

ANOVA for a RCBD trial: SPYLUN2012_MZ-Estacao Agraria do Umbeluzi

reinhardsimon using HIDAP

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This is an automatedly created report.

See more details in section on materials.

Alternate formats:

PDF DOCX

Abstract

This trial has the identifier SPYLUN2012_MZ-Estacao Agraria do Umbeluzi. It was conducted under the supervision of x y as a Advanced Trial as part of a Yield Breeding Program in Estacao Agraria do Umbeluzi, Mozambique, Z in 2016. A total of 59 clones (including reference clones) were evaluated for 34 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 59 treatments, evaluated using a randomized 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, $\epsilon_{ij} \sim N(0, \sigma_e^2)$.

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, Fibers in cooked samples 1 estimating 1-9, 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, Overall taste of cooked sample 1 estimating 1-9, Plants established 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 estimating 1-9, Storage root dry matter content computing percent, Storage root form estimating 1-9, Storage root size estimating 1-9, Storage root starch content measuring percent, Storage root sweetness 1 estimating 1-9, Storage root texture 1 estimating 1-9, Sucrose content measuring percent, Survival index computing percent, Sweet potato weevil symptoms 1 estimating 1-9, Total carotenoids measuring mg per 100g, Vine vigor 1 estimating 1-9, Virus symptoms 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: MUSG11030-9, MUSG11049-5, MUSG11016-16, MUSG11001-2, MUSG11049-7, MUSG11046-18, MUSG11003-10, MUSG11016-2, MUSG11022-10, MUSG11026-11, Resisto, MUSG11010-11, MUSG11049-16, MUSG11048-15, MUSG11023-11, MUSG11022-11, MUSG11016-19, MUSG11021-16, MUSG11016-12, MUSG11004-9, MUSG11012-14, MUSG11016-21, Jonathan, MUSG11046-7, MUSG11036-3, MUSG11006-8, MUSG11033-6, MUSG11010-7, MUSG11044-15, MUSG11040-15, MUSG11050-3, MUSG11011-3, MUSG11016-14, MUSG11022-1, MUSG11002-9, MUSG11044-16, MUSG11046-3, MUSG11008-12, MUSG11040-16, MUSG11001-11, MUSG11042-7, MUSG11016-18, MUSG11046-14, MUSG11019-5, Chingova, MUSG11006-15, MUSG11010-19, MUSG11049-3, MUSG11019-15, MUSG11016-22, MUSG11004-5, MUSG11048-16, MUSG11040-13, MUSG11049-2, MUSG11007-15, MUSG11019-17, MUSG11007-1, MUSG11003-2, MUSG11016-10.

Computational tools

This report was created using x86_64-apple-darwin13.4.0, x86_64, darwin13.4.0, x86_64, darwin13.4.0, , 3, 2.3, 2015, 12, 10, 69752, R, R version 3.2.3 (2015-12-10), Wooden Christmas-Tree on a x86_64-apple-darwin13.4.0 (64-bit) running OS X 10.11.3 (El Capitan) in . The following base packages were loaded: **stats**, **graphics**, **grDevices**, **utils**, **datasets**, **methods**, **base** and the following additional packages: **brapi**, **shinyURL**, **rmdformats**, **knitr**, **qtlcharts**, **d3heatmap**, **rhandsontable**, **dplyr**, **shinydashboard**, **ggplot2**, **leaflet**, **miniUI**, **shiny**.

Results

Raw data

Trait summaries

Trait analyses

The following traits were not analyzed since they had too many missing values ($\geq 10\%$): Sucrose content measuring percent. For the remaining traits missing values were imputed using all available information.

Valid traits: **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**, **Fibers in cooked samples 1 estimating 1-9**, **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**, **Overall taste of cooked sample 1 estimating 1-9**, **Plants established 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 estimating 1-9**, **Storage root dry matter content computing percent**, **Storage root form estimating 1-9**, **Storage root size estimating 1-9**, **Storage root starch content measuring percent**, **Storage root sweetness 1 estimating 1-9**, **Storage root texture 1 estimating 1-9**, **Survival index computing percent**, **Sweet potato weevil symptoms 1 estimating 1-9**, **Total carotenoids measuring mg per 100g**, **Vine vigor 1 estimating 1-9**, **Virus symptoms 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**.

Analysis of Beta carotene content measuring mg per 100g

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

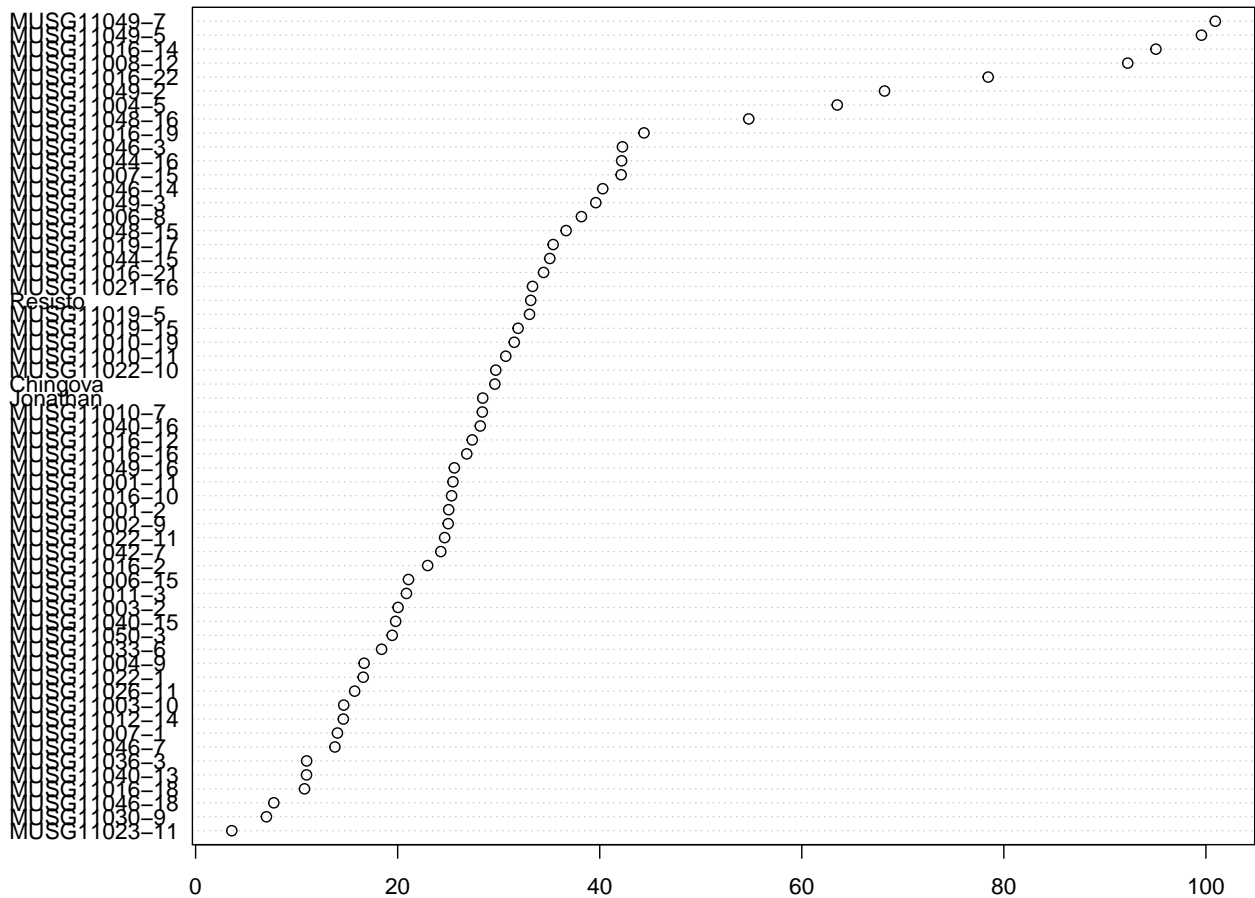
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	58525	1009.05	4.73472	8.78612e-09
REP	1	2.92105	2.92105	0.0137063	0.907206
Residuals	58	12360.8	213.117	NA	NA

The p-value for treatments is 0.00000000878612 which is significant at the 5% level.

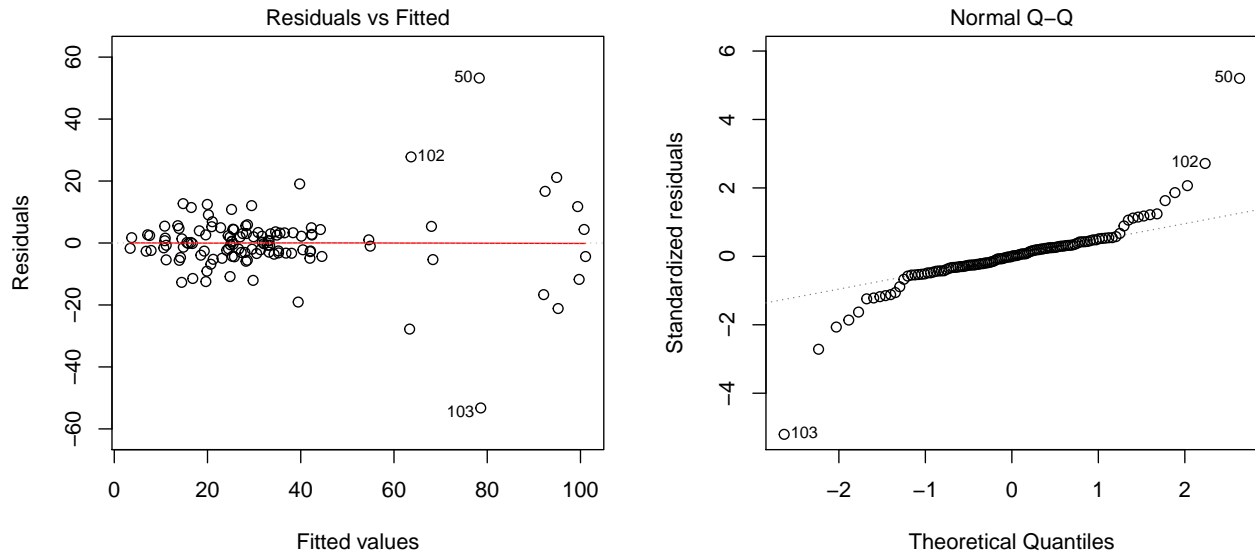
The means of your treatments are:

germplasmName	Beta carotene content measuring mg per 100g
Chingova	29.6
Jonathan	28.4
MUSG11001-11	25.5
MUSG11001-2	25.1
MUSG11002-9	25
MUSG11003-10	14.7
MUSG11003-2	20
MUSG11004-5	63.5
MUSG11004-9	16.7
MUSG11006-15	21.1
MUSG11006-8	38.2
MUSG11007-1	14
MUSG11007-15	42.1
MUSG11008-12	92.3
MUSG11010-11	30.7
MUSG11010-19	31.5
MUSG11010-7	28.4
MUSG11011-3	20.9
MUSG11012-14	14.6
MUSG11016-10	25.3
MUSG11016-12	27.4
MUSG11016-14	95
MUSG11016-16	26.8
MUSG11016-18	10.8
MUSG11016-19	44.4
MUSG11016-2	23
MUSG11016-21	34.4
MUSG11016-22	78.5
MUSG11019-15	31.9
MUSG11019-17	35.4
MUSG11019-5	33
MUSG11021-16	33.4
MUSG11022-1	16.6
MUSG11022-10	29.7
MUSG11022-11	24.6
MUSG11023-11	3.58
MUSG11026-11	15.7
MUSG11030-9	7.01

germplasmName	Beta carotene content measuring mg per 100g
MUSG11033-6	18.4
MUSG11036-3	11
MUSG11040-13	11
MUSG11040-15	19.8
MUSG11040-16	28.2
MUSG11042-7	24.3
MUSG11044-15	35.1
MUSG11044-16	42.2
MUSG11046-14	40.3
MUSG11046-18	7.74
MUSG11046-3	42.2
MUSG11046-7	13.8
MUSG11048-15	36.7
MUSG11048-16	54.8
MUSG11049-16	25.6
MUSG11049-2	68.2
MUSG11049-3	39.6
MUSG11049-5	99.6
MUSG11049-7	101
MUSG11050-3	19.5
Resisto	33.2



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 Content of iron on dry weight basis measuring mg per 100g

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

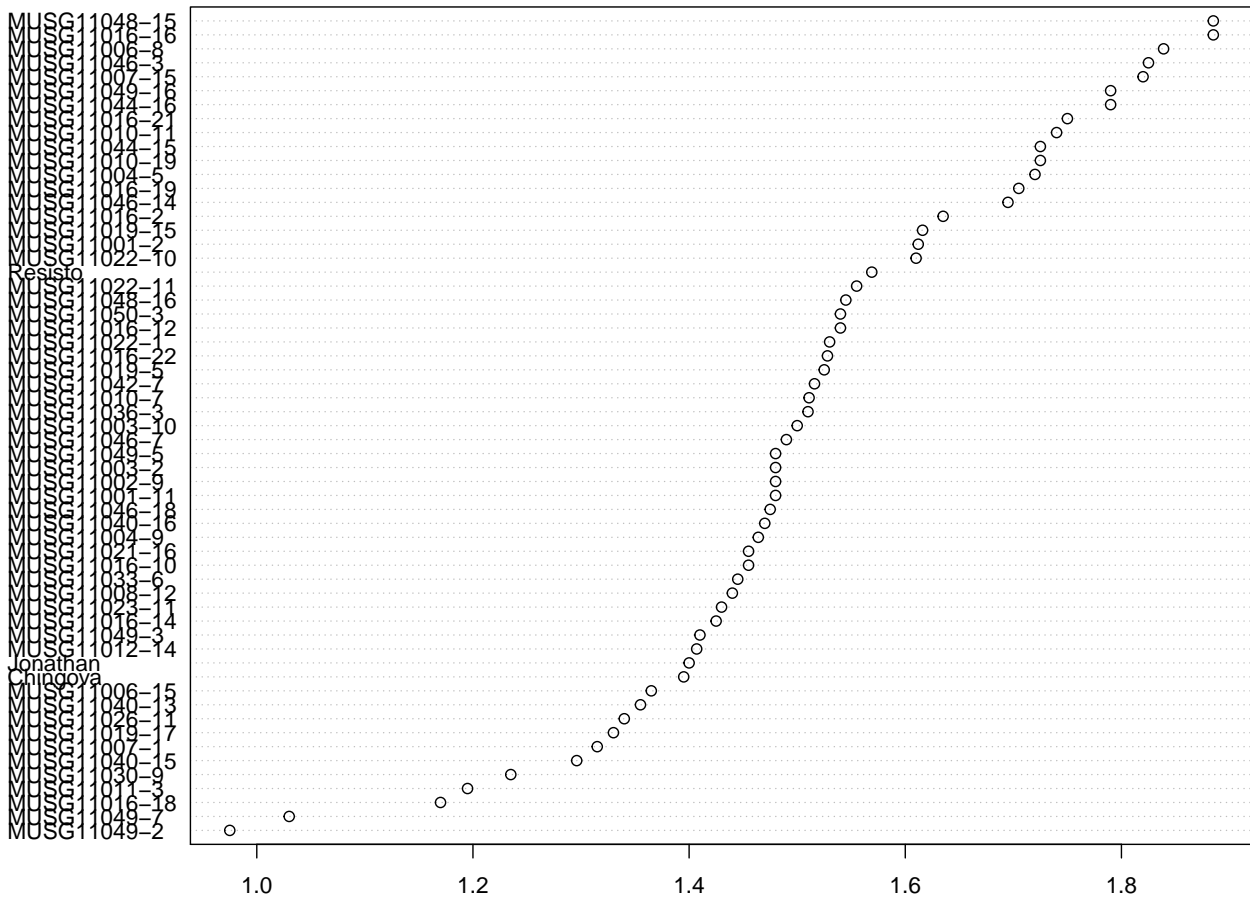
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	4.39317	0.0757443	3.27572	6.01957e-06
REP	1	0.0819172	0.0819172	3.54268	0.0648286
Residuals	58	1.34113	0.0231229	NA	NA

The p-value for treatments is 0.00000601957 which is significant at the 5% level.

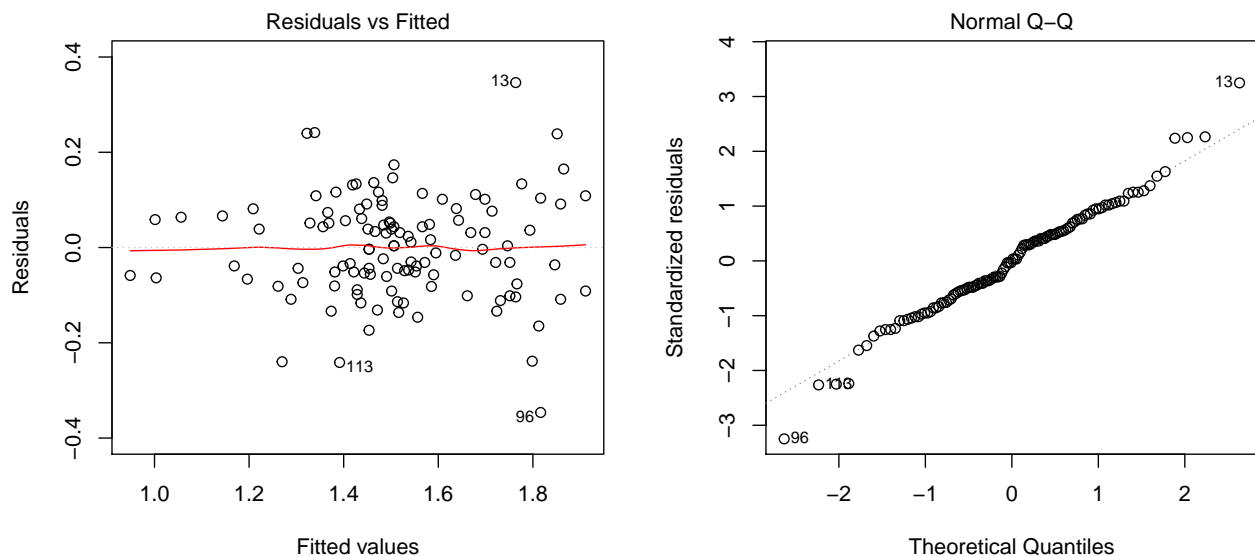
The means of your treatments are:

germplasmName	Content of iron on dry weight basis measuring mg per 100g
Chingova	1.4
Jonathan	1.4
MUSG11001-11	1.48
MUSG11001-2	1.61
MUSG11002-9	1.48
MUSG11003-10	1.5
MUSG11003-2	1.48
MUSG11004-5	1.72
MUSG11004-9	1.46
MUSG11006-15	1.36
MUSG11006-8	1.84
MUSG11007-1	1.31
MUSG11007-15	1.82

germplasmName	Content of iron on dry weight basis measuring mg per 100g
MUSG11008-12	1.44
MUSG11010-11	1.74
MUSG11010-19	1.73
MUSG11010-7	1.51
MUSG11011-3	1.2
MUSG11012-14	1.41
MUSG11016-10	1.46
MUSG11016-12	1.54
MUSG11016-14	1.43
MUSG11016-16	1.89
MUSG11016-18	1.17
MUSG11016-19	1.71
MUSG11016-2	1.64
MUSG11016-21	1.75
MUSG11016-22	1.53
MUSG11019-15	1.62
MUSG11019-17	1.33
MUSG11019-5	1.52
MUSG11021-16	1.46
MUSG11022-1	1.53
MUSG11022-10	1.61
MUSG11022-11	1.55
MUSG11023-11	1.43
MUSG11026-11	1.34
MUSG11030-9	1.24
MUSG11033-6	1.45
MUSG11036-3	1.51
MUSG11040-13	1.35
MUSG11040-15	1.3
MUSG11040-16	1.47
MUSG11042-7	1.52
MUSG11044-15	1.73
MUSG11044-16	1.79
MUSG11046-14	1.7
MUSG11046-18	1.48
MUSG11046-3	1.82
MUSG11046-7	1.49
MUSG11048-15	1.89
MUSG11048-16	1.54
MUSG11049-16	1.79
MUSG11049-2	0.975
MUSG11049-3	1.41
MUSG11049-5	1.48
MUSG11049-7	1.03
MUSG11050-3	1.54
Resisto	1.57



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 Content of zinc on dry weight basis measuring mg per 100g

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

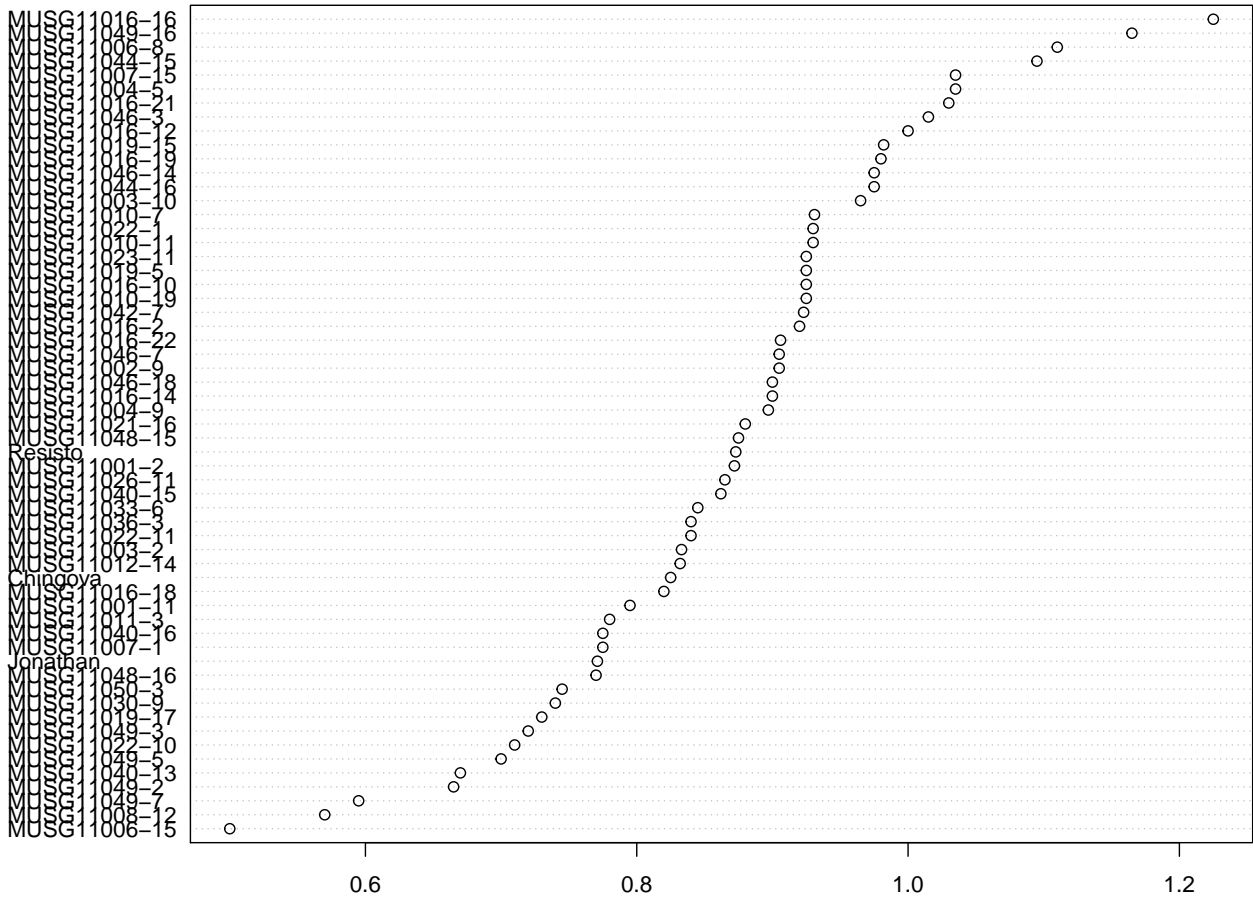
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	2.21006	0.0381046	2.61179	0.000175926
REP	1	0.0744468	0.0744468	5.10279	0.0276623
Residuals	58	0.846187	0.0145894	NA	NA

The p-value for treatments is 0.000175926 which is significant at the 5% level.

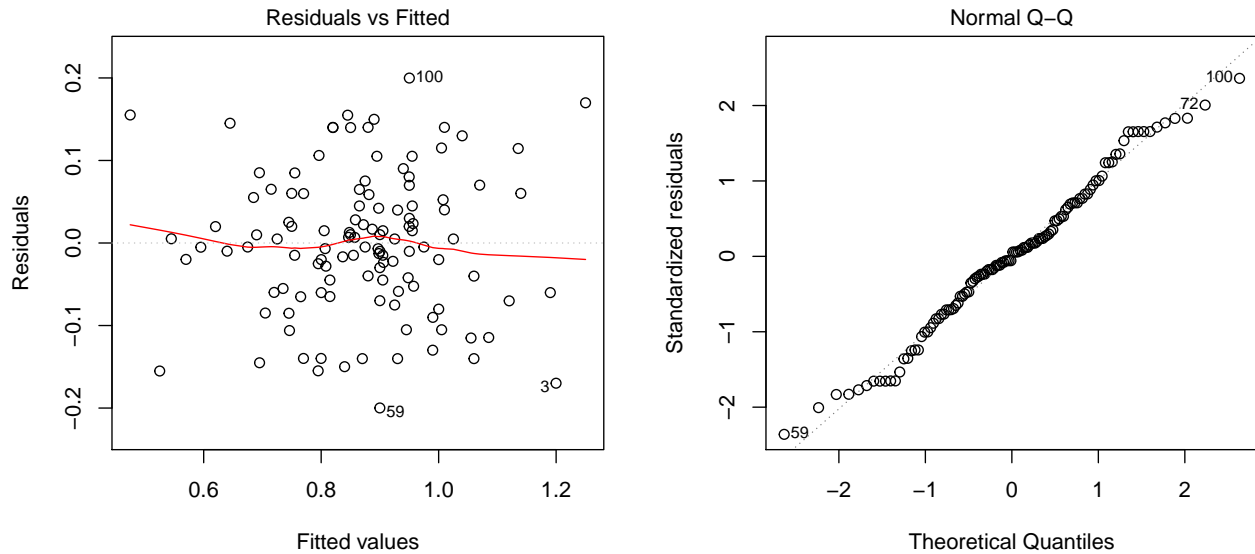
The means of your treatments are:

germplasmName	Content of zinc on dry weight basis measuring mg per 100g
Chingova	0.825
Jonathan	0.771
MUSG11001-11	0.795
MUSG11001-2	0.872
MUSG11002-9	0.905
MUSG11003-10	0.965
MUSG11003-2	0.833
MUSG11004-5	1.03
MUSG11004-9	0.897
MUSG11006-15	0.5
MUSG11006-8	1.11
MUSG11007-1	0.775
MUSG11007-15	1.03
MUSG11008-12	0.57
MUSG11010-11	0.93
MUSG11010-19	0.925
MUSG11010-7	0.931
MUSG11011-3	0.78
MUSG11012-14	0.832
MUSG11016-10	0.925
MUSG11016-12	1
MUSG11016-14	0.9
MUSG11016-16	1.23
MUSG11016-18	0.82
MUSG11016-19	0.98
MUSG11016-2	0.92
MUSG11016-21	1.03
MUSG11016-22	0.906
MUSG11019-15	0.982
MUSG11019-17	0.73
MUSG11019-5	0.925
MUSG11021-16	0.88
MUSG11022-1	0.93
MUSG11022-10	0.71
MUSG11022-11	0.84
MUSG11023-11	0.925
MUSG11026-11	0.865
MUSG11030-9	0.74

germplasmName	Content of zinc on dry weight basis measuring mg per 100g
MUSG11033-6	0.845
MUSG11036-3	0.84
MUSG11040-13	0.67
MUSG11040-15	0.862
MUSG11040-16	0.775
MUSG11042-7	0.923
MUSG11044-15	1.09
MUSG11044-16	0.975
MUSG11046-14	0.975
MUSG11046-18	0.9
MUSG11046-3	1.01
MUSG11046-7	0.905
MUSG11048-15	0.875
MUSG11048-16	0.77
MUSG11049-16	1.17
MUSG11049-2	0.665
MUSG11049-3	0.72
MUSG11049-5	0.7
MUSG11049-7	0.595
MUSG11050-3	0.745
Resisto	0.873



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 Dry weight of storage root samples measuring g of sample

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

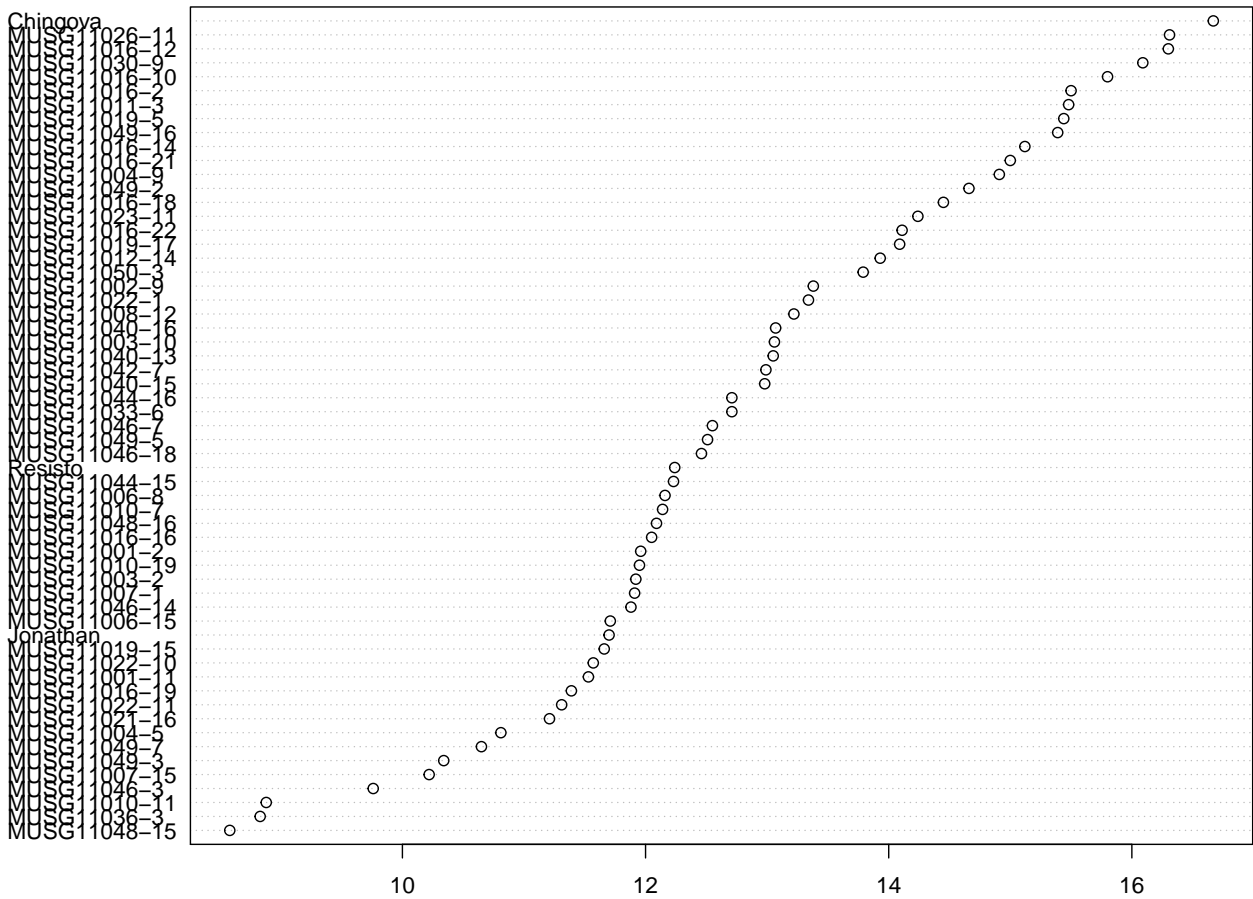
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	433.458	7.47342	5.8768	1.13788e-10
REP	1	0.290215	0.290215	0.228214	0.634647
Residuals	58	73.7575	1.27168	NA	NA

The p-value for treatments is 0.000000000113788 which is significant at the 5% level.

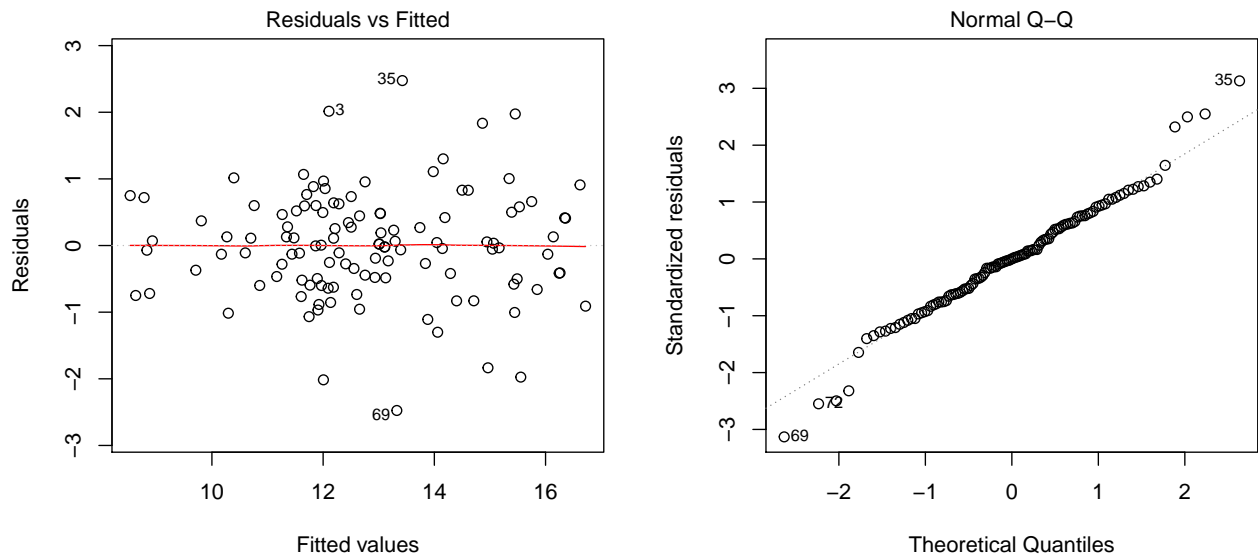
The means of your treatments are:

germplasmName	Dry weight of storage root samples measuring g of sample
Chingova	16.7
Jonathan	11.7
MUSG11001-11	11.5
MUSG11001-2	12
MUSG11002-9	13.4
MUSG11003-10	13.1
MUSG11003-2	11.9
MUSG11004-5	10.8
MUSG11004-9	14.9
MUSG11006-15	11.7
MUSG11006-8	12.2
MUSG11007-1	11.9
MUSG11007-15	10.2

germplasmName	Dry weight of storage root samples measuring g of sample
MUSG11008-12	13.2
MUSG11010-11	8.88
MUSG11010-19	11.9
MUSG11010-7	12.1
MUSG11011-3	15.5
MUSG11012-14	13.9
MUSG11016-10	15.8
MUSG11016-12	16.3
MUSG11016-14	15.1
MUSG11016-16	12.1
MUSG11016-18	14.4
MUSG11016-19	11.4
MUSG11016-2	15.5
MUSG11016-21	15
MUSG11016-22	14.1
MUSG11019-15	11.7
MUSG11019-17	14.1
MUSG11019-5	15.4
MUSG11021-16	11.2
MUSG11022-1	13.3
MUSG11022-10	11.6
MUSG11022-11	11.3
MUSG11023-11	14.2
MUSG11026-11	16.3
MUSG11030-9	16.1
MUSG11033-6	12.7
MUSG11036-3	8.83
MUSG11040-13	13.1
MUSG11040-15	13
MUSG11040-16	13.1
MUSG11042-7	13
MUSG11044-15	12.2
MUSG11044-16	12.7
MUSG11046-14	11.9
MUSG11046-18	12.5
MUSG11046-3	9.76
MUSG11046-7	12.6
MUSG11048-15	8.58
MUSG11048-16	12.1
MUSG11049-16	15.4
MUSG11049-2	14.7
MUSG11049-3	10.3
MUSG11049-5	12.5
MUSG11049-7	10.7
MUSG11050-3	13.8
Resisto	12.2



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 Fibers in cooked samples 1 estimating 1-9

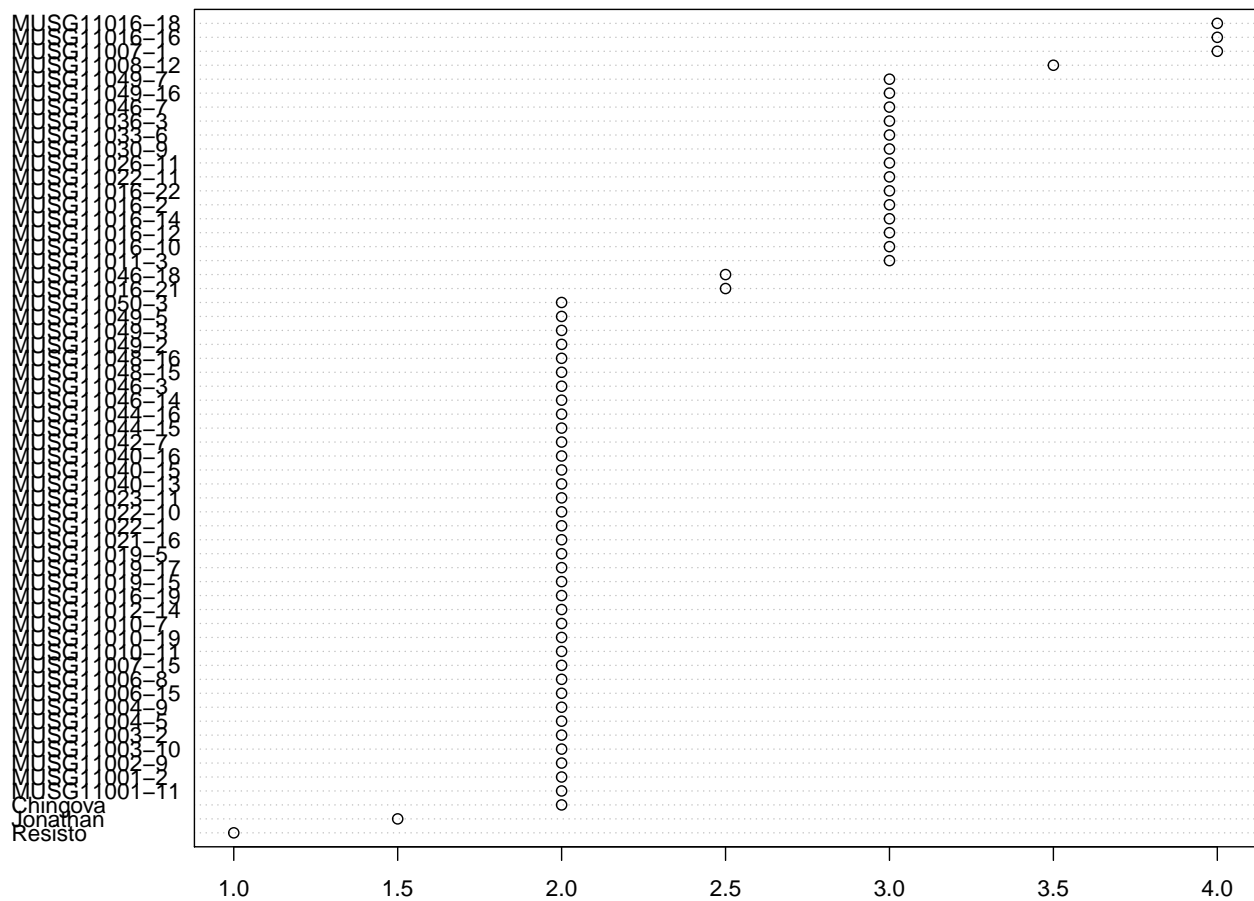
You have fitted a linear model for a RCBD. The ANOVA table for your model is:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	45.0508	0.776739	1.33702	0.135817
REP	1	0.305085	0.305085	0.525151	0.471566
Residuals	58	33.6949	0.580947	NA	NA

The means of your treatments are:

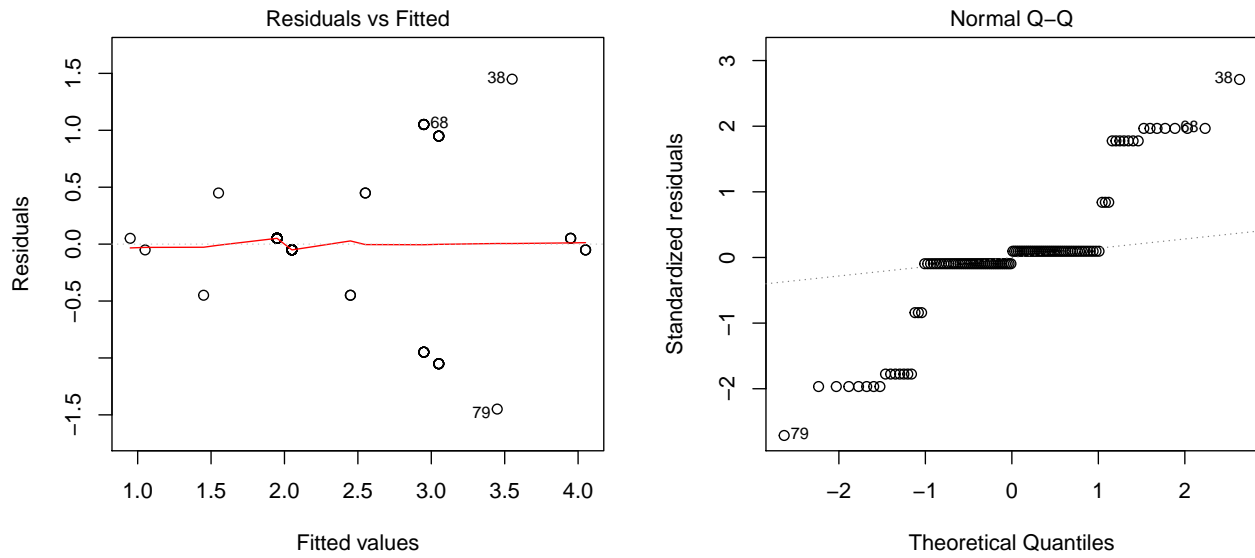
Fibers in cooked samples 1 estimating	
germplasmName	1-9
Chingova	2
Jonathan	1.5
MUSG11001-11	2
MUSG11001-2	2
MUSG11002-9	2
MUSG11003-10	2
MUSG11003-2	2
MUSG11004-5	2
MUSG11004-9	2
MUSG11006-15	2
MUSG11006-8	2
MUSG11007-1	4
MUSG11007-15	2
MUSG11008-12	3.5
MUSG11010-11	2
MUSG11010-19	2
MUSG11010-7	2
MUSG11011-3	3
MUSG11012-14	2
MUSG11016-10	3
MUSG11016-12	3
MUSG11016-14	3
MUSG11016-16	4
MUSG11016-18	4
MUSG11016-19	2
MUSG11016-2	3
MUSG11016-21	2.5
MUSG11016-22	3
MUSG11019-15	2
MUSG11019-17	2
MUSG11019-5	2
MUSG11021-16	2
MUSG11022-1	2
MUSG11022-10	2
MUSG11022-11	3
MUSG11023-11	2
MUSG11026-11	3
MUSG11030-9	3
MUSG11033-6	3

Fibers in cooked samples 1 estimating	
germplasmName	1-9
MUSG11036-3	3
MUSG11040-13	2
MUSG11040-15	2
MUSG11040-16	2
MUSG11042-7	2
MUSG11044-15	2
MUSG11044-16	2
MUSG11046-14	2
MUSG11046-18	2.5
MUSG11046-3	2
MUSG11046-7	3
MUSG11048-15	2
MUSG11048-16	2
MUSG11049-16	3
MUSG11049-2	2
MUSG11049-3	2
MUSG11049-5	2
MUSG11049-7	3
MUSG11050-3	2
Resisto	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 Fresh weight of storage root samples measuring g of sample

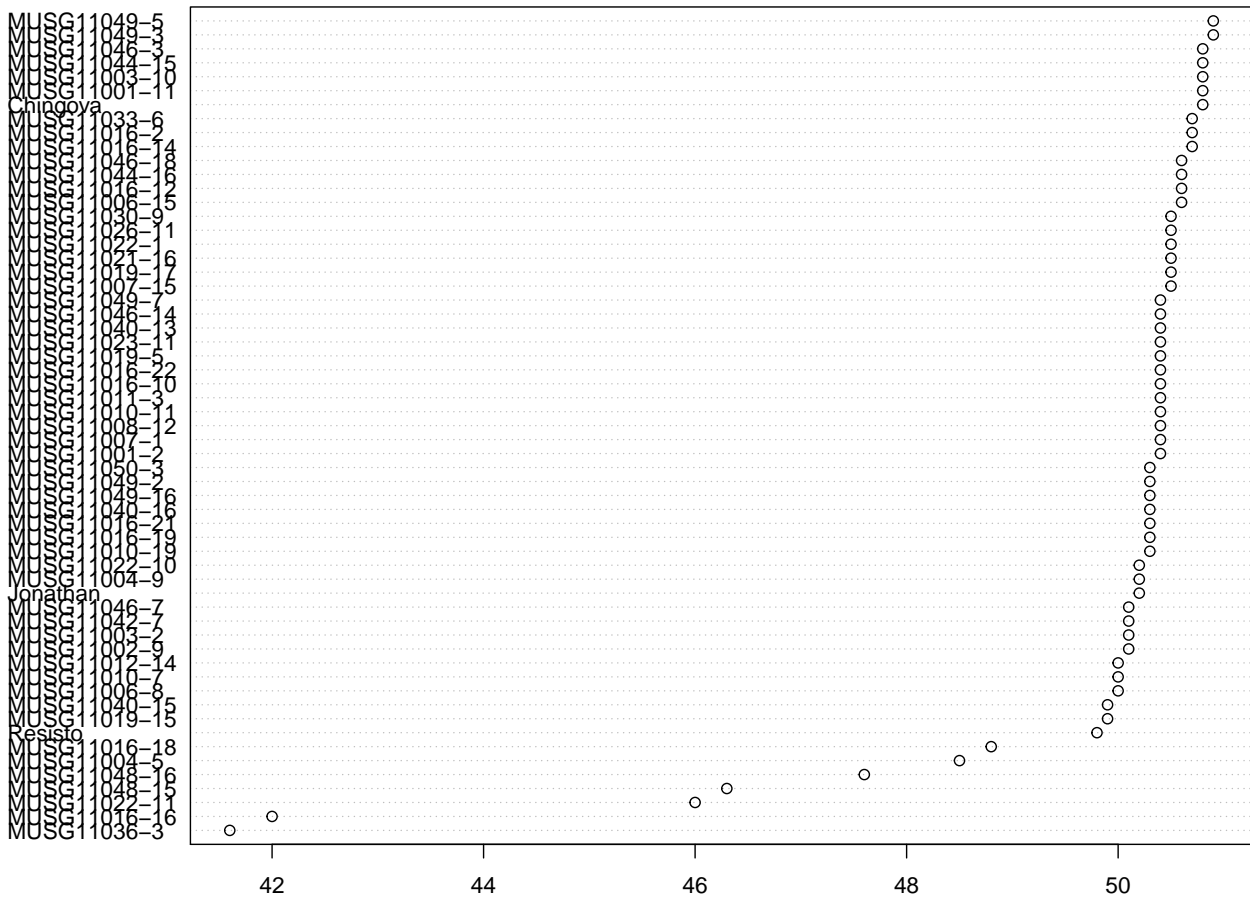
You have fitted a linear model for a RCBD. The ANOVA table for your model is:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	367.991	6.34467	1.44844	0.0806476
REP	1	4.12382	4.12382	0.941435	0.335938
Residuals	58	254.061	4.38036	NA	NA

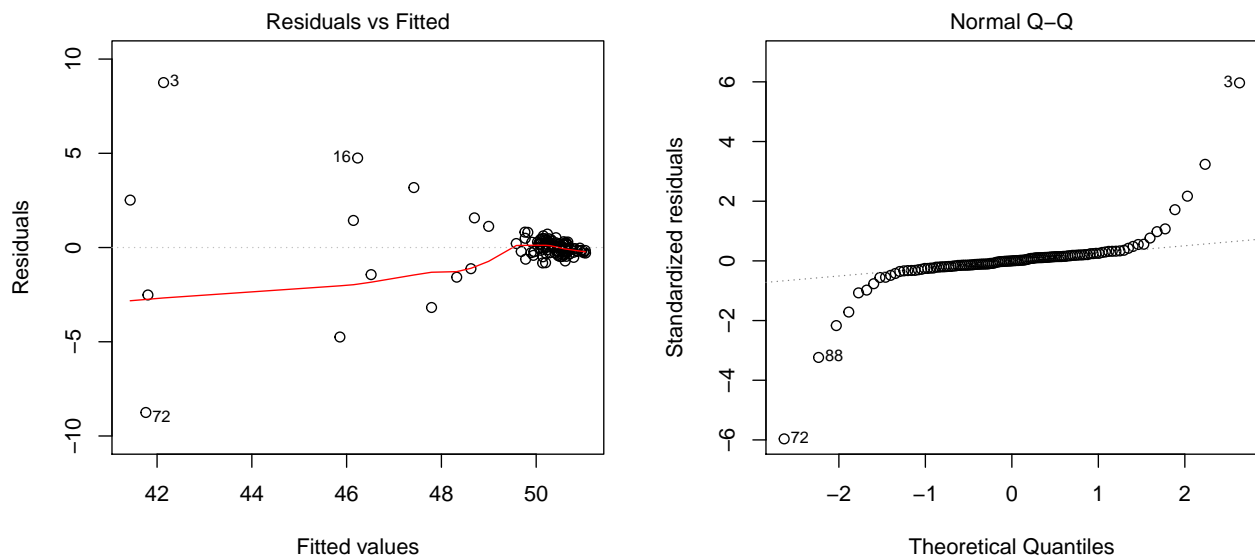
The means of your treatments are:

germplasmName	Fresh weight of storage root samples measuring g of sample
Chingova	50.8
Jonathan	50.2
MUSG11001-11	50.8
MUSG11001-2	50.4
MUSG11002-9	50.1
MUSG11003-10	50.8
MUSG11003-2	50.1
MUSG11004-5	48.5
MUSG11004-9	50.2
MUSG11006-15	50.6
MUSG11006-8	50
MUSG11007-1	50.4
MUSG11007-15	50.5
MUSG11008-12	50.4
MUSG11010-11	50.4
MUSG11010-19	50.3

germplasmName	Fresh weight of storage root samples measuring g of sample
MUSG11010-7	50
MUSG11011-3	50.4
MUSG11012-14	50
MUSG11016-10	50.4
MUSG11016-12	50.6
MUSG11016-14	50.7
MUSG11016-16	42
MUSG11016-18	48.8
MUSG11016-19	50.3
MUSG11016-2	50.7
MUSG11016-21	50.3
MUSG11016-22	50.4
MUSG11019-15	49.9
MUSG11019-17	50.5
MUSG11019-5	50.4
MUSG11021-16	50.5
MUSG11022-1	50.5
MUSG11022-10	50.2
MUSG11022-11	46
MUSG11023-11	50.4
MUSG11026-11	50.5
MUSG11030-9	50.5
MUSG11033-6	50.7
MUSG11036-3	41.6
MUSG11040-13	50.4
MUSG11040-15	49.9
MUSG11040-16	50.3
MUSG11042-7	50.1
MUSG11044-15	50.8
MUSG11044-16	50.6
MUSG11046-14	50.4
MUSG11046-18	50.6
MUSG11046-3	50.8
MUSG11046-7	50.1
MUSG11048-15	46.3
MUSG11048-16	47.6
MUSG11049-16	50.3
MUSG11049-2	50.3
MUSG11049-3	50.9
MUSG11049-5	50.9
MUSG11049-7	50.4
MUSG11050-3	50.3
Resisto	49.8



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 Fructose content measuring percent

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

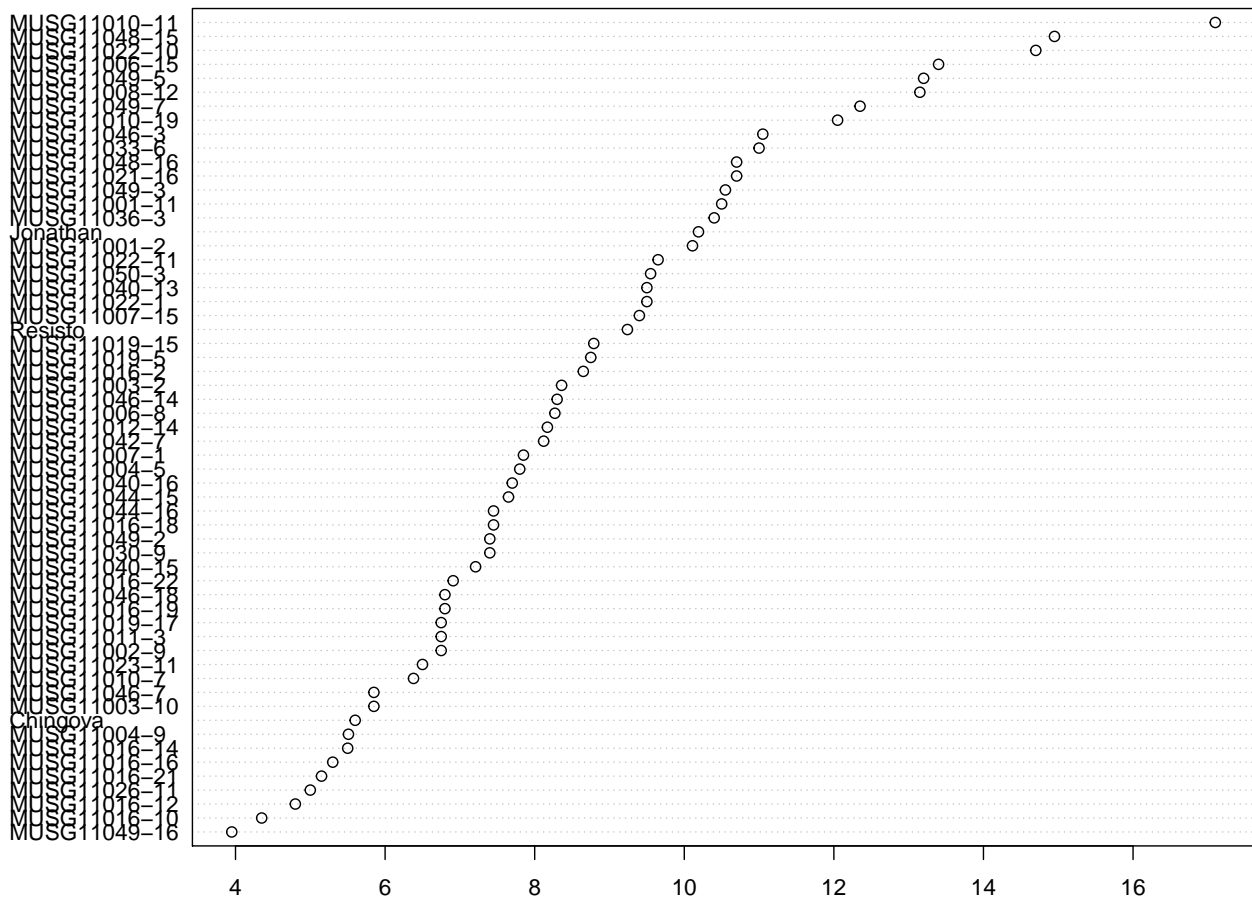
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	909.14	15.6748	4.29775	5.48075e-08
REP	1	14.7369	14.7369	4.04059	0.049077
Residuals	58	211.539	3.64722	NA	NA

The p-value for treatments is 0.0000000548075 which is significant at the 5% level.

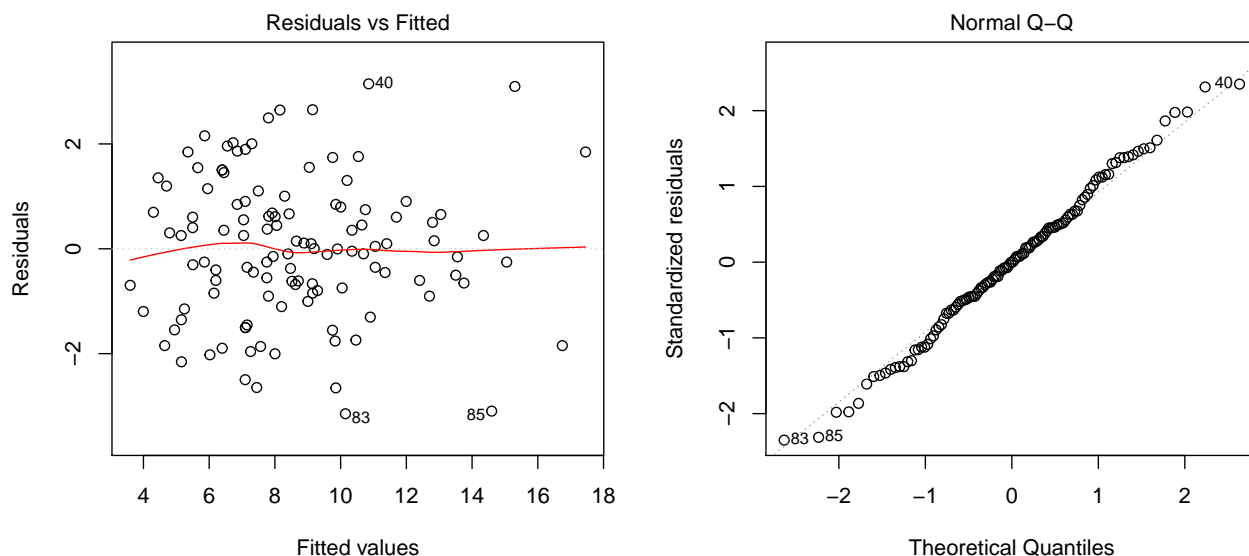
The means of your treatments are:

germplasmName	Fructose content measuring percent
Chingova	5.6
Jonathan	10.2
MUSG11001-11	10.5
MUSG11001-2	10.1
MUSG11002-9	6.75
MUSG11003-10	5.85
MUSG11003-2	8.36
MUSG11004-5	7.8
MUSG11004-9	5.51
MUSG11006-15	13.4
MUSG11006-8	8.27
MUSG11007-1	7.85
MUSG11007-15	9.4
MUSG11008-12	13.2
MUSG11010-11	17.1
MUSG11010-19	12.1
MUSG11010-7	6.38
MUSG11011-3	6.75
MUSG11012-14	8.17
MUSG11016-10	4.35
MUSG11016-12	4.8
MUSG11016-14	5.5
MUSG11016-16	5.3
MUSG11016-18	7.45
MUSG11016-19	6.8
MUSG11016-2	8.65
MUSG11016-21	5.15
MUSG11016-22	6.91
MUSG11019-15	8.79
MUSG11019-17	6.75
MUSG11019-5	8.75
MUSG11021-16	10.7
MUSG11022-1	9.5
MUSG11022-10	14.7
MUSG11022-11	9.65
MUSG11023-11	6.5
MUSG11026-11	5
MUSG11030-9	7.4
MUSG11033-6	11

germplasmName	Fructose content measuring percent
MUSG11036-3	10.4
MUSG11040-13	9.5
MUSG11040-15	7.21
MUSG11040-16	7.7
MUSG11042-7	8.12
MUSG11044-15	7.65
MUSG11044-16	7.45
MUSG11046-14	8.3
MUSG11046-18	6.8
MUSG11046-3	11.1
MUSG11046-7	5.85
MUSG11048-15	14.9
MUSG11048-16	10.7
MUSG11049-16	3.95
MUSG11049-2	7.4
MUSG11049-3	10.6
MUSG11049-5	13.2
MUSG11049-7	12.3
MUSG11050-3	9.55
Resisto	9.24



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 Glucose content measuring percent

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

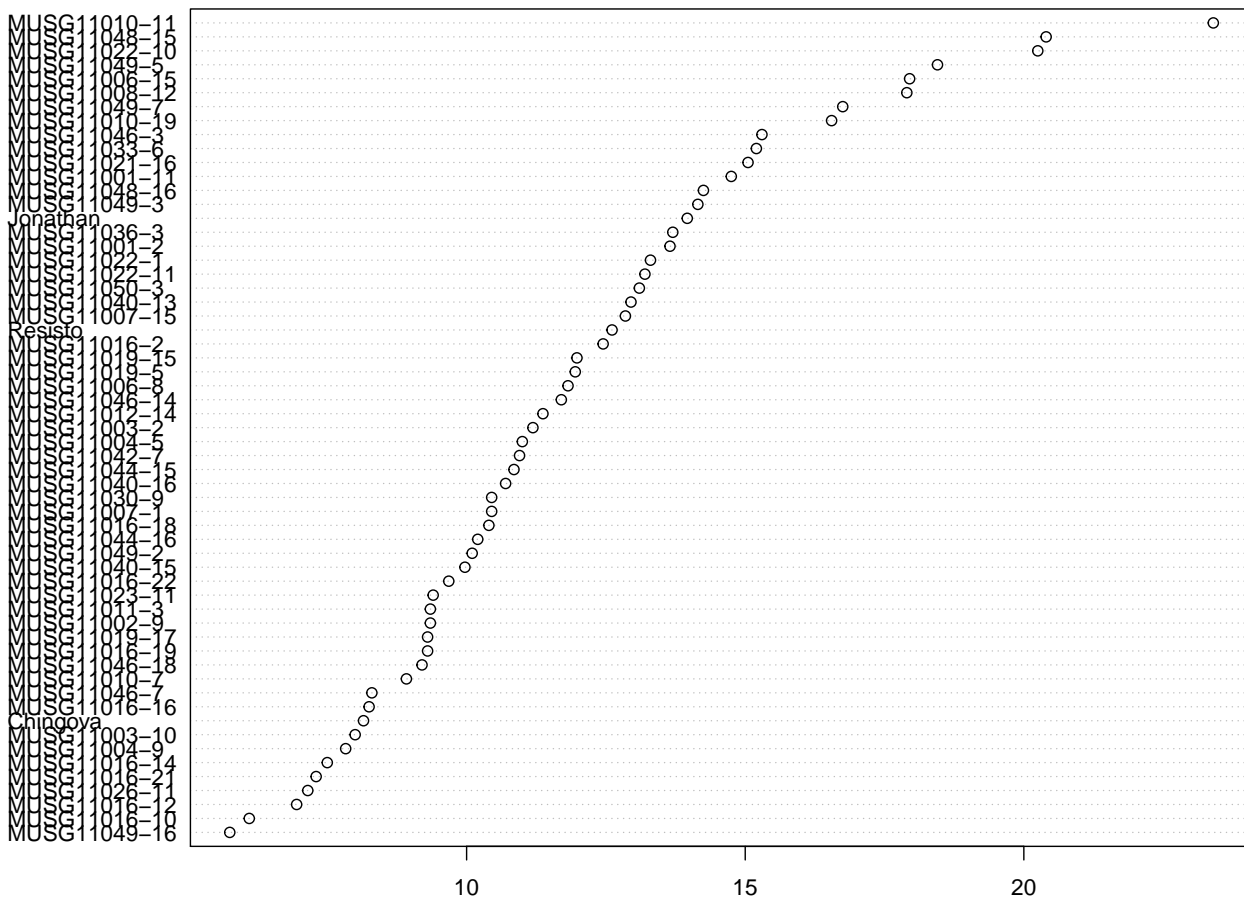
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	1621.76	27.9614	4.19042	8.72822e-08
REP	1	27.6406	27.6406	4.14233	0.0464016
Residuals	58	387.017	6.67271	NA	NA

The p-value for treatments is 0.0000000872822 which is significant at the 5% level.

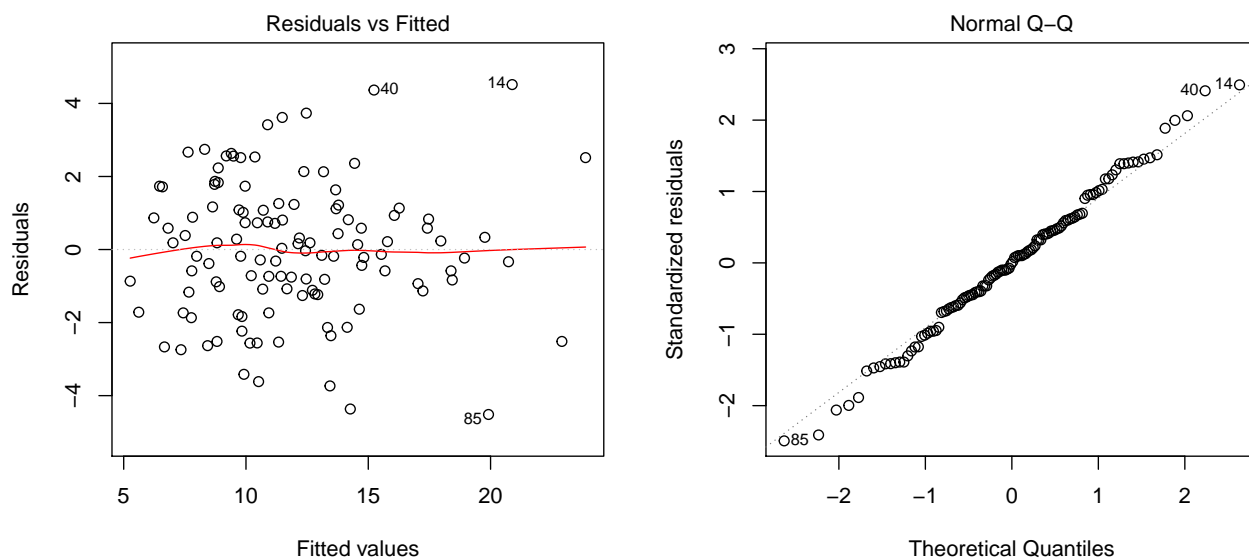
The means of your treatments are:

germplasmName	Glucose content measuring percent
Chingova	8.15
Jonathan	14
MUSG11001-11	14.8
MUSG11001-2	13.7
MUSG11002-9	9.35
MUSG11003-10	8
MUSG11003-2	11.2
MUSG11004-5	11
MUSG11004-9	7.83
MUSG11006-15	17.9
MUSG11006-8	11.8
MUSG11007-1	10.4
MUSG11007-15	12.8
MUSG11008-12	17.9
MUSG11010-11	23.4
MUSG11010-19	16.6
MUSG11010-7	8.92

germplasmName	Glucose content measuring percent
MUSG11011-3	9.35
MUSG11012-14	11.4
MUSG11016-10	6.1
MUSG11016-12	6.95
MUSG11016-14	7.5
MUSG11016-16	8.25
MUSG11016-18	10.4
MUSG11016-19	9.3
MUSG11016-2	12.4
MUSG11016-21	7.3
MUSG11016-22	9.68
MUSG11019-15	12
MUSG11019-17	9.3
MUSG11019-5	11.9
MUSG11021-16	15.1
MUSG11022-1	13.3
MUSG11022-10	20.2
MUSG11022-11	13.2
MUSG11023-11	9.4
MUSG11026-11	7.15
MUSG11030-9	10.4
MUSG11033-6	15.2
MUSG11036-3	13.7
MUSG11040-13	12.9
MUSG11040-15	9.97
MUSG11040-16	10.7
MUSG11042-7	10.9
MUSG11044-15	10.8
MUSG11044-16	10.2
MUSG11046-14	11.7
MUSG11046-18	9.2
MUSG11046-3	15.3
MUSG11046-7	8.3
MUSG11048-15	20.4
MUSG11048-16	14.2
MUSG11049-16	5.75
MUSG11049-2	10.1
MUSG11049-3	14.2
MUSG11049-5	18.4
MUSG11049-7	16.8
MUSG11050-3	13.1
Resisto	12.6



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 Harvest index computing percent

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

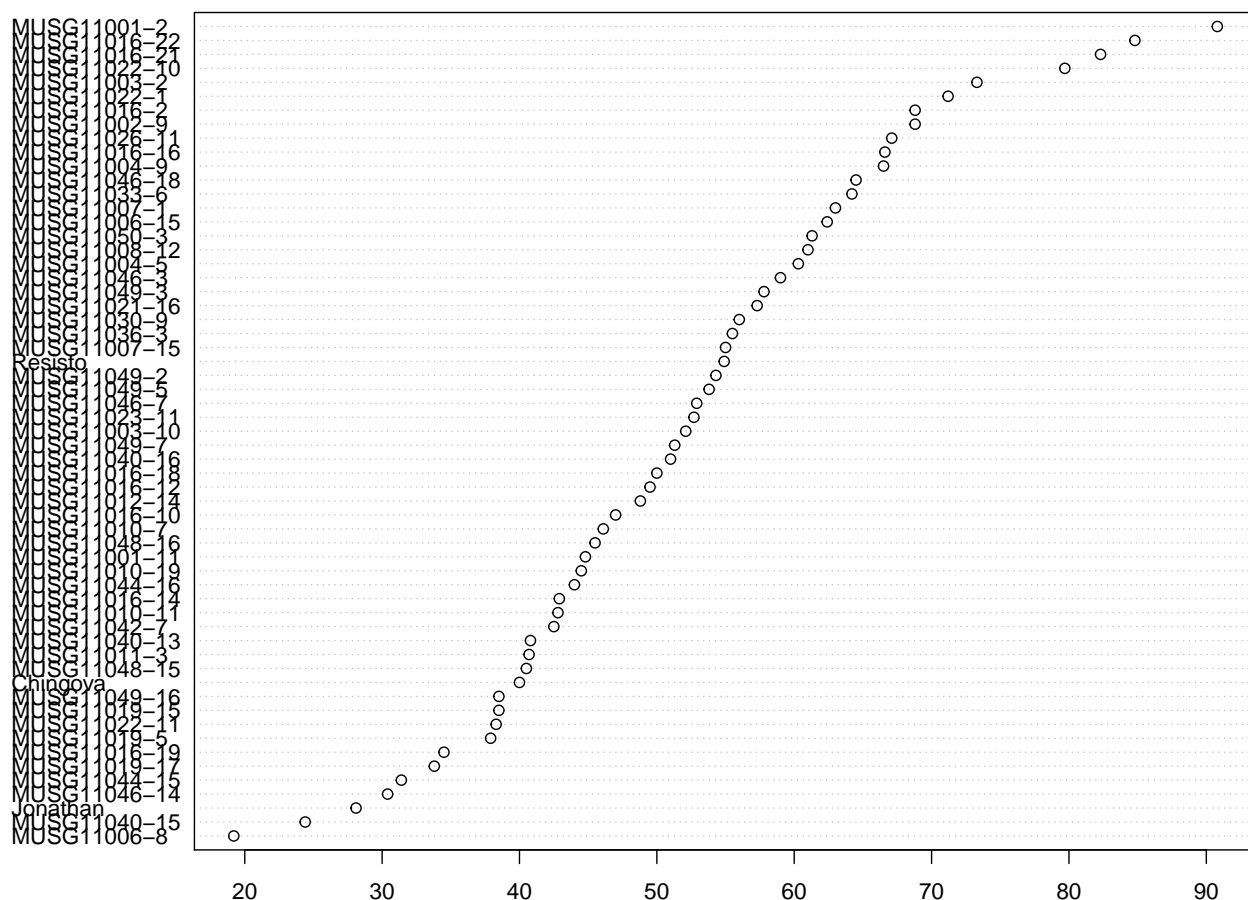
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	26007.1	448.398	3.03258	2.0144e-05
REP	1	185.343	185.343	1.2535	0.267499
Residuals	58	8575.87	147.86	NA	NA

The p-value for treatments is 0.000020144 which is significant at the 5% level.

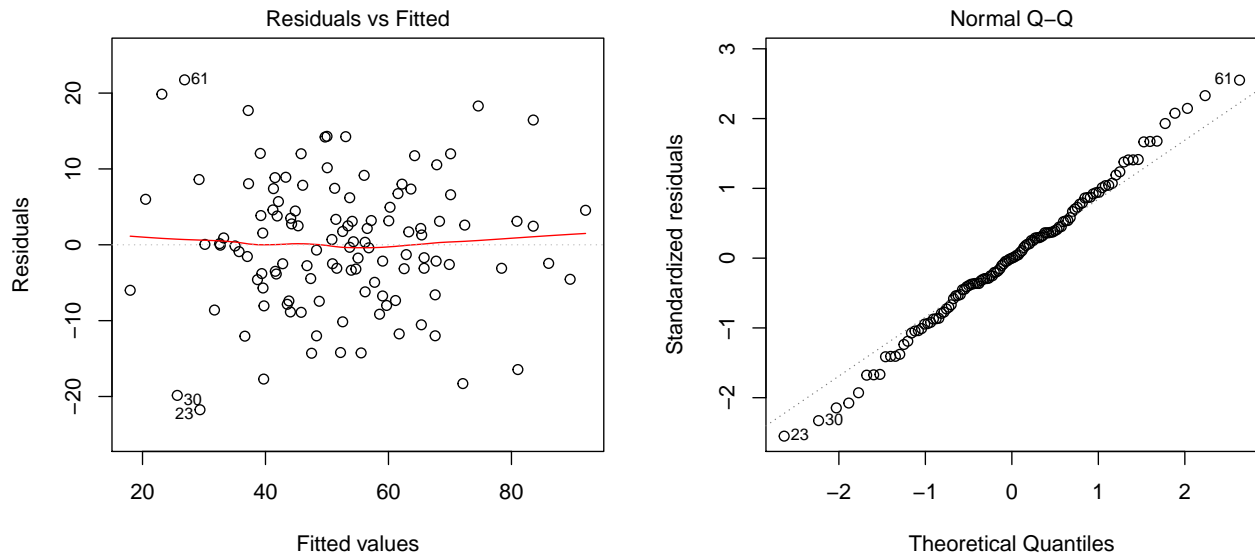
The means of your treatments are:

germplasmName	Harvest index computing percent
Chingova	40
Jonathan	28.1
MUSG11001-11	44.8
MUSG11001-2	90.8
MUSG11002-9	68.8
MUSG11003-10	52.1
MUSG11003-2	73.3
MUSG11004-5	60.3
MUSG11004-9	66.5
MUSG11006-15	62.4
MUSG11006-8	19.2
MUSG11007-1	63
MUSG11007-15	55
MUSG11008-12	61
MUSG11010-11	42.8
MUSG11010-19	44.5
MUSG11010-7	46.1
MUSG11011-3	40.7
MUSG11012-14	48.8
MUSG11016-10	47
MUSG11016-12	49.5
MUSG11016-14	42.9
MUSG11016-16	66.6
MUSG11016-18	50
MUSG11016-19	34.5
MUSG11016-2	68.8
MUSG11016-21	82.3
MUSG11016-22	84.8
MUSG11019-15	38.5
MUSG11019-17	33.8
MUSG11019-5	37.9
MUSG11021-16	57.3
MUSG11022-1	71.2
MUSG11022-10	79.7
MUSG11022-11	38.3
MUSG11023-11	52.7
MUSG11026-11	67.1
MUSG11030-9	56
MUSG11033-6	64.2

germplasmName	Harvest index computing percent
MUSG11036-3	55.5
MUSG11040-13	40.8
MUSG11040-15	24.4
MUSG11040-16	51
MUSG11042-7	42.5
MUSG11044-15	31.4
MUSG11044-16	44
MUSG11046-14	30.4
MUSG11046-18	64.5
MUSG11046-3	59
MUSG11046-7	52.9
MUSG11048-15	40.5
MUSG11048-16	45.5
MUSG11049-16	38.5
MUSG11049-2	54.3
MUSG11049-3	57.8
MUSG11049-5	53.8
MUSG11049-7	51.3
MUSG11050-3	61.3
Resisto	54.9



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 Number of commercial storage roots counting number per plot

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

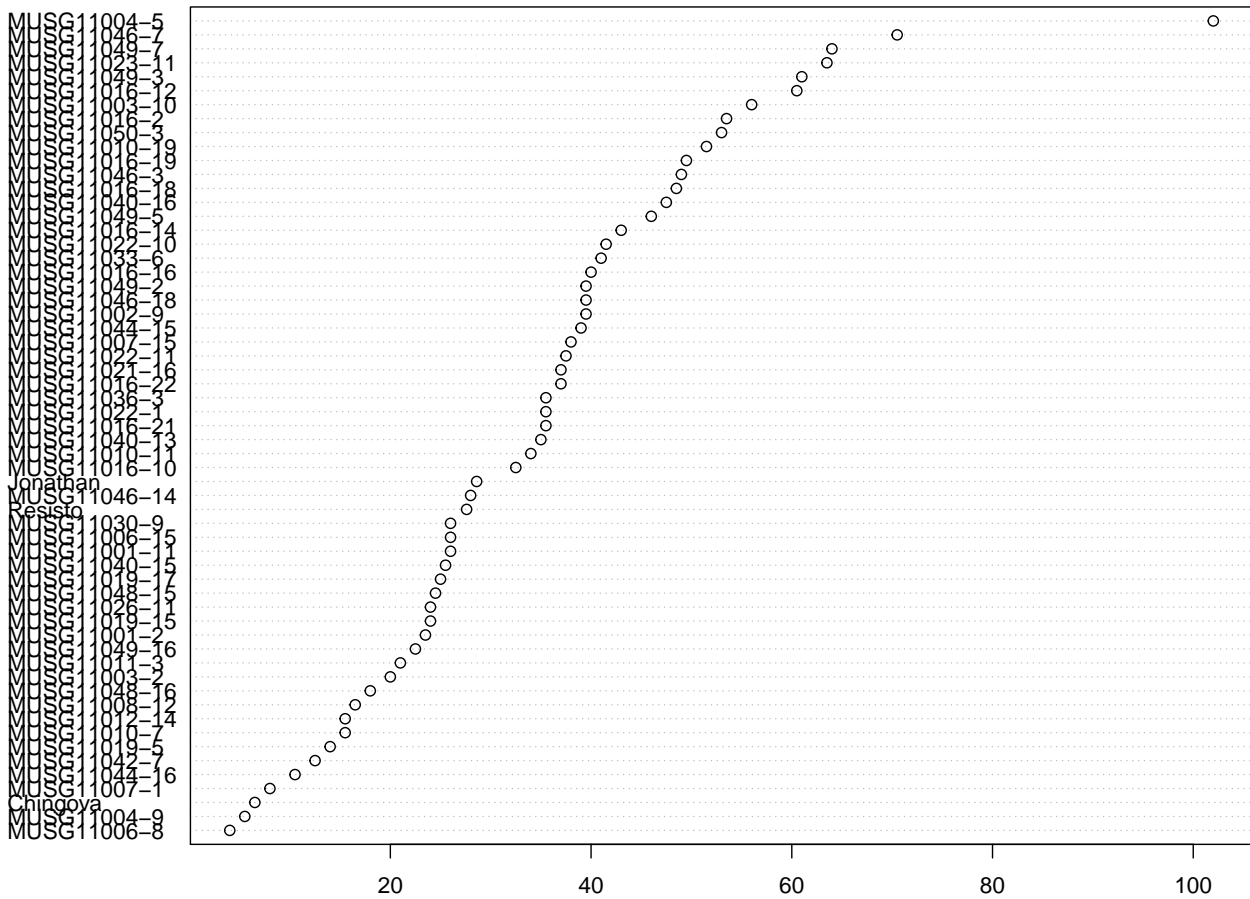
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	38398.6	662.044	3.34039	4.3911e-06
REP	1	7476.61	7476.61	37.7237	7.94121e-08
Residuals	58	11495.2	198.194	NA	NA

The p-value for treatments is 0.0000043911 which is significant at the 5% level.

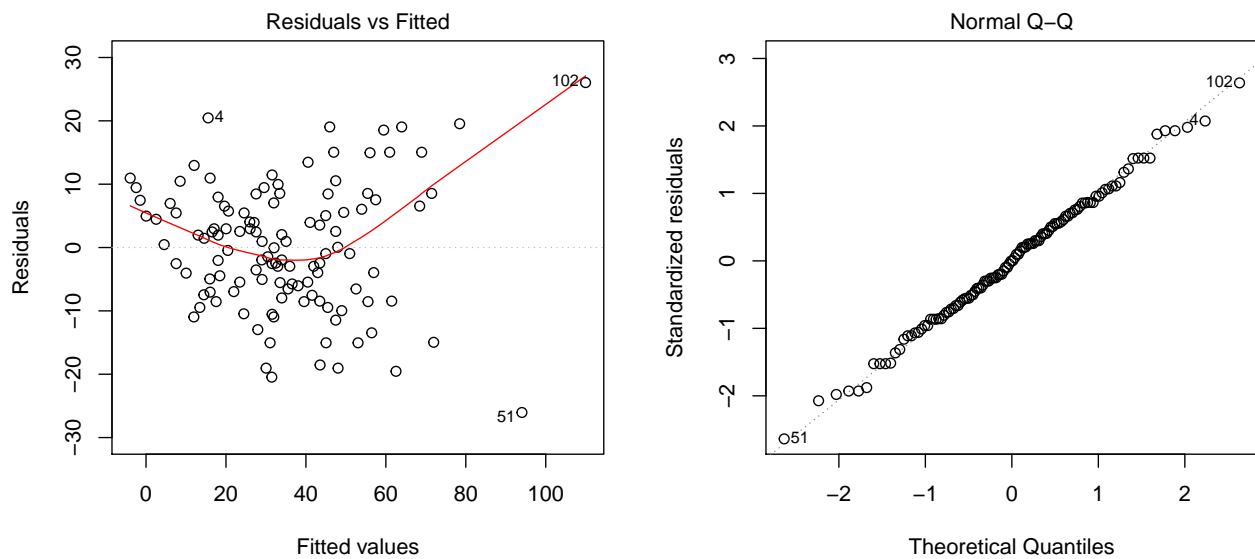
The means of your treatments are:

germplasmName	Number of commercial storage roots counting number per plot
Chingova	6.5
Jonathan	28.6
MUSG11001-11	26
MUSG11001-2	23.5
MUSG11002-9	39.5
MUSG11003-10	56
MUSG11003-2	20
MUSG11004-5	102
MUSG11004-9	5.5
MUSG11006-15	26
MUSG11006-8	4
MUSG11007-1	8
MUSG11007-15	38
MUSG11008-12	16.5
MUSG11010-11	34
MUSG11010-19	51.5

germplasmName	Number of commercial storage roots counting number per plot
MUSG11010-7	15.5
MUSG11011-3	21
MUSG11012-14	15.5
MUSG11016-10	32.5
MUSG11016-12	60.5
MUSG11016-14	43
MUSG11016-16	40
MUSG11016-18	48.5
MUSG11016-19	49.5
MUSG11016-2	53.5
MUSG11016-21	35.5
MUSG11016-22	37
MUSG11019-15	24
MUSG11019-17	25
MUSG11019-5	14
MUSG11021-16	37
MUSG11022-1	35.5
MUSG11022-10	41.5
MUSG11022-11	37.5
MUSG11023-11	63.5
MUSG11026-11	24
MUSG11030-9	26
MUSG11033-6	41
MUSG11036-3	35.5
MUSG11040-13	35
MUSG11040-15	25.5
MUSG11040-16	47.5
MUSG11042-7	12.5
MUSG11044-15	39
MUSG11044-16	10.5
MUSG11046-14	28
MUSG11046-18	39.5
MUSG11046-3	49
MUSG11046-7	70.5
MUSG11048-15	24.5
MUSG11048-16	18
MUSG11049-16	22.5
MUSG11049-2	39.5
MUSG11049-3	61
MUSG11049-5	46
MUSG11049-7	64
MUSG11050-3	53
Resisto	27.6



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 Number of non-commercial storage roots counting number per plot

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

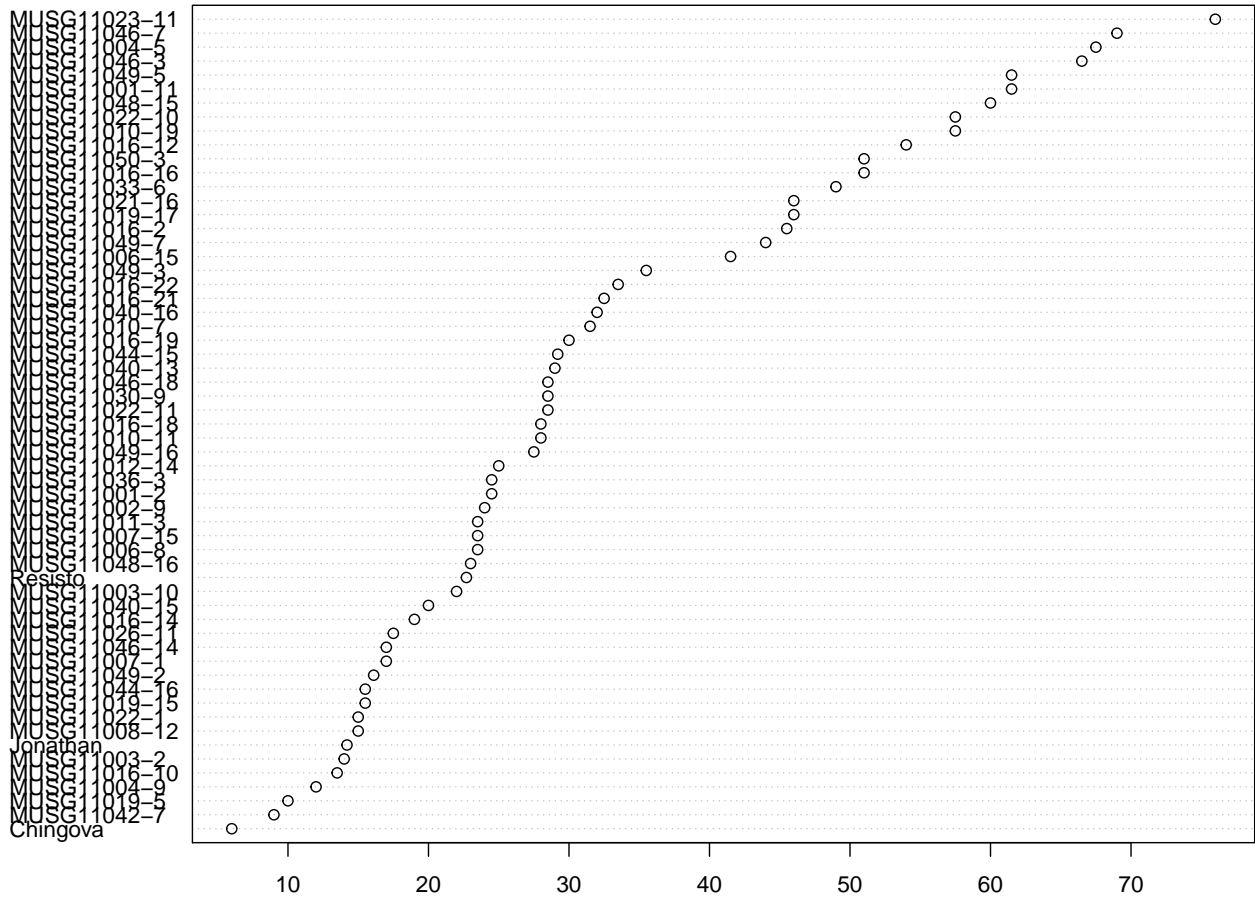
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	36262.1	625.209	2.71391	0.000103119
REP	1	1997.17	1997.17	8.66932	0.00464949
Residuals	58	13361.6	230.372	NA	NA

The p-value for treatments is 0.000103119 which is significant at the 5% level.

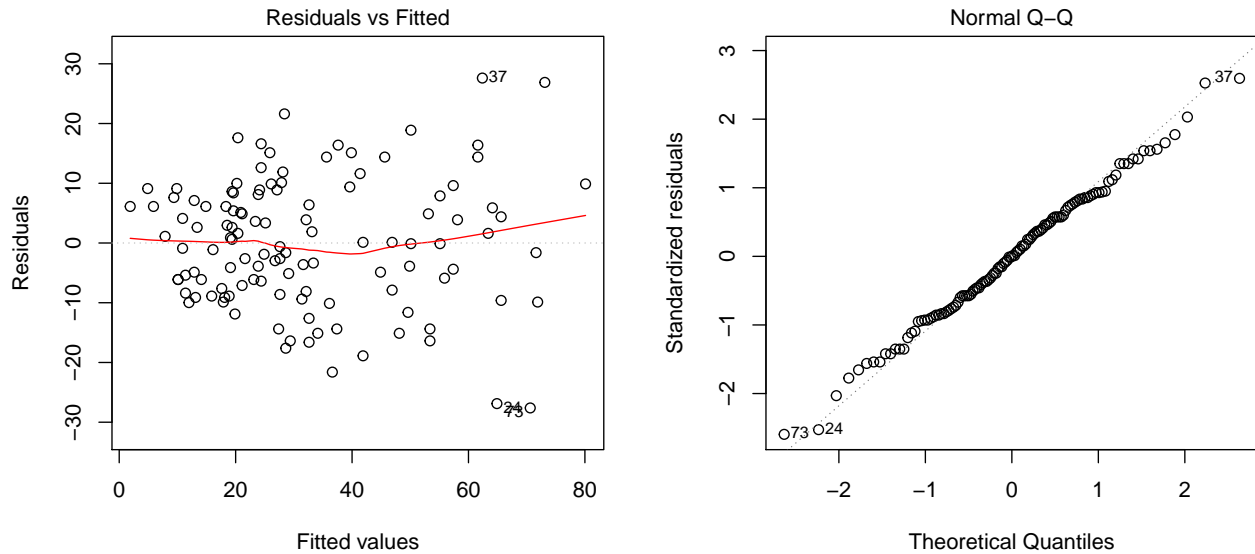
The means of your treatments are:

germplasmName	Number of non-commercial storage roots counting number per plot
Chingova	6
Jonathan	14.2
MUSG11001-11	61.5
MUSG11001-2	24.5
MUSG11002-9	24
MUSG11003-10	22
MUSG11003-2	14
MUSG11004-5	67.5
MUSG11004-9	12
MUSG11006-15	41.5
MUSG11006-8	23.5
MUSG11007-1	17
MUSG11007-15	23.5
MUSG11008-12	15
MUSG11010-11	28
MUSG11010-19	57.5
MUSG11010-7	31.5
MUSG11011-3	23.5
MUSG11012-14	25
MUSG11016-10	13.5
MUSG11016-12	54
MUSG11016-14	19
MUSG11016-16	51
MUSG11016-18	28
MUSG11016-19	30
MUSG11016-2	45.5
MUSG11016-21	32.5
MUSG11016-22	33.5
MUSG11019-15	15.5
MUSG11019-17	46
MUSG11019-5	10
MUSG11021-16	46
MUSG11022-1	15
MUSG11022-10	57.5
MUSG11022-11	28.5
MUSG11023-11	76
MUSG11026-11	17.5
MUSG11030-9	28.5

germplasmName	Number of non-commercial storage roots counting number per plot
MUSG11033-6	49
MUSG11036-3	24.5
MUSG11040-13	29
MUSG11040-15	20
MUSG11040-16	32
MUSG11042-7	9
MUSG11044-15	29.2
MUSG11044-16	15.5
MUSG11046-14	17
MUSG11046-18	28.5
MUSG11046-3	66.5
MUSG11046-7	69
MUSG11048-15	60
MUSG11048-16	23
MUSG11049-16	27.5
MUSG11049-2	16.1
MUSG11049-3	35.5
MUSG11049-5	61.5
MUSG11049-7	44
MUSG11050-3	51
Resisto	22.7



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 Overall taste of cooked sample 1 estimating 1-9

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

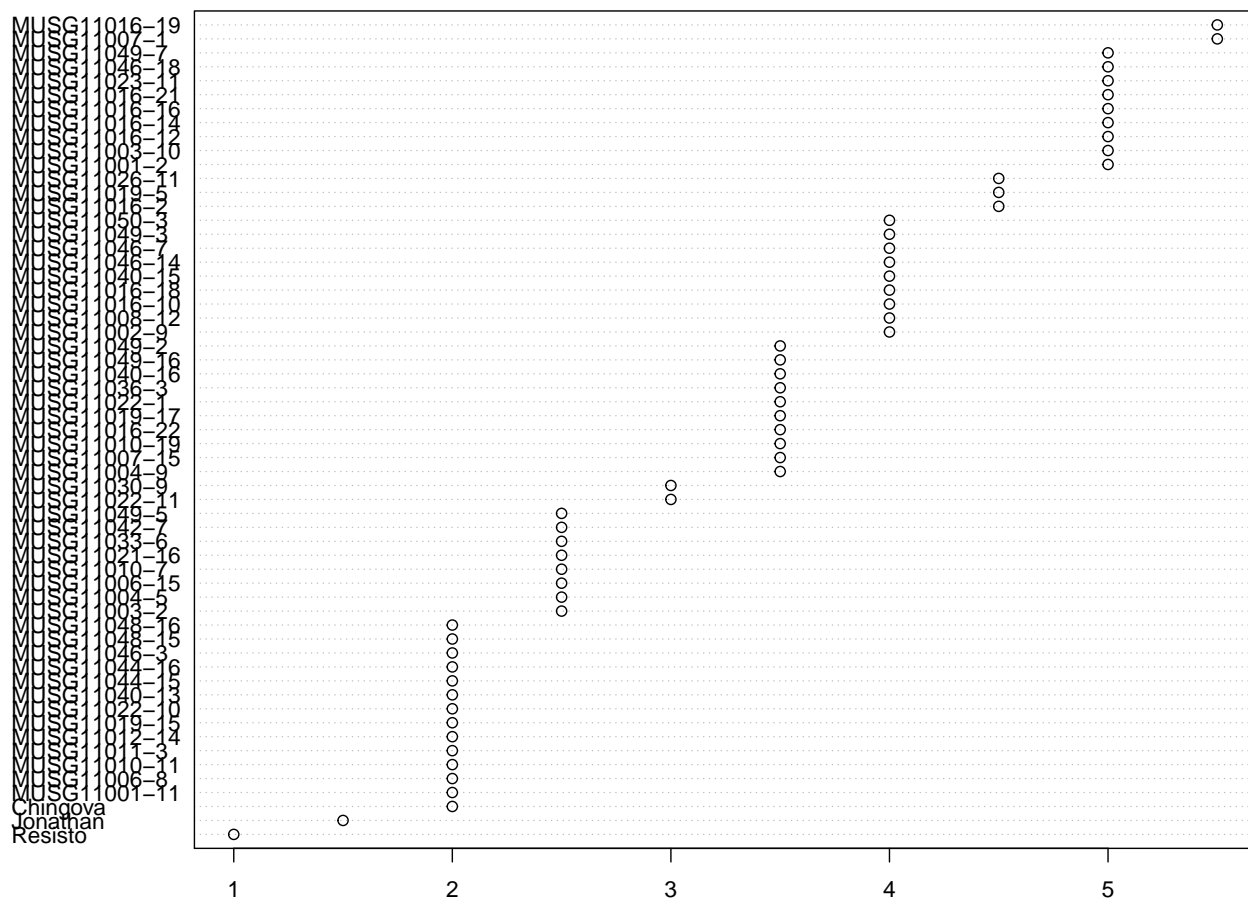
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	164.441	2.83518	2.37445	0.000619079
REP	1	2.74576	2.74576	2.29956	0.134842
Residuals	58	69.2542	1.19404	NA	NA

The p-value for treatments is 0.000619079 which is significant at the 5% level.

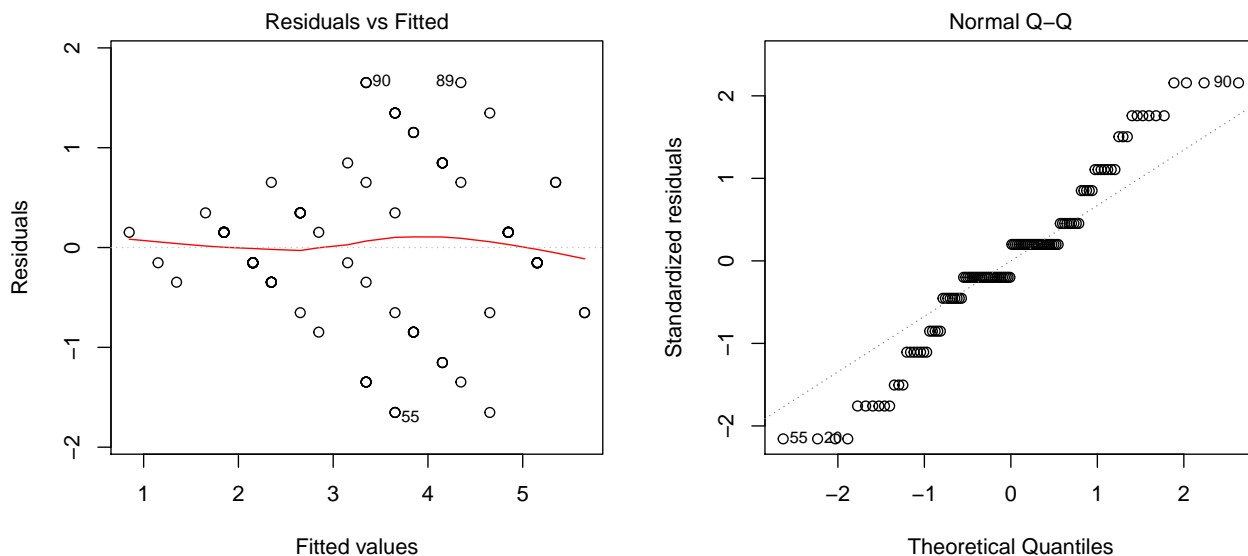
The means of your treatments are:

Overall taste of cooked sample 1 estimating 1-9	
germplasmName	
Chingova	2
Jonathan	1.5
MUSG11001-11	2
MUSG11001-2	5
MUSG11002-9	4
MUSG11003-10	5
MUSG11003-2	2.5
MUSG11004-5	2.5
MUSG11004-9	3.5
MUSG11006-15	2.5
MUSG11006-8	2
MUSG11007-1	5.5
MUSG11007-15	3.5

germplasmName	Overall taste of cooked sample 1 estimating 1-9
MUSG11008-12	4
MUSG11010-11	2
MUSG11010-19	3.5
MUSG11010-7	2.5
MUSG11011-3	2
MUSG11012-14	2
MUSG11016-10	4
MUSG11016-12	5
MUSG11016-14	5
MUSG11016-16	5
MUSG11016-18	4
MUSG11016-19	5.5
MUSG11016-2	4.5
MUSG11016-21	5
MUSG11016-22	3.5
MUSG11019-15	2
MUSG11019-17	3.5
MUSG11019-5	4.5
MUSG11021-16	2.5
MUSG11022-1	3.5
MUSG11022-10	2
MUSG11022-11	3
MUSG11023-11	5
MUSG11026-11	4.5
MUSG11030-9	3
MUSG11033-6	2.5
MUSG11036-3	3.5
MUSG11040-13	2
MUSG11040-15	4
MUSG11040-16	3.5
MUSG11042-7	2.5
MUSG11044-15	2
MUSG11044-16	2
MUSG11046-14	4
MUSG11046-18	5
MUSG11046-3	2
MUSG11046-7	4
MUSG11048-15	2
MUSG11048-16	2
MUSG11049-16	3.5
MUSG11049-2	3.5
MUSG11049-3	4
MUSG11049-5	2.5
MUSG11049-7	5
MUSG11050-3	4
Resisto	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 Plants established counting number per plot

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

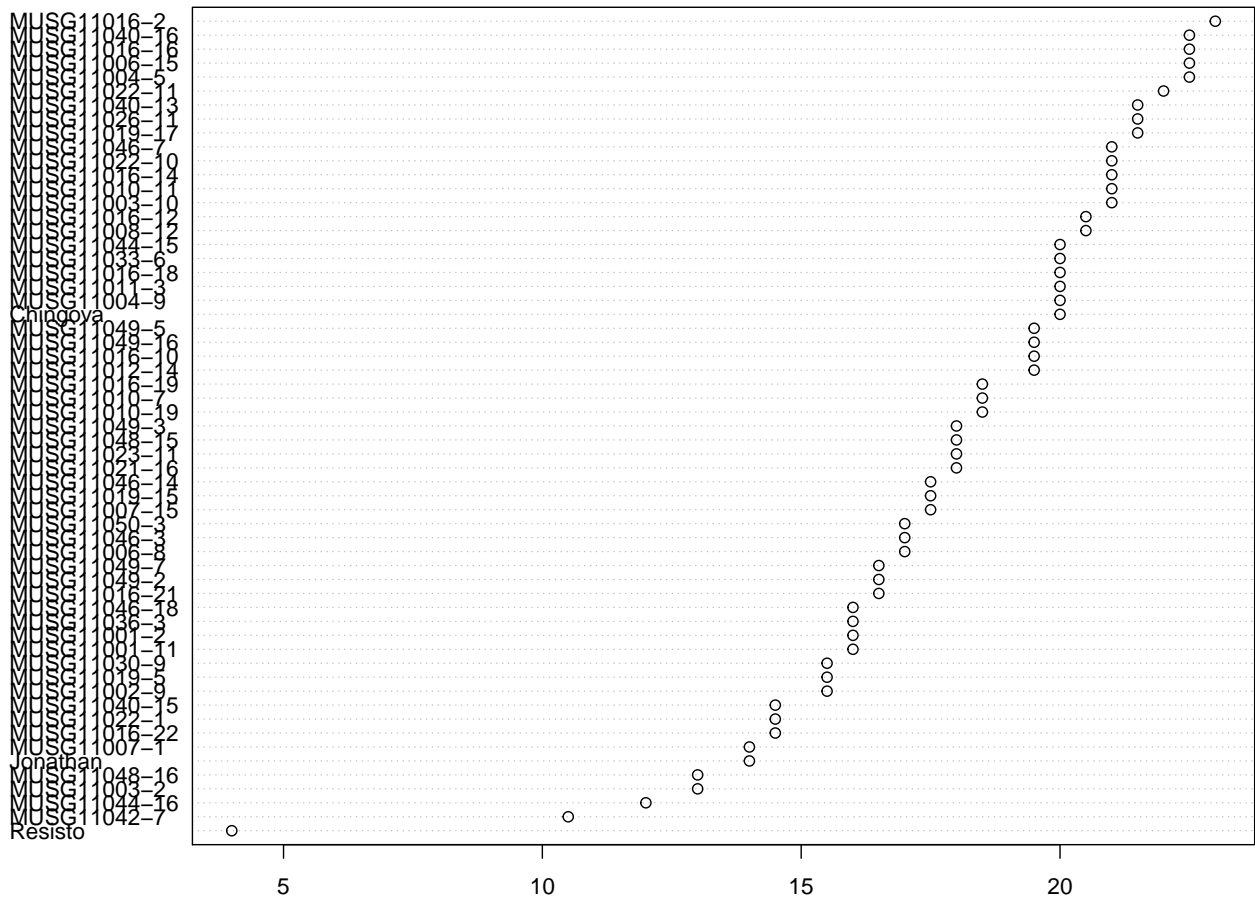
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	1404.08	24.2084	2.02501	0.00404478
REP	1	7.12712	7.12712	0.596177	0.443175
Residuals	58	693.373	11.9547	NA	NA

The p-value for treatments is 0.00404478 which is significant at the 5% level.

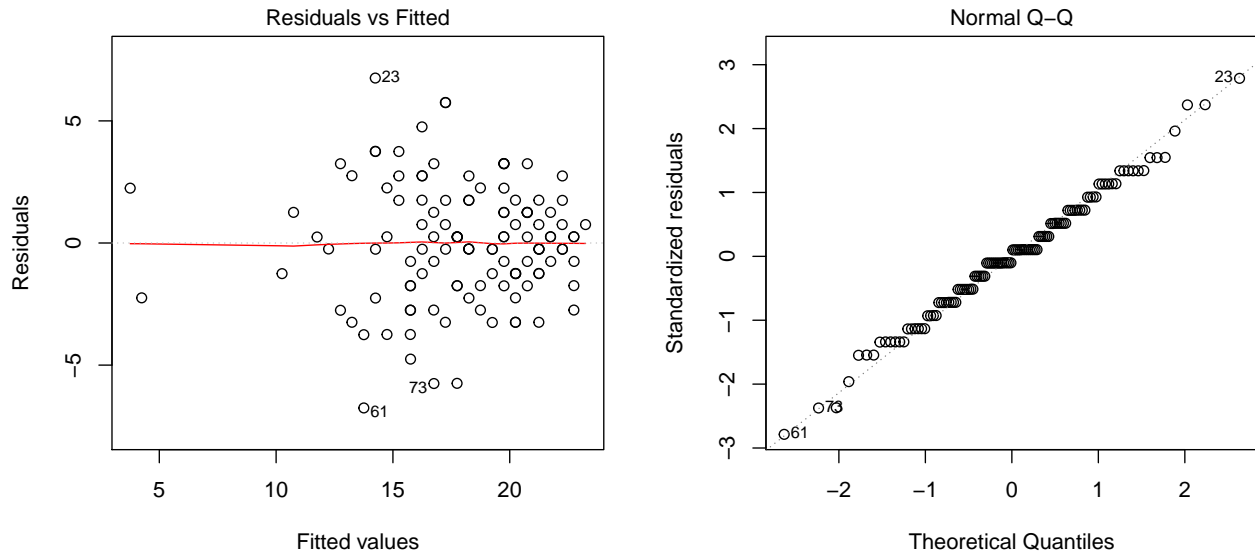
The means of your treatments are:

germplasmName	Plants established counting number per plot
Chingova	20
Jonathan	14
MUSG11001-11	16
MUSG11001-2	16
MUSG11002-9	15.5
MUSG11003-10	21
MUSG11003-2	13
MUSG11004-5	22.5
MUSG11004-9	20
MUSG11006-15	22.5
MUSG11006-8	17
MUSG11007-1	14
MUSG11007-15	17.5
MUSG11008-12	20.5
MUSG11010-11	21
MUSG11010-19	18.5
MUSG11010-7	18.5
MUSG11011-3	20
MUSG11012-14	19.5
MUSG11016-10	19.5
MUSG11016-12	20.5
MUSG11016-14	21
MUSG11016-16	22.5
MUSG11016-18	20
MUSG11016-19	18.5
MUSG11016-2	23
MUSG11016-21	16.5
MUSG11016-22	14.5
MUSG11019-15	17.5
MUSG11019-17	21.5
MUSG11019-5	15.5
MUSG11021-16	18
MUSG11022-1	14.5
MUSG11022-10	21
MUSG11022-11	22
MUSG11023-11	18
MUSG11026-11	21.5
MUSG11030-9	15.5

germplasmName	Plants established counting number per plot
MUSG11033-6	20
MUSG11036-3	16
MUSG11040-13	21.5
MUSG11040-15	14.5
MUSG11040-16	22.5
MUSG11042-7	10.5
MUSG11044-15	20
MUSG11044-16	12
MUSG11046-14	17.5
MUSG11046-18	16
MUSG11046-3	17
MUSG11046-7	21
MUSG11048-15	18
MUSG11048-16	13
MUSG11049-16	19.5
MUSG11049-2	16.5
MUSG11049-3	18
MUSG11049-5	19.5
MUSG11049-7	16.5
MUSG11050-3	17
Resisto	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:



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 harvested counting number per plot

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

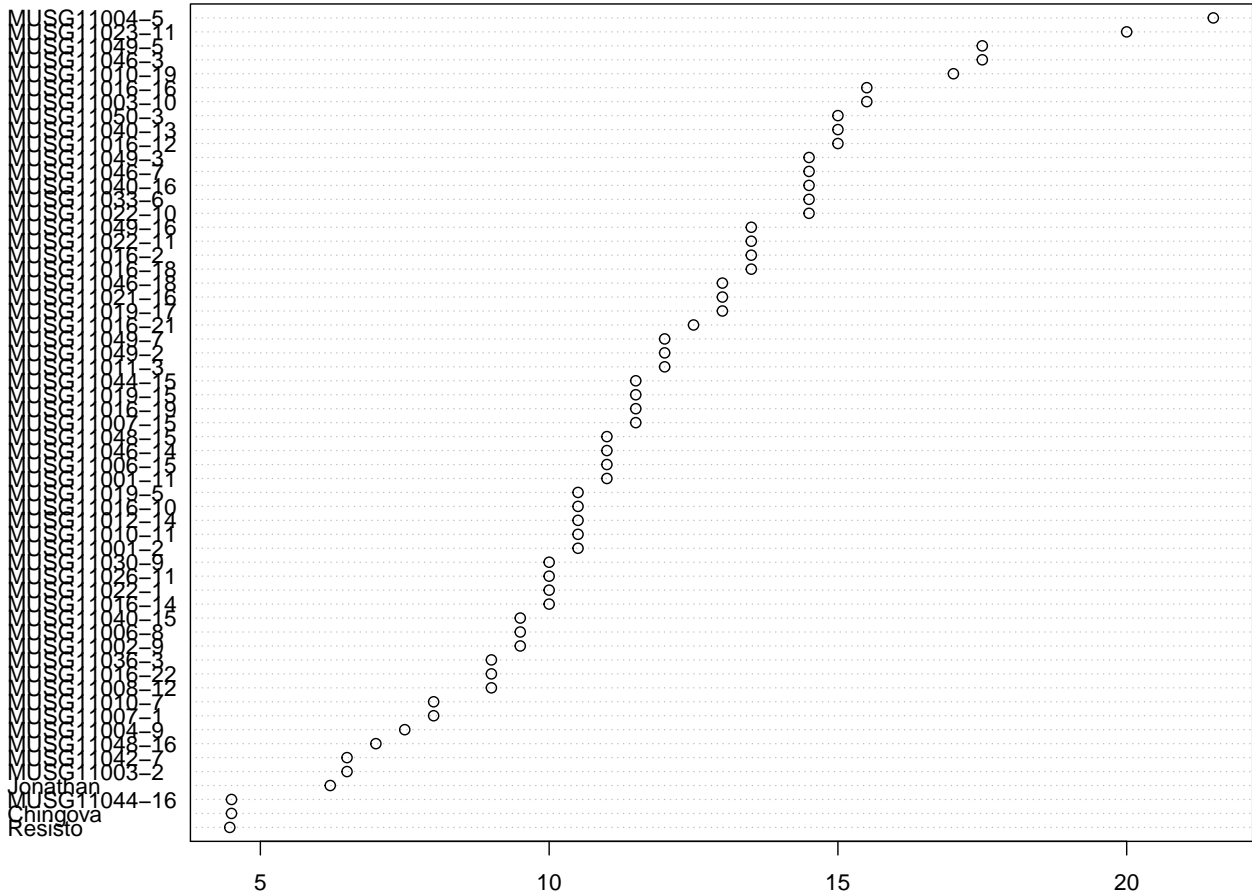
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	1488.04	25.6559	2.33338	0.00077113
REP	1	128.961	128.961	11.7289	0.00113599
Residuals	58	637.719	10.9952	NA	NA

The p-value for treatments is 0.00077113 which is significant at the 5% level.

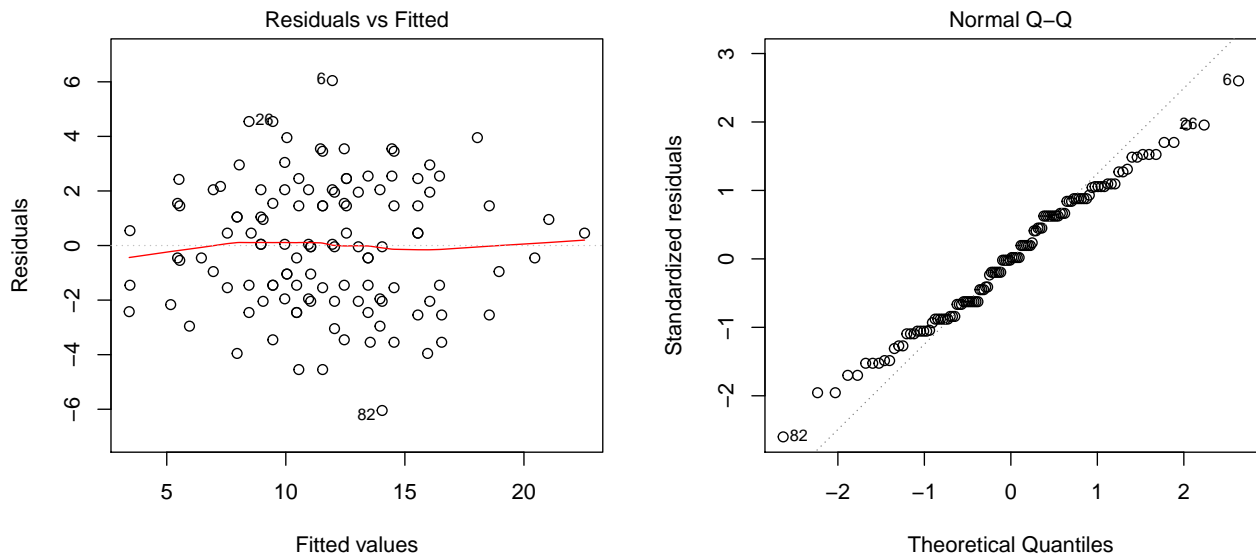
The means of your treatments are:

germplasmName	Plants harvested counting number per plot
Chingova	4.5
Jonathan	6.21
MUSG11001-11	11
MUSG11001-2	10.5
MUSG11002-9	9.5
MUSG11003-10	15.5
MUSG11003-2	6.5
MUSG11004-5	21.5
MUSG11004-9	7.5
MUSG11006-15	11
MUSG11006-8	9.5
MUSG11007-1	8
MUSG11007-15	11.5

germplasmName	Plants harvested counting number per plot
MUSG11008-12	9
MUSG11010-11	10.5
MUSG11010-19	17
MUSG11010-7	8
MUSG11011-3	12
MUSG11012-14	10.5
MUSG11016-10	10.5
MUSG11016-12	15
MUSG11016-14	10
MUSG11016-16	15.5
MUSG11016-18	13.5
MUSG11016-19	11.5
MUSG11016-2	13.5
MUSG11016-21	12.5
MUSG11016-22	9
MUSG11019-15	11.5
MUSG11019-17	13
MUSG11019-5	10.5
MUSG11021-16	13
MUSG11022-1	10
MUSG11022-10	14.5
MUSG11022-11	13.5
MUSG11023-11	20
MUSG11026-11	10
MUSG11030-9	10
MUSG11033-6	14.5
MUSG11036-3	9
MUSG11040-13	15
MUSG11040-15	9.5
MUSG11040-16	14.5
MUSG11042-7	6.5
MUSG11044-15	11.5
MUSG11044-16	4.5
MUSG11046-14	11
MUSG11046-18	13
MUSG11046-3	17.5
MUSG11046-7	14.5
MUSG11048-15	11
MUSG11048-16	7
MUSG11049-16	13.5
MUSG11049-2	12
MUSG11049-3	14.5
MUSG11049-5	17.5
MUSG11049-7	12
MUSG11050-3	15
Resisto	4.47



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

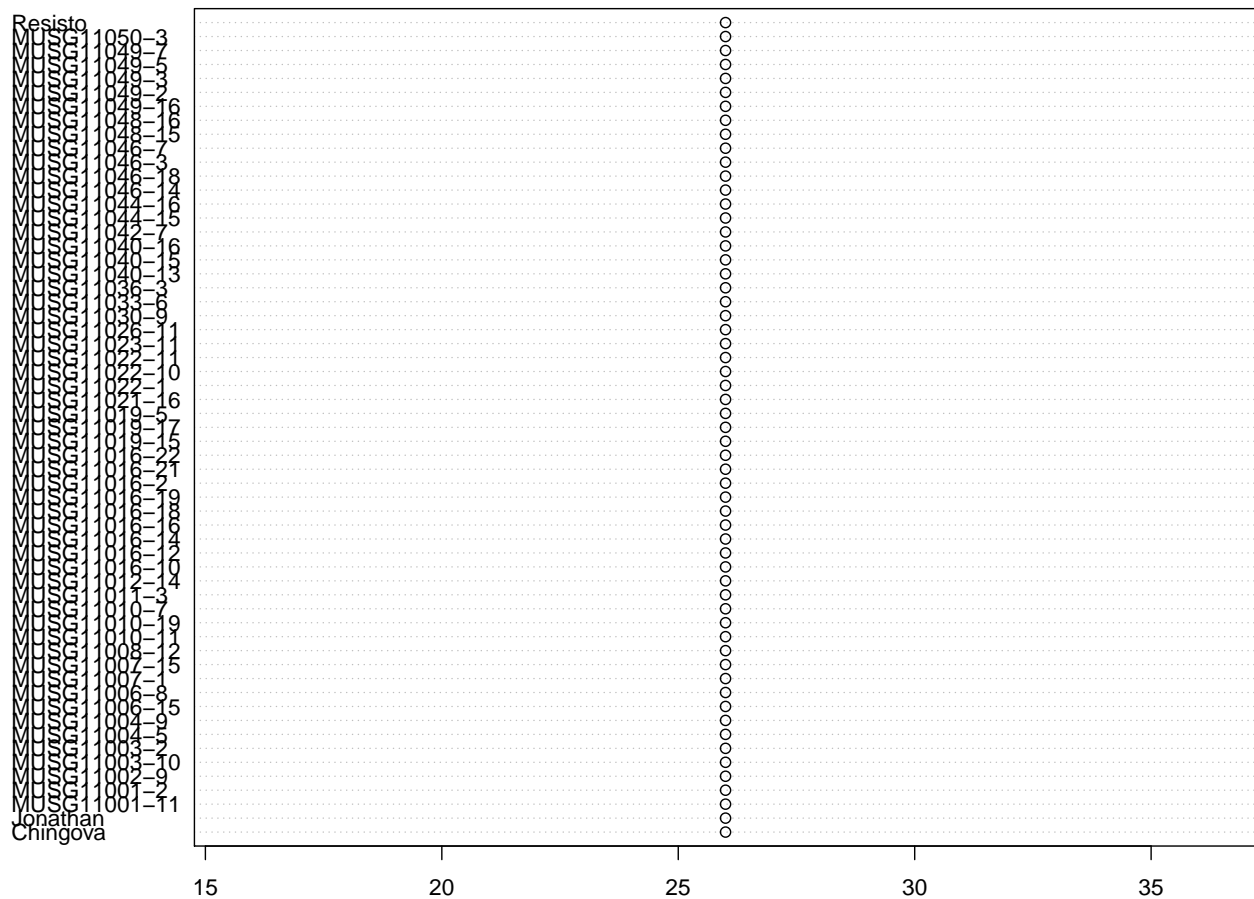
You have fitted a linear model for a RCBD. The ANOVA table for your model is:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	1.83016e-26	3.15544e-28	1	0.5
REP	1	3.15544e-28	3.15544e-28	1	0.321464
Residuals	58	1.83016e-26	3.15544e-28	NA	NA

The means of your treatments are:

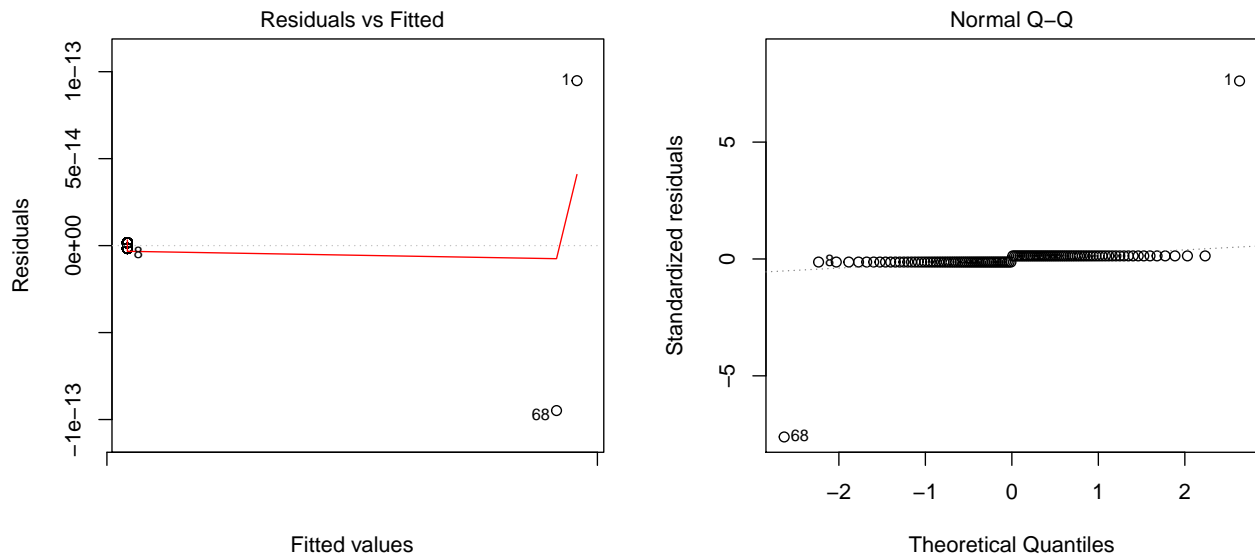
germplasmName	Plants planted counting number per plot
Chingova	26
Jonathan	26
MUSG11001-11	26
MUSG11001-2	26
MUSG11002-9	26
MUSG11003-10	26
MUSG11003-2	26
MUSG11004-5	26
MUSG11004-9	26
MUSG11006-15	26
MUSG11006-8	26
MUSG11007-1	26
MUSG11007-15	26
MUSG11008-12	26
MUSG11010-11	26
MUSG11010-19	26
MUSG11010-7	26
MUSG11011-3	26
MUSG11012-14	26
MUSG11016-10	26
MUSG11016-12	26
MUSG11016-14	26
MUSG11016-16	26
MUSG11016-18	26
MUSG11016-19	26
MUSG11016-2	26
MUSG11016-21	26
MUSG11016-22	26
MUSG11019-15	26
MUSG11019-17	26
MUSG11019-5	26
MUSG11021-16	26
MUSG11022-1	26
MUSG11022-10	26
MUSG11022-11	26
MUSG11023-11	26
MUSG11026-11	26
MUSG11030-9	26
MUSG11033-6	26
MUSG11036-3	26

germplasmName	Plants planted counting number per plot
MUSG11040-13	26
MUSG11040-15	26
MUSG11040-16	26
MUSG11042-7	26
MUSG11044-15	26
MUSG11044-16	26
MUSG11046-14	26
MUSG11046-18	26
MUSG11046-3	26
MUSG11046-7	26
MUSG11048-15	26
MUSG11048-16	26
MUSG11049-16	26
MUSG11049-2	26
MUSG11049-3	26
MUSG11049-5	26
MUSG11049-7	26
MUSG11050-3	26
Resisto	26



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:


```
## Warning in plot.window(...): relative range of values = 17 * EPS, is small
## (axis 1)
```



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 with storage roots counting number per plot

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

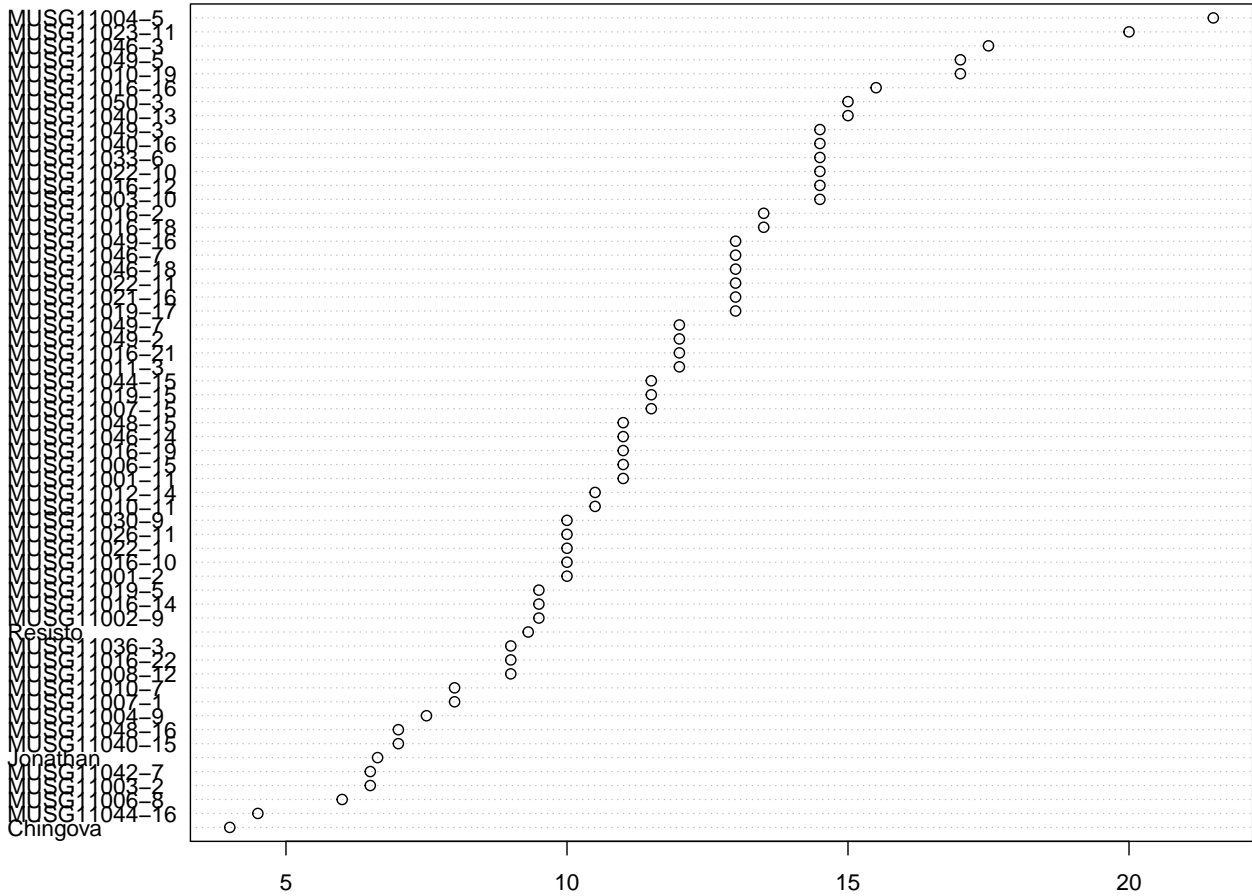
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	1451.77	25.0305	2.33786	0.000752872
REP	1	137.401	137.401	12.8333	0.000697638
Residuals	58	620.983	10.7066	NA	NA

The p-value for treatments is 0.000752872 which is significant at the 5% level.

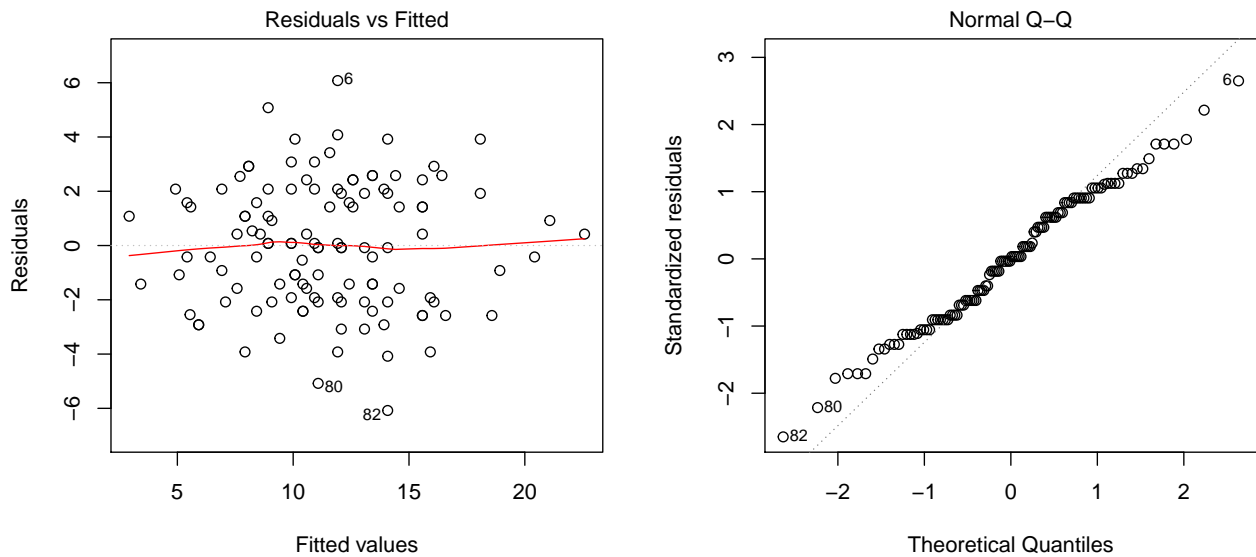
The means of your treatments are:

germplasmName	Plants with storage roots counting number per plot
Chingova	4
Jonathan	6.63
MUSG11001-11	11
MUSG11001-2	10
MUSG11002-9	9.5
MUSG11003-10	14.5
MUSG11003-2	6.5
MUSG11004-5	21.5
MUSG11004-9	7.5
MUSG11006-15	11
MUSG11006-8	6
MUSG11007-1	8
MUSG11007-15	11.5

germplasmName	Plants with storage roots counting number per plot
MUSG11008-12	9
MUSG11010-11	10.5
MUSG11010-19	17
MUSG11010-7	8
MUSG11011-3	12
MUSG11012-14	10.5
MUSG11016-10	10
MUSG11016-12	14.5
MUSG11016-14	9.5
MUSG11016-16	15.5
MUSG11016-18	13.5
MUSG11016-19	11
MUSG11016-2	13.5
MUSG11016-21	12
MUSG11016-22	9
MUSG11019-15	11.5
MUSG11019-17	13
MUSG11019-5	9.5
MUSG11021-16	13
MUSG11022-1	10
MUSG11022-10	14.5
MUSG11022-11	13
MUSG11023-11	20
MUSG11026-11	10
MUSG11030-9	10
MUSG11033-6	14.5
MUSG11036-3	9
MUSG11040-13	15
MUSG11040-15	7
MUSG11040-16	14.5
MUSG11042-7	6.5
MUSG11044-15	11.5
MUSG11044-16	4.5
MUSG11046-14	11
MUSG11046-18	13
MUSG11046-3	17.5
MUSG11046-7	13
MUSG11048-15	11
MUSG11048-16	7
MUSG11049-16	13
MUSG11049-2	12
MUSG11049-3	14.5
MUSG11049-5	17
MUSG11049-7	12
MUSG11050-3	15
Resisto	9.31



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 Protein content measuring percent

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

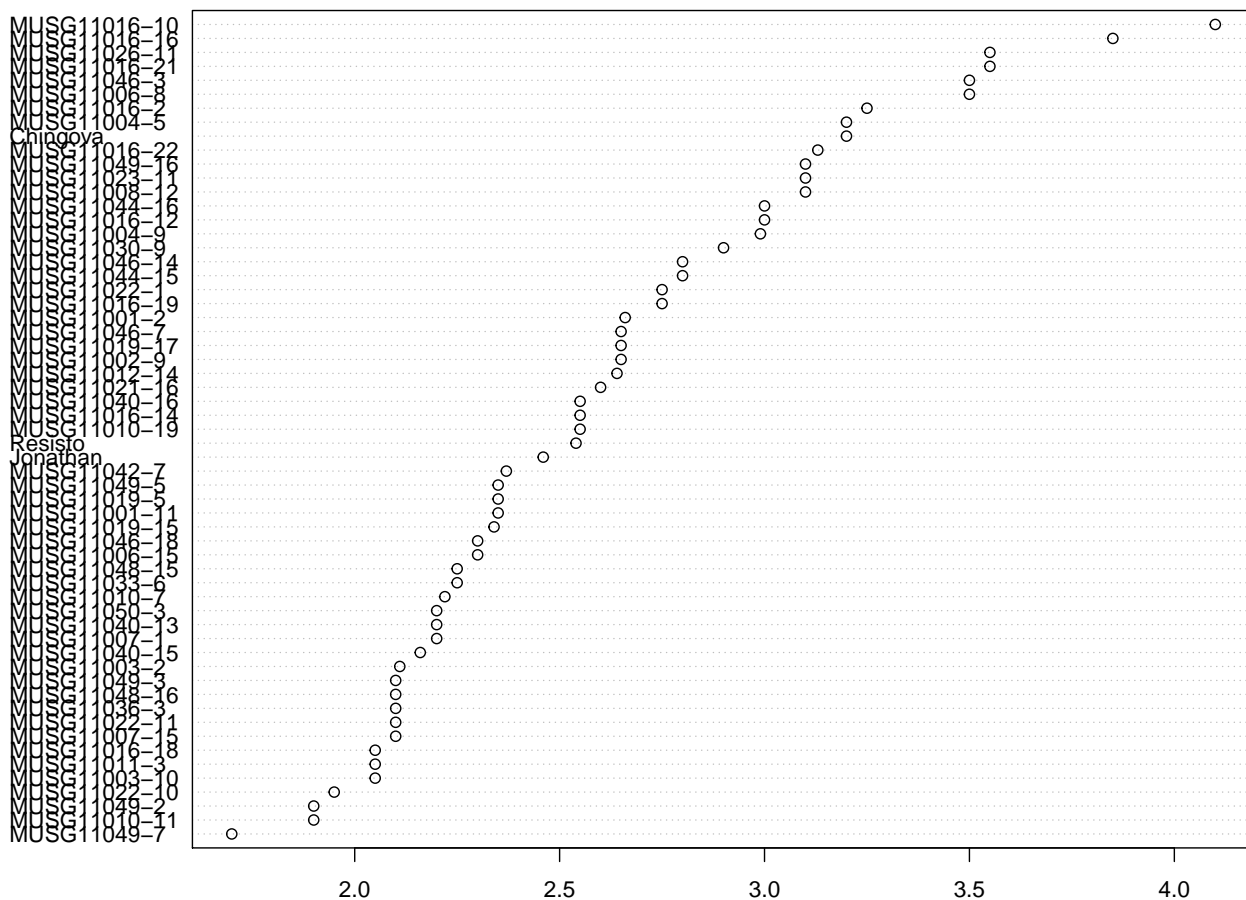
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	32.5712	0.561572	1.87119	0.00921811
REP	1	1.36885	1.36885	4.56109	0.0369399
Residuals	58	17.4066	0.300115	NA	NA

The p-value for treatments is 0.00921811 which is significant at the 5% level.

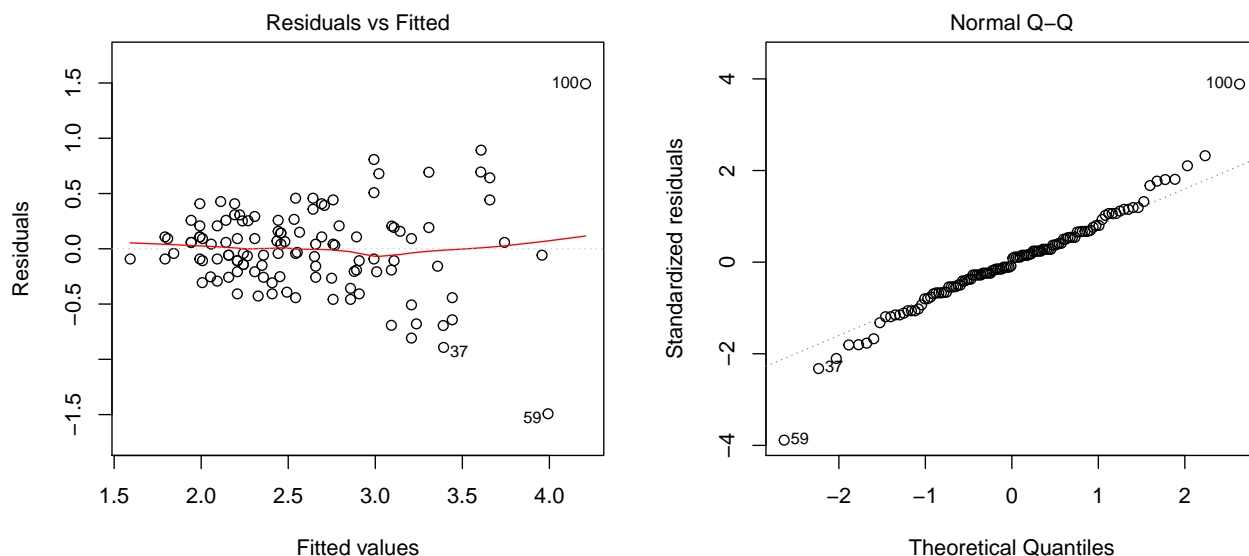
The means of your treatments are:

germplasmName	Protein content measuring percent
Chingova	3.2
Jonathan	2.46
MUSG11001-11	2.35
MUSG11001-2	2.66
MUSG11002-9	2.65
MUSG11003-10	2.05
MUSG11003-2	2.11
MUSG11004-5	3.2
MUSG11004-9	2.99
MUSG11006-15	2.3
MUSG11006-8	3.5
MUSG11007-1	2.2
MUSG11007-15	2.1
MUSG11008-12	3.1
MUSG11010-11	1.9
MUSG11010-19	2.55
MUSG11010-7	2.22
MUSG11011-3	2.05
MUSG11012-14	2.64
MUSG11016-10	4.1
MUSG11016-12	3
MUSG11016-14	2.55
MUSG11016-16	3.85
MUSG11016-18	2.05
MUSG11016-19	2.75
MUSG11016-2	3.25
MUSG11016-21	3.55
MUSG11016-22	3.13
MUSG11019-15	2.34
MUSG11019-17	2.65
MUSG11019-5	2.35
MUSG11021-16	2.6
MUSG11022-1	2.75
MUSG11022-10	1.95
MUSG11022-11	2.1
MUSG11023-11	3.1
MUSG11026-11	3.55
MUSG11030-9	2.9
MUSG11033-6	2.25

germplasmName	Protein content measuring percent
MUSG11036-3	2.1
MUSG11040-13	2.2
MUSG11040-15	2.16
MUSG11040-16	2.55
MUSG11042-7	2.37
MUSG11044-15	2.8
MUSG11044-16	3
MUSG11046-14	2.8
MUSG11046-18	2.3
MUSG11046-3	3.5
MUSG11046-7	2.65
MUSG11048-15	2.25
MUSG11048-16	2.1
MUSG11049-16	3.1
MUSG11049-2	1.9
MUSG11049-3	2.1
MUSG11049-5	2.35
MUSG11049-7	1.7
MUSG11050-3	2.2
Resisto	2.54



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 estimating 1-9

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

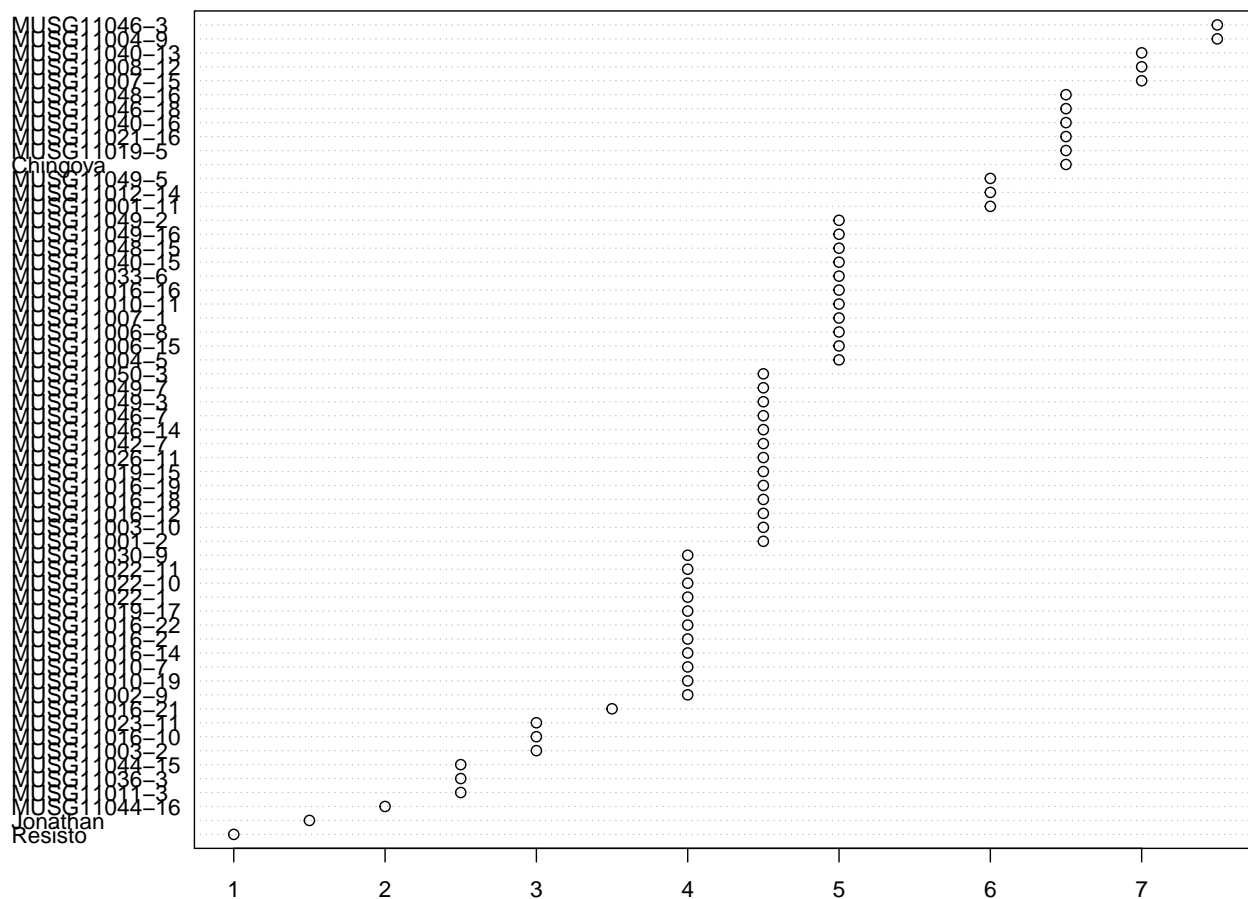
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	237.441	4.0938	2.4487	0.000416731
REP	1	0.0338983	0.0338983	0.0202762	0.887262
Residuals	58	96.9661	1.67183	NA	NA

The p-value for treatments is 0.000416731 which is significant at the 5% level.

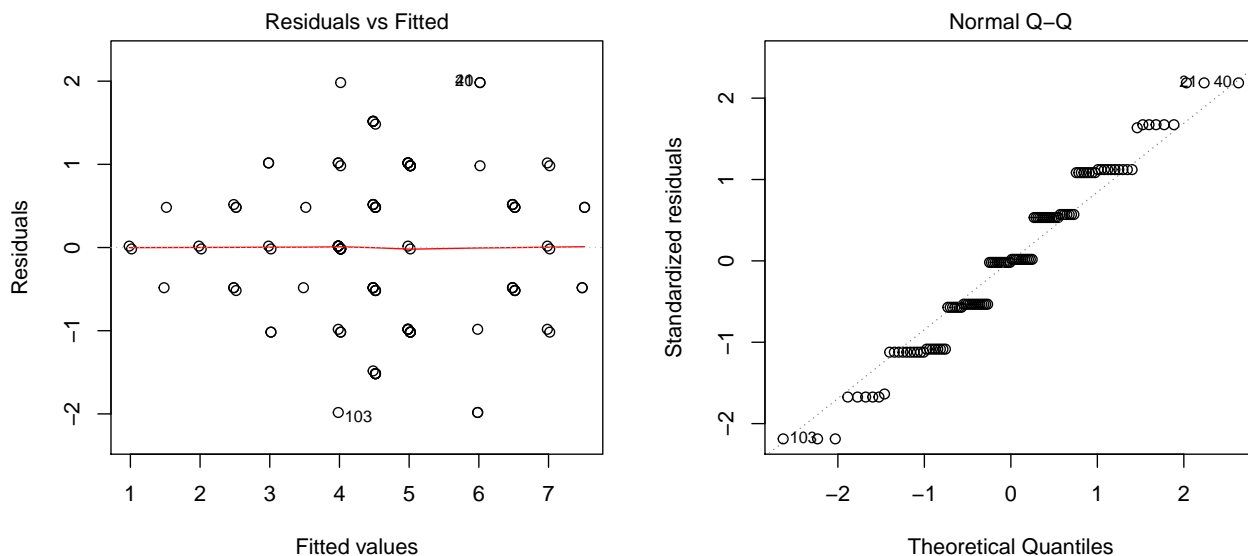
The means of your treatments are:

germplasmName	Storage root damages estimating 1-9
Chingova	6.5
Jonathan	1.5
MUSG11001-11	6
MUSG11001-2	4.5
MUSG11002-9	4
MUSG11003-10	4.5
MUSG11003-2	3
MUSG11004-5	5
MUSG11004-9	7.5
MUSG11006-15	5
MUSG11006-8	5
MUSG11007-1	5
MUSG11007-15	7
MUSG11008-12	7
MUSG11010-11	5
MUSG11010-19	4

germplasmName	Storage root damages estimating 1-9
MUSG11010-7	4
MUSG11011-3	2.5
MUSG11012-14	6
MUSG11016-10	3
MUSG11016-12	4.5
MUSG11016-14	4
MUSG11016-16	5
MUSG11016-18	4.5
MUSG11016-19	4.5
MUSG11016-2	4
MUSG11016-21	3.5
MUSG11016-22	4
MUSG11019-15	4.5
MUSG11019-17	4
MUSG11019-5	6.5
MUSG11021-16	6.5
MUSG11022-1	4
MUSG11022-10	4
MUSG11022-11	4
MUSG11023-11	3
MUSG11026-11	4.5
MUSG11030-9	4
MUSG11033-6	5
MUSG11036-3	2.5
MUSG11040-13	7
MUSG11040-15	5
MUSG11040-16	6.5
MUSG11042-7	4.5
MUSG11044-15	2.5
MUSG11044-16	2
MUSG11046-14	4.5
MUSG11046-18	6.5
MUSG11046-3	7.5
MUSG11046-7	4.5
MUSG11048-15	5
MUSG11048-16	6.5
MUSG11049-16	5
MUSG11049-2	5
MUSG11049-3	4.5
MUSG11049-5	6
MUSG11049-7	4.5
MUSG11050-3	4.5
Resisto	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 Storage root dry matter content computing percent

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

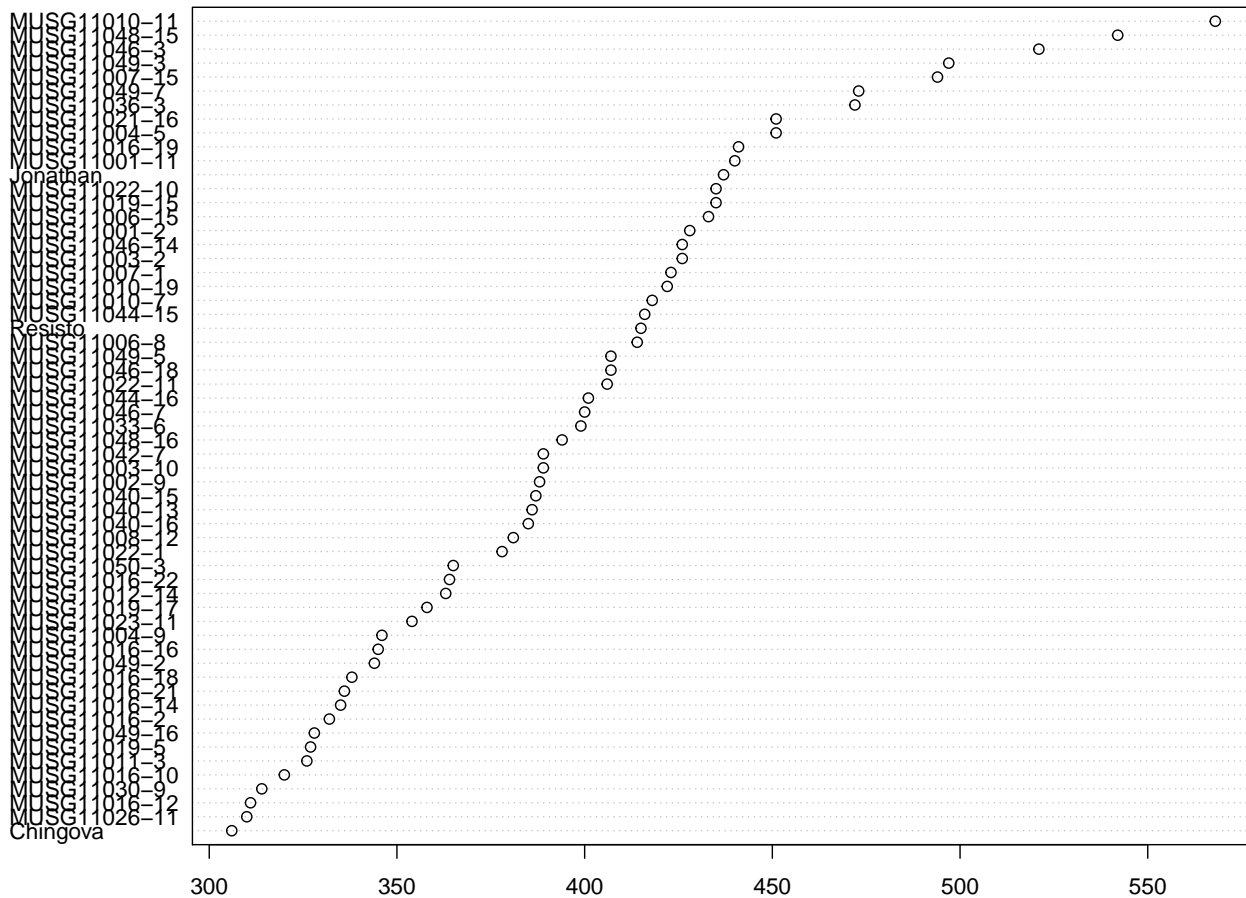
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	399151	6881.91	6.8791	3.90317e-12
REP	1	28.3025	28.3025	0.0282909	0.867012
Residuals	58	58023.7	1000.41	NA	NA

The p-value for treatments is 0.00000000000390317 which is significant at the 5% level.

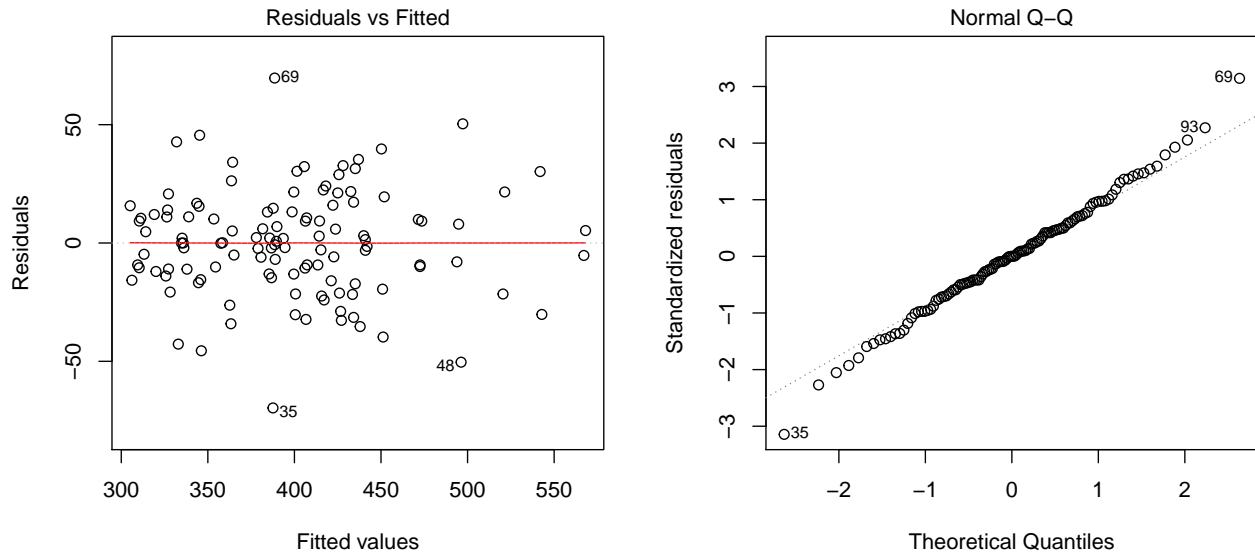
The means of your treatments are:

germplasmName	Storage root dry matter content computing percent
Chingova	306
Jonathan	437
MUSG11001-11	440
MUSG11001-2	428
MUSG11002-9	388
MUSG11003-10	389
MUSG11003-2	426
MUSG11004-5	451
MUSG11004-9	346
MUSG11006-15	433
MUSG11006-8	414
MUSG11007-1	423
MUSG11007-15	494
MUSG11008-12	381
MUSG11010-11	568
MUSG11010-19	422
MUSG11010-7	418
MUSG11011-3	326
MUSG11012-14	363
MUSG11016-10	320
MUSG11016-12	311
MUSG11016-14	335
MUSG11016-16	345
MUSG11016-18	338
MUSG11016-19	441
MUSG11016-2	332
MUSG11016-21	336
MUSG11016-22	364
MUSG11019-15	435
MUSG11019-17	358
MUSG11019-5	327
MUSG11021-16	451
MUSG11022-1	378
MUSG11022-10	435
MUSG11022-11	406
MUSG11023-11	354
MUSG11026-11	310
MUSG11030-9	314

germplasmName	Storage root dry matter content computing percent
MUSG11033-6	399
MUSG11036-3	472
MUSG11040-13	386
MUSG11040-15	387
MUSG11040-16	385
MUSG11042-7	389
MUSG11044-15	416
MUSG11044-16	401
MUSG11046-14	426
MUSG11046-18	407
MUSG11046-3	521
MUSG11046-7	400
MUSG11048-15	542
MUSG11048-16	394
MUSG11049-16	328
MUSG11049-2	344
MUSG11049-3	497
MUSG11049-5	407
MUSG11049-7	473
MUSG11050-3	365
Resisto	415



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 form estimating 1-9

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

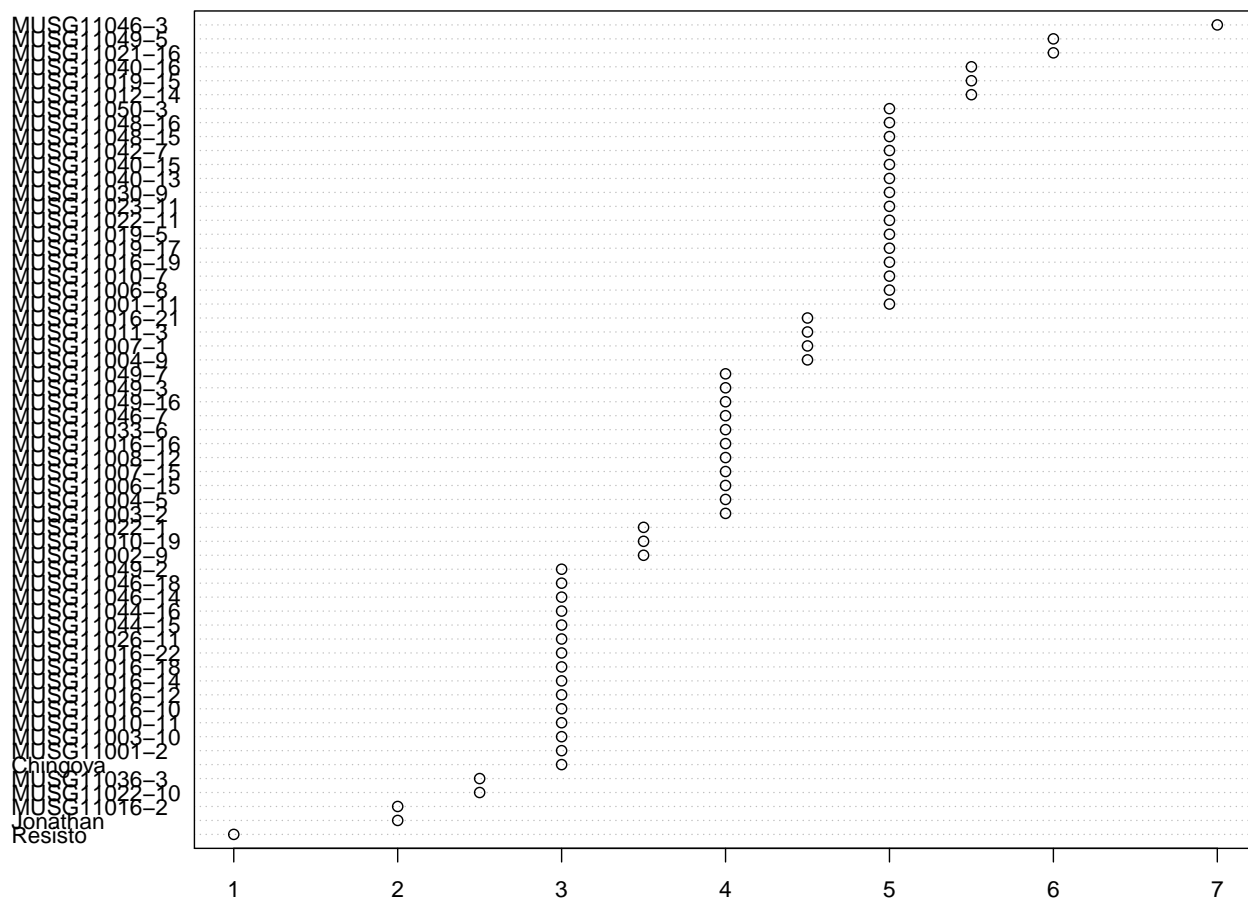
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	153.864	2.65283	3.21687	8.0386e-06
REP	1	2.16949	2.16949	2.63076	0.110236
Residuals	58	47.8305	0.824664	NA	NA

The p-value for treatments is 0.0000080386 which is significant at the 5% level.

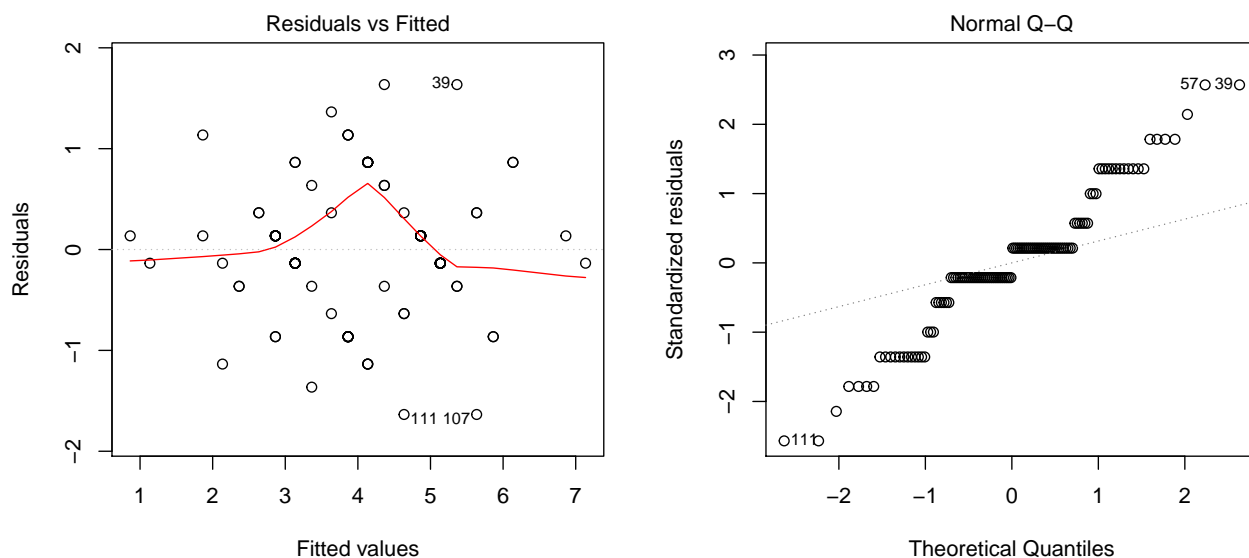
The means of your treatments are:

germplasmName	Storage root form estimating 1-9
Chingova	3
Jonathan	2
MUSG11001-11	5
MUSG11001-2	3
MUSG11002-9	3.5
MUSG11003-10	3
MUSG11003-2	4
MUSG11004-5	4
MUSG11004-9	4.5
MUSG11006-15	4
MUSG11006-8	5
MUSG11007-1	4.5
MUSG11007-15	4
MUSG11008-12	4

germplasmName	Storage root form estimating 1-9
MUSG11010-11	3
MUSG11010-19	3.5
MUSG11010-7	5
MUSG11011-3	4.5
MUSG11012-14	5.5
MUSG11016-10	3
MUSG11016-12	3
MUSG11016-14	3
MUSG11016-16	4
MUSG11016-18	3
MUSG11016-19	5
MUSG11016-2	2
MUSG11016-21	4.5
MUSG11016-22	3
MUSG11019-15	5.5
MUSG11019-17	5
MUSG11019-5	5
MUSG11021-16	6
MUSG11022-1	3.5
MUSG11022-10	2.5
MUSG11022-11	5
MUSG11023-11	5
MUSG11026-11	3
MUSG11030-9	5
MUSG11033-6	4
MUSG11036-3	2.5
MUSG11040-13	5
MUSG11040-15	5
MUSG11040-16	5.5
MUSG11042-7	5
MUSG11044-15	3
MUSG11044-16	3
MUSG11046-14	3
MUSG11046-18	3
MUSG11046-3	7
MUSG11046-7	4
MUSG11048-15	5
MUSG11048-16	5
MUSG11049-16	4
MUSG11049-2	3
MUSG11049-3	4
MUSG11049-5	6
MUSG11049-7	4
MUSG11050-3	5
Resisto	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 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	58	156.78	2.7031	2.06105	0.00333208
REP	1	1.4322	1.4322	1.09202	0.300359
Residuals	58	76.0678	1.31151	NA	NA

The p-value for treatments is 0.00333208 which is significant at the 5% level.

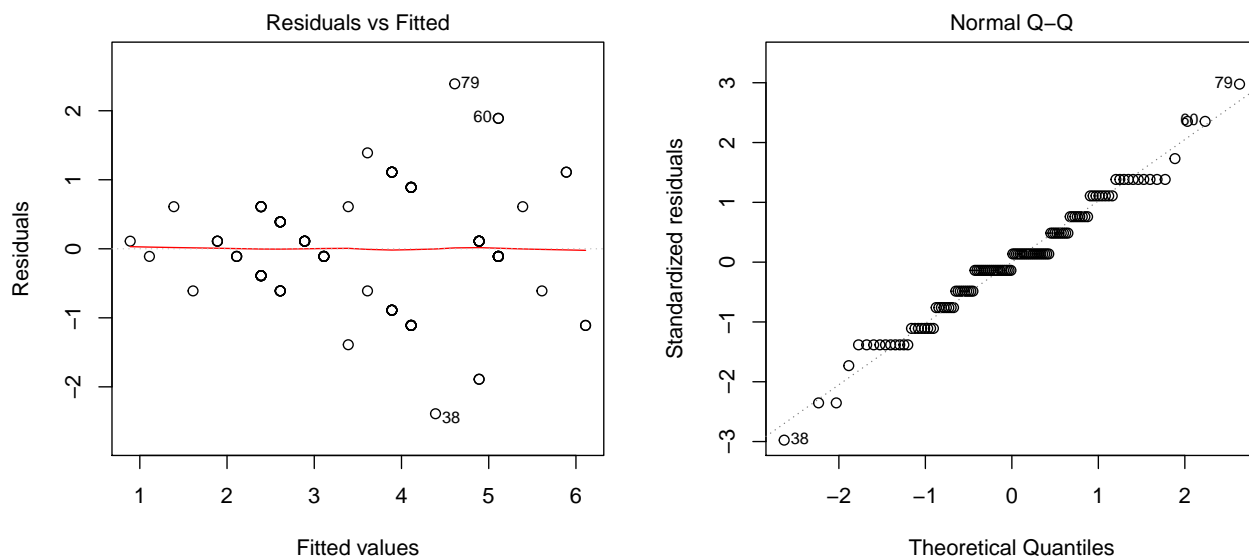
The means of your treatments are:

germplasmName	Storage root size estimating 1-9
Chingova	2.5
Jonathan	1.5
MUSG11001-11	5
MUSG11001-2	3
MUSG11002-9	2.5
MUSG11003-10	4
MUSG11003-2	4
MUSG11004-5	2.5
MUSG11004-9	4
MUSG11006-15	3.5
MUSG11006-8	5.5
MUSG11007-1	4
MUSG11007-15	4
MUSG11008-12	4.5
MUSG11010-11	4
MUSG11010-19	2.5
MUSG11010-7	6
MUSG11011-3	2.5
MUSG11012-14	5
MUSG11016-10	3
MUSG11016-12	2
MUSG11016-14	2.5
MUSG11016-16	4
MUSG11016-18	2.5
MUSG11016-19	2.5
MUSG11016-2	2
MUSG11016-21	2.5
MUSG11016-22	2.5
MUSG11019-15	5
MUSG11019-17	5
MUSG11019-5	5
MUSG11021-16	5
MUSG11022-1	2
MUSG11022-10	3
MUSG11022-11	4
MUSG11023-11	4
MUSG11026-11	2.5
MUSG11030-9	3
MUSG11033-6	5

Scatter plot showing Logarithmic Resistance (Y-axis) versus Frequency (X-axis) for a 100 ohm resistor. The data points show a linear relationship on the log-log scale, indicating a power-law relationship between resistance and frequency.

Frequency (Hz)	Logarithmic Resistance (ohms)
1	1.5
2	2.0
3	2.5
4	3.0
5	3.5
6	4.0

55



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 starch content measuring percent

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

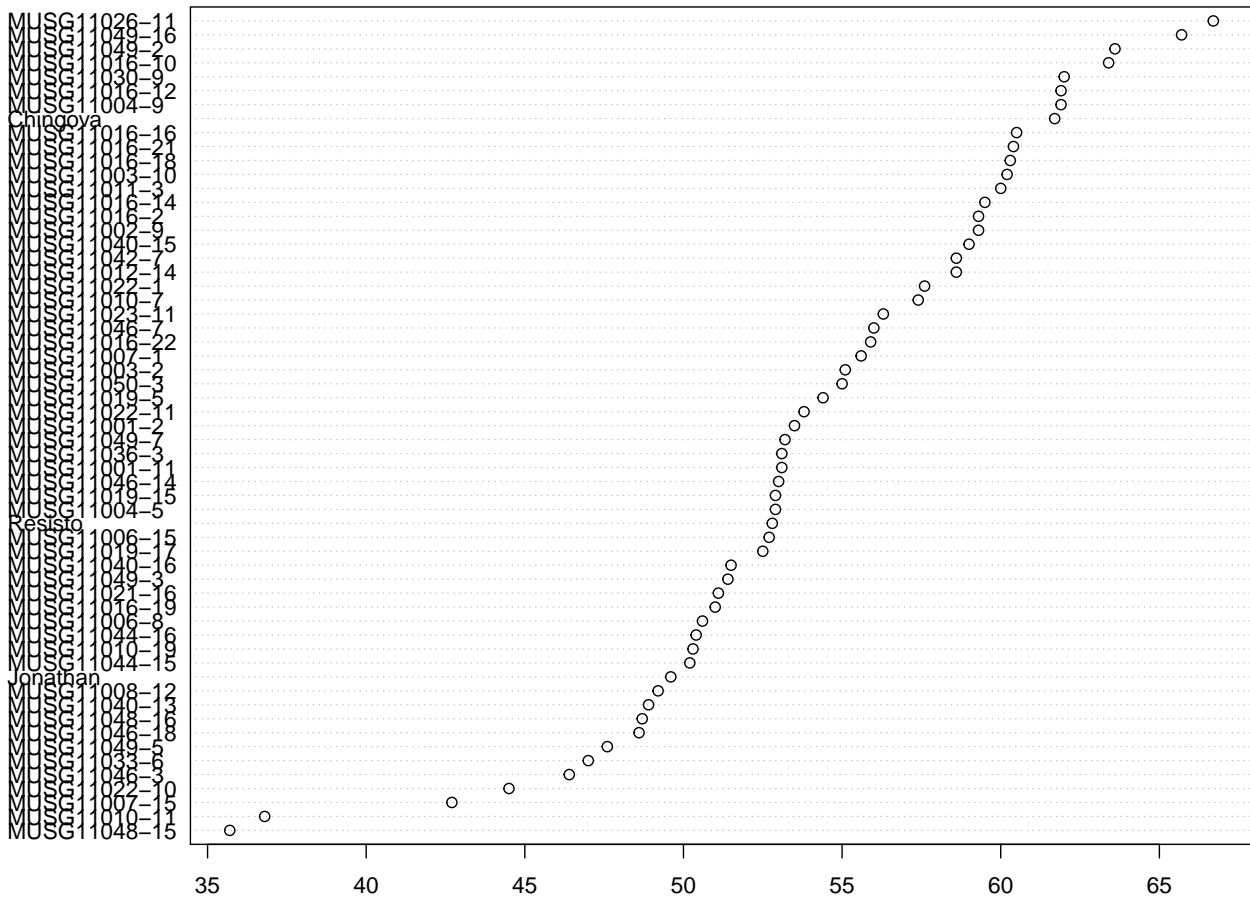
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	4659.19	80.3309	4.74208	8.52671e-09
REP	1	3.80015	3.80015	0.22433	0.637538
Residuals	58	982.52	16.94	NA	NA

The p-value for treatments is 0.00000000852671 which is significant at the 5% level.

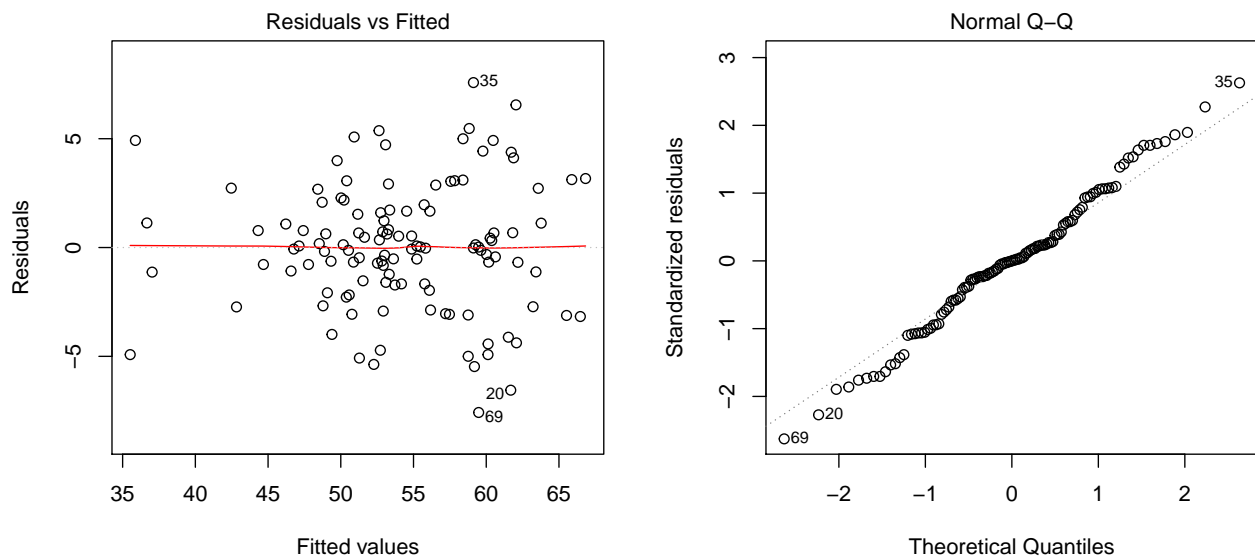
The means of your treatments are:

germplasmName	Storage root starch content measuring percent
Chingova	61.7
Jonathan	49.6
MUSG11001-11	53.1
MUSG11001-2	53.5
MUSG11002-9	59.3
MUSG11003-10	60.2
MUSG11003-2	55.1
MUSG11004-5	52.9
MUSG11004-9	61.9
MUSG11006-15	52.7
MUSG11006-8	50.6
MUSG11007-1	55.6
MUSG11007-15	42.7
MUSG11008-12	49.2
MUSG11010-11	36.8
MUSG11010-19	50.3

germplasmName	Storage root starch content measuring	
	percent	
MUSG11010-7	57.4	
MUSG11011-3	60	
MUSG11012-14	58.6	
MUSG11016-10	63.4	
MUSG11016-12	61.9	
MUSG11016-14	59.5	
MUSG11016-16	60.5	
MUSG11016-18	60.3	
MUSG11016-19	51	
MUSG11016-2	59.3	
MUSG11016-21	60.4	
MUSG11016-22	55.9	
MUSG11019-15	52.9	
MUSG11019-17	52.5	
MUSG11019-5	54.4	
MUSG11021-16	51.1	
MUSG11022-1	57.6	
MUSG11022-10	44.5	
MUSG11022-11	53.8	
MUSG11023-11	56.3	
MUSG11026-11	66.7	
MUSG11030-9	62	
MUSG11033-6	47	
MUSG11036-3	53.1	
MUSG11040-13	48.9	
MUSG11040-15	59	
MUSG11040-16	51.5	
MUSG11042-7	58.6	
MUSG11044-15	50.2	
MUSG11044-16	50.4	
MUSG11046-14	53	
MUSG11046-18	48.6	
MUSG11046-3	46.4	
MUSG11046-7	56	
MUSG11048-15	35.7	
MUSG11048-16	48.7	
MUSG11049-16	65.7	
MUSG11049-2	63.6	
MUSG11049-3	51.4	
MUSG11049-5	47.6	
MUSG11049-7	53.2	
MUSG11050-3	55	
Resisto	52.8	



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 sweetness 1 estimating 1-9

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

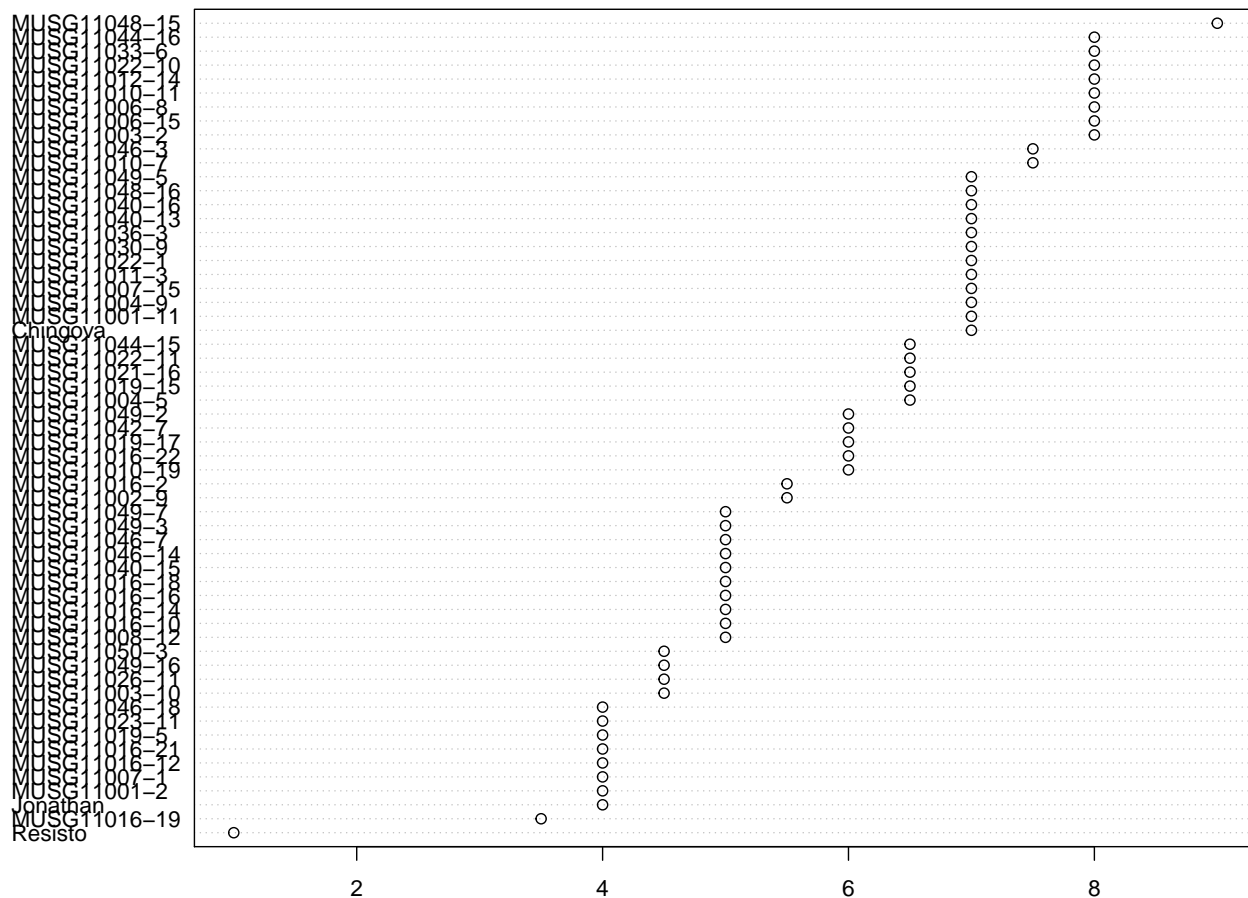
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	282.458	4.86996	1.80065	0.0134052
REP	1	0.135593	0.135593	0.0501351	0.823615
Residuals	58	156.864	2.70456	NA	NA

The p-value for treatments is 0.0134052 which is significant at the 5% level.

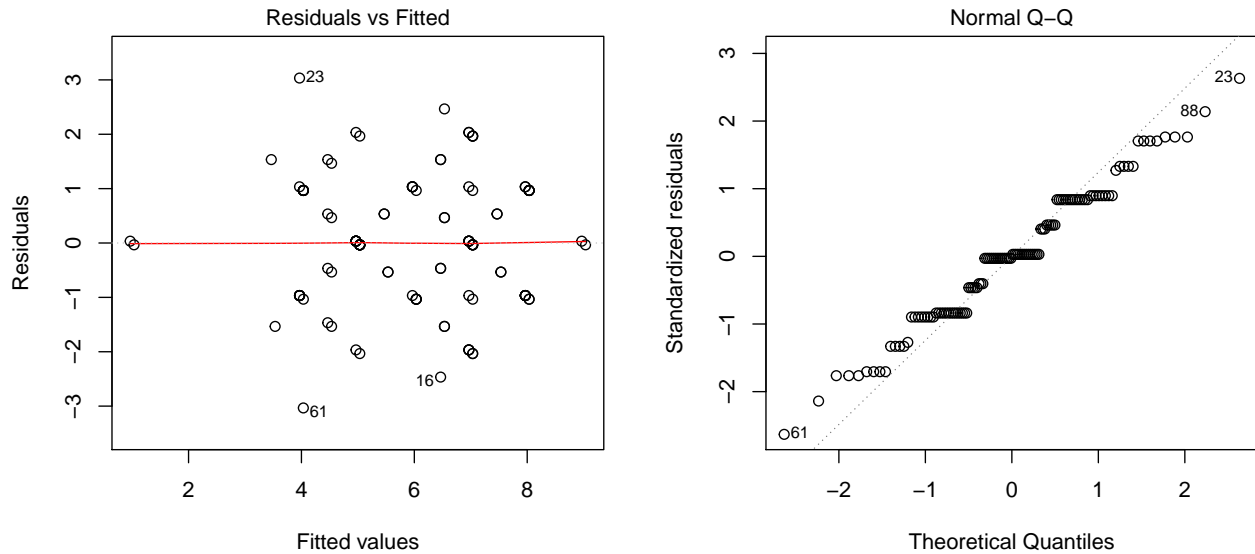
The means of your treatments are:

germplasmName	Storage root sweetness 1 estimating 1-9
Chingova	7
Jonathan	4
MUSG11001-11	7
MUSG11001-2	4
MUSG11002-9	5.5
MUSG11003-10	4.5
MUSG11003-2	8
MUSG11004-5	6.5
MUSG11004-9	7
MUSG11006-15	8
MUSG11006-8	8
MUSG11007-1	4
MUSG11007-15	7
MUSG11008-12	5
MUSG11010-11	8
MUSG11010-19	6
MUSG11010-7	7.5
MUSG11011-3	7
MUSG11012-14	8
MUSG11016-10	5
MUSG11016-12	4
MUSG11016-14	5
MUSG11016-16	5
MUSG11016-18	5
MUSG11016-19	3.5
MUSG11016-2	5.5
MUSG11016-21	4
MUSG11016-22	6
MUSG11019-15	6.5
MUSG11019-17	6
MUSG11019-5	4
MUSG11021-16	6.5
MUSG11022-1	7
MUSG11022-10	8
MUSG11022-11	6.5
MUSG11023-11	4
MUSG11026-11	4.5
MUSG11030-9	7

Storage root sweetness 1 estimating	
germplasmName	1-9
MUSG11033-6	8
MUSG11036-3	7
MUSG11040-13	7
MUSG11040-15	5
MUSG11040-16	7
MUSG11042-7	6
MUSG11044-15	6.5
MUSG11044-16	8
MUSG11046-14	5
MUSG11046-18	4
MUSG11046-3	7.5
MUSG11046-7	5
MUSG11048-15	9
MUSG11048-16	7
MUSG11049-16	4.5
MUSG11049-2	6
MUSG11049-3	5
MUSG11049-5	7
MUSG11049-7	5
MUSG11050-3	4.5
Resisto	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 Storage root texture 1 estimating 1-9

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

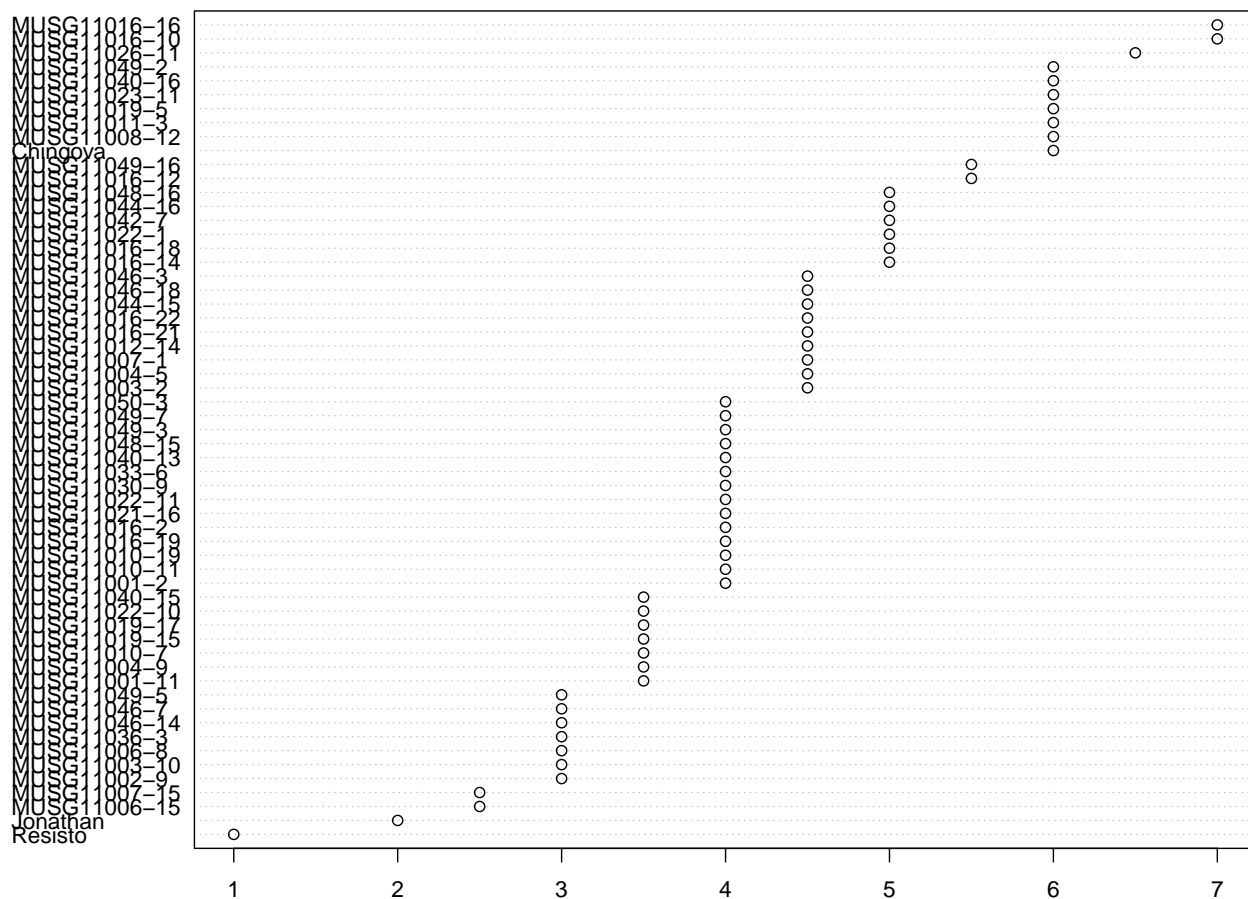
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	172.119	2.96756	1.89001	0.00833833
REP	1	1.4322	1.4322	0.912153	0.343508
Residuals	58	91.0678	1.57013	NA	NA

The p-value for treatments is 0.00833833 which is significant at the 5% level.

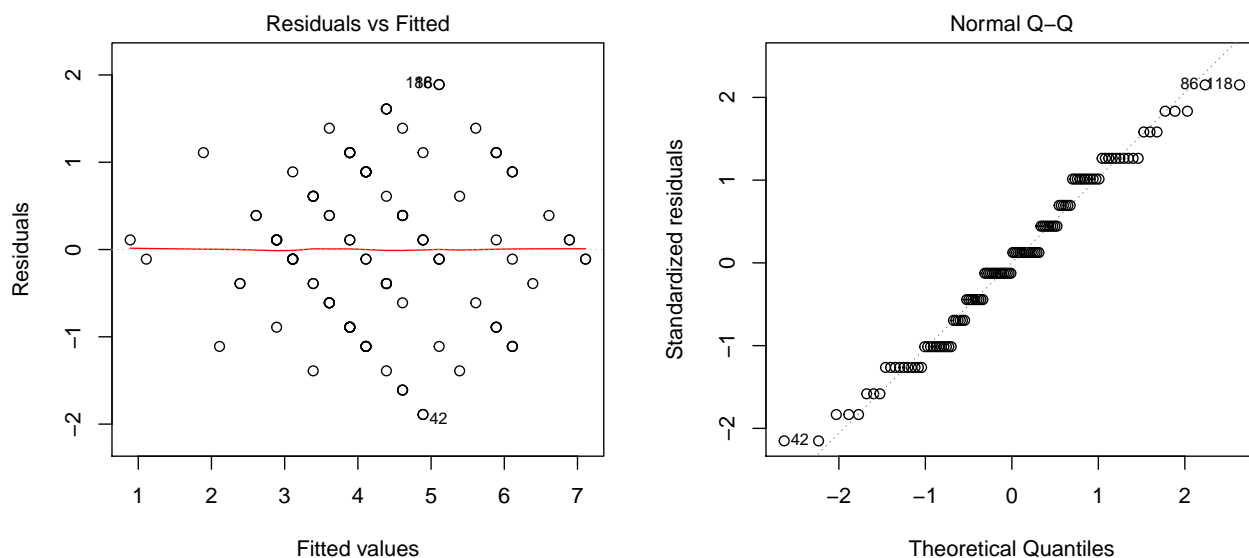
The means of your treatments are:

Storage root texture 1 estimating	
germplasmName	1-9
Chingova	6
Jonathan	2
MUSG11001-11	3.5
MUSG11001-2	4
MUSG11002-9	3
MUSG11003-10	3
MUSG11003-2	4.5
MUSG11004-5	4.5
MUSG11004-9	3.5
MUSG11006-15	2.5
MUSG11006-8	3
MUSG11007-1	4.5
MUSG11007-15	2.5

germplasmName	Storage root texture 1 estimating 1-9
MUSG11008-12	6
MUSG11010-11	4
MUSG11010-19	4
MUSG11010-7	3.5
MUSG11011-3	6
MUSG11012-14	4.5
MUSG11016-10	7
MUSG11016-12	5.5
MUSG11016-14	5
MUSG11016-16	7
MUSG11016-18	5
MUSG11016-19	4
MUSG11016-2	4
MUSG11016-21	4.5
MUSG11016-22	4.5
MUSG11019-15	3.5
MUSG11019-17	3.5
MUSG11019-5	6
MUSG11021-16	4
MUSG11022-1	5
MUSG11022-10	3.5
MUSG11022-11	4
MUSG11023-11	6
MUSG11026-11	6.5
MUSG11030-9	4
MUSG11033-6	4
MUSG11036-3	3
MUSG11040-13	4
MUSG11040-15	3.5
MUSG11040-16	6
MUSG11042-7	5
MUSG11044-15	4.5
MUSG11044-16	5
MUSG11046-14	3
MUSG11046-18	4.5
MUSG11046-3	4.5
MUSG11046-7	3
MUSG11048-15	4
MUSG11048-16	5
MUSG11049-16	5.5
MUSG11049-2	6
MUSG11049-3	4
MUSG11049-5	3
MUSG11049-7	4
MUSG11050-3	4
Resisto	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:

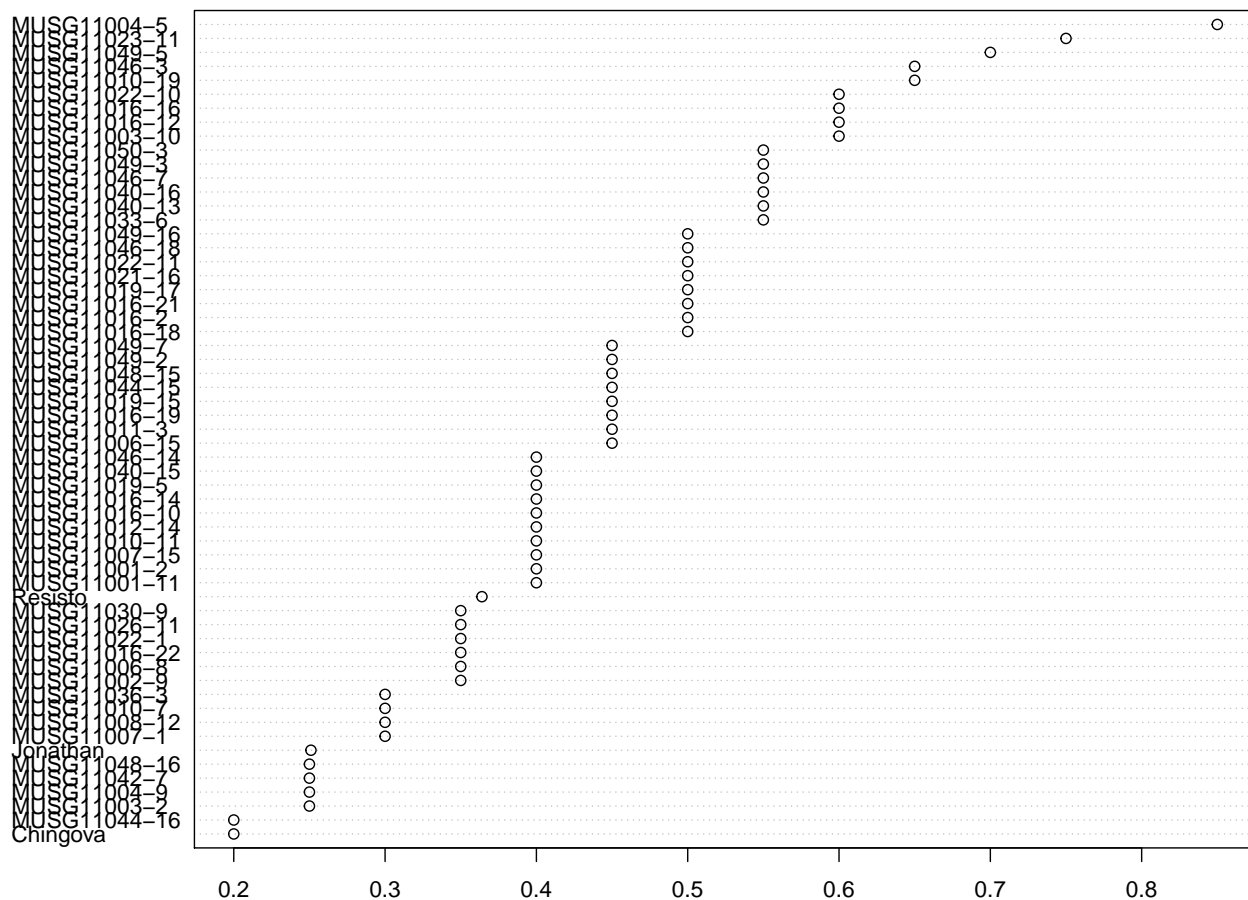
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	2.1349	0.0368087	2.1532	0.00202937
REP	1	0.175407	0.175407	10.2608	0.00220834
Residuals	58	0.991504	0.0170949	NA	NA

The p-value for treatments is 0.00202937 which is significant at the 5% level.

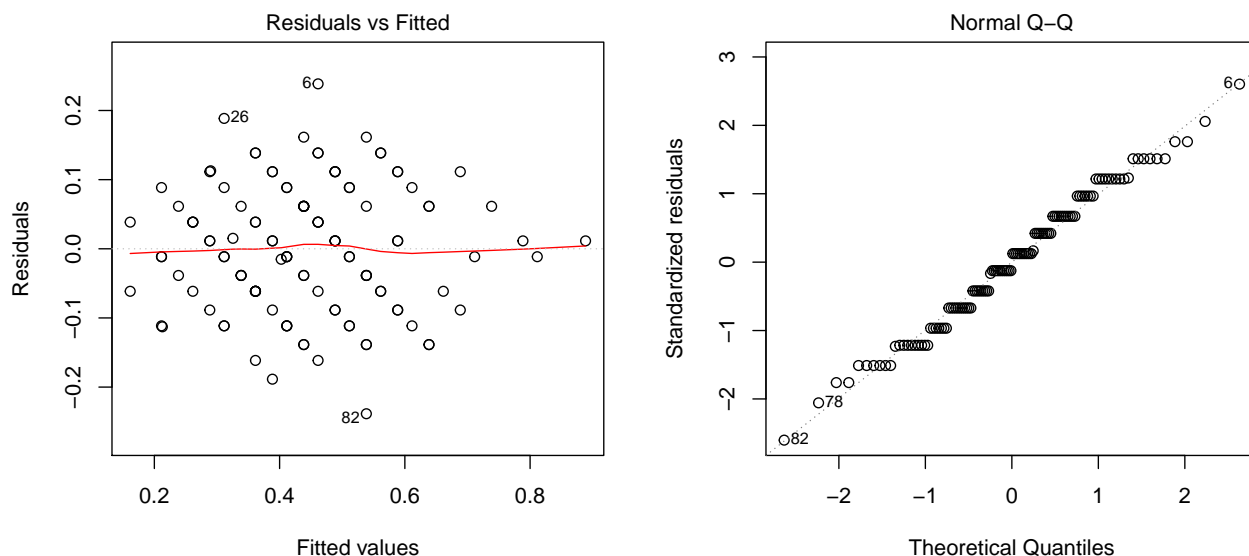
The means of your treatments are:

germplasmName	Survival index computing percent
Chingova	0.2
Jonathan	0.251
MUSG11001-11	0.4
MUSG11001-2	0.4
MUSG11002-9	0.35
MUSG11003-10	0.6
MUSG11003-2	0.25
MUSG11004-5	0.85
MUSG11004-9	0.25
MUSG11006-15	0.45
MUSG11006-8	0.35
MUSG11007-1	0.3
MUSG11007-15	0.4
MUSG11008-12	0.3
MUSG11010-11	0.4
MUSG11010-19	0.65
MUSG11010-7	0.3
MUSG11011-3	0.45
MUSG11012-14	0.4
MUSG11016-10	0.4
MUSG11016-12	0.6
MUSG11016-14	0.4
MUSG11016-16	0.6
MUSG11016-18	0.5
MUSG11016-19	0.45
MUSG11016-2	0.5
MUSG11016-21	0.5
MUSG11016-22	0.35
MUSG11019-15	0.45
MUSG11019-17	0.5
MUSG11019-5	0.4
MUSG11021-16	0.5
MUSG11022-1	0.35
MUSG11022-10	0.6
MUSG11022-11	0.5
MUSG11023-11	0.75
MUSG11026-11	0.35
MUSG11030-9	0.35
MUSG11033-6	0.55

germplasmName	Survival index computing percent
MUSG11036-3	0.3
MUSG11040-13	0.55
MUSG11040-15	0.4
MUSG11040-16	0.55
MUSG11042-7	0.25
MUSG11044-15	0.45
MUSG11044-16	0.2
MUSG11046-14	0.4
MUSG11046-18	0.5
MUSG11046-3	0.65
MUSG11046-7	0.55
MUSG11048-15	0.45
MUSG11048-16	0.25
MUSG11049-16	0.5
MUSG11049-2	0.45
MUSG11049-3	0.55
MUSG11049-5	0.7
MUSG11049-7	0.45
MUSG11050-3	0.55
Resisto	0.364



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

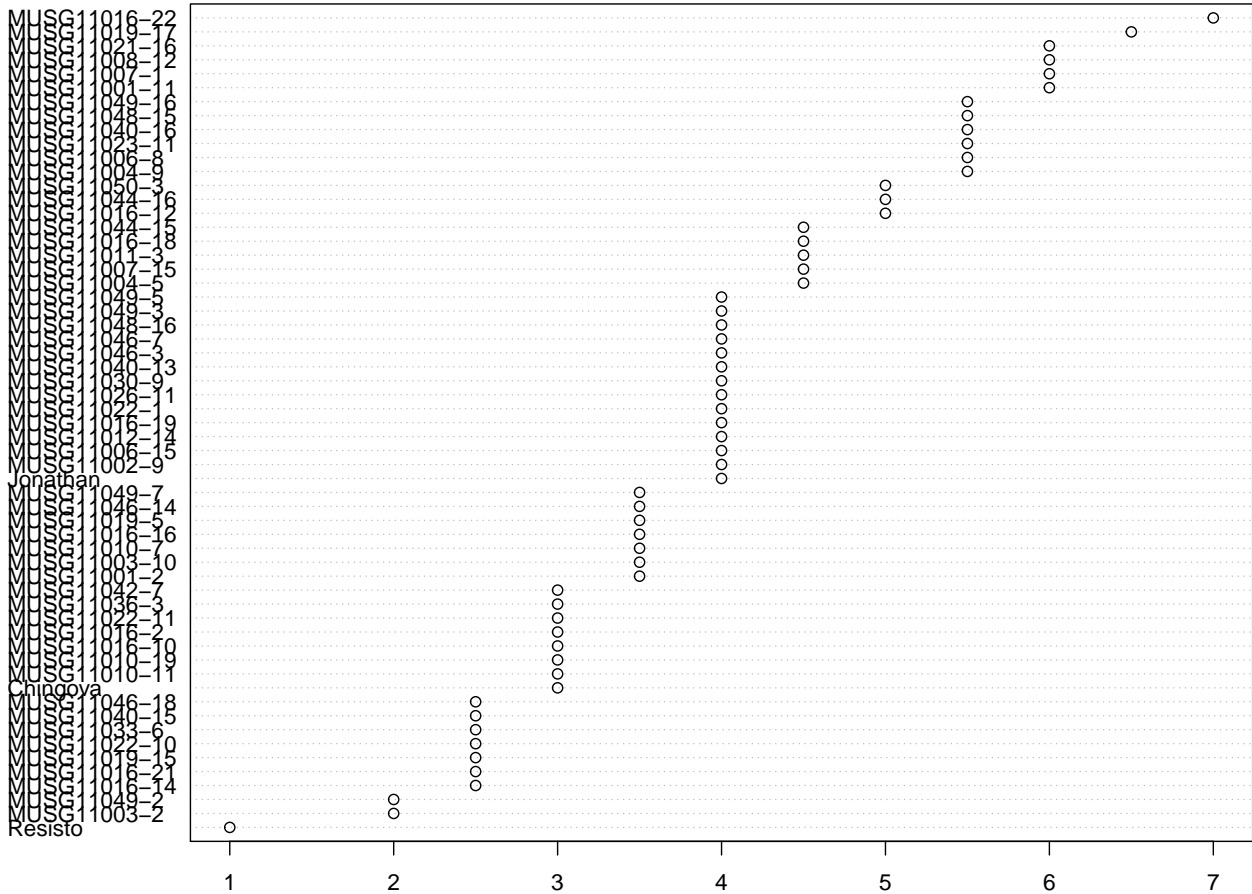
You have fitted a linear model for a RCBD. The ANOVA table for your model is:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	182.966	3.15459	1.37991	0.111553
REP	1	46.4068	46.4068	20.2996	3.25953e-05
Residuals	58	132.593	2.28609	NA	NA

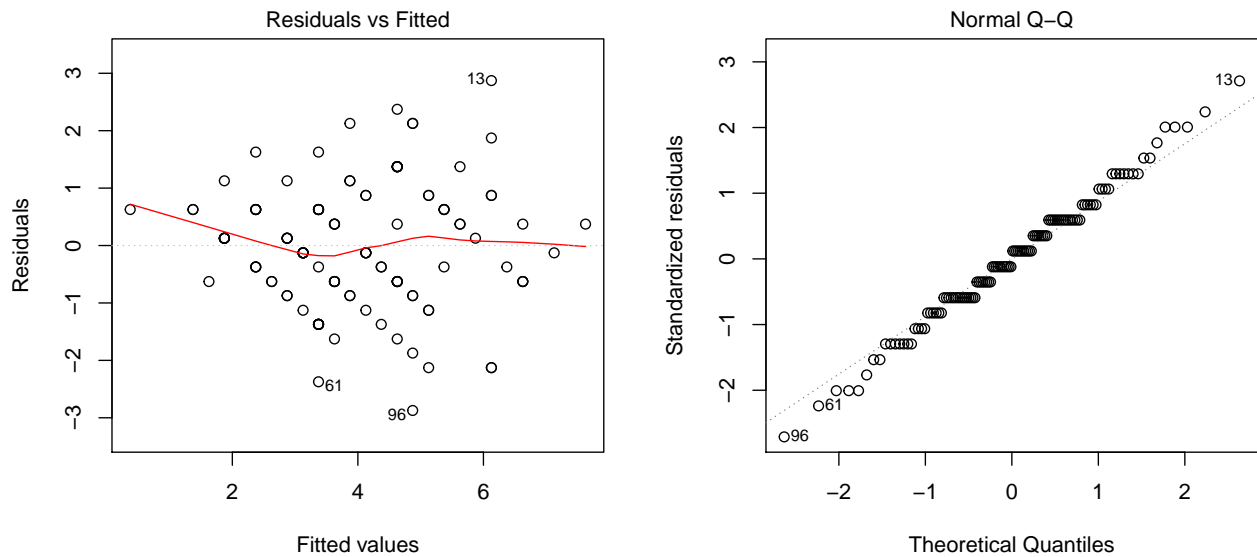
The means of your treatments are:

germplasmName	Sweet potato weevil symptoms 1 estimating 1-9
Chingova	3
Jonathan	4
MUSG11001-11	6
MUSG11001-2	3.5
MUSG11002-9	4
MUSG11003-10	3.5
MUSG11003-2	2
MUSG11004-5	4.5
MUSG11004-9	5.5
MUSG11006-15	4
MUSG11006-8	5.5
MUSG11007-1	6
MUSG11007-15	4.5
MUSG11008-12	6
MUSG11010-11	3
MUSG11010-19	3
MUSG11010-7	3.5
MUSG11011-3	4.5

germplasmName	Sweet potato weevil symptoms 1 estimating 1-9
MUSG11012-14	4
MUSG11016-10	3
MUSG11016-12	5
MUSG11016-14	2.5
MUSG11016-16	3.5
MUSG11016-18	4.5
MUSG11016-19	4
MUSG11016-2	3
MUSG11016-21	2.5
MUSG11016-22	7
MUSG11019-15	2.5
MUSG11019-17	6.5
MUSG11019-5	3.5
MUSG11021-16	6
MUSG11022-1	4
MUSG11022-10	2.5
MUSG11022-11	3
MUSG11023-11	5.5
MUSG11026-11	4
MUSG11030-9	4
MUSG11033-6	2.5
MUSG11036-3	3
MUSG11040-13	4
MUSG11040-15	2.5
MUSG11040-16	5.5
MUSG11042-7	3
MUSG11044-15	4.5
MUSG11044-16	5
MUSG11046-14	3.5
MUSG11046-18	2.5
MUSG11046-3	4
MUSG11046-7	4
MUSG11048-15	5.5
MUSG11048-16	4
MUSG11049-16	5.5
MUSG11049-2	2
MUSG11049-3	4
MUSG11049-5	4
MUSG11049-7	3.5
MUSG11050-3	5
Resisto	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 Total carotenoids measuring mg per 100g

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

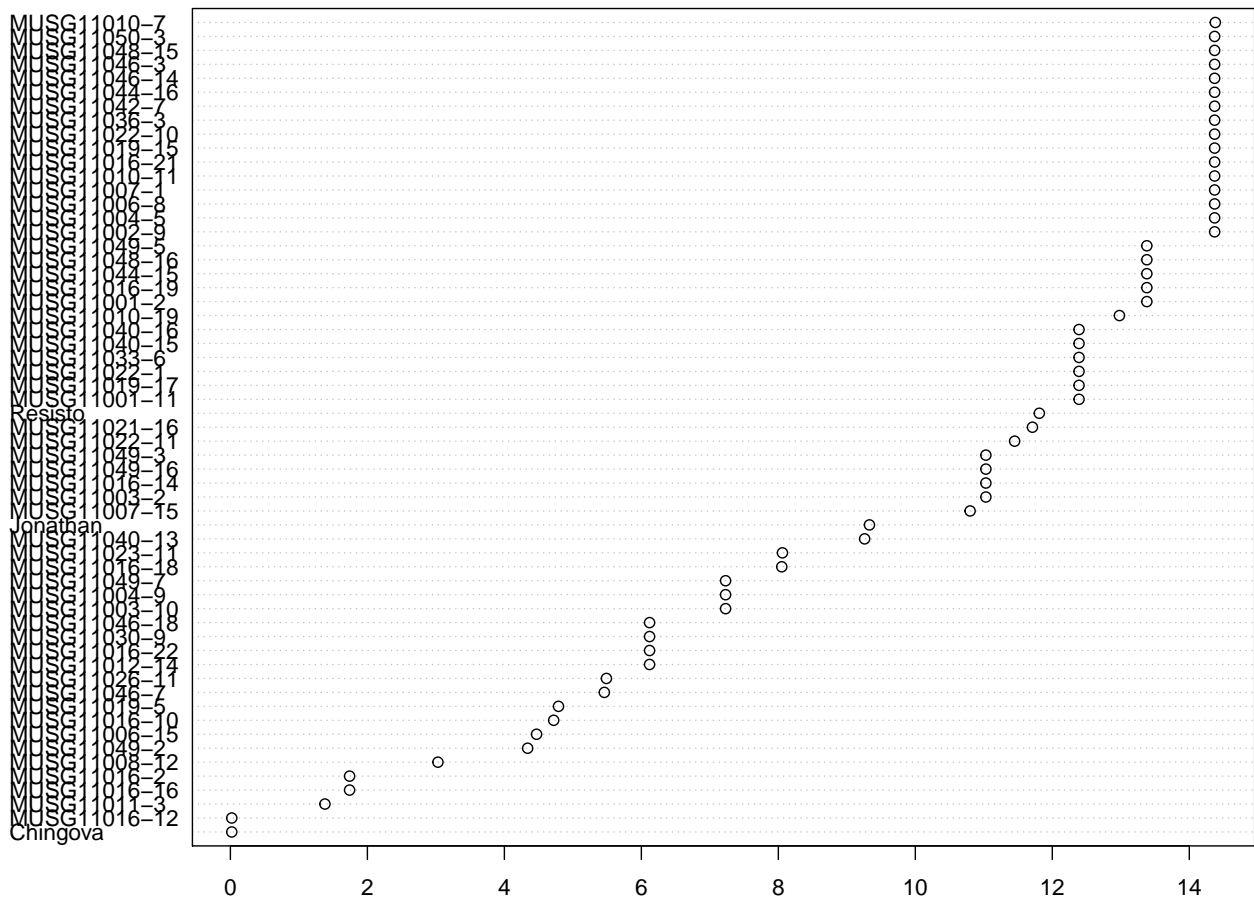
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	2255.84	38.8938	7.08119	2.06387e-12
REP	1	9.13646	9.13646	1.66343	0.20226
Residuals	58	318.568	5.49255	NA	NA

The p-value for treatments is 0.00000000000206387 which is significant at the 5% level.

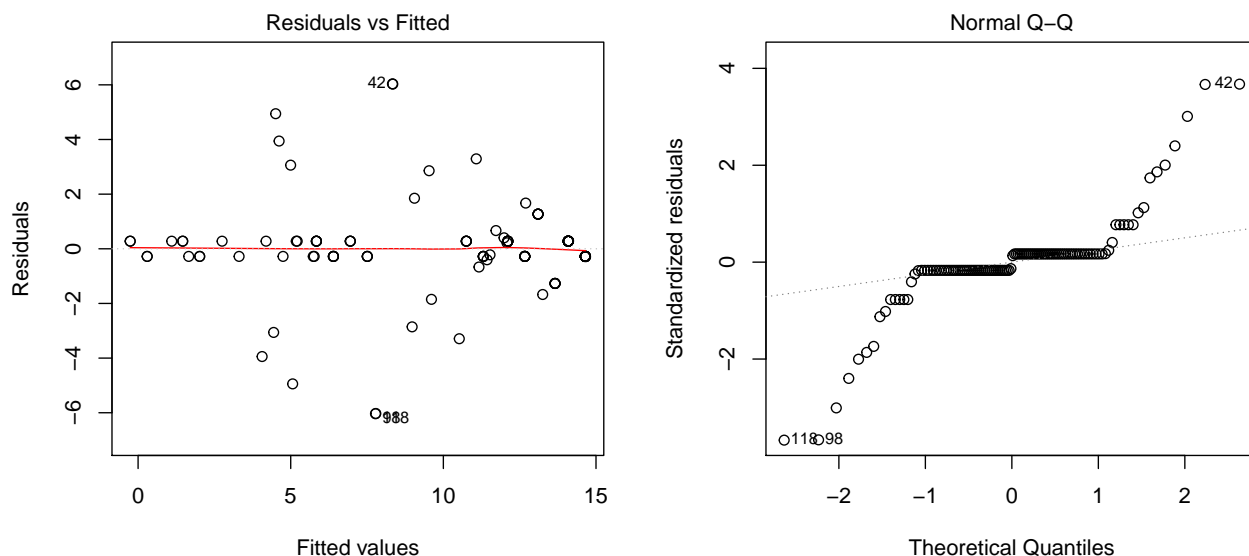
The means of your treatments are:

germplasmName	Total carotenoids measuring mg per 100g
Chingova	0.02
Jonathan	9.33
MUSG11001-11	12.4
MUSG11001-2	13.4
MUSG11002-9	14.4
MUSG11003-10	7.23
MUSG11003-2	11
MUSG11004-5	14.4
MUSG11004-9	7.23
MUSG11006-15	4.47
MUSG11006-8	14.4
MUSG11007-1	14.4
MUSG11007-15	10.8
MUSG11008-12	3.03
MUSG11010-11	14.4
MUSG11010-19	13
MUSG11010-7	14.4
MUSG11011-3	1.38
MUSG11012-14	6.12
MUSG11016-10	4.72
MUSG11016-12	0.02
MUSG11016-14	11
MUSG11016-16	1.74
MUSG11016-18	8.05
MUSG11016-19	13.4
MUSG11016-2	1.74
MUSG11016-21	14.4
MUSG11016-22	6.12
MUSG11019-15	14.4
MUSG11019-17	12.4
MUSG11019-5	4.79
MUSG11021-16	11.7
MUSG11022-1	12.4
MUSG11022-10	14.4
MUSG11022-11	11.4
MUSG11023-11	8.06
MUSG11026-11	5.49
MUSG11030-9	6.12
MUSG11033-6	12.4

germplasmName	Total carotenoids measuring mg per 100g
MUSG11036-3	14.4
MUSG11040-13	9.26
MUSG11040-15	12.4
MUSG11040-16	12.4
MUSG11042-7	14.4
MUSG11044-15	13.4
MUSG11044-16	14.4
MUSG11046-14	14.4
MUSG11046-18	6.12
MUSG11046-3	14.4
MUSG11046-7	5.46
MUSG11048-15	14.4
MUSG11048-16	13.4
MUSG11049-16	11
MUSG11049-2	4.34
MUSG11049-3	11
MUSG11049-5	13.4
MUSG11049-7	7.23
MUSG11050-3	14.4
Resisto	11.8



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:

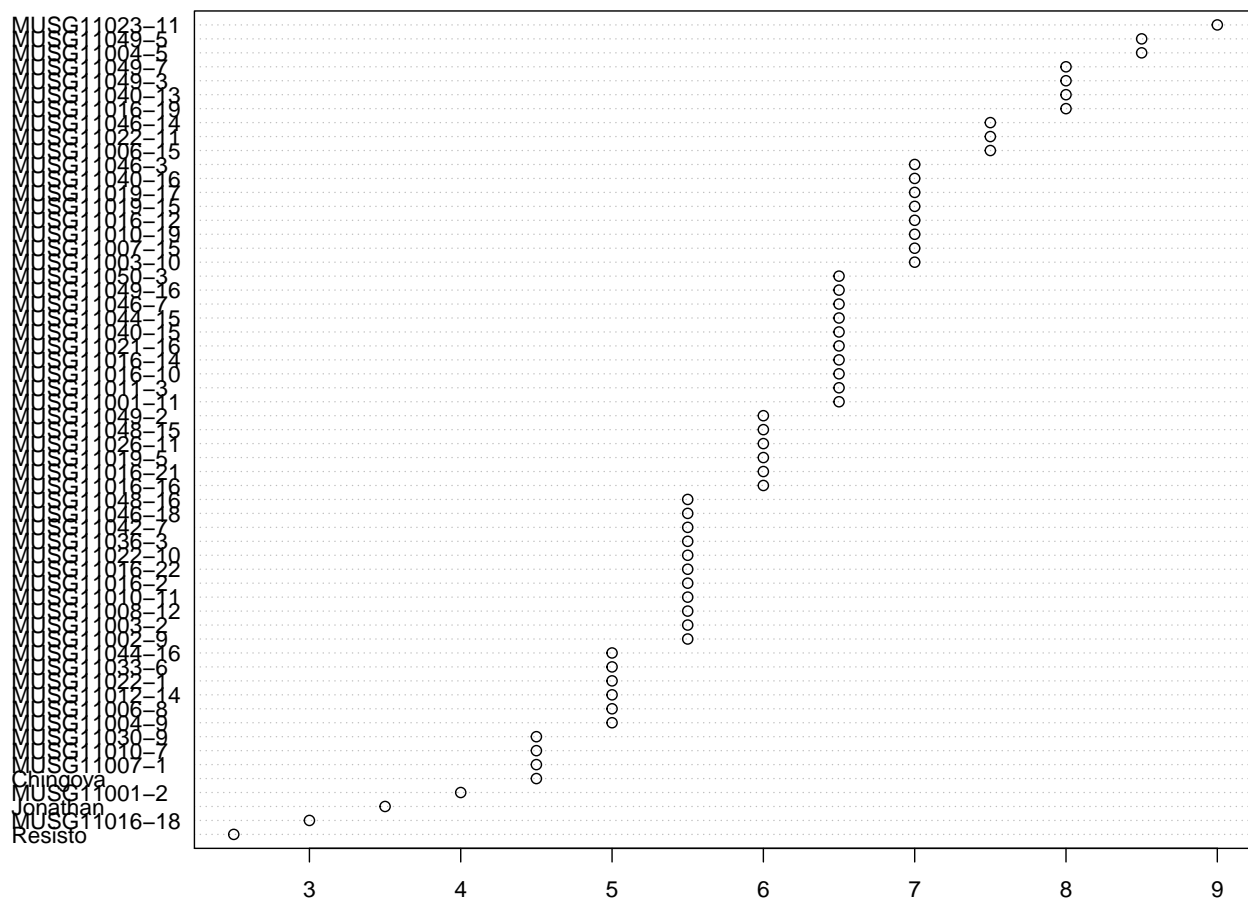
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	207.153	3.5716	3.37998	3.62432e-06
REP	1	34.7119	34.7119	32.8496	3.76116e-07
Residuals	58	61.2881	1.05669	NA	NA

The p-value for treatments is 0.00000362432 which is significant at the 5% level.

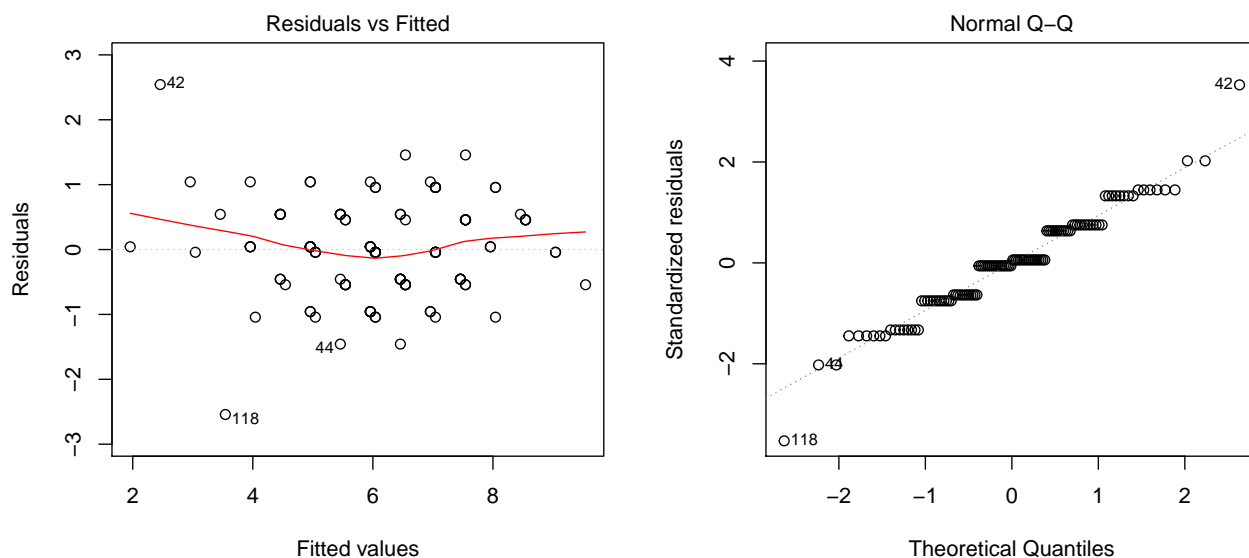
The means of your treatments are:

germplasmName	Vine vigor 1 estimating 1-9
Chingova	4.5
Jonathan	3.5
MUSG11001-11	6.5
MUSG11001-2	4
MUSG11002-9	5.5
MUSG11003-10	7
MUSG11003-2	5.5
MUSG11004-5	8.5
MUSG11004-9	5
MUSG11006-15	7.5
MUSG11006-8	5
MUSG11007-1	4.5
MUSG11007-15	7
MUSG11008-12	5.5
MUSG11010-11	5.5
MUSG11010-19	7
MUSG11010-7	4.5

germplasmName	Vine vigor 1 estimating 1-9
MUSG11011-3	6.5
MUSG11012-14	5
MUSG11016-10	6.5
MUSG11016-12	7
MUSG11016-14	6.5
MUSG11016-16	6
MUSG11016-18	3
MUSG11016-19	8
MUSG11016-2	5.5
MUSG11016-21	6
MUSG11016-22	5.5
MUSG11019-15	7
MUSG11019-17	7
MUSG11019-5	6
MUSG11021-16	6.5
MUSG11022-1	5
MUSG11022-10	5.5
MUSG11022-11	7.5
MUSG11023-11	9
MUSG11026-11	6
MUSG11030-9	4.5
MUSG11033-6	5
MUSG11036-3	5.5
MUSG11040-13	8
MUSG11040-15	6.5
MUSG11040-16	7
MUSG11042-7	5.5
MUSG11044-15	6.5
MUSG11044-16	5
MUSG11046-14	7.5
MUSG11046-18	5.5
MUSG11046-3	7
MUSG11046-7	6.5
MUSG11048-15	6
MUSG11048-16	5.5
MUSG11049-16	6.5
MUSG11049-2	6
MUSG11049-3	8
MUSG11049-5	8.5
MUSG11049-7	8
MUSG11050-3	6.5
Resisto	2.5



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 Virus symptoms 1 estimating 1-9

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

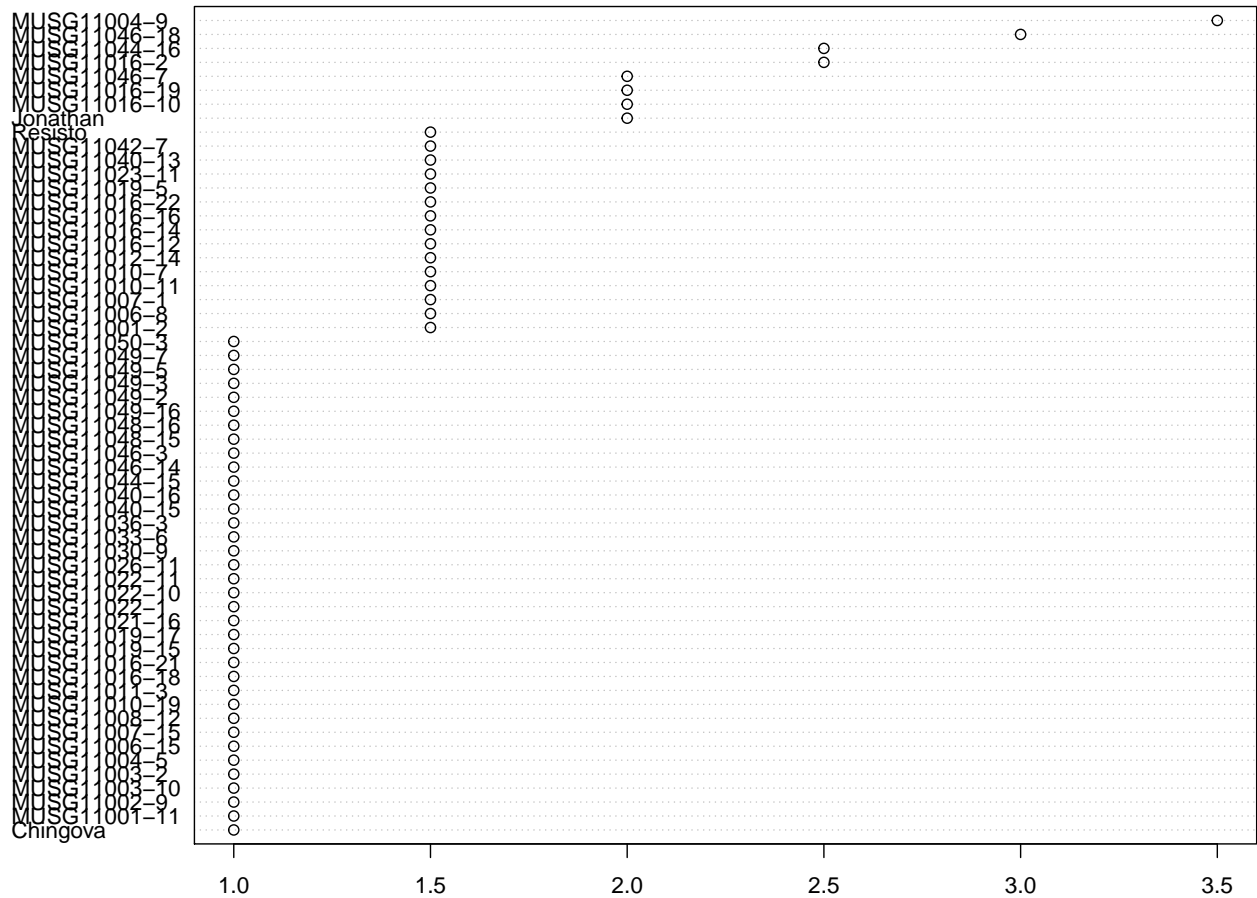
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	32.7627	0.564874	1.58313	0.0414329
REP	1	0.305085	0.305085	0.855037	0.358963
Residuals	58	20.6949	0.356809	NA	NA

The p-value for treatments is 0.0414329 which is significant at the 5% level.

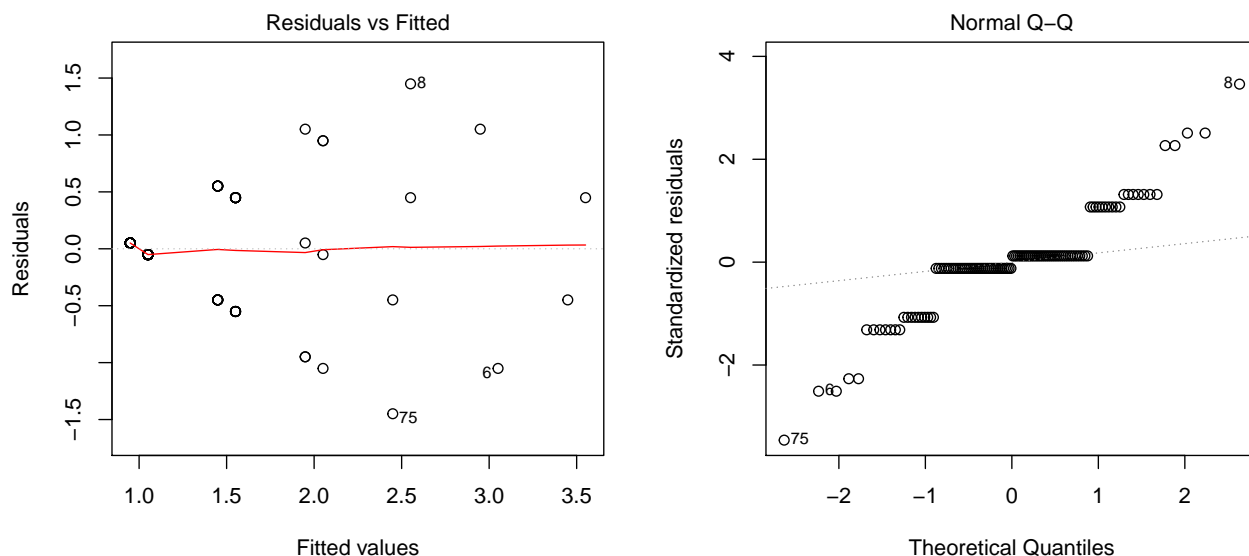
The means of your treatments are:

germplasmName	Virus symptoms 1 estimating 1-9
Chingova	1
Jonathan	2
MUSG11001-11	1
MUSG11001-2	1.5
MUSG11002-9	1
MUSG11003-10	1
MUSG11003-2	1
MUSG11004-5	1
MUSG11004-9	3.5
MUSG11006-15	1
MUSG11006-8	1.5
MUSG11007-1	1.5
MUSG11007-15	1
MUSG11008-12	1
MUSG11010-11	1.5
MUSG11010-19	1
MUSG11010-7	1.5
MUSG11011-3	1
MUSG11012-14	1.5
MUSG11016-10	2
MUSG11016-12	1.5
MUSG11016-14	1.5
MUSG11016-16	1.5
MUSG11016-18	1
MUSG11016-19	2
MUSG11016-2	2.5
MUSG11016-21	1
MUSG11016-22	1.5
MUSG11019-15	1
MUSG11019-17	1
MUSG11019-5	1.5
MUSG11021-16	1
MUSG11022-1	1
MUSG11022-10	1
MUSG11022-11	1
MUSG11023-11	1.5
MUSG11026-11	1
MUSG11030-9	1
MUSG11033-6	1

germplasmName	Virus symptoms 1 estimating 1-9
MUSG11036-3	1
MUSG11040-13	1.5
MUSG11040-15	1
MUSG11040-16	1
MUSG11042-7	1.5
MUSG11044-15	1
MUSG11044-16	2.5
MUSG11046-14	1
MUSG11046-18	3
MUSG11046-3	1
MUSG11046-7	2
MUSG11048-15	1
MUSG11048-16	1
MUSG11049-16	1
MUSG11049-2	1
MUSG11049-3	1
MUSG11049-5	1
MUSG11049-7	1
MUSG11050-3	1
Resisto	1.5



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 Virus symptoms 2 estimating 1-9

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

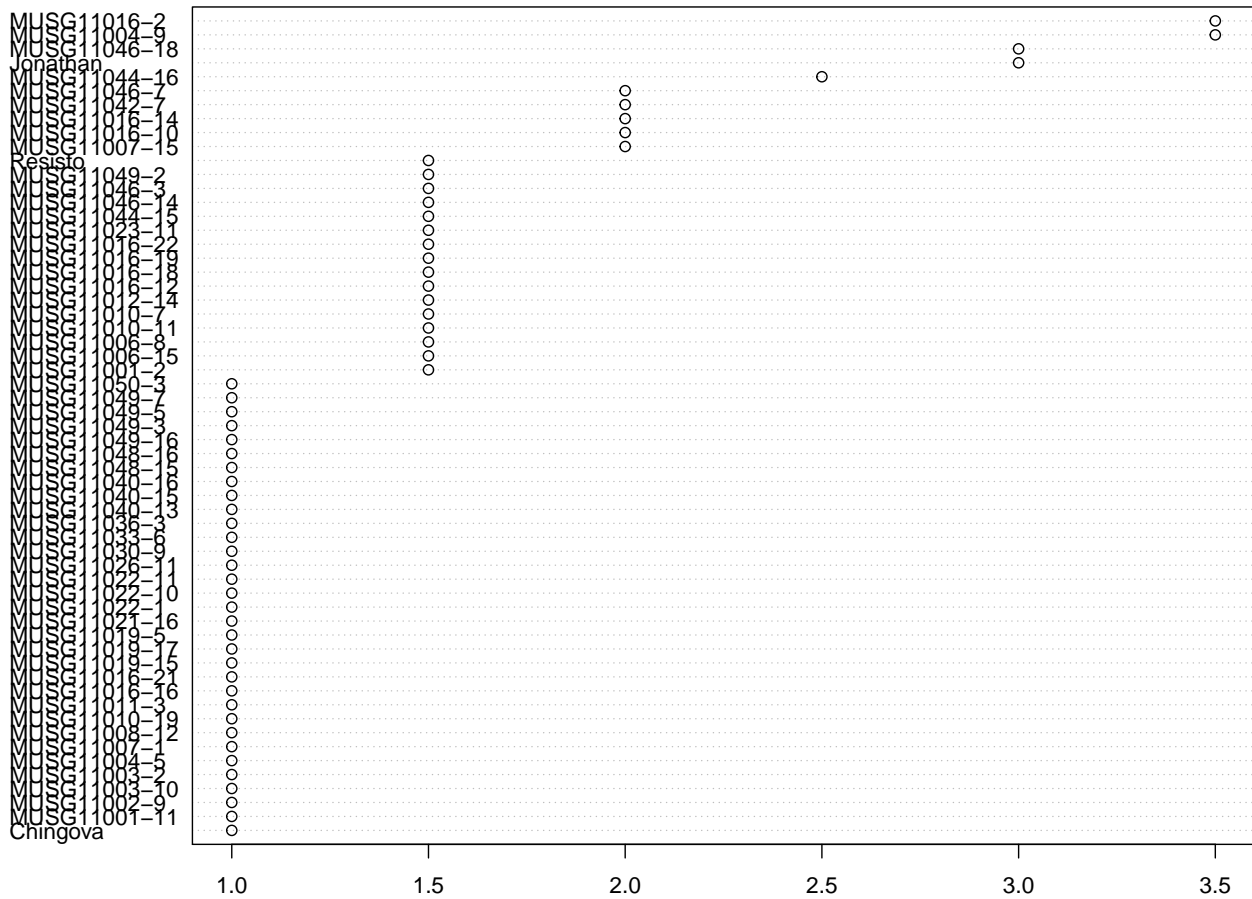
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	44.7797	0.772063	2.66331	0.000134289
REP	1	0.686441	0.686441	2.36794	0.129288
Residuals	58	16.8136	0.289889	NA	NA

The p-value for treatments is 0.000134289 which is significant at the 5% level.

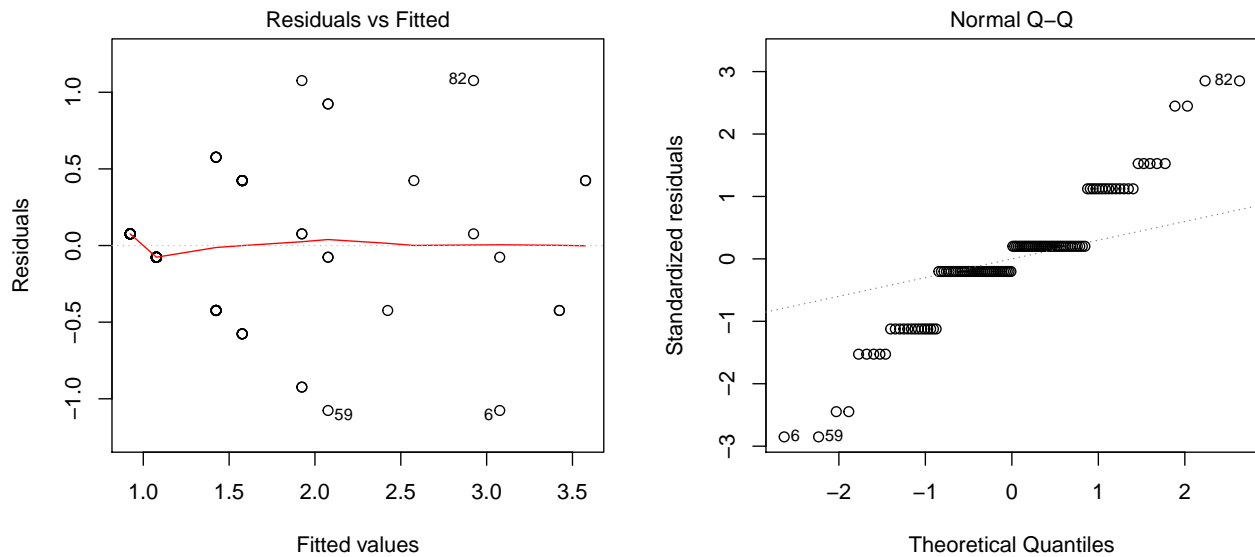
The means of your treatments are:

germplasmName	Virus symptoms 2 estimating 1-9
Chingova	1
Jonathan	3
MUSG11001-11	1
MUSG11001-2	1.5
MUSG11002-9	1
MUSG11003-10	1
MUSG11003-2	1
MUSG11004-5	1
MUSG11004-9	3.5
MUSG11006-15	1.5
MUSG11006-8	1.5
MUSG11007-1	1
MUSG11007-15	2
MUSG11008-12	1
MUSG11010-11	1.5
MUSG11010-19	1
MUSG11010-7	1.5

germplasmName	Virus symptoms 2 estimating 1-9
MUSG11011-3	1
MUSG11012-14	1.5
MUSG11016-10	2
MUSG11016-12	1.5
MUSG11016-14	2
MUSG11016-16	1
MUSG11016-18	1.5
MUSG11016-19	1.5
MUSG11016-2	3.5
MUSG11016-21	1
MUSG11016-22	1.5
MUSG11019-15	1
MUSG11019-17	1
MUSG11019-5	1
MUSG11021-16	1
MUSG11022-1	1
MUSG11022-10	1
MUSG11022-11	1
MUSG11023-11	1.5
MUSG11026-11	1
MUSG11030-9	1
MUSG11033-6	1
MUSG11036-3	1
MUSG11040-13	1
MUSG11040-15	1
MUSG11040-16	1
MUSG11042-7	2
MUSG11044-15	1.5
MUSG11044-16	2.5
MUSG11046-14	1.5
MUSG11046-18	3
MUSG11046-3	1.5
MUSG11046-7	2
MUSG11048-15	1
MUSG11048-16	1
MUSG11049-16	1
MUSG11049-2	1.5
MUSG11049-3	1
MUSG11049-5	1
MUSG11049-7	1
MUSG11050-3	1
Resisto	1.5



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 commercial storage roots measuring kg per plot

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

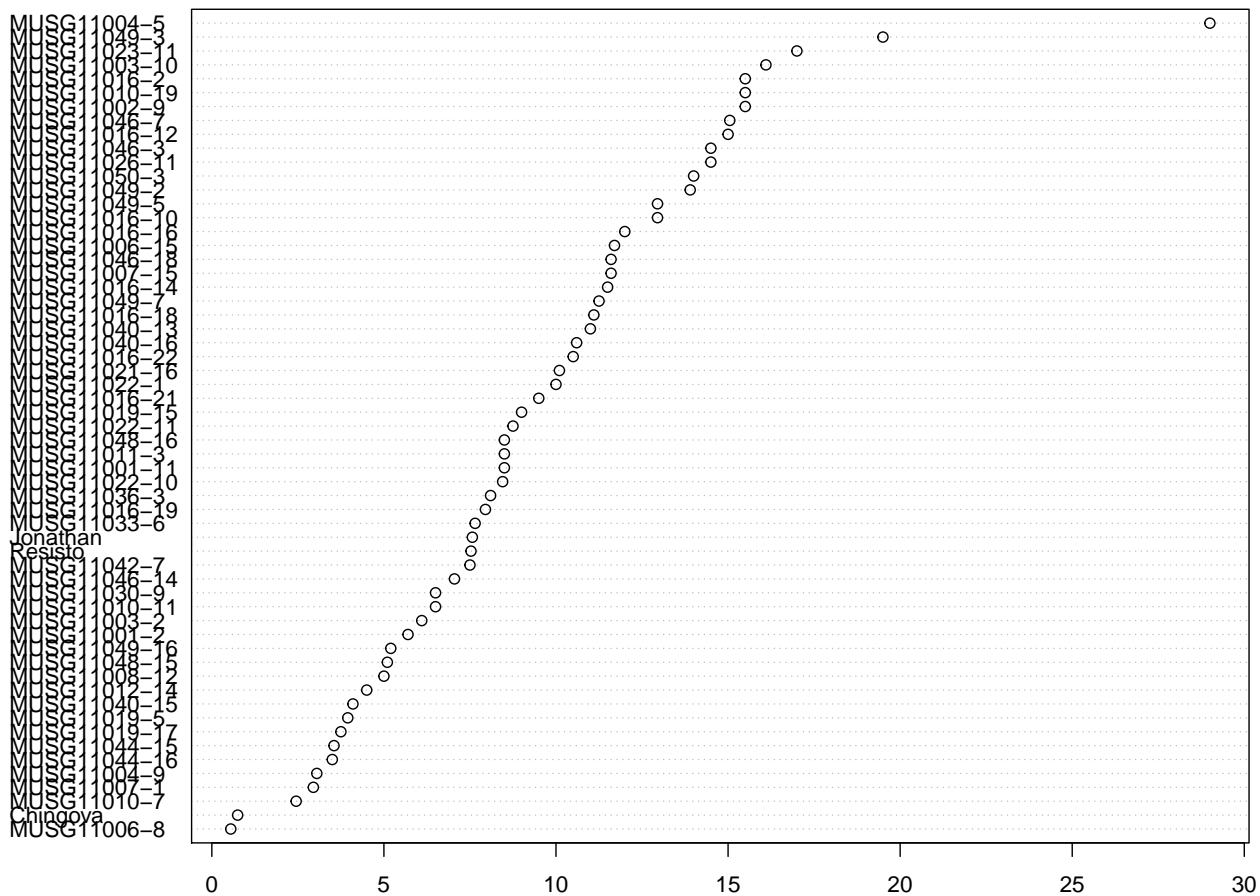
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	3019.61	52.0622	2.92165	3.53462e-05
REP	1	1122.27	1122.27	62.9799	7.84165e-11
Residuals	58	1033.53	17.8194	NA	NA

The p-value for treatments is 0.0000353462 which is significant at the 5% level.

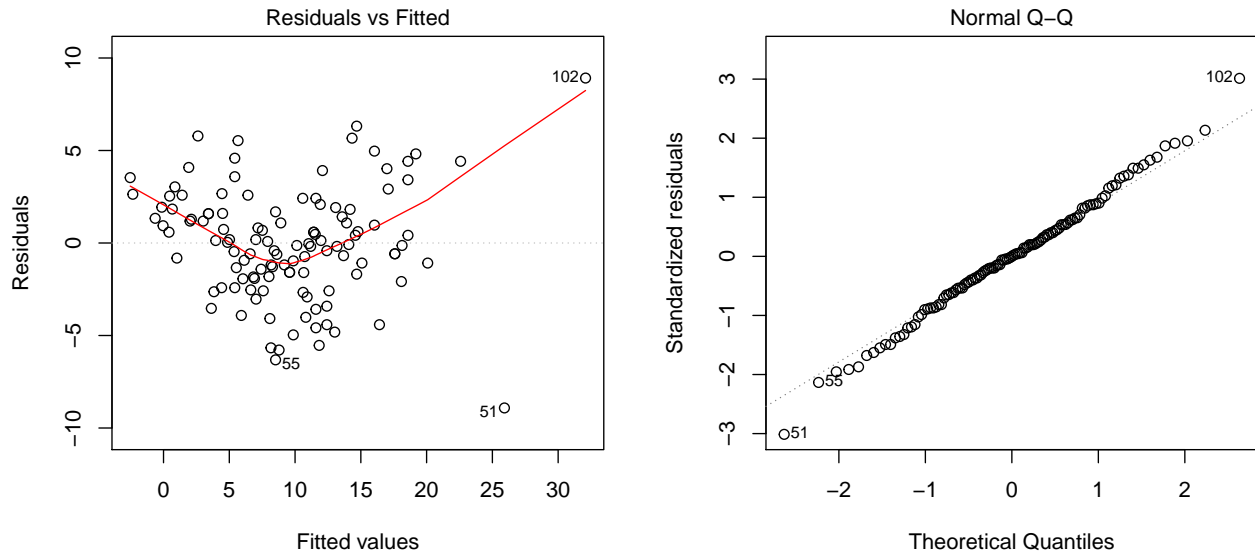
The means of your treatments are:

germplasmName	Weight of commercial storage roots measuring kg per plot
Chingova	0.75
Jonathan	7.57
MUSG11001-11	8.5
MUSG11001-2	5.7
MUSG11002-9	15.5
MUSG11003-10	16.1
MUSG11003-2	6.1
MUSG11004-5	29
MUSG11004-9	3.05
MUSG11006-15	11.7
MUSG11006-8	0.55
MUSG11007-1	2.95
MUSG11007-15	11.6
MUSG11008-12	5
MUSG11010-11	6.5
MUSG11010-19	15.5
MUSG11010-7	2.45
MUSG11011-3	8.5
MUSG11012-14	4.5
MUSG11016-10	12.9
MUSG11016-12	15
MUSG11016-14	11.5
MUSG11016-16	12
MUSG11016-18	11.1
MUSG11016-19	7.95
MUSG11016-2	15.5
MUSG11016-21	9.5
MUSG11016-22	10.5
MUSG11019-15	9
MUSG11019-17	3.75
MUSG11019-5	3.95
MUSG11021-16	10.1
MUSG11022-1	10
MUSG11022-10	8.45
MUSG11022-11	8.75
MUSG11023-11	17
MUSG11026-11	14.5
MUSG11030-9	6.5

germplasmName	Weight of commercial storage roots measuring kg per plot
MUSG11033-6	7.65
MUSG11036-3	8.1
MUSG11040-13	11
MUSG11040-15	4.1
MUSG11040-16	10.6
MUSG11042-7	7.5
MUSG11044-15	3.55
MUSG11044-16	3.5
MUSG11046-14	7.05
MUSG11046-18	11.6
MUSG11046-3	14.5
MUSG11046-7	15.1
MUSG11048-15	5.1
MUSG11048-16	8.5
MUSG11049-16	5.2
MUSG11049-2	13.9
MUSG11049-3	19.5
MUSG11049-5	12.9
MUSG11049-7	11.2
MUSG11050-3	14
Resisto	7.53



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 non-commercial storage roots measuring kg per plot

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

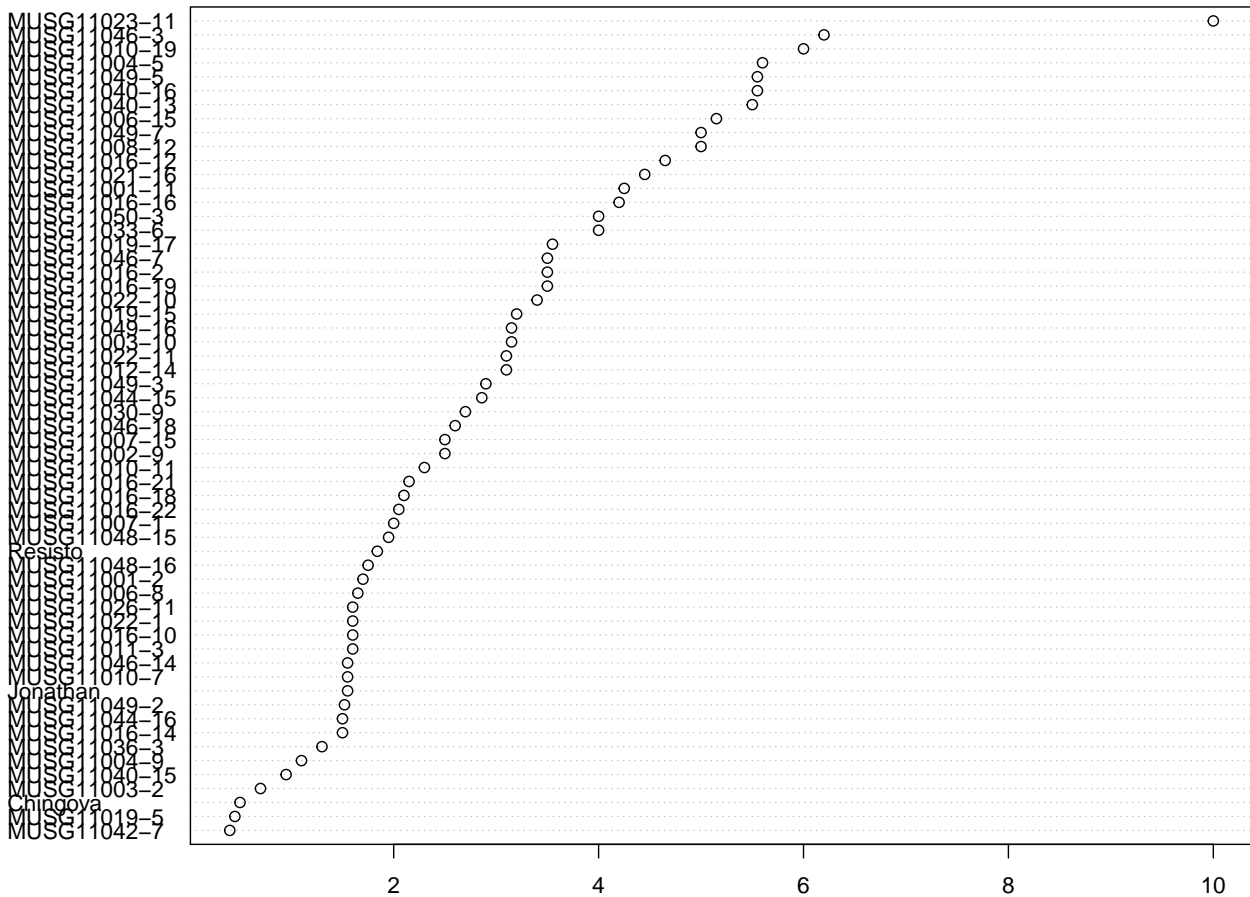
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	373.006	6.43114	2.60792	0.000179544
REP	1	35.5043	35.5043	14.3975	0.000355644
Residuals	58	143.028	2.466	NA	NA

The p-value for treatments is 0.000179544 which is significant at the 5% level.

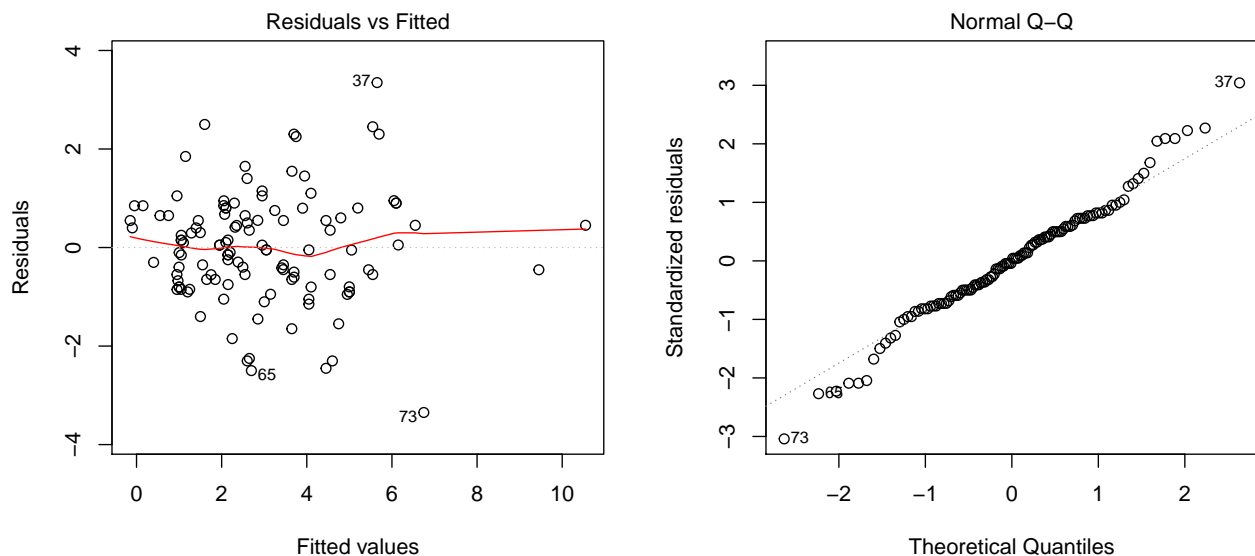
The means of your treatments are:

germplasmName	Weight of non-commercial storage roots measuring kg per plot
Chingova	0.5
Jonathan	1.55
MUSG11001-11	4.25
MUSG11001-2	1.7
MUSG11002-9	2.5
MUSG11003-10	3.15
MUSG11003-2	0.7
MUSG11004-5	5.6
MUSG11004-9	1.1
MUSG11006-15	5.15
MUSG11006-8	1.65
MUSG11007-1	2
MUSG11007-15	2.5

germplasmName	Weight of non-commercial storage roots measuring kg per plot
MUSG11008-12	5
MUSG11010-11	2.3
MUSG11010-19	6
MUSG11010-7	1.55
MUSG11011-3	1.6
MUSG11012-14	3.1
MUSG11016-10	1.6
MUSG11016-12	4.65
MUSG11016-14	1.5
MUSG11016-16	4.2
MUSG11016-18	2.1
MUSG11016-19	3.5
MUSG11016-2	3.5
MUSG11016-21	2.15
MUSG11016-22	2.05
MUSG11019-15	3.2
MUSG11019-17	3.55
MUSG11019-5	0.45
MUSG11021-16	4.45
MUSG11022-1	1.6
MUSG11022-10	3.4
MUSG11022-11	3.1
MUSG11023-11	10
MUSG11026-11	1.6
MUSG11030-9	2.7
MUSG11033-6	4
MUSG11036-3	1.3
MUSG11040-13	5.5
MUSG11040-15	0.95
MUSG11040-16	5.55
MUSG11042-7	0.4
MUSG11044-15	2.86
MUSG11044-16	1.5
MUSG11046-14	1.55
MUSG11046-18	2.6
MUSG11046-3	6.2
MUSG11046-7	3.5
MUSG11048-15	1.95
MUSG11048-16	1.75
MUSG11049-16	3.15
MUSG11049-2	1.52
MUSG11049-3	2.9
MUSG11049-5	5.55
MUSG11049-7	5
MUSG11050-3	4
Resisto	1.84



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:

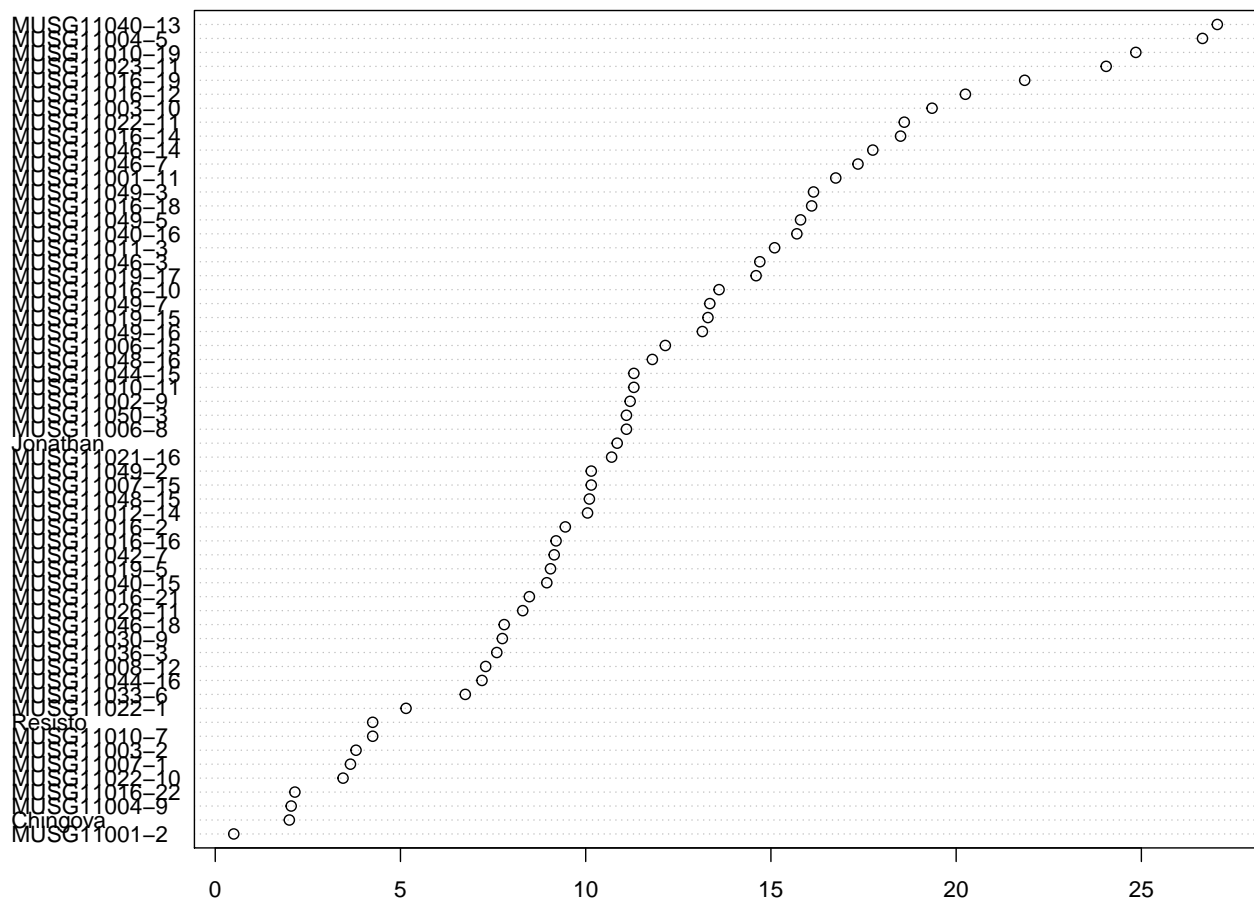
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	58	4502.17	77.6236	2.67463	0.000126567
REP	1	1734.12	1734.12	59.7517	1.73882e-10
Residuals	58	1683.28	29.0222	NA	NA

The p-value for treatments is 0.000126567 which is significant at the 5% level.

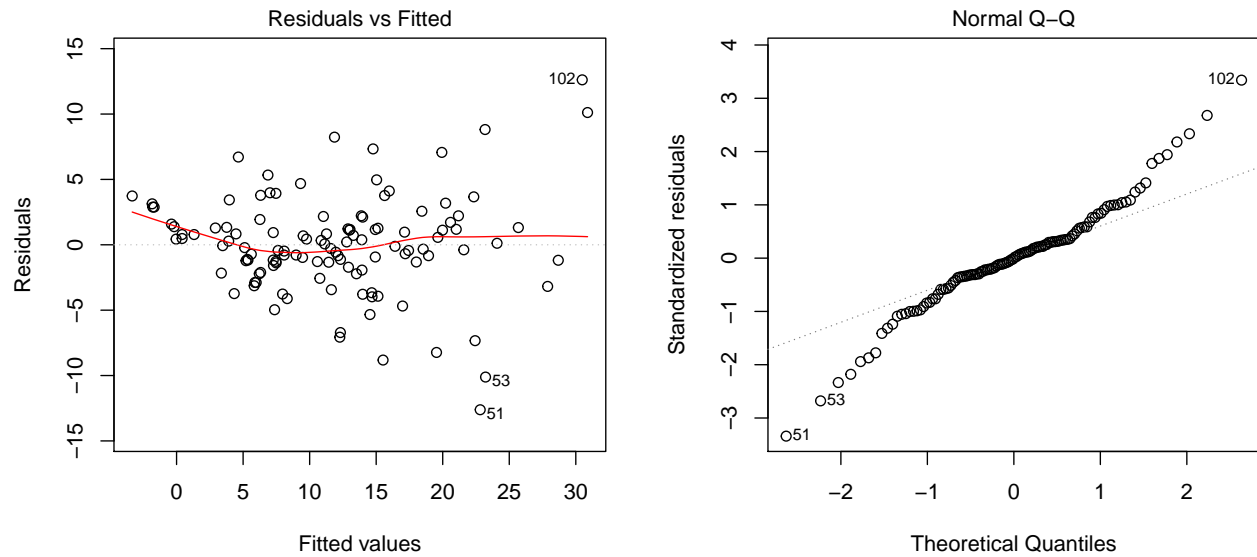
The means of your treatments are:

germplasmName	Weight of vines measuring kg per plot
Chingova	2
Jonathan	10.8
MUSG11001-11	16.8
MUSG11001-2	0.5
MUSG11002-9	11.2
MUSG11003-10	19.4
MUSG11003-2	3.8
MUSG11004-5	26.6
MUSG11004-9	2.05
MUSG11006-15	12.2
MUSG11006-8	11.1
MUSG11007-1	3.65
MUSG11007-15	10.2
MUSG11008-12	7.3
MUSG11010-11	11.3
MUSG11010-19	24.9
MUSG11010-7	4.25
MUSG11011-3	15.1
MUSG11012-14	10.1
MUSG11016-10	13.6
MUSG11016-12	20.2
MUSG11016-14	18.5
MUSG11016-16	9.2
MUSG11016-18	16.1
MUSG11016-19	21.9
MUSG11016-2	9.45
MUSG11016-21	8.48
MUSG11016-22	2.15
MUSG11019-15	13.3
MUSG11019-17	14.6
MUSG11019-5	9.05
MUSG11021-16	10.7
MUSG11022-1	5.15
MUSG11022-10	3.45
MUSG11022-11	18.6
MUSG11023-11	24.1
MUSG11026-11	8.3
MUSG11030-9	7.75
MUSG11033-6	6.75

germplasmName	Weight of vines measuring kg per plot
MUSG11036-3	7.6
MUSG11040-13	27.1
MUSG11040-15	8.95
MUSG11040-16	15.7
MUSG11042-7	9.15
MUSG11044-15	11.3
MUSG11044-16	7.2
MUSG11046-14	17.8
MUSG11046-18	7.8
MUSG11046-3	14.7
MUSG11046-7	17.4
MUSG11048-15	10.1
MUSG11048-16	11.8
MUSG11049-16	13.2
MUSG11049-2	10.2
MUSG11049-3	16.1
MUSG11049-5	15.8
MUSG11049-7	13.3
MUSG11050-3	11.1
Resisto	4.25



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.

Trait correlations

Variety candidate selection

Summary

References

Data sources

Literature