

Table S3 Functional enrichment of regulators based on their target genes under rich medium growth conditions

| Cellular process | Number of genes | | mRNA expression significant changed | Regulators involved in the cellular process | P-value |
|--------------------------------------|-----------------|------------------|---|---|---------|
| | In the process | the cell process | | | |
| ^P Amino acid metabolism | 166 | 148 | swi3,cbf1,mga2,taf14,sin4,arg80,snf5,bas1,rsc2,snf2,snf6,rtg3,ric1,arg81,cdc73,sin3,ngg1,leu3,tup1,ume6,pho23,spt20,,aft1,cse2,cst6,sif2, stp1,eds1,srb2,pho2,gcn4,msn4, zap1,ada2,arp8,asf1,bre1,bre2,bur,caf40,ccr4,cdc73,chs1,cti6,ctr9,dls1,dpb4,eaf5,eaf7,gcn5,htz1,ies2, ies3,ies5,ies6,ite1,leo1,lge1,med1,med15,med16,med18,med2,med20, med3,med31,med5,med9,ngg1,nhp10,not3,not4,npl6,paf1,pho23,rad6,rdp3,rsc1,rsc2,rsc30,rtf1,rtg2, rtt106,rxl2,sap30,set1,sgf29,sif2,sin3,snf12,snf2,snf5,snf6,spt3,spt7,spt8, ssn6,swc3,swd3,swi3,vps71,yaf9,bck1delcla4,dun1delpph3, fab1,hal5delsat4,hsl1delcla4,pho85,ptc1,ptc1delpph3,sit4,sky1,snf1,snf1delrim11,vps15,yck3,ypk1,yvh1 | ≤0.01 | |
| ^P Carbohydrate metabolism | 212 | 195 | cbf1,flo8,mga2,,sin4,gal80,arg80,rgm1,wtm2,ssn2,yer184c,snf6,ric1,mbf1,gcr2,sin3,yer130c,tup1,rds1,cst6,gat3,qis1,rox1,sok2,ada2,bur2,cti6,dls1,dpb4,hda1,hda2,hda3, hfi1,htz1,ies2,ies3,ies6,isw1,med1,med15,med2,med3,med9,ngg1,not3,npl6,rsc1,rsc2,rtg2,rtt109,spt20,spt7,ssn6,sus1,swc5,tup1,yaf9,arkdelprk1,cdk8,cka2,dun1,elm1, hsl1delcla4,ire1,mih1delelm1,ptc1,ptc1delpph3,ptc1delptc2,ptp2delptp3,sit4,vps15 | ≤0.01 | |
| ^P Signal transduction | 71 | 52 | dig1,taf14,hat2,cdc73,phd1,esc2,pho23,gln3,rgt1,sds3,aca1,gis2,msn4,skn7,,ste12,stp2,yhp1,ada2,cti6, gcn5,htl1.med16,nph6,sgf29,sir2,sir3,sir4,spt20,spt7,sus1fab1, fus3,fus3delkss1,hog1,kin3,kss1delfus3delhog1,pbs2,pbs2delptk2,ssk2,ste11,ste20,ste7 | ≤0.01 | |
| ^P mating conjugation | 106 | 78 | dig1,sir3,cdc73,phd1,sir2,rgt1,sds3,skn7,ste12,stp2,,yhp1,chs1,cti6,dep1,dpb4,gcn5,htl1, isw2,ite1,ldb7,not4,pho23,rdp3,rxl2,sgf29,sir2,sir3,sir4,snf6,spt20,spt7,ssn6,sus1, tup1,rsc30,rxl2,sap30,sin3,fus3,fus3delkss1,kss1delfus3delhog1,pbs2,pbs2delptk2,ste11,ste20,ste7 | ≤0.05 | |
| cell organization or biogenesis | 210 | 165 | cbf1,set2,hst1,ric1,hog1,rme1,sum1,yhp1,swi4,rco1,crz1,rgm1,sps18,bre1,cac1,chs1,hst1,htl1,lge1,med15,med2,med3,npl6,rfm1,sdc1,set1,sgf73,snt1,sum1, rsc2,asf1, ark1delprk1,bck1,cdk8,fab1,hsl1delcla4,kin3,mih1delelm1,ptc1,ptc1delpph3,ptc1delptc2,ptp2delptp3,sit4,vps15,yck3,ypk1,slt2delptp3.pho85,fus3 | ≤0.05 | |
| ^P Energy metabolism | 139 | 112 | swi3,sin4,snf6,gal11,pgd1,gcr2,ngg1,pho23,stp1,srb2,zap1,bre1,ccr4,dls1,dpb4,eaf1,hfi1,ies5,lge1,med15,med16,med2,med3,med9,ngg1,nhp10,npl6, rtf1,rtg2,rtt109,sgf29,snf12,snf2,snf6,spt20,spt3,spt8,ssn6,swc3,swi3,swr1,wtypdvswt,yaf9,ark1delprk1,hal5delsat4,sit4,sky1,snf1delrim11 | ≤0.01 | |

| | | | | |
|---|-----|-----|--|-------|
| ^P Nucleotide Metabolism | 115 | 83 | rfx1, taf14, bas1, snf2, snf6, ppr1, gln3, cst6, pho2, sfp1, rfx1, ada2, eaf5, nngg1, snt1, swc3, vps72, yaf9, cka1, oca1, siw14, sky1, snf1 delrim11, tup1, sit4, yvh1 | ≤0.05 |
| ^P Lipid Metabolism | 112 | 92 | mga2, opi1, ric1, spt20, aft1, stp3, cdc73, ctr9, dls1, hfi1, ies2, ies6, med15, med2, sgf73, snf12, snf2, snf5, snf6, spt20, spt7, ssn6, tup1, ark1 delprk1, cdk8, ire1, snf5, bur2, swi3 | ≤0.05 |
| Protein folding | 88 | 70 | sin4, snf6, stb1, aft1, cst6, nut1, skn7, bur2, caf130, eaf7, ies2, nhp10, paf1, snt1, chk1, ire1 | ≤0.05 |
| Ribosome biogenesis, organization | 230 | 169 | snf2, snf6, arg81, spt10, spt20, hal9, cst6, ime1, sfp1, gat4, tos8, rtt109, ark1 delprk1, yrr1, rfx1, hfi1, isw2 | ≤0.05 |
| Mitochondrion relations | 337 | 219 | srb8, mal33, stb1, dal82, nut1, thi2, adr1, ecm22, hac1, mbp1, rgm1, sip4, ccr4, hac1 | ≤0.1 |
| DNA replication, repair | 316 | 188 | jhd1, nut1, gis2, cat8, gis2, mbp1, sut1, tos8 | ≤0.1 |
| response to osmotic stress | 77 | 54 | hog1, pho23, hal9, msn4, spt2, hog1, pbs2, pbs2 delptk2, ptp2 delptp3, ptc1, ste11 | ≤0.05 |
| Sporulation | 131 | 59 | swi6, hst1, sum1, ino2, sps18, bre1, cac1, cac2, cti6, hst1, isw1, med15, med2, med3, msi1, not3, rfm1, rtf1, sdc1, set1, sgf73, sif2, sum1, swd1, swd3, tup1, bck1 delptp3, mck1, stl2 delptp3 | ≤0.05 |
| vesicle organization | 77 | 44 | mig3, cup2, rco1, not4, gat3, arp6, htz1, swc3, swc5, swr1, vps71, vps72, yaf9 | ≤0.1 |
| vitamin metabolic process | 47 | 34 | cac2, set2, sas4, ric1, gzf3, sko1, spt10, sas5, rlf2, hfi1, mot3, tos8, ada2, bre2, caf40, cti6, dep1, dls1, eaf3, eaf5, eaf7, hfi1, htz1, ldb7, med15, not4, npl6, pho23, rsc1, rxt2, sap30, sas2, sas4, sas5, sds3, set1, sgf73, sin3, snf12, snf2, snt1, spt20, spt3, spt7, spt8, ssn6, swd3, cka1, ksp1, mih1 delelm1, sit4, yvh1 | ≤0.05 |
| pseudohyphal growth | 68 | 49 | sip3, sok2, gzf3, phd1, hda1, not3, ste12, ykl222C, ste12, med16, med2, med3, snf12, elm1, ste11, ste20, ste7, yck3 | ≤0.05 |

^P: genes involved in the cellular process were downloaded from the KEGG pathway database, others were downloaded from the GO terms database in SGD