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APPENDICES

APPENDIX A

CHAPTER IV: Code for identification genes significance differential expression

The R code provided for analysis of the six two-color microarray data. The analysis procedure based on the user's guide of limma package that including importing microarray data, preprocessing, normalization and statistical for analysis genes differential expression. The R code for this research is as followed:

Loading packages and read the microarray data that provided on the directory path.

Download library #

```
library(limma)
library(Biobase)
library(base)
library(vsn)
```

Set directory

```
setwd("E:/CRC1")
```

Read data

```
targets <- readTargets("Samples.txt")
files <- targets[,3]
RG <- read.maimages(files, source="scanarrayexpress")
```

Box-plot and density plot of raw intensity and save the plot as picture with png file. R code can be generated as follows:

Intensities of six raw microarray data

```
png("unNormalisedDensities1.png")

    par(mfrow=c(1,3))

    boxplot(data.frame(log2(RG$R)),main="Red", col="red")

    boxplot(data.frame(log2(RG$G)),main="Green", col="green")

    plotDensities(RG)

    dev.off()
```

To assign gene names for each probe in R

Reading the Gene List(Gal file)

```
RG$genes<-readGAL("Human OpArray.gal")

dim(RG$genes)

colnames(RG$genes)

RG$genes[1:10, ]

names(RG$genes)
```

Print Layout

```
RG$printer = getLayout(RG$genes)
```

The Spot Type File

```
spottypes<-readSpotTypes()

RG$genes$Status<-controlStatus(spottypes,RG)
```

To assess the quality of six arrays with R code can be generated as follows

Quality Assessment

```
spottypes <- readSpotTypes()

RG$genes$Status <- controlStatus(spottypes, RG)

plotMA(RG)
```

plotMA(RG, status = RG$genes$Status)

MA-plot for diagnosis six microarray data

The procedure of preprocessing and normalization are separated into three steps, background correction, within-array normalization and between-array normalization. Moreover, the normexp, loess and Aquantile method are chosen to use as three steps respectively.

Background Correction

RG.ne = backgroundCorrect(RG, method = "normexp")

....

Within-array Normalization

MA.loess<-normalizeWithinArrays(RG.ne,method="loess")

....

Between-array Normalization

MA.loess <- normalizeBetweenArrays(MA.loess, method="Aquantile")

MA-plot of between-array normalization

par(mfrow=c(2,3))

plotMA(MA.loess,array=1), plotMA(MA.loess,array=2), plotMA(MA.loess,array=3)

plotMA(MA.loess,array=4), plotMA(MA.loess,array=5), plotMA(MA.loess,array=6)

The accuracy of data after normalized can be consider with densities plot.

Density plot of normalization data

par(mfrow=c(2,3))

plotDensities(MA.loess[,1]), plotDensities(MA.loess[,2]),plotDensities(MA.loess[,3])

plotDensities(MA.loess[,4]), plotDensities(MA.loess[,5]),plotDensities(MA.loess[,6])

Specific design for identified gene differentially expressed between normal and cancer tissues

Design

```
groups<-c("N0.M0","N1.M0","N1.M1","N0.M0","N0.M0","N1.M1")

design<-model.matrix(~groups)
```

Analysis by using Linear Model

```
fit<-lmFit(MA.loess,design)

fit2<-eBayes(fit)
```

Detect genes difference expression

```
tt<-toptable(fit2, coef=2, n=nrow(MA.loess))

rn<-rownames(tt)[tt$P.Value<=0.005]

rn<-as.numeric(rn)

dat.s<-MA.loess[rn,]
```

....

Created file of statistical values specific for design I and writing this data

```
A=toptable(fit2,coef=2,n=nrow(MA.loess),fit2$gene)

write.table(A,"fitstage.xls", append = F,quote = F,

        sep="\t", row.names =F,  col.names=T,na="NA")
```

....

##Merge genes significant differential expression with fitstage.csv to receive logFC values ##

```
X<-read.csv("fitstage.csv",header=T)

Y<-read.csv("Difference Gene Expression_stage.csv",header=T)

TT<-merge(X,Y,by.x="ID",by.y="ID")
```

```
write.table(TT,"Difference Gene Expression_stage&logFC.xls", append = F,

      quote = F,sep ="\t",row.names=F,col.names=T,na="NA")
```

....

Merge genes significant differential expression with Human_whole.csv to receive genes description

```
X<-read.csv("Human_whole.csv",header=T)

Y<-read.csv("Difference Gene Expression_stage&logFC.csv",header=T)

YT<-merge(X,Y,by.x="ID",by.y="ID")

write.table(YT,"descriptionDiff_Stage_logFC.xls", append = F, quote = F,

      sep ="\t",row.names=F,col.names=T,na="NA")
```

....

Merge genes significant differencial expression with 1920 genes from previous research##

```
X<-read.csv("PoolNM.csv")

Y<-read.csv("Oncogene_paperfull.csv")

C<-merge(X,Y,by.x="gene_symbol",by.y="gene_symbol")

write.table(C,"Oncogenes_PoolNM.xls", append = F, quote = F,

      sep ="\t",row.names=F,col.names=T,na="NA")
```

END.

APPENDIX B

Tables of genes significant differential expression of chapter VI

Table B.1: Two hundred and fifty-six genes differentially expressed less than p-value at 0.005, comparing normal and cancer cells from the pooled data set.

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000069869	NEDD4	E3 ubiquitin-protein ligase Nedd-4 (EC 6.3.2.-). [Source:Uniprot/SWISSPROT;Acc:P46934]	4.200375	3.987984	0.002233	0.56824	-1.81865
ENSG00000107317	PTGDS	Prostaglandin-H2 D-isomerase precursor (EC 5.3.99.2) (Lipocalin-type prostaglandin D synthase) (Glutathione-independent PGD synthetase) (Prostaglandin-D synthase) (PGD2 synthase) (PGDS2) (PGDS) (Beta-trace protein) (Cerebrin 28). [Source:Uniprot/SWISSPROT	-4.4632	-3.99233	0.002217	0.56824	-1.81451
ENSG00000110925	NP_110436.1	TGF-beta induced apotosis protein 12 [Source:RefSeq_peptide;Acc:NP_110436]	3.520586	3.62332	0.004161	0.56824	-2.17795
ENSG00000016402	IL20RA	Interleukin-20 receptor alpha chain precursor (IL-20R-alpha) (IL-20R1) (Cytokine receptor family 2 member 8) (Cytokine receptor class-II CRF2-8) (ZcytoR7) (UNQ681/PRO1315). [Source:Uniprot/SWISSPROT;Acc:Q9UHF4]	-3.75974	-3.52742	0.004913	0.56824	-2.27609
ENSG00000181788	SIAH2	Ubiquitin ligase SIAH2 (EC 6.3.2.-) (Seven in absentia homolog 2)	-3.52054	-3.70797	0.003597	0.56824	-2.09254

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
		(Siah-2) (hSiah2). [Source:Uniprot/SWISSPROT;Acc:O43255]					
ENSG00000163686	ABHD6	abhydrolase domain containing 6 [Source:RefSeq_peptide;Acc:NP_065727]	-3.44048	-3.53627	0.004838	0.56824	-2.26697
ENSG00000133424	LARGE	Glycosyltransferase-like protein LARGE (EC 2.4.-.-) (Acetylglucosaminyltransferase-like protein) [Source:Uniprot/SWISSPROT;Acc:O95461]	-3.76618	-3.57006	0.004563	0.56824	-2.23227
ENSG00000109680	TBC1D19	TBC1 domain family member 19. [Source:Uniprot/SWISSPROT;Acc:Q8N5T2]	-3.95396	-3.98513	0.002244	0.56824	-1.82138
ENSG00000158457	NP_848657.1	-	-3.94518	-4.11793	0.001796	0.56824	-1.69621
ENSG00000186020	ZNF529	zinc finger protein 529 [Source:RefSeq_peptide;Acc:NP_066002]	-3.79486	-3.96382	0.002326	0.56824	-1.84175
ENSG00000198288	Q96NM1_HUMAN	-	-3.69254	-3.54561	0.00476	0.56824	-2.25737
ENSG00000175048	ZDHHC14	Zinc finger DHHC domain containing protein 14 (NEW1 domain containing protein) (NEW1CP). [Source:Uniprot/SWISSPROT;Acc:Q8IZN3]	-4.9313	-4.94834	0.00047	0.56824	-0.98605
ENSG00000172201	ID4	DNA-binding protein inhibitor ID-4. [Source:Uniprot/SWISSPROT;Acc:P47928]	4.220407	4.210179	0.00154	0.56824	-1.61113
ENSG00000163743	RCHY1	RING finger and CHY zinc finger domain containing protein 1 (Zinc finger protein 363) (CH-rich interacting match with PLAG1) (Androgen receptor N-terminal-interacting protein). [Source:Uniprot/SWISSPROT;Acc:Q96PM5]	-3.83316	-3.78493	0.003153	0.56824	-2.01593
ENSG00000167580	AQP2	Aquaporin-CD (AQP-CD) (Water channel protein for renal collecting duct) (ADH water channel) (Aquaporin 2) (Collecting duct water channel protein) (WCH-CD).	-4.01667	-4.23486	0.001478	0.56824	-1.58863

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000159208	NP_653298.1	[Source:Uniprot/SWISSPROT;Acc:P41181] -	3.725965	3.569896	0.004564	0.56824	-2.23244
ENSG00000152229	PSTPIP2	Proline-serine-threonine phosphatase-interacting protein 2. [Source:Uniprot/SWISSPROT;Acc:Q9H939]	-4.08081	-4.1543	0.00169	0.56824	-1.66248
ENSG00000131650	KREMEN2	Kremen protein 2 precursor (Kringle-containing protein marking the eye and the nose) (Dickkopf receptor 2). [Source:Uniprot/SWISSPROT;Acc:Q8NCW0]	-4.06864	-3.97988	0.002264	0.56824	-1.82638
ENSG00000161513	FDXR	NADPH:adrenodoxin oxidoreductase, mitochondrial precursor (EC 1.18.1.2) (Adrenodoxin reductase) (AR) (Ferredoxin--NADP(+) reductase). [Source:Uniprot/SWISSPROT;Acc:P22570]	-4.23734	-4.11731	0.001798	0.56824	-1.69678
ENSG00000167182	SP2	Transcription factor Sp2. [Source:Uniprot/SWISSPROT;Acc:Q02086]	4.488072	4.224014	0.001505	0.56824	-1.5985
ENSG00000164120	HPGD	15-hydroxyprostaglandin dehydrogenase [NAD+] [EC 1.1.1.141] (PGDH). [Source:Uniprot/SWISSPROT;Acc:P15428]	4.478824	3.694102	0.003684	0.56824	-2.10646
ENSG00000102007	PLP2	Intestinal membrane A4 protein (Differentiation-dependent protein A4) (Proteolipid protein 2). [Source:Uniprot/SWISSPROT;Acc:Q04941]	3.399667	3.594557	0.004373	0.56824	-2.20723
ENSG00000173581	NP_037433.1	protein predicted by clone 23882 [Source:RefSeq_peptide;Acc:NP_037433]	-4.98162	-4.47129	0.001003	0.56824	-1.3787
ENSG00000149054	ZNF215	Zinc finger protein 215 (BWSCR2 associated zinc-finger protein 2) (BAZ 2). [Source:Uniprot/SWISSPROT;Acc:Q9UL58]	4.016494	3.712248	0.003571	0.56824	-2.08826
ENSG00000110700	RS13_HUMAN	40S ribosomal protein S13.	4.421196	3.885184	0.002658	0.56824	-1.91763

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000172757	CFL1	[Source:Uniprot/SWISSPROT;Acc:P62277] Cofilin, non-muscle isoform (Cofilin-1) (18 kDa phosphoprotein) (p18). [Source:Uniprot/SWISSPROT;Acc:P23528]	4.266179	3.836174	0.002889	0.56824	-1.96547
ENSG00000052835	NP_689671.2	-	-3.95631	-3.89229	0.002626	0.56824	-1.91073
ENSG00000172216	CEBPB	CCAAT/enhancer binding protein beta (C/EBP beta) (Nuclear factor NF-IL6) (Transcription factor 5). [Source:Uniprot/SWISSPROT;Acc:P17676]	3.588977	3.608482	0.004269	0.56824	-2.19304
ENSG00000102984	NP_060000.1	-	-4.52509	-4.35985	0.001203	0.56824	-1.47638
ENSG00000135624	CCT7	T-complex protein 1, eta subunit (TCP-1-eta) (CCT-eta) (HIV-1 Nef interacting protein). [Source:Uniprot/SWISSPROT;Acc:Q99832]	-3.5076	-3.56328	0.004617	0.56824	-2.23922
ENSG00000081320	STK17B	Serine/threonine-protein kinase 17B (EC 2.7.1.37) (DAP kinase-related apoptosis-inducing protein kinase 2). [Source:Uniprot/SWISSPROT;Acc:O94768]	-4.13456	-3.64993	0.003975	0.56824	-2.15097
ENSG00000161973	Q8N6Q0_HUMAN	-	-3.68286	-3.85881	0.00278	0.56824	-1.94333
ENSG00000116661	FBXO2	F-box only protein 2. [Source:Uniprot/SWISSPROT;Acc:Q9UK22]	-3.66176	-3.53539	0.004845	0.56824	-2.26788
ENSG00000100345	MYH9	Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain, type A) (Nonmuscle myosin heavy chain-A) (NMMHC-A). [Source:Uniprot/SWISSPROT;Acc:P35579]	3.863756	3.867277	0.00274	0.56824	-1.93506
ENSG00000114391	RL24_HUMAN	60S ribosomal protein L24 (Ribosomal protein L30). [Source:Uniprot/SWISSPROT;A 1]	4.591827	4.452673	0.001034	0.56824	-1.39486
ENSG00000121764	HCRTR1	Orexin receptor type 1 (Ox1r) (Hypocretin receptor type 1). [Source:Uniprot/SWISSPROT;Acc:O43613]	-3.52249	-3.62832	0.004126	0.56824	-2.17287
ENSG00000141434	MEP1B	Meprin A beta-subunit precursor (EC 3.4.24.18) (Endopeptidase-2)	-4.03437	-3.93904	0.002426	0.56824	-1.86555

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
		(N- benzoyl-L-tyrosyl-P-amino-benzoic acid hydrolase beta subunit) (PABA peptide hydrolase) (PPH beta). [Source:Uniprot/SWISSPROT;Acc:Q16820]					
ENSG00000158859	ADAMTS4	ADAMTS-4 precursor (EC 3.4.24.82) (A disintegrin and metalloproteinase with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS4) (Aggrecanase 1) (ADMP-1). [Source:Uniprot/SWISSPROT;Acc:O75173]	1	-4.05342	0.002001	0.56824	-1.75662
ENSG00000149922	TBX6	T-box transcription factor TBX6 (T-box protein 6). [Source:Uniprot/SWISSPROT;Acc:O95947]	-4.23262	-3.83062	0.002916	0.56824	-1.97091
ENSG00000120055	C10orf95	-	-4.05526	-4.3388	0.001246	0.56824	-1.49508
ENSG00000166603	MC4R	Melanocortin-4 receptor (MC4-R). [Source:Uniprot/SWISSPROT;Acc:P32245]	-4.69067	-4.4838	0.000983	0.56824	-1.36788
ENSG00000164587	RS14_HUMAN	40S ribosomal protein S14 (PRO2640). [Source:Uniprot/SWISSPROT;Acc:P62263]	5.043469	4.173888	0.001636	0.56824	-1.64442
ENSG00000133858	Q96BE7_HUMAN	-	3.647759	3.662652	0.003889	0.56824	-2.13812
ENSG00000008197	NP_758438.1	transcription factor AP-2 beta-like 1 [Source:RefSeq_peptide;Acc:NP_758438]	3.891975	4.149406	0.001704	0.56824	-1.66701
ENSG00000137947	GTF2B	Transcription initiation factor IIB (General transcription factor TFIIB) (S300-II). [Source:Uniprot/SWISSPROT;Acc:Q00403]	-3.89532	-3.78712	0.003141	0.56824	-2.01376
ENSG00000101278	Q9NQ39_HUMAN	OTTHUMP00000029938. [Source:Uniprot/SPTREMBL;Acc:Q9NQ39]	5.177046	4.759809	0.000632	0.56824	-1.13632
ENSG00000172715	XP_070233.3	PREDICTED: similar to ribosomal protein L10a	4.220453	3.822194	0.002958	0.56824	-1.97919

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000168482	CYP21A2	[Source:RefSeq_peptide;Acc:XP_070233] Cytochrome P450 XXIB (EC 1.14.99.10) (Steroid 21-hydroxylase) (P450- C21B). [Source:Uniprot/SWISSPROT;Acc:P08686]	-4.04507	-3.53807	0.004823	0.56824	-2.26511
ENSG00000169340	NP_777584.1	protein disulfide isomerase-like protein of the testi [Source:RefSeq_peptide;Acc:NP_777584]	-4.08851	-3.57603	0.004516	0.56824	-2.22616
ENSG00000197272	IL27	interleukin 27 [Source:RefSeq_peptide;Acc:NP_663634]	-4.20121	-4.46394	0.001015	0.56824	-1.38507
ENSG00000106605	BLVRA	Biliverdin reductase A precursor (EC 1.3.1.24) (Biliverdin-IX alpha-reductase) (BVR A). [Source:Uniprot/SWISSPROT;Acc:P53004]	-3.7144	-3.80097	0.003068	0.56824	-2.00009
ENSG00000198034	RS4X_HUMAN	40S ribosomal protein S4, X isoform (Single copy abundant mRNA protein) (SCR10). [Source:Uniprot/SWISSPROT;Acc:P62701]	3.75622	3.698925	0.003653	0.56824	-2.10161
ENSG00000136986	DERL1	Derlin-1 (Degradation in endoplasmic reticulum protein 1) (Der1-like protein 1) (DERtrin 1) (UNQ243/PRO276). [Source:Uniprot/SWISSPROT;Acc:Q9BUN8]	-3.44797	-3.71942	0.003527	0.56824	-2.08109
ENSG00000173321	XP_370681.1	PREDICTED: similar to ribosomal protein L13a; 60S ribosomal protein L13a; 23 kD highly basic protein [Source:RefSeq_peptide;Acc:XP_370681]	4.409526	4.483272	0.000984	0.56824	-1.36833
ENSG00000198918	RL39_HUMAN	60S ribosomal protein L39. [Source:Uniprot/SWISSPROT;Acc:P62891]	3.877483	4.040135	0.002046	0.56824	-1.76915
ENSG00000168370	-	24 kDa protein [Source:IPI;Acc:IPI00478277]	3.434091	3.517985	0.004994	0.56824	-2.28582
ENSG00000177182	Q8NB32_HUMAN	-	3.553734	3.546573	0.004752	0.56824	-2.25637
ENSG00000168678	XP_172230.2	PREDICTED: similar to ribosomal protein S17 [Source:RefSeq_peptide;Acc:XP_172230]	3.724883	3.53101	0.004882	0.56824	-2.27239

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000178322	-	18 kDa protein [Source:IPI;Acc:IPI00477490]	4.060254	3.550036	0.004724	0.56824	-2.25281
ENSG00000196553	NP_001004331.1	similar to CG32662-PA [Source:RefSeq_peptide;Acc:NP_001004331]	-3.54418	-3.57064	0.004558	0.56824	-2.23168
ENSG00000165509	MAGEC3	Melanoma-associated antigen C3 (MAGE-C3 antigen) (Hepatocellular carcinoma-associated antigen 2). [Source:Uniprot/SWISSPROT;Acc:Q8TD91]	-4.74928	-4.19271	0.001585	0.56824	-1.62713
ENSG00000163301	-	31 kDa protein [Source:IPI;Acc:IPI00479061]	5.615487	4.682709	0.000714	0.56824	-1.19961
ENSG00000198637	RL41_HUMAN	60S ribosomal protein L41 (HG12). [Source:Uniprot/SWISSPROT;Acc:P62945]	4.339314	4.63956	0.000765	0.56824	-1.2355
ENSG00000025772	TOMM34	Mitochondrial import receptor subunit TOM34 (Translocase of outer membrane 34 kDa subunit) (hTom34). [Source:Uniprot/SWISSPROT;Acc:Q15785]	-3.49037	-3.73611	0.003428	0.56824	-2.06441
ENSG00000176219	OR11H6	Olfactory receptor 11H6. [Source:Uniprot/SWISSPROT;Acc:Q8NGC7]	-4.39761	-3.80162	0.003064	0.56824	-1.99945
ENSG00000154148	XP_497998.1	PREDICTED: similar to 60S ribosomal protein L29 (Cell surface heparin binding protein HIP) [Source:RefSeq_peptide;Acc:XP_497998]	4.076665	3.958794	0.002346	0.56824	-1.84657
ENSG00000179082	Q8NAJ2_HUMAN	-	-3.53476	-3.54824	0.004738	0.56824	-2.25466
ENSG00000163682	RPL9	60S ribosomal protein L9. [Source:Uniprot/SWISSPROT;Acc:P32969]	4.338657	4.467555	0.001009	0.56824	-1.38194
ENSG00000177954	RPS27	40S ribosomal protein S27 (Metallopan-stimulin 1) (MPS-1). [Source:Uniprot/SWISSPROT;Acc:P42677]	4.429855	3.701617	0.003637	0.56824	-2.09891

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000172900	-	-	4.38583	4.519004	0.000929	0.56824	-1.33757
ENSG00000180878	NP_775796.1	-	-3.64207	-3.65491	0.003941	0.56824	-2.14594
ENSG00000170088	NP_689894.1	-	-3.38932	-3.54931	0.00473	0.56824	-2.25356
ENSG00000167874	NP_981956.1	similar to RIKEN cDNA 2600017H02 [Source:RefSeq_peptide;Acc:NP_981956]	-4.35033	-4.5159	0.000933	0.56824	-1.34023
ENSG00000143910	-	18 kDa protein [Source:IPI;Acc:IPI00478366]	3.896981	3.548602	0.004735	0.56824	-2.25429
ENSG00000145425	RS3A_HUMAN	40S ribosomal protein S3a. [Source:Uniprot/SWISSPROT;Acc:P61247]	3.807183	3.794179	0.003103	0.56824	-2.00679
ENSG00000198618	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin A) (Cyclosporin A-binding protein). [Source:Uniprot/SWISSPROT;Acc:P62937]	4.160834	4.144413	0.001718	0.56824	-1.67163
ENSG00000197575	-	15 kDa protein [Source:IPI;Acc:IPI00478114]	4.863819	4.931983	0.000482	0.56824	-0.99884
ENSG00000173322	XP_495912.1	PREDICTED: similar to 40S ribosomal protein S6 (Phosphoprotein NP33) [Source:RefSeq_peptide;Acc:XP_495912]	3.791314	3.632402	0.004097	0.56824	-2.16873
ENSG00000087338	GMCL1_HUMAN	Germ cell-less protein-like 1. [Source:Uniprot/SWISSPROT;Acc:Q96IK5]	-3.72991	-3.9918	0.002219	0.56824	-1.81501
ENSG00000163019	Q8N9E7_HUMAN	-	-3.67547	-3.64665	0.003997	0.56824	-2.1543
ENSG00000175267	Q8N7K7_HUMAN	PREDICTED: hypothetical protein LOC146177 [Source:RefSeq_peptide;Acc:XP_370944]	-4.0565	-4.3178	0.001289	0.56824	-1.51383
ENSG00000197495	-	20 kDa protein [Source:IPI;Acc:IPI00478310]	5.424625	5.366693	0.000248	0.56824	-0.67487
ENSG00000198782	RPL17	60S ribosomal protein L17 (L23). [Source:Uniprot/SWISSPROT;Acc:P18621]	4.680867	4.432501	0.01069	0.56824	-1.41244

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000008988	RS20_HUMAN	40S ribosomal protein S20. [Source:Uniprot/SWISSPROT;Acc:P60866]	4.395737	4.529978	0.000912	0.56824	-1.32817
ENSG00000133112	TPT1	Translationally controlled tumor protein (TCTP) (p23) (Histamine-releasing factor) (HRF). [Source:Uniprot/SWISSPROT;Acc:P13693]	4.400243	3.780235	0.003178	0.56824	-2.02057
ENSG00000182997	Q9UHT0_HUMAN	-	3.534986	3.54557	0.00476	0.56824	-2.2574
ENSG00000142937	RS8_HUMAN	40S ribosomal protein S8. [Source:Uniprot/SWISSPROT;Acc:P62241]	4.249802	4.585348	0.000834	0.56824	-1.28107
ENSG00000173908	KRT25D	keratin 25D [Source:RefSeq_peptide;Acc:NP_853513]	-3.69732	-3.88224	0.002671	0.56824	-1.92049
ENSG00000170105	-	44 kDa protein [Source:IPI;Acc:IPI00173839]	-3.98817	-4.15162	0.001698	0.56824	-1.66496
ENSG00000178071	-	11 kDa protein [Source:IPI;Acc:IPI00477391]	3.654631	3.582683	0.004464	0.56824	-2.21936
ENSG00000018312	-	26 kDa protein [Source:IPI;Acc:IPI00402141]	-5.35645	-4.20335	0.001558	0.56824	-1.61738
ENSG00000196546	ENR1_HUMAN	HERV-R_7q21.2 provirus ancestral Env polyprotein precursor (Envelope polyprotein) (ERV3 envelope protein) (ERV-3 envelope protein) (HERV-R envelope protein) (ERV-R envelope protein) [Contains: Surface protein (SU); Transmembrane protein (TM)]. [Source:Uni	-3.87228	-3.79943	0.003076	0.56824	-2.00161
ENSG00000174057	-	25 kDa protein [Source:IPI;Acc:IPI00164838]	4.54163	3.693649	0.003687	0.56824	-2.10691
ENSG00000186676	EEF1G	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) (PRO1608). [Source:Uniprot/SWISSPROT;Acc:P26641]	3.974966	4.164056	0.001663	0.56824	-1.65348
ENSG00000198882	NP_001007540.1	similar to dJ612B15.1 (novel protein similar to 60S ribosomal protein L17 (RPL17)) [Source:RefSeq_peptide;Acc:NP_001007540]	3.402041	3.527183	0.004915	0.56824	-2.27633
ENSG00000132423	COQ3	Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial	-3.63743	-3.65187	0.003962	0.56824	-2.14902

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000170250	-	precursor (EC 2.1.1.114) (Dihydroxyhexaprenylbenzoate methyltransferase) (3,4- dihydroxy-5-hexaprenylbenzoate methyltransferase) (DHHB methyltransferase) (DHHB-MT) (DHHB-MTase) (UG0215E05). [Sou 15 kDa protein [Source:IPI;Acc:IPI00157456]	4.303803	4.130709	0.001758	0.56824	-1.68433
ENSG00000176428	WBSCR24	PREDICTED: similar to Williams-Beuren syndrome critical region protein 24 [Source:RefSeq_peptide;Acc:XP_379866]	4.119402	4.035265	0.002063	0.56824	-1.77375
ENSG00000105887	MTPN	Myotrophin (V-1 protein). [Source:Uniprot/SWISSPROT;Acc:P58546]	-4.11261	-3.61231	0.004241	0.56824	-2.18914
ENSG00000135821	GLUL	Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS). [Source:Uniprot/SWISSPROT;Acc:P15104]	-3.78522	-3.56232	0.004624	0.56824	-2.24021
ENSG00000183569	SERHL	Serine hydrolase-like protein (EC 3.1.-.-). [Source:Uniprot/SWISSPROT;Acc:Q9H418]	-4.46177	-4.34587	0.001231	0.56824	-1.48879
ENSG00000110446	SLC15A3	solute carrier family 15, member 3 [Source:RefSeq_peptide;Acc:NP_057666]	-3.45424	-3.71324	0.003565	0.56824	-2.08727
ENSG00000006712	O75239_HUMAN	-	-4.18249	-4.28462	0.001362	0.56824	-1.5436
ENSG00000108244	KRT23	Keratin, type I cytoskeletal 23 (Cytokeratin 23) (K23) (CK 23). [Source:Uniprot/SWISSPROT;Acc:Q9C075]	-4.13044	-3.91663	0.00252	0.56824	-1.88715
ENSG00000155957	Q9HC19_HUMAN	Z-protein (CGI-119) (SIR protein). [Source:Uniprot/SWISSPROT;Acc:Q9HC24]	4.137597	3.689844	0.003711	0.56824	-2.11073
ENSG00000164879	CA3	Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-III). [Source:Uniprot/SWISSPROT;Acc:P07451]	-3.79955	-3.6085	0.004269	0.56824	-2.19302

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000162775	RBM15	Putative RNA-binding protein 15 (RNA binding motif protein 15) (One- twenty two protein). [Source:Uniprot/SWISSPROT;Acc:Q96T37]	3.730133	3.810163	0.00302	0.56824	-1.99103
ENSG00000156265	C21orf7	TAK1-like protein. [Source:Uniprot/SWISSPROT;Acc:P57077]	-3.55289	-3.77759	0.003193	0.56824	-2.02319
ENSG00000197283	SYNGAP1	Zinc finger and BTB domain containing protein 9. [Source:Uniprot/SWISSPROT;Acc:Q96C00]	-3.91567	-3.77417	0.003211	0.56824	-2.02659
ENSG00000161265	U2AF1L3	U2(RNU2) small nuclear RNA auxiliary factor 1-like 3 [Source:RefSeq_peptide;Acc:NP_659424]	-3.38191	-3.59141	0.004397	0.56824	-2.21045
ENSG00000050130	CN100_HUMAN	Medulloblastoma antigen MU-MB-50.4 (HSPC213/HSPC327) (CDA06). [Source:Uniprot/SWISSPROT;Acc:Q9P055]	-3.54221	-3.60493	0.004296	0.56824	-2.19666
ENSG00000177885	GRB2_HUMAN	Growth factor receptor-bound protein 2 (GRB2 adapter protein) (SH2/SH3 adapter GRB2) (Ash protein). [Source:Uniprot/SWISSPROT;Acc:P62993]	-3.74177	-3.91261	0.002537	0.56824	-1.89105
ENSG00000140280	Q8WTV3_HUMAN	-	-3.63328	-3.74359	0.003384	0.56824	-2.05696
ENSG00000076928	ARHG1_HUMAN	Rho guanine nucleotide exchange factor 1 (p115-RhoGEF) (p115RhoGEF) (115 kDa guanine nucleotide exchange factor (Sub1.5). [Source:Uniprot/SWISSPROT;Acc:Q92888]	-4.20209	-4.43464	0.001065	0.56824	-1.41058
ENSG00000111181	SLC6A12	Sodium- and chloride-dependent betaine transporter (Na+/Cl- betaine/GABA transporter) (BGT-1). [Source:Uniprot/SWISSPROT;Acc:P48065]	-3.45261	-3.54091	0.004799	0.56824	-2.2622
ENSG00000197356	-	similar to RPL23AP7 protein (MGC70863), transcript variant 2, mRNA [Source:RefSeq_dna;Acc:NM_203302]	4.908056	3.697544	0.003662	0.56824	-2.103

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000076382	SPAG5	Sperm associated antigen 5 (Astrin) (Mitotic spindle associated protein p126) (MAP126) (Deepest). [Source:Uniprot/SWISSPROT;Acc:Q96R06]	-3.37005	-3.56479	0.004604	0.56824	-2.23767
ENSG00000033170	FUT8	Alpha-(1,6)-fucosyltransferase (EC 2.4.1.68) (Glycoprotein 6-alpha-L- fucosyltransferase) (GDP-fucose—glycoprotein fucosyltransferase) (GDP-L-Fuc:N-acetyl-beta-D-glucosaminide alpha1,6- fucosyltransferase) (alpha1-6FucT) (Fucosyltransferase 8). [Source:Un	4.239094	3.629168	0.00412	0.56824	-2.17201
ENSG00000119684	MLH3	DNA mismatch repair protein Mlh3 (MutL protein homolog 3). [Source:Uniprot/SWISSPROT;Acc:Q9UHCI]	-3.70479	-3.82847	0.002927	0.56824	-1.97303
ENSG00000170037	Q9C060_HUMAN	LYST-interacting protein LIP8 [Source:RefSeq_peptide;Acc:NP_444279]	-3.67893	-3.72267	0.003507	0.56824	-2.07784
ENSG00000115840	SLC25A12	Calcium-binding mitochondrial carrier protein Aralar1 (Mitochondrial aspartate glutamate carrier 1) (Solute carrier family 25, member 12). [Source:Uniprot/SWISSPROT;Acc:O75746]	-3.88047	-3.93252	0.002453	0.56824	-1.87183
ENSG00000019991	HGF	Hepatocyte growth factor precursor (Scatter factor) (SF) (Hepatopoeitin A). [Source:Uniprot/SWISSPROT;Acc:P14210]	-4.75439	-4.71057	0.000683	0.56824	-1.17662
ENSG00000165891	E2F7	E2F transcription factor 7 [Source:RefSeq_peptide;Acc:NP_976328]	-3.68497	-3.80248	0.00306	0.56824	-1.9986
ENSG00000132185	Q5VXA2_HUMAN	Fc receptor homolog expressed in B cells [Source:RefSeq_peptide;Acc:NP_116127]	-4.43614	-4.60641	0.000807	0.56824	-1.2633
ENSG00000001461	Q7Z354_HUMAN	-	-4.56583	-4.36135	0.0012	0.56824	-1.47504
ENSG00000182180	DNAJC9	DnaJ homolog subfamily C member 9 (DnaJ protein SB73).	-4.07233	-3.74967	0.003349	0.56824	-2.05091

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000111676	DRPLA	Atrophin-1 (Dentatorubral-pallidoluysian atrophy protein). [Source:Uniprot/SWISSPROT;Acc:P54259] [Source:Uniprot/SWISSPROT;Acc:Q8WXX5]	4.323329	3.691904	0.003698	0.56824	-2.10866
ENSG00000105808	RASA4	Ras GTPase-activating protein 4 (RasGAP-activating-like protein 2) (Calcium-promoted Ras inactivator). [Source:Uniprot/SWISSPROT;Acc:O43374]	4.536774	3.93291	0.002451	0.56824	-1.87145
ENSG00000188120	Q6PY97_HUMAN	Deleted in azoospermia 1 (Fragment). [Source:Uniprot/SPTREMBL.Acc:Q96P42]	-10.3856	-9.99907	9.03E-07	0.03393	1.300133
ENSG00000108825	NP_079543.1	-	-4.16141	-4.30442	0.001318	0.56824	-1.5258
ENSG00000108932	SLC16A6	Monocarboxylate transporter 7 (MCT 7) (MCT 6). [Source:Uniprot/SWISSPROT;Acc:O15403]	-3.65794	-3.7618	0.00328	0.56824	-2.03885
ENSG00000110717	NDUFS8	NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex 1-23KD) (CI-23KD) (TYKY subunit). [Source:Uniprot/SWISSPROT;Acc:O00217]	3.552405	3.727576	0.003478	0.56824	-2.07293
ENSG00000105221	AKT2	RAC-beta serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-beta) (Protein kinase Akt-2) (Protein kinase B, beta) (PKB beta). [Source:Uniprot/SWISSPROT;Acc:P31751]	-3.49427	-3.74964	0.003349	0.56824	-2.05094
ENSG00000076108	BAZ2A	Bromodomain adjacent to zinc finger domain 2A (Transcription termination factor-I interacting protein 5) (TTF-I interacting protein 5) (Tip5) (hWALp3). [Source:Uniprot/SWISSPROT;Acc:Q9UIF9]	-5.36122	-4.75485	0.000637	0.56824	-1.14036
ENSG00000100462	SKB1	Protein arginine N-methyltransferase 5 (EC 2.1.1.-) (Shk1 kinase-binding protein 1 homolog) (SKB1Hs) (Jak-binding protein 1) (72	-4.84315	-4.24764	0.001447	0.56824	-1.57702

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
		kDa 1Cln-binding protein). [Source:Uniprot/SWISSPROT;Acc:O14744]					
ENSG00000187949	NDUFB4	NADH-ubiquinone oxidoreductase B15 subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-B15) (CI-B15). [Source:Uniprot/SWISSPROT;Acc:O95168]	-4.68866	-4.77219	0.000619	0.56824	-1.12625
ENSG00000124299	PEPD	Xaa-Pro dipeptidase (EC 3.4.13.9) (X-Pro dipeptidase) (Proline dipeptidase) (Prolidase) (Imidodipeptidase). [Source:Uniprot/SWISSPROT;Acc:P12955]	3.82856	3.530572	0.004886	0.56824	-2.27284
ENSG00000118689	FOXO3A	Forkhead box protein O3A (Forkhead in rhabdomyosarcoma-like 1) (AF6q21 protein). [Source:Uniprot/SWISSPROT;Acc:O43524]	-4.1996	-4.51964	0.000928	0.56824	-1.33702
ENSG00000125386	C4orf8	res4-22 protein [Source:RefSeq_peptide;Acc:NP_003695]	-3.91323	-3.58295	0.00462	0.56824	-2.21909
ENSG00000085831	C1orf34	-	-6.84292	-6.27794	6.71E-05	0.497358	-0.09522
ENSG00000068724	TTC7A	Tetratricopeptide repeat protein 7A (TPR repeat protein 7). [Source:Uniprot/SWISSPROT;Acc:Q9ULT0]	4.850304	4.88087	0.000522	0.56824	-1.0391
ENSG00000110047	EHD1	EH-domain containing protein 1 (Testilin) (hPAST1). [Source:Uniprot/SWISSPROT;Acc:Q9H4M9]	-4.12156	-4.39637	0.001134	0.56824	-1.44411
ENSG00000148120	C9orf3	aminopeptidase O [Source:RefSeq_peptide;Acc:NP_116212]	-6.09722	-5.95062	0.00106	0.497358	-0.28889
ENSG00000153048	CHSP1_HUMAN	Calcium-regulated heat stable protein 1 (Calcium-regulated heat-stable protein of 24 kDa) (CRHSP-24). [Source:Uniprot/SWISSPROT;Acc:Q9Y2V2]	-4.55172	-4.07591	0.001927.	0.56824	-1.73547
ENSG00000197958	RPL12	60S ribosomal protein L12. [Source:Uniprot/SWISSPROT;Acc:P30050]	4.360499	3.534007	0.004857	0.56824	-2.2693

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ENSG00000198506	NM_032890.2	dispatched homolog 1 (Drosophila) (DISP1), mRNA [Source:RefSeq_dna;Acc:NM_032890]	5.450844	4.48118	0.01008	0.56824	-1.38145
ENSG00000158488	CD1E	T-cell surface glycoprotein CD1e precursor (CD1e antigen) (R2G1). [Source:Uniprot/SWISSPROT;Acc:P15812]	-3.98134	-4.02107	0.002112	0.56824	-1.78719
ENSG00000167996	FTH1	Ferritin heavy chain (Ferritin H subunit). [Source:Uniprot/SWISSPROT;Acc:P02794]	4.233539	3.51817	0.004992	0.56824	-2.28563
ENSG00000111143	Q96G13_HUMAN	-	-4.58263	-4.57682	0.000846	0.56824	-1.28829
ENSG00000165487	EFHA1	EF hand domain family, member A1 [Source:RefSeq_peptide;Acc:NP_689939]	-3.97329	-4.02775	0.002089	0.56824	-1.78087
ENSG00000174516	PELI3_HUMAN	Pellino protein homolog 3 (Pellino 3). [Source:Uniprot/SWISSPROT;Acc:Q8N2H9]	-3.4183	-3.66899	0.003846	0.56824	-2.13172
ENSG00000128886	ELL3_HUMAN	RNA polymerase II elongation factor ELL3. [Source:Uniprot/SWISSPROT;Acc:Q9HB65]	3.893789	3.856418	0.002791	0.56824	-1.94566
ENSG00000179889	Q86XE2_HUMAN	-	-4.90098	-4.18666	0.001601	0.56824	-1.63268
ENSG00000181991	MRPS11	28S ribosomal protein S11, mitochondrial precursor (S11mt) (MRP-S11) (Cervical cancer proto-oncogene 2) (HCC-2). [Source:Uniprot/SWISSPROT;Acc:P82912]	3.652945	3.67272	0.003822	0.56824	-2.12797
ENSG00000196628	TCF4	Transcription factor 4 (Immunoglobulin transcription factor 2) (ITF-2) (SL3-3 enhancer factor 2) (SEF-2). [Source:Uniprot/SWISSPROT;Acc:P15884]	-3.73593	-3.55148	0.004712	0.56824	-2.25133
ENSG00000115548	JMJD1A	jumonji domain containing 1A [Source:RefSeq_peptide;Acc:NP_060903]	-5.34283	-4.43953	0.01056	0.56824	-1.4063

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000138709	Q8N7H4_HUMAN	-	-3.43654	-3.62484	0.004151	0.56824	-2.17641
ENSG00000189319	FAM53B	Protein FAM53B. [Source:Uniprot/SWISSPROT;Acc:Q14153]	-5.08715	-5.26273	0.00029	0.56824	-0.74939
ENSG00000095794	CREM	cAMP responsive element modulator. [Source:Uniprot/SWISSPROT;Acc:Q03060]	-3.40643	-3.66346	0.003883	0.56824	-2.1373
ENSG00000124788	ATXN1	Ataxin-1 (Spinocerebellar ataxia type 1 protein). [Source:Uniprot/SWISSPROT;Acc:P54253]	-5.70818	-3.72657	0.003484	0.56824	-2.07393
ENSG00000114867	EIF4G1	Eukaryotic translation initiation factor 4 gamma 1 (eIF-4-gamma 1) (eIF-4G1) (eIF-4G) (p220). [Source:Uniprot/SWISSPROT;Acc:Q04637]	3.542978	3.611957	0.004244	0.56824	-2.1895
ENSG00000130559	CAMSAP1	calmodulin regulated spectrin-associated protein 1 [Source:RefSeq_peptide;Acc:NP_056262]	-3.36276	-3.57533	0.004521	0.56824	-2.22687
ENSG00000124097	NP_001008735.1	high-mobility group (nonhistone chromosomal) protein 1-like 1 [Source:RefSeq_peptide;Acc:NP_001008735]	5.273639	4.916939	0.000493	0.56824	-1.01064
ENSG00000106069	CHN2	Beta-chimaerin (Beta-chimerin) (Rho-GTPase-activating protein 3). [Source:Uniprot/SWISSPROT;Acc:P52757]	5.253497	4.88996	0.000514	0.56824	-1.03191
ENSG00000050165	DKK3	Dickkopf related protein-3 precursor (Dkk-3) (Dickkopf-3) (hDkk-3) (UNQ258/PRO295). [Source:Uniprot/SWISSPROT;Acc:Q9UBP4]	-3.81701	-3.88498	0.002659	0.56824	-1.91783
ENSG00000104728	ARHGEF10	Rho guanine nucleotide exchange factor 10. [Source:Uniprot/SWISSPROT;Acc:O15013]	-3.29064	-3.53515	0.004847	0.56824	-2.26813
ENSG00000142635	-	15 kDa protein [Source:IPI;Acc:IPI00009466]	4.058359	4.003066	0.002177	0.56824	-1.80429
ENSG00000121410	A1BG	Alpha-1-B-glycoprotein precursor (Alpha-1-B glycoprotein). [Source:Uniprot/SWISSPROT;Acc:P04217]	-3.59343	-3.77167	0.003225	0.56824	-2.02906

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ENSG00000155130	MARCKS	Myristoylated alanine-rich C-kinase substrate (MARCKS) (Protein kinase C substrate, 80 kDa protein, light chain) (PKCSL) (80K-L protein). [Source:Uniprot/SWISSPROT;Acc:P29966]	3.995368	3.758017	0.003301	0.56824	-2.04261
ENSG00000121741	Q9H0V5_HUMAN	-	-3.74056	-3.82779	0.00293	0.56824	-1.9737
ENSG00000197907	-	33 kDa protein [Source:IPI;Acc:IPI00479509]	3.763157	4.00198	0.002181	0.56824	-1.80532
ENSG00000147403	RPL10	60S ribosomal protein L10 (QM protein) (Tumor suppressor QM) (Laminin receptor homolog). [Source:Uniprot/SWISSPROT;Acc:P27635]	4.605627	4.426822	0.001079	0.56824	-1.4174
ENSG00000111775	COX6A1	Cytochrome c oxidase polypeptide VIa-liver, mitochondrial precursor (EC 1.9.3.1). [Source:Uniprot/SWISSPROT;Acc:P12074]	4.05343	3.945472	0.0024	0.56824	-1.85936
ENSG00000165730	CJ024_HUMAN	-	-5.06568	-4.03083	0.002078	0.56824	-1.77795
ENSG00000181969	XP_371184.2	PREDICTED: KIAA1183 protein [Source:RefSeq_peptide;Acc:XP_371184]	-3.75702	-3.70857	0.003593	0.56824	-2.09194
ENSG00000182281	-	28 kDa protein [Source:IPI;Acc:IPI00332656]	3.332232	3.57777	0.004502	0.56824	-2.22438
ENSG00000161640	SIGLEC1	Sialic acid binding Ig-like lectin 11 precursor (Siglec-11) (Sialic acid-binding lectin 11) (UNQ9222/PRO28718). [Source:Uniprot/SWISSPROT;Acc:Q96RL6]	-4.03054	-3.94967	0.002383	0.56824	-1.85532
ENSG00000184895	SRY	Sex-determining region Y protein (Testis-determining factor). [Source:Uniprot/SWISSPROT;Acc:Q05066]	4.279836	3.666439	0.003863	0.56824	-2.1343
ENSG00000184085	Q9UHT3_HUMAN	-	-6.38787	-6.57647	4.48E-05	0.497358	0.068403
ENSG00000183405	-	22 kDa protein [Source:IPI;Acc:IPI00478287]	4.468439	4.655183	0.000746	0.56824	-1.22247
ENSG00000182663	-	13 kDa protein [Source:IPI;Acc:IPI00479645]	4.295474	4.485254	0.000981	0.56824	-1.36662

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ENSG00000182912	C21orf90	-	-3.74689	-3.59351	0.004381	0.56824	-2.2083
ENSG00000181404	Q9NQA3_HUMAN	-	-4.04563	-3.66271	0.003888	0.56824	-2.13806
ENSG00000183747	NP_872423.2	-	-3.76011	-3.6235	0.00416	0.56824	-2.17776
ENSG00000186994	Q8IUV2_HUMAN	-	-3.6879	-3.79406	0.003104	0.56824	-2.00691
ENSG00000186994	Q8IUV2_HUMAN	-	-4.21177	-3.52049	0.004972	0.56824	-2.28324
ENSG00000183696	UPP1	Uridine phosphorylase 1 (EC 2.4.2.3) (UrdPase 1) (UPase 1). [Source:Uniprot/SWISSPROT;Acc:Q16831]	-4.04435	-4.16269	0.001667	0.56824	-1.65474
ENSG00000182048	-	13 kDa protein [Source:IPI;Acc:IPI00333671]	-3.41627	-3.69324	0.003689	0.56824	-2.10732
ENSG00000186244	XP_496353.1	PREDICTED: similar to ribosomal protein L21 [Source:RefSeq_peptide;Acc:XP_496353]	5.945581	6.0335	9.42E-05	0.497358	-0.23838
ENSG00000165445	-	17 kDa protein [Source:IPI;Acc:IPI00374706]	-3.48769	-3.60152	0.004321	0.56824	-2.20012
ENSG00000187042	LAMRIP15	Laminin receptor-like protein LAMRL5. [Source:Uniprot/SPTREMBL;Acc:Q96RS2]	3.939894	3.827982	0.002929	0.56824	-1.97351
ENSG00000186729	-	12 kDa protein [Source:IPI;Acc:IPI00472611]	4.304029	3.945034	0.002401	0.56824	-1.85978
ENSG00000187821	-	-	-4.44609	-3.91701	0.002518	0.56824	-1.88679
ENSG00000188442	-	9 kDa protein [Source:IPI;Acc:IPI00414897]	4.121633	3.657763	0.003922	0.56824	-2.14306
ENSG00000189262	NP_898870.1	thymosin-like 3 [Source:RefSeq_peptide;Acc:NP_898870]	3.694497	3.849774	0.002823	0.56824	-1.95215
ENSG00000187899	XP_039702.1	PREDICTED: similar to ribosomal protein S3a; 40S ribosomal protein S3a; v-fos transformation effector protein 1 [Source:RefSeq_peptide;Acc:XP_039702]	5.822773	5.410751	0.000232	0.56824	-0.64383
ENSG00000140988	RPS2	40S ribosomal protein S2 (S4) (LLRep3 protein). [Source:Uniprot/SWISSPROT;Acc:P15880]	4.063239	3.651134	0.003967	0.56824	-2.14976

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ENSG00000188801	NP_945356.1	zinc finger protein 322B [Source:RefSeq_peptide;Acc:NP_945356]	-3.86933	-3.70943	0.003588	0.56824	-2.09109
ENSG00000147604	RPL7	60S ribosomal protein L7. [Source:Uniprot/SWISSPROT;Acc:P18124]	4.743644	4.286033	0.001359	0.56824	-1.54233
ENSG00000189378	Q6ZRY2_HUMAN	-	4.533826	4.142776	0.001723	0.56824	-1.67314
ENSG00000092607	TBX15	T-box transcription factor TBX15 (T-box protein 15). [Source:Uniprot/SWISSPROT;Acc:Q96SF7]	-4.16381	-4.24235	0.00146	0.56824	-1.58182
ENSG00000185386	MAPK11	Mitogen-activated protein kinase 11 (EC 2.7.1.37) (Mitogen-activated protein kinase p38 beta) (MAP kinase p38 beta) (p38b) (p38-2) (Stress- activated protein kinase-2). [Source:Uniprot/SWISSPROT;Acc:Q15759]	-3.41293	-3.57269	0.004542	0.56824	-2.22958
ENSG00000196533	NP_001007545.1	-	-3.94596	-4.00529	0.002169	0.56824	-1.80217
ENSG00000198001	IRAK4_HUMAN	Interleukin-1 receptor-associated kinase-4 (EC 2.7.1.37) (IRAK-4) (NY- REN-64 antigen). [Source:Uniprot/SWISSPROT;Acc:Q9NWZ3]	-4.35439	-3.70916	0.00359	0.56824	-2.09135
ENSG00000196282	-	59 kDa protein [Source:IPI;Acc:IPI00479308]	-5.71637	-4.87889	0.000523	0.56824	-1.04067
ENSG00000196988	ENH5_HUMAN	HERV-H_19p13.11 provirus ancestral Env polyprotein precursor (Envelope polyprotein) (Env protein RGH1) (Env protein RTLV-H) [Includes: Surface protein (SU)]. [Source:Uniprot/SWISSPROT;Acc:P61549]	-5.29682	-5.11212	0.000365	0.56824	-0.86063
ENSG00000198345	-	-	4.360666	4.080318	0.001912	0.56824	-1.73134
ENSG00000019206	-	4 kDa protein [Source:IPI;Acc:IPI00478964]	4.269033	3.538968	0.004815	0.56824	-2.26419
ENSG00000132256	TRIM5_HUMAN	Tripartite motif protein 5 (EC 6.3.2.-) (RING finger protein 88).	-3.51661	-3.69515	0.003677	0.56824	-2.1054

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
		[Source:Uniprot/SWISSPROT:Acc:Q9C035]					
ENSG00000083817	NP_060349.1	zinc finger protein 416 [Source:RefSeq_peptide;Acc:NP_060349]	-3.9578	-4.05594	0.001992	0.56824	-1.75425
ENSG0000019641	NP_003422.2	zinc finger protein 124 [Source:RefSeq_peptide;Acc:NP_003422]	-5.11197	-4.40496	0.00118	0.56824	-1.43656
ENSG0000019906	-	12 kDa protein [Source:IPI;Acc:IPI00515031]	4.930048	4.559196	0.00087	0.56824	-1.30325
ENSG0000019787878	XM_375099.1	-	-3.98487	-3.94693	0.002394	0.56824	-1.85796
ENSG0000019798	-	-	-4.54296	-4.61562	0.000795	0.56824	-1.25556
ENSG0000019694942	-	-	4.07374	3.62988	0.004115	0.56824	-2.17129
ENSG0000019871212	COX2_HUMAN	Cytochrome c oxidase polypeptide II (EC 1.9.3.1). [Source:Uniprot/SWISSPROT;Acc:P00403]	5.158652	4.88299	0.00052	0.56824	-1.03742
ENSG0000019872727	CYB_HUMAN	Cytochrome b. [Source:Uniprot/SWISSPROT:Acc:P00156]	4.252937	3.608091	0.004272	0.56824	-2.19344
ENSG0000019890	PRC1	protein regulator of cytokinesis 1 isoform 3 [Source:RefSeq_peptide;Acc:NP_955446]	-5.69216	-6.13553	8.17E-05	0.497358	-0.17758
ENSG0000013923939	RPL14	60S ribosomal protein L14 (CAG-ISL 7). [Source:Uniprot/SWISSPROT;Acc:P50914]	4.41623	4.523997	0.000921	0.56824	-1.33329
ENSG0000014342020	ENSA	Alpha-endosulfine. [Source:Uniprot/SWISSPROT;Acc:O43768]	-3.62136	-3.68781	0.003724	0.56824	-2.11277
ENSG0000017052323	KRTHB1	Keratin, type II cuticular HB3 (Hair keratin, type II HB3). [Source:Uniprot/SWISSPROT;Acc:P78385]	-3.80594	-3.87363	0.00271	0.56824	-1.92888
ENSG0000010968585	WHSC1	Wolf-Hirschhorn syndrome candidate 1 protein isoform 2 [Source:RefSeq_peptide;Acc:NP_055734]	3.780083	3.763712	0.003269	0.56824	-2.03695
ENSG0000016966868	NP_997357.1	-	-3.42041	-3.56833	0.004576	0.56824	-2.23404
ENSG0000019824747	NP_997368.1	-	-3.57154	-3.83155	0.002912	0.56824	-1.97
ENSG0000013967575	-	heterogeneous nuclear ribonucleoprotein A1-like (LOC144983),	4.088211	4.366584	0.00119	0.56824	-1.47041

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000134758	RNF138	transcript variant 2, mRNA [Source:RefSeq_dna;Acc:NM_001011725] ring finger protein 138 isoform 1 [Source:RefSeq_peptide;Acc:NP_057355]	-4.48509	-4.29982	0.001328	0.56824	-1.52994
ENSG00000125741	OPA3	Optic atrophy 3 protein [Source:Uniprot/SWISSPROT;Acc:Q9H6K4]	-3.70954	-3.81439	0.002998	0.56824	-1.98687
ENSG00000187828	-	25 kDa protein [Source:IPI;Acc:IPI00414723]	-5.08527	-4.69258	0.000703	0.56824	-1.19145
ENSG00000173322	XP_495912.1	PREDICTED: similar to 40S ribosomal protein S6 (Phosphoprotein NP33) [Source:RefSeq_peptide;Acc:XP_495912]	3.497602	3.533493	0.004861	0.56824	-2.26983
HIX0012306	-	Non-protein coding transcript	-3.71176	-3.60407	0.004302	0.56824	-2.19753
HIX0021713	-	Hypothetical protein	-3.64501	-3.91099	0.002544	0.56824	-1.89261
HIX0006727	-	Non-protein coding transcript	-4.03526	-4.3088	0.001309	0.56824	-1.52188
HIX0008703	-	Non-protein coding transcript	-3.55445	-3.55868	0.004654	0.56824	-2.24394
HIX0002024	-	Hypothetical protein	-4.37938	-3.85724	0.002787	0.56824	-1.94486
HIX0011877	-	Hypothetical protein	-5.13745	-4.93263	0.000481	0.56824	-0.99833
HIX0001029	-	Hypothetical protein	-5.98392	-6.22903	7.18E-05	0.497358	-0.12319
HIX0019035	-	Non-protein coding transcript	3.904534	3.979494	0.002266	0.56824	-1.82676
HIX0009215	-	Hypothetical protein	-3.62992	-3.72296	0.003506	0.56824	-2.07754
HIX0006696	-	Non-protein coding transcript	-4.20935	-3.82392	0.00295	0.56824	-1.9775
HIX0022038	-	Similar to Transposase (IS10 transposase)	-3.64862	-3.75291	0.00333	0.56824	-2.04769
HIX0003523	-	Hypothetical protein	-3.46749	-3.57552	0.00452	0.56824	-2.22668
HIX0013987	-	Hypothetical protein	3.865267	4.031106	0.002077	0.56824	-1.77769

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
HIX0007463	-	Non-protein coding transcript	3.42425	3.554664	0.004686	0.56824	-2.24806
HIX0005687	-	Hypothetical protein	-4.2249	-3.92904	0.002467	0.56824	-1.87518
HIX0004105	-	Hypothetical protein	-3.52844	-3.59162	0.004396	0.56824	-2.21023
HIX0018460	-	Hypothetical protein	-5.68738	-4.19827	0.001571	0.56824	-1.62202
HIX0008806	-	Hypothetical protein	-3.48072	-3.63416	0.004084	0.56824	-2.16695
HIX0022990	-	Hypothetical protein	4.603655	3.62029	0.004183	0.56824	-2.18103
HIX0001699	-	Hypothetical protein	3.589937	3.809434	0.003024	0.56824	-1.99175
HIX0016986	-	Hypothetical protein	4.105833	3.703696	0.003624	0.56824	-2.09683
hsa-mir-197	-	Homo sapiens microRNA miR-197 stem-loop	-3.51286	-3.77841	0.003188	0.56824	-2.02238
hsa-mir-222	-	Homo sapiens microRNA miR-222 stem-loop	-4.16922	-3.8385	0.002877	0.56824	-1.96319
AY436380_IE1	IE1	Human herpesvirus 5 strain Towne; p72 protein, alternatively spliced	-4.01992	-4.06322	0.01968	0.56824	-1.74739
M11167_1	-	Human 28S ribosomal RNA	4.949826	4.161412	0.00167	0.56824	-1.65592
M11167_2	-	Human 28S ribosomal RNA	5.698493	4.493624	0.000968	0.56824	-1.35939
MTTA	-	mito_tRNA-Ala	-5.36457	-5.26512	0.000289	0.56824	-0.74766

APPENDIX C

PUBLICATIONS BY AUTHOR

PUBLICATION

Nipaporn Thipmanee, Sukon Prasitwattanaseree, Jeerayut Chaijaruwanich, Nisa Chawapun , Taned Chitapanarux, Imjai Chitapanarux. Identification of Rectal Cancer Genes by Microarray Analysis. Journal of Thai Society of Therapeutic Radiology and Oncology, Thailand, Volume 17:1: Jan-June 2011, 71-78.

ABSTRACT and PRESENTATION

Nipaporn Thipmanee, Sukon Prasitwattanaseree, Jeerayut Chaijaruwanich, Nisa Chawapun , Taned Chitapanarux, Imjai Chitapanarux. Microarray analysis for rectal cancer genes. The proceeding of the 6th Conference on Science and Technology for Youths: 2011 (Abstract and oral presentation); 2011 Mar 17-18: Bangkok, Thailand. 2011.

Nipaporn Thipmanee, Sukon Prasitwattanaseree, Jeerayut Chaijaruwanich, Nisa Chawapun , Taned Chitapanarux, Imjai Chitapanarux. Rectal cancer Classification Using Gene Expression. In press. The symposium "Advance Statistical Method for Healthcare Research". (Abstract and guest speaker), 2011 Aug 22-23; Kantary Hills Hotel, Chiang Mai, Thailand 2011.

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