

Supplemental Table S1. Individual effect of leukocyte telomere length (LTL) related variants on germ cell tumor risk (GCT)

SNP	Chr	Position (GRCh38)	Gene	Rsq	Typed/Imputed	L <sup>2</sup> allele	S <sup>3</sup> allele	Pediatric germ cell tumors (GCT)																	UKB testicular GCT											
								TDT (N = 610)							Case-control analysis <sup>1</sup> (N = 803)										Meta-analysis (N = 1,413)						Case-Control (N = 396)					
								LAF	beta	se	OR <sup>4</sup> (95% CI)	pval	LAF for African ancestry	LAF for Asian ancestry	LAF for Hispanic ancestry	LAF for White ancestry	LAF for White non-trio ancestry	Direction	HetPval	beta	se	OR <sup>4</sup> (95% CI)	pval	Direction	HetPval	beta	se	OR <sup>4</sup> (95% CI)	pval	Rsq	LAF	beta	se	OR <sup>3</sup> (95% CI)	pval	
<b>Codd et al. (2013) – 7 genetic variants predict LTL</b>																																				
rs11125529	2	54248729	ACYP2	0.9913	IMPUTED	A	C	0.129	0.023	0.122	1.02 (0.81, 1.30)	0.855	0.146	0.128	0.096	0.161	0.145	---	0.828	0.020	0.106	1.02 (0.83, 1.26)	0.853	----	0.914	0.021	0.080	1.02 (0.87, 1.19)	0.793	0.9936	0.142	-0.088	0.125	0.92 (0.72, 1.17)	0.480	
rs10936599	3	169774313	TERC	1.0000	TYPED	C	T	0.730	0.109	0.092	1.12 (0.93, 1.34)	0.234	0.904	0.419	0.597	0.779	0.749	++++	0.779	0.155	0.076	1.17 (1.01, 1.36)	0.041	++++	0.864	0.138	0.058	1.15 (1.02, 1.29)	0.018	1.0000	0.758	0.093	0.093	1.10 (0.92, 1.32)	0.315	
rs7675998	4	163086668	NAF1	0.9008	IMPUTED	G	A	0.780	0.219	0.102	1.24 (1.02, 1.52)	0.033	0.830	0.783	0.768	0.747	0.762	---	0.201	-0.060	0.087	0.94 (0.79, 1.12)	0.485	----	0.067	0.056	0.066	1.06 (0.93, 1.20)	0.399	0.9972	0.781	-0.156	0.100	1.17 (0.96, 1.42)	0.118	
rs2736100*	5	1286401	TERT	0.9937	TYPED	C	A	0.472	-0.130	0.082	0.88 (0.75, 1.03)	0.112	0.492	0.473	0.351	0.502	0.464	---	0.574	-0.256	0.072	0.77 (0.67, 0.89)	0.0004	----	0.497	-0.198	0.054	0.82 (0.74, 0.91)	0.0003	1.0000	0.503	-0.183	0.078	0.83 (0.71, 0.97)	0.020	
rs9420907	10	103916707	OBFC1	0.9397	IMPUTED	C	A	0.161	-0.113	0.112	0.89 (0.72, 1.11)	0.313	0.474	0.063	0.119	0.160	0.152	+++	0.309	0.049	0.106	1.05 (0.85, 1.29)	0.645	++++	0.300	-0.033	0.077	0.97 (0.83, 1.13)	0.665	1.0000	0.139	-0.220	0.123	0.80 (0.63, 1.02)	0.073	
rs8105767†	19	22032639	ZNF208	0.9828	IMPUTED	G	A	0.315	0.053	0.087	1.05 (0.89, 1.25)	0.544	0.442	0.288	0.328	0.279	0.308	---	0.421	0.018	0.074	1.02 (0.88, 1.18)	0.804	----	0.555	0.031	0.056	1.03 (0.92, 1.15)	0.580	0.9939	0.295	-0.032	0.087	1.03 (0.87, 1.22)	0.715	
rs755017	20	63790269	RTEL1	0.9996	TYPED	G	A	0.144	0.115	0.120	1.12 (0.89, 1.42)	0.337	0.279	0.436	0.197	0.131	0.117	---	0.375	0.059	0.089	1.06 (0.89, 1.26)	0.508	----	0.497	0.079	0.072	1.08 (0.94, 1.25)	0.270	0.9993	0.138	-0.069	0.118	0.93 (0.74, 1.18)	0.560	
<b>Li et al. (2020) – 20 genetic variants predict LTL</b>																																				
rs3219104	1	226374920	PARP1	0.9384	IMPUTED	C	A	0.779	-0.057	0.102	0.94 (0.77, 1.15)	0.575	0.857	0.569	0.646	0.807	0.805	---	0.748	-0.199	0.082	0.82 (0.70, 0.96)	0.015	----	0.682	-0.144	0.064	0.87 (0.76, 0.98)	0.024	0.9960	0.847	-0.060	0.106	0.94 (0.76, 1.16)	0.570	
rs55749605	3	101513249	SENP7	0.9886	IMPUTED	C	A	0.334	0.092	0.088	1.10 (0.92, 1.30)	0.294	0.231	0.399	0.218	0.387	0.391	++++	0.744	0.029	0.079	1.03 (0.88, 1.20)	0.716	++++	0.816	0.057	0.059	1.06 (0.94, 1.19)	0.331	0.9981	0.375	0.109	0.082	0.90 (0.76, 1.05)	0.183	
rs10936600	3	169796797	TERC	0.9842	IMPUTED	A	T	0.729	0.101	0.092	1.11 (0.92, 1.32)	0.272	0.895	0.438	0.602	0.778	0.756	++++	0.367	0.162	0.077	1.18 (1.01, 1.37)	0.036	++++	0.472	0.136	0.059	1.15 (1.02, 1.29)	0.021	0.9988	0.757	-0.100	0.093	0.90 (0.75, 1.09)	0.282	
rs13137667	4	70908630	MOB1B	0.5887	IMPUTED	C	T	0.963	0.169	0.220	1.18 (0.77, 1.82)	0.442	0.762	0.945	0.940	0.950	0.947	---	0.547	-0.283	0.188	0.75 (0.52, 1.09)	0.131	----	0.357	-0.093	0.143	0.91 (0.69, 1.21)	0.515	0.9928	0.969	-0.110	0.268	0.90 (0.53, 1.52)	0.683	
rs4691895	4	163127047	NAF1	1.0000	TYPED	C	G	0.774	0.208	0.100	1.23 (1.01, 1.50)	0.037	0.853	0.786	0.783	0.757	0.787	---	0.251	-0.119	0.084	0.89 (0.75, 1.05)	0.155	----	0.040	0.016	0.064	1.02 (0.90, 1.15)	0.806	0.9967	0.775	-0.110	0.098	1.12 (0.92, 1.35)	0.263	
rs7705526*	5	1285859	TERT	0.8314	IMPUTED	A	C	0.265	-0.211	0.123	0.81 (0.64, 1.03)	0.086	0.189	0.335	0.229	0.320	0.295	---	0.111	-0.156	0.088	0.86 (0.72, 1.02)	0.077	----	0.177	-0.175	0.072	0.84 (0.73, 0.97)	0.015	0.9705	0.326	-0.201	0.089	0.82 (0.69, 0.97)	0.024	
rs2853677*	5	1287079	TERT	0.8534	IMPUTED	G	A	0.390	-0.159	0.098	0.85 (0.70, 1.03)	0.105	0.326	0.460	0.302	0.432	0.417	---	0.975	-0.263	0.081	0.77 (0.66, 0.90)	0.001	----	0.950	-0.221	0.063	0.80 (0.71, 0.91)	<0.001	1.0000	0.424	-0.225	0.083	0.80 (0.68, 0.94)	0.007	
rs34991172	6	25480100	CARMIL1	0.9762	IMPUTED	T	G	0.960	-0.423	0.209	0.66 (0.44, 0.99)	0.041	0.991	0.999	0.986	0.932	0.939	??-+	0.311	-0.047	0.211	0.95 (0.63, 1.44)	0.826	??-+	0.268	-0.237	0.148	0.79 (0.59, 1.06)	0.111	0.9823	0.920	-0.146	0.168	1.16 (0.83, 1.61)	0.384	
rs2736176	6	31619784	PRRC2A	1.0000	TYPED	C	G	0.319	-0.121	0.090	0.89 (0.74, 1.06)	0.179	0.074	0.308	0.344	0.308	0.305	---	0.139	-0.087	0.077	0.92 (0.79, 1.07)	0.256	----	0.220	-0.102	0.058	0.90 (0.81, 1.01)	0.082	1.0000	0.282	0.075	0.086	1.06 (0.91, 1.28)	0.386	
rs59294613	7	124914213	POT1	0.9883	IMPUTED	C	A	0.713	0.004	0.093	1.00 (0.84, 1.21)	0.963	0.724	0.682	0.771	0.738	0.713	---	0.139	0.184	0.084	1.20 (1.02, 1.42)	0.028	++++	0.109	0.104	0.062	1.11 (0.98, 1.25)	0.096	0.9998	0.713	0.073	0.089	0.93 (0.78, 1.11)	0.411	
rs9419958	10	103916188	STN1 (OBFC1)	0.9393	IMPUTED	T	C	0.161	-0.107	0.113	0.90 (0.72, 1.12)	0.340	0.474	0.063	0.117	0.160	0.152	+++	0.332	0.060	0.106	1.06 (0.86, 1.31)	0.571	++++	0.330	-0.019	0.077	0.98 (0.84, 1.14)	0.809	0.9882	0.139	-0.213	0.123	1.24 (0.97, 1.57)	0.082	
rs228595	11	108234866	ATM	0.9791	IMPUTED	G	A	0.555	-0.099	0.082	0.91 (0.77, 1.06)	0.232	0.753	0.634	0.465	0.553	0.605	+++	0.842	-0.045	0.070	0.96 (0.83, 1.10)	0.522	++++	0.894	-0.068	0.053	0.93 (0.84, 1.04)	0.206	0.9883	0.591	0.117	0.081	0.89 (0.76, 1.04)	0.149	
rs2302588	14	72938044	DCAF4	0.9839	IMPUTED	C	G	0.100	0.086	0.139	1.09 (0.83, 1.43)	0.534	0.066	0.215	0.090	0.099	0.090	0.090	++++	0.943	0.181	0.122	1.20 (0.94, 1.52)	0.138	0++++	0.960	0.140	0.092	1.15 (0.96, 1.38)	0.127	1.0000	0.101	-0.116	0.133	0.89 (0.69, 1.15)	0.382
rs785074	16	69373083	TERF2	0.9802	IMPUTED	G	A	0.254	-0.079	0.093	0.92 (0.77, 1.11)	0.400	0.442	0.106	0.199	0.283	0.264	---	0.534	-0.072	0.086	0.93 (0.79, 1.10)	0.402	----	0.678	-0.075	0.063	0.93 (0.82, 1.05)	0.235	0.9990	0.290	-0.269	0.093	0.76 (0.64, 0.92)	0.004	
rs62053580	16	74646176	RFWD3	0.9229	IMPUTED	A	G	0.868	-0.026	0.130	0.97 (0.76, 1.26)	0.846	0.920	0.757	0.898	0.846	0.825	---	0.773	0.127	0.109	1.14 (0.92, 1.41)	0.243	++++	0.760	0.064	0.083	1.07 (0.91, 1.26)	0.442	0.9890	0.834	0.069	0.111	0.93 (0.75, 1.16)	0.530	
rs7194734	16	82166375	MPHOSPH6	0.8880	IMPUTED	C	T	0.205	-0.239	0.101	0.79 (0.65, 0.96)	0.018	0.215	0.242	0.191	0.236	0.235	----	0.399	-0.055	0.091	0.95 (0.79, 1.13)	0.548	++++	0.319	-0.138	0.068	0.87 (0.76, 1.00)	0.043	0.9997	0.228	0.035	0.092	0.97 (0.81, 1.16)	0.706	
rs8105767†	19	22032639	ZNF208	0.9828	IMPUTED	G	A	0.315	0.053	0.087	1.05 (0.89, 1.25)	0.544	0.442	0.288	0.328	0.279	0.308	---	0.421	0.018	0.074	1.02 (0.88, 1.18)	0.804	----	0.552	0.033	0.056	1.03 (0.93, 1.15)	0.560	0.9939	0.295	0.032	0.087	1.03 (0.87, 1.22)	0.715	
rs75691080	20	63638397	RTEL1/STMN3	0.9180	IMPUTED	C	T	0.923	0.037	0.157	1.04 (0.76, 1.41)	0.814	0.921	0.987	0.939	0.918	0.928	---	0.930	0.070	0.149	1.07 (0.80, 1.44)	0.639	++++	0.971	0.054	0.108	1.06 (0.85, 1.30)	0.616	0.9851	0.915	-0.267	0.134	1.31 (1.00, 1.70)	0.046	
rs34978822	20	63660246	RTEL1	0.8866	IMPUTED	C	G	0.989	0.693	0.408	2.00 (0.90, 4.45)	0.083	0.971	0.992	0.989	0.981	0.982	+++	0.124	-0.078	0.351	0.92 (0.46, 1.84)	0.825	++++	0.099	0.250	0.266	1.28 (0.76, 2.16)	0.348	0.9912	0.979	-0.262	0.260	1.30 (0.78, 2.16)	0.315	
rs73624724	20	63805045	RTEL1/ZBTB46	0.9771	IMPUTED	C	T	0.143	0.095	0.121	1.10 (0.87, 1.39)	0.431	0.255	0.423	0.190	0.131	0.122	---	0.414	0.046	0.091	1.05 (0.88, 1.25)	0.611	----	0.542	0.064	0.073	1.07 (0.92, 1.23)	0.379	0.9998	0.142	-0.033	0.115	0.97 (0.77, 1.21)	0.775	

<sup>1</sup> Model adjusted for ancestry-specific PCs (2 PCs for European Ancestry, 3 PCs for Hispanic and Asian Ancestry, and 4 PCs for African Ancestry), sex (male and female), and study site (COG, Michigan, or California);

<sup>2</sup> L allele = allele associated with longer leukocyte telomere length;

<sup>3</sup>