Library Size 1e6

Loading Data

```
library(tximeta)
dir <- "/fs/cbcb-lab/rob/students/noor/Uncertainity/boot_gibbs/quant_output/Drosophilla/sim_1e6"
source("/fs/cbcb-lab/rob/students/noor/Uncertainity/boot_gibbs/R/helper_func.R")
load("/fs/cbcb-lab/rob/students/noor/Uncertainity/ase-sim/sim_1e6/sim_counts_matrix.rda") ##True Counts

fileNames <- paste("sample", sort(as.vector(outer(c("01", "02"), c("B", "GS"), paste, sep="_"))), sep=
files <- file.path(dir, fileNames, "quant.sf")
coldata <- data.frame(files, names = fileNames, infType = rep(c("Boot", "GS"), times = 2), stringsAsFac
seSamp1 <- tximeta(coldata[c(1:2),])
seSamp2 <- tximeta(coldata[c(3:4),])

seSamp1 <- appTrueCounts(seSamp1, counts_matrix[,1])
seSamp2 <- appTrueCounts(seSamp2, counts_matrix[,2])
```

Computing size factors and confidence intervals

```
seSamp1 <- computeSizeFactors(seSamp1)
```

```
## [1] 1
## [1] 2
```

```
seSamp2 <- computeSizeFactors(seSamp2)
```

```
## [1] 1
## [1] 2
```

```
seSamp1 <- computeConfInt(seSamp1, sf = T)
seSamp2 <- computeConfInt(seSamp2, sf = T)

teSamp1 <- computeAlleleConfInt(seSamp1)
teSamp2 <- computeAlleleConfInt(seSamp2)
```

Coverages for the replicates

```
print(computeCoverage(counts_matrix[,1], seSamp1, list(seq(nrow(seSamp1)/2)), allele = T, trSe = teSamp
```

```
##   sample_01_B sample_01_GS
## 1   0.7084553    0.9957236
```

```
print(computeCoverage(counts_matrix[,2], seSamp2, list(seq(nrow(seSamp2)/2)), allele = T, trSe = teSamp
```

```
##   sample_02_B sample_02_GS
## 1   0.7042937    0.9953504
```

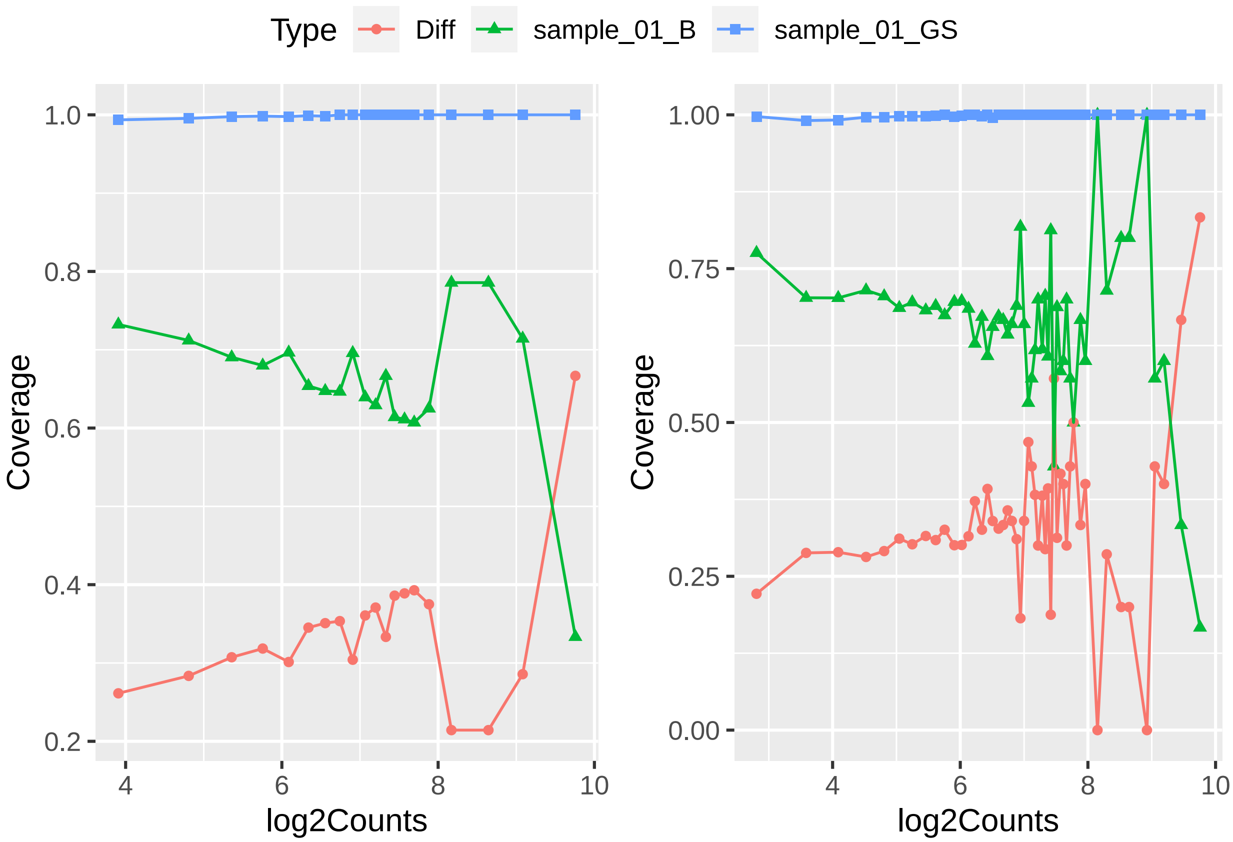
By Counts

Plotting the coverage difference across bins of varying expression

```
nB = c(20,50)
pNb <- vector(mode = "list", length = 2)
for(i in seq_along(pNb))
    pNb[[i]] <- vector(mode = "list", length = length(nB))

m <- nrow(counts_matrix)/2
for(j in seq_along(pNb))
{
    i=1
    for(b in nB)
    {

        cMat <- counts_matrix[,j][1:m] + counts_matrix[,j][m+1:m]
        cInds <- extractBinInds(cMat, breaks = b)
        if(j==1)
            covDf <- createCovDf(seSamp1, counts_matrix[,j], cInds, allele = T, trSe = teSamp1)

        else
            covDf <- createCovDf(seSamp2, counts_matrix[,j], cInds, allele = T, trSe = teSamp2)
        covDf[(b*2+1):(b*3),] = covDf[1:b,]
        covDf[(b*2+1):(b*3),3] = abs(covDf[1:b,3] - covDf[(b*1+1):(b*2),3])
        covDf[,2] = as.character(covDf[,2])
        covDf[(b*2+1):(b*3),2] = "Diff"
        pNb[[j]][[i]] <- plotCovDf(covDf, line=T)
        #print(sort(covDf[(b*2+1):(b*3),3],decreasing=T)[1:20]*100)
        i=i+1
    }
}


p1 <- ggarrange(plotlist = pNb[[1]], common.legend = T)
p2 <- ggarrange(plotlist = pNb[[2]], common.legend = T)
```

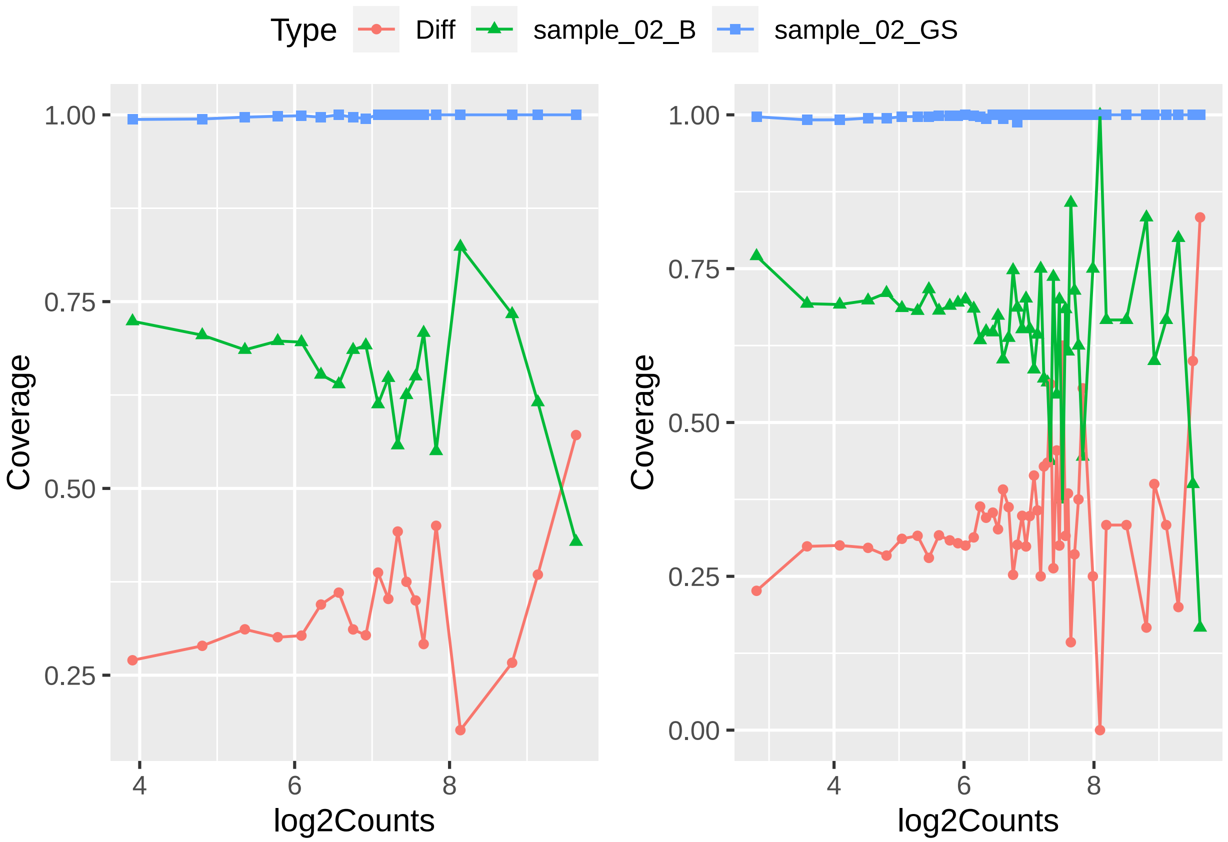
Coverage for Replicate 1 across 20 and 50 bins

```
print(p1)
```



Coverage for Replicate 2 across 20 and 50 bins

```
print(p2)
```



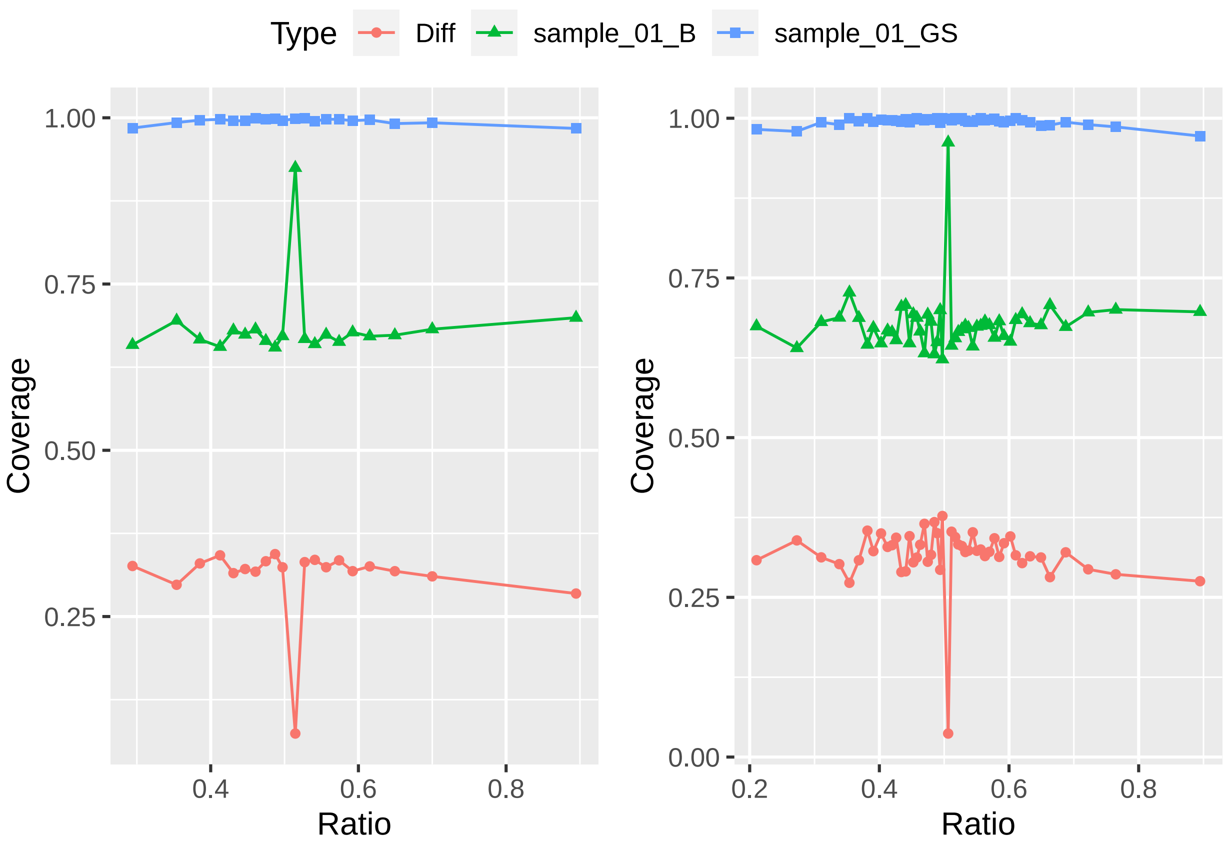
Plotting by ratios

Plotting the coverage difference across bins of varying expression

```
for(j in seq_along(pNb))
{
    i=1
    for(b in nB)
    {
        if(j==1)
        {
            ratio <- computeRatio(counts_matrix[,j])
            cInds <- extractBinInds(ratio, breaks = b)
            covDf <- createCovDf(seSamp1, counts_matrix[,j], cInds, allele = T, trSe = teSamp1, logC =
        }

        else
        {
            ratio <- computeRatio(counts_matrix[,j])
            cInds <- extractBinInds(ratio, breaks = b)
            covDf <- createCovDf(seSamp2, counts_matrix[,j], cInds, allele = T, trSe = teSamp2, logC =
        }
        covDf[(b*2+1):(b*3),] = covDf[1:b,]
        covDf[(b*2+1):(b*3),3] = abs(covDf[1:b,3] - covDf[(b*1+1):(b*2),3])
        covDf[,2] = as.character(covDf[,2])
        covDf[(b*2+1):(b*3),2] = "Diff"
        pNb[[j]][[i]] <- plotCovDf(covDf, line=T,ratio=T)
        #print(sort(covDf[(b*2+1):(b*3),3],decreasing=T)[1:20]*100)
        i=i+1
    }
}

p1 <- ggarrange(plotlist = pNb[[1]], common.legend = T)
p2 <- ggarrange(plotlist = pNb[[2]], common.legend = T)
```

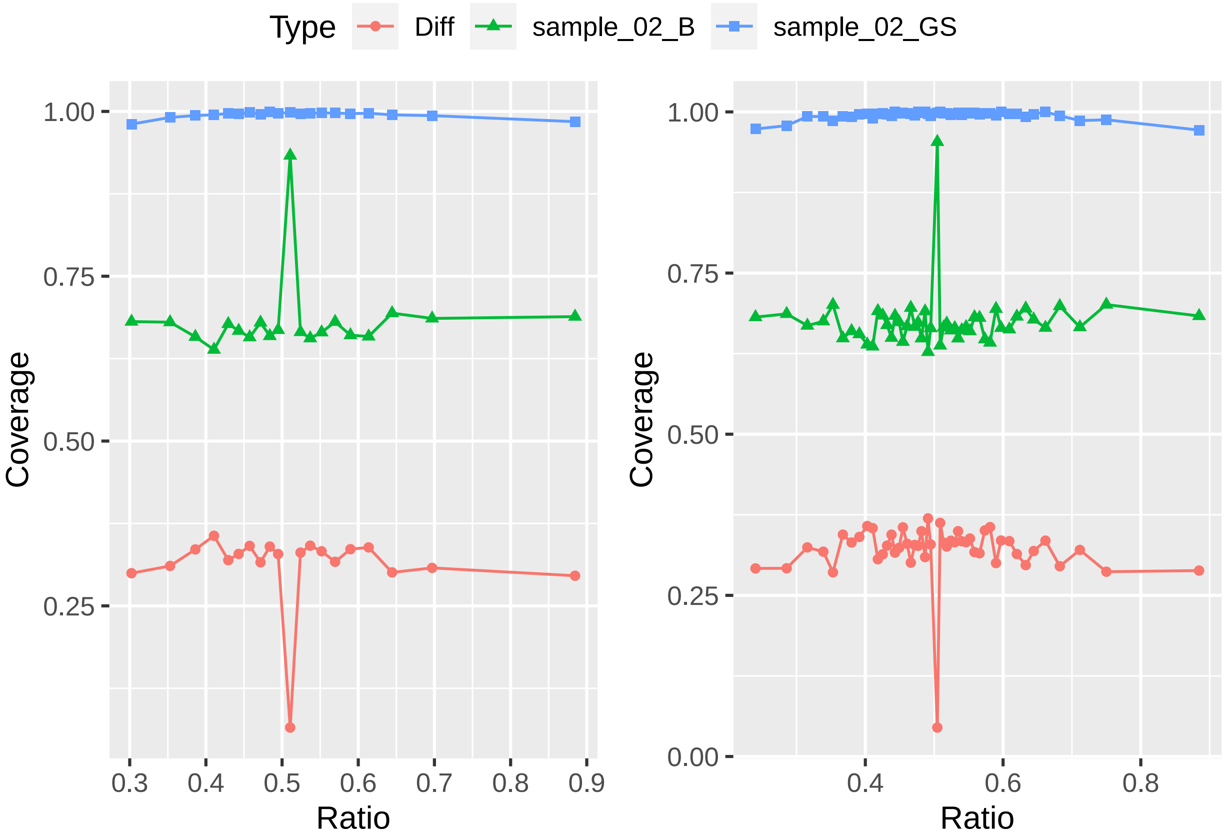
Coverage for Replicate 1 across 20 and 50 bins

```
print(p1)
```



Coverage for Replicate 2 across 20 and 50 bins

```
print(p2)
```


Type
Diff
sample_02_B
sample_02_GS
Coverage
1.00
0.75
0.50
0.25
0.3
0.4
0.5
0.6
0.7
0.8
0.9
Ratio
Coverage
1.00
0.75
0.50
0.25
0.00
0.4
0.6
0.8
Ratio