

Supplementary Figure 2. Sequence alignment

		Section 1																	
		(1)	1	10	20	30	40	50											
ATSAT5Satellite	(1)	TTATGTT	CA	T	TGTTTT	CATGCC	AGATCCG	AACTGCTCT	T	CCAACCGT	TT								
chr.2_SAT5	(1)	TTATGTT	CA	T	TGTTTT	CATGCC	AGATCCG	AACTGCTCT	T	CCAACCGT	TT								
chr.3_SAT5	(1)	TTATGTT	CA	A	TGTTTT	CATGCC	CGATCCG	AACTGCTCT	G	CCAACCGT	AT								
Chr.4_SAT5	(1)	-----																	
Chr.5_SAT5	(1)	-----																	
AT2G18042	(1)	-----																	
AT3G42565	(1)	-----																	
AT4G09545	(1)	-----																	
AT5G60978	(1)	-----																	
Consensus	(1)	TTATGTT	CA	T	TGTTTT	CATGCC	CGATCCG	AACTGCTCT	T	CCAACCGT	TT								
		Section 2																	
		(51)	51	60	70	80	90	100											
ATSAT5Satellite	(51)	AAC	CCGCT	A	T	CA	GAAACTC	T	TCTC	C	TCTAAGTTT	AGTGTTA	ACAAGTCA						
chr.2_SAT5	(1)	-----																	
chr.3_SAT5	(51)	AAT	CCGCA	T	TCTA	C	AAACTC	C	TCTC	G	TCTAAGTTT	AGTGTTA	ACAAGTCA						
Chr.4_SAT5	(1)	-----											ACAAATCA						
Chr.5_SAT5	(1)	-----																	
AT2G18042	(1)	-----																	
AT3G42565	(1)	-----																	
AT4G09545	(1)	-----																	
AT5G60978	(1)	-----																	
Consensus	(51)	AATCCGCT	TTTCT	AGAAACT	C	T	TCTC	G	TCTAAGTTT	AGTGTTA	ACAAGTCA								
		Section 3																	
		(101)	101	110	120	130	140	150											
ATSAT5Satellite	(101)	TGGAGAACC	T	CAT	TGTATAG	AAGTTTT	TACAAACCA	AACTTT	AGATTGAT										
chr.2_SAT5	(1)	-----										GAT							
chr.3_SAT5	(101)	TGGAGAACC	C	CAT	TGTATAG	AAGTTTT	TACAAACCA	AACTTT	AGATTGAT										
Chr.4_SAT5	(9)	TGGAGAACC	-	CAT	TGTATA	AAA	A	TTTTACAAACCA	AACTTT	AGATTGAT	CAAT								
Chr.5_SAT5	(1)	-----																	
AT2G18042	(1)	-----																	
AT3G42565	(1)	-----																	
AT4G09545	(1)	-----																	
AT5G60978	(1)	-----																	
Consensus	(101)	TGGAGAACC	T	CAT	TGTATAG	AAGTTTT	TACAAACCA	AACTTT	AGATTGAT										
		Section 4																	
		(151)	151	160	170	180	190	200											
ATSAT5Satellite	(151)	TCAAATAATTT	-	C	A	G	AAGAAAAT	A	T	TATAAAT	C	G	ATTTATT	G	T	T	T	T	A
chr.2_SAT5	(4)	TCAAATAATTT	T	C	T	A	G	A	A	A	T	T	C	G	A	A	A	A	A
chr.3_SAT5	(151)	TCAAATAATTT	T	C	A	G	A	A	A	A	T	T	C	A	A	A	A	A	A
Chr.4_SAT5	(58)	TCAAATAATTT	T	C	T	A	G	A	A	A	T	A	T	A	T	A	T	A	T
Chr.5_SAT5	(1)	-----																	
AT2G18042	(1)	-----																	
AT3G42565	(1)	-----																	
AT4G09545	(1)	-----																	
AT5G60978	(1)	-----																	
Consensus	(151)	TCAAATAATTT	T	C	T	A	G	A	A	A	T	A	T	A	T	A	T	A	T

Supplementary Figure 2. Sequence alignment

		Section 5											
		201	210	220	230	240	250						
ATSAT5Satellite	(201)	TTT	GAGATATA	AACC	-GATGATTGATTAATTATGTGAAGCC	---	ATT						
chr.2_SAT5	(54)	TTT	TGAGATATA	TACT	-GCTAACTGATTAATTATGTGAAGCC	---	GTT						
chr.3_SAT5	(201)	TTT	GAGATATA	TACC	-GATGAATGATTAATTATGTGAAGCC	---	GTT						
Chr.4_SAT5	(108)	TTT	TGAGATATA	AAACTG	CTGATTGATTAATTATGTGAAGT	CATA	C	GTT					
Chr.5_SAT5	(1)	-----											
AT2G18042	(1)	-----											
AT3G42565	(1)	-----											
AT4G09545	(1)	-----											
AT5G60978	(1)	-----											
Consensus	(201)	TTTTGAGATATATACCTGGTGATTGATTAATTATGTGAAGCCATAGGTTT											
		Section 6											
		251	260	270	280	290	300						
ATSAT5Satellite	(245)	TACTTTTATTTTCTCT	-	TTGTAGTCAATATTTCTTAGTTAATGTTAC	GTG								
chr.2_SAT5	(100)	C	ACTTTTATTG	-CTCT	-TTGTAGTCAATATTTT	CAAGTTAATGTTACTTG							
chr.3_SAT5	(246)	A	ACTTTTGATTTTCTCT	-	TTGTAGTCAATATTTT	TTAGTTAATGTTACTTG							
Chr.4_SAT5	(158)	TACTTTTATTTTCTCTCTT	T	TAATCAATATTTCTTAGTTAATGTT	G	C							
Chr.5_SAT5	(1)	-----											
AT2G18042	(1)	-----											
AT3G42565	(1)	-----											
AT4G09545	(1)	-----											
AT5G60978	(1)	-----											
Consensus	(251)	TACTTTTATTTTCTCTCTTGTAGTCAATATTTCTTAGTTAATGTTACTTG											
		Section 7											
		301	310	320	330	340	350						
ATSAT5Satellite	(294)	TTT	CACACA	TGGAGTTTCAACTATATT	-AAATTT	CTAAAACGGCTAATCA							
chr.2_SAT5	(148)	TTT	T	---CT	TGGAGTTTCAACT	CTATTTAT	CTTATAAAAC	AACTA	T	TGA			
chr.3_SAT5	(295)	TTT	CACACA	TGGAGTTTCAACTATATTTAAATTTATAAAACGGCTAATCA									
Chr.4_SAT5	(208)	TTT	TACACT	TGGAGTTTC	GTCT	TTATTT	TG	ATTTATAAAAC	TG	T	TAATCA		
Chr.5_SAT5	(1)	-----											
AT2G18042	(1)	-----											
AT3G42565	(1)	-----											
AT4G09545	(1)	-----											
AT5G60978	(1)	-----											
Consensus	(301)	TTTTTACACTTGGAGTTTCAACTATATTTAAATTTATAAAACGGCTAATCA											
		Section 8											
		351	360	370	380	390	400						
ATSAT5Satellite	(343)	AATACCTAATTAAAG	T	ATTCAAAGATGTTAAATTA	AAA	-AAAATTAATAT	G						
chr.2_SAT5	(195)	AAT	TTCTAATTAAAG	CAT	C	CAAAGATGTTAAAG	TAAAG	-A	T	AATTAAT	G	T	C
chr.3_SAT5	(345)	AATACCTAATTAAAG	T	ATTCAAAGATGTTAAAG	TTAAAG	AAAAT	CTATAT	G					
Chr.4_SAT5	(258)	AATACCTAATTAA	CC	ATTCAAAGATGTTA	--	TTAAA	-A	T	AATTAAT	A	T	C	
Chr.5_SAT5	(1)	-----											
AT2G18042	(1)	-----											
AT3G42565	(1)	-----											
AT4G09545	(1)	-----											
AT5G60978	(1)	-----											
Consensus	(351)	AATACCTAATTAAAGTATTCAAAGATGTTAAATTAAGATAATTAATATG											

Supplementary Figure 2. Sequence alignment

Section 9

	(401)	401	410	420	430	440	450
ATSAT5Satellite	(392)	A	CAGTTTCACATTTCA	A TC --	CATATAAATAAGCAAG	GATT	TTATTGTTA
chr.2_SAT5	(244)	A	TAGTTTCACATTTCA	TTC --	CATATAAATAAATCAA	AAGTCT	TTATTGTTG
chr.3_SAT5	(395)	A	TAGTTTCACATTTCA	A TATTC	CATATAAATAAGCAAG	GATT	TTATTGTTA
Chr.4_SAT5	(305)	A	CAGTTT	TACATTTCA	TTC --	CATATAAATAAGCAAG	GAATCTTTATTGTTG
Chr.5_SAT5	(1)	-----					
AT2G18042	(1)	-----					
AT3G42565	(1)	-----					
AT4G09545	(1)	-----					
AT5G60978	(1)	-----					
Consensus	(401)	ATAGTTTCACATTTCA TTCATTCATATAAATAAGCAAGGATTTTATTGTTG					

Section 10

	(451)	451	460	470	480	490	500
ATSAT5Satellite	(440)	TTCATCAATCAAAAACAAACAAAGCATTAAAGCATATA	GTTG	-	CTATACTA		
chr.2_SAT5	(292)	TTCATCAATCAAAA	GCAAA	TATAAC	CTT	CAGCATATA	T TTGGCTATACTA
chr.3_SAT5	(445)	TTCATCAATCAAAA	A	AAACAAAGCATTAAAGCATATA	GTTG	-	CTATACTA
Chr.4_SAT5	(353)	TTCATCAATCAAAAACAAACA	G	AGCATTAAAGCATATA	T	TTGGCTATACTA	
Chr.5_SAT5	(1)	-----					
AT2G18042	(1)	-----					
AT3G42565	(1)	-----					
AT4G09545	(1)	-----					
AT5G60978	(1)	-----					
Consensus	(451)	TTCATCAATCAAAAACAAACAAAGCATTAAAGCATATATTTGGCTATACTA					

Section 11

	(501)	501	510	520	530	540	550	
ATSAT5Satellite	(489)	AGA	CTTTTT	A ---	CTCAATTTCTCATT	ATGTCTAT	CAAAAA	TGTGTTTT
chr.2_SAT5	(342)	AGG	TTCTTT	T --	TACTCAATTTCTCATT	ATGTCTAT	AAAAAA	TATGCTTT
chr.3_SAT5	(494)	AGA	CTTT	GT A ---	CTGAATTTCTCATT	ATGTCTAT	CAAAAA	TGTGTTTT
Chr.4_SAT5	(403)	AGG	CTTTTT	TATT	TCTCAGTTTCTCATT	ATGCCTAT	CAAAAA	TGTGTTTT
Chr.5_SAT5	(1)	-----						
AT2G18042	(1)	-----						
AT3G42565	(1)	-----						
AT4G09545	(1)	-----						
AT5G60978	(1)	-----						
Consensus	(501)	AGGCTTTTTTATTTCTCAATTTCTCATTATGTCTATCAAAAAATGTGTTTT						

Section 12

	(551)	551	560	570	580	590	600	
ATSAT5Satellite	(535)	TACT	TCTAGCGGTTCT	TATG	TATCATAGTTTCT	GTAAATGCT	CAATTG	GCC
chr.2_SAT5	(390)	CAC	TCTAGCGGTTCT	TATGC	CATCATCGTTTCT	GTAAATGCT	TAGATG	GCC
chr.3_SAT5	(540)	CCCT	TCTATATGTTCT	TATG	TATCATAGTTTCT	GTAAATGCT	CAATTG	GCC
Chr.4_SAT5	(453)	CAC	TCTAGTGGTTCT	TATGC	CATCATAGTTTCT	GTAAATGCT	CAGTTA	CCT
Chr.5_SAT5	(31)	TTAT	TATAGCGGTT	ATG	TGCGTTT	TGTCTC	GTAAATGCT	CAACTA
AT2G18042	(23)	CAC	TCTAGCGGTTCT	TATGC	CATCATCGTTTCT	GTAAATGCT	TAGATG	GCC
AT3G42565	(23)	CCCT	TCTATATGTTCT	TATG	TATCATAGTTTCT	GTAAATGCT	CAATTG	GCC
AT4G09545	(23)	CAC	TCTAGTGGTTCT	TATGC	CATCATAGTTTCT	GTAAATGCT	CAGTTA	CCT
AT5G60978	(23)	TTAT	TATAGCGGTT	ATG	TGCGTTT	TGTCTC	GTAAATGCT	CAACTA
Consensus	(551)	CACTTCTAGCGGTTCTATGCATCATAGTTTCTGTAAATGCTCAATTG						

Supplementary Figure 2. Sequence alignment

Section 13

	(601)	601	610	620	630	640	650						
ATSAT5Satellite	(585)	CAGTTTCCGGCTC	AAC	TTCC	TTTT	TGTTT	CCGTTCC	AAC	TGATT	CTGG			
chr.2_SAT5	(440)	CAGTTTCCGGCTCCAT	TTCC	TTTT	T	CATTT	CTA	TTCC	GAACC	GATT	CTGG		
chr.3_SAT5	(590)	CAGTTTCCAGCTCAAC	TTCC	TTTT	CC	GTTT	CCGTTCC	AAC	TGATT	TCTGG			
Chr.4_SAT5	(503)	CAGTTTCCGGCTCCGT	TTCT	TTTT	CC	ATTT	T	CGTT	T	CAACC	GATT	CTGG	
Chr.5_SAT5	(81)	CA-----	AT	TTCC	TTTT	CC	ATTT	T	CA	TTCC	TAACC	GATT	TCTGG
AT2G18042	(73)	CAGTTTCCGGCTCCAT	TTCC	TTTT	T	CATTT	CTA	TTCC	GAACC	GATT	CTGG		
AT3G42565	(73)	CAGTTTCCAGCTCAAC	TTCC	TTTT	CC	GTTT	CCGTTCC	AAC	TGATT	TCTGG			
AT4G09545	(73)	CAGTTTCCGGCTCCGT	TTCT	TTTT	CC	ATTT	T	CGTT	T	CAACC	GATT	CTGG	
AT5G60978	(73)	CA-----	AT	TTCC	TTTT	CC	ATTT	T	CA	TTCC	TAACC	GATT	TCTGG
Consensus	(601)	CAGTTTCCGGCTCCATTTCC	TTTT	CC	ATTT	CC	GTTTCC	AACC	GATT	CTGG			

Section 14

	(651)	651	660	670	680	690	700	
ATSAT5Satellite	(635)	A-----	TTACCTGAT	TATAAC	AAAATGTT	TC	TCATCCGTGATGGATA	
chr.2_SAT5	(490)	TATG	T	CAGGAT	TTACCTGAC	ATAAC	AAAATGTTGG	TCATCCGTGATGGATA
chr.3_SAT5	(640)	A-----	TTACCTGAT	TATAAC	AAAATGTT	GG	TCATCCGTGATGGATA	
Chr.4_SAT5	(553)	AATGCCAGGAT	TTACCTGAT	TATAAC	G	AAAATGTTGG	TCATCCGTGATGGATA	
Chr.5_SAT5	(119)	TATGCCAGGAT	TTACCTGAT	TATAAC	A	AAAATGTTGG	TCATCCGTGATGGATA	
AT2G18042	(123)	TATG	T	CAGGAT	TTACCTGAC	ATAAC	AAAATGTTGG	TCATCCGTGATGGATA
AT3G42565	(123)	A-----	TTACCTGAT	TATAAC	AAAATGTT	GG	TCATCCGTGATGGATA	
AT4G09545	(123)	AATGCCAGGAT	TTACCTGAT	TATAAC	G	AAAATGTTGG	TCATCCGTGATGGATA	
AT5G60978	(111)	TATGCCAGGAT	TTACCTGAT	TATAAC	A	AAAATGTTGG	TCATCCGTGATGGATA	
Consensus	(651)	AATGCCAGGATTACCTGAT	TATAAC	AAAATGTTGG	TCATCCGTGATGGATA			

Section 15

	(701)	701	710	720	730	740	750		
ATSAT5Satellite	(676)	TTCC	TGGATGCATTG	CAGAGA	TTTCTCAATC	CATTTT	CACTGGAAA	GTTT	
chr.2_SAT5	(540)	TTCC	TGGATGCATTG	TAGAG	GTTTCTCAATC	TATTTT	CACTGGAAA	ATTC	
chr.3_SAT5	(681)	TTCC	TGGATGCATTG	CAGAGA	TTTCTCAATC	CATTTT	CACTGGAAA	GTTT	
Chr.4_SAT5	(603)	TTCC	TGAATGCATTG	CAGAGA	TTTCTCAATC	CATTTT	TATTGG	CAAATTC	
Chr.5_SAT5	(169)	TTCC	G	GATGCATTG	CAGAGA	TTTCTCAATC	TATTTT	CACAA	GAAAATTT
AT2G18042	(173)	TTCC	TGGATGCATTG	TAGAG	GTTTCTCAATC	TATTTT	CACTGGAAA	ATTC	
AT3G42565	(164)	TTCC	TGGATGCATTG	CAGAGA	TTTCTCAATC	CATTTT	CACTGGAAA	GTTT	
AT4G09545	(173)	TTCC	TGAATGCATTG	CAGAGA	TTTCTCAATC	CATTTT	TATTGG	CAAATTC	
AT5G60978	(161)	TTCC	G	GATGCATTG	CAGAGA	TTTCTCAATC	TATTTT	CACAA	GAAAATTT
Consensus	(701)	TTCC	TGGATGCATTGC	CAGAGATTTCTCAATCC	ATTTT	CACTGGAAA	ATTC		

Section 16

	(751)	751	760	770	780	790	800							
ATSAT5Satellite	(726)	GGT	AATTTAGGT	C	CGG	CTTGTTG	CAAAGCATT	TTTGGA	CGCCGA	---TAA				
chr.2_SAT5	(590)	GGC	AATTTAGGT	C	CA	CTTGTTG	TAAAGCATT	GTTGGA	CGCT	GAAGTCAA				
chr.3_SAT5	(731)	GGT	AATTTAGGT	C	CGG	CTTGTTG	CAAAGCATT	TTTGGA	TGCC	AAAGTCAA				
Chr.4_SAT5	(653)	A	GTAA	TTAGGT	T	CT	GCTTGTTG	CAAAGCATT	TTTGGA	CGCT	GAAGTCAA			
Chr.5_SAT5	(219)	GGT	AA	CTTAGGT	C	CGG	CTTGTTG	CAAAGCATT	TTTGGA	T	GT	CGAA	TC	CAA
AT2G18042	(223)	GGC	AATTTAGGT	C	CA	CTTGTTG	TAAAGCATT	GTTGGA	CGCT	GAAGTCAA				
AT3G42565	(214)	GGT	AATTTAGGT	C	CGG	CTTGTTG	CAAAGCATT	TTTGGA	TGCC	AAAGTCAA				
AT4G09545	(223)	A	GTAA	TTAGGT	T	CT	GCTTGTTG	CAAAGCATT	TTTGGA	CGCT	GAAGTCAA			
AT5G60978	(211)	GGT	AA	CTTAGGT	C	CGG	CTTGTTG	CAAAGCATT	TTTGGA	T	GT	CGAA	TC	CAA
Consensus	(751)	GGTAA	TTAGGT	C	CGG	CTTGTTG	CAAAGCATT	TTTGGA	CGCCGA	GAAGTCAA				

Supplementary Figure 2. Sequence alignment

Section 17

	(801)	801	810	820	830	840	850		
ATSAT5Satellite	(773)	TTG	CATA	CCG	AAAATTCCAT	TTCATTCCAT	TTTTT	TCC	CCGATGCTAAAG
chr.2_SAT5	(640)	TTC	CATG	CCG	AAAATTCCAT	TTCATTCTGTT	TTTTT	TCC	CCGATGCTAAAG
chr.3_SAT5	(781)	TTG	CATA	CCG	AAAATTCCAT	TTCATTCCGTT	ATTTC	TCC	CCGATGCTAAAG
Chr.4_SAT5	(703)	CTG	CATA	CC	AAAATTCCAC	TATTCCG	CTTTTT	TCC	CCGATGCTAAAAG
Chr.5_SAT5	(269)	TTG	CATG	CC	AAAATTCCAT	TTCATTCCGTT	ATTTC	TCC	CCGATGCTAAAAG
AT2G18042	(273)	TTG	CATG	CCG	AAAATTCCAT	TTCATTCTGTT	TTTTT	TCC	CCGATGCTAAAG
AT3G42565	(264)	TTG	CATA	CCG	AAAATTCCAT	TTCATTCCGTT	ATTTC	TCC	CCGATGCTAAAG
AT4G09545	(273)	CTG	CATA	CC	AAAATTCCAC	TATTCCG	CTTTTT	TCC	CCGATGCTAAAAG
AT5G60978	(261)	TTG	CATG	CC	AAAATTCCAT	TTCATTCCGTT	ATTTC	TCC	CCGATGCTAAAAG
Consensus	(801)	TTGC	CATA	CCG	AAAATTCCAT	TTCATTCCGTT	TTTTT	TCC	CCGATGCTAAAG

Section 18

	(851)	851	860	870	880	890	900				
ATSAT5Satellite	(823)	AACAATG	TTC	AAGA	TTG	CCGGTG	CAACTCCTCC	CAT	ACCA	AAATAG	TGT
chr.2_SAT5	(690)	AACAATG	CTC	AAGA	ATTG	TGGTG	CAACTCCTCC	TAT	ACCA	AAATAG	AGT
chr.3_SAT5	(831)	AACAATG	TTC	AAGA	TTG	CCGGTG	CAACTCCTCC	CAT	ACCA	AAATAG	AGT
Chr.4_SAT5	(753)	AACAATG	TTC	AAGA	ATTG	CCGGTG	TAACTCCTCC	TAC	ACCG	AAATAG	AGT
Chr.5_SAT5	(319)	AACAATG	TTC	AAGA	ATTG	CCGGTG	CTAACTCCTCC	TAC	ACCA	AAATAG	AGT
AT2G18042	(323)	AACAATG	CTC	AAGA	ATTG	TGGTG	CAACTCCTCC	TAT	ACCA	AAATAG	---
AT3G42565	(314)	AACAATG	TTC	AAGA	TTG	CCGGTG	CAACTCCTCC	CAT	ACCA	AAATAG	---
AT4G09545	(323)	AACAATG	TTC	AAGA	ATTG	CCGGTG	TAACTCCTCC	TAC	ACCG	AAATAG	---
AT5G60978	(311)	AACAATG	TTC	AAGA	ATTG	CCGGTG	CTAACTCCTCC	TAC	ACCA	AAATAG	---
Consensus	(851)	AACAATG	TTC	AAGA	ATTG	CCGGTG	CAACTCCTCC	TAT	ACCA	AAATAG	AGT

Section 19

	(901)	901	910	920	930	940	950						
ATSAT5Satellite	(873)	TTTA	TCTTATT	-----	TTTAA	AATAGATAA	CTTTTT	-----	CAAC				
chr.2_SAT5	(740)	TTTAG	CCTTAGT	-T-	-----	TTAAAAAT	CTATG	ATTTTTTT	TCTTTT	CAAC			
chr.3_SAT5	(881)	TTTA	ACTTATT	-----	TTTAA	AATAGATA	GC	TTTTTT	-----	CAAC			
Chr.4_SAT5	(803)	TTTA	AAATTATT	A	TT	-----	TTTAA	AATAGATA	ATTTTTTT	---	TCCAAT		
Chr.5_SAT5	(369)	C	TTAG	T	TTATT	T	TTAAAACAT	A	TAAAATA	TGA	ATTTTTT	GTCTTTT	CAAC
AT2G18042	(370)	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AT3G42565	(361)	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AT4G09545	(370)	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AT5G60978	(358)	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Consensus	(901)	TTTAG	CCTT	ATTTTT	TAAAACAT	TTTAA	AATAGATA	AATTTTTTT	TCTTTT	CAAC			

Section 20

	(951)	951	960	970	980	990	1000								
ATSAT5Satellite	(908)	TTATTT	T	TTT	-----	AAAATTTT	-AGCTTACG	T	TACATGTT	TATAA	TAA	T			
chr.2_SAT5	(782)	TTATTT	A	TTT	-----	GAAATTT	GT	-AGCTTAC	T	TACATGTT	TATACT	CCA			
chr.3_SAT5	(916)	TTAT	G	TTT	-----	AAAATTTT	-AGCTT	TAGT	-ACATGTT	TATAA	TAA	T			
Chr.4_SAT5	(844)	TTATTT	C	TT	-----	ACAATTTT	-AGCTTACG	CTACATGTT	TATACT	CCA					
Chr.5_SAT5	(419)	TTCTTT	C	TT	A	AATTTTA	T	AATT	CTCAGA	TTAC	T	CAACATGTT	T	TACT	TAA
AT2G18042	(370)	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AT3G42565	(361)	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AT4G09545	(370)	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AT5G60978	(358)	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Consensus	(951)	TTATTT	TT	AATTTT	T	AATT	CTCAGA	TTAC	T	CAACATGTT	T	TACT	TAA		

Supplementary Figure 2. Sequence alignment

Section 21

	(1001)	1001	1010	1020	1030	1040	1050
ATSAT5Satellite	(951)	AA	TTAAAAA	AGA	GATA	TAGTAATAACATTTGAGAAGTTGC	ATTTG
chr.2_SAT5	(824)	AAAA	GAAAAAA	-AC	GATGATA	CAATAATAACAT	-----AGTTGTATTTG
chr.3_SAT5	(957)	AA	TTAAAAA	----	GAT	TATA	TAGTAATAACATTTGAGAATTTGCATTTG
Chr.4_SAT5	(886)	AAAAAA	TATC	-----	ATATA	AAGTAAA	AACATTTGAGAAGTTGTATTTG
Chr.5_SAT5	(469)	AAAAAA	CGA	-----	TGATA	CATTAATAACATTTGAGAAGT	CGTATTTG
AT2G18042	(370)	-----	-----	-----	-----	-----	-----
AT3G42565	(361)	-----	-----	-----	-----	-----	-----
AT4G09545	(370)	-----	-----	-----	-----	-----	-----
AT5G60978	(358)	-----	-----	-----	-----	-----	-----
Consensus	(1001)	AAAAAAAAAAGACGATGATATAGTAATAACATTTGAGAAGTTGTATTTG					

Section 22

	(1051)	1051	1060	1070	1080	1090	1100
ATSAT5Satellite	(1001)	GGTTC	CATGTTTA	TA	CATTCTTCA	C	TTCTAATGAATAACACCTTGAAACA
chr.2_SAT5	(867)	GGTTCAAT	ACTTACTCATT	T	TTCAATT	A	TAATGAATAACACCTTGAAACA
chr.3_SAT5	(1003)	GGTTCAAT	GTC	TACTCATTCTT	T	AA	TCTAATGAATAACACCTTGAAACA
Chr.4_SAT5	(930)	GGTTCAAT	A	TTTACTCATTCTTCAATT	TCTAATGAATAACAG	C	TTTGAAACA
Chr.5_SAT5	(513)	TGTT	TAA	TTTTA	GTC	G	TTCTTATTTCTAATGAATAA
AT2G18042	(370)	-----	-----	-----	-----	-----	-----
AT3G42565	(361)	-----	-----	-----	-----	-----	-----
AT4G09545	(370)	-----	-----	-----	-----	-----	-----
AT5G60978	(358)	-----	-----	-----	-----	-----	-----
Consensus	(1051)	GGTTCAATGTTTACTCATTCTTCAATTCTAATGAATAACACCTTGAAACA					

Section 23

	(1101)	1101	1110	1120	1130	1140	1150
ATSAT5Satellite	(1051)	TCGAGTCCATAA	TGAATTTAGTCTTACAATGTTACAGA	CC	TTCAAATTG		
chr.2_SAT5	(917)	T	TAACTCCGTAATT	-	AATTTAGTCTT	GCAAT	-----
chr.3_SAT5	(1053)	TCGAG	CCCATAAT	----	G	-----	TTACAATGTTACAGAATTTCAAATTG
Chr.4_SAT5	(980)	TCGAT	TCTATAAAT	-	AACTTT	T	GTCTTACAATGTT
Chr.5_SAT5	(563)	TCGAGT	AGATAAAT	-	AATTTA	A	TGCAATATT
AT2G18042	(370)	-----	-----	-----	-----	-----	-----
AT3G42565	(361)	-----	-----	-----	-----	-----	-----
AT4G09545	(370)	-----	-----	-----	-----	-----	-----
AT5G60978	(358)	-----	-----	-----	-----	-----	-----
Consensus	(1101)	TCGAGTCCATAAATGAAATTTAGTCTTACAATGTTACAGAATTTCAAATTG					

Section 24

	(1151)	1151	1160	1170	1180	1190	1200
ATSAT5Satellite	(1101)	TTT	CATAAATCTTTGAAATATGTCATA	-----	ACACAAAATCTGAGAGT		
chr.2_SAT5	(947)	-----	-----	-----	-----	-----	-----
chr.3_SAT5	(1093)	TTTT	CATAAATCTTTGAAATATGTCATA	-----	ACACAAAATCTGAGAAT		
Chr.4_SAT5	(1013)	-----	-----	-----	-----	-----	-----
Chr.5_SAT5	(609)	TTTT	CATAAATCTTT	T	AGATAC	G	TATAGTAACACAAAATCTGTC
AT2G18042	(370)	-----	-----	-----	-----	-----	-----
AT3G42565	(361)	-----	-----	-----	-----	-----	-----
AT4G09545	(370)	-----	-----	-----	-----	-----	-----
AT5G60978	(358)	-----	-----	-----	-----	-----	-----
Consensus	(1151)	TTTTCATAAATCTTTGAAATATGTCATATAGTAACACAAAATCTGAGAAT					

Supplementary Figure 2. Sequence alignment

		Section 25					
	(1201)	1201	1210	1220	1230	1240	1250
ATSAT5Satellite	(1146)	GGTTTATAATTTTATTAGATAAGACTCGTCTCAAATATGCTGGTGTGAGAA					
chr.2_SAT5	(947)	-----					
chr.3_SAT5	(1138)	GGTTTATAATTTTATTAGATAAGACTCGTCTAA-TAGGCGGGTGTGAGAA					
Chr.4_SAT5	(1013)	-----					
Chr.5_SAT5	(659)	GGTTTATAA CTTT -TTA TATA C GAC -					
AT2G18042	(370)	-----					
AT3G42565	(361)	-----					
AT4G09545	(370)	-----					
AT5G60978	(358)	-----					
Consensus	(1201)	GGTTTATAATTTTATTAGATAAGACTCGTCTAAATATGCTGGTGTGAGAA					
		Section 26					
	(1251)	1251	1260	1270	1280	1290	1300
ATSAT5Satellite	(1196)	ATGTTGTGATGATATAAAAATTCTAAATAGTAATCTGTATTTTCAAAG					
chr.2_SAT5	(947)	-----					
chr.3_SAT5	(1187)	ATGTTGTGATGATATAAAAATTCTAAATAGTAATCTGTATTTT-CAAAG					
Chr.4_SAT5	(1013)	-----					
Chr.5_SAT5	(683)	-----					
AT2G18042	(370)	-----					
AT3G42565	(361)	-----					
AT4G09545	(370)	-----					
AT5G60978	(358)	-----					
Consensus	(1251)	ATGTTGTGATGATATAAAAATTCTAAATAGTAATCTGTATTTTCAAAG					
		Section 27					
	(1301)	1301	1310	1320	1330	1340	1350
ATSAT5Satellite	(1246)	AATATTTCAATTATATACATTCATATACCATGCCTTTACTAATTATATA					
chr.2_SAT5	(947)	-----					
chr.3_SAT5	(1236)	AATATTTCAATTATATACATTCATATACCATGCATTTTCTAATTATATA					
Chr.4_SAT5	(1013)	-----					
Chr.5_SAT5	(683)	-----					
AT2G18042	(370)	-----					
AT3G42565	(361)	-----					
AT4G09545	(370)	-----					
AT5G60978	(358)	-----					
Consensus	(1301)	AATATTTCAATTATATACATTCATATACCATGCCTTTTCTAATTATATA					
		Section 28					
	(1351)	1351	1360	1370	1380	1390	1400
ATSAT5Satellite	(1296)	TAATACGGGATTTCTCAAAGTATAAAGAAAGATAAGACAAGGAAAACAT					
chr.2_SAT5	(947)	-----					
chr.3_SAT5	(1286)	TTATACGGGATTCCTCAAAGCATAACACAAAGATAAGACAAGGAAAACAT					
Chr.4_SAT5	(1013)	-----					
Chr.5_SAT5	(683)	-----					
AT2G18042	(370)	-----					
AT3G42565	(361)	-----					
AT4G09545	(370)	-----					
AT5G60978	(358)	-----					
Consensus	(1351)	TTATACGGGATTTCTCAAAGTATAACAGAAAGATAAGACAAGGAAAACAT					

Supplementary Figure 2. Sequence alignment

Section 29

	(1401)	1401	1410	1420	1430	1440	1450
ATSAT5Satellite (1346)		ACAACA	CTA	TAAAA	GACGCACCA	GACAGAGCCTCTCACTGAATTTTGT	
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----
chr.3_SAT5 (1336)		ACAACA	GCT	TAAAAAGACGCACCA	A	ACAGAGCCTCTCACTGAATTTTGT	
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----
Consensus (1401)		ACAACATCTTTAAAAAGACGCACCAGACAGAGCCTCTCACTGAATTTTGT					

Section 30

	(1451)	1451	1460	1470	1480	1490	1500
ATSAT5Satellite (1395)		GGTAAACGAAT	A	GAACTC	TGTAATTGAGAAAAAA	A	TAAATGAAATAATAT
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----
chr.3_SAT5 (1386)		GGTAAACGAAT	T	GAACTC	CGTAATTGAGAAAAAA	T	GAAATGAAATAA
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----
Consensus (1451)		GGTAAACGAATTGAACTCTGTAATTGAGAAAAAATTAAATGAAATAATAT					

Section 31

	(1501)	1501	1510	1520	1530	1540	1550
ATSAT5Satellite (1445)		TAAGAAATAAAA	A	GAGAGACATATTTAAGTTACAAAATTAGAAAATATTA			
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----
chr.3_SAT5 (1436)		TAAGAAATAAAA	G	GAGAGACATATTTAAGTTACAAAATTAGAAAATATTA			
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----
Consensus (1501)		TAAGAAATAAAAAGGAGAGACATATTTAAGTTACAAAATTAGAAAATATTA					

Section 32

	(1551)	1551	1560	1570	1580	1590	1600
ATSAT5Satellite (1495)		AATCA	CGTATTAATATTTTTCTAAAACAAAATAGGGAAC	TTTTACTTCTG			
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----
chr.3_SAT5 (1486)		AATCA	AGTATTAATATTTTTCTAAAACAAAATAGGGAAC	TTTTACTTCTG			
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----
Consensus (1551)		AATCACGTATTAATATTTTTCTAAAACAAAATAGGGAAC					TTTTACTTCTG

Supplementary Figure 2. Sequence alignment

Section 33

	(1601)	1601	1610	1620	1630	1640	1650
ATSAT5Satellite (1545)		TTTTGAATATATAAACGAT	TT	TTTAATAGAAATTTGTTCAATA	T	TTTAATAT	
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----
chr.3_SAT5 (1536)		TTTTGAATATATAAACGAC	CA	TTTAATAGAAATTTGTTCAATA	G	TTTAATAT	
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----
Consensus (1601)		TTTTGAATATATAAACGAT	TTTTTAATAGAAATTTGTTCAATA	TTTTTAATAT			

Section 34

	(1651)	1651	1660	1670	1680	1690	1700	
ATSAT5Satellite (1595)		AGTAAATAAAA	A	AATTTGT	TATATATGAACTA	--	TTTTTTTTACTTG	TGTAT
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----	-----
chr.3_SAT5 (1586)		AT	TAAATAAAA	C	AATTTG	A	ATATATGAACTAACTTTTTTTACTTA	TGTAT
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----	-----
Consensus (1651)		ATTAAATAAACAA	TTTTGTATATATGAACTAACTTTTTTTACTT	TGTGTAT				

Section 35

	(1701)	1701	1710	1720	1730	1740	1750
ATSAT5Satellite (1643)		ATATCCGATGGGGTTATGAAATTTTTCTATATTTTGT	TTTTTAA	AAATAT			
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----
chr.3_SAT5 (1636)		ATATCCGATGGGGTTATGAAATTTTTCTAT	--	TTTGT	TTT	--	AAAATAT
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----
Consensus (1701)		ATATCCGATGGGGTTATGAAATTTTTCTATATTTTGT	TTTTTAA	AAATAT			

Section 36

	(1751)	1751	1760	1770	1780	1790	1800
ATSAT5Satellite (1693)		AGG	TTTTGTGCAAAACACCCATCTAACTCATCT	AG	TTTTGCAATTTTAC		
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----
chr.3_SAT5 (1682)		AGG	A	TTTTGTGCAAAACACCCATCTAACTCATC	C	T	A
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----
Consensus (1751)		AGGGTTTTGTGCAAAACACCCATCTAACTCATCT	TGTTTTGCAATTTTAC				

Supplementary Figure 2. Sequence alignment

Section 37

	(1801)	1801	1810	1820	1830	1840	1850
ATSAT5Satellite (1743)		CCTA	TATCTCTAACAAA	CA	CATATTAATCTTATGAAGT	CTAAAAA	TAAATAC
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----
chr.3_SAT5 (1732)		CTTC	TATCTCTAACAAA	TGC	CATATTAATCTTATGAAG	A	CTAAAAA
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----
Consensus (1801)		CTTCTATCTCTAACAAATGC	CATATTAATCTTATGAAGTCT	AAAAATAATAC			

Section 38

	(1851)	1851	1860	1870	1880	1890	1900
ATSAT5Satellite (1793)		GCA	AATATGACCCTTATA	C	GTATAT	TGTAAA	CTTTTTTACACTCCATAGA
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----
chr.3_SAT5 (1782)		GTA	AATATGACCCTTATA	TGT	TATATA	GTA	AACTTTTTTACACTCCATAGA
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----
Consensus (1851)		GTA	AATATGACCCTTATA	TGT	TATATTGTA	AACTTTTTTACACTCC	ATAGA

Section 39

	(1901)	1901	1910	1920	1930	1940	1950
ATSAT5Satellite (1843)		TTAG	ATTTTAA	TATTT	C	GAA	GGT
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----
chr.3_SAT5 (1832)		TTAG	ATTTTAA	A	ATTT	TGTT	GGT
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----
Consensus (1901)		TTAG	ATTTTAA	TATTTGTT	GGT	CGATTTGAAGTTTT	TCGTTGCGAGGGC

Section 40

	(1951)	1951	1960	1970	1980	1990	2000
ATSAT5Satellite (1893)		TT	CGATT	AAC	CATATTA	A	ATATCAATAT
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----
chr.3_SAT5 (1882)		TT	C	AATTT	AAC	CATATTA	TATATCAATAT
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----
Consensus (1951)		TT	CGATT	TAA	CATATTTATAT	CAATATTTT	TACAACTTTTGTGGTAGCA

Supplementary Figure 2. Sequence alignment

Section 41

	(2001)	2001	2010	2020	2030	2040	2050
ATSAT5Satellite (1943)		AAA --	TGACGAA	AGGGTTA	CAT	TGCGTATTATTTTAGACTTCA	T
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----
chr.3_SAT5 (1932)		AAAATTGACGAA	GAA	GGTTG	CAATG	GGTATTATTTTAGACTT	CGTA
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----
Consensus (2001)		AAAATTGACGAA	GAGGGGTTGC	ATTGGGTATTATTTTAGACTT	CGT	CGGA	

Section 42

	(2051)	2051	2060	2070	2080	2090	2100
ATSAT5Satellite (1991)		TAATTATGCA	TTT	TTGGAGGTGGAG	AATAAA	GATGCAAAAATAGATGAG	
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----
chr.3_SAT5 (1982)		TAAT -	ATGCA	TTG	TTGGAGGTGGAG	GATAAA	TATGCAAAAATAGATGAG
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----
Consensus (2051)		TAATTATGCA	TTTTTTGGAGGTGGAG	GATAAA	TATGCAAAAATAGATGAG		

Section 43

	(2101)	2101	2110	2120	2130	2140	2150
ATSAT5Satellite (2041)		TTAGAGG	GTTTT	AT -	TTGCACA	AACCCTAAAAATAAC	AAAATTTGATT
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----
chr.3_SAT5 (2031)		TTAGAGA	GTTTT	TCTTTGCACAT	AACCCTAAAAATAAC	GAAATT -	GATT
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----
Consensus (2101)		TTAGAGGGTTTTTTCTTTGCACATAACCCTAAAAATAACGAAATTTGATT					

Section 44

	(2151)	2151	2160	2170	2180	2190	2200
ATSAT5Satellite (2090)		TGATA	AGG	GTGGATA	TTT	CACTAATAAA	TTTGACACGTGTCATGATCAG
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----
chr.3_SAT5 (2080)		TGATA	TGT	GTGGATA	AC	TCACTAATAAA	TTTGACACGTGTCATGATCAGG
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----
Consensus (2151)		TGATATGTGTGGATATTTCACTAATAAATTTTGACACGTGTCATGATCAGG					

Supplementary Figure 2. Sequence alignment

Section 45

	(2201)	2201	2210	2220	2230	2240	2250
ATSAT5Satellite (2140)		TGAGTTAACAATTTT	GAAAGCC	CAACTTT	ATGTA	---	GATATTTGGCAC
chr.2_SAT5 (947)		-----	-----	-----	-----	-----	-----
chr.3_SAT5 (2130)		TGAGTTAACAATTTT	GAAAGCT	CAACTTT	GTA	TATTAAGATATTT	GGCA-
Chr.4_SAT5 (1013)		-----	-----	-----	-----	-----	-----
Chr.5_SAT5 (683)		-----	-----	-----	-----	-----	-----
AT2G18042 (370)		-----	-----	-----	-----	-----	-----
AT3G42565 (361)		-----	-----	-----	-----	-----	-----
AT4G09545 (370)		-----	-----	-----	-----	-----	-----
AT5G60978 (358)		-----	-----	-----	-----	-----	-----
Consensus (2201)		TGAGTTAACAATTTT	GAAAGCT	CAACTTT	GTGTA	TATTAAGATATTT	GGCAC

Section 46

	(2251)	2251	2261
ATSAT5Satellite (2186)		ATATATTGGAT	
chr.2_SAT5 (947)		-----	-----
chr.3_SAT5 (2179)		-----	-----
Chr.4_SAT5 (1013)		-----	-----
Chr.5_SAT5 (683)		-----	-----
AT2G18042 (370)		-----	-----
AT3G42565 (361)		-----	-----
AT4G09545 (370)		-----	-----
AT5G60978 (358)		-----	-----
Consensus (2251)		ATATATTGGAT	

Supplementary Figure 2. Sequence alignments

The 2196 bp SAT5 (ATSAT5) consensus sequence [1] is shown together with the four dispersed SAT5 monomers containing *CRP* genes and the actual coding sequences of the four *CRP* genes or pseudogenes embedded in them (Table 1). Shading indicates sequence identity. Yellow shading indicates *CRP* coding regions. The flanking regions are AT-rich compared to the *CRP* coding sequence (Supplementary Table 2). These AT-rich flanking regions are likely to provide transcriptional regulatory regions and indeed putative TATA boxes (TATAAA between 420 and 430 bp) and poly-adenylation sites (AATAA located between 1021 and 1030 bp) can be detected in these sequences. Alignments were made using Vector NTI Advance11 from Invitrogen. Accession numbers for the single SAT5 monomers containing *CRP* genes or pseudogenes are as follows: chr2 SAT5 fragment containing At2g18042 pseudogene [EMBL:HE610172]; chromosome 3 SAT5 fragment containing At3g42565 gene [EMBL:HE610173]; chromosome 4 SAT5 fragment containing At4g09545 gene [EMBL:HE610174]; chromosome 5 SAT5 fragment containing At5g60978 pseudogene [EMBL:HE610175].

[1] Genetic Information Research Institute: **ATSAT5: A satellite-like sequence from chromosome 5 – a consensus**. *Rebase Reports* 2006, **6**: 50.