

**Table S4 RBC and WBC Parameters in Collaborative Cross Founder Strain and pre-CC Mice**

Strain	RBC (#/uL)	Hb (g/dL)	MCV (fL)	RDW (%)	PLT <sup>1</sup> (#/uL)	MPV (fL)	WBC <sup>1</sup> (#/uL)	LY <sup>1</sup> (#/uL)	NE <sup>1</sup> (#/uL)	MO <sup>1</sup> (#/uL)
<b>A/J</b>	9.70 (0.13)	13.83 (0.21)	48.62 (0.22)	19.47 (0.14)	1016.17 (10.64)	5.25 (0.06)	6.34 (0.48)	4.61 (0.43)	1.27 (0.07)	0.35 (0.03)
<b>C57BL/6J</b>	10.48 (0.25)	15.50 (0.38)	45.97 (0.16)	18.38 (0.16)	946.50 (87.17)	5.32 (0.08v)	10.74 (0.26)	7.03 (0.16)	2.46 (0.09)	1.03 (0.06v)
<b>129S1/SvImJ</b>	9.25 (0.74)	13.47 (1.17)	62.42 (0.38)	17.00 (0.25)	449.17 (29.98)	4.25 (0.07)	5.16 (0.64)	3.72 (0.45)	1.11 (0.14)	0.28 (0.05)
<b>NOD/ShiLtJ</b>	9.44 (0.27)	15.43 (0.46)	55.90 (0.61)	17.14 (0.14)	896.50 (50.82)	5.18 (0.11)	7.11 (0.59)	3.52 (0.30)	2.86 (0.25)	0.49 (0.04)
<b>NZO/HILtJ</b>	10.54 (0.35)	14.93 (0.54)	44.52 (0.30)	20.41 (0.82)	1443.50 (35.41)	5.88 (0.07)	5.90 (0.27)	3.76 (0.20)	1.65 (0.07)	0.48 (0.06)
<b>CAST/EiJ</b>	12.18 (0.22)	16.52 (0.33)	46.32 (0.18)	20.05 (0.44)	659.33 (50.81)	4.28 (0.09)	9.04 (0.92)	6.47 (0.64)	1.83 (0.25)	0.44 (0.08)
<b>PWK/PhJ</b>	12.93 (0.48)	18.54 (0.82)	60.84 (0.67)	18.56 (0.25)	689.00 (141.28)	5.26 (0.12)	8.03 (0.59)	3.87 (0.33)	2.79 (0.20)	0.98 (0.09)
<b>WSB/EiJ</b>	12.47 (0.52)	17.15 (0.68)	57.84 (0.30)	16.51 (0.48)	736.13 (30.40)	3.98 (0.03)	7.06 (0.61)	3.67 (0.37)	2.28 (0.21)	0.82 (0.08)
<b>Pre-CC</b>	10.12 (0.14)	14.49 (0.18)	54.35 (0.61)	18.15 (0.13)	997.78 (34.80)	4.80 (0.04)	8.00 (0.26)	5.27 (0.19)	2.03 (0.08)	0.56 (0.02)
<b>F-statistic<sup>2</sup></b>	10.89 4.49E	5.11 2.29E	260.51 2.29E	13.37 2.88E	14.92 4.56E	58.24 5.11E-	6.46 2.38E	8.91 6.14E	11.83 1.42E	13.55 1.96E
<b>p-value</b>	-08	-04	-35	-09	-10	21	-05	-07	-08	-09
<b>Broad sense heritability<sup>3</sup></b>										
<b>r<sub>1</sub></b>	0.62	0.41	0.98	0.67	0.70	0.91	0.48	0.57	0.64	0.68
<b>g<sup>2</sup></b>	0.45	0.25	0.96	0.51	0.54	0.83	0.31	0.40	0.47	0.51

Values are reported as mean (standard error).

<sup>1</sup> data were log-transformed for statistical analysis and mapping.

<sup>2</sup> ANOVA conducted using only founder strains.

<sup>3</sup>  $r_1$ , the interclass correlation, and  $g^2$ , coefficient of genetic determination, were calculated using founder strains only, as described in (Xing et al., 2009).