Phillipi, Xie, et al: Supplemental Material

Chapter 1

Phenotypes and animals

1.1 Nomenclature, descriptions and transformations

Table 1.1: Phenotype names and transformations used in this document.

Name in analysis	Name in manuscript	Description	Transformation
plusAPCs.Pct	+APCs	Total myeloid cells (+APCs)	logit
minusAPCs.Pct	-APCs	Total lymphoid cells (-APCs)	logit
B.to.T	B/T	Ratio of B-cells to T-cells	log10
CD11cplus.Pct	CD11c+	CD11c+/CD11b- dendritic cells	logit
CD19.Pct	CD19+	Total B-cells (CD19+)	logit
CD23.MFI	CD23 MFI	CD23 antigen density on all B-cells	log10
CD25.Pct.CD4	CD25+	Regulatory T-cells	logit
CD4.Pct.H57	CD4+	Helper and regulatory T-cells	logit
CD4.to.CD8	CD4+/CD8+	Ratio of helper T-cells to cytotoxic T-cells	log10
CD8.Pct.H57	CD8+	Cytotoxic T-cells	logit
DCs.CD11b.MFI	CD11b MFI	CD11b antigen density on dendritic cells	log10
DCs.CD11c.MFI	CD11c MFI	CD11c antigen density on dendritic cells	log10
DCs.Pct	DCs	Classical dendritic cells	logit
FoB.Pct.CD19	FoB	Follicular B-cells (CD19+)	INT
Granulocytes.Pct	Granulocytes	Granulocytes	logit
H57.Pct	H57+	Total T-cells (H57+)	logit
Macrophages.Pct	Macrophages	Macrophages	logit
Monocytes.Pct	Monocytes	Monocytes	logit
Phagocytes.Pct	CD11b Hi	Phagocytes (CD11b Hi)	logit
MZB.Pct.CD19	MZB	Marginal Zone B-cells	INT
TransB.Pct.CD19	TransB	Transitional B-cells	INT

1.2 Gating procedure

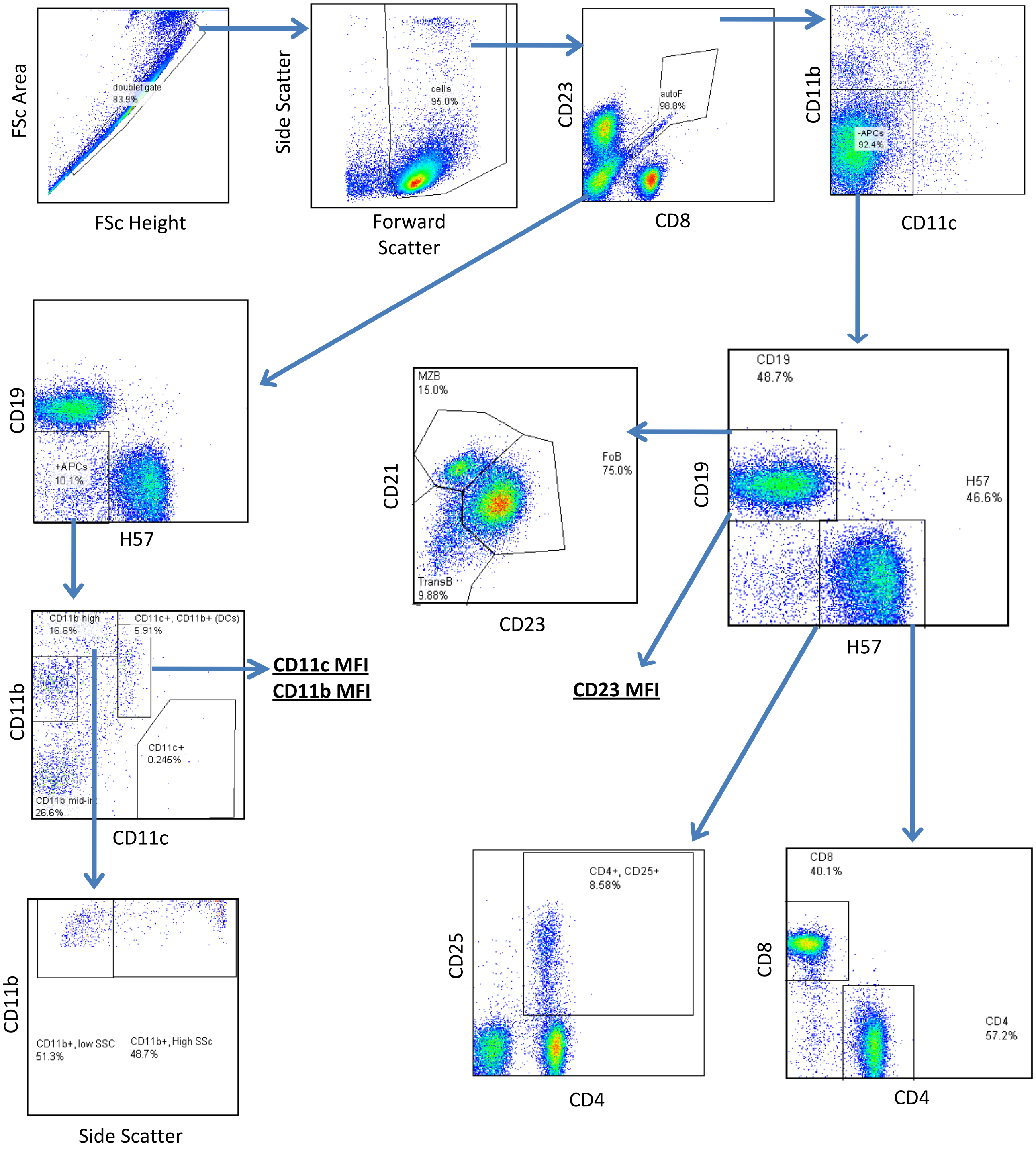

Figure 1.1: Example gating scheme on B6 control spleen

1.3 Mice used in the study

Table 1.2: Number of mice measured. Each strain columns show the number of females, males, and (where applicable) mice for which sex data was unavailable.

Phenotype	AJ	B6	129	NOD	NZO	CAST	PWK	WSB	F1	PreCC
plusAPCs.Pct	4, 2	4, 6, 62	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 66
minusAPCs.Pct	4, 2	4, 6, 62	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 66
B.to.T	4, 2	4, 6, 62	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 66
CD11cplus.Pct	4, 2	4, 6, 61	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 54
CD19.Pct	4, 2	4, 6, 62	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 66
CD23.MFI	4, 2	4, 6, 62	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 66
CD25.Pct.CD4	4, 2	4, 6, 58	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 66
CD4.Pct.H57	4, 2	4, 6, 62	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 66
CD4.to.CD8	4, 2	4, 6, 62	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 66
CD8.Pct.H57	4, 2	4, 6, 62	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 66
DCs.CD11b.MFI	4, 2	4, 6, 61	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 54
DCs.CD11c.MFI	4, 2	4, 6, 61	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 54
DCs.Pct	4, 2	4, 6, 61	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 54
FoB.Pct.CD19	4, 2	4, 6, 58	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 40
Granulocytes.Pct	4, 2	4, 6, 61	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 54
H57.Pct	4, 2	4, 6, 62	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 66
Macrophages.Pct	4, 2	4, 6, 61	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 54
Monocytes.Pct	4, 2	4, 6, 61	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 54
Phagocytes.Pct	4, 2	4, 6, 61	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 54
MZB.Pct.CD19	4, 2	4, 6, 58	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 40
TransB.Pct.CD19	4, 2	4, 6, 58	4, 2	0, 6	0, 10	0, 2	3, 6	2, 8	51, 81	0, 40

Chapter 2

Summary of Results

2.1 Sex and strain effects in the CC founders

Table 2.1: Significance of sex and strain effects on 21 phenotypes in the CC founders. These are calculated using a mixed model that controls for batch as a random effect.

Phenotype	Sex.Effect.Pval	Strain.Effect.Pval
plusAPCs.Pct	3.63e-07	9.58e-05
minusAPCs.Pct	0.00131	0.00144
B.to.T	0.000121	3.44e-05
CD11cplus.Pct	0.595	0.0785
CD19.Pct	0.0137	0.00179
CD23.MFI	0.0108	6.1e-09
CD25.Pct.CD4	2.73e-05	8.15e-06
CD4.Pct.H57	0.588	1.97e-06
CD4.to.CD8	2.34e-05	4.91e-05
CD8.Pct.H57	5.56e-08	0.000242
DCs.CD11b.MFI	0.166	0.00024
DCs.CD11c.MFI	0.00204	1.13e-11
DCs.Pct	0.0846	1.31e-09
FoB.Pct.CD19	0.127	7.88e-07
Granulocytes.Pct	7.23e-05	0.0381
H57.Pct	1.91e-07	0.000195
Macrophages.Pct	0.579	4.63e-05
Monocytes.Pct	0.00971	1.6e-07
Phagocytes.Pct	0.0373	0.00275
MZB.Pct.CD19	0.444	2.56e-10
TransB.Pct.CD19	0.443	4.45e-05

2.2 Diallel analysis

The diallel analysis was confounded by batch effects. Examination of individual phenotypes reveals that, when accounting for uncertainty due to batch, posteriors for most effects in most phenotypes are extremely vague and cover zero.

Chapter 3

Observed Relationships between Immunophenotypes

3.1 Trait correlations within populations: inbreds, F1 hybrids and the PreCC

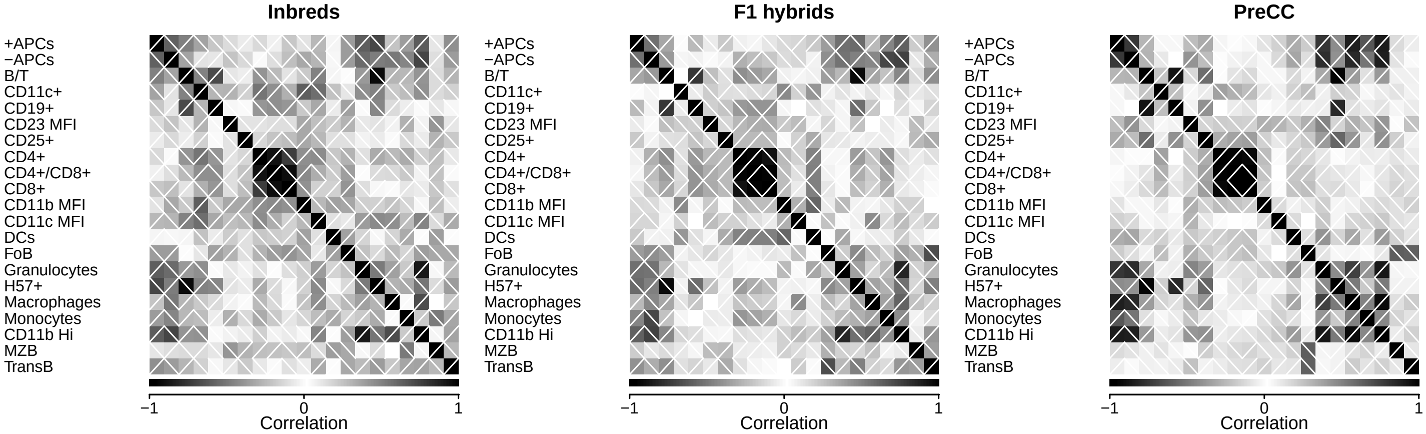

Figure 3.1: Correlations among phenotypes. Each block represents the correlation between two (transformed) phenotypes, with the top-left to bottom-right diagonal of black blocks depicting correlation of +1 (ie, a phenotype with itself). Shading indicates strength of correlation; white diagonal lines indicate positive vs negative correlation. Black crosses indicate missing data.

Chapter 4

plusAPCs.Pct: Total myeloid cells (+APCs)

4.1 Data collected on plusAPCs.Pct

Description: Total myeloid cells (+APCs)

Transformation: logit. Rationale for transformation: Natural range is a proportion between 0 and 1, so logit transformation provides an interpretable scale for effects.

Table 4.1: Number of mice phenotyped for plusAPCs.Pct

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	66	189
Unsexed	0	62	0	0	0	0	0	0	0	0	62
Total	6	72	6	6	10	2	9	10	132	66	319

4.2 Raw and Transformed Data

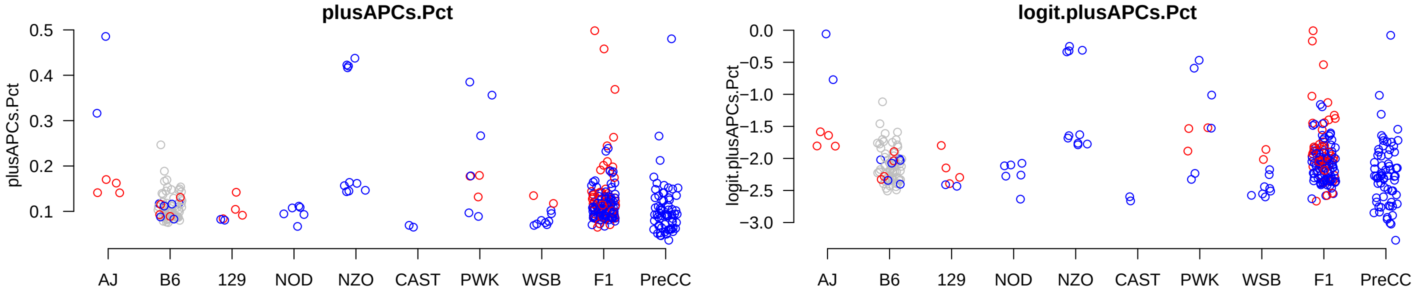

Figure 4.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 4.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	0.236	0.111	0.0975	0.0971	0.261	0.0672	0.207	0.0895	0.127	0.105
SE of Mean	0.0567	0.00348	0.00962	0.00681	0.0444	0.00205	0.0357	0.00708	0.00536	0.00771
Min	0.141	0.0753	0.0806	0.0669	0.143	0.0652	0.0889	0.0691	0.065	0.0364
Max	0.486	0.247	0.142	0.112	0.438	0.0693	0.385	0.135	0.498	0.48
Modeled 95%CI Lower	-1.56	-2.22	-2.34	-2.5	-1.45	-2.98	-1.9	-2.62	-2.05	-2.41
Modeled Mean	-1.23	-2.11	-2.01	-2.1	-1.17	-2.42	-1.58	-2.36	-1.95	-2.24
Modeled 95%CI Upper	-0.892	-2	-1.69	-1.71	-0.891	-1.86	-1.26	-2.09	-1.85	-2.07

Table 4.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	37.7	3.63e-07
Inbred Strain	7	38	5.99	9.58e-05

4.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

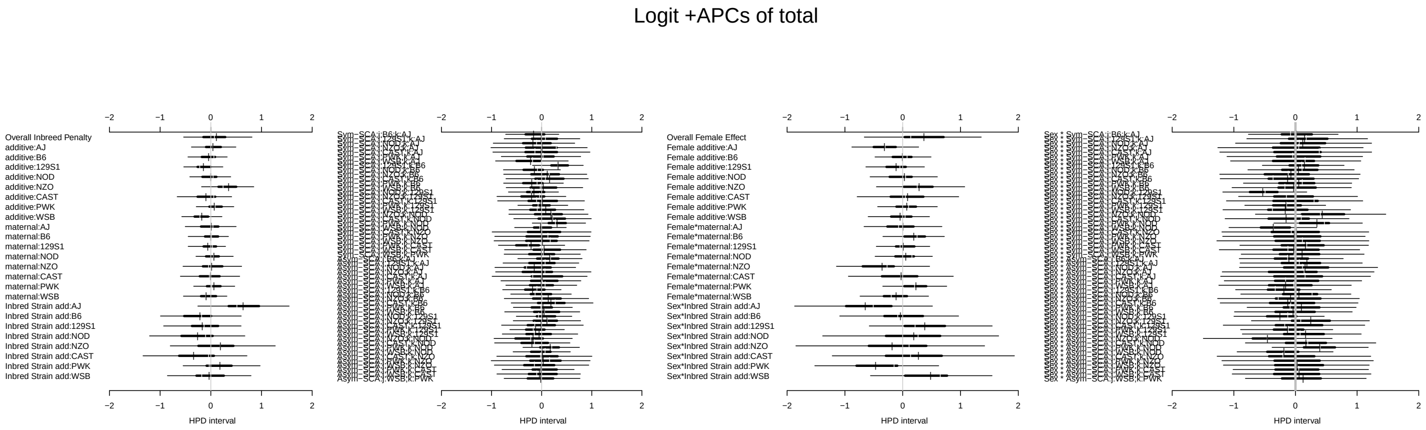

Figure 4.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a logit transformation.

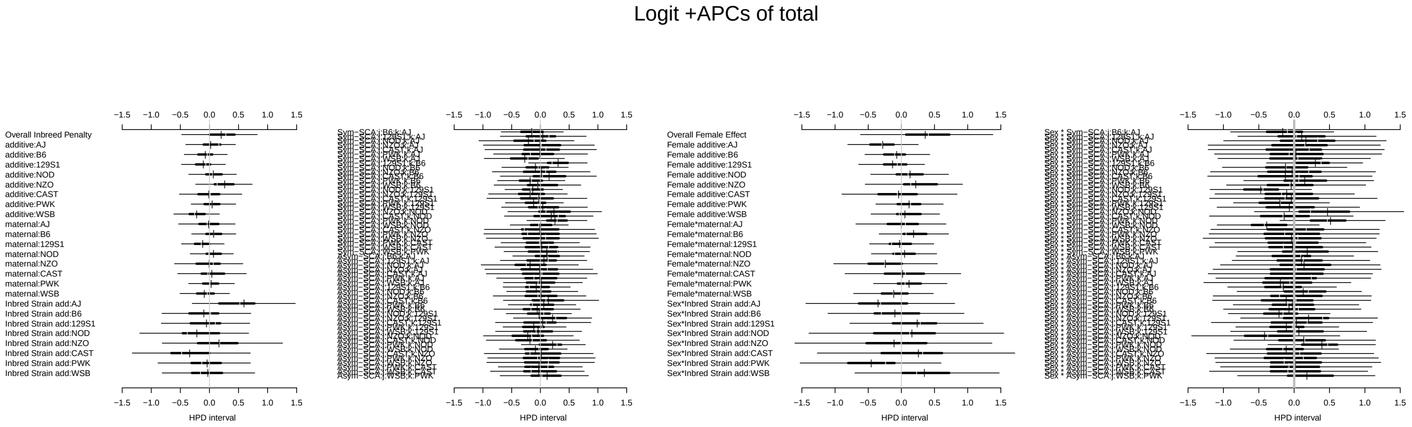

Figure 4.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a logit transformation.

Chapter 5

minusAPCs.Pct: Total lymphoid cells (-APCs)

5.1 Data collected on minusAPCs.Pct

Description: Total lymphoid cells (-APCs)

Transformation: logit. Rationale for transformation: Natural range is a proportion between 0 and 1, so logit transformation provides an interpretable scale for effects.

Table 5.1: Number of mice phenotyped for minusAPCs.Pct

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	66	189
Unsexed	0	62	0	0	0	0	0	0	0	0	62
Total	6	72	6	6	10	2	9	10	132	66	319

5.2 Raw and Transformed Data

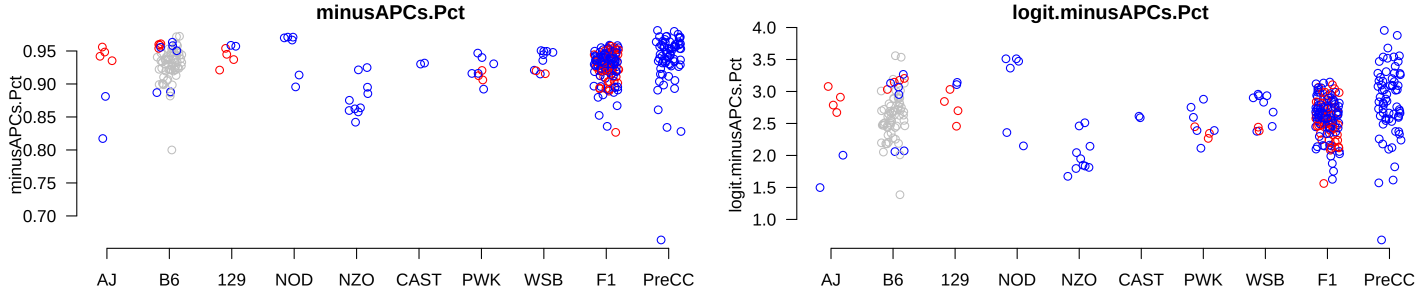

Figure 5.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 5.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	0.913	0.93	0.945	0.948	0.879	0.931	0.92	0.935	0.926	0.936
SE of Mean	0.0221	0.00307	0.00591	0.0139	0.00876	0.00075	0.00564	0.00485	0.00206	0.00564
Min	0.817	0.8	0.921	0.896	0.842	0.93	0.892	0.915	0.827	0.664
Max	0.956	0.972	0.959	0.971	0.925	0.932	0.947	0.951	0.959	0.981
Modeled 95%CI Lower	2.11	2.52	2.36	2.58	2.02	1.95	2.21	2.59	2.47	2.67
Modeled Mean	2.42	2.62	2.66	2.94	2.28	2.47	2.51	2.84	2.56	2.83
Modeled 95%CI Upper	2.73	2.72	2.96	3.3	2.53	2.99	2.8	3.08	2.66	2.98

Table 5.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	12	0.00131
Inbred Strain	7	38	4.28	0.00144

5.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

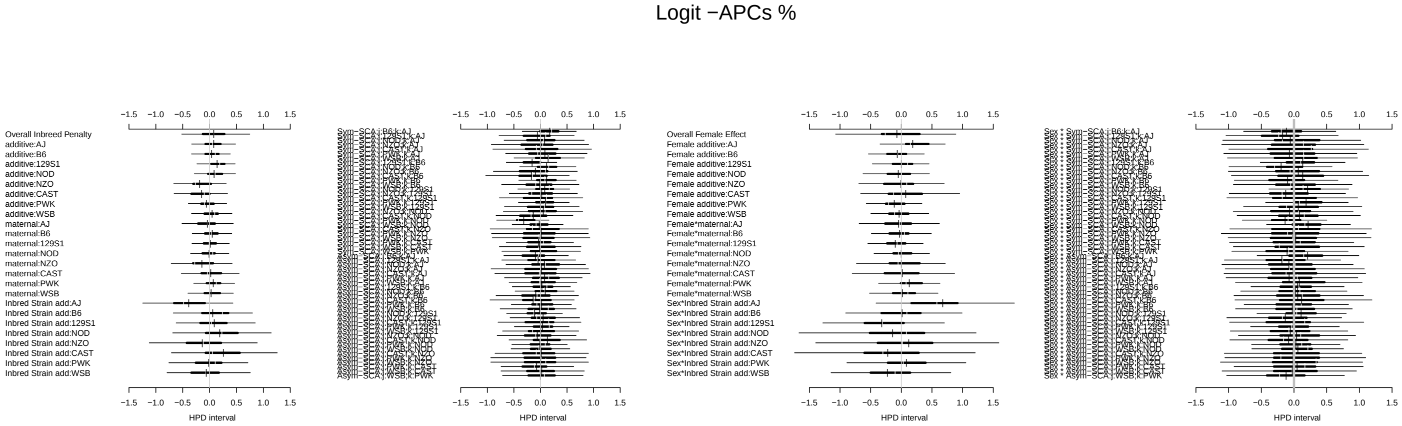

Figure 5.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a logit transformation.

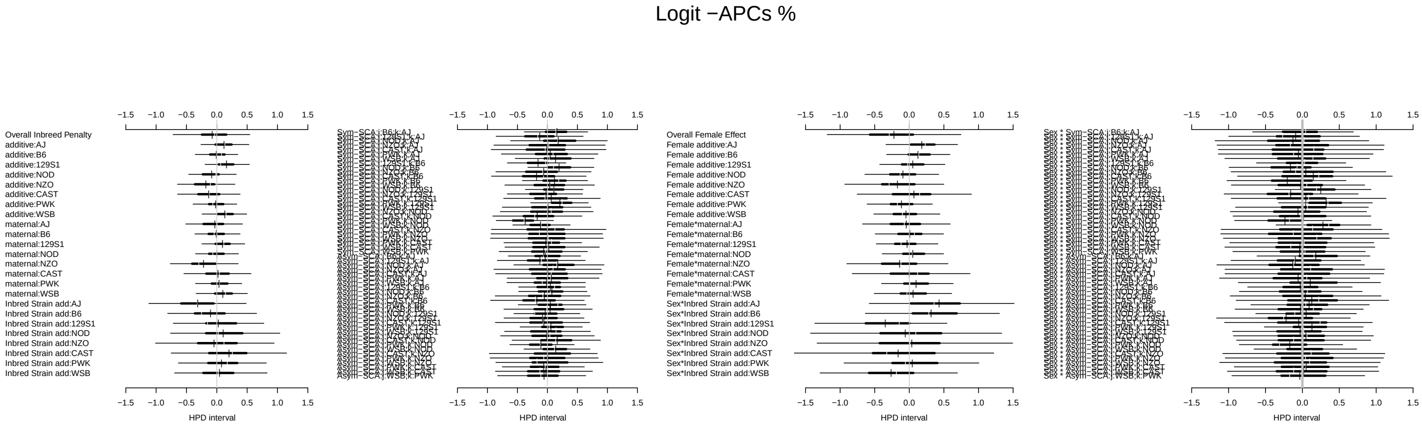

Figure 5.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a logit transformation.

Chapter 6

B.to.T: Ratio of B-cells to T-cells

6.1 Data collected on B.to.T

Description: Ratio of B-cells to T-cells

Transformation: log10. Rationale for transformation: Ratio quantity and therefore highly skewed. Logarithmic transformation brings it onto an additive, symmetric scale. Log to base 10 (log10) is used to provide a more interpretable scale for the effects.

Table 6.1: Number of mice phenotyped for B.to.T

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	66	189
Unsexed	0	62	0	0	0	0	0	0	0	0	62
Total	6	72	6	6	10	2	9	10	132	66	319

6.2 Raw and Transformed Data

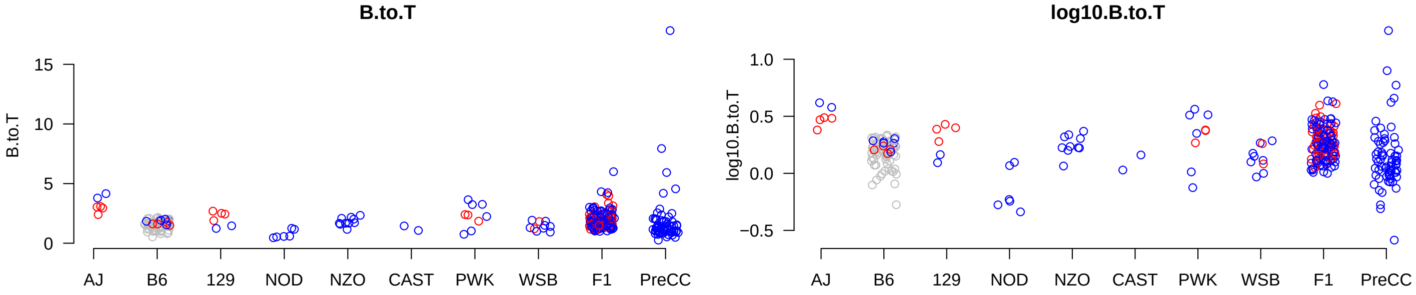

Figure 6.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 6.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	3.24	1.55	2.04	0.762	1.81	1.26	2.31	1.42	1.97	1.83
SE of Mean	0.258	0.043	0.245	0.143	0.109	0.19	0.33	0.111	0.0665	0.288
Min	2.4	0.531	1.24	0.46	1.16	1.07	0.75	0.93	1	0.26
Max	4.16	2.17	2.69	1.25	2.34	1.45	3.65	1.93	6	17.8
Modeled 95%CI Lower	0.378	0.127	0.228	-0.315	0.0791	0.00443	0.182	0.0449	0.235	0.0995
Modeled Mean	0.522	0.171	0.371	-0.155	0.197	0.248	0.313	0.158	0.273	0.165
Modeled 95%CI Upper	0.667	0.214	0.514	0.00497	0.315	0.492	0.443	0.271	0.312	0.23

Table 6.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	18.3	0.000121
Inbred Strain	7	38	6.7	3.44e-05

6.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

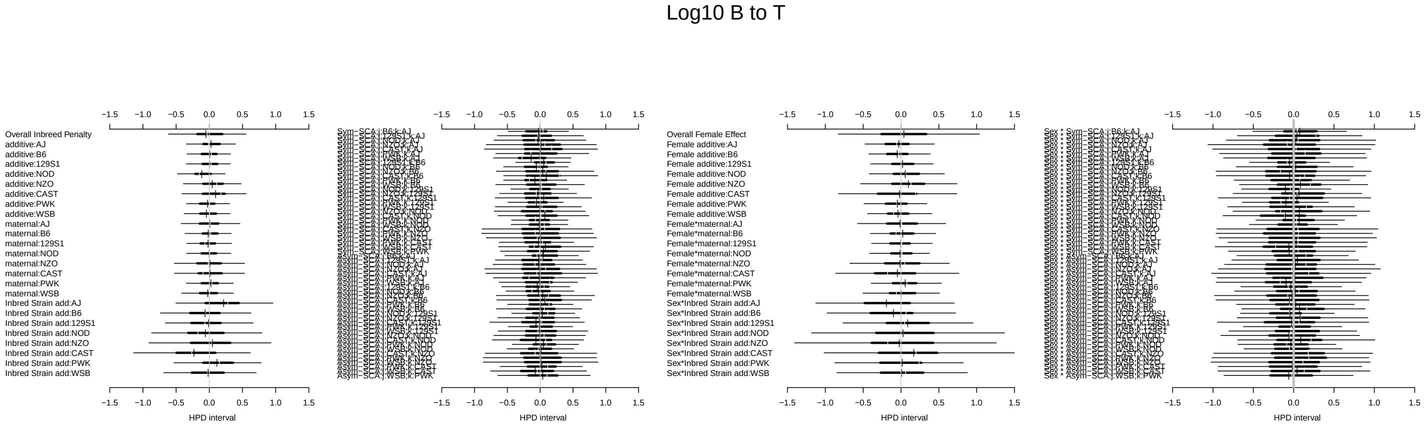

Figure 6.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a log10 transformation.

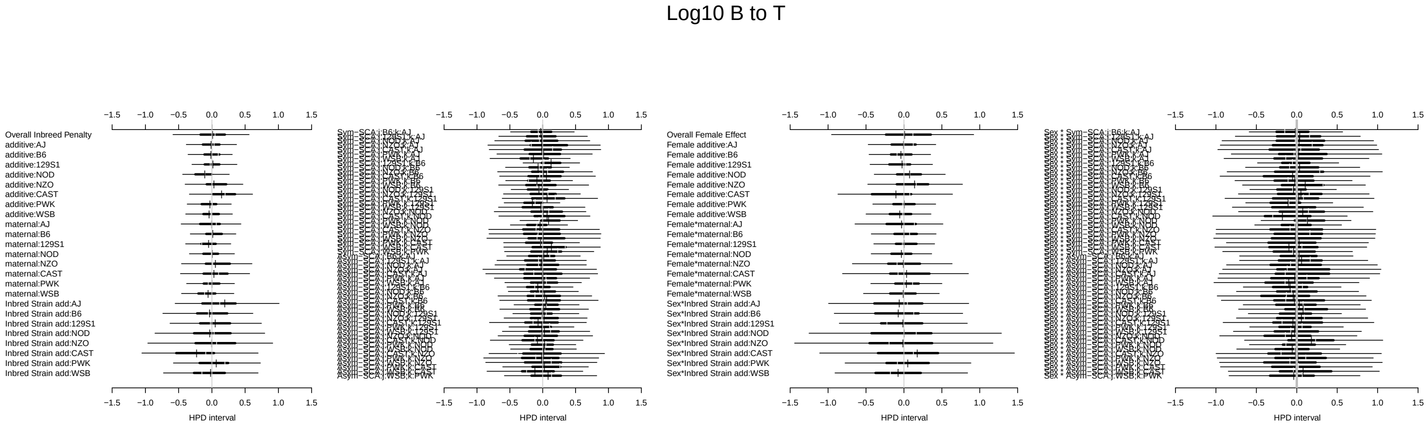

Figure 6.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a log10 transformation.

Chapter 7

CD11cplus.Pct: CD11c+/CD11b- dendritic cells

7.1 Data collected on CD11cplus.Pct

Description: CD11c+/CD11b- dendritic cells

Transformation: logit. Rationale for transformation: Natural range is a proportion between 0 and 1, so logit transformation provides an interpretable scale for effects.

Table 7.1: Number of mice phenotyped for CD11cplus.Pct

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	54	177
Unsexed	0	61	0	0	0	0	0	0	0	0	61
Total	6	71	6	6	10	2	9	10	132	54	306

7.2 Raw and Transformed Data

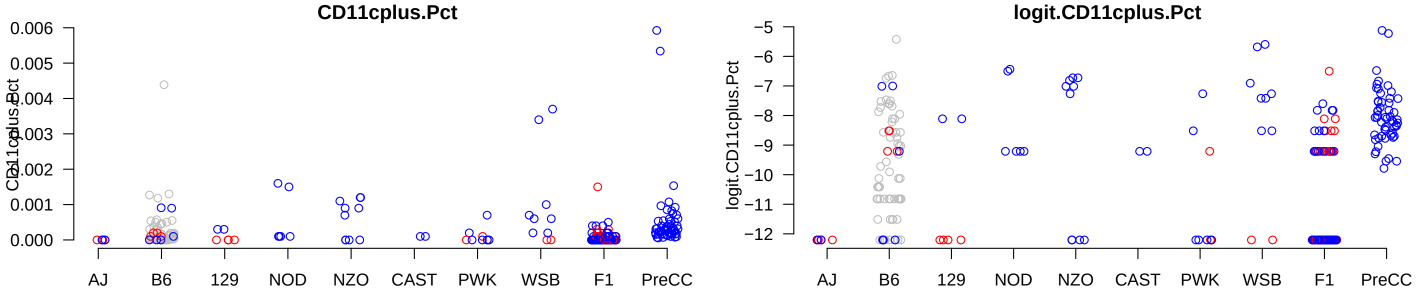

Figure 7.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 7.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	0	0.000255	1e-04	0.000583	6e-04	1e-04	0.000111	0.00104	5.38e-05	0.000572
SE of Mean	0	6.91e-05	6.32e-05	0.000306	0.00017	0	7.72e-05	0.000431	1.37e-05	0.000142
Min	0	0	0	1e-04	0	1e-04	0	0	0	5.62e-05
Max	0	0.00439	3e-04	0.0016	0.0012	1e-04	7e-04	0.0037	0.0015	0.00592
Modeled 95%CI Lower	-11.2	-10.2	-11.1	-10.4	-11	-12.2	-11	-9.9	-11.1	-10.4
Modeled Mean	-10.3	-9.72	-10.2	-9.29	-10.2	-10.8	-9.99	-9.13	-10.6	-9.71
Modeled 95%CI Upper	-9.37	-9.25	-9.34	-8.13	-9.43	-9.35	-8.99	-8.36	-10.1	-9.05

Table 7.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	0.287	0.595
Inbred Strain	7	38	2.01	0.0785

7.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

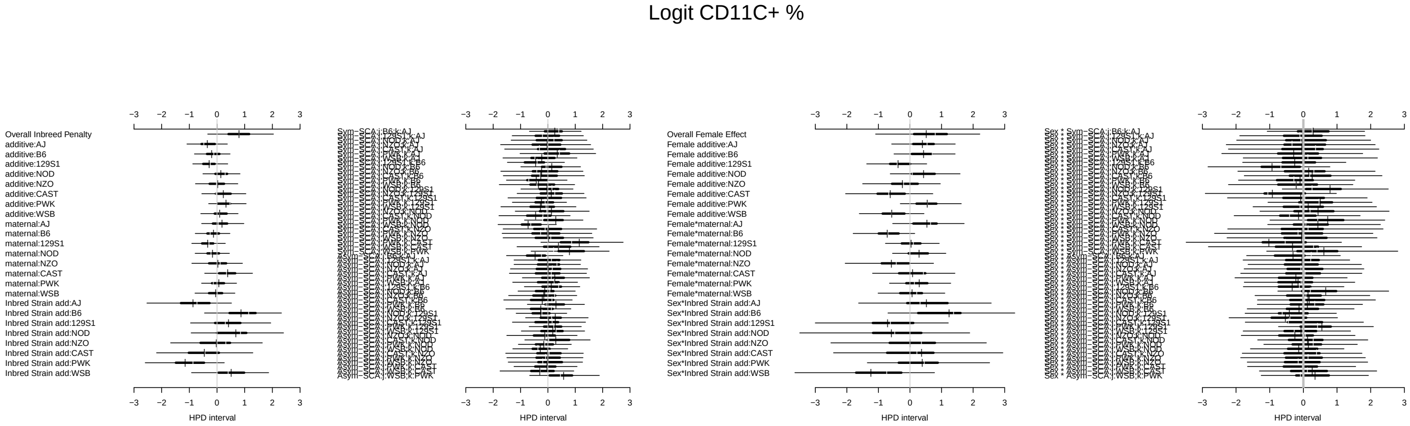

Figure 7.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a logit transformation.

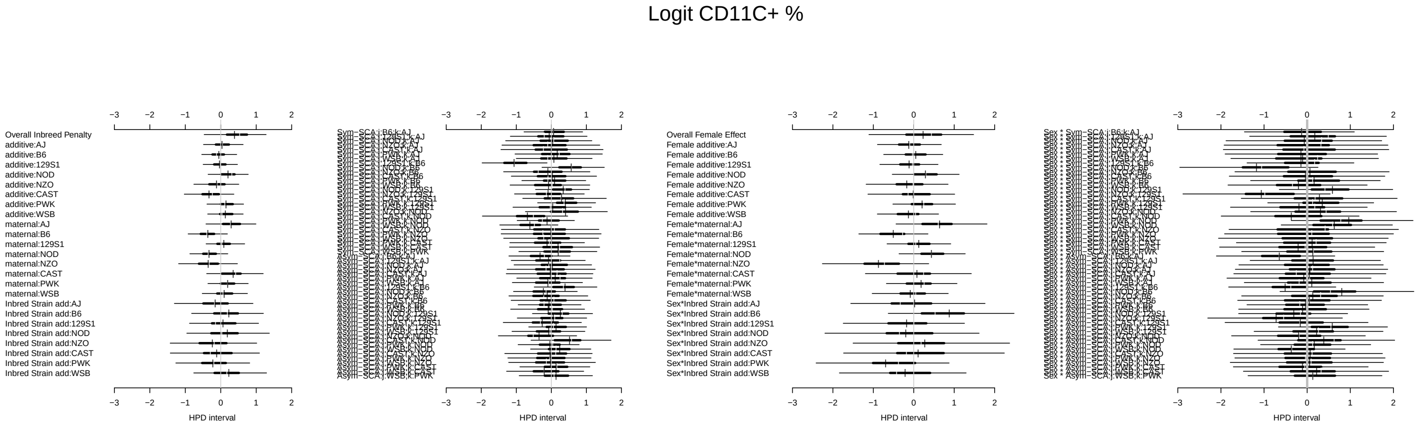

Figure 7.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a logit transformation.

Chapter 8

CD19.Pct: Total B-cells (CD19+)

8.1 Data collected on CD19.Pct

Description: Total B-cells (CD19+)

Transformation: logit. Rationale for transformation: Natural range is a proportion between 0 and 1, so logit transformation provides an interpretable scale for effects.

Table 8.1: Number of mice phenotyped for CD19.Pct

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	66	189
Unsexed	0	62	0	0	0	0	0	0	0	0	62
Total	6	72	6	6	10	2	9	10	132	66	319

8.2 Raw and Transformed Data

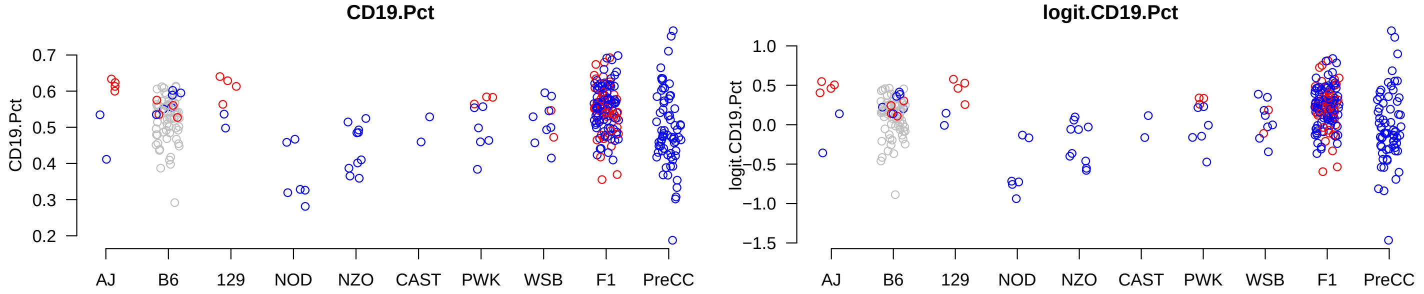

Figure 8.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 8.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	0.569	0.526	0.58	0.363	0.442	0.494	0.516	0.514	0.553	0.493
SE of Mean	0.0347	0.00723	0.0231	0.0322	0.0202	0.0347	0.0231	0.0181	0.00571	0.013
Min	0.412	0.292	0.498	0.281	0.359	0.46	0.384	0.415	0.355	0.188
Max	0.634	0.614	0.64	0.467	0.524	0.529	0.584	0.596	0.698	0.767
Modeled 95%CI Lower	0.041	0.016	0.132	-0.891	-0.502	-0.243	-0.144	-0.101	0.142	-0.0969
Modeled Mean	0.297	0.0927	0.386	-0.608	-0.293	0.19	0.0868	0.0993	0.21	0.0185
Modeled 95%CI Upper	0.554	0.169	0.639	-0.325	-0.0832	0.623	0.318	0.299	0.277	0.134

Table 8.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	6.68	0.0137
Inbred Strain	7	38	4.14	0.00179

8.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

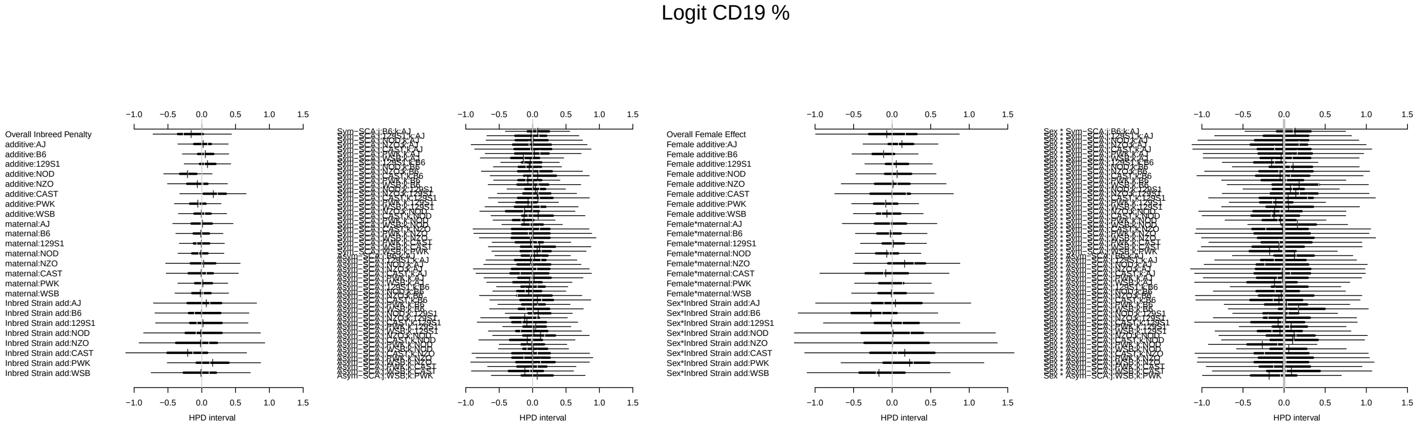

Figure 8.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a logit transformation.

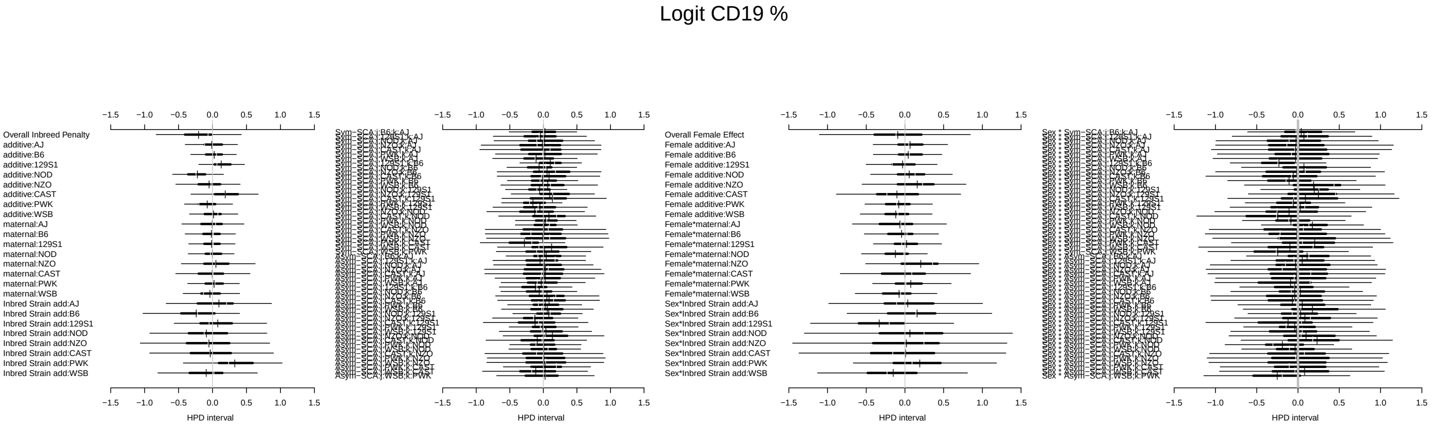

Figure 8.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a logit transformation.

Chapter 9

CD23.MFI: CD23 antigen density on all B-cells

9.1 Data collected on CD23.MFI

Description: CD23 antigen density on all B-cells

Transformation: log10. Rationale for transformation: Dimensionless quantity, but Box-Cox suggests a logarithmic transformation. Log to base 10 (log10) is used to provide a more interpretable scale.

Table 9.1: Number of mice phenotyped for CD23.MFI

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	66	189
Unsexed	0	62	0	0	0	0	0	0	0	0	62
Total	6	72	6	6	10	2	9	10	132	66	319

9.2 Raw and Transformed Data

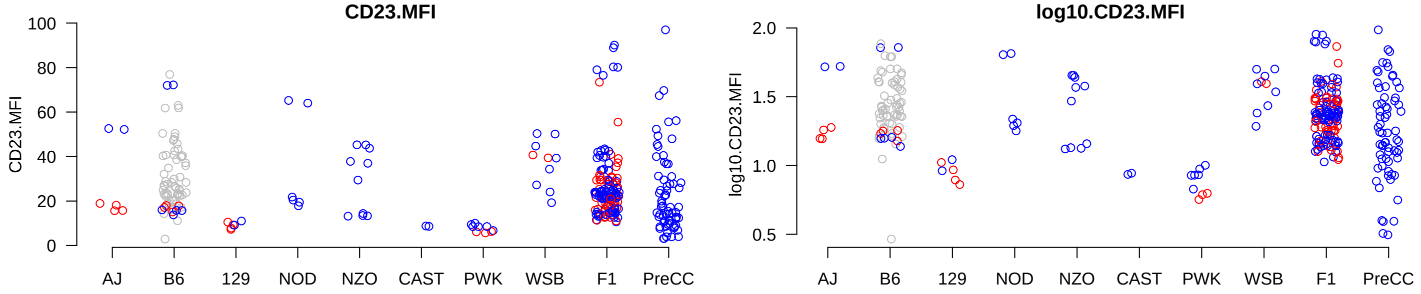

Figure 9.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 9.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	28.9	30.5	9.19	34.8	29.3	8.71	7.76	37	26.8	23.6
SE of Mean	7.46	1.84	0.597	9.44	4.51	0.0845	0.528	3.36	1.35	2.28
Min	15.6	2.92	7.27	17.9	13.2	8.62	5.66	19.3	10.6	3.13
Max	52.6	76.9	11	65.2	45.3	8.79	10	50.3	90.1	96.9
Modeled 95%CI Lower	1.2	1.38	0.878	1.23	1.24	0.767	0.742	1.28	1.29	1.21
Modeled Mean	1.37	1.44	1.04	1.44	1.39	1.05	0.917	1.42	1.35	1.31
Modeled 95%CI Upper	1.54	1.51	1.21	1.65	1.53	1.33	1.09	1.56	1.41	1.41

Table 9.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	7.19	0.0108
Inbred Strain	7	38	14.3	6.1e-09

9.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

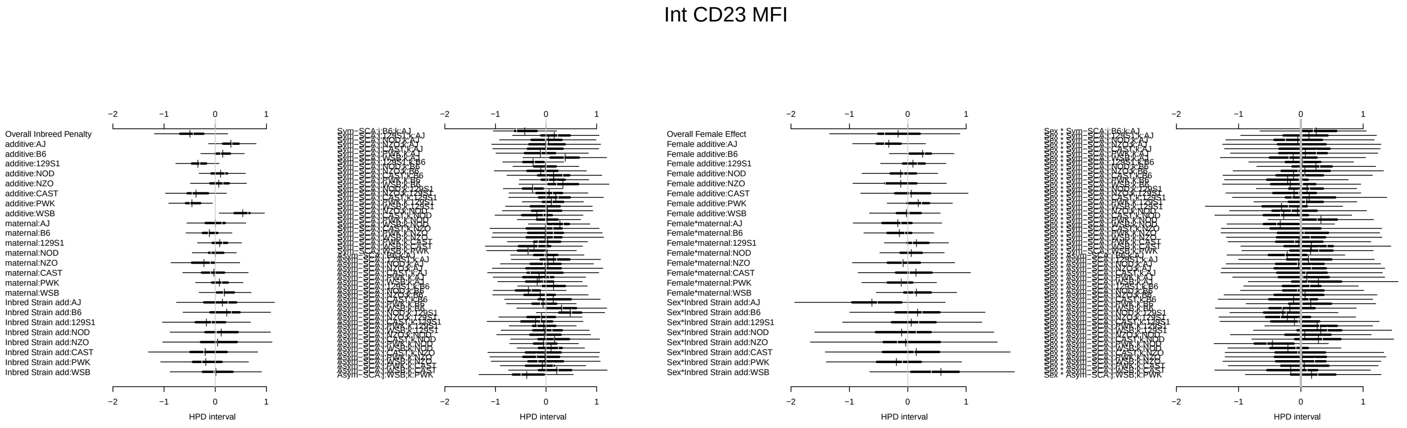

Figure 9.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a log10 transformation.

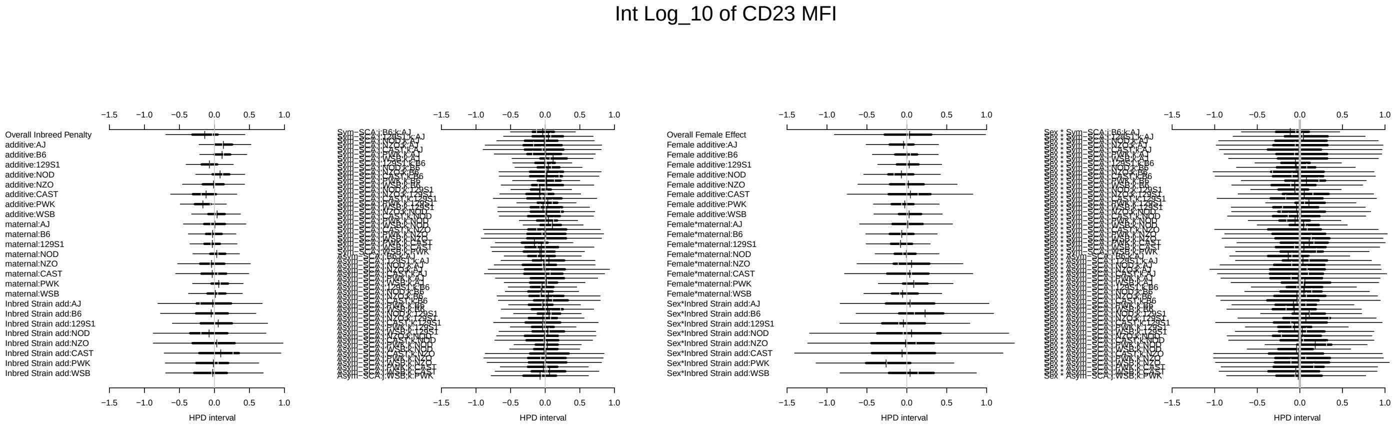

Figure 9.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a log10 transformation.

Chapter 10

CD25.Pct.CD4: Regulatory T-cells

10.1 Data collected on CD25.Pct.CD4

Description: Regulatory T-cells

Transformation: logit. Rationale for transformation: Natural range is a proportion between 0 and 1, so logit transformation provides an interpretable scale for effects.

Table 10.1: Number of mice phenotyped for CD25.Pct.CD4

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	66	189
Unsexed	0	58	0	0	0	0	0	0	0	0	58
Total	6	68	6	6	10	2	9	10	132	66	315

10.2 Raw and Transformed Data

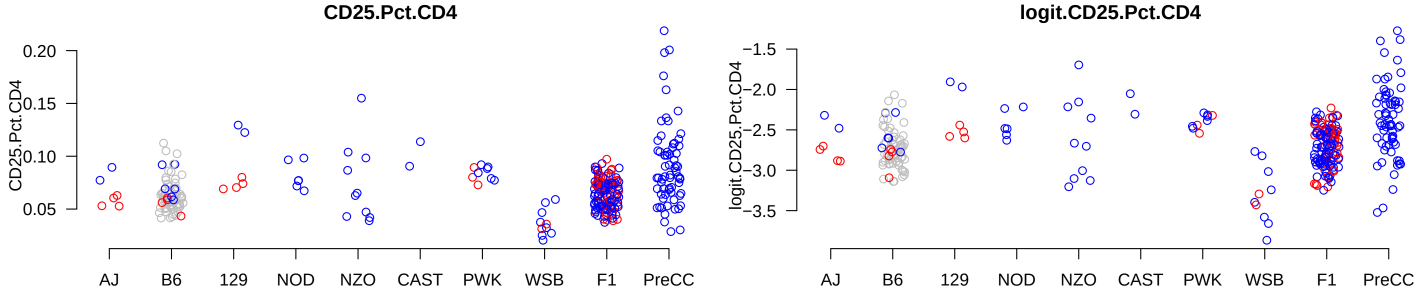

Figure 10.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 10.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 55 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	0.066	0.0633	0.091	0.0813	0.0743	0.102	0.0837	0.0372	0.0645	0.0914
SE of Mean	0.00595	0.00188	0.0112	0.00531	0.0117	0.0116	0.00222	0.00411	0.00119	0.00481
Min	0.0528	0.0415	0.0691	0.0673	0.039	0.0906	0.0729	0.0205	0.0374	0.0287
Max	0.0895	0.112	0.13	0.0983	0.155	0.114	0.092	0.0591	0.0972	0.219
Modeled 95%CI Lower	-2.84	-2.8	-2.53	-2.74	-2.8	-2.69	-2.64	-3.53	-2.73	-2.51
Modeled Mean	-2.59	-2.72	-2.27	-2.47	-2.6	-2.26	-2.42	-3.33	-2.67	-2.41
Modeled 95%CI Upper	-2.34	-2.64	-2.02	-2.2	-2.39	-1.83	-2.19	-3.13	-2.61	-2.3

Table 10.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	22.7	2.73e-05
Inbred Strain	7	38	7.75	8.15e-06

10.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

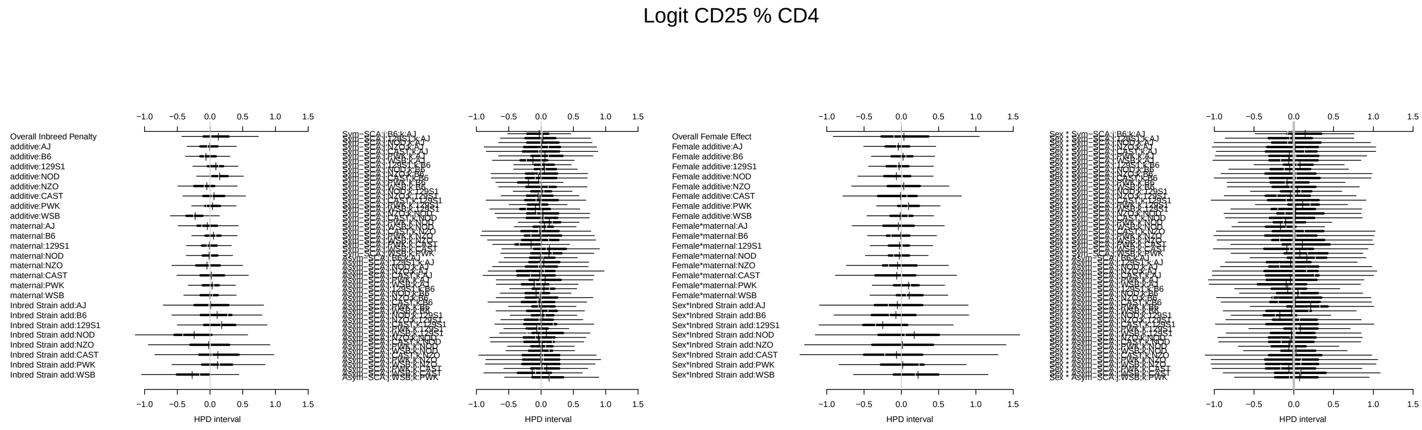

Figure 10.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a logit transformation.

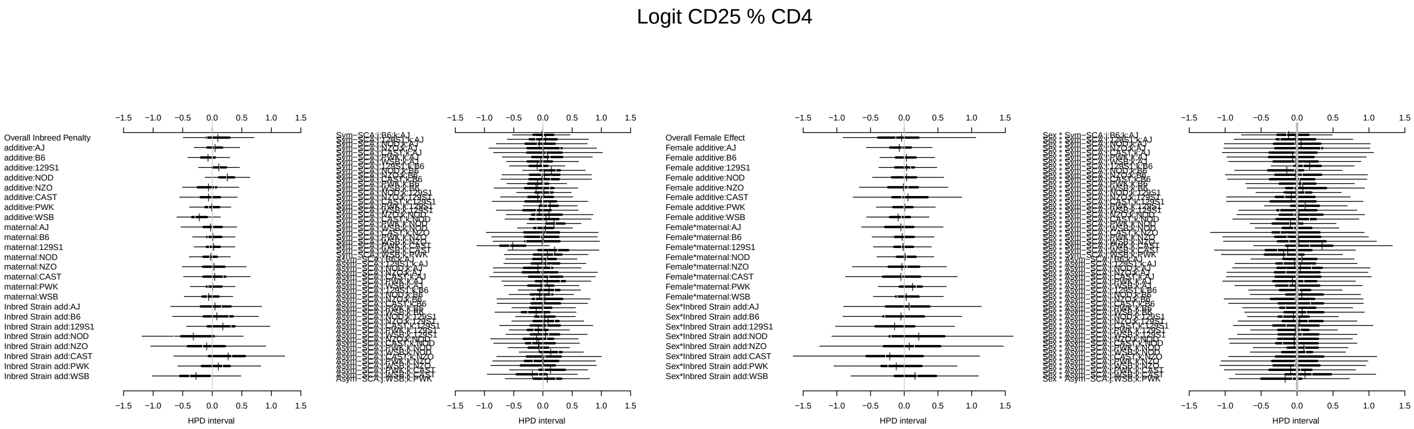

Figure 10.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a logit transformation.

Chapter 11

CD4.Pct.H57: Helper and regulatory T-cells

11.1 Data collected on CD4.Pct.H57

Description: Helper and regulatory T-cells

Transformation: logit. Rationale for transformation: Natural range is a proportion between 0 and 1, so logit transformation provides an interpretable scale for effects.

Table 11.1: Number of mice phenotyped for CD4.Pct.H57

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	66	189
Unsexed	0	62	0	0	0	0	0	0	0	0	62
Total	6	72	6	6	10	2	9	10	132	66	319

11.2 Raw and Transformed Data

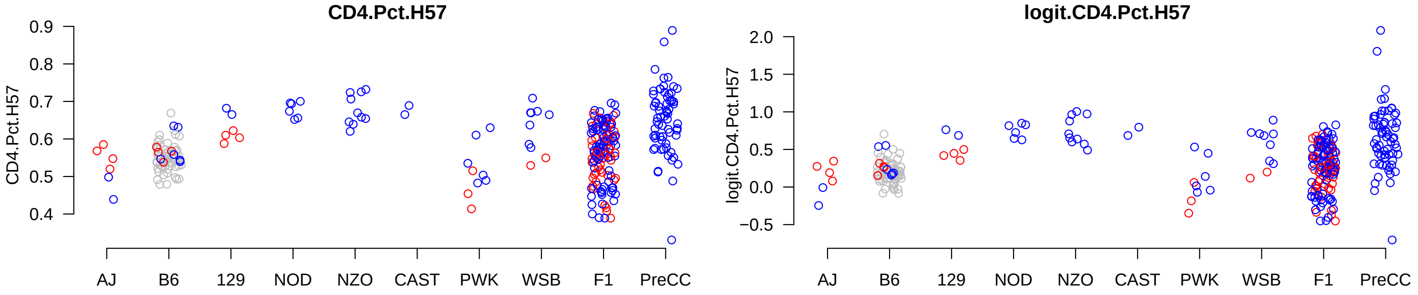

Figure 11.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 11.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	0.526	0.551	0.628	0.679	0.677	0.677	0.515	0.627	0.561	0.651
SE of Mean	0.0217	0.00424	0.0152	0.00866	0.0129	0.0121	0.0231	0.0194	0.0065	0.0108
Min	0.439	0.479	0.588	0.652	0.62	0.665	0.414	0.53	0.389	0.331
Max	0.585	0.669	0.682	0.7	0.732	0.689	0.63	0.709	0.696	0.889
Modeled 95%CI Lower	-0.202	0.129	0.123	0.428	0.612	0.161	-0.148	0.27	0.182	0.435
Modeled Mean	0.0339	0.202	0.354	0.697	0.806	0.557	0.0717	0.455	0.249	0.549
Modeled 95%CI Upper	0.27	0.274	0.586	0.965	1	0.953	0.292	0.64	0.316	0.663

Table 11.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	0.298	0.588
Inbred Strain	7	38	8.87	1.97e-06

11.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

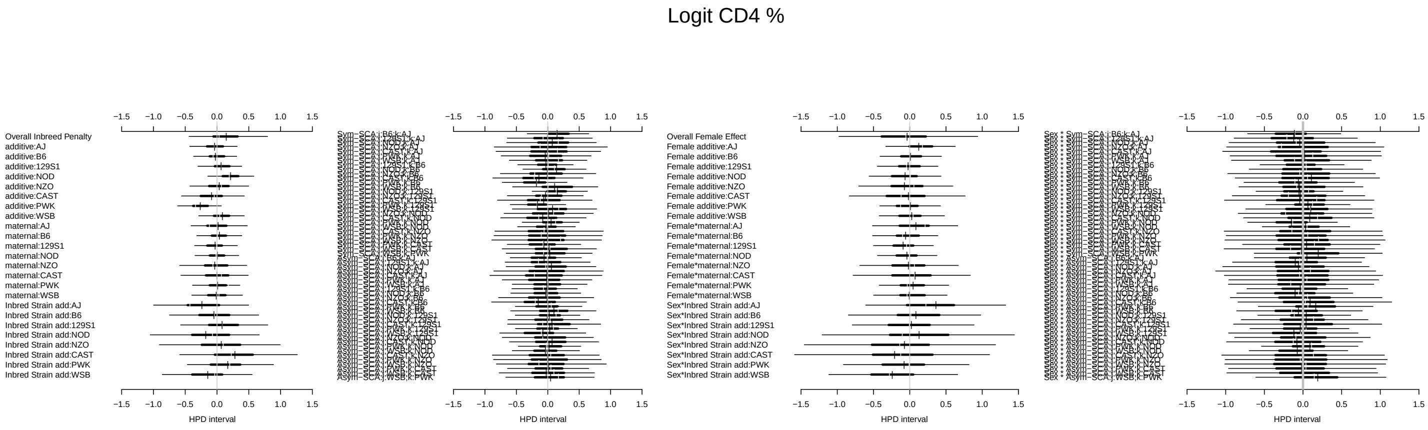

Figure 11.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a logit transformation.

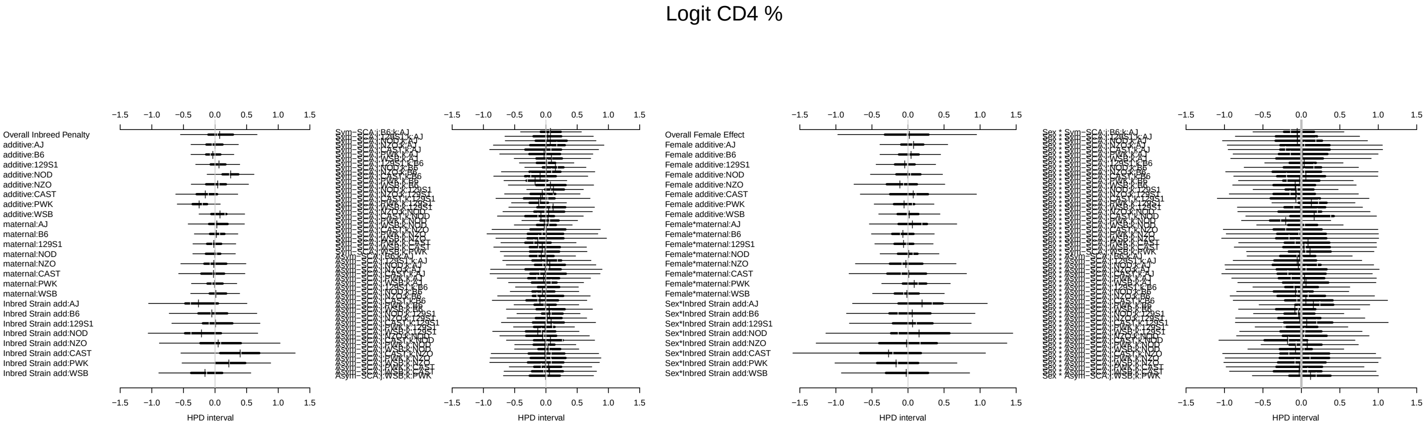

Figure 11.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a logit transformation.

Chapter 12

CD4.to.CD8: Ratio of helper T-cells to cytotoxic T-cells

12.1 Data collected on CD4.to.CD8

Description: Ratio of helper T-cells to cytotoxic T-cells

Transformation: log10. Rationale for transformation: Ratio quantity and therefore highly skewed. Logarithmic transformation brings it onto an additive, symmetric scale. Log to base 10 (log10) is used to provide a more interpretable scale for the effects.

Table 12.1: Number of mice phenotyped for CD4.to.CD8

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	66	189
Unsexed	0	62	0	0	0	0	0	0	0	0	62
Total	6	72	6	6	10	2	9	10	132	66	319

12.2 Raw and Transformed Data

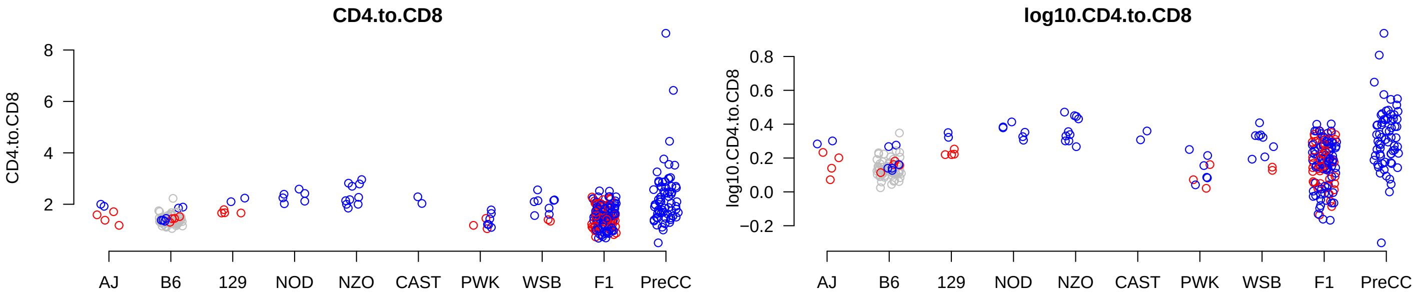

Figure 12.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 12.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	1.63	1.4	1.85	2.3	2.37	2.16	1.34	1.89	1.53	2.31
SE of Mean	0.128	0.0225	0.104	0.0856	0.128	0.13	0.0835	0.126	0.038	0.147
Min	1.18	1.06	1.66	2.02	1.85	2.03	1.05	1.34	0.68	0.5
Max	2	2.23	2.24	2.59	2.96	2.29	1.78	2.56	2.52	8.65
Modeled 95%CI Lower	0.069	0.111	0.117	0.231	0.312	0.114	0.0304	0.151	0.138	0.244
Modeled Mean	0.173	0.142	0.22	0.346	0.397	0.29	0.124	0.233	0.165	0.29
Modeled 95%CI Upper	0.277	0.173	0.323	0.46	0.482	0.466	0.217	0.314	0.192	0.337

Table 12.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	23.2	2.34e-05
Inbred Strain	7	38	6.45	4.91e-05

12.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

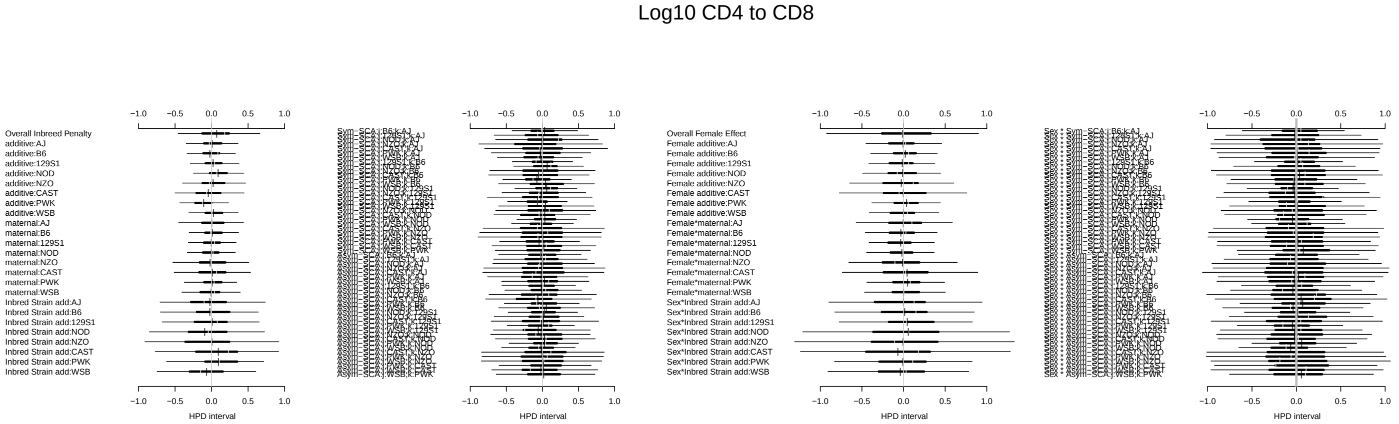

Figure 12.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a log10 transformation.

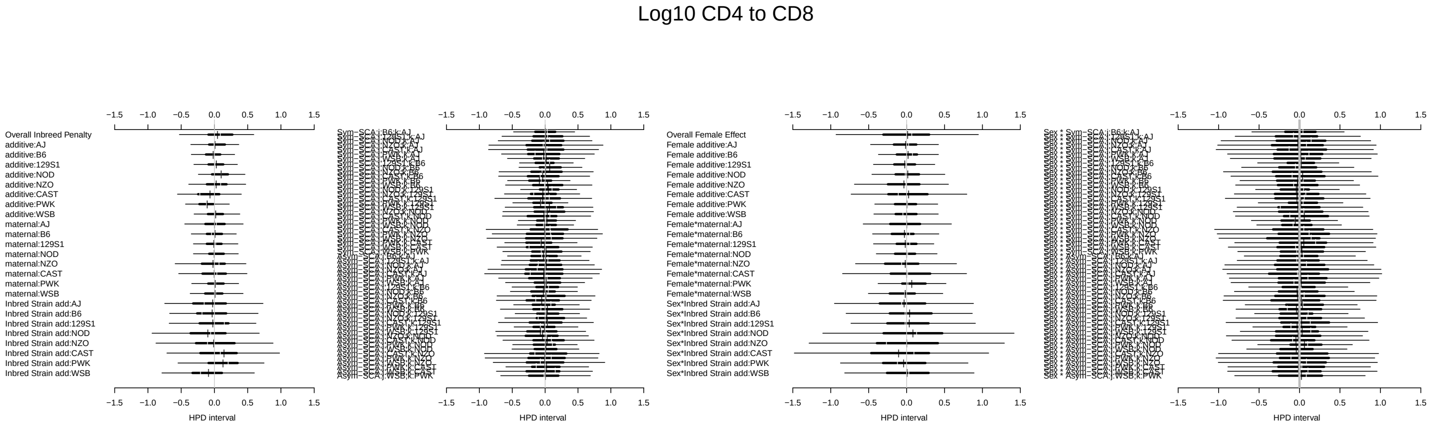

Figure 12.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a log10 transformation.

Chapter 13

CD8.Pct.H57: Cytotoxic T-cells

13.1 Data collected on CD8.Pct.H57

Description: Cytotoxic T-cells

Transformation: logit. Rationale for transformation: Natural range is a proportion between 0 and 1, so logit transformation provides an interpretable scale for effects.

Table 13.1: Number of mice phenotyped for CD8.Pct.H57

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	66	189
Unsexed	0	62	0	0	0	0	0	0	0	0	62
Total	6	72	6	6	10	2	9	10	132	66	319

13.2 Raw and Transformed Data

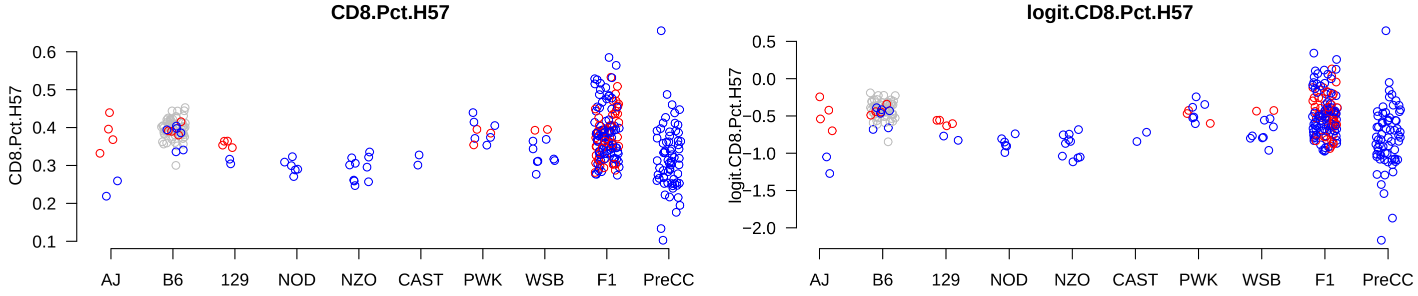

Figure 13.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 13.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	0.336	0.396	0.342	0.297	0.29	0.314	0.388	0.339	0.385	0.318
SE of Mean	0.0341	0.00315	0.0103	0.0074	0.0101	0.0134	0.0095	0.0126	0.00594	0.0107
Min	0.219	0.3	0.304	0.271	0.247	0.301	0.354	0.277	0.274	0.103
Max	0.439	0.453	0.364	0.323	0.336	0.328	0.44	0.395	0.585	0.655
Modeled 95%CI Lower	-0.876	-0.49	-0.833	-1.09	-1.15	-1.13	-0.667	-0.775	-0.534	-0.832
Modeled Mean	-0.642	-0.421	-0.602	-0.843	-0.96	-0.729	-0.462	-0.593	-0.475	-0.732
Modeled 95%CI Upper	-0.409	-0.353	-0.37	-0.591	-0.771	-0.334	-0.257	-0.411	-0.416	-0.633

Table 13.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	45.4	5.56e-08
Inbred Strain	7	38	5.38	0.000242

13.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

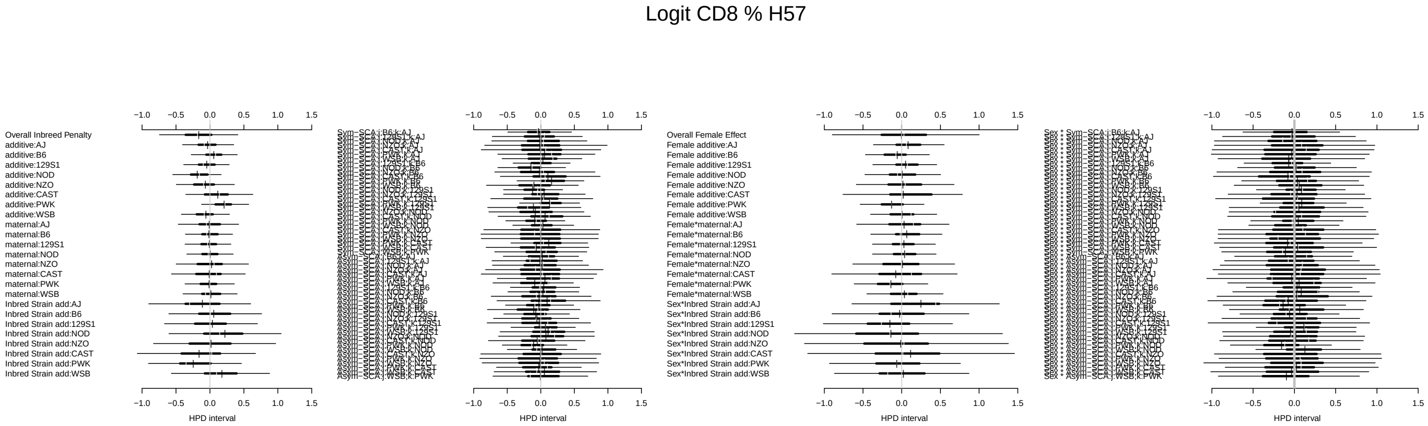

Figure 13.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a logit transformation.

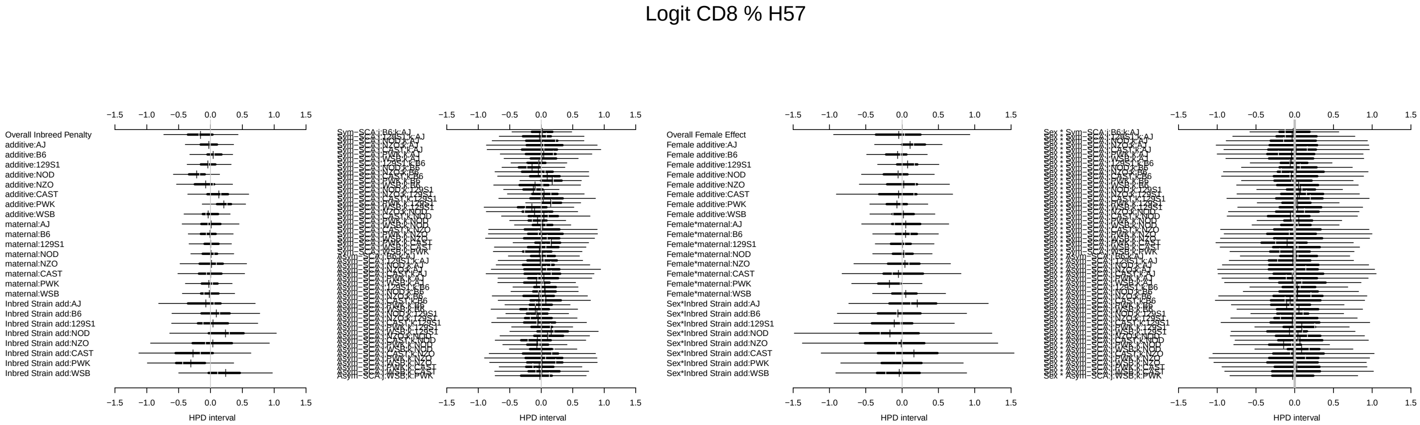

Figure 13.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a logit transformation.

Chapter 14

DCs.CD11b.MFI: CD11b antigen density on dendritic cells

14.1 Data collected on DCs.CD11b.MFI

Description: CD11b antigen density on dendritic cells

Transformation: log10. Rationale for transformation: Dimensionless quantity, but Box-Cox suggests a logarithmic transformation. Log to base 10 (log10) is used to provide a more interpretable scale.

Table 14.1: Number of mice phenotyped for DCs.CD11b.MFI

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	54	177
Unsexed	0	61	0	0	0	0	0	0	0	0	61
Total	6	71	6	6	10	2	9	10	132	54	306

14.2 Raw and Transformed Data

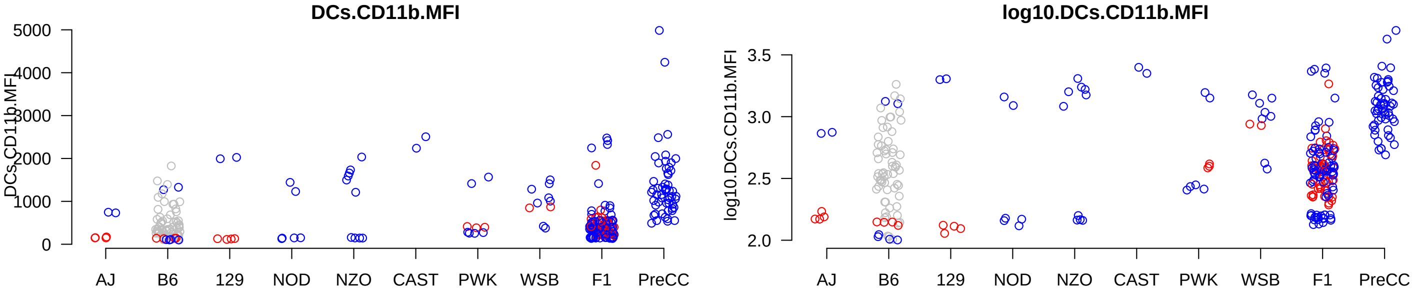

Figure 14.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 14.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	350	467	753	541	1030	2370	583	977	451	1360
SE of Mean	123	45.4	397	253	249	134	173	119	35.7	111
Min	148	101	114	131	145	2240	255	377	134	491
Max	747	1830	2030	1440	2030	2510	1570	1500	2480	4990
Modeled 95%CI Lower	2.52	2.5	2.54	2.27	2.45	2.74	2.48	2.57	2.57	2.7
Modeled Mean	2.67	2.58	2.69	2.45	2.57	2.97	2.64	2.69	2.65	2.81
Modeled 95%CI Upper	2.81	2.66	2.83	2.64	2.7	3.19	2.8	2.81	2.73	2.92

Table 14.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	1.99	0.166
Inbred Strain	7	38	5.39	0.00024

14.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

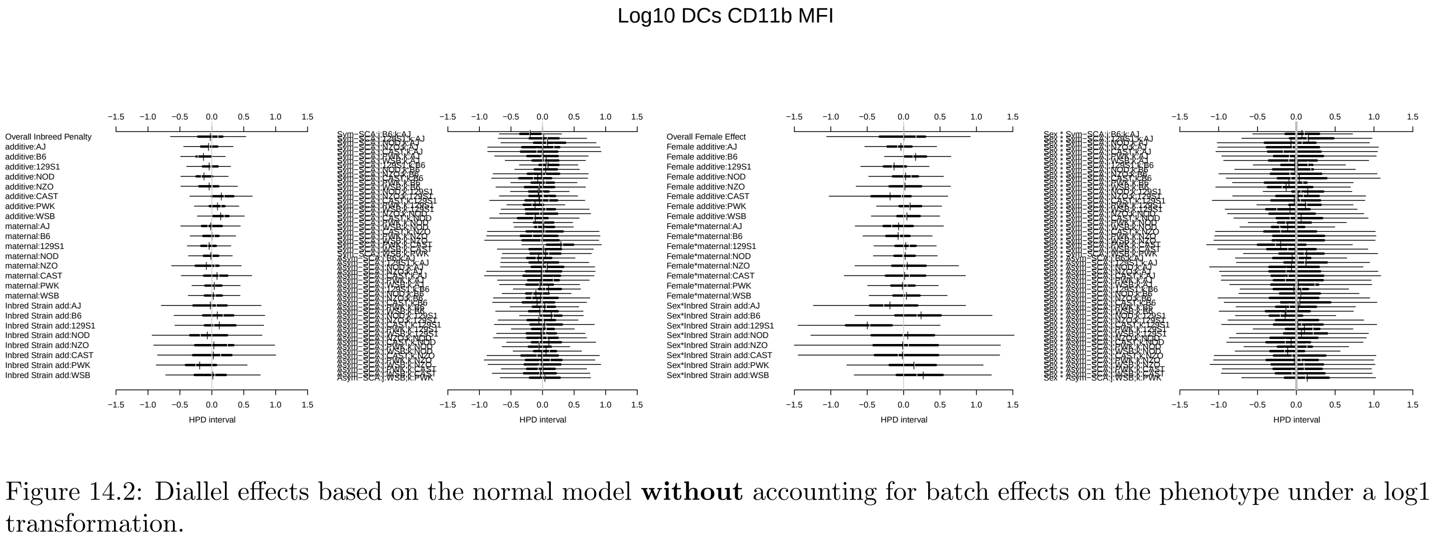

Figure 14.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a log10 transformation.

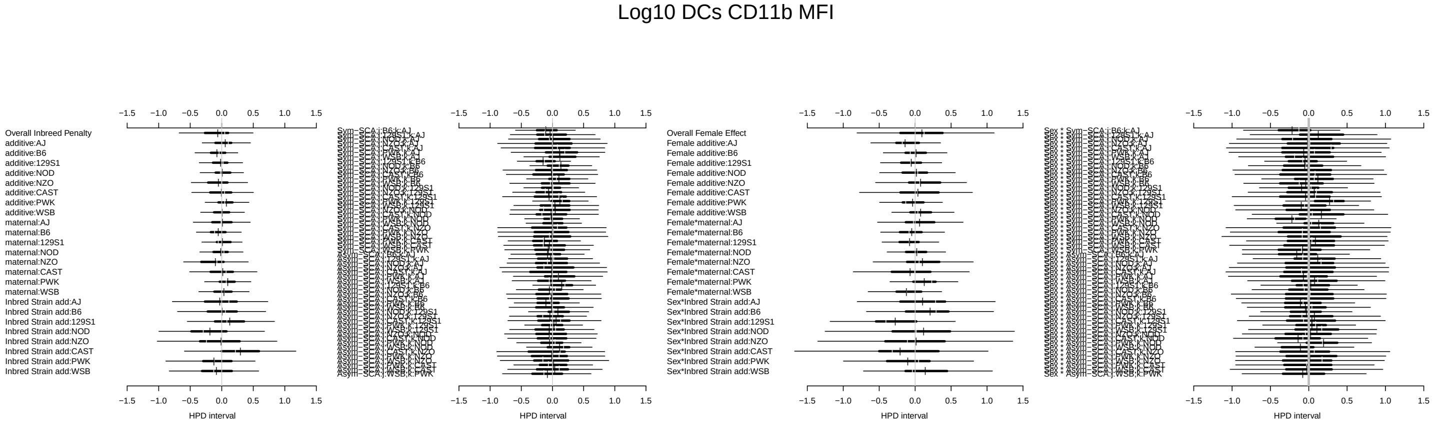

Figure 14.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a log10 transformation.

Chapter 15

DCs.CD11c.MFI: CD11c antigen density on dendritic cells

15.1 Data collected on DCs.CD11c.MFI

Description: CD11c antigen density on dendritic cells

Transformation: log10. Rationale for transformation: Dimensionless quantity, but Box-Cox suggests a logarithmic transformation. Log to base 10 (log10) is used to provide a more interpretable scale.

Table 15.1: Number of mice phenotyped for DCs.CD11c.MFI

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	54	177
Unsexed	0	61	0	0	0	0	0	0	0	0	61
Total	6	71	6	6	10	2	9	10	132	54	306

15.2 Raw and Transformed Data

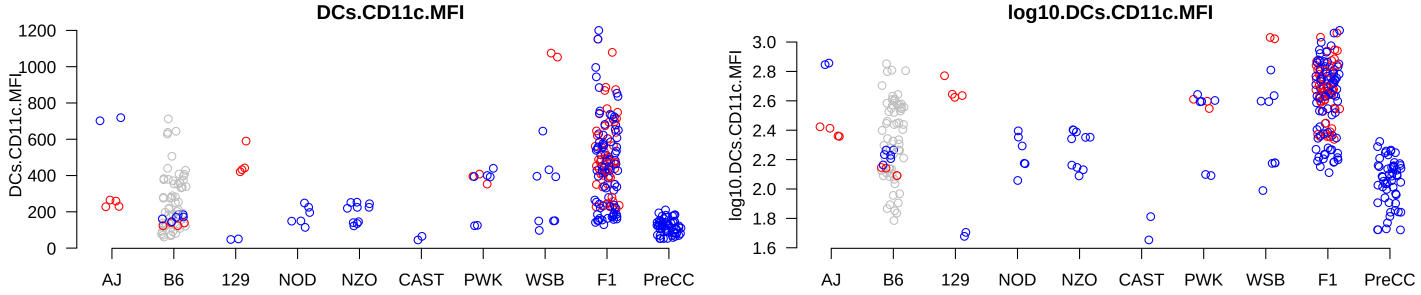

Figure 15.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 15.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	400	248	331	181	196	54.9	337	454	484	119
SE of Mean	98.3	17.7	92.5	21	16.9	9.92	40.8	115	20.5	5.48
Min	228	61	47.6	114	123	45	123	97.6	129	52.7
Max	719	712	590	249	253	64.9	440	1080	1200	211
Modeled 95%CI Lower	2.41	2.28	2.54	2.05	2.26	2.12	2.39	2.39	2.47	2.25
Modeled Mean	2.54	2.35	2.68	2.22	2.38	2.34	2.55	2.51	2.54	2.35
Modeled 95%CI Upper	2.68	2.42	2.81	2.4	2.5	2.56	2.7	2.62	2.61	2.45

Table 15.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	11	0.00204
Inbred Strain	7	38	22.4	1.13e-11

15.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

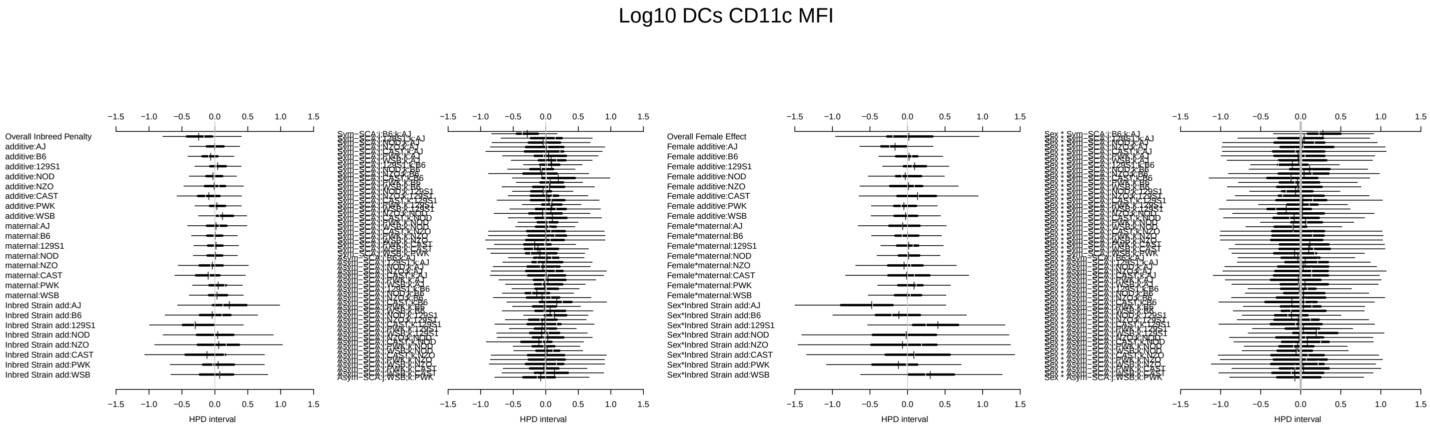

Figure 15.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a log10 transformation.

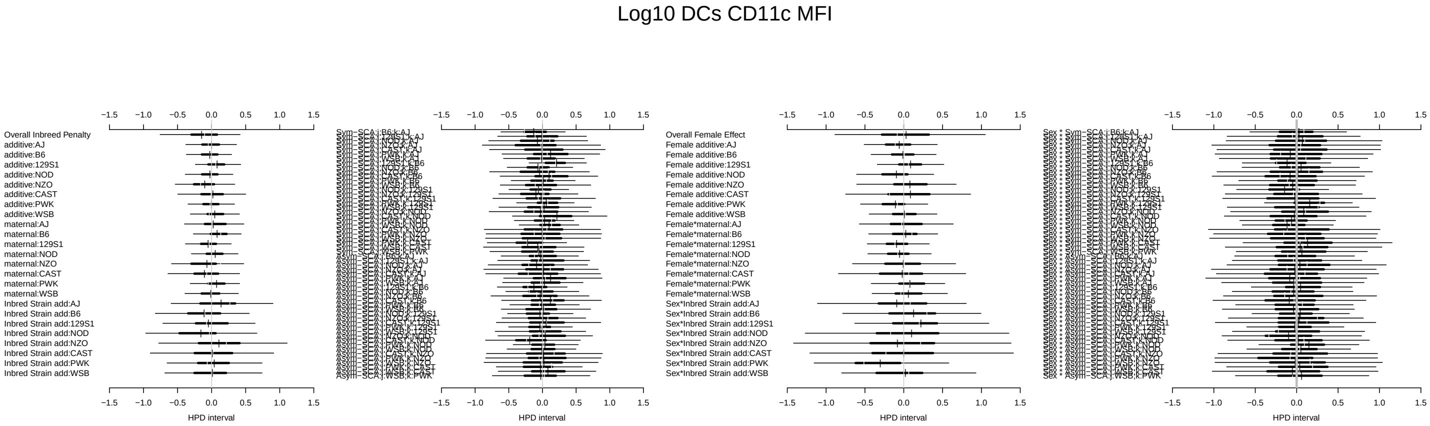

Figure 15.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a log10 transformation.

Chapter 16

DCs.Pct: Classical dendritic cells

16.1 Data collected on DCs.Pct

Description: Classical dendritic cells

Transformation: logit. Rationale for transformation: Natural range is a proportion between 0 and 1, so logit transformation provides an interpretable scale for effects.

Table 16.1: Number of mice phenotyped for DCs.Pct

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	54	177
Unsexed	0	61	0	0	0	0	0	0	0	0	61
Total	6	71	6	6	10	2	9	10	132	54	306

16.2 Raw and Transformed Data

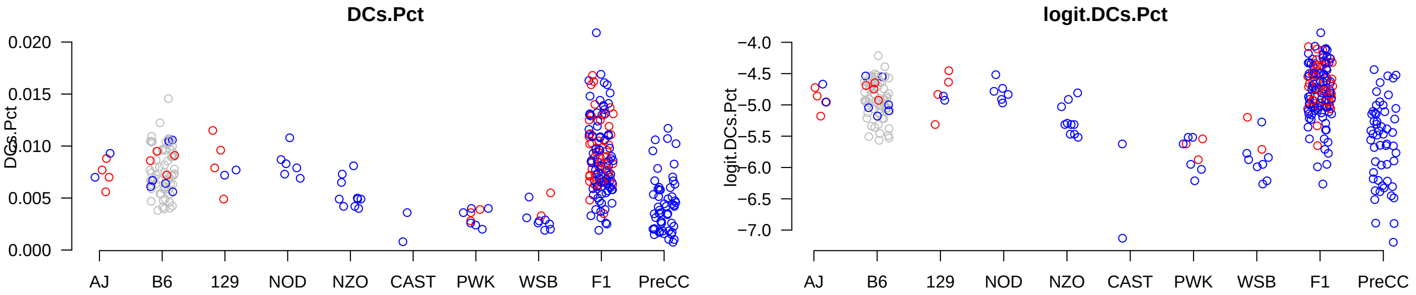

Figure 16.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 16.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	0.00757	0.00773	0.00813	0.00832	0.0054	0.0022	0.00321	0.00317	0.0091	0.00445
SE of Mean	0.000549	0.000265	0.000914	0.000564	0.000445	0.0014	0.000255	0.000382	0.000312	0.000369
Min	0.0056	0.00381	0.0049	0.0069	0.004	8e-04	0.002	0.0019	0.0019	0.00075
Max	0.0093	0.0146	0.0115	0.0108	0.0081	0.0036	0.004	0.0055	0.0209	0.0117
Modeled 95%CI Lower	-5.4	-5	-5.19	-5.18	-5.38	-6.66	-6.08	-5.96	-4.9	-5.7
Modeled Mean	-5.06	-4.89	-4.86	-4.79	-5.1	-6.09	-5.76	-5.69	-4.8	-5.51
Modeled 95%CI Upper	-4.72	-4.78	-4.53	-4.39	-4.82	-5.52	-5.43	-5.43	-4.7	-5.33

Table 16.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	3.14	0.0846
Inbred Strain	7	38	16.1	1.31e-09

16.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

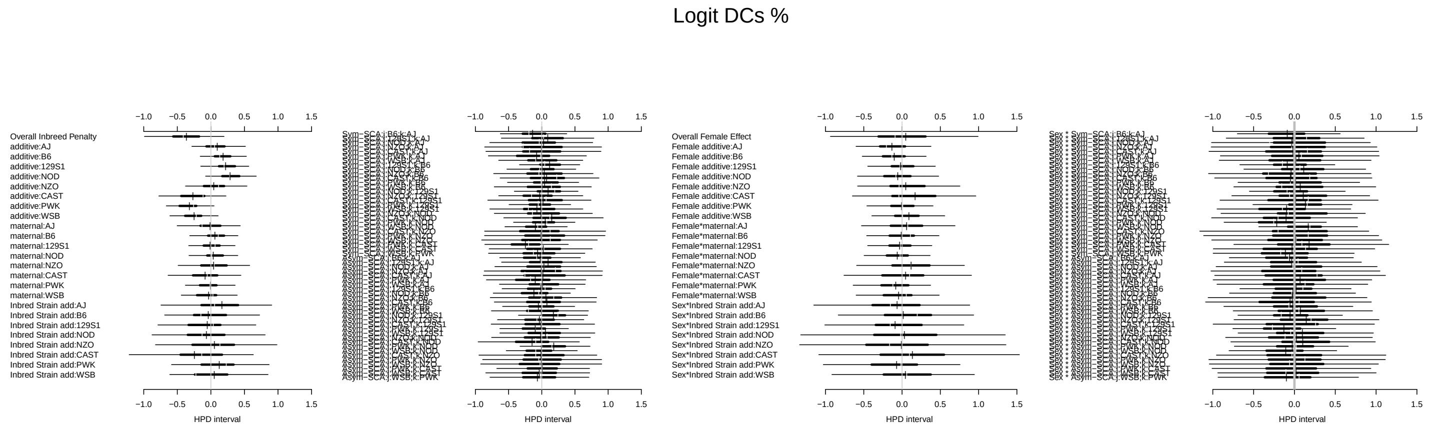

Figure 16.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a logit transformation.

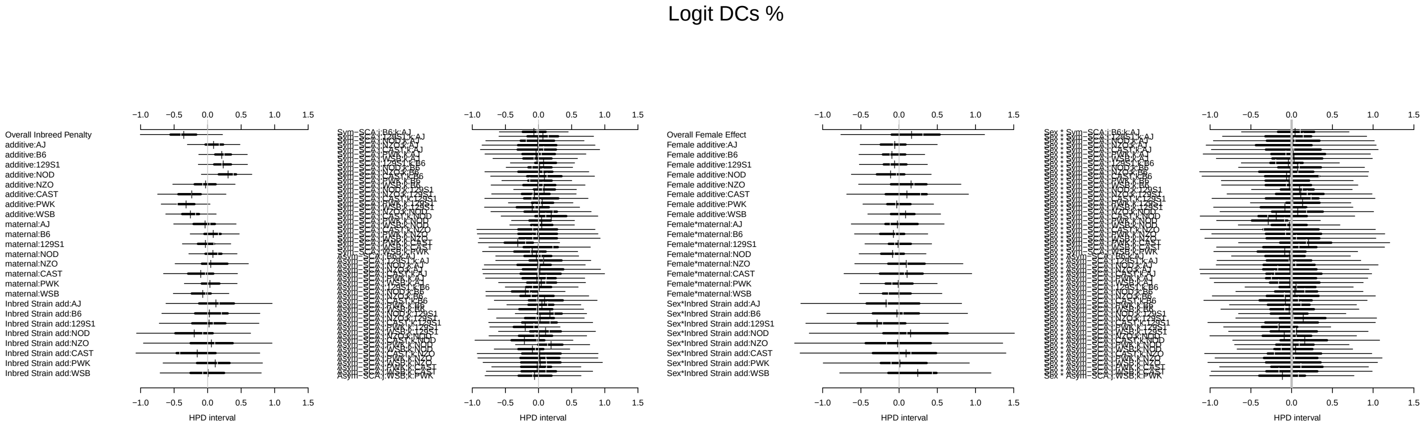

Figure 16.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a logit transformation.

Chapter 17

FoB.Pct.CD19: Follicular B-cells (CD19+)

17.1 Data collected on FoB.Pct.CD19

Description: Follicular B-cells (CD19+)

Transformation: INT. Rationale for transformation: Although natural range is between 0 and 1, outliers and small sample size make a logit transformation unstable for subsequent Gaussian-based analysis. Therefore, the inverse normal transformation using the Bliss correction is used instead.

Table 17.1: Number of mice phenotyped for FoB.Pct.CD19

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	40	163
Unsexed	0	58	0	0	0	0	0	0	0	0	58
Total	6	68	6	6	10	2	9	10	132	40	289

17.2 Raw and Transformed Data

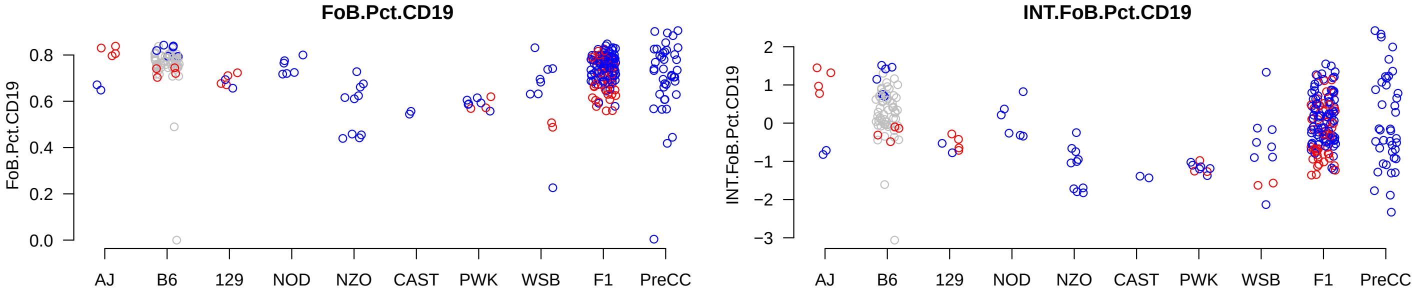

Figure 17.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 17.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 56 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	0.765	0.759	0.689	0.75	0.571	0.551	0.59	0.617	0.736	0.707
SE of Mean	0.034	0.0127	0.0103	0.0141	0.035	0.00605	0.00708	0.0546	0.00562	0.0257
Min	0.648	0	0.656	0.718	0.44	0.544	0.557	0.226	0.559	0.00416
Max	0.838	0.843	0.723	0.8	0.728	0.557	0.62	0.832	0.848	0.906
Modeled 95%CI Lower	-0.22	0.125	-1.36	-0.738	-1.43	-2.19	-1.67	-1.03	-0.21	-0.47
Modeled Mean	0.394	0.325	-0.753	-0.0249	-0.918	-1.16	-1.08	-0.518	-0.0269	-0.1
Modeled 95%CI Upper	1.01	0.526	-0.152	0.688	-0.409	-0.132	-0.497	-0.000574	0.157	0.269

Table 17.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	2.44	0.127
Inbred Strain	7	38	9.63	7.88e-07

17.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

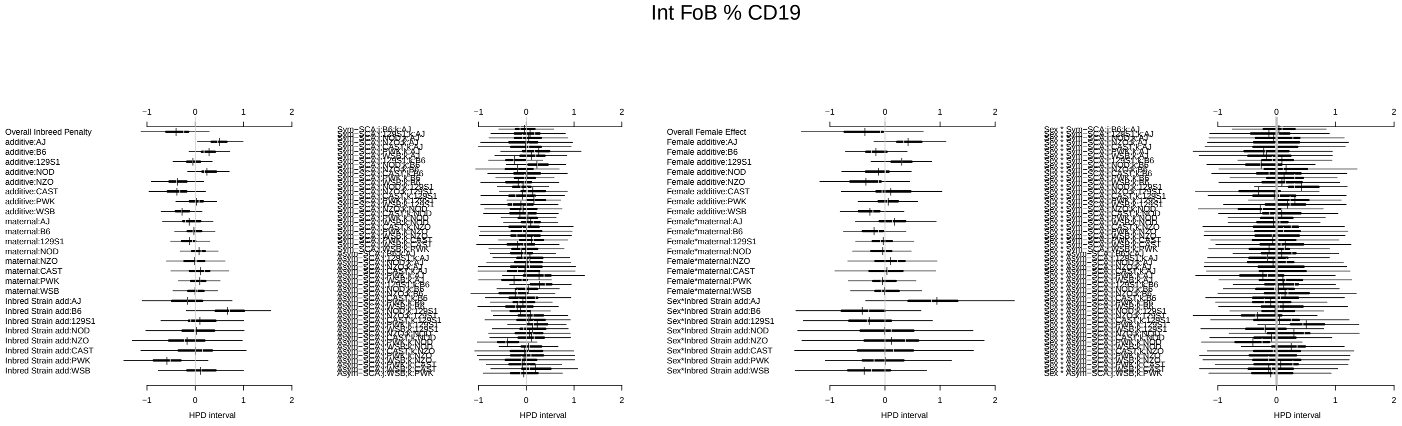

Figure 17.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a INT transformation.

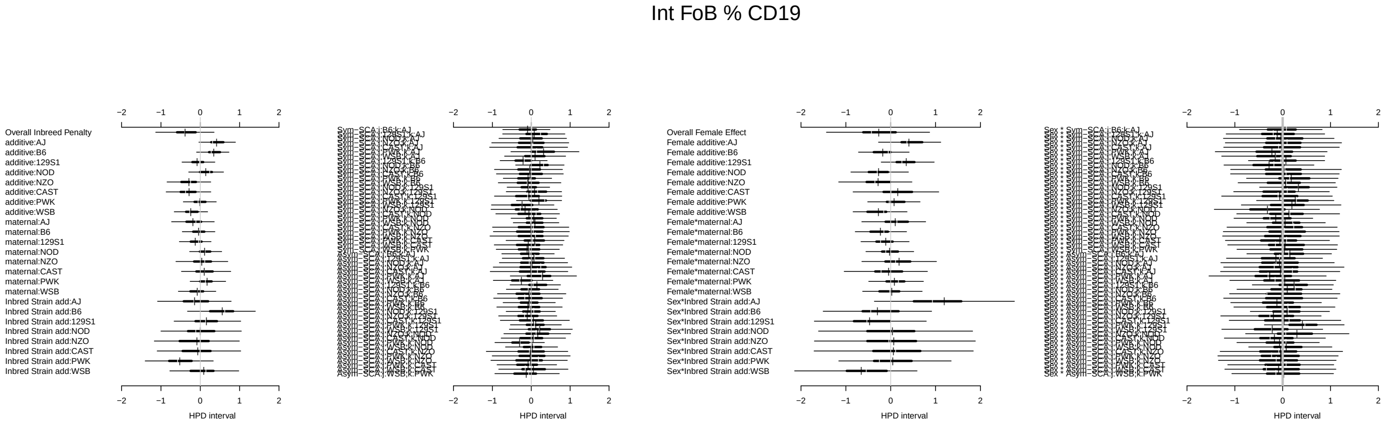

Figure 17.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a INT transformation.

Chapter 18

Granulocytes.Pct: Granulocytes

18.1 Data collected on Granulocytes.Pct

Description: Granulocytes

Transformation: logit. Rationale for transformation: Natural range is a proportion between 0 and 1, so logit transformation provides an interpretable scale for effects.

Table 18.1: Number of mice phenotyped for Granulocytes.Pct

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	54	177
Unsexed	0	61	0	0	0	0	0	0	0	0	61
Total	6	71	6	6	10	2	9	10	132	54	306

18.2 Raw and Transformed Data

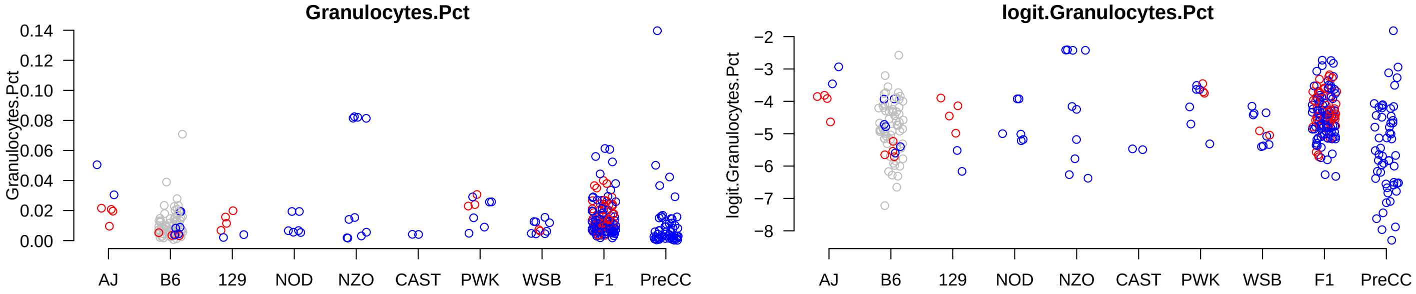

Figure 18.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 18.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	0.0254	0.0109	0.01	0.0105	0.0369	0.00415	0.0208	0.00864	0.0154	0.0106
SE of Mean	0.0057	0.00121	0.00284	0.00282	0.0123	5e-05	0.00301	0.00129	0.00101	0.00282
Min	0.0096	0.00073	0.0021	0.0054	0.0017	0.0041	0.0049	0.0045	0.0018	0.000251
Max	0.0505	0.0708	0.0199	0.0194	0.0825	0.0042	0.0307	0.0155	0.0613	0.14
Modeled 95%CI Lower	-4.36	-5.04	-5.28	-5.55	-4.99	-6.3	-4.82	-5.31	-4.57	-5.71
Modeled Mean	-3.64	-4.81	-4.58	-4.73	-4.4	-5.1	-4.14	-4.75	-4.36	-5.33
Modeled 95%CI Upper	-2.93	-4.59	-3.88	-3.9	-3.81	-3.9	-3.46	-4.18	-4.15	-4.95

Table 18.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	19.8	7.23e-05
Inbred Strain	7	38	2.41	0.0381

18.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

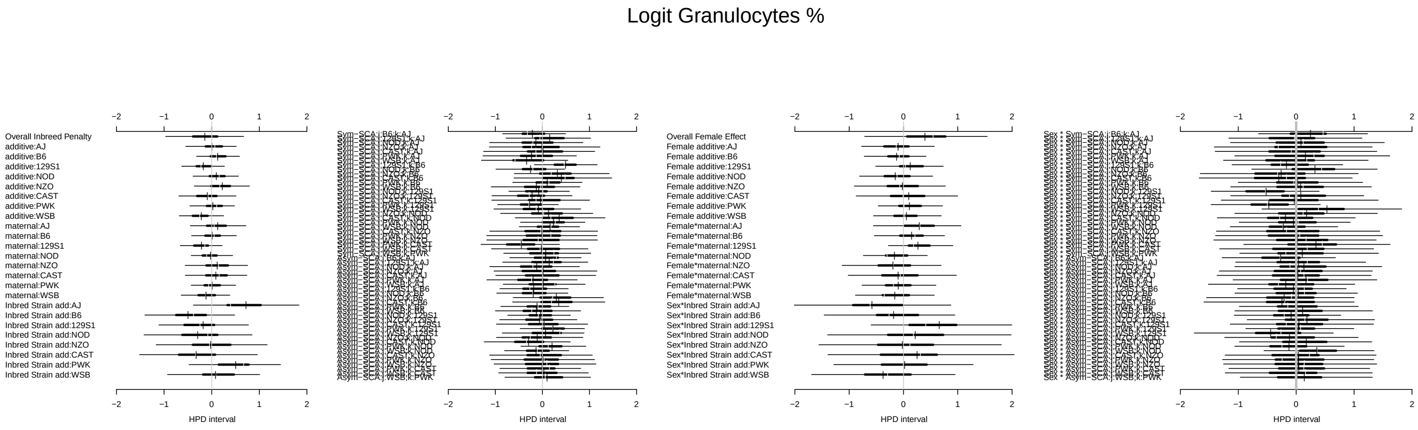

Figure 18.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a logit transformation.

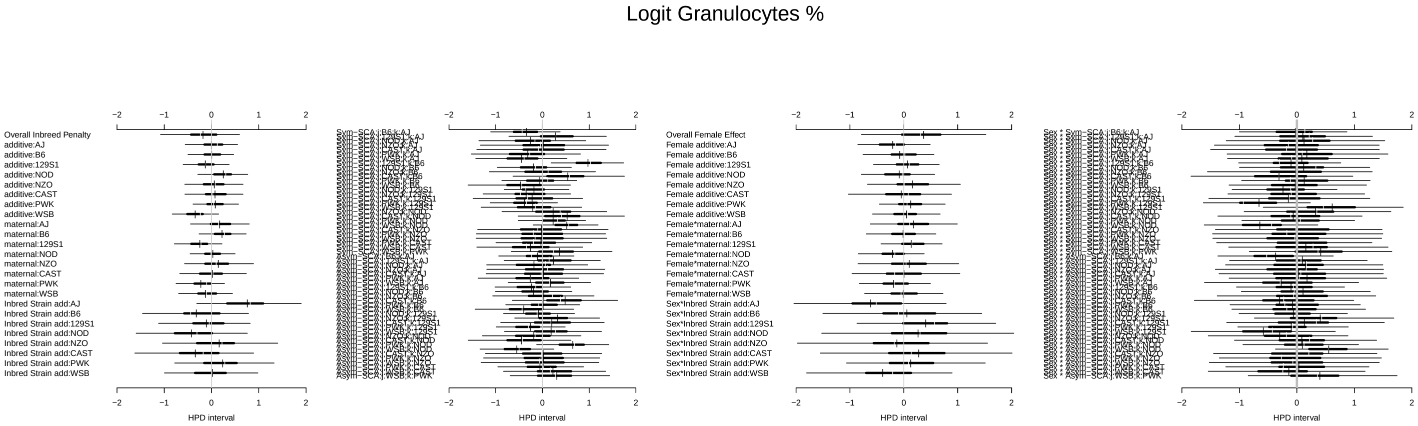

Figure 18.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a logit transformation.

Chapter 19

H57.Pct: Total T-cells (H57+)

19.1 Data collected on H57.Pct

Description: Total T-cells (H57+)

Transformation: logit. Rationale for transformation: Natural range is a proportion between 0 and 1, so logit transformation provides an interpretable scale for effects.

Table 19.1: Number of mice phenotyped for H57.Pct

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	66	189
Unsexed	0	62	0	0	0	0	0	0	0	0	62
Total	6	72	6	6	10	2	9	10	132	66	319

19.2 Raw and Transformed Data

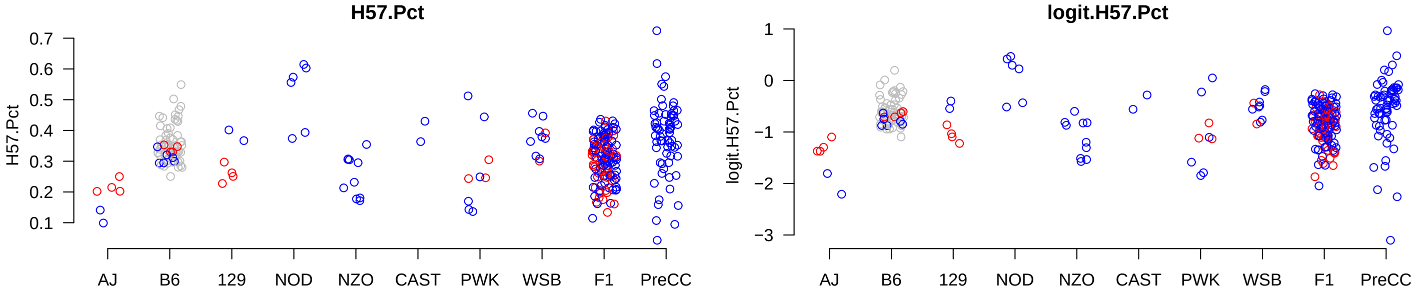

Figure 19.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 19.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	0.185	0.353	0.301	0.519	0.254	0.397	0.272	0.373	0.306	0.376
SE of Mean	0.0224	0.00683	0.0282	0.0437	0.0211	0.0331	0.0434	0.017	0.00629	0.0149
Min	0.099	0.25	0.228	0.374	0.172	0.364	0.136	0.3	0.114	0.043
Max	0.25	0.549	0.402	0.615	0.354	0.43	0.512	0.456	0.436	0.724
Modeled 95%CI Lower	-1.92	-0.709	-1.42	-0.333	-1.23	-1.39	-1.35	-0.818	-0.961	-0.775
Modeled Mean	-1.58	-0.605	-1.09	0.0498	-0.954	-0.813	-1.03	-0.551	-0.867	-0.615
Modeled 95%CI Upper	-1.24	-0.501	-0.751	0.433	-0.673	-0.238	-0.72	-0.283	-0.774	-0.456

Table 19.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	40.3	1.91e-07
Inbred Strain	7	38	5.52	0.000195

19.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

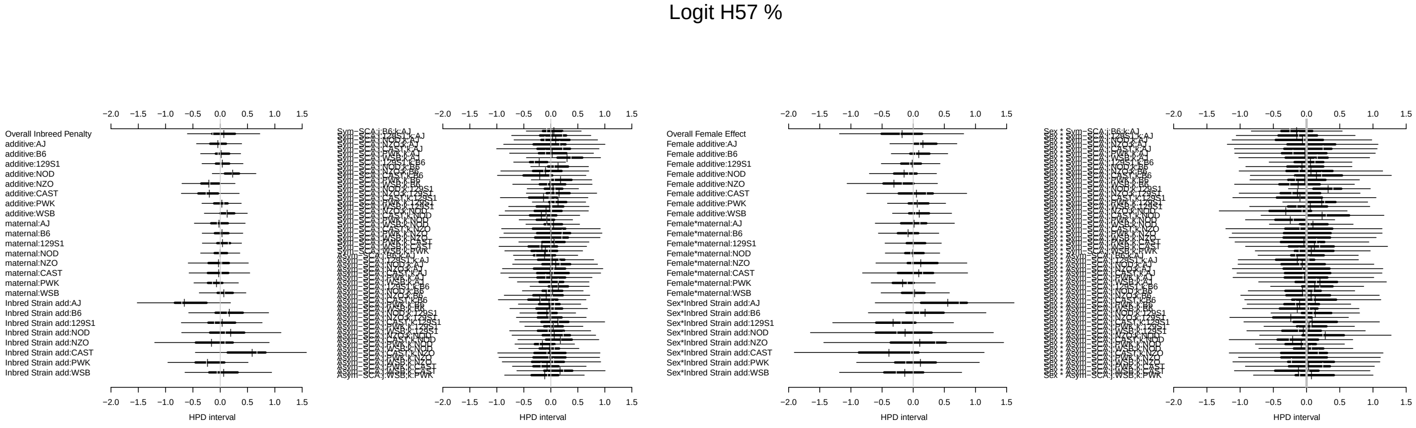

Figure 19.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a logit transformation.

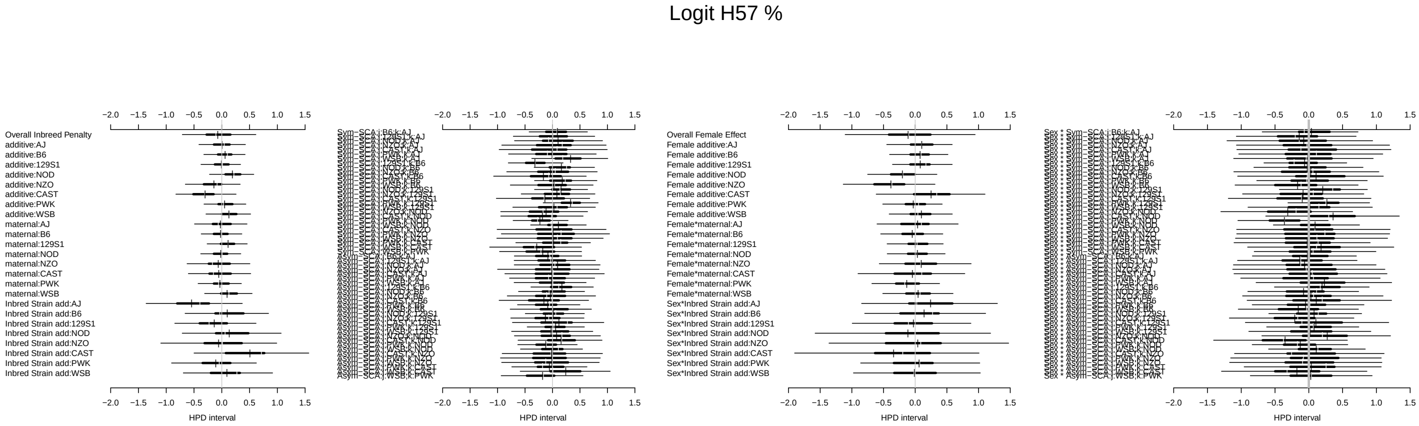

Figure 19.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a logit transformation.

Chapter 20

Macrophages.Pct: Macrophages

20.1 Data collected on Macrophages.Pct

Description: Macrophages

Transformation: logit. Rationale for transformation: Natural range is a proportion between 0 and 1, so logit transformation provides an interpretable scale for effects.

Table 20.1: Number of mice phenotyped for Macrophages.Pct

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	54	177
Unsexed	0	61	0	0	0	0	0	0	0	0	61
Total	6	71	6	6	10	2	9	10	132	54	306

20.2 Raw and Transformed Data

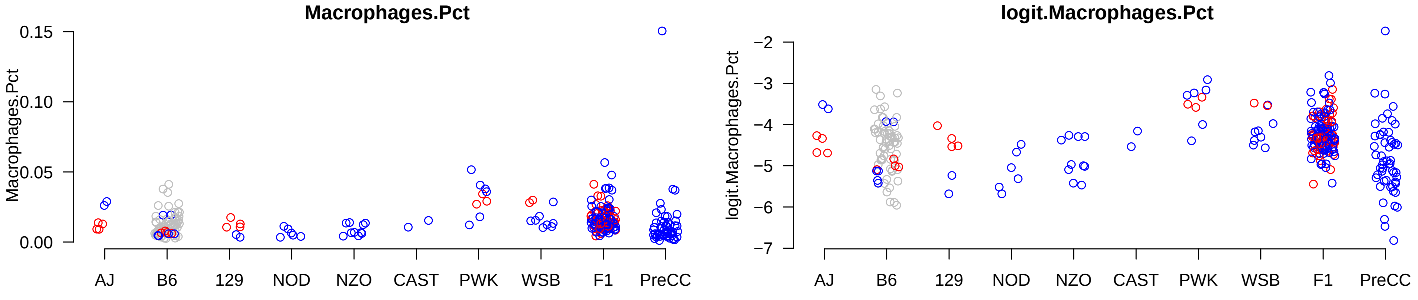

Figure 20.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 20.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	0.0167	0.0125	0.0101	0.00653	0.00882	0.013	0.0318	0.0182	0.0164	0.0125
SE of Mean	0.00353	0.00095	0.00209	0.00127	0.00126	0.0024	0.00397	0.00243	0.000748	0.00282
Min	0.0091	0.00258	0.0034	0.0034	0.0042	0.0106	0.0122	0.0103	0.0043	0.0011
Max	0.0289	0.0412	0.0175	0.0112	0.0139	0.0154	0.0516	0.0299	0.0567	0.151
Modeled 95%CI Lower	-4.72	-4.68	-5.01	-5.69	-5.05	-4.85	-3.86	-4.56	-4.36	-5.08
Modeled Mean	-4.23	-4.53	-4.53	-5.13	-4.65	-4.03	-3.4	-4.18	-4.22	-4.82
Modeled 95%CI Upper	-3.74	-4.37	-4.05	-4.58	-4.25	-3.21	-2.94	-3.8	-4.08	-4.56

Table 20.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	0.313	0.579
Inbred Strain	7	38	6.49	4.63e-05

20.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

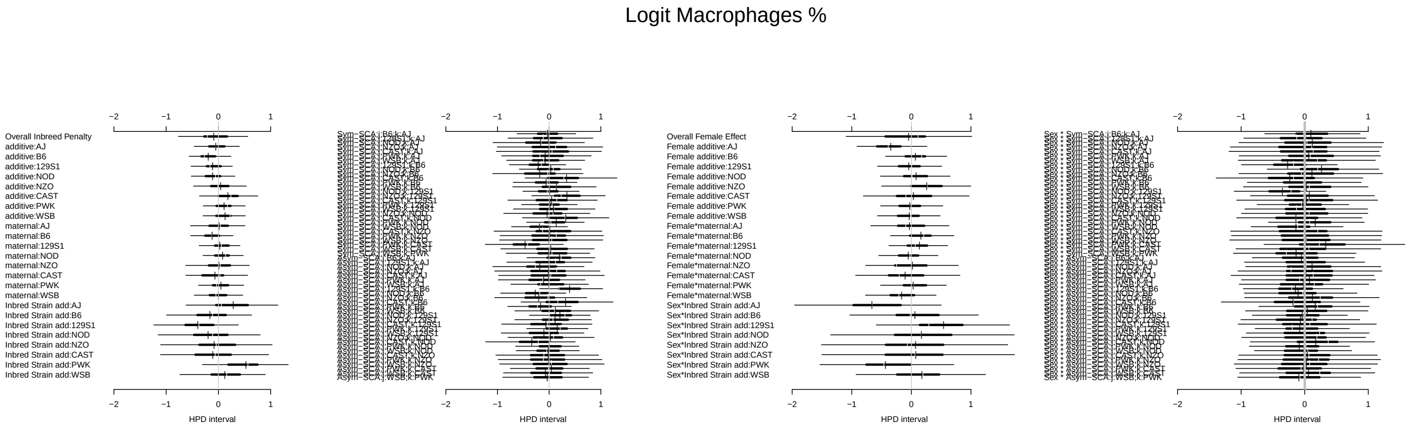

Figure 20.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a logit transformation.

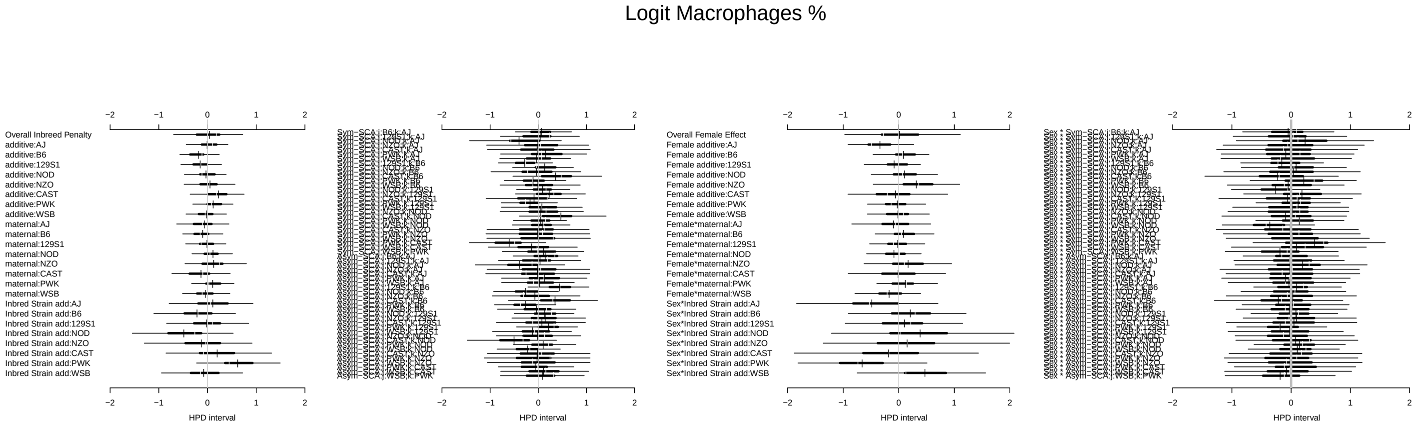

Figure 20.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a logit transformation.

Chapter 21

Monocytes.Pct: Monocytes

21.1 Data collected on Monocytes.Pct

Description: Monocytes

Transformation: logit. Rationale for transformation: Natural range is a proportion between 0 and 1, so logit transformation provides an interpretable scale for effects.

Table 21.1: Number of mice phenotyped for Monocytes.Pct

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	54	177
Unsexed	0	61	0	0	0	0	0	0	0	0	61
Total	6	71	6	6	10	2	9	10	132	54	306

21.2 Raw and Transformed Data

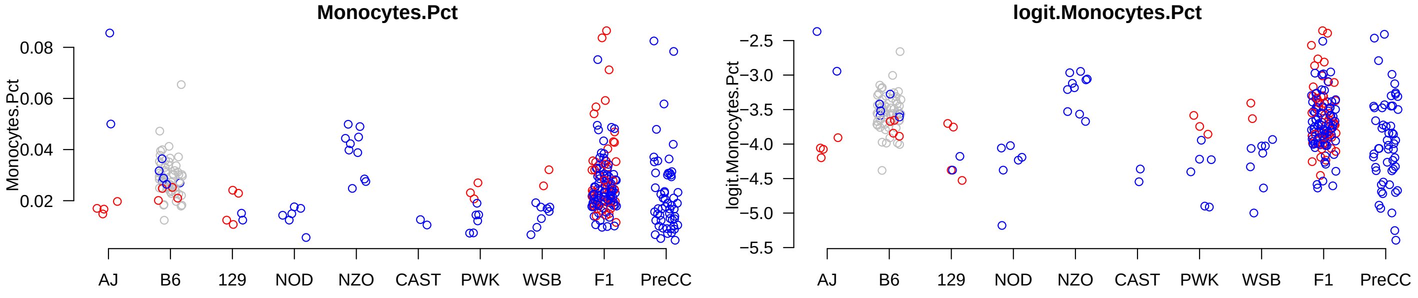

Figure 21.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 21.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	0.034	0.0288	0.0163	0.0136	0.039	0.0116	0.0162	0.0174	0.0275	0.0226
SE of Mean	0.0117	0.000895	0.00236	0.00178	0.00286	0.00105	0.00227	0.00233	0.00117	0.00219
Min	0.0148	0.0124	0.0107	0.0056	0.0248	0.0105	0.0073	0.0067	0.0096	0.00452
Max	0.0856	0.0654	0.0241	0.0176	0.0499	0.0126	0.027	0.0321	0.0865	0.0825
Modeled 95%CI Lower	-3.95	-3.65	-4.31	-4.71	-3.58	-4.89	-4.59	-4.5	-3.74	-4.13
Modeled Mean	-3.59	-3.54	-3.96	-4.3	-3.28	-4.27	-4.26	-4.21	-3.64	-3.94
Modeled 95%CI Upper	-3.22	-3.43	-3.6	-3.89	-2.98	-3.66	-3.92	-3.92	-3.54	-3.76

Table 21.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	7.42	0.00971
Inbred Strain	7	38	11	1.6e-07

21.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

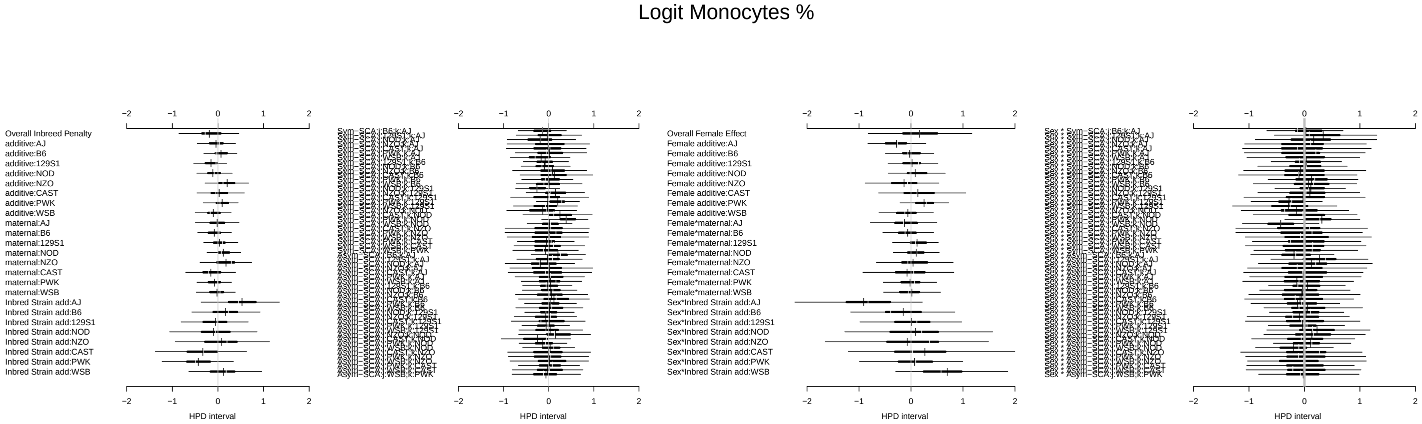

Figure 21.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a logit transformation.

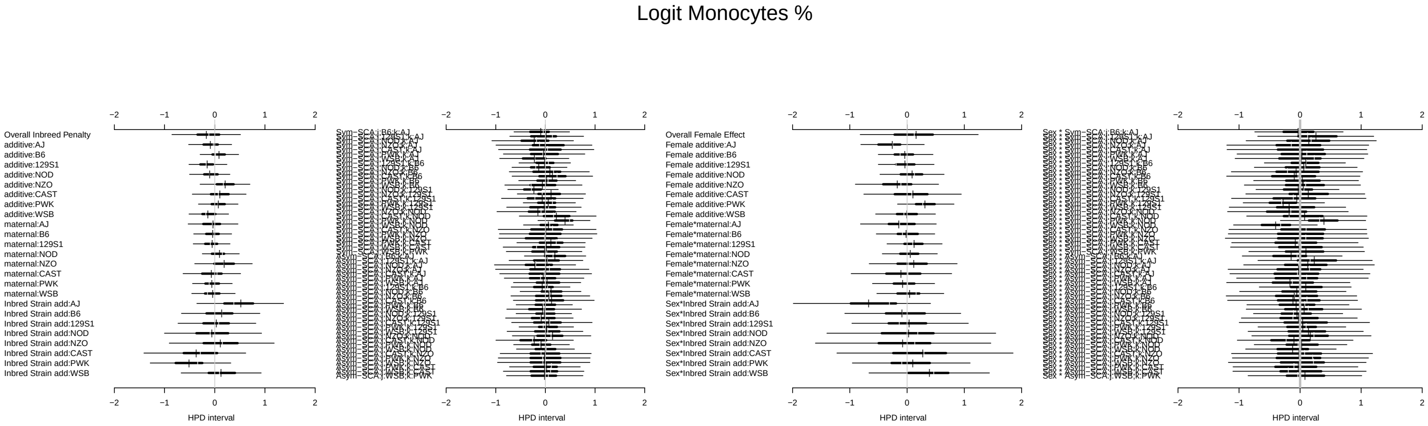

Figure 21.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a logit transformation.

Chapter 22

Phagocytes.Pct: Phagocytes (CD11b Hi)

22.1 Data collected on Phagocytes.Pct

Description: Phagocytes (CD11b Hi)

Transformation: logit. Rationale for transformation: Natural range is a proportion between 0 and 1, so logit transformation provides an interpretable scale for effects.

Table 22.1: Number of mice phenotyped for Phagocytes.Pct

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	54	177
Unsexed	0	61	0	0	0	0	0	0	0	0	61
Total	6	71	6	6	10	2	9	10	132	54	306

22.2 Raw and Transformed Data

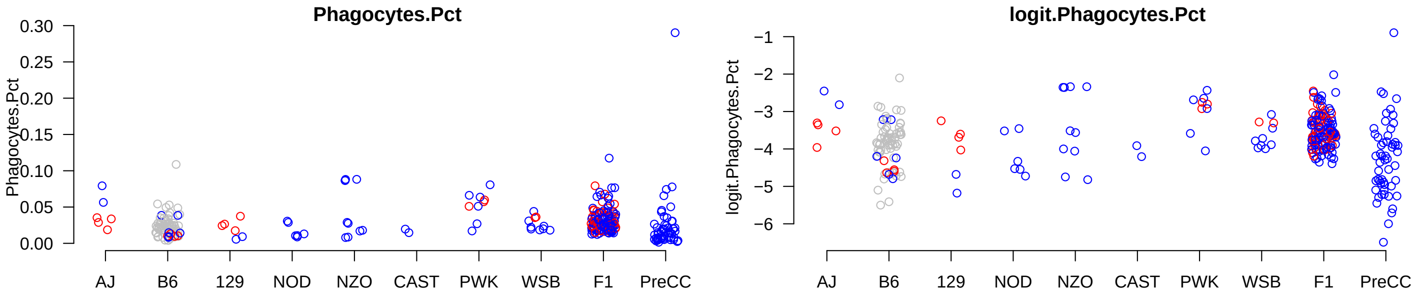

Figure 22.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 22.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 57 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	0.042	0.0235	0.0201	0.0171	0.0458	0.0172	0.0527	0.0269	0.0318	0.0239
SE of Mean	0.009	0.00184	0.00481	0.00404	0.0115	0.00245	0.00655	0.00288	0.00142	0.00556
Min	0.0187	0.00407	0.0056	0.0088	0.008	0.0147	0.0171	0.0181	0.0122	0.00151
Max	0.0793	0.109	0.0374	0.0306	0.0882	0.0196	0.0807	0.044	0.117	0.29
Modeled 95%CI Lower	-3.69	-4.04	-4.32	-4.73	-3.92	-4.59	-3.51	-4.05	-3.66	-4.47
Modeled Mean	-3.17	-3.88	-3.81	-4.14	-3.49	-3.73	-3.03	-3.64	-3.51	-4.2
Modeled 95%CI Upper	-2.66	-3.72	-3.31	-3.55	-3.07	-2.86	-2.55	-3.23	-3.36	-3.93

Table 22.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	4.66	0.0373
Inbred Strain	7	38	3.89	0.00275

22.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

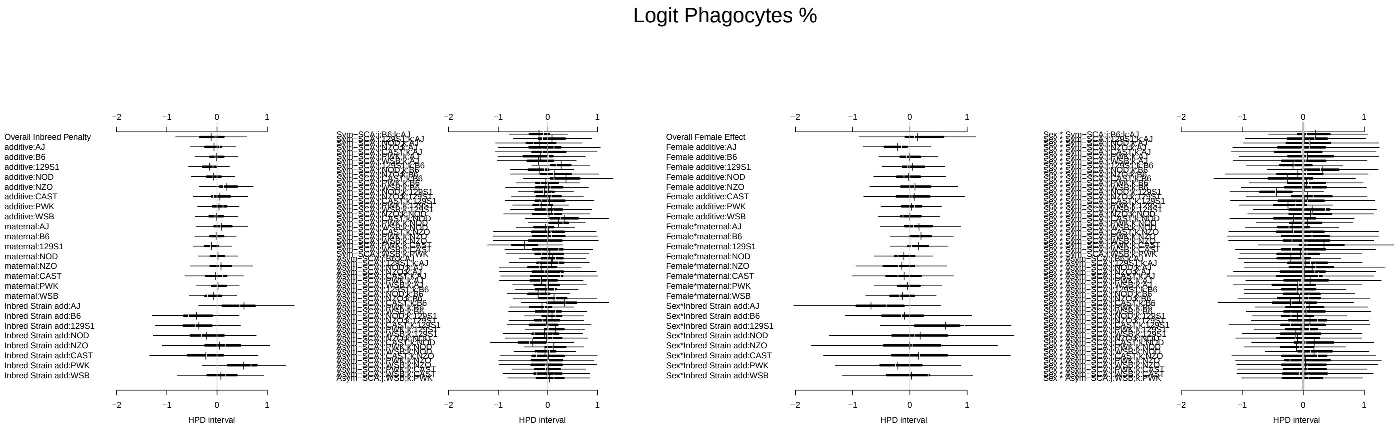

Figure 22.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a logit transformation.

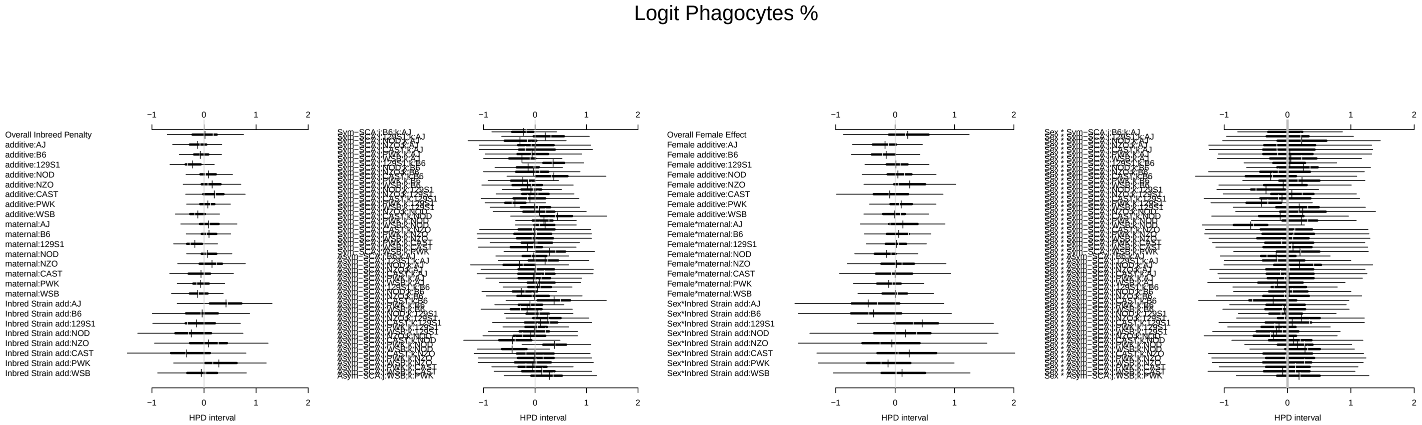

Figure 22.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a logit transformation.

Chapter 23

MZB.Pct.CD19: Marginal Zone B-cells

23.1 Data collected on MZB.Pct.CD19

Description: Marginal Zone B-cells

Transformation: INT. Rationale for transformation: Although natural range is between 0 and 1, outliers and small sample size make a logit transformation unstable for subsequent Gaussian-based analysis. Therefore, the inverse normal transformation using the Bliss correction is used instead.

Table 23.1: Number of mice phenotyped for MZB.Pct.CD19

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	40	163
Unsexed	0	58	0	0	0	0	0	0	0	0	58
Total	6	68	6	6	10	2	9	10	132	40	289

23.2 Raw and Transformed Data

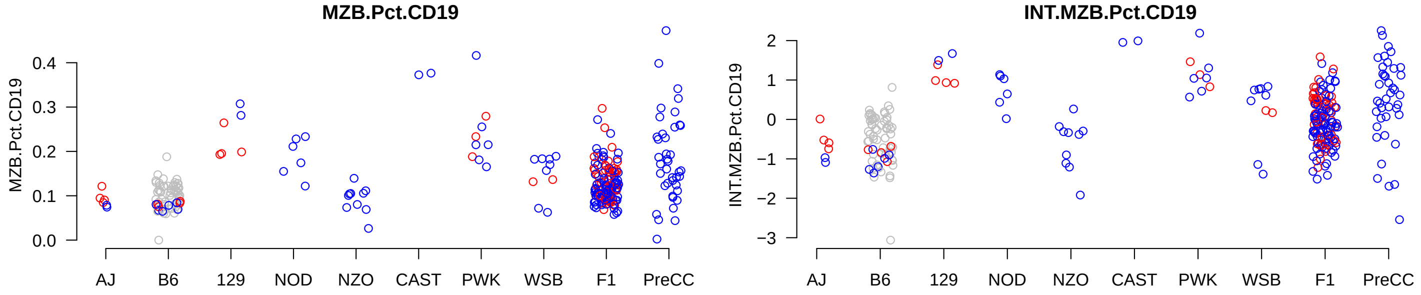

Figure 23.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 23.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 56 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	0.0908	0.0978	0.24	0.187	0.0916	0.375	0.239	0.147	0.126	0.185
SE of Mean	0.00686	0.0034	0.0206	0.0181	0.00972	0.0019	0.0253	0.0147	0.00372	0.0156
Min	0.0744	0	0.193	0.122	0.0264	0.373	0.165	0.0627	0.0578	0.00234
Max	0.122	0.188	0.307	0.233	0.139	0.376	0.416	0.189	0.297	0.472
Modeled 95%CI Lower	-1.18	-0.686	0.535	0.16	-1.05	0.557	0.564	-0.29	-0.191	0.17
Modeled Mean	-0.604	-0.512	1.1	0.78	-0.584	1.53	1.07	0.173	-0.045	0.46
Modeled 95%CI Upper	-0.0305	-0.338	1.67	1.4	-0.119	2.5	1.57	0.636	0.101	0.751

Table 23.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	0.598	0.444
Inbred Strain	7	38	18.1	2.56e-10

23.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

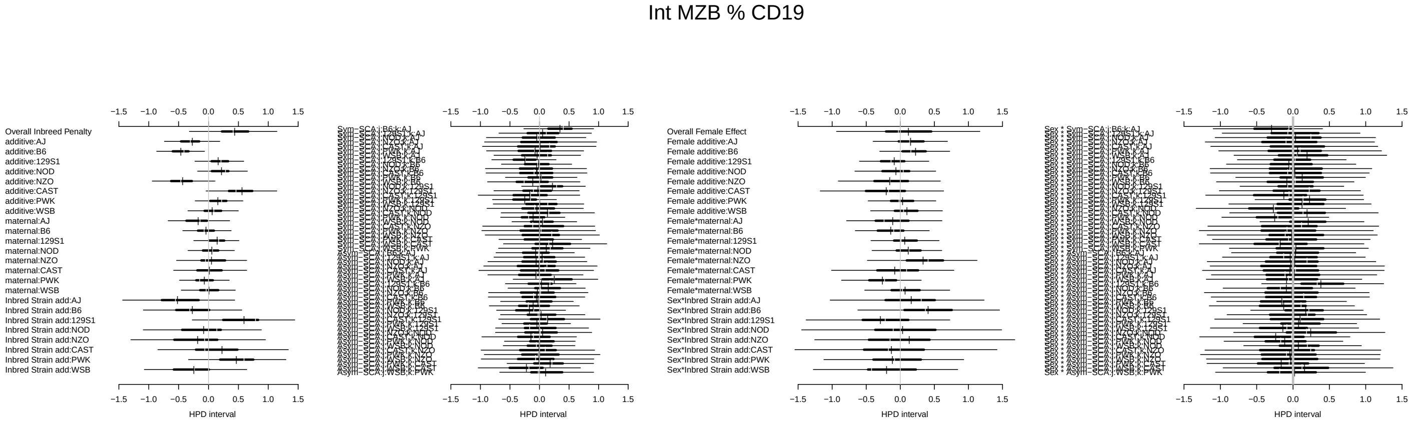

Figure 23.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a INT transformation.

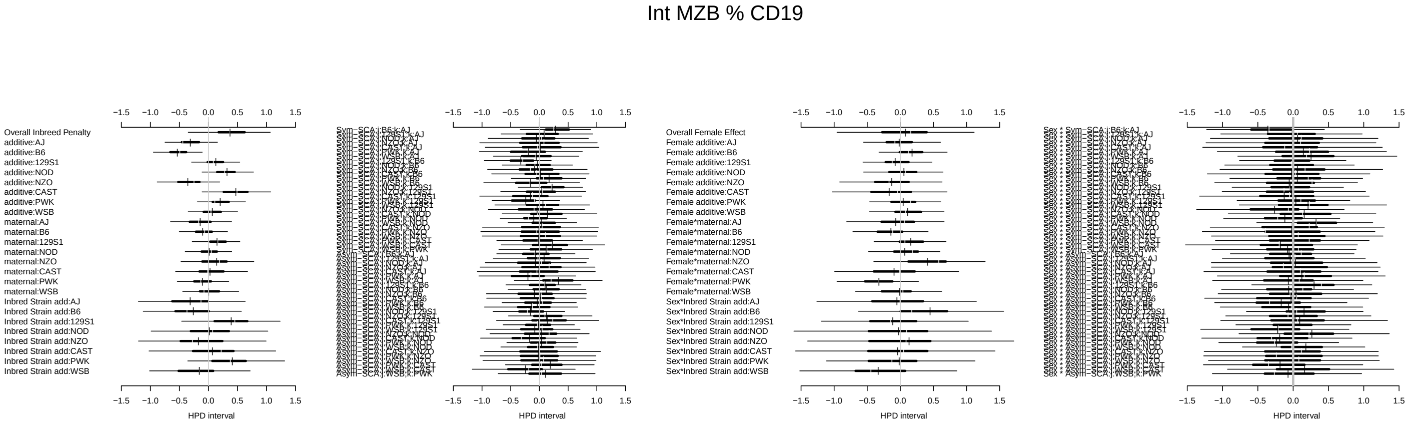

Figure 23.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a INT transformation.

Chapter 24

TransB.Pct.CD19: Transitional B-cells

24.1 Data collected on TransB.Pct.CD19

Description: Transitional B-cells

Transformation: INT. Rationale for transformation: Although natural range is between 0 and 1, outliers and small sample size make a logit transformation unstable for subsequent Gaussian-based analysis. Therefore, the inverse normal transformation using the Bliss correction is used instead.

Table 24.1: Number of mice phenotyped for TransB.Pct.CD19

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC	Total
Female	4	4	4	0	0	0	3	2	51	0	68
Male	2	6	2	6	10	2	6	8	81	40	163
Unsexed	0	58	0	0	0	0	0	0	0	0	58
Total	6	68	6	6	10	2	9	10	132	40	289

24.2 Raw and Transformed Data

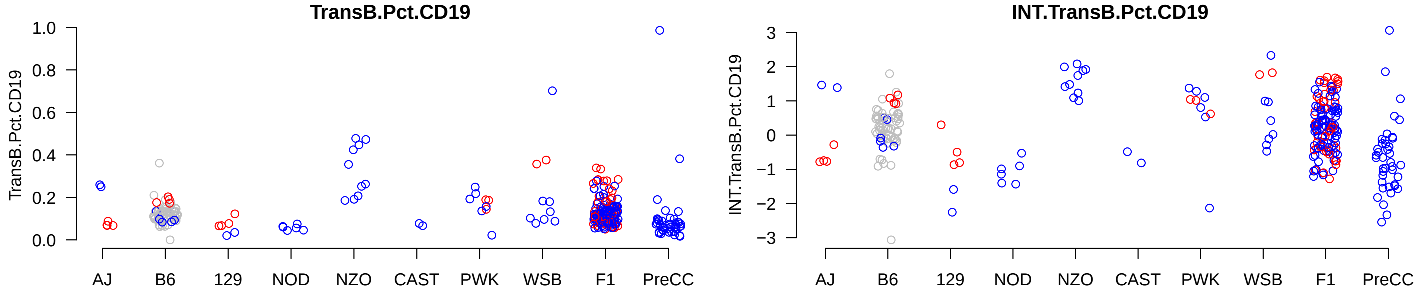

Figure 24.1: Phenotype values: raw and transformed for analysis for founder, F1 hybrid and PreCC mice. Colors distinguish females (red), males (blue), and unsexed (gray) mice.

Table 24.2: Point estimates. Upper table portion: mean and range statistics for raw phenotype values. Lower table portion: strain means and 95% CI on the transformed scale, as estimated from a linear model that includes a random intercept modeling the effects of 56 batches.

	AJ	B6	129S1	NOD	NZO	CAST	PWK	WSB	F1	PreCC
Mean	0.134	0.123	0.0646	0.0574	0.328	0.0721	0.166	0.229	0.133	0.1
SE of Mean	0.0384	0.00556	0.0145	0.00468	0.0382	0.0053	0.0215	0.0625	0.00546	0.0246
Min	0.0676	0	0.0204	0.0443	0.186	0.0668	0.0219	0.0778	0.0503	0.0169
Max	0.259	0.361	0.122	0.0749	0.478	0.0774	0.249	0.702	0.339	0.986
Modeled 95%CI Lower	-0.577	0.00469	-1.07	-2.04	0.781	-0.953	-0.0623	0.0552	0.0236	-0.781
Modeled Mean	0.0156	0.212	-0.492	-1.32	1.28	0.0365	0.531	0.566	0.221	-0.39
Modeled 95%CI Upper	0.608	0.419	0.0862	-0.604	1.78	1.03	1.12	1.08	0.419	0.00156

Table 24.3: Sequential ANOVA table of strain and sex effects, controlling for batch, in the sexed subset of tested inbred strains.

	numerator df	denominator df	F-value	p-value
Sex	1	38	0.602	0.443
Inbred Strain	7	38	6.52	4.45e-05

24.3 Diallel analysis

Diallel analysis including batch effects and Bayesian imputation of missing sex assignments was performed as described in Methods. This diallel arose as a byproduct of another experiment, and suboptimal pairing of batches with F1 hybrid groups in the experimental design means that incorporating batch effects greatly increases uncertainty about estimated genetic parameters.

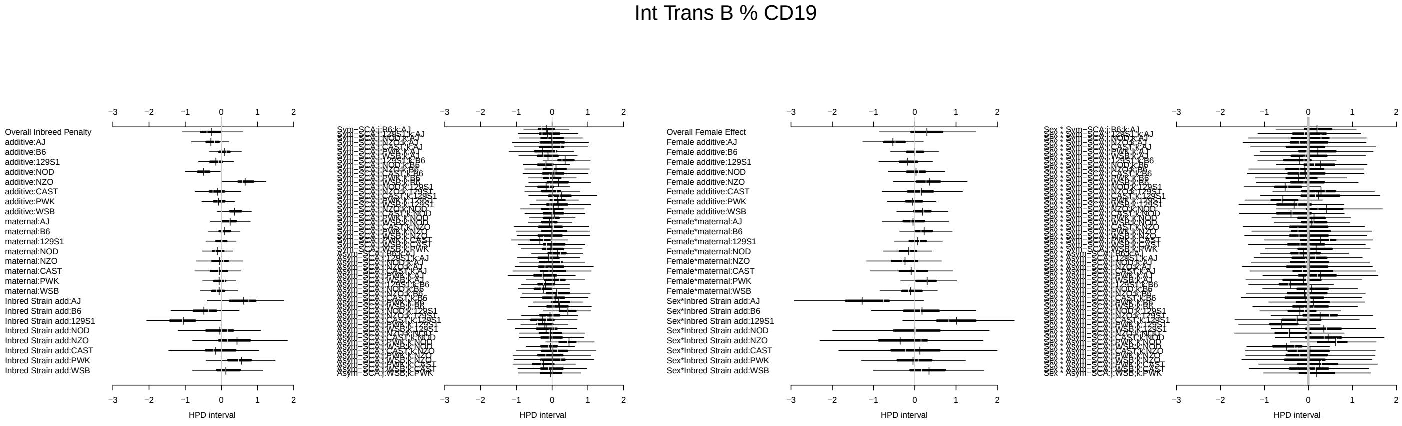

Figure 24.2: Diallel effects based on the normal model **without** accounting for batch effects on the phenotype under a INT transformation.

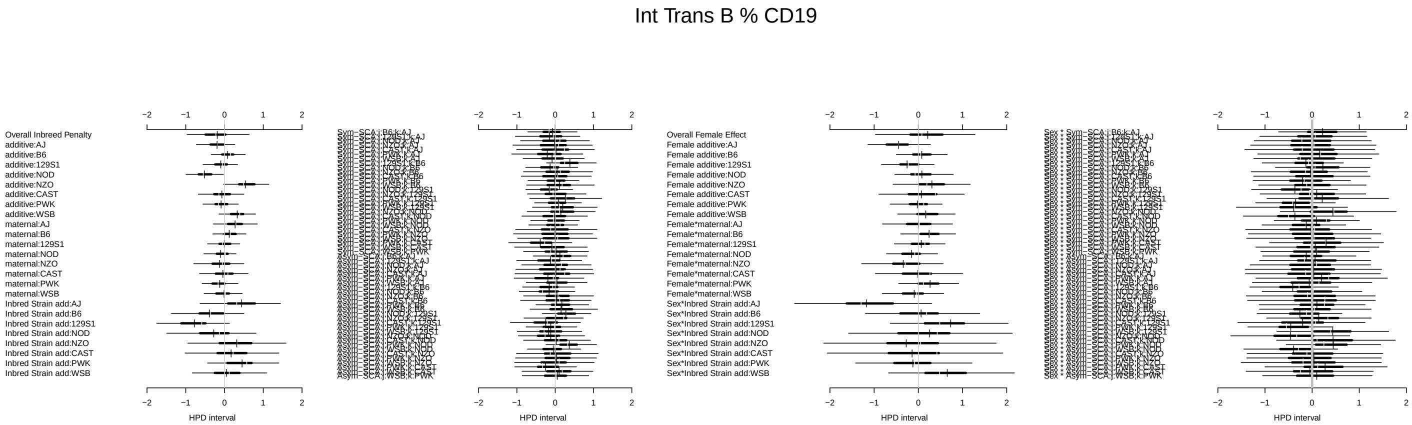

Figure 24.3: Diallel effects based on the normal model **accounting for batch** effects on the phenotype under a INT transformation.