

Table S1. Details of genes and their primers for qRT-PCR analysis

No.	Gene code	Accession number	Nr/Nt description	Primer Sequence (5'-3')	Product Size (bp)	Tm (°C)
1	AsCAT1	F01_transcript_13967	<i>Aegilops tauschii</i> subsp. stragulata catalase isozyme 1	F: ACAGGGATGAGGAGGTGAACTAC R: CGCTGGATGAAACGGTCTTGC	193	58.8 59.7
2	AsPOD1	F01_transcript_67131	<i>Triticum dicoccoides</i> 1-Cys peroxidase	F: GCCCGACAAGAAGGTGAAGC R: GCCGTGAGCAGCGAGTCC	96	58.6 59.9
3	AsPOD12	F01_transcript_17118	<i>A. tauschii</i> peroxidase 12	F: CCCAAGGCAGAGTCCATCGTG R: CCGTCCAGGAGCACTGAAGC	137	60.3 60.1
4	AsMn-SOD	F01_transcript_21558	<i>Stipa purpurea</i> Mn-superoxide dismutase	F: AGAAGCACCACGCCACCTAC R: CGCCGCCGTTGAACITGATG	126	59.4 59.9
5	AsCu/Zn-SOD	F01_transcript_22817	<i>Agrostis stolonifera</i> cytosol Cu/Zn-superoxide dismutase	F: ACCGCCGTGACAGGAAGC R: GCAACACCATCCGCTCCAG	200	59.1 58.1
6	AsFe-SOD	F01_transcript_33161	<i>A. tauschii</i> subsp. stragulata Fe-superoxide dismutase	F: GCTGATGTGCTTGAATCCTTGAAC R: GTGCTTGCTGGTGAACCTCC	150	58.8 59.3
7	AsGR1	F01_transcript_53759	<i>A. tauschii</i> subsp. stragulata glutathione reductase, cytosolic	F: AGAAGCAGCATATCCAAACGACAG R: CAGCCTTGAGTGCGACAGC	142	57.5 58.4
8	AsGR2	F01_transcript_81228	<i>T. dicoccoides</i> glutathione reductase, chloroplastic-like	F: ACGACTACGACCTCTTACCACATC R: GAACACACCCACGAAGCACAC	171	59.4 59.5
9	AsMDHAR	F01_transcript_29627	<i>B. distachyon</i> monodehydroascorbate reductase	F: GCGGAGCAGGCAGTGAAGG R: GCGAGTAGAAGTAGGCGAGGTAG	85	58.4 56.5
10	AsAOX1C	F01_transcript_105355	<i>T. dicoccoides</i> ubiquinol oxidase 1c, mitochondrial-like	F: GCTGGAGGAGGCGGAGAAC R: TCGGTGTAGGAGTGGATGGC	200	59.1 58.3
11	AsLDHA	F01_transcript_70112	<i>T. dicoccoides</i> L-lactate dehydrogenase A-like	F: CCTTGCCACCTCCCTCCTC R: CAGTTCTCCACAGCGTCTTG	213	58.3 58.5
12	AsGLX1	F01_transcript_18206	<i>T. dicoccoides</i> lactoylglutathione lyase	F: AAGTTATGCTCCGTGTTGGTGAC R: TCGGTTGCCCTTGCTATATCTTG	200	59 59.2
13	AsGLX2	F01_transcript_67599	<i>A. tauschii</i> subsp. stragulata probable hydroxyacylglutathione hydrolase 2	F: CTTGAGCGTAGAACCAGGAAAC R: ATTGTTGTGGCACCGTTGG	96	56.8 56.9
14	AsNAC74	F01_transcript_87068	<i>B. distachyon</i> NAC domain-containing protein 74	F: TGCCAAGCCTGCCCTGATATG R: ATTATTGTTGCCACCTCGTTTCC	102	60 59.7
15	AsNAC67	F01_transcript_27463	<i>B. distachyon</i> NAC domain-containing protein 67	F: CCGCCTTGCCGACACCTC R: TCTTCTCCCATTCGTTCTTCTGTC	107	59.8 59
16	AsNAC83	F01_transcript_44175	<i>B. distachyon</i> NAC domain-containing protein 83	F: CGGAAGGCTGGGTGCTCTG R: TCGTGGACGGGATCTTCTTGG	118	59.7 59
17	AsAIL1	F01_transcript_28993	<i>A. tauschii</i> subsp. stragulata AP2-like ethylene-responsive transcription factor AIL1	F: GACGAGACAGGAGTTCATTGCG R: TGCCGTGCTGGTGATGCC	101	59.1 59.8
18	AsBBM1	F01_transcript_63832	<i>A. tauschii</i> subsp. stragulata AP2-like ethylene-responsive transcription factor BBM1	F: CCACCAGTATCTGCCTCCACAAC R: TTCGTCCACTTCCTCATTTCTTCGG	147	60.7 60.5
19	AsRAD2-13	F01_transcript_77110	<i>A. tauschii</i> subsp. stragulata ethylene-responsive transcription factor RAP2-13	F: CCGCCGAGCAGAGGTTTC R: GCGAGAAGCGAGTCCAGTC	124	60.2 59.9
20	AsWNK8	F01_transcript_61751	<i>A. tauschii</i> subsp. stragulata probable serine/threonine-protein kinase WNK8	F: CGTGGAGGTGGCGTGGAAC R: GCGGTGGAAGGCGATGATGG	130	60.2 60.9
21	AsMAPK2	F01_transcript_37493	<i>T. aestivum</i> mitogen-activated protein kinase 2	F: ATAAGTGATACTCCAAGTCCATC R: TATCTATTGCTGGTGTGTAAGTTCG	112	56.2 56.3
22	AsAPX	F01_transcript_31727	<i>Puccinellia tenuiflora</i> ascorbate peroxidase	F: AAGGACTATGCTGAATCACACAAG R: CAACTGCTACGCCGACTGC	133	56.9 58.5
23	AsDHAR	F01_transcript_51051	<i>P. tenuiflora</i> dehydroascorbate reductase	F: AAGACCAAGCCAGCCAAGGAG R: AAGGACAGGACAGAACACAGACG	111	59.8 60.0
24	AsEIF4A	F01_transcript_15006	<i>B. distachyon</i> eukaryotic initiation factor 4A-III homolog A	F: TCTCGCAGGATACGGATGTCTG R: TCCATCGCATTTGGTCGCTCT	88	63.3 63.6

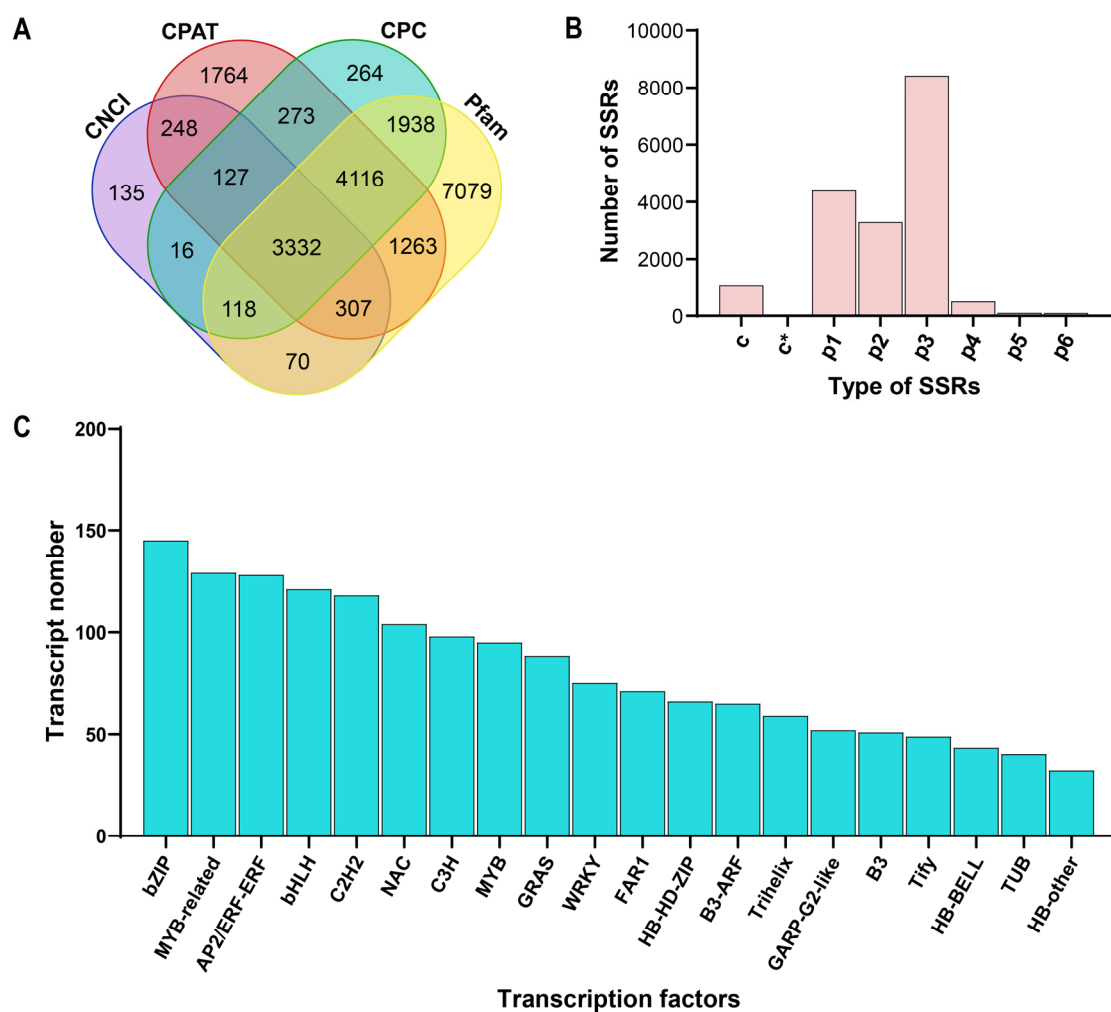


Figure S1. Statistics of identified lncRNAs, SSRs and TFs. **(A)** Venn diagram of identified lncRNAs from the Coding Potential Calculator (CPC), Coding-Non-Coding Index (CNCI), CPAT (Coding Potential Assessment Tool) and Pfam database. **(B)** Density distribution of seven SSR types. c, compound SSR; p1, mono-nucleotide; p2, di-nucleotide; p3, tri-nucleotide; p4, tetra-nucleotide; p5, penta-nucleotide; p6, hexa-nucleotide. **(C)** Statistics of the top 20 TFs; Table S1: Details of genes and their primers for qRT-PCR analysis.