

(A) GFF as GTrack (ad hoc variant)

```
##gtrack version: 1.0
##track type: linked valued segments
##value type: category
##uninterrupted data lines: true
##1-indexed: true
##end inclusive: true
###source value start end score strand phase id name edges
####seqid=ctg123; start=1; end=1497228
. gene 1000 9000 . + . gene00001 EDEN .
. mRNA 1050 7000 . + . mRNA00001 EDEN.1 gene00001
. mRNA 1300 7000 . + . mRNA00002 EDEN.2 gene00001
. exon 1300 1500 . + . exon00001 . mRNA00002
. exon 3000 3902 . + . exon00002 . mRNA00001;mRNA00002
. exon 5000 7000 . + . exon00003 . mRNA00001;mRNA00002
. CDS 1201 1500 . + 0 cds00001.1 edenprotein.1 mRNA00001
. CDS 3000 3902 . + 0 cds00001.2 edenprotein.1 mRNA00001
. CDS 5000 5500 . + 0 cds00001.3 edenprotein.1 mRNA00001
. CDS 3301 3902 . + 0 cds00003.1 edenprotein.2 mRNA00002
. CDS 5000 5500 . + 1 cds00003.2 edenprotein.2 mRNA00002
. CDS 3391 3902 . + 0 cds00004.1 edenprotein.3 mRNA00002
. CDS 5000 5500 . + 1 cds00004.2 edenprotein.3 mRNA00002
```

(B1) BED as GTrack (direct variant)

```
##gtrack version: 1.0
##track type: valued segments
##uninterrupted data lines: true
####seqid start end id value strand thickStart thickEnd itemRgb blockCount blockSizes blockStarts
chr22 1000 5000 cloneA 960 + 1000 5000 0 2 567,488, 0,3512
chr22 2000 6000 cloneB 900 - 2000 6000 0 2 433,399, 0,3601
```

(B2) BED as GTrack (linked variant)

```
##gtrack version: 1.0
##track type: linked valued segments
##uninterrupted data lines: true
####seqid start end id value strand thickStart thickEnd itemRgb edges
chr22 1000 5000 cloneA 960 + 1000 5000 0 .
chr22 1000 1567 cloneA.1 960 + . . cloneA
chr22 4512 5000 cloneA.2 960 + . . cloneA
chr22 2000 6000 cloneB 900 - 2000 6000 0 .
chr22 2000 2433 cloneB.1 900 - . . cloneB
chr22 5601 6000 cloneB.2 900 - . . cloneB
```

(C1 and C2) WIG as GTrack

```
##gtrack version: 1.0
##track type: valued points
##1-indexed: true
##end inclusive: true
###start value
####seqid=chr1
201 25.0
301 26.0
351 25.0
476 23.0
####seqid=chr2
151 10.0
251 11.0
376 13.0
501 14.0

##gtrack version: 1.0
##track type: step function
##1-indexed: true
##end inclusive: true
###end value
####seqid=chr1; start=201; end=600
300 25.0
400 26.0
500 25.0
600 23.0
####seqid=chr2; start=151; end=550
250 10.0
350 11.0
450 13.0
550 14.0
```

(D) Linked genome partition in GTrack

```
##gtrack version: 1.0
##track type: linked genome partition
##edge weights: true
##undirected edges: true

#--original column names--
end id directed undirected
##end id directed edges

####seqid=chr1; start=0; end=300
100 0 2=1.4 2=1.4
200 1 . .
300 2 6=2.3 0=1.4;5=2.3

####seqid=chr2; start=150; end=600
300 3 4=1.2 4=1.2;5=1.7
450 4 . 3=1.2
600 5 3=1.7 2=2.3;3=1.7
```