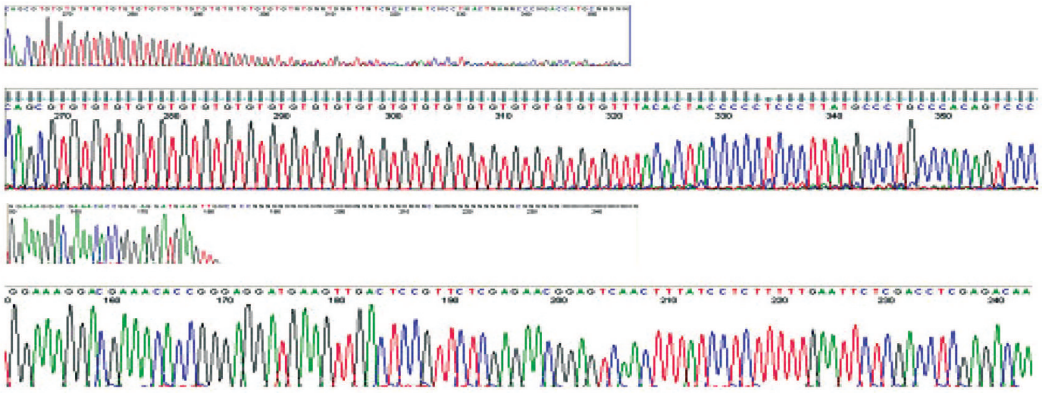
Difficult DNA Templates Sequencing

Description

It is a sequencing method for obtaining high quality results as improving the phenomenon of the signal loss or interruption at a certain point caused by repeated sequence, secondary structure, GC or AT region.

Features

- High quality results are obtained as shown in the below.



*Successful results may not be obtained depending on the sample specificity

Primer Walking Service

Description

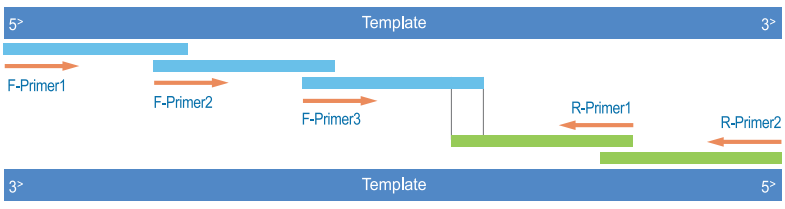
Primer walking service is analyzing the base sequences of PCR products or plasmid, which is not analyzable by single primer extension in one time. Internal primers are designed and prepared with results obtained after performing end sequencing using the primers given or designated by customers. We make extension continuously by designing an internal primer at an appropriate point using he result obtained from the reaction conducted with a new primer and the same template.(for more than 15kb, for large-construct DNA shotgun sequencing is recommended.)

Features

- This service is to read 2~15kb of sequence with PCR product or plasmid DNA that cannot be read fully by single primer extension sequencing. Once performing end sequencing with designated primer by customer, we design internal primers with reference to end sequence data. Necessary walking continues with the same method until the whole region is covered. About one week is taken to read 1~1.5kb by primer walking.

Result

- Providing Ab1file, PDFfile used for primer walking.
- Providing Contig sequence, contig quality.



MACROGEN Advancing through Genomics
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16/18s (ITS 5.8s) rRNA Sequencing

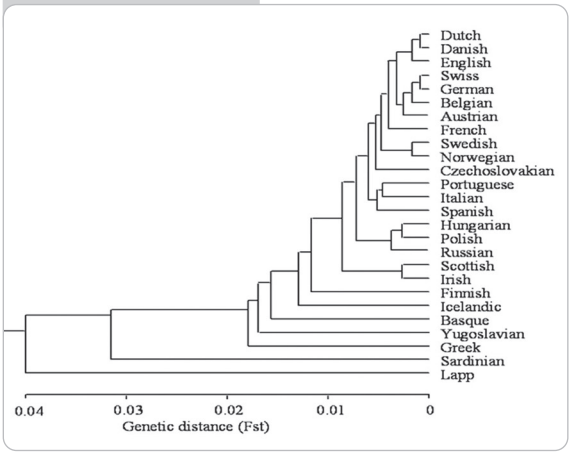
Description

Identify a new bacterial species by using Macorgen·fs 16/18s rRNA sequencing. We provide all inclusive service performing DNA extraction, PCR, sequencing and assembling.1500 base pair or longer sequence is guaranteed for identifying a domain of your bacteria or fungi.
As a value service, we also offer Phylogenetic analysis to enhance your research.

Features

- Performing gDNA extraction, PCR, sequencing, assembling of Bacteria/Fungi (filamentous fungi, yeast).
- For bacteria, results guaranteed for more than 1,300 base pairs of the 16s rRNA genes sequencing.
- For fungi (filamentous fungi, yeast)
  1) Results guaranteed for more than 600 base pairs of the ITS rRNA genes sequencing.
  2) Results guaranteed for more than 1,100 base pairs of the ITS + 26s rRNA gene (D1/D2 region) sequencing.

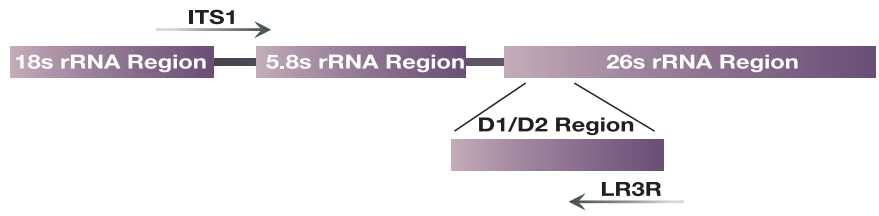
Phylogenetic tree



16s rRNA Region

ITS rRNA Region

ITS and 26s rRNA Region



Order and Result

- Starting material of glycerol cell stock or agar stab is recommended.

DNA preparation → PCR → Purification → Sequencing → Blast N search → Blast N search

- Time required : 4~5 working days after sample QC

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Cloning Service

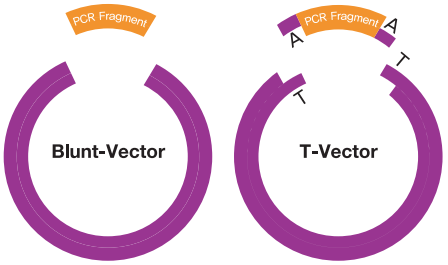
Description

Besides the main purpose of the cloning, we can improve your sequencing results through this cloning service for contaminated PCR products which usually show double peak in chromatogram. This service is given by the following:

Step 1.	Making plasmid by inserting a customer's PCR products into a vector (T-vector or Blunt vector)
Step 2.	Inserting the plasmid into bacteria cell for culture
Step 3.	Cell extraction for the plasmids

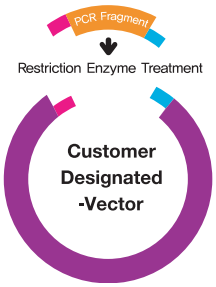
Features

1. PCR fragment cloning (T-vector/Blunt vector cloning)



- Cloning the PCR product (~3Kb) into a vector.
- Cloning after selecting T-vector or Blunt vector depending on DNA polymerase used for PCR (usage of pfu-taq).
- Analyzing the base sequences of the inserted PCR product after cloning.

2. Sub-Cloning

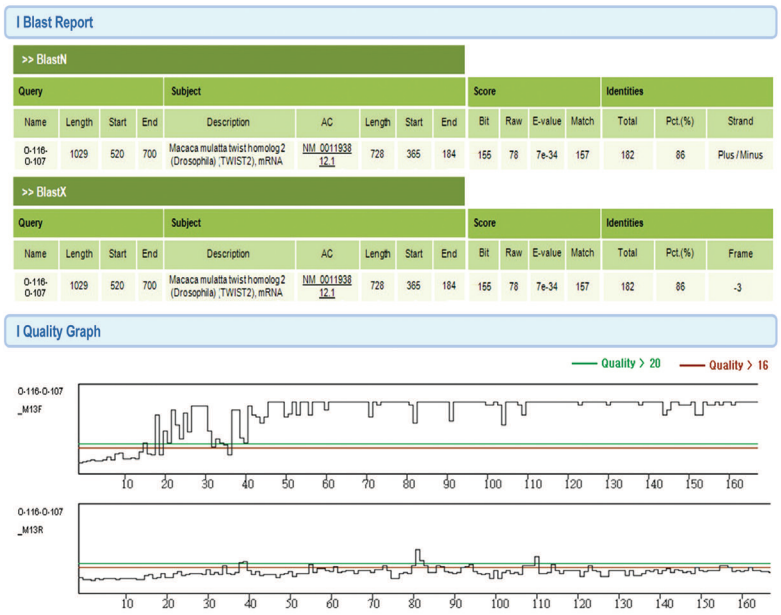


- Sub-cloning the PCR product using a customer-designated vector after specific restriction enzymes treatment.
- Sub-cloning the template DNA and primer using a customer-designated vector after PCR.
- Analyzing the base sequences of the restriction enzyme mapping and the PCR products after cloning.
- The vector for Sub-cloning should be provided by customers.

Value Service

- You can receive full analysis report of your cloning offered by Macrogen's Bioinformatics service. The service scope is included:

  - Contig Chromatogram
  - Analysis Report
  - BlastN / BlastX Report
  - Quality Graph



I Blast Report

>> BlastN

Query				Subject					Score				Identities		
Name	Length	Start	End	Description	AC	Length	Start	End	Bit	Raw	E-value	Match	Total	Pct.(%)	Strand
0-116-0-107	1029	520	700	Macaca mulatta twist homolog 2 (Drosophila) (TWIST2), mRNA	NM_0011938 12.1	728	365	184	155	78	7e-34	157	182	86	Plus / Minus

>> BlastX

Query				Subject					Score				Identities		
Name	Length	Start	End	Description	AC	Length	Start	End	Bit	Raw	E-value	Match	Total	Pct.(%)	Frame
0-116-0-107	1029	520	700	Macaca mulatta twist homolog 2 (Drosophila) (TWIST2), mRNA	NM_0011938 12.1	728	365	184	155	78	7e-34	157	182	86	-3

I Quality Graph

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SNP Discovery Service

Description

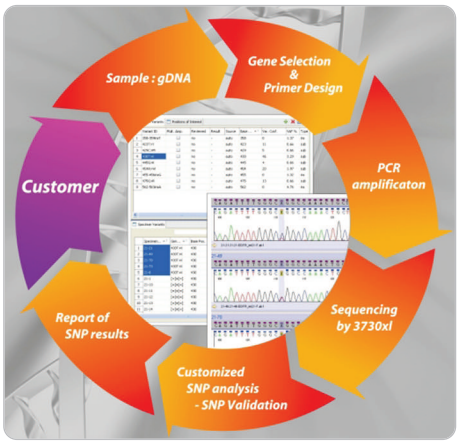
SNP analysis service is highly flexible to any specific project requirements. SNPs (single nucleotide polymorphisms) occurs every 100 to 300 bases along the human genome and account for about 90% of all genetic variations. SNPs could predispose people to disease or influence their response to a drug. Also, we offer a complete package of SNP discovery sequencing services by the following steps:

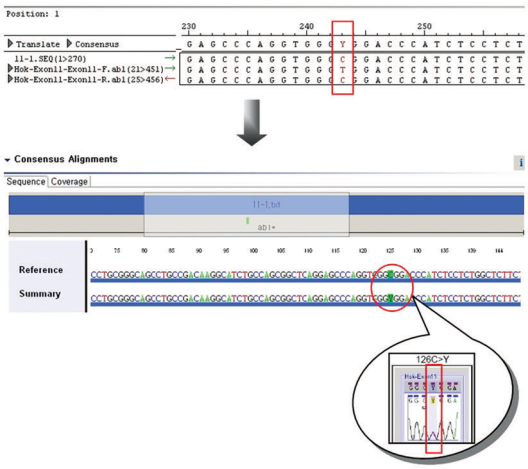
PCR optimization → PCR amplification → Purification → Sequencing → SNP discovery

We provide high-throughput SNP Analysis by using ABI3730XL, automated DNA sequencer, and the result will be available within approximately two (2) weeks.

Features

- Applicable with various samples such as blood, tissue, gDNA, PCR product.
- Secondary confirmation system using DNA star and Varient reporter.
- Providing ABI file, text file, pdf file and report (genotyping file).
- Time required: 4 weeks after sample quality confirmation. (It can be varied depending on sample amount and target genes)





Value Service

- You can receive full annotation of your SNP discovery offered by Macrogen's Bioinformatics service. The service scope is included full SNP summary and Indel summary :

I SNP Summary

Chromosome	Position	Ref	Allele	SNP DB	Annotation Gene	Ref_aa	SNP_aa	Blosum	NS/S	Gkgene_EXON1	Gkgene_EXON2	Gkgene_EXON3	.....
1	59133	A	G	-	CDS : OR4F5	S	S	4	S	GA	GA	GA	.....
1	59374	A	G	rs2691305	Intron : SMAD11	T	A	0	NS	GG	GG	GG	.....
1	60000	T	C	rs4372192	CDS : NPC2L	S	P	-1	NS	-	GT	-	.....
:	:	:	:	:	:	:	:	:	:	:	:	:	:

I Indel Summary

Chromosome	Position	Gkgene_EXON1		Gkgene_EXON2		Gkgene_EXON3			Gkgene_EXON22	
		Annotation Gene	Indel	Annotation Gene	Indel	Annotation Gene	Indel		Annotation Gene	Indel
1	59133	CDS : OR4F5	-A	CDS : OR4F5	-A	CDS : OR4F5	-A	.....	CDS : OR4F5	-A
1	59374	Intron : SMAD11	-G	Intron : SMAD11	-G	Intron : SMAD11	-G	.....	Intron : SMAD11	-G
1	60000	CDS : NPC2L	+T	CDS : NPC2L	+T	CDS : NPC2L	+T	.....	CDS : NPC2L	+T
:	:	:	:	:	:	:	:	:	:	:

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Genotyping-Microsatellite Analysis

Description

Microsatellite Analysis (VNTRs) service encompasses a wide variety of genotyping, DNA profiling, and mutation detection techniques for medical, environmental, and agricultural research. We provide the Microsatellite Analysis (VNTRs) service based on our accumulated experience and know-how in genomics. In general, it is used for amplified fragments' size check only. Since PCR amplification is not available through this service, fluorescent-labeled PCR products should be supplied as Microsatellite Analysis (VNTRs) samples.

Features

- DNA Sources :10~20㎕ of fluorescent labeled PCR product
  (Additional discussion is required when desired to get this service with genomic DNA)
- Time Required : 1 Week after Sample Quality Identification

Standard Dye Sets

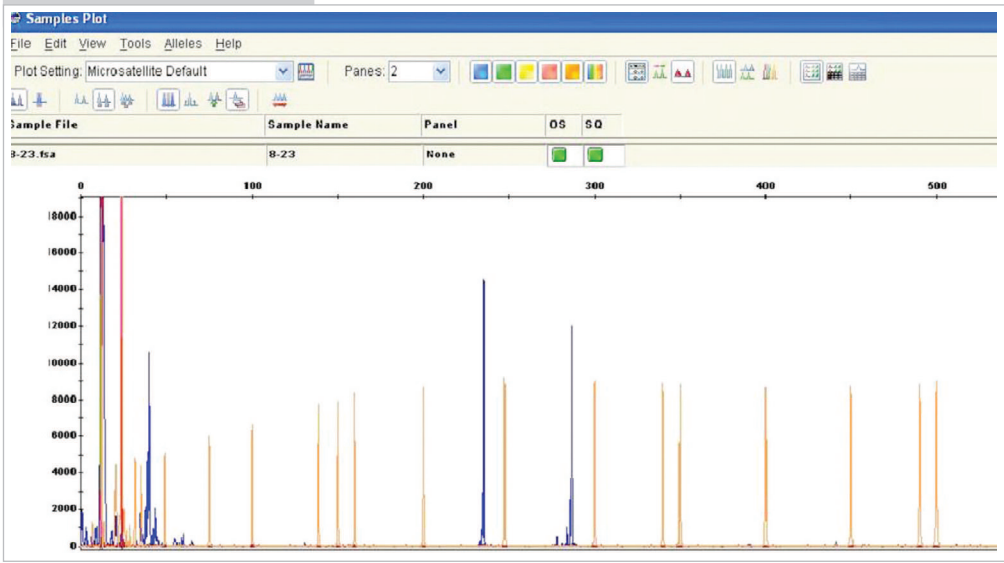
Dye Set (Filter set)	DS-30 (D)	DS-33 (G5)	DS-33 (G5)
Size Standard	400HD-ROX	500LIZ	1200LIZ
Fragment size (bp)	50~400	35~500	20~1200
Size standard Dye	ROX	LIZ	LIZ
Sample Dye	FAM,HEX,NED	FAM,VIC,NED,PET	FAM,VIC,NED,PET

- Accurate information of fluorescent dye and standard size should be given for this service.
- The PCR products mixed by customers should be sent if the multiplex running service is desired after carrying PCR for each dye.

Result

- 3730xl Raw Data (.fsa) / The table against allele values analyzed by Genemapper (v.3.7) / Peaks of allele (.pdf); domestic service, extra charge

Genotyping Raw Data



Mutagenesis Sequencing Service

Description

We provide the essential mutant library preparation for protein structure and function study, gene expression study, and Promotor Change.

Features

- Various mutant preparations such as base pair insertion, substitution, deletion.
- Time required : 14 days after sample QC.

Primer preparation

<Base pair insertion>

GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCAT

TTAACGTCTTAAGTCACTTAGTAGCTTAGAAA

AATTGCAGAATTCAGTGAATCATCGAATCTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCAT

<Substitution>

GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCAT

TTAACGTCTTAAGTCACTTAAGGGCTTAGAA

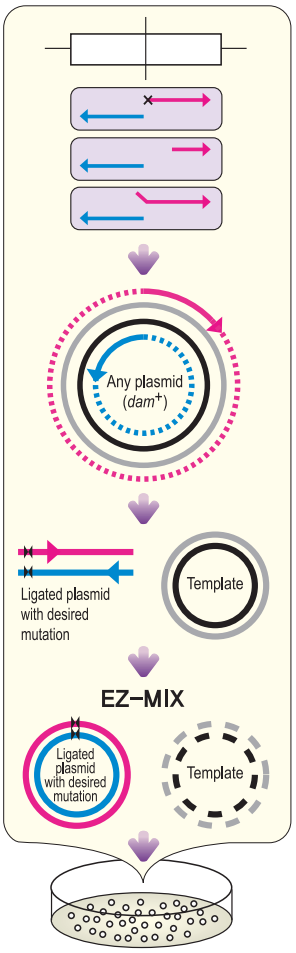
AATTGCAGAATTCAGTGAATCATCGAATCTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCAT

<Deletion>

GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCAT

TTAACGTCTTAAGTCACTTA

AATTGCAGAATTCAGTGAATCATCGAATCTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCAT



1 **Primer preparation**
- Substitution
- Deletion
- Insertion

2 **High fidelity PCR**

3 **Removal of Teplaste and Ligation**
- Ligation with a template and linear plasmid using an enzyme

4 **Transformation**

5 **Confirmation of sequencing results**

Human mtDNA Full Length Sequencing Service

Description

We provide direct sequencing of amplified 16,659 base pair human mitochondria DNA genes.

Features

- Performing whole processes including PCR, sequencing, and assembling.
- Production of PCR products using 14 PCR primer sets, base sequence analysis using 39 sequencing primers, formation of full contig using each sequencing data.
- Time required : 14 days after sample QC.

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