Supplementary Table S2. eQTL-analysis of SNPs associated with T2D

Gene	SNP	Location	SNP type	Alleles	Ancestral	Assessed allele	eQTLGen (blood)		Pancreas	Liver	Adipose - Visceral	Skeletal muscle	Brain	Tibial nerve	Artery/ Aorta	Kidney	sQTLs
							Cis	*Trans*									
GCLC	rs17883901	6:53545239	intron variant	G/A	G	A	-	-	-	-	GCLC(↑)	-	-	--	-	-	
GCLC	rs761142	6:53527310	intron variant	A/C	C	C	GCLC (↓)	-	-	-	-	-	GCLC (↓	-	-	-	-
GCLM	rs7517826	1:93899778	intron variant	C/A	C	A	GCLM (↑) DR1(↑) DNTTIP2 (↓) BCAR3(↓) TMED5(↓)	-	GCLM(↓ RP11-488P3,1(↓	-	GCLM(↓) RP11-488P3,1(↓)	GCLM(↓) RP11-488P3,1(↓)	GCLC (↓	GCLM(↓)	RP11-488P3,1(↓) GCLM(↓) RP11-488P3,1(↓) GCLM(↓) BCAR3(↓)	-	DNTTIP2(Arter
GCLM	rs41303970	1:93909753	TF binding site	G/A	G	A	BCAR3(↓)	-	GCLM (↓	-	GCLM (↓)	GCLM (↓)	GCLM (↓	GCLM(↓)	GCLM (↓)		-
GSS	rs6088660	20:34955093	5 prime UTR variant	C/T	C	T	GSS(↑) TRPC4AP(↑) EDEM2(↑) NCOA6(↑) GGT7(↓) MAP1LC3A (↓ EIF6 (↓) TP53INP2 (↓ MYH7B (↓) RP4-614O4,12(↓)	-	-	-	EDEM2(↑)	GSS(↑) GGT7(↑) NCOA6(↑)	NCOA6(↑)	GSS(↑) TRPC4AP(↑ ACSS2(↑) NCOA6 (↑ MYH7B(↓)	NCOA6(↑) MYH7B(↓) TP53INP2(↓ GSS(↓) PIGU(↓) TRPC4AP(↓	-	TRPC4AP (Pancreas, Live Adipose – Visceral, Skelet muscle, Brain) PROCR Skeleta muscle
GSS	rs13041792	20:34957252	intergenic variant	G/A	G	A	MAP1LC3A(↑ MYH7B(↑) EIF2S2(↑) ITCH(↑) RBM39(↑) TRPC4AP(↓) EDEM2(↓) UQCC(↓) CPNE1(↓) GGT7(↓) RP4-614O4,12(↓) PROCR(↓) MMP24-AS1 CEP250(↓)	-	EDEM2(↑ PROCR(↑ MYH7B(↑	PROCR(↑ TRPC4AI ↓) MYH7B(↑	MAP1LC3A ↑) MYH7B(↑) EDEM2(↓) TRPC4AP(↓	EDEM2(↓) PROCR(↓) GGT7(↑) NFS1(↑)	MYH7B(↑ EDEM2(↓ MAP1LC A(↑) MMP24-AS1(↓) ACSS2(↑	-	EDEM2(↓) MYH7B(↑) PROCR(↓) MAP1LC3A ↑)	-	UQCC1 (Skeleta muscle) TRPC4AP (Brai Artery) PROCR (Artery nerve)
GGT1	rs4820599	22:24594246	intron variant	A/G	G	G	GGT1(↓) FAM211B(↓) BCRP3(↓)	KIR2DL3(↓)	GGT1(↑)	-	-	-	-	-	-	-	BCRP3(Brain)

GGT1	rs5751909	22:24617379	intron variant	G/A	G	A	GGT1(↓) FAM211B(↓) BCRP3(↓) SGSM1(↓)	-	GGT1(↑)	-	-	-	-	BCRP3(↓)	-		BCRP3(Brain)
GGT1	rs5760489	22:24594679	intron variant	A/G	G	G	GGT1(↓) FAM211B(↓) BCRP3(↓)	-	GGT1(↑)	-	-	-	-	LRRC75B(↓	-	-	BCRP3(Brain)
GGT1	rs5760492	22:24599235	non coding transcript exon variant	G/A	G	A	GGT1(↓) FAM211B(↓) BCRP3(↓) SGSM1(↓)	-	GGT1(↑)	GGT1(↑)	-	-	GGT1(↓)	GGT1(↓) LRRC75B(↓	-	-	BCRP3(Brain)
GGT5	rs2275984	22:24226680	missense variant	T/C?	C	C	GGT5(↓) GGT1(↓) GSTT1(↓) UPB1(↓) AP000355,2(↓ DDT(↓) SUSD2(↓) SPECC1L(↓) ADORA2A(↑	-	POM121L P(↓)	-	POM121L9I ↓)	POM121L9I ↓)	POM121L P(↓)	POM121L9 UPB1	POM121L9I ↓) SPECC1L(↑	-	-	
GGT5	rs8140505	22:24220908	intron variant	A/G	G	G	GSTT1(↑) SUSD2(↑) DDT(↑) AP000351,10(' AP000355,2(↓ UPB1(↓)	-	-	-	POM121L9I ↓)	AP000351,4( )	-	POM121L9I ↓)	-	-	-	
GGT5	rs4822473	22:24235823	intron variant	A/G	A	G	GSTT1(↑) SUSD2(↑) AP000351,10(' DDT(↑) SPECC1L(↑) AP000350,6(↑ ADORA2A(↑ UPB1(↓) AP000355,2(↓	-	-	-	POM121L9I ↓)	GGT5(↑)	-	POM121L9I ↓)	POM121L9I ↓)	-	-	
GGT6	rs11657054	17:4559728	missense variant	G/A	G	G	CXCL16(↑) MYBBP1A(↓	-	GGT6(↑)	GGT6(↑)	MYBBP1A('	-	-	MYBBP1A('	MYBBP1A('	-	-	
GGT6	rs2100986	17:4562207	regulatory region variant	C/G/T	T	C	CXCL16(↑) ALOX15(↑) PLD2(↓) MYBBP1A(↓	-	GGT6(↑)	-	MYBBP1A('	-	-	MYBBP1A	MYBBP1A('	-	-	
GGT7	rs11546155	20:34863345	synonymous variant	G/A	G	A	TRPC4AP(↑) NCOA6(↑) EDEM2(↑) EIF6(↑) GSS(↑) PROCR(↑)	-	-	-	GGT7(↓) NCOA6(↑) MAP1LC3A	PIGU(↑) GSS(↑)	NCOA6(↑	NCOA6(↑) MAP1LC3A ↓) FDX1P1(↓)	TP53INP2(↓ NCOA6 MAP1LC3A ↓) GGT7(↓) PIGU		TRPC4AP (adipose)	

						MAP1LC3A(↓) TP53INP2(↓) ITCH(↓) RP4-614O4,12(↓)											
GGT7	rs6119534	20:34853454	intron variant	C/G/T	C	T	MAP1LC3A(↑) ITCH(↑) EIF2S2(↑) MYH7B(↑) EDEM2(↓) GGT7(↓) RP4-614O4,12(↓) UQCC(↓) PROCR(↓) RP5-1125A11,1(↓) TRPC4AP(↓)	-	EDEM2(↑) PROCR(↑) MYH7B(↑)	MAP1LC3A(↑)	MAP1LC3A(↑)	GGT7(↑) ACSS2 (↑) MAP1LC3A(↑) GSS(↑) PROCR(↓) EDEM2(↓)	EDEM2(↓) MYH7B(↑) MAP1LC3A(↑) ACSS2(↑	MAP1LC3A(↑) ACSS2(↑) MYH7B(↑) FDX1P1(↑) EDEM2(↓) RP5-1125A11,7(↓) PROCR(↓)	MAP1LC3A(↑) EDEM2(↓) PROCR(↓) TP53INP2(↑) NCOA6(↑)		TRPC4AP (arter adipose) GSS (skeletal, adipose) MAP1LC3A(Bra n) GGT7 (skeletal
GGCT	rs6462210	7:30499979	intron variant	C/T	T	T	AC005154,8(↓) AC005154,6(↓)	-	AC005154 (↓)	-	-	AC005154,6)	-	AC005154,6)	-	-	AC005154,6 (adipose)
GGCT	rs28679	7:30502181	intron variant	A/G	A	A	GGCT(↑) AC005154,6(↑) AC005154,8(↑) CRHR2(↑) GARS(↑) AC005154,5(↓)	-	GGCT(↓) AC005154 (↓) AC005154 (↓) AC005154 (↓)	AC005154 (↓)	AC005154, (↓) AC005154,7)	GGCT(↓) AC005154,6)	GGCT(↓) AC005154 (↓) AC005154 (↓) CRHR2(↓	GGCT(↓) AC005154,6) AC005154,8) RP4-777O23,1(↓) AC005154,7)	GGCT(↓) AC005154,6) AC005154,7) AC005154,8) RP4-777O23,1(↓	-	AC005154,6 (skeletal, adipos artery, brain, liver, pancreas nerve) GGCT (artery, brain, pancreas GGCT (nerve)
GSTP1	rs1695	11:67585218	missense variant	A/G		G	-	-	DOC2GP( ) NDUFV1( )	NUDT8(↑) CDK2AP2 ↑) RPS6KB2( )	GSTP1(↓) RPS6KB2(↓ NDUFV1(↑	GSTP1(↓) RPS6KB2(↓ AIP(↓) DOC2GP (↓ NUDT8(↑)	GSTP1(↓ DOC2GI (↓)	GSTP1(↓) DOC2GP(↓ NDUFV1(↑ NUDT8(↑)	GSTP1(↓) RPS6KB2(↓ DOC2GP(↑ NUDT8(↑) NDUFV1(↑	-	DOC2GP (artery NDUFV1 (skeletal,pancrea RPS6KB2 (skeletal, artery adipose) NDUFV1 (Brai artery, adipose
GSTP1	rs1138272	11:67586108	missense variant	C/T		T)	DOC2GP(↑) RPS6KB2(↑) ANKRD13D(↑) C11orf80(↑) LRFN4(↑) CCS(↓) CLCF1(↓) SSH3(↓) POLD4(↓) AIP(↓)	-	DOC2GP( ) ANKRD13D(↑)	ANKRD13D(↑)	ANKRD13D(↑) DOC2GP(↓ NDUFV1(↓	ANKRD13D(↑) PC(↑) DOC2GP(↓ RPS6KB2(↓	DOC2GP( )	CLCF1(↓) DOC2GP(↓ RAD9A(↓) NDUFV1(↑ ANKRD13D(↑)	GSTP1(↓) RPS6KB2(↓ ANKRD13D(↑)	-	-

							CORO1B(↓)									
RAC1	rs10951982	7:6382925	intron variant	G/A/T	G	A	DAGLB(↑) FAM220A(↑) ZDHHC4(↓)	-	DAGLB(↑	-	DAGLB(↑)	RAC1(↓) DAGLB(↑)	DAGLB(↑	DAGLB (↑ RAC1(↑)	DAGLB(↑)	-	DAGLB (nerve artery, brain) DAGLB (adipos pancreas, kidne liver,) RAC1 (artery)
RAC1	rs4724800	7:6370897	intergen ic variant	A/G	A	G	DAGLB(↑) FAM220A(↑) CCZ1B(↑) CCZ1(↓)	-	DAGLB(↑	-	DAGLB(↑)	DAGLB(↑)	DAGLB(↑	DAGLB(↑)	DAGLB(↑)	-	DAGLB (adipos nerve, artery) DAGLB (brain kidney, pancreas, skeletal) RAC1 (artery)
RAC1	rs7784465	7:6378644	intron variant	T/C	T	C	RAC1(↑) KDELR2(↑) FAM220A(↑) DAGLB(↓) ZDHHC4(↓)	-	-	-	RAC1(↑)	-	RAC1(↑)	RAC1(↑)	-	-	-
RAC1	rs836478	7:6392059	intron variant	C/T	T	**T**	DAGLB(↑) RAC1(↑) FAM220A(↑) GRID2IP(↑) AC073343,11(- CCZ1B(↓)	-	DAGLB(↑	-	DAGLB(↑)	-	DAGLB(↑	RAC1 DAGLB	DAGLB(↑)	-	RAC1 (skeletal DAGLB (artery brain, skeletal)
RAC1	rs9374	7:6402740	3 prime UTR variant	G/A?	G	A	-	-	DAGLB(↑	DAGLB(↑	DAGLB(↑)	RAC1(↓) DAGLB(↑)	RAC1(↑) DAGLB(↑	RAC1(↑) DAGLB(↑)	DAGLB(↑)	-	DAGLB (artery DAGLB (adipos brain, kidney, liver, skeletal, pancreas)
RAC1	rs10238136	7:6383715	intron variant	A/T	A	T	RAC1(↑) KDELR2(↓) DAGLB(↓)	-	-	-	-	-	-	-	-	-	-
RAC2	rs2239774	22:37241613	synony mous variant	G/C/T	G	C	RAC2(↑) RP1-151B14,9(↑) SSTR3(↑)	-	-	-	-	-	-	-	-	-	-
CYBA	rs9932581	16:88651945	3 prime UTR variant	C/T	C	T	MVD(↑) RNF166(↑) SNAI3-AS1(↑ GALNS(↓) TRAPPC2L(↓	-		-	-	-	MVD(↑)	-	-	-	-
CYBA	rs4673	16:88646828	missens e variant	A/G/T	A	A	SNAI3-AS1(↑ RNF166(↓) SNAI3(↓) MVD(↓)	-	-	-	-	-	-	CYBA (G) (- SNAI3-AS1(G)(↓)	CYBA (G)(↓ SNAI3-AS1(G)(↓)	-	-

CYBB	rs5963327	X:37813966	intron variant	G/T	G	T	-	-	-	-	-	XK(↑)	DYNLT3(	CYBB(↑)	CYBB(↑)	-	-	
CYBB	rs6610650	X:37777261	intron variant	G/A	A	A	-	-	-	-	-	XK (↑) DYNLT3(↓	DYNLT3(	CYBB(↑)	-	-		
NCF2	rs3754515	1:183593647	intron variant	C/A	C	A	NCF2(↑) ARPC5(↑) SMG7(↑) RGL1(↑) RP1-127C7,6(	-	-	ARPC5(↑	ARPC5(↑)	ARPC5(↑) NCF2(↓)	ARPC5(↑	ARPC5(↑)	ARPC5(↑) NCF2(↓)	-	ARPC5 (artery	
NCF2	rs789180	1:183556485	intron variant	A/T?	A	T	NCF2(↑) ARPC5(↓) RGL1(↓)	-	-	-	-	-	-	-	-	-		
NCF2	rs10911363	1:183580622	intron variant	G/T	G	T	NCF2(↑) SMG7(↓) ARPC5(↓) RGL1(↓) SMG7-AS1(↓	-	-	-	SMG7(↓)	NMNAT2(	SMG7(↓)	ARPC5(↓) SMG7(↓)	NCF2(↑) NMNAT2(SMG7(↓)	-	NMNAT2 (Brai	
NCF2	rs17849502	1:183563445	missens e variant	G/A/C /T	G	T	NCF2(↑) SMG7(↓) ARPC5(↓) RGL1(↓)	-	-	-	-	-	-	-	-	-	-	
NCF2	rs796860	1:183555720	3 prime UTR variant	C/A	A	C	SMG7(↑) NCF2(↓) ARPC5(↓) RGL1(↓)	-	-	-	SMG7-AS1(	-	ARPC5(↑	SMG7(↓) SMG7-AS1(	NMNAT2(	-	-	
NCF4	rs2075938	22:36870280	non coding transcrip t exon variant	A/G	G	A	TST(↑) PVALB(↑) CSF2RB(↑) MPST(↑) CSF2RBP1(↑ IFT27(↑) CTA-833B7,2(snoU13(↑)	-	-	-	-	-	-	-	-	-		
NCF4	rs4821544	22:36862461	intron variant	T/A/C	C	C	PVALB(↓) TST(↓) NCF4(↓)	HNRNPA1P2 ↑) RTKN2(↑)	-	-	NCF4(↓)	-	-	NCF4(↓)	NCF4(↓)	-	-	
NCF4	rs2075939	22:36875840	missens e variant	T/C	C	T	PVALB(↑) TST(↑) CSF2RB(↑) NCF4(↓) MPST(↑) IFT27(↑) CSF2RBP1(↑ snoU13(↑)	-	-	-	-	-	-	-	-	-	-	
NCF4	rs5995355	22:36855419	intron variant	A/G/T	G	G	PVALB(↓) TST(↓)	-	-	-	-	-	-	-	-	-	-	
NCF4	rs760519	22:36867664	intron	C/G/T	T	C	PVALB(↑)	-	-	-	-	-	-	-	-	-	-	

			variant				TST(↑) CSF2RB(↑) IFT27(↑) MPST(↑) CSF2RBP1(↑ snoU13(↑) CTA-833B7,2(											
NOXA1	rs28649497	9:137434689	3 prime UTR variant	C/T	T	T	NSMF(↑) NOXA1(↑) EXD3(↑)	-	NOXA1(↑ ENTPD8(-	NOXA1(↑	NOXA1(↑)	NOXA1(↑)	NOXA1(↑	NOXA1(↑) ENTPD8(↓ EXD3(↓)	NOXA1(↑) ENTPD8(↓	-	NOXA1(brain, artery,pancreas skeletal, liver) NOXA1(nerve)	
NOXA1	rs6606588	9:137422367	intron variant	G/A?	G	A	NSMF(↑) NOXA1(↑) EXD3(↑)	-	NOXA1(↑ ENTPD8(-	NOXA1(↑	NOXA1(↑)	NOXA1(↑)	NOXA1(↑	NOXA1(↑) ENTPD8(↓	NOXA1(↑) ENTPD8(↓	-	NOXA1 (artery pancreas, skeletal, liver, brain,adopose) NOXA1(nerve)	
NOX1	rs5921668	X:100847189	intron variant	G/A/C	A	A	-	-	SYTL4(↑	NOX1(↑	SYTL4(↑) TSPAN6(↓	SYTL4(↑) TSPAN6(↓	NOX1(↑) SYTL4(↑	NOX1(↑) TSPAN6(↓	NOX1 (↑) SYTL4(↑) SRPX2(↓) TSPAN6(↓	-	-	
NOX1	rs5921682	X:100875448	intergen ic variant	A/G?	A	G	-	-	SYTL4 (↑	-	-	-	NOX1(↑	-	SYTL4 (↑)	-	-	
NOX4	rs2164521	11:89476817	intron variant	G/A	A	-	-	-	-	-	-	-	-	-	-	-	-	
NOX4	rs2202150	11:89410138	intron variant	A/G	A	-	-	-	-	-	-	-	-	-	-	-	-	
NOX5	rs438866	15:69023103	non coding transcrip t exon variant	C/T	C	-	-	-	-	-	-	-	-	-	-	-	-	
NOX5	rs35672233	15:68930044	intron variant	C/T	C	-	-	-	-	-	-	-	-	-	-	-	-	
BECN1	rs10512488	17:42811886	non coding transcrip t exon variant	G/A	G	A	NT5C3B(↑) FAM134C(↑) NAGLU(↑) TUBG2(↑) NBR2(↑) CTD-3199J23,6(↑) HSD17B1P1(↓ BECN1(↓)	-	-	-	-	HSD17B1P1 ↓) CTD-3014M21,1(- HSD17B1(↓	-	NBR2(↑) EZH1(↑)	RP11-400F19,18(↑ NBR2(↑)	-	MLX (skeletal l, RAMP2-AS1(nerve, TUBG1 (brain) TUBG2 (nerve)	
GLIS3	rs10758593	9:4292083	intron variant	G/A	A	-	-	-	-	-	-	-	-	-	-	-	-	

GLIS3	rs10814916	9:4293150	intron variant	A/C	A	**C**	GLIS3(↓)	-	-	-	-	-	-	-	-	-	-	
GYS2	rs10841855	12:21599174	intron variant	G/T	G	T	GOLT1B(↓) C12orf39(↓)	-	-	-	-	-	-	PYROXD1(´	PYROXD1(´	-	-	
GRK5	rs10886471	10:119389891	intron variant	C/T	C	T	GRK5(↓)	-	-	-	-	-	-	-	-	-	-	
PPARG	rs11709077	3:12295008	intron variant	G/A	G	A	TSEN2(↑) SYN2(↓)	-	-	-	-	SYN2(↑)	-	-	-	-	-	
IGF2BP2	rs11927381	3:185790803	intron variant	T/C	C	C	LIPH(↑) EHHADH(↓	-	-	-	-	-	-	-	-	-	-	
KCNQ1	rs2237896	11:2837210	intron variant	G/A/T	G	A	CDKN1C(↓) NAP1L4(↓)	-	-	-	-	-	-	TSPAN32(↓	-	-	-	
DAAM1	rs35209784	14:59285112	intron variant	C/T	C	T	L3HYPDH(↑	-	-	-	-	-	-	DAAM1(↑	-	-	-	
HNF1B	rs4430796	17:37738049,	intron variant	A/G	G	-	-	-	-	-	-	-	-	-	-	-	-	
CDKAL1	rs4712524	6:20657634	intron variant	A/G	A	G	CDKAL1(↑)	-	-	-	-	-	-	-	-	-	-	
CDKAL1	rs6931514	6:20703721	intron variant	A/G	A	G	CDKAL1(↑)	-	-	-	-	-	-	-	-	-	-	
TCF7L2	rs7903146	10:112998590	intron variant	C/G/T	T	T	-	-	-	-	-	-	-	-	TCF7L2(↓)	-	-	