

Guayule gSaTar terminal inverted repeat sequences.

<i>gSaTar Element</i>	Size bp	Terminal Inverted Repeat Sequence
<i>gSaTar1a</i>	1150	GGGTAA-GGTTAGTGTACAAAGGGTGTGTTTTGTGAGAACGGTAAGAAG GGGTAGAGGTTTGTGTACAAAGGGTGTGTTTTATGAGAAGTGTAGAAG
<i>gSaTar1b</i>	800	GGGTAGGGTTATGTACAAAGGGTGTGTTTTGTAAAAGGGTAAGAAGTGT ----GTGGTTCGTGTACAAAGGGTGAGATTGTGAGAAGGGTAAGAAGATT
<i>gSaTar1c</i>	850	GGATAGGGTTCCTGTATAAAAGGTGTGTTTTTTTAAAAGTGTAAACGTA ----GAGATTCTGTAC-AAAGGGGTGTTATGTGAGAAGTGTAGAAGAA
<i>gSaTar1d</i>	1110	GGGAGAGGCAAGGGATCGGATACAAAATGAAAAGTGTGAGAAGTCAAGAA -----GGGGAGAGTTCCTGTACAAAATGTGTTTTTATGAGAAGGATAAGAA
<i>gSaTar1e</i>	990	GGGTAGGGTTAGTGTACAAAGGGTGTGTTTTGTGAGAATGGTAAGAAGTGTGTTT GGGAAGGGTTCGTGTACAAAGGACAAAAGTGTGAGAAGGTAAAGAGTGTCTTT
<i>gSaTar1f</i>	1090	GGGAGGGTTCCTGTACAAAATAGTTTTTTGTGAGAAATGTA ----GGGATCGGGTACAAAATAGAACTTTTGTGAGAAATGTA
<i>gSaTar1fg</i>	870	GGGTGGGTTAGTGTACAAAGGGTGTGTTTTGTGAGAAGGGTAAGAAG -----GTTCTGTACAAAGGGTGAGATTATGAGAAGGGTAAGAAG
<i>gSaTar2a</i>	400	GGGTAAAGATCAAATACAAAGG-GCTTATCCTATAAACA GGTAAGGTTCTGTATAAATGGTCTTATCCTACAAATA
<i>gSaTar2b</i>	380	GGGTAAGGTTCTGTACAAATGGAA-TTATCGTACGAA GGTAAGGTTATGTACAGTTGGTCTTATCATACAAA
<i>gSaTar2c</i>	360	GGGTAAAGTTCTGTACAAATGGAATTATCGTACGAAGCGTACGAA ----GGACAAAAGATCAAATACAA--AGTAATTTATCGTACGAA
<i>gSaTar3a</i>	430	GGGTGGGGTTCCTGTAAAAGTGTGTTTTTCTAAGAAGTCTAAGAA GGTAAGGAGTTTGTGTAGAAAGTATATTTTCTAAAAGTGTAAAGAA
<i>gSaTar3b</i>	390	GGTAA-GGTTGTTGTACAAAGTACATTTTCGTACAAAGTGTGAGAA GGTAAAGGTTCTGTACAAATTAATTTTCGTACAAAGTGTGGGAA
<i>gSaTar3c</i>	820	GGGTGGGGTTCTCTAGAAAGTGGTGTATTTTAAAGAAAT-TAAGAA GGTTAGGAGTTAGCTTGAAAGTGGGT-TTATCTATAAAGTGTAAAGAA
<i>gSaTar4a</i>	400	GGGTGAG-GTTCCTGTACAAAATGAAAAGTGTGAGAAATTTTAAAT GGGAAAGAGATCGGGTACAAAATGAAAAGTGTGAGAAATGTGAGAAAT
<i>gSaTar4b</i>	400	GGGTTTAGGTTCTGTACAAAGGCCATATTTGTGAGAAGTGTGAGAAGGATTAA GGGTA-AGGTTAGTGTACAAAGGCCATTTTGTGAGAAGTGTGAGAAGGATTAA
<i>gSaTar5a</i>	1630	GGGTCAAGGATCATGTACAAAAAAGGTGTTTTGTGAGAAGGGTAAGAAA ----GGGATCTTGTACAAAAA-TTGGGTTTTGTGAGAAGGGTAAGAAA
<i>gSaTar5b</i>	1050	GGGTCAAGGATCCTGTACAAATGGTGTGTTTTGTGAAAAGGGTAAGAA ----GGGATCTTGTATAAAAATTAGAATTTGTGAGAAGGTAAGAA
<i>gSaTar5c</i>	1050	GTAGATGATCCTGTACAGAGTCTAAGATTGTGAAGAAGGGTAAGAAGCCTTTGTGGAC -----CCTGTACAAAGGAGGTGTTTTGTGAGAAGGGTAAGAAGGCTTTGTGAC
<i>gSaTar6a</i>	500	GTGGAGAGTTCAAATGAGAAGAAATGTATTGTGAAGAAGAAAGAACAAA GGGGA-TGATCAAATAAGAAGAACT-TAGTGTGAGAAATAAAGAAGAGAA
<i>gSaTar6b</i>	460	GGAGAGTTCAAATGAGAAGAAAAAT-ATATCGTAAGAAGAAAAACAAA GGGATAATCAAATGAGAATAAACTCAATGTGAAGAGAAAGAAATGACA
<i>gSaTar7</i>	400	GGGGAAGGATCTACGCAAAACATATATATTGCGGAACACGCGAGAACAA GTGGAAGGATCATTTGAGAACACTAATTATTGCGGAGAACAAAAAGAACAA
<i>gSaTar8a</i>	440	GGGGAGGGTTATCTTGAGAACACTAAATATCGCGAGAACCGTGAGAACAAATAAAA GGGGAGGGTTACTTTGAGAACACTAAATGTGCGAGAACCGTGAGAACAAATGAAAA
<i>gSaTar8b</i>	400	GGGGAGGGTTATCTTGAGAACGCTAAATATC-GCGAGAACCGTGAGAACAAATGAAAA GGGGAGAGTTAATTGAGAACACATGTATTTGTGCGAACCGCAAGAACCCGCTCTAAAA
<i>gSaTar9</i>	520	GGGTAGGGATCATGCGAGAACCA-ACCTTATTGCGAGAACCGGGAGAACCAATGTGAAC -GATTGGATCATTTGAGAACCAACCATTAATTGTGAGAACCGCGAGAACCAAGTGTGAAC
<i>gSaTar10a</i>	530	GGGTAGGGATCCTAAGAGAACCAA-CCCTATTGAGAGCCATGAGAACATTTT -GATTGGATCATTTGAGAACCAAGGCCTAATTGAGAACTGAGAAACCAATCT
<i>gSaTar10b</i>	590	GGGTAGGGATCCTAAGAGAACCAA-CCCTATTGAGAACCAAGAGAACCATCT GGATTGGATCATTTGAGAACCAATTGGCAATTGAGAACTGAGAGAACCATTTT
<i>gSaTar11</i>	1030	GGTA-GGGTTCATGAGAGAACCAAGTAAATGTGAAGAACATAAGAATCAATATGGACC GGATTGGGTTCAAATAAAACCAAGAATTATATAAGAACCATAGAACCAATCTAGACC
<i>gSaTar12</i>	380	GGGAAGTTAAACAGAAAAATCCTAAAAATTTT----AGAAAACCTACTTTCCGAGC GGCTAAGTATAAATAGAAAACCCACTTTTTTTTGGAGAAAACCTACTTCCGAAC
<i>gSaTar13</i>	410	GGGTGAGGATAAAATGAAAACCACTTGAGTTAAGAAAACCGTT---AAAACCATTTATTTTTTTT-ATAAAATTACATG ----GAGAAAACCGTGAAAACCA-----TAGCAAAACCATGTAAAAAACATTTATTTTTTTTGAAGAAATTACATG
<i>gSaTar14a</i>	1120	GGGAGGTTATTGTACA--AGAGAGCTTGACGTACAAAGTGTAGGAGA GGGGAAGGTTAAAAAGAGAGAGCTTAACGTACAAAGTGTACAAAA
<i>gSaTar14b</i>	1120	GGGCTGGTTAAAAATACAGATAAATAATCGTGCAGAGAATATGAGACAAT ----GGTTAACATACAGAAAAATATATCGTGCAGAGGGTAGG-GACAAT
<i>gSaTar15</i>	750	GGGTAAAGTCAAATAAAAAGTTGATTTTGCCTAAGTAGGATAAGAAG GGGGAGAGATCCCCTAAAAATTGGGTTTGTGCTAAGTAGCCTAAGAAG
<i>gSaTar16</i>	840	GGGGAAGTGAATATGGGGCTGTTACGCATCCAA-GTTGTATGCGAAAC GGGT----TGTTACGCATCCAAGTTATATGCAA--AACCAATCAAAAC
Autonomous <i>gSaTar-MULE1</i>	5330	GGGGAAGTGAATATGGTGCTGTTGCGCACCTAACCTTACATGCGCAACCATCAAAACTACGTAGTTTTG GGGGAAGTGAATATGGTACTGTTGCGCACCTAACCTTACATGCGCAACCATCAAAACTACGTAGTTTTG
Autonomous <i>gSaTar-MULE2</i>	3850	GGGAAAAGTGAATA-----TGAGGCTGTTAAGTACCAACCTTACATGTGAAGAACCATCAAAACTACGTAGTTTTG GGGAAAAGTGAATAAGTGAATATGAGGCTGTTAAGTACCAACCTTACATGTGAAGAACCATCAAAACTACGTAGTTTTG
Autonomous <i>gSaTar-MULE3</i>	10800	GGGAGAGTTCTGTACAAATGAGATCTTTTGTGAGAAACGTAGGAACCAATCTGCGAGTGACACATGA GGTAGAGGATCGGGTACAAAATGGCTCTTTTGTGAGAAACGTAGGAACCAATCTGCGAGTGACACATGA
Autonomous <i>gSaTar-MULE4</i>	10500	GGGTGGGGTTAGTGTAGAAATGGTGTGTTTTTGTGAGAATGGTAGGAATCAAT -----GGTTCGGTGAAAACATGAGTTTTTGTGAGAACAGTGAGACCAAT
Autonomous <i>gSaTar-MULE5</i>	10800	GGGTAGGGATCCTAAGAGAACCAACCTAATTTGAGAACCAAGAGAACCAATCT -GGTAGGGATCCTAAGAGAACCAACCTAATTCGAGAACTAAGAGAACCAATCT
Autonomous <i>gSaTar-MULE6</i>	10100	GGGTAGGGATCATGCGAGAACCA-ACCTTATTGCGAGAACCGCGAGAACCA GGATGTGGATCATTTGAGAACCACTTTATTGTGAGAACCGCGAGAACCA

Additional file 1.

Terminal inverted repeats defining non-autonomous and autonomous gSaTar elements. Aligned sequences of 5' and 3' (reverse complement shown) defining TIRs.