

**Table S5: Alignment of stem-loop motifs of all histone genes in *S. constricta***

Gene name/seq position	DIST	Stem-loop		
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ScH1.1-1/34-79	38	ACAAA	GGTCCTTTTCAGGACC	ATCATATCACCCGAAACGACTTACC
ScH1.1-2/34-79	38	ACAAA	GGTCCTTTTCAGGACC	ATCATATCACCCGAAACGACTTACC
ScH1.2/30-75	34	AAAAC	GGCCCTTTTATAGGGCC	ACCAATTAATCAAGAAGAGATTACC
ScH2A.1-1/31-75	34	A-AAC	GGCCCTTTTATAGGGCC	ACCAAATTCCTAGAAACAGATTACA
ScH2A.1-2/31-75	34	A-AAC	GGCCCTTTTATAGGGCC	ACCAATTAATCAAGAAGAGATTACC
ScH2A.1-3/31-75	34	A-AAC	GGCCCTTTTATAGGGCC	ACCAAATTCCTAGAAACAGATTACA
ScH2A.1-4/31-75	34	A-AAC	GGCCCTTTTATAGGGCC	ACCAAATTCCTAGAAACAGATTACA
ScH2A.1-5/31-75	34	A-AAC	GGCCCTTTTATAGGGCC	ACCAATTAATCAAGAAGAGATTACC
ScH2B.1-1/21-66	27	AAAAC	GGCCCTTTTATAGGGCC	ACAAAACGCCTC <b>GAAAAGA</b> AATACC
ScH2B.1-2/21-66	27	AAAAC	GGCCCTTTTATAGGGCC	ACCAAATTCCTAGAAACAGATTACA
ScH2B.1-3/21-66	27	AAAAC	GGCCCTTTTATAGGGCC	ACCAAATTCCTAGAAACAGATTACA
ScH2B.2/22-67	28	AAAAC	GGCCCTTTTATAGGGCC	ACCAAATTCCTAGAAACAGATTACA
ScH3.1-1/24-69	28	ACAAC	GGCCCTTTTATAGGGCC	ACAACCAACCTCGAAATCTATTACC
ScH3.1-2/23-68	27	ACAAC	GGCCCTTTTATAGGGCC	ACAACCAACCTCGAAATCTATTACC
ScH3.3/52-95	56	GAACC	GGTGC-CTCTGGGTCC	TCAAGCTTGAGAGGTGAAAGGCA
ScH4-1/23-68	27	GAAAC	GGCCCTTTTATAGGGCC	ACAACCAACCTCGAAATCTATTACC
ScH4-2/23-68	27	GAAAC	GGCCCTTTTATAGGGCC	ACAAAACGCCTCGAAAAGAAATACC
ScH4-3/23-68	27	GAAAC	GGCCCTTTTATAGGGCC	ACAAAACGCCTCGAAAAGAAATACC
ScH2A.1-6/30-74	33	A-AAC	GGCCCTTTTATAGGGCC	ACCAAATAATCAAGAATAGATTACC
ScH3.1-3/24-67	28	ACAAC	GGCCCTTTTATAGGGCC	ACAAAATTCCTCGAAAAGA--TACC
ScH4-4/23-68	27	GAAAC	GGCCCTTTTATAGGGCC	ACCAACATCCTAGAAACAGATTACA
ScH1.3-6/38-83	42	ACAAA	GGTCCTTTTCAGGACC	ATCAAATAGCACGTAATGAGTTACC
ScH2A.1-18/29-74	33	AAAAC	GGCCCTTTTATAGGGCC	ACCAAATAATCAAGAATAGATTACC
ScH2B.1-21/22-67	28	AAAAC	GGCCCTTTTATAGGGCC	ACCAACATCCTAGAAACAGATTACA
ScH3.1-18/24-69	28	ACAAC	GGCCCTTTTATAGGGCC	ACAACCTCCCTCGAAACATATTACC
ScH4-21/23-66	27	GAAAC	GGCCCTTTTATAGGGCC	ACAAAATTCCTCGAAAAGA--TACC
ScH1oo/15-52	19	CAGAG	AGCTGTT-----C	AATAAATATGCTGTAGAAATAGACA
ScH3.2-2/1-42	5	AAGAT	AACGC-GTTGACACTG	CCACTCACATTAACATTGAATA--
ScH2B.4/1-36	4	GTAA-	-----TTTCTGAGC-	-CACTTTTCTAAAAAAAAAAAA--
ScH3.1-13/24-69	28	ACAAC	GGCCCTTTTATAGGGCC	ACAACCTCCCTCGAAACATATTACC
ScH4-17/23-66	27	GAAAC	GGCCCTTTTATAGGGCC	ACAAAATTCCTCGAAAAGA--TACC

ScH2A.1macro/13-56	17	ATTAT	AGTCCATATCATA—C	ACACATGGAATGAGAAAATATTACA
ScH2A.1-10/30-74	33	A-AAC	GGCCCTTTTTAGGGCC	ACCAAATAATCAAGAATAGATTACC
ScH2B.1-13/22-67	28	AAAAC	GGCCCTTTTTAGGGCC	ACCAACATCCTAGAAACAGATTACA
ScH2B.1-14/22-67	28	AAAAC	GGCCCTTTTTAGGGCC	ACCAACATCCTAGAAACAGATTACA
ScH2B.1-15/22-67	28	AAAAC	GGCCCTTTTTAGGGCC	ACCAACATCCTAGAAACAGATTACA
ScH3.1-9/24-69	28	ACAAC	GGCCCTTTTTAGGGCC	ACAACCTCCCTCGAAACATATTACC
ScH3.4/24-67	28	ACAAC	GGCCCTTTTTAGGGCC	ACAAAATTCTCTCGAAAAGA--TACC
ScH1.3-1/38-83	42	ACAAA	GGTCCTTTTCAGGACC	ATCAAATAGCACGTAATGAGTTACC
ScH1.3-2/38-83	42	ACAAA	GGTCCTTTTCAGGACC	ATCAAATAGCACGTAATGAGTTACC
ScH2A.1-7/29-74	33	AAAAC	GGCCCTTTTTAGGGCC	ACCAAATAATCAAGAATAGATTACC
ScH2B.1-4/22-67	28	AAAAC	GGCCCTTTTTAGGGCC	ACCAACATCCTAGAAACAGATTACA
ScH2B.1-5/22-67	28	AAAAC	GGCCCTTTTTAGGGCC	ACCAACATCCTAGAAACAGATTACA
ScH2B.1-6/24-69	28	CAAAC	GGCCCTTTTTAGGGCC	ACCAACATCCTAGAAACAGATTACA
ScH3.1-4/24-69	28	ACAAC	GGCCCTTTTTAGGGCC	ACAACCTCCCTCGAAACATATTACC
ScH3.1-5/24-69	28	ACAAC	GGCCCTTTTTAGGGCC	ACAACCTCCCTCGAAACATATTACC
ScH4-5/23-66	27	GAAAC	GGCCCTTTTTAGGGCC	ACAAAATTCTCTCGAAAAGA--TACC
ScH4-6/23-66	27	GAAAC	GGCCCTTTTTAGGGCC	ACAAAATTCTCTCGAAAAGA--TACC
ScH4-7/23-66	27	GAAAC	GGCCCTTTTTAGGGCC	ACAAAATTCTCTCGAAAAGA--TACC
ScH1.0/56-99	60	GCATC	GTCGCTCATTATCGCC	AC--ATCACCTCATTGCAGAGTACC
ScH1.1-4/34-79	38	ACAAA	GGTCCTTTTCAGGACC	ATCATATCACCCGAAACGACTTACC
ScH2A.1-11/31-75	34	A-AAC	GGCCCTTTTTAGGGCC	ACCAAATTCCTAGAAACAGATTACA
ScH2A.1-12/31-75	34	A-AAC	GGCCCTTTTTAGGGCC	ACCAAATTCCTAGAAACAGATTACA
ScH2A.1-13/30-75	34	AAAAC	GGCCCTTTTTAGGGCC	ACCAAATTCCTAGAAACAGATTACA
ScH2B.1-16/21-66	27	AAAAC	GGCCCTTTTTAGGGCC	ACAAAACGCCTCGAAAAGAAATACC
ScH3.1-10/23-68	27	ACAAC	GGCCCTTTTTAGGGCC	ACAACCAACCTCGAAATCTATTACC
ScH3.1-11/23-68	27	ACAAC	GGCCCTTTTTAGGGCC	ACAACCAACCTCGAAATCTATTACC
ScH4-14/23-68	27	GAAAC	GGCCCTTTTTAGGGCC	ACAAAACGCCTCGAAAAGAAATACC
ScH3.2-3/23-68	27	AACGC	GTTCTGTCTATCTATCT	ACTATCTATCTATCTATCTACTATC
ScH3.2-4/91-125	95	CAATC	AGCCCTTTTCAGGGC-	-----TATGAAGGGACTACT
ScH3.2-5/18-52	22	CTGTC	TGTCTTCTGTCTGTCT	GCTGTCTGTCTG-----TC
ScH3.1-7/23-68	27	ACAAC	GGCCCTTTTTAGGGCC	ACAAAACGCCTCGAAAAGAAATACC
ScH3.2-1/37-72	41	ACAAT	AACTTTGGTTAAAGC-	-----TTATAAACTGGCAGTT
ScH1.3-5/39-84	43	ACAAA	GGTCCTTTTCAGGACC	ATCAAATAGCACGTAATGAGTTACC
ScH1.3-7/39-84	43	ACAAA	GGTCCTTTTCAGGACC	ATCAAATAGCACGTAATGAGTTACC

ScH1.5/58-103	62	GTAAC	ACGTTTTTTTAAAAAC	AAGAATTCGCCGGAACACACGAGC
ScH2A.1-17/30-75	34	AAAAC	GGCCCTTTTTAGGGCC	ACCAAATAATCAAGAATAGATTACC
ScH2A.1-19/30-75	34	AAAAC	GGCCCTTTTTAGGGCC	ACCAAATAATCAAGAATAGATTACC
ScH2B.1-20/23-68	29	AAAAC	GGCCCTTTTTAGGGCC	ACCAACATCCTAGAAACAGATTACA
ScH2B.1-22/23-68	29	AAAAC	GGCCCTTTTTAGGGCC	ACCAACATCCTAGAAACAGATTACA
ScH3.1-17/25-70	29	ACAAC	GGCCCTTTTTAGGGCC	ACAACCTCCCTCGAAACATATTACC
ScH3.1-19/25-70	29	ACAAC	GGCCCTTTTTAGGGCC	ACAACCTCCCTCGAAACATATTACC
ScH4-20/24-67	28	GAAAC	GGCCCTTTTTAGGGCC	ACAAAATTCCTCGAAAAGA--TACC
ScH4-22/24-67	28	GAAAC	GGCCCTTTTTAGGGCC	ACAAAATTCCTCGAAAAGA--TACC
ScH4-23/24-67	28	GAAAC	GGCCCTTTTTAGGGCC	ACAAAATTCCTCGAAAAGA--TACC
ScH2A.1-15/31-76	35	AAAAC	GGCCCTTTTTAGGGCC	ACCAAATTCCTAGAAACAGATTACA
ScH2Asperm/35-79	39	AAAGC	ATC-CGTGTTATCATC	CGCAACCATATATAAACGACTGTTC
ScH1.1-3/35-80	39	ACAAA	GGTCCTTTTTCAGGACC	ATCATATCACCCGAAACGACTTACC
ScH1.4-1/35-80	39	ACAAA	GGTCCTTTTTCAGGACC	ATCATATCACCCGAAACGACTTACC
ScH1.4-2/35-80	39	ACAAA	GGTCCTTTTTCAGGACC	ATCATATCACCCGAAACGACTTACC
ScH2A.1-8/32-76	35	A-AAC	GGCCCTTTTTAGGGCC	ACCAATTAATCAAGAAGAGATTACC
ScH2A.1-9/32-76	35	A-AAC	GGCCCTTTTTAGGGCC	ACCAAATTCCTAGAAACAGATTACA
ScH2B.1-8/24-69	28	CAAAC	GGCCCTTTTTAGGGCC	ACCAATTAATCAAGAAGAGATTACC
ScH2B.1-9/22-67	28	AAAAC	GGCCCTTTTTAGGGCC	ACCAAATTCCTAGAAACAGATTACA
ScH2B.1-10/22-67	28	AAAAC	GGCCCTTTTTAGGGCC	ACAAAACGCCTCGAAAAGAAATACC
ScH2B.1-11/22-67	28	AAAAC	GGCCCTTTTTAGGGCC	ACAAAACGCCTCGAAAAGAAATACC
ScH2B.1-12/22-67	28	AAAAC	GGCCCTTTTTAGGGCC	ACCAAATTCCTAGAAACAGATTACA
ScH3.1-8/24-69	28	ACAAC	GGCCCTTTTTAGGGCC	ACAACCAACCTCGAAATCTATTACC
ScH4-10/24-69	28	GAAAC	GGCCCTTTTTAGGGCC	ACAAAACGCCTCGAAAAGAAATACC
ScH4-11/24-69	28	GAAAC	GGCCCTTTTTAGGGCC	ACAACCAACCTCGAAATCTATTACC
ScH4-12/24-69	28	GAAAC	GGCCCTTTTTAGGGCC	ACAAAACGCCTCGAAAAGAAATACC
ScH4-13/24-69	28	GAAAC	GGCCCTTTTTAGGGCC	ACAAAACGCCTCGAAAAGAAATACC
ScH3.1-14/25-70	29	ACAAC	GGCCCTTTTTAGGGCC	ACAACCTCCCTCGAAACATATTACC
ScH2A.V/11-41	10	-----	---CCTTATCAGGGA-	-TCAAAATGTACGAACTGAG-----
ScH2A.2/30-75	34	AAAAC	GGCCCTTTTTAGGGCC	ACCAAATAATCAAGAATAGATTACC
ScH2B.1-17/23-68	29	AAAAC	GGCCCTTTTTAGGGCC	ACCAACATCCTAGAAACAGATTACA
ScH4-15/24-67	28	GAAAC	GGCCCTTTTTAGGGCC	ACAAAATTCCTCGAAAAGA--TACC
ScH1.3-3/39-84	43	ACAAA	GGTCCTTTTTCAGGACC	ATCAAATAGCACGTAATGAGTTACC
ScH2A.1-14/30-75	34	AAAAC	GGCCCTTTTTAGGGCC	ACCAAATAATCAAGAATAGATTACC

ScH2B.1-18/23-68	29	AAAAC	GGCCCTTTT TAGGGCC	ACCAACATCCTAGAAACAGATTACA
ScH3.1-12/25-70	29	ACAAC	GGCCCTTTT TAGGGCC	ACAACCTCCCTCGAAACATATTACC
ScH4-16/24-67	28	GAAAC	GGCCCTTTT TAGGGCC	ACAAAATTCCTCGAAAAGA--TACC
ScH2B.3/28-73	32	CAAAC	GGCCCTTTT TAGGGCC	ACAAAACGCCTCGAAAAGAAATACC
ScH1.3-4/39-84	43	ACAAA	GGTCCTTTT CAGGACC	ATCAAATAGCACGTAATGAGTTACC
ScH2A.1-16/30-75	34	AAAAC	GGCCCTTTT TAGGGCC	ACCAAATAATCAAGAATAGATTACC
ScH2B.1-19/23-68	29	AAAAC	GGCCCTTTT TAGGGCC	ACCAACATCCTAGAAACAGATTACA
ScH3.1-15/25-70	29	ACAAC	GGCCCTTTT TAGGGCC	ACAACCTCCCTCGAAACATATTACC
ScH3.1-16/25-70	29	ACAAC	GGCCCTTTT TAGGGCC	ACAACCTCCCTCGAAACATATTACC
ScH4-18/24-67	28	GAAAC	GGCCCTTTT TAGGGCC	ACAAAATTCCTCGAAAAGA--TACC
ScH4-19/24-67	28	GAAAC	GGCCCTTTT TAGGGCC	ACAAAATTCCTCGAAAAGA--TACC
ScH2B.1-7/24-69	28	CAAAC	GGCCCTTTT TAGGGCC	ACAAAACGCCTCGAAAAGAAATACC
ScH3.1-6/25-70	29	ACAAC	GGCCCTTTT TAGGGCC	ACAACCAACCTCGAAATCTATTACC
ScH4-8/24-69	28	GAAAC	GGCCCTTTT TAGGGCC	ACAAAACGCCTCGAAAAGAAATACC
ScH4-9/24-69	28	GAAAC	GGCCCTTTT TAGGGCC	ACAACCAACCTCGAAATCTATTACC

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Note: DIST (Distance between stop codon and stem-loop structure). The gray shaded background is the gene without stem-loop structure.