

Supplementary Table S3 Impact of genes encoding enzymes for glutathione biosynthesis on expression levels of genes for protein folding and unfolded protein response in pancreatic β -cells of non-diabetics and diabetic patients (Dataset 1)

Independent gene (glutathione biosynthesis)	Dependent gene (protein folding /unfolded protein response)	<i>beta</i>	Standard error of <i>beta</i>	R ²	P-value	FDR adjusted P- value (Q- value)
Diabetic patients						
GCLC	<i>EP300</i>	-0.872	0.173	0.761	0.001	0.10
GCLC	<i>HSPA1L</i>	0.854	0.184	0.729	0.0016	0.10
GCLC	<i>MTOR</i>	-0.764	0.228	0.584	0.01	0.40
GCLC	<i>CALR</i>	0.724	0.244	0.524	0.018	0.54
GCLC	<i>DDIT3</i>	0.647	0.270	0.419	0.043	0.73
GCLC	<i>CREBRF</i>	-0.664	0.264	0.441	0.036	0.71
GCLC	<i>TM7SF4</i>	0.699	0.253	0.489	0.024	0.57
GCLM	<i>ATR</i>	-0.652	0.268	0.426	0.04	0.99
GCLM	<i>NUP153</i>	0.723	0.244	0.522	0.018	0.99
GCLM	<i>RAE1</i>	-0.697	0.254	0.485	0.025	0.99
GSS	<i>GSK3B</i>	0.653	0.268	0.427	0.04	0.26
GSS	<i>HSBP1</i>	0.691	0.256	0.477	0.026	0.21
GSS	<i>HSP90AA1</i>	0.634	0.274	0.401	0.049	0.29
GSS	<i>HSPA14</i>	-0.690	0.256	0.476	0.027	0.21
GSS	<i>NUP153</i>	-0.723	0.244	0.523	0.018	0.21
GSS	<i>NUP214</i>	0.643	0.271	0.413	0.045	0.28
GSS	<i>NUP58</i>	-0.677	0.260	0.458	0.03	0.22
GSS	<i>RANBP2</i>	-0.919	0.139	0.845	0.00016	0.019
GSS	<i>CRYAB</i>	0.664	0.264	0.441	0.036	0.25
GSS	<i>CTDSP2</i>	0.791	0.216	0.625	0.006	0.21
GSS	<i>ATF4</i>	0.710	0.249	0.504	0.021	0.21
GSS	<i>BID</i>	0.695	0.254	0.483	0.026	0.21
GSS	<i>CALR</i>	0.716	0.247	0.513	0.019	0.21
GSS	<i>DDIT3</i>	0.701	0.252	0.491	0.02	0.21
GSS	<i>CKAP4</i>	-0.712	0.248	0.507	0.02	0.21
GSS	<i>CREB3L2</i>	-0.771	0.225	0.595	0.009	0.21
GSS	<i>DNAJB11</i>	0.719	0.246	0.516	0.019	0.21
GSS	<i>EDEM1</i>	-0.879	0.169	0.773	0.0008	0.047
GSS	<i>EIF2AK3</i>	-0.752	0.233	0.566	0.01	0.21
GSS	<i>XBP1</i>	0.702	0.252	0.493	0.02	0.21
Non-diabetic patients						
GCLM	<i>BAG1</i>	0.733	0.241	0.537	0.015	0.13
GCLM	<i>BAG2</i>	0.841	0.191	0.707	0.002	0.046
GCLM	<i>DNAJB6</i>	0.863	0.178	0.745	0.001	0.048
GCLM	<i>DNAJC7</i>	0.670	0.262	0.449	0.03	0.18
GCLM	<i>HSPA14</i>	0.825	0.199	0.681	0.003	0.059
GCLM	<i>HSPA8</i>	0.821	0.202	0.674	0.0036	0.059
GCLM	<i>HSPA9</i>	0.720	0.245	0.518	0.02	0.15
GCLM	<i>NDC1</i>	0.669	0.263	0.447	0.03	0.18
GCLM	<i>NDC1</i>	0.669	0.263	0.447	0.03	0.18
GCLM	<i>NUP153</i>	0.763	0.228	0.583	0.01	0.09
GCLM	<i>NUP160</i>	0.849	0.187	0.722	0.0018	0.047
GCLM	<i>NUP205</i>	0.810	0.207	0.656	0.004	0.059
GCLM	<i>NUP214</i>	-0.876	0.171	0.767	0.0009	0.048
GCLM	<i>NUP54</i>	0.765	0.228	0.585	0.0099	0.09
GCLM	<i>NUP58</i>	0.761	0.230	0.578	0.01	0.09
GCLM	<i>POM121C</i>	0.651	0.268	0.424	0.04	0.20
GCLM	<i>PTGES3</i>	0.782	0.221	0.611	0.008	0.09

GCLM	SIRT1	0.783	0.220	0.613	0.007	0.09
GCLM	ST13	0.644	0.270	0.415	0.04	0.20
GCLM	EEF1A1	0.647	0.270	0.418	0.04	0.20
GCLM	ASNS	0.683	0.258	0.466	0.029	0.18
GCLM	EDEM2	-0.645	0.270	0.416	0.04	0.20
GCLM	EIF2S2	0.730	0.242	0.532	0.016	0.13
GCLM	PDIA6	0.675	0.261	0.456	0.03	0.18
GCLM	SSR1	0.843	0.190	0.711	0.002	0.048
GSS	BAG1	-0.771	0.225	0.595	0.009	0.15
GSS	BAG2	-0.703	0.251	0.494	0.02	0.20
GSS	BAG4	0.763	0.229	0.582	0.01	0.15
GSS	DNAJB6	-0.755	0.232	0.570	0.01	0.15
GSS	HSPA14	-0.722	0.244	0.522	0.018	0.20
GSS	NDC1	-0.709	0.249	0.503	0.02	0.20
GSS	NUP133	-0.699	0.253	0.489	0.02	0.20
GSS	NUP153	-0.654	0.267	0.428	0.04	0.28
GSS	NUP160	-0.666	0.264	0.444	0.035	0.26
GSS	NUP210	0.782	0.220	0.611	0.007	0.15
GSS	NUP214	0.637	0.273	0.405	0.047	0.29
GSS	NUP37	-0.686	0.257	0.471	0.028	0.26
GSS	NUP50	0.633	0.274	0.401	0.049	0.29
GSS	NUP54	-0.670	0.263	0.448	0.03	0.26
GSS	NUP88	-0.792	0.216	0.627	0.006	0.15
GSS	RANBP2	-0.780	0.221	0.608	0.008	0.15
GSS	RPA1	-0.641	0.271	0.411	0.045	0.29
GSS	ST13	-0.792	0.216	0.627	0.006	0.15
GSS	TPR	-0.844	0.190	0.712	0.002	0.15
GSS	CRYAB	-0.667	0.264	0.444	0.035	0.26

Beta, the regression coefficient; R², R-squared; FDR adjusted P-value was calculated with FDR online calculator (<https://www.sdmproject.com/utilities/?show=FDR>, assessed 10.06.2023);
Bold depicts statistically significant P- and Q-values.