Table S3: Characteristics and distribution of the detected SSR motifs (without MNRs) across the non-redundant 56 SSR+ive sequences generated using SSR enrichment approach.

SSR motif type/ length	AG[T]	AC[T]	AT[NT]	DNRs	AAC[T]	AAG[T]	TNRs[T]	All detected SSRs (without MNRs)
6 to 7-mer	5	4	1	10	1	1	2	12
8 to 10-mer	11	8	1	20	1	--	1	21
11 to 13-mer	6	5	--	11	--	--	--	11
14 to 16-mer	3	3	--	6	--	--	--	6
17 to 19-mer	2	1	--	3	--	--	--	3
20 to 22-mer	3	2	--	5	--	--	--	5
23 to 25-mer	7	0	--	7	--	--	--	7
26 to 28-mer	3	1	--	4	--	--	--	4
29 to 31-mer	1	0	--	1	--	--	--	1
Total number	41	24	2	67	2	1	3	70
Total length (RIs)	632	298	14	944	16	6	22	966
Mean length (RIs)	15.4	12.4	7	14.2	8	6	7.3	13.8

Note: [T]: Targeted SSR motifs; [NT]: Non-targeted SSR motifs; --: Not detected; RI: Repeat Iterations