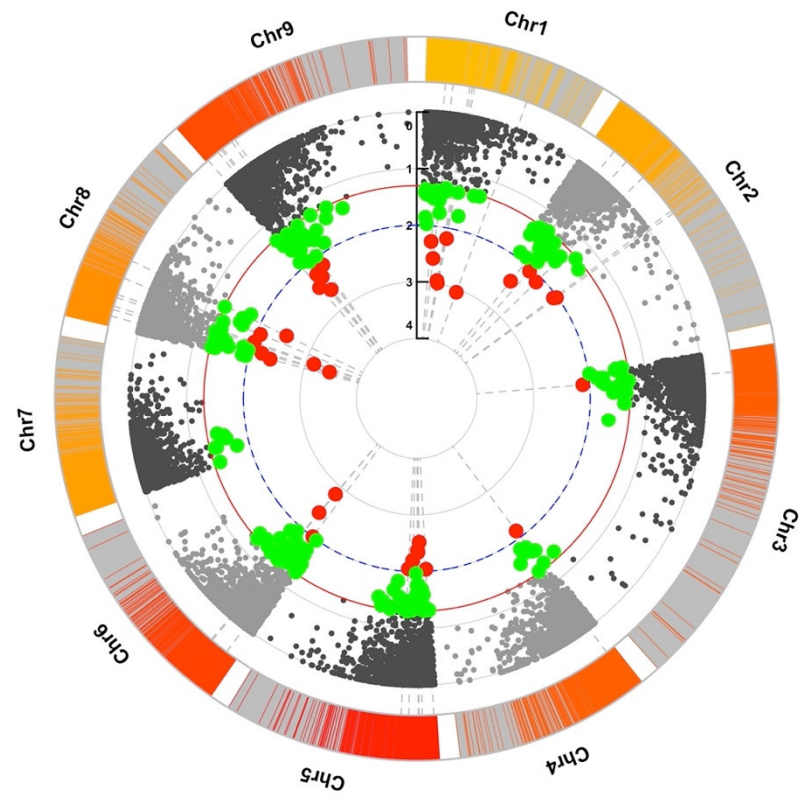
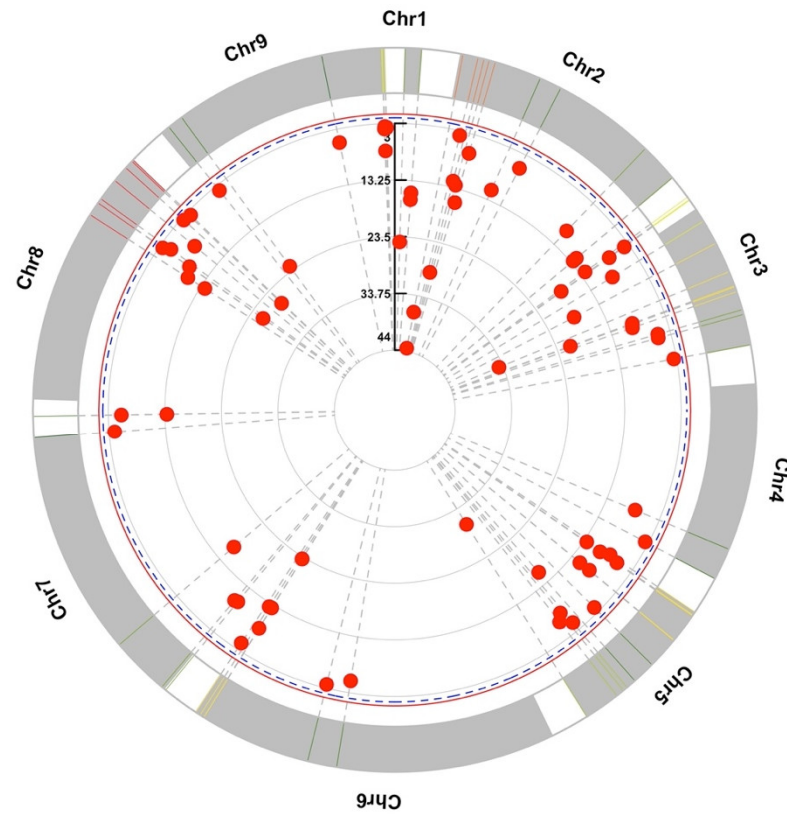




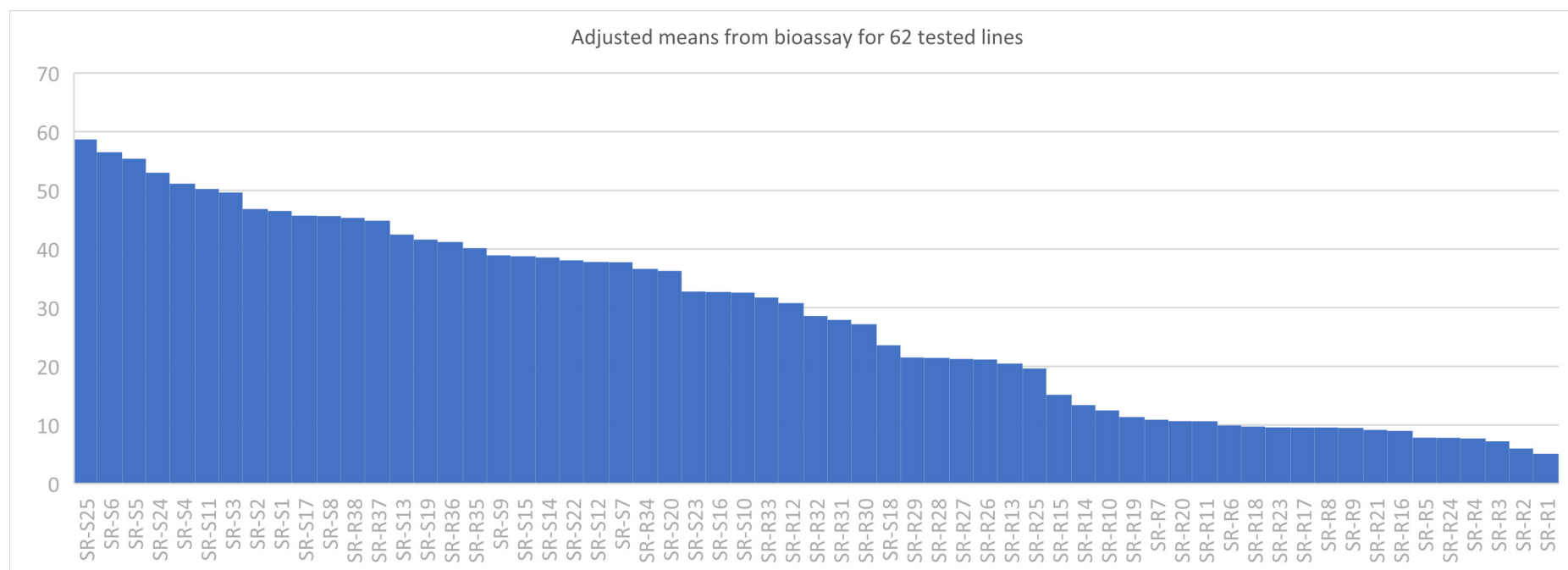
Supplementary Figure S1: *Rhizoctonia* scoring scale for phenotyping done in SBSI, Iran.



Supplementary Figure S2: Circular Manhattan plot from association analysis showing significantly associated SNPs from SBSI dataset distributed across the EL10 sugar beet reference genome. SNPs highlighted in green have a p-value ≤ 0.05 and SNPs highlighted in red have a p-value ≤ 0.01 .



Supplementary Figure S3: Circular Manhattan plot from association analysis on Strube Research germplasm highlighting mutually occurring significant SNPs with the association analysis from SBSI dataset. SNPs highlighted in red were identified as strongly discriminating the contrasting phenotypes with a p-value ≤ 0.01 .



Supplementary Figure S4: Adjusted means of 62 breeding lines (including standards and controls) from *Rhizoctonia* bioassay.

Supplementary Table S1: Sequences of top 60 significantly associated SNPs discriminating resistant and susceptible phenotypes from the bioinformatics analyses.

SNP	Sequence	SNP position	Reference allele	Alternate allele
SNP26	TGCAGTGATCTCTTTTCATGTTGTATTGCTCTATAGCGTACACGACCATGTTGGCACTCCAA CCACTTGA	61	A	T
SNP32	TGCAGAAGATGGAAGGCAGCAAAATATTTCTTCATACCATCATCGTCATAATCATCTAAA TATCTGGGG	66	G	A
SNP125	TGCAGATCATACAAGGTATTCCAAATGCAACTGCTGTGCAGCTTGATGTGTCAGACCAAG AGAGTTTGC	6	A	G
SNP116	TGCAGGTTCGTCTACCACTAAACGTCTTCTTACCAGTTCTGTTACAGATCGGAAGAGCGGT TCAGCAGG	9	C	T
SNP4	TGCAGAGCCGCTACTCACCGCTGCCTGTTCTTATCTCTCCTCTGTTGAAGTTCCTTTTTCTT CTTTTAT	62	T	C
SNP81	TGCAGTATGTACACAAAAGGATCAGCCAATCTTAGACTACAGCTAACCAAGCAAAACAA AGAACTTCAA	30	T	C

SNP12 6	TGCAGTGGTACCGAGTGTGCCCTTTGGTTTTTGCAATACTGCATAATTTTACCTGGTTTGC CTCCATTA	12	C	T
SNP47	TGCAGAAGAACATATATCATTAGCTTACCAAAATTACAGATCGGAAGAGCGGTTTCAGCAG GAATGCCGA	20	T	C
SNP62	TGCAGAAGCACAAGATGAAGAGGAGCAAGATGAGGAGATGCTGCGCAGTTCGTGCTGCA ACCAGAGTAC	45	G	A
SNP75	TGCAGTTTTGGGACACTTGACTTGTATATCAACTGAACTTTCGCCACAAGTTTGGTACAGA TTACTCAG	13	A	G
SNP43	TGCAGTTTTGGGGCACTTGACTTGTATATCAACTGAACTTTGGCCACAAGTTTGGTACAGA TTACTCAG	21	C	A
SNP53	TGCAGTCAGAAGAAATGCAGCAGCCCAGGTGATCGCCAGACCCAAGGGAACCTGACAAC AGCTTATTAG	34	C	T
SNP16	TGCAGATTTTTCTCCACGCATCTAGCAAACTCTGAAAGCTACCAGTGGTGAATTGCTGAT TTTTCAAC	27	A	T
SNP19	TGCAGTCTTGTGGAGATAAGGCTGGATTAGCGTGTTTTGAATATTTACAGATCGGAAGAG CGGTTTCAGC	30	G	C
SNP86	TGCAGCTGAAGCACGACCCACAGACCACCAAGGAGCATGGGCCTTGTGACATATACAGC CACTAGCATC	51	A	G

SNP21	TGCAGCCAATTCACTGGTGGGCTTTTGCTGATACAATGTTTCATAGAAAATCCTCAAAGG ATCTCTCTG	52	C	T
SNP91	TGCAGTTTTGTTAGATTCTGAAGATTCATGATGCCAATAAATTGACATTTATTGTTCTTGA TTGAATTG	66	A	C
SNP18	TGCAGTTATGACATGGCAACATGCATAGCAGAAAAATTACAGATCGGAAGAGCGGTTCA GCAGGAATGC	31	G	C
SNP15	TGCAGTAAAAAAGTTCCAAAGATGGGAATGGCACCTTCTTTTTTACAGATCGGAAGAGCG GTTTCAGCAG	32	C	T
SNP71	TGCAGACTATAATGCAAATCTTAGTTGCTTCCCTCTTCTCTTCTATTATTCTATGAGGTGT GATGATA	51	T	A
SNP17	TGCAGTCTAAGTACTTGATATTTATTTGCTTCCTAAAATACACCTTTCCTGTAATTATGT GAGTATT	27	T	C
SNP11 3	TGCAGGCCTTGGCAATCCTGAGCTTTCTCATTACAAGTTGAACCTACAAGAAAGTGCTTCT AACAGAAG	47	C	A
SNP72	TGCAGGCATAGAGAGGAATGATGCAAATTGTCTGAGAAGGCTATATTACAGATCGGAAG AGCGGTTTCAG	29	T	C
SNP58	TGCAGATCCAAAGACAAAAGAGGATGTACACAAAGTGCCTAACAGGGAGACGCTCACCT TGTAAGTTCT	51	C	A

SNP20	TGCAGTGATCGCTCCCAAGAAGGCCTGGACAGGGGATGGGGTTTTAGATTCAATCGAGAC TGATCCAAT	10	C	T
SNP34	TGCAGCAGGAGTTGTCTGCTGCTAAAACAGAAGTAAACAGAGTTGAGTCAAGTATGGCTG ATGCATTAT	14	G	A
SNP29	TGCAGCCGCGACTAGCTGCACCGGTGGAGTACCAACAGAGATTTGCATAAGGAAATCTCC CTCATTAGG	63	C	G
SNP1	TGCAGCCGTTTTCTTACTTTTCCTACTCTACTATCTTTCCAGCCACAACGAGGCAAAAACA CCAAACTC	24	T	C
SNP55	TGCAGTTACATTTTTGCCCTCTTTATTCGTCGCTTTCTCCACTATTTACGTTTCATTCCAA GTATCCA	57	T	A
SNP12	TGCAGATGATTTGGCTTGCTCCCTGAACCCCTCCTAGAAAGGTGGCAGGAAGTTACAGATC GGAAGAGCG	6	A	G
SNP23	TGCAGTCTGATGACCATTGTTGCAACTCTTGTGAAGAAGTTCGTGAGGCTTACAGAAAGA AGGGCTGGG	65	C	A
SNP50	TGCAGAAAACTTGACTTCAGAAGATTTACTACCCTCTTTGTGGGATAAATGCAAGGTGA GCAAAATCA	26	T	C
SNP96	TGCAGATTATGAAATACACATGTATGATTGTATAAATTGATGGTATATTGTGGTGTATTTT TAGGTGGA	17	C	T

SNP24	TGCAGAAAATGTATTTTCCTTCCTTCCAACATTTTCCCATATCAACTTCATTACAGATCGGA AGAGCGGT	30	A	G
SNP42	TGCAGAAATTGCTTTACGGTTATCCAGATAAACAAGAAGATGACTAAAATATTCTCTAAC CATGAGGTC	54	C	T
SNP69	TGCAGCATCAGCGATGCTTATTTGCATTGAGTGGATTACAGATCGGAAGAGCGGTTCAGC AGGAATGCC	11	G	A
SNP11 0	TGCAGCATCAGTGATGCTTATTTGCATTGAGTGGATTACAGATCGGAAGAGCGGTTCAGC AGGAATGCC	12	T	C
SNP64	TGCAGCATCTGACATTTGAGAACTGGTGAAATATTTTCAGCACATATTCTTGCGACAACA ATGCGCTCA	65	G	A
SNP8	TGCAGACTACATAAATGCACGGGGGTTAGAATATATGTGTGCCTCTGAAAGACTGAAACA ACATTTTAC	69	C	G
SNP67	TGCAGATATCTCAAATCTGGATAACAGAAAATCAAAGATCCGTGGATGCGTATTACAGA TCGGAAGAG	12	C	G
SNP59	TGCAGATATCTGAAAATCTGGATAACAGAAAATCAAACATCCGTGGATGCGTATTACAGA TCGGAAGAG	38	C	G
SNP56	TGCAGCCACCTATTCCATTTTCATGGACGTATCACTCTGACCTCATTAGAGCTGCTCATCA GACTGGAG	29	G	T

SNP13 0	TGCAGAAAGCTTCAGCTTTGCTCTACCTAAATTTCAATCTTTCTTGAGTTCGTAGGGGTTC AAGCCTGC	23	C	T
SNP10 4	TGCAGATATGGAATCGAGAGTGAATGAAAATGTATGGCAACGATTTGGGATTGAGCAAC ATCCTCCGCG	41	C	A
SNP49	TGCAGGGTTGCTTGGAGCTTGTTGCCAGGTACTGGTGCTCGGATTATTGCTTTGGTGGGT GGTCCTTG	67	T	A
SNP41	TGCAGAGTTGTCTTTCCTGCAACTCTAATCTTTAGGGAAATCCCCAATGATAGGCTCCTAT TTTTTAGA	24	T	C
SNP60	TGCAGCAAGGACAACCTCCGTGCACATTGGATGTTGGGCAAAAACCAATAGCTGACATTTG ATTCAGCAA	18	C	T
SNP46	TGCAGAAGTTTGGATTCTGAGAATAATAGTTGCTATGTTTTTTATGGTGGAATTCTCAAT ACTCCGAA	49	G	A
SNP51	TGCAGGATATTGCATTTTCATCGGTATAATGGGGTTCACGTTATTGGAAGATGCACAGGAG AATTTGTAC	55	C	T
SNP57	TGCAGCTATGGTGCATAAACAAAAGGGGTCCAGTTTTTGCTGCAATGTTTACAGATCGGA AGAGCGGT	41	T	C
SNP70	TGCAGCCCAGATTCCCTCCTTAGAACAACACTCATTTATTAGGTTACAGATCGGAAGAGC GGTTCAGCA	14	C	T

SNP11 9	TGCAGAACTTCGTTTACTCTTATGATTCCCCGAGCTAGCTTTGCAACATCCATGGAAAGGG AGTTGGAA	56	A	C
SNP10 9	TGCAGGTACTTACGGGCGAAGCAAGTCTACCATCAGTCCCTTTTGAGAAGCCTGCCTTTGT ATGGCCAG	14	G	A
SNP94	TGCAGGAGTCGATTCCAACCAACGCCACAAATTTTAGATGGTTGCATTTCACTGTTGGCA GAAGGTATT	10	C	T
SNP22	TGCAGTATAGAATGATAATTCCTAGTCTTGGTGATAATGTCCGGGTAATAAAATCTAATT CCTAGTTT	43	G	A
SNP7	TGCAGAAAAAAGCGCAGATGAAAGAAAAGAAACATATTCTTTACAGATCGGAAGAGCGG TTCAGCAGGA	13	C	T
SNP27	TGCAGCAAGTTCAATACCAACCGTTACTATATCCAAGATTTCTAAAAGGGGATAGAAGTA GCTTTACAG	41	T	C
SNP76	TGCAGGTACATATGATAATTGATATGGCAGAAATGATTGCTTCAAGTAGTGTCCATTTAG GGAATTTTA	38	T	A
SNP93	TGCAGATACAAGATATACCAAAAACAAAAAACAAAAACATAGCATATCTTGTA AAAAGAT GGATCTAATT	24	C	T
SNP10 2	TGCAGCACAAATAAATGGCGTGCTTTATGTTGTTGGTGGATATGATGGAAGTGTATACCT AGGGTAAGC	23	A	C

Supplementary Table S2: Ruppel scores (Scholten et al., 2001) of USDA releases from field rating done in 2018 used for validation of SNP93.

<i>Release</i>	<i>FC709-2</i>	<i>FC709-2</i>	<i>FC709-2</i>	<i>FC703</i>	<i>FC703</i>	<i>FC703</i>	<i>FC901/C817</i>	<i>FC901/C817</i>	<i>FC901/C817</i>
<i>genotype</i>	20121034	20121034	20121034	20041005	20041005	20041005	20141002	20141002	20141002
<i>Replicate</i>	Rep1	Rep2	Rep3	Rep1	Rep2	Rep3	Rep1	Rep2	Rep3
<i>field plot</i>	2002	2040	2070	2001	2041	2063	2000	2034	2064
<i>Plant 1</i>	1	3	1	1	3	4	5	6	5
<i>Plant 2</i>	1	2	2	2	3	3	6	5	1
<i>Plant 3</i>	1	2	1	1	2	3	5	7	2
<i>Plant 4</i>	1	1	2	1	2	3	5	6	4
<i>Plant 5</i>	2	2	1	3	1	3	5	5	4
<i>Plant 6</i>	1	1	3	4	3	3	4	7	3
<i>Plant 7</i>	2	2	2	1	2	4	6	4	4
<i>Plant 8</i>	0	4	2	3	4	4	6	6	4

Supplementary Table S3: rhAmp allelic discrimination assay details for SNP93 testing.

Primer	Sequence
Allele Specific Primer 1 :	TGCTGCAGATACAAGATATATCAAAAC
Allele Specific Primer 2 :	ATGCTGCAGATACAAGATATATCAAAAT
Locus Specific Primer :	GCAAGTCTGAATTTCTGATCTCATCTTTA