Untitled

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```
## Global options
options(max.print="75")
knitr::opts_chunk$set(echo=TRUE,
                      cache=FALSE,
                   prompt=FALSE,
                   tidy=TRUE,
                   comment=NA,
                   message=FALSE,
                   warning=FALSE)
knitr::opts_knit$set(width=75)
```

```
# BiocManager::install() # Actualiza paquetes instalados
if (!require(BiocManager)) install.packages("BiocManager")

installifnot <- function(pkg) {
    if (!require(pkg, character.only = T)) {
        BiocManager::install(pkg)
    }
}
installifnot("oligo")
installifnot("limma")
installifnot("Biobase")
installifnot("arrayQualityMetrics")
installifnot("genefilter")
installifnot("annotate")
installifnot("xtable")
installifnot("gplots")
installifnot("GOstats")
installifnot("mogene10sttranscriptcluster.db")
library("BiocManager")
library("affy")
library("oligo")
library("pd.ht.hg.u133.plus.pm")
library("hgu133plus2.db")
library("ggplot2")
library("hgu133plus2.db")
library(org.Hs.eg.db)
library("mogene10sttranscriptcluster.db")
library(knitr)
library(rmdformats)
library("AnnotationDbi")
```

```r
library("org.Mm.eg.db")
library(genekitr)
```

```r
markers_kidney.sc <- read.csv2("/home/nrb/Escritorio/perAnna/20_sc_kidney/markers.csv")
kidney.sc <- markers_kidney.sc$X
# write.csv(kidney.sc, '/home/nrb/Escritorio/perAnna/Vennplot/kidney.sc.csv')

markers_liver.sc <- read.csv2("/home/nrb/Escritorio/perAnna/18_hepato/markers41.csv")
liver.sc <- markers_liver.sc$X
# write.csv(liver.sc, '/home/nrb/Escritorio/perAnna/Vennplot/liver.sc.csv')

DEG_bulk_kidney <- read.delim("/home/nrb/Documentos/R/kidney/DEG.txt")
kidney.bulk <- DEG_bulk_kidney$Gene

# write.csv(kidney.bulk,
# '/home/nrb/Escritorio/perAnna/Vennplot/kidney.bulk.csv')

DEG_bulk_liver <- read.delim("/home/nrb/Documentos/R/liver/DEG_liver.txt")
liver.bulk <- DEG_bulk_liver$Gene
# write.csv(liver.bulk, '/home/nrb/Escritorio/perAnna/Vennplot/liver.bulk.csv')
```

```r
library(biomaRt)
human <- useEnsembl("ensembl", dataset = "hsapiens_gene_ensembl")

liver.sc <- getBM(attributes = c("hgnc_symbol", "ensembl_gene_id"), filters = "hgnc_symbol",
    values = liver.sc, mart = human)
write.csv2(liver.sc, "/home/nrb/Escritorio/perAnna/Vennplot/liver.sc2.csv")

kidney.bulk <- getBM(attributes = c("hgnc_symbol", "ensembl_gene_id"), filters = "ensembl_gene_id",
    values = kidney.bulk, mart = human)
write.csv2(kidney.bulk, "/home/nrb/Escritorio/perAnna/Vennplot/kidney.bulk2.csv")
```

```r
kidney.sc <- mapIds(org.Mm.eg.db, keys = kidney.sc, column = "ENSEMBL", keytype = "SYMBOL")
kidney.sc <- as.data.frame(kidney.sc)
kidney.sc$symbol <- rownames(kidney.sc)
kidney.sc$ensembl <- kidney.sc$kidney.sc
kidney.sc <- kidney.sc[, -1]

write.csv2(kidney.sc, "/home/nrb/Escritorio/perAnna/Vennplot/kidney.sc2.csv")


liver.bulk <- mapIds(org.Mm.eg.db, keys = liver.bulk, column = "SYMBOL", keytype = "ENSEMBL")
liver.bulk <- as.data.frame(liver.bulk)
liver.bulk$ensembl <- rownames(liver.bulk)
liver.bulk$symbol <- liver.bulk$liver.bulk
liver.bulk <- liver.bulk[, -1]
write.csv2(liver.bulk, "/home/nrb/Escritorio/perAnna/Vennplot/liver.bulk2.csv")
```

```r
library(VennDetail)
library(VennDiagram)
library(venn)
```

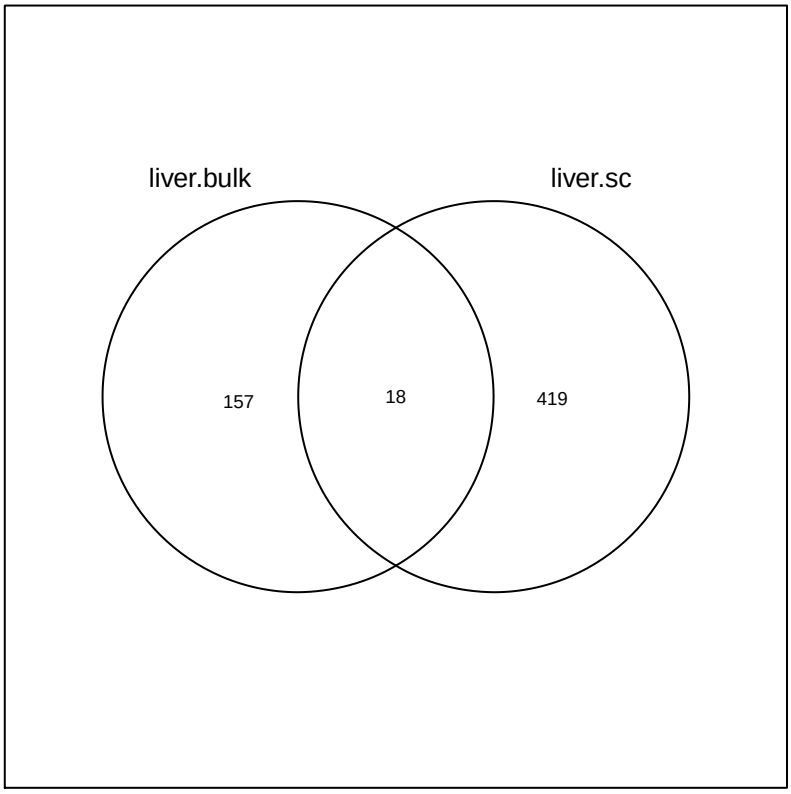
```
liver.bulk.mouse <- read.csv("/home/nrb/Escritorio/perAnna/Vennplot/both/liver.bulk.mouse.csv")
liver.bulk.mouse <- subset(liver.bulk.mouse, !is.na(liver.bulk.mouse[, 3]) & liver.bulk.mouse[,
    3] != "")
liver.bulk.human <- liver.bulk.mouse[, 3]

liver.sc.human <- read.csv("/home/nrb/Escritorio/perAnna/Vennplot/both/liver.sc.human.csv")
liver.sc.human <- subset(liver.sc.human, !is.na(liver.sc.human[, 1]) & liver.sc.human[,
    1] != "")
liver.sc.human <- liver.sc.human[, 1]

kidney.bulk.human <- read.csv("/home/nrb/Escritorio/perAnna/Vennplot/both/kidney.bulk.human.csv")
kidney.bulk.human <- subset(kidney.bulk.human, !is.na(kidney.bulk.human[, 1]) & kidney.bulk.human[,
    1] != "")
kidney.bulk.human <- kidney.bulk.human[, 1]

kidney.sc.mouse <- read.csv("/home/nrb/Escritorio/perAnna/Vennplot/both/kidney.sc.mouse.csv")
kidney.sc.mouse <- subset(kidney.sc.mouse, !is.na(kidney.sc.mouse[, 3]) & kidney.sc.mouse[,
    3] != "")
kidney.sc.human <- kidney.sc.mouse[, 3]
```

Venn Diagrams

humà symbol

Comparació fetge (bulk-sc)

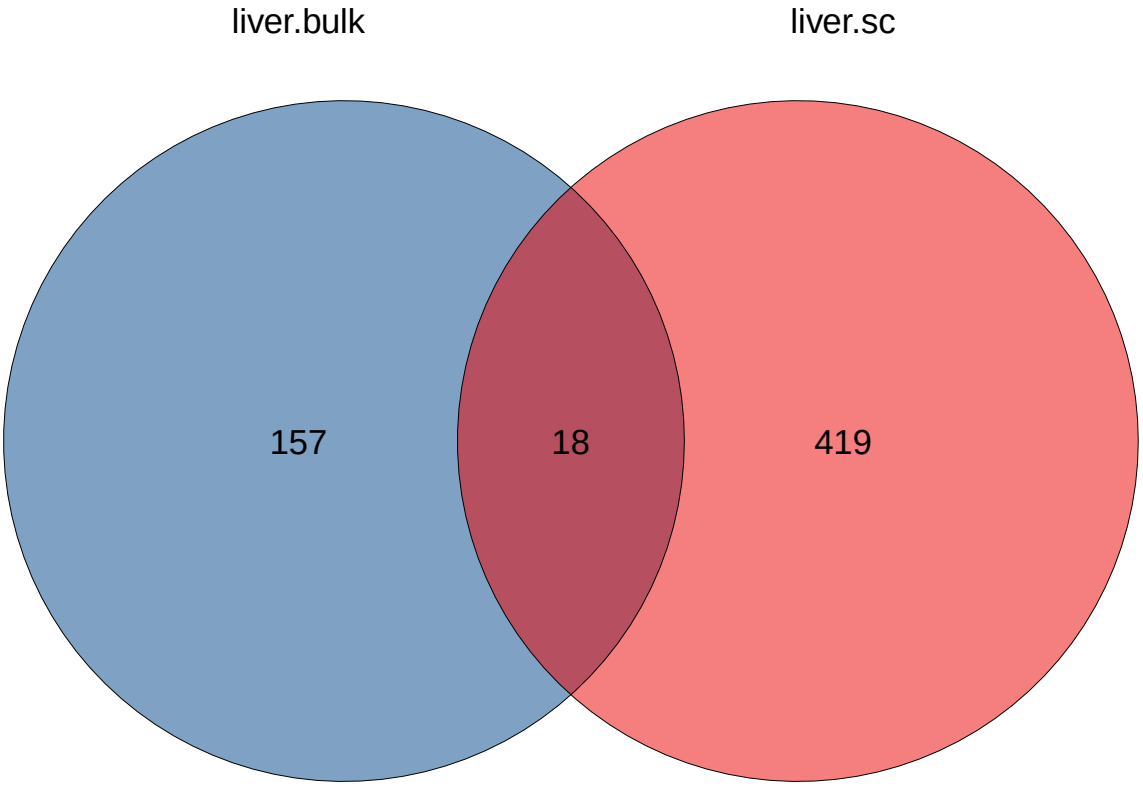
```
# liver human
ven <- venn(list(liver.bulk = liver.bulk.human, liver.sc = liver.sc.human))
```




```
vendetail <- venndetail(list(liver.bulk = liver.bulk.human, liver.sc = liver.sc.human))
res <- result(vendetail)
df.gens <- res[res$Subset == "Shared", ]
(gens_fetge_human <- as.vector(df.gens$Detail))
```

```
 [1] "UQCRQ"   "SULT2A1" "SPINK1"  "PTP4A1"  "MT-ND5"  "MT-ND4L" "MT-ND4"
 [8] "MT-ND3"  "MT-ND2"  "MT-ND1"  "MT-CYB"  "MT-CO3"  "MT-CO2"  "MT-CO1"
[15] "MT-ATP8" "MT-ATP6" "GCHFR"   "FABP1"
```

```
plotVenn(list(liver.bulk = liver.bulk.human, liver.sc = liver.sc.human), use_venn = TRUE,
    color = (ggsci::pal_lancet())(2), alpha_degree = 0.5, main_text_size = 4.5, border_thick = 0)
```



Llistat en comparar bulk-Fetge vs scsn-Fetge

```
library(biomaRt)
mart <- useMart(biomart = "ENSEMBL_MART_ENSEMBL", dataset = "hsapiens_gene_ensembl")
listAttributes(mart)
```

	name	description
1	ensembl_gene_id	Gene stable ID
2	ensembl_gene_id_version	Gene stable ID version
3	ensembl_transcript_id	Transcript stable ID
4	ensembl_transcript_id_version	Transcript stable ID version
5	ensembl_peptide_id	Protein stable ID
6	ensembl_peptide_id_version	Protein stable ID version
7	ensembl_exon_id	Exon stable ID
8	description	Gene description
9	chromosome_name	Chromosome/scaffold name
10	start_position	Gene start (bp)
11	end_position	Gene end (bp)
12	strand	Strand
13	band	Karyotype band
14	transcript_start	Transcript start (bp)
15	transcript_end	Transcript end (bp)
16	transcription_start_site	Transcription start site (TSS)
17	transcript_length	Transcript length (including UTRs and CDS)
18	transcript_tsl	Transcript support level (TSL)
19	transcript_gencode_basic	GENCODE basic annotation

```
20             transcript_appris                              APPRIS annotation
21       transcript_is_canonical                              Ensembl Canonical
22        transcript_mane_select          RefSeq match transcript (MANE Select)
23 transcript_mane_plus_clinical RefSeq match transcript (MANE Plus Clinical)
24            external_gene_name                                      Gene name
25          external_gene_source                            Source of gene name
           page
1  feature_page
2  feature_page
3  feature_page
4  feature_page
5  feature_page
6  feature_page
7  feature_page
8  feature_page
9  feature_page
10 feature_page
11 feature_page
12 feature_page
13 feature_page
14 feature_page
15 feature_page
16 feature_page
17 feature_page
18 feature_page
19 feature_page
20 feature_page
21 feature_page
22 feature_page
23 feature_page
24 feature_page
25 feature_page
 [ reached 'max' / getOption("max.print") -- omitted 3144 rows ]
```

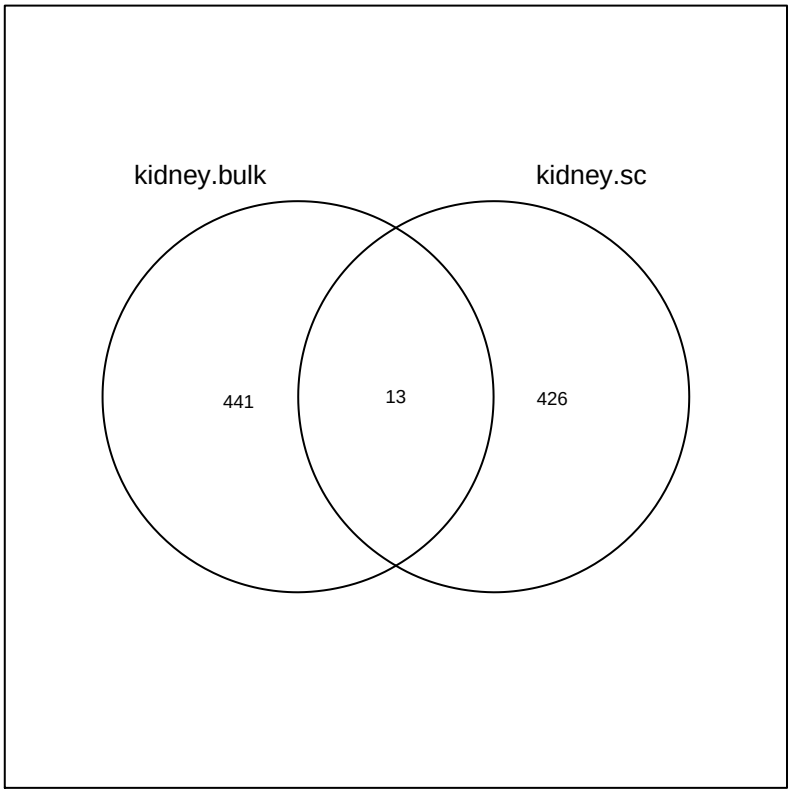
```r
# Query the database for annotation information
fetge <- getBM(attributes = c("entrezgene_id", "hgnc_symbol", "ensembl_gene_id",
    "description"), filters = "hgnc_symbol", values = gens_fetge_human, mart = mart)
print(kable(fetge))
```

```
| entrezgene_id|hgnc_symbol |ensembl_gene_id |description
|-------------:|:-----------|:---------------|:----------------------------------------------------------
|          2168|FABP1       |ENSG00000163586 |fatty acid binding protein 1 [Source:HGNC Symbol;Acc:HGNC
|          2644|GCHFR       |ENSG00000137880 |GTP cyclohydrolase I feedback regulator [Source:HGNC Symbo
|          4508|MT-ATP6     |ENSG00000198899 |mitochondrially encoded ATP synthase membrane subunit 6 [S
|          4509|MT-ATP8     |ENSG00000228253 |mitochondrially encoded ATP synthase membrane subunit 8 [S
|          4512|MT-CO1      |ENSG00000198804 |mitochondrially encoded cytochrome c oxidase I [Source:HGN
|          4513|MT-CO2      |ENSG00000198712 |mitochondrially encoded cytochrome c oxidase II [Source:HG
|          4514|MT-CO3      |ENSG00000198938 |mitochondrially encoded cytochrome c oxidase III [Source:H
|          4519|MT-CYB      |ENSG00000198727 |mitochondrially encoded cytochrome b [Source:HGNC Symbol;A
|          4535|MT-ND1      |ENSG00000198888 |mitochondrially encoded NADH:ubiquinone oxidoreductase cor
|          4536|MT-ND2      |ENSG00000198763 |mitochondrially encoded NADH:ubiquinone oxidoreductase cor
|          4537|MT-ND3      |ENSG00000198840 |mitochondrially encoded NADH:ubiquinone oxidoreductase cor
```

```
|          4538|MT-ND4      |ENSG00000198886 |mitochondrially encoded NADH:ubiquinone oxidoreductase co
|          4539|MT-ND4L     |ENSG00000212907 |mitochondrially encoded NADH:ubiquinone oxidoreductase co
|          4540|MT-ND5      |ENSG00000198786 |mitochondrially encoded NADH:ubiquinone oxidoreductase co
|          7803|PTP4A1      |ENSG00000112245 |protein tyrosine phosphatase 4A1 [Source:HGNC Symbol;Acc:
|          6690|SPINK1      |ENSG00000164266 |serine peptidase inhibitor Kazal type 1 [Source:HGNC Symb
|          6822|SULT2A1     |ENSG00000105398 |sulfotransferase family 2A member 1 [Source:HGNC Symbol;A
|         27089|UQCRQ       |ENSG00000164405 |ubiquinol-cytochrome c reductase complex III subunit VII
```

Comparació ronyó (bulk-sc)

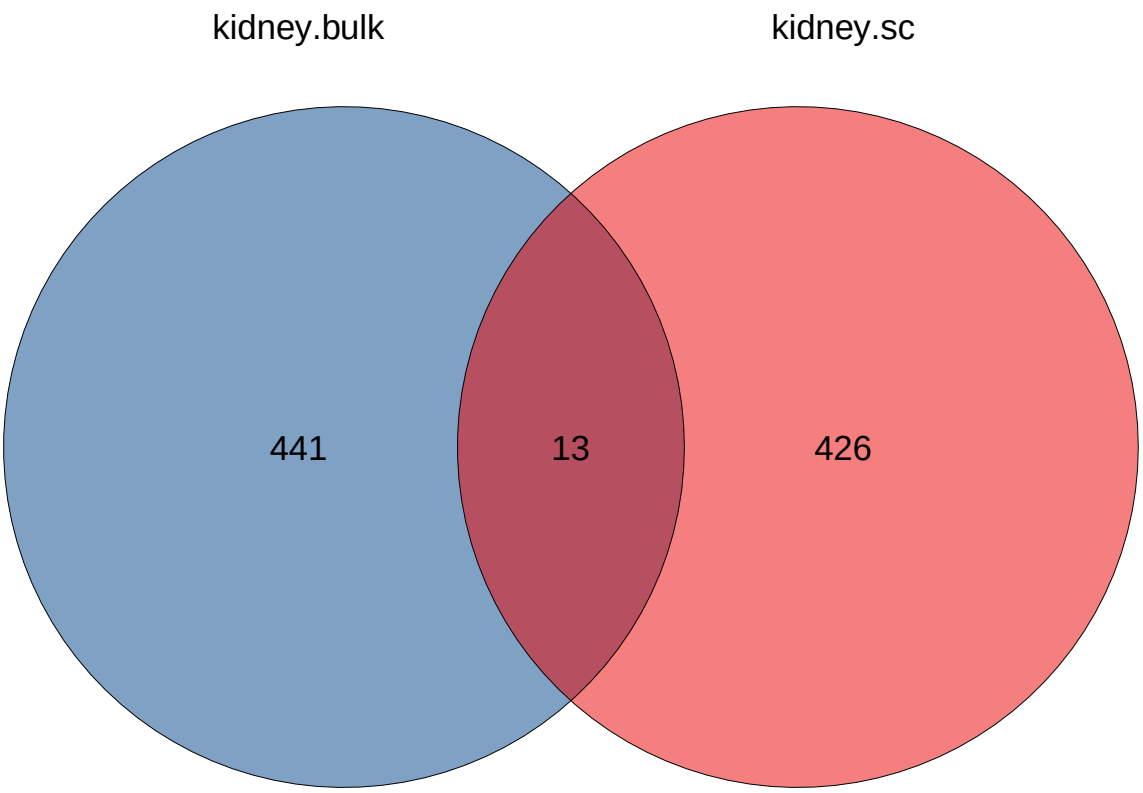
```
ven <- venn(list(kidney.bulk = kidney.bulk.human, kidney.sc = kidney.sc.human))
```




```
vendetail <- venndetail(list(kidney.bulk = kidney.bulk.human, kidney.sc = kidney.sc.human))
res <- result(vendetail)
df.gens <- res[res$Subset == "Shared", ]
(gens_ronyo_human <- as.vector(df.gens$Detail))
```

```
 [1] "SYP"      "RSRP1"    "PROCA1"   "OGT"      "NKTR"     "MT-ND6"
 [7] "MT-ND5"   "MT-ND4L"  "MT-ND2"   "MT-ND1"   "MT-CYB"   "CATSPER2"
[13] "ANLN"
```

```
library(genekitr)
plotVenn(list(kidney.bulk = kidney.bulk.human, kidney.sc = kidney.sc.human), use_venn = TRUE,
    color = (ggsci::pal_lancet())(2), alpha_degree = 0.5, main_text_size = 4.5, border_thick = 0)
```



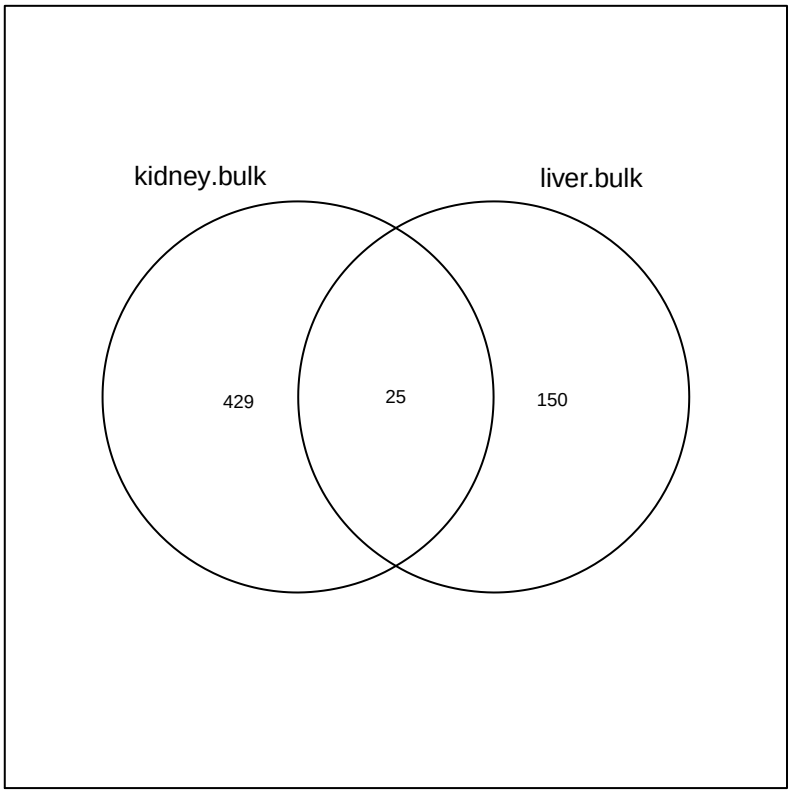
Llistat en comparar bulk-Ronyó vs scsn-Ronyó

```
ronyo <- getBM(attributes = c("entrezgene_id", "hgnc_symbol", "ensembl_gene_id",
    "description"), filters = "hgnc_symbol", values = gens_ronyo_human, mart = mart)
print(kable(ronyo))
```

entrezgene_id	hgnc_symbol	ensembl_gene_id	description
54443	ANLN	ENSG00000011426	anillin, actin binding protein [Source:HGNC Symbol;Acc:HGN
117155	CATSPER2	ENSG00000166762	cation channel sperm associated 2 [Source:HGNC Symbol;Acc
4519	MT-CYB	ENSG00000198727	mitochondrially encoded cytochrome b [Source:HGNC Symbol;A
4535	MT-ND1	ENSG00000198888	mitochondrially encoded NADH:ubiquinone oxidoreductase cor
4536	MT-ND2	ENSG00000198763	mitochondrially encoded NADH:ubiquinone oxidoreductase cor
4539	MT-ND4L	ENSG00000212907	mitochondrially encoded NADH:ubiquinone oxidoreductase cor
4540	MT-ND5	ENSG00000198786	mitochondrially encoded NADH:ubiquinone oxidoreductase cor
4541	MT-ND6	ENSG00000198695	mitochondrially encoded NADH:ubiquinone oxidoreductase cor
4820	NKTR	ENSG00000114857	natural killer cell triggering receptor [Source:HGNC Symbo
8473	OGT	ENSG00000147162	O-linked N-acetylglucosamine (GlcNAc) transferase [Source
147011	PROCA1	ENSG00000167525	protein interacting with cyclin A1 [Source:HGNC Symbol;Acc
57035	RSRP1	ENSG00000117616	arginine and serine rich protein 1 [Source:HGNC Symbol;Acc
6855	SYP	ENSG00000102003	synaptophysin [Source:HGNC Symbol;Acc:HGNC:11506]

Comparació bulks (ronyo-fetge)

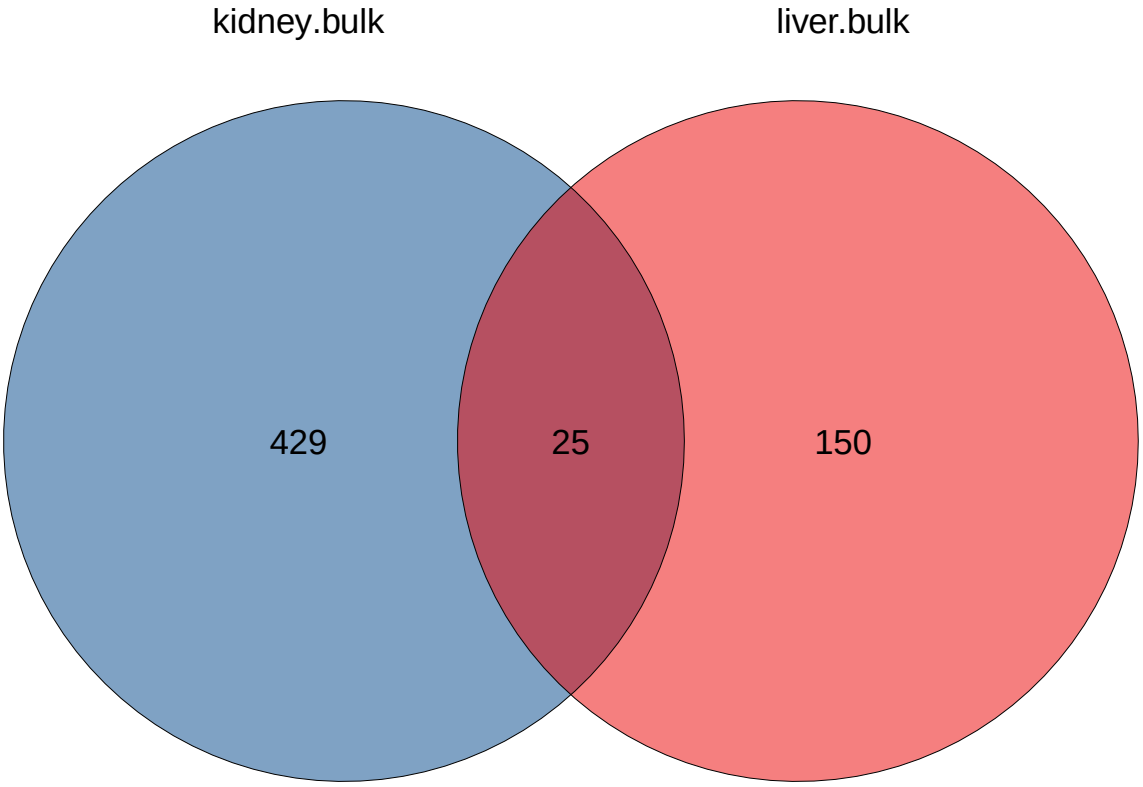
```
ven <- venn(list(kidney.bulk = kidney.bulk.human, liver.bulk = liver.bulk.human))
```




```
vendetail <- venndetail(list(kidney.bulk = kidney.bulk.human, liver.bulk = liver.bulk.human))
res <- result(vendetail)
df.gens <- res[res$Subset == "Shared", ]
(gens_bulks_human <- as.vector(df.gens$Detail))
```

```
 [1] "TTLL3"    "SYNGAP1"  "MT-ND6"   "MT-ND5"   "MT-ND4L"  "MT-ND4"
 [7] "MT-ND3"   "MT-ND2"   "MT-ND1"   "MT-CYB"   "MT-CO3"   "MT-CO2"
[13] "MT-CO1"   "MT-ATP8"  "MT-ATP6"  "MLXIPL"   "MAPK8IP3" "LENG8"
[19] "KCNC3"    "DOCK3"    "COL27A1"  "CDH24"    "CCNL2"    "ASIC3"
[25] "ABCC10"
```

```
library(genekitr)
plotVenn(list(kidney.bulk = kidney.bulk.human, liver.bulk = liver.bulk.human), use_venn = TRUE,
    color = (ggsci::pal_lancet())(2), alpha_degree = 0.5, main_text_size = 4.5, border_thick = 0)
```



Llistat en comparar bulk-Ronyó vs bulk-Fetge

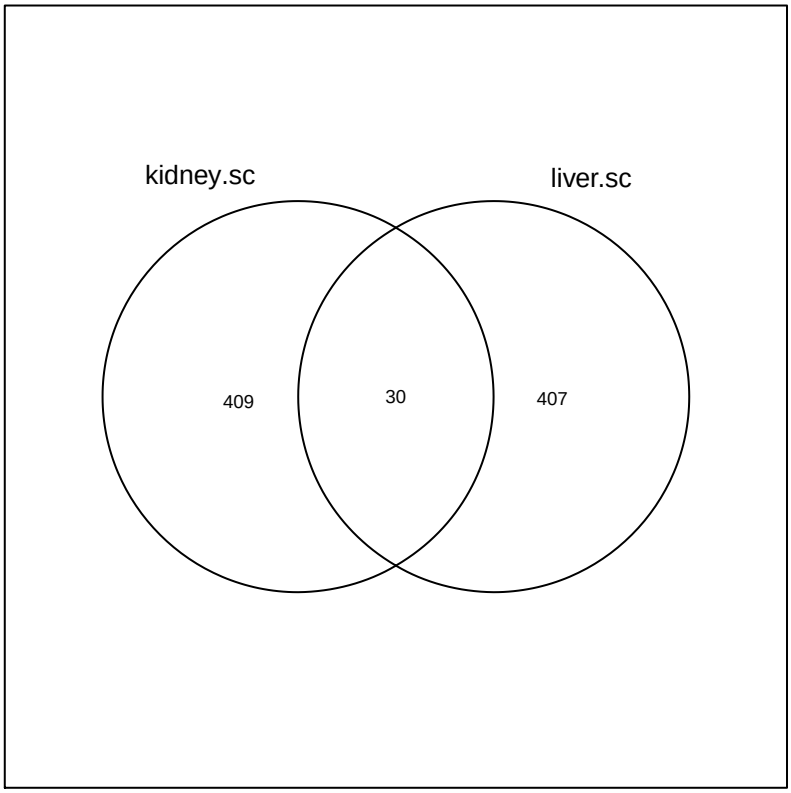
```
bulks <- getBM(attributes = c("entrezgene_id", "hgnc_symbol", "ensembl_gene_id",
    "description"), filters = "hgnc_symbol", values = gens_bulks_human, mart = mart)
print(kable(bulks))
```

entrezgene_id	hgnc_symbol	ensembl_gene_id	description
89845	ABCC10	ENSG00000124574	ATP binding cassette subfamily C member 10 [Source:HGNC Sy
9311	ASIC3	ENSG00000213199	acid sensing ion channel subunit 3 [Source:HGNC Symbol;Ac
81669	CCNL2	ENSG00000221978	cyclin L2 [Source:HGNC Symbol;Acc:HGNC:20570]
64403	CDH24	ENSG00000139880	cadherin 24 [Source:HGNC Symbol;Acc:HGNC:14265]
85301	COL27A1	ENSG00000196739	collagen type XXVII alpha 1 chain [Source:HGNC Symbol;Acc
1795	DOCK3	ENSG00000088538	dedicator of cytokinesis 3 [Source:HGNC Symbol;Acc:HGNC:2
3748	KCNC3	ENSG00000131398	potassium voltage-gated channel subfamily C member 3 [Sou
114823	LENG8	ENSG00000276458	leukocyte receptor cluster member 8 [Source:HGNC Symbol;A
114823	LENG8	ENSG00000274305	leukocyte receptor cluster member 8 [Source:HGNC Symbol;A
114823	LENG8	ENSG00000276681	leukocyte receptor cluster member 8 [Source:HGNC Symbol;A
114823	LENG8	ENSG00000167615	leukocyte receptor cluster member 8 [Source:HGNC Symbol;A
23162	MAPK8IP3	ENSG00000138834	mitogen-activated protein kinase 8 interacting protein 3
51085	MLXIPL	ENSG00000009950	MLX interacting protein like [Source:HGNC Symbol;Acc:HGNC
4508	MT-ATP6	ENSG00000198899	mitochondrially encoded ATP synthase membrane subunit 6 [
4509	MT-ATP8	ENSG00000228253	mitochondrially encoded ATP synthase membrane subunit 8 [
4512	MT-CO1	ENSG00000198804	mitochondrially encoded cytochrome c oxidase I [Source:HG
4513	MT-CO2	ENSG00000198712	mitochondrially encoded cytochrome c oxidase II [Source:H
4514	MT-CO3	ENSG00000198938	mitochondrially encoded cytochrome c oxidase III [Source:
4519	MT-CYB	ENSG00000198727	mitochondrially encoded cytochrome b [Source:HGNC Symbol;

```
|          4535|MT-ND1      |ENSG00000198888 |mitochondrially encoded NADH:ubiquinone oxidoreductase co
|          4536|MT-ND2      |ENSG00000198763 |mitochondrially encoded NADH:ubiquinone oxidoreductase co
|          4537|MT-ND3      |ENSG00000198840 |mitochondrially encoded NADH:ubiquinone oxidoreductase co
|          4538|MT-ND4      |ENSG00000198886 |mitochondrially encoded NADH:ubiquinone oxidoreductase co
|          4539|MT-ND4L     |ENSG00000212907 |mitochondrially encoded NADH:ubiquinone oxidoreductase co
|          4540|MT-ND5      |ENSG00000198786 |mitochondrially encoded NADH:ubiquinone oxidoreductase co
|          4541|MT-ND6      |ENSG00000198695 |mitochondrially encoded NADH:ubiquinone oxidoreductase co
|          8831|SYNGAP1     |ENSG00000227460 |synaptic Ras GTPase activating protein 1 [Source:HGNC Syml
|          8831|SYNGAP1     |ENSG00000197283 |synaptic Ras GTPase activating protein 1 [Source:HGNC Syml
|         26140|TTLL3       |ENSG00000214021 |tubulin tyrosine ligase like 3 [Source:HGNC Symbol;Acc:HGN
```

Comparació scs (ronyo-fetge)

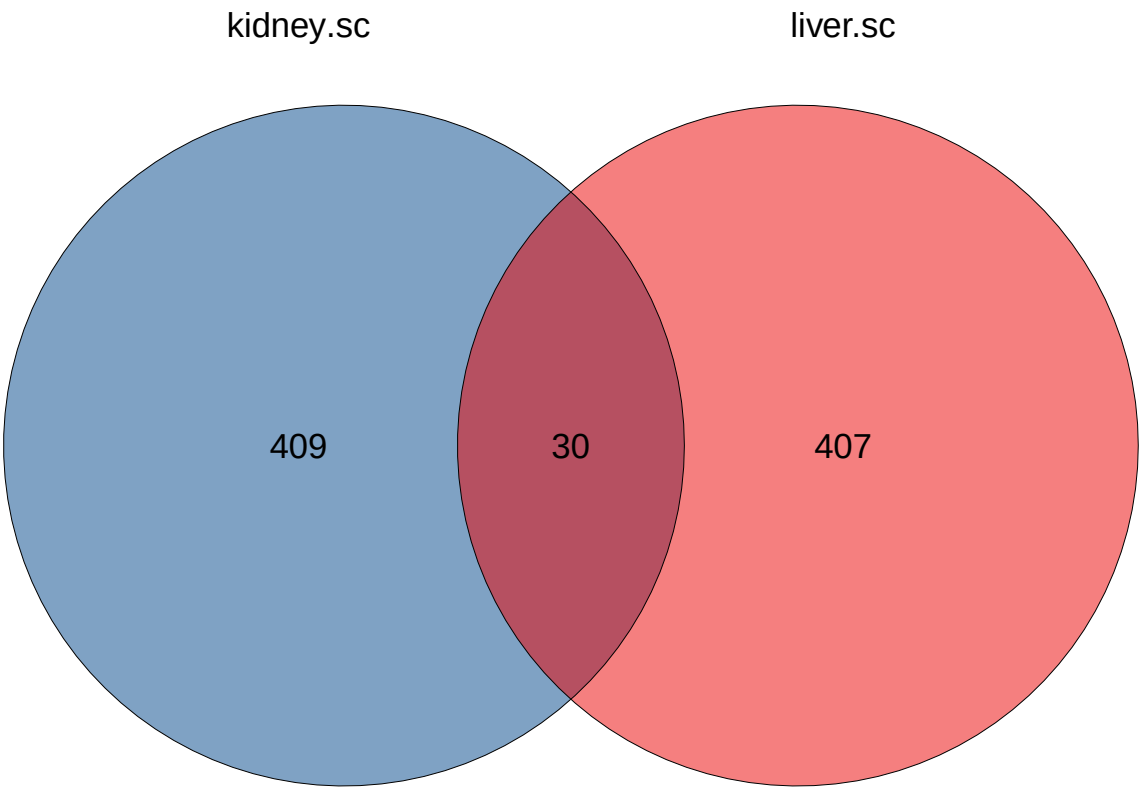
```
ven <- venn(list(kidney.sc = kidney.sc.human, liver.sc = liver.sc.human))
```




```
vendetail <- venndetail(list(kidney.sc = kidney.sc.human, liver.sc = liver.sc.human))
res <- result(vendetail)
df.gens <- res[res$Subset == "Shared", ]
(gens.sc_human <- as.vector(df.gens$Detail))
```

```
 [1] "ZEB2"    "UPP2"    "SRC"     "SMC2"    "SLC27A2" "SDC4"    "PTPRD"
 [8] "PRKCB"   "PDE4D"   "PAG1"    "MT1M"    "MT-ND5"  "MT-ND4L" "MT-ND2"
[15] "MT-ND1"  "MT-CYB"  "MGST1"   "MAGI2"   "GRAMD1B" "GPX3"    "GNG2"
[22] "FUT2"    "FGG"     "CYP2E1"  "CD74"    "CD320"   "BNC2"    "ANTXR2"
[29] "ADH1B"   "ABCC2"
```

```
library(genekitr)
plotVenn(list(kidney.sc = kidney.sc.human, liver.sc = liver.sc.human), use_venn = TRUE,
    color = (ggsci::pal_lancet())(2), alpha_degree = 0.5, main_text_size = 4.5, border_thick = 0)
```



Llistat

en comparar scsn-Ronyó vs scsn-Fetge

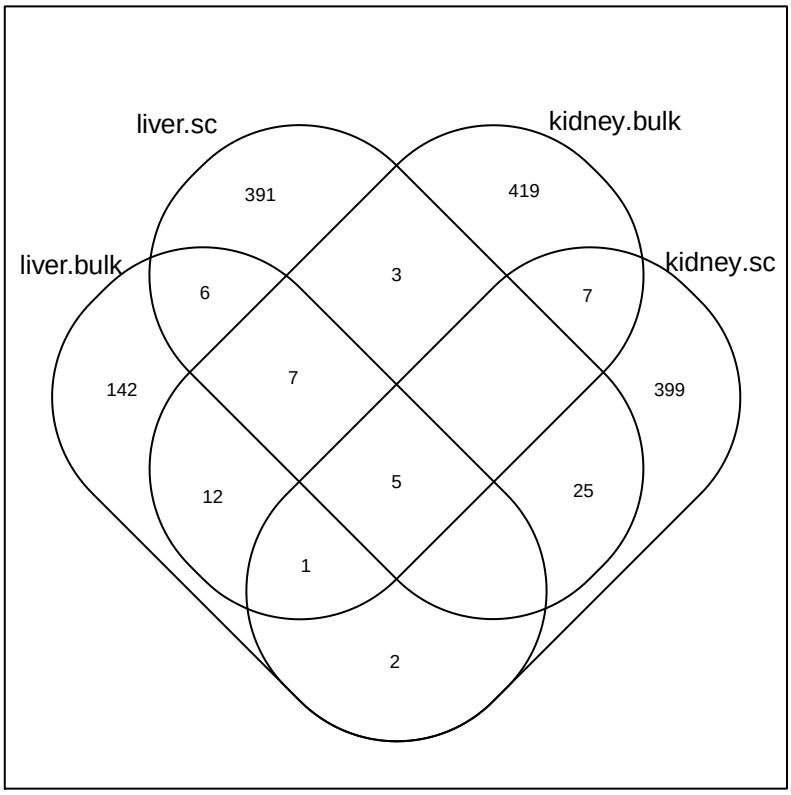
```
scs <- getBM(attributes = c("entrezgene_id", "hgnc_symbol", "ensembl_gene_id", "description"),
    filters = "hgnc_symbol", values = gens.sc_human, mart = mart)
print(kable(scs))
```

entrezgene_id	hgnc_symbol	ensembl_gene_id	description
1244	ABCC2	ENSG00000023839	ATP binding cassette subfamily C member 2 [Source:HGNC Sy
125	ADH1B	ENSG00000196616	alcohol dehydrogenase 1B (class I), beta polypeptide [Sou
118429	ANTXR2	ENSG00000163297	ANTXR cell adhesion molecule 2 [Source:HGNC Symbol;Acc:HG
54796	BNC2	ENSG00000173068	basonuclin 2 [Source:HGNC Symbol;Acc:HGNC:30988]
51293	CD320	ENSG00000167775	CD320 molecule [Source:HGNC Symbol;Acc:HGNC:16692]
972	CD74	ENSG00000019582	CD74 molecule [Source:HGNC Symbol;Acc:HGNC:1697]
1571	CYP2E1	ENSG00000130649	cytochrome P450 family 2 subfamily E member 1 [Source:HGN
2266	FGG	ENSG00000171557	fibrinogen gamma chain [Source:HGNC Symbol;Acc:HGNC:3694]
2524	FUT2	ENSG00000176920	fucosyltransferase 2 [Source:HGNC Symbol;Acc:HGNC:4013]
54331	GNG2	ENSG00000186469	G protein subunit gamma 2 [Source:HGNC Symbol;Acc:HGNC:44
2878	GPX3	ENSG00000211445	glutathione peroxidase 3 [Source:HGNC Symbol;Acc:HGNC:455
57476	GRAMD1B	ENSG00000023171	GRAM domain containing 1B [Source:HGNC Symbol;Acc:HGNC:29
9863	MAGI2	ENSG00000187391	membrane associated guanylate kinase, WW and PDZ domain c
4257	MGST1	ENSG00000008394	microsomal glutathione S-transferase 1 [Source:HGNC Symbol

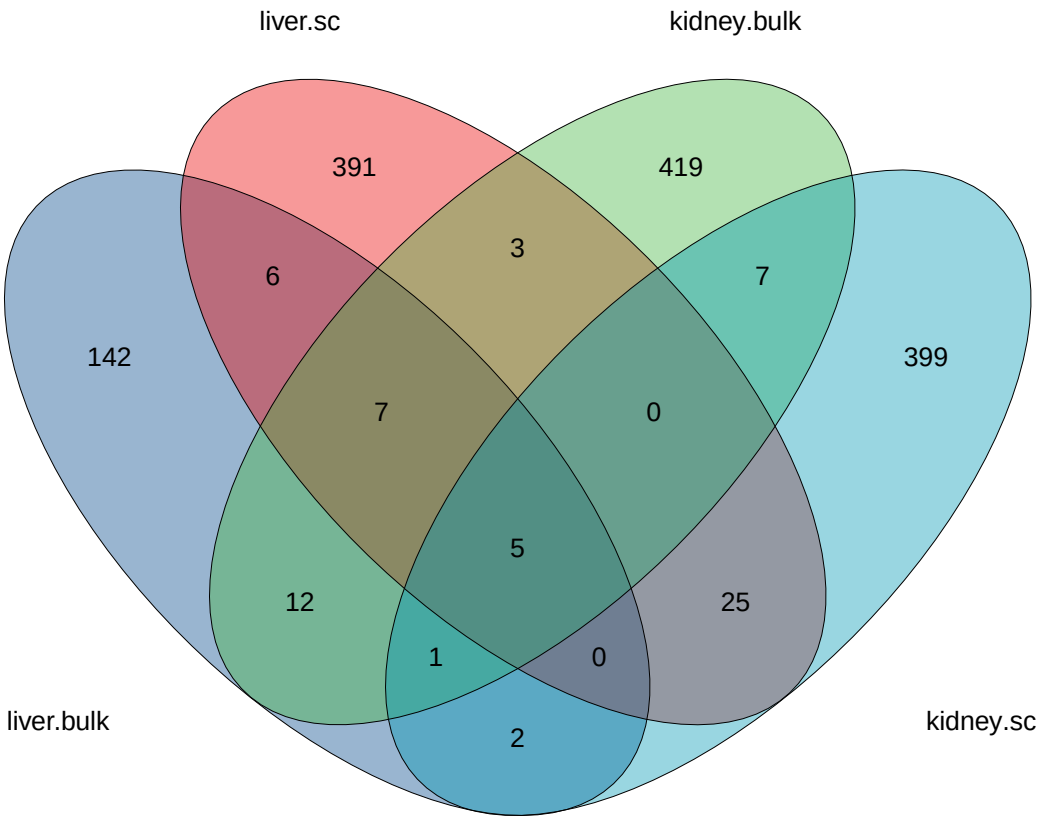
	4519	MT-CYB	ENSG00000198727 |mitochondrially encoded cytochrome b [Source:HGNC Symbol;A
	4535	MT-ND1	ENSG00000198888 |mitochondrially encoded NADH:ubiquinone oxidoreductase co
	4536	MT-ND2	ENSG00000198763 |mitochondrially encoded NADH:ubiquinone oxidoreductase co
	4539	MT-ND4L	ENSG00000212907 |mitochondrially encoded NADH:ubiquinone oxidoreductase co
	4540	MT-ND5	ENSG00000198786 |mitochondrially encoded NADH:ubiquinone oxidoreductase co
	4499	MT1M	ENSG00000205364 |metallothionein 1M [Source:HGNC Symbol;Acc:HGNC:14296]
	55824	PAG1	ENSG00000076641 |phosphoprotein membrane anchor with glycosphingolipid mic
	5144	PDE4D	ENSG00000113448 |phosphodiesterase 4D [Source:HGNC Symbol;Acc:HGNC:8783]
	5579	PRKCB	ENSG00000166501 |protein kinase C beta [Source:HGNC Symbol;Acc:HGNC:9395]
	5789	PTPRD	ENSG00000153707 |protein tyrosine phosphatase receptor type D [Source:HGNC
	6385	SDC4	ENSG00000124145 |syndecan 4 [Source:HGNC Symbol;Acc:HGNC:10661]
	11001	SLC27A2	ENSG00000140284 |solute carrier family 27 member 2 [Source:HGNC Symbol;Acc
	10592	SMC2	ENSG00000136824 |structural maintenance of chromosomes 2 [Source:HGNC Symb
	6714	SRC	ENSG00000291971 |SRC proto-oncogene, non-receptor tyrosine kinase [Source:H
	6714	SRC	ENSG00000197122 |SRC proto-oncogene, non-receptor tyrosine kinase [Source:H
	151531	UPP2	ENSG00000007001 |uridine phosphorylase 2 [Source:HGNC Symbol;Acc:HGNC:2306
	9839	ZEB2	ENSG00000169554 |zinc finger E-box binding homeobox 2 [Source:HGNC Symbol;A

Comparació tot

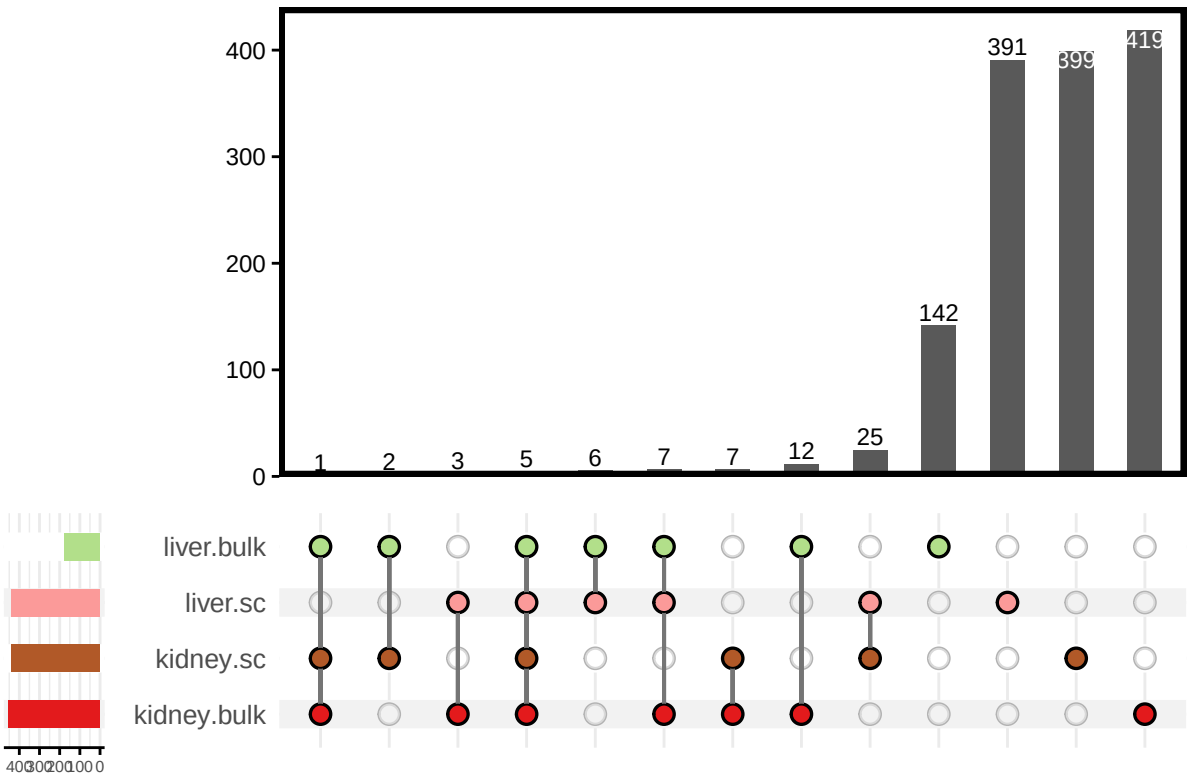
```
ven <- venn(list(liver.bulk = liver.bulk.human, liver.sc = liver.sc.human, kidney.bulk = kidney.bulk.hu
    kidney.sc = kidney.sc.human))
```




```
plotVenn(list(liver.bulk = liver.bulk.human, liver.sc = liver.sc.human, kidney.bulk = kidney.bulk.human
    kidney.sc = kidney.sc.human), use_venn = TRUE, color = (ggsci::pal_lancet())(4),
    alpha_degree = 0.4, main_text_size = 3.5, border_thick = 0)
```




```
plotVenn(list(liver.bulk = liver.bulk.human, liver.sc = liver.sc.human, kidney.bulk = kidney.bulk.human
    kidney.sc = kidney.sc.human), use_venn = FALSE, main_text_size = 12, legend_text_size = 6,
    legend_position = "left")
```


400
300
200
100
0
1
2
3
5
6
7
7
12
25
142
391
399
419
liver.bulk
liver.sc
kidney.sc
kidney.bulk
400
300
200
100
0