Table S1. DNA sequences containing 12 randomly selected SNPs identified by GBS to be validated for STARP marker design.

SNP name	SNP allele	Chromosome	Pseudomolecule position (bp)*	DNA sequence containing SNP site*
SNP1	G/A	2	6,683,897	AGTAACTGCTTGTAAGCTGTTTCTATTTGCCTAATACCTACTTGGCACGATTCACAG TCAACCACATTTCCAGATGCATCTTTCAAGATCACAACCAGC**[G/A]**CGTACAGATTT GGCTGCAATTATACAAAGAAGGACAGATAGAAGAGAGATCAGAAACCTAAAACTA TTATTTTAAATACACTCAAACAAGAAGATATTTG
SNP2	C/T	2	6,699,473	TTTCGAGCCCATTATTCACTTAAGAAAACTAGTAAAAAAACTGCACATGTAACAAGA AGCATATTGATTTATTTTTCTGCAAGGATACACCAAAAATCT**[C/T]**ACCATGCATACG TTGAAGTAATGTTCCCAGTTTCCCACATAGAAGTAAAGAATAAGATGTACCAATGGT CATTTTAGTATCTCTACTTGCTTAAGGTACT
SNP3	G/T	2	15,405,209	GCAAAACTAGAATGTACGAGTCTTACTTGGCATCGAACATCATCTAAACTGTACATA ATTTTCAAGTGCCTCTTCAGCTTCCAAAGGAGCTGAAGAGTA**[G/T]**TAGCTGCAAGAC ATACAGCCTATACAAACACCAAAACCTTGATATCACTGGATGCATTACAAACACAGA CAGCCACAAACACCAAAATCTTAATATCACT
SNP4	C/T	2	20,510,300	CACCTCACTTCAAACTAGTTTGCTTTTTTTGCAATACTCCGTTTTATCAAGTTCTACA TATATTCATCAGAGACAGTCAGATGGAATGTCCACATCATT**[C/T]**GATTTGACAACT ATGATGTTGAGCATCAATGCATTGCACGGACTGTGTATGTGAACGATATTCTTTACT ATATTATTTGAACCACTTCTTCTCAGTGTTG
SNP5	A/G	2	25,049,866	CACCTTCCTCCAACGACCGGCGACAACCCATTTTCTCTCTCTCCTTGCCAACGGTAA TGCATGAAGCTTCATATTTCTAATTTTTTTTGGTTACTCATC**[A/G]**AACCCTAATAAT TGGGTGTTTGGGATATAGGTGGCCTAACAGCACCGTACGCCGACCGTATGACTGTC GTCCCTTCTAATTATGTCTCCTCGCCGTCGAT
SNP6	A/G	2	36,998,366	TTCCCTTAATTGCTGCGCGGCCAAAACCACTGCAACAGGCCACTTAACGATAGTAG CAATAAGCATTCGTTCTACTAGTGAGGTTTGAGGACCTAGAGA**[A/G]**AGAATGCCC ACACTACCACAATCTTGACAAGTGGTTCATCACCCATGCATTCTACAATGGTCTCC ATCCCCATCTCAAGAGTATAACTGATTCATCTGCA
SNP7	C/T	2	46,993,083	AATAAGCTAATCAAGAAAACAAACAAAATTCAAGAAAATGCATACATGTAGAGATTA GGAAGTAGCGAATGGTGTGTCAACCTATGTAGAGAATTTGCG**[C/T]**AGAAAAAATTAT TTTAGTGGAAAAAAATTATCTTGAGTGGCACATGTAGACTCTAGTGTTTAGGCGGGGT TTGTGTTGCTTAGATTAGGATGGGTGATGA
SNP8	C/T	2	54,738,552	AGTATTTTGGGTCCGCAGATAGACCAAAATATTCCCAAATGCTGGAAGCGATTAGGT GTTTGCGATCTCAAATGGATCAAATGGCAACCATGCATAATT**[C/T]**GATGATAACTTA TTTAATGGCTTGCAGCCAACAACAAGGCAGCCAATTCACCCAGGAGAAATTGAGAAA GTTCGTGATTCATGGTTCTGGGCTTGGCCAA
SNP9	T/C	6	18,347,119	AAGAGAGCTGGGATTTCCCACCCCAACCCCAAACACATGTACGCAAGCGATGCGCA

				CACATGCATTGGGCATAAAGCAGGAACAGATAGAACGCTGTCC**[T/C]**AAACAATGT CGACTAAGGTAAGCTACAATCAAATTCTATTTTCCAGTAATATATACTAGAAATATC TGACAAGCATTCAGACAAAAGCCCAGTAGCTCGC
SNP10	T/C	6	21,725,867	AAACCACAGCCACGCTAAGAATTCATCTTTCCTGTAAAGACCTTGCTTCGCAAATGC ATCTGCCACAAAGTTTGCATTTCGACATTTGTGAATTATTGA**[T/C]**ATGTCAAGGCCT TCCTTCTAGCATTTCTGATGAAATTTAACTGGAAATTTAAATTCCAAGGTCCTCCGCT TTCACTATTGCACCATGAGACCGCATTGAA
SNP11	T/A	6	63,509,596	AGCAATTTGACGCGATTAAGTTGACTAACTGTCTTTGAGCCTCTGGTGAACTGATGCA TAGTTACTATTTGTGACGAAACTGTGTCTGAAGTGTAGAAT**[T/A]**ATGTAGTTTTCTTT ATATAATAAGTTGAATTGTATACTATTGAAATCAAACTTAGTGGTGACTGTAAGATT GTTACTGCTGAATTGCAGCTCGCACTGAA
SNP12	C/T	6	67,233,702	TCCACAAAAATGAAGCAATTGCAATTAAATTTCGTATAGATCAAAACTAGTTTAGCA AATGTGAGCAACTAACAAGAGACGAAATGTCACAAGTTTGCT**[C/T]**TGTAAGGGTAA TTCACTTCCTACTAAATCATGGTAATAAATCTCGGCCACAACACTACATGCATTGTA AAGGTTCTTAAGCTTATCGCGAAAACCATCTG

* Pseudomolecule position (bp) of each SNP and DNA sequences containing each SNP are according to genomic sequence assembly EL10.2 [28].

Table S2. Validation of F_1 plants using STARP markers developed from the validated SNPs among parental sugarbeet lines.

Cross	Total seed harvested	False F_1s detected
F1024/CR933	11	2
F1024/F1028	9	1
F1024/F1029	24	3
F1024/F1056	4	2
F1024/FC1019	9	0
F1024/FC1740	5	0
F1024/L19	7	2
F1024/L29	6	0
F1024/SP8030	3	1
F1028/F1029	4	0
F1057/F1056	31	4
F1057/L29	7	0
Total	**120**	**15**