Table S6: GO pathway enrichment of significantly rewired CRE combinations (p<0.01)

CRE			
Pair	C agravisia a Dathyyay	Concerned Dethyvey	S. hayanya Dothyyoy
	S. cerevisiae Pathway	Conserved Pathway	S. bayanus Pathway
ABF1x	poly(A)+ mRNA export	protein O-linked	
HAC1	from nucleus	glycosylation	isoprenoid biosynthetic process
A DE1		proteasomal ubiquitin-	
ABF1x		dependent protein catabolic	
RPN4		process	chromatin silencing
ABF1x			mitotic spindle organization in
STB1		spindle pole body separation	nucleus
AFT2x	nitrogen catabolite		
CAT8	activation of transcription		activation of Rab GTPase activity
AFT2x			positive regulation of translational
MIG1	histone demethylation	oxidation-reduction process	elongation
AFT2x		positive regulation of	
ZMS1	histone demethylation	translational elongation	leukotriene biosynthetic process
	negative regulation of		
ARG80x	actin filament		
GCN4	polymerization	arginine biosynthetic process	lysine biosynthetic process
CAT8x	phenylalanyl-tRNA	ATP synthesis coupled proton	regulation of ergosterol biosynthetic
UME6	aminoacylation	transport	process
CBF1x	cysteine biosynthetic	glutathione biosynthetic	
CRZ1	process via cystathionine	process	ammonium transport
CBF1x	regulation of nitrogen	ER-associated protein	positive regulation of translational
PHD1	utilization	catabolic process	elongation
CRZ1x		•	
STP1	thiamine transport		uridine transport
CRZ1x	nitrogen catabolite		
SUT1	activation of transcription	tricarboxylic acid cycle	cellular response to hypoxia
CRZ1x	cysteine biosynthetic	, , ,	
TYE7	process via cystathionine		telomere maintenance via telomerase
DAL80xG	gamma-aminobutyric acid	nitrogen catabolite repression	
AT1	transport	of transcription	leucine biosynthetic process
DAL80xG	gamma-aminobutyric acid	nitrogen catabolite repression	
LN3	transport	of transcription	leucine biosynthetic process
DAL80xG	gamma-aminobutyric acid	nitrogen catabolite repression	
ZF3	transport	of transcription	adenine catabolic process
DAL82xP	rRNA pseudouridine	or wantsorie won	musimis sumsome process
HD1	synthesis		lagging strand elongation
EDS1x	positive regulation of	tRNA-type intron splice site	
MBP1	histone acetylation	recognition and cleavage	glycolysis
EDS1x	box H/ACA snoRNP	ribosomal large subunit	8-yxyx
PBF2	assembly	biogenesis	rRNA processing
FKH1x	premeiotic DNA	orogeneous	Tit it processing
STB1	replication		cellular response to heat
FKH1x	premeiotic DNA	mitotic chromosome	conditi response to neut
SWI4	replication	condensation	telomere capping
FKH1x	premeiotic DNA	mitotic chromosome	teromere cupping
SWI6	replication	condensation	telomere capping
2 1/10	replication	Condensation	teromere capping

FKH2x	premeiotic DNA	mitotic chromosome	
STB1	replication	condensation	telomere capping
FKH2x	premeiotic DNA	mitotic chromosome	telomere capping
SWI4	_ _		4-1
FKH2x	replication premeiotic DNA	condensation	telomere capping
	1 1	mitotic chromosome	4-1
SWI6	replication	condensation	telomere capping
GIS1x	protein	1 1 1 1 1	
MIG3	monoubiquitination	glycogen biosynthetic process	energy reserve metabolic process
GIS1x	regulation of translational		negative regulation of sphingolipid
RDS2	fidelity		biosynthetic process
GIS1x			regulation of fungal-type cell wall
STP1	uridine transport	TOR signaling cascade	1,3-alpha-glucan biosynthetic process
GIS1x			
SUT1	uridine transport	glycogen biosynthetic process	thiamine transport
		dolichol-linked	
HAC1x	proline biosynthetic	oligosaccharide biosynthetic	protein import into peroxisome
SWI6	process	process	matrix, receptor recycling
HAP2x	mitochondrial magnesium		
RSC3	ion transport	heme transport	uridine transport
MBP1x	tryptophan biosynthetic		
REB1	process	chitin biosynthetic process	nucleotide-sugar transport
	regulation of	negative regulation of	
	establishment or	ubiquitin-protein ligase	
MBP1x	maintenance of cell	activity involved in mitotic	
STB1	polarity	cell cycle	DNA repair
		negative regulation of	_
		ubiquitin-protein ligase	
MDD1		activity involved in mitotic	
MBP1x	post-Golgi vesicle-	activity involved in initotic	
MBP1x SWI6	post-Golgi vesicle- mediated transport		GDP-mannose biosynthetic process
	mediated transport threonine biosynthetic	cell cycle glutathione biosynthetic	GDP-mannose biosynthetic process
SWI6	mediated transport	cell cycle	GDP-mannose biosynthetic process drug transmembrane transport
SWI6 MET32xP	mediated transport threonine biosynthetic	cell cycle glutathione biosynthetic	
SWI6 MET32xP HO4	mediated transport threonine biosynthetic process	cell cycle glutathione biosynthetic process sporulation resulting in	drug transmembrane transport
SWI6 MET32xP HO4 MIG1x	mediated transport threonine biosynthetic process disaccharide catabolic	cell cycle glutathione biosynthetic process sporulation resulting in formation of a cellular spore	
SWI6 MET32xP HO4 MIG1x PDR1	mediated transport threonine biosynthetic process disaccharide catabolic process	cell cycle glutathione biosynthetic process sporulation resulting in formation of a cellular spore nucleotide-excision repair,	drug transmembrane transport
SWI6 MET32xP HO4 MIG1x PDR1 MIG1x RCS1	mediated transport threonine biosynthetic process disaccharide catabolic	cell cycle glutathione biosynthetic process sporulation resulting in formation of a cellular spore	drug transmembrane transport
SWI6 MET32xP HO4 MIG1x PDR1 MIG1x RCS1 MIG1x	mediated transport threonine biosynthetic process disaccharide catabolic process histone demethylation	cell cycle glutathione biosynthetic process sporulation resulting in formation of a cellular spore nucleotide-excision repair, DNA incision, 3'-to lesion	drug transmembrane transport
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SWI6 MET32xP HO4 MIG1x PDR1 MIG1x RCS1 MIG1x STP1 MIG1x	mediated transport threonine biosynthetic process disaccharide catabolic process histone demethylation cellular respiration	cell cycle glutathione biosynthetic process sporulation resulting in formation of a cellular spore nucleotide-excision repair, DNA incision, 3'-to lesion	drug transmembrane transport glycolysis
SWI6 MET32xP HO4 MIG1x PDR1 MIG1x RCS1 MIG1x STP1 MIG1x STP2	mediated transport threonine biosynthetic process disaccharide catabolic process histone demethylation	cell cycle glutathione biosynthetic process sporulation resulting in formation of a cellular spore nucleotide-excision repair, DNA incision, 3'-to lesion	drug transmembrane transport
SWI6 MET32xP HO4 MIG1x PDR1 MIG1x RCS1 MIG1x STP1 MIG1x STP2 MIG1x	mediated transport threonine biosynthetic process disaccharide catabolic process histone demethylation cellular respiration	cell cycle glutathione biosynthetic process sporulation resulting in formation of a cellular spore nucleotide-excision repair, DNA incision, 3'-to lesion acetyl-CoA catabolic process	drug transmembrane transport glycolysis inositol biosynthetic process
SWI6 MET32xP HO4 MIG1x PDR1 MIG1x RCS1 MIG1x STP1 MIG1x STP2 MIG1x UME6	mediated transport threonine biosynthetic process disaccharide catabolic process histone demethylation cellular respiration cellular respiration	cell cycle glutathione biosynthetic process sporulation resulting in formation of a cellular spore nucleotide-excision repair, DNA incision, 3'-to lesion	drug transmembrane transport glycolysis
SWI6 MET32xP HO4 MIG1x PDR1 MIG1x RCS1 MIG1x STP1 MIG1x STP2 MIG1x UME6 MIG3x	mediated transport threonine biosynthetic process disaccharide catabolic process histone demethylation cellular respiration cellular respiration vacuole inheritance UDP-glucose metabolic	cell cycle glutathione biosynthetic process sporulation resulting in formation of a cellular spore nucleotide-excision repair, DNA incision, 3'-to lesion acetyl-CoA catabolic process acetyl-CoA catabolic process	drug transmembrane transport glycolysis inositol biosynthetic process hydrogen peroxide catabolic process
SWI6 MET32xP HO4 MIG1x PDR1 MIG1x RCS1 MIG1x STP1 MIG1x STP2 MIG1x UME6 MIG3x MSN4	mediated transport threonine biosynthetic process disaccharide catabolic process histone demethylation cellular respiration cellular respiration vacuole inheritance UDP-glucose metabolic process	cell cycle glutathione biosynthetic process sporulation resulting in formation of a cellular spore nucleotide-excision repair, DNA incision, 3'-to lesion acetyl-CoA catabolic process	drug transmembrane transport glycolysis inositol biosynthetic process
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ZMS1	MIG3x	protein		
MSN2x Process proces			glycogen biosynthetic process	
MSN2x				
MSN2x				cell shape checkpoint
Materials Mate		1	•	
PHDIX PHO4 Phosphate transport diadenosine polyphosphate catabolic process mitochondrial electron transport, ubiquinol to eytochrome c mitochondrial fusion polyphosphate catabolic process process polyphosphate catabolic process pr			tricarboxylic acid cycle	1 1 7
PHO4 phosphate transport tricarboxylic acid cycle clongation mitochondrial electron transport, ubiquinol to cytochrome c mitochondrial fusion mi		1		
diadenosine mitochondrial electron transport, ubiquinol to cytochrome c mitochondrial fusion megative regulation of transcription megative regulation of ell ubiquitin-process mitochondrial fusion mitochondrial fus		phosphate transport	tricarboxylic acid cycle	
SUT1 process cytochrome c mitochondrial fusion				
SUT1 process cytochrome c mitochondrial fusion	PHD1x	polyphosphate catabolic	transport, ubiquinol to	
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