

Table S1. Best hit contigs that exhibit significant identity with the coding DNA sequences of *TaSUT2s*.

Query sequence ^a										
E value ^b	<i>TaSUT2A</i>		<i>TaSUT2B</i>			<i>TaSUT2D</i>			Best hit contig	Contig's chromosomal location
	Identity (%)	Match length (bp)	E value	Identity (%)	Match length (bp)	E value	Identity (%)	Match length (bp)		
0	100	739	0	100	739	0	99	741	#2683050	5D
0	97	739	0	97	739	0	97	741	#2242458	5B
0	92	526	0	92	526	0	93	526	#2270208	5B
2e ⁻⁸⁶	99	183	2e ⁻⁸⁶	99	183	2e ⁻⁸⁶	99	185	#1490385	5A
3e ⁻⁷⁷	99	168	3e ⁻⁷⁷	99	168	3e ⁻⁷⁷	99	168	#1540422	5A
3e ⁻⁷⁷	99	168	3e ⁻⁷⁷	99	168	3e ⁻⁷⁷	99	168	#1508214	5A
4e ⁻⁴⁴	83	182	4e ⁻⁴⁴	83	182	2e ⁻⁴²	81	186	#2749442	5D

^aThe IWGSC survey sequence repository was searched for contiguous DNA sequences (contigs) with the cDNA sequences of *TaSUT2A*, *TaSUT2B* and *TaSUT2D* as queries. ^bE Value determines the significance of the alignment score.