ANOVA for a RCBD trial: SPYLPT2013_GH-Tono

RSIMON using HIDAP

May 06, 2016, 14:44h

Contents

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## Warning: package 'knitr' was built under R version 3.2.5
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## Warning: package 'magrittr' was built under R version 3.2.5
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# This is an automatedly created report.

# See more details in section on materials.
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Alternate formats:

PDF DOCX

Abstract

This trial has the identifier SPYLPT2013_GH-Tono. It was conducted under the supervision of x y as a Advanced Trial as part of a Yield Breeding Program in Tono, Ghana, Z in 2016. A total of 163 clones (including reference clones) were evaluated for 26 traits.

Materials and Methods

Location characterization

Installation

Geographic and climate characterization

Weather during planting season

Soil

Field management

Observations on special events

Materials

Trait descriptions (from ontology)

Model specification and data description

There is data from 163 treatments, evaluated using a randomize complete block design with 1, 2 blocks. The statistical model is

$$y_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij}$$

where

- y_{ij} is the observed response with treatment i and block j.
- μ is the mean response over all treatments and blocks.
- τ_i is the effect for treatment i.
- β_j is the effect for block j.
- ϵ_{ij} is the error term.

In this model we assume that the errors are independent and have a normal distribution with common variance, that is, $\epsilon_{ij} \sim N(0, \sigma_\epsilon^2)$.

The following traits are analyzed: **Beta carotene content measuring mg per 100g, Content of iron on dry weight basis measuring mg per 100g, Content of zinc on dry weight basis measuring mg per 100g, Dry weight of storage root samples measuring g of sample, Fresh weight of storage root samples measuring g of sample, Fructose content measuring percent, Glucose content measuring percent, Harvest index computing percent, Number of commercial storage roots counting number per plot, Number of non-commercial storage roots counting number per plot, Plants harvested counting number per plot, Plants planted counting number per plot, Plants with storage roots counting number per plot, Protein content measuring percent, Storage root damages estimatimg 1-9, Storage root dry matter content computing percent, Storage root**

size estimating 1-9, Storage root starch content measuring percent, Sucrose content measuring percent, Survival index computing percent, Sweet potato weevil symptoms 1 estimating 1-9, Vine vigor 1 estimating 1-9, Virus symptoms 2 estimating 1-9, Weight of commercial storage roots measuring kg per plot, Weight of non-commercial storage roots measuring kg per plot, Weight of vines measuring kg per plot.

The following germplasm was analyzed: PG12012-1, PG12012-2, PG12151-19, PG12151-73, PG12088-10, PG12085-16, PG12149-5, PG12166-4, PG12151-75, PG12149-18, PG12155-30, PG12155-50, PG12005-88, PG12005-52, PG12165-42, PG12078-4, PG12149-9, PG12165-36, PG12165-20, PG12086-5, Ogyefo, PG12005-1, PG12155-110, PG12167-5, PG12078-3, PG12165-31, PG12005-24, PG12155-32, PG12083-11, PG12005-82, PG12086-11, PG12165-3, PG12165-43, PG12086-17, PG12165-30, PG12151-4, PG12005-35, PG12084-10, PG12149-20, PG12149-49, PG12150-7, PG12146-13, PG12146-27, PG12089-5, PG12012-4, PG12011-7, PG12089-14, PG12160-51, PG12080-15, PG12160-104, PG12163-151, PG12162-10, PG12162-39, PG12162-9, PG12162-43, PG12162-3, PG12162-5, PG12160-72, PG12071-6, PG12146-23, PG12162-19, PG12118-5, PGB12162-4, PG12162-56, Sauti, PG12047-3, PG12163-163, PG12163-117, PG12164-21, PG12081-3, PG12076-5, PG12089-13, PG12163-173, PG12070-14, PG12162-16, PG12163-167, PG12162-54, PG12162-31, PG12160-47, PG12058-15, PG12153-2, PG12163-133, PG12153-21, PG12010-15, PG12149-40, PG12136-2, PG12153-14, PG12151-32, PG12021-10, PG12149-8, PG12079-29, PG12168-2, PG12164-26, PG12086-18, PG12153-35, PG12166-30, PG12059-14, PG12005-55, PG12153-29, PG12061-13, PG12155-22, PG12151-88, PG12151-61, PG12170-4, PG12082-18, PG12108-3, PG12059-8, PG12153-24, PG12147-5, PG12135-2, PG12076-13, PG12005-79, PG12166-11, PG12151-65, PG12149-28, PG12078-17, PG12145-2, PG12164-43, PG12005-105, PG12147-1, PG12028-4, PG12014-2, PG12088-29, PG12088-2, PG12088-4, PG12146-19, PG12021-7, PG12148-6, PG12153-16, PG12108-4, PG12154-1, PG12055-14, PG12088-27, PG12088-8, PG12057-14, PG12150-53, PG12101-3, PG12151-36, PG12064-5, PG12169-5, PG12089-3, PG12175-3, PG12149-19, PG12088-19, PG12148-26, PG12090-31, PG12148-39, PG12155-8, PG12073-12, PG12155-17, PG12155-20, PG12155-12, PG12083-20, PG12155-106, PG12151-53, PG12151-24, PG12166-26, PG12152-29, PG12152-33, PG12151-26, PG12069-11, PG12146-21, Apomuden.

Computational tools

This report was created using i386-w64-mingw32, i386, mingw32, i386, mingw32, Revised, 3, 2.4, 2016, 03, 16, 70336, R, R version 3.2.4 Revised (2016-03-16 r70336), Very Secure Dishes on a i386-w64-mingw32/i386 (32-bit) running Windows 7 x64 (build 7601) Service Pack 1 in . The following base packages were loaded: **stats, graphics, grDevices, utils, datasets, methods, base** and the following additional packages: **magrittr, knitr, shiny**.

Results

Raw data

Trait summaries

Trait analyses

The following traits were not analyzed since they had too many missing values ($>= 10\%$): Beta carotene content measuring mg per 100g, Content of iron on dry weight basis measuring mg per 100g, Content of zinc on dry weight basis measuring mg per 100g, Dry weight of storage root samples measuring g of sample, Fresh weight of storage root samples measuring g of sample, Fructose content measuring percent, Glucose content measuring percent, Harvest index computing percent, Number of commercial storage roots counting number per plot, Number of non-commercial storage roots counting number per plot, Plants with storage roots counting number per plot, Protein content measuring percent, Storage root dry matter content computing percent, Storage root starch content measuring percent, Sucrose content measuring percent, Weight of

commercial storage roots measuring kg per plot, Weight of non-commercial storage roots measuring kg per plot. For the remaining traits missing values were imputed using all available information.

Valid traits: **Plants harvested counting number per plot, Plants planted counting number per plot, Storage root damages estimatimg 1-9, Storage root size estimating 1-9, Survival index computing percent, Sweet potato weevil symptoms 1 estimating 1-9, Vine vigor 1 estimating 1-9, Virus symptoms 2 estimating 1-9, Weight of vines measuring kg per plot**.

Analysis of Plants harvested counting number per plot

You have fitted a linear model for a RCBD. The ANOVA table for your model is:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	162	1696.66	10.4732	2.37905	2.90496e-08
REP	1	7.25015	7.25015	1.64691	0.201213
Residuals	162	713.169	4.40228	NA	NA

The p-value for treatments is 0.0000000290496 which is significant at the 5% level.

The means of your treatments are:

germplasmName	Plants harvested counting number per plot
Apomuden	8.5
Ogyefo	7.5
PG12005-1	8.5
PG12005-105	5
PG12005-24	5
PG12005-35	8
PG12005-52	10
PG12005-55	2
PG12005-79	4.5
PG12005-82	8.5
PG12005-88	7.5
PG12010-15	8
PG12011-7	2.54
PG12012-1	4.5
PG12012-2	3.5
PG12012-4	2
PG12014-2	2
PG12021-10	5
PG12021-7	3.18
PG12028-4	2
PG12047-3	7.5
PG12055-14	4.49
PG12057-14	3
PG12058-15	3.15
PG12059-14	3.5
PG12059-8	4
PG12061-13	7
PG12064-5	3.34
PG12069-11	1.6

germplasmName	Plants harvested counting number per plot
PG12070-14	1
PG12071-6	5
PG12073-12	2.09
PG12076-13	4.86
PG12076-5	2
PG12078-17	3.88
PG12078-3	3.62
PG12078-4	5
PG12079-29	1.41
PG12080-15	3
PG12081-3	2.5
PG12082-18	2.98
PG12083-11	1.86
PG12083-20	6
PG12084-10	1
PG12085-16	10
PG12086-11	3.43
PG12086-17	5
PG12086-18	10
PG12086-5	1.5
PG12088-10	7
PG12088-19	5.15
PG12088-2	5
PG12088-27	3.05
PG12088-29	4.5
PG12088-4	2.61
PG12088-8	4.65
PG12089-13	5.5
PG12089-14	7
PG12089-3	7.5
PG12089-5	2
PG12090-31	3.41
PG12101-3	9.5
PG12108-3	3.31
PG12108-4	3.5
PG12118-5	3.23
PG12135-2	3
PG12136-2	7
PG12145-2	9.5
PG12146-13	4.5
PG12146-19	2
PG12146-21	5.34
PG12146-23	1.8
PG12146-27	1.21
PG12147-1	8.5
PG12147-5	3
PG12148-26	2.5
PG12148-39	6.5
PG12148-6	4.9
PG12149-18	4.02
PG12149-19	4.5

germplasmName	Plants harvested counting number per plot
PG12149-20	5.5
PG12149-28	5.5
PG12149-40	2.5
PG12149-49	7.5
PG12149-5	4
PG12149-8	10
PG12149-9	6
PG12150-53	4.46
PG12150-7	5.5
PG12151-19	2.64
PG12151-24	4
PG12151-26	4.54
PG12151-32	6.35
PG12151-36	7.35
PG12151-4	2.47
PG12151-53	6
PG12151-61	8.5
PG12151-65	4
PG12151-73	10
PG12151-75	3.24
PG12151-88	1
PG12152-29	5.3
PG12152-33	7.5
PG12153-14	4
PG12153-16	2
PG12153-2	2
PG12153-21	5
PG12153-24	7
PG12153-29	4
PG12153-35	2.89
PG12154-1	5.34
PG12155-106	9
PG12155-110	2.43
PG12155-12	5
PG12155-17	3.5
PG12155-20	5
PG12155-22	8
PG12155-30	5.5
PG12155-32	4.05
PG12155-50	3.45
PG12155-8	3.96
PG12160-104	3.52
PG12160-47	5
PG12160-51	3
PG12160-72	6.5
PG12162-10	4.5
PG12162-16	2
PG12162-19	4
PG12162-3	2
PG12162-31	2.5
PG12162-39	5

germplasmName	Plants harvested counting number per plot
PG12162-43	2.5
PG12162-5	2.85
PG12162-54	3.27
PG12162-56	4
PG12162-9	4
PG12163-117	2.5
PG12163-133	4.31
PG12163-151	7.5
PG12163-163	5
PG12163-167	5
PG12163-173	4.4
PG12164-21	10
PG12164-26	9
PG12164-43	6.5
PG12165-20	5.09
PG12165-3	3.5
PG12165-30	1.57
PG12165-31	3.5
PG12165-36	8
PG12165-42	4
PG12165-43	4
PG12166-11	5
PG12166-26	5.5
PG12166-30	6.05
PG12166-4	2.84
PG12167-5	2.5
PG12168-2	8.5
PG12169-5	5.5
PG12170-4	8
PG12175-3	2.55
PGB12162-4	3.5
Sauti	7.97
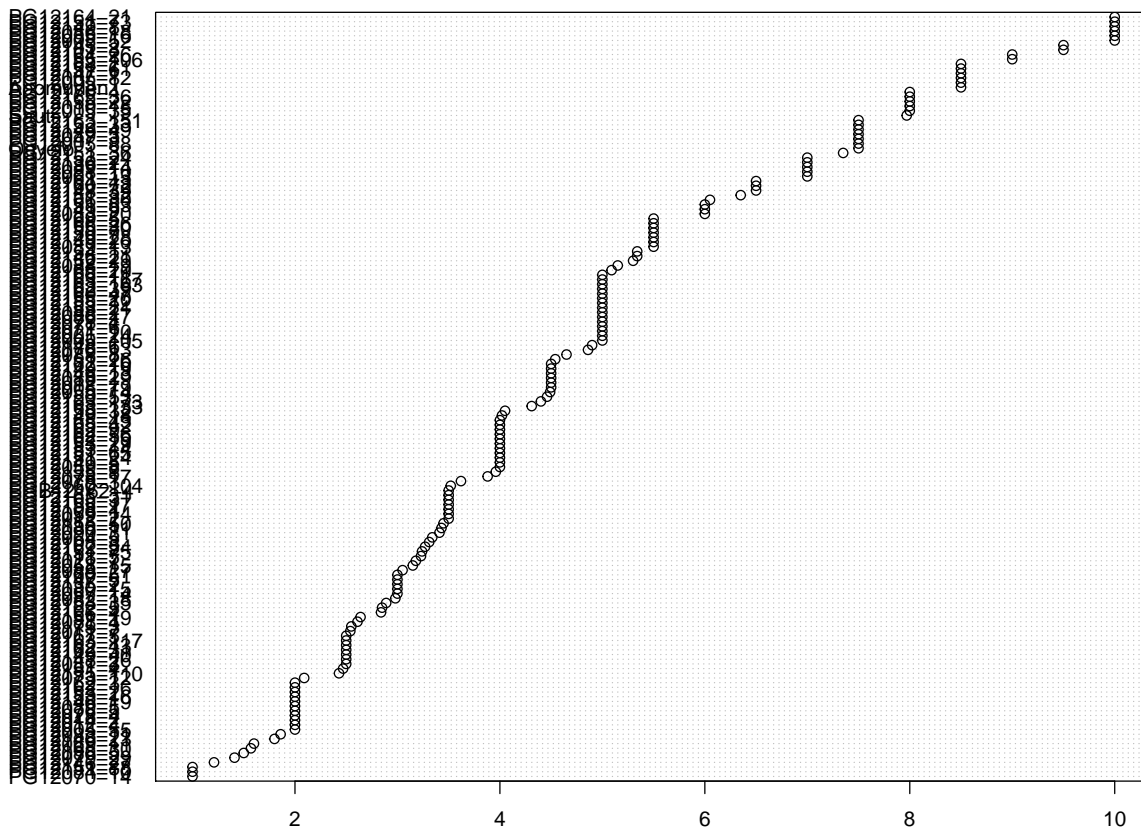
Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:
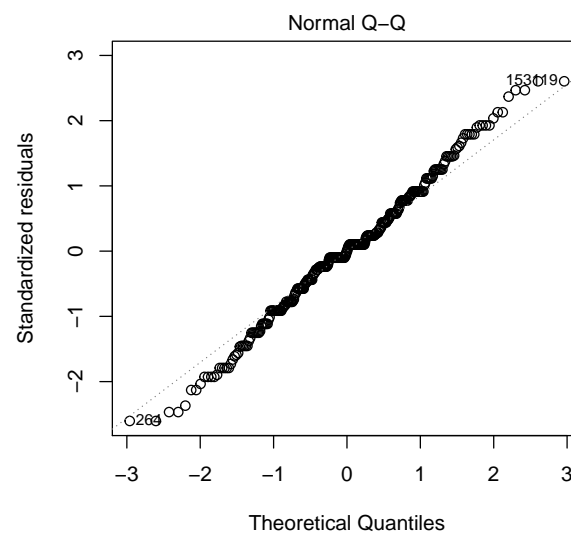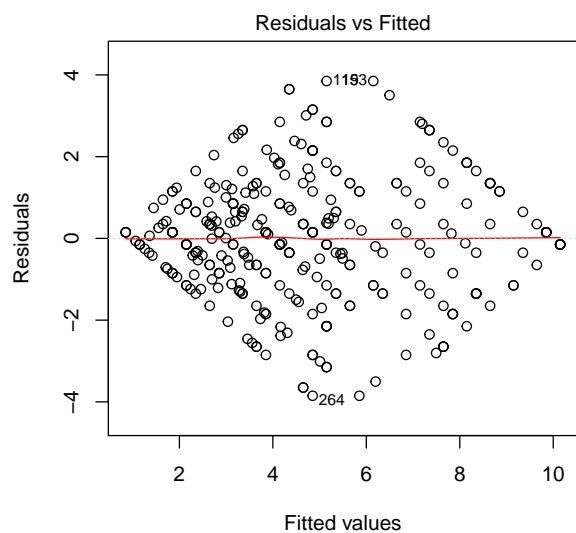
Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Analysis of Plants planted counting number per plot

You have fitted a linear model for a RCBD. The ANOVA table for your model is:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	162	3.91816e-29	2.41861e-31	1	0.5
REP	1	2.41861e-31	2.41861e-31	1	0.318802
Residuals	162	3.91816e-29	2.41861e-31	NA	NA

The means of your treatments are:

germplasmName	Plants planted counting number per plot
Apomuden	10
Ogyefo	10
PG12005-1	10
PG12005-105	10
PG12005-24	10
PG12005-35	10
PG12005-52	10
PG12005-55	10
PG12005-79	10
PG12005-82	10
PG12005-88	10
PG12010-15	10
PG12011-7	10
PG12012-1	10
PG12012-2	10
PG12012-4	10
PG12014-2	10
PG12021-10	10
PG12021-7	10
PG12028-4	10
PG12047-3	10
PG12055-14	10
PG12057-14	10
PG12058-15	10
PG12059-14	10
PG12059-8	10
PG12061-13	10
PG12064-5	10
PG12069-11	10
PG12070-14	10
PG12071-6	10
PG12073-12	10
PG12076-13	10
PG12076-5	10
PG12078-17	10
PG12078-3	10

germplasmName	Plants planted counting number per plot
PG12078-4	10
PG12079-29	10
PG12080-15	10
PG12081-3	10
PG12082-18	10
PG12083-11	10
PG12083-20	10
PG12084-10	10
PG12085-16	10
PG12086-11	10
PG12086-17	10
PG12086-18	10
PG12086-5	10
PG12088-10	10
PG12088-19	10
PG12088-2	10
PG12088-27	10
PG12088-29	10
PG12088-4	10
PG12088-8	10
PG12089-13	10
PG12089-14	10
PG12089-3	10
PG12089-5	10
PG12090-31	10
PG12101-3	10
PG12108-3	10
PG12108-4	10
PG12118-5	10
PG12135-2	10
PG12136-2	10
PG12145-2	10
PG12146-13	10
PG12146-19	10
PG12146-21	10
PG12146-23	10
PG12146-27	10
PG12147-1	10
PG12147-5	10
PG12148-26	10
PG12148-39	10
PG12148-6	10
PG12149-18	10
PG12149-19	10
PG12149-20	10
PG12149-28	10
PG12149-40	10
PG12149-49	10
PG12149-5	10
PG12149-8	10
PG12149-9	10
PG12150-53	10

germplasmName	Plants planted counting number per plot
PG12150-7	10
PG12151-19	10
PG12151-24	10
PG12151-26	10
PG12151-32	10
PG12151-36	10
PG12151-4	10
PG12151-53	10
PG12151-61	10
PG12151-65	10
PG12151-73	10
PG12151-75	10
PG12151-88	10
PG12152-29	10
PG12152-33	10
PG12153-14	10
PG12153-16	10
PG12153-2	10
PG12153-21	10
PG12153-24	10
PG12153-29	10
PG12153-35	10
PG12154-1	10
PG12155-106	10
PG12155-110	10
PG12155-12	10
PG12155-17	10
PG12155-20	10
PG12155-22	10
PG12155-30	10
PG12155-32	10
PG12155-50	10
PG12155-8	10
PG12160-104	10
PG12160-47	10
PG12160-51	10
PG12160-72	10
PG12162-10	10
PG12162-16	10
PG12162-19	10
PG12162-3	10
PG12162-31	10
PG12162-39	10
PG12162-43	10
PG12162-5	10
PG12162-54	10
PG12162-56	10
PG12162-9	10
PG12163-117	10
PG12163-133	10
PG12163-151	10
PG12163-163	10

germplasmName	Plants planted counting number per plot
PG12163-167	10
PG12163-173	10
PG12164-21	10
PG12164-26	10
PG12164-43	10
PG12165-20	10
PG12165-3	10
PG12165-30	10
PG12165-31	10
PG12165-36	10
PG12165-42	10
PG12165-43	10
PG12166-11	10
PG12166-26	10
PG12166-30	10
PG12166-4	10
PG12167-5	10
PG12168-2	10
PG12169-5	10
PG12170-4	10
PG12175-3	10
PGB12162-4	10
Sauti	10
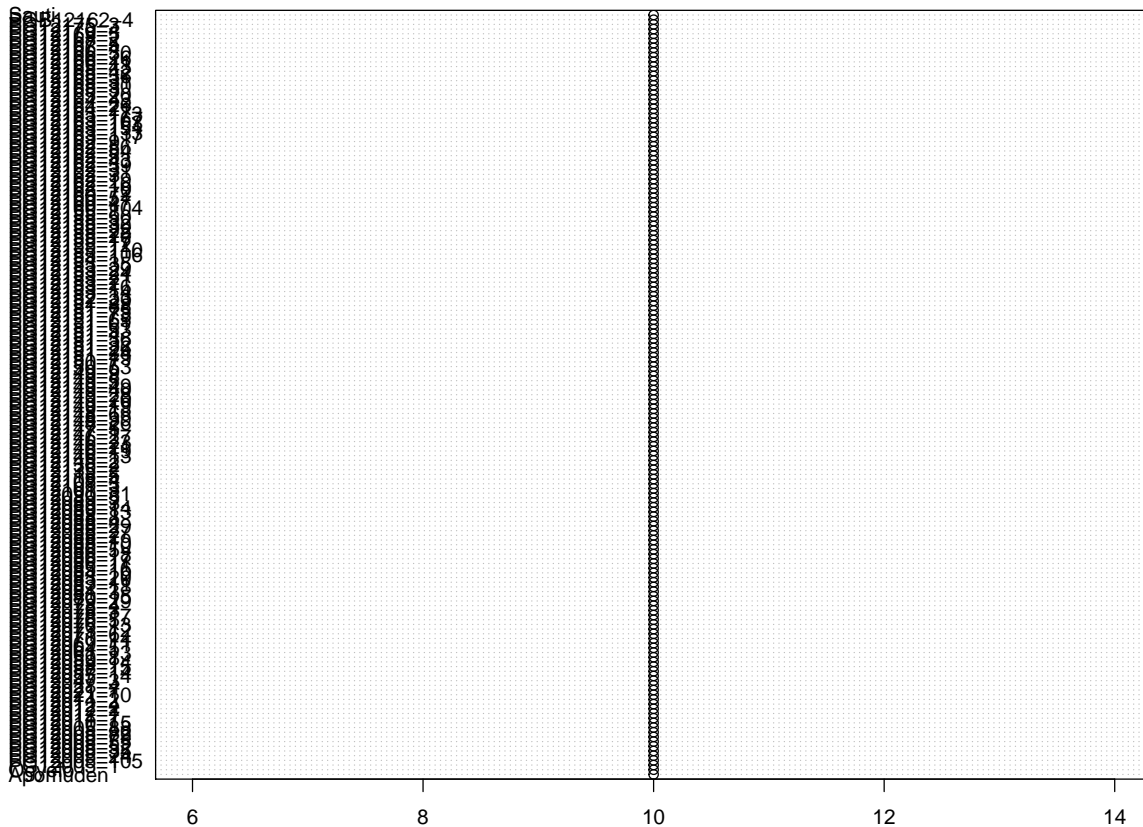
Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:
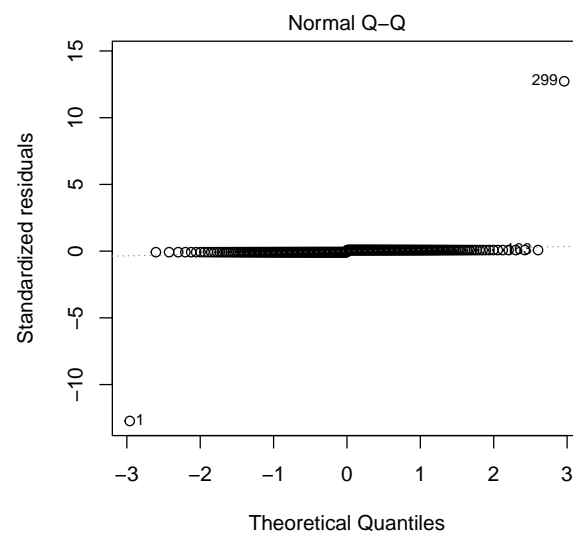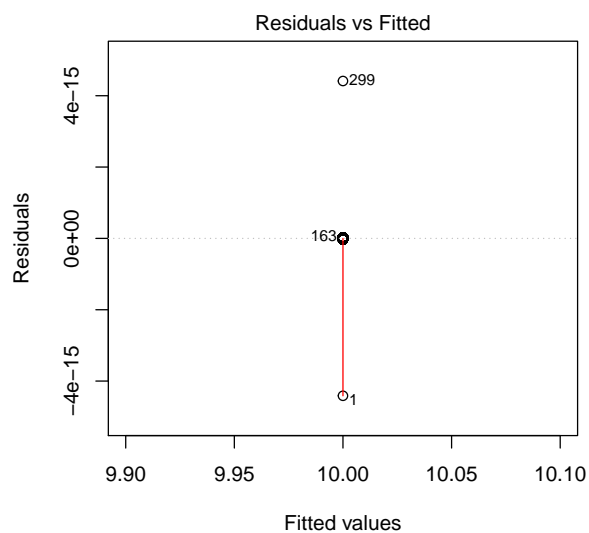
Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Analysis of Storage root damages estimatimg 1-9

You have fitted a linear model for a RCBD. The ANOVA table for your model is:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	162	458.331	2.82921	2.1394	8.93278e-07
REP	1	1.76687	1.76687	1.33608	0.249428
Residuals	162	214.233	1.32243	NA	NA

The p-value for treatments is 0.000000893278 which is significant at the 5% level.

The means of your treatments are:

germplasmName	Storage root damages estimatimg 1-9
Apomuden	6.5
Ogyefo	1.5
PG12005-1	2
PG12005-105	1.5
PG12005-24	1
PG12005-35	1.5
PG12005-52	1
PG12005-55	4
PG12005-79	1.5
PG12005-82	1
PG12005-88	2
PG12010-15	1.5
PG12011-7	1
PG12012-1	1.5
PG12012-2	1.5
PG12012-4	1.5
PG12014-2	2
PG12021-10	1
PG12021-7	1
PG12028-4	1
PG12047-3	2
PG12055-14	1
PG12057-14	1
PG12058-15	1
PG12059-14	1
PG12059-8	2
PG12061-13	1
PG12064-5	1
PG12069-11	1
PG12070-14	1
PG12071-6	1.5
PG12073-12	1
PG12076-13	1
PG12076-5	1

germplasmName	Storage root damages estimatimg 1-9
PG12078-17	1.5
PG12078-3	1.5
PG12078-4	2
PG12079-29	1
PG12080-15	2
PG12081-3	1.5
PG12082-18	1
PG12083-11	1
PG12083-20	2
PG12084-10	1
PG12085-16	2.5
PG12086-11	1
PG12086-17	4
PG12086-18	4.5
PG12086-5	3
PG12088-10	1.5
PG12088-19	1
PG12088-2	2
PG12088-27	1
PG12088-29	1.5
PG12088-4	1.5
PG12088-8	1.5
PG12089-13	2
PG12089-14	2
PG12089-3	2
PG12089-5	1.5
PG12090-31	1
PG12101-3	4
PG12108-3	1
PG12108-4	1
PG12118-5	1.5
PG12135-2	1.5
PG12136-2	1.5
PG12145-2	6
PG12146-13	1
PG12146-19	1
PG12146-21	1.5
PG12146-23	1
PG12146-27	1
PG12147-1	5
PG12147-5	1
PG12148-26	1.5
PG12148-39	1.5
PG12148-6	1
PG12149-18	1.5
PG12149-19	1
PG12149-20	2
PG12149-28	1.5
PG12149-40	1
PG12149-49	1.5
PG12149-5	2.5

germplasmName	Storage root damages estimatimg 1-9
PG12149-8	1
PG12149-9	2
PG12150-53	1.5
PG12150-7	2
PG12151-19	1
PG12151-24	1.5
PG12151-26	3.5
PG12151-32	1.5
PG12151-36	1.5
PG12151-4	1
PG12151-53	6.5
PG12151-61	7.5
PG12151-65	1.5
PG12151-73	2
PG12151-75	1
PG12151-88	1
PG12152-29	1
PG12152-33	2
PG12153-14	1.5
PG12153-16	3.5
PG12153-2	1.5
PG12153-21	3
PG12153-24	1
PG12153-29	2
PG12153-35	1
PG12154-1	1
PG12155-106	1.5
PG12155-110	1.5
PG12155-12	1
PG12155-17	1.5
PG12155-20	2
PG12155-22	2
PG12155-30	2
PG12155-32	1.5
PG12155-50	1
PG12155-8	1
PG12160-104	1.5
PG12160-47	2
PG12160-51	1
PG12160-72	3.5
PG12162-10	2
PG12162-16	1
PG12162-19	3.5
PG12162-3	1.5
PG12162-31	1
PG12162-39	1.5
PG12162-43	1
PG12162-5	4
PG12162-54	1
PG12162-56	3
PG12162-9	1.5

germplasmName	Storage root damages estimating 1-9
PG12163-117	1.5
PG12163-133	1
PG12163-151	2
PG12163-163	2.5
PG12163-167	3
PG12163-173	1.5
PG12164-21	4.5
PG12164-26	4
PG12164-43	3.5
PG12165-20	1
PG12165-3	1.5
PG12165-30	1
PG12165-31	2
PG12165-36	3.5
PG12165-42	2
PG12165-43	2
PG12166-11	3
PG12166-26	1
PG12166-30	1.5
PG12166-4	1.5
PG12167-5	5.5
PG12168-2	3.5
PG12169-5	1.5
PG12170-4	2.5
PG12175-3	1
PGB12162-4	2
Sauti	1
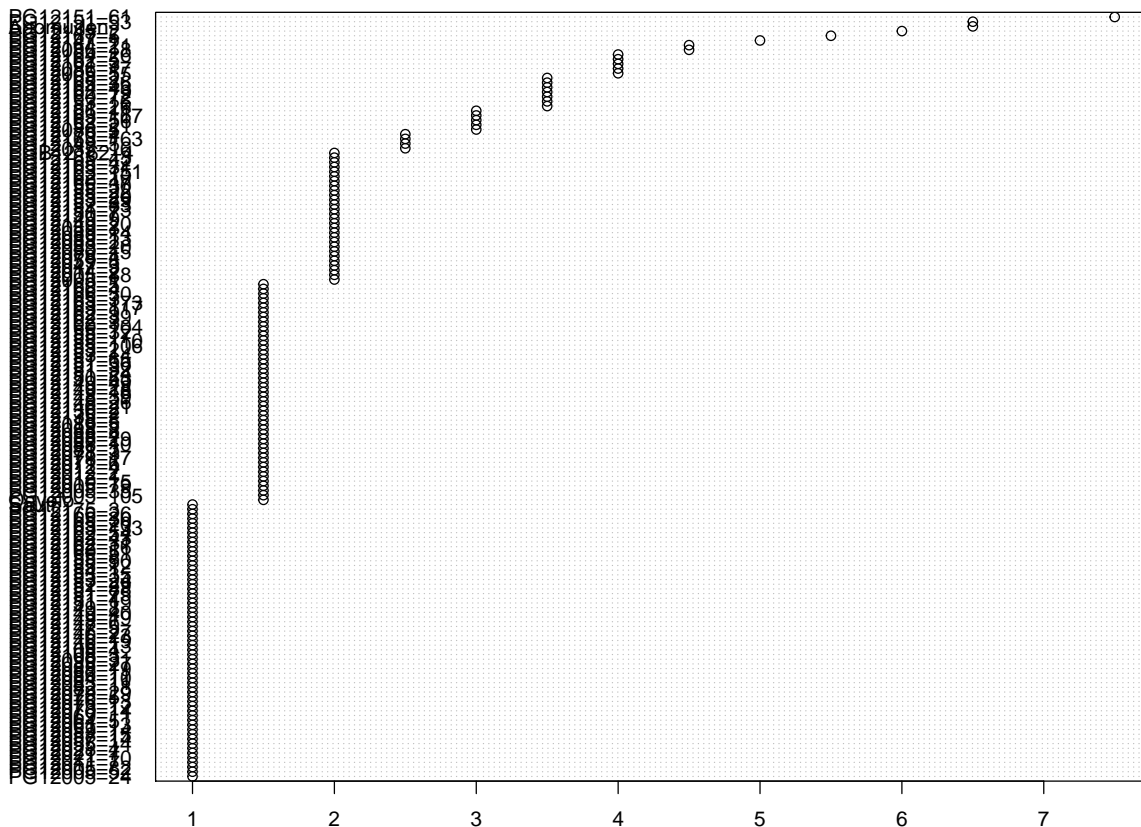
Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:

Residuals vs Fitted

Normal Q–Q

18
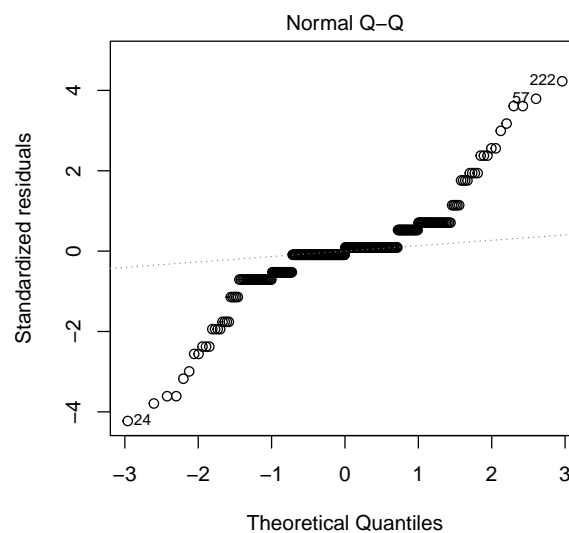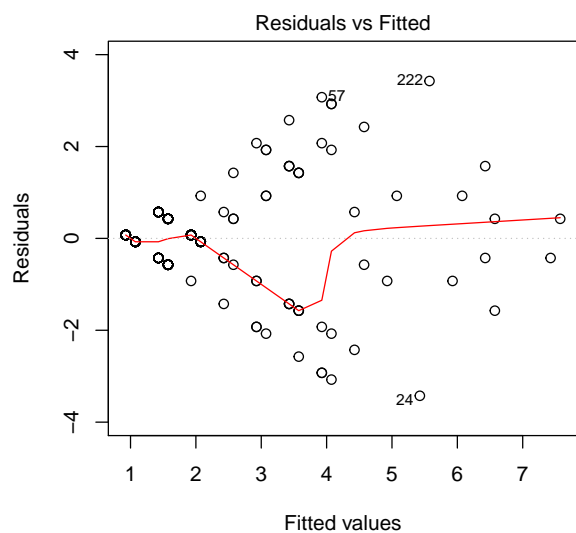
Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Analysis of Storage root size estimating 1-9

You have fitted a linear model for a RCBD. The ANOVA table for your model is:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	162	876.81	5.41241	2.03898	3.72307e-06
REP	1	3.97546	3.97546	1.49765	0.222811
Residuals	162	430.025	2.65447	NA	NA

The p-value for treatments is 0.00000372307 which is significant at the 5% level.

The means of your treatments are:

germplasmName	Storage root size estimating 1-9
Apomuden	6
Ogyefo	2.5
PG12005-1	4
PG12005-105	2
PG12005-24	1
PG12005-35	2
PG12005-52	1
PG12005-55	1.5
PG12005-79	2
PG12005-82	1
PG12005-88	2.5
PG12010-15	4
PG12011-7	1
PG12012-1	3
PG12012-2	2.5
PG12012-4	2
PG12014-2	2.5
PG12021-10	1
PG12021-7	1
PG12028-4	1
PG12047-3	3
PG12055-14	1
PG12057-14	1
PG12058-15	1
PG12059-14	1
PG12059-8	3.5
PG12061-13	1
PG12064-5	1
PG12069-11	1
PG12070-14	1
PG12071-6	2.5
PG12073-12	1
PG12076-13	1
PG12076-5	1
PG12078-17	1.5

germplasmName	Storage root size estimating 1-9
PG12078-3	1.5
PG12078-4	2.5
PG12079-29	1
PG12080-15	4
PG12081-3	2
PG12082-18	1
PG12083-11	1
PG12083-20	2
PG12084-10	1
PG12085-16	7
PG12086-11	1
PG12086-17	3
PG12086-18	3.5
PG12086-5	1.5
PG12088-10	2.5
PG12088-19	1
PG12088-2	5
PG12088-27	1
PG12088-29	1.5
PG12088-4	1.5
PG12088-8	2
PG12089-13	5.5
PG12089-14	6
PG12089-3	3.5
PG12089-5	3.5
PG12090-31	1
PG12101-3	5
PG12108-3	1
PG12108-4	1
PG12118-5	2.5
PG12135-2	3
PG12136-2	3
PG12145-2	6
PG12146-13	1
PG12146-19	1
PG12146-21	2
PG12146-23	1
PG12146-27	1
PG12147-1	6
PG12147-5	1
PG12148-26	2
PG12148-39	3
PG12148-6	1
PG12149-18	2.5
PG12149-19	1
PG12149-20	2
PG12149-28	3
PG12149-40	1
PG12149-49	2.5
PG12149-5	6.5
PG12149-8	1
PG12149-9	2

germplasmName	Storage root size estimating 1-9
PG12150-53	2
PG12150-7	2.5
PG12151-19	1
PG12151-24	2
PG12151-26	3.5
PG12151-32	3
PG12151-36	4
PG12151-4	1
PG12151-53	6
PG12151-61	2.5
PG12151-65	1.5
PG12151-73	8.5
PG12151-75	1
PG12151-88	1
PG12152-29	1
PG12152-33	2.5
PG12153-14	2.5
PG12153-16	3
PG12153-2	2
PG12153-21	4
PG12153-24	1
PG12153-29	3
PG12153-35	1
PG12154-1	1
PG12155-106	4
PG12155-110	1.5
PG12155-12	1
PG12155-17	3
PG12155-20	5.5
PG12155-22	3.5
PG12155-30	3.5
PG12155-32	1.5
PG12155-50	1
PG12155-8	1
PG12160-104	3
PG12160-47	5
PG12160-51	1
PG12160-72	5
PG12162-10	2.5
PG12162-16	1
PG12162-19	4
PG12162-3	1.5
PG12162-31	1
PG12162-39	1.5
PG12162-43	1
PG12162-5	1.5
PG12162-54	1
PG12162-56	2.5
PG12162-9	2
PG12163-117	2
PG12163-133	1
PG12163-151	6

germplasmName	Storage root size estimating 1-9
PG12163-163	4.5
PG12163-167	6
PG12163-173	1.5
PG12164-21	6.5
PG12164-26	5
PG12164-43	3.5
PG12165-20	1
PG12165-3	3.5
PG12165-30	1
PG12165-31	5
PG12165-36	3.5
PG12165-42	2.5
PG12165-43	4.5
PG12166-11	2
PG12166-26	1
PG12166-30	2
PG12166-4	2
PG12167-5	3
PG12168-2	5
PG12169-5	4
PG12170-4	3.5
PG12175-3	1
PGB12162-4	6
Sauti	1
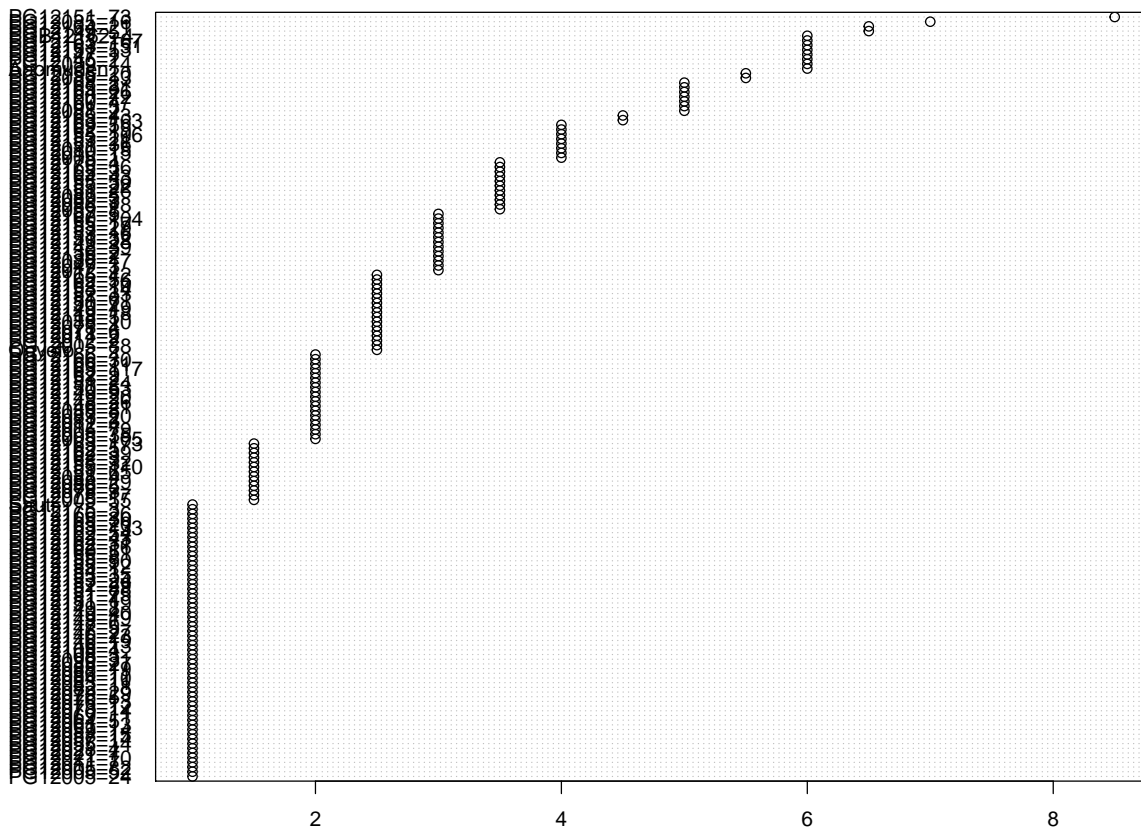
Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:
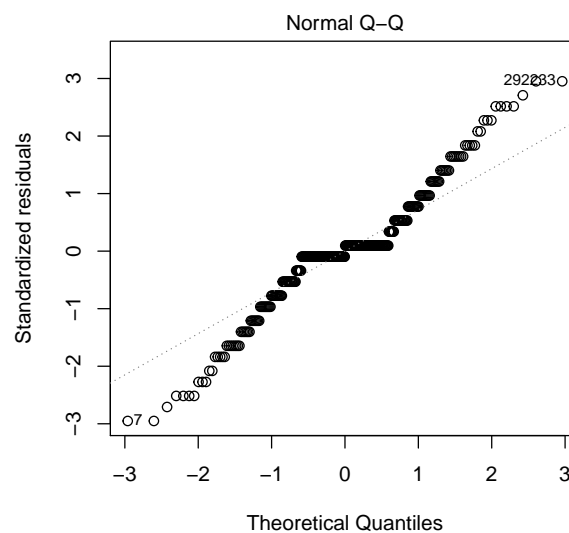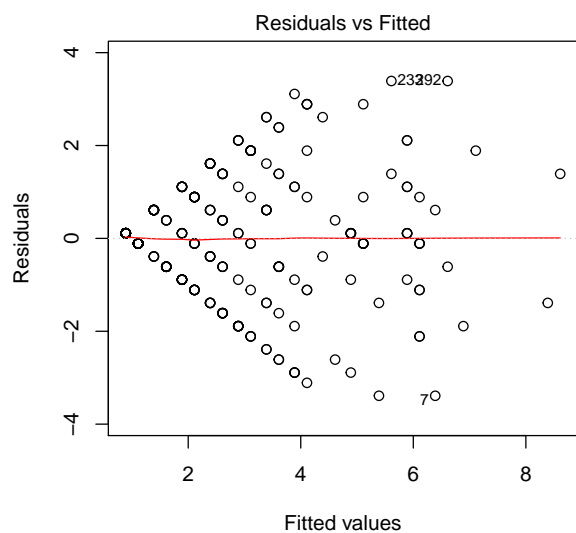
Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Analysis of Survival index computing percent

You have fitted a linear model for a RCBD. The ANOVA table for your model is:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	162	16.9666	0.104732	2.37905	2.90496e-08
REP	1	0.0725015	0.0725015	1.64691	0.201213
Residuals	162	7.13169	0.0440228	NA	NA

The p-value for treatments is 0.0000000290496 which is significant at the 5% level.

The means of your treatments are:

germplasmName	Survival index computing percent
Apomuden	0.85
Ogyefo	0.75
PG12005-1	0.85
PG12005-105	0.5
PG12005-24	0.5
PG12005-35	0.8
PG12005-52	1
PG12005-55	0.2
PG12005-79	0.45
PG12005-82	0.85
PG12005-88	0.75
PG12010-15	0.8
PG12011-7	0.254
PG12012-1	0.45
PG12012-2	0.35
PG12012-4	0.2
PG12014-2	0.2
PG12021-10	0.5
PG12021-7	0.318
PG12028-4	0.2
PG12047-3	0.75
PG12055-14	0.449
PG12057-14	0.3
PG12058-15	0.315
PG12059-14	0.35
PG12059-8	0.4
PG12061-13	0.7
PG12064-5	0.334
PG12069-11	0.16
PG12070-14	0.1
PG12071-6	0.5
PG12073-12	0.209
PG12076-13	0.486
PG12076-5	0.2
PG12078-17	0.388

germplasmName	Survival index computing percent
PG12078-3	0.362
PG12078-4	0.5
PG12079-29	0.141
PG12080-15	0.3
PG12081-3	0.25
PG12082-18	0.298
PG12083-11	0.186
PG12083-20	0.6
PG12084-10	0.1
PG12085-16	1
PG12086-11	0.343
PG12086-17	0.5
PG12086-18	1
PG12086-5	0.15
PG12088-10	0.7
PG12088-19	0.515
PG12088-2	0.5
PG12088-27	0.305
PG12088-29	0.45
PG12088-4	0.261
PG12088-8	0.465
PG12089-13	0.55
PG12089-14	0.7
PG12089-3	0.75
PG12089-5	0.2
PG12090-31	0.341
PG12101-3	0.95
PG12108-3	0.331
PG12108-4	0.35
PG12118-5	0.323
PG12135-2	0.3
PG12136-2	0.7
PG12145-2	0.95
PG12146-13	0.45
PG12146-19	0.2
PG12146-21	0.534
PG12146-23	0.18
PG12146-27	0.121
PG12147-1	0.85
PG12147-5	0.3
PG12148-26	0.25
PG12148-39	0.65
PG12148-6	0.49
PG12149-18	0.402
PG12149-19	0.45
PG12149-20	0.55
PG12149-28	0.55
PG12149-40	0.25
PG12149-49	0.75
PG12149-5	0.4
PG12149-8	1
PG12149-9	0.6

germplasmName	Survival index computing percent
PG12150-53	0.446
PG12150-7	0.55
PG12151-19	0.264
PG12151-24	0.4
PG12151-26	0.454
PG12151-32	0.635
PG12151-36	0.735
PG12151-4	0.247
PG12151-53	0.6
PG12151-61	0.85
PG12151-65	0.4
PG12151-73	1
PG12151-75	0.324
PG12151-88	0.1
PG12152-29	0.53
PG12152-33	0.75
PG12153-14	0.4
PG12153-16	0.2
PG12153-2	0.2
PG12153-21	0.5
PG12153-24	0.7
PG12153-29	0.4
PG12153-35	0.289
PG12154-1	0.534
PG12155-106	0.9
PG12155-110	0.243
PG12155-12	0.5
PG12155-17	0.35
PG12155-20	0.5
PG12155-22	0.8
PG12155-30	0.55
PG12155-32	0.405
PG12155-50	0.345
PG12155-8	0.396
PG12160-104	0.352
PG12160-47	0.5
PG12160-51	0.3
PG12160-72	0.65
PG12162-10	0.45
PG12162-16	0.2
PG12162-19	0.4
PG12162-3	0.2
PG12162-31	0.25
PG12162-39	0.5
PG12162-43	0.25
PG12162-5	0.285
PG12162-54	0.327
PG12162-56	0.4
PG12162-9	0.4
PG12163-117	0.25
PG12163-133	0.431
PG12163-151	0.75

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germplasmName	Survival index computing percent
PG12163-163	0.5
PG12163-167	0.5
PG12163-173	0.44
PG12164-21	1
PG12164-26	0.9
PG12164-43	0.65
PG12165-20	0.509
PG12165-3	0.35
PG12165-30	0.157
PG12165-31	0.35
PG12165-36	0.8
PG12165-42	0.4
PG12165-43	0.4
PG12166-11	0.5
PG12166-26	0.55
PG12166-30	0.605
PG12166-4	0.284
PG12167-5	0.25
PG12168-2	0.85
PG12169-5	0.55
PG12170-4	0.8
PG12175-3	0.255
PGB12162-4	0.35
Sauti	0.797
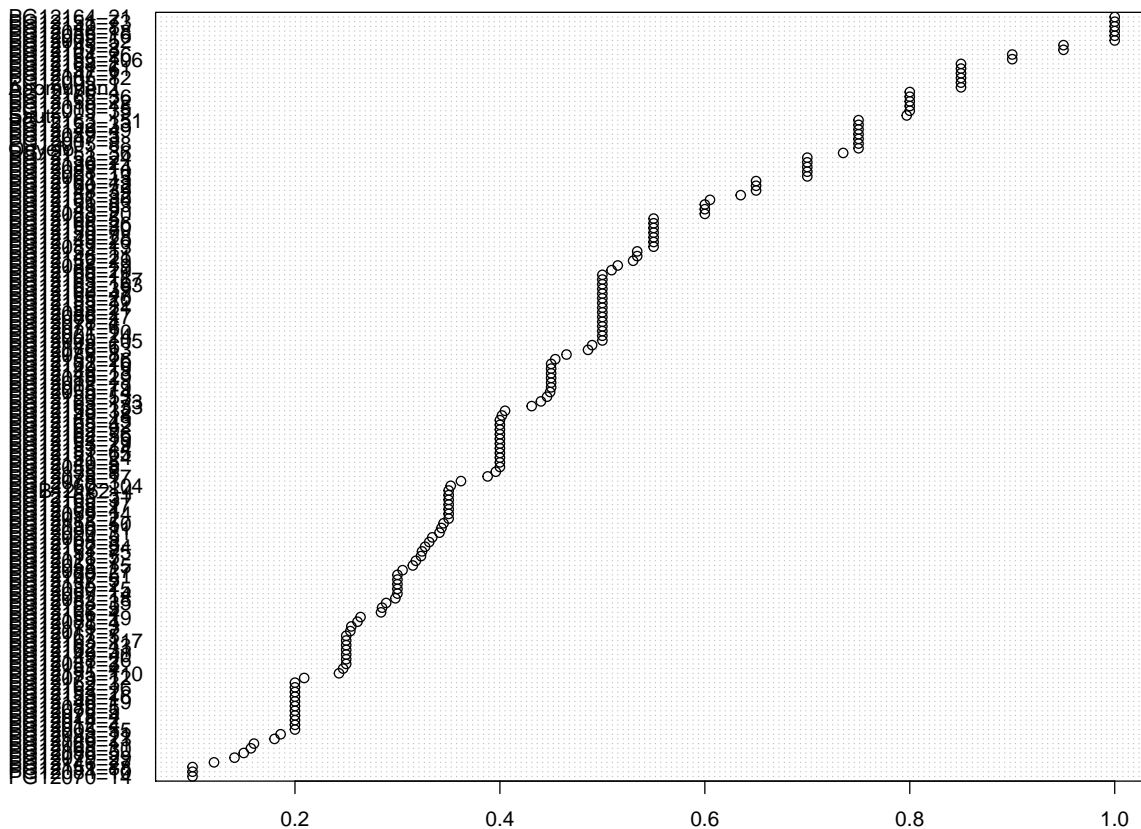
Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:
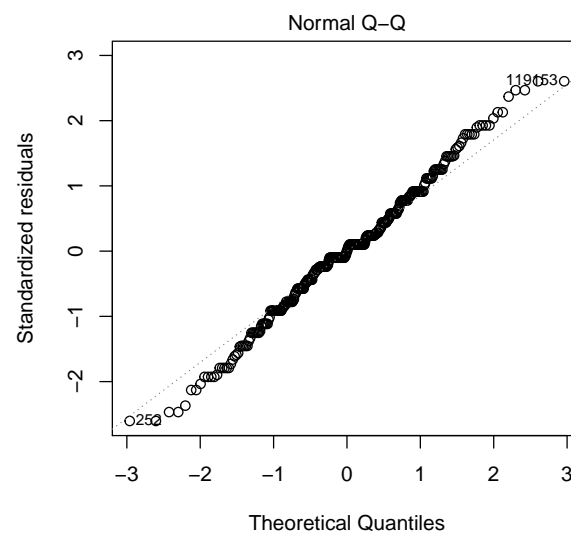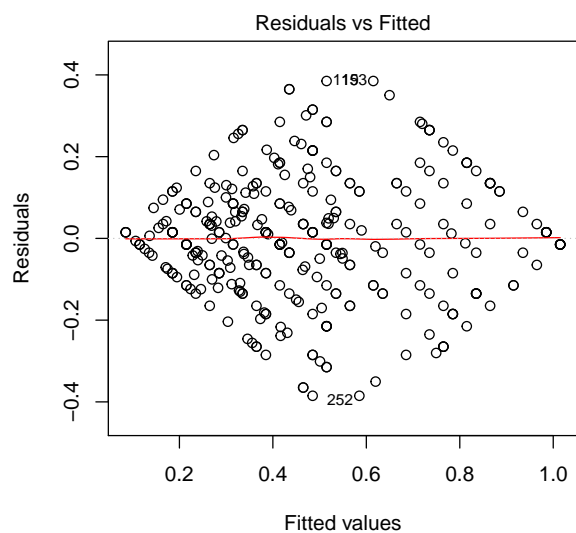
Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Analysis of Sweet potato weevil symptoms 1 estimating 1-9

You have fitted a linear model for a RCBD. The ANOVA table for your model is:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	162	149.16	0.920738	1.41742	0.013518
REP	1	1.76687	1.76687	2.71999	0.101036
Residuals	162	105.233	0.649587	NA	NA

The p-value for treatments is 0.013518 which is significant at the 5% level.

The means of your treatments are:

germplasmName	Sweet potato weevil symptoms 1 estimating 1-9
Apomuden	4
Ogyefo	1.5
PG12005-1	2
PG12005-105	1.5
PG12005-24	1
PG12005-35	1.5
PG12005-52	1
PG12005-55	1.5
PG12005-79	1.5
PG12005-82	1
PG12005-88	2
PG12010-15	1.5
PG12011-7	1
PG12012-1	1.5
PG12012-2	1.5
PG12012-4	1.5
PG12014-2	1.5
PG12021-10	1
PG12021-7	1
PG12028-4	1
PG12047-3	2
PG12055-14	1
PG12057-14	1
PG12058-15	1
PG12059-14	1
PG12059-8	4
PG12061-13	1
PG12064-5	1
PG12069-11	1
PG12070-14	1
PG12071-6	1.5
PG12073-12	1
PG12076-13	1
PG12076-5	1

germplasmName	Sweet potato weevil symptoms 1 estimating 1-9
PG12078-17	1.5
PG12078-3	1.5
PG12078-4	2
PG12079-29	1
PG12080-15	2
PG12081-3	3
PG12082-18	1
PG12083-11	1
PG12083-20	2
PG12084-10	1
PG12085-16	3
PG12086-11	1
PG12086-17	3.5
PG12086-18	2
PG12086-5	2
PG12088-10	1.5
PG12088-19	1
PG12088-2	2
PG12088-27	1
PG12088-29	1.5
PG12088-4	1.5
PG12088-8	1.5
PG12089-13	2
PG12089-14	3.5
PG12089-3	2
PG12089-5	1.5
PG12090-31	1
PG12101-3	2
PG12108-3	1
PG12108-4	1
PG12118-5	1.5
PG12135-2	1.5
PG12136-2	1.5
PG12145-2	2
PG12146-13	1
PG12146-19	1
PG12146-21	1.5
PG12146-23	1
PG12146-27	1
PG12147-1	3
PG12147-5	1
PG12148-26	1.5
PG12148-39	1.5
PG12148-6	1
PG12149-18	1.5
PG12149-19	1
PG12149-20	2
PG12149-28	1.5
PG12149-40	1
PG12149-49	1.5
PG12149-5	2

germplasmName	Sweet potato weevil symptoms 1 estimating 1-9
PG12149-8	1
PG12149-9	2
PG12150-53	1.5
PG12150-7	2
PG12151-19	1
PG12151-24	1.5
PG12151-26	1.5
PG12151-32	1.5
PG12151-36	1.5
PG12151-4	1
PG12151-53	2
PG12151-61	2
PG12151-65	1.5
PG12151-73	2
PG12151-75	1
PG12151-88	1
PG12152-29	1
PG12152-33	2
PG12153-14	3
PG12153-16	2
PG12153-2	1.5
PG12153-21	2
PG12153-24	1
PG12153-29	2
PG12153-35	1
PG12154-1	1
PG12155-106	2
PG12155-110	1.5
PG12155-12	1
PG12155-17	1.5
PG12155-20	2
PG12155-22	2
PG12155-30	2
PG12155-32	1.5
PG12155-50	1
PG12155-8	1
PG12160-104	1.5
PG12160-47	3.5
PG12160-51	1
PG12160-72	2
PG12162-10	2
PG12162-16	1
PG12162-19	2
PG12162-3	1.5
PG12162-31	1
PG12162-39	1.5
PG12162-43	1
PG12162-5	1.5
PG12162-54	1
PG12162-56	1.5
PG12162-9	1.5

germplasmName	Sweet potato weevil symptoms 1 estimating 1-9
PG12163-117	1.5
PG12163-133	1
PG12163-151	2
PG12163-163	2
PG12163-167	3.5
PG12163-173	1.5
PG12164-21	2
PG12164-26	2
PG12164-43	3.5
PG12165-20	1
PG12165-3	1.5
PG12165-30	1
PG12165-31	2
PG12165-36	3.5
PG12165-42	2
PG12165-43	2
PG12166-11	1.5
PG12166-26	1
PG12166-30	1.5
PG12166-4	1.5
PG12167-5	3.5
PG12168-2	2
PG12169-5	1.5
PG12170-4	1.5
PG12175-3	1
PGB12162-4	3
Sauti	1
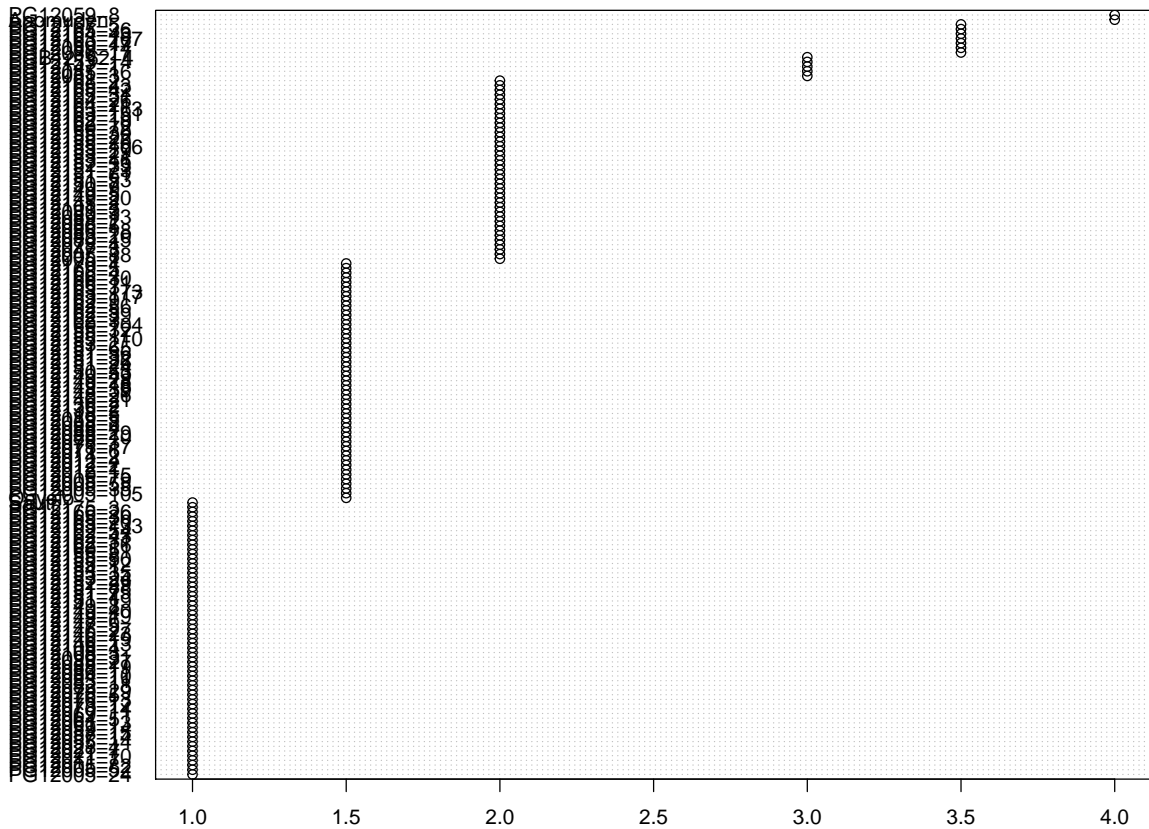
Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:
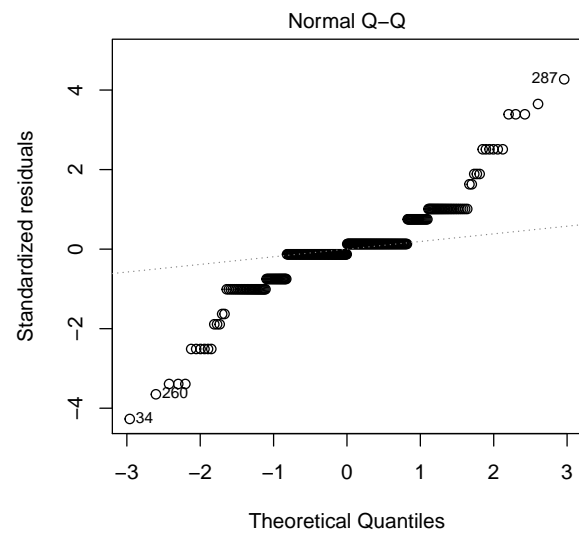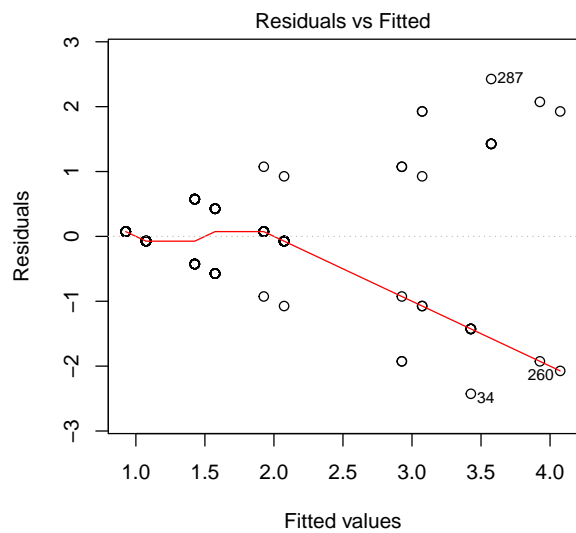
Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Analysis of Vine vigor 1 estimating 1-9

You have fitted a linear model for a RCBD. The ANOVA table for your model is:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	162	2434.2	15.0259	3.3211	6.07441e-14
REP	1	0.0490798	0.0490798	0.0108478	0.917177
Residuals	162	732.951	4.52439	NA	NA

The p-value for treatments is 0.0000000000000607441 which is significant at the 5% level.

The means of your treatments are:

germplasmName	Vine vigor 1 estimating 1-9
Apomuden	7.5
Ogyefo	10
PG12005-1	6.5
PG12005-105	9
PG12005-24	3
PG12005-35	5
PG12005-52	6.5
PG12005-55	3.5
PG12005-79	2
PG12005-82	8.5
PG12005-88	9
PG12010-15	7
PG12011-7	2
PG12012-1	3
PG12012-2	6.5
PG12012-4	2
PG12014-2	2
PG12021-10	5.5
PG12021-7	1
PG12028-4	2.5
PG12047-3	5
PG12055-14	1
PG12057-14	8.5
PG12058-15	3.5
PG12059-14	5.5
PG12059-8	6.5
PG12061-13	9
PG12064-5	1.5
PG12069-11	2
PG12070-14	2
PG12071-6	2
PG12073-12	5
PG12076-13	1.5
PG12076-5	5
PG12078-17	2

germplasmName	Vine vigor 1 estimating 1-9
PG12078-3	1.5
PG12078-4	6
PG12079-29	2
PG12080-15	5
PG12081-3	2.5
PG12082-18	2
PG12083-11	2
PG12083-20	5.5
PG12084-10	2
PG12085-16	7
PG12086-11	1.5
PG12086-17	5
PG12086-18	10
PG12086-5	4
PG12088-10	5
PG12088-19	3.5
PG12088-2	5.5
PG12088-27	2
PG12088-29	2
PG12088-4	1.5
PG12088-8	3
PG12089-13	5.5
PG12089-14	5
PG12089-3	4
PG12089-5	2
PG12090-31	1.5
PG12101-3	9.5
PG12108-3	1.5
PG12108-4	8
PG12118-5	2.5
PG12135-2	6
PG12136-2	7.5
PG12145-2	10
PG12146-13	6
PG12146-19	7
PG12146-21	8.5
PG12146-23	2.5
PG12146-27	3
PG12147-1	8.5
PG12147-5	2.5
PG12148-26	2
PG12148-39	8
PG12148-6	1
PG12149-18	2.5
PG12149-19	7
PG12149-20	4.5
PG12149-28	4.5
PG12149-40	2.5
PG12149-49	7
PG12149-5	5
PG12149-8	10
PG12149-9	4

germplasmName	Vine vigor 1 estimating 1-9
PG12150-53	5
PG12150-7	7.5
PG12151-19	2
PG12151-24	2
PG12151-26	8
PG12151-32	4.5
PG12151-36	5.5
PG12151-4	1
PG12151-53	4.5
PG12151-61	8
PG12151-65	2
PG12151-73	9.5
PG12151-75	3
PG12151-88	4
PG12152-29	1.5
PG12152-33	3
PG12153-14	2
PG12153-16	4.5
PG12153-2	7.5
PG12153-21	5.5
PG12153-24	9.5
PG12153-29	2
PG12153-35	4
PG12154-1	1
PG12155-106	8
PG12155-110	3
PG12155-12	3.5
PG12155-17	10
PG12155-20	7
PG12155-22	2
PG12155-30	7.5
PG12155-32	2
PG12155-50	1.5
PG12155-8	1.5
PG12160-104	5
PG12160-47	3.5
PG12160-51	2
PG12160-72	8
PG12162-10	5
PG12162-16	3
PG12162-19	3
PG12162-3	7.5
PG12162-31	3.5
PG12162-39	2.5
PG12162-43	2.5
PG12162-5	4.5
PG12162-54	4
PG12162-56	5.5
PG12162-9	7.5
PG12163-117	2.5
PG12163-133	1.5
PG12163-151	6

germplasmName	Vine vigor 1 estimating 1-9
PG12163-163	8
PG12163-167	9.5
PG12163-173	1.5
PG12164-21	10
PG12164-26	10
PG12164-43	8.5
PG12165-20	3.5
PG12165-3	2
PG12165-30	2
PG12165-31	3
PG12165-36	7
PG12165-42	4
PG12165-43	4.5
PG12166-11	7.5
PG12166-26	9.5
PG12166-30	7
PG12166-4	3.5
PG12167-5	4.5
PG12168-2	9.5
PG12169-5	8.5
PG12170-4	9
PG12175-3	1
PGB12162-4	5
Sauti	10
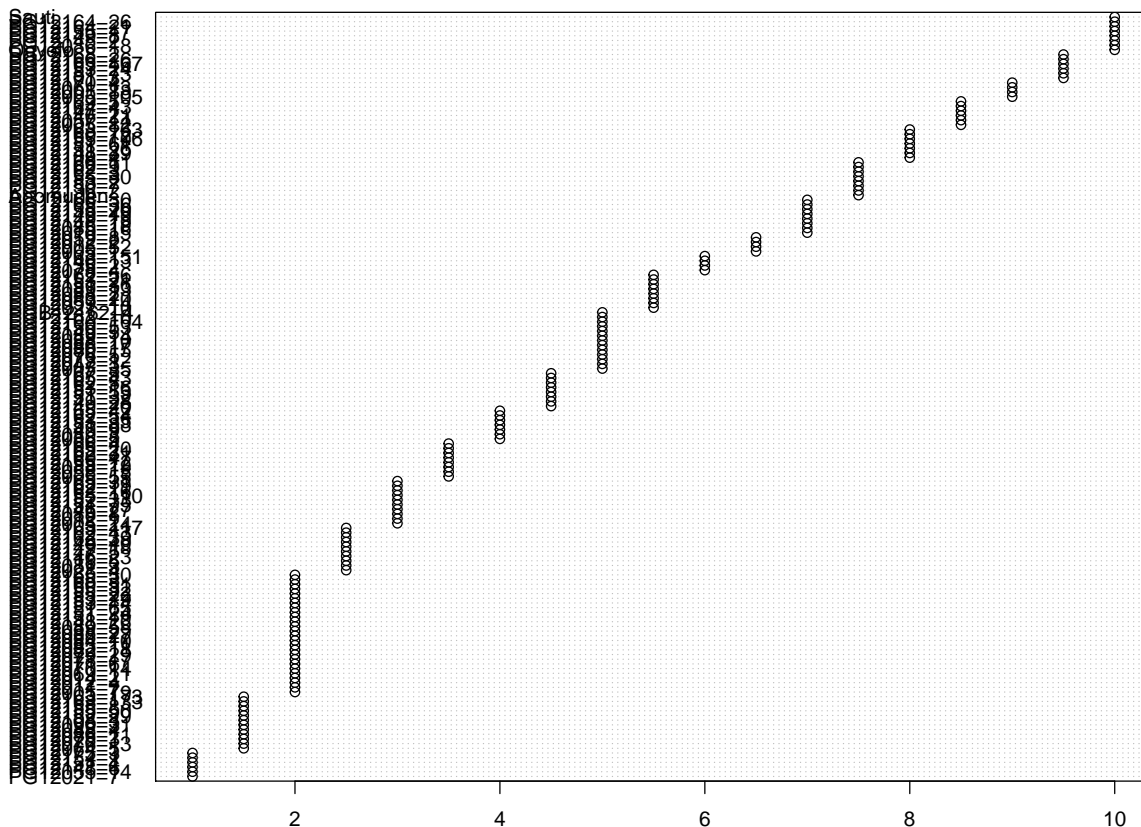
Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:

38
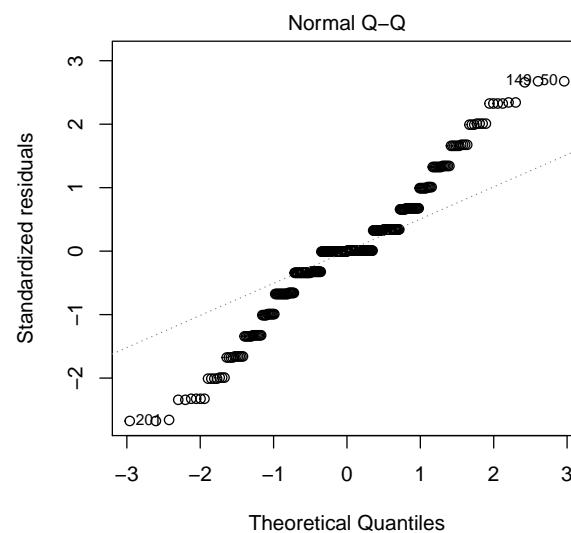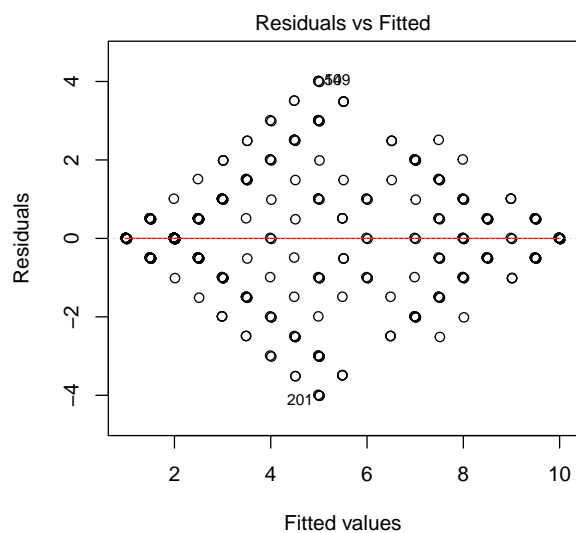
Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Analysis of Virus symptoms 2 estimating 1-9

You have fitted a linear model for a RCBD. The ANOVA table for your model is:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	162	1991.15	12.291	1.98412	8.07863e-06
REP	1	12.9601	12.9601	2.09213	0.149991
Residuals	162	1003.54	6.19469	NA	NA

The p-value for treatments is 0.00000807863 which is significant at the 5% level.

The means of your treatments are:

germplasmName	Virus symptoms 2 estimating 1-9
Apomuden	4.5
Ogyefo	5
PG12005-1	6
PG12005-105	4
PG12005-24	9.5
PG12005-35	8.5
PG12005-52	6.5
PG12005-55	9.5
PG12005-79	10
PG12005-82	7
PG12005-88	4.5
PG12010-15	5.5
PG12011-7	10
PG12012-1	9.5
PG12012-2	6
PG12012-4	10
PG12014-2	5
PG12021-10	8.5
PG12021-7	1
PG12028-4	9.5
PG12047-3	8.5
PG12055-14	1
PG12057-14	5
PG12058-15	9
PG12059-14	6.5
PG12059-8	5.5
PG12061-13	4.5
PG12064-5	5.5
PG12069-11	10
PG12070-14	10
PG12071-6	10
PG12073-12	2.5
PG12076-13	5.5
PG12076-5	8
PG12078-17	10

germplasmName	Virus symptoms 2 estimating 1-9
PG12078-3	5.5
PG12078-4	7
PG12079-29	10
PG12080-15	8
PG12081-3	9.5
PG12082-18	10
PG12083-11	10
PG12083-20	7.5
PG12084-10	10
PG12085-16	6.5
PG12086-11	5.5
PG12086-17	8
PG12086-18	4.5
PG12086-5	9
PG12088-10	8.5
PG12088-19	3
PG12088-2	7.5
PG12088-27	10
PG12088-29	10
PG12088-4	5.5
PG12088-8	3.5
PG12089-13	8
PG12089-14	9
PG12089-3	9.5
PG12089-5	10
PG12090-31	5.5
PG12101-3	5
PG12108-3	5.5
PG12108-4	7
PG12118-5	9.5
PG12135-2	6.5
PG12136-2	5
PG12145-2	5.5
PG12146-13	6
PG12146-19	4
PG12146-21	7.5
PG12146-23	9.5
PG12146-27	4
PG12147-1	4.5
PG12147-5	9.5
PG12148-26	10
PG12148-39	7
PG12148-6	1
PG12149-18	5
PG12149-19	5.5
PG12149-20	9
PG12149-28	9
PG12149-40	9.5
PG12149-49	6.5
PG12149-5	7
PG12149-8	3.5
PG12149-9	9

germplasmName	Virus symptoms 2 estimating 1-9
PG12150-53	2
PG12150-7	7.5
PG12151-19	10
PG12151-24	10
PG12151-26	5.5
PG12151-32	3.5
PG12151-36	8
PG12151-4	1
PG12151-53	8.5
PG12151-61	5.5
PG12151-65	10
PG12151-73	3.5
PG12151-75	3.5
PG12151-88	8
PG12152-29	5.5
PG12152-33	9.5
PG12153-14	10
PG12153-16	8
PG12153-2	7
PG12153-21	8.5
PG12153-24	4.5
PG12153-29	10
PG12153-35	4
PG12154-1	1
PG12155-106	7.5
PG12155-110	9
PG12155-12	9
PG12155-17	6
PG12155-20	6.5
PG12155-22	10
PG12155-30	6
PG12155-32	10
PG12155-50	5.5
PG12155-8	5.5
PG12160-104	3
PG12160-47	9
PG12160-51	10
PG12160-72	7
PG12162-10	8.5
PG12162-16	9.5
PG12162-19	9.5
PG12162-3	6
PG12162-31	7.5
PG12162-39	9.5
PG12162-43	9.5
PG12162-5	3.5
PG12162-54	4
PG12162-56	6.5
PG12162-9	7
PG12163-117	10
PG12163-133	5.5
PG12163-151	8

germplasmName	Virus symptoms 2 estimating 1-9
PG12163-163	7.5
PG12163-167	5.5
PG12163-173	5.5
PG12164-21	4
PG12164-26	4.5
PG12164-43	5
PG12165-20	4.5
PG12165-3	10
PG12165-30	10
PG12165-31	9.5
PG12165-36	6
PG12165-42	9.5
PG12165-43	8.5
PG12166-11	4.5
PG12166-26	6.5
PG12166-30	7.5
PG12166-4	9
PG12167-5	8
PG12168-2	5
PG12169-5	6
PG12170-4	4
PG12175-3	1
PGB12162-4	9
Sauti	3.5
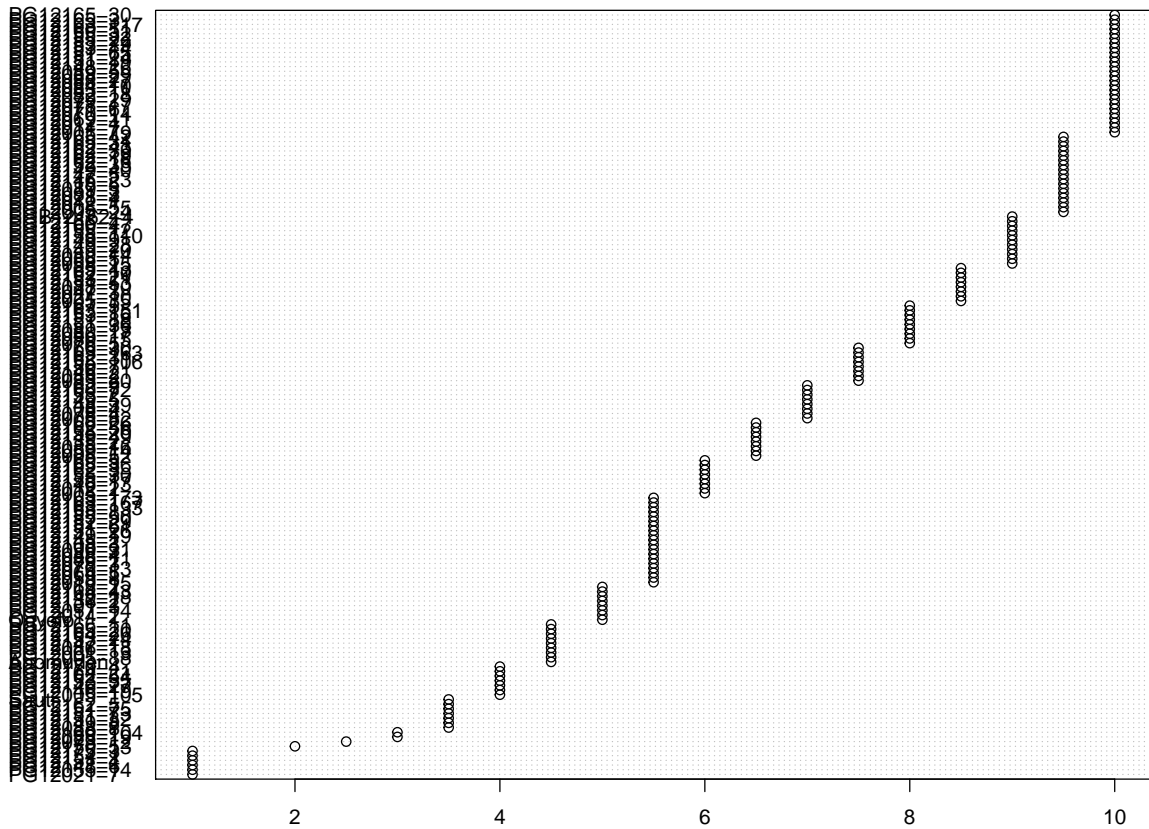
Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:
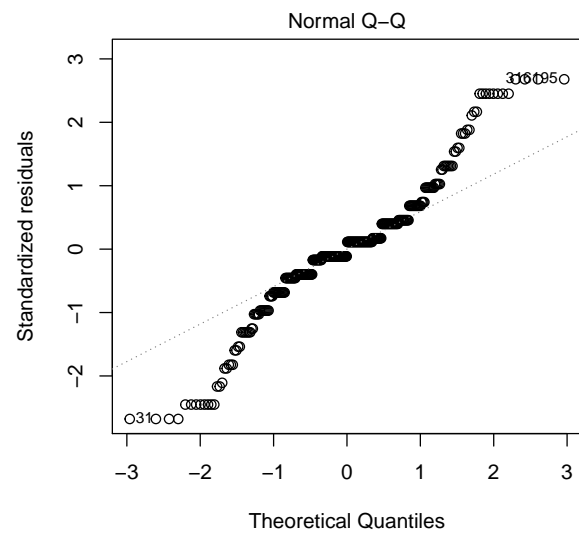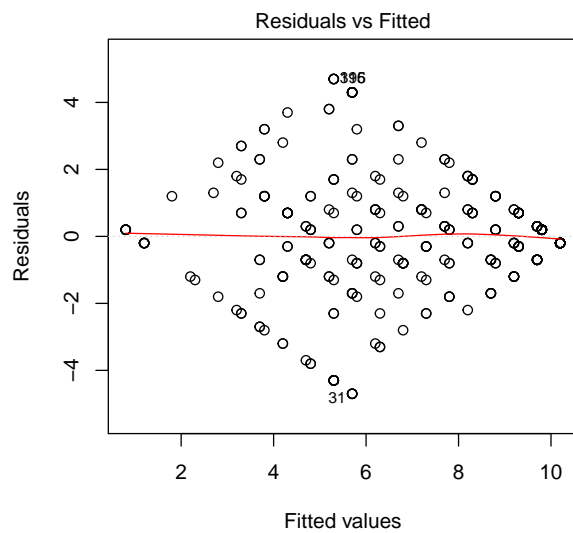
Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Analysis of Weight of vines measuring kg per plot

You have fitted a linear model for a RCBD. The ANOVA table for your model is:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	162	4005.84	24.7274	2.95805	8.31124e-12
REP	1	77.7463	77.7463	9.3005	0.00267688
Residuals	162	1354.22	8.35937	NA	NA

The p-value for treatments is 0.00000000000831124 which is significant at the 5% level.

The means of your treatments are:

germplasmName	Weight of vines measuring kg per plot
Apomuden	5.85
Ogyefo	9.4
PG12005-1	6.15
PG12005-105	9.6
PG12005-24	3
PG12005-35	5
PG12005-52	16.4
PG12005-55	1.85
PG12005-79	2.5
PG12005-82	9.92
PG12005-88	10.8
PG12010-15	5.3
PG12011-7	1.63
PG12012-1	0.9
PG12012-2	2.25
PG12012-4	1.57
PG12014-2	2.37
PG12021-10	2
PG12021-7	2.28
PG12028-4	1.35
PG12047-3	2.83
PG12055-14	3.04
PG12057-14	3.65
PG12058-15	1.38
PG12059-14	5.85
PG12059-8	6.75
PG12061-13	9.35
PG12064-5	2.77
PG12069-11	0.673
PG12070-14	0.75
PG12071-6	0.75
PG12073-12	2.15
PG12076-13	3.03
PG12076-5	1.65
PG12078-17	1.24

germplasmName	Weight of vines measuring kg per plot
PG12078-3	2.16
PG12078-4	1.5
PG12079-29	1
PG12080-15	0.75
PG12081-3	4.2
PG12082-18	2.11
PG12083-11	1.05
PG12083-20	2.55
PG12084-10	0.7
PG12085-16	7.35
PG12086-11	2.3
PG12086-17	0.75
PG12086-18	15.9
PG12086-5	1.05
PG12088-10	2.75
PG12088-19	4.82
PG12088-2	4.65
PG12088-27	1.23
PG12088-29	1.55
PG12088-4	0.975
PG12088-8	2.94
PG12089-13	1.8
PG12089-14	2.45
PG12089-3	2.8
PG12089-5	1.05
PG12090-31	1.91
PG12101-3	7.6
PG12108-3	2.69
PG12108-4	6.25
PG12118-5	1.52
PG12135-2	2.1
PG12136-2	4.95
PG12145-2	15.4
PG12146-13	2.6
PG12146-19	2.3
PG12146-21	8.1
PG12146-23	0.892
PG12146-27	1.42
PG12147-1	4.5
PG12147-5	0.985
PG12148-26	1.1
PG12148-39	3.8
PG12148-6	4.32
PG12149-18	2.04
PG12149-19	4.65
PG12149-20	1.8
PG12149-28	3.85
PG12149-40	0.99
PG12149-49	4.15
PG12149-5	5.19
PG12149-8	15.2
PG12149-9	4.55

germplasmName	Weight of vines measuring kg per plot
PG12150-53	4.62
PG12150-7	5.2
PG12151-19	1.19
PG12151-24	2.65
PG12151-26	4.95
PG12151-32	2.59
PG12151-36	5.31
PG12151-4	1.8
PG12151-53	3.63
PG12151-61	5.7
PG12151-65	0.988
PG12151-73	16.9
PG12151-75	1.86
PG12151-88	0.95
PG12152-29	5.17
PG12152-33	3.05
PG12153-14	0.8
PG12153-16	1.45
PG12153-2	2.35
PG12153-21	8.9
PG12153-24	8.9
PG12153-29	1.4
PG12153-35	3.27
PG12154-1	4.34
PG12155-106	9.7
PG12155-110	1.11
PG12155-12	5.5
PG12155-17	9.4
PG12155-20	4.95
PG12155-22	3.9
PG12155-30	5.7
PG12155-32	1.61
PG12155-50	1.83
PG12155-8	3.01
PG12160-104	3.05
PG12160-47	1
PG12160-51	1
PG12160-72	5.85
PG12162-10	1.2
PG12162-16	0.5
PG12162-19	1.25
PG12162-3	2.2
PG12162-31	0.5
PG12162-39	0.75
PG12162-43	0.75
PG12162-5	2.45
PG12162-54	2.67
PG12162-56	3.55
PG12162-9	2.75
PG12163-117	1.76
PG12163-133	3.75
PG12163-151	3.15

germplasmName	Weight of vines measuring kg per plot
PG12163-163	4.7
PG12163-167	5.45
PG12163-173	3.02
PG12164-21	9.4
PG12164-26	11.5
PG12164-43	5.25
PG12165-20	3.43
PG12165-3	1.45
PG12165-30	0.7
PG12165-31	1.75
PG12165-36	2.95
PG12165-42	1.85
PG12165-43	2.95
PG12166-11	5.25
PG12166-26	8.2
PG12166-30	4.6
PG12166-4	2
PG12167-5	1.75
PG12168-2	12.2
PG12169-5	7.9
PG12170-4	5.1
PG12175-3	1.32
PGB12162-4	1.1
Sauti	17.4
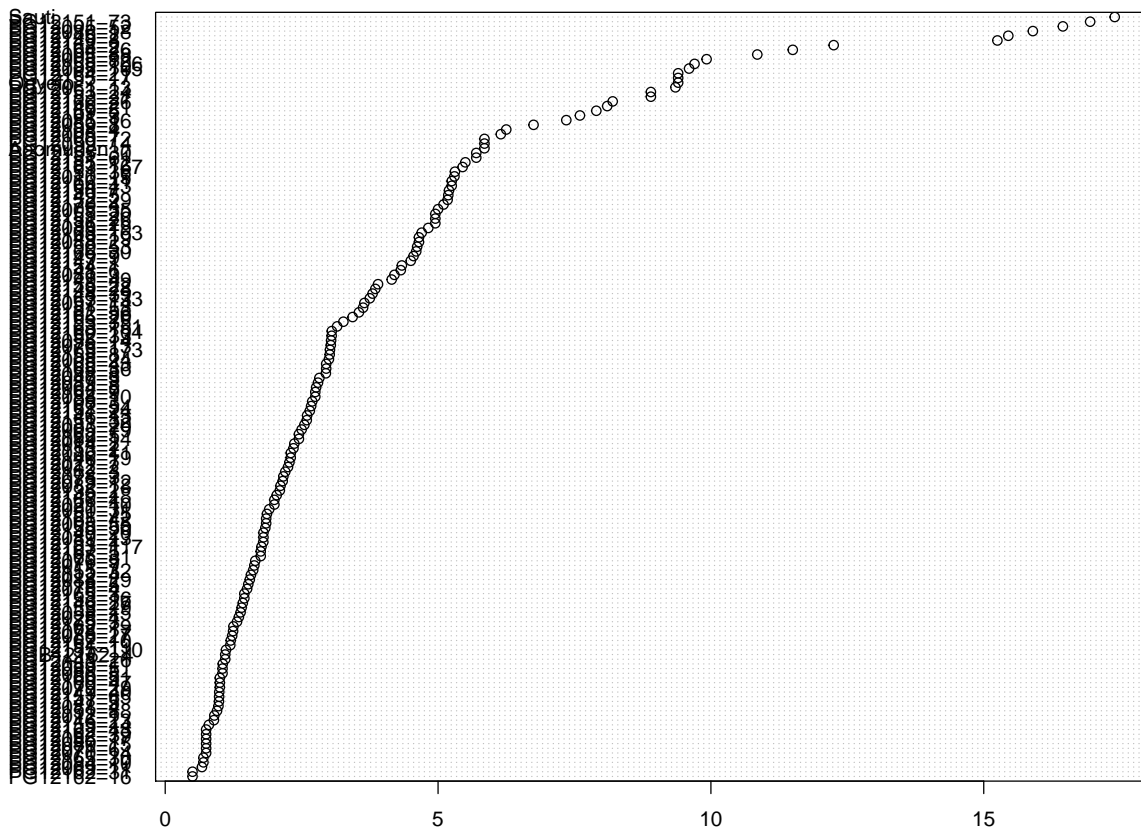
Do not forget the assumptions of the model. It is supposed that the error has a normal distribution with the same variance for all the treatments. The following plots must help you evaluate this:

Residuals vs Fitted

Residuals

Fitted values

Normal Q–Q

Standardized residuals

Theoretical Quantiles
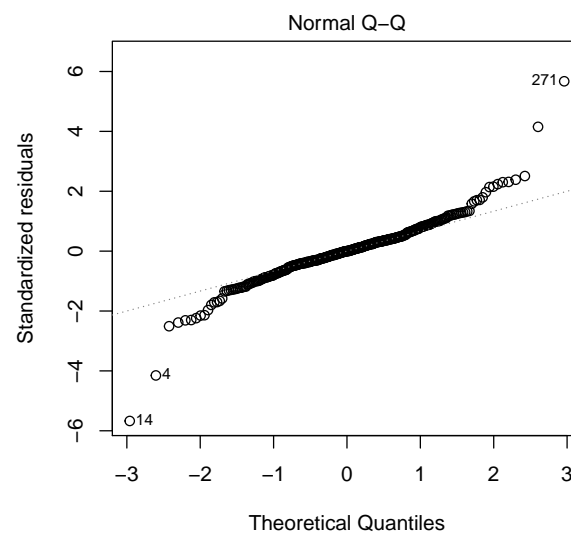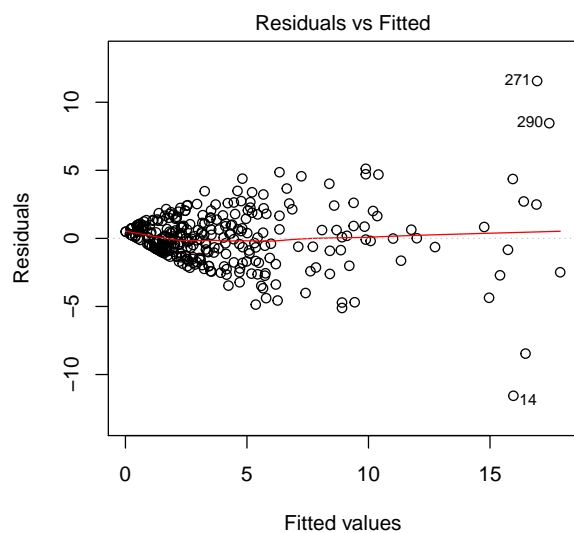
Funnel shapes for the first plot may suggest heterogeneity of variances while departures from the theoretical normal line are symptoms of lack of normality.

Trait correlations

Variety candidate selection

Summary

References

Data sources

Literature