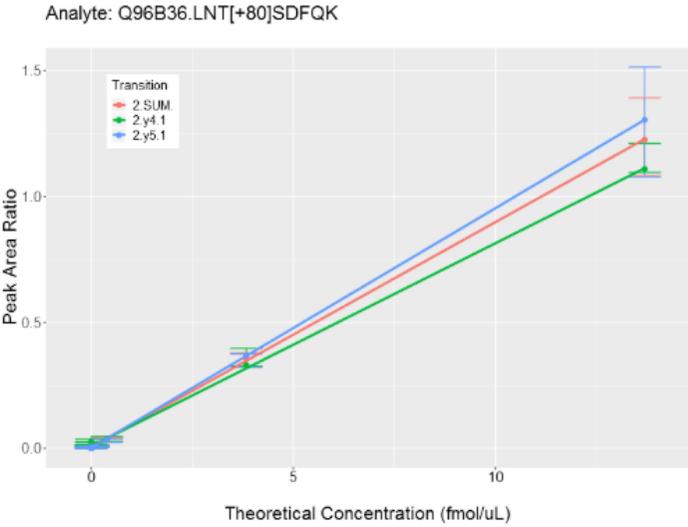
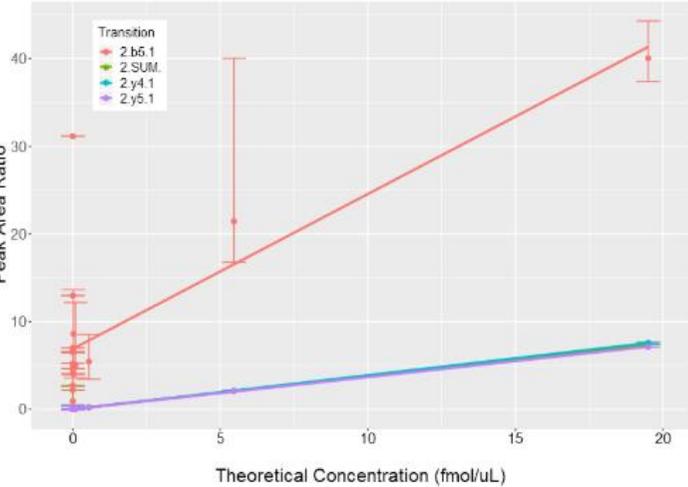
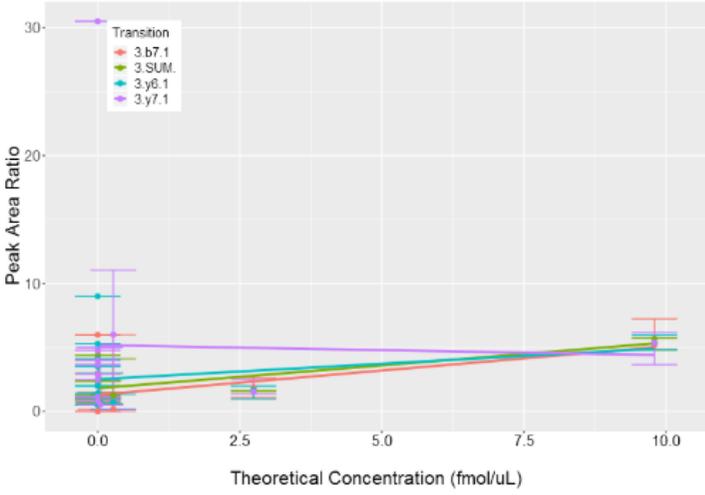


Response Curve (Experiment 1)

Error category	Error message	Example case	Solution to the issue						
Internal standard	Internal standard is set to be none.	<table border="1"> <thead> <tr> <th>Skyline File Name</th> <th>Internal Standard Type</th> <th>Quality</th> </tr> </thead> <tbody> <tr> <td>MousePlasmaV2Exp1B3_refined.sky</td> <td>none</td> <td>The internal standard in the skyline file is set to be none. Errors happen for all the peptides.</td> </tr> </tbody> </table>	Skyline File Name	Internal Standard Type	Quality	MousePlasmaV2Exp1B3_refined.sky	none	The internal standard in the skyline file is set to be none. Errors happen for all the peptides.	In Skyline, settings -> Peptide Settings -> Modifications -> Internal standard type , set Internal standard.
Skyline File Name	Internal Standard Type	Quality							
MousePlasmaV2Exp1B3_refined.sky	none	The internal standard in the skyline file is set to be none. Errors happen for all the peptides.							
Internal standard	Internal standard is incorrect according to the inferred internal standard.	<table border="1"> <thead> <tr> <th>Skyline File Name</th> <th>Internal Standard Type</th> <th>Quality</th> </tr> </thead> <tbody> <tr> <td>MousePlasmaV2Exp1B3_refined.sky</td> <td>heavy</td> <td>The internal standard in the skyline file is set to be heavy, while the inferred internal standard is light. Errors happen for all the peptides.</td> </tr> </tbody> </table>	Skyline File Name	Internal Standard Type	Quality	MousePlasmaV2Exp1B3_refined.sky	heavy	The internal standard in the skyline file is set to be heavy, while the inferred internal standard is light. Errors happen for all the peptides.	In Skyline, settings -> Peptide Settings -> Modifications -> Internal standard type , set Internal standard to be the correct type.
Skyline File Name	Internal Standard Type	Quality							
MousePlasmaV2Exp1B3_refined.sky	heavy	The internal standard in the skyline file is set to be heavy, while the inferred internal standard is light. Errors happen for all the peptides.							
Attribute	Essential attributes have missing values.	<table border="1"> <thead> <tr> <th>Skyline File Name</th> <th>Peptide sequence with errors</th> <th>Issue reason</th> </tr> </thead> <tbody> <tr> <td>DDRpanel_052316_curves_05_QCTEST.sky</td> <td>DLSHIGDAVVISC[+57]JAK[+114]DGVK</td> <td> <ul style="list-style-type: none"> Essential attribute(s) has (have) missing values, including ReplicateName; Replicate; SampleGroup. Essential attribute(s) has (have) missing values, including ISSpike or PeptideConcentrationIS. </td> </tr> </tbody> </table>	Skyline File Name	Peptide sequence with errors	Issue reason	DDRpanel_052316_curves_05_QCTEST.sky	DLSHIGDAVVISC[+57]JAK[+114]DGVK	<ul style="list-style-type: none"> Essential attribute(s) has (have) missing values, including ReplicateName; Replicate; SampleGroup. Essential attribute(s) has (have) missing values, including ISSpike or PeptideConcentrationIS. 	<ol style="list-style-type: none"> In Skyline, for the old template, View -> Document Grid -> Views -> Replicates, check the corresponding attributes; for the new template, View -> Document Grid -> Views -> Assay Curve Replicates, check the corresponding attributes. If the corresponding attributes are normal in step 1, in Skyline, View -> Targets -> By Name, in Targets panel, navigate to the peptide sequence, check the fragment ions from precursors of light and heavy isotopes, find the fragment ions with no data, and delete them.
Skyline File Name	Peptide sequence with errors	Issue reason							
DDRpanel_052316_curves_05_QCTEST.sky	DLSHIGDAVVISC[+57]JAK[+114]DGVK	<ul style="list-style-type: none"> Essential attribute(s) has (have) missing values, including ReplicateName; Replicate; SampleGroup. Essential attribute(s) has (have) missing values, including ISSpike or PeptideConcentrationIS. 							
Attribute	Essential attributes are annotated in unqualified data type.	None	In Skyline, for the old template, View -> Document Grid -> Views -> Replicates , check the data types of corresponding attributes; for the new template, View -> Document Grid -> Views -> Assay Curve Replicates , check the data types of corresponding attributes.						
Internal standard peptide concentration	The annotation of the concentration of the internal standard peptide has issues.	<table border="1"> <thead> <tr> <th>Skyline File Name</th> <th>Peptide sequence with errors</th> <th>Issue reason</th> </tr> </thead> <tbody> <tr> <td>MousePlasmaV2Exp1B3_refined.sky</td> <td>LPLPALFK</td> <td> <ul style="list-style-type: none"> The annotation of the concentration of the internal standard peptide has issues. Please check the annotation of IS Spike or PeptideConcentrationIS. </td> </tr> </tbody> </table>	Skyline File Name	Peptide sequence with errors	Issue reason	MousePlasmaV2Exp1B3_refined.sky	LPLPALFK	<ul style="list-style-type: none"> The annotation of the concentration of the internal standard peptide has issues. Please check the annotation of IS Spike or PeptideConcentrationIS. 	In Skyline, for the old template, View -> Document Grid -> Views -> Replicates , check the attribute of IS Spike, then View -> Document Grid -> Views -> Peptides , check the attribute of PeptideConcentrationIS; for the new template, View -> Document Grid -> Views -> Assay Peptides , check the attribute of Internal Standard Concentration.
Skyline File Name	Peptide sequence with errors	Issue reason							
MousePlasmaV2Exp1B3_refined.sky	LPLPALFK	<ul style="list-style-type: none"> The annotation of the concentration of the internal standard peptide has issues. Please check the annotation of IS Spike or PeptideConcentrationIS. 							
Concentration	More than one concentration levels are	None	In Skyline, for the old template, View -> Document Grid -> Views -> Replicates , check the attribute of Concentration; for the new						

	needed.		template, View -> Document Grid -> Views -> Assay Curve Replicates , check the attribute of Analyte Concentration.						
Light and Medium isotope	Both light and medium isotope labels are found in the peptide.	None	In Skyline, in the Targets panel, navigate to the peptide with errors, click each fragment ion to check its isotope label type.						
Area values of heavy or light Isotope	More than one area values of heavy or light isotope exist for the combination of protein, peptidemodifiedsequence, precursorcharge, productcharge, fragmentation, replicate, concentration, samplegroup, isspike and isotopelabel.	<table border="1"> <thead> <tr> <th>Skyline File Name</th> <th>Peptide sequence with errors</th> <th>Issue reason</th> </tr> </thead> <tbody> <tr> <td>20160720_MousePlasmaExp1Batch5_refined.sky</td> <td>ETPAASEAPSSAAK</td> <td> <ul style="list-style-type: none"> More than one area values of heavy or light isotope exist for the combination of protein, peptidemodifiedsequence, precursorcharge, productcharge, fragmentation, replicate, concentration, samplegroup, isspike and isotopelabel. </td> </tr> </tbody> </table>	Skyline File Name	Peptide sequence with errors	Issue reason	20160720_MousePlasmaExp1Batch5_refined.sky	ETPAASEAPSSAAK	<ul style="list-style-type: none"> More than one area values of heavy or light isotope exist for the combination of protein, peptidemodifiedsequence, precursorcharge, productcharge, fragmentation, replicate, concentration, samplegroup, isspike and isotopelabel. 	In Skyline, in the Targets panel, navigate to the peptide with errors, click each fragment ion and check the Peak Areas – Replicate Comparison panel, more than one Peak Area value could be observed in one Replicate . Re-import the data related to the peptide into the current Skyline document to make sure there is one area value of heavy or light isotope kept.
Skyline File Name	Peptide sequence with errors	Issue reason							
20160720_MousePlasmaExp1Batch5_refined.sky	ETPAASEAPSSAAK	<ul style="list-style-type: none"> More than one area values of heavy or light isotope exist for the combination of protein, peptidemodifiedsequence, precursorcharge, productcharge, fragmentation, replicate, concentration, samplegroup, isspike and isotopelabel. 							
Fragment ion	In response curve, no fragment ion with both heavy and light isotopes exists.	None	In Skyline, in the Targets panel, navigate to the peptide with errors, click each fragment ion (heavy or light isotope) and check the Peak Area value in Peak Areas – Replicate Comparison panel. Re-import the data related to the peptide into the current Skyline document to make sure the heavy and light isotope appear only one time for the fragment ions of the peptide.						

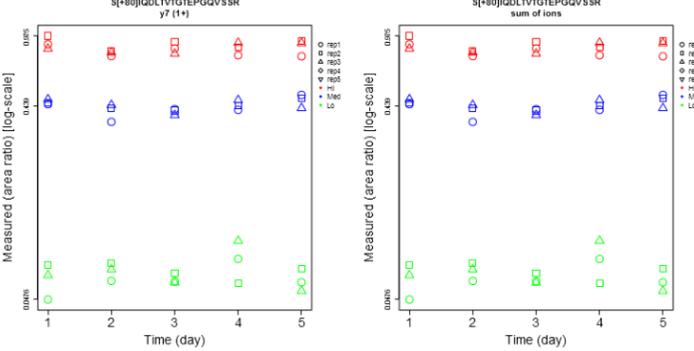
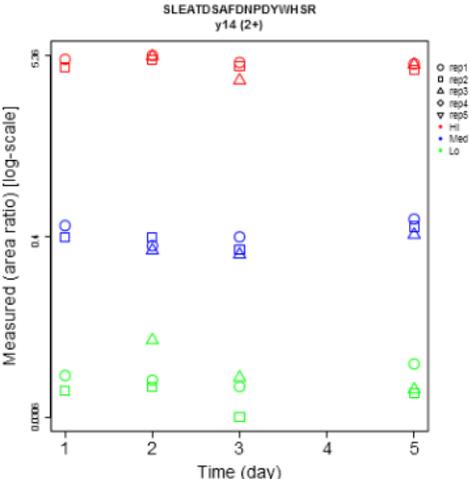
Warning category	Warning message	Example case	Solution to the issue
Fragment ion	In response curve, the number of fragment ions with both heavy and light isotopes is less than 3.	<p>In response curve, only two fragment ions 2.y4.1, 2.y5.1 (with both heavy and light isotopes) exist.</p> 	Check the response curve graph to make further decisions.
Bad linear regression fit	The coefficient of variance of slopes of the fragment ions is larger than 0.5.	<p>Analyte: O95819.VYPLINR</p> 	Check the slopes of the fragment ions in the response curve graph to make further decisions.

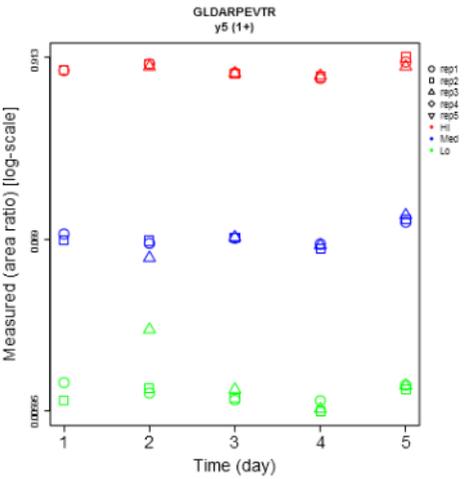
<p>Bad linear regression fitting</p>	<p>The fit of the linear regression model is poor due to $R^2 < 0.5$ or $p > 0.05$ in the significance test for linear regression.</p>		<p>Check the response curve graph to make further decisions.</p>
<p>Bad linear regression fitting</p>	<p>The exponent of the fitted power function for the fragment ion data is not between 0.75 and 1.25</p>	<p>None</p>	<p>Check the response curve graph to make further decisions.</p>
<p>High variance</p>	<p>Not all of the transition ratios of the fragment ion are within 30% of the mean when checking the samples above the LLOQ</p>	<p>None</p>	<p>Check the response curve graph to make further decisions.</p>

Repeatability (Experiment 2)

Error category	Error message	Example case	Solution to the issue						
Internal standard	Internal standard is set to be none.	None	In Skyline, settings -> Peptide Settings -> Modifications -> Internal standard type , set Internal standard.						
Internal standard	Internal standard is incorrect according to the inferred internal standard.	<table border="1"> <thead> <tr> <th>Skyline File Name</th> <th>Internal Standard Type</th> <th>Quality</th> </tr> </thead> <tbody> <tr> <td>TCGA glyco 26 peps_repeatability.sky</td> <td>light</td> <td>The internal standard in the skyline file is set to be light, while the inferred internal standard is heavy. Errors happen for all the peptides.</td> </tr> </tbody> </table>	Skyline File Name	Internal Standard Type	Quality	TCGA glyco 26 peps_repeatability.sky	light	The internal standard in the skyline file is set to be light, while the inferred internal standard is heavy. Errors happen for all the peptides.	In Skyline, settings -> Peptide Settings -> Modifications -> Internal standard type , set Internal standard to be the correct type.
Skyline File Name	Internal Standard Type	Quality							
TCGA glyco 26 peps_repeatability.sky	light	The internal standard in the skyline file is set to be light, while the inferred internal standard is heavy. Errors happen for all the peptides.							
Attribute	Essential attributes have missing values.	<table border="1"> <thead> <tr> <th>Skyline File Name</th> <th>Peptide sequence with errors</th> <th>Issue reason</th> </tr> </thead> <tbody> <tr> <td>DDRpanel_052316_repeatability_03_QCTEST.sky</td> <td>LSLEFPGYPYNAPTVK, precursor charge: 2</td> <td> <ul style="list-style-type: none"> Essential attribute(s) has (have) missing values, including Replicate; Concentration; SampleGroup. </td> </tr> </tbody> </table>	Skyline File Name	Peptide sequence with errors	Issue reason	DDRpanel_052316_repeatability_03_QCTEST.sky	LSLEFPGYPYNAPTVK, precursor charge: 2	<ul style="list-style-type: none"> Essential attribute(s) has (have) missing values, including Replicate; Concentration; SampleGroup. 	In Skyline, for the old template, View -> Document Grid -> Views -> Replicates , check the corresponding attributes; for the new template, View -> Document Grid -> Views -> Assay Repeatability Replicates , check the corresponding attributes.
Skyline File Name	Peptide sequence with errors	Issue reason							
DDRpanel_052316_repeatability_03_QCTEST.sky	LSLEFPGYPYNAPTVK, precursor charge: 2	<ul style="list-style-type: none"> Essential attribute(s) has (have) missing values, including Replicate; Concentration; SampleGroup. 							
Attribute	Essential attributes are using uncontrolled terms.	None	In Skyline, for the old template, View -> Document Grid -> Views -> Replicates , check the corresponding attributes; for the new template, View -> Document Grid -> Views -> Assay Repeatability Replicates , check the corresponding attributes.						
Attribute	Essential attributes are annotated in unqualified data type.	None	In Skyline, for the old template, View -> Document Grid -> Views -> Replicates , check the data type of the corresponding attributes; for the new template, View -> Document Grid -> Views -> Assay Repeatability Replicates , check the data type of the corresponding attributes.						
Light and Medium isotope	Both light and medium isotope labels are found in the peptide with a specific charge.	None	In Skyline, in the Targets panel, navigate to the peptide with errors, click each fragment ion to check its isotope label type.						

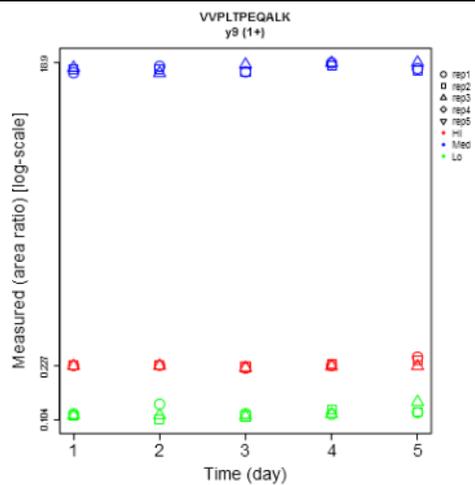
<p>Area values of heavy or light Isotope</p>	<p>The number of light isotopes or heavy isotopes is not one due to wrongly annotated values in attributes.</p>	<table border="1"> <thead> <tr> <th data-bbox="658 92 889 188">Skyline File Name</th> <th data-bbox="889 92 1019 188">Peptide sequence with errors</th> <th data-bbox="1019 92 1393 188">Issue reason</th> </tr> </thead> <tbody> <tr> <td data-bbox="658 188 889 448">MousePlasmaExp2B3_Refined.sky</td> <td data-bbox="889 188 1019 448">DFALQNPQVPR, precursor charge: 2</td> <td data-bbox="1019 188 1393 448"> <ul style="list-style-type: none"> For b2 (1+): 2 heavy isotopes 2 light isotopes due to multiple values in attributes: replicate_name (Day4_Std3_R01 Day4_Std3_R03). For b3 (1+): 2 heavy isotopes 2 light isotopes due to multiple values in attributes: replicate_name (Day4_Std3_R01 Day4_Std3_R03). For y2 (1+): 2 heavy isotopes 2 light isotopes due to multiple values in attributes: replicate_name (Day4_Std3_R01 Day4_Std3_R03). For y3 (1+): 2 heavy isotopes 2 light isotopes due to multiple values in attributes: replicate_name (Day4_Std3_R01 Day4_Std3_R03). For y6 (1+): 2 heavy isotopes 2 light isotopes due to multiple values in attributes: replicate_name (Day4_Std3_R01 Day4_Std3_R03). </td> </tr> </tbody> </table>	Skyline File Name	Peptide sequence with errors	Issue reason	MousePlasmaExp2B3_Refined.sky	DFALQNPQVPR, precursor charge: 2	<ul style="list-style-type: none"> For b2 (1+): 2 heavy isotopes 2 light isotopes due to multiple values in attributes: replicate_name (Day4_Std3_R01 Day4_Std3_R03). For b3 (1+): 2 heavy isotopes 2 light isotopes due to multiple values in attributes: replicate_name (Day4_Std3_R01 Day4_Std3_R03). For y2 (1+): 2 heavy isotopes 2 light isotopes due to multiple values in attributes: replicate_name (Day4_Std3_R01 Day4_Std3_R03). For y3 (1+): 2 heavy isotopes 2 light isotopes due to multiple values in attributes: replicate_name (Day4_Std3_R01 Day4_Std3_R03). For y6 (1+): 2 heavy isotopes 2 light isotopes due to multiple values in attributes: replicate_name (Day4_Std3_R01 Day4_Std3_R03). 	<p>In Skyline, for the old template, View -> Document Grid -> Views -> Replicates, check the values of the attribute of Replicate for the problematic replicate names, for example, correct the values of the attribute of Replicate for the replicate name of Day4_Std3_R01 and Day4_Std3_R03. In Skyline, for the old template, View -> Document Grid -> Views -> Replicates, check the values of the attribute of Replicate for the problematic replicate names; for the new template, View -> Document Grid -> Views -> Assay Repeatability Replicates, check the values of the attribute of Replicate Number for the problematic replicate names.</p>
Skyline File Name	Peptide sequence with errors	Issue reason							
MousePlasmaExp2B3_Refined.sky	DFALQNPQVPR, precursor charge: 2	<ul style="list-style-type: none"> For b2 (1+): 2 heavy isotopes 2 light isotopes due to multiple values in attributes: replicate_name (Day4_Std3_R01 Day4_Std3_R03). For b3 (1+): 2 heavy isotopes 2 light isotopes due to multiple values in attributes: replicate_name (Day4_Std3_R01 Day4_Std3_R03). For y2 (1+): 2 heavy isotopes 2 light isotopes due to multiple values in attributes: replicate_name (Day4_Std3_R01 Day4_Std3_R03). For y3 (1+): 2 heavy isotopes 2 light isotopes due to multiple values in attributes: replicate_name (Day4_Std3_R01 Day4_Std3_R03). For y6 (1+): 2 heavy isotopes 2 light isotopes due to multiple values in attributes: replicate_name (Day4_Std3_R01 Day4_Std3_R03). 							

Warning category	Warning message	Example case	Solution to the issue
Fragment ion	In repeatability graph, the number of fragment ions with both heavy and light isotopes is less than 3.	<p>In the repeatability graph below, the number of fragment ions is 1 < 3; the only fragment ion is: y7 (1+).</p> 	Check the repeatability graph to make further decisions.
Missing points	In repeatability graph, for the fragment ion, there is no point on at least one day.	<p>For fragment ion y14 (2+), there are no points on day 4.</p> 	Check the repeatability graph to make further decisions.
Missing points	In repeatability graph, fragment ion doesn't have three concentrations: Hi, Med, and Low on a specific	None	Check the repeatability graph to make further decisions.

	day.		
Missing points	In repeatability graph, fragment ion has less than 3 replicates for a specific concentration on the specific day.	For fragment ion y5 (1+), there are less than 3 replicates in concentration(s) Hi, Lo, Med on day 1. 	Check the repeatability graph to make further decisions.
Bad distribution of points	In repeatability graph, for the fragment ion, the intra-assay, inter-assay or total coefficient of variance is larger than the threshold of 0.2.	None	Check the repeatability graph to make further decisions.
High variance	Not of all the transition ratios of the fragment ion in the specific concentration are within 30% of the mean.	None.	Check the repeatability graph to make further decisions.

Abnormal display of points

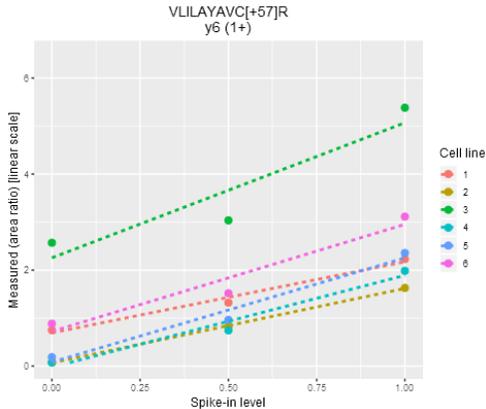
In repeatability graph, for the fragment ion, the points are not displayed by the sequence of Hi, Med and low from top to bottom



In Skyline, for the old template, **View -> Document Grid -> Views -> Replicates**, check the attribute of Sample Group; for the new template, **View -> Document Grid -> Views -> Assay Repeatability Replicates**, check the attribute of Sample Group.

Selectivity (Experiment 3)

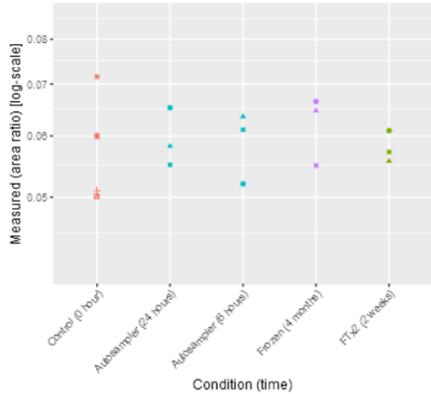
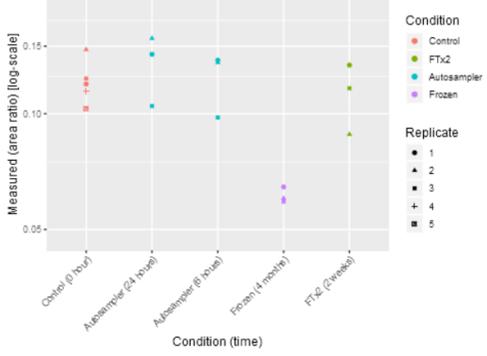
Error category	Error message	Example case	Solution to the issue						
Internal standard	Internal standard is set to be none.	<table border="1"> <thead> <tr> <th>Skyline File Name</th> <th>Internal Standard Type</th> <th>Quality</th> </tr> </thead> <tbody> <tr> <td>CPTAC_TemplateDoc_Exp3_Selectivity_DRAFT02.sky</td> <td>none</td> <td>The internal standard in the skyline file is set to be none. Please set it to be heavy. Errors happen for all the peptides.</td> </tr> </tbody> </table>	Skyline File Name	Internal Standard Type	Quality	CPTAC_TemplateDoc_Exp3_Selectivity_DRAFT02.sky	none	The internal standard in the skyline file is set to be none. Please set it to be heavy. Errors happen for all the peptides.	In Skyline, settings -> Peptide Settings -> Modifications -> Internal standard type , set Internal standard.
Skyline File Name	Internal Standard Type	Quality							
CPTAC_TemplateDoc_Exp3_Selectivity_DRAFT02.sky	none	The internal standard in the skyline file is set to be none. Please set it to be heavy. Errors happen for all the peptides.							
Internal standard	Internal standard is incorrect.	<table border="1"> <thead> <tr> <th>Skyline File Name</th> <th>Internal Standard Type</th> <th>Quality</th> </tr> </thead> <tbody> <tr> <td>Batch1_Exp3_20160519_M1.sky</td> <td>heavy</td> <td>The internal standard in the skyline file is set to be heavy, while the inferred internal standard is light. Errors happen for all the peptides.</td> </tr> </tbody> </table>	Skyline File Name	Internal Standard Type	Quality	Batch1_Exp3_20160519_M1.sky	heavy	The internal standard in the skyline file is set to be heavy, while the inferred internal standard is light. Errors happen for all the peptides.	In Skyline, settings -> Peptide Settings -> Modifications -> Internal standard type , set Internal standard to be the correct type.
Skyline File Name	Internal Standard Type	Quality							
Batch1_Exp3_20160519_M1.sky	heavy	The internal standard in the skyline file is set to be heavy, while the inferred internal standard is light. Errors happen for all the peptides.							
Attribute	Essential attributes have missing values.	None	In Skyline, View -> Document Grid -> Views -> Assay Selectivity Replicates , check the corresponding attributes.						
Attribute	Essential attributes are annotated in unqualified data type.	None	In Skyline, View -> Document Grid -> Views -> Assay Selectivity Replicates , check the data types of corresponding attributes.						
Light and Medium isotope	Both light and medium isotope labels are found in the peptide with a specific charge.	None	In Skyline, in the Targets panel, navigate to the peptide with errors, click each fragment ion to check its isotope label type.						
Concentration	More than one concentration levels are needed.	None	In Skyline, View -> Document Grid -> Views -> Assay Selectivity Replicates , check the attribute of Analyte Concentration.						
Area values of heavy or light Isotope	The number of light isotopes or heavy isotopes is not one due to wrongly annotated values in attributes.	<table border="1"> <thead> <tr> <th>Skyline File Name</th> <th>Peptide sequence with errors</th> <th>Issue reason</th> </tr> </thead> <tbody> <tr> <td>CPTAC_TemplateDoc_Exp3_Selectivity_DRAFT02_2019-11-20_10-11-50.sky.ctb</td> <td>LDQDQLPCGAR, precursor charge: 2</td> <td> <ul style="list-style-type: none"> For y5 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate, analyte concentration on sample group. For y6 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate, analyte concentration on sample group. For y8 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate, analyte concentration on sample group. For y9 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate, analyte concentration on sample group. For y9 (2+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate, analyte concentration on sample group. </td> </tr> </tbody> </table>	Skyline File Name	Peptide sequence with errors	Issue reason	CPTAC_TemplateDoc_Exp3_Selectivity_DRAFT02_2019-11-20_10-11-50.sky.ctb	LDQDQLPCGAR, precursor charge: 2	<ul style="list-style-type: none"> For y5 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate, analyte concentration on sample group. For y6 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate, analyte concentration on sample group. For y8 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate, analyte concentration on sample group. For y9 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate, analyte concentration on sample group. For y9 (2+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate, analyte concentration on sample group. 	In Skyline, View -> Document Grid -> Views -> Assay Selectivity Replicates , check the values of the attribute of Replicate Number, Analyte Concentration and Exp3 SampleGroup.
Skyline File Name	Peptide sequence with errors	Issue reason							
CPTAC_TemplateDoc_Exp3_Selectivity_DRAFT02_2019-11-20_10-11-50.sky.ctb	LDQDQLPCGAR, precursor charge: 2	<ul style="list-style-type: none"> For y5 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate, analyte concentration on sample group. For y6 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate, analyte concentration on sample group. For y8 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate, analyte concentration on sample group. For y9 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate, analyte concentration on sample group. For y9 (2+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate, analyte concentration on sample group. 							

Warning category	Warning message	Example case	Solution to the issue																												
Fragment ion	The number of fragment ions is less than 3.	None	Check the selectivity graph to make further decisions.																												
Sample group	The number of sample group is less than 6.	None	Check the selectivity graph to make further decisions.																												
Bad linear regression fit	The coefficient of variance of slopes of the fragment ion is larger than 0.5.	None	Check the selectivity graph to make further decisions.																												
Bad linear regression fitting	The fit of the linear regression model is poor due to $R^2 < 0.5$ for some fragment ions in the significance test for linear regression.	None	Check the selectivity graph to make further decisions.																												
Bad linear regression fitting	The RMSE of intercepts at y axis of the fit lines is larger than 1.0.	<p data-bbox="674 874 1386 943">For fragment ion of y6 (1+), the RMSE of intercepts at y axis of is $1.008 > 1$.</p>  <table border="1" data-bbox="674 997 1160 1406"> <caption>Approximate data points from the selectivity graph</caption> <thead> <tr> <th>Spike-in level</th> <th>Cell line 1</th> <th>Cell line 2</th> <th>Cell line 3</th> <th>Cell line 4</th> <th>Cell line 5</th> <th>Cell line 6</th> </tr> </thead> <tbody> <tr> <td>0.00</td> <td>0.2</td> <td>0.3</td> <td>2.2</td> <td>0.1</td> <td>0.2</td> <td>1.0</td> </tr> <tr> <td>0.50</td> <td>0.5</td> <td>0.6</td> <td>3.5</td> <td>0.4</td> <td>0.5</td> <td>1.8</td> </tr> <tr> <td>1.00</td> <td>0.8</td> <td>0.9</td> <td>5.5</td> <td>0.7</td> <td>0.8</td> <td>3.0</td> </tr> </tbody> </table>	Spike-in level	Cell line 1	Cell line 2	Cell line 3	Cell line 4	Cell line 5	Cell line 6	0.00	0.2	0.3	2.2	0.1	0.2	1.0	0.50	0.5	0.6	3.5	0.4	0.5	1.8	1.00	0.8	0.9	5.5	0.7	0.8	3.0	Check the area values for the fragment ion y6 (1+) in Skyline.
Spike-in level	Cell line 1	Cell line 2	Cell line 3	Cell line 4	Cell line 5	Cell line 6																									
0.00	0.2	0.3	2.2	0.1	0.2	1.0																									
0.50	0.5	0.6	3.5	0.4	0.5	1.8																									
1.00	0.8	0.9	5.5	0.7	0.8	3.0																									

High variance	Not all of the area ratios of the fragment ion in the non-blank spike level are within 30% of the mean.	None	Check the area values for the fragment ion in Skyline.
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Stability (Experiment 4)

Error category	Error message	Example case	Solution to the issue						
Internal standard	Internal standard is set to be none.	<table border="1"> <thead> <tr> <th>Skyline File Name</th> <th>Internal Standard Type</th> <th>Quality</th> </tr> </thead> <tbody> <tr> <td>CPTAC_TemplateDoc_Exp4_Stability_DRAFT02_2020-01-06_16-35-35.sky.zip</td> <td>none</td> <td>The internal standard in the skyline file is set to be none. Please set it to be heavy. Errors happen for all the peptides.</td> </tr> </tbody> </table>	Skyline File Name	Internal Standard Type	Quality	CPTAC_TemplateDoc_Exp4_Stability_DRAFT02_2020-01-06_16-35-35.sky.zip	none	The internal standard in the skyline file is set to be none. Please set it to be heavy. Errors happen for all the peptides.	In Skyline, settings -> Peptide Settings -> Modifications -> Internal standard type , set Internal standard.
Skyline File Name	Internal Standard Type	Quality							
CPTAC_TemplateDoc_Exp4_Stability_DRAFT02_2020-01-06_16-35-35.sky.zip	none	The internal standard in the skyline file is set to be none. Please set it to be heavy. Errors happen for all the peptides.							
Attribute	Essential attributes have missing values.	<table border="1"> <thead> <tr> <th>Skyline File Name</th> <th>Peptide sequence with errors</th> <th>Issue reason</th> </tr> </thead> <tbody> <tr> <td>CPTAC_TemplateDoc_Exp4_Stability_DRAFT02_2020-01-09_10-45-35.sky.zip</td> <td>LDQPGNLPGSNR, precursor charge: 2</td> <td> <ul style="list-style-type: none"> Essential attribute(s) has (have) missing values, including ReplicateNumber. </td> </tr> </tbody> </table>	Skyline File Name	Peptide sequence with errors	Issue reason	CPTAC_TemplateDoc_Exp4_Stability_DRAFT02_2020-01-09_10-45-35.sky.zip	LDQPGNLPGSNR, precursor charge: 2	<ul style="list-style-type: none"> Essential attribute(s) has (have) missing values, including ReplicateNumber. 	1. In Skyline, View -> Document Grid -> Views -> Assay Stability Replicates , check the corresponding attributes.
Skyline File Name	Peptide sequence with errors	Issue reason							
CPTAC_TemplateDoc_Exp4_Stability_DRAFT02_2020-01-09_10-45-35.sky.zip	LDQPGNLPGSNR, precursor charge: 2	<ul style="list-style-type: none"> Essential attribute(s) has (have) missing values, including ReplicateNumber. 							
Attribute	Essential attributes are annotated in unqualified data type.	None	In Skyline, View -> Document Grid -> Views -> Assay Stability Replicates , check the data types of corresponding attributes.						
Attribute	Incorrect annotations in the attribute of Exp4 Sample Group or Freeze Thaw Cycles.	None	In Skyline, View -> Document Grid -> Views -> Assay Stability Replicates , check the corresponding attributes.						
Light and Medium isotope	Both light and medium isotope labels are found in the peptide with a specific charge.	None	In Skyline, in the Targets panel, navigate to the peptide with errors, click each fragment ion to check its isotope label type.						
Area values of heavy or light isotope	The number of light isotopes or heavy isotopes is not one due to wrongly annotated values in attributes.	<table border="1"> <thead> <tr> <th>Skyline File Name</th> <th>Peptide sequence with errors</th> <th>Issue reason</th> </tr> </thead> <tbody> <tr> <td>CPTAC_TemplateDoc_Exp4_Stability_DRAFT02_2020-01-16_10-45-35.sky.zip</td> <td>LDQPGNLPGSNR, precursor charge: 2</td> <td> <ul style="list-style-type: none"> For y5 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. For y6 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. For y8 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. For y8 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. For y9 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. For y9 (2+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. </td> </tr> </tbody> </table>	Skyline File Name	Peptide sequence with errors	Issue reason	CPTAC_TemplateDoc_Exp4_Stability_DRAFT02_2020-01-16_10-45-35.sky.zip	LDQPGNLPGSNR, precursor charge: 2	<ul style="list-style-type: none"> For y5 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. For y6 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. For y8 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. For y8 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. For y9 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. For y9 (2+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. 	In Skyline, View -> Document Grid -> Views -> Assay Stability Replicates , check the values of the attribute of Replicate Number, Time, Time Units and Exp4 SampleGroup.
Skyline File Name	Peptide sequence with errors	Issue reason							
CPTAC_TemplateDoc_Exp4_Stability_DRAFT02_2020-01-16_10-45-35.sky.zip	LDQPGNLPGSNR, precursor charge: 2	<ul style="list-style-type: none"> For y5 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. For y6 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. For y8 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. For y8 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. For y9 (1+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. For y9 (2+): 2 heavy isotopes 2 light isotopes due to wrongly annotated values in attributes: replicate number, time or sample group. 							

Warning category	Warning message	Example case	Solution to the issue
Attribute	Attributes of Time or Time Units have missing values.	None	In Skyline, View -> Document Grid -> Views -> Assay Stability Replicates , check the corresponding attributes.
Sample storage conditions and times	The number of sample storage conditions and times is less than 6.	<p data-bbox="680 300 1016 357">GTFC[+57]SFDTPDDSIR y10 (1+) P-value from ANOVA: 0.94</p> 	Check the stability graph to make further decisions.
Replicate Number	The number of replicate is less than 2.	None	Check the stability graph to make further decisions.
Significant changes observed	The ANOVA p value is less than 0.05.	<p data-bbox="680 944 994 1002">VGFLPSAGK y7 (1+) P-value from ANOVA: 0.0046</p> 	Check the stability graph to make further decisions.
Bad distribution of points	In stability table, for the fragment ion under the	None	Check the stability table to make further decisions.

	storage condition, the intra-assay of variance is larger than the threshold of 0.2.		
Bad distribution of points	In stability table, for the fragment ion, according to time zero analysis, the RMSE(s) is larger than the threshold of 0.2.	None	Check the stability table to make further decisions.

Endogenous (Experiment 5)

Error category	Error message	Example case	Solution to the issue						
Internal standard	Internal standard is set to be none.	<table border="1"> <thead> <tr> <th>Skyline File Name</th> <th>Internal Standard Type</th> <th>Quality</th> </tr> </thead> <tbody> <tr> <td>CPTAC_TemplateDoc_Exp5_Reproducibility_DRAFT01_2020-03-26_09-58-55.sky.zip</td> <td>none</td> <td>The internal standard in the skyline file is set to be none. Errors happen for all the peptides.</td> </tr> </tbody> </table>	Skyline File Name	Internal Standard Type	Quality	CPTAC_TemplateDoc_Exp5_Reproducibility_DRAFT01_2020-03-26_09-58-55.sky.zip	none	The internal standard in the skyline file is set to be none. Errors happen for all the peptides.	In Skyline, settings -> Peptide Settings -> Modifications -> Internal standard type , set Internal standard.
Skyline File Name	Internal Standard Type	Quality							
CPTAC_TemplateDoc_Exp5_Reproducibility_DRAFT01_2020-03-26_09-58-55.sky.zip	none	The internal standard in the skyline file is set to be none. Errors happen for all the peptides.							
Attribute	Essential attributes have missing values.	<table border="1"> <thead> <tr> <th>Skyline File Name</th> <th>Peptide sequence with errors</th> <th>Issue reason</th> </tr> </thead> <tbody> <tr> <td>CPTAC_TemplateDoc_Exp5_Reproducibility_DRAFT01_2020-03-25_09-58-55.sky.zip</td> <td>LDQFGHLPGSNR, precursor charge: 2</td> <td> <ul style="list-style-type: none"> Essential attribute(s) has (have) missing values, including Day. Essential attribute(s) has (have) missing values, including SampleGroup. </td> </tr> </tbody> </table>	Skyline File Name	Peptide sequence with errors	Issue reason	CPTAC_TemplateDoc_Exp5_Reproducibility_DRAFT01_2020-03-25_09-58-55.sky.zip	LDQFGHLPGSNR, precursor charge: 2	<ul style="list-style-type: none"> Essential attribute(s) has (have) missing values, including Day. Essential attribute(s) has (have) missing values, including SampleGroup. 	In Skyline, View -> Document Grid -> Views -> Assay Endogenous Replicates , check the corresponding attributes.
Skyline File Name	Peptide sequence with errors	Issue reason							
CPTAC_TemplateDoc_Exp5_Reproducibility_DRAFT01_2020-03-25_09-58-55.sky.zip	LDQFGHLPGSNR, precursor charge: 2	<ul style="list-style-type: none"> Essential attribute(s) has (have) missing values, including Day. Essential attribute(s) has (have) missing values, including SampleGroup. 							
Attribute	Essential attributes are annotated in unqualified data type.	None	In Skyline, View -> Document Grid -> Views -> Assay Endogenous Replicates , check the data types of corresponding attributes.						
Light and Medium isotope	Both light and medium isotope labels are found in the peptide with a specific charge.	None	In Skyline, in the Targets panel, navigate to the peptide with errors, click each fragment ion to check its isotope label type.						
Area values of heavy or light isotope	The number of light isotopes or heavy isotopes is not one due to wrongly annotated values in attributes.	None	In Skyline, View -> Document Grid -> Views -> Assay Endogenous Replicates , check the values of the attribute of Replicate Number, Day and SampleGroup.						

Warning category	Warning message	Example case	Solution to the issue
Fragment ion	In reproducible detection of endogenous analyte graph, the number of fragment ions with both heavy and light isotopes is less than 3.	None	Check the reproducible detection of endogenous analyte graph to make further decisions.
Missing points	In reproducible detection of endogenous analyte graph, for the fragment ion, there is no point on at least one day.	None	Check the reproducible detection of endogenous analyte graph to make further decisions.
Missing points	In reproducible detection of endogenous analyte graph, fragment ion has less than 3 replicates on the specific day.	None	Check the reproducible detection of endogenous analyte graph to make further decisions.