Electronic supplementary material

Supplementary Fig. 1. Multiple sequence alignment of the WRKY domain in Tartary buckwheat.

Supplementary Table 1. Number of WRKY genes identified in various species.

| Group | F.tatarium | Arabidopsis thaliana | Oryza sativa | Triticum aestivum | Apium graveolens | Camellia sinensis | Populus trichocarpa | Glycine max |
|-------|------------|----------------------|--------------|-------------------|------------------|-------------------|--------------------|------------|
| I     | 16         | 32                   | 34           | 25                | 10               | 13                | 50                 | 32         |
| II a  | 6          | 3                    | 4            | 5                 | 6                | 4                 | 5                  | 14         |
| II b  | 10         | 8                    | 8            | 1                 | 8                | 3                 | 9                  | 33         |
| II c  | 17         | 7                    | 7            | 12                | 21               | 12                | 13                 | 42         |
| II d  | 12         | 8                    | 11           | 12                | 6                | 7                 | 13                 | 21         |
| II e  | 10         | -                    | -            | 5                 | 12               | 5                 | 4                  | 20         |
| III   | 7          | 14                   | 36           | 33                | 6                | 6                 | 10                 | 26         |
| Total | 78         | 72                   | 100          | 93                | 69               | 50                | 104                | 188        |
**Supplementary Table 2.** The 14 representative WRKYS in *Arabidopsis thaliana* included in this study.

| Name     | Gene ID   | Subfamily |
|----------|-----------|-----------|
| AtWRKY6  | At1g62300 | II b      |
| AtWRKY8  | At5g46350 | II c      |
| AtWRKY9  | At1g68150 | II b      |
| AtWRKY12 | At2g44745 | II c      |
| AtWRKY14 | At1g30650 | II e      |
| AtWRKY15 | At2g23320 | II d      |
| AtWRKY18 | At4g31800 | II a      |
| AtWRKY21 | At2g30590 | II d      |
| AtWRKY25 | At2g30250 | I         |
| AtWRKY33 | At2g38470 | I         |
| AtWRKY40 | At1g80840 | II a      |
| AtWRKY46 | At2g46400 | III       |
| AtWRKY54 | At2g40750 | III       |
| AtWRKY65 | At1g29280 | II e      |

**Supplementary Table 3.** FtWRKY primers used in the expression pattern analysis.

| Gene name | Forward (5'-3') | Reverse (5'-3') |
|-----------|-----------------|-----------------|
| FtWRKY6   | ATCCTCTGCTTCCATGGCTT | AGACCTGCTTCTCTGTGACC |
| FtWRKY7   | CCGACGAGCACAACAAATCAT | TGAAACAGGAGCAAGGAAG |
| FtWRKY31  | CCCAGAGTGTCCACACATC | CATGCGGAATCTTGGCTT |
| FtWRKY74  | ACCGGAGAGGCTGTTACAAA | ACTTGCTTGATTGCTTGCA |
| Histone3  | AAGGAGCAATTGGCAAC | TCAGAAAGGACCAACGTA |

**Supplementary Table 4.** Details of the identified motif sequences.

| Motif | E value   | Width | Site | Best possible match                                                                 |
|-------|-----------|-------|------|-------------------------------------------------------------------------------------|
| 1     | 1.0E-1685 | 29    | 76   | LEDGYRWRKYGQVKVGKYPYPRSVYKYKCTH                                                    |
| 2     | 7.0E-716  | 24    | 56   | GCPRVRKQVQRCADERSUJTTYG                                                             |
| 3     | 4.80E-276 | 41    | 11   | DGYVWRKYGQVKQVKASEFPRSVYKYKCTHPNCVKKVEHSGD                                       |
| 4     | 1.2E-166  | 21    | 31   | KRKKKKEREPRIATMKTEDVH                                                             |
| 5     | 8.5E-166  | 49    | 10   | NHNLPLPAAMAMASTTTAAAASMLSGSMPADGLMNPFLALTLPSC                                 |
| 6     | 8.6E-162  | 15    | 29   | ITEIYKGAHNHPKP                                                                  |
| 7     | 1.4E-137  | 21    | 14   | GRCSSRKRRKSRVRRVRRVPA                                                            |
| 8     | 5.5E-105  | 29    | 14   | FLVEQMASSLLKPFPTTAALAAASGRFM                                                      |
| 9     | 1.40E-94  | 15    | 17   | GCAPKHERVQLDP                                                                  |
| 10    | 3.70E-89  | 48    | 10   | TELAKLQVELEQMNIEERLKMLAQVQSQNYTALQMHVVAIMQQHQNQ                                |