

Table S1: The most significant gene-gene combinations associated with coronary heart disease in patients with severe COVID-19.

Combinations of genotypes (1)	Beta (2)	<i>p</i> (3)	Risk (4)
Two-locus models			
rs7949972 <i>ELF5</i> × rs17078346 <i>SLC6A20-LZTFL1</i>			
rs7949972 <i>ELF5</i> T/T×rs17078346 <i>SLC6A20-LZTFL1</i> A/A	0.24601	0.04468	H
rs7949972 <i>ELF5</i> C/C ×rs17078346 <i>SLC6A20-LZTFL1</i> A/A	-0.14525	0.04757	L
rs7949972 <i>ELF5</i> T/C×rs17078346 <i>SLC6A20-LZTFL1</i> C/A	0.24961	0.00722	H
rs9636867 <i>IFNAR2</i> × rs12610495 <i>DPP9</i>			
rs9636867 <i>IFNAR2</i> A/G×rs12610495 <i>DPP9</i> A/A	-0.2002	0.008286	L
rs9636867 <i>IFNAR2</i> G/G×rs12610495 <i>DPP9</i> G/A	0.1552	0.080176	H
rs9636867 <i>IFNAR2</i> A/G×rs12610495 <i>DPP9</i> G/A	0.17587	0.054566	H
rs9636867 <i>IFNAR2</i> G/G×rs12610495 <i>DPP9</i> G/G	0.267026	0.081992	H
rs7949972 <i>ELF5</i> × rs12610495 <i>DPP9</i>			
rs7949972 <i>ELF5</i> T/C×rs12610495 <i>DPP9</i> A/A	-0.15258	0.05622	L
rs7949972 <i>ELF5</i> C/C ×rs12610495 <i>DPP9</i> A/A	-0.14242	0.05503	L
rs7949972 <i>ELF5</i> T/T×rs12610495 <i>DPP9</i> G/A	0.30104	0.02864	H
rs7949972 <i>ELF5</i> T/C×rs12610495 <i>DPP9</i> G/A	0.18543	0.01752	H
Three-locus models			
rs7949972 <i>ELF5</i> × rs61882275 <i>ELF5</i> × rs12610495 <i>DPP9</i>			
rs7949972 <i>ELF5</i> T/C×rs618822758 <i>ELF5</i> A/A×rs12610495 <i>DPP9</i> A/A	-0.32512	0.013279	L
rs7949972 <i>ELF5</i> C/C ×rs618822758 <i>ELF5</i> G/G×rs12610495 <i>DPP9</i> A/A	-0.14242	0.055029	L
rs7949972 <i>ELF5</i> T/T×rs618822758 <i>ELF5</i> A/A×rs12610495 <i>DPP9</i> G/A	0.30104	0.028638	H
rs7949972 <i>ELF5</i> T/C×rs618822758 <i>ELF5</i> A/G×rs12610495 <i>DPP9</i> G/A	0.23456	0.005411	H
rs9636867 <i>IFNAR2</i> × rs61882275 <i>ELF5</i> × rs17078346 <i>SLC6A20-LZTFL1</i>			
rs9636867 <i>IFNAR2</i> A/A×rs618822758 <i>ELF5</i> A/A×rs17078346 <i>SLC6A20-LZTFL1</i> A/A	0.579875	0.05525	H
rs9636867 <i>IFNAR2</i> A/G×rs618822758 <i>ELF5</i> G/G×rs17078346 <i>SLC6A20-LZTFL1</i> A/A	-0.21304	0.0495	L
rs9636867 <i>IFNAR2</i> A/G×rs618822758 <i>ELF5</i> A/A×rs17078346 <i>SLC6A20-LZTFL1</i> C/A	0.408984	0.09917	H
rs9636867 <i>IFNAR2</i> G/G×rs618822758 <i>ELF5</i> A/G×rs17078346 <i>SLC6A20-LZTFL1</i> C/A	0.342103	0.02595	H
rs9636867 <i>IFNAR2</i> A/A×rs618822758 <i>ELF5</i> A/G×rs17078346 <i>SLC6A20-LZTFL1</i> C/A	0.57068	0.05927	H
rs9636867 <i>IFNAR2</i> A/A×rs618822758 <i>ELF5</i> G/G×rs17078346 <i>SLC6A20-LZTFL1</i> C/A	-0.39216	0.06846	L

rs9636867 IFNAR2 × rs12610495 DPP9 × rs12585036 ATP11A			
rs9636867 IFNAR2 A/G×rs12610495 DPP9 A/A×rs12585036 ATP11A C/C	-0.22195	0.03523	L
rs9636867 IFNAR2 A/G×rs12610495 DPP9 G/A×rs12585036 ATP11A C/C	0.39442	0.00112	H
rs9636867 IFNAR2 A/A×rs12610495 DPP9 G/A×rs12585036 ATP11A C/T	0.3759	0.08003	H
rs9636867 IFNAR2 A/G×rs12610495 DPP9 G/A×rs12585036 ATP11A T/T	-0.55255	0.06713	L
Four-locus models			
rs7949972 ELF5 × rs9636867 IFNAR2 × rs61882275 ELF5 × rs17078346 SLC6A20-LZTFL1			
rs7949972 ELF5 T/T×rs9636867 IFNAR2 G/G×rs61882275 ELF5 A/A×rs17078346 SLC6A20-LZTFL1 A/A	0.31893	0.07073	H
rs7949972 ELF5 T/T×rs9636867 IFNAR2 A/A×rs61882275 ELF5 A/A×rs17078346 SLC6A20-LZTFL1 A/A	0.576824	0.05612	H
rs7949972 ELF5 C/C ×rs9636867 IFNAR2 A/G×rs61882275 ELF5 G/G×rs17078346 SLC6A20-LZTFL1 A/A	-0.21654	0.04551	L
rs7949972 ELF5 T/T×rs9636867 IFNAR2 G/G×rs61882275 ELF5 A/A×rs17078346 SLC6A20-LZTFL1 C/A	0.590393	0.05052	H
rs7949972 ELF5 T/C×rs9636867 IFNAR2 A/G×rs61882275 ELF5 A/A×rs17078346 SLC6A20-LZTFL1 C/A	0.761212	0.07405	H
rs7949972 ELF5 T/C×rs9636867 IFNAR2 G/G×rs61882275 ELF5 A/G×rs17078346 SLC6A20-LZTFL1 C/A	0.338995	0.02709	H
rs7949972 ELF5 T/C×rs9636867 IFNAR2 A/A×rs61882275 ELF5 A/G×rs17078346 SLC6A20-LZTFL1 C/A	0.567628	0.0602	H
rs7949972 ELF5 C/C ×rs9636867 IFNAR2 A/A×rs61882275 ELF5 G/G×rs17078346 SLC6A20-LZTFL1 C/A	-0.39533	0.06576	L
rs9636867 IFNAR2 × rs12610495 DPP9 × rs12585036 ATP11A × rs17713054 SLC6A20-LZTFL1			
rs9636867 IFNAR2 A/G×rs12610495 DPP9 A/A×rs12585036 ATP11A C/C×rs17713054 SLC6A20-LZTFL1 G/G	-0.25409	0.031298	L
rs9636867 IFNAR2 A/G×rs12610495 DPP9 G/A×rs12585036 ATP11A C/C×rs17713054 SLC6A20-LZTFL1 G/G	0.3989	0.005714	H
rs9636867 IFNAR2 A/A×rs12610495 DPP9 G/A×rs12585036 ATP11A C/T×rs17713054 SLC6A20-LZTFL1 G/G	0.375895	0.080029	H
rs9636867 IFNAR2 G/G×rs12610495 DPP9 G/A×rs12585036 ATP11A C/C×rs17713054 SLC6A20-LZTFL1 A/G	0.387439	0.07111	H
rs9636867 IFNAR2 A/A×rs12610495 DPP9 G/G×rs12585036 ATP11A C/C×rs17713054 SLC6A20-LZTFL1 A/G	-0.71834	0.091679	L
rs9636867 IFNAR2 G/G×rs12610495 DPP9 G/A×rs12585036 ATP11A C/T×rs17713054 SLC6A20-LZTFL1 A/G	0.358154	0.028338	H
rs7949972 ELF5 × rs9636867 IFNAR2 × rs12610495 DPP9 × rs17713054 SLC6A20-LZTFL1			
rs7949972 ELF5 T/C×rs9636867 IFNAR2 A/G×rs12610495 DPP9 A/A×rs17713054 SLC6A20-LZTFL1 G/G	-0.20761	0.06929	L
rs7949972 ELF5 T/T×rs9636867 IFNAR2 A/A×rs12610495 DPP9 G/A×rs17713054 SLC6A20-LZTFL1 G/G	0.775899	0.06761	H
rs7949972 ELF5 C/C ×rs9636867 IFNAR2 G/G×rs12610495 DPP9 G/G×rs17713054 SLC6A20-LZTFL1 G/G	0.476249	0.05324	H
rs7949972 ELF5 C/C ×rs9636867 IFNAR2 A/G×rs12610495 DPP9 G/G×rs17713054 SLC6A20-LZTFL1 G/G	-0.66382	0.02712	L
rs7949972 ELF5 T/T×rs9636867 IFNAR2 G/G×rs12610495 DPP9 G/A×rs17713054 SLC6A20-LZTFL1 A/G	0.586785	0.05113	H
rs7949972 ELF5 T/C×rs9636867 IFNAR2 G/G×rs12610495 DPP9 G/A×rs17713054 SLC6A20-LZTFL1 A/G	0.293298	0.09561	H
rs7949972 ELF5 C/C ×rs9636867 IFNAR2 G/G×rs12610495 DPP9 G/A×rs17713054 SLC6A20-LZTFL1 A/G	0.389189	0.06913	H
rs7949972 ELF5 T/C×rs9636867 IFNAR2 A/G×rs12610495 DPP9 G/A×rs17713054 SLC6A20-LZTFL1 A/G	0.36837	0.08553	H
rs7949972 ELF5 C/C ×rs9636867 IFNAR2 A/A×rs12610495 DPP9 G/G×rs17713054 SLC6A20-LZTFL1 A/G	-0.72358	0.08851	L

Note: obtained by the MB-MDR method, taking into account correction for covariates (age and physical activity);

1 – combination of genotypes;

2 – beta – logistic regression coefficients for combinations of genotypes;

3 – p – level of significance;

4 – Risk: H – high, L – low

Table S2: The most significant gene-environmental combinations associated with coronary heart disease in patients with severe COVID-19.

Combinations of genotypes (1)	Beta (2)	p (3)	Risk (4)
rs12610495 <i>DPP9</i> × SMOKE			
rs12610495 <i>DPP9</i> A/A×0	-0.22356	0.000656	L
rs12610495 <i>DPP9</i> G/A×1	0.22563	0.011911	H
rs17078346 <i>SLC6A20-LZTFL1</i> × SMOKE			
rs17078346 <i>SLC6A20-LZTFL1</i> A/A ×0	-0.21431	0.000638	L
rs17078346 <i>SLC6A20-LZTFL1</i> A/A ×1	0.15985	0.043807	H
rs17713054 <i>SLC6A20-LZTFL1</i> × SMOKE			
rs17713054 <i>SLC6A20-LZTFL1</i> G/G×0	-0.21315	0.000671	L
rs17713054 <i>SLC6A20-LZTFL1</i> G/G×1	0.164088	0.032551	H
rs61882275 <i>ELF5</i> × rs17078346 <i>SLC6A20-LZTFL1</i> × SMOKE			
rs61882275 <i>ELF5</i> G/G×rs17078346 <i>SLC6A20-LZTFL1</i> A/A ×0	-0.1674	0.04141	L
rs61882275 <i>ELF5</i> A/G×rs17078346 <i>SLC6A20-LZTFL1</i> C/A ×0	0.401734	0.002264	H
rs61882275 <i>ELF5</i> A/G×rs17078346 <i>SLC6A20-LZTFL1</i> A/A ×1	0.248542	0.035968	H
rs7949972 <i>ELF5</i> × rs17713054 <i>SLC6A20-LZTFL1</i> × SMOKE			
rs7949972 <i>ELF5</i> T/C×rs17713054 <i>SLC6A20-LZTFL1</i> G/G×0	-0.16255	0.03011	L
rs7949972 <i>ELF5</i> C/C ×rs17713054 <i>SLC6A20-LZTFL1</i> G/G×0	-0.18079	0.02385	L
rs7949972 <i>ELF5</i> T/C×rs17713054 <i>SLC6A20-LZTFL1</i> A/G×0	0.23411	0.04103	H
rs7949972 <i>ELF5</i> T/T×rs17713054 <i>SLC6A20-LZTFL1</i> G/G×1	0.36877	0.03644	H
rs9636867 <i>IFNAR2</i> × rs61882275 <i>ELF5</i> × rs17078346 <i>SLC6A20-LZTFL1</i> × SMOKE			
rs9636867 <i>IFNAR2</i> A/G×rs61882275 <i>ELF5</i> A/A×rs17078346 <i>SLC6A20-LZTFL1</i> A/A ×0	-0.23661	0.08801	L

rs9636867 <i>IFNAR2</i> A/G×rs618822758 <i>ELF5</i> G/G×rs17078346 <i>SLC6A20-LZTFL1</i> A/A ×0	-0.21628	0.05247	L
rs9636867 <i>IFNAR2</i> G/G×rs618822758 <i>ELF5</i> A/G×rs17078346 <i>SLC6A20-LZTFL1</i> C/A ×0	0.31815	0.07207	H
rs9636867 <i>IFNAR2</i> A/A×rs618822758 <i>ELF5</i> A/G×rs17078346 <i>SLC6A20-LZTFL1</i> C/A ×0	0.57261	0.05855	H
rs9636867 <i>IFNAR2</i> A/A×rs618822758 <i>ELF5</i> A/A×rs17078346 <i>SLC6A20-LZTFL1</i> A/A ×1	0.58132	0.05478	H
rs9636867 <i>IFNAR2</i> A/G×rs618822758 <i>ELF5</i> A/G×rs17078346 <i>SLC6A20-LZTFL1</i> A/A ×1	0.58464	0.01801	H
rs9636867 <i>IFNAR2</i> A/A×rs618822758 <i>ELF5</i> A/G×rs17078346 <i>SLC6A20-LZTFL1</i> A/A ×1	0.45042	0.0693	H
rs9636867 <i>IFNAR2</i> A/G×rs618822758 <i>ELF5</i> A/A×rs17078346 <i>SLC6A20-LZTFL1</i> C/A ×1	0.76842	0.07199	H
rs9636867 <i>IFNAR2</i> × rs61882275 <i>ELF5</i> × rs17713054 <i>SLC6A20-LZTFL1</i> × SMOKE			
rs9636867 <i>IFNAR2</i> A/G×rs618822758 <i>ELF5</i> A/A×rs17713054 <i>SLC6A20-LZTFL1</i> G/G×0	-0.22757	0.08619	L
rs9636867 <i>IFNAR2</i> A/G×rs618822758 <i>ELF5</i> G/G×rs17713054 <i>SLC6A20-LZTFL1</i> G/G×0	-0.21628	0.05247	L
rs9636867 <i>IFNAR2</i> A/A×rs618822758 <i>ELF5</i> A/G×rs17713054 <i>SLC6A20-LZTFL1</i> A/G×0	0.572612	0.05855	H
rs9636867 <i>IFNAR2</i> A/A×rs618822758 <i>ELF5</i> A/A×rs17713054 <i>SLC6A20-LZTFL1</i> G/G×1	0.581316	0.05478	H
rs9636867 <i>IFNAR2</i> A/G×rs618822758 <i>ELF5</i> A/G×rs17713054 <i>SLC6A20-LZTFL1</i> G/G×1	0.584637	0.01801	H
rs9636867 <i>IFNAR2</i> A/A×rs618822758 <i>ELF5</i> A/G×rs17713054 <i>SLC6A20-LZTFL1</i> G/G×1	0.450423	0.0693	H
rs9636867 <i>IFNAR2</i> A/G×rs618822758 <i>ELF5</i> A/A×rs17713054 <i>SLC6A20-LZTFL1</i> A/G×1	0.768424	0.07199	H
Note: obtained by the MB-MDR method, taking into account correction for covariates (age); 1 – combination of genotypes; 2 – beta – logistic regression coefficients for combinations of genotypes; 3 – <i>p</i> – level of significance; 4 – Risk: H – high, L – low			

Table S3: The most significant gene-gene combinations associated with cerebral stroke in patients with severe COVID-19.

Combinations of genotypes (1)	Beta (2)	<i>p</i> (3)	Risk (4)
Two-locus models			
rs17078346 <i>SLC6A20-LZTFL1</i> × rs12610495 <i>DPP9</i>			
rs17078346 <i>SLC6A20-LZTFL1</i> A/A ×rs12610495 <i>DPP9</i> A/A	-0.15211	0.029586	L
rs17078346 <i>SLC6A20-LZTFL1</i> A/A ×rs12610495 <i>DPP9</i> G/A	0.29149	0.000166	H
rs12610495 <i>DPP9</i> × rs17713054 <i>SLC6A20-LZTFL1</i>			
rs12610495 <i>DPP9</i> A/A×rs17713054 <i>SLC6A20-LZTFL1</i> G/G	-0.15762	0.0225	L
rs12610495 <i>DPP9</i> G/A×rs17713054 <i>SLC6A20-LZTFL1</i> G/G	0.263833	0.000498	H

Three-locus models			
rs7949972 <i>ELF5</i> × rs9636867 <i>IFNAR2</i> × rs12610495 <i>DPP9</i>			
rs7949972 <i>ELF5</i> T/T×rs9636867 <i>IFNAR2</i> A/G×rs12610495 <i>DPP9</i> A/A	0.38174	0.08798	H
rs7949972 <i>ELF5</i> T/T×rs9636867 <i>IFNAR2</i> G/G×rs12610495 <i>DPP9</i> G/A	0.43161	0.0311	H
rs7949972 <i>ELF5</i> T/T×rs9636867 <i>IFNAR2</i> A/G×rs12610495 <i>DPP9</i> G/A	0.47426	0.06543	H
rs7949972 <i>ELF5</i> T/C×rs9636867 <i>IFNAR2</i> A/G×rs12610495 <i>DPP9</i> G/A	0.4091	0.00078	H
rs7949972 <i>ELF5</i> C/C ×rs9636867 <i>IFNAR2</i> A/A×rs12610495 <i>DPP9</i> G/A	0.55315	0.013	H
Four-locus models			
rs7949972 <i>ELF5</i> × rs9636867 <i>IFNAR2</i> × rs12610495 <i>DPP9</i> × rs143334143 <i>CCHCR1</i>			
rs7949972 <i>ELF5</i> T/T×rs9636867 <i>IFNAR2</i> A/G×rs12610495 <i>DPP9</i> A/A×rs143334143 <i>CCHCR1</i> G/G	0.381736	8.80E-02	H
rs7949972 <i>ELF5</i> T/T×rs9636867 <i>IFNAR2</i> G/G×rs12610495 <i>DPP9</i> G/A×rs143334143 <i>CCHCR1</i> G/G	0.431614	3.11E-02	H
rs7949972 <i>ELF5</i> T/C×rs9636867 <i>IFNAR2</i> A/G×rs12610495 <i>DPP9</i> G/A×rs143334143 <i>CCHCR1</i> G/G	0.508207	9.23E-05	H
rs7949972 <i>ELF5</i> T/T×rs9636867 <i>IFNAR2</i> A/G×rs12610495 <i>DPP9</i> G/A×rs143334143 <i>CCHCR1</i> A/G	1.800464	3.45E-05	H
rs7949972 <i>ELF5</i> C/C ×rs9636867 <i>IFNAR2</i> A/A×rs12610495 <i>DPP9</i> G/A×rs143334143 <i>CCHCR1</i> A/G	1.724019	7.57E-05	H
rs7949972 <i>ELF5</i> C/C ×rs9636867 <i>IFNAR2</i> A/G×rs12610495 <i>DPP9</i> G/G×rs143334143 <i>CCHCR1</i> A/G	0.771505	8.20E-02	H
rs7949972 <i>ELF5</i> × rs9636867 <i>IFNAR2</i> × rs12610495 <i>DPP9</i> × rs11183780 <i>CCHCR1</i>			
rs7949972 <i>ELF5</i> T/T×rs9636867 <i>IFNAR2</i> A/G×rs12610495 <i>DPP9</i> A/A×rs11183780 <i>CCHCR1</i> T/T	0.380363	8.98E-02	H
rs7949972 <i>ELF5</i> T/T×rs9636867 <i>IFNAR2</i> G/G×rs12610495 <i>DPP9</i> G/A×rs11183780 <i>CCHCR1</i> T/T	0.430254	3.20E-02	H
rs7949972 <i>ELF5</i> T/C×rs9636867 <i>IFNAR2</i> A/G×rs12610495 <i>DPP9</i> G/A×rs11183780 <i>CCHCR1</i> T/T	0.506926	9.97E-05	H
rs7949972 <i>ELF5</i> T/T×rs9636867 <i>IFNAR2</i> A/G×rs12610495 <i>DPP9</i> G/A×rs11183780 <i>CCHCR1</i> C/T	1.799124	3.62E-05	H
rs7949972 <i>ELF5</i> C/C ×rs9636867 <i>IFNAR2</i> A/A×rs12610495 <i>DPP9</i> G/A×rs11183780 <i>CCHCR1</i> C/T	1.722676	7.93E-05	H
Note: obtained by the MB-MDR method, taking into account correction for covariates (age and physical activity); 1 – combination of genotypes; 2 – beta – logistic regression coefficients for combinations of genotypes; 3 – <i>p</i> – level of significance; 4 – Risk: H – high, L – low			

Table S4: The most significant gene-environmental combinations associated with cerebral stroke in patients with severe COVID-19.

Combinations of genotypes (1)	Beta (2)	<i>p</i> (3)	Risk (4)
rs12610495 <i>DPP9</i> × SMOKE			
rs12610495 <i>DPP9</i> A/A×0	-0.11622	0.093188	L

rs12610495 <i>DPP9</i> G/A×1	0.26708	0.004179	H
rs61882275 <i>ELF5</i> × rs12585036 <i>ATP11A</i> × SMOKE			
rs618822758 <i>ELF5</i> A/A×rs12585036 <i>ATP11A</i> C/C×1	0.76397	4.36E-06	H
rs61882275 <i>ELF5</i> × rs12610495 <i>DPP9</i> × rs11183780 <i>CCHCR1</i> × VEGET			
rs618822758 <i>ELF5</i> A/A×rs12610495 <i>DPP9</i> G/A×rs11183780 <i>CCHCR1</i> C/T×1	1.75055	6.01E-05	H
rs618822758 <i>ELF5</i> G/G×rs12610495 <i>DPP9</i> G/A×rs11183780 <i>CCHCR1</i> C/T×1	1.69391	1.06E-04	H
rs9636867 <i>IFNAR2</i> × rs12585036 <i>ATP11A</i> × rs11183780 <i>CCHCR1</i> × VEGET			
rs9636867 <i>IFNAR2</i> A/G×rs12585036 <i>ATP11A</i> C/C×rs11183780 <i>CCHCR1</i> C/T×1	1.23532	6.29E-05	H
rs9636867 <i>IFNAR2</i> A/A×rs12585036 <i>ATP11A</i> C/C×rs11183780 <i>CCHCR1</i> C/T×1	1.69473	1.01E-04	H
Note: obtained by the MB-MDR method, taking into account correction for covariates (age); 1 – combination of genotypes; 2 – beta – logistic regression coefficients for combinations of genotypes; 3 – <i>p</i> – level of significance; 4 – Risk: H – high, L – low			

Table S5: Analysis of the effect of rs17713054 *SLC6A20-LZTFL1* on the binding of DNA to transcription factors.

Nº	Ref/SNP allele ¹	TF ²	GAIN /LOSS ³	Motif ⁴	P-Value SNP impact ⁵	P-Value Ref ⁶	P-Value SNP ⁷
1	G/A	CEBPB	gain	CEBPB_2	0	0.754	0
2	G/A	CEBP	gain	CEBP_5	0	0.258	0
3	G/A	CEBPA	gain	CEBPA_1	0	0.794	0
4	G/A	ATF1	gain	CEBPB_2	0	0.754	0
5	G/A	CEBPB	gain	CEBP_5	0	0.258	0
6	G/A	EP300	gain	CEBPA_1	0	0.794	0
7	G/A	CEBPB	gain	CEBPB_1	0	0.396	0.000003
8	G/A	TLX2	gain	CEBPB_1	0	0.396	0.000003
9	G/A	CEBPB	gain	CEBPB_4	0.0003	0.086	0.0001
10	G/A	TEF	gain	CEBPB_4	0.0003	0.086	0.0001
11	G/A	CEBPG	gain	CEBPG_3	0.003	0.091	0.002
12	G/A	Ddit3::Cebp a	gain	CEBPG_3	0.003	0.091	0.002
13	G/A	CEBPB	gain	CEBPB_5	0.002	0.096	0.003
14	G/A	ATF4	gain	CEBPB_5	0.002	0.096	0.003
15	G/A	STAT	gain	STAT_disc4	0.004	0.075	0.003
16	G/A	CEBPG	gain	CEBPG_2	0.003	0.106	0.004
17	G/A	MLX	gain	CEBPG_2	0.003	0.106	0.004
18	G/A	SRF	gain	SRF_3	0.001	0.061	0.004
19	G/A	NFIL3	gain	SRF_3	0.001	0.061	0.004
20	G/A	CEBPB	gain	CEBPB_3	0.001	0.355	0.005
21	G/A	RFX5	gain	CEBPB_3	0.001	0.355	0.005
22	G/A	CEBPE	gain	CEBPE_1	0.001	0.304	0.005
23	G/A	DBP	gain	CEBPE_1	0.001	0.304	0.005
24	G/A	CEBPA	gain	MA0102.3	0.002	0.110	0.005
25	G/A	IRF5	gain	MA0102.3	0.002	0.110	0.005
26	G/A	CEBPA	gain	CEBPA_2	0.001	0.629	0.005
27	G/A	MAFB	gain	CEBPA_2	0.001	0.629	0.005
28	G/A	CEBPD	gain	CEBPD_2	0.001	0.752	0.006
29	G/A	ZFX	gain	CEBPD_2	0.001	0.752	0.006
30	G/A	DBP	gain	DBP_1	0.001	0.232	0.008
31	G/A	CEBP	gain	DBP_1	0.001	0.232	0.008
32	G/A	CEBPB	gain	MA0466.1	0.003	0.130	0.008
33	G/A	RFX5	gain	MA0466.1	0.003	0.130	0.008
34	G/A	SOX5	gain	SOX5_1	0.007	0.153	0.009
35	G/A	PITX2	gain	PITX2_1	0.004	0.200	0.018
36	G/A	CUX2	gain	CUX2_2	0.007	0.253	0.018
37	G/A	CEBP	gain	CEBP_3	0.005	0.199	0.018
38	G/A	DBP	gain	DBP_4	0.015	0.213	0.021
39	G/A	MYC	gain	MYC_disc5	0.004	0.376	0.021
40	G/A	AR	gain	MYC_disc5	0.004	0.376	0.021
41	G/A	ONECUT1	gain	ONECUT1_3	0.004	0.796	0.023
42	G/A	TEF	gain	ONECUT1_3	0.004	0.796	0.023
43	G/A	CUX1	gain	CUX1_10	0.013	0.300	0.028
44	G/A	HSF	gain	HSF_disc1	0.007	0.392	0.029
45	G/A	ATF4	gain	ATF4_3	0.006	0.429	0.035

46	G/A	Sox5	gain	MA0087.1	0.007	0.355	0.039
47	G/A	AP1	gain	AP1 disc1	0.013	0.440	0.042
48	G/A	ONECUT2	gain	ONECUT2 1	0.009	0.539	0.045
49	G/A	NR3C1	loss	NR3C1 2	0.008	0.004	0.066
50	G/A	MSX1	loss	MSX1 1	0.012	0.004	0.075
51	G/A	MYF	loss	MYF 1	0.002	0.008	0.089
52	G/A	AR	loss	MYF 1	0.002	0.008	0.089
53	G/A	PAX9	loss	PAX9 1	0.006	0.012	0.132
54	G/A	RAD21	loss	RAD21 disc8	0.008	0.031	0.196
55	G/A	STAT	loss	STAT disc7	0.009	0.028	0.204
56	G/A	RUNX3	loss	RUNX3 3	0.001	0.011	0.233
57	G/A	MYC	loss	RUNX3 3	0.001	0.011	0.233
58	G/A	ETS	loss	ETS disc7	0.012	0.031	0.235
59	G/A	HNF4	loss	HNF4 disc2	0.004	0.033	0.267
60	G/A	RAD21	loss	RAD21 disc5	0.006	0.041	0.277
61	G/A	RUNX2	loss	RUNX2 5	0.007	0.017	0.284
62	G/A	BCL	loss	BCL disc9	0.013	0.048	0.285
63	G/A	REST	loss	REST disc5	0.009	0.048	0.285
64	G/A	ELF1	loss	ELF1 disc3	0.004	0.039	0.306
65	G/A	MXI1	loss	ELF1 disc3	0.004	0.039	0.306
66	G/A	HINFP	loss	HINFP 4	0.005	0.034	0.319
67	G/A	TFCP2	loss	TFCP2 3	0.007	0.022	0.323
68	G/A	TP73	loss	TP73 1	0.015	0.044	0.331
69	G/A	NRF1	loss	NRF1 disc2	0.009	0.045	0.335
70	G/A	E2F1	loss	E2F1 22	0.007	0.046	0.475
71	G/A	CEBP	loss	CEBP 2	0	0.172	0.0000004
72	G/A	HLF	loss	CEBP 2	0	0.172	0.0000004
	A ⁸	transforming growth factor beta receptor signaling pathway (GO:0007179; FDR = 4.94×10 ⁻²)					
	G ⁹	response to hypoxia (GO:0001666; FDR = 2.8×10 ⁻²); myoblast differentiation (GO:0045445; FDR = 2.56×10 ⁻³); response to growth factor (GO:0070848; FDR = 1.79×10 ⁻³)					
1 – reference (Ref) / alternative (SNP) allele; 2 – TF - transcription factor; 3 – binding of TF to the reference (LOSS) / alternative (GAIN) allele; 4 – binding sites with high affinity for TF; 5 – p value statistically confirming the potential gain or loss of function of the genomic region with SNP in terms of transcription factor binding; 6 – p-value for assessing the binding of TF to the Ref allele; 7 – p-value for assessing the binding of TF to the SNP allele; 8 – biological processes pathogenetically significant for IS, in which TFs that bind to the SNP allele are jointly involved (data from the Gene Ontology resource; http://geneontology.org/); 9 – biological processes pathogenetically significant for IS, in which TFs that bind to reference allele are jointly involved (data from the Gene Ontology resource; http://geneontology.org/)							

Table S6: Analysis of the effect of rs12610495 *DPP9* on the binding of DNA to transcription factors.

№	Ref/SNP allele ¹	TF ²	GAIN /LOSS ³	Motif ⁴	P-Value SNP impact ⁵	P-Value Ref ⁶	P-Value SNP ⁷
1	A/G	NFE2	gain	NFE2 disc3	0	0.228	3.9×10 ⁻⁷

2	A/G	Gata4	gain	NFE2_disc3	0	0.228	3.9×10 ⁻⁷
3	A/G	E2F1	gain	E2F1_17	0.002	0.110	0.002
4	A/G	TEAD3	gain	E2F1_17	0.002	0.110	0.002
5	A/G	PITX2	gain	PITX2_1	0.004	0.119	0.003
6	A/G	HMG3	gain	PITX2_1	0.004	0.119	0.003
7	A/G	MZF1	gain	MZF1_3	0.002	0.125	0.004
8	A/G	TAL1	gain	MZF1_3	0.002	0.125	0.004
9	A/G	MZF1_1-4	gain	MA0056.1	0	0.128	0.005
10	A/G	RFX1	gain	MA0056.1	0	0.128	0.005
11	A/G	E2F1	gain	E2F1_16	0.0001	0.213	0.009
12	A/G	ELK3	gain	E2F1_16	0.0001	0.213	0.009
13	A/G	IRF	gain	IRF_disc5	0.002	0.110	0.009
14	A/G	ELK1	gain	IRF_disc5	0.002	0.110	0.009
15	A/G	E2F1	gain	E2F1_19	0.001	0.221	0.011
16	A/G	TCF12	gain	E2F1_19	0.001	0.221	0.011
17	A/G	SP1	gain	SP1_5	0.001	0.538	0.012
18	A/G	FLI1	gain	SP1_5	0.001	0.538	0.012
19	A/G	ZNF589	gain	ZNF589_1	0.006	0.203	0.015
20	A/G	ETV5	gain	ZNF589_1	0.006	0.203	0.015
21	A/G	ZIC3	gain	ZIC3_2	0.004	0.100	0.015
22	A/G	ERG	gain	ZIC3_2	0.004	0.100	0.015
23	A/G	EGR1	gain	EGR1_disc6	0.009	0.192	0.015
24	A/G	ZIC2	gain	ZIC2_2	0.002	0.135	0.018
25	A/G	HDAC2	gain	ZIC2_2	0.002	0.135	0.018
26	A/G	ZIC1	gain	ZIC1_2	0.004	0.124	0.019
27	A/G	ELF3	gain	ZIC1_2	0.004	0.124	0.019
28	A/G	BCL6B	gain	BCL6B_2	0.004	0.154	0.019
29	A/G	SRF	gain	BCL6B_2	0.004	0.154	0.019
30	A/G	SP1	gain	SP1_3	0.002	0.777	0.024
31	A/G	EWSR1-FLI1	gain	SP1_3	0.002	0.777	0.024
32	A/G	EGR1	gain	EGR1_disc1	0.003	0.248	0.025
33	A/G	BDP1	gain	EGR1_disc1	0.003	0.248	0.025
34	A/G	USF	gain	USF_1	0.014	0.360	0.029
35	A/G	ETS	gain	ETS_1	0.005	0.265	0.030
36	A/G	ETV4	gain	ETS_1	0.005	0.265	0.030
37	A/G	SP1	gain	MA0079.3	0.008	0.390	0.043
38	A/G	HIC2	gain	HIC2_1	0.012	0.884	0.043
39	A/G	SP1	gain	SP1_4	0.008	0.466	0.043
40	A/G	ZBTB7A	gain	ZBTB7A_1	0.007	0.469	0.044
41	A/G	ELK4	gain	ZBTB7A_1	0.007	0.469	0.044
42	A/G	MAX	gain	MAX_2	0.018	0.356	0.045
43	A/G	ELF4	loss	ELF4_1	0.010	0.003	0.051
44	A/G	SPDEF	loss	SPDEF_5	0.008	0.004	0.069
45	A/G	GATA3	loss	MA0037.2	0.002	0.004	0.091
46	A/G	ELK1	loss	MA0037.2	0.002	0.004	0.091
47	A/G	RUNX1	loss	RUNX1_4	0.006	0.009	0.092
48	A/G	NHLH1	loss	RUNX1_4	0.006	0.009	0.092
49	A/G	EHF	loss	EHF_2	0.004	0.004	0.101
50	A/G	E2F4	loss	EHF_2	0.004	0.004	0.101

51	A/G	REST	loss	REST_disc2	0.015	0.012	0.104
52	A/G	ELF1	loss	ELF1_disc1	0.013	0.008	0.139
53	A/G	Gata1	loss	MA0035.3	0.002	0.007	0.180
54	A/G	E2F1	loss	MA0035.3	0.002	0.007	0.180
55	A/G	ETS1	loss	ETS1_4	0.007	0.008	0.190
56	A/G	GATA4	loss	ETS1_4	0.007	0.008	0.190
57	A/G	GATA	loss	GATA_disc1	0.008	0.011	0.221
58	A/G	Mecom	loss	GATA_disc1	0.008	0.011	0.221
59	A/G	SPDEF	loss	SPDEF_6	0.006	0.008	0.223
60	A/G	MZF1	loss	SPDEF_6	0.006	0.008	0.223
61	A/G	FEV	loss	MA0156.1	0.014	0.024	0.225
62	A/G	ETS	loss	ETS_disc2	0.009	0.013	0.229
63	A/G	GABPA	loss	MA0062.2	0.011	0.023	0.232
64	A/G	GATA1	loss	GATA1_5	0.013	0.045	0.247
65	A/G	GATA1	loss	GATA1_6	0.016	0.021	0.261
66	A/G	ZBTB6	loss	ZBTB6_1	0.005	0.012	0.285
67	A/G	FEV	loss	ZBTB6_1	0.005	0.012	0.285
68	A/G	ELK4	loss	MA0076.2	0.003	0.022	0.288
69	A/G	E2F1	loss	MA0076.2	0.003	0.022	0.288
70	A/G	GATA2	loss	MA0036.2	0.013	0.028	0.301
71	A/G	MEF2	loss	MEF2_disc2	0.008	0.042	0.338
72	A/G	EHF	loss	MEF2_disc2	0.008	0.042	0.338
	A/G	ELF1	loss	MA0473.1	0.014	0.024	0.352
	A/G	TATA	loss	TATA_disc6	0.006	0.032	0.360
	A/G	E2F4	loss	TATA_disc6	0.006	0.032	0.360
	A/G	ETS	loss	ETS_disc4	0.013	0.033	0.376
	A/G	GABPA	loss	GABPA_2	0.003	0.020	0.486
	A/G	SOX10	loss	GABPA_2	0.003	0.020	0.486
	A/G	GABPA	loss	GABPA_3	0.001	0.002	0.629
	A/G	BCL	loss	GABPA_3	0.001	0.002	0.629
	A/G	CREB1	loss	CREB1_10	0.011	0.048	0.633
	G ⁸	heart looping GO:0001947 0.0445					
	A ⁹	positive regulation of endothelial cell migration (GO:0010595; FDR = 0.04); positive regulation of angiogenesis (GO:0045766; FDR = 0.001); cardiac muscle tissue regeneration (GO:0061026; FDR = 0.002); cardiac right ventricle morphogenesis (GO:0003215; FDR = 0.03); response to xenobiotic stimulus (GO:0009410; FDR = 0.03)					

1 – reference (Ref) / alternative (SNP) allele;
2 – TF - transcription factor;
3 – binding of TF to the reference (LOSS) / alternative (GAIN) allele;
4 – binding sites with high affinity for TF;
5 – p value statistically confirming the potential gain or loss of function of the genomic region with SNP in terms of transcription factor binding;
6 – p-value for assessing the binding of TF to the Ref allele;
7 – p-value for assessing the binding of TF to the SNP allele;
8 – biological processes pathogenetically significant for IS, in which TFs that bind to the SNP allele are jointly involved (data from the Gene Ontology resource; <http://geneontology.org/>);
9 – biological processes pathogenetically significant for IS, in which TFs that bind to reference allele are jointly involved (data from the Gene Ontology resource; <http://geneontology.org/>)

Table S7: Analysis of the effect of rs7949972 *ELF5* on the binding of DNA to transcription factors.

Nº	Ref/SNP allele ¹	TF ²	GAIN /LOSS ³	Motif ⁴	P-Value SNP impact ⁵	P-Value Ref ⁶	P-Value SNP ⁷
1	C/T	EN1	gain	EN1_2	0	0.145	1.1×10 ⁻⁶
2	C/T	NR4A2	gain	EN1_2	0	0.145	1.1×10 ⁻⁶
3	C/T	SOX14	gain	SOX14_3	0.0003	0.068	0.001
4	C/T	CREB1	gain	SOX14_3	0.0003	0.068	0.001
5	C/T	STAT	gain	STAT_disc5	0.0001	0.059	0.002
6	C/T	TBX1	gain	STAT_disc5	0.0001	0.059	0.002
7	C/T	FOXA	gain	FOXA_disc4	0.002	0.053	0.002
8	C/T	AR	gain	FOXA_disc4	0.002	0.053	0.002
9	C/T	SPI1	gain	SPI1_disc1	0.004	0.062	0.004
10	C/T	SPIB	gain	SPIB_2	0.002	0.104	0.005
11	C/T	TFCP2	gain	SPIB_2	0.002	0.104	0.005
12	C/T	SOX2	gain	SOX2_3	0.024	0.052	0.009
13	C/T	SOX1	gain	SOX1_3	0.003	0.130	0.010
14	C/T	NR6A1	gain	SOX1_3	0.003	0.130	0.010
15	C/T	ESRRB	gain	ESRRB_2	0.024	0.071	0.010
16	C/T	NR5A1	gain	NR5A1_2	0.009	0.170	0.010
17	C/T	SOX8	gain	SOX8_6	0.009	0.145	0.012
18	C/T	SOX8	gain	SOX8_5	0.023	0.060	0.012
19	C/T	Esrrb	gain	MA0141.2	0.005	0.144	0.012
20	C/T	ESRRB	gain	ESRRB_1	0.013	0.149	0.012
21	C/T	ESRRG	gain	ESRRG_2	0.017	0.122	0.014
22	C/T	EP300	gain	EP300_disc2	0.004	0.430	0.014
23	C/T	PBX	gain	PBX_1	0.006	0.220	0.016
24	C/T	EGR1	gain	EGR1_disc4	0.005	0.161	0.017
25	C/T	SPI1	gain	SPI1_3	0.010	0.348	0.022
26	C/T	ELF1	gain	ELF1_1	0.008	0.296	0.022
27	C/T	HNF4A	gain	HNF4A_7	0.025	0.142	0.023
28	C/T	ZNF652	gain	ZNF652_1	0.003	0.567	0.024
29	C/T	CEBPB	gain	MA0466.1	0.014	0.258	0.026
30	C/T	ESRRA	gain	ESRRA_4	0.013	0.216	0.028
31	C/T	ESRRG	gain	ESRRG_3	0.023	0.290	0.029
32	C/T	CREB3	loss	CREB3_2	0.024	0.242	0.029
33	C/T	STAT6	loss	STAT6_2	0.009	0.316	0.034
34	C/T	SOX10	loss	SOX10_5	0.020	0.180	0.037
35	C/T	SIX5	loss	SIX5_disc3	0.019	0.178	0.043
36	C/T	EWSR1::FLI1	loss	EWSR1::FLI1_1	0.001	0.312	0.046
37	C/T	NR2F6	loss	EWSR1::FLI1_1	0.001	0.312	0.046
38	C/T	POU3F2	loss	POU3F2_2	0.024	0.211	0.048
39	C/T	IRF2	loss	IRF2_1	0.0001	0.003	0.055
40	C/T	REST	loss	IRF2_1	0.0001	0.003	0.055
41	C/T	ZBTB33	loss	ZBTB33_disc4	0.001	0.002	0.058
42	C/T	ESRRA	loss	ZBTB33_disc4	0.001	0.002	0.058
43	C/T	CREB1	loss	CREB1_2	0.001	0.002	0.084
44	C/T	IRF5	loss	CREB1_2	0.001	0.002	0.084

45	C/T	STAT	loss	STAT_disc3	0.016	0.022	0.141
46	C/T	TEAD2	loss	TEAD2_1	0.0007	0.008	0.170
47	C/T	RXRA	loss	TEAD2_1	0.0007	0.008	0.170
48	C/T	IRF1	loss	IRF1_1	0.014	0.016	0.180
49	C/T	IRF9	loss	IRF9_1	0.011	0.017	0.203
50	C/T	IRF9	loss	IRF9_2	0.010	0.017	0.227
51	C/T	CREB1	loss	CREB1_8	0.021	0.019	0.250
52	C/T	PATZ1	loss	PATZ1_1	0.0002	0.025	0.271
53	C/T	CEBPA	loss	PATZ1_1	0.0002	0.025	0.271
54	C/T	ZNF740	loss	ZNF740_3	0.014	0.046	0.326
55	C/T	IRF3	loss	IRF3_1	0.022	0.048	0.333
56	C/T	RUNX2	loss	RUNX2_6	0.003	0.016	0.341
57	C/T	RUNX2	loss	RUNX2_1	0.002	0.005	0.381
58	C/T	NR2F1	loss	RUNX2_1	0.002	0.005	0.381
59	C/T	RUNX1	loss	RUNX1_7	0.013	0.035	0.382
60	C/T	Gfi1b	loss	MA0483.1	0.025	0.044	0.391
61	C/T	REST	loss	REST_disc4	0.007	0.045	0.624
62	C/T	RUNX3	loss	RUNX3_2	0.004	0.021	0.813
63	C/T	OVOL2	loss	OVOL2_1	0.009	0.048	0.865
	T ⁸	glial cell fate commitment (GO:0021781; FDR = 0.02); neural crest cell migration (GO:0001755; FDR = 0.01); regulation of neuron apoptotic process (GO:0043523; FDR = 0.04)					
	C ⁹	positive regulation of CD8-positive, alpha-beta T cell differentiation (GO:0043378; FDR = 0.002); negative regulation of CD4-positive, alpha-beta T cell differentiation (GO:0043371; FDR = 0.03)					
1 – reference (Ref) / alternative (SNP) allele; 2 – TF - transcription factor; 3 – binding of TF to the reference (LOSS) / alternative (GAIN) allele; 4 – binding sites with high affinity for TF; 5 – p value statistically confirming the potential gain or loss of function of the genomic region with SNP in terms of transcription factor binding; 6 – p-value for assessing the binding of TF to the Ref allele; 7 – p-value for assessing the binding of TF to the SNP allele; 8 – biological processes pathogenetically significant for IS, in which TFs that bind to the SNP allele are jointly involved (data from the Gene Ontology resource; http://geneontology.org/); 9 – biological processes pathogenetically significant for IS, in which TFs that bind to reference allele are jointly involved (data from the Gene Ontology resource; http://geneontology.org/)							

Table S8: Analysis of the effect of rs61882275 *ELF5* on the binding of DNA to transcription factors.

№	Ref/SNP allele ¹	TF ²	GAIN /LOSS ³	Motif ⁴	P-Value SNP impact ⁵	P-Value Ref ⁶	P-Value SNP ⁷
1	G/A	SRF	gain	SRF_2	0.002	0.068	0.002
2	G/A	HNF4	gain	HNF4_5	0.001	0.525	0.003
3	G/A	NANOG	gain	NANOG_disc3	0.001	1.000	0.006
4	G/A	EGR2	gain	EGR2_2	0.030	0.091	0.009
5	G/A	HNF4A	gain	HNF4A_8	0.047	0.054	0.010
6	G/A	SRF	gain	SRF_4	0.014	0.103	0.011

7	G/A	SRF	gain	SRF_6	0.024	0.081	0.013
8	G/A	ZBTB33	gain	ZBTB33_1	0.049	0.135	0.016
9	G/A	VDR	gain	VDR_3	0.004	0.264	0.022
10	G/A	YY1	gain	YY1_6	0.013	0.429	0.022
11	G/A	SOX8	gain	SOX8_6	0.009	0.263	0.023
12	G/A	LHX8	gain	LHX8_2	0.019	0.195	0.031
13	G/A	TCF12	gain	TCF12_disc6	0.015	0.243	0.033
14	G/A	VDR	gain	VDR_2	0.019	0.311	0.036
15	G/A	CUX1	gain	CUX1_5	0.011	0.476	0.040
16	G/A	RAD21	gain	RAD21_disc5	0.005	0.245	0.043
17	G/A	HNF4	gain	HNF4_disc5	0.008	0.352	0.049
18	G/A	AHR::ARNT	loss	AHR::ARNT_2	0.004	0.003	0.064
19	G/A	HIC1	loss	HIC1_1	0.040	0.015	0.080
20	G/A	HIF1A	loss	HIF1A_1	0.014	0.005	0.084
21	G/A	SMC3	loss	SMC3_disc3	0.013	0.022	0.114
22	G/A	CTCF	loss	CTCF_disc9	0.000	0.001	0.136
23	G/A	HNF4	loss	HNF4_disc3	0.015	0.018	0.144
24	G/A	NFE2	loss	NFE2_disc4	0.006	0.016	0.149
25	G/A	HIF1A::ARNT	loss	MA0259.1	0.008	0.005	0.151
26	G/A	SIN3A	loss	SIN3A_disc6	0.008	0.021	0.163
27	G/A	HINFP	loss	MA0131.1	0.003	0.009	0.165
28	G/A	HIF1A::ARNT	loss	HIF1A::ARNT_1	0.001	0.003	0.166
29	G/A	RAD21	loss	RAD21_disc8	0	0.00001	0.175
30	G/A	ETS	loss	ETS_disc8	0.007	0.011	0.190
31	G/A	SIN3A	loss	SIN3A_disc5	0.010	0.033	0.194
32	G/A	PTF1A	loss	PTF1A_1	0.022	0.045	0.200
33	G/A	TATA	loss	TATA_disc8	0.034	0.027	0.203
34	G/A	HIF1A	loss	HIF1A_2	0.024	0.020	0.209
35	G/A	SOX10	loss	SOX10_9	0.020	0.037	0.213
36	G/A	BHLHE40	loss	BHLHE40_disc2	0.000	0.001	0.214
37	G/A	HF1H3B	loss	HF1H3B_1	0.015	0.045	0.255
38	G/A	CTCF	loss	CTCF_disc5	0.007	0.035	0.255
39	G/A	BCL	loss	BCL_disc10	0.005	0.022	0.265
40	G/A	BCL	loss	BCL_disc9	0.012	0.046	0.293
41	G/A	YY1	loss	YY1_disc5	0	0.000	0.295
42	G/A	ELF1	loss	ELF1_disc3	0.0002	0.001	0.326
43	G/A	HEY1	loss	HEY1_1	0.010	0.022	0.354
44	G/A	TATA	loss	TATA_disc10	0	0.000	0.378
45	G/A	AHR::ARNT	loss	AHR::ARNT_1	0.009	0.020	0.392
46	G/A	MYC	loss	MYC_1	0.021	0.030	0.410
47	G/A	ZBTB7A	loss	ZBTB7A_disc2	0.009	0.049	0.438
48	G/A	HES7	loss	HES7_1	0.005	0.024	0.548
49	G/A	HINFP	loss	HINFP_2	0.0001	0.001	0.676
	A ⁸	-					
	G ⁹	regulation of neurogenesis (GO:0050767; FDR = 0.003)					
1 – reference (Ref) / alternative (SNP) allele;							

- 2 – TF - transcription factor;
- 3 – binding of TF to the reference (LOSS) / alternative (GAIN) allele;
- 4 – binding sites with high affinity for TF;
- 5 – p value statistically confirming the potential gain or loss of function of the genomic region with SNP in terms of transcription factor binding;
- 6 – p-value for assessing the binding of TF to the Ref allele;
- 7 – p-value for assessing the binding of TF to the SNP allele;
- 8 – biological processes pathogenetically significant for IS, in which TFs that bind to the SNP allele are jointly involved (data from the Gene Ontology resource; <http://geneontology.org/>);
- 9 – biological processes pathogenetically significant for IS, in which TFs that bind to reference allele are jointly involved (data from the Gene Ontology resource; <http://geneontology.org/>)