**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