ANALYSIS OF GENE EXPRESSIONS DATA

GOAL

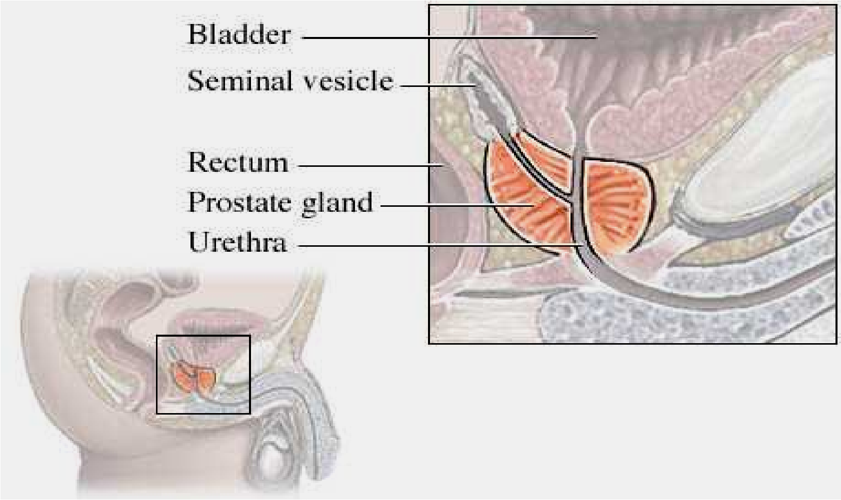
The goal of this project is to identify genes differentially expressed between recurrent and non-recurrent prostate tumors and how different ways of calculating gene expressions influenced this finding.

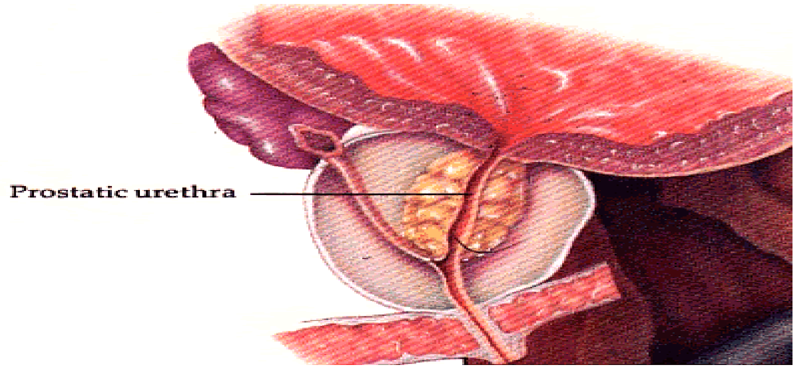
What are the factors the influence cancer recurrences? To answer this question, we rely on the methods of *biostatistics*. What is statistics? *Statistics* explores the collection, organization, analysis, and interpretation of numerical data. When the focus of statistics is on biological and medical science it is called *biostatistics.* The aim of *biostatical* study is to assess the information available in the data about a hypothesis of interest and to present them in a way that valid interpretations can be potential. In this study the information given are gene expression data of patients with prostate cancer recurrence, and non recurrent prostate cancer patients. We are going to analyze the gene expression data to find out which genes may provide a reason for prostate cancer recurrences.

What is gene expression? Genes are expressed when the cell decides that it wants to use some particular segment of DNA. How are levels of gene expression obtained? Expressions levels are obtained using oligonucleotide arrays.

What is Prostate Cancer? Prostate cancer is the abnormal growth of cells (tumor) in the tissues of the Prostate Gland "The prostate gland is a small walnut shaped organ that lies just below a man's bladder". [See figure 1] (Refers to the figure below)

Figure1.Prostate Gland (**www.prostate.com.ph/anatomy_prostate_diseases.htm**)





A recurrent Prostate Cancer patient is a patient who has been diagnosed with a primary prostate cancer, had radical prostatectomy to remove the tumor, and has been found to have a cancer recurrence during the follow-up period. A non-recurrent Prostate Cancer patient is a patient who has been diagnosed with prostate cancer and after the tumor is removed, there are no cancer recurrences during the follow-up period.

GENE EXPRESSION DATA

In this project we are going to compare gene expressions in recurrent and non-recurrent patients, using two computer programs: Microsoft Excel and the R Statistical Package. We will use the t-test statistic to compare the gene expressions. The data available to us consists of the expression levels of more than 44,000 genes from each of 37 recurrent patients and 42 non-recurrent patients. Gene expressions are obtained using the HU133A and the HU133B affymetrix oligonucleotide arrays (www.affymetrix..com). Each array consists of approximately 22,000 genes or probes. The methods for processing patients RNA and obtaining data from oligonucleotide arrays are described in the summer project report of Ms. Christina Wassel (2001).

Briefly, the RNA sample from each patient is hybridized to an array. Every gene is represented using approximately 16 pairs of perfect match and mismatch probe sets in the array. The intensity measurements of these probe sets are obtained using a scanner, and represent the RNA expression of the genes. The expression level of each gene is finally calculated as the summary of the perfect match and mismatch intensities of that gene. There are various methods for calculating gene expressions. We consider two methods known as MAS 5.0 and the robust multiarray (RMA) method. These methods are discussed by Irizarry et al (2003).

Our final data consist of four large files. The first two files give the MAS5.0 and the RMA gene expression measures on all the genes from HU133A array for the patients. The last two files provide similar data for the HU133B array. Our goal is to compare gene expression between the recurrent and non-recurrent patients using the MAS 5.0 and RMA methods for the genes in HU133A array, and likewise for HU133B array. If MAS 5.0 and RMA methods for calculating gene expressions are similar, then one would expect the same genes to be identified as being differentially expressed in our analysis.

T-TEST STATISTIC

Microsoft Excel is a spreadsheet application developed by Microsoft. On Excel we are going to find the logs of gene expressions of the 37 recurrent prostate cancer patients and 42 non-recurrent prostate cancer patients, with gene levels in about 22283 genes in each patient. After finding the logs we find the averages of the logs in both the recurrent and non recurrent values. Following the averages we find the variance and the standard deviation. We then calculate the t-test statistic. The T-test compares the standardized mean of two groups. We then calculate the p-value. When we use Excel we go according to some formulas, the formula's are below. What is a P Value? The p-value measures the probability of observing the results from the given data under the null hypothesis**.** The null hypothesis states that there is no difference in the expression level of that gene between the recurrent and nom-recurrent patients. The smaller the p-value, the greater likelihood that the null hypothesis is incorrect, i.e. there is a difference between the recurrent and non-recurrent with regards to the expression level of that gene.

The standard deviation is sometimes expressed as a percent of the mean, in which case it's known as a **coefficient of variation**. The **coefficient of variation** is the degree to which a set of data points varies. It is often called the relative standard deviation, since it takes into account the mean (average) of the array a data. It is also the statistical measure of the deviation of the variable from its mean. To calculate the coefficient of variance you, use the formula below:

Coefficient of Variance =

Standard Deviation of the Gene in the Group\Mean of the Gene in the group.

MY FORMULA OF A IN RECURRENT AND NON-RECURRENT GROUP

Calculating Logs (LN)
Ln of 42=LN (42) =3.7377
Ln of (165.0736) =5.106392.

Calculate $\overline{R}$ = the average expression of a single gene for recurrent patients

$$= \left(r_1 + r_2 + \ldots\ldots. + r_{37}\right) \Big/ 37$$

Calculate $\overline{N}$ = the average expression of a single gene for non-recurrent patients

$$= \left(n_1 + n_2 + \ldots\ldots. + n_{42}\right) \Big/ 42$$

Calculate Variance of the recurrent value =

$$\sigma_r = \left\{\left(r_1 - \bar{r}\right)^2 + \ldots\ldots.. + \left(r_{37} - \bar{r}\right)^2\right\} \Big/ (37-1)$$

Calculating Standard Deviation of R's=

$$\sigma_r = \sqrt{\sigma_n^2}$$

Calculating Variance of the non-recurrent values=

$$\sigma_n^2 = \left\{(n_1 - \overline{n})^2 + ... + (n_{42} - \overline{n})^2\right\} \Big/ (42 - 1)$$

Calculating the Standard Deviation of the N's=

$$\sigma_n = \sqrt{\sigma_n^2}$$

Calculating the t-test for the Gene=

The T-Statistic:

$$T = \overline{R} - \overline{N} \Big/ \sqrt{\frac{(37-1)\sigma_r^2 + (42-1)\sigma_n^2}{37+42-2}}$$

R is a language and the environment for statistical computing and graphics. To use R, the first thing you do is to save your excel data recurrent and non-recurrent data as a text file. After you have done that then you can go to R and read the data you have saved as a text file. The first thing we are going to do after we have read our data on excel is to calculate the t-test. It is desirable that in using R, you must always write you command in a notebook file and save the command there, before transferring it to R, to avoid any mistakes. Then we find the mean, variance and the standard deviation of both recurrent and non-recurrent data of the array a data after finding the standard deviation, we plot the recurrent mean with the RMA recurrent mean, non-recurrent mean and the RMA non-recurrent mean, recurrent standard deviation and RMA recurrent standard deviation, non-recurrent standard deviation.

We calculate the coefficient of Variation, after the computation of the coefficient of variance we plot the ranks of the MAS 5.0 recurrent mean and the recurrent coefficient of variance, ranks of the MAS 5.0 non-recurrent mean and the non-recurrent coefficient of variance, rank of the RMA recurrent mean and RMA recurrent coefficient of variance, rank of the RMA non-recurrent mean and the RMA non-recurrent coefficient of variance.

RESULTS FOR APPENDIX A [1:8]: PLOTS OF DATA SUMMERIES

Appendix 1 represents the plot of MAS 5.0 recurrent mean and the RMA recurrent mean for the HU133A data. The vertical axes represent the plot of the RMA mean of the recurrent patients in the HU133A array. The horizontal line axes represent the plot of the MAS 5.0 mean in recurrent patients for the HU133A array. The plot shows that the values of the MAS recurrent means are higher than the values of the RMA recurrent mean. This is because, when you take a point like 6 on the MAS recurrent mean and compare it to the RMA recurrent mean is going to have values between 4 and 6, therefore MAS recurrent mean have higher mean value than RMA recurrent mean values. Appendix 2 represents the plot of the MAS 5.0 mean of the non-recurrent patients and the RMA mean of the non-recurrent patients in the HU133A array. The same interpretation reached on appendix 1 can be reach on this plot. This plot shows that MAS 5.0 non-recurrent mean has higher mean values than RMA. Again these is because when you take a point like point like 8 on the MAS 5.0 non-recurrent mean and compare it to a point on the RMA recurrent men it tends to have a higher mean. Appendix 3 represents the plot of the MAS5.0 recurrent standard deviation and the RMA recurrent standard deviation of the HU133A array. We plotted it to see the difference between the MAS5.0 standard deviation in the recurrent patients and the RMA standard deviation of the recurrent patients. This plot illustrates that MAS5.0 standard deviation values are higher than RMA standard deviation values. This is because, when you look at the point plotted for MAS 5.0, they tend to go higher than RMA standard deviation, because values of the MAS 5.0 recurrent standard deviation go up 2.0 while the values for RMA only go up to1.5. Appendix 4 represents the plot of the MAS5.0 non-recurrent standard deviation and the RMA non-recurrent standard deviation in the HU133A array. It shows the difference between the MAS standard deviation in the non-recurrent patients and the RMA standard deviation on the non-recurrent patients in the HU133A array. The interpretation reached for appendix 3 can also be reach for this plot.

Appendix 5 represents the plots of the ranks of the recurrent mean versus the recurrent coefficient of variance. The pattern shown in this graph is that the higher the values of the ranks of the recurrent mean, the lower the values of the ranks of the recurrent coefficient of variation, and the higher the values of the ranks of the coefficient of variation of the recurrent patients, the lower the values of the ranks of the recurrent mean. This is because the plots of the ranks show a line. Appendix 6 represents the plots of the ranks of the non-recurrent mean and the non-recurrent coefficient of variance. This plot as appendix 5 also shows the pattern that, the higher ranks of the non-recurrent mean, the lower the values of the ranks of the non-recurrent coefficient of variation, and the higher the values of the ranks of the coefficient of variation, the lower the values of the ranks of the non-recurrent mean. Appendix 7 represents the plot of the ranks of the RMA recurrent mean and the RMA recurrent coefficient of variance. This pattern is different form those seen in appendix 5 and 6. This graph does not show any pattern, because the plots of the ranks are scatted around. It illustrates however that the higher the values of the non-recurrent mean, it's coefficient of variation can be anything, and the higher the ranks of the non-recurrent coefficient of variation, it's ranks of the non-recurrent mean can be anything The last appendix, appendix 8 represents the plot of the ranks RMA non-recurrent mean and the RMA non-recurrent coefficient of variance. The interpretation reached for appendix7 can be reached for this appendix. Similar interpretations can be seen for data from HU133B array.

APPENDIX D: **Description of the Genes Identified from T-Statistics**

[1]

In our results, we found that gene **216396_s_at,** with a p value 0.0000000604 rank first in the MAS 5.0 data of the HU133A array and ranked 129 in RMA with RMA P Value of 0.0000000494. **GO Biological Process:** 6917 // induction of apoptosis //

traceable author statement. **Gene Title:** etoposide induced 2.4 mRNA. And gene **204505_s_at,** ranked second in MAS 5.0 data of the HU133A array, with P value 0.00000176 and ranked 17879 in RMA with RMA P value of 0.3106558. **GO Biological Process:** 7010 // cytoskeleton organization and biogenesis // traceable author statement /// 51017 // actin filament bundle formation // traceable author statement. **Gene Title:** erythrocyte membrane protein band 4.9 (dematin**)**

[2] Gene **209196_at** ranked first in RMA data of the HU133A array, with P value 0.0000000000561, and ranked 1950 in MAS 5.0 with MAS 5.0 p Value of 0.021580564. **Gene Symbol:** C6orf11. **Gene Title:** chromosome 6 open reading frame 11. Gene **212388_at,** with P Value of 0.000000000153 **ranked** second in RMA and ranked 477 in MAS 5.0 with P value of 0.00273711. **GO Biological Process:** 6511 // ubiquitin-dependent protein catabolism // inferred from electronic annotation /// 6512 // ubiquitin cycle // inferred from electronic annotation. **Gene Tittle**: ubiquitin specific protease 24

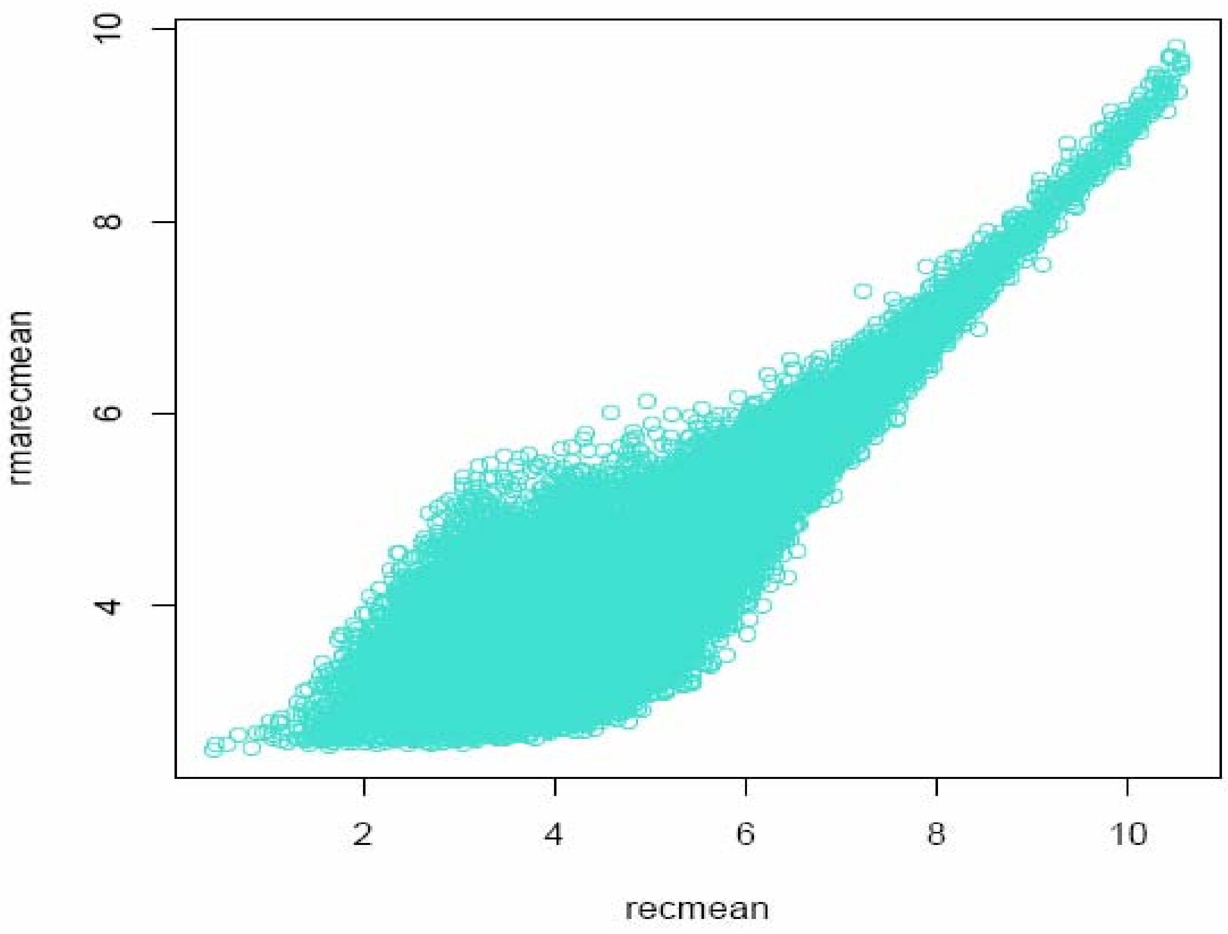
[3] Gene **244677**_at with P Value 0.0000038011569742924 ranked first in MAS 5.0 I HU133B array and ranked 70 in RMA, with RMA P Value of 0.000026747578998787. **Transcript Assignment**: AA416756 // /DB_XREF=zu08h08.s1 /CLONE=IMAGE:731295 // gb // --- // ---. **Alignment**: chr17:7997493-7998118 (-) // 78.64 // p13.1. And Gene **242424_at** with P value 4.06232646188442E-06 Ranked second in MAS 5.0 HU133B array and ranked 47 in RMA with RMA with RMA P 0.0000174011899405357. **Transcript Assignment**: AA345855 // /DB_XREF=EST51947 // gb // --- // --- /// AI687578 // /DB_XREF=tp97d06.x1 /CLONE=IMAGE:2207243 // gb // --- // --- /// AW811065 // /DB_XREF=MR2-ST0131-211099-008-e08 // gb // --- // --- /// AW811149 // /DB_XREF=MR2-ST0131-111199-003-h03 // gb

[4] Gene **232134_at**, with P value 1.01686129960754E-07 ranked first in RMA data of the HU133B array and ranked 7 in MAS 5.0 with MAS 5.0 P Value of 9.52524804986865E-06. **Transcript Assignment**: AK021714 // Homo sapiens cDNA FLJ11652 fis, clone HEMBA1004461. // gb // 10 // ---. **Alignment**: chr5:6781969-6783951 (+) // 91.52 // p15.31. Gene **239264_at** with P Value 1.95097149768841E-07 ranked second In RMA HU133B array, and ranked 7210 in MAS 5.0 with MAS 5.0 P Value of 0.179045869512288. **Go Biological Process**: 6904 // vesicle docking during exocytosis // inferred from electronic annotation /// 15031 // protein transport // inferred from electronic annotation. **Transcript Assignment**: AA531562 // nj64e05.s1 Homo sapiens cDNA /clone=IMAGE-997280 /gb=AA531562 /gi=2274268 /ug=Hs.125010 /len=415 // gb // --- // --- /// AA531562 // /DB_XREF=nj64e05.s1 /CLONE=IMAGE:997280 // gb // --- // --- /// AI240025 // qh39a06.x1 Homo sapiens cDNA, 3' e.

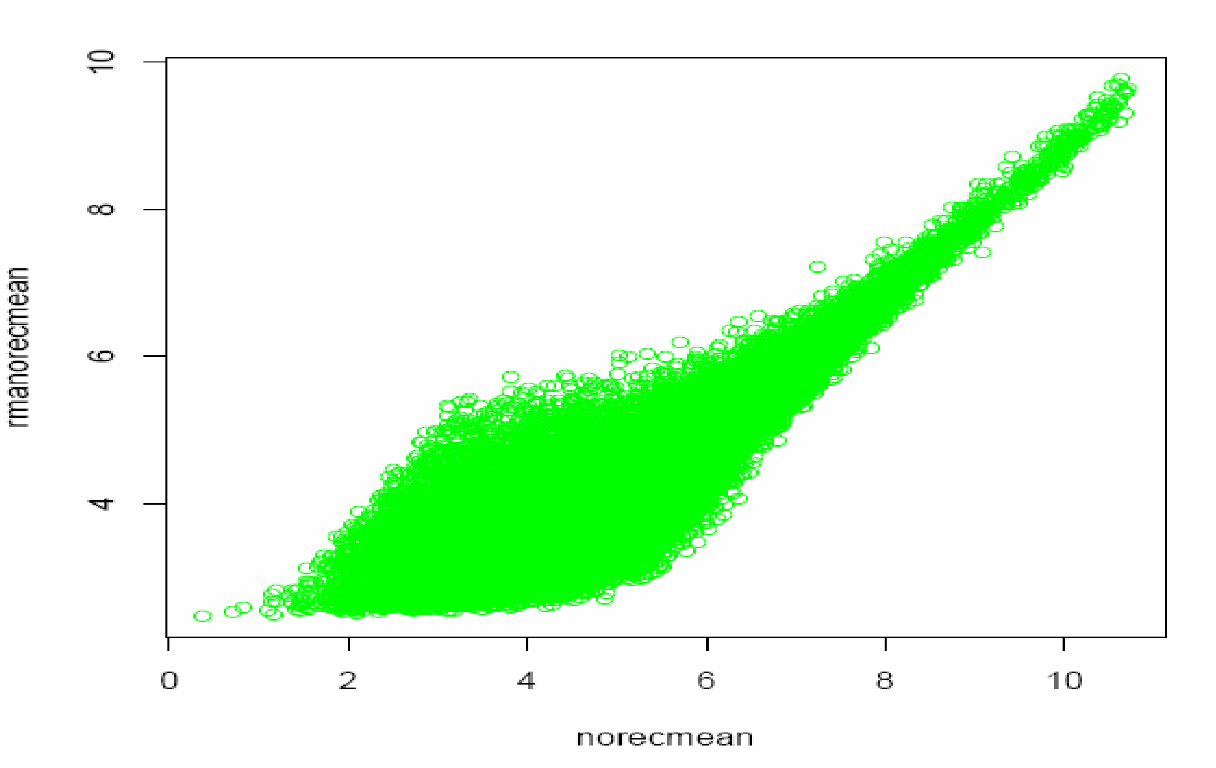
CONCLUSION

In conclusion, we have determined with our results that the RMA data for both the HU133A and the HU133B arrays may be more useful than the MAS 5.0 format, because we determined that that MAS5.0 data for both arrays had higher variances and the RMA data for both array had smaller variances. The mean expressions were similar for both methods for larger expression values. Further research with additional data will be needed to reach more definitive conclusions.

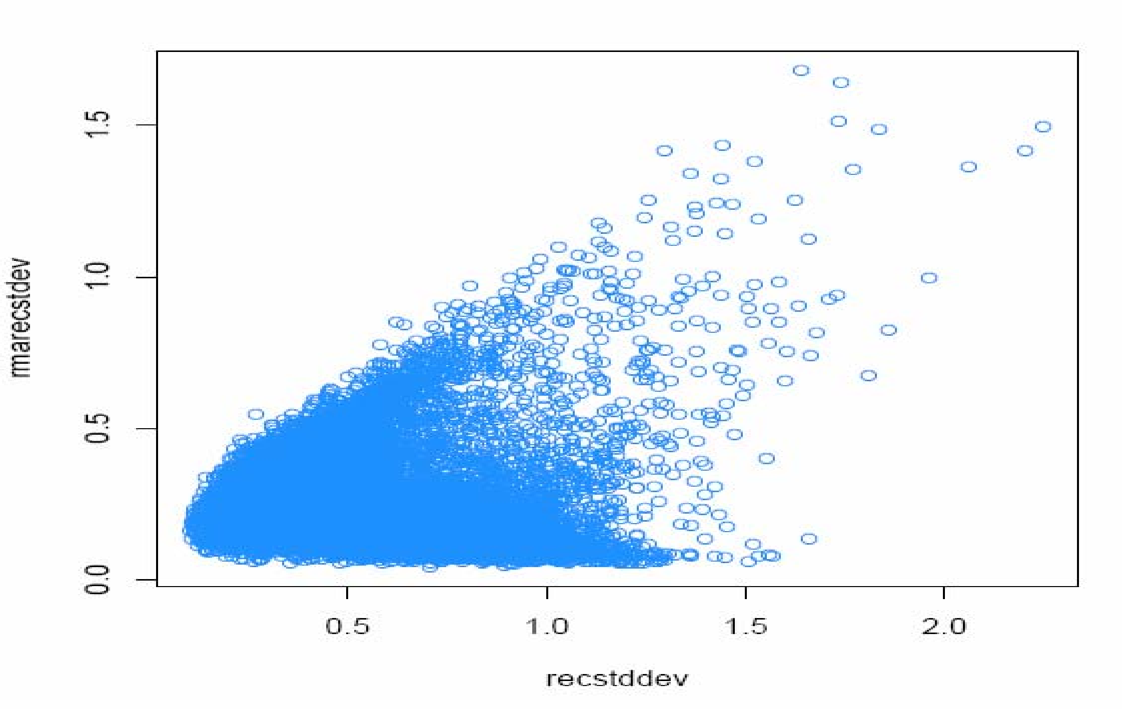
[A] Appendix 1: [Mean gene expressions of recurrent patients from HU133A array. MAS 5.0 versus RMA methods for calculating gene expressions]



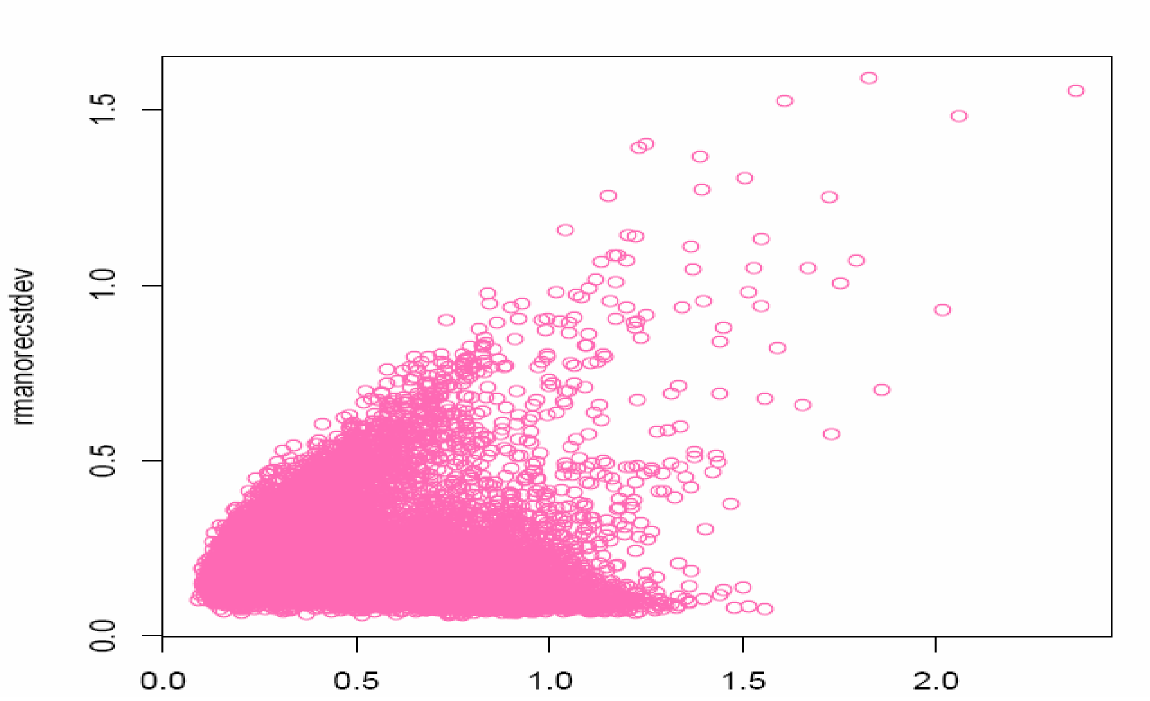
[A] Appendix 2: [Mean gene expression of non-recurrent patients from HU133A array. MAS 5.0 versus RMA Methods for calculating gene expression.



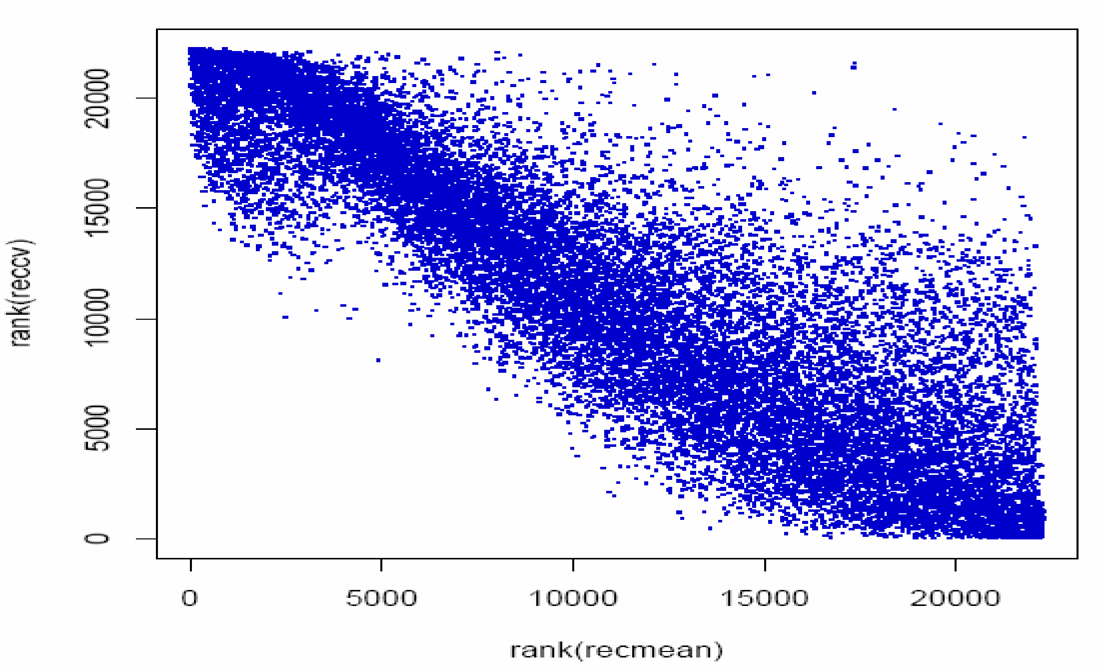
[A] Appendix 3: [Standard deviation gene expressions of recurrent patients form HU133A array. MAS 5.0 versus RMA methods for calculating gene expression]



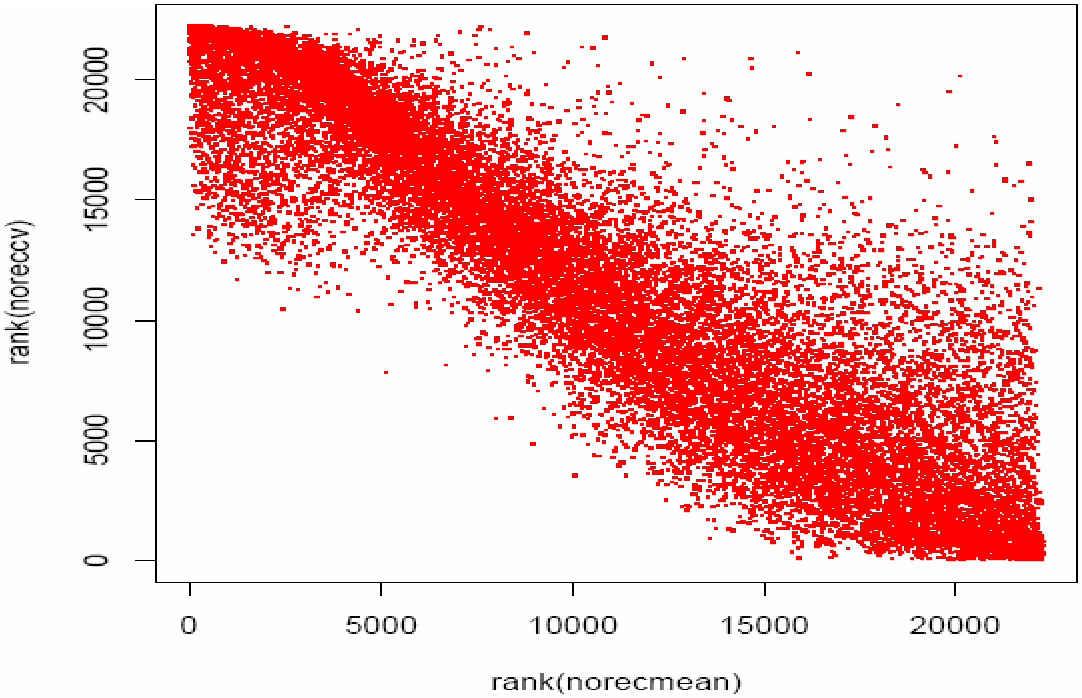
[A] Appendix 4: [Standard deviation gene expressions for non-recurrent patients from HU133A array. MAS 5.0 and RMA methods for calculating gene expressions]



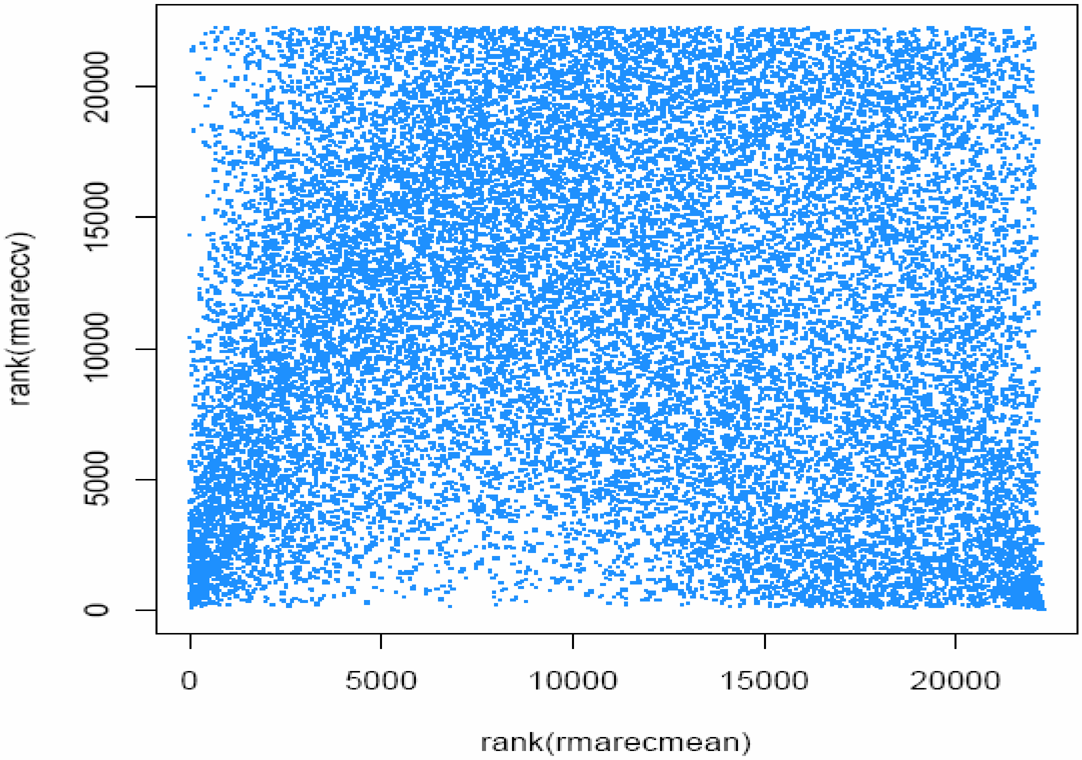
[A] Appendix 5: [Ranks of recurrent patients MAS 5.0mean and recurrent patients MAS 5.0 coefficient of variance from HU133A array]



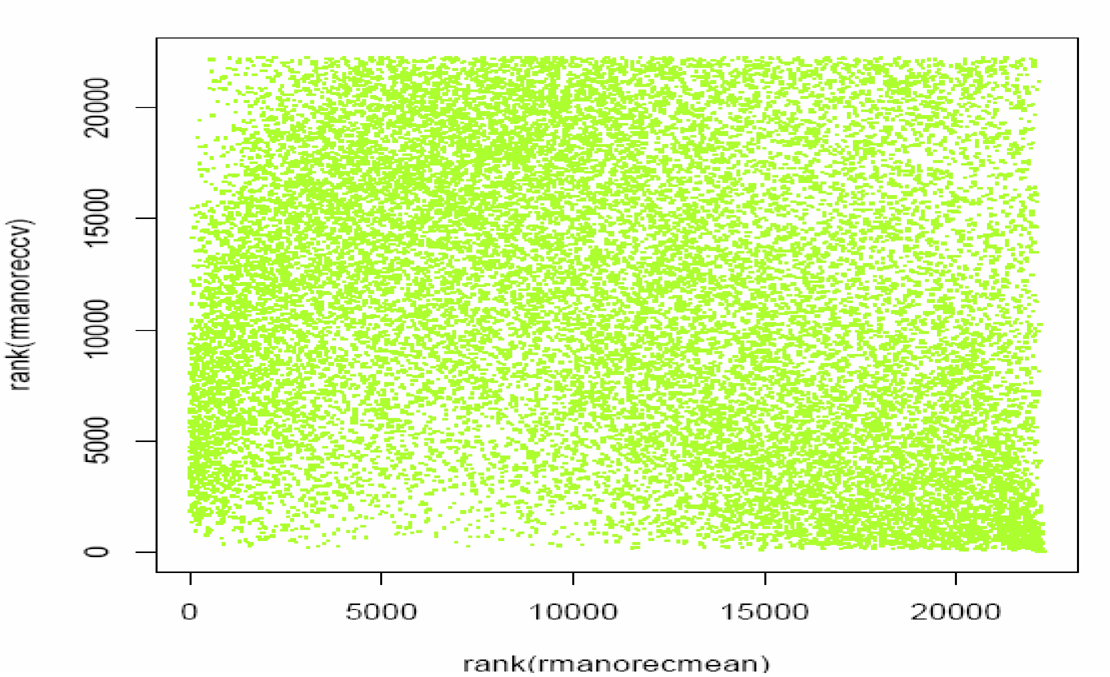
[A] Appendix 6: [Ranks of non-recurrent patients MAS 5.0 mean and non-recurrent patients MAS 5.0 coefficient of variance from HU133A array]



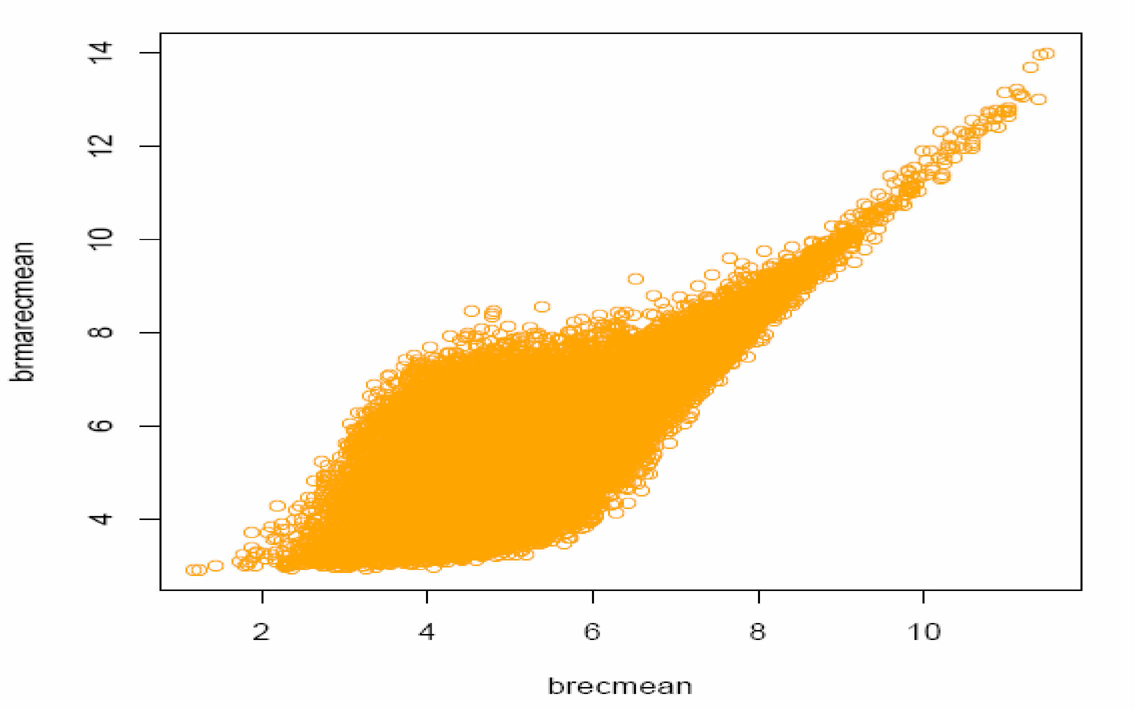
[A] Appendix 7: [Ranks of recurrent patients RMA mean and recurrent patients RMA coefficient of Variance from HU133A array]



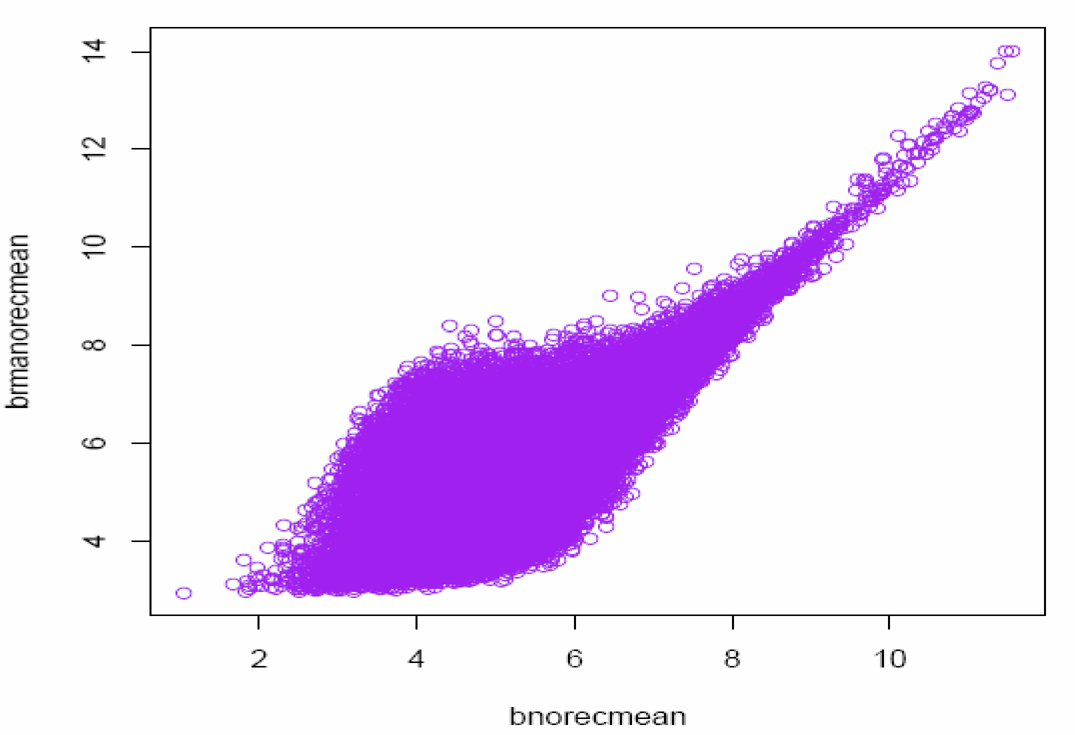
[A] Appendix 8: [Ranks of non-recurrent patients RMA mean and non-recurrent patients RMA coefficient of Variance from HU133A array.



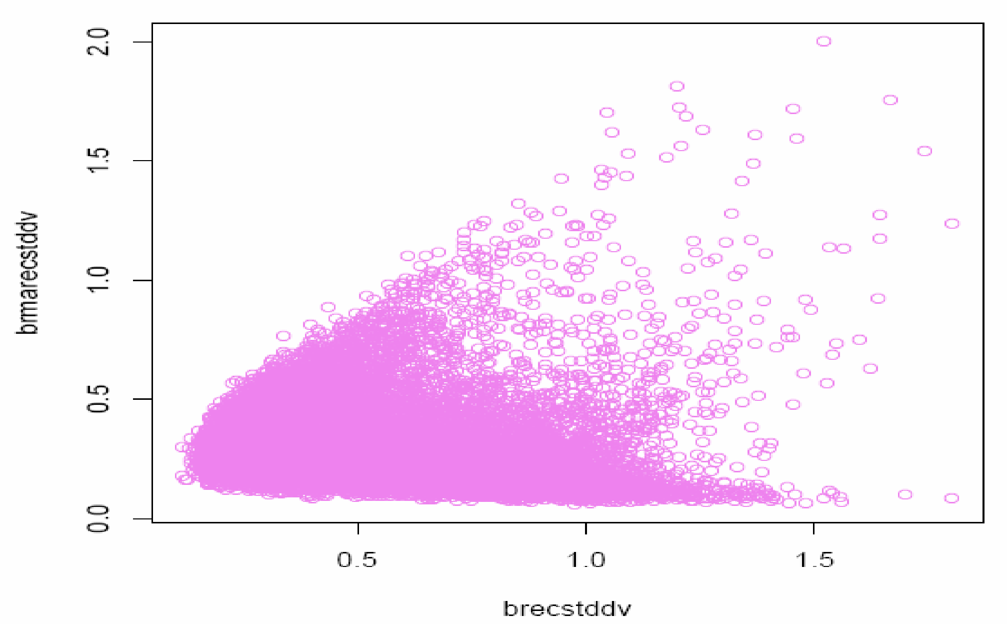
[B] Appendix 1: [Mean gene expressions of recurrent patients from HU133B array. MAS 5.0 versus RMA methods for calculating gene expressions]



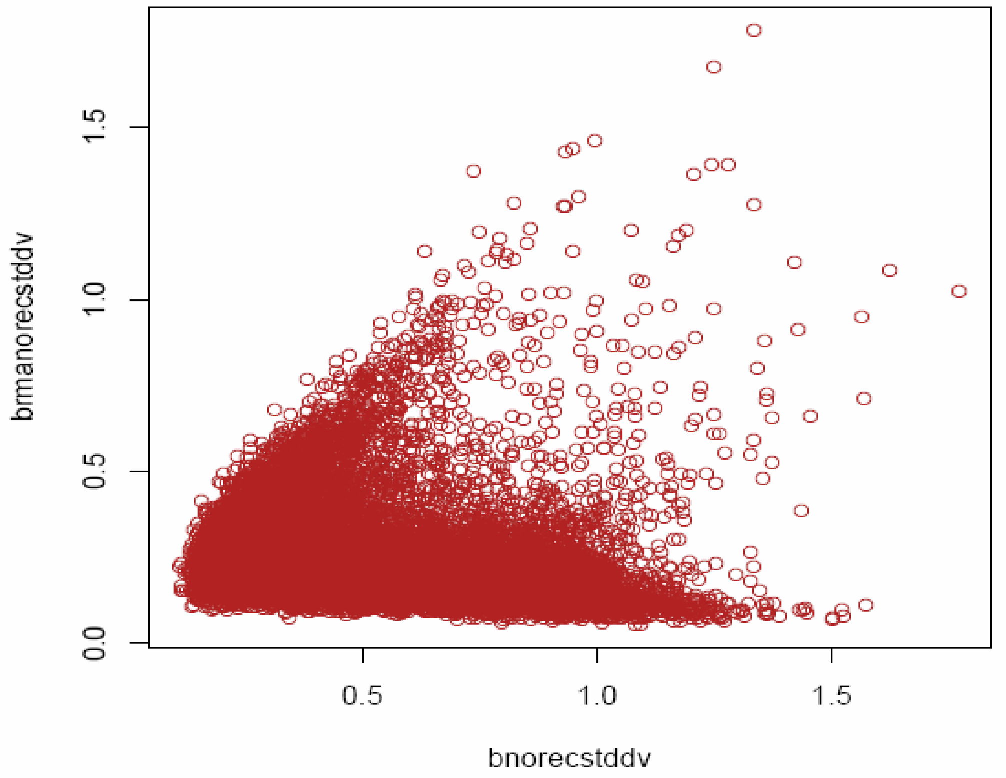
[B] Appendix 2: [Mean gene expression of non-recurrent patients from HU133B array. MAS 5.0 versus RMA Methods for calculating gene expression]



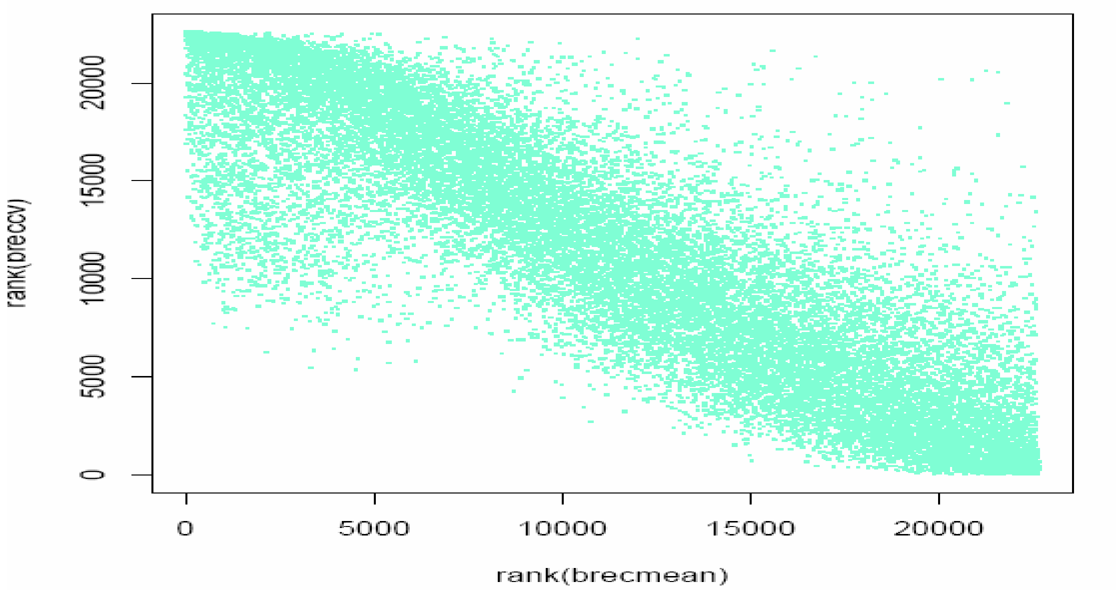
[B] Appendix 3: [Standard deviation gene expressions of recurrent patients form HU133B array. MAS 5.0 versus RMA methods for calculating gene expression]



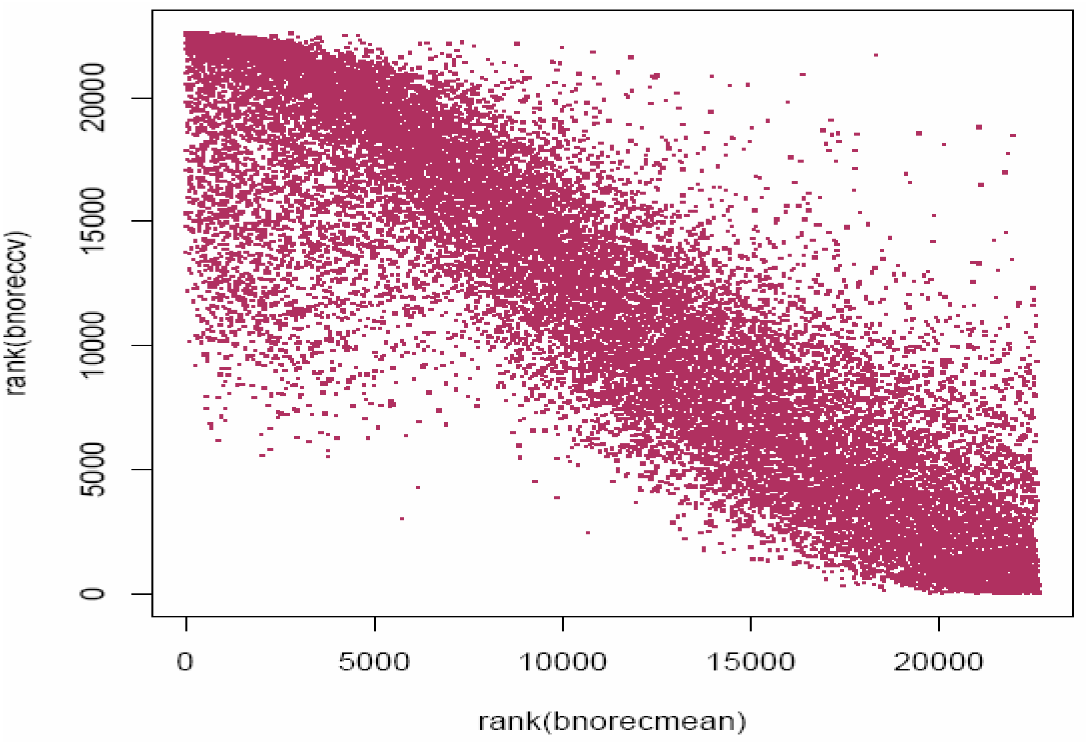
[B] Appendix 4: [Standard deviation gene expressions for non-recurrent patients from HU133B array. MAS 5.0 and RMA methods for calculating gene expressions]



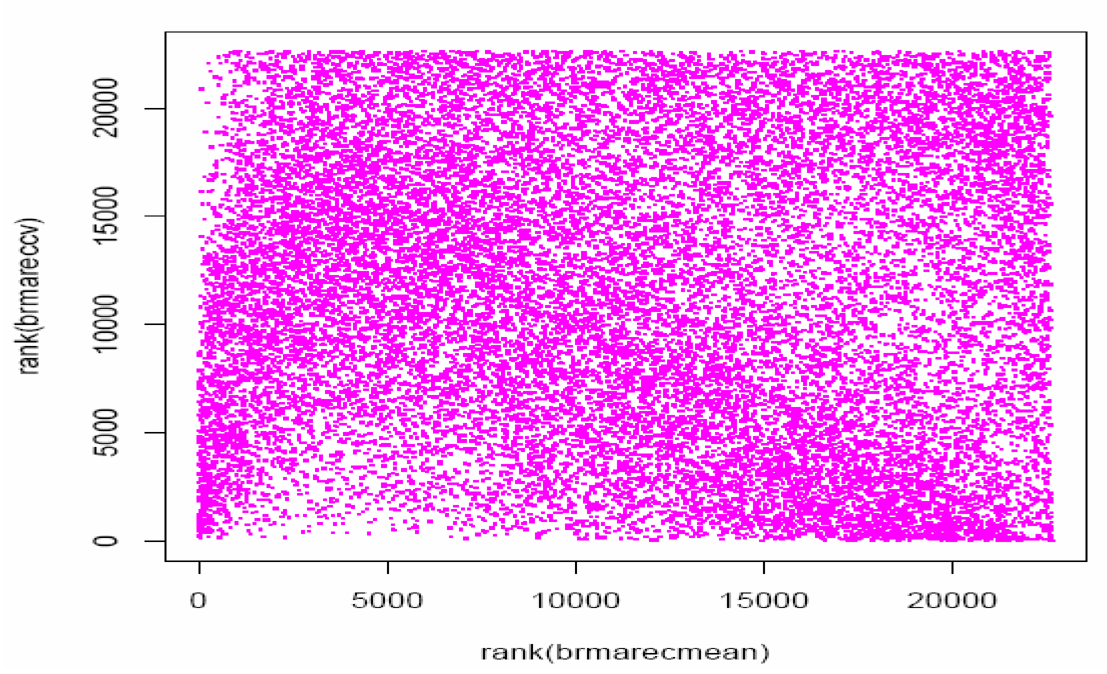
[B] Appendix 5: [Ranks of recurrent patients MAS 5.0mean and recurrent patients MAS 5.0 coefficient of variance from HU133B array]



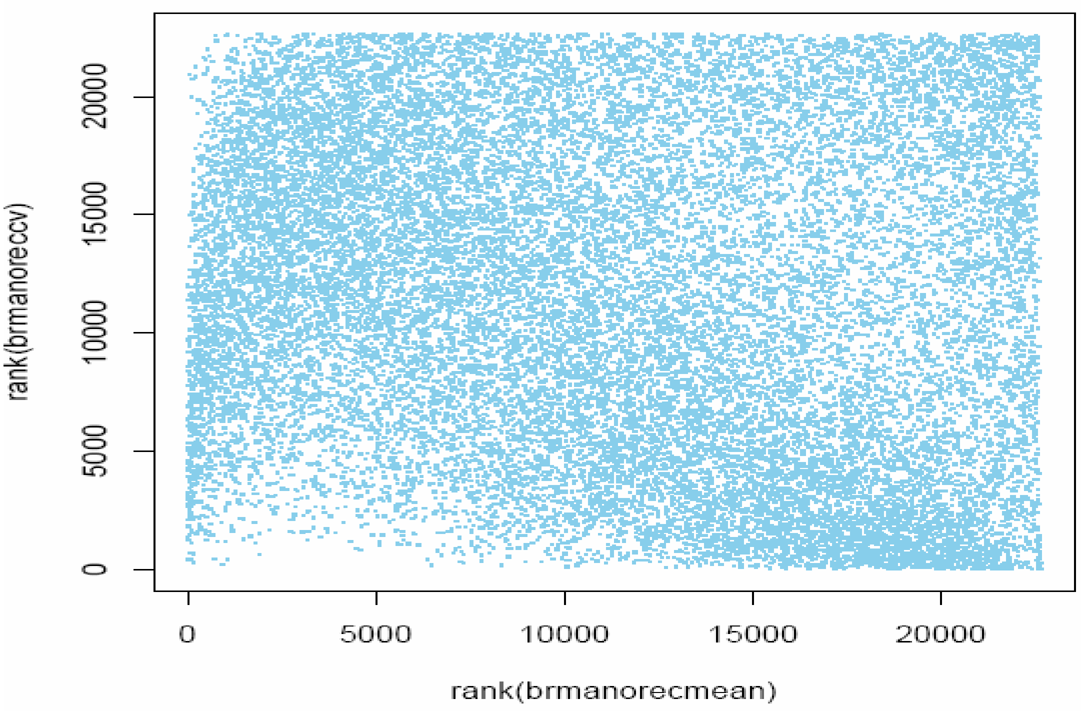
[B] Appendix 6: [Ranks of non-recurrent patients MAS 5.0 mean and non-recurrent patients MAS 5.0 coefficient of variance from HU133A array]



[B] Appendix 7: [Ranks of recurrent patients RMA mean and recurrent patients RMA coefficient of Variance from HU133B array]



[B] Appendix 8: [Ranks of non-recurrent patients RMA mean and non-recurrent patients RMA coefficient of Variance from HU133B array.



APPENDIX C (The commands I used for the R statistical package)

Reading MAS 5.0 Recurrent Data

```
recurdata←read.table(“g:/data/recvsnorec/recur2.txt”,header=T)
names(recurdata)
recurdata[1:5,1:5]
genename←recurdata[,1]
recurdata←recurdata[,-1]
dim(recurdata)
```

Reading MAS 5.0 Non-Recurrent Data

```
norecdata←read.table(“g:/data/recvsnorec/norec2.txt”,header=T)
names(norecdata)
norecdata[1:5,1:5]
genename←norecdata[,1]
norecdata←norecdata[,-1]
dim(norecdata)
```

Calculating MAS 5.0 Logs

```
logrec←log(recurdata)

lognorec←log(norecdata)
```

Calculating MAS 5.0 T-Test

```
recnorec←cbind(logrec,lognorec)

dim(recnorec)
recnorec[1:5,1:5]
rownames(recnorec)←genename

tresults←apply(recnorec,1,
    function(X){
    x1←x[1:37]
    x2←[38:79]
    temp←t.test(x1,x2)$statistic
    return(temp)})
length(tresults)
tresults[1:10]
ls()
save.image("g:/data/recvsnorec/first")
```

Quit from R.

```
q()
```

Calculating P Value:

```
load("g:/data/recvsnorec/first")
tresulstspvalue←2*(1-pt(abs(tresults),df=77))
tresults[1:10]
```

MAS5.0

```
btresults<-apply(brecnorec,1,
function(x){
x1<-x[1:37]
x2<-x[38:79]
temp<-t.test(x1,x2)$statistic
return(temp)})

brecmean<-apply(brecnorec[,1:37],1,mean)
bnorecmean<-apply(brecnorec[38:79],1,mean)
brecvar<-apply(brecnorec[,1:37],1,var)
bnorecvar<-apply(brecnorec[,38:79],1,var)
brecstddv<-sqrt(brecvar)
bnorecstddv<-sqrt(bnorecvar)
```

RMA

```
rmabtresults<-apply(rmabrecnorec,1,
function(x){
x1<-x[1:37]
x2<-x[38:79]
temp<-t.test(x1,x2,)$statistic
return(temp)})
```

```
brmarecmean<-apply(rmabrecnorec[,1:37],1,mean)
brmanorecmean<-apply(rmabrecnorec[,38:79],1,mean)
brmarecvar<-apply(rmabrecnorec[,1:37],1,var)
brmanorecvar<-apply(rmabrecnorec[,38:79],1,var)
brmarecstddv<-sqrt(brmarecvar)
brmanorecstddv<-sqrt(brmanorecvar)
```

PLoTS

```
plot(brecmean,brmarecmean)
plot(bnorecmean,brmanorecmean)
plot(brecstddv,brmarecstddv)
plot(bnorecstddv,brmanorecstddv)
```

Calculate B Array Coefficient of Variance

```
breccv<-brecstddv/brecmean
bnoreccv<-bnorecstddv/bnorecmean
brmareccv<-brmarecstddv/brmarecmean
brmanoreccv<-brmanorecstddv/brmanorecmean
```

Plot CV

```
plot(rank(brecmean),rank(breccv),pch=”.”)
plot(rank(bnorecmean),rank(bnoreccv),pch=”.”)
plot(rank(brmarecmean),rank(brmareccv),pch=”.”)
plot(rank(brmanorecmean),rank(brmanoreccv),pch=”.”)
```

APPENDIX D (Final Rsults)

MAS 5.0 DATA

Gene 1:

Gene Name: 216396_s_at, P Value: 0.0000000604
Ranked 129 in RMA, RMA P Value: 0.0000000494
Sequence source: GenBank
Transcript ID (Array Design): Hs.286027.3
GO Biological Process: 6917 // induction of apoptosis // traceable author statement
GO Cellular Process: None
GO Molecular Function: None
Pathway: None
Chromosomal Location: chr11q24
Gene Symbol: EI24
Gene Title: etoposide induced 2.4 mRNA
Alignment: chr11:124957742-124959334 (+) // 84.1 // q24.2 /// chr10:85646028-85646666 (+) // 37.76 // q23.1

Uni Gene ID: Hs.343911

Gene 2:

Gene Name: 204505_s_at, P Value: 0.00000176
Ranked 17878 in RMA, RMA P Value: 0.3106558
Sequence source: GenBank
Transcript ID (Array Design): g4503580
GO Biological Process: 7010 // cytoskeleton organization and biogenesis // traceable author statement /// 51017 // actin filament bundle formation // traceable author statement

GO Cellular Process: 15629 // actin cytoskeleton // traceable author statement
GO Molecular Function: 3779 // actin binding // inferred from electronic annotation
Pathway: None
Chromosomal Location: chr8p21.1
Gene Symbol: EPB49
Gene Title: erythrocyte membrane protein band 4.9 (dematin**)**
Alignment: chr8:21972679-21995982 (+) // 98.09 // p21.3
Uni Gene ID: Hs.274122

Gene 3:

Gene Name: 217844_at, P Value: 0.00000201
Ranked 12939 in RMA, RMA P Value: 0.053411857
Sequence source: GenBank
Transcript ID (Array Design): g10864008
GO Biological Process: None
GO Cellular Process: 5634 // nucleus // traceable author statement
GO Molecular Function: 4721 // phosphoprotein phosphatase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation

Pathway: None
Chromosomal Location: chr2q35
Gene Symbol: CTDSP1
Gene Title: CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1
Alignment: chr2:219089982-219096168 (+) // 91.79 // q35
Uni Gene ID: Hs.444468

Gene 4:

Gene Name: 201611_s_at, P Value: 0.0000033
Ranked 15051 in RMA, RMA P Value: 0.119600775
Sequence source: GenBank
Transcript ID (Array Design): g6912429
GO Biological Process: 6464 // protein modification // traceable author statement /// 6481 // C-terminal protein amino acid methylation // inferred from electronic annotation /// 6481 // C-terminal protein amino acid methylation // traceable author statement /// 6612 // protein-membrane targeting // traceable author statement

GO Cellular Process: 5624 // membrane fraction // traceable author statement /// 5783 // endoplasmic reticulum // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation

GO Molecular Function: 3880 // C-terminal protein carboxyl methyltransferase activity // traceable author statement /// 4671 // protein-S-isoprenylcysteine O-methyltransferase activity // inferred from electronic annotation /// 8168 // methyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation

Pathway: None
Chromosomal Location: chr1p36.21
Gene Symbol: ICMT
Gene Title: isoprenylcysteine carboxyl methyltransferase
Alignment: chr1:6215520-6230272 (-) // 89.66 // p36.31
Uni Gene ID: Hs.515688

Gene 5:

Gene Name: 202555_s_at, P Value: 0.00000489
Ranked 4449 in RMA, RMA P Value: 0.000555137
Sequence source: GenBank
Transcript ID (Array Design): g5174600
GO Biological Process: 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6468 // protein amino acid phosphorylation // traceable author statement

GO Cellular Process: None

GO Molecular Function: 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4687 // myosin-light-chain kinase activity // traceable author statement /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 4871 // signal transducer activity // not recorded /// 5516 // calmodulin binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation

Pathway: None
Chromosomal Location: chr3q21
Gene Symbol: MYLK
Gene Title: myosin, light polypeptide kinase /// myosin, light polypeptide kinase
Alignment: None
Uni Gene ID: Hs.477375

Gene 6:

Gene Name: 206689_x_at, P Value: 0.00000655
Ranked 15003 in RMA, RMA P Value: 0.117297674
Sequence source: GenBank
Transcript ID (Array Design): g5454127
GO Biological Process: 1558 // regulation of cell growth // inferred from electronic annotation /// 6302 // double-strand break repair // inferred from mutant phenotype /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of

transcription, DNA-dependent // inferred from electronic annotation /// 6366 // transcription from RNA polymerase II promoter // traceable author statement /// 16568 // chromatin modification // inferred from electronic annotation /// 16573 // histone acetylation // inferred from direct assay

GO Cellular Process: 5634 // nucleus // traceable author statement /// 35267 // TIP60 histone acetyltransferase complex // inferred from direct assay

GO Molecular Function: 3713 // transcription coactivator activity // traceable author statement /// 4402 // histone acetyltransferase activity // inferred from electronic annotation /// 8415 // acyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation

Pathway: None
Chromosomal Location: chr11q13
Gene Symbol: HTATIP
Gene Title: HIV-1 Tat interacting protein, 60kDa
Alignment: chr11:65236073-65243650 (+) // 99.23 // q13.1
Uni Gene ID: Hs.528299

Gene 7:

Gene Name: 207138_at, P Value: 0.0000109
Ranked 10208 in RMA, RMA P Value: 0.016773997
Sequence source: GenBank
Transcript ID (Array Design): g4885546
GO Biological Process: 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation

GO Cellular Process: 5634 // nucleus // traceable author statement

GO Molecular Function: 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // not recorded

Pathway: None
Chromosomal Location: chr9q22.31
Gene Symbol: PHF2
Gene Title: PHD finger protein 2
Alignment: chr9:93418241-93519591 (+) // 77.37 // q22.31
Uni Gene ID: Hs.211441

Gene 8:

Gene Name: 203431_s_at, P Value: 0.000011
Ranked 311 in RMA, RMA P Value: 0.000000291
Sequence source: GenBank
Transcript ID (Array Design): g7662261
GO Biological Process: None
GO Cellular Process: None

GO Molecular Function: 5096 // GTPase activator activity // inferred from electronic annotation
Pathway: None
Chromosomal Location: chr11q24-q25
Gene Symbol: RICS
Gene Title: Rho GTPase-activating protein
Alignment: chr11:128343051-128399219 (-) // 99.98 // q24.3
Uni Gene ID: Hs.440379

Gene 9:

Gene Name: 213675_at, P Value: 0.0000126
Ranked 19446 in RMA, RMA P Value: 0.514612383
Sequence source: GenBank
Transcript ID (Array Design): Hs.14896.1
GO Biological Process: None
GO Cellular Process: None
GO Molecular Function: None
Pathway: None
Chromosomal Location: None
Gene Symbol: None
Gene Title: CDNA FLJ25106 fis, clone CBR01467
Alignment: chr11:12512733-12513794 (+) // 93.41 // p15.3
Uni Gene ID: Hs.432914

Gene 10:

Gene Name: 201933_at, P Value: 0.000016
Ranked 14733 in RMA, RMA P Value: 0.106794585
Sequence source: GenBank
Transcript ID (Array Design): g4506138
GO Biological Process: 6350 // transcription // inferred from electronic annotation /// 6508 // proteolysis and peptidolysis // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 7076 // mitotic chromosome condensation // inferred from direct assay /// 16192 // vesicle-mediated transport // inferred from direct assay /// 16458 // gene silencing // inferred from direct assay /// 45014 // negative regulation of transcription by glucose // inferred from direct assay /// 45749 // negative regulation of S phase of mitotic cell cycle // inferred from mutant phenotype /// 45892 // negative regulation of transcription, DNA-dependent // inferred from direct assay

GO Cellular Process: 794 // condensed nuclear chromosome // inferred from direct assay /// 5769 // early endosome // inferred from direct assay /// 5815 // microtubule organizing center // inferred from direct assay /// 12505 // endomembrane system // inferred from direct assay /// 16363 // nuclear matrix // inferred from direct assay

GO Molecular Function: 5515 // protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from sequence or structural similarity /// 8237 //

metallopeptidase activity // traceable author statement /// 8270 // zinc ion binding // traceable author statement

Pathway: None
Chromosomal Location: chr16q24.3
Gene Symbol: PCOLN3
Gene Title: procollagen (type III) N-endopeptidase
Alignment: chr16:88238345-88251754 (-) // 98.71 // q24**.**3
Uni Gene ID: Hs.461777

Gene 11:

Gene Name: 212518_at, P Value: 0.0000176
Ranked 14089 in RMA, RMA P Value: 0.083808345
Sequence source: GenBank
Transcript ID (Array Design): Hs.275182.0
GO Biological Process: None
GO Cellular Process: None
GO Molecular Function: 16308 // 1-phosphatidylinositol-4-phosphate 5-kinase activity // inferred from electronic annotation

Pathway: None
Chromosomal Location: chr19p13.3
Gene Symbol: PIP5K1C
Gene Title: phosphatidylinositol-4-phosphate 5-kinase, type I, gamma
Alignment: chr19:3581180-3651445 (-) // 97.74 // p13.3
Uni Gene ID: Hs.282177

Gene 12:

Gene Name: 206571_s_at, P Value: 0.0000191
Ranked 1553 in RMA, RMA P Value: 0.000018
Sequence source: GenBank
Transcript ID (Array Design): g4758523
GO Biological Process: 6468 // protein amino acid phosphorylation // inferred from direct assay /// 6950 // response to stress // inferred from direct assay /// 7165 // signal transduction // traceable author statement /// 7243 // protein kinase cascade // inferred from direct assay

GO Cellular Process: None

GO Molecular Function: 4674 // protein serine/threonine kinase activity // inferred from direct assay /// 5083 // small GTPase regulator activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from direct assay /// 16740 // transferase activity // inferred from electronic annotation

Chromosomal Location: chr2q11.2-q12
Gene Symbol: MAP4K4
Gene Title: mitogen-activated protein kinase kinase kinase kinase 4

Alignment: chr2:101773005-101966474 (+) // 94.1 // q11.2
Uni Gene ID: Hs.431550

Gene 13:

Gene Name: 222182_s_at, P Value: 0.0000232
Ranked 96 in RMA, RMA P Value: 0.0000000299
Sequence source: GenBank
Transcript ID (Array Design): Hs.239720.1
GO Biological Process: 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6358 // regulation of global transcription from RNA polymerase II promoter // non-traceable author statement

GO Cellular Process: 5634 // nucleus // non-traceable author statement

GO Molecular Function: 16455 // RNA polymerase II transcription mediator activity // traceable author statement /// 30528 // transcription regulator activity // inferred from electronic annotation

Pathway: None
Chromosomal Location: chr12q15
Gene Symbol: CNOT2
Gene Title: CCR4-NOT transcription complex, subunit 2
Alignment: chr12:68923477-69034139 (+) // 91.01 // q15
Uni Gene ID: Hs.133350

Gene 14:

Gene Name: 221426_s_at, P Value: 0.0000297
Ranked 17280 in RMA, RMA P Value: 0.256467209
Sequence source: GenBank
Transcript ID (Array Design): g13562103
GO Biological Process: 7165 // signal transduction // non-traceable author statement /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7608 // perception of smell // inferred from electronic annotation

GO Cellular Process: 5887 // integral to plasma membrane // not recorded

GO Molecular Function: 4872 // receptor activity // not recorded /// 4984 // olfactory receptor activity // inferred from electronic annotation

Pathway: None
Chromosomal Location: chr17p13.3
Gene Symbol: OR3A3
Gene Title: olfactory receptor, family 3, subfamily A, member 3 /// olfactory receptor, family 3, subfamily A, member 3

Alignment: chr17:3270611-3271577 (+) // 99.69 // p13.2 /// chr17:3128013-3128979 (-) // 91.82 // p13.3

Uni Gene ID: Hs.532689

Gene 15:

Gene Name: 201497_x_at, P Value: 0.0000306
Ranked 8165 in RMA, RMA P Value: 0.005935145
Sequence source: GenBank
Transcript ID (Array Design): g13124874
GO Biological Process: 6941 // striated muscle contraction // inferred from electronic annotation /// 7517 // muscle development // inferred from electronic annotation

GO Cellular Process: 5859 // muscle myosin // traceable author statement /// 5863 // striated muscle thick filament // inferred from electronic annotation /// 16459 // myosin // inferred from electronic annotation

GO Molecular Function: 3774 // motor activity // inferred from electronic annotation /// 3779 // actin binding // inferred from electronic annotation /// 5516 // calmodulin binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation

Pathway: None
Chromosomal Location: chr16p13.13-p13.12
Gene Symbol: MYH11
Gene Title: myosin, heavy polypeptide 11, smooth muscle
Alignment: chr16:15704494-15858369 (-) // 96.36 // p13.11
Uni Gene ID: Hs.460109

Gene 16:

Gene Name: 204358_s_at, P Value: 0.000031
Ranked 20868 in RMA, RMA P Value: 0.740771754
Sequence source: GenBank
Transcript ID (Array Design): g6808604
GO Biological Process: 7155 // cell adhesion // inferred from electronic annotation
GO Cellular Process: 5578 // extracellular matrix (sensu Metazoa) // non-traceable author statement /// 5887 // integral to plasma membrane // non-traceable author statement

GO Molecular Function: 5057 // receptor signaling protein activity // non-traceable author statement /// 30674 // protein binding, bridging // non-traceable author statement

Pathway: None
Chromosomal Location: chr14q24-q32
Gene Symbol: FLRT2
Gene Title: fibronectin leucine rich transmembrane protein 2
Alignment: chr14:85157554-85159807 (+) // 99.96 // q31.3
Uni Gene ID: Hs.533710

Gene 17:

Gene Name: 214743_at, P Value: 0.0000368
Ranked 128 in RMA, RMA P Value: 0.0000000493
Sequence source: GenBank
Transcript ID (Array Design): Hs.147049.1
GO Biological Process: 122 // negative regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7275 // development // traceable author statement

GO Cellular Process: 5634 // nucleus // inferred from electronic annotation

GO Molecular Function: 3700 // transcription factor activity // inferred from electronic annotation /// 3702 // RNA polymerase II transcription factor activity // traceable author statement

Pathway: None
Chromosomal Location: chr7q22.1
Gene Symbol: CUTL1
Gene Title: cut-like 1, CCAAT displacement protein (Drosophila**)**
Alignment: chr7:101054316-101486779 (+) // 98.03 // q22.1
Uni Gene ID: Hs.438974

Gene 18:

Gene Name: 209747_at, P Value: 0.0000386
Ranked 10101 in RMA, RMA P Value: 0.015951442
Sequence source: GenBank
Transcript ID (Array Design): g339551
GO Biological Process: 74 // regulation of cell cycle // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement /// 7267 // cell-cell signaling // traceable author statement /// 8283 // cell proliferation // inferred from electronic annotation /// 9887 // organogenesis // traceable author statement /// 16049 // cell growth // inferred from electronic annotation

GO Cellular Process: None

GO Molecular Function: 5160 // transforming growth factor beta receptor binding // traceable author statement /// 8083 // growth factor activity // inferred from electronic annotation

Pathway: None
Chromosomal Location: chr14q24
Gene Symbol: TGFB3
Gene Title: transforming growth factor, beta **3**
Alignment: chr14:75494252-75517251 (-) // 99.8 // q24.3

Uni Gene ID: Hs.2025

Gene 19:

Gene Name: 217696_at, P Value: 0.0000396
Ranked 9771 in RMA, RMA P Value: 0.013836891
Sequence source: GenBank
Transcript ID (Array Design): Hs.325905.0
GO Biological Process: 6486 // protein amino acid glycosylation // traceable author statement /// 42355 // L-fucose catabolism // non-traceable author statement

GO Cellular Process: 5794 // Golgi apparatus // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement

GO Molecular Function: 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 46920 // alpha (1, 3)-fucosyltransferase activity // traceable author statement

Pathway: None
Chromosomal Location: chr9q34.3
Gene Symbol: FUT7
Gene Title: fucosyltransferase 7 (alpha (1,3) fucosyltransferase)
Alignment: chr9:137200643-137202013 (-) // 85.29 // q34.3
Uni Gene ID: Hs.457

Gene 20:

Gene Name: 206866_at, P Value: 0.0000421
Ranked 16770 in RMA, RMA P Value: 0.216948881
Sequence source: GenBank
Transcript ID (Array Design): g4502724
GO Biological Process: 7155 // cell adhesion // inferred from electronic annotation /// 7155 // cell adhesion // traceable author statement /// 7156 // homophilic cell adhesion // inferred from electronic **annotation**

GO Cellular Process: 5886 // plasma membrane // not recorded /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation

GO Molecular Function: 5509 // calcium ion binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation

Pathway: None
Chromosomal Location: chr20q13.3
Gene Symbol: CDH4
Gene Title: cadherin 4, type 1, R-cadherin (retinal)
Alignment: chr20:59260953-59945678 (+) // 99.05 // q13.33
Uni Gene ID: Hs.217754

RMA DATA

Gene 1:

Gene Name: **209196_at**, P Value: 0.0000000000561
Ranked 1950 in MAS 5.0, MAS P Value: 0.021580564
Sequence Source: GenBank
Transcript ID (Array Design): g12653238
GO Biological Process: None
GO Cellular Process: None
GO Molecular Function: None
Pathway: None
Chromosomal Location: chr6p21.3
Gene Symbol: C6orf11
Gene Title: chromosome 6 open reading frame 11
Alignment: chr6:33354863-33364969 (-) // 98.51 // p21.32
Uni Gene ID: Hs.520063

Gene 2:

Gene Name: 212388_at, P Value: 0.000000000153
Ranked 477 in MAS 5.0, MAS P Value: 0.00273711
Sequence Source: GenBank
Transcript ID (Array Design): Hs.7243.0
GO Biological Process: 6511 // ubiquitin-dependent protein catabolism // inferred from electronic annotation /// 6512 // ubiquitin cycle // inferred from electronic annotation

GO Cellular Process: None

GO Molecular Function: 4197 // cysteine-type endopeptidase activity // inferred from electronic annotation /// 4221 // ubiquitin thiolesterase activity // inferred from electronic annotation

Pathway: None
Chromosomal Location: chr1p32.3
Gene Symbol: USP24
Gene Tittle: ubiquitin specific protease 24
Alignment: chr1:55244054-55326194 (-) // 93.86 // p32.3
Uni Gene ID: Hs.477009

Gene 3:

Gene Name: 212804_s_at, P Value: 0.000000000233
Ranked 3704 in MAS 5.0, MAS P Value: 0.059180047
Sequence Source: GenBank
Transcript ID (Array Design): Hs.172069.0
GO Biological Process: None
GO Cellular Process: None

GO Molecular Function: 5096 // GTPase activator activity // inferred from electronic annotation
Pathway: None
Chromosomal Location: chr9q33.3
Gene Symbol: GAPVD1
Gene Tittle: GTPase activating protein and VPS9 domains 1
Alignment: chr9:125163350-125206839 (+) // 91.88 // q33.3
Uni Gene ID: Hs.495134

Gene 4:
Gene Name: 220175_s_at, P Value: 0.000000000253
Ranked 11169 in MAS 5.0, MAS P Value: 0.343331356
Sequence Source: GenBank
Transcript ID (Array Design): g10190707
GO Biological Process: None
GO Cellular Process: None
GO Molecular Function: None
Pathway: None
Chromosomal Location: chr9p24.3 /// chr2q14.1 /// chr9q13 /// chr9q21.13
Gene Symbol: CBWD1 /// CBWD2 /// LOC220869 /// DC36
Gene Tittle: COBW domain containing 1 /// COBW domain containing 2/// dopamine responsive protein/// COBW-like placental proteins

Alignment: chr2:113936236-113969606 (+) // 92.99 // q14.1 /// chr9:68110711-68144113 (+) // 93.43 // q13 /// chr9:67940859-67974259 (-) // 93.14 // q13 /// chr9:111410-144773 (-) // 92.7 // p24.3

Uni Gene ID: Hs.355950

Gene 5
Gene Name: 205787_x_at, P Value: 0.000000000294
Ranked 503 in MAS 5.0, MAS P Value: 0.002929395
Sequence Source: GenBank
Transcript ID (Array Design): Hs.17969.0
GO Biological Process: None
GO Cellular Process: None
GO Molecular Function: 3676 // nucleic acid binding // inferred from electronic annotation
Pathway: None
Chromosomal Location: chr1q32.1
Gene Symbol: KIAA0663
Gene Tittle: KIAA0663 gene product
Alignment: chr1:200517708-200554903 (+) // 98.28 // q32.1 /// chr6:66068990-66073272 (+) // 95.26 // q12 /// chr1:216169664-216173944 (-) // 95.17 // q41

Uni Gene ID: Hs.532399

Gene 6:

Gene Name: 212729_at, P Value: 0.000000000394
Ranked 8146 in MAS 5.0, MAS P Value: 0.209572613
Sequence Source: GenBank
Transcript ID (Array Design): Hs.11101.0
GO Biological Process: 8285 // negative regulation of cell proliferation // non-traceable author statement
GO Cellular Process: None
GO Molecular Function: 4385 // guanylate kinase activity // non-traceable author statement /// 5515 // protein binding // inferred from electronic annotation

Pathway: None
Chromosomal Location: chrXq13.1
Gene Symbol: DLG3
Gene Tittle: discs, large homolog 3 (neuroendocrine-dlg, Drosophila**)**
Alignment: chrX: 69455175-69508357 (+) // 96.6 // q13.1
Uni Gene ID: Hs.522680

Gene 7:

Gene Name: 203693_s_at, P Value: 0.000000000432
Ranked 6290 in MAS 5.0, P Value: 0.136848216
Sequence Source: GenBank
Transcript ID (Array Design): g12669913
GO Biological Process: 74 // regulation of cell cycle // inferred from electronic annotation /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent **//** inferred from electronic annotation /// 6367 // transcription initiation from RNA polymerase II promoter // traceable author statement

GO Cellular Process: 5634 // nucleus // inferred from electronic annotation /// 5667 // transcription factor complex // inferred from electronic annotation

GO Molecular Function: 3700 // transcription factor activity // traceable author statement /// 5515 // protein binding // traceable author statement

Pathway: Cell_cycle_KEGG // GenMAPP /// G1_to_S_cell_cycle_Reactome // GenMAPP
Chromosomal Location: chr6p22
Gene Symbol: E2F3
Gene Tittle: E2F transcription factor 3
Alignment: chr6:20510376-20601921 (+) // 95.89 // p22.3
Uni Gene ID: Hs.269408

Gene 8:

Gene Name: **218318_s_at**, P Value: 0.000000000462
Ranked 20864 in MAS 5.0, MAS P Value: 0.909864385
Sequence Source: GenBank
Transcript ID (Array Design): g7706444

GO Biological Process: 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6468 // protein amino acid phosphorylation // inferred from sequence or structural similarity /// 7243 // protein kinase cascade // inferred from sequence or structural similarity /// 30178 // negative regulation of Wnt receptor signaling pathway // inferred from sequence or structural similarity

GO Cellular Process: 5634 // nucleus // inferred from sequence or structural similarity

GO Molecular Function: 287 // magnesium ion binding // inferred from sequence or structural similarity /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4707 // MAP kinase activity // inferred from sequence or structural similarity /// 5524 // ATP binding // inferred from sequence or structural similarity /// 16740 // transferase activity // inferred from electronic annotation

Pathway: None
Chromosomal Location: chr17q11.2
Gene Symbol: NLK
Gene Tittle: nemo like kinase
Alignment: chr17:23393814-23546710 (+) // 92.56 // q11.2
Uni Gene ID: Hs.208759

Gene 9:
Gene Name: 202200_s_at, P Value: 0.000000000486
Ranked 22 in MAS 5.0, MAS P Value: 0.0000481
Sequence Source: GenBank
Transcript ID (Array Design): g4507218
GO Biological Process: 74 // regulation of cell cycle // traceable author statement /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 8380 // RNA splicing // traceable author statement

GO Cellular Process: 5634 // nucleus // traceable author statement

GO Molecular Function: 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation

Pathway: mRNA_processing_Reactome // GenMAPP
Chromosomal Location: chr6p21.3-p21.2
Gene Symbol: SRPK1
Gene Tittle: SFRS protein kinase 1
Alignment: chr6:35908788-35996285 (-) // 96.37 // p21.31
Uni Gene ID: Hs.443861

Gene 10:
Gene Name: 214020_x_at, P Value: 0.0000000005
Ranked 8242 in MAS 5.0, MAS P Value: 0.212828844
Sequence Source: GenBank
Transcript ID (Array Design): Hs.149846.1

GO Biological Process: 7160 // cell-matrix adhesion // inferred from electronic annotation /// 7229 // integrin-mediated signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation

GO Cellular Process: 8305 // integrin complex // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation

GO Molecular Function: 4872 // receptor activity // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation

Pathway: Integrin-mediated_cell_adhesion_KEGG // GenMAPP
Chromosomal Location: chr3q21.2
Gene Symbol: ITGB5
Gene Tittle: Integrin, beta 5
Alignment: chr3:125964699-125964806 (-) // 46.54 // q21.2
Uni Gene ID: Hs.13155

Gene 11:
Gene Name: 215099_s_at, P Value: 0.000000000601
Ranked 445 in MAS 5.0, MAS P Value: 0.002480536
Sequence Source: GenBank
Transcript ID (Array Design): Hs.79372.1
GO Biological Process: 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation

GO Cellular Process: 5634 // nucleus // not recorded

GO Molecular Function: 3700 // transcription factor activity // non-traceable author statement /// 3707 // steroid hormone receptor activity // inferred from electronic annotation /// 3713 // transcription coactivator activity // traceable author statement /// 4886 // retinoid-X receptor activity // traceable author statement /// 5496 // steroid binding // inferred from electronic annotation

Pathway: Nuclear Receptors // GenMAPP
Chromosomal Location: chr6p21.3
Gene Symbol: RXRB
Gene Tittle: retinoid X receptor, beta
Alignment: chr6:33271166-33274324 (-) // 98.31 // p21.32
Uni Gene ID: Hs.388034

Gene 12:
Gene Name: 220086_at, P Value: 0.000000000663
Ranked 640 in MAS 5.0, MAS P Value: 0.004288133
Sequence Source: GenBank
Transcript ID (Array Design): g11968012
GO Biological Process: None
GO Cellular Process: 5634 // nucleus // inferred from electronic annotation
GO Molecular Function: 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation

Pathway: None
Chromosomal Location: chr10q26
Gene Symbol: ZNFN1A5
Gene Tittle: zinc finger protein, subfamily 1A, 54758301 (-) // 93.11 // q26.13
Uni Gene ID: Hs.501289
Alignment: chr10:124743188-12

Gene 13:
Gene Name: **217027_x_at**, P Value: 0.000000000715
Ranked 21862 in MAS 5.0, P Value: 0.972958532
Sequence Source: GenBank
Transcript ID (Array Design): Hs.283758.0
GO Biological Process: 59 // protein-nucleus import, docking // inferred from electronic annotation /// 60 // protein-nucleus import, translocation // traceable author statement /// 6607 // NLS-bearing substrate-nucleus import // traceable author statement /// 15031 // protein transport // inferred from electronic annotation

GO Cellular Process: 5634 // nucleus // inferred from electronic annotation /// 5643 // nuclear pore // traceable author statement /// 5737 // cytoplasm // traceable author statement

GO Molecular Function: 5488 // binding // inferred from electronic annotation /// 8139 // nuclear localization sequence binding // traceable author statement /// 8270 // zinc ion binding // traceable author statement /// 8565 // protein transporter activity // inferred from electronic annotation

Pathway: None
Chromosomal Location: chr17q21.32
Gene Symbol: KPNB1
Gene Tittle: karyopherin (importin) beta 1
Alignment: chr17:43112431-43113034 (+) // 94.37 // q21.32 /// chr7:148456600-148456831 (-) // 100.0 // q36.1

Uni Gene ID: Hs.532793

Gene 14:
Gene Name: 208930_s_at, P Value: 0.000000000938
Ranked 2009 in MAS 5.0, MAS P Value: 0.022608488
Sequence Source: GenBank
Transcript ID (Array Design): Hs.256583.1
GO Biological Process: 279 // M phase // non-traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation

GO Cellular Process: 5634 // nucleus // non-traceable author statement

GO Molecular Function: 3677 // DNA binding // inferred from electronic annotation /// 3725 // double-stranded RNA binding // inferred from electronic annotation

Pathway: None

Chromosomal Location: chr19p13.2
Gene Symbol: ILF3
Gene Tittle: interleukin enhancer binding factor 3, 90kDa
Alignment: chr19:10625973-10657441 (+) // 97.99 // p13.2
Uni Gene ID: Hs.465885

Gene 15:

Gene Name: 219129_s_at, P Value: 0.00000000101
Ranked 10320 in MAS 5.0, MAS P Value: 0.30441394
Sequence Source: GenBank
Transcript ID (Array Design): g13375861
GO Biological Process: None
GO Cellular Process: None
GO Molecular Function: None
Pathway: None
Chromosomal Location: chr5q33.2
Gene Symbol: SAP30L
Gene Tittle: Sin3A associated protein p30-like
Alignment: chr5:153805709-153815864 (+) // 94.15 // q33.2
Uni Gene ID: Hs.483906

Gene 16:

Gene Name: 207605_x_at, P Value: 0.00000000105
Ranked 3343 in MAS 5.0, MAS P Value: 0.050772082
Sequence Source: GenBank
Transcript ID (Array Design): g13374556
GO Biological Process: 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // non-traceable author statement

GO Cellular Process: 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement

GO Molecular Function: 3676 // nucleic acid binding // inferred from electronic annotation /// 3700 // transcription factor activity // non-traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 8270 // zinc ion binding // non-traceable author statement

Pathway: None
Chromosomal Location: chr7q11.2
Gene Symbol: ZNF117
Gene Tittle: zinc finger protein 117 (HPF9)
Alignment: chr7:63881312-63886547 (-) // 98.63 // q11.21
Uni Gene ID: Hs.250693

Gene 17:

Gene Name: 202884_s_at, P Value: 0.00000000109

Ranked 1141 in MAS 5.0, MAS P Value: 0.00978175
Sequence Source: GenBank
Transcript ID (Array Design): g11386166
GO Biological Process: 74 // regulation of cell cycle // inferred from sequence or structural similarity /// 188 // inactivation of MAPK // inferred from sequence or structural similarity /// 6275 // regulation of DNA replication // inferred from sequence or structural similarity /// 6445 // regulation of translation // inferred from sequence or structural similarity /// 6461 // protein complex assembly // inferred from sequence or structural similarity /// 6470 // protein amino acid dephosphorylation // inferred from sequence or structural similarity /// 6672 // ceramide metabolism // inferred from sequence or structural similarity /// 6917 // induction of apoptosis // inferred from sequence or structural similarity /// 8380 // RNA splicing // inferred from sequence or structural similarity /// 10033 // response to organic substance // inferred from sequence or structural similarity /// 19932 // second-messenger-mediated signaling // inferred from sequence or structural similarity /// 30111 // regulation of Wnt receptor signaling pathway // inferred from sequence or structural similarity /// 30155 // regulation of cell adhesion // inferred from sequence or structural similarity /// 30308 // negative regulation of cell growth // inferred from sequence or structural similarity /// 40008 // regulation of growth // inferred from sequence or structural similarity /// 42518 // negative regulation of tyrosine phosphorylation of Stat3 protein // inferred from sequence or structural similarity /// 45449 // regulation of transcription // inferred from sequence or structural similarity /// 45595 // regulation of cell differentiation // inferred from sequence or structural similarity

GO Cellular Process: 159 // protein phosphatase type 2A complex // inferred from sequence or structural similarity /// 5625 // soluble fraction // inferred from sequence or structural similarity /// 5634 // nucleus // inferred from sequence or structural similarity /// 5739 // mitochondrion // inferred from sequence or structural similarity /// 5829 // cytosol // inferred from sequence or structural similarity /// 15630 // microtubule cytoskeleton // inferred from sequence or structural similarity /// 16020 // membrane // inferred from sequence or structural similarity

GO Molecular Function: 158 // protein phosphatase type 2A activity // not recorded /// 3823 // antigen binding // inferred from sequence or structural similarity /// 4721 // phosphoprotein phosphatase activity // inferred from electronic annotation /// 5488 // binding // inferred from electronic annotation /// 5515 // protein binding // inferred from sequence or structural similarity /// 8601 // protein phosphatase type 2A regulator activity // inferred from sequence or structural similarity /// 16787 // hydrolase activity // inferred from electronic annotation /// 46982 // protein heterodimerization activity // inferred from sequence or structural similarity

Pathway: Glycogen_Metabolism // GenMAPP
Chromosomal Location: chr11q23.2
Gene Symbol: PPP2R1B
Gene Tittle: protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform
Alignment: chr11:111117442-111142323 (-) // 99.95 // q23.1
Uni Gene ID: Hs.269128

Gene 18:

Gene Name: 203536_s_at, P Value: 0.00000000137
Ranked 16317 in MAS 5.0, MAS P Value: 0.00978175
Sequence Source: GenBank
Transcript ID (Array Design): g4757987
GO Biological Process: 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement /// 8284 // positive regulation of cell proliferation // traceable author statement

GO Cellular Process: 5634 // nucleus // inferred from electronic annotation
GO Molecular Function: None
Pathway: None
Chromosomal Location: chr2q11.2
Gene Symbol: WDR39
Gene Tittle: WD repeat domain 39
Alignment: chr2:96353806-96359170 (+) // 97.38 // q11.2
Uni Gene ID: Hs.12109

Gene 19:

Gene Name: 201048_x_at, P Value: 0.0000000015
Ranked 12528 in MAS 5.0, MAS P Value: 0.413603435
Sequence Source: GenBank
Transcript ID (Array Design): g4506372
GO Biological Process: 7264 // small GTPase mediated signal transduction // inferred from electronic annotation /// 15031 // protein transport // inferred from electronic annotation

GO Cellular Process: 5794 // Golgi apparatus // inferred from electronic annotation

GO Molecular Function: 3924 // GTPase activity // traceable author statement /// 5525 // GTP binding // inferred from electronic annotation

Pathway: None
Chromosomal Location: chr11q13.3
Gene Symbol: RAB6A
Gene Tittle: RAB6A, member RAS oncogene family
Alignment: chr2:130453849-130454579 (+) // 90.14 // q21.1 /// chr2:131954364-131955094 (-) // 90.41 // q21.1 /// chr11:73066547-73149397 (-) // 99.46 // q13.4

Uni Gene ID: Hs.503222

Gene 20:

Gene Name: 218294_s_at, P Value: 0.00000000178
Ranked 41 in MAS 5.0, MAS P Value: 0.000102256
Sequence Source: GenBank
Transcript ID (Array Design): g12006056
GO Biological Process: 15031 // protein transport // inferred from electronic annotation
GO Cellular Process: 5634 // nucleus // inferred from electronic annotation /// 5643 // nuclear pore // traceable author statement /// 16021 // integral to membrane // inferred

from electronic annotation /// 19867 // outer membrane // inferred from electronic annotation

GO Molecular Function: 15288 // porin activity // inferred from electronic annotation
Pathway: None
Chromosomal Location: chr22q13.31
Gene Symbol: NUP50
Gene Tittle: nucleoporin 50kDa
Alignment: chr22:43902363-43903836 (+) // 95.35 // q13.31 /// chr14:64133957-64135423 (-) // 94.07 // q23.3

Uni Gene ID: Hs.475103

B mas rank

GENE 1
Gene Name: 244677_at, P Value: 0.0000038011569742924
Ranked 70 in RMA, RMA P Value: 0.000026747578998787
Target Description: Consensus includes gb:AA416756 /FEA=EST /DB_XREF=gi:2077710 /DB_XREF=est:zu08h08.s1 /CLONE=IMAGE:731295 /UG=Hs.161051 ESTs, Moderately similar to ALU6_HUMAN ALU SUBFAMILY SP SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: None
Transcript Assignment: AA416756 // /DB_XREF=zu08h08.s1 /CLONE=IMAGE:731295 // gb // --- // ---
Annotation Notes: None
Uni Gene ID: None
Gene Title: None
Chromosomal Location: None
Gene Symbol: None
Alignment: chr17:7997493-7998118 (-) // 78.64 // p13.1

GENE 2

Gene Name: 242424_at, P Value: 4.06232646188442E-06

Ranked 47 in RMA, RMAP Value: 0.0000174011899405357

Target Description: Consensus includes gb:AA345855 /FEA=EST /DB_XREF=gi:1998113 /DB_XREF=est:EST51947 /UG=Hs.273613 ESTs, Moderately similar to ALUB_HUMAN !!!! ALU CLASS B WARNING ENTRY !!! H.sapiens

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: None
Pathway: None

Annotation Transcript Cluster: AI687578,AW811065,AW811149,AA345855
Transcript Assignment: AA345855 // /DB_XREF=EST51947 // gb // --- // --- /// AI687578 // /DB_XREF=tp97d06.x1 /CLONE=IMAGE:2207243 // gb // --- // --- /// AW811065 // /DB_XREF=MR2-ST0131-211099-008-e08 // gb // --- // --- /// AW811149 // /DB_XREF=MR2-ST0131-111199-003-h03 // gb

Annotation Notes: None
Uni Gene ID: Hs.370457
Gene Title: LETM1 domain containing 1
Chromosomal Location: chr12q13.12
Gene Symbol: LETMD1
Alignment: chr12:49734921-49735668 (+) // 39.02 // q13.12

GENE 3

Gene Name: 237356_at, P Value: 4.92269710261617E-06

Ranked 1321 in RMA, RMA P Value: 0.00235842684237642

Target Description: Consensus includes gb:AI697714 /FEA=EST /DB_XREF=gi:4985614 /DB_XREF=est:we16e06.x1 /CLONE=IMAGE:2341282 /UG=Hs.202512 ESTs

Go Biological Process: 6508 // proteolysis and peptidolysis // inferred from electronic annotation

Go Cellular Process: 5578 // extracellular matrix (sensu Metazoa) // inferred from electronic annotation /// 31012 // extracellular matrix // inferred from electronic annotation

Go Molecular Function: 4222 // metalloendopeptidase activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation

Pathway: None

Annotation Transcript Cluster: BF511173,AW860192,BE327108,AI693812,AI697714,BE220068,AW341356,AI702158,BF433567,BE328891,AW860134,AW770767

Transcript Assignment: AI693812 // wd87b06.x1 Homo sapiens cDNA, 3’ end /clone=IMAGE-2338547 /clone_end=3’ /gb=AI693812 /gi=4971152 /ug=Hs.202512 /len=501 // gb // --- // --- /// AI693812 // /DB_XREF=wd87b06.x1 /CLONE=IMAGE:2338547 // gb // --- // --- /// AI697714 // we16e06.x1

Annotation Notes: None
Uni Gene ID: Hs.188746
Gene Title: A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18
Chromosomal Location: chr16q23
Gene Symbol: ADAMTS18
Alignment: chr16:75928186-75929131 (-) // 80.46 // q23.1

GENE 4

Gene Name: 228567_at, P Value: 5.44402046487313E-06
Ranked 360 in RMA, RMA P Value: 0.000295270711898832
Target Description: Consensus includes gb:BG109230 /FEA=EST /DB_XREF=gi:12602736 /DB_XREF=est:602281257F1 /CLONE=IMAGE:4368663 /UG=Hs.46824 ESTs

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: AK095707(11)
Transcript Assignment: AK095707 // Homo sapiens cDNA FLJ38388 fis, clone FEBRA2004485. // gb // 11 // ---

Annotation Notes: GENSCAN00000060676 // ensembl // 4 // Negative Strand Matching Probes
Uni Gene ID: Hs.374278
Gene Title: CDNA FLJ38388 fis, clone FEBRA2004485
Chromosomal Location: None
Gene Symbol: None
Alignment: chr16:79980865-79981990 (+) // 99.91 // q23.2

GENE 5

Gene Name: 223676_at, P Value: 6.82701510101857E-06

Ranked 9309 in RMA, RMA P Value: 0.134096776552327

Target Description: gb:BC001256.1 /DEF=Homo sapiens, hypothetical protein RP4-622L5, clone MGC:4996, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein RP4-622L5 /DB_XREF=gi:12654826 /UG=Hs.272299 hypothetical protein RP4-622L5 /FL=gb:BC001256.1

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: AK075260(11),BC001256(11),BC038842(11),NM_019118(11)
Transcript Assignment: AK075260 // Homo sapiens cDNA FLJ90779 fis, clone THYRO1001205. // gb // 11 // --- /// BC001256 // Homo sapiens hypothetical protein RP4-622L5, mRNA (cDNA clone IMAGE:3463478), complete cds. // gb // 11 // --- /// BC038842 // Homo sapiens hypothetical pro

Annotation Notes: BC041458 // gb // 4 // Negative Strand Matching Probes /// GENSCAN00000011904 // ensembl // 4 // Negative Strand Matching Probes

Uni Gene ID: Hs.272299
Gene Title: hypothetical protein RP4-622L5
Chromosomal Location: chr1p36.11-p34.2
Gene Symbol: RP4-622L5

GENE 6

Gene Name: 237206_at, P Value: 7.00296578171056E-06

Ranked 76 in RMA, RMA P Value: 0.0000284573676381239

Target Description: Consensus includes gb:AI452798 /FEA=EST /DB_XREF=gi:4287873 /DB_XREF=est:tj50f07.x1 /CLONE=IMAGE:2144965 /UG=Hs.165892 ESTs

Go Biological Process: 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation

Go Cellular Process: 5634 // nucleus // inferred from electronic annotation
Go Molecular Function: 3677 // DNA binding // inferred from electronic annotation
Pathway: None
Annotation Transcript Cluster: AK128608(11),BX640673(11)
Transcript Assignment: AK096753 // Homo sapiens cDNA FLJ39434 fis, clone PROST2004161. // gb // 9 // --- /// AK128608 // Homo sapiens cDNA FLJ46767 fis, clone TRACH3024823. // gb // 11 // --- /// BX640673 // Homo sapiens mRNA; cDNA DKFZp686O15128 (from clone DKFZp686O15128). //

Annotation Notes: None
Uni Gene ID: Hs.462257
Gene Title: myocardin
Chromosomal Location: chr17p11.2
Gene Symbol: MYOCD
Alignment: chr17:12608893-12609359 (+) // 99.79 // p12

GENE 7
Gene Name: 232134_at, P Value: 9.52524804986865E-06
Ranked 1 in MAS, MAS P Value: 1.01686129960754E-07
Target Description: Consensus includes gb:AW139789 /FEA=EST /DB_XREF=gi:6144507 /DB_XREF=est:UI-H-BI1-aeb-h-10-0-UI.s1 /CLONE=IMAGE:2718955 /UG=Hs.16370 Homo sapiens cDNA FLJ11652 fis, clone HEMBA1004461

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: AK021714(10)
Transcript Assignment: AK021714 // Homo sapiens cDNA FLJ11652 fis, clone HEMBA1004461. // gb // 10 // ---

Annotation Notes: None
Uni Gene ID: Hs.16370
Gene Title: CDNA FLJ11652 fis, clone HEMBA1004461
Chromosomal Location: None

Gene Symbol: None
Alignment: chr5:6781969-6783951 (+) // 91.52 // p15.31

GENE 8

Gene Name: 231843_at, P Value: 9.80191715282963E-06

Ranked 310 in MAS, MAS P Value: 0.000237696911618013

Target Description: Consensus includes gb:AB046815.1 /DEF=Homo sapiens mRNA for KIAA1595 protein, partial cds. /FEA=mRNA /GEN=KIAA1595 /PROD=KIAA1595 protein /DB_XREF=gi:10047264 /UG=Hs.286173 KIAA1595 protein

Go Biological Process: None

Go Cellular Process: None

Go Molecular Function: 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 8026 // ATP-dependent helicase activity // inferred from

Pathway: None

Annotation Transcript Cluster: AB046815(9),BC035911(9),NM_020936(11)

Transcript Assignment: AB046815 // Homo sapiens mRNA for KIAA1595 protein, partial cds. // gb // 9 // --- /// BC035911 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 55, mRNA (cDNA clone IMAGE:5493465), complete cds. // gb // 9 // --- /// NM_020936 // Homo sapiens DEAD

Annotation Notes: GENSCAN00000036846 // ensembl // 1 // Cross Hyb Matching Probes
Uni Gene ID: Hs.286173
Gene Title: DEAD (Asp-Glu-Ala-Asp) box polypeptide 55
Chromosomal Location: chr12q24.31
Gene Symbol: DDX55
Alignment: chr12:122163642-122630097 (+) // 56.03 // q24.31

GENE 9

Gene Name: 224269_at, P Value: 0.0000112624698742625

Ranked 2175 in RMA, RMA P Value: 0.00576322129954776

Target Description: gb:BC004180.1 /DEF=Homo sapiens, Similar to RIKEN cDNA 1110054P19 gene, clone MGC:2782, mRNA, complete cds. /FEA=mRNA /PROD=Similar to RIKEN cDNA 1110054P19 gene /DB_XREF=gi:13278824 /UG=Hs.307016 Homo sapiens, Similar to RIKEN cDNA 1110054P19

Go Biological Process: None
Go Cellular Process: 45095 // keratin filament // inferred from electronic annotation
Go Molecular Function: None
Pathway: None

Annotation Transcript Cluster: NM_031854(11)
Transcript Assignment: NM_031854 // Homo sapiens keratin associated protein 4-12 (KRTAP4-12), mRNA. // refseq // 11 // ---

Annotation Notes: GENSCAN00000041898 // ensembl // 1 // Cross Hyb Matching Probes /// GENSCAN00000002262 // ensembl // 1 // Cross Hyb Matching Probes

Uni Gene ID: Hs.307016
Gene Title: keratin associated protein 4-12
Chromosomal Location: chr17q12-q21
Gene Symbol: KRTAP4-12
Alignment: chr17_random:2436180-2437233 (+) // 83.06 // /// chr17:36532872-36533925 (-) // 83.06 // q21.2 /// chr17:36549649-36570491 (-) // 46.67 // q21.2 /// chr17:36507306-36550287 (-) // 46.39 // q21.2

GENE 10

Gene Name: 225689_at, P Value: 0.000012292306550199
Ranked 11999 in RMA, RMA P Value: 0.246064984366905
Target Description: Consensus includes gb:BE856822 /FEA=EST /DB_XREF=gi:10370235 /DB_XREF=est:7f69d08.x1 /CLONE=IMAGE:3299919 /UG=Hs.12313 Homo sapiens, clone IMAGE:3926450, mRNA, partial cds

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: 16740 // transferase activity // inferred from electronic annotation
Pathway: None
Annotation Transcript Cluster: AK124737(11),NM_032806(11)
Transcript Assignment: AK124737 // Homo sapiens cDNA FLJ42747 fis, clone BRAWH3000314. // gb // 11 // --- /// NM_032806 // Homo sapiens hypothetical protein FLJ14566 (FLJ14566), mRNA. // refseq // 11 // --- /// ENST00000344697 // cdna:ccds chromosome:NCBI35:3:43095735:43122569:

Annotation Notes: GENSCAN00000017975 // ensembl // 2 // Cross Hyb Matching Probes
Uni Gene ID: Hs.12313
Gene Title: glycosyltransferase
Chromosomal Location: chr3p22.1
Gene Symbol: AGO61
Alignment: chr3:43095729-43122554 (-) // 98.02 // p22.1

GENE 11

Gene Name: 229422_at, P Value: 0.0000177023276415333

Ranked 8 in RMA, RMA P Value: 1.76902731663375E-06

Target Description: Consensus includes gb:AA448346 /FEA=EST /DB_XREF=gi:2162016 /DB_XREF=est:zw98g12.s1 /CLONE=IMAGE:785062 /UG=Hs.309734 ESTs, Moderately similar to NRD2 convertase H.sapiens

Go Biological Process: 6508 // proteolysis and peptidolysis // non-traceable author statement /// 7528 // neuromuscular junction development // traceable author statement

Go Cellular Process: None
Go Molecular Function: 16919 // nardilysin activity // non-traceable author statement
Pathway: None
Annotation Transcript Cluster: AK090844(9)
Transcript Assignment: AK090844 // Homo sapiens cDNA FLJ33525 fis, clone BRAMY2006779. // gb // 9 // ---

Annotation Notes: ENSESTT00000083586 // ensembl // 1 // Cross Hyb Matching Probes /// ENSESTT00000083587 // ensembl // 1 // Cross Hyb Matching Probes /// ENSESTT00000083588 // ensembl // 1 // Cross Hyb Matching Probes /// ENSESTT00000083589 // ensembl // 1 // Cross Hyb Mat

Uni Gene ID: Hs.551509
Gene Title: Nardilysin (N-arginine dibasic convertase)
Chromosomal Location: chr1p32.2-p32.1
Gene Symbol: NRD1
Alignment: chr1:52014657-52015643 (-) // 87.11 // p32.3

GENE 12

Gene Name: 239886_at, P Value: 0.0000194843919563148

Ranked 117 in RMA, RMA P Value: 0.0000591091690456125

Target Description: Consensus includes gb:N72610 /FEA=EST /DB_XREF=gi:1229714 /DB_XREF=est:za46h03.s1 /CLONE=IMAGE:295637 /UG=Hs.183834 ESTs

Go Biological Process: 6508 // proteolysis and peptidolysis // inferred from electronic annotation /// 6915 // apoptosis // inferred from electronic annotation /// 16567 // protein ubiquitination // inferred from electronic annotation

Go Cellular Process: 151 // ubiquitin ligase complex // inferred from electronic annotation /// 16021 // integral to membrane // inferred from sequence or structural similarity

Go Molecular Function: 4842 // ubiquitin-protein ligase activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation

Pathway: None

Annotation Transcript Cluster: N72610,AA659457,H69022,AW152217,AW452073

Transcript Assignment: AA659457 // nu24e03.s1 Homo sapiens cDNA /clone=IMAGE-1208956 /gb=AA659457 /gi=2595611 /ug=Hs.183834 /len=450 // gb // --- // --- /// AA659457 // /DB_XREF=nu24e03.s1 /CLONE=IMAGE:1208956 // gb // --- // --- /// AW152217 // /DB_XREF=xf03g06.x1 /CLONE=IMAGE

Annotation Notes: None
Uni Gene ID: Hs.484363

Gene Title: Ring finger protein 130
Chromosomal Location: chr5q35.3
Gene Symbol: RNF130
Alignment: chr5:179367614-179368041 (-) // 51.69 // q35.3

GENE 13

Gene Name: 226412_at, P Value: 0.0000221454400251009

Ranked 860in RMA, RMA P Value: 0.00120277430096172

Target Description: Consensus includes gb:N66397 /FEA=EST /DB_XREF=gi:1218522 /DB_XREF=est:yz39g04.s1 /CLONE=IMAGE:285462 /UG=Hs.18368 DKFZP564B0769 protein

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: AJ420570(11)
Transcript Assignment: AJ420570 // Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1623397. // gb // 11 // --- /// BX648520 // Homo sapiens mRNA; cDNA DKFZp686F0485 (from clone DKFZp686F0485). // gb // 11 // ---

Annotation Notes: ENSESTT00000056786 // ensembl // 5 // Cross Hyb Matching Probes
Uni Gene ID: Hs.520287
Gene Title: chromosome 6 open reading frame 111
Chromosomal Location: chr6q16.3
Gene Symbol: C6orf111
Alignment: chr6:99966396-99979889 (-) // 93.77 // q16.2

GENE 14

Gene Name: 236692_at, P Value: 0.000022231288075325

Ranked 1785 in RMA, RMA P Value: 0.00405376151400838

Target Description: Consensus includes gb:AI523391 /FEA=EST /DB_XREF=gi:4437526 /DB_XREF=est:ar72c09.x1 /CLONE=IMAGE:2128144 /UG=Hs.88550 ESTs

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: ENSESTT00000062022
Transcript Assignment: ENSESTT00000062022 // --- // ensembl // 0 // chr17:30757995-30758366(-)
Annotation Notes: BX648369 // gb // 2 // Cross Hyb Matching Probes /// NM_173666 // refseq // 2 // Cross Hyb Matching Probes /// ENST00000304058 // ensembl // 2 // Cross Hyb Matching Probes

Uni Gene ID: None
Gene Title: None
Chromosomal Location: None
Gene Symbol: None
Alignment: chr17:30757818-30758263 (-) // 98.45 // q12

GENE 15

Gene Name: 239701_at, P Value: 0.0000227555250149614

Ranked 7143 in RMA, RMA P Value: 0.0738590190447246

Target Description: Consensus includes gb:BF508564 /FEA=EST /DB_XREF=gi:11591862 /DB_XREF=est:UI-H-BI4-aoo-b-07-0-UI/CLONE=IMAGE:3085404 /UG=Hs.199310 ESTs

Go Biological Process: 7155 // cell adhesion // non-traceable author statement /// 7267 // cell-cell signaling // not recorded /// 7596 // blood coagulation // traceable author statement /// 19735 // antimicrobial humoral response (sensu Vertebrata) // not recorded

Go Cellular Process: 5886 // plasma membrane // non-traceable author statement /// 5887 // integral to plasma membrane // traceable author statement

Go Molecular Function: 287 // magnesium ion binding // inferred from electronic annotation /// 4050 // apyrase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation

Pathway: Purine metabolism // KEGG /// Pyrimidine metabolism // KEGG

Annotation Transcript Cluster: AI187945,AI762649,AA347954

Transcript Assignment: AA347954 // EST54362 Homo sapiens cDNA, 3’ end /clone=ATCC-149033 /clone_end=3’ /gb=AA347954 /gi=2000211 /ug=Hs.199310 /len=112 // gb // --- // --- /// AA347954 // /DB_XREF=EST54362 // gb // --- // --- /// AI187945 // qe13e09.x1 Homo sapiens cDNA, 3’ end

Annotation Notes: None
Uni Gene ID: Hs.550467
Gene Title: Ectonucleoside triphosphate diphosphohydrolase 1
Chromosomal Location: chr10q24
Gene Symbol: ENTPD1
Alignment: chr10:97532868-97533457 (+) // 97.01 // q24.1

GENE 16

Gene Name: 234622_at, P Value: 0.0000237203943009856

Ranked 161 in RMA, RMA P Value: 0.0000898130549125131

Target Description: Consensus includes gb:AK025167.1 /DEF=Homo sapiens cDNA: FLJ21514 fis, clone COL05780. /FEA=mRNA /DB_XREF=gi:10437629 /UG=Hs.306775 Homo sapiens cDNA: FLJ21514 fis, clone COL05780

Go Biological Process: None

Go Cellular Process: None
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: AK025167
Transcript Assignment: AK025167 // /DEF=Homo sapiens cDNA: FLJ21514 fis, clone COL05780. // gb // --- // ---

Annotation Notes: None
Uni Gene ID: Hs.128586
Gene Title: Hypothetical protein LOC221814
Chromosomal Location: chr7p21.3
Gene Symbol: LOC221814
Alignment: chr7:15947003-15948943 (+) // 67.83 // p21.1

GENE 17

Gene Name: 227561_at, P Value: 0.0000255056728555303

Ranked 771 in RMA, RMA P Value: 0.00103275248044499

Target Description: Consensus includes gb:W73819 /FEA=EST /DB_XREF=gi:1383972 /DB_XREF=est:zd52e11.s1 /CLONE=IMAGE:344300 /UG=Hs.42392 ESTs

Go Biological Process: 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 7155 // cell adhesion // traceable author statement /// 7165 // signal transduction // traceable author statement /// 7169 // transmembrane receptor protein tyrosine kin

Go Cellular Process: 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation

Go Molecular Function: 4714 // transmembrane receptor protein tyrosine kinase activity // traceable author statement /// 4872 // receptor activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase acti

Pathway: None
Annotation Transcript Cluster: AK092374(11),BX537651(10)
Transcript Assignment: AK092374 // Homo sapiens cDNA FLJ35055 fis, clone OCBBF2018563. // gb // 11 // --- /// BX537651 // Homo sapiens mRNA; cDNA DKFZp686C0390 (from clone DKFZp686C0390). // gb // 10 // ---

Annotation Notes: None
Uni Gene ID: Hs.275757
Gene Title: Discoidin domain receptor family, member 2
Chromosomal Location: chr1q12-q23
Gene Symbol: DDR2
Alignment: chr1:159484461-159485774 (+) // 99.32 // q23.3 /// chr10:38677607-38678927 (+) // 96.66 // p11.21

GENE 18

Gene Name: 234668_at, P Value: 0.0000266262625550073
Ranked 53 in RMA, RMA P Value: 0.0000200056245918123
Target Description: Consensus includes gb:AK026828.1 /DEF=Homo sapiens cDNA: FLJ23175 fis, clone LNG10438. /FEA=mRNA /DB_XREF=gi:10439774 /UG=Hs.306886 Homo sapiens cDNA: FLJ23175 fis, clone LNG10438

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: AK026828(11)
Transcript Assignment: AK026828 // Homo sapiens cDNA: FLJ23175 fis, clone LNG10438. // gb // 11 // ---

Annotation Notes: None
Uni Gene ID: Hs.443061
Gene Title: Chromosome X open reading frame 45
Chromosomal Location: chrXq23
Gene Symbol: CXorf45
Alignment: chrX:110794958-110796042 (+) // 30.22 // q23

GENE 19

Gene Name: 244024_at, P Value: 0.0000266510727575664

Ranked 595 in RMA, RMA P Value: 0.000695031785357125

Target Description: Consensus includes gb:T67481 /FEA=EST /DB_XREF=gi:678629 /DB_XREF=est:yd12d12.s1 /CLONE=IMAGE:66935 /UG=Hs.189690 ESTs

Go Biological Process: 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation

Go Cellular Process: 5634 // nucleus // inferred from electronic annotation

Go Molecular Function: 3676 // nucleic acid binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation

Pathway: None

Annotation Transcript Cluster: BX648401(11),NM_001007088(11),NM_006962(11)

Transcript Assignment: BX648401 // Homo sapiens mRNA; cDNA DKFZp686E12229 (from clone DKFZp686E12229). // gb // 11 // --- /// NM_006962 // Homo sapiens zinc finger protein 21 (KOX 14) (ZNF21), transcript variant 1, mRNA. // refseq // 11 // --- /// NM_001007088 // Homo sapiens z

Annotation Notes: None
Uni Gene ID: Hs.189690
Gene Title: zinc finger protein 21 (KOX 14)
Chromosomal Location: chrXp22.11-p11.23
Gene Symbol: ZNF21

Alignment: chrX:47591182-47591593 (-) // 95.57 // p11.23

GENE 20

Gene Name: 236883_at, P Value: 0.0000269925019009687

Ranked 1750 in RMA, RMA P Value: 0.00390181422224734

Target Description: Consensus includes gb:AI769104 /FEA=EST /DB_XREF=gi:5235613 /DB_XREF=est:wg32g09.x1 /CLONE=IMAGE:2366848 /UG=Hs.211167 ESTs

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: AA808388
Transcript Assignment: AA808388 // /DB_XREF=oa90d10.s1 /CLONE=IMAGE:1319539 // gb // --- // ---

Annotation Notes: None
Uni Gene ID: Hs.537931
Gene Title: Transcribed locus
Chromosomal Location: None
Gene Symbol: None
Alignment: chr1:111382820-111383572 (-) // 39.38 // p13.3

B RMA RANKS

GENE 1

Gene Name: 232134_at, P Value: 1.01686129960754E-07

Ranked 7 in MAS, MAS P Value: 9.52524804986865E-06

Target Description: Consensus includes gb: AW139789 /FEA=EST /DB_XREF=gi: 6144507 /DB_XREF=est: UI-H-BI1-aeb-h-10-0-UI.s1 /CLONE=IMAGE: 2718955 /UG=Hs.16370 Homo sapiens cDNA FLJ11652 fis, clone HEMBA1004461

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: AK021714(10)
Transcript Assignment: AK021714 // Homo sapiens cDNA FLJ11652 fis, clone HEMBA1004461. // gb // 10 // ---

Annotation Notes: None
Uni Gene ID: Hs.16370
Gene Title: CDNA FLJ11652 fis, clone HEMBA1004461
Chromosomal Location: None
Gene Symbol: None

Alignment: chr5:6781969-6783951 (+) // 91.52 // p15.31

GENE 2

Gene Name: 239264_at, P Value: 1.95097149768841E-07

Ranked 7210 in MAS, MAS P Value: 0.179045869512288

Target Description : Consensus includes gb:AW973078 /FEA=EST /DB_XREF=gi:8162924 /DB_XREF=est:EST385175 /UG=Hs.293039 ESTs

Go Biological Process: 6904 // vesicle docking during exocytosis // inferred from electronic annotation /// 15031 // protein transport // inferred from electronic annotation

Go Cellular Process: 145 // exocyst // inferred from electronic annotation
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: AW973078,AI791652,H93340,AI240025,AA531562,AI247774,AI821511

Transcript Assignment: AA531562 // nj64e05.s1 Homo sapiens cDNA /clone=IMAGE-997280 /gb=AA531562 /gi=2274268 /ug=Hs.125010 /len=415 // gb // --- // --- /// AA531562 // /DB_XREF=nj64e05.s1 /CLONE=IMAGE:997280 // gb // --- // --- /// AI240025 // qh39a06.x1 Homo sapiens cDNA, 3' e

Annotation Notes: None
Uni Gene ID: Hs.321273
Gene Title: SEC8-like 1 (S. cerevisiae)
Chromosomal Location: chr7q31
Gene Symbol: SEC8L1
Alignment: chr7:132803294-132803696 (+) // 52.95 // q33

GENE 3:
Gene Name: 224233_s_at, P Value: 4.42660007760054E-07
Ranked 4574 in MAS, MAS P Value: 0.0829377670490903
Target Description: gb:BC002535.1 /DEF=Homo sapiens, hypothetical protein FLJ10504, clone MGC:959, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein FLJ10504 /DB_XREF=gi:12803422 /UG=Hs.279763 hypothetical protein FLJ10504 /FL=gb:BC002535.1

Go Biological Process: 6508 // proteolysis and peptidolysis // inferred from electronic annotation
Go Cellular Process: None
Go Molecular Function: 4289 // subtilase activity // inferred from electronic annotation
Pathway: None

Annotation Transcript Cluster: AF111708(11),AK056128(11),BC002535(11),NM_018116(11)

Transcript Assignment: AF111708 // Homo sapiens SLTP005 (LST005) mRNA, complete cds. // gb // 11 // --- /// BC002535 // Homo sapiens misato, mRNA (cDNA clone

MGC:959 IMAGE:3140498), complete cds. // gb // 11 // --- /// CR936872 // Homo sapiens mRNA; cDNA DKFZp686B1757 (from clo

Annotation Notes: AB046826 // gb // 6 // Negative Strand Matching Probes /// ENST00000271883 // ensembl // 6 // Negative Strand Matching Probes /// GENSCAN00000033383 // ensembl // 7 // Cross Hyb Matching Probes

Uni Gene ID: Hs.279763
Gene Title: misato
Chromosomal Location: chr1q22
Gene Symbol: MST
Alignments: chr1:152393088-152397190 (+) // 96.03 // q22 /// chr1:152528668-152533054 (+) // 95.65 // q22

GENE 4:
Gene Name: 238842_at, P Value: 4.64825831825166E-07
Ranked 240 in MAS, P Value: 0.00103853843447377
Target Description: Consensus includes gb:BE000242 /FEA=EST /DB_XREF=gi:8260475 /DB_XREF=est:MR0-BN0070-260400-017-b09 /UG=Hs.192068 ESTs

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: GENSCAN00000019553
Transcript Assignment: GENSCAN00000019553 // cdna:Genscan chromosome:NCBI35:10:98709543:98742932:1 // ensembl // 0 // chr10:98709542-98742932(+)

Annotation Notes: None
Uni Gene ID: None
Gene Title: None
Chromosomal Location: None
Gene Symbol: None
Alignment: chr10:98740302-98740791 (+) // 81.85 // q24.1

GENE 5

Gene Name: 224595_at, P Value: 5.20085010391469E-07

Ranked 26 in MAS, MAS P Value: 0.0000379032345965147

Target Description: Consensus includes gb:AK022549.1 /DEF=Homo sapiens cDNA FLJ12487 fis, clone NT2RM2000609, highly similar to Homo sapiens CTL1 gene. /FEA=mRNA /DB_XREF=gi:10434002 /UG=Hs.179902 transporter-like protein /FL=gb:NM_022109.1

Go Biological Process: 15871 // choline transport // traceable author statement
Go Cellular Process: 16021 // integral to membrane // traceable author statement

Go Molecular Function: 15220 // choline transporter activity // traceable author statement
Pathway: None
Annotation Transcript Cluster: BC018213(11),NM_080546(11)
Transcript Assignment: BC018213 // Homo sapiens CDW92 antigen, mRNA (cDNA clone IMAGE:3882479), partial cds. // gb // 11 // --- /// NM_080546 // Homo sapiens CDW92 antigen (CDW92), mRNA. // refseq // 11 // --- /// ENST00000185520 // cdna:ccds chromosome:NCBI35:9:105086666:10523

Annotation Notes: AJ272365 // gb // 8 // Cross Hyb Matching Probes
Uni Gene ID: Hs.494700
Gene Title: CDW92 antigen
Chromosomal Location: chr9q31.2
Gene Symbol: CDW92
Alignment: chr9:105086584-105233239 (+) // 96.06 // q31.1

GENE 6:

Gene Name: 226442_at, P Value: 1.11737398955647E-06

Ranked 1527 in MAS, MAS P Value: 0.0149357535264563

Target Description: Consensus includes gb:H06267 /FEA=EST /DB_XREF=gi:869819 /DB_XREF=est:yl79a05.s1 /CLONE=IMAGE:44083 /UG=Hs.321640 ESTs, Highly similar to JC7326 bood POZ containing protein H.sapiens

Go Biological Process: None

Go Cellular Process: None

Go Molecular Function: 3746 // translation elongation factor activity // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation

Pathway: None
Annotation Transcript Cluster: AB053325
(11), AF447886 (9), NM_032548 (11), NM_172027 (11), NM_172028 (11)
Transcript Assignment: AF447886 // Homo sapiens PP2259 mRNA, complete cds. // gb // 9 // --- /// AB053325 // Homo sapiens mRNA for BPOZ splice variant type2, complete cds. // gb // 11 // --- /// NM_172028 // Homo sapiens ankyrin repeat and BTB (POZ) domain containing 1 (ABTB1),

Annotation Notes: AK090422 // gb // 8 // Cross Hyb Matching Probes /// ENSESTT00000075389 // ensembl // 7 // Cross Hyb Matching Probes

Uni Gene ID: Hs.107812
Gene Title: ankyrin repeat and BTB (POZ) domain containing 1
Chromosomal Location: chr3q21
Gene Symbol: ABTB1
Alignment: chr3:128877724-128881614 (+) // 99.89 // q21.3

Gene 7:

Gene Name: 244290_at, P Value: 1.50647897778633E-06

Ranked 777 in MAS, MAS P Value: 0.00549653474902367

Target Description: Consensus includes gb: AW293174 /FEA=EST /DB_XREF=gi: 6699810 /DB_XREF=est: UI-H-BW0-aii-c-12-0-UI.s1 /CLONE=IMAGE:2729470 /UG=Hs.252627 ESTs

Go Biological Process: None
Go Cellular Process: 16021 // integral to membrane // inferred from electronic annotation
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: AA808306,AW293174,AI857762
Transcript Assignment: AA808306 // /DB_XREF=oc41g02.s1 /CLONE=IMAGE:1352306 // gb // --- // --- /// AI857762 // /DB_XREF=wl21g06.x1 /CLONE=IMAGE:2425594 // gb // --- // --- /// AW293174 // /DB_XREF=UI-H-BW0-aii-c-12-0-UI.s1 /CLONE=IMAGE:2729470 // gb // --- // ---

Annotation Notes: None
Uni Gene ID: Hs.3781
Gene Title: Leucine rich repeat neuronal 3
Chromosomal Location: chr7q31.1
Gene Symbol: LRRN3
Alignment: chr7:110466396-110466926 (-) // 66.61 // q31.1

GENE 8:

Gene Name: 229422_at, P Value: 1.76902731663375E-06

Ranked 11 in MAS, MAS P Value: 0.0000177023276415333

Target Description: Consensus includes gb:AA448346 /FEA=EST /DB_XREF=gi:2162016 /DB_XREF=est:zw98g12.s1 /CLONE=IMAGE:785062 /UG=Hs.309734 ESTs, Moderately similar to NRD2 convertase H.sapiens

Go Biological Process: 6508 // proteolysis and peptidolysis // non-traceable author statement /// 7528 // neuromuscular junction development // traceable author statement

Go Cellular Process: None
Go Molecular Function: 16919 // nardilysin activity // non-traceable author statement
Pathway: None
Annotation Transcript Cluster: AK090844(9)
Transcript Assignment: AK090844 // Homo sapiens cDNA FLJ33525 fis, clone BRAMY2006779. // gb // 9 // ---

Annotation Notes: ENSESTT00000083586 // ensembl // 1 // Cross Hyb Matching Probes /// ENSESTT00000083587 // ensembl // 1 // Cross Hyb Matching Probes /// ENSESTT00000083588 // ensembl // 1 // Cross Hyb Matching Probes /// ENSESTT00000083589 // ensembl // 1 // Cross Hyb Mat

Uni Gene ID: Hs.551509
Gene Title: Nardilysin (N-arginine dibasic convertase)
Chromosomal Location: chr1p32.2-p32.1

Gene Symbol: NRD1
Alignment: chr1:52014657-52015643 (-) // 87.11 // p32.3

GENE 9:

Gene Name: 232310_at, P Value: 1.93133009984692E-06

Ranked 988 in MAS, MAS P Value: 0.00776839139759833

Target Description: Consensus includes gb:AK026502.1 /DEF=Homo sapiens cDNA: FLJ22849 fis, clone KAIA987. /FEA=mRNA /DB_XREF=gi:10439376 /UG=Hs.4786 Homo sapiens cDNA: FLJ22849 fis, clone KAIA987

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: AW835376,AK026502,Z45264,R19241,H55196
Transcript Assignment: AK026502 // /DEF=Homo sapiens cDNA: FLJ22849 fis, clone KAIA987. // gb // --- // --- /// AW835376 // /DB_XREF=QV0-LT0014-250200-130-h05 // gb // --- // --- /// H55196 // /DB_XREF=CHR220135 /CLONE=C22_172 // gb // --- // --- /// R19241 // /DB_XREF=yg24f04.

Annotation Notes: AK026502 // gb // 11 // Negative Strand Matching Probes /// AK127256 // gb // 2 // Negative Strand Matching Probes /// XM_373952 // refseq // 6 // Negative Strand Matching Probes /// ENSESTT00000095000 // ensembl // 6 // Negative Strand Matching Probes //

Uni Gene ID: Hs.517502
Gene Title: Hypothetical gene supported by AK098833
Chromosomal Location: chr22q12.1
Gene Symbol: None
Alignment: chr22:25393326-25442689 (-) // 62.91 // q12.1

GENE 10:
Gene Name: 238789_at, P Value: 2.09047469024171E-06
Ranked 852 in MAS, MAS P Value: 0.00621527738815075
Target Description: Consensus includes gb:BF343843 /FEA=EST /DB_XREF=gi:11291036 /DB_XREF=est:602015518F1 /CLONE=IMAGE:4150996 /UG=Hs.127402 ESTs

Go Biological Process: 6955 // immune response // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 45786 // negative regulation of cell cycle // inferred from electronic annotation

Go Cellular Process: None

Go Molecular Function: 3924 // GTPase activity // inferred from electronic annotation /// 5525 // GTP binding // inferred from electronic annotation

Pathway: None

Annotation Transcript Cluster: D79994(9)
Transcript Assignment: D79994 // Homo sapiens KIAA0172 mRNA, complete cds. // gb // 9 // --- /// ENSESTT00000045572 // --- // ensembl // 9 // ---

Annotation Notes: BC037495 // gb // 1 // Cross Hyb Matching Probes /// ENSESTT00000045573 // ensembl // 7 // Cross Hyb Matching Probes

Uni Gene ID: Hs.493272
Gene Title: ankyrin repeat domain 15
Chromosomal Location: chr9p24.3
Gene Symbol: ANKRD15
Alignment: chr9:494492-539535 (+) // 67.4 // p24.3

GENE 11

Gene Name: 240652_at, P Value: 2.43714276937368E-06

Ranked 2433 in MAS, MAS P Value: 0.0297714054348048

Target Description: Consensus includes gb:BF343843 /FEA=EST /DB_XREF=gi:11291036 /DB_XREF=est:602015518F1 /CLONE=IMAGE:4150996 /UG=Hs.127402 ESTs

Go Biological Process: 6955 // immune response // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 45786 // negative regulation of cell cycle // inferred from electronic annotation

Go Cellular Process: None
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: GENSCAN00000067228
Transcript Assignment: GENSCAN00000067228 // cdna:Genscan chromosome:NCBI35:2:145089729:145119439:-1 // ensembl // 0 // chr2:145089728-145119439(-)

Annotation Notes: None
Uni Gene ID: None
Gene Title: None
Chromosomal Location: None
Gene Symbol: None
Alignment: chr2:145100274-145100912 (-) // 94.19 // q22.3

GENE 12:

Gene Name: 226767_s_at, P Value: 2.64451742415517E-06

Ranked 1790 in MAS, MAS P Value: 0.0189193613088874

Target Description: Consensus includes gb:AI341467 /FEA=EST /DB_XREF=gi:4078394 /DB_XREF=est:qq94a09.x1 /CLONE=IMAGE:1939000 /UG=Hs.322482 Homo sapiens mRNA; cDNA DKFZp566J2046 (from clone DKFZp566J2046); complete cds

Go Biological Process: 8152 // metabolism // inferred from electronic annotation
Go Cellular Process: None
Go Molecular Function: None
Pathway: 3824 // catalytic activity // inferred from electronic annotation
Annotation Transcript Cluster: NM_031208(11)

Transcript Assignment: NM_031208 // Homo sapiens fumarylacetoacetate hydrolase domain containing 1 (FAHD1), mRNA. // refseq // 11 // --- /// ENST00000326061 // cdna:ccds chromosome:NCBI35:16:1817226:1818909:1 gene:ENSG00000180185 CCDS10448.1 // ensembl // 11 // ---

Annotation Notes: CR600899 // gb // 6 // Cross Hyb Matching Probes /// BC063017 // gb // 6 // Cross Hyb Matching Probes /// GENSCAN00000010122 // ensembl // 7 // Cross Hyb Matching Probes

Uni Gene ID: Hs.513265
Gene Title: fumarylacetoacetate hydrolase domain containing 1
Chromosomal Location: chr16p13.3
Gene Symbol: FAHD1
Alignment: chr16:1816972-1818276 (+) // 78.13 // p13.3

GENE 13
Gene Name: 228182_at, P Value: 2.80395270313427E-06
Ranked 2882 in MAS, MAS P Value: 0.0389118083989646
Target Description: Consensus includes gb:AI935802 /FEA=EST /DB_XREF=gi:5674672 /DB_XREF=est:wp04c12.x1 /CLONE=IMAGE:2463862 /UG=Hs.9572 ESTs

Go Biological Process: 6171 // cAMP biosynthesis // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation

Go Cellular Process: 16021 // integral to membrane // inferred from electronic annotation

Go Molecular Function: 287 // magnesium ion binding // inferred from electronic annotation /// 4016 // adenylate cyclase activity // inferred from electronic annotation

Pathway: G_Protein_Signaling // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP /// Purine metabolism // KEGG

Annotation Transcript Cluster: AK098381(11)

Transcript Assignment: AK098381 // Homo sapiens cDNA FLJ25515 fis, clone CBR06479. // gb // 11 // ---

Annotation Notes: ENSESTT00000094922 // ensembl // 7 // Negative Strand Matching Probes
Uni Gene ID: Hs.129493
Gene Title: adenylate cyclase 5
Chromosomal Location: chr3q13.2-q21
Gene Symbol: ADCY5
Alignment: chr3:124483832-124484478 (-) // 94.02 // q21.1

GENE 14:

Gene Name: 228274_at, P Value: 3.12869738894328E-06

Ranked 2394 in MAS, MAS P Value: 0.0290924697619266

Target Description: Consensus includes gb:BE963955 /FEA=EST /DB_XREF=gi:11767283 /DB_XREF=est:601657722R1 /CLONE=IMAGE:3875860 /UG=Hs.152510 ESTs, Weakly similar to DWHUT L-serine dehydratase H.sapiens

Go Biological Process: 6520 // amino acid metabolism // inferred from electronic annotation /// 8152 // metabolism // inferred from electronic annotation

Go Cellular Process: None
Go Molecular Function: 3824 // catalytic activity // inferred from electronic annotation
Pathway: None
Annotation Transcript Cluster: NM_138432(10)
Transcript Assignment: NM_138432 // Homo sapiens serine dehydratase-like (SDSL), mRNA. // refseq // 10 // --- /// ENST00000345635 // cdna:ccds chromosome:NCBI35:12:112322970:112338800:1 gene:ENSG00000139410 CCDS9170.1 // ensembl // 10 // --- /// ENSESTT00000050225 // --- //

Annotation Notes: None
Uni Gene ID: Hs.337594
Gene Title: serine dehydratase-like
Chromosomal Location: chr12q24.13
Gene Symbol: SDSL
Alignment: chr12:112335915-112338801 (+) // 91.95 // q24.13

GENE 15

Gene Name: 237483_at, P Value: 3.31932476282937E-06

Ranked 1731 in MAS, MAS P Value: 0.0180037768105208

Target Description: Consensus includes gb:AI990790 /FEA=EST /DB_XREF=gi:5837671 /DB_XREF=est:ws23g11.x1 /CLONE=IMAGE:2498084 /UG=Hs.188614 ESTs

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: 5545 // phosphatidylinositol binding // non-traceable author statement
Pathway: None
Annotation Transcript Cluster: BF438424,N67553,AW237245,AI990790,AI654883,T91767,BE550293
Transcript Assignment: AI654883 // wb52a08.x1 Homo sapiens cDNA, 3’ end /clone=IMAGE-2309270 /clone_end=3’ /gb=AI654883 /gi=4738862 /ug=Hs.188614 /len=323 // gb // --- // --- /// AI654883 // /DB_XREF=wb52a08.x1 /CLONE=IMAGE:2309270 // gb // --- // --- /// AI990790 // ws23g11.x1

Annotation Notes: None

Uni Gene ID: Hs.188614
Gene Title: Pleckstrin homology domain containing, family A member 5
Chromosomal Location: chr12p12
Gene Symbol: PLEKHA5
Alignment: chr12:19295623-19295940 (+) // 90.45 // p12.3

GENE 16:
Gene Name: 239718_at, P Value: 3.88875067391936E-06
Ranked 4096 in MAS, MAS P Value: 0.0691904721704044
Target Description: Consensus includes gb:R42552 /FEA=EST /DB_XREF=gi:817314 /DB_XREF=est:yg01a09.s1 /CLONE=IMAGE:30807 /UG=Hs.17554 ESTs

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: AK124303(11)
Transcript Assignment: AK124303 // Homo sapiens cDNA FLJ42310 fis, clone TRACH2007733. // gb // 11 // ---

Annotation Notes: None
Uni Gene ID: Hs.444400
Gene Title: CDNA FLJ42310 fis, clone TRACH2007733
Chromosomal Location: None
Gene Symbol: None
Alignment: chr4:4304810-4305630 (+) // 48.56 // p16.3 /// chr2:91234299-91235117 (-) // 52.16 // p11.1

GENE 17:
Gene Name: 241662_x_at, P Value: 3.99086581848174E-06
Ranked 22386 in MAS, MAS P Value: 0.3179874480898
Target Description: Consensus includes gb:AW063472 /FEA=EST /DB_XREF=gi:8887409 /DB_XREF=est:TN0965 /UG=Hs.313518 ESTs

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: None
Transcript Assignment: AW063472 // /DB_XREF=TN0965 // gb // --- // ---
Annotation Notes: None
Uni Gene ID: None
Gene Title: None
Chromosomal Location: None
Gene Symbol: None
Alignment: None

Gene 18

Gene Name: 229206_at, P Value: 4.43077202905151E-06
Ranked 216 in MAS, MAS P Value: 0.000921262960729363
Target Description: Consensus includes gb:BE551650 /FEA=EST /DB_XREF=gi:9793262 /DB_XREF=est:hx96d01.x1 /CLONE=IMAGE:3195649 /UG=Hs.158126 Homo sapiens cDNA FLJ13350 fis, clone OVARC1002143

Go Biological Process: None
Go Cellular Process: None
Go Molecular Function: None
Pathway: None
Annotation Transcript Cluster: AK021558(10),AK023412(10)
Transcript Assignment: AK021558 // Homo sapiens cDNA FLJ11496 fis, clone HEMBA1001964. // gb // 10 // --- /// AK023412 // Homo sapiens cDNA FLJ13350 fis, clone OVARC1002143. // gb // 10 // ---

Annotation Notes: None
Uni Gene ID: Hs.158126
Gene Title: CDNA FLJ13350 fis, clone OVARC1002143
Chromosomal Location: None
Gene Symbol: None
Alignment: chr6:151805058-151807378 (+) // 70.49 // q25.1

GENE 19:
Gene Name: 230443_at, P Value: 4.47065660891255E-06
Ranked 126 in MAS, MAS P Value: 0.000443094622267992
Target Description: Consensus includes gb:AI288202 /FEA=EST /DB_XREF=gi:3931922 /DB_XREF=est:ql90f02.x1 /CLONE=IMAGE:1879611 /UG=Hs.120453 ESTs

Go Biological Process: 74 // regulation of cell cycle // traceable author statement /// 398 // nuclear mRNA splicing, via spliceosome // inferred from electronic annotation /// 6412 // protein biosynthesis // inferred from electronic annotation /// 42254 // ribosome biogenesis

Go Cellular Process: 5681 // spliceosome complex // inferred from electronic annotation /// 5730 // nucleolus // traceable author statement /// 5840 // ribosome // inferred from electronic annotation

Go Molecular Function: 3723 // RNA binding // traceable author statement /// 3735 // structural constituent of ribosome // inferred from electronic annotation

Pathway: None
Annotation Transcript Cluster: AK124020(11)
Transcript Assignment: AK124020 // Homo sapiens cDNA FLJ42026 fis, clone SPLEN2036501. // gb // 11 // ---

Annotation Notes: ENSESTT00000053933 // ensembl // 1 // Cross Hyb Matching Probes

Uni Gene ID: Hs.182255

Gene Title: NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)

Chromosomal Location: chr22q13.2-q13.31
Gene Symbol: NHP2L1
Alignment: chr22:40408222-40408946 (-) // 84.2 // q13.2

GENE 20
Gene Name: 227507_at, P Value: 0.0000055255744519922
Ranked 420 in MAS, MAS P Value: 0.00231120250730577
Target Description: Consensus includes gb:BF593899 /FEA=EST /DB_XREF=gi:11686223 /DB_XREF=est:nab46h06.x1 /CLONE=IMAGE:3269218 /UG=Hs.23970 ESTs

Go Biological Process: 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation

Go Cellular Process: 5634 // nucleus // inferred from electronic annotation

Go Molecular Function: 3677 // DNA binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation

Pathway: None
Annotation Transcript Cluster: AK090507(9)
Transcript Assignment: AK090507 // Homo sapiens cDNA FLJ33188 fis, clone ADRGL2004749. // gb // 9 // ---

Annotation Notes: None
Uni Gene ID: Hs.79347
Gene Title: Zinc finger protein 592
Chromosomal Location: chr15q25.3
Gene Symbol: ZNF592
Alignment: chr15:83149632-83150265 (+) // 44.14 // q25.3

References.

http://www.tufts.edu/~gdallal/pval.htm
http://www.cmh.edu/stats/definitions/pvalue.htm
www.affymetrix..com
www.bioconductor.org
R Irrizarry, Exploration, normalization, and summaries of high density oligonucleotide array probe level data
Biostatistics. 2003 Apr;4(2):249-64.
Christina Wassel (2001): Summer Project Report MSKCC.