

Additional file 8 Alignment of nucleotide sequences of the three *BjSultr1;2* forms. Shared nucleotides are highlighted in grey.

<i>BjSultr1; 2a</i>	1	ATGTC	TGGGAGAGCTCATCC	TGTGGACGCTGAT	TAAGTCCAGCAACGGACGGTGGAGAT	CTCCGAT	CAAAATCGTGCCTCACCCGCCATAAAAGTTGGGG																	
<i>BjSultr1; 2b</i>	1	ATGTC	TGGGAGAGCTCATCC	TG-----	ATGTAAATCCGGTGACGGATGGTGGAGAT	CTTCT	TATCAAAATCGTGCCTCACCCGGCATAAAAGTTGGGG																	
<i>BjSultr1; 2c</i>	1	ATGTC	TGGGAGAGCTCATCC	TG-----	ATGTGAAATCCCTGTGTACGGATGGTGGAGAT	CTTCCGAT	CAAAATCGTGCCTCACCCGGCATAAAAGTTGGGTG																	
<i>BjSultr1; 2a</i>	101	TCC	CACCGAAGCAGAAACATG	TTCATGAC	TTCATGTACACGTTCAAAGAAACTTT	CTTCC	CATGATGATCCCTCTCAGAGATTTTAAAGATCAGCCTAAAGTC																	
<i>BjSultr1; 2b</i>	92	TCC	CACCGAAGCAGAAACATG	TTCATGAC	TTCATGTACACGTTCAAAGAAACTTT	CTTCC	CATGATGATCCCTCTCAGACATTTTAAAGATCAGCCTAAAGTC																	
<i>BjSultr1; 2c</i>	92	TCC	CACCGAAGCAGAAACATG	TTCATGAC	TTCATGTACACGTTCAAAGAAAGCTTT	CTTCC	CATGATGATCCCTCTCAGACACTTAAAGATCAGCCTAAAGTC																	
<i>BjSultr1; 2a</i>	201	CAAA	CAGTTCAATGCTCCAGT	CTGTCT	CCCGTTTTCGAT	TGGGAC	GTAGCTACAACTCAAGAAGTTTCGTGGTGATCTAAATTCGCCGGTTTA																	
<i>BjSultr1; 2b</i>	192	CAAAA	AGTTCAATGCTCCAGT	CTGTCT	CCCGTTTTCGAT	TGGGAC	GTAGCTACAACTCAAGAAGTTTCGTGGTGATCTAAATTCGCCGGTTTA																	
<i>BjSultr1; 2c</i>	192	TAA	GAAAGTTCAATGCTCCAGT	CTGTCT	CCCGTTTTCGAT	TGGGAC	GTAGCTACAACTCAAGAAGTTTCGTGGTGATCTAAATTCGCCGGTTTA																	
<i>BjSultr1; 2a</i>	301	ACT	AT	TGCCAGTCT	TGTAATCC	TCAGGAT	ATTTGGATA	CGCTAAGCTCGTAAATTTGGATCCTAAATACGGTTTATATTCGAGTTTGTACCTCCATTGG																
<i>BjSultr1; 2b</i>	292	ACT	AT	TGCCAGTCT	TGTAATCC	TCAGGAT	ATTTGGATA	CGCTAAGCTCGTAAATTTGGATCCTAAATACGGTTTATATTCGAGTTTGTACCTCCATTGG																
<i>BjSultr1; 2c</i>	292	ACT	AT	TGCCAGTCT	TGTAATCC	TCAGGAT	ATTTGGATA	CGCTAAGCTCGTAAATTTGGATCCTAAATACGGTTTATATTCGAGTTTGTACCTCCATTGG																
<i>BjSultr1; 2a</i>	401	TGT	AT	GCA	TGTA	TGGGAGT	TCTAGGCA	TAGCAATAGGACCCGTGCGTGTGGTTTCTCTGTCTGCTAGGTA	CTCCTCAAGCTGAGGTCGACCCAGT															
<i>BjSultr1; 2b</i>	392	TGT	AT	GCA	TGTA	TGGGAGT	TCTAGGCA	TAGCAATAGGACCCGTGCGTGTGGTTTCTCTGTCTGCTAGGTA	CTCCTCAAGCTGAGGTCGACCCAGT															
<i>BjSultr1; 2c</i>	392	TGT	AT	GCA	TGTA	TGGGAGT	TCTAGGCA	TAGCAATAGGACCCGTGCGTGTGGTTTCTCTGTCTGCTAGGTA	CTCCTCAAGCTGAGGTCGACCCAGT															
<i>BjSultr1; 2a</i>	501	CACA	AAACCC	TGAT	GAGTAC	CTCCGAC	TTTCCCTT	CACCGCCAGT	TTTTCGCCGGTGTCACTGAAGCAGCCCTTGGATTTCTTAGGTTAGGTTCTTTGATT															
<i>BjSultr1; 2b</i>	492	CACA	AAACCC	TGAT	GAGTAC	CTCCGAC	TTTCCCTT	CACCGCCAGT	TTTTCGCCGGTGTCACTGAAGCAGCCCTTGGATTTCTTAGGTTAGGTTCTTTGATT															
<i>BjSultr1; 2c</i>	492	CACA	AAACCC	TGAT	GAGTAC	CTCCGAC	TTTTCGCCGGTGTCACTGAAGCAGCCCTTGGATTTCTTAGGTTAGGTTCTTTGATT																	
<i>BjSultr1; 2a</i>	601	GAT	TTCC	TTT	CACAC	GGGCT	GTGTGGAT	TTTCAT	GGGTGGTGCAGCCATCACAAATAGCTCTTCAAGCTCAAAAGGGTTTCTTAGGATCAAAAAATTTCA															
<i>BjSultr1; 2b</i>	592	GAT	TTCC	TTT	CACAC	GGGCT	GTGTGGAT	TTTCAT	GGGTGGTGCAGCCATCACAAATAGCTCTTCAAGCTCAAAAGGGTTTCTTAGGATCAAAAAATTTCA															
<i>BjSultr1; 2c</i>	592	GAT	TTCC	TTT	CACAC	GGGCT	GTGTGGAT	TTTCAT	GGGTGGTGCAGCCATCACAAATAGCTCTTCAAGCTCAAAAGGGTTTCTTAGGATCAAAAAATTTCA															
<i>BjSultr1; 2a</i>	701	CCA	AGAAA	AC	CGAT	AT	CA	TTGCT	TTTTAGATTTCTGTCTT	CAGCGCAGCTCAT	CATGGTTGGAAT	TGGCAGACT	TATAC	TCAT	TGGTGCAT	CTTCTTTGAC								
<i>BjSultr1; 2b</i>	692	CCA	AGAAA	AC	CGAT	AT	CA	TTGCT	TTTTAGATTTCTGTCTT	CAGCGCAGCTCAT	CATGGTTGGAAT	TGGCAGACT	TATAC	TCAT	TGGTGCAT	CTTCTTTGAC								
<i>BjSultr1; 2c</i>	692	CCA	AGAAA	AC	CGAT	AT	CA	TTGCT	TTTTAGATTTCTGTCTT	CAGCGCAGCTCAT	CATGGTTGGAAT	TGGCAGACT	TATAC	TCAT	TGGTGCAT	CTTCTTTGAC								
<i>BjSultr1; 2a</i>	801	CTT	CC	TTCT	CACT	CT	TAAA	CT	AT	TGGGAAAAGAA	CAAGAAA	CTGTT	CC	GGG	TTCC	GGG	TTGCAC	CCGTTGATATCAGTTATCAATTTCCACCTTCTTT						
<i>BjSultr1; 2b</i>	792	CTT	CC	TTCT	CACT	CT	TAAA	CT	AT	TGGGAAAAGAA	CAAGAAA	CTGTT	CC	GGG	TTCC	GGG	TTGCAC	CCGTTGATATCAGTTATCAATTTCCACCTTCTTT						
<i>BjSultr1; 2c</i>	792	ATT	CC	TTCT	CACT	CT	TAAA	CT	AT	TGGGAAAAGAA	CAAGAAA	CTGTT	CC	GGG	TTCC	GGG	TTGCAC	CCGTTGATATCAGTTATCAATTTCCACATTTCTTT						
<i>BjSultr1; 2a</i>	901	GTC	TAC	ATA	TAA	CCCG	GAG	CCAA	AAAC	AAGG	AT	CTT	GA	AAA	CA	AT	CTT	TCT	CTTTT	TTGATCAAAATTTTGA	TCAAAATTTT	TACT	CT	CCGGAG
<i>BjSultr1; 2b</i>	892	GTT	TAC	ATA	TAA	CCCG	GAG	CCAA	AAAC	AAGG	AT	CTT	GA	AAA	CA	AT	CTT	TCT	CTTTT	TTGATCAAAATTTTGA	TCAAAATTTT	TACT	CT	CCGGCC
<i>BjSultr1; 2c</i>	892	GTC	TAC	ATA	TAA	CCCG	GAG	CCAA	AAAC	AAGG	AT	CTT	GA	AAA	CA	AT	CTT	TCT	CTTTT	TTGATCAAAATTTTGA	TCAAAATTTT	TACT	CT	CCGGAC

BjSultr1; 2a 1001 ATAACTTGGCAAAGGGGATTCCCATCGGTGTTGTCGGTGGAAATGGTCGCCCTAACAGAAAGCTGTAGCGAATGGAAAGAAACCTTTGCTGCAATGAAAGACTA
BjSultr1; 2b 992 ATTACCTAGCTAAAGGGCATTCCCATCGGTAGTCCCTGGAAATGGTTGCCCTAACGGAACTGTGGCTATTGGAAAGAAACAATTTGCTGCAATGAAAGACTA
BjSultr1; 2c 992 ATTACCTTGCFAAGGGCATTCCGTATCGGTGAGTCCCTGGAAATGGTCGCCCTAACGGAAAGCTGTGGCTATTGGAAAGAAACCTTTGCTGCAATGAAAGACTA

BjSultr1; 2a 1101 TCAAAATCGACGGTAAACAAAGAGATGGTAGACTAGGTGTTAAGAACCTTGTGTTGGAACAATGTCCTTTCTTGTACTAGTGGCAGAGATCGTTCTCAAGATCA
BjSultr1; 2b 1092 TCAAAATAGATGGTAAACAAAGAGATGGTAGACTAGGTGTTAAGAACCTTGTGTTGGAACAATGTCCTTTCTTGTACTAGTGGCAGAGATCGTTCTCAAGATCA
BjSultr1; 2c 1092 TCAAAATCGATGGTAAACAAAGAGATGGTAGACTAGGTGTTAAGAACCTTGTGTTGGAACAATGTCCTTTCTTGTACTAGTGGCAGAGATCGTTCTCAAGATCA

BjSultr1; 2a 1201 GCTGTAAACTTCATGGCTGGATGTCAAAACHTGGTGTTCACCAACATCAATAATGTCCTTTCTTGTGACACTGCTCTTCCCTCACTCCCTCTTTTCAAGT
BjSultr1; 2b 1192 GCTGTAAACTTCATGGCTGGATGTCAAAACHTGGTGTTCACCAACATCAATAATGTCCTTTCTTGTGACACTGCTCTTCCCTCACTCCCTCACTTTTAAAGT
BjSultr1; 2c 1192 GCTGTAAACTTCATGGCTGGATGTCAAAACHTGGTGTTCACCAACATCAATAATGTCCTTTCTTGTGACACTGCTCTTCCCTCACTCCCTCACTTTTAAAGT

BjSultr1; 2a 1301 ACACACCAAAACGCCATCCITAGCAGCTATTATATCATCAACGCCAGTGAATCCCTGTGATGATVATCCAAAGCAGTATTTTGAATCTTCAAGGTCGATAAGCTCGA
BjSultr1; 2b 1292 ACACACCAAAACGCCAATCCITCGCAGCTATTATATCATCAATGCTGTGATTCCTTTGATGATVATCCAAAGCAGTATTTGATCTTCAAGGTCGATAAGCTTTGA
BjSultr1; 2c 1292 ACACACCAAAACGCCATCCITCGCAGCTATTATATCATCAATGCTGTGATTCCTTTGATGATVATCCAAAGCAGTATTTGATCTTCAAGGTCGATAAGCTTTGA

BjSultr1; 2a 1401 CTTTCATCGCTTGTATGGGAGCTTTCTTTTGGCGTCACTCTTTTCCGTTGAGATCGGACTTCTTATTTGTCCTCTCTATATCGTTTGGCTTAAGATTCCTCTTG
BjSultr1; 2b 1392 TTTTCGTTGCTGTATGGGAGCTTTCTTTTGGCGTCACTCTTTTCCGTTGAGATGGGCTTCTCATTTGCCGTTCTATATCATTTGCAAGATTCCTCTTG
BjSultr1; 2c 1392 CTTTCGTTGCTTGTATGGGAGCTTTCTTTTGGCGTCACTCTTTTCCGTTGAGATGGGCTTCTCATTTGCCGTTCTATATCATTTGCTTAAGATTCCTCTTG

BjSultr1; 2a 1501 CAAAGTAAACAAGACTAGAACCCGAGTTCTTTGGAAACATCCCAAACCTTCAGTATATCCGGAAACATCCAACAGTATCCTGAAGCCACCATGTTCCAGGGG
BjSultr1; 2b 1492 CAAAGTAAACAAGACTAGAACCCGAGTTCTTTGGAAACATCCCAAACCTTCAGTATATAGAAACATCCAACAGTATCCTGAAGCCACCATGTTCCAGGGG
BjSultr1; 2c 1492 CAAAGTAAACAAGACTAGAACCCGAGTTCTTTGGAAACATCCCAAACCTTCAGTATATAGAAACATCCAACAGTATCCTGAAGCCACCATGTTCCAGGGG

BjSultr1; 2a 1601 TTCCTAACCTCGTGTGACTCGCGGATTTACTTCTCCAACTCAAATACGTCAGAGAAAGGATCCAAAGATGGTTACTAGAGGAAGAAAGAGAAAGGTTGAA
BjSultr1; 2b 1592 TTCCTAACCTCGTGTGACTCGCGGATTTACTTCTCCAACTCAAATACGTCAGAGAAAGGATCCAAAGATGGTTACTAGAGGAAGAAAGAGAAAGTGA
BjSultr1; 2c 1592 TTCCTAACCTCGTGTGACTCGCGGATTTACTTCTCCAACTCAAATACGTCAGAGAAAGGATCCAAAGATGGTTACTAGAGGAAGAAAGAGAAAGGTTGAA

BjSultr1; 2a 1701 AGCAGCAAGCCTACCTAGGATCCAGTTTCTGATCATGAAATGTCACCTGTTACGGACATCGACACAAGTGGTATTCACGCCCTAGAAAGCTTATACAAA
BjSultr1; 2b 1692 AGCAGCAAGCCTACCTAGGATCCAGTTTCTGAAATGTCACCTGTTACGGACATCGATACAAGTGGTATCCACGCCCTAGAAAGCTTATATAAG
BjSultr1; 2c 1692 AGCAGCAAGCCTACCTAGGATCCAGTTTCTGAAATGTCACCTGTTACGGACATCGATACAAGTGGTATCCACGCCCTAGAAAGCTTATACAAA

BjSultr1; 2a 1801 TCTCTCCAGAAAAGAGATATTCAGTTGGTTCTTCCGAAACCTTGGACCGTTGGTGAATGGCAAGCTACATTTGTTCGCACITTTGCTGACATGCTAGGACACG
BjSultr1; 2b 1792 TCTCTACAGAAAGAGATATTCAGTTGGTTCTTCCGAAACCTTGGTAAATGGCAAGCTACATTTGTTCGCACITTTGCTGATATGTTAGGACACG
BjSultr1; 2c 1792 TCTCTCCAGAAAGAGATATTCAGTTGGTTCTTCCGAAACCTTGGTAAATGGTGAATGGCAAGCTTACACTTGTCTCACITTTGCTGACATGTTGGATATG

BjSultr1; 2a 1901 ACCATATCTTTCTGACGGTGGCTGATGCCCTGGAAAGCTTGGTGTCCAAAACCTCTCCGACGAGGTTCTGA 1968
BjSultr1; 2b 1892 ACAATATATTTCTGACGGTGGCTGATGCCCTGGAAATCTTGTGTCCAAAACCTCTCCGACGAGGTTCTGA 1959
BjSultr1; 2c 1892 ACCATATCTTTCTGACGGTGGCTGATGCCCTGGAAAGCTTGGTGTCCAAAACCTCTCCGACGAGGTTCTGA 1959