

Supplemental Table 1. Infection response of nine oat lines to 15 *Pyrenophora avenae* isolates to evaluate virulence phenotype.

	<i>Pyrenophora avenae</i> Isolate*															Mean
	PA101	PA102	PA103	PA104	PA105	PA108	PA109	PA110	PA111	PA112	PA114	PA115	PA116	PA117	PA118	
CDC Dancer	6.3	5.0	7.0	7.3	7.0	7.0	7.3	7.0	8.0	6.3	7.3	5.0	6.3	5.7	5.3	6.5a
AC Morgan	4.3	3.0	6.3	4.3	4.3	7.3	5.7	5.0	7.7	7.0	4.3	5.0	5.0	4.7	3.3	5.2b
CDC Morrison	5.0	2.3	5.0	4.3	3.0	5.7	4.0	5.0	2.7	2.0	2.3	2.0	2.3	4.0	3.0	3.5e
BetaGene	4.3	3.0	5.7	6.3	4.3	5.0	5.0	5.0	6.3	3.7	5.7	4.3	3.7	3.7	4.0	4.7c
Triactor	4.3	2.7	3.7	4.3	3.7	5.7	4.3	7.0	5.3	4.3	5.0	3.0	4.7	4.7	3.3	4.4cd
CDC Weaver	3.0	2.7	5.7	4.3	5.0	7.3	7.3	6.3	8.0	6.7	3.0	2.0	2.3	3.0	3.7	4.7c
CDC Sol-Fi	3.7	2.3	3.7	4.3	3.3	6.3	5.7	5.0	6.7	6.3	2.3	2.0	2.3	3.0	3.0	4.0d
HiFi	4.3	2.7	5.0	4.3	5.7	6.3	5.7	5.3	7.0	5.3	5.3	5.7	5.0	4.7	4.3	5.1b
Aslak	4.3	2.7	4.3	5.7	4.3	6.3	7.0	5.7	7.7	7.0	6.3	5.0	5.7	3.7	3.0	5.2b
Mean**	4.4efg	2.9i	5.1cde	5.0cde	4.5efg	6.3ab	5.8bc	5.7bc	6.6a	5.4cd	4.6def	3.8gh	4.1fgh	4.1fgh	3.7hi	

**Pyrenophora avenae* isolates collected from commercial oat fields in Saskatchewan.

**Means followed by the same letter were not significantly different ($P < 0.05$).

Supplemental Table 2. Infection response of nine oat lines to 17 *Cochliobolus sativus* isolates to evaluate virulence phenotype.

	<i>Cochliobolus sativus</i> Isolate*																	Mean
	CS301	CS302	CS303	CS304	CS305	CS306	CS307	CS308	CS309	CS310	CS311	CS312	CS313	CS314	CS315	CS316	CS317	
CDC Dancer	3.0	7.7	3.3	5.0	6.7	7.7	7.3	3.7	2.3	5.0	4.0	7.0	3.0	4.0	3.3	5.7	5.7	5.0a
AC Morgan	3.0	5.7	3.0	3.0	3.3	6.7	6.7	2.7	2.0	4.3	2.3	4.0	2.7	3.7	3.0	4.0	4.7	3.8b
CDC Morrison	3.0	5.3	3.3	3.0	3.7	5.7	6.7	3.0	2.0	4.7	3.3	4.3	3.0	3.7	2.7	3.7	3.0	3.8b
BetaGene	3.0	7.0	3.7	3.3	4.3	3.3	5.7	2.3	1.7	2.7	4.3	3.3	2.0	3.3	3.3	2.0	3.7	3.5c
Triactor	2.7	6.0	3.0	3.3	3.3	4.3	4.3	3.0	2.0	3.0	3.0	4.3	2.0	3.0	3.3	2.7	2.7	3.3c
CDC Weaver	3.0	7.7	4.0	3.0	4.3	4.3	7.0	2.3	1.0	4.3	3.0	3.7	3.0	3.3	3.0	2.7	3.7	3.7b
CDC Sol-Fi	2.0	6.7	3.0	2.7	3.7	3.6	5.0	2.0	2.0	3.7	3.0	4.7	2.7	3.0	2.0	2.3	3.0	3.2c
HiFi	3.0	6.3	4.7	3.0	3.0	5.7	4.3	3.0	2.7	3.7	4.0	5.0	3.0	3.3	3.0	3.0	4.0	3.8b
Aslak	1.7	5.7	3.0	3.7	3.3	4.0	5.7	2.3	2.0	3.3	3.0	3.7	2.0	3.3	3.0	3.0	3.0	3.3c
Mean**	2.7h	6.5a	3.4efg	3.3g	4.0e	5.0c	5.9b	2.7h	2.0i	3.9ef	3.3g	4.4d	2.6h	3.4fg	3.0h	3.2g	3.7efg	

**Cochliobolus sativus* isolates collected from commercial oat fields in Saskatchewan.

**Means followed by the same letter were not significantly different (P < 0.05).

Supplemental Table 3. Infection response of 32 oat lines to three *Pyrenophora teres* isolates to identify bi-parental mapping parents and parents for resistance breeding.

Oat Line	<i>Pyrenophora avenae</i> Isolate			Mean
	PA101	PA102	PA114	
CDC Dancer	7.7	5.0	6.3	6.3ab
AC Morgan	6.3	3.0	3.0	4.1fghi
CDC Morrison	4.3	2.7	3.7	3.6hijk
BetaGene	5.0	2.7	5.0	4.2efgh
Triactor	4.3	2.0	4.0	3.4ijkl
CDC Weaver	3.7	2.0	2.3	2.7mno
CDC Sol-Fi	3.3	2.3	2.3	2.6mno
HiFi	5.0	2.7	5.0	4.2efgh
Aslak	6.0	2.7	5.0	4.6de
Matilda	5.3	2.7	4.7	4.2efgh
Aigorudo	2.0	1.0	2.7	1.9pqr
Iowa N2052	7.7	6.3	7.0	7.0a
OT3011	3.7	2.0	2.7	2.8lmno
96-21Cn19	1.7	1.0	1.0	1.2r
SA99572	2.7	2.0	2.7	2.5nop
OT3028	2.3	2.7	2.3	2.4nop
Provena B	5.7	2.7	3.3	3.9ghij
Boyer	6.3	3.3	5.0	4.9de
Ave 117.02	2.3	2.0	2.3	2.2opq
OT3033	2.7	2.3	3.0	2.7mno
Bw 1103	2.7	1.7	2.0	2.1opq
OT3031	3.3	2.0	2.0	2.4nop
CDC Seabiscuit	5.7	4.3	3.7	4.6efg
MN06212	3.7	2.3	3.7	3.2jklm
CDC Minstrel	3.7	3.0	3.0	3.2jklm
OT3050	2.3	3.7	3.0	3.0klmn
Robust	6.3	2.3	3.0	3.9ghij
ND061868	1.7	1.0	2.0	1.6qr
Vista	7.3	5.0	5.0	5.8bc
AC Ass/S42	1.3	2.0	2.3	1.9pqr
CDC ProFi	7.0	5.0	4.3	5.4cd
SA060539	4.3	5.0	4.7	4.7ef
Mean*	4.3a	2.8c	3.5b	

*Means followed by the same letter were not significantly different (P < 0.05).

Supplemental Table 4. Infection response of 32 oat lines to six *Cochliobolus sativus* isolates to evaluate bi-parental mapping parents and parents for resistance breeding.

Oat line	<i>Cochliobolus sativus</i> Isolate						Mean
	CS301	CS302	CS305	CS307	CS312	CS316	
CDC Dancer	2.0	7.0	7.0	7.3	5.7	6.3	5.9ab
AC Morgan	3.0	6.7	6.7	6.0	5.0	5.3	5.5bc
CDC Morrison	2.7	5.0	5.7	5.7	5.0	5.7	5.0cd
BetaGene	2.3	6.7	4.3	3.7	2.0	3.0	3.7hijkl
Triactor	2.3	6.3	3.7	4.0	2.3	4.3	3.8hijk
CDC Weaver	3.0	7.0	3.0	5.0	3.7	3.3	4.2efgh
CDC Sol-Fi	2.7	6.0	5.7	4.7	2.7	3.0	4.1efghi
HiFi	3.0	7.3	5.3	5.0	5.0	4.7	5.1cd
Aslak	1.0	6.3	4.7	6.3	2.7	3.3	4.1fghij
Matilda	2.0	4.3	3.7	6.3	2.7	2.0	3.5ijklmn
Aigorudo	2.0	5.0	4.0	4.3	2.7	2.0	3.3klmn
Iowa N2052	1.0	8.3	4.7	5.0	4.3	3.7	4.5defg
OT3011	1.3	7.7	3.3	5.0	2.7	2.0	3.7hijkl
96-21Cn19	1.0	6.3	1.7	4.3	2.7	2.3	3.1lmn
SA99572	2.7	9.0	4.0	7.0	6.3	3.7	5.5bc
OT3028	2.7	4.7	4.3	4.7	2.7	2.7	3.6hijklm
Provena B	1.3	4.3	3.0	5.0	5.0	3.3	3.7hijkl
Boyer	1.7	7.3	5.0	2.3	4.3	4.3	4.2efgh
Ave 117.02	1.0	6.7	3.3	2.0	2.7	2.3	3.0mn
OT3033	2.3	7.3	3.0	3.3	3.0	3.0	3.7hijkl
Bw 1103	2.0	5.7	4.3	3.7	2.3	2.0	3.3klmn
OT3031	2.0	7.0	5.0	3.7	1.0	2.7	3.6hijklmn
CDC Seabiscuit	2.3	8.3	5.0	6.7	3.0	3.0	4.7de
MN06212	2.0	7.7	3.3	3.0	3.0	1.7	3.5jklmn
CDC Minstrel	2.0	7.3	5.0	5.7	3.7	4.0	4.6def
OT3050	2.3	5.7	3.7	5.0	3.0	4.3	4.0fghij
Robust	2.7	7.7	5.3	6.0	3.0	2.7	4.6defg
ND061868	1.3	4.3	3.3	4.3	2.0	2.3	2.9n
Vista	3.0	5.7	4.3	4.3	2.7	3.7	4.0ghijk
AC Ass/S42	1.7	4.7	3.3	7.0	3.7	2.7	3.9hijk
CDC ProFi	2.0	7.0	4.3	4.7	2.3	2.0	3.7hijk
SA060539	4.0	6.3	6.3	7.3	6.3	6.3	6.1a
Mean*	2.1e	6.5a	4.4c	4.9b	3.4d	3.4d	

*Means followed by the same letter were not significantly different ($P < 0.05$).

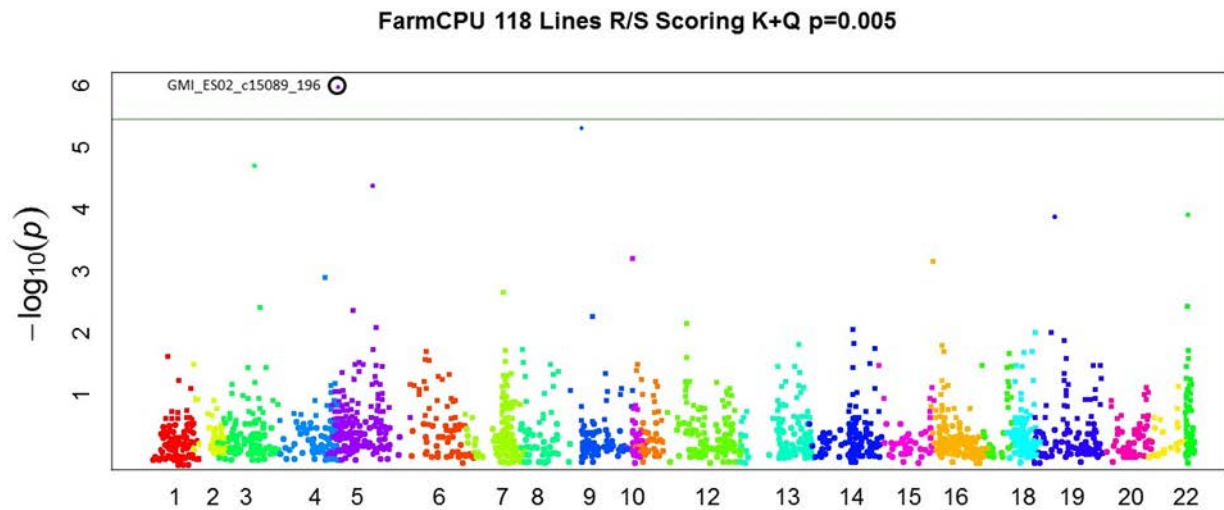
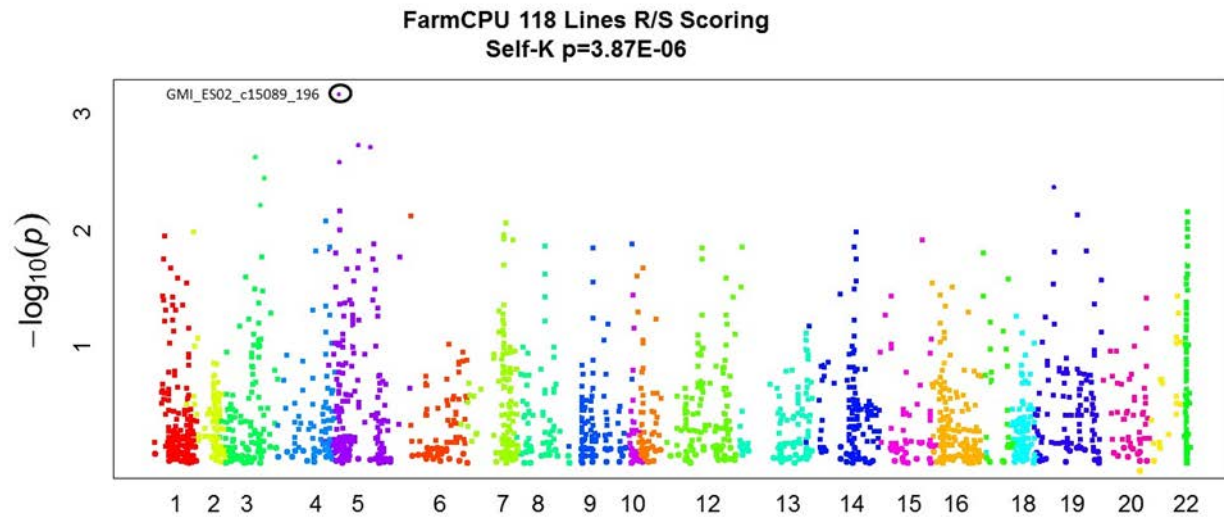
Supplemental Table 5. Consensus map location and annotation for genetic markers underlying the QTL peak identified as being associated with resistance to *P. avenae* isolates PA102 and PA114 in the OT3011 x Iowa N2052 population. Information from Chaffin et al. (2016).

Marker ID	Chrom.	Position (cM)	Gene	Gene Ontology Annotation	Protein ID	Product Name
ES22_c18205_366	5C	89.6	arginyl-trna--protein transferase 1-like	P:arginyl-tRNA aminoacylation; P:regulation of seed germination; P:regulation of lipid catabolic process; P:protein arginylation; F:arginyltransferase activity; F:ATP binding; P:response to abscisic acid stimulus; F:arginine-tRNA ligase activity; P:leaf s	BAJ96636.1	predicted protein
ES15_c10501_398	5C	89.6	histone deacetylase 8-like	F:histone deacetylase activity; P:histone deacetylation	XP_003568360.1	histone deacetylase 8-like
ES14_c2496_651	5C	89.5	phosphatidate phosphatase lpin3-like	F:phosphatidate phosphatase activity; P:cellular response to phosphate starvation; P:lipid metabolic process	XP_003568284.1	phosphatidate phosphatase LPIN3-like
ES22_c1052_894	5C	89.5	ribosome production factor 1-like	P:seed dormancy process; C:cytosol; P:regulation of cell cycle process; P:seed germination; P:meristem structural organization; P:regulation of flower development; P:photomorphogenesis; P:protein targeting to mitochondrion; P:cell division; P:vegetative t	BAK03924.1	predicted protein
ES22_c8057_338	5C	89.1	deoxycytidine kinase	F:phosphotransferase activity, alcohol group as acceptor; F:kinase activity; P:phosphorylation; P:nucleobase-containing compound metabolic process; F:ATP binding; C:nucleus	XP_003568392.1	uncharacterized protein LOC100842339
ES15_c3003_520	5C	83.9	nadh dehydrogenase	P:response to oxidative stress; F:NAD binding; P:ubiquitin-dependent protein catabolic process; F:zinc ion binding; F:2 iron, 2 sulfur cluster binding; F:NADH dehydrogenase (ubiquinone) activity; C:mitochondrial respiratory chain complex I; P:response to	BAJ89234.1	predicted protein
GBS_90539		89.6			XP_003568344.1	protein BUD31 homolog 2-like
ES15_lrc9414_222		89.5	aldose reductase	P:response to cadmium ion; C:cytosol; F:oxidoreductase activity; C:nucleus; P:oxidation-reduction process	XP_002441209.1	hypothetical protein
ES22_c4473_396		89.5	atp-dependent zinc metalloprotease ftsh mitochondrial-like	F:nucleoside-triphosphatase activity; F:zinc ion binding; C:integral to membrane; C:mitochondrial inner membrane; F:metalloendopeptidase activity; P:proteolysis; F:ATP binding; C:chloroplast thylakoid membrane; P:protein catabolic process	BAK03446.1	predicted protein
ES17_c10995_455		87.1	zinc finger protein 830-like	F:zinc ion binding; C:intracellular	XP_003568196.1	zinc finger protein 830-like
ES15_c3296_521		83.7	upf0586 protein c9orf41 homolog		XP_003568132.1	UPF0586 protein C9orf41 homolog

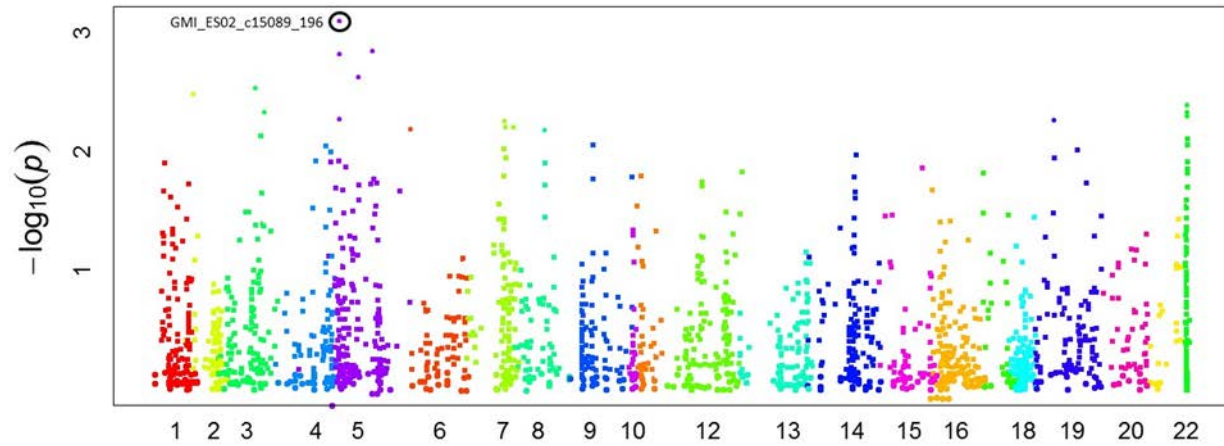
Supplemental Table 6. Consensus map location and annotation for genetic markers associated with resistance to *P. avenae* isolate PA114 in the association mapping population. Information from Chaffin et al. (2016).

Marker ID	Chrom.	Position (cM)	Gene	Gene Ontology Annotation	Protein ID	Product Name
GMI_ES02_c15089_196	5C	23.6	splicing factor u2af 50 kda subunit	F:nucleic acid binding; F:nucleotide binding; F:transferase activity, transferring phosphorus- containing groups	XP_003558854.1	uncharacterized protein LOC100840355
GMI_ES14_c2536_539	8A	41.8	protein phosphatase 2a structural subunit	P:positive regulation of abscisic acid mediated signaling pathway; F:protein phosphatase type 2A regulator activity; C:cell wall; P:auxin polar transport; P:regulation of stomatal movement; P:response to ethylene stimulus; P:response to cadmium ion	AAM94368.1	protein phosphatase 2A regulatory A subunit
GMI_ES22_c1163_38	21D	26.3	splicing factor 3a subunit 3- like	P:G2 phase of mitotic cell cycle; P:mitotic recombination; P:response to freezing; F:zinc ion binding; P:karyogamy; P:embryo development ending in seed dormancy; P:mRNA export from nucleus; P:protein deubiquitination; P:histone methylation	BAJ88091.1	predicted protein
GMI_ES03_c10561_484	9D	87.3	zinc finger (c3hc4-type ring finger) protein family-like	F:ligase activity; C:integral to membrane	XP_003573320.1	UPF0392 protein Os08g0121900- like

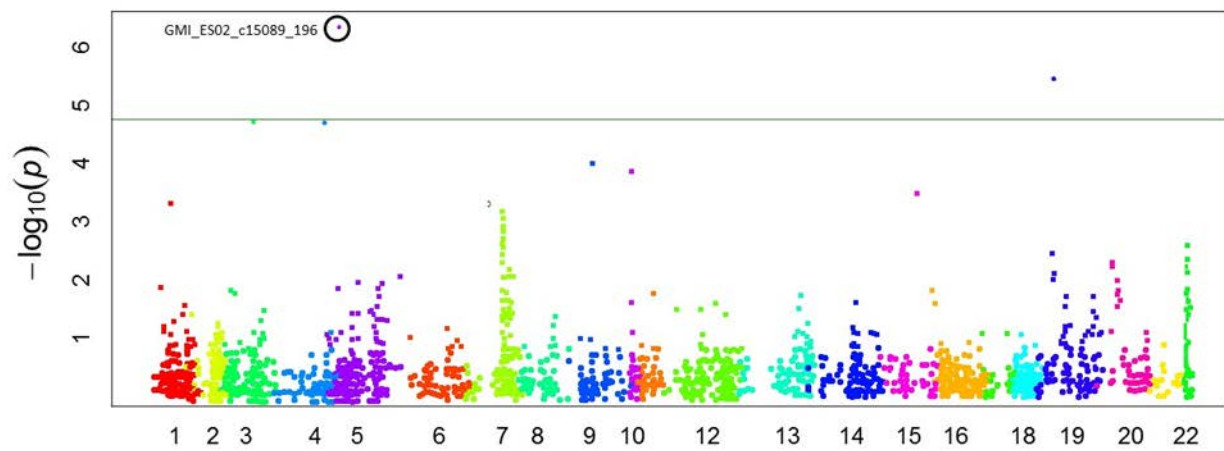
Supplemental Figure 1. The following figures represent Manhattan plots identifying markers (circled and labelled in each figure) significantly associated with resistance to *P. avenae* isolate PA114 in the 150 member association mapping panel. Each Manhattan plot is derived from one of the various analysis methods indicated and summarized in Table 14 within the final report file. Details of the analysis for each Manhattan plot are provided above each figure.



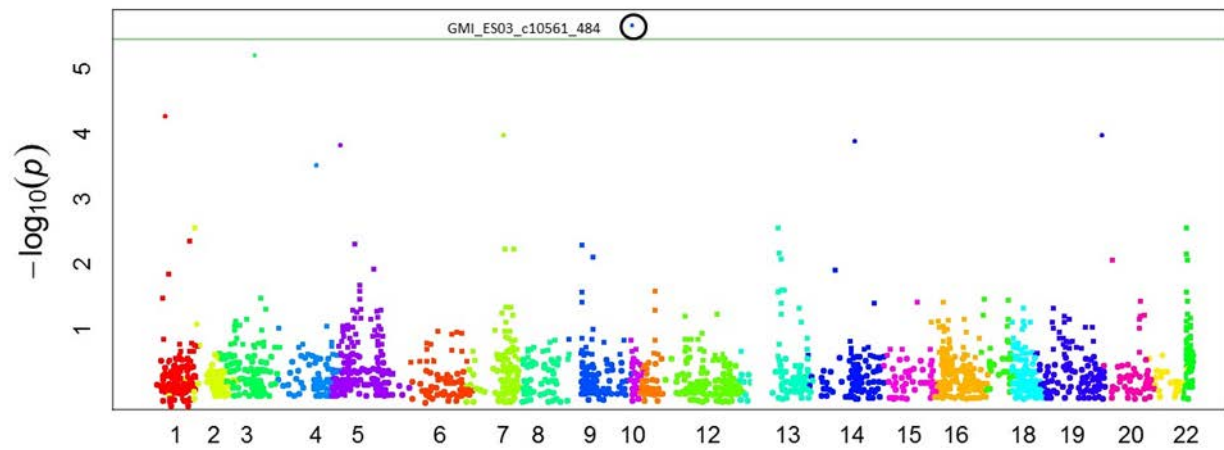
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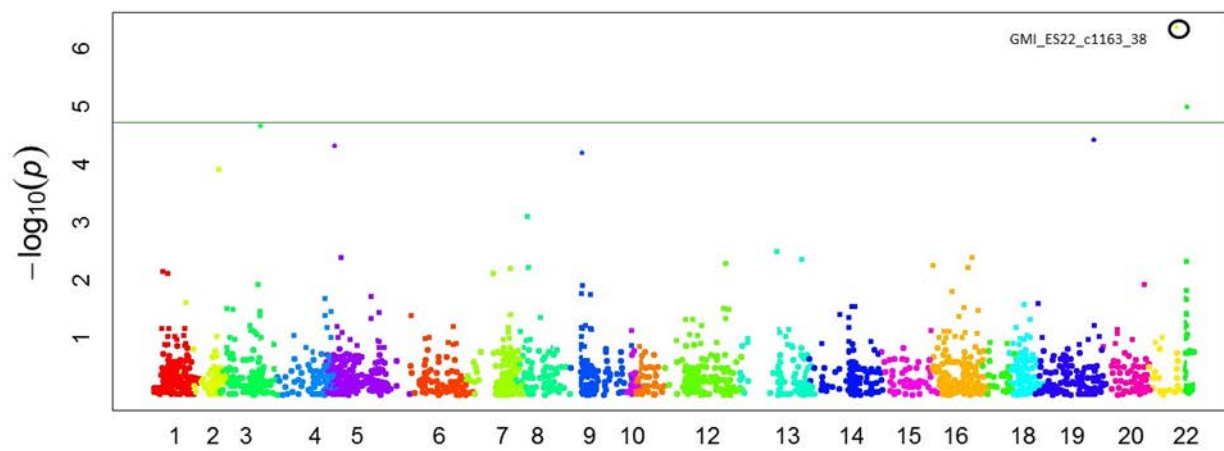
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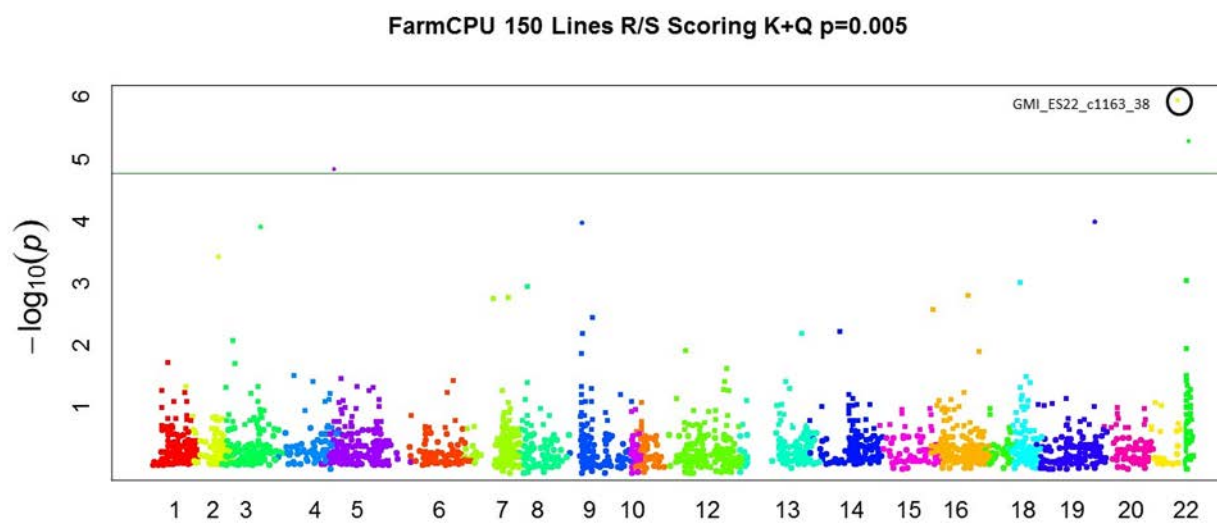
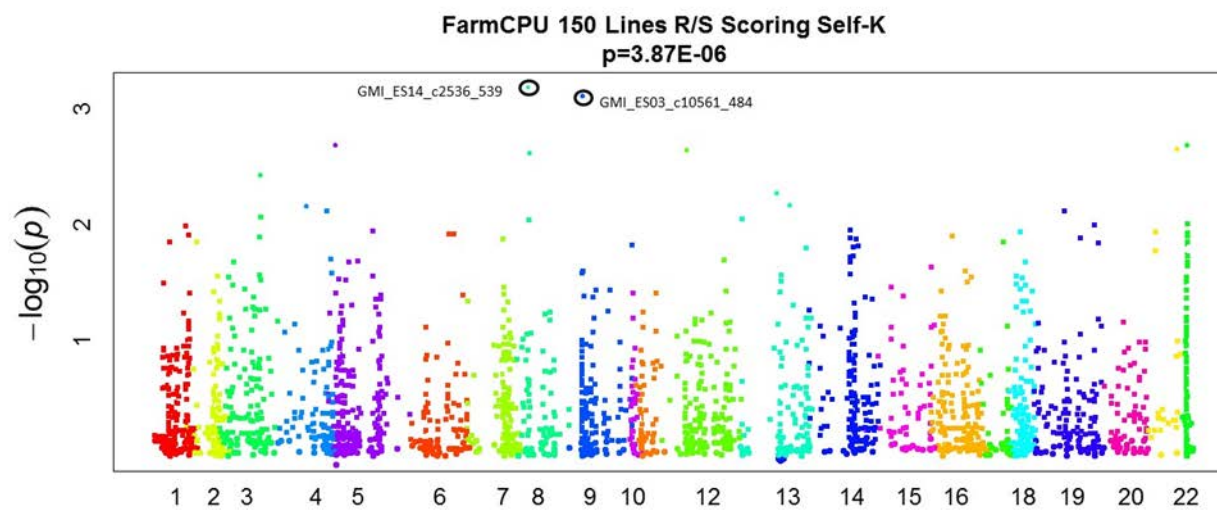


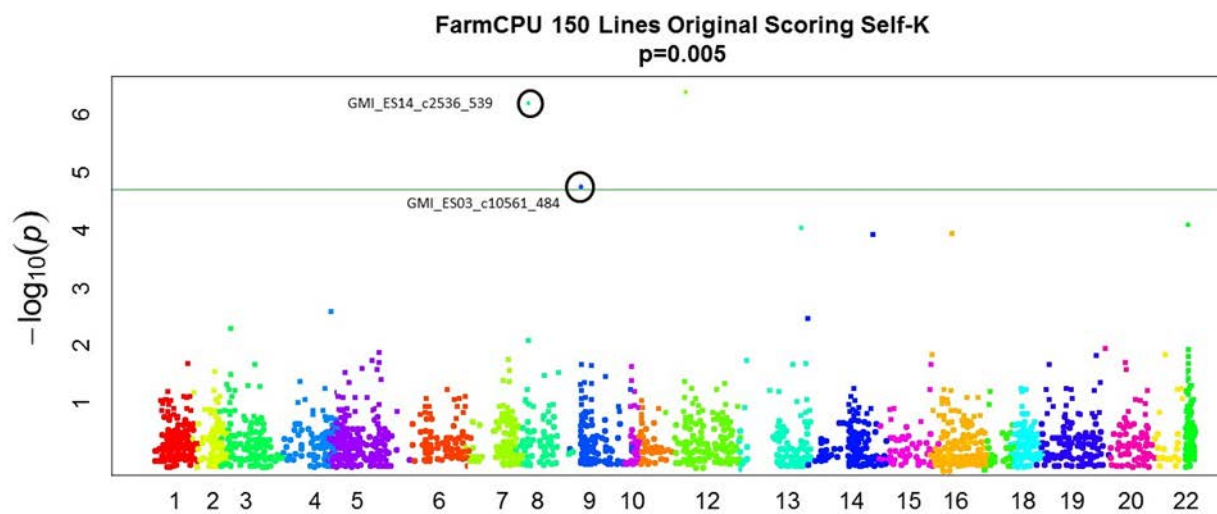
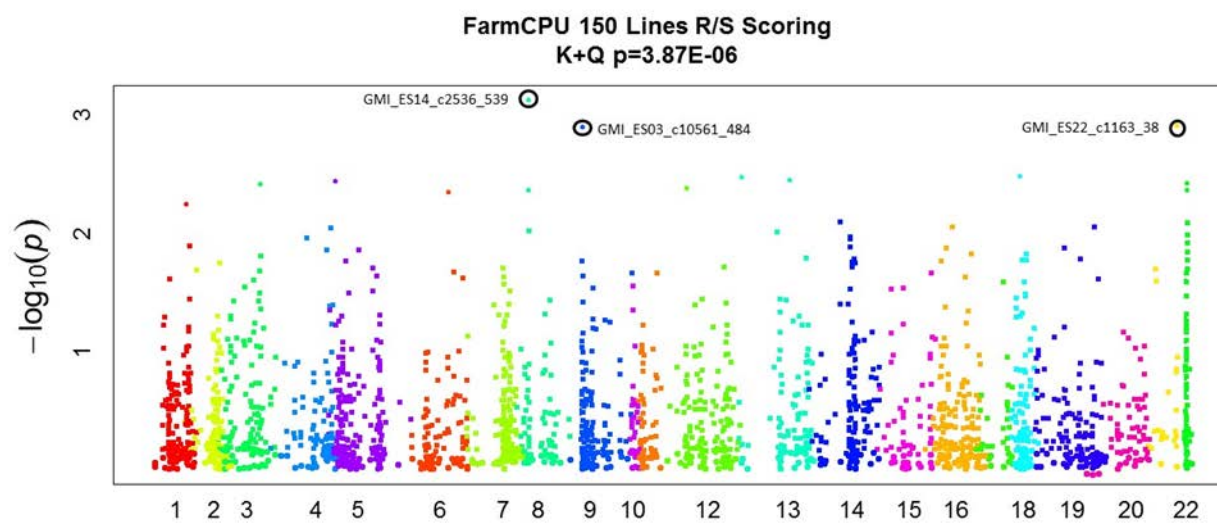
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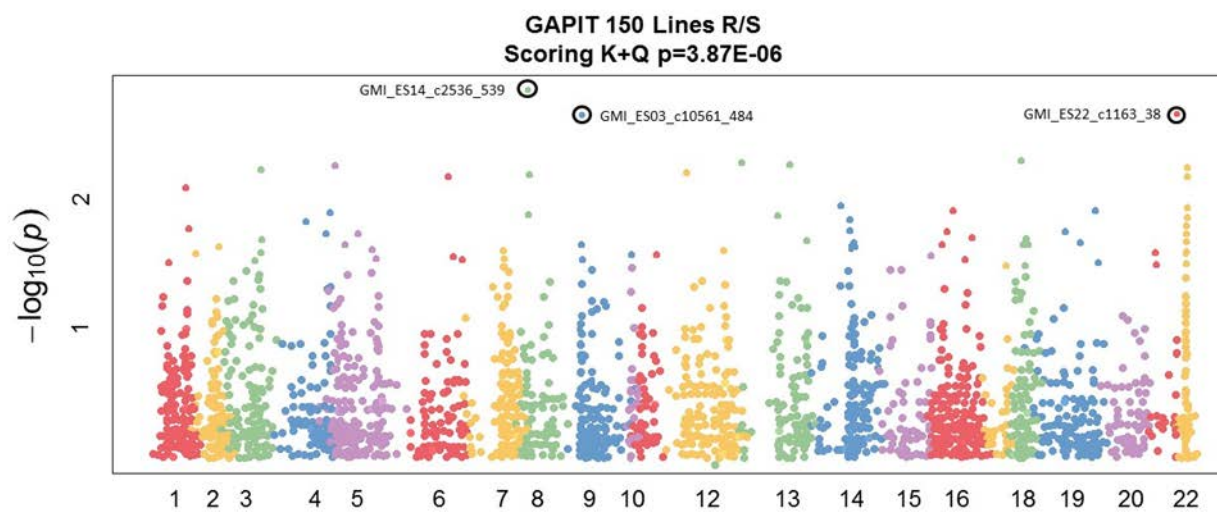
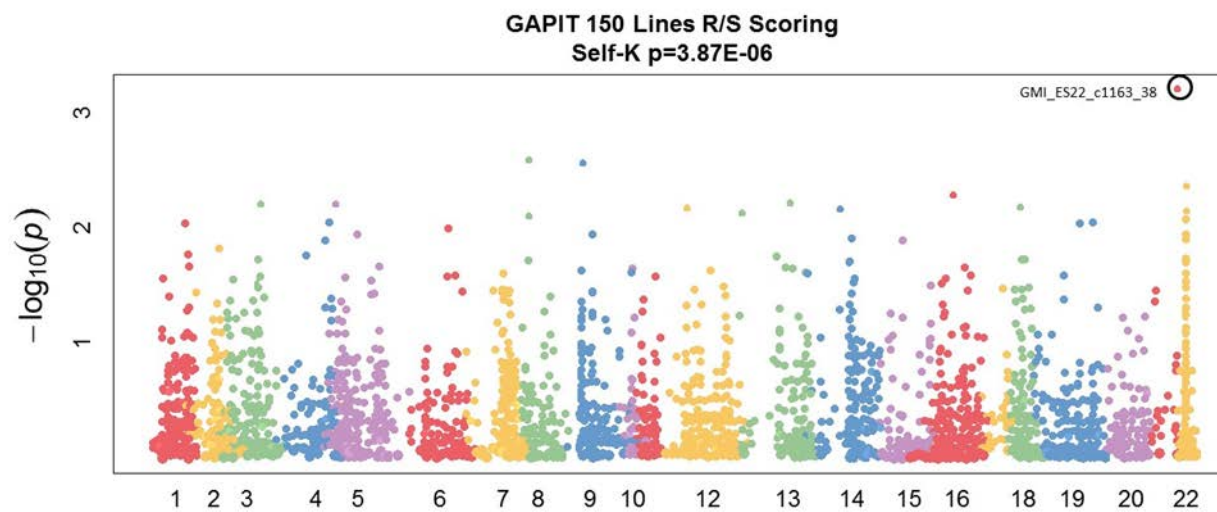


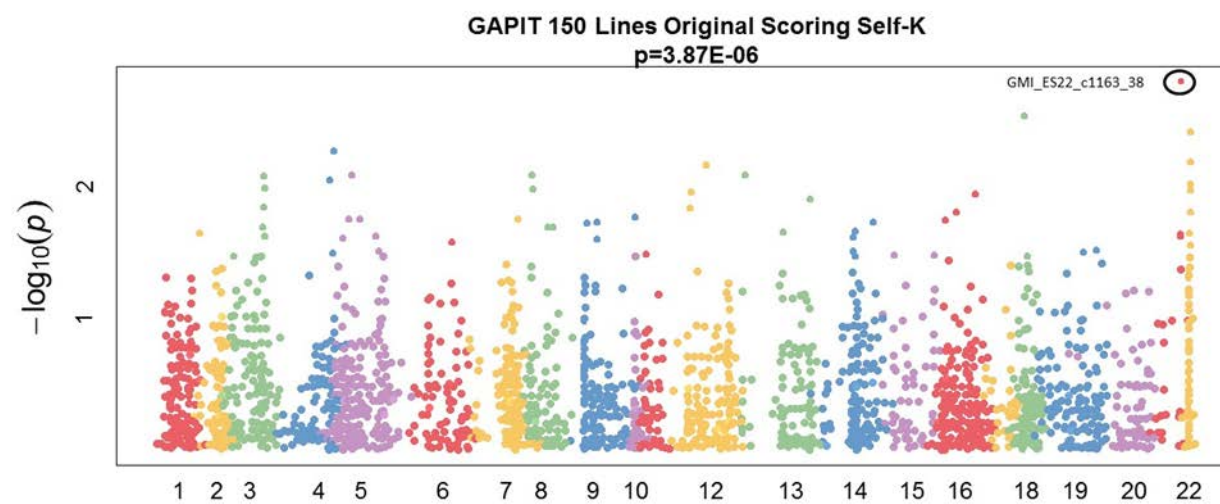
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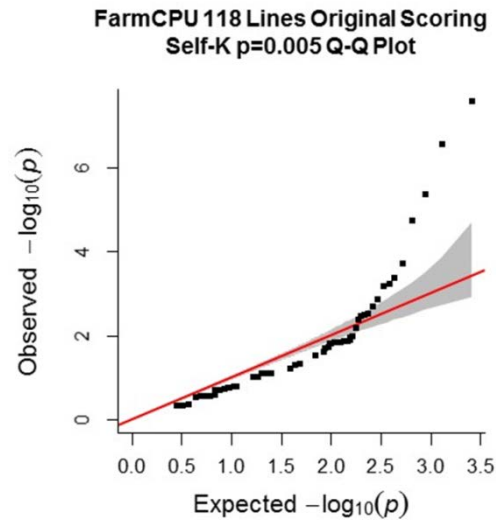
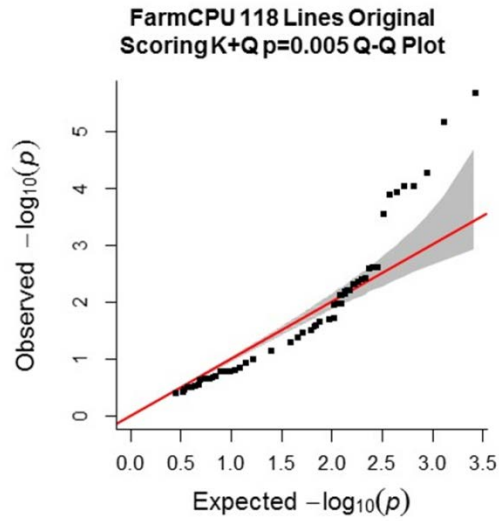




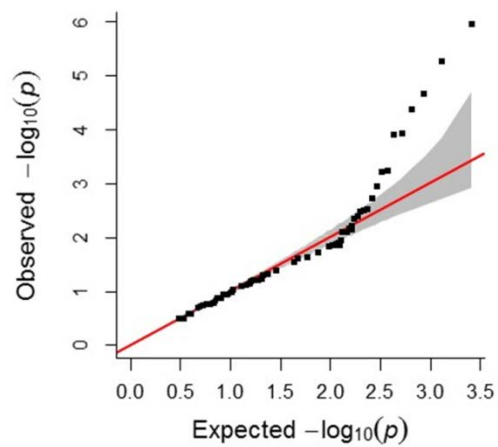




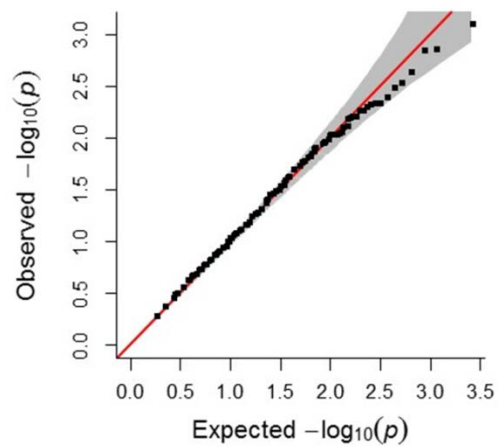
Supplemental Figure 2. The following figures represent Q-Q plots derived from one of the various analysis methods indicated and summarized in Table 14 within the final report file. Details of the analysis for each Q-Q plot are provided above each figure.



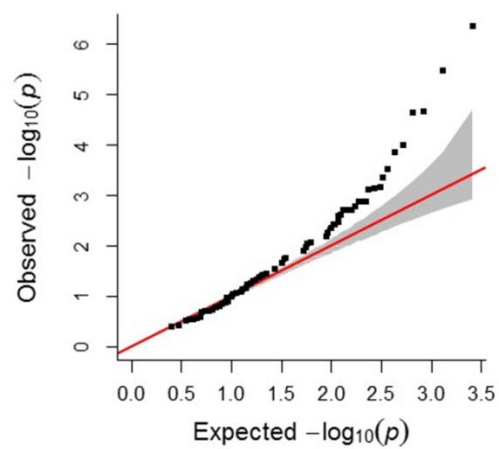
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Q-Q Plot



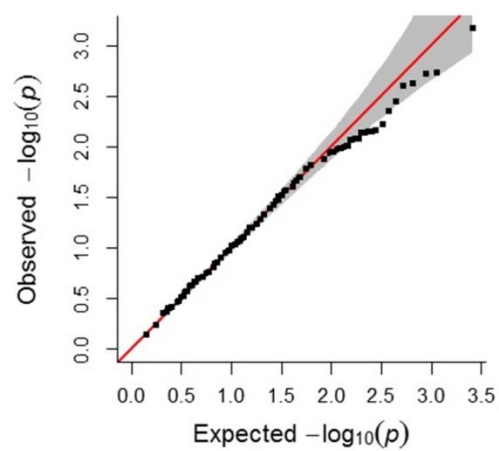
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Q-Q Plot



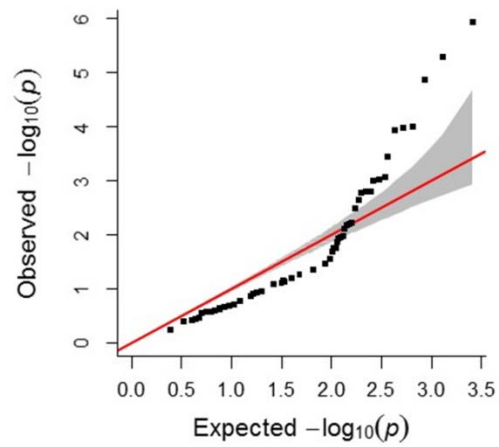
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Q-Q Plot



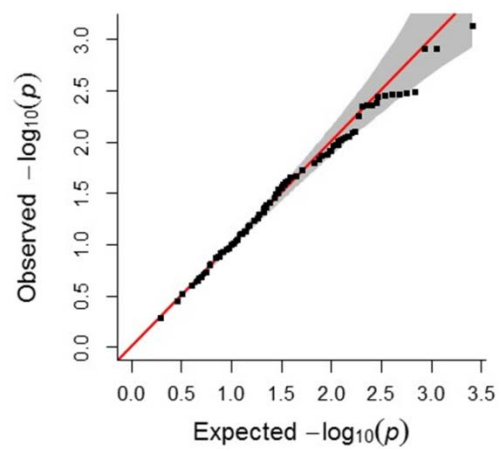
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 $p=3.87E-06$ Q-Q Plot



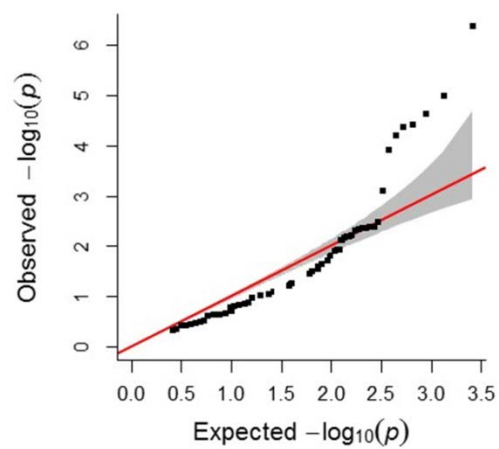
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Q-Q Plot



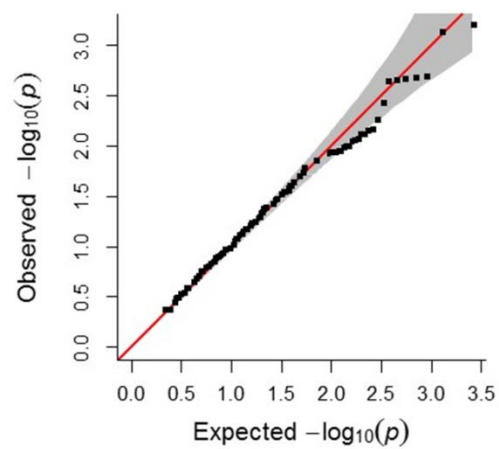
FarmCPU 150 Lines R/S Scoring K+Q $p=3.87E-06$
Q-Q Plot



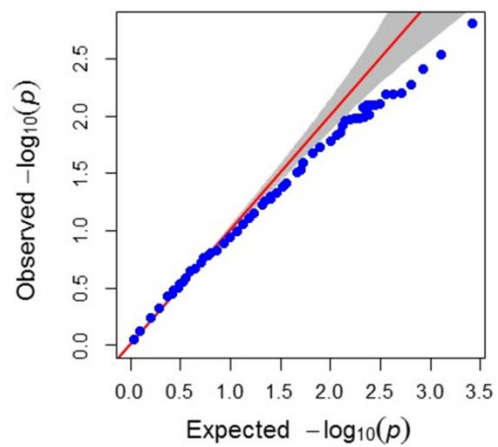
FarmCPU 150 Lines R/S Scoring Self-K
p=0.005 Q-Q Plot



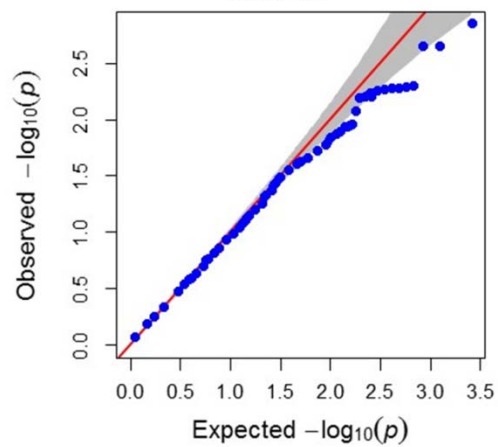
FarmCPU 150 Lines R/S Scoring Self-K p=3.87E-06
Q-Q Plot



**GAPIT 150 Lines Original Score Self-K
p=3.87E-06 Q-Q Plot**



**GAPIT 150 Lines R/S Scoring K+Q p=3.87E-06
Q-Q Plot**



GAPIT 150 Lines R/S Scoring Self-K p=3.87E-06
Q-Q Plot

