



SeqScape Software v2.5

Quick Reference Guide

Applied Biosystems SeqScape Software v2.5 is expressly designed for mutation detection and analysis, SNP discovery and validation, pathogen subtyping, allele identification, and sequence confirmation.

This Quick Reference Guide describes the four workflows performed in these types of studies:



Workflow for Creating a Project



Workflow for Reviewing Data



Workflow for Modifying Settings



Workflow for Exporting and Printing

Workflow for Creating a Project

All analysis in SeqScape software occurs in a project. Before you can create a project you must create a project template that contains:

- A Reference Data Group (RDG)
- Analysis Defaults
- Display Settings

Once a project is created, the project template can be used recurrently.

Note: VariantSEQr customers should proceed directly to Step 4 "Add Sample Files" on Page 7.

Creating a project requires that you follow these steps:

Creating a Project
1. Import the Reference Sequence
2. Define Analysis and Display Settings
3. Create a Project Template
4. Add Sample Files
5. Analyze the Data

Step 1: Import a Reference Sequence

IMPORTANT! The Reference Sequence format can be any of the following:

- .txt, ab1, .seq, .fsta files
- Genbank format files
- Aligned sequences in .fsta (FASTA format)

The workflow described below uses a Genbank file for your reference data. To begin, first download a Genbank file, then create a known variants table.

Note: If you download a Genbank file in the NCBI web interface, select **Display as Genbank**, then **Send to File** to save it as a text file that can be imported.



To use a Genbank file as your reference:

- 1. Open the **SeqScape Manager** from the Tools menu.
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- 2. Select the **Reference Data Group** tab.
- 3. Click **New**, then enter a name.
- 4. Select the **ROI** (Regions of Interest) tab.

Note: For information on any of the four panes in the ROI tab (Layer, ROI, Reference Sequence, Reference Segment), click **Info**.

5. Click on the **Add Ref. Segment** button.

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6. Select the Genbank file, then click **Import**.

Note: When the Genbank file imports, information from the feature table populates the Regions of Interest (ROI) table in the SeqScape software and layers are automatically created.

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/organism="Homo sapiens"
/db xref="taxon:9606"
/map="6p21.3"
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/gene="HLA-C"
/allele="HLA-Cw*0802"
join(<1270,517>792)
/gene="HLA-C"
/product="HLA-C class I antigen"
join(<1270,517>792)
/gene="HLA-C"
/codon_start=3
/product="HLA-C class I antigen"
/protein id="AAG53742.1"
/db_xref="GI:12483747"
/translation="SHSMRYFYTAVSRPGRGEPRFIAVGYVDDTQFVQFDSDAASPRG
EPRAPWVEQEGPEYWDRETQKYKRQAQTDRVSLRNLRGYYNQSEAGSHTLQRMYGCDL
GPDGRLLRGYNQFAYDGKDYIALNEDLRSWTAADKAAQITQRKWEAAREAEQRRAYLE
GTCVEWLRRYLENGKKTLQRA"
1270
/gene="HLA-C"
/number=2
517792
/gene="HLA-C"
/number=3

7. Select the **NT Variants** tab (RDG Properties) and select the NT Variants you want to add to the reference sequence, then click **Import** to import a tabdelimited variants file or a multi-aligned sequences (.fsta) file.

Note: When importing an AA variants file, use a tab delimited variants format.

8. Click **OK**.

You have now completed importing the reference sequence.

Step 2: Define Analysis and Display Settings

To define analysis defaults:

- 1. Select Tools > SeqScape Manager.
- 2. Select the **Analysis Protocols** tab.
- 3. Click New, then enter a name.
- 4. Select the **Basecalling** tab, then select the Basecaller file and Dye/Primer file from the drop-down lists.
- 5. Keep the default settings for Processed Data, Ending Base and Quality Threshold options unless a custom setting is required.
- 6. Select the **Mixed Bases** tab to define the secondary peak threshold for mixed base identification.

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4	change base	PLAB_target_	56	С	Y	Cyan		yes
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	Change Base	PLAB_target_e				Oyan		yes
	Change Base	PLAB_target_p	511	Т	C	Oyan		yes





- 7. Select the Clear Range tab.
- 8. Keep the default settings for Quality Value and Reference Trimming.
- × General Basecalling Mixed Bases Clear Range Filter Clear Range Methods First bp Last bp 🔽 Use quality values Nbases Nbases Remove bases from the ends until fewer than 4 bases out of 20 have QVs < 20 Qv5x αv₅̂x Use identification of N calls < X N's per Z bases until there are fewer than 4 Ns out of 20 bases < X N's per Z bases Mask M13 universal sequencing primers Use reference trimming Multiple clear range methods are applied in order αγື⇒) Smallest clear range is the result. ОК Cancel
- Select the Filter tab. Keep the default Filter settings as shown.
- 10. Click OK.
- 11. Select the **Analysis Defaults** tab in the SeqScape Manager.
- 12. Click **New,** then enter an Analysis Defaults name.
- 13. Select the Sample tab.
- 14. In the drop-down list, select the Analysis Protocol you created.
- 15. In the **Project** and **Specimen** tabs, keep the default settings.
- 16. Click Save.

Generally you will keep the defaults for **Display Settings** and proceed to Step 3, "Creating a Project Template."

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ew Analysis Settings		×
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Step 3: Create a Project Template

To create a project template:

- 1. Select Tools > SeqScape Manager.
- 2. Select the **Project Templates** tab.
- 3. Click **New**, then enter a Project Templates name.
- 4. In the drop-down lists, select the Reference Data Group and Analysis Defaults that you previously created in Steps 1 and 2.
- 5. Keep the default Display Settings.
- 6. Click OK.
- 7. Close the SeqScape Manager.

You now have created the Project Template.

Step 4: Add Sample Files

To create a project:

- 1. In SeqScape software, select File > New Project.
- 2. Enter a name for the project.
- 3. In the Project Template list, select the project template you previously created (in Step 3).
- 4. Click New.

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ype the first few letters of the project tem	plate you are loo	oking for. HLA					

5. To add data to your project, select File > Import Samples.

IMPORTANT! Groups of sample files from the **same** biological source must be grouped together (into one specimen) in SeqScape software.

- 6. Navigate to your data folder, then group your sample files into specimens.
- 7. For manual specimen creation:
 - a. Click New Specimen.
 - b. Select files belonging to the specimen, then click **Add Samples**.
- 8. For automatic specimen creation:
 - a. Define the delimiters by assigning alphanumeric values in the **Start** and **End** fields.
 - b. Select the data folder, then click **Auto Add**.

Note: It is recommended that you use a sample naming convention such as:

IndividualID_Gene_Exon_ WellLoc_F/R.ab1

9. Click **OK**.

You now have created a project with samples and you are ready to analyze the data.



Step 5: Analyze the Data

To analyze your data:

1. Click 🕨 (Analyze) for analysis to begin.

Note: A progress bar indicates that the software is performing basecalling, trimming, assembly, consensi alignment and reference comparison on your data.

After a successful analysis, your data appear assembled in the Project view.

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Workflow for Reviewing Data

Reviewing data require that you follow these steps:

Reviewing Data and Results
1. Review Data per Specimen and Assign Pass/Fail Status
2. Review All Data in Project View
3. View Variant Results in Mutations/AA Variants Reports
4. View Resequencing Results in the Genotyping Report

Step 1: Review Data per Specimen and Assign Pass/Fail Status

To review data by specimen:

1. In the Project Navigator (Project view), select a specimen.

> **Note:** The specimen view shows the sample distribution within the specimen across the reference sequence. Forward and reverse orientations are indicated by arrows representing sequence coverage.

 In the Project Navigator, open the Analysis QC Report to view failed sample traces (Unassembled).

Note: SeqScape software automatically filters out low quality sample traces based on the settings in the Filter tab of the Analysis Protocol. These samples are grouped in the unassembled node after analysis. Descriptions of the failed samples appear in the Sample Analysis Table (QC Report).



Note: The Analysis QC Report provides a list of sample traces with possible heterozygous indel mutations (HIMs). HIMs are detected when two alleles differ by an insertion or deletion in a sample trace.

3. Adjust analysis settings to allow failed samples to assemble in the project (see Modifying Settings Workflow for more detail).

Note: You may need to modify your Filter and/or Clear Range analysis settings and then reanalyze data to allow failed samples to pass (Assembled).

4. Select a Segment name, then select the **Assembly** tab to view passed sample traces (Assembled).

Note: The Segment Assembly displays the assembly of sample traces within a specimen for a specific region of the reference sequence. To zoom in/out, select **Cntl +/-**.

- 5. Edit bases with low quality values if necessary.
 - a. You can customize the bar colors for the quality values (in Display Settings) and flag bases with low quality values in red, for example.

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- b. When switching between the Project view and the Assembly view, the base position is bookmarked for easier editing.
- c. Make sure **Discrepancy** is checked in Multiple Tab Jump Settings, if required.

Note: The algorithm automatically corrects for sequencing errors by reviewing data quality in both directions (forward and reverse) to arrive at an accurate consensus.



- 6. Right-click the specimen name to assign Pass/Fail review status.
- 7. Repeat Steps 1 to 6 for all specimens in the project.

You are now ready to review your data at the project level.

Step 2: Review all Data in Project View

To review all data:

- 1. Examine variants between the specimen consensus and the reference sequence by either of the following methods:
 - a. Select the Character/ Dots view. In this view, dots appear for all bases as in the reference, and characters appear for variants.
 - b. View data by layers. Select a layer from the Active Layer drop-down list.



Reference:

PLAB SegScape Webinar

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- c. Select the **Tab Jump to Next** field. In this setting, you can select **Known/ Unknown Variant**.
- 2. To add a Known Variant rightclick a base, then select **Add Variant**.
- Click **OK**. The variant is displayed in the Overview pane as a red bar.
- 4. To view Amino Acid translation, click on the **Amino Acid** view.

You are now ready to review the variant results in reports.

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Step 3: View Variant Results in Mutations/AA Variants Reports

To view variant results in reports:

1. Select the desired layer using the **Active Layer** drop-down list, and highlight the project name within the Project Navigator.

Note: To view results at the specimen level, highlight the specimen name.

- 2. Select **Analysis**, then select **Report Manager**.
- 3. In the left pane, select the **Mutations Report**.
- 4. In the right pane, view mutations in the Mutations Table.
- In the Mutations Table, click on a base change to link the mutation to a specimen consensus in the Project view.

Note: You can review the mutation by looking at its quality value and its position in a region of interest (ROI).



Note: You can sort mutations by quality value, type, and so on by double-clicking any of the column headers. To remove a column, right-click, then deselect the column name.

6. Click the triangle icon next to the specimen name to view the sample electropherogram.

Note: Look for mutations at the specimen level or "confirmed" mutations due to bidirectional coverage.

- Open the Mutations report to view the amino acid effect (AA Change/Effect column) for translated regions.
- 8. Click any of the amino acids in the AA Change column to navigate to the AA Variants Report.
- 9. Click an AA Change to link the AA variant to a specimen consensus in the Amino Acid view.

Note: To adjust how the report displays text results, click **Report Settings**, then deselect **Wrap Text**.

To view reports and data simultaneously, select **Window > Tile** in the main menu.



			AA V	ariants				
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Specimen1	V14L	14	1	Sub	no	40G>C ROI: NM_004864_exon_1		•
Specimen1	\$53[T,S]	53	1	Sub	no	157 T>W ROI: NM_004864_exon_1		
Specimen1	E3260	326	1	Sub	no	685A>G ROI: NM_004864_exon_2		
Specimen1	D327[D.E]	327	1	Sub	no	689C>S ROI: NM_004864_exon_2		
Specimen2	V14[L,V]	14	1	Sub	no	406>S ROI: NM_004864_exon_1; 406>C ROI: NM_004864_exon_1		
Specimen2	E3260	326	1	Sub	no	685A>9 ROI:		▼

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Step 4: View Resequencing Results in the Genotyping Report

IMPORTANT! The Genotyping Report contains some tables that are filled with the VariantSEQr[™] Resequencing System project templates.

To view resequencing results in a report:

1. In the Navigation pane, select the project name.

Note: To view results at the specimen level, select the specimen name.

- 2. Select **Analysis**, then select **Report Manager**.
- 3. In the left pane, select **Genotyping Report**.

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Specim en2	100.0	46.2	100.0	95.8	0.0	0.0	0.0	0.0	100.0	46.2	100.0	95.8	0.0	0.0	0.0	0.0	
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Specime	in .							т.	(167 / NM	_004864	_exon_1						
Specime	in2							т	(41)								

4. In the Resequencing Coverage Table, review the resequencing coverage percentage for each specimen.

Note: The resequencing coverage is based on the target regions.

 In the Project view, add genotypes in the Genotyping Report by right-clicking a base, then selecting Add Genotype.

Note: To view the genotypes for each specimen, open the Genotyping Report.

6. Review the genotypes to compare variants or bases across specimens in a project.

If you completed reviewing your data, and reanalysis is required, go to "Workflow on Modifying Settings" on the next page. If reanalysis is *not* required, you can go directly to "Workflow on Exporting and Printing."



Workflow for Modifying Settings

You can make modifications to your analyzed project by changing the settings (analysis, reference or display) after reviewing your analysis results.

Modifying settings requires that you follow these steps:

Modifying Analysis Settings
1. Modify Analysis Settings in the Project
2. Modify Reference Settings in the Project
3. Modify Display Settings in the Project
4. Apply a Project Template to an Existing Project

Step 1: Modify Analysis Setting in the Project

To modify analysis settings for *all* samples in a Project or Specimen:

- 1. Select **Project** or **Specimen Name** in the Project Navigator.
- 2. Select Analysis > Sample Manager.

File Edit View Tools	Analysis	DBSearch	Window	Help
* 🚅 🔲 🖾		e	Ctrl	+R
	Sampl	le Manager		
ds 🚹 🔛 📓 📰 🗌	Repor	t Manager	Ctrl	+1
RLAB_SeqScape_Web	Apply I	Project Temp	late	
Project Navigator	RDG F	Properties	Ctrl	+D [
E-SPLAB_SeqScape_\	Analys	is Defaults		
🕀 🚺 Specimen1	Analys	is Settings	Ctrl	+B
다 루 Unassembl	Displa	y Settings	Ctrl	+Y

- If you want to adjust the Basecaller and Dye Set/Primer file, select the desired settings, then click **Apply**.
- 4. Click **OK** to close the Sample Manager.

Note: In the project, a red slash through the files that you adjusted indicates the samples are ready to be reanalyzed.

5. Click (Analyze) to analyze the specimen.

If you need to adjust *more* than the Basecaller and Dye Set/Primer File:

1. Create a new Analysis Protocol in the SeqScape Manager. (See Step 2 on Page 4).

Sample File Name	Specimen	Sample Name	BaseCaller	DyeSetPrimer	Spacing	Peak 1	Start	Stop	Assembled
Specimen1_PLA	Specimen1	00000019866	KB.bcp	KB_3730_POP7_BDTv3.mob	10.97	1497	1526	6082	
Specimen1_PLA	Specimen1	00000019866	KB.bcp	KB_3730_POP7_BDTv3.meb	11.25	1652	1581	7744	
Specimen1_PLA	Specimen1	00000019866	KB.bcp	KB_3730_POP7_BDTv3.meb	11.16	1551	1580	6820	
Specimen1_PLA	Specimen1	00000019866	KB.bcp	KB_3730_POP7_BDTv3.mob	10.97	1495	1524	6682	
Specimen1_PLA	Specimen1	00000019866	KB bcp	KB_3730_POP7_BDTv3.mob	11.25	1541	1570	7885	
Specimen1_PLA	Specimen1	00000019866	KB.bcp	KB_3730_POP7_BDTv3.mob	11.15	1514	1543	7747	
Specimen1_PLA	Specimen1	00000019866	KB.bcp	KB_3730_POP7_BDTv3.meb	11.26	1574	1603	7621	
Specimen1_PLA	Specimen1	00000019866	K8 bcp	KB_3730_POP7_BDTv3.mob	11.22	1557	1586	7584	
Specimen1_PLA	Specimen1	00000019866	KB.bcp	KB_3730_POP7_BDTv3.mob	11.24	1557	1586	7630	
Specimen1_PLA	Specimen1	00000019866	KB.bcp	KB_3730_POP7_BDTv3.mob	10.98	1503	1532	7471	
Specimen1_PLA	Specimen1	00000019866	KB.bcp	KB_3730_POP7_BDTv3.mob	11.25	1562	1591	7909	
Specimen1_PLA	Specimen1	00000019866	KB bcp	KB_3730_POP7_BDTv3.mob	11.19	1538	1567	7861	
Specimen1_PLA	Specimen1	00000019866	KB.bcp	KB_3730_POP7_BDTv3.mob	11.04	1509	1538	7774	
Specimen1_PLA Specimen1_PLA Specimen1_PLA	Specimen1 Specimen1 Specimen1	00000019866 00000019866 00000019866	КВ.bcp КВ.bcp КВ.bcp	KB_3730_POP7_BDTv3 meb KB_3730_POP7_BDTv3 meb KB_3730_POP7_BDTv3.meb	11.25 11.19 11.04	1562 1538 1509	1591 1567 1538	7909 7861 7774	

- 2. Select the desired samples in the Sample Manager, then click **Apply** to apply the Analysis Protocol.
- 3. Click **OK** to close the Sample Manager.

Note: In the project, a red slash through the specimen/ files that you adjusted indicates that the samples are ready to be reanalyzed.

4. Click (Analyze) to reanalyze the data.

If you are adjusting the Analysis Settings in a Project for just **one** sample:

- 1. Select the sample in the Project Navigator.
- Go to Analysis > Analysis Settings and make your modifications to the settings.

IMPORTANT! The change applies only to the selected sample and does not modify the Analysis protocol created in the SeqScape Manager.

Note: A red slash through the selected sample indicates the sample is ready to be analyzed.

3. Click on the **▶** icon to reanalyze the data.

Apply Analysis Protocol

Choose an Analysis Protocol that will be applied to the set of selected samples.

Analysis Protocol:	3100 🔽
	3100
	3100_SR_POP6_BDTv1_mixed_v2
	3130_ResequencingProtocol
	3700LR POP5 BDTv1 v2
	3730_ReSequencingProtocol
	test

Sample Manager								×
Edit, DBSearch								
Sample File Name Specim	n Sample Name	BaseCaller	DyeSet/Primer	Spacing	Peak 1	Start	Stop	Assembled
😫 Specimen1_PLASpecime	m1 00000019866	. KB.bcp	KB_3130_POP7_BDTv3.mob	0.00				i 🔶
😫 Specimen1_PLASpecime	en1 00000019866.	. KB.bcp	KB_3130_POP7_BDTv3.mob	0.00				/ 🔴
😫 Specimen1_PLASpecime	m1 00000019866.	. KB.bcp	KB_3130_P0P7_BDTv3.mob	0.00				
😫 Specimen1_PLASpecime	n1 00000019866	. KB.bcp	KB_3130_POP7_BDTv3.mob	0.00				i 🔴
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😫 Specimen1_PLASpecime	m1 00000019866.	. KB.bcp	KB_3130_P0P7_BDTv3.mob	0.00	0	0	0	
😫 Specimen1_PLASpecime	n1 00000019866.	. KB.bcp	KB_3130_POP7_BDTv3.mob	0.00	0	0	0	i 🔴
😫 Specimen1_PLASpecime	n1 00000019866.	. KB.bcp	KB_3130_POP7_BDTv3.mob	0.00	0	0	0	•
😫 Specimen1_PLASpecime	m1 00000019866.	. KB.bcp	KB_3130_P0P7_BDTv3.mob	0.00	0	0	0	•
😫 Specimen1_PLASpecime	n1 00000019866.	. KB.bcp	KB_3130_POP7_BDTv3.mob	0.00	0	0	0	i 🔴
😫 Specimen1_PLASpecime	n1 00000019866.	. KB.bcp	KB_3130_POP7_BDTv3.mob	0.00	0	0	0	•
😫 Specimen1_PLASpecime	n1 00000019866.	. KB.bcp	KB_3130_POP7_BDTv3.mob	0.00				•
😫 Specimen1_PLASpecime	m1 00000019866.	. KB.bcp	KB_3130_POP7_BDTv3.mob	0.00	0	0	0	

×

File Edit View Tools	Analysis	DBSearch	Window	Hel
r* 🚅 📓 🗐 🔿	Analyz	e	Ctrl	+R
	Samp	e Manager		
ds 🔛 🖂 🚊 📃	Repor	t Manager	Ctrl	+1
🞇 PLAB_SeqScape_Web	Apply I	Project Temp	late	
Project Navigator	RDG F	Properties	Ctrl	+D
E- 🗳 PLAB_SeqScape_\	Analys	is Defaults		
🗄 🚺 Specimen1	Analys	is Settings	Ctrl	+B
E-U Specimen2	Displa	y Settings	Ctrl	ι+Υ
 → PLAB_segm → Specime 	nen_1 n2_PLAB n2_PLAB n2_PLAB n2_PLAB n2_PLAB n2_PLAB n2_PLAB n2_PLAB n2_PLAB n2_PLAB nent_2 ed ent_1 nent_2	28_A7.r 27_A1.r 27_A4.f 42_A2.r 42_A5.f 25_A9.f 24_A6.r 24_A1.f 24_A1.f		

Step 2: Modify Reference Settings in the Project

To make changes such as adding variants to an existing reference:

- 1. Click rdg in the project view.
- 2. Select the ROI tab.
- 3. Modify the reference settings within a project by:
 - Changing the Codon Start Number for amino acid translation
 - Modifying the translation frames
 - Changing the ROI Start numbering in the ROI pane
 - Adding variants and changing variant styles or colors

Note: These modifications are saved only within the *existing* project. They do not change in the original Reference Data Group that you created in the SeqScape Manager.

Step 3: Modify Display Settings in the Project

To modify the Display Settings within a project:

- 1. In the Project view, click **ds** (Display Settings) to modify viewing options.
- 2. Select the **Bases** tab.
- 3. Change the color scale as desired to modify the quality value bars.
- 4. Select the Views tab.

Eile Edit View	Tools	Analysis	DBSearch	Window	Help	_	1	-		
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a 🙌 🛃 😹	121			UH 14			Active Layer	LAB_Target 💌 Tab ju	mps to next Unknown Varia	ant 💌



Eile Edit Yiew Tools Analysis DBSearch Window Help	
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🐻 🕂 🖬 💩 🖄 💷 📰 🖼 📓 🗮 🗮 🛄 📴 🕼 🖉 🔤 🔟 Active Layer; PLAB_Target 🝸 Tab jumps to next Unk	nown Variant 💌

General Bases Electropherogram Views	
Base Font Font Size: 12 Font Style: PLAIN	Ouality Values Bar Color: 0 50 15 25
Base Scale Show base number every 10 bases	The color scale for the Quality Value bars can be modified.
Base Colors Base Style: Colored Text	
A: C: G: T:	

- 5. Increase the number of bases you want to display in the Project view as indicated in the EP Window field.
- 6. (Optional) Select Italicize Reverse Strand.

Note: The display settings show 70 bases and italicize reverse strands by default.

Edit Display Settings	
General Bases Electropherogram Views	
General View Settings	Project View Settings
Characters/Dots:	Display Mode: 🔛 🔟 💩
Electropherograms: 🔟 🛄	EP Window (bp): 70 Shown GT Pos. on
Confidence Bars:	Hidden GT Pos. on Expanded NT
NT Tab Jump: Multiple AA Tab Jump: Multiple	Summary
View Column Selector:	IV variants IV Index
Sample View Settings Original Sequence:	Reference-AA
Shorimon View Softings	Collapsed NT
Italicize Reverse Strand	☑ Summary ☑ NT Variants
Clear Range:	I Index
Show All:	Reference
	Expanded AA
Amplicon View Settings	Summary
Amplicon Coverage:	I⊻ AA Variants
Zoom Factor: 100% 💌	I Index I Reference-AA

Step 4: Apply a Project Template to an Existing Project

To make changes to an existing Project Template:

- 1. Select Tools > SeqScape Manager, or simply click Tooltip.
- 2. Modify the data objects within SeqScape Manager and reselect the same data objects within the Project Template to apply changes.
- 3. Click **Open Folders** to verify your modifications.
- 4. Click **OK** to close the Project Template editor.



To apply the modified Project Template:

- 1. Open the project.
- 2. Select **Apply Project Template** (Analysis menu).
- 3. Select the appropriate Project Template from the drop-down menu.
- Click (Analyze) to reanalyze the data with the modified template.

Note: All previous edits are lost.



Workflow for Exporting and Printing

In this workflow we review optional selections for exporting and printing your analysis results.

Exporting and Printing

1. Select Export Options for an Analyzed Project

2. Set Print Options at Project/Specimen/Segment Levels

To determine which printing and exporting options are available in SeqScape, select a level in the Project Navigator from one of the four choices:

- Project
- Specimen
- Reference Segment
- Sample
- 1. Select File > Export, File > Print.

File	Edit	View	Tools	Analysis	DBSearch	Window
N	ew Pro	oject				Ctrl+N
ð	þen Pi	roject				Ctrl+0
N	ew Pro	oject Wi	zard			
С	lose P	roject				Ctrl+W
S	ave Pr	oject				Ctrl+S
S	ave Pr	oject As				Alt+A
In	nport S	Sample	s To Pro	ject		Ctrl+M
In	nport T	ext Seg	iment			Ctrl+T
E:	xport	_	1			•
P	rint					Ctrl+P

Step 1: Select Export Options for an Analyzed Project

To export a selected report from a Project:

- 1. Open the project.
- 2. Select **Report Manager** (Analysis Menu).
- 3. Select Export > Report.
- When the Export window opens, select for the format tab-delimited text (Microsoft Excel[®]), PDF, HTML, or XML.

Export	•	Sample Sequence File	
Print	Ctrl+I	Report	

To export all reports automatically after analysis:

- 1. Select Tools > Options.
- 2. Select **Export Reports After Analysis**, then in the Format drop-down list, select a format to export.



- 3. Browse to set a target directory for the file.
- 4. Click OK.

Note: Once a project is reanalyzed, the reports will *automatically* export to the set directory.

To export alignment files:

 Select the project (Project Navigator), then select File > Export. You can export the nucleotides project alignment or the amino acid project alignment.

Note: The reference sequence and the specimen consensus sequences also export.

- (Optional) Select File > Export for the Specimen level/ Reference Segment level to export the consensus sequence or the aligned sample sequence.
- 3. (Optional) Select **Electropherogram** to export the Sample Sequence.

File Edit View Tools Analysis	DBSear	ch Window Help
New Project	Ctrl+N	
Open Project	Ctrl+O	
New Project Wizard		🛛 뒢 🔛 🛄 🔛 Active L
Close Project	Ctrl+W	
Save Project	Ctrl+S	sequencingPrimerSet
Save Project As	Alt+A	View AmpliconView
Import Samples To Project	Ctrl+M	
Import Text Segment	Ctrl+T	arnet ROIsPLAB_target_promoter
Export	Þ	Project Alignment - Nucleotides
Print	Ctrl+P	Project Alignment - Amino Acid
1 PLAB-ResequencingPrimerSet		Library Search Results

Import Samples To Project	Ctrl+M	
Import Text Segment	Ctrl+T	
Export	N 1	Consensus Sequence
Print	Ctrl+P	Aligned Sample Sequence

Step 2: Set Print Options at the Project, Specimen, Segment Levels

Print Specimen

Header/Footer...

Rint Segment Assembly

Print.

Only the visible data
 O All data
 Print Properties
 Potrait
 C Landscape
Paper Letter 8.5 by 11 inches

Print

Print

C On All Print F C Po C La Paper Hea

Select **All Data** to print the specimen consensus sequences and the reference sequence. Selecting **All Data** does *not* print the Electropherogram data.

Select **Only the Visible Data** to print only visible data. Consequentially, only the *displayed* electropherogram data (specimens) are printed.

Note: The electropherogram data for the full project are *not* printed. Only the data that display in the Project window prints.

From the Specimen view, you can print only the data that are displayed.

From the Segment Assembly view, you can print all data *and* the visible data that are displayed.

ly the visible data data	Bases per par	nel: 50
roperties rtrait ndscape		
Letter 8.5 by 11 inches 💌	1	
den/Footer	Print	Cancel

x

٠

Print Settings for Project

×

Cancel

By selecting a sample you can print the sample electropherogram.



For more information on Using SeqScape software v2.5, refer to the SeqScape Software User Manual.



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