

	<i>Mean Age</i>	<i>p - value</i>
t(1;11) Carriers	49	0.045
t(1;11) Non-carriers	37	

**Supplementary Table 1** Comparison of ages between t(1;11) carriers and non-carriers

Shown are the mean ages of t(1;11) carriers and non-carriers, and unpaired t-test *p*-value comparing between-group age.

	<i>Males</i>	<i>Females</i>	<i>p-value</i>
t(1;11) Carriers	8	9	1
t(1;11) Non-carriers	12	12	

**Supplementary Table 2** Comparison of gender between t(1;11) carriers and non-carriers

Shown are the counts for male and females amongst t(1;11) carriers and non-carriers, and Fisher's exact *p*-value.

	<i>CD8<sup>+</sup> T-Cells</i>	<i>CD4<sup>+</sup> T-Cells</i>	<i>Natural Killer Cells</i>	<i>B-Cells</i>	<i>Monocytes</i>	<i>Granulocytes</i>
Mean proportion in t(1;11) Carriers	0.05	0.15	0.06	0.06	0.07	0.62
Mean proportion in t(1;11) Non-carriers	0.05	0.16	0.06	0.05	0.07	0.62
<i>p- value</i>	0.7	0.58	0.5	0.41	0.85	0.87

**Supplementary Table 3** Comparison of estimated cellular composition of whole blood between (1;11) carriers and non-carriers

Shown are the mean estimated proportions for blood cell types in t(1;11) carriers and non-carriers, and unpaired t-test *p*-values for each cell type.

<i>GO Term</i>	<i>Description</i>	<i>Class</i>	<i>Enrichment</i>	<i>p-value</i>	<i>q-value</i>
GO:0043005	neuron projection	Component	1.73	2.29 X 10 <sup>-9</sup>	3.72 X 10 <sup>-6</sup>
GO:0042995	cell projection	Component	1.44	3.63 X 10 <sup>-7</sup>	0.0003
GO:0030425	dendrite	Component	1.43	2.10 X 10 <sup>-6</sup>	0.0009
GO:0009653	anatomical structure morphogenesis	Process	1.5	6.49 X 10 <sup>-8</sup>	0.0009
GO:0097458	neuron part	Component	1.96	1.93 X 10 <sup>-6</sup>	0.001
GO:0009987	cellular process	Process	1.33	5.98 X 10 <sup>-7</sup>	0.002
GO:0048562	embryonic organ morphogenesis	Process	4.36	4.93 X 10 <sup>-7</sup>	0.0022
GO:0048856	anatomical structure development	Process	1.07	4.14 X 10 <sup>-7</sup>	0.0028
GO:0048731	system development	Process	1.72	1.04 X 10 <sup>-6</sup>	0.0028
GO:0030424	axon	Component	1.12	3.05 X 10 <sup>-5</sup>	0.0083
GO:0044444	cytoplasmic part	Component	4.26	2.75 X 10 <sup>-5</sup>	0.0089
GO:0032502	developmental process	Process	1.3	6.12 X 10 <sup>-6</sup>	0.0093
GO:0010646	regulation of cell communication	Process	1.25	4.91 X 10 <sup>-6</sup>	0.0096
GO:0044763	single-organism cellular process	Process	1.1	5.69 X 10 <sup>-6</sup>	0.0097
GO:0050793	regulation of developmental process	Process	1.21	4.54 X 10 <sup>-6</sup>	0.01
GO:0048812	neuron projection morphogenesis	Process	2.26	8.99 X 10 <sup>-6</sup>	0.012
GO:0009887	organ morphogenesis	Process	2.15	8.55 X 10 <sup>-6</sup>	0.017
GO:0051960	regulation of nervous system development	Process	1.25	1.29 X 10 <sup>-5</sup>	0.014
GO:0023051	regulation of signaling	Process	1.54	1.52 X 10 <sup>-5</sup>	0.014
GO:0051094	positive regulation of developmental process	Process	1.41	1.43 X 10 <sup>-5</sup>	0.014
GO:0048583	regulation of response to stimulus	Process	1.25	1.24 X 10 <sup>-5</sup>	0.014
GO:0050807	regulation of synapse organisation	Process	6.99	2.31 X 10 <sup>-5</sup>	0.02
GO:0044424	intracellular part	Component	1.07	8.74 X 10 <sup>-5</sup>	0.02
GO:0070588	calcium ion transmembrane transport	Process	1.21	4.33 X 10 <sup>-5</sup>	0.021
GO:0051962	positive regulation of nervous system development	Process	1.93	2.97 X 10 <sup>-5</sup>	0.021
GO:0044708	single-organism behavior	Process	1.68	4.57 X 10 <sup>-5</sup>	0.022
GO:2000026	regulation of multicellular organismal development	Process	1.38	3.19 X 10 <sup>-5</sup>	0.022
GO:0045595	regulation of cell differentiation	Process	1.56	3.52 X 10 <sup>-5</sup>	0.022
GO:2001030	negative regulation of cellular glucuronidation	Process	1.34	4.33 X 10 <sup>-5</sup>	0.022
GO:0048858	cell projection morphogenesis	Process	1.98	2.90 X 10 <sup>-5</sup>	0.022
GO:0009888	tissue development	Process	1.63	3.75 X 10 <sup>-5</sup>	0.022
GO:0050767	regulation of neurogenesis	Process	25.57	3.46 X 10 <sup>-5</sup>	0.023q
GO:0031344	regulation of cell projection organisation	Process	25.57	3.98 X 10 <sup>-5</sup>	0.023

GO:1904224	negative regulation of glucuronosyltransferase activity	Process	25.57	4.33 X 10 <sup>-5</sup>	0.023
GO:0044767	single-organism developmental process	Process	2.35	2.87 X 10 <sup>-5</sup>	0.023
GO:1904223	regulation of glucuronosyltransferase activity	Process	1.79	4.33 X 10 <sup>-5</sup>	0.024
GO:0021852	pyramidal neuron migration	Process	17,640	5.67 X 10 <sup>-5</sup>	0.026
GO:0051239	regulation of multicellular organismal process	Process	1.29	6.25 X 10 <sup>-5</sup>	0.028
GO:0032990	cell part morphogenesis	Process	1.84	6.46 X 10 <sup>-5</sup>	0.028
GO:0003197	endocardial cushion development	Process	1.45	7.97 X 10 <sup>-5</sup>	0.028
GO:2001029	regulation of cellular glucuronidation	Process	2.01	7.94 X 10 <sup>-5</sup>	0.029
GO:0045597	positive regulation of cell differentiation	Process	1.75	7.08 X 10 <sup>-5</sup>	0.029
GO:0052697	xenobiotic glucuronidation	Process	46.22	7.94 X 10 <sup>-5</sup>	0.029
GO:2000467	positive regulation of glycogen (starch) synthase activity	Process	22.72	7.90 X 10 <sup>-5</sup>	0.03
GO:0046578	regulation of Ras protein signal transduction	Process	22.72	7.55 X 10 <sup>-5</sup>	0.03
GO:0048598	embryonic morphogenesis	Process	21.83	7.86 X 10 <sup>-5</sup>	0.031
GO:0051240	positive regulation of multicellular organismal process	Process	1.35	9.01 X 10 <sup>-5</sup>	0.031
GO:0048513	organ development	Process	1.43	0.0001	0.034
GO:0034702	ion channel complex	Component	1.81	0.0002	0.035
GO:0072300	positive regulation of metanephric glomerulus development	Process	213.82	0.0001	0.037
GO:0005783	endoplasmic reticulum	Component	5.76	0.0003	0.041
GO:0005768	endosome	Component	1.64	0.0003	0.042
GO:0014069	postsynaptic density	Component	35.18	0.0003	0.043
GO:0048167	regulation of synaptic plasticity	Process	1.79	0.0001	0.044
GO:0044699	single-organism process	Process	1.07	0.0001	0.044
GO:0044216	other organism cell	Component	5.29	0.0003	0.044
GO:0044297	cell body	Component	1.43	0.0002	0.045
GO:0050804	modulation of synaptic transmission	Process	2.5	0.0001	0.045
GO:0043524	negative regulation of neuron apoptotic process	Process	2.63	0.0002	0.046
GO:0033387	putrescine biosynthetic process from ornithine	Process	22.88	0.0002	0.047
GO:0031225	anchored component of membrane	Component	1.38	0.0004	0.048
GO:0044463	cell projection part	Component	4.34	0.0004	0.049

**Supplementary Table 4** Summary of GO terms enriched amongst differentially methylated genes in t(1;11) carriers

For each GO term, Supplementary Table summarises the GO identifier, the GO description, the GO class, enrichment, the enrichment p-values, and enrichment FDR q-values for genes showing the most differential methylation in t(1,11) carriers compared to non-carriers. Enrichment is defined as  $(b/n) / (B/N)$ , where  $b$  = the number of genes at the top of the p-value ranked list that is associated with a given GO term,  $n$  = the number of genes at the top of the p-value-ranked gene list,  $B$  = the total number of genes associated with a given GO term, and  $N$  = the total number of genes.

Gene(s)	Feature(s)	Region	Probes	DMR <i>p</i> -value
<i>TNXB</i>	Body	Chr6:32063516-32065113	51	2.46 x 10 <sup>-13</sup>
NA	IGR	Chr3:196704439-196707088	5	7.89 x 10 <sup>-10</sup>
<i>C11orf75</i>	TSS1500	Chr11:93277097-93277255	3	1.67 x 10 <sup>-9</sup>
NA; <i>PRRT1</i>	IGR, 3'UTR	Chr6:32115866-32116728	14	2.60 x 10 <sup>-9</sup>
<i>RNF5P1;AGPAT1</i>	TSS1500, TSS200	Chr6:32145233-32145902	20	6.26 x 10 <sup>-9</sup>
<i>GABRG1</i>	TSS1500, TSS200, 5'UTR	Chr4:46125801-46126455	7	7.27 x 10 <sup>-9</sup>
<i>KRTAP5-9</i>	TSS1500, TSS200, 5'UTR	Chr11:71259142-71259846	5	3.17 x 10 <sup>-8</sup>
<i>CYP2E1</i>	Body	Chr10:135343047-135343426	3	5.93 x 10 <sup>-8</sup>
<i>XRR1</i>	TSS200	Chr11:74660246-74660274	4	6.07 x 10 <sup>-8</sup>
<i>RHOD</i>	3'UTR	Chr11:66839183-66839543	3	8.99 x 10 <sup>-8</sup>
<i>TUBGCP5</i>	TSS1500, TSS200	Chr15:22833108-22833236	3	1.58 x 10 <sup>-7</sup>
<i>TRAK1</i>	TSS1500, Body, 1stExon	Chr3:42201087-42202130	6	1.64 x 10 <sup>-7</sup>
<i>PSMB8</i>	3'UTR, Body	Chr6:32807898-32810304	22	3.32 x 10 <sup>-7</sup>
NA	IGR	Chr1:209526301-209528771	3	3.46 x 10 <sup>-7</sup>
NA	IGR	Chr6:159359910-159360236	3	1.48 x 10 <sup>-6</sup>
<i>RTKN</i>	TSS1500	Chr2:74669347-74669415	4	1.94 x 10 <sup>-6</sup>
NA; <i>KLHL30</i>	IGR, TSS1500, TSS200	Chr2:239043942-239047460	9	2.67 x 10 <sup>-6</sup>
<i>PCSK6</i>	Body	Chr15:101991031-101992367	5	2.8 x 10 <sup>-6</sup>
<i>MIR663</i>	TSS1500	Chr20:26190290-26190418	3	3.66 x 10 <sup>-6</sup>
<i>ZNF385D</i>	Body, 1stExon	Chr3:21791767-21792729	4	3.82 x 10 <sup>-6</sup>
<i>TNF</i>	1stExon	Chr6:31543557-31543767	6	4.05 x 10 <sup>-6</sup>
<i>BNIP3</i>	Body	Chr10:133793398-133793556	3	9.21 x 10 <sup>-6</sup>
<i>TMEM131</i>	Body	Chr2:98377310-98378420	3	9.58 x 10 <sup>-6</sup>
<i>LTA</i>	TSS200, 5'UTR, 1stExon	Chr6:31540040-31540705	11	9.59 x 10 <sup>-6</sup>
NA	IGR	Chr17:41380728-41383399	5	9.98 x 10 <sup>-6</sup>
<i>MIXL1</i>	TSS1500	Chr1:226411005-226411085	4	1.06 x 10 <sup>-5</sup>
<i>C17orf98</i>	Body, 1stExon	Chr17:36997274-36997566	3	1.3 x 10 <sup>-5</sup>
<i>FAM83A</i>	Body	Chr8:124217614-124217906	3	1.42 x 10 <sup>-5</sup>
<i>SPI40</i>	TSS200, 5'UTR, Body	Chr2:231090159-231091121	5	1.56 x 10 <sup>-5</sup>
<i>MEST</i>	5'UTR	Chr7:130131819-130131937	8	3 x 10 <sup>-5</sup>
<i>MOV10L1</i>	TSS200, Body	Chr22:50584735-50585710	7	3.02 x 10 <sup>-5</sup>
NA	IGR	Chr5:101117938-101120956	5	3.37 x 10 <sup>-5</sup>
NA	IGR	Chr2:54934730-54938012	4	3.42 x 10 <sup>-5</sup>

<i>LOC399815</i>	TSS200	Chr10:124638974-124638992	3	3.43 x 10 <sup>-5</sup>
<i>STX6</i>	TSS200	Chr1:180992101-180992126	3	3.44 x 10 <sup>-5</sup>
NA	IGR	Chr7:156888064-156890971	5	3.65 x 10 <sup>-5</sup>
NA	IGR	Chr14:54814555-54817362	4	5.68 x 10 <sup>-5</sup>
NA	IGR	Chr7:73001195-73003686	3	6.35 x 10 <sup>-5</sup>
NA	IGR	Chr4:77341749-77342075	3	6.66 x 10 <sup>-5</sup>
<i>TDH</i>	Body	Chr8:11203736-11204163	4	7.48 x 10 <sup>-5</sup>
<i>SMYD2</i>	Body	Chr1:214476582-214477761	3	9.03 x 10 <sup>-5</sup>
<i>IGSF9B</i>	Body	Chr11:133820356-133821733	4	9.05 x 10 <sup>-5</sup>
<i>TAP1</i>	Body	Chr6:32819956-32820360	7	9.06 x 10 <sup>-5</sup>
NA	IGR	Chr1:39281563-39282050	4	9.11 x 10 <sup>-5</sup>
NA	IGR	Chr10:134898718-134899190	3	9.24 x 10 <sup>-5</sup>
NA	IGR	Chr11:123939376-123941869	3	0.0001
NA	IGR	Chr1:147799913-147804738	9	0.0001
<i>HLA-DPA1</i>	Body, 3'UTR	Chr6:33033283-33037541	16	0.0001
<i>MIR548N</i>	Body	Chr2:179387372-179388545	3	0.0001
<i>LIME1</i>	Body	Chr20:62369366-62369583	3	0.0001
NA	IGR	Chr7:1208305-1210932	3	0.0001
<i>VSTM1</i>	TSS200, Body, 1stExon	Chr19:54566357-54567319	3	0.0001
NA	IGR	Chr5:61027075-61030044	6	0.0001
<i>ZNF677</i>	TSS200	Chr19:53758279-53758315	3	0.0001
NA	IGR	Chr11:8290652-8290978	3	0.0002
<i>ACP5</i>	TSS1500	Chr19:11689791-11689944	5	0.0002
<i>PSKH2</i>	TSS1500, TSS200	Chr8:87082001-87082129	5	0.0002
<i>ATP8A2</i>	Body	Chr13:26586108-26586400	3	0.0002
<i>VAX2</i>	TSS1500	Chr2:71126945-71127001	3	0.0002
<i>LRP1B</i>	TSS200	Chr2:142889366-142889402	3	0.0003
<i>C2orf54</i>	TSS1500	Chr2:241836300-241836518	3	0.0003
<i>KCNIP1; KCNMB1</i>	TSS200, Body	Chr5:169815897-169816859	4	0.0003
NA	IGR	Chr8:832849-833211	4	0.0003
<i>C6orf48</i>	5'UTR	Chr6:31802972-31803220	9	0.0004
<i>NHEDC1</i>	TSS200, 1stExon	Chr4:103940811-103940897	3	0.0004
<i>HEATR2</i>	Body, 3'UTR	Chr7:824351-826059	6	0.0004
NA	IGR	Chr10:115860117-115860473	3	0.0004

<i>OR2L13</i>	1stExon	Chr1:248100542-248100657	4	0.0005
<i>RPTOR</i>	Body	Chr17:78809217-78810354	3	0.0005
<i>ADARB2</i>	Body	Chr10:1452489-1453586	3	0.0005
<i>KLHL29</i>	Body	Chr2:23885619-23886838	3	0.0005
NA	IGR	Chr6:33870717-33874881	16	0.0006
<i>C2CD4D</i>	Body	Chr1:151810808-151810978	4	0.0006
<i>KATNAL2</i>	5'UTR	Chr18:44561939-44562173	5	0.0006
NA	IGR	Chr1:46632418-46632744	4	0.0007
NA	IGR	Chr1:117316713-117319422	6	0.0007
<i>RHOV</i>	Body	Chr1:228872106-228872264	3	0.0007
<i>ADAMTS2</i>	Body	Chr5:178594504-178594662	3	0.0007
<i>NFE2L1</i>	TSS1500	Chr17:46124661-46124789	3	0.0007
<i>TBCD</i>	Body	Chr17:80759197-80760159	3	0.0007
<i>RPI</i>	Body	Chr8:55533808-55534034	4	0.0007
<i>DPYSL3</i>	Body	Chr5:146832152-146832444	5	0.0008
<i>DZIP1L</i>	TSS1500	Chr3:137834643-137834771	3	0.0009
NA	IGR	Chr12:29302148-29302314	3	0.0009
NA	IGR	Chr12:114916775-114919883	6	0.0010
<i>MSXI</i>	Body	Chr4:4864284-4864576	6	0.0010
NA	IGR	Chr6:32848233-32852184	3	0.0011
<i>MAPT</i>	1stExon	Chr17:43971863-43971971	4	0.0011
<i>ERMAP</i>	5'UTR, Body	Chr1:43295986-43296972	4	0.0012
<i>TRIM10</i>	3'UTR, Body	Chr6:30118914-30123074	24	0.0012
NA; <i>RPRM</i>	IGR, 3'UTR	Chr2:15433734-154334094	5	0.0013
NA	IGR	Chr1:160950485-160953893	5	0.0013
NA	IGR	Chr10:133528532-133530912	4	0.0016
<i>HOXC11</i>	3'UTR	Chr12:54369487-54373005	6	0.0017
<i>TSPAN19;LRR1Q1</i>	TSS200, 5'UTR	Chr12:85430071-85430601	8	0.0018
<i>TRIM15</i>	3'UTR	Chr6:30140125-30140546	8	0.0019
<i>PRICKLE1</i>	Body, 3'UTR	Chr12:42850912-42854914	7	0.0019
<i>STAT3</i>	Body	Chr17:40489088-40490266	5	0.0021
NA; <i>COX19</i>	IGR, 3'UTR	Chr7:1001886-1005509	9	0.0022
NA	IGR	Chr8:53325115-53327858	8	0.0023
<i>SI00A13; SI00A14</i>	TSS1500, 3'UTR	Chr1:153589312-153593314	5	0.0036

<i>MICB</i>	Body	Chr6:31466095-31466266	4	0.0039
NA	IGR	Chr6:30094973-30095632	25	0.0040
<i>SLC6A12</i>	TSS200, 5'UTR	Chr12:322249-322914	9	0.0044
<i>TNXB</i>	Body	Chr6:32054900-32055225	8	0.0063
NA	IGR	Chr5:3102528-3106063	4	0.0064
<i>TMCO3</i>	Body	Chr13:114192835-114194543	11	0.0064
<i>ASCL2</i>	TSS1500	Chr11:2293053-2293275	9	0.0064
<i>VARS2</i>	Body	Chr6:30883736-30885444	14	0.0074
<i>B3GALT4</i>	1stExon	Chr6:33245445-33245846	20	0.0090
<i>NOM1</i>	Body	Chr7:156755232-156756616	6	0.0092
<i>ALPL</i>	5'UTR	Chr1:21877057-21877844	6	0.0105
<i>HLA-DPA1</i>	Body	Chr6:33040054-33041250	8	0.0121
<i>EHMT2</i>	Body	Chr6:31858853-31861146	20	0.0124
NA	IGR	Chr12:131700432-131703053	5	0.0166
<i>KLC2</i>	3'UTR	Chr11:66034892-66035327	14	0.0169
<i>CNTN4</i>	Body	Chr3:3079716-3080819	4	0.0224
<i>GNL1</i>	3'UTR	Chr6:30507466-30511643	15	0.0289
<i>PRDM16</i>	Body	Chr1:3209038-3210391	5	0.0380
<i>HCP5</i>	TSS1500, TSS200, 1stExon, Body, 3'UTR	Chr6:31429311-31433970	18	0.0392
NA	IGR	Chr5:170762452-170765146	9	0.0408
<i>ARHGAP25</i>	TSS1500, 5'UTR, Body	Chr2:69001334-69002335	10	0.0428
<i>HSPAIL</i>	5'UTR, Body	Chr6:31778918-31782134	19	0.0498

**Supplementary Table 5** Summary of t(1;11)-associated DMRs identified by the probe lasso algorithm

Summary of the genes (if applicable), genomic features, hg19 genomic coordinates, number of probes and FDR-corrected p-value (q-value) associated with each DMR. “NA” in the “Gene” column represents intergenic regions (i.e. regions not annotated to a RefSeq gene). Genomic features are coded “IGR” for intergenic regions, “TSS200” and “TSS1500” for probes occurring within 200 and 1500 of a gene’s transcription start site, respectively; “5’UTR” and “3’UTR” for probes occurring within a gene’s 5’ and 3’ untranslated region, respectively, “1stExon” for probes occurring within the first exon of a gene, and “Body” for probes occurring within the gene body.



	<i>t(1;11) Non-carriers</i>	<i>t(1;11) Carriers</i>
Unaffected	18	
Recurrent MDD	2	3
Single episode MDD	2	3
Single episode MDD + generalised anxiety	1	
Generalised anxiety	1	
Conduct disorder (adolescent)		2
Single episode MDD + Conduct disorder (adolescent)		1
Cyclothymia		3
Bipolar Disorder I		2
Schizophrenia		2
Schizoaffective disorder		1

**Supplementary Table 6** Diagnosis counts within each group

Shown is a summary of psychiatric diagnoses in the family and the number of *t(1;11)* carriers and non-carriers with a given diagnosis.