Supplementary Table 4. Variance explained by chromosome 5 or all autosomes, as estimated by REML

Hemangiosarcoma	variance explained	SE	p	variance explained, sex as covariate	SE	p
all autosomes	0.37	0.18	2.40E-03	0.40	0.18	1.32E-03
only chr 5	0.26	0.10	3.45E-04	0.25	0.10	2.91E-04
chr 5, 25-40 Mb	0.18	0.10	7.08E-05	0.18	0.10	4.23E-05
B-cell lymphoma						
all autosomes	1.11	0.48	6.55E-03	1.12	0.46	2.41E-03
only chr 5	0.22	0.18	7.72E-02	0.13	0.15	1.86E-01
chr 5, 25-40 Mb	0.63	0.25	1.66E-04	0.60	0.25	5.76E-04
combined dataset						
all autosomes	0.41	0.17	8.52E-04	0.43	0.17	6.58E-04
only chr 5	0.21	0.09	6.79E-04	0.19	0.09	1.19E-03
chr 5, 25-40 Mb	0.23	0.11	2.17E-05	0.22	0.11	2.76E-05