```
> # load the human transcripts DB to hg
> library(TxDb.Hsapiens.UCSC.hg38.knownGene)
> hg <- TxDb.Hsapiens.UCSC.hg38.knownGene
>
> # prefilter chromosome X "chrX" using seqlevels()
> seqlevels(hg) <- c("chrX")
>
> # get all transcripts by gene and print it
> hg_chrXt <- transcriptsBy(hg, by = "gene")
> hg_chrXt
GRangesList object of length 985:
$10009
GRanges object with 2 ranges and 2 metadata columns:
    seqnames              ranges strand |    tx_id    tx_name
       <Rle>           <IRanges> <Rle> | <integer> <character>
  [1]    chrX [120250752, 120258398]     + |   178656  uc004esn.2
  [2]    chrX [120250755, 120255434]     + |   178657  uc010nqm.2

$100093698
GRanges object with 1 range and 2 metadata columns:
    seqnames              ranges strand | tx_id    tx_name
  [1]    chrX [13310652, 13319933]     + | 176971 uc031tgt.1

$100124540
GRanges object with 1 range and 2 metadata columns:
    seqnames              ranges strand | tx_id    tx_name
  [1]    chrX [47388649, 47388777]     + | 177448 uc010nhr.2

...
<982 more elements>
-------
seqinfo: 1 sequence from hg38 genome
>
> # select gene `215` from the transcripts
> hg_chrXt$`215`
GRanges object with 3 ranges and 2 metadata columns:
    seqnames              ranges strand |    tx_id    tx_name
       <Rle>           <IRanges> <Rle> | <integer> <character>
  [1]    chrX [153724868, 153744762]     + |   179161  uc004fif.2
  [2]    chrX [153725817, 153729897]     + |   179162  uc065bvz.1
  [3]    chrX [153735344, 153740604]     + |   179163  uc065bwa.1
  -------
  seqinfo: 1 sequence from hg38 genome
```