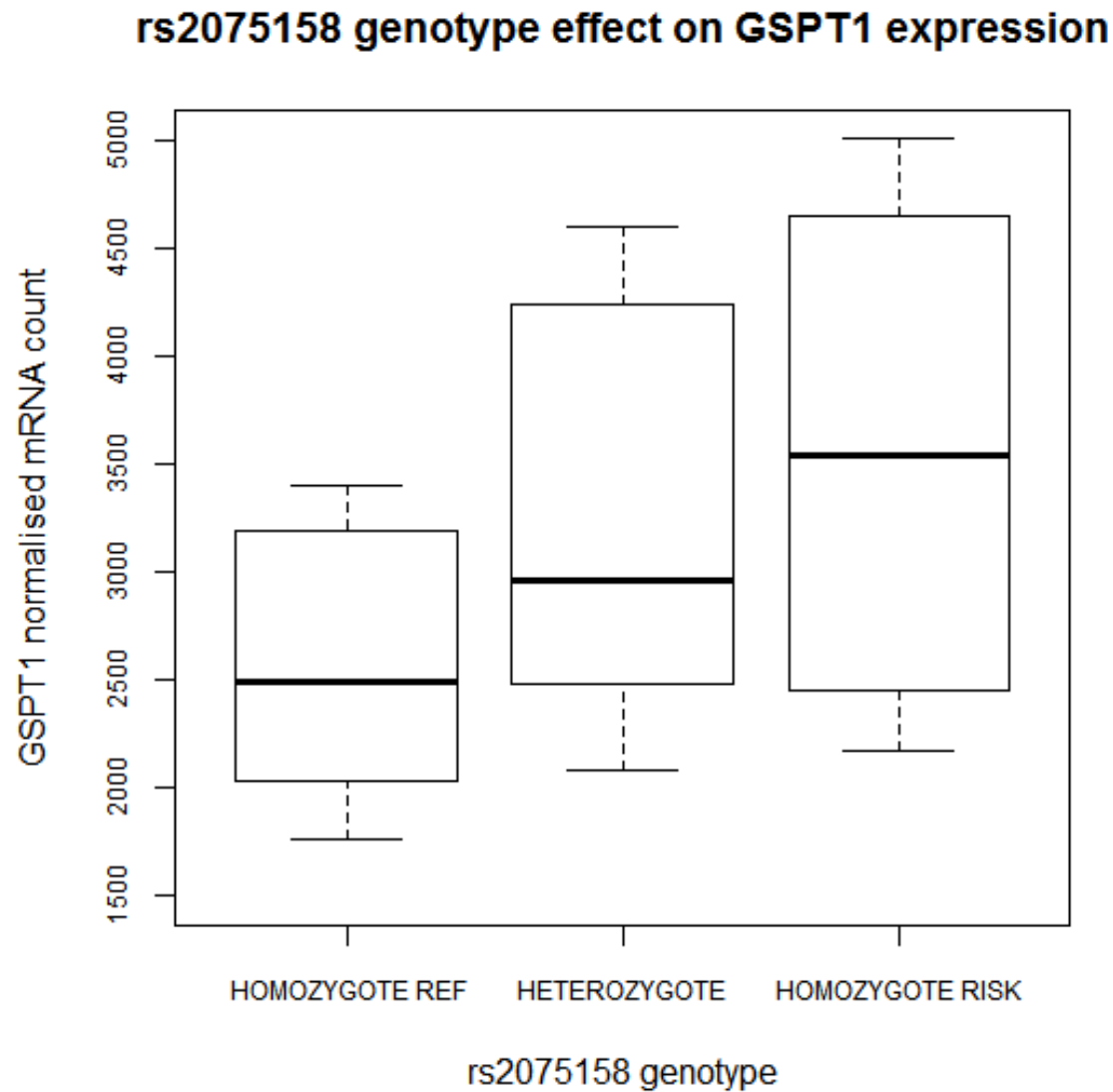
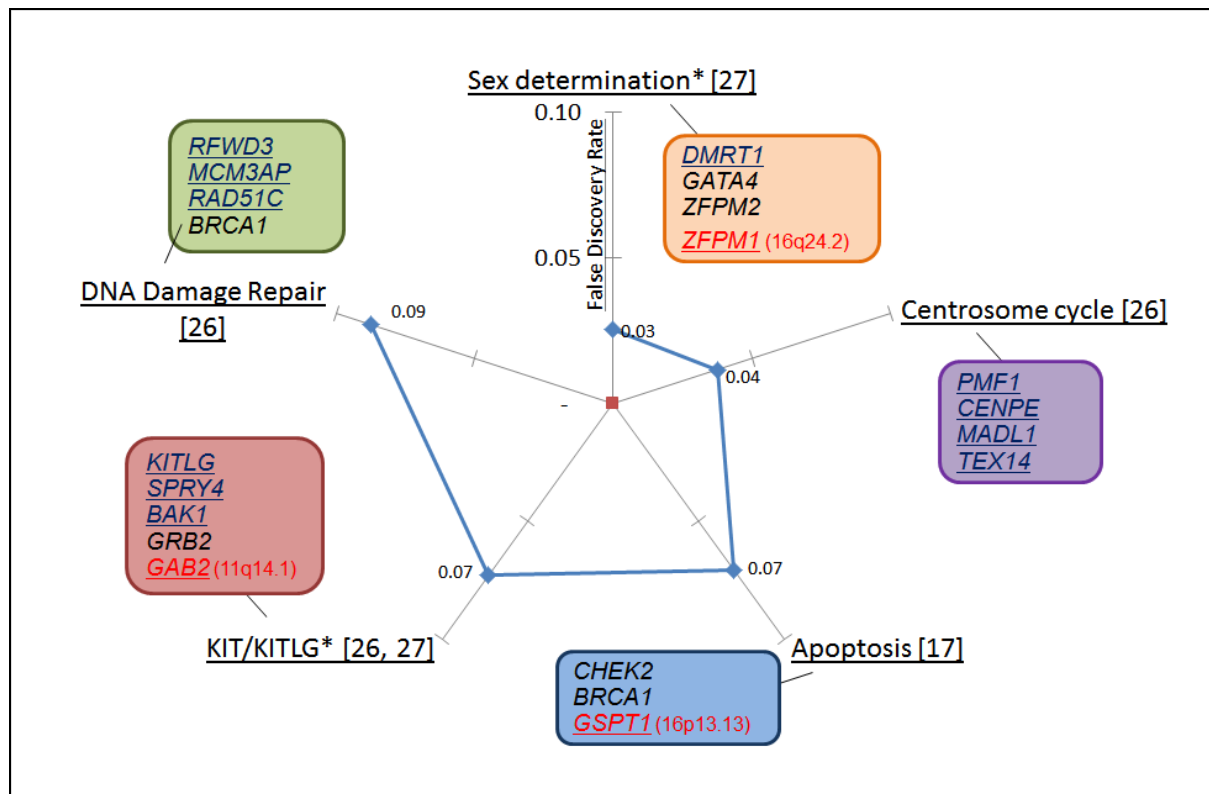


Supplementary Figures

Supplementary figure 1 – Boxplot of eQTL at 16p13.13. The dark black line represents the median expression value for each genotype and the box represents the upper and lower quartiles of data above/below the median. The whiskers extend out to 0.2 times the interquartile range.



Supplementary figure 2 - Significantly enriched TGCT Pathways, implicated in this paper and at least one other study (references in brackets). Gene set names are in underlined black text, ordered with the most significant pathway first (Sex Determination) and then subsequent pathways presented in clockwise order with decreasing significance. The values on the blue line represent the false discovery rate for each pathway as calculated by the iGSEA4GWAS algorithm. In the text boxes are selected genes related to each pathway, colour-coded as follows: dark blue underlined text = genes in LD with risk SNPs identified in previous TGCT GWAS, red underlined text = genes in LD with the four new loci identified in this study, black plain text = genes not yet in LD with any TGCT risk SNPs but highlighted as significant by the iGSEA4GWAS algorithm. Pathways marked with an asterisk are custom gene sets, with “Sex determination” pathway defined as per ¹ and the “KIT/KITLG” pathway defined based on known interacting partners of KIT/KITLG using the STRING database².



Supplementary Tables

Supplementary table 1 – *P*-values from eQTL tests performed. *P*-value threshold 0.0028 considered significant, corrected for 18 multiple tests.

	11q14.1		3q23	16q24.2		16p13.13	
	rs2450140	rs11237477	rs11705932	rs3859027	rs12597021	rs2018199	rs2075158
GAB2	0.909	0.7395					
USP35	0.1896	0.04572					
TFDP2			0.3403				
ATP1B3			0.7273				
ZFPM1				0.2993	0.1304		
BCAR4						0.2793	0.1407
GSPT1						0.00059	0.00051
TNFRSF17	0.5626	0.4104					
RSL1D1	0.05329	0.0431					

Supplementary table 2 - TGCT predisposition loci identified to date, presented in chronological order with functional grouping based on previous review paper³. For loci with multiple reported SNPs the marker listed is taken from first study in the reference column.

SNP	Locus	Candidate Gene(s)	Functional Grouping	Reference(s)
rs995030	12q21	<i>KITLG</i>	1) <i>KIT/KITLG</i> signalling	4,5
rs210138	6p21	<i>BAK1</i>	1) <i>KIT/KITLG</i> signalling 2) Apoptosis	4,5
rs4624820	5q31	<i>SPRY4</i>	1) <i>KIT/KITLG</i> signalling	4
rs4635969	5p15	<i>TERT</i>	3) Telomerase function	6
		<i>CLPTM1L</i>	2) Apoptosis	
rs755383	9p24	<i>DMRT1</i>	7) Sex determination	6
rs2900333	12p13	<i>ATF7IP</i>	3) Telomerase function	6,7
rs8046148	16q12.1	<i>HEATR3</i>	unknown/other	8
rs2839243	21q22.3	<i>non-coding</i>	unknown/other	8
rs3805663	5q31.1	<i>CATSPER3</i>	unknown/other	8
		<i>PITX1</i>	3) Telomerase function	
rs10510452	3p24.3	<i>DAZL</i>	4) Male germ cell development	8
rs2720460	4q24	<i>CENPE</i>	5) Centrosome cycle	8

rs7010162	8q13.3	<i>PRDM14</i>	4) Male germ cell development	8
rs9905704	17q22	<i>RAD51C</i>	6) DNA Repair	9
		<i>PPM1E</i>	unknown/other	
		<i>TEX14</i>	5) Centrosome cycle	
rs3790672	1q24.1	non-coding	unknown/other	8,10
rs2072499	1q22	<i>PMF1</i>	5) Centrosome cycle	8,9
rs4888262 ^c	16q22.3	<i>RFWD3</i>	6) DNA Repair	9
rs12699477	7p22.3	<i>MAD1L1</i>	5) Centrosome cycle	9
rs17021463	4q22.2	<i>HPGDS</i>	4) Male germ cell development	9
rs1510272	3q25	<i>SSR3</i>	unknown/other	11
		<i>TIPARP</i>	unknown/other	
rs7501939	17q12	<i>HNF1B</i>	unknown/other	12
rs2195987	19p12	non-coding	unknown/other	12
rs11705932	3q24	<i>TFDP2</i>	unknown/other	new
		<i>ATP1B3</i>	unknown/other	
rs7107174	11q14	<i>GAB2</i>	1) KIT/KITLG signalling	new
		<i>USP35</i>	unknown/other	
rs4561483	16p13	<i>BCAR4</i>	unknown/other	new
		<i>RSL1D1</i>	unknown/other	
		<i>GSPT1</i>	2) Apoptosis	
		<i>TNFRSF17</i>	unknown/other	
rs55637647	16q24	<i>ZFPM1</i>	7) Sex determination	new

Supplementary table 3 – Pathway associations with FDR < 0.1

Pathway/Gene set name	P-value	False Discovery Rate
CELLULAR COMPONENT DISASSEMBLY	< 0.001	0.0210
Sex determination gene set (Custom Set)	< 0.001	0.0252
CENTROSOME CYCLE	< 0.001	0.0375
INDUCTION OF APOPTOSIS BY INTRACELLULAR SIGNALS	< 0.001	0.0706
KIT/KITLG Signalling (Custom Set)	< 0.001	0.0729
PROTEIN COMPLEX DISASSEMBLY	< 0.001	0.0738
MACROMOLECULAR COMPLEX DISASSEMBLY	< 0.001	0.0738
CONDENSED CHROMOSOME	0.001	0.0784
SINGLE STRANDED RNA BINDING	< 0.001	0.0796
TRANSCRIPTION FROM RNA POLYMERASE III PROMOTER	0.001	

		0.0798
CHROMOSOME	0.003	0.0806
TRANSITION METAL ION BINDING	0.004	0.0806
INTRA GOLGI VESICLE MEDIATED TRANSPORT	0.001	0.0806
ZINC ION BINDING	0.001	0.0808
CELLULAR PROTEIN COMPLEX DISASSEMBLY	< 0.001	0.0812
NKCELLSPATHWAY	< 0.001	0.0823
DNA DAMAGE RESPONSE SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	< 0.001	0.0826
HSA04120 UBIQUITIN MEDIATED PROTEOLYSIS	< 0.001	0.0826
IL17PATHWAY	0.001	0.0837
RESPONSE TO ABIOTIC STIMULUS	0.001	0.0840
RESPONSE TO IONIZING RADIATION	0.001	0.0855
SMALL PROTEIN CONJUGATING ENZYME ACTIVITY	< 0.001	0.0871
DNA DAMAGE RESPONSE SIGNAL TRANSDUCTION RESULTING IN INDUCTION OF APOPTOSIS	< 0.001	0.0873
HYPERTROPHY MODEL	0.001	0.0878
MANNOSYLTRANSFERASE ACTIVITY	< 0.001	0.0891
CELLULAR PROTEIN METABOLIC PROCESS	< 0.001	0.0901
CELLULAR MACROMOLECULE METABOLIC PROCESS	< 0.001	0.0921
G2PATHWAY	0.002	0.0928
DNA DAMAGE RESPONSE SIGNAL TRANSDUCTION	0.002	0.0935
IGF1PATHWAY	0.001	0.0991
RESPONSE TO RADIATION	< 0.001	0.0997

Supplementary Note

Supplementary note 1: The UK Testicular Cancer Collaboration (UKTCC)

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Dr Thiagarajan Sreenivasan	United Lincolnshire Hospitals NHS Trust	Pilgrim Hospital, Boston, Lincolnshire PE21 9QS
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