

## **Supplementary text and figures**

### **1. Supplementary figures**

S1 - Liability-scale heritability explained vs chromosome size.

S2 – SNP beta estimate comparison for the 156 LOY loci in discovery analyses including or excluding cancer cases

S3 – The impact of sample size and Y chromosome PAR1 / Non-PAR ratio on PAR-LOY power over mLRR-Y

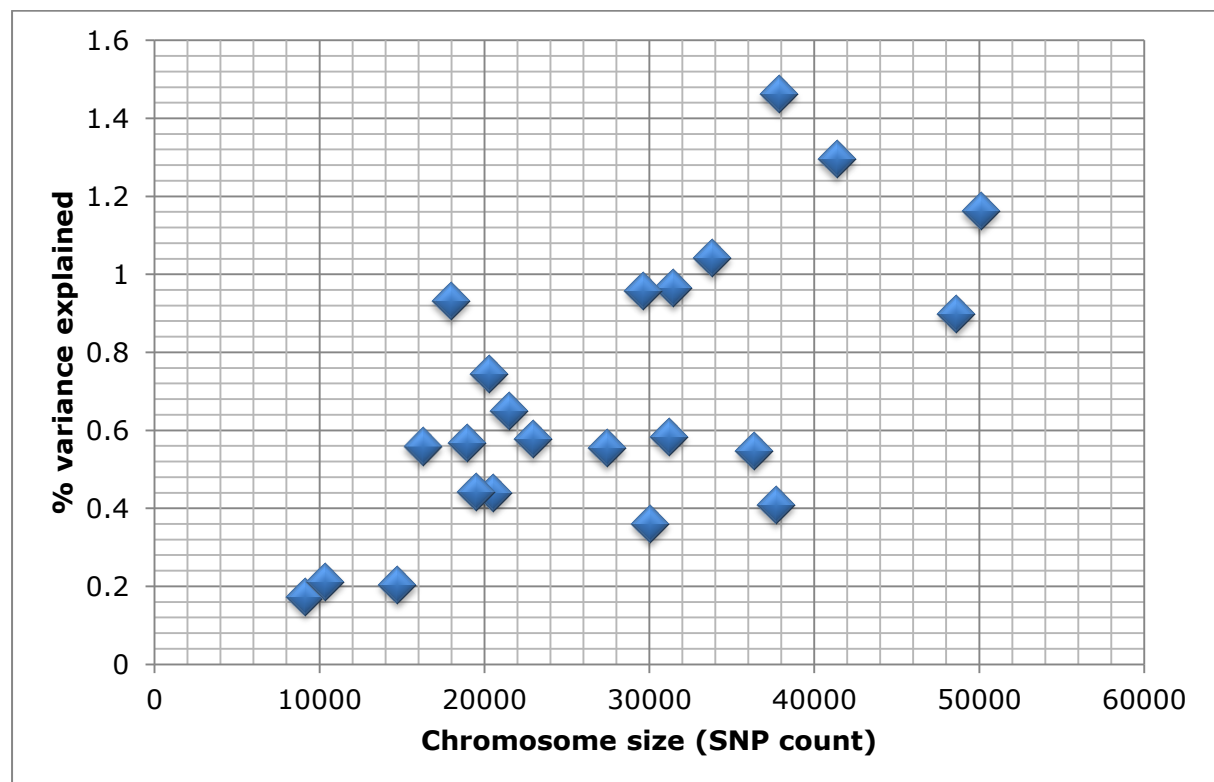
S4 - Cell and tissue type enrichment estimated using LDSC-SEG

S5 - Differential expression of the *TCL1A* gene in B-lymphocytes with and without the Y chromosome within individual subjects

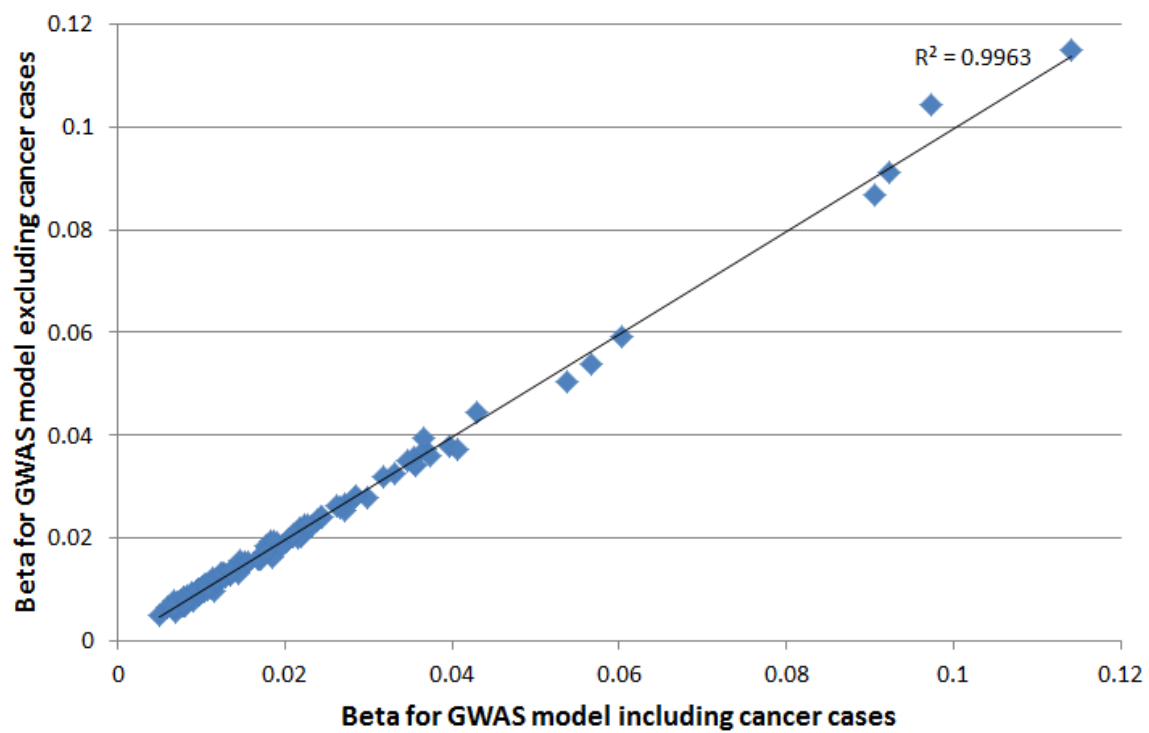
### **2. Consortium authorship**

### **3. Acknowledgements**

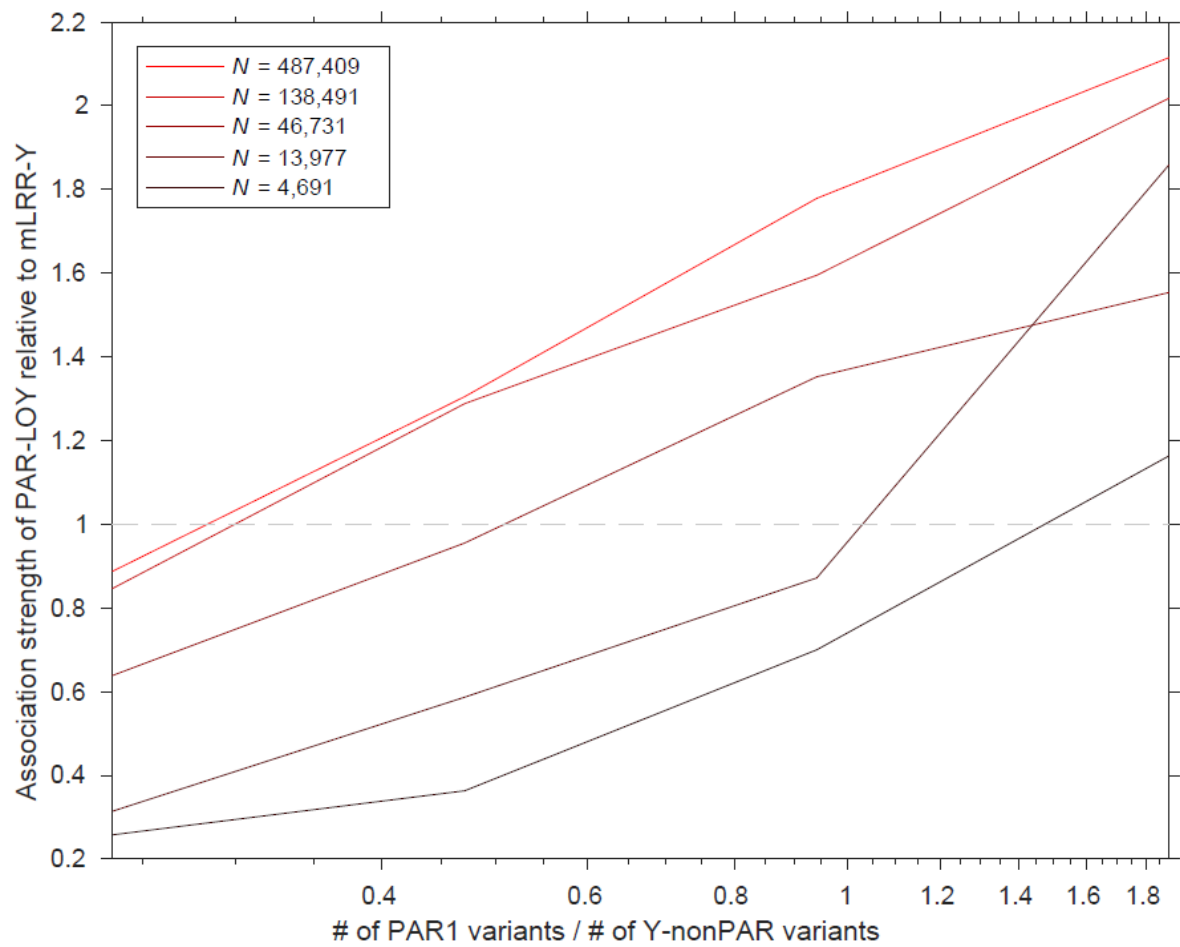
**Figure S1 | Liability-scale heritability explained vs chromosome size.**



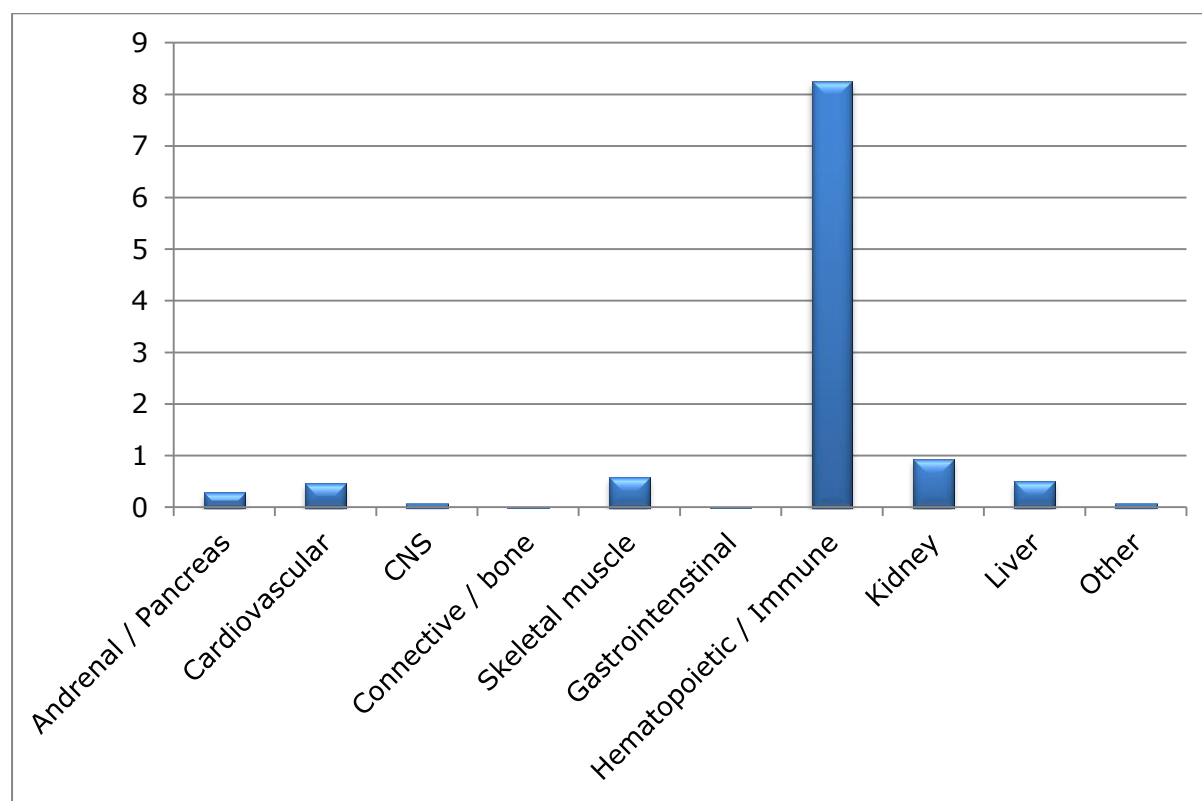
**Figure S2 | SNP beta estimate comparison for the 156 LOY loci in discovery analyses including or excluding cancer cases**



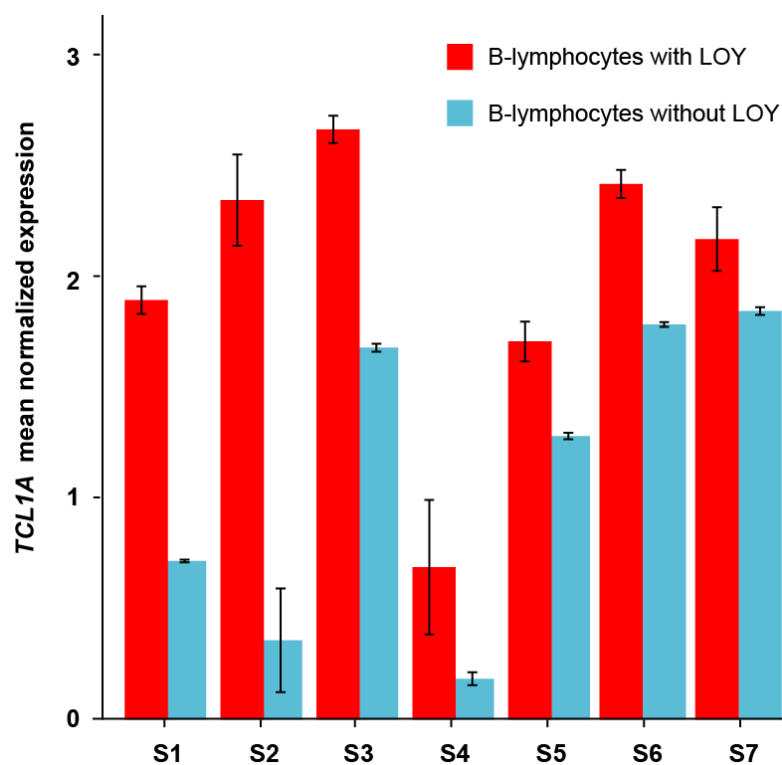
**Figure S3 | The impact of sample size and Y chromosome PAR1 / Non-PAR ratio on PAR-LOY power over mLRR-Y.**



**Figure S4 | Cell and tissue type enrichment estimated using LDSC-SEG**



**Supplementary Figure 5.** Differential expression of the *TCL1A* gene in B-lymphocytes with and without the Y chromosome within individual subjects. Error bars indicate the 95% confidence interval of the mean normalized expression of *TCL1A* within each group. To avoid stochastic effects that might occur in estimations using a small number of cells, results are shown for individuals with LOY in at least 10% of the B-lymphocytes and with LOY in more than five individual B-lymphocytes. Within each of the seven individuals (S1-S7) meeting this criteria, *TCL1A* showed a higher expression in the LOY cells compared to normal cells. This suggests that the observed *TCL1A* overexpression in B-lymphocytes without a Y chromosome is independent from the individual genotypes at the lead GWAS-SNP (rs2887399).



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### Kidney Cancer GWAS Meta-Analysis Project

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### **Colorectal Cancer UK GWAS**

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## **Glioma GWAS**

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