

Table S1. Primer sequences designed for reference gene and each of 6 tested *TaCKX* genes and amplicon length.

Gene	Forward primer	Reverse primer	Amplicon length
<i>Ref2</i>	GCTCTCCAACAACATTGCCAAC	GCTTCTGCCTGTCACATACGC	165
<i>TaCKX1</i>	GTCTACCCGCTCAACAAATCC	CCCAGGTACTCCTTGTACCCTAT	188
<i>TaCKX2.1</i>	TCTACCCCATGAACCGGGAC	TCTCCTCGTTCTGCTCCTCC	144
<i>TaCKX2.2</i>	TTGATCGCGGAGCTAATCCA	TATCACATACGCCATCCATGC	205
<i>TaCKX3</i>	TTGTCAAGGGACTGTAGTAGGG	GAATTAGAGTTCACGGCTTGATG	150
<i>TaCKX5</i>	GTCCGATTTTGTAGAAGACTGATT	CATACATGACACCAACGTACATCTT	150
<i>TaCKX10</i>	GAGCTAAGGGCTTGTGGGA	ACATAAAGCAATTACCTGGACTTG	167

Table S2. Phenotypic traits and ratio indicator in silent T₁ and non-silent, control plants.

T ₁ (mean expression of <i>TaCKX1</i>)	plant height (cm) [SD]	number of spikes [SD]	spike length [SD]	grain number [SD]	grain yield (g) [SD]	TGW (g) [SD]	SPAD first spike [SD]	SPAD next spikes [SD]
Silent (0.58)	71.00 [3.91]	3.88 [1.27]	9.58 [0.98]	125.00 [47.88]	5.64 [1.93]	45.87 [3.2]	53.75 [1.55]	46.48 [5.67]
Non-silent (1.00)	71.00 [2.69]	4.88 [1.05]	9.94 [0.59]	178.13 [48.48]	7.91 [2.39]	44.36 [4.92]	53.39 [3.37]	46.81 [7.26]
Ratio indicator ¹	1.00	0.79	0.96	0.70	0.71	1.03	1.05	0.99

¹ ratio indicator (mean value in silent / mean value in not silent, control plants)

Table S3. Phenotypic traits and ratio indicator in silent T₂ and non-silent, control plants.

T ₂ (mean expression of <i>TaCKX1</i>)	plant height (cm) [SD]	number of spikes [SD]	spike length [SD]*	grain number [SD]	grain yield (g) [SD]	TGW (g) [SD]*	SPAD first spike [SD]	SPAD next spikes [SD]	Root weight (mg) [SD]
Silent (0.28)	70.33 [5.06]	7.83 [2.54]	7.78* [0.96]	127.33 [44.69]	4.80 [2.01]	36.59* [9.24]	40.10 [3.65]	44.08 [16.8]	92.00 [15.89]
Non-silent (1.00)	76.00 [3.51]	5.00 [1.91]	9.06* [0.68]	98.50 [40.43]	4.65 [1.93]	47.09* [2.01]	42.27 [3.13]	40.33 [4.56]	86.00 [18.00]
Ratio indicator	0.93	1.57	0.86	1.29	1.03	0.78	0.95	1.09	1.07

* significantly different ($p \leq 0.05$)

¹ ratio indicator (mean value in silent / mean value in non-silent, control plants)

Table S4 A. B. Correlation coefficients among expression of all tested *TaCKX* genes and enzyme activity, and phenotypic traits in non-silent (A) and highly silent T₂ plants (B). * non-parametric analysis; in bold - significant at p<0.01

silent	spike number *	spike length	grain number *	grain yield (g)	TGW	root mass	CKX activity	TaCKX 1	TaCKX 2.1	TaCK X 2.2	TaCKX 11 (3)	TaCKX 5*	TaCKX 9 (10)	tZ	tZGs	cZ	cZOG	DZGs	iP	BA	IAA	ABA	GA	SPAD first spike
plant height	0.03	0.31	0.38	0.34	0.32	-0.26	0.11	-0.32	-0.52	0.25	0.06	-0.15	0.43	-0.64	-0.7	-0.19	-0.24	-0.19	-0.45	0.3	-0.47	0.31	-0.22	0.42
spike number*		-0.03	0.88	-0.33	-0.39	-0.33	-0.03	-0.52	0.52	-0.21	-0.33	0.52	-0.15	0.52	-0.15	0.39	0.03	0.52	0.76	0.58	0.46	0.15	0.58	-0.27
spike length			0.2	0.61	0.55	0.12	0.85	0.33	-0.38	0.62	0.14	0.77	0.41	-0.42	-0.82	-0.62	-0.04	-0.52	-0.37	-0.48	0.13	-0.43	-0.53	0.52
grain number*				0.03	-0.09	-0.2	0.2	-0.54	0.14	-0.26	-0.14	0.6	-0.14	0.09	-0.54	0.03	0.26	0.26	0.43	0.54	0.54	0.14	0.2	0.2
grain yield (g)					0.82	0.66	0.81	-0.16	-0.6	-0.21	0.75	0.03	-0.34	-0.42	-0.76	-0.66	0.6	0.03	-0.53	0.07	0.36	0.39	-0.59	0.61
TGW						0.77	0.53	0.24	-0.85	-0.2	0.79	0.2	-0.33	-0.61	-0.55	-0.78	0.59	-0.27	-0.9	-0.33	0.09	0.22	-0.77	0.58
root mass							0.36	0.13	-0.54	-0.65	0.85	0.26	-0.82	-0.2	-0.06	-0.59	0.91	0.08	-0.57	-0.21	0.46	0.35	-0.58	0.34
CKX activity								0.03	-0.24	0.25	0.37	0.77	0.01	-0.19	-0.78	-0.56	0.28	-0.12	-0.16	-0.15	0.47	-0.1	-0.44	0.49
TaCKX1									0.02	0.39	0.12	0.2	0.14	0.14	0.19	-0.06	-0.23	-0.34	-0.29	-0.8	-0.35	-0.59	-0.04	-0.32
TaCKX2.1										0.18	-0.47	0.14	0.13	0.91	0.52	0.84	-0.52	0.52	0.93	0.29	-0.06	-0.18	0.89	-0.8
TaCKX2.2											-0.58	0.03	0.93	-0.09	-0.38	0.02	-0.76	-0.54	0.14	-0.42	-0.31	-0.76	0.07	0.00
TaCKX11 (3)												0.26	-0.73	-0.09	-0.22	-0.34	0.66	0.35	-0.59	0.08	0.07	0.6	-0.32	0.12
TaCKX5*													-0.14	0.03	-0.26	-0.43	0.54	-0.26	0.37	-0.09	0.71	-0.43	-0.14	0.09
TaCKX9 (10)														-0.22	-0.34	0.09	-0.82	-0.54	0.16	-0.23	-0.41	-0.63	0.1	0.06
tZ															0.59	0.8	-0.28	0.71	0.76	0.28	-0.05	0.03	0.85	-0.88
tZGs																0.56	-0.04	0.3	0.39	-0.02	-0.08	-0.04	0.5	-0.67
cZ																	-0.61	0.66	0.71	0.52	-0.48	0.16	0.99	-0.9
cZOG																		0.07	-0.41	-0.02	0.69	0.42	-0.62	0.5
DZGs																			0.46	0.78	-0.06	0.71	0.68	-0.61
iP																				0.41	0.18	-0.14	0.75	-0.55
BA																					-0.06	0.79	0.51	-0.21
IAA																						-0.05	-0.43	0.48
ABA																							0.13	-0.02
GA																								-0.91

[illegible]