2012

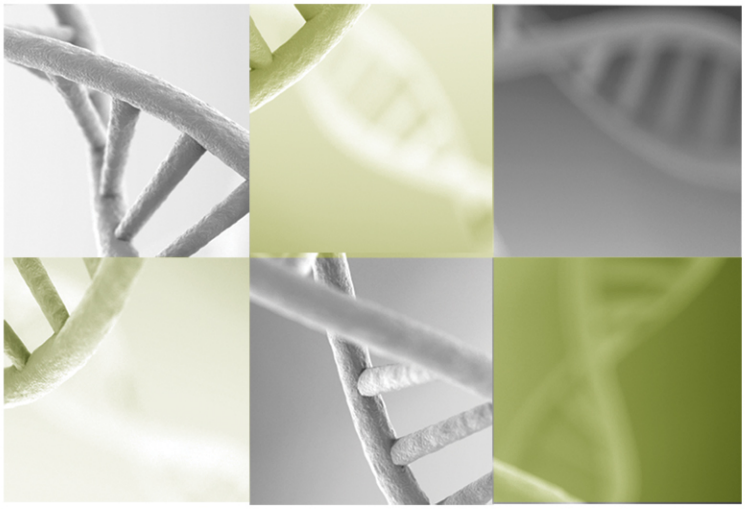
SolGent Service

Sequencing service
Next Generation Sequencing service
Microarray service
Genotyping service

SolGent Co., Ltd.
Solutions for Genetic Technologies

SolGent Service

SolGent. located in South Korea, is founded in 2000 and SolGent is growing stable for a over 10-year based on our strong relationship with our valued customers and SolGent's passion for quality. SolGent Services are accuracy, fast turnaround, and cost effective.The biggest merit of our services is that our excellent technology support team provides FREE consulting from when you select appropriate instrument to troubleshooting for all analysis. You can experience outstanding performance with SolGent™ Services. Apply SolGent service for your novel project!



Sequencing service

- *Guaranteed accuracy : 99%*
- *Fast turnaround : within 48hrs*
- *Long read through length : 700~750bp*
- *Free consulting : troubleshooting and data analysis by experts bioinformatics*
- *Free universal primer*

1. Description

SolGent™ Sequencing service includes general sequencing, primer walking and microorganism identification(16s/18s). SolGent provides accuracy and rapid service utilizing concentrated know how for over a decade. And customer can get the results within 48hrs. SolGent boast minimum background and clear peak using innovative technology such as RCA solution or high-GC solution. SolGent™primer walking service is the method for medium-large scale of DNA sequencing up to 10Kb. Customer can get sequencing data within a week (in case of 3kb of sequencing) with free consulting and analysis service using bioinformatics. 16s/18s rRNA full sequencing is a service to classify and identify microbe species by comparing the homology with GeneBank database after analyzing the ribosomal RNAgene sequencing of microbes not only with prokaryotic cells including bacteria but also with eukaryotic cells including fungus.

2. Application

- General sequencing service
- Primer walking
- Microorganism identification (16s / 18s)

3. Feature

Platform	Read length	Capillary Seperation Distance
ABI3730XL	700~750bp	50cm

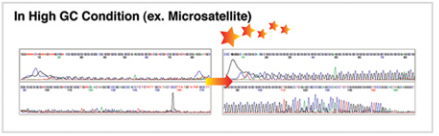
4. Work flow

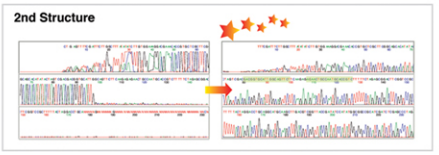
Sample submit → Quality confirmation → Analysis → Results

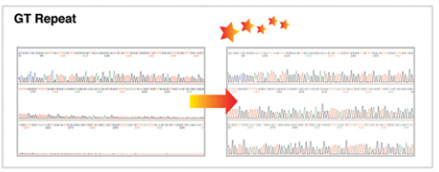
Sequencing service

5. Technology

SolGent offers high quality sequencing with experienced know how.







6. Sample preparation

- We accept sample in the form of gDNA, PCR fragments and plasmid the DNA.
- Required template concentration

Template	Quantity	
Product	100 ~ 200bp	
	200 ~ 500bp	3ng ~ 10 ng
	500 ~ 1000bp	5ng ~ 20 ng
	1000 ~ 2000bp	10ng ~ 40 ng
	> 2000bp	20ng ~ 50 ng
	Single - stranded	25ng ~ 50 ng
	Double - stranded	150ng ~ 300 ng
	Cosmid, BAC	0.5ng ~ 1.0 ug
	Bacterial genomic DNA	2ug ~ 3 ug

- Sample storage duration : 1 month

7. Results

You can get the results By Advanced System for Sequence Analysis (within 48hrs)

* ASSA Service : Easy result connection
  Vector screening
  Blast search
  Data Storage : for a 6 month

Sequencing service

8. SolGent Universal sequencing primer list

Vector Name	Primer Name
GFP/GFP(Cycle-3-mutant)	GFP-CF, GFP-NR
p426-GAL	GAL1-ProF
pACT	T7, EBV-R
pBacPAK8,9	BaculoVF, BaculoVR
pBacPAK-HIS1	BaculoVF, BaculoVR
pBAD-Myc-His	pBAD-3', pBAD-5'
pBAD-Thio	pBAD-3', pBAD-5'
pBAD-TOPO	pBAD-3', pBAD-5'
pBIND	T7, GAL4-BD-F, EBV-R
pBIND	T7, GAL4-BD-F, EBV-R
pBlueBac4.5	BaculoVF, BaculoVR
pBluescript	T3, T7, M13F(-20), M13R(-20), M13R(-48)
pBlue-TOPO	T7
pBrige	GAL4-BDF, pGAL4_BD_3
pCAT-Basic	M13F(-20)
pCDNA1	T7, SP6
pCDNA2.1	M13F(-20), T7, M13R(-20)
pCDNA3	T7, SP6, CmV-ProF, BGH-R
pCDNA3.1	T7, CMV-ProF, BGH-R
pCDNA4/HisMax-TOPO	T7, XpressF
pCDNA4-Myc-His	CMV-ProF, T7, c-myc-R
pCDNA6-Myc-His	CMV-ProF, T7, c-myc-R
pCEP4	CMV-ProF, EBV-R
pCI	T7, EBV-R
pCMV6	CMV-ProF
pCMV6-XL4	CMV-ProF, T7, pCMV6-3'
pCMV-HA	CMV-ProF
pCMVmyc-nuc	CMV-ProF, c-myc-R
pCR2.1-TOPO	M13F(-20), M13R(-20), M13F(-47), M13R(-48), T7
pCR3.1	T7
pCR4Blunt-TOPO	M13F(-20), M13R(-20), M13F(-47), M13R(-48), T7
pCR4-TOPO	M13F(-20), M13R(-20), M13F(-47), M13R(-48), T7, T3
pCR II-TOPO	T7, SP6, M13F(-20), M13F(-47), M13R(-48)
pCRT7/CT-TOPO	T7
pCRT7/NT-TOPO	T7, T7ter, XpressF
pEBFP-C1	SV40-pAR, EGFP-CF
pEGFP	SV40-pAR, EGFP-CF
pEGFP-C1,C2,F	SV40-pAR, EGFP-CF
pEGFP-N1,N3	EGFP-NR, CMV-Pro-F
pENTR/D-TOPO	M13F(-20), M13R(-20), T7
pENTR1A	pENTR-5', SeqL-A, SeqL-B
pENTR4	pENTR-5', SeqL-A, SeqL-B

Vector Name	Primer Name
pGEM-T easy	T7, SP6, M13F(-47), M13(-48)
pGEX	pGEX-5', pGEX-3'
pGilda	LexAF, pGAL4_BD_3
pGL2-Basic	GLprimer1, GLprimer2
pGL2-Control	GLprimer1, GLprimer2
pGL2-Enhancer	GLprimer1, GLprimer2
pGL2-Promoter	GLprimer1, GLprimer2
pGL3-Basic(MCS I)	RVprimer3, GLprimer2
pGL3-Basic(MCS II)	RVprimer4, GLprimer2
pGL3-Control(MCS I)	RVprimer3, GLprimer2
pGL3-Control(MCS II)	RVprimer4, GLprimer2
pGL3-Enhancer(MCS I)	RVprimer3, GLprimer2
pGL3-Enhancer(MCS II)	RVprimer4, GLprimer2
pGL3-Promoter(MCS I)	RVprimer3, GLprimer2
pGL3-Promoter(MCS II)	RVprimer4, GLprimer2
pGL4.10	RVprimer3
pGL4.70	RVprimer3
pGL4.71	RVprimer3
pLexA	LexAF, pGAL4_BD_3
pMAL-c	malEF, M13F(-47)
pMAL-d	malEF, M13F(-47)
pMAL-e	malEF, M13F(-47)
pProEX-Hta	pTrcHIS-3', pBAD-3', M13R(-48)
pQE	pQE-F, pQE-R
pSE420	pTrcHIS-3', pTrcHIS-5'
pTrcHIS	pTrcHIS-3', pTrcHIS-5', XpressF
pTrcHIS-TOPO	pTrcHIS-3', pTrcHIS-5'
pTrcHIS-TOPO/lacZ	pTrcHIS-3', pTrcHIS-5'
pUC18/19	M13F(-20), M13F(-47), M13R(-20), M13R(-48)
T&A vector (RBC)	T7, M13F(-20), M13R(-20)
16s rRNA gene 동정 primer	27F, 1492R, 518R, 785F, 337F
18s rRNA gene 동정 primer	ITS1, ITS4
pENTR-D(TOPO)	M13R(-20), T7, M13F(-20), SeqL-A
pENTR-U6	M13R(-20), M13F(-20)
pET-32a(+)	T7, T7ter
pET-41EK-LIC	GST-C-F, T7ter
pEYFP-C1	SV40-pAR
pFlag-CMV	pFlag-CMV-30, pFlag-CMV-24
pGADt24	GAL4-ADF, pGAL4_AD_3
pGADT7	GAL4-ADF, pGAL4_AD_3
pGBKT7	T7, GAL4-BD-F, pGAL4_BD_3
pGBT9	GAL4-BDF, qGAL4_BD_3

Primer Name	Primer Sequence (5'-3')
T7	TAA TAC GAC TCA CTA TAG GG
SP6	ATT TAG GTG ACA CTA TAG
M13F(-20)	GTA AAA CGA CGG CCA GT
M13F(-47)	CGC CAG GGT TTT CCC AGT CAC GA
M13R(-20)	GGA AAC AGC TAT GAC CAT G
M13R(-48)	AGC GGA TAA CAA TTT CAC ACA GGA
T3	AAT TAA CCC TCA CTA AAG GG
BGH-R	TAG AAG GCA CAG TCG AGG
SeqL-A	GCA GTT CCC TAC TCT CGC
SeqL-B	CAT CAG AGA TTT TGA GAC AC
pENTR-5'	CTA CAA ACT CTT CCT GTT AGT TAG
T7 ter	GCT AGT TAT TGC TCA GCG
pQE-F	CAA TTT CAC ACA GAA TTC ATT AAA G
pQE-R	GAG CGT TCT GAA CAA ATC CAG
pGEX-5'	GGG CTG GCA AGC CAC GTT TGG TG
pGEX-3'	CCG GGA GCT GCA TGT GTC AGA GG
pFlag-CMV-30	AAT GTC GTA ATA ACC CCG CCC CGT TGA CGC
pFlag-CMV-24	TAT TAG GAC AAG GCT GGT GGG CAC
pBAD-3'	ATC TGT ATC AGG CTG AAA ATC
pBAD-5'	CCA TAG GAT TTT TAT CCA TAA G
BaculoVF	TTT ACT GTT TTC GTA ACA GTT TTG
BaculoVR	AAC GCA CAG AAT CTA GCG C
c-myc-R	CTC TTC TGA GAT GAG TTT TTG
CMV-ProF	AAA TGG GCG GTA GGC GTG
malEF	GGT CGT CAG ACT GTC GAT GAA GCC
pTrcHis-3'	ATC TGT ATC AGG CTG AAA ATC
pTrcHis-5'	TTA AAG AGG TAT ATA TTA ATG TAT CG
EBVR	GTG GTT TGT CCA AAC TCA TC
GAL1-ProF	AAC ATT TTC GGT TTG TAT TAC TTC

Primer Name	Primer Sequence (5'-3')
GST-CF	GCA TGG CCT TTG CAG GG
pCMV6-3'	CTG GGG AGG GGT CAC AGG G
XpressF	AGC ATG ACT GGT GGA CAG
RVprimer3	CTA GCA AAA TAG GCT GTC CC
Rvprimer4	GAC GAT AGT CAT GCC CCG CG
SV40-pAR	GAA ATT TGT GAT GCT ATT GC
EGFP-CF	AGC ACC CAG TCC GCC CTG AGC
EGFP-CR	CGT CCA TGC CGA GAG TG
EGFP-NR	CGT CGC CGT CCA GCT C
GFP-CF	GGT CCT TCT TGA GTT TGT AAC
GFP-NR	CAT CAC CAT CTA ATT CAA CAA G
GLprimer1	TGT ATC TTA TGG TAC TGT AAC TG
GLprimer2	CTT TAT GTT TTT GGC GTC TTC CA
LexAF	CGT CAG CAG AGC TTC ACC ATT G
GAL4-ADF	TAC CAC TAC AAT GGA TGA TG
GAL4-BD-NR	TTT CTT TGG AGC ACT TGA GC
GAL4-BDF	TCA TCG GAA GAG AGT A
pGAL4_AD-3	GAA CTT GCG GGG TTT TTC
pGAL4_BD-3	AAT CAT AAG AAA TTC GCC C
CMV-ProR	TGC TTG GGC GGT CAG C
LacZa-NR	CCT CTT CGC TAT TAC GC
SV40-pAF	AAA TAA AGC AAT AGC ATC AC
27F	AGA GTT TGA TCC TGG CTC AG
1492R	GGT TAC CTT GTT ACG ACT T
ITS1	TCC GTA GGT GAA CCT GCG G
ITS4	TCC TCC GCT TAT TGA TAT GC

Memo

Next Generation Sequencing service

- *High throughput*
- *Possession Roche454 GS FLX Ti, Illumina GAIIx and Illumina HiSeq2000 platform*
- *Free consulting*
  : Recommend appropriate a platform in accordance with your research
- *Customized data analysis by well-trained bioinformatics team*
- *Fast Turnaround*

1. Description

The latest, many scientist use next generation sequencing technology to identify or utilize nature of whole genome. Next generation sequencing technology is required high technical skills and accuracy bioinformatics technical supports. SolGent, has experienced know how, provides high throughput and high quality output with state of the art instrument including Roche 454 GS FLX ti, Illumina GAIIx, Illumina HiSeq2000 and target capture system of NimbleGen and Agilent. And we offer FREE consulting not only troubleshooting but also when you select appropriate instrument for your research. And advanced bioinformatics services including basic analysis such as BLAST search are available in accordance with customer demands. Customer can apply various research utilizing SolGent™ Next Generation Sequencing service.

2. Application

1) Whole Genome Sequencing (Prokaryote)

- Draft sequencing
- De Novo Assembly (chromosone~11Mbp)
- Reference Mapping
- Chloroplast sequencing
- Gap filling
- Methylation

2) Genome Annotation

- ORF find
- COG category
- CDS information
- Structural RNA (tRNA/rRNA)
- GC contents / GC skew

3) cDNA Sequencing

- Transcriptome analysis
- COG, GO analysis

4) Microsatellite

- SSR (Simple Sequence Repeat) detection

5) Metagenome analysis

6) SNP Discovery

3. Platform

- GS FLX 454, Illumina GAIIx, Illumina HiSeq2000
- Roche NimbleGen SeqCap, Agilent SureSelect, Fluidigm Biomark, RainDance

4. Feature

▫ GSFLX Titanium

Run Format	Throughput	
	#Reads / Lane	#Bases / Lane
2 Lanes (1/2 plate)	450 ~ 650 K	180 ~ 280 M
4 Lanes (1/4 plate)	160 ~ 250 K	60 ~ 110 M
8 Lanes (1/8 plate)	80 ~ 120 K	30 ~ 50 M

▫ Illumina GAIIx

Run Format	Read Lengrh	Run time (Day)	High-Quality Output (Gb)		# of Reads
			/ Lane	/ Run (2FlowCell)	
Single Read	1 x 35 bp	2	1.0 Gb	8 ~ 9 Gb	27 ~31 million/Lane
	1 x 75 bp	4	2.1 Gb	17 ~ 19 Gb	
	1 x 100 bp	5	2.8 Gb	22 ~ 25 Gb	
	1 x 150 bp	7	4.5 Gb	36 ~ 40 Gb	
Paired End	2 x 35 bp	4	2.0 Gb	16 ~ 18 Gb	225 ~250 million/FC
	2 x 75 bp	8	4.2 Gb	34 ~ 38 Gb	
	2 x 100 bp	10	5.6 Gb	45 ~ 50 Gb	
	2 x 150 bp	14	9.0 Gb	80 ~ 90 Gb	

▫ Illumina HiSeq2000

Run Format	Read Lengrh	Run time (Day)	High-Quality Output (Gb)		# of Reads
			/ Lane	/ Run (2FlowCell)	
Single Read	1 x 50 bp	2	1.0 Gb	37 ~ 50 Gb	46 ~58 million/Lane
	1 x 100 bp	4	2.1 Gb	75 ~ 100 Gb	
Paired End	2 x 50 bp	4	2.0 Gb	75 ~ 100 Gb	375 ~470 million/FC
	2 x 100 bp	8	4.2 Gb	150 ~ 200 Gb	

Next Generation Sequencing service

5. Available service

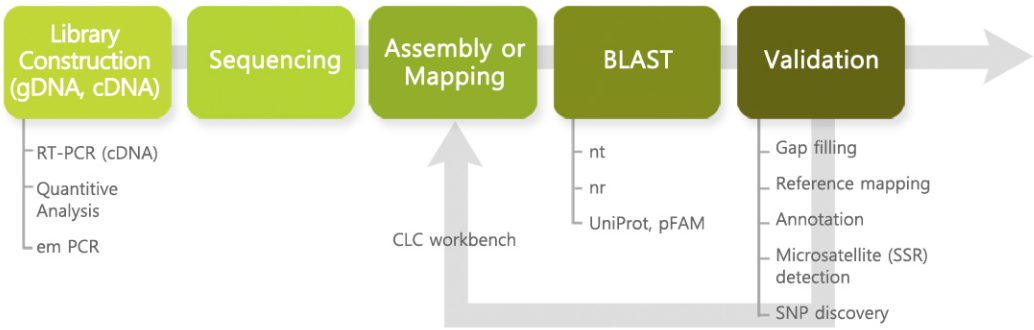
▫ Sequencing

Library type	HiSeq 2000	GAIIx	GSFLX
DNA single read (shotgun)	●	●	●
DNA paired end	Insert size 100 ~ 600 bp	Insert size 100 ~ 600 bp	—
DNA Mate pair	1 ~ 5 kb	1 ~ 5 kb	3, 8, 20 kb
Multiplexing	~ 12 plex	~ 12 plex	~ 20 plex
Amplicon	—	—	Fusion primer is available
mRNA Seq	●	●	●
Small RNA Seq	●	●	—
ChIP Seq	●	●	—
Sequence capture	●	●	●

▫ Sequencing capture

Method	Platform	Product	Capture size
Hybridzation	Agilent SureSelect	Human All Exons	38 Mb or 50 Mb Exons
		Custom	250 Kb ~ 3 Mb
	NimbleGen SeqCap	Exome	35 Mb
		385 K / 2.1 M	~ 10 Mb
Multiplex PCR	Fludigim BioMark	Access Array	10 kb ~ 2Mb
	Rain Dance	Cancer panel	2 Mb, Cancer related genes
		Custom	~ 2 Mb

6. Workflow



Next General Sequencing service

7. Sample preparation

- We accept in the form of gDNA, cDNA, amplicon, Chloroplast and Mitochondria DNA for NGS service.
- Required sample concentration

For GAIIx, HiSeq2000	Material	Amount	Conc(ng/ul)	A260/280	A260/23	DNA size
DNA seq (Single or Paired)	gDNA	5.5 ug	100 ng / ul	1.8 ~ 2.0	> 1.5	intact DNA
Mate Pair (1 ~ 5 kb)	gDNA	20 ug	100 ng / ul	1.8 ~ 2.0	> 1.5	intact DNA
Transcriptome	Total RNA	10.5 ug	200 ng / ul	—	—	RIN > 8
Transcriptome	mRNA	1 ug	200 ng / ul	—	—	—
ChIP Seq	ChIPed DNA	50 ug	1 ng / ul	—	—	—
Small RNA	Total RNA	10.5 ug	1 ug / ul	—	—	RIN > 8
Target resequencing (Agilent SureSelect)	gDNA	3.5 ug	30 ng / ul	1.8 ~ 2.0	> 1.5	non-degraded
Target resequencing (NimbleGen SeqCap)	gDNA	5.5 ug	50 ng / ul	≥ 1.8	> 1.5	> 1.5 kb

For GSFLX	Material	Amount	Conc(ng/ul)	A260/280	A260/23	DNA size
Shotgun sequencing	gDNA	5.5 ug	50 ng / ul	≥ 1.8	> 1.5	> 1.5 kb
3K Paired end	gDNA	5.5 ug	25 ng / ul	≥ 1.8	> 1.5	> 15 kb : non degraded
8K Paired end	gDNA	15.5 ug	200 ng / ul	≥ 1.8	> 1.5	> 24 kb : non degraded
20K Paired end	gDNA	30.5 ug	200 ng / ul	≥ 1.8	> 1.5	> 60 kb : non degraded
Amplicon	PCR Product using Fusion primer			—	—	—
Transcriptome (W DSN normalization)	Total RNA	2 ug	—	—	—	—
Transcriptome (W / O normalization)	Total RNA	2 ug	—	—	—	—
Target resequencing (NimbleGen SeqCap)	gDNA	5.5 ug	50 ng / ul	≥ 1.8	> 1.5	> 1.5 kb

- Sample storage duration : 1month

8. Results

- Basic report (Raw reads, Assembly, Blast) : Contig sequence file(.fna,.ual,.sff) and Blast results (.html)

  *** We supply a basic reports with free of charge, And if customer requests any analysis, it will be additional charged in accordance with kind of validation service.*

- You can download results on-line or get it as potable drive or CD/DVD.
- Results storage duration : 6 months

Microarray service

- *Certified services provider of Affymetrix and Agilent*
- *Customized data analysis by accustomed SolGent bioinformatics*

1. Description

SolGent provides analysis services for SNP, mRNA, miRNA, aCGH, and CNV among many other areas of molecular biology research. To optimize the quality of the experiment results, our quality control process starts with each sample itself, and continues throughout the experimental steps. Based on the needs of our client, we also provide from basic data analysis to advanced statistical analysis services.

2. Application

1) DNA analysis (SNP / aCGH / CNV analysis services)

- GWAS
- Linkage Analysis
- Pharcogenomics
- Cytogenetics
- Cancer Genomics

2) RNA analysis (Expression analysis service)

- Gene expression profiling
- microRNA

3. Platform

- Affymetirx GeneChip platform
- Affymetirx GeneTitan platform
- Agilent platform

Microarray service

4. Platform approach guide

	Platform	Description	
DNA analysis solution	Affymetrix GeneChip platform	Genome-wide Human SNP Array 6.0	
		Genome-wide Human SNP Array 5.0	
		DMET Plus Array	
		Human Mitochondrial Resequencing Array 2.0	
		Mouse Genotyping Array	
		Rice 44K SNP Genotyping Array	
	Affymetrix GeneTitan platform	Axiom™ Genome-Wide ASI 1 Array Plate	
		Axiom™ myDesign™ Array	
		Axiom™ Bovine Array	
	Agilent platform	CGH	Human, Mouse, Rat, Custom
		CNV	Human
		Methylation	Human, Mouse
RNA analysis solution	Affymetrix GeneChip platform	Gene Array	Human, Mouse, Rat
		3' IVT Array	Human U133+, Mouse 430, Rat 230, Arabidopsis, Barley, Bovine, C. elegans, Canine, Chicken, Citrus, Cotton, Drosophila, E. coli, Maize, Medicago, P. aeruginosa, Plasmodium/Anopheles, Poplar, Porcine, Rhesus Macaque, Rice, S. aureus, Soybean, Sugar Cane, Tomato, Vitis vinifera (Grape), Wheat, Xenopus laevis, Xenopus tropicalis, Yeast, Zebrafish
		miRNA 2.0 Array	131 organisms
	Affymetirx GeneTitan platform	3' IVT Array	Human U219, Human U133+ PM, Mouse 430 PM, Rat 230 PM
		Gene Array	Human, Mouse, Rat
	Agilent platform	Gene expression	Arabidopsis (V4), Barley, Bovine (V2), Brassica, C. elegans (V2), Canine (V2), Chicken (V2), Cotton, Drosophila, E. coli, Horse, Magnaporthe (V2), Medicago, Mosquito, Rabbit, Porcine (V2), Rhesus Macaque (V2), Rice, Salmon, Sheep, Tobacco, Tomato, Wheat, Xenopus (V2), Yeast (V2), Zebrafish (V3)
		miRNA	Human, Mouse, Rat, Custom

5. Workflow

Microarray service

6. Sample preparation

1) DNA analysis (SNP/aCGH/CNV analysis services)

- Affymetirx

Type	Total gDNA
Array 6.0	1ug(50ng/ul)~1.5ug(100ng/ul)
Axiom	500ng(25ng/ul)~1ug(50ng/ul)
DMET	2ug(60ng/ul)~3ug(100ng/ul)
Cytogenetics 2.7M	500ng(50ng/ul)~1ug(100ng/ul)

- Agilent

Type	Total gDNA
aCGH,CNV	3.5ug(50ng/ul)~6.5ug(200ng/ul)

2) RNA analysis (Expression analysis services)

- Affymetirx

Type	Total gDNA
3'IVT (Eukaryotic organism)	500ng(50ng/ul)~1ug(100ng/ul)
Gene Array (Prokaryotic organism)	15ug(600ng/ul)~20ug(1ng/ul)
miRNA	500ng(50ng/ul)~1ug(100ng/ul)
	500ng(50ng/ul)~2ug(200ng/ul)

- Agilent

Type	Total gDNA
One-color expression array	300ng(50ng/ul)~2ug(200ng/ul)
miRNA	200ng(50ng/ul)~1ug(100ng/ul)

7. Results

DNA analysis services

● Standard analysis report
- Marker information(HWE, Call rate, MAF etc)
- In case of Case/control study
  : Association study(Supply various analysis report in accordance with genetic model)
  Clinical information and association study about case/control)
  Additional report Haplotype detection and association study in accordance with results

● Advanced analysis report * * *There are additional charge*
- Survival analysis
- Gene-Gene interaction analysis (including MDR)
  Furthermore we can provide customized reports with consulting by our accustomed bioinformatics.

● GWAS
- QC report(Marker, Sample)
- Association Study
- Gene review

RNA analysis services

● Standard analysis report
- QC & Basic statistics reports
- Basic statistical process support(T-test, One-way ANOVA)
- Clustering (Hierarchical, K-mean)
- Ontology, Pathway grouping
- Target gene analysis report after miRNA analysis

● Advanced analysis report * * *There are additional charge*
- GSEA(Gene Set Enrichment Analysis)
- Survival analysis
- Classification analysis
- eQTL analysis
- Analysis method setting and support

- Results storage duration : 6months

Genotyping service

- *One-stop service*
- *Expertise & Know-how*
- *Customized service*
- *Low error rate using automatic system*
- *Possession 39,000 assay*
- *High resolution and high quality data*

1. Description

SolGent Genotyping service encompasses a range of application used to confirmation a genetic mutation relating disease and analysis of phylogenetic classification, genetic difference between individual and microbial variety and structure. SolGent have lots of platforms and we can supply customized analysis as well as basic analysis service according to customer requests.

2. Application

- Singleplex Genotyping : TaqMan assay, SNaPShot™ assay
- Multiplex Genotyping : BioMark™ (48 or96 plex), SNP-IT assay (12-plex)
- Resequencing (SNP discovery)

3. Platform

- ABI PRISM 7900HT real-time PCR system
- ABI 3130xl DNA Analyzer
- SNPstream UHT Array Imager
- Fluidigm BioMark System

Genotyping service

4. Feature

▫ Study design service

- We provide SNP allele frequency information and LD analysis information between SNPs and it will be helpful that customer selects SNP.
- If customer give us target SNP, we will provide service from primer design to final results.
- We possess 39,000 assay

▫ Quality assurance

- Minimizing error rate through automated scalable system
- High resolution and high quality data

▫ Express service

- Within 2 weeks in case of possessing an assay

▫ DNA preparation service

- Extracting and quantify high-purity DNA preparation from buffy coat and whole blood(up to 20ul) using automatic system FUJIFILM and QuickGene-mini80)

5. Workflow

Genotyping service

6. Platform Approach guide

Platform	Assay	Feature
ABI PRISM 7900HT real-time PCR system	TaqMan® assay	- Easy to analyze large sample set - Low sample input - Sample requirement : 10ng / genotype - timeline 5 ~ 6 weeks
Fludigm BioMark™ system	TaqMan® assay	- Multiplexed genotyping using existing Tagman assay (48 x 48, 96 standard format) - proven assay, high throughput - flexbility of analysis format - timeline 5 ~ 6 weeks
ABI 3130xl DNA Analyzer	Resequencing (SNP Discovery)	- From target gene design to data analysis - Novel SNP discovery, LD analysis and TagSNP selection - timeline 6 weeks
	AFLP	- Avaliable information within short time - Sample requirement 100ng / genotype - Timeline 5 ~ 6 weeks
	SSR	- Easy to confirm repeat sequence with statistical data - Sample requirement 25ng / genotyping - Timeline 5 ~ 6 weeks
SNPsteam® UHT Array Image™	SNP-IT® assay AFLP SSR	- Easy to analyze large sample set (You can order in multiple 348 smaple) - 12-multiplexed genotyping - Low sample input (10ng / 12 genotyping) - timeline 5 ~ 6 weeks
Veriti	RFLP	- Easy to analyze small sample set - Sample reqirement 25ng / genotyping - Timeline 5 ~ 6 weeks
	ASP (Allele Specific PCR)	- Easy to analyze small sample set - Advantage for additional sample order - Sample requirement 25ng / genotype - Timeline 6 weeks

7. Results

▫ Raw data & result analysis reports (.fsa) as excel format

- We can also provide peak scanner software of ABI.
- You can be available 'SolGent advanced analysis service' with additional charge.

▫ Results storage duration : 6 months

How to order

How to order for all SolGent Services

Fill out order sheet

Ship your sample

Get the result

1. Fill out order sheet : You can be available order sheet from our homepage www.solgent.com

2. Ship your sample

- Policy for freight charge

  Freight charge ,in case of general sequencing for over 20rxns and other SolGent services will be paid by SolGent.

  Before sending your samples, contact us. order@solgent.com

3. Get the results

You can get the results according to each results format.

4. Sample storage duration : 1 month

If storage duration of samples is terminated, we will discard it. But if customer requests other terms, we can do as customer requests.

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