

## Supplemental Material

### **Tandem inactivation of inositol pyrophosphatases Asp1, Siw14, and Aps1 illuminates functional redundancies in inositol pyrophosphate catabolism in fission yeast**

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Supplemental Table S1. Lists of protein-coding transcripts that are downregulated or upregulated by  $\geq 2$ -fold (expressed as log<sub>2</sub> Fold Change) in *aps1-H397A siw14 $\Delta$  asp1 $\Delta$  tgp1 $\Delta$*  cells vis-à-vis wild-type cells.

Supplemental Table S2. List of *S. pombe* strains used in this study.

| Systematic ID | Gene name  | Product                                                                                                 | log2FoldChange |
|---------------|------------|---------------------------------------------------------------------------------------------------------|----------------|
| SPBC359.02    | alr2       | alanine racemase Alr2                                                                                   | -4.26          |
| SPAPB8E5.05   | mfm1       | M-factor precursor Mfm1                                                                                 | -3.78          |
| SPBPB21E7.04c | cmt2       | O-methyltransferase, human COMT catechol homolog 2                                                      | -3.27          |
| SPBC359.01    |            | amino acid transmembrane transporter                                                                    | -2.88          |
| SPBP26C9.02c  | car1       | arginase Car1                                                                                           | -2.73          |
| SPAC1039.09   | isp5       | amino acid transmembrane transporter Isp5                                                               | -2.66          |
| SPBPB10D8.02c |            | arylsulfatase                                                                                           | -2.65          |
| SPBPB2B2.01   | nrg1       | amino acid transmembrane transporter Nrg1                                                               | -2.54          |
| SPAC11D3.06   |            | MatE family transmembrane transporter                                                                   | -2.40          |
| SPBC839.06    | cta3       | P-type ATPase, potassium exporting Cta3                                                                 | -2.39          |
| SPAPB24D3.03  | agm2       | agmatinase 2, Agm2                                                                                      | -2.30          |
| SPAC513.03    | mfm2       | M-factor precursor Mfm2                                                                                 | -2.21          |
| SPBC1683.06c  | urh1       | uridine ribohydrolase Urh1                                                                              | -2.15          |
| SPBC1683.08   | ght4       | plasma membrane hexose:proton symporter, unknown specificity Ght4                                       | -2.09          |
| SPAC27D7.03c  | mei2       | RNA-binding protein involved in meiosis Mei2                                                            | -2.04          |
| SPAC11H11.04  | mam2       | pheromone p-factor receptor Mam2                                                                        | -2.02          |
| SPAC11E3.06   | map1       | DNA-binding transcription factor, MADS-box Map1                                                         | -1.97          |
| SPAC11D3.03c  |            | aminomethyltransferase-like and DUF1989 family protein, implicated in urea metabolism                   | -1.94          |
| SPAC977.13c   |            | hydrolase, pseudogene (4 frameshifts)                                                                   | -1.89          |
| SPBC8E4.03    | agm3       | agmatinase 3, Agm3                                                                                      | -1.81          |
| SPBPB2B2.02   | say1       | ER sterol deacetylase Say1                                                                              | -1.78          |
| SPAC1399.04c  | uck2       | uracil phosphoribosyltransferase Uck2                                                                   | -1.77          |
| SPBC359.04c   | pfl7       | cell surface glycoprotein, flocculin Pfl7, DIPSY family                                                 | -1.66          |
| SPAC1002.17c  | urg2       | uracil phosphoribosyltransferase                                                                        | -1.64          |
| SPAC1002.19   | urg1       | GTP cyclohydrolase II Urg1                                                                              | -1.62          |
| SPCC1223.09   | uro1       | uricase Uro1                                                                                            | -1.62          |
| SPBC32C12.02  | ste11      | DNA-binding transcription factor Ste11                                                                  | -1.61          |
| SPCC548.07c   | ght1       | plasma membrane high-affinity glucose:proton symporter Ght1                                             | -1.60          |
| SPAP11E10.01  |            | ornithine cyclodeaminase-like protein                                                                   | -1.58          |
| SPCC737.04    |            | UPF0300 family protein 6                                                                                | -1.56          |
| SPAPJ695.02   |            | Schizosaccharomyces pombe specific protein                                                              | -1.54          |
| SPAC977.15    |            | dienelactone hydrolase family, implicated in cellular detoxification                                    | -1.54          |
| SPAC1556.04c  | cdd1       | cytidine deaminase Cdd1                                                                                 | -1.52          |
| SPAC1399.06   |            | dubious                                                                                                 | -1.51          |
| SPAC1565.04c  | ste4       | MAPK cascade adaptor protein Ste4                                                                       | -1.49          |
| SPAC56F8.15   |            | Schizosaccharomyces pombe specific protein                                                              | -1.48          |
| SPAC1F8.01    | ght3       | plasma membrane gluconate:proton symporter Ght3                                                         | -1.48          |
| SPAC922.07c   | atd2       | aldehyde dehydrogenase                                                                                  | -1.48          |
| SPAC869.05c   | sul2       | plasma membrane sulfate transmembrane transporter Sul2                                                  | -1.47          |
| SPAC31G5.09c  | spk1       | MAP kinase Spk1                                                                                         | -1.44          |
| SPBC359.03c   | aat1       | plasma membrane amino acid transmembrane transporter Aat1                                               | -1.43          |
| SPCC569.07    |            | aromatic aminotransferase                                                                               | -1.43          |
| SPAC1039.01   |            | amino acid transmembrane transporter                                                                    | -1.42          |
| SPCC338.12    | pbi2       | vacuolar proteinase B inhibitor Pbi2                                                                    | -1.39          |
| SPAC11D3.19   |            | Schizosaccharomyces pombe specific protein                                                              | -1.37          |
| SPBC16A3.13   | meu7       | alpha-amylase homolog Aah4                                                                              | -1.36          |
| SPAC664.13    |            | Schizosaccharomyces pombe specific protein                                                              | -1.36          |
| SPBPB2B2.05   |            | class I glutamine amidotransferase family protein                                                       | -1.34          |
| SPAC1399.05c  | toe1       | DNA-binding transcription factor, zf-fungal binuclear cluster type                                      | -1.33          |
| SPAC977.16c   | dak2       | dihydroxyacetone kinase Dak2                                                                            | -1.32          |
| SPBPB10D8.01  |            | cysteine transmembrane transporter                                                                      | -1.32          |
| SPAC1039.10   | mmf2       | mitochondrial matrix protein, YjgF family protein Mmf2, reactive intermediate imine deaminase A homolog | -1.31          |
| SPCC794.02    | wtf5       | wtf antidote-like meiotic drive suppressor Wtf5                                                         | -1.29          |
| SPCC417.02    | dad5       | DASH complex subunit Dad5                                                                               | -1.26          |
| SPAC1002.18   | urg3       | DUF1688 family fungal conserved protein, implicated in uracil or riboflavin metabolism                  | -1.24          |
| SPBC725.03    |            | pyridoxamine 5'-phosphate oxidase                                                                       | -1.24          |
| SPAP7G5.06    | per1       | plasma membrane amino acid transmembrane transporter Per1                                               | -1.22          |
| SPAC521.03    |            | short chain dehydrogenase, human DHRS7 family                                                           | -1.21          |
| SPAC1F8.05    | isp3       | spore wall structural constituent Isp3                                                                  | -1.19          |
| SPBC36.02c    |            | spermidine family transmembrane transporter                                                             | -1.17          |
| SPAC869.10c   | put4       | plasma membrane proline transmembrane transporter Put4                                                  | -1.17          |
| SPBPB21E7.07  | aes1       | phenazine biosynthesis PhzF protein family                                                              | -1.15          |
| SPBPB21E7.08  |            | pseudogene                                                                                              | -1.14          |
| SPBC1683.12   |            | carboxylic acid transmembrane transporter                                                               | -1.12          |
| SPBC365.12c   | ish1       | nuclear envelope Ish domain protein Ish1                                                                | -1.11          |
| SPAC23H3.15c  | ddr48      | DNA damage-responsive protein Ddr48                                                                     | -1.11          |
| SPAC110.05    | SPAC110.06 | dubious                                                                                                 | -1.10          |
| SPAC167.06c   | mug143     | Schizosaccharomyces specific protein Mug143                                                             | -1.09          |
| SPAC30D11.01c | gto2       | extracellular alpha-glucosidase Gto2                                                                    | -1.06          |
| SPBC23G7.13c  |            | plasma membrane urea transmembrane transporter                                                          | -1.04          |
| SPBC21C3.19   | rtc3       | SBD5 family protein Rtc3                                                                                | -1.01          |

| Systematic ID | Gene name | Product                                                  | log2FoldChange |
|---------------|-----------|----------------------------------------------------------|----------------|
| SPBCPT2R1.08c | tlh2      | RecQ type DNA helicase Tlh1                              | 2.78           |
| SPAC27D7.09c  |           | But2 family protein, similar to cell surface molecules   | 2.26           |
| SPAC186.05c   | gdt1      | Golgi calcium and manganese antiporter Gdt1              | 2.07           |
| SPBC947.04    | pfl3      | cell surface glycoprotein, flocculin Pfl3, DIPSY family  | 1.75           |
| SPCC191.11    | inv1      | external invertase, beta-fructofuranosidase Inv1         | 1.67           |
| SPBC530.02    |           | transmembrane transporter                                | 1.29           |
| SPBC1711.15c  |           | Schizosaccharomyces pombe specific protein               | 1.25           |
| SPCC622.19    | jmj4      | histone demethylase Jmj4                                 | 1.17           |
| SPAC23D3.05c  |           | alcohol dehydrogenase pseudogene                         | 1.07           |
| SPAC1B3.16c   | vht1      | plasma membrane vitamin H transmembrane transporter Vht1 | 1.06           |
| SPAC4H3.08    | fox2      | 3-hydroxyacyl-CoA dehydrogenase Fox2                     | 1.05           |
| SPBC409.08    |           | spermine family transmembrane transporter                | 1.05           |
| SPCC364.06    | nap1      | histone H2A-H2B chaperone Nap1                           | 1.02           |

Table S2. List of *S. pombe* strains used in this study.

| Strain  | Genotype                                                                                        |
|---------|-------------------------------------------------------------------------------------------------|
| AS612   | <i>h+ ssu72-C13S::natMX</i>                                                                     |
| AS2308  | <i>h- asp1-H397A::kanMX aps1Δ::hygMX ssu72-C13S::natMX</i>                                      |
| BS54    | <i>h- spx1Δ::kanMX</i>                                                                          |
| BS400   | <i>h+ asp1-H397A::natMX spx1Δ::kanMX aps1Δ::hygMX</i>                                           |
| BS828   | <i>h- aps1Δ::hygMX spx1Δ::kanMX siw14Δ::natMX</i>                                               |
| AGP237  | <i>h- tgp1Δ::ura4<sup>+</sup></i>                                                               |
| BS957   | <i>h+ tgp1Δ::ura4<sup>+</sup> aps1Δ::hygMX</i>                                                  |
| BS958   | <i>h+ tgp1Δ::ura4<sup>+</sup> siw14Δ::hygMX</i>                                                 |
| BS971   | <i>h+ tgp1Δ::ura4<sup>+</sup> aps1Δ::kanMX siw14Δ::hygMX</i>                                    |
| BS1011  | <i>h+ asp1-H397A::natMX aps1Δ::hygMX tgp1Δ::ura4<sup>+</sup> [Hat]</i>                          |
| BS1452  | <i>h+ siw14Δ::hygMX asp1-H397A::natMX aps1Δ::kanMX spx1Δ::ura4MX</i>                            |
| BS1454  | <i>h- asp1-H397A::natMX aps1Δ::hygMX spx1-Y26A-K30A-K34A::kanMX</i>                             |
| BS1456  | <i>h- asp1-H397A::natMX aps1Δ::hygMX spx1-C374A-C377A::kanMX</i>                                |
| BS1402  | <i>h- asp1-H397A::natMX aps1Δ::hygMX tgp1Δ::ura4<sup>+</sup> nab2-R192L kcs1-Q739K [Hat-S1]</i> |
| BS1403  | <i>h+ asp1-H397A::natMX aps1Δ::hygMX tgp1Δ::ura4<sup>+</sup> kcs1-Q739K [Hat-S2]</i>            |
| BS1404  | <i>h- asp1-H397A::natMX aps1Δ::hygMX tgp1Δ::ura4<sup>+</sup> kcs1-R738T [Hat-S3]</i>            |
| BS1405  | <i>h+ asp1-H397A::natMX aps1Δ::hygMX tgp1Δ::ura4<sup>+</sup> spx1-F393V [Hat-S4]</i>            |
| BS1406  | <i>h- asp1-H397A::natMX aps1Δ::hygMX tgp1Δ::ura4<sup>+</sup> kcs1-G765R [Hat-S5]</i>            |
| BS1407  | <i>h+ asp1-H397A::natMX aps1Δ::hygMX tgp1Δ::ura4<sup>+</sup> kcs1-Q739K [Hat-S6]</i>            |
| BS1408  | <i>h- asp1-H397A::natMX aps1Δ::hygMX tgp1Δ::ura4<sup>+</sup> spx1-(298fs) [Hat-S7]</i>          |
| BS1409  | <i>h+ asp1-H397A::natMX aps1Δ::hygMX tgp1Δ::ura4<sup>+</sup> swd22-S125R [Hat-S8]</i>           |
| BS1505  | <i>h+ siw14Δ::kanMX aps1Δ::hygMX asp1Δ::kanMX</i>                                               |
| BS1509  | <i>h+ siw14-C189S::hygMX aps1-E89A-E93A::kanMX spx1Δ::ura4MX</i>                                |
| BS1511  | <i>h+ siw14-C189S::hygMX aps1-E89A-E93A::kanMX tgp1Δ::ura4<sup>+</sup></i>                      |
| BS1513  | <i>h+ asp1-H397A::natMX siw14-C189S::hygMX aps1-E89A-E93A::kanMX spx1Δ::ura4MX</i>              |
| ASY236  | <i>h- nab2Δ::kanMX</i>                                                                          |
| JTB1047 | <i>h+ asp1-H397A::natMX aps1Δ::hygMX tgp1Δ::ura4<sup>+</sup> nab2Δ::kanMX</i>                   |

The strains are *leu1-32 ura4-D18 his3-D1* and either *ade6-m216* or *ade6-m210*. Mating types were determined by mixing cells with each of the parental *h+* and *h-* strains on malt agar and observing tetrads after 24-48 h of incubation. Abbreviations of the strain names used in the text and figures text are provided in [ ] brackets.