

Sparctm1a(EUCOMM)Wtsi

DEXA mixed model analysis

Variable	Unit of analysis
Weight	g
Nose to tail length	cm
Bone mineral density	g/cm ²
Bone mineral content	g
Lean mass	g
Fat mass	g
Fat percentage	%

Abbreviations:

LRT: Likelihood ratio test

ML: Maximum likelihood

REML: Residual maximum likelihood

BMC: Bone mineral content

BMD: Bone mineral density

LM: Lean mass

FM: Fat mass

Fat %: Fat percentage

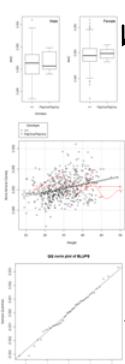
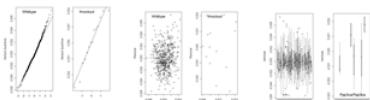
SE: Standard Error

Information on diagnostic graphs presented for each model

Bone Mineral Density: Final model values and diagnostics

Parameter estimates:

	Value	Std. Error	D.F.	t-value	p-value
(Intercept)	0.043279	0.000951	505	45.75092	0.0000
GenotypeP001/P002	-0.1948	0.000782	505	-0.7641	0.3717
GenotypeVal	0.000611	0.000254	505	2.40495	0.0185
Weight	0.000187	1.968e-05	505	6.3225	0.0000



A: A boxplot comparison of the dependent variable for each genotype for each sex.

B: Weight versus dependent variable scatterplot
For each genotype a regression and a Loess line is fitted. A Loess line is a locally weighted linear line. Graph only relevant for models that include weight as a fixed effect.

C: Normal Q-Q plot of the best linear unbiased prediction of random effects (BLUPS).

D: For each genotype group, conditional raw residues are plotted versus batch.

E: For each genotype group, a plot of conditional raw residue versus predicted values.

F: Normal Q-Q plots of conditional raw residues for each genotype.

Mixed Model results 1

Starting model:

$$Y_{ij} = \beta_0 + \beta_1 \text{Genotype1}_{ij} + \beta_2 \text{Sex1}_{ij} + \\ \beta_3 \text{Genotype1}_{ij} \text{Sex1}_{ij} + u_j + e_{ij}.$$

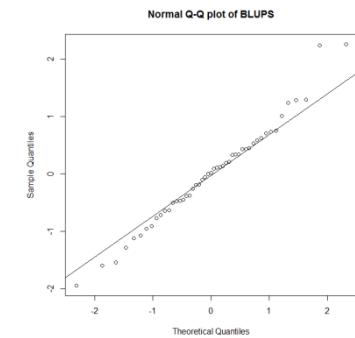
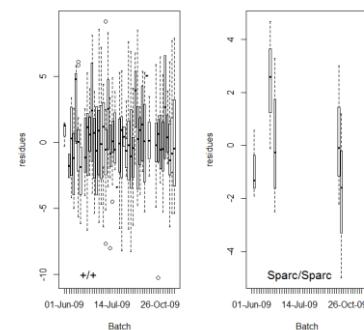
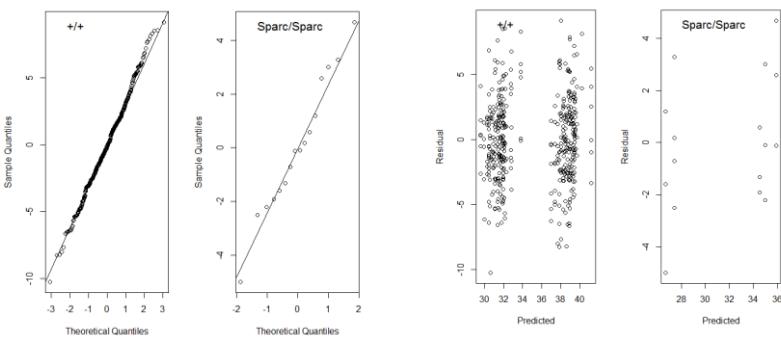
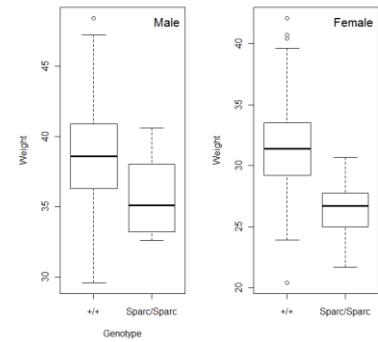
Weight: Top down modelling output

Hypothesis	Model1	Model 2	Test	Estimation method	Test statistic value	p-value
Is batch significant?	Batch	No batch	LRT	REML	$\chi^2(0:1)=11.17$	8e-4
Is variance homogenous?	Homogenous	Heterogeneous	LRT	REML	$\chi^2(2)=1.43$	0.2311
Testing fixed effects – sex			Type 1 F-test	REML	$F(1,417)=23.400$	0.0000
Testing fixed effects – sex*genotype			Type 1 F-test	REML	$F(1,47)=0.9351$	0.3545
Testing treatment - Is genotype significant?	With genotype	Without genotype	LRT	ML	$\chi^2(2)=16.97$	3.792e-05

Weight: Final model values and diagnostics

Parameter estimates:

	Value	Std.Error	DF	t-value	p-value
(Intercept)	31.554	0.296	417	106.534	0.0000
GenotypeSpArc/SpArc	-4.082	0.979	417	-4.168	0.0000
GenderMale	7.430	0.311	417	23.888	0.0000



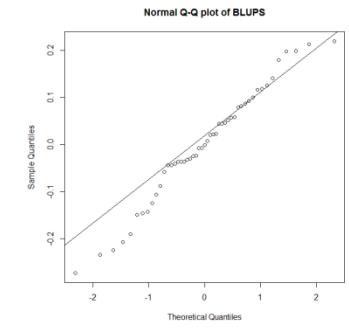
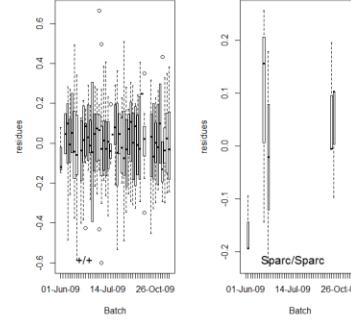
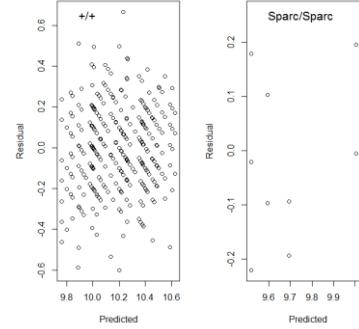
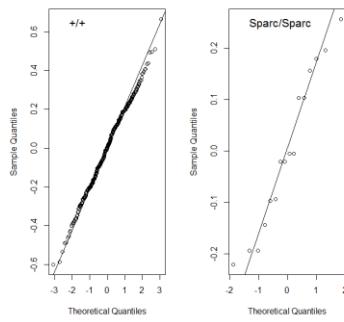
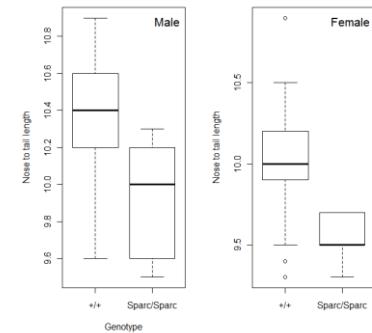
Nose to tail length: Top down modelling output

Hypothesis	Model1	Model 2	Test	Estimation method	Test statistic value	<i>p</i> -value
Is batch significant?	Batch	No batch	LRT	REML	$\chi^2(0:1)=91.568$	<.0001
Is variance homogenous?	Homogenous	Heterogeneous	LRT	REML	$\chi^2(2)=01.372$	0.2414
Testing fixed effects – sex			Type 1 <i>F</i> -test	REML	$F(1,417)=-4.9781$	0.0000
Testing fixed effects – sex*genotype			Type 1 <i>F</i> -test	REML	$F(1,47)=-0.0900$	0.9287
Testing treatment - Is genotype significant?	With genotype	Without genotype	LRT	ML	$\chi^2(2)=41.667$	1.081e-10

Nose to tail length: Final model values and diagnostics

Parameter estimates:

	Value	Std.Error	DF	t-value	p-value
(Intercept)	10.036	0.026	417	390.738	0.0000
GenotypeSparc/Sparsc	-0.491	0.073	417	-6.728	0.0000
GenderMale	0.373	0.020	417	18.965	0.0000



Bone mineral Density:

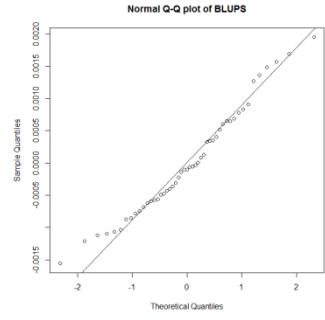
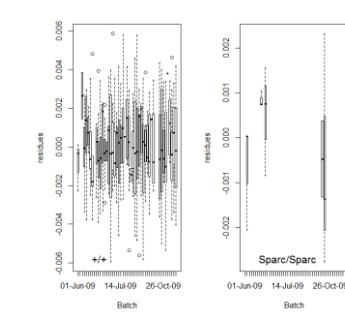
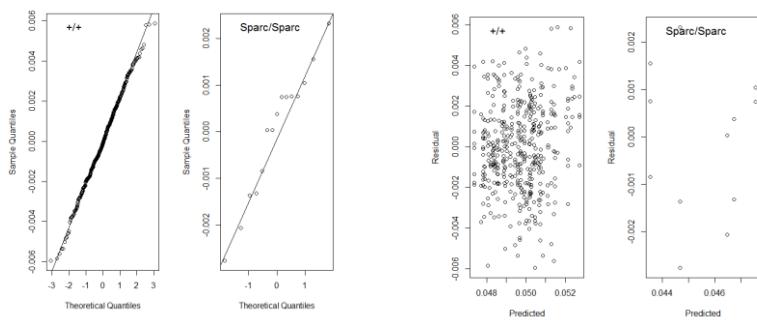
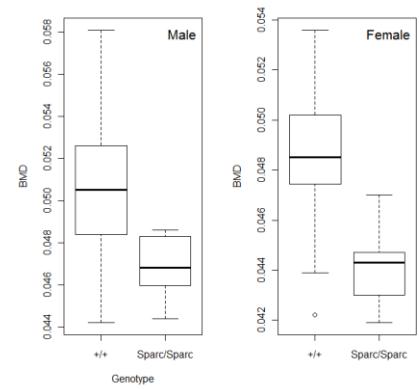
Top down modelling output

Hypothesis	Model1	Model 2	Test	Estimation method	Test statistic value	<i>p</i> -value
Is batch significant?	Batch	No batch	LRT	REML	$\chi^2(0:1)=33.815$	<0.0001
Is variance homogenous?	Homogenous	Heterogeneous	LRT	REML	$\chi^2(2)=0.7423$	0.3889
Testing fixed effects – sex			Type 1 F-test	REML	$F(1,412)=8.744$	0.0000
Testing fixed effect – genotype*sex			Type 1 F-test	REML	$F(1,47)=-0.129$	0.8978
Testing treatment - Is genotype significant?	With genotype	Without genotype	LRT	ML	$\chi^2(2)=26.479$	2.66e-7

Bone Mineral Density: Final model values and diagnostics

Parameter estimates:

	Value	Std.Error	DF	t-value	p-value
(Intercept)	0.049	0.000	412	217.665	0.0000
GenotypeSparc/Sparc	-0.004	0.001	412	-5.377	0.0000
GenderMale	0.002	0.000	412	8.831	0.0000



Bone Mineral Content:

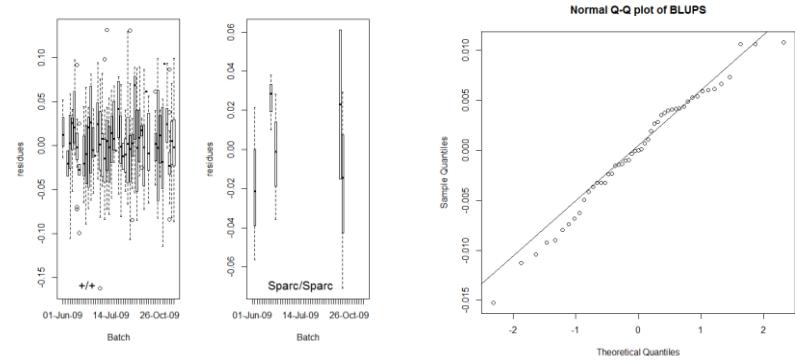
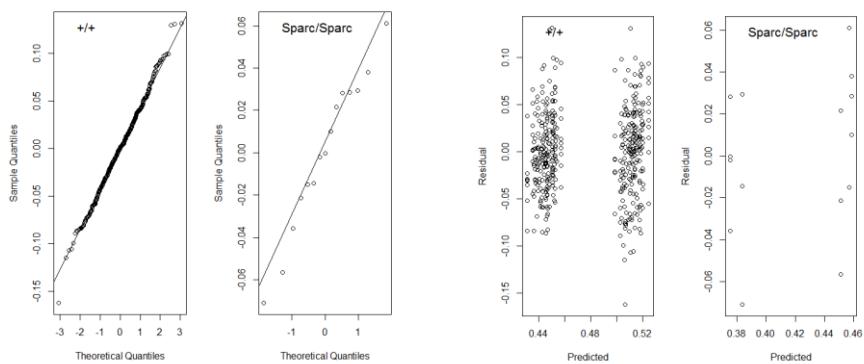
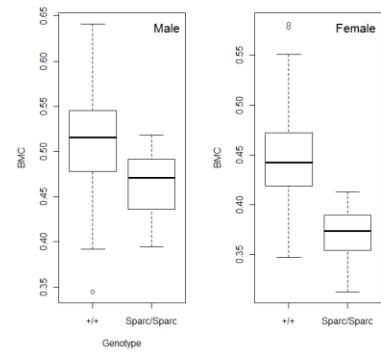
Top down modelling output

Hypothesis	Model1	Model 2	Test	Estimation method	Test statistic value	<i>p</i> -value
Is batch significant?	Batch	No batch	LRT	REML	$\chi^2(0:1)=3.49327$	0.0616
Is variance homogenous?	Homogenous	Heterogeneous	LRT	REML	$\chi^2(2)=0.742$	0.3889
Testing fixed effects – sex			Type 1 <i>F</i> -test	REML	$F(1,412)=15.82$	0.0000
Testing fixed effect – genotype*sex			Type 1 <i>F</i> -test	REML	$F(1,47)=0.8496$	0.3998
Testing treatment - Is genotype significant?	With genotype	Without genotype	LRT	ML	$\chi^2(2)=21.760$	3.089e-6

Bone Mineral Content: Final model values and diagnostics

Parameter estimates:

	Value	Std.Error	DF	t-value	p-value
(Intercept)	0.446	0.003	412	130.326	0.0000
GenotypeSpars/Sparc	-0.060	0.013	412	-4.759	0.0000
GenderMale	0.068	0.004	412	16.222	0.0000



Lean Mass:

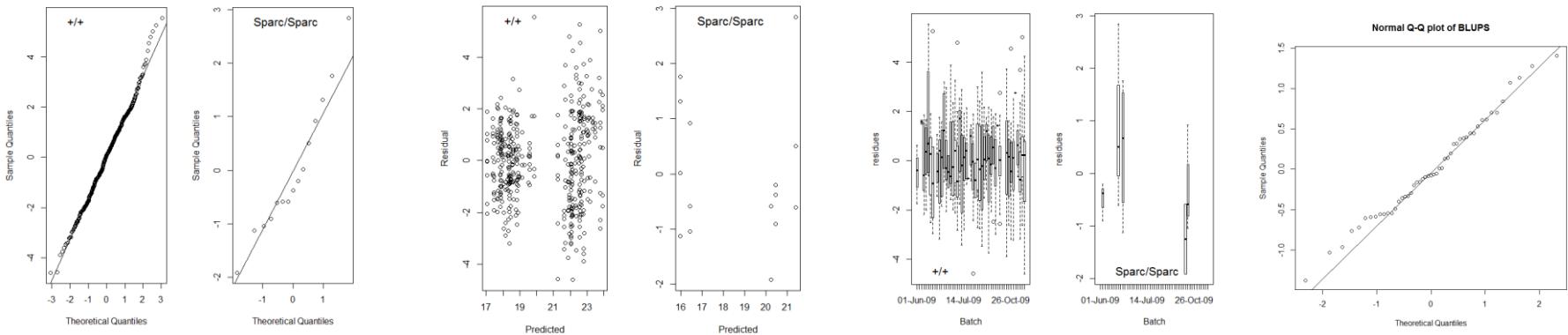
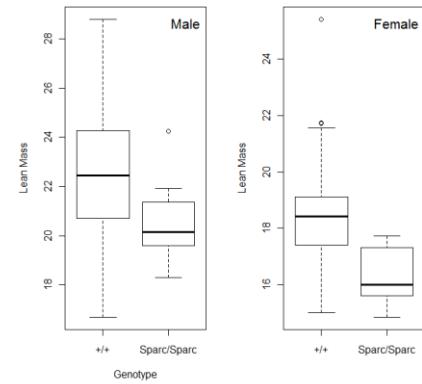
Top down modelling output

Hypothesis	Model1	Model 2	Test	Estimation method	Test statistic value	<i>p</i> -value
Is batch significant?	Batch	No batch	LRT	REML	$\chi^2(0:1)=31.43$	<.0001
Is variance homogenous?	Homogenous	Heterogeneous	LRT	REML	$\chi^2(2)=4.052$	0.0441
Testing fixed effects – sex			Type 1 <i>F</i> -test	REML	$F(1,412)=25.95$	0.0000
Testing fixed effect – genotype*sex			Type 1 <i>F</i> -test	REML	$F(1,47)=-0.480$	0.6331
Testing treatment - Is genotype significant?	With genotype	Without genotype	LRT	ML	$\chi^2(2)=11.556$	0.000675

Lean Mass: Final model values and diagnostics

Parameter estimates:

	Value	Std.Error	DF	t-value	p-value
(Intercept)	18.441	0.170	412	108.679	0.0000
GenotypeSparc/Sparc	-1.862	0.542	412	-3.436	0.0006
GenderMale	4.210	0.161	412	26.190	0.0000



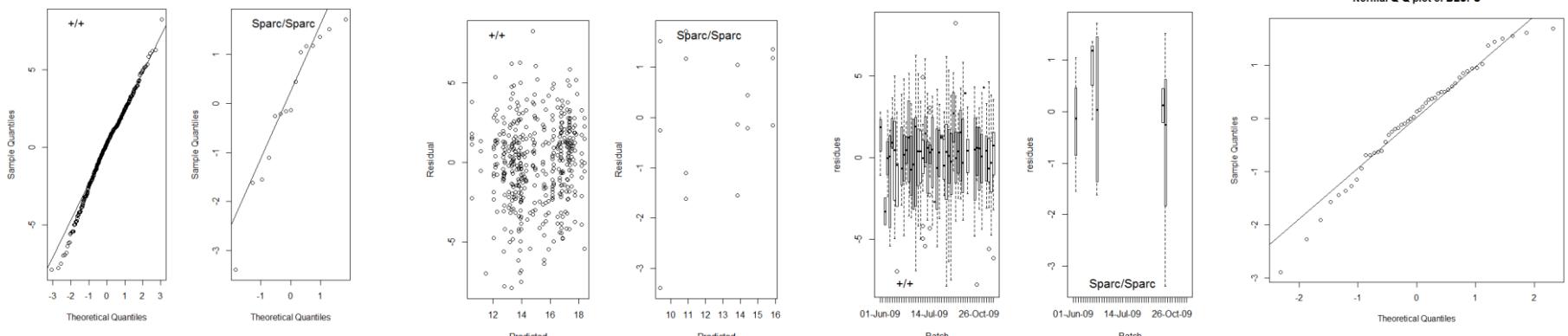
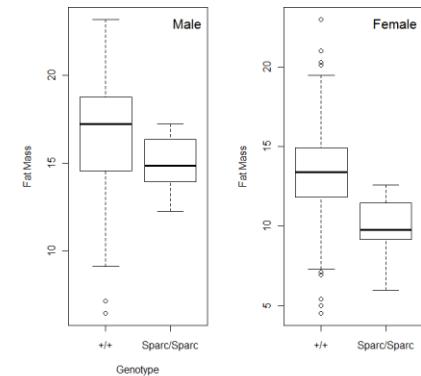
Fat Mass: Final model values and diagnostics

Hypothesis	Model1	Model 2	Test	Estimation method	Test statistic value	p-value
Is batch significant?	Batch	No batch	LRT	REML	$\chi^2(0:1)=28.715$	<.0001
Is variance homogenous?	Homogenous	Heterogeneous	LRT	REML	$\chi^2(2)=4.0524$	0.0441
Testing fixed effects – sex			Type 1 F-test	REML	$F(1,412)=13.048$	0.0000
Testing fixed effect – genotype*sex			Type 1 F-test	REML	$F(1,47)=1.0322$	0.3072
Testing treatment - Is genotype significant?	With genotype	Without genotype	LRT	ML	$\chi^2(2)=13.586$	0.00022 77

Fat Mass: Final model values and diagnostics

Parameter estimates:

	Value	Std.Error	DF	t-value	p-value
(Intercept)	13.411	0.273	412	49.122	0.0000
GenotypeSparc/Sparsc	-2.583	0.649	412	-3.979	0.0001
GenderMale	3.419	0.252	412	13.541	0.0000



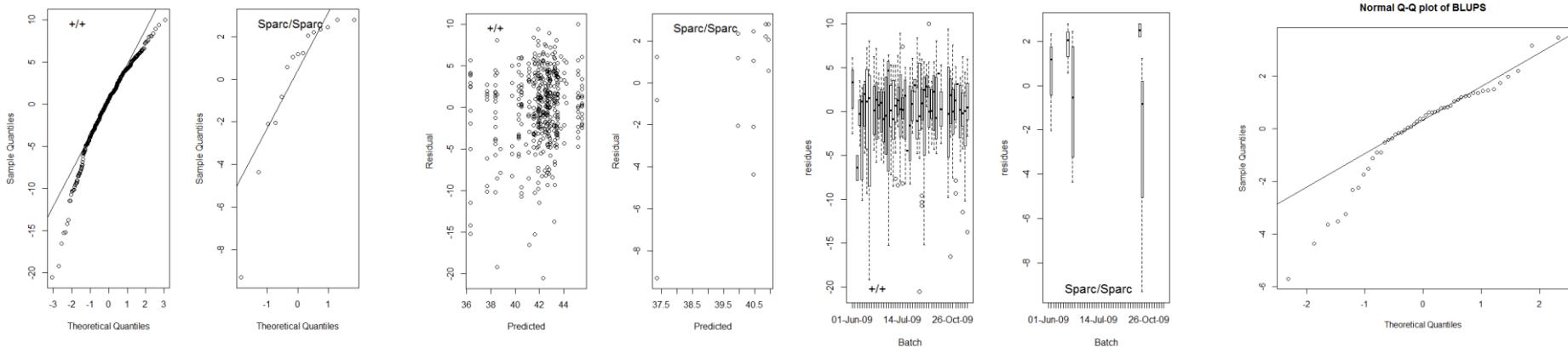
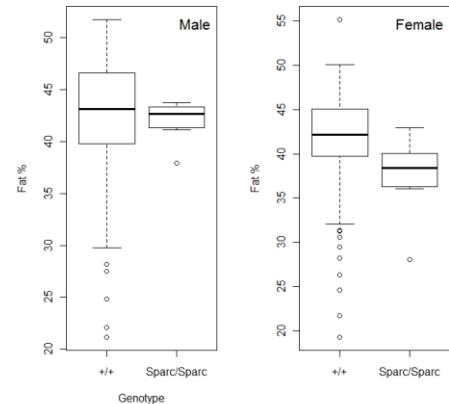
Dependent variable: Fat Percentage (Fat %)

Hypothesis	Model1	Model 2	Test	Estimation method	Test statistic value	p-value
Is batch significant?	Batch	No batch	LRT	REML	$\chi^2(0:1)=42.334$	<.0001
Is variance homogenous?	Homogenous variance	Heterogeneous	LRT	REML	$\chi^2(2)=2.6767$	0.1018
Testing fixed effects – sex			Type 1 F-test	REML	$F(1,411)=1.371$	0.1711
Testing fixed effect – genotype*sex			Type 1 F-test	REML	$F(1,47)=1.418$	0.1627
Is genotype significant?	With genotype	Without genotype	LRT	ML	$\chi^2(2)=2.5998$	0.10687

Fat %: Final model values and diagnostics

Parameter estimates:

	Value	Std.Error	DF	t-value	p-value
(Intercept)	42.036	0.430	413	97.850	0.0000
GenotypeSparc/SpArc	-2.443	1.519	413	-1.608	0.1086



Summary

Variable	<i>p</i> value	Adjusted <i>p'</i> value	Genotype Estimate ± SE	Sex
Weight	1.58e-7	7.52E-07	Y↓ -4.08±0.979	Y↑
Nose to tail length	1.08e-10	7.02E-10	Y↓ -0.491±0.073	Y↑
BMD	2.66e-7	1.15E-06	Y↓ -0.004±0.001	N
BMC	3.09e-6	1.24E-05	Y↓ -0.060±0.0013	Y↑
LM	0.0006	0.0017	Y↓ -1.862±0.542	Y↑
FM	0.0002	0.0006	Y↓ -2.583±0.649	Y↓
Fat %	0.1068	0.1501	N	Y↓

Y denotes a statistically significant effect and N indicates a non significant effect. The ↑ symbol indicates a positive estimated regression coefficient such that this effect leads to an increase in the dependent variable. Whilst, the ↓ symbol indicates a negative estimated regression coefficient such that this effect leads to a decrease in the dependent variable.

Mixed Model results 2

Starting model:

$$Y_{ij} = \beta_0 + \beta_1 \text{Genotype1}_{ij} + \beta_2 \text{Sex1}_{ij} + \\ \beta_3 \text{Weight1}_{ij} + \beta_4 \text{Genotype1}_{ij} \text{Sex1}_{ij} + u_j + \\ e_{ij}.$$

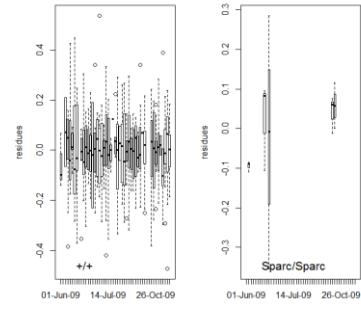
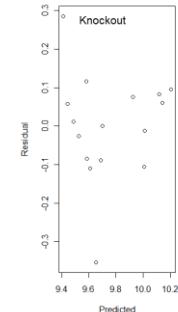
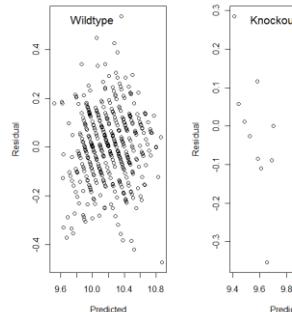
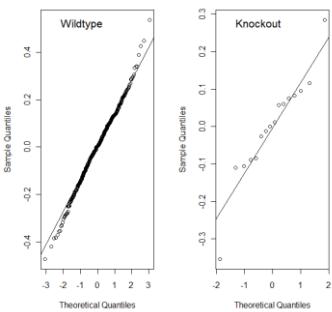
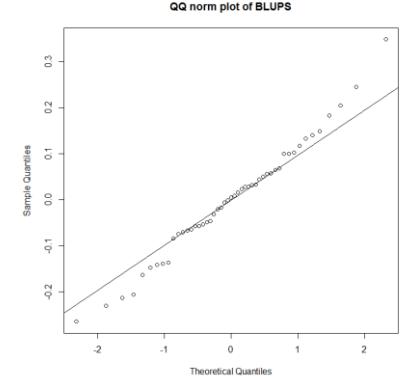
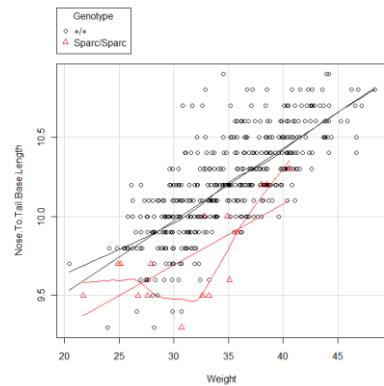
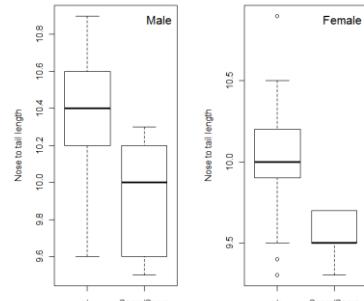
Nose to tail length: Top down modelling output

Hypothesis	Model1	Model 2	Test	Estimation method	Test statistic value	<i>p</i> -value
Is batch significant?	Batch	No batch	LRT	REML	$\chi^2(0:1)=170.49$	<0.0001
Is variance homogenous?	Homogenous	Heterogeneous	LRT	REML	$\chi^2(2)=0.007$	0.9319
Testing fixed effects – sex			Type 1 <i>F</i> -test	REML	$F(1,416)=7.981$	0.0050
Testing fixed effects – sex*genotype			Type 1 <i>F</i> -test	REML	$F(1,47)=0.219$	0.6418
Testing fixed effects – Weight			Type 1 <i>F</i> -test	REML	$F(1,416)=340.48$	<0.0001
Testing treatment - Is genotype significant?	With genotype	Without genotype	LRT	ML	$\chi^2(2)=27.48$	1.587e-07

Nose to tail length: Final model values and diagnostics

Parameter estimates:

	Value	Std.Error	DF	t-value	p-value
(Intercept)	8.728943	0.074709	416	116.839	0.0000
GenotypeSparc/Spard	-0.32514	0.060934	416	-5.33603	0.0000
sexMale	0.062747	0.022384	416	2.80322	0.0053
Weight	0.041395	0.002243	416	18.45883	0.0000



Bone mineral Density:

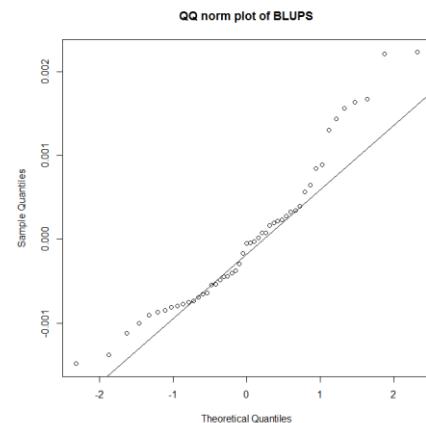
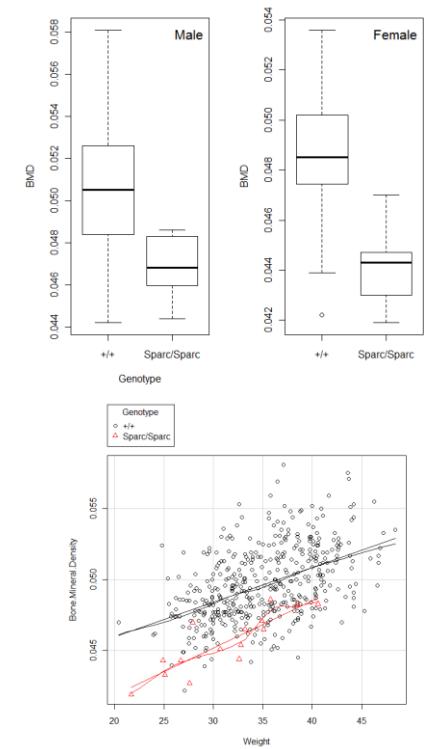
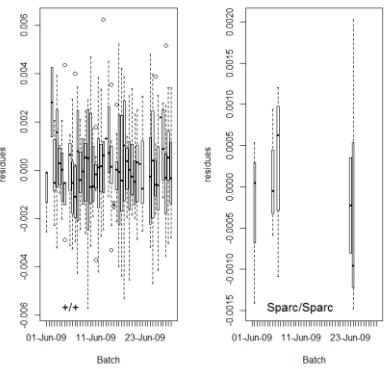
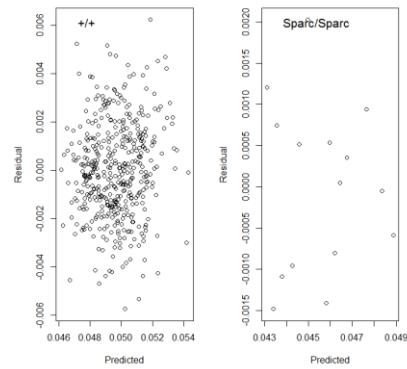
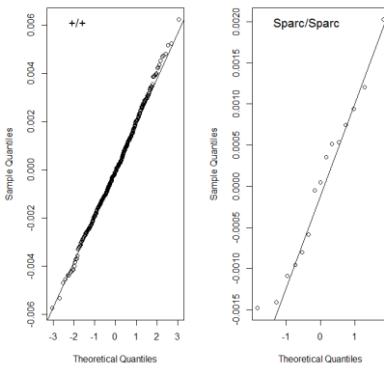
Top down modelling output

Hypothesis	Model1	Model 2	Test	Estimation method	Test statistic value	p-value
Is batch significant?	Batch	No batch	LRT	REML	$\chi^2(0:1)=50.79$	<0.0001
Is variance homogenous?	Homogenous	Heterogeneous	LRT	REML	$\chi^2(2)=5.10$	0.0239
Testing fixed effects – sex			Type 1 F-test	REML	$F(1,411)=0.257$	0.6122
Testing fixed effects – weight			Type 1 F-test	REML	$F(1,411)=88.00$	<0.0001
Testing fixed effect – genotype*sex			Type 1 F-test	REML	$F(1,47)=0.47$	0.4947
Testing treatment - Is genotype significant?	With genotype	Without genotype	LRT	ML	$\chi^2(2)=20.180$	7.04e-06

Bone Mineral Density: Final model values and diagnostics

Parameter estimates:

	Value	Std.Error	DF	t-value	p-value
(Intercept)	0.040777	0.000706	412	57.72091	0.0000
GenotypeSparc/Sparsc	-0.00259	0.000513	412	-5.04827	0.0000
Weight	0.000257	1.92E-05	412	13.39569	0.0000



Bone Mineral Content:

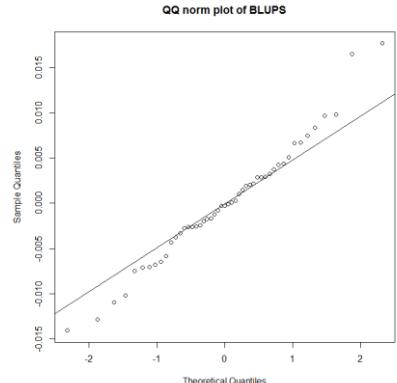
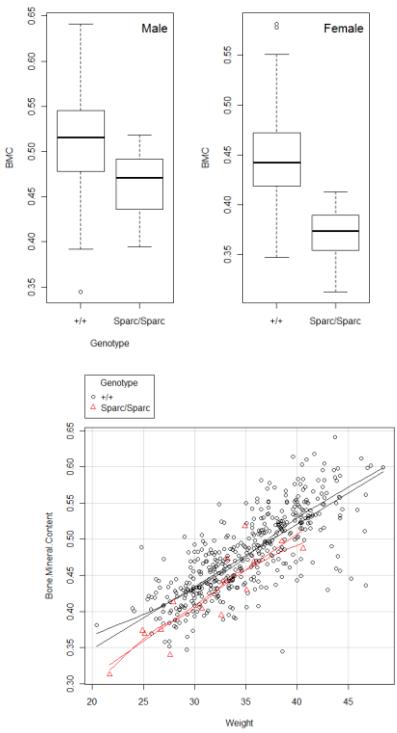
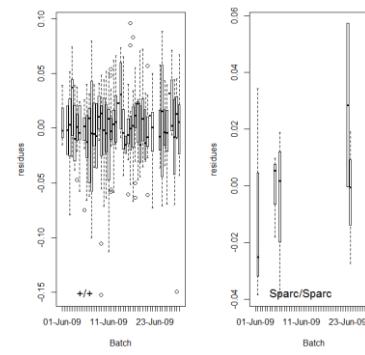
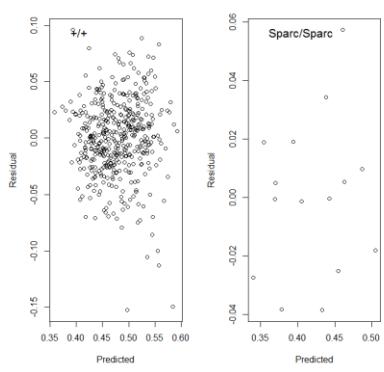
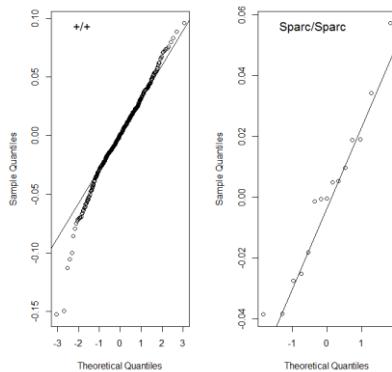
Top down modelling output

Hypothesis	Model1	Model 2	Test	Estimation method	Test statistic value	p-value
Is batch significant?	Batch	No batch	LRT	REML	$\chi^2(0:1)=8.26$	0.004
Is variance homogenous?	Homogenous	Heterogeneous	LRT	REML	$\chi^2(2)=0.951$	0.3292
Testing fixed effects – sex			Type 1 F-test	REML	$F(1,411)=2.072$	0.1507
Testing fixed effects – weight			Type 1 F-test	REML	$F(1,411)=285.8$	<0.0001
Testing fixed effect – genotype*sex			Type 1 F-test	REML	$F(1,47)=0.087$	0.7688
Testing treatment - Is genotype significant?	With genotype	Without genotype	LRT	ML	$\chi^2(2)=4.709$	0.03

Bone Mineral Content: Final model values and diagnostics

Parameter estimates:

	Value	Std.Error	DF	t-value	p-value
(Intercept)	0.19	0.02	411	12.16	0.0000
GenotypeSparc/Sparsc	-0.02	0.01	411	-2.39	0.0175
Weight	0.01	0.00	411	16.95	0.0000
sexMale	0.01	0.00	411	1.47	0.1420



Lean Mass:

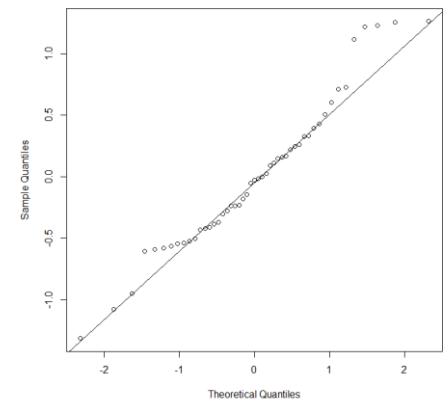
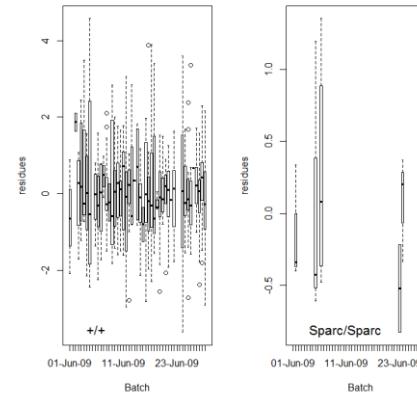
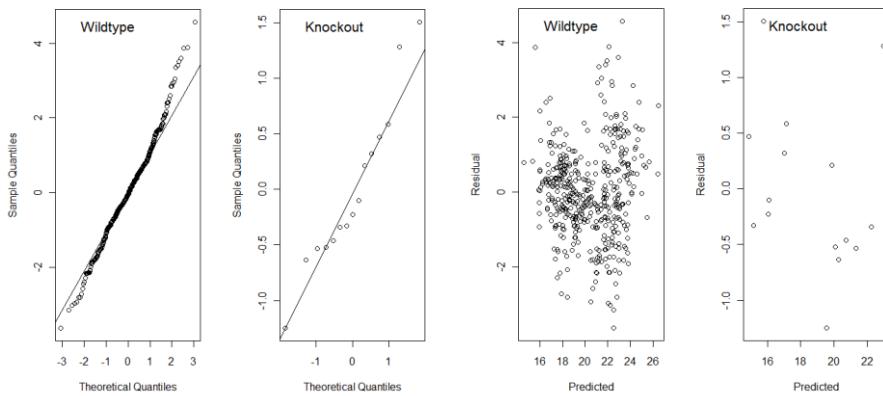
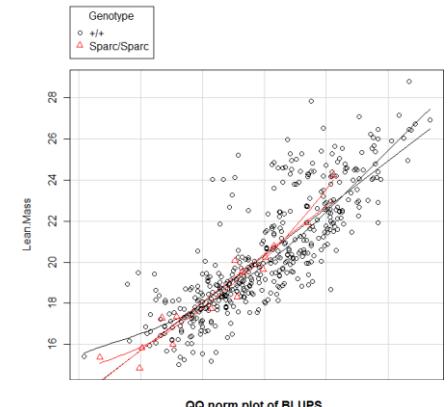
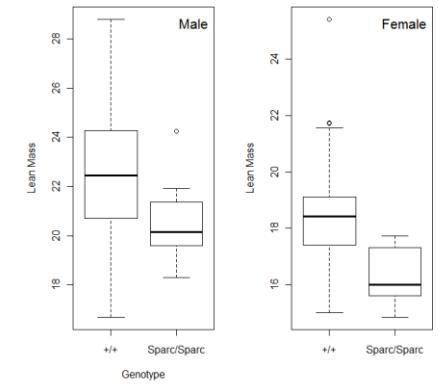
Top down modelling output

Hypothesis	Model1	Model 2	Test	Estimation method	Test statistic value	p-value
Is batch significant?	Batch	No batch	LRT	REML	$\chi^2(0:1)=60.57$	<0.0001
Is variance homogenous?	Homogenous	Heterogeneous	LRT	REML	$\chi^2(2)=5.55$	0.0185
Testing fixed effects – sex			Type 1 F-test	REML	$F(1,411)=84.703$	<0.0001
Testing fixed effects – weight			Type 1 F-test	REML	$F(1,411)=363.67$	<0.0001
Testing fixed effect – genotype*sex			Type 1 F-test	REML	$F(1,47)=2.777$	0.1022
Testing treatment - Is genotype significant?	With genotype	Without genotype	LRT	ML	$\chi^2(2)=0.798$	0.3715

Lean Mass: Final model values and diagnostics

Parameter estimates:

	Value	Std.Error	DF	t-value	p-value
(Intercept)	7.611139	0.588627	411	12.93034	0.0000
GenotypeSparc/SpArc	-0.29144	0.33048	411	-0.88186	0.3784
sexMale	1.640734	0.180809	411	9.074391	0.0000
Weight	0.34305	0.018081	411	18.97274	0.0000



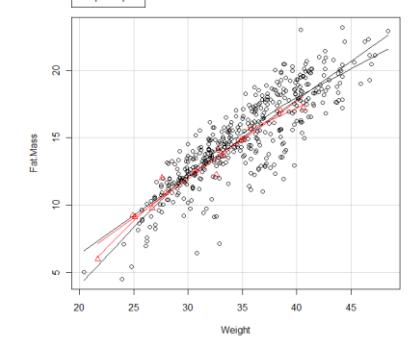
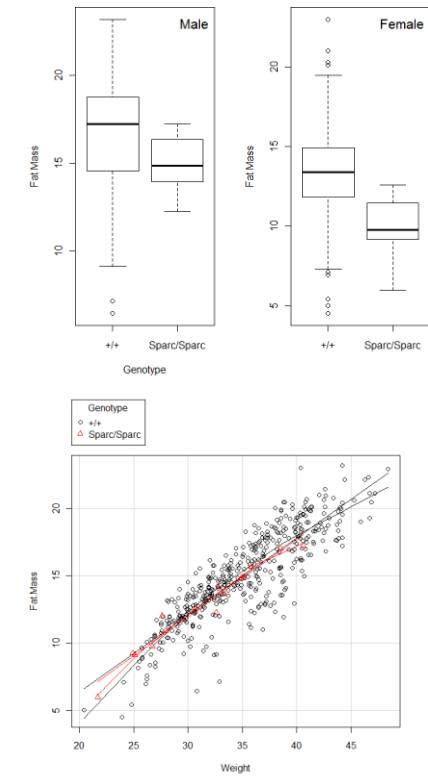
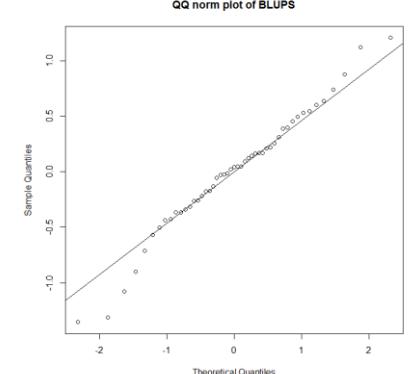
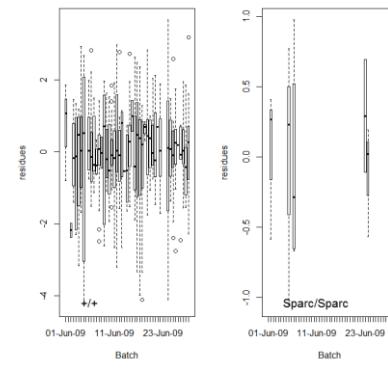
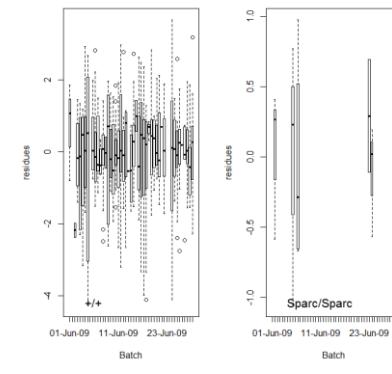
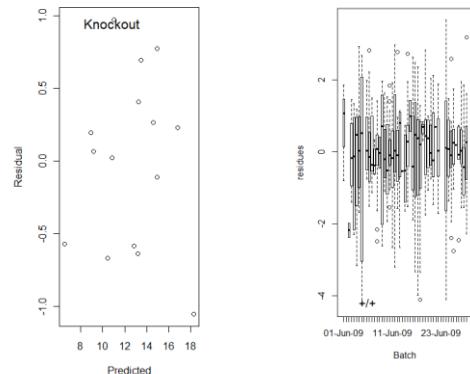
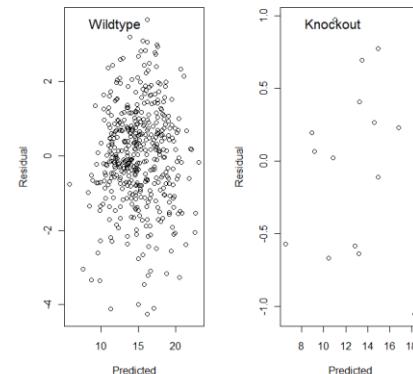
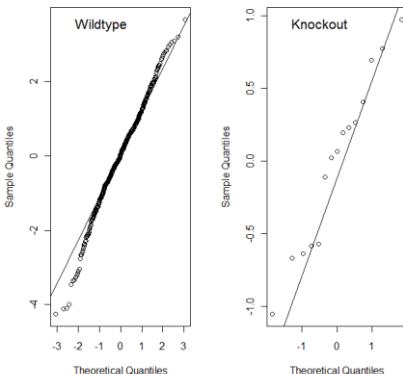
Fat Mass: Final model values and diagnostics

Hypothesis	Model1	Model 2	Test	Estimation method	Test statistic value	p-value
Is batch significant?	Batch	No batch	LRT	REML	$\chi^2(0:1)=52.79$	<0.0001
Is variance homogenous?	Homogenous	Heterogeneous	LRT	REML	$\chi^2(2)=7.515$	0.0061
Testing fixed effects – sex			Type 1 F-test	REML	$F(1,411)=84.754$	<0.0001
Testing fixed effects – weight			Type 1 F-test	REML	$F(1,411)=1309.60$	<0.0001
Testing fixed effect – genotype*sex			Type 1 F-test	REML	$F(1,47)= 0.744$	0.3927
Testing treatment - Is genotype significant?	With genotype	Without genotype	LRT	ML	$\chi^2(2)=1.554$	0.2125

Fat Mass: Final model values and diagnostics

Parameter estimates:

	Value	Std.Error	DF	t-value	p-value
(Intercept)	-8.58667	0.62306	411	-13.7815	0.0000
GenotypeSparc/Sparc	0.393943	0.320326	411	1.22982	0.2195
sexMale	-1.7669	0.192659	411	-9.17113	0.0000
Weight	0.696697	0.019222	411	36.24525	0.0000



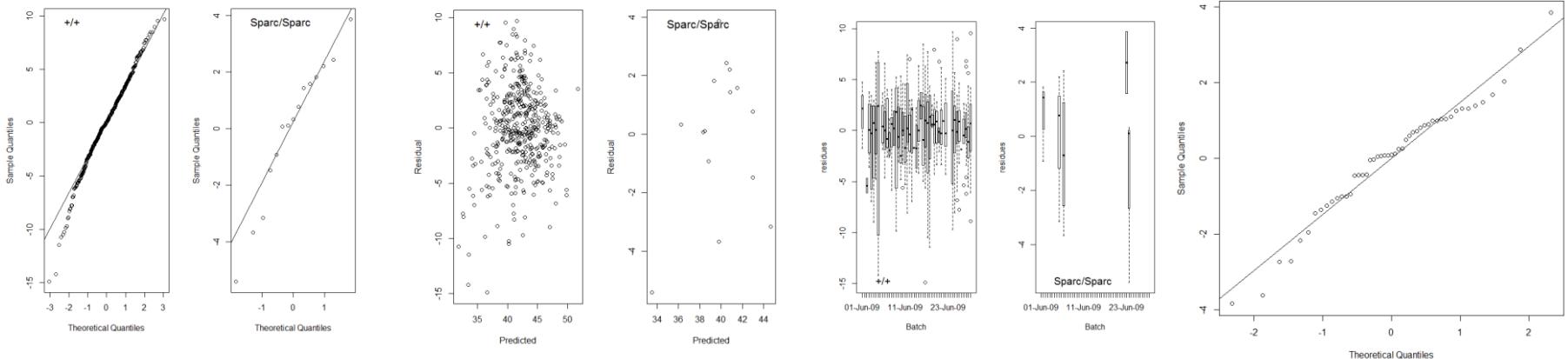
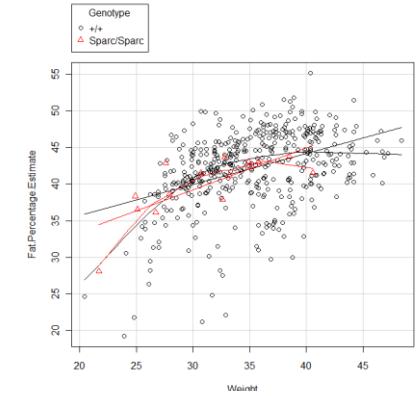
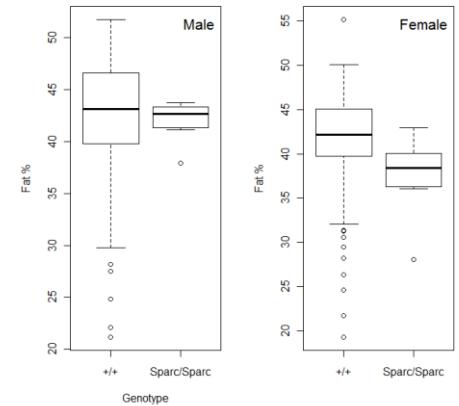
Dependent variable: Fat Percentage (Fat %)

Hypothesis	Model1	Model 2	Test	Estimation method	Test statistic value	p-value
Is batch significant?	Batch	No batch	LRT	REML	$\chi^2(0:1)=48.536$	<.0001
Is variance homogenous?	Homogenous variance	Heterogeneous	LRT	REML	$\chi^2(2)=3.3473$	0.0673
Testing fixed effects – sex			Type 1 F-test	REML	$F(1,411)=94.90$	<.0001
Testing fixed effects – weight			Type 1 F-test	REML	$F(1,411)=214.93$	<.0001
Testing fixed effect – genotype*sex			Type 1 F-test	REML	$F(1,47)=1.672$	0.2023
Is genotype significant?	With genotype	Without genotype	LRT	ML	$\chi^2(2)=0.6899$	0.4062

Fat %: Final model values and diagnostics

Parameter estimates:

	Value	Std.Error	DF	t-value	p-value
(Intercept)	16.13209	1.784149		411	9.041899
GenotypeSparc/Sparsc	1.047678	1.275536		411	0.821363
sexMale	-5.30435	0.548967		411	-9.66241
Weight	0.808772	0.055044		411	14.69329



Summary

Variable	<i>p</i> value	Adjusted <i>p'</i> value	Genotype Estimate ± SE	Sex	Weight
Nose to tail length	1.587e-7	7.52E-07	Y↓ -0.325±0.060	Y↑	Y↑
BMD	7.048e-6	2.44E-05	Y↓ -0.002±0.0005	N	Y↑
BMC	0.03	0.0472	Y↓ -0.02±0.01	Y↑	Y↑
LM	0.3715	0.4024	N	Y↑	Y↑
FM	0.2125	0.2569	N	Y↓	Y↑
Fat %	0.4062	0.4310	N	Y↓	Y↑

Y denotes a statistically significant effect and N indicates a non significant effect. The ↑ symbol indicates a positive estimated regression coefficient such that this effect leads to an increase in the dependent variable. Whilst, the ↓ symbol indicates a negative estimated regression coefficient such that this effect leads to a decrease in the dependent variable.