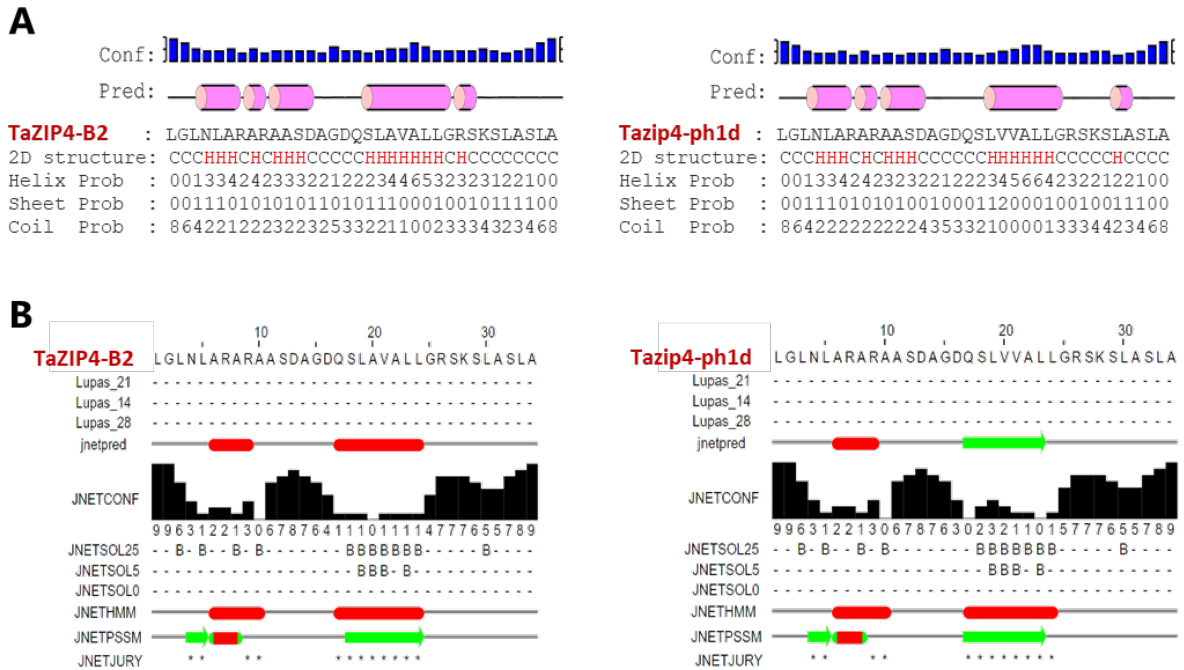**Supplementary Figure S1.** The differential pollen size distribution data collected by coulter counter (Multiziser 4e) for each plant (biological replicate) from the *zip4-ph1d* mutant and its corresponding wild type (cv. Cadenza). Five anther samples were collected from florets in the middle portion of the first spike of each plant. Each sample contains three anthers collected from the same floret. Pollen profiles are consistent within the same genotype and very similar in both genotypes.
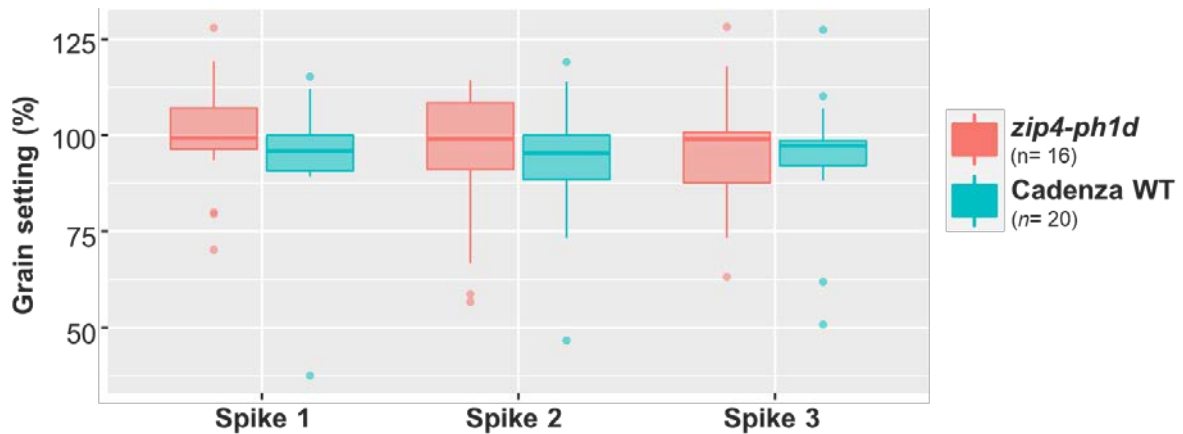
Supplementary Figure S2. Grain setting (normalized grain number per spike) in the first three spikes of the plant for the *zip4-ph1d* mutant and the wild type control (cv. Cadenza) under CER growth conditions. *n* refers to the number of plants (biological replicates) used in the experiment.

A

```
Conf: [blue bars]
Pred: [helix/coil diagram]
TaZIP4-B2      : LGLNLARARAASDAGDQSLAVALLGRSKSLASLA
2D structure:  CCCHHHCHCHHHCCCCCHHHHHHHCHCCCCCCCC
Helix Prob  : 00133424233322122234465323231222100
Sheet Prob  : 00111010101011010111000100010111100
Coil  Prob  : 86422122232232533221100233343234668
```

```
Conf: [blue bars]
Pred: [helix/coil diagram]
Tazip4-ph1d : LGLNLARARAASDAGDQSLVVALLGRSKSLASLA
2D structure: CCCHHHCHCHHHCCCCCCHHHHHCCCCCHCCCC
Helix Prob  : 00133424232322122234566423221222100
Sheet Prob  : 00111010101001000112000100010011100
Coil  Prob  : 86422222222224353321000013334423468
```

B

TaZIP4-B2   LGLNLARARAASDAGDQSLAVALLGRSKSLASLA
```
Lupas_21   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Lupas_14   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Lupas_28   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
jnetpred
JNETCONF
           99631221306787641110111147776557 89
JNETSOL25  - - B - - B - - B - B - - - - - - - BBBBBBB - - - - B - - - -
JNETSOL5   - - - - - - - - - - - - - - - - - - - BBB - B - - - - - - - - - - -
JNETSOL0   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
JNETHMM
JNETPSSM
JNETJURY       * *     * *           * * * * * * * *
```

Tazip4-ph1d   LGLNLARARAASDAGDQSLVVALLGRSKSLASLA
```
Lupas_21   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Lupas_14   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Lupas_28   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
jnetpred
JNETCONF
           9963122130678763023211015777655789
JNETSOL25  - - B - B - - B - B - - - - - - - BBBBBBB - - - - B - - - -
JNETSOL5   - - - - - - - - - - - - - - - - - - BBB - B - - - - - - - - - - - -
JNETSOL0   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
JNETHMM
JNETPSSM
JNETJURY       * *     * *           * * * * * * * *
```

Supplementary Figure S3. Prediction of the secondary structure of the TPR2 of in the wild type TaZIP4-B2 protein and mutant (Tazip4-ph1d). (A) 2D structure prediction using the PEP2D server based on PSSM random forest model. Helix is represented in cylindrical shape in pink colour and coil is represented as black line. **(B)** 2D structure prediction using the Jpred 4 server. Key: Jnet: Final secondary structure prediction for query; Jalign: Jnet alignment prediction; Jhmm: Jnet hmm profile prediction; Jpssm: Jnet PSIBLAST pssm profile prediction; Lupas: Lupas Coil prediction (window size of 14, 21 and 28). Jnet_25: Jnet prediction of burial, less than 25% solvent accessibility; Jnet_5: Jnet prediction of burial, less than 5% exposure; Jnet_0: Jnet prediction of burial, 0% exposure; Jnet Rel: Jnet reliability of prediction accuracy, ranges from 0 to 9, higher scores indicate greater significance.

Supplementary Table S6. Analysis of the level of micronuclei (MN) at the tetrad stage in (**A**) Cadenza wild type (WT) and (**B**) the *zip4-ph1d* mutant. Three individual plants were used from each genotype.

A

	Cadenza WT-1	Cadenza WT-2	Cadenza WT-3	All Cadenza WT
% Tetrads with MN	8.02	4.50	2.91	5.49
Total No. Tetrads	324	111	275	710
No. Tetrads with MN	26	5	8	39

B

	zip4-ph1d-1	*zip4-ph1d*-2	*zip4-ph1d*-3	All *zip4-ph1d*
% Tetrads with MN	10.52	13.91	11.82	12.26
Total No. Tetrads	190	273	279	742
No. Tetrads with MN	20	38	33	91

Supplementary Table S7. Frequencies of rod bivalents, ring bivalents, multivalents and total chiasmata in three haploid Cadenza wild type (Cad-WT) and three haploid Cadenza *zip4-ph1d* mutant plants. Mean number per cell and range of variation between cells are indicated.

A

Line	No. of cells examined	Rod bivalents		Ring bivalents		Multivalents		Chiasma frequency per cell	
		Mean	Range	Mean	Range	Mean	Range	Mean	Range
Haploid Cad-WT-1	**135**	0.585	0-3	0.007	0-1	0.015	0-1	0.630	0-5
Haploid Cad-WT-2	**158**	0.677	0-3	0.006	0-1	0.000	0	0.690	0-3
Haploid Cad-WT-3	**273**	0.549	0-2	0.015	0-1	0.000	0	0.579	0-3

B

Line	No. of cells examined	Rod bivalents		Ring bivalents		Multivalents		Chiasma frequency per cell	
		Mean	Range	Mean	Range	Mean	Range	Mean	Range
Haploid *zip4-ph1d-1*	104	3.288	0-6	0.760	0-4	0.788	0-3	6,423	2-10
Haploid *zip4-ph1d-2*	102	3.363	0-6	0.529	0-4	0.529	0-3	6.020	1-11
Haploid *zip4-ph1d-3*	227	3.441	0-6	0.696	0-3	0.718	0-3	6.326	0-12