

FFPE 샘플이용 total RNA-Seq 실험분석



2017
Never Ending Service



BIO-Experiment & Analysis Service

Microarray

- ❖ Gene Expression
- ❖ miRNA
- ❖ CGH / CNV
- ❖ ChIP on chip
- ❖ Methylation
- ❖ Agilent/Affymetrix
- ❖ Exiqon

NGS

- ❖ RNA-Seq
- ❖ small RNA-Seq
- ❖ ChIP-Seq
- ❖ MBD-Seq
- ❖ Exome-Seq
- ❖ Target DNA-Seq
- ❖ Illumina/IonProton

qRT-PCR

- ❖ mRNA
- ❖ microRNA
- ❖ PCR Array
- ❖ Qiagen
- ❖ Genosensor
- ❖ Others

Antibody Array

- ❖ Protein Profiling
- ❖ Phosphorylation
- ❖ FullmoonBio
- ❖ RayBiotech
- ❖ Others

nature COMMUNICATIONS

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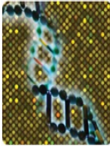
NATURE COMMUNICATIONS | ARTICLE

Metabolic engineering of *Corynebacterium glutamicum* for L-arginine production

Seok Hyun Park, Hyun Uk Kim, Tae Yong Kim, Jun Seok Park, Suok-Su Kim


Affiliations | Contributions | Corresponding author

Microarray



❖ Meaningful Data from Any Genome

NGS



❖ Next Generation Sequencing



DNA

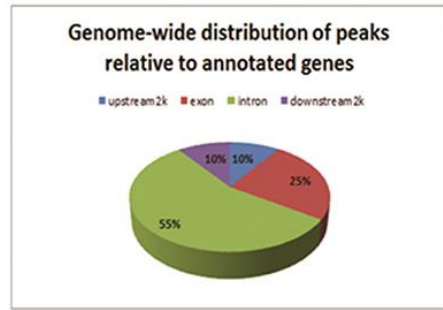
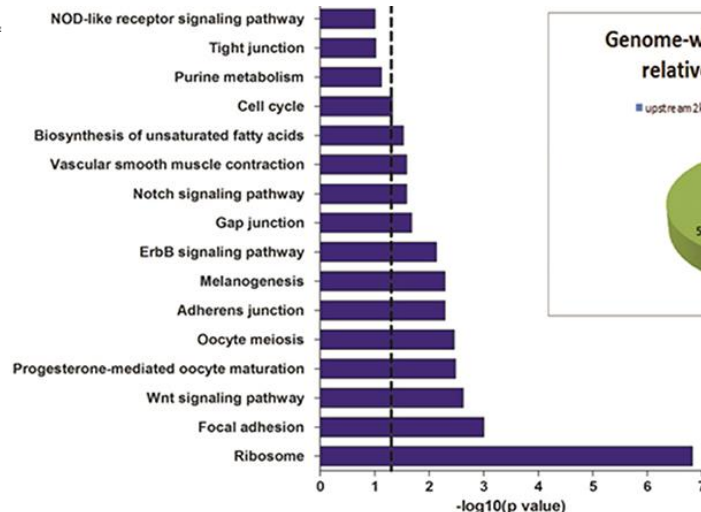
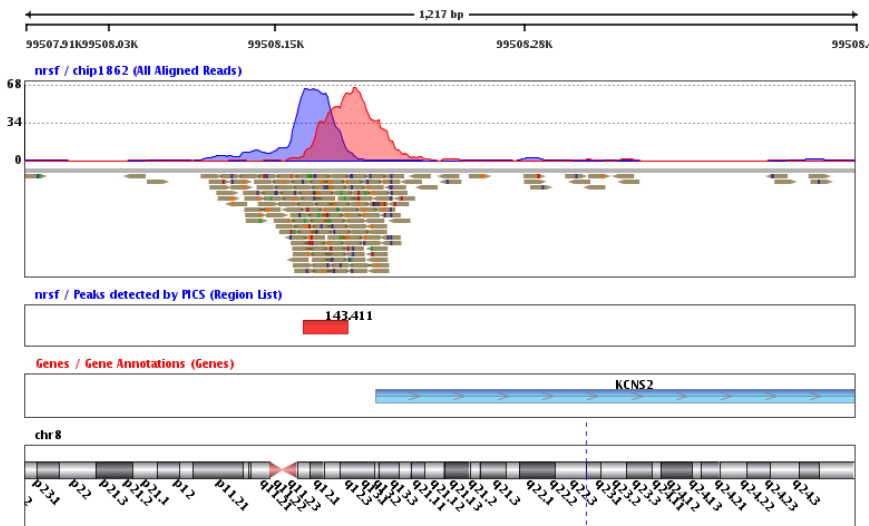


- MBD-Seq**
 - DNA Methylation Profiling
 - Epigenome 분석
 - gDNA 샘플준비
- ChIP-Seq**
 - DNA-Protein Interactions
 - Histone modifications
 - IP-DNA 샘플준비
- Target DNA-Seq**
 - 특정영역 DNA 위치를 집중적으로 Sequencing
 - SNP, CNV 분석외
 - gDNA 샘플준비

RNA



- total RNA RNA-Seq**
 - mRNA-Seq 분석외 LncRNA 분석가능
 - Whole transcriptome
 - total RNA 샘플준비
- mRNA RNA-Seq**
 - Gene Expression, Isoform, GO/Pathway
 - Splicing, Gene Fusion외
 - total RNA 샘플준비
- Quant RNA-Seq**
 - DEG 분석에 집중
 - 극미량, FFPE 샘플도 실험 가능
 - total RNA 샘플준비

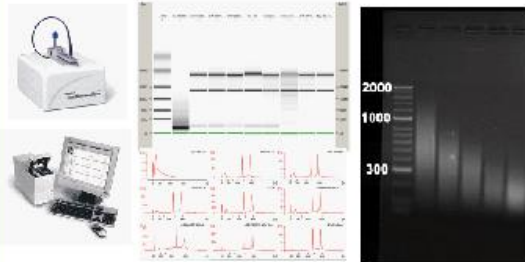


RNA-Seq Process

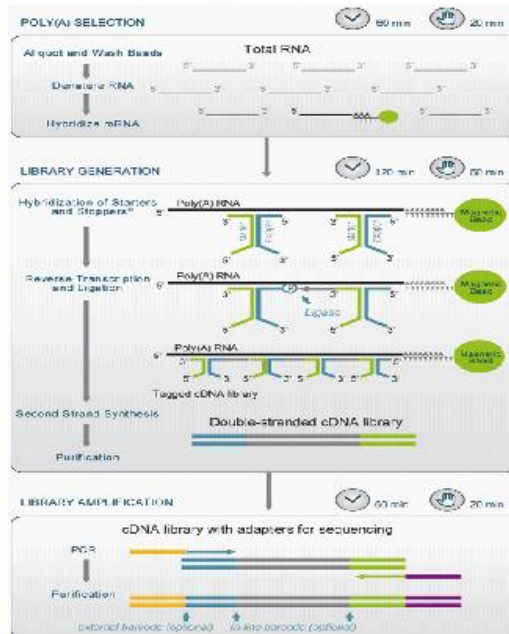


Sample Preparation

Sample Prep & QC

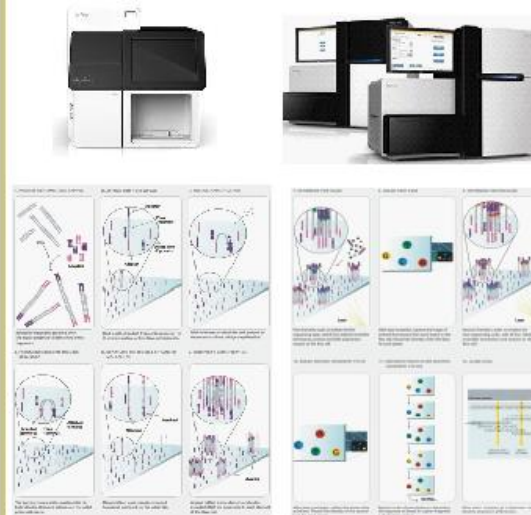


Library Prep & QC

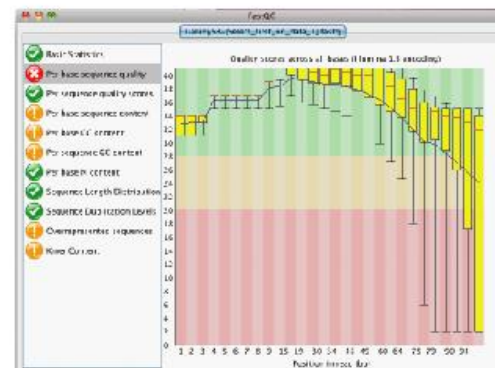


Sequencing

Cluster Generation & Sequencing

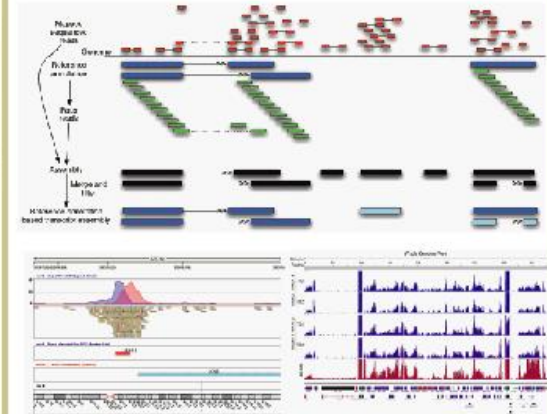


FastQC

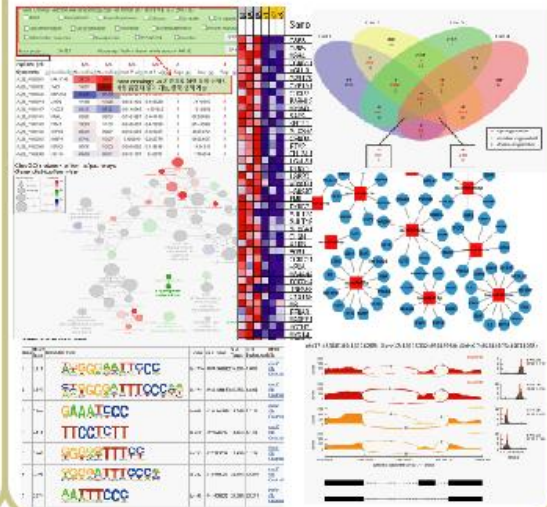


Data Analysis

Genome Mapping & Analysis



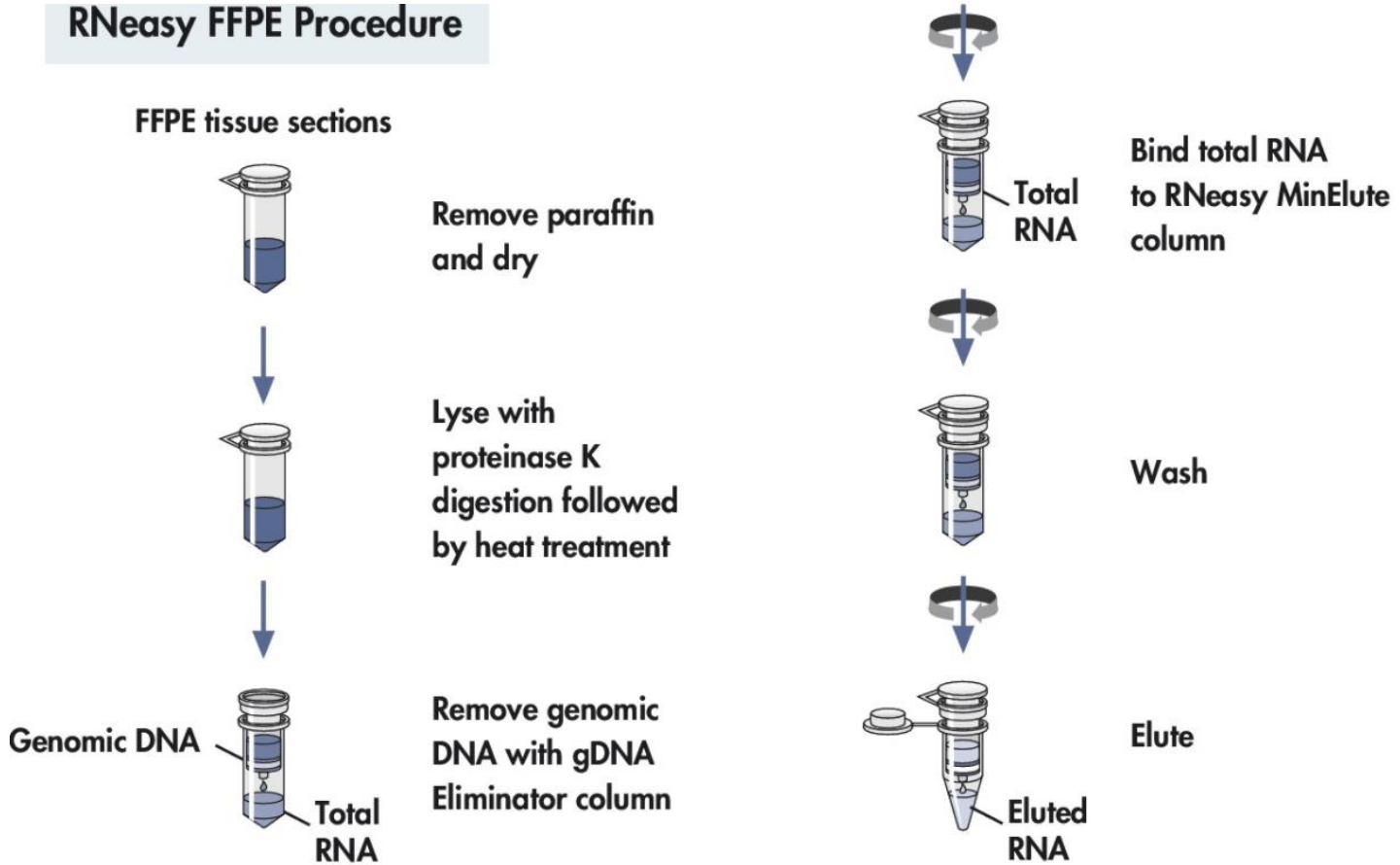
Data Mining & Visualization



RNA Sample Prep. (Qiagen's RNeasy FFPE)



RNeasy FFPE Procedure

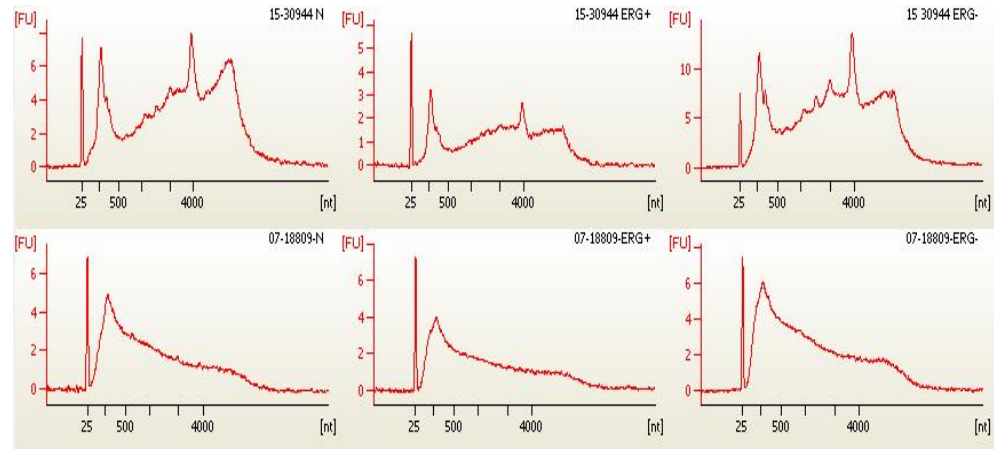
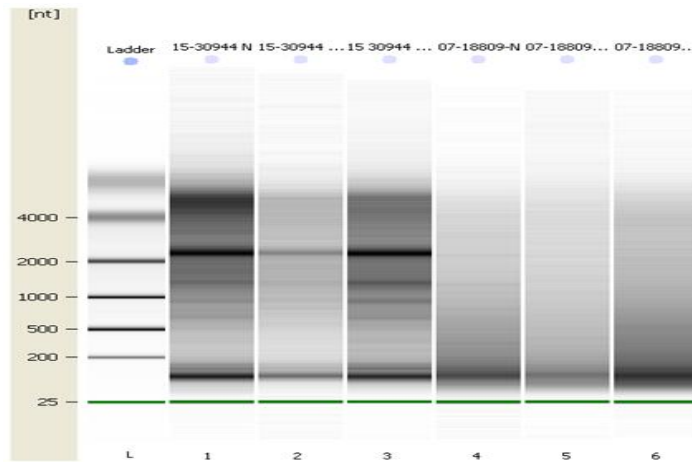


- FFPE samples에서 최적화된 결과 — formalin crosslinking을 제거하는 참신한 방법
- High RNA yields — efficient release of RNA without compromising RNA integrity
- 빠른 처리 과정 — 약 70분 정도만에 RNA를 얻을 수 있는 프로토콜

RNA Quality Control



Sample	ng/μl	OD _{260/280}	OD _{260/230}	Total (ng)	Ratio(28s/18s)	RIN	Result
15-30944 N	92.3	1.92	2.2	2307.5	0.0	2.9	Check
15-30944 ERG+	61	1.91	2.33	1525	0.2	3.0	Check
15-30944 ERG-	178.9	1.91	1.9	4472.5	0.2	3.2	Check
07-18809 N	88.9	1.87	2.3	2222.5	0.0	2.4	Check
07-18809 ERG+	63.6	1.82	2.05	1590	0.0	2.4	Check
07-18809 ERG-	109.9	1.85	2.07	2747.5	0.0	2.3	Check



- RIN(RNA Integrity Number) :

Agilent社에서 제공하는 software tool로 Eukaryote total RNA sample에 적용되며, electrophoretic trace에 의해 integrity가 결정됩니다. 1~10까지의 값을 가지며, RIN값에 대한 다양한 결과는 <http://www.chem.agilent.com/rin/rinSearch.aspx> 에서 찾아 보실 수 있습니다.

RiboGone™ rRNA removal & SMARTer cDNA synthesis

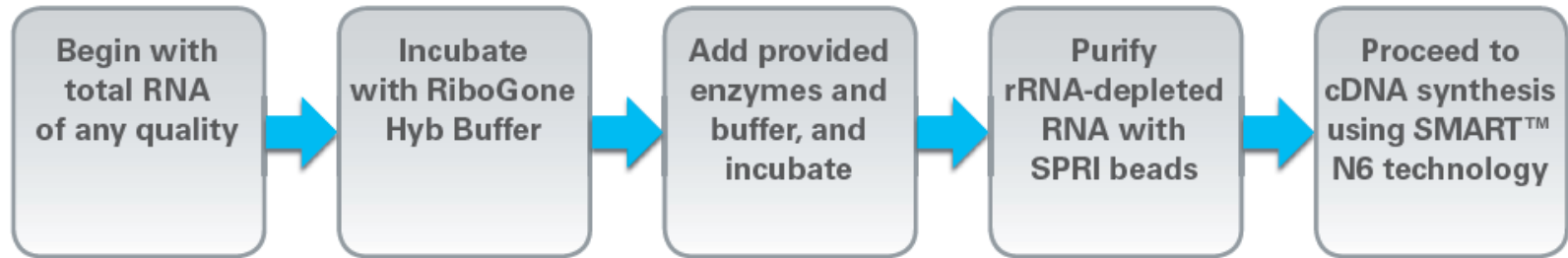


Figure 1. Workflow for RiboGone rRNA depletion. This kit is designed for use with low input samples containing 10–100 ng of total RNA, and works with full-length or degraded RNA. Samples processed using the RiboGone kit are ready for cDNA synthesis with any random-primed SMARTer RNA-Seq kit, including the SMARTer Stranded RNA-Seq Kit, SMARTer Universal Low Input RNA Kit for Sequencing, and SMARTer Universal Low Input RNA Library Prep Kit.

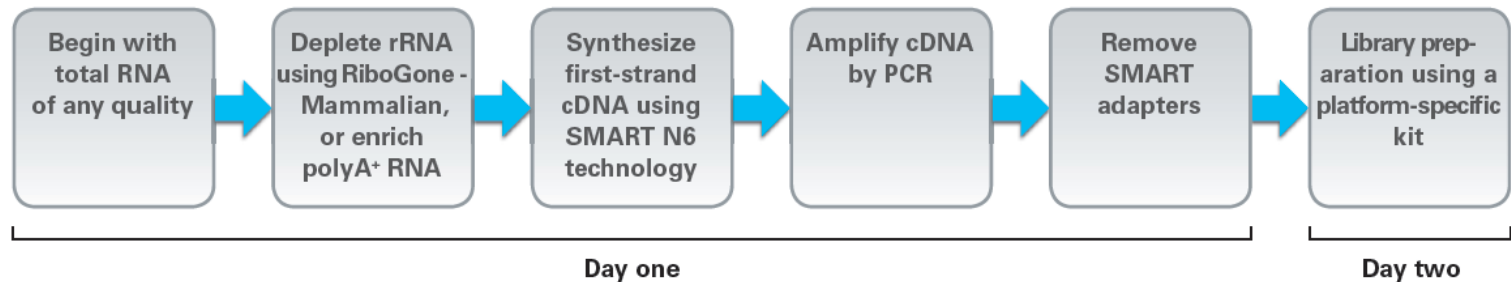
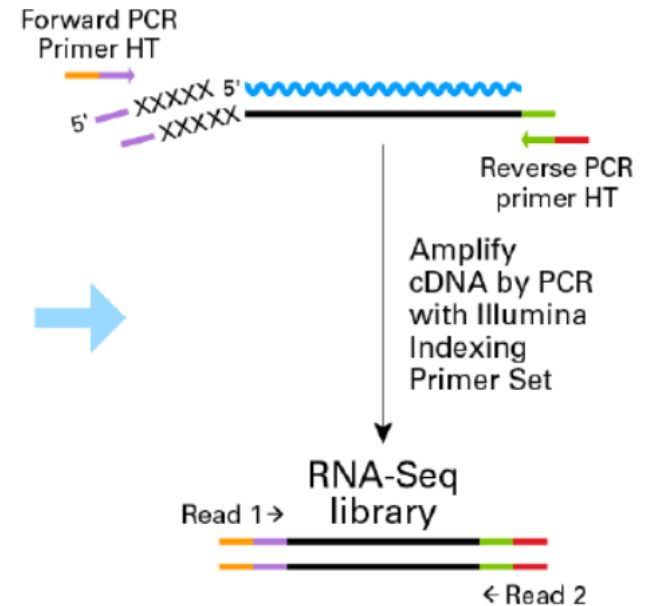
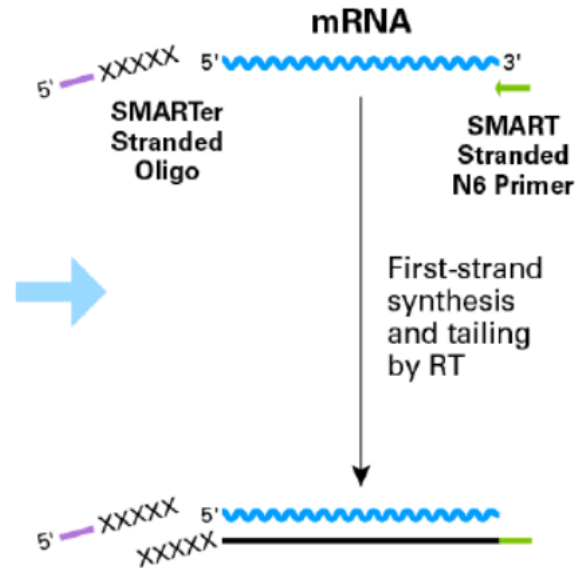
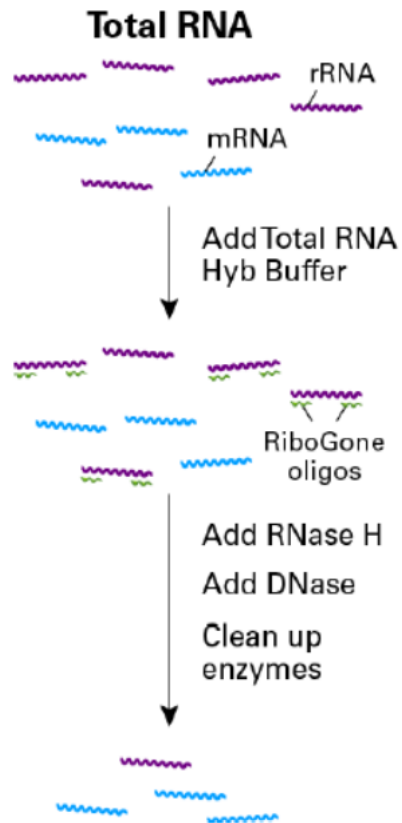


Figure 3. Workflow for random-primed cDNA synthesis with SMARTer Universal Low Input RNA kits. SMARTer Universal cDNA synthesis is random-primed, which makes it ideal for use with compromised mammalian RNA samples, e.g. RNA from FFPE tissue. Ribosomal RNA must be removed with RiboGone - Mammalian prior to SMARTer Universal cDNA synthesis.

RiboGone™ rRNA removal & SMARTer cDNA synthesis

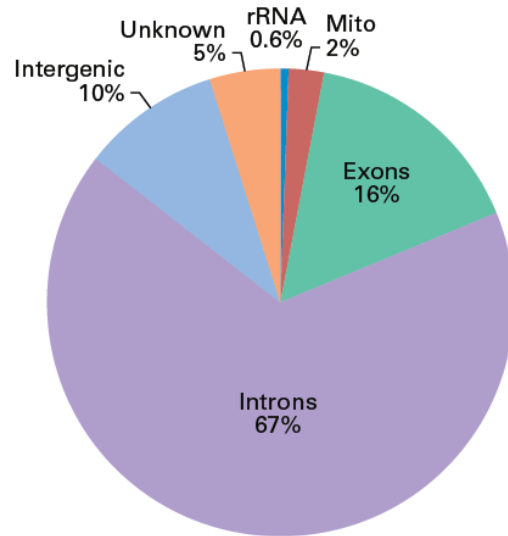


Two configurations:

Low Input (10 ng–100 ng) = RiboGone - Mammalian + SMARTer Stranded Total RNA Sample Prep

High Input (100 ng–1 mg) = SMARTer Stranded Total RNA Sample Prep Kit - HI

Summary for SMARTer Kit Using



High quality RNA-seq data from FFPE samples

The library was sequenced on an Illumina MiSeq® instrument with ~6M 1 x 50 bp paired end reads. rRNA reads were reduced to 0.6% of total reads, and 16,463 genes were identified. The number of reads that mapped to introns, exons, intergenic regions, rRNA, mitochondrial RNA, and unknown sources are shown as percentages of the total reads (Figure 4).

Figure 4. RiboGone treatment and random-primed SMARTer cDNA synthesis preserve transcriptome data while eliminating rRNA. Total RNA was extracted, cleared of rRNA, converted to cDNA and prepared for Illumina sequencing as described above. The cDNA was sequenced on an Illumina MiSeq Platform with 1 x 50 bp reads, and the reads were trimmed by CLC Genomics Workbench and mapped to rRNA, the mitochondrial genome, and the human genome with RefSeq masking using CLC (% reads indicated). 16,463 genes were identified with an RPKM (reads per kilobase of exon per million of reads) of at least 0.1. The number of reads that map to introns or exons is a percentage of the total reads.

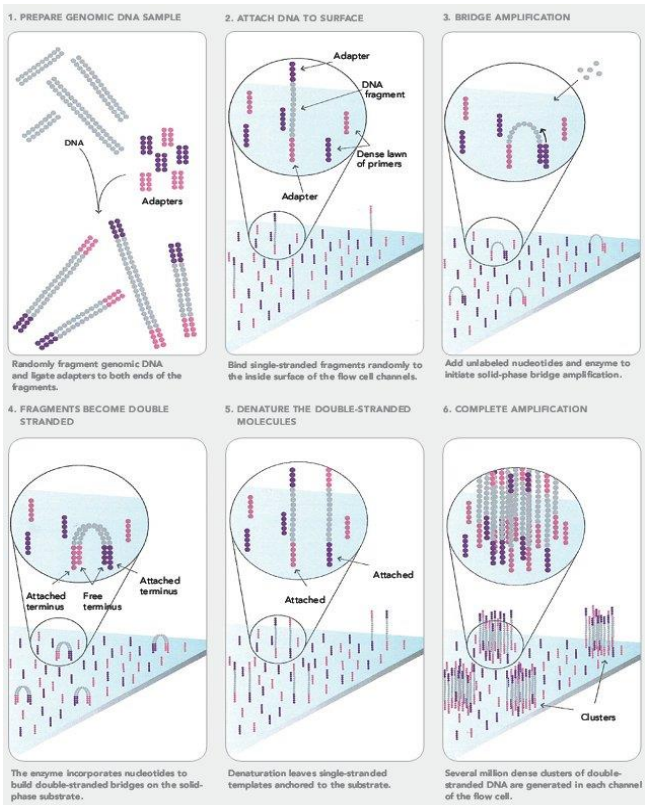
Summary

Random priming extends the applicability of transcriptome analysis to include samples which contain non-polyadenylated and/or compromised input RNA. However, in order to maximize RNA-Seq data quality and quantity, random primed RNA-Seq kits must be paired with rRNA removal methods. The RiboGone - Mammalian kit specifically removes 5S, 5.8S, 18S, and 28S rRNA sequences (as well as 12S mitochondrial rRNA sequences) from human, mouse, or rat total RNA. In this study, 16,463 genes were identified with an RPKM ≥ 0.1 , while rRNA and mtRNA reads were reduced to <1% and ~2% of the RNA-Seq library reads, respectively (Figure 4). These data indicate that SMARTer random-primed cDNA synthesis paired with RiboGone rRNA depletion yields high-value RNA-Seq data, even from challenging samples such as small quantities of FFPE tissue.

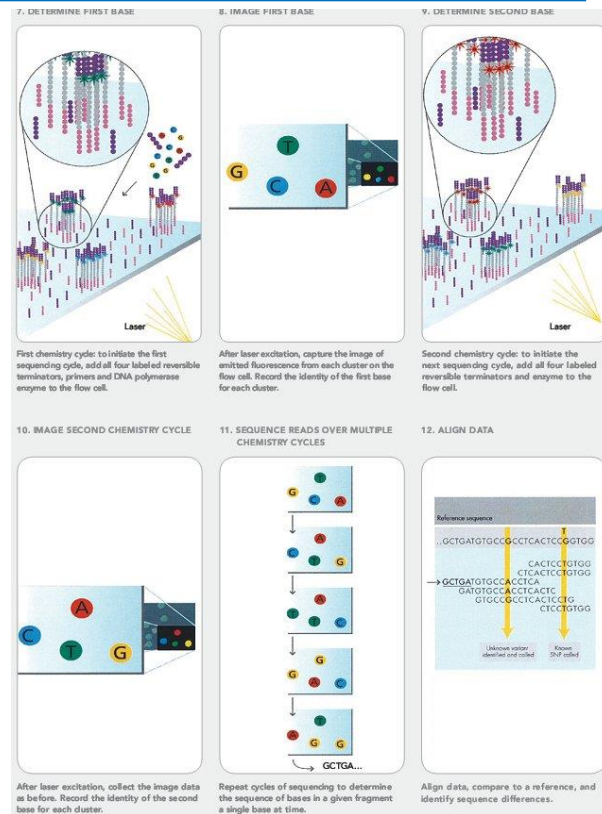
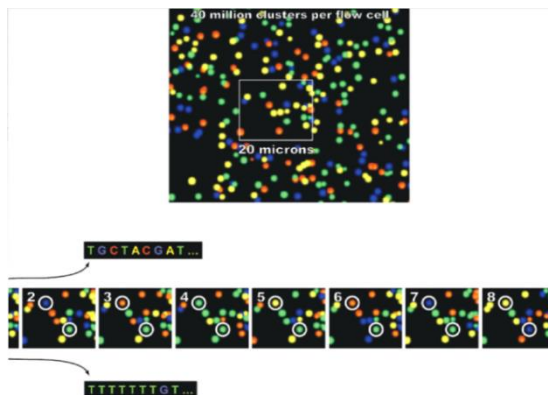
Sequencing



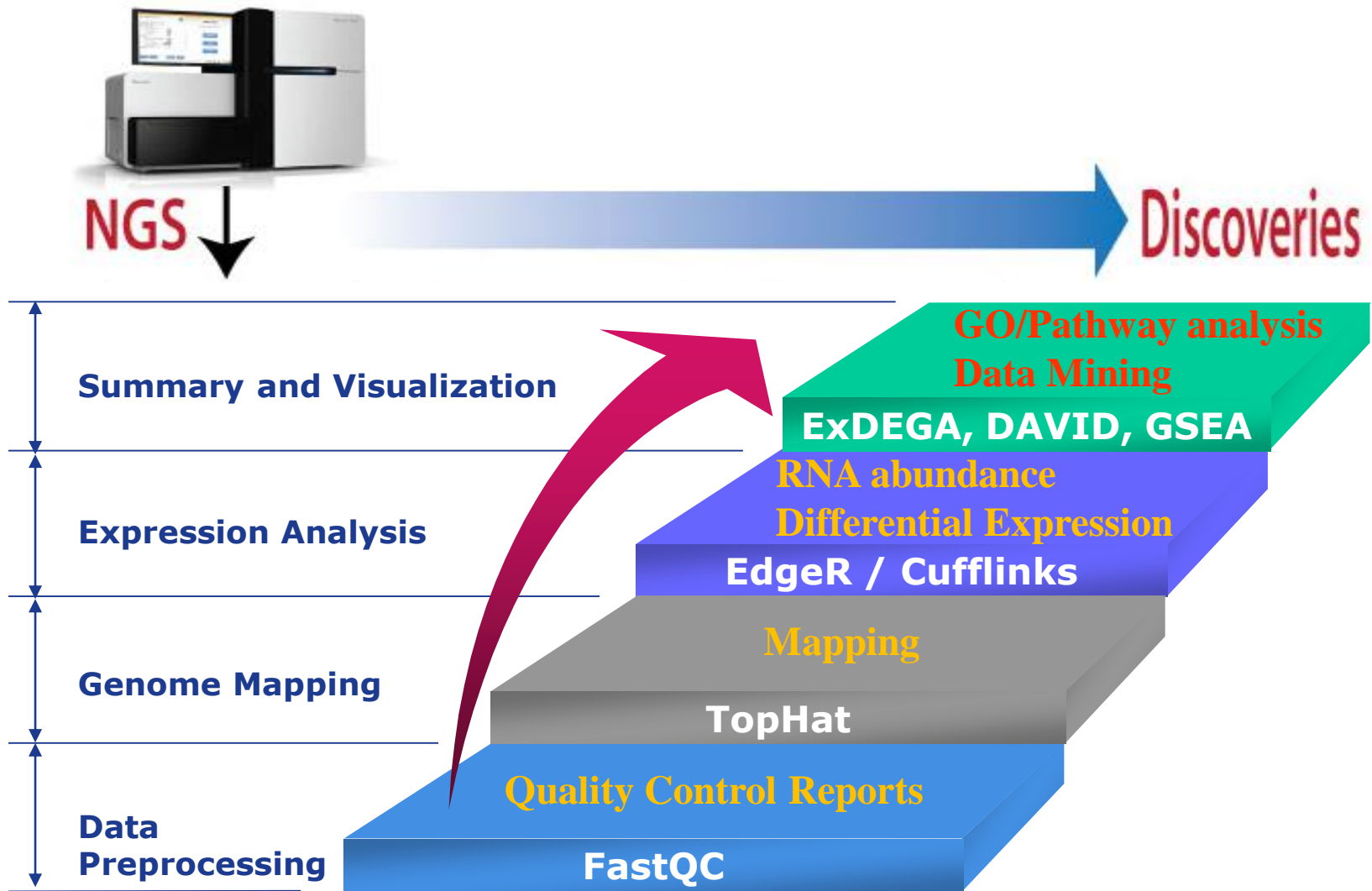
Run Format	Read Length	# of Reads	High-Quality Output (Gb)	
			/lane	/FlowCell
Single End	1 x 50bp	~150 million/lane	7.5 Gb	135-150 Gb
	1 x 100bp		15 Gb	270-300 Gb
Paired End	2 x 50bp	~300 million/lane	15 Gb	270-300 Gb
	2 x 100bp		30 Gb	540-600 Gb



Illumina HiSeq-2000/2500 Illumina NextSeq 500



Work Flow of Data Analysis



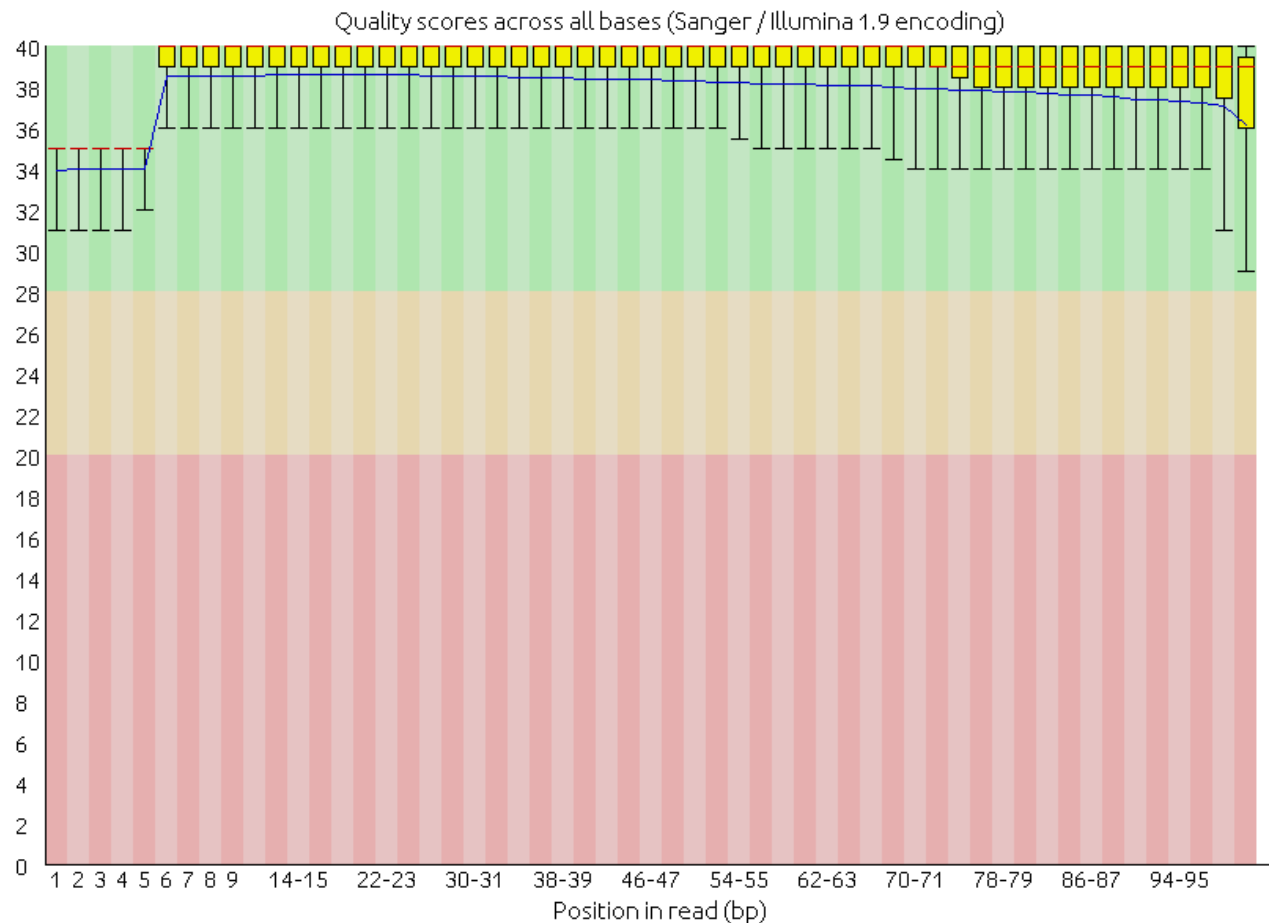
Other Data Analysis Tools for Data Processing, Mining, Visualization : MISO, Quick GO, ClueGO, CytoScape, DAVID, GSEA, UCSC Genome, IGV, IPA, Others

FastQ 파일 안에서 각 position의 base에 대한 quality 값의 영역을 보여 줌

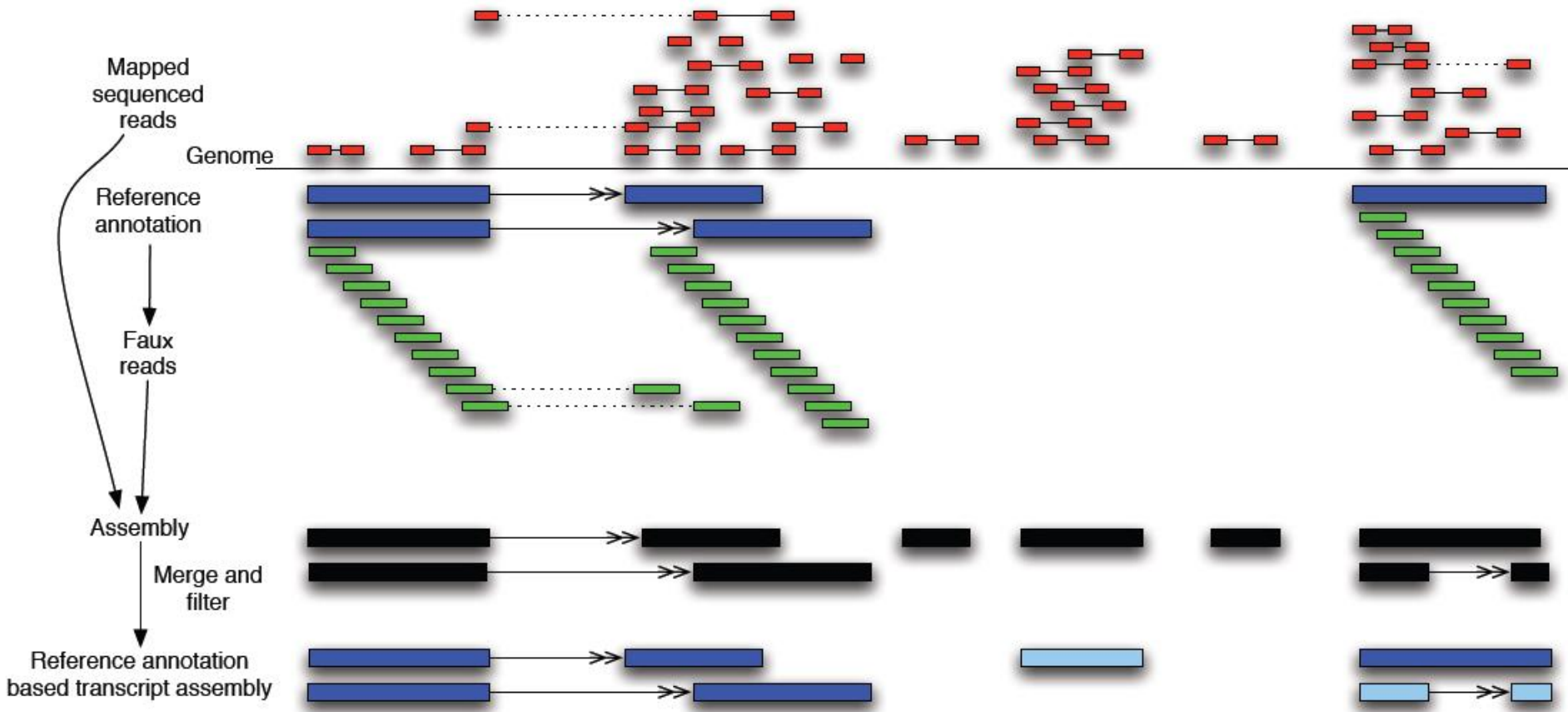
Summary

- ✔ [Basic Statistics](#)
- ✔ [Per base sequence quality](#)
- ✔ [Per tile sequence quality](#)
- ✔ [Per sequence quality scores](#)
- ✘ [Per base sequence content](#)
- ! [Per sequence GC content](#)
- ✔ [Per base N content](#)
- ✔ [Sequence Length Distribution](#)
- ✔ [Sequence Duplication Levels](#)
- ✔ [Overrepresented sequences](#)
- ✔ [Adapter Content](#)
- ✘ [Kmer Content](#)

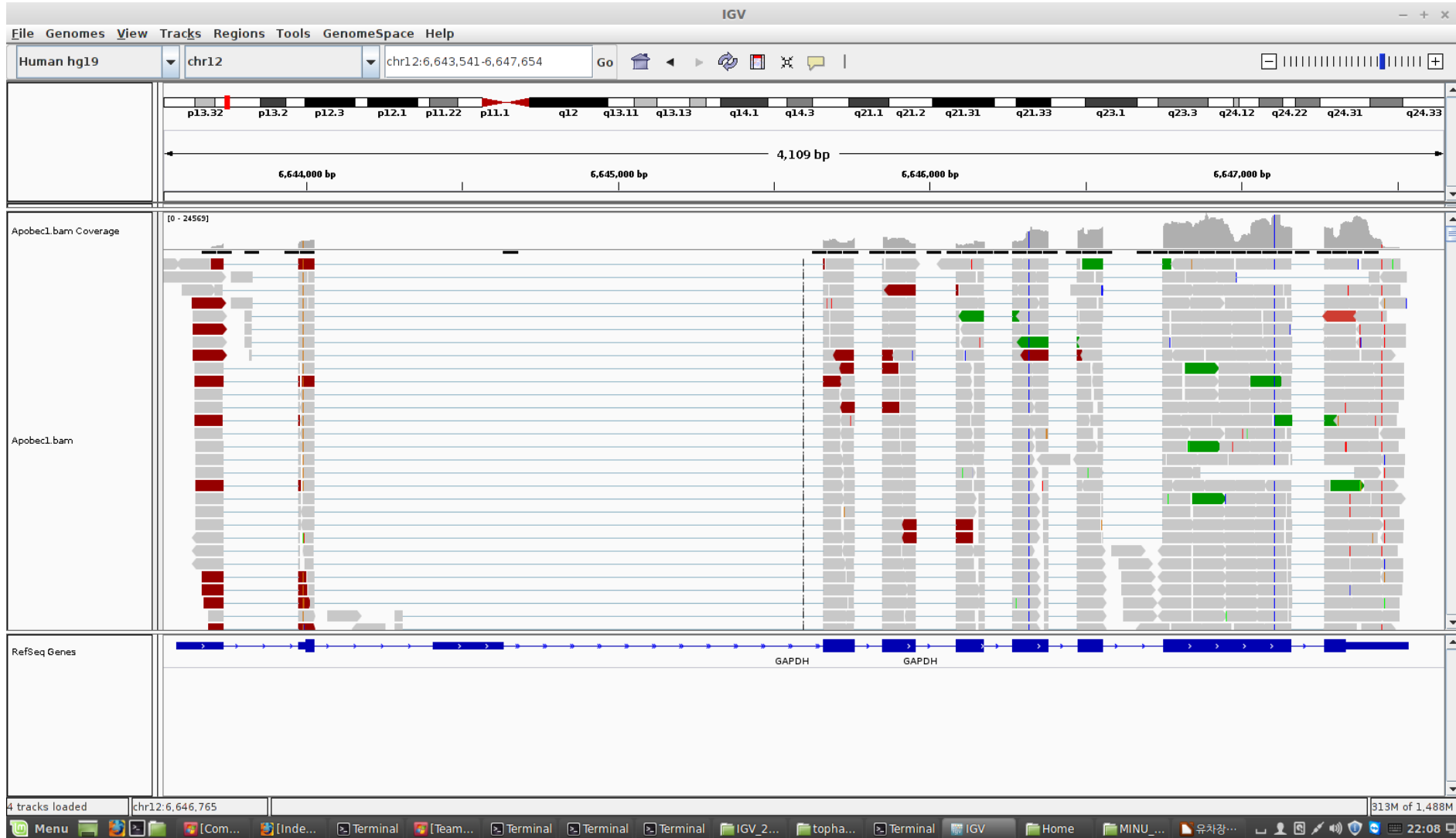
✔ Per base sequence quality



Data Analysis – TopHat, Cufflinks



Data Analysis – IGV



Data Analysis – ExDEGA



ExDEGA : Excel based Differentially Expressed Gene Analysis tool

View All Data

Gene Category

ANI OR

Aging

Angiogenesis

Apoptotic process

Cell cycle

Cell death

Cell differentiation

Cell migration

Cell proliferation

DNA repair

Gene Category Settings

Gene Symbol	AD_TG_LI / AD_LT_LI	AD_FMT_LI / AD_LT_LI	AD_FMT_LI / AD_TG_LI	AD_FMT_LI / AD_TG_LI	AD_TG_LI / AD_LT_LI	AD_FMT_LI / AD_LT_LI	AD_FMT_LI / AD_TG_LI	AD_FMT_LI / AD_TG_LI	AD_FMT_LI / AD_TG_LI	AD_LT_LI	AD_TG_LI	AD_FMT_LI	AD_FMT_LI	AD_LT_LI
22 Mybl1	0.561	0.401	0.715	0.857	0.053	0.004	0.115	0.670	7.279	6.445	5.961	6.224		
41 Slco5a1	0.752	0.419	0.557	0.779	0.230	0.005	0.049	0.711	4.923	4.513	3.669	4.151		
253 Pms1	0.669	0.497	0.742	0.871	0.017	0.009	0.218	0.891	6.274	5.694	5.264	5.495		
288 Aux3	0.571	0.203	0.356	0.678	0.090	0.000	0.101	0.936	4.389	3.581	2.091	3.021		
326 Icus	0.654	0.472	0.722	0.861	0.222	0.201	0.989	7.292	6.679	6.209	6.463			
489 Ccl20	0.612	0.191	0.313	0.656	0.655	0.035	0.045	0.392	5.343	4.635	2.957	4.027		
499 A530032D15Rik	1.175	0.408	0.348	0.674	0.974	0.001	0.021	0.166	7.769	8.002	6.477	7.432		
501 C130026I21Rik	1.033	0.256	0.248	0.624	0.958	0.005	0.010	0.168	10.417	10.465	8.452	9.784	1	
502 Sp110	1.000	0.378	0.378	0.689	0.854	0.037	0.017	0.172	12.297	12.297	10.893	11.759	1	
503 Sp140	0.914	0.259	0.284	0.642	0.886	0.016	0.023	0.292	11.258	11.128	9.310	10.488	1	
505 A630001G21Rik	1.266	0.471	0.372	0.686	0.478	0.016	0.008	0.057	7.612	7.952	6.527	7.408		
729 Trincm163	0.739	0.412	0.557	0.779	0.369	0.019	0.254	0.857	5.292	4.855	4.012	4.494		
742 Cxcr4	0.833	0.379	0.455	0.727	0.463	0.001	0.003	0.267	10.017	9.754	8.617	9.294		
752 Fcarnr	1.143	0.470	0.411	0.705	0.599	0.042	0.010	0.094	8.873	9.066	7.783	8.562		
754 Fcrrr	1.867	0.176		0.547	0.452	0.009	0.008	0.050	9.491	10.392	6.984	9.522		
890 Rgs13	0.638	0.396	0.620	0.810	0.253	0.044	0.320	1.000	6.491	5.843	5.153	5.539		
894 Brinp3	1.245	2.003	1.489	1.245	0.064	0.006	0.089	0.854	4.884	5.312	5.887	5.628		
1025 Sell	1.312	0.166	0.127	0.563	0.565	0.001	0.001	0.040	9.018	9.409	6.428	8.581		
1036 Xcl1	0.643	0.425	0.660	0.830	0.162	0.011	0.475	0.710	5.871	5.234	4.636	4.966		
1081 Sh2d1b1	0.841	0.418	0.497	0.748	0.369	0.016	0.081	0.488	5.672	5.422	4.412	5.004		
1089 Furla	1.216	0.270	0.222	0.611	0.884	0.001	0.007	0.112	10.526	10.808	8.636	10.097		
1163 BC094916	1.709	0.363	0.212	0.606	0.412	0.008	0.008	0.043	5.384	6.157	3.922	5.435		
1165 Pyhin1	1.150	0.350	0.302	0.651	0.445	0.029	0.003	0.050	7.123	7.336	5.609	6.717		
1186 Mpx1			0.787	0.893	0.049	0.036	0.939	0.198	10.700	7.242	6.896	7.079		
1195 Kmo	0.908	0.374	0.412	0.706	0.580	0.001	0.007	0.248	7.697	7.547	6.278	7.055		
1354 Cr2	1.329	0.167	0.126	0.563	0.693	0.013	0.013	0.100	8.763	9.173	6.183	8.344		
1442 Il2ra2	0.697	0.431	0.618	0.809	0.191	0.014	0.162	0.930	7.708	7.187	6.494	6.882		
1558 Hs3st5	1.230	2.410	1.959	1.480	0.809	0.015	0.065	0.349	4.720	5.028	5.999	5.594		
1672 Eclar	0.578	0.425	0.736	0.868	0.066	0.003	0.617	0.440	4.949	4.159	3.716	3.955		

DEG Analysis

Significant Gene Selection

Fold change: 2

Average of Normalized RC (log2): 4

p-value: 0.05

Sample Comparison / Filter

ADTG_LI / AD_LT_LI

ADFMT_LI / AD_LT_LI

ADFMT_LI / AD_TG_LI

ADLT_LI + AD_FMT_LI / AD_TG_LI

Gene Category Graph

총 24421개 중 200개의 레코드가 있습니다.

- ❖ Add Another GO 기능을 통해 사용자가 원하는 GO를 자유롭게 구성할수 있습니다.
- ❖ Significant gene을 매우 빠르고 쉽게 데이터를 취할수 있고 그래프로 표현할수 있습니다.

Data Analysis – ExDEGA



파일 홈 삽입 페이지 레이아웃 수식 네이터 검토 보기 ExDEGA Acrobat 어떤 작업을 하시나요?

Calibri 11 가 가 텍스트 주 바꿈 숫사 표준 2 표준 나뉨 샵입 삭제 서지 사용 회계 새우기 지우기 정렬 및 찾기 및 필터 선택 편집

E7 1.05156170330382

	A	B	C	D	E	F	G	H	I	J	K	L	M
	Filter: 200	Fold change			p-value					Average of Normalized RC (log2)			
						AD LT LI+							
1195	Krno	0.908	0.374	0.412	0.706	0.580	0.001	0.007	0.248	7.607	7.557	6.278	7.055
1354	Cr2	1.329	0.167	0.136	0.563	0.693	0.013	0.013	0.100	8.763	9.173	6.183	8.344
1442	Il22ra2	0.697	0.431	0.618	0.809	0.191	0.014	0.162	0.930	7.708	7.187	6.494	6.882
1558	Hs3sl5	1.230	2.410	1.959	1.480	0.809	0.015	0.065	0.349	4.730	5.028	5.999	5.594
1672	Edar	0.578	0.425	0.736	0.868	0.065	0.003	0.617	0.440	4.949	4.159	3.716	3.955

Gene Ontology Graph

% of Total Significant

Bar graph showing the percentage of up and down significant genes for various BioFunction categories. The y-axis represents the percentage (0% to 4%), and the x-axis lists the BioFunction categories. The number of genes for each category is indicated above the bars.

BioFunction	% Up Significant	% Dn Significant	Count
Aging	~0.5%	~0.5%	2
Angiogenesis	~0.5%	~0.5%	1
Apoptotic process	~0.5%	~0.5%	3
Cell cycle	~0.5%	~0.5%	5
Cell death	~0.5%	~0.5%	5
Cell differentiation	~0.5%	~0.5%	4
Cell migration	~0.5%	~0.5%	12
Cell proliferation	~0.5%	~0.5%	6
DNA repair	~0.5%	~0.5%	2
Extracellular matrix	~0.5%	~0.5%	4
Immune response	~0.5%	~0.5%	30
Inflammatory response	~0.5%	~0.5%	14
Neurogenesis	~0.5%	~0.5%	8
RNA splicing	~0.5%	~0.5%	0
Secretion	~0.5%	~0.5%	2

DEG Analysis

Significant Gene Selection

Fold change: 2

Average of Normalized RC (log2): 4

p-value: 0.05

Sample Comparison / Filter

ADTG_LI / AD_LT_LI

ADFMT_LI / AD_LT_LI

ADFMT_LI / AD_TG_LI

ADLT_LI+ AD_FMT_LI/AD_TG_LI

Gene Category Graph

순번 24421개 중 200개의 레코드가 있습니다.

- ❖ Pie chart를 통해 Significant gene 대상으로 BioFunction 분포를 확인하고 영역을 클릭하면 해당 up/down 유전자가 필터링됨.
- ❖ Bar graph를 통해 BioFunction 별로 up/down의 분포를 확인하고 bar를 클릭하면 해당 유전자를 확인할 수 있음.

Data Analysis – ExDEGA



파일 홈 삽입 페이지 레이아웃 수식 데이터 검토 보기 ExDEGA Acrobat 어떤 작업을 원하시나요?

Calibri 11 가 가 텍스트 주 바꿈

숫사 표준 2 표준 나뉨

사용 집계 새우기

Venn Diagram Analysis

A - AD_TG_LI / AD_LT_LI
B - AD_FMT_LI / AD_LT_LI
C - AD_FMT_LI / AD_TG_LI

0 up-regulated
1 contra regulated
2 down-regulated

Venn Diagram tool

Sample Comparison

ADTG_LI / AD_LT_LI
 ADFMT_LI / AD_LT_LI
 ADFMT_LI / AD_TG_LI
 ADLT_LI + AD_FMT_LI

Fold change: 1.5
Average of Normalized RC (log2): 4
p-value: 0.05

Diagram View

All Save Image

Volcano Plot

순비 24421개 중 16개의 레코드가 있습니다.

Gene Symbol	AD_TG_LI / AD_LT_LI	AD_FMT_LI / AD_LT_LI	AD_FMT_LI / AD_TG_LI	AD_LT_LI + AD_FMT_LI / AD_TG_LI
2761 Gabrg2	1.693	2.506	1.480	1.240
4366 Gm6682	1.838	1.518	0.826	0.913
4728 Arg2	1.620	1.772	1.094	1.047
6797 Pdlim2	1.511	1.581	1.046	1.023
8284 Ctdc58	1.581	1.531	0.968	0.984
9538 Ai661453	1.501	1.516	1.010	1.005
11529 Adamts12	1.710	2.147	1.256	1.128
11637 Lcn2	1.507	1.832	1.216	1.108
13673 Fltc1	1.583	1.807	1.141	1.071
15046 Abcb4	1.573	1.535	0.976	0.988
18860 Hif3a	1.585	1.618	1.021	1.010
19258 Lrn3	1.560	1.606	1.030	1.015
20336 Trnc7	1.767	2.518	1.425	1.213
20734 Mti483	1.625	1.838	1.131	1.065
21806 Osgin1	1.547	1.585	1.024	1.012
24366 Mid1	2.092	1.641	0.784	0.892
24424				
24425				
24426				
24427				
24428				
24429				
24430				
24431				
24432				
24433				
24434				
24435				
24436				

Data Analysis – ExDEGA



Microsoft Word ribbon: 파일, 홈, 삽입, 레이아웃, 수식, 네이터, 검토, 보기, ExDEGA, Acrobat, 이면 작업을 원하시나요?, 공용

Font: Calibri, Size: 11, Bold, Italic, Underline, Paragraph: 들여쓰기, 줄바꿈, 글꼴, 맞춤, 표시 형식, 스타일: 표준 2, 표준, 나뭇잎, 보통, 좋음, 경고문

Worksheet: A11637, Lcn2

Gene Symbol	AD_TG_LI / AD_LT_LI	AD_FMT_LI / AD_LT_LI	AD_FMT_LI / AD_TG_LI	AD_LT_LI+ / AD_FMT_LI / AD_TG_LI	p-value	Average of Normalized RC (log2)
Lcn2	~10.5	~10.5	~10.5	~10.5	~0.8	~0.8
Fhd1	~10.5	~10.5	~10.5	~10.5	~0.8	~0.8
Abcb4	~10.5	~10.5	~10.5	~10.5	~0.8	~0.8
Hif3a	~10.5	~10.5	~10.5	~10.5	~0.8	~0.8
Lfn3	~10.5	~10.5	~10.5	~10.5	~0.8	~0.8
Tmc7	~10.5	~10.5	~10.5	~10.5	~0.8	~0.8
Mir483	~4.2	~4.8	~4.8	~4.8	~0.8	~0.8
Osgin1	~10.5	~10.5	~10.5	~10.5	~0.8	~0.8

Gene Graph Tool: Average of Normalized RC (log2) vs. AD conditions. Legend: Lcn2, Fhd1, Abcb4, Hif3a, Lfn3, Tmc7, Mir483, Osgin1.

Analysis Graph: Fold Change (log2) vs. AD conditions. Legend: Lcn2, Fhd1, Abcb4, Hif3a, Lfn3, Tmc7, Mir483, Osgin1.

DEG Analysis Panel: Gene Category Graph, Analysis Graph (Venn Diagram, Volcano Plot), Selected Gene Graph (Gene Symbol: Abcb4, Hif3a, Lfn3, Tmc7, Mir483, Osgin1), Graph View, Gene Search.

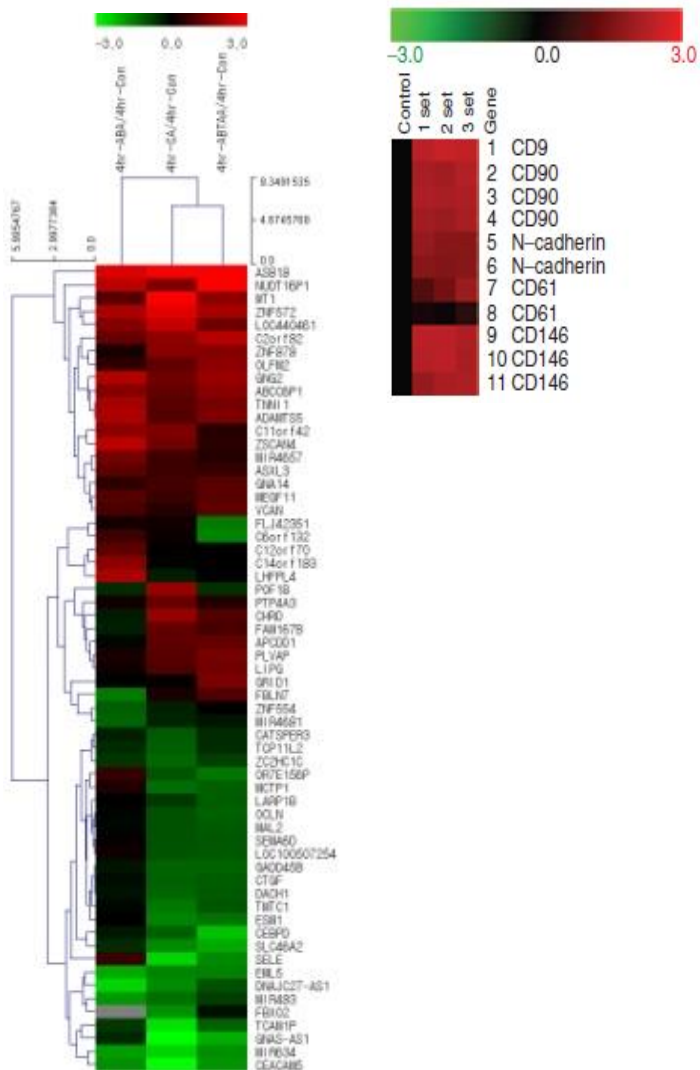
대상을 선택한 다음 <Enter> 키를 누르거나 [붙여넣기]를 선택합니다.

개수: 8 83%

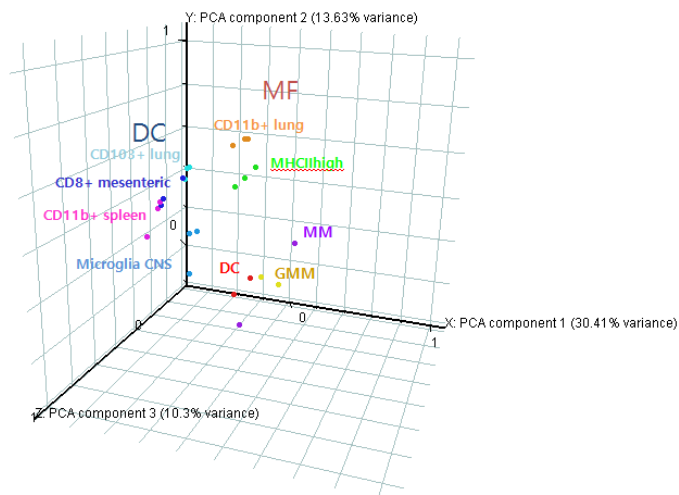
Data Analysis – Clustering



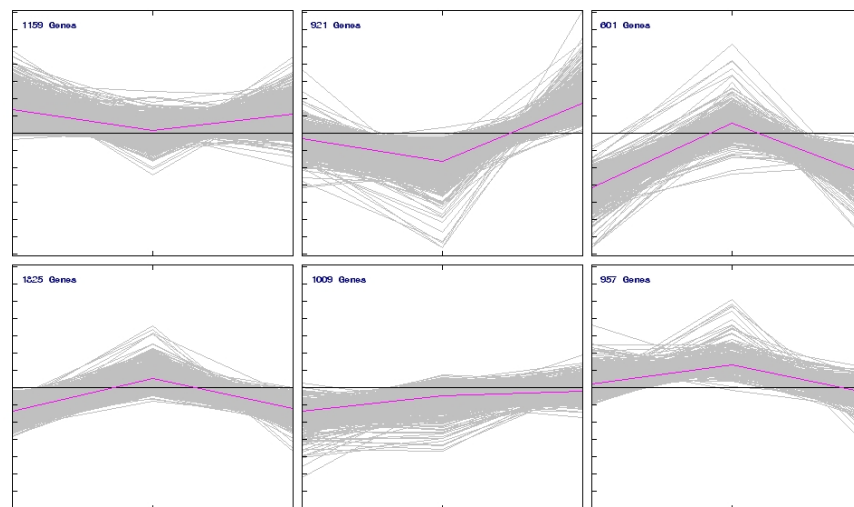
Hierarchical Clustering (HCL)



Principal Component Analysis (PCA)



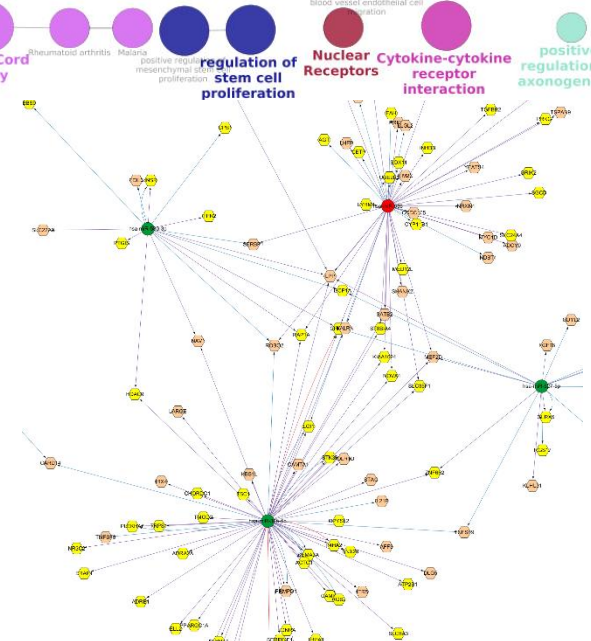
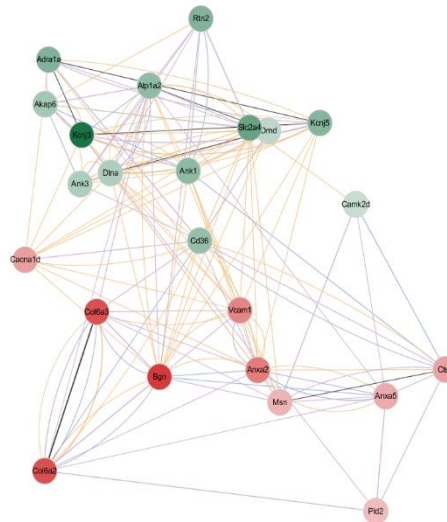
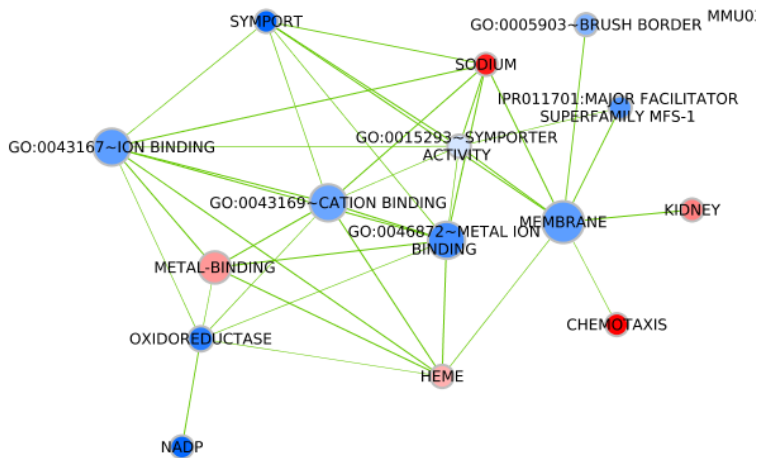
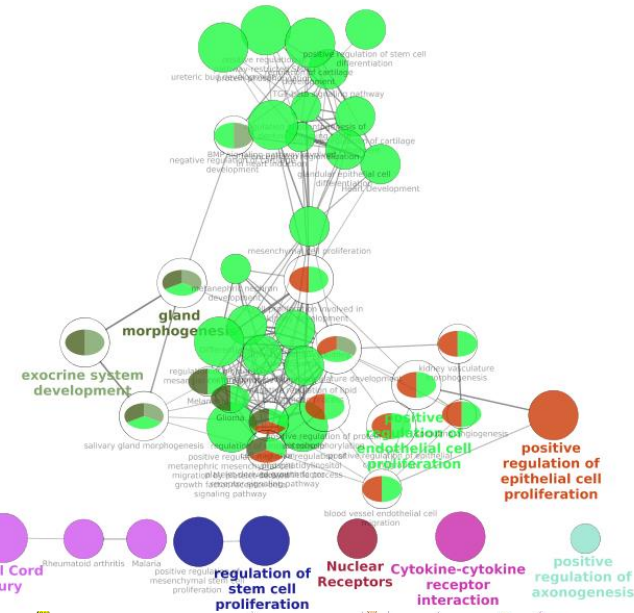
K-means clustering (KMC)



Data Analysis – Networks



- ❖ Gene Network Generation : **String**
- ❖ GO & Pathway Analysis with **ClueGO**
- ❖ Gene Set Enrichment Analysis with **DAVID**
- ❖ Gene Set Enrichment Analysis with **GeneMania**
- ❖ Transcription Factor Analysis with **iRegulon**
- ❖ miRNA Target Analysis : **CyTargetLinker**



Data Analysis – Exon skipping



Nat Methods. 2010 Dec;7(12):1009-15. doi: 10.1038/nmeth.1528. Epub 2010 Nov 7.

Analysis and design of RNA sequencing experiments for identifying isoform regulation.

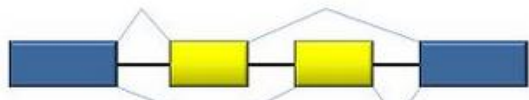
Katz Y¹, Wang ET, Airoidi EM, Burge CB.

⊕ Author information

Splicing Patterns



Exon skipping



Mutually exclusive exons



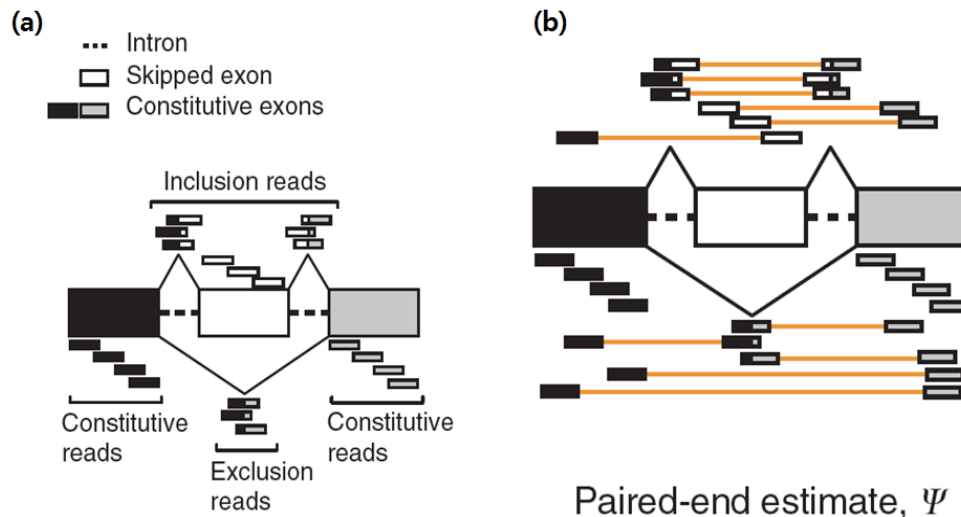
Alternative 5' donor sites



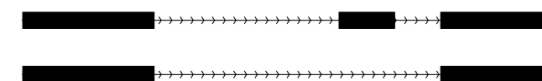
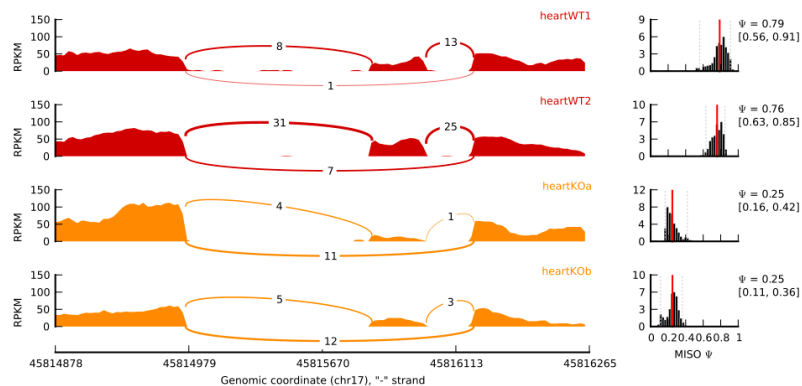
Alternative 3' acceptor sites



Intron retention



chr17:45816186:45816265:-@chr17:45815912:45815950:-@chr17:45814875:45814965:-



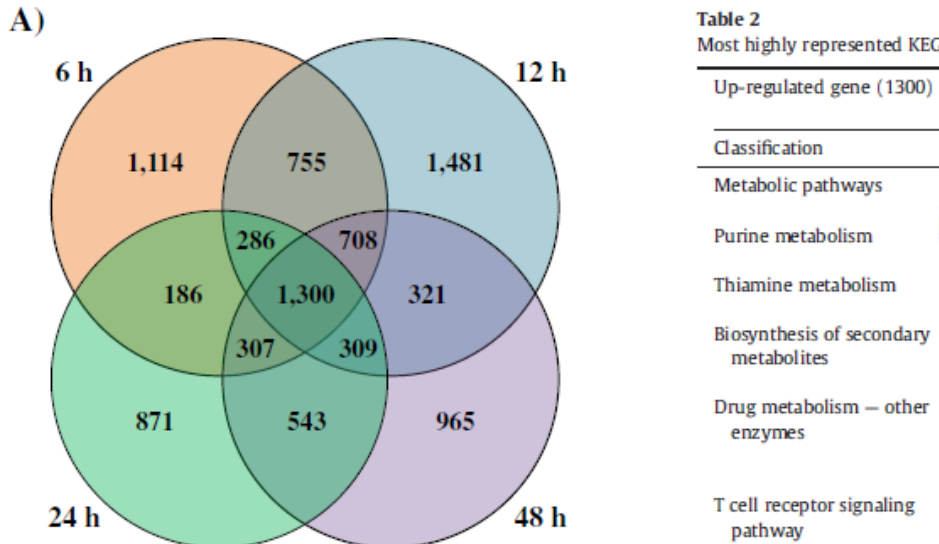
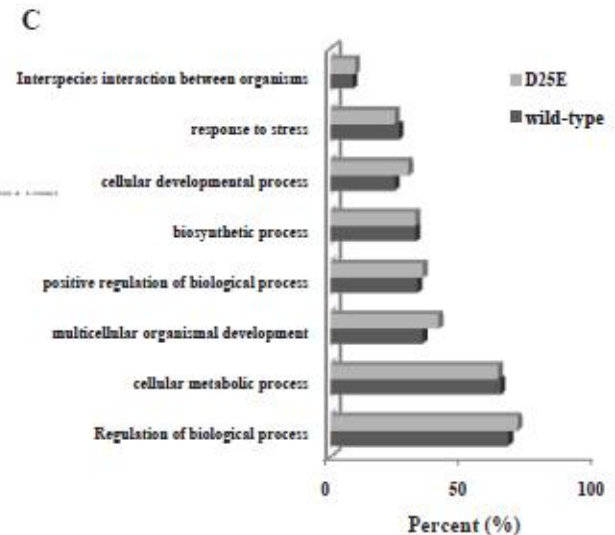
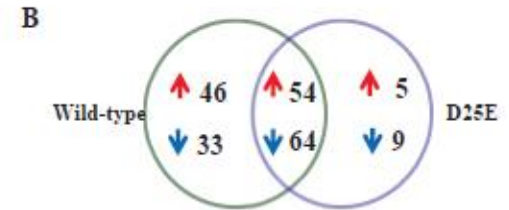
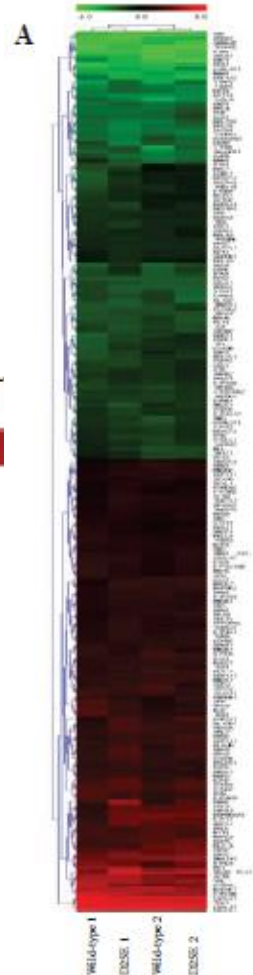
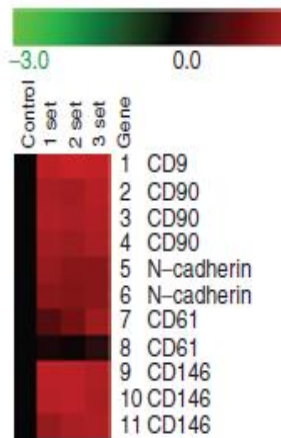
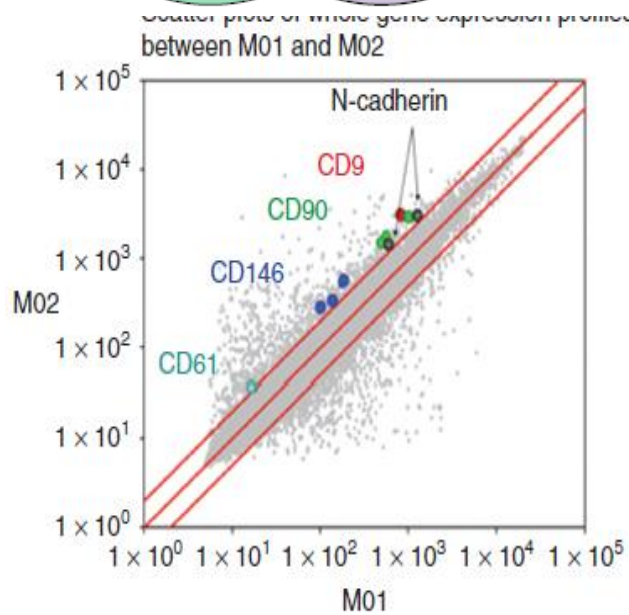


Table 2
Most highly represented KEGG classifications in up- and down-regulated transcripts.

Classification	#	%	Classification	#	%	t2.1
						t2.2
Up-regulated gene (1300)			Down-regulated genes (588)			t2.3
Metabolic pathways						t2.4
Purine metabolism						
Thiamine metabolism						
Biosynthesis of secondary metabolites						
Drug metabolism – other enzymes						
T cell receptor signaling pathway						



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Gene Expression Omnibus: a public functional genomics data repository supporting MIAME submissions. Array- and sequence-based data are accepted. Tools are provided to help download experiments and curated gene expression profiles. [More information »](#)

GEO navigation

A	B
1	SERIES
2	title Murine ES Cells: Control vs. Triple-Fusion Transfected
3	summary Transcriptional profiling of mouse embryonic stem cells comp
4	overall design Two-condition experiment, ES vs. TF-ES cells. Biological repl
5	contributor Jane,Doe
6	contributor John,A,Smith
7	
8	SAMPLES
9	# The corresponding example matrix table is included in the next worksheet.
10	Sample name title
11	ES-rep1 Control Embyronic Stem Cell Replicate 1
12	ES-rep2 Control Embyronic Stem Cell Replicate 2
13	ES-rep3 Control Embyronic Stem Cell Replicate 3
14	ES-rep4 Control Embyronic Stem Cell Replicate 4
15	TF-ES-rep1 Triple-Fusion Transfected Embryonic Stem Cells Replicate 1
16	TF-ES-rep2 Triple-Fusion Transfected Embryonic Stem Cells Replicate 2
17	TF-ES-rep3 Triple-Fusion Transfected Embryonic Stem Cells Replicate 3
18	

Jang et al. *Virology Journal* 2011, 8:453
<http://www.virologyj.com/content/8/1/453>



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Gene Expression Profiles are Altered in Human Papillomavirus-16 E6 D25E-Expressing Cell Lines

Mi Jang[†], Jee Eun Rhee[†], Dai-Ho Jang and Sung Soon Kim^{*}

N-cadherin Determines Individual Variations in the Therapeutic Efficacy of Human Umbilical Cord Blood-derived Mesenchymal Stem Cells in a Rat Model of Myocardial Infarction

Eun Ju Lee¹, Eue-Keun Choi^{1,2}, Soo Kyoung Kang¹, Gi-Hwan Kim¹, Ju Young Park¹, Hyun-Jae Kang^{1,2}, Sae-Won Lee¹, Keum-Hyun Kim¹, Jin Sook Kwon³, Ki Hong Lee⁴, Youngkeun Ahn⁴, Ho-Jae Lee¹, Hyun-Jai Cho^{1,2}, Soo Jin Choi⁵, Won Il Oh⁵, Young-Bae Park^{1,2} and Hyo-Soo Kim^{1,2,6}

Hepatology Research

Hepatology Research 2011; 41: 170-183 doi: 10.1111/j.1872-034X.2010.007

Original Article

Expression profiles of miRNAs in human embryonic stem cells during hepatocyte differentiation

Nury Kim,¹ Hyemin Kim,¹ Inkyung Jung,² Yeji Kim,¹ Dongsup Kim² and Yong-Mahn Han¹

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