

10 20 30 40 50 60 70 80 90 100

AhSCRpro -----GTT AATAACTCC AAAAT--TG AGTCACTCTG GGTAATITC AGTTATTAAA AAGCAATAT CAAAGTITIT ITTCTTTGG
AtSCRpro GTAATCTAT AATATATGG GTCAATGT AAAATATAA ACTAAAGAT ATTAATATAT AAAATAGAAA TAGAATAATIT CTAAATAAT TCTTTTAAA

110 120 130 140 150 160 170 180 190 200

AhSCRpro AAACAGAT ATGGATATA TTT-----CAGATTTCG CACTATCAA ACAGTAACG GTAGAACAG AGGCAAGTAA CCAATATAT TTTGTACTT
AtSCRpro AGTAGAATAT A-BAGATATA TATTGGAGAG TAGAATATAG AGCTAT--AC ATTGGAGATG GTCTAAACT CTCGACCTTA TAAA--AGT GAACTATCT

210 220 230 240 250 260 270 280 290 300

AhSCRpro GATCCATCG CTTGTACTG CAGGTATTCA AAAATTTGTA CTGTTACTG GCCTTGTCTA TTAGGGATAC TAGGGTTGGG CAAAGTA--CTCGTAACTC
AtSCRpro GATCGATCG TCCCACTAAA AACTAGAAA AAACTATAGG CATATGCTTA TCGTATACT TTTAATCCT TTBATCTCTE TAGCAAGGAC CTCTCTGGTC

310 320 330 340 350 360 370 380 390 400

AhSCRpro GTCGTGATG CGT-TACTTG TCTGTACTC GCGTGAAGA ATAAAGTATT TGTGTGTCG AAGGCAAGTA TCAAGAGTAA TAAITTAGAT ACTTGCAGT
AtSCRpro CCTCCGAGC AATATGGACA AGAAGCAGA GACCTACCCG ATACCTCAC T-CACITATT CGATTTTTT TCTGAAATG -AACATATGT ACTTGTCA--

410 420 430 440 450 460 470 480 490 500

AhSCRpro ACAAGCCAA CAAACAGTAG TGGAAAAAA ATTAACAATC GGCTTGTTC ACCCGTACTT CGTAAATATT TTAGCATTT ATATACATAT AATTCATATT
AtSCRpro ACTAGTGTG AATTAATATT ATCCAAAGTA ATTGAA----T-TAGCTG AATTTGGGT TTAATTTAAA TAAATTATTT ATATACATAT TGTGAACTCT

510 520 530 540 550 560 570 580 590 600

AhSCRpro AATATGTTT TAAACATAT TTTAATAGT ACATCAAGG TAAATGAA--AATTTAAAT AT-GTAAAA ATTTGAGGT GTTCTCTGCA AATTCATATC
AtSCRpro TTTATAAAAT AATTCCTCAA AATGTAACT GTTATAAAA GAATGTACTT GGCAATTAAT ATTAACAATT ATTTAATATT CCTAATATG AAC-ATTTCG

610 620 630 640 650 660 670 680 690 700

AhSCRpro AAGTAATCG TAAATCTTG CAGTAACTC GCAAGTACA AGTAAAGCG CAAGGCAAGT AACTGGCAAG TCGGCAATG TTTAGCAAGT ACTCGAATAT
AtSCRpro --TTATCTAA GTATATCTC CA--TCAAT CTAATTCGA AAAAATGAG AATTTTTAG CAAATATTAA TA--TTATAC TTTAATAAA GATAAATATT

710 720 730 740 750 760 770 780 790 800

AhSCRpro AAAGTACTT GGTTTACAA CAGCCACCA CAAAACTAA TTTTTATTG TCAACAGG CAAGCCAGT AATACCTATT CTAATAAG CAACTACTCG
AtSCRpro GTAAATGTTT AAGTGTAAAT AAT--ATTT TGAATATTA ACGGAAC--TATTGAA TATTAGAT ATGTGAAT ATATATAAT TAAATACTA

810 820 830 840 850 860 870 880 890 900

AhSCRpro TCTGTGZAT ATTATTTTT TTAGACBAG T-ACGGGGG AATGACG--GTAC---GG GACAGTAC CAGTACTGT CTCAGTCTT ACCTTATCC
AtSCRpro TTTGAAAGAA AACTTTAAA AAGTATTGAA TTTAATAATG TTTAATAAA GTATTATTAA AACAAAAAT AAAAAAAT GTTTAATTTT ACTGAACGAG

910 920 930 940 950 960 970 980 990 1,000

AhSCRpro TCTCG--BAC ATACCAAAA AAAAAAGTG AAGC-TACT CTGTTGATGG GTCCCAAC AAGCTAGAAC AAAACTTAG CCAATGCTG CCTCCTAAT
AtSCRpro ATCAAAATGTT ATGTGAGGTG TAAATATTA TATATATGA AATTTAACA AATTAAGAT AATTTGAA GAAAACTTT ---TAAATG ATTTGATTTA

1,010 1,020 1,030 1,040 1,050 1,060 1,070 1,080 1,090 1,100

AhSCRpro TATCTTCA ACCCTTGTAT CTCTGTA--G AAGGACCTCT CTCTCCGCG TCCAGAGTCC CCA-GCCAT AAGGATTAG GACATATAGC AAGAGACCTA
AtSCRpro TAAATTTAA ATATTATTA AAAAAATAA AATATATGT TAATTTAGT TAAAGAGT AGATGGCA ACGGCTTBA GTGATAGTA ATATGAGG

1,110 1,120 1,130 1,140 1,150 1,160 1,170 1,180 1,190 1,200

AhSCRpro AAACATTCT TAGACATGT TTTTGGGA TCGTGGATTT CAG--GAG CCACTATATT TAAAAAAC TAGTATTGT ATTTATGCT AATTTAAGT
AtSCRpro ATAACTCC--AGGTGAAAT CCAATTAGATA T-GTTAATT TCACTAACG GGTTAGATG GTAGGAGGG TTTGGTCTBA TAGTAAACG AGACAGTATA

1,210 1,220 1,230 1,240 1,250 1,260 1,270 1,280 1,290 1,300

AhSCRpro GTGTACTG TAAATCTCTA AACTCCCA TAAAAATTA -BATTATTG GTTAAATTT ATCTTCTCG TAAAGTTTC TCAATGCTT TCAACACG
AtSCRpro CCAGGCTGA TATCATTAG ATATTTTTA TTTACTGAA CAGGATTAAT GTAGAGCGG ATTTGGATCG -ATAGTAATA CGAGACGTA TACCATAT

1,310 1,320 1,330 1,340 1,350 1,360 1,370 1,380 1,390 1,400

AhSCRpro GACTGCTGA GCTTCAAAA-CAAAGTATGG AAGGTGCGG TAATATCTC AGTATTCCA AATTTTATT ATTAAGCG CAGGCAAG AATCATGAG
AtSCRpro GAAATCAAG ATATACCAAT CAAATAACA TATTTATGCT TTAATAGTA AACAGAA--AAACAATTT AACAAAAA ATATAATTA AATTTAATT

1,410 1,420 1,430 1,440 1,450 1,460 1,470 1,480 1,490 1,500

AhSCRpro ATATAAAAA AAGTAAAAA GAAG--AA TCATAGCAAT TTTTGGTTT CAGTCCAGT CTCACGAC -TAAATTCG AACATGCT- TTGTTGAT
AtSCRpro ATTTAGTTAT AATCTAGATC TGTATTTTA CTTATGAAAT TGTATGTAAT TGTTCCTATA CTTTAAACA GTAAAAATCA AACATAGTAA TTGTTACTTA

1,510 1,520 1,530 1,540 1,550 1,560 1,570 1,580 1,590 1,600

AhSCRpro TTTTATC TGATATGGT AT-ATTACT TGTCCGAGC TGTGTGAA AATTTACGA ATT-TAAT GAAATGAGT GAAATTTAAT TT-TAGTTA
AtSCRpro ATATATAT ATATATAABA ATGTACTAT TACAAAATA AACAATTA ATATATTT ATATTAACA AATTAATTT TTTTAAA AAAATAGTTT

1,610 1,620 1,630 1,640 1,650 1,660 1,670 1,680 1,690 1,700

AhSCRpro AACGGT--ACTBA-AA AATTTATGA ATTTGCATG ATTTAATTGA TGT---TTT TTAGTTACT ATTTAAGAC AATATTTT TTA
AtSCRpro TACGGTTTAC CAGGTTAA AATCTAGTTG ATTTGCATAA ATTTAAGCAA GCTCGTTTT TTAGTTACT ATTTAGACCT ATAAATTTT TTAATGGCA

1,710 1,720 1,730 1,740 1,750 1,760 1,770 1,780 1,790 1,800

AhSCRpro -----TTA TCATTGAAT TAA-----TT ATTTAA TATATACCTT ATGGATACAG ATGCATATT CGTTTGTAA ACTGTTTCA CGTTATCACT
AtSCRpro TCAGGTTAG TAAATAAAT TTGATTATCA TTTATTTAC TATATACCTT ATGGATACAG ATGCATATT CGTTTGTAA ATGTGTTCA CGTTATCACT

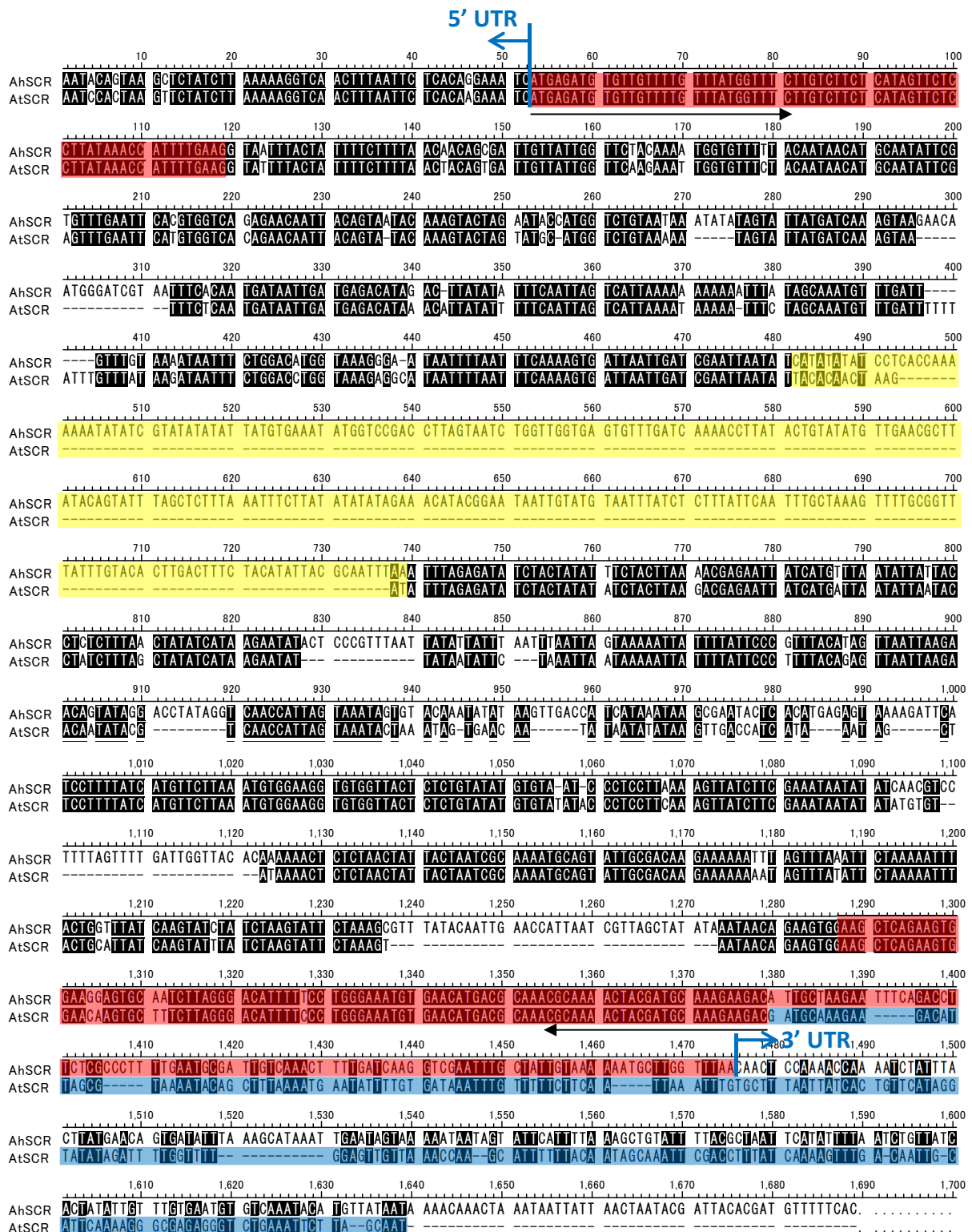
1,810 1,820 1,830 1,840 1,850 1,860 1,870 1,880 1,890 1,900

AhSCRpro TAGCACATT TGTGTGTG ACACATATAT TACGTGTTG TATATGAAT ATTTTGTAA TCTTTTATA CGTAAACA TAAACATAC ACAGGTTTG
AtSCRpro TAGCACATT TGTATTGTG ACACATATAT TATGTGTTG TATATGAAT ATTTTGTAA TCTTTTATA CGTAAACA-----CTAC ACAGGTTTG

1,910 1,920 1,930 1,940 1,950 1,960 1,970 1,980 1,990 2,000

AhSCRpro GGTTATGTT ACCCTATAT AAAGACAAA CTTCACAT AAT
AtSCRpro GGTTATGTT ACCCTATAT AAAGACAAA CTTCACAT GCAC

Promoter region of SCR-A



Coding region of SCR-A

Nucleotide sequence comparison of SCR-A between *A. thaliana* and *A. halleri*.

Supplementary Figure S1
(continued)