A QuickStart Guide for the Creation and Ordering of SureSelect Target Enrichment Oligo Sets

without the Wizard

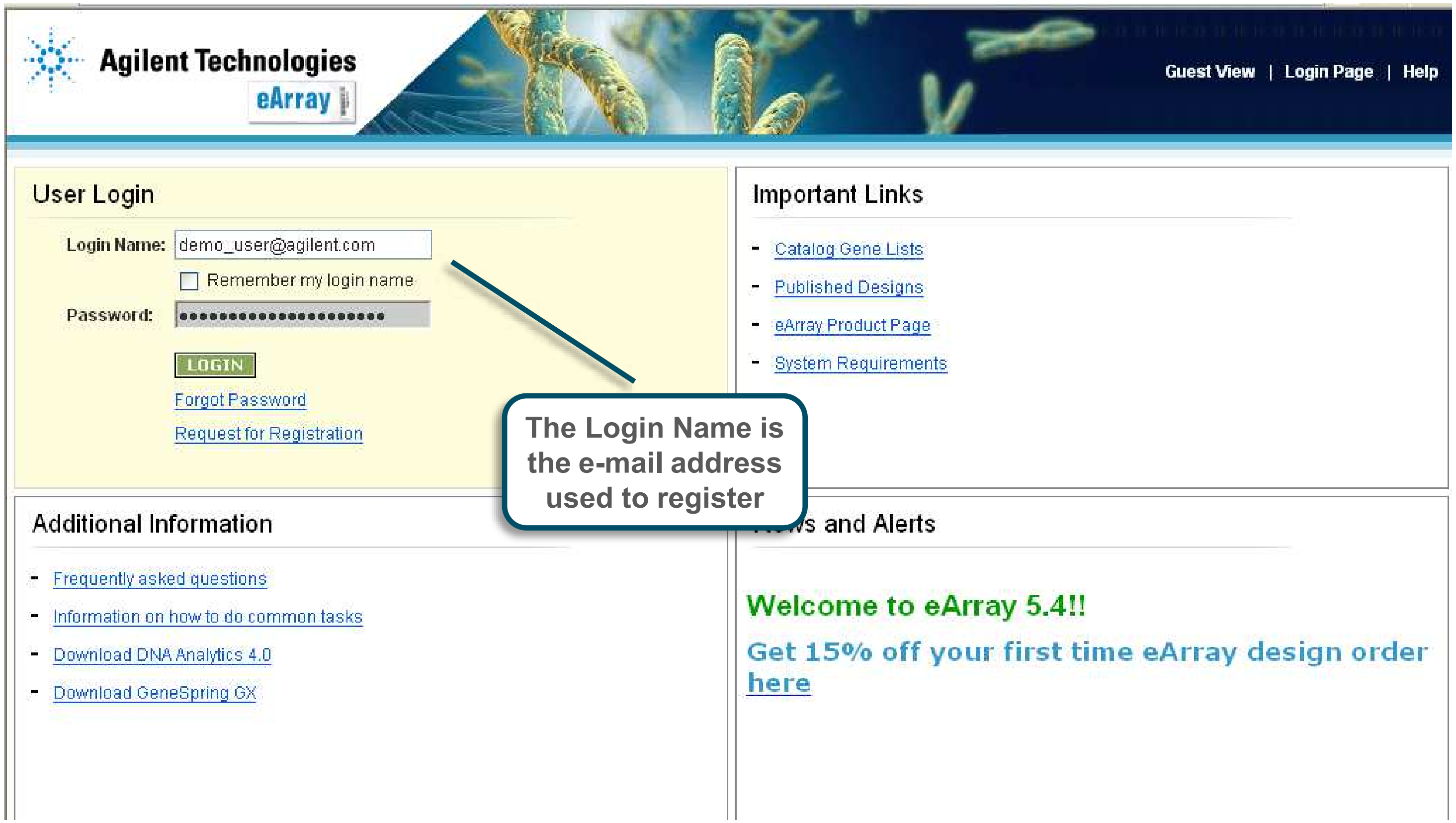
Using **eArray**,
a free web-based
design tool

Table of Contents

Getting Started

Access eArray

- Access eArray at: https://earray.chem.agilent.com/earray/
- Log in to eArray, if this is your first time visiting, click Request for Registration



Login Name: demo_user@agilent.com

☐ Remember my login name

Password: ••••••••••••••••••••••

Welcome to eArray 5.4!!

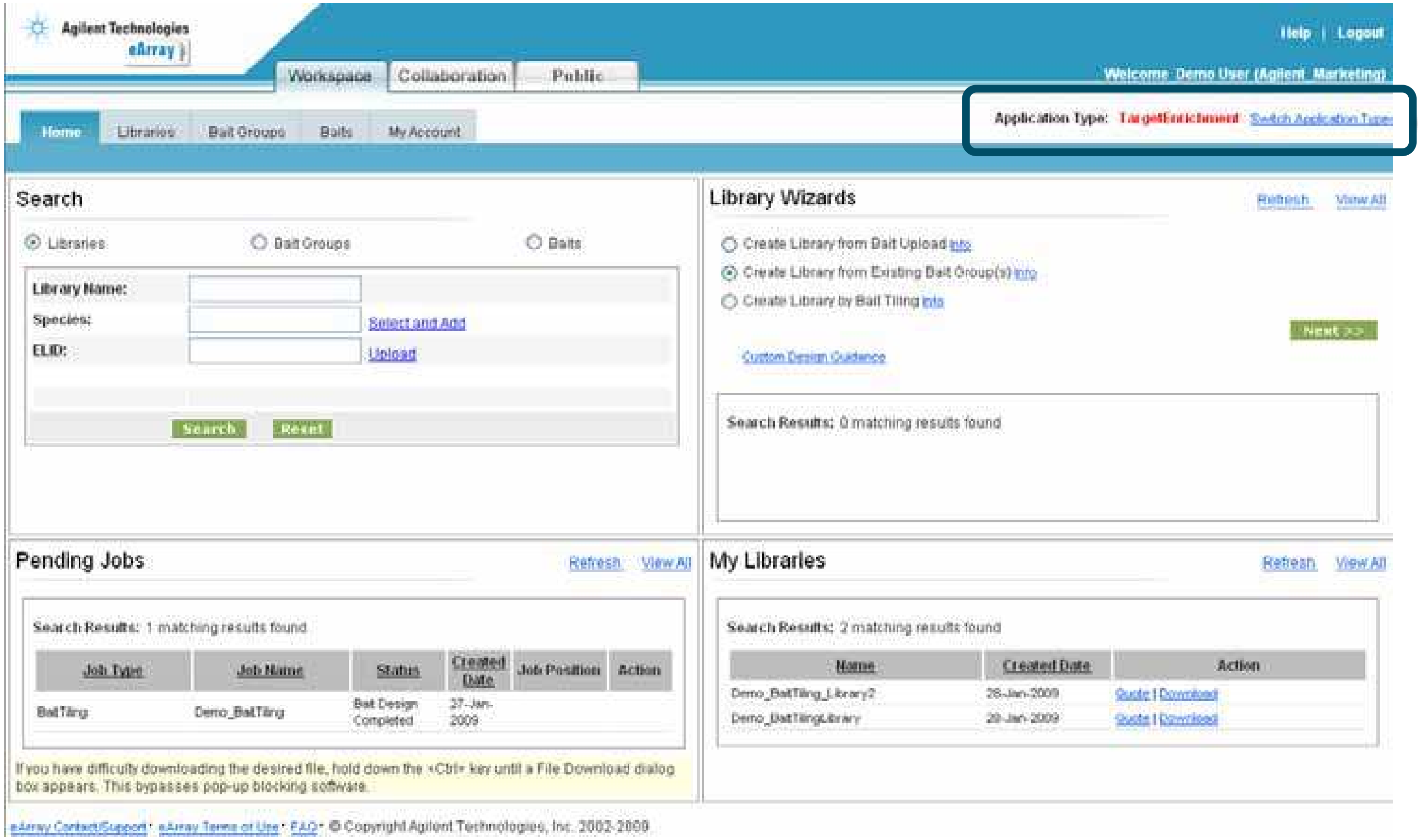
Get 15% off your first time eArray design order here

The Login Name is the e-mail address used to register

Getting Started

Confirm Application Type

- Confirm that the Application Type is TargetEnrichment



Welcome Demo User (Agilent Marketing)

Application Type: TargetEnrichment Switch Application Type

Search

● Libraries ○ Bait Groups ○ Baits

Library Name:

Species:

ELID:

Library Wizards

○ Create Library from Bait Upload info

● Create Library from Existing Bait Group(s) info

○ Create Library by Bait Tiling info

Search Results: 0 matching results found

Pending Jobs

Search Results: 1 matching results found

Job Type	Job Name	Status	Created Date	Job Position	Action
BaitTiling	Demo_BaitTiling	Bait Design Completed	27-Jan-2009		

If you have difficulty downloading the desired file, hold down the <Ctrl> key until a File Download dialog box appears. This bypasses pop-up blocking software.

My Libraries

Search Results: 2 matching results found

Name	Created Date	Action
Demo_BaitTiling_Library2	28-Jan-2009	Quote | Download
Demo_BaitTilingLibrary	29-Jan-2009	Quote | Download

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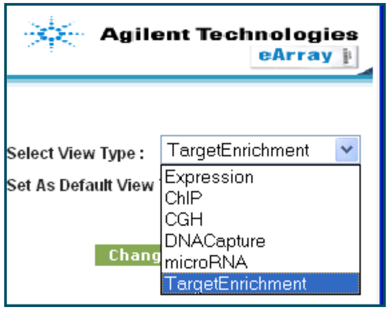
If necessary, select **Switch Application Type** to select Target Enrichment



Select View Type : TargetEnrichment

Set As Default View

Getting Started

Select Method

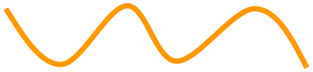
- Choose between two methods for creating a SureSelect Target Enrichment Set

	Benefits	Caveats	When to Use
Following the Wizard*	• Easy, stream-lined method • The Wizard takes the user from initiation of design to submission	• The user will only be able to download the library details after the library is completed • The user will not have access to a "fate" file	When a simple or straightforward design is planned
Independent of the Wizard	• User can download additional files, including a Fate file that lists the # of baits tiled for each target interval • User can fine-tune the design, creating and combining multiple bait groups with a variety of parameter settings • User can easily track the success of bait tiling for individual targets during the process of design	• User will not be guided by a Wizard	When iterations may be desired to get an optimal design for a target set

*** This tutorial guides the user on how to create a design independent of the Wizard. If desired, please see the tutorial on how to create a design with the Wizard.**

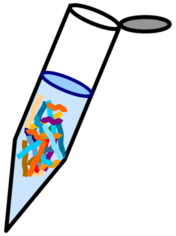
Terms and Definitions

- **Bait**:
  - A single oligo sequence of pre-determined length (120 bp) that complements a targeted region of the genome

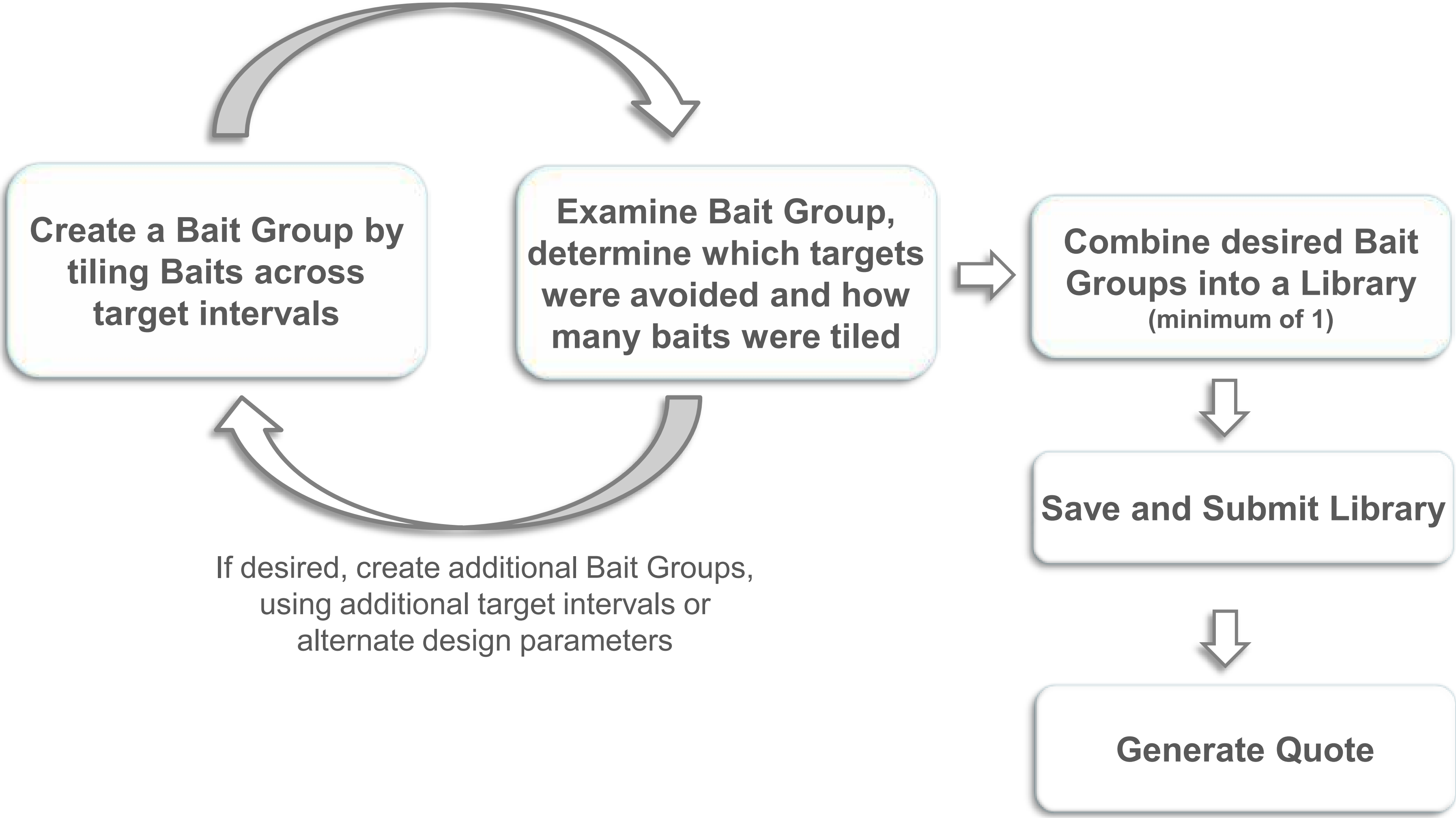


- **Bait Group**:
  - Consists of a group of Baits designed to complement a single or set of targeted intervals
  - May be formed from baits generated within eArray, baits uploaded into eArray, or bait search results within eArray

- **Library**:
  - Consists of one or more Bait Groups
  - Represents the set of oligos that will be produced for the kit



Workflow Summary



Create a Bait Group by tiling Baits across target intervals

Examine Bait Group, determine which targets were avoided and how many baits were tiled

If desired, create additional Bait Groups, using additional target intervals or alternate design parameters

Combine desired Bait Groups into a Library
(minimum of 1)

Save and Submit Library

Generate Quote

Create a Bait Group

Design Baits

- To create a Bait Group, go to the Baits page, and select Bait Tiling

Click on **Baits**

Application Type: TargetEnrichment

Click on **Bait Tiling**

- This will bring you to the page where you can define design parameters for a Bait Group

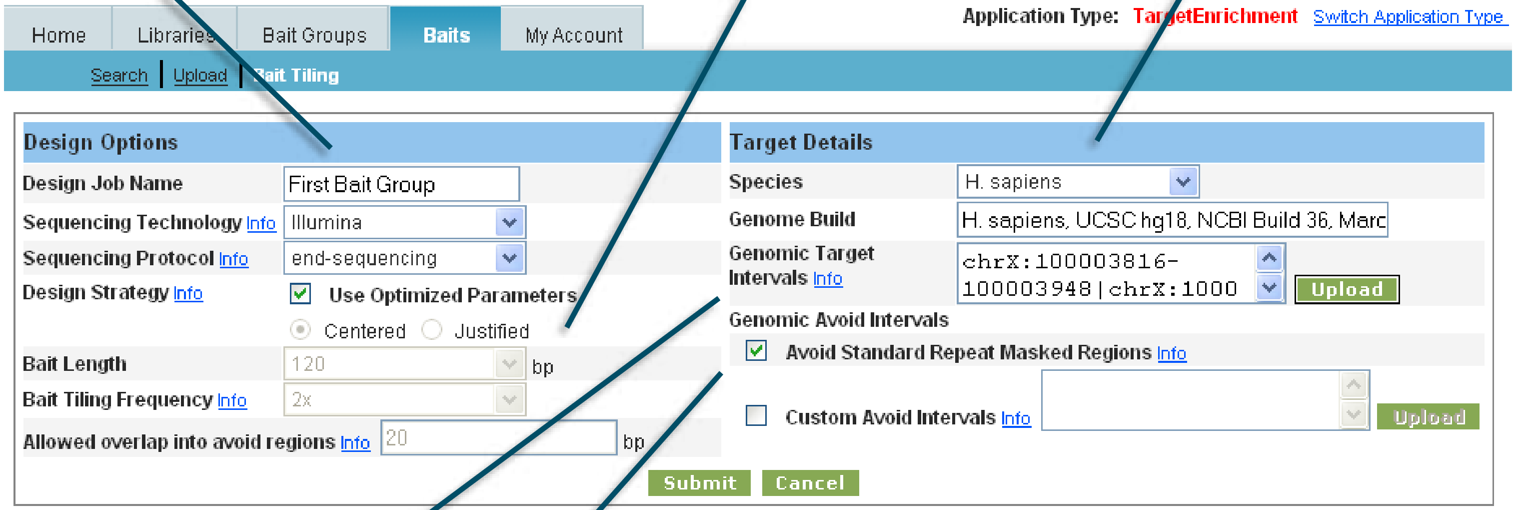
Create a Bait Group

Design Options

1. Enter a name for the design job.

2. Design Strategy: To use the parameters previously optimized for general bait tiling, leave the checkmark on this option. To change the parameters, uncheck this option. The next slide describes the parameter changes that can be applied.

3. Species: Select the species for which the target intervals were designed. The Genome Build will then automatically be populated by eArray.



Application Type: TargetEnrichment

Design Options

Design Job Name	First Bait Group
Sequencing Technology	Illumina
Sequencing Protocol	end-sequencing
Design Strategy	☑ Use Optimized Parameters ● Centered ○ Justified
Bait Length	120 bp
Bait Tiling Frequency	2x
Allowed overlap into avoid regions	20 bp

Target Details

Species	H. sapiens
Genome Build	H. sapiens, UCSC hg18, NCBI Build 36, Marc
Genomic Target Intervals	chrX:100003816-100003948|chrX:1000

Genomic Avoid Intervals

☑ Avoid Standard Repeat Masked Regions

☐ Custom Avoid Intervals

4. Genomic Target Intervals: Either type in or upload the genomic intervals for the targets to be enriched. Examples are provided on a later slide.

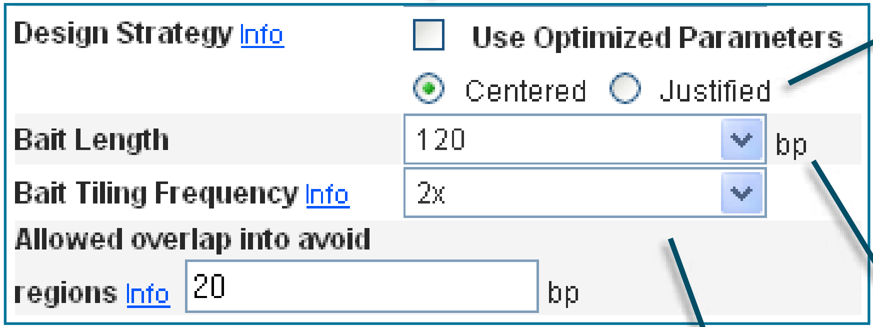
5. Genomic Avoid Intervals:
- Choose to avoid the standard repeat masked regions by leaving a checkmark next to this option (based on the UCSC RepeatMasker track).
- Add additional intervals to avoid with the baits by typing those intervals in or uploading them in the same format as the target intervals.

6.Submit:
Select Submit when Options and Details are completed.

Create a Bait Group

Design Strategy

1. Change the parameters: To be able to change these parameters, first remove the checkbox from the "Use Optimized Parameters" option.



Design Strategy Info ☐ Use Optimized Parameters

● Centered ○ Justified

Bait Length: 120 bp

Bait Tiling Frequency Info: 2x

Allowed overlap into avoid regions Info: 20 bp

2. Centered versus Justified: (see next slide for visuals)

Centered:
Baits are centered, and evenly distributed, across each target region. Baits may overlap to regions outside of the target.

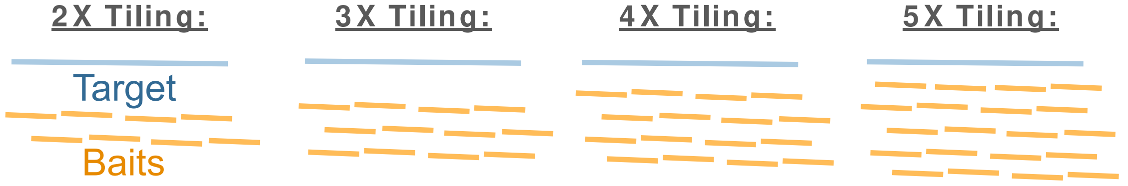
Why use this? This is the method tested most extensively.

Justified:
Baits are first tiled across the target. If baits extend past the target interval, all baits are shifted inward so that there will be no overlap with adjacent but un-targeted genomic regions.

Why use this? If it is desired to avoid having baits to any region adjacent to targets, for example, if sequencing cDNA.

3. Bait Length: Currently, 120 bp is available as the only bait length option. All baits will be designed to be 120 bp in length.

4. Bait Tiling Frequency:
Options include 2X, 3X, 4X, and 5X and indicate the amount of bait overlap. Tiling frequency is not enforced at target edges. Increasing the frequency will lead to the ability to cover fewer or smaller regions in a library.



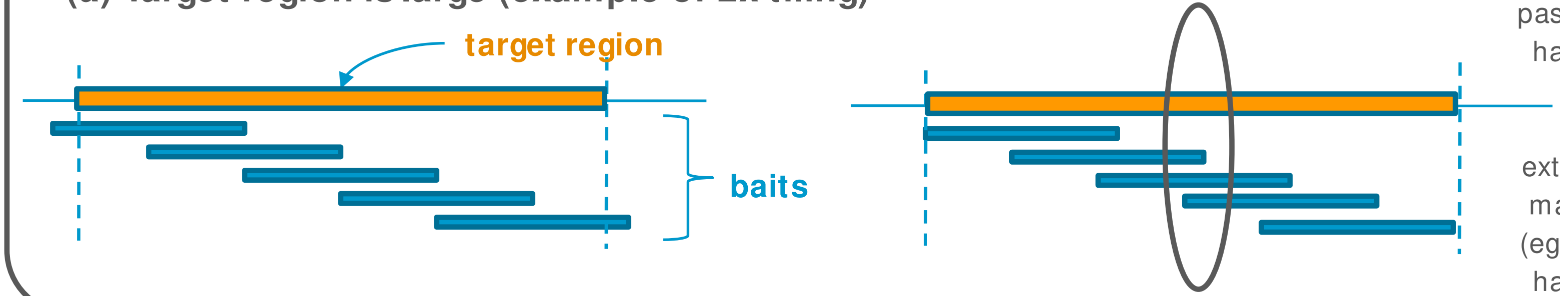
5. Allowed overlap into avoid regions: Centered baits may overlap with regions adjacent to the target. In case the targets are adjacent to Avoid Regions, enter the acceptable amount of overlap with these in bp. To ensure that there is no overlap in any Avoid Regions, select '0 bp'.

Create a Bait Group

Centered versus Justified

Centered **Justified**

(a) Target region is large (example of 2x tiling)



Centered baits extend past interval boundaries, but have even coverage across entire region

Justified baits do not extend past boundaries, but may have uneven coverage (eg, see circle where regions have both 2x and 3x tiling)

(b) Target region is 2 times the bait length

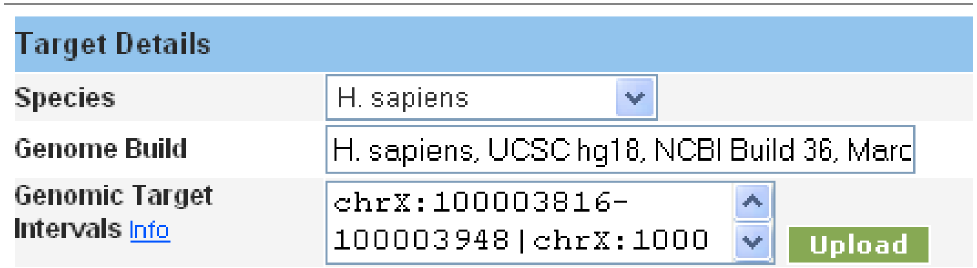
Design is the same for Centered and Justified

(c) Target region is shorter than the bait length

Design is the same for Centered and Justified

Create a Bait Group

Formats for describing Target Intervals



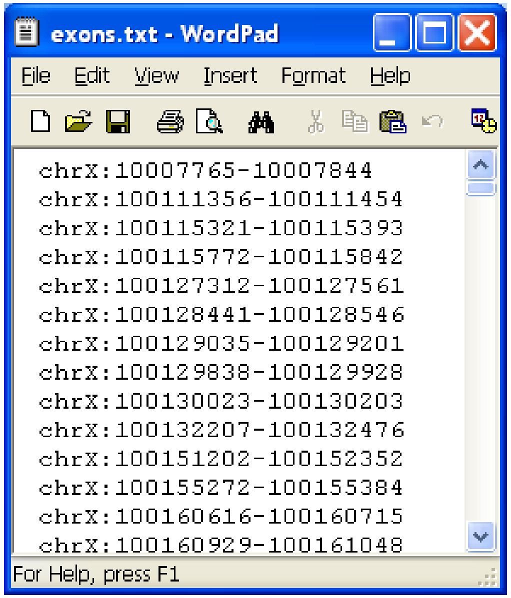
Target Details	
Species	H. sapiens
Genome Build	H. sapiens, UCSC hg18, NCBI Build 36, Marc
Genomic Target Intervals Info	chrX:100003816-100003948|chrX:1000

Option 1: Type in the genomic intervals to be targeted.
The format for typing in the intervals is as follows:

chrX:100003816-100003948|chrX:100004037-100004218|chrX:100004314-100004465|chrX:100004329-100004465|chrX:100004804-100004888

Each interval should be separated by the | character. If there is a long list of intervals, it would be better to use option 2.

Option 2: Upload a file that includes the genomic intervals to be targeted:
The format for uploading the intervals is as follows:



```
chrX:10007765-10007844
chrX:100111356-100111454
chrX:100115321-100115393
chrX:100115772-100115842
chrX:100127312-100127561
chrX:100128441-100128546
chrX:100129035-100129201
chrX:100129838-100129928
chrX:100130023-100130203
chrX:100132207-100132476
chrX:100151202-100152352
chrX:100155272-100155384
chrX:100160616-100160715
chrX:100160929-100161048
```

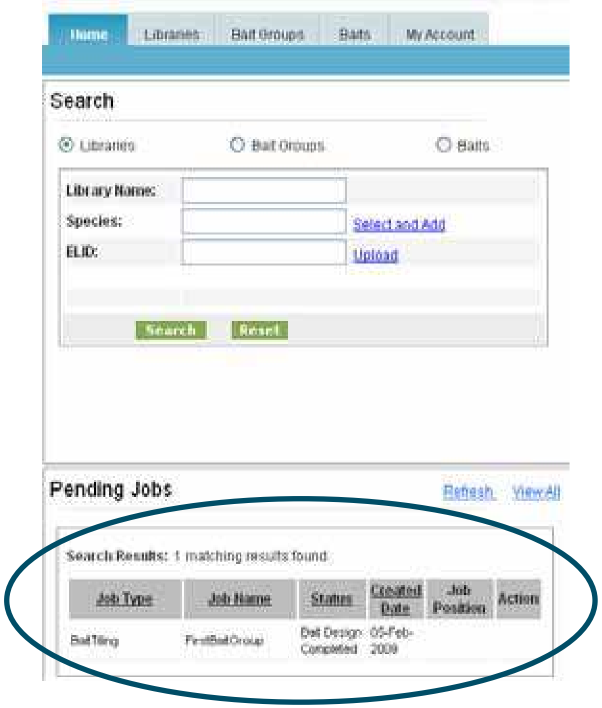
Each interval should be presented on a separate line, and the file should be saved as a text file.

When using this option, select Upload, Browse to find the saved file, and then select Upload File.

Create a Bait Group

Check Bait Group Status

- The status of your Bait Group can be viewed in the Pending Jobs quadrant on the Home page (see left), or at the bottom of the Baits page (see right)
- To continue, you must be on the Baits page



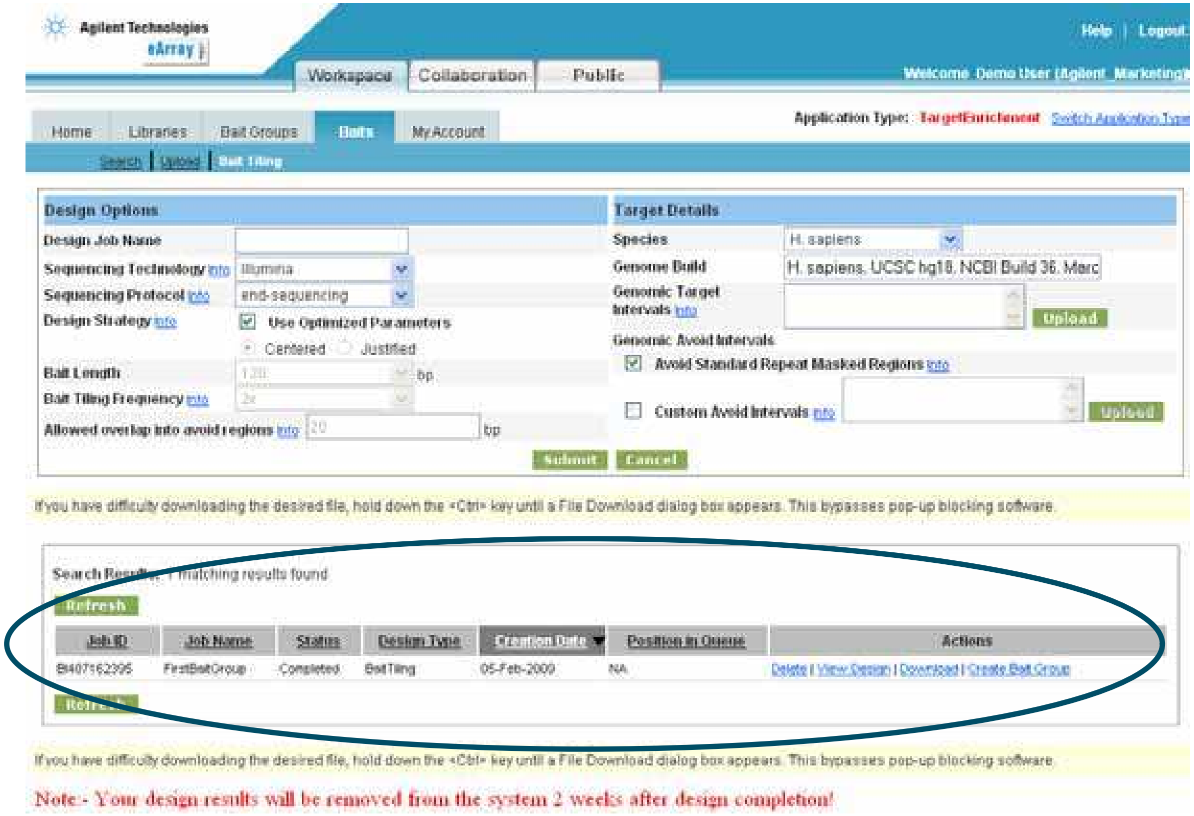
● Libraries ○ Bait Groups ○ Baits

Library Name:
Species:
ELID:

Pending Jobs

Search Results: 1 matching results found

Job Type	Job Name	Status	Created Date	Job Position	Action
BaitTiling	FirstBaitGroup	Bait Design Completed	05-Feb-2009		



Welcome Demo User (Agilent_Marketing

Application Type: TargetEnrichment

Design Options

Design Job Name:
Sequencing Technology: Illumina
Sequencing Protocol: end-sequencing
Design Strategy: ☑ Use Optimized Parameters
● Centered ○ Justified
Bait Length: 120 bp
Bait Tiling Frequency: 2x
Allowed overlap into avoid regions: 20 bp

Target Details

Species: H. sapiens
Genome Build: H. sapiens, UCSC hg18, NCBI Build 36, Marc
Genomic Target Intervals:
Genomic Avoid Intervals
☑ Avoid Standard Repeat Masked Regions
☐ Custom Avoid Intervals

If you have difficulty downloading the desired file, hold down the <Ctrl> key until a File Download dialog box appears. This bypasses pop-up blocking software.

Search Results: 1 matching results found

Job ID	Job Name	Status	Design Type	Creation Date	Position in Queue	Actions
BI407162396	FirstBaitGroup	Completed	BaitTiling	05-Feb-2009	NA	Delete | View Design | Download | Create Bait Group

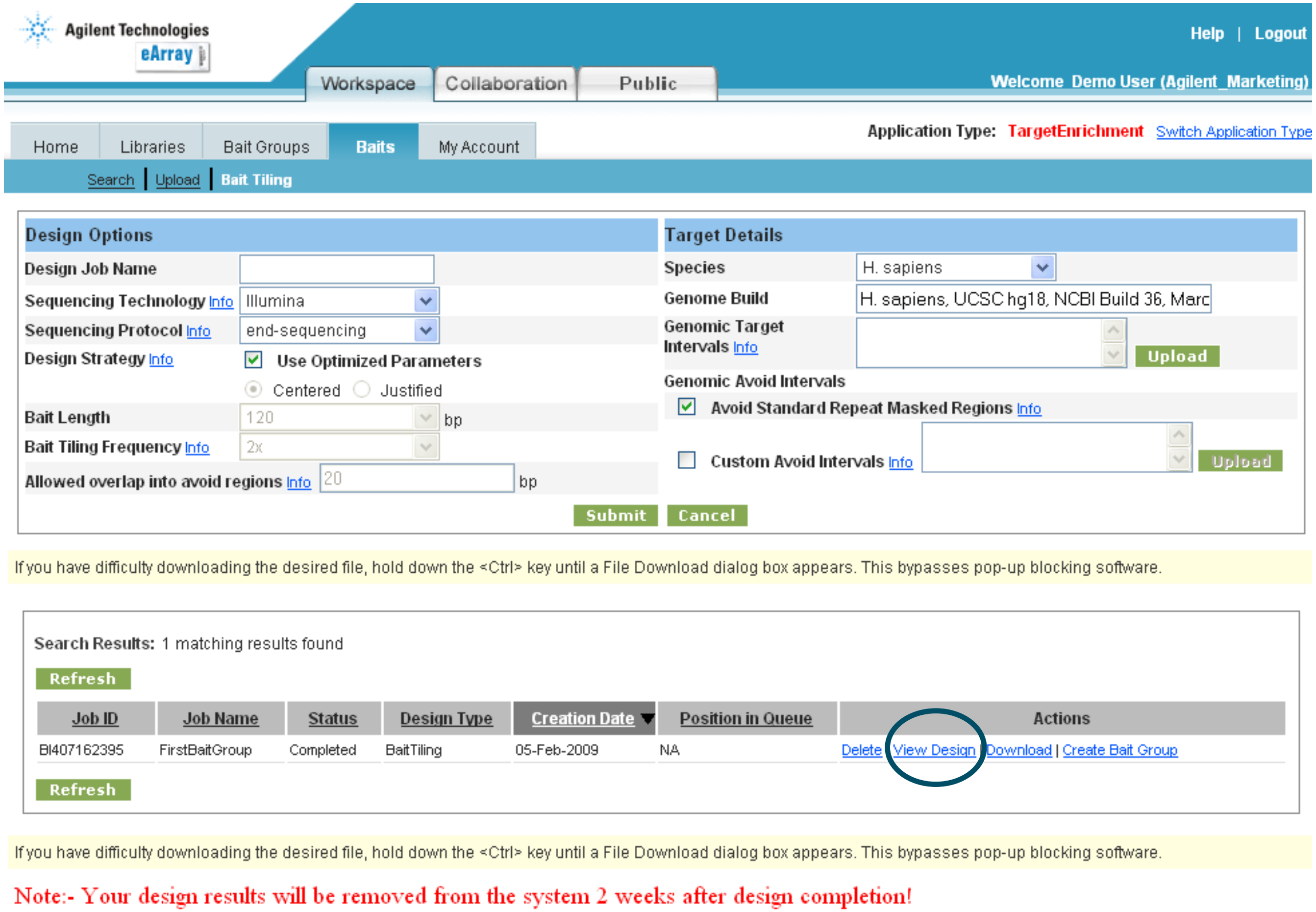
If you have difficulty downloading the desired file, hold down the <Ctrl> key until a File Download dialog box appears. This bypasses pop-up blocking software.

Note:- Your design results will be removed from the system 2 weeks after design completion!

Create a Bait Group

View Design Details (I)

- To view the Bait Group design, click on View Design on the Baits page



Welcome Demo User (Agilent_Marketing)

Application Type: TargetEnrichment Switch Application Type

Design Options

Design Job Name	
Sequencing Technology Info	Illumina
Sequencing Protocol Info	end-sequencing
Design Strategy Info	☑ Use Optimized Parameters ● Centered ○ Justified
Bait Length	120 bp
Bait Tiling Frequency Info	2x
Allowed overlap into avoid regions Info	20 bp

Target Details

Species	H. sapiens
Genome Build	H. sapiens, UCSC hg18, NCBI Build 36, Marc
Genomic Target Intervals Info	

Genomic Avoid Intervals

☑ Avoid Standard Repeat Masked Regions Info

☐ Custom Avoid Intervals Info

If you have difficulty downloading the desired file, hold down the <Ctrl> key until a File Download dialog box appears. This bypasses pop-up blocking software.

Search Results: 1 matching results found

Job ID	Job Name	Status	Design Type	Creation Date	Position in Queue	Actions
BI407162395	FirstBaitGroup	Completed	BaitTiling	05-Feb-2009	NA	Delete | View Design | Download | Create Bait Group

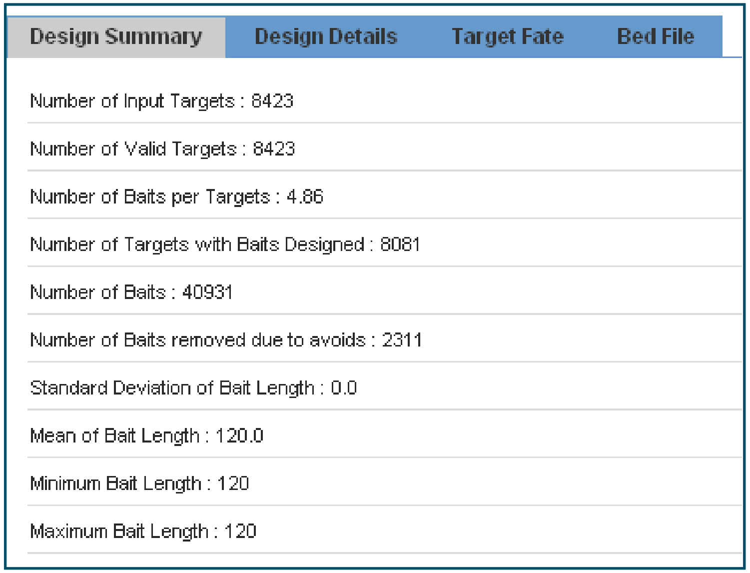
If you have difficulty downloading the desired file, hold down the <Ctrl> key until a File Download dialog box appears. This bypasses pop-up blocking software.

Note:- Your design results will be removed from the system 2 weeks after design completion!

Create a Bait Group

View Design Details (II)

- Toggle between Design Summary, Design Details, Target Fate, and Bed File to view the details of the bait design (only the first 100 lines will be presented).



Number of Input Targets : 8423

Number of Valid Targets : 8423

Number of Baits per Targets : 4.86

Number of Targets with Baits Designed : 8081

Number of Baits : 40931

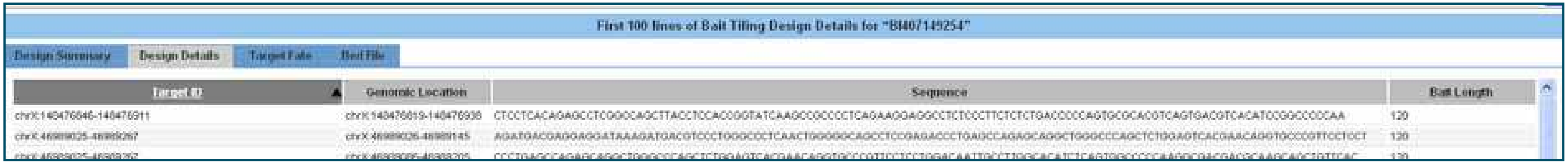
Number of Baits removed due to avoids : 2311

Standard Deviation of Bait Length : 0.0

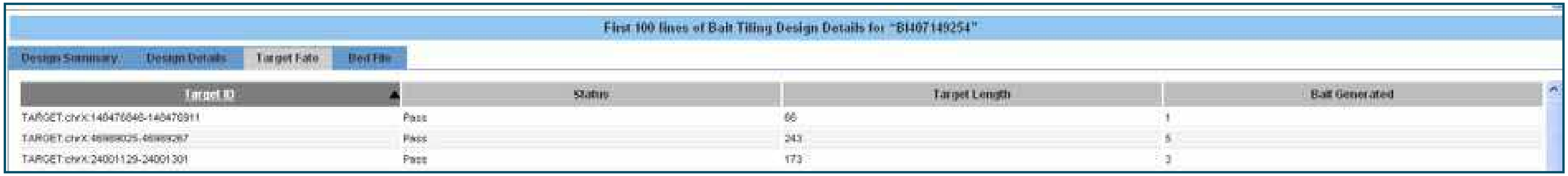
Mean of Bait Length : 120.0

Minimum Bait Length : 120

Maximum Bait Length : 120


First 100 lines of Bait Tiling Design Details for "BI407149254"

Target ID	Genomic Location	Sequence	Bait Length
chrX:140476846-140476911	chrX:140476819-140476938	CTCCTCACAGAGCCTCGGGCAGCTTACCTCCACCGGTATCAAGCCGCCCCTCAGAAGGAGGCCTCTCCCTTCTCTCTGACCCCCAGTGCGCACGTCAGTGACGTCACATCCGGCCCCCAA	120
chrX:46989025-46989267	chrX:46989026-46989145	AGATGACGAGGAGGATAAAGATGACGTCCCTGGGCCCTCAACTGGGGGCAGCCTCCGAGACCCTGAGCCAGAGCAGGCTGGGCCCAGCTCTGGAGTCACGAACAGGTGCCCGTTCCTCCT	120


First 100 lines of Bait Tiling Design Details for "BI407149254"

Target ID	Status	Target Length	Bait Generated
TARGET:chrX:140476846-140476911	Pass	66	1
TARGET:chrX:46989025-46989267	Pass	243	5
TARGET:chrX:24001129-24001301	Pass	173	3


First 100 lines of Bait Tiling Design Details for "BI407149254"

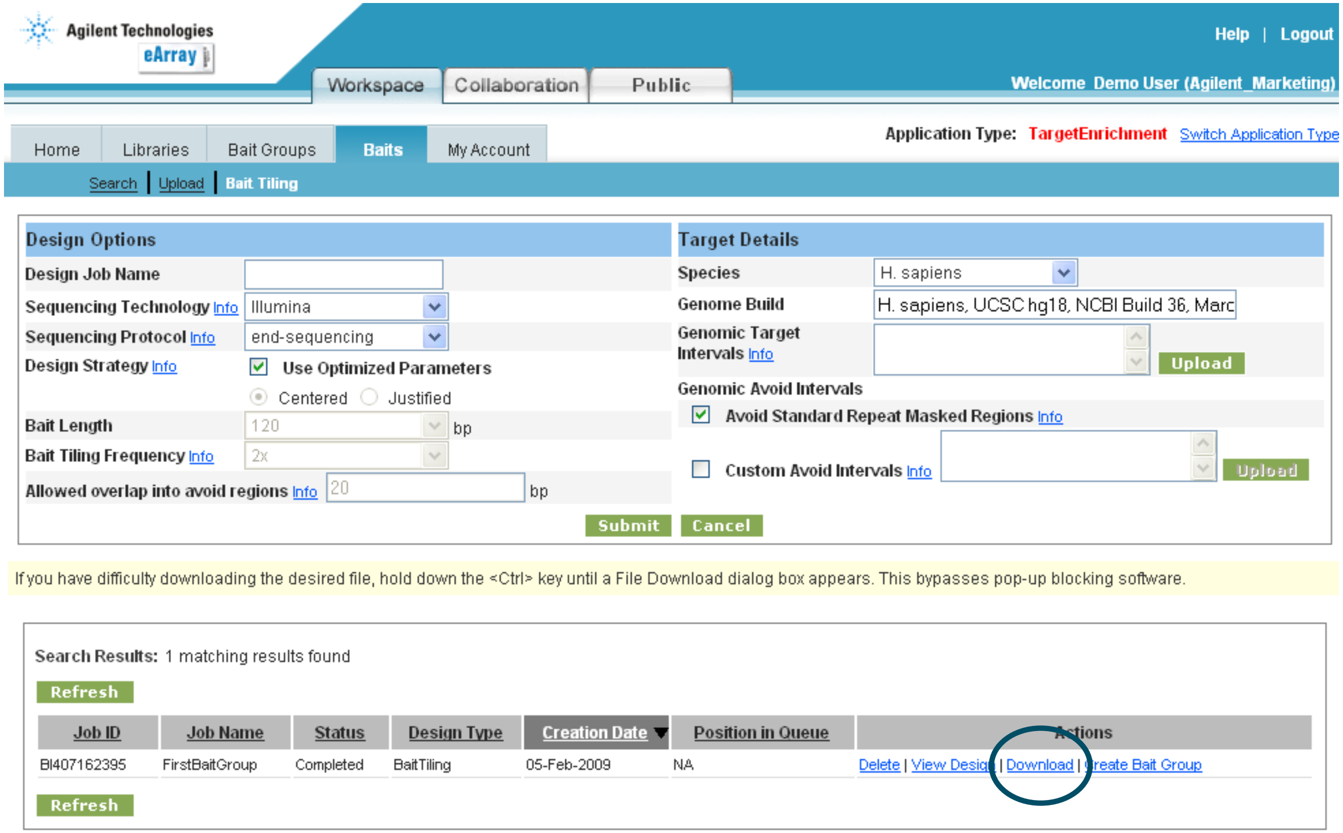
Chromosome	Chromosome Start	Chromosome Stop	Bait Name	Score	Strand
chrX	140476819	140476938	BI407149254_0	1000	+
chrX	046989026	046989145	BI407149254_2	1000	+
chrX	046989086	046989205	BI407149254_3	1000	+
chrX	046989206	046989325	BI407149254_5	1000	+

Agilent Technologies

Create a Bait Group

Download the Design (I)

- To download the design results files, click on Download on the Baits page.
- It may be necessary to hold down the Ctrl key until the File Download dialog box appears



Application Type: TargetEnrichment Switch Application Type

Design Options

Design Job Name	
Sequencing Technology Info	Illumina
Sequencing Protocol Info	end-sequencing
Design Strategy Info	☑ Use Optimized Parameters ● Centered ○ Justified
Bait Length	120 bp
Bait Tiling Frequency Info	2x
Allowed overlap into avoid regions Info	20 bp

Target Details

Species	H. sapiens
Genome Build	H. sapiens, UCSC hg18, NCBI Build 36, Marc
Genomic Target Intervals Info	

Genomic Avoid Intervals

☑ Avoid Standard Repeat Masked Regions Info

☐ Custom Avoid Intervals Info

If you have difficulty downloading the desired file, hold down the <Ctrl> key until a File Download dialog box appears. This bypasses pop-up blocking software.

Search Results: 1 matching results found

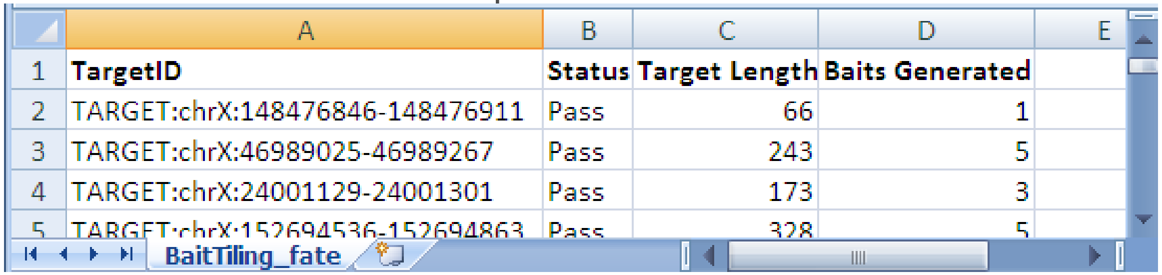
Job ID	Job Name	Status	Design Type	Creation Date	Position in Queue	Actions
BI407162395	FirstBaitGroup	Completed	BaitTiling	05-Feb-2009	NA	Delete | View Design | Download | Create Bait Group

Create a Bait Group

Download the Design (II)

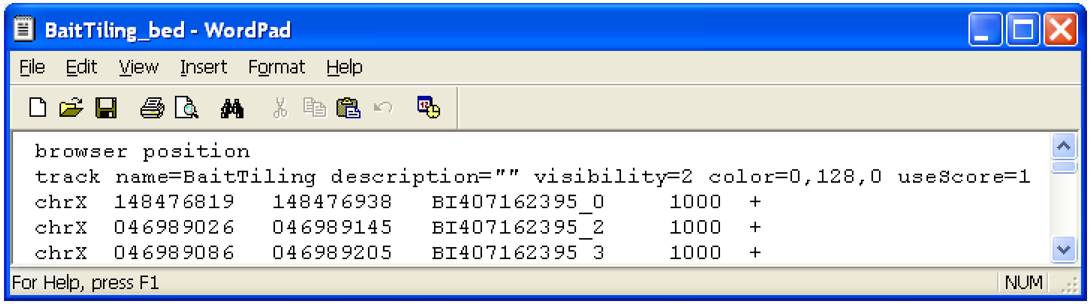
There are four files included in the downloaded zip:

Example of a Fate file:



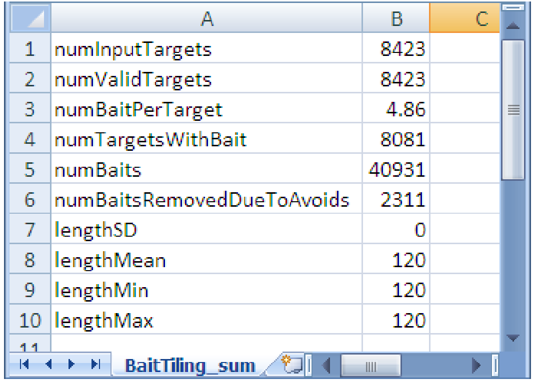
	A	B	C	D	E
1	**TargetID**	**Status**	**Target Length**	**Baits Generated**	
2	TARGET:chrX:148476846-148476911	Pass	66	1	
3	TARGET:chrX:46989025-46989267	Pass	243	5	
4	TARGET:chrX:24001129-24001301	Pass	173	3	
5	TARGET:chrX:152694536-152694863	Pass	328	5	

Example of a BED file:



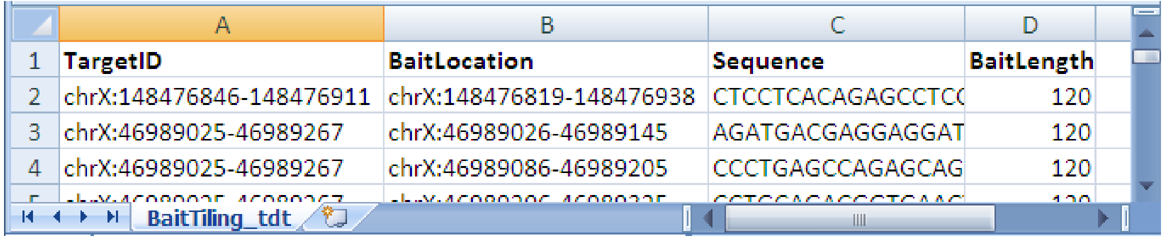
```
browser position
track name=BaitTiling description="" visibility=2 color=0,128,0 useScore=1
chrX  148476819  148476938  BI407162395_0   1000  +
chrX  046989026  046989145  BI407162395_2   1000  +
chrX  046989086  046989205  BI407162395_3   1000  +
```

Example of a Summary file:



	A	B	C
1	numInputTargets	8423	
2	numValidTargets	8423	
3	numBaitPerTarget	4.86	
4	numTargetsWithBait	8081	
5	numBaits	40931	
6	numBaitsRemovedDueToAvoids	2311	
7	lengthSD	0	
8	lengthMean	120	
9	lengthMin	120	
10	lengthMax	120	

Example of a TDT (tab delimited table) file:



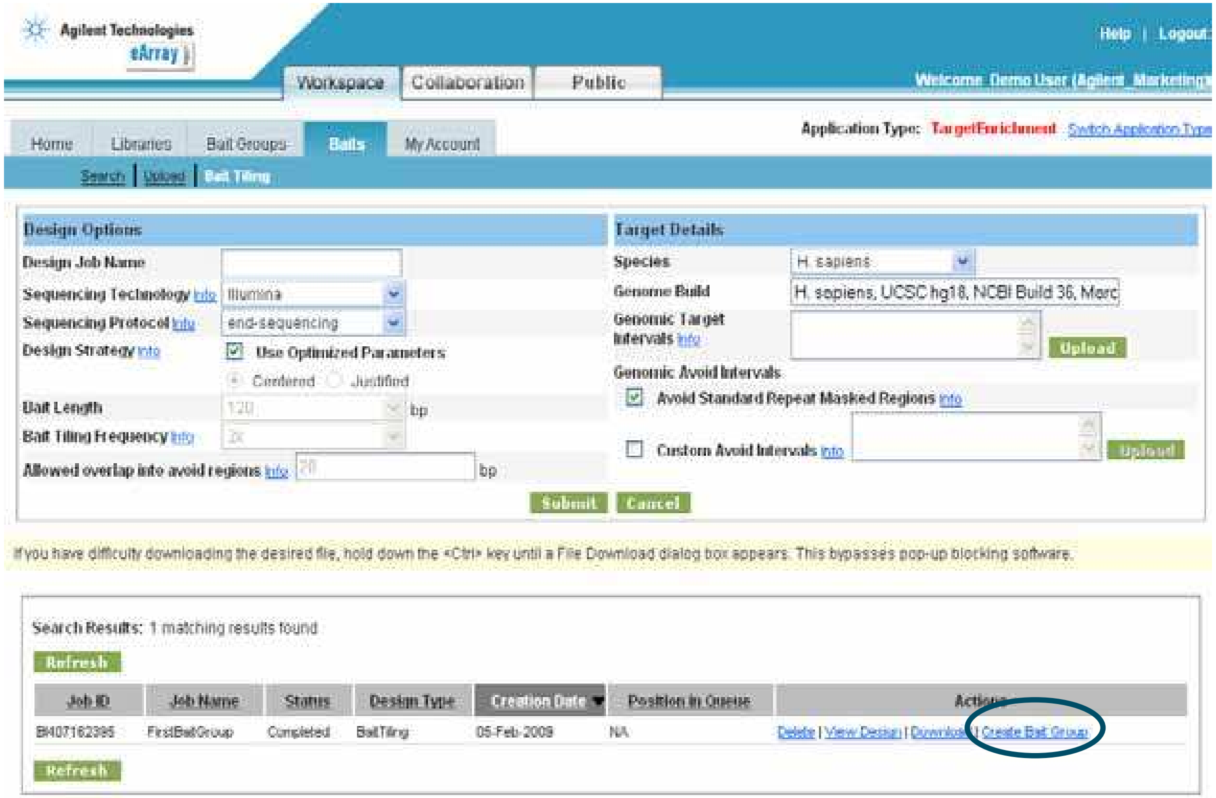
	A	B	C	D
1	**TargetID**	**BaitLocation**	**Sequence**	**BaitLength**
2	chrX:148476846-148476911	chrX:148476819-148476938	CTCCTCACAGAGCCTC	120
3	chrX:46989025-46989267	chrX:46989026-46989145	AGATGACGAGGAGGAT	120
4	chrX:46989025-46989267	chrX:46989086-46989205	CCCTGAGCCAGAGCAG	120

Create Bait Group

Create Bait Group

Once satisfied with the Bait Group Design, select **Create Bait Group**

Check the status of the Bait Group creation in the Pending Jobs quadrant of the **Home** page



Application Type: TargetEnrichment Switch Application Type

Design Options

Design Job Name	
Sequencing Technology info	Illumina
Sequencing Protocol info	end-sequencing
Design Strategy info	☑ Use Optimized Parameters ● Centered ○ Justified
Bait Length	120 bp
Bait Tiling Frequency info	2x
Allowed overlap into avoid regions info	20 bp

Target Details

Species	H. sapiens
Genome Build	H. sapiens, UCSC hg18, NCBI Build 36, Marc
Genomic Target Intervals info	

Genomic Avoid Intervals

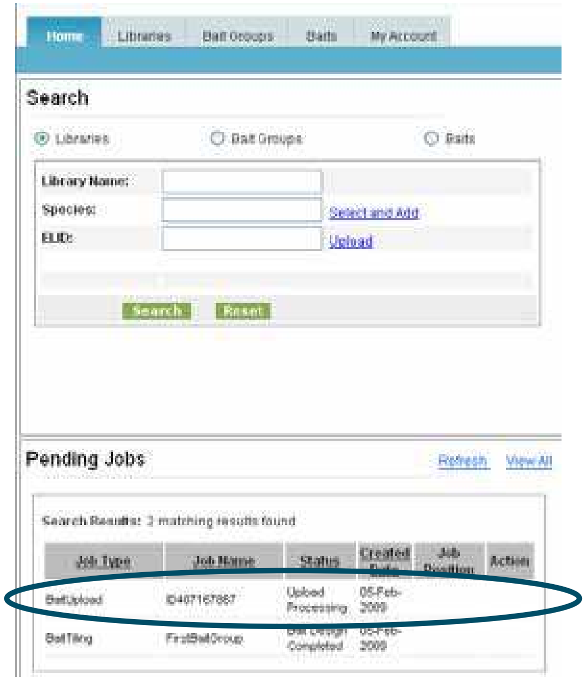
☑ Avoid Standard Repeat Masked Regions info

☐ Custom Avoid Intervals info

If you have difficulty downloading the desired file, hold down the <Ctrl> key until a File Download dialog box appears. This bypasses pop-up blocking software.

Search Results: 1 matching results found

Job ID	Job Name	Status	Design Type	Creation Date	Position in Queue	Actions
BI407162395	FirstBaitGroup	Completed	BaitTiling	05-Feb-2009	NA	Delete | View Design | Download | Create Bait Group



Search

● Libraries ○ Bait Groups ○ Baits

Library Name:	
Species:	
ELID:	

Pending Jobs

Search Results: 3 matching results found

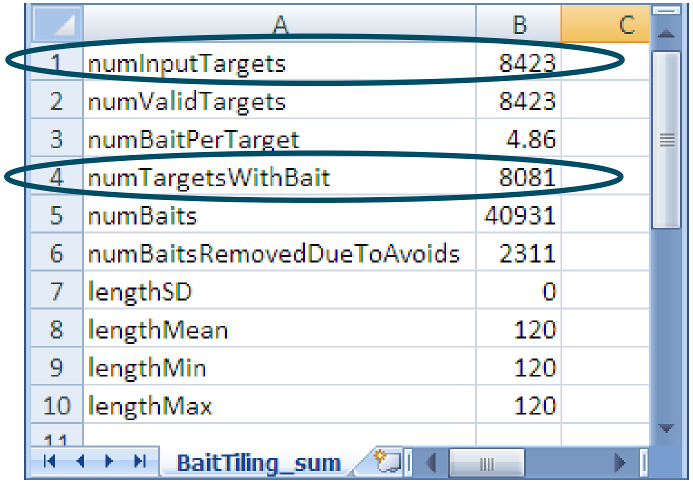
Job Type	Job Name	Status	Created Date	Job Position	Action
BaitUpload	I0407167867	Upload Processing	05-Feb-2009		
BaitTiling	FirstBaitGroup	Bait Design Completed	05-Feb-2009		

While waiting for the Bait Group to be created, design additional Bait Groups, if desired

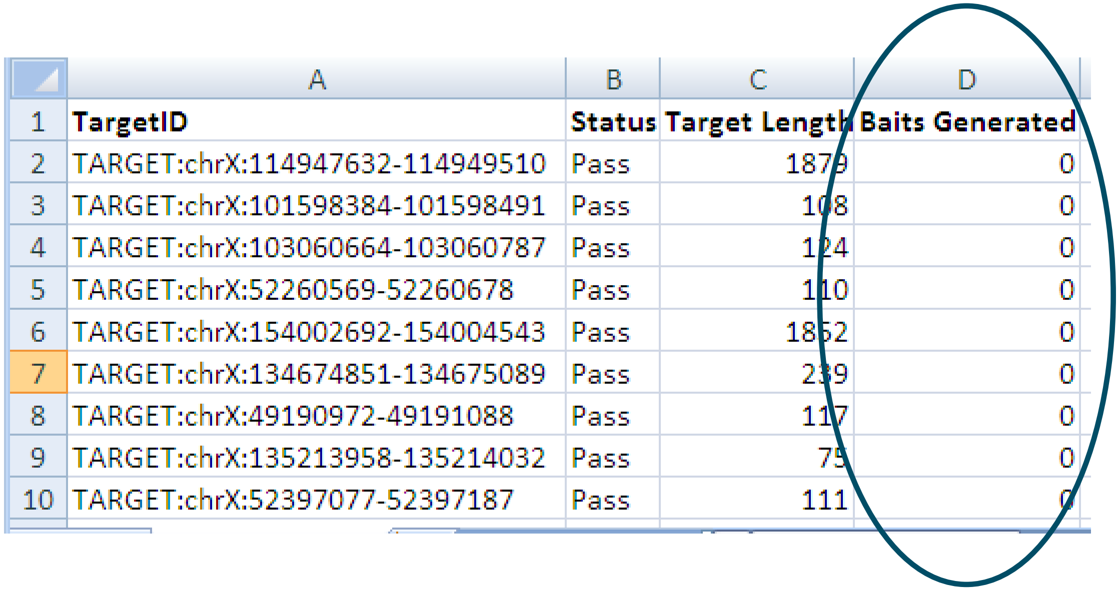
Examine Bait Group

Look for Missed Targets

- Open the BaitTiling_fate file in Excel
- Sort the file for Status to identify invalid (failed) genomic coordinates
  - These are targets for which the genomic coordinates could not be correctly assigned
- Sort the file for Baits Generated to identify targets for which no baits were assigned
  - In this example, according to the BaitTiling_sum file (left): 8423 - 8081 = 342 targets were not assigned baits; these can be viewed on the right in the BaitTiling_fate file



	A	B	C
1	numInputTargets	8423	
2	numValidTargets	8423	
3	numBaitPerTarget	4.86	
4	numTargetsWithBait	8081	
5	numBaits	40931	
6	numBaitsRemovedDueToAvoids	2311	
7	lengthSD	0	
8	lengthMean	120	
9	lengthMin	120	
10	lengthMax	120	



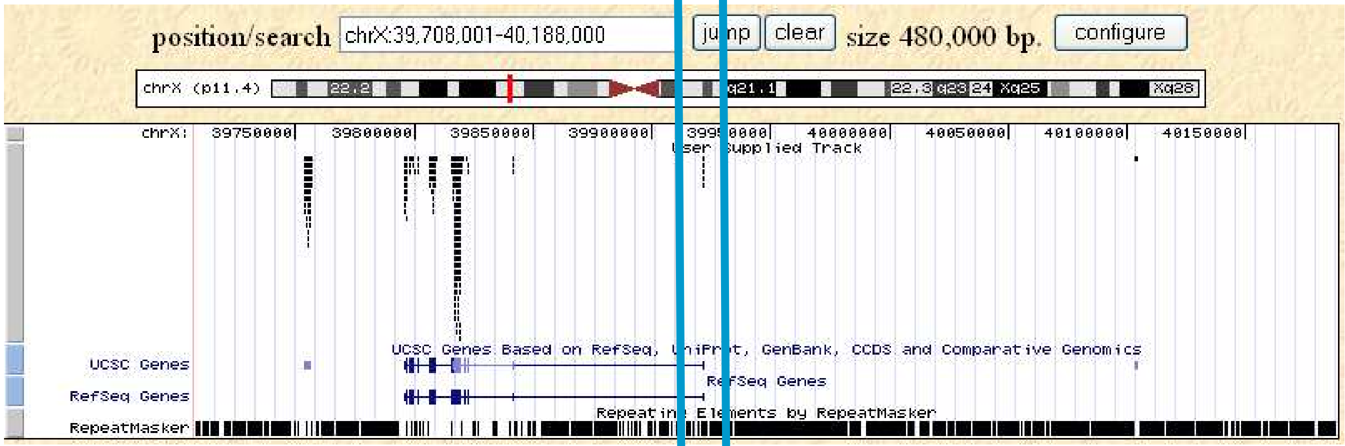
	A	B	C	D
1	**TargetID**	**Status**	**Target Length**	**Baits Generated**
2	TARGET:chrX:114947632-114949510	Pass	1879	0
3	TARGET:chrX:101598384-101598491	Pass	108	0
4	TARGET:chrX:103060664-103060787	Pass	124	0
5	TARGET:chrX:52260569-52260678	Pass	110	0
6	TARGET:chrX:154002692-154004543	Pass	1852	0
7	TARGET:chrX:134674851-134675089	Pass	239	0
8	TARGET:chrX:49190972-49191088	Pass	117	0
9	TARGET:chrX:135213958-135214032	Pass	75	0
10	TARGET:chrX:52397077-52397187	Pass	111	0

Examine Bait Group

View Design in UCSC Browser

- The BED file can be uploaded into the UCSC browser as an easy method to visualize the probes tiled across targets of interest

Segment of chrX with baits tiled across exons (target intervals)



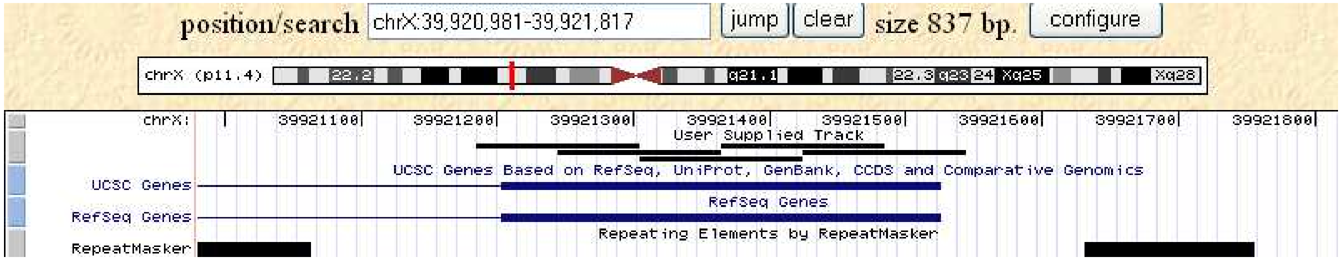
position/search chrX:39,708,001-40,188,000 size 480,000 bp.

Baits

Genes

RepeatMasker

Zoomed in view of baits tiled across a single exon



position/search chrX:39,920,981-39,921,817 size 837 bp.

Baits

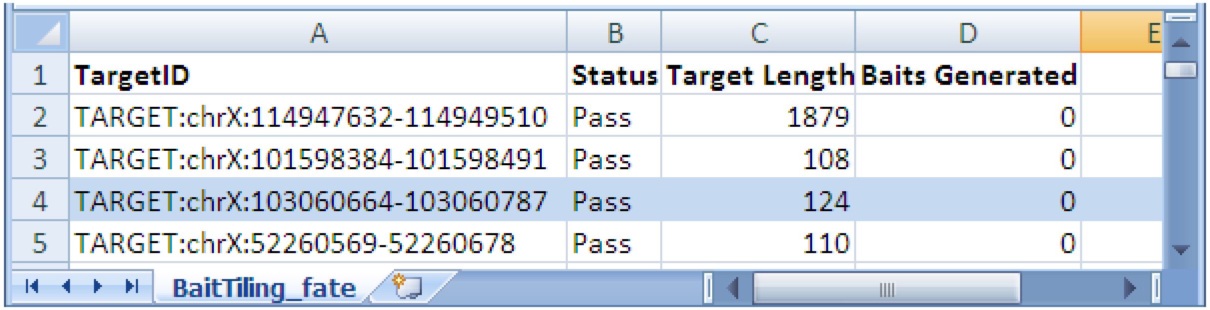
Genes

RepeatMasker

Examine Bait Group

Identify Targets for Potential Re-Tiling

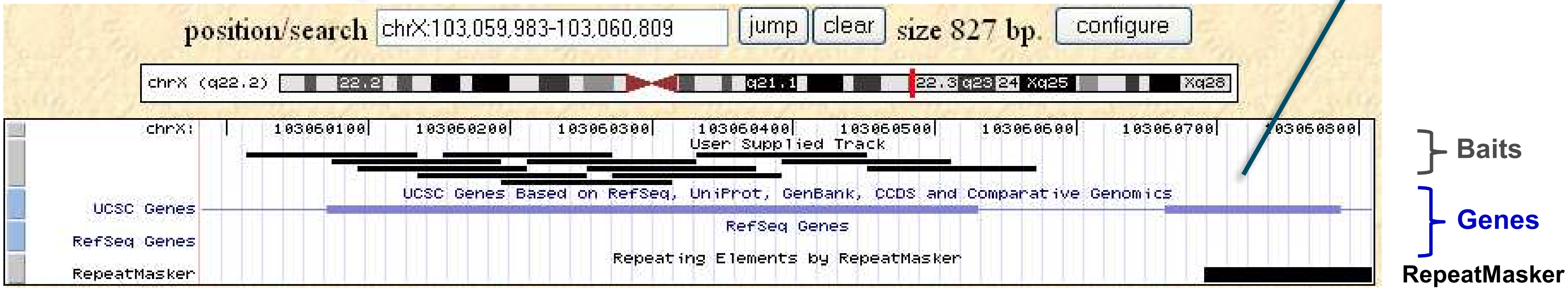
1. Select targets not assigned baits in the Fate file.



	A	B	C	D
1	**TargetID**	**Status**	**Target Length**	**Baits Generated**
2	TARGET:chrX:114947632-114949510	Pass	1879	0
3	TARGET:chrX:101598384-101598491	Pass	108	0
4	TARGET:chrX:103060664-103060787	Pass	124	0
5	TARGET:chrX:52260569-52260678	Pass	110	0

2. Upload BED file to the UCSC browser, and zoom in on the target to identify the reason that it was provided zero baits.

3. In this example, the exon on the right is covered by a section identified as "repeats" by the RepeatMasker track, and design parameters had specified to avoid these regions. Therefore, this target received zero baits.

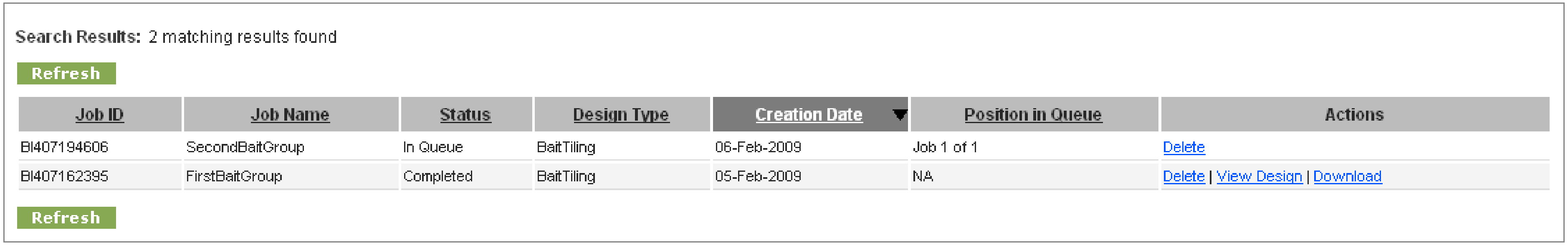


position/search chrX:103,059,983-103,060,809 size 827 bp.

If the target is still desired, it is possible to create a new, additional Bait Group for this target with new design parameters that allow repeat regions. Both Bait Groups can later be included in the final library.

Complete Design for all Bait Groups

- Before proceeding to create the Library, complete the design for all Bait Groups that might be included in that Library
- Reasons for using multiple Bait Groups include:
  - To use different design options for different targets
  - To include Bait Groups from previous projects
  - To maintain separate Bait Groups based on target types; for example, a Bait Group of chrX exons, a Bait Group for Kinases, and so on



Search Results: 2 matching results found

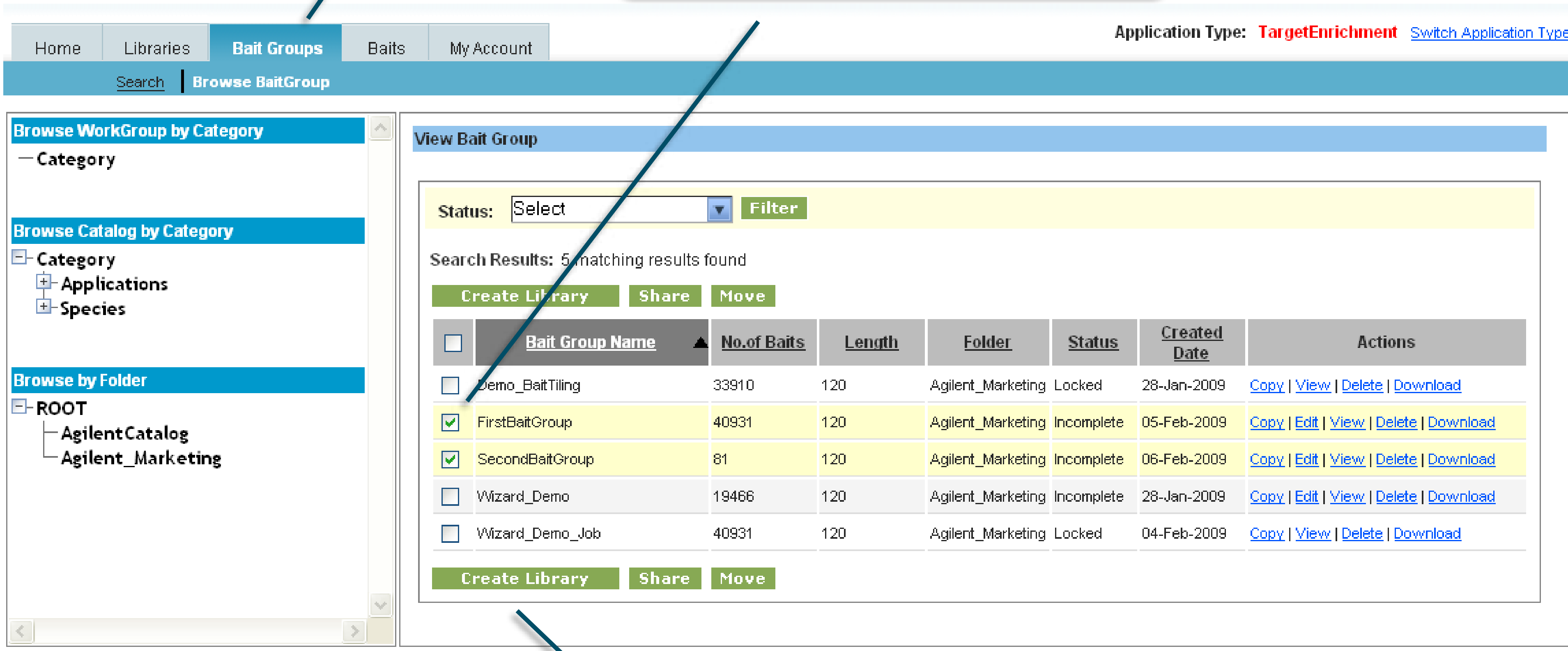
Job ID	Job Name	Status	Design Type	Creation Date	Position in Queue	Actions
BI407194606	SecondBaitGroup	In Queue	BaitTiling	06-Feb-2009	Job 1 of 1	Delete
BI407162395	FirstBaitGroup	Completed	BaitTiling	05-Feb-2009	NA	Delete | View Design | Download

Create the Library

Select Bait Groups to Include in the Library

1. Go to the **Bait Groups** page, and select **Browse BaitGroup**

2. Place a check next to any Bait Groups that should be included in the Library



Application Type: TargetEnrichment Switch Application Type

Status: Select

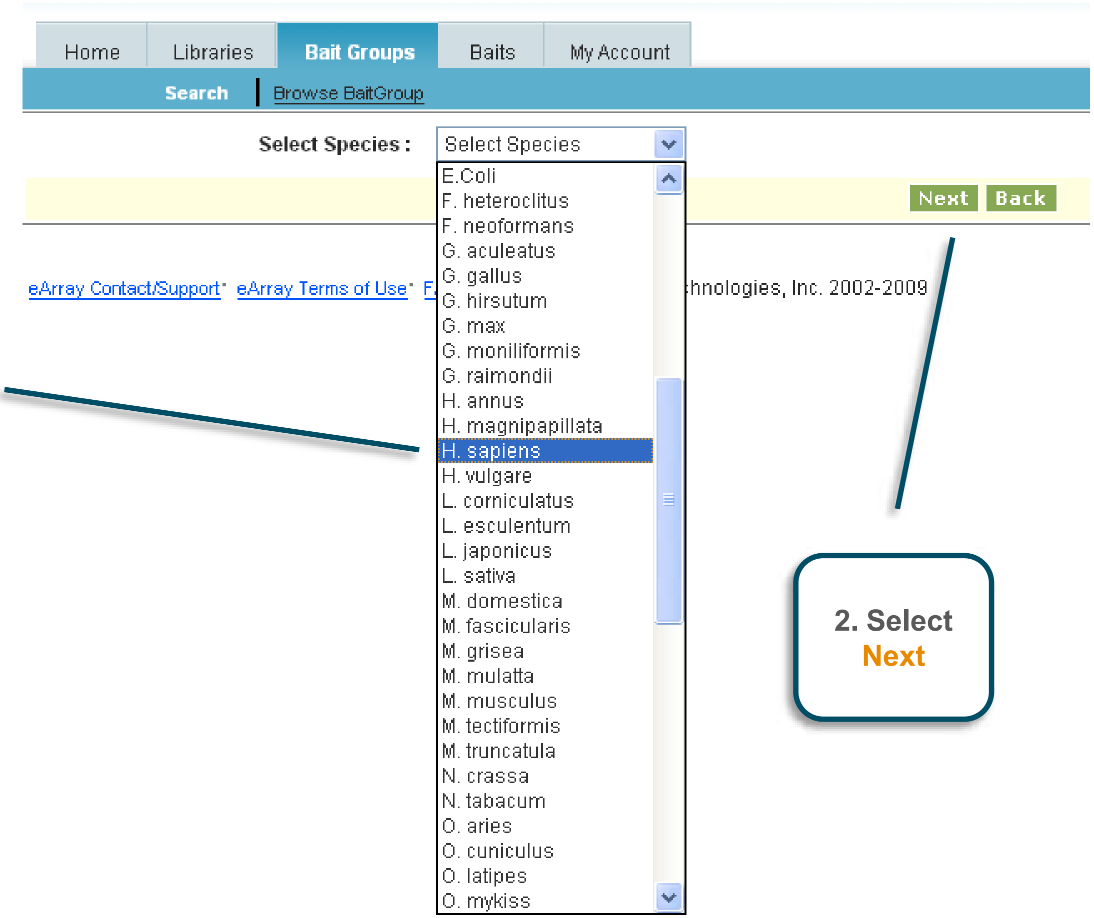
Search Results: 5 matching results found

☐	Bait Group Name	No.of Baits	Length	Folder	Status	Created Date	Actions
☐	Demo_BaitTiling	33910	120	Agilent_Marketing	Locked	28-Jan-2009	Copy | View | Delete | Download
☑	FirstBaitGroup	40931	120	Agilent_Marketing	Incomplete	05-Feb-2009	Copy | Edit | View | Delete | Download
☑	SecondBaitGroup	81	120	Agilent_Marketing	Incomplete	06-Feb-2009	Copy | Edit | View | Delete | Download
☐	Wizard_Demo	19466	120	Agilent_Marketing	Incomplete	28-Jan-2009	Copy | Edit | View | Delete | Download
☐	Wizard_Demo_Job	40931	120	Agilent_Marketing	Locked	04-Feb-2009	Copy | View | Delete | Download

3. Select **Create Library**

Create the Library

Select the Species



1. Select the species

2. Select Next

Create the Library

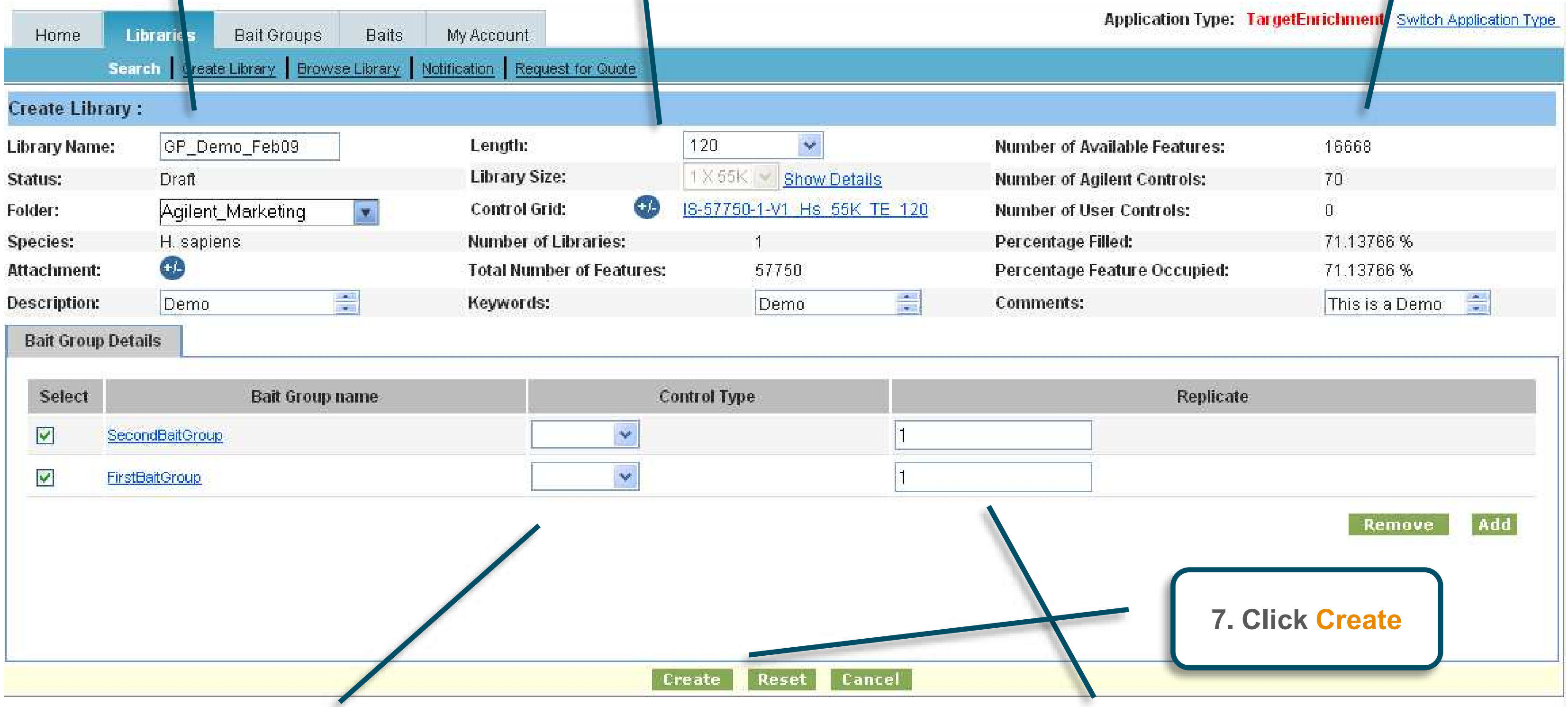
Define the Library

1. Provide a name for the library

2. Set the length for the baits

3. Provide a Description, Keywords, and Comments

4. View the Library statistics



Application Type: TargetEnrichment

Create Library :

Library Name:	GP_Demo_Feb09	**Length:**	120	**Number of Available Features:**	16668
Status:	Draft	**Library Size:**	1 X 55K	**Number of Agilent Controls:**	70
Folder:	Agilent_Marketing	**Control Grid:**	IS-57750-1-V1_Hs_55K_TE_120	**Number of User Controls:**	0
Species:	H. sapiens	**Number of Libraries:**	1	**Percentage Filled:**	71.13766 %
Attachment:		**Total Number of Features:**	57750	**Percentage Feature Occupied:**	71.13766 %
Description:	Demo	**Keywords:**	Demo	**Comments:**	This is a Demo

Select	Bait Group name	Control Type	Replicate
☑	SecondBaitGroup		1
☑	FirstBaitGroup		1

7. Click Create

5. Set the Control Type for each Bait Group. If these are not controls, leave the Control Type blank.

6. Determine the number of replicates desired per Bait Group. Use the Percentage Filled statistic above to help decide on replicate #, and to monitor the effect of changing the #.

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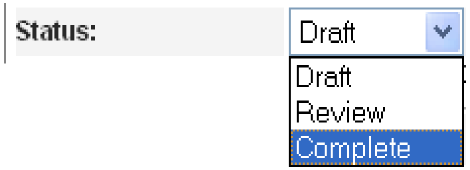
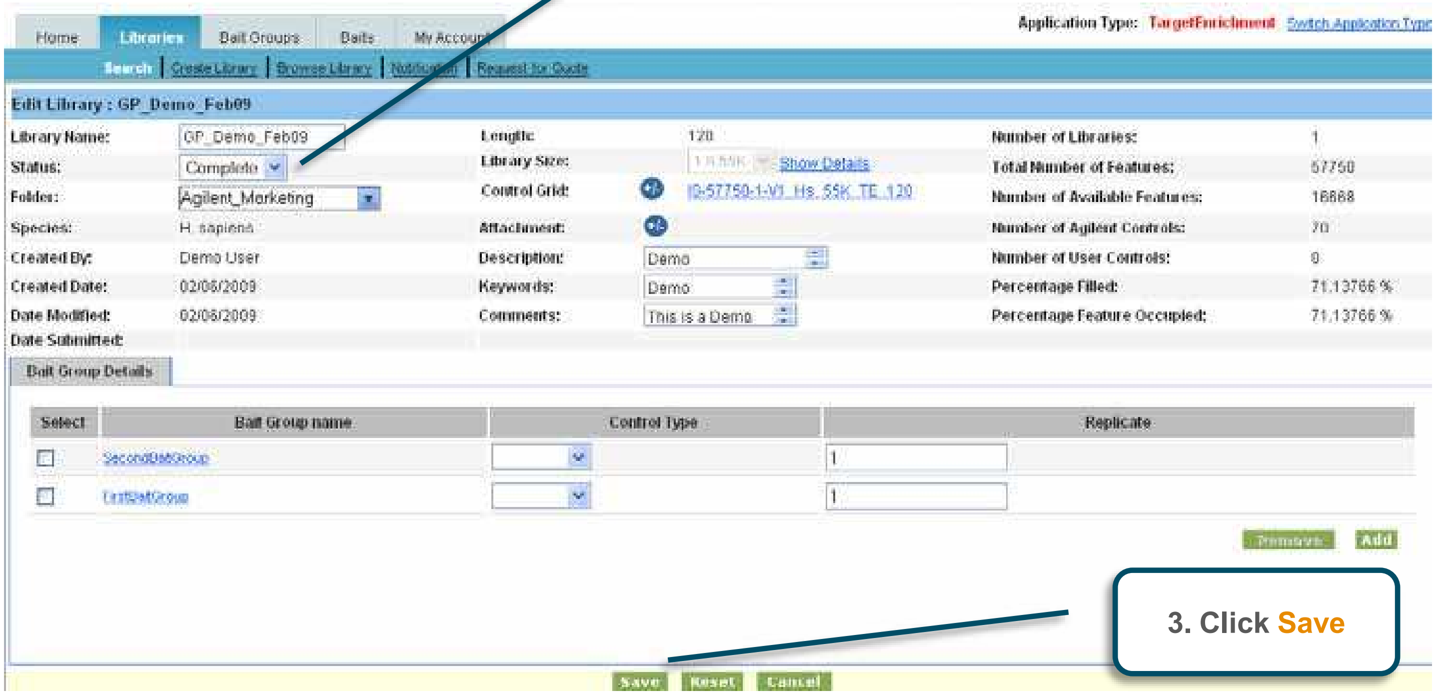
Create the Library

Review Library Details and Submit as Complete

1. **Review the Library Details**
If desired, replicate #s can be edited at this time

2. Determine the status for the Library
If the library is to be submitted, it must be set as Complete.





Application Type: TargetEnrichment

Edit Library : GP_Demo_Feb09

Library Name:	GP_Demo_Feb09	**Length:**	120	**Number of Libraries:**	1
Status:	Complete	**Library Size:**	1 x 55K	**Total Number of Features:**	57750
Folder:	Agilent_Marketing	**Control Grid:**	IG-57750-1-V1_Hs_55K_TE_120	**Number of Available Features:**	16668
Species:	H. sapiens	**Attachment:**		**Number of Agilent Controls:**	70
Created By:	Demo User	**Description:**	Demo	**Number of User Controls:**	0
Created Date:	02/06/2009	**Keywords:**	Demo	**Percentage Filled:**	71.13766 %
Date Modified:	02/06/2009	**Comments:**	This is a Demo	**Percentage Feature Occupied:**	71.13766 %
Date Submitted:					

Bait Group Details

Select	Bait Group name	Control Type	Replicate
☐	SecondBaitGroup		1
☐	FirstBaitGroup		1

3. Click Save

Create the Library

Finalize Submission

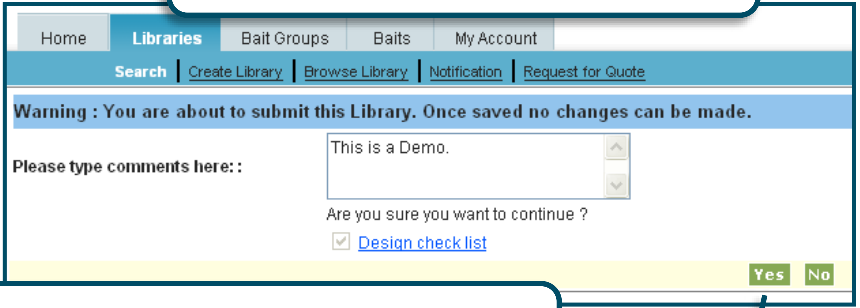
1. Provide a comment and click **Yes**

Warning : You are about to complete this Library. Once saved no changes can be made.

Please type comments here: : This is a Demo

Are you sure you want to continue ?

2. Provide a comment in the next window and click on **Design check list**



Warning : You are about to submit this Library. Once saved no changes can be made.

Please type comments here: : This is a Demo.

Are you sure you want to continue ?

☑ Design check list

3. Read and check off the Design check list, and click **Done**

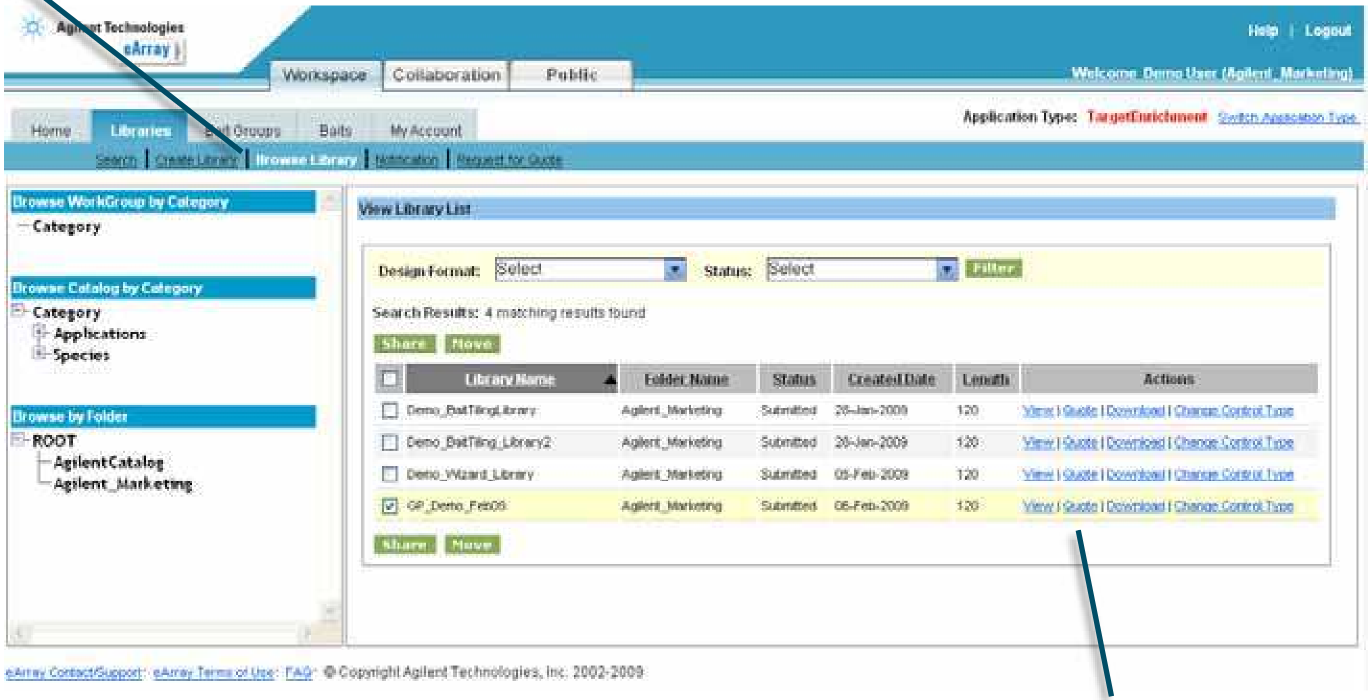
4. Click **Yes** to finalize the submission of the Library, making it available for getting a quote.

This is not a kit order, this is only a submission so that the kit can be ordered.

Generate a Quote

Select Library

1. Select Browse Library on the **Libraries** page to find the Library



Design Format: Select
Status: Select

Search Results: 4 matching results found

☐	Library Name	Folder Name	Status	Created Date	Length	Actions
☐	Demo_BaitTilingLibrary	Agilent_Marketing	Submitted	28-Jan-2009	120	View | Quote | Download | Change Control Type
☐	Demo_BaitTiling_Library2	Agilent_Marketing	Submitted	28-Jan-2009	120	View | Quote | Download | Change Control Type
☐	Demo_Wizard_Library	Agilent_Marketing	Submitted	05-Feb-2009	120	View | Quote | Download | Change Control Type
☑	GP_Demo_Feb09	Agilent_Marketing	Submitted	06-Feb-2009	120	View | Quote | Download | Change Control Type

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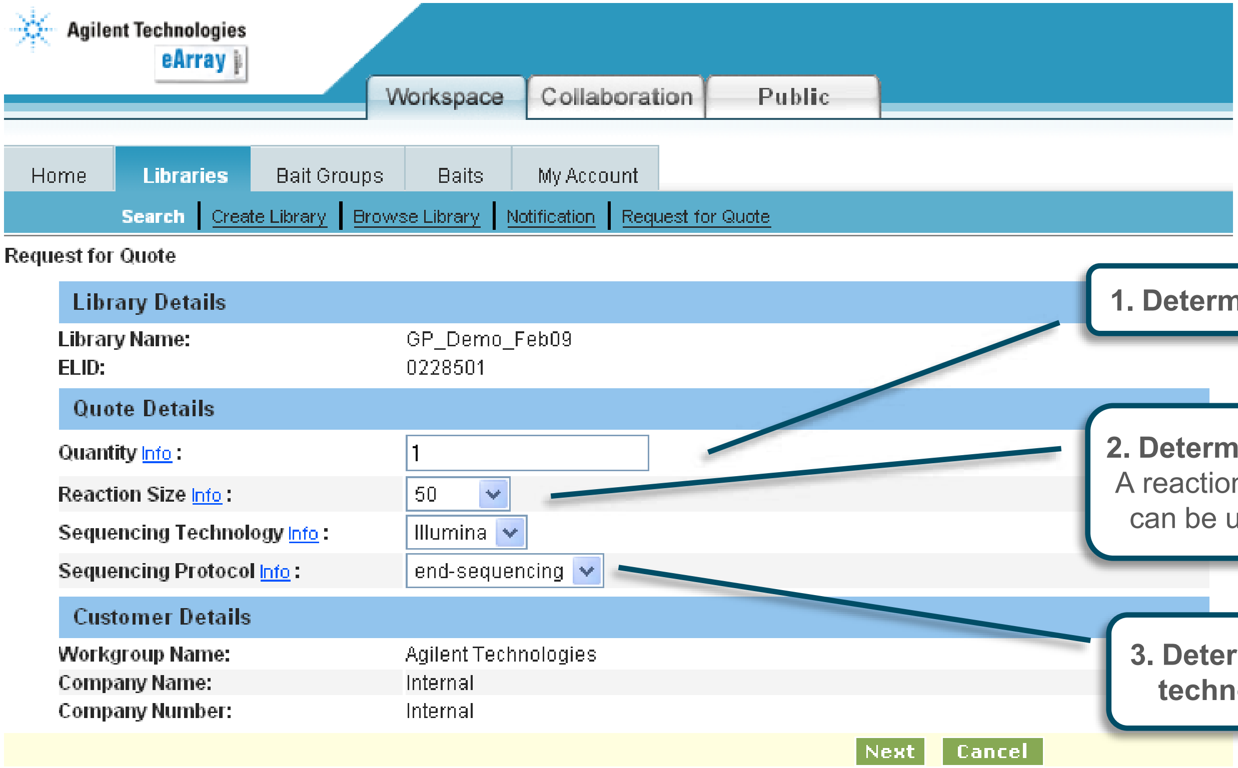
2. Click on **Quote**

Generate a Quote

Describe Order



Request for Quote

Library Details

Library Name:	GP_Demo_Feb09
ELID:	0228501

Quote Details

Quantity Info :	1
Reaction Size Info :	50
Sequencing Technology Info :	Illumina
Sequencing Protocol Info :	end-sequencing

Customer Details

Workgroup Name:	Agilent Technologies
Company Name:	Internal
Company Number:	Internal

1. Determine the number of Libraries desired

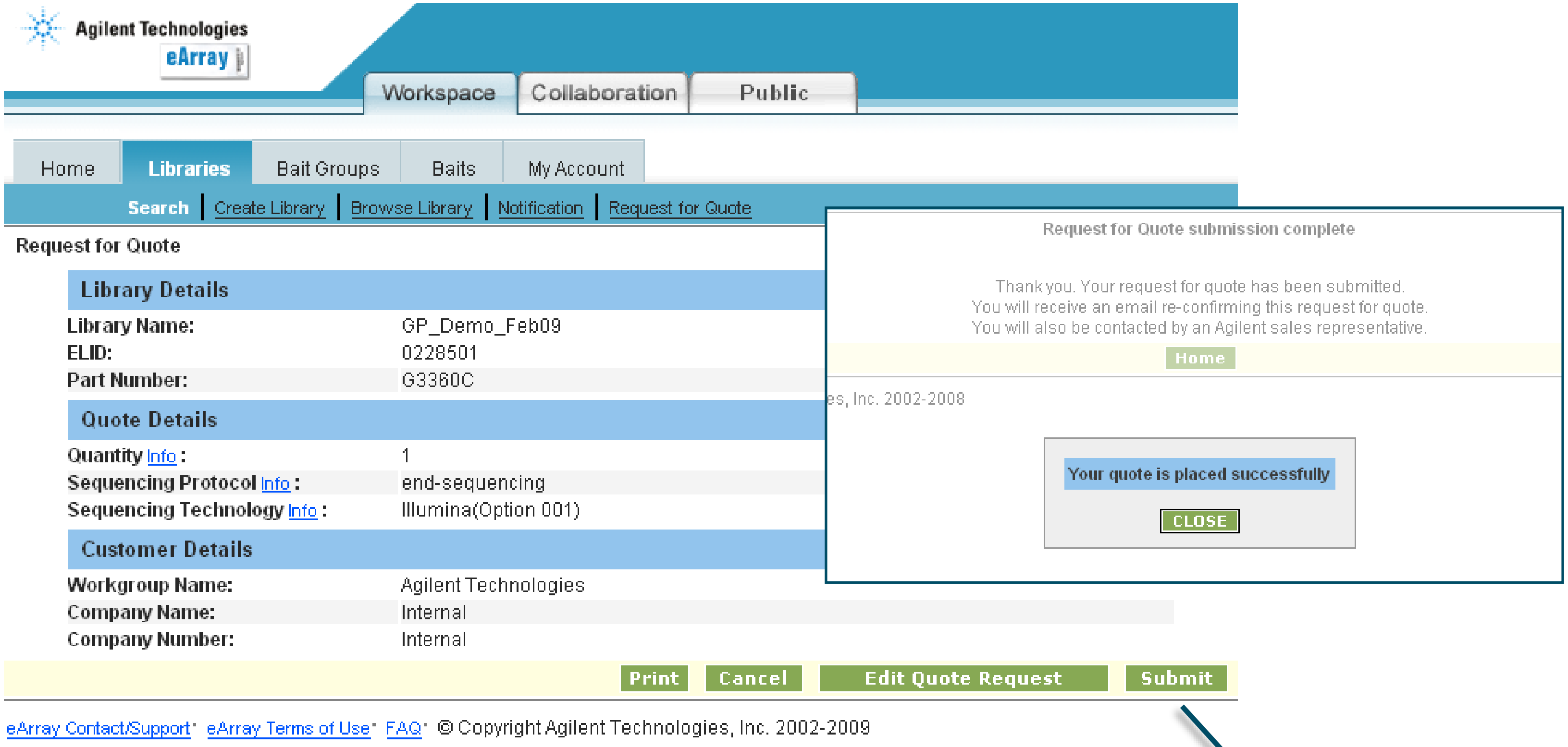
2. Determine the number reactions per library:
A reaction size of 50 means that a single Library can be used for capture with 50 DNA samples

3. Determine the sequencing technology and protocol

4. Click Next

Generate a Quote

Review and Submit Quote



Request for Quote

Library Details

Library Name:	GP_Demo_Feb09
ELID:	0228501
Part Number:	G3360C

Quote Details

Quantity Info :	1
Sequencing Protocol Info :	end-sequencing
Sequencing Technology Info :	Illumina(Option 001)

Customer Details

Workgroup Name:	Agilent Technologies
Company Name:	Internal
Company Number:	Internal

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Request for Quote submission complete

Thank you. Your request for quote has been submitted.
You will receive an email re-confirming this request for quote.
You will also be contacted by an Agilent sales representative.

es, Inc. 2002-2008

Your quote is placed successfully

Click **Submit**