SUPPLEMENTARY MATERIALS

Tissue-specific alternative splicing of *TCF7L2*

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Supplementary Table 1. Expression of assay "ex7-8"of *TCF7L2*, normalized by expression of reference genes *B2M* (ß-2 microglobulin), *GAPDH* (Glyceraldehyde-3-phosphate dehydrogenase) or both genes

Tissues, cells	dCt (Log2) relative to expression of reference genes *		
	B2M	GAPDH	B2M and GAPDH
pancreas	-3.22	-3.75	-3.48
colon	-3.37	-3.94	-3.66
brain	-1.96	-6.21	-4.09
small intestine	-3.74	-4.59	-4.16
monocytes, CD14+	-5.24	-3.09	-4.16
lung	-5.24	-3.61	-4.42
cultured adipocytes	-3.89	-6.28	-5.08
kidney	-3.97	-6.32	-5.15
spleen	-6.35	-4.00	-5.18
liver	-4.88	-5.80	-5.34
pancreatic islets	-4.96	-6.01	-5.48
heart	-4.31	-7.41	-5.86
skeletal muscle	-3.66	-10.46	-7.06
blood mononuclear cells	-8.76	-6.30	-7.53
T cells, CD8+	-9.36	-5.92	-7.64
B cells, CD19+	-10.41	-6.98	-8.69
T cells, CD4+	-11.45	-7.89	-9.67
lymphoblastoid cells, CEPH	-12.01	-14.11	-13.06
activated B cells, CD19+	-13.96	-13.63	-13.80
activated blood mononuclear cells	-14.02	-13.93	-13.98
activated T cells, CD4+	-13.35	-14.90	-14.12
activated T cells, CD8+	-16.32	-15.11	-15.71

* calculated according to formula: dCt =Ct $_{\text{reference}}$ – Ct $_{\text{target,}}$ where "reference" represents levels of expression (Ct values) of B2M, GAPDH or both genes and "target" represents level of expression of TCF7L2; negative Ct means that a target is expressed lower than a reference gene; fold difference in expression between a reference and a target can be calculated as 2 $^{(\text{dCt})}$. Each tissue is represented by one sample or a mix of several samples.

Supplementary Table 2. Alternative splicing within *TCF7L2*

Alternative feature	Position, Build 36.1	Sequence of alternative features Underlined – position of transcriptions start sites (**BOLD**) – short alternative fragments	Detected by assay
TSS1 -536 bp promoter	chr10:114,699,999	AATAATCTCCGCTCCCAGACTACTCCGTTCCTCCGGATTTCGATCCCCCCTTTTTCTATCTGTC	TSS1
TSS2 +83 bp, ex1	chr10:114,700,588	AGGAGAAGAGCTCCGAAAACTCCTCGGCAGAGAGGGATTTAGCTG	TSS2
TSS3 +200 bp, intron1	chr10:114,700,723	TTTTTATCTTTTTCCTGGGCTTGGCAAATGTTGCTGAAAGGGGAGA	TSS3
TSS_P2intr1 +239 bp, intron1	chr10:114,700,744	TTGGCAAATGTTGATGAAAGGGGAGAAATCGGGGCTGGGGGCGGC	TSS3
TSS_P2intr1 +302 bp, intron1	chr10:114,700,807	GCGTGTGCGTACGGTGCCACCATTGCAAAAACTTGTAACCCTGTTT	TSS3
TSS_P2intr1 +338 bp, intron1	chr10:114,700,842	TAACCCTGTTTTTTTCTACCCCCCCTCGACCTCGCCGATTCTTTTTCT	TSS3
Ex3a, 69bp	chr10:114,714,305-114,714,373	CTCCATTTTCAGTCCGGCAGCACACATTACTCTGCGTACAAAACGATTGAACACCAGATTGCAGTTCAG	ex3a-4
Exon 4a, 141bp	chr10:114,839,149-114,839,289	AGCCCCCTCCCTTGCTGCACTCAGGGACATGACTGTCAGCACTTCTACCCCCCCTCAGACTTCACTGTCAGCACTCAAGTCTTCAGGGACATGAAAAGGAGCCACTCCTTACAAAAAGTTGGGGAGCCCTGGTGTATTGAG	ex4-4a
Exon 4a, 144bp, with extra 3bp	chr10:114,839,146-114,839,289	**(CAG)**AGCCCCCTCCCTTGCTGCACTCAGGGACATGACTGTCAGCACTTCTACCCCCCCTCAGACTTCACTGTCAGCACTCAAGTCTTCAGGGACATGAAAAGGAGCCACTCCTTACAAAAAGTTGGGGAGCCCTGGTGTATTGAG	ex4-4a
Exon 6, 103 bp,with/without 12 bp in the end	chr10:114,893,672-114,893,774	GAATCCCACGGCCTCCGCACCCTCCAGATATATCCCCGTATTACCCACTATCGCCTGGCACCGTAGGACAAATCCCCCATCCGCTAGGATG**(GTTAGTACCACA)**	Not measured
Exon 8, 141 bp, with/without extra 15 bp in the beginning	chr10:114,900,732-114,900,872	**(CTTTCTGTCTTCTAG)**GTTCCCTCCCCATATGGTCCCACCACATCATACGCTACACACGACGGGCATTCCGCATCCGGCCATAGTCACACCAACAGTCAAACAGGAATCGTCCCAGAGTGATGTCGGCTCACTCCATAGTTC	Not measured
Ex12, 51 bp	chr10:114,908,416-114,908,466	AACACAGCGAATGTTTCCTAAATCCTTGCCTTTCACTTCCTCCGATTACAG	Ex12-13
Ex13, 73 bp	chr10:114,909,669-114,909,741	ACCTGAGCGCTCCTAAGAAATGCCGAGCGCGCTTTGGCCTTGATCAACAGAATAACTGGTGCGGCCCTTGCAG	ex11-13, ex13-14, ex13-13a
Ex13a, 73 bp	chr10:114,910,368-114,910,440	ATGCAAATACTCCAAAGAAGTGTCGGGCACTGTTCGGGCTTGACCGACAGACTTTATGGTGCAAACCGTGCAG	ex11-13a, ex13-13a
Ex13b, 25 bp	chr10:114,911,328-114,911,352	TCTTTGAATTTGGAATATTACAATG	ex13-13b

Supplementary Table 3. Characteristics of splicing forms of *TCF7L2*

GenBank accession number	Structure *	Detected by assay	Type of C-terminal end (short, nedium, long) Location of stop codon	Expression, tissues
FJ010166	Ex1-11,12,13,13a	Ex13-13a	short, stop codon in exon 13a	Low expression, highest expression in liver, lowest in pancreas
FJ010167	Ex1-11,13a, 14	Ex11-13a	long, stop codon in end of ex14	First/ second common splicing form, lowest expression in skeletal muscles
FJ010168	Ex1-11,13,13b	Ex13-13b	short, stop codon in ex 13b	Low expression, detectable in pancreatic islets, colon and at a lower level in pancreas but negative in many other tissues
FJ010169	Ex1-11,12,13,13b	Ex13-13b	short, stop codon in ex 13b	Low expression, detectable in pancreatic islets, colon and at a lower level in pancreas but negative in many other tissues
FJ010172	Ex1-11,14	Ex11-14	medium, stop codon in beginning of ex14	First/ second common splicing form
FJ010173	Ex1-11,12,13,14	Ex12-13	long, stop codon in end of ex14	Highest expression in monocytes, lowest in lymphoblasts
FJ010174	Ex1-11,13,14	Ex11-13	long, stop codon in end of ex 14	Highest expression in skeletal muscles, lowest in lymphoblasts

* - combinatorial use of alternative start sites and alternative exons 3a and 4a and inclusion of 3, 12 and 15 bp within exons 4a,, 6 and 8 was not evaluated

Supplementary Table 4. Relative abundance of *TCF7L2* splicing forms with different C-terminal ends in human tissues, compared to highest expressing form in each tissue

Tissue, Type of C-terminal end	Ex11,14 Medium	Ex11,12,13,14 Long	Ex11,13,14 Long	Ex11,13a,14 Long	Ex11,12,13,13a Short	Ex11,12,13,13b Short
Detected by assays	Ex11-14	Ex12-13	Ex11-13	Ex11-13a	Ex13-13a	Ex13-13b
Pancreatic islets n=22	**1.0**	0.33	0.20	0.62	0.08	0.04
Pancreas n=36	**1.0**	0.27	0.15	0.88	0.008	0.0015
Colon n=81	0.89	0.21	0.12	**1.0**	0.02	<0.001
Liver n=30	0.66	0.45	0.25	**1.0**	0.19	Negative
Monocytes n=61	0.77	**1.00**	0.10	0.29	0.08	Negative
Subcutaneous adipose tissue n=14	**1.0**	0.56	0.36	0.25	0.10	Negative
Skeletal muscles, N=27	**1.0**	0.57	0.50	0.13	0.08	Negative
Lymphoblasts, n=17	**1.0**	0.10	0.09	0.34	0.01	Negative

Supplementary Table 5A. Effects of age, sex, BMI, CMV infection and islet purity on expression of *TCF7L2* and other genes in pancreatic islets, Set 1, US, n=18

Expression assay	factors, p-value for multiple linear regression				
	Age, years	Sex	BMI, kg/m2	CMV	Islets Purity, %
TSS1	0.545	0.214	0.292	0.264	0.912
TSS2	0.663	0.193	0.698	0.318	0.865
TSS3	0.232	0.122	0.817	0.120	0.810
ex3a-4	0.730	0.105	0.152	0.197	0.818
ex7-8	0.750	0.328	0.683	0.205	0.986
ex11-13	0.444	0.202	0.750	0.108	0.913
ex12-13	0.609	0.320	0.399	**0.029** higher with CMV	0.623
ex13-13a	0.634	0.396	0.306	0.054	0.718
ex11-13a	0.729	0.418	0.116	0.421	0.622
ex11-14	0.909	0.337	0.992	0.360	0.851
ex13-14	0.640	0.829	0.574	0.075	0.541
ex13-13b	0.217	0.574	0.227	**0.008** higher with CMV	0.981
Proinsulin	0.571	0.732	0.497	0.988	0.424
Proglucagon	0.160	**0.025**	0.423	0.172	0.437
Ghrelin/ obestatin	0.454	0.282	0.238	0.588	0.393
Somatostatin	0.328	0.163	0.089	0.526	0.473
Chromogranin A	0.221	0.730	0.845	0.097	0.690
PDX1	0.685	0.134	0.157	0.542	0.877
PCNA	0.679	0.127	0.159	0.731	0.811
VIP	0.353	0.831	0.487	0.610	0.275

For each trait, the association of all listed variables was jointly evaluated using multiple linear regression; only samples that include all of the evaluated factors are included into analysis. In bold p-values <0.05

Supplementary Table 5B. Effects of age, sex and BMI on expression of *TCF7L2* and other genes in pancreas, n=34

Expression assay	factors, p-value for multiple linear regression		
	Age, years	Sex	BMI, Kg/m2
TSS1	0.352	0.327	0.263
TSS2	0.537	0.540	0.372
TSS3	0.218	0.939	0.341
ex3a-4	0.088	0.718	0.721
ex7-8	0.230	0.960	0.747
ex11-13	0.619	0.503	0.208
ex12-13	0.239	0.420	0.974
ex13-13a	0.409	0.126	0.899
ex11-13a	0.437	0.919	0.512
ex11-14	0.318	0.948	0.649
ex13-14	0.744	0.159	0.433
ex13-13b	**0.025**	0.106	0.667
Proinsulin	0.091	0.054	0.890
Proglucagon	**0.009**	0.657	0.722
Ghrelin/obestatin	0.217	**0.007**	**0.045**
Somatostatin	0.035	0.209	0.959
Chromogranin A	0.083	0.096	0.485

For each trait, the association of all listed variables was jointly evaluated using multiple linear regression; only samples that include all of the evaluated factors are included into analysis. In bold p-values <0.05

Supplementary Table 5C. Effects of age, sex and BMI on expression of *TCF7L2* and other genes in colon, n= 51

Expression assay	factors, p-value for multiple linear regression		
	Age, years	Sex	BMI, Kg/m2
TSS1	0.814	0.199	0.684
TSS2	0.986	0.237	0.983
TSS3	0.655	0.430	0.259
ex3a-4	0.548	0.791	0.912
ex7-8	0.926	0.168	0.663
ex11-13	0.101	0.856	0.792
ex12-13	0.612	0.189	0.110
ex13-13a	0.600	0.732	0.650
ex11-13a	0.535	0.774	0.265
ex11-14	0.240	0.599	0.195
ex13-14	0.124	0.671	0.455
ex13-13b	0.661	0.673	0.127
Proglucagon (Glucagon-Like Peptide 1, GLP-1)	0.484	**<0.001** higher in males	0.236
Somatostatin	0.048	0.174	0.744
Chromogranin A	0.587	0.573	0.413

For each trait, the association of all listed variables was jointly evaluated using multiple linear regression; only samples that include all of the evaluated factors are included into analysis. In bold p-values <0.05

Supplementary Table 5D. Effects of age and sex on expression of *TCF7L2* in peripheral blood monocytes, n=63

Expression assay	factors, p-value for multiple linear regression	
	Age, years	Sex
TSS1	0.366	0.086
TSS2	0.267	0.091
TSS3	0.270	0.205
ex3a-4	0.279	0.192
ex7-8	0.877	0.163
ex11-13	0.353	0.684
ex12-13	0.410	0.294
ex13-13a	0.597	0.597
ex11-13a	0.337	0.954
ex11-14	0.207	0.429
ex13-14	0.125	0.871

For each trait, the association of all listed variables was jointly evaluated using multiple linear regression; only samples that include all of the evaluated factors are included into analysis. In bold p-values <0.05

Supplementary Table 5E. Effects of age and sex on expression of *TCF7L2* in liver, n=59

Expression assay	factors, p-value for multiple linear regression	
	Age, years	Sex
TSS1	**0.017**	0.483
TSS2	0.065	0.395
TSS3	0.182	0.144
ex3a-4	0.211	0.912
ex7-8	**0.020**	0.949
ex11-13	0.184	0.260
ex12-13	0.317	0.071
ex13-13a	0.158	0.056
ex11-13a	0.232	0.184
ex11-14	0.227	0.221
ex13-14	**0.022**	0.618

For each trait, the association of all listed variables was jointly evaluated using multiple linear regression; only samples that include all of the evaluated factors are included into analysis. In bold p-values <0.05

Supplementary Table 5F. Effects of age and sex on expression of *TCF7L2* in subcutaneous adipose tissue, n=14

Expression assay	factors, p-value for multiple linear regression	
	Age, years	BMI, Kg/m2
TSS1	**0.008**	0.400
TSS2	0.981	0.658
TSS3	0.484	0.827
ex3a-4	0.907	0.743
ex7-8	0.947	0.365
ex11-13	0.400	0.473
ex12-13	0.696	0.634
ex13-13a	0.721	0.292
ex11-13a	0.737	0.424
ex11-14	0.600	0.964
ex13-14	0.210	0.593

For each trait, the association of all listed variables was jointly evaluated using multiple linear regression; only samples that include all of the evaluated factors are included into analysis. In bold p-values <0.05

Supplementary Table 5G. Effects of age, sex and diagnosis on expression of *TCF7L2* in skeletal muscles, n=25

Expression assay	factors, p-value for multiple linear regression		
	Age, years	Sex	Diagnosis: healthy/ muscular degeneration
TSS1	0.703	0.476	0.538
TSS2	0.748	0.729	0.979
TSS3	0.812	0.398	**0.009** lower in disease
ex3a-4	0.577	0.697	0.504
ex7-8	0.667	0.828	0.758
ex11-13	0.671	0.818	0.083
ex12-13	0.710	0.363	0.817
ex13-13a	0.220	0.186	0.884
ex11-13a	0.724	0.753	0.635
ex11-14	0.555	0.790	0.852
ex13-14 *	0.270	0.613	0.802

For each trait, the association of all listed variables was jointly evaluated using multiple linear regression; only samples that include all of the evaluated factors are included into analysis. In bold p-values <0.05

Supplementary Table 6A. Sample characteristics and *T2F7L2* expression by genotypes of SNPs in pancreatic islets, Set 1, US, n=26

Traits, expression assays	**rs7903146**					**rs12255372**				
	geno types	n	mean	fold	p-value **	geno types	n	mean	fold	p-value **
BMI, kg/m2	CC	10	26.41	ref	0.418	GG	5	27.08	ref	0.751
	TT	7	28.34	1.07		TG	13	27.24	1.01	
	TT	5	28.30	1.07		TT	4	28.62	1.06	
Age, years	CC	10	38.30	ref	0.457	GG	5	39.60	ref	0.732
	TC	7	43.48	1.14		TG	13	41.62	1.05	
	TT	5	48.20	1.26		TT	4	47.25	1.19	
Islets viability, %	CC	9	90.89	ref	0.454	GG	4	92.50	ref	0.676
	TC	6	93.17	1.03		TG	12	91.17	0.99	
	TT	5	88.20	0.97		TT	4	88.50	0.96	
Islets purity, %	CC	9	85.56	ref	0.830	GG	4	85.00	ref	0.825
	TC	6	86.67	1.01		TG	12	86.25	1.01	
	TT	5	84.00	0.98		TT	4	83.75	0.99	
Cold time, h	CC	9	11.99	ref	0.541	GG	4	13.31	ref	0.834
	TC	5	15.75	1.31		TG	11	13.76	1.03	
	TT	4	13.00	1.08		TT	3	11.33	0.85	
CMV infection frequency	CC	10	0.80	ref	0.413	GG	5	1.00	ref	0.131
	TC	6	0.50	0.63		TG	12	0.58	0.58	
	TT	4	0.50	0.63		TT	3	0.33	0.33	
TSS1 *	CC	12	-2.67	ref	0.747	GG	6	-2.07	ref	0.246
	TC	7	-2.62	1.04		TG	14	-2.87	0.57	
	TT	5	-3.14	0.72		TT	4	-3.33	0.42	
TSS2 *	CC	12	-4.64	ref	0.760	GG	6	-4.08	ref	0.355
	TC	7	-4.46	1.13		TG	14	-4.78	0.62	
	TT	5	-4.99	0.78		TT	4	-5.11	0.49	
TSS3 *	CC	12	-9.18	ref	0.839	GG	6	-8.30	ref	0.353
	TC	7	-8.77	1.33		TG	14	-9.30	0.50	
	TT	5	-9.09	1.06		TT	4	-9.26	0.51	
ex3a-4 *	CC	12	-5.86	ref	0.591	GG	6	-5.48	ref	0.213
	TC	7	-6.01	0.90		TG	14	-6.10	0.65	
	TT	5	-6.39	0.69		TT	4	-6.51	0.49	
ex7-8 *	CC	12	-4.87	ref	0.746	GG	6	-4.34	ref	0.198
	TC	7	-4.82	1.04		TG	14	-5.07	0.60	
	TT	5	-5.23	0.78		TT	4	-5.33	0.50	
ex11-13 *	CC	12	-8.39	ref	0.848	GG	6	-7.71	ref	0.244
	TC	7	-8.19	1.15		TG	14	-8.54	0.56	
	TT	5	-8.58	0.88		TT	4	-8.76	0.48	
ex12-13 *	CC	12	-7.21	ref	0.169	GG	6	-6.58	ref	**0.010**
	TC	7	-7.72	0.70		TG	14	-7.69	0.46	
	TT	5	-8.50	0.41		TT	4	-8.96	0.19	
ex13-13a *	CC	12	-9.24	ref	0.242	GG	6	-8.66	ref	**0.022**
	TC	7	-9.86	0.65		TG	14	-9.76	0.47	
	TT	5	-10.23	0.50		TT	4	-10.60	0.26	
ex11-13a *	CC	12	-6.52	ref	0.619	GG	6	-6.08	ref	0.181
	TC	7	-6.93	0.75		TG	14	-6.93	0.55	
	TT	5	-6.94	0.75		TT	4	-6.99	0.53	
ex11-14 *	CC	12	-5.99	ref	0.848	GG	6	-5.52	ref	0.357
	TC	7	-5.94	1.04		TG	14	-6.18	0.63	
	TT	5	-6.30	0.81		TT	4	-6.30	0.58	
ex13-14 *	CC	12	-6.07	ref	0.144	GG	6	-5.06	ref	**0.002**
	TC	7	-6.52	0.73		TG	14	-6.82	0.30	
	TT	5	-7.46	0.38		TT	4	-7.49	0.19	
ex13-13b *	CC	13	-10.89	ref	0.244	GG	6	-9.84	ref	**0.003**
	TC	6	-11.82	0.52		TG	14	-11.71	0.27	

	TT	6	-11.79	0.54		TT	5	-12.06	0.21	
Proinsulin *	CC	13	2.09	ref	0.129	GG	6	1.52	ref	**0.037**
	TC	6	2.09	1.00		TG	14	2.34	1.77	
	TT	6	0.57	0.35		TT	5	0.27	0.42	
Proglucagon *	CC	13	5.10	ref	0.363	GG	6	5.93	ref	0.063
	TC	6	4.11	0.50		TG	14	4.42	0.35	
	TT	5	4.83	0.83		TT	4	4.45	0.36	
Ghrelin/obestatin *	CC	13	-7.97	ref	0.478	GG	6	-8.52	ref	0.563
	TC	6	-8.42	0.73		TG	14	-8.02	1.41	
	TT	6	-9.00	0.49		TT	5	-8.95	0.74	
Somatostatin *	CC	13	0.43	ref	0.651	GG	6	-0.16	ref	0.670
	TC	6	0.22	0.86		TG	14	0.42	1.49	
	TT	6	-0.27	0.62		TT	5	-0.14	1.01	
Chromogranin A *	CC	13	1.44	ref	0.544	GG	6	2.03	ref	**0.063**
	TC	6	0.94	0.71		TG	14	1.02	0.50	
	TT	6	1.04	0.76		TT	5	0.83	0.44	
PDX1 *	CC	13	-5.87	ref	0.674	GG	6	-5.77	ref	0.601
	TC	6	-6.42	0.68		TG	14	-6.10	0.80	
	TT	6	-6.49	0.65		TT	5	-6.76	0.50	
PCNA1 *	CC	13	-5.12	ref	0.577	GG	6	-4.82	ref	0.419
	TC	7	-5.44	0.80		TG	15	-5.50	0.62	
	TT	6	-5.66	0.69		TT	5	-5.44	0.65	
VIP *	CC	13	-9.93	ref	0.571	GG	6	-9.61	ref	0.643
	TC	5	-10.81	0.54		TG	13	-10.80	0.44	
	TT	6	-11.18	0.42		TT	5	-10.42	0.57	

* expression of assays, normalized to expression level of reference gene B2M, Log 2 scale

** p-values for univariate linear regression under an additive genetic model for SNPs not adjusted for covariates; in bold p-values <0.05

Supplementary Table 6B. Sample characteristics and *T2F7L2* expression by genotypes of SNPs in pancreatic islets, Set 2, Sweden, n=24

Traits, expression assays	rs7903146					rs12255372				
	geno types	n	mean	fold	p-value **	geno types	n	mean	fold	p-value **
BMI, kg/m2	CC	13	26.29	ref	0.738	GG	13	26.47	ref	0.313
	TT	10	25.15	0.96		TG	11	25.04	0.95	
	TT	1	26.30	1.0		TT	0			
Age, years	CC	13	57.23	ref	0.622	GG	13	60.00	ref	0.053
	TC	10	52.30	0.91		TG	11	49.82	0.83	
	TT	1	61.00	1.07		TT	0			
Islets purity, %	CC	13	69.23	ref	0.296	GG	13	63.85	ref	0.786
	TC	10	53.80	0.78		TG	11	61.18	0.96	
	TT	1	65.00	0.94		TT	0			
HbA1c	CC	10	5.35	ref	0.918	GG	9	5.47	ref	0.681
	TC	7	5.47	1.03		TG	9	5.34	0.98	
	TT	1	5.50	1.00		TT	0			
ex11-13 *	CC	11	-8.68	ref	**0.007**	GG	11	-8.68	ref	0.891
	TC	8	-8.22	1.38		TG	9	-8.60	1.06	
	TT	1	-11.7	0.12		TT	0			
ex12-13 *	CC	9	-7.75	ref	0.058	GG	9	-7.56	ref	0.290
	TC	7	-6.68	2.10		TG	7	-6.93	1.55	
	TT	0				TT	0			
ex13-13a *	CC	12	-9.83	ref	**0.011**	GG	12	-9.67	ref	0.726
	TC	8	-8.70	2.19		TG	9	-9.41	1.20	
	TT	1	-13.28	0.09		TT	0			
ex11-13a *	CC	8	-7.23	ref	**0.003**	GG	8	-7.10	ref	0.933
	TC	7	-6.60	1.55		TG	8	-7.14	0.97	
	TT	1	-9.89	0.16		TT	0			
ex11-14 *	CC	11	-6.46	ref	**0.007**	GG	11	-6.45	ref	0.907
	TC	8	-6.11	1.27		TG	9	-6.51	0.96	
	TT	1	-9.65	0.11		TT	0			
ex13-14 *	CC	11	-7.06	ref	**0.044**	GG	11	-7.06	ref	0.759
	TC	8	-6.90	1.12		TG	9	-7.23	0.89	
	TT	1	-9.92	0.14		TT	0			
ex13-13b *	CC	11	-10.91	ref	**0.017**	GG	10	-10.99	ref	0.372
	TC	6	-11.30	0.76		TG	8	-11.58	0.66	
	TT	1	-14.69	0.07		TT	0			

* expression of assays, normalized to expression level of reference gene B2M, Log 2 scale

** p-values for univariate linear regression under an additive genetic model for SNPs not adjusted for covariates; in bold p-values <0.05

Supplementary Table 6C. Sample characteristics and *T2F7L2* expression by genotypes of SNPs in pancreas, n=46

Traits and assays	rs7903146					rs12255372				
	geno types	n	mean	fold	p-value **	geno types	n	mean	fold	p-value **
BMI, kg/m2	CC	24	27.89	ref	0.578	GG	24	27.92	ref	0.418
	TC	11	27.99	1.00		TG	11	27.57	0.99	
	TT	3	33.42	1.20		TT	3	34.70	1.24	
Age, years	CC	29	56.86	Ref	0.093	GG	31	53.64	ref	0.511
	TC	15	52.33	0.92		TG	13	52.69	0.98	
	TT	3	36.00	0.63		TT	3	64.66	1.21	
TSS1 *	CC	27	-2.88	ref	0.599	GG	28	-2.85	ref	0.903
	TC	13	-2.75	1.09		TG	11	-2.78	1.05	
	TT	2	-2.66	1.16		TT	3	-2.80	1.04	
TSS2 *	CC	27	-4.67	ref	0.698	GG	28	-4.63	ref	0.941
	TC	13	-4.55	1.09		TG	11	-4.57	1.04	
	TT	2	-4.48	1.14		TT	3	-4.64	0.99	
TSS3 *	CC	27	-12.00	ref	0.685	GG	28	-12.01	ref	0.982
	TC	13	-12.08	0.95		TG	11	-12.02	0.99	
	TT	2	-11.70	1.23		TT	3	-11.94	1.05	
ex3a-4*	CC	27	-7.55	ref	0.800	GG	28	-7.55	ref	0.948
	TC	13	-7.62	0.95		TG	11	-7.60	0.97	
	TT	2	-7.18	1.29		TT	3	-7.47	1.06	
ex7-8 *	CC	27	-4.94	ref	0.171	GG	28	-4.98	ref	1.000
	TC	13	-5.21	0.83		TG	11	-4.99	0.99	
	TT	2	-4.20	1.67		TT	3	-4.99	0.99	
ex11-13 *	CC	27	-9.48	ref	0.545	GG	28	-9.47	ref	0.611
	TC	13	-9.38	1.07		TG	11	-9.40	1.05	
	TT	2	-8.98	1.41		TT	3	-9.08	1.31	
ex12-13 *	CC	27	-8.59	ref	0.642	GG	28	-8.54	ref	0.933
	TC	13	-8.38	1.16		TG	11	-8.49	1.04	
	TT	2	-8.38	1.16		TT	3	-8.39	1.11	
ex13-13a *	CC	27	-13.69	ref	0.190	GG	28	-13.65	ref	0.941
	TC	13	-13.72	0.98		TG	11	-13.63	1.01	
	TT	2	-12.32	2.58		TT	3	-13.42	1.17	
ex11-13a *	CC	27	-6.90	ref	0.448	GG	28	-6.89	ref	0.437
	TC	13	-6.87	1.02		TG	11	-6.90	0.99	
	TT	2	-6.35	1.47		TT	3	-6.44	1.37	
ex11-14 *	CC	27	-6.72	ref	0.515	GG	28	-6.71	ref	0.491
	TC	13	-6.66	1.04		TG	11	-6.68	1.02	
	TT	2	-6.26	1.38		TT	3	-6.31	1.32	
ex13-14 *	CC	27	-7.98	ref	0.347	GG	28	-8.02	ref	0.922
	TC	14	-7.91	1.05		TG	13	-7.93	1.06	
	TT	3	-8.51	0.69		TT	3	-7.96	1.04	
ex13-13b *	CC	24	-14.34	ref	0.455	GG	26	-14.48	ref	0.766

	TC	14	-14.68	0.79		TG	12	-14.44	1.03	
	TT	2	-15.21	0.55		TT	2	-15.01	0.69	
Proinsulin *	CC	27	-1.19	ref	0.851	GG	28	-1.04	ref	0.640
	TC	14	-1.35	0.90		TG	13	-1.47	0.74	
	TT	3	-.80	1.31		TT	3	-1.64	0.66	
Proglucagon *	CC	26	-1.62	ref	0.374	GG	28	-1.44	ref	0.770
	TC	15	-1.76	0.91		TG	13	-1.82	0.77	
	TT	3	-.31	2.48		TT	3	-1.79	0.78	
Ghrelin/ obestatin *	CC	27	-8.38	ref	0.749	GG	29	-8.34	ref	0.923
	TC	15	-8.52	0.91		TG	13	-8.53	0.88	
	TT	3	-7.72	1.58		TT	3	-8.18	1.12	
Somatostatin *	CC	27	-2.38	ref	0.212	GG	29	-2.30	ref	0.617
	TC	15	-2.89	0.70		TG	13	-2.78	0.72	
	TT	3	-1.26	2.17		TT	3	-2.80	0.71	
Chromogranin A *	CC	27	-3.01	ref	0.705	GG	29	-2.95	ref	0.963
	TC	15	-2.94	1.05		TG	13	-2.88	1.05	
	TT	3	-2.37	1.56		TT	3	-3.10	0.90	

* expression of assays, normalized to expression level of reference gene B2M, Log 2 scale

** p-values for univariate linear regression under an additive genetic model for SNPs, not adjusted for covariates

Supplementary Table 6D. Sample characteristics and *T2F7L2* expression by genotypes of SNPs in colon, n=128

Traits and assays	**rs7903146**					**rs12255372**				
	geno types	n	mean	fold	p-value **	geno types	n	mean	fold	p-value **
BMI, kg/m2	CC	48	27.06	ref	0.547	GG	46	27.38	ref	0.933
	TC	25	27.74	1.03		TG	28	27.58	1.01	
	TT	7	30.04	1.11		TT	6	28.47	1.04	
Age, years	CC	73	57.92	ref	0.991	GG	70	56.50	ref	0.336
	TC	44	57.66	1.00		TG	48	60.50	1.07	
	TT	10	57.20	1.00		TT	9	53.11	0.94	
TSS1 *	CC	49	-2.94	ref	0.313	GG	47	-2.89	ref	0.839
	TC	29	-2.98	0.97		TG	31	-2.98	0.94	
	TT	5	-2.46	1.39		TT	5	-2.93	0.97	
TSS2 *	CC	49	-5.65	ref	0.843	GG	45	-5.63	ref	0.962
	TC	28	-5.69	0.97		TG	31	-5.67	0.97	
	TT	4	-5.47	1.13		TT	5	-5.71	0.95	
TSS3 *	CC	49	-13.12	ref	0.722	GG	45	-13.08	ref	0.568
	TC	28	-13.25	0.91		TG	31	-13.31	0.85	
	TT	4	-13.51	0.76		TT	5	-13.41	0.80	
ex3a-4 *	CC	49	-6.68	ref	0.400	GG	45	-6.65	ref	0.728
	TC	28	-6.87	0.88		TG	31	-6.83	0.88	
	TT	4	-6.25	1.35		TT	5	-6.76	0.93	
ex7-8 *	CC	49	-5.21	ref	0.538	GG	45	-5.22	ref	0.509
	TC	28	-5.40	0.88		TG	31	-5.34	0.92	
	TT	4	-5.53	0.80		TT	5	-5.66	0.74	
ex11-13 *	CC	52	-11.59	ref	0.999	GG	50	-11.55	ref	0.644
	TC	29	-11.60	0.99		TG	31	-11.71	0.90	
	TT	5	-11.60	0.99		TT	8	-11.35	1.15	
ex12-13 *	CC	51	-10.81	ref	0.834	GG	49	-10.74	ref	0.920
	TC	29	-10.68	1.09		TG	31	-10.85	0.93	
	TT	5	-10.75	1.04		TT	5	-10.71	1.02	
ex13-13a *	CC	49	-13.95	ref	0.507	GG	47	-13.90	ref	0.431
	TC	29	-13.73	1.16		TG	31	-13.78	1.09	
	TT	5	-14.21	0.84		TT	5	-14.41	0.70	
ex11-13a *	CC	52	-8.53	ref	0.798	GG	50	-8.53	ref	0.264
	TC	30	-8.52	1.01		TG	31	-8.37	1.12	
	TT	5	-8.25	1.21		TT	5	-9.04	0.70	
ex11-14 *	CC	52	-8.73	ref	0.577	GG	50	-8.72	ref	0.752
	TC	31	-8.62	1.08		TG	32	-8.62	1.07	
	TT	5	-8.45	1.28		TT	5	-8.53	1.14	
ex13-14 *	CC	57	-8.45	ref	0.215	GG	54	-8.36	ref	0.294
	TC	33	-8.45	1.00		TG	37	-8.70	0.79	
	TT	8	-9.10	0.64		TT	8	-8.64	0.82	
ex13-13b *	CC	59	-12.55	ref	0.290	GG	56	-12.40	ref	0.200

	TC	33	-12.56	0.99		TG	37	-12.83	0.74	
	TT	9	-12.63	0.95		TT	8	-13.33	0.52	
VIP *	CC	58	-5.92	ref	0.211	GG	55	-5.81	ref	0.540
	TC	34	-5.79	1.09		TG	38	-6.11	0.81	
	TT	9	-6.71	0.58		TT	8	-6.19	0.77	
Proglucagon *	CC	56	-7.82	ref	0.173	GG	54	-7.61	ref	0.892
	TC	32	-7.21	1.53		TG	36	-7.63	0.99	
	TT	9	-7.66	1.12		TT	7	-7.34	1.21	
Somatostatin *	CC	58	-8.61	ref	0.565	GG	55	-8.44	ref	0.419
	TC	33	-8.25	1.28		TG	37	-8.66	0.86	
	TT	9	-8.55	1.04		TT	8	-7.89	1.46	
Chromogranin A *	CC	58	-4.52	ref	0.214	GG	55	-4.27	ref	0.912
	TC	33	-3.99	1.44		TG	37	-4.37	0.93	
	TT	9	-4.12	1.32		TT	8	-4.17	1.07	

* expression of assays, normalized to expression level of reference gene B2M, Log 2 scale

** p-values for univariate linear refression under an additive genetic model for SNPs, not adjusted for covariates

Supplementary Table 6E. Sample characteristics and *T2F7L2* expression by genotypes of SNPs in peripheral blood monocytes, n=65

	rs7903146					**rs12255372**				
Traits and assays	geno types	n	mean	fold	p-value **	geno types	n	mean	fold	p-value **
Age, years	CC	33	43.07	ref	0.057	GG	38	44.32	ref	0.129
	TC	23	50.74	1.18		TG	22	49.73	1.12	
	TT	7	51.29	1.19		TT	3	56.33	1.27	
TSS1 *	CC	33	-3.20	ref	0.909	GG	38	-3.24	ref	0.516
	TC	23	-3.08	1.09		TG	24	-2.96	1.21	
	TT	7	-3.12	1.06		TT	3	-3.40	0.90	
TSS2 *	CC	33	-5.02	ref	0.781	GG	38	-5.06	ref	0.283
	TC	23	-4.84	1.13		TG	24	-4.70	1.28	
	TT	7	-4.90	1.09		TT	3	-5.25	0.88	
TSS3 *	CC	33	-9.01	ref	0.731	GG	38	-9.16	ref	0.115
	TC	23	-8.90	1.08		TG	24	-8.61	1.46	
	TT	7	-8.80	1.16		TT	3	-8.98	1.13	
ex3a-4 *	CC	33	-6.48	ref	0.759	GG	38	-6.51	ref	0.129
	TC	23	-6.32	1.12		TG	24	-6.19	1.25	
	TT	7	-6.50	0.99		TT	3	-7.03	0.70	
ex7-8 *	CC	33	-5.63	ref	0.550	GG	38	-5.60	ref	0.595
	TC	23	-5.44	1.14		TG	24	-5.48	1.09	
	TT	7	-5.85	0.86		TT	3	-6.06	0.73	
ex11-13 *	CC	33	-10.13	ref	0.930	GG	38	-10.16	ref	0.284
	TC	23	-10.10	1.02		TG	24	-10.02	1.10	
	TT	7	-10.18	0.97		TT	3	-10.49	0.80	
ex12-13 *	CC	33	-7.48	ref	0.969	GG	38	-7.49	ref	0.577
	TC	23	-7.52	0.97		TG	24	-7.47	1.01	
	TT	7	-7.51	0.98		TT	3	-7.88	0.76	
ex13-13a *	CC	33	-10.33	ref	0.762	GG	38	-10.33	ref	0.551
	TC	23	-10.42	0.94		TG	24	-10.43	0.93	
	TT	7	-10.51	0.88		TT	3	-10.72	0.76	
ex11-13a *	CC	33	-8.58	ref	0.915	GG	38	-8.60	ref	0.804
	TC	23	-8.60	0.99		TG	24	-8.57	1.02	
	TT	7	-8.66	0.95		TT	3	-8.76	0.90	
ex11-14 *	CC	33	-7.19	ref	0.834	GG	38	-7.17	ref	0.837
	TC	23	-7.14	1.04		TG	24	-7.17	1.00	
	TT	7	-7.27	0.95		TT	3	-7.34	0.89	
ex13-14 *	CC	33	-6.95	ref	0.293	GG	38	-6.94	ref	0.259
	TC	23	-6.69	1.20		TG	24	-6.60	1.27	
	TT	7	-6.53	1.34		TT	3	-6.72	1.16	

* expression of assays, normalized to expression level of reference gene B2M, Log 2 scale
** p-values for univariate linear regression under an additive genetic model for SNPs, not adjusted for covariates

Supplementary Table 6F. Sample characteristics and *T2F7L2* expression by genotypes of SNPs in liver, n=62

Traits and assays	rs7903146					rs12255372				
	geno types	n	mean	fold	p-value **	geno types	n	mean	fold	p-value **
Age, years	CC	29	49.03	ref	0.841	GG	33	49.60	ref	0.820
	TC	27	48.96	0.99		TG	23	48.13	0.97	
	TT	3	40.67	0.83		TT	3	40.67	0.82	
TSS1 *	CC	31	-4.97	ref	0.656	GG	34	-5.00	ref	0.651
	TC	28	-4.99	0.99		TG	25	-4.95	1.04	
	TT	3	-4.32	1.57		TT	3	-4.32	1.60	
TSS2 *	CC	31	-4.31	ref	0.605	GG	34	-4.33	ref	0.616
	TC	28	-4.36	0.97		TG	25	-4.35	0.99	
	TT	3	-3.71	1.52		TT	3	-3.71	1.54	
TSS3 *	CC	31	-10.96	ref	0.912	GG	34	-10.91	ref	0.716
	TC	28	-11.07	0.93		TG	25	-11.14	0.85	
	TT	3	-10.93	1.02		TT	3	-10.93	0.99	
ex3a-4 *	CC	31	-4.09	ref	0.455	GG	34	-4.09	ref	0.404
	TC	28	-4.37	0.82		TG	25	-4.41	0.80	
	TT	3	-3.62	1.39		TT	3	-3.62	1.39	
ex7-8 *	CC	31	-0.66	ref	0.998	GG	34	-0.62	ref	0.857
	TC	28	-0.67	0.99		TG	25	-0.74	0.92	
	TT	3	-0.65	1.01		TT	3	-0.67	0.97	
ex11-13 *	CC	31	-8.65	ref	0.967	GG	34	-8.63	ref	0.973
	TC	28	-8.62	1.02		TG	25	-8.64	0.99	
	TT	3	-8.53	1.09		TT	3	-8.53	1.07	
ex12-13 *	CC	31	-8.09	ref	0.579	GG	34	-8.10	ref	0.561
	TC	28	-8.36	0.83		TG	25	-8.38	0.82	
	TT	3	-7.88	1.16		TT	3	-7.88	1.16	
ex13-13a *	CC	31	-9.37	ref	0.859	GG	34	-9.37	ref	0.862
	TC	28	-9.47	0.93		TG	25	-9.47	0.93	
	TT	3	-9.11	1.20		TT	3	-9.11	1.20	
ex11-13a *	CC	31	-7.28	ref	0.751	GG	34	-7.28	ref	0.756
	TC	28	-7.31	0.98		TG	25	-7.31	0.98	
	TT	3	-6.84	1.36		TT	3	-6.84	1.36	
ex11-14 *	CC	31	-7.08	ref	0.522	GG	34	-7.07	ref	0.516
	TC	28	-6.91	1.13		TG	25	-6.90	1.13	
	TT	3	-6.28	1.74		TT	3	-6.28	1.73	
ex13-14 *	CC	31	-8.30	ref	0.619	GG	34	-8.29	ref	0.504
	TC	28	-8.52	0.86		TG	25	-8.56	0.83	
	TT	3	-8.18	1.09		TT	3	-8.18	1.08	

* expression of assays, normalized to expression level of reference gene B2M, Log 2 scale

** p-values for univariate linear regression under an additive genetic model for SNPs, not adjusted for covariates

Supplementary Table 6G. Sample characteristics and *T2F7L2* expression by genotypes of SNPs in subcutaneous adipose tissue, n=14

Traits and assays	rs7903146					rs12255372				
	geno types	n	mean	fold	p-value **	geno types	n	mean	fold	p-value **
BMI, kg/m2	CC	7	32.09	ref	0.206	GG	6	32.07	ref	0.252
	TC	6	27.63	0.86		TG	7	28.29	0.88	
	TT	1	20.00	0.62		TT	1	20.00	0.62	
Age, years	CC	7	45.71	ref	0.331	GG	6	46.33	ref	0.508
	TC	5	50.40	1.10		TG	6	49.00	1.06	
	TT	1	40.00	0.88		TT	1	40.00	0.86	
P1ex1 *	CC	7	-1.13	ref	0.606	GG	6	-1.18	ref	0.561
	TC	6	-0.84	1.22		TG	7	-0.85	1.26	
	TT	1	-1.55	0.75		TT	1	-1.55	0.77	
P2ex1 *	CC	7	-2.34	ref	0.900	GG	6	-2.28	ref	0.816
	TC	6	-2.49	0.90		TG	7	-2.52	0.85	
	TT	1	-2.18	1.12		TT	1	-2.18	1.07	
P2intr1 *	CC	7	-6.67	ref	0.254	GG	6	-6.71	ref	0.233
	TC	6	-7.00	0.80		TG	7	-6.92	0.86	
	TT	1	-5.04	3.10		TT	1	-5.04	3.18	
ex3a-4 *	CC	7	-4.30	ref	0.242	GG	6	-4.22	ref	0.423
	TC	6	-4.27	1.02		TG	7	-4.34	0.92	
	TT	1	-2.89	2.66		TT	1	-2.89	2.51	
ex7-8 *	CC	7	-4.25	ref	0.523	GG	6	-4.20	ref	0.539
	TC	6	-4.20	1.04		TG	7	-4.25	0.97	
	TT	1	-3.22	2.04		TT	1	-3.22	1.97	
ex11-13 *	CC	7	-6.64	ref	0.704	GG	6	-6.59	ref	0.781
	TC	6	-6.50	1.10		TG	7	-6.56	1.02	
	TT	1	-6.20	1.36		TT	1	-6.20	1.31	
ex12-13 *	CC	7	-6.00	ref	0.291	GG	6	-5.93	ref	0.272
	TC	6	-6.00	1.00		TG	7	-6.06	0.91	
	TT	1	-4.85	2.22		TT	1	-4.85	2.11	
ex13-13a *	CC	7	-8.57	ref	0.113	GG	6	-8.47	ref	0.113
	TC	6	-8.47	1.07		TG	7	-8.57	0.93	
	TT	1	-6.72	3.61		TT	1	-6.72	3.36	
ex11-13a *	CC	7	-7.34	ref	0.504	GG	6	-7.32	ref	0.591
	TC	6	-6.94	1.32		TG	7	-7.02	1.23	
	TT	1	-6.39	1.93		TT	1	-6.39	1.91	
ex11-14 *	CC	7	-5.07	ref	0.992	GG	6	-4.96	ref	0.811
	TC	6	-5.12	0.97		TG	7	-5.20	0.85	
	TT	1	-5.10	0.98		TT	1	-5.10	0.91	
ex13-14 *	CC	7	-5.20	ref	0.557	GG	6	-5.16	ref	0.614
	TC	6	-5.04	1.12		TG	7	-5.10	1.04	
	TT	1	-4.51	1.61		TT	1	-4.51	1.57	

* expression of assays, normalized to expression level of reference gene B2M, Log 2 scale; ** p-values for univariate linear regression under an additive genetic model for SNPs, not adjusted for covariates

Supplementary Table 6H. Sample characteristics and *T2F7L2* expression by genotypes of SNPs in skeletal muscles, n=25

	rs7903146					**rs12255372**				
Traits and assays	geno types	n #	mean	fold	**p-value	geno types	n #	mean	fold	** p-value
Age, years	CC	16	18.19	ref	0.436	GG	12	18.75	ref	0.849
	TC	4	28.00	1.53		TG	9	21.33	1.13	
	TT	5	15.80	0.87		TT	4	16.25	0.87	
TSS1 *	CC	18	-2.09	ref	0.970	GG	13	-2.20	ref	0.227
	TC	4	-2.05	1.03		TG	10	-1.85	1.27	
	TT	6	-2.04	1.04		TT	5	-2.19	1.01	
TSS2 *	CC	18	-3.49	ref	0.547	GG	13	-3.57	ref	0.182
	TC	4	-3.26	1.17		TG	10	-3.23	1.27	
	TT	6	-3.32	1.12		TT	5	-3.39	1.14	
TSS3 *	CC	17	-8.71	ref	0.558	GG	12	-8.79	ref	0.397
	TC	4	-8.42	1.22		TG	10	-8.38	1.33	
	TT	6	-8.39	1.25		TT	5	-8.56	1.18	
ex3a-4 *	CC	18	-4.91	ref	0.346	GG	13	-5.00	ref	0.110
	TC	4	-4.46	1.36		TG	10	-4.55	1.38	
	TT	6	-4.85	1.04		TT	5	-4.94	1.05	
ex7-8 *	CC	18	-4.43	ref	0.749	GG	13	-4.59	ref	**0.049**
	TC	4	-4.27	1.12		TG	10	-4.10	1.40	
	TT	6	-4.29	1.10		TT	5	-4.41	1.13	
ex11-13 *	CC	18	-6.92	ref	**0.009**	GG	13	-7.03	ref	**0.005**
	TC	4	-6.10	1.76		TG	10	-6.33	1.63	
	TT	6	-6.44	1.39		TT	5	-6.56	1.39	
ex12-13 *	CC	18	-6.62	ref	0.474	GG	13	-6.71	ref	0.370
	TC	4	-6.62	1.00		TG	10	-6.45	1.20	
	TT	6	-6.26	1.28		TT	5	-6.29	1.34	
ex13-13a *	CC	18	-9.51	ref	0.831	GG	13	-9.55	ref	0.800
	TC	4	-9.46	1.03		TG	10	-9.38	1.12	
	TT	6	-9.32	1.14		TT	5	-9.40	1.11	
ex11-13a *	CC	18	-8.74	ref	0.735	GG	13	-8.81	ref	0.481
	TC	4	-8.50	1.18		TG	10	-8.53	1.21	
	TT	6	-8.70	1.03		TT	5	-8.74	1.05	
ex11-14 *	CC	18	-5.88	ref	0.094	GG	13	-6.03	ref	**0.008**
	TC	4	-5.34	1.45		TG	10	-5.39	1.56	
	TT	6	-5.50	1.30		TT	5	-5.59	1.36	
ex13-14 *	CC	17	-6.44	ref	0.357	GG	12	-6.51	ref	0.170
	TC	4	-5.95	1.40		TG	10	-6.05	1.38	
	TT	6	-6.30	1.10		TT	5	-6.48	1.02	

* expression of assays, normalized to expression level of reference gene B2M, Log 2 scale

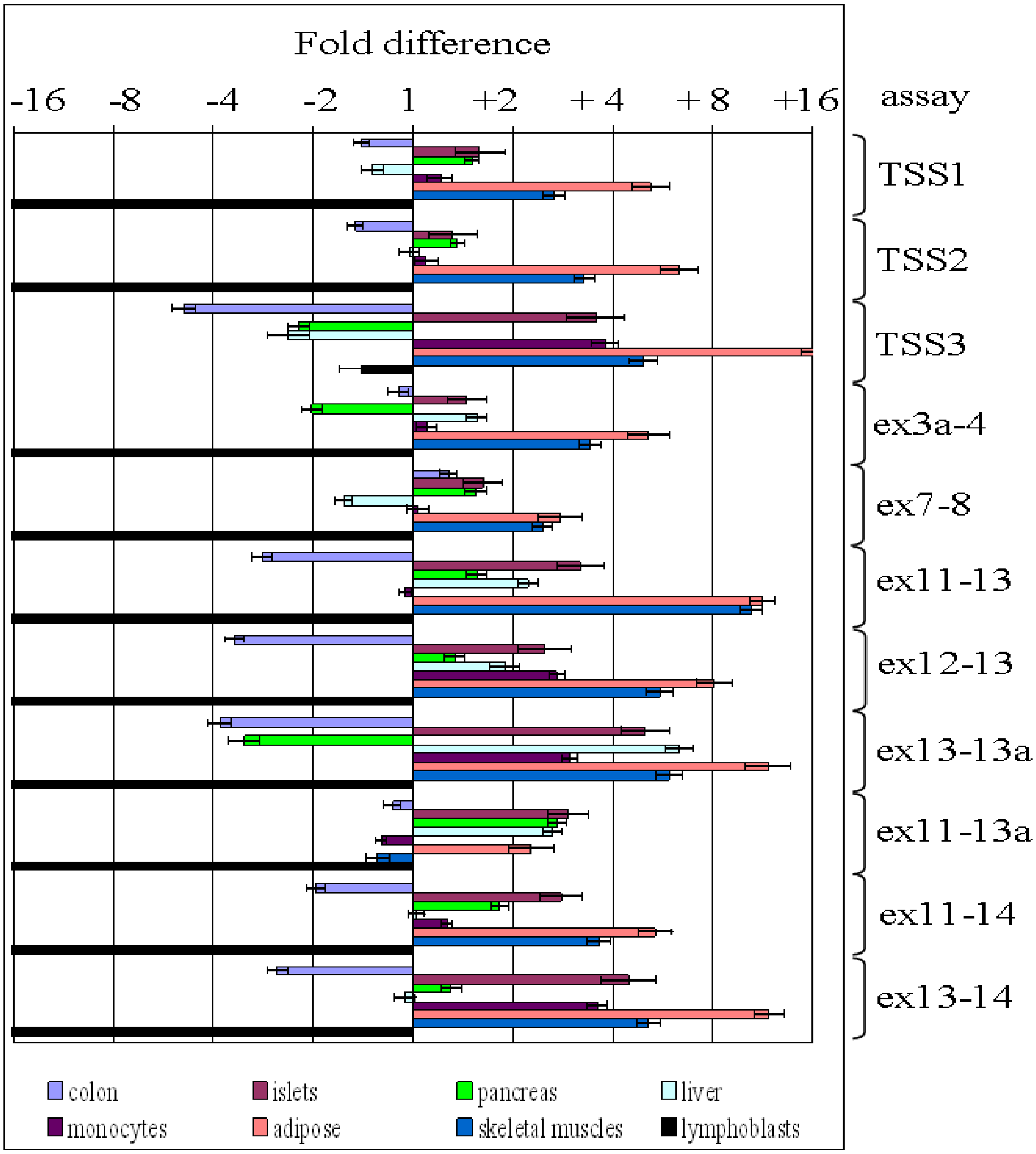
** p-values for univariate linear regression under an additive genetic model for SNPs not adjusted for covariates; in bold p-values <0.05; # - samples for expression analysis were selected based on genotypes

Supplementary Table 7. Primers and probes for expression assays used in this study

Expression assays, Type	Primers, probes or commercial assays from Applied Biosystems	Amplicon size, bp
TCF7L2,TSS1 SYBR Green	P1ex1F: GGTGGAGGGGATGACCTA Ex3R: GGGATCATGATGAAGGGGTA	307 bp
TCF7L2, TSS2 SYBR Green	P2ex1F: AAACGAATCAAAACAGCTCCT Ex3R: GGGATCATGATGAAGGGGTA	168 bp
TCF7L2, TSS3 SYBR Green	P2intr1F: TTCTTTTTCTCCCCCTTCTCC Ex3R: GGGATCATGATGAAGGGGTA	211 bp
TCF7L2, ex3a SYBR Green	Ex3aF: ACTCTGCGTACAAAACGATTGA Ex4R: AGCAGTGGCCATTTCATCTG	66 bp
TCF7L2, ex4a SYBR Green	Ex4F: GGCCACTGCTTGATGTCC Ex4aR: TGAGTGCTGACAGTGAAGTCTG	162 bp
TCF7L2, ex7-8, TaqMan	Hs00181036_m1	
TCF7L2, ex11-13, TaqMan	Ex11F: GAAGAAGAGGAAAAGGGACAAGCA Ex13R: GCGCTCGGCATTTCTTAGGA FAM-probe: CAGGTCATTGGTCTCTCC	70 bp
TCF7L2, ex11-13a, TaqMan	Ex11F: GAAGAAGAGGAAAAGGGACAAGCA Ex13aR: CGGTCAAGCCCGAACAGT FAM-probe: ACCAATGATGCAAATACT	86 bp
TCF7L2, ex11-14, TaqMan	Ex11F: CGCGGGATAACTATGGAAAGAAGAA Ex14R: CTTGTATGTAGCGAACGCACTTTT FAM-probe: TTTTCTCATTGGTCTCTCCCGGCTG	94 bp
TCF7L2, ex12-13, TaqMan	Ex12F: ACACAGCGAATGTTTCCTAAATCCT Ex13R: CGCGCTCGGCATTTCTTAG FAM-probe: TTCCTCCGATTACAGACCTG	80 bp
TCF7L2, ex13-13a, TaqMan	Ex13F: GCTTTGGCCTTGATCAACAGAATAA Ex13aR: CGGTCAAGCCCGAACAGT FAM-probe: TTGCAGATGCAAATACT	88 bp
TCF7L2, ex13-14, TaqMan	Ex13F: GCTTTGGCCTTGATCAACAGAATAA Ex14R: CTTGTATGTAGCGAACGCACTTTT FAM-probe: TCTCCTGCAAGGGCC	74 bp

TCF7L2, ex13-13b, TaqMan	Ex13F: GCTTTGGCCTTGATCAACAGAATAA Ex13bR: CGAACGCACTTTTTTTTTCTCCATT FAM-probe: CCCTTGCAGTCTTTG	88 bp
Proinsulin	Hs02741908_m1	
Proglucagon	HS00174967_m1	
Somatostatin	HS00356144_m1	
Ghrelin/obestatin	HS00175082_m1	
Chromogranin A	HS00900373_m1	
PDX1 (Insulin –promoter Factor 1, IPF1)	Hs00236830_m1	
Vasoactive Intestinal Peptide (VIP)	HS00175021_m1	
Proliferating Cell Nuclear Antigen (PCNA)	HS00427214_g1	
GAPDH	4333764F	
B2M	HS00173470_m1	

Supplementary Figure 1. Relative expression of *TCF7L2* assays in 289 samples from 8 human tissues



Expression in each tissue is normalized to levels of endogenous control B2M and presented as fold difference relative to the mean expression of all tissue samples (on log2 scale) for each assay. Low expression in lymphoblastoid cell lines is not shown in full scale. Error bars indicate mean values with 95% confidence intervals. This figure illustrates lower variation in expression of some assays – TSS1, “ex7-8”, “ex11-13a” and higher variation in expression of other assays – TSS3, “ex11-13”, ex12-13”, “ex13-13a”, “ex13-14”.

Supplementary Figure 2.

Difference in expression of *TCF7L2* assays between pancreas and pancreatic islets.
A “zero” dotted line represents similar expression between the tissues. Error bars show 95% confidence intervals in expression.