S1 Suplementary material. Search strategy applied in each database.

DATABASE	SEARCH STRATEGY
PubMed/NCBI	#1((“COVID-19” [MeSH Terms]) OR "COVID 19" [All Fields] OR "SARS-CoV-2 Infection" [All Fields] OR "Infection, SARS-CoV-2" [All Fields] OR "SARS CoV 2 Infection" [All Fields] OR "SARS-CoV-2 Infections" [All Fields] OR "2019 Novel Coronavirus Disease" [All Fields] OR "2019 Novel Coronavirus Infection" [All Fields] OR "2019-nCoV Disease" [All Fields] OR "2019 nCoV Disease" [All Fields] OR "2019-nCoV Diseases" [All Fields] OR "Disease, 2019-nCoV" [All Fields] OR "COVID-19 Virus Infection" [All Fields] OR "COVID 19 Virus Infection" [All Fields] OR "COVID-19 Virus Infections" [All Fields] OOR "Virus Infection, COVID-19" [All Fields] OR "Coronavirus Disease 2019" [All Fields] OR "Disease 2019, Coronavirus" [All Fields] OR "Coronavirus Disease-19" [All Fields] OR "Coronavirus Disease 19" [All Fields] OR "Severe Acute Respiratory Syndrome Coronavirus 2 Infection" [All Fields] OR "SARS Coronavirus 2 Infection" [All Fields] OR "COVID-19 Virus Disease" [All Fields] OR "COVID 19 Virus Disease" [All Fields] OR "Disease, COVID-19 Virus" [All Fields] OR "Virus Disease, COVID-19" [All Fields] OR "2019-nCoV Infection" [All Fields] OR "2019 nCoV Infection" [All Fields] OR "2019-nCoV Infections" [All Fields] "Infection, 2019-nCoV" [All Fields] OR "COVID19" [All Fields] OR "COVID-19 Pandemic" [All Fields] OR "COVID 19 Pandemic" [All Fields] OR "Pandemic, COVID-19" [All Fields] OR "COVID-19 Pandemics" [All Fields] OR "SARS-CoV-2 variants" #2"diabetes"[All Fields]) OR "diabetes mellitus" [All Fields]) OR “Complications of Diabetes Mellitus” [All Fields]) OR “Diabetes Complication” [All Fields]) OR “Diabetes Mellitus Complication” [All Fields]) OR “Diabetes Mellitus Complications” [All Fields]) OR “Diabetes Related Complications” [All Fields]) OR “Diabetes-Related Complication” [All Fields]) OR “Diabetes-Related Complications” [All Fields]) OR “Diabetic Complication” [All Fields]) OR “Diabetic Complications”

	#3“polymorphism” [All Fields] OR “polymorphism genetic” [All Fields]) OR “Amplified Fragment Length Polymorphism Analysis” [All Fields]) OR “Polymorphism, Single-Stranded Conformational” [All Fields]) OR “Polymorphism, Restriction Fragment Length” [All Fields]) OR “Polymorphism, Single Nucleotide” [All Fields]) OR “DNA Copy Number Variations” #4= #1 AND #2 AND #3 Filters: Full text, Humans, from 2019 – 2023
EMBASE	'coronavirus disease 2019' AND 'diabetes mellitus' AND polymorphism:ti,ab,kw AND [2019-2023]/py
Web of Science	((((ALL=(Covid 19)) OR ALL=(Coronavirus disease)) OR ALL=(Sars cov 2)) AND ALL=(Diabetes mellitus)) AND ALL=(polymorphism)
SCOPUS	(TITLE-ABS-KEY (coronavirus AND disease) OR TITLE-ABS-KEY (covid 19) OR TITLE-ABS-KEY (sars AND cov2) AND TITLE-ABS-KEY (diabetes AND mellitus) AND TITLE-ABS-KEY (polymorphism) OR TITLE-ABS-KEY (polymorphism AND genetic))

VHL	(coronavirus disease) OR (covid 19) OR (sars cov2) AND (diabetes mellitus) AND (polymorphism) AND (year_cluster:[2019 TO 2023])

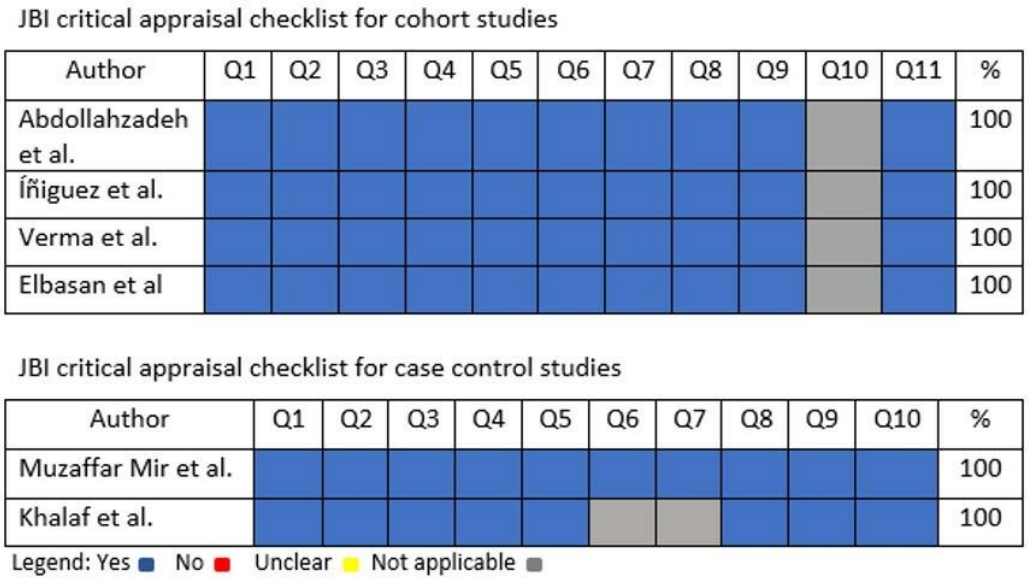
S2 Suplementary material. PECOS criteria for inclusion and exclusion of studies.

Parameter	Inclusion criteria	Exclusion criteria
Population	Adults with DM who had COVID-19	Studies conducted with non-diabetic populations. Non-human studies including *in vitro* observations or research concentrating on animal experiments
Exposure	Genetic polymorphisms	Studies without data on genetic polymorphisms
Comparison	Adults with DM who had COVID-19	None
Outcomes	Susceptibility in the development of symptoms and progression of COVID-19 and complications	Studies with insufficient data on symptoms and progression of COVID-19
Study design	Observational	Case reports, letters, reviews, conference abstracts, personal opinions, book chapters

FIGURA S3 – CHECKLIST FOR COHORT STUDIES (pdf file)

FIGURA S4 – CHECKLIST FOR CASE CONTROL STUDIES (pdf file)

FIGURA S5 - JBI critical appraisal checklist for cohort studies



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S6 Suplementary material. Main characteristics of the included studies

Reference, Country	Type of study	Data collection period	Gene	Polymorphism	Genotyping method	Polymorphisms and genotypes	Type of polymorphisms	N (Control)	N (Case)		
								Asymptomatic	Mild/ moderate symptoms	Severe/ critical symptoms	Total symptoms
Abdollahzadeh et al. [20], Iran	Cohort	Between May 5 and September 25, 2020	*VDR*	rs4516035	PCR-RFLP	T>C: TT, TC and CC	SNP	16	44	32	92
				rs7975232	PCR-RFLP	C>A: CC, CA and AA	SNP				
				rs1544410	PCR-RFLP	G>A: GG, GA and AA	SNP				
				rs739837	PCR-RFLP	C>T: CC, CT and TT	SNP				
				rs731236	PCR-RFLP	A>G: AA, AG and GG	SNP				
				rs757343	PCR-RFLP	G>A: GG, GA and AA	SNP				
				rs2228570	PCR-RFLP	C>T: CC, CT and TT	SNP				
				rs11568820	PCR-RFLP	G>A: GG, GA and AA	SNP				
Íñiguez et al. [21], Spain	Cohort	17 April - 29 May 2020)	*ACE*	rs4341	qPCR	C>G: CC, CG and GG	SNP	0	12	3	30
				rs4343	qPCR	A>G: AA, AG and GG	SNP	0	12	3	
Muzaffar Mir et al. [22], Saudi Arabia	Case-control (prospective cohort)	Between September 2020 and April 2021.	*ACE2*	rs4646994	ARMS-PCR	I/D: II, ID and DD	Insertion/ Deletion	Healthy	Not available	47	47
				rs4240157	ARMS-PCR	C>T: CC, CT and TT	SNP				
Verma et al. [23], India	Cohort	From August 2020 to September 2020	*ACE*	rs4646994	PCR- AFLP	I/D: II, ID and DD	Insertion/ Deletion	Not available	13	24	37
Elbasan et al. [24], Turkey	Cohort (cross-sectional)	Between April and October 2020	*ACE*	rs4646994	PCR	I/D: II, ID and DD	Insertion/ Deletion	Not available	50	25	75

Khalaf et al. [18], Iraq	Case-control	Not reported	*IL 6*	rs1800795	PCR	G>C: GG, GC, CC	SNP	Not available	Not available	6	6
			IL 17A	rs2275913		G>A: GG, GA, AA	SNP			6	6
										Total	293

PCR = Polymerase Chain Reaction; RFLP = Restriction Fragment Length Polymorphism; qPCR = Real Time Polymerase Chain Reaction; SNP = Single Nucleotide Polymorphism; ARMS = amplification refractory mutation system; AFLP = amplified fragment length polymorphism.

S7 Suplementary material - Details of the selection of studys included

Reference	**Abdollahzadeh et al. [19], Iran**
Diagnostic method	Positive result of real-time reverse transcriptase- polymerase chain reaction (RT-PCR) assay of nasal and/or pharyngeal swabs, following WHO interim guidance.
Analysis period	Between May 5 and September 25, 2020
Techniques for identifying polymorphisms	Peripheral blood was taken from each of the participants and DNA extraction was applied by High Pure PCR Template Preparation Kit (Roche Applied Science, USA) following the manufacturer's recommendations. The target SNPs were genotyped using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP).
Asymptomatic	Subjects with absence of clinical symptoms and no need for hospitalization or ventilation.
Mild /moderate symptoms	Patients with a wide range of symptoms, including fever, sore throat, dry cough, headache, shortness of breath, diarrhea, myalgia, fatigue, nausea, vomiting, and parageusia.
Severe/critical symptoms	Regarding respiratory impairment, severe cases require non-invasive ventilation, while critical patients, defined as respiratory failure, requiring invasive ventilation and intensive care unit (ICU) admission.

Reference	**Íñiguez et al. [20], Spain**
Diagnostic method	Patients positive were confirmed by PCR from nasopharyngeal swabs,
Analysis period	From the first epidemic wave (17 April -29 May 2020).
Techniques for identifying polymorphisms	The rs4341 and rs4343 genotyping of the DNA samples was carried out in an Applied Biosciences (ABI) 7300 RT-PCR system using predesigned TaqMan SNP Genotyping Human Assays.
Asymptomatic	Patients with any of the following non-life-threatening symptoms such as fever, myalgia, fatigue, rhinorrhea, vomits, sickness, diarrhea, dry cough, cephalalgia, anosmia, ageusia (they had no lung involvement in chest X-ray and had not required oxygen supplement. Since none of them required hospital admission.
Mild /moderate symptoms	Patients hospitalized in the normal ward were patients with symptoms requiring oxygen therapy or patients presenting a high decompensation of their underlying diseases due to the SARS-CoV-2 infection.
Severe/critical symptoms	ICU group were patients that required invasive mechanical ventilation.

Reference	**Muzaffar Mir et al. [21], Saudi Arabia**
Diagnostic method	COVID-19 laboratory confirmation was defined as a positive result on RT-qPCR (SARS-CoV-2 RT-qPCR detection kit) of nasal and oropharyngeal swab specimens. We selected COVID-19 positive cases confirmed by a real-time reverse transcription polymerase chain reaction (rRT-PCR) test.
Analysis period	September 2020 and April 2021.
Techniques for identifying	Genomic DNA was extracted using DNeasy Blood K (Qiagen, Hilden, Germany) as per the manufacturer's instructions. The extracted DNA was dissolved in nuclease- free water and stored at 4 ◦C until use. Quality and integrity of DNA

polymorphisms	were checked by NanoDropTM (Thermo Scientific, Waltham, MA, USA). All DNA samples from COVID-19 and controls were screened for purity by measuring optical density (OD) at 260 nm (OD260) and 280 nm (OD280). The λ260/λ280 ratios ranged from 1.83–1.99 indicating good quality DNA. The target SNPs were genotyped using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP).
Asymptomatic	150 matched healthy controls.
Mild /moderate symptoms	There was no such group of patients in this study.
Severe/critical symptoms	The COVID-19 patients who had oxygen saturation was less than 60 and needed mechanical ventilatory support in ICU were classified as having severe COVID-19 disease.

Reference	**Verma et al. [22], Spain**
Diagnostic method	COVID-19 patients confirmed by RT-PCR with age more than 20 years), and exclusion criteria (Pregnant patients, patients with known malignant disease) were selected.
Analysis period	from August 2020 to September 2020.
Techniques for identifying polymorphisms	High molecular weight genomic DNA was extracted from peripheral blood leucocytes using commercially available kit (Nucleospin Blood) and quality/quantity was assessed by using spectrophotometer quantification and analyzed on gel electrophoresis. ACE1 gene polymorphisms (rs4646994) were done in COVID-19 patients via polymerase chain reaction amplified fragment length polymorphism (PCR- AFLP) using specific primers (forward primer- 5' - CTGGAGACCACTCCCATCCTTTCT- 3' and reverse primer- 5' - GATGTGGCCATCACATTCGTCAGAT-3'). Reactions were performed in 15 µL volume containing 10 pmol of each primer, 1× PCR master mix (EmeraldAmp GT PCR master mix), 3 mM MgCl2, and 2 U Taq polymerase (G Biosciences). PCR sequence amplification was performed under the conditions: Initial denaturation at 95 ◦C for 5 min, followed by 35 cycles of denaturation at 95 ◦C for 45 s, annealing at 60 ◦ C for 1.15 min, extension at 72 ◦ C for 2.30 min and final extension at 72 ◦C for 10 min. PCR products were checked on 2.5% agarose gel and visualized by gel documentation system EZ, BIO-RAD (California), 481 bp product for allele I and 194 bp for allele D.
Asymptomatic	Only hospitalized patients were analyzed.
Mild /moderate symptoms	Patients with respiratory rate less than 24 per minute and SpO2 > 94% on room air were considered as mild patient.
Severe/critical symptoms	Patients with respiratory rate more than 30 per minute OR SpO2 < 90% on room air with pneumonia were categorized into severe patients.

Reference	**Elbasan et al., [23], Iran**
Diagnostic method	Positive result of real-time reverse transcriptase- polymerase chain reaction (RT-PCR) assay of nasal and/or pharyngeal swabs, following WHO interim guidance.
Analysis period	April and October 2020.
Techniques for identifying	D and I alleles in intron 16 of the ACE gene were determined on the basis of polymerase chain reaction (PCR) and the products were visualized by agarose gel electrophoresis. Genomic DNA was isolated from 5 mL of

polymorphisms	peripheral blood using the ZeeSan Lab-Aid1 824 sBlood DNA isolation kit. The quality and concentration of genomic DNA samples were measured by a NanoDrop (NanoDropTM 2000/2000c spectrophotometers). For PCR, 100 ng genomic DNA was added to 10x PCR Buffer, 2 mM MgCl2, 0.5 mM dNTP, 0.1 pmol primers and 1 unit of Thermus aquaticus DNA polymerase with a total reaction volume of 25 µL. The amplicon sizes of the first primer pair for the detection of D and I alleles were 319 bp and 597 bp, respectively (hace3s, 5', GCCCTGCAGGTGTCTGCAGCATGT3'; hace3as, 5'GGATGGCTCTCCCCGCCT TGTCTC3'). PCR (BIO-RAD T100) conditions included denaturation at 94 Ċ for 30 seconds, annealing at 56 Ċ for 45 seconds, and extension at 72 Ċ for two minutes, repeated for 35 cycles, followed by a final extension at 72 Ċ for seven minutes. PCR products were conducted at 98 V and 36 min. on 1.5% agarose gel electrophoresis. Amplicons were visualized by spec- trophotometer (Gel Doc XR+ System, BIO-RAD). The second primer pair (hace5a, 5'TGGGA CCACAGCGCCCGCCACTAC3'; hace5c, 5'TCGCCAGCCCTCCCATGCCCATAA3') was used for the DD allele control due to the predominance of D allele amplifications in heterozygous samples. All samples that showed the DD allele pattern were amplified a second time with this primer pair. The PCR conditions were same as the previous conditions except for an annealing temperature of 67 Ċ. PCR products that included the I allele had an amplicon size of 335-bp. The homozygous DD allele did not show any band under UV. We grouped the patients according to the determination of ACE 1 alleles as DD, ID, or II.
Asymptomatic	There was no such group of patients in this study.
Mild /moderate symptoms	Group 1. Mild ambulatory disease. Group 2. Hospitalized with moderate disease.
Severe/critical symptoms	Group 3. Hospitalized with severe disease and dead. Group 4. The need for noninvasive mechanical ventilation (NIMV), reservoir mask, admission to the ICU.

Reference	**Khalaf et al., [17], Spain**
Diagnostic method	COVID-19 was identified by PCR, CT scan; furthermore, the infection was confirmed by IgG and IgM levels investigation by fluorescence immuno-assay (FIA).
Analysis period	Ethical Clearence research in approval in December 1, 2021. Only this information.
Techniques for identifying polymorphisms	The IL-6 and IL-17A genes were amplified using a traditional polymerase chain reaction (PCR) thermal cycler Tc-3000X (Techne, USA). The PCR mixture contains 5 µl AccuPower PCR Premix (Bioneer, Korea). that is ready to use, 1 µl each of forward and reverse primers, 13 µl of DNAse-free water, and 5 µl of ex- tracted DNA for a total volume of 25 µl. Depending on the insertion program, the mixture was moved to a thermal cycler to initiate the reaction. Thermocycling was designed to operate under the following conditions: an initial denaturation at 95◦C for 5 min, 30 cycles of denaturation at 95◦C for 30 sec., annealing at 60◦C for 30 sec., and elongation at 72◦C for 30 sec., and final single extension step at 72◦C for 1 min for one cycle. On a 2% agarose gel, the PCR products were electrophoresed. DNA migrating bands were detected using a gel documentation system.
Asymptomatic	Healthy volunteers made up the fourth group.

Mild /moderate symptoms	There was no such group of patients in this study.
Severe/critical symptoms	Six severely ill patients with COVID-19 and T2DM made up the first group "G1". Six patients with COVID-19 only made up the second group "G2", six T2DM patients made up the third group "G3".

S8 Supplementary material. Genotypic and allelic distribution, and association of symptoms with genetic variants in the *VDR* gene, for SNPs which did not present a statistically significant difference between the groups (Abdollahzadeh et al. [20]).

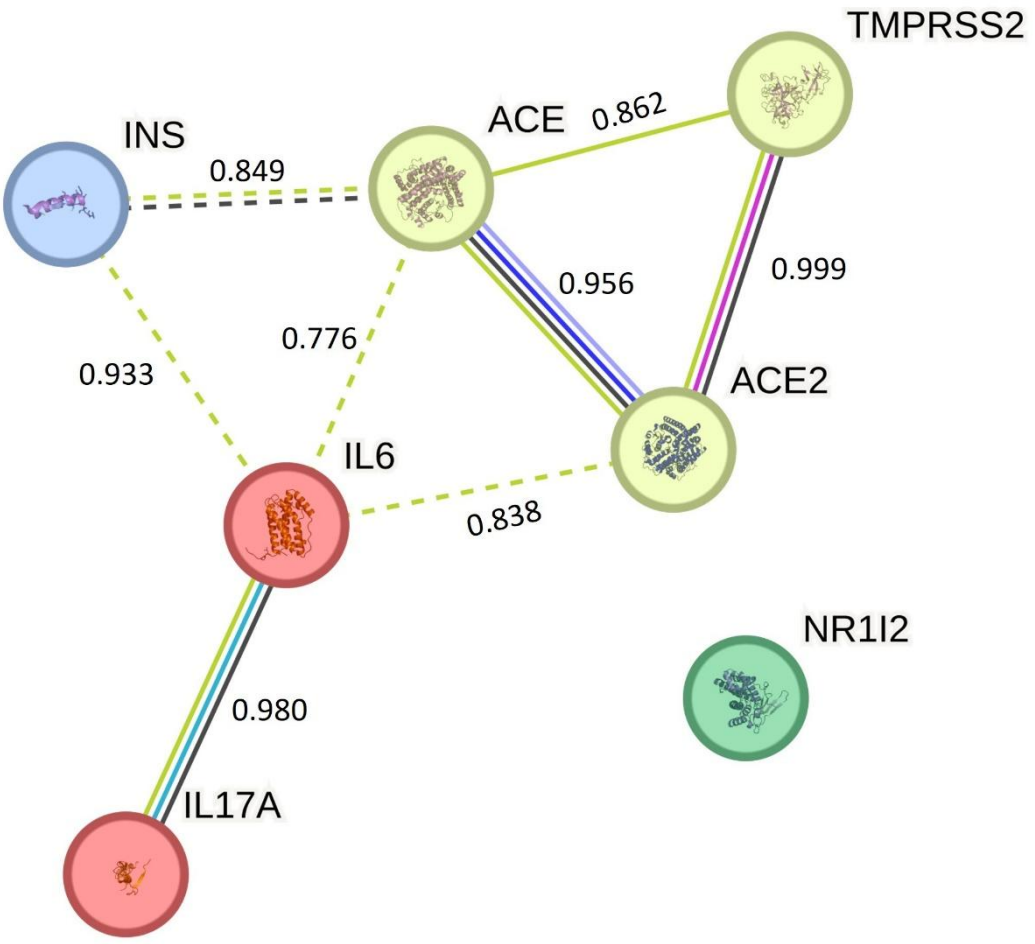
Genes	Models	Genotype	Control, n (%)	Case, n (%)	OR (CI 95%)	p
rs11568820	Codominant	GG	5 (31.250%)	20 (26.316%)	Ref	-
		GA	8 (50.000%)	32 (42.105%)	0.500 (0.101 - 1.935)	0.341
		AA	3 (18.750%)	24 (31.579%)	0.500 (0.09 -2.229)	0.380
	Recessive	GG+GA	13 (81.250%)	52 (68.421%)	Ref	-
		AA	3 (18.750%)	24 (31.579%)	0.785 (0.251 - 2.744)	0.687
	Dominant	GG	5 (31.250%)	20 (26.316%)	Ref	-
		GA+AA	11 (68.750%)	56 (73.684%)	0.500 (0.107 - 1.729)	0.312
	Overdominant	GG+AA	8 (50.000%)	44 (57.895%)	Ref	-
		GA	8 (50.000%)	32 (42.105%)	0.727 (0.242 - 2.173)	0.564
			Alleles			
		G	18 (56.250%)	72 (47.368%)	-	0.845
		A	14 (43.750%)	80 (52.632%)		
rs1544410	Codominant	GG	8 (50.000%)	32 (42.105%)	Ref	-
		GA	7 (43.750%)	36 (47.368%)	1.285 (0.416 - 4.050)	0.660
		AA	1 (6.250%)	8 (10.526%)	2.000 (0.298 - 39.861)	0.540
	Recessive	GG+GA	15 (93.750%)	68 (89.474%)	Ref	-
		AA	1 (6.250%)	8 (10.526%)	1.764 (0.290 - 34.003)	0.605
	Dominant	GG	8 (50.000%)	32 (42.105%)	Ref	-
		GA+AA	8 (50.000%)	44 (57.895%)	1.375 (0.460 - 4.116)	0.563
	Overdominant	GG+AA	9 (56.250%)	40 (52.632%)	Ref	-
		GA	7 (43.750%)	36 (47.368%)	1.157 (0.391 - 3.541)	0.792
			Alleles			
		G	23 (71.875%)	100 (65.789%)	-	0.0001
		A	9 (28.125%)	52 (34.211%)		
rs2228570	Codominant	CC	6 (37.500%)	26 (34.211%)	Ref	-
		CT	6 (37.500%)	35 (46.053%)	1.346 (0.380 - 4.768)	0.638
		TT	4 (25.000%)	15 (19.737%)	0.865 (0.211 - 3.842)	0.841
	Recessive	CC+CT	12 (75.000%)	61 (80.263%)	Ref	-
		TT	4 (25.000%)	15 (19.737%)	0.737 (0.219 - 2.924)	0.637
	Dominant	CC	6 (37.500%)	26 (34.211%)	Ref	-
		CT+TT	10 (62.500%)	50 (65.789%)	1.153 (0.358 - 3.469)	0.801
	Overdominant	CC+TT	10 (62.500%)	41 (53.947%)	Ref	-
		CT	6 (37.500%)	35 (46.053%)	1.422 (0.478 - 4.549)	0.533

		Alleles				
		C	18 (56.250%)	87 (57.237%)	-	0.176
		T	14 (43.750%)	65 (42.763%)		
rs731236	Codominant	AA	6 (37.500%)	36 (47.368%)	Ref	-
		AG	9 (56.250%)	31 (40.789%)	0.574 (0.174 - 1.770)	0.340
		GG	1 (6.250%)	9 (11.842%)	1.500 (0.215 - 30.200)	0.723
	Recessive	AA+AG	15 (93.750%)	67 (88.158%)	Ref	-
		GG	1 (6.250%)	9 (11.842%)	2.014 (0.338 - 38.586)	0.521
	Dominant	AA	6 (37.500%)	36 (47.368%)	Ref	-
		AG+GG	10 (62.500%)	40 (52.632%)	0.666 (0.208 - 1.980)	0.473
	Overdominant	AA+GG	7 (43.750%)	45 (59.211%)	Ref	-
		AG	9 (56.250%)	31 (40.789%)	0.535 (0.174 - 1.586)	0.261
		Alleles				
		A	21 (65.625%)	103 (67.763%)	-	0.837
		G	11 (34.375%)	49 (32.237%)		
rs739837	Codominant	CC	8 (50.000%)	50 (65.789%)	Ref	-
		CT	8 (50.000%)	21 (27.632%)	-	0.124
		TT	0 (0.000%)	5 (6.579%)	-	0.993
	Recessive	CC+CT	16 (100.000%)	71 (93.421%)	Ref	-
		TT	0 (0.000%)	5 (6.579%)	-	0.993
	Dominant	CC	8 (50.000%)	50 (65.789%)	Ref	-
		CT+TT	8 (50.000%)	26 (34.211%)	0.520 (0.172 - 1.564)	0.239
	Overdominant	CC+TT	8 (50.000%)	55 (72.368%)	Ref	-
		CT	8 (50.000%)	21 (27.632%)	0.381 (0.124 - 1.161)	0.086
		Alleles				
		C	24 (75.000%)	121 (79.605%)	-	0.634
		T	8 (25.000%)	31 (20.395%)		
rs757343	Codominant	GG	13 (81.250%)	58 (76.316%)	Ref	-
		GA	3 (18.750%)	14 (18.421%)	-	0.949
		AA	0 (0.000%)	4 (5.263%)	-	0.994
	Recessive	GG+GA	16 (100.000%)	72 (94.737%)	Ref	-
		AA	0 (0.000%)	4 (5.263%)	-	0.994
	Dominant	GG	13 (81.250%)	58 (76.316%)	Ref	-
		GA+AA	3 (18.750%)	18 (23.684%)	1.344 (0.380 - 6.333)	0.670
	Overdominant	GG+AA	13 (81.250%)	62 (81.579%)	Ref	-
		GA	3 (18.750%)	14 (18.421%)	0.978 (0.269 - 4.674)	0.975
		Alleles				
		G	29 (90.625%)	130 (85.526%)	-	0.577
		A	3 (9.375%)	22 (14.474%)		
rs7975232	Codominant	CC	5 (31.250%)	30 (39.474%)	Ref	-

	CA	8 (50.000%)	40 (52.632%)	0.833 (0.231 - 2.755)	0.768
	AA	3 (18.750%)	6 (7.895%)	0.333 (0.061 - 1.964)	0.199
Recessive	CC+CA	13 (81.250%)	70 (92.105%)	Ref	-
	AA	3 (18.750%)	6 (7.895%)	0.371 (0.085 - 1.930)	0.198
Dominant	CC	5 (31.250%)	30 (39.474%)	Ref	-
	CA+AA	11 (68.750%)	46 (60.526%)	0.696 (0.202 - 2.124)	0.539
Overdominant	CC+AA	8 (50.000%)	36 (47.368%)	Ref	-
	CA	8 (50.000%)	40 (52.632%)	1.111 (0.372 - 3.317)	0.848
Alleles					
	C	18 (56.250%)	100 (65.789%)	-	0.317
	A	14 (43.750%)	52 (34.211%)		

* Chi-Square; %, relative frequency; CI, confidence interval; N, Absolute Frequency; OR, Odds ratio

Figure S9



S10 Supplementary material. Characteristics of proteins used for interaction networks and clustering.

Code	Protein Uniprot	Protein STRING	Location Celullar	Identity	p-value	Cluster

P11473	VDR	NR1I2	Nucleus and Cytoplasm	42,00%	1,20E-77	1
P12821	ACE1	ACE	Cytoplasm, Cell membrane and Secreted	100,00%	0,00	2
Q9BYF1	ACE2	ACE2	Cytoplasm, Cell membrane and Secreted	100,00%	0,00	2
P05231	IL6	IL6	Secreted	100,00%	3,80E-114	3
Q16552	IL17	IL17A	Secreted	100,00%	2,20E-87	3
P01308	INS	INS	Secreted	100,00%	5,70E-61	4
O15393	TMPS2	TMPRSS2	Cell membrane and Secreted	100,00%	6,50E-306	2