Table S1. List of primers used in complementation assay. Bold text indicates the pDR195 recombination sequences.

PRIMER	UmZRT1 PRIMER SEQUENCES	UmZRT2 PRIMER SEQUENCES
1 Forward	**GAAAGAAAAAAAATATACCC CAGCCTCGACCCAGCCTCGA** GATGGCTGACGAAATTCAGTG	**GAAAGAAAAAAAATATACCC CAGCCTCGACCCAGCCTCGA** GATGTTGGGGATCAATGTTAA GAG
2 Reverse	**GAGACTTGACCAAACCTCTG GCGAAGAAGTCCAAAGCTGG ATCC**CTGTAGAGAGGAAAGAA TCGAGGT	**GAGACTTGACCAAACCTCTG GCGAAGAAGTCCAAAGCTGG ATCC**GGTTGCTATGCCAGACCT TAG
3 Forward	CAATCGTTAATAATTAATTAAT TGGAAAATAAC	CAATCGTTAATAATTAATTAAT TGGAAAATAAC
4 Reverse	CTACCAACGATTTGACCC	ACAATCTGCCACTTCACATTG
5 Reverse		CTACCAACGATTTGACCC

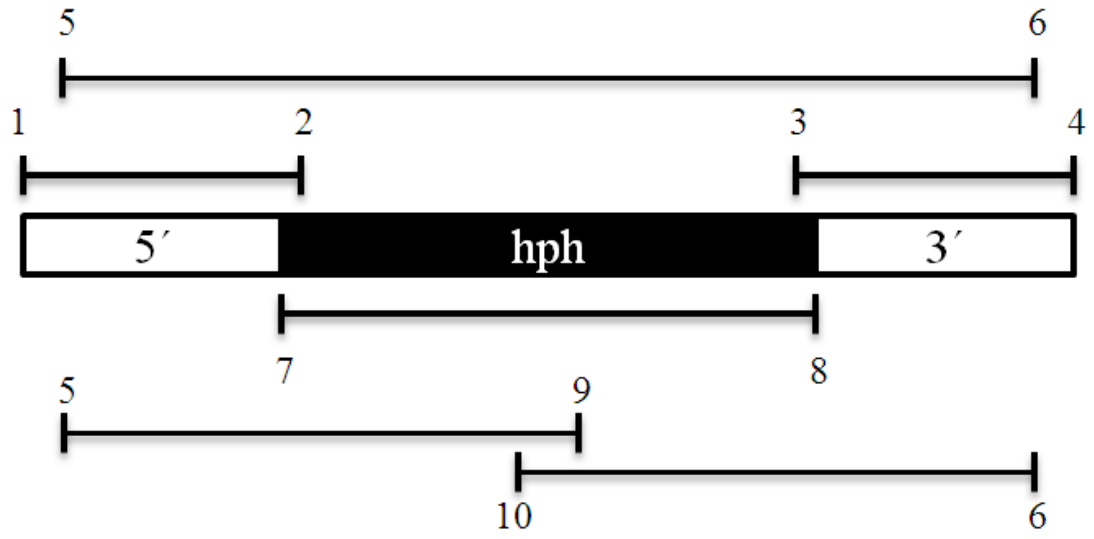

Figure S1. Representation of the gene replacement cassette. The construction is composed of 5´ and 3´regions localized approximately 1000bp upstream and downstream respectively from the open reading frame of the interest gene ORF, and the hph (hygromicin phosphotransferase) as resistance gene. The numbers represent the primers used to amplify the delimited region, and they are described in the Table S2.

Table S2. List of primers used to generate the replacement cassettes.

PRIMER	UmZRT1 PRIMER SEQUENCES	UmZRT2 PRIMER SEQUENCES
1	TCGAATGGACCAACTGTCTG	GCTCAAGCAGCTCGAAACTTG
2	GCACACGACTCACATCTGCCGC CACTC **TAACAGGGAAAGGGCCGAAC**	GCACACGACTCACATCTGCCGC CACTC**GCTACAGACTGGATCG GTTC**
3	AGTCTGCCAACGTGGAGTAAG TGAACC **CTTCGGACCTCGATTCTTTC**	AGTCTGCCAACGTGGAGTAAG TGAACC**GTTGCGTGATGTTCC GAGT**
4	AATGGACAGGACACATGGAG	CCTGGAAGCACACCGAGACT
5	GAACAGCAGCGGTTTCTGACC	GTGACTCTAGCACAAGCGGAC
6	GGATGACGAAGGGTTGGC	GGATACAACACGTTGGGCATC T
7	CTCGAGTGGCGGCAGATGTGA GTCG	CTCGAGTGGCGGCAGATGTGA GTCG
8	GGTTCACTTACTCCACGTTG	GGTTCACTTACTCCACGTTG
9	GAT TTG TGT ACG CCC GAC AG	
10		CGAGAGCCTGACCTATTGCATC

Table S3. Primers used in qRT-PCR.

GEN	FORWARD	REVERSE
UmZRT1	CTTCCTCTCGGCATGAAGTC	ATGAACTCGTGTGCAAGCAG
UmZRT2	CGTCTCTCCCTGCTAAGGTG	TCTTCTGCATCTGCCTGTTG
Rim101	GACTCGCACATGGCTGAGAGG	GCCGAGGGATCAAAGGCGG
Nrg1	ACTTGACCACCTCGACCTTG	AAAGGCGACACCATTCAATC
Actin	CTCBATCATGAAGTGTGA	BTGCTTYGARATCCACAT

Table S4. Differences in predicted transmembrane domains according to the prediction software used. All programs used predicted 8 transmembranal domains with slight variations in the endpoints of each domain.

Protein	Domain	PSIPRED	ExpasyTMpred	Protter version 1.0	UniProt database	HMMTOP
UmZrt1p	1	20-41	22-41	18-40	18-40	22-41
	2	57-75	60-79	60-78	60-78	60-79
	3	97-117	98-118	98-118	98-118	98-116
	4	212-227	209-227	206-227	206-227	206-225
	5	234-249	215-249	233-257	233-257	234-252
	6	269-286	265-288	269-288	269-288	265-288
	7	303-322	301-318	308-329	308-329	297-320
	8	341-358	341-359	341-361	341-361	341-359
UmZrt2p	1	185-206	13-33	183-207	183-207	193-212
	2	229-247	190-213	228-248	228-248	233-252
	3	267-286	226-248	268-290	268-290	267-286
	4	357-372	266-287	352-372	352-372	355-374
	5	382-397	364-387	378-397	378-397	379-398
	6	413-431	412-432	409-432	409-432	413-432
	7	447-466	444-463	444-464	444-464	445-464
	8	485-502	485-505	485-505	485-505	485-504

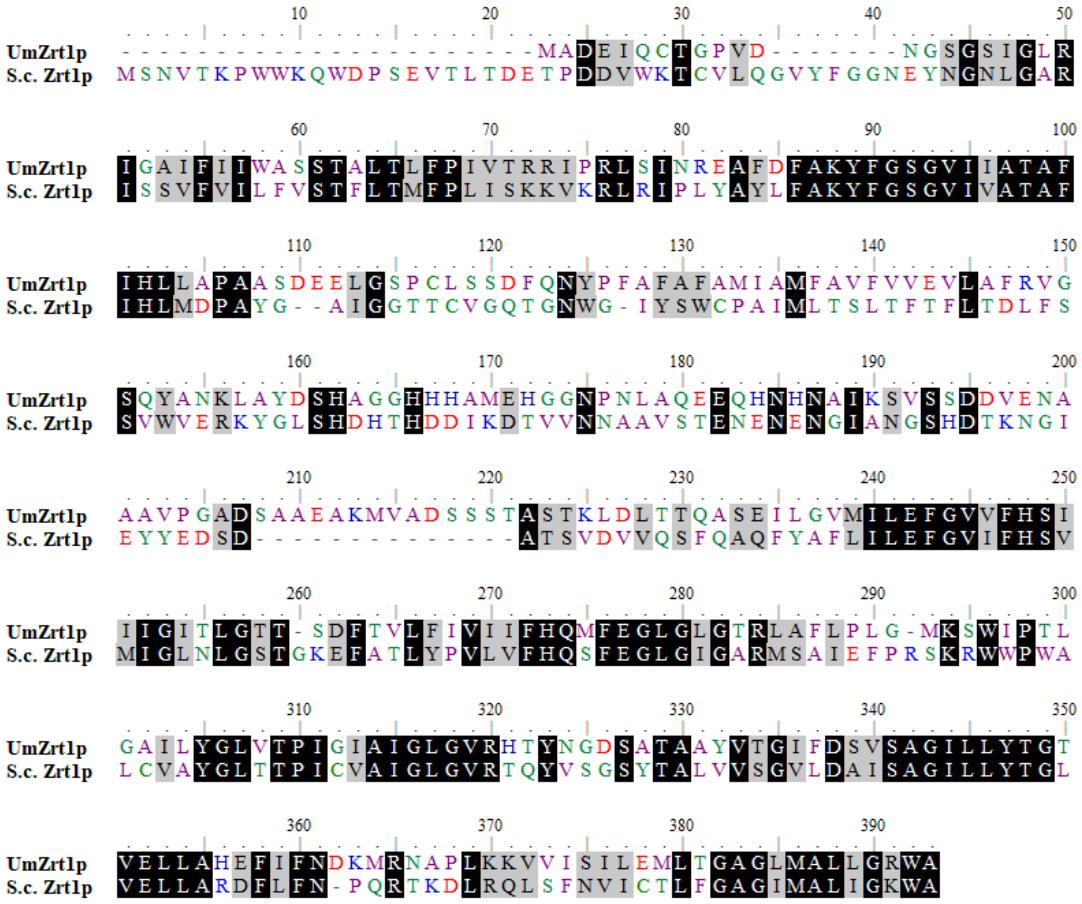

Figure S2. UmZrt1p and *Saccharomyces cerevisiae* Zrt1p alignment. Identical amino acids shared between the sequences are marked in black. Similar amino acids (same charge or hydrophobicity) are shown in gray. Polar amino acids are exhibited in green (G, S, T, Y, C, Q, and N), basic in blue (K, R, and H), acidic in red (D and E), and hydrophobic in purple (A, V, L, I, P, W, F, and M).

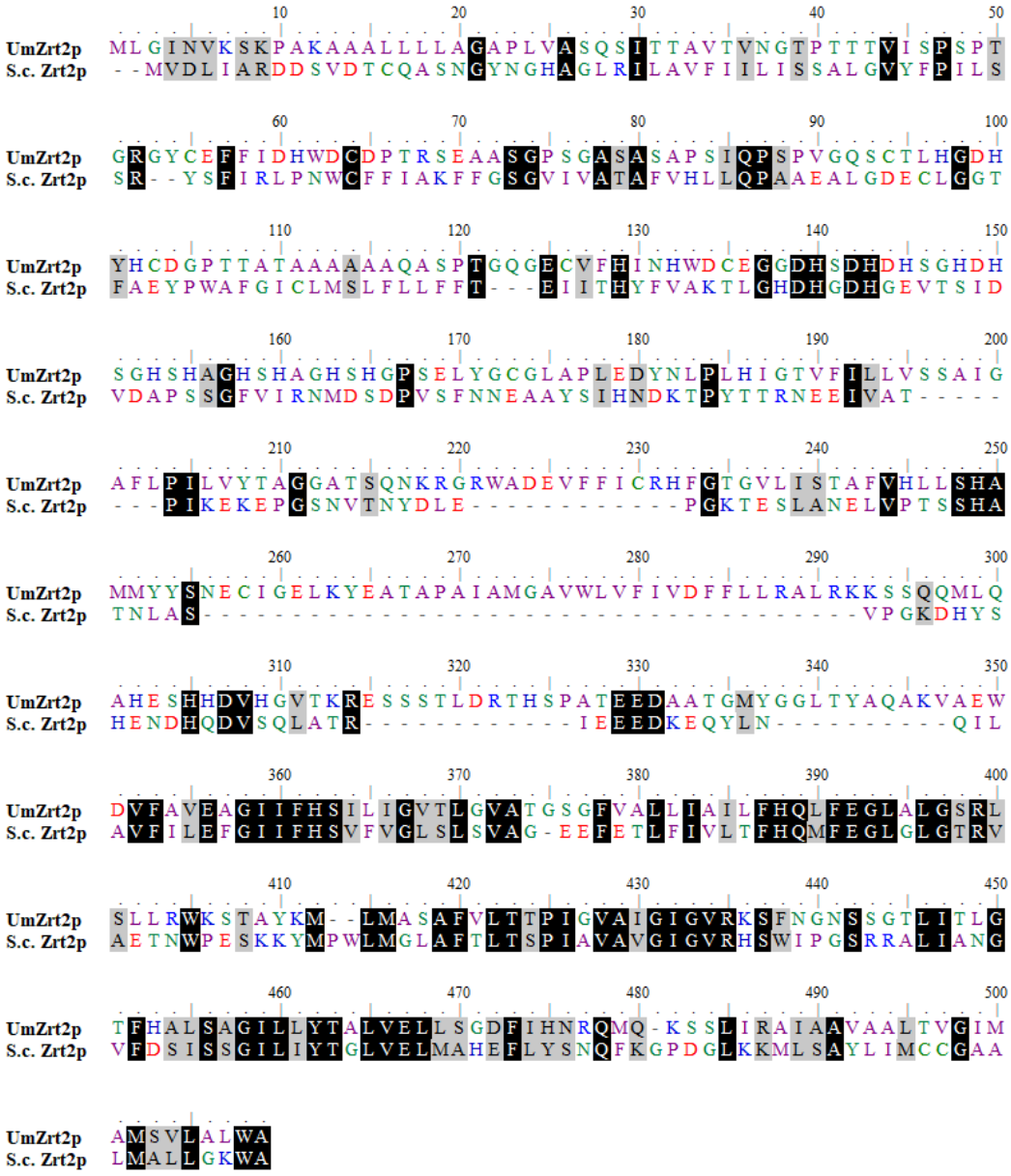

Figure S3. UmZrt2p and *Saccharomyces cerevisiae* Zrt2p alignment. Identical amino acids shared between the sequences are marked in black. Similar amino acids (same charge or hydrophobicity) are shown in gray. Polar amino acids are exhibited in green (G, S, T, Y, C, Q, and N), basic in blue (K, R, and H), acidic in red (D and E), and hydrophobic in purple (A, V, L, I, P, W, F, and M).

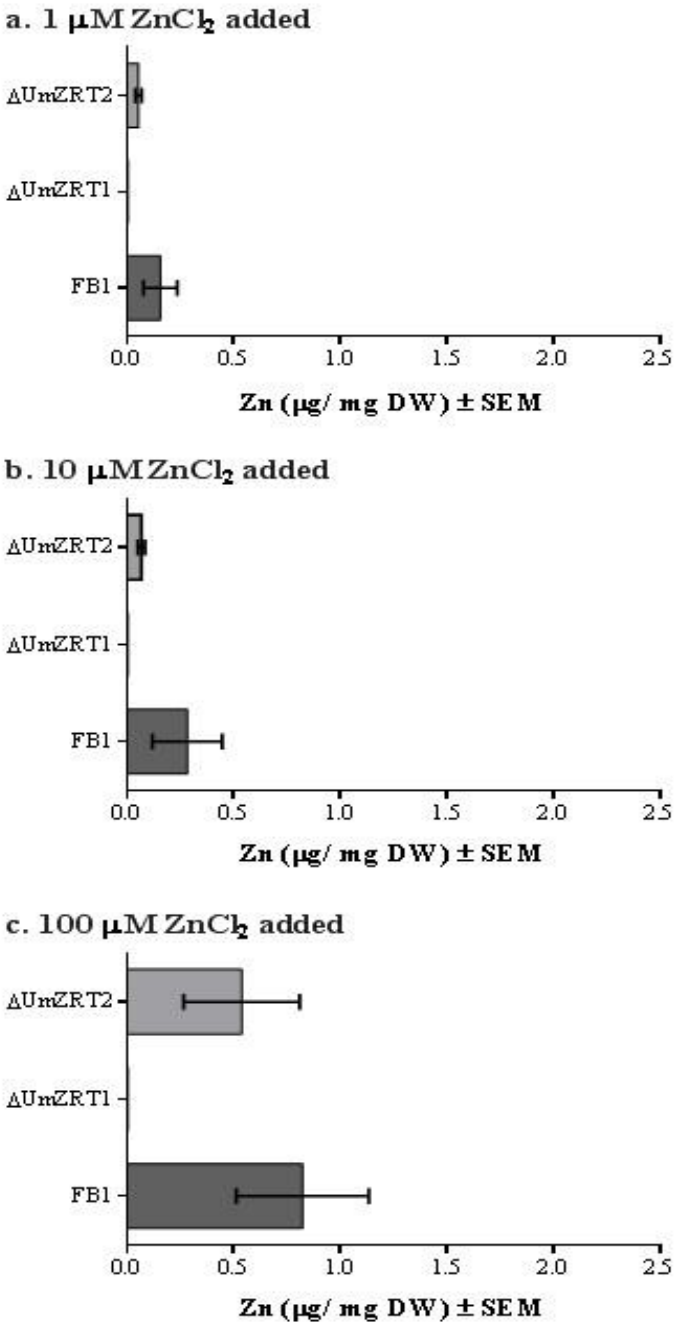

Figure S4. Quantification of zinc by ICP-OES. Determination of zinc concentration in dry weight of cells grown in YNB supplemented with 1, 10 and 100 µM of $ZnCl_2$ corresponding with a, b and c respectively.

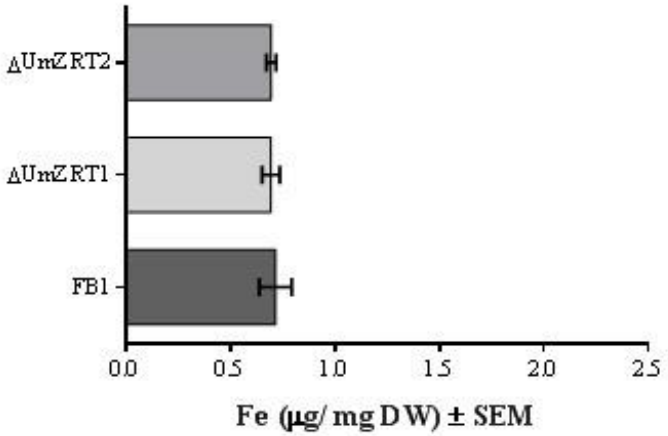

Figure S5. Quantification of iron by ICP-OES. Determination of iron concentration in dry weight of cells grown at YNB + 1 µM of $ZnCl_2$. All the strains showed the similar amount of iron.