```
> # load human reference genome hg38
> library(TxDb.Hsapiens.UCSC.hg38.knownGene)
> # assign hg38 to hg, then print it
> hg <- TxDb.Hsapiens.UCSC.hg38.knownGene
> hg
TxDb object:
# Db type: TxDb
# Supporting package: GenomicFeatures
# Data source: UCSC
# Genome: hg38
# Organism: Homo sapiens
# Taxonomy ID: 9606
# UCSC Table: knownGene
# UCSC Track: GENCODE v24
# Resource URL: http://genome.ucsc.edu/
# Type of Gene ID: Entrez Gene ID
# Full dataset: yes
# miRBase build ID: NA
# transcript nrow: 197782
# exon_nrow: 581036
# cds nrow: 293052
# Db created by: GenomicFeatures package from Bioconductor
# Creation time: 2016-09-29 13:02:09 +0000 (Thu, 29 Sep 2016)
# GenomicFeatures version at creation time: 1.25.18
# RSQLite version at creation time: 1.0.0
# DBSCHEMAVERSION: 1.1
> # filter 1: extract all the genes in chromosome X as hg_chrXg, then print it
> hg_chrXg <- genes(hg, filter = list(tx_chrom = c("chrX")))</pre>
> hg chrXg
GRanges object with 983 ranges and 1 metadata column:
                         ranges strand
      segnames
                                          gene id
        <Rle>
                      <IRanges> <Rle> | <character>
   10009
          chrX [120250752, 120258398]
                                          + |
                                                 10009
 100093698
             chrX [ 13310652, 13319933]
                                           + | 100093698
 100124540 chrX [ 47388649, 47388777]
                                           + | 100124540
 100126270 chrX [147909431, 147911817] - | 100126270
 100126302
             chrX [134540161, 134540272] - | 100126302
    9823
           chrX [101655281, 101659891]
                                          - |
                                                9823
    9843
           chrX [ 66162549, 66268867]
                                         + |
                                               9843
    9947
           chrX [141903894, 141909388]
                                                9947
```

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9949
           chrX [110194186, 110440233]
                                                9949
           chrX [ 71118556, 71142454]
    9968
                                        +|
                                               9968
 seqinfo: 455 sequences (1 circular) from hg38 genome
> # filter 2: extract all positive stranded genes in chromosome X as hg_chrXgp, then sort it
> hg_chrXgp <- genes(hg, filter = list(tx_chrom = c("chrX"), tx_strand = "+"))
> sort(hg chrXgp)
GRanges object with 533 ranges and 1 metadata column:
      seqnames
                         ranges strand |
                                         gene_id
        <Rle>
                     <IRanges> <Rle> | <character>
   55344
           chrX [ 276322, 303356]
                                      + |
                                            55344
    6473
           chrX [624344, 659411]
                                      +|
                                            6473
    1438
           chrX [1268800, 1310381]
                                              1438
                    [1293918, 1293992] + | 100500894
 100500894
             chrX
    3563
           chrX
                 [1336616, 1382689]
                                       + |
                                              3563
                      ... ... .
 100302111
             chrX [155457517, 155457615]
                                            + | 100302111
 100507404
             chrX [155466540, 155611616]
                                            + | 100507404
           chrX [155767812, 155782459]
   10251
                                          + |
                                                10251
   6845
           chrX [155881293, 155943769]
                                         +|
                                                6845
    3581
           chrX [155997581, 156022236]
                                         + |
                                                3581
```

seqinfo: 455 sequences (1 circular) from hg38 genome