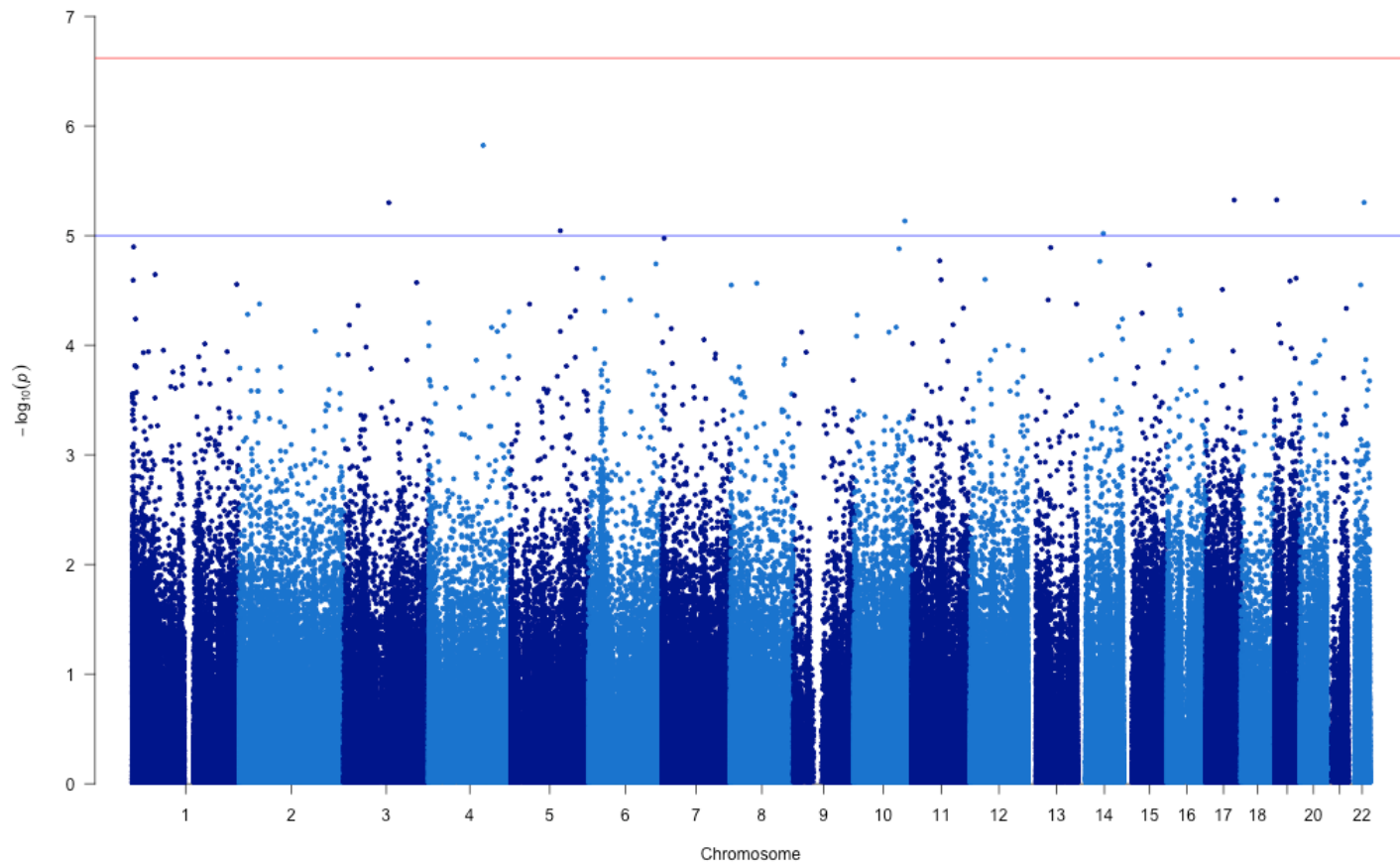
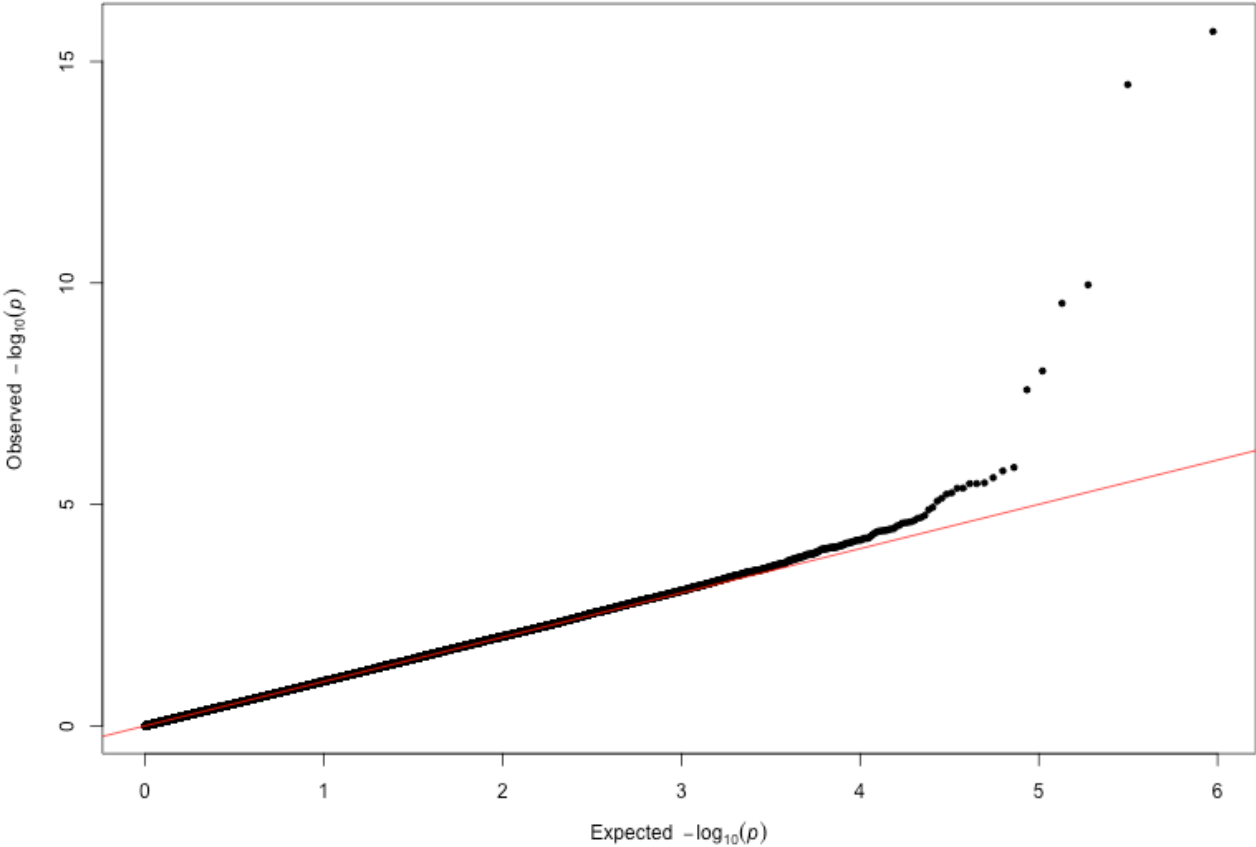


**Supplemental Figure 1:** Manhattan plot of meta-analysis of EWAS for fT4. The x-axis shows chromosome position, and the y-axis  $-\log_{10} P$ -values. The epigenome-wide significance threshold is represented by the horizontal red line ( $P=2.4E-7$ ) and the threshold for suggestive association shown by the horizontal blue line ( $P=1.0E-5$ ).

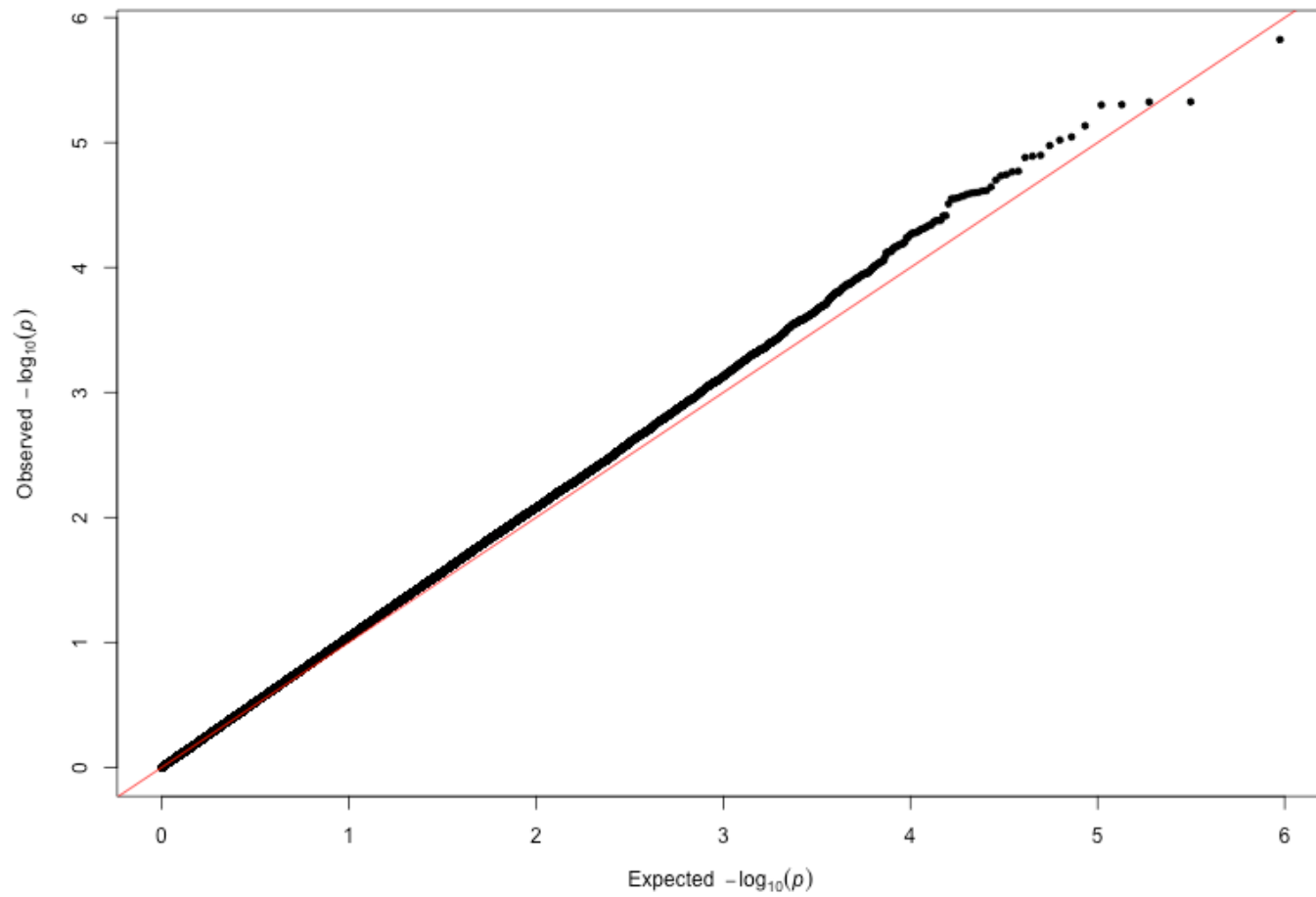


Supplemental Figure 2: QQ plot of a) fT3, b) fT4 and c) TSH meta-analysis results.

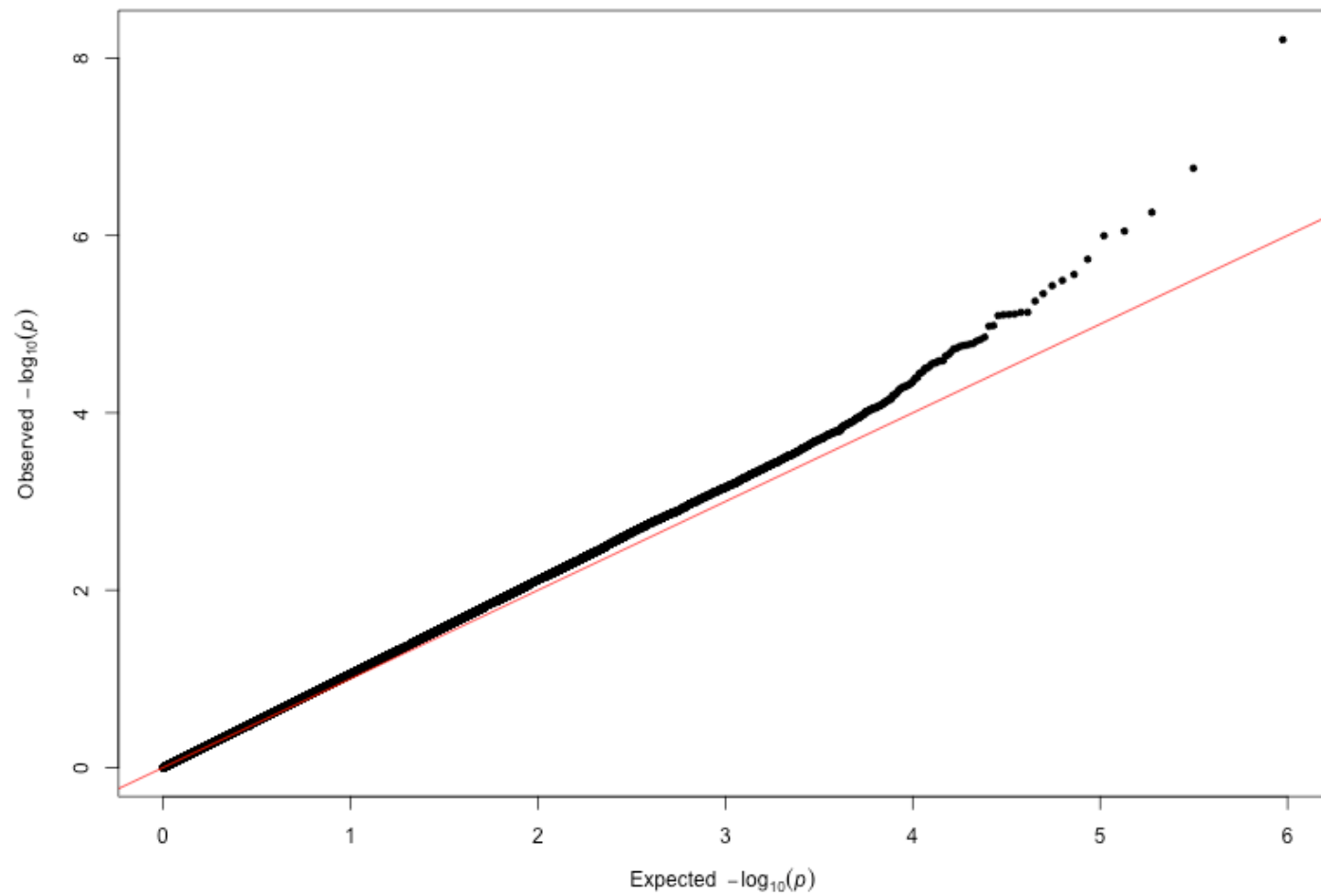
a)



b)

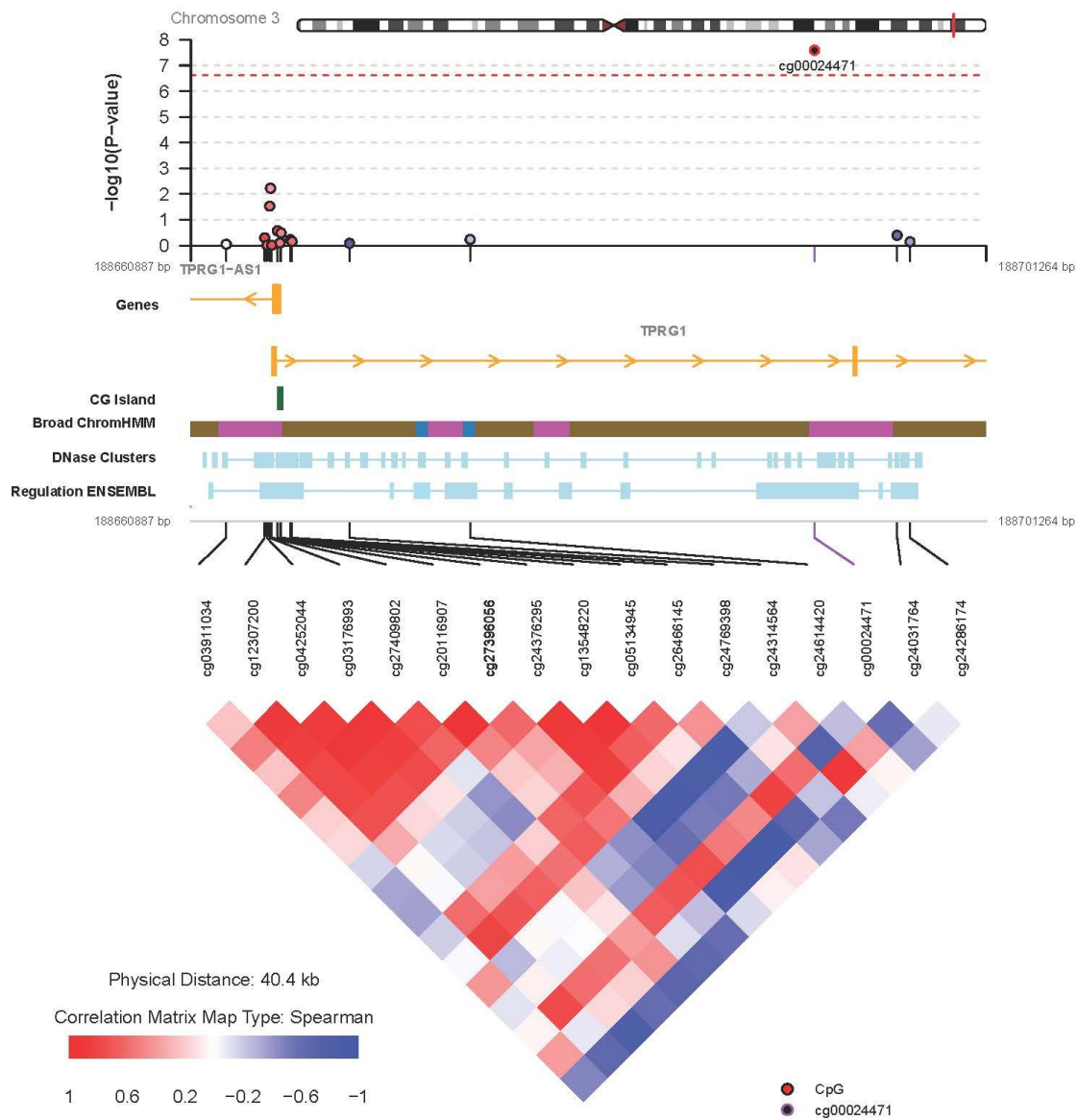


c)

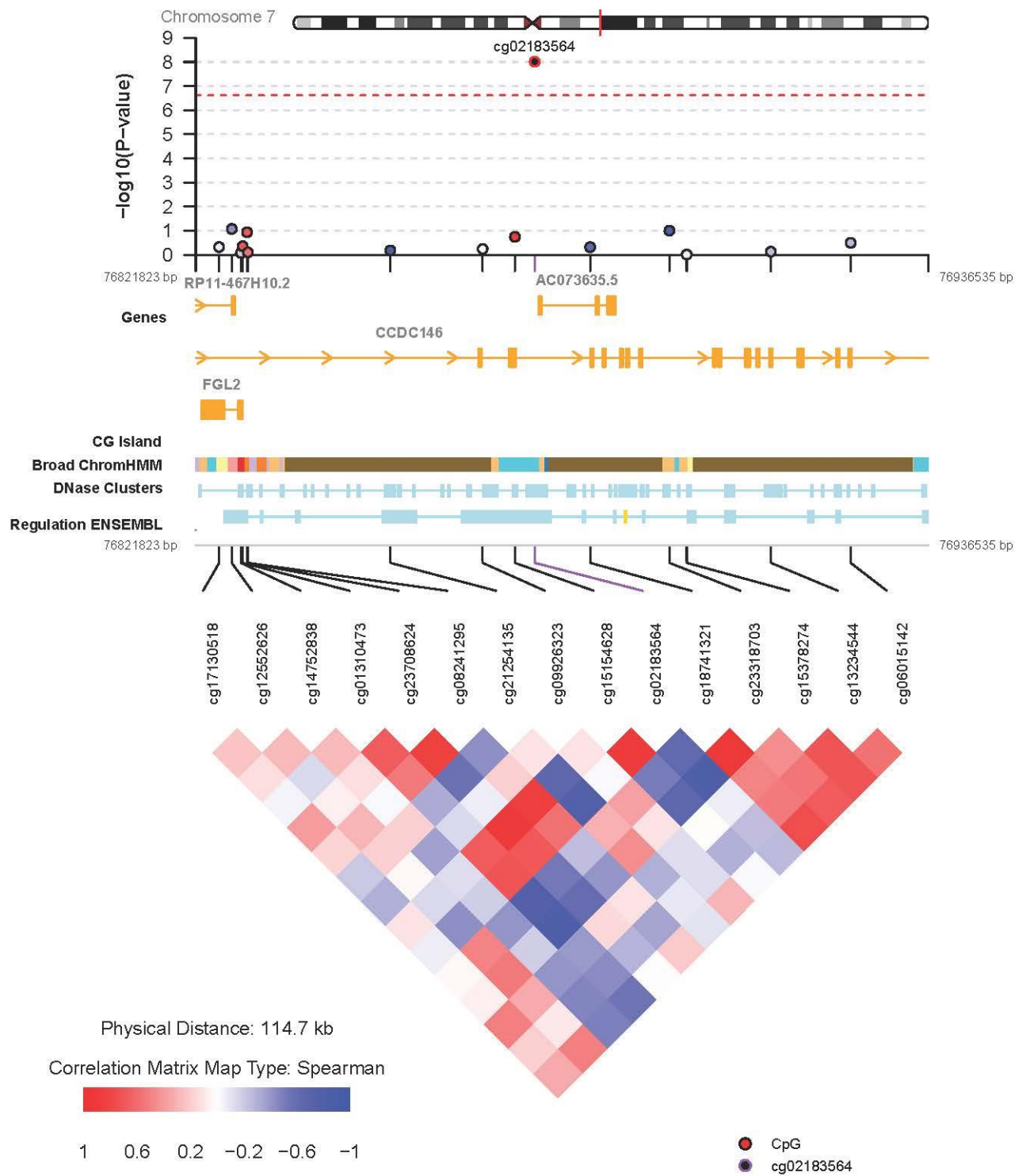


**Supplemental Figure 3:** Local association plots describing the genomic region for each of the significant DMP (top panel), the functional annotation (middle panel) and the pattern of co-methylation at individual CpG sites at a) cg00024471, b) cg02183564, c) cg01695994, d) cg19837174, e) cg03445151 and f) cg20065905. Co-methylation relationships are derived from BSGS participants.

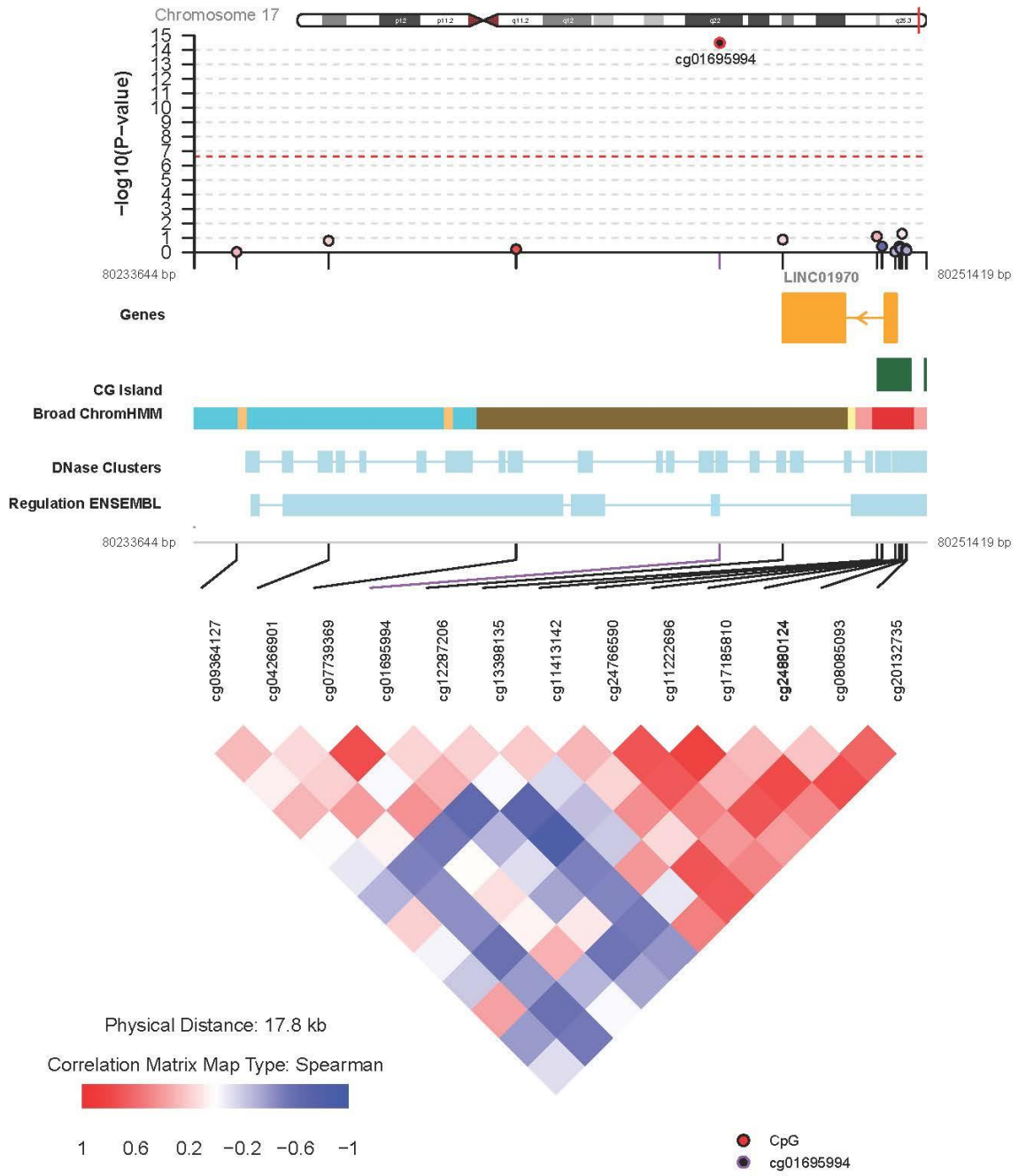
a)



b)

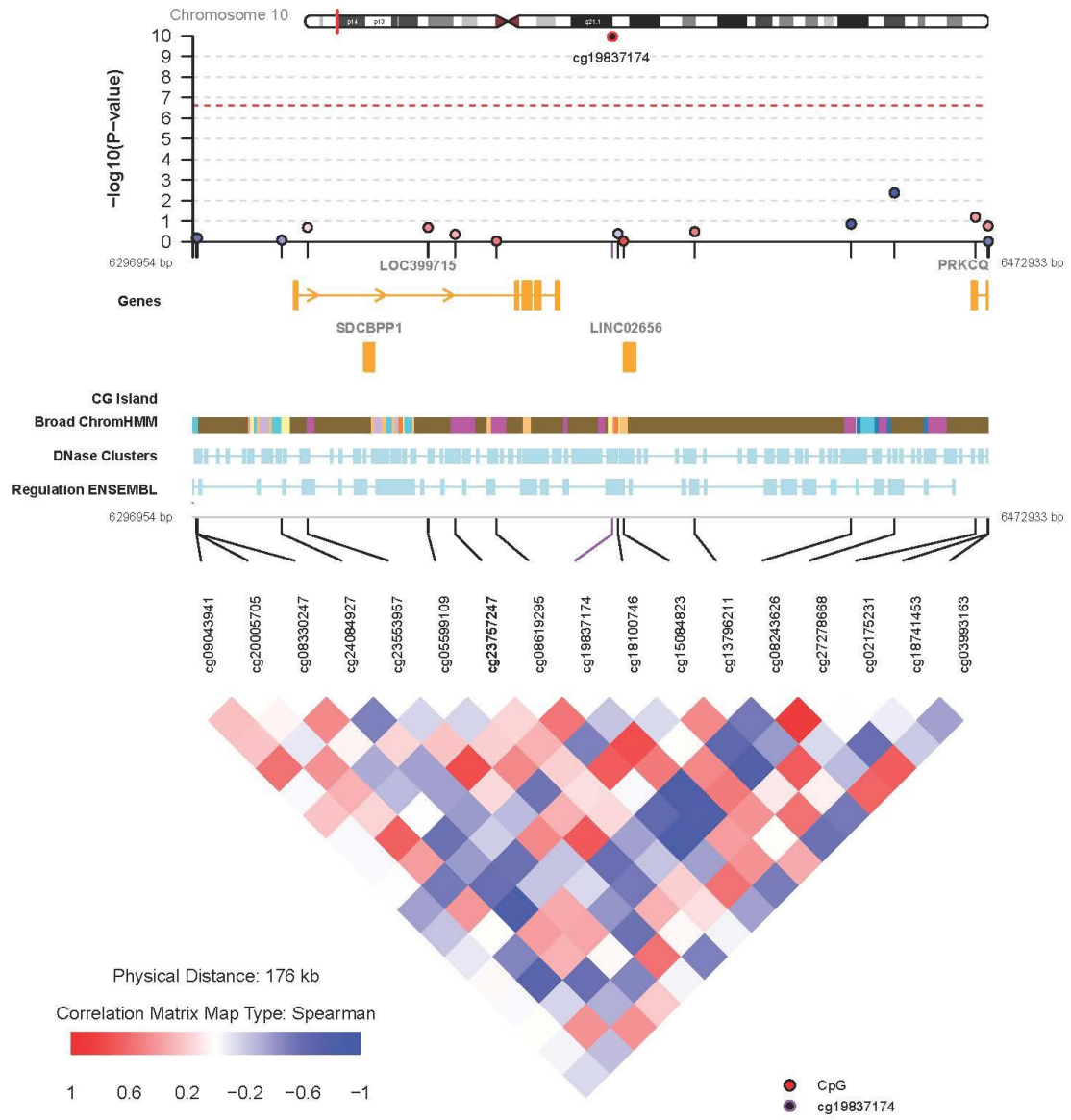


c)



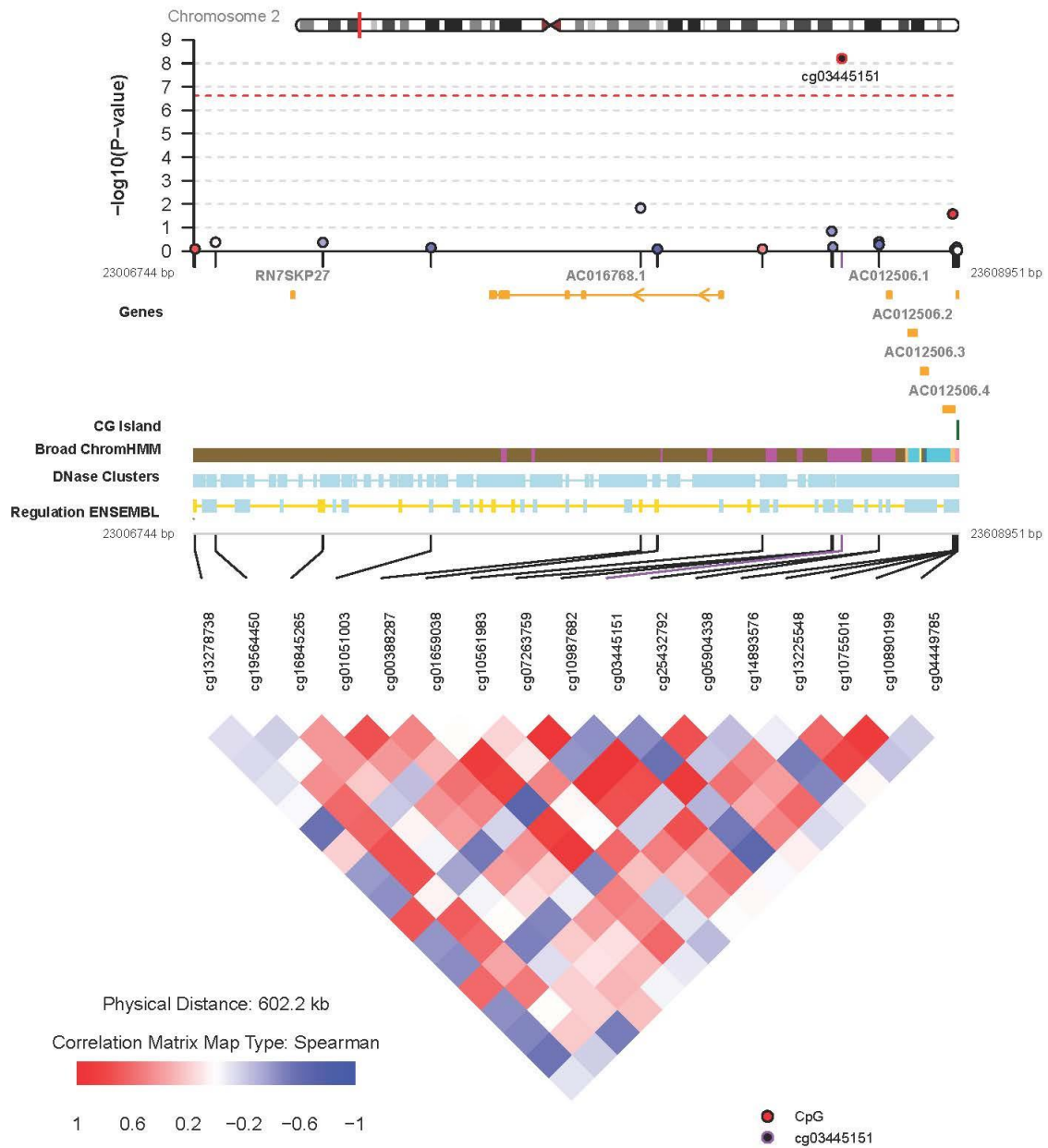
d)

d)

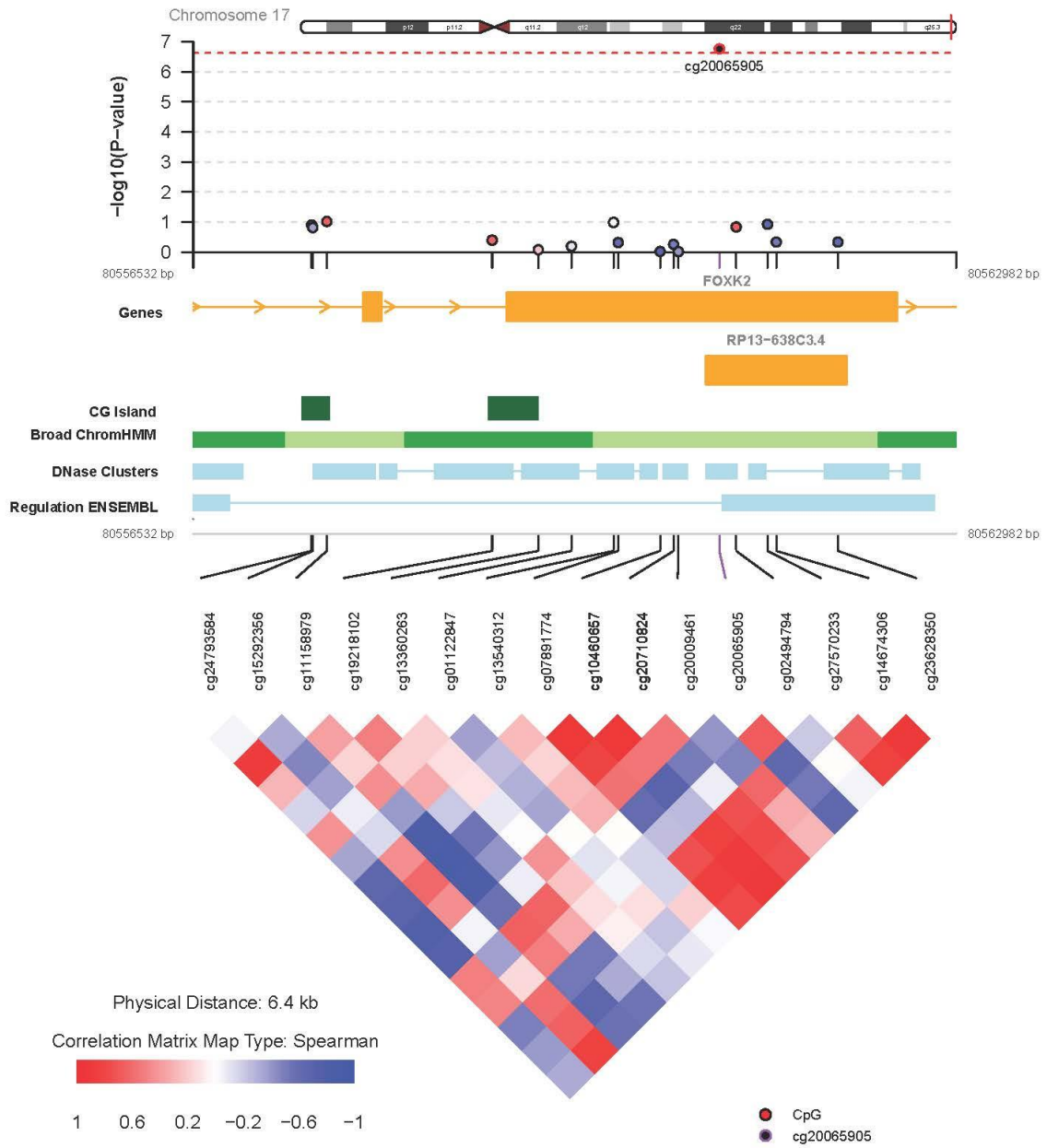




e)



f)



**Supplemental table 1.** Differentially methylated positions associated with fT3 meeting suggestive threshold

CpG site	Chr	Position (hg19)	Gene	Location	BSGS (n)	BSGS $\beta$	BSGS P-value	Raine (n)	Raine $\beta$	Raine P-value	Meta-analysis (n)	Meta-analysis $\beta$	Meta-analysis P-value
cg00414041	6	166944284	<i>RPS6KA2</i>	Intron	563	1.84	4.62E-6	863	0.68	3.65E-2	1426	1.16	4.28E-6
cg02311864	6	47215645	<i>TNFRSF21</i>	Intron 4	562	-1.55	7.44E-5	863	-0.84	4.85E-3	1425	-1.10	3.26E-6
cg06983052	1	90288099	<i>LRRC8D</i>	Intron 1	563	-1.53	3.81E-9	863	-0.21	2.66E-1	1426	-0.69	8.43E-6
cg09737870	6	33036717	<i>HLA-DPA1</i>	Intron	562	-1.39	6.06E-4	863	-1.06	2.35E-3	1425	-1.21	5.48E-6
cg13821176	8	126448338	<i>TRIB1</i>	Exon	563	-1.38	8.56E-7	863	-0.43	2.43E-2	1426	-0.74	3.41E-6
cg14108380	9	139299357	<i>SDCCAG3/ ENTR1</i>	Intron	563	1.21	7.10E-6	863	0.51	7.88E-2	1426	0.88	7.27E-6
cg18518074	11	64642317	<i>EHD1</i>	Intron	563	-0.91	8.98E-5	863	-0.58	7.12E-3	1426	-0.73	3.38E-6
cg18828762	15	90791294	<i>CIB1</i>	Intron 1	563	1.58	8.35E-7	863	0.49	9.54E-2	1426	1.00	4.32E-6
cg19495013	12	52214119	<i>FIGNL2</i>	Exon 2	555	1.77	7.37E-6	863	0.72	3.74E-2	1418	1.18	5.87E-6
cg20146909	1	90289611	<i>LRRC8D</i>	Intron 1	563	-1.88	2.41E-8	863	-0.44	8.53E-2	1426	-0.98	1.76E-6
cg24842354	1	2004058	<i>PRKCZ</i>	Intron 4	563	1.39	7.56E-6	863	0.62	1.77E-2	1426	0.94	2.49E-6
cg26313511	3	125053816	<i>ZNF148</i>	Intron	563	0.55	4.82E-4	863	0.47	8.73E-4	1426	0.51	1.46E-6

Abbreviations: Chr, chromosome; BSGS, Brisbane Systems Genetics Study.

**Supplemental table 2.** Differentially methylated positions associated with fT4 meeting suggestive threshold

CpG site	Chr	Position (hg19)	Gene	Location	BSGS (n)	BSGS $\beta$	BSGS <i>P</i> -value	Raine (n)	Raine $\beta$	Raine <i>P</i> -value	Meta-analysis (n)	Meta-analysis $\beta$	Meta-analysis <i>P</i> -value
cg01033822	4	126572326	Intergenic	-	563	-1.31	9.53E-5	863	-0.88	2.79E-3	1426	-1.08	1.50E-6
cg03638180	17	65373764	<i>PITPNC1</i>	Exon 1	563	0.63	7.29E-2	863	1.31	7.89E-6	1426	1.03	4.73E-6
cg06898279	14	60629192	<i>DHRS7/ PCNXL4</i>	Intron	563	1.56	1.62E-7	863	0.26	4.01E-1	1426	0.94	9.54E-6
cg16886828	19	5032663	<i>KDM4B</i>	Intron	563	1.39	3.63E-4	863	0.89	2.17E-3	1426	1.06	4.72E-6
cg19097648	5	115117462	<i>ATG12</i>	Exon 1	563	1.14	1.61E-5	863	0.53	5.06E-2	1426	0.84	9.02E-6
cg25314532	22	38349562	<i>C22orf23</i>	Various	562	1.14	1.05E-3	863	0.95	1.30E-3	1425	1.03	4.98E-6
cg25758137	3	105145479	<i>ALCAM</i>	Intron 1	563	-1.75	6.11E-6	863	-0.66	2.22E-2	1426	-1.05	5.01E-6
cg26747948	10	118390498	<i>PNLIPRP2</i>	Intron	563	-0.99	2.22E-4	863	-0.78	8.64E-3	1426	-0.90	7.35E-6

Abbreviations: Chr, chromosome; BSGS, Brisbane Systems Genetics Study.

**Supplemental table 3.** Differentially methylated positions associated with TSH meeting suggestive threshold

CpG site	Chr	Position (hg19)	Gene	Location	BSGS (n)	BSGS $\beta$	BSGS P-value	Raine (n)	Raine $\beta$	Raine P-value	Meta-analysis (n)	Meta-analysis $\beta$	Meta-analysis P-value
cg02883161	12	120807618	Intergenic	-	563	-0.15	3.60E-2	863	-0.30	3.09E-6	1426	-0.24	1.01E-6
cg03720100	6	30720264	Intergenic	-	563	-0.09	3.57E-4	863	-0.08	6.99E-3	1426	-0.09	8.01E-6
cg04222728	7	138549666	<i>KIAA1549</i>	Intron	563	0.21	1.02E-3	863	0.18	2.17E-3	1426	0.20	7.79E-6
cg06233738	16	89459257	<i>ANKRD11</i>	Intron	561	0.22	3.82E-3	863	0.23	4.04E-5	1424	0.23	5.49E-7
cg09226051	1	247611503	<i>NLRP3</i>	Intron	561	0.21	2.77E-3	863	0.25	5.34E-4	1424	0.23	5.50E-6
cg12930262	18	12283427	Intergenic	-	563	0.31	1.57E-5	863	0.15	4.05E-2	1426	0.23	7.35E-6
cg18355146	13	46550832	<i>ZC3H13</i>	Intron	563	0.23	1.57E-3	863	0.22	4.91E-4	1426	0.22	2.75E-6
cg18527751	18	43756134	<i>C18orf25</i>	Intron 1	560	0.16	1.33E-2	863	0.21	1.50E-4	1423	0.19	7.38E-6
cg18990365	2	183106125	<i>PDE1A</i>	Intron	563	0.19	2.39E-4	863	0.16	5.43E-3	1426	0.18	4.54E-6
cg21429780	4	140779949	<i>MAML3</i>	Intron	563	0.18	3.35E-4	863	0.17	2.70E-3	1426	0.17	3.21E-6
cg22798925	20	57464129	<i>GNAS</i>	Intron	563	-0.20	3.37E-3	863	-0.22	7.36E-4	1426	-0.21	7.70E-6
cg22801866	7	5459420	<i>TNRC18</i>	Intron	563	-0.31	1.59E-5	863	-0.13	9.80E-3	1426	-0.20	3.68E-6
cg25829531	20	2648594	Intergenic	-	562	0.37	3.81E-7	863	0.13	7.53E-2	1425	0.25	8.94E-7
cg25951934	5	172711054	Intergenic	-	563	-0.24	4.70E-4	863	-0.18	4.30E-3	1426	-0.21	7.85E-6

Abbreviations: Chr, chromosome; BSGS, Brisbane Systems Genetics Study.