

## APPENDIX

<b>Name</b>	<b>Sequence</b>
XLG1GO <sub>w</sub> SF	AGGAAGACTCTACG GGTCTCTCACCATGCCATTGAAAGAAGATG
XLG1 GOR	ACGAAGACGTCAGAGGTCTCACCTTATTTGAGAAGGAACTGG
XLG1GI1F	TGGAAGACTCGTCGTCGAATCCGTTAGTACC
XLG1GI1R	ACGAAGACGACGACGACTCATTCAAGTCTAAAC
XLG1GI2F	GAGAAGACGAAAACGAGAGGTTTTGTGAAGC
XLG1GI2R	AAGAAGACCAGTTTTTCATAATCTGTTTAACTCC
XLG1GI4F	GAGAAGACTGAGGACGTCGGAATGGTTGTGTTG
XLG1G4R	CAGAAGACCGTCCTCAAACATATCTATCCACTTGC
XLG3 GowSF	GCGAAGACTGTACGGGTCTCACACCATGGAGAAGAAAGATGAAGG
XLG3 GOR	AGGAAGACCACAGAGGTCTCACCTTCTCCTCCGGTC TATATGG
XLG3 GI1F	ACGAAGACCGGTTTTCTCGTATAGCGGGAGGAGTC
XLG3 GI1R	GCGAAGACAGAAACCGGTAATGGTATCGG
XLG3 GI2F	GAGAAGACGGTTTCTGTGTTGCATAATAACCC
XLG3 GI2R	ATGAAGACCAGAAACCACAGACTCAGAGCTAGC
XLG3 GI3F	AAGAAGACGAGGCCTGAGCAGCTGATTGTGAATGG
XLG3 GI3R	CAGAAGACCAGGCCTCAGCTGATTAGCAGTACAC
XLG3 GI4F	TGGAAGACTGTCTACTACCGCCTCAGAAGTTG
XLG3 GI4R	GAGAAGACAGTAGACAGTTGAGCAAGTCAGCC
SPX1 GO <sub>w</sub> sF	AAGAAGACCATACGGGTCTCGCACCATGAAGTTTGGTAAGAGTC
SPX1 GOR	AGGAAGACTGCAGAGGTCTCACCTTTTTGGCTTCTTGCTCCAAC
SPX1 GI1F	CCGAAGACTAGAGGACGAGTTGGAGAAAATTCAAC
SPX1 GI1R	TCGAAGACGTCTCTAACAATTGGATGAAATTG
SPX1 GI2F	TCGAAGACAGTCTCCATATGAAGAGCACAATCGC
SPX1 GI2R	TCGAAGACTGGAGACTCTCCATGAACTTATGC
SPX3 O <sub>w</sub> sF	GGGAAGACCTTACGGGTCTCTCACCATGAAGTTTGGAAAGAGG
SPX3 OR	TGGAAGACAACAGAGGTCTCGCCTTTGGAATAGGAATCGGAGAAG

Table S1. List of primers used for Golden Gate cloning.

Name	Sequence
MR001_LBb1.3	ATTTTGCCGATTTTCGGAAC
MR002_LP_xlg1-2	TGGAAACAGTGGTTCTGGAAC
MR003_RP_xlg1-2	TTGGTTCCATCTTCTGACACC
MR004_LP_xlg3-1	ATATCCGAGGAAACATTTGGG
MR005_RP_xlg3-1	TGAGTGTTAACCGACTTTGGC
MR295_SALK_059139_LP	CTCACCATCACCACCTTCTTC
MR296_SALK_059139_RP	CTTGATTGCTCCAAGTGTTT
MR297_SALK_062645_LP	ATGACAGAGTTTCGGATGTGG
MR298_SALK_062645_RP	AACTGGCAGAGAGAACACAGC
MR303_SALK_141914_LP	TCGATGGAAGAGAACGATTTG
MR304_SALK_141914_RP	AATCGCTGAACCAGTCACAAG
MR305_SALK_107656_LP	CCCTTCTTCCTCATAACGTCC
MR306_SALK_107656_RP	AATCCGATACCATTACCGGTC
MR307_SALK_025392_LP	ATAATAGACAGGGTGGGTCGC
MR308_SALK_025392_RP	TCCACTACCGAATCGAACTTG
MR012_LP_phr1-2	GAGAGACCTCACACGCACTTC
MR013_RP_phr1-2	CTTTCTGGCGAACCTGTAGTG
SPX1-1 (SALK_092030C)_LP	AGAGATAGAATTGCGAAAGC
SPX1-1 (SALK_092030C)_RP	CTATTTGGCTTCTTGCTCC
SPX2-1 (SALK_080503C)_LP	CACCATCAATCCTGTAACCAA
SPX2-1 (SALK_080503C)_RP	TGGCCGGAGTCATTCGTCAT

Table S2. List of primers used for genotyping.

Name	Sequence
ACT8-F	GACTCAGATCATGTTTGAGACCTTT
ACT8-R	CCAGAGTCCAACACAATACCG
SPX3-F	CGCCGGTGGAAATCTATTTTCG
SPX3-R	CAGAACCATTTGCCATGGAA
MGD3-F	GGTACGATTGCGGAAGCACTG
MGD3-R	GTCGAACACGGCTTCAGGTTG

Table S3. List of primers used for q-RT-PCR.

Description	Mating type	Genotype	Name
pB29 AtBRI1 828-1196 + pP6 AtBKI1 1-337	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa pP6-pADH1- Gal4_AD_pP6_AtBKI1_1-337-tADH1-LEU2- ampR pB29-pADH1-AtBRI1_828-1196-LexA- tADH1-TRP1-TetR	8a
pB29 AtSPX1 1-252 + pP6	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa pP6-pADH1- Gal4_AD_pP6_tADH1-LEU2-ampR pB29- pADH1-AtSPX1_1-252 -LexA-tADH1-TRP1- TetR	1a
pB29 AtSPX1 1-252 + pP6 AtXLG1 1-888	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa pP6-pADH1- Gal4_AD_pP6_AtXLG1_1-888-tADH1-LEU2- ampR pB29-pADH1-AtSPX1_1-252-LexA- tADH1-TRP1-TetR	9a
pB29 AtSPX1 1-252 + pP6 AtXLG1 210-430	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa pP6-pADH1- Gal4_AD_pP6_AtXLG1_210-430-tADH1- LEU2-ampR pB29-pADH1-AtSPX1_1-252- LexA-tADH1-TRP1-TetR	22a
pB29 AtSPX1 1-252 + pP6 AtXLG3 130-360	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa pP6-pADH1- Gal4_AD_pP6_AtXLG3_130-360-tADH1- LEU2-ampR pB29-pADH1-AtSPX1_1-252- LexA-tADH1-TRP1-TetR	28a
pB29 AtSPX-MFS1 1-240 + pP6 AtXLG3 130-360	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa pP6-pADH1- Gal4_AD_pP6_AtXLG3_130-360-tADH1- LEU2-ampR pB29-pADH1-AtSPX-MFS1_1- 240-LexA-tADH1-TRP1-TetR	37a
pB29 AtBRI1 828-1196 + pP6 AtBKI1 1-337	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa vip1::natNT2 pP6-pADH1- Gal4_AD_pP6_AtBKI1_1-1011-tADH1-LEU2- ampR pB29-pADH1-AtBRI1_2484-3588-LexA- tADH1-TRP1-TetR	RW420
L40 strain	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa	RW184
L40 ΔVIP1 c1	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa vip1::natNT2	RW196

Table S4.1 List of *Saccharomyces cerevisiae* strains used in this study.

Description	Mating type	Genotype
pB29 AtSPX1 1-252 + pP6 AtXLG3 1-848	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa pP6-pADH1-Gal4_AD_pP6_AtXLG3_1-848-tADH1-LEU2-ampR pB29-pADH1-AtSPX1_1-252 -LexA-tADH1-TRP1-TetR
pB29 AtSPX-MFS1 1-240 + pP6 AtXLG3 1-848	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa pP6-pADH1-Gal4_AD_pP6_AtXLG3_1-848-tADH1-LEU2-ampR pB29-pADH1-AtSPX-MFS1_1-240 -LexA-tADH1-TRP1-TetR
pB29 AtSPX1 1-252 + pP6 AtXLG1 210-410	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa pP6-pADH1-Gal4_AD_pP6_AtXLG1_210-410-tADH1-LEU2-ampR pB29-pADH1-AtSPX1_1-252-LexA-tADH1-TRP1-TetR
pB29 AtSPX1 1-252 + pP6 AtXLG3 160-360	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa pP6-pADH1-Gal4_AD_pP6_AtXLG3_160-360-tADH1-LEU2-ampR pB29-pADH1-AtSPX1_1-252-LexA-tADH1-TRP1-TetR
pB29 AtSPX-MFS1 1-240 + pP6 AtXLG3 160-360	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa pP6-pADH1-Gal4_AD_pP6_AtXLG3_160-360-tADH1-LEU2-ampR pB29-pADH1-AtSPX-MFS1_1-240-LexA-tADH1-TRP1-TetR
pB29 AtSPX1 1-252 + pP6	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa vip1::natNT2 pP6-pADH1-Gal4_AD_pP6-tADH1-LEU2-ampR pB29-pADH1-AtSPX1_1-252-LexA-tADH1-TRP1-TetR
pB29 AtSPX-MFS1 1-240 + pP6	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa vip1::natNT2 pP6-pADH1-Gal4_AD_pP6-tADH1-LEU2-ampR pB29-pADH1-AtSPX-MFS1_1-240 -LexA-tADH1-TRP1-TetR
pB29 AtSPX1 1-252 + pP6 AtXLG1 1-844	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa vip1::natNT2 pP6-pADH1-Gal4_AD_pP6_AtXLG1_1-844-tADH1-LEU2-ampR pB29-pADH1-AtSPX1_1-252 -LexA-tADH1-TRP1-TetR

pB29 AtSPX1 1-252 + pP6 AtXLG3 1-848	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa vip1::natNT2 pP6-pADH1-Gal4_AD_pP6_AtXLG3_1-848 -tADH1-LEU2-ampR pB29-pADH1-AtSPX1_1-252 -LexA-tADH1-TRP1-TetR
pB29 AtSPX-MFS1 1-240 + pP6 AtXLG3 1-848	a	MATa ade2 trp1-901 leu2-3,112 lys2-801am his3D200 lys2::(lexAop)4-HIS3 ura3-52::URA3 (lexAop)8-lacZa vip1::natNT2 pP6-pADH1-Gal4_AD_pP6_AtXLG3_1-848 -tADH1-LEU2-ampR pB29-pADH1-AtSPX-MFS1_1-240 -LexA-tADH1-TRP1-TetR

Table S4.2 List of *Saccharomyces cerevisiae* strains used in this study.

<b>Synthetic gene fragment</b>	<b>Module</b>	<b>Antibiotic resistance</b>
cSPX1_1-240	L0	Ampicillin
cSPX1_241-677	L0	Ampicillin
cSPX1_678-867	L0	Ampicillin
cXLG1_1-461	L0	Ampicillin
cXLG1_462-967	L0	Ampicillin
cXLG1_968-2807	L0	Ampicillin
cXLG1_2808-3339	L0	Ampicillin
cXLG3_1-240	L0	Ampicillin
cXLG3_241-330	L0	Ampicillin
cXLG3_331-873	L0	Ampicillin
cXLG3_874-964	L0	Ampicillin
cXLG3_965-2694	L0	Ampicillin

Table S5. L0 modules carrying *SPX* and *XLG* synthetic genes fragment created using the GG cloning toolkit.

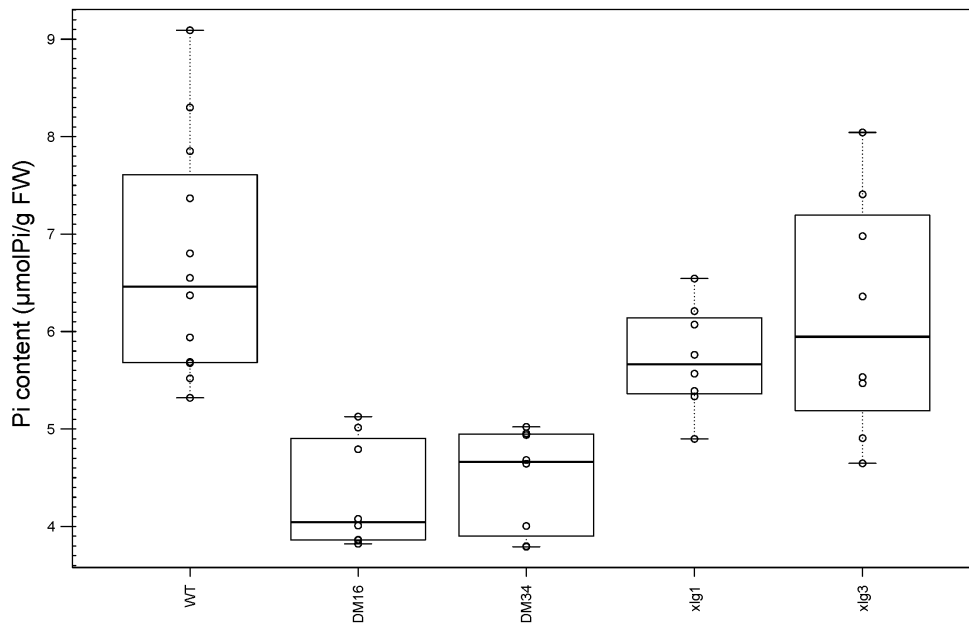


Figure S1. Boxplot showing the Pi levels in wild-type (WT), *xlg1-2* and *xlg3-2* single mutants and *xlg1-2 xlg3-2* double mutants (DM16 and DM34) grown in sufficient Pi condition for 20 days. Raw data is represented as dots

	Estimate	Std. Error	t value	Pr(> t )
DM16 - wt	-2.3857	0.4187	-5.697	< 0.001 ***
DM34 - wt	-2.2270	0.4187	-5.318	< 0.001 ***
<i>xlg1</i> - wt	-0.9842	0.4187	-2.350	0.082 .
<i>xlg3</i> - wt	-0.5383	0.4187	-1.285	0.543

Table S6. Dunnett's t test comparing each single and double *xlg* mutants with wild-type (wt). Significant codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1