Cross-platform validation of a mouse blood gene signature for quantitative reconstruction of radiation dose

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B cells

Coefficients:

	Value	Std.Error	t-value	p-value
(Intercept)	5.431439	0.2449634	22.172452	0.0000
Dose	-0.661612	0.0670307	-9.870276	0.0000
Sex	-0.454254	0.3451976	-1.315925	0.1928
Sex_Dose	0.110583	0.0917816	1.204850	0.2326

T cells

Coefficients:

	Value	Std.Error	t-value	p-value
(Intercept)	6.038787	0.14741720	40.96393	0.0000
Dose	-0.539373	0.04852854	-11.11455	0.0000
Sex	-0.400618	0.21230775	-1.88697	0.0636
Sex_Dose	0.076703	0.06827473	1.12345	0.2653

Supplementary Fig1A Comparison of B and T cell counts after radiation, effects of dose and sex only and then dose and sex together. In both cases, p-values for Sex and Sex+Dose were not significant, p values >0.05

1B T cells

1C B cells
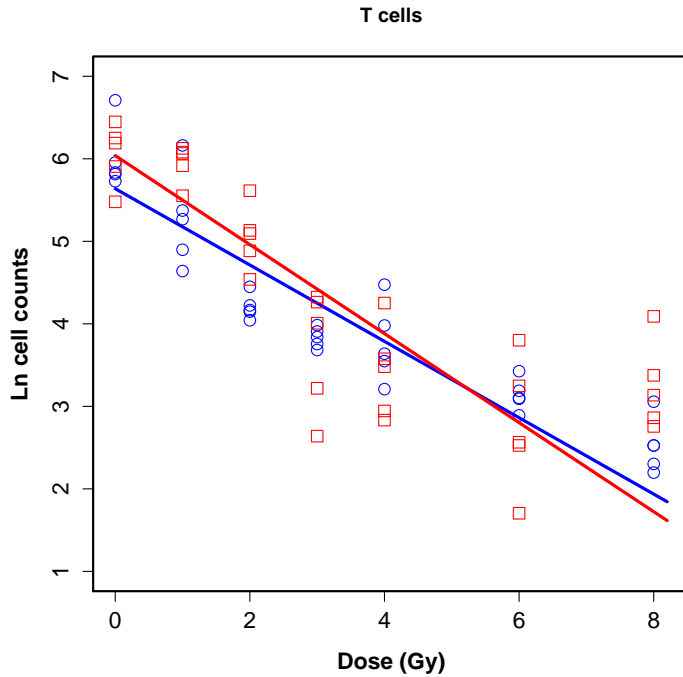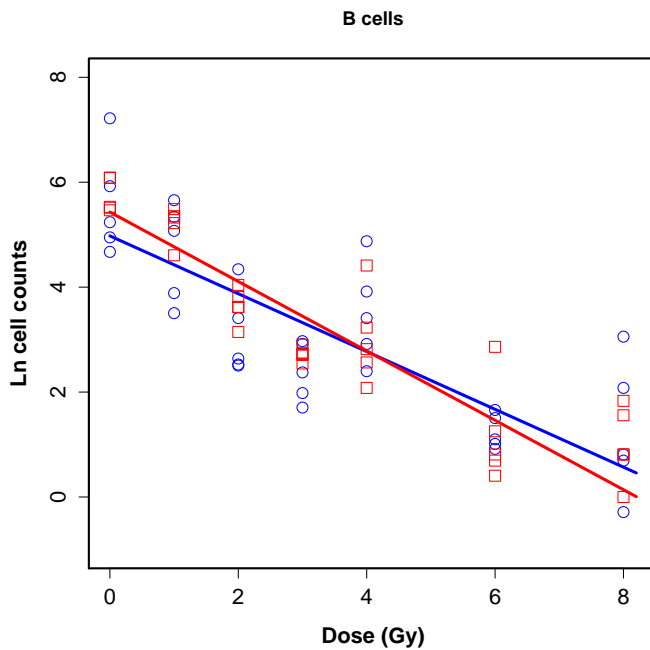
Graph shows individual data for each mouse.
**Blue = males**
Red = females

Supplementary figures 1B and 1C Comparison of B and T cell counts after radiation, effects of dose and sex only and then dose and sex together. In both cases, p-values for Sex and Sex+Dose were not significant, p values >0.05
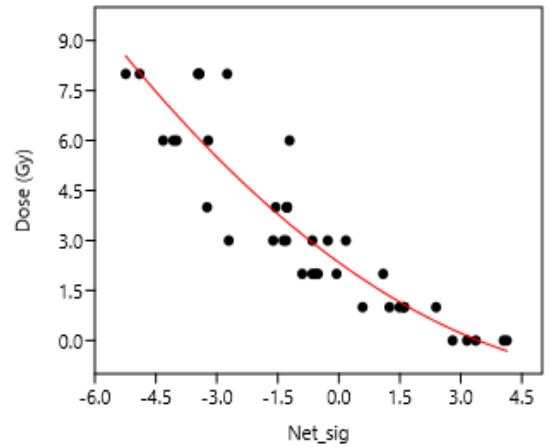
2A. Male Mice

2B. Female Mice

Legend:
- Phlda3
- Rhoc
- Lrg1
- Ccr7
- Ly6d
- Cd19
- Cxcr5
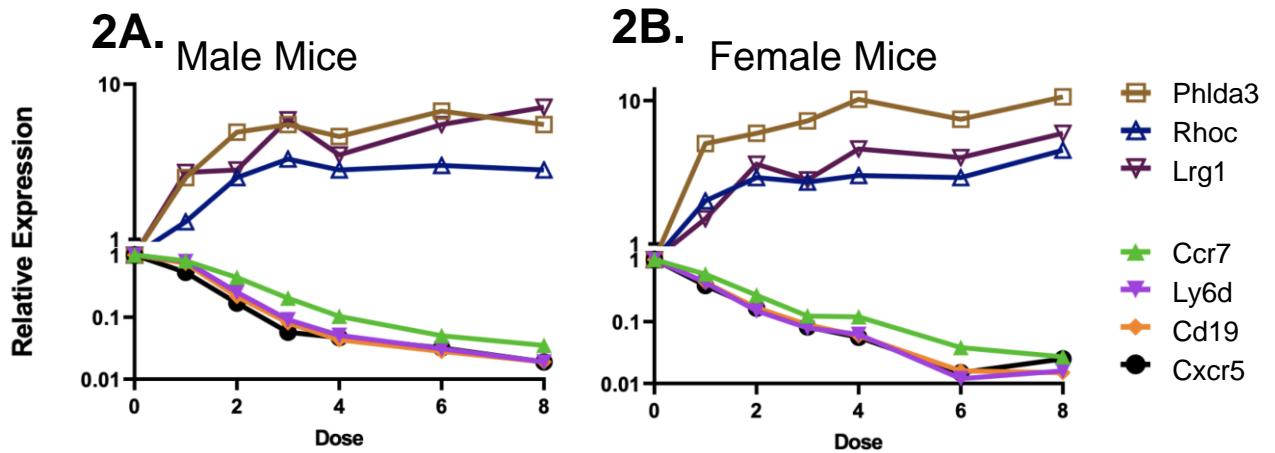
Supplementary figures 2 Relative gene expression fold changes of 7 signature mRNA by qRT-PCR , dose vs sham calibrator (using geomean of Actb and Gapdh housekeeping genes), n=5 males (**2A**) and n=5 females (**2B**).
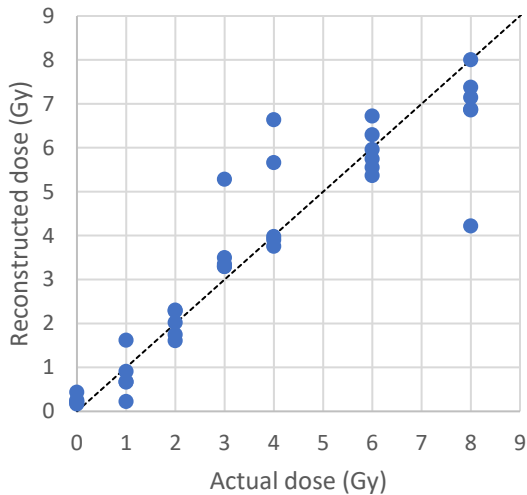
3A. $0.1016x^2 - 0.8844x + 2.053$
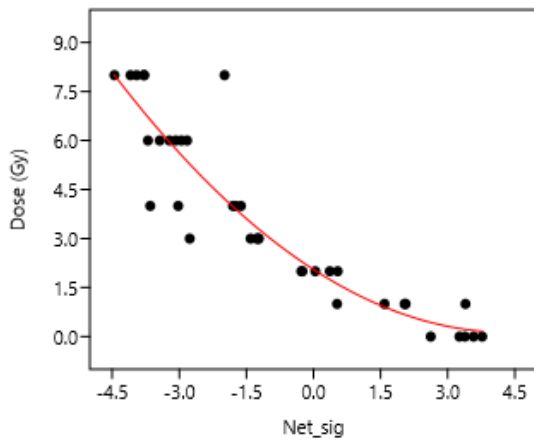
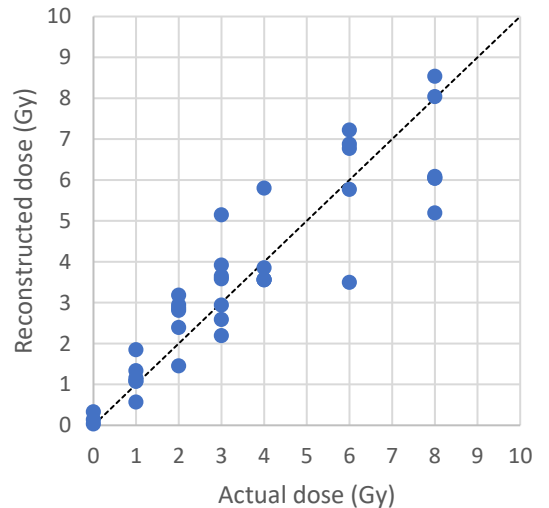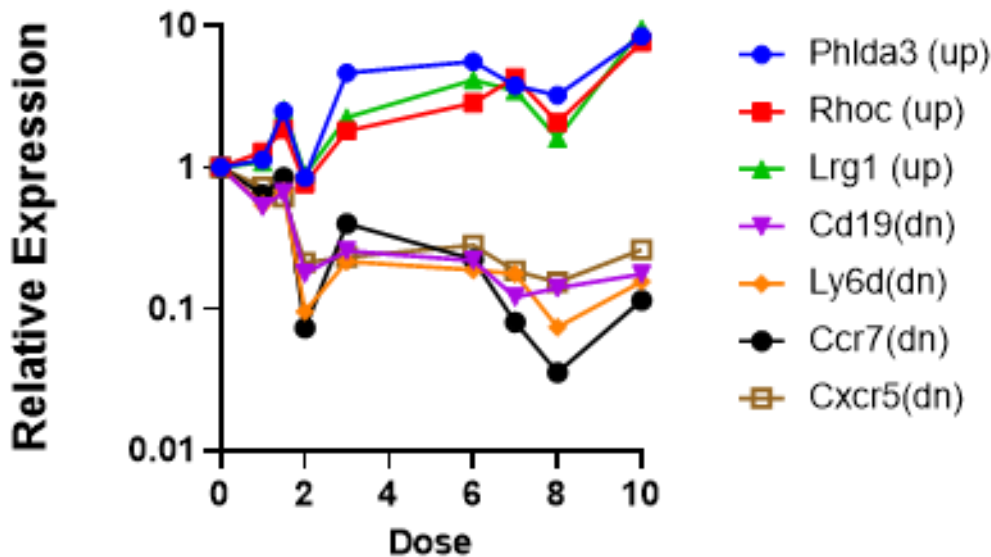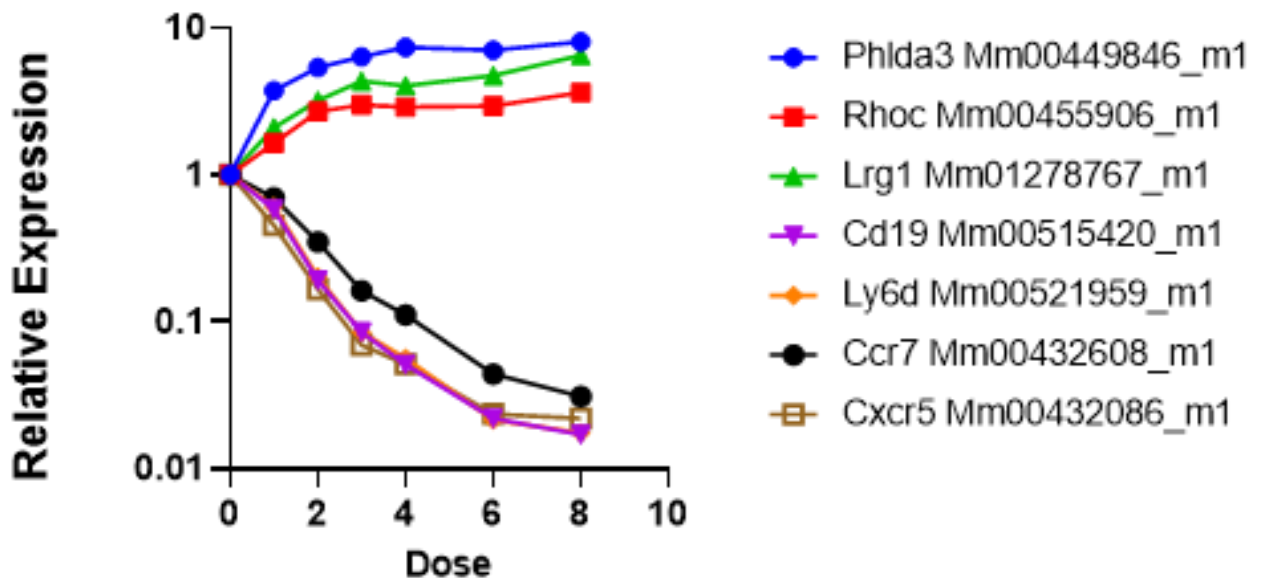**3B.** $0.05756x^2 - 0.8805x + 2.342$

3C. Males

3D. Females

Supplementary figures 3. Male (**3A** and **3C**) gene expression results for dose reconstruction. **3A** plot Net_sig (N) independent variable and dose as dependent variable in males, and equation for the regression line. **3C** plot of reconstructed dose vs actual dose delivered and fit line using the regression model. Female (**3B** and **3D**) gene expression results for dose reconstruction. **3B** plot Net_sig (N) independent variable and dose as dependent variable in males, and equation for the regression line . **3D** plot of reconstructed dose vs actual dose delivered and fit line using the regression model.

4A. Microarray 7genes average

Legend:
- Phlda3 (up)
- Rhoc (up)
- Lrg1 (up)
- Cd19(dn)
- Ly6d(dn)
- Ccr7(dn)
- Cxcr5(dn)

4B. PCR 7genes average

Legend:
- Phlda3 Mm00449846_m1
- Rhoc Mm00455906_m1
- Lrg1 Mm01278767_m1
- Cd19 Mm00515420_m1
- Ly6d Mm00521959_m1
- Ccr7 Mm00432608_m1
- Cxcr5 Mm00432086_m1

Supplementary figures 4. Relative gene expression curves, mean of n=10 (5 males and 5 females) for the 7mRNA signature genes, by microarray (**4A**) fold changes mean of irradiated vs sham, and qRT-PCR (**4B**) fold changes dose vs sham calibrator (using geomean of Actb and Gapdh housekeeping genes)