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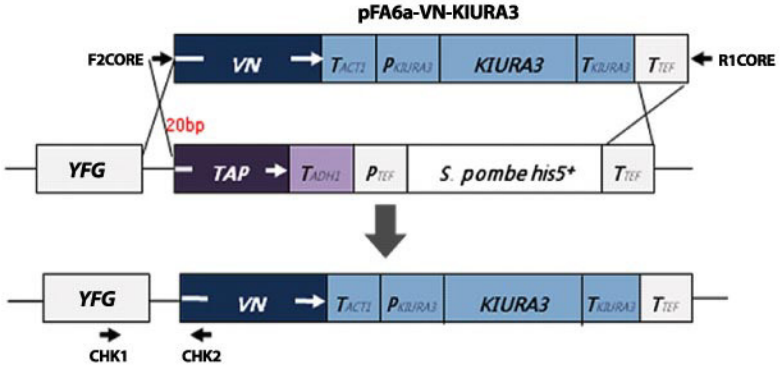
S. cerevisiae VN-Fusion Library

The yeast *saccharomyces cerevisiae* is now recognized as a model system representing a simple eukaryote whose genome can be easily manipulated. The *S. cerevisiae* VN-Fusion Library was created by Dr. Won-Ki Huh at Seoul National University (School of Biological Sciences, Korea). The VN-Fusion Library consists of 5,809 VN-tagged Open Reading Frames (ORFs) covering 93% of the yeast proteome.

Most biological processes are carried out and regulated by dynamic networks of protein-protein interactions. The bimolecular fluorescence complementation (BiFC) assay is now regarded as one of the most advanced and powerful tools for studying *in vivo* detection of 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.



***S. cerevisiae* VN-Fusion Library Specification**	
No. of strains	5,809 strains
Selection Marker	KIURA3
Genotype	All *S. cerevisiae* VN-Fusion strains were derived from BY4741 *(MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0)*
	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 ℃ (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)

Features and Benefits

- A powerful tool for studying protein-protein interactions in living cells
  (Non-invasive method for analyzing fluorescence without the need for any external cofactors)
- Clear visualization of subcellular protein-protein interaction localization
  (Formation of a fluorescent complex)
- Stronger signal and direct readout measurable with relatively simple equipment
  (Using a fluorescence microscope)
- Genome-wide high-throughput screening possible
  (93% yeast proteome coverage)
- Unknown protein function analysis through functional complementation is possible
- Analysis of proteinylation (ubiquitination, sumoylation, neddylation) is possible

Product Lists

Cat. No.	Product	Details	Contents
S. cerevisiae VN-Fusion Library			
V-1010VN-A	_S. cerevisiae_ VN-Fusion Individual Strains	Agar Type	Individual strain Strain information sheet
V-1010VN-G	_S. cerevisiae_ VN-Fusion Individual Strains	Glycerol Type	
V-1030VN	_S. cerevisiae_ VN-Fusion Set (5,809 strains)	63 plates (96-well) Glycerol Type	5,809 strains supplied in 96-well plate List of strains on CD Product manual
Validation Primer			
V-1030VN-P	_AccuOligo®_ _S. cerevisiae_ VN-Fusion Validation Primer Set	63 plates (96-well)	Primers in 96-well plate (1 nmole) List of Primer on CD Product manual
Yeast protein tagging vectors for BiFC analysis			
V-1010-V1	pFA6a-VN173-HIS3MX6	5 ug	Vector Vector information sheet
V-1010-V2	pFA6a-VC155-HIS3MX6	5 ug	
V-1010-V3	pFA6a-VN173-TRP1	5 ug	
V-1010-V4	pFA6a-VC155-TRP1	5 ug	
V-1010-V5	pFA6a-VN173-KanMX6	5 ug	
V-1010-V6	pFA6a-VC155-KanMX6	5 ug	
V-1010-V7	pFA6a-HIS3MX6-PGAL1-VN173	5 ug	
V-1010-V8	pFA6a-HIS3MX6-PGAL1-VC155	5 ug	
V-1010-V9	pFA6a-TRP1-PGAL1-VN173	5 ug	
V-1010-V10	pFA6a-TRP1-PGAL1-VC155	5 ug	
V-1010-V11	pFA6a-KanMX6-PGAL1-VN173	5 ug	
V-1010-V12	pFA6a-KanMX6-PGAL1-VC155	5 ug	
V-1010-V13	pFA6a-HIS3MX6-PCET1-VN173	5 ug	
V-1010-V14	pFA6a-HIS3MX6-PCET1-VC155	5 ug	
V-1010-V15	pFA6a-TRP1-PCET1-VN173	5 ug	
V-1010-V16	pFA6a-TRP1-PCET1-VC155	5 ug	
V-1010-V17	pFA6a-KanMX6-PCET1-VN173	5 ug	
V-1010-V18	pFA6a-KanMX6-PCET1-VC155	5 ug	

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