Block 2: Visualization and normalization

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First we loaded the data into dataframe (skin.df) then recreated the transposed format (tdata).

# load in the data  
skin.df <- read.table("get\_normal\_vs\_tumor2\_RAW\_Skin.out",sep=" ",header=TRUE)  
# Create a reversed data frame  
# Transpose just the gene expression  
tdata <- data.frame(t(skin.df[,-2562]))  
# Add sample type as column name  
colnames(tdata)<-paste0(skin.df$tissue,1:72)

Then we inspect the data using functions as dim(), summary(), and so on.

dim(tdata)

## [1] 2561 72

str(tdata)

## 'data.frame': 2561 obs. of 72 variables:  
## $ tumor1 : num 16 82.6 366.4 1351.1 44 ...  
## $ tumor2 : num 15.3 86.7 344.5 1361.4 47.2 ...  
## $ tumor3 : num 13.4 109.7 227.1 468.5 44.7 ...  
## $ tumor4 : num 15.9 112.9 239.6 642.6 49.4 ...  
## $ tumor5 : num 13.2 56.4 120.5 771.6 75.1 ...  
## $ tumor6 : num 12.3 45.6 142.8 703.9 54.3 ...  
## $ tumor7 : num 15.6 42.8 136.2 800.6 50.7 ...  
## $ tumor8 : num 12.2 46 239 462.5 35.9 ...  
## $ tumor9 : num 13.3 50 249.2 417.1 42.1 ...  
## $ tumor10 : num 13.6 43.8 256.7 537.5 43.2 ...  
## $ tumor11 : num 12.9 89.1 255.1 621.2 59.3 ...  
## $ tumor12 : num 14.2 97.2 214.8 793.3 80.1 ...  
## $ tumor13 : num 15.1 73.2 222.3 474.4 64.8 ...  
## $ tumor14 : num 14.9 51.8 237.3 690.3 56.4 ...  
## $ tumor15 : num 13.3 60 296.5 750.8 49.7 ...  
## $ tumor16 : num 15.2 91.3 316.6 535.4 36.3 ...  
## $ tumor17 : num 18.5 62.9 297.1 573 43.3 ...  
## $ tumor18 : num 15.5 95.6 311.3 709.5 37.6 ...  
## $ tumor19 : num 14.4 43 527.1 1148 43.5 ...  
## $ tumor20 : num 13.6 35.4 652.4 1241.3 45.7 ...  
## $ tumor21 : num 13.3 72.2 249.5 948.2 70.8 ...  
## $ tumor22 : num 15.5 106.5 199.3 933.8 84.5 ...  
## $ tumor23 : num 14.5 45 287.1 1007 47.1 ...  
## $ tumor24 : num 12.9 47.6 285.2 851.6 42.1 ...  
## $ tumor25 : num 13.8 51.4 303.1 1066.4 45.2 ...  
## $ tumor26 : num 14.1 54.1 308.4 771 60.7 ...  
## $ tumor27 : num 14.6 55.4 241 665 44.2 ...  
## $ tumor28 : num 13 52 297.7 643.6 45.3 ...  
## $ tumor29 : num 14.9 61.8 291.4 627.9 51.1 ...  
## $ tumor30 : num 15.6 122.7 254.2 363.5 62.7 ...  
## $ tumor31 : num 14.8 99.5 222.2 274.8 50 ...  
## $ tumor32 : num 16.3 87.7 211.6 274.6 51.2 ...  
## $ tumor33 : num 14.7 72.5 357 420 47.6 ...  
## $ tumor34 : num 14.7 72.8 347 466.3 68.4 ...  
## $ tumor35 : num 17.4 53.1 345.8 999 51.7 ...  
## $ tumor36 : num 16.4 44.6 330.2 967.6 46.7 ...  
## $ tumor37 : num 15.4 38.2 371 1154.9 38.8 ...  
## $ tumor38 : num 13.3 56.3 343.9 1248 44.8 ...  
## $ tumor39 : num 18.2 74.3 324.2 611.8 61.6 ...  
## $ tumor40 : num 17.3 68.2 257.7 828.9 53.1 ...  
## $ tumor41 : num 16.2 73.1 380.5 841.5 66.4 ...  
## $ tumor42 : num 13.8 43.9 474.7 730.5 74.8 ...  
## $ tumor43 : num 13.6 51.8 459.1 670.4 63 ...  
## $ normal44: num 13 50.8 171.7 350.8 49.8 ...  
## $ normal45: num 16.1 50.3 198.8 286.9 40.7 ...  
## $ normal46: num 17.7 50.2 200.6 268.7 56.4 ...  
## $ normal47: num 16.6 72 93 309.6 44.6 ...  
## $ normal48: num 17.8 149.3 208 290.6 59.4 ...  
## $ normal49: num 16.1 93.4 147.4 309.7 45.2 ...  
## $ normal50: num 17.6 67.6 106.7 200.9 54 ...  
## $ normal51: num 15.3 70.8 159.1 274.7 45.6 ...  
## $ normal52: num 13.8 68.5 145.6 276.5 54.2 ...  
## $ normal53: num 17.9 68 182.2 319.4 42.7 ...  
## $ normal54: num 15 69.7 149.1 320.1 51.9 ...  
## $ normal55: num 17.4 68.7 106.7 191.4 46.9 ...  
## $ normal56: num 14.8 63 164.2 385.1 44.4 ...  
## $ normal57: num 16.7 115 422.6 330.1 59.1 ...  
## $ normal58: num 17 72.7 295.6 294.4 49.1 ...  
## $ normal59: num 14.5 78.7 245.6 325.5 49.8 ...  
## $ normal60: num 15.4 85.3 256.5 299.8 42.4 ...  
## $ normal61: num 15.7 67.9 219 321.3 49.5 ...  
## $ normal62: num 14.1 89.5 146.9 238.4 49.2 ...  
## $ normal63: num 26.4 82.8 159.3 539.6 45.6 ...  
## $ normal64: num 24.9 105.1 268.9 300.9 75.8 ...  
## $ normal65: num 15.6 99 183.2 395.5 45.5 ...  
## $ normal66: num 18.4 86.6 152.4 349.4 47.8 ...  
## $ normal67: num 15.1 74.1 111.2 304.6 45.8 ...  
## $ normal68: num 17.7 81.7 178.3 288.3 52.5 ...  
## $ normal69: num 17 75.1 181.5 338.6 49.8 ...  
## $ normal70: num 14.9 102.8 137.1 380.8 49.9 ...  
## $ normal71: num 18.1 83.3 245.9 250.6 44.5 ...  
## $ normal72: num 20.3 91.7 154.6 352.6 45.7 ...

names(tdata)

## [1] "tumor1" "tumor2" "tumor3" "tumor4" "tumor5" "tumor6"   
## [7] "tumor7" "tumor8" "tumor9" "tumor10" "tumor11" "tumor12"   
## [13] "tumor13" "tumor14" "tumor15" "tumor16" "tumor17" "tumor18"   
## [19] "tumor19" "tumor20" "tumor21" "tumor22" "tumor23" "tumor24"   
## [25] "tumor25" "tumor26" "tumor27" "tumor28" "tumor29" "tumor30"   
## [31] "tumor31" "tumor32" "tumor33" "tumor34" "tumor35" "tumor36"   
## [37] "tumor37" "tumor38" "tumor39" "tumor40" "tumor41" "tumor42"   
## [43] "tumor43" "normal44" "normal45" "normal46" "normal47" "normal48"  
## [49] "normal49" "normal50" "normal51" "normal52" "normal53" "normal54"  
## [55] "normal55" "normal56" "normal57" "normal58" "normal59" "normal60"  
## [61] "normal61" "normal62" "normal63" "normal64" "normal65" "normal66"  
## [67] "normal67" "normal68" "normal69" "normal70" "normal71" "normal72"

quantile(tdata, na.rm=TRUE)

## 0% 25% 50% 75% 100%   
## 9.6200 40.2775 106.7700 323.1450 21891.7600

summary(tdata)

## tumor1 tumor2 tumor3   
## Min. : 10.40 Min. : 10.32 Min. : 10.39   
## 1st Qu.: 36.69 1st Qu.: 37.69 1st Qu.: 36.46   
## Median : 102.43 Median : 98.89 Median : 103.49   
## Mean : 443.14 Mean : 449.55 Mean : 388.55   
## 3rd Qu.: 387.14 3rd Qu.: 385.08 3rd Qu.: 358.07   
## Max. :18651.45 Max. :18504.65 Max. :20513.70   
## tumor4 tumor5 tumor6   
## Min. : 9.9 Min. : 9.70 Min. : 9.77   
## 1st Qu.: 34.1 1st Qu.: 36.78 1st Qu.: 35.13   
## Median : 110.2 Median : 105.30 Median : 101.81   
## Mean : 398.0 Mean : 427.35 Mean : 420.53   
## 3rd Qu.: 379.9 3rd Qu.: 389.69 3rd Qu.: 378.96   
## Max. :19562.5 Max. :11786.93 Max. :15517.41   
## tumor7 tumor8 tumor9   
## Min. : 10.06 Min. : 10.34 Min. : 9.97   
## 1st Qu.: 35.08 1st Qu.: 34.82 1st Qu.: 34.32   
## Median : 104.79 Median : 103.12 Median : 107.75   
## Mean : 441.60 Mean : 368.15 Mean : 365.05   
## 3rd Qu.: 399.60 3rd Qu.: 336.02 3rd Qu.: 342.82   
## Max. :12676.77 Max. :19423.29 Max. :19335.98   
## tumor10 tumor11 tumor12   
## Min. : 10.26 Min. : 9.97 Min. : 10.54   
## 1st Qu.: 33.33 1st Qu.: 35.85 1st Qu.: 35.89   
## Median : 103.08 Median : 101.95 Median : 106.87   
## Mean : 376.56 Mean : 383.91 Mean : 386.62   
## 3rd Qu.: 353.80 3rd Qu.: 352.19 3rd Qu.: 363.32   
## Max. :20424.31 Max. :21891.76 Max. :20027.57   
## tumor13 tumor14 tumor15   
## Min. : 9.80 Min. : 10.21 Min. : 10.24   
## 1st Qu.: 36.59 1st Qu.: 35.48 1st Qu.: 34.67   
## Median : 105.42 Median : 105.69 Median : 106.23   
## Mean : 366.23 Mean : 365.59 Mean : 373.83   
## 3rd Qu.: 331.16 3rd Qu.: 361.34 3rd Qu.: 377.23   
## Max. :20526.50 Max. :14467.22 Max. :14773.25   
## tumor16 tumor17 tumor18   
## Min. : 10.50 Min. : 9.91 Min. : 9.89   
## 1st Qu.: 35.03 1st Qu.: 35.58 1st Qu.: 36.20   
## Median : 113.61 Median : 109.31 Median : 110.88   
## Mean : 401.06 Mean : 393.86 Mean : 407.54   
## 3rd Qu.: 362.42 3rd Qu.: 359.41 3rd Qu.: 355.72   
## Max. :16305.83 Max. :15891.86 Max. :16572.46   
## tumor19 tumor20 tumor21   
## Min. : 10.12 Min. : 10.79 Min. : 9.80   
## 1st Qu.: 34.25 1st Qu.: 34.36 1st Qu.: 35.25   
## Median : 100.13 Median : 100.98 Median : 111.04   
## Mean : 419.83 Mean : 406.70 Mean : 428.77   
## 3rd Qu.: 371.86 3rd Qu.: 360.66 3rd Qu.: 385.16   
## Max. :16480.82 Max. :14936.97 Max. :20527.92   
## tumor22 tumor23 tumor24   
## Min. : 10.25 Min. : 10.13 Min. : 10.80   
## 1st Qu.: 36.78 1st Qu.: 39.97 1st Qu.: 39.78   
## Median : 111.28 Median : 101.56 Median : 102.27   
## Mean : 367.14 Mean : 407.61 Mean : 400.18   
## 3rd Qu.: 340.66 3rd Qu.: 344.20 3rd Qu.: 347.31   
## Max. :13464.75 Max. :17153.32 Max. :15912.80   
## tumor25 tumor26 tumor27   
## Min. : 10.56 Min. : 10.59 Min. : 10.46   
## 1st Qu.: 41.46 1st Qu.: 40.25 1st Qu.: 34.99   
## Median : 102.34 Median : 99.95 Median : 102.33   
## Mean : 420.33 Mean : 402.58 Mean : 402.62   
## 3rd Qu.: 349.83 3rd Qu.: 340.14 3rd Qu.: 351.70   
## Max. :18311.98 Max. :15073.22 Max. :17725.02   
## tumor28 tumor29 tumor30   
## Min. : 10.46 Min. : 10.10 Min. : 10.64   
## 1st Qu.: 33.76 1st Qu.: 34.65 1st Qu.: 42.65   
## Median : 103.10 Median : 108.37 Median : 107.52   
## Mean : 428.75 Mean : 400.60 Mean : 376.01   
## 3rd Qu.: 380.91 3rd Qu.: 348.83 3rd Qu.: 325.23   
## Max. :18777.27 Max. :17551.42 Max. :17270.23   
## tumor31 tumor32 tumor33   
## Min. : 10.54 Min. : 10.26 Min. : 10.20   
## 1st Qu.: 36.22 1st Qu.: 43.63 1st Qu.: 35.06   
## Median : 101.16 Median : 103.42 Median : 103.01   
## Mean : 363.19 Mean : 340.57 Mean : 424.48   
## 3rd Qu.: 338.15 3rd Qu.: 304.75 3rd Qu.: 366.05   
## Max. :15834.68 Max. :15211.77 Max. :19246.39   
## tumor34 tumor35 tumor36   
## Min. : 9.97 Min. : 10.58 Min. : 10.57   
## 1st Qu.: 35.65 1st Qu.: 35.36 1st Qu.: 36.49   
## Median : 106.54 Median : 99.42 Median : 97.34   
## Mean : 399.09 Mean : 378.30 Mean : 392.02   
## 3rd Qu.: 351.26 3rd Qu.: 361.11 3rd Qu.: 350.05   
## Max. :21143.11 Max. :14950.44 Max. :15570.20   
## tumor37 tumor38 tumor39   
## Min. : 10.33 Min. : 10.47 Min. : 10.33   
## 1st Qu.: 33.72 1st Qu.: 32.13 1st Qu.: 39.57   
## Median : 98.68 Median : 100.02 Median : 103.42   
## Mean : 442.97 Mean : 432.84 Mean : 386.12   
## 3rd Qu.: 406.64 3rd Qu.: 389.37 3rd Qu.: 347.65   
## Max. :18078.66 Max. :16253.92 Max. :16338.64   
## tumor40 tumor41 tumor42   
## Min. : 10.56 Min. : 10.90 Min. : 10.19   
## 1st Qu.: 37.61 1st Qu.: 38.53 1st Qu.: 35.38   
## Median : 101.79 Median : 107.04 Median : 104.76   
## Mean : 404.27 Mean : 418.55 Mean : 412.62   
## 3rd Qu.: 348.30 3rd Qu.: 369.31 3rd Qu.: 369.77   
## Max. :15727.48 Max. :15753.67 Max. :18594.65   
## tumor43 normal44 normal45   
## Min. : 10.58 Min. : 10.35 Min. : 10.09   
## 1st Qu.: 37.03 1st Qu.: 43.14 1st Qu.: 42.07   
## Median : 108.82 Median : 104.25 Median : 115.94   
## Mean : 389.47 Mean : 328.62 Mean : 383.56   
## 3rd Qu.: 341.35 3rd Qu.: 289.98 3rd Qu.: 329.77   
## Max. :17248.70 Max. :12148.58 Max. :13111.09   
## normal46 normal47 normal48   
## Min. : 10.27 Min. : 10.98 Min. : 11.11   
## 1st Qu.: 44.13 1st Qu.: 44.95 1st Qu.: 50.35   
## Median : 114.67 Median : 103.31 Median : 104.86   
## Mean : 395.63 Mean : 279.84 Mean : 256.08   
## 3rd Qu.: 351.24 3rd Qu.: 247.57 3rd Qu.: 229.49   
## Max. :9414.05 Max. :10849.94 Max. :11771.41   
## normal49 normal50 normal51   
## Min. : 10.02 Min. : 10.19 Min. : 10.60   
## 1st Qu.: 46.87 1st Qu.: 46.94 1st Qu.: 48.05   
## Median : 108.26 Median : 111.04 Median : 110.03   
## Mean : 331.35 Mean : 335.57 Mean : 398.88   
## 3rd Qu.: 269.59 3rd Qu.: 293.70 3rd Qu.: 271.39   
## Max. :12276.40 Max. :12648.69 Max. :17824.82   
## normal52 normal53 normal54   
## Min. : 10.56 Min. : 10.28 Min. : 10.33   
## 1st Qu.: 49.37 1st Qu.: 44.82 1st Qu.: 48.86   
## Median : 115.99 Median : 110.94 Median : 111.42   
## Mean : 421.42 Mean : 336.88 Mean : 345.48   
## 3rd Qu.: 301.27 3rd Qu.: 304.54 3rd Qu.: 249.26   
## Max. :16587.40 Max. :10135.99 Max. :16166.28   
## normal55 normal56 normal57   
## Min. : 10.85 Min. : 10.49 Min. : 9.62   
## 1st Qu.: 50.10 1st Qu.: 48.23 1st Qu.: 54.07   
## Median : 109.61 Median : 110.83 Median : 116.44   
## Mean : 297.21 Mean : 403.92 Mean : 321.14   
## 3rd Qu.: 256.71 3rd Qu.: 278.71 3rd Qu.: 266.61   
## Max. :11084.84 Max. :16519.70 Max. :17158.07   
## normal58 normal59 normal60   
## Min. : 10.08 Min. : 10.23 Min. : 10.50   
## 1st Qu.: 41.83 1st Qu.: 42.15 1st Qu.: 43.17   
## Median : 107.91 Median : 106.58 Median : 109.78   
## Mean : 369.55 Mean : 353.18 Mean : 337.89   
## 3rd Qu.: 308.94 3rd Qu.: 301.23 3rd Qu.: 298.03   
## Max. :14442.17 Max. :13555.59 Max. :13667.86   
## normal61 normal62 normal63   
## Min. : 10.62 Min. : 10.19 Min. : 10.60   
## 1st Qu.: 45.01 1st Qu.: 43.45 1st Qu.: 46.55   
## Median : 107.92 Median : 98.69 Median : 106.13   
## Mean : 351.54 Mean : 260.83 Mean : 328.21   
## 3rd Qu.: 278.96 3rd Qu.: 233.23 3rd Qu.: 275.25   
## Max. :13818.37 Max. :11009.03 Max. :10758.58   
## normal64 normal65 normal66   
## Min. : 10.27 Min. : 10.76 Min. : 10.60   
## 1st Qu.: 49.13 1st Qu.: 48.18 1st Qu.: 45.89   
## Median : 108.49 Median : 106.71 Median : 113.01   
## Mean : 325.05 Mean : 291.99 Mean : 351.83   
## 3rd Qu.: 270.43 3rd Qu.: 254.50 3rd Qu.: 295.76   
## Max. :9407.53 Max. :10837.92 Max. :11863.98   
## normal67 normal68 normal69   
## Min. : 11.12 Min. : 10.71 Min. : 10.73   
## 1st Qu.: 50.75 1st Qu.: 48.67 1st Qu.: 48.77   
## Median : 110.09 Median : 110.78 Median : 111.21   
## Mean : 364.16 Mean : 395.22 Mean : 429.94   
## 3rd Qu.: 263.16 3rd Qu.: 284.58 3rd Qu.: 262.18   
## Max. :16084.68 Max. :16604.65 Max. :19013.02   
## normal70 normal71 normal72   
## Min. : 10.81 Min. : 10.47 Min. : 9.96   
## 1st Qu.: 53.62 1st Qu.: 45.05 1st Qu.: 42.44   
## Median : 116.99 Median : 105.59 Median : 105.98   
## Mean : 404.74 Mean : 322.44 Mean : 336.61   
## 3rd Qu.: 244.96 3rd Qu.: 276.38 3rd Qu.: 285.33   
## Max. :19013.02 Max. :11436.83 Max. :14932.83

This data frame has 2561 rows (genes) and 72 column (samples).The maximal value is 21891.76, the mininal value is 9.62, and median is 106.77.

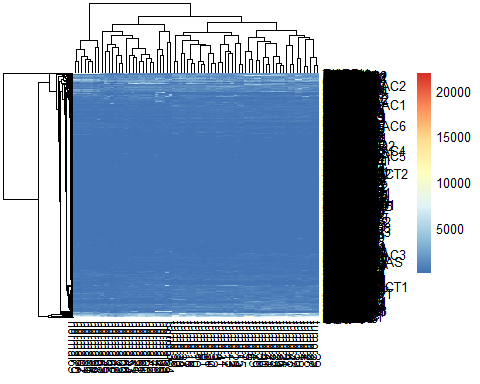
## Task 1

First we generate heatmaps for both log-transformed data with the original data. For task one the log of the data is used to create a heatmap using the pheatmap function. This log function is used because all the variables are right-skew. This can be seen in the histograms created in the block one project. Because the data is reght-skewed it can be influenced a lot by a few outliers. Taking the log will help by reducing the skew.

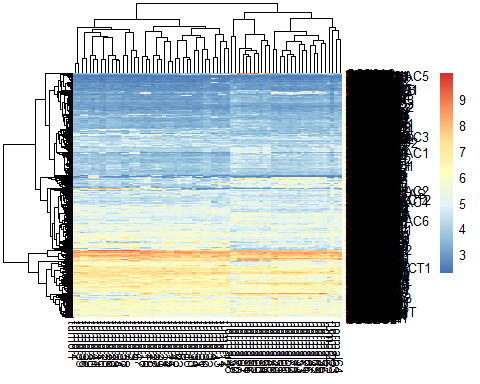
# Generate a heatmap for both log-transformed data with the original data.  
library(pheatmap)

## Warning: package 'pheatmap' was built under R version 3.4.2

# for original data  
pheatmap(tdata)



# for log-transformed data  
pheatmap(log(tdata))



Then we also visualize the sample correlation matrix.

# create correlation matrix for both log-transformed data with the original data.  
cor(tdata)

## tumor1 tumor2 tumor3 tumor4 tumor5 tumor6  
## tumor1 1.0000000 0.9959747 0.8200759 0.8231901 0.8330841 0.8251239  
## tumor2 0.9959747 1.0000000 0.8142107 0.8202314 0.8380307 0.8305948  
## tumor3 0.8200759 0.8142107 1.0000000 0.9833068 0.7011787 0.6835361  
## tumor4 0.8231901 0.8202314 0.9833068 1.0000000 0.7029619 0.6816784  
## tumor5 0.8330841 0.8380307 0.7011787 0.7029619 1.0000000 0.9778747  
## tumor6 0.8251239 0.8305948 0.6835361 0.6816784 0.9778747 1.0000000  
## tumor7 0.8440737 0.8495522 0.7277355 0.7316856 0.9582441 0.9463439  
## tumor8 0.8335290 0.8250135 0.8479638 0.8456655 0.7747707 0.7714963  
## tumor9 0.8482113 0.8400888 0.8711026 0.8714261 0.7775574 0.7651228  
## tumor10 0.8437516 0.8338615 0.8461882 0.8466432 0.7741867 0.7797105  
## tumor11 0.8155592 0.8156381 0.8833481 0.8907968 0.7045404 0.6860528  
## tumor12 0.8602807 0.8576486 0.9221140 0.9327737 0.7476036 0.7207100  
## tumor13 0.8623458 0.8655401 0.8903768 0.8975925 0.7605153 0.7464539  
## tumor14 0.8325022 0.8258641 0.7863415 0.7961415 0.7955443 0.7993858  
## tumor15 0.8320178 0.8268852 0.7859375 0.7897943 0.8014799 0.8096626  
## tumor16 0.8782828 0.8748913 0.8305877 0.8316784 0.8253120 0.8156455  
## tumor17 0.8910036 0.8883465 0.8274220 0.8300485 0.8315045 0.8328274  
## tumor18 0.8830760 0.8819229 0.8420203 0.8442802 0.8332940 0.8169275  
## tumor19 0.8309915 0.8355937 0.6902547 0.6957912 0.8659197 0.8806824  
## tumor20 0.8312215 0.8333946 0.6986771 0.7040597 0.8611640 0.8701896  
## tumor21 0.8924826 0.8914265 0.8060385 0.8072847 0.8618893 0.8547591  
## tumor22 0.7807902 0.7761609 0.7810312 0.8037199 0.7619552 0.7390556  
## tumor23 0.8763009 0.8817772 0.7670473 0.7731552 0.8716314 0.8679326  
## tumor24 0.8725400 0.8786616 0.7580070 0.7690539 0.8682933 0.8643468  
## tumor25 0.8783241 0.8819634 0.7815312 0.7870133 0.8703564 0.8678575  
## tumor26 0.8661265 0.8730861 0.7458023 0.7531899 0.8662713 0.8648564  
## tumor27 0.8761954 0.8758595 0.8005936 0.7974986 0.8173242 0.7933798  
## tumor28 0.8857478 0.8816448 0.8178667 0.8179883 0.8210064 0.7920140  
## tumor29 0.8793854 0.8781719 0.8157016 0.8156853 0.8280580 0.8037147  
## tumor30 0.8627751 0.8621911 0.8481644 0.8452350 0.8046127 0.8062738  
## tumor31 0.8374932 0.8361954 0.8595526 0.8586972 0.7683327 0.7652599  
## tumor32 0.8540902 0.8532735 0.8349646 0.8352152 0.7961370 0.8032466  
## tumor33 0.8417779 0.8401415 0.8156061 0.8097616 0.7959191 0.7991428  
## tumor34 0.8124168 0.8077367 0.8574418 0.8574721 0.7485952 0.7331125  
## tumor35 0.8497053 0.8480315 0.7987042 0.7984000 0.8087628 0.8083995  
## tumor36 0.8430277 0.8436532 0.7739411 0.7749047 0.8034659 0.8122367  
## tumor37 0.8841055 0.8834346 0.7599403 0.7545442 0.8472093 0.8553696  
## tumor38 0.8744215 0.8753600 0.7526357 0.7498364 0.8583175 0.8537777  
## tumor39 0.8290275 0.8396722 0.7007168 0.7088010 0.8578003 0.8483114  
## tumor40 0.8740134 0.8837500 0.7473872 0.7532337 0.8797333 0.8707763  
## tumor41 0.8777156 0.8850398 0.7625175 0.7669632 0.8801225 0.8648614  
## tumor42 0.8728967 0.8764225 0.8223681 0.8212546 0.8260402 0.8464428  
## tumor43 0.8771996 0.8797360 0.8258716 0.8270763 0.8289491 0.8494278  
## normal44 0.7977750 0.8042564 0.7748192 0.7788760 0.7411438 0.7209441  
## normal45 0.7434836 0.7479590 0.7120658 0.7131366 0.6922697 0.6706858  
## normal46 0.7053507 0.7091780 0.6690683 0.6726151 0.6729792 0.6499615  
## normal47 0.8080762 0.8060947 0.7785381 0.7804267 0.7623526 0.7501071  
## normal48 0.7118493 0.7050844 0.7273069 0.7151630 0.6971578 0.6859018  
## normal49 0.7699187 0.7766252 0.7160980 0.7269868 0.7444747 0.7215496  
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## normal51 0.6782186 0.6801657 0.6422476 0.6451971 0.6200771 0.6002931  
## normal52 0.6720213 0.6743269 0.6419104 0.6460502 0.6158857 0.5951727  
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## normal57 0.6370375 0.6353390 0.6570524 0.6477102 0.6036550 0.5776195  
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## normal59 0.7880610 0.7958813 0.7520600 0.7626175 0.7489756 0.7325629  
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## normal61 0.7801841 0.7870234 0.7494969 0.7575153 0.7234828 0.7052371  
## normal62 0.8026144 0.8058365 0.7757360 0.7818310 0.7089102 0.6939009  
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## normal72 0.7948779 0.8018927 0.7776932 0.7863854 0.7458214 0.7226656  
## tumor7 tumor8 tumor9 tumor10 tumor11 tumor12  
## tumor1 0.8440737 0.8335290 0.8482113 0.8437516 0.8155592 0.8602807  
## tumor2 0.8495522 0.8250135 0.8400888 0.8338615 0.8156381 0.8576486  
## tumor3 0.7277355 0.8479638 0.8711026 0.8461882 0.8833481 0.9221140  
## tumor4 0.7316856 0.8456655 0.8714261 0.8466432 0.8907968 0.9327737  
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## tumor13 tumor14 tumor15 tumor16 tumor17 tumor18  
## tumor1 0.8623458 0.8325022 0.8320178 0.8782828 0.8910036 0.8830760  
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## tumor16 0.8783286 0.8687920 0.8699689 1.0000000 0.9789537 0.9869318  
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## tumor19 tumor20 tumor21 tumor22 tumor23 tumor24  
## tumor1 0.8309915 0.8312215 0.8924826 0.7807902 0.8763009 0.8725400  
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## normal55 0.6750840 0.6898089 0.7333243 0.7375127 0.7108709 0.7099436  
## normal56 0.5866998 0.5997212 0.6935214 0.6612115 0.6541015 0.6466798  
## normal57 0.5646372 0.5649592 0.6802739 0.6527564 0.6263573 0.6133855  
## normal58 0.7073290 0.7182668 0.7871854 0.7950930 0.7671933 0.7650139  
## normal59 0.7336230 0.7440229 0.7782138 0.7749431 0.7733120 0.7747715  
## normal60 0.7402858 0.7518129 0.7662211 0.7517187 0.7763734 0.7770722  
## normal61 0.6952633 0.7100918 0.7599727 0.7673687 0.7519154 0.7522133  
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## normal63 0.5668433 0.5970080 0.6092391 0.7457550 0.5995454 0.6007776  
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## normal67 0.5655293 0.5750709 0.6697989 0.6363573 0.6292213 0.6218517  
## normal68 0.5230349 0.5315174 0.6285188 0.6580066 0.5877453 0.5873920  
## normal69 0.5370454 0.5448540 0.6513191 0.6123763 0.5985113 0.5922939  
## normal70 0.5410575 0.5502980 0.6581175 0.6192615 0.6068963 0.5997490  
## normal71 0.7020500 0.7184283 0.7406777 0.7488795 0.7518573 0.7559201  
## normal72 0.7186806 0.7293735 0.7886549 0.7924901 0.7715865 0.7704519  
## tumor25 tumor26 tumor27 tumor28 tumor29 tumor30  
## tumor1 0.8783241 0.8661265 0.8761954 0.8857478 0.8793854 0.8627751  
## tumor2 0.8819634 0.8730861 0.8758595 0.8816448 0.8781719 0.8621911  
## tumor3 0.7815312 0.7458023 0.8005936 0.8178667 0.8157016 0.8481644  
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## tumor8 0.8343497 0.8011317 0.8525864 0.8689075 0.8696881 0.8890208  
## tumor9 0.8424151 0.8115630 0.8669839 0.8852734 0.8858778 0.8940560  
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## tumor27 0.8469535 0.8561292 1.0000000 0.9701602 0.9916964 0.8499821  
## tumor28 0.8553111 0.8512976 0.9701602 1.0000000 0.9748519 0.8623606  
## tumor29 0.8494858 0.8572608 0.9916964 0.9748519 1.0000000 0.8661554  
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## tumor42 0.8740879 0.8346832 0.8354237 0.8499395 0.8515198 0.9107236  
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## tumor31 tumor32 tumor33 tumor34 tumor35 tumor36  
## tumor1 0.8374932 0.8540902 0.8417779 0.8124168 0.8497053 0.8430277  
## tumor2 0.8361954 0.8532735 0.8401415 0.8077367 0.8480315 0.8436532  
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## tumor37 tumor38 tumor39 tumor40 tumor41 tumor42  
## tumor1 0.8841055 0.8744215 0.8290275 0.8740134 0.8777156 0.8728967  
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## normal61 0.7492339 0.7428014 0.6995951 0.7528523 0.7593219 0.7824171  
## normal62 0.7501344 0.7415105 0.7054942 0.7512209 0.7636845 0.7965535  
## normal63 0.6062453 0.6044262 0.5568989 0.5921414 0.6068662 0.6395884  
## normal64 0.6109343 0.6076205 0.5807257 0.6139463 0.6263753 0.6455726  
## normal65 0.7804390 0.7778963 0.7313754 0.7735696 0.7839768 0.8081720  
## normal66 0.7182742 0.7108432 0.6560292 0.7067225 0.7168047 0.7416771  
## normal67 0.6369093 0.6358562 0.6049049 0.6464572 0.6581587 0.6642626  
## normal68 0.5866931 0.5874498 0.5736437 0.6058702 0.6180066 0.6172351  
## normal69 0.6067413 0.6096395 0.5807821 0.6217987 0.6363276 0.6430139  
## normal70 0.6185987 0.6172219 0.5832990 0.6251404 0.6405040 0.6484016  
## normal71 0.7426892 0.7342843 0.7103957 0.7570922 0.7586487 0.7565213  
## normal72 0.7656515 0.7651777 0.7288364 0.7743723 0.7798566 0.7952557  
## tumor43 normal44 normal45 normal46 normal47 normal48  
## tumor1 0.8771996 0.7977750 0.7434836 0.7053507 0.8080762 0.7118493  
## tumor2 0.8797360 0.8042564 0.7479590 0.7091780 0.8060947 0.7050844  
## tumor3 0.8258716 0.7748192 0.7120658 0.6690683 0.7785381 0.7273069  
## tumor4 0.8270763 0.7788760 0.7131366 0.6726151 0.7804267 0.7151630  
## tumor5 0.8289491 0.7411438 0.6922697 0.6729792 0.7623526 0.6971578  
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## tumor7 0.8160674 0.7665167 0.7071929 0.6888651 0.7838141 0.7129198  
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## tumor9 0.8901107 0.8416044 0.7730060 0.7136700 0.8455501 0.7773153  
## tumor10 0.8926539 0.8049482 0.7380807 0.6849965 0.8214281 0.7469033  
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## tumor13 0.8685629 0.8670171 0.7944235 0.7424688 0.8510272 0.7612775  
## tumor14 0.8942509 0.7500494 0.7048209 0.6688311 0.7837254 0.7256784  
## tumor15 0.9064110 0.7432254 0.6962639 0.6589309 0.7692896 0.7272842  
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## tumor28 0.8533771 0.8040002 0.7571561 0.7251860 0.8241695 0.7507139  
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## tumor32 0.9027824 0.8181878 0.7566953 0.7373465 0.8334560 0.7531428  
## tumor33 0.8819619 0.7999064 0.7518092 0.7176525 0.8144848 0.7617450  
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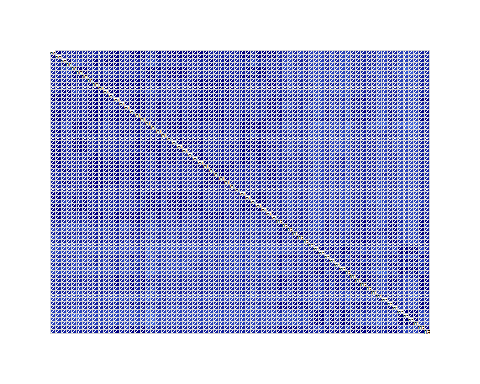
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## normal71 0.7952419 0.7961015 0.8183806 0.8297415 0.8132343 0.8096187  
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## tumor10 0.8974692 0.9876368 0.9886299 1.0000000 0.9178245 0.9139446  
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## normal71 0.8020237 0.8204275 0.8190495 0.8321048 0.8171458 0.8256672  
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## tumor25 tumor26 tumor27 tumor28 tumor29 tumor30  
## tumor1 0.9112742 0.9041425 0.9035659 0.9044658 0.8962315 0.8909557  
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## tumor8 0.8989080 0.8912548 0.9098631 0.9153952 0.9153062 0.9196654  
## tumor9 0.8958750 0.8863970 0.9067953 0.9170002 0.9216391 0.9140336  
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## tumor12 0.8819891 0.8819987 0.8937432 0.9053664 0.9090618 0.9207911  
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## tumor14 0.9104403 0.9150715 0.9269818 0.9279727 0.9363324 0.9273692  
## tumor15 0.9155908 0.9165176 0.9295106 0.9279051 0.9341686 0.9276834  
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## tumor17 0.9001889 0.8909155 0.9136069 0.9231656 0.9341612 0.8925437  
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## tumor28 0.9182713 0.9173076 0.9827091 1.0000000 0.9846422 0.9130746  
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## tumor43 normal44 normal45 normal46 normal47 normal48  
## tumor1 0.9030357 0.8232075 0.7888118 0.7811121 0.8076996 0.7144906  
## tumor2 0.9016669 0.8240383 0.7897708 0.7813340 0.8052779 0.7080774  
## tumor3 0.9011404 0.8357408 0.8038972 0.7958691 0.8283155 0.7325788  
## tumor4 0.9100706 0.8437671 0.8172561 0.8112242 0.8319270 0.7238533  
## tumor5 0.9130029 0.8390813 0.8035785 0.7948158 0.8214129 0.7388285  
## tumor6 0.9098163 0.8360149 0.7957581 0.7882315 0.8218606 0.7399735  
## tumor7 0.9207555 0.8365804 0.8032716 0.8001606 0.8280640 0.7373586  
## tumor8 0.9341498 0.8509014 0.8139403 0.8082326 0.8443679 0.7472614  
## tumor9 0.9442880 0.8857490 0.8541148 0.8464359 0.8638748 0.7586345  
## tumor10 0.9387808 0.8661187 0.8334260 0.8280278 0.8450240 0.7335483  
## tumor11 0.9140798 0.8294484 0.8037248 0.8045668 0.8305826 0.7265233  
## tumor12 0.9202986 0.8341970 0.8121534 0.8162988 0.8365415 0.7233775  
## tumor13 0.9273615 0.9004825 0.8784265 0.8703668 0.8722760 0.7426041  
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## tumor15 0.9266832 0.8252669 0.8018131 0.7988255 0.8353477 0.7439342  
## tumor16 0.9328535 0.9352245 0.9005771 0.8795665 0.8826900 0.7857575  
## tumor17 0.9323934 0.9171990 0.8903389 0.8700252 0.8735056 0.7628328  
## tumor18 0.9356023 0.9314963 0.9040229 0.8847882 0.8932485 0.7983759  
## tumor19 0.9056490 0.8236948 0.7901040 0.7856835 0.8100997 0.7213540  
## tumor20 0.9081544 0.8357108 0.8043936 0.8106256 0.8266888 0.7301110  
## tumor21 0.9407683 0.8370007 0.8102125 0.8078008 0.8414502 0.7532630  
## tumor22 0.9079918 0.8273405 0.8085120 0.8310039 0.8589745 0.7709265  
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## tumor24 0.9216066 0.8443595 0.8094985 0.8027599 0.8262310 0.7291885  
## tumor25 0.9219122 0.8410314 0.8061539 0.8013661 0.8306491 0.7503614  
## tumor26 0.9139140 0.8280820 0.7933493 0.7902952 0.8188853 0.7250452  
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## tumor30 0.9301077 0.8513668 0.8177775 0.8207003 0.8520599 0.7665206  
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## tumor33 0.9313834 0.8638462 0.8326721 0.8317662 0.8417507 0.7338798  
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## tumor36 0.8965422 0.8086057 0.7719826 0.7647802 0.7990375 0.7068609  
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## normal47 0.8651091 0.9090544 0.8962757 0.8896007 1.0000000 0.9098384  
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## tumor3 0.8018465 0.8014784 0.7505780 0.7689266 0.8253657 0.7747916  
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## tumor5 0.8004703 0.7857069 0.7532116 0.7623170 0.8072267 0.7596495  
## tumor6 0.7950231 0.7816881 0.7528504 0.7609380 0.8048077 0.7584717  
## tumor7 0.7996331 0.7979337 0.7607399 0.7724109 0.8077334 0.7752797  
## tumor8 0.8136642 0.8179754 0.7655271 0.7821733 0.8312280 0.7864994  
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## tumor2 0.7908535 0.8174311 0.7948144 0.7632719 0.7800697 0.7911513  
## tumor3 0.8197848 0.8280845 0.8235034 0.7967186 0.8067953 0.8141309  
## tumor4 0.8361235 0.8311806 0.8316297 0.8085617 0.8082515 0.8226269  
## tumor5 0.8074656 0.7999145 0.7973423 0.7774914 0.8017993 0.8083039  
## tumor6 0.8022783 0.8000558 0.7994621 0.7742106 0.8001856 0.8026951  
## tumor7 0.8122241 0.8172327 0.8104076 0.7989466 0.8072352 0.8102397  
## tumor8 0.8293964 0.8290324 0.8257178 0.7980112 0.8190395 0.8232694  
## tumor9 0.8737977 0.8344066 0.8540119 0.8154492 0.8411265 0.8549426  
## tumor10 0.8477269 0.8256049 0.8362022 0.8021603 0.8201211 0.8334253  
## tumor11 0.8186119 0.8344517 0.8316131 0.8222228 0.8063143 0.8155369  
## tumor12 0.8312131 0.8590343 0.8533247 0.8477644 0.8088588 0.8237020  
## tumor13 0.8965547 0.8396772 0.8607067 0.8315521 0.8442344 0.8726142  
## tumor14 0.8144320 0.8541096 0.8328271 0.8281946 0.8087042 0.8208951  
## tumor15 0.8065700 0.8466081 0.8229316 0.8184831 0.8061615 0.8170928  
## tumor16 0.9052786 0.8315719 0.8462863 0.8077522 0.8670375 0.8877083  
## tumor17 0.8908955 0.8322548 0.8441329 0.8043758 0.8505097 0.8737448  
## tumor18 0.9067173 0.8424762 0.8552292 0.8228015 0.8793290 0.8941610  
## tumor19 0.7902306 0.7994214 0.7927863 0.7754288 0.7846887 0.7913544  
## tumor20 0.8075638 0.8060012 0.8161790 0.8030231 0.7993641 0.8076833  
## tumor21 0.8199850 0.8494277 0.8337996 0.8190217 0.8152641 0.8199331  
## tumor22 0.8341091 0.8639296 0.8759260 0.8935020 0.8343338 0.8311151  
## tumor23 0.8119207 0.8244233 0.8059207 0.7881461 0.7960991 0.8025789  
## tumor24 0.8206203 0.8301342 0.8092587 0.7929937 0.7973833 0.8082213  
## tumor25 0.8143430 0.8294338 0.8146290 0.8014167 0.8087043 0.8098379  
## tumor26 0.8057552 0.8307382 0.8067989 0.7959737 0.7898930 0.7972211  
## tumor27 0.8165609 0.8395138 0.8136743 0.8022071 0.8047811 0.8103952  
## tumor28 0.8230430 0.8319830 0.8171508 0.8011399 0.8055944 0.8170238  
## tumor29 0.8466473 0.8509047 0.8387877 0.8221233 0.8268880 0.8358707  
## tumor30 0.8335031 0.8503442 0.8489472 0.8438533 0.8304061 0.8285553  
## tumor31 0.8221313 0.8366590 0.8454649 0.8347044 0.8162416 0.8190617  
## tumor32 0.8495658 0.8555336 0.8654243 0.8570342 0.8425627 0.8429140  
## tumor33 0.8422704 0.8130354 0.8282494 0.8040732 0.8151792 0.8295071  
## tumor34 0.8093194 0.8223087 0.8337963 0.8278772 0.8015373 0.8033833  
## tumor35 0.7838478 0.8205933 0.7967323 0.7830885 0.7854050 0.7907074  
## tumor36 0.7751533 0.8073633 0.7865493 0.7696522 0.7709269 0.7787952  
## tumor37 0.8096708 0.8261686 0.8113889 0.7899511 0.8125531 0.8234532  
## tumor38 0.7859618 0.8196268 0.7940313 0.7759025 0.7893428 0.7943034  
## tumor39 0.7708504 0.8050649 0.7816821 0.7732211 0.7889152 0.7785592  
## tumor40 0.8102987 0.8226178 0.8066374 0.7920528 0.8036353 0.8057439  
## tumor41 0.8027113 0.8228426 0.8058368 0.7922609 0.8017391 0.8011765  
## tumor42 0.8492398 0.8418248 0.8317017 0.8084606 0.8236514 0.8364821  
## tumor43 0.8737164 0.8568541 0.8495902 0.8235309 0.8424144 0.8544815  
## normal44 0.9379535 0.8411809 0.8715975 0.8194147 0.8929702 0.9169335  
## normal45 0.9124811 0.8086934 0.8532730 0.8009316 0.8970976 0.9576870  
## normal46 0.8958973 0.7948417 0.8903438 0.8622564 0.8874443 0.9389889  
## normal47 0.9070042 0.8891353 0.9071068 0.8699033 0.9688515 0.9467066  
## normal48 0.8045073 0.8030436 0.8219619 0.7891847 0.9433917 0.8666591  
## normal49 0.9478065 0.8538200 0.8880739 0.8273969 0.9312402 0.9303835  
## normal50 0.8860016 0.8564461 0.8624198 0.8310587 0.8666713 0.8767491  
## normal51 0.8524001 0.8176067 0.8378252 0.8169492 0.8545012 0.8426752  
## normal52 0.8610924 0.8268953 0.8496043 0.8273610 0.8581374 0.8486545  
## normal53 0.9252296 0.8555252 0.8992246 0.8477090 0.9328971 0.9620522  
## normal54 0.8429269 0.8403004 0.8745774 0.8603216 0.8660041 0.8404593  
## normal55 0.8995236 0.8562229 0.9040812 0.8487929 0.9340239 0.9191974  
## normal56 0.8719939 0.8274385 0.8516134 0.8293358 0.8644654 0.8569768  
## normal57 0.7900412 0.7977430 0.7818270 0.7979093 0.8608465 0.7998203  
## normal58 0.9800690 0.8595257 0.8838221 0.8505163 0.9076259 0.9227958  
## normal59 0.9725119 0.8303926 0.8754609 0.8334524 0.9082689 0.9274565  
## normal60 0.9640663 0.8396094 0.8713481 0.8310509 0.9189468 0.9313964  
## normal61 1.0000000 0.8461175 0.8747571 0.8374887 0.8901012 0.9149988  
## normal62 0.8461175 1.0000000 0.8548409 0.8402133 0.8506420 0.8470206  
## normal63 0.8747571 0.8548409 1.0000000 0.9086741 0.8882324 0.8859243  
## normal64 0.8374887 0.8402133 0.9086741 1.0000000 0.8481199 0.8374207  
## normal65 0.8901012 0.8506420 0.8882324 0.8481199 1.0000000 0.9538273  
## normal66 0.9149988 0.8470206 0.8859243 0.8374207 0.9538273 1.0000000  
## normal67 0.8600991 0.8341267 0.8419102 0.8157575 0.8632382 0.8494977  
## normal68 0.8027651 0.8131918 0.8358254 0.8295595 0.8412929 0.8156095  
## normal69 0.8250978 0.8095519 0.8349863 0.8273936 0.8350925 0.8203158  
## normal70 0.8032115 0.8054001 0.8153287 0.8114811 0.8396935 0.8066784  
## normal71 0.9352508 0.8302004 0.8860206 0.8535363 0.9055444 0.9408313  
## normal72 0.9667323 0.8448223 0.8858540 0.8521094 0.9124930 0.9234059  
## normal67 normal68 normal69 normal70 normal71 normal72  
## tumor1 0.7482626 0.7545352 0.7424701 0.7164082 0.7952419 0.8034933  
## tumor2 0.7463160 0.7517780 0.7414670 0.7137476 0.7961015 0.8038589  
## tumor3 0.7520424 0.7633918 0.7446480 0.7173360 0.8183806 0.8371804  
## tumor4 0.7522267 0.7663633 0.7463186 0.7135369 0.8297415 0.8511014  
## tumor5 0.7530275 0.7554250 0.7471971 0.7222006 0.8132343 0.8246311  
## tumor6 0.7520358 0.7549206 0.7477581 0.7237970 0.8096187 0.8231327  
## tumor7 0.7596233 0.7723367 0.7603429 0.7300925 0.8115386 0.8317157  
## tumor8 0.7659124 0.7738298 0.7618678 0.7349389 0.8264764 0.8432358  
## tumor9 0.7819241 0.7811980 0.7713997 0.7415947 0.8614295 0.8781955  
## tumor10 0.7642588 0.7691540 0.7596202 0.7262107 0.8418308 0.8573682  
## tumor11 0.7546973 0.7821356 0.7569115 0.7257247 0.8211227 0.8374427  
## tumor12 0.7610281 0.7801724 0.7607111 0.7277542 0.8254930 0.8405950  
## tumor13 0.7870875 0.7843427 0.7766745 0.7354072 0.8979936 0.9060626  
## tumor14 0.7542746 0.7772442 0.7538106 0.7259808 0.8187586 0.8295463  
## tumor15 0.7542717 0.7784209 0.7530506 0.7266812 0.8129316 0.8248298  
## tumor16 0.8064580 0.7791508 0.7838310 0.7527868 0.9052541 0.9129700  
## tumor17 0.7911368 0.7739647 0.7746735 0.7387344 0.9006981 0.9010003  
## tumor18 0.8120157 0.7955867 0.7951382 0.7666615 0.9075721 0.9153644  
## tumor19 0.7356309 0.7426883 0.7336098 0.7021126 0.8020237 0.8090367  
## tumor20 0.7494992 0.7579897 0.7491661 0.7152388 0.8204275 0.8249959  
## tumor21 0.7670113 0.7824633 0.7672516 0.7401283 0.8190495 0.8343793  
## tumor22 0.7759827 0.8005824 0.7772826 0.7526934 0.8321048 0.8480840  
## tumor23 0.7578270 0.7598530 0.7499644 0.7252446 0.8171458 0.8236664  
## tumor24 0.7553982 0.7585174 0.7468424 0.7174407 0.8256672 0.8314162  
## tumor25 0.7640200 0.7698775 0.7574609 0.7348237 0.8216269 0.8282094  
## tumor26 0.7539374 0.7599208 0.7486580 0.7218999 0.8097289 0.8158779  
## tumor27 0.7635016 0.7713439 0.7606847 0.7345308 0.8198800 0.8319575  
## tumor28 0.7575687 0.7661980 0.7549084 0.7241041 0.8264565 0.8367965  
## tumor29 0.7769589 0.7821371 0.7720331 0.7417615 0.8484894 0.8599033  
## tumor30 0.7862804 0.8016915 0.7846313 0.7627600 0.8387718 0.8463795  
## tumor31 0.7697699 0.7907384 0.7677743 0.7392724 0.8323485 0.8430623  
## tumor32 0.8005308 0.8102295 0.7959022 0.7715915 0.8609814 0.8642123  
## tumor33 0.7695862 0.7749905 0.7692369 0.7343305 0.8462022 0.8532533  
## tumor34 0.7525467 0.7824536 0.7579617 0.7263400 0.8089699 0.8253479  
## tumor35 0.7372968 0.7532072 0.7373207 0.7127610 0.7921987 0.8021796  
## tumor36 0.7303828 0.7464044 0.7345393 0.7085970 0.7879281 0.7920854  
## tumor37 0.7631952 0.7695374 0.7617833 0.7344627 0.8192296 0.8255328  
## tumor38 0.7464817 0.7551684 0.7455600 0.7225208 0.7858334 0.8006811  
## tumor39 0.7405470 0.7645075 0.7383751 0.7177197 0.7834323 0.7971061  
## tumor40 0.7568226 0.7677618 0.7523876 0.7245721 0.8201713 0.8312926  
## tumor41 0.7594878 0.7729305 0.7567652 0.7323628 0.8079181 0.8220733  
## tumor42 0.7715311 0.7746152 0.7672333 0.7365514 0.8411162 0.8554501  
## tumor43 0.7883453 0.7807941 0.7785205 0.7496714 0.8598360 0.8752632  
## normal44 0.8473329 0.8009642 0.8101224 0.7863293 0.9416300 0.9400215  
## normal45 0.8155550 0.7753641 0.7869417 0.7586916 0.9470956 0.9126804  
## normal46 0.8170911 0.7901133 0.8031595 0.7720864 0.9291150 0.8957609  
## normal47 0.8726400 0.8535994 0.8497572 0.8424331 0.9219129 0.9294890  
## normal48 0.8203139 0.8032352 0.7847831 0.8133393 0.8090990 0.8328285  
## normal49 0.8749482 0.8158212 0.8360332 0.8301780 0.9106087 0.9344977  
## normal50 0.9159590 0.9226981 0.9023727 0.8844435 0.8677385 0.8776662  
## normal51 0.9764801 0.9245812 0.9718350 0.9643903 0.8274174 0.8480119  
## normal52 0.9719534 0.9424908 0.9736855 0.9606055 0.8368073 0.8554247  
## normal53 0.8613028 0.8286994 0.8350842 0.8148725 0.9619486 0.9375368  
## normal54 0.9397389 0.9443274 0.9527268 0.9506918 0.8217304 0.8393428  
## normal55 0.9081167 0.8657948 0.8810582 0.8783848 0.9098547 0.9084419  
## normal56 0.9755338 0.9195810 0.9681073 0.9543738 0.8509320 0.8711631  
## normal57 0.9009240 0.8650479 0.8836539 0.9101966 0.7596083 0.7941032  
## normal58 0.8608378 0.8130888 0.8285161 0.8087501 0.9361877 0.9771993  
## normal59 0.8467842 0.8031751 0.8146416 0.7872177 0.9475926 0.9810980  
## normal60 0.8555549 0.8044155 0.8186516 0.7970542 0.9506541 0.9760153  
## normal61 0.8600991 0.8027651 0.8250978 0.8032115 0.9352508 0.9667323  
## normal62 0.8341267 0.8131918 0.8095519 0.8054001 0.8302004 0.8448223  
## normal63 0.8419102 0.8358254 0.8349863 0.8153287 0.8860206 0.8858540  
## normal64 0.8157575 0.8295595 0.8273936 0.8114811 0.8535363 0.8521094  
## normal65 0.8632382 0.8412929 0.8350925 0.8396935 0.9055444 0.9124930  
## normal66 0.8494977 0.8156095 0.8203158 0.8066784 0.9408313 0.9234059  
## normal67 1.0000000 0.9195807 0.9648543 0.9553271 0.8341110 0.8580968  
## normal68 0.9195807 1.0000000 0.9413491 0.9332592 0.7987970 0.8155759  
## normal69 0.9648543 0.9413491 1.0000000 0.9727037 0.8095718 0.8267769  
## normal70 0.9553271 0.9332592 0.9727037 1.0000000 0.7829807 0.7995332  
## normal71 0.8341110 0.7987970 0.8095718 0.7829807 1.0000000 0.9497693  
## normal72 0.8580968 0.8155759 0.8267769 0.7995332 0.9497693 1.0000000

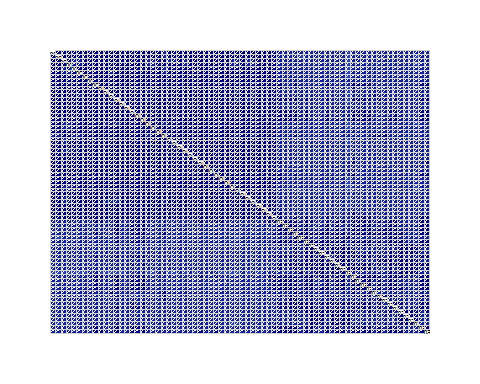
# visualize the correlation matrix  
library(corrgram)

## Warning: package 'corrgram' was built under R version 3.4.2

corrgram(tdata)



corrgram(log(tdata))



Based on the heatmaps we generated, there is no missing value in out data. We confirmed this by using the code below.

# Check missing values  
any(is.na(tdata))

## [1] FALSE

What do you observe? differences between two heatmaps(original data and log-transformed data).

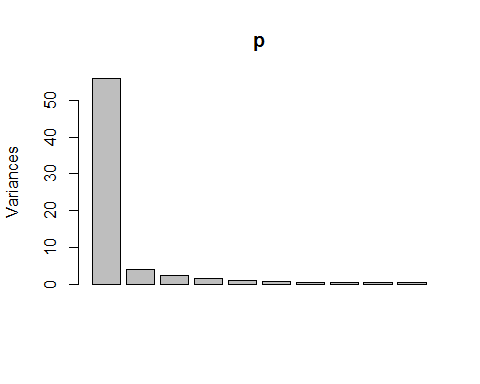
## Task 2

We used prcomp() to generate a PCA and use plot() and summary() to inspect the results. We also created biplots.

p <- prcomp(tdata,scale=TRUE)  
summary(p)

## Importance of components%s:  
## PC1 PC2 PC3 PC4 PC5 PC6  
## Standard deviation 7.4807 2.02059 1.48838 1.25235 0.92381 0.81535  
## Proportion of Variance 0.7772 0.05671 0.03077 0.02178 0.01185 0.00923  
## Cumulative Proportion 0.7772 0.83393 0.86470 0.88648 0.89833 0.90757  
## PC7 PC8 PC9 PC10 PC11 PC12  
## Standard deviation 0.71572 0.69210 0.65840 0.62961 0.61872 0.6119  
## Proportion of Variance 0.00711 0.00665 0.00602 0.00551 0.00532 0.0052  
## Cumulative Proportion 0.91468 0.92133 0.92735 0.93286 0.93818 0.9434  
## PC13 PC14 PC15 PC16 PC17 PC18  
## Standard deviation 0.57203 0.54433 0.52665 0.50654 0.48816 0.46302  
## Proportion of Variance 0.00454 0.00412 0.00385 0.00356 0.00331 0.00298  
## Cumulative Proportion 0.94792 0.95204 0.95589 0.95945 0.96276 0.96574  
## PC19 PC20 PC21 PC22 PC23 PC24  
## Standard deviation 0.45885 0.44133 0.42979 0.41682 0.4072 0.37662  
## Proportion of Variance 0.00292 0.00271 0.00257 0.00241 0.0023 0.00197  
## Cumulative Proportion 0.96866 0.97137 0.97394 0.97635 0.9787 0.98062  
## PC25 PC26 PC27 PC28 PC29 PC30  
## Standard deviation 0.34652 0.33637 0.31306 0.30382 0.28715 0.26650  
## Proportion of Variance 0.00167 0.00157 0.00136 0.00128 0.00115 0.00099  
## Cumulative Proportion 0.98229 0.98386 0.98522 0.98650 0.98765 0.98864  
## PC31 PC32 PC33 PC34 PC35 PC36  
## Standard deviation 0.25683 0.24991 0.23622 0.2238 0.21747 0.19653  
## Proportion of Variance 0.00092 0.00087 0.00078 0.0007 0.00066 0.00054  
## Cumulative Proportion 0.98955 0.99042 0.99119 0.9919 0.99255 0.99308  
## PC37 PC38 PC39 PC40 PC41 PC42  
## Standard deviation 0.19073 0.18260 0.17597 0.17105 0.16638 0.15902  
## Proportion of Variance 0.00051 0.00046 0.00043 0.00041 0.00038 0.00035  
## Cumulative Proportion 0.99359 0.99405 0.99448 0.99489 0.99527 0.99562  
## PC43 PC44 PC45 PC46 PC47 PC48  
## Standard deviation 0.15601 0.14272 0.14095 0.13999 0.13605 0.12614  
## Proportion of Variance 0.00034 0.00028 0.00028 0.00027 0.00026 0.00022  
## Cumulative Proportion 0.99596 0.99624 0.99652 0.99679 0.99705 0.99727  
## PC49 PC50 PC51 PC52 PC53 PC54  
## Standard deviation 0.12412 0.1210 0.1205 0.11745 0.11039 0.10582  
## Proportion of Variance 0.00021 0.0002 0.0002 0.00019 0.00017 0.00016  
## Cumulative Proportion 0.99749 0.9977 0.9979 0.99808 0.99825 0.99841  
## PC55 PC56 PC57 PC58 PC59 PC60  
## Standard deviation 0.10351 0.10121 0.09749 0.09511 0.09123 0.08946  
## Proportion of Variance 0.00015 0.00014 0.00013 0.00013 0.00012 0.00011  
## Cumulative Proportion 0.99856 0.99870 0.99883 0.99896 0.99907 0.99918  
## PC61 PC62 PC63 PC64 PC65 PC66  
## Standard deviation 0.08558 0.07934 0.07769 0.07665 0.07314 0.07267  
## Proportion of Variance 0.00010 0.00009 0.00008 0.00008 0.00007 0.00007  
## Cumulative Proportion 0.99928 0.99937 0.99945 0.99954 0.99961 0.99968  
## PC67 PC68 PC69 PC70 PC71 PC72  
## Standard deviation 0.07037 0.06779 0.06536 0.06066 0.05686 0.04477  
## Proportion of Variance 0.00007 0.00006 0.00006 0.00005 0.00004 0.00003  
## Cumulative Proportion 0.99975 0.99982 0.99988 0.99993 0.99997 1.00000

plot(p)

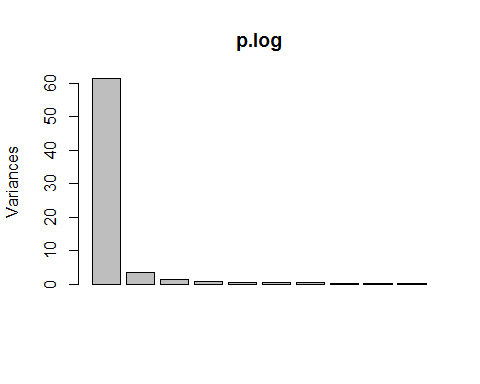


Based on these results, the first six PCs are needed to explain at least 90% of the variation.

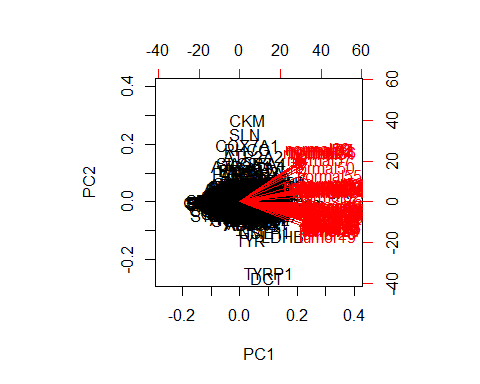
p.log <- prcomp(log(tdata),scale=TRUE)  
summary(p.log)

## Importance of components%s:  
## PC1 PC2 PC3 PC4 PC5 PC6  
## Standard deviation 7.8300 1.84983 1.14255 0.86721 0.71614 0.59917  
## Proportion of Variance 0.8515 0.04753 0.01813 0.01045 0.00712 0.00499  
## Cumulative Proportion 0.8515 0.89903 0.91716 0.92761 0.93473 0.93972  
## PC7 PC8 PC9 PC10 PC11 PC12  
## Standard deviation 0.5631 0.53948 0.5231 0.50293 0.47144 0.44985  
## Proportion of Variance 0.0044 0.00404 0.0038 0.00351 0.00309 0.00281  
## Cumulative Proportion 0.9441 0.94816 0.9520 0.95548 0.95856 0.96137  
## PC13 PC14 PC15 PC16 PC17 PC18  
## Standard deviation 0.44215 0.4240 0.41427 0.38085 0.37406 0.3700  
## Proportion of Variance 0.00272 0.0025 0.00238 0.00201 0.00194 0.0019  
## Cumulative Proportion 0.96409 0.9666 0.96897 0.97098 0.97293 0.9748  
## PC19 PC20 PC21 PC22 PC23 PC24  
## Standard deviation 0.35377 0.34548 0.34086 0.32470 0.31525 0.30910  
## Proportion of Variance 0.00174 0.00166 0.00161 0.00146 0.00138 0.00133  
## Cumulative Proportion 0.97657 0.97822 0.97984 0.98130 0.98268 0.98401  
## PC25 PC26 PC27 PC28 PC29 PC30  
## Standard deviation 0.29058 0.28306 0.26334 0.24568 0.2403 0.22856  
## Proportion of Variance 0.00117 0.00111 0.00096 0.00084 0.0008 0.00073  
## Cumulative Proportion 0.98518 0.98629 0.98726 0.98810 0.9889 0.98962  
## PC31 PC32 PC33 PC34 PC35 PC36  
## Standard deviation 0.2082 0.20289 0.19712 0.18647 0.18384 0.18051  
## Proportion of Variance 0.0006 0.00057 0.00054 0.00048 0.00047 0.00045  
## Cumulative Proportion 0.9902 0.99080 0.99134 0.99182 0.99229 0.99274  
## PC37 PC38 PC39 PC40 PC41 PC42  
## Standard deviation 0.17759 0.1707 0.16389 0.15658 0.15629 0.15198  
## Proportion of Variance 0.00044 0.0004 0.00037 0.00034 0.00034 0.00032  
## Cumulative Proportion 0.99318 0.9936 0.99396 0.99430 0.99464 0.99496  
## PC43 PC44 PC45 PC46 PC47 PC48  
## Standard deviation 0.1475 0.14305 0.13765 0.13604 0.13257 0.13087  
## Proportion of Variance 0.0003 0.00028 0.00026 0.00026 0.00024 0.00024  
## Cumulative Proportion 0.9953 0.99554 0.99581 0.99606 0.99631 0.99655  
## PC49 PC50 PC51 PC52 PC53 PC54  
## Standard deviation 0.12830 0.12631 0.12277 0.1203 0.11620 0.11605  
## Proportion of Variance 0.00023 0.00022 0.00021 0.0002 0.00019 0.00019  
## Cumulative Proportion 0.99678 0.99700 0.99721 0.9974 0.99760 0.99778  
## PC55 PC56 PC57 PC58 PC59 PC60  
## Standard deviation 0.11298 0.11124 0.10899 0.10791 0.10302 0.10181  
## Proportion of Variance 0.00018 0.00017 0.00016 0.00016 0.00015 0.00014  
## Cumulative Proportion 0.99796 0.99813 0.99830 0.99846 0.99861 0.99875  
## PC61 PC62 PC63 PC64 PC65 PC66  
## Standard deviation 0.09927 0.09691 0.09378 0.09228 0.09059 0.08702  
## Proportion of Variance 0.00014 0.00013 0.00012 0.00012 0.00011 0.00011  
## Cumulative Proportion 0.99889 0.99902 0.99914 0.99926 0.99937 0.99948  
## PC67 PC68 PC69 PC70 PC71 PC72  
## Standard deviation 0.08522 0.08398 0.08263 0.07899 0.07686 0.06651  
## Proportion of Variance 0.00010 0.00010 0.00009 0.00009 0.00008 0.00006  
## Cumulative Proportion 0.99958 0.99968 0.99977 0.99986 0.99994 1.00000

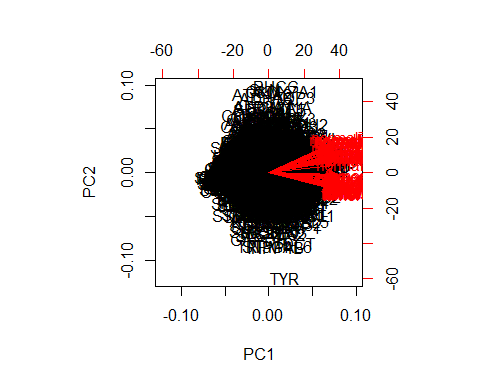
plot(p.log)

 Based on these results, the first three PCs are needed to explain at least 90% of the variation.

# original data  
biplot(p)



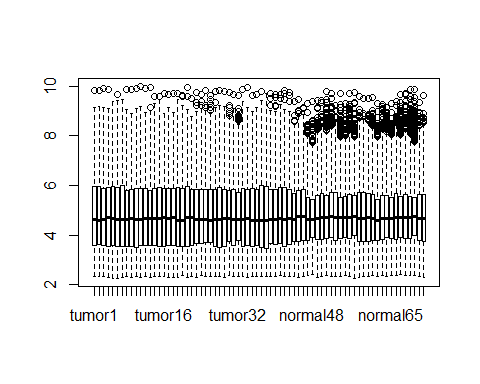
# log-transformed data  
biplot(p.log)

 These biplots shows that most variation is capured by PC1. This can be stated because all of the arrows range from 0.1 to 0.4 over the PC1 axis. PC2 shows more variation, about half of the samples are grouped on the positive side of the PC2 axix, these are all the samples derived from healthy tissue.The other half is grouped on the negative side of the PC2 axix, these are all the samples derived form tumor samples.

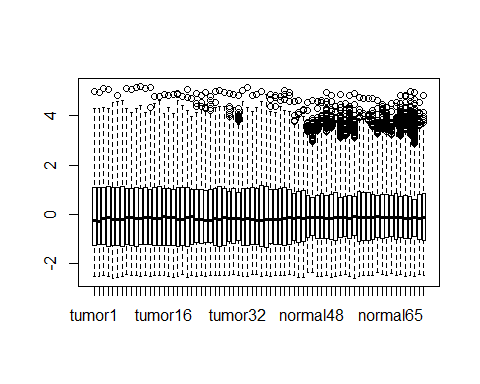
## Task 3

Here we try different normalisation methods to help us decide which is best. The data was mean normalised (assigned to the mn\_tdata variable) and mean/variance normalised (assigned to the mvn\_tdata variable). Boxplots were created to visualise the difference between these normalisation methods. The first boxplot created in the following block of code produces a plot of the non-normalised log of the original data. This can be used to compare to the normalised plots and visualise the difference between the not nomalised and the normalised data. The plots here

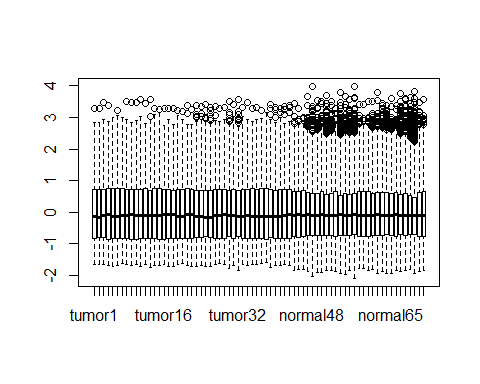
# mean normalisation  
mn\_tdata <- scale(log(tdata), center=TRUE, scale=FALSE)  
# mean/variance normalisation  
mvn\_tdata <- scale(log(tdata), center=TRUE, scale=TRUE)  
# boxplot on log-transformed data  
boxplot(log(tdata))



# boxplot on mean normalised data  
boxplot(mn\_tdata)

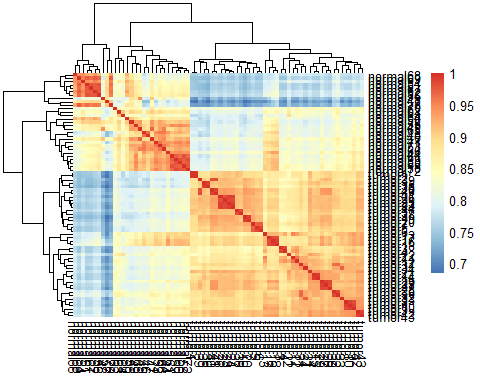


# boxplot on mean/variance normalised data  
boxplot(mvn\_tdata)

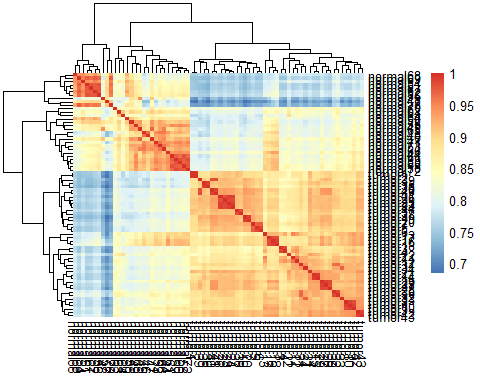


In our opinion, the mean normalisation is in this case the better option. Because the purpose of this project is to analyze human transcriptome variation across healthy tissues and diseased (cancer) tissues. Therefore we expect there would be differences between tumor and mormal samples. The mean/variance normalisation could remove the biological variation we are looking for. Whilest the mean normalisation minimilises the techical variaton it will not interfere with the potentialy interesting biological variation.

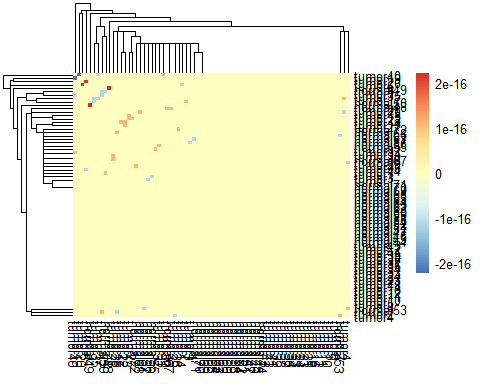
#Comparing correlation  
cor.matrix.log <- cor(log(tdata))  
cor.mn\_tdata <- cor(mn\_tdata)  
pheatmap(cor.matrix.log)



pheatmap(cor.mn\_tdata)



# calculate changes  
change <- cor.matrix.log - cor.mn\_tdata  
pheatmap(change)

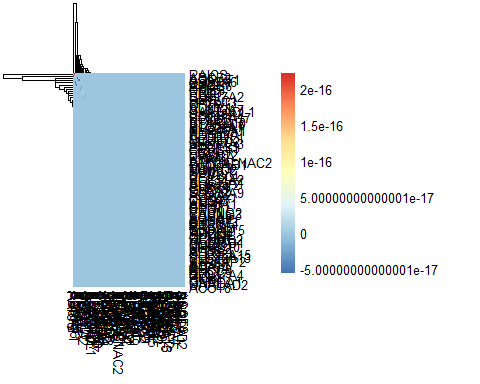


We also inspected the correlation between normalized and original values across first 100 genes and isualized the change induced by the normalization

# select first 100 genes out of the tdata  
genes <- skin.df[,1:100]  
cor.genes <- cor(log(genes))  
#normalise the genes data frame   
mn\_genes <- scale(log(genes),center=TRUE, scale=FALSE)  
# calculate the difference and visualize the change  
cor.mn\_genes <- cor(mn\_genes)  
genes.diff <- cor.genes - cor.mn\_genes  
summary(genes.diff)

## NAALAD2 NAALADL1 ACOT8 GNPDA1   
## Min. :0 Min. :0.000e+00 Min. :0 Min. :0   
## 1st Qu.:0 1st Qu.:0.000e+00 1st Qu.:0 1st Qu.:0   
## Median :0 Median :0.000e+00 Median :0 Median :0   
## Mean :0 Mean :4.337e-21 Mean :0 Mean :0   
## 3rd Qu.:0 3rd Qu.:0.000e+00 3rd Qu.:0 3rd Qu.:0   
## Max. :0 Max. :4.337e-19 Max. :0 Max. :0   
## KCNE3 GNE HCN4 PIGK SLC17A4   
## Min. :-5.421e-20 Min. :0 Min. :0 Min. :0 Min. :0   
## 1st Qu.: 0.000e+00 1st Qu.:0 1st Qu.:0 1st Qu.:0 1st Qu.:0   
## Median : 0.000e+00 Median :0 Median :0 Median :0 Median :0   
## Mean :-5.421e-22 Mean :0 Mean :0 Mean :0 Mean :0   
## 3rd Qu.: 0.000e+00 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0   
## Max. : 0.000e+00 Max. :0 Max. :0 Max. :0 Max. :0   
## ABCC5 ABCB6 ABCC9 ABCF2   
## Min. :0 Min. :-5.551e-17 Min. :0 Min. :0.00e+00   
## 1st Qu.:0 1st Qu.: 0.000e+00 1st Qu.:0 1st Qu.:0.00e+00   
## Median :0 Median : 0.000e+00 Median :0 Median :0.00e+00   
## Mean :0 Mean :-5.551e-19 Mean :0 Mean :2.22e-18   
## 3rd Qu.:0 3rd Qu.: 0.000e+00 3rd Qu.:0 3rd Qu.:0.00e+00   
## Max. :0 Max. : 0.000e+00 Max. :0 Max. :2.22e-16   
## ATP9A KCNK7 UST ADA   
## Min. :0 Min. :-5.551e-17 Min. :-1.388e-17 Min. :0   
## 1st Qu.:0 1st Qu.: 0.000e+00 1st Qu.: 0.000e+00 1st Qu.:0   
## Median :0 Median : 0.000e+00 Median : 0.000e+00 Median :0   
## Mean :0 Mean :-5.551e-19 Mean :-1.388e-19 Mean :0   
## 3rd Qu.:0 3rd Qu.: 0.000e+00 3rd Qu.: 0.000e+00 3rd Qu.:0   
## Max. :0 Max. : 0.000e+00 Max. : 0.000e+00 Max. :0   
## AASS ATP6AP2 LPCAT3 CHST4 SLC25A13  
## Min. :0 Min. :0 Min. :-3.469e-18 Min. :0 Min. :0   
## 1st Qu.:0 1st Qu.:0 1st Qu.: 0.000e+00 1st Qu.:0 1st Qu.:0   
## Median :0 Median :0 Median : 0.000e+00 Median :0 Median :0   
## Mean :0 Mean :0 Mean :-3.469e-20 Mean :0 Mean :0   
## 3rd Qu.:0 3rd Qu.:0 3rd Qu.: 0.000e+00 3rd Qu.:0 3rd Qu.:0   
## Max. :0 Max. :0 Max. : 0.000e+00 Max. :0 Max. :0   
## SLC25A15 DHRS9 ALG3 NME6 DHRS2   
## Min. :0 Min. :0 Min. :0 Min. :-2.776e-17 Min. :0   
## 1st Qu.:0 1st Qu.:0 1st Qu.:0 1st Qu.: 0.000e+00 1st Qu.:0   
## Median :0 Median :0 Median :0 Median : 0.000e+00 Median :0   
## Mean :0 Mean :0 Mean :0 Mean :-2.776e-19 Mean :0   
## 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0 3rd Qu.: 0.000e+00 3rd Qu.:0   
## Max. :0 Max. :0 Max. :0 Max. : 0.000e+00 Max. :0   
## MFSD10 COQ7 SLC35B1 KCNMB2 GPHN   
## Min. :0 Min. :0 Min. :0 Min. :0 Min. :0   
## 1st Qu.:0 1st Qu.:0 1st Qu.:0 1st Qu.:0 1st Qu.:0   
## Median :0 Median :0 Median :0 Median :0 Median :0   
## Mean :0 Mean :0 Mean :0 Mean :0 Mean :0   
## 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0   
## Max. :0 Max. :0 Max. :0 Max. :0 Max. :0   
## SLC17A2 GLYAT ABCC4 TCIRG1 B3GALT5   
## Min. :-1.388e-17 Min. :0 Min. :0 Min. :0 Min. :0   
## 1st Qu.: 0.000e+00 1st Qu.:0 1st Qu.:0 1st Qu.:0 1st Qu.:0   
## Median : 0.000e+00 Median :0 Median :0 Median :0 Median :0   
## Mean :-1.388e-19 Mean :0 Mean :0 Mean :0 Mean :0   
## 3rd Qu.: 0.000e+00 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0   
## Max. : 0.000e+00 Max. :0 Max. :0 Max. :0 Max. :0   
## RRAGB AKR1A1 B3GNT3 ABCA7 ABCA9 ABCA8   
## Min. :0 Min. :0 Min. :0 Min. :0 Min. :0 Min. :0   
## 1st Qu.:0 1st Qu.:0 1st Qu.:0 1st Qu.:0 1st Qu.:0 1st Qu.:0   
## Median :0 Median :0 Median :0 Median :0 Median :0 Median :0   
## Mean :0 Mean :0 Mean :0 Mean :0 Mean :0 Mean :0   
## 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0   
## Max. :0 Max. :0 Max. :0 Max. :0 Max. :0 Max. :0   
## CACNG3 CACNG2 CDO1 BPNT1 CEPT1 ATP8A1   
## Min. :0 Min. :0 Min. :0 Min. :0 Min. :0 Min. :0   
## 1st Qu.:0 1st Qu.:0 1st Qu.:0 1st Qu.:0 1st Qu.:0 1st Qu.:0   
## Median :0 Median :0 Median :0 Median :0 Median :0 Median :0   
## Mean :0 Mean :0 Mean :0 Mean :0 Mean :0 Mean :0   
## 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0   
## Max. :0 Max. :0 Max. :0 Max. :0 Max. :0 Max. :0   
## PEMT ST3GAL6 CDS1 CDIPT   
## Min. :0 Min. :0.000e+00 Min. :0 Min. :-2.168e-19   
## 1st Qu.:0 1st Qu.:0.000e+00 1st Qu.:0 1st Qu.: 0.000e+00   
## Median :0 Median :0.000e+00 Median :0 Median : 0.000e+00   
## Mean :0 Mean :2.711e-22 Mean :0 Mean :-2.168e-21   
## 3rd Qu.:0 3rd Qu.:0.000e+00 3rd Qu.:0 3rd Qu.: 0.000e+00   
## Max. :0 Max. :2.711e-20 Max. :0 Max. : 0.000e+00   
## LYPLA1 ACAA2 ECI2 SLC30A9   
## Min. :0 Min. :0 Min. :0.000e+00 Min. :0   
## 1st Qu.:0 1st Qu.:0 1st Qu.:0.000e+00 1st Qu.:0   
## Median :0 Median :0 Median :0.000e+00 Median :0   
## Mean :0 Mean :0 Mean :1.388e-19 Mean :0   
## 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0.000e+00 3rd Qu.:0   
## Max. :0 Max. :0 Max. :1.388e-17 Max. :0   
## SLC25A17 SLC9A6 ENOX2 GLRX3   
## Min. :-5.421e-20 Min. :-5.551e-17 Min. :0 Min. :0   
## 1st Qu.: 0.000e+00 1st Qu.: 0.000e+00 1st Qu.:0 1st Qu.:0   
## Median : 0.000e+00 Median : 0.000e+00 Median :0 Median :0   
## Mean :-5.421e-22 Mean :-5.551e-19 Mean :0 Mean :0   
## 3rd Qu.: 0.000e+00 3rd Qu.: 0.000e+00 3rd Qu.:0 3rd Qu.:0   
## Max. : 0.000e+00 Max. : 0.000e+00 Max. :0 Max. :0   
## PRDX4 AGPAT1 AGPAT2 SPTLC1   
## Min. :0 Min. :-5.551e-17 Min. :0 Min. :-3.469e-18   
## 1st Qu.:0 1st Qu.: 0.000e+00 1st Qu.:0 1st Qu.: 0.000e+00   
## Median :0 Median : 0.000e+00 Median :0 Median : 0.000e+00   
## Mean :0 Mean :-5.551e-19 Mean :0 Mean :-3.469e-20   
## 3rd Qu.:0 3rd Qu.: 0.000e+00 3rd Qu.:0 3rd Qu.: 0.000e+00   
## Max. :0 Max. : 0.000e+00 Max. :0 Max. : 0.000e+00   
## SLC35A1 SLC19A2 SLC34A2 CEL DPYSL4   
## Min. :0 Min. :-2.168e-19 Min. :0 Min. :0 Min. :0   
## 1st Qu.:0 1st Qu.: 0.000e+00 1st Qu.:0 1st Qu.:0 1st Qu.:0   
## Median :0 Median : 0.000e+00 Median :0 Median :0 Median :0   
## Mean :0 Mean :-2.168e-21 Mean :0 Mean :0 Mean :0   
## 3rd Qu.:0 3rd Qu.: 0.000e+00 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0   
## Max. :0 Max. : 0.000e+00 Max. :0 Max. :0 Max. :0   
## NPC2 POMT1 TXNRD2 MTHFS SLCO1B1   
## Min. :0 Min. :0 Min. :0 Min. :0 Min. :0   
## 1st Qu.:0 1st Qu.:0 1st Qu.:0 1st Qu.:0 1st Qu.:0   
## Median :0 Median :0 Median :0 Median :0 Median :0   
## Mean :0 Mean :0 Mean :0 Mean :0 Mean :0   
## 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0   
## Max. :0 Max. :0 Max. :0 Max. :0 Max. :0   
## PAICS ST6GALNAC2 ATP5L PMVK RRAGA   
## Min. :0.00e+00 Min. :0 Min. :0 Min. :0 Min. :0   
## 1st Qu.:0.00e+00 1st Qu.:0 1st Qu.:0 1st Qu.:0 1st Qu.:0   
## Median :0.00e+00 Median :0 Median :0 Median :0 Median :0   
## Mean :2.22e-18 Mean :0 Mean :0 Mean :0 Mean :0   
## 3rd Qu.:0.00e+00 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0   
## Max. :2.22e-16 Max. :0 Max. :0 Max. :0 Max. :0   
## B3GNT2 EBP FUT9 CERS1   
## Min. :0 Min. :-2.776e-17 Min. :0 Min. :0   
## 1st Qu.:0 1st Qu.: 0.000e+00 1st Qu.:0 1st Qu.:0   
## Median :0 Median : 0.000e+00 Median :0 Median :0   
## Mean :0 Mean :-2.776e-19 Mean :0 Mean :0   
## 3rd Qu.:0 3rd Qu.: 0.000e+00 3rd Qu.:0 3rd Qu.:0   
## Max. :0 Max. : 0.000e+00 Max. :0 Max. :0   
## SLC12A7 PTGES3 AHCYL1 SLC17A3 MTHFD2   
## Min. :-4.337e-19 Min. :0 Min. :0 Min. :0 Min. :0   
## 1st Qu.: 0.000e+00 1st Qu.:0 1st Qu.:0 1st Qu.:0 1st Qu.:0   
## Median : 0.000e+00 Median :0 Median :0 Median :0 Median :0   
## Mean :-4.337e-21 Mean :0 Mean :0 Mean :0 Mean :0   
## 3rd Qu.: 0.000e+00 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0   
## Max. : 0.000e+00 Max. :0 Max. :0 Max. :0 Max. :0   
## ADCY1 STARD10 CFTR NEU3   
## Min. :0.000e+00 Min. :0.000e+00 Min. :-4.337e-19 Min. :0   
## 1st Qu.:0.000e+00 1st Qu.:0.000e+00 1st Qu.: 0.000e+00 1st Qu.:0   
## Median :0.000e+00 Median :0.000e+00 Median : 0.000e+00 Median :0   
## Mean :4.337e-21 Mean :2.711e-22 Mean :-4.337e-21 Mean :0   
## 3rd Qu.:0.000e+00 3rd Qu.:0.000e+00 3rd Qu.: 0.000e+00 3rd Qu.:0   
## Max. :4.337e-19 Max. :2.711e-20 Max. : 0.000e+00 Max. :0   
## ALDH1L1 FTCD PDE10A HPSE CYP46A1   
## Min. :0 Min. :0.000e+00 Min. :0 Min. :0 Min. :0   
## 1st Qu.:0 1st Qu.:0.000e+00 1st Qu.:0 1st Qu.:0 1st Qu.:0   
## Median :0 Median :0.000e+00 Median :0 Median :0 Median :0   
## Mean :0 Mean :1.388e-19 Mean :0 Mean :0 Mean :0   
## 3rd Qu.:0 3rd Qu.:0.000e+00 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0   
## Max. :0 Max. :1.388e-17 Max. :0 Max. :0 Max. :0   
## SLC26A1 SLC22A7   
## Min. :0 Min. :0   
## 1st Qu.:0 1st Qu.:0   
## Median :0 Median :0   
## Mean :0 Mean :0   
## 3rd Qu.:0 3rd Qu.:0   
## Max. :0 Max. :0

pheatmap(genes.diff)



## Task 4

We normalize all three datasets in Table 1, and we also created the transposed format for all the dataset. then we saved the results for using later on in the project.

# open all the datasets  
RAW.all <- read.table("get\_normal\_vs\_tumor\_RAW.out", header = TRUE, sep = " ", stringsAsFactors = FALSE)  
RAW.breast <- read.table("get\_normal\_vs\_tumor2\_RAW\_Breast.out", header = TRUE, sep = " ", stringsAsFactors = FALSE)  
RAW.FeReSy <- read.table("get\_normal\_vs\_tumor2\_RAW\_Female.Reproductive.System.out", header = TRUE, sep = " ", stringsAsFactors = FALSE)  
  
# create the transposed format  
tRAW.all <- data.frame(t(RAW.all[,-2562]))  
colnames(tRAW.all)<-paste0(RAW.all$tissue,1:2132)  
tRAW.breast <- data.frame(t(RAW.breast[,-2562]))  
colnames(tRAW.breast)<-paste0(RAW.breast$tissue,1:503)  
tRAW.FeReSy <- data.frame(t(RAW.FeReSy[,-2562]))  
colnames(tRAW.FeReSy)<-paste0(RAW.FeReSy$tissue,1:130)  
  
# normalize all the datasets  
mn.tRAW.all <- scale(log(tRAW.all), center=TRUE, scale=FALSE)  
mn.tRAW.breast <- scale(log(tRAW.breast), center=TRUE, scale=FALSE)  
mn.tRAW.FeReSy <- scale(log(tRAW.FeReSy), center=TRUE, scale=FALSE)