

Genes whose expression is altered following speciation in *Spartina*

<i>Spartina</i> contig	length (bp)	Number of regions in the Sorghum genome	Gene annotation	GO accession number	Biological process function
contig29975	480	3 regions	bhlh transcription factor	GO:0030528	transcription regulator activity
contig09805	1100	1 region	ccaat-box transcription factor complex expressed	GO:0003700	transcription factor activity
contig10492	320	2 regions	cytochrome c oxidase polypeptide vib	GO:0006123	mitochondrial electron transport, cytochrome c to oxygen
contig29230	469	1 region	cytochrome c oxidase subunit 1	GO:0005507	copper ion binding
contig32516	493	5 regions	global transcription factor group	GO:0006357	regulation of transcription from RNA polymerase II promoter
contig06826	841	2 regions	glutathione s-transferase	GO:0046686	response to cadmium ion
contig16114	472	5 regions	glutathione s-transferase gstu6	GO:0004364	glutathione transferase activity
contig20419	1088	2 regions	hexokinase 2	GO:0030528	transcription regulator activity
contig13824	1145	2 regions	myb family transcription factor	GO:0045449	regulation of transcription
contig04589	563	2 regions	myb transcription factor	GO:0003677	DNA binding
contig18882	1230	1 region	peptide transporter ptr2	GO:0000325	plant-type vacuole
contig05684	428	3 regions	peroxidase 1	GO:0006979	response to oxidative stress
contig15367	883	1 region	retrotransposon protein	GO:0005739	mitochondrion
contig13583	1064	2 regions	seuss transcriptional co-regulator	GO:0009790	embryonic development
contig31047	311	2 regions	transcription factor iia small subunit	GO:0005672	transcription factor TFIIA complex
contig30693	780	1 region	transcription initiation factor iib	GO:0003743	translation initiation factor activity
contig08620	1174	3 regions	vacuolar h ⁺ -atpase catalytic subunit	GO:0005618	cell wall