

Supplemental Figure S3. Coverage of the *C. albicans* mtDNA reference sequence with one of two identical copies of the inverted repeat region removed by forward and reverse RNA-seq reads in wild-type (BWP17, WT), homozygous *pet127Δ* strain (KO), and two independent isolates of *Capet127_{D375A}*/*Capet127_{D375A}* point mutant strain (mut3, mut4). Forward (fwd) and reverse (rev) mapping reads are shown separately. Note that for TU02 and TU04 the sense strand is the reverse strand. Transcription units and gene annotations are according to Kolondra et al. 2015. BWA files obtained using bamCompare were visualized in pyGenomeTracks. The maximum value on the depth coverage axis was set to better visualize low-coverage regions, truncating the highest values. General coverage graphs for the entire mtDNA are followed by detailed graphs for selected regions.

CamtDNA

5

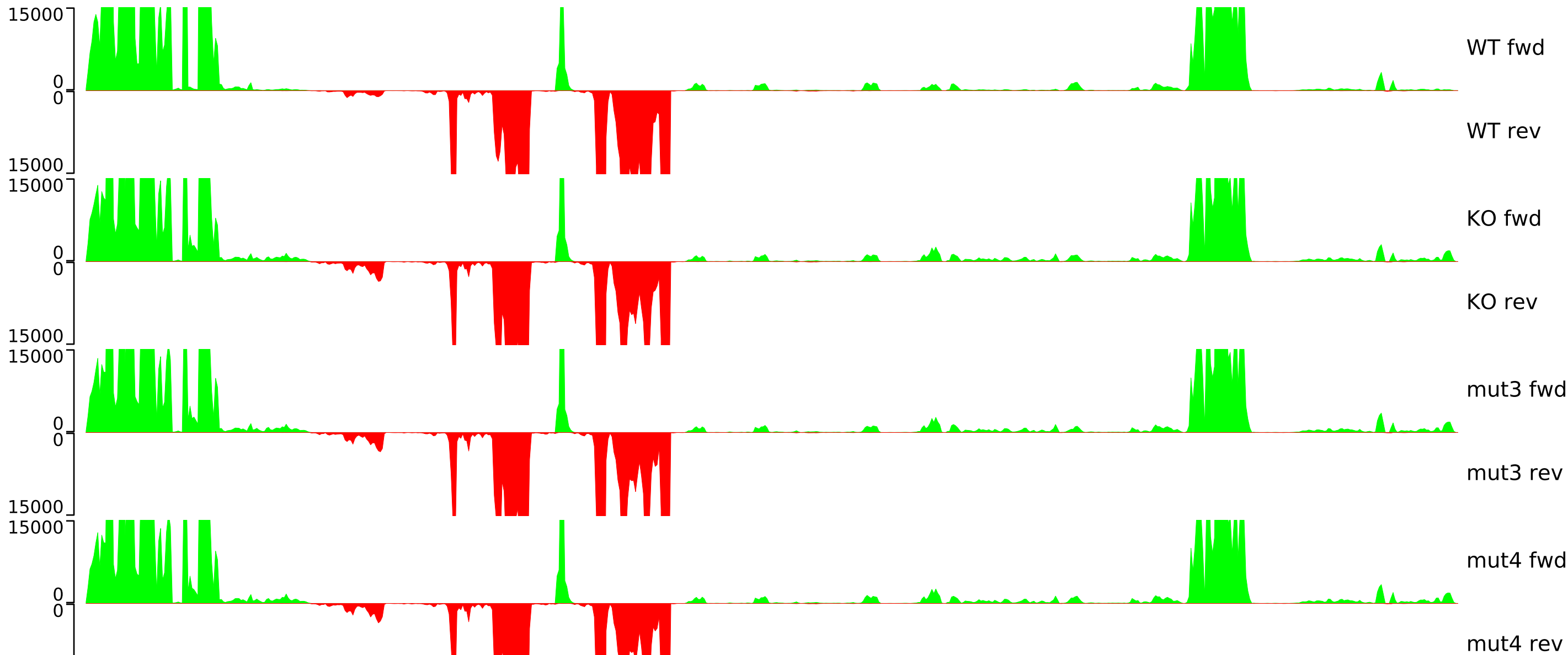
10

15

20

25

30 Kb



WT fwd

WT rev

KO fwd

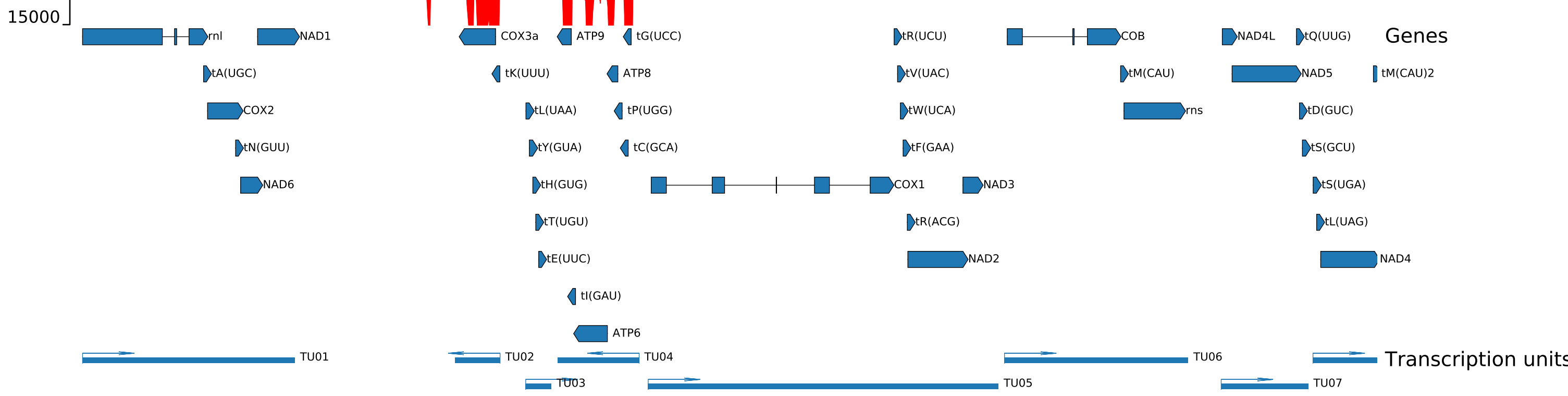
KO rev

mut3 fwd

mut3 rev

mut4 fwd

mut4 rev



CamtDNA

5

10

15

20

25

30 Kb

5000

0

WT fwd

0

WT rev

5000

0

KO fwd

0

KO rev

5000

0

mut3 fwd

0

mut3 rev

5000

0

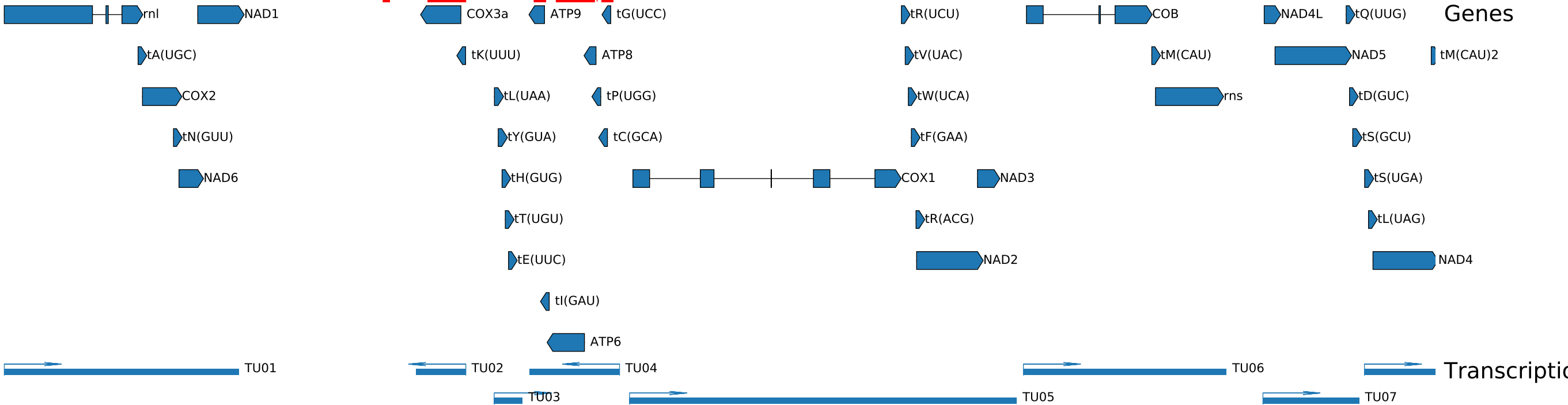
mut4 fwd

0

mut4 rev

5000

Genes



Transcription units

CamtDNA

0

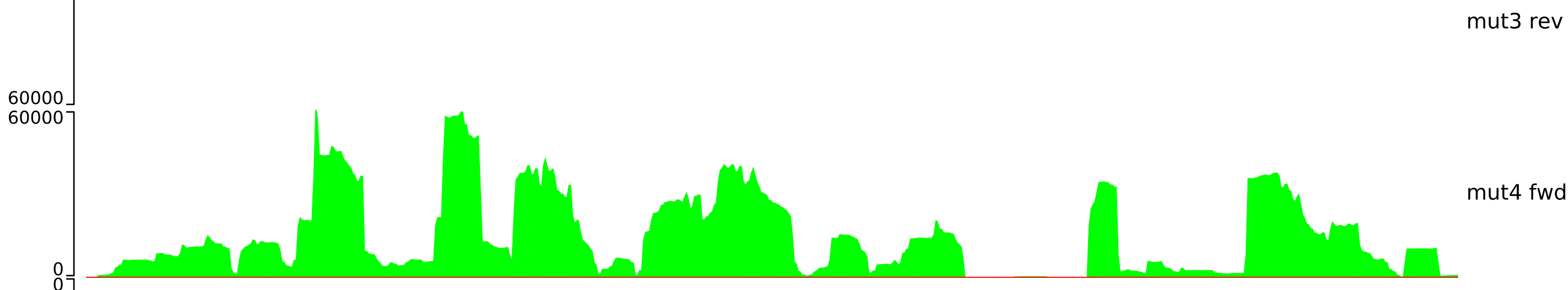
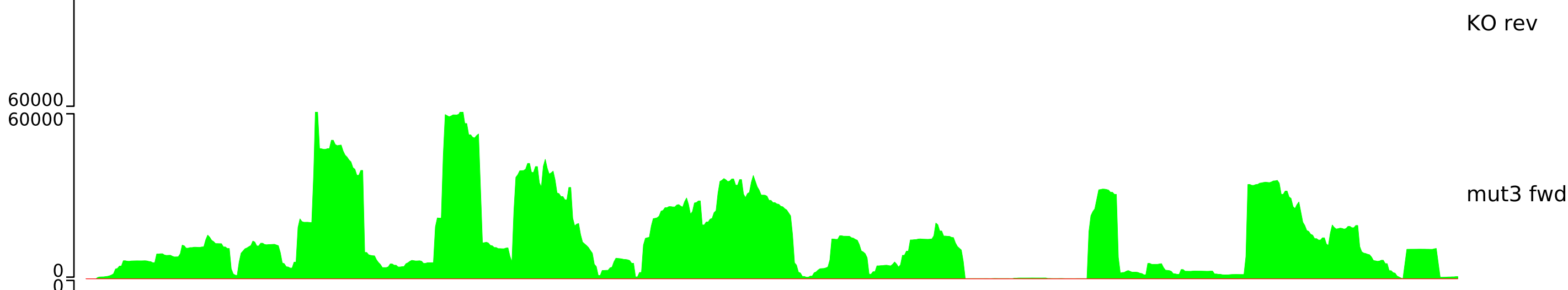
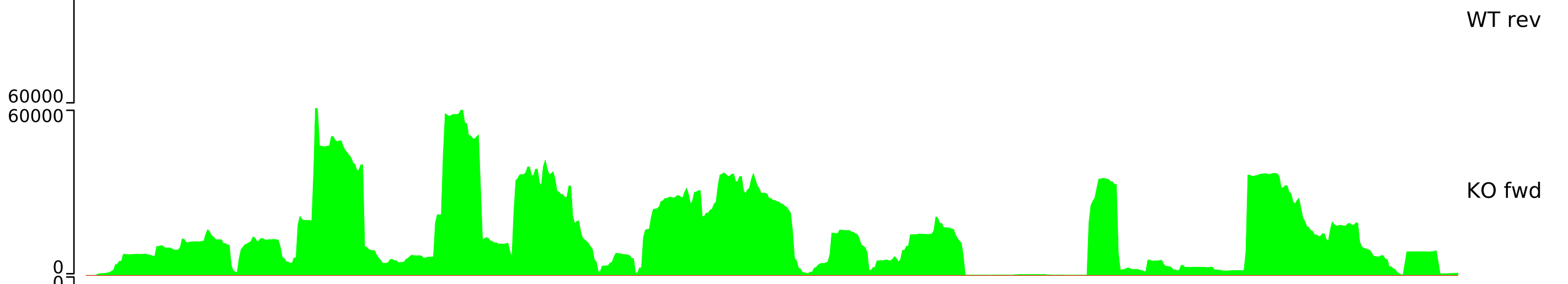
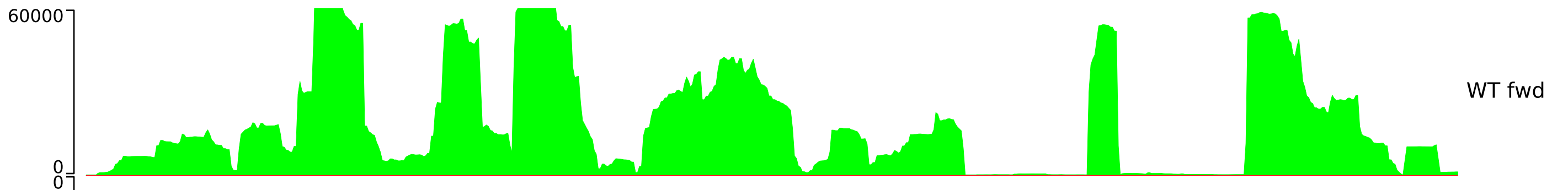
1

2

2

2

3 Kb



CamtDNA

3,200 3,400 3,600 3,800 4,000 b 4,200

WT fwd

WT rev

KO fwd

KO rev

mut3 fwd

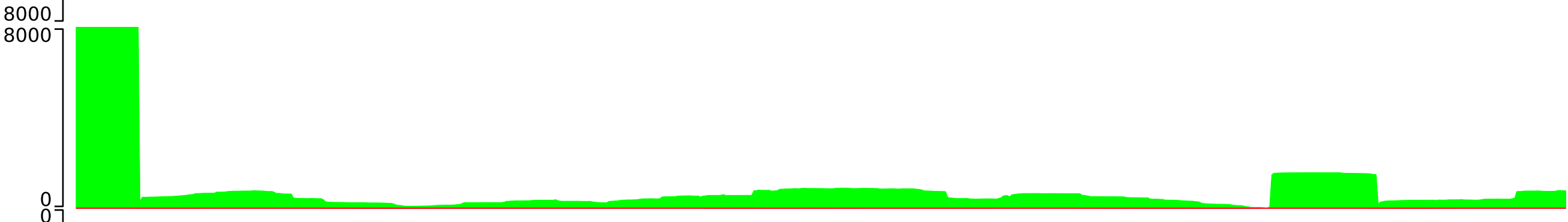
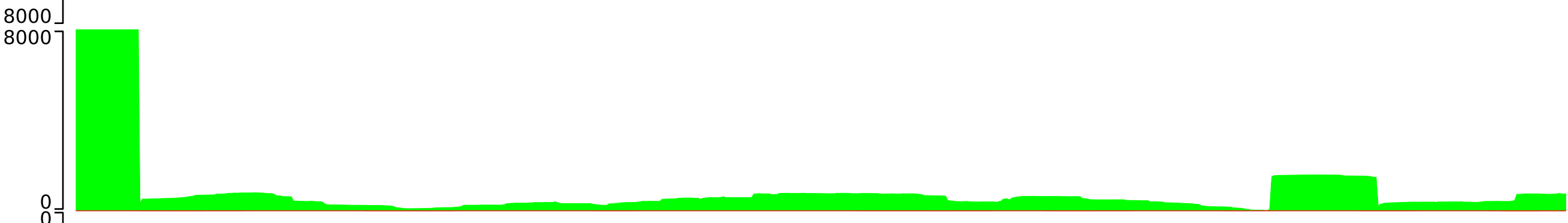
mut3 rev

mut4 fwd

mut4 rev

Genes

Transcription units



CamtDNA

4,100 4,200 4,300 4,400 4,500 b

WT fwd

WT rev

KO fwd

KO rev

mut3 fwd

mut3 rev

mut4 fwd

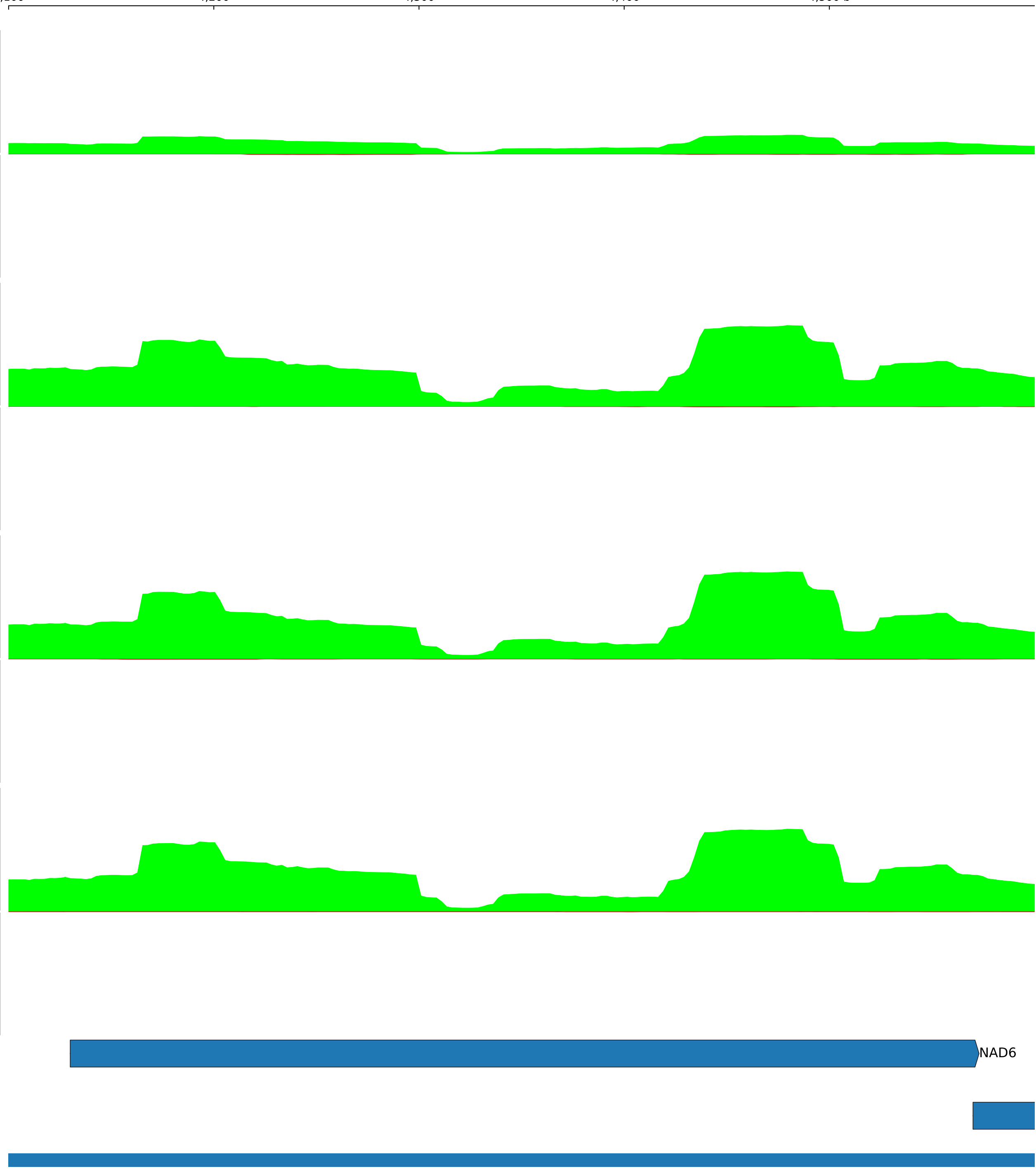
mut4 rev

NAD6

Genes

Transcription units

1400
0
1400
0
1400
0
1400
0
1400
0
1400



CamtDNA

4,600

4,800

5,000

5,200

5,400 b

WT fwd

WT rev

KO fwd

KO rev

mut3 fwd

mut3 rev

mut4 fwd

mut4 rev

Genes

NAD1

TU01

1600

0

1600

0

1600

0

1600

0

1600

NAD6

NAD1

TU01

Transcription units

CamtDNA

10,000

10,200

10,400

10,600

10,800 b

11,000

50000

0

50000

0

50000

0

50000

0

50000

WT fwd

WT rev

KO fwd

KO rev

mut3 fwd

mut3 rev

mut4 fwd

mut4 rev

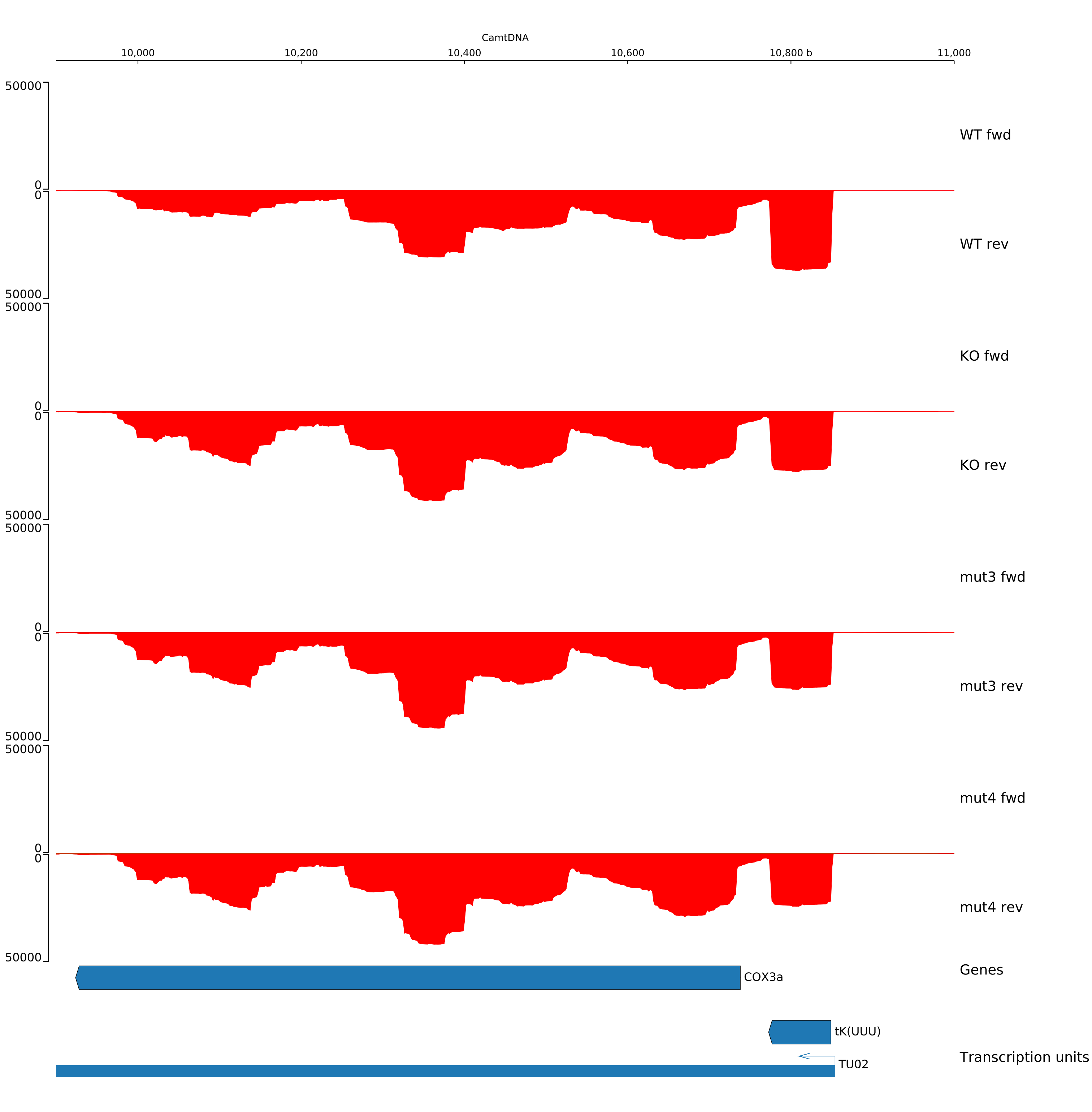
Genes

COX3a

tK(UUU)

TU02

Transcription units



CamtDNA

12,900

13,000

13,100

13,200

13,300

13,400

13,500

13,600 b

40000

0

40000

0

40000

0

40000

0

40000

WT fwd

WT rev

KO fwd

KO rev

mut3 fwd

mut3 rev

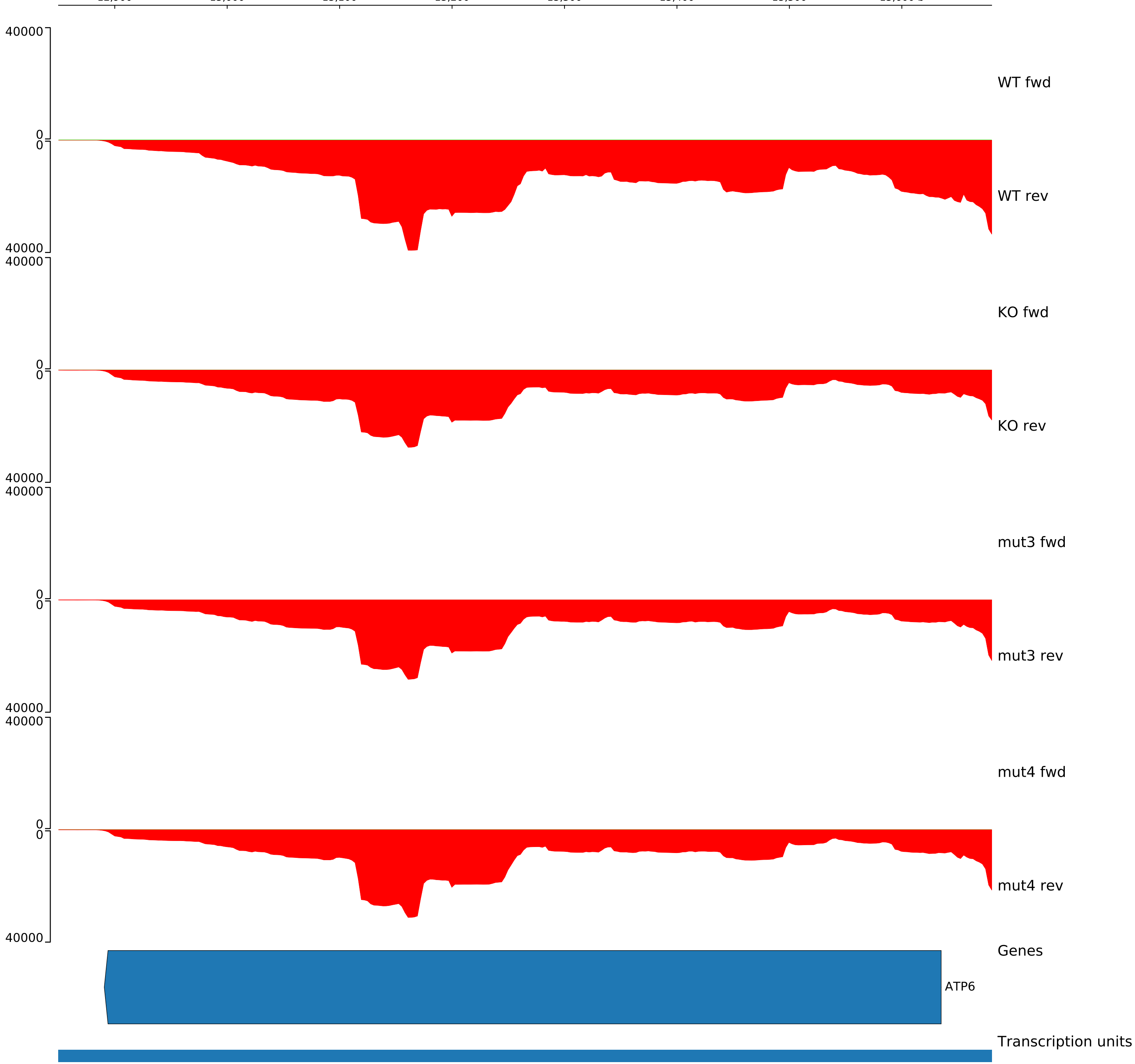
mut4 fwd

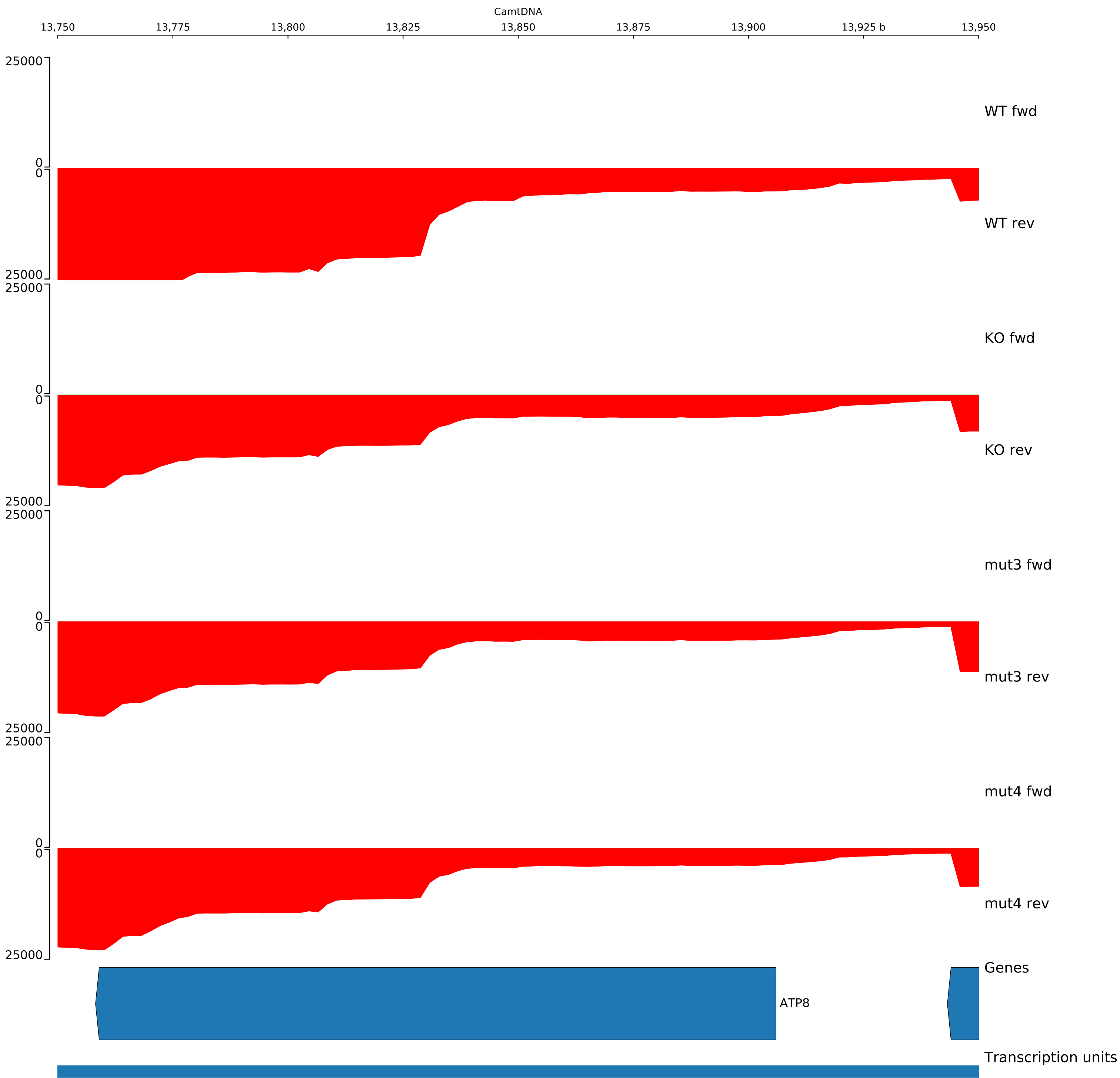
mut4 rev

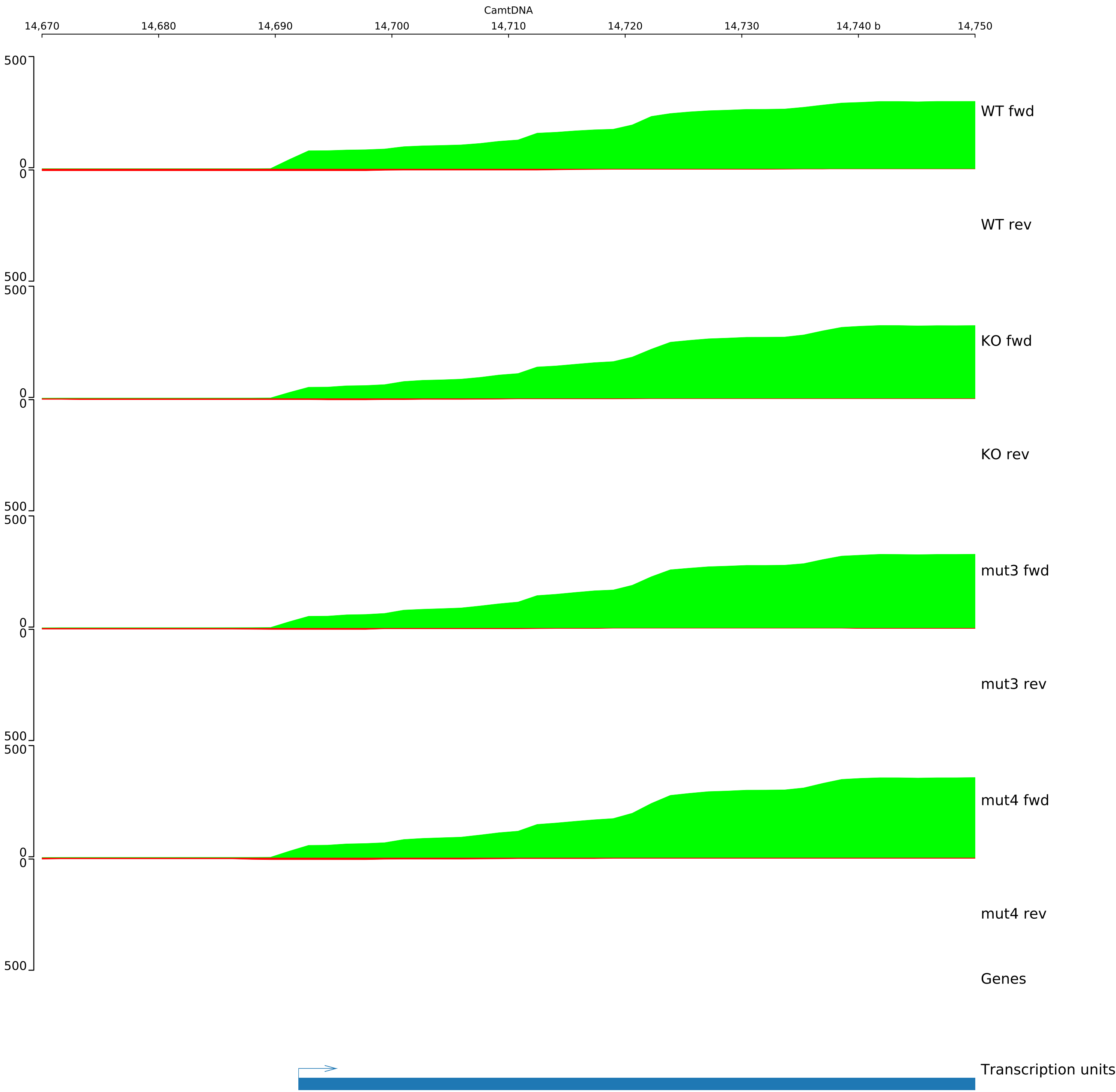
Genes

ATP6

Transcription units







CamtDNA

15

16

17

18

19

20 Kb

21

WT fwd

WT rev

KO fwd

KO rev

mut3 fwd

mut3 rev

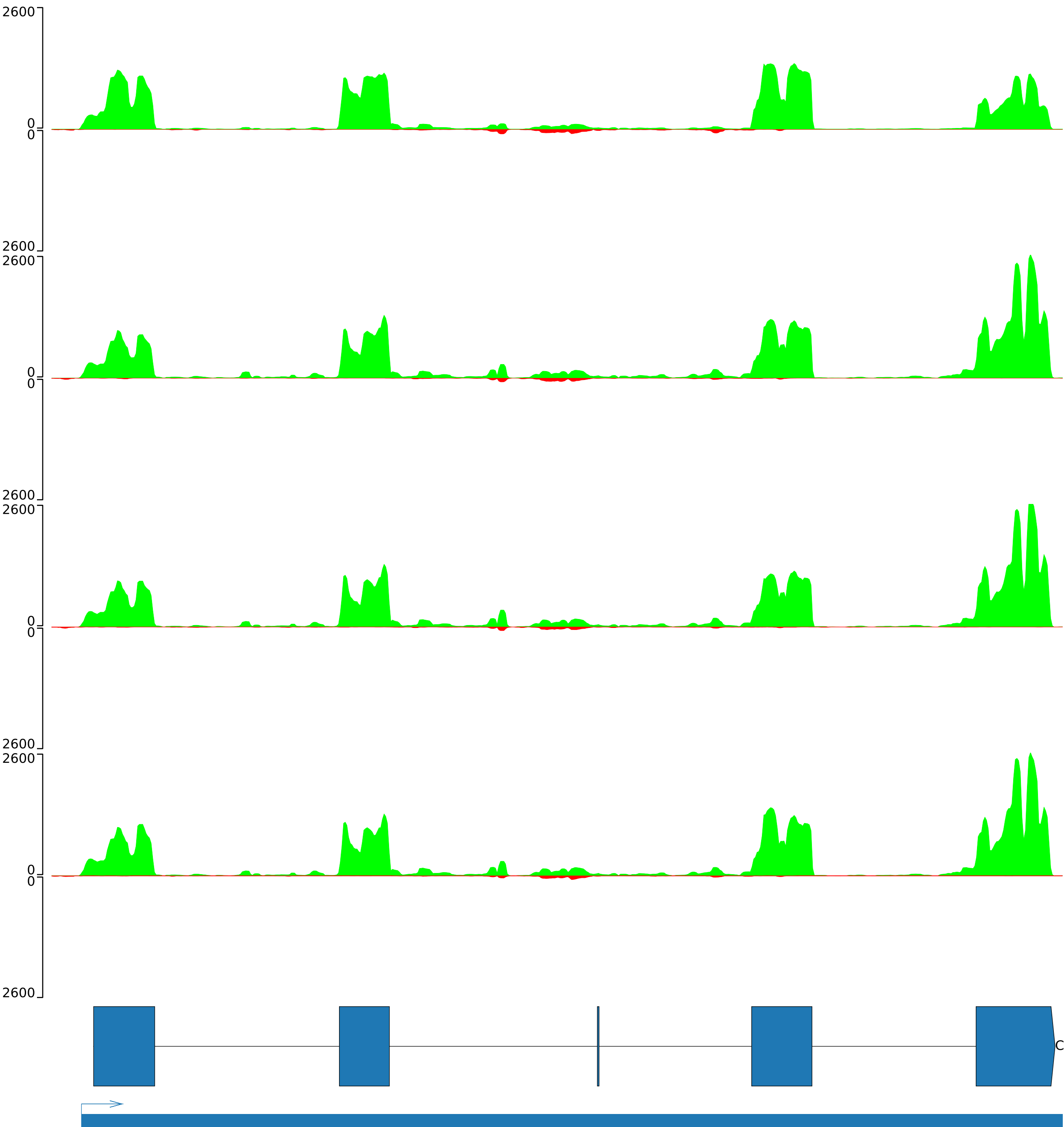
mut4 fwd

mut4 rev

Genes

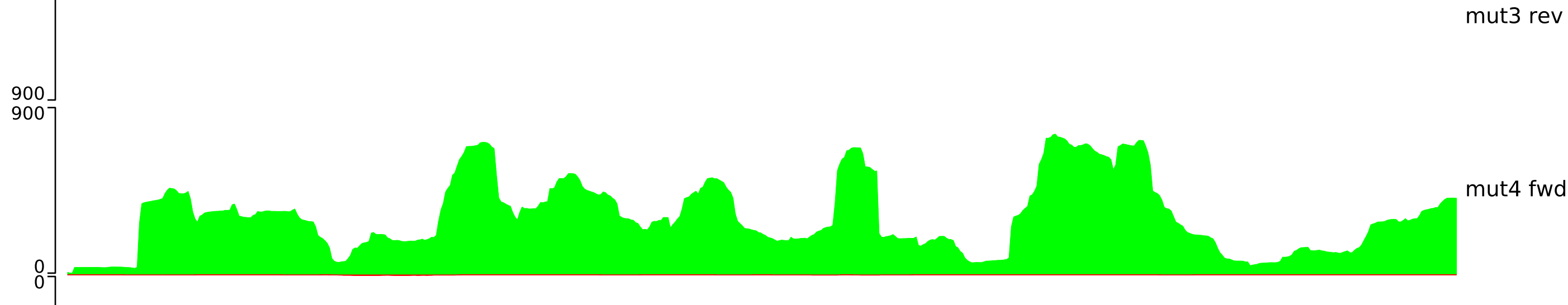
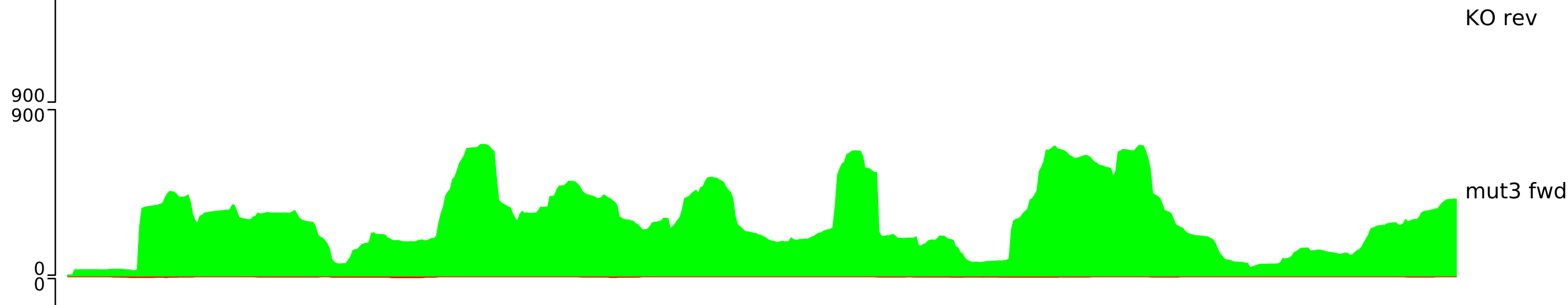
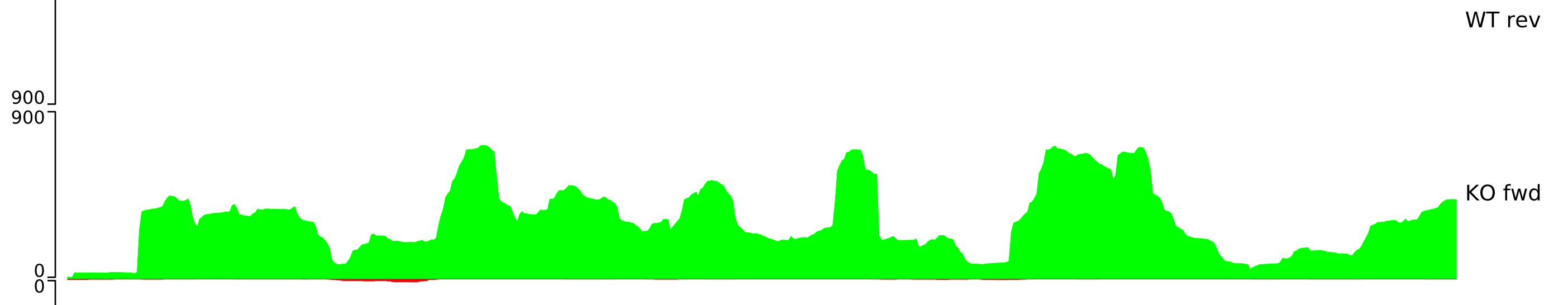
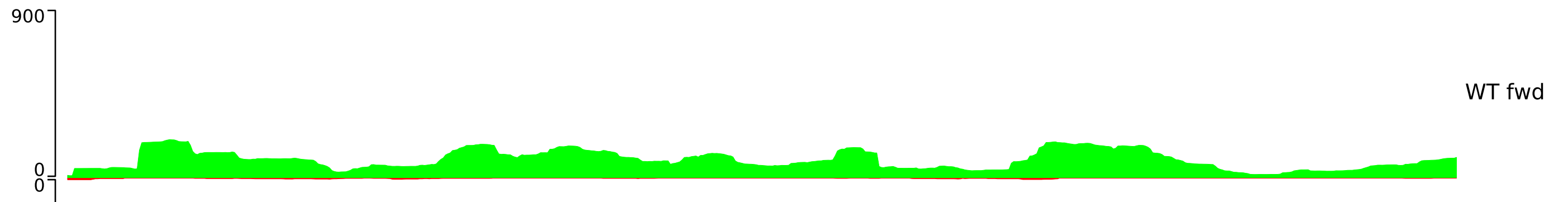
COX1

Transcription units



CamtDNA

21 22 22 22 22 23 23 Kb



tR(ACG)

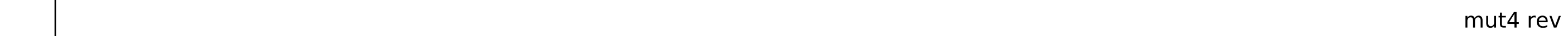
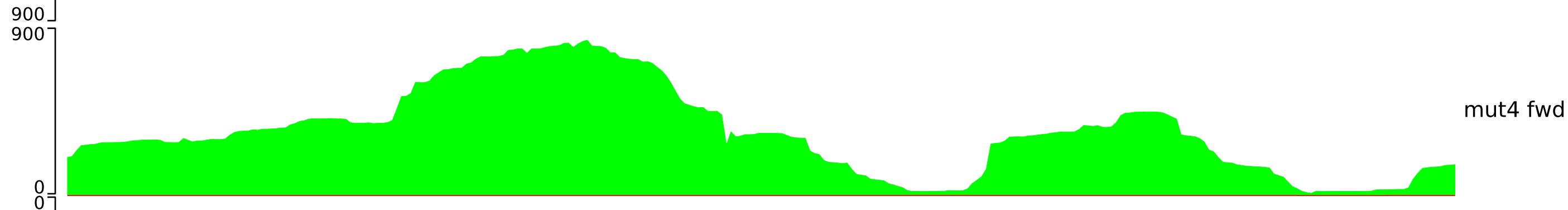
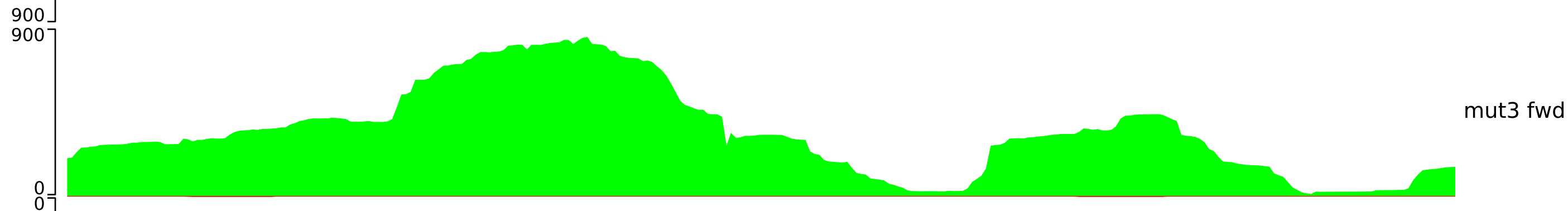
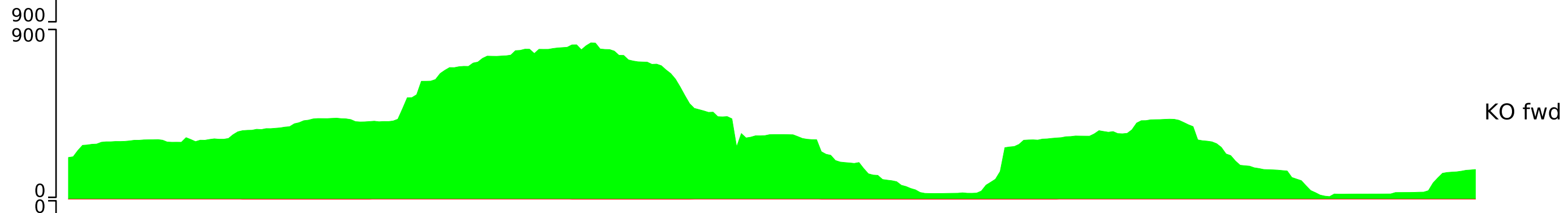
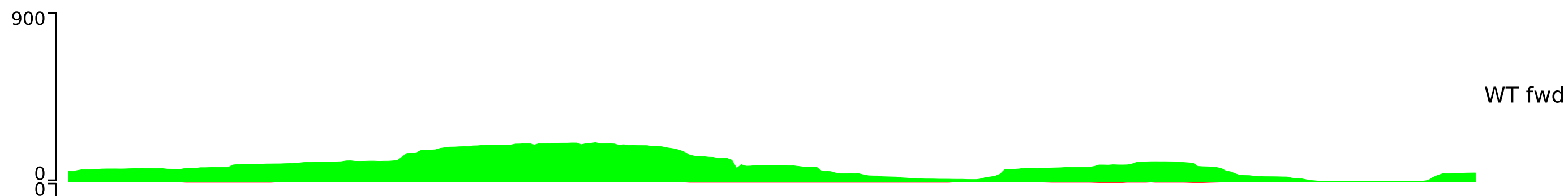
Genes

NAD2

Transcription units

22,800 22,900 23,000 23,100 23,200 b 23,300

CamtDNA



Transcription units

CamtDNA

24

24

25

26

26

26 Kb

WT fwd

WT rev

KO fwd

KO rev

mut3 fwd

mut3 rev

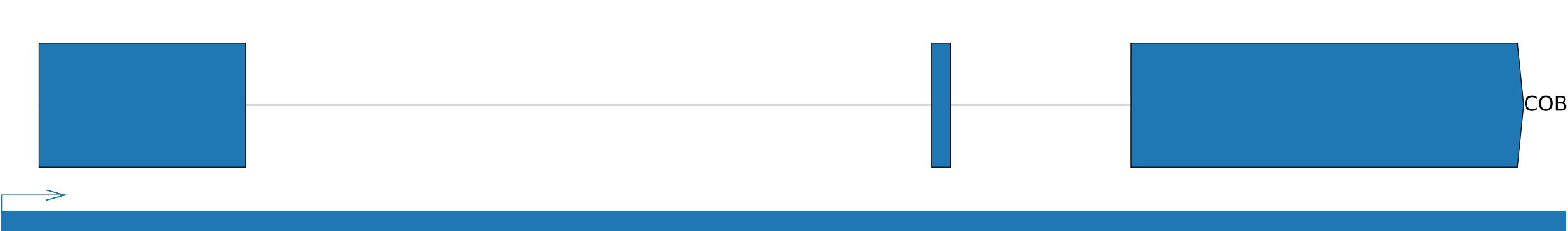
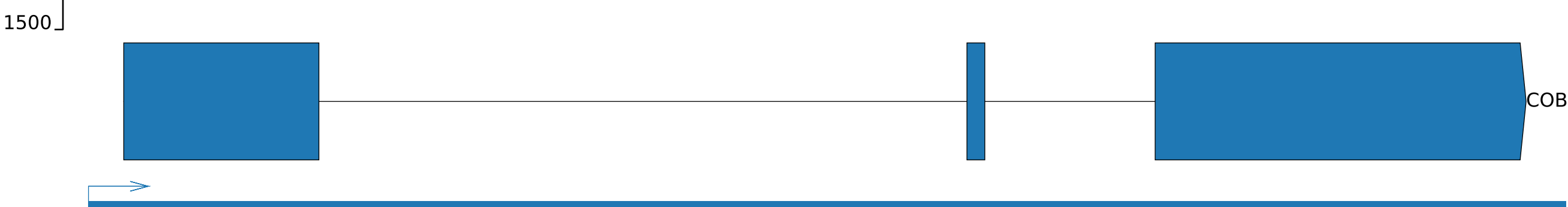
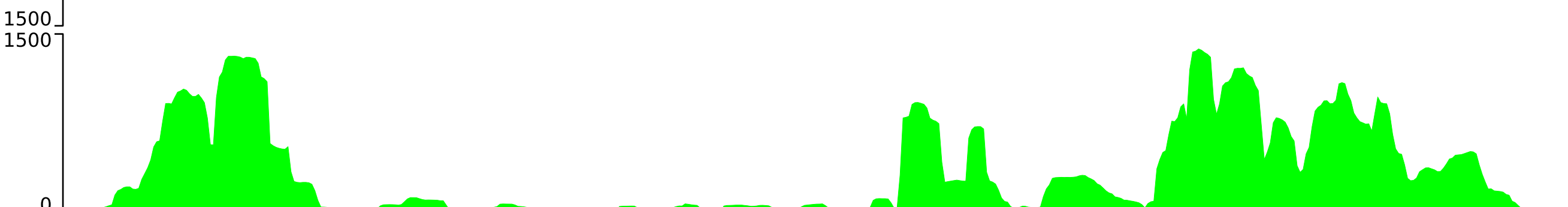
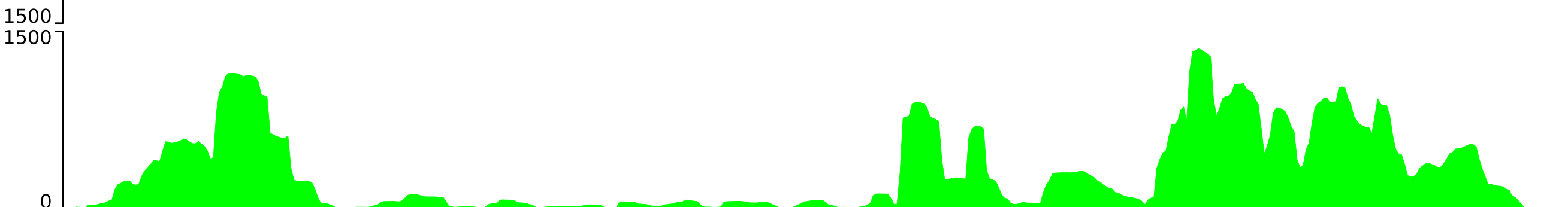
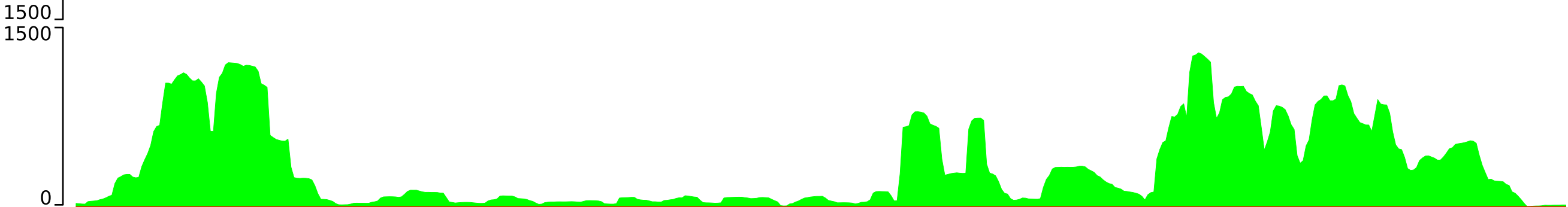
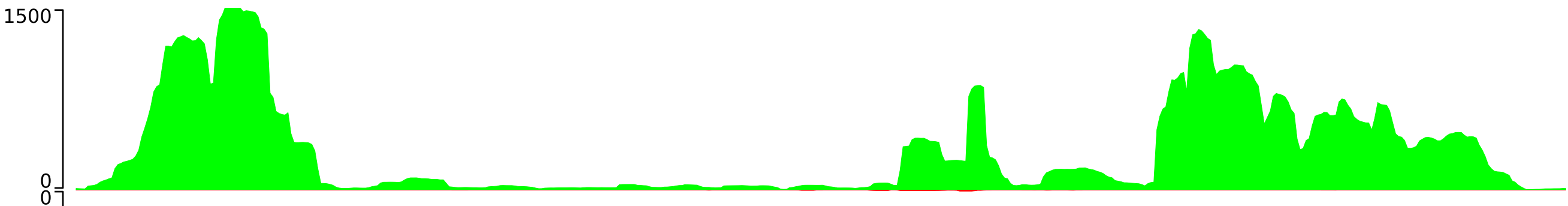
mut4 fwd

mut4 rev

Genes

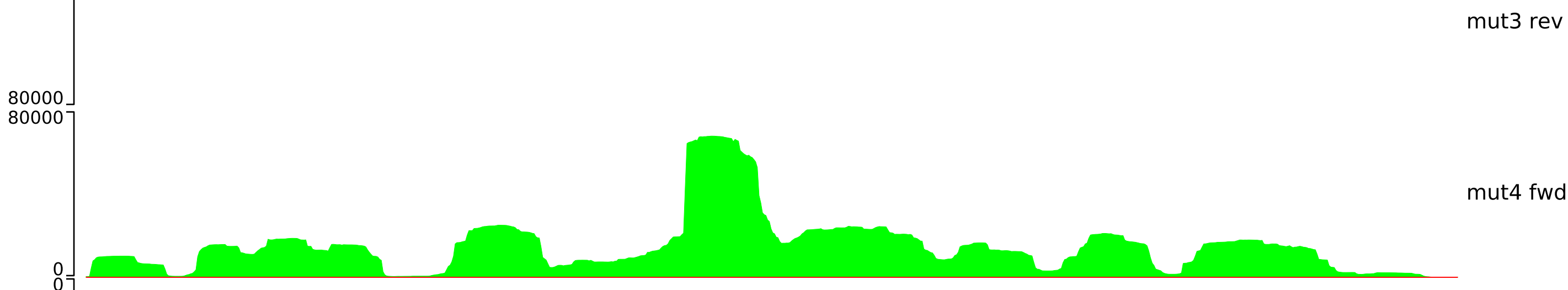
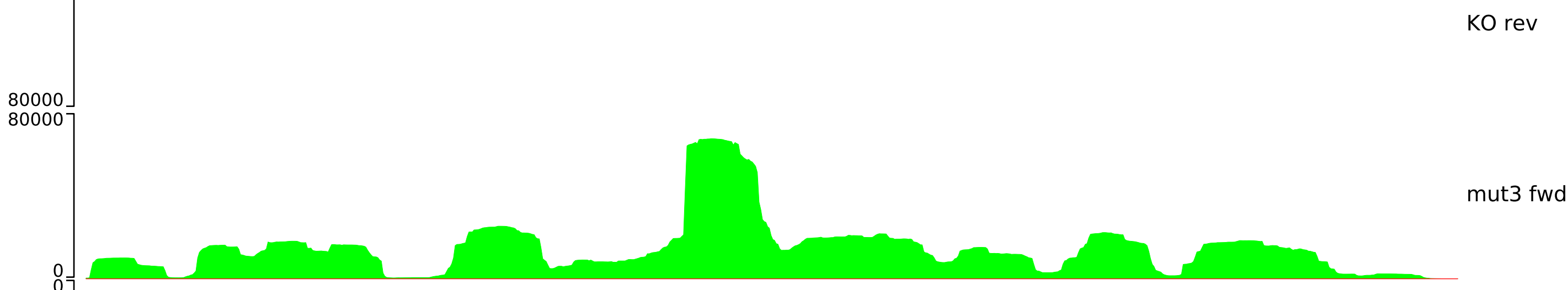
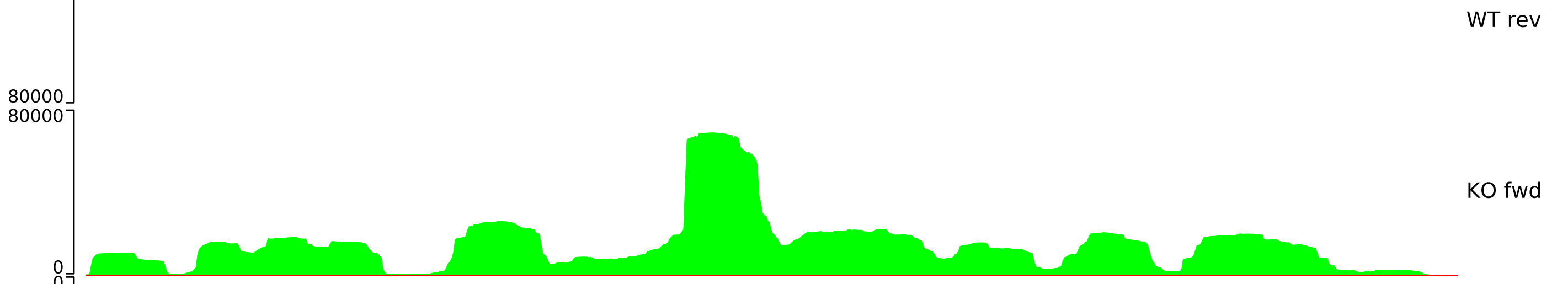
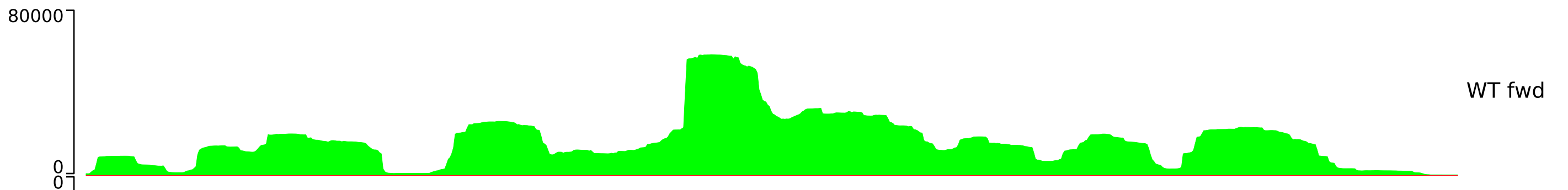
COB

Transcription units



CamtDNA

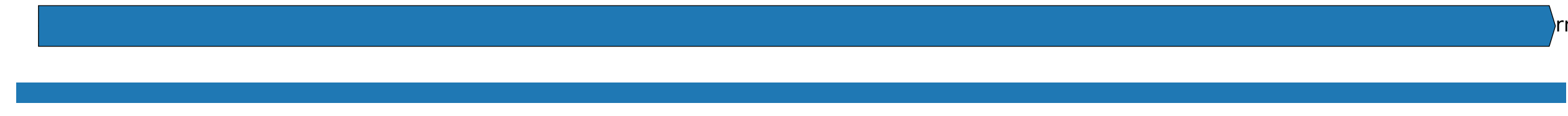
27 27 27 28 28 28 28 28 Kb



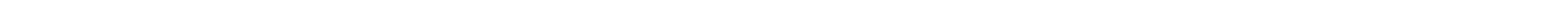
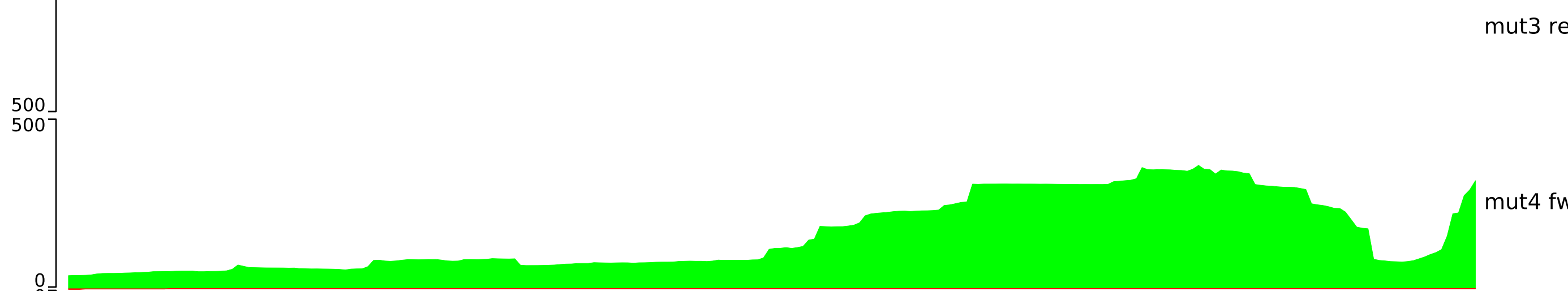
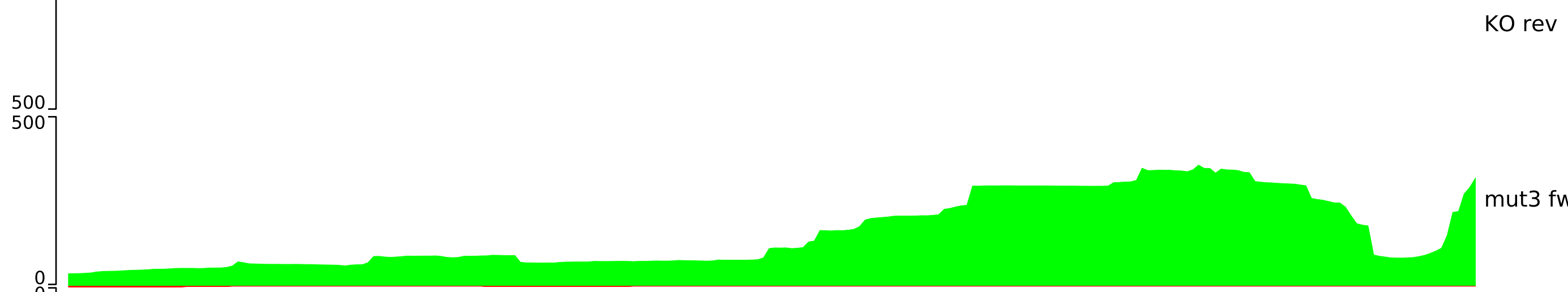
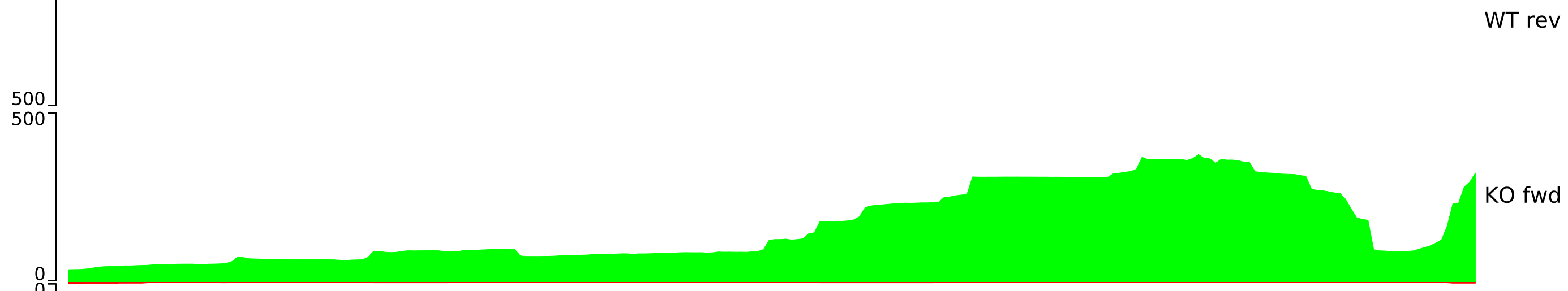
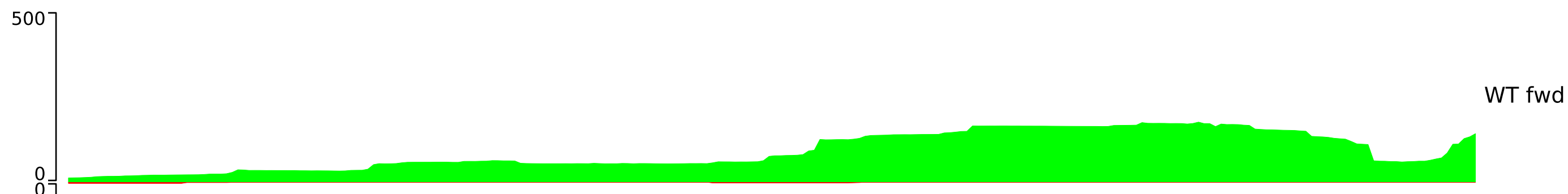
tM(CAU)

Genes

Transcription units

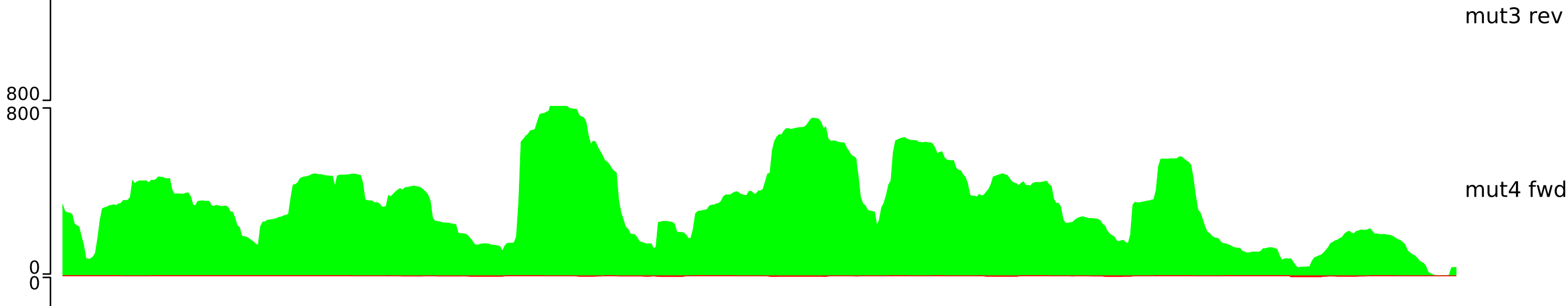
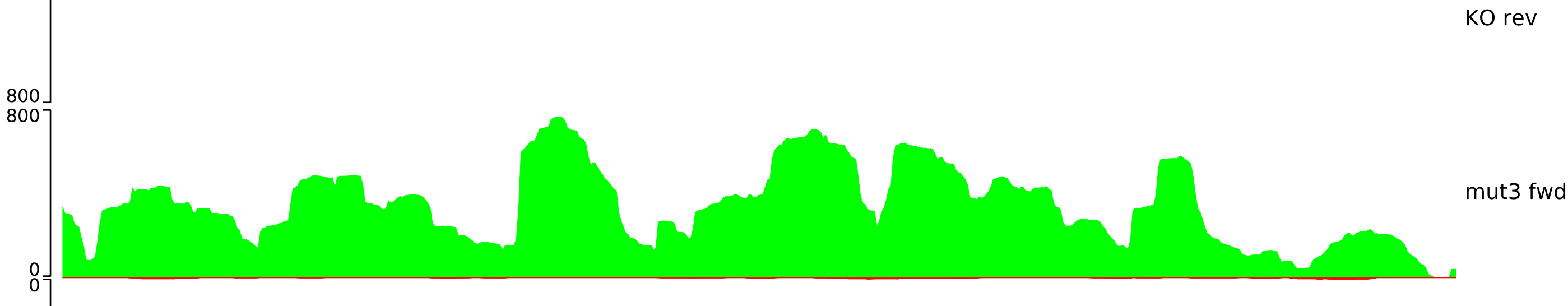
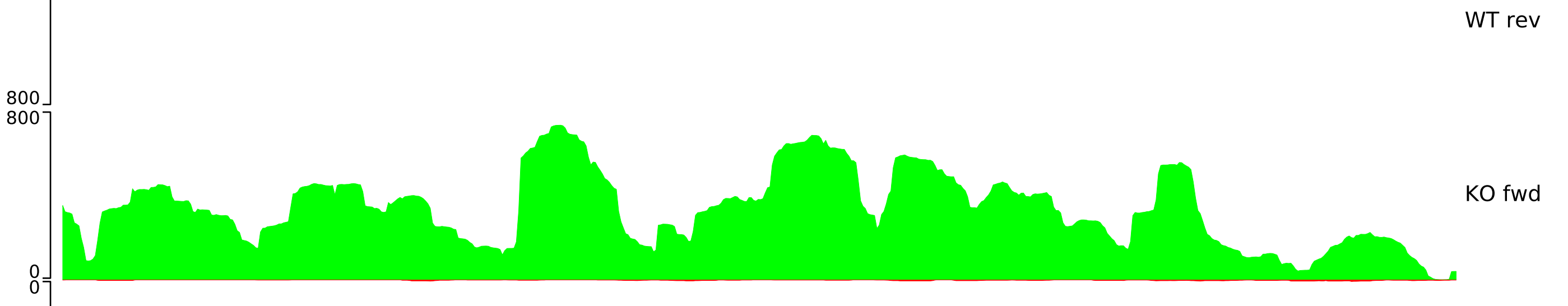
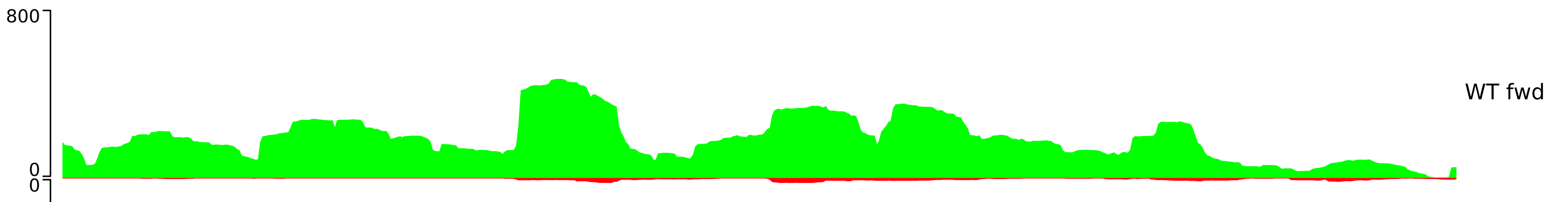


29,550 29,600 29,650 29,700 29,750 29,800 b 29,850
CamtDNA



CamtDNA

30 30 30 30 31 31 31 31 31 Kb



NAD4L

Genes

NAD5

Transcription units

