SUPPLEMENTAL FIGURE LEGENDS

Suppl Figure 1. Linker scan analysis of *ARS319*. (A) Plasmid loss rates per generation are plotted for wild type *ARS319* (pFJ9) and mutant versions of pFJ9 containing GGTCGAC linker substitutions and additional mutations. (B) Detailed view of wild type *ARS319* sequence and mutant derivatives, marked as in Fig. 2B.

Suppl Figures 2-10. Overview of nucleosome positions generated from various genome-wide datasets (Suppl Table 2). Four individual nucleosome studies are highlighted using colored lines or ovals. The solid grey ovals indicate the consensus positions of nucleosomes determined from six genome-wide studies (see (1)). A vertical line indicates the dyad position for each positioned nucleosome. There are two clear discrepancies between (1) and the four nucleosome studies we highlight (2-5) that are indicated by grey ovals with a white asterisk. These two nucleosomes, one completely overlapping *ARS1* and the other overlapping the B2 element of *ARS309*, also had a low occupancy value of 22/100 and 45/100 in (1) are therefore not shown in Figure 7.

Suppl Figure 11. The average ATCG composition of the B-region of 228 conserved ARS elements identified by Nieduszynski et al. (6) is plotted as a percentage relative to distance from the EACS in bp. Nucleotide 1 in this graph is the last base pair of the 3' EACS, GT<u>T</u>.

SUPPLEMENTAL REFERENCES

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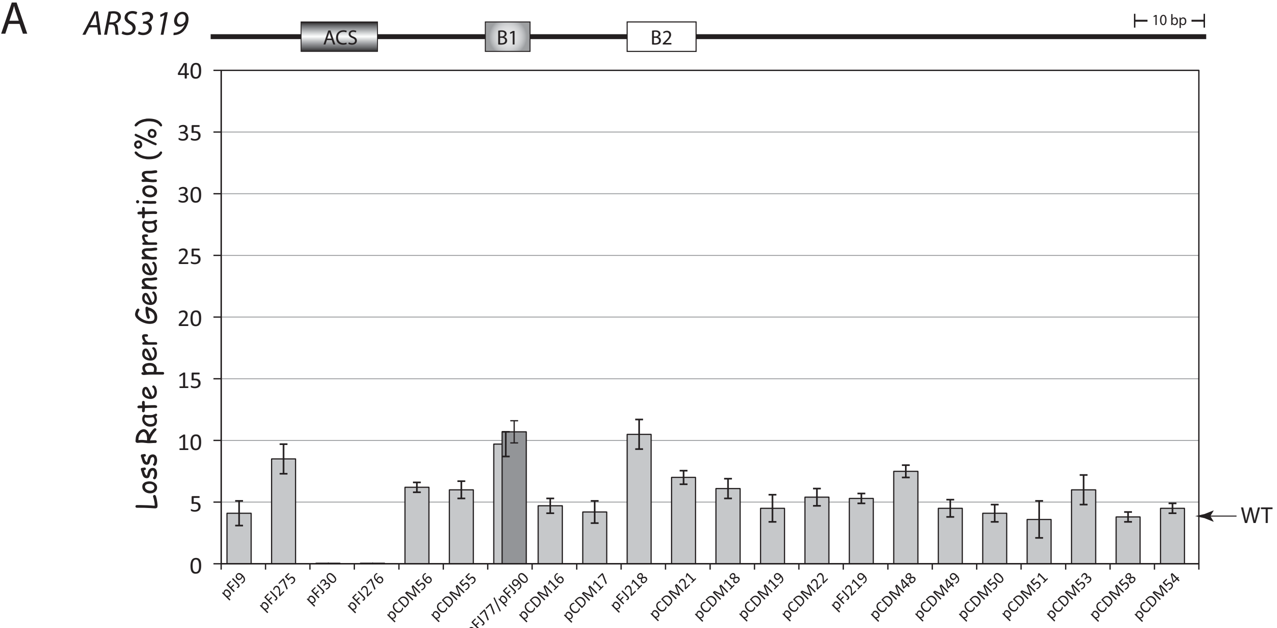

B

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pFJ9      GAATATTTTTATGTTTAGGTGATTTTAGTGGTGATTTTTCTGTAATATTGACATAAGTGTATATAAATTAAGTGGTTAGTATACGGTGAAAAAGAGGTACAACGTATGTATTAAGGGAATTTATACGATATTTGGGCCCGCCG
pFJ275    ---ggg-----------------------------------------------------------------------------------------------------------------------------------------
pFJ30     ------ggTcgac----------------------------------------------------------------------------------------------------------------------------------
pFJ276    ----------ggtcgac------------------------------------------------------------------------------------------------------------------------------
pCDM56    ------------------Ggtcgac----------------------------------------------------------------------------------------------------------------------
pCDM55    -------------------------ggtcGac---------------------------------------------------------------------------------------------------------------
pFJ77     ----------------------------------gg-----------------------------------------------------------------------------------------------------------
pFJ90     ---------------------------------ggg-----------------------------------------------------------------------------------------------------------
pCDM16    ------------------------------------ggTCgac----------------------------------------------------------------------------------------------------
pCDM17    -------------------------------------------ggTcgac---------------------------------------------------------------------------------------------
pFJ218    --------------------------------------------------ggtcgAc--------------------------------------------------------------------------------------
pCDM21    --------------------------------------------------------Ggtcgac--------------------------------------------------------------------------------
pCDM18    ---------------------------------------------------------------ggtcgac-------------------------------------------------------------------------
pCDM19    -----------------------------------------------------------------------Ggtcgac-----------------------------------------------------------------
pCDM22    ------------------------------------------------------------------------------Ggtcgac----------------------------------------------------------
pFJ219    -------------------------------------------------------------------------------------GgtcgAc---------------------------------------------------
pCDM48    --------------------------------------------------------------------------------------------gGtcGac--------------------------------------------
pCDM49    ---------------------------------------------------------------------------------------------------ggtCGac-------------------------------------
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pCDM51    -----------------------------------------------------------------------------------------------------------------gGtcgAc-----------------------
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pCDM58    -------------------------------------------------------------------------------------------------------------------------------ggtcgac---------
pCDM54    ----------------------------------------------------------------------------------------------------------------------------------------ggtcgac
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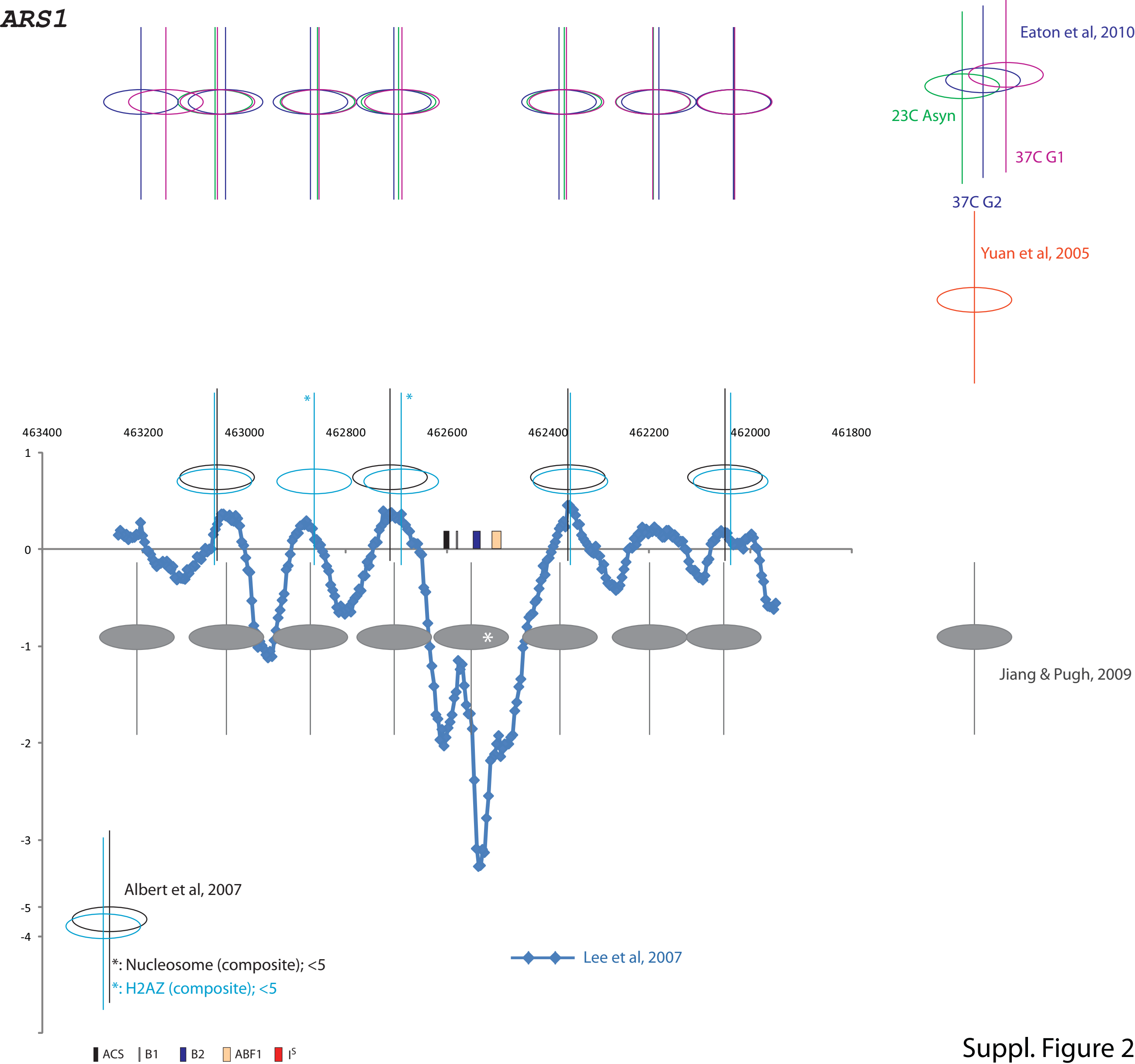
Suppl. Figure 1



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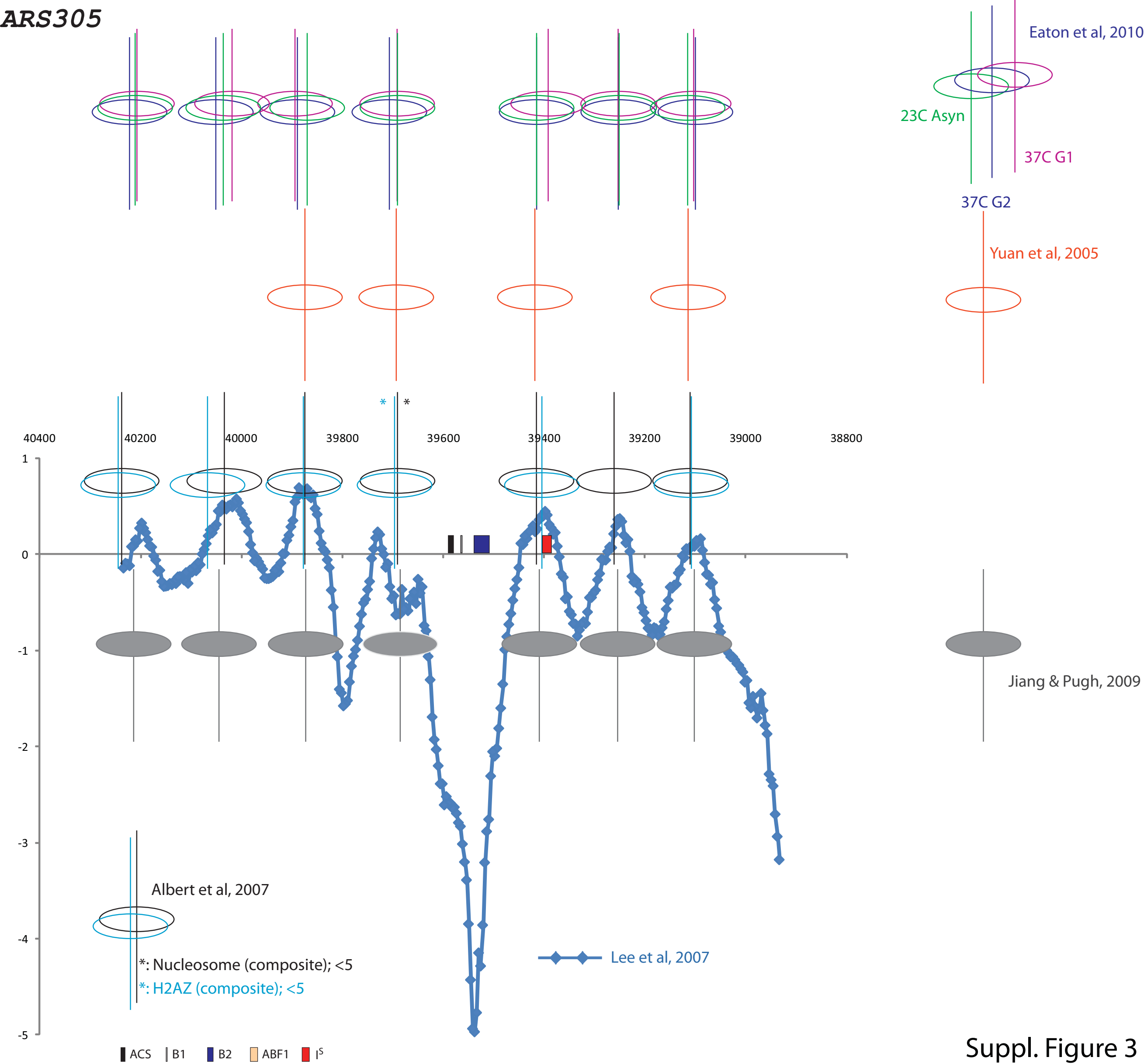

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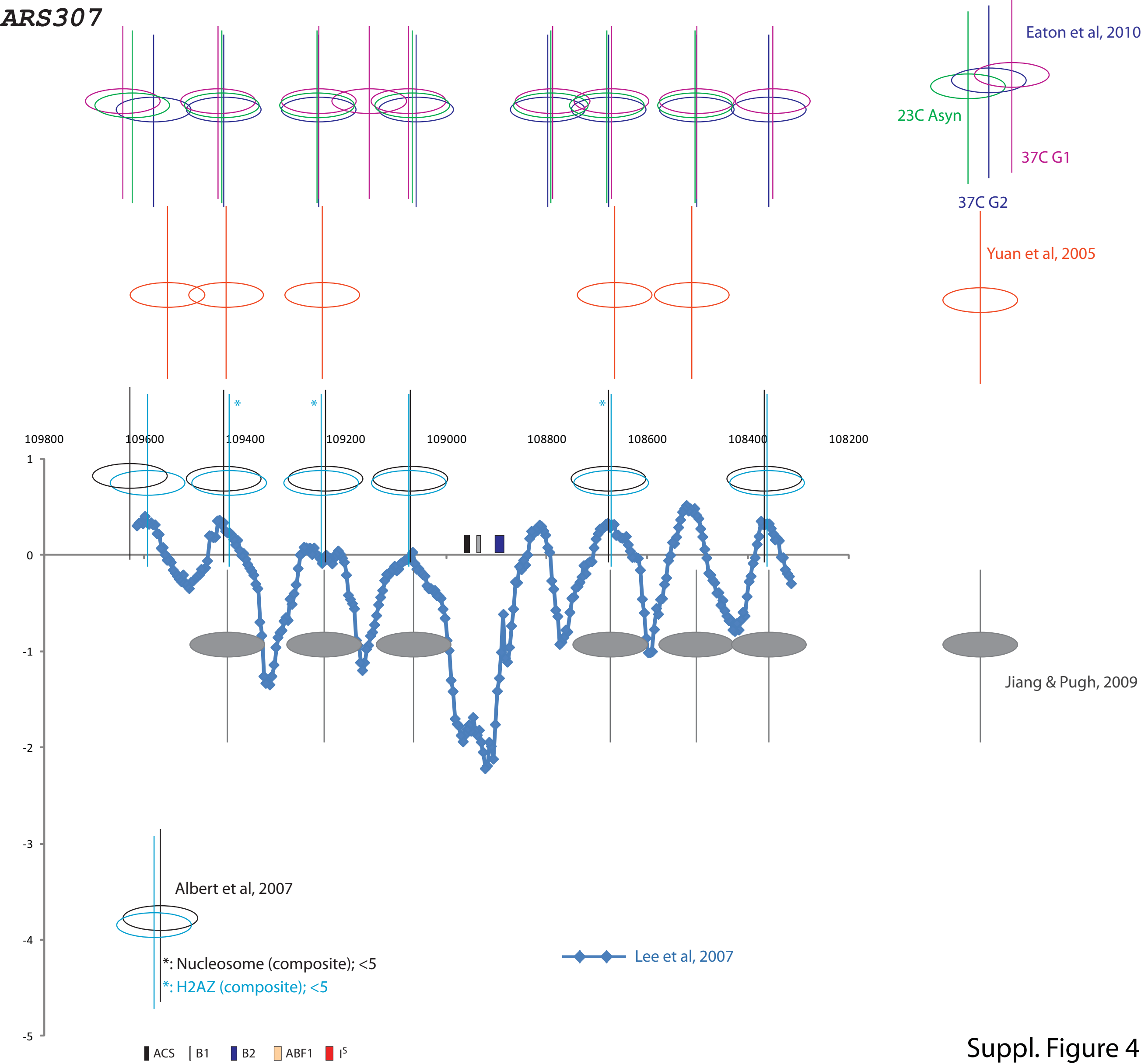
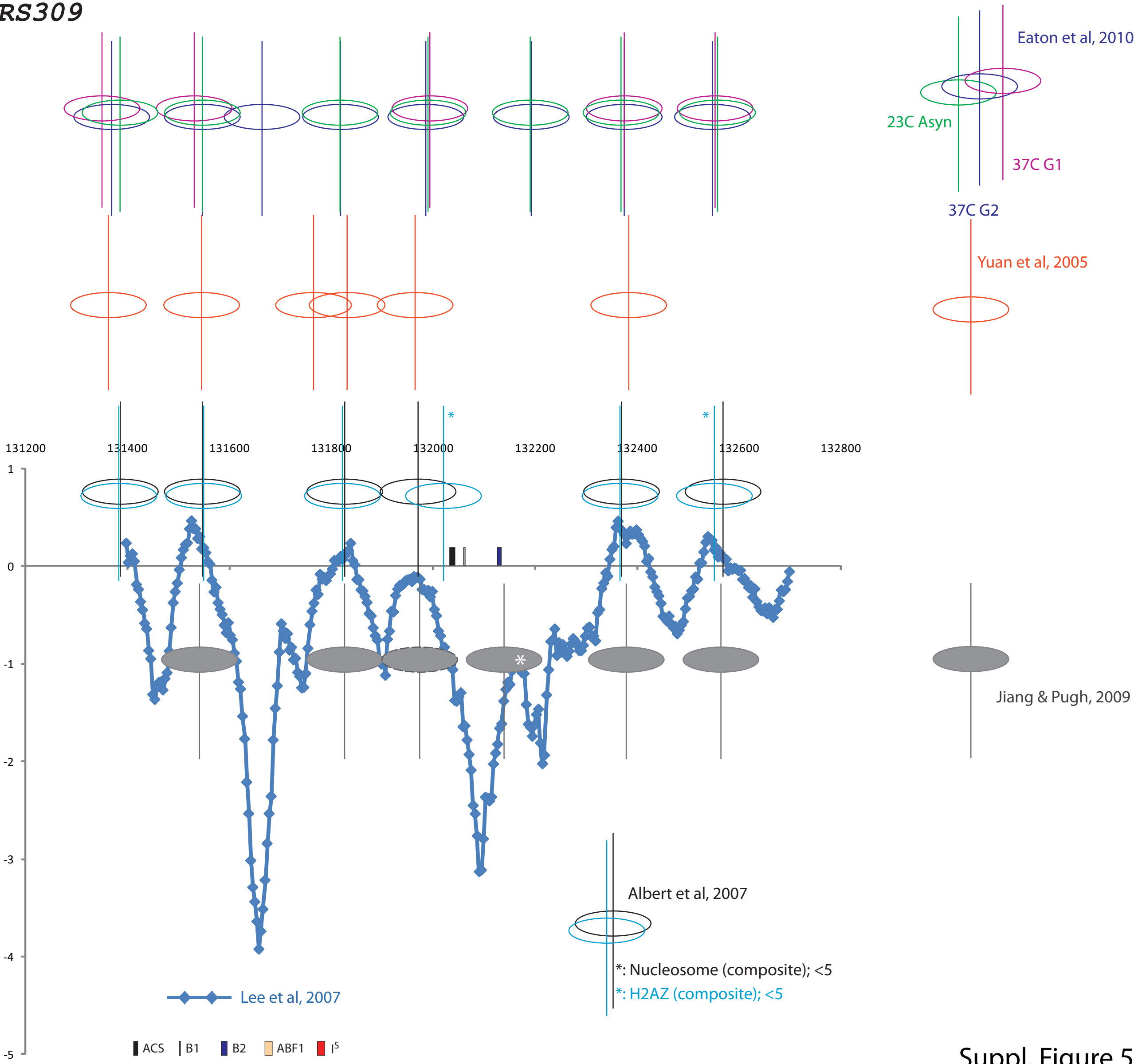


Suppl. Figure 4

ARS309



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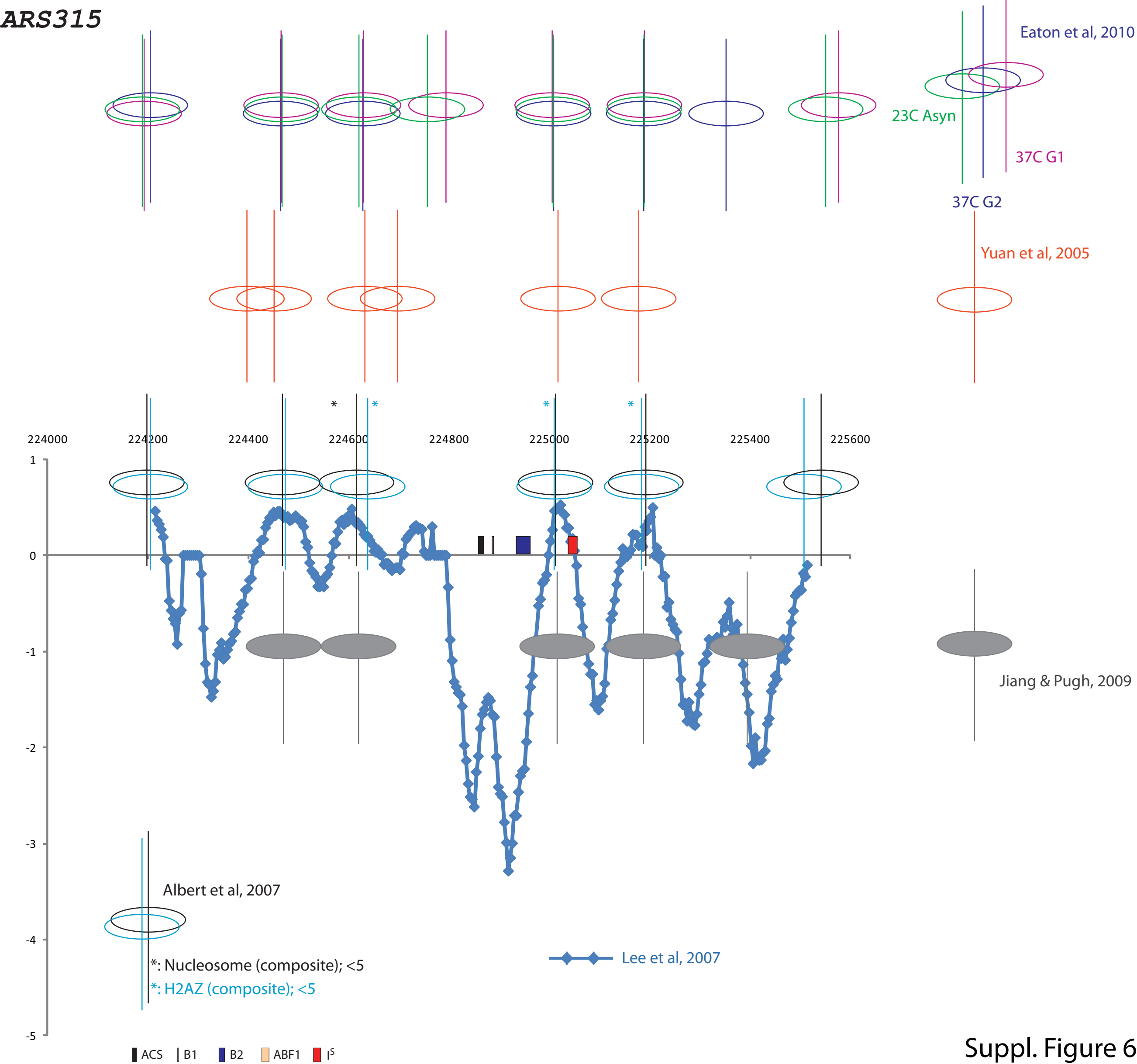

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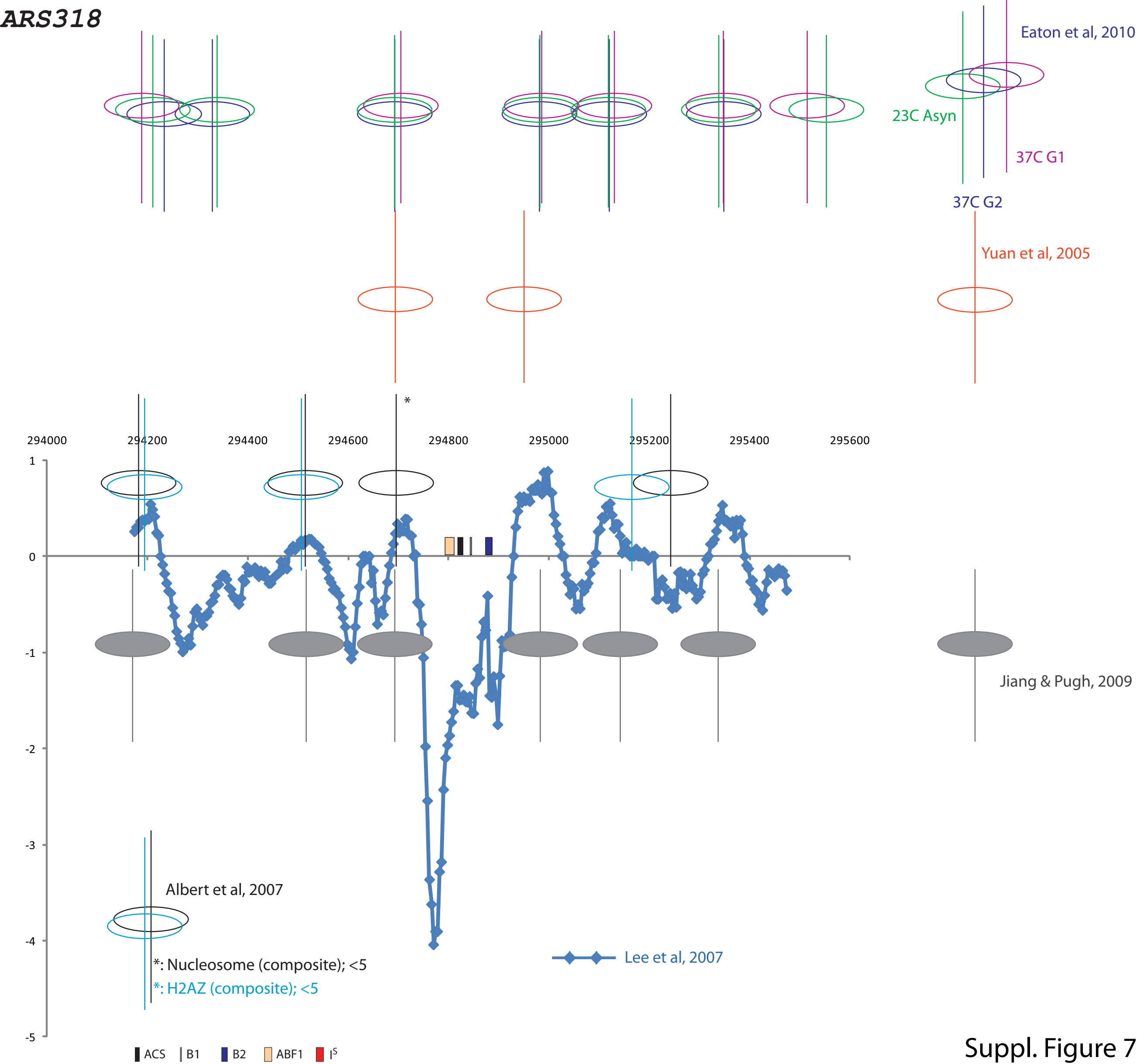
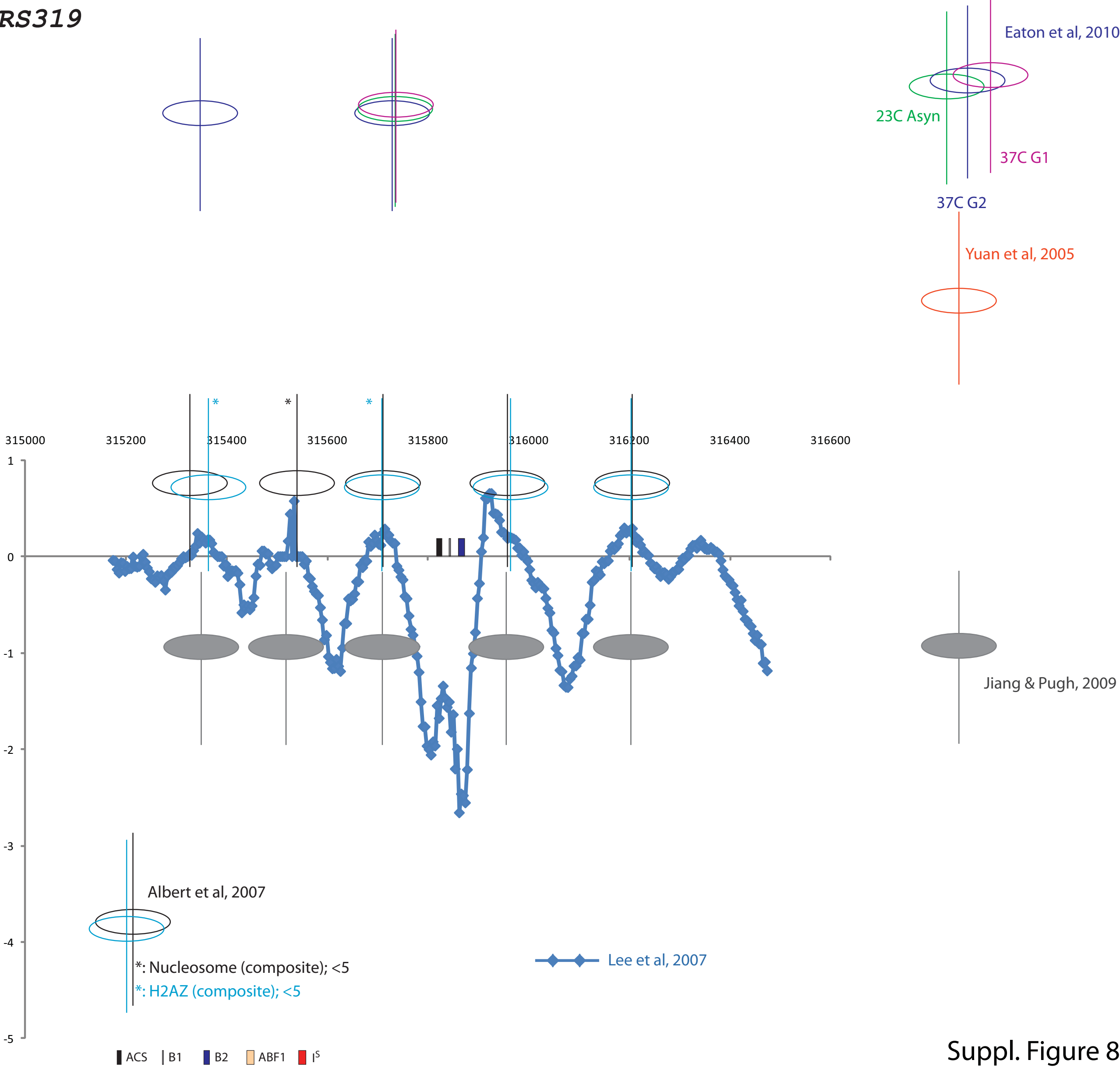


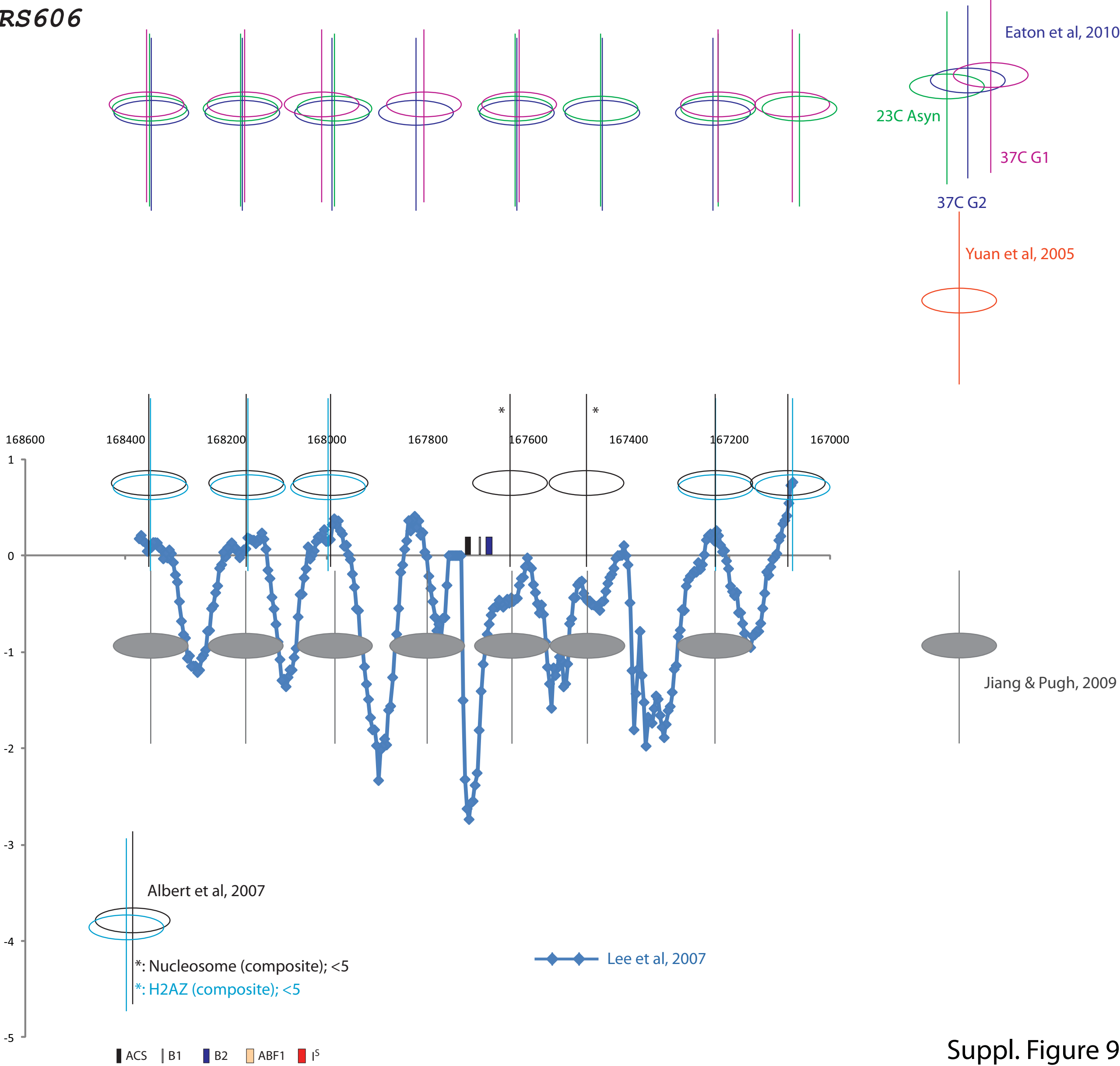
Suppl. Figure 7

ARS319



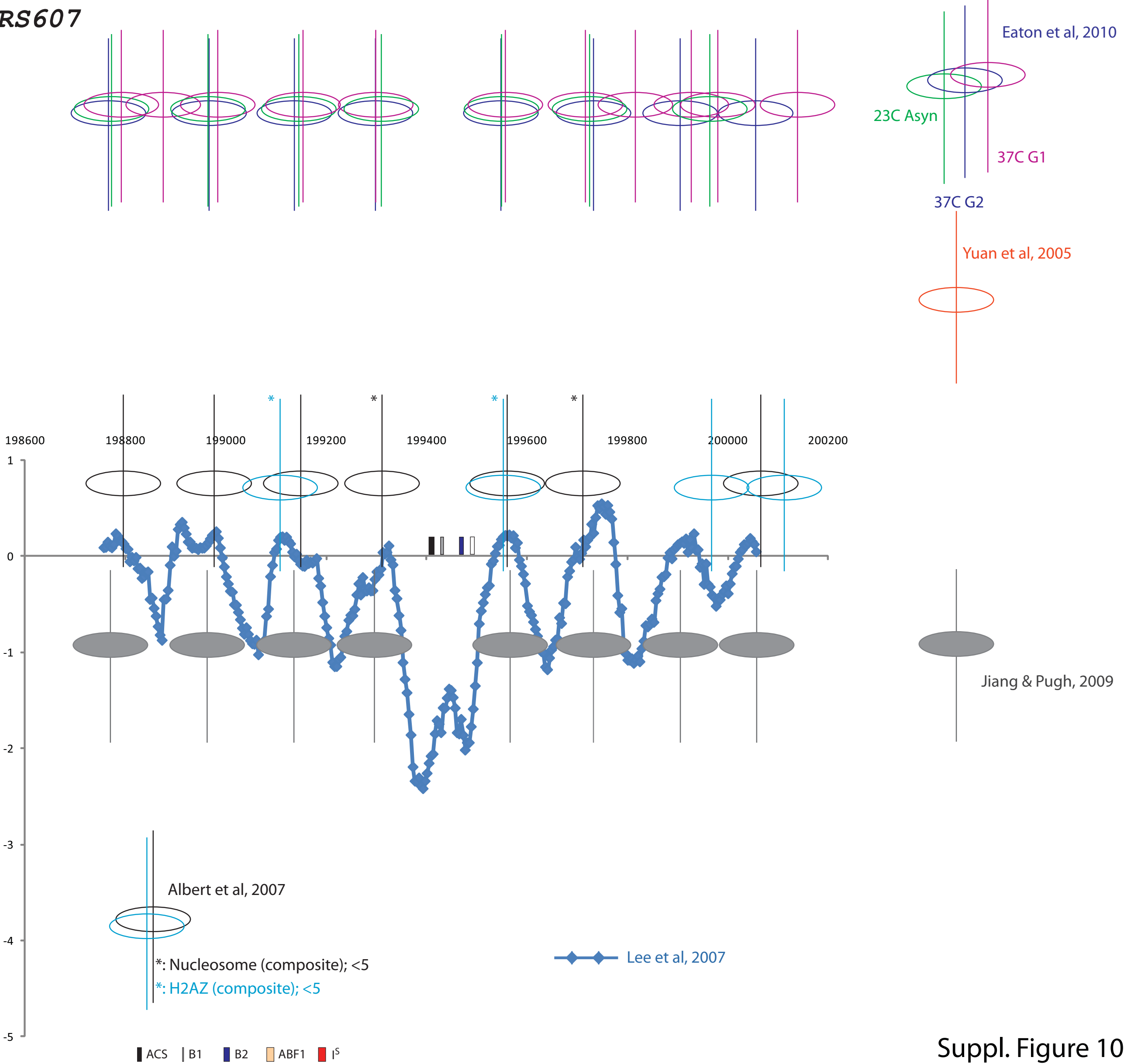
Suppl. Figure 8

ARS606

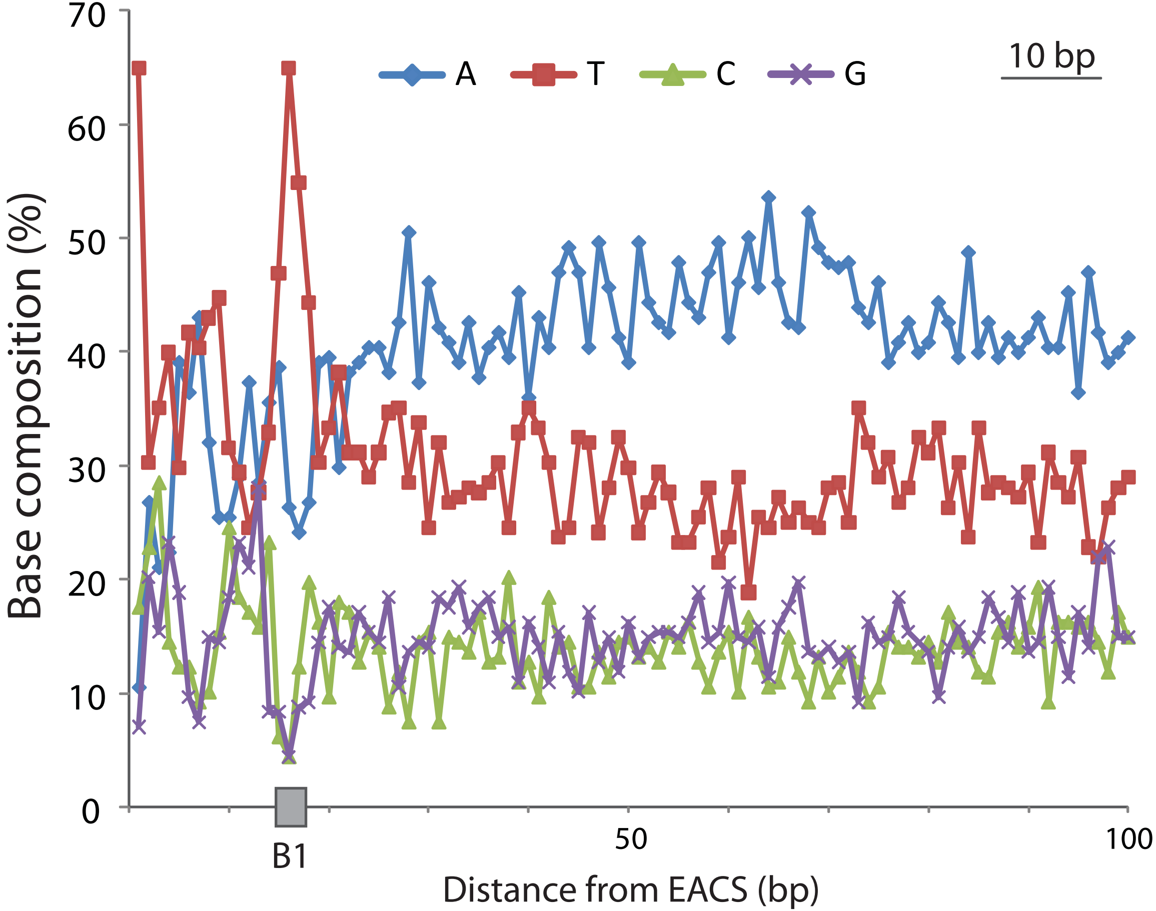


Suppl. Figure 9

ARS607



Suppl. Figure 10



Suppl. Figure 11

Suppl Table 1

Systematic name	proARS	Chr	Position / bp	proACS	100 nucleotides after 15bp proACS
ARSI-31	104	1	31002	ATTTTTAAGTTTTGT	TGGGTCTCTGAGAACTTTCAAAAAAAGAAAAAGTAAAGTATGATAAAACGGAGCACTTGCCAAAGTAATTAACGCCCATTAAAAAGAAGGCATAGGAGGC
ARSI-70	106	1	70433	TTTTTTATGTTTAGA	AACAAAATTTCCCCGAGAGAAAGGGAAAATATGTGGAAAAAGAAAAAGCACTTCCTTACCAAACGTCATTCCATCCATGAAATACTTGGCCGATTGAACT
ARSI-125	107	1	124522	ATATTTAAGTCTTGA	TTAACTGCTTTGGATGCTGTATTTTTATCATATTAACATTTTGATTAAAGAAAGAAAGTACATATTGATTTATTCATATTTAAATAGAGAAAACTACCAA
ARSI-160	109	1	159951	TTATTTATATTTAGT	GGGAGCAAAACAGTTTATTGAATGTTTACCAGAACCGAAAAAAAAGCTCTTCTAAACTGTTGACATCCAGTTCATTTACTTCCACGTGTAGATGTGAAGG
ARSI-176	110	1	176232	CTTTTTATGTTTTCT	TATGATTGAATTATTTATATTCTAAATTCCTCACGAATTTATACTGAAGATTTCCTTCCAGGCGAGAATAATAAACACATATTTATGATGATAACAAGAC
ARSII-29	201.5	2	28985	TTTTTTATAATTTGG	TCTAACAAACTTGATATCAGAACCACGTAGAAGAAAAAGAGACTAATAGTAAAAATATCAAGAAAGTTGACCAATTTTTGTTATATATGTCCGTAAAAGT
ARSII-63	202	2	63370	TTTTTTAATTTTTGT	CACGAAATCCTGGTATTTATTCTTGGAATGTATTTTTTTCTTTTGAAACACATTACCAACTCTTTTCAAAATCTCCAGGAATGGCAGAGAAGAAAACAAA
ARSII-170	207	2	170222	AGTTTTATATTTAGT	GAACATATGGGCAATTCCAGTGAACGCTTAAAAGCTGGGCAAAGAAATATATAAATTTAAAGATATAATGACAAGATAGCTCAAAATAACCGGAGAGTAA
ARSII-198	207.5	2	198385	AATTTAATGATTAGG	CAAGCTTATTGTTAAACAAGAAAAAACTTCAAAGTACATTGAAAAAAAAAGGAAATGTAATCAATTCCCCTCAAAATAAATTTTCTTACAAACCCATGAT
ARSII-238	208	2	237834	CTTTTTACTTTTAGT	TAAACTATTAAAGAATAATTTCCGCAAGGTACATAGCGATTTAAGTAGTTCAGAAAAGAAATTATTTAAAAATTACTCGCTCTCTTATTTGAAATGAAGA
ARSII-255	209	2	255040	ATTTTTATGTTTTGT	ATTTGGATTTTAGAAAGTAAATAAAGAAGGTAGAAGAGTTACGGAATGAAGAAAAAAAAATAAACAAAGGTTTAAAAAATTTCAACAAAAAGCGTACTTT
ARSII-326	211	2	326153	TTTTTTACATTTTTT	TAAGCCATAACGGATTTTAGTTACCGAGATTTTCAATCCTATAAGAATTACCTAAACTATTAAAAGCGGACCCATCTAAAACATAACGTTCGGCAAGTAG
ARSII-408	214	2	408003	TTATTTATATTTTGT	TCTGGAAGCTCTTTACAGAATGGAGTAGGAAAATATATAGAGAGGAAAAGCGAAATCGTTACGAGAATAAATAATCAAGAAAAGAAACTTGAACTTGGCT
ARSII-418	215	2	417972	TTTTTCATACTATGT	CTTTCATTTCCAACGTCCACAAGTACTGTAGAAATGTCTAGCGAAAATTATGAGAAAATAATGGTGTAATCGTTATAAAGTTTGCTAAATTTTTGTCTTG
ARSII-487	216	2	486858	ATATTCATGTTTAGT	TTTCCTTTTACATAATTTGGTCTTAGTACAGAGAAGTCCTCTTCTTCGCTTCTTCGCTTTTGGTCTTTCTGAAAAAGATCGATAAATAACATCCTAAAGA
ARSII-623	220	2	622713	TTATTTATATTTTTC	TTCAAATGTAAAGTTGGGTACCTAAGCTTAAATTCACCTGAAAATGAATTATATGAAAGATTTTACACCACATGTAAAAAAAAACGTACAAAAAGCCAAA
ARSII-704	222	2	704298	ATATATATATTTAGG	TAAATCATTTACACTTTTCGTCGATCTAAAAGCTCATCGCATTTTTTCGGTCCTGATGTTAAAAATTTATTTCGTTTATTAAAAAAAAAAAAAACATTAC
ARSII-742	224	2	741741	TTTTTAACGTTTTGT	TTGTCCCACTTGGTATTCCCCAGGCGAAAAGATATGTGGGAACTATCATGTTTTTGTTGGTACAAAATAAGGCATTATGCTAAAAACATACTATTTAACC
ARSII-757	225	2	757442	TTTTTAACGATTTGT	AAAGGATTACAGCAGTTCGTTATACTTGGCTGATAGCGTTAATTTTGCATACTTTTCTTATAATTGGTAATTTTCCTACGTATTATACAGTTGTACGTAT
ARSII-792	228	2	792173	GAAATTATGTTTTGT	TATGAATCTGAAAAGAAAAATACTATTTTAGCAATACAATGAATTTAAAAAGTTACCCTGTACTTTAATCCTTCAATTAAAACACTTCTTAAAATAGTAT
ARSIII-11	301	3	11254	TTTTTTATGTTTTTT	TAAAACATTAAAGTTTTCGGCACGGACTTATTTGGAATTCAAATTATTAATGAAAGAACAATTAACTAATTAATGTACTTAGTATTTGGCCATTATTATC
ARSIII-40	305	3	39591	TTTTATATGTTTTGT	TATGTATTGTTTATTTTCCCTTTAATTTTAGGATATGAAAACAAGAATTTATCAAAGAAAAAAATCTTAGCTTTAAGAACTACAAAGTAAATAAAAAATA
ARSIII-75	306	3	74522	TTATATTTATTTAGT	ACTTCTTGAGTTTACATATCCTTCGTAAAAATGCAACTTTTGTCGAAAAACACTTCCAAAAAAAAATAATAATGAATTTATGAAGCATACTAACGAGCGA
ARSIII-109	307	3	108968	TTATTTATGTTTTCT	TCTTCACACATGGGTTACTGGCAGAAAATAAAGAAGAGAGAGGATCAATATATATATATATATGCTAAAAGATTATAATATGAAACTTATTTAAAATCAG
ARSIII-132	309	3	132037	TTGTTTATATCTTGT	TTTGAAGTTTTAGCTTTGAAAAACATTTAATTGCGAAGTAACATAATGTTATTAATAGTGTACGACTGAAACAGCCATTCTATTTAAACATATAAAAGTA
ARSIII-167	310	3	166652	TTATTTATGTTATGT	ATATATAATCGTAACTCTTAGAGCAAAAAGTAAAAAAAAAGGTGGTACTTACCGAGGGAGAATATATACAAATTTATTCGTAAATGTAAATAATTAATTG
ARSIII-194	313	3	194302	TTTTTTACTTTTAGT	TTGTTAAATTTTAGTTTTCGTCATATATATAAAGTTTAAAAAGGTACAAAGAATGCAGTAATAAGAAATGTAATTACATGAGGGCAGTTTAAGTGCTACC
ARSIII-198	314	3	197551	ATATTCATGTTTAGT	ACTGAAAATTAAGAATACTTGCATAACTACAGTAGATAATATTTTTTGATAAGAAACCAGACGTAAATTAGATGTAATCTTTTACAGATATTACAGTCAA
ARSIII-225	315	3	224854	TTTTTTATGTTTTTC	TTCGCGCGTCAACTTTCTACCAAGAGAAAAACAATATAAGGTCTCCTTACTCTATAGGAGAATAAAACAAACAAAAATAAAAAGCACATCGTAGCGCCAA
ARSIII-273	316	3	273023	TTTTTCAAATTTAGT	TCTTCGTTGCCTACATTTTCTTAATTTTGTTTCCATTGCTTGTATCAAAAACTTATGAAATTACAAGCGTCAAGAAGCTGTTTATAAGAAGTAATGAAAA
ARSIII-293	317	3	292591	TTGTTTACTTTTTCT	ATCAGTGTTTTCAATTTTTTATTAAACAATGTTTGATTTTTTAAATCGCAATTTAATACCTAAATATAAAAAATGTTATTATATTGCAAAAACCCATCAA
ARSIII-316	319	3	315873	ATTTTTATGTTTAGG	TGATTTTAGTGGTGATTTTTCTGTAATATTGACATAAGTGTATATAAATTAAGTGGTTAGTATACGGTGAAAAAGAGGTATAACGTATGTATTAAGGGAA
ARSIV-16	403	4	15681	TTTTTTACGTTTTCT	CCATATTTCGAATTGTTCCTTCTTCAATCAAAATAATAAAAAAAAAAAATCACAAAAATGACTATAGTATTTTGAGCCCAACATGACTGCGAAATTGCTA
ARSIV-86	405	4	86124	ATTTTTATGTTTGGG	CGCAGAAAACAAGCTAAAACGGTGAGATAGGATAAACTATAATATAATTAAATTAAAAATACTGACTATATAAGCTAGACCTTATAAACTCTGAATATAA
ARSIV-124	406	4	123676	TTGTTTTCACTTTGT	GTTCGAAAAAATAAGTATTTGAAAACGAAAAAATAGTTTGTATGTTTGTATATAAGTTGTTATTATCAAAAATTAGAGGGAAAAAGTAACTAAATATATA
ARSIV-213	409	4	212593	TTTTTTATATTTTGT	TGTTGGTTTCAGGAAAAAGGGAGCTTTGCAAAAAAAAATAAAAAAAAATTGACAGGATGATCTATAAATATATTAATTGACCTATATAATGGTTTACACT
ARSIV-254	410	4	253840	TTTTTATAGTTTTGC	TTTGAATCTTTGTGTTTCCACACCGGAGAAAAAAAAGTTCATGAAGTGAAAAAGCGGTTAAACATGAATTTTCTACTATCTAAAGATAAAATTACAGATG
ARSIV-330	413	4	329741	ATTTTTATTTTTTTG	TTCAAGTAGGTTCATGCCGACAGTAAATCCTTATGCCCTACCTAAATATAAACACCCAAATATATATATATATATATATATATATAAATAATAAAAACGG
ARSIV-408	414	4	408131	TATATTATATTTAGC	GATGTAATGAAAGTAAAAAAACAAAAAAAAAAAACAACAATAATCAAATGACGCATATCTAAATATTCCAGAAAAGAATATAAATAACGAGGGTGATAAA
ARSIV-484	417	4	484034	TTTTTTATATTTATG	TAGCTTTTTGTATATTCTTAAGGACTTGTTTGATCTTTTACCCCTTCGCGTGGAGATAGGCTGCGCGGTTACTTTTATTAGAACGTACCCCAGATCTGTC
ARSIV-506	417.5	4	505517	TTTTTTATATTTTTG	CCTATATTCTTCTTTTTCTTTTTCTGTCTTGGGACGAAAGACAACAAAAAAAACCACCAGTAGCAAGAAATAAAAGAAGAGCCACTTAAATCGAGATAAT
ARSIV-555	418	4	555396	AAGTTTATGTTTTTT	CACTGGAGGCGTCATTTTCGCGTTGAGAAGATGTTCTTATCCAAATTTCAACTGTTATATAGAAGAGCAAAAAATTGCCAAAAAAAACAACATTTATTCA
ARSIV-568	419	4	567676	TTTTTTATGTTTTGA	GCCTACACCTGTTGGTGTCGGTAAAGAAAAAGTCAGAAATATAAATATTTAATCGGTATATAAAAGGCAAAACGTGAAAAAAAAAAATTAAAAGTTTATA
ARSIV-640	421	4	640062	TTTTTAAAGTTTTGG	TCGTTGAAAAAGGATTCAGAACAGGCAAAGATTATATATTAACGATATATATGAAAAATGAATGACAAATTTATAAGGAATAAGTTGAACATTAATAGCT
ARSIV-703	422	4	702924	TAATTAATGTTTTGG	TCTGAATTTTTATTTTTCAAAAATGAGGTGAAAACCTCCAACGAAACTTTTTAATTAAAACCATCCGATACAGAATTTTAAATCATCTAAAGCATTTATT
ARSIV-748	422.5	4	748456	TAATTAATATTTTGT	ATCTAAAGTGTTCATACTATATTATTTACTTAGATTATACATAATTAAAAAAAAAAAAAACTTTTTTTCCTTGTTTTCATTTTGTTTTTATTATTAAATA
ARSIV-753	423	4	753332	TTTTTTACATTTTGC	TTCAAAATAATGACTTTCCATTGACCTAACATGTTGAAAAACACAATTTTATCGCAGTGAATAGAAAAATACTTGATTGTGTATACAGCTTAAAAAATAA
ARSIV-806	425	4	806100	TTTTTAATATTTAGC	TGGGGTTGGGTAACAAGTGAGCAAGGGAAAAAGTGAACATTTTAAGAAGAACAATAAAATAGCAAGAGATGGAATGGTAATGCTTGGCTCTCGAGAAGAG
ARSIV-914	428	4	913856	ATTTTTATATTTTGT	TTCTTGCGTGGAGTTTTTACAGGAAGTTAATCACAACAGAGGGTTCAATCTCCAAGGCATAAAATAAACAAAAATTGTAATAGTTAGCAACTGCAATACG
ARSIV-922	429	4	921736	ATTTTAATGATTAGT	TGGGCTTTTGGCTACATATGTAAAATTACATATAATATAATGGACACATAAGCAAAAAAAAAAAAAAAAAAAATAAACAAATGAGCAACCCATCAAATAC
ARSIV-1017	430	4	1016845	TTGTTTACGTTTTGG	AGGAAAACTAATTATTTTTTTAATAAAGTAAACATAGCATTTCCAAGGTGCAAACCGATCCCTACCACCAAAATAAGCATACAAGACCGTTACAGCGTTA

Systematic name	proARS	Chr	Position / bp	proACS	100 nucleotides after 15bp proACS
ARSIV-1058	431	4	1057887	TTTTTTATGTTTATT	CCATATATACACTTATAATTTTTTTTTTTTGCGATTAATATAAGTTTGCCTGGATACACGAACATATATATGATTAAAATGGTTGTCTCGAACAAAAAAT
ARSIV-1110	431.5	4	1110132	TTTTTTATATTTTTA	TTCAAAAATAACATTCAAAATTTAATTTTAATAAACTCATTTAAAAAAAACCTCTAAAAACATGAAGATAGAACTATAATAACGGCTTCAGTATTCAAGA
ARSIV-1159	432	4	1159450	TTTTTTTTCTTTTCT	AAGCTTTGAAGAAAAGTTAACAGCTTTACCCTTCAAAGTTATTGTTTTGTAGCGCTAGAAGCGAAGTAGGCGCTCTTTCTCGCATAAGCTACCTTAGGAG
ARSIV-1166	432.5	4	1166170	TTATTTACATTTTGT	CGGAATATTATTTCTTCTCTACAGAAAAATGAAAGCAACAGAATTGAATTTCGACAAGTCACAAACAAACTTTGTAGACTTTTTATTACAAAAATTTATT
ARSIV-1241	433	4	1240919	TGATTTATATTTAGT	CCAAATATTACAGAAAAAAAAAAAAAAGATGCCTAAGCCTTGGGTCTTATTTCGAACAAATCCATCCATCGGTAACAATTCAAAAAAAGAATATTTCGTC
ARSIV-1276	434	4	1276267	TTTTTCTCATTTTTT	TATGTTTCCCCCCCAAAGTTCTGATTTTATAATATTTTATTTCACACAATTCCATTTAACAGAGGGGGAATAGATTCTTTAGCTTAGAAAATTAGTGATC
ARSIV-1303	435	4	1302755	AAATATATATTTAGT	TAATGAAAATGGAATTAACGAAAGAGAAGTAAAAAAAATGAACATAAACCACATATAAAATAACAACTGATACACACTATCTTAGTTTATTATTTTAAAA
ARSIV-1404	440	4	1404322	CTTTTTATATTTTGG	AATGTTTTTGTGCTAAAAAAATCATTATTCTGGGCGACATACAGTAAAATAATATTTAATATGAAACAAAGCGTATCATTTTGTAGACACCGATATCACG
ARSIV-1462	443	4	1461899	TTGTTCATAATTTGT	AGCCAAGTTGTAGTGATAAATAATAATTTAGGCAGATATTCTTATATGCTTGAGTGGAACTTCTAGCATATTCAGTATACTTGATATTAAAGCCTTTAAC
ARSIV-1487	446	4	1487091	CTTTTTAAATTTAGT	TTTTTTACTAGCTAATTCATTTACTAAACAACAAAAGAAAATAGCACAAAATGGAAAGCAAAGAAATATCAATTAGGTCAAGAACCCCTCCATCGAAGCT
ARSV-59	507	5	59469	ATATTTACATTTTGA	TACTGTCCATCAGATTTTAGTCACTAACATCTAAGTTAAGGAAGTAAGAGATTCAGACTCCGGTAAGGAAAAAAAAAAAAAAGAAAAAAAAAAAACAAAC
ARSV-94	508	5	94056	AAGTTTATATTTTGT	TGCTAGCGTTACGGTTATGTTTTTACGATACATATCGCCTAAGCAGGTCTCTGCGCCTAAAAAAAGTAAACATATAAATTGGGAAAGCAATATAATTAAA
ARSV-146	510	5	145713	AGTTTTTTGTTTAGT	TTTTTAATCTGGATATTCAGCAGCTATTTCGGCAGTGCACACCCGCAAGAAAAATATACATAATGCTACAATACTCCTAAAATATTATATAAAGTATGAA
ARSV-174	511	5	173807	AATTTTATATTTTGC	CTTGAAATTTAATCATGAAATTATATCTGTAAAGGAAAATTAGGGAATGAAATACAAACAATACGAACATAATCCGTAAAAGTATAAATAATCCAAATAC
ARSV-212	512	5	212455	AAAATTATGTTTAGG	TAATGAAAAAATAGTAAAAAAATGCTTCCTTAAGTTAATTATGAATTTCCCTATTAACACACATGCGTACACAAAAAAAGTATACGGAAACTATATTAGA
ARSV-288	514	5	287565	TTATTTATGTTTTGT	TCCCAGCGGGCATCTTTCAATAAAATGAACTCAAGAAGAAGTAAATAATAACAAGCTATAATGGGTGGCCATTTGTGATCAAATTTGGAGTGAAACACGT
ARSV-354	516	5	353582	ATATTTACTTTTTGG	TGCGGAAATCTGTAATATTTTAAAACAAAATCTCATCCTTTTGAAAAGAAACGATGAAGAAAAAAAATAATAACATACATTGTACCTTCACTAACACTTG
ARSV-407	517	5	406902	TTTTTTATATATAGT	CCCGCTCTCAAGTGAATTAGAAAAGTAAAGTATACACGCAAAACAAGGGCGTAAATAAAAGAAAACGAAAAAGCAACTAAATAAAAGCTTACATCCAAGT
ARSV-439	518	5	439101	TTTTTTAAGTTTTGC	GCCTTTAGCTCATGTTTAGTTTCTGGTGGGGGAAGCGGTAATTATTTTAAAGTAGCCAACATAAGCAAAATATATGGAGAAAAAGAAGAATACCGTCGGA
ARSV-550	522	5	549585	TTATTAATATCTTGT	TATGATTCTTTGTTTTAGCAGCTCCAAAAGAAAGGAATATTATAATATAATTGTTGTAATTCGGAAAAAAAATATTAAATTACTATGGTGCATATGCGTA
ARSVI-168	606	6	167731	ATATTTATATTTTCG	TTTGCAATTTCGCAATTTTAATATGTCACAAAAAAAGCGCCCACAGAATTATCAAGAAGACCAACCAAATCAATAATAAAATTCGGCAAATAACATTATT
ARSVI-199	607	6	199401	TTGTTTATATTTAGT	TACGTTGGGATCAAGTTTTAAAAAACTAGATCTGGAGTGACCAAAAAAAAAATACCCAGCGTAAGGTAAATATTATGGATATGCTTTGGAAGAAAAGAAT
ARSVI-216	608	6	216469	TTTTTTACTTTTAGT	TTTCTTCTATGCGCAAGCTTTTCTATTGGCTGCCAAATAGAAAATTATTGAAATATGATTACATTACAATATTTATTTGTCTTATGAAAACTAACCATCA
ARSVI-256	609	6	256374	TTTTTTATGTTTTTT	CCGGAATTGGCTAAATTCACAAAAAAAAAGAGCATAAAGCGAATTGAATTGTCTCGCCAAGAAAACGCACTGAGAGGACGATTGATCCTCCAGACAAGAT
ARSVII-64	702	7	64457	TTTTTAATATTTTGT	TTCTCGTTTTGCCTTATTTAATTTTGTGACATGTAAAAATTACGAAGCCTATTGGGGGCCAATTGAAGTAAACTAAATATAACAATAGTCCTTTGTAGTT
ARSVII-112	704	7	112127	TTTTATACGTTTATG	TCTATTTCAATGCAATTACGTGAAAAATAAAAGAACGCTACCATAAAAATGTTAAAAACTGGTTAAAAATGTCAAAAAATGGTCCGAAAACTGAAAAAAT
ARSVII-163	707	7	163240	CATTTTATAATTTGT	TGTTACAAACAGTATTTTACAAGTCATAATAAACGTTCAAAAACAAACACAATATTAAAAGAATTGGTATTAGGATCCGACATGACAATTAACTTAGATC
ARSVII-204	710	7	203975	TTTTTTATATTTATT	AAAAGAATAAAAGTAAAGTGCAGAAAGAAAACAACATCATAAAATATGAAAGAAAAAAAAAGGCAATGTTAGTGTTATGAAGGGAGAAACAATTACCGTA
ARSVII-286	714	7	286007	TTATTTACTTTTAGT	CCGTATACTTTTATTTTGTTTTGTTAGACAATCTCGAAGAACAAAAAAAAAAGATAAAACAGAAAGATAAATGTGCACTCTTTTGTACCTCGTTCTGCTA
ARSVII-353	716	7	352864	TTAATTACGTTTAGT	TTTCCTACTGAAACTTTTTTTTTAAAAGACCCTGAGAATTTCATCTCGAGAATAATGAAGACCAATATATAAGTAATGAATCATAAAAGTACAAGAGCAG
ARSVII-389	717	7	388847	TTATTTAACTTTTGT	TCCTAATTATGTATTAGTATTTACTGGTCGTCAAAAAATAGGAAAGGTAAATAAATAAGATTCGGGTATATTATACATTATAAATGAGAACTAACCGGTT
ARSVII-421	718	7	421284	AAATTATTGTTTAGT	TTTGATTAGCTTTACTTTAATTCGCACAAAAAAAAGCCTGCATTGTCACGAGAACATTGAAACATATACAAAAAACAAATTTGAAATAGAAAACAAAGCA
ARSVII-485	719	7	485113	TTATTTATGTTTTGC	CGTAAGATCGATACTTTTCTTATTCTCATCAAGAAAACACAAACTGCCAAGAACTAAGAAAAGAAGAGCCGTAAACAATGCTTGTAAACCGAAGTATGAA
ARSVII-509	720	7	508909	ATTTTAATGTTTGGT	TGTGAATTGAAAGAATACCATTCGGGCACGCAATAGTTATGAACTTAACCGAGCTCAAATAATTTAAAGATAAAAGATAAAAGATAAAAGATAAAAGACA
ARSVII-569	721	7	568661	GTATTTATATTTAGC	CCCTCCTCAGTCTTTTGTTTCCAAAAAACGTGAAGCAGAAGCTCTTGTTGTGACTATTCGAAAAGTATCGCTATAGTAATCACCAGAAACTACAAAGTTC
ARSVII-575	722	7	574702	GTATTTATGTTTTGT	CATTCTTTTCTACATAATCTTGAAACTAGGTAGATCTACAATTGAAAAGTAAATACTAACATTATTTACTAAATTTAAGTTAGAAATCGGCACGAAAAAA
ARSVII-660	727	7	660002	TATTTTATGTTTACT	TATGTTAACCTGCATTATTTCCATAAATAACAAAAGGCAAAAAAGTAACAAATGAAGTTATTAGGAAACAATAAAAAAACAATATCGAGAAAAAAACGAC
ARSVII-715	728	7	715315	TTGTTTATATTTTGT	TTCTATAATAATGTATTGAAGATATAAACAAACATAATTTTACTGTTAACATTTAGGCGCAACAAAAGGACGATCTTTTTTTATTTATCACAAGTTAAAG
ARSVII-778	729	7	778015	TTTTTTACCTTTTGT	TCCGTTATTGATTTTTCGCAGCAAGGTTGAAGCTTCAAATTTGAAAATGAAATTAAGACGTAGAGATGAAAAACAGCGATGAAATTACTTTTTATAGCTT
ARSVII-835	731	7	834667	TGTATATAGTTTAGT	TACCATTTCCGTACTTTGGATGTAAATTAAAATTAAAGAGAGACATTATTTTTAGTTGCGAATACATAACAGCGAATGTTCATGGGGAAAAGTTAAAAAC
ARSVII-888	731.5	7	888415	ATTTTAATATTTTGT	TCTTTAGTTTTAAAAATTCAGAAGAGAAAAAAATTTTATTTGTCACAAGGAAATAAAACATAAACAAAAAAGAAAAATTAAGATTTGCAATTCTGCCGCT
ARSVII-978	733	7	977906	TTTTTTAATTTTTTT	ATATTTTTCCATCTTTTGATGTAATATAGAGGTTATATAATGAAAGAATATATAAGAGGTCATAAAAAATCATTAAAAAAATGCGAGTTCAGGAACATAT
ARSVII-999	734	7	999470	TTTTTTACTTTTTGG	GCTACATTATTCTTGAAAAAAGTTCATGTTTTGTTATTTCTTTCTCACATACTTTATAAAAAAAGATAATTTTTTTAAAAAAAAAAAAAAATACAAGTGG
ARSVIII-8	802	8	7754	ATTTTTATATTTAGG	TGATTTTAGTGGTTATTTTTCTATAACAAATATTGAAAATAAGTGTTTTTGAATTTAGTGGTTATTGTATGGTGTAAAGTGATAAAACATATGCGAAAAG
ARSVIII-64	805	8	64300	AATTTTAATTTTAGT	TATTGATTTCAATGAAACAAAAGGAAACTGACGGCTTCTTAAAATAAATATATTTAACATGAAACATTAAAAAAAAATTGTCACTACACAGAGAGAAAAT
ARSVIII-134	807	8	133530	ATTTTAACATTTAGT	TTGTGATTTCCGGTAAAAGGGTAGTGTTGTTTTTTTGAGAGCCTTTTCTGACGGACAAATGGTCGCAGGAAATATAAATTTATATTTAGTAATACGCAAT
ARSVIII-169	809	8	168596	ATTTAGACATTTAGT	TTAGTATTCTAGGTGCTTAAATAATGAATATTGTCTATAGATGACTAATCATAAATGAACGAAAAGAAAGAATTCAAGAGGCGATAACAAACTTCCGCGG
ARSVIII-246	813	8	245789	TATTTTATGATTAGT	TGCAAAACTTGAAAAAAACAATAGAATTTCATCACATAATTGAAAGATAATGAACTCTTTCAGTCAGTTAGATCCATGTTTTTTGAAGAAAAGTTTACGA
ARSVIII-392	818	8	392253	CTTTTCATGTTTTGT	TGTAGAGAGCCCATTTAAAACAAAGATGTTTACCAGAAAACAAAAGAAAAGATCAAATAAGTGAGTAAATGAAATGCTGTACCTTCCAATTTCTCGAACT
ARSVIII-448	820	8	447792	ATGTTTATGTTTTGT	GAGTAAAGTCAAGAATTTGTCTTCTTGTTAAAACTACAAAAAATAATGTATGCAAAATAGTATAGCAAGATCATTTTAATAATTCAATGTTATAAACGTT
ARSVIII-502	822	8	501945	GTTTATACATTTTGT	TTCTTTTTACCAATATTCAACTTCTGAACACATAGATTTTAATTAAGATACAATTTGGCGAACTTAATTTGCAAACGATTTTACATGTAAGAAATTGTTG
ARSVIII-556	824	8	556137	ATTTTTACGTTTAGG	TGATTTTGGTGGTGATTTTTCTATAATATTGAAATAAGTGTATATAAATTGAGTGGTTAGTATATGGTGAAAAAGTGGTATAACGTATGTATTAAGAGCA
ARSIX-106	909	9	105966	TTATTCATGTTTTCT	TTTAATTATCGAGCTTTTGAAGGTGAGGTAGTTTAGGAAGTGAGGCTGATAAGTAAAAATTGGATTTTAGGGAAAACTAGATCCAGGATTGGTACTATTT

Systematic name	proARS	Chr	Position / bp	proACS	100 nucleotides after 15bp proACS
ARSIX-136	911	9	136287	CAGTTTATGTTTTGT	TTACTTGGACAGCCAAAAAGAGAAAAAGAAGGTGAAAATTTTTTATGTGATCTCTTCAAAGAAATTTTAGATACTTTAAATGATGCCGTACGTCTTTGTT
ARSIX-175	912	9	175170	TGTTTTATGTTTTGT	CTGGAAAAACATATAGTACGGATATTTTTGAAAAACTTTGAAATAATATGTAAATTATGTAAAAAAATTAAAGAACCATTATAAAAGAATATTACCAAAA
ARSIX-215	913	9	214732	TAATTTATGTTTTGT	AAAGAATAAAATGAGTATGATGAAGGAATCTTACCTCTATTAACTATTTCTTCTTTTTTTTTCCTTCGATAAGATGTGCGCGAATTCAATATGGAAGAAA
ARSIX-246	913.5	9	245879	TTTTTAATGTTTTGT	CCTTATAACGCGACTTATTCAAAAGAAAAAAAGAAGTCCCATGCAAAAATCTTGTCATTATTGCGAATGGATATATCAGTGAGACCTTTTTAAGGTTGTA
ARSIX-248	914	9	247751	TTTTTAATGTTTTGT	CGTCACAACGCGACCTTAAATAAAAGAATTCCACGCTAGATTCATGCTACTATCACGAACAATACGTACCAATTAAGCTTTCTTGGTGTAATAAAAAAAG
ARSIX-342	919	9	342028	TTTTTAATGTTTAGC	TTTCAAAAAAGCTAAAATAAACCATAAGCGTTATTCTTATTATATTGATAGTAGAAGAGGAAGAGTGGTTATCTTTACTCAAATTAACGATTGCTTTTAT
ARSIX-357	920	9	357222	ATTTTTATATTTTGT	TGCTTCAAAAACAGTGCCGTATCCTTAATGAATGAAAAATTCTAAAGAAAATAAGTTGATACTAAAAATATAATGTCCTTGAAGTATTTATGCGATATAT
ARSIX-412	922	9	412000	ATTTTAATGTTTTGT	CGTGAAGAAGAAGAAGTAAATAAAGTAGCGTGGGGATAGCGAAATGAAAACATTCAATTATCAAAACAAAAACTTTTAACTACATTTATACCTTTACTTT
ARSX-8	1002	10	7731	ATTTTTATGTTTAGG	TGATTTTGGTGGTGATTTTTATGTAATATTGGCATAAGTGTATATAAATTAAGTGGTTAGTATATGGTGAAAAAGTGGTATAACGTATGTATTAAGGGCA
ARSX-68	1005	10	67713	TTTTTTATTTTTTTT	TTGGAATGTCGCGCCCAGGACAAAAACATATAATTTATTAGCCTAGGCAGTAAATAGTAGGCGAAAAAGATTGAAAAGTATTATACATGTGGAAATTTAT
ARSX-100	1006	10	99505	TTTTTAATTTTTTTT	TTTTAATTTTTTTTTTTCATAGACTTTTATTTAAATAAATCACGTCTATATATGTATCAGTATATAACGTAAAAAAAAAAACACCGTCAGTTAAACAAA
ARSX-299	1010	10	298616	TTATTTACCTCTTTT	CCCAGCAAGCGGGCAACTTCTTTAAGAAAAGTAATCTTTTTTGTACGTCGAATTATCAAAGCTTGGTTACTATATTTAACATTATTGTTTAGTAACAGTA
ARSX-337	1011	10	337048	TTTTTTATGTTTAGC	TAAGTAAAAGCAGCTTGGAGTAAAAAAAAAAAATGAGTAAATTTCTCGATGGATTAGTTTCTCACAGGTAACATAACAAAAACCAAGAAAAGCCCGCTTCT
ARSX-375	1012	10	374639	TTATTTATAGTTTCT	ATCTTTCAGCTTTCAAAAAATAATATATATGGCGCTTCATGAAAAGAGAGCTAGCTACAGAAATATAAACAGTCATGGATGAATAGGCGGCGGCAGCTAT
ARSX-376	1013	10	375580	TTTTTTTTGCTTTTT	TAAAGACTATAAAAGTGTAAACTGTCAGTAAAAAAAATAGACACCACAAAACAATAAGTGAAGATAAAAGAGCCTAGTGAAGTAAACTAATTCAAATGAG
ARSX-417	1014	10	417089	TTTTTTATATTTAGT	TTACTTTCCAGTCAATTCTTTCCGCCCTTTGCATCTATAAATTTAAATAGAAGGATAAAAAAGTGGTTATGAATAGGTAAATAATACTAGAGTAGGACGA
ARSX-540	1018	10	540302	ATTTTTACATTTAGT	AATATCTAATAACATATACACAAAAAAGGGACAGATTTTTGAATTAAATAAACCAAGCGTAAATCAGTATTGCTCTTACCGCAGTAGGGGGAGTTATCTA
ARSX-613	1019	10	612772	TTTTTTATCTTTAGT	TGCCTAAATACTATTTATTTCGTCAATTTTACAACCTCTTTTATATACACCATTCGATTTCCCACGAAGTAAAATAATAATTCTATAAACAGATTTATCT
ARSX-654	1020	10	654244	TTATTTACATTTTGG	TCATTTGAAAATACTTTACTTAAAAAGACGAGGAAGAAACTGTAAATCCATAGTTCGAGAGTTGAAGTGCCCTTCAAAACAAAAACTCCTGACTTTTTTT
ARSX-684	1021	10	683706	TTGTTTAACATTAGT	TTCAAATTAACAGCTTTTGTGAGAAAATATATTTTGGATGAATAGCAGAAAATAGAAATCTGGAAATAAACAAAACAGAGCCAAAATTCTAAGCTTAATA
ARSX-712	1022	10	711661	TTTTTAATGTTTTCT	TAGAAAAATTAAAAAACTTCTCAATTAAATGTAAAATTTTACTTGTTGGCGATACCTTAGAGGATTCAAATTTAACTAGTGTTAATATACGAACTGGTAA
ARSX-730	1023	10	729813	TTTTTTACGTTTTCT	CCATATTTCGAATTGTTCCTTCTTCAATCAAAATAATAAAAAAAAAAAAATCACAAAAATGACTATAGTATTTTGAGCCCAACATGACTGCGAAATTGCTA
ARSX-737	1024	10	736905	ATTTTTATTTTTCGG	TGTTATTTTCAAGTATTACTGCTTTTGAATTGGTCTATATATATGGACATGAACCAGTGCCGAAAAGTATTCACTTTTCATTCAGGACCAAAGATAATAG
ARSX-745	1025	10	744632	ATTTTTATGTTTAGG	TGATTTTAGTGGTGATTTTTTTGTAATATTGGCATAAGTGTATATAAATTGAGTGGTTAGTATACGGTGTAAAAGTGGTATAACGTATGTATTAAGAGCA
ARSXI-56	1103	11	55865	TCATTAATGTTTAGT	TCCGAGCGTGACGTTACTAACTGCGAAAAAAGTTCCTTCGACTAGTAAATATCAAAGGCGAAAACATAAGTATATGGGAGAATTATAACAAGTTAAGTGA
ARSXI-98	1104.5	11	98386	TTTTTTATGTTTAGT	GTATATTTGCTAGAAAGAAACAAGATCTTTTTTGGTAGTGTAAATGCTTAAACTTTGTCTCTTTTTCCTTTTTACTTTGGAAAAATGCCGACGCAAGAAC
ARSXI-153	1106	11	153121	ATTTTTACAATTTGT	CACCGAAATAGCAGTTTTTGTTTAATTTTAACGCTATGGGGTAAAAATTTTGGGCCCAATTTCAACTGAAAGAAGAGATATTTTAAATATGATAAGATAA
ARSXI-196	1106.3	11	196213	TTTTTCATTTTTTGT	TTGTATTTTCCCGTTTTGAAAAACTCCCACTTTAATGCAGGACATCGTTCAAAACAAGCTTTAAAGATTTGACAGTAAAATCCTCACTTTACTCAAGACA
ARSXI-213	1106.7	11	213308	TTTTAAATATTTAGT	TATTGAATGATTAAATTAGAAGGATTGATCATAAACAACACAAGAGAAACAAAGAGTATGGGGGATAATTAGTACTTTCATTTCTTTACCTGTGTACGGC
ARSXI-329	1109	11	329499	TTTTTTATGTTTTTT	TACGTTTTGAGATCATAAATATTTGGAAATATAAATAATCACAAATTCATAACAACTCTTTTTTTAGATAAAGTAAAAACACAGTTATGTATGTAAAGTA
ARSXI-389	1112	11	388662	TTGTTTATGTTTATT	TGTAAAATTACATTATTTAATTTCTTGAAAGTAAAAAACTTGAATTTCTGAAATAAATAAAAACTAGAGAAAAATTAACGATGAGGCATGCGACGGAAAT
ARSXI-417	1113	11	416878	AAGTTTAATTTTAGG	TGTCGGGAGAAACATTTTAATCCCTTTTTATGAATATAATTTAAGTACTAAAAAAATCACCATAATTATACAAAGTAACTGCAATTTAAAAGTACGTTTA
ARSXI-448	1114	11	447837	CTTTTTATGTTTTGT	TCTTGATTTTAATACTACATTTAGTTCAGCTCTTTTTCACTTATTTTTGCACATGGAAGATCAAATACATGAAAAGTACACAAAAGAACAAACAAAAGCC
ARSXI-517	1116	11	516680	TTTTTTACTTTTTGT	TATTTTATTTATGTTTTTCTAGGAAATGTAAAAATAAATCTTTTAGTAGACAGCGAGATGAAAACTAATCTGTGTGAGCTTCAATCAATCAATATGATTT
ARSXI-582	1118	11	581532	TTTTTTACATTTAGT	TTCATTATTATGCAAATTAGAGGGTATACAGTTGAGATTTTAACACTTTGAATTAAAAAGTGTTACAGAGGAAACCGACGCAAAAGGCTTGGTGACGCAA
ARSXI-612	1120	11	612045	TTTTTTATGTTTTTG	GCTCCTAGAGGTGAATATTTTCTTTTTCTTTCTTCGCAGCTATATACTAAATATTAGTGATATAAACAGCAAGAACTATAAACCTAAAAGTAGCCAAAGC
ARSXI-642	1123	11	642412	GATTTTATATTTAGT	TGGCGAACTAGCTCATCCTAATTATAATTAAACTTATATATAGCATAAACCGACAATAATGCGTGGGTGGTCCTCCATGCCGAATTTGTGAACTGAATTA
ARSXII-91	1206	12	91466	ATTTTAACGTTTAGT	TCATCTTGCTGTGAATAATCTAAAAGTAAACAATGGACAAAAAAGTCCACTGGACGTCAAATCTTTTTTTATTGTATTTGGGACATATGGCGTTGATAAC
ARSXII-157	1209	12	156700	GATTTTACTTTTTGG	AAGGGCTTTGGACAATTTAAAGAAGATAATTTGAAGTACCCCATCAAATGCTAGAATGAAATATTTAATATACTAAATTAAGGCTGGTATTTAAAAACGT
ARSXII-231	1211	12	231250	TTGTTTATATTTTTG	TTCAAAAAATGAGTTAATAATGATTTTTCATCTTCGGCTTACCGGTCTTGAAAATATTTGTTAAGACAACAGTGGATAAAATAAAACTAAACAACTCAAG
ARSXII-289	1212	12	289421	AAATTAATGTTTTGC	TGCTTTTACTGTCGCGTTTAACAGTTGATTTTCCCAAAAAAAAAAAAAGAAGTTAACAGCATCTATATAAAGAAGGATATAGATAACATGCACATTTTCG
ARSXII-373	1213	12	373328	TTTTTTATATTTTCT	CCGTATTTATGAAAATTCCTCTTCGGTAAAAGCACAGAATTAGACTTGAAATGTAAACAATATAAGACAGACAAACCTTTATCGAAGATAGAAGTGCTGA
ARSXII-413	1215	12	412854	TGTTTTTTGTTTTGT	TGTAGTATTCGAGCATTAAGGATAAAAAAAGCTTGTGAATAAAAATCTTTCGCTAAAAATCAATATAAGAAAATGGTAAGCAGCTGAAAGATAATAAGGT
ARSXII-451	1216	12	450660	TTTTTTATATCTTGC	TTATAAAGCAGAAGGTGATTTATTTAATTTTCGTCTGATACCATCCATTAACTGAAAATTACTGACAAACAGAAATACGTTAGATAGTATGTTAACGAAA
ARSXII-459	1216.5	12	459091	TTGTTTATGTTTTGT	GTGATGATTTTACATTTTTGCATAGTATTAGGTAGTCAGATGAAAGATGAATAGACATAGGAGTAAGAAAACATAGAATAGTTACCGTTATTGGTAGGAG
ARSXII-513	1217	12	513085	TTATTTATGTTTTTG	TCACAAACGCGCACATGTTTGTAGGGAGTAATGTCATTGTCAAACAAAACACATAAGAAAAACATGGTGAGATTATTAAAAAAGTGTATAAGTTTATAAA
ARSXII-603	1218	12	603110	TTTTTAATGTTTATG	TTCAACATACCCGAAACCACTACAAGACGGAAAATACTAGAGAAACATCAACAAATGAAAAAAAAAGGCTACAATCCTCGGATGAAACTGATAAAAACGA
ARSXII-660	1220	12	659892	CTTTTTATGTTTATT	TCATGGATTACGAAATTTGCTGGCTTTTTAGAGTGACCGATGAGTTGCATGTACATATGTGCGAAATAAAACAATACGGTAGTAAAACATGAATACTTCG
ARSXII-745	1223	12	745115	ATCTTTATGTTTTGT	TTGCCTTTACTGGCCAGAAATTTTATACTTATTTTGAATAGAACACATTAAGTTCTACAGGTACCTGCAAAATATCGAGACAAAAGTTTGAACGAGAATA
ARSXII-794	1226	12	794207	AAGTTTAAGTTTAGT	TACGGGGTTTAATGTAATGCGAAGGAACCTAAAAGAAAGGCTGAAATAATCAACCAATAAACAAACCATTAAAGAGGTGGAAATAATTATGATCAAAGAA
ARSXII-889	1227.5	12	888741	TTTTTTATGTTTAGA	TGTAAAAATTAATTTTTTTTTCAAATATGCTGCCGTGAAAACGAATTCAAATAGACGATTACACAATATTTTGAATAATTACATGAAGAAACATTAATTA
ARSXII-1007	1232	12	1007235	ATTTTTATATTTTGT	GTTTGCTAAGGTCTAATCGTTCAGCTAAGTTAAAGCTAAGTATAAGAAGCAAAAAATACTAAATTATACTAAATTATAAATTTTCGTACATAAATAATCA
ARSXII-1014	1233	12	1013785	TTTTTTATGTTTTCT	CGTTTCTTTTCTTTTTTTTGTTTTATATCTTACACATTTTTAATATACTAAAGTAAAATAAAAAAATACGTACTGTTTCCCTTTGTTTTCTCCTCCTCT

Systematic name	proARS	Chr	Position / bp	proACS	100 nucleotides after 15bp proACS
ARSXII-1024	1234	12	1024151	TTAATGATGTTTAGT	TCTGAAATAACGATTTTTTAAGCGCTTGGCAATTTCACAAGAAAAAGGTGAAAAAAGAAAAATAAGATTAAACGATGAATGCGATTTTTTGTTTCTGTTA
ARSXIII-32	1303	13	31767	TAGTTTATTATTAGT	TGCCAAAACGAAACATTTAACATGTGAATTAAAAATACAAAAAAAAGCCTATTAACGATCTAAATTTATGACAAAAGACATATAATTATTTTAATGATGC
ARSXIII-94	1305	13	94390	TTAATTATATTTAGA	TATATATTCGTATTTTATTAATAATTAGGAGGAATAAAGTCCGACATTTTTTTCAAAAAAAAAAAAAATAATATTTCACAACGAAAAATCTATAAATAAAA
ARSXIII-137	1307	13	137321	ATATTTATGTTTTGT	TAATCTCCTCTACCCTTTCAATGCTTGAAAAATACTTTCAACTTTTCGATTGGGTGATGAAAAAAAGACAAATAGTGTAAAGGGTTCAAAAATAAATAAC
ARSXIII-184	1308	13	184017	TTATATATGGTTAGT	TAACTCTATGTTCCAACAAATACCAATAAAGATCGCGCAAGTGGTTTAGTGGTAAAATCCAACGTTGCCATCGTTGGGCCCCCGGTTCGATTCCGGGCTT
ARSXIII-263	1309	13	263126	TTTTTTATATTTTGT	GATAAAGGGATAACTCGTCTTGCCTTCACTGCGCTTCGATTCTACTTTAGCTAAACTAAGCGTTACTTTGTTTGAGAATCTCTCAGCCGTTAAATCAACG
ARSXIII-287	1310	13	286845	TTTTTCTTATTTAGT	TTTTGTAGGCGGCATAGTATTACTTGCAGATTTTTTTAAAGTCCCTGAGCCCCAAAGTTCCAAAGCAACAAAAAAACATAAATCCTTTGCAGGAAAAGTA
ARSXIII-371	1312	13	371020	ATTTTATTGTTTAGT	TCATGATAAAAAACTTCAAATCACTTTTAATCTGGTAGACAGAGAAAACAAATCGAAACGAAAATAGAGAACTACGAATAAAAAAATATAAGTGGAGAAG
ARSXIII-468	1316	13	468236	TTTTTTATTTTTTGT	TCCTAATTTTTTTTTTTTTACATTTTATTAGCTATACACTTGGCGCAAGGATATTTTATATACCGGATATAATAGATAATTAAAAGACTACTAATTAAA
ARSXIII-536	1320	13	535769	TAATTTATATTTAGT	TTAGGATATAGATTATCCTAGGCTTTAATATTTTAATGGAAAAAAACTACAATAAGATTGAAACAAAGAACTTGGATAAAAAAACAAAACAACTCTGTAG
ARSXIII-611	1323	13	611318	TTGTTTATGTTTATG	TTCTTTATACTCAAAATCAATAAGTGCTTATTTTAGCGAATTTTCTTCTACGAATATATATAAGTCATATCTAAGACTTCCATCCGTGCTTTATTACGTT
ARSXIII-635	1324	13	634522	ATTTTTACTATTTGT	AATAATGATTCTGCTTTACGCGCCTTTAAAAAAGTTGGTCTTAATGTAAACATGAACCATAGCACACAATTTAAGACATCAGCTGTCAAATGACCATAAA
ARSXIII-649	1325	13	649361	TATTTCATATTTTGT	TGACATTTGAGAGCTTCAATTGTATAAAGTTGCAAGATAATATATGAGGTTAGGGAAGCCGGATAAAGAAAATAGAGTACTTTAAAACTGTTCATGGACT
ARSXIII-758	1327	13	758417	AATTTTATGTTTTTT	TCTTCGTTTTGCGAAAATTCGCATGAGTGTCTCTGTATATATATATAACAAAAAGATGAAAAAAGGGAAGGTAGAAAAAACCGCGCTAAGTTTTGGCAGT
ARSXIII-773	1328	13	772677	TTTTTTACTATTACT	TTCTTTTTCAAGCTTTTAAGCGCCGAAATGATATTTAAGGGAAGATGACTAAAGGGACAGCGACGAGGATTCAGCCTGGACAGTGATAGAAAAGTTATGC
ARSXIII-805	1329	13	805162	ATTTTTGTATTTAGT	CTTTGTTTTCGAACTTTTATTAATATTAAATTTCAGTAAGTAAATTAAAAGAACATCTTTAAAAGAGTATATTTATTGTTACATATGTTGATCTTAAAAG
ARSXIII-815	1330	13	815391	AATTCTATGTTTTGT	TCCTGAAATCTCGATATTTTAGTAACTTAAAATAAAGGTAATAAAATCATCAAAGGTTTTCCATCCAGTGGTCCAAAAAAAAAAAAATACAGAAGCAACA
ARSXIII-898	1332	13	897977	TTTTTTATGTTTGGT	TCTTGTTATTGAACAAAAAAATGAATTAACCCGAACACTACCAAATCAATAGCAGAAGAAAAGAAGAAAATGATAAAATAAAGGTGAGAACCATTTTAAA
ARSXIV-29	1405	14	28653	TTTTTTATTTTTAGG	TGCTAAAGGCTATTTCAACTTAAATTTAAAATTGAAAATTTCCTTGTTTCATTGAATGTATAAGAAACTTTATATTCTTCAGCGTTATTAAGCGCATCTT
ARSXIV-62	1406	14	61694	TTTTTAATGTTTTGT	AGAGGAAAACTTAAAAGTTGTCATTTTTATTCAGATCGCAATCCATGGTTTGACACATTCTATCTTAAAAAAACAAAATCTATTTATTTTGGTTTCGGCT
ARSXIV-90	1407	14	89754	ATTTTTAAGTTTTGT	TTGTTTTTTTTATTGTTTTGCTTCGTAGTTTCAATTTTAAACATTAATGTGTGCAAAAACTATAAGACAATGGTATACGCAAGAAAAACTATAAGTAGCA
ARSXIV-170	1411	14	169747	AATTTAACGTTTTGT	TTCTTCCGTCATCATATCCAGTGGGAAAGGTGTATTTCTAGAAAATAATGTTAACCTTCAAGGTTATGCTTTGCGATATTTGACACTTTCCAAAGAAACA
ARSXIV-196	1412	14	196224	TTTTTAACTTTTAGC	CGCGGTCAGTGACATTTTGGCTTTCCCACCATTCCACGTCTGAAAAAAAAAAAAAAAAAAGAGATAAAATATGAATTGAATATATATCAAAAATGTCTGC
ARSXIV-250	1413	14	250464	ATTTTTACGGTTTTT	TGAAAAGAACCCGTTATGAAATTAAGAAAAACAGTAATTCAAAAATGTGAAGAAATTAGGAAACAAAATATCTTAAAAAGATTGAACGAACACTCTGTTA
ARSXIV-280	1414	14	280062	TTATTTATGTTTTTC	TCTCAGAAGCCATTTTTTTTTGGTTTTATGGTAAAGGCACCCTTTAAAAATAATACTAAATGTTTCTTTGAAAAATACCATACTTACAACTAATTAATTA
ARSXIV-322	1415	14	322000	TTGTTTACGTTTAGG	CGAAATACTCACCTCTTTACTATTAAAATAATAGAATTTATCAGAAAAAAAGTCAGCAACATCAAAAATAACAGATGGATGGCTCTAGGATAAAGGATTC
ARSXIV-412	1417	14	412438	TTTTTTATATTTCTG	CCCAAAAAACGTAGTTCAAAGAAAAGGAACTATCCCAAAATAGAAGCAAGTTATGTTTAAGGAATTAAAAAATGTACCTATAAAGCACGTTTTTCTGATA
ARSXIV-450	1419	14	449533	ATATTTACATTTAGC	CCTTCTATAACCGTTTTTTTAATTTCCCGATCTGATGAAAAGGATGCAACATCACTCTAAAACGTTGAAAATGGCTCCAATTCATAAGGTCACTTTAGTG
ARSXIV-499	1420	14	499038	TTCTTTATGTTTAGC	TCTTTTTTCATCACTTCTAATTCGCAAATAGAAGGGGAAGGAGGACAGCAATTATGTAAAAATTAATTAGTATGTCAGTAACAAAAAGAAGAGATAACAG
ARSXIV-546	1421	14	546145	ATTTTTACGTTTTGG	CACGTGAATCTTCAGTAATTGATTGCACGCTTGATAAACGAAAAAAACATAAACAAATAAGGTAAGACTGCATTGTAAATCCTAGGAATGAGAAAGAACA
ARSXIV-561	1422	14	561326	TTGTTCACATTTAGT	TTTTGAAAAGAAGTAATCAAAAAAAAATAAAAAACAAATAAACACATATGCAAATATGTTCTATCAAAGAGGTATATGAAACTGTTTGAATGTAAATCAA
ARSXIV-610	1424	14	609532	TTTTTTATGTTTATT	TTCTATTACTGATTTTCACAAAGAAAGGTAAAAAAAAACATACTTCAGCGGCTATACAACCATATTTAAGTAAATGCACTCAGAGAAAGTATACAAGTAA
ARSXIV-636	1426	14	635830	TTTTTTAATTTTAGT	TAAGTTTTCTTCTAATTTTGAATATAAAAAGTCATCTTATAACTAGTACATTTTATATGAAGGAGTTTCTATAGGTTTTAAAGGTGTGCAAAAAAAAAAA
ARSXIV-692	1427	14	691677	TAATTAACATTTTGT	TTCAATCTCTCACTTCGCTTAAGACCAAATAATCTCCTTGAAAGAAAAGAAAACTTAAAAGCATGCTTTTCTCTTAGCGGAAGCCATAGGTCCAAAAGGG
ARSXV-36	1506.5	15	35713	ATATTTATATTTAGA	GGCCTATATTGCGCATCGAACTTTTCAAAATCCGCGGAAAATTATAGAATTCATCATATATAATGAAGGAACTGTGTTCCTGAAAAGAACAAAAAAAGGA
ARSXV-73	1507	15	72688	TTTTTTACTTTTAGT	TTATTTTTTTAGACTTTAATGTCGTTCTCCCTTTTTAAAGAGTAAATACATATTTAAAAAAGTGACTATGGCTATTGCTAAACGTGATAAAAATCAGAGC
ARSXV-85	1508	15	85365	ATATTTATGTTTATG	TTCCATCATGTAGAAAAGTTTCATTTAAAATTAATAGCCCGTCAAAAATACAAGTGAAAAAAAATAAAAATTAAAAGCTCTCTATTTCTTATAAACTAAC
ARSXV-114	1509	15	113894	TTGTTTATATTTTTG	TACCACAAACATCATTAGAAGCTGCAAATGAAGTGAATCAGAAAATTTAAAAATGAAACTAAATACTAAATATTATTGTTCTTTTTCTAACAGTTGAAGT
ARSXV-167	1510	15	167002	TTATTTATGTTTTCG	TTATATTTTCAACATTTCCGGAAAATAAAAAAGCGACTTTTTGAGGATATTATCCTATCATCTGTTGAGAAACCTAAGACAGTTAGTTTCTATGATAATA
ARSXV-278	1511	15	277732	TTGTTTATCTTTTGT	TATTAAAGCTCTACTTTTGAAATCCAAATCGTGTTTCCTTATGCTAAGGTGGAAAAAAATAATAATAAATAAAATGGCCAACAATAAACAATAGCCTCTC
ARSXV-337	1513	15	337483	CTTTTTACCTTTTGT	CACCATATTAAATCTTTAAACAAATCTAACTATGAAAAAATCCTTTAAACATATGTTAATATGTGGAAAATAAATACTAAAATAAAAATCTAGAACTGAA
ARSXV-437	1513.5	15	436792	ATATTTATTTTTATT	CACTTCTGAGAAATACAAGTTGCATGTCTCAAAACTTTTACTTTTCAACAAAATATTAATCAAAAAAAATAAATGAAAAAAGAAGACCATATTGAAGAAC
ARSXV-490	1514	15	490061	TTGTTTTTCTTTTCT	TCTTATAATTTGTAAATTTTTTAACTGCATTAGATCATTATATTATCTTTCAAAACGCCAGTCGTTTTTATTAGACCTTTATATACGTTTCAAAGTGGTT
ARSXV-567	1516	15	566597	AATTTTACCTTTTGA	TGCGGAATTGACTTTTTCTTGAATAATACATAACTTTTCTTAAAAGAATCAAAGACAGATAAAATTTAAGAGATATTAAATATTAGTGAGAAGCCGAGAA
ARSXV-657	1519	15	656702	TATTTAATGATTAGT	AAGACAAAAATGACATTTAAGCATCTATAAAATAAGAAAAATAAAAAAATGAAGGGAAAAAGCTAAACACTAACTTCTTGACCAAACAAACAAGGAAAAG
ARSXV-730	1521	15	729795	ATTTTTATATTTTGG	CCGGTTTATGGATAGAAAACACGTCAAACGTTCGATGGATCTTATAAAAAGTAATGATGTAAAGCAAGGTACAAAAATGAAAGAAGTACGGTTTACTGTT
ARSXV-767	1523	15	766690	TATTTTACGTTTTTT	CATAATCATATACTTTCTGCCGAAATTTTTTGCCTTCATTATGCACACTAATGTTATTAATCAGATAAAAATACAGAAATTTAAAATAAATACTGAGAAT
ARSXV-783	1524	15	783387	ATTTTTAACTTTTGG	TTTTGAAGCTCGTAATTCAACAAAAAAGAATTAAATAATCTTCAAGTCCGATAACAAGATGTAGAAAAAACATCCCAATGAAGTTACAAGTCAAACCATT
ARSXV-874	1526	15	874367	ATTTTAATATTTGTT	AGGATTCGCCTTTATTTCACAATCAAAAGGAAACACATAAAAAAAGTGTCATGCTCTACGTGAATAAAGAATTAGTGAAATAATAATAAGGCAATCAGAA
ARSXV-908	1528	15	908307	TTGTTTATGTTTAGG	TTAACGATAGACATATTTATTTTTTTTTCTAGGAATAAAAATGAAGAACGGGAAGAAAAGGAAAAATGAAAATGAAGAATATGAAGAGTAAACCTACTTA
ARSXV-982	1529	15	981505	TTATTTATATTTTTC	TTCAGTGAAGCGATTTTTTTTTTACACAGACCAAGACGGAAAAAAGTAGCTAAGGAAGAAAACAAAATCATGAAAAAAATGTGAAGTGATCATGCACATC
ARSXV-1054	1529.5	15	1053692	TTGTTTAAATTTTGT	TCGGTCTCGGCTATATTTGGAAGAAAAATAGCCAGTACATACTTTCTACCACTTTCGCTCAATTATCAATAAAAACATTTAATCGAAAGTCATTCAAACT
ARSXVI-43	1604	16	43150	TTGTTTATATTTTTG	AATTTAAACTGTTTTATAGAAATGTATGTAATATATAAATTTTATTTTCCTTGAAAAAATGGGTATTTTTCTTTCTATTTTTTCAAGAAAATCTTCCTGT

Systematic name	proARS	Chr	Position / bp	proACS	100 nucleotides after 15bp proACS
ARSXVI-73	1605	16	73105	TTTTTTTTGTTTTTT	CAGTTCTTTGTTTACCTATTTTTTCTTTGCCGCAATTGCAAATATTATTAACTTAATTGCGATTATTGAGACTAAACAATAAAGACCTGGCAGTGGAGGC
ARSXVI-117	1607	16	116593	ATTTTTATGTTTTGT	TCCATACTAAATGCAGTTTATAAAATTTTTCAAATGAGTCAAGCTATGTATAATCAGTGCTACAAAAATGATAAGATGCAATTGCAAGAAAAAATCCCTT
ARSXVI-290	1614	16	289531	TAATTAATGTTTACT	TCAGACAATAAAACATTAAAAACAAATTTTTAGAAAAACAAAAGCTGAAGTAAAGACTAAATATTACACAATTTATTCATACATTTCCGCCCCAAACTCA
ARSXVI-385	1618	16	384592	AAATTTATGTTTATG	TGGCGTAAAATATCTTTCTTCTGAAAACACATGCAGCAGTTACTCCCATCATAAAAGGAATTAATAAATGAATAGTATAAACAATTATTTACTTAAATAT
ARSXVI-418	1619	16	418178	TTATTTACAATTAGT	TTTCTCAGAACGATATTCAATACAGTTCTCCGGATTTTTGCTTACTATATTGGCCCCAAAAAAATGAAATAAAAAAAGAAAACAAAATAATATACTTGGG
ARSXVI-457	1620.5	16	456759	TTTATTATTTTTTGT	TCTTATTTTCCGGCTTTCGGAAGATGTAGAGTGGTCCGGTATATTAATGCTTGAACTAGGAAAAACTATGGATGGGGCGGCTCTTCATTCATGACAGTAT
ARSXVI-512	1621	16	511704	ATTTTTATGTTTTTT	GAGATATTTCGAGCTTTCTATTTTTTTAAAATGCCTGAATTTCCATCTTCAAAAAAAACATAAAAAAGGTACTTTACCACCAAATAAATGATAACCACAA
ARSXVI-564	1622	16	563877	TCTTTTATATTTAGT	CCGCTTTACACCGAAAAGGTCATTTTTAAAAAGGCAAGAGAACTAGGAAAAGTAAAACGTGCCCCCTTCAAAGCGAAGAGATGAATATATTTAGAAGTTA
ARSXVI-565	1622.5	16	565115	TTTTTAATTTTTAGT	TAGTAGATTTTCGTTCGAGGCCCTAAAAATGTACCGAAAAGTCATAATAAACGGGCGGAGTCACATCGTAAGAGTAACATATACAATATGCGAGCAGACT
ARSXVI-634	1623	16	633921	TTTTTATAGTTTAGT	TGGTTTTGTTTAATTTCTAGAATCCTGTTCGGCGCTTTTGTTAAAAGTAAAAAATGAAAATTCAAACGAAATGAACCTAATCACGTTAGAATTTAAATCT
ARSXVI-684	1624	16	684405	TTTTTTACTTTTTGT	TTCTTTATTAATTTTTTAGTTTTTTTCATATTCTATTTTATTATAAGTAGTAATATGAAGAAATTTCCCAAGCAAAGCTCAATAAAATTATTTAGCTAAA
ARSXVI-696	1625	16	695618	TTTTTTTAATTTTCT	GACTACTGTTCAGCCATCAAGGTATGTCTAAATTAATAATATTCAGCATTTTCAACGTGCGCTTACCATCTGCTAATACACAGCTCCTCTGAAAGTTTCT
ARSXVI-749	1626	16	749117	ATTTTTAAGTTTAGT	AATCTTTTTCGGGATGAGATGTTTTGAAGAGTTTTATGCTATTAAAGTAGTAATATGATTTATATATTCAAATAAAATGTAAATTATGAAAGAAAAATAC
ARSXVI-777	1626.5	16	777094	TTATTTATATTTTGG	CATTACTCTTCATCATTTTTTTCCCTCTAAGAAGCTTCCTTTCTTTTTATAAGGATAACAAAACCAAAAGGAATATTGGGTCAGATGAATGGACGCGAAT
ARSXVI-819	1627	16	819339	ATTTTTATATTTATT	CATGATATATTAATATTAATATATCGATGGTGAAGGACACCACACCTGTATTTCTTTGATTGAAAACAATTTTGTAACATTGGCTGCAAAAGTTTTTGCA
ARSXVI-843	1628	16	842851	TTATTTAGATTTAGT	TGCGATCAAGTGTAGAAACACATTAAAAACTATGTTGAAAAACATAAAAAGTATTTGCAGATCATTAAACATTAGAATTAACTATTTATCATTAACTATT
ARSXVI-881	1630	16	880906	TATTTTATGTTTAGG	TTAATAACTTTGGTAATGCTAAATTATCTTAATTTGACGTACACAAATTCTTCCTACTGTTATATATGTTCGAATTATCTTTTAAATTGTTGCTAAAAAA
ARSXVI-933	1631	16	933164	TTATTTACGTTTAGC	TTTGCTGTGGTTCTTTTATACTTAATCATATAAGATACATGCATCTAGATTGCCACTATATAGCAGCACATGTTACAGTTAACTATCGATTGTCCAAAAT

Suppl Table 2. Nucleosome positioning datasets

		Author(s)	Journal	Title
Compiled		Jiang & Pugh	Genome Biology 10:R109, 2009	A compiled and systematic reference map of nucleosome positions across the *S. cerevisiae* genome
	1	Mavrich et al. (Pugh)	Genome Research 18:1073-1083, 2008	A barrier nucleosome model for statistical positioning of nucleosomes throughout the yeast genome
	2	Albert et al. (Pugh)	Nature 446:572-576, 2007	Translational and rotational settings of H2A.Z nucleosomes across the *Saccharomyces cerevisiae* genome
	3	Field et al. (Segal)	PLoS Comp Biology 4(11):e1000216, 2008	Distinct modes of regulation by chromatin encoded through nucleosome positioning signals
	4	Shivaswamy et al. (Iyer)	PLoS Biology 6(3): e65, 2008	Dynamic remodeling of individual nucleosomes across a eukaryotic genome in response to transcriptional perturbation
	5	Whitehouse et al. (Tsukiyama)	Nature 450:1031-1036, 2007	Chromatin remodeling at promoters suppresses antisense transcription
	6	Lee et al. (Nislow)	Nature Genetics 39(10):1235-1244, 2007	A high-resolution atlas of nucleosome occupancy in yeast
Individual		Eaton et al. (MacAlpine)	Genes & Dev 24:748-753, 2010	Conserved nucleosome positioning defines replication origins
Individual		Yuan et al. (Rando)	Science 309:626-630, 2005	Genome-scale identification of nucleosome positions in *S. cerevisiae*
Individual		Albert et al. (Pugh)	Nature 446:572-576, 2007	Translational and rotational settings of H2A.Z nucleosomes across the *Saccharomyces cerevisiae* genome
Individual		Lee et al. (Nislow)	Nature Genetics 39(10):1235-1244, 2007	A high-resolution atlas of nucleosome occupancy in yeast