**Figure S4. Alignment of nucleotide sequences corresponding to *sgk2a* and *sgk2b*.**

 1 50

sgk2a\_NM\_001139943 (1) --------------------CAACAGTGCTGTGCCCTGAGCTG-GGACAC

 sgk2b\_BT059352 (1) CTCTGGTCTTCTCCTTTTAGCGCAAGAAGTATGAA---AGCTCTGGAGGC

 51 100

sgk2a\_NM\_001139943 (30) TTGACTCGATCTGCGGGG-CTTCAGTCAGTCGACAAGACATCGCTCCGGC

 sgk2b\_BT059352 (48) TGTAAATGCTGTACGGCCACTACAGACGGCGGATT-GACCAAGCAGAGCC

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 101 150

sgk2a\_NM\_001139943 (79) TGCACGCACCTGCGACAGGTGGCCT---AAGCTTC-GTTTTAACCTTCAC

 sgk2b\_BT059352 (97) TATAACTAGGCTTTGCACGTTCGCTGTCACGCAGCAGTGTCAGAGAGGAA

 151 200

sgk2a\_NM\_001139943 (125) AAAAGGTCTATGAAACACTGATGTAGGCACCCCGGTGAGCACGGAATGGA

 sgk2b\_BT059352 (147) AAAAGGTCTGTGAAGCACTGATGTAGGCTCCCCGGTGTGCAAGGAATGGA

 201 250

sgk2a\_NM\_001139943 (175) CCAAGACCATGGCAAATTCTAATCCACTTAGATCACCATCCTCCACCCTC

 sgk2b\_BT059352 (197) CCAAGACCATGGCAAATTGTAATCCACTTAGATCACCGTCCTCCACCCTC

 251 300

sgk2a\_NM\_001139943 (225) AGTGAGGTCAACCTGGGACCTTCAGCAAACCCACATGCCAAGCCCACTGA

 sgk2b\_BT059352 (247) AGTGAGGTCAACCTGGGACCCTCGGCAAACCCACATGCCAAGCCCACTGA

 301 350

sgk2a\_NM\_001139943 (275) CTTTGACTTTTTGGCTGTTATTGGAAAAGGGACCTTTGGGAAGGTCCTGC

 sgk2b\_BT059352 (297) CTTTGACTTCTTGGCTGTTATTGGAAAAGGGACCTATGGGAAGGTCCTGC

 351 400

sgk2a\_NM\_001139943 (325) TCGCCAAGCTCAAAGCTGACAATAAATTCTATGCTGTGAAAGTTCTACAG

 sgk2b\_BT059352 (347) TCGCCAAGCTCAAAGCTGACAACAAATTCTATGCGGTCAAAGTTTTACAG

 401 450

sgk2a\_NM\_001139943 (375) AAGAAAGTAATCCTGAAGAAAAAGGAGCAAAAGAACATCATGGCAGAGAG

 sgk2b\_BT059352 (397) AAGAAAGTCATCCTGAAGAAAAAGGAGCAAAAGAACATCATGGCAGAGAG

 451 500

sgk2a\_NM\_001139943 (425) GAACGTGCTGCTGAAGAGCCTGAAGCATCCTTTCCTGGTGGGCCTCCACT

 sgk2b\_BT059352 (447) GAACGTGCTGCTGAAGAGCCTGAAGCACCCTTTCCTGGTGGGCCTCCACT

 501 550

sgk2a\_NM\_001139943 (475) ACTCCTTCCAGACCCCAGAGAAGCTCTACTTTGTCCTCGACTATGTCAAC

 sgk2b\_BT059352 (497) ACTCCTTCCAGACCCCAGAGAAGCTCTACTTTGTCCTGGACTATGTCAAC

 551 600

sgk2a\_NM\_001139943 (525) GGGGGAGAGCTCTTCTTCCACCTGCAGAGGGAGCGGTGCTTCTTGGAGCC

 sgk2b\_BT059352 (547) GGGGGAGAGATCTTCTTCCACCTGCAGAGGGAGCGGTGCTTCTTGGAGCC

 601 650

sgk2a\_NM\_001139943 (575) GAGGGCTCGGTTCTATGCTGCTGAGGTAGCCAGTGCCATCGGCTACCTTC

 sgk2b\_BT059352 (597) GAGGGCTCGGTTCTACGCTGCTGAGGTAGCCAGTGCCATCGGCTACCTTC

 651 700

sgk2a\_NM\_001139943 (625) ACTCCCTCAACATCGTTTACAGAGATCTAAAGCCAGAGAATATTCTCTTA

 sgk2b\_BT059352 (647) ACTCCCTCAACATCGTTTACAGAGATCTGAAGCCAGAGAATATTCTCTTA

 701 750

sgk2a\_NM\_001139943 (675) GACTCTCAGGGCCATGTGGTACTTACAGACTTTGGGCTGTGTAAAGAGGG

 sgk2b\_BT059352 (697) GACTCTCAGGGCCACGTGGTGCTTACGGACTTTGGGCTGTGTAAAGAGGG

 751 800

sgk2a\_NM\_001139943 (725) AGTTGAGCCGGAGACCACCACGTCCACTTTCTGTGGAACCCCTGAGTATT

 sgk2b\_BT059352 (747) AGTGGAGCCGGATACCACCACGTCCACTTTCTGTGGAACCCCTGAGTATT

 801 850

sgk2a\_NM\_001139943 (775) TGGCCCCTGAGGTTCTGCGTAAGGAGCCCTATGACCGCACAGTGGACTGG

 sgk2b\_BT059352 (797) TGGCCCCTGAGATTCTGCGTAAGGAGCCCTATGACCGCACTGTGGACTGG

 851 900

sgk2a\_NM\_001139943 (825) TGGTGTCTGGGAGCTGTGCTCTATGAGATGATCTATAGTCTTCCCCCATT

 sgk2b\_BT059352 (847) TGGTGTCTAGGAGCTGTGCTCTATGAGATGATCTATAGTCTTCCTCCTTT

 901 950

sgk2a\_NM\_001139943 (875) CTACAGCCGGGACGTGTCTGAAATGTACGATGGCATCCTACACAAGCCTC

 sgk2b\_BT059352 (897) TTACAGCCGGGACATGTCTGAGCTGTATGATGGTATCCTGCACAAGCCTC

 951 1000

sgk2a\_NM\_001139943 (925) TGCCGCTGCCCCCAGGGAAGTCAGGCGCTGTCTGTAGTCTGCTCCAGGGC

 sgk2b\_BT059352 (947) TGCCTCTGCCCCCAGGGAAGTCAGACGCTGTCTGTAGTCTGCTCCAGAGC

 1001 1050

sgk2a\_NM\_001139943 (975) CTCCTGCAGAAAGACCAGCACTGCAGGTTGGG**AGCCATCGCTGACTTTCT**

 sgk2b\_BT059352 (997) CTCCTGCAGAAGGACCAGCACTGCAGGCTGGGAGCCATCGACGACTTTTT

 1051 1100

sgk2a\_NM\_001139943 (1025) **ACA**AATAAAGAACCATGTGTTCTTCTCCCCGATTAACTGGGATGACCTGT

 sgk2b\_BT059352 (1047) AGAAATCAAGAACCATGTGTTCTTCTCCCCGATTAACTGGGATGACCTGT

 1101 1150

sgk2a\_NM\_001139943 (1075) ACCACAAGAGAATCACTCCTCCATACAACCCCAATGTGAAAGGGCCAGCG

 sgk2b\_BT059352 (1097) ACCACAAGCGGATCACTCCTCCGTACTACCCCAATGTGAAAGGGCCAGCG

 1151 1200

sgk2a\_NM\_001139943 (1125) GACACACAGCACATAGACCCAGAGTTCACCAGAGAG**ATGGTGCCTAACTC**

 sgk2b\_BT059352 (1147) GACACGCAGCACATAGACCCAGAGTTCACCAGAGAGATGGTGCCTAACTC

 1201 1250

sgk2a\_NM\_001139943 (1175) **AGTGGG**CCGCACCCCTGAGCTCAACGCCGGCACCAGCAGCTCTAACGCAT

 sgk2b\_BT059352 (1197) GGTGGGCCGCACCCCTGAGCTGAACGCCAGCACCAGCAGCAGCAACGCCT

 1251 1300

sgk2a\_NM\_001139943 (1225) TCAATGGCTTCTCCTACGTTTCTGGTGAAGA---CAGCTTCCTTTGAGAC

 sgk2b\_BT059352 (1247) TCAATGGCTTCTCCTACGTCTGTGGTGAAGAAGACAGCTTCCTCTAAGAC

 1301 1350

sgk2a\_NM\_001139943 (1272) AGGGAGGAAGGTTCCTCACAGCACCACCACTGCC-------GAGGCCGAG

 sgk2b\_BT059352 (1297) AGGGAAGAAGGTCCCTCACAGCACAACCACTGCCTGAGCTCGAGGTAGAA

 1351 1400

sgk2a\_NM\_001139943 (1315) GTAGAAGTTACCCGTAACCACATATCTACAATTCGATTCCTTAACCGTAA

 sgk2b\_BT059352 (1347) GTAGAAGTTACCCCTAACCACATATCTAGGATTC**AATTCCTCAACCCCAA**

 1401 1450

sgk2a\_NM\_001139943 (1365) ATCCTAACCTTAACCTTTAAGTCAGGAGGATAAAACATATATTTTACCCT

 sgk2b\_BT059352 (1397) **ATCC**TAACCTTAACCTCTAAGTCAGGAGG-TGAAAAAGATATTTGGCCCT

 1451 1500

sgk2a\_NM\_001139943 (1415) GGATTCAACAGTTAGTGGCAACCTCTATCAACTTCATTGGCCACGGTCAT

 sgk2b\_BT059352 (1446) TGAT----CAGTTAGTGGCAACCTCGATCAACTTCATTGGCCACAGCTAT

 1501 1550

sgk2a\_NM\_001139943 (1465) AGAAATGGAGCACATTGAATATCATGCATTTTTATGTAGGTGAAGCAA--

 sgk2b\_BT059352 (1492) AGAAATGGAGCACATTGAACAGAATGCATT**TTTGTGTAGGCTATGCGCAG**

 1551 1600

sgk2a\_NM\_001139943 (1513) -GAAAGAGATGTAAG-----------------AAAACATTTAAATGCACC

 sgk2b\_BT059352 (1542) TGCATGCCACGTCTGTTCATCTAGACCTCATTAGAACAGGCAGACGCAGC

 1601 1650

sgk2a\_NM\_001139943 (1545) ACCCA--ACTGTTGCTTTTG---CTGTAGGTGA----------CTGCCCT

 sgk2b\_BT059352 (1592) AGGCACTAATGATATCTGTGAAACTCTAGTCGAAACCATATTTCTGCTCT

 1651 1700

sgk2a\_NM\_001139943 (1580) ATGAATTCTATTTATAT-------------GCCCTT--------------

 sgk2b\_BT059352 (1642) TAAAGTGCTGTTTTTAATACAAACACGGTGGACCTTCCAAACATTTGTTA

 1701 1750

sgk2a\_NM\_001139943 (1603) ------------------GACTCTGC------------TTGATTTCTCA-

 sgk2b\_BT059352 (1692) TTTTAAATGAAATGTGATGATTGTCCAACAATACATTATTGATTTGAAAA

 1751 1800

sgk2a\_NM\_001139943 (1622) -------TTTCAGGA--CAAAGTCTTTTTGCACATCCAATCGT--GCTGG

 sgk2b\_BT059352 (1742) CATGCTGTTTCTGTTATCACTGACTTTGTGTAGATTAGATTAGAGGCTTG

 1801 1850

sgk2a\_NM\_001139943 (1661) ACTTTTTATTTGCTAGCAG--ATG-TTGA---------------------

 sgk2b\_BT059352 (1792) ACTCTATTGTTGCATCCAGGCATGCTTGAGGGGATAGCTCACTCAAATTA

 1851 1900

sgk2a\_NM\_001139943 (1687) ----TTTACTTCTCCTTTCACTA--CAAT-GTAAAG--TCAACAGTGTGA

 sgk2b\_BT059352 (1842) CAAATTTCCTTTCCCTGTCAGTAGTCTATAGAAAAGGTTTGACGGCAATT

 1901 1950

sgk2a\_NM\_001139943 (1728) CTACATAAA--GGACATGT-----AAATA-------CAGTACACGCTCCT

 sgk2b\_BT059352 (1892) CTAGATGATTTGAACATGCGTGGAAAATGTGCGTATCAGTACCATGACTT

 1951 2000

sgk2a\_NM\_001139943 (1764) AGATGCTATGTGT------------AGAAGGTAAAGCATCAGGT------

 sgk2b\_BT059352 (1942) GAATGGGATTTGTGCCACAGGTGCCACAAAGTCATGGTACCGATATAAGC

 2001 2050

sgk2a\_NM\_001139943 (1796) --TCTATGGAAA-GTTGTGGT-GTATGGATTAAGATGGTCTGATTATCAC

 sgk2b\_BT059352 (1992) AATCTATGGAAAAGGTATGACAGCAATCGGTGCTTTGGTTTTATT-TCCC

 2051 2100

sgk2a\_NM\_001139943 (1842) TAGAACAGG-----AAGACACAAATGTGTGTGAAACTCTAGTCGAACCC-

 sgk2b\_BT059352 (2041) TGGCACTGTTTCTAAATGTACAAAAGCTGAAGAACATCCTCACATACAGG

 2101 2150

sgk2a\_NM\_001139943 (1886) -ATT-------CCTCTGCTC----TTTAAGTGCTGCTTTT----AATACA

 sgk2b\_BT059352 (2091) TATTGTTTTTGCCACTGCTTGGAGTTAAAGGGAAACTCGTGAAAAATGTA

 2151 2200

sgk2a\_NM\_001139943 (1920) AACACTGTGGACTT---TCCAAACATT---TCT-TAACTCGTTTGTTGAA

 sgk2b\_BT059352 (2141) AACACTGCACACTGCTGTTCAACCCTTAGGTCTGTTCCACAAATGCTAAA

 2201 2250

sgk2a\_NM\_001139943 (1963) AATATAAATTTTTG---CATTGATTTGAGAATATG--CTG---------T

 sgk2b\_BT059352 (2191) ACCTTAGCATTTGGAGGCATTTCCAGGGGAAGTGGGACCGGAGCACGGAT

 2251 2300

sgk2a\_NM\_001139943 (1999) TTCTATTAT--CACTGACTTTTAGTAGATTAGAGTACATAAAGGCTTGAC

 sgk2b\_BT059352 (2241) TGCTGTTATACCATAGACTGCTTACAGGGTAAGGAAACCAACGTGTTATT

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 2301 2350

sgk2a\_NM\_001139943 (2047) T-GAAATGTTGCGTCCAGGGATGC--TTAACAGCAACATAAACCTATGCC

 sgk2b\_BT059352 (2291) TTGTGATGTGGGGG--AGCTATCCCTTTAACAGCAACATAAACCTACGCC

 2351 2400

sgk2a\_NM\_001139943 (2094) AGATTATTCTCACAGCTGTAAAGGTGCGTGCCATGGTGCTATTAACCTTG

 sgk2b\_BT059352 (2339) A---TCTTCTTACAACTGTAAAAGTGCGTGCCATGGTGTTCTTAACCTTG

 2401 2450

sgk2a\_NM\_001139943 (2144) TTAAACAAAACATGTGACTGTGTCAGCACAATGGGTGACATTAAAGACTG

 sgk2b\_BT059352 (2386) TGCAACAAGCCATATAATTGTGTCAACACGACGGGTAACATT--CGACTG

 2451 2500

sgk2a\_NM\_001139943 (2194) TTGAC--ATGCCAACACCATCTTAAAGATGACTGACATTCAATGAGGCAC

 sgk2b\_BT059352 (2434) TTGACTTATGCCAGCACCGTGTTAAAGGTGACTGATGCGCAATGATG---

 2501 2550

sgk2a\_NM\_001139943 (2242) AGTTACAAGTATGTGTACATAA---CTTCACAATAAATCACT-TCCCTAT

 sgk2b\_BT059352 (2481) ---------TATGTGTACATAAAAACGTTACAATAAATAACTATCCCTA-

 2551 2573

sgk2a\_NM\_001139943 (2288) CAAAAAAAAAAAAAAAAAAAAGA

 sgk2b\_BT059352 (2521) -AAAAAAAAAAAAAAAAAAAAGA