

MAVID Alignment - HOMO vs. All

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Criteria: 75%, 100 bp
Regions: 0

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Seqs: homo/cow
Criteria: 95%, 100 bp
Regions: 8

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Seqs: homo/mouse
Criteria: 89%, 100 bp
Regions: 4

Alignment 4
Seqs: homo/frog
Criteria: 81%, 100 bp
Regions: 8

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Regions: 7

Alignment 6
Seqs: homo/trout
Criteria: 79%, 100 bp
Regions: 3

Alignment 7
Seqs: homo/danio
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Regions: 13

Alignment 8
Seqs: homo/fly
Criteria: 67%, 100 bp
Regions: 5

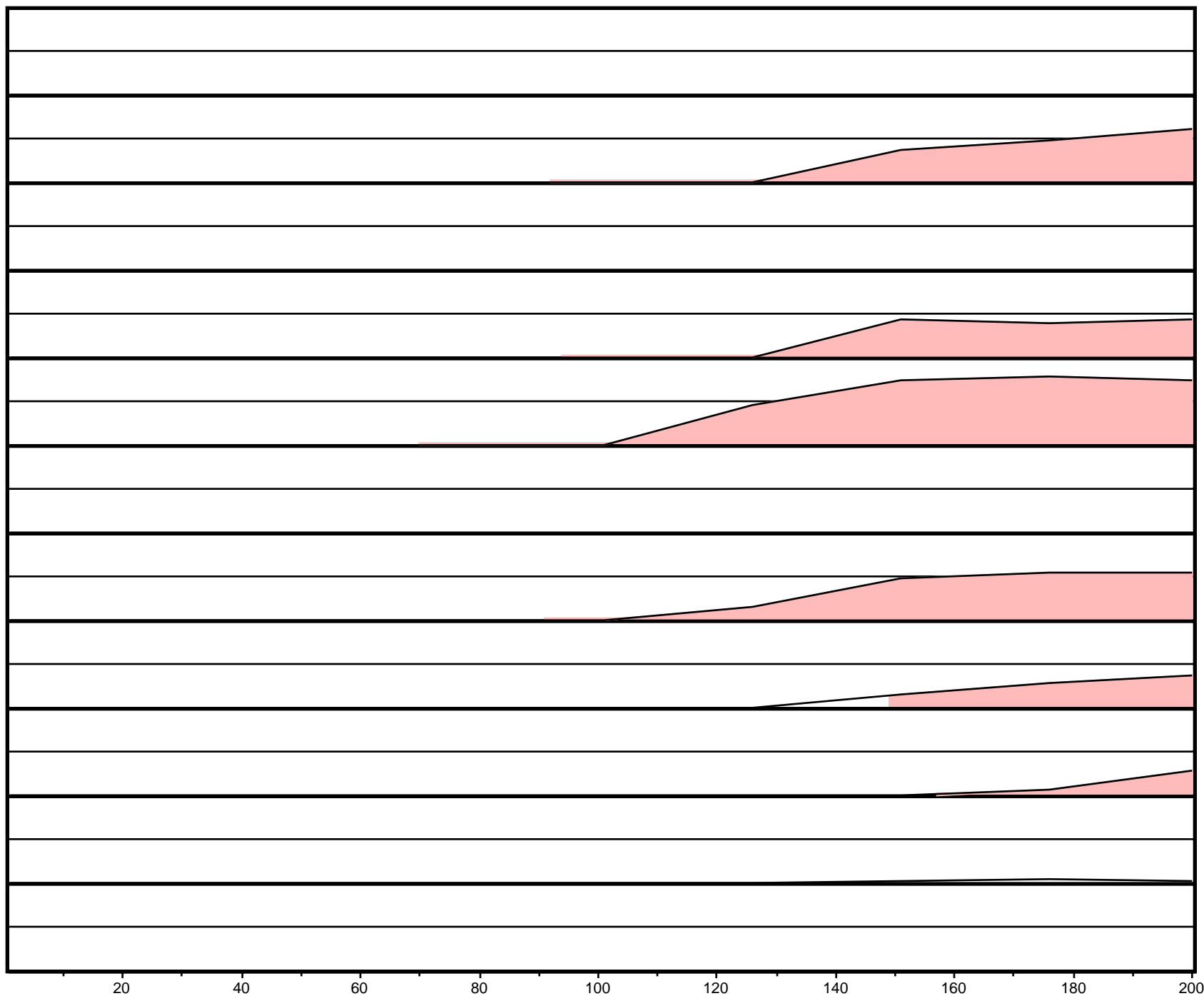
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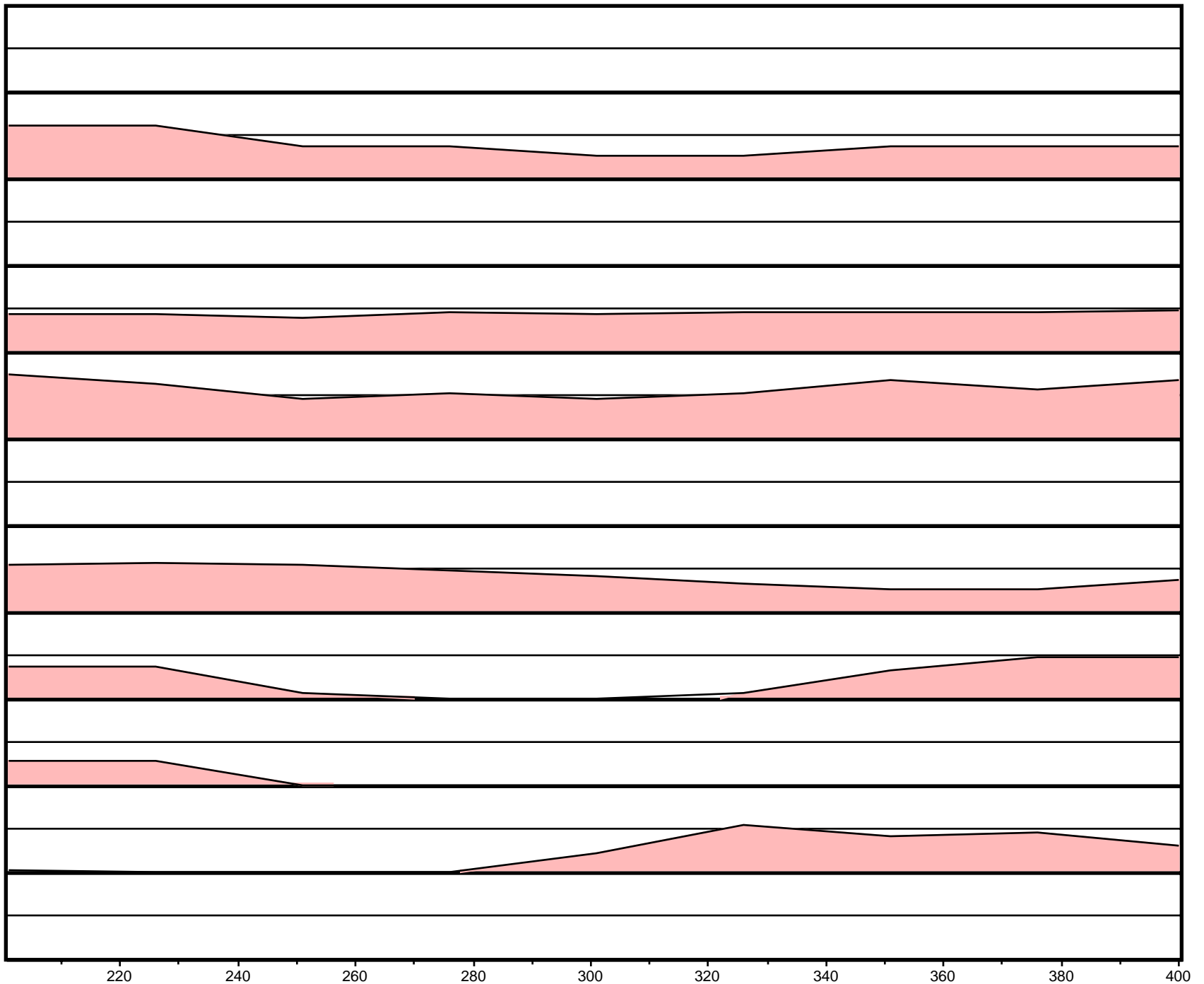
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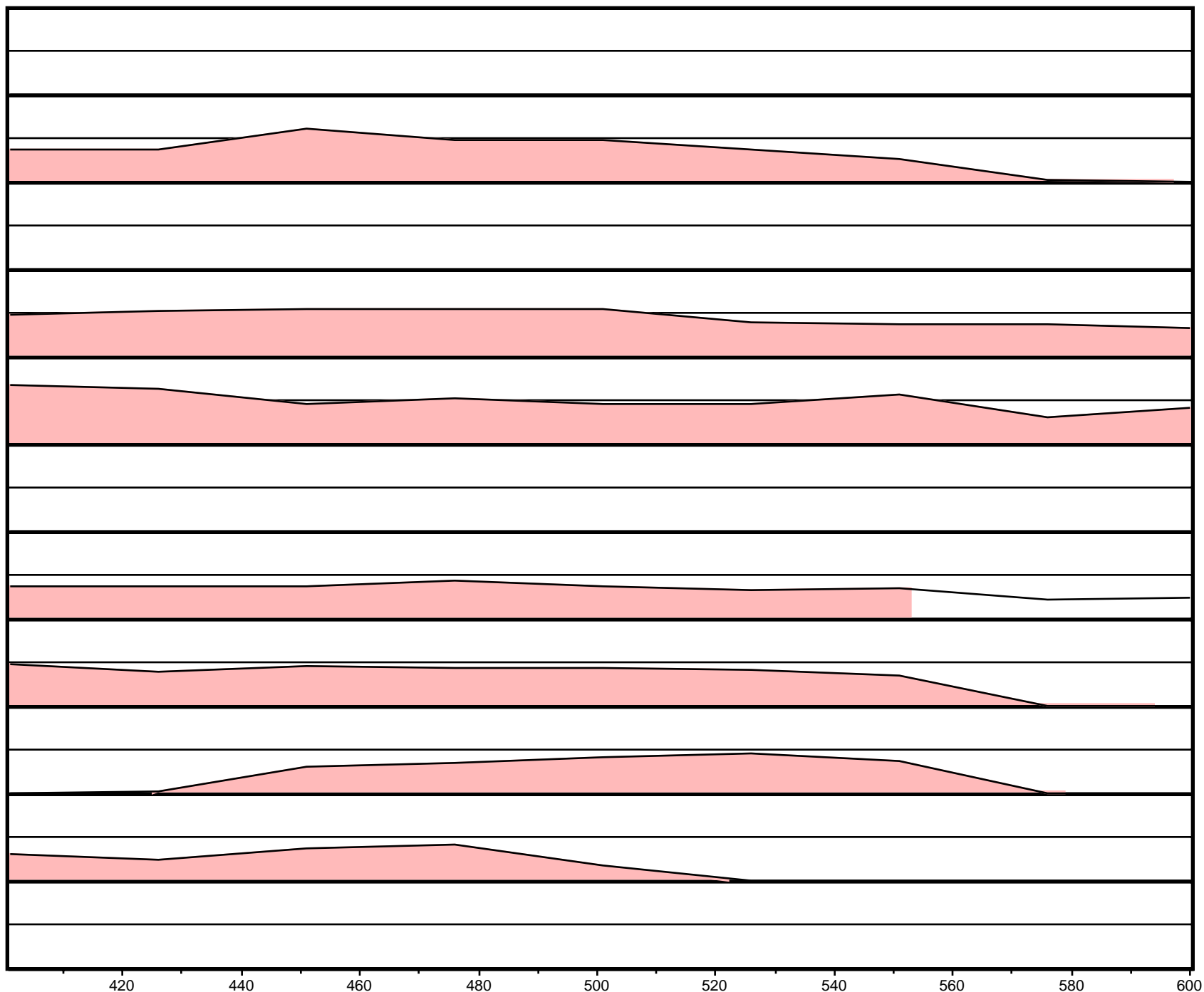
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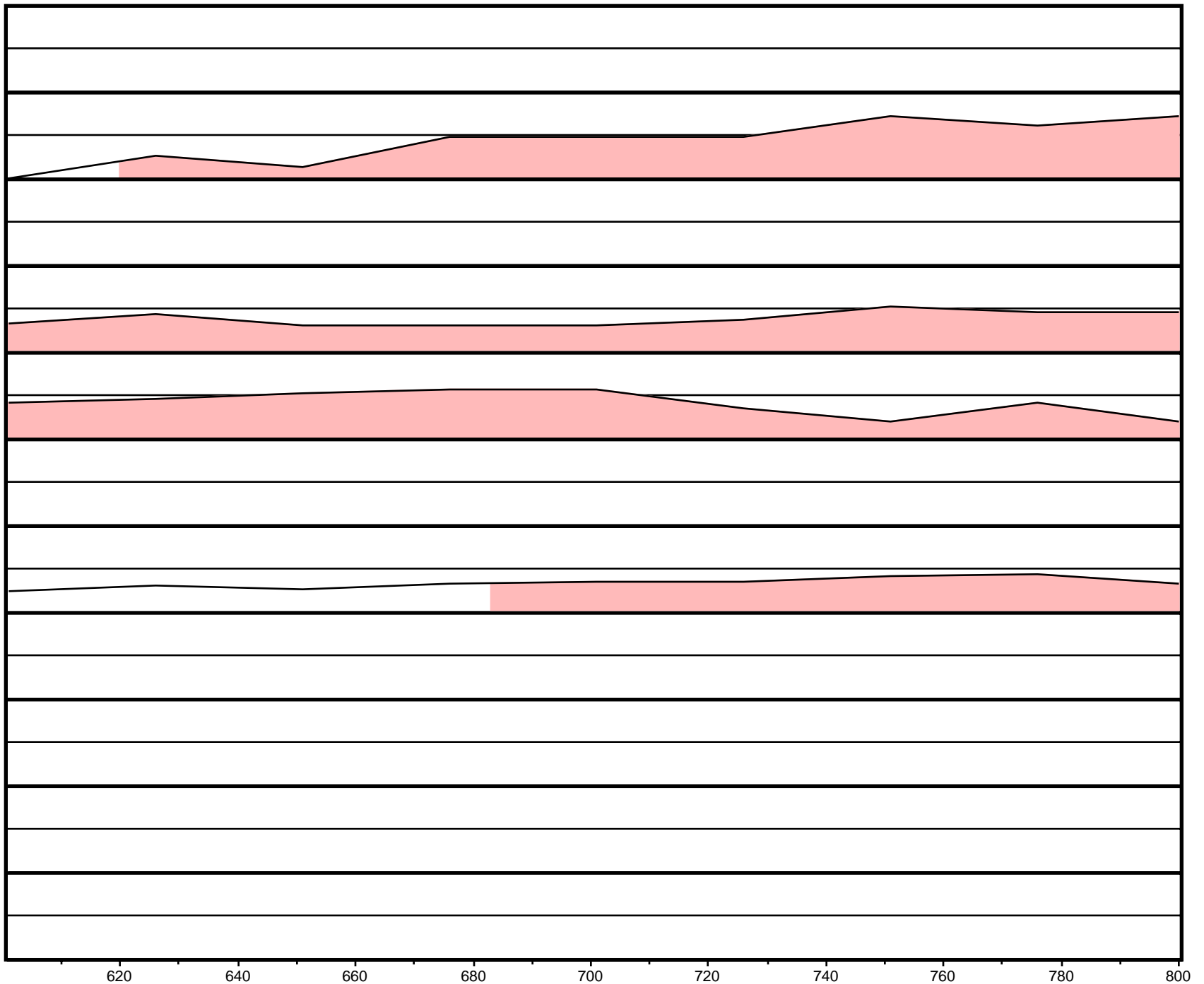
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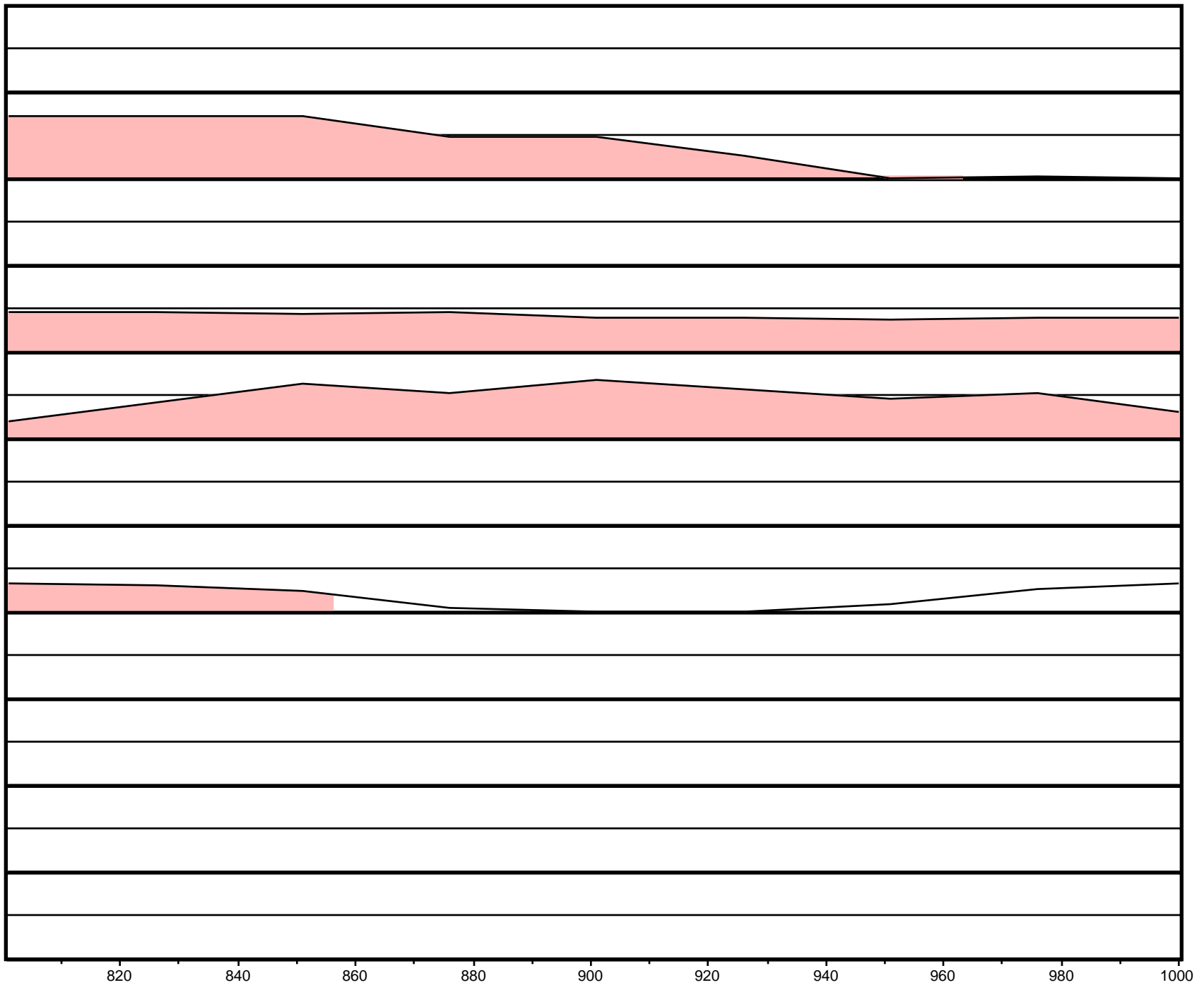
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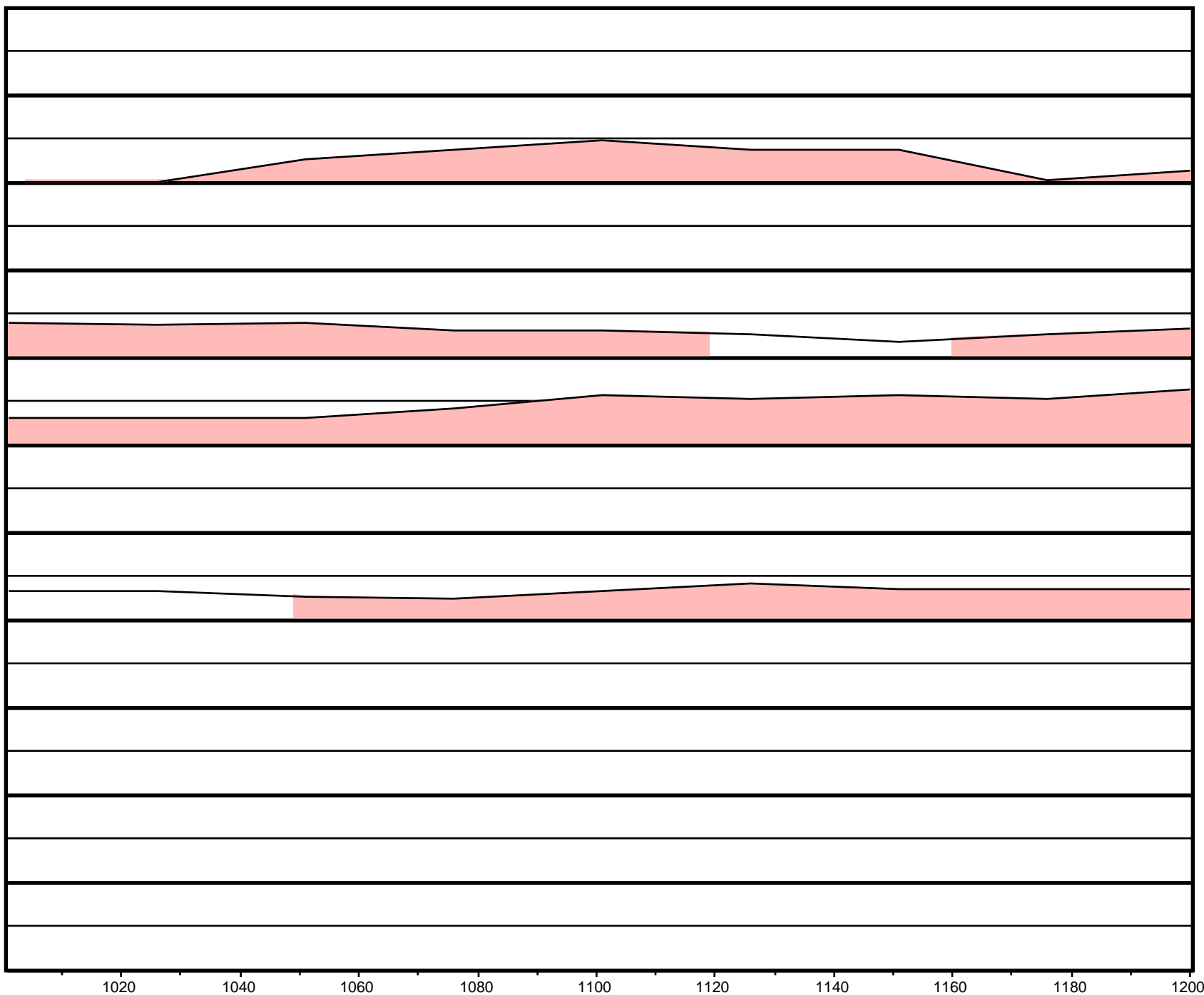
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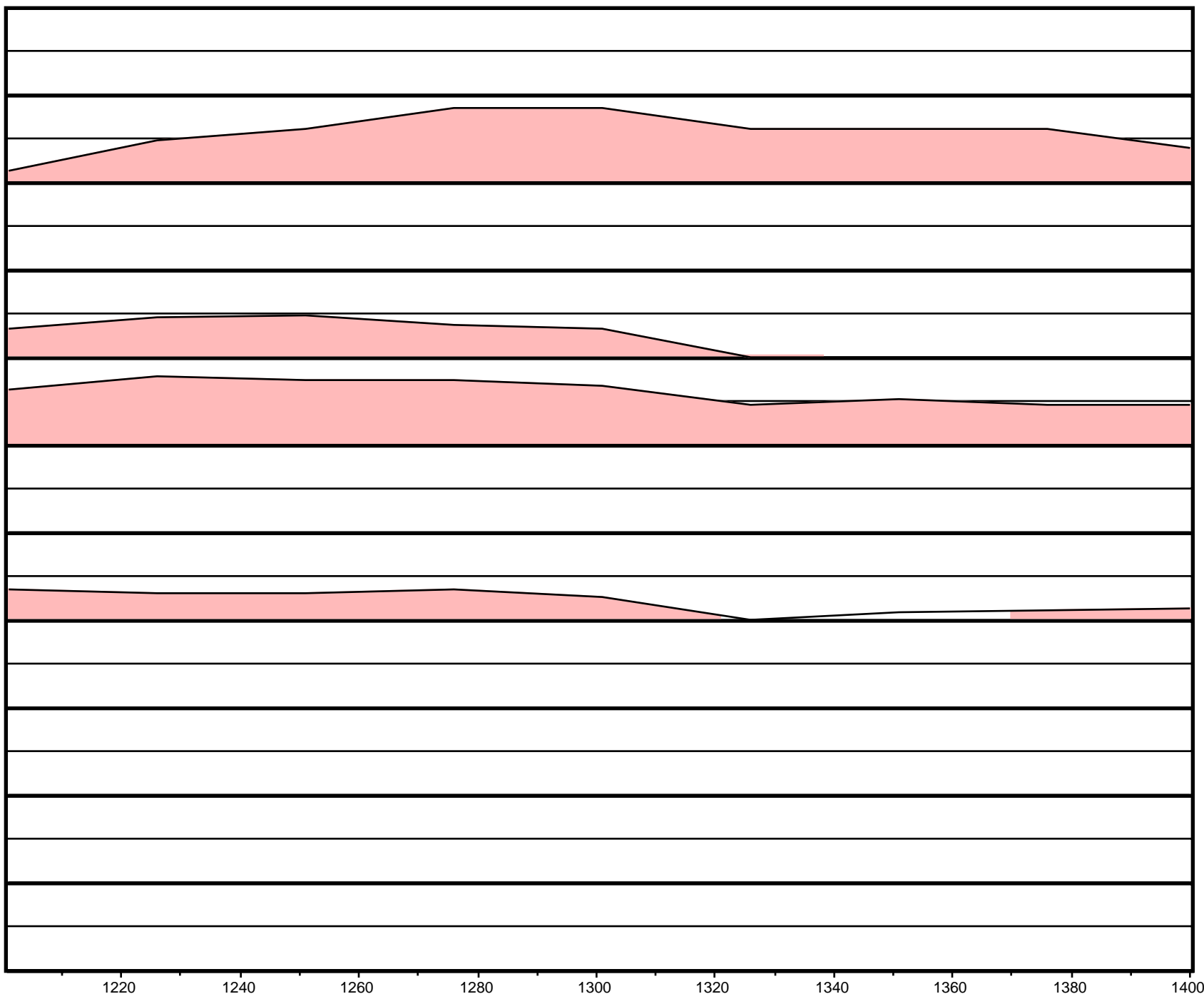
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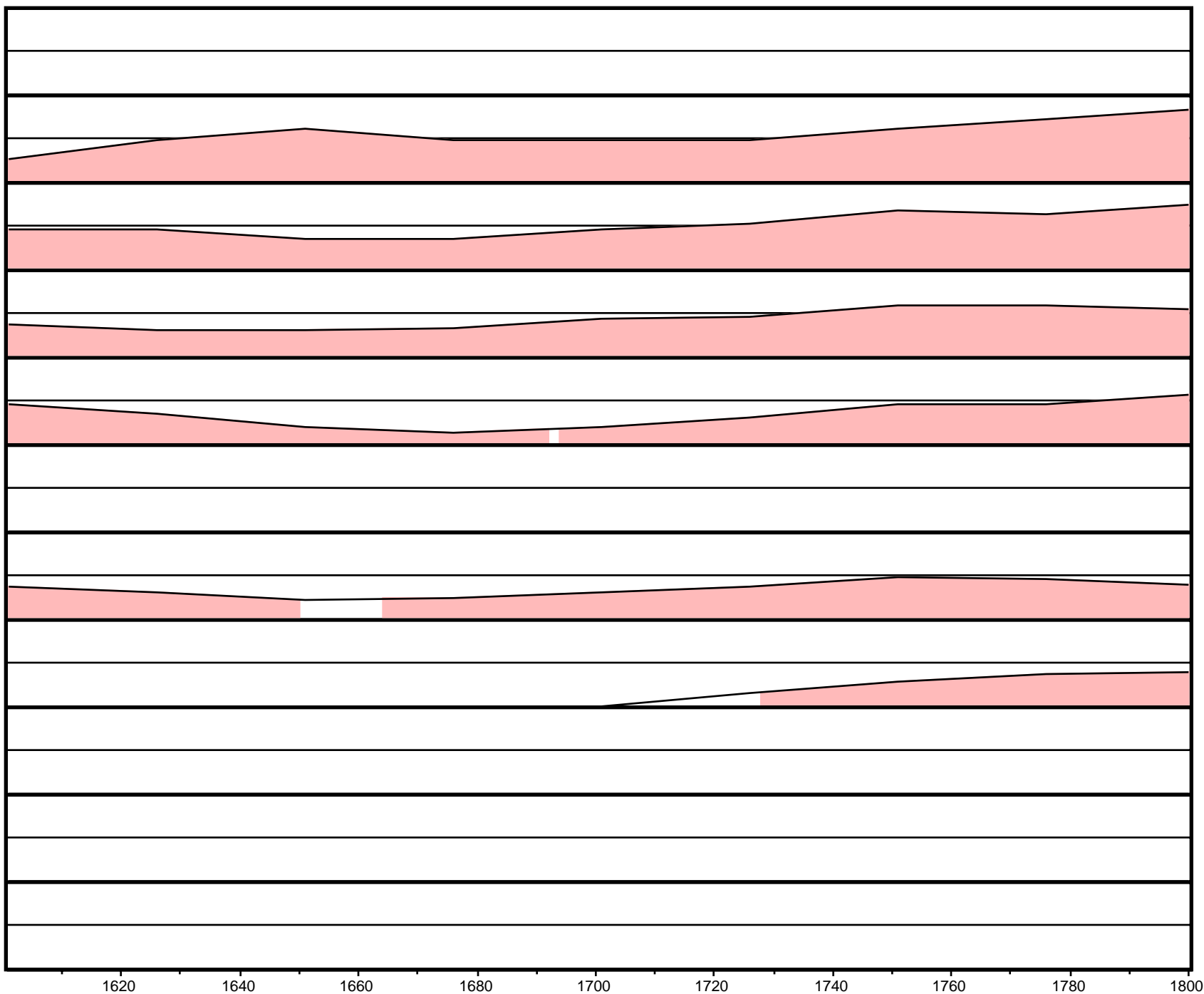
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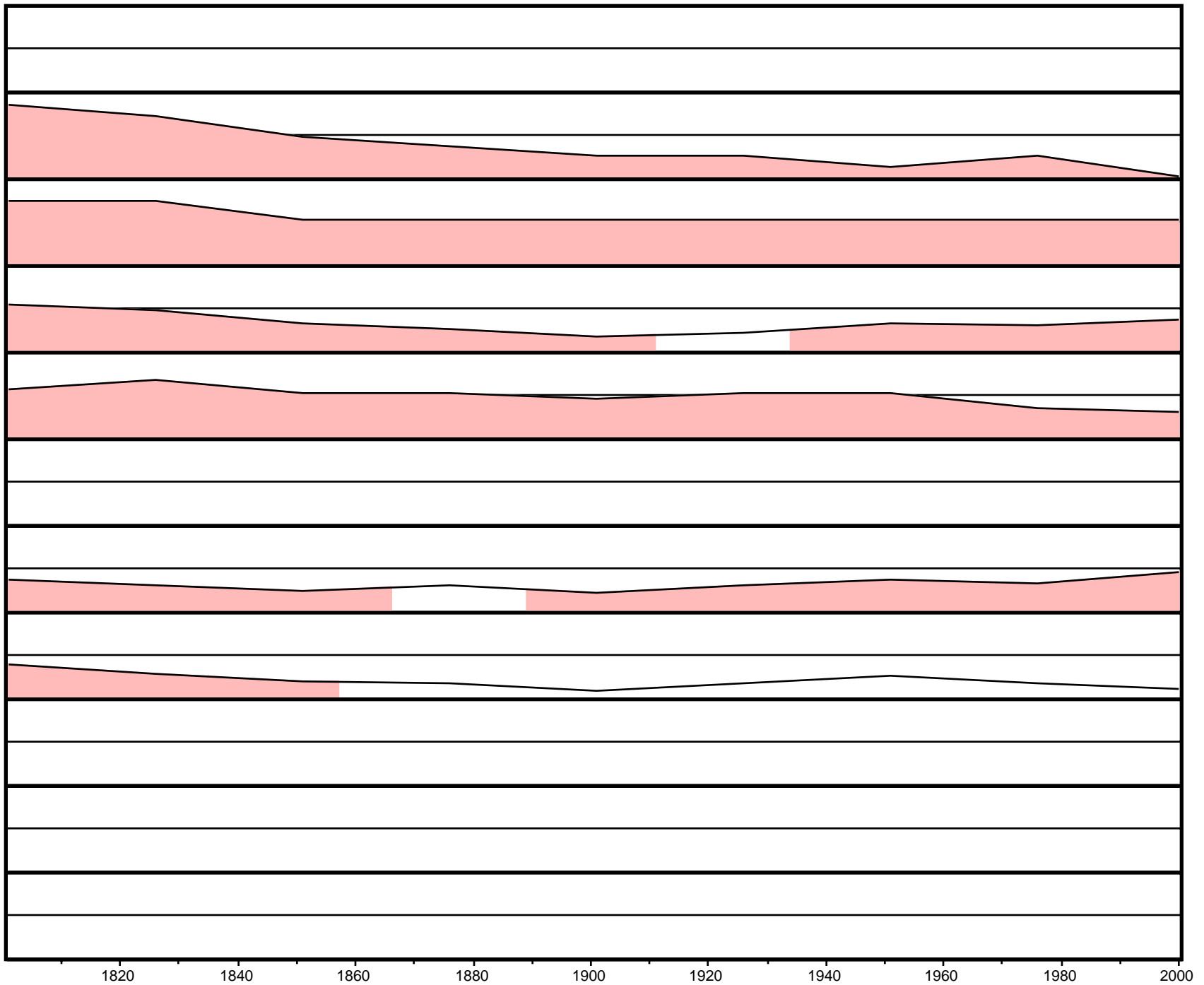
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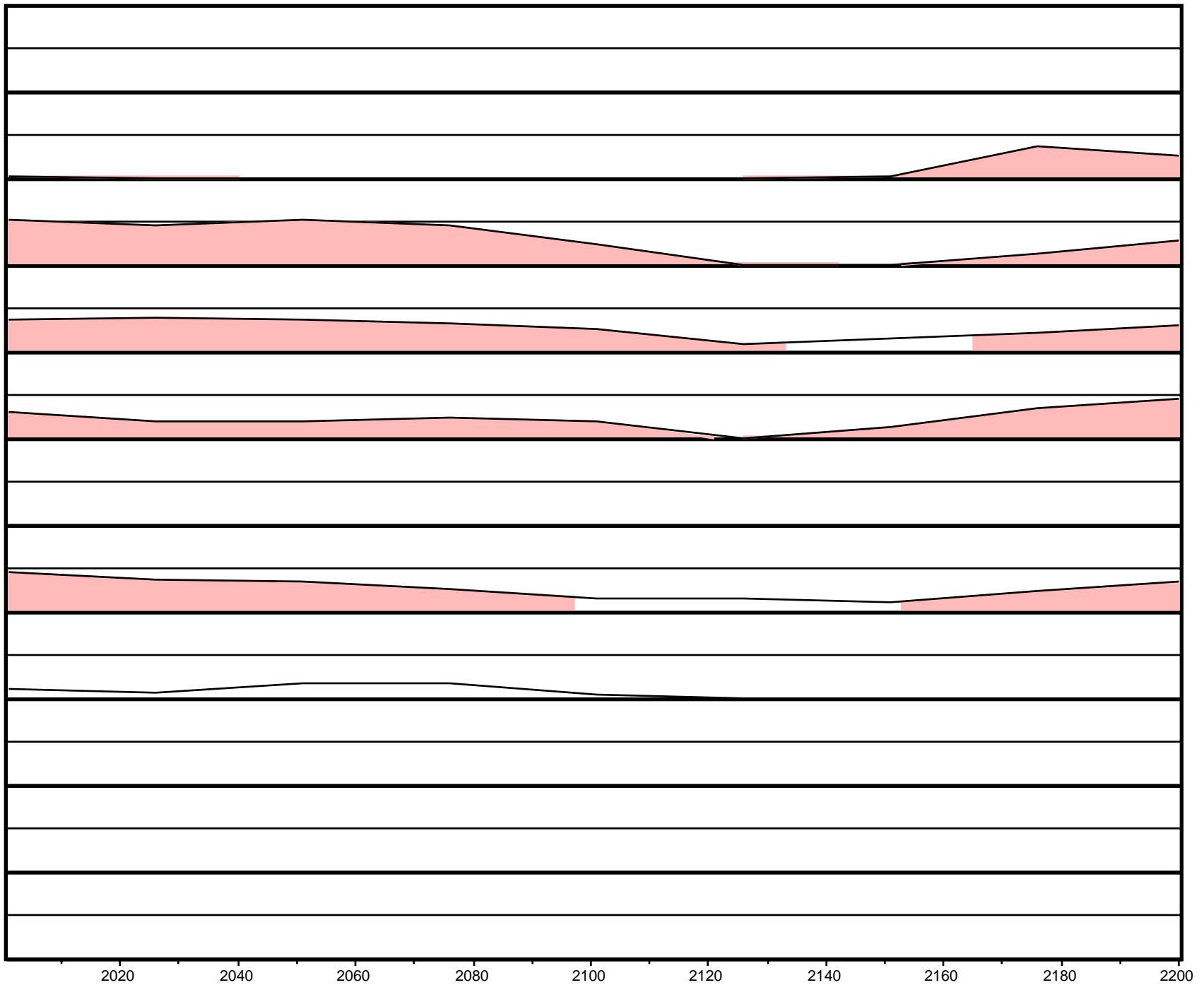
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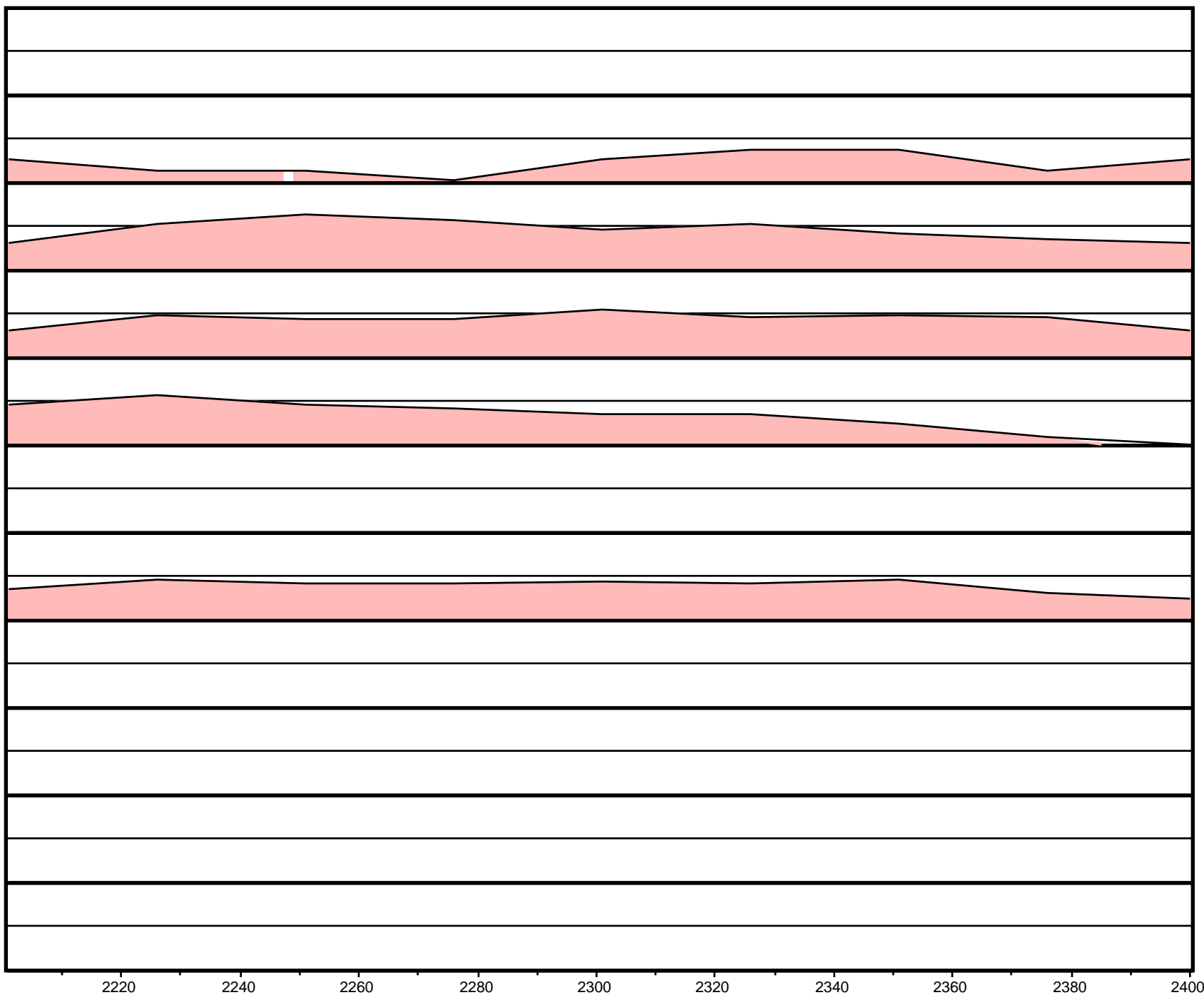
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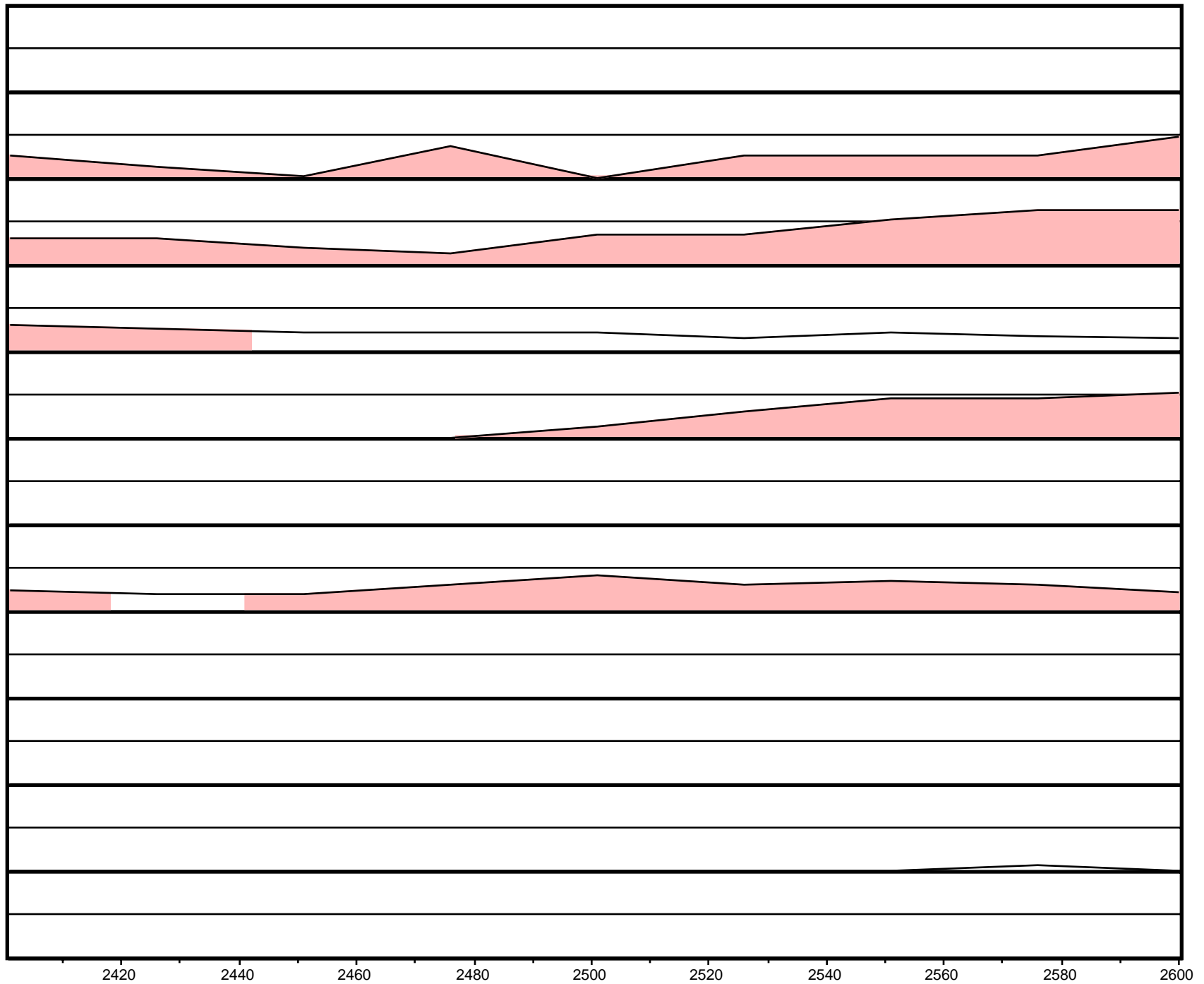
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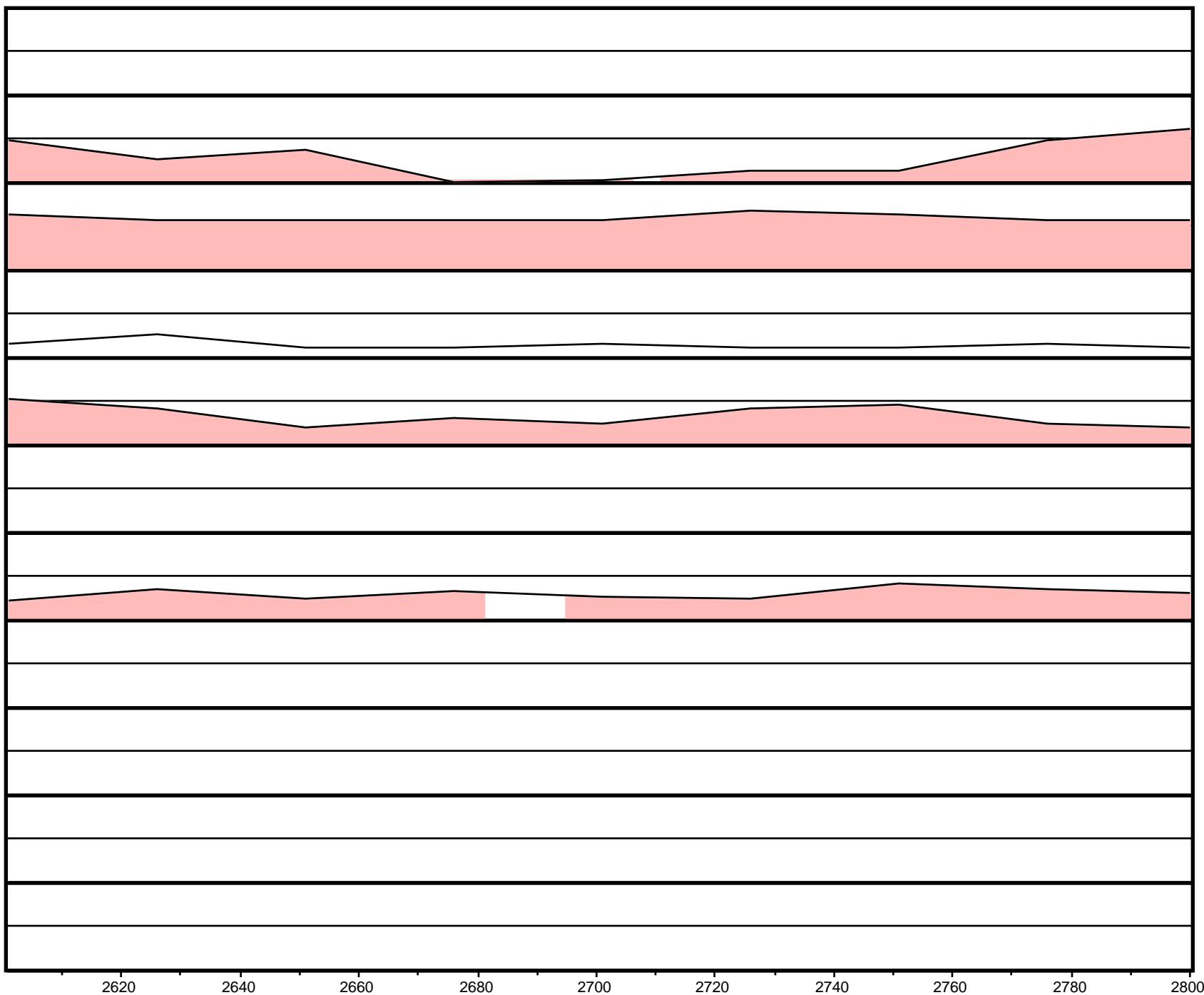
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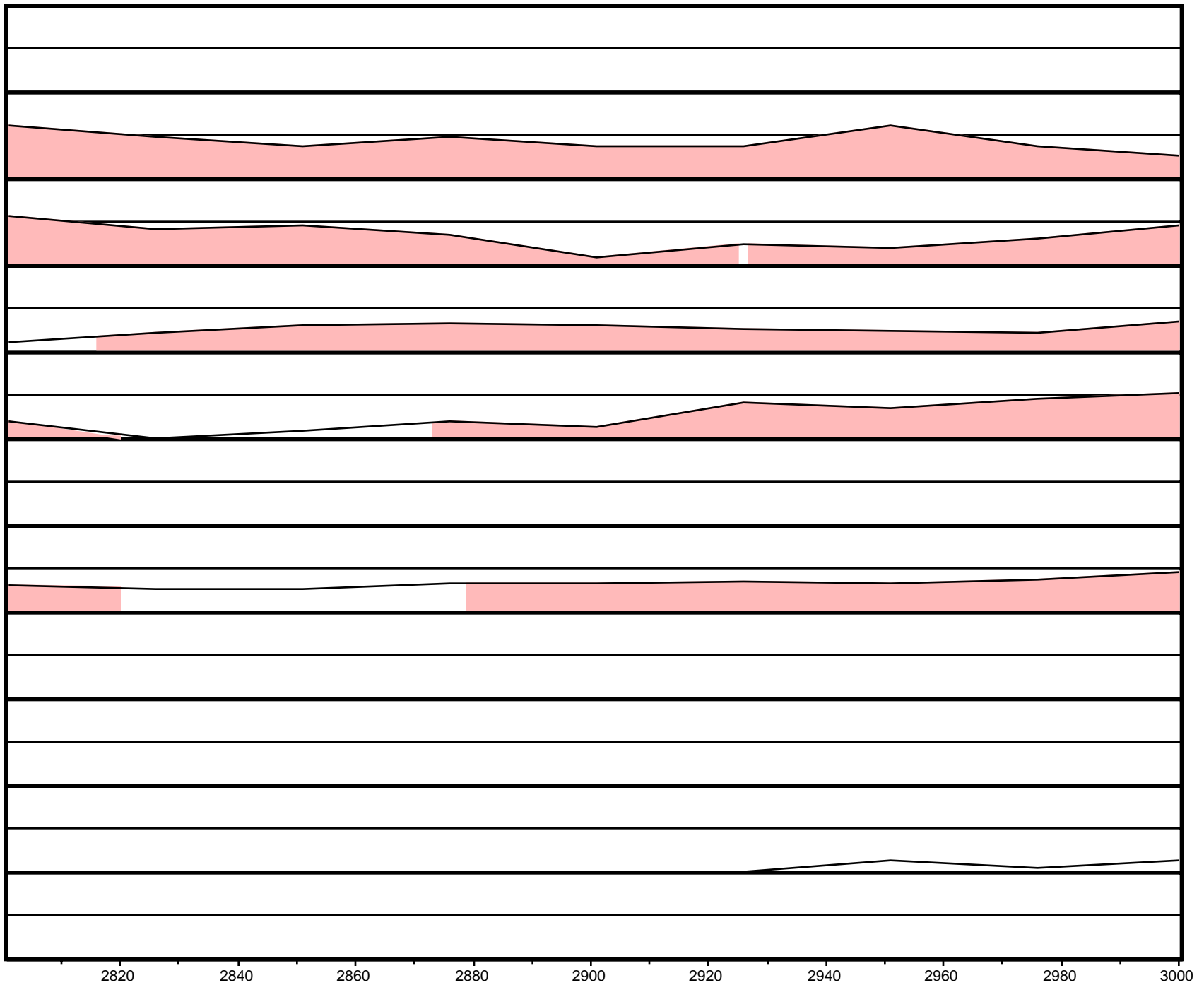
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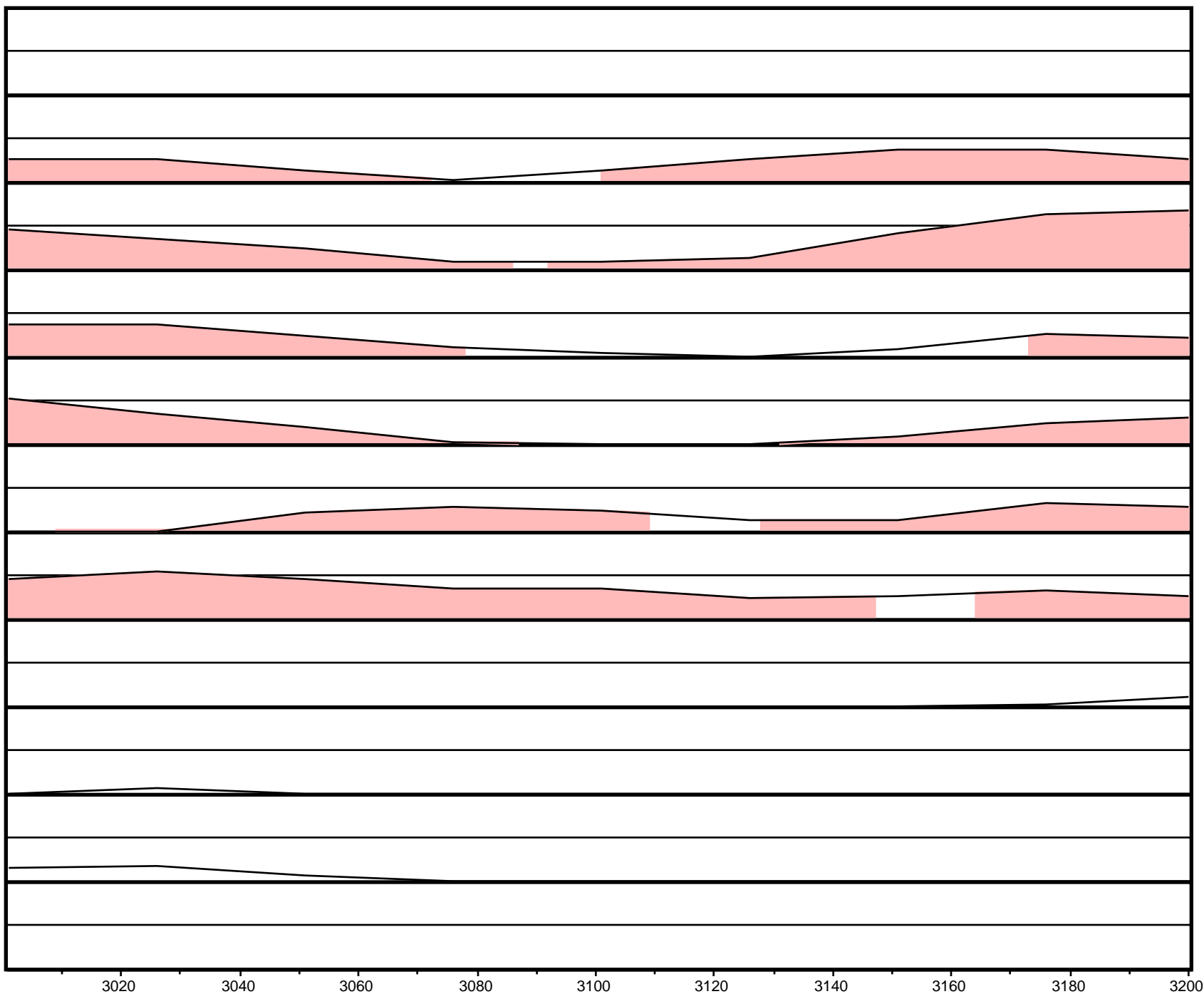
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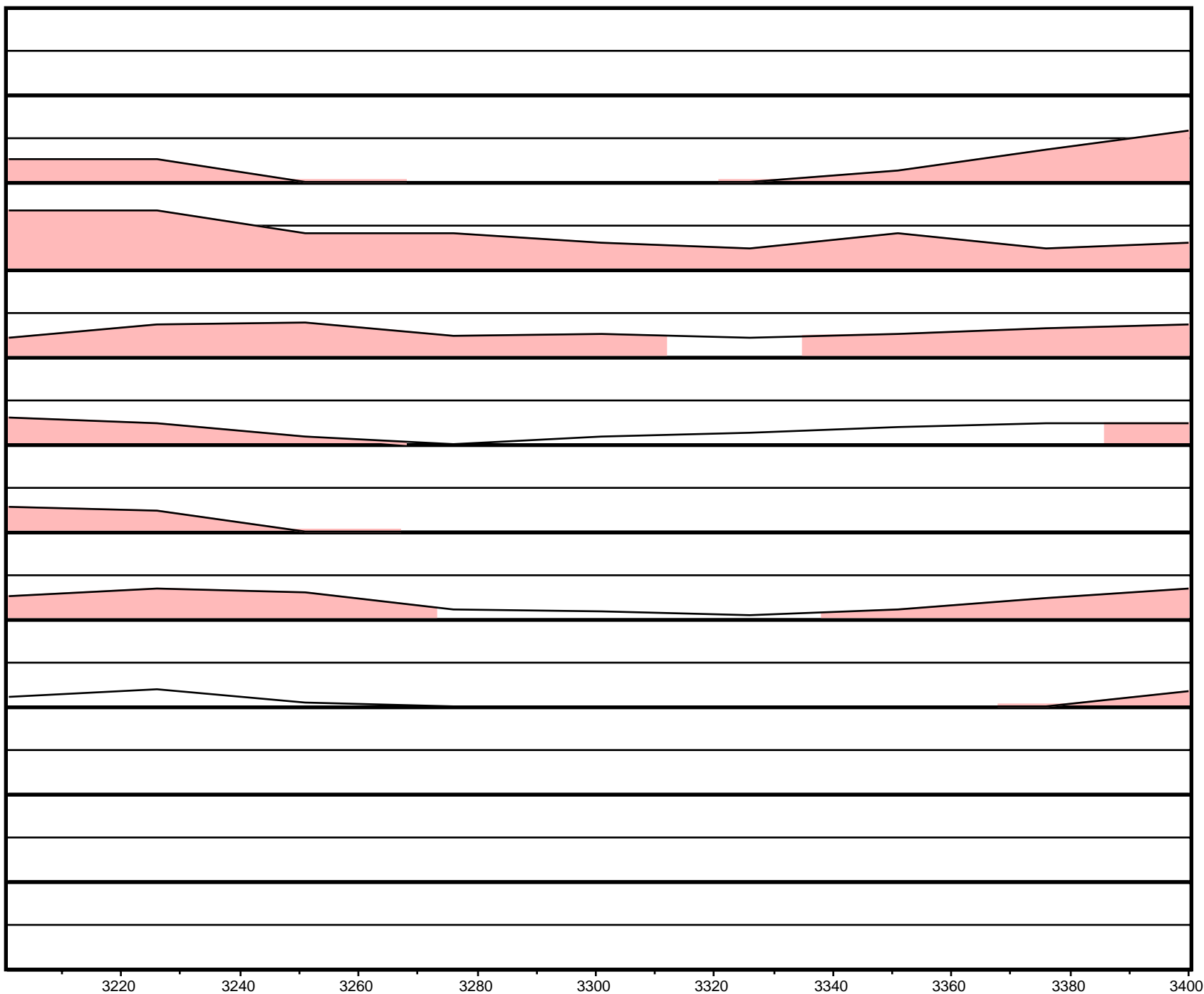
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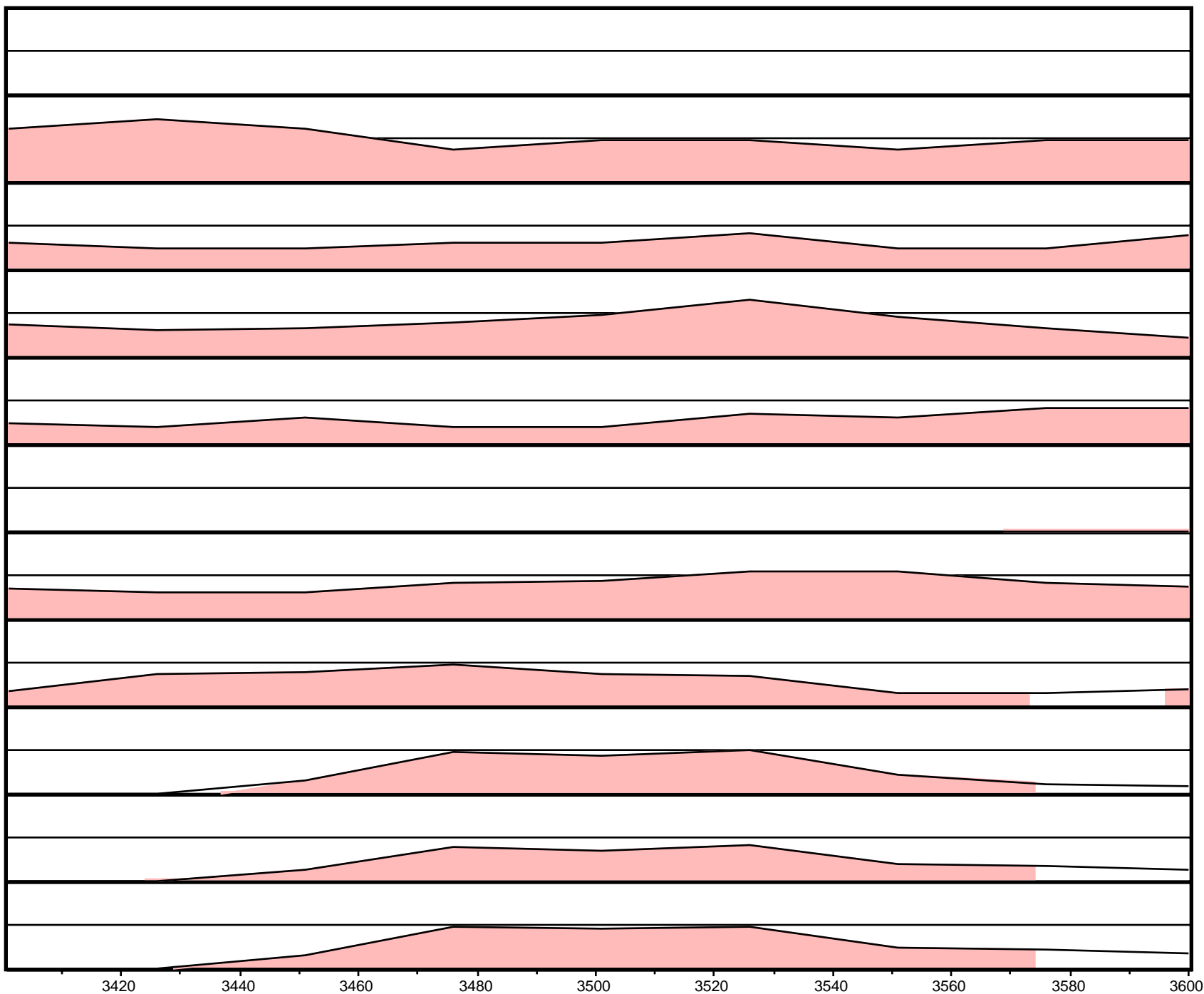
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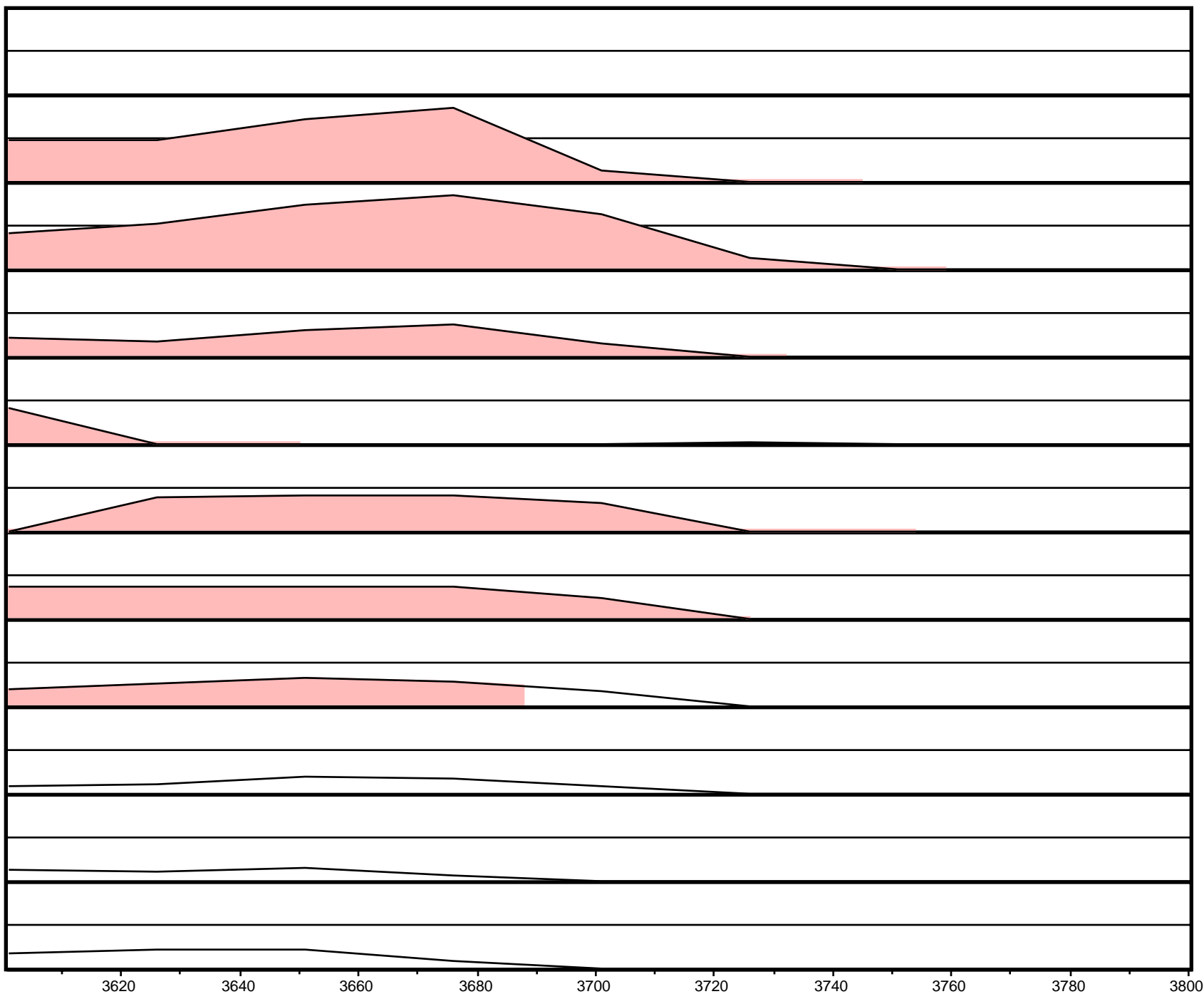
Alignment 9
Seqs: homo/celegans
Criteria: 68%, 100 bp
Regions: 3

Alignment 10
Seqs: homo/flower
Criteria: 66%, 100 bp
Regions: 2

Alignment 11
Seqs: homo/soy
Criteria: 66%, 100 bp
Regions: 1

X-axis: homo
Resolution: 25
Window size: 100 bp

▶ gene
■ exon
■ UTR
■ CNS



MAVID Alignment - HOMO vs. All

Alignment 1
Seqs: homo/pig
Criteria: 75%, 100 bp
Regions: 0

Alignment 2
Seqs: homo/cow
Criteria: 95%, 100 bp
Regions: 8

Alignment 3
Seqs: homo/mouse
Criteria: 89%, 100 bp
Regions: 4

Alignment 4
Seqs: homo/frog
Criteria: 81%, 100 bp
Regions: 8

Alignment 5
Seqs: homo/rat
Criteria: 89%, 100 bp
Regions: 7

Alignment 6
Seqs: homo/trout
Criteria: 79%, 100 bp
Regions: 3

Alignment 7
Seqs: homo/danio
Criteria: 79%, 100 bp
Regions: 13

Alignment 8
Seqs: homo/fly
Criteria: 67%, 100 bp
Regions: 5

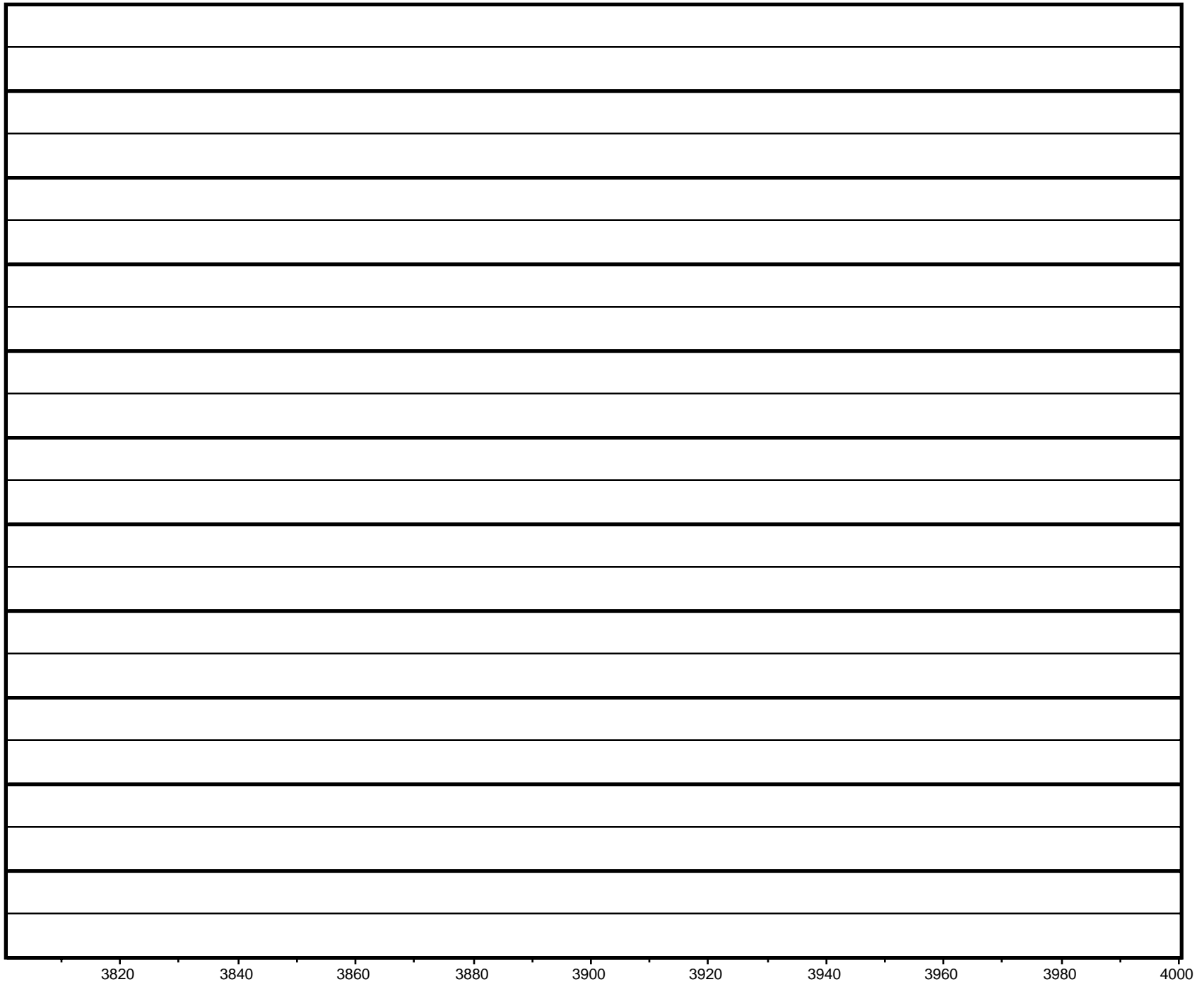
Alignment 9
Seqs: homo/celegans
Criteria: 68%, 100 bp
Regions: 3

Alignment 10
Seqs: homo/flower
Criteria: 66%, 100 bp
Regions: 2

Alignment 11
Seqs: homo/soy
Criteria: 66%, 100 bp
Regions: 1

X-axis: homo
Resolution: 25
Window size: 100 bp

► gene
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Alignment 7
Seqs: homo/danio
Criteria: 79%, 100 bp
Regions: 13

Alignment 8
Seqs: homo/fly
Criteria: 67%, 100 bp
Regions: 5

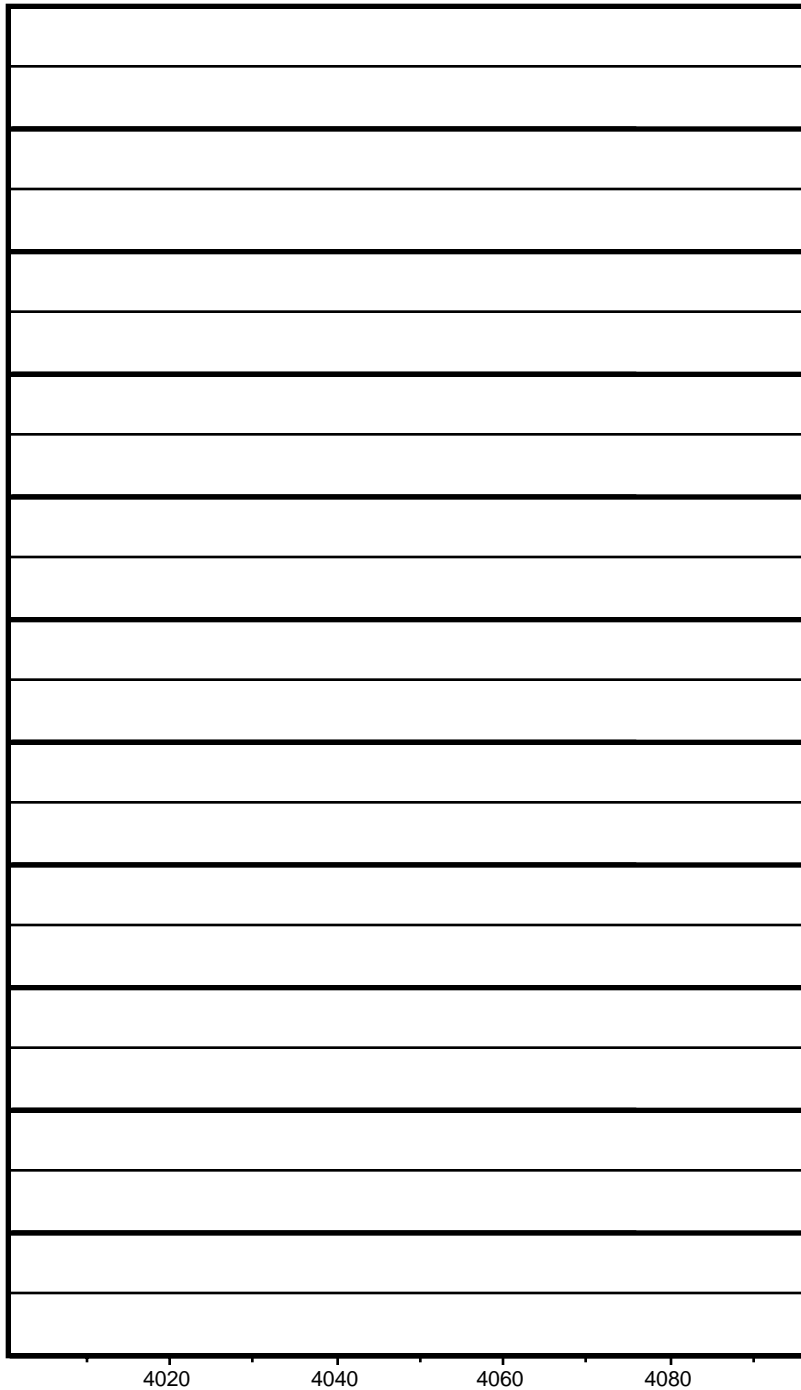
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Seqs: homo/celegans
Criteria: 68%, 100 bp
Regions: 3

Alignment 10
Seqs: homo/flower
Criteria: 66%, 100 bp
Regions: 2

Alignment 11
Seqs: homo/soy
Criteria: 66%, 100 bp
Regions: 1

X-axis: homo
Resolution: 25
Window size: 100 bp

► gene
■ exon
■ UTR
■ CNS



4020 4040 4060 4080