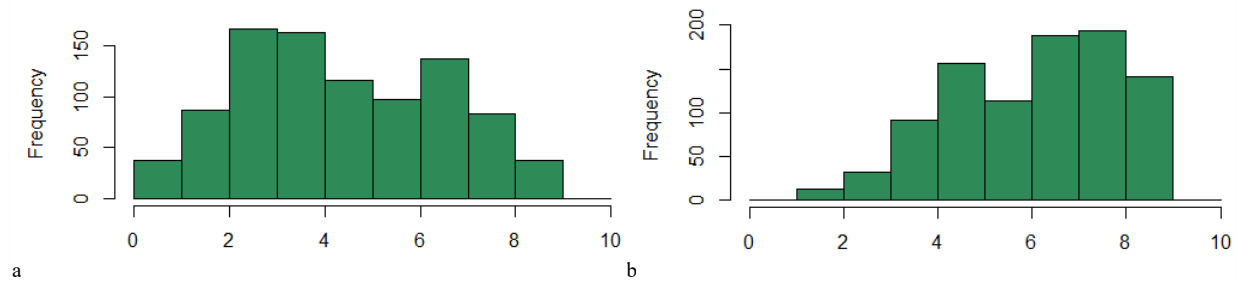
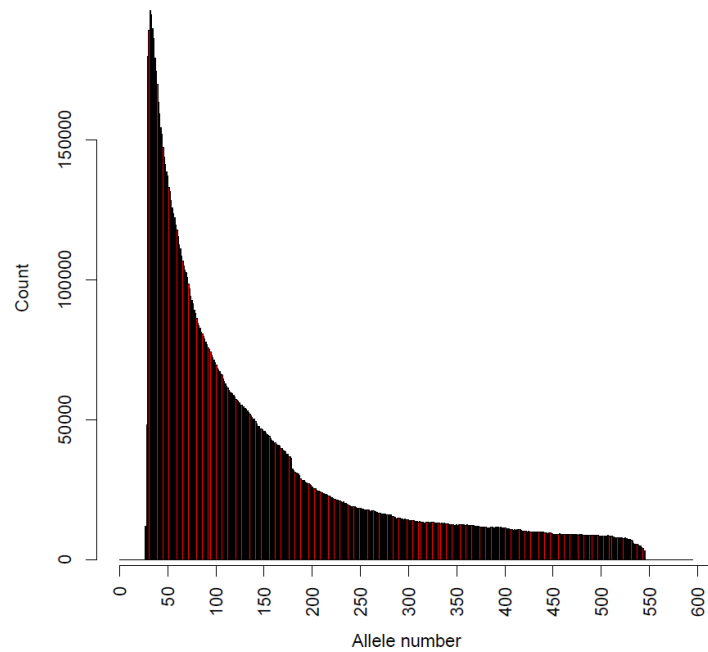


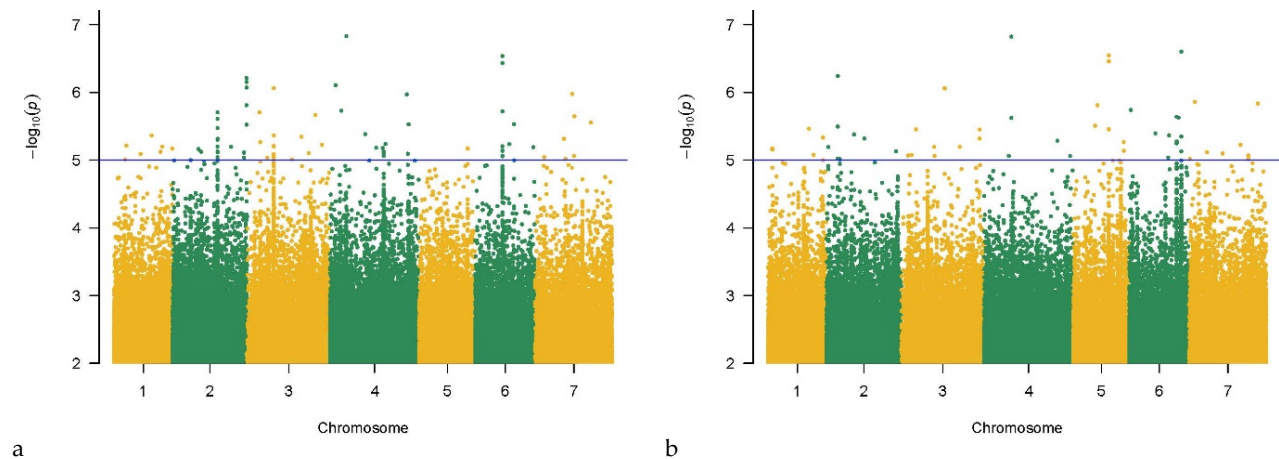
**Figure S1.** Flowchart of population development.



**Figure S2.** Phenotypic distribution among the 1,000 genotypes of crown (a) and brown rust (b). The x-axis refers to the scale used for the disease scoring, where 1 refers to heavy attack (high susceptibility of perennial ryegrass) and 9 corresponds to no rust infection (high tolerance).



**Figure S3.** Site Frequency Spectrum (SFS) plot. Distribution of allele frequencies of the SNP loci in the population



**Figure S4.** Manhattan plot GWAS results of CRR (a) and BRR (b). On the x-axis, the 7 chromosomes are reported in alternating colours. The blue horizontal line indicates the arbitrary cutoff of  $-\log_{10}(p\text{-value})=5$ .

**Table S1.** List of SNPs associated with CR. Selected markers with a  $p$ -value above the arbitrary threshold  $-\log_{10}(p\text{-value})>5$ .

SNPs ID	Chr	Position (bp)	p-value
Gcta-snp-1.1	1	50,888,681	8.82976e-06
Gcta-snp-1.2	1	57,202,120	6.85289e-06
Gcta-snp-1.3	1	123,289,042	7.1705e-06
Gcta-snp-1.4	1	17,455,1781	4.39621e-06
Gcta-snp-1.5	1	216,254,732	7.8503e-06

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Gcta-snp-1.6	1	223,812,092	6.54172e-06
Gcta-snp-1.7	1	270,501,016	7.68761e-06
Gcta-snp-2.1	2	84,442,240	9.82199e-06
Gcta-snp-2.2	2	120,467,462	7.239e-06
Gcta-snp-2.3	2	132,102,685	8.4921e-06
Gcta-snp-2.4	2	208,763,776	1.8167e-06
Gcta-snp-2.5	2	208,763,879	6.0652e-06
Gcta-snp-2.6	2	208,765,282	8.73605e-06
Gcta-snp-2.7	2	208,806,413	9.51495e-06
Gcta-snp-2.8	2	208,810,723	9.9128e-06
Gcta-snp-2.9	2	208,811,051	3.20473e-06
Gcta-snp-2.10	2	208,829,396	8.9686e-06
Gcta-snp-2.11	2	208,834,020	2.23917e-06
Gcta-snp-2.12	2	208,834,440	4.63526e-06
Gcta-snp-2.13	2	208,848,996	7.28031e-06
Gcta-snp-2.14	2	209,769,507	4.5522e-06
Gcta-snp-2.15	2	271,678,020	6.66405e-06
Gcta-snp-2.16	2	331,778,177	9.69674e-06
Gcta-snp-2.17	2	331,831,873	8.31896e-06
Gcta-snp-2.18	2	343,028,606	8.33522e-07
Gcta-snp-2.19	2	343,028,650	6.93544e-07
Gcta-snp-2.20	2	343,029,116	5.74696e-07
Gcta-snp-3.1	3	56,959,112	1.83089e-06
Gcta-snp-3.2	3	123,400,748	7.75118e-07
Gcta-snp-3.3	3	123,493,806	4.20124e-06
Gcta-snp-3.4	3	123,499,279	9.91972e-06
Gcta-snp-3.5	3	123,511,283	5.67409e-06
Gcta-snp-3.6	3	251,948,944	4.38419e-06
Gcta-snp-3.7	3	285,814,253	7.77014e-06
Gcta-snp-3.8	3	316,837,904	2.28292e-06
Gcta-snp-3.9	3	347,482,523	6.66388e-06
Gcta-snp-4.1	4	26,602,446	8.24678e-07
Gcta-snp-4.2	4	53,000,213	2.20674e-06
Gcta-snp-4.3	4	76,349,694	1.57119e-07
Gcta-snp-4.4	4	163,621,753	3.93225e-06
Gcta-snp-4.5	4	214,582,294	6.8227e-06
Gcta-snp-4.6	4	244,680,870	7.4836e-06
Gcta-snp-4.7	4	249,794,945	4.76004e-06
Gcta-snp-4.8	4	257,511,725	5.6311e-06
Gcta-snp-4.9	4	356,839,682	1.14406e-06
Gcta-snp-4.10	4	361,318,775	8.68191e-06
Gcta-snp-4.11	4	365,157,378	3.22589e-06
Gcta-snp-5.1	5	224,633,296	6.94505e-06
Gcta-snp-6.1	6	126,252,299	8.77432e-06
Gcta-snp-6.2	6	126,253,264	7.34757e-06
Gcta-snp-6.3	6	126,253,475	6.38375e-06
Gcta-snp-6.4	6	126,254,672	3.6641e-07

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<b>Gcta-snp-6.5</b>	6	126,255,271	4.86194e-06
<b>Gcta-snp-6.6</b>	6	158,207,491	6.63217e-06
<b>Gcta-snp-6.7</b>	6	270,303,728	5.81906e-06
<b>Gcta-snp-7.1</b>	7	43,143,239	9.11627e-06
<b>Gcta-snp-7.2</b>	7	172,435,701	1.07606e-06
<b>Gcta-snp-7.3</b>	7	181,138,453	9.07996e-06
<b>Gcta-snp-7.4</b>	7	183,420,642	2.32578e-06
<b>Gcta-snp-7.5</b>	7	259,535,462	2.9603e-06

**Table S2.** List of genes associated with CRR. Gene ID refers to the name of the gene, Chr refers to the chromosome where the gene is located, START and STOP refer to the gene's first and last nucleotide position on the chromosome, and Gene size refers to the gene size in bp.

<b>Gene ID</b>	<b>Chr</b>	<b>START</b>	<b>STOP</b>	<b>Gene size (bp)</b>
<b>Lp_chr1_0.12850</b>	chr1	174,544,889	174,548,709	3820
<b>Lp_chr1_0.12851</b>	chr1	174,550,364	174,551,550	1186
<b>Lp_chr1_0.16593</b>	chr1	223,810,306	223,812,121	1815
<b>Lp_chr2_0.6271</b>	chr2	84,445,123	84,448,803	3680
<b>Lp_chr2_0.8753</b>	chr2	120,466,171	120,468,611	2440
<b>Lp_chr2_0.24844</b>	chr2	343,028,981	343,029,284	303
<b>Lp_chr2_0.24845</b>	chr2	343,029,675	343,033,480	3805
<b>Lp_chr3_0.8551</b>	chr3	123,396,008	123,396,638	630
<b>Lp_chr3_0.8552</b>	chr3	123,400,198	123,400,828	630
<b>Lp_chr3_0.17611</b>	chr3	251,942,496	251,944,253	1757
<b>Lp_chr3_0.20045</b>	chr3	285,813,172	285,815,144	1972
<b>Lp_chr3_0.24613</b>	chr3	347,481,574	347,482,756	1182
<b>Lp_chr3_0.24615</b>	chr3	347,485,871	347,488,371	2500
<b>Lp_chr4_0.2271</b>	chr4	26,600,949	26,602,802	1853
<b>Lp_chr4_0.6124</b>	chr4	76,351,602	76,351,911	309
<b>Lp_chr4_0.6125</b>	chr4	76,353,862	76,356,228	2366
<b>Lp_chr4_0.18309</b>	chr4	244,684,987	244,688,942	3955
<b>Lp_chr4_0.19179</b>	chr4	257,503,274	257,507,594	4320
<b>Lp_chr4_0.19180</b>	chr4	257,508,178	257,509,165	987
<b>Lp_chr4_0.19181</b>	chr4	257,513,104	257,514,895	1791
<b>Lp_chr6_0.9029</b>	chr6	126,251,598	126,256,062	4464
<b>Lp_chr7_0.1.18459</b>	chr7	259,529,572	259,531,605	2033

**Table S3.** BLAST-N information of genes identified using GCTA and MAGMA for CRR. Expected Value (E-value) refers to the number of expected hits of similar quality that could found just by chance with the calculated score. Coverage (Cov) refers to the percent of the query length included in the aligned segments. Identity (I) refers to the highest percent identity for a set of aligned segments to the same subject sequence.

<b>Gene ID</b>	<b>Organism</b>	<b>E-value</b>	<b>Cov (%)</b>	<b>I (%)</b>	<b>Accession number</b>	<b>Putative function</b>
<b>Lp_chr1_0.12850 (GCTA)</b>	<i>A. tauschii</i>	0	100	90.53	XM_020337866.1	protein root UVB sensitive 6-like

Lp_chr1_0.12851 (GCTA)	<i>A. tauschii</i>	3.00e-112	66	80.22	XM_020323781.1	wall-associated receptor kinase
Lp_chr1_0.16593 (GCTA)	<i>B. distachyon</i>	0	99	87.55	XM_003568324.4	tubby-like protein
Lp_chr2_0.6271 (GCTA)	<i>A. tauschii</i>	0	99	93.76	XM_020335834.1	cinnamate 4-monooxygenase-like
Lp_chr2_0.22569 (MAGMA)	-	-	-	-	-	
Lp_chr2_0.24844 (GCTA, MAGMA)	-	-	-	-	-	
Lp_chr2_0.24845 (GCTA)	<i>A. tauschii</i>	0	47	86.75	XM_020322177.1	a transmembrane receptor protein kinase TMK1
Lp_chr2_0.8753 (GCTA, MAGMA)	<i>B. distachyon</i>	3.00e-04	2	97.14	XM_024461354.1	
Lp_chr3_0.8552 (GCTA)	<i>A. tauschii</i>	0	100	91.08	XM_020298474.1	VQ motif
Lp_chr3_0.8555 (GCTA- MAGMA)	<i>Avena strigosa</i>	0	62	84.90	DQ680849.1½	Sad1 and Sad2
Lp_chr3_0.17805 (GCTA, MAGMA)	<i>A. tauschii</i>	0	96	80	XM_020296375.1	oxygenase called indole-3-pyruvate monooxygenase (YUCCA10)
Lp_chr3_0.20704 (GCTA)	<i>L. perenne</i>	0	97	94.15	KY771172.1	beta-1-6-glucanase-like protein
Lp_chr3_0.20827 (MAGMA)	<i>A. tauschii</i>	0	91	81.12	XM_020342790.1	4hydroxyphenylacetaldehyde oxime monooxygenase-like
Lp_chr4_0.2271 (GCTA, MAGMA)	<i>A. tauschii</i>	0	96	87.01	XM_020293186.1	NRT1/PTR family 5.7-like
Lp_chr4_0.6084 (GCTA)	<i>A. tauschii</i>	0	64	86.05	XM_003560396.4	phosphatidylinositol transfer
Lp_chr4_0.6125 (GCTA)	<i>A. tauschii</i>	0	91	77.39	XM_020318203.1	chaperone protein ClpB1-like.
Lp_chr4_0.18630 (GCTA, MAGMA)	<i>A. tauschii</i>	0	99	87.81	XM_020306365.1	metacaspase-1-like.
Lp_chr4_0.18634 (GCTA, MAGMA)	<i>A. tauschii</i>	0	100	84.44	XM_020298243.1	metacaspase-1-like.
Lp_chr4_0.19180 (GCTA)	<i>A. tauschii</i>	0	100	87.78	XM_020343272.1	pentatricopeptide repeat (PRR) proteins
Lp_chr4_0.20313 (GCTA)	<i>A. tauschii</i>	0	66	86.02	XM_020296375.1	oxygenase called indole-3-pyruvate monooxygenase (YUCCA10)

<b>Lp_chr5_0.16081 (MAGMA)</b>	<i>A. tauschii</i>	2.00e-33	8	82.97	KY771172.1	beta-1-6-glucanase-like protein.
<b>Lp_chr6_0.9029 (GCTA, MAGMA)</b>	<i>A. tauschii</i>	0	100	93.39	XM_020321879.1	plastid casein kinase 2 (CK2)
<b>Lp_chr7_0.1.9979 (GCTA)</b>	<i>L. perenne</i>	6.00e-07	2	100	KY771172.1	beta-1-6-glucanase-like protein.
<b>Lp_chr7_0.1.11324 (GCTA)</b>	<i>B. distachyon</i>	0	100	86.13	XM_003574460.4	ubiquitin receptor RAD23.
<b>Lp_chr7_0.1.24966 (MAGMA)</b>	<i>Triticum dicoccoides</i>	0	96	82.60	XM_037607392.1	Disease resistance protein Pik-2.

**Table S4.** List of SNPs associated with BRR. Selected markers with a  $p$ -value above the arbitrary threshold  $-\log_{10}(p\text{-value}) > 5$ .

<b>SNP ID</b>	<b>Chr</b>	<b>position</b>	<b>p-value</b>
BR-Gcta-snp-1.1	1	20,121,295	6.98e-01
BR-Gcta-snp-1.2	1	20,121,300	6.57e-01
BR-Gcta-snp-1.3	1	189,974,240	3.56e-01
BR-Gcta-snp-1.4	1	211,929,165	9.57e-01
BR-Gcta-snp-1.5	1	255,276,992	4.56e-01
BR-Gcta-snp-2.1	2	8,243,648	6.30e-01
BR-Gcta-snp-2.2	2	52,157,077	3.17e-01
BR-Gcta-snp-2.3	2	52,180,401	9.51e-01
BR-Gcta-snp-2.4	2	52,180,410	6.12e-02
BR-Gcta-snp-2.5	2	61,858,721	9.92e-01
BR-Gcta-snp-2.6	2	127,577,619	4.62e-01
BR-Gcta-snp-2.7	2	175,999,676	4.94e-01
BR-Gcta-snp-2.8	2	323,147,284	8.09e-01
BR-Gcta-snp-3.1	3	32,254,304	8.91e-01
BR-Gcta-snp-3.2	3	48,819,030	7.89e-01
BR-Gcta-snp-3.3	3	68,544,650	3.42e-01
BR-Gcta-snp-3.4	3	152,867,482	6.66e-02
BR-Gcta-snp-3.5	3	154,994,124	9.03e-01
BR-Gcta-snp-3.6	3	201,638,596	8.82e-02
BR-Gcta-snp-3.7	3	271,821,353	6.63e-01
BR-Gcta-snp-3.8	3	363,850,690	5.40e-01
BR-Gcta-snp-4.1	4	116,156,855	8.11e-01
BR-Gcta-snp-4.2	4	127,117,474	2.39e-02
BR-Gcta-snp-4.3	4	127,117,513	1.44e-02
BR-Gcta-snp-4.4	4	339,683,441	5.37e-01
BR-Gcta-snp-4.5	4	399,341,149	8.16e-01
BR-Gcta-snp-5.1	5	101,345,714	3.42e-01
BR-Gcta-snp-5.2	5	112,656,442	1.69e-01
BR-Gcta-snp-5.3	5	164,117,281	3.77e-01
BR-Gcta-snp-5.4	5	164,899,699	3.58e-02

BR-Gcta-snp-5.5	5	233,960,573	5.79e-01
BR-Gcta-snp-5.6	5	234,361,710	7.44e-01
BR-Gcta-snp-6.1	6	7,336,647	1.86e-01
BR-Gcta-snp-6.2	6	121,008,266	4.23e-01
BR-Gcta-snp-6.3	6	180,310,095	9.58e-01
BR-Gcta-snp-6.4	6	184,483,550	4.34e-01
BR-Gcta-snp-6.5	6	219,585,587	2.51e-01
BR-Gcta-snp-6.6	6	219,586,506	5.76e-01
BR-Gcta-snp-6.7	6	227,975,953	2.51e-01
BR-Gcta-snp-6.8	6	241,419,154	7.54e-01
BR-Gcta-snp-7.1	7	27,365,296	1.38e-01
BR-Gcta-snp-7.2	7	83,124,103	7.53e-01
BR-Gcta-snp-7.3	7	156,537,933	8.19e-01
BR-Gcta-snp-7.4	7	238,806,220	6.23e-01
BR-Gcta-snp-7.5	7	275,454,738	9.88e-01
BR-Gcta-snp-7.6	7	27,5494,480	8.77e-01
BR-Gcta-snp-7.7	7	319,181,966	1.44e-01

**Table S5.** List of genes associated with BRR. Gene ID refers to the name of the gene Chr refers to the chromosome where the gene is located, START and STOP refer to the gene's first and last nucleotide position on the chromosome, and Gene size refers to the gene size in bp.

Gene ID	Chr	START	STOP	Gene size (bp)
Lp_chr1_0.1542	chr1	20,120,371	20,121,325	954
Lp_chr1_0.18994	chr1	255,276,205	255,278,383	2,178
Lp_chr1_0.18995	chr1	255,281,635	255,290,751	9,116
Lp_chr2_0.622	chr2	8,234,314	8,239,230	4,916
Lp_chr2_0.623	chr2	8,240,880	8,244,851	3,971
Lp_chr2_0.3894	chr2	52,178,587	52,182,215	3,628
Lp_chr2_0.3895	chr2	52,184,051	52,184,678	627
Lp_chr2_0.23247	chr2	323,143,203	323,146,714	3,511
Lp_chr2_0.23248	chr2	323,151,743	323,152,142	399
Lp_chr3_0.3323	chr3	48,815,776	48,816,132	356
Lp_chr3_0.25825	chr3	363,840,342	363,847,474	7,132
Lp_chr3_0.25826	chr3	363,848,840	363,852,037	3,197
Lp_chr4_0.29466	chr4	399,338,819	399,341,984	3,165
Lp_chr4_0.29467	chr4	399,343,955	399,344,255	300
Lp_chr5_0.11861	chr5	164,112,771	164,114,235	1,464
Lp_chr5_0.11862	chr5	164,117,453	164,119,064	1,611
Lp_chr5_0.11921	chr5	164,901,677	164,902,350	673
Lp_chr5_0.16787	chr5	234,358,978	234,359,638	660
Lp_chr6_0.596	chr6	7,338,230	7,341,436	3,206
Lp_chr6_0.15799	chr6	219,584,326	219,586,833	2,507
Lp_chr6_0.15800	chr6	219,587,444	219,589,409	1,965
Lp_chr7_0.1.1922	chr7	27,361,869	27,366,349	4,480
Lp_chr7_0.1.6143	chr7	83,126,037	83,126,433	396

Lp_chr7_0.1.11390	chr7	156,531,318	156,533,534	2,216
Lp_chr7_0.1.19634	chr7	275,454,123	275,455,236	1,113
Lp_chr7_0.1.19642	chr7	275,494,595	275,495,775	1,180
Lp_chr7_0.1.22707	chr7	319,181,319	319,183,513	2,194

**Table S6.** BLAST-N information of genes identified using GCTA and MAGMA for BRR. Expected Value (E-value) refers to the number of hits of similar quality that could be found just by chance. Coverage (Cov) refers to the percent of the query length included in the aligned segments. Identity (I) refers to the highest percent identity for a set of aligned segments to the same subject sequence.

Gene ID	Organism	E value	Cov (%)	I (%)	Accession number	Putative function
evm.model.Lp_chr1_0.1542 (GCTA)	<i>A. tauschii</i>	8e-153	88	78.87	XM_020345349.1	wall-associated receptor kinase (WAK)
evm.model.Lp_chr1_0.1598 (MAGMA)	<i>A. tauschii</i>	0	94	82.97	XM_020341457.1	disease resistance protein RPM1-like
evm.model.Lp_chr1_0.2823 (MAGMA)	-	-	-	-	-	-
evm.model.Lp_chr1_0.18994 (GCTA)	<i>A. tauschii</i>	7e-157	48	77.05	XM_020327116.1	BPT/POZ and MATH domain-containing protein
evm.model.Lp_chr1_0.18995 (GCTA)	<i>A. tauschii</i>	0	92	91.49	XM_020296114.1	Protein timeless homolog
evm.model.Lp_chr2_0.622 (GCTA)	<i>T. dicoccoides</i>	0	82	79.78	XM_037619652.1	Putative FBD-associated F-box protein At3g50710
evm.model.Lp_chr2_0.623 (GCTA)	<i>T. dicoccoides</i>	0	85	8538.66	XM_037619698.1	Beta-1,4-xylosyltransferase IRX9
evm.model.Lp_chr2_0.3894 (GCTA, MAGMA)	<i>B. distachyon</i>	1e-141	63	82.52	XM_003562573.3	serine/arginine-rich SC35-like
evm.model.Lp_chr2_0.3895 (GCTA)	<i>B. distachyon</i>	1e-48	89	79.57	XM_003572657.4	S-noroclaurine synthase.
evm.model.Lp_chr2_0.19756 (MAGMA)	<i>A. tauschii</i>	0	99	87.23	XM_020329468.1	uncharacterized
evm.model.Lp_chr2_0.23247 (GCTA)	<i>A. tauschii</i>	0	100	84.17	XM_020330933.1	codifies for AP2-like ethylene-responsive



						transcription factor AIL5
evm.model.Lp_chr2_0.23248 (GCTA)	-	-	-	-	-	-
evm.model.Lp_chr3_0.8432 (MAGMA)	-	-	-	-	-	-
evm.model.Lp_chr3_0.8507 (MAGMA)	<i>A. tauschii</i>	0	51	86.23	XM_020315688.1	xaa-Pro dipeptidase-like
evm.model.Lp_chr3_0.25825 (GCTA)	<i>A. tauschii</i>	0	96	88.79	XM_020339997.1	NAD kinase 1
evm.model.Lp_chr3_0.25826 (GCTA, MAGMA)	<i>A. tauschii</i>	0	97	87.16	XM_020339996.1	inactive leucine-rich repeat receptor-like protein kinase At5g48380.
evm.model.Lp_chr3_0.3323 (GCTA)	-	-	-	-	-	-
evm.model.Lp_chr3_0.8509 (MAGMA)	<i>Setaria viridis</i>	3e-46	77	74.08	XM_034736952.1	glutathione S-transferase GSTF1
evm.model.Lp_chr3_0.9565 (MAGMA)	<i>A. tauschii</i>	0	91	88.60	XM_020335608.1	serine incorporator
evm.model.Lp_chr3_0.23458 (MAGMA)	<i>B. distachyon</i>	0	98	86.21	XM_003570476.4	Uncharacterized protein
evm.model.Lp_chr4_0.29466 (GCTA)	-	-	-	-	-	-
evm.model.Lp_chr4_0.29467 (GCTA)	-	-	-	-	-	-
evm.model.Lp_chr5_0.11861 (GCTA)	<i>A. tauschii</i>	0	97	80.93	XM_010232430.2	F-box/LRR-repeat protein 14.
evm.model.Lp_chr5_0.11862 (GCTA)	<i>A. tauschii</i>	0	87	88.51	XM_020343219.1	
evm.model.Lp_chr5_0.11920 (MAGMA)	<i>B. distachyon</i>	0	100	93.18	XM_003577987.4	heavy metal-associated (HMA) isoprenylated plant protein (HIPP) 23.
evm.model.Lp_chr5_0.11921 (GCTA)	<i>A. tauschii</i>	0	100	86.72	XM_020300496.1	GTP-binding protein
evm.model.Lp_chr5_0.16787 (GCTA)	<i>Festuca arundinacea</i>	0	90	90.79	MH796656.1	Dehydration responsive element binding protein 1B-like protein.
evm.model.Lp_chr6_0.596 (GCTA)	-	-	-	-	-	-

<b>evm.model.Lp_chr6_0.1579 9 (MAGMA)</b>	<i>B. distachyon</i>	0	98	85.29	XM_003570583. 4	Type I inositol polyphosphate 5- phosphatase 5.
<b>evm.model.Lp_chr6_0.1580 0 (GCTA, MAGMA)</b>	<i>A. tauschii</i>	0	100	87.02	XM_020300272. 1	random slug protein 5-like isoform X1
<b>evm.model.Lp_chr7_0.1.192 2 (GCTA)</b>	<i>A. tauschii</i>	0	90	78.60	XM_020304986. 1	chloride intracellular channel protein 6-like
<b>evm.model.Lp_chr7_0.1.614 3 (GCTA)</b>	<i>Sorghum bicolor</i>	2e-55	75	80.91	XM_002438295. 2	glycine-rich cell wall structural proteins
<b>evm.model.Lp_chr7_0.1.113 90 (GCTA)</b>	<i>B. distachyon</i>	1e-97	90	74.35	XM_003574454. 4	codifying for a TIFY protein
<b>evm.model.Lp_chr7_0.1.227 07 (GCTA, MAGMA)</b>	<i>A. tauschii</i>	0	100	91.76	XM_020344125. 1	cytochrome P450 77A3
<b>evm.model.Lp_chr7_0.1.196 34 (GCTA)</b>	<i>A. tauschii</i>	0	96	90.76	XM_020291380. 1	peroxidase P7- like
<b>evm.model.Lp_chr7_0.1.196 42 (GCTA)</b>	<i>A. tauschii</i>	0	100	91.76	XM_020344125. 1	



**Figure S5.** Symptoms of crown rust infection of perennial ryegrass.