SUPPLEMENTAL MATERIAL

Table S1. Clinical characteristics of non-diabetic participants in the Diabetes Genetics Initiative (DGI) and the Prevalence, Prediction and Prevention of Diabetes (PPP-Botnia).

Characteristics	DGI	PPP-Botnia
N (male/female)	1467 (707/760)	4323 (2043/2280)
Age (years)	58.8 ± 10.1	47.6 ± 15.2
BMI (kg/m^2)	26.6 ± 3.7	26.3 ± 4.3
Fasting plasma glucose (mmol/l)	5.3 ± 0.5	5.3 ± 0.6
Glucose 30min (mmol/l)	8.3 ± 1.5	8.3 ± 1.6
Glucose 120 min (mmol/l)	5.6 ± 1.3	5.2 ± 1.6
Fasting insulin (mU/l)	5.2 (4.3)	5.3 (4.2)
Insulin 30 min (mU/l)	50.2 (48.9)	50.4 (38.3)
Insulin 120min (mU/l)	36.2 (29.7)	23.7 (26.2)
Insulinogenic index	14.1 (14.8)	15.9 (16.1)
HOMA-IR	1.46 (1.08)	1.26 (1.04)

Data are expressed as mean ± S.D or median (IQR). Insulinogenic index; calculated as ((insulin at 30 min – insulin at 0 min) / (glucose at 30 min – glucose at 0 min)). HOMA-IR; calculated as ((glucose at 0 min * insulin at 0 min)/22.5)).

Table S2 Spearman correlations (**ρ**) between expression of exocytotic genes and HbA1c, GSIS and BIS in human donors.

Gene	HbA1c (n=44)		GSIS (n=41)		BIS (n=43)	
	ρ	p-value	ρ	p-value	ρ	p-value
RIMS2	**-0.375**	**0.012**	0.156	0.331	0.265	0.069
SNAP25	**-0.289**	**0.057**	**0.289**	**0.067**	0.157	0.315
STX1A	**-0.259**	**0.089**	**0.345**	**0.027**	0.186	0.234
STXBP1	**-0.347**	**0.021**	0.208	0.193	0.058	0.711
STXBP2	**0.324**	**0.032**	-0.234	0.142	0.078	0.618
SYT4	**-0.260**	**0.089**	0.252	0.112	0.103	0.511
SYT7	-0.228	0.137	0.138	0.391	0.071	0.653
SYT11	-0.165	0.284	0.251	0.418	0.157	0.316
SYT13	**-0.287**	**0.059**	**0.347**	**0.026**	0.141	0.368
VAMP2	-0.185	0.229	0.174	0.277	-0.035	0.823

Data were obtained from non-diabetic donors and are presented by the Spearman correlation factor (**ρ**) and p-value of the association. Significant correlations (p<0.05) are indicated in bold black and almost significant in bold-grey (p<0.09). Notice that the correlations are in the same direction as results obtained from non-diabetic and T2D altogether. GSIS-Glucose Stimulated Insulin Secretion; BIS- Basal Insulin Secretion

Table S3. Genome locations used in SNP analysis.

Gene	CHR	Start	Stop position	Size (kbp)	n
RIMS1	6	72 643 371	73 179 229	535 859	61
RIMS2	8	104 572 152	105 344 627	772 476	78
SNAP25	20	10 147 477	10 236 065	108 589	28
STX1A	7	72 548 192	72 588 639	23 829	1
STXBP1	9	127 444 122	127 544 549	100 428	3
STXBP2	19	7 597 991	7 628 759	30 769	4
STXBP3	1	108 991 327	109 074 181	82 855	13
SYT1	12	77 750 241	78 358 255	608 015	88
SYT2	1	199 281 384	199 354 238	72 855	12
SYT3	19	55 807 048	55 843114	36 067	1
SYT4	18	39 091 855	39 121 613	29 759	2
SYT5	19	60 366 281	06 393 532	27 252	6
SYT6	1	114 333 956	114 418 514	84 559	21
SYT7	11	61 029 364	61 114 874	85 511	6
SYT8	11	1 802 250	1 825 326	23 077	1
SYT9	11	7 219 757	7 456 844	237 088	43
RAB3A	19	18 158 611	18 185 874	27 264	1
VAMP2	17	7 993 190	8 017 018	23 829	1
UNC13B	9	35 141 989	35 405 331	263 343	23

UCSC Genome Browser on Human May 2004 Assembly. An additional 10 kb has been added upstream and downstream of each gene. Where multiple ref seq entries have been available we have chosen the longest. CHR-chromosome, n-number of SNPs investigated for each gene.

Table S4. Candidate SNPs in the *RIMS1* gene

SNP	GENE	CHR	POSITION	MAF	LD	A1/A2	2h glc p-value	2h glc BETA	IGI p-value	IGI BETA
rs6926634	*RIMS1*	6	72800435	0.138		A/G	0.006	0.15±0.055	0.046	0.14±0.068
rs12524886	*RIMS1*	6	72762605	0.138		A/G	0.005	0.15±0.055	0.039	0.14±0.067
rs12524194	***RIMS1***	**6**	**72962342**	**0.248**		**A/G**	**0.021**	**0.10±0.043**	**0.004**	**0.15±0.051**
rs17746778	*RIMS1*	6	73111992	0.275		A/G	0.018	0.10±0.043	0.003	0.15±0.051
rs1339226	***RIMS1***	**6**	**73113269**	**0.275**		**C/T**	**0.011**	**0.11±0.043**	**0.003**	**0.15±0.051**
rs1546914	*RIMS1*	6	73114364	0.279		T/C	0.010	0.11±0.043	0.004	0.15±0.051
rs1883822	*RIMS1*	6	73093086	0.292		G/C	0.024	0.09±0.041	0.004	0.15±0.049
rs17690774	*RIMS1*	6	73129122	0.274		A/G	0.021	0.10±0.043	0.003	0.16±0.051
rs1416545	*RIMS1*	6	73178710	0.205		A/G	0.006	0.13±0.047	0.011	0.15±0.057

Candidate SNPs in *RIMS1* with MAF >0.05 and p-value < 0.05 in either 2 hour glucose (2h glc) or insulinogenic index (IGI), out of which at least one phenotypic trait must be < 0.01. Top-candidate SNPs (bold) were selected for replication. CHR-chromosome; POSITION- position of SNP; MAF-Minor Allele Frequency; LD- Linkage Disequilibrium where gray areas represent SNPs within the same LD-block; A1- minor allele; A2-major allele; p-value - GC corrected p-values from DGI were used; BETA-beta-coefficient which represent the proportion of 1 s.d. change (in standardized 2h glc and IGI with mean=0 and s.d.=1 after adjustment for age, gender, log BMI, recruitment centre and for IGI also including type of insulin measurement) per copy of the allele model.