
uAnalyze v2.0

Beta

dna.utah.edu | Department of Pathology | University of Utah

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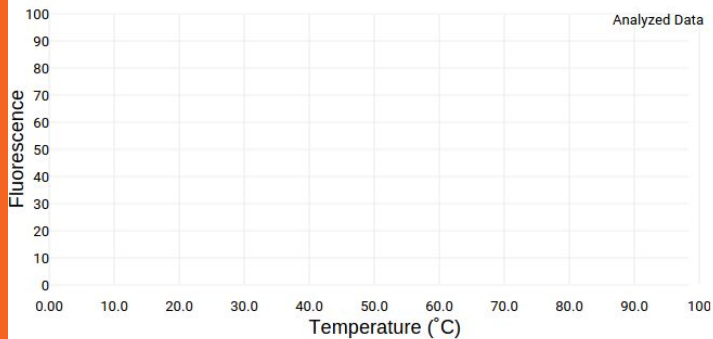
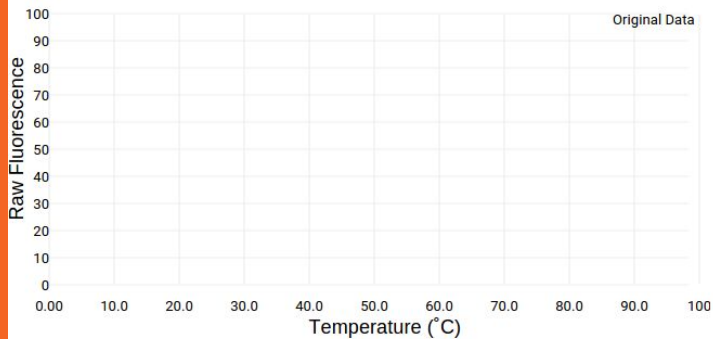
**uAnalyze 2.0 is a
from scratch update
of the publication
version.**

Interface

Generic ▾ Choose Files No file chosen

Derivative Normalize Overlay

Load Demo Files ▾



Select All Select None

Predicted Curve

```
ACGACGTTGTAACACGACAGAAGCATA
GTATAGAAGAAAAACAGCGCGCGCG
GCGCCAACACATTCAACCTTGCCACC
ATGGGGAAC TGGGCTGTAATGAGGG
GCTCTCCATTTTGTCTTGAAGTACC
ACAAGAGATAAGTTATAAATTCTCTGA
```

Reaction Conditions

Mono+: 20 Free Mg⁺⁺: 2.2

DMSO%: 0

Curve Name Prediction1

Cursors - Low:

High:

File name: meltcurves.csv

Save

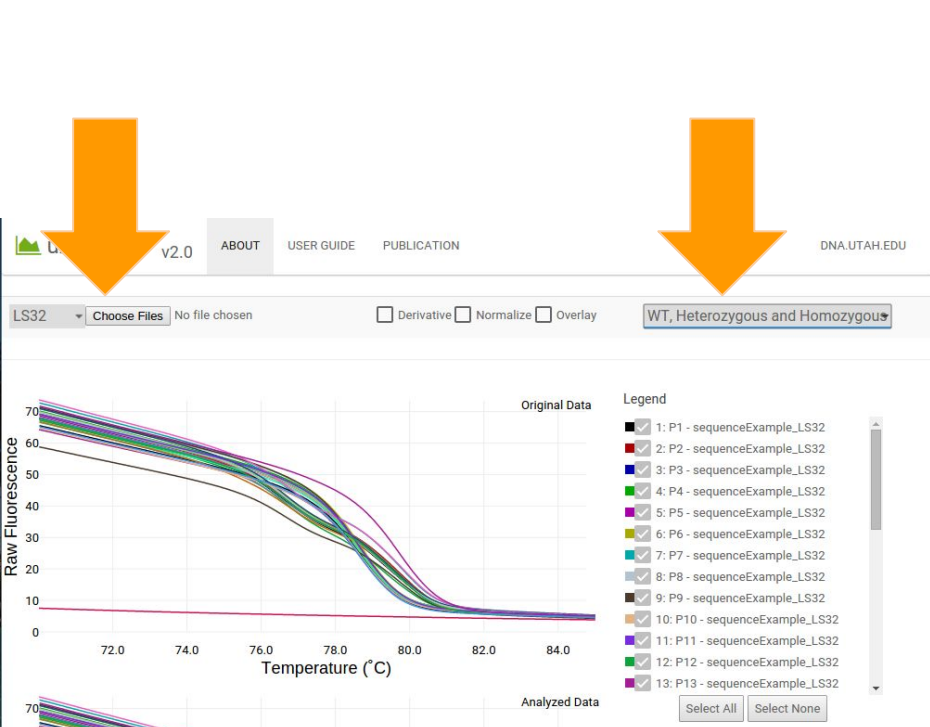
+ Add Curve

Walkthrough

Normalizing Data

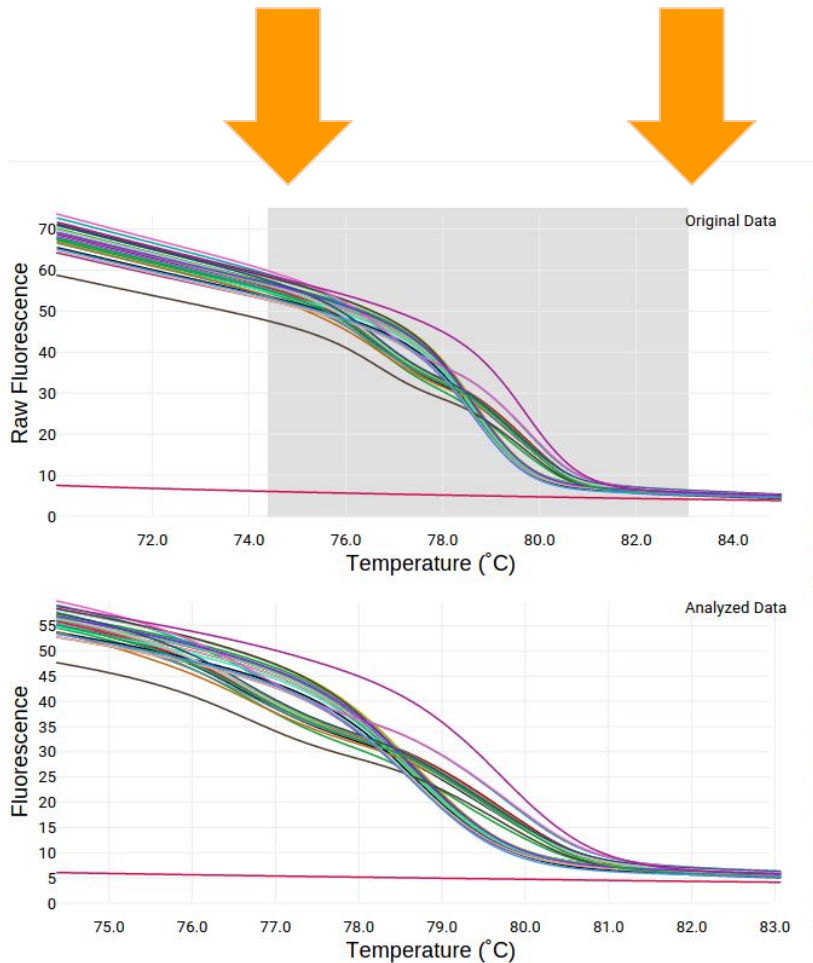
- Upload File
- Drag Cursor
- Select Normalize
- Export Data





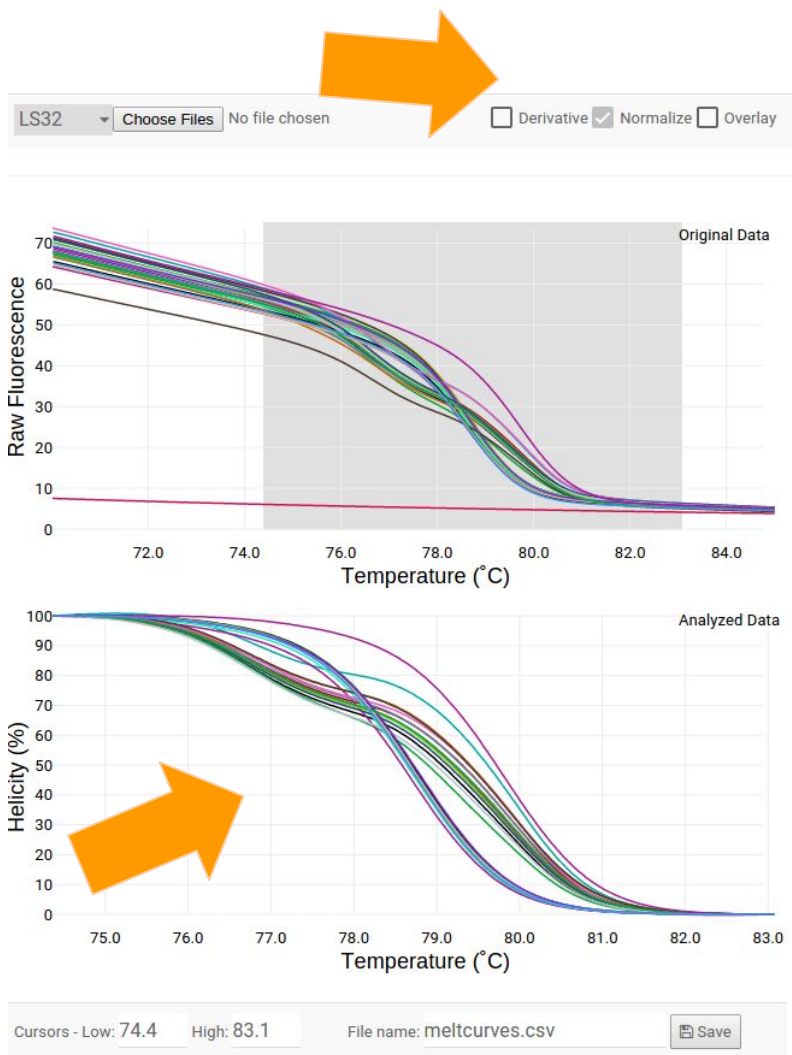
• Upload File

- Use the drop down on the left to select file type
- Click the file upload button
- For example data, use the Load Demo Files drop down on the far right



- Drag Cursor (top chart)

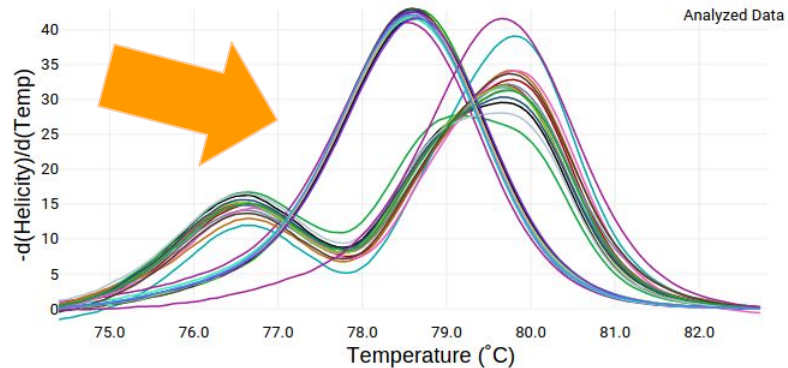
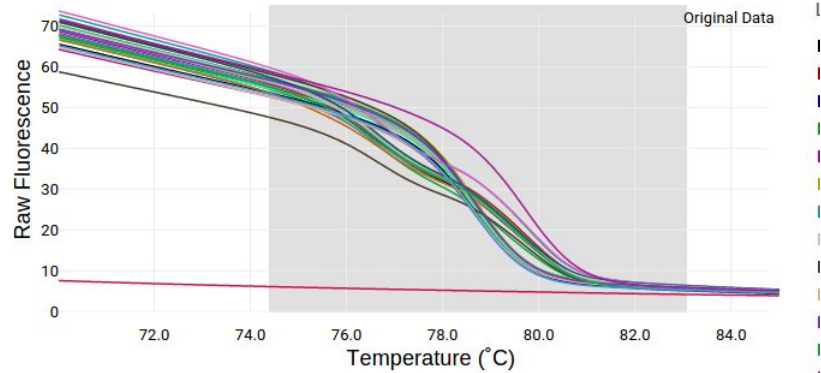

- Using the mouse, hold and drag a click across the region in which normalizing should be applied
- Release the click when done
- You will immediately see the updated region of interest on the analyzed chart (bottom)



- Normalization

- Click normalize on the top navigation once cursor region is set
- The bottom chart will immediately normalize the region of interest

LS32 Choose Files No file c Derivative Normalize Overlay



Cursors - Low: 74.4 High: 83.1

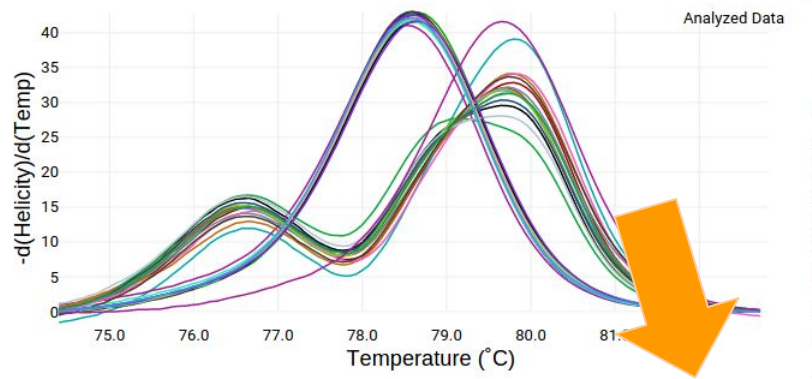
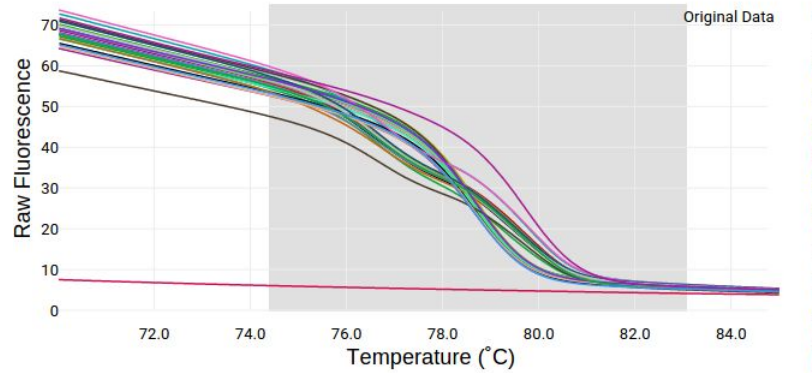
File name: meltcurves.csv

Save

- Normalization II

- Click derivative on the top navigation to update the analyzed data

LS32 No file chosen Derivative Normalize Overlay



Cursors - Low: 74.4 High: 83.1 File name: meltcurves.csv

- Data Export to .CSV
 - Click the save icon button to save export the analyzed chart as a .csv file for quick import into Excel.
 - The file can be named with the input box to the left of the save button

WT, Heterozygous and Homozygous

Legend

- 1: P1 - sequenceExample_LS32
- 2: P2 - sequenceExample_LS32
- 3: P3 - sequenceExample_LS32
- 4: P4 - sequenceExample_LS32
- 5: P5 - sequenceExample_LS32
- 6: P6 - sequenceExample_LS32
- 7: P7 - sequenceExample_LS32
- 8: P8 - sequenceExample_LS32
- 9: P9 - sequenceExample_LS32
- 10: P10 - sequenceExample_LS32
- 11: P11 - sequenceExample_LS32
- 12: P12 - sequenceExample_LS32
- 13: P13 - sequenceExample_LS32

Select All

Select None

Predicted Curve

```
ACGACGTTGTAAAACGACAGAAGCATA
GTATAGAAGAAAAACAGCGCGCGCG
GCGCCAACACATTCAACCTCTGCCACC
ATGGGGAAGTGGGCTGTGAATGAGGG
GCTCTCCATTTTTGTCAATTGTAAGTACC
AACAAGAGATAAGTTATAAATTCTCTGA
```

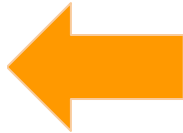
Reaction Conditions

Mono+: 20 Free Mg⁺⁺: 2.2

DMSO%: 0

Curve Name Prediction1

+ Add Curve



- Visibility of Samples

- Use the legend on the right to change visibility of a sample using the checkboxes provided next to the sample name

WT, Heterozygous and Homozygous

Legend

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- 13: P13 - sequenceExample_LS32

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Predicted Curve

```

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GTATAGAAGAAAAACAGCGCGCGG
GCGCCAACACATTCAACCTGTGCCACC
ATGGGGAAC TGGGCTGTGAATGAGGG
GCTCTCCATTTTGTCAATTGTAAGTACC
AACAAAGAGATAAGTTATAAATTCTCTGA

```

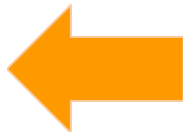
Reaction Conditions

Mono+: 20 Free Mg++: 2.2

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Curve Name Prediction1

+ Add Curve



- Add uMelt Prediction

- A prediction may be added via the uMelt web service and may be added any time for comparison to experimental
- Once parameters and sequence are set, simply push the Add Curve button below
- The predicted curve can be named accordingly (such as “Pred - Exon 1 - 15mM Salt”)

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**Questions or
feedback may be
sent to zach.dwight
at path.utah.edu**

Thanks!

uAnalyzeSM v2.0

ABOUT

USER GUIDE

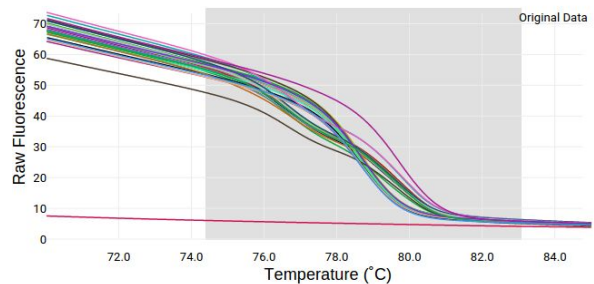
PUBLICATION

DNA.UTAH.EDU

LS32 Choose Files No file chosen

Derivative Normalize Overlay

WT, Heterozygous and Homozygous

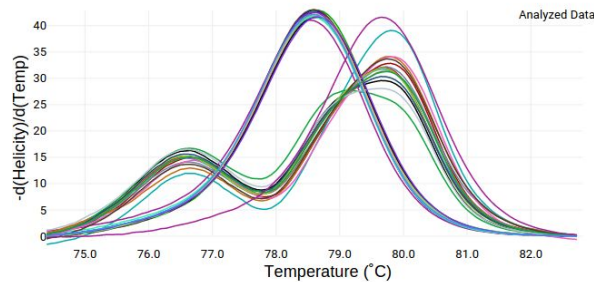


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Predicted Curve

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GTATAGAAAGAAAACAGCGCGCGG
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