

**Genome-Wide Association Study Identifies Novel Type II Diabetes Risk Loci in Jordan  
Subpopulations**

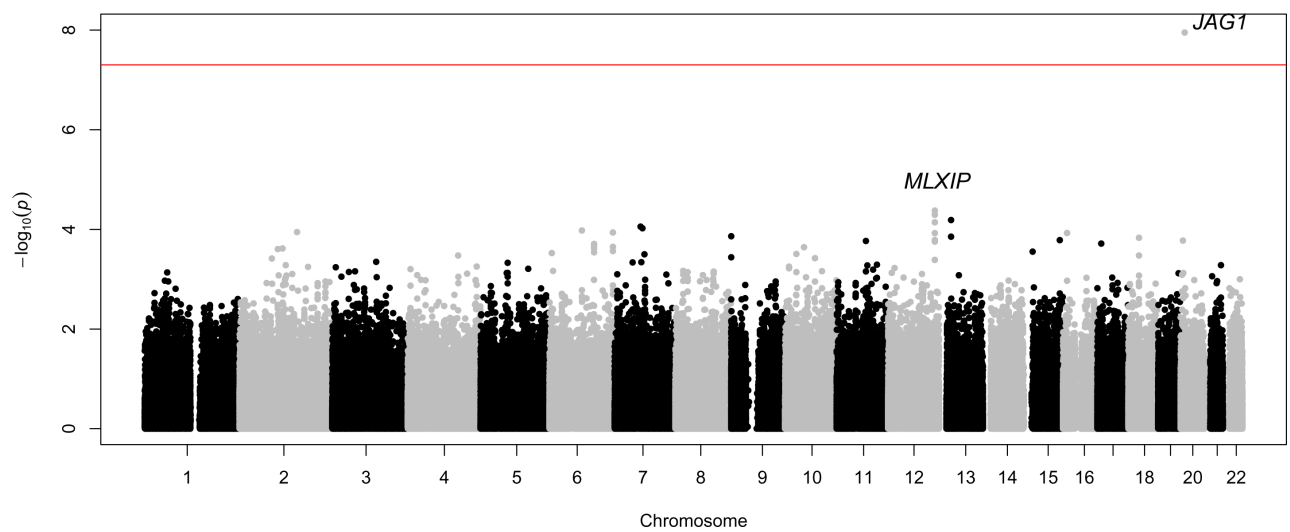
Rana Dajani, Jin Li, Zhi Wei, Michael E. March, Qianghua Xia, Yousef Khader, Nancy Hakooz, Raja Fatahallah, Mohammed El-Khateeb, Ala Arafat, Tareq Saleh, Abdel Rahman Dajani, Zaid Al-Abbadi, Mohamed Abdul Qader, Abdel Halim Shiyab, Anwar Bateiha, Kamel Ajlouni, Hakon Hakonarson

Supplementary Information

## Supplementary Figures

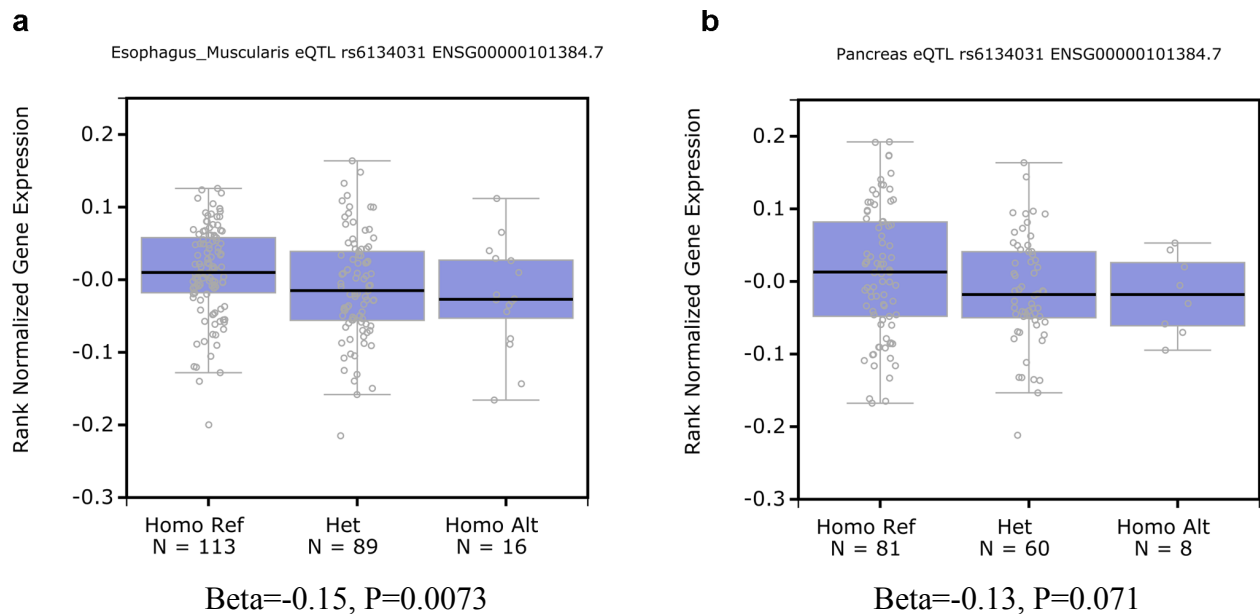
### Supplementary Figure 1. Manhattan plot of the result from the meta-analysis of Chechen and Circassian groups.

SNPs are sorted by chromosomal location along X axis against their  $-\log_{10}(P\text{-value})$  shown on Y axis. The horizontal line represents the genome-wide significance level  $p=5 \times 10^{-8}$ .



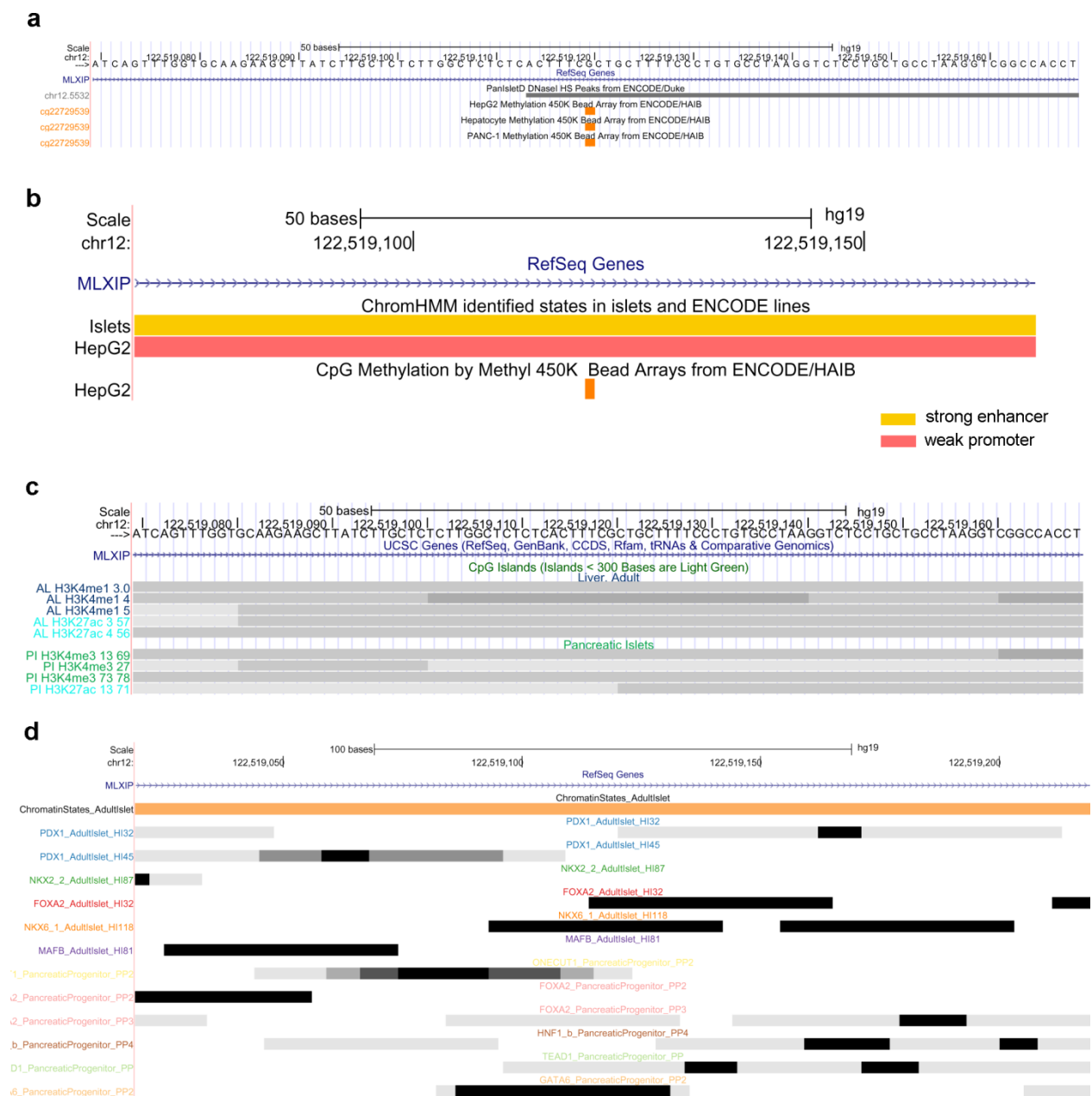
**Supplementary Figure 2: The association between SNP rs6134031 genotype and gene *JAG1* expression level in esophagus muscularis and pancreas.**

The relationship between SNP rs6134031 genotype and gene *JAG1* expression level was evaluated in GTEx Portal (GTEx Consortium 2015). Their correlation in **(a)** Esophagus muscularis and **(b)** Pancreas are shown. The different genotype groups of SNP rs6134031 are indicated on the X-axis, with C being the reference allele and T being the alternative allele. The Rank Normalized gene expression level of gene *JAG1* is shown on the Y-axis. The black line in the box plot denotes the median expression level in each genotype group. The bottom and the top border of each box represent the first quartile and the third quartile of the rank normalized gene expression level, respectively. The end of the lower whisker and that of the upper whisker represent the 1.5 interquartile range (IQR). The small grey circles denote *JAG1* expression level of each individual.



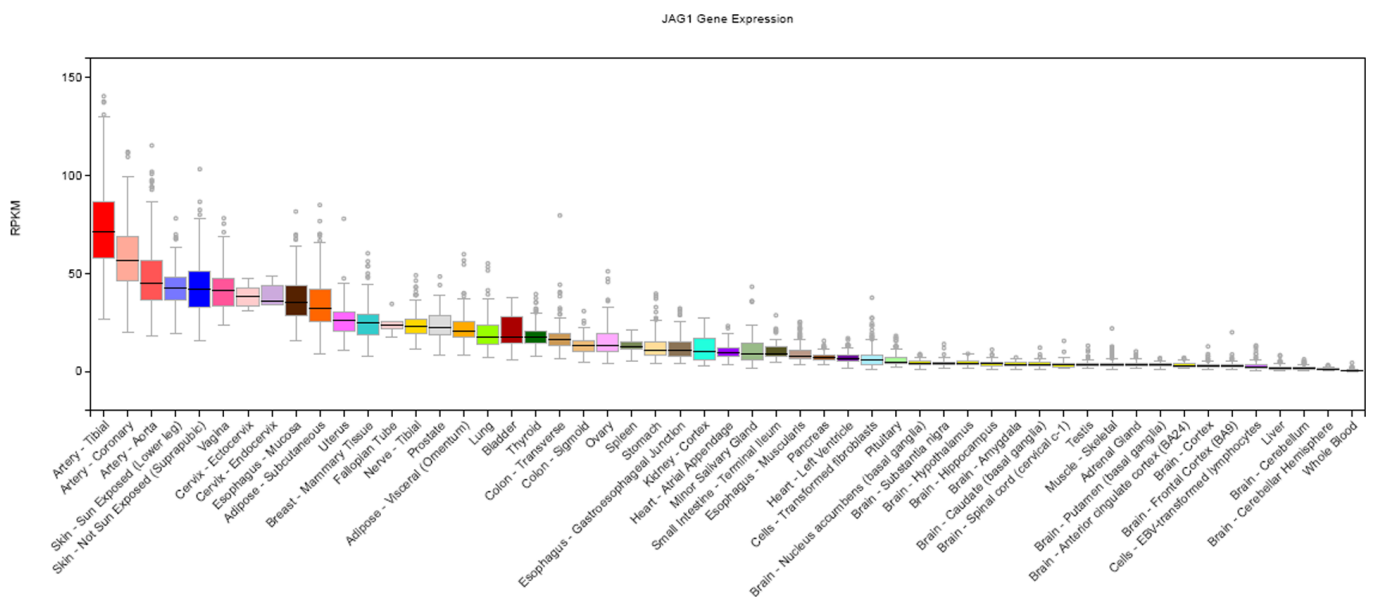
**Supplementary Figure 3.** Epigenetics profiles of the immediate genomic region of cg22729539.

**(a)** DNase hypersensitivity peaks in pancreatic islets; **(b)** chromatin states in pancreatic islets and human liver carcinoma cells HepG2; **(c)** histone markers in adult liver and pancreatic islets; **(d)** Transcription factor binding sites in pancreatic islets and pancreatic progenitor cells.



**Supplementary Figure 4: Box plot showing the expression level of *JAG1* gene in different human tissue/cell types, based on GTEx RNA-seq data.**

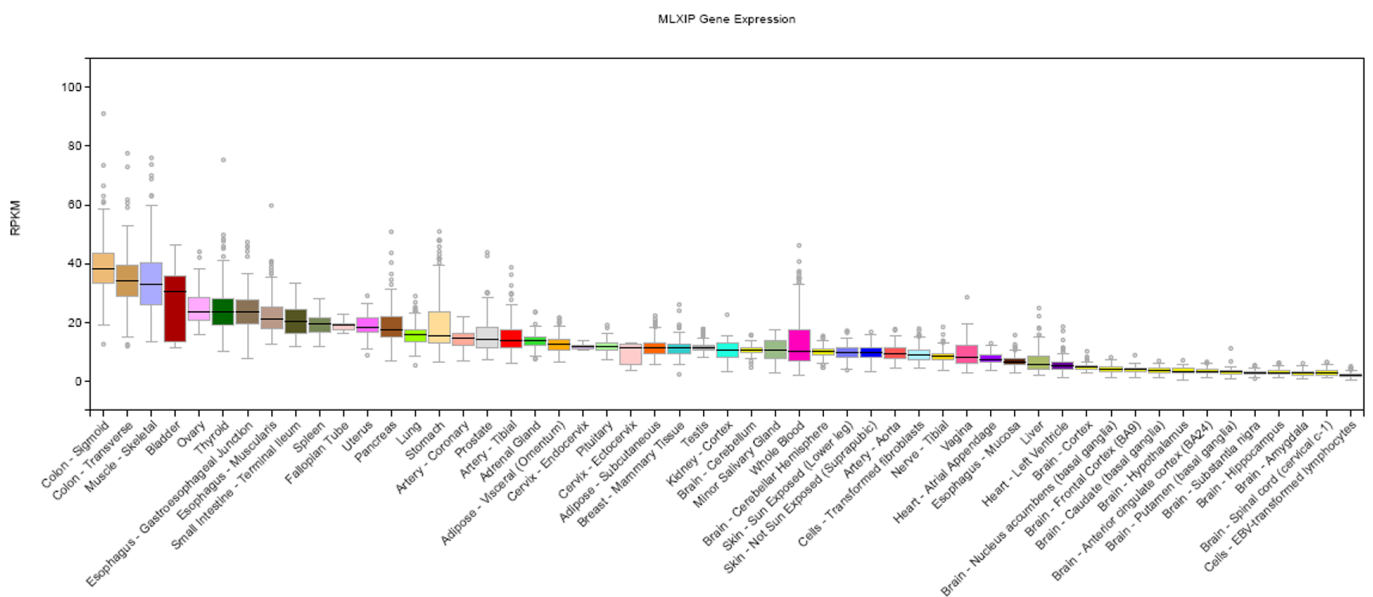
The plot was generated via GTEx (GTEx Consortium 2015) online portal. Tissue/cell types are indicated on the X-axis, and the normalized gene expression levels are indicated by the RPKM (Reads Per Kilobase of transcript per Million mapped reads) values on the Y-axis. The dark black line in each box shows the median expression level in each cell/tissue type, and the bottom/top border of each box indicates the first/third quartile of the RPKM. The end of the lower whisker and that of the upper whisker represent the lowest and the highest datum within the 1.5 interquartile range (IQR) of the lower quartile and the upper quartile, respectively; and the grey circles represent data points outside of this range.





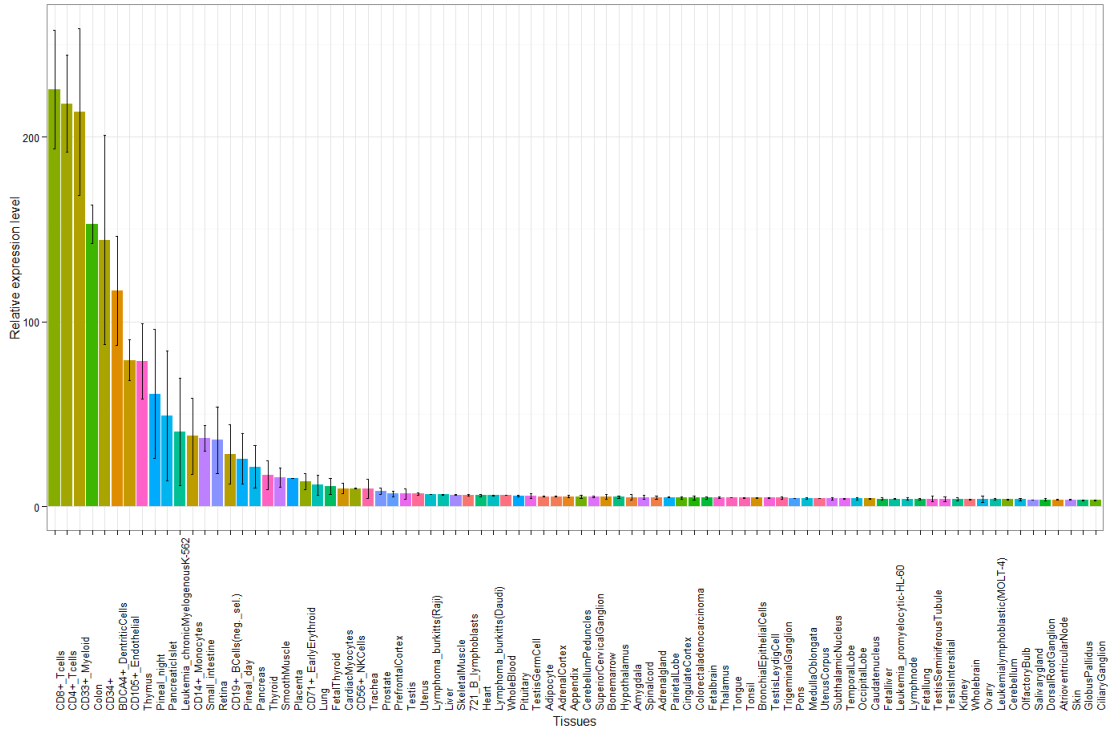
**Supplementary Figure 6: Box plot showing the expression level of *MLXIP* gene in different human tissue/cell types, based on GTEx RNA-seq data.**

The box plot was generated via GTEx (GTEx Consortium 2015) online portal. Tissue/cell types are indicated on the X-axis, and the normalized gene expression levels are indicated by the RPKM (Reads Per Kilobase of transcript per Million mapped reads) values on the Y-axis. The dark black line in each box shows the median expression level in each cell/tissue type, and the bottom/top border of each box indicates the first/third quartile of the RPKM. The end of the lower whisker and that of the upper whisker represent the lowest and the highest datum within the 1.5 interquartile range (IQR) of the lower quartile and the upper quartile, respectively; and the grey circles represent data points outside of this range.



**Supplementary Figure 7: Bar graph showing the expression level of *MLXIP* gene in different human tissue/cell types, based on BioGPS microarray data.**

The expression data were downloaded from BioGPS (Wu et al. 2016; Wu et al. 2009) web portal (<http://biogps.org/#goto=welcome>)

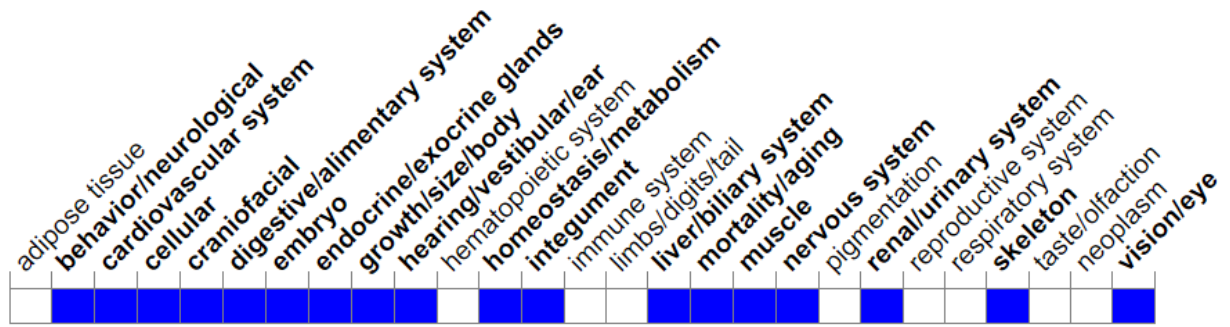




### Supplementary Figure 8: Summary of *JAG1* knockout mice phenotype.

The blue boxes indicate the presence of the defects. Information was extracted from

<http://www.informatics.jax.org/marker/MGI:1095416> (Blake et al. 2017; Finger et al. 2017).



## Supplementary Tables

**Supplementary Table 1: Top associations from Type 2 Diabetes GWAS of Circassian subpopulation.**

SNP	Chr	Pos(hg19)	Closest Gene	A1	OR (95% CI)	P-value
rs6134031	20	10752610	<i>JAG1</i>	T	9.48 (3.09,29.07)	8.36x10 <sup>-5</sup>
rs12403551	1	101864215	<i>RNU6-6</i>	A	4.09 (1.76,9.51)	1.06x10 <sup>-3</sup>
rs349488	5	62557698	<i>IPO11</i>	A	4.17 (1.77,9.80)	1.06x10 <sup>-3</sup>
rs11760752	7	73023062	<i>MLXIPL</i>	A	5.16 (1.92,13.89)	1.15x10 <sup>-3</sup>
rs11770924	7	122659240	<i>TAS2R16</i>	G	0.20 (0.07,0.53)	1.29x10 <sup>-3</sup>
rs11704261	22	33206863	<i>SYN3,TIMP3</i>	T	7.49 (2.19,25.69)	1.35x10 <sup>-3</sup>
rs7290713	22	33188545	<i>SYN3</i>	T	7.49 (2.19,25.69)	1.35x10 <sup>-3</sup>
rs2617892	18	28142539	<i>MIR302F</i>	C	2.74 (1.48,5.08)	1.36x10 <sup>-3</sup>
rs2433086	8	25530161	<i>CDCA2</i>	A	0.20 (0.08,0.54)	1.38x10 <sup>-3</sup>
rs10486867	7	70071920	<i>AUTS2</i>	A	0.27 (0.12,0.61)	1.54x10 <sup>-3</sup>

SNP – single nucleotide polymorphism; Chr – chromosome; Pos – Position; A1 – minor allele; OR – odds ratio; CI – confidence interval

**Supplementary Table 2: Top associations from Type 2 Diabetes GWAS of Chechen subpopulation.**

SNP	Chr	Pos(hg19)	Closest Gene	A1	OR (95% CI)	P-value
rs6134031	20	10752610	<i>JAG1</i>	T	9.84 (3.33,29.02)	3.45x10 <sup>-5</sup>
rs4398502	4	174819200	<i>FBXO8</i>	G	0.14 (0.06,0.36)	3.87x10 <sup>-5</sup>
rs12283277	11	80399178	<i>intergenic</i>	C	5.96 (2.55,13.96)	3.88x10 <sup>-5</sup>
rs203035	17	50069517	<i>CA10</i>	A	6.55 (2.67,16.08)	4.07x10 <sup>-5</sup>
rs203038	17	50070614	<i>CA10</i>	T	6.55 (2.67,16.08)	4.07x10 <sup>-5</sup>
rs188028	17	49991836	<i>CA10</i>	A	6.94 (2.73,17.64)	4.71x10 <sup>-5</sup>
rs203049	17	50078989	<i>CA10</i>	A	6.16 (2.56,14.82)	4.96x10 <sup>-5</sup>
rs12617659	2	121309759	<i>LOC84931</i>	T	11.43 (3.51,37.18)	5.17x10 <sup>-5</sup>
rs7264874	20	56045814	<i>CTCF</i>	T	14.65 (3.99,53.82)	5.27x10 <sup>-5</sup>
rs1945378	11	80429527	<i>intergenic</i>	G	6.08 (2.53,14.57)	5.28x10 <sup>-5</sup>

SNP – single nucleotide polymorphism; Chr – chromosome; Pos – Position; A1 – minor allele; OR – odds ratio; CI – confidence interval

**Supplementary Table 3: The histone marks, DNase hypersensitive sites near  
cg22729539 (chr12:122081214-122081214, hg38).**

Only cell lines which are biologically relevant to Type II Diabetes are shown. Data were extracted via Haploreg (Ward & Kellis 2012), based on Roadmap (Leung et al. 2015) and ENCODE datasets (Encode Project Consortium 2012).

Chr	Pos (hg38)	H3K4me1	H3K4me3	H3K27ac	H3K9ac	DNase	Proteins bound
12	122080733	E025,E063,E066,E087, E098,E107,E108,E120, E121	E025,E063,E066,E09 8,E107,E108,E120,E 121	E063,E066,E087,E0 98,E108,E120,E121	E025,E063,E066,E 087,E107,E108,E12 0,E121	E098,E120,E 121	CJUN, POL2, P300, RAD21
12	122080829	E025,E063,E066,E087, E098,E107,E108,E120, E121	E025,E063,E066,E09 8,E107,E108,E120,E 121	E063,E066,E087,E0 98,E108,E120,E121	E025,E063,E066,E 087,E107,E108,E12 0,E121	E121	POL2
12	122080943	E025,E063,E066,E087, E098,E107,E108,E120, E121	E025,E063,E066,E09 8,E107,E108,E120,E 121	E063,E066,E087,E0 98,E108,E120,E121	E025,E063,E066,E 087,E107,E108,E12 0,E121	E098	
12	122081053	E025,E063,E066,E087, E098,E107,E108,E120, E121	E025,E063,E066,E08 7,E098,E107,E108,E 120,E121	E063,E066,E087,E0 98,E108,E120,E121	E025,E063,E066,E 087,E107,E108,E12 0,E121		CEBPB
12	122081110	E025,E063,E066,E087, E098,E107,E108,E120, E121	E025,E063,E066,E08 7,E098,E107,E108,E 120,E121	E063,E066,E087,E0 98,E108,E120,E121	E025,E063,E066,E 087,E107,E108,E12 0,E121	E098,E121	CEBPB
12	122081119	E025,E063,E066,E087, E098,E107,E108,E120, E121	E025,E063,E066,E08 7,E098,E107,E108,E 120,E121	E063,E066,E087,E0 98,E108,E120,E121	E025,E063,E066,E 087,E107,E108,E12 0,E121	E098,E120,E 121	CEBPB
12	122081164	E025,E063,E066,E087, E098,E107,E108,E120, E121	E025,E063,E066,E08 7,E098,E107,E108,E 120,E121	E063,E066,E087,E0 98,E108,E120,E121	E025,E063,E066,E 087,E107,E108,E12 0,E121	E098,E120,E 121	CEBPB
12	122081182	E025,E063,E066,E087, E098,E107,E108,E120, E121	E025,E063,E066,E08 7,E098,E107,E108,E 120,E121	E063,E066,E087,E0 98,E108,E120,E121	E025,E063,E066,E 087,E107,E108,E12 0,E121	E098,E120,E 121	CEBPB
12	122081287	E025,E063,E066,E087, E098,E107,E108,E120, E121	E025,E063,E066,E08 7,E098,E107,E108,E 120,E121	E063,E066,E087,E0 98,E108,E120,E121	E025,E063,E066,E 087,E107,E108,E12 0,E121	E120,E121	
12	122081427	E025,E063,E066,E087, E098,E107,E108,E120, E121	E025,E063,E066,E08 7,E098,E107,E108,E 120,E121	E063,E066,E087,E0 98,E108,E120,E121	E025,E063,E066,E 087,E107,E108,E12 0,E121	E098,E120,E 121	
12	122081486	E025,E063,E066,E087, E098,E107,E108,E120, E121	E025,E063,E066,E08 7,E098,E107,E108,E 120,E121	E063,E066,E087,E0 98,E108,E120,E121	E025,E063,E066,E 087,E107,E108,E12		

		E121	120,E121		0,E121
12	122081564	E025,E063,E066,E087, E098,E107,E108,E120, E121	E025,E063,E066,E08 7,E098,E107,E108,E	E063,E066,E087,E0 98,E108,E120,E121	E025,E063,E066,E 087,E107,E108,E12
12	122081573	E025,E063,E066,E087, E098,E107,E108,E120, E121	E025,E063,E066,E08 7,E098,E107,E108,E	E063,E066,E087,E0 98,E108,E120,E121	E025,E063,E066,E 087,E107,E108,E12

Cell line description: E025= Adipose Derived Mesenchymal Stem Cell Cultured Cells; E063= Adipose Nuclei; E066=Liver; E087= Pancreatic Islets; E098= Pancreas; E107= Skeletal Muscle Male; E108= Skeletal Muscle Female; E120= HSMM Skeletal Muscle Myoblasts Cells; E121= HSMM cell derived Skeletal Muscle Myotubes Cells.

**Supplementary Table 4: The association statistics of genes that have been reported to be associated with T2D in previous genetic or genomic studies.**

Nominally significant associations are highlighted.

Gene	SNP	Chr	Pos (hg19)	A1	OR	P
<i>FAF1</i>	rs17387024	1	50993178	C	2.19	<b>5.26x10<sup>-3</sup></b>
<i>TGFBR3</i>	rs17881430	1	92327707	A	1.82	<b>4.56x10<sup>-2</sup></b>
<i>F3</i>	rs17111996	1	95122518	T	0.63	<b>4.99x10<sup>-2</sup></b>
<i>SLC44A3</i>	rs735937	1	95335769	C	0.58	<b>3.80x10<sup>-2</sup></b>
<i>ADAM30</i>	rs10923918	1	120412885	T	0.59	9.57x10 <sup>-2</sup>
<i>NOTCH2</i>	rs17258579	1	120469077	C	1.63	0.20
<i>CR2</i>	rs2182911	1	207660071	C	1.78	6.97x10 <sup>-2</sup>
<i>PROX1</i>	rs3767848	1	214173840	A	1.72	<b>3.51x10<sup>-2</sup></b>
<i>LYPLAL1</i>	rs12123734	1	219577622	A	1.65	<b>3.51x10<sup>-2</sup></b>
<i>DUSP5P,RHOU</i>	rs12407568	1	228783329	T	1.92	0.55
<i>RHOU</i>	rs496663	1	229098232	C	1.80	<b>1.95x10<sup>-2</sup></b>
<i>PCNXL2</i>	rs6693854	1	233215885	C	0.48	<b>2.77x10<sup>-2</sup></b>
<i>TMEM18</i>	rs4241319	2	603079	G	1.91	<b>1.28x10<sup>-2</sup></b>
<i>THADA</i>	rs1549723	2	43460514	A	0.58	9.24x10 <sup>-2</sup>
<i>BCL11A</i>	rs356993	2	60750560	T	1.46	0.15
<i>TMEM163</i>	rs4953921	2	135286448	G	1.40	0.17
<i>RND3</i>	rs193046	2	150904778	C	7.35	<b>1.13x10<sup>-4</sup></b>
<i>RBM43</i>	rs11675356	2	151931005	A	0.55	5.71x10 <sup>-2</sup>
<i>ITGB6</i>	rs10202454	2	161044155	G	4.19	<b>3.04x10<sup>-2</sup></b>
<i>RBMS1</i>	rs532146	2	161622892	G	2.12	<b>2.65x10<sup>-2</sup></b>
<i>GRB14</i>	rs12474679	2	165346592	G	1.66	5.70x10 <sup>-2</sup>
<i>IRS1</i>	rs16822601	2	227616748	C	2.63	6.28x10 <sup>-2</sup>
<i>DNER</i>	rs977041	2	230350848	A	1.68	<b>3.64x10<sup>-2</sup></b>
<i>SYN2</i>	rs4684093	3	12025330	C	1.56	0.10
<i>SYN2,TIMP4</i>	rs17035943	3	12194584	C	0.21	0.16
<i>PPARG</i>	rs12485478	3	12351223	G	5.66	7.00x10 <sup>-2</sup>
<i>UBE2E2</i>	rs13096681	3	22686512	A	2.70	<b>6.00x10<sup>-3</sup></b>
<i>MIR548AC,UBE2E2</i>	rs1353322	3	23390301	G	0.61	5.67x10 <sup>-2</sup>
<i>PSMD6-AS2</i>	rs4688181	3	63989456	G	9.40	<b>9.30x10<sup>-3</sup></b>
<i>PSMD6,PSMD6-AS2</i>	rs2280162	3	63997491	A	1.92	5.63x10 <sup>-2</sup>
<i>PSMD6</i>	rs166229	3	64021228	G	1.27	0.37
<i>ADAMTS9</i>	rs9871177	3	64480785	C	0.29	<b>1.60x10<sup>-3</sup></b>
<i>ADAMTS9-AS2,MIR548A2</i>	rs318725	3	64755337	G	0.62	<b>4.76x10<sup>-2</sup></b>
<i>ADAMTS9-AS2</i>	rs9790242	3	65103850	A	2.81	<b>1.91x10<sup>-2</sup></b>
<i>ZPLD1</i>	rs9854367	3	102259425	C	1.90	<b>3.75x10<sup>-2</sup></b>
<i>ADCY5</i>	rs4678005	3	123021298	C	1.78	<b>3.20x10<sup>-2</sup></b>
<i>PLS1</i>	rs1983434	3	142347757	G	0.67	0.12

<i>PEX5L</i>	rs2003004	3	179836036	G	2.33	<b>1.27x10<sup>-2</sup></b>
<i>C3orf65,IGF2BP2</i>	rs17826758	3	185431283	G	0.96	0.91
<i>IGF2BP2</i>	rs12639517	3	185574131	T	1.43	0.16
<i>ST6GAL1</i>	rs10513809	3	186667250	T	0.19	5.28x10 <sup>-2</sup>
<i>LPP-AS2</i>	rs7651169	3	187814477	G	1.94	<b>1.51x10<sup>-2</sup></b>
<i>FLJ42393,LPP</i>	rs4577458	3	187897424	C	0.69	0.15
<i>LPP</i>	rs2278096	3	188590650	T	2.30	<b>9.35x10<sup>-3</sup></b>
<i>MAEA</i>	rs3817604	4	1291337	T	0.61	0.31
<i>WFS1</i>	rs10002743	4	6276581	G	0.51	<b>4.73x10<sup>-2</sup></b>
<i>PPP2R2C</i>	rs7377185	4	6407801	T	2.03	<b>8.57x10<sup>-3</sup></b>
<i>COX7B2</i>	rs9291290	4	46878105	T	0.56	<b>3.08x10<sup>-2</sup></b>
<i>GABRA4</i>	rs2055940	4	46997913	A	2.47	<b>1.05x10<sup>-3</sup></b>
<i>TMEM154</i>	rs6849505	4	153573491	T	0.57	0.25
<i>ANP32C,MARCH1</i>	rs2288675	4	165118652	T	1.30	0.27
<i>ARL15</i>	rs154021	5	53463117	C	1.85	<b>3.03x10<sup>-2</sup></b>
<i>MAP3K1</i>	rs3736430	5	56180480	G	2.69	<b>2.09x10<sup>-2</sup></b>
<i>ZBED3</i>	rs2914141	5	76378192	T	1.58	0.12
<i>ZBED3-AS1</i>	rs7708285	5	76425867	G	1.80	<b>4.80x10<sup>-2</sup></b>
<i>CETN3</i>	rs16868525	5	89640426	A	4.42	<b>1.36x10<sup>-2</sup></b>
<i>ZNF608</i>	rs7705693	5	124084365	T	1.94	<b>1.25x10<sup>-2</sup></b>
<i>PCBD2</i>	rs9285933	5	134257519	A	0.43	5.24x10 <sup>-2</sup>
<i>RREB1</i>	rs7757080	6	6929780	C	2.77	<b>1.67x10<sup>-2</sup></b>
<i>SSR1</i>	rs9968917	6	7267002	A	0.46	0.25
<i>CDKAL1</i>	rs16884481	6	21076048	T	3.06	<b>1.31x10<sup>-2</sup></b>
<i>TCF19</i>	rs1044870	6	31130821	T	0.54	0.20
<i>POU5F1</i>	rs9263796	6	31132883	T	0.54	0.20
<i>HLA-DQA2</i>	rs3957146	6	32681530	C	3.20	<b>1.97x10<sup>-3</sup></b>
<i>PPARD</i>	rs4713854	6	35381099	C	2.79	5.39x10 <sup>-2</sup>
<i>ZFAND3</i>	rs12529345	6	37755453	T	2.21	<b>3.16x10<sup>-3</sup></b>
<i>KCNK16</i>	rs11758206	6	39296416	T	3.08	0.22
<i>VEGFA</i>	rs4714696	6	43719993	C	1.63	7.78x10 <sup>-2</sup>
<i>C6orf57</i>	rs9455167	6	71291087	G	0.06	0.11
<i>RPS12,SNORD100</i>	rs9389034	6	133138010	C	1.01	0.97
<i>RPS12</i>	rs12193474	6	133186168	C	0.54	0.18
<i>IL20RA</i>	rs276550	6	137401777	C	0.61	6.92x10 <sup>-2</sup>
<i>SASH1</i>	rs6570846	6	148682423	A	2.11	<b>3.80x10<sup>-3</sup></b>
<i>ETV1</i>	rs9792016	7	13857235	G	2.53	<b>1.89x10<sup>-3</sup></b>
<i>DGKB</i>	rs10487790	7	15042907	C	2.22	<b>2.08x10<sup>-2</sup></b>
<i>AGR2</i>	rs11773294	7	16839835	C	2.13	<b>3.29x10<sup>-2</sup></b>
<i>AGR3</i>	rs3944100	7	17054346	C	1.92	<b>1.76x10<sup>-2</sup></b>
<i>JAZF1</i>	rs10258887	7	27940578	C	3.67	<b>1.85x10<sup>-2</sup></b>
<i>JAZF1-AS1</i>	rs4722772	7	28285903	C	1.52	0.14
<i>CRHR2</i>	rs255125	7	30743011	A	0.70	0.23
<i>ELMO1</i>	rs10488653	7	37491704	C	3.22	<b>2.04x10<sup>-2</sup></b>

<i>ACHE</i>	rs6980219	7	100542445	T	0.67	0.13
<i>GCCI</i>	rs17714284	7	127147205	A	2.39	5.28x10 <sup>-2</sup>
<i>PAX4</i>	rs327510	7	127257894	G	1.26	0.40
<i>SND1,SND1-IT1</i>	rs1362897	7	127638703	A	1.28	0.43
<i>SND1</i>	rs6467157	7	127660763	C	0.64	0.17
<i>LRRC4,SND1</i>	rs6944446	7	127667516	A	0.84	0.50
<i>LEP</i>	rs1116656	7	127910047	A	1.64	5.64x10 <sup>-2</sup>
<i>KLF14</i>	rs1364422	7	130445981	T	1.72	6.04x10 <sup>-2</sup>
<i>GFRA2</i>	rs17060577	8	21673762	G	0.38	<b>1.73x10<sup>-2</sup></b>
<i>DOK2</i>	rs11780601	8	21717841	T	1.84	<b>4.78x10<sup>-2</sup></b>
<i>ANK1</i>	rs12549902	8	41509259	G	0.55	<b>1.83x10<sup>-2</sup></b>
<i>TP53INP1</i>	rs493506	8	95965135	G	2.01	0.12
<i>SLC30A8</i>	rs7828267	8	118236041	C	2.20	<b>1.34x10<sup>-2</sup></b>
<i>WISP1</i>	rs13256058	8	134195513	A	1.54	8.47x10 <sup>-2</sup>
<i>GLIS3</i>	rs10973736	9	3838888	T	2.43	<b>7.17x10<sup>-3</sup></b>
<i>GLIS3,GLIS3-AS1</i>	rs10974067	9	3900982	C	1.14	0.65
<i>PTPRD</i>	rs10441691	9	8125336	A	2.48	<b>6.65x10<sup>-3</sup></b>
<i>CDKN2A</i>	rs3731217	9	21984661	C	1.41	0.30
<i>CDKN2B,CDKN2B-AS1</i>	rs1063192	9	22003367	G	0.83	0.48
<i>CDKN2B-AS1</i>	rs10965267	9	22161828	G	0.39	6.77x10 <sup>-2</sup>
<i>LINGO2</i>	rs12347591	9	28342014	C	2.37	<b>6.15x10<sup>-3</sup></b>
<i>TLE4</i>	rs10123659	9	83235735	G	0.35	<b>1.37x10<sup>-2</sup></b>
<i>TLE1</i>	rs10491932	9	83333000	A	0.40	<b>1.44x10<sup>-2</sup></b>
<i>SYK</i>	rs10993708	9	93606091	A	45.95	<b>2.62x10<sup>-2</sup></b>
<i>AUH</i>	rs7025567	9	93969769	A	1.54	0.23
<i>PALM2</i>	rs10979994	9	112438399	T	2.59	<b>6.75x10<sup>-3</sup></b>
<i>PALM2-AKAP2</i>	rs7030564	9	112778952	C	1.46	0.15
<i>AKAP2,PALM2-AKAP2</i>	rs496709	9	112879944	G	0.63	0.16
<i>SVEP1</i>	rs17733560	9	113124562	C	0.43	<b>2.42x10<sup>-2</sup></b>
<i>MUSK</i>	rs10980575	9	113585503	A	2.09	<b>3.37x10<sup>-2</sup></b>
<i>GPSM1</i>	rs28380074	9	139225139	G	0.64	6.24x10 <sup>-2</sup>
<i>CDC123</i>	rs7916879	10	12300790	A	1.62	6.29x10 <sup>-2</sup>
<i>CAMK1D</i>	rs7899150	10	12509131	T	1.93	<b>2.68x10<sup>-2</sup></b>
<i>VPS26A</i>	rs12256853	10	70930360	G	1.52	0.25
<i>C10orf35</i>	rs12569387	10	71460661	T	1.55	0.12
<i>ZMIZ1</i>	rs10824715	10	80858151	C	1.74	<b>2.77x10<sup>-2</sup></b>
<i>PTEN</i>	rs7079271	10	89833307	G	1.92	<b>2.02x10<sup>-2</sup></b>
<i>IDE</i>	rs11187061	10	94305409	T	1.65	6.10x10 <sup>-2</sup>
<i>KIF11</i>	rs12256435	10	94353278	T	2.35	<b>4.19x10<sup>-2</sup></b>
<i>HHEX</i>	rs2497313	10	94480391	T	1.85	9.71x10 <sup>-2</sup>
<i>TCF7L2</i>	rs12098403	10	115006062	A	2.94	<b>2.31x10<sup>-2</sup></b>
<i>GRK5</i>	rs11198929	10	121207272	T	0.56	<b>3.37x10<sup>-2</sup></b>
<i>PLEKHA1</i>	rs1998345	10	124124306	A	1.44	0.15
<i>TCERG1L</i>	rs4751353	10	133078257	A	2.07	<b>1.25x10<sup>-2</sup></b>



<i>KCNQ1</i>	rs12274567	11	2474956	A	2.39	<b>4.68x10<sup>-2</sup></b>
<i>KCNQ1,KCNQ1OT1</i>	rs10832514	11	2688526	A	1.49	0.11
<i>GALNTL4</i>	rs4441010	11	11269086	G	2.02	<b>1.38x10<sup>-2</sup></b>
<i>CSNK2A1P,GALNTL4</i>	rs2071460	11	11374269	G	1.12	0.63
<i>KCNJ11</i>	rs2074314	11	17411821	C	1.54	0.11
<i>MTNR1B</i>	rs6483208	11	92705844	G	5.47	<b>1.42x10<sup>-2</sup></b>
<i>ATM</i>	rs17412803	11	108217384	G	3.61	<b>4.29x10<sup>-2</sup></b>
<i>BARX2</i>	rs3019806	11	129374559	T	2.11	<b>2.13x10<sup>-2</sup></b>
<i>TMEM45B</i>	rs10894138	11	129657401	T	1.33	0.22
<i>KLHDC5</i>	rs11829884	12	27994433	A	4.06	7.93x10 <sup>-2</sup>
<i>DCD</i>	rs4759097	12	55075774	G	1.38	0.19
<i>MSRB3</i>	rs10878260	12	65724724	A	0.39	<b>5.81x10<sup>-3</sup></b>
<i>HMGA2</i>	rs1480468	12	66342117	A	1.84	9.06x10 <sup>-2</sup>
<i>TSPAN8</i>	rs10506627	12	71666552	C	4.00	0.18
<i>LGR5</i>	rs1298142	12	71941490	C	2.03	<b>3.26x10<sup>-2</sup></b>
<i>HNFLA-ASI</i>	rs11065374	12	121400205	C	1.89	<b>1.01x10<sup>-2</sup></b>
<i>HNFLA</i>	rs1169302	12	121432302	G	0.58	<b>3.16x10<sup>-2</sup></b>
<i>MPHOSPH9</i>	rs1727301	12	123664514	A	1.45	0.14
<i>SGCG</i>	rs17078439	13	23766378	C	2.30	<b>2.60x10<sup>-2</sup></b>
<i>SACS</i>	rs9578601	13	24018842	T	1.88	6.50x10 <sup>-2</sup>
<i>RNF6</i>	rs11619338	13	26745831	T	0.45	<b>2.55x10<sup>-2</sup></b>
<i>SPRY2</i>	rs9574595	13	80772435	T	0.43	5.73x10 <sup>-2</sup>
<i>RASGRP1</i>	rs4465567	15	38798246	C	0.50	<b>1.53x10<sup>-2</sup></b>
<i>HMG20A</i>	rs16953967	15	77836521	T	0.64	9.54x10 <sup>-2</sup>
<i>ZFAND6</i>	rs4778745	15	80363413	G	1.58	0.25
<i>AP3S2,C15orf38-AP3S2</i>	rs12440213	15	90366032	T	0.66	0.20
<i>C15orf38-AP3S2</i>	rs3803533	15	90441937	T	1.19	0.70
<i>C15orf38,C15orf38-AP3S2</i>	rs1702161	15	90480586	G	1.45	0.44
<i>PRC1</i>	rs4932182	15	91508803	A	1.13	0.61
<i>LOC100507118,PRC1</i>	rs8042680	15	91521337	A	1.19	0.45
<i>TNRC6A</i>	rs12103149	16	24673898	A	1.58	0.13
<i>FTO</i>	rs17236708	16	54128426	A	0.63	6.98x10 <sup>-2</sup>
<i>CCDC102A</i>	rs9922763	16	57546146	A	1.40	0.22
<i>WWOX</i>	rs7200433	16	78955140	T	3.12	<b>5.72x10<sup>-3</sup></b>
<i>CMIP</i>	rs4888159	16	81646894	T	2.09	<b>2.95x10<sup>-3</sup></b>
<i>CMIP,LOC100129617</i>	rs1128658	16	81700808	A	1.34	0.53
<i>NXN</i>	rs910922	17	710317	A	2.23	<b>1.46x10<sup>-2</sup></b>
<i>SRR</i>	rs12450028	17	2207425	T	1.74	<b>2.35x10<sup>-2</sup></b>
<i>SLC16A13</i>	rs11078663	17	6942108	C	0.84	0.49
<i>SLC16A11</i>	rs193399	17	6962272	A	2.24	0.27
<i>HNFB1B</i>	rs17138522	17	36043734	G	4.61	<b>1.92x10<sup>-2</sup></b>
<i>LPIN2</i>	rs3826637	18	2937646	G	0.59	6.09x10 <sup>-2</sup>
<i>LOC727896,LPIN2</i>	rs643507	18	2946291	C	0.63	0.44
<i>LAMA1</i>	rs679668	18	7039943	A	2.74	<b>3.29x10<sup>-3</sup></b>

<i>MC4R</i>	rs11152221	18	58017249	T	1.95	<b>3.08x10<sup>-2</sup></b>
<i>PEPD</i>	rs891035	19	34060938	G	0.49	<b>1.94x10<sup>-2</sup></b>
<i>GIPR</i>	rs12976464	19	46162399	A	0.82	0.65
<i>R3HDML</i>	rs3746570	20	42965863	T	1.58	0.12
<i>HNF4A</i>	rs2425640	20	43028037	A	0.63	6.00x10 <sup>-2</sup>
<i>MIR5095,RBM38</i>	rs439749	20	55968113	G	0.64	0.10
<i>CTCF</i>	rs7264874	20	56045814	T	4.53	<b>3.39x10<sup>-3</sup></b>
<i>PCK1</i>	rs1543375	20	56130620	G	1.67	<b>3.47x10<sup>-2</sup></b>
<i>HUNK</i>	rs2833579	21	33328529	G	1.53	8.47x10 <sup>-2</sup>
<i>LIMK2</i>	rs5997917	22	31621792	A	1.76	0.11
<i>SULT4A1</i>	rs470085	22	44219716	C	4.61	<b>1.95x10<sup>-2</sup></b>
<i>FAM58A</i>	rs4898361	X	152872445	A	2.33	5.11x10 <sup>-2</sup>
<i>DUSP9</i>	rs3761536	X	152906292	T	0.58	0.22

SNP – single nucleotide polymorphism; Chr – chromosome; Pos – Position; A1 – minor allele; OR – odds ratio

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