

Supplemental Table S1. Sequence differences between *ZmOXS2* homologs from sweet corn and information from NCBI. Black lettering shows sequences from NCBI and the red lettering from sweet corn cultivar FengTian 1. Predicted domains where SNPs reside shown in parentheses.

	DNA			Protein		
ZmOXS2b	C	186	G			
	T	303	C			
	A	307	G	T	103	A (ANK)
	T	317	C	V	106	A (ANK)
	G	340	T	A	114	S
	T	399	C			
	C	441	T			
	A	555	G			
	T	561	C			
	G	775	A	V	259	I (ZnF_C3H1)
	C	930	G			
	G	958	A	A	320	T
	G	1179	C			
	T	1416	C			
T	1530	C				
ZmO2L1	C	1854	G	D	618	E

Supplemental Table S3. Significantly enriched Gene Ontology (GO) terms of DEGs. Expression patterns of some DEGs of C1 and C2 annotated to the given GO-term. Corrected P-value ≤ 0.05 defined as significantly enriched GO terms in DEGs.

	Gene Ontology term	Cluster frequency	Genome frequency of use	Corrected P-value
Terms for C1	oxidoreductase activity	19 out of 63 genes, 30.2%	1737 out of 16587 genes, 10.5%	0.00083
	iron ion binding	8 out of 63 genes, 12.7%	432 out of 16587 genes, 2.6%	0.01271
Terms for C2	arsenate reductase activity	2 out of 51 genes, 3.9%	8 out of 16587 genes, 0.0%	0.01051
	oxidoreductase activity	14 out of 51 genes, 27.5%	1737 out of 16587 genes, 10.5%	0.02289

Supplemental Table S4. RNA-seq and qRT-PCR values of 30 DEGs in intersection of C1 and C2. Values of RNA-seq and qRT-PCR are the fold change of DEG expression. Check marks indicate promoters of these genes contain BOXS2 motif. DEGs selected for tolerance test shown in numbers with parentheses. Value with asterisk indicates expression level differ between RNA-seq and qRT-PCR results.

C1					C2				
DEG#	AGI Code	BOXS2	RNA-seq	qRT-PCR	DEG#	AGI Code	BOXS2	RNA-seq	qRT-PCR
(11)	AT1G14960	✓	2.83	6.28	(11)	AT1G14960	✓	2.64	13.98
(19)	AT5G48850		2.50	5.95	(7)	AT5G26260		1.98	9.67
(20)	AT2G43535		5.99	5.65	(24)	AT5G48000		2.55	7.74
(24)	AT5G48000		3.81	5.43	(21)	AT4G13420	✓	3.61	7.62
(30)	AT5G39110		0.49 ★	5.25 ★	8	AT3G45140	✓	1.90	6.02
(7)	AT5G26260		2.35	4.82	(19)	AT5G48850		2.21	5.32
(21)	AT4G13420	✓	7.52	4.23	(23)	AT5G37990	✓	2.82	4.86
(23)	AT5G37990	✓	4.69	3.70	(30)	AT5G39110		1.96	4.07
12	AT3G49580		2.68	3.51	(20)	AT2G43535		2.79	3.62
4	AT5G24660		2.10	2.86	3	AT2G39310	✓	1.89	3.17
5	AT3G49570	✓	2.09	2.75	12	AT3G49580		2.60	3.08
1	AT1G75280	✓	2.22	2.68	25	AT2G05540		0.48 ★	3.01 ★
14	AT3G08860		2.57	2.53	16	AT4G13860	✓	2.51	2.94
8	AT3G45140	✓	1.72	2.19	5	AT3G49570	✓	2.00	2.73
17	AT5G23020		2.22	2.15	14	AT3G08860		2.96	2.72
18	AT5G26220		2.73	2.14	18	AT5G26220		2.18	2.68
6	AT4G04610	✓	2.12	2.01	4	AT5G24660		1.85	2.62
25	AT2G05540		0.53 ★	1.76 ★	10	AT1G16410		3.17	2.40
2	AT1G78370		2.18	1.76	1	AT1G75280	✓	1.91	2.35
3	AT2G39310	✓	2.08	1.70	13	AT3G19710		2.81	2.32
28	ATCG00800		0.38 ★	1.60 ★	6	AT4G04610	✓	2.05	2.17
10	AT1G16410		2.90	1.57	17	AT5G23020		2.40	2.11
15	AT3G02020	✓	2.53	1.55	15	AT3G02020	✓	2.47	2.07
16	AT4G13860	✓	2.35	1.54	28	ATCG00800		0.56 ★	1.98 ★
13	AT3G19710		2.72	1.51	2	AT1G78370		1.88	1.96
22	AT1G18100	✓	3.99	1.38	26	AT5G18600	✓	0.38 ★	1.85 ★
9	AT5G23010		1.83	1.06	9	AT5G23010		2.03	1.81
27	AT3G15450		0.35	0.65	22	AT1G18100	✓	3.37	1.60
29	ATCG00440		0.27	0.64	29	ATCG00440		0.42	0.69
26	AT5G18600	✓	0.43	0.64	27	AT3G15450		0.45	0.59

Supplemental Table S5. Primer Sequences. Capital lettering indicates sequences from genes, lower case from vectors.

primer name	Sequence	primer name	Sequence
ZmOXS2b-1F	5' gtaccocgggatcctATGGGGGAAGCCTCCGAC 3'	DEG23 (pro) R	5' ttggcgtctccatTGTTCCTTAGAGGCGAGAGA 3'
ZmOXS2b-1R	5' gcaggtgactctagCTAGACTACCATCTCATCCAGCTGG 3'	DEG24 (pro) F	5' gtaccocgggatcctCGAGATCGTGAATCCTTCTAGGTA 3'
ZmO2L1-1F	5'gtaccocgggatcctATGGGGGACCTTGCTGAT 3'	DEG24 (pro) R	5' ttggcgtctccatGCCCAAAACATATCGAGATCAATG 3'
ZmO2L1-1R	5' gcaggtgactctagCTAAAAGCTCAGGTGAGCTTG 3'	DEG30 (pro) F	5' gtaccocgggatcctATTTCGATTAGACATTATAGACATT 3'
ZmOXS2b-2F	5' gtaccocgggatcctclagaATGGGGGAAGCCTCCGAC 3'	DEG30 (pro) R	5' ttggcgtctccatTTTCAAAACAAAAGTTATGCTA 3'
ZmOXS2b-2R	5' gcaggtgactctclagaGACTACCATCTCATCCAGCTGG 3'	firefly luciferase F	5' ATGGAAGACGCCAAAAACATAAGA 3'
ZmO2L1-2F	5'gtaccocgggatcctclagaATGGGGGACCTTGCTGAT 3'	firefly luciferase R	5' gcaggtgactctagTTACACGGCGATCTTTCCGCC 3'
ZmO2L1-2R	5' gcaggtgactctclagaAAAGCTCAGGTGAGCTTG 3'	double 35S-Rluc F	5' cgggggactctagCCTGCAGGTCAACATGGTGG 3'
35S-DEGs constructs		double35S-Rluc R	5' gcaggtgactctagTCACTGGATTTTGGTTTTAGGAATT 3'
DEG 7 (AT5G26260) F	5' gtaccocgggatcctACAAAAACAAAAAAGATCTCA 3'	qRT-PCR analysis	
DEG 7 (AT5G26260) R	5' gcaggtgactctagCGTGCTTTAAACTATTTTGTCTAT 3'	DEG1 AT1G75280 q F	5' AACCAAGATCATTTCGCCA 3'
DEG 11(AT1G14960) F	5' gtaccocgggatcctGCATCAGAAAAACAGGAATAAAGCA 3'	DEG1 AT1G75280 q R	5' CCGCACTCGTCTTATCCACA 3'
DEG11(AT1G14960) R	5' gcaggtgactctagTAAGTTTGGGCTCATACCAGATTG 3'	DEG2 AT1G78370 q F	5' ACACCTCGTTTGTTCACGCAC 3'
DEG 19(AT5G48850) F	5' gtaccocgggatcctCTGTCAACAGACATCTTTATAATTA 3'	DEG2 AT1G78370 q R	5' GCAACGCAACTCTAGCCCTC 3'
DEG 19(AT5G48850) R	5' gcaggtgactctagACTTCTAGAGATTTTCATGGTTTTTC 3'	DEG3 AT2G39310 q F	5' ACATCATAGCAGTGGAGGGA 3'
DEG20 (AT2G43535) F	5' gtaccocgggatcctATAATAGTTATGACAGCTAATGACT 3'	DEG3 AT2G39310 q R	5' TTGACCAACCAATGGAGAC 3'
DEG20 (AT2G43535) R	5' gcaggtgactctagCCGTCAAATCAATCTGC 3'	DEG4 AT5G24660 q F	5' AAGAACCGAGAGATGGAGAA 3'
DEG21 (AT2G43535) P1 F	5' gtaccocgggatcctACAGCCGGCAATACGTGTTTGAGAC 3'	DEG4 AT5G24660 q R	5' GGCTAGCTGTGAGCAGAGAC 3'
DEG21 (AT2G43535) P1 R	5' CGTCACATAATAAAAAGTCAACAGT 3'	DEG5 AT3G49570 q F	5' AAGCAGCAAAACCACCTAAC 3'
DEG21 (AT2G43535) P2 F	5' TTTTATTATGTGACGCACGCTCCTCC 3'	DEG5 AT3G49570 q R	5' CCATTTCTCTCTCAACTCTC 3'
DEG21 (AT2G43535) P2 R	5' GCCTTTAAGACGGTAATGTCATGCT 3'	DEG6 AT4G04610 q F	5' CTCTCGTTTCGGTGTTCAT 3'
DEG21 (AT2G43535) P3 F	5' TACCGTCTTAAAGCCTTAATCCA 3'	DEG6 AT4G04610 q R	5' TGTCTTGGTTCAGCGTTTA 3'
DEG21 (AT2G43535) P3 R	5' gcaggtgactctagTAGATAAATGACAAATGTTAAAGCT 3'	DEG7 AT5G26260 q F	5' CCCGACAGAAAAAAGAGAAAG 3'
DEG 23(AT5G37990) F	5' gtaccocgggatcctAAAACAATAACCAATTCTCCTAAAG 3'	DEG7 AT5G26260 q R	5' TCCAACAAGAAAATCATCAGAGT 3'
DEG 23(AT5G37990) R	5' gcaggtgactctagAAATATAGTATGTAATCCAACCA 3'	DEG8 AT3G45140 q F	5' AGATGACTTGATTGGTGTGT 3'
DEG 24(AT5G48000) F	5' gtaccocgggatcctCCCTAATACGCCCCCTCG 3'	DEG8 AT3G45140 q R	5' TCTTATCCTTGTTCGTGGT 3'
DEG 24(AT5G48000) R	5' gcaggtgactctagTGAATACCTTATCGATATATTCATC 3'	DEG9 AT5G23010 q F	5' CCGACAGCTCGCTAACTCC 3'
DEG30 (AT5G39110) F	5' gtaccocgggatcctATGAGGTTTTCCAAGTCTCTCATCC 3'	DEG9 AT5G23010 q R	5' CATCCACCTCATTCCCAACA 3'
DEG30 (AT5G39110) R	5' gcaggtgactctagTATCCAAGAAAATGTTAATACCCCG 3'	DEG10 AT1G16410 q F	5' AGAAGGTGGTAAGGCTGCTGT 3'
Luciferase assay constructs		DEG10 AT1G16410 q R	5' GCTTTGATTTCTGTGTGTG 3'
DEG7 (pro) F	5' gtaccocgggatcctGAAGTCAGGGATATTCTTCTTCTC 3'	DEG11 AT1G14960 q F	5' CTCGTGATGGGAAAGAGGAA 3'
DEG7 (pro) R	5' ttggcgtctccatTTTTGAGACTTTTTTGTGTTT 3'	DEG11 AT1G14960 q R	5' GGACTCGGGGATGAAATGTA 3'
DEG11(pro) F	5' gtaccocgggatcctAGCGAGAGCGAGACAGAGAGG 3'	DEG12 AT3G49580 q F	5' ACAGGCACGTGACTATCAGAT 3'
DEG11(pro) R	5' ttggcgtctccatTGATGAATCAATTAGCTTTGGATTG 3'	DEG12 AT3G49580 q R	5' GGAAGAGACGACAGAAGAAGAA 3'
DEG19(pro) F	5' gtaccocgggatcctTATTACTAGACTAAGCCACTGTTAT 3'	DEG13 AT3G19710 q F	5' AAACACATCCATGGCTCTTCT 3'
DEG19(pro) R	5' ttggcgtctccatCTTTTTTCTCTGTTTTTCT 3'	DEG13 AT3G19710 q R	5' CTCTTCCCACTGACATTCGCA 3'
DEG20 (pro) F	5' gtaccocgggatcctTGAATGGTCCACCAAGTAATAATGA 3'	DEG14 AT3G08860 q F	5' AATGCTAACCTCGTGGCTCAC 3'
DEG20 (pro) R	5' ttggcgtctccatGGCGATTCTCTATCTTCTCTCTCT 3'	DEG14 AT3G08860 q R	5' AATCTCTCCCTCTCACGCTC 3'
DEG21(pro) F	5' gtaccocgggatcctGTGAAAAATCATATGCTATGCATCG 3'	DEG15 AT3G02020 q F	5' CTCAAAGGGGCTCAACTTCTCA 3'
DEG21(pro) R	5' ttggcgtctccatTTTTTGCTGTGTTTTTTTTTTTT 3'	DEG15 AT3G02020 q R	5' CTCACTCTTCCGCTTCAACA 3'
DEG23 (pro) F	5' gtaccocgggatcctAGGATAATATGTATGACGTATGAGT 3'	DEG16 AT4G13860 q F	5' GATATGTTGAGGGAAGCCTTT 3'

primer name	Sequence	primer name	Sequence
DEG16 AT4G13860 q R	5' CGGAGTGACTGCTGTATGTGAC 3'	DEG11 F3 F	5' CGAGAGCGAGACAGAGAGGAC 3'
DEG17 AT5G23020 q F	5' GCAGCACTTACTCCACCGCA 3'	DEG11 F3 R	5' CAGAAACAAACGTGGGAACATA 3'
DEG17 AT5G23020 q R	5' TTCTTCCCTCAGACGACACCG 3'	DEG11 F4 F	5' TGTTAACGTAGCTTGGTGTGA 3'
DEG18 AT5G26220 q F	5' TGCTTATTGTGTCTGGAG 3'	DEG11 F4 R	5' AGTGCTTTTATTCCTGTTTTCT 3'
DEG18 AT5G26220 q R	5' GATTGGCGTGAAGTGCAT 3'	DEG19 F5 F	5' ACTAGACTAAGCCACTGTTATGT 3'
DEG19 AT5G48850 q F	5' GCTATCAAATCTTTCCGTCC 3'	DEG19 F5 R	5' GTAAAACGGTCCATTAGAACATC 3'
DEG19 AT5G48850 q R	5' ACAACTCAACTTGCTCCTCC 3'	DEG19 F6 F	5' ATATTGTCCAAATTCATTCTTA 3'
DEG20 AT2G43535 q F	5' CGCCTAAGATATTTCCGACG 3'	DEG19 F6 R	5' CTTTTTTCCTCTGTTTTCTCT 3'
DEG20 AT2G43535 q R	5' AGCATTCACTTTACCGCCC 3'	DEG20 F7 F	5' ATATTGTCCAAATTCATTCTTA 3'
DEG21 AT4G13420 q F	5' GCAAAAAATGGATGGTGGAG 3'	DEG20 F7 R	5' CTTTTTTCCTCTGTTTTCTCT 3'
DEG21 AT4G13420 q R	5' ATGATGAAAAGATCGGGTGC 3'	DEG20 F8 F	5' TTATTTGATTTTTTTGTTGT 3'
DEG22 AT1G18100 q F	5' TCGTGAGAGTTTGGTGAAGA 3'	DEG20 F8 R	5' CTCATTGTGTTGTGTAGTGGT 3'
DEG22 AT1G18100 q R	5' AAATCGCAGAATACGGTGTG 3'	DEG21 F9 F	5' TCGCAAAAGTTAATTATGAAA 3'
DEG23 AT5G37990 (CIMT1) q F	5' AAGCCACTAACCAACGACTT 3'	DEG21 F9 R	5' AACCAGAAAGGAAGATACCGCAT 3'
DEG23 AT5G37990 (CIMT1) q R	5' GCTCATTGACCACACCATCT 3'	DEG21 F10 F	5' CTATTACGCCTATAAAGCCACT 3'
DEG24 AT5G48000 q F	5' GTGTTGGAGGTGGAGTGGAG 3'	DEG21 F10 R	5' TTTTTGTGTTGTGATATTGTGAC 3'
DEG24 AT5G48000 q R	5' TTTGGGAAGTATGGGAGTG 3'	DEG23 F11 F	5' GTTGTTCCTTTTTTTTTTCTTT 3'
DEG25 AT2G05540 q F	5' ATACTACCAGTTCTTTCTTCCA 3'	DEG23 F11 R	5' AGTTTAGCTGTCAGCTCTTCT 3'
DEG25 AT2G05540 q R	5' TTTTCTGCTCTGCCGATTTCTC 3'	DEG23 F12 F	5' GTTAATAAATACGAGGTGGC 3'
DEG26 AT5G18600 q F	5' GAGGGAGGGAGATCGAGCAG 3'	DEG23 F12 R	5' AGAGAAAAACAACTTTAGGAGAA 3'
DEG26 AT5G18600 q R	5' TTAAGCATGGAATCAAGGA 3'	DEG24 F13 F	5' TACAAGAAAAATAAAAAACACA 3'
DEG27 AT3G15450 q F	5' ATCGTTTGCTCCTTCCCTAA 3'	DEG24 F13 R	5' TAGCCATAACAAAAGATTGA 3'
DEG27 AT3G15450 q R	5' CCTTCACTATCAATCCTCGGC 3'	DEG24 F14 F	5' GATGATAAATAATGTGTGTTGA 3'
DEG28 ATCG00800 q F	5' GGACAATTAATAAATCGCGTT 3'	DEG24 F14 R	5' AGTTGAGTAGGATCTTAAGTGT 3'
DEG28 ATCG00800 q R	5' TTCTCTGATCCATTCAACAGC 3'	DEG30 F15 F	5' TCTTATATTCTTTTTGGTTTT 3'
DEG29 ATCG00440 q F	5' GATGTACTGGGGTATCTGCT 3'	DEG30 F15 R	5' ACTTGGTCTTAGCAATTTGT 3'
DEG29 ATCG00440 q R	5' CCATTCCAATGCTCCTTTTCG 3'	DEG30 F16 F	5' ACAATTGCAATCCCGTAAAAACAT 3'
DEG30 AT5G39110 q F	5' TATCGGCTTTGGTCAATTCCT 3'	DEG30 F16 R	5' AAACCCGTCGGTAAAAAAA 3'
DEG30 AT5G39110 q R	5' ATCTTCTGCCCTTGGCTTCT 3'	DEG23 F17 F	5' AAAGAGGAATTGAGAGAAAAGAA 3'
actin1(AT2G37620) Forward	5' GATTGGCATCACACTTTCTACAATG 3'	DEG23 F17 R	5' ATACCAAAAAATAGCATAACAGA 3'
actin1(AT2G37620) Reverse	5' GTTCCACCACTGAGCACAATG 3'	DEG23 F18 F	5' AAAGACAAACCATAAATAA 3'
ZmOXS2b forward qRT	5' CCCCCGAGCACACCAGATT 3'	DEG23 F18 R	5' GGCAGATCTCAAATCAATAA 3'
ZmOXS2b reverse qRT	5' CCTTACAAGGGTATTGACCCAT 3'	DEG23 F19 F	5' GTTTATAAGTCTTCTTGGTCCC 3'
ZmO2L1 forward qRT	5' ATCCTCGCAAGCACCCATACA 3'	DEG23 F19 R	5' TCATTTAGCATAATCGACATCCA 3'
ZmO2L1 reverse qRT	5' AGCCAGCTCTCGAAAAACCA 3'	DEG23 F20 F	5' GAGGTGGCCCGATTTTTTA 3'
ZmEF1-α forward qRT	5' TGATGAGATTGTGAAGGAAGTC 3'	DEG23 F20 R	5' AAGGCACTCAACATTGTTCTTA 3'
ZmEF1-α reverse qRT	5' CAGAGATTGGAACGAAGTGG 3'	AtOXS2 -F	5' GGGGTACCATGTGCTGGATCAGACCG 3'
ChIP-qPCR analysis		AtOXS2 -R	5' AACTGCAGATTCTGCTGAGCCACAAGCTGATC 3'
actin2 F	5' GTTAGCAACTGGGATGATATGG 3'	ZmOXS2b-3F	5' GGGGTACCATGGGGAAGCCCTCCGACGC 3'
actin2 R	5' CAGCACCAATCGTGATGACTTGCCC 3'	ZmOXS2b-3R	5' GGACTAGTCAGATCTACGACTACCATCTCATCCAG 3'
DEG7 F1 F	5' TTCTTAGTTTTTTTTTTGTGAT 3'	ZmO2L1-3F	5' GCTCTAGAATGGGCGACCTTGCTGAT 3'
DEG7 F1 R	5' ACCCTGGAGTTTTCTTTTTTAT 3'	ZmO2L1-3R	5' GAAGATCTACAAAGCTCAGGTGAGCTGTGTA 3'
DEG7 F2 F	5' AACATCTACCTTTCCCAATGGAC 3'	CIMT1 F	5' GCGGAGCTCATGTTGAGTGCCTTTTTGGG 3'
DEG7 F2 R	5' TATCAAAATACCGACGAAATCA 3'	CIMT1 R	5' GCGGATCCTTTTTTTTAAAGCAGATAAAATAATC 3'