Supplementary Table.

Table S1. Yeast strains used in this study.

Strain	Relevant Genotype	Genotype	Reference/Source
JW81	WT	*h- ade6-M210 leu1-32 ura4-D18*	(1)
idn1Δ	*idn1Δ*	*h+ ade6-M210 leu1-32 ura4-D18 SPAC4G9.12Δ::kanMX4*	Bioneer
gcd1Δ	*gcd1Δ*	*h+ ade6-M210 leu1-32 ura4-D18 SPCC794.01cΔ::kanMX4*	Bioneer
ABY540	*loz1Δ*	*h+ ade6-M210 leu1-32 ura4-D18 SPAC25B8.19cΔ::kanMX6*	(2)
ABY84	*loz1-1*	*h+ ade6-M210 leu1-32 ura4-D18 loz1-1*	(2)
ABY880	*idn1Δ loz1Δ*	*h- ade6-M216 leu1-32 ura4-D18 SPAC25B8.19cΔ::kanMX6 SPAC4G9.12Δ::kanMX4*	This study
ABY1098	*idn1Δ* idn1-GFP	*h+ ade6-M210 leu1-32 ura4-D18 SPAC4G9.12Δ::kanMX4 JK148-pgk1-idn1GFP::LEU2+*	This study
ABY1050	*idn1Δ* JK148	*h+ ade6-M210 leu1-32 ura4-D18 SPAC4G9.12Δ::kanMX4 JK148::LEU2+*	This study
ABY1067	*idn1Δ loz1Δ* idn1-GFP	h? *ade6-M? leu1-32 ura4-D18 SPAC25B8.19cΔ::kanMX6 SPAC4G9.12Δ::kanMX4 JK148-pgk1-idn1GFP::LEU2+*	This study
ABY991	*gcd1Δ loz1Δ*	h? *ade6-M? leu1-32 ura4-D18 SPAC25B8.19cΔ::kanMX6 SPCC794.01cΔ::kanMX4*	This study
ABY1115	JW81 *gcd1-lacZ*	*h- ade6-M210 leu1-32 ura4-D18 JK148 gcd1-lacZ::LEU2+*	This study
ABY1095	*loz1Δ gcd1-lacZ*	*h- ade6-M216 leu1-32 ura4-D18 SPAC25B8.19cΔ::kanMX6 JK148-gcd1-lacZ::LEU2+*	This study
ABY1116	*Gcd1*-13myc	*h- ade6-M210 leu1-32 ura4-D18 SPCC794.01c*-13xmyc*::kanMX6*	This study
ABY1100	*idn1Δ gcd1Δ*	h? *ade6-M? leu1-32 ura4-D18 SPAC4G9.12Δ::kanMX4 SPCC794.01cΔ::kanMX4*	This study
ABY1395	*zwf1Δ*	*h+ ade6-M? leu1-32 ura4-D18 SPAC3A12.18Δ::kanMX6*	This study
ABY1382	*zwf1Δ gcd1Δ*	h? *ade6-M? leu1-32 ura4-D18 SPAC3A12.18Δ::kanMX6 SPCC794.01cΔ::kanMX4*	

References

1. Wu, J. Q., Kuhn, J. R., Kovar, D. R., and Pollard, T. D. (2003) Spatial and temporal pathway for assembly and constriction of the contractile ring in fission yeast cytokinesis. *Dev Cell* **5**, 723-734
2. Corkins, M. E., May, M., Ehrensberger, K. M., Hu, Y. M., Liu, Y. H., Bloor, S. D., Jenkins, B., Runge, K. W., and Bird, A. J. (2013) Zinc finger protein Loz1 is required for zinc-responsive regulation of gene expression in fission yeast. *Proc Natl Acad Sci U S A* **110**, 15371-15376

Supplemental Figures.

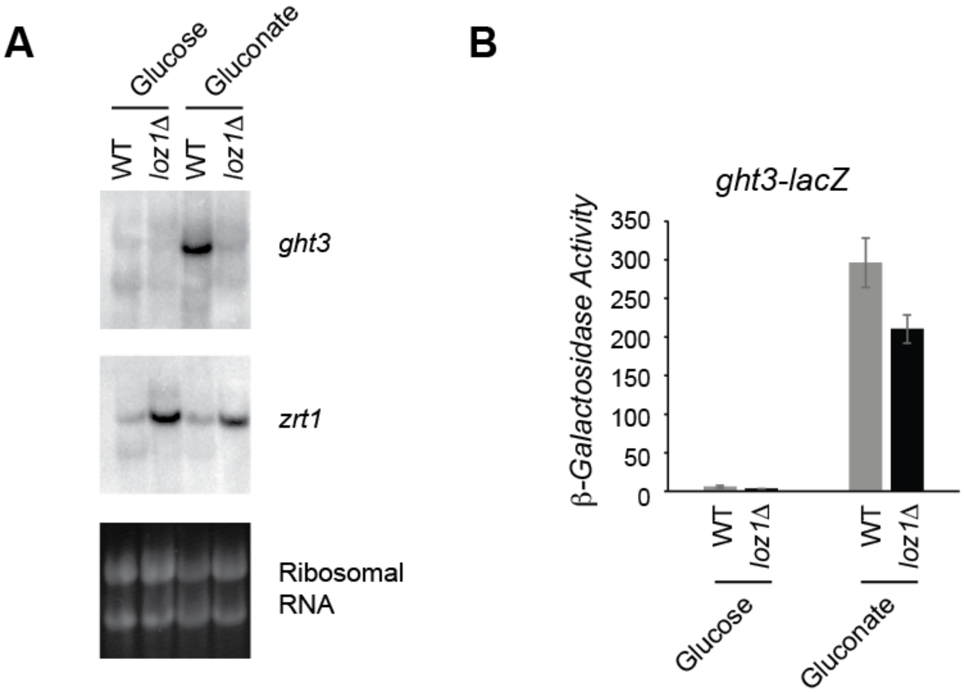


Figure S1. *ght3* is not expressed at high levels in cells grown using glucose as the carbon source.

A. Wild-type and *loz1*Δ cells pregrown in YES medium were inoculated to an OD_{600} of ~0.1 in fresh YES medium. Cells were grown for 1 hr in YES medium containing 3% glucose as the carbon source. Cells were then spun down, washed, and were transferred to YES medium containing 3% glucose or 4% gluconate. After 4 hrs growth, cells were spun down and total RNA extracted for RNA blot analysis. RNA blots were probed for *ght3* and the Loz1 target *zrt1*. Ribosomal RNAs are shown as the loading control. B. Wild-type and *loz1*Δ cells expressing a *ght3-lacZ* reporter were grown as above and β-Galactosidase activity measure by standard methods. Results show the average values for 3 independent repeats and error bars represent standard deviations.

```
S.pombe          MTVTPINPTNQPYKYVFVVIGPAGSGKTTMAKAVSEKLGFEYIEGDDLHPKANIEKMSQG
H.sapiens        ----------MAAPGALLVMGVSGSGKSTVGALLASELGWKFYDADDYHPEENRRKMGKG
E.coli           -----------MAGESFILMGVSGSGKTLIGSKVAALLSAKFIDGDDLHPAKNIDKMSQG
                                 ::::* :****: :.  ::  *. :: :.** **  *  **.:*

S.pombe          HPLNDNDRWGWLHNCGGACAMELDKESIKGVVLTCSALKRSYRDILRSSLEHR-------
H.sapiens        IPLNDQDRIPWLCNLHDILLRD--VASGQRVVLACSALKKTYRDILTQGKDGVALKCEES
E.coli           IPLSDEDRLPWLERLNDASYSL--YKKNETGFIVCSSLKKHYRDILRKGSPHV-------
                  **.*:**  ** .            . :  .:.**:**: ***** ..

S.pombe          -------PAILRFIYLAASRETLIKRTTSRKNHYMKADMVESQLAILEAPTADEKDVITI
H.sapiens        GKEAKQAEMQLLVVHLSGSFEVISGRLLKREGHFMPPELLQSQFETLEPPAAPEN-FIQI
E.coli           -----------HFLWLDGDYETILARMQRRAGHFMPVALLKSQFEALERPQEDEQDIVRI
                             .: * .. *.:  *   *  *:*   :::**:  ** *   *: .: *

S.pombe          SVENGKEQSEEECLDIVHKMVNENKQP-----------
H.sapiens        SVDKNVSEIIATIMETL-KMK-----------------
E.coli           DINHDIANVTEQCRQAVLAIRQNRICAKEGSASDQRCE
                 .::.   :      : :  :
```

Figure S2. Idn1 from *S. pombe* shares sequence homology with characterized gluconate kinases.

An alignment of Idn1 from *S. pombe* with IdnK from *Escherichia coli* and *Homo sapiens*. Alignments were performed using Clustal Omega (EMBL-EBI).

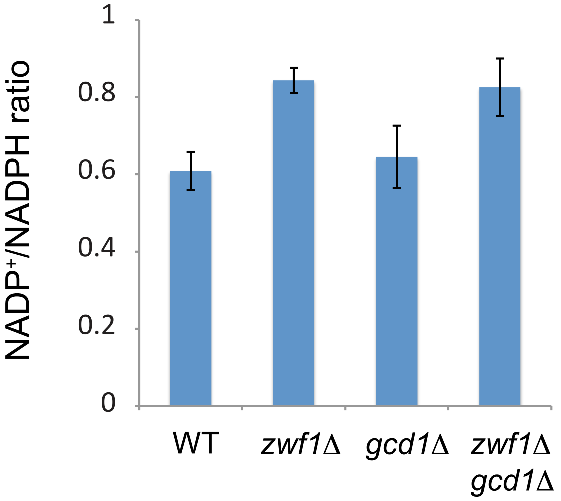
```
HsH6PD             MLAEPFNWHPGMWNMLIVAMCLALLG---CLQAQELQGHVSIILLGATGDLAKKYLWQGL 57
LmG6PD             ----------------------------------VSEIKTLVTFFGGTGDLAKRKLYPSV 26
DmCG7140           ----------------------------MISMDPHNEEAYSIVVFGASGGLAKKKVFPAL 32
SpSPAC3C7.13C      --------------------------------------MVTFMVFGASGNLANKKTFPAL 22
SpSPCC794.01C      --------------------------------------MLSIIVFGASGDLATKMTFPAL 22
HsG6PD             -MAEQV-------ALSRTQVCGILREELFQGDAFHQSDTHIFIIMGASGDLAKKKIYPTI 52
SpZWF1             ----------------------------MSSANLSIKENGAMVVFGASGDLSKKKTFPAL 32
ScZWF1             ----------------------------MSEGPVKFEKNTVISVFGASGDLAKKKTFPAL 32
                                                            . .:*.:* *:.:  :  :

HsH6PD             FQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALESLSCPKDMAPSHCAEHKDQFLQLS 117
LmG6PD             FNLYKKGYLQK-HFAIVGTARQALNDDEFK-QLVRD--CIK---DFTDDQAQAEAFIEHF 79
DmCG7140           WALFRENRLPQ-GTKIFTFTRSPLQTKTYR-LQILP--YMELDKHR--DPKKYNLFWTTV 86
SpSPAC3C7.13C      FHLFKRNLVDRSSFYVLGYARSKIPIGEFR-ESIRE--SVK---PDTESKQVFQDFIDRV 76
SpSPCC794.01C      FALYVRKIIPE-DFQIIGYARSKLSQEAAN-KIVTA--HIPIDDTVGASQKALNTFVEHY 78
HsG6PD             WWLFRDGLLPE-NTFIVGYARSRLTVADIR-KQSEP--FFK---ATPEEKLKLEDFFARN 105
SpZWF1             FSLFSEGRLPK-DIRIVGYARSKIEHEDFL-DRITQ--NIKIDEEDSQAKEKLEEFKKRC 88
ScZWF1             FGLFREGYLDP-STKIFGYARSKLSMEEDL-KSRVL--PHLKKPHGEADDSKVEQFFKMV 88
                   : *:           .   :                                 : *

HsH6PD             QYR--QLKTAEDYQALNKDIEAQLQHAGLREAGRIFYFSVPPFAYEDIARNINSSCRPGP 175
LmG6PD             SYRAHDVTDAASYAVLKEAIEEAADKF-DIDGNRIFYMSVAPRFFGTIAKYLKSEGLLAD 138
DmCG7140           HCVQGEYDKPENYVALTEAMVHQETKHNQVRANRIFYLALPPIVFDQVTLNVSRKCSST- 145
SpSPAC3C7.13C      SYFSGQYDQSSSYVEFRKHLESVEKKADSSKALRIFYIALPPSVYVTVSSHIYENLYL-- 134
SpSPCC794.01C      KYVPGTYDKPESFEMLNSIIAEKE-TAPASECTRIFYLVLPPHLFAPVSELIKSKAHPN- 136
HsG6PD             SYVAGQYDDAASYQRLNSHMNALHL---GSQANRLFYLALPPTVYEAVTKNIHESCMSQI 162
SpZWF1             SYYRGSYDKPEDFEGLNSHLCE--REGDRSTHNRIFYLALPPDVFVSVATNLKKKCVPE- 145
ScZWF1             SYISGNYDTDEGFDELRTQIEKFEKSANVDVPHRLFYLALPPSVFLTVAKQIKSRVYAE- 147
                               :  :   :             *:**: : *  :  ::  :

HsH6PD             GAWLRVVLEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQILPFRDQNRKA 235
LmG6PD             TGYNRLMIEKPFGTSYDTAAELQNDLENAFDDNQLFRIDHYLGKEMVQNIAALRFGNP-I 197
DmCG7140           TGWNRIIVEKPFARDDISYKAFQTSLCNCFRESQIYLMDHLLSRQVMQNFFALRYSNH-L 204
SpSPAC3C7.13C      PGKSRLVIEKPFGKNYQSAVKLKEEVHKHWKEEEIYRIDHYTAKDMVNNFFTLRFANSSS 194
SpSPCC794.01C      GMVTRLIVEKPIGFDYKSADAILSDLSKHWSAKDTFKVDHFLGEDMIDGFTAIRFANS-M 195
HsG6PD             RGWNRIIVEKPFGRDLQSSDRLSNHISSLFREDQIYRIDHYLGKEMVQNLMVLRFANR-I 221
SpZWF1             KGIARLVIEKPFGVDLKSAQELQSQLAPLFDEKEIYRIDHYLGKEMVQNLVHLRFCNP-V 204
ScZWF1             NGITRVIVEKPFGHDLASARELQKNLGPLFKEEELYRIDHYLGKELVKNLLVLRFGNQ-F 206
                       *:::***:. .  :   :   :   :  .: : :**  ..: :  :  :*  *

HsH6PD             LDGLWNRHHVERVEIIMKETV-DAEGRTSFYEEYGVIRDVLQNHLTEVLTLVAMELPHNV 294
LmG6PD             FDAAWNKDYIKNVQVTLSEVL-GVEERAGYYDTAGALLDMIQNHTMQIVGWLAMEKPESF 256
DmCG7140           WAETLNHRHVAAVMISIKCELPVSVNRADYFNQFGIIRDLMTNHMIQMLAMLAMDQPYAN 264
SPSPAC3C7.13C      IDAVLNRHSIQSVEIHMYETG-GCEGRIGYYDANGVVRDVVQNHLTQIFCIAAMNEPKSA 253
SpSPCC794.01C      FEPIWNREHIESVRVDFREDF-GCEGRGGYFEGAGILRDVVQNHLLQLLTLLCIEEPKSQ 254
HsG6PD             FGPIWNRDNIACVILTFKEPF-GTEGRGGYFDEFGIIRDVMQNHLLQMLCLVAMEKPAST 280
SpZWF1             ISHLWDKNSISSVQITFKEPI-GTEGRGGYFDSSTIVRDIVQNHLVQILTLLTMETPTTF 263
ScZWF1             LNASWNRDNIQSVQISFKERF-GTEGRGGYFDSIGIIRDVMQNHLLQIMTLLTMERPVSF 265
                        ::  :  * : :         *   :::     : *:: **  ::.    :: *

HsH6PD             SSAEAVLRHKLQVFQALRGLQRGS----AVVGQYQSYSEQV---RRELQ--KPDSFHSLT 345
LmG6PD             T-DKDIRAAKNAAFNALKIYDEAEVNKYFVRAQYGAGDSAD---FKPYLEELDVPADSKN 312
DmCG7140           T-ADDLRAERLKVLRQVLTPNIGD----VVLAQYRNNRRETDPAKCGYTEHTYIPKDSFT 319
SpSPAC3C7.13C      S-ASDVRAEKVNLLKATRPASLKE----SMLGQYTTSEDGK---IPGYLDLEGVPKDSKA 305
SpSPCC794.01C      D-AEDIIKCKVDFLKSLHPVSKED----IVYGQYTKSANGK---VPGYRELDGVADDSEV 306
HsG6PD             N-SDDVRDEKVKVLKCISEVQANN----VVLGQYVGNPDGEGEATKGYLDDPTVPRGSTT 335
SpZWF1             S-ADDLRDEKVKVLRRTRLGDLKD----IVLGQYVKSKDGK---KPGYLDDETVPKGSRC 315
ScZWF1             D-PESIRDEKVKVLKAVAPIDTDD----VLLGQYGKSEDGS---KPAYVDDDTVDKDSKC 317
                      . :   :   :.     .  .     : .**                       *
```

```
HsH6PD             PTFAAVLVHIDNLRWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQSQCL 405
LmG6PD             NTFIAGELQFDLPRWEGVPFYVRSGKRLAAKQTRVDIVFKAGTFNF-GSE------QEAQ 365
DmCG7140           PTFALVVLHINNRRWTGVPFILRAGKALNDTKSEVRIQYKPVDCDTFHSD------STDI 373
SpSPAC3C7.13C      TTFAASTLHVDNDRWKGVPFVFVSGKRMKKGEVYIKYYFRLKDSGIFSDV--------KR 357
SpSPCC794.01C      STFCALQLRSEAPRWKGIPIIISAGKGLDRDYFEARITFKRREGGMFPTV--------DS 358
HsG6PD             ATFAAVVLYVENERWDGVPFILRCGKALNERKAEVRLQFHDVAGDIFHQQ--------CK 387
SpZWF1             PTYSAIPCFIDTERWRGVPFLLKAGKAMDIGKVEIRVQFKAAANGLFKD---------AY 366
ScZWF1             VTFAAMTFNIENERWEGVPIMMRAGKALNESKVEIRLQYKAVASGVFKD---------IP 368
                    *:       :  ** *:*: . .** :          ::

HsH6PD             PRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPGLRLFGSPLSDYYAYSPVRE 465
LmG6PD             EAVLSIIIDPKG----AIELKLNAKSVEDA-------FNTRTIDLGWTVSDEDK---KNT 411
DmCG7140           RNELVLRSFPTE----EVFMRMRLKRQGED-------ICLRESEINLRVDDRGPKG---- 418
SpSPAC3C7.13C      RRYLILHVQPEE----FVNLTCTINKPMTTD------LQPIDAYASLNYNEQFKDLMKEK 407
SpSPCC794.01C      SNVLVLRVYPKE----FIALKGHIKQPGFS-------RQIVPVTLDVKYPEAFPDTWI-- 405
HsG6PD             RNELVIRVQPNE----AVYTKMMTKKPGMF-------FNPEESELDLTYGNRYKNVKL-- 434
SpZWF1             HNELVIRVQPDE----AIYFKMNIKQPGLS-------EAPLLTDLDLTYSRRFKNMKL-- 413
ScZWF1             NNELVIRVQPDA----AVYLKFNAKTPGLS-------NATQVTDLNLTYASRYQDFWI-- 415
                      * :           :

HsH6PD             RDAHSVLLSHIFHGRKNFFITTENLLASWNFWTPLLESLAH---KAPRLYPGGAENGRLL 522
LmG6PD             PEPYERMIHDTMNGDGSNFADWNGVSIAWKFVDAISAVYTA-DKAPLETYKSGSM-GPEA 469
DmCG7140           LQGLPGYLLNVFQGDQTLFMRSDEQCEIWRIFSPVLATIDS-DRPRPLHYDFGSR-GPLL 476
SpSPAC3C7.13C      RDGYEILFEDAIRGDPTKFIRYDEVEYAWKIWDEILDSP-----KKPIPYPAGSD-GPEG 461
SpSPCC794.01C      HKAYEVVIADAINGKHTHFISDDEVRTSWKIFDDVLDTT---GDLSPLPYAFGSHHGPDA 462
HsG6PD             PDAYERLILDVFCGSQMHFVRSDELREAWRIFTPLLHQIEL-EKPKPIPYIYGSR-GPTE 492
SpZWF1             HEAYEALFLDAFAGDQSRFARIDELECAWSLVDPLLKYMEE-EKPVPEPYEYGSD-GPEC 471
ScZWF1             PEAYEVLIRDALLGDHSNFVRDDELDISWGIFTPLLKHIERPDGPTPEIYPYGSR-GPKG 474
                    .     : . : *    *   :     * :   :              *  *:  *

HsH6PD             DFEFSSGRLFFSQQ-----QPEQLVPGPGPAPMPSDFQVLRAKYRESPLVSAWSEELISK 577
LmG6PD             SDKLLAANGDAWVFKG-------------------------------------------- 485
DmCG7140           AYRKAERAGFVFFATDEWHQSEETLEYTVK----NSKQLIGPHTALKPVRDPRSKR---- 528
SpSPAC3C7.13C      LEAYMKRHLGHE------------------------------------------------ 473
SpSPCC794.01C      TLEFFKKRNLEWD----------------------------------------------- 475
HsG6PD             ADELMKRVGFQYEGTYKWVNPHKL------------------------------------ 516
SpZWF1             LYSFLKKFGYIYDSPDYYDYPVMSVPSDH------------------------------- 500
ScZWF1             LKEYMQKHKYVMPEKHPYAWPVTKPEDTKD----N*------------------------ 505


HsH6PD             LANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPWAHTHLWLVDERCVPL 637
LmG6PD             ------------------------------------------------------------ 485
DmCG7140           ------------------------SNSNP------------------------------- 533
SpSPAC3C7.13C      ------------------------------------------------------------ 473
SpSPCC794.01C      ------------------------------------------------------------ 475
HsG6PD             ------------------------------------------------------------ 516
SpZWF1             ------------------------------------------------------------ 500
ScZWF1             ------------------------------------------------------------ 505
```

Figure S3. SPCC794.01c shares sequence homology with characterized glucose 6-phosphate dehydrogenases.

An alignment of human hexose 6 phosphate dehydrogenase (HsH6PD), *Leuconostoc mesenteroides* glucose 6 phosphate dehydrogenase (LmG6PD), *Drosophila melanogaster* CG7140, *S. pombe* SPAC3C7.13c (SpSPAC3C7.13C), *S. pombe* SPCC794.01c (SpSPCC794.01C), human glucose 6 phosphate dehydrogenase (HsG6PD), *S. pombe* Zwf1 (SpZWF1), and *S. cerevisiae* Zwf1 (ScZWF1). The sequence of HsH6PD was truncated at amino acid 637. Residues that are predicted to coordinate the 6-phosphate (of G6P) and glucose (of G6P) are highlighted in green and yellow, respectively. Predictions were based of the structure of human glucose 6-phosphate dehydrogenase (1).

Figure S4. Deletion of *zwf1* or *zwf1 gcd1* increases the NADP$^+$/NADPH ratio in exponentially growing cells.



The indicated strains were grown to an A600 ~1.0 and the levels of NADP$^+$ and NADPH levels measured using the 3-(4,5-dimethylthiazolyl-2)-2,5-diphenyltetrazolium bromide and phenazine ethosulfate cycling assay. The data shown is the average NADP$^+$/NADPH ratio from three independent experiments, with error bars representing the standard deviations.

References

1. Kotaka M, Gover S, Vandeputte-Rutten L, Au SW, Lam VM, Adams MJ. Structural studies of glucose-6-phosphate and NADP$^+$ binding to human glucose-6-phosphate dehydrogenase. Acta Crystallogr D Biol Crystallogr. 2005;61(Pt 5):495-504.