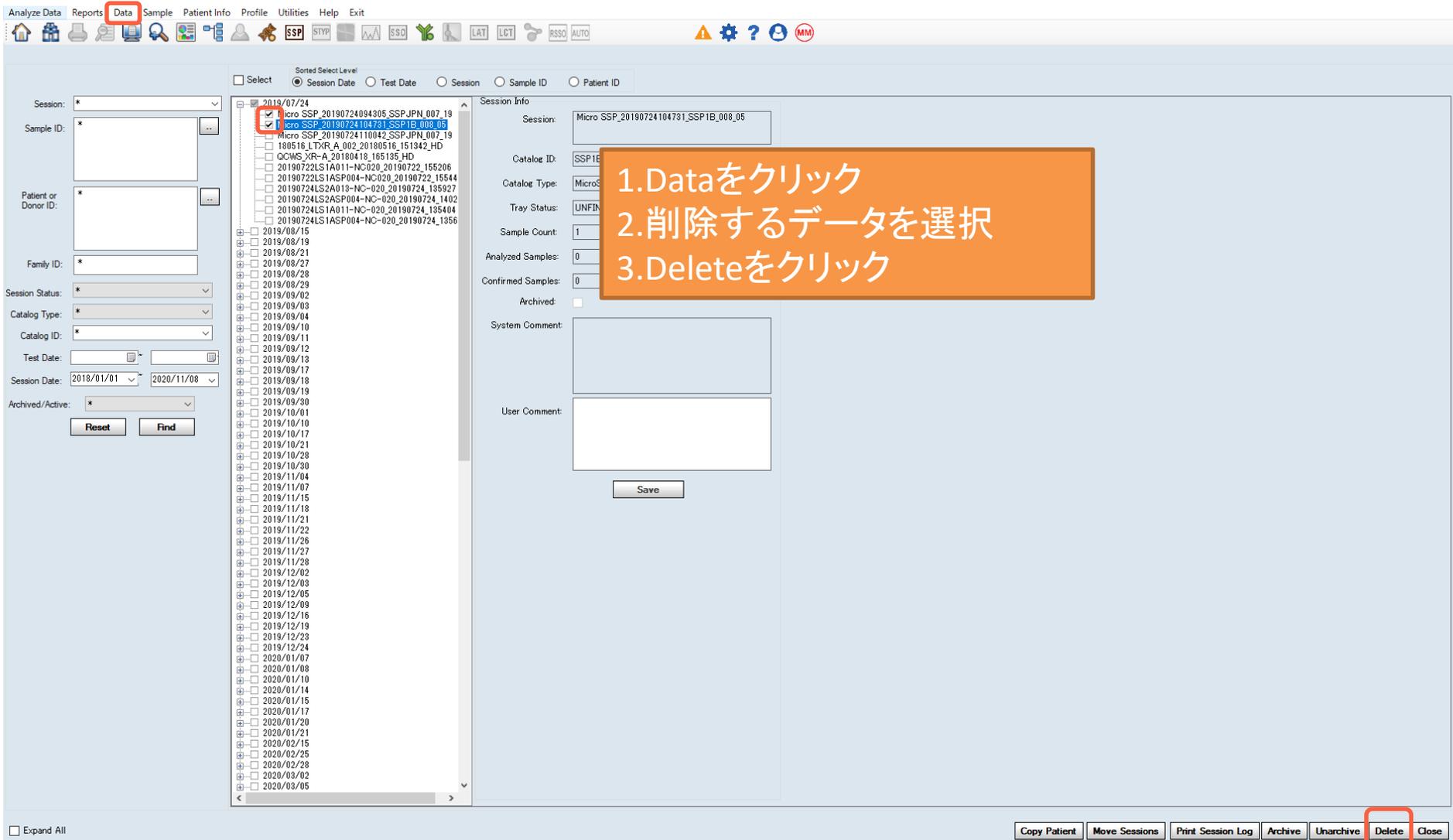
The screenshot shows the HLA Fusion software interface. The top menu bar includes 'Analyze Data', 'Reports', 'Data', 'Sample', 'Patient Info', 'Profile', 'Utilities', 'Help', and 'Exit'. The 'Data' menu is highlighted with a red box. Below the menu is a toolbar with various icons. The main interface is divided into several sections: a search filter section on the left, a central Navigator panel, and a 'Session Info' section on the right. The Navigator panel shows a list of sessions with checkboxes and dates. The search filter section includes fields for 'Session Date', 'Test Date', 'Session', 'Sample ID', and 'Patient ID'. The 'Session Date' field is highlighted with a red box, and the 'Find' button is also highlighted. A yellow box highlights the 'Test Date', 'Session Date', and 'Archived/Active' fields, along with 'Reset' and 'Find' buttons. An orange box contains a list of instructions in Japanese.

1. Dataをクリック
2. Session Date欄で表示する日にちを選択
3. Findをクリック
4. 2で選択した期間のデータがNavigatorに表示

Test Date: [] []
Session Date: 2018/01/01 [] ~ 2020/11/08 []
Archived/Active: * []
Reset Find

Expand All Copy Patient Move Sessions Print Session Log Archive Unarchive Delete Close

データの削除



Analyze Data Reports **Data** Sample Patient Info Profile Utilities Help Exit

Sorted Select Level
 Select Session Date Test Date Session Sample ID Patient ID

Session: *
Sample ID: *
Patient or Donor ID: *
Family ID: *
Session Status: *
Catalog Type: *
Catalog ID: *
Test Date:
Session Date: 2018/01/01 ~ 2020/11/08
Archived/Active: *

2019/07/24
 Micro SSP_20190724104781_SSP1B_008_05
 Micro SSP_20190724110042_SSP1B_007_19
 180516_LTXR_A_002_20180516_151342_HD
 QCWS_XR-A_20180418_165135_HD
 20190722LSIA011-NC020_20190722_155206
 20190722LSIASP004-NC020_20190722_15544
 20190724LS2A015-NC-020_20190724_135927
 20190724LS2ASP004-NC-020_20190724_1402
 20190724LSIA011-NC-020_20190724_135404
 20190724LSIASP004-NC-020_20190724_1356

Session Info
Session: Micro SSP_20190724104781_SSP1B_008_05
Catalog ID: SSP1B
Catalog Type: MicroS
Tray Status: UNFIN
Sample Count: 1
Analyzed Samples: 0
Confirmed Samples: 0
Archived:
System Comment:
User Comment:
Save

1. Dataをクリック
2. 削除するデータを選択
3. Deleteをクリック

Expand All

Copy Patient Move Sessions Print Session Log Archive Unarchive **Delete** Close

レポートの作成

作成方法

The screenshot displays the software's main interface with the 'Reports' menu highlighted in red. A dropdown menu is open, showing options: 'Antibody Custom' (highlighted in red), 'Antibody Screening/Identification', 'Antibody Screening Results', and 'Single Antigen Report'. The 'Antibody Custom' option is selected, leading to the 'Custom Antibody Screening Report Setup' dialog box.

The dialog box, titled 'HLA Fusion™', contains several sections for configuring the report:

- Lab Information:** Includes a dropdown for 'LABScreen' and a 'Setup' button (highlighted in red).
- Patient Information:** Features 'Check All' and 'Uncheck All' buttons, and a list of checkboxes for fields like Patient ID, Project Type, SSN, Ethnicity, etc.
- Test Configuration:** Includes 'Check All' and 'Uncheck All' buttons, and checkboxes for 'User Settings' and 'NJ and PC Values'.
- Overall Results/Assignments:** Features 'Check All' and 'Uncheck All' buttons, and checkboxes for 'Overall Pos/Neg', '% PRA', and 'New Antibody'.
- Epitope Analysis Results:** Includes 'Check All' and 'Uncheck All' buttons, and checkboxes for 'Antibody Specificity' and 'CREG Analysis Details'.
- Tail Analysis Results:** Features 'Check All' and 'Uncheck All' buttons, and checkboxes for 'Antibody Specificity' and 'Tail Analysis Details'.
- Test and Catalog Details:** Includes 'Check All' and 'Uncheck All' buttons, and checkboxes for 'Bead ID or Test Well', 'Test Values', and 'Sero Specificity'.
- Cutoff Summary:** Features checkboxes for 'Bead MFI Chart', 'Raw Data', and 'Sort Antigen Using HLA Order'.

At the bottom of the dialog box, there are buttons for 'Check All', 'Uncheck All', 'Save', 'Delete', and 'Cancel'. An orange callout box at the bottom right of the dialog contains the text: レポートに出力する項目を選択 (Select items to output to the report).

表示例-2

Epitope Analysis

Class I	Specificity DSA	TP	FN	Mean (Baseline) of Positives
B45		1	0	26434.08
B76		1	0	24681.3
B44		2	0	23915
A33		2	0	21937.27
A68				
A34				
A26		1	0	19445.58
A31		1	0	19219.48
A66		2	0	18255.89
A25		1	0	17949.33
B82		1	0	17663.97
A69		1	0	17441.25
A74		1	0	16800.00
A29				
A3				

DSA情報はドナー情報を入力したときのみ表示

CREG Table

A Locus:

- Strong Cross-reactivity
- Cross-reactivity
- CREG (Cross-reactivity Group)

B Locus:

- Strong Cross-reactivity
- Cross-reactivity
- CREG (Cross-reactivity Group)

○ Red Circle: DSA Positive
○ Blue Circle: Non DSA Positive
○ Yellow Circle: DSA Negative

Epitope Analysis Results

Antibody Specificity (REQUIRED for this group)

CREG Analysis Details:
TP, FN, Mean (Raw) of Positives

CREG Chart, Circle DSA

Test Configuration

User Settings:
Excluded Antigens, Positive Re-Threshold, Normalization Formula Level

NC and PC Values, % PRA Threshold and Cutoffs by Region

Overall Results/Assignments

Overall Pos/Neg Other
 % PRA % Donor
 Antibody New
 Possible Epitope Amino Acid

Epitope Analysis Results

Allele Specificity
 Cutoff Summary
 Bead MFI Chart
 Raw Data
 Sort Antigens
 Rxn Score

表示例-3

×

Tail Analysis Results

Antibody Specificity (REQUIRED for this)

Tail Analysis Details:
TP/FP/FN/TN, R Value, Average Score, % Inclusion, Strength Index

Manual Tail Assignment

Test and Catalog Details

Bead ID or Test Well (REQUIRED for this)

Test Values: Rxn, Raw, Normalized, Count

SFI Raw, SFI Normal

Sero Specificity

Allele Specificity

Sort by: Bead ID ▼

ASC DESC

Test and Catalog Details

Bead ID or Test Well (REQUIRED for this)

Test Values: Rxn, Raw, Normalized, Count

SFI Raw, SFI Normal

Sero Specificity

Allele Specificity

Sort by: Normalized ▼

ASC DESC

ソートする項目の変更可能

Test Details							Patient Type	
Bead	Rxn	Raw	SFI Raw	Normal	SFINormal	Cnt	Specificity	Allele Specificity
001		20.77					157	
002		12569.04					161	
003	1	48.44		27.67		171	A1	A*01:01
004	8	21913.96		21893.19		146	A2	A*02:01
005	8	10781.83		10761.06		149	A2	A*02:03
006	8	22007.99		21987.22		139	A2	A*02:06
007	1	33.59		12.82		166	A3	A*03:01
008	1	50.34		14.13		168	A11	A*11:01
009	1	56.35		9.06		186	A11	A*11:02
010	4	699.61		676.73		169	A23	A*23:01
011	4	1355.66		1334.89		181	A24	A*24:02
012	4	1330.94		1310.17		145	A24	A*24:03
013	1	54.05		16.87		152	A25	A*25:01
014	1	70.53		7.29		172	A26	A*26:01
015	2	162.38		141.61		166	A29	A*29:01
016	4	1443.46		1422.69		170	B27, Bw4	B*27:05

ビーズID順

Test Details							Patient Type	
Bead	Rxn	Raw	SFI Raw	Normal	SFINormal	Cnt	Specificity	Allele Specificity
077	8	27684.38		27619.76		146	B73, Bw6	B*73:01
089	8	27331.31		27250.91		100	Cw7	C*07:02
006	8	22007.99		21987.22		139	A2	A*02:06
004	8	21913.96		21893.19		146	A2	A*02:01
095	8	20273.42		20169.45		155	Cw17	
031	8	19961.05		19909.16		163	A69	A*69:01
030	8	17258.31		17154.54		138	A68	A*68:02
096	8	16771.27		16715.59		151	Cw18	
090	8	13528.64		13482.14		130	Cw8	C*18:02
088	8	12753.6		12601.14		139	Cw6	C*08:01
005	8	10781.83		10761.06		149	A2	C*06:02
8		8232.9		8212.13		146	A68	A*02:03
8		5319.59		5256.5		149	Cw12	A*68:01
8		4882.13		4828.42		137	Cw16	
034	8	4312.45		4291.68		159	B7, Bw6	C*12:03
073	6	3658.86		3608.32		157	B57, Bw4	C*16:01
								B*07:02
								B*57:03

nMFIの値順

表示例-4

✕

Tail Analysis Results

Antibody Specificity (REQUIRED for this)

Tail Analysis Details:

Manual Tail Assignment

Test and Catalog Details

Bead ID or Test Well (REQUIRED for this)

Test Values: Rxn, Raw, Normalized, Count

SFI Raw, SFI Normal

Sero Specificity Sort by: Bead ID

Allele Specificity ASC DESC

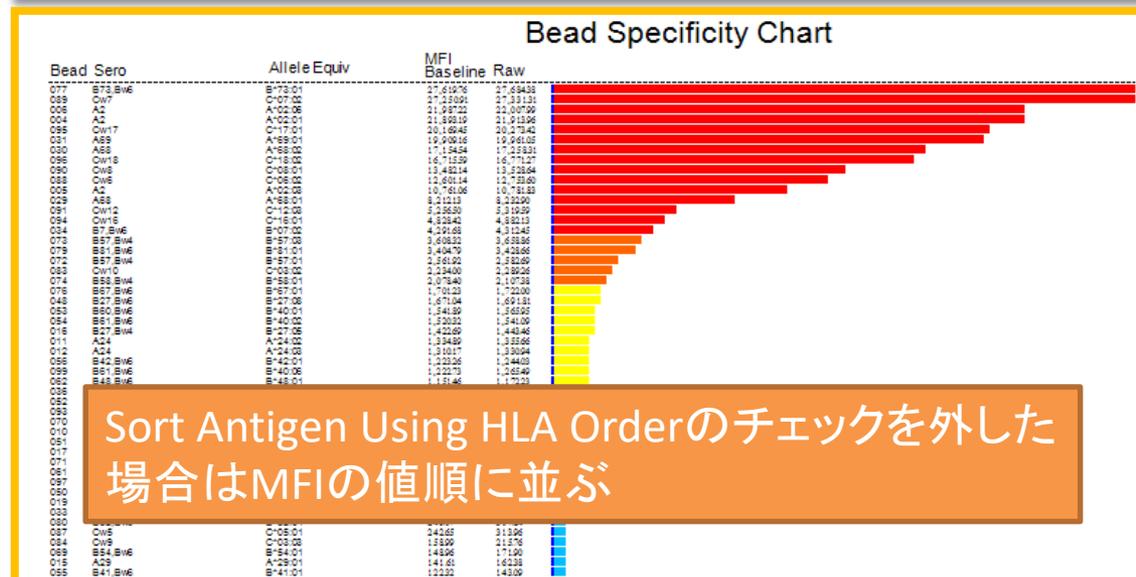
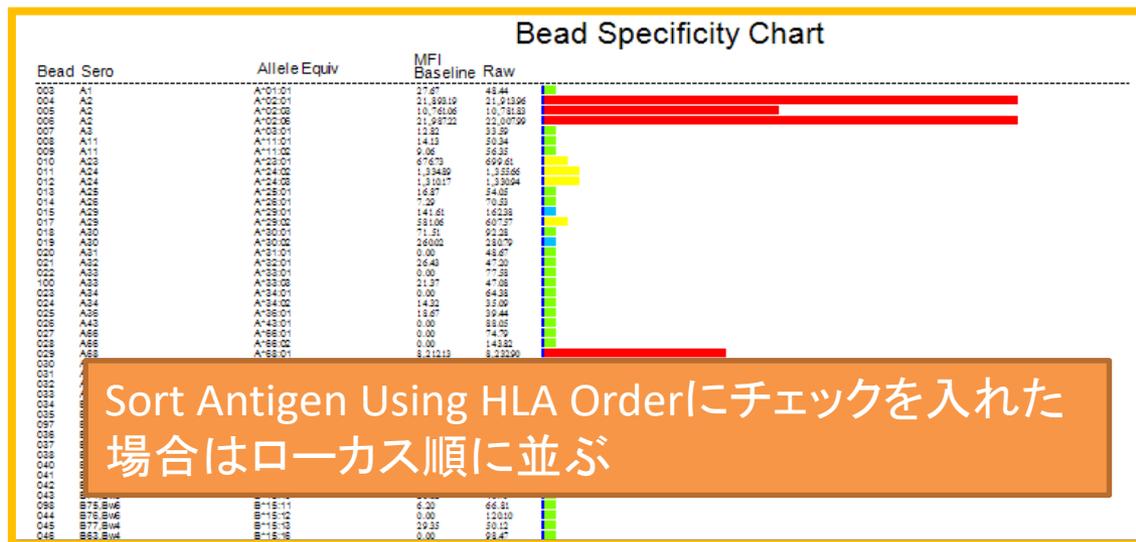
Cutoff Summary

Bead MFI Chart

Raw Data Baseline

Sort Antigen Using HLA Order

Rxn Score Sort Alphanumerically



設定例

Custom Antibody Screening Report Setup

HLA Fusion™

Type or enter the report name*:
LABScreen

Lab Information

Patient Information
Check All **Uncheck All**

- Patient ID, Name (REQUIRED for this group)
- Project Type
- SSN
- Ethnicity, DOB, Gender
- Disease, Status, Blood, Transplant Type
- Address, Phone, Email
- Spouse, Emg. Contact, Employer
- DCN, Hospital, Division
- UNOS CPRA
- Donor Info
- Molecular Typing Sero Typing
- Antibody Assignment
- Match / Mismatch
 - Add MFI Baseline
- Acceptable Antigens
- Unacceptable Antigens
- AM DFC ETKAS DFC
- Unacceptable Epitopes

Sample Information
Check All **Uncheck All**

- Sample ID (REQUIRED) Barcode
- System Comments User Comments
- Sample Source Dilution Factor

Session Information
Check All **Uncheck All**

- Session ID/Date (REQUIRED for this group)
- Luminex Info
- Session Details: Catalog ID, Locus Type, Test Position, Date, NS Sample
- More Tests and Tests Remarks
- Quantiplex/SFI

Test Configuration
Check All **Uncheck All**

- User Settings:
 - Excluded Antigens, Positive Region Threshold, Normalization Formula, Allele Level
- NG and PC Values, % PRA -or- %SA and Cutoffs by Region

Overall Results/Assignments
Check All **Uncheck All**

- Overall Pos/Neg Other
- % PRA % Donor PRA
- Antibody New Antibody
- Possible Epitope Amino Acid Position

Epitope Analysis Results
Check All **Uncheck All**

- Antibody Specificity (REQUIRED for this group)
- CREG Analysis Details:
 - TP, FN, Mean (Raw) of Positives
- CREG Chart, Circle DSA

Tail Analysis Results
Check All **Uncheck All**

- Antibody Specificity (REQUIRED for this)
- Tail Analysis Details:
 - TP/FP/FN/TN, R Value, Average Score, % Inclusion, Strength Index
- Manual Tail Assignment

Test and Catalog Details
Check All **Uncheck All**

- Bead ID or Test Well (REQUIRED for this)
- Test Values: Rxn, Raw, Normalized, Count
- SFI Raw, SFI Normal
- Sero Specificity **Sort by:** Normalized ASC DESC
- Allele Specificity

Cutoff Summary

- Bead MFI Chart
 - Raw Data Baseline
 - Sort Antigen Using HLA Order
- Rxn Score Sort Alphanumerically

Check All **Uncheck All** **Save** **Delete** **Cancel**

ONE LAMBDA

Mixedのレポート-1



Analyze Data **Reports** Data Sample Patient Info Profile Utilities Help Exit

Home Print Search Help SSP STYP SSO LAT LCT

Patient Generic Typing LABType MicroSSP Generic Antibody LABScreen Specialty Statistical Miscellaneous

Patient or Donor ID: * ...
 Session: * ...
 Batch: * ...
 Sample ID: * ...

Sample Summary **LSM Details** Info Close
 LSM Summary

SessionID: _____
 WellPosition: _____
 SampleID: _____
 PatientID: _____

LSM Detail Approved By: _____ Date: _____

Session ID: 20201021_LSM12_021_NC16_20201021_210635
 Catalog: LSM12NC16_021_00

NS Sample: NC16

Background Values											
003	0.29	004	0.46	005	0.53	007	0.52	009	0.48	012	0.57
019	0.5	023	0.31	025	0.57	033	0.59	035	0.55	050	0.5
065	0.61	068	2.12	097	2.16	NC	0.45				

PC 0.46

Class I	Positive Cutoff:	1.5	Negative Cutoff:	1.2	NC Threshold:	50	Class I	Sensitivity/MFI:	0
Class II	Positive Cutoff:	1.5	Negative Cutoff:	1.2	NC Threshold:	50	Class II	Sensitivity/MFI:	0
MIC	Positive Cutoff:	1.5	Negative Cutoff:	1.2	NC Threshold:	50	HNA	Sensitivity/MFI:	0

Patient ID:	Patient Name:	Local ID:
Status:	Transplant Type:	
	Class I:	Class II:

Overall	Bead	Result	Raw Data	Ratio	Count	Overall	Bead	Result	Raw Data	Ratio	Count	Sample Date
Negative	003	Negative	0.5	0.00	142	Negative	025	Negative	0.78	0.01	121	NC 0.42 148
	004	Negative	0.4	0.00	145		033	Negative	0.48	0.00	153	PC 0.29 148
	005	Negative	0.44	0.00	140		035	Negative	0.49	0.00	142	PC/NC Ratio 0.69
	007	Negative	0.38	0.00	157		050	Negative	0.48	0.00	124	
	009	Negative	0.5	0.00	151		065	Negative	0.64	0.00	143	
	012	Negative	0.54	0.00	142							
	013	Negative	0.44	0.00	183							
	014	Negative	0.45	0.00	153							
	016	Negative	0.55	0.00	122							
	017	Negative	0.56	0.00	155							
	019	Negative	0.72	0.01	100							
	023	Negative	0.36	0.00	139							
	MIC											
Overall	Bead	Result	Raw Data	Ratio	Count							
Negative	068	Negative	2.14	0.03	140							
	097	Negative	1.53	0.02	121							

Sec. Ab: _____ Treatment: _____
 Saved By: 1,1 Saved Date: 10/26, 2020
 Confirmed By: _____ Confirmed Date: _____
 Comment: Low PC <=500 (002=0.29). Low PC/NC Ratio.
 User Comment: _____

1, 1

11/8/2020 HLA Fusion™ 4.4.0.13925 Page 1 of 1

Mixedのレポート-2



Analyze Data **Reports** Data Sample Patient Info Profile Utilities Help Exit

Patient Generic Typing LABType MicroSSP Generic Antibody LABScreen Specialty Statistics

Sample Summary

- LSM Details
- LSM Summary**
- LSM Overview

Patient or Donor ID: *
 Session: *
 Batch: *
 Sample ID: *

SessionID
 WellPosition
 SampleID
 CatalogID

LSM Summary

Approved By: _____ Date: _____

Session ID: 20201021_LSM12_021_NC16_20201021_210635
 Catalog ID: LSM12NC16_021_00

NS Sample: NC16

Background Value

003	0.29	004	0.46	005	0.53	007	0.52	009	0.48	012	0.57	013	0.42	014	0.38	016	0.52	017	0.51
019	0.5	023	0.31	025	0.57	033	0.59	035	0.55	050	0.5	065	0.61	068	2.12	097	2.16	NC	0.45
PC 0.46																			

Class I Positive Cutoff: 1.5 Negative Cutoff: 1.2 NC Threshold 50 Class I Sensitivity/MFI: 0
 Class II Positive Cutoff: 1.5 Negative Cutoff: 1.2 NC Threshold 50 Class II Sensitivity/MFI: 0
 MIC Positive Cutoff: 1.5 Negative Cutoff: 1.2 NC Threshold 50 HNA Sensitivity/MFI: 0

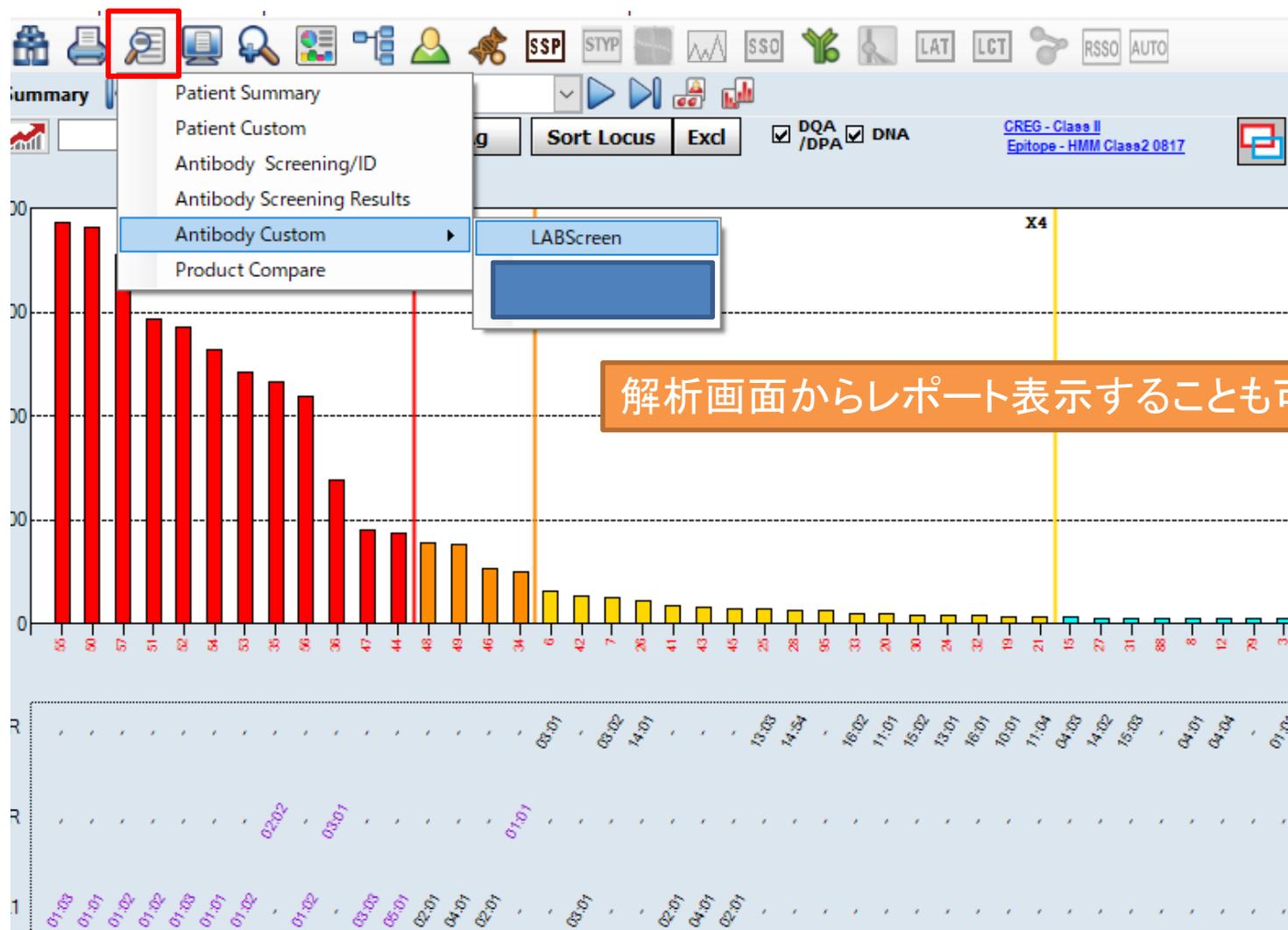
[WellPosition] Sample ID	Class I	Class II	MIC	←NC→		←PC→		PCNC
				Raw	Count	Raw	Count	
[28(1,D) 24S3	Negative	Negative	Negative	0.42	148	0.29	148	0.69

PatientID: _____ Patient Name: _____
 Sec. Ab: _____ Treatment Saved Date: 10/26/2020
 Saved By: 1,1 Confirmed Date: _____ Sample Date: _____
 Comment: Low PC <500 (002=0.29). Low PCNC Ratio.

User Comment

1,1

解析画面からレポートの表示

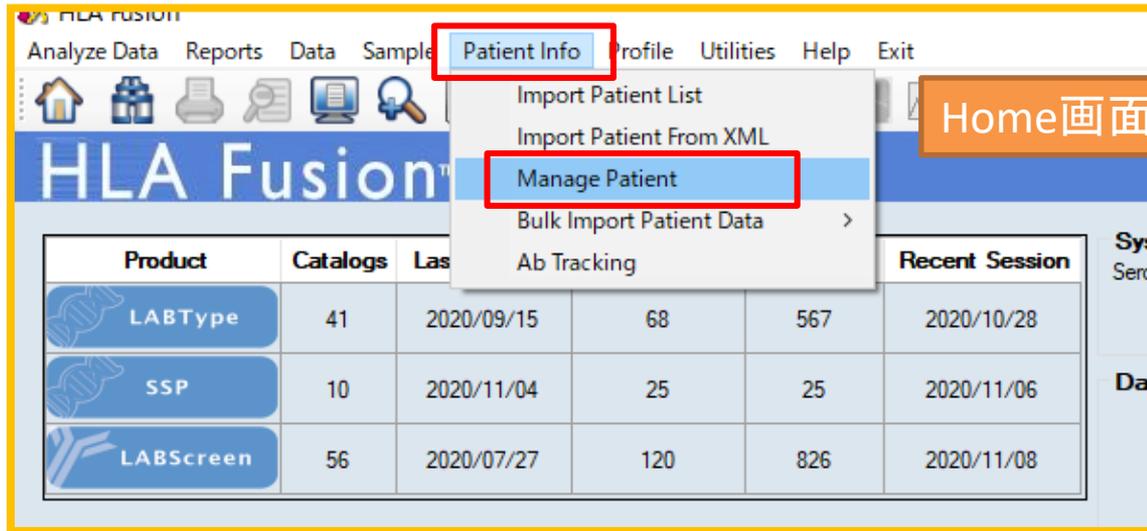


患者情報の登録

登録方法

- マニュアルで入力
 - Home画面より登録
 - 解析画面より登録
 - 解析している結果に関連づけされる
 - 同じサンプルIDのデータにまとめて関連づけされる
- csvファイルを使用してまとめてインポート

マニュアルでの入力方法



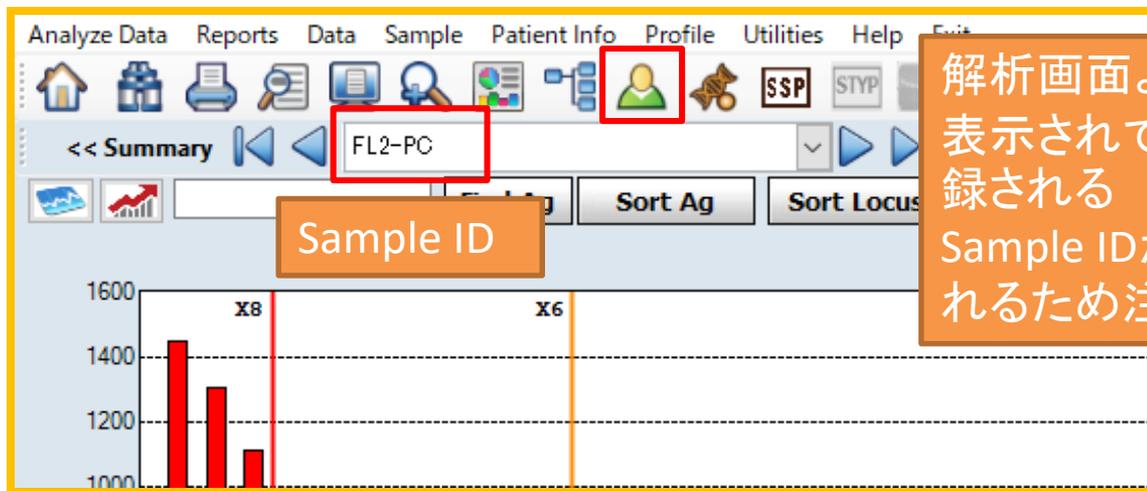
HLA Fusion

Analyze Data Reports Data Sample Patient Info Profile Utilities Help Exit

Import Patient List
Import Patient From XML
Manage Patient
Bulk Import Patient Data
Ab Tracking

Product	Catalogs	Last			Recent Session
LABType	41	2020/09/15	68	567	2020/10/28
SSP	10	2020/11/04	25	25	2020/11/06
LABScreen	56	2020/07/27	120	826	2020/11/08

Home画面より入力



Analyze Data Reports Data Sample Patient Info Profile Utilities Help Exit

FL2-PC

Sample ID

Sort Ag Sort Locus

1600
1400
1200
1000

X8 X6

解析画面より入力

表示されているデータに患者情報が登録される

Sample IDが同じ他のデータにも登録されるため注意

患者情報の入力

Patient/Donor Information

General Info

Enforce ISBT format for Patient/Donor ID

Patient/Donor Info

Patient or Donor ID * ... C

Patient/Donor Flag Patient

Family ID

First Name *

Middle Name

Last Name *

Birthdate <Select Date>

Gender Male Female LINK

City

State/Province

Country

Postal Code

Region

Phone

Mobile

Work

Histo PatientID

MRN

Spouse Info

Spouse Name

Emergency

Blood Type

Phone

Donor ID

Relat with

ONE LAMBDA

赤枠は必須項目
IDは一度登録すると変更が
できないため注意

Patient/Donor Information

General Info HLA Tests Creatinine Tests Notable Events Treatment History Crossmatch Result

ID: Patient 160 Name: mitoe, nishimoto

Antibody Tested:

HLA Assignments Molecular

Class I			Class II							
A	B	C	DRB1	DRB3	DRB4	DRB5	DQB1	DQA1	DPB1	DPA1
02:10	46:01	01:02	13:02				03:03		03:01	
24:02	39:01	07:02	13:02				04:01		03:01	

HLA Assignments Serology Only digits, "BLANK", "Low", "-" and "/" are accepted in serology fields.

Class I				Class II			
A	B	Bw	Cw	DR	DR(51,52,53)	DQ	DP
2	46		1	13		9	3
24	39		7	13		4	3

Show UNOS Web Calculator

Other

MICA MICB KIR

Antibody

Class I

Class II

MIC Ar

Unacce

Accept

Unaccept

Class I

Class II

MIC

HLA Test Comments

Edit / Update

ONE LAMBDA

必須項目を入力するとタブが表示されるため、
タイピング情報を入力してSave
「*」は不要

ドナー情報の入力

Patient/Donor Information

General Info | HLA Tests

Enforce ISBT format for Patient/Donor ID

Patient/Donor Info

Patient or Donor ID * 111

Patient/Donor Flag Donor

Family ID

First Name * 1a

Middle Name

Last Name * 1b1

Birthdate <Select Date>

Gender

City

State/Province

Country

Postal Code

Region

Phone

Mobile

Work

Histo PatientID

MRN

Spouse Info

Spouse Name

Emergency

Blood Type

Phone

ONE LAMBDA

赤枠は必須項目
IDは一度登録すると変更が
できないため注意

Patient/Donor Information

General Info | HLA Tests

ID: Donor228 Name: yosuke do, harada

Associate Sample IDs View Sample Summary

AM DFC ETKAS DFC

Export to UNet Antibody Tested:

HLA Assignments Molecular

Class I			Class II							
A	B	C	DRB1	DRB3	DRB4	DRB5	DQB1	DQA1	DPB1	DPA1
02:06	07:02	03:04	01:01				05:01			
24:02	35:01	03:04	04:05				04:01			

HLA Assignments Serology Only dirits, "BLANK", "Low" - and / are accepted in serology fields.

Class I				Class II			
A	B	Bw	Ow	DR	DR(51,52,53)	DQ	DP
2	7	10		1		5	
24	35	10		4		4	

NMDP HaploStats

CPRA Show UNOS Web Calculator

Other

MICA MICB KIR

Antibody Assignments

Class I Antibody

Class II Antibody

MIC Antibody Specimen

Unacceptable Antigen

Acceptable Antigen

Unacceptable Epitope

Class I

Class II

MIC

HLA Test Comments

Edit / Update

Save Close

ONE LAMBDA

必須項目を入力するとタブが表示されるため、
タイピング情報を入力してSave
「*」は不要

ドナー情報との関連づけ

必ずを入れる

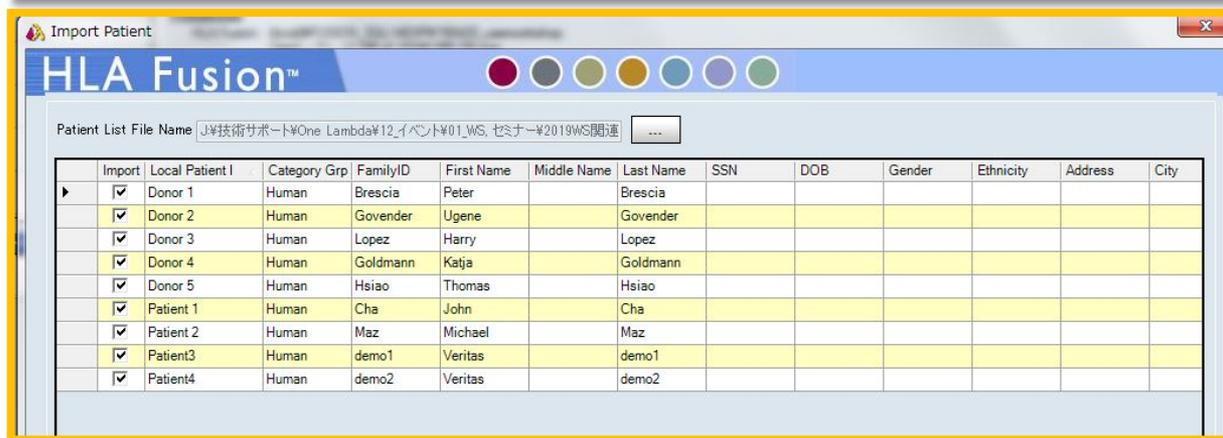
患者情報を表示し「Associate Donor IDs」をクリック
事前に登録したドナーIDを選択し、右側に移動して
OKをクリック
複数ドナーの登録可能

Donor ID	Relationship with patient	Association Comments	Comments
1235	with patient		

CSVファイルの作成

	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る
* ひな型をご希望の方はご連絡ください *



Import Patient

HLA Fusion™

Patient List File Name: [日本語サポート#One_Lambda#12_イベント#01_WS_セミナー#2019WS関連] ...

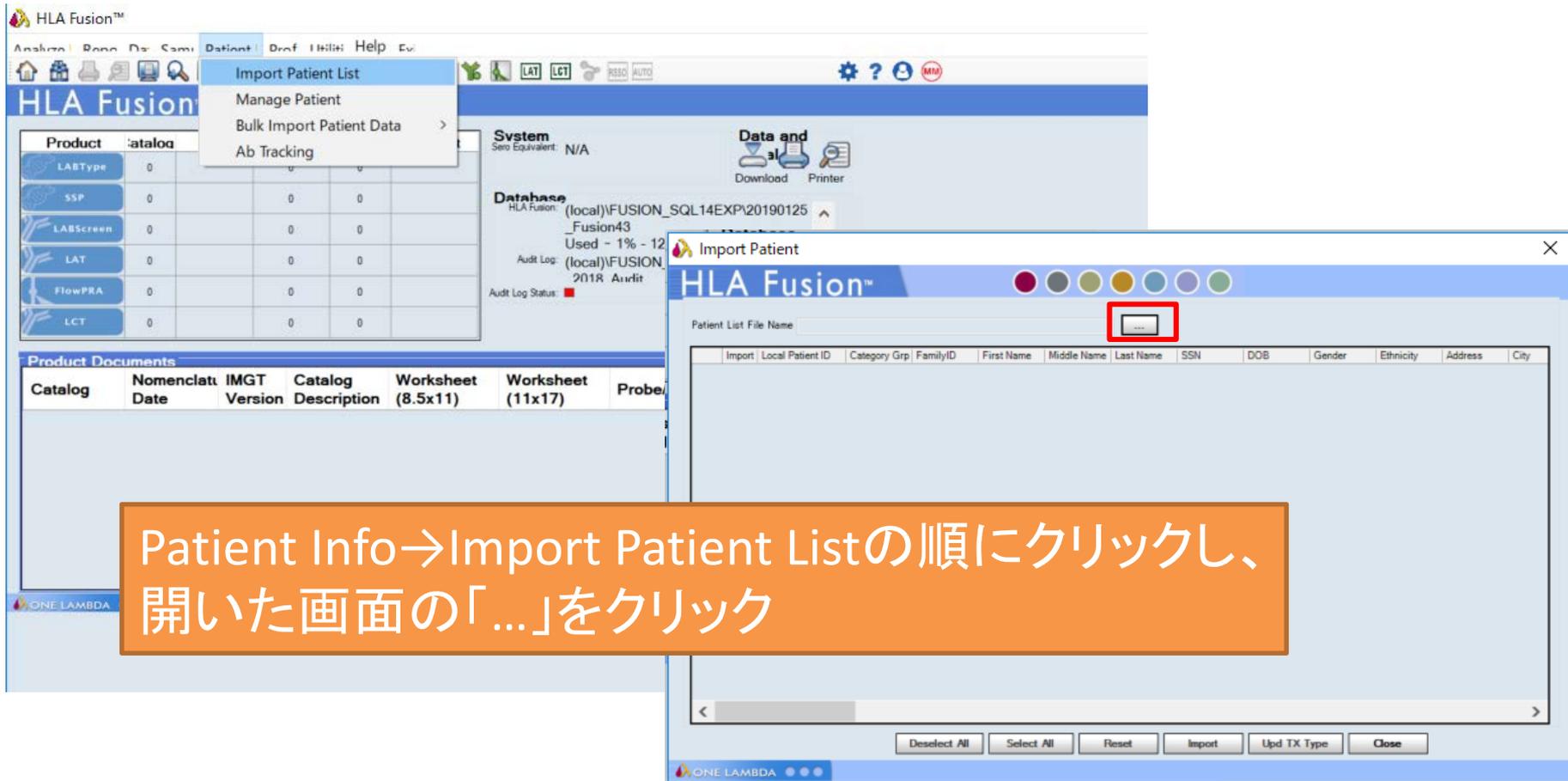
Import	Local Patient I	Category Grp	FamilyID	First Name	Middle Name	Last Name	SSN	DOB	Gender	Ethnicity	Address	City
<input checked="" type="checkbox"/>	Donor 1	Human	Brescia	Peter		Brescia						
<input checked="" type="checkbox"/>	Donor 2	Human	Govender	Ugene		Govender						
<input checked="" type="checkbox"/>	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。

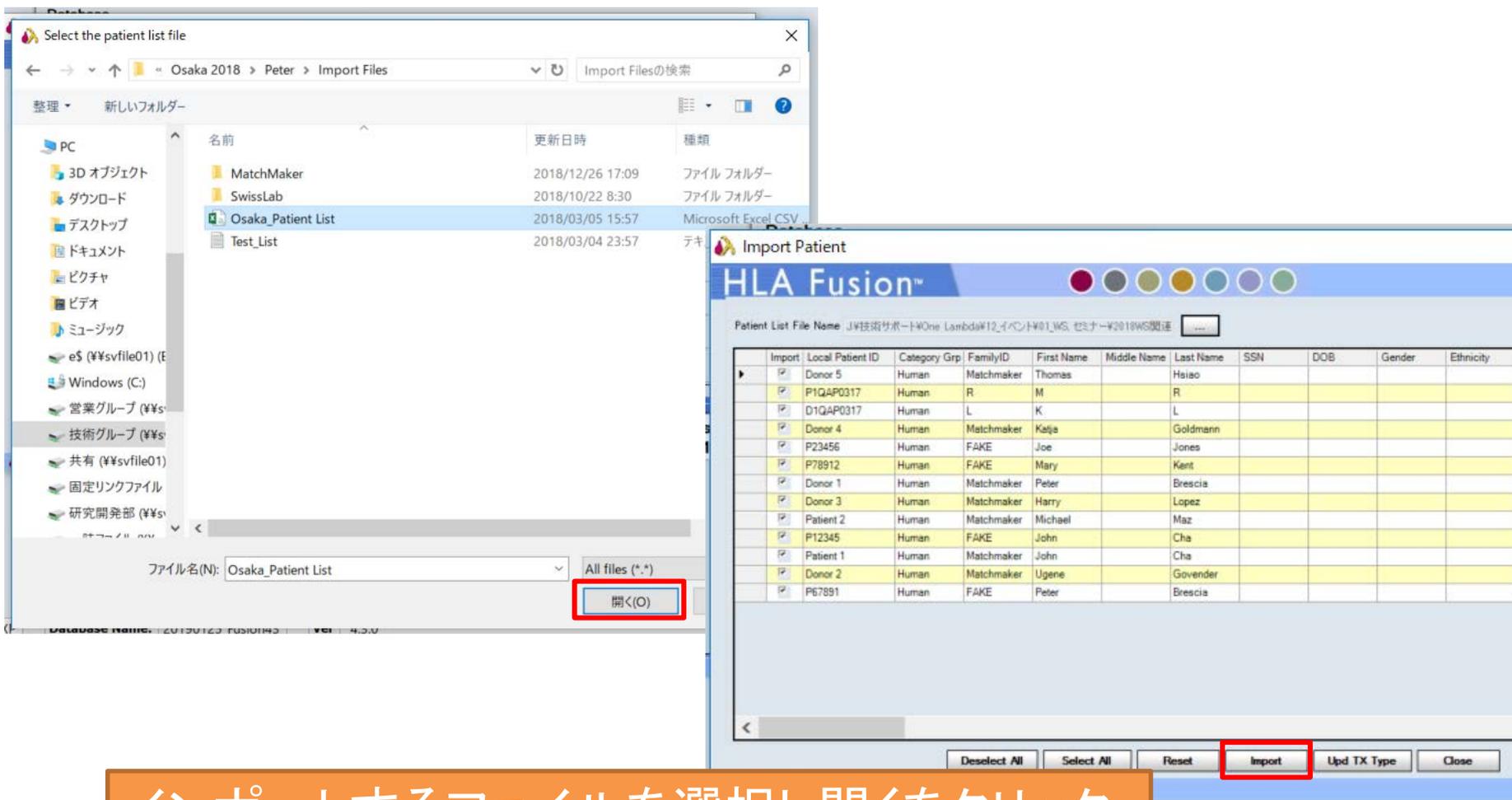
CSVファイルのインポート-1



The screenshot shows the HLA Fusion software interface. The 'Patient' menu is open, highlighting 'Import Patient List'. An 'Import Patient' dialog box is open in the foreground, with a red box around the '...' button next to the 'Patient List File Name' field. The dialog box contains a table with columns: Import, Local Patient ID, Category Grp, FamilyID, First Name, Middle Name, Last Name, SSN, DOB, Gender, Ethnicity, Address, City. At the bottom of the dialog are buttons: 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

CSVファイルのインポート-2

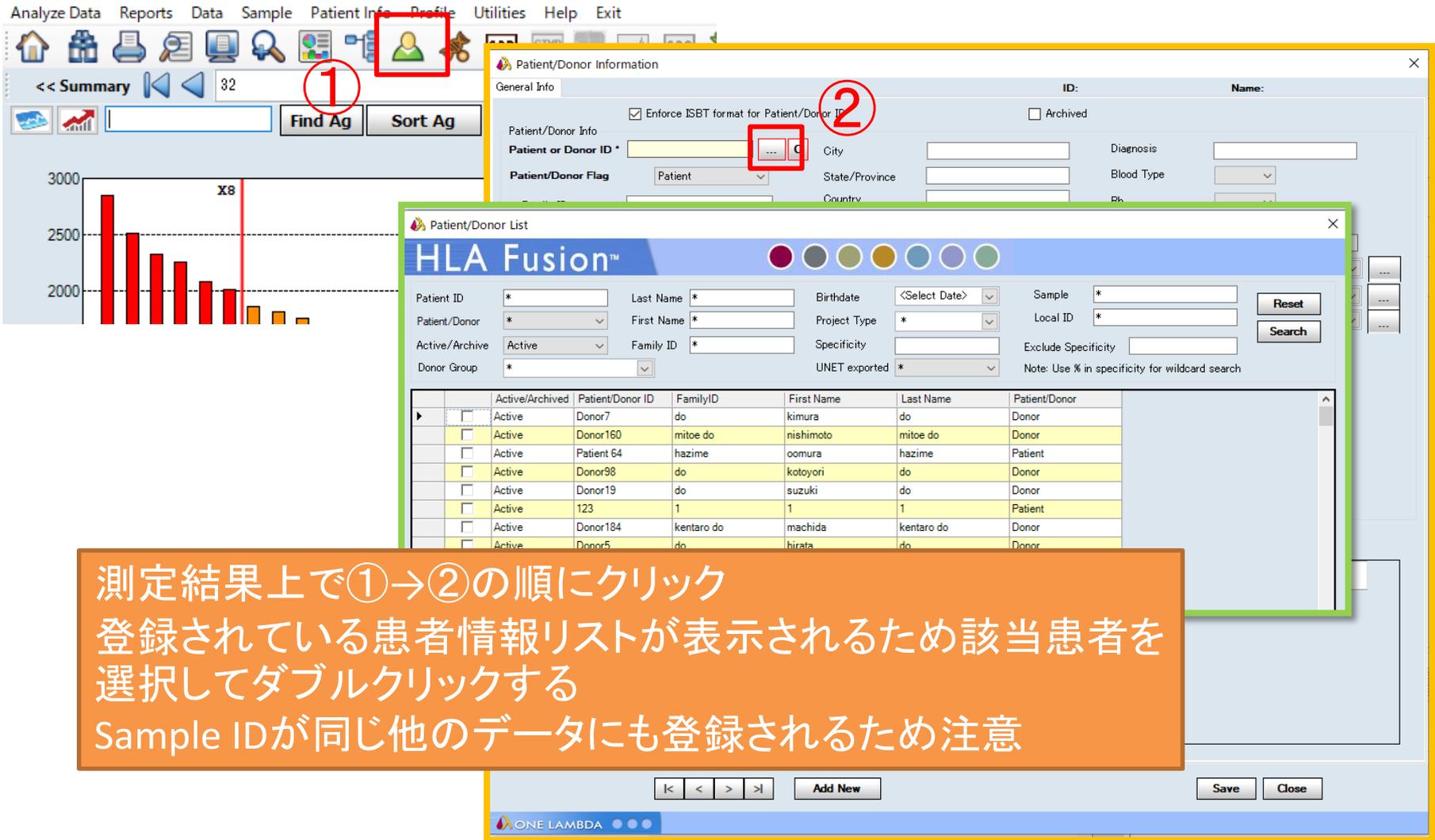


The image shows two overlapping windows from the HLA Fusion software. The left window is a file explorer titled "Select the patient list file" showing a directory structure with "Osaka_Patient List" selected. The right window is the "Import Patient" dialog, which displays a table of patient data. The "Import" button in the bottom right of the dialog is highlighted with a red box.

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

過去のデータとの関連づけ-1



Analyze Data Reports Data Sample Patient Info Profile Utilities Help Exit

<< Summary < < 32

Find Ag Sort Ag

3000
2500
2000

X8

1

2

Patient/Donor Information

General Info

Enforce ISBT format for Patient/Donor ID Archived

ID: Name:

Patient/Donor Info

Patient/Donor ID * ... City

Patient/Donor Flag Patient State/Province Blood Type

Country

Patient/Donor List

HLA Fusion™

Patient ID * Last Name * Birthdate <Select Date> Sample * Reset

Patient/Donor * First Name * Project Type * Local ID * Search

Active/Archive Active Family ID * Specificity Exclude Specificity

Donor Group * UNET exported * Note: Use % in specificity for wildcard search

	Active/Archived	Patient/Donor ID	FamilyID	First Name	Last Name	Patient/Donor
▶	<input type="checkbox"/>	Active Donor7	do	kimura	do	Donor
	<input type="checkbox"/>	Active Donor160	mitoe do	nishimoto	mitoe do	Donor
	<input type="checkbox"/>	Active Patient 64	hazime	oomura	hazime	Patient
	<input type="checkbox"/>	Active Donor98	do	kotoyori	do	Donor
	<input type="checkbox"/>	Active Donor19	do	suzuki	do	Donor
	<input type="checkbox"/>	Active 123	1	1	1	Patient
	<input type="checkbox"/>	Active Donor184	kentarodo	machida	kentarodo	Donor
	<input type="checkbox"/>	Active Donor5	do	hirata	do	Donor

ONE LAMBDA

Add New Save Close

測定結果上で①→②の順にクリック

登録されている患者情報リストが表示されるため該当患者を選択してダブルクリックする

Sample IDが同じ他のデータにも登録されるため注意

過去のデータとの関連づけ-2

Patient/Donor Information

General Info | HLA Tests | Creatinine Tests | Notable Events | Treatment History | Crossmatch Result | ID: Patient_93 | Name: PPP, XXX

Enforce ISBT format for Patient/Donor ID Archived

Patient/Donor Info

Patient or Donor ID * Patient_93 ... C City State/Province Diagnosis

Patient/Donor Flag Patient Blood Type

Family ID PPP Country Rh

First Name * XXX Postal Code From Other Facility

Middle Name Region Facility Name

Last Name * PPP Phone Mobile Project Type

Birthdate <Select Date> Work Status

Gender Male Female UNK Fax Transplant Type

Category Group Human Animal Email Address

SSN Employer

Ethnicity

Associate Donor IDs

Spouse Info

Spouse Name Emergency Blood Type Phone

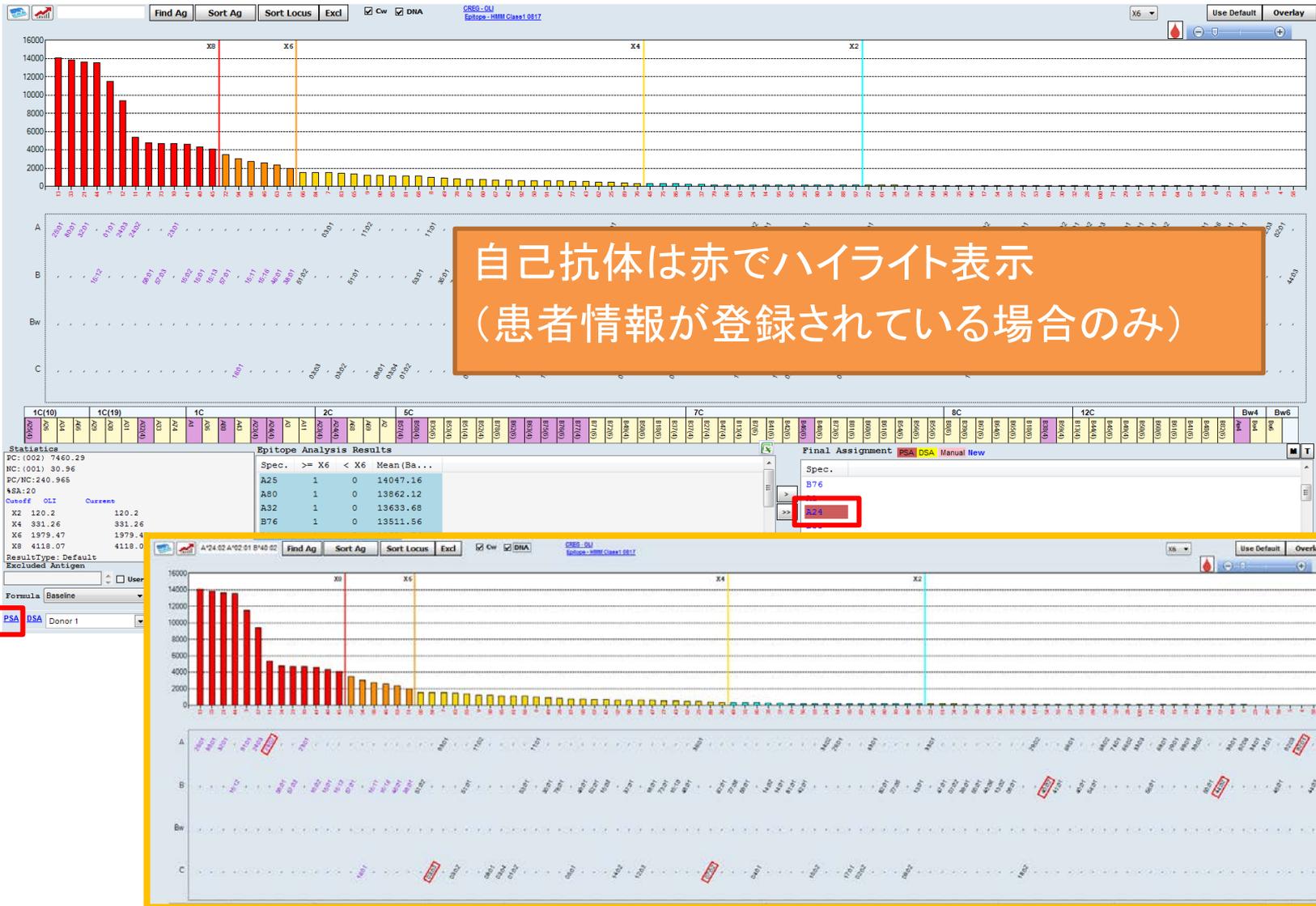
Donor ID	Relationship with patient	Association Comments	Comments
----------	---------------------------	----------------------	----------

Edit / Update | < | << | >> | > | Add New | Export | Delete | Print | Save | Close

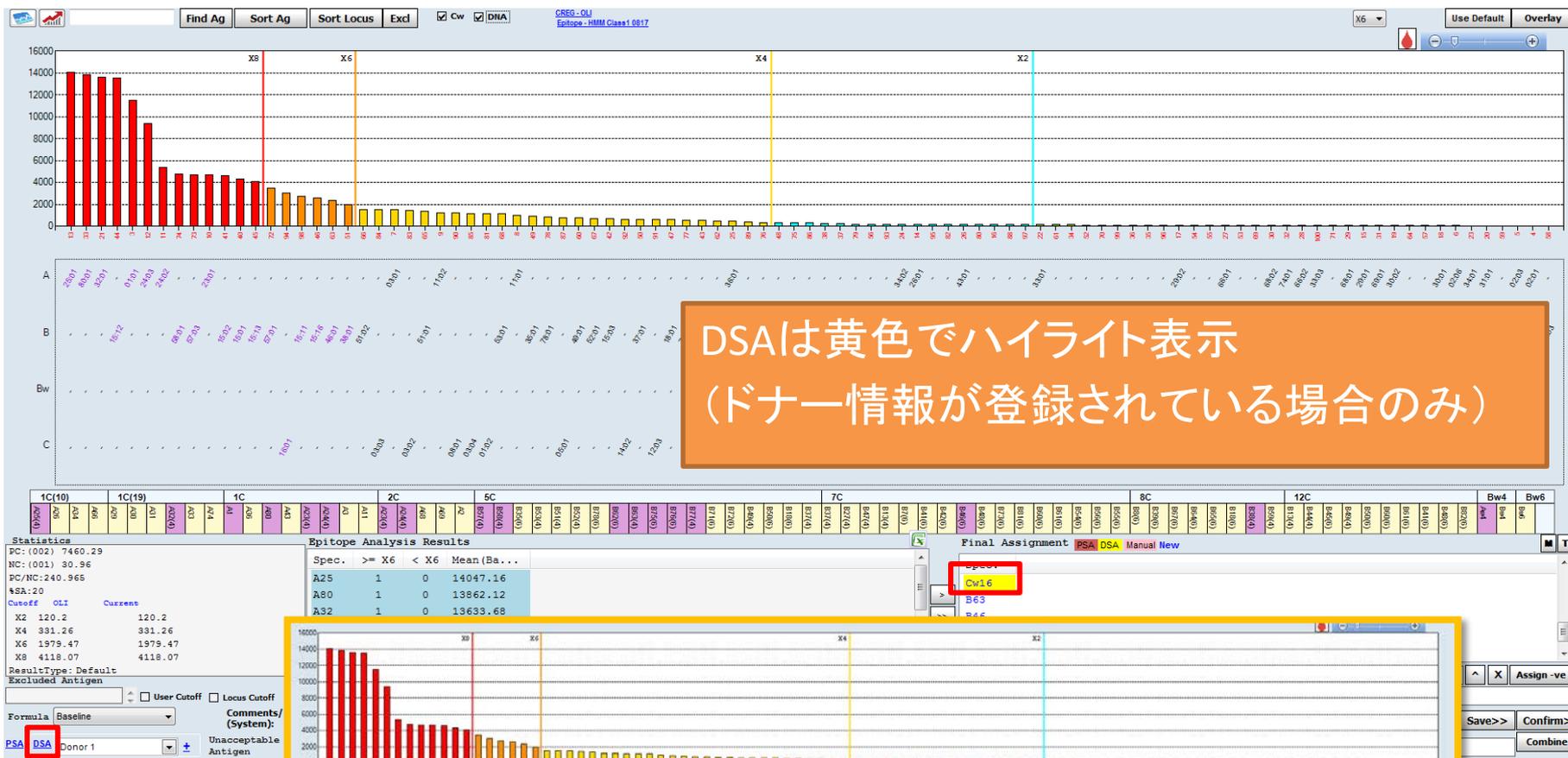
ONE LAMBDA

選択した患者情報が入力されていることを確認し、Edit/Updateにを入れSaveをクリックして終了

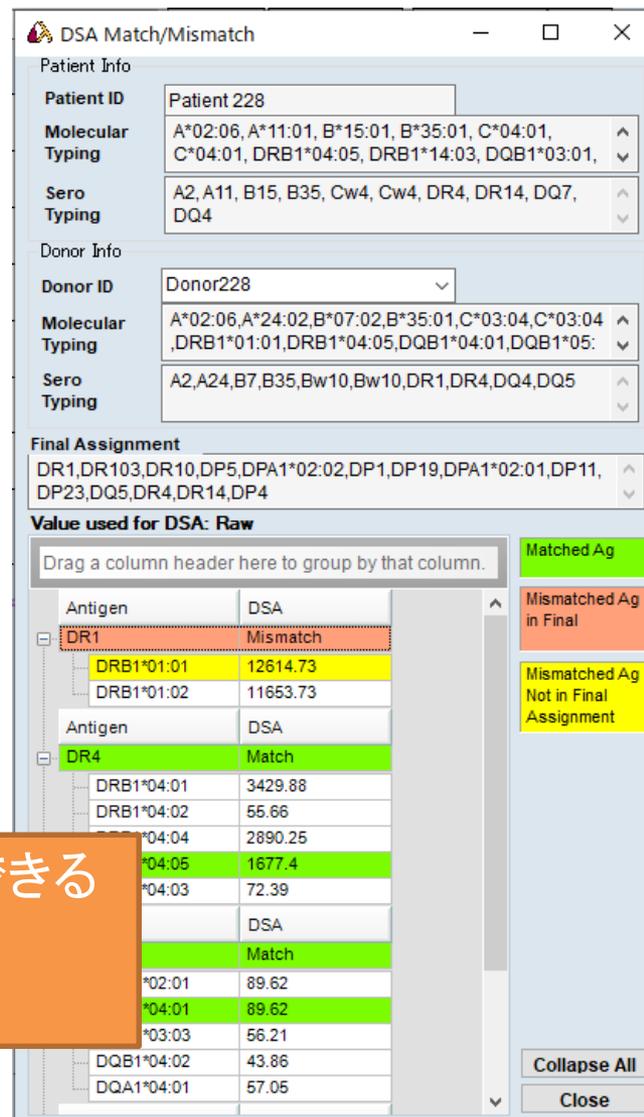
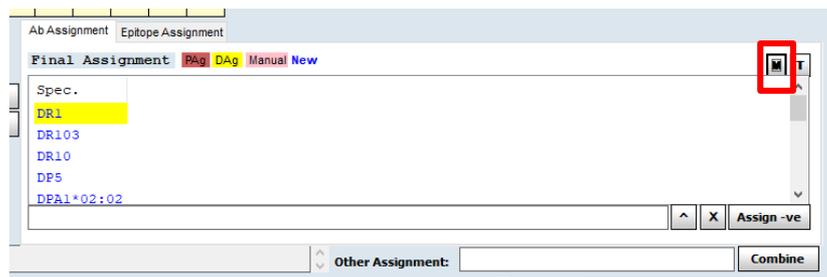
自己抗体の表示



DSAの表示



DSA情報の確認



DSA Match/Mismatch

Patient Info

Patient ID: Patient 228

Molecular Typing: A*02:06, A*11:01, B*15:01, B*35:01, C*04:01, C*04:01, DRB1*04:05, DRB1*14:03, DQB1*03:01

Sero Typing: A2, A11, B15, B35, Cw4, Cw4, DR4, DR14, DQ7, DQ4

Donor Info

Donor ID: Donor228

Molecular Typing: A*02:06, A*24:02, B*07:02, B*35:01, C*03:04, C*03:04, DRB1*01:01, DRB1*04:05, DQB1*04:01, DQB1*05:01

Sero Typing: A2, A24, B7, B35, Bw10, Bw10, DR1, DR4, DQ4, DQ5

Final Assignment: DR1, DR103, DR10, DP5, DPA1*02:02, DP1, DP19, DPA1*02:01, DP11, DP23, DQ5, DR4, DR14, DP4

Value used for DSA: Raw

Drag a column header here to group by that column.

Antigen	DSA
DR1	Mismatch
DRB1*01:01	12614.73
DRB1*01:02	11653.73
DR4	Match
DRB1*04:01	3429.88
DRB1*04:02	55.66
DRB1*04:04	2890.25
DRB1*04:05	1677.4
DRB1*04:03	72.39
	DSA
	Match
	89.62
	89.62
	56.21
DQB1*04:02	43.86
DQA1*04:01	57.05

Matched Ag (Green)

Mismatched Ag in Final (Red)

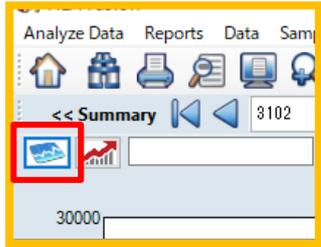
Mismatched Ag Not in Final Assignment (Yellow)

Collapse All

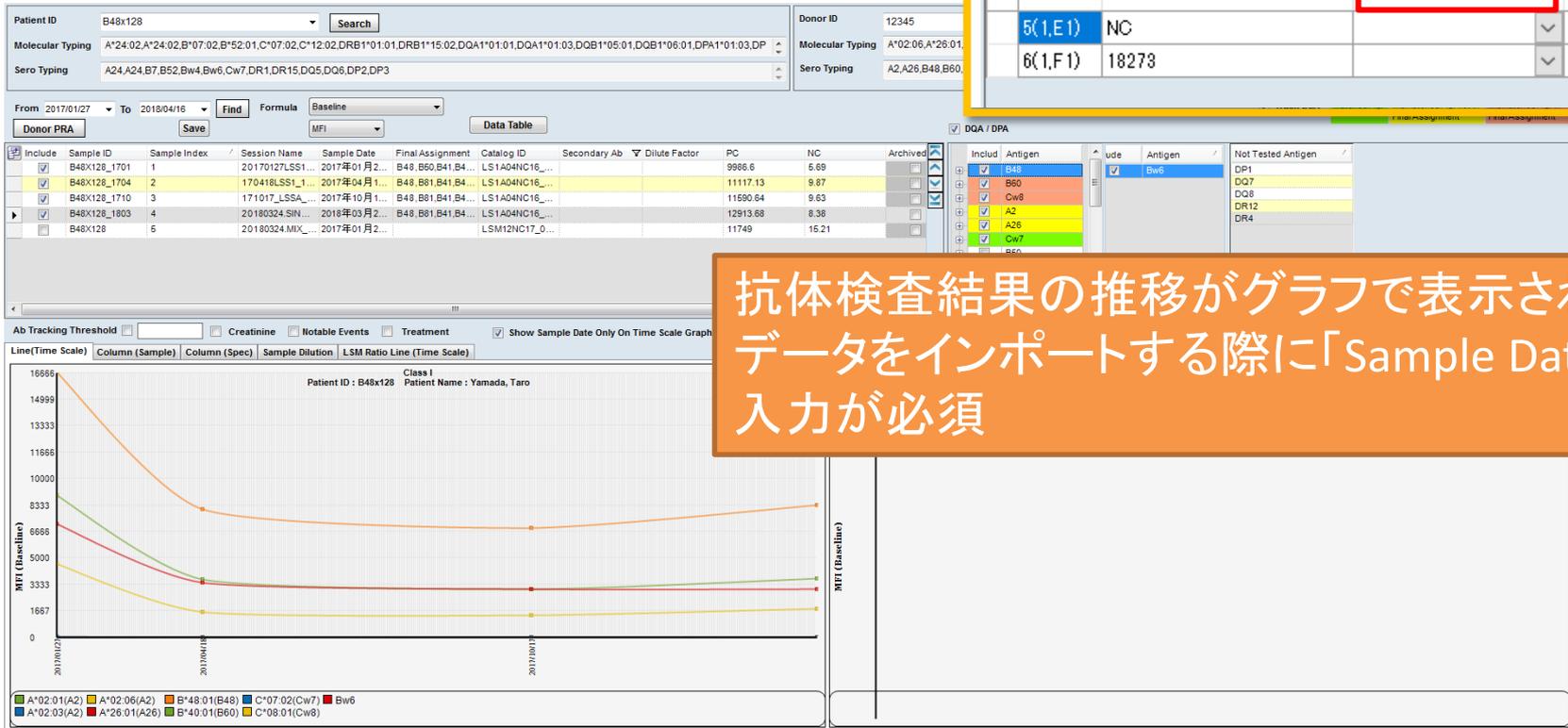
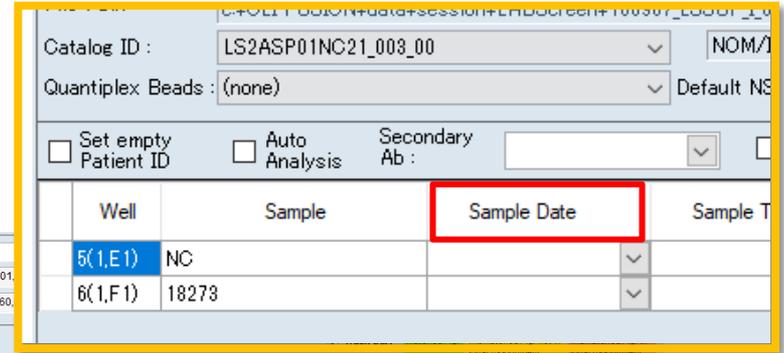
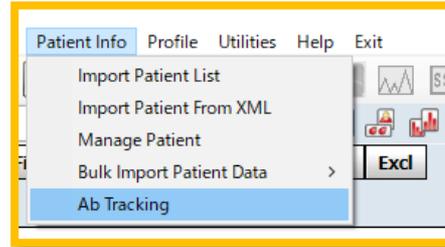
Close

「M」ボタンを押すとDSA情報が確認できる
赤：陽性と判定したDSA
黄：陽性と判定していないDSA

モニタリング



または



抗体検査結果の推移がグラフで表示されるデータをインポートする際に「Sample Date」の入力が必須



アッセイの注意点



安定したデータを取得するために

- LABScanのメンテナンス
 - Calibration/Verification
 - プローブ洗浄、高さ調節
- 検体の前処理は常に同じ方法を
 - 凍結融解 & 遠心は必須
 - Adsorb out、EDTA処理を推奨
- 洗浄操作の与える影響は大きい
 - フリッキングの強さ
 - ドライボルテックスの時間

LABScanのメンテナンス

メンテナンスが適切に行われていないと正確なデータが得られませんので、定期的にメンテナンスを行ってください

メンテナンス	項目	内容
測定毎	<ul style="list-style-type: none">Performance Verification	レーザーの確認
Weekly Maintenance	<ul style="list-style-type: none">CalibrationPerformance VerificationWeekly Maintenanceプローブ洗浄	レーザーの補正 レーザーの確認 流路の洗浄 プローブの洗浄
Monthly Maintenance	<ul style="list-style-type: none">Monthly Maintenance	流路の洗浄
Yearly Maintenance	<ul style="list-style-type: none">Luminex Japanによるメンテナンス	フィルター、チューブ類の交換、レーザー調整など

凍結融解 & 遠心

- 背景
 - 患者血清・血漿中には不純物が含まれる
- 操作方法
 - 血清・血漿の凍結 (-70°C 以下、15分)
 - 解凍後遠心 (8,000~10,000G、10分間以上)
 - 遠心後、中間層より検体を回収する
- 注意点
 - 高速回転の遠心機を使用するとなお良い
 - 不純物が多い検体は、遠心速度、時間を増やす



- 背景

- ラテックスに対する非特異な抗体をもつ検体は、バックグラウンドが高くなることがある
- ラテックス抗体を吸着するビーズ試薬

- 注意点

- バックグラウンドが高い検体の70-80%で有効であると考えられている
- 複数回行くと抗体が減弱するので要注意(3回程度が限度)
- 検体によっては処理をすることでNCビーズが上がる場合もある

- Adsorb Outビーズをボルテックス
- 検体血清30 μ LにAdsorb Outビーズ3 μ L加えボルテックス
- 室温で30分間、振とうさせながらインキュベート
- 15,000rpmで5分間遠心
- 上清を新しいチューブに回収
 - チューブ底のAdsorb Outビーズを吸わないように注意
 - 使用したビーズは再利用不可
 - Adsorb Out ビーズが混入した場合は、再度遠心して上清を回収

Adsorb Outを繰り返した時の蛍光値

	Neat	1x ADS	2x ADS	3x ADS	4x ADS
<i>Bead #1</i>	4451	804	579	538	471
<i>Bead #2</i>	7516	5115	3508	3833	3935
<i>PC/NC Ratio</i>	1.7	6.4	6.1	7.1	8.4
<i>Top Beads</i>	19, 4, 18, 75, 91, 23, 69, 15	19, 4, 18, 75, 91, 23, 15, 81	19, 4, 75, 91, 23, 15, 81, 69	19, 4, 75, 91, 18, 23, 69, 17	19, 4, 75, 18, 91, 23, 69, 17

減弱した抗体

データ: One Lambda

Adsorb outでNCが下がらない場合

- 原因ははっきりとはわかっていませんが、Adsorb outでは取り除けない非特異タンパク質があるためと考えられております
- 対処方法としましては、Adsorb outを使用していない血清を用い、別の前処理方法で検査をしていただくことをお勧めします
 - FBS、希釈、凍結融解等をお試してください

- 背景

- 補体成分がHLA抗体に結合することで、二次抗体の結合が阻害され、偽陰性となることがある(この現象をプロゾーン現象と呼びます)
- 補体活性に必要な Ca^{2+} をキレートすることで除去します

プロゾーン現象

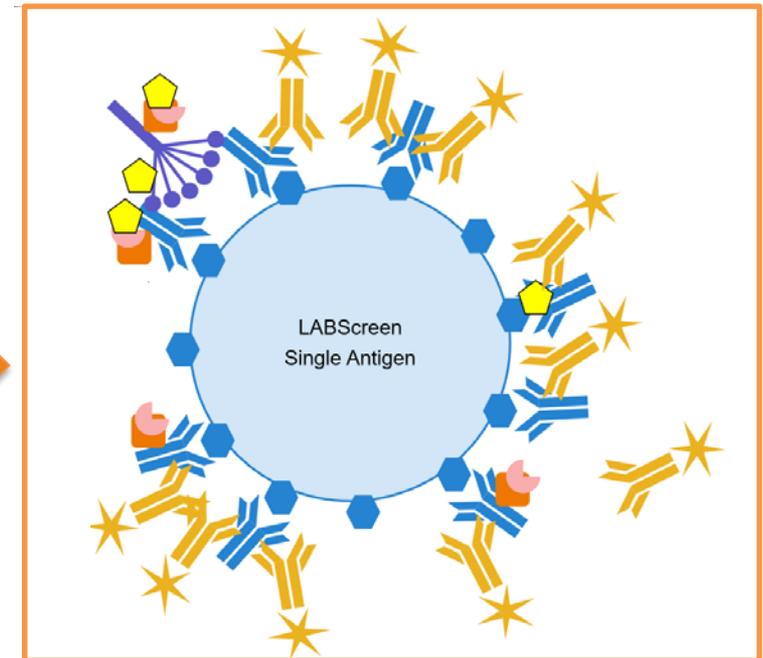
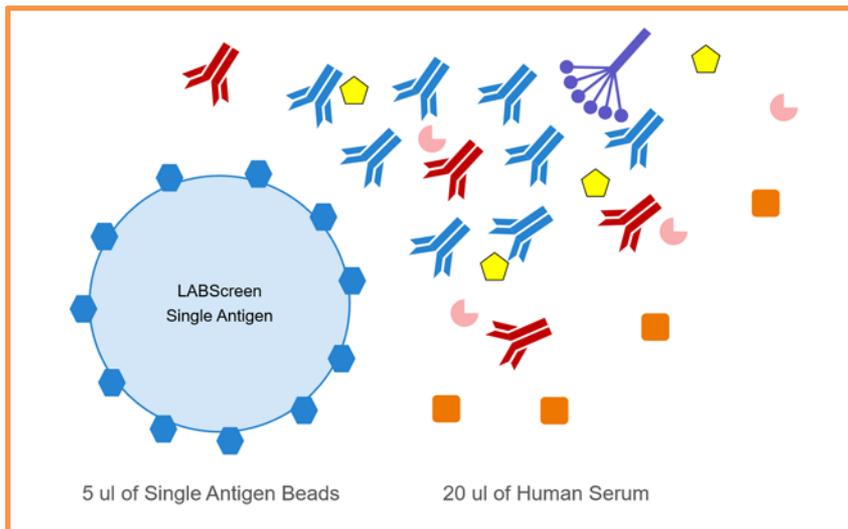
- 検体中に過剰なHLA抗体や補体が存在することで、二次抗体の反応が阻害され、偽陰性となる現象
- 測定結果からプロゾーン現象が起こっているか否かは判断できません
- 前処理を行い測定結果に変化が見られればプロゾーン現象が起こっていたことがわかります

試薬と血清の反応(通常)

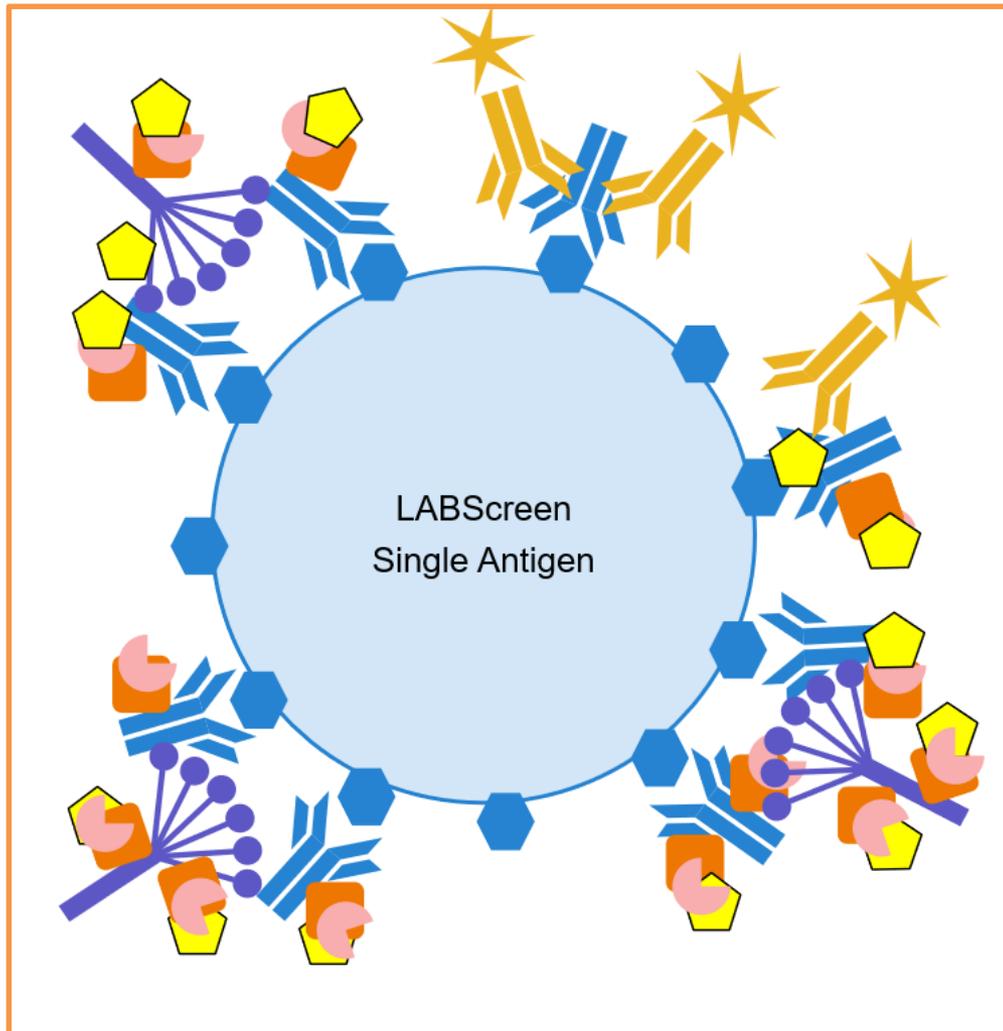
アイコンの説明

-  HLA抗原
-  抗HLA抗体
-  非特異抗HLA抗体
-  補体(C1q)
-  補体(C4)
-  補体(C2)
-  補体(C3)
-  二次抗体

補体活性が低い場合は、二次抗体が問題なくHLA抗体に結合するため、MFIの値に影響を与えない

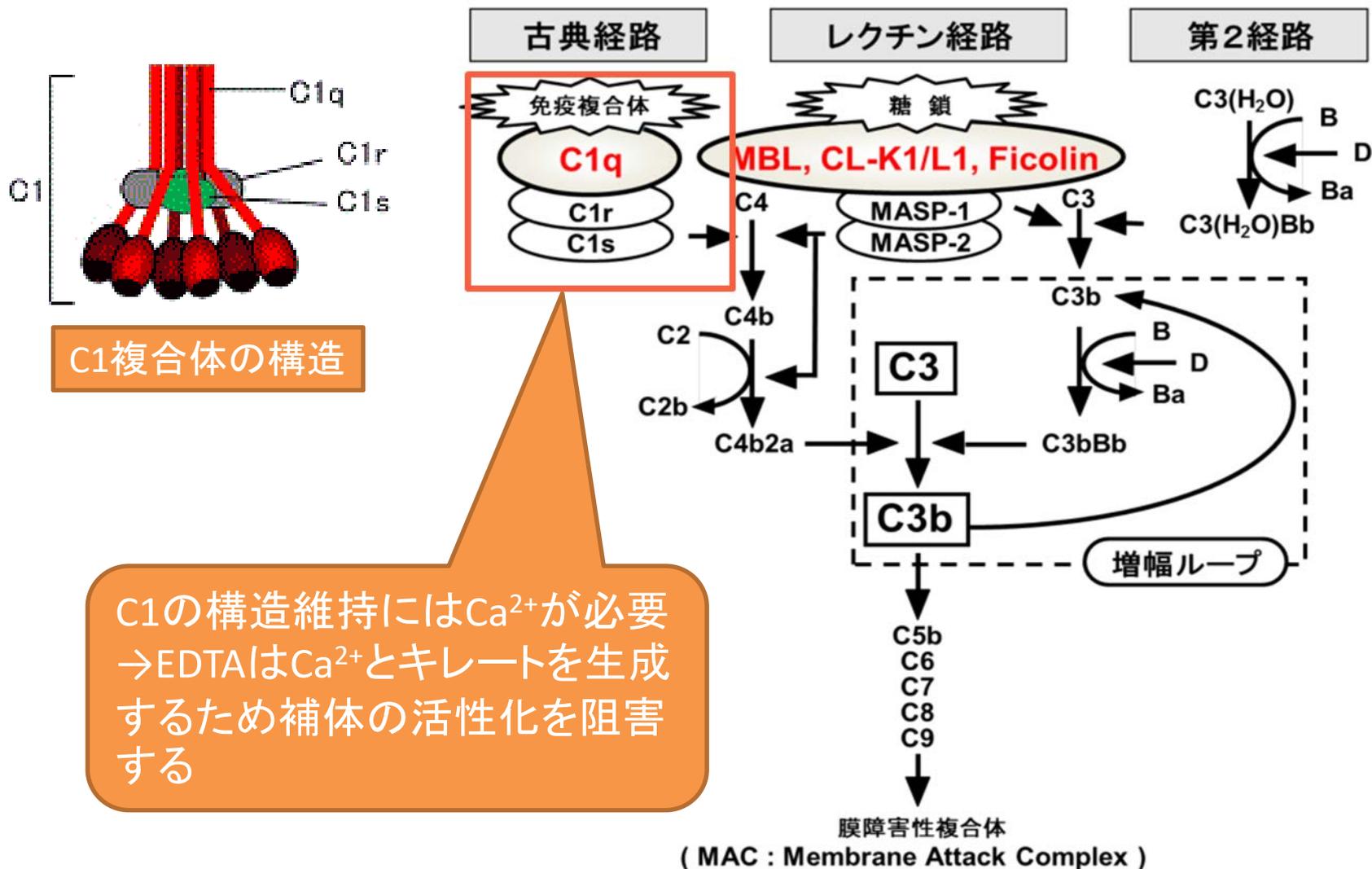


試薬と血清の反応(補体活性が高い)



補体がHLA抗体に結合するため、二次抗体が結合できなくなる
→MFIの値が下がる(偽陰性となる可能性がある)

補体活性経路



C1複合体の構造

C1の構造維持にはCa²⁺が必要
 →EDTAはCa²⁺とキレートを生成
 するため補体の活性化を阻害
 する

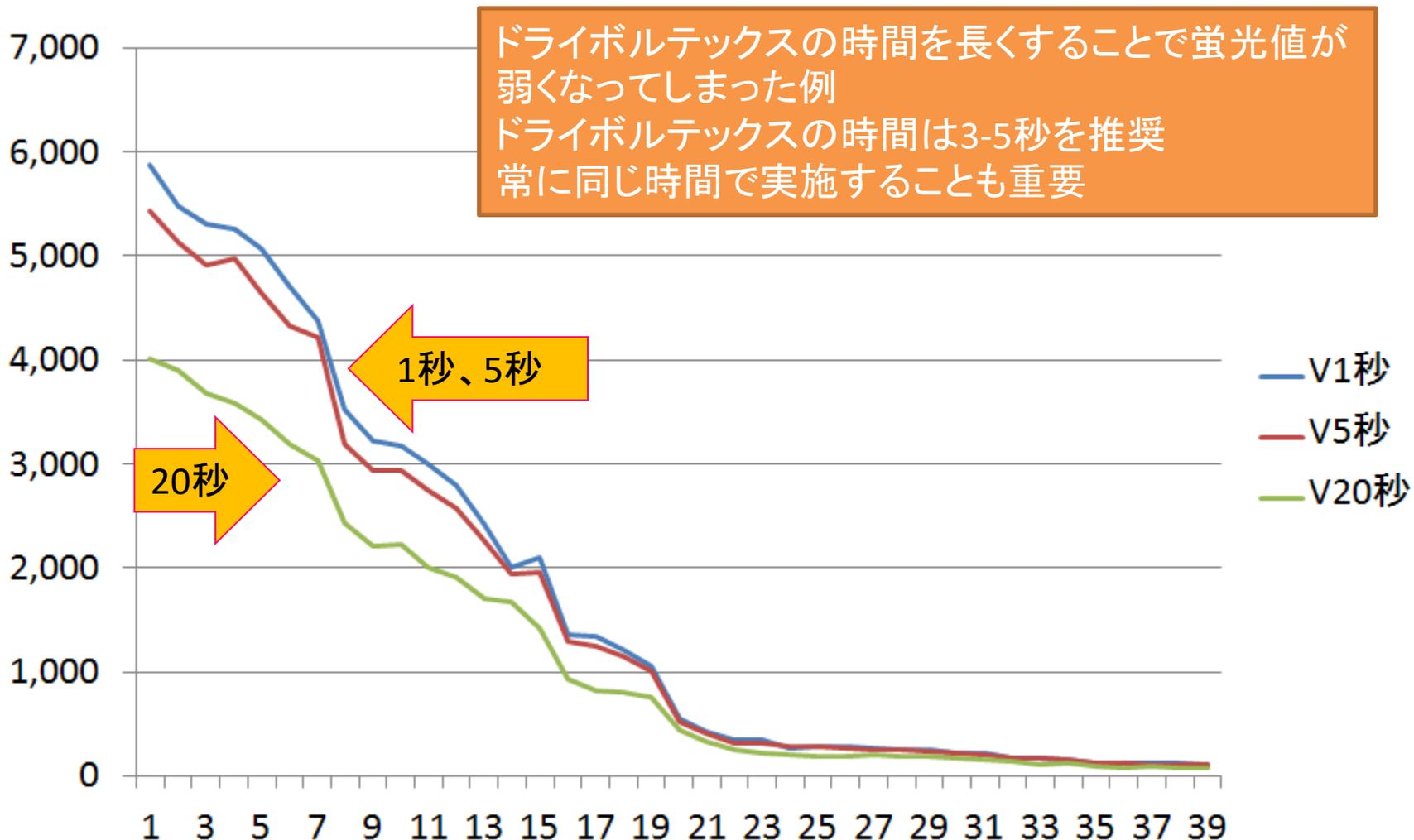
- 血清90 μ Lに0.5M EDTA(メーカー不問)2 μ L添加
 - EDTAの最終濃度を約10mMとなるように調整する
 - 溶液状態のEDTAの利用を推奨
- 室温で30分間振とうしながら反応させる
- 20,000 gで10分間遠心、上清を使用

- 参考文献
 - HLA Antibody Specification Using Single-Antigen Beads—A Technical Solution for the Prozone Effect (*Transplantation* 2011;92: 510–515)

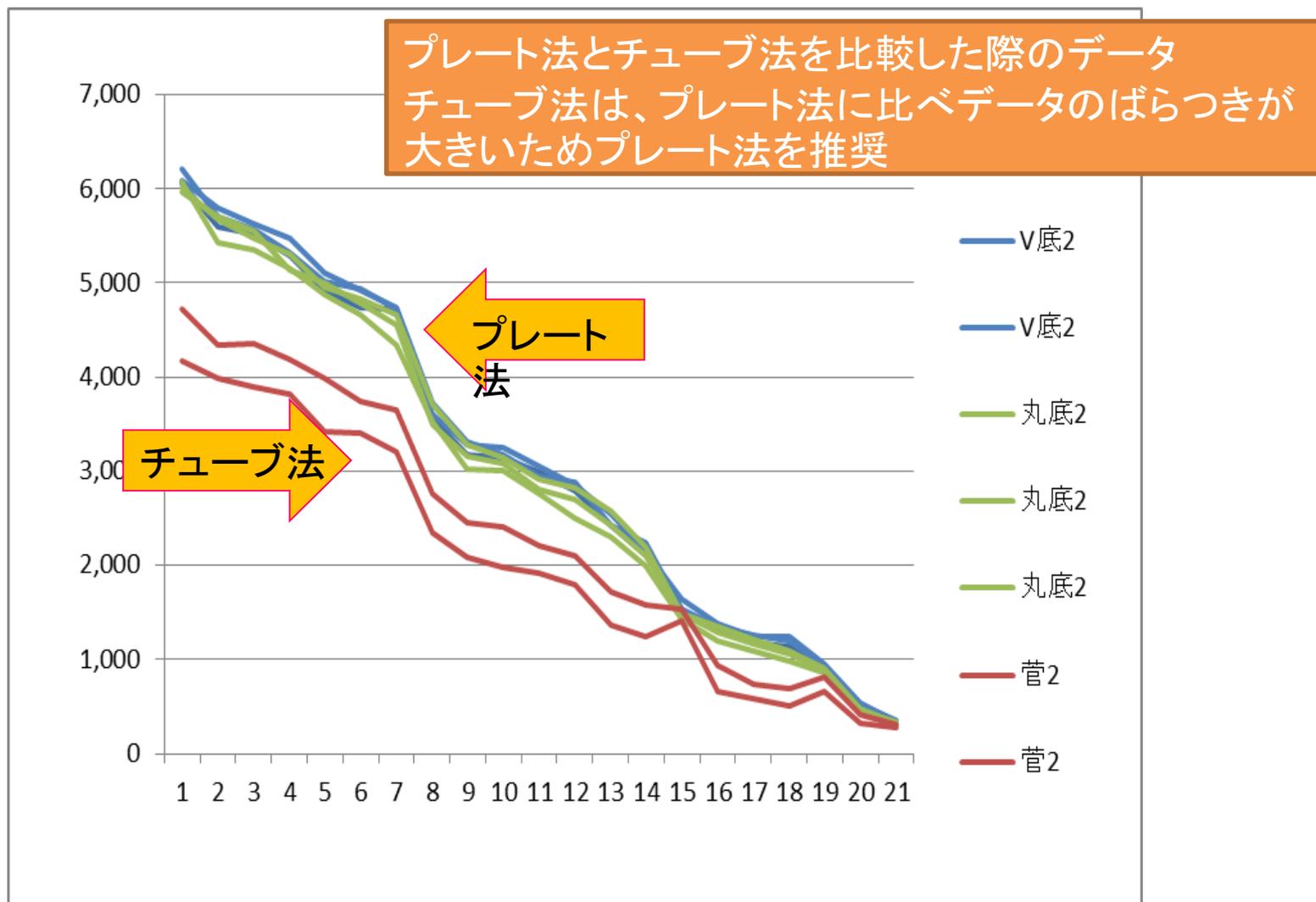
洗淨操作

- フリッキング
 - 遠心力をかけずに垂直に振り下ろす
 - 動画公開中
 - <https://www.youtube.com/watch?v=eQrg6z00ERg>
- ドライボールテックス
 - 時間は常に一定にする
 - 動画公開中
 - <https://www.youtube.com/watch?v=F3RQxamJTW4>

ドライボルトテックスの時間の影響

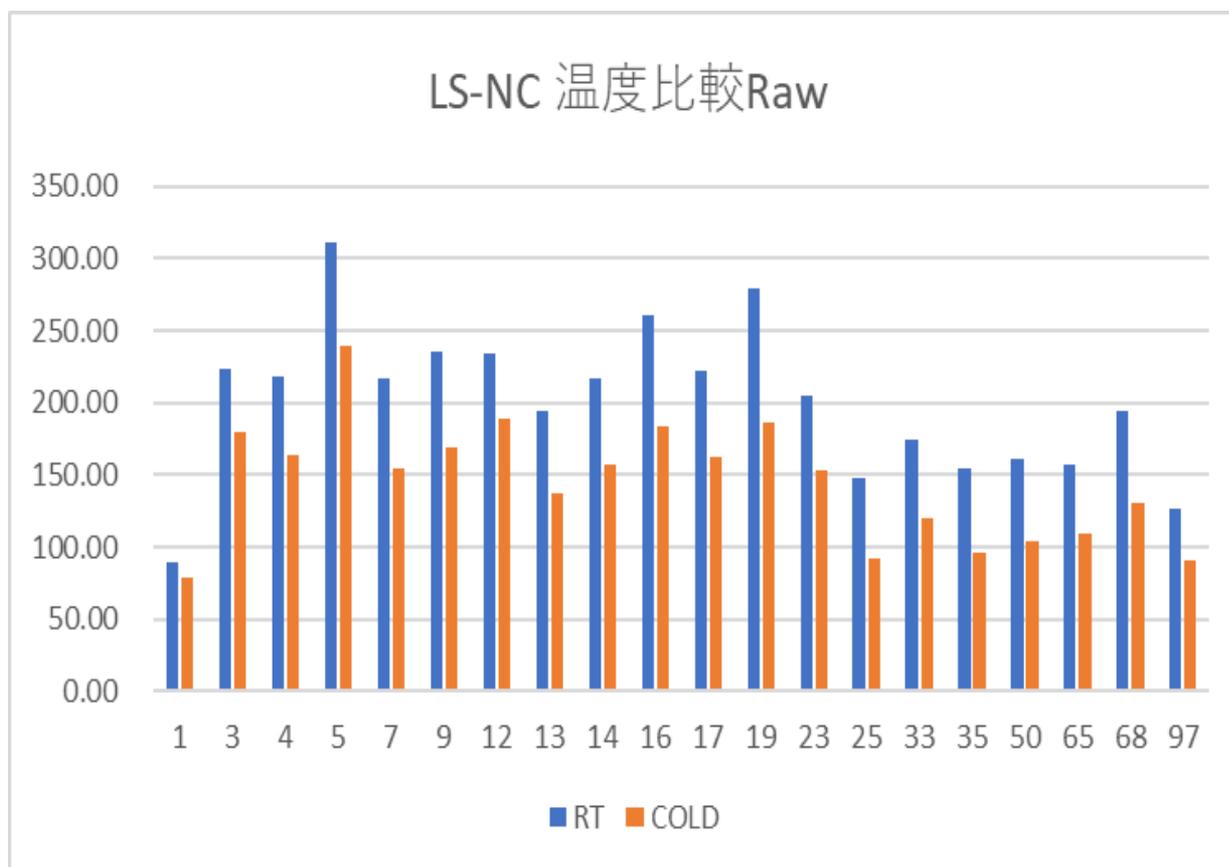


プレート法とチューブ法の比較

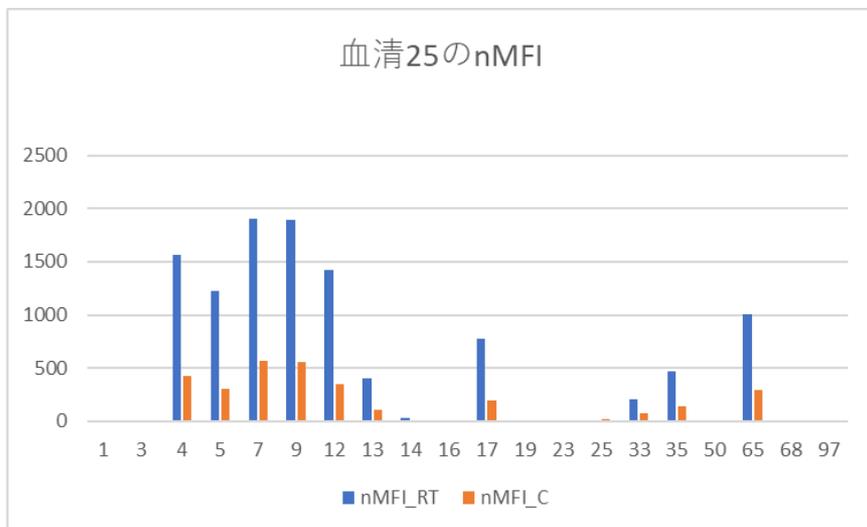
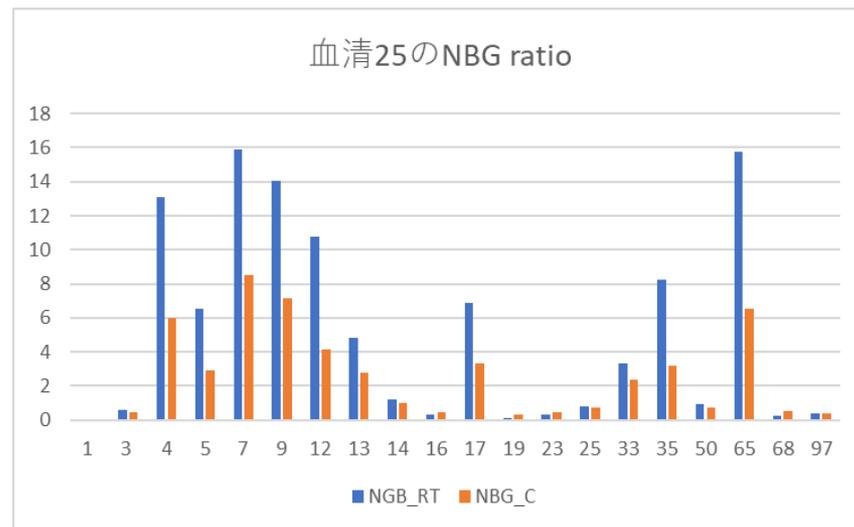
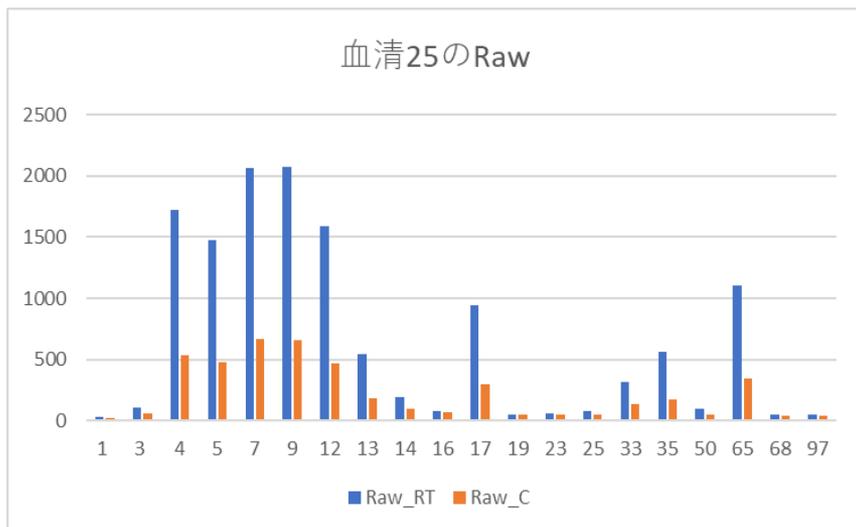


WashBufferの温度の影響-1

陰性コントロール血清の蛍光値を比較すると
全てのビーズで室温の方が高い



WashBufferの温度の影響-2



蛍光値(Raw)、NBG Ratio、nMFI全てにおいて室温の方が高い
Product InsertにはWBの使用温度の記載はないが、メーカーのQC資料には operation temperature は25℃と記載されているため、必ずWash Bufferは室温に戻してから使用する

ご質問はありますでしょうか??

