Supplementary Material for

Thyroid cancer susceptibility polymorphisms: confirmation of loci on chromosomes 9q22, 5q24 and 14q13, validation of a recessive 8q24 locus and failure to replicate a locus on 5q24

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Supplementary Table 1. Kaspar probe sequences used to genotype the markers examined in this study

SNP	Probe	Sequence
rs2910164	Allele C	GAAGGTGACCAAGTTCATGCTGGTTGTGTCAGTGTCAGACCTC
	Allele G	GAAGGTCGGAGTCAACGGATTGGTTGTGTCAGTGTCAGACCTG
	Common	CGATGACAGAGATATCCCAGCTGAA
rs6983267	Allele G	GAAGGTGACCAAGTTCATGCTCATAAAAATTCTTTGTACTTTTCTCAGTGC
	Allele T	GAAGGTCGGAGTCAACGGATTCACATAAAAATTCTTTGTACTTTTCTCAGTGA
	Common	CCAGAGTTAATACCCTCATCGTCCTT
rs965513	Allele A	GAAGGTGACCAAGTTCATGCTGTGGCTGGAATGGAACAGATCAAAA
	Allele G	GAAGGTCGGAGTCAACGGATTGGCTGGAATGGAACAGATCAAAG
	Common	GTCTTTGTTAGCATTGTGAGAACAGACTA
	Allele A	GAAGGTGACCAAGTTCATGCTCCAGAGTCCAGTCCCGGTCA
	Allele G	GAAGGTCGGAGTCAACGGATTCAGAGTCCCGGTCG
	Common	GGTGCTTCTCGAGGCGGGCA
rs944289	Allele C	GAAGGTGACCAAGTTCATGCTCAATTTAATTTGGTTGAAAGATAGTCATTGC
	Allele T	GAAGGTCGGAGTCAACGGATTGCAATTTAATTTGGTTGAAAGATAGTCATTGT
	Common	GGACATTAGATTATTTTAAATTCCCAGCTA

Supplementary Table 2. 9q22 SNPs that are in high linkage disequilibrium (r^2 >0.5) with both rs1867277 and rs965513. Data from the 1000 Genomes Project Phase 1, Interim release, May 11 2011.

SNP	**Location on chromosome 9**	**r^2 with rs955513**	**r^2 with rs1877277**
rs6478413	100,582,024	0.54	0.64
rs10124220	100,583,074	0.59	0.71
rs1443432	100,583,195	0.54	0.64
rs7848973	100,588,839	0.58	0.70

Supplementary Table 3. Association between rs2910164 genotypes and thyroid cancer risk using genotypic, Cochran-Armitage trend, allelic, dominant, recessive and heterozygous disease models

Test	**Counts in all TC cases**	**Counts in All controls**	**P all cases**	**P papillary cases**
Genotypic	41/277/436	339/2179/3540	0.913	0.938
Trend	360/1156	2857/9259	0.846	0.919
Allelic	359/1149	2857/9259	0.846	0.919
Dominant	318/439	2518/3540	0.749	0.825
Recessive	41/713	339/5719	0.858	0.836
Heterozygous	277/477	2179/3879	0.708	0.784

Supplementary Table 4. Proportion of thyroid cancer heritability explained by four SNPs at chromosome 8q24, 9q22 and 14q13.

SNP	**OR per allele**[1]	**Attributable sibling relative risk**
rs6983267	1.140	0.007
rs965513	1.780 (1.981)	0.045
rs1867277	1.29- (1.749)	0.043
rs944289	1.330	0.018
Combined	3.760	0.111
No effect of rs1867277	3.995	0.066
No effect of rs965513	3.813	0.064

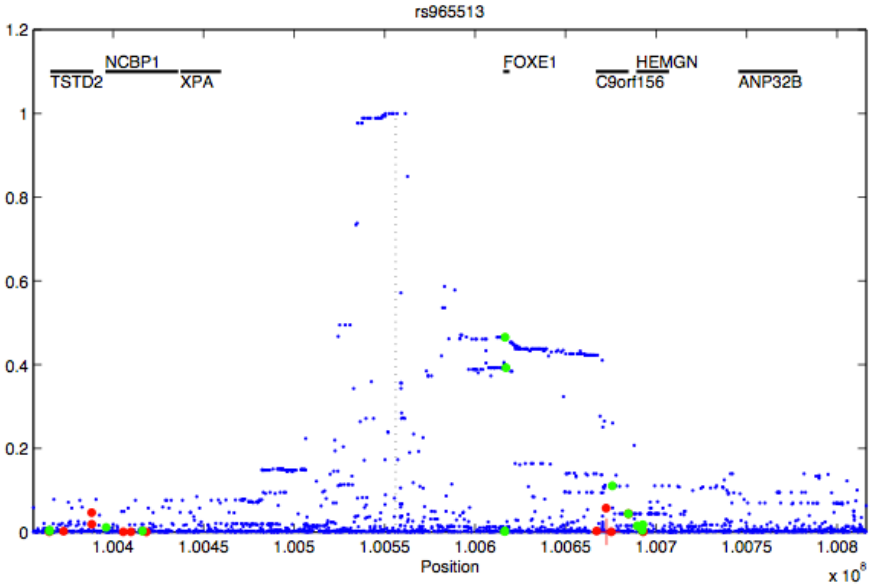
[1]. For the 9q22 markers we show their ORs obtained from the logistic regression testing when both genotypes are incorporated models and the ORs when they are analyses separately (in parenthesis)

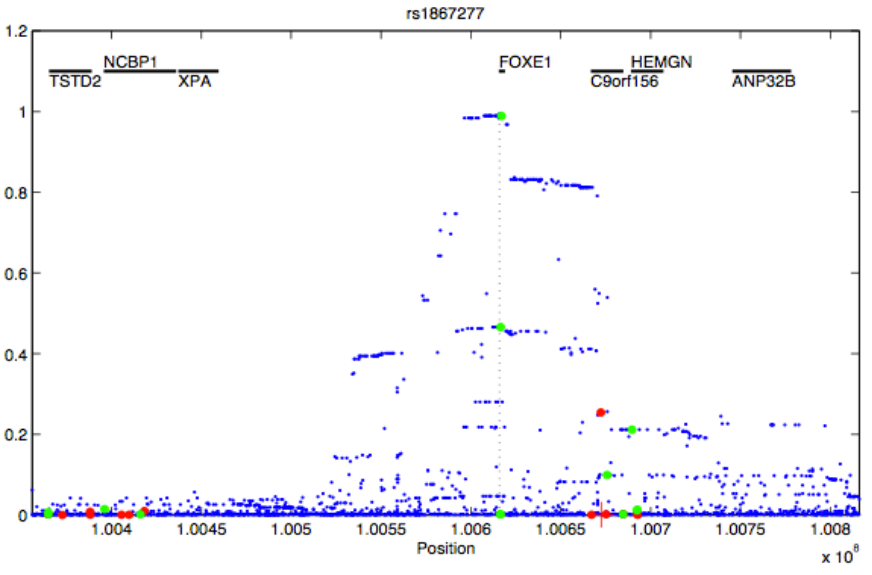
Supplementary Table 5. Number of risk alleles at rs6983267, rs965513, rs1867277 and rs944289 in thyroid cases and controls.

Number of alleles	**Cases (n=755)**	**Controls (=6076)**
0	2 (0.3%)	84 (1.4%)
1	19(2.5%)	389(6.4%)
2	61(8.1%)	1008(16.6%)
3	123(16.3%)	1439(23.7%)
4	182(24.1%)	1371(22.6%)
5	171(22.6%)	969(15.9%)
6	121 (16%)	562(9.2%)
7	59 (7.8%)	213(3.5%)
8	17(2.3%)	41(0.7%)

Supplementary Figure 1. Linkage disequilibrium plots for rs965513 (A) and rs1867277 (B). The approximate location of the seven 9q22 genes is shown on top of the figure. The vertical dotted lines in the middle of each figure indicate the position of rs965513 and rs1867277, respectively. r^2 values between either rs965513 or rs1867277 and surrounding markers are shown in the y-axis. The x-axis shows the physical positions of markers on chromosome 9q22. Synonymous variants are highlighted in green circles, non-synonymous variants are highlighted in red circles and premature stop generating variants are highlighted with red crosses.

A)





Supplementary Figure 2. Meta-analysis of associations between the rs6983267G allele and thyroid cancer