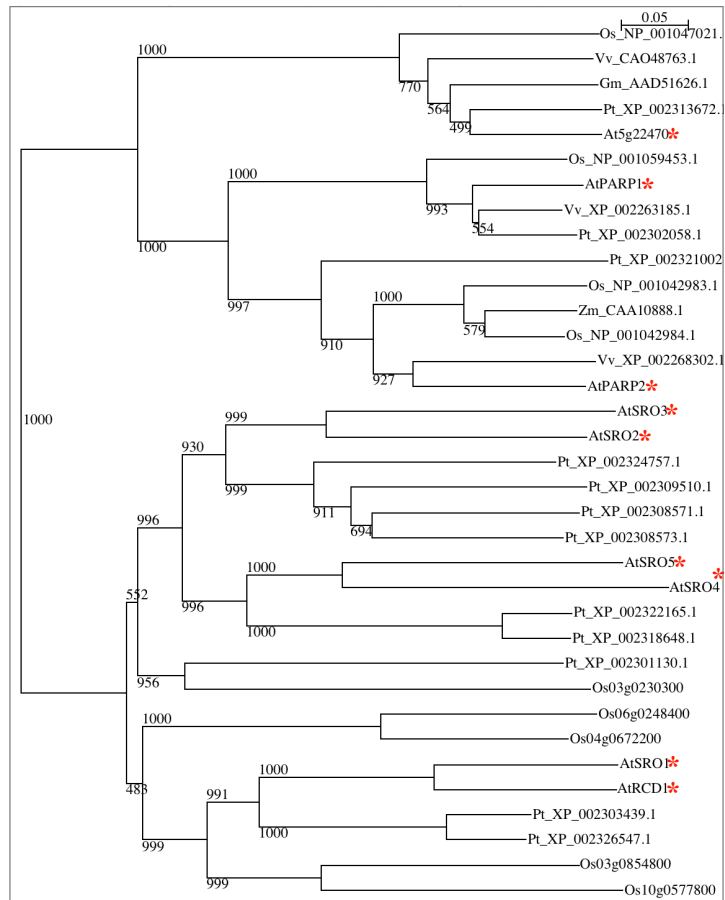
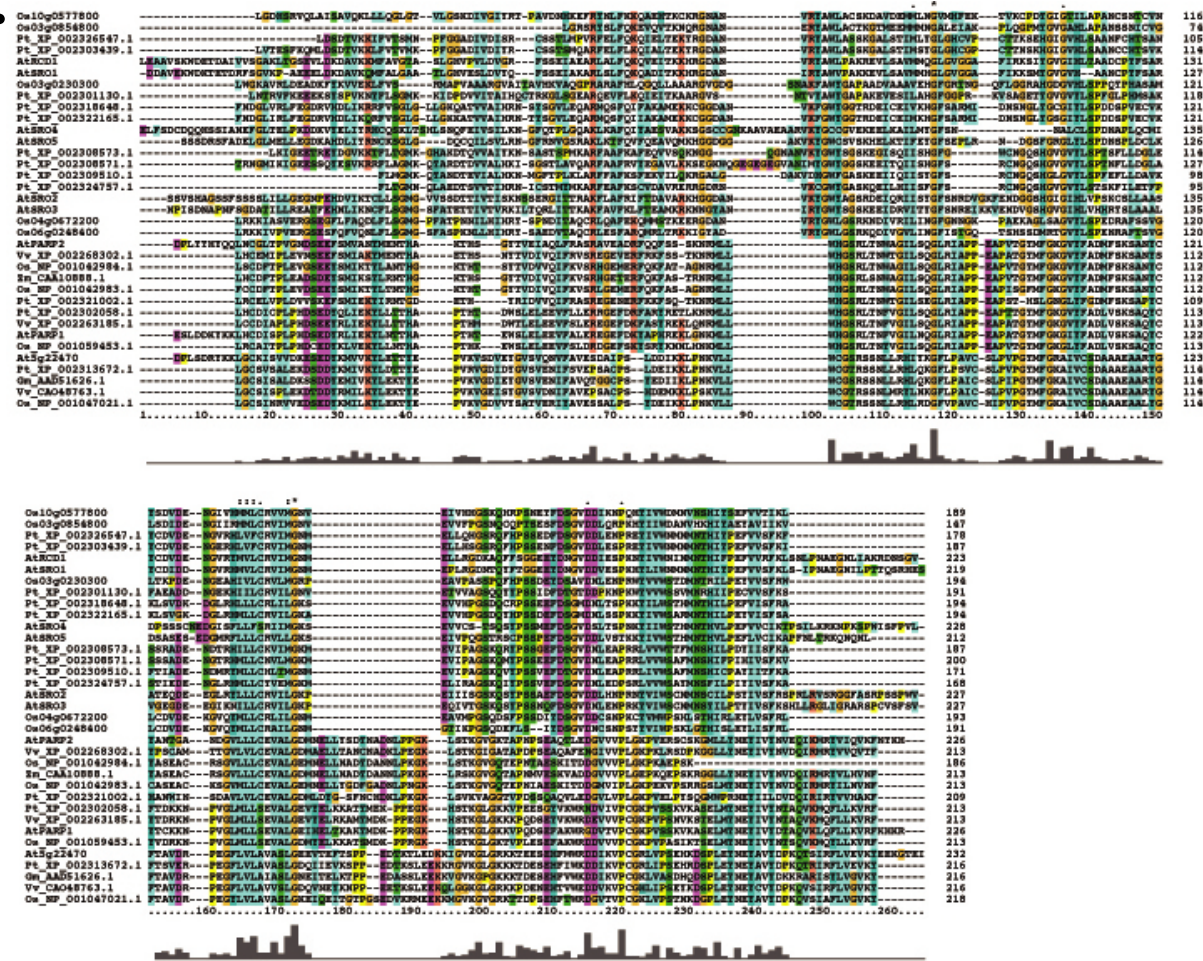


A.**B.**

Supplemental Fig. 1. Phylogenetic tree of the PARP family in angiosperms. **A.** Phylogenetic tree of PARP signature containing proteins from across the angiosperms. The tree was generated using the neighbor joining method. Numbers indicate bootstrap values. Arabidopsis genes mentioned in the text are indicated by asterisks. **B.** Alignment of the PARP signatures of selected plant PARP proteins used to generate the phylogenetic tree. Dashes indicate gaps introduced to improve the alignment. Length of the PARP signatures in amino acids are indicated on the right. Species used: *Os*, *Oryza sativa*; *Vv*, *Vitis vinifera*; *Gm*, *Glycine max*; *Pt*, *Populus trichocarpa*; *At*, *Arabidopsis thaliana*; *Zm*, *Zea mays*.

A.

| | | | | | | |
|---------------|----|------------|-------------|------------|------------|------------|
| RCD1 | 96 | ENGEWNDL-P | E-HVICAIQN | ELEEKs---- | --AAIEFKLC | GHSFILDFLH |
| SRO1 | 95 | ENGEWIDL-P | D-HILCDIRN | DLEAKR---- | --ATIEFNWC | GRHFLDLFLH |
| PARP11 | 34 | ECGKWHMFQP | DTNSQCSVSS | EDIEKSFKTN | PCGSISFTTS | KFSYKIDFAE |
| Con. | | E G+W+ P | * + C++ + + | +K+ | +I F | + +DF |

| | | | |
|---------------|-----|------------|-------|
| RCD1 | 138 | MQRLDMETGA | KTP-L |
| SRO1 | 137 | MYRLDLETGV | KTQ-L |
| PARP11 | 84 | MKQMNLTG- | K-QRL |
| Con. | | M++++* TG | K * L |

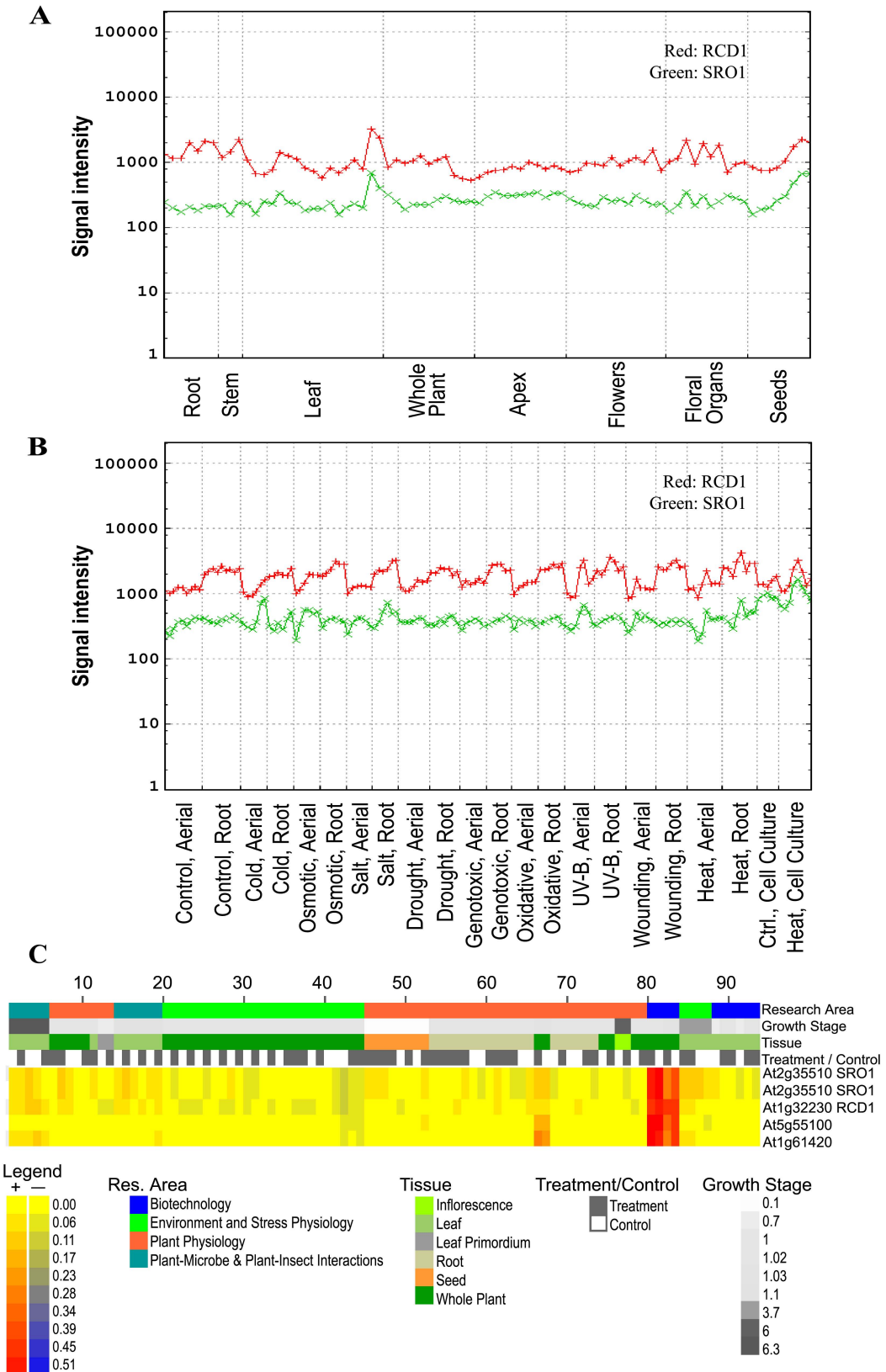
B.

| | | | | | | |
|---------------|-----|------------|------------|------------|------------|------------|
| RCD1 | 313 | QKQVEITKKH | RG--DANVRY | AWLPAKREVL | SAVMMQGLG- | -VGGAFIRKS |
| SRO1 | 309 | QKQADITKKH | RG--DANIRY | AWVPAKKEVL | SAVMMHGLG- | -VGGAFIKKS |
| PARP11 | 176 | RKKAQLKKK- | RGVPOINEQM | LFHGTSSEFV | EAICIHNFWD | RING--IHGA |
| Con. | | +K+A + KK | RG N + | + + E + | A+ +* | + G I + |

| | | | | | | |
|---------------|-----|------------|------------|------------|------------|------------|
| RCD1 | 359 | IYGVGIHLTA | ADCPYFSARY | CDVDENGVRY | MVLCRVIMGN | MELLRGDKAQ |
| SRO1 | 357 | MYGVGVH--A | ANCPYFSARY | CDIDDNGVRH | MVLCRVIMGN | MEPLRGDNTQ |
| PARP11 | 223 | VFGKGTy--F | ARDAAYSSRF | CK-DD--IKS | MFLARVLIGD | Y--INGDSKY |
| Con. | | ++G G + | A +S+R+ | C D* ++ | M L RV++G+ | + GD |

| | | | | | | |
|---------------|-----|------------|------------|--------------|------------|---------|
| RCD1 | 409 | FFSGGEE--- | ---YDNGVDD | IESPKNYIVW | NINMNTHIFP | EFVVRFK |
| SRO1 | 403 | YFTGGEE--- | ---YDNGVDD | VESPKHYLIW | NMNMNTHIYP | EFVVSFK |
| PARP11 | 288 | MRPPSKDGSY | VNLYDSCVDD | TWNPkIFVVF | DANQ---IYP | EYLIDFH |
| Con. | | ++ | YD+ VDD | +PK ++++ + N | I*P | E+++ F |

Supplemental Figure 2. RCD/SRO are similar to human PARP-11. Sequences aligned were Arabidopsis RCD1 and SRO1 and human PARP11. (A) Alignment of the WWE domain of the three proteins. (B) Alignment of the PARP catalytic domain and surrounding sequences. Dashes indicate gaps introduced to improve the alignment. Identical residues are indicated by the one letter code for amino acids while residues similar between PARP11 and RCD1/SRO1 are indicated by + signs. Asterisks indicate residues that are identical between PARP11 and one of the Arabidopsis proteins.



Supplemental Figure 3. Expression patterns of *RCD1* and *SRO1*. Expression profile of *RCD1* and *SRO1* in different developmental tissues and stages (A); and in different abiotic stress conditions (B). The data were generated by AtGenExpress (Development) and (Abiotic stress), respectively, and presented using the AtGenExpression Visualization Tool. *RCD1* (red) and *SRO1* (green) showed similar expression patterns. (C) Pearson Correlation Coefficients for expression of the top 5 gene expression vectors as compared to that for *SRO1* using Expression Angler on the Botany Array Resource data set.

Supplemental Table I.

| <i>Name of the primer</i> | <i>Sequence (5' to 3')</i> |
|---------------------------|---|
| RCD1-F | CACCATGGAAGCCAAGATCGTCAAG |
| RCD1-R | TTACAATCCACCTGCACCTTC |
| SRO1-F | CACCATGGAAGCCAAAATCGTCAAGGTATCG |
| SRO1-R | TTACAATCCACCTGCACCTTC |
| SRO1-1600F | AATTGCTCGTAAAGACATGGATTTG |
| SRO1-1360R | CCGAACTCTCGTGCCTACTCTGAGTAG |
| SRO1-150F | ATGGGTGCTTTCACCCAACAGTTTCCAC |
| S432-LP | CCAAGCTTACGGGAAGCGAAG |
| S432-RP | CCCCGGATGATGAATCAGAGA |
| S383-LP | TTCACGACAGCAAAGAGAGTCG |
| S383-RP | TCCCAATGCTGAAGGTGATT |
| pSRO1-F | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCTTCAAAGACTGACCAACACAGGCAC |
| pSRO1-R | GGGGACAACTTTTGTATACAAAAGTTGTTTTCTCTACTAACAACACTAAACC |
| SRO1g-F | GGGGACAACTTTGTATACAAAAGTTGATGGAAGCCAAAATCGTCAAGGTATC |
| SRO1g-R | GGGGACCACTTTGTACAAGAAAGCTGGGTTCTTGTTGCCCTATTCTTAGAGCATCGG |
| pRCD1-F | GGGGACAAGTTTGTACAAAAAAGCAGGCTTGGTGGTGAATTCAATCTGGTTGG |
| pRCD1-R | GGGGACAACTTTTGTATACAAAAGTTGTTCTATATATTAACAATACTAAACCTATAACC |
| RCD1c-F | GGGGACAACTTTGTATACAAAAGTTGATGGAAGCCAAGATCGTCAAGGTG |
| RCD1c-R | GGGGACCACTTTGTACAAGAAAGCTGGGTTTACAATCCACCTGCACCTTCTTCATG |
| Actin-F | GGCGATGAAGCTCAATCCAAA |
| Actin-R | GGTCACGACCAGCAAGATCAA |
| FLC-F | TTCTCCTCCGGCGATAACCTGGT |
| FLC-R | TCAACCGCCGATTTAAGGTGGCT |
