

Table S1. Primers for real-time PCR analysis and vector construction of *SaPCR2*.

| Primer ID | Primer sequence (5' to 3') | Function | Reference |
|---------------------------|--|---------------------|-----------|
| <i>SaACTIN1</i> -qF1 | TGTGCTTTCCCTCTATGCC | Real-time PCR | [1] |
| <i>SaACTIN1</i> -qR1 | CTGCTCCATACAAGCCAACCACG | | |
| <i>SaPCR2</i> -qF1 | GCGGTGGGATGTGGTCTAC | Real-time PCR | [2] |
| <i>SaPCR2</i> -qR1 | CGATAATCTCGGCTATTTGGC | | |
| pDR196- <i>SaPCR2</i> -F1 | tataccccagcctcgactagtATGTATCCATCTTTGTCTG | Vector construction | [2] |
| pDR196- <i>SaPCR2</i> -R1 | gataagcttgatatcgaattcTCATCTACTCATCCCCTGC | | |

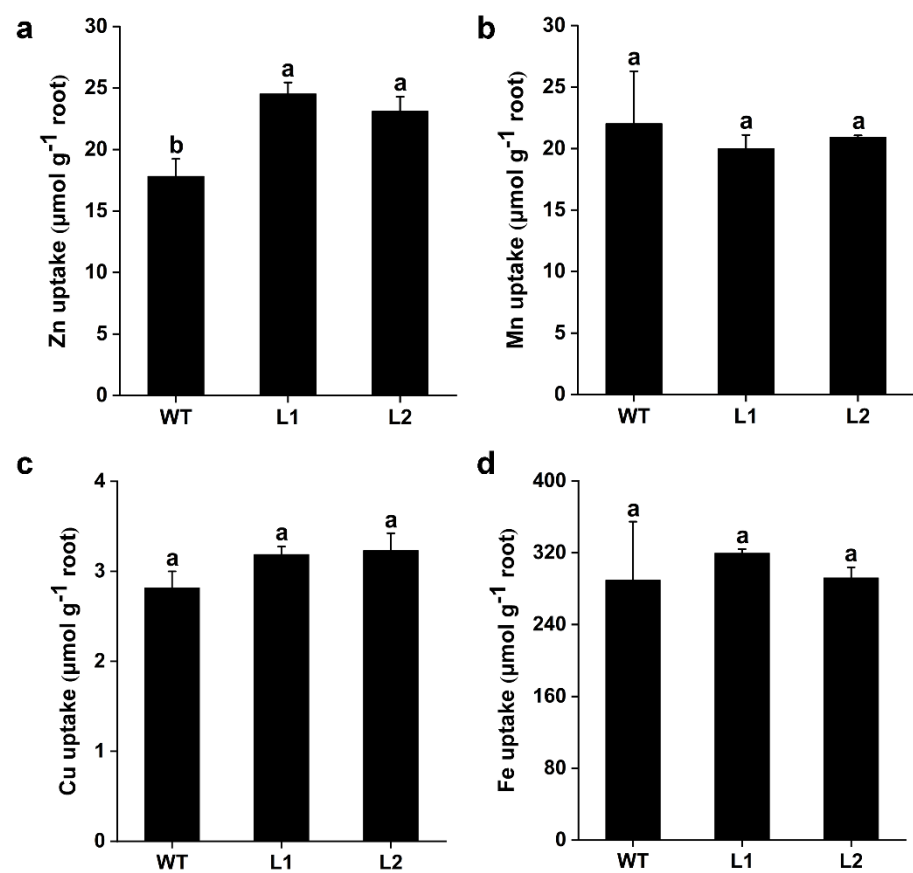


Figure S1. Trace elements uptake, including (a) Zn, (b) Mn, (c) Cu, and (d) Fe, in the non-hyperaccumulating ecotype (NHE) *Sedum alfredii* wild type (WT) and *SaPCR2* overexpressing lines (L1 and L2) after five-week-preculturing. Uptake was calculated in terms of the root dry weight. Different letters indicate significant differences between genotype in a treatment ($P < 0.05$). Error bars = mean \pm standard error (SE; $n = 3$).

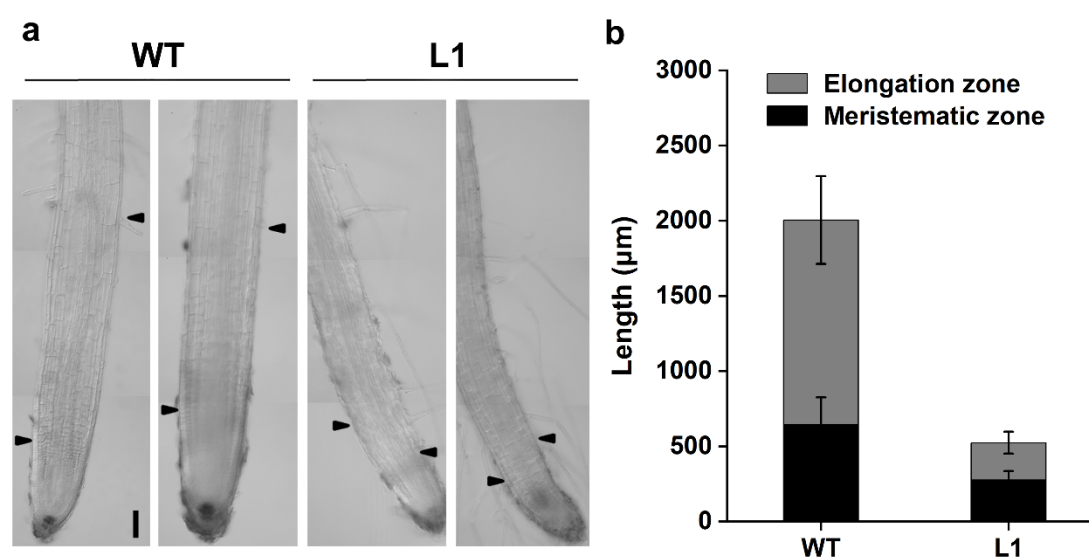


Figure S2. Root tip structures of the non-hyperaccumulating ecotype (NHE) *Sedum alfredii* wild type (WT) and *SaPCR2* overexpressing lines (L1 and L2) grown in normal nutrient solution. (a) Growth of root tips. Bar=200 μm. (b) Length of meristematic zone and elongation zone. Error bars = mean ± SE (n=5).

| | | |
|----------------|---|-----|
| SaPCR2-protein |MYP S LENEHDQK Y TPSR G | 20 |
| AtZIP1 | .MSECGCFSAITMLRICVVL I ICLHMCCASDCTSHDDPV S QDEAEK..ATK L KLGS I AL | 57 |
| AtZIP2 | MALSSKTLKSTLFFLSIIFLCFSLILAHGGIDDGDEEETNQPPATGTTTVVNLRSKSL | 60 |
| NcZNT1 |MASSPTK I LCDAGESDLCRDDAA...AFL L KFVA I AS | 34 |
| Consensus | | |
| SaPCR2-protein | LQRGIPAPVELY.....PPY I PPQ....LRPR L TGG M W S TGL C HCCDDPANSFI | 68 |
| AtZIP1 | LLVAGGVGVSLP....LIGKRIPALQ P ENDIFFMVKAFAAGVILCTGFV H LPDAFERLS | 113 |
| AtZIP2 | VLVKIYCIILFFSTFLAGVSPYFYRWNESFLLGTQFSGIFLATALIHFLSDANETFR | 120 |
| NcZNT1 | ILLAGAAGVAIP....LIGKNRRFLQTEGNLFVAAKAFAGVILATGFV H LAGGTEALT | 90 |
| Consensus | | |
| SaPCR2-protein | TCC C PCITF.....GQIA E IIDKGSPNCATHGAIYGLILMTG.....CAC | 108 |
| AtZIP1 | SPC L EDTTAGK F PFAGFVAMLSAMGTLMDTFATGYKRQHFSN.....NHG S K | 162 |
| AtZIP2 | GLKHKEYPY.AFMLAAAGCYCLTMLADVAVAFVAAGSNNNHVGAS.....VGESRE | 169 |
| NcZNT1 | NPCLPDYPWSKEFPFGFFAMVAALITLLVDFMGTOY Y ESKQQRNEVAGGGEAAVVE T SS | 150 |
| Consensus | | |
| SaPCR2-protein | LYSCFYRS.....KMRAQYDLQ.....E S PCVD C L | 133 |
| AtZIP1 | QNVVV V DE.....EEH A G.....HVHI H THAS.....HG H THG S TEL | 194 |
| AtZIP2 | DDDVAVKE.....EG.....RREIKSGVD.....V S QALIR T | 196 |
| NcZNT1 | VLPVVVERGND S KAFGEEDGGGMHIVGIRAAAHNHSHSNAHGTFDGHAGQ S HGHV H | 210 |
| Consensus | | |
| SaPCR2-protein | V.....HFCCKTCALCQEYRELKSRGLDMGIGWEANIERQRRGTVTSPVVPQ G MS | 183 |
| AtZIP1 | I.....RRRIVSQVLEIGIVVHSV I IGISLGASQSIDIKPLMAALS F HQFFEG L G | 245 |
| AtZIP2 | S.....GFGDTALLIFALCFHSIFEGIAIGLSDTKSDAWRNLT I SLHKVFAAVA | 246 |
| NcZNT1 | HGSHDVENGARHVVSQILELGIVSHS I IIGLSLGV S QSPCTIRPLIAALS F HQFFEG F A | 270 |
| Consensus | | |
| SaPCR2-protein | R..... | 184 |
| AtZIP1 | LGG C ISLADMK S KSTVLMATFFSVTAP L GIGIGLGMSSGLGYRKESKEAIMVEGMLNAAS | 305 |
| AtZIP2 | MG..IALLKLIPKRPFFLTVVYSFAFGISS P IGVGIGIGINATSQAGAGDWTYAISM L A | 304 |
| NcZNT1 | LGG C ISQAQFKNKSAIIMACFFALTAP I GIGIGITAVAS..SFNSHSPGALVTEGILDSLS | 328 |
| Consensus | | |
| SaPCR2-protein | | 184 |
| AtZIP1 | AGIL I YMSLV D LLATDFMNPRLQSNLWHLAAAYLSLVLAGAGSM S LLAIW | 354 |
| AtZIP2 | CGVFVYVAVNH L ISKGYK.PREECYFDKPIYKFI A VF L GVALLSV V MIW | 352 |
| NcZNT1 | AGIL T YMALVDLIAADFLSKRMSCNVRLQVVS Y VML F LGA L MSALAIW | 377 |
| Consensus | | |

Figure S3. Alignment of protein sequences of SaPCR2, AtZIP1, AtZIP2, and NcZNT1. Red box indicated a highly conserved sequence region.

References

1. Chao, Y.; Zhang, M.; Feng, Y.; Yang, X.; Islam, E. cDNA-AFLP analysis of inducible gene expression in zinc hyperaccumulator *Sedum alfredii* Hance under zinc induction. *Environ. Exp. Bot.* **2010**, *68*, 107–112, <https://doi:10.1016/j.envexpbot.2009.11.013>.
2. Lin, J.; Gao, X.; Zhao, J.; Zhang, J.; Chen, S.; Lu, L. Plant Cadmium Resistance 2 (SaPCR2) facilitates cadmium efflux in the roots of hyperaccumulator *Sedum alfredii* Hance. *Front. Plant Sci.* **2020**, *11*, 568887, <https://doi:10.3389/fpls.2020.568887>.