

Diversity in the pre-immune immunoglobulin repertoire of SHR lines susceptible and resistant to end organ injury.

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Supplementary Figure 2

Distribution of sequence read coverage density across the rat IGH locus on chromosome 6. Read coverage was binned over 100kbase bins and plotted for both SHR lines. Genome-wide average coverage for SHR-A3 was 43.6 and for SHR-B2 was 48.5.

