

**S3A Table.**

Primers for 3C validation of 4C interactions, and 3C results.

Primer name indicates if the 4C cis-interaction was unique to one or common to both 4C replicates.

\*: 3C positive control; previously reported interaction between scs' and scs.

\*\* : Region selected for FISH analysis.

Viewpoint	Primer name	Chr	Primer sequence	Distance from viewpoint	3C result	
					Rep1	Rep2
scs'	scs'_VP_5	3R	GTCACGATATTCTTCAACCAACCGATAGTATCGC	viewpoint		
	scs'_scs_common_cis_3*	3R	ATCGTTTACGGTAGCCATTCTCACGT	~ 11 kb	+	+
	scs'_common_cis1_3	3R	TAATCTCCACCTGCCATTTG	~ 49 kb	+	+
	scs'_common_cis2_3	3R	CGAAGCAGACTCGCAATTA	~ 201 kb	-	-
	scs'_common_cis3_3**	3R	CAACTCTCGCTCTCGTTTC	~ 203 kb	+	-
	scs'_common_cis4_3	3R	CAGGAGAAGAAGGTGGTTAAG	~ 204 kb	-	-
	scs'_common_cis5_3	3R	ACAGTGAACCTCGTCGTC	~ 457 kb	-	-
	scs'_common_cis6_3	3R	ACGTCCACCAGTCCCTTCAACAAT	~ 527 kb	+	+
	scs'_common_cis7_3**	3R	CGAACTCCATTGTGAACAAGCTGATGG	~ 748 kb	+	+
	scs'_common_cis8_3	3R	CCTCAAAATGAGATGTAGCCGT	~ 930 kb	+	-
	scs'_unique_cis1_R1	3R	GCTGCTGCTAACTCAATTATAC	~ 1.28 Mb	-	+
	scs'_unique_cis1_R2	3R	ATTGCCATTGCCGTTGTGCATCATATC	~ 2.46 Mb	-	+
	scs'_unique_cis2_R2	3R	TGACTCACCGAAGCTTTATTC	~ 3.84 Mb	-	-
scs'_unique_cis2_R1	3R	GCTTGTCACTCATCATTCTATC	~ 17.1 Mb	-	+	
hts	hts'_VP_5	2R	ATCTGAGGCGGCACCTTACACT	viewpoint		
	hts'_common_cis1_3	2R	TAAGCTCCAGAGACGCTTTAGTGC	~ 62 kb	+	-
	hts'_common_cis2_3	2R	TGAATTTCCCAATGCCCAATCAACAGGT	~ 67 kb	+	+
	hts'_common_cis3_3	2R	GGGTTTCCTTATTGCAAGGG	~ 115 kb	+	-
	hts'_common_cis4_3**	2R	TCACAATGGCCTTACATC	~ 850 kb	+	+
	hts'_common_cis5_3	2R	GCGCCACAAGAACCTTA	~ 896 kb	+	+
	hts'_common_cis6_3	2R	CTGTGTCTCAGTGCATAGAAG	~ 1.29 Mb	+	-
	hts'_common_cis7_3	2R	CCTATTAAACGCGGTCAATCCT	~ 1.39 Mb	-	-
	hts'_common_cis8_3	2R	CAATGTCGGCGTGTATGT	~ 1.69 Mb	-	-
	hts'_common_cis9_3	2R	CTTAACCGGCTTTGCCTT	~ 1.73 Mb	-	-
	hts'_unique_cis1_R2	2R	AATCCGAAGAACTTTGGCAATA	~ 3.45 Mb	-	-
	hts'_common_cis10_3	2R	GCACCTTGCCGTAGGA	~ 4.49 Mb	-	-
	hts'_common_cis11_3	2R	CCGCATTCTGTTGTATTG	~ 4.85 Mb	-	-
	hts'_unique_cis1_R1	2R	CCGTGGTTCTCGGTGATAACAGCATAG	~ 5.47 Mb	-	-
	hts'_unique_cis2_R2	2R	CTCGTACTTGCTATCCAGTCCAGTA	~ 11.2 Mb	-	+
	hts'_unique_cis2_R1	2R	GTTATGGTGATTATTGGTAGATTCCG	~ 12.8 Mb	-	+
	hts'_trans1_3	X	GGAAAGACCGGTTATATCTG	trans	+	-
hts'_trans2_3	3L	GTTGATAGTAGCCCGGTTGA	trans	-	-	
hts'_trans3_3	2L	TGCACTCCTCAGAACATAAAC	trans	+	-	
snf	snf'_VP_5	X	CACCGGTGCGATAACATATCGATAGACC	viewpoint		
	snf'_common_cis1_3	X	AATGGTGGACGATTGGG	~ 7 kb	+	-
	snf'_common_cis2_3	X	AACGGTTGAAGCATGGAC	~ 14 kb	+	+
	snf'_common_cis3_3	X	CTAAGTGAGCACAGCCACA	~ 105 kb	+	-
	snf'_common_cis4_3	X	ATGCCGAGCATAAGTGCCTCTGTG	~ 112 kb	+	+
	snf'_common_cis5_3	X	GAAATCACCACCGACGT	~ 231 kb	-	-
	snf'_common_cis6_3	X	GCAACACAAGCAACATACAACCTGTGGT	~ 370 kb	+	+
	snf'_common_cis7_3**	X	GTAATACGGCTCCTGCATGA	~ 405 kb	+	-
	snf'_unique_cis1_R2	X	GCTATCCATTAAACCAACTCCCGAGCGA	~ 1.21 Mb	-	+
	snf'_common_cis8_3	X	GCAGATTATGTTTGGCTTGTG	~ 4.75 Mb	-	-
	snf'_unique_cis2_R2	X	ATGTACATACATCCATCCATTCCG	~ 6.51 Mb	-	+
	snf'_common_cis9_3	X	CCAATAAGCGCATTCTACACA	~ 9.49 Mb	-	-
	snf'_unique_cis1_R1	X	GTGCCTTCTCGAATCCATCGGTCA	~ 10.4 Mb	-	-
	snf'_unique_cis2_R1	X	ATCGAATCGTTTCATTGTTGTG	~ 12.1 Mb	-	+
	snf'_trans1_3	3L	TTCGCTCCACTTGAACCTGTGCT	trans	+	+
snf'_trans2_3	2L	ACTGAGTCTAGGAAATATGAAACC	trans	-	-	
snf'_trans3_3	2R	GCTGACCCATGAAGCTCCACTT	trans	-	-	
RpS6	RpS6'_VP_5	X	GACCGATAGGAGGAAGTAGAGATGACAGAT	viewpoint		
	RpS6'_common_cis1_3	X	ATCCCGTCGATCCTCCAGGA	~ 7 kb	+	+
	RpS6'_common_cis2_3	X	ACCGCTAAACCAATGTCCAAGTCATCGT	~ 9 kb	+	+
	RpS6'_common_cis3_3	X	ATACGATCGGAAGAGCGATG	~ 10 kb	+	+
	RpS6'_common_cis4_3	X	GCTATACATTACTTATCTGGAAAGG	~ 13 kb	+	+
	RpS6'_common_cis5_3	X	GTGTTTAGGATCTCGACCAGTG	~ 14 kb	+	+
	RpS6'_common_cis6_3	X	GTATAAACAGCACCGGCACTGCT	~ 142 kb	+	-
	RpS6'_common_cis7_3	X	CACAAATCTATGCATTACATCCC	~ 167 kb	+	-
	RpS6'_common_cis8_3	X	CCCAAATCCTGATGATCCTTATC	~ 172 kb	-	-
	RpS6'_common_cis9_3	X	AAGTCCGTTGCTTCTTCTC	~ 1.61 Mb	-	-
	RpS6'_common_cis10_3**	X	CGATAAACAGAGCACCAAAGA	~ 3.05 Mb	+	+
	RpS6'_unique_cis1_R2	X	GCACAACAAAGGACTAGAAGTA	~ 3.05 Mb	-	+
	RpS6'_unique_cis1_R1	X	CAATCGGCAATTCTATTGTTGA	~ 3.20 Mb	-	+
	RpS6'_common_cis11_3	X	TAGTGTGAGCACTTGGCTGTCCACA	~ 5.05 Mb	-	-
	RpS6'_common_cis12_3	X	GTAATACTTGTAGCCAGAACCAACAGCAG	~ 6.15 Mb	+	+
	RpS6'_unique_cis2_R1	X	CTACTATTGTCGACCACTGTGCGAT	~ 7.58 Mb	-	+
	RpS6'_unique_cis2_R2	X	CTCGTGCATCACCTCCAGCAGATA	~ 11.8 Mb	-	+
	RpS6'_trans1_3	2L	CACCTCAGGTTATAAAATCCACTCAAGGCAAA	trans	-	-
	RpS6'_trans2_3	2L	TACTTGGCTGACTCCGG	trans	+	-
	RpS6'_trans3_3	3L	GATCATTAGCACTAGCAATTAGTCTGCGC	trans	+	+

**S3B Table: 3C cross-check.**

Primers for 3C validation of 4C interactions, and 3C results.

Primer name indicates if the 4C cis-interaction was unique to one or common to both 4C replicates.

\*: 3C positive control; previously reported interaction between scs' and scs.

\*\* : Region selected for FISH analysis.

3C viewpoint cross-check: viewpoint, primer name, chr, sequence, original viewpoint interaction, and results						
Viewpoint	Primer name	Chr	Primer sequence	Distance from viewpoint	3C result	
					Rep1	Rep2
scs'	hts_common_cis1_3	2R	TAAGCTCCAGAGAACGCTTTAGTGC	hts	-	-
	hts_common_cis2_3	2R	TGAATTTCCCAATGCCCAATCAACAGGT	hts	-	-
	snf_common_cis4_3	X	ATGCCGAGCATAAGTGCCTGTGTG	snf	-	-
	snf_common_cis6_3	X	GCAACACAAGCAACATACAACCTGTGGT	snf	-	-
	snf_trans3_3	2R	GCTGACCCATGAAGCTCCACTT	snf	-	-
	RpS6_common_cis1_3	X	ATCCCGTCGATCCTCCAGGA	RpS6	-	-
	RpS6_common_cis2_3	X	ACCGCTAAACCAATGTCCAAGTCATCGT	RpS6	-	-
	RpS6_trans3_3	3L	GATCATTAGCACTAGCAATTAGCTGCGC	RpS6	-	-
hts	scs'_common_cis6_3	3R	ACGTCCACCAGTCCCTTCACAAT	scs'	-	-
	scs'_common_cis7_3	3R	CGAACTCCATTGTGAACAAGCTGATGG	scs'	-	-
	snf_common_cis4_3	X	ATGCCGAGCATAAGTGCCTGTGTG	snf	-	-
	snf_common_cis6_3	X	GCAACACAAGCAACATACAACCTGTGGT	snf	-	-
	snf_trans3_3	2R	GCTGACCCATGAAGCTCCACTT	snf	-	-
	RpS6_common_cis1_3	X	ATCCCGTCGATCCTCCAGGA	RpS6	-	-
	RpS6_common_cis2_3	X	ACCGCTAAACCAATGTCCAAGTCATCGT	RpS6	-	-
	RpS6_trans3_3	3L	GTAATACTTTGTAGCCAGAACACAACAGCAG	RpS6	-	-
snf	scs'_common_cis6_3	3R	ACGTCCACCAGTCCCTTCACAAT	scs'	-	-
	scs'_common_cis7_3	3R	CGAACTCCATTGTGAACAAGCTGATGG	scs'	-	-
	hts_common_cis1_3	2R	TAAGCTCCAGAGAACGCTTTAGTGC	hts	-	-
	hts_common_cis2_3	2R	TGAATTTCCCAATGCCCAATCAACAGGT	hts	-	-
	RpS6_common_cis1_3	X	ATCCCGTCGATCCTCCAGGA	RpS6	-	-
	RpS6_common_cis2_3	X	ACCGCTAAACCAATGTCCAAGTCATCGT	RpS6	-	-
	RpS6_trans3_3	3L	GTAATACTTTGTAGCCAGAACACAACAGCAG	RpS6	-	-
	RpS6	scs'_common_cis6_3	3R	ACGTCCACCAGTCCCTTCACAAT	scs'	-
scs'_common_cis7_3		3R	CGAACTCCATTGTGAACAAGCTGATGG	scs'	-	-
hts_common_cis1_3		2R	TAAGCTCCAGAGAACGCTTTAGTGC	hts	-	-
hts_common_cis2_3		2R	TGAATTTCCCAATGCCCAATCAACAGGT	hts	-	-
snf_common_cis4_3		X	ATGCCGAGCATAAGTGCCTGTGTG	snf	-	-
snf_common_cis6_3		X	GCAACACAAGCAACATACAACCTGTGGT	snf	-	-
snf_trans3_3		2R	GCTGACCCATGAAGCTCCACTT	snf	-	-