G-TWYST
GM PLANTS TWO YEAR SAFETY TESTING

G-TwYST Study B

a 90-day toxicity study in rats fed GM maize NK603

Statistical report appendices

Paul W. Goedhart & Hilko van der Voet

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Biometris, one of the largest groups of quantitative scientists in North-Western Europe, develops statistical and mathematical methods for the quantification of biological processes and processes in our living environment. These methods are applied and validated in practice and are often available as software packages. In addition, we provide education at the undergraduate, Master, PhD, and PostDoc levels, as well as training and consultancy for industry. We cover a wide range of application areas, from gene to ecosystem and from product to production chain. Our goal is to bring quantitative methods to life.

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Appendices

Appendix 1. Initial data processing and preparation of data files

The following data files were obtained from the test site Slovak Medical University (SZU).

Design of the study	**File Size**
Design Study B.xlsx	26,530
Weights and Feed intake	**File Size**
Tab_1_1-13 week_Body weight_90_day_st_1B_G_TwYST_Mal.xlsx	175,972
Tab_2_1_13 week_Body weight_90_day_st_1B_G_TwYST_Femal.xlsx	99,598
Tab_3_1-13 week_Feed consump_90_day_st_1B_G_TwYST_Mal.xlsx	174,281
Tab_4_1-13 week_Feed consump_90_day_st_1B_G_TwYST_Femal.xlsx	179,254
Haematology	**File Size**
Tab_5_Haemat_90-day_st_1B_G_TwYST_Mal.xlsx	42,453
Tab_6_Haemat_90-day_st_1B_G_TwYST_Femal.xlsx	42,262
diffWBC	**File Size**
GTwYSt-B Differential WBC Jun 2016 final JT.xlsx	24,952
Clinical Biochemistry	**File Size**
Tab_7a_Clin_Chem_bl _90-day_st_1B_G_TwYST_Mal.xlsx	68,415
Tab_8a_Clin_Chem_bl_90-day_st_1B_G_TwYST_Femal.xlsx	67,818
Urine	**File Size**
Tab_7b_Clin_Chem_ur_90-day_st_1B_G_TwYST_Mal.xlsx	62,374
Tab_8b_Clin_Chem_ur_90-day_st_1B_G_TwYST_Femal.xlsx	60,177
Blood_urine_3 month_MC_G_TwYST_90day st1_B_Males_time	81.648
Blood_urine_3 month_MC_G_TwYST_90day st1_B_Females_time	77.106
Organ weights	**File Size**
Tab_9_Absolute_organ weights_90_day_st_1B_G_TwYST_Mal.xlsx	46,025
Tab_11_Absolute_organ weights_90_day_st_1B_G_TwYST_Femal.xlsx	36,691
Immunology	**File Size**
G-TwYST - Study B - Phagocyt and resp burst final.xlsx	16,934
GTwYSt-B ltt jun2016 final.xlsx	24,430
Cytokines	**File Size**
G-TwYST - Study B - Cytokines - Final.xlsx	41,519
CellPhenotype	**File Size**
CD markers DB - G-TwYST study B - final 7.8.2017 (002).xlsx	29,302
Hormone	**File Size**
Steinberg Ratten_valid080317_MS.xlsx	22,611
eCycle	**File Size**
MONITORING of ESTROUS CYCLICITY_G-TwYST_B 2016.xlsx	37,948

GenStat programs ***01-Read-Females.gen*** and ***01-Read-Males.gen*** combine all these data files into single Excel files, separately for Females and Males (these Excel files have the same name as the GEN files). The design of the experiment is represented by means of the following design factors:

Animal:	animal number (1-80 for males and 101-180 for females)
Cage:	cage number (1-40 for males and 44-83 for females)
Treat:	blinded feeding group (XA, XB, XC, XD, XE)
Week:	week at which the cage was started
Row:	row in the experimental design (1-4)
Block:	block in the experimental design (1-8 for males and 9-16 for females)
Group:	un-blinded feed group (Control, NK11-, NK11+, NK33-, NK33+)
Maize:	maize of feed group (Control, NK603)
AmountNK:	amount of NK603 in feed group (0, 11, 33)
Roundup:	whether roundup was used in the feed group (No, Yes)

The levels of the treatment factors are linked in the following way:

Factor	Levels / Labels				
Treat (blinded)	XA	XB	XC	XD	XE
Group	NK11-	NK33+	NK33-	NK11+	Control
Maize	NK603	NK603	NK603	NK603	Control
AmountNK	11	33	33	11	0
RoundUp	No	Yes	No	Yes	No

Since Cage is the experimental unit and since the data are statistically analysed on the LOG scale the data are stored in several ways in the following Excel sheets:

Raw:	raw data on the original scale as given in the original Excel files
MeanRaw:	cage means on the original scale
LogRaw:	raw data on the log-scale
MeanLogRaw:	cage means on the log-scale (first log-transform then take the mean)

In addition to these sheets the combined Excel files contain a sheet “Response” with the grouping of the variables, a sheet “Cytokines” with limiting values for the cytokine measurements (see below), a sheet “ GrowthRate” with the estimates parameters of the growth curves which are fitted to the animal weights (see main text), and finally a sheet “GrowthRateMeans” with the cage means of these estimated parameters.

Data values that are set to missing

Some of the response variables are not measured for every animal and are therefore missing, i.e. an empty cell in the resulting Excel file. In addition some of the values are set to missing either because something went wrong at the experimental station (see remarks below), or because the measurement was considered to be an outlier (see the outlier section in the main text). The original values in the original Excel files are stored in sheets with the same names as above and the prefix “org”, e.g. orgRaw. The original values in these sheets, which are set to missing, have a golden coloured background.

Cytokine data and limiting values

The Cytokine data contain many “Out of Range” values which are too small or too large for the measurement device. Such values are replaced by the limiting value in which the assays really work. Moreover values outside these limits are also replaced by the limits. The limiting values are given in the table below, along with the number of values that are set to the minimum (nMin) or maximum (nMax), and the number of values that are within the range (nWithin). From this table it is clear that only cytokines IL2, IL4, IL10, IL17A, TFNa and IFNg are informative. The other cytokines mostly have values outside the assay range.

Assay limits			Males			Females		
Cytokine	minimum	maximum	nMin	nMax	nWithin	nMin	nMax	nWithin
IL1a	12.2	50000	47	-	2	31	-	1
IL1b	15.9	65000	48	-	1	32	-	-
IL2	4.9	20000	-	-	49	-	-	32
IL4	1.2	5000	-	-	49	1	-	31
IL5	2.4	10000	47	-	2	29	-	3
IL6	4.9	20000	48	-	1	32	-	-
IL10	9.8	40000	-	2	47	-	4	28
IL12p70	9.8	40000	37	-	12	18	-	14
IL13	4.9	20000	38	-	11	28	-	4
IL17A	3.7	15000	-	-	49	-	-	32
GCSF	3.7	15000	49	-	0	32	-	-
GMCSF	9.8	40000	42	-	7	29	-	3
TNFa	4.9	20000	2	-	47	3	-	29
IFNg	9.8	40000	-	-	49	-	-	32

Further remarks on data pre-processing

Further remarks with comments from Slovak Medical University (SZU). i.e. Jana Tulinská and Dagmar Zeljenková, in italics:

1. Feed intake is only available at the cage level. Feed intake is rescaled to gram/animal/day units, taking account of the number of animals still alive in the cage. The mean of the feed intake is added to the feed intake data.
2. The following measured weights were set to missing due to what CZU called “*Incorrectly resetted weights*”: for males the following animal numbers and week numbers (14,9), (30,12), (75,8) and (80,8), and for females (107,9), (151,8), (170,8) and (176,10). Further checking revealed the following typing errors: for female rat 175 in week 6 the weight 220.01 was changed in 202.71, for male rat 44 in week 12 the weight 470.68 was changed to 420.68.
3. All female rats have completed the experiment. Male rat 41 in Cage 21 (feed NK33-) is removed from the experiment at the end of week 8. This rat seems to be already sick in week 7 since the feed consumption in week 7 for the cage is very low. Therefore the weight of the rat in week 7 and the feed consumption in weeks 7 and 8 for cage 21 are set to missing.
4. Organ weights were expressed as a percentage of the final body weight.
5. Urine pH (upH) is not log transformed as pH is already measured on a log scale.
6. Basophils (diffWBC) was zero for all rats and is thus not statistically analysed.

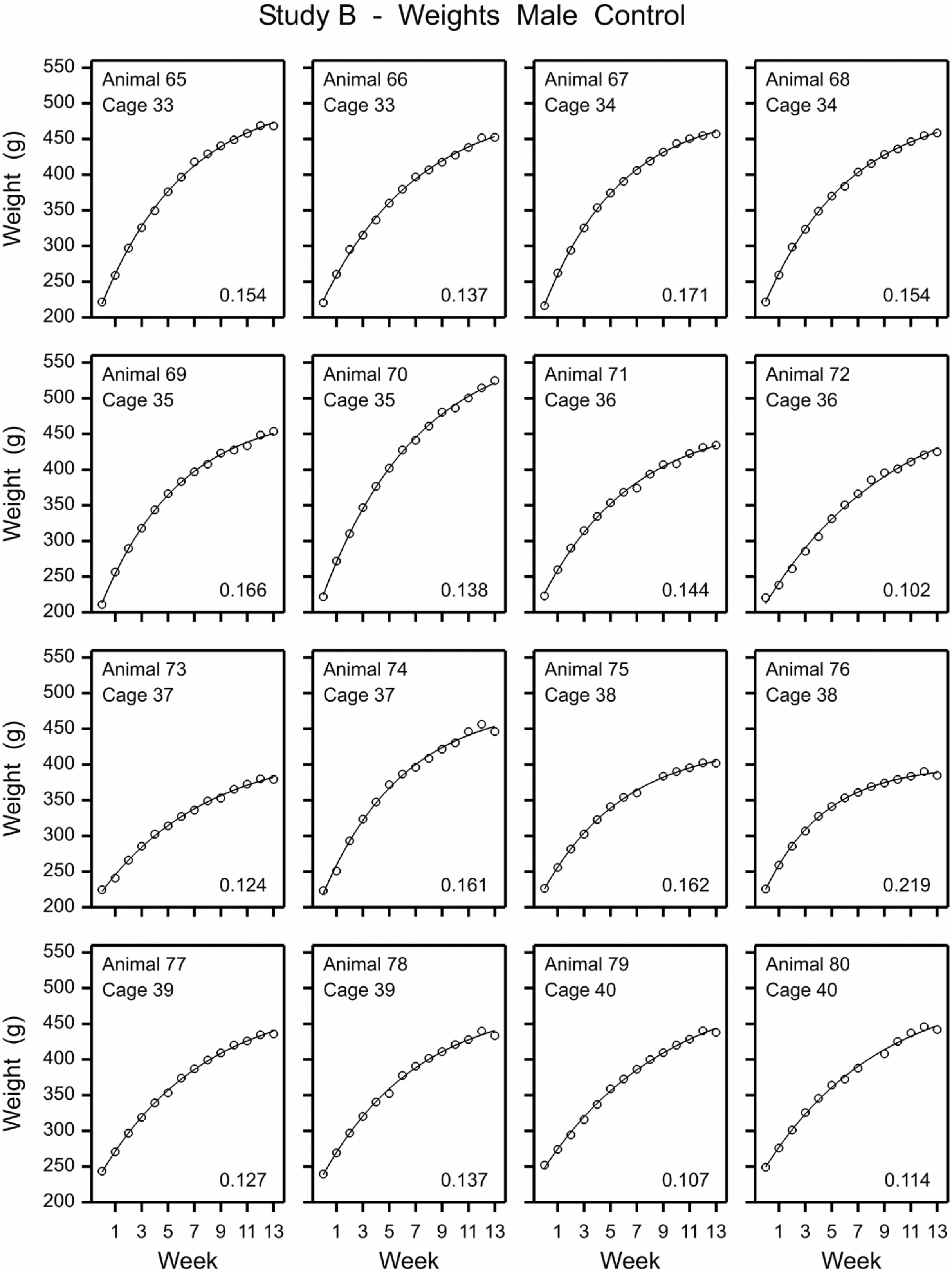
7. Haematology PLT for female rats 110/117/119/124/157/160/176 are likely to be wrong (see remarks in original Excel file “Tab_6_Haemat_90-day_st_1B_G_TwYST_Femal.xlsx”). SZU remarked that “*Problem with Platelets – The same problem occurred during the GRACE project. In peripheral blood of rats is substantially higher number of thrombocytes (platelets) than in human blood. Study personal is experienced and familiar with the problem. They took available tool how to prevent the clotting (immediate gentle mixing on roller); however in several samples clotting occurred. Remarks from Dr. Relka Líšková are included directly in the database*”. PLT for these rats are therefore set to missing.
8. HGB for several female rats: '< 27.5' is replaced by 27.5. *This is agreed by SZU*.
9. Organ weights Thymus for female rat 122 is missing. SZU remarked that “*There was macroscopic pathological finding on the thymus. Person was so focused on the problem, that colleague forgot to weight the organ*”.
10. Haematology PLT for male rat 20 is likely to be wrong (see remarks in the original Excel file “Tab_5_Haemat_90-day_st_1B_G_TwYST_Mal.xlsx”). PLT for this rat is therefore set to missing. *This is implicitly agreed by SZU*.
11. HGB for male rat 74: '< 27.5' in the original data is replaced by 27.5. *Implicitly agreed by SZU*.
12. Urine U-keton for male rat 5: '0,5l' in the original data is replaced by 0.5. *This is agreed by SZU*.
13. The following Urine data are not statistically analysed because they are largely uninformative: **uColour** (all measurements equal 2, i.e. yellow, except for two female rats 179 and 180 in the control group which have the value 1, i.e. light yellow), **uBil** (all measurements equal 0), **uNit** (all measurements equal 0 except for male rats 16, 48, 63, 64, 79 which have the value 1), **uProtein** (all measurements equal 0), **uGlu** (all measurements equal 1), **uHemogl** (all measurements equal 0 except for male rat 47 which has a value 25 and for female rat 147 which has a value 10), and **uUrobili** (all measurements are equal to 1). The following Urine variables remained and were statistically analysed: uVol, uVolW, uLeu, uOsmoll, uKeton and upH.
14. Organ Heart weight for male rat 73 is missing. *SZU remarked that “Person forgot to weight the organ and placed it directly to the cassette”*.
15. Some of the Hormone data were repeated. The chief of the Endocrinology Lab in Hannover, Marion Schmicke, wrote about these repeated values: “*Where the values are similar, it makes sense to keep the original value, since these examinations were determined in a test routine.*” For male rats only two T4 measurements were repeated: for rat 15 the first measurement is 33.1, the second equals 44.1. Following the advice of Dr Schmicke, the second value (44.1) is used in the statistical analysis. For rat 63 the first measurement is 51.8, the second equals 52.3; the first measurement (51.8) is used because there is hardly any difference. For female rats the original and repeated measurement are given below. The values with the yellow background are used. These choices are confirmed by Pablo Steinberg.

Rat	17β	17β REP	Rat	T3	T3 REP	Rat	T4	T4 REP
144	7.47	4.83	162	0.75	0.83	139	19.97	32.10
158	7.24	6.90	175	0.66	0.68			
159	8.24	8.00						
160	5.28	6.10						
162	3.30	3.14						
164	15.18	7.10						
180	4.20	3.88						

16. Some of the 17β and T4 Hormone measurements for females were censored, i.e. they are lower than the lower limit of the measurement device. The reported limit value for 17β equals 2.0 for rats 119 and 153, and 0.01 for rat 152. The limiting value for rat 152 was considered to be too low and has been replaced by 2.0. The censored values were replaced by half the limiting value, i.e. by 1, which is common practice when there are few censored values. Furthermore for T4 a lower limiting value of 10 was reported for female rats 109, 124 and 142. Again these were replaced by half the limiting value, i.e. by 5.
17. For the CellPhenotype data both the CD3- as well as the CD3+ marker data are reported. These should theoretically add up to 100%; however due to measurement error there are some small deviations from 100%. Only the CD3+ marker are therefore statistically analysed. Note that the CellPhenotype data are percentages.
18. The following stages (in days) of the oestrous cycle are reported: proestrous, estrous, metestrous and diestrous. It was decided to not statistically analyse these. Instead the duration of the first and second cycle were analysed, as well as the number of irregular cycles (out of 2).

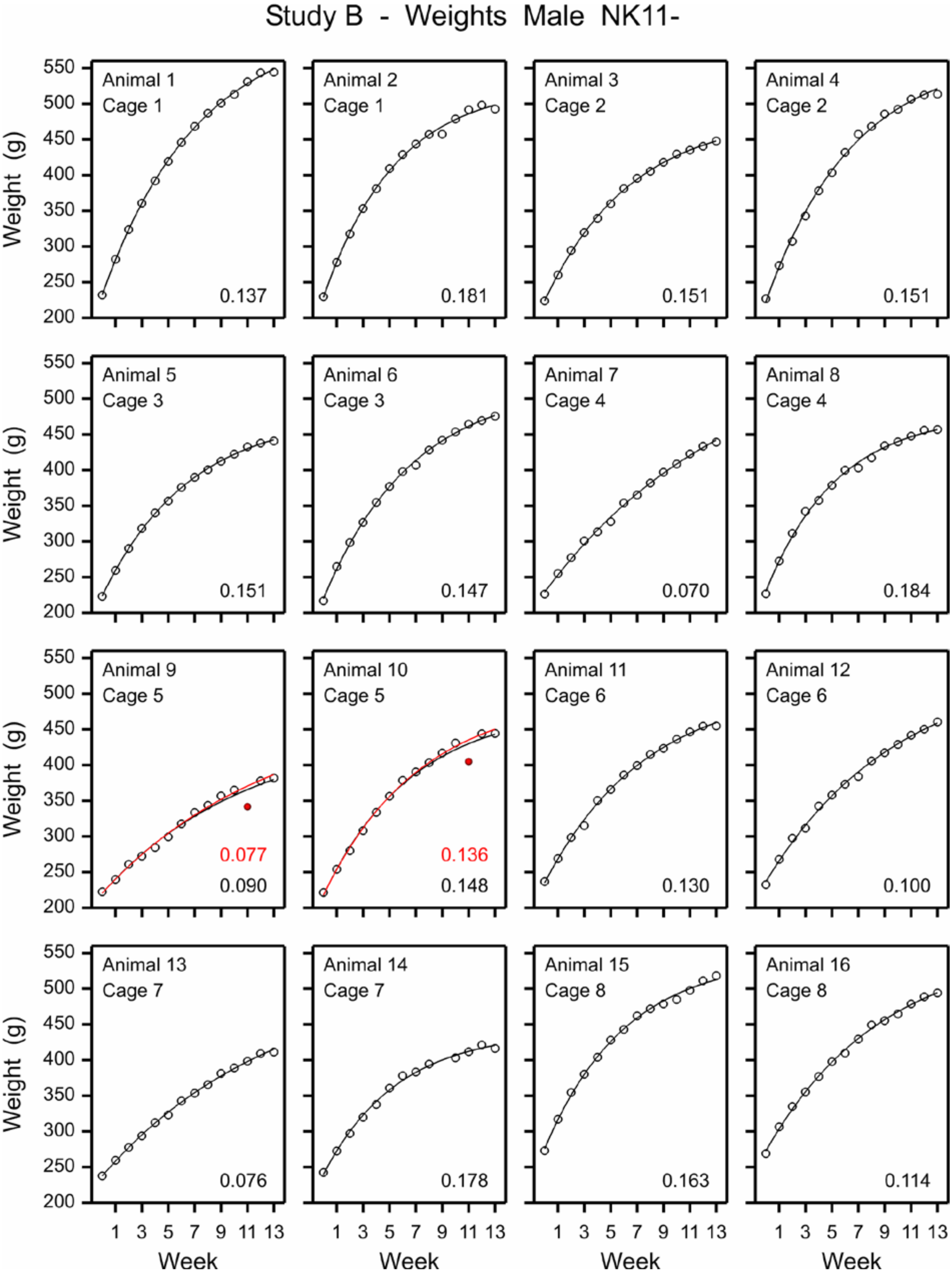
Appendix 2. Growth curves per animal

The estimated growth rate, i.e. $\gamma = -\log(R)$, is given in the right-bottom corner of each graph. In case an absolute standardized residual is larger than 3, the accompanying weight is set to missing and the curve is fitted again with results given in red.



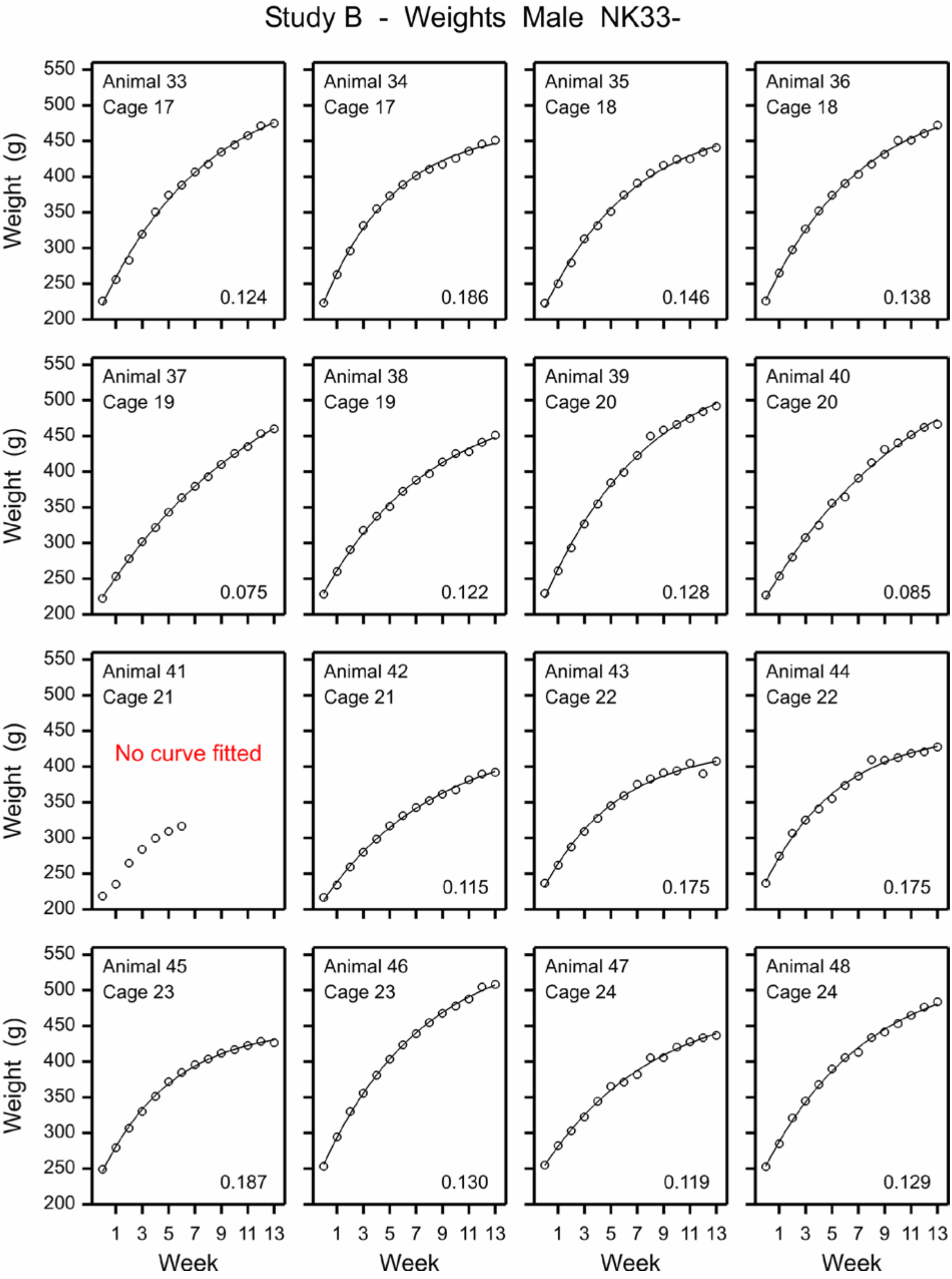
Appendix 2. Growth curves per animal (continued)

The estimated growth rate, i.e. $\gamma = -\log(R)$, is given in the right-bottom corner of each graph. In case an absolute standardized residual is larger than 3, the accompanying weight is set to missing and the curve is fitted again with results given in red.



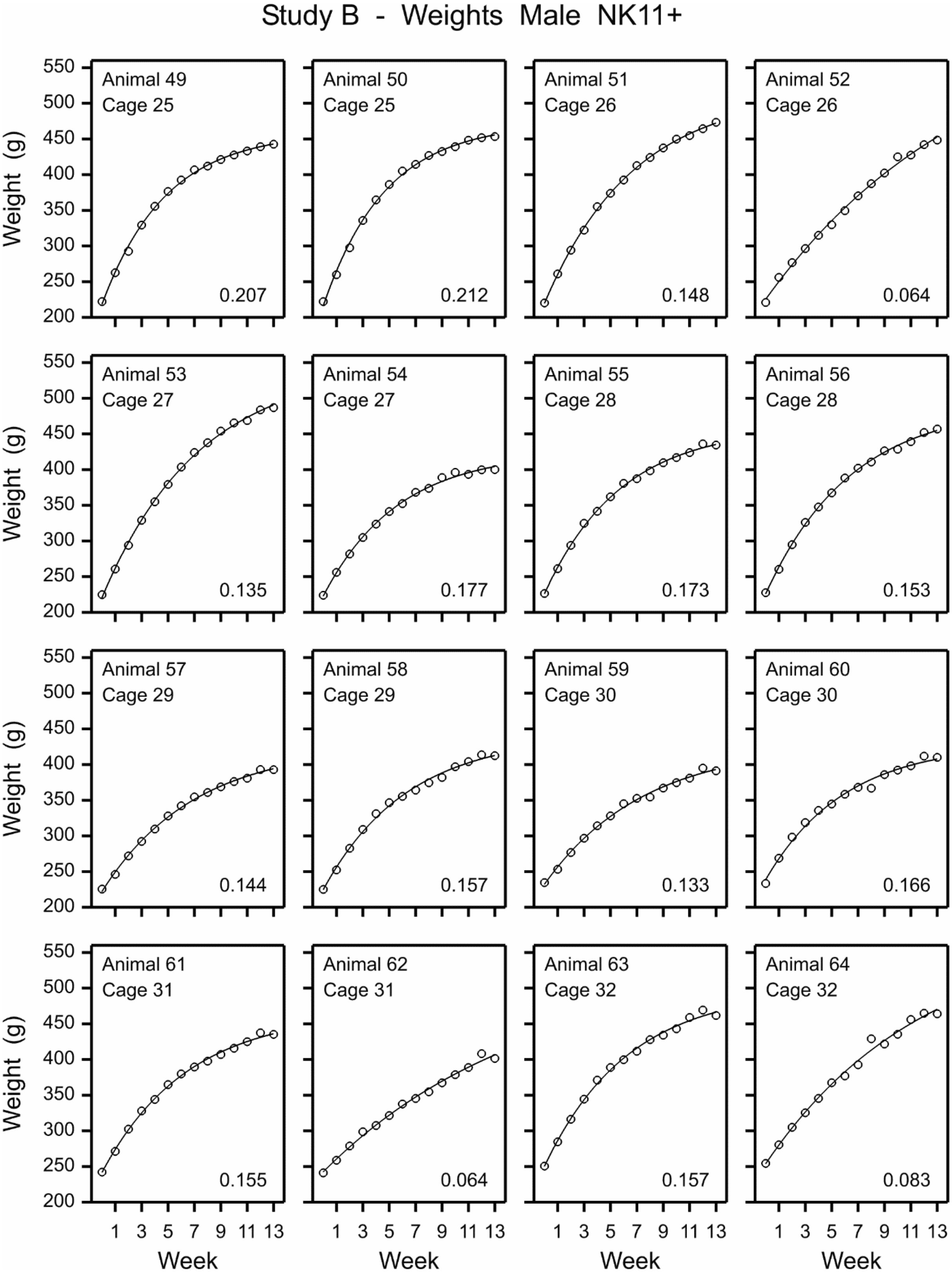
Appendix 2. Growth curves per animal (continued)

The estimated growth rate, i.e. $\gamma = -\log(R)$, is given in the right-bottom corner of each graph. In case an absolute standardized residual is larger than 3, the accompanying weight is set to missing and the curve is fitted again with results given in red.



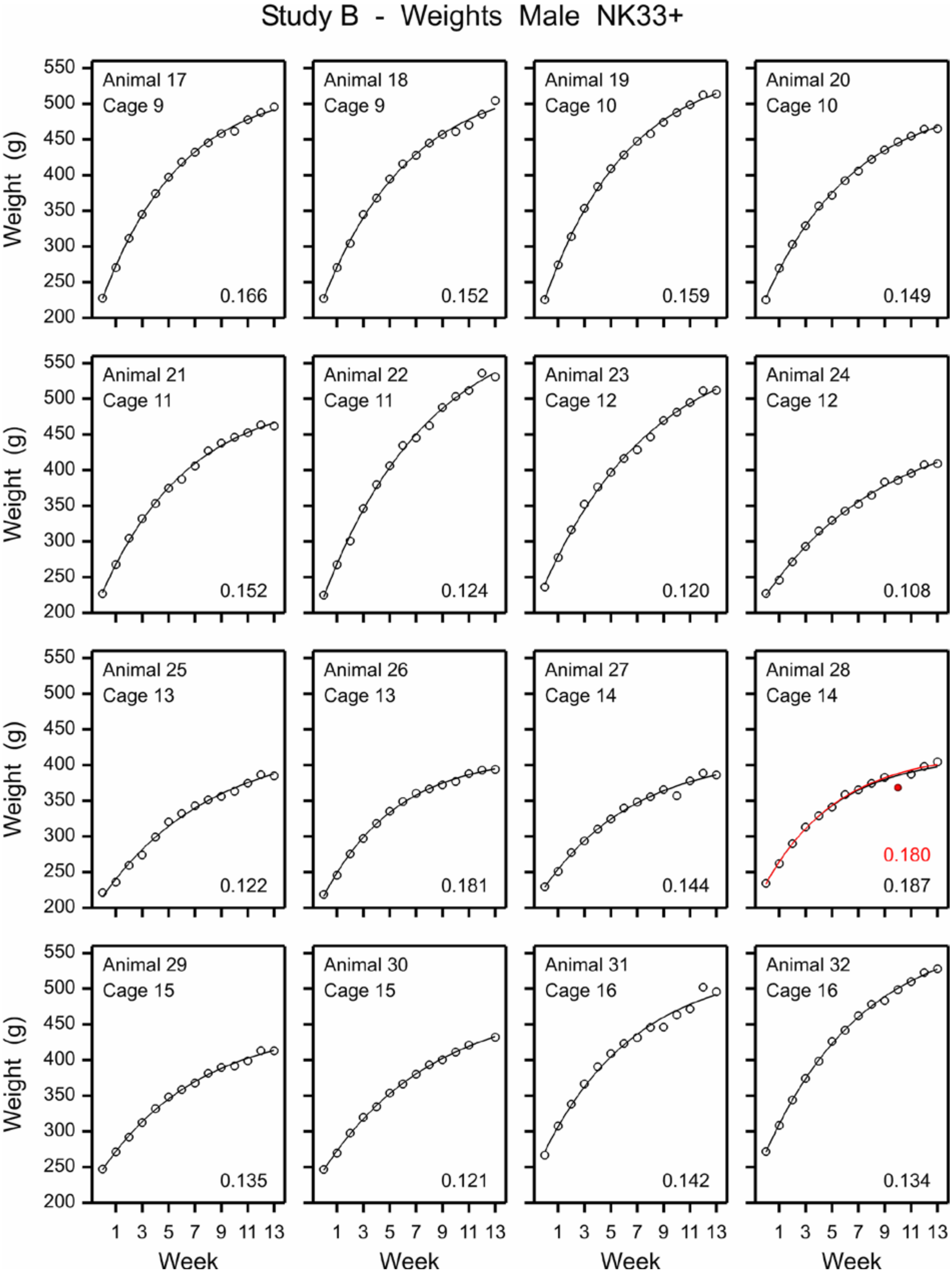
Appendix 2. Growth curves per animal (continued)

The estimated growth rate, i.e. $\gamma = -\log(R)$, is given in the right-bottom corner of each graph. In case an absolute standardized residual is larger than 3, the accompanying weight is set to missing and the curve is fitted again with results given in red.



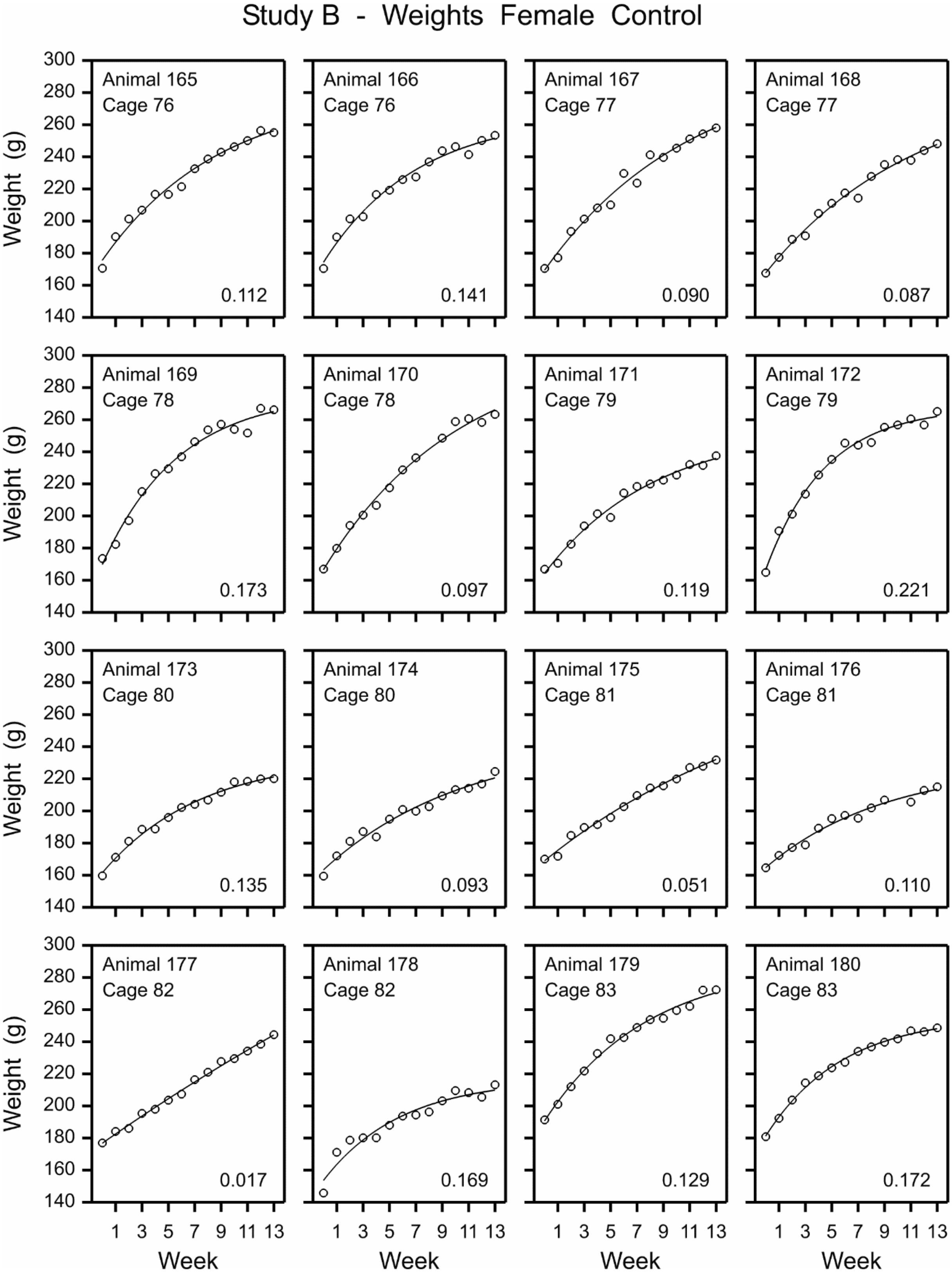
Appendix 2. Growth curves per animal (continued)

The estimated growth rate, i.e. $\gamma = -\log(R)$, is given in the right-bottom corner of each graph. In case an absolute standardized residual is larger than 3, the accompanying weight is set to missing and the curve is fitted again with results given in red.



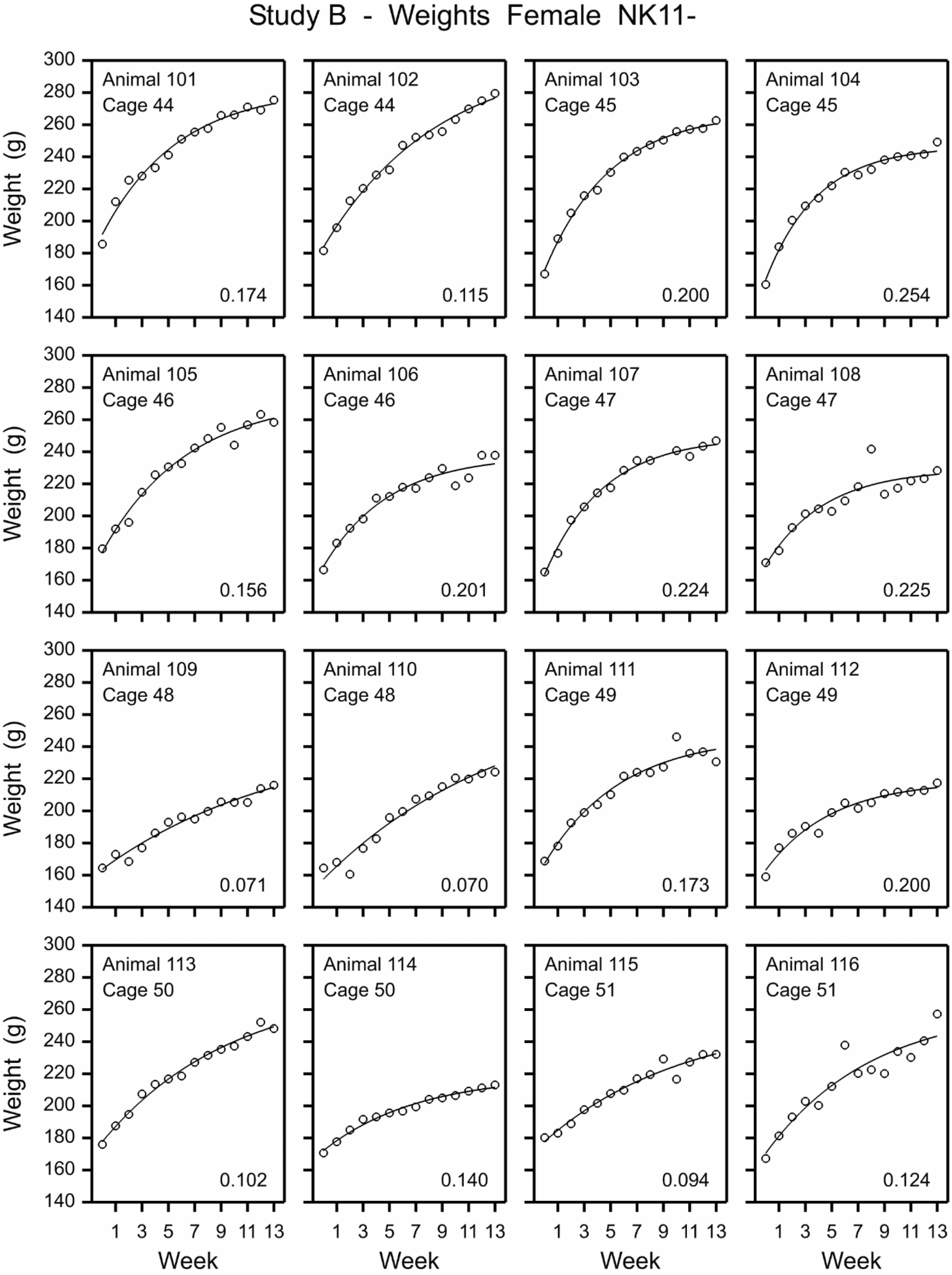
Appendix 2. Growth curves per animal (continued)

The estimated growth rate, i.e. $\gamma = -\log(R)$, is given in the right-bottom corner of each graph. In case an absolute standardized residual is larger than 3, the accompanying weight is set to missing and the curve is fitted again with results given in red.



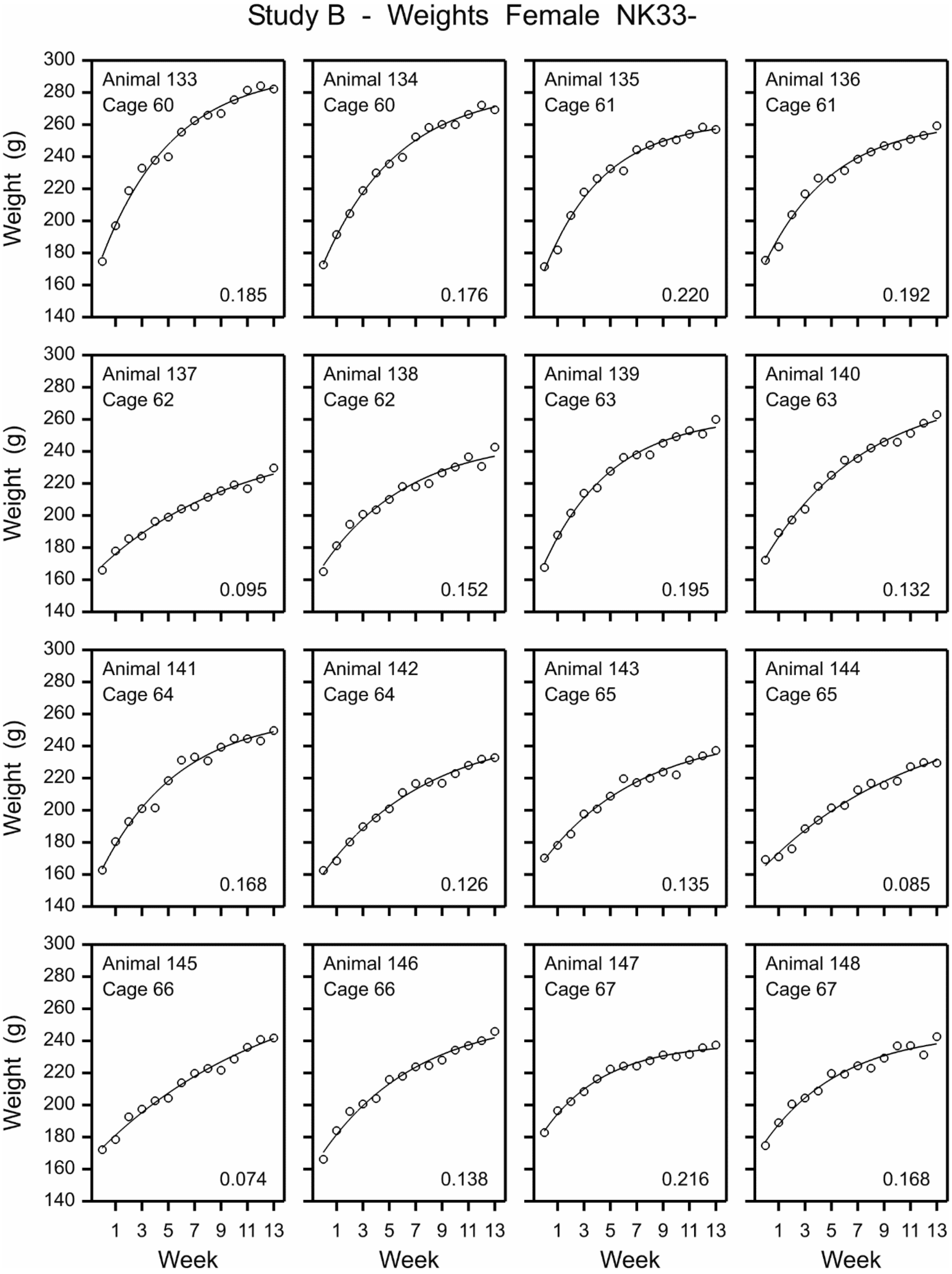
Appendix 2. Growth curves per animal (continued)

The estimated growth rate, i.e. $\gamma = -\log(R)$, is given in the right-bottom corner of each graph. In case an absolute standardized residual is larger than 3, the accompanying weight is set to missing and the curve is fitted again with results given in red.



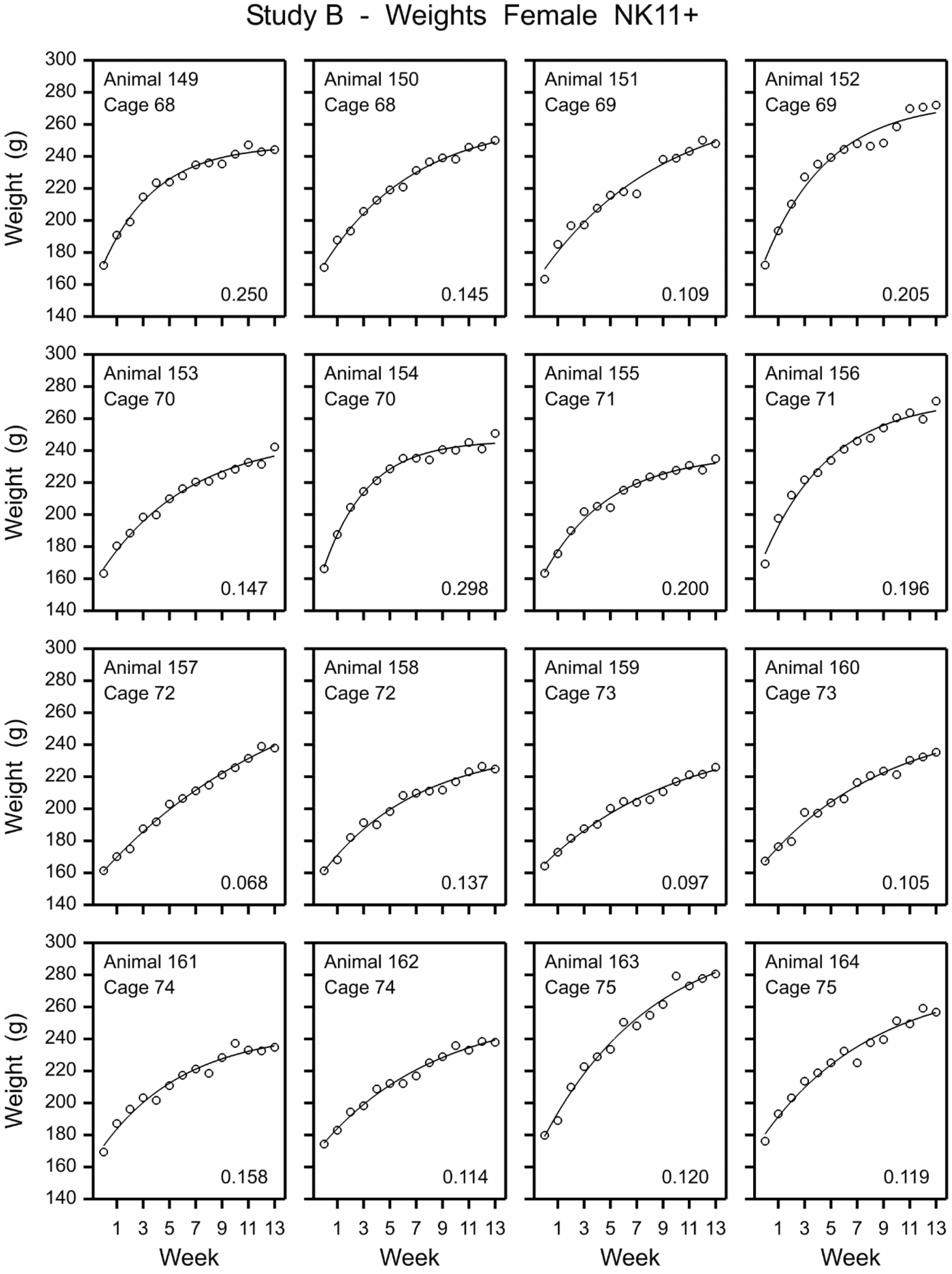
Appendix 2. Growth curves per animal (continued)

The estimated growth rate, i.e. $\gamma = -\log(R)$, is given in the right-bottom corner of each graph. In case an absolute standardized residual is larger than 3, the accompanying weight is set to missing and the curve is fitted again with results given in red.



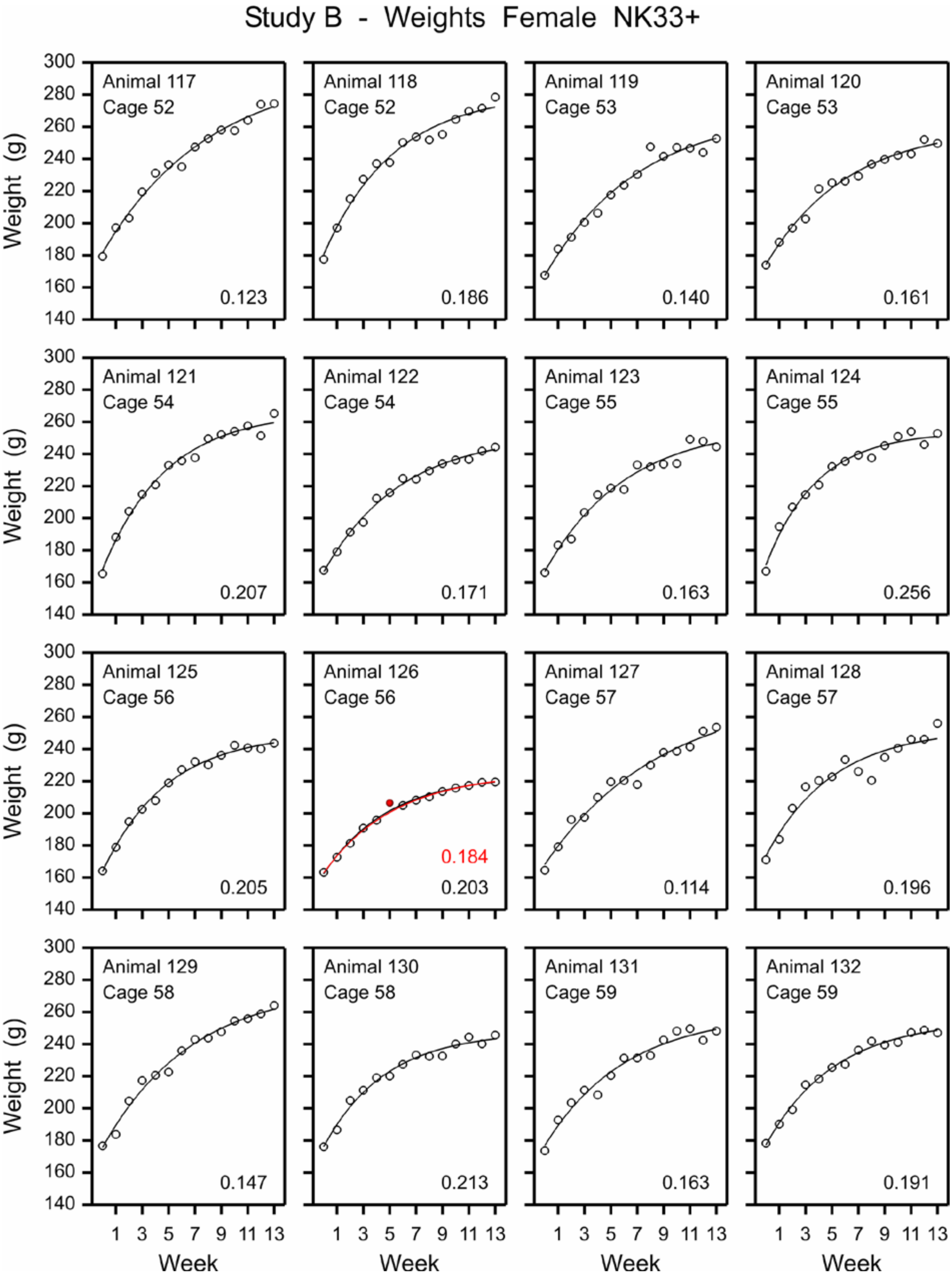
Appendix 2. Growth curves per animal (continued)

The estimated growth rate, i.e. $\gamma = -\log(R)$, is given in the right-bottom corner of each graph. In case an absolute standardized residual is larger than 3, the accompanying weight is set to missing and the curve is fitted again with results given in red.

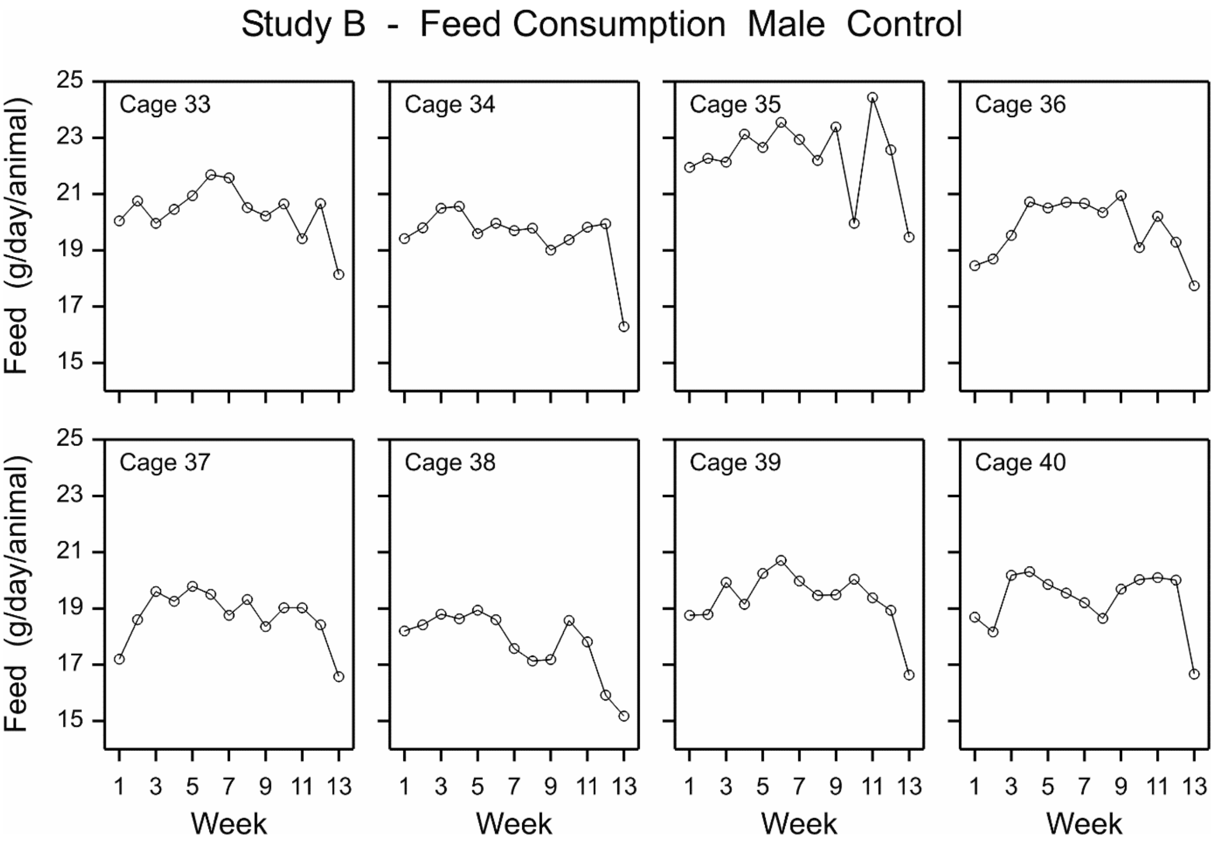


Appendix 2. Growth curves per animal (continued)

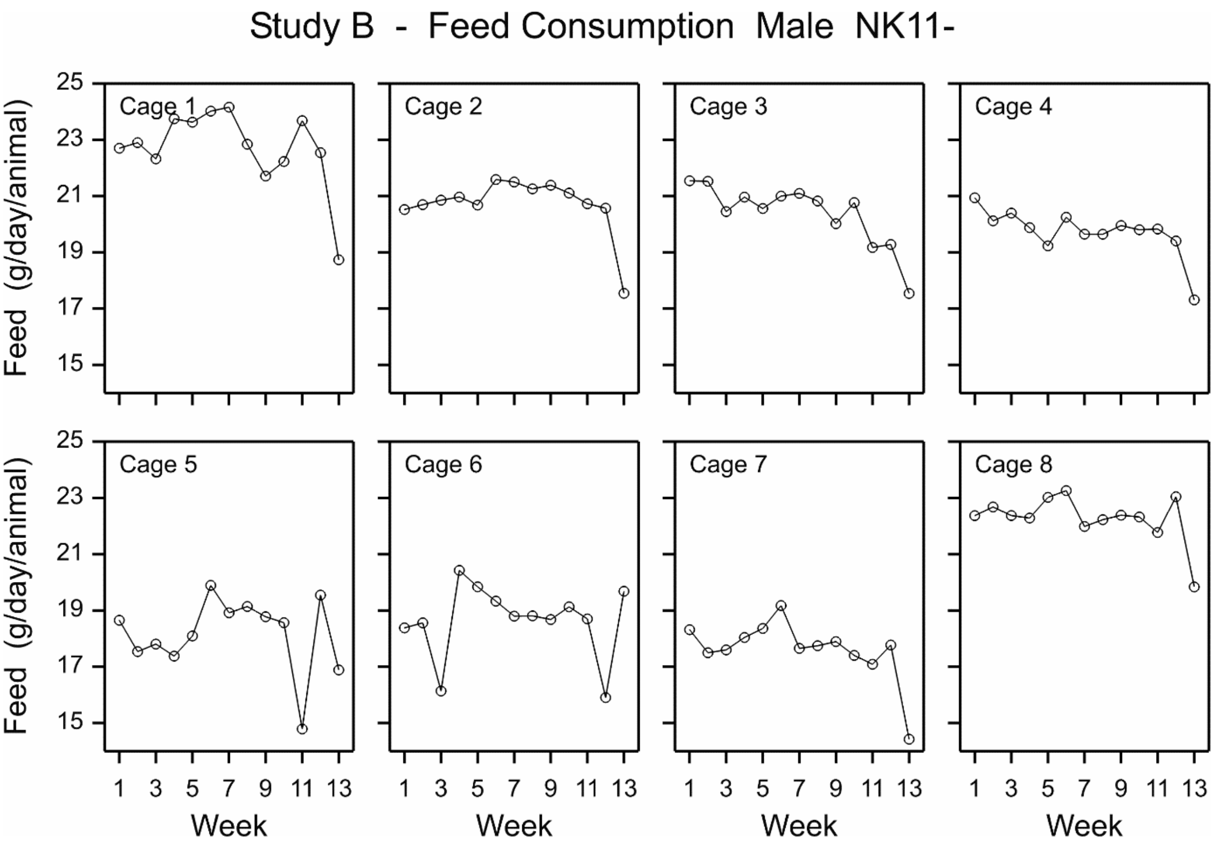
The estimated growth rate, i.e. $\gamma = -\log(R)$, is given in the right-bottom corner of each graph. In case an absolute standardized residual is larger than 3, the accompanying weight is set to missing and the curve is fitted again with results given in red.



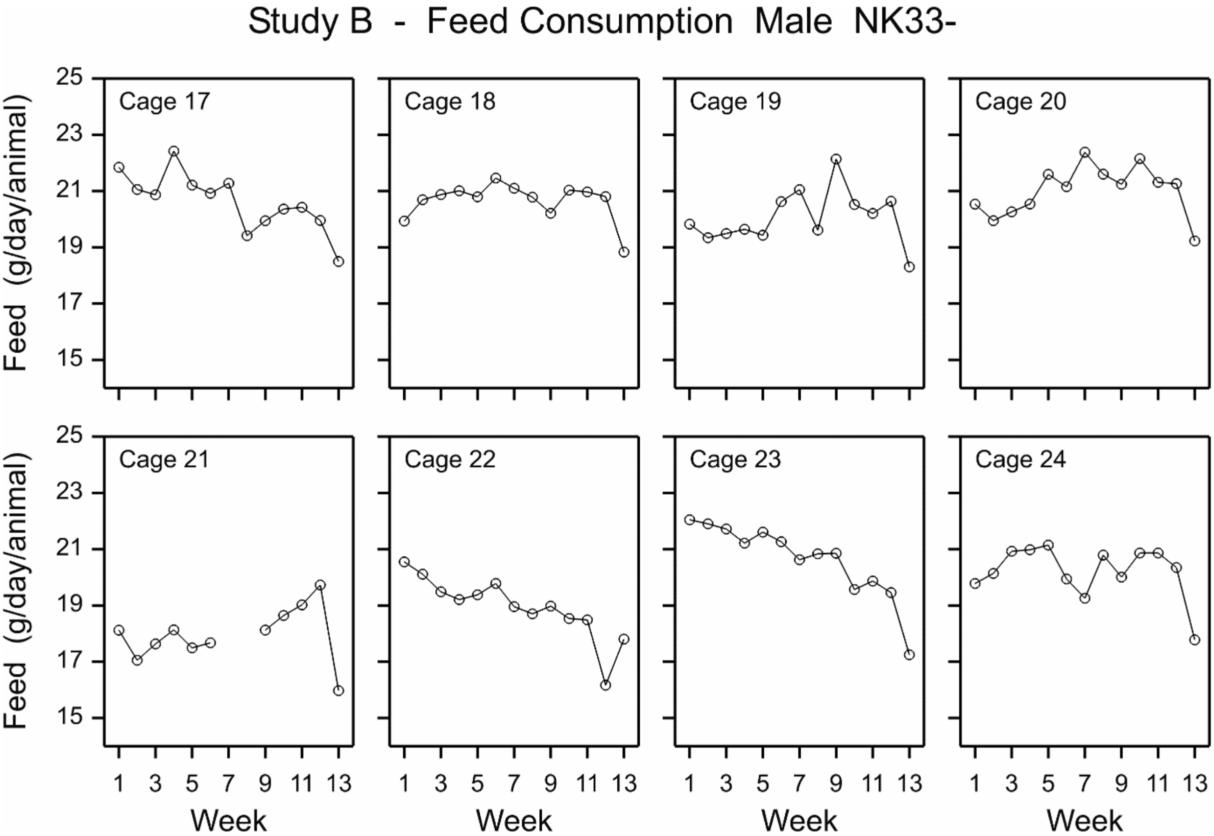
Appendix 3. Feed consumption per cage



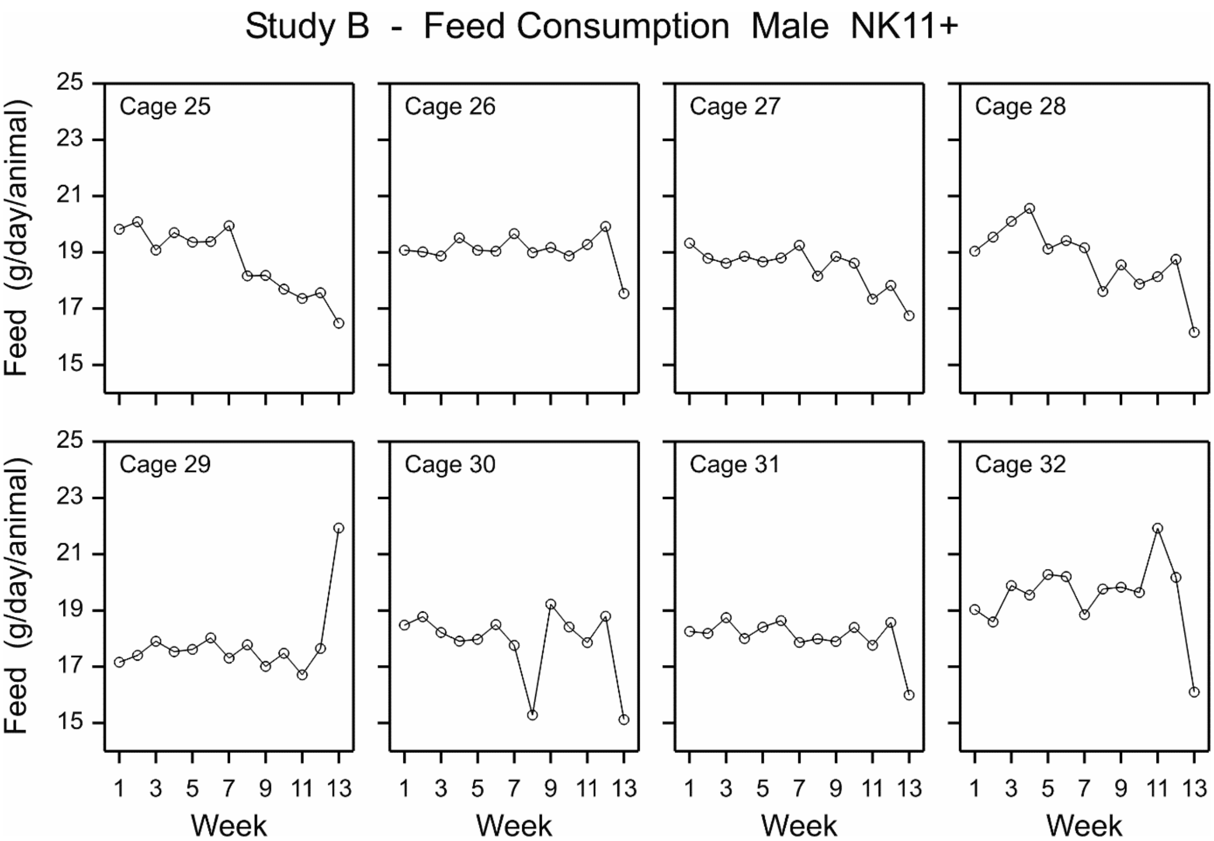
Appendix 3. Feed consumption per cage (continued)



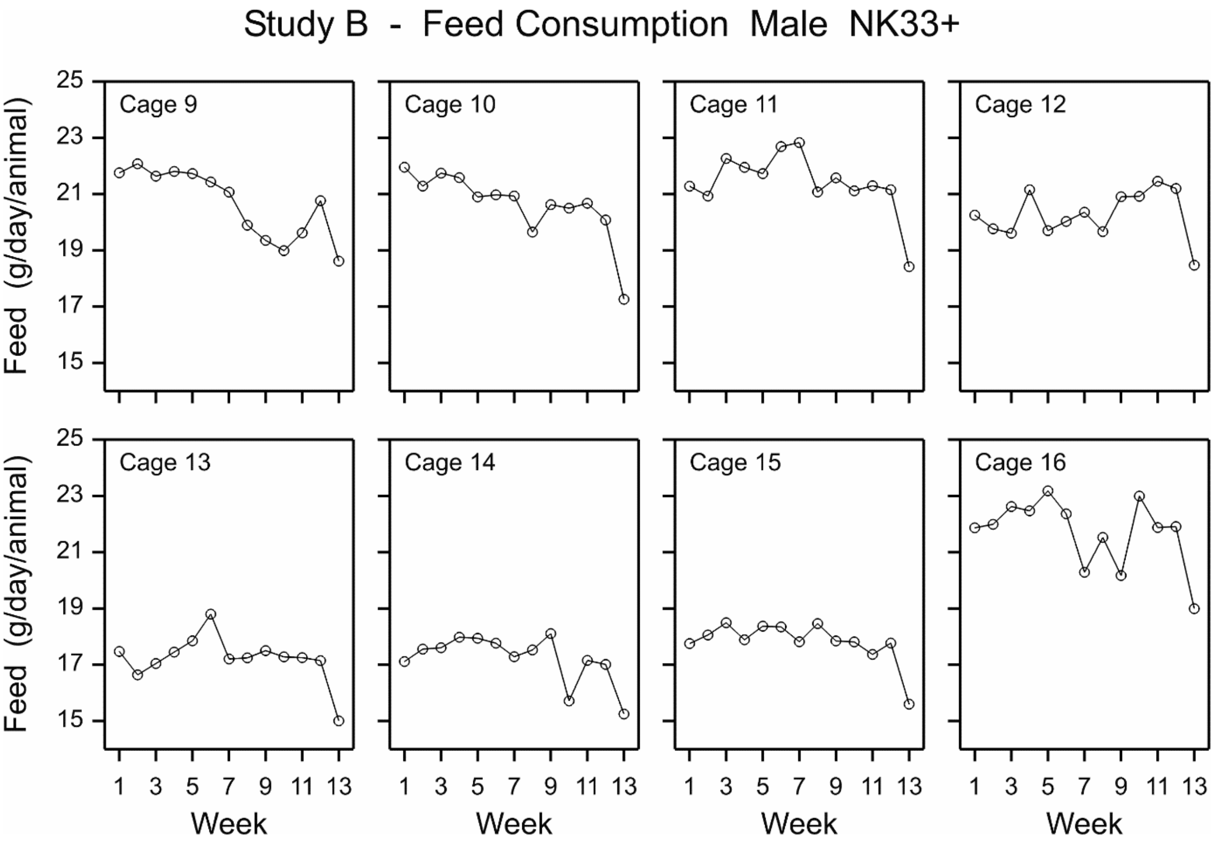
Appendix 3. Feed consumption per cage (continued)



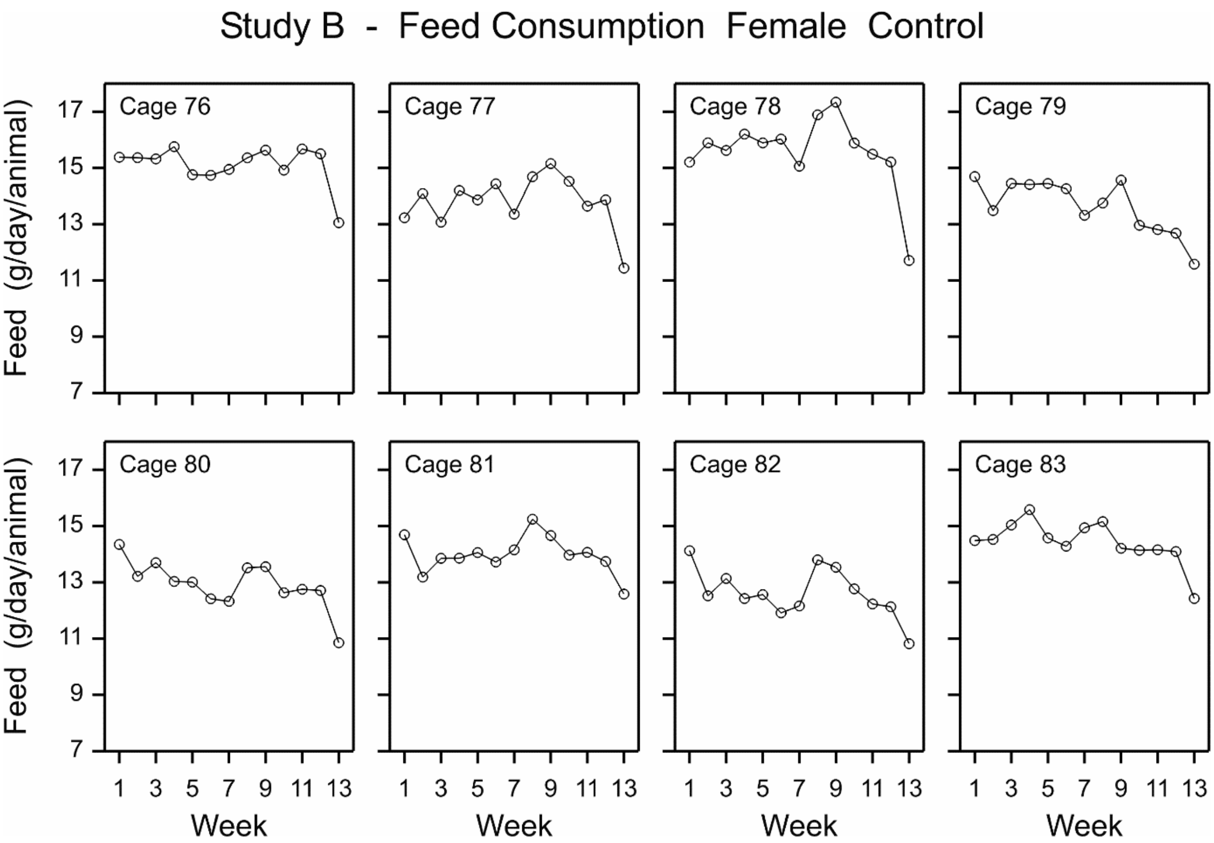
Appendix 3. Feed consumption per cage (continued)



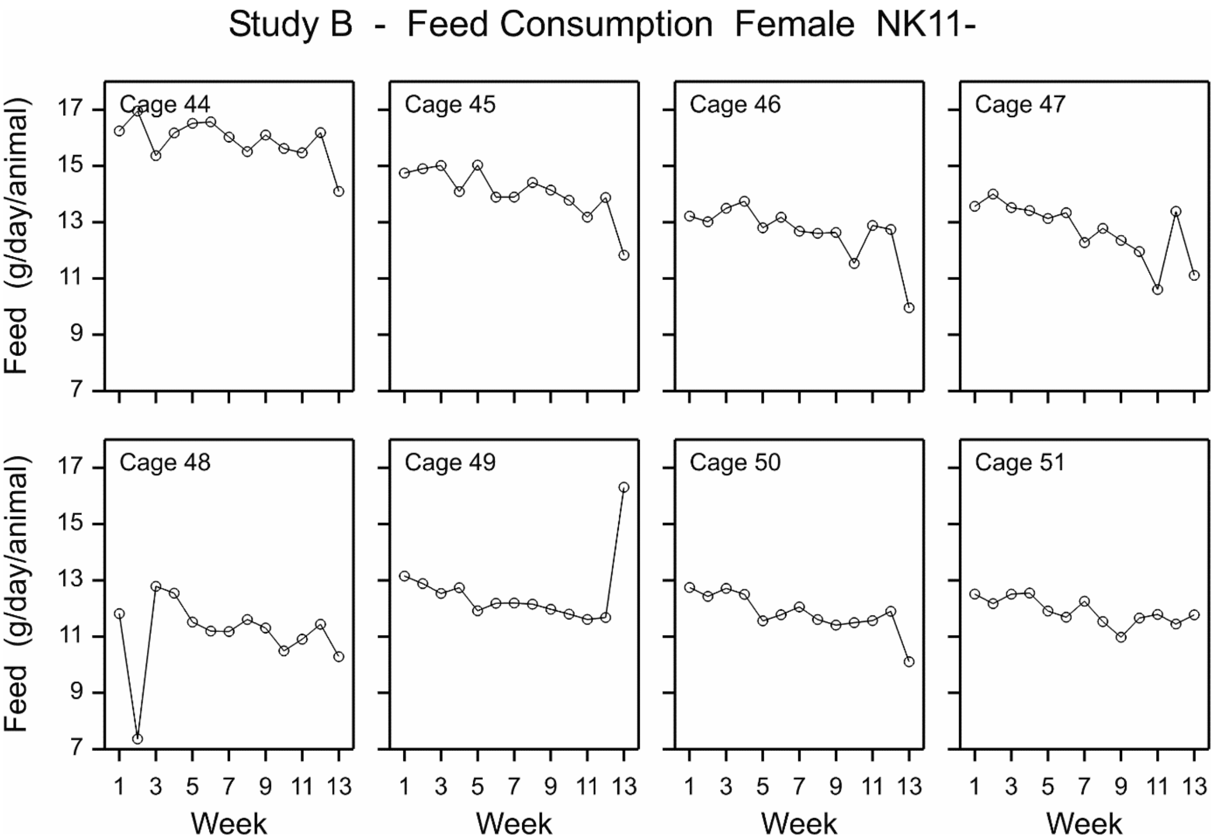
Appendix 3. Feed consumption per cage (continued)



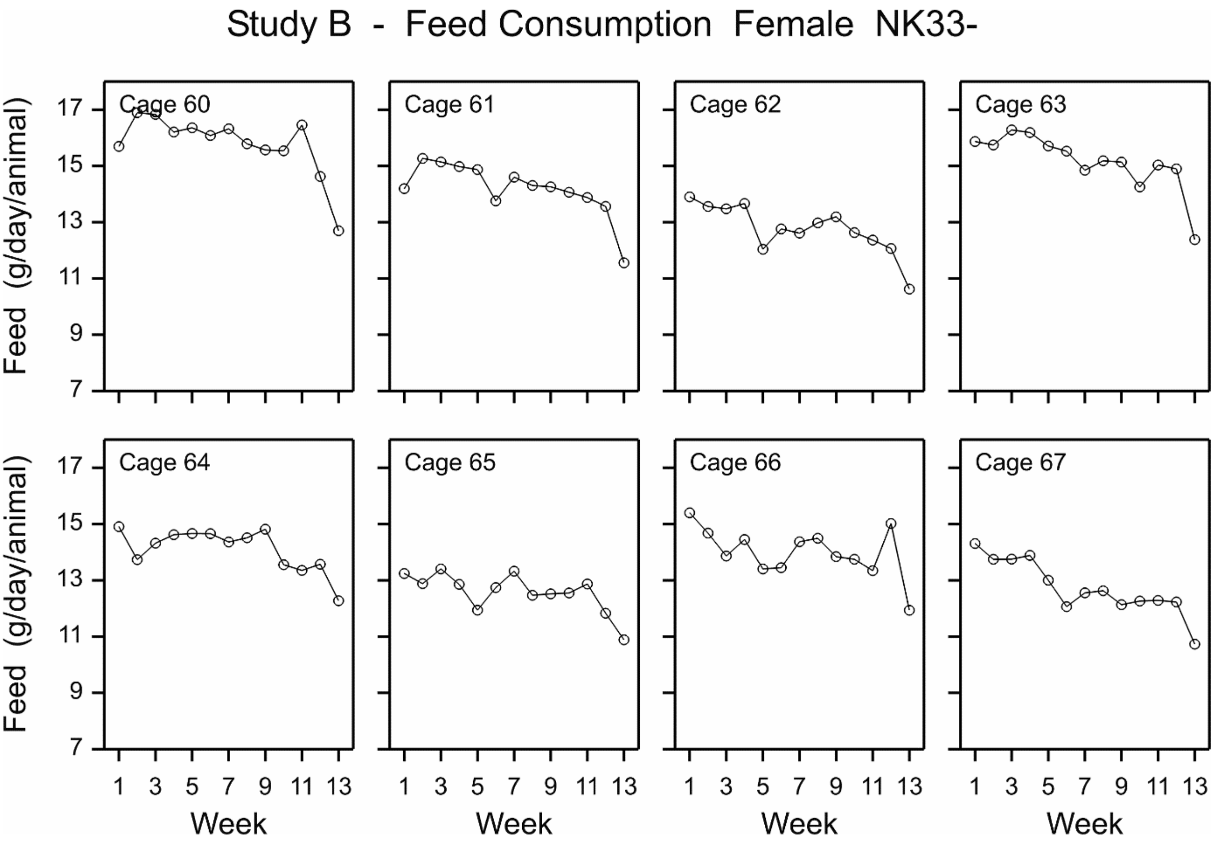
Appendix 3. Feed consumption per cage (continued)



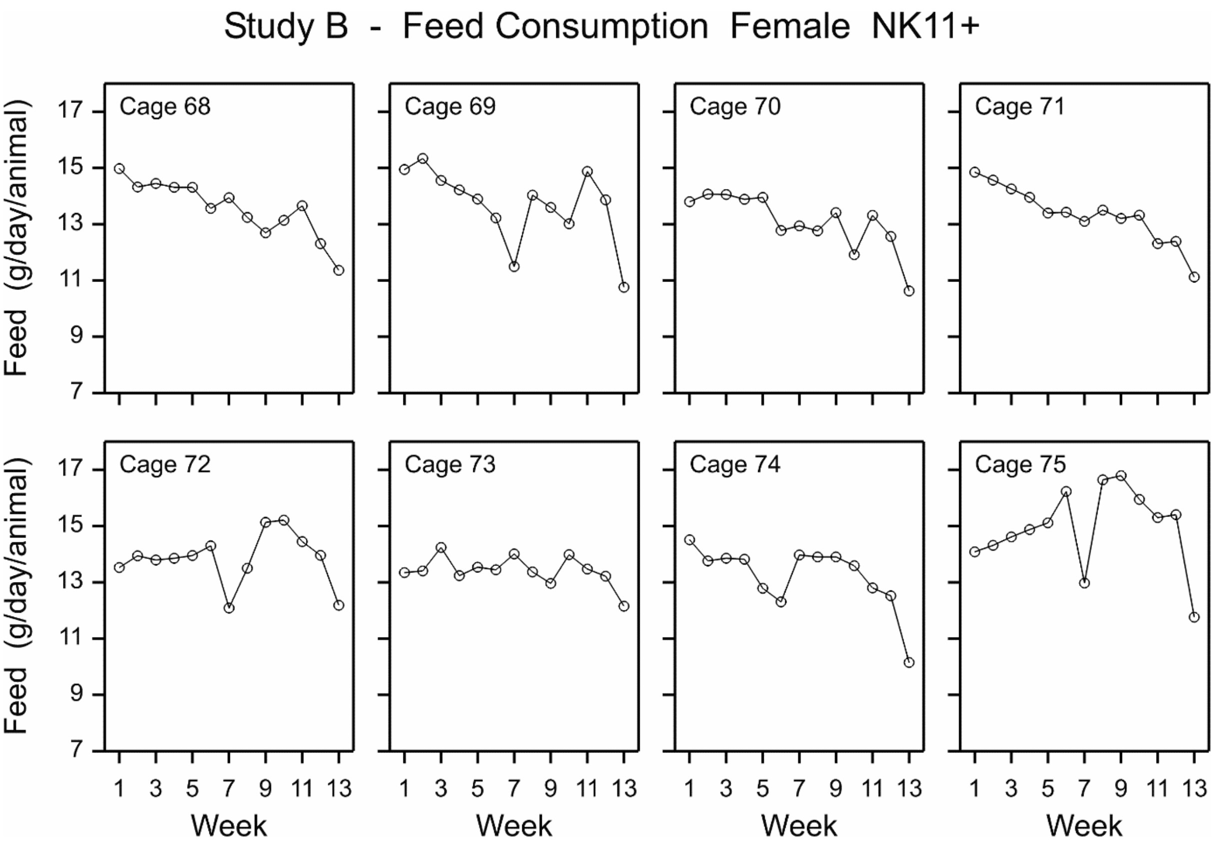
Appendix 3.   Feed consumption per cage (continued)



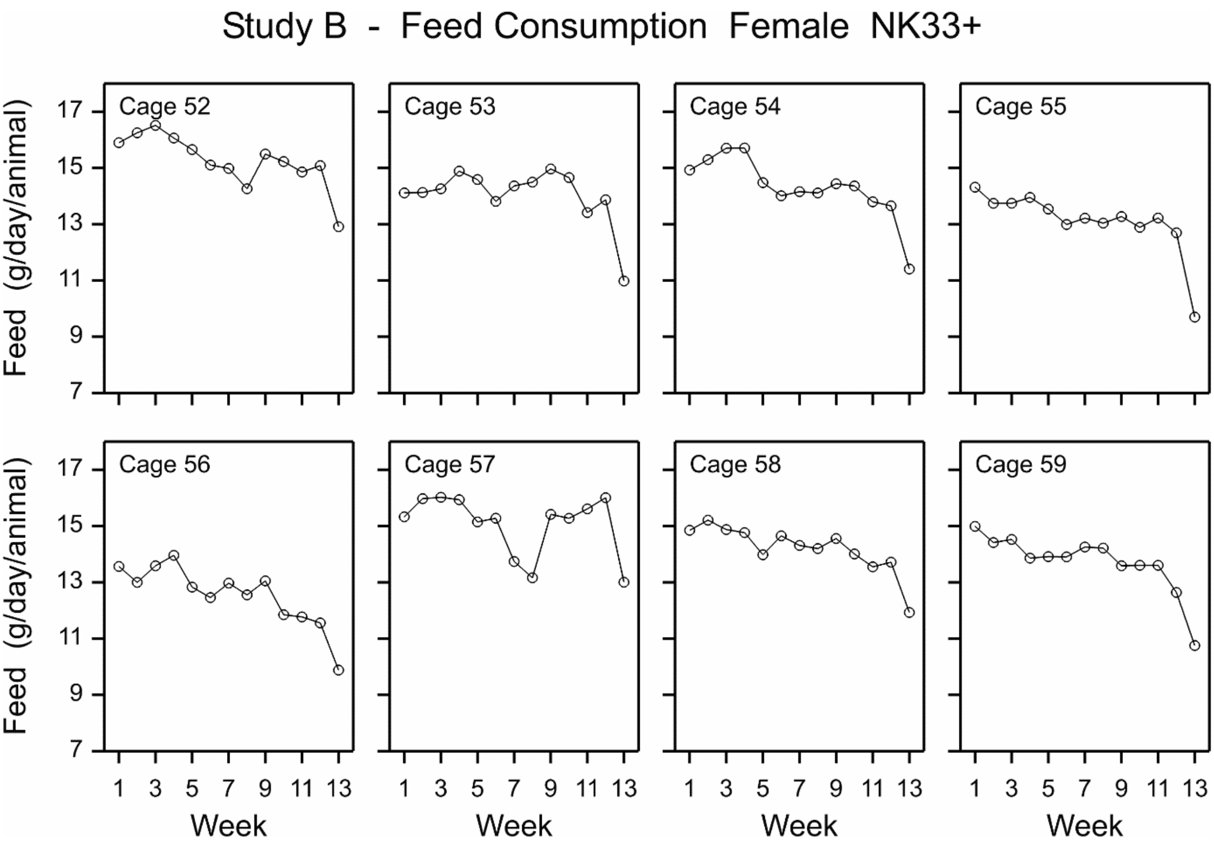
Appendix 3.   Feed consumption per cage (continued)



Appendix 3. Feed consumption per cage (continued)

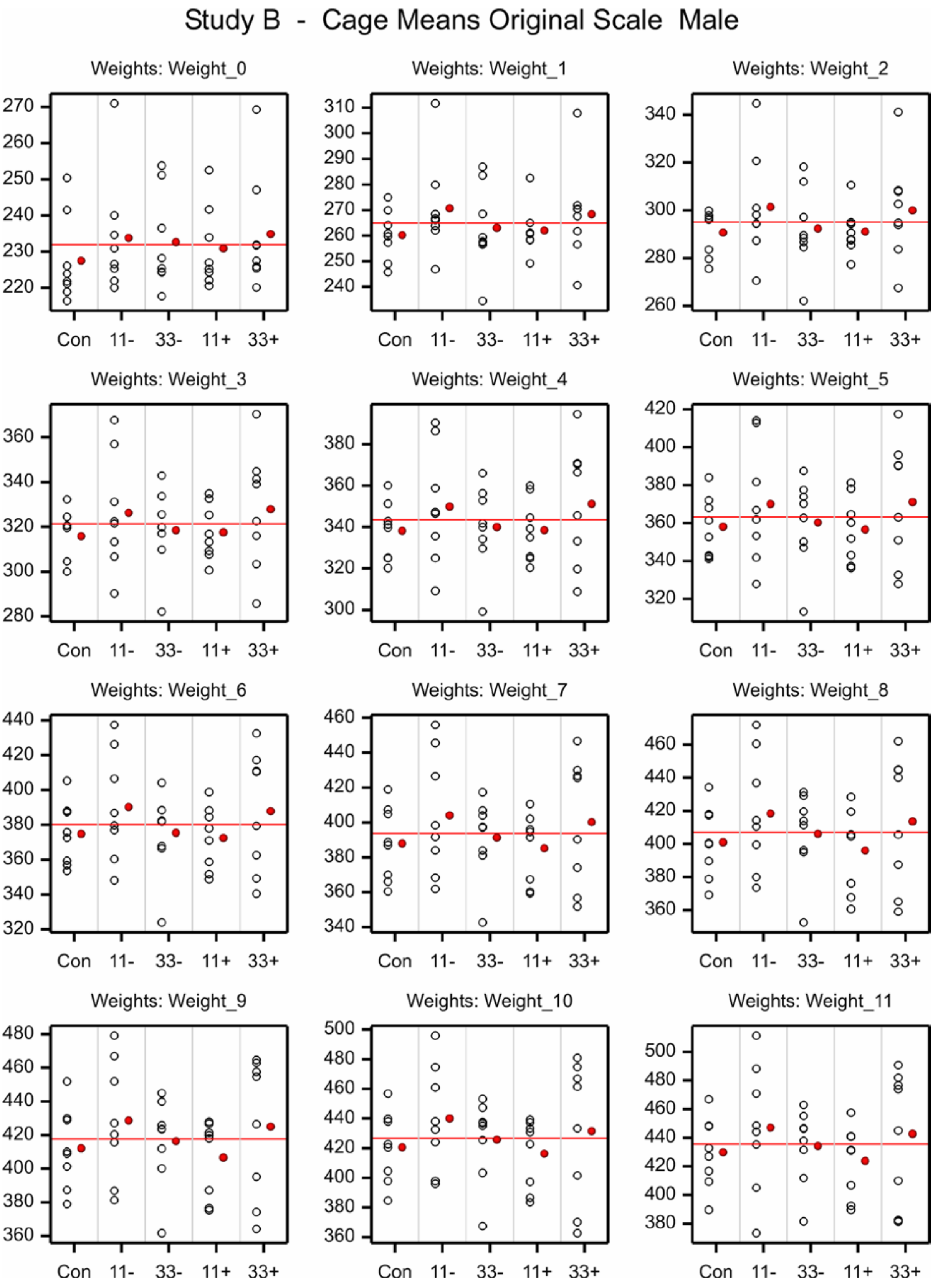


Appendix 3. Feed consumption per cage (continued)



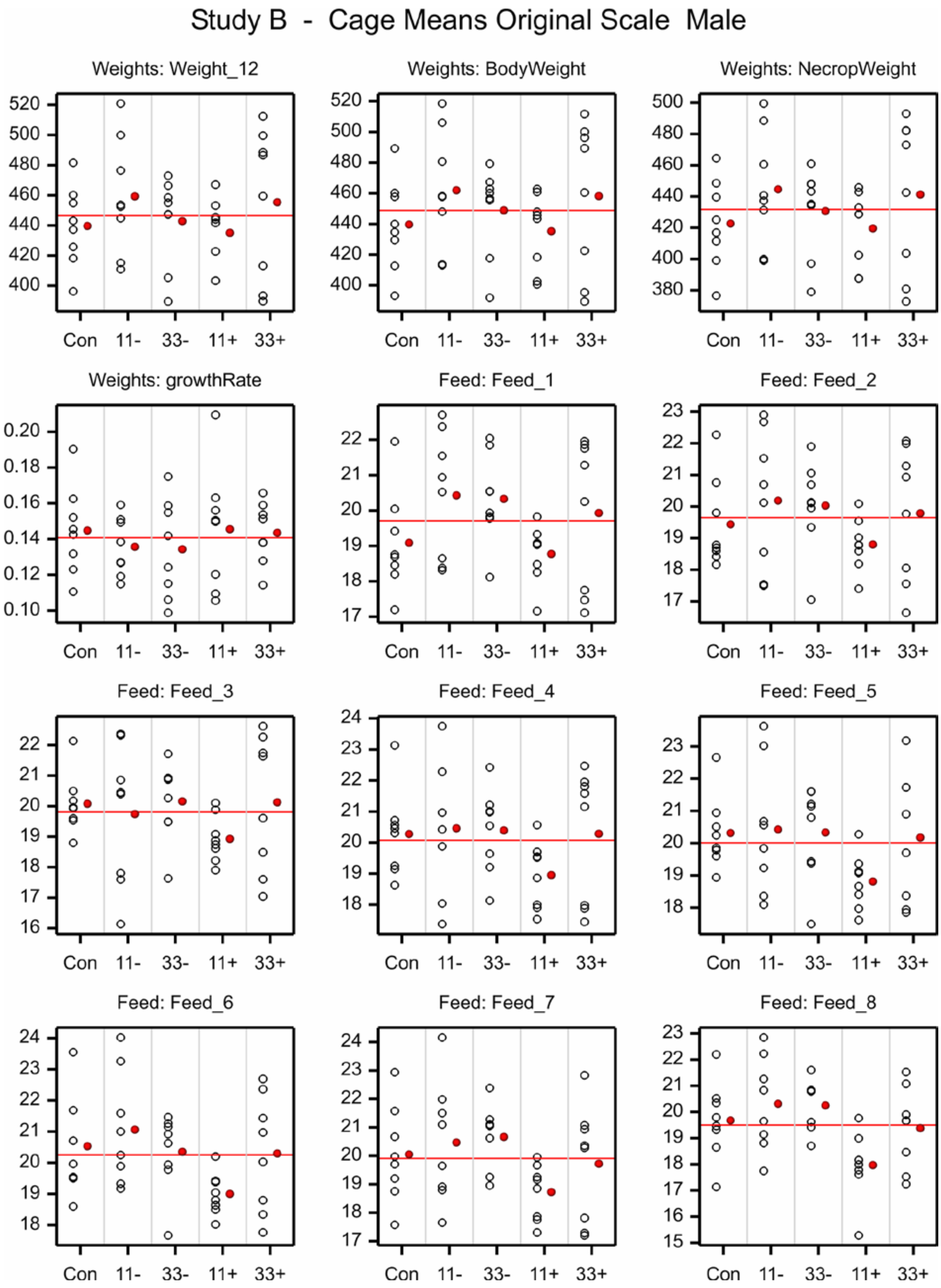
Appendix 4. Graphs of cage means on the original scale

Red symbols denote means for feeding groups while the red line denotes the overall mean.



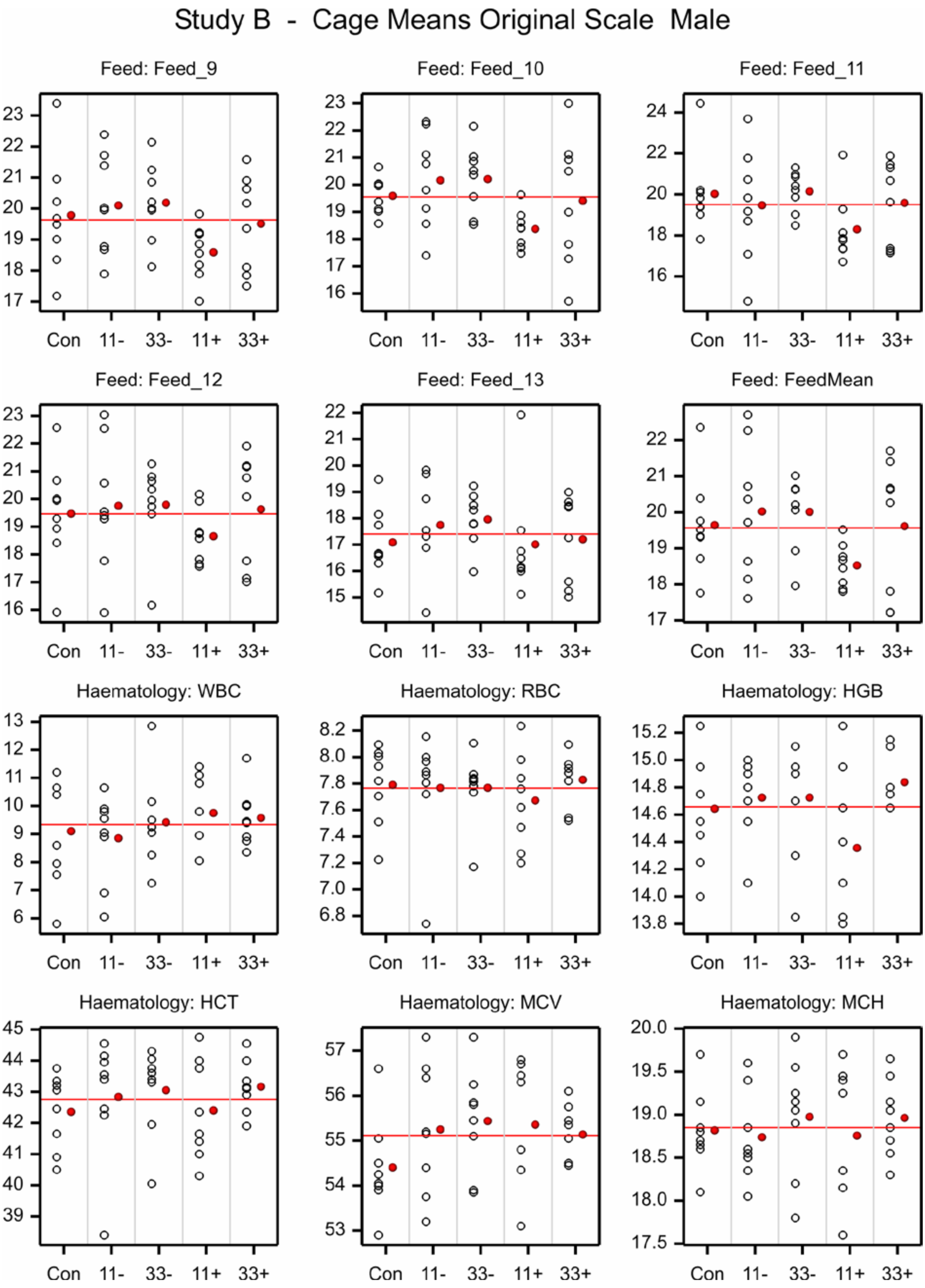
Appendix 4. Graphs of cage means on the original scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



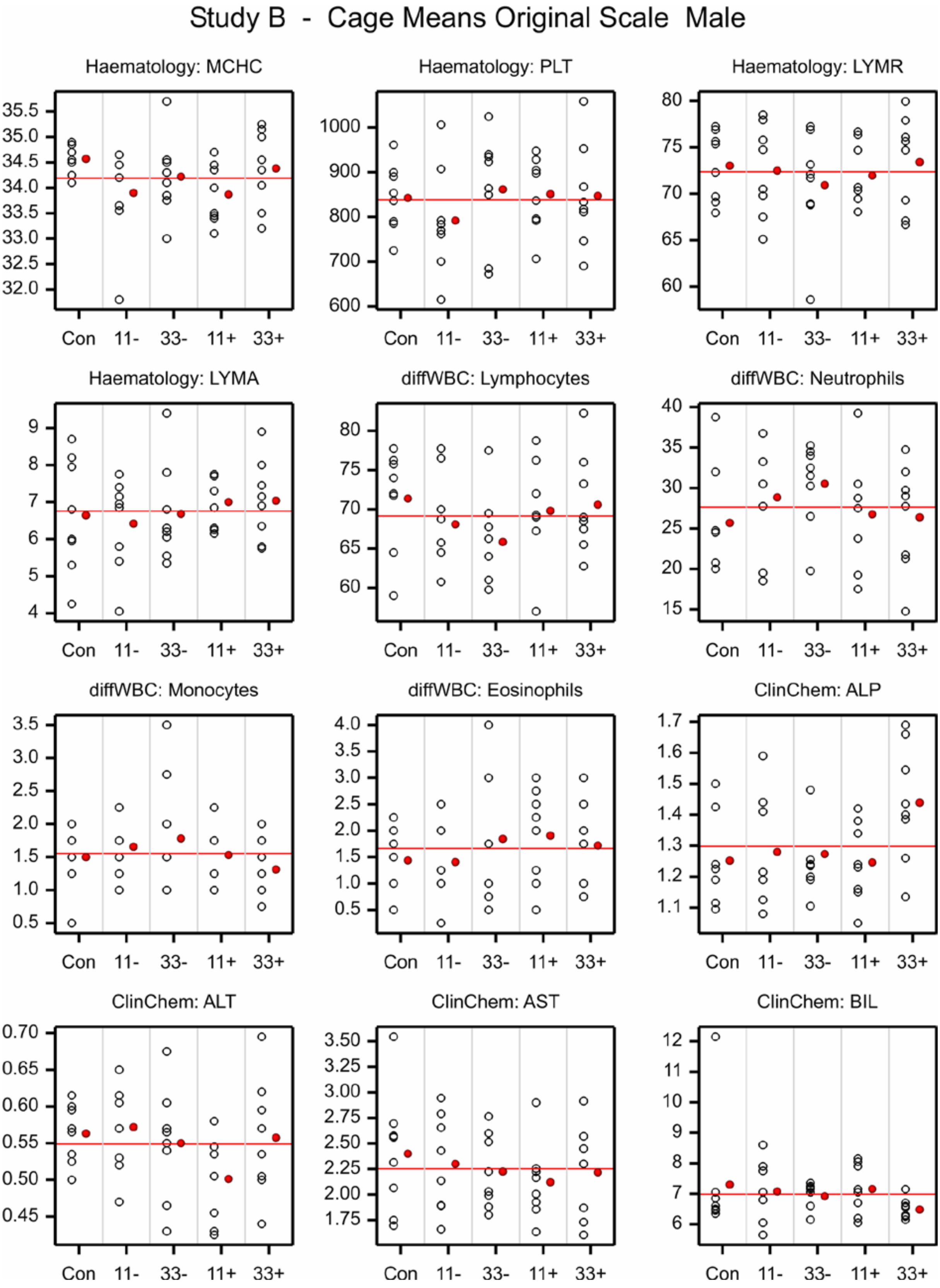
Appendix 4. Graphs of cage means on the original scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



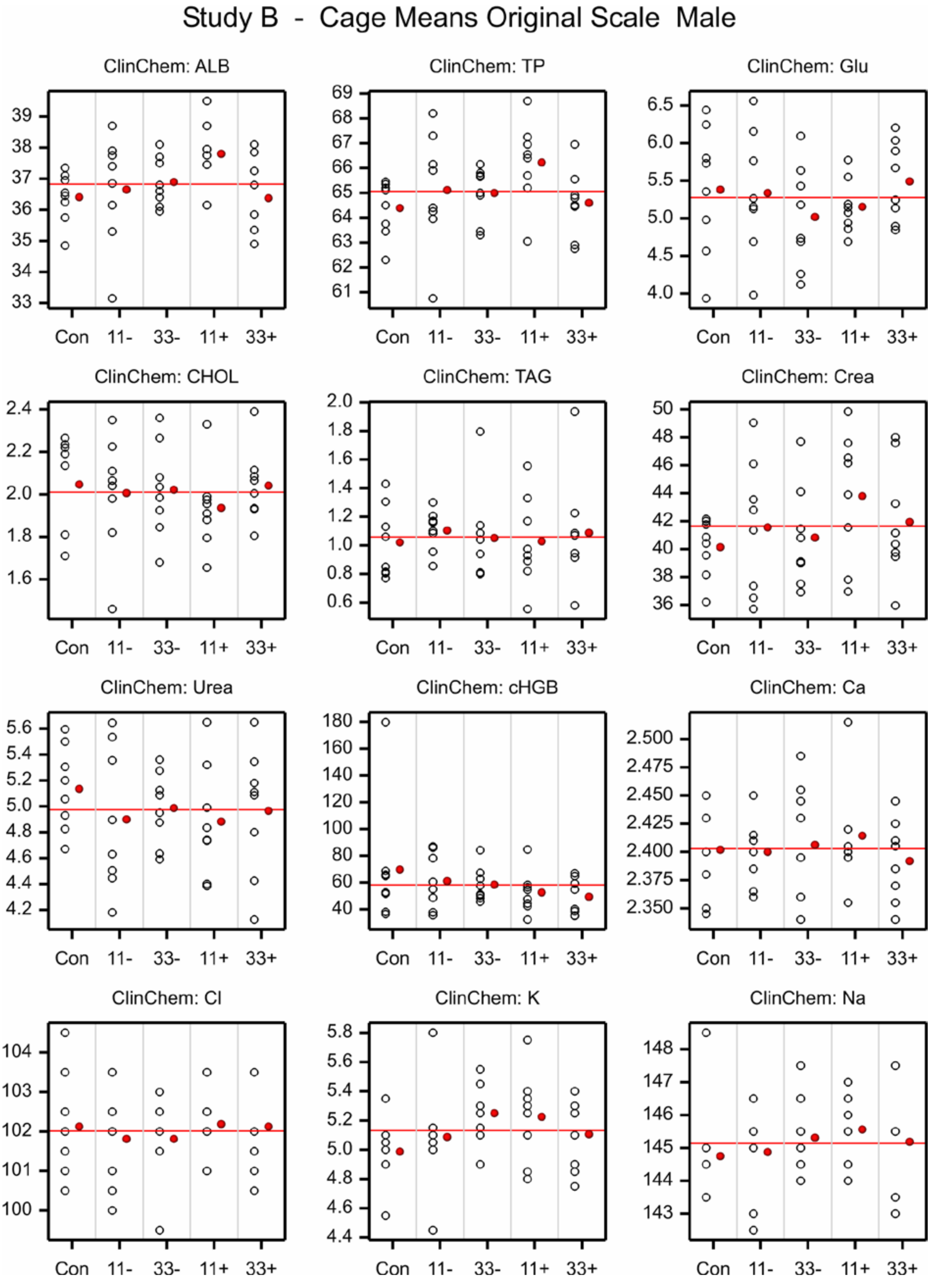
Appendix 4. Graphs of cage means on the original scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



Appendix 4. Graphs of cage means on the original scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



Appendix 4. Graphs of cage means on the original scale (continued)

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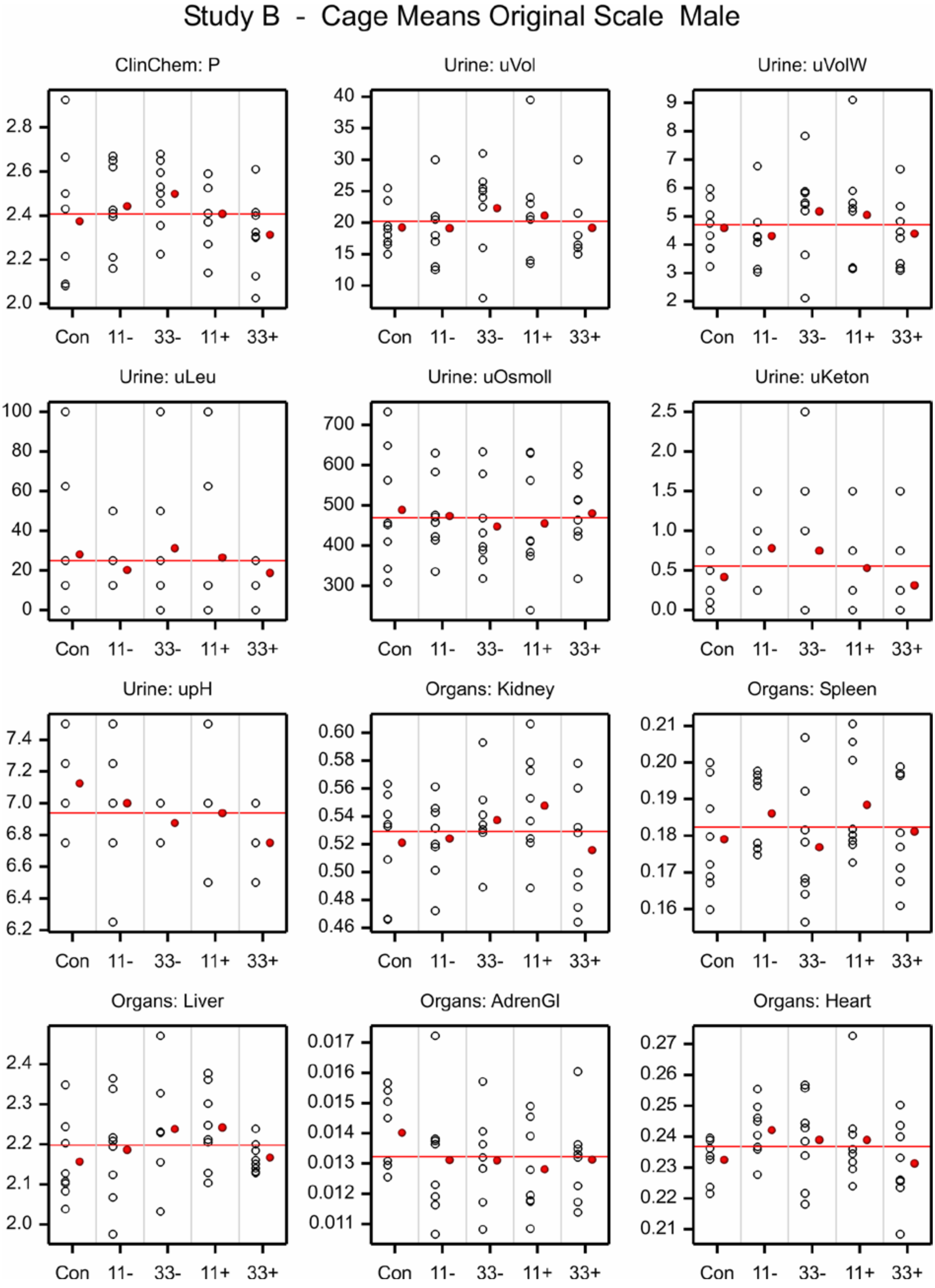
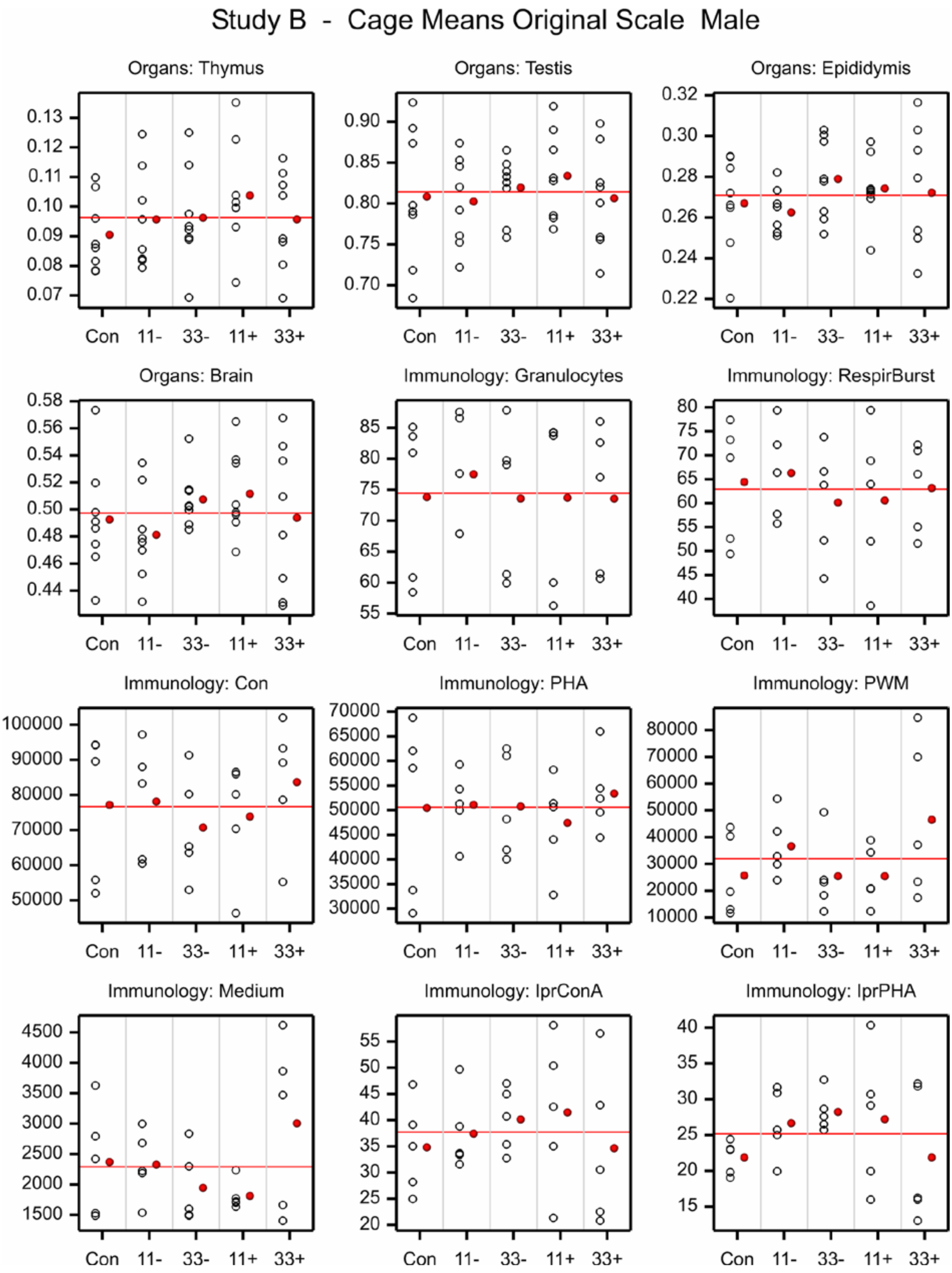


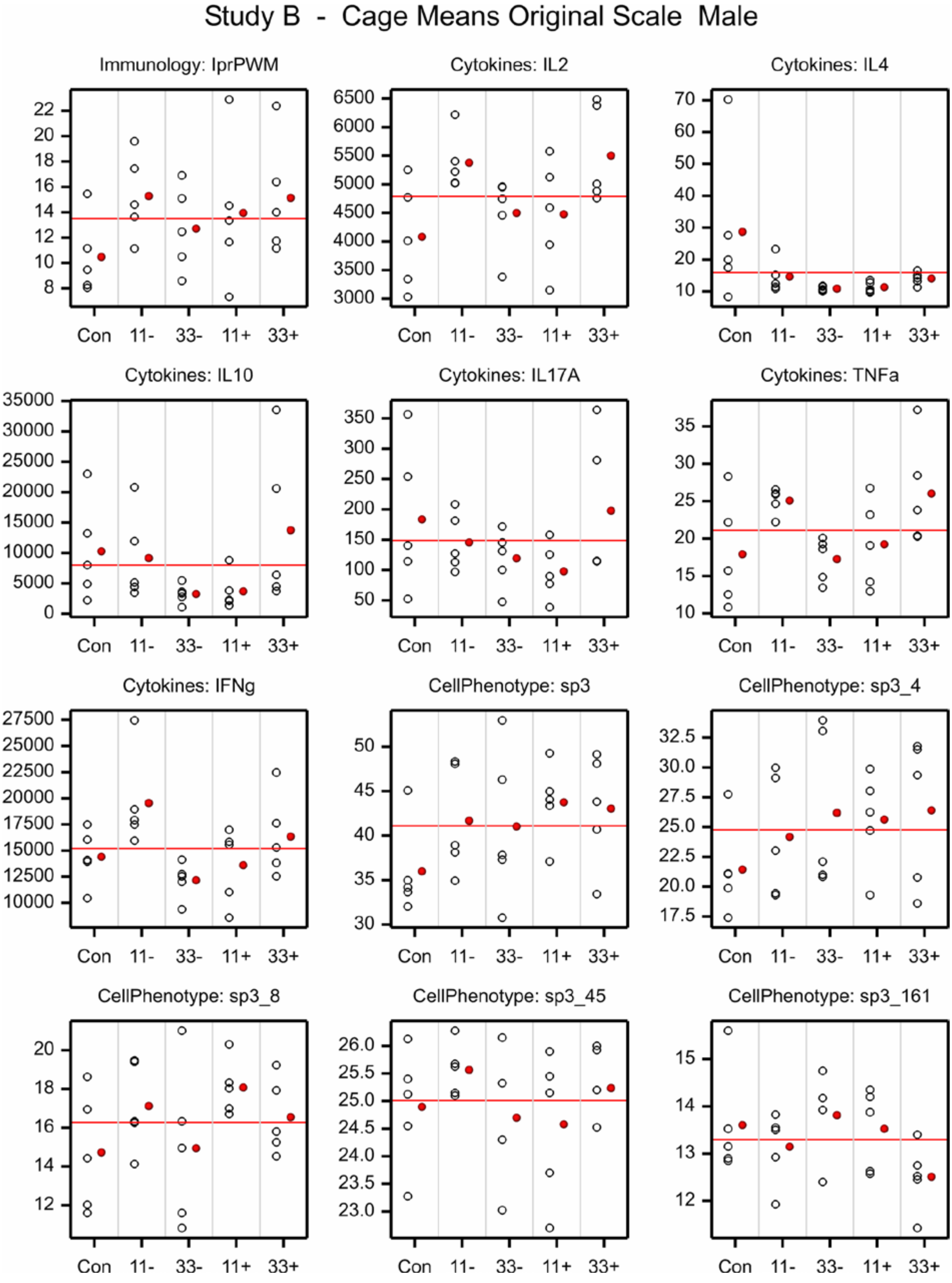
Appendix 4. Graphs of cage means on the original scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



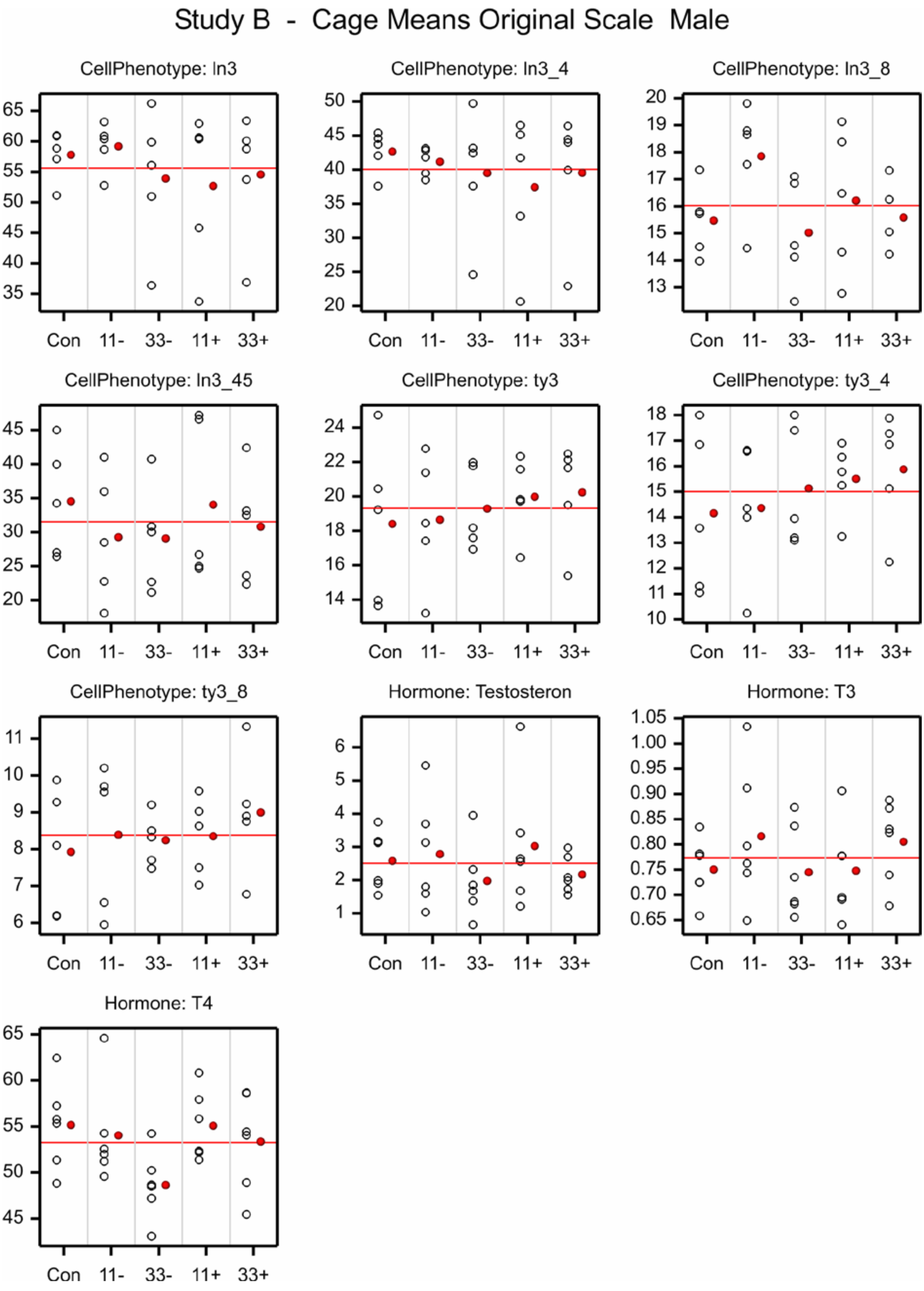
Appendix 4. Graphs of cage means on the original scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



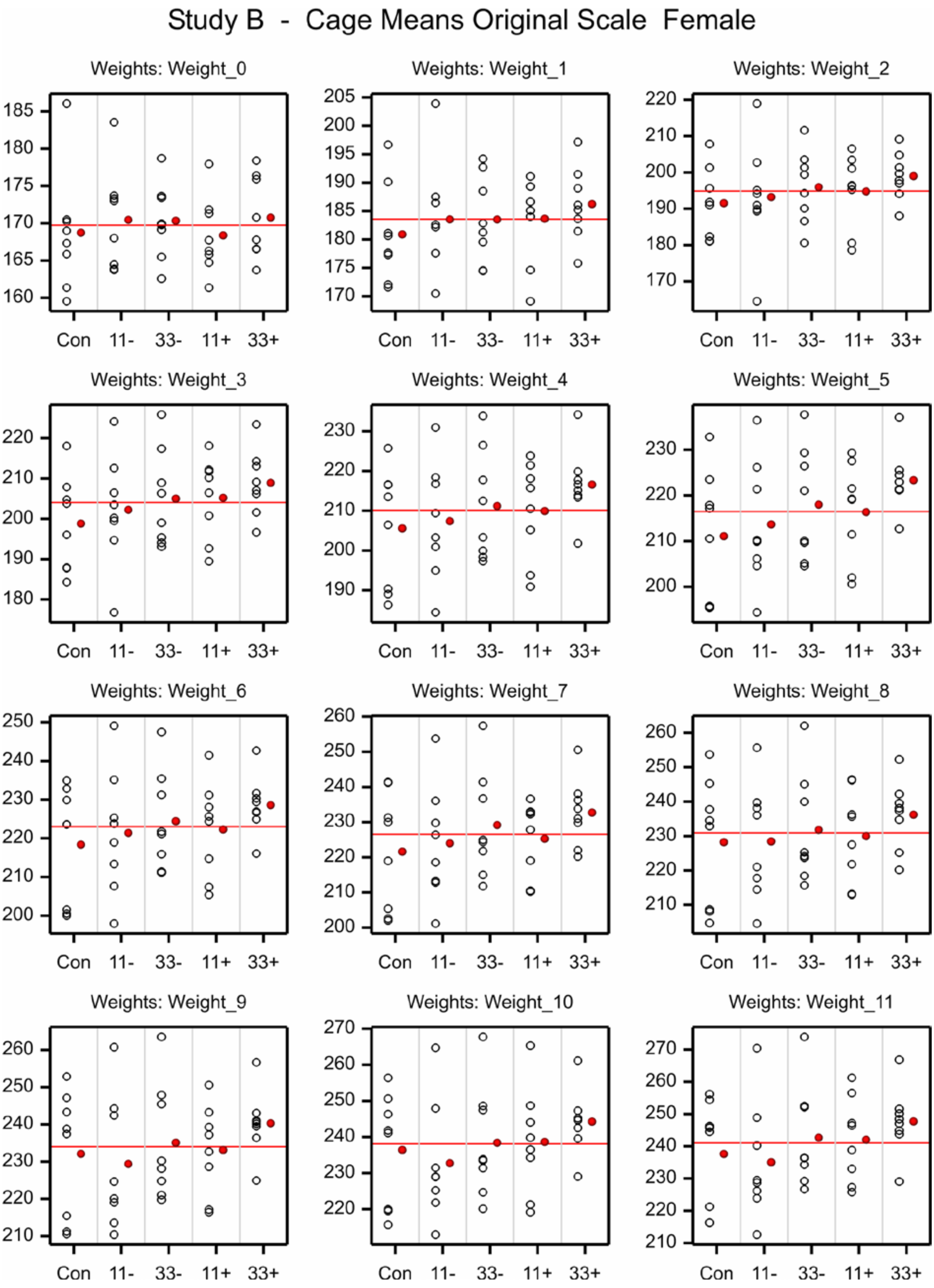
Appendix 4. Graphs of cage means on the original scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



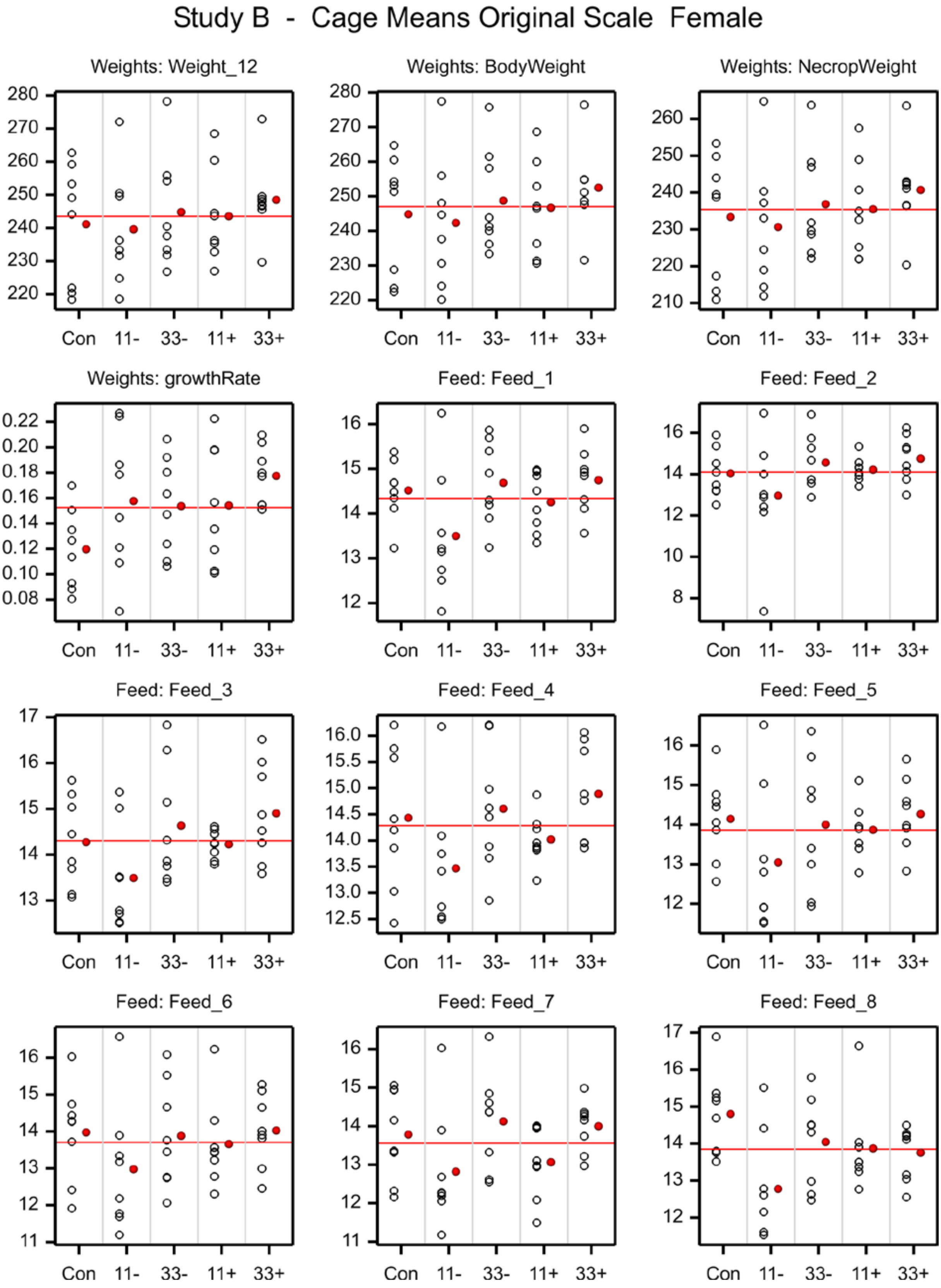
Appendix 4. Graphs of cage means on the original scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



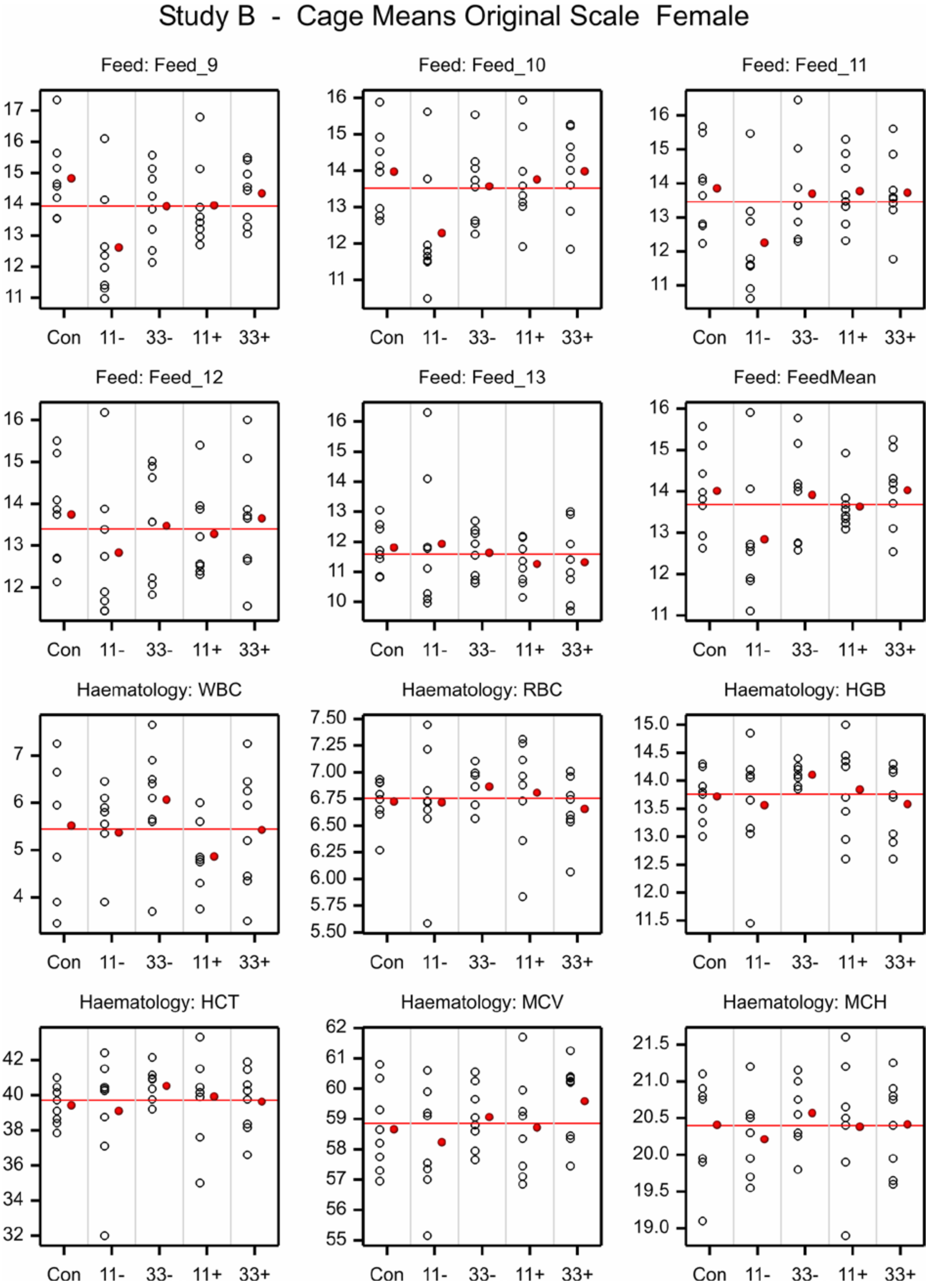
Appendix 4. Graphs of cage means on the original scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



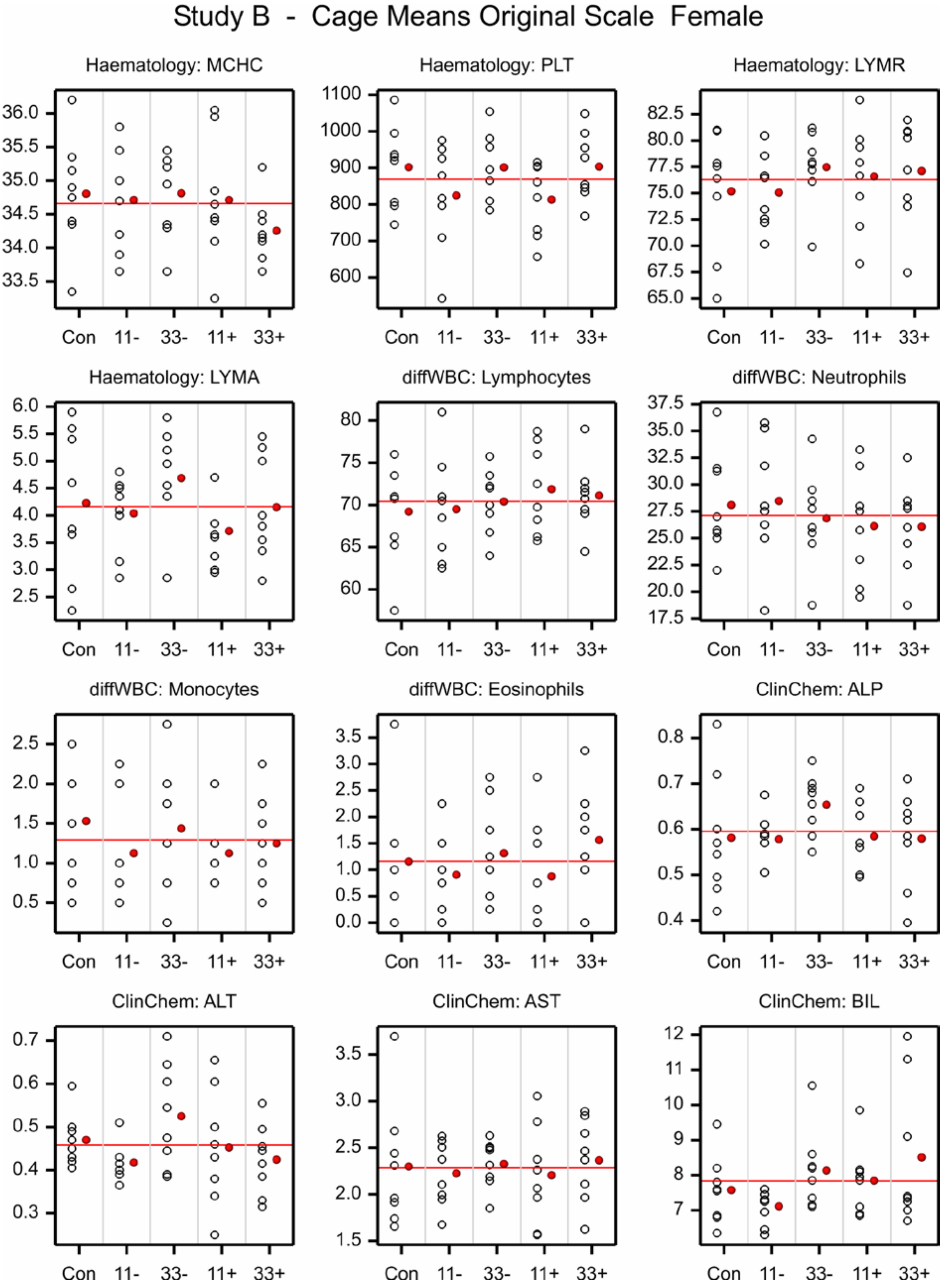
Appendix 4. Graphs of cage means on the original scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



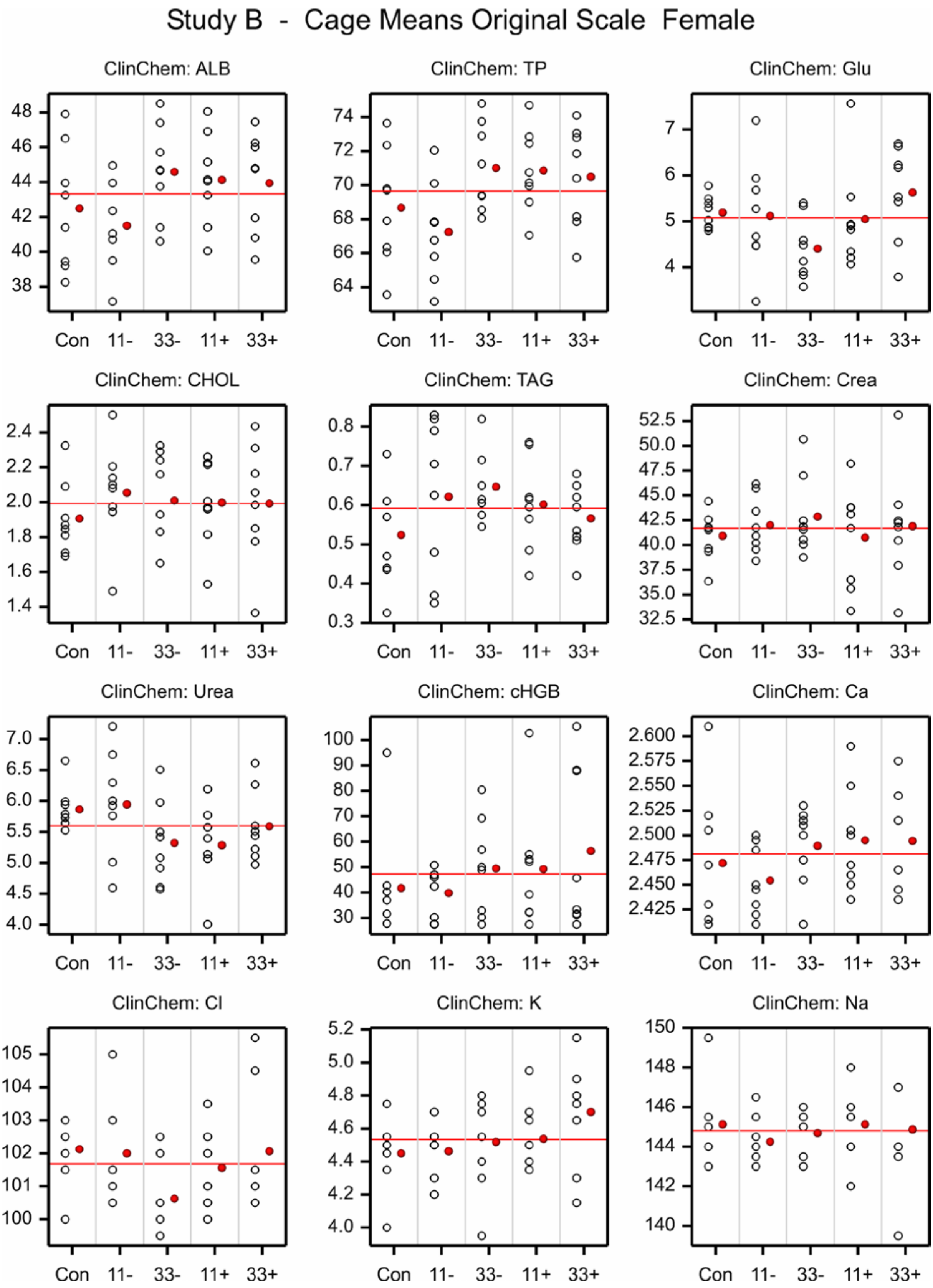
Appendix 4. Graphs of cage means on the original scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



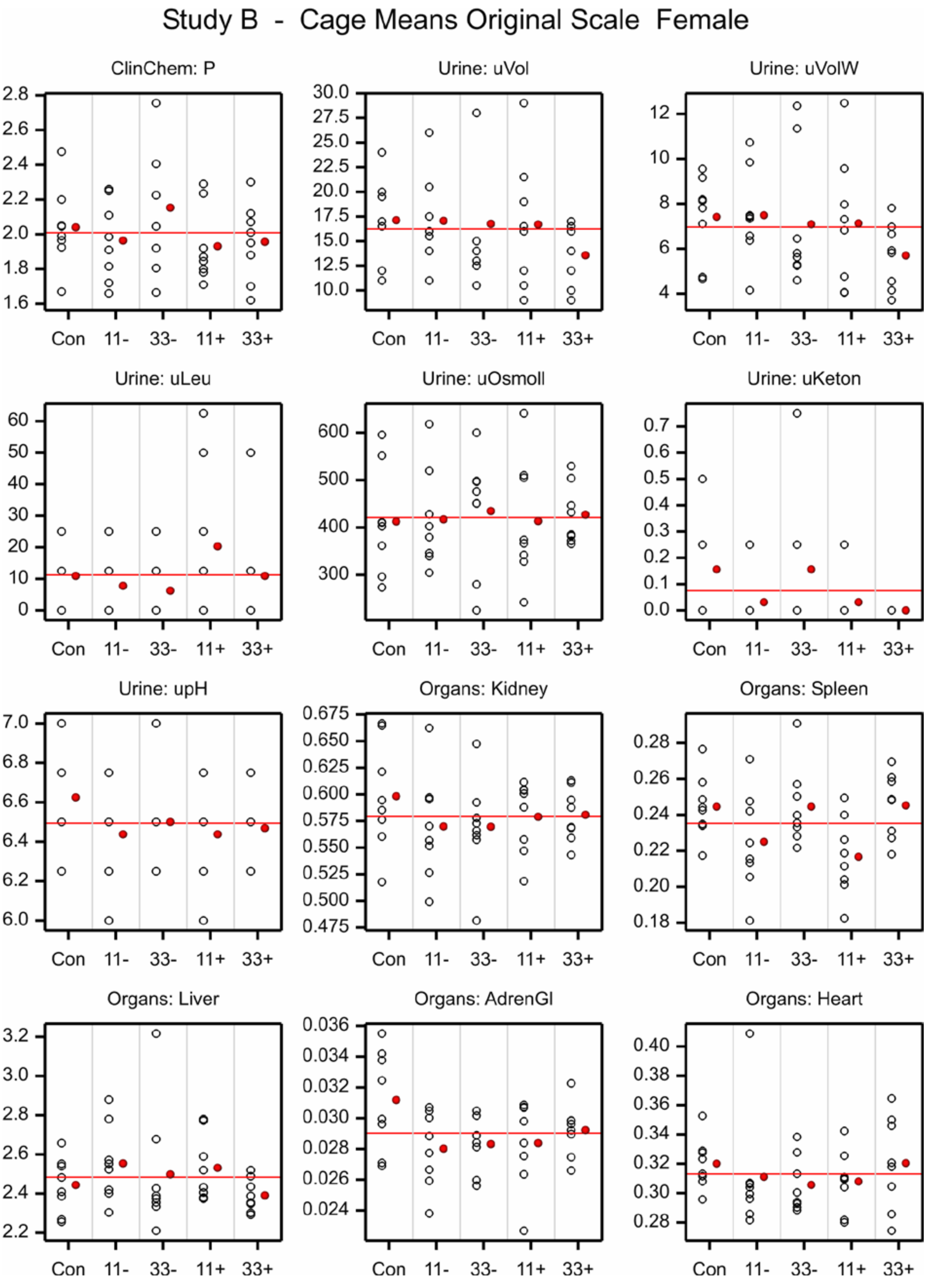
Appendix 4. Graphs of cage means on the original scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



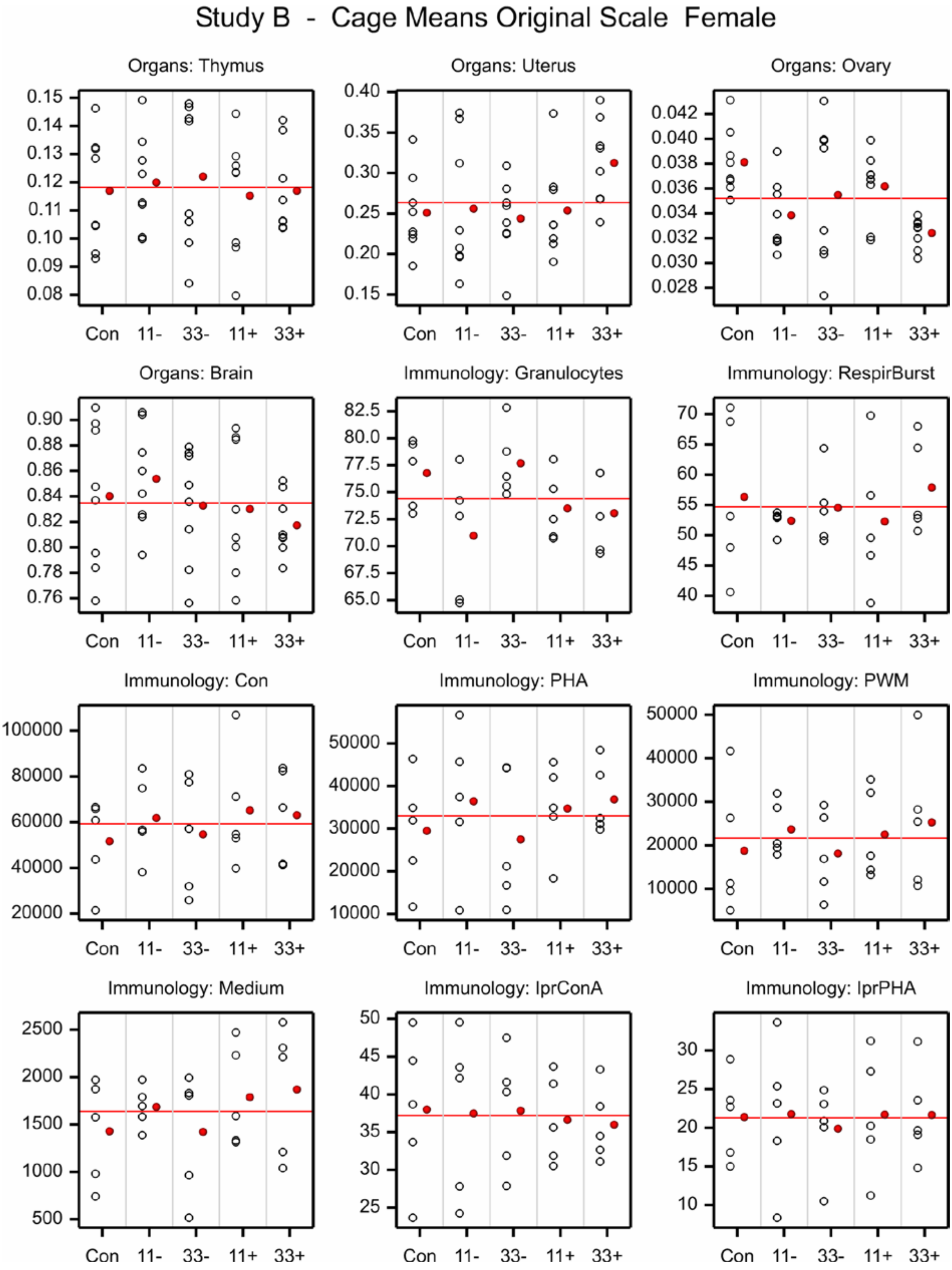
Appendix 4. Graphs of cage means on the original scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



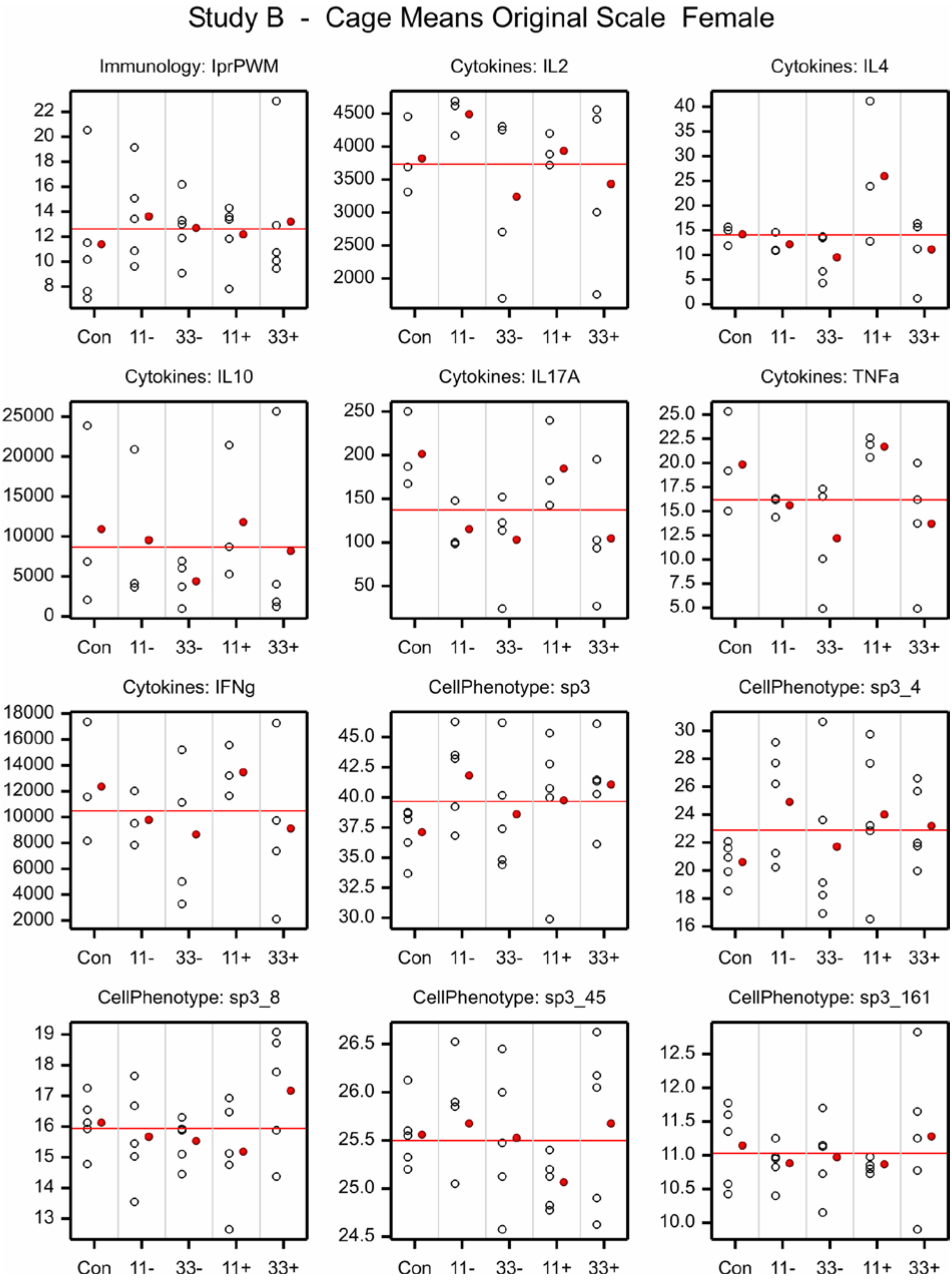
Appendix 4. Graphs of cage means on the original scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



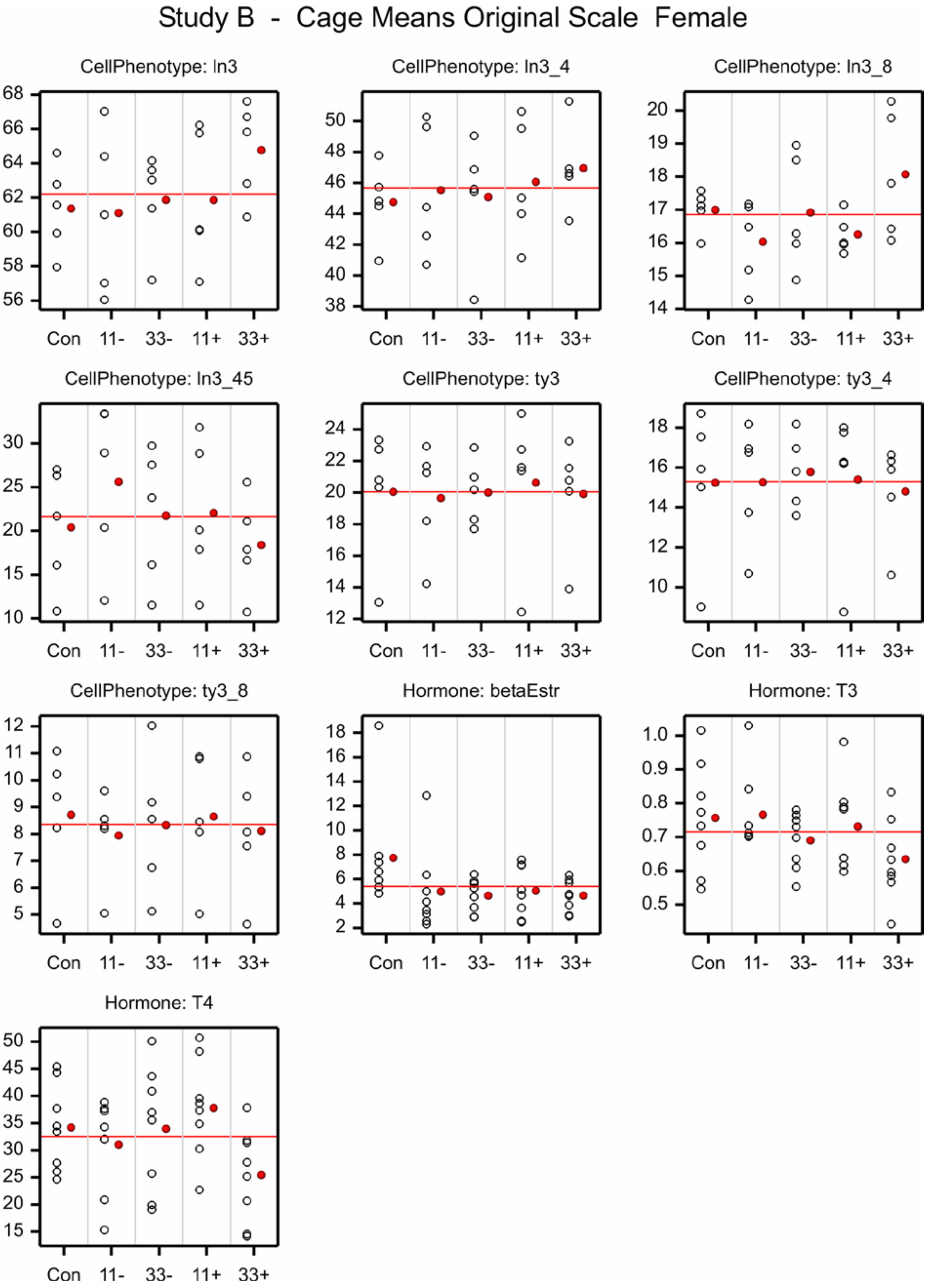
Appendix 4. Graphs of cage means on the original scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



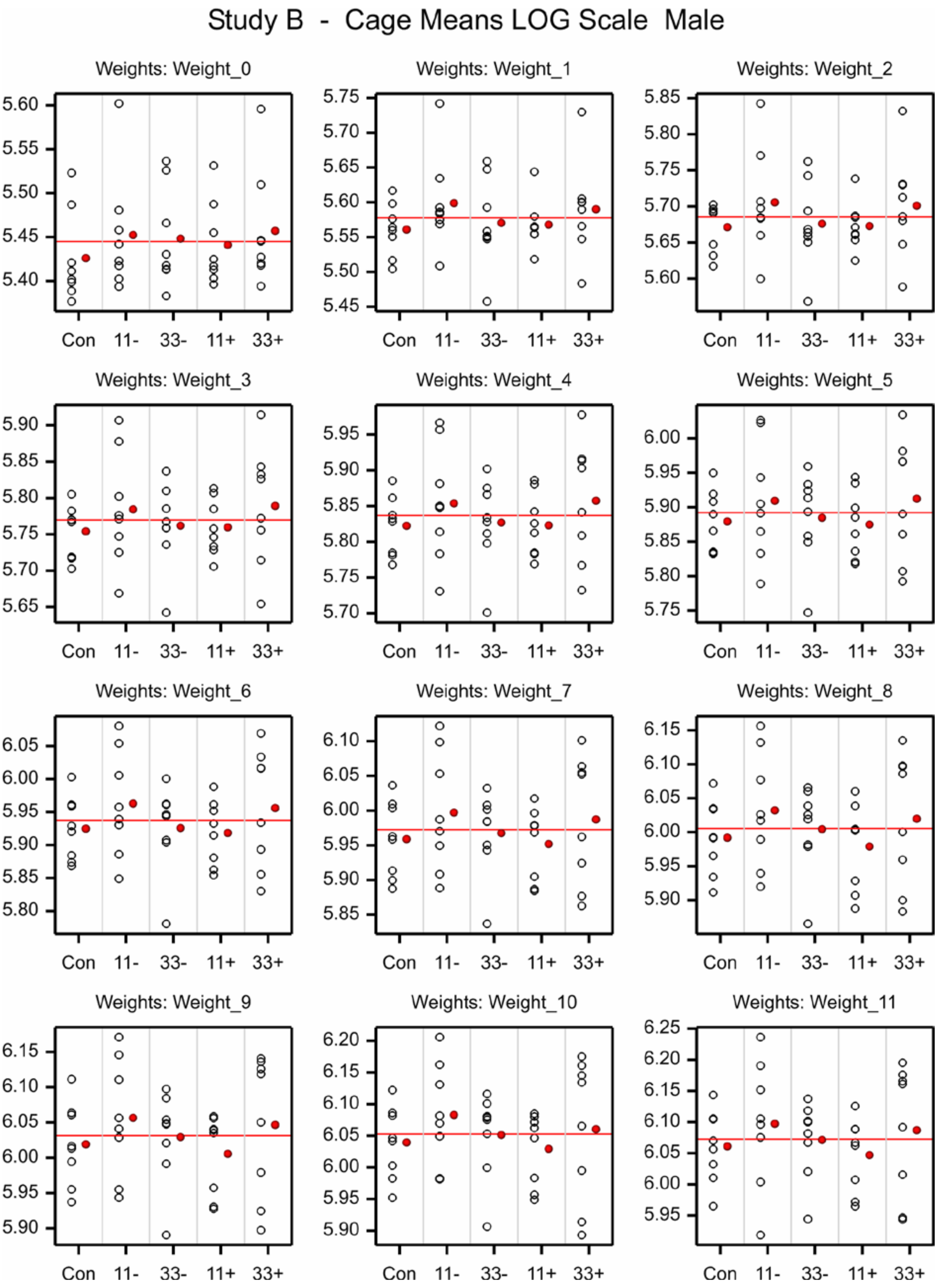
Appendix 4. Graphs of cage means on the original scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



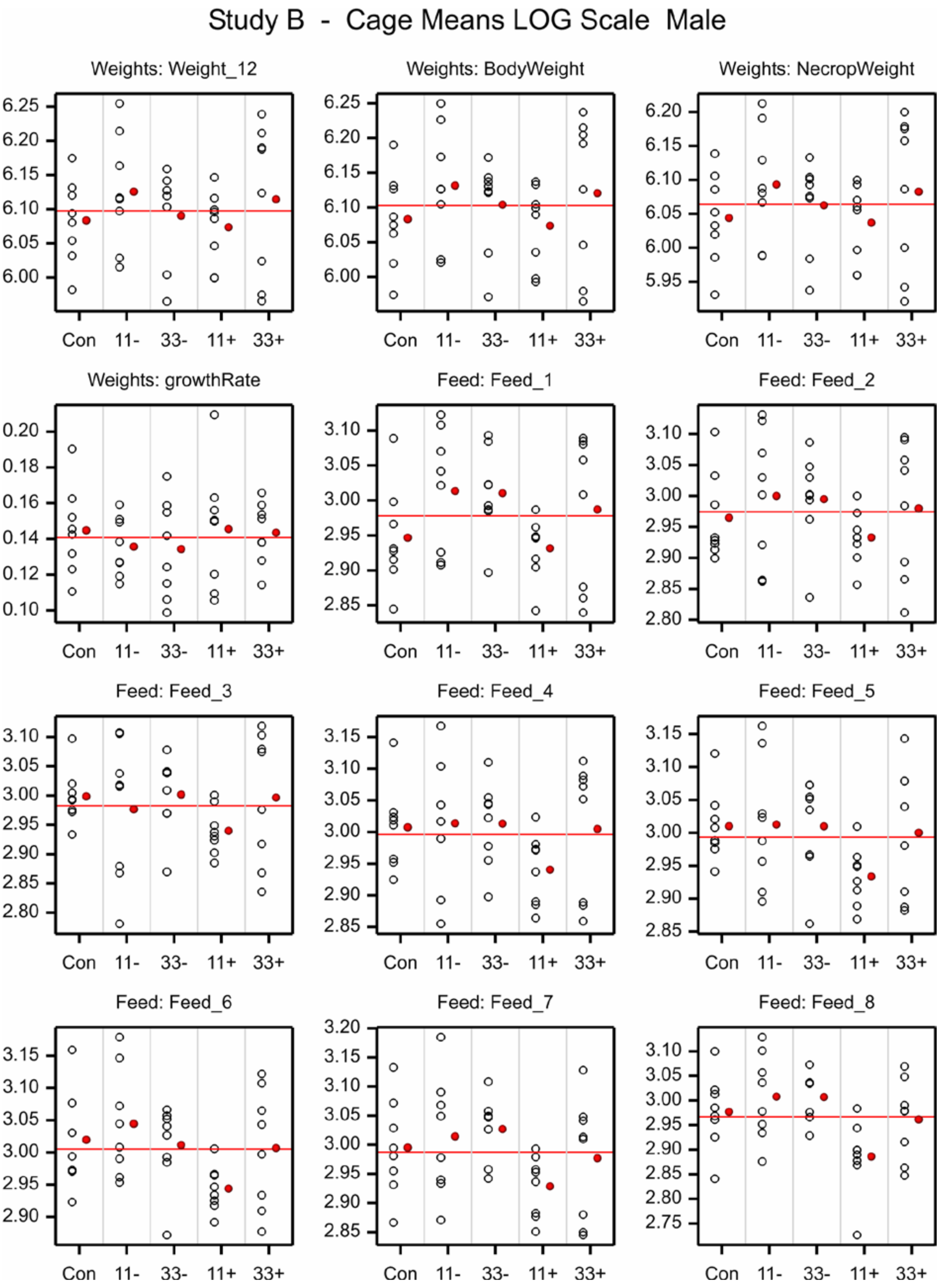
Appendix 5. Graphs of cage means on the log scale

Red symbols denote means for feeding groups while the red line denotes the overall mean.



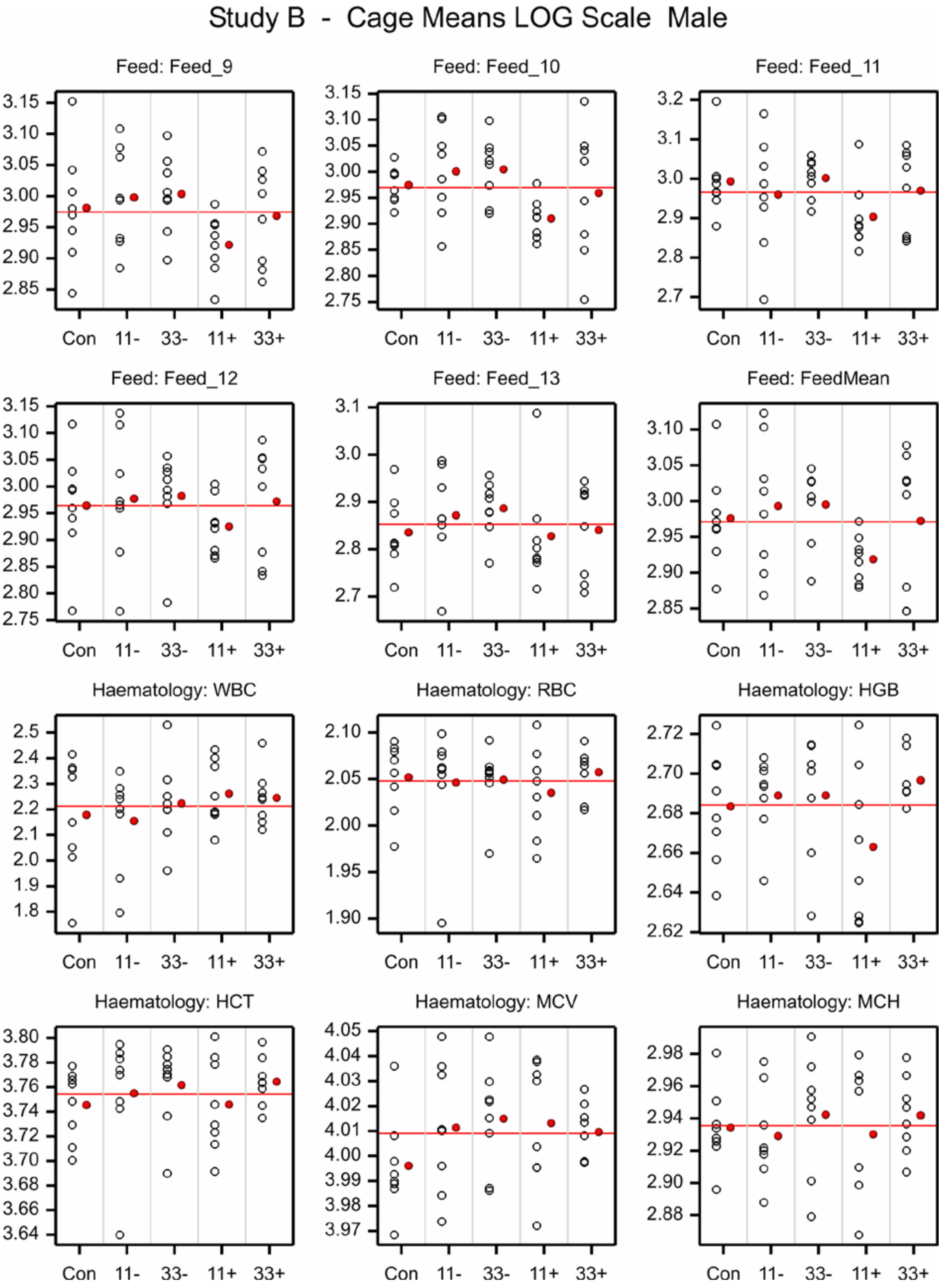
Appendix 5. Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



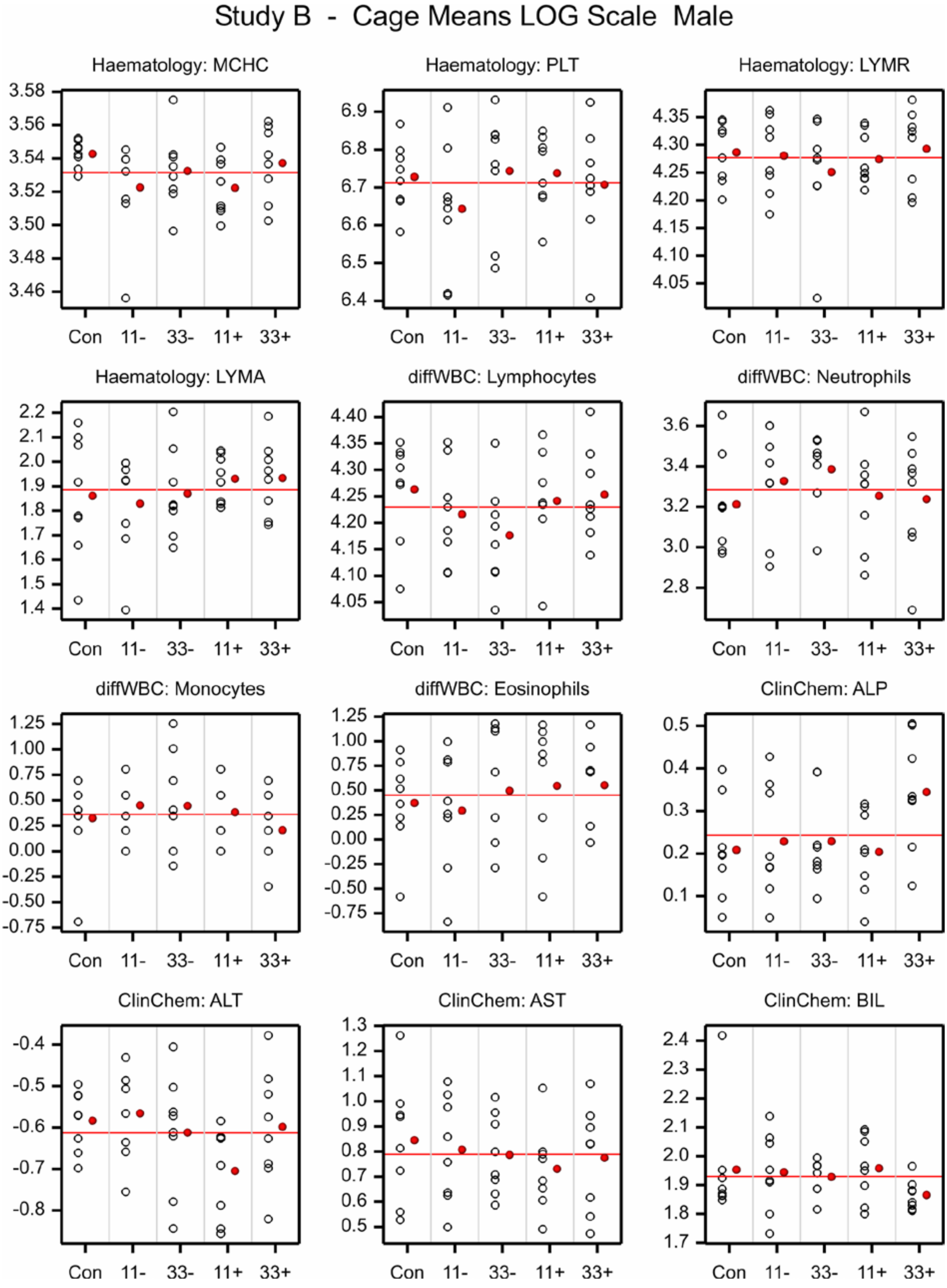
Appendix 5. Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



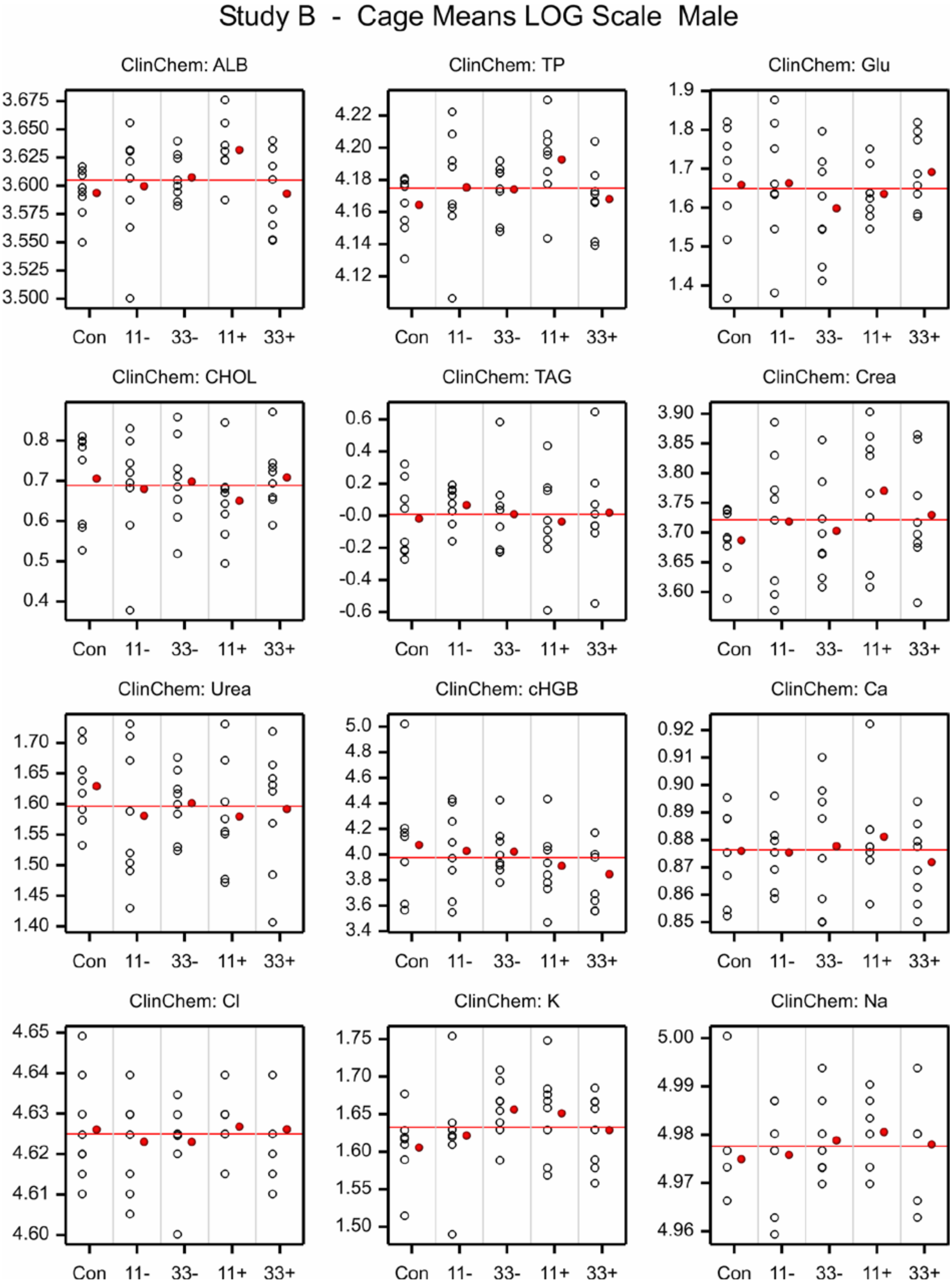
Appendix 5. Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



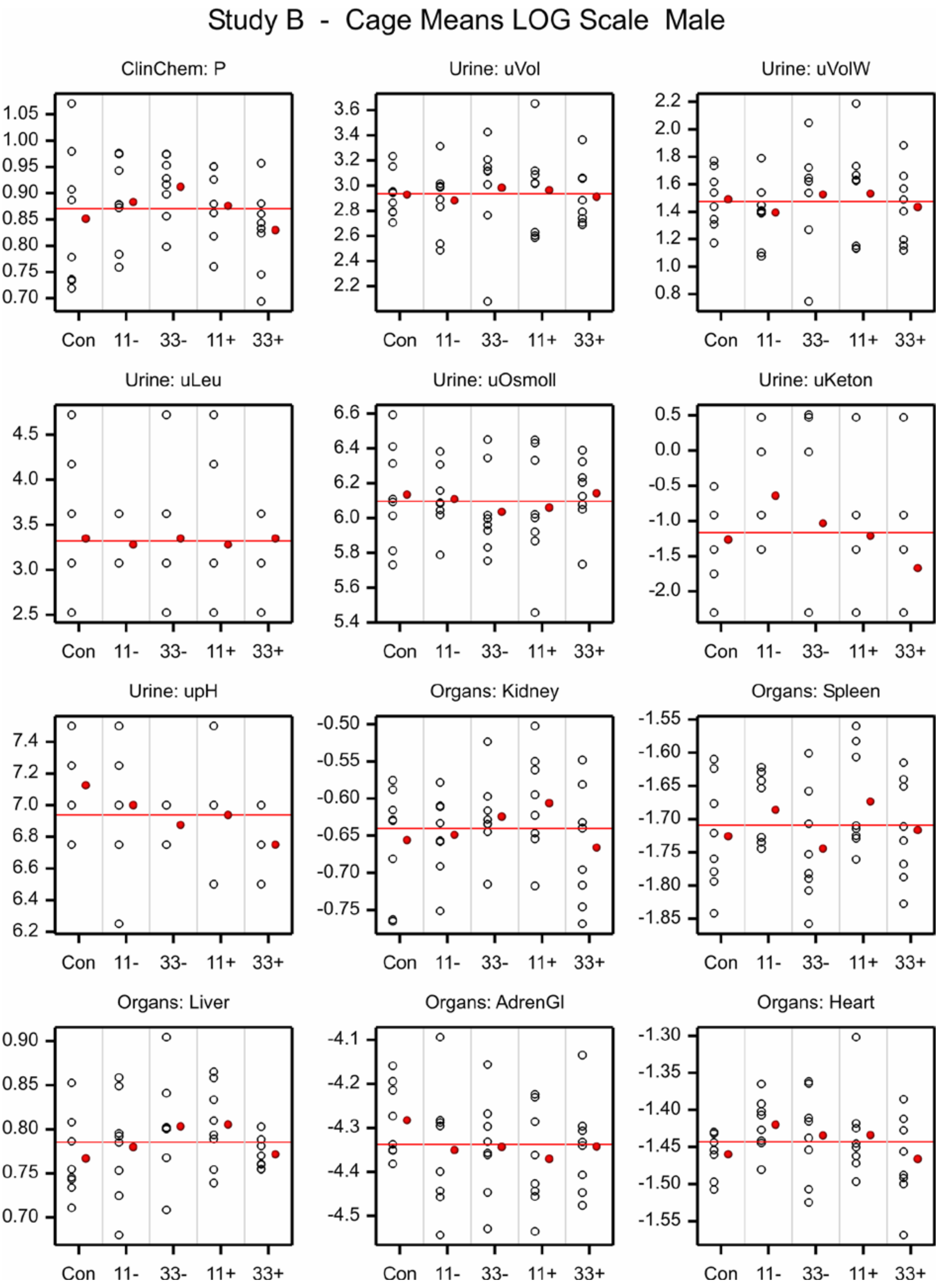
Appendix 5.   Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



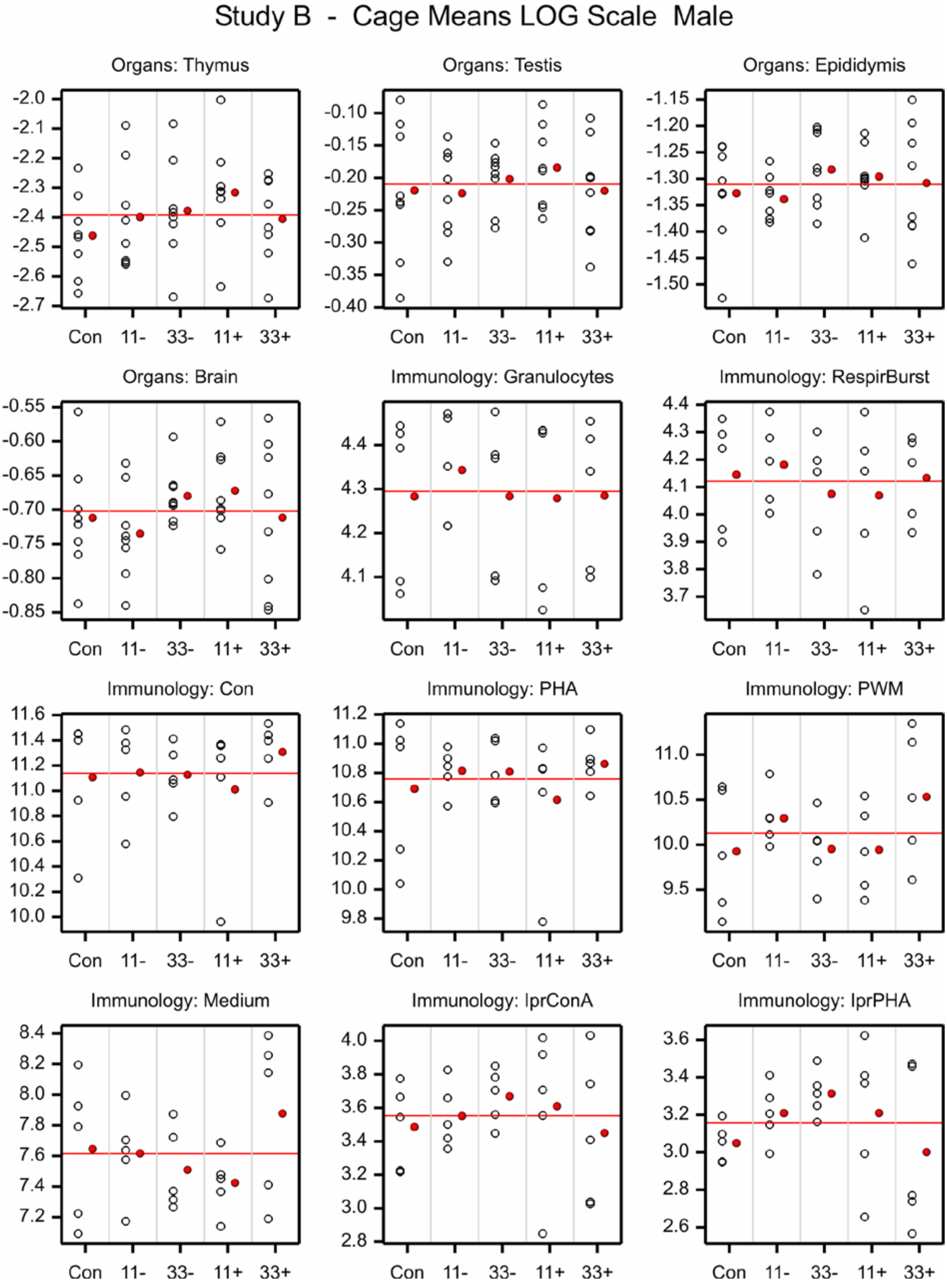
Appendix 5. Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



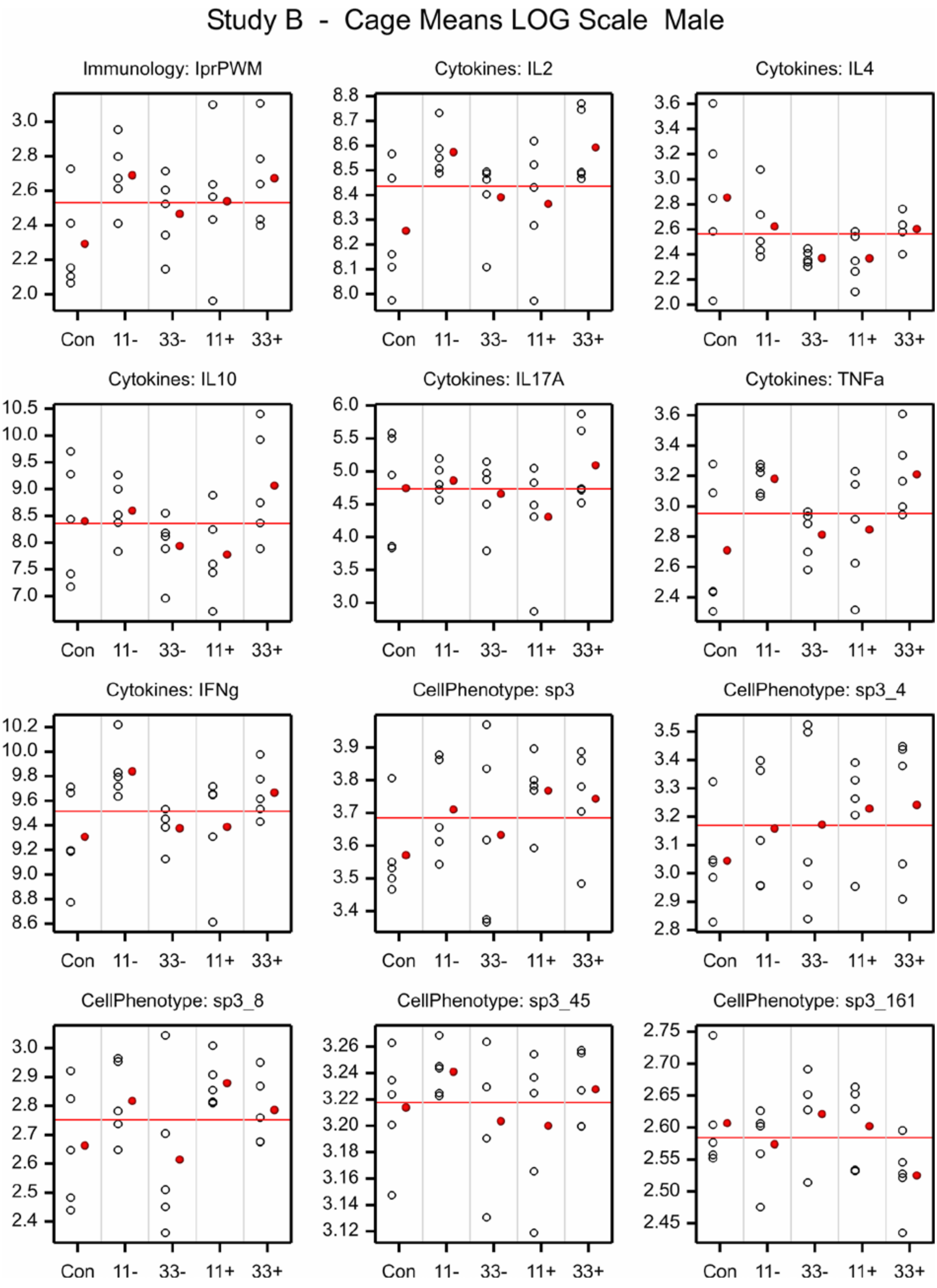
Appendix 5. Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



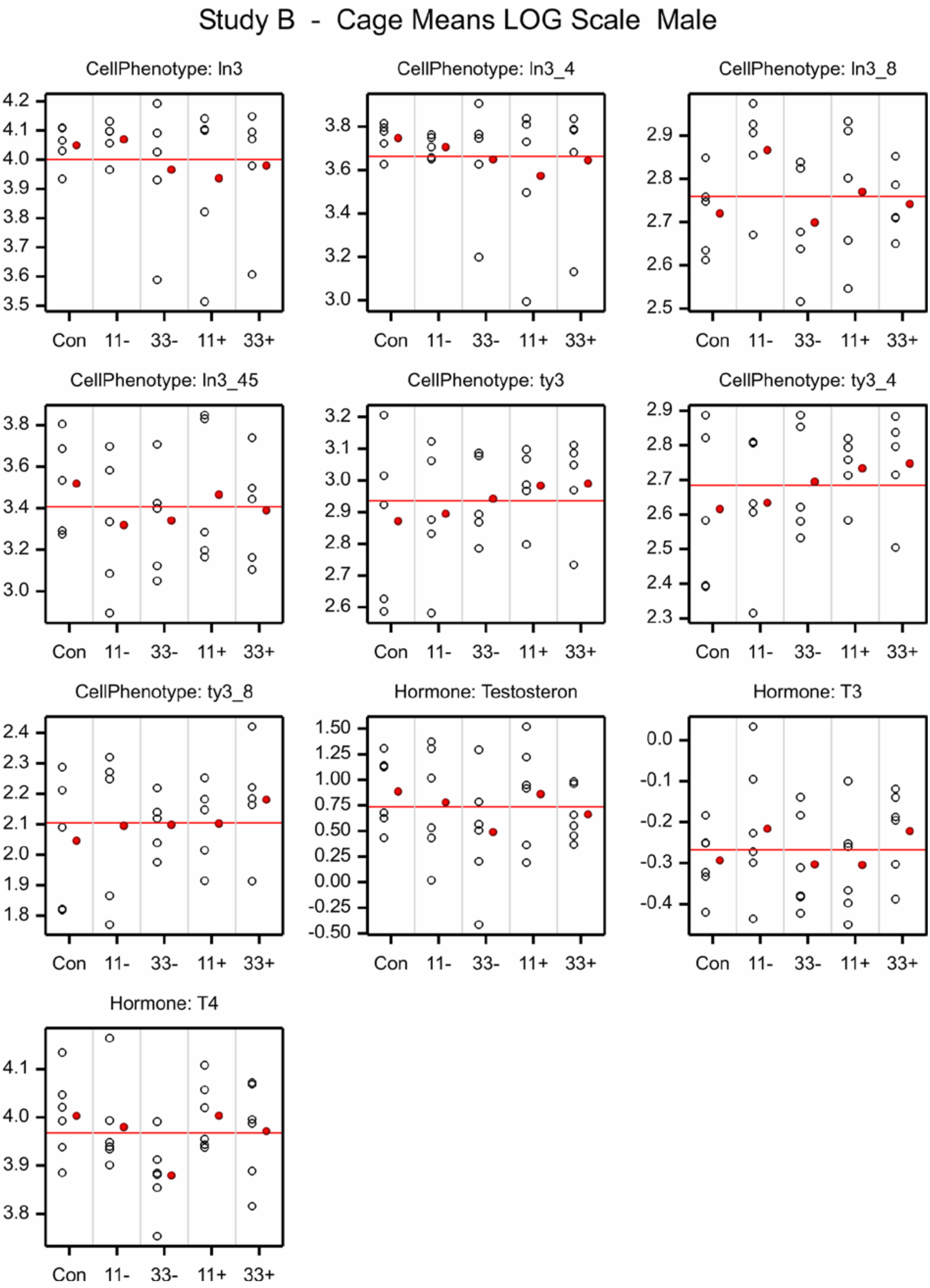
Appendix 5. Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



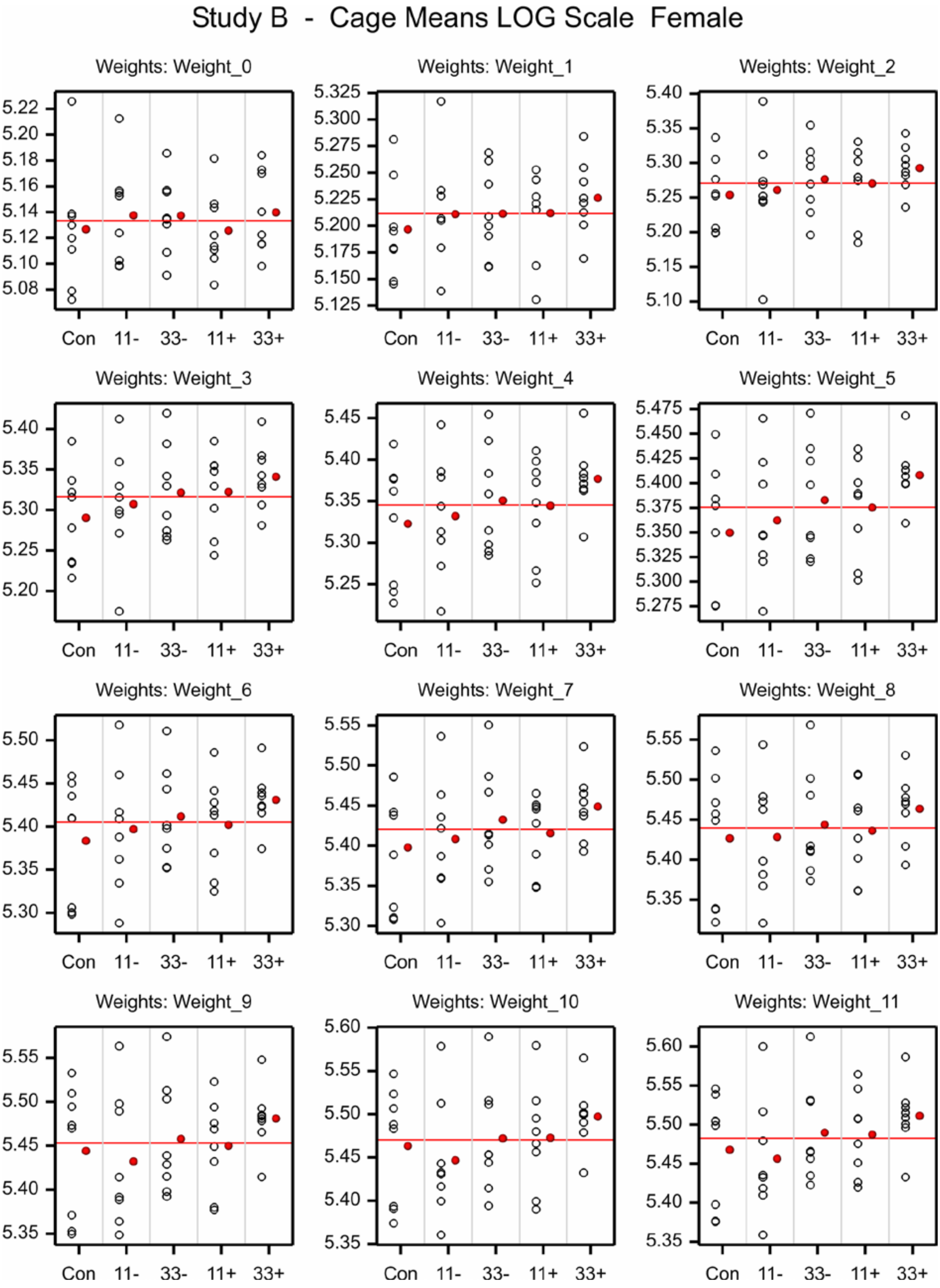
Appendix 5. Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



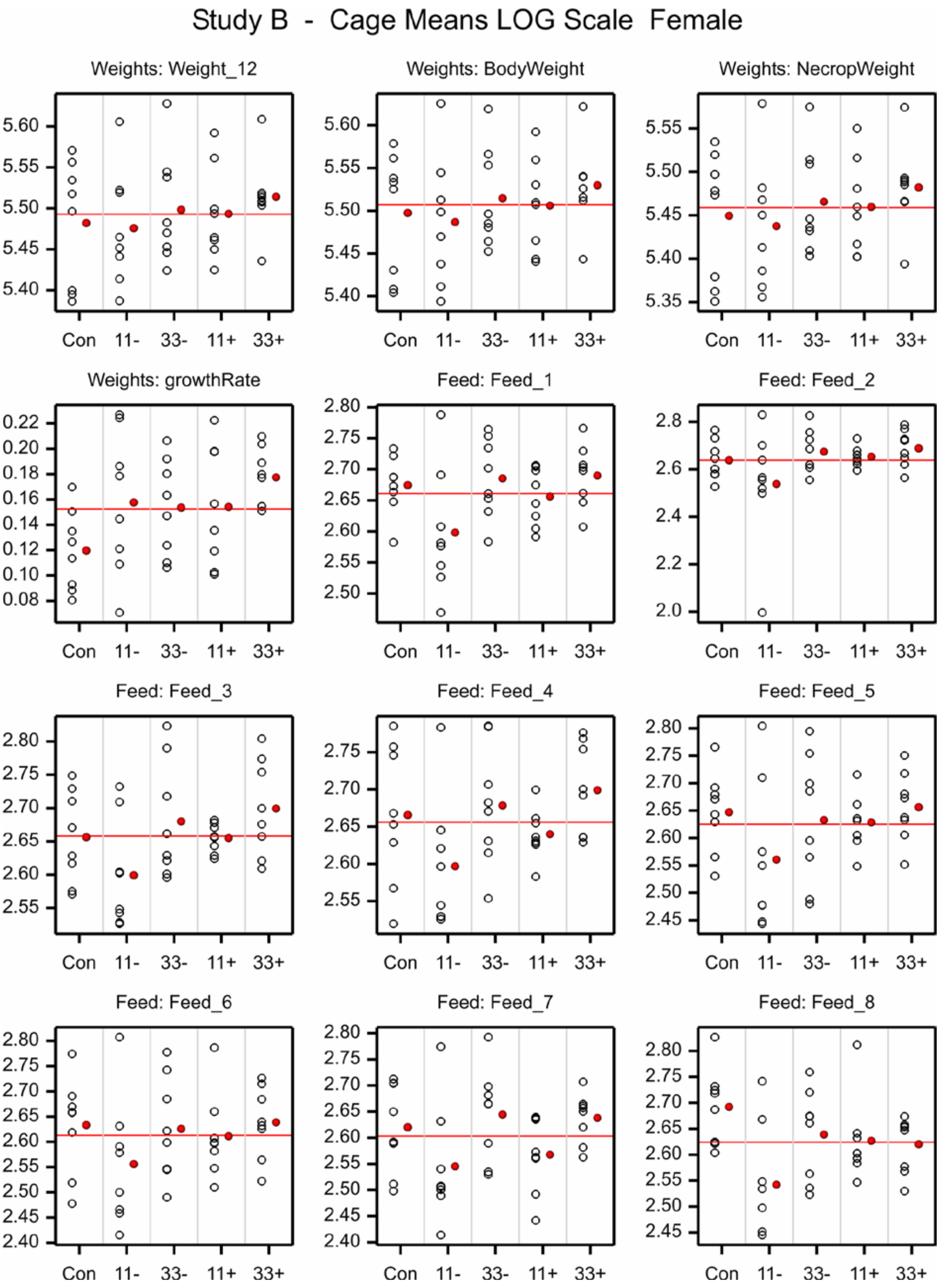
Appendix 5. Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



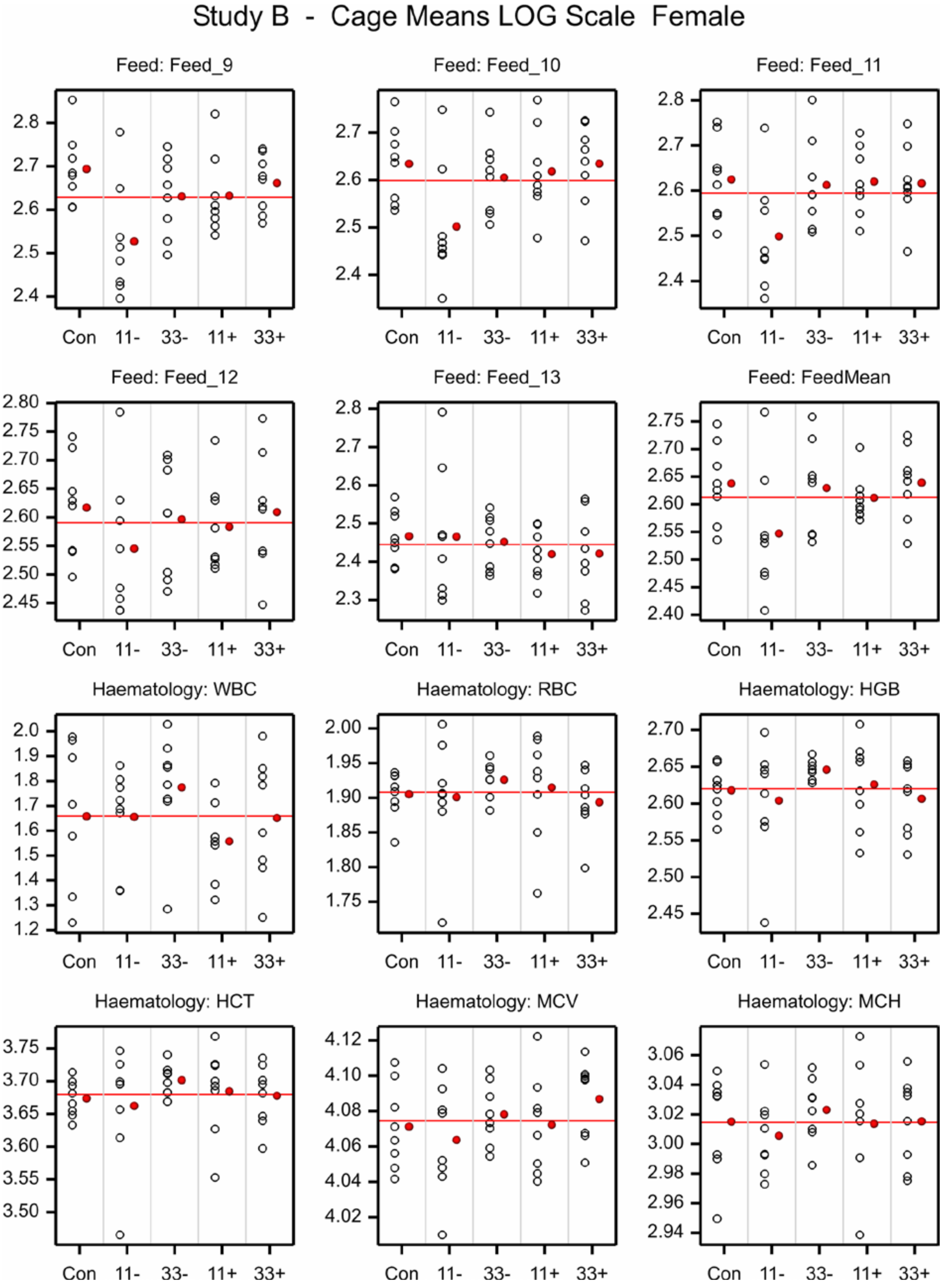
Appendix 5. Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



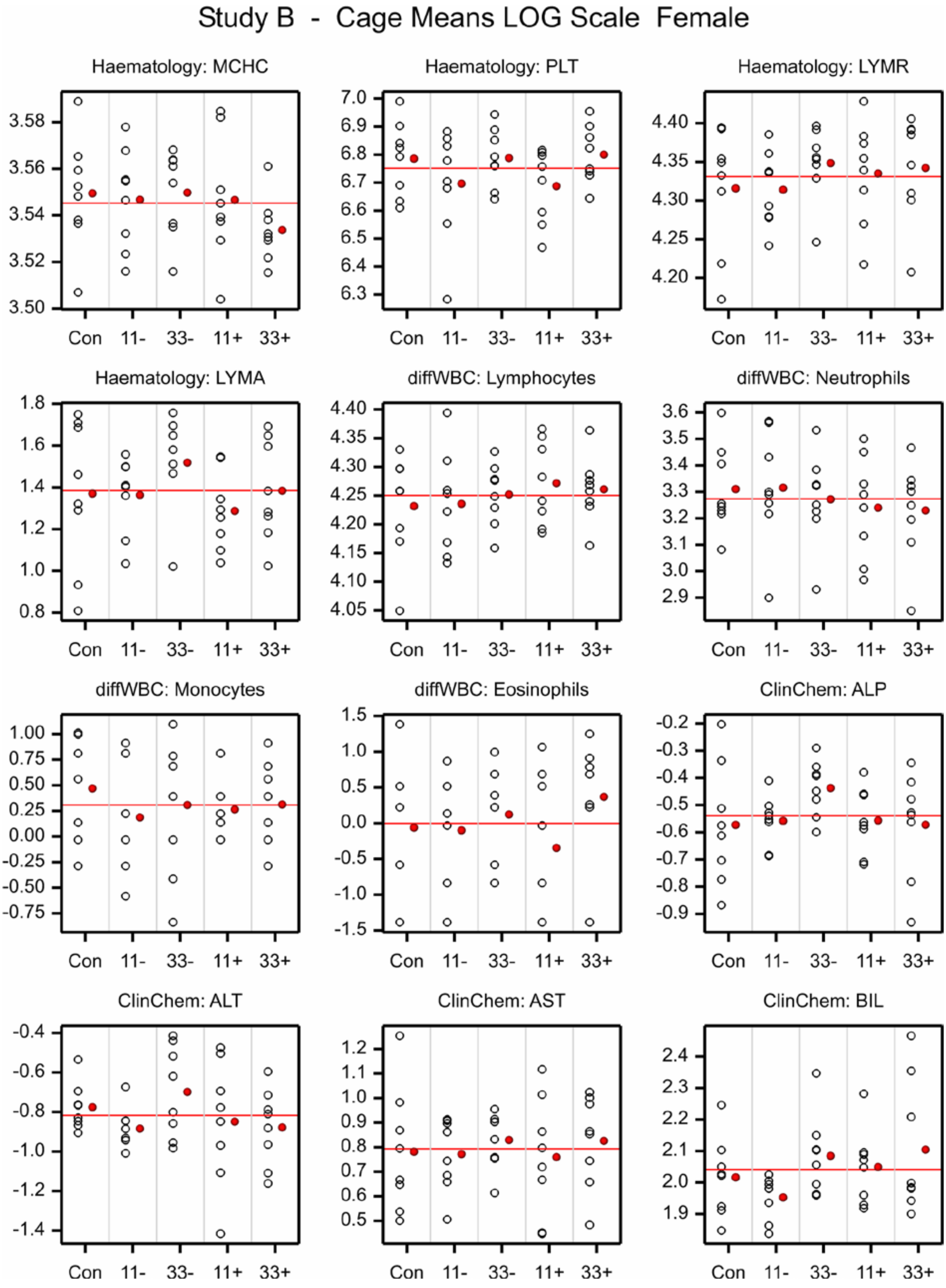
Appendix 5. Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



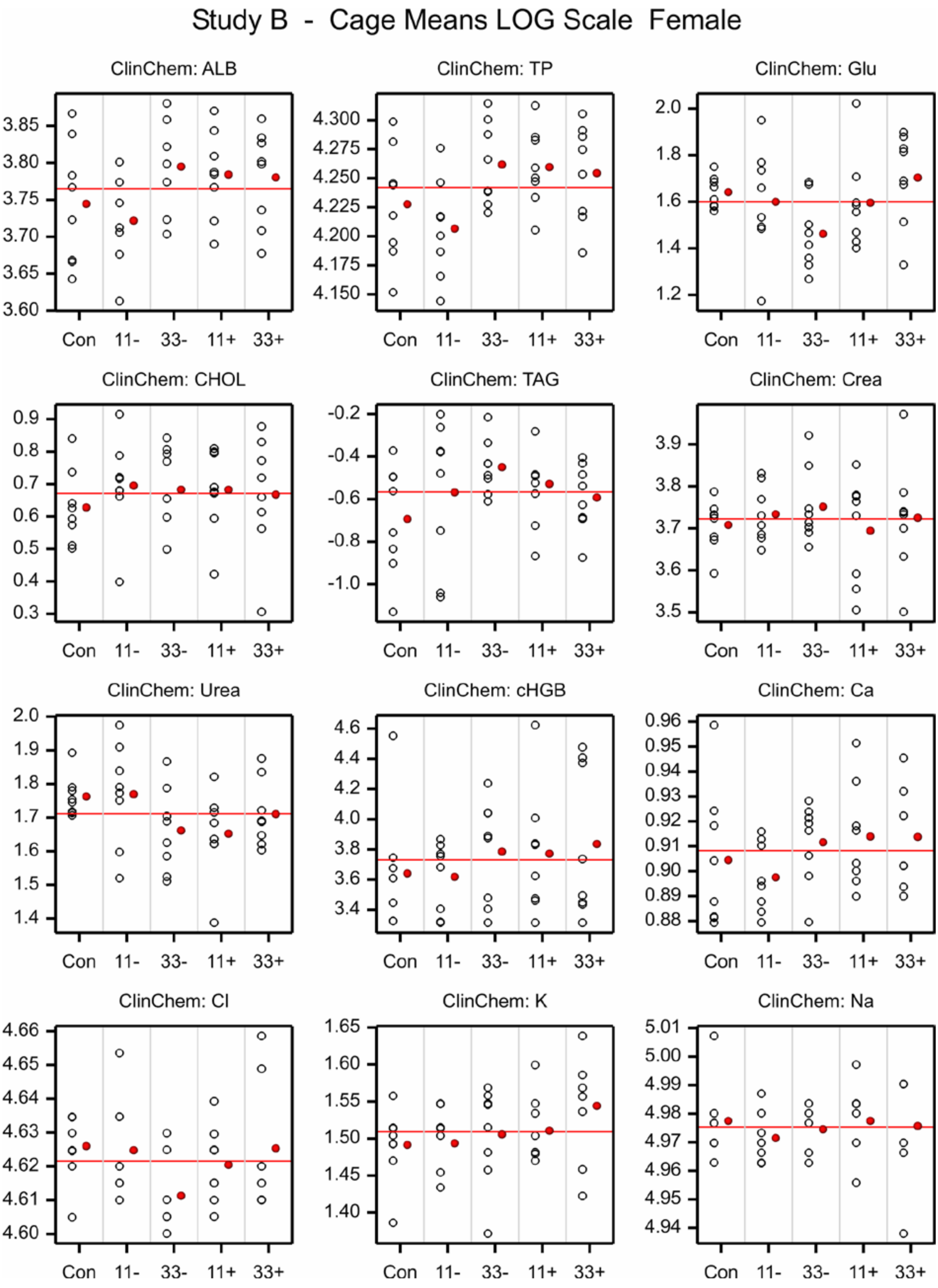
Appendix 5. Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



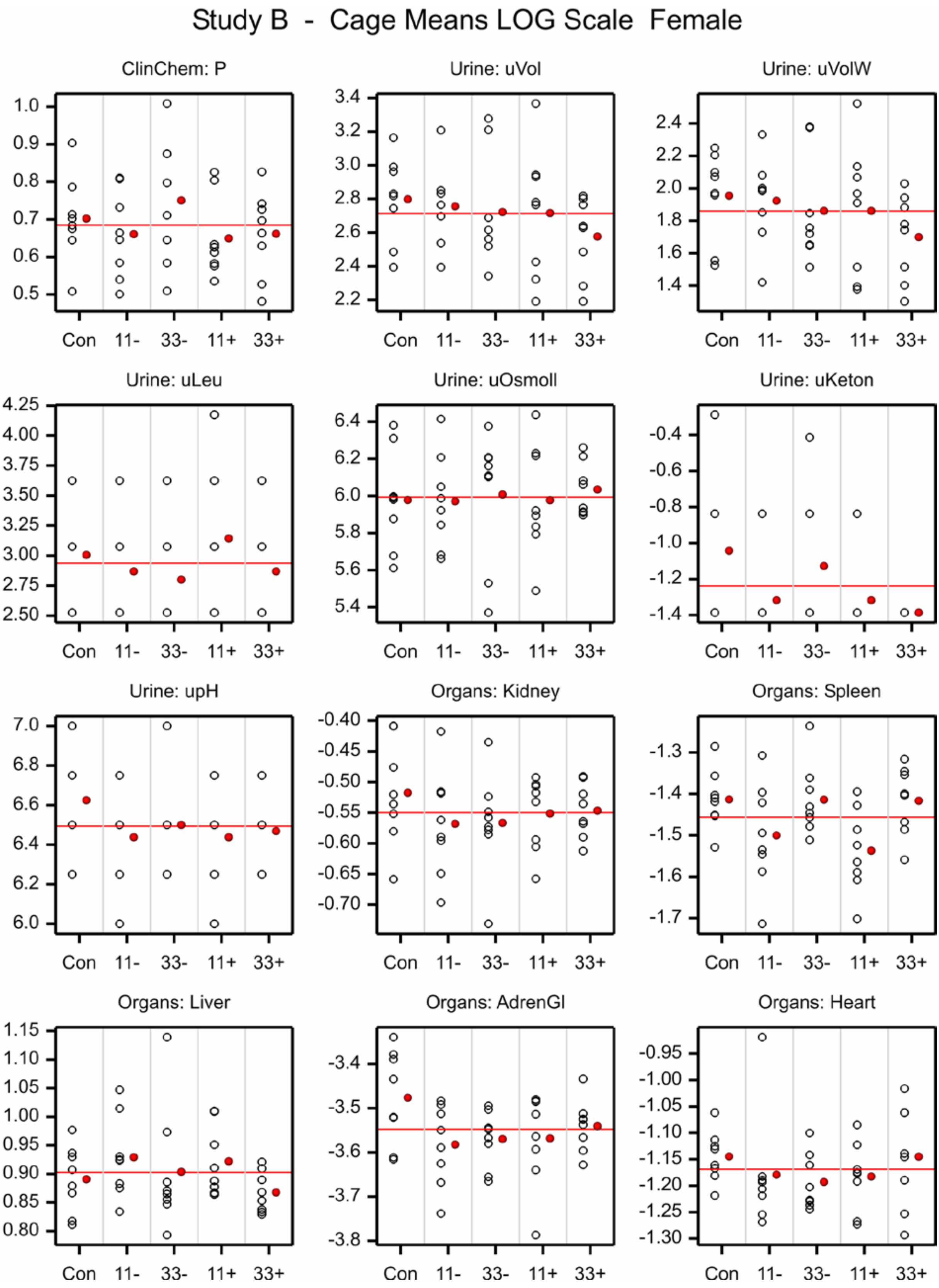
Appendix 5. Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



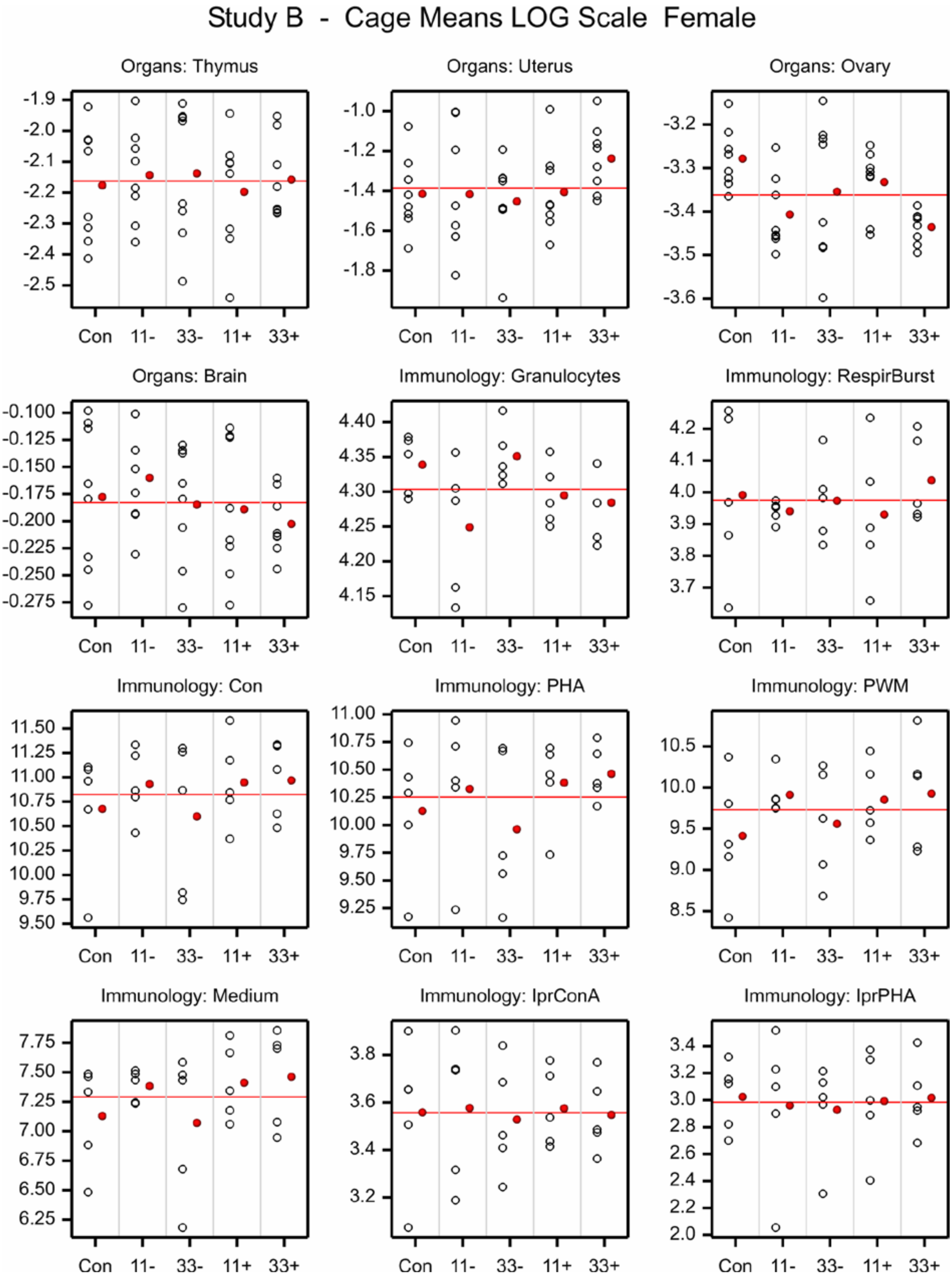
Appendix 5. Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



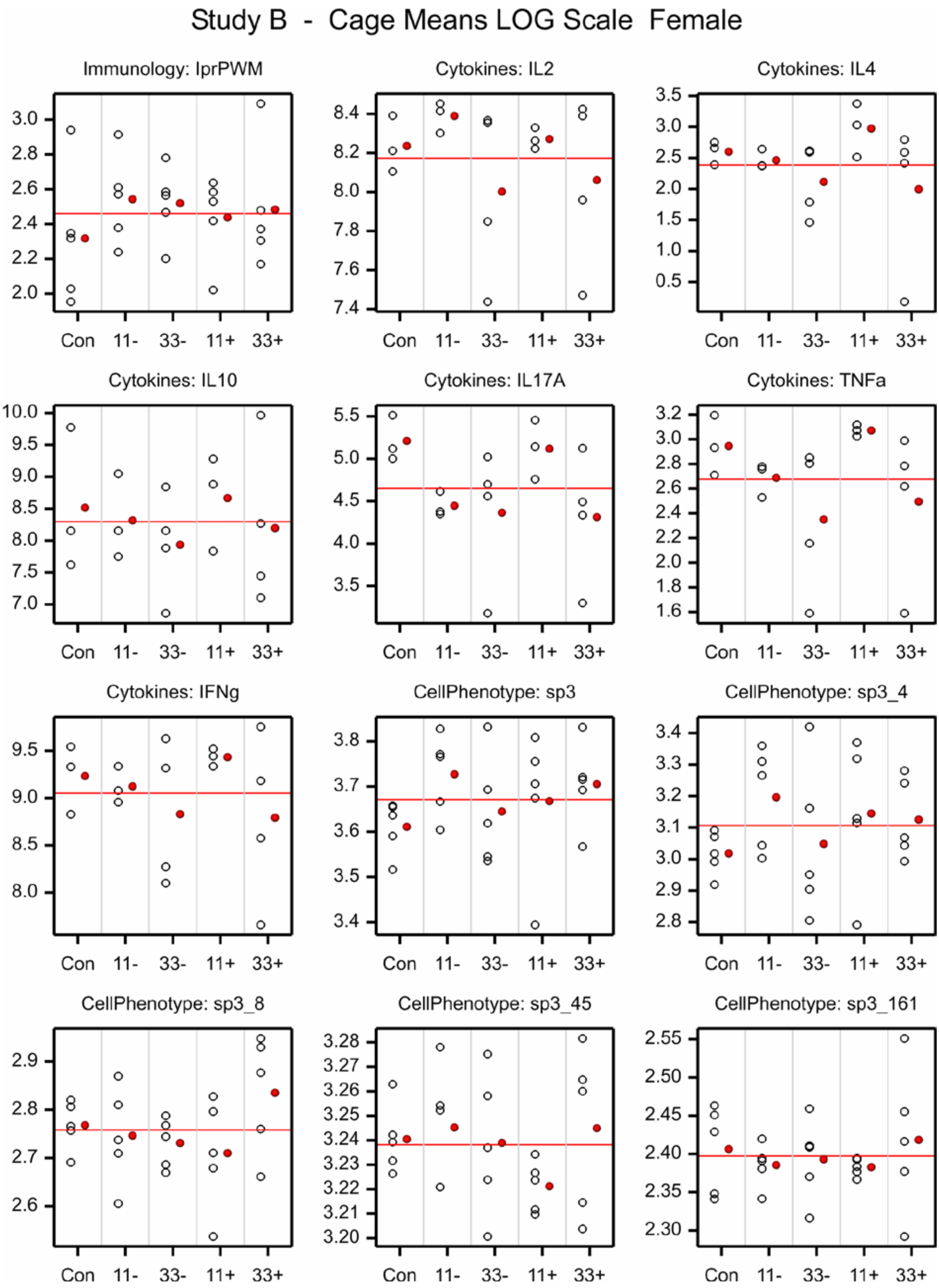
Appendix 5. Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



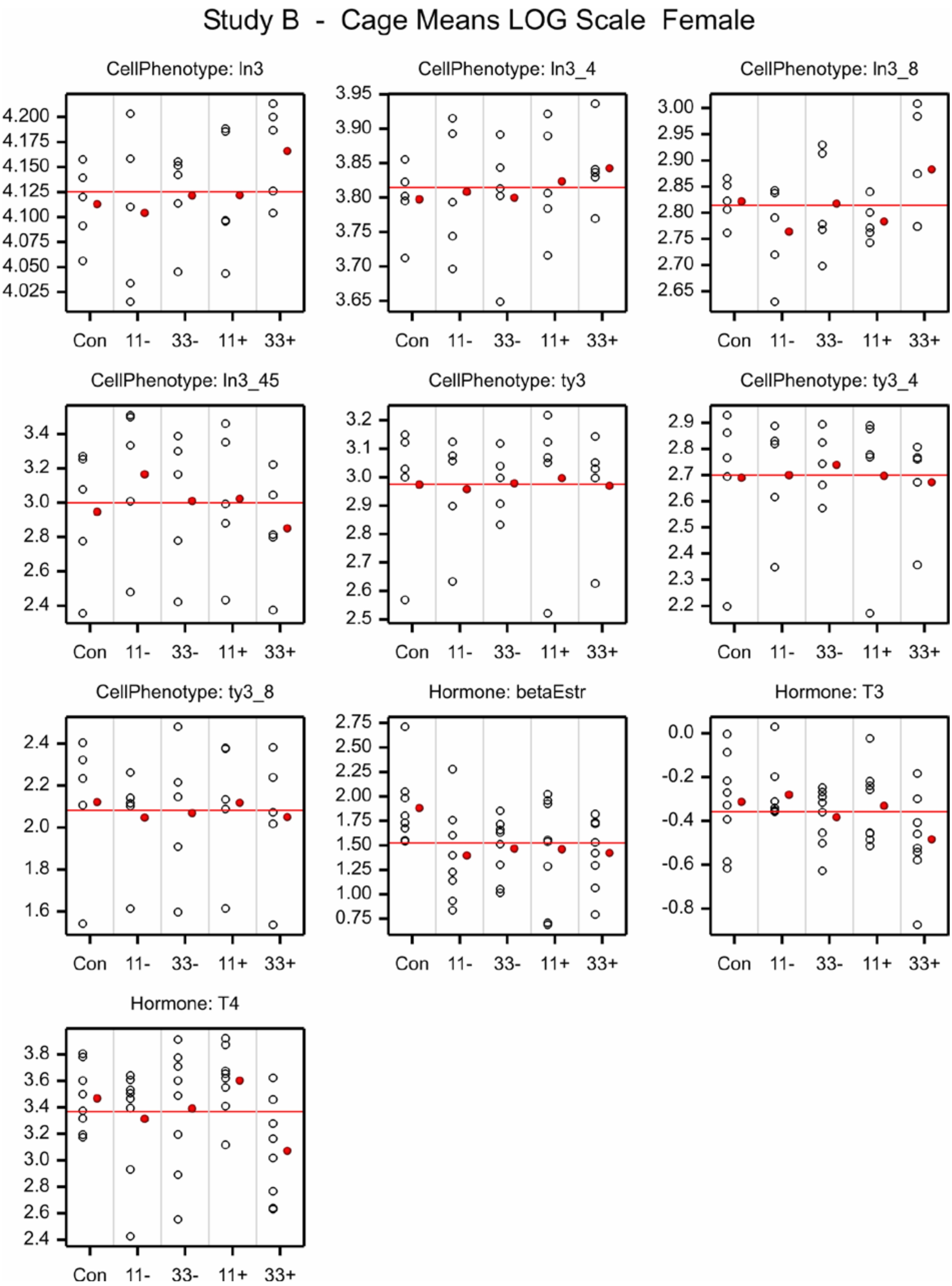
Appendix 5. Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



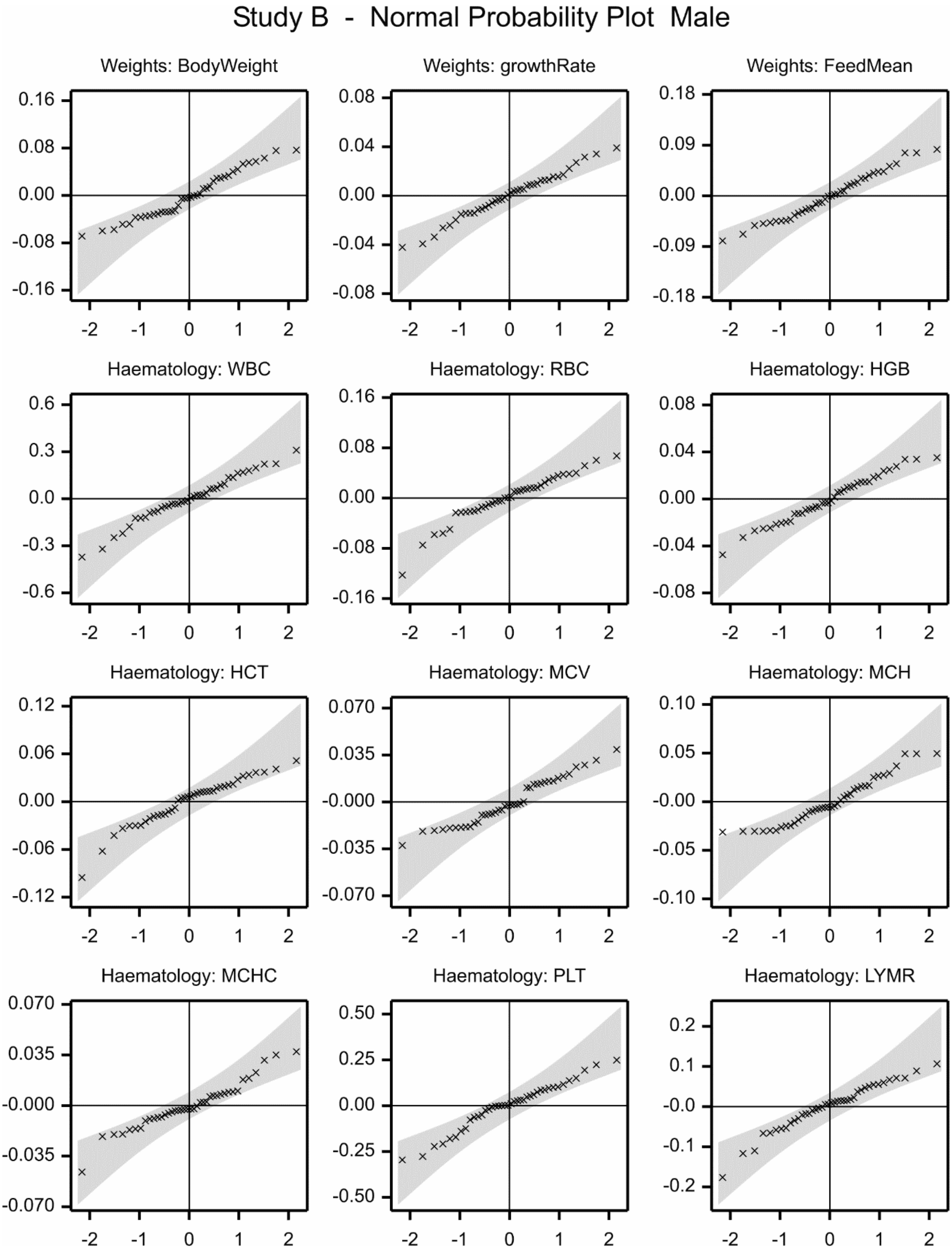
Appendix 5. Graphs of cage means on the log scale (continued)

Red symbols denote means for feeding groups while the red line denotes the overall mean.



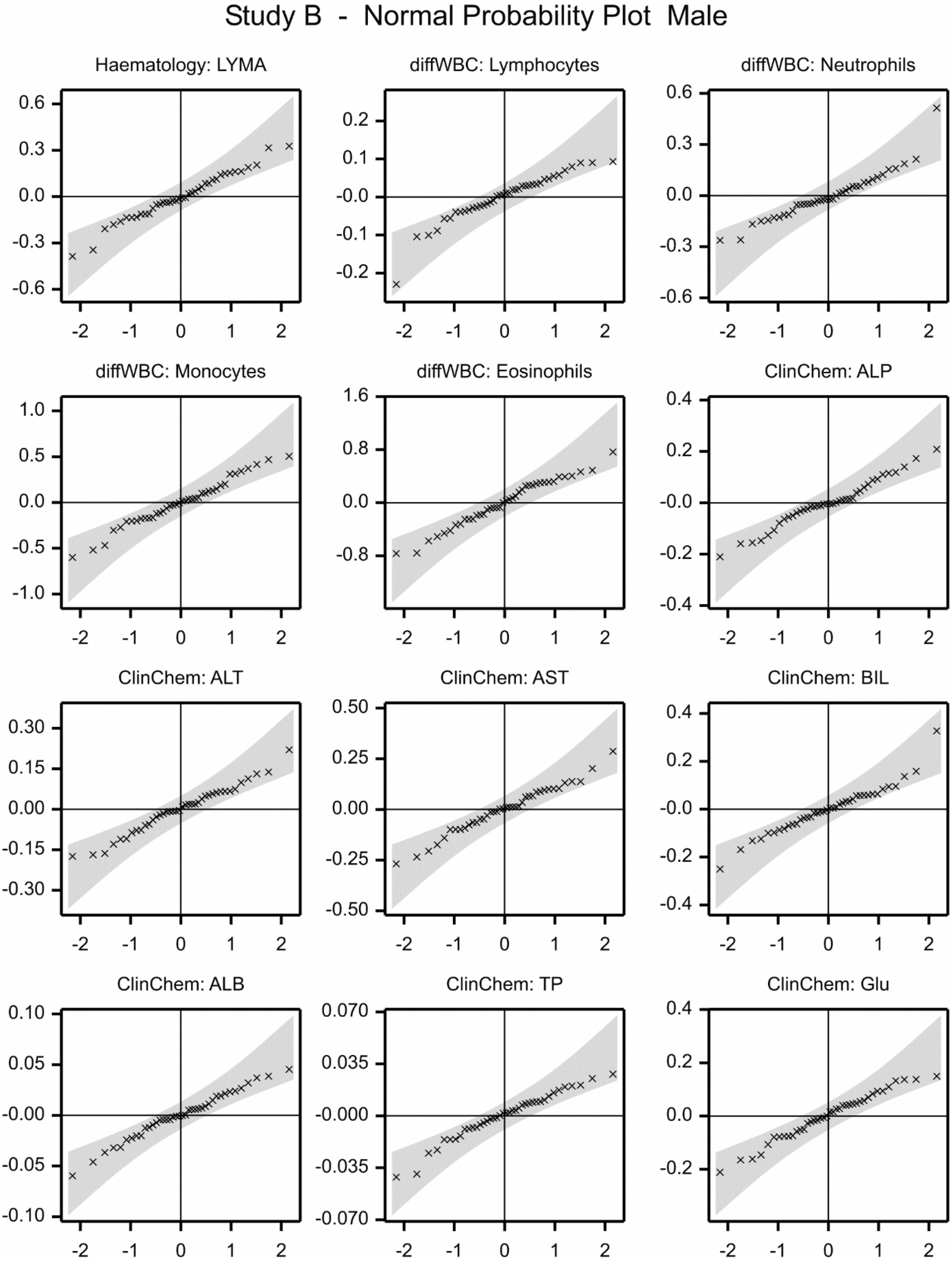
Appendix 6. Normal probability plots of residuals after ANOVA

Residuals are obtained from ANOVA of cage means (log scale). A 99% confidence envelop is added.



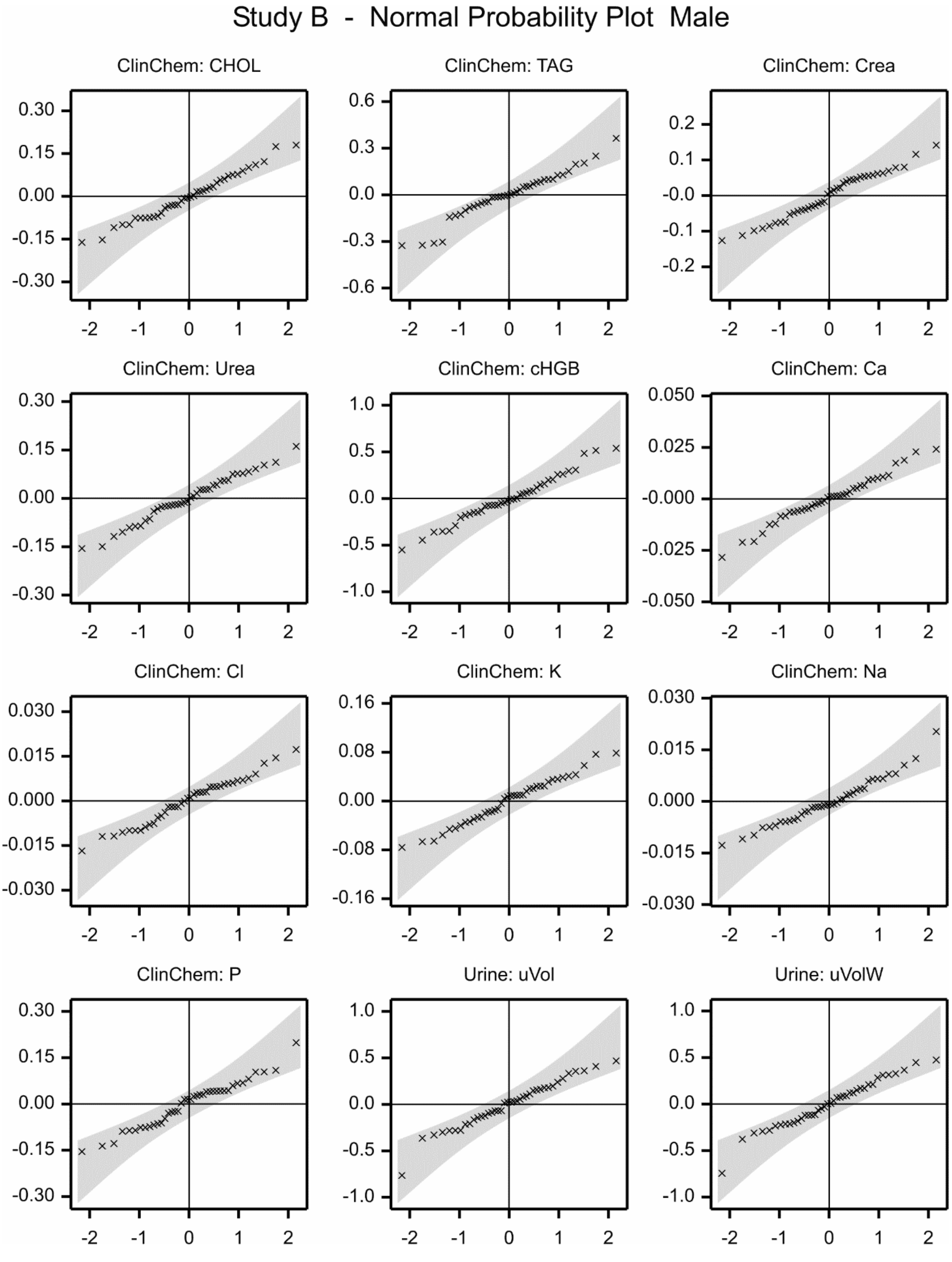
Appendix 6. Normal probability plots of residuals after ANOVA (continued)

Residuals are obtained from ANOVA of cage means (log scale). A 99% confidence envelop is added.



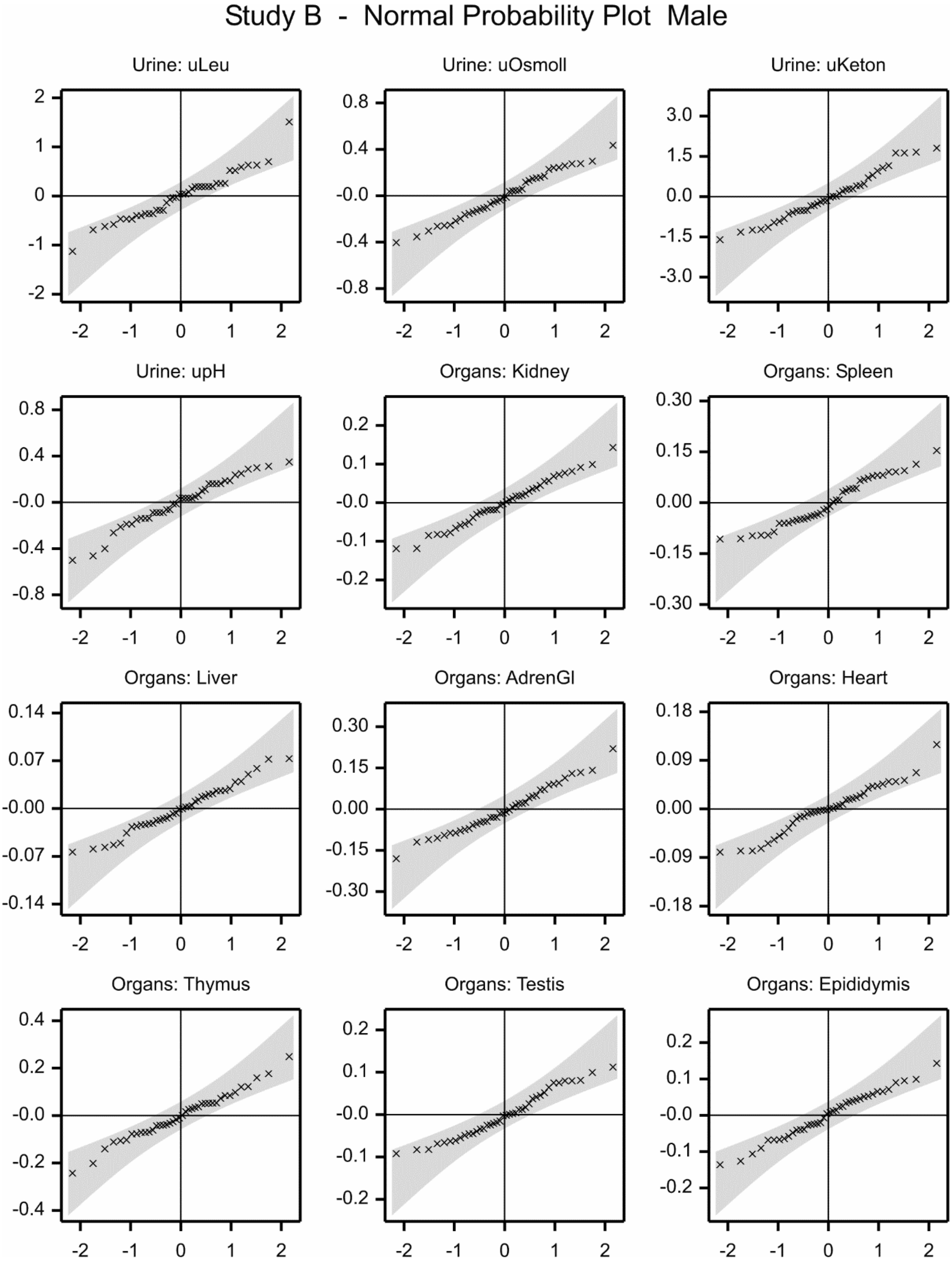
Appendix 6. Normal probability plots of residuals after ANOVA (continued)

Residuals are obtained from ANOVA of cage means (log scale). A 99% confidence envelop is added.



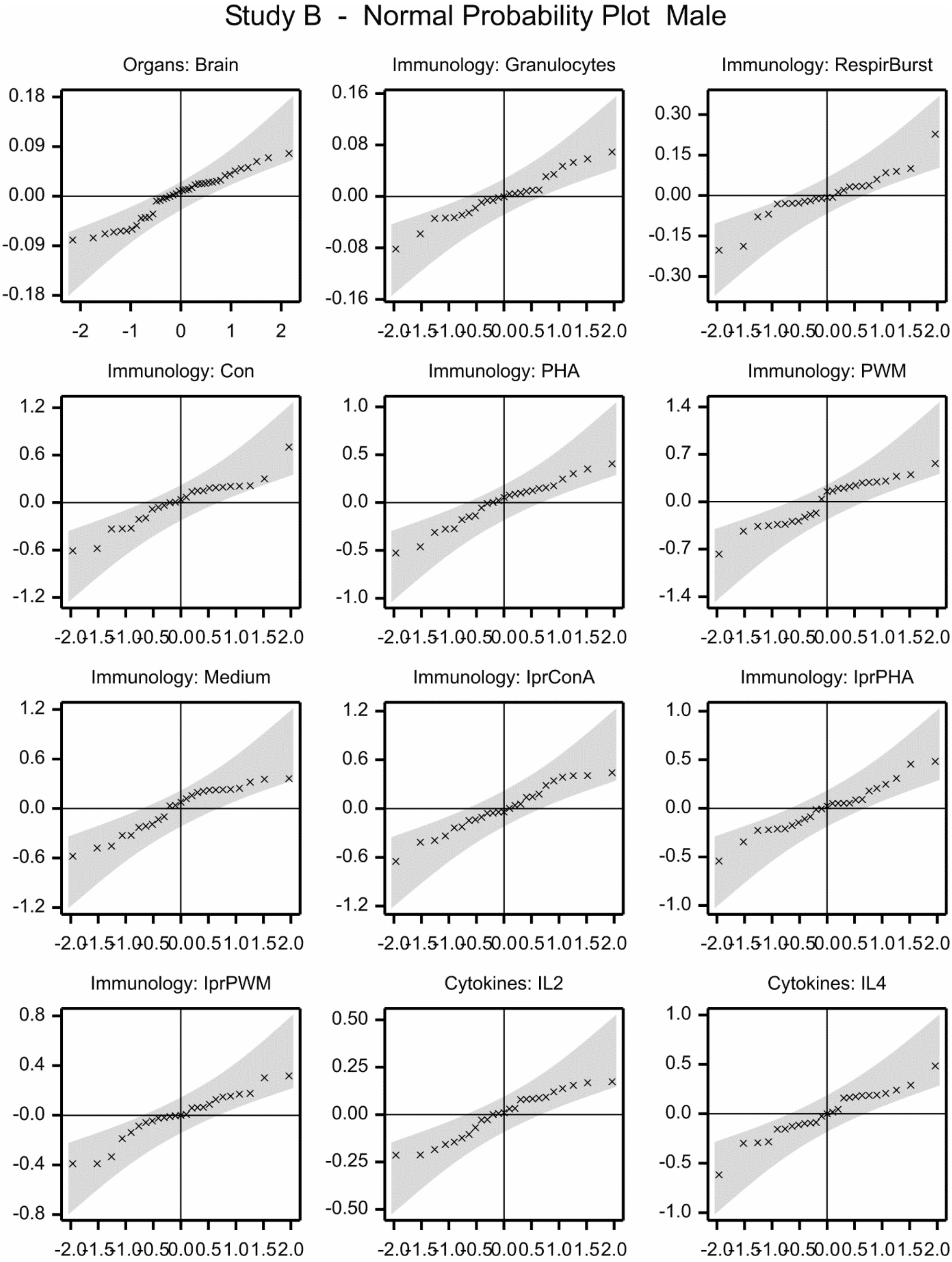
Appendix 6. Normal probability plots of residuals after ANOVA (continued)

Residuals are obtained from ANOVA of cage means (log scale). A 99% confidence envelop is added.



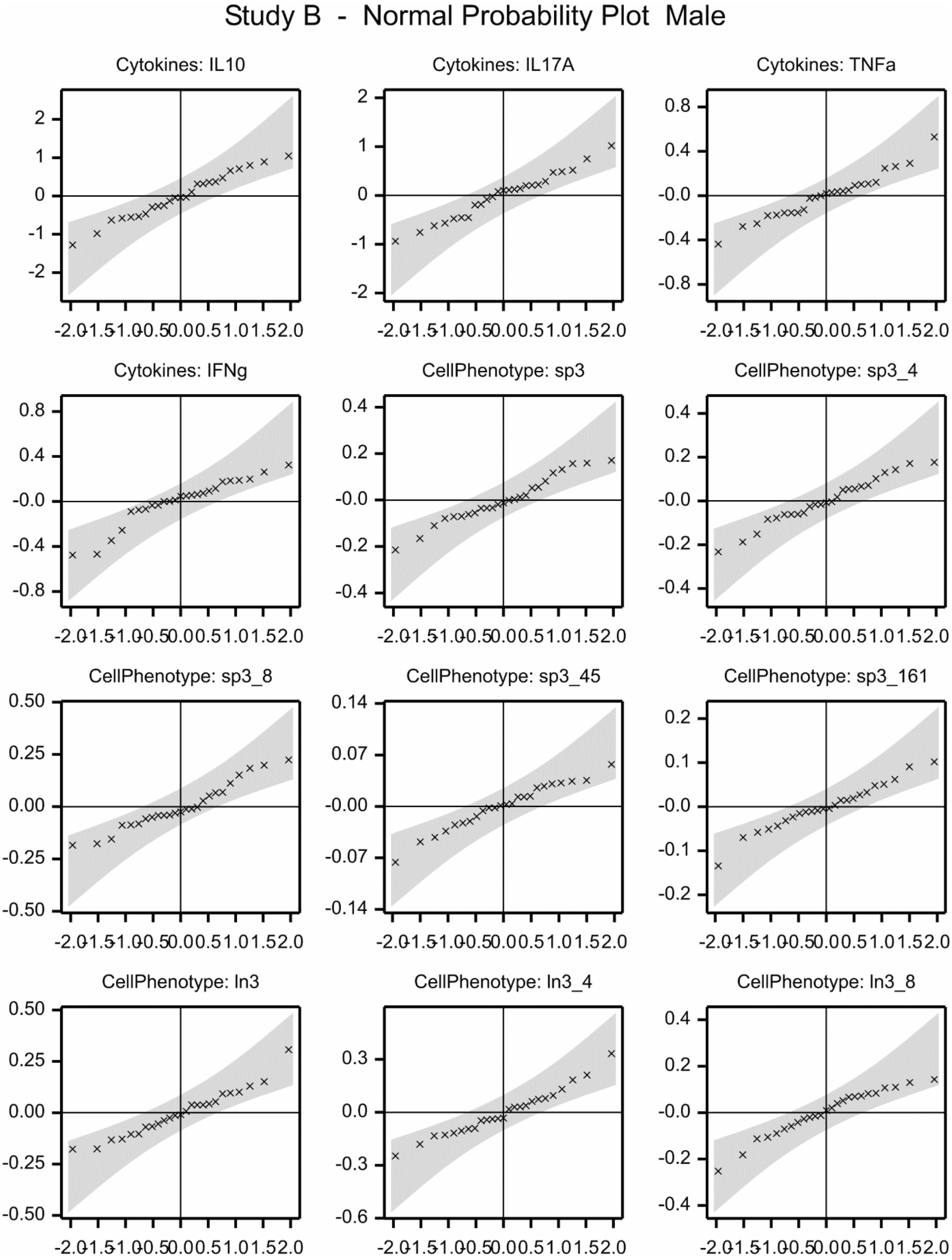
Appendix 6. Normal probability plots of residuals after ANOVA (continued)

Residuals are obtained from ANOVA of cage means (log scale). A 99% confidence envelop is added.



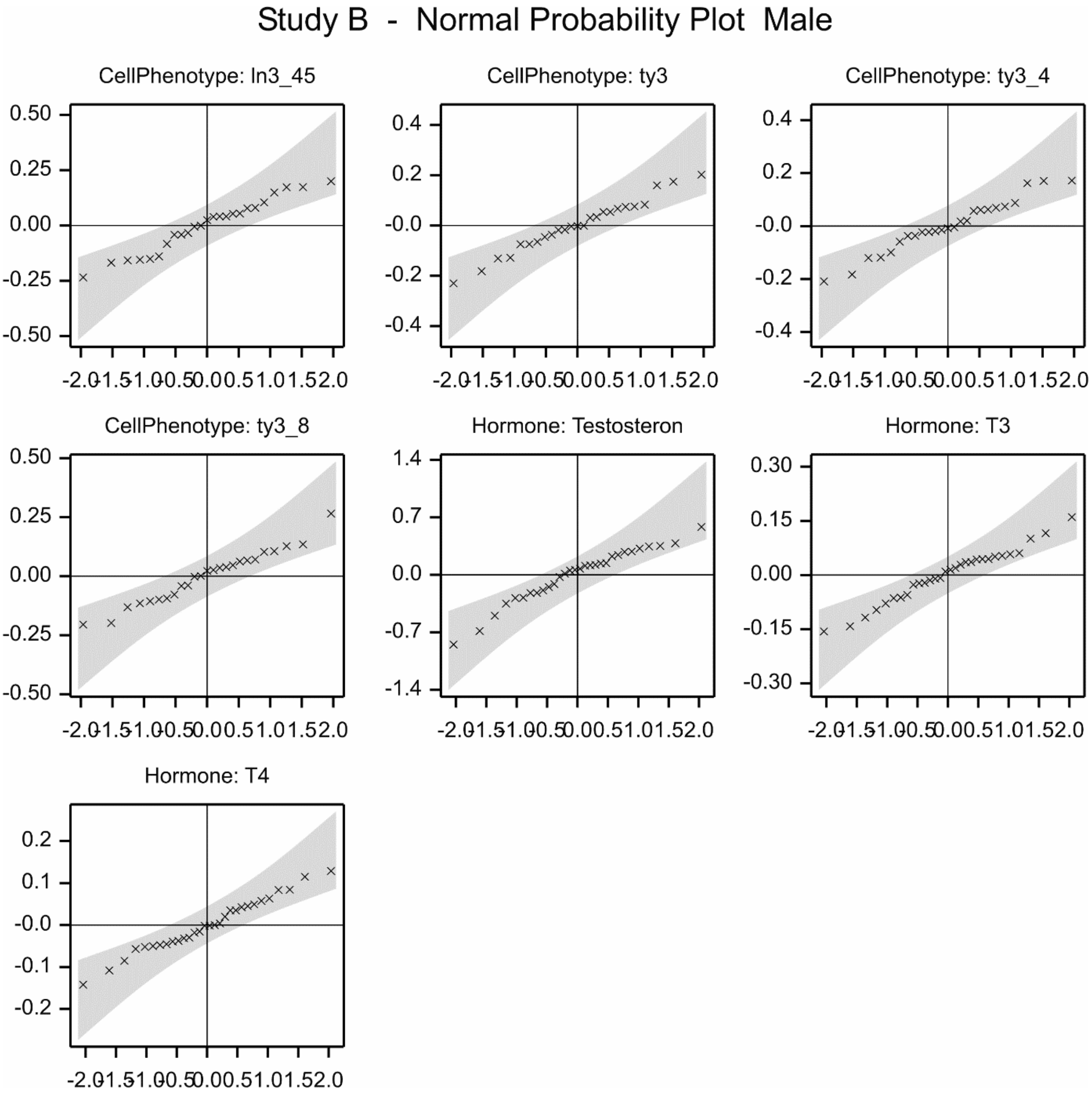
Appendix 6. Normal probability plots of residuals after ANOVA (continued)

Residuals are obtained from ANOVA of cage means (log scale). A 99% confidence envelop is added.



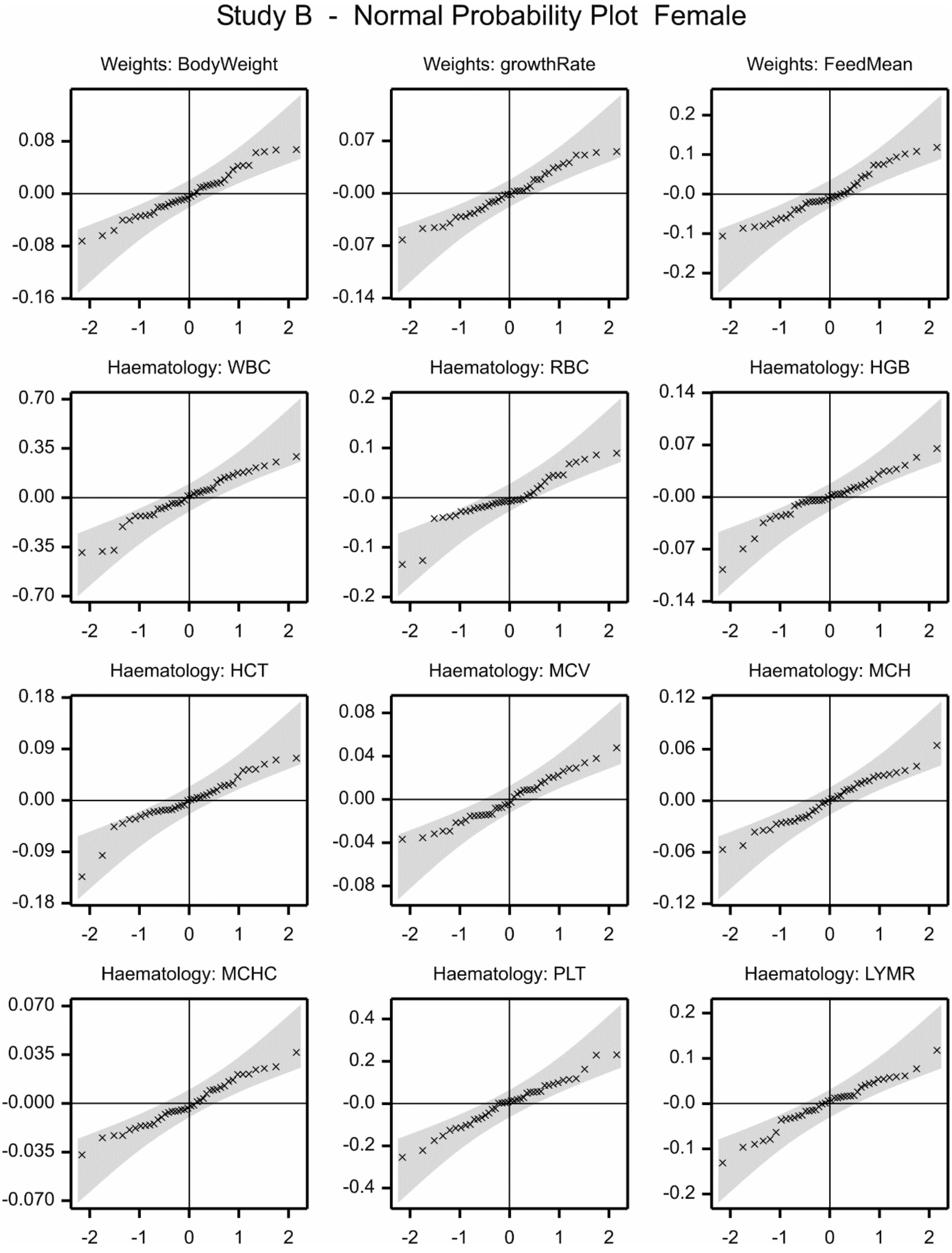
Appendix 6. Normal probability plots of residuals after ANOVA (continued)

Residuals are obtained from ANOVA of cage means (log scale). A 99% confidence envelop is added.



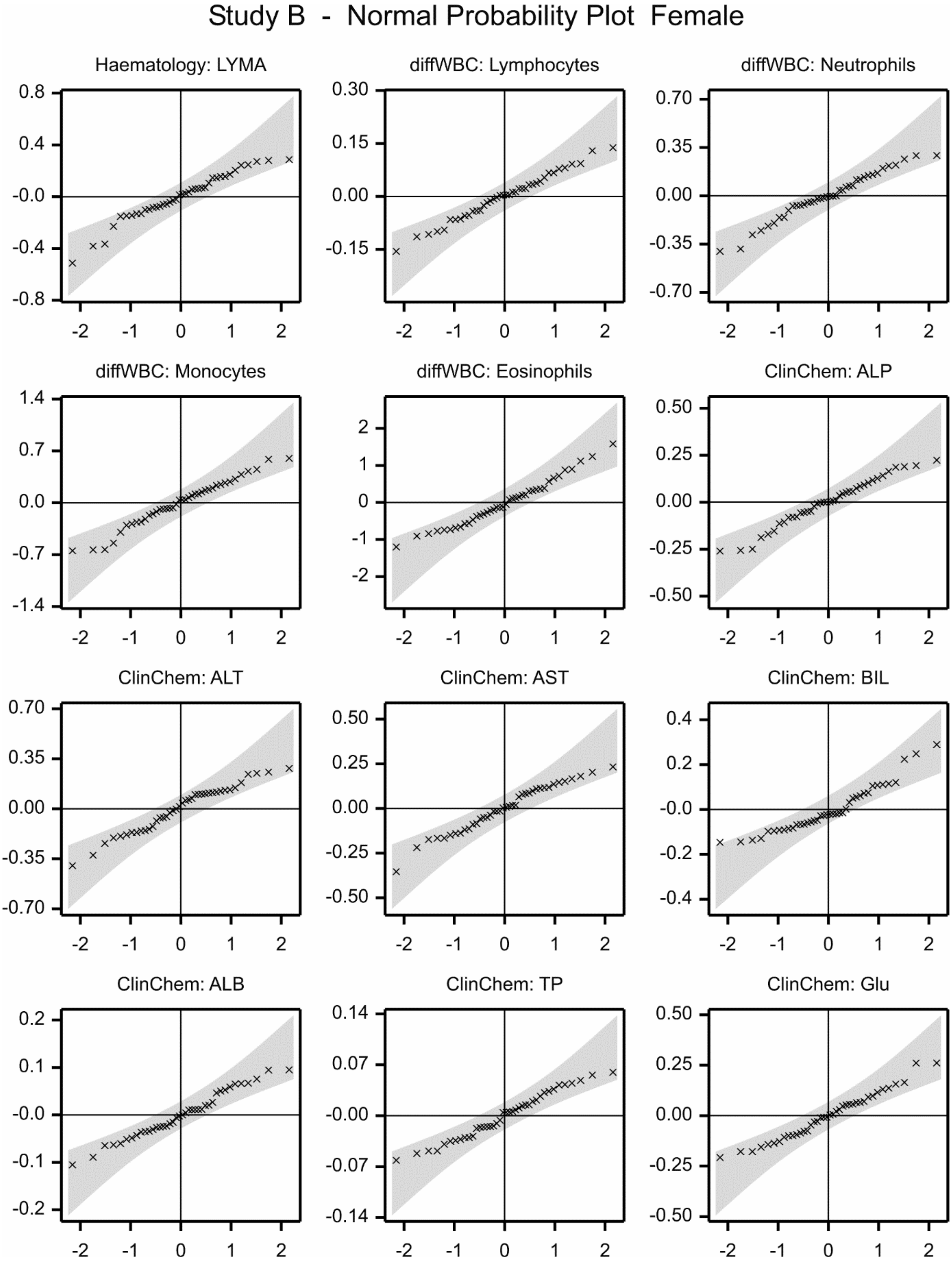
Appendix 6. Normal probability plots of residuals after ANOVA (continued)

Residuals are obtained from ANOVA of cage means (log scale). A 99% confidence envelop is added.



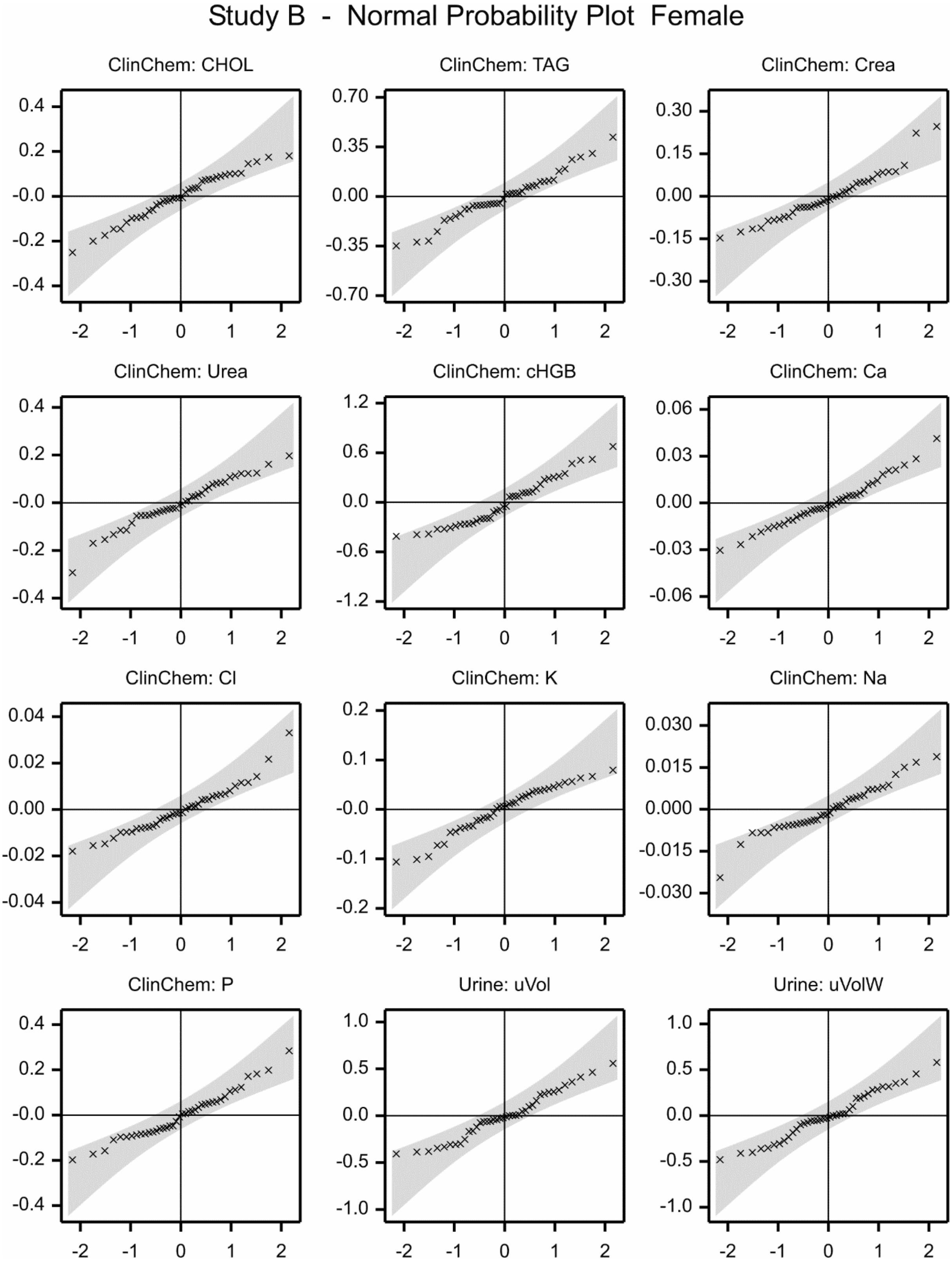
Appendix 6. Normal probability plots of residuals after ANOVA (continued)

Residuals are obtained from ANOVA of cage means (log scale). A 99% confidence envelop is added.



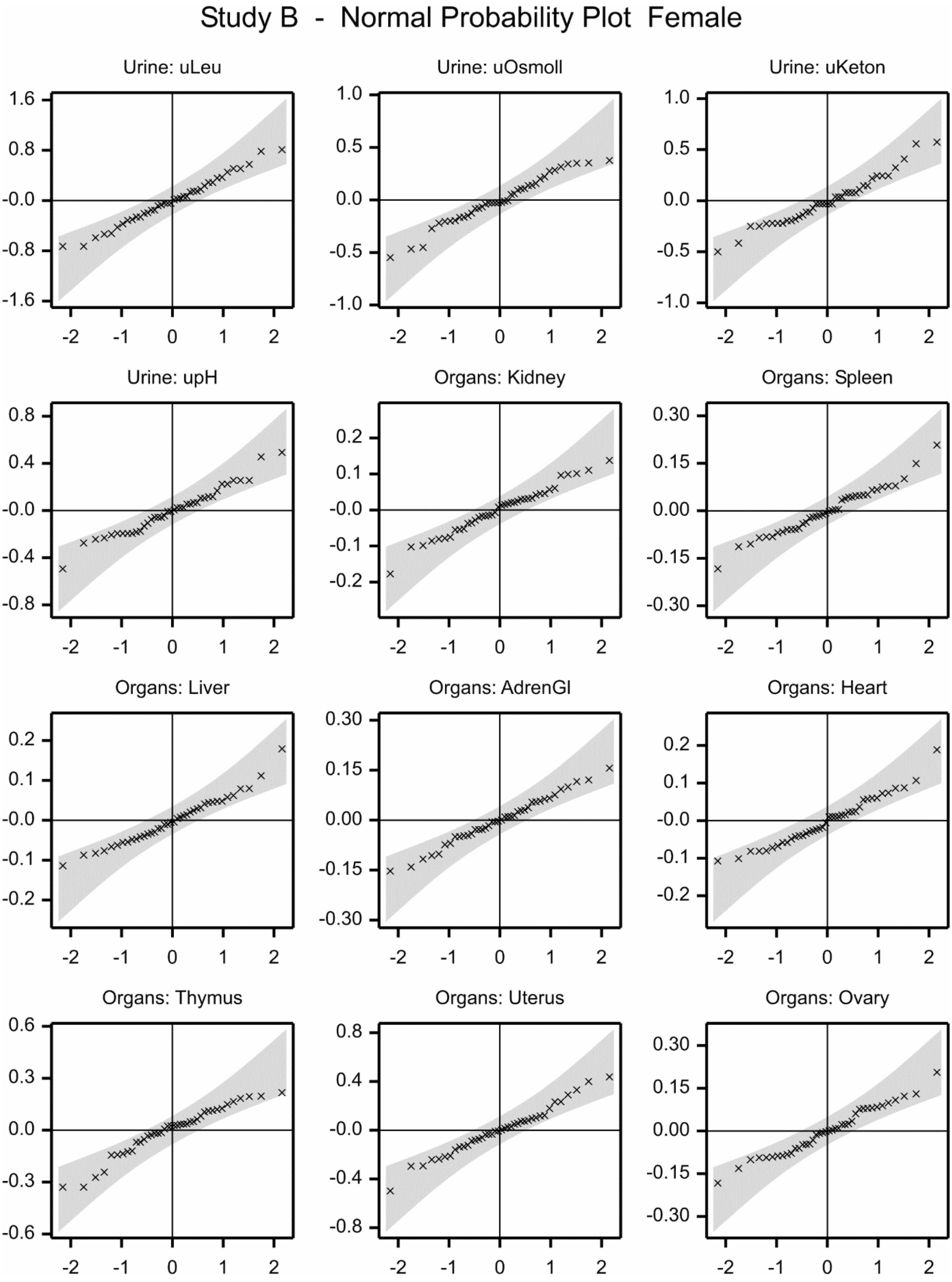
Appendix 6. Normal probability plots of residuals after ANOVA (continued)

Residuals are obtained from ANOVA of cage means (log scale). A 99% confidence envelop is added.



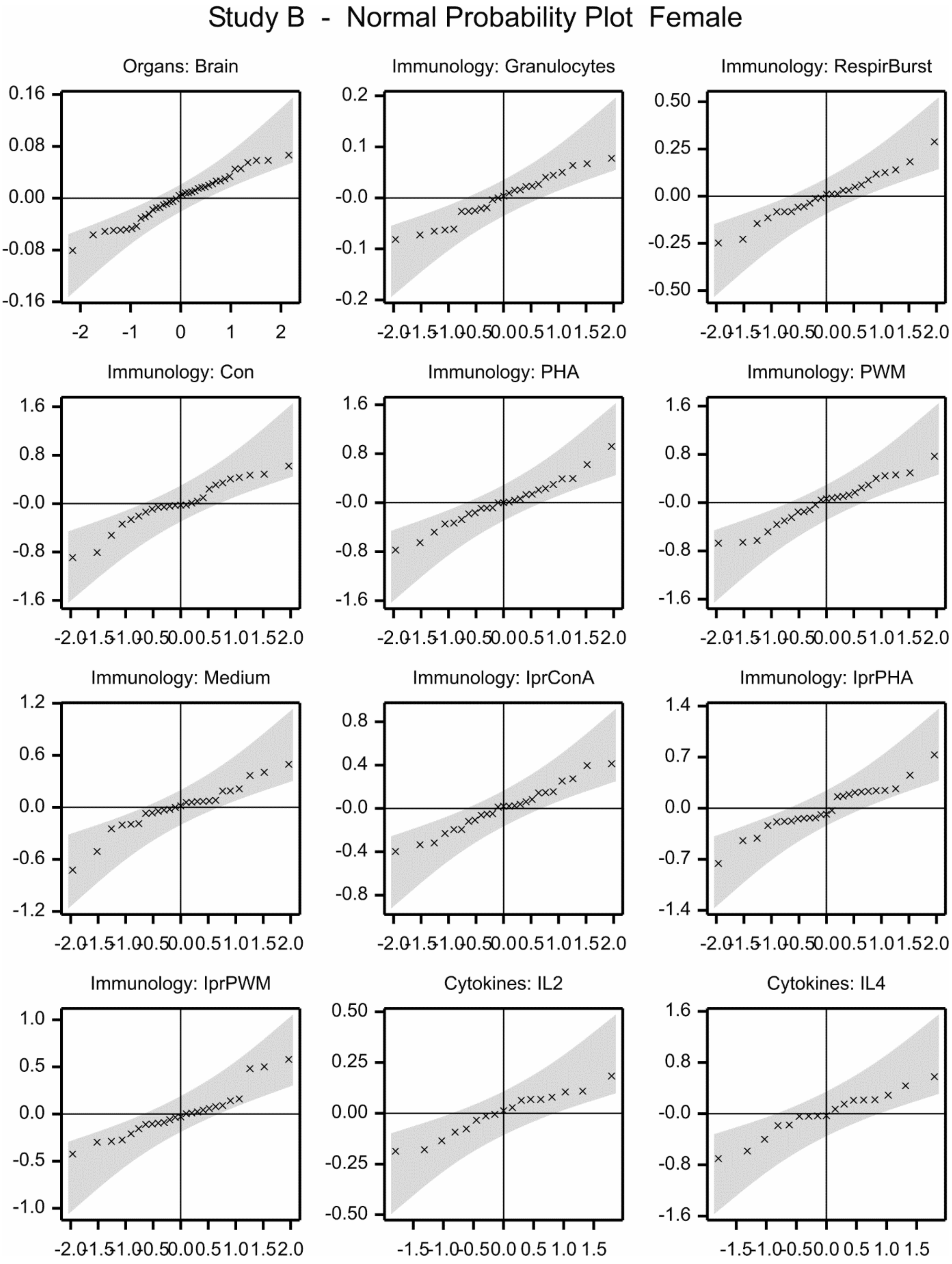
Appendix 6. Normal probability plots of residuals after ANOVA (continued)

Residuals are obtained from ANOVA of cage means (log scale). A 99% confidence envelop is added.



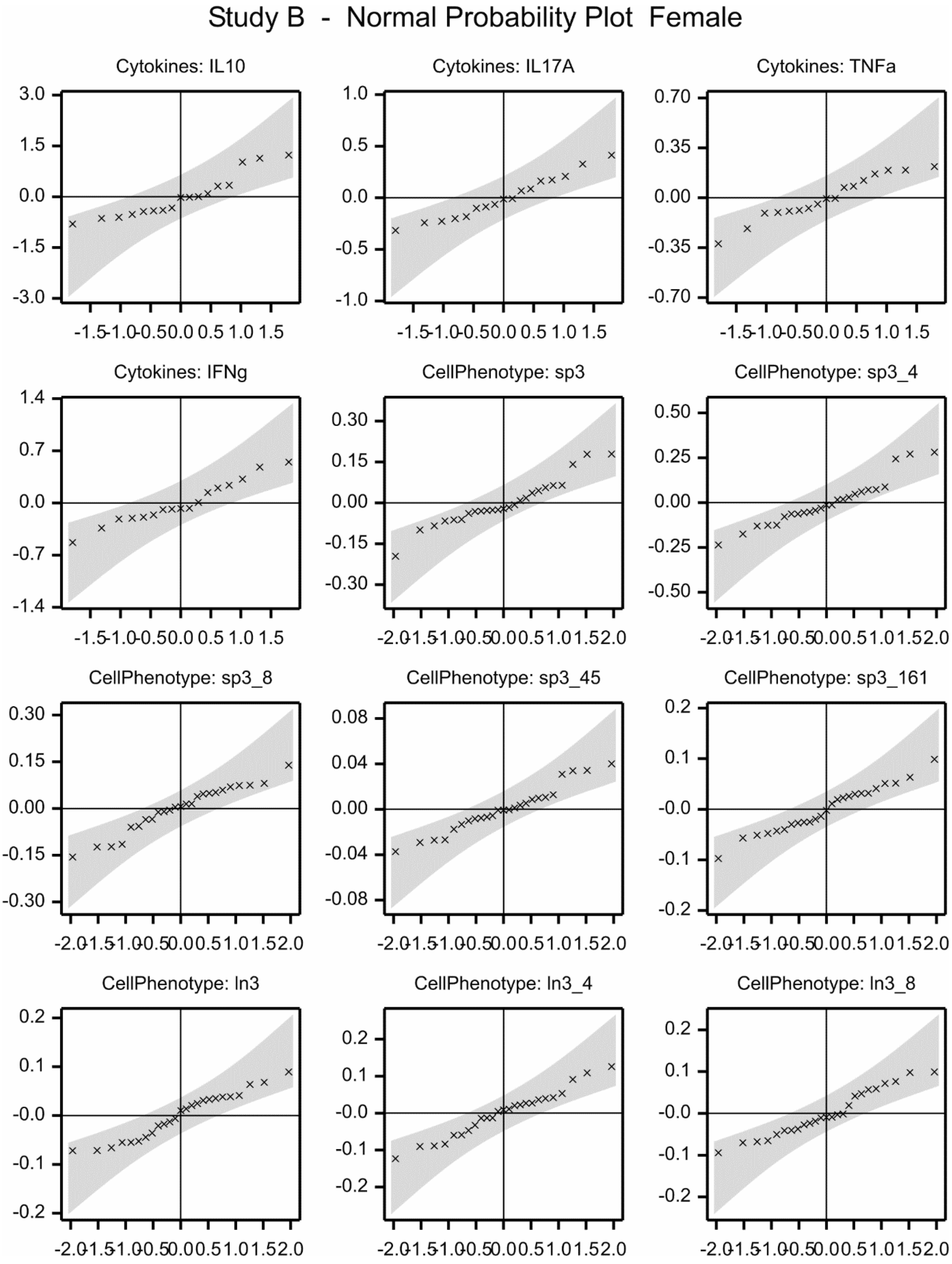
Appendix 6. Normal probability plots of residuals after ANOVA (continued)

Residuals are obtained from ANOVA of cage means (log scale). A 99% confidence envelop is added.



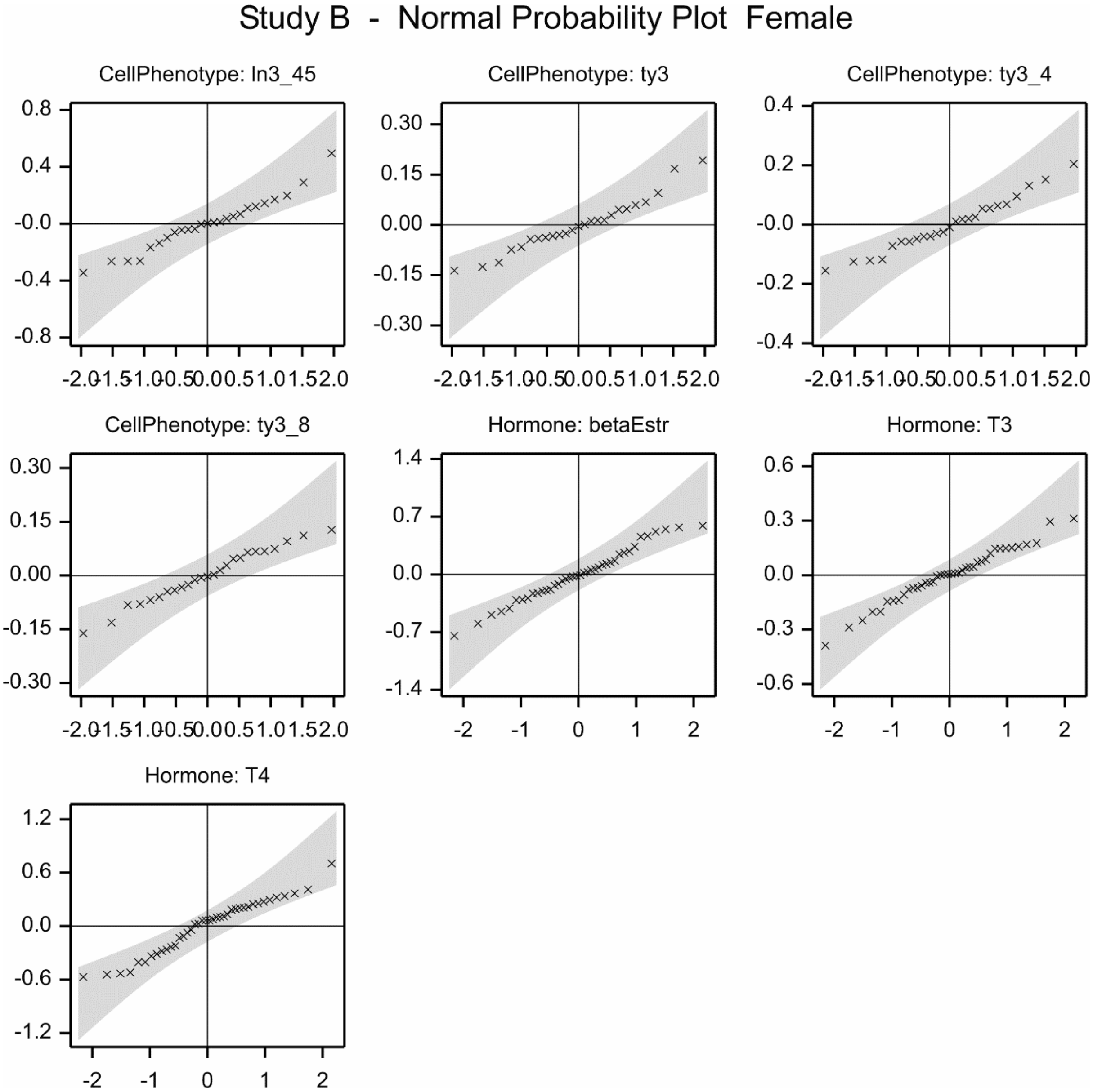
Appendix 6. Normal probability plots of residuals after ANOVA (continued)

Residuals are obtained from ANOVA of cage means (log scale). A 99% confidence envelop is added.



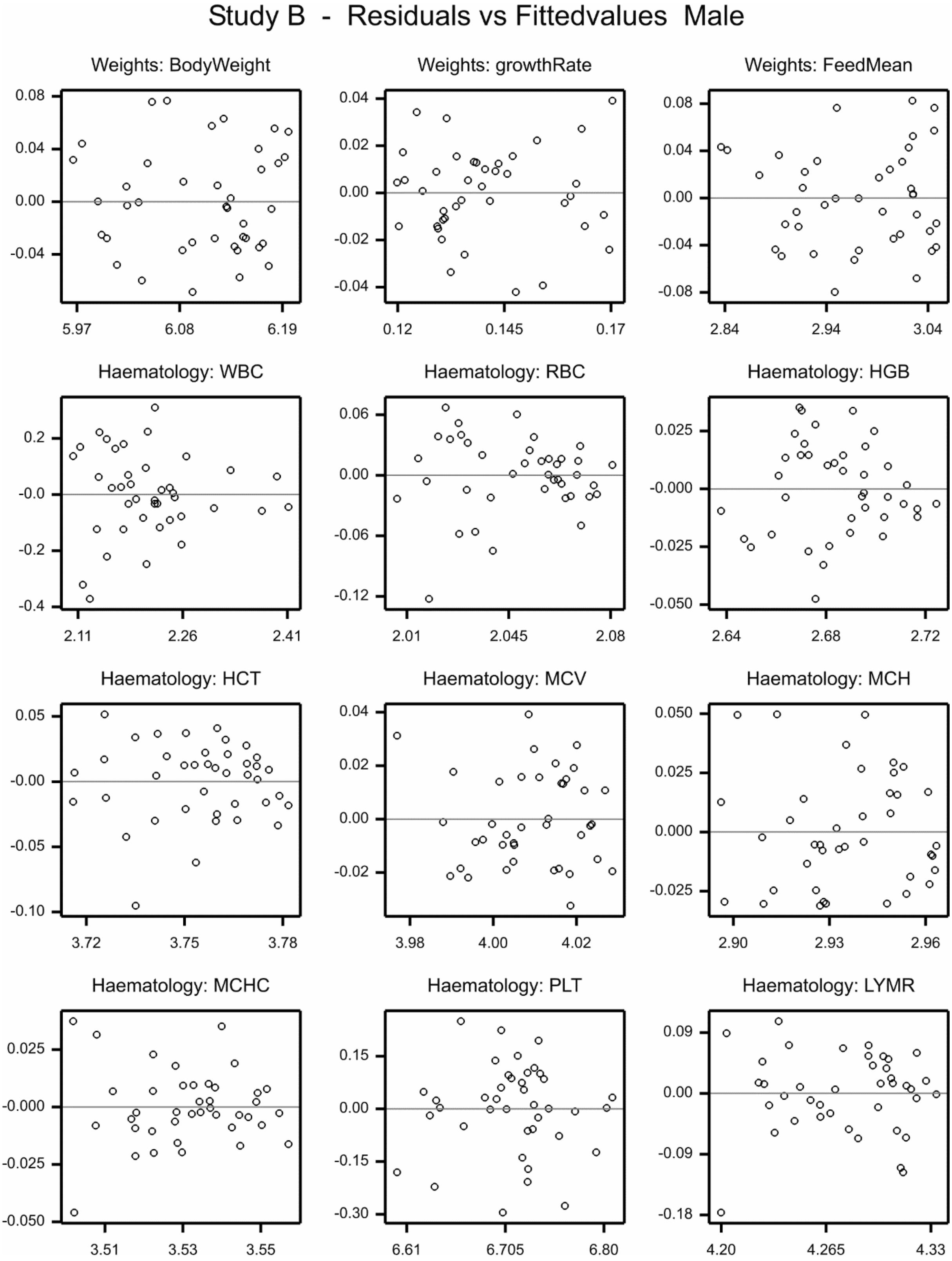
Appendix 6. Normal probability plots of residuals after ANOVA (continued)

Residuals are obtained from ANOVA of cage means (log scale). A 99% confidence envelop is added.



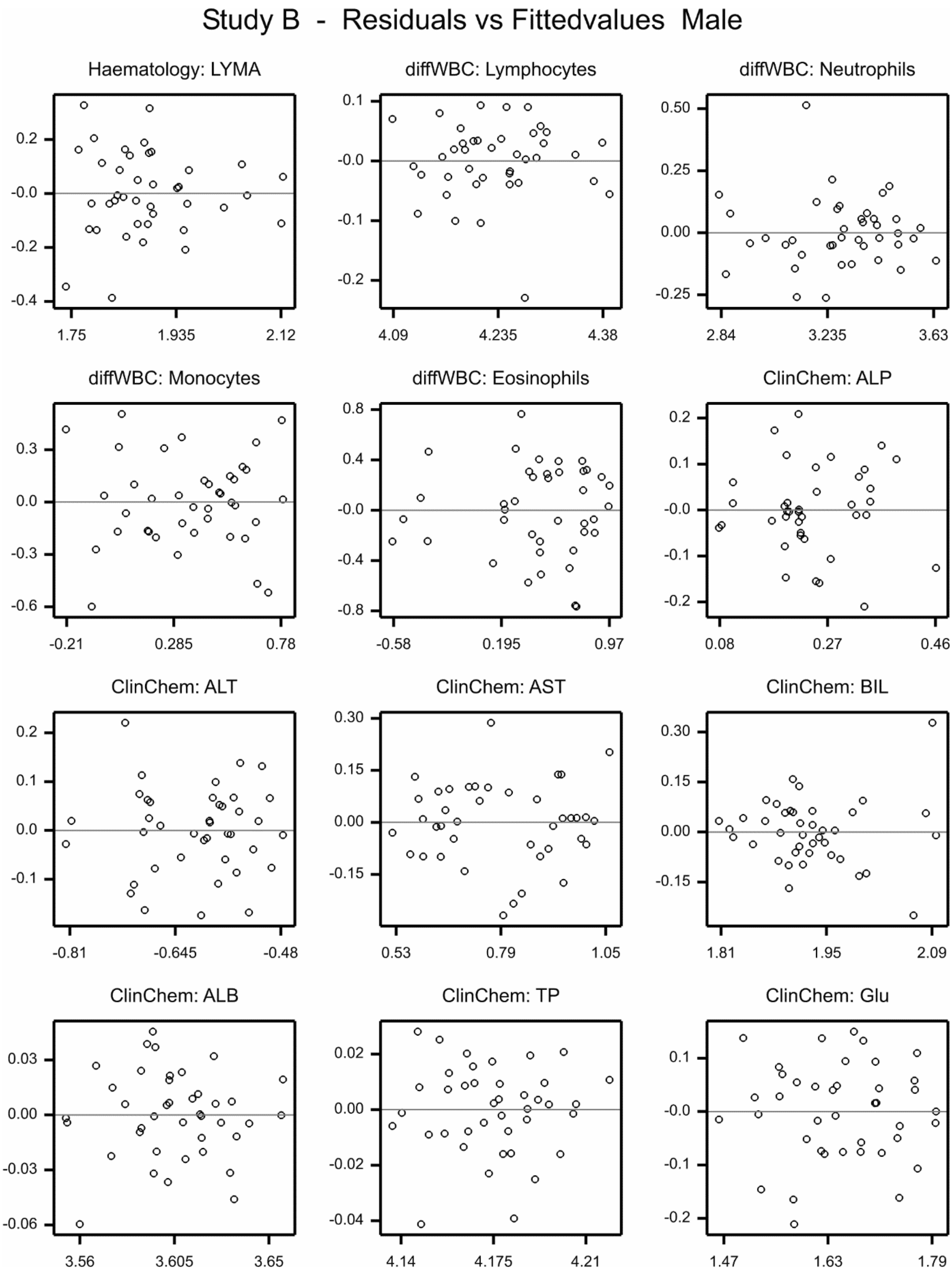
Appendix 7. Graphs of residuals versus fitted values after ANOVA

Residuals and fitted values are obtained from ANOVA of cage means (after a log transformation).



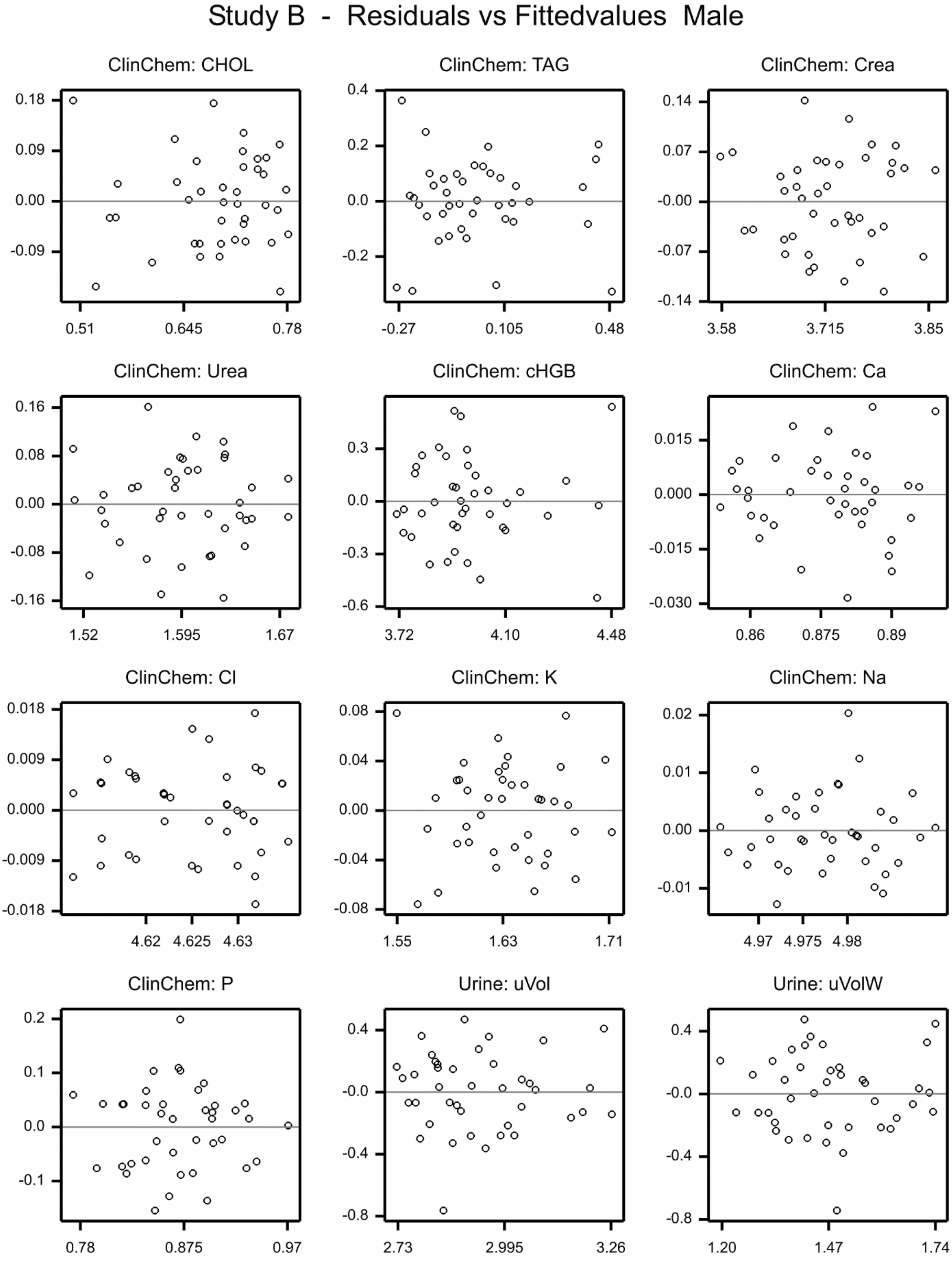
Appendix 7. Graphs of residuals versus fitted values after ANOVA (continued)

Residuals and fitted values are obtained from ANOVA of cage means (after a log transformation).



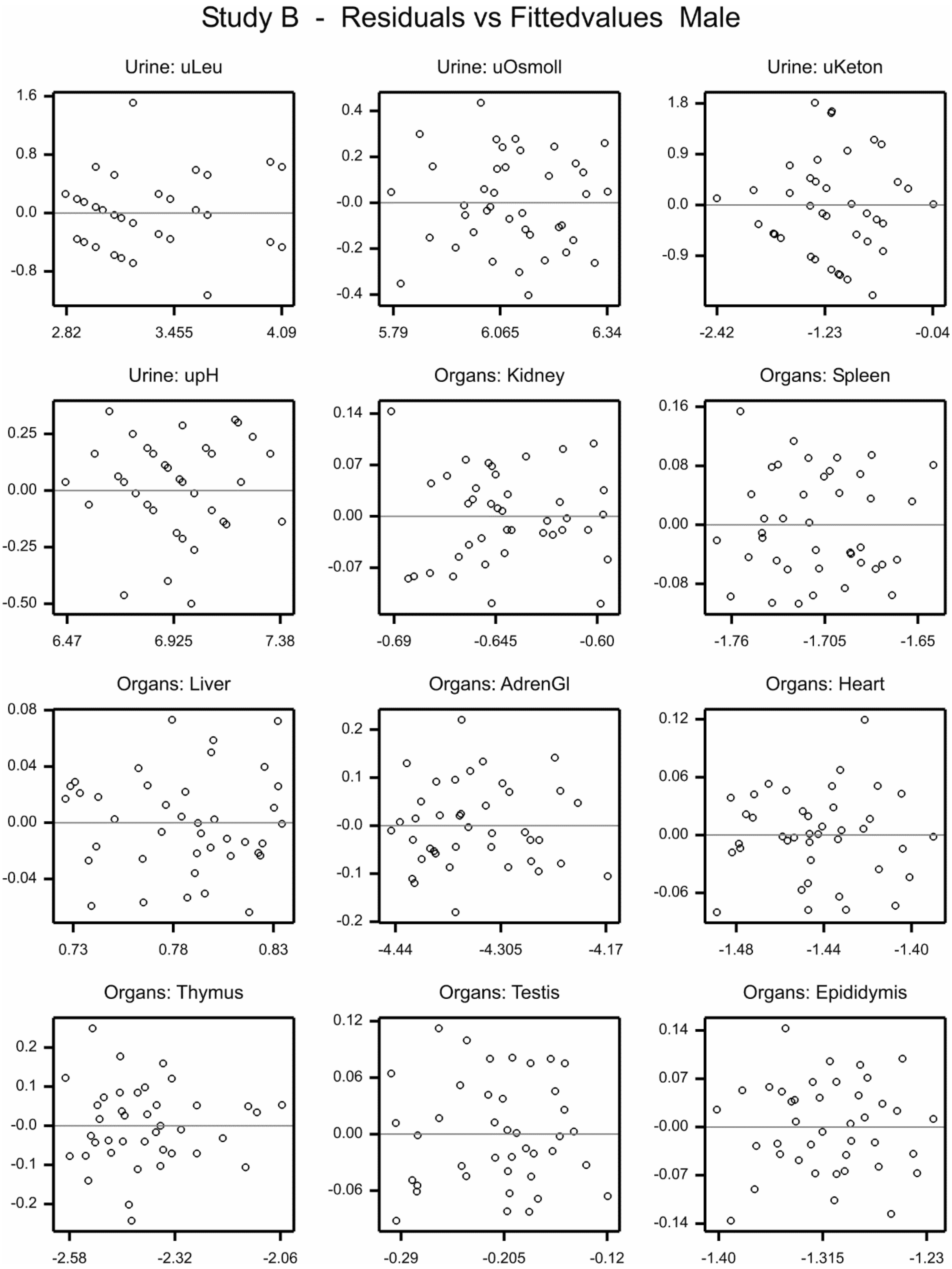
Appendix 7. Graphs of residuals versus fitted values after ANOVA (continued)

Residuals and fitted values are obtained from ANOVA of cage means (after a log transformation).



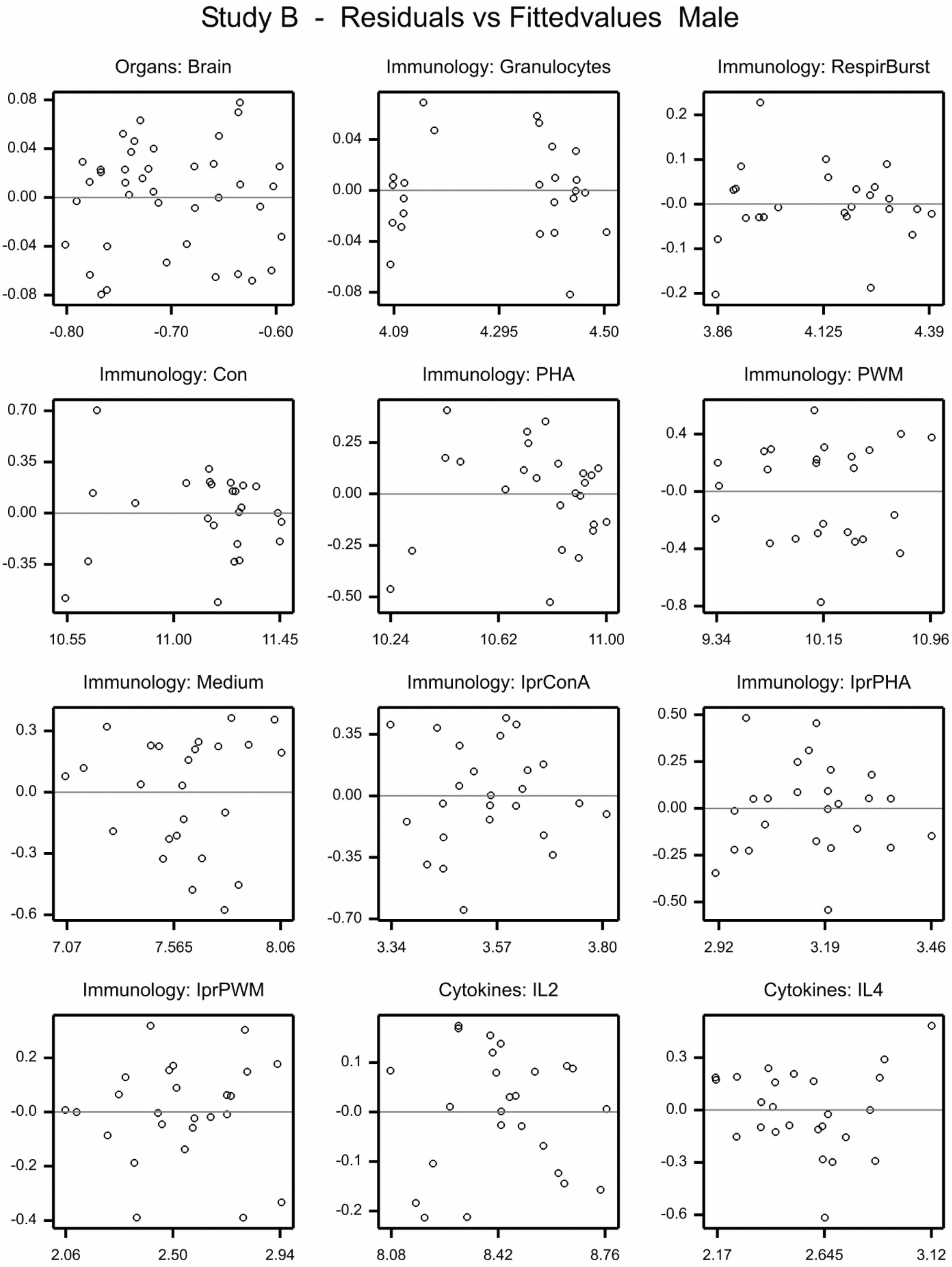
Appendix 7. Graphs of residuals versus fitted values after ANOVA (continued)

Residuals and fitted values are obtained from ANOVA of cage means (after a log transformation).



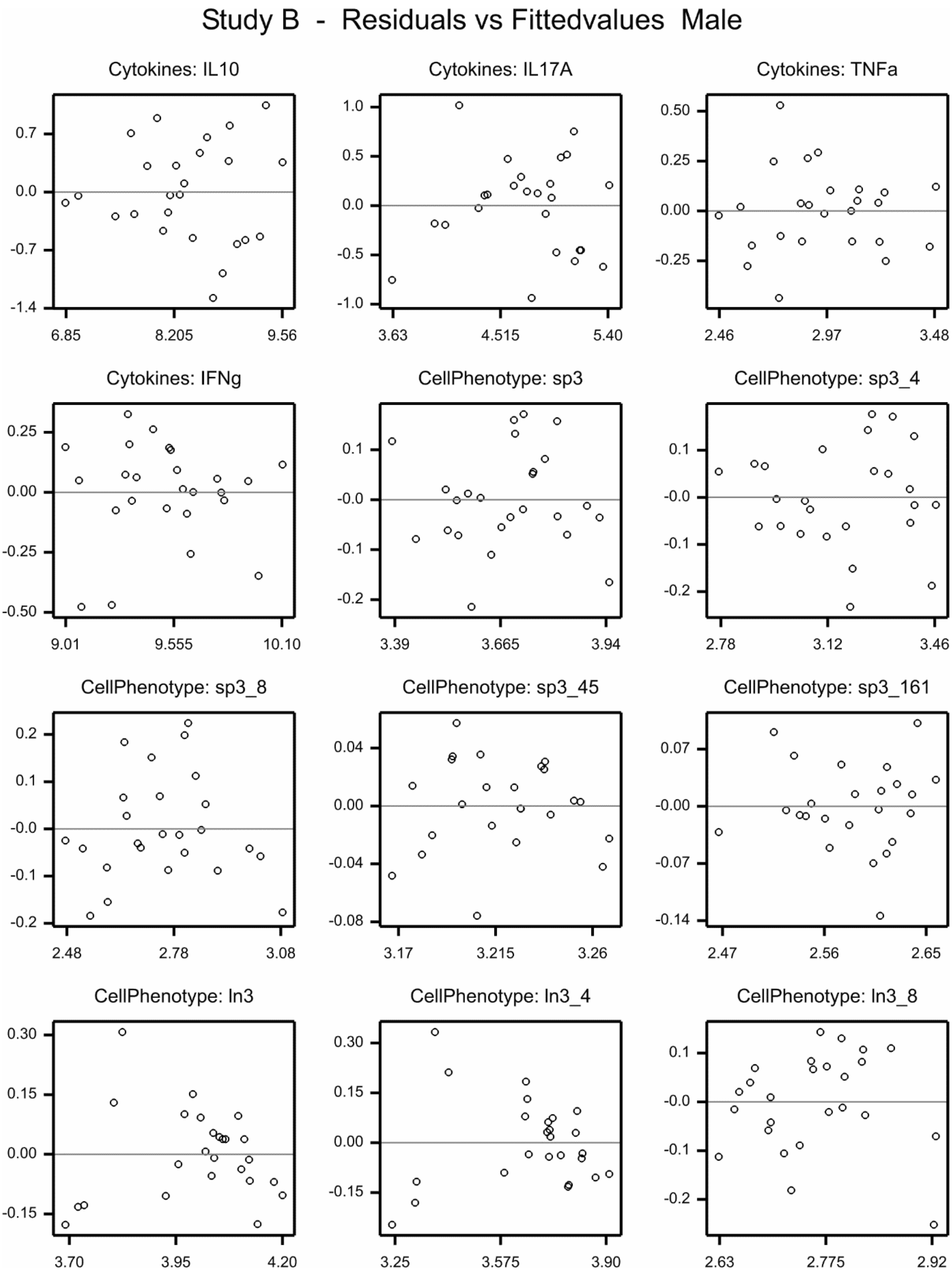
Appendix 7. Graphs of residuals versus fitted values after ANOVA (continued)

Residuals and fitted values are obtained from ANOVA of cage means (after a log transformation).



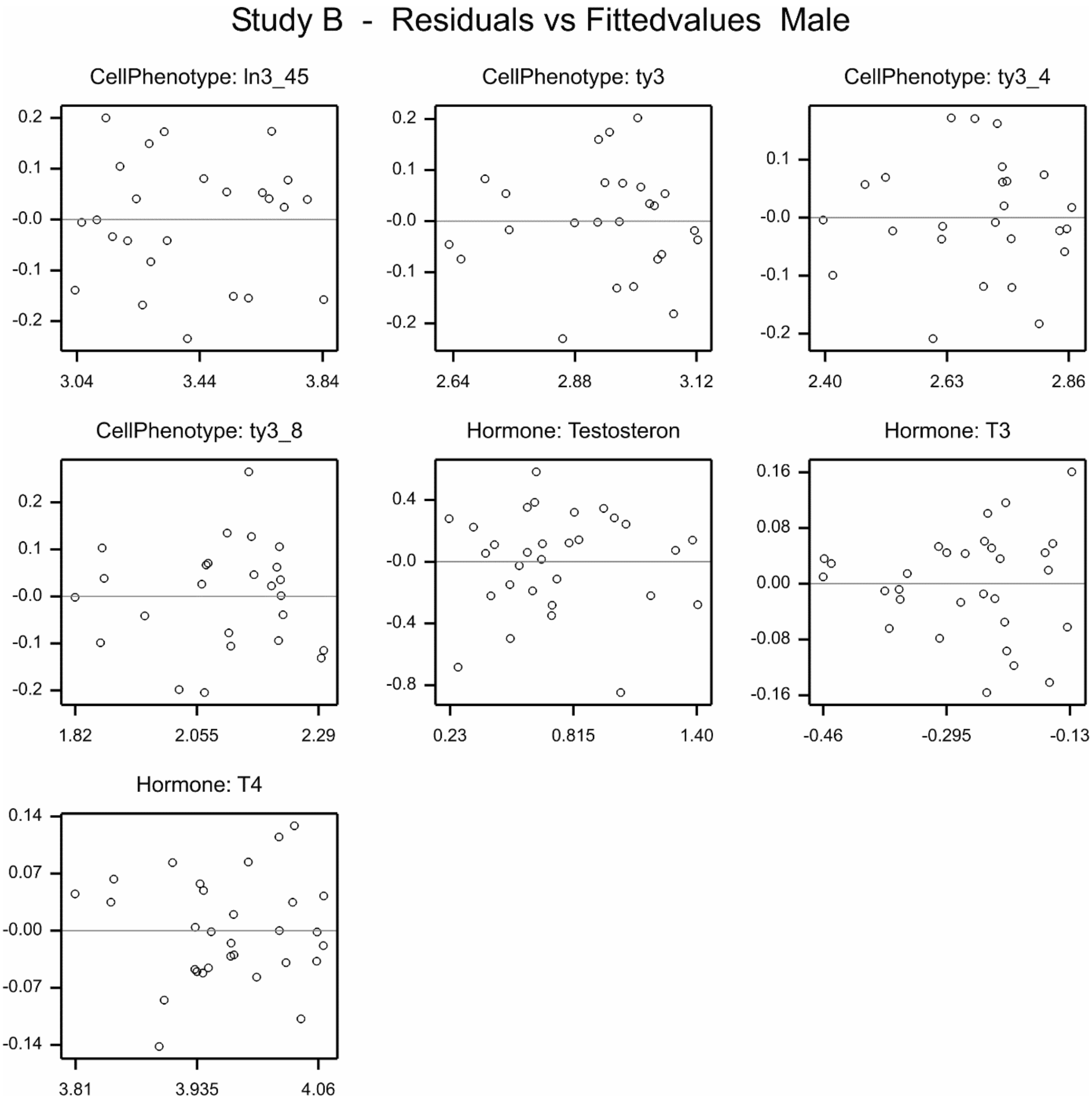
Appendix 7. Graphs of residuals versus fitted values after ANOVA (continued)

Residuals and fitted values are obtained from ANOVA of cage means (after a log transformation).



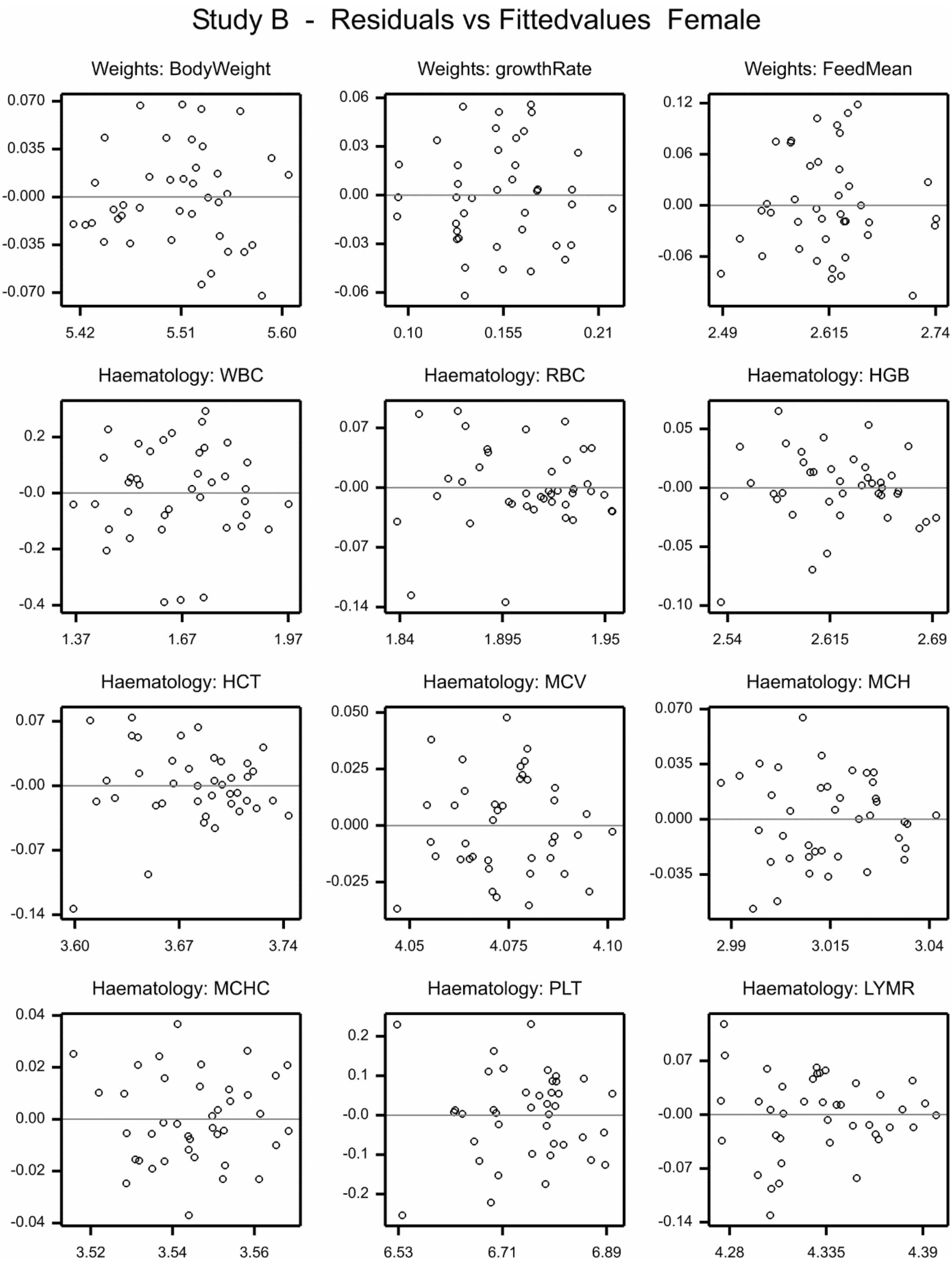
Appendix 7. Graphs of residuals versus fitted values after ANOVA (continued)

Residuals and fitted values are obtained from ANOVA of cage means (after a log transformation).



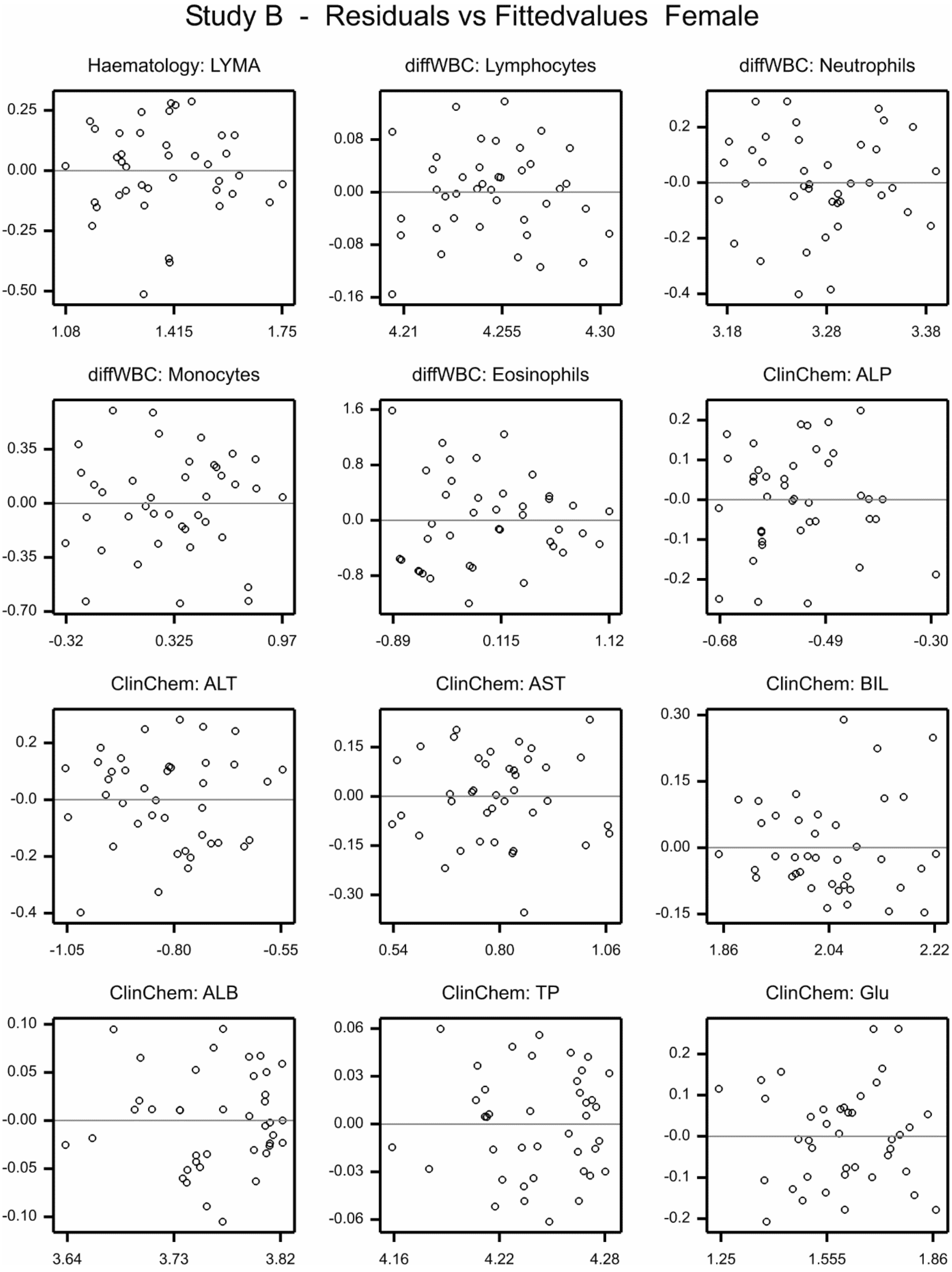
Appendix 7. Graphs of residuals versus fitted values after ANOVA (continued)

Residuals and fitted values are obtained from ANOVA of cage means (after a log transformation).



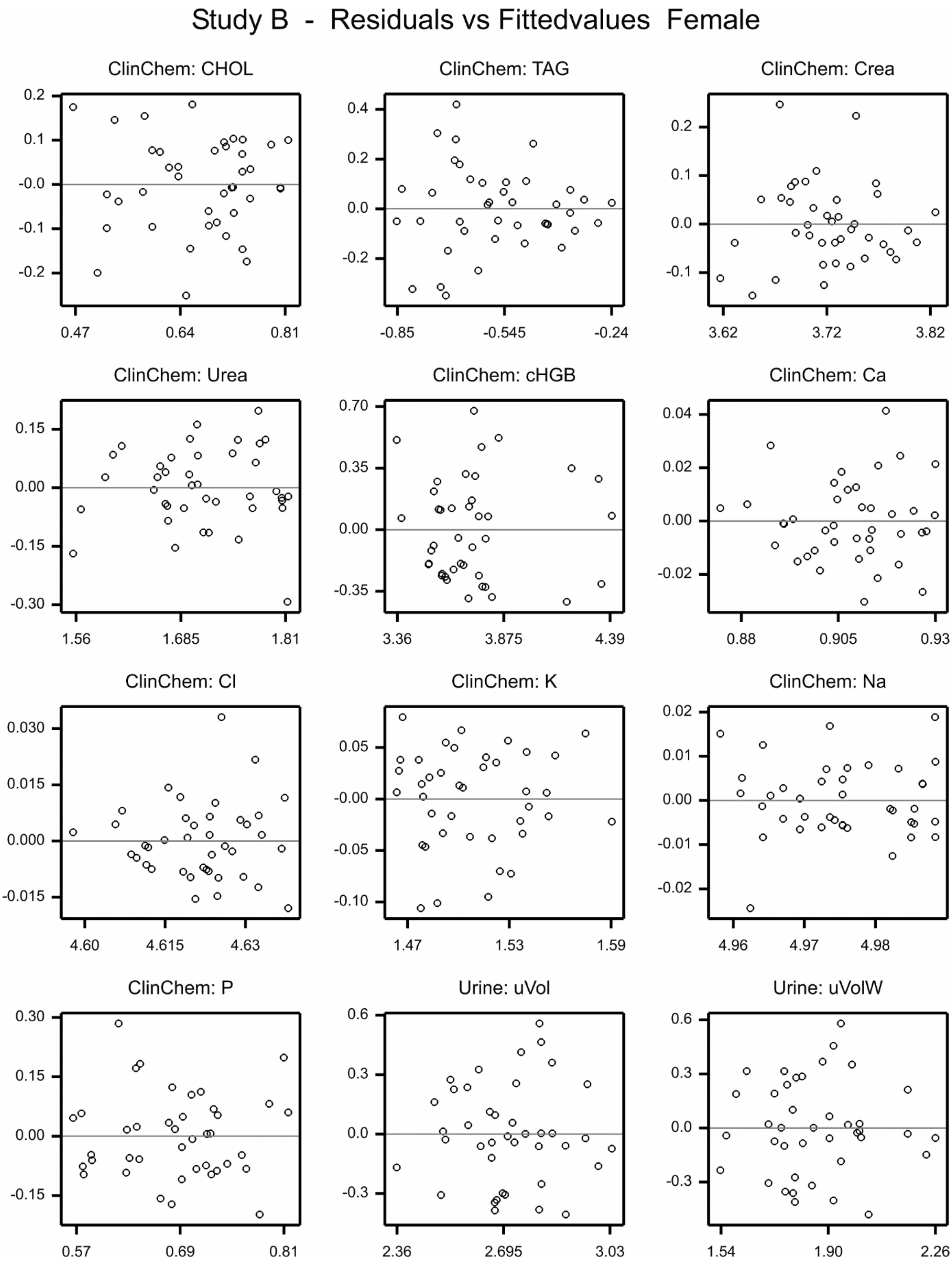
Appendix 7. Graphs of residuals versus fitted values after ANOVA (continued)

Residuals and fitted values are obtained from ANOVA of cage means (after a log transformation).



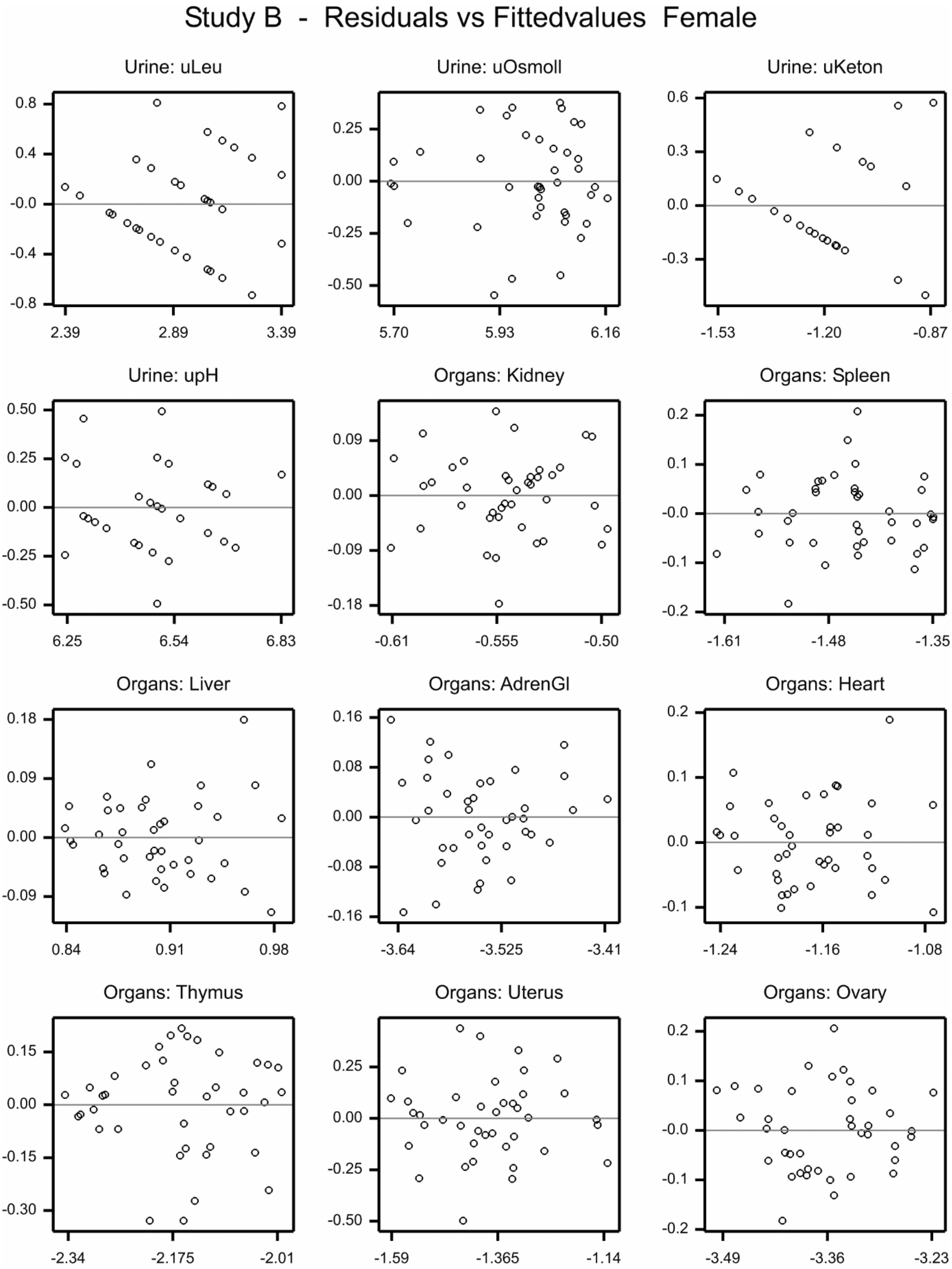
Appendix 7. Graphs of residuals versus fitted values after ANOVA (continued)

Residuals and fitted values are obtained from ANOVA of cage means (after a log transformation).



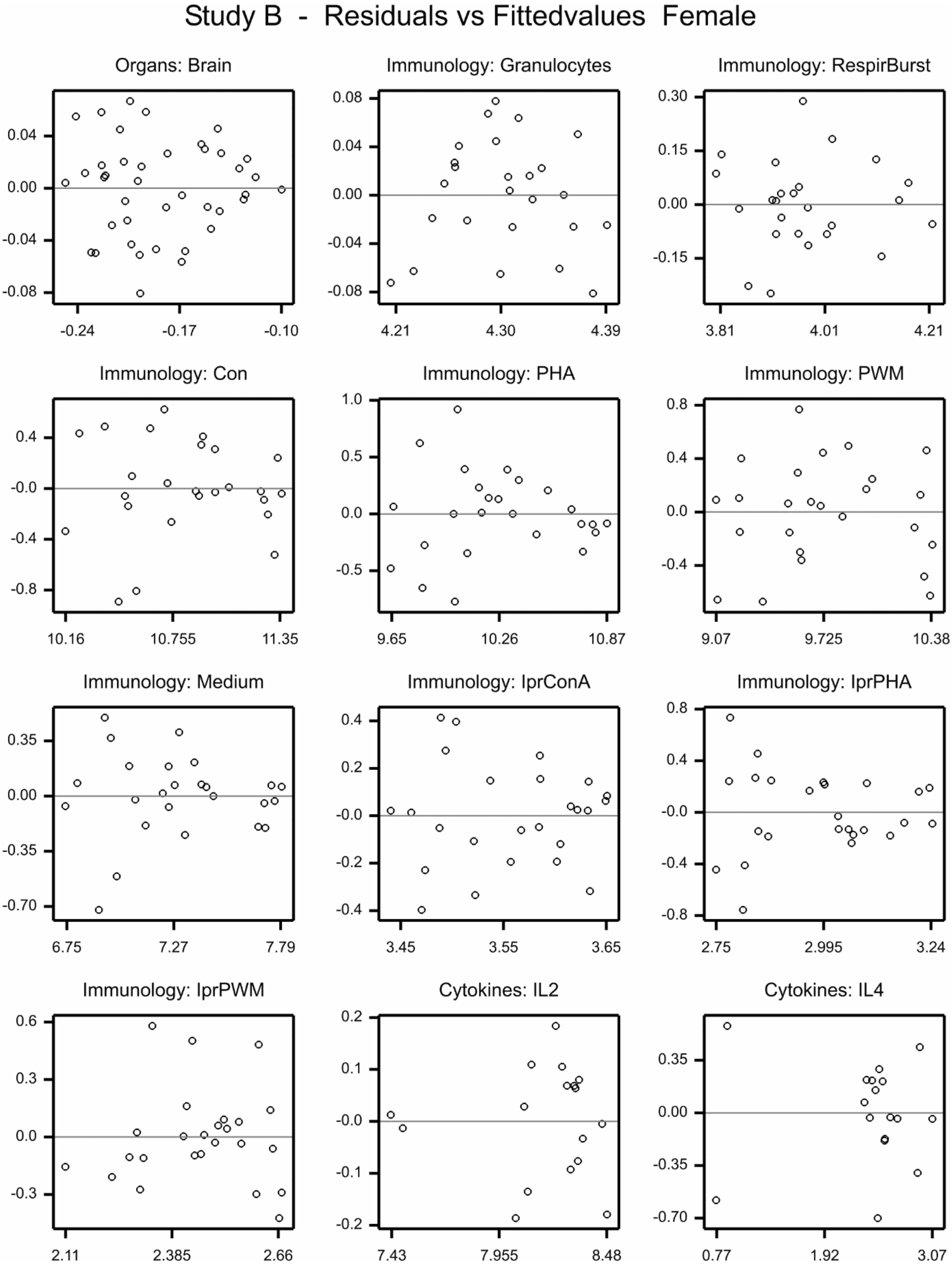
Appendix 7. Graphs of residuals versus fitted values after ANOVA (continued)

Residuals and fitted values are obtained from ANOVA of cage means (after a log transformation).



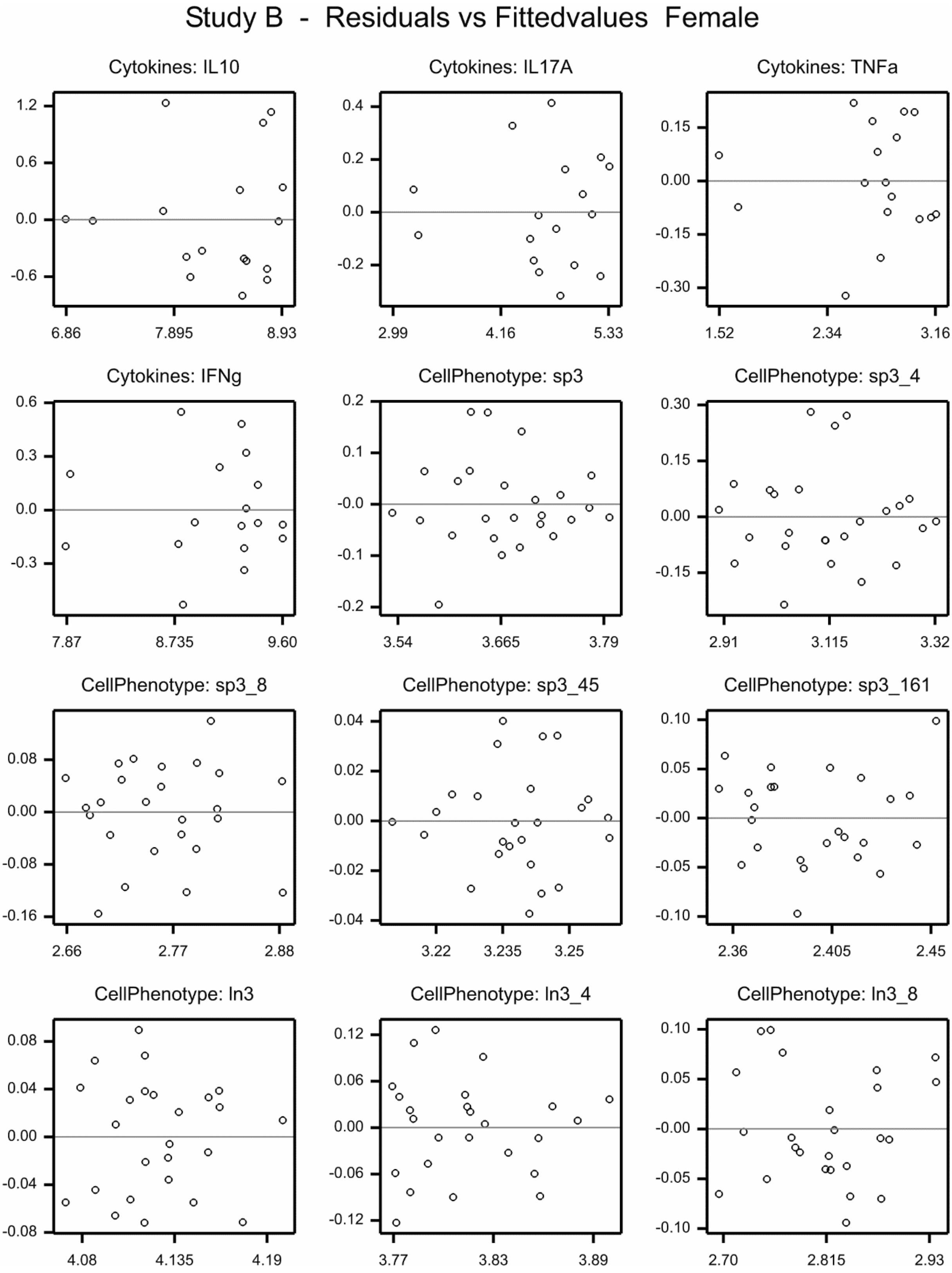
Appendix 7. Graphs of residuals versus fitted values after ANOVA (continued)

Residuals and fitted values are obtained from ANOVA of cage means (after a log transformation).



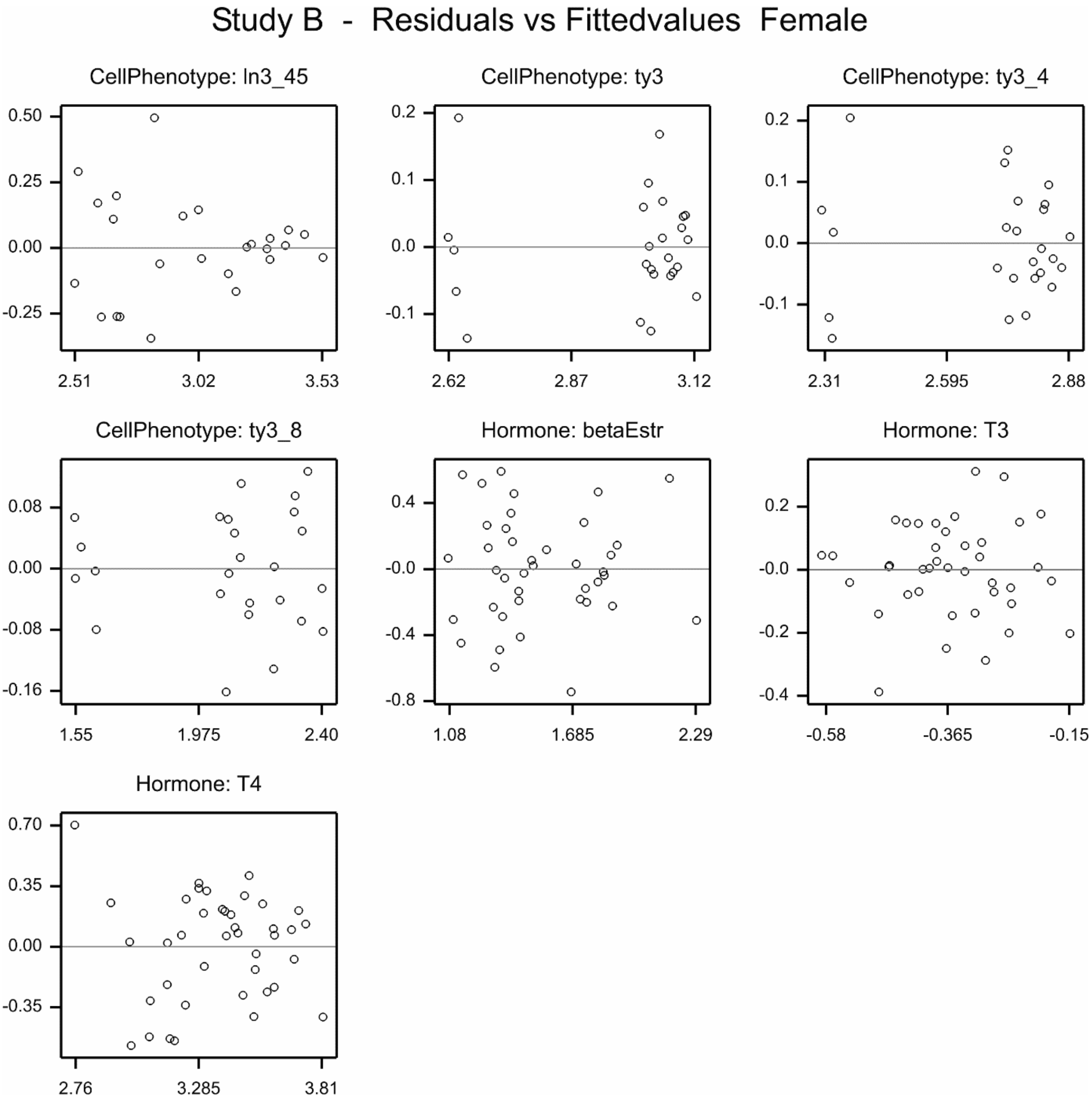
Appendix 7. Graphs of residuals versus fitted values after ANOVA (continued)

Residuals and fitted values are obtained from ANOVA of cage means (after a log transformation).



Appendix 7. Graphs of residuals versus fitted values after ANOVA (continued)

Residuals and fitted values are obtained from ANOVA of cage means (after a log transformation).



Appendix 8. Re-analysis of the GRACE data

The following GRACE data files have been retrieved from the CADIMA website at 29-11-2016:

- Study A: “20161121 Grace Data Trial A (Data Definition V4).xlsx”
- Study B: “20161121 Grace Data Trial B (Data Definition V4).xlsx”
- Study C: “20161121 Grace Data Trial C (Data Definition V4).xlsx”
- Study D: “20161121 Grace Data Trial D (Data Definition V4).xlsx”
- Study E: “20161121 Grace Data Trial E (Data Definition V4).xlsx”

These data files were combined into a single Excel file using GenStat with separate sheets for males and females. Note the following:

- All values which were read from the data files were sorted according to Trial_ID and Animal_ID to make sure that the order of the observations is the same.
- Original cage and animal numbers are not unique across studies. They have been made unique such that cage numbers start at 100, 200, 300, 400 and 500 for the respective studies A to E, while animal numbers start at 1000, 2000, 3000, 4000 and 5000.
- Organ weights in study C are not available after 13 weeks since study C is a one-year study.
- For study C animal weights are available for all 160 animals while haematology and clinical biochemistry measurements are only available for a limited set of 80 animals.
- Values in sheet “Data exclusions” for all studies were already set to missing in the original Excel files. Note that this is not the case when the comment in that sheet reads “will be considered”. This implies that for study A 2 of these values are set to missing, for study B none, for study C only one as the other values are for observations beyond week 13. For studies D and C all values given in “Data exclusions” were set to missing in the original Excel files.
- Organ Weights are expressed as a percentage of the body weight at week 13. This is done for each individual rat.
- The percentage organ weights for Left and Right were summed before analysis.
- There are two HGB variables; one in the haematology group and one in clinical biochemistry. The latter is called cHGB.
- All measurements were LOG transformed, using the natural logarithm. The response variables “Monocyte” and “Eosinophil” contain 3 respectively 28 zeroes. Therefore the value of 0.5 was added to these before taking the logarithm.
- The exponential growth curve was fitted to the weights to obtain an estimate of the growth rate parameter γ. Some weights seems to be outlying although most outliers did not affect the fitted curve that much. Outlying weights were therefore not removed.

Not all cage means are based on two values due to missing observations. These missing observations are listed in Table 1. Only for Cage 170 in Study A (Female rats with feed Conv-1) both values of Ca and Na are missing and these are thus the only missing values for the cage means. The fact that some means are based on one observation rather than two is ignored in the statistical analysis.

Table 1 Missing observations in the five GRACE studies.

Study	Cage	Animal	Sex	Feed	Missing
A	120	1039	M	Conv2	ALP ALT AST Alb Glu Krea TP Urea CHOL Ca Cl K Na P TAG
A	123	1045	M	Conv2	K
A	141	1082	F	GMO-33	ALP ALT AST Alb Glu Krea TP Urea CHOL Ca Cl K Na P TAG
A	162	1123	F	Conv2	ALP ALT AST Alb Glu Krea TP Urea CHOL Ca Cl K Na P TAG
A	163	1125	F	Conv2	Ovary_L Ovary
A	168	1135	F	Conv1	P
A	170	1139	F	Conv1	Ca Na
A	170	1140	F	Conv1	CHOL Ca K Na P TAG
A	176	1152	F	Control	Ca K Na P TAG
B	216	2232	M	GMO-11	ALP ALT AST Alb Glu Krea TP Urea CHOL Ca Cl K Na P TAG
B	220	2240	M	Conv2	PLT
B	240	2280	M	Control	Ca K Na P TAG Kidney_R Kidney
B	255	2310	F	GMO-11	CHOL Ca Cl K Na P TAG
B	257	2314	F	Conv2	ALP ALT AST Alb Glu Krea TP Urea CHOL Ca Cl K Na P TAG
B	264	2327	F	Conv2	Ca K Na P
C	305	3009	M	GMO-33	ALT
C	315	3029	M	GMO-11	ALT
C	325	3050	M	Control	WBC RBC HGB HCT MCV MCH MCHC PLT LYMcount Lymphocyte Neutrophil Monocyte Eosinophil
C	352	3103	F	GMO-33	ALP
C	370	3139	F	GMO-11	ALT
C	374	3147	F	Control	HGB
C	381	3161	F	Conv2	CHOL
D	407	4013	M	GMO-11	Alb TP K
D	408	4016	M	GMO-11	Alb TP K
D	410	4020	M	GMO-11	Alb TP K
D	433	4101	F	GMO-33	Alb TP K
D	437	4109	F	GMO-33	CHOL
D	440	4116	F	GMO-11	Alb TP K
D	443	4122	F	Control	CHOL
E	523	5045	M	GMO-11	Alb TP K
E	525	5050	M	GMO-11	Alb TP K

After compilation of a single Excel data file Tables 3 and 6 of Schmidt et al (2017) were generated in order to check whether the same data have been used. For both tables first cage means were calculated and then the relevant means in Tables 3 and 6. A difference of 1 in the last printed number was ignored in comparing the tables. The following discrepancies were found:

- For Alb, TP and K large discrepancies are found in Table 6. This is due to the fact that Schmidt *et al* (2017) calculated Table 6 **including** the outliers listed in sheet “Data exclusions” for trials D and E. To put it otherwise, when these “Data exclusions” outliers are copied to the sheet “Clinical biochemistry” in the original Excel files, the values in Table 6 are obtained. The outliers are excluded in the analysis presented here.
- For Na a small discrepancy was found in Table 6. This is due to non-rounding of 5 Na values when Table 6 was calculated by Schmidt *et al* (2017).

The cage means on the log scale were subjected to analysis of variance for each trial and sex separately with feed as treatment and no blocking effect (the design is completely randomized). Grubbs’ outlier test at the 1% level was applied to the residuals to detect outliers. This was done repeatedly, i.e. outliers were set to missing, the data were re-analysed and Grubbs’ test was performed again, until no further outliers were found. In the second cycle one extra outlier was found for Males and the third cycle did not detect any further outliers. The outliers thus found are given in Table 2. These outlier are set to missing.

Table 2 Outliers in GRACE studies according to Grubbs' test at the 1% level on the residuals of an analysis of variance for each study and sex separately.

Males: outliers in GRACE studies				
Study	Variable	Feed	Cage	LOG value
A	HGB	Control	135	2.464
A	MCH	Control	135	2.776
A	MCHC	Control	135	3.353
A	ALT	Conv2	123	0.9449
A	AST	Conv2	123	1.321
B	growthR	Conv2	220	-0.2835
B	ALT	Conv2	217	0.04217
B	Alb	Conv2	220	3.310
B	P	Conv2	217	1.523
B	Liver	Control	240	1.075
B	Liver	Conv2	217	1.023
B	Pancreas	Control	235	-2.443
C	MCH	GMO-11	317	3.090
C	MCHC	GMO-11	317	3.702
D	PLT	GMO-11	407	5.005
E	Ca	Control	528	1.094
E	Testis	GMO-11	524	0.1140
E	Epididymis	GMO-11	524	-0.9447
Females: outliers in GRACE studies				
Study	Variable	Feed	Cage	Value
A	MCHC	Conv1	170	3.649
A	PLT	Conv1	170	5.615
A	AST	Conv1	168	0.9291
A	Glu	Conv1	168	1.238
A	K	Conv1	168	2.004
A	Heart	GMO-33	148	-1.512
B	Weight_4	Conv2	257	5.130
B	CHOL	GMO-11	255	1.115
B	Lung	GMO-33	248	-0.5240
B	Uterus	Conv2	262	-3.028
C	MCH	Control	374	1.634
C	MCHC	Control	374	2.223
D	Weight_3	Control	443	5.058
D	PLT	Control	443	5.190

Appendix 9. Sums of squares, degrees of freedom and effective replication for the GRACE data

The values below are based on a simultaneous statistical analysis of the five GRACE studies A-E on cage means after a log-transform and after removal of outliers. The columns have the following interpretation:

- SS_R the between reference feeds sums of squares
- SS_E the residual sums of squares
- df_E the degrees of freedom for the residual sums of squares
- n_{eff} the effective replication
- %R/S the between reference feeds estimated standard error (σ_R) as a percentage of the estimated residual standard error (σ_E), where empty cells denote zero values.

Variable	Male rats					Female rats				
	SS_R	SS_E	df_E	n_{eff}	%R/S	SS_R	SS_E	df_E	n_{eff}	%R/S
BodyWeight	0.008387	0.19554	69	10.50		0.014574	0.26913	69	10.50	
growthRate	0.000206	0.02434	68	10.33		0.000751	0.06011	69	10.50	
FeedMean	0.022190	0.16515	69	10.50	35	0.032193	0.24197	69	10.50	35
WBC	0.489441	2.61275	59	9.25	44	0.356101	3.36561	59	9.25	25
RBC	0.004304	0.14638	59	9.25		0.007652	0.07286	59	9.25	24
HGB	0.008819	0.09808	58	9.08	18	0.003452	0.05478	59	9.25	
HCT	0.005987	0.13627	59	9.25		0.004400	0.04452	59	9.25	22
MCV	0.000242	0.01864	59	9.25		0.000925	0.02226	59	9.25	
MCH	0.001610	0.03980	58	9.08		0.002266	0.05291	58	9.11	
MCHC	0.001347	0.01505	58	9.08	18	0.000187	0.01436	57	8.94	
PLT	0.056905	3.74573	59	9.25		0.057845	1.66444	57	9.08	
LYMA	0.402469	2.53641	59	9.25	38	0.320270	3.15442	59	9.25	23
Lymphocytes	0.008561	0.11920	59	9.25	8	0.012897	0.12741	59	9.25	23
Neutrophils	0.101555	1.54710	59	9.25		0.214056	1.72788	59	9.25	30
Monocytes	0.932225	6.25457	59	9.25	36	0.948050	4.73942	59	9.25	46
Eosinophils	1.831756	12.92053	59	9.25	34	1.006901	14.28882	59	9.25	7
ALP	0.058075	1.80285	59	9.25		0.050742	1.41079	59	9.25	
ALT	0.040433	0.76309	57	8.90		0.143187	3.83379	59	9.25	
AST	0.082408	1.33797	58	9.08		0.108613	2.28004	58	9.08	
ALB	0.003719	0.16461	58	9.08		0.002401	0.49386	59	9.25	
TP	0.003316	0.09254	59	9.25		0.044110	0.30963	59	9.25	35
Glu	0.137923	1.20832	59	9.25	27	0.068248	1.26028	58	9.08	
CHOL	0.157821	0.72566	59	9.25	49	0.066835	0.91290	59	9.25	9
TAG	1.512480	4.78566	59	9.25	63	0.455467	6.38891	59	9.25	7
Crea	0.100802	1.01337	59	9.25	22	0.169402	0.84663	59	9.25	46
Urea	0.162169	0.56082	59	9.25	59	0.212305	0.68252	59	9.25	62
Ca	0.021413	0.21007	58	9.25	23	0.069969	0.13967	58	9.08	83
Cl	0.010708	0.13568	59	9.25	13	0.001771	0.04791	59	9.25	
K	0.025453	0.68615	59	9.25		0.063943	0.62498	58	9.08	23
Na	0.011611	0.16216	59	9.25	8	0.003438	0.04081	58	9.08	16
P	0.071064	0.54837	58	9.08	31	0.084107	0.93345	59	9.25	19

Variable	**Male rats**					**Female rats**				
	SS_R	SS_E	df_E	n_{eff}	%R/S	SS_R	SS_E	df_E	n_{eff}	%R/S
Kidney	0.008755	0.15764	50	8.00		0.002113	0.14971	50	8.00	
Spleen	0.028870	0.32638	50	8.00	11	0.007828	0.48420	50	8.00	
Liver	0.011485	0.10964	48	7.66	18	0.021902	0.24719	50	8.00	12
AdrenGl	0.054960	0.63981	50	8.00	10	0.021734	0.71168	50	8.00	
Heart	0.015268	0.12327	50	8.00	26	0.005002	0.16094	50	8.00	
Thymus	0.135724	1.59675	50	8.00	9	0.168167	0.75330	50	8.00	47
Testis	0.012233	0.26694	50	8.00		-	-	-	-	
Epididymis	0.012314	0.28836	50	8.00		-	-	-	-	
Uterus	-	-	-	-		0.063741	1.37482	49	7.83	
Ovary	-	-	-	-		0.187232	0.81620	50	8.00	48
Brain	0.017742	0.11613	50	8.00	34	0.012478	0.19660	50	8.00	

Appendix 10. Estimated differences between GMO feeds and the control feed

The differences are given along with the residual sums of squares SS_F based on ANOVA on cage means after a log-transform. All residual sums of squares have 28 degrees of freedom.

Variable	Male rats					Female rats				
	NK11-	NK33-	NK11+	NK33+	SS_F	NK11-	NK33-	NK11+	NK33+	SS_F
BodyWeight	0.0483	0.0209	-0.0095	0.0374	0.0607	-0.0107	0.0172	0.0085	0.0323	0.0496
growthRate	-0.0091	-0.0105	0.0007	-0.0013	0.0140	0.0381	0.0340	0.0346	0.0579	0.0376
FeedMean	0.0173	0.0192	-0.0571	-0.0036	0.0661	-0.0906	-0.0081	-0.0260	0.0015	0.1357
WBC	-0.0239	0.0448	0.0829	0.0663	0.8516	-0.0024	0.1167	-0.1006	-0.0067	1.0721
RBC	-0.0057	-0.0026	-0.0167	0.0053	0.0541	-0.0042	0.0208	0.0097	-0.0117	0.0862
HGB	0.0055	0.0056	-0.0204	0.0132	0.0152	-0.0139	0.0283	0.0080	-0.0114	0.0383
HCT	0.0095	0.0162	0.0004	0.0190	0.0342	-0.0113	0.0280	0.0110	0.0041	0.0660
MCV	0.0153	0.0188	0.0171	0.0135	0.0117	-0.0075	0.0070	0.0010	0.0156	0.0179
MCH	-0.0051	0.0081	-0.0040	0.0077	0.0221	-0.0096	0.0080	-0.0015	0.0002	0.0288
MCHC	-0.0202	-0.0103	-0.0205	-0.0056	0.0101	-0.0027	0.0003	-0.0028	-0.0158	0.0110
PLT	-0.0846	0.0156	0.0101	-0.0204	0.6369	-0.0894	0.0020	-0.0983	0.0144	0.4736
LYMA	-0.0318	0.0094	0.0697	0.0725	0.9315	-0.0067	0.1485	-0.0828	0.0139	1.2956
Lymphocytes	-0.0471	-0.0870	-0.0217	-0.0099	0.1512	0.0040	0.0204	0.0400	0.0293	0.1769
Neutrophils	0.1155	0.1734	0.0419	0.0257	0.7460	0.0052	-0.0386	-0.0703	-0.0806	1.1428
Monocytes	0.1252	0.1199	0.0573	-0.1193	2.5522	-0.2828	-0.1615	-0.2051	-0.1566	3.9057
Eosinophils	-0.0785	0.1244	0.1743	0.1810	4.9363	-0.0386	0.1836	-0.2838	0.4304	15.8918
ALP	0.0200	0.0203	-0.0046	0.1359	0.3257	0.0146	0.1354	0.0161	0.0005	0.6179
ALT	0.0178	-0.0286	-0.1214	-0.0150	0.2984	-0.1082	0.0775	-0.0728	-0.1022	1.0551
AST	-0.0378	-0.0585	-0.1142	-0.0700	0.5260	-0.0098	0.0476	-0.0219	0.0441	0.6787
ALB	0.0060	0.0137	0.0381	-0.0006	0.0211	-0.0227	0.0503	0.0396	0.0357	0.0952
TP	0.0109	0.0096	0.0282	0.0036	0.0097	-0.0210	0.0341	0.0319	0.0267	0.0410
Glu	0.0041	-0.0607	-0.0234	0.0324	0.3072	-0.0418	-0.1791	-0.0457	0.0621	0.5302
CHOL	-0.0259	-0.0078	-0.0556	0.0026	0.2605	0.0672	0.0547	0.0545	0.0396	0.4268
TAG	0.0850	0.0283	-0.0182	0.0375	0.8801	0.1253	0.2439	0.1649	0.1011	1.0755
Crea	0.0315	0.0159	0.0832	0.0428	0.1664	0.0255	0.0435	-0.0139	0.0170	0.2758
Urea	-0.0484	-0.0278	-0.0495	-0.0371	0.2073	0.0069	-0.1009	-0.1103	-0.0522	0.3836
Ca	-0.0006	0.0018	0.0052	-0.0041	0.0051	-0.0069	0.0072	0.0095	0.0093	0.0089
Cl	-0.0031	-0.0031	0.0007	0.0001	0.0024	-0.0012	-0.0147	-0.0055	-0.0006	0.0041
K	0.0159	0.0506	0.0457	0.0232	0.0569	0.0021	0.0142	0.0193	0.0526	0.0884
Na	0.0009	0.0039	0.0056	0.0030	0.0018	-0.0060	-0.0029	0.0000	-0.0018	0.0027
P	0.0318	0.0609	0.0248	-0.0217	0.2243	-0.0414	0.0485	-0.0526	-0.0404	0.4356
Kidney	0.0071	0.0316	0.0497	-0.0101	0.1481	-0.0505	-0.0490	-0.0337	-0.0290	0.1704
Spleen	0.0397	-0.0187	0.0523	0.0092	0.1901	-0.0868	-0.0005	-0.1236	-0.0032	0.2242
Liver	0.0129	0.0365	0.0385	0.0048	0.0465	0.0385	0.0130	0.0315	-0.0229	0.1381
AdrenGl	-0.0678	-0.0607	-0.0878	-0.0599	0.2868	-0.1060	-0.0935	-0.0921	-0.0643	0.2015
Heart	0.0399	0.0253	0.0259	-0.0064	0.0755	-0.0342	-0.0481	-0.0378	-0.0003	0.1601
Thymus	0.0628	0.0841	0.1459	0.0563	0.3881	0.0331	0.0385	-0.0208	0.0182	0.7489
Testis	-0.0043	0.0176	0.0353	-0.0005	0.1208	-	-	-	-	-
Epididymis	-0.0114	0.0447	0.0314	0.0194	0.1643	-	-	-	-	-
Uterus	-	-	-	-	-	-0.0016	-0.0379	0.0094	0.1773	1.4886
Ovary	-	-	-	-	-	-0.1285	-0.0760	-0.0539	-0.1577	0.2725
Brain	-0.0232	0.0320	0.0397	0.0003	0.0721	0.0178	-0.0070	-0.0112	-0.0248	0.0509

Appendix 11. Intervals for equivalence tests

95% Confidence interval plus estimate for the ratio Δ of a GMO feed versus the control feed, 95% Confidence interval plus median for (upper) equivalence limits, and the confidence interval plus median for Δ on the ELSD scale. Red background colouring indicates significant differences, green background colouring indicates significant equivalences (in all remaining cases equivalence is still more likely than not).

Males NK11- versus Control									
Weights	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK11-	lower	esti	upper	lower	median	upper	lower	median	upper
BodyWeight	1.001	1.049	1.101	1.131	1.166	1.220	0.004	0.310	0.590
growthRate	0.968	0.991	1.014	1.035	1.050	1.064	-0.623	-0.186	0.298
FeedMean	0.968	1.017	1.069	1.123	1.163	1.272	-0.219	0.110	0.404
Haematology	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK11-	lower	esti	upper	lower	median	upper	lower	median	upper
WBC	0.817	0.976	1.167	1.728	2.017	3.253	-0.269	-0.032	0.224
RBC	0.951	0.994	1.040	1.120	1.154	1.201	-0.333	-0.040	0.281
HGB	0.982	1.006	1.030	1.112	1.139	1.201	-0.142	0.041	0.202
HCT	0.974	1.010	1.046	1.124	1.155	1.204	-0.186	0.064	0.283
MCV	0.994	1.015	1.037	1.034	1.048	1.063	-0.125	0.322	0.749
MCH	0.967	0.995	1.024	1.055	1.075	1.100	-0.445	-0.071	0.342
MCHC	0.961	0.980	0.999	1.032	1.046	1.070	-0.870	-0.437	-0.017
PLT	0.787	0.919	1.072	1.864	2.131	2.544	-0.286	-0.111	0.093
LYMA	0.804	0.969	1.168	1.681	1.952	2.953	-0.301	-0.046	0.235
diffWBC	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK11-	lower	esti	upper	lower	median	upper	lower	median	upper
Lymphocytes	0.885	0.954	1.029	1.042	1.108	1.178	-1.837	-0.467	0.347
Neutrophils	0.950	1.122	1.327	1.426	1.593	1.900	-0.113	0.243	0.568
Monocytes	0.832	1.133	1.544	2.217	2.810	5.268	-0.180	0.117	0.382
Eosinophils	0.601	0.925	1.421	3.161	4.410	10.705	-0.314	-0.051	0.241
ClinChem	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK11-	lower	esti	upper	lower	median	upper	lower	median	upper
ALP	0.914	1.020	1.139	1.544	1.696	1.944	-0.172	0.037	0.224
ALT	0.916	1.018	1.131	1.301	1.400	1.568	-0.269	0.051	0.339
AST	0.837	0.963	1.108	1.417	1.560	1.833	-0.366	-0.083	0.235
ALB	0.978	1.006	1.035	1.143	1.175	1.222	-0.138	0.036	0.190
TP	0.992	1.011	1.030	1.107	1.130	1.166	-0.067	0.088	0.222
Glu	0.902	1.004	1.118	1.441	1.576	1.967	-0.231	0.009	0.240
CHOL	0.883	0.974	1.076	1.336	1.457	1.919	-0.301	-0.065	0.195
TAG	0.908	1.089	1.305	2.291	2.910	7.169	-0.090	0.074	0.227
Crea	0.954	1.032	1.117	1.407	1.521	1.821	-0.113	0.073	0.237
Urea	0.872	0.953	1.041	1.303	1.416	1.901	-0.362	-0.131	0.114
Ca	0.986	0.999	1.013	1.178	1.219	1.323	-0.070	-0.003	0.067
Cl	0.988	0.997	1.006	1.139	1.169	1.234	-0.071	-0.019	0.041
K	0.970	1.016	1.064	1.322	1.397	1.522	-0.090	0.047	0.165
Na	0.993	1.001	1.009	1.152	1.185	1.253	-0.043	0.005	0.049
P	0.942	1.032	1.131	1.263	1.353	1.602	-0.202	0.101	0.370
Organs	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK11-	lower	esti	upper	lower	median	upper	lower	median	upper
Kidney	0.935	1.007	1.085	1.097	1.158	1.233	-0.508	0.049	0.574
Spleen	0.956	1.040	1.132	1.194	1.268	1.417	-0.193	0.163	0.484
Liver	0.972	1.013	1.056	1.121	1.158	1.243	-0.200	0.085	0.338
AdrenGl	0.842	0.934	1.037	1.301	1.406	1.629	-0.469	-0.194	0.104
Heart	0.987	1.041	1.098	1.117	1.162	1.264	-0.090	0.258	0.594
Thymus	0.944	1.065	1.201	1.567	1.751	2.190	-0.105	0.109	0.297
Testis	0.931	0.996	1.065	1.179	1.237	1.326	-0.331	-0.019	0.308
Epididymis	0.914	0.989	1.069	1.174	1.239	1.333	-0.397	-0.052	0.324
Brain	0.928	0.977	1.029	1.116	1.161	1.276	-0.465	-0.148	0.195

Appendix 11. Intervals for equivalence tests (continued)

Males NK33- versus Control									
Weights	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK33-	lower	esti	upper	lower	median	upper	lower	median	upper
BodyWeight	0.974	1.021	1.071	1.131	1.166	1.220	-0.179	0.134	0.404
growthRate	0.967	0.990	1.013	1.035	1.050	1.065	-0.649	-0.215	0.271
FeedMean	0.970	1.019	1.071	1.123	1.163	1.271	-0.209	0.123	0.417
Haematology	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK33-	lower	esti	upper	lower	median	upper	lower	median	upper
WBC	0.875	1.046	1.250	1.728	2.016	3.253	-0.194	0.061	0.288
RBC	0.954	0.997	1.043	1.120	1.154	1.201	-0.325	-0.018	0.308
HGB	0.982	1.006	1.030	1.112	1.139	1.201	-0.143	0.041	0.204
HCT	0.981	1.016	1.053	1.124	1.155	1.204	-0.137	0.111	0.326
MCV	0.998	1.019	1.041	1.034	1.048	1.063	-0.049	0.399	0.830
MCH	0.980	1.008	1.038	1.055	1.075	1.101	-0.297	0.111	0.475
MCHC	0.971	0.990	1.009	1.032	1.046	1.070	-0.626	-0.222	0.209
PLT	0.870	1.016	1.185	1.866	2.130	2.545	-0.185	0.020	0.211
LYMA	0.837	1.009	1.217	1.682	1.952	2.965	-0.272	0.013	0.286
diffWBC	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK33-	lower	esti	upper	lower	median	upper	lower	median	upper
Lymphocytes	0.850	0.917	0.988	1.043	1.106	1.179	-2.000	-0.862	-0.122
Neutrophils	1.006	1.189	1.406	1.426	1.593	1.905	0.012	0.366	0.706
Monocytes	0.827	1.127	1.536	2.213	2.809	5.270	-0.185	0.112	0.380
Eosinophils	0.737	1.132	1.741	3.169	4.405	10.538	-0.210	0.081	0.339
ClinChem	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK33-	lower	esti	upper	lower	median	upper	lower	median	upper
ALP	0.914	1.020	1.140	1.544	1.696	1.944	-0.173	0.038	0.225
ALT	0.874	0.972	1.080	1.301	1.400	1.569	-0.365	-0.083	0.234
AST	0.820	0.943	1.085	1.415	1.559	1.828	-0.404	-0.129	0.191
ALB	0.986	1.014	1.043	1.143	1.175	1.222	-0.090	0.084	0.234
TP	0.991	1.010	1.029	1.107	1.130	1.166	-0.077	0.078	0.212
Glu	0.845	0.941	1.048	1.440	1.577	1.974	-0.335	-0.129	0.102
CHOL	0.899	0.992	1.095	1.336	1.457	1.926	-0.270	-0.020	0.246
TAG	0.858	1.029	1.234	2.288	2.907	7.293	-0.145	0.024	0.181
Crea	0.939	1.016	1.099	1.408	1.522	1.832	-0.152	0.037	0.203
Urea	0.891	0.973	1.062	1.302	1.417	1.911	-0.301	-0.074	0.173
Ca	0.988	1.002	1.016	1.178	1.219	1.321	-0.060	0.009	0.072
Cl	0.988	0.997	1.006	1.139	1.169	1.236	-0.072	-0.019	0.041
K	1.004	1.052	1.102	1.322	1.397	1.522	0.013	0.149	0.272
Na	0.996	1.004	1.012	1.152	1.185	1.254	-0.025	0.023	0.063
P	0.970	1.063	1.165	1.262	1.352	1.606	-0.105	0.194	0.470
Organs	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK33-	lower	esti	upper	lower	median	upper	lower	median	upper
Kidney	0.958	1.032	1.112	1.097	1.158	1.233	-0.312	0.212	0.710
Spleen	0.902	0.981	1.068	1.194	1.268	1.413	-0.401	-0.076	0.286
Liver	0.995	1.037	1.081	1.121	1.159	1.243	-0.037	0.242	0.505
AdrenGl	0.848	0.941	1.044	1.302	1.407	1.627	-0.447	-0.172	0.126
Heart	0.973	1.026	1.082	1.117	1.162	1.264	-0.187	0.163	0.486
Thymus	0.964	1.088	1.227	1.567	1.752	2.192	-0.064	0.146	0.337
Testis	0.952	1.018	1.089	1.179	1.237	1.325	-0.242	0.081	0.363
Epididymis	0.967	1.046	1.131	1.174	1.239	1.333	-0.164	0.205	0.537
Brain	0.980	1.032	1.088	1.116	1.161	1.278	-0.137	0.205	0.527

Appendix 11. Intervals for equivalence tests (continued)

Males NK11+ versus Control									
Weights	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK11+	lower	esti	upper	lower	median	upper	lower	median	upper
0.944	0.991	1.039	1.131	1.166	1.219	-0.340	-0.061	0.254	0.944
0.978	1.001	1.024	1.035	1.050	1.064	-0.490	0.015	0.511	0.978
0.899	0.945	0.993	1.123	1.163	1.272	-0.684	-0.367	-0.047	0.899
Haematology	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK11+	lower	esti	upper	lower	median	upper	lower	median	upper
0.909	1.086	1.299	1.729	2.017	3.245	-0.137	0.113	0.339	0.909
0.940	0.983	1.029	1.120	1.154	1.200	-0.391	-0.116	0.202	0.940
0.957	0.980	1.003	1.112	1.139	1.201	-0.316	-0.153	0.027	0.957
0.965	1.000	1.037	1.124	1.155	1.203	-0.249	0.002	0.253	0.965
0.996	1.017	1.039	1.034	1.048	1.063	-0.084	0.361	0.790	0.996
0.968	0.996	1.025	1.055	1.075	1.101	-0.432	-0.055	0.356	0.968
0.961	0.980	0.999	1.032	1.046	1.069	-0.882	-0.446	-0.021	0.961
0.866	1.010	1.179	1.866	2.130	2.543	-0.195	0.013	0.210	0.866
0.889	1.072	1.292	1.682	1.952	2.949	-0.178	0.101	0.348	0.889
diffWBC	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK11+	lower	esti	upper	lower	median	upper	lower	median	upper
Lymphocytes	0.908	0.979	1.055	1.042	1.108	1.178	-1.487	-0.216	0.771
Neutrophils	0.882	1.043	1.233	1.426	1.593	1.906	-0.275	0.089	0.414
Monocytes	0.777	1.059	1.443	2.219	2.808	5.264	-0.248	0.053	0.326
Eosinophils	0.774	1.190	1.830	3.157	4.399	10.454	-0.173	0.114	0.369
ClinChem	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK11+	lower	esti	upper	lower	median	upper	lower	median	upper
ALP	0.891	0.995	1.112	1.543	1.696	1.942	-0.214	-0.009	0.204
ALT	0.797	0.886	0.984	1.302	1.400	1.567	-0.653	-0.356	-0.047
AST	0.775	0.892	1.027	1.416	1.560	1.826	-0.539	-0.251	0.061
ALB	1.010	1.039	1.068	1.143	1.175	1.222	0.060	0.233	0.391
TP	1.009	1.029	1.048	1.107	1.130	1.166	0.072	0.229	0.371
Glu	0.878	0.977	1.088	1.441	1.577	1.966	-0.259	-0.049	0.187
CHOL	0.857	0.946	1.044	1.336	1.457	1.919	-0.378	-0.140	0.114
TAG	0.819	0.982	1.178	2.293	2.908	7.230	-0.176	-0.015	0.154
Crea	1.004	1.087	1.176	1.407	1.521	1.824	0.009	0.193	0.365
Urea	0.871	0.952	1.039	1.302	1.416	1.902	-0.365	-0.134	0.108
Ca	0.991	1.005	1.019	1.178	1.219	1.324	-0.044	0.026	0.086
Cl	0.991	1.001	1.010	1.139	1.169	1.233	-0.057	0.004	0.062
K	1.000	1.047	1.096	1.321	1.397	1.522	-0.001	0.135	0.256
Na	0.997	1.006	1.014	1.152	1.185	1.253	-0.015	0.032	0.074
P	0.935	1.025	1.124	1.263	1.353	1.601	-0.226	0.079	0.350
Organs	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK11+	lower	esti	upper	lower	median	upper	lower	median	upper
Kidney	0.975	1.051	1.132	1.098	1.158	1.233	-0.181	0.334	0.841
Spleen	0.968	1.054	1.146	1.194	1.268	1.412	-0.137	0.214	0.541
Liver	0.997	1.039	1.084	1.120	1.159	1.244	-0.023	0.254	0.518
AdrenGl	0.826	0.916	1.016	1.300	1.406	1.627	-0.530	-0.252	0.047
Heart	0.973	1.026	1.082	1.117	1.162	1.263	-0.185	0.166	0.489
Thymus	1.026	1.157	1.305	1.566	1.752	2.186	0.044	0.255	0.455
Testis	0.969	1.036	1.108	1.179	1.237	1.327	-0.152	0.163	0.444
Epididymis	0.954	1.032	1.116	1.174	1.239	1.332	-0.226	0.144	0.471
Brain	0.988	1.041	1.096	1.116	1.161	1.278	-0.081	0.257	0.586

Appendix 11. Intervals for equivalence tests (continued)

Males NK33+ versus Control									
Weights	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK33+	lower	esti	upper	lower	median	upper	lower	median	upper
BodyWeight	0.990	1.038	1.089	1.131	1.166	1.220	-0.066	0.240	0.517
growthRate	0.976	0.999	1.022	1.035	1.050	1.064	-0.515	-0.025	0.484
FeedMean	0.948	0.996	1.047	1.123	1.163	1.270	-0.342	-0.021	0.315
Haematology	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK33+	lower	esti	upper	lower	median	upper	lower	median	upper
WBC	0.894	1.069	1.278	1.727	2.017	3.245	-0.158	0.090	0.315
RBC	0.961	1.005	1.052	1.119	1.154	1.201	-0.287	0.037	0.333
HGB	0.989	1.013	1.038	1.113	1.139	1.200	-0.082	0.099	0.257
HCT	0.983	1.019	1.056	1.124	1.155	1.204	-0.117	0.130	0.346
MCV	0.993	1.014	1.035	1.034	1.048	1.063	-0.164	0.285	0.703
MCH	0.979	1.008	1.037	1.055	1.075	1.100	-0.304	0.105	0.467
MCHC	0.975	0.994	1.014	1.032	1.046	1.070	-0.520	-0.120	0.322
PLT	0.840	0.980	1.143	1.867	2.129	2.547	-0.214	-0.027	0.180
LYMA	0.892	1.075	1.296	1.682	1.953	2.966	-0.173	0.104	0.350
diffWBC	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK33+	lower	esti	upper	lower	median	upper	lower	median	upper
Lymphocytes	0.918	0.990	1.068	1.043	1.108	1.178	-1.363	-0.095	1.045
Neutrophils	0.868	1.026	1.213	1.427	1.593	1.907	-0.310	0.054	0.386
Monocytes	0.651	0.888	1.209	2.218	2.808	5.218	-0.379	-0.110	0.186
Eosinophils	0.780	1.198	1.842	3.161	4.408	10.572	-0.170	0.117	0.375
ClinChem	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK33+	lower	esti	upper	lower	median	upper	lower	median	upper
ALP	1.026	1.146	1.279	1.543	1.695	1.940	0.047	0.255	0.445
ALT	0.886	0.985	1.095	1.301	1.399	1.566	-0.336	-0.044	0.279
AST	0.810	0.932	1.073	1.416	1.559	1.829	-0.435	-0.154	0.161
ALB	0.972	0.999	1.028	1.143	1.176	1.222	-0.175	-0.004	0.172
TP	0.985	1.004	1.023	1.107	1.130	1.165	-0.128	0.028	0.168
Glu	0.928	1.033	1.150	1.439	1.576	1.966	-0.167	0.069	0.274
CHOL	0.908	1.003	1.107	1.336	1.457	1.919	-0.263	0.006	0.271
TAG	0.866	1.038	1.245	2.291	2.906	7.158	-0.135	0.033	0.185
Crea	0.964	1.044	1.129	1.407	1.521	1.822	-0.084	0.100	0.263
Urea	0.882	0.964	1.052	1.302	1.417	1.904	-0.328	-0.100	0.145
Ca	0.982	0.996	1.010	1.178	1.219	1.324	-0.080	-0.020	0.049
Cl	0.991	1.000	1.010	1.139	1.169	1.235	-0.061	0.000	0.061
K	0.977	1.023	1.072	1.322	1.397	1.522	-0.068	0.069	0.186
Na	0.995	1.003	1.011	1.152	1.185	1.253	-0.030	0.018	0.059
P	0.893	0.979	1.073	1.263	1.353	1.602	-0.341	-0.070	0.234
Organs	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
MalesNK33+	lower	esti	upper	lower	median	upper	lower	median	upper
Kidney	0.919	0.990	1.067	1.097	1.158	1.234	-0.585	-0.067	0.487
Spleen	0.928	1.009	1.098	1.194	1.268	1.413	-0.330	0.037	0.379
Liver	0.964	1.005	1.048	1.121	1.158	1.243	-0.256	0.032	0.300
AdrenGl	0.849	0.942	1.045	1.301	1.406	1.627	-0.443	-0.170	0.129
Heart	0.942	0.994	1.048	1.117	1.162	1.264	-0.380	-0.039	0.326
Thymus	0.938	1.058	1.193	1.567	1.752	2.189	-0.115	0.098	0.285
Testis	0.935	1.000	1.069	1.179	1.237	1.327	-0.329	-0.002	0.326
Epididymis	0.943	1.020	1.103	1.174	1.239	1.332	-0.286	0.090	0.419
Brain	0.950	1.000	1.054	1.116	1.161	1.276	-0.362	0.002	0.364

Appendix 11. Intervals for equivalence tests (continued)

Females NK11- versus Control									
Weights	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK11-	lower	esti	upper	lower	median	upper	lower	median	upper
BodyWeight	0.948	0.989	1.033	1.169	1.208	1.279	-0.256	-0.057	0.172
growthRate	1.001	1.039	1.079	1.052	1.077	1.102	0.006	0.507	1.016
FeedMean	0.851	0.913	0.981	1.134	1.190	1.330	-0.927	-0.504	-0.102
Haematology	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK11-	lower	esti	upper	lower	median	upper	lower	median	upper
WBC	0.816	0.998	1.219	1.792	2.091	2.977	-0.278	-0.003	0.274
RBC	0.941	0.996	1.054	1.040	1.089	1.157	-0.920	-0.050	0.828
HGB	0.950	0.986	1.024	1.058	1.085	1.124	-0.601	-0.169	0.310
HCT	0.941	0.989	1.039	1.021	1.063	1.113	-2.000	-0.196	2.000
MCV	0.967	0.992	1.019	1.032	1.050	1.071	-0.660	-0.151	0.409
MCH	0.958	0.990	1.024	1.065	1.087	1.118	-0.466	-0.113	0.290
MCHC	0.977	0.997	1.018	1.027	1.041	1.055	-0.576	-0.068	0.474
PLT	0.800	0.915	1.045	1.500	1.655	1.904	-0.407	-0.175	0.089
LYMA	0.797	0.993	1.238	1.717	2.005	2.809	-0.325	-0.009	0.315
diffWBC	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK11-	lower	esti	upper	lower	median	upper	lower	median	upper
Lymphocytes	0.925	1.004	1.089	1.040	1.112	1.203	-1.878	0.040	2.000
Neutrophils	0.817	1.005	1.236	1.421	1.640	2.207	-0.431	0.010	0.444
Monocytes	0.514	0.754	1.105	1.754	2.344	4.710	-0.770	-0.317	0.119
Eosinophils	0.445	0.962	2.081	1.737	3.206	6.159	-0.892	-0.034	0.831
ClinChem	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK11-	lower	esti	upper	lower	median	upper	lower	median	upper
ALP	0.872	1.015	1.182	1.399	1.545	1.761	-0.332	0.033	0.370
ALT	0.736	0.897	1.095	1.832	2.117	2.611	-0.373	-0.141	0.123
AST	0.844	0.990	1.161	1.601	1.797	2.152	-0.279	-0.017	0.259
ALB	0.921	0.978	1.038	1.249	1.311	1.396	-0.273	-0.083	0.140
TP	0.942	0.979	1.018	1.215	1.272	1.447	-0.226	-0.084	0.075
Glu	0.833	0.959	1.104	1.392	1.531	1.768	-0.390	-0.096	0.238
CHOL	0.942	1.070	1.214	1.315	1.432	1.659	-0.167	0.183	0.498
TAG	0.927	1.133	1.385	2.306	2.776	3.989	-0.075	0.120	0.292
Crea	0.927	1.026	1.136	1.365	1.493	1.975	-0.194	0.060	0.287
Urea	0.893	1.007	1.135	1.312	1.455	2.060	-0.311	0.018	0.335
Ca	0.975	0.993	1.011	1.170	1.230	1.514	-0.109	-0.031	0.054
Cl	0.987	0.999	1.011	1.076	1.092	1.117	-0.145	-0.014	0.126
K	0.946	1.002	1.061	1.313	1.396	1.612	-0.168	0.006	0.176
Na	0.984	0.994	1.004	1.073	1.089	1.124	-0.171	-0.069	0.048
P	0.844	0.959	1.090	1.326	1.446	1.711	-0.419	-0.110	0.238
Organs	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK11-	lower	esti	upper	lower	median	upper	lower	median	upper
Kidney	0.878	0.951	1.030	1.071	1.139	1.201	-1.102	-0.387	0.246
Spleen	0.837	0.917	1.005	1.242	1.324	1.436	-0.606	-0.305	0.019
Liver	0.967	1.039	1.117	1.169	1.231	1.353	-0.161	0.181	0.495
AdrenGl	0.825	0.899	0.981	1.330	1.428	1.579	-0.518	-0.294	-0.052
Heart	0.894	0.966	1.044	1.089	1.153	1.220	-0.787	-0.239	0.329
Thymus	0.874	1.034	1.222	1.278	1.459	2.015	-0.383	0.083	0.518
Uterus	0.788	0.998	1.264	1.268	1.517	1.822	-0.659	-0.005	0.653
Ovary	0.795	0.879	0.973	1.406	1.557	2.174	-0.506	-0.279	-0.056
Brain	0.974	1.018	1.063	1.167	1.213	1.295	-0.136	0.090	0.287

Appendix 11. Intervals for equivalence tests (continued)

Females NK33- versus Control

Weights	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK33-	lower	esti	upper	lower	median	upper	lower	median	upper
BodyWeight	0.974	1.017	1.062	1.169	1.208	1.280	-0.137	0.089	0.286
growthRate	0.997	1.035	1.074	1.052	1.077	1.102	-0.044	0.455	0.962
FeedMean	0.924	0.992	1.065	1.135	1.190	1.330	-0.440	-0.043	0.383
Haematology	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK33-	lower	esti	upper	lower	median	upper	lower	median	upper
WBC	0.920	1.124	1.373	1.792	2.090	2.978	-0.113	0.153	0.394
RBC	0.965	1.021	1.081	1.040	1.089	1.157	-0.523	0.240	1.091
HGB	0.990	1.029	1.068	1.058	1.085	1.123	-0.119	0.340	0.796
HCT	0.978	1.028	1.081	1.021	1.063	1.136	-0.587	0.485	2.000
MCV	0.981	1.007	1.033	1.031	1.050	1.070	-0.417	0.139	0.656
MCH	0.975	1.008	1.042	1.064	1.087	1.118	-0.305	0.094	0.451
MCHC	0.980	1.000	1.021	1.027	1.041	1.055	-0.546	0.008	0.555
PLT	0.877	1.002	1.145	1.500	1.655	1.903	-0.266	0.004	0.271
LYMA	0.931	1.160	1.446	1.714	2.005	2.808	-0.103	0.208	0.495
diffWBC	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK33-	lower	esti	upper	lower	median	upper	lower	median	upper
Lymphocytes	0.941	1.021	1.107	1.040	1.112	1.204	-1.048	0.195	2.000
Neutrophils	0.782	0.962	1.183	1.419	1.640	2.218	-0.469	-0.076	0.354
Monocytes	0.580	0.851	1.247	1.755	2.341	4.718	-0.609	-0.180	0.266
Eosinophils	0.555	1.202	2.599	1.733	3.199	6.089	-0.644	0.157	0.981
ClinChem	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK33-	lower	esti	upper	lower	median	upper	lower	median	upper
ALP	0.983	1.145	1.333	1.398	1.545	1.761	-0.038	0.306	0.628
ALT	0.886	1.081	1.318	1.831	2.117	2.609	-0.163	0.102	0.333
AST	0.894	1.049	1.230	1.602	1.798	2.151	-0.192	0.081	0.318
ALB	0.991	1.052	1.116	1.249	1.310	1.396	-0.034	0.184	0.378
TP	0.995	1.035	1.076	1.215	1.272	1.448	-0.021	0.137	0.283
Glu	0.726	0.836	0.963	1.391	1.530	1.768	-0.732	-0.415	-0.086
CHOL	0.931	1.056	1.199	1.315	1.432	1.656	-0.203	0.149	0.465
TAG	1.044	1.276	1.560	2.308	2.778	3.966	0.040	0.234	0.414
Crea	0.943	1.044	1.156	1.365	1.493	1.975	-0.147	0.103	0.327
Urea	0.802	0.904	1.019	1.312	1.454	2.065	-0.568	-0.254	0.048
Ca	0.989	1.007	1.026	1.170	1.230	1.514	-0.053	0.032	0.111
Cl	0.973	0.985	0.998	1.076	1.092	1.117	-0.291	-0.165	-0.026
K	0.958	1.014	1.074	1.313	1.396	1.621	-0.131	0.041	0.192
Na	0.987	0.997	1.007	1.073	1.089	1.125	-0.136	-0.033	0.084
P	0.924	1.050	1.193	1.325	1.447	1.714	-0.218	0.128	0.434
Organs	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK33-	lower	esti	upper	lower	median	upper	lower	median	upper
Kidney	0.879	0.952	1.031	1.071	1.139	1.201	-1.078	-0.374	0.270
Spleen	0.912	0.999	1.095	1.242	1.324	1.437	-0.340	-0.002	0.339
Liver	0.943	1.013	1.089	1.169	1.231	1.352	-0.292	0.061	0.382
AdrenGl	0.835	0.911	0.993	1.331	1.428	1.578	-0.482	-0.259	-0.017
Heart	0.882	0.953	1.030	1.089	1.153	1.220	-0.894	-0.334	0.225
Thymus	0.879	1.039	1.229	1.279	1.458	2.035	-0.365	0.095	0.527
Uterus	0.760	0.963	1.219	1.268	1.518	1.822	-0.696	-0.090	0.543
Ovary	0.838	0.927	1.025	1.406	1.557	2.163	-0.374	-0.164	0.054
Brain	0.951	0.993	1.037	1.167	1.212	1.296	-0.242	-0.036	0.190

Appendix 11. Intervals for equivalence tests (continued)

Females NK11+ versus Control									
Weights	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK11+	lower	esti	upper	lower	median	upper	lower	median	upper
BodyWeight	0.966	1.009	1.053	1.169	1.208	1.281	-0.183	0.045	0.247
growthRate	0.997	1.035	1.075	1.052	1.077	1.102	-0.039	0.460	0.964
FeedMean	0.907	0.974	1.046	1.134	1.190	1.329	-0.518	-0.143	0.266
Haematology	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK11+	lower	esti	upper	lower	median	upper	lower	median	upper
WBC	0.740	0.904	1.105	1.792	2.091	2.978	-0.371	-0.132	0.136
RBC	0.954	1.010	1.069	1.041	1.089	1.156	-0.714	0.113	0.961
HGB	0.971	1.008	1.047	1.058	1.085	1.123	-0.395	0.095	0.540
HCT	0.962	1.011	1.063	1.021	1.063	1.116	-2.000	0.188	2.000
MCV	0.975	1.001	1.027	1.032	1.050	1.070	-0.565	0.020	0.590
MCH	0.966	0.999	1.032	1.064	1.087	1.118	-0.412	-0.016	0.395
MCHC	0.977	0.997	1.018	1.027	1.041	1.055	-0.574	-0.072	0.468
PLT	0.793	0.906	1.035	1.500	1.654	1.900	-0.428	-0.192	0.068
LYMA	0.738	0.920	1.147	1.714	2.007	2.815	-0.396	-0.115	0.202
diffWBC	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK11+	lower	esti	upper	lower	median	upper	lower	median	upper
Lymphocytes	0.959	1.041	1.129	1.040	1.112	1.226	-0.588	0.388	2.000
Neutrophils	0.758	0.932	1.146	1.419	1.640	2.214	-0.523	-0.139	0.286
Monocytes	0.556	0.815	1.194	1.755	2.344	4.760	-0.665	-0.229	0.214
Eosinophils	0.348	0.753	1.629	1.734	3.201	6.133	-1.057	-0.243	0.508
ClinChem	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK11+	lower	esti	upper	lower	median	upper	lower	median	upper
ALP	0.873	1.016	1.183	1.400	1.545	1.761	-0.323	0.035	0.371
ALT	0.762	0.930	1.134	1.831	2.117	2.614	-0.327	-0.096	0.170
AST	0.834	0.978	1.147	1.601	1.797	2.149	-0.288	-0.038	0.241
ALB	0.980	1.040	1.104	1.248	1.310	1.395	-0.074	0.145	0.338
TP	0.993	1.032	1.074	1.215	1.272	1.447	-0.031	0.128	0.275
Glu	0.830	0.955	1.100	1.391	1.529	1.769	-0.400	-0.105	0.230
CHOL	0.931	1.056	1.198	1.315	1.431	1.656	-0.208	0.148	0.464
TAG	0.965	1.179	1.441	2.304	2.776	3.987	-0.035	0.158	0.333
Crea	0.891	0.986	1.092	1.365	1.493	1.980	-0.269	-0.033	0.223
Urea	0.794	0.896	1.010	1.312	1.454	2.059	-0.598	-0.279	0.021
Ca	0.991	1.010	1.028	1.170	1.230	1.511	-0.042	0.042	0.123
Cl	0.982	0.994	1.007	1.076	1.092	1.116	-0.182	-0.062	0.078
K	0.962	1.019	1.080	1.312	1.396	1.617	-0.116	0.056	0.204
Na	0.990	1.000	1.010	1.073	1.089	1.125	-0.118	0.001	0.119
P	0.835	0.949	1.078	1.325	1.447	1.714	-0.447	-0.138	0.205
Organs	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK11+	lower	esti	upper	lower	median	upper	lower	median	upper
Kidney	0.893	0.967	1.047	1.071	1.138	1.200	-0.935	-0.257	0.411
Spleen	0.806	0.884	0.969	1.242	1.324	1.435	-0.753	-0.436	-0.112
Liver	0.960	1.032	1.109	1.169	1.231	1.353	-0.196	0.148	0.460
AdrenGl	0.836	0.912	0.995	1.330	1.428	1.579	-0.478	-0.255	-0.015
Heart	0.891	0.963	1.040	1.089	1.153	1.219	-0.812	-0.262	0.304
Thymus	0.828	0.979	1.158	1.278	1.458	2.020	-0.494	-0.053	0.420
Uterus	0.797	1.009	1.278	1.270	1.518	1.824	-0.632	0.021	0.661
Ovary	0.856	0.947	1.048	1.406	1.558	2.161	-0.321	-0.116	0.106
Brain	0.947	0.989	1.033	1.167	1.213	1.295	-0.255	-0.057	0.169

Appendix 11. Intervals for equivalence tests (continued)

Females NK33+ versus Control									
Weights	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK33+	lower	esti	upper	lower	median	upper	lower	median	upper
BodyWeight	0.989	1.033	1.078	1.169	1.209	1.280	-0.056	0.168	0.368
growthRate	1.021	1.060	1.100	1.052	1.077	1.102	0.273	0.772	1.333
FeedMean	0.933	1.001	1.075	1.134	1.191	1.330	-0.422	0.007	0.431
Haematology	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK33+	lower	esti	upper	lower	median	upper	lower	median	upper
WBC	0.813	0.993	1.214	1.794	2.092	2.978	-0.278	-0.009	0.268
RBC	0.934	0.988	1.046	1.040	1.089	1.156	-0.979	-0.136	0.676
HGB	0.952	0.989	1.027	1.058	1.085	1.123	-0.569	-0.136	0.345
HCT	0.955	1.004	1.055	1.021	1.063	1.113	-2.000	0.072	2.000
MCV	0.990	1.016	1.042	1.032	1.050	1.071	-0.223	0.313	0.840
MCH	0.968	1.000	1.034	1.065	1.087	1.118	-0.408	0.003	0.411
MCHC	0.965	0.984	1.004	1.026	1.041	1.055	-0.892	-0.389	0.118
PLT	0.888	1.014	1.159	1.499	1.655	1.900	-0.240	0.029	0.276
LYMA	0.814	1.014	1.264	1.715	2.007	2.823	-0.306	0.019	0.329
diffWBC	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK33+	lower	esti	upper	lower	median	upper	lower	median	upper
Lymphocytes	0.949	1.030	1.117	1.040	1.112	1.212	-0.785	0.282	2.000
Neutrophils	0.750	0.923	1.135	1.421	1.641	2.210	-0.539	-0.156	0.265
Monocytes	0.583	0.855	1.253	1.754	2.344	4.835	-0.603	-0.174	0.274
Eosinophils	0.711	1.538	3.327	1.737	3.202	7.127	-0.352	0.368	1.220
ClinChem	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK33+	lower	esti	upper	lower	median	upper	lower	median	upper
ALP	0.859	1.001	1.165	1.400	1.545	1.762	-0.364	0.001	0.364
ALT	0.740	0.903	1.101	1.833	2.116	2.607	-0.365	-0.134	0.128
AST	0.891	1.045	1.226	1.602	1.798	2.152	-0.199	0.074	0.314
ALB	0.976	1.036	1.100	1.248	1.311	1.395	-0.089	0.131	0.323
TP	0.988	1.027	1.068	1.215	1.272	1.449	-0.051	0.107	0.251
Glu	0.924	1.064	1.225	1.391	1.530	1.769	-0.191	0.143	0.435
CHOL	0.917	1.040	1.181	1.316	1.433	1.659	-0.245	0.108	0.422
TAG	0.905	1.106	1.352	2.308	2.775	3.975	-0.096	0.097	0.267
Crea	0.919	1.017	1.126	1.366	1.493	1.982	-0.213	0.040	0.272
Urea	0.842	0.949	1.070	1.311	1.454	2.061	-0.424	-0.130	0.182
Ca	0.991	1.009	1.028	1.170	1.230	1.519	-0.043	0.041	0.122
Cl	0.987	0.999	1.012	1.076	1.092	1.117	-0.142	-0.007	0.134
K	0.995	1.054	1.116	1.313	1.396	1.612	-0.016	0.154	0.308
Na	0.988	0.998	1.008	1.073	1.089	1.124	-0.125	-0.020	0.098
P	0.845	0.960	1.091	1.325	1.447	1.719	-0.415	-0.105	0.243
Organs	Interval for ratio Δ			Interval for EQ limit			Interval for Δ ELSD scale		
Females NK33+	lower	esti	upper	lower	median	upper	lower	median	upper
Kidney	0.897	0.971	1.052	1.071	1.139	1.201	-0.888	-0.224	0.455
Spleen	0.909	0.997	1.092	1.242	1.324	1.435	-0.341	-0.011	0.329
Liver	0.910	0.977	1.050	1.169	1.231	1.353	-0.418	-0.108	0.241
AdrenGl	0.860	0.938	1.023	1.331	1.428	1.580	-0.394	-0.178	0.064
Heart	0.925	1.000	1.080	1.089	1.153	1.219	-0.618	-0.002	0.618
Thymus	0.861	1.018	1.204	1.278	1.458	2.026	-0.422	0.045	0.489
Uterus	0.943	1.194	1.512	1.268	1.518	1.839	-0.143	0.421	1.051
Ovary	0.772	0.854	0.945	1.406	1.557	2.173	-0.581	-0.345	-0.110
Brain	0.934	0.976	1.019	1.167	1.212	1.294	-0.324	-0.127	0.100

Appendix 12. R-script for the classical statistical analysis.

```
# Classical Statistical analysis of a single response for G-TwYST Study B
# Define some settings
alpha <- 0.95            # Confidence level for intervals
friedman.mc <- 20000     # Number of MC samples for p.value of Friedman test
friedman.limit <- 0.25   # Do MC when Asymptotic p.value is smaller than limit
set.seed(492193917)      # Initialize random generator
alpha2 <- (1+alpha)/2

# Define a dataframe to save results of test-statistics
testStats <- as.data.frame(matrix(nrow=9,ncol=2))
colnames(testStats) <- c("statistic", "value")
rownames(testStats) <- c("fAnova", "pAnova", "pKS", "pSW",
    "pFriedmanAs", "pFriedmanMc","pBartlett", "pLeveneMean", "pLeveneMedian")
testStats[,1] <- c("fAnova", "pAnova", "pKS", "pSW",
    "pFriedmanAs", "pFriedmanMc","pBartlett", "pLeveneMean", "pLeveneMedian")

# Get data, define factors and sort (necessary for wilcox.test())
data <- read.csv("RscriptInput.csv")
data$block <- as.factor(data$block)
data$treat <- as.factor(data$treat)
newlevels <- levels(data$treat)[c(1,2,4,3,5)]
data$treat <- factor(data$treat, newlevels)
data <- data[order(data$block, data$treat),]

# Load libraries
suppressMessages(library(multcomp))  # For Dunnett multiple comparison after ANOVA
suppressMessages(library(MBESS))     # For SES intervals
suppressMessages(library(NSM3))      # For p.value of non-parametric Friedman test
suppressMessages(library(car))       # For Levene test for homogeneity of variance
library(broom)                       # For the tidy() function

# ================================================================================
# Randomized block ANOVA; note that lm() takes proper account of any unbalance
# Estimates for treat are differences between GMO feeds and the Control feed
# ================================================================================
lm0 <- lm(response ~ block, data)
lm  <- lm(response ~ block + treat, data)
aov <- anova(lm, lm0)
testStats["fAnova","value"] <- aov$F[2]
testStats["pAnova","value"] <- aov$'Pr(>F)'[2]
estimates <- tidy(lm)
estimates

# Extract results for treatment differences, rename columns, add Residual Df and Se
tAnova <- estimates[startsWith(estimates[,1],"treat"),
    c("term", "estimate", "std.error", "statistic", "p.value")]
colnames(tAnova)[c(3,4,5)] <- c("se", "tvalue", "pvalue")
tAnova$term <- gsub("treat", "", tAnova$term)
tAnova$term <- gsub("'", "", tAnova$term)
tAnova$dfRes <- df.residual(lm)
tAnova$seRes <- summary(lm)$sigma

# Add confidence interval for differences
edt <- qt(alpha2, tAnova$dfRes)
tAnova$CIlower <- tAnova$estimate - edt*tAnova$se
tAnova$CIupper <- tAnova$estimate + edt*tAnova$se

# Add Dunnett p.values
dunnett <- glht(lm, linfct=mcp(treat="Dunnett"))
tAnova$pdunnett <- summary(dunnett)$test$pvalues
```

```
# Add SES and its confidence interval
tAnova$SES <- tAnova$estimate/tAnova$seRes
tAnova$SESlower <- NA * tAnova$SES
tAnova$SESupper <- NA * tAnova$SES
tnobs <- aggregate(response ~ treat, data=data, FUN=function(x) sum( !is.na(x) ))
nobs  <- as.vector(tnobs[,2])
mult  <- sqrt( (nobs[1] + nobs[c(2,3,4,5)]) / (nobs[1]*nobs[c(2,3,4,5)]) )
for (ii in 1:4) {
  CInct <- conf.limits.nct(tAnova$tvalue[ii], tAnova$dfRes[ii], conf.level=alpha)
  tAnova$SESlower[ii] <- mult[ii] * CInct$Lower.Limit
  tAnova$SESupper[ii] <- mult[ii] * CInct$Upper.Limit
}

# Do normality checks for lm() residuals
# This is only approximate because residuals are not independent
res <- residuals(lm)
ks <- ks.test(res, "pnorm", mean(res), sd(res))
testStats["pKS","value"] <- ks$p.value
sw <- shapiro.test(res)
testStats["pSW","value"] <- sw$p.value


# ==================================================================================
# Non-parametric Friedman test and pairwise Wilcoxon signed rank tests
# ==================================================================================
fried <- friedman.test(data$response, groups=data$treat, blocks=data$block)
testStats["pFriedmanAs","value"] <- fried$p.value

if (fried$p.value < friedman.limit) {
  blk <- as.numeric(data$block)
  trt <- as.numeric(data$treat)
  pFrd <- pFrd(x=data$response, b=blk, trt=trt, method="Monte Carlo",
n.mc=friedman.mc)
  testStats["pFriedmanMc","value"] <- pFrd$p.val
} else {
  testStats["pFriedmanMc","value"] <- NA
}

# Pairwise Wilcoxon signed rank test. Note that ordering of data is (block,treat)
# Also note that wilcox.test() can handle NA
sublevels <- levels(data$treat)[1]
controlData <- data$response[data$treat %in% sublevels]
for (ii in 1:4) {
  sublevels <- levels(data$treat)[1+ii]
  treatData <- data$response[data$treat %in% sublevels]
  wt <- wilcox.test(controlData, treatData, paired=TRUE, exact=TRUE)
  tPairwise$pwilcoxon[ii] <- wt$p.value
}

# ==================================================================================
# Bartlett test for homogeneity of variance
# ==================================================================================
bt <- bartlett.test(response ~ treat, data=data)
testStats["pBartlett","value"] <- bt$p.value
lv <- levene.test(response ~ treat, data=data, center=mean)
testStats["pLeveneMean","value"] <- lv$'Pr(>F)'[1]
lv <- leveneTest(response ~ treat, data=data, center=median)
testStats["pLeveneMedian","value"] <- lv$'Pr(>F)'[1]
```

```
# =================================================================================
# Kolomogorov-Smirnov & Shapiro-Wilks tests for normality
# =================================================================================
normality <- as.data.frame(matrix(nrow=5,ncol=3))
colnames(normality) <- c("term", "pKS", "pSW")
normality$term <- levels(data$treat)
normality[, seq(2,ncol(normality))] <- NA
for (ii in 1:5) {
  sublevels <- levels(data$treat)[ii]
  treatData <- data$response[data$treat %in% sublevels]
  treatData <- treatData[!is.na(treatData)]
  if (var(treatData) > 0) {
    ks <- ks.test(treatData, "pnorm", mean(treatData), sd(treatData))
    normality$pKS[ii] <- ks$p.value
    sw <- shapiro.test(treatData)
    normality$pSW[ii] <- sw$p.value
  }
}

# =================================================================================
# Output results for further processing in GenStat
# =================================================================================
for (ii in 1:1) {
  cat("\n")
  print(testStats);  cat("\n\n")
  print(tAnova);     cat("\n\n")
  print(tPairwise);  cat("\n\n")
  print(normality);  cat("\n\n")
}
write.csv(testStats, file="RscriptTest.csv",      row.names=FALSE, quote=FALSE)
write.csv(tAnova,    file="RscriptAnova.csv",     row.names=FALSE, quote=FALSE)
write.csv(tPairwise, file="RscriptPairwise.csv",  row.names=FALSE, quote=FALSE)
write.csv(normality, file="RscriptNormality.csv", row.names=FALSE, quote=FALSE)
```

Appendix 13. Example input file for the R-script in Appendix 12.

The data below should be copied to file “RscriptInput.csv” before running the R script. The response is the cage mean after a log transformation for bodyweights of males.

```
block, treat,     response
1,    'NK11-',    6.2496415506357
3,    'NK11-',    6.17278862957348
5,    'NK11-',    6.12657203771323
7,    'NK11-',    6.10471889354237
2,    'NK11-',    6.02085190889498
4,    'NK11-',    6.12610756622776
6,    'NK11-',    6.02523136685413
8,    'NK11-',    6.2263041096267
1,    'NK33+',    6.21488917440368
3,    'NK33+',    6.19187429093509
5,    'NK33+',    6.20460981658788
7,    'NK33+',    6.12608346907439
2,    'NK33+',    5.9648620526416
4,    'NK33+',    5.97964419724186
6,    'NK33+',    6.0460681545403
8,    'NK33+',    6.23717574027201
1,    'NK33-',    6.13734732239293
3,    'NK33-',    6.12322077222906
5,    'NK33-',    6.12131408829246
7,    'NK33-',    6.17197443073755
2,    'NK33-',    5.97121081808071
4,    'NK33-',    6.03444059351441
6,    'NK33-',    6.14312752333845
8,    'NK33-',    6.13034866785079
1,    'NK11+',    6.10467806948035
3,    'NK11+',    6.13282610850054
5,    'NK11+',    6.08971253690092
7,    'NK11+',    6.09918289342016
2,    'NK11+',    5.99765989327377
4,    'NK11+',    5.99272521960128
6,    'NK11+',    6.03555160256235
8,    'NK11+',    6.13732407276488
1,    'Control',  6.13154510722597
3,    'Control',  6.12631138706038
5,    'Control',  6.19015909005954
7,    'Control',  6.06263273304877
2,    'Control',  6.01950644928912
4,    'Control',  5.97426001205971
6,    'Control',  6.07469820771048
8,    'Control',  6.08668458603948
```

Appendix 14. P-values for difference tests between GMO feeds and the control feed

Difference tests are based on log transformed cage means. P-values are given for Dunnett tests (Dunnet), for t-tests and for Wilcoxon signed rank tests (Wilcox). P-values smaller than 0.01/0.05 have a gold/yellow background.

Weights	NK11-			NK33-			NK11+			NK33+		
Males	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
BodyWeight	0.144	0.047	0.250	0.781	0.377	0.461	0.982	0.686	0.742	0.328	0.119	0.148
growthRate	0.832	0.423	0.641	0.757	0.358	0.250	1.000	0.949	0.945	1.000	0.910	0.945
FeedMean	0.886	0.483	0.641	0.844	0.435	0.312	0.084	0.026	0.039	1.000	0.883	0.844

Haematology	NK11-			NK33-			NK11+			NK33+		
Males	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
WBC	0.996	0.786	0.945	0.960	0.611	0.547	0.747	0.350	0.641	0.861	0.453	0.383
RBC	0.997	0.796	0.742	1.000	0.907	0.547	0.861	0.454	0.742	0.997	0.810	0.641
HGB	0.970	0.640	0.641	0.969	0.637	0.641	0.260	0.091	0.461	0.626	0.269	0.109
HCT	0.952	0.592	0.250	0.762	0.362	0.312	1.000	0.981	1.000	0.656	0.287	0.055
MCV	0.392	0.148	0.250	0.223	0.076	0.148	0.297	0.106	0.109	0.496	0.197	0.078
MCH	0.988	0.718	0.742	0.940	0.567	0.742	0.995	0.775	1.000	0.950	0.588	0.383
MCHC	0.130	0.042	0.055	0.656	0.288	0.195	0.123	0.040	0.039	0.938	0.563	0.641
PLT	0.630	0.271	0.250	0.999	0.837	0.844	1.000	0.895	0.461	0.996	0.789	0.547
LYMR	0.999	0.865	0.945	0.689	0.309	0.742	0.989	0.722	1.000	0.999	0.854	1.000
LYMA	0.990	0.730	0.945	1.000	0.919	0.844	0.859	0.451	0.742	0.842	0.433	0.383

diffWBC	NK11-			NK33-			NK11+			NK33+		
Males	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
Lymphocytes	0.521	0.210	0.195	0.080	0.025	0.109	0.936	0.559	0.933	0.996	0.789	0.742
Neutrophils	0.437	0.168	0.195	0.131	0.043	0.055	0.960	0.612	0.945	0.993	0.755	0.461
Monocytes	0.822	0.414	0.326	0.843	0.434	0.483	0.986	0.707	0.798	0.844	0.436	0.483
Eosinophils	0.987	0.711	0.547	0.936	0.558	0.641	0.822	0.413	0.310	0.803	0.396	0.383

ClinCheml	NK11-			NK33-			NK11+			NK33+		
Males	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
ALP	0.988	0.713	0.641	0.987	0.710	0.945	1.000	0.933	0.945	0.058	0.018	0.109
ALT	0.990	0.733	0.383	0.948	0.584	0.844	0.083	0.026	0.016	0.995	0.774	0.844

AST	0.949	0.586	0.742	0.808	0.401	0.461	0.298	0.107	0.148	0.699	0.316	0.461
BIL	1.000	0.883	0.945	0.979	0.670	0.195	1.000	0.935	0.844	0.382	0.143	0.195
ALB	0.977	0.665	0.844	0.713	0.325	0.109	0.033	0.010	0.016	1.000	0.965	0.742
TP	0.599	0.253	0.461	0.693	0.311	0.078	0.018	0.005	0.078	0.986	0.703	0.945
Glu	1.000	0.939	1.000	0.605	0.256	0.148	0.976	0.659	0.945	0.926	0.541	0.742
CHOL	0.953	0.595	0.547	0.999	0.873	0.641	0.609	0.259	0.250	1.000	0.957	0.945
TAG	0.741	0.346	0.250	0.993	0.752	0.844	0.999	0.839	0.383	0.980	0.676	0.547
Crea	0.829	0.420	0.383	0.982	0.683	0.742	0.122	0.039	0.109	0.638	0.276	0.250
Urea	0.629	0.271	0.250	0.914	0.523	0.195	0.611	0.260	0.383	0.803	0.396	0.383
cHGB	0.993	0.751	0.844	0.989	0.723	1.000	0.636	0.275	0.250	0.354	0.130	0.195
Ca	1.000	0.933	0.742	0.997	0.797	0.945	0.854	0.446	0.641	0.931	0.551	0.383
Cl	0.909	0.515	0.441	0.908	0.513	0.574	1.000	0.884	0.742	1.000	0.991	0.933
K	0.889	0.487	0.547	0.103	0.033	0.078	0.158	0.052	0.195	0.693	0.312	0.272
Na	0.998	0.825	1.000	0.724	0.333	0.272	0.436	0.168	0.195	0.857	0.449	0.447
P	0.886	0.483	0.547	0.471	0.185	0.195	0.948	0.584	0.461	0.967	0.632	1.000
Urine	NK11-			NK33-			NK11+			NK33+		
Males	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
uVol	0.993	0.752	0.641	0.988	0.716	0.383	0.998	0.817	0.742	1.000	0.905	0.673
uVolW	0.914	0.523	0.461	0.998	0.812	0.547	0.996	0.782	0.742	0.986	0.707	0.641
uLeu	0.998	0.810	0.569	1.000	1.000	0.916	0.998	0.810	0.414	1.000	1.000	1.000
uOsmoll	0.998	0.832	0.844	0.824	0.416	0.547	0.925	0.539	0.547	1.000	0.949	0.945
uKeton	0.573	0.238	0.029	0.975	0.658	0.844	1.000	0.918	0.889	0.850	0.441	0.281
upH	0.694	0.312	0.203	0.149	0.049	0.098	0.361	0.134	0.396	0.016	0.004	0.012
Organs	NK11-			NK33-			NK11+			NK33+		
Males	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
Kidney	0.999	0.847	0.844	0.799	0.393	0.742	0.467	0.183	0.461	0.996	0.783	0.547
Spleen	0.738	0.343	0.312	0.974	0.653	0.641	0.530	0.215	0.250	0.998	0.826	0.844
Liver	0.919	0.530	0.742	0.243	0.084	0.109	0.203	0.069	0.250	0.998	0.817	0.945
AdrenGl	0.484	0.191	0.312	0.576	0.240	0.195	0.266	0.094	0.195	0.588	0.247	0.250
Heart	0.366	0.136	0.039	0.730	0.338	0.461	0.716	0.327	0.844	0.997	0.808	0.844
Thymus	0.668	0.295	0.078	0.428	0.164	0.250	0.063	0.019	0.016	0.743	0.347	0.641

Testis	1.000	0.898	1.000	0.954	0.596	0.641	0.663	0.292	0.461	1.000	0.989	0.945
Epididymis	0.994	0.768	0.641	0.600	0.253	0.312	0.827	0.419	0.461	0.962	0.616	0.547
Brain	0.770	0.368	0.547	0.536	0.218	0.383	0.350	0.129	0.312	1.000	0.991	0.945
Immunology	NK11-			NK33-			NK11+			NK33+		
Males	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
Granulocytes	0.140	0.047	0.312	1.000	0.988	1.000	1.000	0.885	0.812	1.000	0.953	0.625
RespirBurst	0.950	0.594	0.625	0.680	0.308	0.062	0.624	0.272	0.312	0.999	0.861	0.625
Con	0.999	0.870	1.000	1.000	0.930	1.000	0.978	0.673	0.625	0.787	0.388	0.438
PHA	0.908	0.518	0.812	0.920	0.538	0.625	0.981	0.687	0.625	0.770	0.374	0.812
PWM	0.453	0.179	0.438	1.000	0.922	1.000	1.000	0.949	1.000	0.105	0.034	0.125
Medium	1.000	0.897	1.000	0.921	0.539	0.812	0.705	0.325	0.312	0.672	0.302	0.438
IprConA	0.994	0.769	0.812	0.824	0.421	0.312	0.946	0.585	0.438	0.999	0.875	1.000
IprPHA	0.802	0.401	0.312	0.442	0.174	0.062	0.801	0.400	0.438	0.997	0.798	0.812
IprPWM	0.044	0.014	0.062	0.575	0.243	0.188	0.285	0.103	0.312	0.055	0.017	0.125
Cytokines	NK11-			NK33-			NK11+			NK33+		
Males	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
IL2	0.013	0.004	0.062	0.437	0.171	0.812	0.618	0.268	0.312	0.009	0.003	0.062
IL4	0.545	0.227	0.438	0.058	0.018	0.188	0.056	0.018	0.125	0.477	0.191	0.438
IL10	0.979	0.677	0.812	0.714	0.331	0.312	0.484	0.194	0.125	0.437	0.171	0.438
IL17A	0.993	0.760	0.625	0.998	0.817	0.625	0.595	0.255	0.312	0.755	0.362	0.812
TNFa	0.032	0.010	0.188	0.914	0.528	1.000	0.811	0.408	0.625	0.023	0.007	0.125
IFNg	0.014	0.004	0.125	0.978	0.671	0.812	0.960	0.617	0.812	0.116	0.038	0.062
CellPhenotype	NK11-			NK33-			NK11+			NK33+		
Males	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
sp3	0.248	0.088	0.062	0.835	0.431	0.625	0.065	0.020	0.125	0.120	0.039	0.125
sp3_4	0.463	0.184	0.125	0.366	0.138	0.312	0.119	0.039	0.125	0.089	0.029	0.062
sp3_8	0.258	0.092	0.125	0.943	0.577	0.812	0.073	0.023	0.125	0.438	0.172	0.312
sp3_45	0.648	0.284	0.312	0.999	0.870	0.875	0.945	0.579	0.438	0.945	0.580	1.000
sp3_161	0.838	0.433	0.625	0.987	0.716	1.000	1.000	0.909	1.000	0.189	0.064	0.125
ln3	0.998	0.821	1.000	0.740	0.350	0.312	0.516	0.211	0.312	0.839	0.436	0.625
ln3_4	0.981	0.684	0.438	0.733	0.345	0.312	0.290	0.105	0.188	0.705	0.325	0.812

ln3_8	0.212	0.074	0.312	0.995	0.783	0.625	0.912	0.525	0.438	0.995	0.782	0.625
ln3_45	0.140	0.047	0.312	0.209	0.073	0.125	0.941	0.574	1.000	0.462	0.183	0.188
ty3	0.995	0.777	0.812	0.799	0.398	0.625	0.472	0.188	0.312	0.424	0.165	0.312
ty3_4	0.998	0.816	0.812	0.699	0.321	0.625	0.383	0.146	0.312	0.296	0.108	0.125
ty3_8	0.942	0.577	0.438	0.929	0.553	0.812	0.912	0.524	0.812	0.365	0.138	0.438
Hormone	NK11-			NK33-			NK11+			NK33+		
Males	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
Testosteron	0.971	0.646	0.562	0.269	0.096	0.312	1.000	0.914	0.844	0.725	0.337	0.062
T3	0.390	0.148	0.562	0.999	0.854	0.844	0.998	0.834	0.438	0.458	0.180	0.031
T4	0.958	0.609	0.688	0.038	0.011	0.031	1.000	0.993	0.844	0.884	0.484	0.219

Weights	NK11-			NK33-			NK11+			NK33+		
Females	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
BodyWeight	0.961	0.614	0.742	0.830	0.422	0.641	0.983	0.688	0.383	0.366	0.136	0.383
growthRate	0.144	0.047	0.148	0.215	0.074	0.039	0.205	0.070	0.078	0.014	0.004	0.008
FeedMean	0.048	0.015	0.039	0.998	0.818	0.742	0.867	0.461	0.641	1.000	0.967	0.945
Haematology	NK11-			NK33-			NK11+			NK33+		
Females	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
WBC	1.000	0.981	0.945	0.582	0.243	0.742	0.694	0.313	0.195	1.000	0.946	0.742
RBC	1.000	0.880	0.844	0.866	0.460	0.078	0.990	0.729	0.641	0.980	0.676	0.945
HGB	0.865	0.458	0.742	0.369	0.137	0.039	0.978	0.668	0.461	0.927	0.544	0.641
HCT	0.972	0.645	0.945	0.609	0.259	0.055	0.974	0.655	0.461	0.999	0.866	0.742
MCV	0.934	0.555	0.641	0.950	0.587	0.547	1.000	0.935	0.945	0.553	0.227	0.383
MCH	0.934	0.556	0.547	0.965	0.624	0.461	1.000	0.929	1.000	1.000	0.989	0.844
MCHC	0.996	0.783	0.641	1.000	0.977	0.945	0.995	0.775	0.641	0.334	0.122	0.250
PLT	0.462	0.180	0.383	1.000	0.976	0.742	0.379	0.142	0.461	0.998	0.827	0.742
LYMR	1.000	0.955	0.945	0.664	0.292	0.312	0.920	0.532	0.742	0.799	0.393	0.945
LYMA	1.000	0.951	0.945	0.457	0.178	0.641	0.856	0.448	0.312	1.000	0.898	0.641

diffWBC	NK11-			NK33-			NK11+			NK33+		
Females	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
Lymphocytes	1.000	0.921	0.844	0.960	0.612	0.844	0.709	0.322	0.547	0.873	0.467	0.742
Neutrophils	1.000	0.959	1.000	0.986	0.705	0.844	0.893	0.492	0.461	0.840	0.432	0.742
Monocytes	0.378	0.141	0.250	0.801	0.394	0.641	0.646	0.281	0.326	0.817	0.409	0.461
Eosinophils	1.000	0.919	1.000	0.967	0.630	0.641	0.865	0.458	0.673	0.616	0.263	0.272
ClinChem	NK11-			NK33-			NK11+			NK33+		
Females	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
ALP	0.999	0.845	1.000	0.229	0.079	0.250	0.998	0.830	0.742	1.000	0.995	0.945
ALT	0.635	0.274	0.078	0.840	0.431	0.383	0.866	0.459	0.641	0.678	0.302	0.461
AST	1.000	0.900	0.945	0.929	0.546	0.641	0.996	0.780	0.945	0.944	0.576	0.547
BIL	0.700	0.316	0.109	0.649	0.283	0.383	0.957	0.603	0.148	0.439	0.169	0.641
ALB	0.850	0.442	0.641	0.271	0.096	0.250	0.471	0.185	0.312	0.560	0.231	0.547
TP	0.645	0.281	0.461	0.245	0.085	0.250	0.298	0.107	0.250	0.448	0.174	0.312
Glu	0.930	0.549	0.641	0.048	0.015	0.016	0.907	0.512	0.461	0.778	0.375	0.312
CHOL	0.653	0.286	0.312	0.788	0.383	0.461	0.790	0.385	0.461	0.917	0.526	0.641
TAG	0.524	0.212	0.461	0.062	0.019	0.008	0.290	0.104	0.109	0.692	0.311	0.250
Crea	0.960	0.612	0.383	0.794	0.389	0.641	0.996	0.781	0.844	0.991	0.734	0.800
Urea	1.000	0.907	0.844	0.271	0.096	0.109	0.205	0.070	0.055	0.784	0.380	0.195
cHGB	1.000	0.893	0.945	0.808	0.401	0.461	0.854	0.446	0.250	0.610	0.259	0.547
Ca	0.852	0.444	0.742	0.838	0.430	0.461	0.673	0.298	0.250	0.686	0.307	0.547
Cl	0.999	0.841	0.800	0.069	0.021	0.039	0.768	0.367	0.383	1.000	0.915	0.833
K	1.000	0.940	0.933	0.962	0.617	0.945	0.898	0.498	0.383	0.209	0.071	0.109
Na	0.567	0.235	0.250	0.934	0.556	0.725	1.000	0.998	0.945	0.989	0.722	0.742
P	0.908	0.512	0.641	0.851	0.443	0.641	0.814	0.406	0.461	0.915	0.523	0.844
Urine	NK11-			NK33-			NK11+			NK33+		
Females	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
uVol	0.995	0.775	0.844	0.958	0.606	0.844	0.945	0.577	0.742	0.379	0.142	0.148
uVolW	0.999	0.841	0.945	0.929	0.546	0.742	0.928	0.545	0.547	0.293	0.105	0.195
uLeu	0.929	0.547	0.595	0.770	0.368	0.520	0.929	0.547	0.595	0.929	0.547	0.679
uOsmoll	1.000	0.960	1.000	0.998	0.827	0.844	1.000	0.995	0.742	0.980	0.676	0.742

uKeton	0.173	0.058	0.203	0.930	0.548	0.746	0.173	0.058	0.203	0.064	0.020	0.089
upH	0.343	0.126	0.048	0.678	0.302	0.330	0.343	0.126	0.250	0.500	0.199	0.168
Organs	NK11-			NK33-			NK11+			NK33+		
Females	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
Kidney	0.513	0.206	0.078	0.539	0.220	0.641	0.802	0.395	0.547	0.869	0.463	0.547
Spleen	0.186	0.062	0.109	1.000	0.991	0.641	0.034	0.010	0.016	1.000	0.943	0.641
Liver	0.648	0.282	0.250	0.987	0.713	0.945	0.782	0.378	0.461	0.912	0.519	0.547
AdrenGl	0.060	0.019	0.078	0.112	0.036	0.078	0.120	0.039	0.055	0.377	0.141	0.078
Heart	0.776	0.373	0.195	0.527	0.213	0.039	0.714	0.326	0.383	1.000	0.993	0.945
Thymus	0.983	0.689	0.547	0.970	0.641	0.383	0.997	0.801	0.641	0.998	0.825	0.742
Uterus	1.000	0.989	1.000	0.992	0.745	0.844	1.000	0.935	0.844	0.365	0.135	0.148
Ovary	0.048	0.015	0.016	0.364	0.135	0.383	0.650	0.284	0.195	0.012	0.003	0.008
Brain	0.818	0.410	0.383	0.992	0.746	0.844	0.956	0.602	0.195	0.604	0.256	0.461
Immunology	NK11-			NK33-			NK11+			NK33+		
Females	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
Granulocytes	0.067	0.021	0.312	0.990	0.737	0.625	0.551	0.230	0.312	0.376	0.143	0.312
RespirBurst	0.950	0.593	0.812	0.999	0.852	1.000	0.910	0.522	1.000	0.966	0.634	1.000
Con	0.803	0.402	1.000	0.996	0.796	1.000	0.767	0.371	0.625	0.720	0.335	0.125
PHA	0.899	0.506	0.812	0.944	0.579	0.812	0.797	0.397	0.188	0.617	0.267	0.188
PWM	0.305	0.111	0.312	0.965	0.631	1.000	0.407	0.157	0.062	0.283	0.102	0.188
Medium	0.557	0.233	0.312	0.995	0.779	1.000	0.466	0.185	0.125	0.331	0.123	0.062
IprConA	1.000	0.911	1.000	0.999	0.857	1.000	1.000	0.917	0.625	1.000	0.952	0.625
IprPHA	0.996	0.795	0.812	0.983	0.697	0.438	1.000	0.900	0.812	1.000	0.978	1.000
IprPWM	0.590	0.251	0.438	0.670	0.301	0.188	0.917	0.533	0.438	0.794	0.394	0.438
Cytokines	NK11-			NK33-			NK11+			NK33+		
Females	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
IL2	0.502	0.214	0.500	0.985	0.720	0.750	0.992	0.764	0.750	0.999	0.877	0.750
IL4	0.985	0.719	0.500	0.998	0.838	0.250	0.704	0.338	0.500	0.946	0.601	1.000
IL10	0.994	0.779	1.000	0.990	0.748	1.000	0.998	0.833	0.750	1.000	0.953	1.000
IL17A	0.025	0.008	0.250	0.158	0.057	0.250	0.980	0.694	0.750	0.111	0.039	0.500
TNFa	0.390	0.157	0.500	0.216	0.080	0.250	0.856	0.470	0.750	0.667	0.312	0.500

IFNg	0.988	0.734	1.000	0.993	0.765	0.750	0.911	0.540	0.500	0.975	0.677	1.000
CellPhenotype	NK11-			NK33-			NK11+			NK33+		
Females	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
sp3	0.269	0.096	0.188	0.959	0.614	1.000	0.804	0.402	0.438	0.437	0.171	0.188
sp3_4	0.258	0.092	0.188	0.994	0.764	0.812	0.535	0.221	0.312	0.663	0.296	0.312
sp3_8	0.986	0.712	0.812	0.915	0.529	0.625	0.710	0.328	0.125	0.602	0.259	0.312
sp3_45	0.994	0.765	0.812	1.000	0.925	1.000	0.567	0.238	0.062	0.995	0.779	0.812
sp3_161	0.934	0.561	0.438	0.986	0.709	0.812	0.903	0.512	0.312	0.991	0.738	1.000
ln3	0.998	0.814	0.812	0.998	0.816	0.812	0.997	0.810	1.000	0.427	0.166	0.188
ln3_4	0.998	0.827	0.812	1.000	0.962	1.000	0.954	0.602	0.438	0.765	0.370	0.312
ln3_8	0.488	0.196	0.312	1.000	0.922	1.000	0.781	0.383	0.312	0.438	0.172	0.312
ln3_45	0.395	0.151	0.625	0.976	0.666	0.062	0.955	0.604	0.188	0.909	0.521	0.625
ty3	0.997	0.797	1.000	1.000	0.937	1.000	0.988	0.720	0.812	1.000	0.944	0.812
ty3_4	1.000	0.884	0.812	0.884	0.487	0.625	1.000	0.917	0.812	0.997	0.811	1.000
ty3_8	0.522	0.214	0.438	0.774	0.377	0.812	1.000	0.955	1.000	0.548	0.228	0.312
Hormone	NK11-			NK33-			NK11+			NK33+		
Females	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox	Dunnet	t-test	Wilcox
betaEstr	0.059	0.018	0.148	0.126	0.041	0.039	0.116	0.037	0.039	0.078	0.024	0.008
T3	0.987	0.713	0.945	0.838	0.429	0.547	0.999	0.834	0.945	0.185	0.062	0.312
T4	0.800	0.393	0.383	0.978	0.669	0.641	0.865	0.458	0.383	0.110	0.035	0.039

Appendix 15. Tests for normality and homogeneity of variance

P-values for the Shapiro-Wilks (SW) normality test are given separately for each feeding group, and also for the ANOVA residuals. In addition P-values for Bartlett and Levene test for homogeneity of variance are given. P-values smaller than 0.01/0.05 have a gold/yellow background.

Male Weights	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
BodyWeight	0.989	0.565	0.040	0.188	0.146	0.195	0.468	0.181
growthRate	0.939	0.563	0.720	0.410	0.827	0.924	0.282	0.319
FeedMean	0.570	0.726	0.050	0.716	0.056	0.635	0.066	0.013
Male Haematology	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
WBC	0.266	0.072	0.678	0.434	0.422	0.779	0.303	0.189
RBC	0.259	0.001	0.011	0.984	0.149	0.057	0.209	0.580
HGB	0.967	0.082	0.049	0.280	0.027	0.787	0.080	0.039
HCT	0.298	0.008	0.024	0.713	0.925	0.065	0.211	0.410
MCV	0.315	0.793	0.627	0.183	0.287	0.154	0.330	0.210
MCH	0.589	0.556	0.628	0.256	0.988	0.023	0.529	0.148
MCHC	0.565	0.007	0.782	0.442	0.514	0.160	0.049	0.227
PLT	0.994	0.523	0.125	0.419	0.699	0.302	0.392	0.698
LYMR	0.291	0.542	0.039	0.124	0.279	0.197	0.323	0.630
LYMA	0.683	0.037	0.555	0.215	0.799	0.759	0.207	0.178
Male diffWBC	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
Lymphocytes	0.083	0.442	0.945	0.265	0.806	0.007	0.999	0.992
Neutrophils	0.204	0.179	0.015	0.741	0.286	0.012	0.849	0.743
Monocytes	0.005	0.638	0.518	0.334	0.931	0.738	0.394	0.464
Eosinophils	0.429	0.482	0.149	0.142	0.380	0.593	0.787	0.451
Male ClinChem	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
ALP	0.580	0.490	0.095	0.551	0.572	0.659	0.932	0.830
ALT	0.560	0.595	0.705	0.110	0.997	0.751	0.485	0.566
AST	0.745	0.635	0.569	0.704	0.617	0.870	0.802	0.615
BIL	0.000	0.897	0.216	0.425	0.371	0.165	0.007	0.251
ALB	0.360	0.329	0.561	0.603	0.317	0.876	0.122	0.089
TP	0.162	0.667	0.109	0.737	0.572	0.269	0.236	0.296

Glu	0.421	0.867	0.828	0.667	0.355	0.518	0.214	0.229
CHOL	0.031	0.158	0.978	0.634	0.657	0.862	0.730	0.663
TAG	0.258	0.325	0.075	0.908	0.446	0.135	0.165	0.559
Crea	0.288	0.636	0.532	0.420	0.537	0.477	0.366	0.215
Urea	0.923	0.436	0.677	0.639	0.469	0.889	0.329	0.168
cHGB	0.166	0.580	0.442	0.905	0.111	0.802	0.305	0.511
Ca	0.207	0.702	0.398	0.047	0.948	0.800	0.564	0.264
Cl	0.643	0.511	0.026	0.248	0.120	0.621	0.590	0.288
K	0.405	0.074	0.931	0.674	0.302	0.755	0.535	0.889
Na	0.008	0.179	0.330	0.408	0.070	0.441	0.853	0.992
P	0.275	0.325	0.400	0.534	0.803	0.400	0.269	0.071
Male Urine	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
uVol	0.479	0.522	0.044	0.165	0.191	0.461	0.259	0.552
uVolW	0.827	0.423	0.218	0.155	0.639	0.536	0.429	0.511
uLeu	0.239	0.000	0.283	0.045	0.004	0.200	0.058	0.089
uOsmoll	0.896	0.745	0.219	0.434	0.500	0.778	0.501	0.408
uKeton	0.558	0.188	0.006	0.064	0.003	0.367	0.180	0.006
upH	0.274	0.413	0.001	0.037	0.093	0.300	0.067	0.116
Male Organs	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
Kidney	0.135	0.723	0.372	0.991	0.776	0.955	0.805	0.371
Spleen	0.706	0.037	0.819	0.094	0.731	0.089	0.820	0.792
Liver	0.503	0.795	0.440	0.736	0.253	0.655	0.069	0.313
AdrenGl	0.288	0.689	0.966	0.493	0.525	0.806	0.795	0.730
Heart	0.186	0.983	0.552	0.053	0.868	0.319	0.252	0.380
Thymus	0.937	0.131	0.750	0.534	0.416	0.973	0.952	0.968
Testis	0.692	0.735	0.164	0.591	0.793	0.196	0.323	0.271
Epididymis	0.132	0.318	0.315	0.171	0.577	0.927	0.134	0.061
Brain	0.833	0.791	0.147	0.677	0.379	0.069	0.146	0.054
Male Immunology	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
Granulocytes	0.052	0.155	0.173	0.019	0.197	0.770	0.910	0.153
RespirBurst	0.189	0.779	0.656	0.753	0.281	0.058	0.752	0.384

Con	0.069	0.336	0.876	0.009	0.330	0.179	0.320	0.305
PHA	0.159	0.699	0.186	0.032	0.885	0.540	0.061	0.021
PWM	0.316	0.426	0.858	0.688	0.736	0.085	0.449	0.156
Medium	0.527	0.762	0.222	0.893	0.222	0.044	0.321	0.016
lprConA	0.301	0.696	0.785	0.293	0.448	0.581	0.191	0.181
lprPHA	0.507	0.997	0.979	0.645	0.099	0.863	0.020	0.000
lprPWM	0.208	0.992	0.831	0.873	0.550	0.161	0.692	0.803
Male Cytokines	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
IL2	0.513	0.308	0.020	0.632	0.038	0.141	0.394	0.131
IL4	0.995	0.272	0.839	0.699	0.644	0.477	0.001	0.018
IL10	0.520	0.904	0.373	0.960	0.605	0.897	0.597	0.209
IL17A	0.139	0.915	0.340	0.187	0.174	0.874	0.243	0.166
TNFa	0.141	0.205	0.339	0.674	0.639	0.721	0.074	0.005
IFNg	0.444	0.196	0.319	0.057	0.839	0.030	0.217	0.153
Male CellPhenotype	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
sp3	0.047	0.277	0.398	0.444	0.380	0.590	0.458	0.139
sp3_4	0.560	0.171	0.190	0.422	0.113	0.751	0.732	0.086
sp3_8	0.556	0.420	0.416	0.313	0.379	0.294	0.204	0.091
sp3_45	0.801	0.453	0.907	0.443	0.154	0.816	0.261	0.112
sp3_161	0.041	0.227	0.488	0.098	0.641	0.881	0.968	0.931
ln3	0.292	0.330	0.431	0.107	0.074	0.502	0.037	0.086
ln3_4	0.349	0.359	0.256	0.124	0.014	0.822	0.005	0.090
ln3_8	0.588	0.258	0.550	0.529	0.749	0.314	0.671	0.370
ln3_45	0.447	0.769	0.655	0.051	0.650	0.439	0.935	0.576
ty3	0.559	0.706	0.302	0.475	0.150	0.928	0.505	0.234
ty3_4	0.244	0.274	0.196	0.419	0.355	0.575	0.548	0.280
ty3_8	0.262	0.106	0.945	0.738	0.673	0.788	0.406	0.058
Male Hormone	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
Testosteron	0.399	0.573	0.947	0.727	0.349	0.237	0.468	0.443
T3	0.864	0.915	0.272	0.696	0.393	0.737	0.667	0.596
T4	0.991	0.033	0.773	0.315	0.415	0.953	0.937	0.897

Female Weights	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
BodyWeight	0.085	0.815	0.289	0.655	0.222	0.539	0.776	0.328
growthRate	0.748	0.708	0.561	0.325	0.335	0.501	0.205	0.043
FeedMean	0.903	0.393	0.336	0.059	0.814	0.193	0.167	0.295
Female Haematology	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
WBC	0.426	0.063	0.098	0.647	0.753	0.146	0.610	0.320
RBC	0.141	0.124	0.673	0.214	0.318	0.006	0.012	0.219
HGB	0.769	0.218	0.912	0.817	0.242	0.104	0.001	0.017
HCT	0.918	0.039	0.835	0.367	0.758	0.030	0.004	0.107
MCV	0.682	0.763	0.793	0.640	0.158	0.537	0.667	0.449
MCH	0.099	0.716	0.888	0.875	0.372	0.836	0.517	0.505
MCHC	0.946	0.854	0.161	0.558	0.604	0.843	0.533	0.616
PLT	0.783	0.135	0.825	0.189	0.900	0.883	0.394	0.525
LYMR	0.149	0.807	0.097	0.912	0.127	0.596	0.605	0.529
LYMA	0.302	0.181	0.087	0.545	0.571	0.143	0.381	0.229
Female diffWBC	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
Lymphocytes	0.268	0.656	0.938	0.350	0.698	0.978	0.556	0.380
Neutrophils	0.575	0.373	0.604	0.734	0.419	0.448	0.963	0.970
Monocytes	0.445	0.629	0.428	0.065	0.961	0.545	0.188	0.078
Eosinophils	0.360	0.479	0.254	0.115	0.069	0.674	0.792	0.315
Female ClinChem	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
ALP	0.897	0.380	0.944	0.573	0.309	0.460	0.086	0.157
ALT	0.300	0.246	0.297	0.768	0.882	0.276	0.030	0.024
AST	0.578	0.205	0.297	0.709	0.438	0.488	0.259	0.272
BIL	0.797	0.141	0.189	0.282	0.079	0.008	0.090	0.028

ALB	0.527	0.866	0.821	0.946	0.467	0.673	0.875	0.553
TP	0.928	0.987	0.371	0.979	0.568	0.446	0.868	0.736
Glu	0.539	0.875	0.441	0.113	0.240	0.569	0.062	0.251
CHOL	0.474	0.215	0.184	0.166	0.525	0.608	0.815	0.767
TAG	0.679	0.145	0.739	0.558	0.673	0.525	0.104	0.014
Crea	0.503	0.535	0.157	0.271	0.540	0.062	0.161	0.235
Urea	0.090	0.779	0.767	0.242	0.269	0.552	0.251	0.400
cHGB	0.012	0.073	0.332	0.281	0.038	0.056	0.434	0.237
Ca	0.139	0.406	0.224	0.486	0.537	0.806	0.435	0.325
Cl	0.082	0.095	0.070	0.866	0.018	0.117	0.462	0.294
K	0.160	0.149	0.153	0.128	0.432	0.168	0.677	0.612
Na	0.029	0.361	0.083	0.718	0.026	0.216	0.175	0.222
P	0.698	0.587	0.919	0.056	0.844	0.376	0.733	0.410
Female Urine	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
uVol	0.744	0.644	0.051	0.747	0.240	0.276	0.613	0.464
uVolW	0.120	0.681	0.035	0.471	0.576	0.554	0.750	0.558
uLeu	0.067	0.027	0.004	0.197	0.027	0.920	0.758	0.601
uOsmoll	0.511	0.790	0.028	0.795	0.112	0.297	0.282	0.348
uKeton	0.027	0.000	0.005	0.000	*	0.346	0.000	0.000
upH	0.120	0.114	0.010	0.408	0.037	0.543	0.650	0.215
Female Organs	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
Kidney	0.719	0.959	0.227	0.148	0.666	0.840	0.435	0.708
Spleen	0.863	0.987	0.304	0.966	0.688	0.758	0.634	0.547
Liver	0.774	0.524	0.031	0.077	0.337	0.528	0.090	0.298
AdrenGl	0.367	0.572	0.341	0.077	0.805	0.984	0.412	0.201
Heart	0.976	0.002	0.198	0.502	0.731	0.317	0.131	0.544
Thymus	0.283	0.964	0.147	0.496	0.036	0.061	0.725	0.201

Uterus	0.934	0.256	0.063	0.457	0.815	0.909	0.564	0.252
Ovary	0.785	0.175	0.356	0.090	0.644	0.717	0.007	0.000
Brain	0.394	0.641	0.287	0.277	0.530	0.618	0.292	0.134
Female Immunology	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
Granulocytes	0.176	0.422	0.471	0.630	0.223	0.498	0.365	0.021
RespirBurst	0.578	0.634	0.751	0.970	0.100	0.968	0.021	0.041
Con	0.034	0.731	0.112	0.952	0.241	0.198	0.545	0.197
PHA	0.556	0.264	0.279	0.145	0.734	0.961	0.360	0.318
PWM	0.979	0.019	0.563	0.734	0.380	0.731	0.342	0.198
Medium	0.221	0.140	0.169	0.630	0.143	0.166	0.144	0.006
IprConA	0.518	0.330	0.860	0.366	0.740	0.868	0.589	0.362
IprPHA	0.605	0.421	0.074	0.571	0.842	0.389	0.579	0.715
IprPWM	0.347	0.877	0.792	0.137	0.154	0.056	0.741	0.866
Female Cytokines	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
IL2	0.715	0.467	0.304	0.735	0.352	0.623	0.035	0.015
IL4	0.466	0.035	0.221	0.778	0.036	0.686	0.049	0.044
IL10	0.458	0.593	0.878	0.515	0.455	0.048	0.869	0.725
IL17A	0.422	0.195	0.187	0.886	0.741	0.768	0.183	0.315
TNFa	0.912	0.135	0.365	0.974	0.201	0.486	0.032	0.051
IFNg	0.562	0.614	0.307	0.824	0.934	0.689	0.060	0.016
Female CellPhenotype	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
sp3	0.195	0.627	0.434	0.158	0.655	0.177	0.434	0.567
sp3_4	0.787	0.246	0.542	0.462	0.299	0.136	0.196	0.144
sp3_8	0.610	0.959	0.508	0.667	0.433	0.335	0.319	0.223
sp3_45	0.515	0.338	0.976	0.572	0.356	0.452	0.194	0.035
sp3_161	0.162	0.682	0.854	0.618	0.996	0.870	0.010	0.053
ln3	0.877	0.643	0.104	0.280	0.326	0.232	0.670	0.266

ln3_4	0.522	0.579	0.309	0.802	0.420	0.824	0.773	0.522
ln3_8	0.816	0.383	0.374	0.733	0.216	0.297	0.176	0.025
ln3_45	0.311	0.214	0.449	0.730	0.764	0.638	0.985	0.907
ty3	0.058	0.196	0.954	0.047	0.082	0.425	0.605	0.778
ty3_4	0.134	0.209	0.954	0.012	0.047	0.845	0.531	0.681
ty3_8	0.147	0.047	0.946	0.220	0.536	0.902	0.981	0.973

Female Hormone	SW Control	SW NK11-	SW NK33-	SW NK11+	SW NK33+	SW residual	Bartlett	Levene
betaEstr	0.065	0.733	0.348	0.155	0.529	0.776	0.645	0.567
T3	0.777	0.001	0.307	0.212	0.792	0.762	0.618	0.612
T4	0.442	0.012	0.411	0.618	0.543	0.180	0.366	0.230