Table 2. List of gene-pair characteristics

short name of characteristic (description)	**# gene pairs with characteristic**
2h H-S (2h Homology BLAST E < e-3 - SSL)	120614
2h P-S (2h Physical interaction - SSL)	30340
2h S-S (2h SSL - SSL)	90799
2h S-X (2h mRNA expression correlation coefficent >0.7 - SSL)	332829
2h H-H (2h Homology BLAST E < e-3 - Homology BLAST E < e-3)	521210
2h H-P (2h Homology BLAST E < e-3 - Physical interaction)	207820
2h H-R (2h Homology BLAST E < e-3 - Common upstream regulator p-value <= 0.001)	1862552
2h H-X (2h Homology BLAST E < e-3 - mRNA expression correlation coefficent >0.7)	2303659
2h P-P (2h Physical interation - Physical interaction)	96511
2h P-R (2h Physical interaction - Common upstream regulator p-value <= 0.001)	739278
2h X-X (2h Common upstream regulator p-value <= 0.001 - Common upstream regulator p-value <= 0.001)	1897278
physical (physical interaction)	109433
stable (stable physical complex)	42391
TAP (TAP matrix interaction detected by Gavin et al)	17314
TAP-Gavin-all (TAP matrix interaction detected by Gavin et al)	17314
TAP-Gavin-spoke (TAP spoke interaction detected by Gavin et al)	3225
TAP-Gavin-matrix (TAP matrix interaction detected by Gavin et al)	17314
HMS-PCI (HMS-PCI matrix interaction detected by Ho et al)	26649
HMS-PCI (HMS-PCI matrix interaction detected by Ho et al)	26649
HMS-PCI-spoke (HMS-PCI spoke interaction detected by Ho et al)	3618
HMS-PCI-matrix (HMS-PCI matrix interaction detected by Ho et al)	26649
binary interaction (yeast-two-hybrid interaction)	5126
two-hybrid (yeast-two-hybrid interaction)	5126
YTH-Ito (yeast-two-hybrid interaction detected by Ito et al)	4393
YTH-Ito1 (Ito1 yeast-two-hybrid interaction detected by Ito et al)	4393
YTH-Ito2 (Ito2 yeast-two-hybrid interaction detected by Ito et al)	1417
YTH-Ito3 (Ito3 yeast-two-hybrid interaction detected by Ito et al)	754
YTH-Uetz (yeast-two-hybrid interaction detected by Uetz et al)	905
YTH-UI3 (combination of yeast-two-hybrid interaction detected by Uetz or Ito3)	1536
MIPS complex (same MIPS complex)	64792
MIPS sub-complex (same MIPS sub-complex)	8707
MIPS complex (same MIPS complex)	64792
phys-IUGH (Ito3, Uetz, TAP-spoke, HMS-PCI-spoke interaction)	8044
mRNA coexpression (correlated mRNA expression) {cc}	374822
Affymetrix (Affymetrix mRNA expression correlation coefficent >0.7 or < -0.7)	294416
Cell cycle (cell cycle mRNA expression correlation coefficent >0.7 or < -0.7)	294416
cc >0.9 (cell cycle mRNA expression correlation coefficent >0.9)	2381
cc >0.8 (cell cycle mRNA expression correlation coefficent >0.8)	53426
cc >0.7 (cell cycle mRNA expression correlation coefficent >0.7)	221757
cc <-0.7 (cell cycle mRNA expression correlation coefficent < -0.7)	72669
cc <-0.8 (cell cycle mRNA expression correlation coefficent < -0.8)	5632
cc <-0.9 (cell cycle mRNA expression correlation coefficent < -0.9)	6
cDNA microarray (cDNAarray mRNA expression correlation coefficent >0.6 or < -0.6)	84873
Rosetta (Rosetta mRNA expression correlation coefficent >0.6 or < -0.6)	84873
cc >0.9 (Rosetta mRNA expression correlation coefficent >0.9)	304
cc >0.8 (Rosetta mRNA expression correlation coefficent >0.8)	4714
cc >0.7 (Rosetta mRNA expression correlation coefficent >0.7)	20071
cc >0.6 (Rosetta mRNA expression correlation coefficent >0.6)	57367
cc <-0.6 (Rosetta mRNA expression correlation coefficent < -0.6)	27506
cc <-0.7 (Rosetta mRNA expression correlation coefficent < -0.7)	10833
cc <-0.8 (Rosetta mRNA expression correlation coefficent < -0.8)	2467
cc <-0.9 (Rosetta mRNA expression correlation coefficent < -0.9)	19
homology e<-3 (sequence homology BLAST E <e-3)	40438
homology e<-3 (sequence homology BLAST E <e-3)	40438
homology e<-6 (sequence homology BLAST E <e-6)	22170

homology e<-12 (sequence homology BLAST E <e-12)	13182
C: same localization (same subcellular localization)	50009
C: extracellular	171
C: cell wall	741
C: plasma membrane	12561
C: cytoplasm	175528
C: cytoskeleton	6555
C: actin cytoskeleton	666
C: tubulin cytoskeleton	253
C: spindle pole body	630
C: intermediate filaments	3
C: ER	13031
C: ER membrane	6903
C: ER lumen	36
C: golgi	3486
C: golgi membrane	1596
C: transport vesicles	1225
C: ER-golgi transport vesicles	55
C: golgi-ER transport vesicles	55
C: inter-golgi transport vesicles	1
C: golgi-plasma membrane transport vesicles	6
C: golgi-vacuole transport vesicles	36
C: endocytotic transport vesicles	6
C: nucleus	349030
C: nuclear envelope	990
C: nuclear matrix	595
C: nucleolus	1225
C: nuclear pore	465
C: chromosome structure	253
C: mitochondria	71631
C: mitochondrial outer membrane	153
C: mitochondrial intermembrane space	28
C: mitochondrial inner membrane	6105
C: mitochondrial matrix	1035
C: peroxisome	780
C: peroxisomal membrane	136
C: peroxisomal matrix	171
C: endosome	55
C: vacuole	1431
C: vacuolar membrane	741
C: vacuolar lumen	15
C: microsomes	3
C: lipid particles	6
function (same MIPS function)	229775
phenotype (same phenotype)	74660
protein class (same MIPS protein class)	53038
predicted complex (same predicted physical complex)	37861
com reg <= 0.01 (common upstream regulator p-value <= 0.01)	896504
com reg <= 0.01 (commmon upstream regulator p-value <= 0.01)	896504
com reg <= 0.005 (commmon upstream regulator p-value <= 0.005)	502684
com reg <= 0.001 (commmon upstream regulator p-value <= 0.001)	181767
dist < 7kb (chromosomal distance < 7kb)	26473
dist < 7kb (chromosomal distance < 7kb)	26473
dist < 5kb (chromosomal distance < 5kb)	19838
dist < 3kb (chromosomal distance < 3kb)	13083
dist < 1kb (chromosomal distance < 1kb)	6561
gene fusion	358
conserved gene neighborhood	6387
gene cooccurence	997

MCC >0 (mutual clustering coefficent >0)	126245
Curagen mcc >0 (Curagen mcc >0)	8350
Curagen mcc >= 3 (Curagen mcc >3)	8328
Curagen mcc >= 5 (Curagen mcc >5)	7815
Curagen mcc >= 7 (Curagen mcc >7)	4933
Curagen mcc >= 10 (Curagen mcc >10)	300
UI1 mcc >0 (Uetz + Ito1 mcc >0)	120833
UI1 mcc >= 3 (Uetz + Ito1 mcc >3)	117355
UI1 mcc >= 5 (Uetz + Ito1 mcc >5)	104071
UI1 mcc >= 7 (Uetz + Ito1 mcc >7)	40750
UI1 mcc >= 10 (Uetz + Ito1 mcc >10)	1615
UI3 mcc >0 (Uetz + Ito3 mcc >0)	7815
UI3 mcc >= 3 (Uetz + Ito3 mcc >3)	7514
UI3 mcc >= 5 (Uetz + Ito3 mcc >5)	5412
UI3 mcc >= 7 (Uetz + Ito3 mcc >7)	1411
UI3 mcc >= 10 (Uetz + Ito3 mcc >10)	298
posterior (posterior probability of physical interaction > 0)	9826
post >= 0.7 (posterior probability of physical interaction >= 0.7)	326
post >= 0.5 (posterior probability of phyiscal interaction >= 0.5)	326
post >= 0.3 (posterior probability of phyiscal interaction >= 0.3)	338