E

Genome-wide Functional Analysis

S. pombe Genome-wide Deletion Mutant Library
S. cerevisiae VN-Fusion Library
Genome-wide Drug Target Identification(*GP Screen*™)

S. cerevisiae Mutant Library
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S.pombe Genome-wide Deletion Mutant Library

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S. pombe Genome-wide Deletion Mutant Library

S. pombe Genome-wide Deletion Mutant Library

Overview

Bioneer's exclusive *S. pombe* (Schizosaccharomyces pombe) Genome-wide Deletion Mutant Library is a powerful tool for large-scale genetic functional analysis, for identification and verification of drug targets, and for integrated systemic research of cell function. Co-developed by Bioneer and KRIBB (Korea Research Institute of Biotechnology and Bioscience) in collaboration with Dr. Paul Nurse of the CRC (Cancer Research Center) in the UK, the *S. pombe* Genome-wide Deletion Mutant Library (*S. pombe* Library) can be used for genetic and chemical screening such as drug target identification, gene expression profiling, and synthetic lethal profiling. *S. pombe* Library offers higher homology with mammalian cells and human genes than those of *S. pombe*. *S. pombe* Library targets every 4,914 ORF (Open Reading Frame) in the S. pombe genome via targeted mutagenesis. A total of 4,840 heterozygous diploid deletion mutants representing 98.5% of the organism genome and 3,400 haploid deletion mutants with 95.3% genome coverage are available. Since there are different tag sequences (barcode) for each individual mutant, the library provides an ideal way to approach research in gene function and drug target screening for large number of genes by using pools of mutants. It is also possible to analyze biological gene functions through phenotype research with the deletion mutant having specific genes absent.

■ Characteristics of *S. pombe* Deletion Mutant Library

Strains	Diploid 4,840 strains, Haploid 3,400 strains		
Selection Marker	KanMX4, G418		
Genotype	**Diploid**: SP286	h+/h+	ade6-M210/ade6-M216 ura4-D18/ura4-D18 leu1-32/leu1-32
	Haploid: ED666	h+	ade6-M210 ura4-D18 leu1-32
	ED668	h+	ade6-M216 ura4-D18 leu1-32
Culture media	**YES**: for rich complete medium		
	EMM: for minimal medium		
Strain verification	Check PCR, Sequencing		
Storage	Store at -70℃ (Glycerol type) /Store at 22℃ to 25℃ (Agar type)		
References	**Analysis of a genome-wide set of gene deletions in the fission yeast *Schizosaccharomyces pombe* Nat Biotechnol**. 2010 Jun;28(6): 617-623. **Stc1: A Critical Link between RNAi and Chromatin Modification Required for Heterochromatin Integrity Cell.** 2010 Mar 5;140(5):666-677. **Conservation and Rewiring of Functional Modules Revealed by an Epistasis Map in Fission Yeast Science.** 2008 Oct 17;322(5900):405-410. Epub 2008 Sep 25.		
Patent	10-2008-037420, 12/989,192		

01 S. pombe Genome-wide Deletion Mutant Library

S. pombe Genome-wide Deletion Mutant Library

■ S. pombe Deletion Mutant Construction

• *S. pombe* Diploid Deletion Mutant Construction:

The Genome-wide Deletion Mutants (diploid) has been generated through homologous recombination in *S. pombe*. The deletion mutants were constructed through PCR-based mutagenesis using *S. pombe* genome sequence information provided by The Wellcome Trust Sanger Institute.

The protocol of deletion mutant construction is as follows:

All of the deletion cassettes for mutant construction were designed to contain an antibiotic-resistant gene as a selection marker, tag sequences to identify each mutant, and universal sequences to amplify the tag sequences. As a selection marker, KanMX4 module that gives Geneticin (G418) resistance to transformant was used (Figure 1). A deletion cassette amplified by PCR was then inserted into S. pombe SP286 (h+/h+ ade6-M210/ade6-M216 ura4-D18/ura4-D18 leu1-32/leu1-32) through homologous recombination (Figure 2), followed by insertion into a deletion site simultaneously (Figure 3).

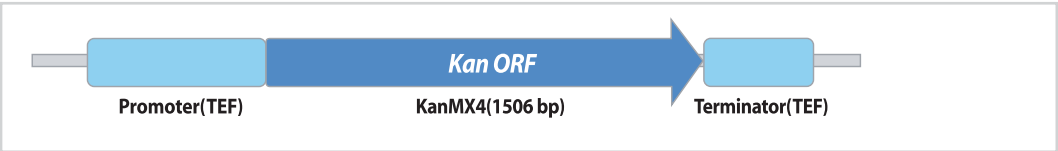


Figure 1. KanMX4 as a selection marker

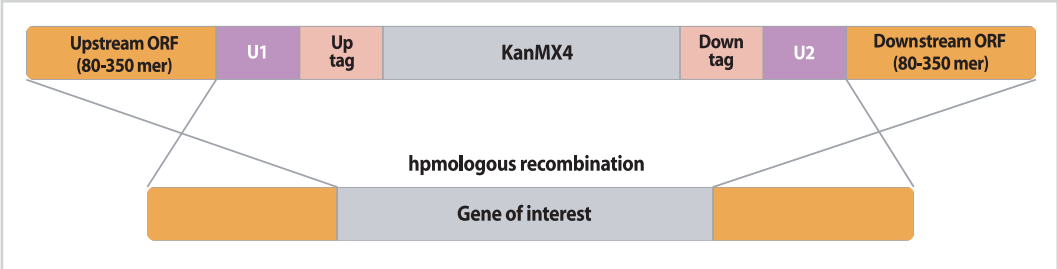


Figure 2. The scheme of a deletion cassette

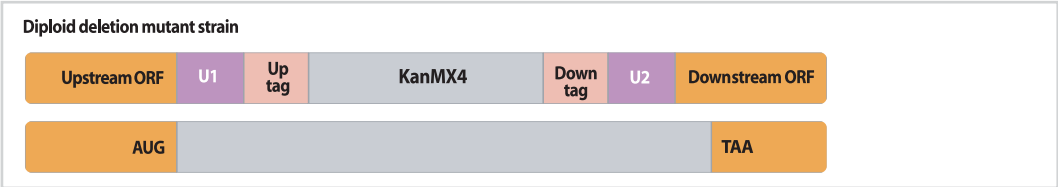


Figure 3. Diploid mutant strain construction

- *S. pombe* Haploid Deletion Mutant Construction:

We have constructed haploid mutants from diploid mutants as follows (Figure 4, 5):

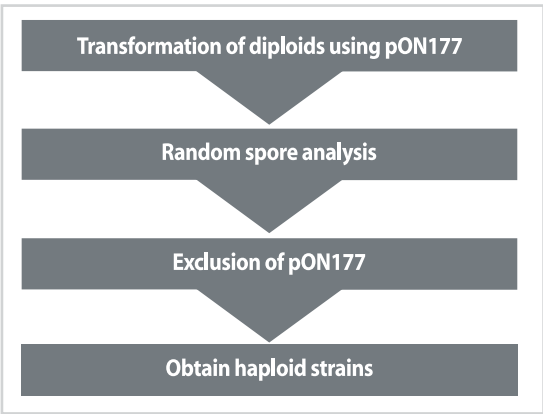


Figure 4. Workflow of haploid strain construction

S. pombe Genome-wide Deletion Mutant Library

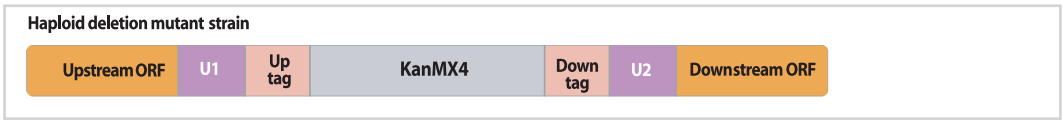


Figure 5. Haploid mutant strain construction

■ *S. pombe* Deletion Mutant Verification

To confirm proper deletion mutant generation, colony PCR was performed by using both specific primers for the target gene and for the KanMX module. CP5-CPN1 and CPC3-CP3 PCR products must be present. Bioneer provides primer sets for mutant verification (Figure 6).

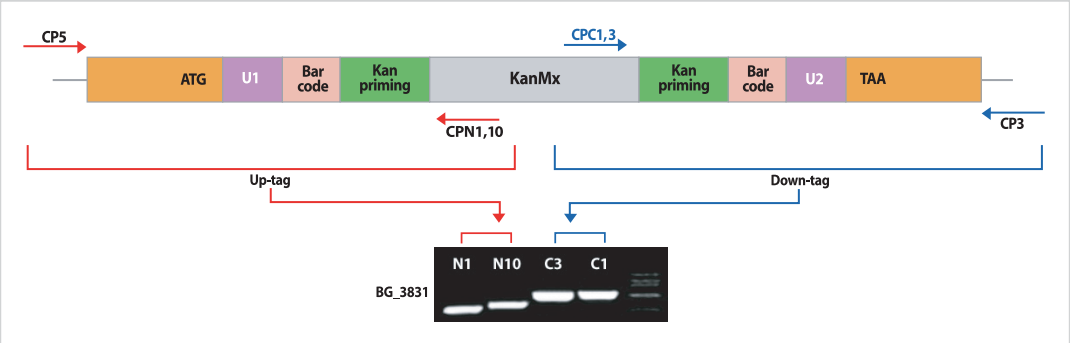


Figure 6. Example of strain verification using colony PCR

■ Ordering & Technical Support

For more information or technical assistance, contact us via phone (+82-42-930-8777), fax (+82-42-930-8688) or email (spombe-support@bioneer.com). Additional international offices are listed on our web page (www.bioneer.com).

01 S. pombe Genome-wide Deletion Mutant Library

S. pombe Individual Deletion Mutant Strains

Description

S. pombe has been an important model system to study cell division and signal transduction mechanisms. It was reported that not only its genes are highly homologous to human one but also the signaling pathways are similar between the two species. Gene deletion inside a cell is an essential tool to study gene function through phenotype investigation and drug target validation. Bioneer created *S. pombe* Deletion Mutants through collaborations with KRIBB and CRC. 3,400 of haploid and 4,840 of heterozygous diploid single-gene deletion strains have been constructed as of October 2012 and new strains are being added on an ongoing basis.

Features and Benefits

- One of two Genome-wide deletion mutants library (Only 2 kinds exist: *S. pombe* & *S. cerevisiae*).
- It has physiological processes Similar to.
- It has human cancer gene with over 30% of homology.
- It has the rapid cell cycle to make it simple to analyze molecular biological mechanism and pathway.
- Phenotype analysis is possible due to its recessive mutant type.
- Unknown genomic function analysis through functional complementation is possible.
- Functional analysis of biological gene cluster is possible through Genome-wide pool set.
- Cell-based HCS drug target screening is possible.

Specifications

- Contents
- Note

Individual Deletion Mutant Strain	1 tube
Strain information sheet	1 copy
Product manual	1 copy

- Agar Type

The individual Deletion Mutant Strain is supplied in a 2.0 ml tube containing 1 ml YES agar medium with Geneticin (G418) at a concentration of 100 µg/ml. The strain in agar type is shipped at room temperature and viable up to 2 weeks when stored at 4°C. For long-term storage, Keep your strain into glycerol stocks upon receipt.

- Glycerol Type

The individual Deletion Mutant Strain can be also supplied in a 2.0 ml tube containing 0.5 ml YES / 25% glycerol media with Geneticin (G418) at a concentration of 100 µg/ml. The mutant in this glycerol type is shipped on dry ice and can be maintained at -70°C for over 2 years.
Dry ice shipping and handling charge will be added.

S. pombe Individual Deletion Mutant Strains

Application

- Biological mechanism and toxicity research of drug candidate
- Discovery of target molecule
- Identification of drug candidate
  (Especially, it could establish bridge-head in the anticancer drug research)

Ordering Information

Cat No.	Type	Ship Format	Product Description
M-1010D-A	Diploid	Agar	*S. pombe* Individual Heterozygous Diploid Deletion Mutant Strain, Agar
M-1010D-G		Glycerol	*S. pombe* Individual Heterozygous Diploid Deletion Mutant Strain, Glycerol
M-1010H-A	Haploid	Agar	*S. pombe* Individual Haploid Deletion Mutant Strain, Agar
M-1010H-G		Glycerol	*S. pombe* Individual Haploid Deletion Mutant Strain, Glycerol

01 S. pombe Genome-wide Deletion Mutant Library

S. pombe Deletion Mutant Sets

Description

In vivo screening technology using yeast is very essential to discover the pathway of bioactive materials like drug target candidate, as well as to identify target proteins. Bioneer generated the *S. pombe* Deletion Mutants through collaborations with KRIBB and CRC. 3,400 of haploid and 4,840 of heterozygous diploid single-gene deletion strains have been constructed as of October 2012 and new strains are being added on an ongoing basis. As haploinsufficiency-typed mutants, they are very effective to research drug target candidate because it is possible to analyze phenotype through the pattern matching with Bioneer's *S. pombe* Deletion Mutant Sets.

Features and Benefits

- The only Genome-wide deletion mutants library (Only 2 kinds exist: *S. pombe* & *S. cerevisiae*).
- It has physiological processes similar to mammalian cells.
- It has human cancer gene with over 30% of homology.
- It has the rapid cell cycle to make it simple to analyze molecular biological mechanism and pathway.
- Phenotype analysis is possible due to its recessive mutant type.
- Unknown genomic function analysis through functional complementation is possible.
- Functional analysis of biological gene cluster is possible through Genome-wide pool set.
- Cell-based HCS drug target screening is possible.
- Storage

Specifications

- Contents

A. *S. pombe* Heterozygous Diploid Deletion Mutant Set

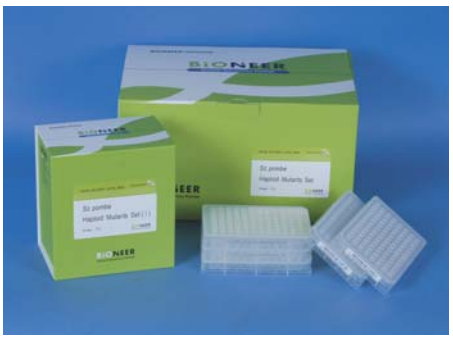
4,840 strains supplied in 96-well plate	54 plates total
Wild type Strain (SP286)	1 well
List of diploid strains on CD	1 copy
Product manual	1 copy

B. *S. pombe* Haploid Deletion Mutant Set Ver 4.0

3,400 strains supplied in 96-well plate	36 plates total
Wild type Strains (ED666 and ED668)	2 wells
List of haploid strains on CD	1 copy
Product manual	1 copy
Validation Primer Set (optional)	1 set

S. pombe Deletion Mutant Sets

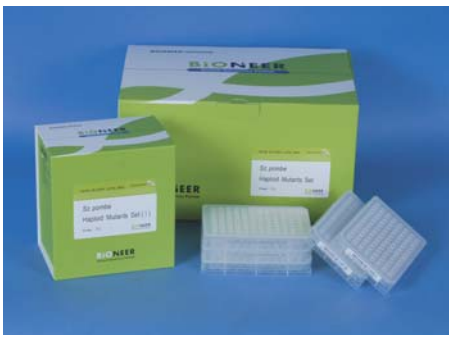
C. *S. pombe* Haploid Deletion Mutant ver 3.0 to 4.0 Upgrade Package



278 strains supplied in 96-well plate	3 plates total
Wild type Strains (ED666 and ED668)	2 wells
List of haploid strains on CD	1 copy
Product manual	1 copy
Validation Primer Set* (optional)	1 set

* Sequence information is not provided.

D. *S. pombe* Haploid Deletion Mutant ver 2.0 to 4.0 Upgrade Package



743 strains supplied in 96-well plate	8 plates total
Wild type Strain (ED666 and ED668)	2 wells
List of haploid strains on CD	1 copy
Product manual	1 copy
Validation Primer Set* (optional)	1 set

* Sequence information is not provided.

The *S. pombe* Deletion Mutant Sets are supplied in 96-well plates containing 100 µl of YES media (25% glycerol & 100 µg/ml Geneticin (G418)). The set is shipped on dry ice and is viable for over 1 year when stored at -70 °C.

Application

- Biological mechanism and toxicity research of drug candidate
- Discovery of target molecule
- Identification of drug candidate
  (Especially, it could establish bridge-head in the anticancer drug research)

Ordering Information

Cat No.	Type	Product Description	Quantity
M-1030D	Diploid	*S. pombe* Heterozygous Diploid Deletion Mutant Set	54 plates (96-well)
M-4030H	Haploid	*S. pombe* Haploid Deletion Mutant Set Ver 4.0	36 plates (96-well)
M-4030H-L*		*S. pombe* Haploid Deletion Mutant Set Ver 4.0 Licensing	36 plates (96-well)
M-3030H-U4		*S. pombe* Haploid Deletion Mutant ver 3.0 to ver 4.0 Upgrade Package	3 plates (96-well)
M-2030H-U4		*S. pombe* Haploid Deletion Mutant ver 2.0 to ver 4.0 Upgrade Package	8 plates (96-well)

Up to 3 Sets of M-4030H-L can be purchased under the name of purchaser or organization. Please refer to the MTA on our website http://www.bioneer.co.kr/products/YeastGenome/Library-overview.aspx regarding the details of the license limitations.

01 S. pombe Genome-wide Deletion Mutant Library

AccuOligo® S. pombe Validation Primer Set

Description

Bioneer provides the primer set for mutant validation.

Features and Benefits

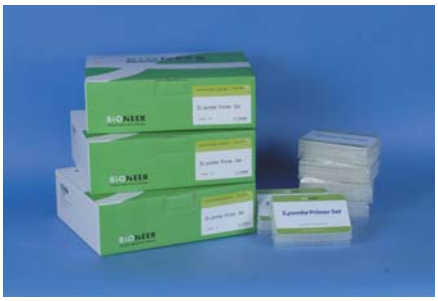
- Complete QC: All the manufactured oligos are checked by MALDI-TOF mass spec.
- High purity: By applying Bio-RP purification system, all the impurities, especially (N-1)mer, can be removed very efficiently.

- Storage

The validation primer set is lyophilized in 96-well plates and shipped at room temperature. Resuspend each primer in 10 mm Tris buffer(pH 8.0) or distilled H_2O to the concentration of 10 pmol/50 ul. The primer in Tris buffer or dH_2O is stable for one year at -20 ℃.

Specifications

- Contents



AccuOligo® primers in 96-well plate (CP3-CPC3)	36 plates total
AccuOligo® primers in 96-well plate (CP5-CPN1)	36 plates total
List of primers on CD	1 copy
Product manual	1 copy

Experimental Data

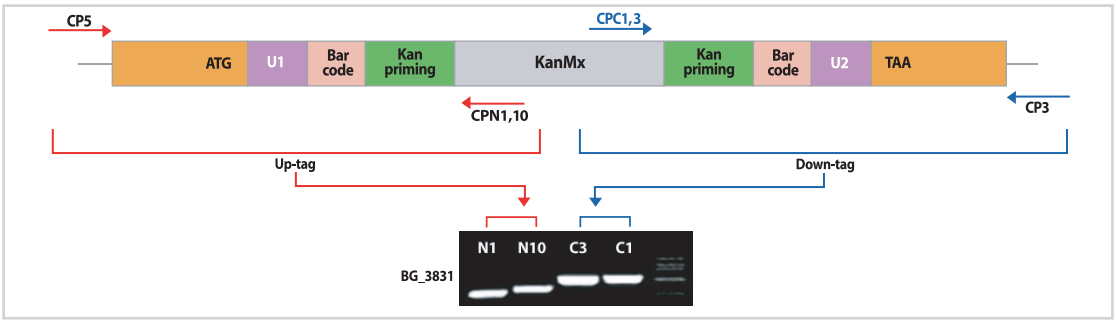


Figure 1. Example of strain verification using *AccuOligo*® *S. pombe* Validation Primer

Ordering Information

Cat. No.	Product Description	Quantity
M-3030P	*AccuOligo*® *S. pombe* Validation Primer Set	72 plates (96-well)
M-3030-U4	*AccuOligo*® *S. pombe* Validation Primer ver 3.0 to ver 4.0 Upgrade Package	6 plates (96-well)

S. pombe Genomic DNA

Description

S. pombe Genomic DNA is isolated from the *S. pombe* parent strain used to generate the deletion library.

Features and Benefits

- Genomic DNA purified with the *AccuPrep*® Genomic DNA Extraction Kit provides high quality and yield.

Specifications

- Contents

S. pombe Genomic DNA in 2.0 ml tube	1 tube
List of Genomic DNA on CD	1 copy
Product manual	1 copy

- Storage

The *S. pombe* Genomic DNA is supplied in 2.0 ml tube and shipped on dry ice. The product should be stored at -20 °C.

Ordering Information

Cat. No.	Product Description	Quantity
M-1030-D	*S. pombe* Genomic DNA	2 µg

02 *S.cerevisiae* VN-Fusion Library

S.cerevisiae VN-Fusion Library

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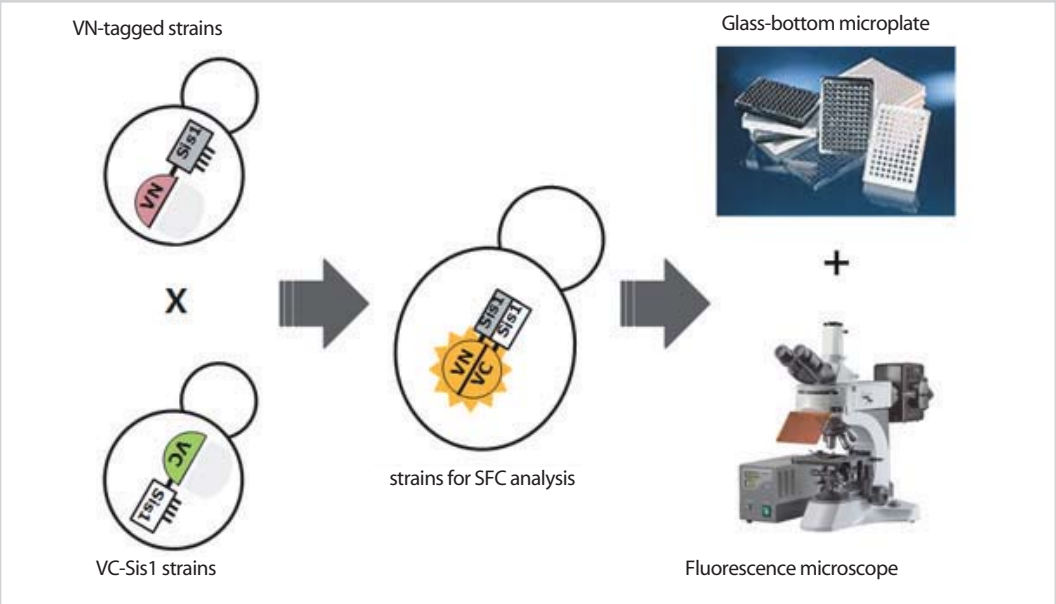
S. cerevisiae VN-Fusion Library

Overview

Most biological processes are carried out and regulated by dynamic networks of protein-protein interactions. Thus, identification and visualization of protein-protein interactions provide significant insight into the individual roles of cellular proteins. Advanced technologies are producing large scale protein-protein interaction data at an ever increasing pace. The Bimolecular Fluorescence Complementation (BiFC) assay is now regarded as one of the most advanced and effective tools for studying in vivo protein-protein interactions in several organisms. The BiFC assay is based on the formation of a fluorescent complex by fragments of yellow fluorescent protein, brought together by association of two interacting partners fused to the fragments. This approach enables visualization of the subcellular localizations of specific protein complexes in the normal intracellular environment.

The yeast *S. cerevisiae* (*Saccharomyces cerevisiae*) is a widely used simple eukaryotic model system whose genome can be easily manipulated. The *S. cerevisiae* VN-Fusion Library was created by Dr. Won-Ki Huh of Seoul National University (Korea). The *S. cerevisiae* VN-Fusion Library consists of 5,809 VN-tagged Open Reading Frames (ORFs) covering 93% of the yeast proteome.



<Non-invasive analysis of protein-protein interaction in living cells>

■ Characteristics of *S. cerevisiae* VN-Fusion Library

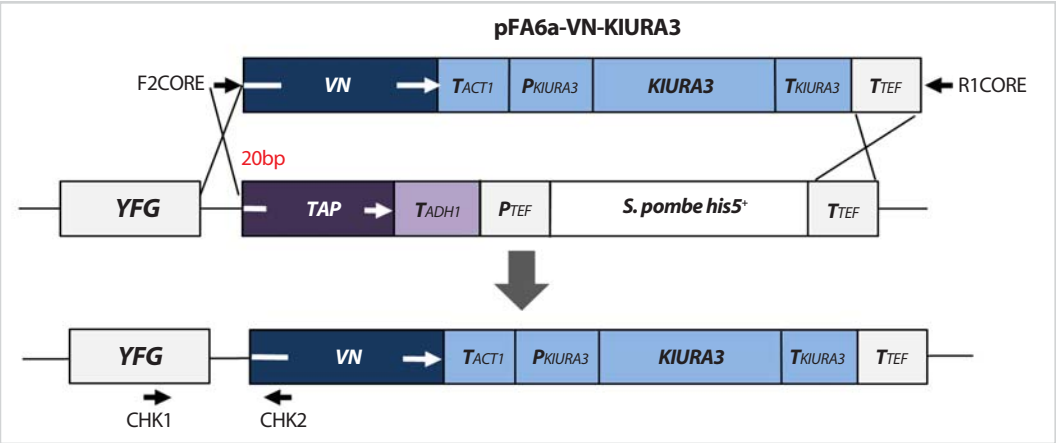
No. of Strains	5,809 strains
Selection Marker	KIURA3
Genotype	All *S. cerevisiae* VN-Fusion strains were derived from BY4741 (*MATa his3△1 leu2△0 met15△0 ura3△0*) Haploid
Culture Media	YPD: for general culture and maintenance medium SC-Ura or SC-His: for medium selection & counter selection (auxotrophic culture)
Strain Verification	Medium selection & Counter selection, Check PCR
Storage	Store at -70°C (Glycerol type) / Store at room temperature (Agar type)
References	1) Sung MK., *et al., J. Microbiol. Methods*, 83(2): 194-201 (2010) 2) Sung MK., *et al., Yeast*, 24: 767-775 (2007) 3) Huh, W., *et al., Nature*, 425: 686-691 (2003)
Patent	10-2009-0048746

02
S. cerevisiae
VN-Fusion Library

S. cerevisiae VN-Fusion Library

■ Construction of *S. cerevisiae* VN-Fusion Library

A ~2.5 kb DNA cassette including the VN and KlURA3 marker gene was amplified by PCR using pFA6a-VN-KlURA3 as a template, and the "universal" F2CORE and R1CORE primers. The obtained DNA cassette was transformed into ~6,000 yeast strains from the TAP-tagged collection (Ghaemmaghami et al., 2003). The transformed cells were spread on SC-Ura plates and incubated at 30°C for 3 days. Among several colonies, 10 colonies were picked, streaked on fresh SC-Ura plates, and incubated at 30°C for 24 hours. To check correct switching to the VN tag, cells grown on SC-Ura plates were replica-plated onto SC-His plates. Cells also growing on SC-His plates were discarded.

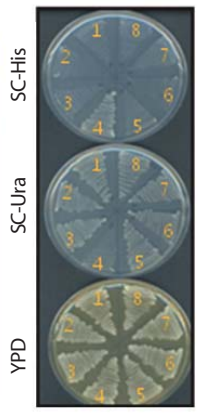


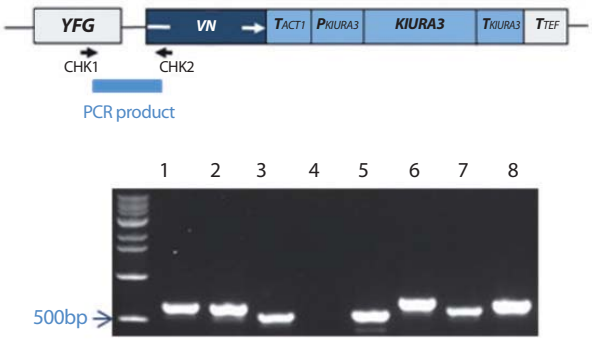
■ Validation of *S. cerevisiae* VN-Fusion

- Medium selection/Counter-selection & Check PCR:

To confirm that the TAP tag was successfully switched to the VN tag, the colonies selected by SC-Ura medium were checked by the colony PCR method using CHK1 and CHK2 primers.

No.	ORF
1	YIL095W
2	YBR276C
3	YLR182W
4	YBR198C
5	YOR133W
6	YKR079C
7	YMR102C
8	YDR251W





<Medium selection/Counter-selection> <Check PCR>

[Results: *S. cerevisiae* VN-Fusion strains- 1, 2, 3, 5, 6, 7, 8 / TAP-fusion strain-4]

S. cerevisiae VN-Fusion Library

■ Experimental Data

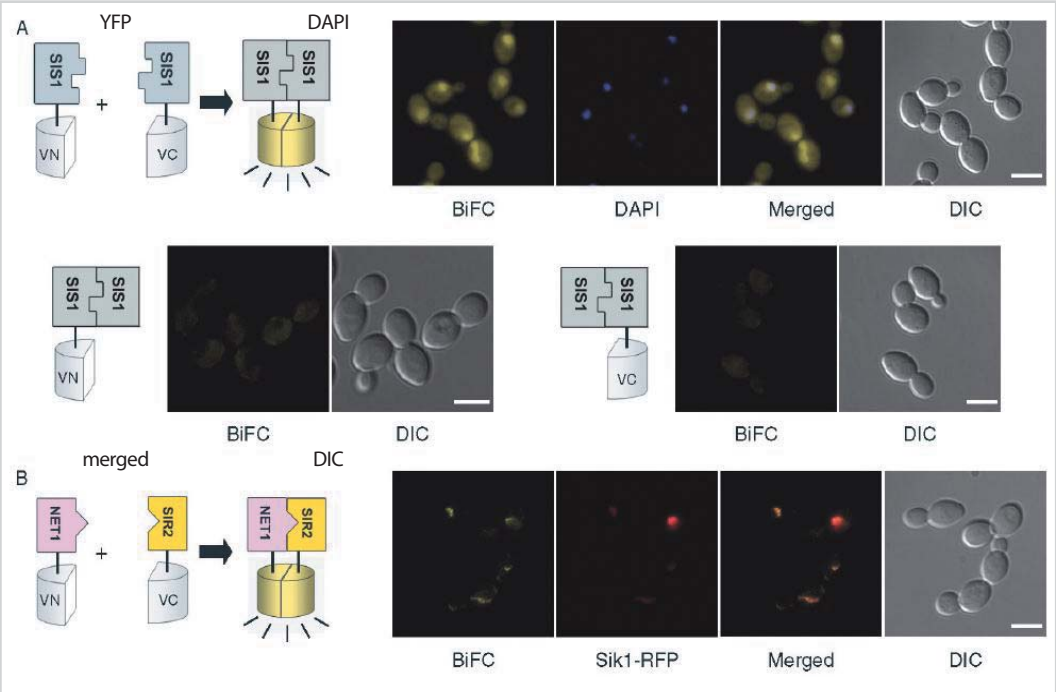


Figure 1. Visualization of subcellular localization of protein–protein interaction (Yeast 2007; 24: 767–775.)
- Sis1 is a Type II HSP40 co-chaperone that interacts with the HSP70 protein Ssa1 (Luke et al., 1991).
The BiFC signal was clearly detected in the nucleus and the cytoplasm, indicating that the VN-tagged Sis1 interacted with the VC-tagged Sis1 in the nucleus and the cytoplasm, where Sis1 is reported to be localized to (Huh et al., 2003).

02
S. cerevisiae
VN-Fusion Library

S. cerevisiae VN-Fusion Library

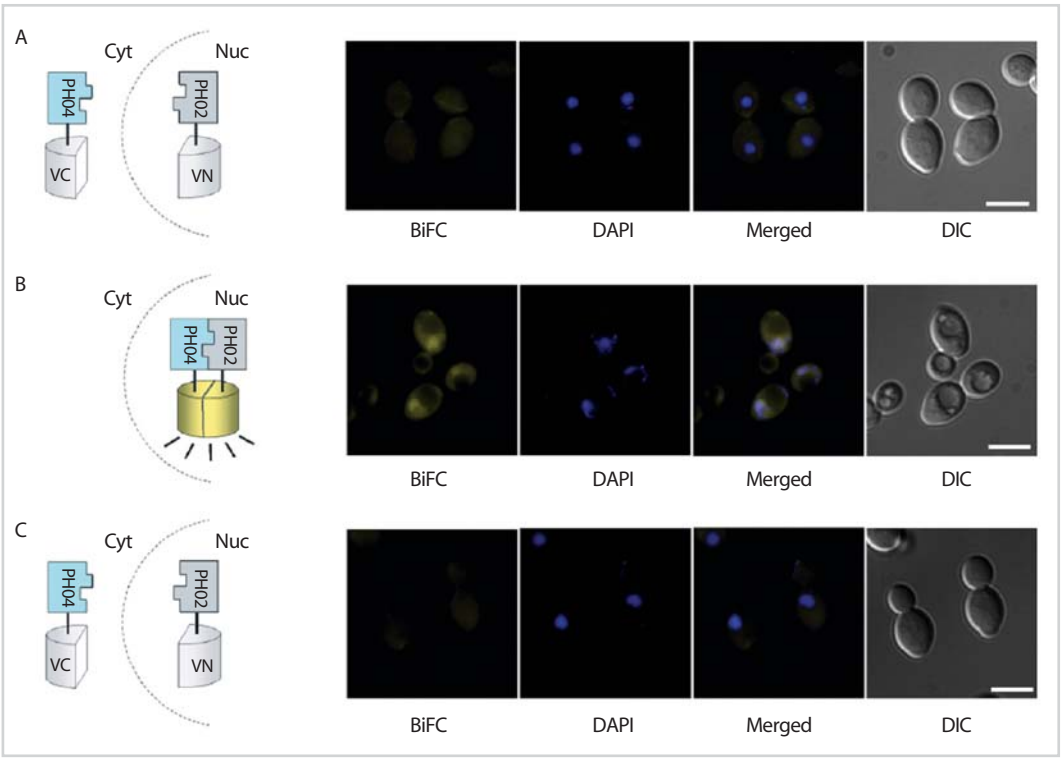


Figure 2. Visualization of induced protein–protein interaction (Yeast 2007; 24: 767–775.)

- Pho2, Pho4: transcription factors involved in phosphate metabolism

(A) In medium containing a high concentration of phosphate: did not show any BiFC signal

(B) Phosphate starvation: detected BiFC signal accumulating in the nucleus (Pho2-Pho4 interaction in the nucleus)

(C) Medium lacking phosphate to medium containing a high concentration of phosphate: the BiFC signal disappeared from the nucleus

■ Ordering & Technical Support

For more information or technical assistance, contact us via phone (+82-42-930-8777), fax (+82-42-930-8688) or email (vn-support@bioneer.com). Additional international offices are listed on our web page (www.bioneer.com).

S. cerevisiae Individual VN-Fusion Strains

■ Description

Protein-protein interaction is a fundamental mechanism for integrating cellular signals and generating the regulatory specificity of cellular processes. BiFC assay is used to analyze protein-protein interaction in living cells. Bioneer provides the *S. cerevisiae* Individual VN-Fusion Strains for BiFC analysis.

■ Features and Benefits

- Non-invasive method for analyzing fluorescence without the need for any external cofactors or cell lysis
- Clear visualization of subcellular protein-protein interaction localization (formation of a fluorescent complex)
- Strong signal and direct readout measurable with relatively simple equipment (using a fluorescence microscope)
- Genome-wide high-throughput screening is possible (93% yeast proteome coverage)
- Unknown protein function analysis through functional complementation is possible
- Analysis of proteinylation (ubiquitination, sumoylation, neddylation…) is possible

■ Application

- The field of basic biological research
  - Identification of binding proteins, investigation of novel functional roles of proteins, global dynamic analysis of protein-protein interaction under the various conditions, and creating database for post-translational modifications information of proteins under the various conditions
- The field of basic Medicine and Pharmacy
  - Drug discovery, target validation, genome-wide high-throughput screening, pathway mapping, drug mechanism-of-action studies, and diagnostics

■ Specifications

- Contents

Individual strain in 2.0 ml tube	1 tube
Strain information sheet	1 copy

- Products information

- Agar Type

The individual strain is supplied in a 2.0 ml tube containing 1 ml YPD agar medium. The strain in agar type is shipped at room temperature and is viable up to 2 weeks when stored at 4°C.

- Glycerol Type

The individual strain is supplied in a 2.0 ml tube containing 0.5 ml YPD / 25% glycerol media. The strain in glycerol type is shipped on dry ice and can be stored at -70 °C over 2 years. Dry ice shipping and handling charge will be added.

■ Ordering Information

Cat. No.	Product Description	Ship Format
V-1010VN-A	*S. cerevisiae* Individual VN-Fusion Strain, Agar	Agar
V-1010VN-G	*S. cerevisiae* Individual VN-Fusion Strain, Glycerol	Glycerol

02
S. cerevisiae
VN-Fusion Library

S. cerevisiae VN-Fusion Set

Description

Protein-protein interaction is a fundamental mechanism for integrating cellular signals and generating the regulatory specificity of cellular processes. BiFC assay is used to analyze protein-protein interaction in living cells. Bioneer provides the *S. cerevisiae* VN-Fusion Set for BiFC analysis. The *S. cerevisiae* VN-Fusion Library consists of 5,809 VN-tagged Open Reading Frames (ORFs) covering 93% of the yeast proteome.

Features and Benefits

- Non-invasive method for analyzing fluorescence without the need for any external cofactors or cell lysis.
- Clear visualization of subcellular protein-protein interaction localization (formation of a fluorescent complex).
- Strong signal and direct readout measurable with relatively simple equipment (using a fluorescence microscope).
- Genome-wide high-throughput screening is possible (93% yeast proteome coverage).
- Unknown protein function analysis through functional complementation is possible.
- Analysis of proteinylation (ubiquitination, sumoylation, neddylation…) is possible.

Application

- The field of basic biological research.
  - Identification of binding proteins, investigation of novel functional roles of proteins, global dynamic analysis of protein-protein interaction under the various conditions, and creating database for post-translational modifications information of proteins under the various conditions.
- The field of basic Medicine and Pharmacy.
  - Drug discovery, target validation, genome-wide high-throughput screening, pathway mapping, drug mechanism of action studies, and diagnostics.

Specifications

- Contents

5,809 strains supplied in 96-well plate	63 plates total
List of strains on CD	1 copy
Product manual	1 copy

- Storage

The *S. cerevisiae* VN-Fusion Set is supplied in 96-well plate format containing 100 µl YPD medium with 25% glycerol. Store the plates at -70 °C.

Ordering Information

Cat. No.	Product Description	Quantity
V-1030VN	*S. cerevisiae* VN-Fusion Set (5,809 strains)	63 plates (96-well)

AccuOligo® S. cerevisiae Validation Primer Set

Description

Bioneer provides the primer set for *S. cerevisiae* VN-Fusion Library validation.

Features and Benefits

- **QC:** All the manufactured oligos are checked by MALDI-TOF mass spec.
- **High purity**: applying Bio-RP purification system impurities, especially (N-1) mer, can be removed very efficiently.

Specifications

- Contents

AccuOligo® primers in 96-well plate	63 plates total
List of primers on CD	1 copy
Product manual	1 copy

- Primer sequences:

CHK1	gene-specific primer
CHK2	5′-CACCATGGTGGCGATGGATC-3′

- Storage

The validation primer set is lyophilized in 96-well plates and shipped at room temperature. Resuspend each primer in 10 mm Tris buffer (pH 8.0) or distilled H_2O to the concentration of 10 pmol/50 µl. The primer in Tris buffer or dH_2O is stable for one year at -20 ℃.

Experimental Data

No.	ORF
1	YIL095W
2	YBR276C
3	YLR182W
4	YBR198C
5	YOR133W
6	YKR079C
7	YMR102C
8	YDR251W

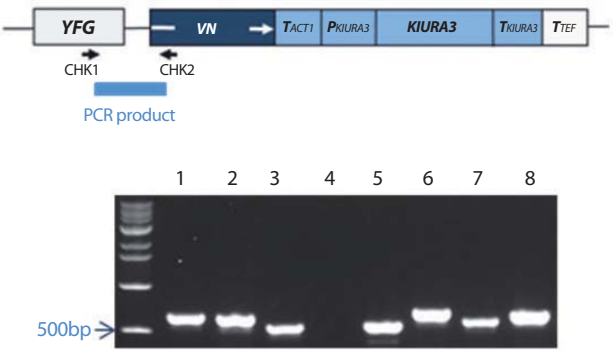


Figure 1. Example of strain verification using *AccuOligo*® *S. cerevisiae* Validation Primer Set

Ordering Information

Cat. No.	Product Description	Quantity
V-1030VN-P	*AccuOligo*® *S. cerevisiae* VN-Fusion Validation Primer Set	63 plates (96-well)

02
S. cerevisiae
VN-Fusion Livrary

S. cerevisiae protein tagging vectors for BiFC analysis

■ Description

S. cerevisiae protein tagging vectors for BiFC analysis are used to create the VN- or VC-fusion proteins. The plasmids contain one of three selectable markers - the kanMX6 module, the His3MX6 module and the *S. cerevisiae* TRP1 gene, for selection with G418, growth media lacking histidine or tryptophan, respectively.

■ Features and Benefits

- Plasmid DNA purified with the *AccuPrep*® Plasmid Extraction Kit (K-3030-1) provides high yields of plasmid DNA.
- The BiFC vector system is useful for the development of a high-throughput platform to study protein-protein interactions in living yeast cells.

■ Specifications

- Contents

Vector	1 tube
Vector information sheet	1 copy

- Storage

The individual vector is supplied in a 2.0 ml tube and shipped at room temperature. The dry vector pellet can be dissolved in Tris buffer (10 mm Tris-HCl, pH 8.0, 1 mm EDTA; C-9005) or distilled H_2O. Store the dissolved vector at -20 ℃.

■ Ordering Information

Cat. No.	Product Description	Quantity
V-1010-V1	pFA6a-VN173-HIS3MX6	5 μg
V-1010-V2	pFA6a-VC155-HIS3MX6	5 μg
V-1010-V3	pFA6a-VN173-TRP1	5 μg
V-1010-V4	pFA6a-VC155-TRP1	5 μg
V-1010-V5	pFA6a-VN173-KanMX6	5 μg
V-1010-V6	pFA6a-VC155-KanMX6	5 μg
V-1010-V7	pFA6a-HIS3MX6-PGAL1-VN173	5 μg
V-1010-V8	pFA6a-HIS3MX6-PGAL1-VC155	5 μg
V-1010-V9	pFA6a-TRP1-PGAL1-VN173	5 μg
V-1010-V10	pFA6a-TRP1-PGAL1-VC155	5 μg
V-1010-V11	pFA6a-KanMX6-PGAL1-VN173	5 μg
V-1010-V12	pFA6a-KanMX6-PGAL1-VC155	5 μg
V-1010-V13	pFA6a-HIS3MX6-PCET1-VN173	5 μg
V-1010-V14	pFA6a-HIS3MX6-PCET1-VC155	5 μg
V-1010-V15	pFA6a-TRP1-PCET1-VN173	5 μg
V-1010-V16	pFA6a-TRP1-PCET1-VC155	5 μg
V-1010-V17	pFA6a-KanMX6-PCET1-VN173	5 μg
V-1010-V18	pFA6a-KanMX6-PCET1-VC155	5 μg

03 Genome-wide DrugTarget Identifiation Service

Genome-wide Drug Target Identifiation Service

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03 Genome-wide Drug Target Identification

Primary Test Service for *GPScreen*™

Description

Primary Test is the first step to determine the biological activity of drugs or drug candidates in *S. pombe*, which is required for the proceeding the following *GPScreen*™ Service.

The following information will be acquired in this step.

1. Solubility of Customer's compounds in cultured solution of *S. pombe*.
2. Determination of Growth-inhibitory activity (GI_{50}) in wild-type *S. pombe*.
   - GI_{50} means the concentration of drugs for 50% inhibition of cell growth.
   - *GPScreen*™ will be performed only to the compounds that show growth-inhibitory activity in wild-type *S. pombe* in this primary activity test.

Experimental Data

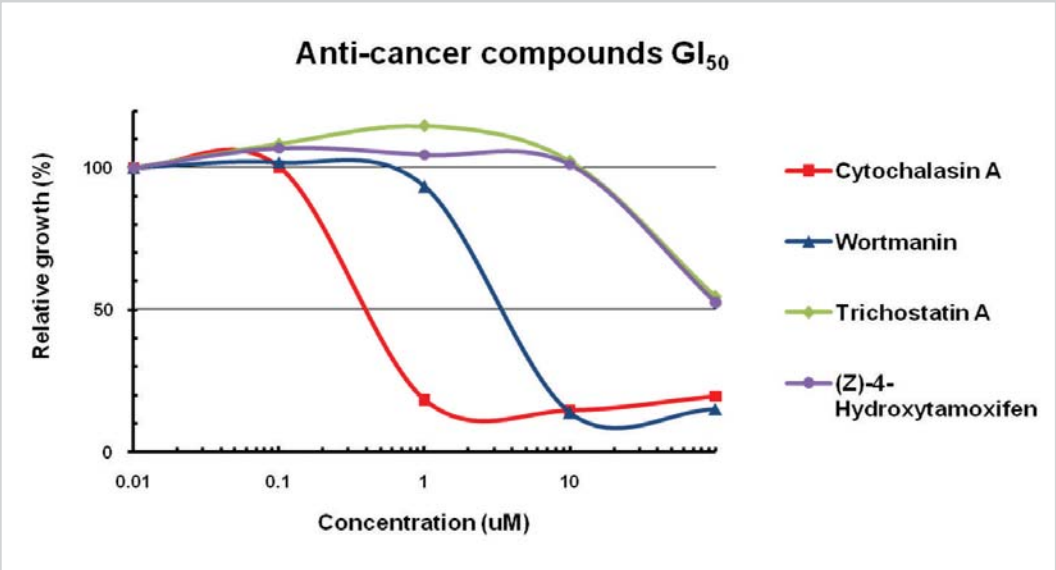


Figure 1. Determination of Growth-Inhibitory Activity (GI_{50}) of customer's compounds

Ordering Information

Cat No.	Product Description	Cell type
GPS-00	Primary Test Service in Wild Type *S. pombe*	SP286 (*S. pombe* wild-type)

- This service takes about 2-3 days.
- The service price may vary depending on the number of your compounds requested.

GPScreen™ Service using *S. pombe* Genome-wide Mutant Set

■ Description

Precise Drug Target Identification is the first step for improving efficacy, tracing and avoiding side-effects as well as understanding the mode-of-actions of drug candidates. However, until now, effective systematic approaches for the precise drug target identification at genome levels have not been commercially available.

GPScreen™ is a genome-wide HTS drug target screening system using drug-induced haploinsufficiency (DIH) in the World's first *S. pombe* genome-wide heterozygous deletion mutant library (http://pombe.bioneer.com, Nat. Biotech, 28, 617–623 (2010)). Fission yeast S. pombe is considered a superior model organism of mammalian cells as its cell division pattern is similar to that of mammalian cells.

Bioneer's *GPScreen*™ Custom Service analyzes the drug effects on 4840 genes individually, which covers almost 98% of genome of *S. pombe*, thereby providing a systemic screening solution for drug target identification of drug candidates which would accommodate customer's drug discovery and development in a quick and cost effective way.

More detailed information is described in the following website; http://eng.bioneer.com/products/GPScreen/GPScreen-overview.aspx.

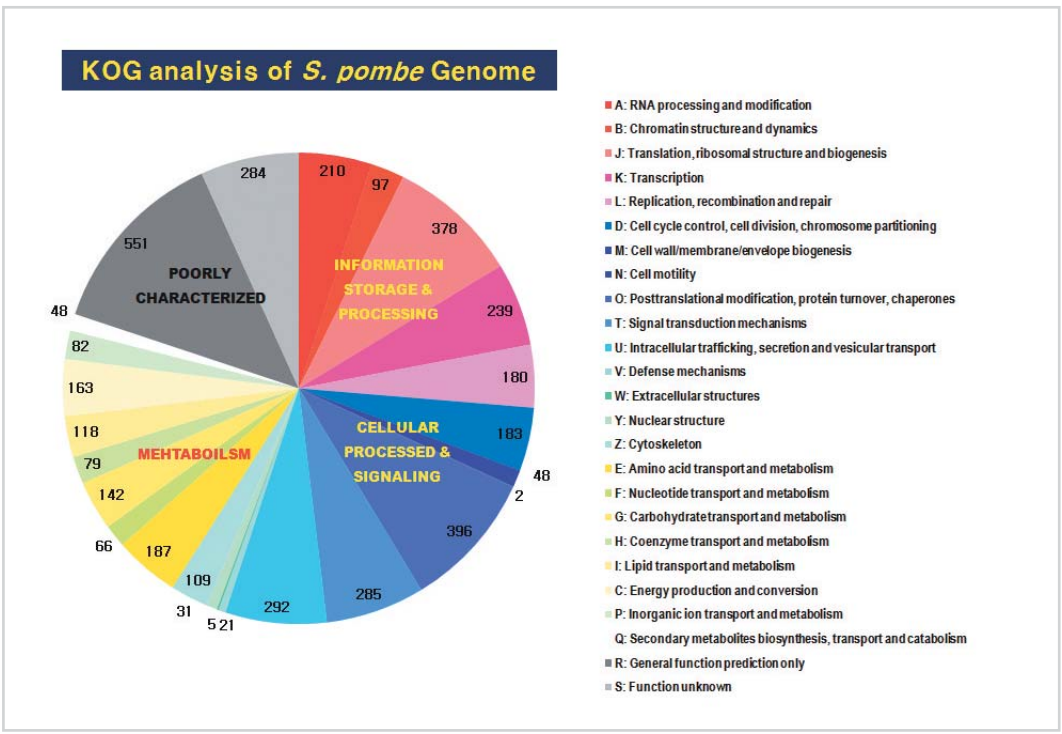


Figure 2. Schematic Diagram of *GPScreen*™ Custom Service

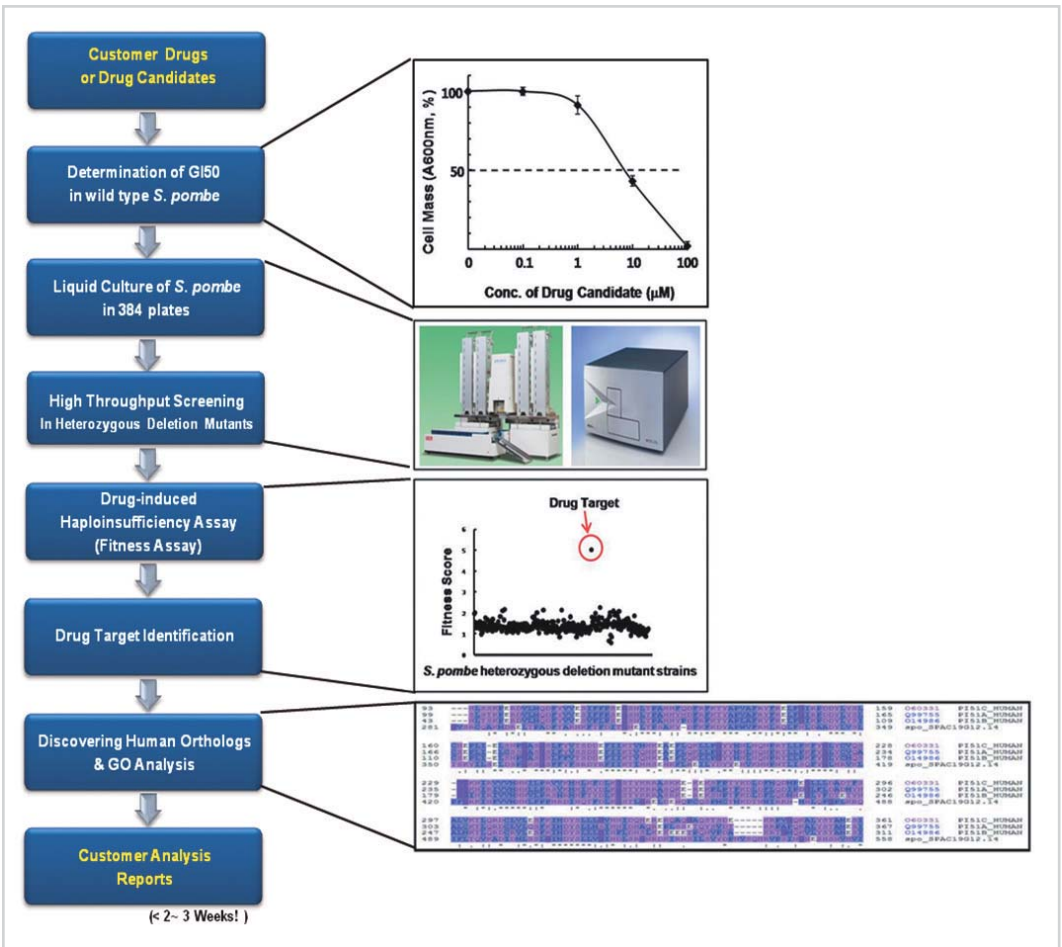
03
Genome-wide Drug Target Identification

GPScreen™ Service using *S. pombe* Genome-wide Mutant Set

Applications

- Drug repositioning; New drug target discovery of known compounds.
- Natural drug target identification.
- Mode-of-action.
- Comparison of compounds with similar modes of action.
- Evaluation of side effects.

Procedure



GPScreen™ Service using *S. pombe* Genome-wide Mutant Set

■ Experimental Data

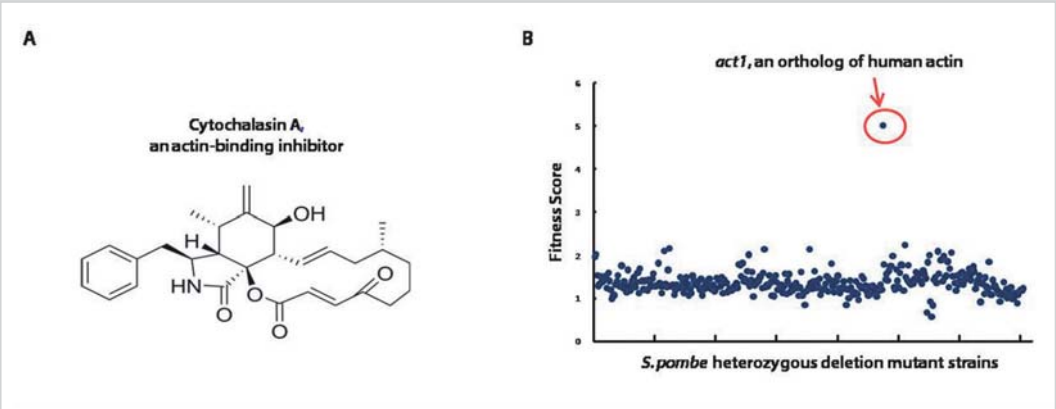


Figure 3. Drug Target Identification of cytochalasin A using *GPScreen*™

In the presence of cytochalasin A, a heterozygous deletion mutant of act1 shows decreased growth as a result of a decrease in "functional" Act1 protein. was the only gene in the genome-wide screen to show this effect, demonstrating that act1 is a target of cytochalasin A.

■ Ordering Information

GPScreen™ Service using *S. pombe* Genome-wide Mutant Set

Cat No.	Full Screening Service	No. of genes
GPS-01-GW	*S. pombe* Genome-wide Heterozygous Deletion Mutant Screening Service	4,840

GPScreen™ Service using *S. pombe* Essential gene Mutant Set

Cat No.	Essential Gene Screening Service	No. of genes
GPS-02-ESS	*S. pombe* Essential Gene Heterozygous Deletion Mutant Screening Service	1,259

GPScreen™ Service using KOG analysis-based Functional Group Subsets

Cat No.	Functional Group-based Subset Services	No. of genes
INFORMATION STORAGE AND PROCESSING		
GPS-03K-A	A: RNA processing and modification Screening Service	210
GPS-03K-B	B: Chromatin structure and dynamics Screening Service	97
GPS-03K-J	J: Translation, ribosomal structure and biosis Screening Service	378
GPS-03K-K	K: Transcription Screening Service	239
GPS-03K-L	L: Replication, recombination and repair Screening Service	180
CELLULAR PROCESSES AND SIGNALING		
GPS-03K-D	D: Cell cycle control, cell division, chromosome partitioning Screening Service	183
GPS-03K-M	M: Cell wall/membrane/envelope biosis Screening Service	48
GPS-03K-N	N: Cell motility Service	2
GPS-03K-O	O: Posttranslational modification, protein turnover, chaperones Screening Service	396

03 Genome-wide Drug Target Identification

GPScreen™ Service using *S. pombe* Genome-wide Mutant Set

GPS-03K-T	T: Signal transduction mechanisms Screening Service	285
GPS-03K-U	U: Intracellular trafficking, secretion, and vesicular transport Screening Service	292
GPS-03K-V	V: Defense mechanisms Screening Service	21
GPS-03K-W	W: Extracellular structures Screening Service	5
GPS-03K-Y	Y: Nuclear structure Screening Service	31
GPS-03K-Z	Z: Cytoskeleton Screening Service	109
METABOLISM		
GPS-03K-E	E: Amino acid transport and metabolism Screening Service	187
GPS-03K-F	F: Nucleotide transport and metabolism Screening Service	66
GPS-03K-G	G: Carbohydrate transport and metabolism Screening Service	142
GPS-03K-H	H: Coenzyme transport and metabolism Screening Service	79
GPS-03K-I	I: Lipid transport and metabolism Screening Service	118
GPS-03K-C	C: Energy production and conversion Screening Service	163
GPS-03K-P	P: Inorganic ion transport and metabolism Screening Service	82
GPS-03K-Q	Q: Secondary metabolites biosynthesis, transport and catabolism Screening Service	48
POORLY CHARACTERIZED		
GPS-03K-R	R: General function prediction only Screening Service	551
GPS-03K-S	S: Function unknown Screening Service	284

GPScreen™ Service using Human Disease-related Subsets

Cat. No.	Human Diseaes-related Subset Services	No. of genes
GPS-04H-A	Cell Cycle Regulator Screening Service	321
GPS-04H-B	DNA Damage Repair Screening Service	376
GPS-04H-C	Cytokinesis Screening Service	124
GPS-04H-D	Chromatin Remodeling Screening Service	257
GPS-04H-E	Histone Modification Screening Service	63
GPS-04H-F	Protein Kinase Screening Service	223
GPS-04H-G	GTPase Proteins Screening Service	90
GPS-04H-H	ABC Transporter Screening Service	31
GPS-04H-I	Transcription Factor Screening Service	362
GPS-04H-J	Neurological Disease Screening Service	19

■ Contact Us

Please let us (gpscreen@bioneer.com) know the details about your compounds/ candidate drugs, so that we can provide you with a more accurate quotations and timeline estimate. The service price may vary depending on the number of your compounds requested.