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")
```

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```
## Within-array Normalization ##
MA.loess<-normalizeWithinArrays(RG.ne,method="loess")
```

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```
## 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,]
```

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```
## 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")
```

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```
##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
		[Source:Uniprot/SWISSPROT;Acc:P41181]					
ENSG00000159208	NP_653298.1	-	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
		[Source:Uniprot/SWISSPROT;Acc:P62277]					
ENSG00000172757	CFL1	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;Acc:P83731]	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

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000141434	MEP1B	Meprin A beta-subunit precursor (EC 3.4.24.18) (Endopeptidase-2) (N- benzoyl-L-tyrosyl-P-amino-benzoic acid hydrolase beta subunit) (PABA peptide hydrolase) (PPH beta). [Source:Uniprot/SWISSPROT;Acc:Q16820]	-4.03437	-3.93904	0.002426	0.56824	-1.86555
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

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000172715	XP_070233.3	PREDICTED: similar to ribosomal protein L10a [Source:RefSeq_peptide;Acc:XP_070233]	4.220453	3.822194	0.002958	0.56824	-1.97919
ENSG00000168482	CYP21A2	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	3.724883	3.53101	0.004882	0.56824	-2.27239

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
		[Source:RefSeq_peptide;Acc:XP_172230]					
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).	4.429855	3.701617	0.003637	0.56824	-2.09891

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
		[Source:Uniprot/SWISSPROT;Acc:P42677]					
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).	4.680867	4.432501	0.001069	0.56824	-1.41244

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
		[Source:Uniprot/SWISSPROT;Acc:P18621]					
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
ENSG00000181312	-	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

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000132423	COQ3	Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial precursor (EC 2.1.1.114) (Dihydroxyhexaprenylbenzoate methyltransferase) (3,4- dihydroxy-5-hexaprenylbenzoate methyltransferase) (DHHB methyltransferase) (DHHB-MT) (DHHB-MTase) (UG0215E05). [Sou	-3.63743	-3.65187	0.003962	0.56824	-2.14902
ENSG00000170250	-	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:Q9H4I8]	-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) (S1R 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-	-3.79955	-3.6085	0.004269	0.56824	-2.19302

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
		III). [Source:Uniprot/SWISSPROT;Acc:P07451]					
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,	4.908056	3.697544	0.003662	0.56824	-2.103

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
		mRNA [Source:RefSeq_dna;Acc:NM_203302]					
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:Q9UHC1]	-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

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000182180	DNAJC9	DnaJ homolog subfamily C member 9 (DnaJ protein SB73). [Source:Uniprot/SWISSPROT;Acc:Q8WXX5]	-4.07233	-3.74967	0.003349	0.56824	-2.05091
ENSG00000111676	DRPLA	Atrophin-1 (Dentatorubral-pallidoluysian atrophy protein). [Source:Uniprot/SWISSPROT;Acc:P54259]	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 I-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-	-4.84315	-4.24764	0.001447	0.56824	-1.57702

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
		binding protein 1 homolog) (SKB1Hs) (Jak-binding protein 1) (72 kDa ICln-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	0.004462	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	0.000106	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.	4.360499	3.534007	0.004857	0.56824	-2.2693

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
		[Source:Uniprot/SWISSPROT;Acc:P30050]					
ENSG00000198506	NM_032890.2	dispatched homolog 1 (Drosophila) (DISP1), mRNA [Source:RefSeq_dna;Acc:NM_032890]	5.450844	4.468118	0.001008	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
ENSG00000011143	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	-5.34283	-4.43953	0.001056	0.56824	-1.4063

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
		[Source:RefSeq_peptide;Acc:NP_060903]					
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-1B-glycoprotein precursor (Alpha-1-B glycoprotein).	-3.59343	-3.77167	0.003225	0.56824	-2.02906

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
		[Source:Uniprot/SWISSPROT;Acc:P04217]					
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	4.001981	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	SIGLEC11	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

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000182663	-	13 kDa protein [Source:IPI;Acc:IPI00479645]	4.295474	4.485254	0.000981	0.56824	-1.36662
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	LAMR1P15	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).	4.063239	3.651134	0.003967	0.56824	-2.14976

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
		[Source:Uniprot/SWISSPROT;Acc:P15880]					
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
ENSG00000198206	-	4 kDa protein [Source:IPI;Acc:IPI00478964]	4.269033	3.538968	0.004815	0.56824	-2.26419

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000132256	TRIM5_HUMAN	Tripartite motif protein 5 (EC 6.3.2.-) (RING finger protein 88). [Source:Uniprot/SWISSPROT;Acc:Q9C035]	-3.51661	-3.69515	0.003677	0.56824	-2.1054
ENSG00000083817	NP_060349.1	zinc finger protein 416 [Source:RefSeq_peptide;Acc:NP_060349]	-3.9578	-4.05594	0.001992	0.56824	-1.75425
ENSG00000196418	NP_003422.2	zinc finger protein 124 [Source:RefSeq_peptide;Acc:NP_003422]	-5.11197	-4.40496	0.001118	0.56824	-1.43656
ENSG00000198906	-	12 kDa protein [Source:IPI;Acc:IPI00515031]	4.930048	4.559196	0.00087	0.56824	-1.30325
ENSG00000197878	XM_375099.1	-	-3.98487	-3.94693	0.002394	0.56824	-1.85796
ENSG00000197988	-	-	-4.54296	-4.61562	0.000795	0.56824	-1.25556
ENSG00000196942	-	-	4.07374	3.62988	0.004115	0.56824	-2.17129
ENSG00000198712	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
ENSG00000198727	CYB_HUMAN	Cytochrome b. [Source:Uniprot/SWISSPROT;Acc:P00156]	4.252937	3.608091	0.004272	0.56824	-2.19344
ENSG00000198901	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
ENSG00000139239	RPL14	60S ribosomal protein L14 (CAG-ISL 7). [Source:Uniprot/SWISSPROT;Acc:P50914]	4.441623	4.523997	0.000921	0.56824	-1.33329
ENSG00000143420	ENSA	Alpha-endosulfine. [Source:Uniprot/SWISSPROT;Acc:O43768]	-3.62136	-3.68781	0.003724	0.56824	-2.11277
ENSG00000170523	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
ENSG00000109685	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
ENSG00000169668	NP_997357.1	-	-3.42041	-3.56833	0.004576	0.56824	-2.23404
ENSG00000198247	NP_997368.1	-	-3.57154	-3.83155	0.002912	0.56824	-1.97

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
ENSG00000139675	-	heterogeneous nuclear ribonucleoprotein A1-like (LOC144983), transcript variant 2, mRNA [Source:RefSeq_dna;Acc:NM_001011725]	4.088211	4.366584	0.00119	0.56824	-1.47041
ENSG00000134758	RNF138	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

Name	Gene_symbol	Description	logFC	t	P.Value	adj.P.Val	B
HIX0013987	-	Hypothetical protein	3.865267	4.031106	0.002077	0.56824	-1.77769
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	0.001968	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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