ПРИЛОЖЕНИЕ

к статье Н.С. Юдина, Н.Л. Подколодного, Т.А. Агарковой, Е.В. Игнатьевой «Приоритизация генов, ассоциированных с патогенезом лейкоза у крупного рогатого скота»

Таблица S1.
Данные по полногеномному анализу ассоциаций.
Гены КРС, которые содержат аллельные варианты, ассоциированные с чувствительностью/устойчивостью к инфекции ВЛКРС по результатам полногеномного анализа ассоциаций. Все гены собраны из экспериментальных статей

Обозначение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Идентификатор SNP в базе данных dbSNP/аллели BOLA-DRB3	Ссылка	Локализация SNP	Порода	Фенотипический признак
ZBTB20	zinc finger and BTB domain containing 20	508864	rs43241193	[Brym et al., 2016]	Интрон	Holstein-Frisian	Based on serological (ELISA), molecular(nested-PCR proviral detection) and hematological assays, the casegroup was composed of 43 BLV-infected individuals, approx. 5-year-old, with apparent hematological alterations characteristic forthe lymphoproliferative stage of enzootic bovine leukosis (averageWBC
TRIM45	tripartite motif containing 45	539091	rs110785500	[Brym et al., 2016]	5' фланкирующая область	Holstein-Frisian	Based on serological (ELISA), molecular(nested-PCR proviral detection) and hematological assays, the casegroup was composed of 43 BLV-infected individuals, approx. 5-year-old, with apparent hematological alterations characteristic forthe lymphoproliferative stage of enzootic bovine leukosis (averageWBC
AP4B1	adaptor related protein complex 4 subunit beta 1	512078	rs109405425	[Brym et al., 2016]	Интрон	Holstein-Frisian	Based on serological (ELISA), molecular(nested-PCR proviral detection) and hematological assays, the casegroup was composed of 43 BLV-infected individuals, approx. 5-year-old, with apparent hematological alterations characteristic forthe lymphoproliferative stage of enzootic bovine leukosis (averageWBC
HGF	hepatocyte growth factor	282879	rs42993006	[Brym et al., 2016]	Межгенный район	Holstein-Frisian	Based on serological (ELISA), molecular(nested-PCR proviral detection) and hematological assays, the casegroup was composed of 43 BLV-infected individuals, approx. 5-year-old, with apparent hematological alterations characteristic forthe lymphoproliferative stage of enzootic bovine leukosis (averageWBC

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CDCA2	cell division cycle associated 2	515287	rs43564499	[Brym et al., 2016]	Интрон	Holstein-Frisian	Based on serological (ELISA), molecular(nested-PCR proviral detection) and hematological assays, the casegroup was composed of 43 BLV-infected individuals, approx. 5-year-old, with apparent hematological alterations characteristic forthe lymphoproliferative stage of enzootic bovine leukosis (averageWBC
LOC101907861	uncharacterized	-	rs42014447	[Brym et al., 2016]	Межгенный район	Holstein-Frisian	Based on serological (ELISA), molecular(nested-PCR proviral detection) and hematological assays, the casegroup was composed of 43 BLV-infected individuals, approx. 5-year-old, with apparent hematological alterations characteristic forthe lymphoproliferative stage of enzootic bovine leukosis (averageWBC
DAG1	dystroglycan 1	281439	rs42012947	[Brym et al., 2016]	Интрон	Holstein-Frisian	Based on serological (ELISA), molecular(nested-PCR proviral detection) and hematological assays, the casegroup was composed of 43 BLV-infected individuals, approx. 5-year-old, with apparent hematological alterations characteristic forthe lymphoproliferative stage of enzootic bovine leukosis (averageWBC
COL21A1	collagen type XXI alpha 1 chain	533456	rs110601061	[Brym et al., 2016]	Интрон	Holstein-Frisian	Based on serological (ELISA), molecular(nested-PCR proviral detection) and hematological assays, the casegroup was composed of 43 BLV-infected individuals, approx. 5-year-old, with apparent hematological alterations characteristic forthe lymphoproliferative stage of enzootic bovine leukosis (averageWBC
PNPLA1	patatin like phospholipase domain containing 1	786888	rs41583098	[Brym et al., 2016]	Экзон, 5' UTR	Holstein-Frisian	Based on serological (ELISA), molecular(nested-PCR proviral detection) and hematological assays, the casegroup was composed of 43 BLV-infected individuals, approx. 5-year-old, with apparent hematological alterations characteristic forthe lymphoproliferative stage of enzootic bovine leukosis (averageWBC
ADGRF2	adhesion G protein-coupled receptor F2	539131	rs110155623	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
CD2AP	CD2 associated protein	533188	rs110155623	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
CRISP1	cysteine rich secretory protein 1	616774	rs41587216	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
TFAP2D	transcription factor AP-2 delta	539910	rs41566363	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
PKHD1	fibrocystin/polyductin	5314	rs41641297	[Carignano et al., 2018]	Интрон	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
TRAM2	translocation associated membrane protein 2	617287	rs109343703	[Carignano et al., 2018]	Интрон	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.

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TRAM2	translocation associated membrane protein 2	617287	rs110499907	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
GCM1	glial cells missing homolog 1	317779	rs110473048	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
BOLA-DQA1	major histocompatibility complex, class II, DQ alpha, type 1	282534	rs110525467	[Carignano et al., 2018]	Экзон, синонимичная замена	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
BOLA-DRB3	major histocompatibility complex, class II, DRB3	282530	rs110579760	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
TNXB	tenascin XB	282654	rs110836188	[Carignano et al., 2018]	Экзон, синонимичная замена	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
SLC44A4	solute carrier family 44 member 4	520625	rs41255514	[Carignano et al., 2018]	3' UTR	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
NEU1	neuraminidase 1	505554	rs17872223	[Carignano et al., 2018]	Интрон	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
C23H6orf47	chromosome 23 C6orf47 homolog	617546	rs110861313	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
ABHD16A	abhydrolase domain containing 16A	513252	rs110861313	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
LY6G5C	lymphocyte antigen 6 family member G5C	100848062	rs110861313	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
LY6G5B	lymphocyte antigen 6 family member G5B	539236	rs110861313	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
CSNK2B	casein kinase 2 beta	539235	rs110861313	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
GPANK1	G-patch domain and ankyrin repeats 1	617553	rs110861313	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
APOM	apolipoprotein M	505830	rs110861313	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
BAG6	BCL2 associated athanogene 6	508605	rs110861313	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
PRRC2A	proline rich coiled-coil 2A	538553	rs17871874	[Carignano et al., 2018]	Экзон, синонимичная замена	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
LTA	lymphotoxin alpha	280845	rs110260956	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
NFKBIL1	NFKB inhibitor like 1	514369	rs110260956	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
ATP6V1G2	ATPase H+ transporting V1 subunit G2	514368	rs110260956	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
LTB	lymphotoxin beta	529757	rs110260956	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.

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TNF	tumor necrosis factor	280943	rs110260956	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
LOC616942	major histocompatibility complex, class I, A-like	616942	rs110350951	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
LOC616942	major histocompatibility complex, class I, A-like	616942	rs110794231	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
SFTA2	surfactant associated 2	616978	rs41587536	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
TUBB	tubulin beta class I	615087	rs110742604	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
IER3	immediate early response 3	505455	rs110742604	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
FLOT1	flotillin 1	532573	rs110742604	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
TRIM31	tripartite motif containing 31	517666	rs109856572	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
TRIM40	tripartite motif containing 40	786497	rs109856572	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
LOC516273	olfactory receptor 2G6-like	516273	rs110769723	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
LOC618064	olfactory receptor 2G3	618064	rs110769723	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
LOC785162	olfactory receptor, family 2, subfamily H, member 2-like	785162	rs110769723	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
LOC784787	olfactory receptor 10C1	784787	rs109015676	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
LOC511103	olfactory receptor 2J3	511103	rs109015676	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
LOC784858	olfactory receptor 10C1	784858	rs109015676	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
LOC522315	putative olfactory receptor 2W6	522315	rs110034224	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
ABT1	activator of basal transcription 1	539270	rs110277740	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
NRSN1	neurensin 1	510831	rs109754326	[Carignano et al., 2018]	Межгенный район	Holstein and Holstein x Jersey cows	The anti-p24 ELISA assay was used to discriminate BLV infected animals, followed by total WBC counts.
CNTN3	contactin 3	526697	rs110616206	[Takeshima et al., 2017]	Межгенный район	Japanese Black	We categorized the 444 BLV-infected cows into four groups according to proviral load: Low (0 < provirus load ≤ 13,819, 266 heads), Medium (14,237 < provirus load ≤ 40,698, 85 heads), High (42,605 < provirus load ≤ 73,145, 60 heads), and Very High (76,397 < provirus

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							load ≤ 132,230, 33 heads).
ABHD16A	abhydrolase domain containing 16A	513252	rs29026690	[Takeshima et al., 2017]	Межгенный район	Japanese Black	We categorized the 444 BLV-infected cows into four groups according to proviral load: Low (0 < provirus load ≤ 13,819, 266 heads), Medium (14,237 < provirus load ≤ 40,698, 85 heads), High (42,605 < provirus load ≤ 73,145, 60 heads), and Very High (76,397 < provirus load ≤ 132,230, 33 heads).
PRR3	proline rich 3	525344	rs17872126	[Takeshima et al., 2017]	Интрон	Japanese Black	We categorized the 444 BLV-infected cows into four groups according to proviral load: Low (0 < provirus load ≤ 13,819, 266 heads), Medium (14,237 < provirus load ≤ 40,698, 85 heads), High (42,605 < provirus load ≤ 73,145, 60 heads), and Very High (76,397 < provirus load ≤ 132,230, 33 heads).

Литература к таблице **S1**

REF	PubMedID	Авторы	Название	Данные о журнале
[Brym et al., 2016]	27269789	Brym P, Bojarojć-Nosowicz B, Oleński K, Hering DM, Ruść A, Kaczmarczyk E, Kamiński S.	Genome-wide association study for host response to bovine leukemia virus in Holstein cows.	Vet Immunol Immunopathol. 2016 Jul;175:24-35. doi: 10.1016/j.vetimm.2016.04.012. Epub 2016 Apr 29.
[Carignano et al., 2018]	29439661	Carignano HA, Roldan DL, Beribe MJ, Raschia MA, Amadio A, Nani JP, Gutierrez G, Alvarez I, Trono K, Poli MA, Miretti MM.	Genome-wide scan for commons SNPs affecting bovine leukemia virus infection level in dairy cattle.	BMC Genomics. 2018 Feb 13;19(1):142. doi: 10.1186/s12864-018-4523-2.
[Takeshima et al., 2017]	28376881	Takeshima SN, Sasaki S, Meripet P, Sugimoto Y, Aida Y.	Single nucleotide polymorphisms in the bovine MHC region of Japanese Black cattle are associated with bovine leukemia virus proviral load.	Retrovirology. 2017 Apr 4;14(1):24. doi: 10.1186/s12977-017-0348-3.

Таблица S2.

Данные по аллельным вариантам.

Гены КРС, которые содержат аллельные варианты, ассоциированные с чувствительностью/устойчивостью к инфекции ВЛКРС. Все гены собраны из экспериментальных статей.

Обозначение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Идентификатор SNP в базе данных dbSNP/аллели BOLA-DRB3	Ссылка	Локализация SNP	Порода	Фенотипический признак	Комментарии
TNF	tumor necrosis factor	280943	rs800546346	[Lendez et al., 2013]	TNF, promoter	Holstein	Animals were classified as high or low proviral load by a semiquantitative PCR technique	In the low proviral load group, there was a significant association between the proviral load and a low frequency of the G/G genotype at position -824.
TNF	tumor necrosis factor	280943	rs800546346	[Konnai et al., 2006]	TNF, promoter	Japanese black, Holstein-Friesian and First filial of Japanese black/Holstein-Friesian	BLV-infected cells were quantified based on viral genome amplification by real-time PCR as described previously [14]. Twenty-five animals with lymphoma were diagnosed clinically, and confirmed by microscopic and histological examinations.	We found that the frequency of the TNF-alpha -824G allele, which has been associated with low transcription activity of the promoter/predicted enhancer region of the bovine TNF-alpha gene, was higher in individuals with BLV-induced lymphoma than in asymptomatic carrier individuals.
BOLA-DRB3	major histocompatibility complex, class II, DRB3	282530	*0902	[Juliarena et al., 2008]	BOLA-DRB3 gene	Holstein	BLV-infected Holstein cattle were classified into two infection profiles characterized by low and high proviral loads	Allele ISAG*0902 appears to be the best BLV resistance marker in Holstein cattle
BOLA-DRB3	major histocompatibility complex, class II, DRB3	282530	*0902	[Miyasaka et al., 2013]	BOLA-DRB3 gene	Japanese Black	BLV proviral load	
BOLA-DRB3	major histocompatibility complex, class II, DRB3	282530	*1101	[Miyasaka et al., 2013]	BOLA-DRB3 gene	Japanese Black	BLV proviral load	
BOLA-DRB3	major histocompatibility complex, class II, DRB4	282530	*1601	[Miyasaka et al., 2013]	BOLA-DRB3 gene	Japanese Black	BLV proviral load	
BOLA-DRB3	major histocompatibility	282530	*0902	[Carignano et al., 2017]	BOLA-DRB3 gene	Holstein and Holstein × Jersey	Level of infection by assessing differences in proviral load in peripheral blood.	

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	complex, class II, DRB4							
BOLA-DRB3	major histocompatibility complex, class II, DRB4	282530	*1001	[Carignano et al., 2017]	BOLA-DRB3 gene	Holstein and Holstein × Jersey	Level of infection by assessing differences in proviral load in peripheral blood.	
BOLA-DRB3	major histocompatibility complex, class II, DRB4	282530	*1201	[Carignano et al., 2017]	BOLA-DRB3 gene	Holstein and Holstein × Jersey	Level of infection by assessing differences in proviral load in peripheral blood.	
BOLA-DRB3	major histocompatibility complex, class II, DRB4	282530	*0101	[Nikbakht Brujeni et al., 2016]	BOLA-DRB3 gene	Holstein	The studied cattle were categorized into three groups: BLV seronegative, BLV seropositive with persistent lymphocytosis (PL), and BLV seropositive with lymphosarcoma (LS).	
BOLA-DRB3	major histocompatibility complex, class II, DRB4	282530	*4201	[Nikbakht Brujeni et al., 2016]	BOLA-DRB3 gene	Holstein	The studied cattle were categorized into three groups: BLV seronegative, BLV seropositive with persistent lymphocytosis (PL), and BLV seropositive with lymphosarcoma (LS).	
BOLA-DRB3	major histocompatibility complex, class II, DRB4	282530	*1101	[Nikbakht Brujeni et al., 2016]	BOLA-DRB3 gene	Holstein	The studied cattle were categorized into three groups: BLV seronegative, BLV seropositive with persistent lymphocytosis (PL), and BLV seropositive with lymphosarcoma (LS).	
BOLA-DRB3	major histocompatibility complex, class II, DRB4	282530	*3202	[Nikbakht Brujeni et al., 2016]	BOLA-DRB3 gene	Holstein	The studied cattle were categorized into three groups: BLV seronegative, BLV seropositive with persistent lymphocytosis (PL), and BLV seropositive with lymphosarcoma (LS).	
BOLA-DRB3	major histocompatibility complex, class II, DRB4	282530	*1802	[Nikbakht Brujeni et al., 2016]	BOLA-DRB3 gene	Holstein	The studied cattle were categorized into three groups: BLV seronegative, BLV seropositive with persistent lymphocytosis (PL), and BLV seropositive with lymphosarcoma (LS).	
BOLA-DRB3	major histocompatibility complex, class II, DRB4	282530	*0901	[Nikbakht Brujeni et al., 2016]	BOLA-DRB3 gene	Holstein	The studied cattle were categorized into three groups: BLV seronegative, BLV seropositive with persistent lymphocytosis (PL), and BLV seropositive with lymphosarcoma (LS).	
BOLA-DQA1	major histocompatibility complex, class II,	282534	*0204	[Miyasaka et al., 2013]	BOLA-DQA1 gene	Japanese Black	BLV proviral load	

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	DQ alpha, type 1							
BOLA-DQA1	major histocompatibility complex, class II, DQ alpha, type 2	282534	*10012	[Miyasaka et al., 2013]	BOLA-DQA1 gene	Japanese Black	BLV proviral load	

Литература к таблице **S2**

REF	PubMedID	Авторы	Название	Данные о журнале
[Juliarena et al., 2008]	18573126	Juliarena MA, Poli M, Sala L, Ceriani C, Gutierrez S, Dolcini G, Rodríguez EM, Mariño B, Rodríguez-Dubra C, Esteban EN.	Association of BLV infection profiles with alleles of the BoLA-DRB3.2 gene.	Anim Genet. 2008 Aug;39(4):432-8. doi: 10.1111/j.1365-2052.2008.01750.x. Epub 2008 Jun 28.
[Miyasaka et al., 2013]	23216331	Miyasaka T, Takeshima SN, Jimba M, Matsumoto Y, Kobayashi N, Matsuhashi T, Sentsui H, Aida Y.	Identification of bovine leukocyte antigen class II haplotypes associated with variations in bovine leukemia virus proviral load in Japanese Black cattle.	Tissue Antigens. 2013 Feb;81(2):72-82. doi: 10.1111/tan.12041. Epub 2012 Dec 6.
[Lendez et al., 2013]	26051703	Lendez PA, Passucci JA, Poli MA, Gutierrez SE, Dolcini GL, Ceriani MC.	Association of TNF-α gene promoter region polymorphisms in bovine leukemia virus (BLV)-infected cattle with different proviral loads.	Arch Virol. 2015 Aug;160(8):2001-7. doi: 10.1007/s00705-015-2448-5. Epub 2015 Jun 9.
[Konnai et al., 2006]	16839795	Konnai S, Usui T, Ikeda M, Kohara J, Hirata T, Okada K, Ohashi K, Onuma M.	Tumor necrosis factor-alpha genetic polymorphism may contribute to progression of bovine leukemia virus-infection.	Microbes Infect. 2006 Jul;8(8):2163-71. Epub 2006 Jun 2.
[Carignano et al., 2017]	28568505	Carignano HA, Beribe MJ, Caffaro ME, Amadio A, Nani JP, Gutierrez G, Alvarez I, Trono K, Miretti MM, Poli MA.	BOLA-DRB3 gene polymorphisms influence bovine leukaemia virus infection levels in Holstein and Holstein × Jersey crossbreed dairy cattle.	Anim Genet. 2017 Aug;48(4):420-430. doi: 10.1111/age.12566. Epub 2017 May 31.
[Nikbakht Brujeni et al., 2016]	26782666	Nikbakht Brujeni G, Ghorbanpour R, Esmailnejad A.	Association of BoLA-DRB3.2 Alleles with BLV Infection Profiles (Persistent Lymphocytosis/Lymphosarcoma) and Lymphocyte Subsets in Iranian Holstein Cattle.	Biochem Genet. 2016 Apr;54(2):194-207. doi: 10.1007/s10528-016-9712-6. Epub 2016 Jan 19.

Таблица S3.

Данные по нокаутам.

Ген КРС: нокаут этого гена у мышей повышает смертность при заражении ВЛКРС. Ген взят из экспериментальной статьи

Обозначение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Ссылка	Модельный организм	Эксперимент	Эффект	Роль гена	Альтернативные названия
TNF	tumor necrosis factor	280943	[Muller et al., 2003]	Мышь	We infected TNF(-/-) mice with a plasmid encoding infectious BLV to further elucidate the role of TNF in BLV infection. [Muller et al., 2003]	TaqMan quantitative PCR showed that proviral DNA was present in genomic DNA isolated from spleen cells of TNF(-/-) mice 4 weeks post-infection, whereas it was not detected in wild-type mice. [Muller et al., 2003]	It showing that the lack of TNF enables the plasmid encoded BLV to persist longer, and therefore rendering the mice more susceptible to an infection with BLV [Muller et al., 2003]	TNFa; TNF-a; TNF-alpha

Литература к таблице **S3**

REF	PubMedID	Авторы	Название	Данные о журнале
[Muller et al., 2003]	12628760	Müller C, Coffey TJ, Koss M, Teifke JP, Langhans W, Werling D.	Lack of TNF alpha supports persistence of a plasmid encoding the bovine leukaemia virus in TNF(-/-) mice.	Vet Immunol Immunopathol. 2003 Mar 20;92(1-2):15-22.

Таблица S4.

Данные по экспрессии

Гены КРС, кодирующие мРНК/белки, которые индуцируются или репрессируются в ответ на инфекцию ВЛКРС. Все гены собраны из экспериментальных статей.

Обозначение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Ссылка	Метод	Эксперимент	Индуктор (ВЛКРС или белок)	Эффект	мРНК или белок	Роль в патогенезе
IL6	interleukin 6	280826	[Iwan et al., 2017]	Dendritic cell precursors were isolated with the use of immunomagnetic beads from BLV-infected and BLV-free cows. From these precursors cultures of monocyte derived dendritic cells (MoDCs) were generated with the use of a cytokine cocktail (IL-4 and GM-CSF). Additionally, parallel DCs from BLV-negative animals were infected in vitro.	The level of cytokines: IL-6, IL-10, IL-12(p40), IL-12(p70) was determined in dendritic cell cultures: infected in vitro, originating from naturally infected cattle and BLV-free cattle.	ВЛКРС	Expression is upregulated	protein	In the case of spleen MoDCs and lymph node MoDCs a decrease in production of IL-12(p40) and IL-12(p70) in favour of IL-6 and IL-10 was noted, suggesting promotion of BLV infection development.
IL10	interleukin 10	281246	[Iwan et al., 2017]	Dendritic cell precursors were isolated with the use of immunomagnetic beads from BLV-infected and BLV-free cows. From these precursors cultures of monocyte derived dendritic cells (MoDCs) were generated with the use of a cytokine cocktail (IL-4 and GM-CSF). Additionally, parallel DCs from BLV-negative animals were infected in vitro.	The level of cytokines: IL-6, IL-10, IL-12(p40), IL-12(p70) was determined in dendritic cell cultures: infected in vitro, originating from naturally infected cattle and BLV-free cattle.	ВЛКРС	Expression is upregulated	protein	In the case of spleen MoDCs and lymph node MoDCs a decrease in production of IL-12(p40) and IL-12(p70) in favour of IL-6 and IL-10 was noted, suggesting promotion of BLV infection development.
IL12A	interleukin 12A	281856	[Iwan et al., 2017]	Dendritic cell precursors were isolated with the use of immunomagnetic beads from BLV-infected and BLV-free cows. From these precursors cultures of monocyte derived dendritic cells (MoDCs) were generated with the use of a cytokine cocktail (IL-4 and	The level of cytokines: IL-6, IL-10, IL-12(p40), IL-12(p70) was determined in dendritic cell cultures: infected in vitro, originating from naturally infected cattle and BLV-free cattle.	ВЛКРС	Expression is downregulated	protein	In the case of spleen MoDCs and lymph node MoDCs a decrease in production of IL-12(p40) and IL-12(p70) in favour of IL-6 and IL-10 was noted, suggesting promotion of BLV infection development.

Обозна-чение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Ссылка	Метод	Эксперимент	Индуктор (ВЛКРС или белок)	Эффект	мРНК или белок	Роль в патогенезе
				GM-CSF). Additionally, parallel DCs from BLV-negative animals were infected in vitro.					
IL12B	interleukin 12B	281857	[Iwan et al., 2017]	Dendritic cell precursors were isolated with the use of immunomagnetic beads from BLV-infected and BLV-free cows. From these precursors cultures of monocyte derived dendritic cells (MoDCs) were generated with the use of a cytokine cocktail (IL-4 and GM-CSF). Additionally, parallel DCs from BLV-negative animals were infected in vitro.	The level of cytokines: IL-6, IL-10, IL-12(p40), IL-12(p70) was determined in dendritic cell cultures: infected in vitro, originating from naturally infected cattle and BLV-free cattle.	ВЛКРС	Expression is downregulated	protein	In the case of spleen MoDCs and lymph node MoDCs a decrease in production of IL-12(p40) and IL-12(p70) in favour of IL-6 and IL-10 was noted, suggesting promotion of BLV infection development. IFN-γ expression was significantly higher in LPL animals.
IFNG	interferon gamma	281237	[Farias et al., 2016]	This is the first report concerning the patterns of TLRs 3, 7–9 expression on PBMC from BLV infected animals with high proviral load (HPL) and low proviral load (LPL).	We aimed to characterize cytokines and toll-like receptors (TLR) expression related to the proviral load profiles.	ВЛКРС	Expression is upregulated	mRNA	IFN-γ and IL-12 mRNA expression level was significantly higher in PBMC from infected cattle (LPL n=6 and HPL n=7) compared to uninfected animals (n=5). While no significant differences were observed in IL-12 expression between LPL and HPL group, IFN-γ expression was significantly higher in LPL animals.
IL12B	interleukin 12B	281857	[Farias et al., 2016]	This is the first report concerning the patterns of TLRs 3, 7–9 expression on PBMC from BLV infected animals with high proviral load (HPL) and low proviral load (LPL).	We aimed to characterize cytokines and toll-like receptors (TLR) expression related to the proviral load profiles.	ВЛКРС	Expression is upregulated	mRNA	IFN-γ and IL-12 mRNA expression level was significantly higher in PBMC from infected cattle (LPL n=6 and HPL n=7) compared to uninfected animals (n=5). While no significant differences were observed in IL-12 expression between LPL and HPL group, IFN-γ expression was significantly higher in LPL animals.
TLR3	toll like receptor 3	281535	[Farias et al., 2016]	This is the first report concerning the patterns of TLRs 3, 7–9 expression on PBMC from BLV infected animals with high proviral load	We aimed to characterize cytokines and toll-like receptors (TLR) expression related to the proviral load profiles.	ВЛКРС	Expression is upregulated	mRNA	Infected cattle exhibited higher expression levels of TLR3, 7-9. TLR8 and TLR9 were up-regulated in HPL group, and TLR3 was up-regulated in LPL group.

Обозна-чение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Ссылка	Метод	Эксперимент	Индуктор (ВЛКРС или белок)	Эффект	мРНК или белок	Роль в патогенезе
				(HPL) and low proviral load (LPL).					
TLR7	toll like receptor 7	493686	[Farias et al., 2016]	This is the first report concerning the patterns of TLRs 3, 7–9 expression on PBMC from BLV infected animals with high proviral load (HPL) and low proviral load (LPL).	We aimed to characterize cytokines and toll-like receptors (TLR) expression related to the proviral load profiles.	ВЛКРС	Expression is upregulated	mRNA	Infected cattle exhibited higher expression levels of TLR3, 7-9. Animals with HPL had significantly higher expression of TLR7/8 than uninfected cattle.
TLR8	toll like receptor 8	532262	[Farias et al., 2016]	This is the first report concerning the patterns of TLRs 3, 7–9 expression on PBMC from BLV infected animals with high proviral load (HPL) and low proviral load (LPL).	We aimed to characterize cytokines and toll-like receptors (TLR) expression related to the proviral load profiles.	ВЛКРС	Expression is upregulated	mRNA	Infected cattle exhibited higher expression levels of TLR3, 7-9. Animals with HPL had significantly higher expression of TLR7/8 than uninfected cattle. TLR8 and TLR9 were up-regulated in HPL group, and TLR3 was up-regulated in LPL group.
TLR9	toll like receptor 9	282602	[Farias et al., 2016]	This is the first report concerning the patterns of TLRs 3, 7–9 expression on PBMC from BLV infected animals with high proviral load (HPL) and low proviral load (LPL).	We aimed to characterize cytokines and toll-like receptors (TLR) expression related to the proviral load profiles.	ВЛКРС	Expression is upregulated	mRNA	Infected cattle exhibited higher expression levels of TLR3, 7-9. TLR8 and TLR9 were up-regulated in HPL group, and TLR3 was up-regulated in LPL group.
TNFRSF1B	TNF receptor superfamily member 1B	338033	[Stachura et al., 2016]	A single T>C nucleotide polymorphism (rs42686850) of bovine tumor necrosis factor receptor type II gene (TNF-RII) is located within a sequence with allele-specific affinity to bind E2F transcription factors	The objective of the study was to determine the effect of this SNP and BLV infection on the TNF-RII gene expression at the mRNA and protein levels in peripheral blood mononuclear cells (PBMC).	ВЛКРС	Expression is downregulated	mRNA	Statistical analysis demonstrated significantly lower amounts of mRNA TNF-RII in BLV-positive animals as compared to BLV-negative cows (p<0.001).
IFNG	interferon gamma	281237	[Ohira et al., 2016]	CD4(+)CD25(high)Foxp3(+) T cells suppress excess immune responses that lead to autoimmune and/or inflammatory diseases, and maintain host immune homeostasis. However, CD4(+)CD25(high)Foxp3(+) T cells reportedly contribute to	In this study, kinetic and functional analyses of CD4(+)CD25(high)Foxp3(+) T cells were performed in cattle with bovine leukemia virus (BLV) infections, which have reported immunosuppressive	ВЛКРС	Expression is downregulated	protein	Production of the Th1 cytokines IFN-γ and TNF-α was reduced in BLV-infected cattle compared with uninfected cattle, and numbers of IFN-γ or TNF-α producing CD4(+) T cells decreased with disease progression. In contrast, IFN-γ production by NK cells was inversely correlated with BLV

Обозна-чение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Ссылка	Метод	Эксперимент	Индуктор (ВЛКРС или белок)	Эффект	мРНК или белок	Роль в патогенезе
				disease progression by over suppressing immune responses in some chronic infections.	characteristics.				proviral loads in infected cattle.
TNF	tumor necrosis factor	280943	[Ohira et al., 2016]	CD4(+)CD25(high)Foxp3(+) T cells suppress excess immune responses that lead to autoimmune and/or inflammatory diseases, and maintain host immune homeostasis. However, CD4(+)CD25(high)Foxp3(+) T cells reportedly contribute to disease progression by over suppressing immune responses in some chronic infections.	In this study, kinetic and functional analyses of CD4(+)CD25(high)Foxp3(+) T cells were performed in cattle with bovine leukemia virus (BLV) infections, which have reported immunosuppressive characteristics.	ВЛКРС	Expression is downregulated	protein	Production of the Th1 cytokines IFN-γ and TNF-α was reduced in BLV-infected cattle compared with uninfected cattle, and numbers of IFN-γ or TNF-α producing CD4(+) T cells decreased with disease progression.
TNF	tumor necrosis factor	280943	[Bojarojć-Nosowicz et al., 2015]	Nested PCR test, hematological analysis, immunophenotypic analysis	The aim of this study was to determine whether SNP at position -824 (promoter region) of the TNFα gene significantly differentiates the size of IgM+, CD5+ and CD11b+ cell subpopulations and affects the expression of membrane-bound TNFα protein (mTNFα) on these cells and their susceptibility to BLV infections.	ВЛКРС	Expression is upregulated	protein	In this study, significant differences were determined for the first time between TNFα genotypes and the percentage of cells with the CD11b+TNFα+p24+ immunophenotype. Furthermore, greater expansion of lymphocytes with the IgM+TNFα+p24+ immunophenotype was reported in cows with the G/G genotype than in A/A homozygotes. Cells with the above immunophenotype were more frequently observed in cows with persistent leukocytosis than in aleukemic cattle.
CTLA4	cytotoxic T-lymphocyte associated protein 4	281732	[Suzuki et al., 2015]	To test for differences in the protein expression level of CTLA-4, we measured the proportion of CTLA-4-expressing cells by flow cytometry.	Here the kinetics of CTLA-4(+) cells were analyzed in BLV-infected cattle.	ВЛКРС	Expression is upregulated	protein	CTLA-4 mRNA was predominantly expressed in CD4(+) T cells in BLV-infected cattle, and the expression was positively correlated with Foxp3 mRNA expression.
FOXP3	forkhead box P3	506053	[Suzuki et al., 2013]	nested-PCR, qRT-PCR,	We monitored Foxp3(+) T cells in bovine leukemia virus (BLV)-infected cattle.	ВЛКРС	Expression is upregulated	protein	By flow cytometric analysis, the proportion of Foxp3(+) CD4(+) cells from persistent lymphocytotic cattle was significantly increased compared to control and AL cattle.

Обозна-чение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Ссылка	Метод	Эксперимент	Индуктор (ВЛКРС или белок)	Эффект	мРНК или белок	Роль в патогенезе
PDCD1	programmed cell death 1	613842	[Ikebuchi et al., 2013]	First, in this study, to establish a method for the expression and functional analysis of bovine PD-1, hybridomas producing monoclonal antibodies (mAb) specific for bovine PD-1 were established.	Next, to examine whether PD-1 blockade by anti-PD-1 mAb could upregulate the immune reaction during chronic infection, the expression and functional analysis of PD-1 in PBMC isolated from BLV-infected cattle with or without lymphoma were performed using anti-PD-1 mAb.	ВЛКРС	Expression is upregulated	protein	The frequencies of both PD-1+ CD4+ T cells in blood and lymph node and PD-1+ CD8+ T cells in lymph node were higher in BLV-infected cattle with lymphoma than those without lymphoma or control uninfected cattle.
LAG3	lymphocyte activating 3	515155	[Konnai et al., 2013]	Functional analysis of LAG-3	In this study, bovine LAG-3 expression was analyzed in bovine leukemia virus (BLV)-infected cattle.	ВЛКРС	Expression is upregulated	protein	The mean fluorescence intensity (MFI) for LAG-3 on PBMCs from PL cattle was significantly increased compared to control and asymptomatic (AL) cattle. Specifically, the LAG-3 expression level was significantly increased in both CD4(+) and CD8(+) T cells from PL cattle. LAG-3 expression correlated positively with increased numbers of lymphocytes and MHC class II(+) cells in infected animals.
IL2RA	interleukin 2 receptor subunit alpha	281861	[Tawfeeq et al., 2012]	A 49-month-old Holstein cow with anorexia, tachypnea, enlarged peripheral lymph nodes, and difficulty standing up was suspected of bovine leukosis. Hematological examination revealed lymphocytosis with the presence of neoplastic cells. Cytological findings of fine needle aspiration of subiliac lymph nodes indicated lymphosarcoma. Histopathology and antibody analysis confirmed the diagnosis of enzootic bovine leukosis, a B-cell bovine lymphoma caused by bovine	Gene expressions known as biomarkers of hematopoietic neoplasia in human were also examined in the present case.	ВЛКРС	Expression is upregulated	mRNA	Increased messenger RNA expression of interleukin 2 receptor, thymidine kinase, and immunoglobulin-associated alpha-1 was observed in the case animal.

Обозна-чение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Ссылка	Метод	Эксперимент	Индуктор (ВЛКРС или белок)	Эффект	мРНК или белок	Роль в патогенезе
				leukemia virus.					
CD79A	CD79a molecule	281674	[Tawfeeq et al., 2012]	A 49-month-old Holstein cow with anorexia, tachypnea, enlarged peripheral lymph nodes, and difficulty standing up was suspected of bovine leukosis. Hematological examination revealed lymphocytosis with the presence of neoplastic cells. Cytological findings of fine needle aspiration of subiliac lymph nodes indicated lymphosarcoma. Histopathology and antibody analysis confirmed the diagnosis of enzootic bovine leukosis, a B-cell bovine lymphoma caused by bovine leukemia virus.	Gene expressions known as biomarkers of hematopoietic neoplasia in human were also examined in the present case.	ВЛКРС	Expression is upregulated	mRNA	Increased messenger RNA expression of interleukin 2 receptor, thymidine kinase, and immunoglobulin-associated alpha-1 was observed in the case animal.
TK1	thymidine kinase 1	504652	[Tawfeeq et al., 2012]	A 49-month-old Holstein cow with anorexia, tachypnea, enlarged peripheral lymph nodes, and difficulty standing up was suspected of bovine leukosis. Hematological examination revealed lymphocytosis with the presence of neoplastic cells. Cytological findings of fine needle aspiration of subiliac lymph nodes indicated lymphosarcoma. Histopathology and antibody analysis confirmed the diagnosis of enzootic bovine leukosis, a B-cell bovine lymphoma caused by bovine leukemia virus.	Gene expressions known as biomarkers of hematopoietic neoplasia in human were also examined in the present case.	ВЛКРС	Expression is upregulated	mRNA	Increased messenger RNA expression of interleukin 2 receptor, thymidine kinase, and immunoglobulin-associated alpha-1 was observed in the case animal.
HAVCR2	hepatitis A virus	768047	[Okagawa et al., 2012]	The immunoinhibitory receptor T cell immunoglobulin domain	In this study, cDNA encoding for bovine Tim-3	ВЛКРС	Expression is upregulated	mRNA	Tim-3 mRNA expression in CD4+ and CD8+ cells was upregulated

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	cellular receptor 2			and mucin domain-3 (Tim-3) and its ligand, galectin-9 (Gal-9), are involved in the immune evasion mechanisms for several pathogens causing chronic infections. Quantitative real-time PCR analysis showed that bovine Tim-3 mRNA is mainly expressed in T cells such as CD4+ and CD8+ cells, while Gal-9 mRNA is mainly expressed in monocyte and T cells.	and Gal-9 were cloned and sequenced, and their expression and role in immune reactivation were analyzed in bovine leukemia virus (BLV)-infected cattle.				during disease progression of BLV infection.
LAG3	lymphocyte activating 3	515155	[Shirai et al., 2012]	Lymphocyte activation gene-3 (LAG-3), a major histocompatibility complex (MHC) class II binding CD4 homologue has recently been shown as one of the mechanisms for down-regulating immune responses during chronic disease progression. We found that the bovine LAG-3 mRNA transcripts were expressed predominantly on T-cells such as CD4(+) and CD8(+) cells, among peripheral blood mononuclear cells.	For the first time, we cloned LAG-3 from two breeds of cattle (Holstein and Japanese Black), and analyzed its expression levels in cattle infected with bovine leukemia virus (BLV), a chronic viral infection that leads to immuno-suppression.	ВЛКРС	Expression is upregulated	mRNA	LAG-3 mRNA expression on CD4(+) T-cells from BLV-infected cattle was upregulated compared to that in normal cattle.
CD274	CD274 molecule	533834	[Ikebuchi et al., 2011]	The inhibitory receptor programmed death-1 (PD-1) and its ligand, programmed death-ligand 1 (PD-L1) are involved in immune evasion mechanisms for several pathogens causing chronic infections. In a previous report, we showed that, in bovine leukemia virus (BLV) infection, the expression of bovine PD-1 is closely associated with disease	To investigate the role of PD-L1 in BLV infection, we identified the bovine PD-L1 gene, and examined PD-L1 expression in BLV-infected cattle in comparison with uninfected cattle.	ВЛКРС	Expression is upregulated	protein	The proportion of PD-L1 positive cells, especially among B cells, was upregulated in cattle with the late stage of the disease compared to cattle at the aleukemic infection stage or uninfected cattle. The proportion of PD-L1 positive cells correlated positively with prediction markers for the progression of the disease such as leukocyte number, virus load and virus titer whilst on the contrary, it inversely correlated with the degree of interferon-

Обозна-чение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Ссылка	Метод	Эксперимент	Индуктор (ВЛКРС или белок)	Эффект	мРНК или белок	Роль в патогенезе
				progression. However, the functions of bovine PD-L1 are still unknown.					gamma expression.
SYK	spleen associated tyrosine kinase	515515	[Murakami et al., 2011]	In B-cells, Syk is involved in early B-cell receptor signaling, which affects cellular survival, proliferation and differentiation. Although the kinetics of Syk mRNA and its activity are variable in different types of tumor cells, Syk may have a relation to tumor progression in many human tumors, including B-cell lymphoma/leukemia.	In this study we examined whether Syk mRNA expression was changed in bovine leukemia virus (BLV)-induced persistent lymphocytosis (PL) and lymphoma.	ВЛКРС	Expression is upregulated	mRNA	As a result, we demonstrated that the Syk mRNA expression was significantly increased in PL samples, whereas it was decreased in tumor samples. Moreover one cow, which Syk mRNA expression has been lowest among PL cattle, developed lymphoma three months later and the expression significantly decreased. These data suggest that Syk mRNA expression dynamics is closely related to BLV-induced disease.
TNF	tumor necrosis factor	280943	[Usui et al., 2006]	Freshly isolated IgM(+) B-cells from three sheep with lymphocytosis constitutively transcribed TNF-alpha mRNA.	In this study, the expression of TNF-alpha in IgM(+) B-cells from BLV-infected sheep with or without lymphocytosis was determined.	ВЛКРС	Expression is upregulated	mRNA	TNF-alpha mRNA expression was markedly higher in lymphocytotic sheep when compared to that of non-lymphocytotic sheep or uninfected sheep. Expression of membrane-bound TNF-alpha on IgM(+) B-cells was also augmented in lymphocytotic sheep.
TNF	tumor necrosis factor	280943	[Konnai et al., 2006]	The TNF-alpha protein level in the PBMCs was determined by flow cytometric analysis, and it was noted that most of the cells expressing membrane-bound TNF-alpha in the spontaneously proliferating cells were CD5+ or sIgM+-cells.	o determine if the spontaneous cell proliferation observed in the late disease stages, such as persistent lymphocytosis and lymphosarcoma, correlated with the expression level of TNF-alpha, we analyzed the mRNA expression levels for TNF-alpha in spontaneously proliferating PBMCs derived from BLV-infected cattle.	ВЛКРС	Expression is upregulated	mRNA	The mean mRNA expression level for TNF-alpha was higher in the spontaneously proliferating PBMCs derived from BLV-infected cattle than in non-spontaneously proliferating PBMCs from normal cattle.
TNFRSF1B	TNF receptor superfamily member 1B	338033	[Konnai et al., 2005]	Most cells expressing TNF-RII in PL cattle were CD5+ or sIgM+ cells and these cells showed resistance to TNF-	In order to investigate the different TNF-alpha-induced responses, in this study we examined the	ВЛКРС	Expression is upregulated	mRNA	The proliferative response of PBMC isolated from those cattle with PL in the presence of recombinant bovine TNF-alpha

Обозна-чение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Ссылка	Метод	Эксперимент	Индуктор (ВЛКРС или белок)	Эффект	мРНК или белок	Роль в патогенезе
				alpha-induced apoptosis.	TNF-alpha-induced proliferative response and the expression levels of two distinct TNF receptors on peripheral blood mononuclear cells (PBMC) derived from BLV-uninfected cattle and BLV-infected cattle that were aleukemic (AL) or had persistent lymphocytosis (PL).				(rTNF-alpha) was significantly higher than those from AL cattle and uninfected cattle and the cells from PL cattle expressed significantly higher mRNA levels of TNF receptor type II (TNF-RII) than those from AL and BLV-uninfected cattle.
IFNG	interferon gamma	281237	[Amills et al., 2002]	The role of T-helper (Th) responses in the subclinical progression of bovine leukemia virus (BLV) infection was explored by determining the contribution of CD4+ T cells to the expression of mRNAs encoding interferon-gamma (IFN-gamma), interleukin-2 (IL-2), interleukin-4 (IL-4), and interleukin-10 (IL-10) in BLV-infected cattle.	Relative levels of mRNA encoding IFN-gamma, IL-2, IL-4, and IL-10 were measured in fresh and concanavalin A (Con A) activated peripheral blood mononuclear cells (PBMCs) and purified CD4+ T cells from cows seronegative to BLV (BLV-), seropositive without persistent lymphocytosis (BLV+PL-), and seropositive with PL (BLV+PL+) using a semiquantitative reverse transcription-polymerase chain reaction (RT-PCR) assay	ВЛКРС	Expression is downregulated	mRNA	The expressions of IFN-gamma, IL-2, and IL-4 mRNAs were significantly reduced in the PBMCs from BLV+PL+ cows as compared to BLV- cows. In contrast, Con A stimulated PBMCs and CD4+ T cells did not differ significantly in expression of IFN-gamma, IL-2, IL-10, or IL-4 mRNAs among the BLV infection groups.
IL2	interleukin 2	280822	[Amills et al., 2002]	The role of T-helper (Th) responses in the subclinical progression of bovine leukemia virus (BLV) infection was explored by determining the contribution of CD4+ T cells to the expression of mRNAs encoding interferon-gamma (IFN-gamma), interleukin-2 (IL-2), interleukin-4 (IL-4), and interleukin-10 (IL-10) in BLV-	Relative levels of mRNA encoding IFN-gamma, IL-2, IL-4, and IL-10 were measured in fresh and concanavalin A (Con A) activated peripheral blood mononuclear cells (PBMCs) and purified CD4+ T cells from cows seronegative to BLV (BLV-), seropositive	ВЛКРС	Expression is downregulated	mRNA	The expressions of IFN-gamma, IL-2, and IL-4 mRNAs were significantly reduced in the PBMCs from BLV+PL+ cows as compared to BLV- cows. In contrast, Con A stimulated PBMCs and CD4+ T cells did not differ significantly in expression of IFN-gamma, IL-2, IL-10, or IL-4 mRNAs among the BLV infection groups.

Обозна-чение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Ссылка	Метод	Эксперимент	Индуктор (ВЛКРС или белок)	Эффект	мРНК или белок	Роль в патогенезе
				infected cattle.	without persistent lymphocytosis (BLV+PL-), and seropositive with PL (BLV+PL+) using a semiquantitative reverse transcription-polymerase chain reaction (RT-PCR) assay				
IL4	interleukin 4	280824	[Amills et al., 2002]	The role of T-helper (Th) responses in the subclinical progression of bovine leukemia virus (BLV) infection was explored by determining the contribution of CD4+ T cells to the expression of mRNAs encoding interferon-gamma (IFN-gamma), interleukin-2 (IL-2), interleukin-4 (IL-4), and interleukin-10 (IL-10) in BLV-infected cattle.	Relative levels of mRNA encoding IFN-gamma, IL-2, IL-4, and IL-10 were measured in fresh and concanavalin A (Con A) activated peripheral blood mononuclear cells (PBMCs) and purified CD4+ T cells from cows seronegative to BLV (BLV-), seropositive without persistent lymphocytosis (BLV+PL-), and seropositive with PL (BLV+PL+) using a semiquantitative reverse transcription-polymerase chain reaction (RT-PCR) assay	ВЛКРС	Expression is downregulated	mRNA	The expressions of IFN-gamma, IL-2, and IL-4 mRNAs were significantly reduced in the PBMCs from BLV+PL+ cows as compared to BLV- cows. In contrast, Con A stimulated PBMCs and CD4+ T cells did not differ significantly in expression of IFN-gamma, IL-2, IL-10, or IL-4 mRNAs among the BLV infection groups.
TNFRSF1B	TNF receptor superfamily member 1B	338033	[Kabeya et al., 2001]	Sheep inoculated with BLV were divided into two groups; one was BLV-positive and the other BLV-negative based on the detection in peripheral blood mononuclear cells (PBMC).	To examine whether tumor necrosis factor alpha (TNF alpha) contributes to the pathogenesis of bovine leukemia virus (BLV) infection, the mRNA expression patterns of TNF alpha and its receptors, type 1 (TNF R1) and type 2 (TNF R2) were investigated	ВЛКРС	Expression is downregulated	mRNA	Expression of TNF R1 mRNA was down-regulated in PBMC from the BLV-positive compared to BLV-negative sheep.
TNF	tumor necrosis factor	280943	[Kabeya et al., 2001]	Sheep inoculated with BLV were divided into two groups; one was BLV-positive and the other BLV-negative based on	To examine whether tumor necrosis factor alpha (TNF alpha) contributes to the pathogenesis of bovine	ВЛКРС	Expression is upregulated	mRNA	Membrane-bound TNF alpha (mTNF alpha) is thought to be one of the ligands, inducing B-cell activation. Flow cytometric analysis

Обозна-чение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Ссылка	Метод	Эксперимент	Индуктор (ВЛКРС или белок)	Эффект	мРНК или белок	Роль в патогенезе
				the detection in peripheral blood mononuclear cells (PBMC).	leukemia virus (BLV) infection, the mRNA expression patterns of TNF alpha and its receptors, type 1 (TNF R1) and type 2 (TNF R2) were investigated				demonstrated that the number of PBMC, that were positive for mTNF alpha expression, was increased in the BLV-positive sheep.
IFNG	interferon gamma	281237	[Yakobson et al., 2000]	We have established experimental models of bovine leukemia virus (BLV) infection followed by progression to persistent lymphocytosis (PL) positive (BLV+PL+) or PL negative (BLV+PL-) stages of infection.	Two out of six BLV infected animals developed PL+ 4 weeks after BLV infection. One other animal became PL+ late in the course of infection and three infected animals stayed PL-. These animals (PL-) exhibited transient lymphocytosis 3-4 weeks after infection and sustained PL- lymphocyte counts up to 24 weeks after infection.	ВЛКРС	Expression is upregulated	mRNA	Competitive RT-PCR analysis of IFN-gamma mRNA expression revealed that peripheral blood mononuclear cells (PBMC) of animals with PL+ status developed by 4 weeks after infection had augmented IFN-gamma mRNA expression 3-4 weeks after BLV infection.
IL2	interleukin 2	280822	[Yakobson et al., 2000]	We have established experimental models of bovine leukemia virus (BLV) infection followed by progression to persistent lymphocytosis (PL) positive (BLV+PL+) or PL negative (BLV+PL-) stages of infection.	Two out of six BLV infected animals developed PL+ 4 weeks after BLV infection. One other animal became PL+ late in the course of infection and three infected animals stayed PL-. These animals (PL-) exhibited transient lymphocytosis 3-4 weeks after infection and sustained PL- lymphocyte counts up to 24 weeks after infection.	ВЛКРС	Expression is upregulated	mRNA	Competitive RT-PCR analysis of IL-2 mRNA expression showed an increase in the levels of IL-2 mRNA in PL animals.
IL10	interleukin 10	281246	[Yakobson et al., 2000]	We have established experimental models of bovine leukemia virus (BLV) infection followed by progression to persistent lymphocytosis (PL) positive (BLV+PL+) or PL negative (BLV+PL-) stages of	Two out of six BLV infected animals developed PL+ 4 weeks after BLV infection. One other animal became PL+ late in the course of infection and three infected animals	ВЛКРС	Expression is upregulated	mRNA	Interleukin-10 (IL-10) mRNAs expression were elevated both in PL+ and PL- animals from 3 and 12 weeks after infection respectively.

Обозна-чение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Ссылка	Метод	Эксперимент	Индуктор (ВЛКРС или белок)	Эффект	мРНК или белок	Роль в патогенезе
				infection.	stayed PL-. These animals (PL-) exhibited transient lymphocytosis 3-4 weeks after infection and sustained PL- lymphocyte counts up to 24 weeks after infection.				
TNF	tumor necrosis factor	280943	[Kabeya et al., 1999]	Protective immune responses were analyzed in eight sheep vaccinated with BLV envelope peptides and experimentally infected with bovine-leukemia virus (BLV). Five of eight peptide-immunized sheep showed a high T-cell proliferative response to the BLV peptides and all of these were protected from the infection. The other three peptide-immunized sheep showed no T-cell proliferative responses to any BLV antigens similar to control sheep, though they also exhibited resistance to BLV challenge.	To investigate other mechanisms which suppress BLV expansion in these non-responding sheep, we measured the levels of the cytokine expressions before, and after, BLV challenge using competitive reverse-transcriptase polymerase chain-reaction systems.	BLV envelope peptides	Expression is upregulated	mRNA	It was revealed that the expression of tumor necrosis factor alpha (TNFalpha) was higher in BLV-resistant sheep than in BLV-susceptible sheep.
IL2RA	interleukin 2 receptor subunit alpha	281861	[Isaacson et al., 1998]	Dual-color flow cytometry	In order to investigate the potential mechanisms of BLV-induced immune activation, dual-color flow cytometry was used to compare the expression of MHC class II (MHC II) molecules and the inducible IL-2 receptor alpha chain, CD25, on lymphocyte subsets in freshly isolated and cultured PBMC from these same BLV-infected cattle (n=5) with that of age-matched, uninfected controls (n=3).	ВЛКРС	Expression is upregulated	protein	Although CD25 expression was not increased on freshly isolated lymphocytes from BLV-infected cattle, an increased percentage of B cells from BLV-infected cattle expressed CD25 after 20 h of culture, either in the presence ($p<0.05$) or absence ($p<0.01$) of Con A.

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IL12B	interleukin 12B	281857	[Pyeon, Splitter, 1998]	Quantitative competitive PCR	Here, by using quantitative competitive PCR, we show that peripheral blood mononuclear cells from bovine leukemia virus-infected animals in the alymphocytotic stage of disease express an increased amount of IL-12 p40 mRNA. In contrast, IL-12 p40 mRNA expression by cells from animals with late-stage disease, termed persistent lymphocytosis, was significantly decreased compared to that by normal and alymphocytotic animals.	ВЛКРС	Expression is up/downregulated	mRNA	Here, by using quantitative competitive PCR, we show that peripheral blood mononuclear cells from bovine leukemia virus-infected animals in the alymphocytotic stage of disease express an increased amount of IL-12 p40 mRNA. In contrast, IL-12 p40 mRNA expression by cells from animals with late-stage disease, termed persistent lymphocytosis, was significantly decreased compared to that by normal and alymphocytotic animals.
IL2	interleukin 2	280822	[Trueblood et al., 1998]	The expression of interleukin-2 (IL-2), IL-4, IL-10, and gamma interferon (IFN-gamma) mRNA, was measured in stimulated peripheral blood mononuclear cells	To examine the role of the cytokine microenvironment in this virus-induced B-lymphocyte expansion, the expression of interleukin-2 (IL-2), IL-4, IL-10, and gamma interferon (IFN-gamma) mRNA, was measured in stimulated peripheral blood mononuclear cells from persistently lymphocytotic BLV-infected cows, nonlymphocytotic BLV-infected cows, and uninfected cows.	ВЛКРС	Expression is upregulated	mRNA	IL-2 and IL-10 mRNA expression and IL-2 functional activity were significantly increased when peripheral blood mononuclear cells from persistently lymphocytotic cows were stimulated with concanavalin A (ConA). Additionally, during persistent lymphocytosis, peak IL-2 and IL-10 mRNA expression was delayed, and elevated expression was prolonged.
IL10	interleukin 10	281246	[Trueblood et al., 1998]	The expression of interleukin-2 (IL-2), IL-4, IL-10, and gamma interferon (IFN-gamma) mRNA, was measured in stimulated peripheral blood mononuclear cells	To examine the role of the cytokine microenvironment in this virus-induced B-lymphocyte expansion, the expression of interleukin-2	ВЛКРС	Expression is upregulated	mRNA	IL-2 and IL-10 mRNA expression and IL-2 functional activity were significantly increased when peripheral blood mononuclear cells from persistently lymphocytotic cows were stimulated with

Обозна-чение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Ссылка	Метод	Эксперимент	Индуктор (ВЛКРС или белок)	Эффект	мРНК или белок	Роль в патогенезе
					(IL-2), IL-4, IL-10, and gamma interferon (IFN-gamma) mRNA, was measured in stimulated peripheral blood mononuclear cells from persistently lymphocytotic BLV-infected cows, nonlymphocytotic BLV-infected cows, and uninfected cows.				concanavalin A (ConA). Additionally, during persistent lymphocytosis, peak IL-2 and IL-10 mRNA expression was delayed, and elevated expression was prolonged.
IFNG	interferon gamma	281237	[Keefe et al., 1997]	Mesenteric and supra-mammary lymph nodes were obtained from a panel of nine cattle. Three were non-infected controls, three were BLV-positive aleukemic (AL), and three were BLV-positive persistent lymphocytotic (PL).	Mononuclear cells were perfused from the organs and total RNA extracted from either 1 x 10(8) unseparated cells or 1 x 10(7) purified CD4/CD8 T-cells. cDNA was generated and subjected to RT-PCR to analyze cytokine transcription during disease progression. cDNA levels were normalized using beta-actin PCR at sub-plateau cycle number, enabling a semi-quantitative assessment of cytokine gene transcripts.	ВЛКРС	Expression is upregulated	mRNA	Using this approach, IL-2, IL-10 and IFN-gamma message was detected in the T-cell fractions of all of the BLV-infected animals, but not in the non-infected controls.
IL2	interleukin 2	280822	[Keefe et al., 1997]	Mesenteric and supra-mammary lymph nodes were obtained from a panel of nine cattle. Three were non-infected controls, three were BLV-positive aleukemic (AL), and three were BLV-positive persistent lymphocytotic (PL).	Mononuclear cells were perfused from the organs and total RNA extracted from either 1 x 10(8) unseparated cells or 1 x 10(7) purified CD4/CD8 T-cells. cDNA was generated and subjected to RT-PCR to analyze cytokine transcription during disease progression. cDNA levels were normalized using beta-	ВЛКРС	Expression is upregulated	mRNA	Using this approach, IL-2, IL-10 and IFN-gamma message was detected in the T-cell fractions of all of the BLV-infected animals, but not in the non-infected controls.

Обозна-чение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Ссылка	Метод	Эксперимент	Индуктор (ВЛКРС или белок)	Эффект	мРНК или белок	Роль в патогенезе
					actin PCR at sub-plateau cycle number, enabling a semi-quantitative assessment of cytokine gene transcripts.				
IL10	interleukin 10	281246	[Keefe et al., 1997]	Mesenteric and supra-mammary lymph nodes were obtained from a panel of nine cattle. Three were non-infected controls, three were BLV-positive aleukemic (AL), and three were BLV-positive persistent lymphocytotic (PL).	Mononuclear cells were perfused from the organs and total RNA extracted from either 1 x 10(8) unseparated cells or 1 x 10(7) purified CD4/CD8 T-cells. cDNA was generated and subjected to RT-PCR to analyze cytokine transcription during disease progression. cDNA levels were normalized using beta-actin PCR at sub-plateau cycle number, enabling a semi-quantitative assessment of cytokine gene transcripts.	ВЛКРС	Expression is upregulated	mRNA	Using this approach, IL-2, IL-10 and IFN-gamma message was detected in the T-cell fractions of all of the BLV-infected animals, but not in the non-infected controls.
IL6	interleukin 6	280826	[Meirom et al., 1997]	Flow cytometry	An approach which might help in the elucidation of some immune impairment phenomena is the investigation of the role that cytokines play in the pathogenesis and immune response of BLV infected animals. Here we describe our findings on IL-6 and TNF.	ВЛКРС	Expression is upregulated	protein	We have found that the levels of IL-6 in the sera of BLV infected cows which show persistent lymphocytosis (BLV+ PL+) were significantly higher than those of BLV infected with no lymphocytosis (BLV+ PL-) or BLV negative cows (BLV-).
PRIM1	DNA primase subunit 1	506240	[Stone et al., 1996]	RT-PCR	We analyzed the expression of two proto-oncogenes, pim-1 and c-myc, proto-oncogenes deregulated in some human B cell leukemias and lymphomas, in peripheral blood mononuclear	ВЛКРС	Expression is upregulated	mRNA	These results suggest that pim-1 and c-myc are upregulated in B lymphocytes from BLV-infected PL cows

Обозна-чение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Ссылка	Метод	Эксперимент	Индуктор (ВЛКРС или белок)	Эффект	мРНК или белок	Роль в патогенезе
					leukocytes (PBML) from BLV-infected PL cows.				
MYC	MYC proto-oncogene, bHLH transcription factor	511077	[Stone et al., 1996]	RT-PCR	We analyzed the expression of two proto-oncogenes, pim-1 and c-myc, proto-oncogenes deregulated in some human B cell leukemias and lymphomas, in peripheral blood mononuclear leukocytes (PBML) from BLV-infected PL cows.	ВЛКРС	Expression is upregulated	mRNA	These results suggest that pim-1 and c-myc are upregulated in B lymphocytes from BLV-infected PL cows
IL10	interleukin 10	281246	[Pyeon et al., 1996]	RT-PCR	Here, we show that peripheral blood mononuclear cells (PBMCs) from bovine leukemia virus-infected animals with late-stage disease express considerably more IL-10 mRNA than animals that are not infected or that are in the early stages of disease.	ВЛКРС	Expression is upregulated	mRNA	These findings suggest that IL-10 produced by monocytes/macrophages may influence the progression of bovineleukosis in animals that develop persistent lymphocytosis of B cells or B-cell lymphosarcoma.
IL2	interleukin 2	280822	[Sordillo et al., 1994]	Peripheral blood mononuclear cells were used in blastogenesis assays to assess the functional ability of lymphocytes.	The effects of bovine leukosis virus (BLV) on the phenotypic and functional characteristics of peripheral blood mononuclear cells were investigated.	ВЛКРС	Expression is upregulated	protein	Cultures of lymphocytes obtained from BLV+PL animals produced greater amounts of interleukin-2 (IL-2) than BLV+AL and BLV- groups, although no differences were observed in the expression of IL-2 receptors.

Литература к таблице **S4**

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Таблица S5.

Данные по экспрессии, полученные с помощью ДНК-микрочипа

Гены КРС, экспрессия которых повышается/снижается у животных с персистентным лимфоцитозом. Все гены собраны из экспериментальной статьи Brym, Kaminski, 2017

Обозначение гена	Полное название гена	Идентификатор Refseq	Повышение/снижение экспрессии	Ссылка
CFD	complement factor D (adipsin)	NM_001034255	Понижение	[Brym, Kaminski, 2017]
ITCH	itchy E3 ubiquitin protein ligase homolog (mouse)	NM_001082428	Понижение	[Brym, Kaminski, 2017]
CD63	CD63 molecule	NM_205803	Понижение	[Brym, Kaminski, 2017]
AIF1	allograft inflammatory factor 1	NM_173985	Понижение	[Brym, Kaminski, 2017]
F5	coagulation factor V (proaccelerin, labile factor)	NM_173879	Понижение	[Brym, Kaminski, 2017]
S100A4	S100 calcium binding protein A4	NM_174595	Понижение	[Brym, Kaminski, 2017]
LGALS1	lectin, galactoside-binding, soluble, 1	NM_175782	Понижение	[Brym, Kaminski, 2017]
SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1	NM_001077970	Понижение	[Brym, Kaminski, 2017]
SIRPA	signal-regulatory protein alpha	NM_175788	Понижение	[Brym, Kaminski, 2017]
CST3	cystatin C	NM_174029	Понижение	[Brym, Kaminski, 2017]
LGMN	legumain	NM_174101	Понижение	[Brym, Kaminski, 2017]
NFAM1	NFAT activating protein with ITAM motif 1	XM_002687969	Понижение	[Brym, Kaminski, 2017]
CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	NM_176784	Понижение	[Brym, Kaminski, 2017]
PLA2G7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	NM_174578	Понижение	[Brym, Kaminski, 2017]
CD2	CD2 molecule	NM_001011676	Понижение	[Brym, Kaminski, 2017]
STAT4	signal transducer and activator of transcription 4	NM_001083692	Понижение	[Brym, Kaminski, 2017]
TGFBI	transforming growth factor, beta-induced, 68kDa	NM_001205402	Понижение	[Brym, Kaminski, 2017]
AMICA1	adhesion molecule, interacts with CXADR antigen 1	NM_001080250	Понижение	[Brym, Kaminski, 2017]
PLA2G16	phospholipase A2, group XVI	NM_001075280	Понижение	[Brym, Kaminski, 2017]
MTMR9	myotubularin related protein 9-like	NM_001046256	Понижение	[Brym, Kaminski, 2017]
TYROBP	TYRO protein tyrosine kinase binding protein	NM_174627	Понижение	[Brym, Kaminski, 2017]
ANXA3	annexin A3	NM_001035325	Понижение	[Brym, Kaminski, 2017]
LGALS3	lectin, galactoside-binding, soluble, 3	NM_001102341	Понижение	[Brym, Kaminski, 2017]
CAPN2	calpain 2, (m/II) large subunit	NM_001103086	Понижение	[Brym, Kaminski, 2017]
ITGB7	integrin, beta 7	NM_001105365	Понижение	[Brym, Kaminski, 2017]
IPCEF1	interaction protein for cytohesin exchange factor 1	XM_595033	Понижение	[Brym, Kaminski, 2017]
CD9	CD9 molecule	NM_173900	Понижение	[Brym, Kaminski, 2017]
MITF	microphthalmia-associated transcription factor	NM_001001150	Понижение	[Brym, Kaminski, 2017]
S100A10	S100 calcium binding protein A10	NM_174650	Понижение	[Brym, Kaminski, 2017]
DUSP6	dual specificity phosphatase 6	NM_001046195	Понижение	[Brym, Kaminski, 2017]
CTSC	cathepsin C	NM_001033617	Понижение	[Brym, Kaminski, 2017]
CD44	CD44 molecule	NM_174013	Понижение	[Brym, Kaminski, 2017]
PTGER4	prostaglandin E receptor 4	NM_174589	Понижение	[Brym, Kaminski, 2017]
KIAA1598	KIAA1598 ortholog	XR_139692	Понижение	[Brym, Kaminski, 2017]
TIMP1	TIMP metallopeptidase inhibitor 1	NM_174471	Понижение	[Brym, Kaminski, 2017]
IGHA1	Bos taurus IgM	NM_001205186	Понижение	[Brym, Kaminski, 2017]

Обозначение гена	Полное название гена	Идентификатор Refseq	Повышение/снижение экспрессии	Ссылка
VIM	vimentin	NM_173969	Понижение	[Brym, Kaminski, 2017]
SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member	NM_177521	Понижение	[Brym, Kaminski, 2017]
IL17R	nterleukin 17 receptor	XM_005895201	Понижение	[Brym, Kaminski, 2017]
FCN2	ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin)	NM_001010996	Понижение	[Brym, Kaminski, 2017]
WIPF1	AS/WASL interacting protein family, member 1	NM_001076923	Понижение	[Brym, Kaminski, 2017]
S100A8	S100 calcium binding protein A8 (S100A8)	NM_001113725	Понижение	[Brym, Kaminski, 2017]
KIR3DL3	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 3	XR_138959	Понижение	[Brym, Kaminski, 2017]
USP11	ubiquitin specific peptidase 11	NM_001080308	Понижение	[Brym, Kaminski, 2017]
TXK	TXK tyrosine kinase	NM_001206148	Понижение	[Brym, Kaminski, 2017]
HRSP12	heat-responsive protein 12	NM_001034208	Понижение	[Brym, Kaminski, 2017]
COTL1	coactosin-like 1 (Dictyostelium)	NM_001046593	Понижение	[Brym, Kaminski, 2017]
SMIM10	small integral membrane protein 10	NM_001163442	Понижение	[Brym, Kaminski, 2017]
RHBDL1	rhomboid, veinlet-like 1 (Drosophila)	XM_002697968	Понижение	[Brym, Kaminski, 2017]
THBD	thrombomodulin	NM_001166522	Понижение	[Brym, Kaminski, 2017]
PDE2A	phosphodiesterase 2A, cGMP-stimulated	NM_001143846	Понижение	[Brym, Kaminski, 2017]
ANG	angiogenin, ribonuclease, RNase A family, 5	NM_001078144	Понижение	[Brym, Kaminski, 2017]
QSOX1	quiescin Q6 sulfhydryl oxidase 1	NM_001102074	Понижение	[Brym, Kaminski, 2017]
IL1B	interleukin 1, beta	NM_174093	Понижение	[Brym, Kaminski, 2017]
PTK2B	PTK2B protein tyrosine kinase 2 beta	NM_001102252	Понижение	[Brym, Kaminski, 2017]
FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)(FCGR3A)	NM_001077402	Понижение	[Brym, Kaminski, 2017]
FCHO2	FCH domain only 2	NM_001098119	Понижение	[Brym, Kaminski, 2017]
PGRMC1	progesterone receptor membrane component 1	NM_001075133	Понижение	[Brym, Kaminski, 2017]
SORL1	sortilin-related receptor, L(DLR class) A repeats containing	NM_001192757	Понижение	[Brym, Kaminski, 2017]
TKT	transketolase	NM_001003906	Понижение	[Brym, Kaminski, 2017]
DYNLT1	dynein, light chain, Tctex-type 1	NM_174620	Понижение	[Brym, Kaminski, 2017]
NDEL1	nudE nuclear distribution gene E homolog (A.nidulans)-like 1	NM_001191246	Понижение	[Brym, Kaminski, 2017]
FYN	FYN oncogene related to SRC	NM_001077972	Понижение	[Brym, Kaminski, 2017]
ANXA1	annexin A1	NM_175784	Понижение	[Brym, Kaminski, 2017]
PYCARD	PYD and CARD domain containing	NM_174730	Понижение	[Brym, Kaminski, 2017]
LYZ2	lysozyme C-2	NM_180999	Понижение	[Brym, Kaminski, 2017]
STOM	stomatin	NM_001105473	Понижение	[Brym, Kaminski, 2017]
MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	NM_001034779	Понижение	[Brym, Kaminski, 2017]
SPSB2	splA/ryanodine receptor domain and SOCS box containing 2	NM_001076280	Понижение	[Brym, Kaminski, 2017]
GLIPR2	GLI pathogenesis-related 2	NM_001076112	Понижение	[Brym, Kaminski, 2017]
ATP6AP2	ATPase, H+ transporting, lysosomal accessory protein 2	NM_001098022	Понижение	[Brym, Kaminski, 2017]
ATXN1	ataxin 1	XM_005223825	Понижение	[Brym, Kaminski, 2017]
CSK	c-src tyrosine kinase	NM_001075397	Понижение	[Brym, Kaminski, 2017]
CXCR2	interleukin 8 receptor, beta	NM_174360	Понижение	[Brym, Kaminski, 2017]
RHOQ	ras homolog gene family, member Q	NM_001205498	Понижение	[Brym, Kaminski, 2017]
C1orf21	BTA 16 open reading frame, human C1orf21	NM_001081547	Понижение	[Brym, Kaminski, 2017]
ANXA2	annexin A2	NM_174716	Понижение	[Brym, Kaminski, 2017]
CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	NM_001046050	Понижение	[Brym, Kaminski, 2017]
ITGA6	integrin, alpha 6	NM_001109981	Понижение	[Brym, Kaminski, 2017]

Обозначение гена	Полное название гена	Идентификатор Refseq	Повышение/снижение экспрессии	Ссылка
RNASE6	ribonuclease, RNase A family, k6	NM_174594	Понижение	[Brym, Kaminski, 2017]
PCK2	phosphoenolpyruvate carboxykinase 2	NM_001205594	Понижение	[Brym, Kaminski, 2017]
CTSW	cathepsin W	NM_001110070	Понижение	[Brym, Kaminski, 2017]
CD2BP2	CD2 (cytoplasmic tail) binding protein 2	NM_001083682	Понижение	[Brym, Kaminski, 2017]
MACROD1	MACRO domain containing 1	NM_001046509	Понижение	[Brym, Kaminski, 2017]
GNG5	guanine nucleotide binding protein (G protein), gamma 5	NM_174811	Понижение	[Brym, Kaminski, 2017]
CERKL	ceramide kinase-like	XM_003581805	Понижение	[Brym, Kaminski, 2017]
P4HB	prolyl 4-hydroxylase, beta polypeptide	NM_174135	Понижение	[Brym, Kaminski, 2017]
SELPLG	P-selectin glycoprotein ligand 1 mRNA	NM_001037628	Понижение	[Brym, Kaminski, 2017]
LCK	lymphocyte-specific protein tyrosine kinase	NM_001034334	Понижение	[Brym, Kaminski, 2017]
ADIPOQ	adiponectin, C1Q and collagen domain	NM_174742	Понижение	[Brym, Kaminski, 2017]
SLC7A7	solute carrier family 7 (amino acid transporter light chain, y+L system) member 7	NM_001075151	Понижение	[Brym, Kaminski, 2017]
GPT2	glutamic pyruvate transaminase (alanine aminotransferase)	XM_005218738	Понижение	[Brym, Kaminski, 2017]
MEF2BNB	MEF2B neighbor (MEF2BNB)	NM_001145792	Понижение	[Brym, Kaminski, 2017]
LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	NM_001076844	Понижение	[Brym, Kaminski, 2017]
KMT2C	lysine (K)-specific methyltransferase 2C	XM_005198184	Понижение	[Brym, Kaminski, 2017]
DUSP1	dual specificity phosphatase 1	NM_001046452	Понижение	[Brym, Kaminski, 2017]
IGF1R	insulin-like growth factor 1 receptor	NM_001244612	Понижение	[Brym, Kaminski, 2017]
XBP1	X-box binding protein 1	NM_001034727	Понижение	[Brym, Kaminski, 2017]
RABGAP1L	RAB GTPase activating protein 1-like	XM_003587088	Понижение	[Brym, Kaminski, 2017]
LXN	latexin	NM_001080340	Понижение	[Brym, Kaminski, 2017]
ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	XM_005224830	Понижение	[Brym, Kaminski, 2017]
WLS	wntless homolog (Drosophila)	XM_005204461	Понижение	[Brym, Kaminski, 2017]
SDCBP	syndecan binding protein (syntenin)	NM_001075483	Понижение	[Brym, Kaminski, 2017]
CD3E	CD3e molecule, epsilon (CD3-TCR complex)	NM_174011	Понижение	[Brym, Kaminski, 2017]
CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	NM_174512	Понижение	[Brym, Kaminski, 2017]
A2M	alpha-2-macroglobulin	NM_001109795	Понижение	[Brym, Kaminski, 2017]
TSPAN13	tetraspanin 13	NM_001035362	Понижение	[Brym, Kaminski, 2017]
TBC1D2B	TBC1 domain family, member 2B	XM_002696662	Понижение	[Brym, Kaminski, 2017]
SELL	selectin L, CD62, LECAM1	NM_174182	Понижение	[Brym, Kaminski, 2017]
CD3G	CD3g molecule, gamma (CD3-TCR complex)	NM_001040472	Понижение	[Brym, Kaminski, 2017]
VAV3	vav 3 guanine nucleotide exchange factor	XM_002686162	Понижение	[Brym, Kaminski, 2017]
KIF2C	kinesin family member 2C	NM_001101147	Понижение	[Brym, Kaminski, 2017]
ARRB2	arrestin, beta 2	XM_005220181	Понижение	[Brym, Kaminski, 2017]
EFHD2	EF-hand domain family, member D2	NM_001103245	Понижение	[Brym, Kaminski, 2017]
RASGEF1B	RasGEF domain family, member 1B	NM_001083649	Понижение	[Brym, Kaminski, 2017]
CD244	CD244 molecule, natural killer cell receptor 2B4	NM_001192350	Понижение	[Brym, Kaminski, 2017]
C1QC	complement component 1, q subcomponent, C chain (C1QC)	NM_001206396	Понижение	[Brym, Kaminski, 2017]
RNF130	ring finger protein 130	NM_001099708	Понижение	[Brym, Kaminski, 2017]
NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like, E3 ubiquitin protein ligase	XM_005199752	Понижение	[Brym, Kaminski, 2017]

Обозначение гена	Полное название гена	Идентификатор Refseq	Повышение/снижение экспрессии	Ссылка
CYP27A1	cytochrome P450, family 27, subfamily A, polypeptide 1	NM_001083413	Понижение	[Brym, Kaminski, 2017]
CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	NM_174267	Понижение	[Brym, Kaminski, 2017]
UAP1	UDP-N-acteylglucosamine pyrophosphorylase 1	XM_005203527	Понижение	[Brym, Kaminski, 2017]
CHI3L1	chitinase 3-like 1	NM_001080219	Понижение	[Brym, Kaminski, 2017]
SOAT1	sterol O-acyltransferase 1	NM_001034206	Понижение	[Brym, Kaminski, 2017]
KLF4	Kruppel-like factor 4	NM_001105385	Понижение	[Brym, Kaminski, 2017]
CPD	carboxypeptidase D	XM_003587391	Понижение	[Brym, Kaminski, 2017]
NFE2	nuclear factor (erythroid-derived 2), 45kDa	NM_001014923	Понижение	[Brym, Kaminski, 2017]
HK3	hexokinase 3	NM_001101929	Понижение	[Brym, Kaminski, 2017]
NRSN2	neurensin 2	NM_001101269	Понижение	[Brym, Kaminski, 2017]
RARA	retinoic acid receptor, alpha	NM_001014942	Понижение	[Brym, Kaminski, 2017]
MXD4	MAX dimerization protein 4	NM_001076256	Понижение	[Brym, Kaminski, 2017]
CYB5R1	cytochrome b5 reductase 1	NM_001034518	Понижение	[Brym, Kaminski, 2017]
TALDO1	transaldolase 1	NM_001035283	Понижение	[Brym, Kaminski, 2017]
FGL2	fibrinogen-like 2	NM_001046097	Понижение	[Brym, Kaminski, 2017]
NRN1	neuritin 1	NM_001046438	Понижение	[Brym, Kaminski, 2017]
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	NM_001034034	Понижение	[Brym, Kaminski, 2017]
ZMYM6	zinc finger, MYM-type 6	NM_001206292	Понижение	[Brym, Kaminski, 2017]
DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	XM_003582915	Понижение	[Brym, Kaminski, 2017]
SLAMF1	signaling lymphocytic activation molecule family member 1	NM_174184	Понижение	[Brym, Kaminski, 2017]
LRRC25	leucine rich repeat containing 25	NM_174688	Понижение	[Brym, Kaminski, 2017]
STK40	serine/threonine kinase 40	NM_001075727	Понижение	[Brym, Kaminski, 2017]
LAT	linker for activation of T cells	NM_001104978	Понижение	[Brym, Kaminski, 2017]
CTSS	cathepsin S	NM_001033615	Понижение	[Brym, Kaminski, 2017]
PPP1R3B	protein phosphatase 1, regulatory subunit 3B	NM_001103247	Понижение	[Brym, Kaminski, 2017]
EMR3	egf-like module containing, mucin-like, hormone receptor-like 3	XM_005228632	Понижение	[Brym, Kaminski, 2017]
RGS2	regulator of G-protein signaling 2, 24kDa	NM_001075596	Понижение	[Brym, Kaminski, 2017]
ALAS2	aminolevulinate, delta-, synthase 2	NM_001035103	Понижение	[Brym, Kaminski, 2017]
CSF2RA	granulocyte-macrophage colony-stimulating factor receptor subunit alpha-like	XM_005192580	Понижение	[Brym, Kaminski, 2017]
GSN	gelsolin	NM_001113284	Понижение	[Brym, Kaminski, 2017]
SLC46A2	solute carrier family 46, member 2	NM_001024519	Понижение	[Brym, Kaminski, 2017]
MAFB	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog B	XM_610891	Понижение	[Brym, Kaminski, 2017]
KLKB1	kallikrein B, plasma (Fletcher factor) 1	NM_001046352	Понижение	[Brym, Kaminski, 2017]
PLBD1	phospholipase B domain containing 1	NM_001166298	Понижение	[Brym, Kaminski, 2017]
SORCS3	sortilin-related VPS10 domain containing receptor 3	XM_005225556	Понижение	[Brym, Kaminski, 2017]
DAZAP2	DAZ associated protein 2	XM_005206320	Понижение	[Brym, Kaminski, 2017]
LEF1	lymphoid enhancer-binding factor 1	XM_005207653	Понижение	[Brym, Kaminski, 2017]
CCR3	chemokine (C-C motif) receptor 3	XM_005223027	Понижение	[Brym, Kaminski, 2017]
MEX3A	mex-3 RNA binding family member A	NM_001206290	Понижение	[Brym, Kaminski, 2017]
C1QA	complement component 1, q subcomponent, A chain	NM_001014945	Понижение	[Brym, Kaminski, 2017]
OSBPL7	oxysterol binding protein-like 7	NM_001205647	Понижение	[Brym, Kaminski, 2017]
ATPIF1	ATPase inhibitory factor 1	NM_175816	Понижение	[Brym, Kaminski, 2017]
IL18	interleukin 18 (interferon-gamma-inducing factor)	XM_005215801	Понижение	[Brym, Kaminski, 2017]

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NCF1	neutrophil cytosolic factor 1	NM_174119	Понижение	[Brym, Kaminski, 2017]
MZB1	marginal zone B and B1 cell-specific protein	NM_001098930	Понижение	[Brym, Kaminski, 2017]
YPEL5	yippee-like 5 (Drosophila)	NM_001079793	Понижение	[Brym, Kaminski, 2017]
DST	dystonin	XM_001252266	Понижение	[Brym, Kaminski, 2017]
PF4,CXCL4	platelet factor 4	NM_001101062	Понижение	[Brym, Kaminski, 2017]
CFP	complement factor properdin	NM_001076178	Понижение	[Brym, Kaminski, 2017]
ACTN4	actinin, alpha 4	NM_001098052	Понижение	[Brym, Kaminski, 2017]
CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	NM_001046444	Понижение	[Brym, Kaminski, 2017]
TSPAN17	tetraspanin 17	NM_001014880	Понижение	[Brym, Kaminski, 2017]
NUDT3	nudix (nucleoside diphosphate linked moiety X)-type motif 3	NM_001082466	Понижение	[Brym, Kaminski, 2017]
IL6R	interleukin 6 receptor	NM_001110785	Понижение	[Brym, Kaminski, 2017]
CFB	complement factor B	NM_001040526	Понижение	[Brym, Kaminski, 2017]
LPAR6	lysophosphatidic acid receptor 6	NM_001101284	Понижение	[Brym, Kaminski, 2017]
SLC31A2	solute carrier family 31 (copper transporters)	NM_001034556	Понижение	[Brym, Kaminski, 2017]
PHF12	PHD finger protein 12	NM_001192131	Понижение	[Brym, Kaminski, 2017]
IGG1C	IgG1 heavy chain constant region (IgC-gamma)	S82409	Понижение	[Brym, Kaminski, 2017]
HNMT	histamine N-methyltransferase	NM_001035434	Понижение	[Brym, Kaminski, 2017]
KLRC1	killer cell lectin-like receptor subfamily C, member 1	NM_001168587	Понижение	[Brym, Kaminski, 2017]
IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	NM_175773	Понижение	[Brym, Kaminski, 2017]
CA2	carbonic anhydrase II	NM_178572	Понижение	[Brym, Kaminski, 2017]
CD96	CD96 molecule	NM_001035072	Понижение	[Brym, Kaminski, 2017]
CARD9	caspase recruitment domain family, member 9	NM_001077111	Понижение	[Brym, Kaminski, 2017]
BAP1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	NM_001102549	Понижение	[Brym, Kaminski, 2017]
PDE4A	phosphodiesterase 4A, cAMP-specific	NM_001101081	Понижение	[Brym, Kaminski, 2017]
JUN	jun proto-oncogene	NM_001077827	Понижение	[Brym, Kaminski, 2017]
NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	NM_175820	Понижение	[Brym, Kaminski, 2017]
PRDM1	PR domain containing 1, with ZNF domain	NM_001192936	Понижение	[Brym, Kaminski, 2017]
LGALSL	lectin, galactoside-binding-like	NM_001205831	Понижение	[Brym, Kaminski, 2017]
DEFB7	defensin beta 7	NM_001102362	Понижение	[Brym, Kaminski, 2017]
TIMP2	TIMP metallopeptidase inhibitor 2	NM_174472	Понижение	[Brym, Kaminski, 2017]
CXCL8	interleukin 8	NM_173925	Понижение	[Brym, Kaminski, 2017]
CC2D1B	coiled-coil and C2 domain containing 1B	XM_588670	Понижение	[Brym, Kaminski, 2017]
MKNK1	MAP kinase interacting serine/threonine kinase 1	NM_001035358	Понижение	[Brym, Kaminski, 2017]
ISG20	interferon stimulated exonuclease gene 20kDa	XM_005911016	Понижение	[Brym, Kaminski, 2017]
HBA	hemoglobin, alpha 2	NM_001077422	Понижение	[Brym, Kaminski, 2017]
ARHGAP9	Rho GTPase activating protein 9	XM_005192327	Понижение	[Brym, Kaminski, 2017]
LAMP1	lysosomal-associated membrane protein 1	NM_001075124	Понижение	[Brym, Kaminski, 2017]
SNX10	sorting nexin 10	NM_001075375	Понижение	[Brym, Kaminski, 2017]
DSTN	destrin (actin depolymerizing factor)	XM_005904567	Понижение	[Brym, Kaminski, 2017]
PARP8	poly (ADP-ribose) polymerase family, member 8	NM_001192298	Понижение	[Brym, Kaminski, 2017]
G6PD	glucose-6-phosphate dehydrogenase	NM_001244135	Понижение	[Brym, Kaminski, 2017]
CD84	CD84 molecule	XM_002685862	Понижение	[Brym, Kaminski, 2017]
HSPB1	heat shock 27kDa protein 1	NM_001025569	Понижение	[Brym, Kaminski, 2017]

Обозначение гена	Полное название гена	Идентификатор Refseq	Повышение/снижение экспрессии	Ссылка
MOSPD1	motile sperm domain containing 1	NM_001038137	Понижение	[Brym, Kaminski, 2017]
ATF3	activating transcription factor 3	NM_001046193	Понижение	[Brym, Kaminski, 2017]
TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	NM_001034647	Понижение	[Brym, Kaminski, 2017]
PCYOX1	prenylcysteine oxidase 1	NM_001105474	Понижение	[Brym, Kaminski, 2017]
SLC44A1	solute carrier family 44 (choline transporter), member 1	XM_002689908	Понижение	[Brym, Kaminski, 2017]
FKBP11	FK506 binding protein 11, 19 kDa	NM_001045932	Понижение	[Brym, Kaminski, 2017]
GUCY1B3	guanylate cyclase 1, soluble, beta 3	NM_174641	Понижение	[Brym, Kaminski, 2017]
MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	NM_001034584	Повышение	[Brym, Kaminski, 2017]
KBTBD8	T cell activation kelch repeat protein	NM_001192696	Повышение	[Brym, Kaminski, 2017]
ADRA2A	alpha2A adrenergic receptor	NM_174499	Повышение	[Brym, Kaminski, 2017]
MS4A1,	membrane-spanning 4-domains, subfamily A, member 1	NM_001077854	Повышение	[Brym, Kaminski, 2017]
ADORA2B	adenosine A2b receptor	NM_001075925	Повышение	[Brym, Kaminski, 2017]
PPA2	pyrophosphatase (inorganic) 2	NM_001076396	Повышение	[Brym, Kaminski, 2017]
CD19	CD19 molecule	NM_001245998	Повышение	[Brym, Kaminski, 2017]
APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	NM_176609	Повышение	[Brym, Kaminski, 2017]
HIF1A	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	NM_174339	Повышение	[Brym, Kaminski, 2017]
SLC4A10	Solute carrier family 4, sodium bicarbonate transporter-like, member 10	NM_001038128	Повышение Повышение	[Brym, Kaminski, 2017] [Brym, Kaminski, 2017]
CCT5	T-complex protein 1, chaperonin containing TCP1, subunit 5 (epsilon)	NM_001034595	Повышение	[Brym, Kaminski, 2017]
SH3GLB2	SH3-domain GRB2-like endophilin B2	NM_001076802	Повышение	[Brym, Kaminski, 2017]
LMO2	LIM domain only 2 (rhombotin-like 1)	NM_001076352	Повышение	[Brym, Kaminski, 2017]
CCNG1	cyclin G1	NM_001013364	Повышение	[Brym, Kaminski, 2017]
BANK1	B-cell scaffold protein with ankyrin repeats 1	XM_002688119	Повышение	[Brym, Kaminski, 2017]
HADH	hydroxyacyl-CoA dehydrogenase	NM_001046334	Повышение	[Brym, Kaminski, 2017]
HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	NM_001007809	Повышение	[Brym, Kaminski, 2017]
DYNLL1	cytoplasmic dynein light polypeptide 1	NM_001003901	Повышение	[Brym, Kaminski, 2017]
SIRT5	sirtuin 5	NM_001034295	Повышение	[Brym, Kaminski, 2017]
C1QBP	complement component 1, q subcomponent binding protein (C1QBP), nuclear gene encoding mitochondrial protein	NM_001034527	Повышение	[Brym, Kaminski, 2017]
GMPS	guanine monphosphate synthetase	BC111273	Повышение	[Brym, Kaminski, 2017]
HSD17B10	hydroxysteroid (17-beta) dehydrogenase 10	NM_174334	Повышение	[Brym, Kaminski, 2017]
TRMT112	tRNA methyltransferase 11-2 homolog (S. cerevisiae)	NM_001045981	Повышение	[Brym, Kaminski, 2017]
SRSF9	serine/arginine-rich splicing factor 9	NM_001083398	Повышение	[Brym, Kaminski, 2017]
ZNF106 / zfp106	zinc finger protein 106 homolog (mouse)	XM_002690810	Повышение	[Brym, Kaminski, 2017]
C12orf57	chromosome 5 open reading frame, human C12orf57	NM_001075525	Повышение	[Brym, Kaminski, 2017]
BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	NM_001076121	Повышение	[Brym, Kaminski, 2017]
TEP1	telomerase-associated protein 1	NM_001206912	Повышение	[Brym, Kaminski, 2017]
MRPS18B	mitochondrial ribosomal protein S18B	NM_001038524	Повышение	[Brym, Kaminski, 2017]
VBP1	von Hippel-Lindau binding protein 1	NM_001038516	Повышение	[Brym, Kaminski, 2017]
PACSIN1	protein kinase C and casein kinase substrate in neurons 1	NM_001101101	Повышение	[Brym, Kaminski, 2017]
SYK	spleen tyrosine kinase	NM_001037465	Повышение	[Brym, Kaminski, 2017]
PPP2CB	protein phosphatase 2, catalytic subunit, beta isozyme	NM_001075857	Повышение	[Brym, Kaminski, 2017]
EEF1B2	eukaryotic translation elongation factor 1 beta 2	NM_001014936	Повышение	[Brym, Kaminski, 2017]

Обозначение гена	Полное название гена	Идентификатор Refseq	Повышение/снижение экспрессии	Ссылка
SORCS1	sortilin-related VPS10 domain containing receptor 1	NM_001191207	Повышение	[Brym, Kaminski, 2017]
PHGDH	phosphoglycerate dehydrogenase	NM_001035017	Повышение	[Brym, Kaminski, 2017]
GDI2	GDP dissociation inhibitor 2	NM_001033762	Повышение	[Brym, Kaminski, 2017]
BCCIP	BRCA2 and CDKN1A interacting protein	NM_001046122	Повышение	[Brym, Kaminski, 2017]
RTN4	reticulon 4	XM_005212571	Повышение	[Brym, Kaminski, 2017]
NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa (NDUFB5), nuclear gene encoding mitochondrial protein	NM_176656	Повышение	[Brym, Kaminski, 2017]
MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3	NM_001191162	Повышение	[Brym, Kaminski, 2017]
TCF4	transcription factor 4	NM_001034621	Повышение	[Brym, Kaminski, 2017]
SDHA	succinate dehydrogenase complex, subunit A, flavoprotein	NM_174178	Повышение	[Brym, Kaminski, 2017]
WDFY4	WDFY family member 4	NM_001205945	Повышение	[Brym, Kaminski, 2017]
ELOVL5	ELOVL fatty acid elongase 5	NM_001046597	Повышение	[Brym, Kaminski, 2017]
NMI	N-myc (and STAT) interactor	NM_001035098	Повышение	[Brym, Kaminski, 2017]
SYNGR2	synaptogyrin 2	NM_001100358	Повышение	[Brym, Kaminski, 2017]
CXXC5	CXXC finger protein 5	NM_001038176	Повышение	[Brym, Kaminski, 2017]
SMIM20	small integral membrane protein 20	NM_001145428	Повышение	[Brym, Kaminski, 2017]
HMGN1	high mobility group nucleosome binding domain 1	NM_001034772	Повышение	[Brym, Kaminski, 2017]
LUZP6	leucine zipper protein 6	XM_005198116	Повышение	[Brym, Kaminski, 2017]
FAM53B	family with sequence similarity 53, member B	-	Повышение	[Brym, Kaminski, 2017]
GLMN	glomulin, FKBP associated protein	NM_001192020	Повышение	[Brym, Kaminski, 2017]
MAT2A	methionine adenosyltransferase II, alpha	NM_001101131	Повышение	[Brym, Kaminski, 2017]
FCGR2B, CD32	Fc fragment of IgG, low affinity IIb, receptor (CD32)	NM_174539	Повышение	[Brym, Kaminski, 2017]
SOX5	SRY (sex determining region Y)-box 5	NM_001083471	Повышение	[Brym, Kaminski, 2017]
SUMO2	SMT3 suppressor of mif two 3 homolog 2 (yeast)	BT021041	Повышение	[Brym, Kaminski, 2017]
MDH2	malate dehydrogenase 2, NAD (mitochondrial)	NM_001013587	Повышение	[Brym, Kaminski, 2017]
ACTL6A	actin-like 6A	NM_001105035	Повышение	[Brym, Kaminski, 2017]
CYB5R3	cytochrome b5 reductase 3	NM_001103250	Повышение	[Brym, Kaminski, 2017]
B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	NM_001076979	Повышение	[Brym, Kaminski, 2017]
CD79B	CD79b molecule, immunoglobulin-associated beta, transcript variant 2	XM_586841	Повышение	[Brym, Kaminski, 2017]
TMEM134	transmembrane protein 134	NM_001080254	Повышение	[Brym, Kaminski, 2017]
SLC35F2	solute carrier family 35, member F2	XM_612258	Повышение	[Brym, Kaminski, 2017]
PABPC4	poly(A) binding protein, cytoplasmic 4	XM_005204784	Повышение	[Brym, Kaminski, 2017]
HSPA9	heat shock 70kDa protein 9 (mortalin)	NM_001034524	Повышение	[Brym, Kaminski, 2017]
DNASE2	deoxyribonuclease II, lysosomal	NM_001075127	Повышение	[Brym, Kaminski, 2017]
SNRPA1	small nuclear ribonucleoprotein polypeptide A	NM_001098948	Повышение	[Brym, Kaminski, 2017]
EIF4A2	eukaryotic translation initiation factor 4A2	NM_001034044	Повышение	[Brym, Kaminski, 2017]
HAT1	histone acetyltransferase 1	NM_001034347	Повышение	[Brym, Kaminski, 2017]
RHNO1	chromosome 5 open reading frame, human C12orf32, RAD9-HUS1-RAD1 interacting nuclear orphan 1	NM_001075631	Повышение	[Brym, Kaminski, 2017]
STX7	syntaxin 7	NM_001077864	Повышение	[Brym, Kaminski, 2017]
SP100	SP100 nuclear antigen	XM_001789440	Повышение	[Brym, Kaminski, 2017]
MIEN1	migration and invasion enhancer 1	NM_001075221	Повышение	[Brym, Kaminski, 2017]
RPL19	ribosomal protein L19	NM_001040516	Повышение	[Brym, Kaminski, 2017]
ARPC5L	actin related protein 2/3 complex, subunit 5-like	NM_001034737	Повышение	[Brym, Kaminski, 2017]

Обозначение гена	Полное название гена	Идентификатор Refseq	Повышение/снижение экспрессии	Ссылка
MRPL50	mitochondrial ribosomal protein L50	NM_001046180	Повышение	[Brym, Kaminski, 2017]
MAT2B	methionine adenosyltransferase II, beta	NM_001046526	Повышение	[Brym, Kaminski, 2017]
PAIP2	poly(A) binding protein interacting protein 2	NM_001034636	Повышение	[Brym, Kaminski, 2017]
YWHAG	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	NM_174793	Повышение	[Brym, Kaminski, 2017]
THAP9	THAP domain containing 9	NM_001244183	Повышение	[Brym, Kaminski, 2017]
GLRX3	glutaredoxin 3	NM_001035101	Повышение	[Brym, Kaminski, 2017]
TERF2	telomeric repeat binding factor 2	NM_001205589	Повышение	[Brym, Kaminski, 2017]
TMBIM6	transmembrane BAX inhibitor motif containing 6	NM_001076414	Повышение	[Brym, Kaminski, 2017]
SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	XM_589161	Повышение	[Brym, Kaminski, 2017]
RBBP7	retinoblastoma binding protein 7	NM_001034638	Повышение	[Brym, Kaminski, 2017]
LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	NM_001177740	Повышение	[Brym, Kaminski, 2017]
ADAM9	ADAM metallopeptidase domain 9	NM_001192818	Повышение	[Brym, Kaminski, 2017]
PEBP1	phosphatidylethanolamine binding protein 1	NM_001033623	Повышение	[Brym, Kaminski, 2017]
C15H11orf31	chromosome 15 open reading frame, human C11orf31	NM_001164092	Повышение	[Brym, Kaminski, 2017]
NAE1	NEDD8 activating enzyme E1 subunit 1	NM_001193033	Повышение	[Brym, Kaminski, 2017]
TES	testis derived transcript (3 LIM domains)	XM_005205431	Повышение	[Brym, Kaminski, 2017]
SEC31A	SEC31 homolog A (S. cerevisiae)	NM_001191274	Повышение	[Brym, Kaminski, 2017]
GNL3	guanine nucleotide binding protein-like 3 nucleolar	XM_005898122	Повышение	[Brym, Kaminski, 2017]
CDCA7L	cell division cycle associated 7-like	NM_001104977	Повышение	[Brym, Kaminski, 2017]
ATP5F1A / ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1	NM_174684	Повышение	[Brym, Kaminski, 2017]
TPD52	tumor protein D52	NM_001076922	Повышение	[Brym, Kaminski, 2017]
GMPS	guanine monphosphate synthetase	NM_001206436	Повышение	[Brym, Kaminski, 2017]
DEXI	Dexi homolog (mouse)	NM_001191169	Повышение	[Brym, Kaminski, 2017]
CABIN1	calcineurin binding protein 1	XM_002694694	Повышение	[Brym, Kaminski, 2017]
PPM1E	protein phosphatase, Mg2+/Mn2+ dependent, 1E	XM_002695602	Повышение	[Brym, Kaminski, 2017]
SNRPD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa	NM_001076479	Повышение	[Brym, Kaminski, 2017]
EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	NM_001046117	Повышение	[Brym, Kaminski, 2017]
RRP7A	ribosomal RNA processing 7 homolog A (S. cerevisiae)	NM_001110074	Повышение	[Brym, Kaminski, 2017]
ZCCHC11)	uridylyltransferase 4-like	NM_001206930	Повышение	[Brym, Kaminski, 2017]
CXXC5	CXXC finger protein 5	NM_001038176	Повышение	[Brym, Kaminski, 2017]
CIITA	major histocompatibility complex class II transactivator	XM_002697962	Повышение	[Brym, Kaminski, 2017]
ERH	enhancer of rudimentary homolog (Drosophila)	NM_001034336	Повышение	[Brym, Kaminski, 2017]
NIFK	MKI67 (FHA domain) interacting nucleolar phosphoprotein	NM_001034354	Повышение	[Brym, Kaminski, 2017]
AVEN	Bos taurus apoptosis, caspase activation inhibitor	XM_002690781	Повышение	[Brym, Kaminski, 2017]
CMTM7	CKLF-like MARVEL transmembrane domain containing 7	NM_001075960	Повышение	[Brym, Kaminski, 2017]
GPN3	GPN-loop GTPase 3	NM_001075272	Повышение	[Brym, Kaminski, 2017]
RPF1	ribosome production factor 1 homolog (S. cerevisiae)	NM_001083417	Повышение	[Brym, Kaminski, 2017]
NACA	nascent polypeptide-associated complex alpha subunit	NM_001014916	Повышение	[Brym, Kaminski, 2017]
DOB	major histocompatibility complex, class II, DO beta	NM_001013600	Повышение	[Brym, Kaminski, 2017]
EHHADH	enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase	NM_001075780	Повышение	[Brym, Kaminski, 2017]
APIP	APAF1 interacting protein	NM_001075352	Повышение	[Brym, Kaminski, 2017]
HSPA14	heat shock 70kDa protein 14	NM_001046388	Повышение	[Brym, Kaminski, 2017]

Обозначение гена	Полное название гена	Идентификатор Refseq	Повышение/снижение экспрессии	Ссылка
BMS1	BMS1 homolog, ribosome assembly protein (yeast)	NM_001206147	Повышение	[Brym, Kaminski, 2017]
SPIB	Spi-B transcription factor (Spi-1/PU.1 related)	NM_001205444	Повышение	[Brym, Kaminski, 2017]
HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	NM_001034696	Повышение	[Brym, Kaminski, 2017]
ENOPH1	enolase-phosphatase 1	NM_001075875	Повышение	[Brym, Kaminski, 2017]
HSPA4	heat shock 70kDa protein 4	NM_001114192	Повышение	[Brym, Kaminski, 2017]
JDP2	Jun dimerization protein 2	NM_001193245	Повышение	[Brym, Kaminski, 2017]
IPO4	importin 4	NM_001083661	Повышение	[Brym, Kaminski, 2017]
CTPS	CTP synthase	NM_001077858	Повышение	[Brym, Kaminski, 2017]
IFI30	interferon, gamma-inducible protein 30	NM_001101251	Повышение	[Brym, Kaminski, 2017]
NCOA7	nuclear receptor coactivator 7	XM_003586458	Повышение	[Brym, Kaminski, 2017]
NAT1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	NM_001075572	Повышение	[Brym, Kaminski, 2017]
PIGO	phosphatidylinositol glycan anchor biosynthesis, class O	XM_001251645	Повышение	[Brym, Kaminski, 2017]
STARD7	StAR-related lipid transfer (START) domain containing 7	NM_001102086	Повышение	[Brym, Kaminski, 2017]
ACAT1	acetyl-CoA acetyltransferase 1	NM_001046075	Повышение	[Brym, Kaminski, 2017]
CRTC3	CREB regulated transcription coactivator 3	XM_591546	Повышение	[Brym, Kaminski, 2017]
TRMT5	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	NM_001034565	Повышение	[Brym, Kaminski, 2017]
PTCD3	Pentatricopeptide repeat domain 3	NM_001046034	Повышение	[Brym, Kaminski, 2017]
CDC16	cell division cycle 16 homolog (S. cerevisiae)	NM_001192990	Повышение	[Brym, Kaminski, 2017]
RSRC1	arginine/serine-rich coiled-coil 1	NM_001075404	Повышение	[Brym, Kaminski, 2017]
UBA2	ubiquitin-like modifier activating enzyme 2	NM_001083381	Повышение	[Brym, Kaminski, 2017]
AP1B1	adaptor-related protein complex 1, beta 1 subunit	NM_001045938	Повышение	[Brym, Kaminski, 2017]
LCN2	lipocalin 2	XM_005908492	Повышение	[Brym, Kaminski, 2017]
ITPR1	inositol 1,4,5-trisphosphate receptor, type 1	NM_174841	Повышение	[Brym, Kaminski, 2017]
HMGB1	high mobility group box 1	NM_176612	Повышение	[Brym, Kaminski, 2017]
CFL2	cofilin 2	XM_005891814	Повышение	[Brym, Kaminski, 2017]
CXCL10	chemokine (C-X-C motif) ligand 10	NM_001046551	Повышение	[Brym, Kaminski, 2017]
CBX6	chromobox homolog 6	NM_001103094	Повышение	[Brym, Kaminski, 2017]
KAT6B	K(lysine) acetyltransferase 6B	XM_005226509	Повышение	[Brym, Kaminski, 2017]
DYNLL1	dynein, light chain, LC8-type 1	NM_001003901	Повышение	[Brym, Kaminski, 2017]
CXHXorf57	chromosome X open reading frame, human CXorf57	-	Повышение	[Brym, Kaminski, 2017]
ZBTB32	zinc finger and BTB domain containing 32	NM_001191224	Повышение	[Brym, Kaminski, 2017]
BBIP1	BBSome interacting protein 1	XM_003584100	Повышение	[Brym, Kaminski, 2017]
TUBB4B	tubulin, beta 2C	NM_001034663	Повышение	[Brym, Kaminski, 2017]
NR2F6	nuclear receptor subfamily 2, group F, member 6	XM_002704716	Повышение	[Brym, Kaminski, 2017]
ATM	ataxia telangiectasia mutated	NM_001205935	Повышение	[Brym, Kaminski, 2017]
RBM34	RNA binding motif protein 34	NM_001110082	Повышение	[Brym, Kaminski, 2017]
PKM	pyruvate kinase	NM_001205727	Повышение	[Brym, Kaminski, 2017]
SLC7A5	solute carrier family 7 (amino acid transporter light chain, L system), member 5	NM_174613	Повышение	[Brym, Kaminski, 2017]
SNRNP70	small nuclear ribonucleoprotein 70kDa (U1	NM_001076046	Повышение	[Brym, Kaminski, 2017]
ITPR3	inositol 1,4,5-trisphosphate receptor, type 3	NM_174370	Повышение	[Brym, Kaminski, 2017]

Литература к таблице **S5**

REF	PubMedID	Авторы	Название	Данные о журнале
[Brym, Kaminski, 2017]	27812893	Brym P., Kaminski S.	Microarray analysis of differential gene expression profiles in blood cells of naturally BLV-infected and uninfected Holstein-Friesian cows.	Mol. Biol. Rep. 2017;44:109-127. DOI: 10.1007/s11033-016-4088-6.

Таблица S6.

Данные по белок-белковым взаимодейстаиям.

Гены/белки КРС, которые непосредственно физически взаимодействуют с белками ВЛКРС. Все гены собраны из экспериментальных статей.

Обозначение гена в базе Entrez Gene	Полное название гена	Идентификатор гена в базе Entrez Gene	Ссылка	Метод	Интерактант: вирион, белок или РНК	Значение для патогенеза
AP3D1	adaptor related protein complex 3 subunit delta 1	281023	[Corredor et al., 2018]	in vitro, Madin-Darby bovine kidney (MDBK) cells	gp51	It was found that rNgp51 preferentially bound to MDBK cells, suggesting this domain's functional role during invasion.
ATF2	activating transcription factor 2	509827	[Willems et al., 1992]	in vitro, a vector expressing CREB2 was transfected into D17 osteosarcoma cells.	lambda-gt11 cDNA library was constructed with mRNA isolated from a BLV-induced tumor	In the absence of the tax transactivator, the CREB2 protein and the cyclic AMP-dependent protein kinase A activate the BLV long terminal repeat at a basal expression level: trans activation reached 10% of the values obtained in the presence of tax alone.
FDPS	farnesyl diphosphate synthase	281156	[Lefèbvre et al., 2002]	in vitro, we utilized the yeast two-hybrid system to identify protein partners of G4	G4 is accessory protein encoded by the X region of bovine leukemia virus	Results revealed that G4 interacts with farnesyl pyrophosphate synthetase (FPPS), a protein involved in the mevalonate/squalene pathway and in synthesis of FPP, a substrate required for prenylation of Ras.

Литература к таблице **S6**

REF	PubMedID	Авторы	Название	Данные о журнале
[Corredor et al., 2018]	29928016	Corredor AP, González J, Baquero LA, Curtidor H, Olaya-Galán NN, Patarroyo MA, Gutiérrez MF.	In silico and in vitro analysis of boAP3d1 protein interaction with bovine leukaemia virus gp51.	PLoS One. 2018 Jun 21;13(6):e0199397. doi: 10.1371/journal.pone.0199397.
[Willems et al., 1992]	1309910	Willems L, Kettmann R, Chen G, Portetelle D, Burny A, Derse D.	A cyclic AMP-responsive DNA-binding protein (CREB2) is a cellular transactivator of the bovine leukemia virus long terminal repeat.	J Virol. 1992 Feb;66(2):766-72.
[Lefèbvre et al., 2002]	11773414	Lefèbvre L, Vanderplasschen A, Ciminale V, Heremans H, Dangoisse O, Jauniaux JC, Toussaint JF, Zelnik V, Burny A, Kettmann R, Willems L.	Oncoviral bovine leukemia virus G4 and human T-cell leukemia virus type 1 p13(II) accessory proteins interact with farnesyl pyrophosphate synthetase.	J Virol. 2002 Feb;76(3):1400-14.

Таблица S7.

Каталог генов КРС и других видов млекопитающих, вовлеченных в процесс инфицирования ВЛКРС

Gene Symbol (Bos taurus)	Gene Symbol (Homo sapiens)	Evidence	Ensembl Gene ID (human)
A2M	*A2M*	Expr_Chip	ENSG00000175899
ABHD16A	*ABHD16A*	GWAS	ENSG00000204427
ABT1	*ABT1*	GWAS	ENSG00000146109
ACAT1	*ACAT1*	Expr_Chip	ENSG00000075239
ACTL6A	*ACTL6A*	Expr_Chip	ENSG00000136518
ACTN4	*ACTN4*	Expr_Chip	ENSG00000130402
ADAM9	*ADAM9*	Expr_Chip	ENSG00000168615
ADGRF2	*ADGRF2*	GWAS	ENSG00000164393
ADIPOQ	*ADIPOQ*	Expr_Chip	ENSG00000181092
ADORA2B	*ADORA2B*	Expr_Chip	ENSG00000170425
ADRA2A	*ADRA2A*	Expr_Chip	ENSG00000150594
AIF1	*AIF1*	Expr_Chip	ENSG00000204472
ALAS2	*ALAS2*	Expr_Chip	ENSG00000158578
AMICA1	*JAML*	Expr_Chip	ENSG00000160593
ANG	*ANG*	Expr_Chip	ENSG00000214274
ANXA1	*ANXA1*	Expr_Chip	ENSG00000135046
ANXA2	*ANXA2*	Expr_Chip	ENSG00000182718
ANXA3	*ANXA3*	Expr_Chip	ENSG00000138772
AP1B1	*AP1B1*	Expr_Chip	ENSG00000100280
AP3D1	*AP3D1*	PPI	ENSG00000065000
AP4B1	*AP4B1*	GWAS	ENSG00000134262
APEX1	*APEX1*	Expr_Chip	ENSG00000100823
APIP	*APIP*	Expr_Chip	ENSG00000149089
APOM	*APOM*	GWAS	ENSG00000204444
ARHGAP9	*ARHGAP9*	Expr_Chip	ENSG00000123329
ARPC5L	*ARPC5L*	Expr_Chip	ENSG00000136950
ARRB2	*ARRB2*	Expr_Chip	ENSG00000141480
ATF2	*ATF2*	PPI	ENSG00000115966
ATF3	*ATF3*	Expr_Chip	ENSG00000162772
ATM	*ATM*	Expr_Chip	ENSG00000149311
ATP5F1A	*ATP5F1A*	Expr_Chip	ENSG00000152234
ATP6AP2	*ATP6AP2*	Expr_Chip	ENSG00000182220
ATP6V1G2	*ATP6V1G2*	GWAS	ENSG00000213760
ATPIF1	*ATP5IF1*	Expr_Chip	ENSG00000130770
ATXN1	*ATXN1*	Expr_Chip	ENSG00000124788
AVEN	*AVEN*	Expr_Chip	ENSG00000169857
B3GNT5	*B3GNT5*	Expr_Chip	ENSG00000176597
BAG6	*BAG6*	GWAS	ENSG00000204463
BANK1	*BANK1*	Expr_Chip	ENSG00000153064
BAP1	*BAP1*	Expr_Chip	ENSG00000163930
BBIP1	*BBIP1*	Expr_Chip	ENSG00000214413
BCCIP	*BCCIP*	Expr_Chip	ENSG00000107949
BCL11A	*BCL11A*	Expr_Chip	ENSG00000119866
BMS1	*BMS1*	Expr_Chip	ENSG00000165733
BOLA-DQA1	*HLA-DPA1*	GWAS Alleles	ENSG00000231389
BOLA-DRB3	*HLA-DRB1*	GWAS Alleles	ENSG00000196126
C12orf57	*C12orf57*	Expr_Chip	ENSG00000111678
C15H11orf31	*SELENOH*	Expr_Chip	ENSG00000211450
C1orf21	*C1orf21*	Expr_Chip	ENSG00000116667
C1QA	*C1QA*	Expr_Chip	ENSG00000173372
C1QBP	*C1QBP*	Expr_Chip	ENSG00000108561
C1QC	*C1QC*	Expr_Chip	ENSG00000159189
C23H6orf47	*C6orf47*	GWAS	ENSG00000204439
CA2	*CA2*	Expr_Chip	ENSG00000104267
CABIN1	*CABIN1*	Expr_Chip	ENSG00000099991
CAPN2	*CAPN2*	Expr_Chip	ENSG00000162909
CARD9	*CARD9*	Expr_Chip	ENSG00000187796
CBX6	*CBX6*	Expr_Chip	ENSG00000183741
CC2D1B	*CC2D1B*	Expr_Chip	ENSG00000154222
CCNG1	*CCNG1*	Expr_Chip	ENSG00000113328
CCR3	*CCR3*	Expr_Chip	ENSG00000183625
CCT5	*CCT5*	Expr_Chip	ENSG00000150753
CD19	*CD19*	Expr_Chip	ENSG00000177455
CD2	*CD2*	Expr_Chip	ENSG00000116824
CD244	*CD244*	Expr_Chip	ENSG00000122223
CD274	*CD274*	Expr_Articles	ENSG00000120217

Gene Symbol (Bos taurus)	Gene Symbol (Homo sapiens)	Evidence	Ensembl Gene ID (human)
CD2AP	*CD2AP*	GWAS	ENSG00000198087
CD2BP2	*CD2BP2*	Expr_Chip	ENSG00000169217
CD3E	*CD3E*	Expr_Chip	ENSG00000198851
CD3G	*CD3G*	Expr_Chip	ENSG00000160654
CD44	*CD44*	Expr_Chip	ENSG00000026508
CD63	*CD63*	Expr_Chip	ENSG00000135404
CD79A	*CD79A*	Expr_Articles	ENSG00000105369
CD79B	*CD79B*	Expr_Chip	ENSG00000007312
CD84	*CD84*	Expr_Chip	ENSG00000066294
CD9	*CD9*	Expr_Chip	ENSG00000010278
CD96	*CD84*	Expr_Chip	ENSG00000066294
CDC16	*CDC16*	Expr_Chip	ENSG00000130177
CDC42EP3	*CDC42EP3*	Expr_Chip	ENSG00000163171
CDCA2	*CDCA2*	GWAS	ENSG00000184661
CDCA7L	*CDCA7L*	Expr_Chip	ENSG00000164649
CDK5R1	*CDK5R1*	Expr_Chip	ENSG00000176749
CDKN2D	*CDKN2D*	Expr_Chip	ENSG00000129355
CEBPA	*CEBPA*	Expr_Chip	ENSG00000245848
CEBPD	*CEBPD*	Expr_Chip	ENSG00000221869
CERKL	*CDKN2D*	Expr_Chip	ENSG00000129355
CFB	*CFB*	Expr_Chip	ENSG00000243649
CFD	*CFD*	Expr_Chip	ENSG00000197766
CFL2	*CFL2*	Expr_Chip	ENSG00000165410
CFP	*CFP*	Expr_Chip	ENSG00000126759
CHI3L1	*CHI3L1*	Expr_Chip	ENSG00000133048
CIITA	*CIITA*	Expr_Chip	ENSG00000179583
CMTM7	*CMTM7*	Expr_Chip	ENSG00000153551
CNTN3	*CNTN3*	GWAS	ENSG00000113805
COL21A1	*COL21A1*	GWAS	ENSG00000124749
COTL1	*COTL1*	Expr_Chip	ENSG00000103187
CPD	*CPD*	Expr_Chip	ENSG00000108582
CRISP1	*CRISP1*	GWAS	ENSG00000124812
CRTC3	*CRTC3*	Expr_Chip	ENSG00000140577
CSF2RA	*CSF2RA*	Expr_Chip	ENSG00000198223
CSK	*CSK*	Expr_Chip	ENSG00000103653
CSNK2B	*CSNK2B*	GWAS	ENSG00000204435
CST3	*CST3*	Expr_Chip	ENSG00000101439
CTLA4	*CTLA4*	Expr_Articles	ENSG00000163599
CTPS	*CTPS1*	Expr_Chip	ENSG00000171793
CTSC	*CTSC*	Expr_Chip	ENSG00000109861
CTSS	*CTSS*	Expr_Chip	ENSG00000163131
CTSW	*CTSW*	Expr_Chip	ENSG00000172543
CXCL10	*CXCL10*	Expr_Chip	ENSG00000169245
CXCL8	*CXCL8*	Expr_Chip	ENSG00000169429
CXCR2	*CXCR2*	Expr_Chip	ENSG00000180871
CXHXorf57	*RADX*	Expr_Chip	ENSG00000147231
CXXC5	*CXXC5*	Expr_Chip	ENSG00000171604
CYB5R1	*RADX*	Expr_Chip	ENSG00000147231
CYB5R3	*CYB5R3*	Expr_Chip	ENSG00000100243
CYP27A1	*CYP27A1*	Expr_Chip	ENSG00000135929
DAG1	*DAG1*	GWAS	ENSG00000173402
DAZAP2	*DAZAP2*	Expr_Chip	ENSG00000183283
DEFB7	*DEFB107A*	Expr_Chip	ENSG00000186572
DEXI	*DEXI*	Expr_Chip	ENSG00000182108
DNAJC1	*DNAJC1*	Expr_Chip	ENSG00000136770
DNASE2	*DNASE2*	Expr_Chip	ENSG00000105612
DOB	*HLA-DOB*	Expr_Chip	ENSG00000241106
DST	*DST*	Expr_Chip	ENSG00000151914
DSTN	*DSTN*	Expr_Chip	ENSG00000125868
DUSP1	*DUSP1*	Expr_Chip	ENSG00000120129
DUSP6	*DUSP6*	Expr_Chip	ENSG00000139318
DYNLL1	*DYNLL1*	Expr_Chip	ENSG00000088986
DYNLT1	*DYNLT1*	Expr_Chip	ENSG00000146425
EEF1B2	*EEF1B2*	Expr_Chip	ENSG00000114942
EFHD2	*EFHD2*	Expr_Chip	ENSG00000142634
EHHADH	*EHHADH*	Expr_Chip	ENSG00000113790
EIF2S3	*EIF2S3*	Expr_Chip	ENSG00000130741
EIF4A2	*EIF4A2*	Expr_Chip	ENSG00000156976
ELOVL5	*ELOVL5*	Expr_Chip	ENSG00000012660
EMR3	*ADGRE3*	Expr_Chip	ENSG00000131355
ENOPH1	*ENOPH1*	Expr_Chip	ENSG00000145293

Gene Symbol (Bos taurus)	Gene Symbol (Homo sapiens)	Evidence	Ensembl Gene ID (human)
ERH	*ERH*	Expr_Chip	ENSG00000100632
F5	*F5*	Expr_Chip	ENSG00000198734
FAM53B	*FAM53B*	Expr_Chip	ENSG00000189319
FCGR2B	*FCGR2B*	Expr_Chip	ENSG00000072694
FCGR3A	*FCGR3A*	Expr_Chip	ENSG00000203747
FCHO2	*FCHO2*	Expr_Chip	ENSG00000157107
FCN2	*FCN1*	Expr_Chip	ENSG00000085265
FDPS	*FDPS*	PPI	ENSG00000160752
FGL2	*FGL2*	Expr_Chip	ENSG00000127951
FKBP11	*FKBP11*	Expr_Chip	ENSG00000134285
FLOT1	*FLOT1*	GWAS	ENSG00000137312
FOXP3	*FOXP3*	Expr_Articles	ENSG00000049768
FYN	*FYN*	Expr_Chip	ENSG00000010810
G6PD	*G6PD*	Expr_Chip	ENSG00000160211
GAPDH	*GAPDH*	Expr_Chip	ENSG00000111640
GCM1	*GCM1*	GWAS	ENSG00000137270
GDI2	*GDI2*	Expr_Chip	ENSG00000057608
GLIPR2	*GLIPR2*	Expr_Chip	ENSG00000122694
GLMN	*GLMN*	Expr_Chip	ENSG00000174842
GLRX3	*GLRX3*	Expr_Chip	ENSG00000108010
GMPS	*GMPS*	Expr_Chip	ENSG00000163655
GNG5	*GNG5*	Expr_Chip	ENSG00000174021
GNL3	*GNL3*	Expr_Chip	ENSG00000163938
GPANK1	*GPANK1*	GWAS	ENSG00000204438
GPN3	*GPN3*	Expr_Chip	ENSG00000111231
GPT2	*GPT2*	Expr_Chip	ENSG00000166123
GSN	*GSN*	Expr_Chip	ENSG00000148180
GUCY1B3	*GUCY1B1*	Expr_Chip	ENSG00000061918
HADH	*HADH*	Expr_Chip	ENSG00000138796
HAT1	*HAT1*	Expr_Chip	ENSG00000128708
HAVCR2	*HAVCR2*	Expr_Articles	ENSG00000135077
HBA	*HBA1*	Expr_Chip	ENSG00000206172
HGF	*HGF*	GWAS	ENSG00000019991
HIF1A	*HIF1A*	Expr_Chip	ENSG00000100644
HK3	*HK3*	Expr_Chip	ENSG00000160883
HMGB1	*HMGB1*	Expr_Chip	ENSG00000189403
HMGN1	*HMGN1*	Expr_Chip	ENSG00000205581
HNMT	*HNMT*	Expr_Chip	ENSG00000150540
HRSP12	*RIDA*	Expr_Chip	ENSG00000132541
HSD17B10	*HSD17B10*	Expr_Chip	ENSG00000072506
HSD17B4	*HSD17B4*	Expr_Chip	ENSG00000133835
HSD3B7	*HSD3B7*	Expr_Chip	ENSG00000099377
HSPA14	*HSPA14*	Expr_Chip	ENSG00000284024
HSPA4	*HSPA4*	Expr_Chip	ENSG00000170606
HSPA9	*HSPA9*	Expr_Chip	ENSG00000113013
HSPB1	*HSPB1*	Expr_Chip	ENSG00000106211
IER3	*IER3*	GWAS	ENSG00000137331
IFI30	*IFI30*	Expr_Chip	ENSG00000216490
IFNG	*IFNG*	Expr_Articles	ENSG00000111537
IGF1R	*IGF1R*	Expr_Chip	ENSG00000140443
IGG1C		Expr_Chip	
IGHA1	*IGHA1*	Expr_Chip	ENSG00000211895
IGJ	*JCHAIN*	Expr_Chip	ENSG00000132465
IL10	*IL10*	Expr_Articles	ENSG00000136634
IL12A	*IL12A*	Expr_Articles	ENSG00000168811
IL12B	*IL12B*	Expr_Articles	ENSG00000113302
IL17R	*IL17RA*	Expr_Chip	ENSG00000177663
IL18	*IL18*	Expr_Chip	ENSG00000150782
IL1B	*IL1B*	Expr_Chip	ENSG00000125538
IL2	*IL2*	Expr_Articles	ENSG00000109471
IL2RA	*IL2RA*	Expr_Articles	ENSG00000134460
IL4	*IL4*	Expr_Articles	ENSG00000113520
IL6	*IL6*	Expr_Articles	ENSG00000136244
IL6R	*IL6R*	Expr_Chip	ENSG00000160712
IPCEF1	*IPCEF1*	Expr_Chip	ENSG00000074706
IPO4	*IPO4*	Expr_Chip	ENSG00000196497
ISG20	*ISG20*	Expr_Chip	ENSG00000172183
ITCH	*ITCH*	Expr_Chip	ENSG00000078747
ITGA6	*ITGA6*	Expr_Chip	ENSG00000091409
ITGAL	*ITGAL*	Expr_Chip	ENSG00000005844
ITGB7	*ITGB7*	Expr_Chip	ENSG00000139626

Gene Symbol (Bos taurus)	Gene Symbol (Homo sapiens)	Evidence	Ensembl Gene ID (human)
ITPR1	*ITPR1*	Expr_Chip	ENSG00000150995
ITPR3	*ITPR3*	Expr_Chip	ENSG00000096433
JDP2	*JDP2*	Expr_Chip	ENSG00000140044
JUN	*JUN*	Expr_Chip	ENSG00000177606
KAT6B	*KAT6B*	Expr_Chip	ENSG00000156650
KBTBD8	*KBTBD8*	Expr_Chip	ENSG00000163376
KIAA1598	*SHTN1*	Expr_Chip	ENSG00000187164
KIF2C	*KIF2C*	Expr_Chip	ENSG00000142945
KIR3DL3	*KIR3DL3*	Expr_Chip	ENSG00000242019
KLF4	*KLF4*	Expr_Chip	ENSG00000136826
KLKB1	*KLKB1*	Expr_Chip	ENSG00000164344
KLRC1	*KLRC1*	Expr_Chip	ENSG00000134545
KMT2C	*KMT2C*	Expr_Chip	ENSG00000055609
LAG3	*LAG3*	Expr_Articles	ENSG00000089692
LAMP1	*LAMP1*	Expr_Chip	ENSG00000185896
LAT	*LAT*	Expr_Chip	ENSG00000213658
LCK	*LCK*	Expr_Chip	ENSG00000182866
LCN2	*LCN2*	Expr_Chip	ENSG00000148346
LCP2	*LCP2*	Expr_Chip	ENSG00000043462
LEF1	*LEF1*	Expr_Chip	ENSG00000138795
LGALS1	*LGALS1*	Expr_Chip	ENSG00000100097
LGALS3	*LGALS3*	Expr_Chip	ENSG00000131981
LGALSL	*LGALSL*	Expr_Chip	ENSG00000119862
LGMN	*LGMN*	Expr_Chip	ENSG00000100600
LMO2	*LMO2*	Expr_Chip	ENSG00000135363
LOC101907861		GWAS	
LOC511103		GWAS	
LOC516273		GWAS	
LOC522315		GWAS	
LOC616942	*HLA-F*	GWAS	ENSG00000204642
LOC618064		GWAS	
LOC784787	*HCG4*	GWAS	ENSG00000176998
LOC784858		GWAS	
LOC785162		GWAS	
LPAR6	*LPAR6*	Expr_Chip	ENSG00000139679
LRRC25	*LRRC25*	Expr_Chip	ENSG00000175489
LTA	*LTA*	GWAS	ENSG00000226979
LTB	*LTB*	GWAS	ENSG00000227507
LUZP6	*LUZP6*	Expr_Chip	ENSG00000267697
LXN	*LXN*	Expr_Chip	ENSG00000079257
LY6G5B	*LY6G5B*	GWAS	ENSG00000240053
LY6G5C	*LY6G5C*	GWAS	ENSG00000204428
LYN	*LYN*	Expr_Chip	ENSG00000254087
LYZ2	*LYZ*	Expr_Chip	ENSG00000090382
MACROD1	*MACROD1*	Expr_Chip	ENSG00000133315
MAFB	*MAFB*	Expr_Chip	ENSG00000204103
MAP4K3	*MAP4K3*	Expr_Chip	ENSG00000011566
MAPKAPK3	*MAPKAPK3*	Expr_Chip	ENSG00000114738
MAT2A	*MAT2A*	Expr_Chip	ENSG00000168906
MAT2B	*MAT2B*	Expr_Chip	ENSG00000038274
MDH2	*MDH2*	Expr_Chip	ENSG00000146701
MEF2BNB	*BORCS8*	Expr_Chip	ENSG00000254901
MEX3A	*MEX3A*	Expr_Chip	ENSG00000254726
MIEN1	*MIEN1*	Expr_Chip	ENSG00000141741
MITF	*MITF*	Expr_Chip	ENSG00000187098
MKNK1	*MKNK1*	Expr_Chip	ENSG00000079277
MOSPD1	*MOSPD1*	Expr_Chip	ENSG00000101928
MRPL50	*MRPL50*	Expr_Chip	ENSG00000136897
MRPS18B	*MRPS18B*	Expr_Chip	ENSG00000204568
MS4A1	*MS4A1*	Expr_Chip	ENSG00000156738
MSH2	*MSH2*	Expr_Chip	ENSG00000095002
MTMR9	*MTMR9*	Expr_Chip	ENSG00000104643
MXD4	*MXD4*	Expr_Chip	ENSG00000123933
MYC	*MYC*	Expr_Articles	ENSG00000136997
MZB1	*MZB1*	Expr_Chip	ENSG00000170476
NACA	*NACA*	Expr_Chip	ENSG00000196531
NAE1	*NAE1*	Expr_Chip	ENSG00000159593
NAT1	*NAT1*	Expr_Chip	ENSG00000171428
NCF1	*NCF1*	Expr_Chip	ENSG00000158517
NCOA7	*NCOA7*	Expr_Chip	ENSG00000111912
NDEL1	*NDEL1*	Expr_Chip	ENSG00000166579

Gene Symbol (Bos taurus)	Gene Symbol (Homo sapiens)	Evidence	Ensembl Gene ID (human)
NDUFA4	*NDUFA4*	Expr_Chip	ENSG00000189043
NDUFB5	*NDUFB5*	Expr_Chip	ENSG00000136521
NEDD4L	*NEDD4L*	Expr_Chip	ENSG00000049759
NEU1	*NEU1*	GWAS	ENSG00000204386
NFAM1	*NFAM1*	Expr_Chip	ENSG00000235568
NFE2	*NFE2*	Expr_Chip	ENSG00000123405
NFKBIL1	*NFKBIL1*	GWAS	ENSG00000204498
NIFK	*NIFK*	Expr_Chip	ENSG00000155438
NMI	*NMI*	Expr_Chip	ENSG00000123609
NR2F6	*NR2F6*	Expr_Chip	ENSG00000160113
NRN1	*NRN1*	Expr_Chip	ENSG00000124785
NRSN1	*NRSN1*	GWAS	ENSG00000152954
NRSN2	*NRSN2*	Expr_Chip	ENSG00000125841
NUDT3	*NUDT3*	Expr_Chip	ENSG00000272325
OSBPL7	*OSBPL7*	Expr_Chip	ENSG00000006025
P4HB	*P4HB*	Expr_Chip	ENSG00000185624
PABPC4	*PABPC4*	Expr_Chip	ENSG00000090621
PACSIN1	*PACSIN1*	Expr_Chip	ENSG00000124507
PAIP2	*PAIP2*	Expr_Chip	ENSG00000120727
PARP8	*PARP8*	Expr_Chip	ENSG00000151883
PCK2	*PCK2*	Expr_Chip	ENSG00000100889
PCYOX1	*PCYOX1*	Expr_Chip	ENSG00000116005
PDCD1	*PDCD1*	Expr_Articles	ENSG00000188389
PDE2A	*PDE2A*	Expr_Chip	ENSG00000186642
PDE4A	*PDE4A*	Expr_Chip	ENSG00000065989
PEBP1	*PEBP1*	Expr_Chip	ENSG00000089220
PF4	*PF4*	Expr_Chip	ENSG00000163737
PGRMC1	*PGRMC1*	Expr_Chip	ENSG00000101856
PHF12	*PHF12*	Expr_Chip	ENSG00000109118
PHGDH	*PHGDH*	Expr_Chip	ENSG00000092621
PIGO	*PIGO*	Expr_Chip	ENSG00000165282
PKHD1	*PKHD1*	GWAS	ENSG00000170927
PKM	*PKM*	Expr_Chip	ENSG00000067225
PLA2G16	*PLA2G16*	Expr_Chip	ENSG00000176485
PLA2G7	*PLA2G7*	Expr_Chip	ENSG00000146070
PLBD1	*PLBD1*	Expr_Chip	ENSG00000121316
PNPLA1	*PNPLA1*	GWAS	ENSG00000180316
PPA2	*PPA2*	Expr_Chip	ENSG00000138777
PPM1E	*PPM1E*	Expr_Chip	ENSG00000175175
PPP1R3B	*PPP1R3B*	Expr_Chip	ENSG00000173281
PPP2CB	*PPP2CB*	Expr_Chip	ENSG00000104695
PRDM1	*PRDM1*	Expr_Chip	ENSG00000057657
PRIM1	*PRIM1*	Expr_Articles	ENSG00000198056
PRR3	*PRR3*	GWAS	ENSG00000204576
PRRC2A	*PRRC2A*	GWAS	ENSG00000204469
PTCD3	*PTCD3*	Expr_Chip	ENSG00000132300
PTGER4	*PTGER4*	Expr_Chip	ENSG00000171522
PTK2B	*PTK2B*	Expr_Chip	ENSG00000120899
PYCARD	*PYCARD*	Expr_Chip	ENSG00000103490
QSOX1	*QSOX1*	Expr_Chip	ENSG00000116260
RABGAP1L	*RABGAP1L*	Expr_Chip	ENSG00000152061
RARA	*RARA*	Expr_Chip	ENSG00000131759
RASGEF1B	*RASGEF1B*	Expr_Chip	ENSG00000138670
RBBP7	*RBBP7*	Expr_Chip	ENSG00000102054
RBM34	*RBM34*	Expr_Chip	ENSG00000188739
RGS2	*RGS2*	Expr_Chip	ENSG00000116741
RHBDL1	*RHBDL1*	Expr_Chip	ENSG00000103269
RHNO1	*RHNO1*	Expr_Chip	ENSG00000171792
RHOQ	*RHOQ*	Expr_Chip	ENSG00000119729
RNASE6	*RNASE6*	Expr_Chip	ENSG00000169413
RNF130	*RNF130*	Expr_Chip	ENSG00000113269
RPF1	*RPF1*	Expr_Chip	ENSG00000117133
RPL19	*RPL19*	Expr_Chip	ENSG00000108298
RRP7A	*RRP7A*	Expr_Chip	ENSG00000189306
RSRC1	*RSRC1*	Expr_Chip	ENSG00000174891
RTN4	*RTN4*	Expr_Chip	ENSG00000115310
S100A10	*S100A10*	Expr_Chip	ENSG00000197747
S100A4	*S100A4*	Expr_Chip	ENSG00000196154
S100A8	*S100A8*	Expr_Chip	ENSG00000143546
SDCBP	*SDCBP*	Expr_Chip	ENSG00000137575
SDHA	*SDHA*	Expr_Chip	ENSG00000073578

Gene Symbol (Bos taurus)	Gene Symbol (Homo sapiens)	Evidence	Ensembl Gene ID (human)
SEC31A	*SEC31A*	Expr_Chip	ENSG00000138674
SELL	*SELL*	Expr_Chip	ENSG00000188404
SELPLG	*SELPLG*	Expr_Chip	ENSG00000110876
SFTA2	*SFTA2*	GWAS	ENSG00000196260
SH3GLB2	*SH3GLB2*	Expr_Chip	ENSG00000148341
SIRPA	*SIRPA*	Expr_Chip	ENSG00000198053
SIRT5	*SIRT5*	Expr_Chip	ENSG00000124523
SLAMF1	*SLAMF1*	Expr_Chip	ENSG00000117090
SLC31A2	*SLC31A2*	Expr_Chip	ENSG00000136867
SLC35F2	*SLC35F2*	Expr_Chip	ENSG00000110660
SLC40A1	*SLC40A1*	Expr_Chip	ENSG00000138449
SLC44A1	*SLC44A1*	Expr_Chip	ENSG00000070214
SLC44A4	*SLC44A4*	GWAS	ENSG00000204385
SLC46A2	*SLC46A2*	Expr_Chip	ENSG00000119457
SLC4A10	*SLC4A10*	Expr_Chip	ENSG00000144290
SLC7A5	*SLC7A5*	Expr_Chip	ENSG00000103257
SLC7A7	*SLC7A7*	Expr_Chip	ENSG00000155465
SMIM10	*SMIM10*	Expr_Chip	ENSG00000184785
SMIM20	*SMIM20*	Expr_Chip	ENSG00000250317
SNRNP70	*SNRNP70*	Expr_Chip	ENSG00000104852
SNRPA1	*SNRPA1*	Expr_Chip	ENSG00000131876
SNRPD3	*SNRPD3*	Expr_Chip	ENSG00000100028
SNX10	*SNX10*	Expr_Chip	ENSG00000086300
SOAT1	*SOAT1*	Expr_Chip	ENSG00000057252
SORCS1	*SORCS1*	Expr_Chip	ENSG00000108018
SORCS3	*SORCS3*	Expr_Chip	ENSG00000156395
SORL1	*SORL1*	Expr_Chip	ENSG00000137642
SOX5	*SOX5*	Expr_Chip	ENSG00000134532
SP100	*SP100*	Expr_Chip	ENSG00000067066
SPIB	*SPIB*	Expr_Chip	ENSG00000269404
SPSB2	*SPSB2*	Expr_Chip	ENSG00000111671
SRSF9	*SRSF9*	Expr_Chip	ENSG00000111786
STARD7	*STARD7*	Expr_Chip	ENSG00000084090
STAT4	*STAT4*	Expr_Chip	ENSG00000138378
STK40	*STK40*	Expr_Chip	ENSG00000196182
STOM	*STOM*	Expr_Chip	ENSG00000148175
STX7	*STX7*	Expr_Chip	ENSG00000079950
SULT1A1	*SULT1A1*	Expr_Chip	ENSG00000196502
SUMO2	*SUMO2*	Expr_Chip	ENSG00000188612
SYK	*SYK*	Expr_Articles Expr_Chip	ENSG00000165025
SYNCRIP	*SYNCRIP*	Expr_Chip	ENSG00000135316
SYNGR2	*SYNGR2*	Expr_Chip	ENSG00000108639
TALDO1	*TALDO1*	Expr_Chip	ENSG00000177156
TBC1D2B	*TBC1D2B*	Expr_Chip	ENSG00000167202
TCF4	*TCF4*	Expr_Chip	ENSG00000196628
TEP1	*TEP1*	Expr_Chip	ENSG00000129566
TERF2	*TERF2*	Expr_Chip	ENSG00000132604
TES	*TES*	Expr_Chip	ENSG00000135269
TFAP2D	*TFAP2D*	GWAS	ENSG00000008197
TGFBI	*TGFBI*	Expr_Chip	ENSG00000120708
THAP9	*THAP9*	Expr_Chip	ENSG00000168152
THBD	*THBD*	Expr_Chip	ENSG00000178726
TIMP1	*TIMP1*	Expr_Chip	ENSG00000102265
TIMP2	*TIMP2*	Expr_Chip	ENSG00000035862
TK1	*TK1*	Expr_Articles	ENSG00000167900
TKT	*TKT*	Expr_Chip	ENSG00000163931
TLR3	*TLR3*	Expr_Articles	ENSG00000164342
TLR7	*TLR7*	Expr_Articles	ENSG00000196664
TLR8	*TLR8*	Expr_Articles	ENSG00000101916
TLR9	*TLR9*	Expr_Articles	ENSG00000239732
TMBIM6	*TMBIM6*	Expr_Chip	ENSG00000139644
TMEM134	*TMEM134*	Expr_Chip	ENSG00000172663
TNF	*TNF*	GWAS Knockout Expr_Articles Alleles	ENSG00000232810
TNFRSF1B	*TNFRSF1B*	Expr_Articles	ENSG00000028137
TNFSF13	*TNFSF13*	Expr_Chip	ENSG00000161955
TNXB	*TNXB*	GWAS	ENSG00000168477
TPD52	*TPD52*	Expr_Chip	ENSG00000076554
TRAM2	*TRAM2*	GWAS	ENSG00000065308
TRIM31	*TRIM31*	GWAS	ENSG00000204616
TRIM40	*TRIM40*	GWAS	ENSG00000204614

Gene Symbol (Bos taurus)	Gene Symbol (Homo sapiens)	Evidence	Ensembl Gene ID (human)
TRIM45	*TRIM45*	GWAS	ENSG00000134253
TRMT112	*TRMT112*	Expr_Chip	ENSG00000173113
TRMT5	*TRMT5*	Expr_Chip	ENSG00000126814
TSPAN13	*TSPAN13*	Expr_Chip	ENSG00000106537
TSPAN17	*TSPAN17*	Expr_Chip	ENSG00000048140
TUBB	*TUBB*	GWAS	ENSG00000196230
TUBB4B	*TUBB4B*	Expr_Chip	ENSG00000188229
TXK	*TXK*	Expr_Chip	ENSG00000074966
TYROBP	*TYROBP*	Expr_Chip	ENSG00000011600
UAP1	*UAP1*	Expr_Chip	ENSG00000117143
UBA2	*UBA2*	Expr_Chip	ENSG00000126261
USP11	*USP11*	Expr_Chip	ENSG00000102226
VAV3	*VAV3*	Expr_Chip	ENSG00000134215
VBP1	*VBP1*	Expr_Chip	ENSG00000155959
VIM	*VIM*	Expr_Chip	ENSG00000026025
WDFY4	*WDFY4*	Expr_Chip	ENSG00000128815
WIPF1	*WIPF1*	Expr_Chip	ENSG00000115935
WLS	*WLS*	Expr_Chip	ENSG00000116729
XBP1	*XBP1*	Expr_Chip	ENSG00000100219
YPEL5	*YPEL5*	Expr_Chip	ENSG00000119801
YWHAG	*YWHAG*	Expr_Chip	ENSG00000170027
ZBTB20	*ZBTB20*	GWAS	ENSG00000181722
ZBTB32	*ZBTB32*	Expr_Chip	ENSG00000011590
ZCCHC11	*TUT4*	Expr_Chip	ENSG00000134744
ZMYM6	*ZMYM6*	Expr_Chip	ENSG00000163867
ZNF106	*ZNF106*	Expr_Chip	ENSG00000103994

Таблица S8.

Перепредставленные (FDR<0.05, Fold Enrichment>3) термины из словаря биологических процессов (GOTERM_BP_ALL) базы Gene Ontology, выявленные при анализе списка из 446 генов системой DAVID.

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0045349~interferon-alpha biosynthetic process	5	1.1	2.4E-06	*NMI, TLR3, TLR7, TLR8, TLR9*	37.4	1.2E-02	5.3E-05	4.7E-03
GO:0045354~regulation of interferon-alpha biosynthetic process	5	1.1	2.4E-06	*NMI, TLR3, TLR7, TLR8, TLR9*	37.4	1.2E-02	5.3E-05	4.7E-03
GO:0042095~interferon-gamma biosynthetic process	9	1.9	6.2E-10	*IL18, IL12A, TLR3, IL12B, FOXP3, TLR7, TLR8, IL10, TLR9*	24.0	3.1E-06	3.3E-08	1.2E-06
GO:0045072~regulation of interferon-gamma biosynthetic process	7	1.5	2.8E-07	*TLR3, IL12B, FOXP3, TLR7, TLR8, IL10, TLR9*	21.8	1.4E-03	8.1E-06	5.3E-04
GO:0002643~regulation of tolerance induction	6	1.3	9.0E-06	*HMGB1, IL2RA, CD3E, ITCH, FOXP3, PDCD1*	18.7	4.3E-02	1.6E-04	1.7E-02
GO:0002507~tolerance induction	6	1.3	2.2E-05	*IL2RA, LYN, CD3E, ITCH, FOXP3, PDCD1*	16.0	1.0E-01	3.5E-04	4.1E-02
GO:0042104~positive regulation of activated T cell proliferation	8	1.7	1.1E-06	*IL4, IL2RA, IL18, IL12A, PYCARD, IL12B, SLAMF1, IL2*	13.6	5.5E-03	2.6E-05	2.1E-03
GO:0050798~activated T cell proliferation	10	2.1	7.5E-08	*IL4, IL2RA, FYN, IL18, CD274, IL12A, PYCARD, IL12B, SLAMF1, IL2*	12.1	3.7E-04	2.4E-06	1.4E-04
GO:0046006~regulation of activated T cell proliferation	9	1.9	6.3E-07	*IL4, IL2RA, IL18, CD274, IL12A, PYCARD, IL12B, SLAMF1, IL2*	11.6	3.1E-03	1.6E-05	1.2E-03
GO:0032729~positive regulation of interferon-gamma production	16	3.4	3.4E-12	*CD244, TNF, CD3E, IL18, TLR3, SLAMF1, TLR7, TLR8, TLR9, CD2, IL12A, PYCARD, TXK, IL12B, LTA, IL2*	11.5	1.7E-08	3.3E-10	6.5E-09
GO:0046635~positive regulation of alpha-beta T cell activation	12	2.6	3.6E-09	*CD244, IL6, CD3E, IL18, IFNG, IL12A, ANXA1, AP3D1, RARA, IL12B, FOXP3, SYK*	11.5	1.8E-05	1.6E-07	6.9E-06
GO:0032649~regulation of interferon-gamma production	22	4.7	2.7E-16	*CD244, TNF, CD3E, IL18, TLR3, FOXP3, SLAMF1, TLR7, IL10, TLR8, TLR9, CD96, C1QBP, CD274, CD2, PYCARD, IL12A, RARA, TXK, IL12B, LTA, IL2*	11.0	1.1E-12	6.5E-14	4.2E-13
GO:0032609~interferon-gamma production	22	4.7	9.8E-16	*CD244, TNF, CD3E, IL18, TLR3, FOXP3, SLAMF1, TLR7, IL10, TLR8, TLR9, CD96, C1QBP, CD274, CD2, PYCARD, IL12A, RARA, TXK, IL12B, LTA, IL2*	10.4	5.0E-12	2.6E-13	1.9E-12
GO:0042089~cytokine biosynthetic process	22	4.7	1.3E-15	*IL4, IL6, CARD9, TNF, NMI, CD3E, IL18, TLR3, FOXP3, TLR7, IL10, TLR8, TLR9, IFNG, IL12A, HSPB1, GLMN, IL12B, LTB, KLF4, LAG3, SYK*	10.3	6.1E-12	3.0E-13	2.3E-12
GO:0046634~regulation of alpha-beta T cell activation	14	3.0	5.4E-10	*IL4, CD244, IL6, CD3E, IL18, IFNG, IL12A, ANXA1, AP3D1, RARA, ITCH, IL12B, FOXP3, SYK*	10.3	2.7E-06	2.9E-08	1.0E-06
GO:0050853~B cell receptor signaling pathway	9	1.9	1.8E-06	*VAV3, CD19, LYN, LCK, CTLA4, CD79B, CD79A, NFAM1, SYK*	10.2	9.1E-03	4.2E-05	3.5E-03
GO:0032945~negative regulation of	11	2.4	8.7E-08	*IL2RA, LYN, CD274, CTLA4, GLMN, PRDM1,*	10.0	4.3E-04	2.7E-06	1.7E-04

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
mononuclear cell proliferation				*ITCH, FOXP3, ATM, IL10, IL2*				
GO:0050672~negative regulation of lymphocyte proliferation	11	2.4	8.7E-08	*IL2RA, LYN, CD274, CTLA4, GLMN, PRDM1, ITCH, FOXP3, ATM, IL10, IL2*	10.0	4.3E-04	2.7E-06	1.7E-04
GO:0042035~regulation of cytokine biosynthetic process	20	4.3	5.8E-14	*IL4, IL6, CARD9, NMI, TNF, CD3E, TLR3, FOXP3, TLR7, IL10, TLR8, TLR9, IFNG, HSPB1, GLMN, IL12B, LTB, KLF4, LAG3, SYK*	10.0	2.9E-10	8.8E-12	1.1E-10
GO:0042108~positive regulation of cytokine biosynthetic process	13	2.8	4.1E-09	*IL4, TNF, CD3E, TLR3, TLR7, TLR8, TLR9, IFNG, GLMN, HSPB1, IL12B, LTB, SYK*	9.9	2.1E-05	1.8E-07	7.9E-06
GO:0042107~cytokine metabolic process	22	4.7	2.8E-15	*IL4, IL6, CARD9, TNF, NMI, CD3E, IL18, TLR3, FOXP3, TLR7, IL10, TLR8, TLR9, IFNG, IL12A, HSPB1, GLMN, IL12B, LTB, KLF4, LAG3, SYK*	9.9	1.4E-11	6.0E-13	5.3E-12
GO:0002294~CD4-positive, alpha-beta T cell differentiation involved in immune response	10	2.1	5.1E-07	*IL4, IL6, PTGER4, IFNG, IL12A, ANXA1, LEF1, RARA, IL12B, FOXP3*	9.8	2.5E-03	1.4E-05	9.8E-04
GO:0070664~negative regulation of leukocyte proliferation	11	2.4	1.1E-07	*IL2RA, LYN, CD274, CTLA4, GLMN, PRDM1, ITCH, FOXP3, ATM, IL10, IL2*	9.8	5.5E-04	3.3E-06	2.1E-04
GO:0002293~alpha-beta T cell differentiation involved in immune response	10	2.1	6.5E-07	*IL4, IL6, PTGER4, IFNG, IL12A, ANXA1, LEF1, RARA, IL12B, FOXP3*	9.6	3.2E-03	1.7E-05	1.2E-03
GO:0002287~alpha-beta T cell activation involved in immune response	10	2.1	6.5E-07	*IL4, IL6, PTGER4, IFNG, IL12A, ANXA1, LEF1, RARA, IL12B, FOXP3*	9.6	3.2E-03	1.7E-05	1.2E-03
GO:0032755~positive regulation of interleukin-6 production	14	3.0	1.9E-09	*HMGB1, IL6, ZBTB20, CARD9, ZCCHC11, TNF, ADORA2B, XBP1, IFNG, PYCARD, TLR3, IL6R, TLR7, TLR9*	9.3	9.4E-06	9.1E-08	3.6E-06
GO:0042531~positive regulation of tyrosine phosphorylation of STAT protein	10	2.1	8.2E-07	*IL4, IL6, LYN, FYN, IL18, IFNG, IL12A, IL12B, IL6R, IL2*	9.3	4.1E-03	2.0E-05	1.6E-03
GO:0032608~interferon-beta production	9	1.9	3.8E-06	*HMGB1, ZBTB20, NMI, FLOT1, PYCARD, TLR3, TLR7, TLR8, TLR9*	9.3	1.8E-02	7.6E-05	7.1E-03
GO:0032655~regulation of interleukin-12 production	9	1.9	3.8E-06	*ARRB2, C1QBP, IFNG, TLR3, IL12B, SLAMF1, LTB, IL10, TLR9*	9.3	1.8E-02	7.6E-05	7.1E-03
GO:0002637~regulation of immunoglobulin production	10	2.1	1.0E-06	*IL4, IL6, TNF, XBP1, TMBIM6, MZB1, IFNG, TNFSF13, FOXP3, IL2*	9.1	5.1E-03	2.5E-05	2.0E-03
GO:0032722~positive regulation of chemokine production	10	2.1	1.0E-06	*IL4, IL6, TNF, ADORA2B, IFNG, PYCARD, TLR3, IL6R, ADIPOQ, TLR7*	9.1	5.1E-03	2.5E-05	2.0E-03
GO:0032648~regulation of interferon-beta production	9	1.9	4.7E-06	*HMGB1, ZBTB20, NMI, FLOT1, PYCARD, TLR3, TLR7, TLR8, TLR9*	9.1	2.3E-02	9.1E-05	8.9E-03
GO:0042093~T-helper cell differentiation	9	1.9	4.7E-06	*IL4, IL6, PTGER4, IL12A, ANXA1, LEF1, RARA, IL12B, FOXP3*	9.1	2.3E-02	9.1E-05	8.9E-03
GO:0032760~positive regulation of tumor necrosis factor production	10	2.1	1.3E-06	*HMGB1, ZBTB20, CARD9, IFNG, CD2, PYCARD, HSPB1, TLR3, IL12B, TLR9*	8.9	6.3E-03	3.0E-05	2.4E-03
GO:0032615~interleukin-12 production	9	1.9	5.8E-06	*ARRB2, C1QBP, IFNG, TLR3, IL12B, SLAMF1, LTB, IL10, TLR9*	8.8	2.8E-02	1.1E-04	1.1E-02
GO:1903557~positive regulation of	10	2.1	1.6E-06	*HMGB1, ZBTB20, CARD9, IFNG, CD2, PYCARD,*	8.7	7.8E-03	3.7E-05	3.0E-03

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
tumor necrosis factor superfamily cytokine production				*HSPB1, TLR3, IL12B, TLR9*				
GO:0042102~positive regulation of T cell proliferation	16	3.4	3.6E-10	*IL4, CD244, IL6, IL2RA, AIF1, CD3E, IL18, ANXA1, FOXP3, SLAMF1, IFNG, IL12A, PYCARD, IL12B, SYK, IL2*	8.5	1.8E-06	2.1E-08	6.8E-07
GO:0002292~T cell differentiation involved in immune response	10	2.1	1.9E-06	*IL4, IL6, PTGER4, IFNG, IL12A, ANXA1, LEF1, RARA, IL12B, FOXP3*	8.5	9.6E-03	4.3E-05	3.7E-03
GO:0032675~regulation of interleukin-6 production	19	4.1	7.4E-12	*HMGB1, ZBTB20, IL6, CARD9, TNF, ZCCHC11, ADORA2B, TLR3, IL6R, HGF, FOXP3, SLAMF1, TLR7, IL10, TLR9, ARRB2, XBP1, IFNG, PYCARD*	8.4	3.7E-08	6.4E-10	1.4E-08
GO:1904894~positive regulation of STAT cascade	12	2.6	1.4E-07	*IL4, IL6, LYN, PTK2B, FYN, IL18, IFNG, IL12A, IL12B, IL6R, IL10, IL2*	8.3	7.2E-04	4.3E-06	2.7E-04
GO:0046427~positive regulation of JAK-STAT cascade	12	2.6	1.4E-07	*IL4, IL6, LYN, PTK2B, FYN, IL18, IFNG, IL12A, IL12B, IL6R, IL10, IL2*	8.3	7.2E-04	4.3E-06	2.7E-04
GO:0032479~regulation of type I interferon production	10	2.1	2.4E-06	*HMGB1, ZBTB20, NMI, FLOT1, PYCARD, TLR3, TLR7, TLR8, TLR9, SYK*	8.3	1.2E-02	5.2E-05	4.5E-03
GO:0032640~tumor necrosis factor production	17	3.6	1.8E-10	*HMGB1, ZBTB20, CARD9, TLR3, FOXP3, SLAMF1, ADIPOQ, NFKBIL1, IL10, TLR9, ARRB2, IFNG, CD2, PYCARD, HSPB1, RARA, IL12B*	8.1	9.1E-07	1.2E-08	3.5E-07
GO:0042509~regulation of tyrosine phosphorylation of STAT protein	10	2.1	2.9E-06	*IL4, IL6, LYN, FYN, IL18, IFNG, IL12A, IL12B, IL6R, IL2*	8.1	1.4E-02	6.1E-05	5.5E-03
GO:1903555~regulation of tumor necrosis factor superfamily cytokine production	18	3.9	5.0E-11	*HMGB1, ZBTB20, CARD9, TLR3, FOXP3, SLAMF1, ADIPOQ, NFKBIL1, IL10, TLR9, ARRB2, CD274, IFNG, CD2, PYCARD, HSPB1, RARA, IL12B*	8.1	2.5E-07	3.6E-09	9.6E-08
GO:0032635~interleukin-6 production	19	4.1	1.4E-11	*HMGB1, ZBTB20, IL6, CARD9, TNF, ZCCHC11, ADORA2B, TLR3, IL6R, HGF, FOXP3, SLAMF1, TLR7, IL10, TLR9, ARRB2, XBP1, IFNG, PYCARD*	8.1	6.8E-08	1.1E-09	2.6E-08
GO:0048659~smooth muscle cell proliferation	9	1.9	1.3E-05	*IL6, TNF, AIF1, ANG, IFNG, IL12A, IL12B, IL6R, ADIPOQ*	8.0	6.1E-02	2.1E-04	2.4E-02
GO:0032677~regulation of interleukin-8 production	10	2.1	3.5E-06	*CD244, TNF, CD2, ANXA1, PYCARD, TLR3, ADIPOQ, TLR7, KLF4, TLR8*	7.9	1.7E-02	7.1E-05	6.6E-03
GO:0043367~CD4-positive, alpha-beta T cell differentiation	10	2.1	3.5E-06	*IL4, IL6, PTGER4, IFNG, IL12A, ANXA1, LEF1, RARA, IL12B, FOXP3*	7.9	1.7E-02	7.1E-05	6.6E-03
GO:0071706~tumor necrosis factor superfamily cytokine production	18	3.9	7.5E-11	*HMGB1, ZBTB20, CARD9, TLR3, FOXP3, SLAMF1, ADIPOQ, NFKBIL1, IL10, TLR9, ARRB2, CD274, IFNG, CD2, PYCARD, HSPB1, RARA, IL12B*	7.9	3.7E-07	5.3E-09	1.4E-07
GO:0032637~interleukin-8 production	11	2.4	9.5E-07	*CD244, TNF, CHI3L1, CD2, ANXA1, PYCARD, TLR3, ADIPOQ, TLR7, KLF4, TLR8*	7.9	4.7E-03	2.3E-05	1.8E-03
GO:0032680~regulation of tumor necrosis factor production	17	3.6	3.3E-10	*HMGB1, ZBTB20, CARD9, TLR3, FOXP3, SLAMF1, ADIPOQ, NFKBIL1, IL10, TLR9, ARRB2, IFNG, CD2, PYCARD, HSPB1, RARA, IL12B*	7.8	1.7E-06	2.0E-08	6.3E-07

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0030888~regulation of B cell proliferation	10	2.1	4.2E-06	*IL4, VAV3, LYN, MZB1, IFNG, CTLA4, PRDM1, ATM, IL10, IL2*	7.8	2.0E-02	8.3E-05	7.9E-03
GO:0048660~regulation of smooth muscle cell proliferation	9	1.9	1.8E-05	*IL6, TNF, AIF1, ANG, IFNG, IL12A, IL12B, IL6R, ADIPOQ*	7.6	8.7E-02	3.0E-04	3.5E-02
GO:0032606~type I interferon production	10	2.1	5.0E-06	*HMGB1, ZBTB20, NMI, FLOT1, PYCARD, TLR3, TLR7, TLR8, TLR9, SYK*	7.6	2.4E-02	9.5E-05	9.5E-03
GO:0045582~positive regulation of T cell differentiation	10	2.1	5.9E-06	*IL4, IL6, XBP1, IFNG, IL12A, ANXA1, AP3D1, RARA, FOXP3, SYK*	7.5	2.9E-02	1.1E-04	1.1E-02
GO:0035710~CD4-positive, alpha-beta T cell activation	10	2.1	5.9E-06	*IL4, IL6, PTGER4, IFNG, IL12A, ANXA1, LEF1, RARA, IL12B, FOXP3*	7.5	2.9E-02	1.1E-04	1.1E-02
GO:0002705~positive regulation of leukocyte mediated immunity	14	3.0	4.8E-08	*IL4, STX7, TNF, ADORA2B, TNFSF13, FOXP3, LAMP1, IFNG, IL12A, IL12B, LTA, LAG3, SYK, IL2*	7.3	2.4E-04	1.6E-06	9.2E-05
GO:0002708~positive regulation of lymphocyte mediated immunity	12	2.6	6.3E-07	*IL4, LAMP1, STX7, TNF, IFNG, IL12A, TNFSF13, IL12B, FOXP3, LTA, LAG3, IL2*	7.2	3.1E-03	1.7E-05	1.2E-03
GO:0050864~regulation of B cell activation	17	3.6	1.2E-09	*IL4, IL6, VAV3, LYN, MZB1, CTLA4, TNFSF13, NFAM1, FOXP3, IL10, ATM, TLR9, XBP1, IFNG, PRDM1, SYK, IL2*	7.2	6.0E-06	5.9E-08	2.3E-06
GO:0042129~regulation of T cell proliferation	20	4.3	3.0E-11	*IL4, CD244, IL6, IL2RA, LGALS3, AIF1, CD3E, IL18, ANXA1, FOXP3, SLAMF1, CD274, IFNG, PYCARD, IL12A, GLMN, IL12B, ITCH, SYK, IL2*	7.2	1.5E-07	2.2E-09	5.7E-08
GO:0007260~tyrosine phosphorylation of STAT protein	10	2.1	8.3E-06	*IL4, IL6, LYN, FYN, IL18, IFNG, IL12A, IL12B, IL6R, IL2*	7.2	4.1E-02	1.5E-04	1.6E-02
GO:0002275~myeloid cell activation involved in immune response	10	2.1	8.3E-06	*CD84, IL4, HMGB1, ADORA2B, LYN, PYCARD, SLAMF1, ANXA3, TYROBP, SYK*	7.2	4.1E-02	1.5E-04	1.6E-02
GO:0002698~negative regulation of immune effector process	13	2.8	2.1E-07	*CD84, IL4, CD96, A2M, TNF, ARRB2, C1QBP, TMBIM6, ANXA1, ITCH, FOXP3, SLAMF1, IL10*	7.1	1.0E-03	6.1E-06	3.9E-04
GO:0002700~regulation of production of molecular mediator of immune response	16	3.4	5.2E-09	*IL4, IL6, CD244, TNF, TMBIM6, MZB1, TLR3, TNFSF13, FOXP3, SLAMF1, IL10, TLR9, CD96, XBP1, IFNG, IL2*	7.1	2.6E-05	2.2E-07	9.9E-06
GO:0050670~regulation of lymphocyte proliferation	27	5.8	6.0E-15	*CD244, AIF1, IL18, IL10, IFNG, PYCARD, ITCH, SYK, IL4, IL6, VAV3, IL2RA, LYN, LGALS3, CD3E, MZB1, CTLA4, ANXA1, FOXP3, SLAMF1, ATM, CD274, IL12A, GLMN, IL12B, PRDM1, IL2*	7.1	3.0E-11	1.2E-12	1.1E-11
GO:0002703~regulation of leukocyte mediated immunity	22	4.7	3.2E-12	*IL4, HMGB1, STX7, TNF, ADORA2B, LYN, TLR3, TNFSF13, FOXP3, SLAMF1, TLR9, CD84, CD96, LAMP1, ARRB2, IFNG, IL12A, IL12B, LAG3, LTA, SYK, IL2*	7.1	1.6E-08	3.2E-10	6.2E-09
GO:0032602~chemokine production	11	2.4	2.7E-06	*IL4, IL6, TNF, ADORA2B, IFNG, PYCARD, TLR3, IL6R, ADIPOQ, TLR7, KLF4*	7.1	1.3E-02	5.9E-05	5.2E-03
GO:0032944~regulation of mononuclear cell proliferation	27	5.8	7.1E-15	*CD244, AIF1, IL18, IL10, IFNG, PYCARD, ITCH, SYK, IL4, IL6, VAV3, IL2RA, LYN, LGALS3, CD3E, MZB1, CTLA4, ANXA1, FOXP3, SLAMF1, ATM, CD274, IL12A, GLMN, IL12B, PRDM1, IL2*	7.1	3.5E-11	1.4E-12	1.4E-11
GO:0002312~B cell activation	10	2.1	9.8E-06	*IL4, HMGB1, XBP1, PTK2B, MSH2, LGALS1,*	7.0	4.7E-02	1.7E-04	1.9E-02

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
involved in immune response				*IFNG, TNFSF13, FOXP3, IL2*				
GO:0050715~positive regulation of cytokine secretion	13	2.8	2.5E-07	*HMGB1, CD244, TNF, PTGER4, SLAMF1, IL10, XBP1, CD274, IFNG, PYCARD, CD2, GLMN, SYK*	7.0	1.2E-03	7.2E-06	4.7E-04
GO:1903039~positive regulation of leukocyte cell-cell adhesion	24	5.1	3.5E-13	*IL4, CD244, IL6, IL2RA, TNF, AIF1, CD3E, IL18, LGALS1, ANXA1, FOXP3, SLAMF1, CD44, XBP1, CD274, LCK, IFNG, PYCARD, IL12A, AP3D1, RARA, IL12B, SYK, IL2*	7.0	1.7E-09	3.7E-11	6.6E-10
GO:0002821~positive regulation of adaptive immune response	12	2.6	8.8E-07	*IL4, STX7, TNF, IFNG, IL12A, ANXA1, PYCARD, TNFSF13, IL12B, FOXP3, LTA, IL2*	7.0	4.4E-03	2.2E-05	1.7E-03
GO:0032642~regulation of chemokine production	11	2.4	3.2E-06	*IL4, IL6, TNF, ADORA2B, IFNG, PYCARD, TLR3, IL6R, ADIPOQ, TLR7, KLF4*	7.0	1.6E-02	6.6E-05	6.1E-03
GO:0046631~alpha-beta T cell activation	16	3.4	1.0E-08	*IL4, CD244, IL6, PTGER4, CD3E, IL18, ANXA1, LEF1, FOXP3, IFNG, IL12A, AP3D1, RARA, IL12B, ITCH, SYK*	6.8	5.0E-05	4.0E-07	1.9E-05
GO:0070663~regulation of leukocyte proliferation	27	5.8	2.0E-14	*CD244, AIF1, IL18, IL10, IFNG, PYCARD, ITCH, SYK, IL4, IL6, VAV3, IL2RA, LYN, LGALS3, CD3E, MZB1, CTLA4, ANXA1, FOXP3, SLAMF1, ATM, CD274, IL12A, GLMN, IL12B, PRDM1, IL2*	6.8	9.9E-11	3.4E-12	3.8E-11
GO:0002699~positive regulation of immune effector process	22	4.7	8.9E-12	*IL4, CD244, IL6, STX7, TNF, ADORA2B, LYN, MZB1, ANXA1, TNFSF13, FOXP3, CD84, LAMP1, XBP1, IFNG, IL12A, RARA, IL12B, LAG3, LTA, SYK, IL2*	6.7	4.4E-08	7.7E-10	1.7E-08
GO:0045621~positive regulation of lymphocyte differentiation	11	2.4	4.4E-06	*IL4, IL6, XBP1, IFNG, IL12A, ANXA1, AP3D1, RARA, PRDM1, FOXP3, SYK*	6.7	2.1E-02	8.6E-05	8.3E-03
GO:0002706~regulation of lymphocyte mediated immunity	16	3.4	1.2E-08	*IL4, HMGB1, STX7, TNF, TNFSF13, FOXP3, SLAMF1, LAMP1, CD96, ARRB2, IFNG, IL12A, IL12B, LTA, LAG3, IL2*	6.7	5.9E-05	4.6E-07	2.3E-05
GO:0050870~positive regulation of T cell activation	22	4.7	1.1E-11	*IL4, CD244, IL6, IL2RA, AIF1, CD3E, IL18, LGALS1, ANXA1, FOXP3, SLAMF1, XBP1, CD274, LCK, IFNG, PYCARD, IL12A, AP3D1, RARA, IL12B, SYK, IL2*	6.7	5.2E-08	8.7E-10	2.0E-08
GO:0002824~positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	11	2.4	5.1E-06	*IL4, STX7, TNF, IFNG, IL12A, ANXA1, TNFSF13, IL12B, FOXP3, LTA, IL2*	6.6	2.5E-02	9.7E-05	9.7E-03
GO:0046632~alpha-beta T cell differentiation	12	2.6	1.7E-06	*IL4, IL6, PTGER4, IFNG, IL12A, ANXA1, LEF1, AP3D1, RARA, IL12B, FOXP3, SYK*	6.6	8.2E-03	3.8E-05	3.1E-03
GO:0022409~positive regulation of cell-cell adhesion	26	5.6	1.4E-13	*IL4, CD244, IL6, TNF, IL2RA, CD3E, AIF1, LGALS1, IL18, FLOT1, ANXA1, FOXP3, SLAMF1, ITGA6, CD44, XBP1, IFNG, LCK, CD274, PYCARD, IL12A, AP3D1, RARA, IL12B, IL2, SYK*	6.6	6.9E-10	1.8E-11	2.6E-10
GO:0050671~positive regulation of lymphocyte proliferation	17	3.6	7.2E-09	*IL4, CD244, IL6, IL2RA, VAV3, AIF1, CD3E, IL18, ANXA1, FOXP3, SLAMF1, IFNG, PYCARD, IL12A, IL12B, SYK, IL2*	6.4	3.6E-05	3.0E-07	1.4E-05

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0001818~negative regulation of cytokine production	26	5.6	2.6E-13	*NMI, TNF, CD2AP, IL10, TLR9, CD96, IFNG, PYCARD, RARA, LAG3, IL6, PTGER4, ANXA1, LEF1, HGF, FOXP3, SLAMF1, ADIPOQ, NFKBIL1, CD84, C1QBP, ARRB2, CD274, IL12A, IL12B, KLF4*	6.4	1.3E-09	2.9E-11	5.0E-10
GO:0032946~positive regulation of mononuclear cell proliferation	17	3.6	8.4E-09	*IL4, CD244, IL6, IL2RA, VAV3, AIF1, CD3E, IL18, ANXA1, FOXP3, SLAMF1, IFNG, PYCARD, IL12A, IL12B, SYK, IL2*	6.4	4.2E-05	3.4E-07	1.6E-05
GO:0070665~positive regulation of leukocyte proliferation	18	3.9	2.8E-09	*IL4, CD244, IL6, VAV3, IL2RA, LYN, AIF1, CD3E, IL18, ANXA1, FOXP3, SLAMF1, IFNG, PYCARD, IL12A, IL12B, SYK, IL2*	6.3	1.4E-05	1.2E-07	5.2E-06
GO:1902106~negative regulation of leukocyte differentiation	10	2.1	2.4E-05	*IL4, LYN, MAFB, CTLA4, ANXA1, RARA, FOXP3, ADIPOQ, C1QC, MYC*	6.3	1.1E-01	3.8E-04	4.6E-02
GO:0001776~leukocyte homeostasis	11	2.4	9.1E-06	*LAT, HMGB1, IL6, IL2RA, HIF1A, LYN, IFNG, ANXA1, FOXP3, SLC40A1, SLC46A2*	6.2	4.4E-02	1.6E-04	1.7E-02
GO:0071222~cellular response to lipopolysaccharide	17	3.6	1.3E-08	*IL6, TNF, LYN, IL18, CXCL8, NFKBIL1, IL10, CXCL10, TNFRSF1B, XBP1, IFNG, IL12A, PYCARD, RARA, PRDM1, IL12B, ADAM9*	6.2	6.5E-05	5.0E-07	2.5E-05
GO:0051250~negative regulation of lymphocyte activation	14	3.0	3.7E-07	*IL4, IL2RA, LYN, CD274, CTLA4, ANXA1, GLMN, ITCH, PRDM1, FOXP3, LAG3, ATM, IL10, IL2*	6.2	1.8E-03	1.0E-05	7.0E-04
GO:0050851~antigen receptor-mediated signaling pathway	14	3.0	3.7E-07	*VAV3, LYN, CD3E, CTLA4, NFAM1, FOXP3, CD19, FYN, LCK, IFNG, CD79B, CD79A, SYK, LCP2*	6.2	1.8E-03	1.0E-05	7.0E-04
GO:0042098~T cell proliferation	20	4.3	5.3E-10	*IL4, CD244, IL6, IL2RA, AIF1, CD3E, IL18, ANXA1, FOXP3, SLAMF1, FYN, CD274, IFNG, PYCARD, IL12A, GLMN, IL12B, ITCH, SYK, IL2*	6.1	2.6E-06	2.9E-08	1.0E-06
GO:0002274~myeloid leukocyte activation	17	3.6	1.5E-08	*CRTC3, IL4, HMGB1, CD244, ADORA2B, LYN, CXCL8, SLAMF1, IL10, ANXA3, CD84, JUN, PYCARD, TYROBP, ADAM9, SYK, LCP2*	6.1	7.5E-05	5.7E-07	2.9E-05
GO:0002761~regulation of myeloid leukocyte differentiation	13	2.8	1.3E-06	*IL4, TNF, LYN, MAFB, MITF, LEF1, ADIPOQ, C1QC, IFNG, RARA, IL12B, MYC, TYROBP*	6.1	6.4E-03	3.0E-05	2.4E-03
GO:0050707~regulation of cytokine secretion	18	3.9	5.7E-09	*HMGB1, CD244, TNF, PTGER4, LYN, ANXA1, FOXP3, SLAMF1, TLR8, IL10, TLR9, XBP1, CD274, IFNG, CD2, PYCARD, GLMN, SYK*	6.1	2.8E-05	2.4E-07	1.1E-05
GO:0071887~leukocyte apoptotic process	12	2.6	3.9E-06	*IL6, IL2RA, HIF1A, CD3G, LGALS3, LYN, IFNG, ANXA1, PDCD1, IL10, IL2, SLC46A2*	6.1	1.9E-02	7.8E-05	7.4E-03
GO:1903037~regulation of leukocyte cell-cell adhesion	32	6.9	1.4E-15	*CD244, TNF, AIF1, IL18, CD44, XBP1, IFNG, PYCARD, AP3D1, RARA, ITCH, LAG3, SYK, IL4, IL6, IL2RA, LGALS3, CD3E, LGALS1, CTLA4, ANXA1, FOXP3, SLAMF1, LAT, LCK, CD274, IL12A, GLMN, IL12B, KLF4, SLC46A2, IL2*	6.0	6.6E-12	3.2E-13	2.5E-12
GO:0050663~cytokine secretion	19	4.1	2.8E-09	*HMGB1, CD244, TNF, PTGER4, CHI3L1, ANXA1, FOXP3, SLAMF1, IL10, XBP1, CD274, IFNG, CD2, IL12A, PYCARD, GLMN, IL12B, SYK, LCP2*	5.9	1.4E-05	1.3E-07	5.4E-06
GO:0050863~regulation of T cell	29	6.2	8.0E-14	*CD244, AIF1, IL18, XBP1, IFNG, PYCARD,*	5.9	4.0E-10	1.2E-11	1.5E-10

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
activation				*AP3D1, RARA, ITCH, LAG3, SYK, IL4, IL6, IL2RA, LGALS3, CD3E, LGALS1, CTLA4, ANXA1, FOXP3, SLAMF1, LAT, LCK, CD274, IL12A, GLMN, IL12B, SLC46A2, IL2*				
GO:0071219~cellular response to molecule of bacterial origin	17	3.6	3.0E-08	*IL6, TNF, LYN, IL18, CXCL8, NFKBIL1, IL10, CXCL10, TNFRSF1B, XBP1, IFNG, IL12A, PYCARD, RARA, PRDM1, IL12B, ADAM9*	5.8	1.5E-04	1.1E-06	5.7E-05
GO:0002366~leukocyte activation involved in immune response	29	6.2	1.2E-13	*ITGAL, HMGB1, CD244, ADORA2B, TNFSF13, XBP1, PTK2B, IFNG, PYCARD, RARA, TYROBP, SYK, IL4, IL6, LYN, PTGER4, MSH2, LGALS1, ANXA1, LEF1, FOXP3, SLAMF1, ANXA3, CD84, LAMP1, IL12A, IL12B, IL2*	5.8	6.0E-10	1.6E-11	2.3E-10
GO:0002263~cell activation involved in immune response	29	6.2	1.6E-13	*ITGAL, HMGB1, CD244, ADORA2B, TNFSF13, XBP1, PTK2B, IFNG, PYCARD, RARA, TYROBP, SYK, IL4, IL6, LYN, PTGER4, MSH2, LGALS1, ANXA1, LEF1, FOXP3, SLAMF1, ANXA3, CD84, LAMP1, IL12A, IL12B, IL2*	5.7	7.9E-10	2.0E-11	3.0E-10
GO:0002695~negative regulation of leukocyte activation	15	3.2	3.5E-07	*IL4, IL2RA, LYN, CTLA4, ANXA1, FOXP3, IL10, ATM, CD84, CD274, GLMN, PRDM1, ITCH, LAG3, IL2*	5.7	1.8E-03	1.0E-05	6.7E-04
GO:0001819~positive regulation of cytokine production	43	9.2	6.9E-20	*HMGB1, CD244, TNF, ADORA2B, IL18, TLR3, TLR7, TLR8, IL10, ATF2, TLR9, XBP1, IFNG, CD2, PYCARD, RARA, LTB, LTA, SYK, IL4, IL6, ZBTB20, CARD9, ZCCHC11, PTGER4, CD3E, FLOT1, ANXA1, HGF, IL6R, NFAM1, FOXP3, SLAMF1, ADIPOQ, HIF1A, C1QBP, CD274, IL12A, HSPB1, GLMN, TXK, IL12B, IL2*	5.7	3.4E-16	3.1E-17	1.3E-16
GO:0051251~positive regulation of lymphocyte activation	26	5.6	4.5E-12	*IL4, CD244, IL6, IL2RA, VAV3, CD3E, AIF1, IL18, LGALS1, ANXA1, TNFSF13, FOXP3, SLAMF1, LAMP1, XBP1, IFNG, CD274, LCK, PYCARD, IL12A, AP3D1, RARA, PRDM1, IL12B, IL2, SYK*	5.6	2.3E-08	4.2E-10	8.6E-09
GO:0051249~regulation of lymphocyte activation	39	8.4	6.6E-18	*CD244, AIF1, IL18, TNFSF13, IL10, TLR9, XBP1, IFNG, PYCARD, AP3D1, RARA, ITCH, LAG3, SYK, IL4, IL6, IL2RA, VAV3, LGALS3, LYN, CD3E, LGALS1, MZB1, ANXA1, CTLA4, NFAM1, FOXP3, SLAMF1, ATM, LAMP1, LAT, LCK, CD274, IL12A, GLMN, IL12B, PRDM1, IL2, SLC46A2*	5.6	3.3E-14	2.5E-15	1.3E-14
GO:0050777~negative regulation of immune response	12	2.6	8.5E-06	*CD84, IL4, CD96, A2M, TNF, NMI, ARRB2, ANXA1, IL12B, FOXP3, SLAMF1, IL10*	5.6	4.1E-02	1.5E-04	1.6E-02
GO:0045580~regulation of T cell differentiation	12	2.6	8.5E-06	*IL4, IL6, XBP1, IFNG, IL12A, CTLA4, ANXA1, AP3D1, RARA, FOXP3, SLC46A2, SYK*	5.6	4.1E-02	1.5E-04	1.6E-02
GO:0002285~lymphocyte activation involved in immune response	21	4.5	1.0E-09	*IL4, ITGAL, HMGB1, CD244, IL6, PTGER4, MSH2, LGALS1, ANXA1, LEF1, TNFSF13,*	5.6	5.1E-06	5.1E-08	1.9E-06

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
				FOXP3, LAMP1, XBP1, PTK2B, IFNG, IL12A, RARA, IL12B, IL2				
GO:0002377~immunoglobulin production	11	2.4	2.6E-05	*IL4, IL6, TNF, XBP1, MSH2, TMBIM6, MZB1, IFNG, TNFSF13, FOXP3, IL2*	5.6	1.2E-01	4.0E-04	4.9E-02
GO:0046651~lymphocyte proliferation	32	6.9	2.3E-14	*HMGB1, CD244, AIF1, IL18, IL10, IFNG, PYCARD, ITCH, SYK, IL4, IL6, VAV3, IL2RA, LGALS3, LYN, CD3E, MZB1, CTLA4, ANXA1, LEF1, FOXP3, SLAMF1, ATM, FYN, CD274, IL12A, GLMN, IL12B, PRDM1, CD79A, IL2*	5.5	1.2E-10	3.9E-12	4.5E-11
GO:0032943~mononuclear cell proliferation	32	6.9	2.7E-14	*HMGB1, CD244, AIF1, IL18, IL10, IFNG, PYCARD, ITCH, SYK, IL4, IL6, VAV3, IL2RA, LGALS3, LYN, CD3E, MZB1, CTLA4, ANXA1, LEF1, FOXP3, SLAMF1, ATM, FYN, CD274, IL12A, GLMN, IL12B, PRDM1, CD79A, IL2*	5.4	1.3E-10	4.3E-12	5.1E-11
GO:0071216~cellular response to biotic stimulus	18	3.9	3.1E-08	*IL6, TNF, LYN, IL18, CXCL8, NFKBIL1, IL10, CXCL10, TNFRSF1B, XBP1, IFNG, IL12A, PYCARD, RARA, PRDM1, IL12B, ADAM9, SYK*	5.4	1.6E-04	1.1E-06	6.0E-05
GO:0002429~immune response-activating cell surface receptor signaling pathway	14	3.0	1.7E-06	*VAV3, LYN, CD3E, CTLA4, NFAM1, FOXP3, CD19, FYN, LCK, IFNG, CD79B, CD79A, SYK, LCP2*	5.4	8.6E-03	4.0E-05	3.3E-03
GO:0002696~positive regulation of leukocyte activation	27	5.8	6.1E-12	*IL4, CD244, IL6, IL2RA, VAV3, ADORA2B, CD3E, AIF1, IL18, LGALS1, ANXA1, TNFSF13, FOXP3, SLAMF1, LAMP1, XBP1, IFNG, CD274, LCK, PYCARD, IL12A, AP3D1, RARA, PRDM1, IL12B, IL2, SYK*	5.3	3.0E-08	5.4E-10	1.2E-08
GO:0031348~negative regulation of defense response	15	3.2	7.4E-07	*A2M, NMI, IL2RA, PTGER4, HGF, FOXP3, ADIPOQ, IL10, CD96, TNFRSF1B, ARRB2, C1QBP, IL12B, ITCH, IL2*	5.3	3.7E-03	1.9E-05	1.4E-03
GO:0002822~regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	13	2.8	5.2E-06	*IL4, HMGB1, STX7, TNF, IFNG, IL12A, ANXA1, TNFSF13, IL12B, FOXP3, SLAMF1, LTA, IL2*	5.3	2.5E-02	9.8E-05	9.8E-03
GO:0022407~regulation of cell-cell adhesion	37	7.9	3.0E-16	*CD244, TNF, AIF1, IL18, CD44, XBP1, IFNG, PYCARD, AP3D1, RARA, ITCH, LAG3, SYK, IL4, IL6, IL2RA, LGALS3, LYN, CD3E, LGALS1, FLOT1, CTLA4, ANXA1, LEF1, FOXP3, SLAMF1, ADIPOQ, LAT, ITGA6, LCK, CD274, IL12A, GLMN, IL12B, KLF4, IL2, SLC46A2*	5.3	1.7E-12	9.2E-14	6.3E-13
GO:0050778~positive regulation of immune response	46	9.9	3.9E-20	*HMGB1, A2M, TNF, STX7, ADORA2B, MAPKAPK3, TLR3, TNFSF13, TLR7, TLR8, TLR9, XBP1, IFNG, PYCARD, RARA, CFD, LTA, LAG3, SYK, IL4, IL6, CARD9, VAV3, LYN, CD3E, CFB, FLOT1, ANXA1, CTLA4, NFAM1, FOXP3, NFKBIL1, C1QA, LAMP1, CD19, ARRB2, C1QBP,*	5.3	2.0E-16	2.2E-17	7.5E-17

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
				FYN, LCK, IL12A, CD79B, TXK, IL12B, CD79A, IL2, LCP2				
GO:0002819~regulation of adaptive immune response	14	3.0	2.2E-06	*IL4, HMGB1, STX7, TNF, IFNG, PYCARD, IL12A, ANXA1, TNFSF13, IL12B, FOXP3, SLAMF1, LTA, IL2*	5.3	1.1E-02	4.9E-05	4.2E-03
GO:0050714~positive regulation of protein secretion	19	4.1	1.9E-08	*HMGB1, CD244, IL6, TNF, PTGER4, WLS, SLAMF1, IL10, HIF1A, XBP1, ANG, CD274, IFNG, CD2, PYCARD, GLMN, ADAM9, SYK, IL2*	5.3	9.5E-05	7.0E-07	3.7E-05
GO:0070661~leukocyte proliferation	32	6.9	9.2E-14	*HMGB1, CD244, AIF1, IL18, IL10, IFNG, PYCARD, ITCH, SYK, IL4, IL6, VAV3, IL2RA, LGALS3, LYN, CD3E, MZB1, CTLA4, ANXA1, LEF1, FOXP3, SLAMF1, ATM, FYN, CD274, IL12A, GLMN, IL12B, PRDM1, CD79A, IL2*	5.2	4.6E-10	1.3E-11	1.7E-10
GO:1902107~positive regulation of leukocyte differentiation	14	3.0	2.8E-06	*IL4, IL6, TNF, XBP1, IFNG, IL12A, ANXA1, LEF1, AP3D1, RARA, IL12B, PRDM1, FOXP3, SYK*	5.2	1.4E-02	5.9E-05	5.3E-03
GO:0050867~positive regulation of cell activation	27	5.8	1.3E-11	*IL4, CD244, IL6, IL2RA, VAV3, ADORA2B, CD3E, AIF1, IL18, LGALS1, ANXA1, TNFSF13, FOXP3, SLAMF1, LAMP1, XBP1, IFNG, CD274, LCK, PYCARD, IL12A, AP3D1, RARA, PRDM1, IL12B, IL2, SYK*	5.2	6.3E-08	1.0E-09	2.4E-08
GO:1903707~negative regulation of hemopoiesis	13	2.8	7.3E-06	*IL4, LYN, MAFB, ANXA1, CTLA4, PF4, FOXP3, ADIPOQ, C1QC, PTK2B, RARA, MYC, HSPA9*	5.2	3.6E-02	1.3E-04	1.4E-02
GO:0045089~positive regulation of innate immune response	18	3.9	7.2E-08	*HMGB1, CARD9, LYN, FLOT1, MAPKAPK3, TLR3, TLR7, NFKBIL1, TLR8, TLR9, LAMP1, ARRB2, C1QBP, IL12A, PYCARD, TXK, IL12B, LAG3*	5.1	3.6E-04	2.3E-06	1.4E-04
GO:0002694~regulation of leukocyte activation	41	8.8	2.1E-17	*CD244, ADORA2B, AIF1, IL18, TNFSF13, IL10, TLR9, XBP1, IFNG, PYCARD, AP3D1, RARA, ITCH, LAG3, SYK, IL4, IL6, IL2RA, VAV3, LGALS3, LYN, CD3E, LGALS1, MZB1, ANXA1, CTLA4, NFAM1, FOXP3, SLAMF1, ATM, CD84, LAMP1, LAT, CD274, LCK, IL12A, GLMN, IL12B, PRDM1, IL2, SLC46A2*	5.1	1.0E-13	7.3E-15	3.9E-14
GO:0002443~leukocyte mediated immunity	27	5.8	1.8E-11	*HMGB1, STX7, TNF, ADORA2B, TLR3, TNFSF13, TLR9, CD96, IFNG, LTA, LAG3, SYK, IL4, LYN, MSH2, FOXP3, SLAMF1, ANXA3, C1QA, CD84, LAMP1, ARRB2, C1QBP, IL12A, CTSC, IL12B, IL2*	5.1	8.9E-08	1.3E-09	3.4E-08
GO:0050866~negative regulation of cell activation	15	3.2	1.3E-06	*IL4, IL2RA, LYN, CTLA4, ANXA1, FOXP3, IL10, ATM, CD84, CD274, GLMN, PRDM1, ITCH, LAG3, IL2*	5.1	6.5E-03	3.1E-05	2.5E-03
GO:0045619~regulation of lymphocyte differentiation	14	3.0	3.5E-06	*IL4, IL6, XBP1, IFNG, IL12A, CTLA4, ANXA1, AP3D1, RARA, PRDM1, NFAM1, FOXP3, SLC46A2, SYK*	5.1	1.7E-02	7.1E-05	6.6E-03

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:1902105~regulation of leukocyte differentiation	24	5.1	3.3E-10	*IL4, IL6, TNF, LYN, MAFB, MITF, CTLA4, ANXA1, LEF1, NFAM1, FOXP3, ADIPOQ, C1QC, XBP1, IFNG, IL12A, AP3D1, RARA, PRDM1, IL12B, MYC, TYROBP, SYK, SLC46A2*	5.1	1.7E-06	2.0E-08	6.4E-07
GO:0002286~T cell activation involved in immune response	12	2.6	2.4E-05	*IL4, ITGAL, IL6, PTGER4, IFNG, IL12A, ANXA1, LEF1, RARA, IL12B, FOXP3*	5.0	1.1E-01	3.8E-04	4.5E-02
GO:0045088~regulation of innate immune response	21	4.5	6.2E-09	*HMGB1, A2M, CARD9, NMI, LYN, FLOT1, MAPKAPK3, TLR3, TLR7, NFKBIL1, TLR8, TLR9, CD96, LAMP1, ARRB2, C1QBP, PYCARD, IL12A, TXK, IL12B, LAG3*	5.0	3.1E-05	2.6E-07	1.2E-05
GO:0002449~lymphocyte mediated immunity	20	4.3	1.6E-08	*IL4, HMGB1, STX7, TNF, MSH2, TNFSF13, FOXP3, SLAMF1, C1QA, CD96, LAMP1, ARRB2, C1QBP, IFNG, IL12A, CTSC, IL12B, LAG3, LTA, IL2*	5.0	8.1E-05	6.0E-07	3.1E-05
GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	15	3.2	1.6E-06	*IL4, IL6, LYN, CD3E, IL18, IL6R, HGF, CD44, FYN, PTK2B, IFNG, IL12A, IL12B, SYK, IL2*	5.0	8.1E-03	3.8E-05	3.1E-03
GO:0002253~activation of immune response	29	6.2	5.6E-12	*HMGB1, A2M, MAPKAPK3, TLR3, TLR7, TLR8, TLR9, IFNG, PYCARD, CFD, SYK, VAV3, LYN, CD3E, CFB, FLOT1, CTLA4, NFAM1, FOXP3, NFKBIL1, C1QA, CD19, ARRB2, C1QBP, FYN, LCK, CD79B, CD79A, LCP2*	4.9	2.8E-08	5.1E-10	1.1E-08
GO:0002757~immune response-activating signal transduction	24	5.1	5.9E-10	*HMGB1, VAV3, LYN, CD3E, FLOT1, CTLA4, MAPKAPK3, TLR3, NFAM1, FOXP3, TLR7, NFKBIL1, TLR8, TLR9, CD19, ARRB2, C1QBP, FYN, LCK, IFNG, CD79B, CD79A, SYK, LCP2*	4.9	2.9E-06	3.2E-08	1.1E-06
GO:0002440~production of molecular mediator of immune response	17	3.6	3.3E-07	*IL4, CD244, IL6, TNF, MSH2, TMBIM6, MZB1, TLR3, TNFSF13, FOXP3, SLAMF1, IL10, TLR9, CD96, XBP1, IFNG, IL2*	4.9	1.6E-03	9.4E-06	6.3E-04
GO:0042100~B cell proliferation	13	2.8	1.3E-05	*IL4, HMGB1, IL6, VAV3, LYN, IFNG, CTLA4, LEF1, CD79A, PRDM1, ATM, IL10, IL2*	4.9	6.0E-02	2.1E-04	2.4E-02
GO:0002768~immune response-regulating cell surface receptor signaling pathway	14	3.0	5.3E-06	*VAV3, LYN, CD3E, CTLA4, NFAM1, FOXP3, CD19, FYN, LCK, IFNG, CD79B, CD79A, SYK, LCP2*	4.9	2.6E-02	1.0E-04	1.0E-02
GO:0002683~negative regulation of immune system process	35	7.5	3.4E-14	*A2M, TNF, NMI, PF4, C1QC, PDCD1, IL10, CD96, PTK2B, RARA, ITCH, MYC, LAG3, HSPA9, IL4, IL2RA, PTGER4, LYN, MAFB, TMBIM6, CTLA4, ANXA1, FOXP3, SLAMF1, ADIPOQ, ATM, NFKBIL1, CD84, ARRB2, C1QBP, CD274, GLMN, IL12B, PRDM1, IL2*	4.9	1.7E-10	5.3E-12	6.4E-11
GO:0050865~regulation of cell activation	42	9.0	5.3E-17	*CD244, ADORA2B, AIF1, IL18, TNFSF13, IL10, TLR9, XBP1, IFNG, PYCARD, AP3D1, RARA, ITCH, LAG3, SYK, IL4, IL6, IL2RA, VAV3, LGALS3, LYN, CD3E, LGALS1, MZB1, ANXA1, CTLA4, NFAM1, FOXP3, SLAMF1, ATM, CD84, LAMP1, LAT, CD274, LCK, IL12A, GLMN, TXK,*	4.9	2.6E-13	1.8E-14	1.0E-13

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
				IL12B, PRDM1, IL2, SLC46A2				
GO:0042113~B cell activation	26	5.6	1.3E-10	*IL4, HMGB1, IL6, VAV3, LYN, MSH2, LGALS1, MZB1, CTLA4, LEF1, TNFSF13, NFAM1, TPD52, FOXP3, ATM, IL10, XBP1, PTK2B, IFNG, CMTM7, CD79B, CD79A, PRDM1, SYK, IL2*	4.9	6.5E-07	8.3E-09	2.5E-07
GO:0002460~adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	20	4.3	3.1E-08	*IL4, HMGB1, IL6, STX7, TNF, MSH2, IL18, ANXA1, LEF1, TNFSF13, FOXP3, SLAMF1, C1QA, C1QBP, IFNG, IL12A, CTSC, IL12B, LTA, IL2*	4.8	1.5E-04	1.1E-06	5.9E-05
GO:0001817~regulation of cytokine production	54	11.6	1.4E-21	*IL18, TLR3, CD2AP, TLR7, TLR8, IL10, TLR9, CD96, IFNG, RARA, CSK, LTB, LTA, LAG3, SYK, ZBTB20, ZCCHC11, PTGER4, LYN, CD3E, FLOT1, LEF1, IL6R, NFAM1, CD84, HIF1A, C1QBP, ARRB2, IL12A, HSPB1, TXK, IL12B, HMGB1, CD244, NMI, TNF, ADORA2B, ATF2, XBP1, CD2, PYCARD, IL4, IL6, CARD9, ANXA1, HGF, FOXP3, SLAMF1, ADIPOQ, NFKBIL1, CD274, GLMN, KLF4, IL2*	4.8	7.0E-18	1.2E-18	2.7E-18
GO:0031349~positive regulation of defense response	25	5.4	7.2E-10	*HMGB1, TNF, ADORA2B, S100A8, MAPKAPK3, TLR3, TLR7, TLR8, TLR9, PYCARD, LAG3, LTA, IL6, CARD9, LYN, PTGER4, FLOT1, NFKBIL1, LAMP1, PDE2A, C1QBP, ARRB2, IL12A, TXK, IL12B*	4.7	3.6E-06	3.8E-08	1.4E-06
GO:0045637~regulation of myeloid cell differentiation	18	3.9	2.9E-07	*IL4, HMGB1, TNF, LYN, MAFB, MITF, LEF1, PF4, ADIPOQ, C1QC, HIF1A, PTK2B, IFNG, RARA, IL12B, MYC, TYROBP, HSPA9*	4.7	1.4E-03	8.3E-06	5.5E-04
GO:1903708~positive regulation of hemopoiesis	16	3.4	1.8E-06	*IL4, HMGB1, IL6, TNF, ANXA1, LEF1, FOXP3, HIF1A, XBP1, IFNG, IL12A, AP3D1, RARA, IL12B, PRDM1, SYK*	4.6	8.7E-03	4.0E-05	3.4E-03
GO:0050776~regulation of immune response	52	11.1	4.3E-20	*A2M, TLR3, TNFSF13, TLR7, TLR8, IL10, TLR9, CD96, IFNG, RARA, CSK, CFD, LTA, LAG3, SYK, LYN, CD3E, FLOT1, NFAM1, C1QA, CD84, C1QBP, ARRB2, LCK, IL12A, TXK, IL12B, LCP2, HMGB1, NMI, TNF, STX7, ADORA2B, MAPKAPK3, XBP1, PYCARD, IL4, IL6, CARD9, VAV3, CFB, ANXA1, CTLA4, FOXP3, SLAMF1, NFKBIL1, LAMP1, CD19, FYN, CD79B, CD79A, IL2*	4.6	2.2E-16	2.2E-17	8.3E-17
GO:0002764~immune response-regulating signaling pathway	24	5.1	2.1E-09	*HMGB1, VAV3, LYN, CD3E, FLOT1, CTLA4, MAPKAPK3, TLR3, NFAM1, FOXP3, TLR7, NFKBIL1, TLR8, TLR9, CD19, ARRB2, C1QBP, FYN, LCK, IFNG, CD79B, CD79A, SYK, LCP2*	4.6	1.0E-05	9.9E-08	4.0E-06
GO:0002573~myeloid leukocyte differentiation	18	3.9	4.3E-07	*CEBPA, IL4, TNF, LYN, MAFB, MITF, LEF1, ADIPOQ, C1QC, ANXA2, JUN, IFNG, RARA, SPIB, IL12B, MYC, SNX10, TYROBP*	4.5	2.1E-03	1.2E-05	8.2E-04

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0001816~cytokine production	55	11.8	1.4E-20	*IL18, TLR3, CD2AP, TLR7, TLR8, IL10, TLR9, CD96, IFNG, RARA, LTB, LTA, LAG3, SYK, ZBTB20, ZCCHC11, PTGER4, LYN, CD3E, FLOT1, LEF1, IL6R, NFAM1, CD84, HIF1A, C1QBP, ARRB2, IL12A, HSPB1, TXK, IL12B, LCP2, HMGB1, CD244, NMI, TNF, ADORA2B, ATF2, XBP1, CD2, PYCARD, IL4, IL6, CARD9, ANXA1, CHI3L1, HGF, FOXP3, SLAMF1, ADIPOQ, NFKBIL1, CD274, GLMN, KLF4, IL2*	4.5	6.7E-17	8.4E-18	2.6E-17
GO:0002250~adaptive immune response	27	5.8	3.5E-10	*IL4, HMGB1, IL6, TNF, STX7, MSH2, IL18, ANXA1, LEF1, TNFSF13, CTSS, FOXP3, SLAMF1, C1QA, C1QBP, FYN, IFNG, PYCARD, IL12A, CTSC, IL12B, CD79A, CSK, LTA, IL2, SYK*	4.5	1.7E-06	2.1E-08	6.7E-07
GO:0002697~regulation of immune effector process	35	7.5	4.7E-13	*HMGB1, CD244, A2M, TNF, STX7, ADORA2B, TLR3, TNFSF13, IL10, TLR9, CD96, XBP1, IFNG, PYCARD, RARA, ITCH, LAG3, LTA, SYK, IL4, IL6, LYN, TMBIM6, MZB1, ANXA1, FOXP3, SLAMF1, STOM, CD84, LAMP1, ARRB2, C1QBP, IL12A, IL12B, IL2*	4.5	2.3E-09	4.9E-11	8.9E-10
GO:0002684~positive regulation of immune system process	66	14.1	1.0E-24	*A2M, AIF1, IL18, TLR3, TNFSF13, TLR7, TLR8, CXCL10, TLR9, IFNG, RARA, ITCH, CFD, LTA, LAG3, SYK, LYN, CD3E, FLOT1, LEF1, NFAM1, C1QA, CD84, HIF1A, C1QBP, ARRB2, LCK, PLA2G7, IL12A, TXK, PRDM1, IL12B, LCP2, HMGB1, CD244, STX7, TNF, ADORA2B, MAPKAPK3, CXCL8, PF4, XBP1, PTK2B, PYCARD, AP3D1, IL4, IL6, CARD9, IL2RA, VAV3, LGALS3, CFB, LGALS1, MZB1, ANXA1, CTLA4, FOXP3, SLAMF1, NFKBIL1, LAMP1, CD19, FYN, CD274, CD79B, CD79A, IL2*	4.5	5.1E-21	1.7E-21	2.0E-21
GO:0045785~positive regulation of cell adhesion	31	6.6	1.4E-11	*CD244, TNF, AIF1, IL18, CD44, PTK2B, XBP1, IFNG, PYCARD, AP3D1, RARA, ADAM9, SYK, IL4, IL6, VAV3, IL2RA, CD3E, LGALS1, FLOT1, ANXA1, S100A10, FOXP3, SLAMF1, ITGA6, C1QBP, LCK, CD274, IL12A, IL12B, IL2*	4.5	6.7E-08	1.1E-09	2.6E-08
GO:0002237~response to molecule of bacterial origin	23	4.9	1.2E-08	*IL6, CARD9, TNF, PTGER4, LYN, IL18, MAPKAPK3, CXCL8, PF4, NFKBIL1, IL10, CXCL10, TLR9, CD96, TNFRSF1B, XBP1, IFNG, PYCARD, IL12A, RARA, PRDM1, IL12B, ADAM9*	4.4	5.9E-05	4.6E-07	2.3E-05
GO:1903706~regulation of hemopoiesis	29	6.2	1.0E-10	*HMGB1, TNF, MITF, PF4, C1QC, PTK2B, XBP1, IFNG, AP3D1, RARA, MYC, TYROBP, SYK, HSPA9, IL4, IL6, LYN, MAFB, CTLA4, ANXA1, LEF1, NFAM1, FOXP3, ADIPOQ, HIF1A, IL12A, IL12B, PRDM1, SLC46A2*	4.4	5.1E-07	6.8E-09	1.9E-07
GO:0032496~response to lipopolysaccharide	21	4.5	7.2E-08	*IL6, TNF, PTGER4, LYN, IL18, MAPKAPK3, CXCL8, PF4, NFKBIL1, IL10, CXCL10, CD96,*	4.4	3.6E-04	2.3E-06	1.4E-04

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
				TNFRSF1B, XBP1, IFNG, PYCARD, IL12A, RARA, PRDM1, IL12B, ADAM9				
GO:0045321~leukocyte activation	61	13.1	1.7E-21	*AIF1, IL18, TNFSF13, TPD52, IL10, TLR9, IFNG, RARA, ITCH, LAG3, SYK, ADAM9, PTGER4, LYN, CD3E, LEF1, NFAM1, CD84, JUN, LCK, IL12A, PRDM1, IL12B, LCP2, CRTC3, HMGB1, ITGAL, CD244, ADORA2B, CXCL8, XBP1, PTK2B, PYCARD, AP3D1, TYROBP, IL4, IL6, IL2RA, VAV3, LGALS3, MSH2, MAFB, LGALS1, MZB1, ANXA1, CTLA4, FOXP3, SLAMF1, ANXA3, ATM, LAMP1, LAT, FYN, CD274, CMTM7, GLMN, CD79B, CD79A, IL2, SLC46A2*	4.2	8.7E-18	1.2E-18	3.3E-18
GO:0046649~lymphocyte activation	52	11.1	5.7E-18	*AIF1, IL18, TNFSF13, TPD52, IL10, TLR9, IFNG, RARA, ITCH, LAG3, SYK, LYN, PTGER4, CD3E, LEF1, NFAM1, LCK, IL12A, PRDM1, IL12B, HMGB1, ITGAL, CD244, XBP1, PTK2B, PYCARD, AP3D1, IL4, IL6, IL2RA, VAV3, LGALS3, MSH2, MAFB, LGALS1, MZB1, ANXA1, CTLA4, FOXP3, SLAMF1, ATM, LAMP1, LAT, FYN, CD274, GLMN, CMTM7, CD79B, CD79A, IL2, SLC46A2*	4.1	2.8E-14	2.4E-15	1.1E-14
GO:1903532~positive regulation of secretion by cell	23	4.9	3.9E-08	*IL4, HMGB1, CD244, IL6, TNF, ADORA2B, PTGER4, WLS, SLAMF1, IL10, LAMP1, HIF1A, XBP1, ANG, CD274, IFNG, CD2, PYCARD, GLMN, SDCBP, ADAM9, SYK, IL2*	4.1	1.9E-04	1.3E-06	7.4E-05
GO:0050727~regulation of inflammatory response	22	4.7	8.3E-08	*A2M, IL6, TNF, IL2RA, ADORA2B, LYN, S100A8, PTGER4, ANXA1, TLR3, HGF, FOXP3, ADIPOQ, IL10, TLR9, TNFRSF1B, PDE2A, C1QBP, PYCARD, IL12B, LTA, IL2*	4.1	4.1E-04	2.6E-06	1.6E-04
GO:0030098~lymphocyte differentiation	30	6.4	2.1E-10	*TPD52, PTK2B, XBP1, IFNG, AP3D1, RARA, SYK, IL4, IL6, PTGER4, MSH2, CD3E, MAFB, LGALS1, CTLA4, ANXA1, LEF1, NFAM1, FOXP3, SLAMF1, ATM, LCK, IL12A, CMTM7, CD79B, IL12B, PRDM1, CD79A, SLC46A2*	4.1	1.0E-06	1.3E-08	3.9E-07
GO:0030595~leukocyte chemotaxis	16	3.4	8.3E-06	*HMGB1, VAV3, S100A8, LYN, LGALS3, AIF1, ANXA1, CXCL8, PF4, CXCL10, C1QBP, PTK2B, IFNG, PLA2G7, IL12A, SYK*	4.1	4.0E-02	1.5E-04	1.6E-02
GO:0051047~positive regulation of secretion	24	5.1	2.6E-08	*IL4, HMGB1, CD244, IL6, TNF, ADORA2B, PTGER4, S100A8, WLS, SLAMF1, IL10, LAMP1, HIF1A, XBP1, ANG, CD274, IFNG, CD2, PYCARD, GLMN, SDCBP, ADAM9, SYK, IL2*	4.1	1.3E-04	9.2E-07	4.9E-05
GO:0001775~cell activation	68	14.6	5.4E-23	*AIF1, IL18, TNFSF13, TPD52, IL10, CXCL10, TLR9, IFNG, RARA, ITCH, LAG3, SYK, ADAM9, PTGER4, LYN, CD3E, LEF1, NFAM1, CD84, F5, JUN, LCK, IL12A, HSPB1, TXK, PRDM1, IL12B, LCP2, CRTC3, HMGB1, ITGAL, CD244,*	4.0	2.7E-19	5.4E-20	1.0E-19

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
				ADORA2B, CXCL8, PF4, XBP1, PTK2B, ADRA2A, PYCARD, AP3D1, TCF4, TYROBP, IL4, IL6, IL2RA, VAV3, LGALS3, MSH2, MAFB, LGALS1, MZB1, ANXA1, CTLA4, FOXP3, SLAMF1, ANXA3, ATM, LAMP1, LAT, FYN, CD274, CMTM7, GLMN, CD79B, CD79A, IL2, SLC46A2				
GO:0007159~leukocyte cell-cell adhesion	40	8.6	2.4E-13	*ITGAL, CD244, TNF, S100A8, AIF1, IL18, CD44, XBP1, ITGB7, IFNG, PYCARD, AP3D1, RARA, ITCH, LAG3, SYK, IL4, IL6, IL2RA, LGALS3, PTGER4, CD3E, MAFB, LGALS1, CTLA4, ANXA1, LEF1, FOXP3, SLAMF1, LAT, FYN, LCK, CD274, IL12A, GLMN, IL12B, KLF4, IL2, SLC46A2*	4.0	1.2E-09	2.9E-11	4.6E-10
GO:0050708~regulation of protein secretion	26	5.6	8.6E-09	*HMGB1, CD244, TNF, IL10, TLR8, TLR9, XBP1, ANG, IFNG, CD2, PYCARD, DNAJC1, SYK, ADAM9, IL6, LYN, PTGER4, TMBIM6, ANXA1, WLS, FOXP3, SLAMF1, HIF1A, CD274, GLMN, IL2*	4.0	4.3E-05	3.5E-07	1.6E-05
GO:0050900~leukocyte migration	23	4.9	8.3E-08	*HMGB1, VAV3, TNF, LGALS3, LYN, S100A8, PTGER4, AIF1, SELL, MITF, ANXA1, CXCL8, PF4, CXCL10, ITGA6, C1QBP, PTK2B, ITGB7, IFNG, PLA2G7, PYCARD, IL12A, SYK*	4.0	4.1E-04	2.6E-06	1.6E-04
GO:0002521~leukocyte differentiation	42	9.0	9.3E-14	*TNF, MITF, TPD52, C1QC, PTK2B, XBP1, IFNG, AP3D1, RARA, SPIB, MYC, TYROBP, SYK, IL4, CEBPA, IL6, PTGER4, LYN, CD3E, MSH2, MAFB, LGALS1, ANXA1, CTLA4, LEF1, NFAM1, FOXP3, SLAMF1, ADIPOQ, ATM, ANXA2, JUN, LCK, IL12A, CMTM7, CD79B, IL12B, PRDM1, CD79A, SNX10, SLC46A2*	3.9	4.6E-10	1.3E-11	1.8E-10
GO:0070486~leukocyte aggregation	36	7.7	9.6E-12	*ITGAL, CD244, S100A8, AIF1, IL18, CD44, XBP1, IFNG, PYCARD, AP3D1, RARA, ITCH, LAG3, SYK, IL4, IL6, IL2RA, LGALS3, PTGER4, CD3E, MAFB, LGALS1, CTLA4, ANXA1, LEF1, FOXP3, SLAMF1, FYN, LCK, CD274, IL12A, GLMN, IL12B, SLC46A2, IL2*	3.9	4.8E-08	8.1E-10	1.8E-08
GO:0060326~cell chemotaxis	20	4.3	1.1E-06	*HMGB1, VAV3, LGALS3, S100A8, LYN, AIF1, ANXA1, CXCL8, LEF1, PF4, HGF, CXCL10, ARRB2, C1QBP, PTK2B, IFNG, PLA2G7, IL12A, HSPB1, SYK*	3.9	5.4E-03	2.6E-05	2.1E-03
GO:0030217~T cell differentiation	17	3.6	8.8E-06	*IL4, IL6, PTGER4, MAFB, CD3E, ANXA1, CTLA4, LEF1, FOXP3, XBP1, LCK, IFNG, IL12A, AP3D1, RARA, IL12B, SYK*	3.8	4.3E-02	1.6E-04	1.7E-02
GO:0042110~T cell activation	34	7.3	1.0E-10	*ITGAL, CD244, AIF1, IL18, XBP1, IFNG, PYCARD, AP3D1, RARA, ITCH, LAG3, SYK, IL4, IL6, IL2RA, LGALS3, PTGER4, CD3E, MAFB,*	3.8	5.0E-07	6.8E-09	1.9E-07

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
				LGALS1, CTLA4, ANXA1, LEF1, FOXP3, SLAMF1, FYN, LCK, CD274, IL12A, GLMN, IL12B, SLC46A2, IL2				
GO:0070489~T cell aggregation	34	7.3	1.0E-10	*ITGAL, CD244, AIF1, IL18, XBP1, IFNG, PYCARD, AP3D1, RARA, ITCH, LAG3, SYK, IL4, IL6, IL2RA, LGALS3, PTGER4, CD3E, MAFB, LGALS1, CTLA4, ANXA1, LEF1, FOXP3, SLAMF1, FYN, LCK, CD274, IL12A, GLMN, IL12B, SLC46A2, IL2*	3.8	5.0E-07	6.8E-09	1.9E-07
GO:0071593~lymphocyte aggregation	34	7.3	1.1E-10	*ITGAL, CD244, AIF1, IL18, XBP1, IFNG, PYCARD, AP3D1, RARA, ITCH, LAG3, SYK, IL4, IL6, IL2RA, LGALS3, PTGER4, CD3E, MAFB, LGALS1, CTLA4, ANXA1, LEF1, FOXP3, SLAMF1, FYN, LCK, CD274, IL12A, GLMN, IL12B, SLC46A2, IL2*	3.8	5.4E-07	7.1E-09	2.1E-07
GO:0018108~peptidyl-tyrosine phosphorylation	19	4.1	3.1E-06	*IL4, IL6, LYN, CD3E, IL18, HGF, IL6R, IGF1R, CD44, FYN, PTK2B, LCK, IFNG, IL12A, TXK, IL12B, CSK, SYK, IL2*	3.8	1.5E-02	6.6E-05	5.9E-03
GO:0030099~myeloid cell differentiation	27	5.8	1.5E-08	*HMGB1, TNF, MITF, PF4, C1QC, ALAS2, PTK2B, IFNG, RARA, SPIB, MYC, TYROBP, HSPA9, CEBPA, IL4, LYN, MAFB, LEF1, ADIPOQ, ANXA2, DNASE2, HIF1A, G6PD, JUN, ATPIF1, IL12B, SNX10*	3.8	7.3E-05	5.5E-07	2.8E-05
GO:0002252~immune effector process	53	11.3	1.9E-16	*A2M, TLR3, TNFSF13, TLR7, TLR8, IL10, CXCL10, TLR9, ISG20, CD96, IFNG, RARA, ITCH, CFD, LTA, LAG3, SYK, LYN, PTGER4, LEF1, C1QA, STOM, CD84, C1QBP, ARRB2, IL12A, CTSC, IL12B, HMGB1, ITGAL, CD244, TNF, STX7, ADORA2B, XBP1, PTK2B, PYCARD, TYROBP, IL4, IL6, CARD9, MSH2, CFB, TMBIM6, LGALS1, MZB1, ANXA1, FOXP3, SLAMF1, ANXA3, LAMP1, IL2*	3.7	1.1E-12	6.9E-14	4.2E-13
GO:0018212~peptidyl-tyrosine modification	19	4.1	3.6E-06	*IL4, IL6, LYN, CD3E, IL18, HGF, IL6R, IGF1R, CD44, FYN, PTK2B, LCK, IFNG, IL12A, TXK, IL12B, CSK, SYK, IL2*	3.7	1.8E-02	7.3E-05	6.9E-03
GO:0006954~inflammatory response	38	8.1	1.4E-11	*HMGB1, A2M, TNF, S100A8, ADORA2B, AIF1, IL18, CXCL8, TLR3, PF4, TLR7, IL10, TLR8, CXCL10, TLR9, CD96, TNFRSF1B, KLKB1, PYCARD, IL1B, LTA, SYK, IL6, IL2RA, PTGER4, LYN, ANXA1, CHI3L1, HGF, FOXP3, ADIPOQ, LAT, HIF1A, PDE2A, C1QBP, CCR3, IL12B, IL2*	3.7	7.0E-08	1.1E-09	2.7E-08
GO:0002682~regulation of immune system process	85	18.2	6.4E-26	*A2M, AIF1, IL18, MITF, TLR3, TNFSF13, C1QC, TLR7, TLR8, IL10, PDCD1, TLR9, CXCL10, CD96, IFNG, RARA, ITCH, CFD, CSK, MYC, LAG3, LTA, SYK, PTGER4, LYN, CD3E, FLOT1, LEF1, NFAM1, C1QA, CD84, STOM, HIF1A,*	3.6	3.2E-22	1.6E-22	1.2E-22

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
				C1QBP, ARRB2, LCK, PLA2G7, IL12A, TXK, PRDM1, IL12B, LCP2, HMGB1, CD244, STX7, NMI, TNF, ADORA2B, MAPKAPK3, CXCL8, PF4, PTK2B, XBP1, PYCARD, AP3D1, HSPA9, TYROBP, IL4, IL6, CARD9, IL2RA, VAV3, LGALS3, CFB, MAFB, TMBIM6, LGALS1, MZB1, CTLA4, ANXA1, FOXP3, SLAMF1, ADIPOQ, ATM, NFKBIL1, LAT, LAMP1, CD19, FYN, CD274, GLMN, CD79B, CD79A, SLC46A2, IL2				
GO:0030155~regulation of cell adhesion	44	9.4	5.1E-13	*CD244, TNF, AIF1, IL18, CXCL8, CD44, XBP1, PTK2B, IFNG, PYCARD, AP3D1, RARA, ITCH, LAG3, SYK, ADAM9, IL4, IL6, IL2RA, VAV3, LGALS3, LYN, ACTN4, CD3E, LGALS1, FLOT1, ANXA1, CTLA4, LEF1, S100A10, FOXP3, SLAMF1, ADIPOQ, LAT, ITGA6, C1QBP, CD274, LCK, IL12A, GLMN, IL12B, KLF4, IL2, SLC46A2*	3.6	2.6E-09	5.3E-11	9.8E-10
GO:0009306~protein secretion	29	6.2	1.2E-08	*HMGB1, CD244, TNF, TLR8, IL10, TLR9, XBP1, ANG, IFNG, CD2, PYCARD, ADAM9, SYK, IL6, LYN, PTGER4, TMBIM6, CHI3L1, ANXA1, WLS, FOXP3, SLAMF1, HIF1A, CD274, IL12A, GLMN, IL12B, LCP2, IL2*	3.6	5.8E-05	4.5E-07	2.2E-05
GO:0032103~positive regulation of response to external stimulus	18	3.9	1.3E-05	*IL6, TNF, ADORA2B, S100A8, PTGER4, AIF1, CXCL8, TLR3, PF4, TLR9, CXCL10, PDE2A, C1QBP, PTK2B, PLA2G7, IL12A, HSPB1, LTA*	3.6	6.1E-02	2.1E-04	2.4E-02
GO:0051222~positive regulation of protein transport	30	6.4	9.1E-09	*HMGB1, CD244, CYB5R1, CDK5R1, TNF, IL18, SORL1, TLR3, BAP1, TLR7, IL10, HNMT, STARD7, XBP1, ANG, IFNG, CD2, PYCARD, ACTL6A, ADAM9, SYK, IL6, PTGER4, WLS, SLAMF1, STOM, HIF1A, CD274, GLMN, IL2*	3.5	4.5E-05	3.6E-07	1.7E-05
GO:0006955~immune response	83	17.8	5.0E-24	*A2M, S100A8, AIF1, IL18, TLR3, SYNCRIP, TNFSF13, TLR7, TLR8, IL10, TLR9, CXCL10, CD96, IFNG, IL1B, RARA, CFD, CSK, BOLA-DRB3, LTB, LAG3, LTA, SYK, PTGER4, LYN, CD3E, FLOT1, LEF1, CTSS, NFAM1, CTSW, C1QA, CD84, BOLA-DQA1, C1QBP, ARRB2, TRIM31, LCK, IL12A, TXK, CTSC, IL12B, LCP2, ITGAL, HMGB1, CD244, STX7, NMI, TNF, ADORA2B, MAPKAPK3, CXCL8, PF4, IGF1R, TNFRSF1B, PTK2B, XBP1, PYCARD, GAPDH, TYROBP, IL4, IL6, CARD9, VAV3, IL2RA, CFB, MSH2, LGALS1, CTLA4, ANXA1, FOXP3, SLAMF1, ANXA3, NFKBIL1, LAT, LAMP1, CD19, FYN, CD274, CD79B, CD79A, IL2*	3.5	2.5E-20	6.2E-21	9.6E-21
GO:0016337~single organismal cell-cell adhesion	49	10.5	2.6E-13	*ITGAL, CD244, CDK5R1, TNF, S100A8, AIF1, IL18, CD44, XBP1, ITGB7, IFNG, CD2, PYCARD, AP3D1, RARA, ITCH, LAG3, ADAM9, SYK, IL4,*	3.4	1.3E-09	2.9E-11	4.9E-10

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
				IL6, TNXB, IL2RA, LGALS3, PTGER4, LYN, MAFB, CD3E, LGALS1, FLOT1, CTLA4, ANXA1, LEF1, FOXP3, SLAMF1, ADIPOQ, LAT, ITGA6, FYN, CD274, LCK, IL12A, HSPB1, GLMN, IL12B, KLF4, SLC46A2, IL2				
GO:1904951~positive regulation of establishment of protein localization	31	6.6	1.7E-08	*HMGB1, CD244, CYB5R1, CDK5R1, TNF, IL18, SORL1, TLR3, BAP1, TLR7, IL10, HNMT, STARD7, XBP1, ANG, IFNG, CD2, PYCARD, ACTL6A, ADAM9, SYK, IL6, PTGER4, WLS, SLAMF1, STOM, CCT5, HIF1A, CD274, GLMN, IL2*	3.3	8.4E-05	6.2E-07	3.2E-05
GO:0031347~regulation of defense response	38	8.1	3.4E-10	*HMGB1, A2M, TNF, NMI, S100A8, ADORA2B, MAPKAPK3, TLR3, TLR7, IL10, TLR8, TLR9, CD96, TNFRSF1B, PYCARD, ITCH, LTA, LAG3, IL6, CARD9, IL2RA, PTGER4, LYN, FLOT1, ANXA1, HGF, FOXP3, ADIPOQ, NFKBIL1, STOM, LAMP1, PDE2A, ARRB2, C1QBP, IL12A, TXK, IL12B, IL2*	3.3	1.7E-06	2.0E-08	6.5E-07
GO:0045087~innate immune response	37	7.9	7.6E-10	*HMGB1, A2M, NMI, S100A8, AIF1, MAPKAPK3, TLR3, SYNCRIP, TLR7, TLR8, TLR9, CD96, PTK2B, PYCARD, CFD, CSK, GAPDH, LAG3, SYK, IL4, IL6, CARD9, LYN, CFB, FLOT1, ANXA1, NFKBIL1, C1QA, LAMP1, ARRB2, C1QBP, FYN, TRIM31, LCK, IL12A, TXK, IL12B*	3.3	3.8E-06	4.0E-08	1.4E-06
GO:0098602~single organism cell adhesion	52	11.1	1.1E-13	*S100A8, AIF1, IL18, CD44, IFNG, RARA, ITCH, LAG3, SYK, ADAM9, LYN, ACTN4, PTGER4, CD3E, FLOT1, LEF1, C1QBP, LCK, IL12A, HSPB1, IL12B, ITGAL, CDK5R1, CD244, TNF, XBP1, ITGB7, CD2, PYCARD, AP3D1, IL4, IL6, TNXB, IL2RA, LGALS3, MAFB, LGALS1, ANXA1, CTLA4, S100A10, FOXP3, SLAMF1, ADIPOQ, LAT, ITGA6, FYN, CD274, GLMN, KLF4, IL2, SLC46A2*	3.3	5.7E-10	1.5E-11	2.2E-10
GO:0002520~immune system development	59	12.6	2.8E-15	*MITF, TNFSF13, TPD52, C1QC, PDCD1, ALAS2, IFNG, SPIB, RARA, ITCH, LTB, MYC, LTA, SYK, PTGER4, LYN, CD3E, LEF1, NFAM1, G6PD, HIF1A, JUN, LCK, IL12A, ATPIF1, PRDM1, IL12B, SLC40A1, SNX10, HMGB1, TNF, PF4, XBP1, PTK2B, AP3D1, HSPA9, TYROBP, IL4, CEBPA, IL6, IL2RA, MSH2, MAFB, LGALS1, ANXA1, CTLA4, FOXP3, SLAMF1, ADIPOQ, ATM, ANXA2, DNASE2, CMTM7, CD79B, CD79A, KLF4, IL2, SLC46A2*	3.2	1.4E-11	6.3E-13	5.3E-12
GO:0048534~hematopoietic or lymphoid organ development	54	11.6	2.5E-13	*MITF, TPD52, C1QC, ALAS2, IFNG, SPIB, RARA, LTB, MYC, LTA, SYK, LYN, PTGER4, CD3E, LEF1, NFAM1, G6PD, HIF1A, JUN, LCK, IL12A,*	3.1	1.2E-09	2.9E-11	4.8E-10

Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
				ATPIF1, PRDM1, IL12B, SLC40A1, SNX10, HMGB1, TNF, PF4, XBP1, PTK2B, AP3D1, HSPA9, TYROBP, IL4, CEBPA, IL6, MSH2, MAFB, LGALS1, ANXA1, CTLA4, FOXP3, SLAMF1, ADIPOQ, ATM, ANXA2, DNASE2, CMTM7, CD79B, CD79A, KLF4, SLC46A2				
GO:0030097~hemopoiesis	51	10.9	1.4E-12	*MITF, TPD52, C1QC, ALAS2, IFNG, RARA, SPIB, MYC, SYK, LYN, PTGER4, CD3E, LEF1, NFAM1, G6PD, HIF1A, JUN, LCK, IL12A, ATPIF1, PRDM1, IL12B, SNX10, HMGB1, TNF, PF4, XBP1, PTK2B, AP3D1, TYROBP, HSPA9, IL4, CEBPA, IL6, MSH2, MAFB, LGALS1, ANXA1, CTLA4, FOXP3, SLAMF1, ADIPOQ, ATM, ANXA2, DNASE2, CMTM7, CD79B, CD79A, KLF4, SLC46A2*	3.1	7.2E-09	1.5E-10	2.7E-09
GO:0009617~response to bacterium	28	6.0	4.4E-07	*TNF, IL18, MAPKAPK3, CXCL8, PF4, IL10, CXCL10, TLR9, CD96, TNFRSF1B, DEFB7, XBP1, IFNG, PYCARD, RARA, LTA, ADAM9, SYK, LYZ2, IL6, CARD9, LYN, PTGER4, NFKBIL1, ANXA3, IL12A, IL12B, PRDM1*	3.1	2.2E-03	1.2E-05	8.4E-04
GO:0034097~response to cytokine	36	7.7	7.7E-09	*TNF, NMI, AIF1, MAPKAPK3, SYNCRIP, CXCL8, PF4, TIMP2, CXCL10, TIMP1, STAT4, PTK2B, XBP1, IFNG, PYCARD, IL1B, SELPLG, GAPDH, ADAM9, SYK, IL6, ZCCHC11, IL2RA, CSNK2B, CHI3L1, LEF1, ADIPOQ, MAP4K3, HIF1A, PDE2A, JUN, CD274, TXK, IL12B, KLF4*	3.1	3.8E-05	3.2E-07	1.5E-05
GO:0030335~positive regulation of cell migration	24	5.1	4.9E-06	*ACTN4, LGALS3, LYN, AIF1, CXCL8, LEF1, PF4, HGF, MIEN1, ANXA3, CXCL10, GLIPR2, IGF1R, HIF1A, C1QBP, PTK2B, JUN, IFNG, PLA2G7, PYCARD, IL12A, HSPB1, SDCBP, ADAM9*	3.0	2.4E-02	9.4E-05	9.3E-03

Таблица S9.

Список 162 генов, связанных со всеми 200 перепредставленными GO терминами (FDR<0.05, Fold Enrichment>3), выявленными системой DAVID.

NMI
TLR3
TLR7
TLR8
TLR9
IL18
IL12A
IL12B
FOXP3
IL10
HMGB1
IL2RA
CD3E
ITCH
PDCD1
LYN
IL4
PYCARD
SLAMF1
IL2
FYN
CD274
CD244
TNF
CD2
TXK
LTA
IL6
IFNG
ANXA1
AP3D1
RARA
SYK
CD96
C1QBP
CARD9
HSPB1
GLMN
LTB
KLF4
LAG3

VAV3
CD19
LCK
CTLA4
CD79B
CD79A
NFAM1
PRDM1
ATM
PTGER4
LEF1
ZBTB20
ZCCHC11
ADORA2B
XBP1
IL6R
FLOT1
ARRB2
TMBIM6
MZB1
TNFSF13
ADIPOQ
AIF1
HGF
PTK2B
NFKBIL1
ANG
CHI3L1
STX7
LAMP1
LGALS3
CD84
ANXA3
TYROBP
A2M
MSH2
LGALS1
CD44
ITGA6
CD2AP
MAFB
C1QC
MYC
LAT

HIF1A
SLC40A1
SLC46A2
CXCL8
CXCL10
TNFRSF1B
ADAM9
LCP2
CRTC3
JUN
MITF
CD3G
ITGAL
ATF2
MAPKAPK3
CFD
CFB
C1QA
WLS
PF4
HSPA9
CTSC
TPD52
CMTM7
CSK
S100A8
PDE2A
CEBPA
ANXA2
SPIB
SNX10
CTSS
STOM
PLA2G7
S100A10
SDCBP
F5
ADRA2A
TCF4
ITGB7
DNAJC1
SELL
IGF1R
ALAS2

DNASE2
G6PD
ATPIF1
ISG20
KLKB1
IL1B
CCR3
ACTN4
CYB5R1
CDK5R1
SORL1
BAP1
HNMT
STARD7
ACTL6A
SYNCRIP
BOLA-DRB3
CTSW
BOLA-DQA1
TRIM31
GAPDH
TNXB
CCT5
DEFB7
LYZ2
TIMP2
TIMP1
STAT4
SELPLG
CSNK2B
MAP4K3
MIEN1
GLIPR2

Таблица S10.

Перепредставленные (FDR<0.05, Fold Enrichment>3) биологические пути из баз KEGG и REACTOME, выявленные при анализе списка из 446 генов системой DAVID.

Category	Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	bta05321:Inflammatory bowel disease (IBD)	15	3.2	2.6E-08	*IL4, IL6, TNF, IL18, FOXP3, IL10, BOLA-DQA1, STAT4, JUN, IFNG, IL12A, IL1B, IL12B, BOLA-DRB3, IL2*	6.8E+00	5.9E-06	5.9E-06	3.3E-05
KEGG_PATHWAY	bta05142:Chagas disease (American trypanosomiasis)	17	3.6	4.7E-07	*IL6, CD3G, TNF, CD3E, CXCL8, C1QC, IL10, TLR9, C1QA, JUN, PPP2CB, IFNG, IL12A, IL1B, IL12B, IL2*	4.7E+00	1.1E-04	5.3E-05	6.0E-04
KEGG_PATHWAY	bta05144:Malaria	12	2.6	5.7E-07	*ITGAL, HBA, IL6, TNF, IL18, IFNG, IL12A, IL1B, CXCL8, HGF, IL10, TLR9*	7.2E+00	1.3E-04	4.3E-05	7.3E-04
KEGG_PATHWAY	bta05143:African trypanosomiasis	10	2.1	1.5E-06	*HBA, IL6, TNF, IL18, IFNG, IL12A, IL1B, IL12B, IL10, TLR9*	8.5E+00	3.4E-04	8.5E-05	1.9E-03
KEGG_PATHWAY	bta05152:Tuberculosis	20	4.3	3.7E-06	*CIITA, IL6, CARD9, TNF, IL18, CTSS, IL10, TLR9, LAMP1, BOLA-DQA1, FCGR2B, IFNG, IL12A, IL1B, IL12B, FCGR3A, BOLA-DRB3, HSPA9, SYK*	3.5E+00	8.4E-04	1.7E-04	4.8E-03
KEGG_PATHWAY	bta04060:Cytokine-cytokine receptor interaction	23	4.9	5.2E-06	*IL4, IL6, IL2RA, TNF, IL18, CXCL8, CXCR2, TNFSF13, PF4, HGF, IL6R, IL10, CXCL10, TNFRSF1B, CCR3, IFNG, IL12A, IL1B, IL12B, LTB, LTA, IL2*	3.1E+00	1.2E-03	2.0E-04	6.7E-03
KEGG_PATHWAY	bta04640:Hematopoietic cell lineage	14	3.0	5.3E-06	*IL4, IL6, TNF, IL2RA, CD3G, CD3E, IL6R, CD9, CD19, CD44, ITGA6, CD2, MS4A1, IL1B*	4.8E+00	1.2E-03	1.7E-04	6.8E-03
KEGG_PATHWAY	bta04660:T cell receptor signaling pathway	15	3.2	6.5E-06	*IL4, TNF, CD3G, VAV3, CD3E, CTLA4, IL10, PDCD1, LAT, FYN, JUN, LCK, IFNG, LCP2, IL2*	4.4E+00	1.5E-03	1.8E-04	8.3E-03
KEGG_PATHWAY	bta05162:Measles	17	3.6	7.5E-06	*IL4, IL6, IL2RA, CD3G, CD3E, CSNK2B, SLAMF1, TLR7, TLR9, FCGR2B, FYN, IFNG, IL12A, IL1B, IL12B, IL2*	3.8E+00	1.7E-03	1.9E-04	9.6E-03
KEGG_PATHWAY	bta05164:Influenza A	19	4.1	7.7E-06	*CIITA, IL6, TNF, IL18, FDPS, CXCL8, TLR3, TLR7, CXCL10, ATF2, BOLA-DQA1, JUN, IFNG, IL12A, PYCARD, IL1B, IL12B, BOLA-DRB3*	3.5E+00	1.7E-03	1.7E-04	9.8E-03
KEGG_PATHWAY	bta05323:Rheumatoid arthritis	14	3.0	7.7E-06	*ITGAL, IL6, TNF, IL18, CTLA4, CXCL8, TNFSF13, ATP6V1G2, BOLA-DQA1, JUN, IFNG, IL1B, BOLA-DRB3, LTB*	4.7E+00	1.7E-03	1.6E-04	9.8E-03
KEGG_PATHWAY	bta05140:Leishmaniasis	12	2.6	1.2E-05	*IL4, BOLA-DQA1, TNF, NCF1, JUN, IFNG, IL12A, IL1B, IL12B, FCGR3A, BOLA-DRB3, IL10*	5.3E+00	2.6E-03	2.2E-04	1.5E-02
KEGG_PATHWAY	bta05150:Staphylococcus aureus infection	11	2.4	1.3E-05	*C1QA, ITGAL, BOLA-DQA1, FCGR2B, CFB, CFD, FCGR3A, SELPLG, C1QC,*	5.9E+00	2.9E-03	2.2E-04	1.7E-02

Category	Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
					BOLA-DRB3, IL10				
KEGG_PATHWAY	bta05133:Pertussis	12	2.6	2.6E-05	*C1QA, IL6, TNF, CFL2, JUN, IL12A, PYCARD, IL1B, CXCL8, IL12B, C1QC, IL10*	4.9E+00	5.8E-03	4.1E-04	3.3E-02
KEGG_PATHWAY	bta05168:Herpes simplex infection	19	4.1	2.8E-05	*HMGN1, IL6, SP100, TNF, CSNK2B, TLR3, TLR9, CFP, BOLA-DQA1, C1QBP, SRSF9, JUN, IFNG, IL12A, IL1B, IL12B, BOLA-DRB3, LTA*	3.2E+00	6.2E-03	4.2E-04	3.6E-02
REACTOME_PATHWAY	R-BTA-202733:R-BTA-202733 (Cell surface interactions at the vascular wall)	12	2.6	2.48E-07	*CD84, ITGAL, CD244, THBD, CD44, LYN, FYN, SELL, CD2, PF4, SELPLG, SIRPA*	7.7E+00	8.74E-05	8.74E-05	3.39E-04
REACTOME_PATHWAY	R-BTA-114604:R-BTA-114604 (GPVI-mediated activation cascade)	10	2.1	1.53E-05	*LAT, IL2RA, VAV3, LYN, FYN, LCK, CSF2RA, IL2, LCP2, SYK*	6.5E+00	5.39E-03	2.70E-03	2.10E-02

Таблица S11.

Список 81 генов, связанных со всеми со всеми 17-ю перепредставленными (FDR<0.05, Fold Enrichment>3) биологическими путями, выявленными системой DAVID.

IL4
IL6
TNF
IL18
FOXP3
IL10
BOLA-DQA1
STAT4
JUN
IFNG
IL12A
IL1B
IL12B
BOLA-DRB3
IL2
CD3G
CD3E
CXCL8
C1QC
TLR9
C1QA
PPP2CB
ITGAL
HBA
HGF
CIITA
CARD9
CTSS
LAMP1
FCGR2B
FCGR3A
HSPA9
SYK
IL2RA
CXCR2
TNFSF13
PF4
IL6R
CXCL10
TNFRSF1B
CCR3

LTB
LTA
CD9
CD19
CD44
ITGA6
CD2
MS4A1
VAV3
CTLA4
PDCD1
LAT
FYN
LCK
LCP2
CSNK2B
SLAMF1
TLR7
FDPS
TLR3
ATF2
PYCARD
ATP6V1G2
NCF1
CFB
CFD
SELPLG
CFL2
HMGN1
SP100
CFP
C1QBP
SRSF9
CD84
CD244
THBD
LYN
SELL
SIRPA
CSF2RA

Таблица S12.

Оценка индекса значимости (или веса) w_i, на основе анализа сетей белок-белковых взаимодействий H_PPI и L_PPI.

CORR(rang,gold)	pValue
0.187243607	**0.001**

GeneSymbol	Gold list	degreeE	n-degreeE	degree	N-degree	oddsratio	pValue	n11	n12	n21	n22	ratioR	ln(ratioR)	Sig0,05(ln(R))	pValueR	minLNR	maxLNR	w_i (rang)
SLC7A7	0	15	413	79	18785	8.6363	2.28E-09	15	413	64	18372	10.4260	2.3453	0.5705	2.44E-10	1.7748	2.9158	**1.77**
TYROBP	0	34	394	284	18580	5.6456	3.35E-14	34	394	250	18186	6.2774	1.8385	0.3719	2.17E-15	1.4667	2.2104	**1.47**
CD79A	0	24	404	189	18675	5.8699	7.23E-11	24	404	165	18271	6.5782	1.8853	0.4393	8.88E-12	1.4460	2.3246	**1.45**
MS4A1	0	11	417	74	18790	6.6981	2.75E-06	11	417	63	18373	7.6930	2.0416	0.6475	8.35E-07	1.3941	2.6892	**1.39**
CTSS	0	27	401	235	18629	5.3375	3.70E-11	27	401	208	18228	5.9006	1.7767	0.4129	4.79E-12	1.3638	2.1896	**1.36**
CD3E	1	49	379	495	18369	4.7977	6.32E-17	49	379	446	17990	5.2150	1.6535	0.3120	3.20E-18	1.3414	1.9655	**1.34**
C1QA	0	36	392	355	18509	4.7882	5.47E-13	36	392	319	18117	5.2157	1.6536	0.3588	5.69E-14	1.2948	2.0124	**1.29**
TLR8	0	17	411	146	18718	5.3029	1.38E-07	17	411	129	18307	5.8700	1.7715	0.5150	3.72E-08	1.2566	2.2865	**1.26**
IL2RA	1	19	409	169	18695	5.1389	4.21E-08	19	409	150	18286	5.6631	1.7357	0.4871	1.05E-08	1.2486	2.2229	**1.25**
CD2	0	47	381	517	18347	4.3777	5.61E-15	47	381	470	17966	4.7155	1.5530	0.3165	4.63E-16	1.2364	1.8695	**1.24**
FGL2	0	19	409	171	18693	5.0782	5.00E-08	19	409	152	18284	5.5880	1.7224	0.4868	1.27E-08	1.2356	2.2092	**1.24**
IL6R	0	41	387	448	18416	4.3550	2.80E-13	41	387	407	18029	4.6930	1.5482	0.3365	3.11E-14	1.2117	1.8847	**1.21**
CD63	0	20	408	187	18677	4.8959	3.96E-08	20	408	167	18269	5.3625	1.6813	0.4739	1.02E-08	1.2074	2.1552	**1.21**
TNFRSF1B	0	43	385	480	18384	4.2777	1.39E-13	43	385	437	17999	4.6002	1.5283	0.3291	1.50E-14	1.1992	1.8574	**1.20**
NFAM1	0	35	393	379	18485	4.3437	1.33E-11	35	393	344	18092	4.6839	1.5463	0.3618	2.00E-12	1.1845	1.9080	**1.18**
CTLA4	0	21	407	204	18660	4.7196	3.31E-08	21	407	183	18253	5.1465	1.6402	0.4620	8.62E-09	1.1782	2.1023	**1.18**
IL10	0	32	396	350	18514	4.2745	1.31E-10	32	396	318	18118	4.6040	1.5291	0.3768	2.39E-11	1.1523	1.9059	**1.15**
LCP2	0	43	385	515	18349	3.9794	1.25E-12	43	385	472	17964	4.2508	1.4495	0.3281	1.73E-13	1.1214	1.7776	**1.12**
SELPLG	0	9	419	73	18791	5.5291	8.38E-05	9	419	64	18372	6.1660	1.8207	0.7041	3.94E-05	1.1166	2.5248	**1.12**
ATF2	1	51	377	641	18223	3.8458	4.88E-14	51	377	590	17846	4.0918	1.4114	0.3037	5.58E-15	1.1077	1.7151	**1.11**
IL6	1	30	398	339	18525	4.1190	1.03E-09	30	398	309	18127	4.4219	1.4888	0.3877	2.27E-10	1.1011	1.8765	**1.10**
C1QC	0	25	403	275	18589	4.1933	1.61E-08	25	403	250	18186	4.5127	1.5091	0.4227	4.32E-09	1.0864	1.9318	**1.09**
CD19	0	21	407	225	18639	4.2743	1.53E-07	21	407	204	18232	4.6114	1.5307	0.4597	4.83E-08	1.0710	1.9904	**1.07**
BANK1	0	2	426	8	18856	11.0657	0.019641	2	426	6	18430	14.4210	2.6694	1.5999	1.31E-02	1.0695	4.2693	**1.07**
S100A4	0	28	400	324	18540	4.0056	6.12E-09	28	400	296	18140	4.2899	1.4586	0.3999	1.57E-09	1.0587	1.8585	**1.06**
RNASE6	0	13	415	125	18739	4.6960	1.26E-05	13	415	112	18324	5.1250	1.6361	0.5823	5.39E-06	1.0538	2.2184	**1.05**
HLA-DPA1	0	27	401	313	18551	3.9906	1.19E-08	27	401	286	18150	4.2730	1.4546	0.4068	3.23E-09	1.0479	1.8614	**1.05**
IL1B	0	37	391	466	18398	3.7360	1.90E-10	37	391	429	18007	3.9720	1.3818	0.3504	4.01E-11	1.0314	1.7322	**1.03**
LTB	0	15	413	154	18710	4.4126	5.71E-06	15	413	139	18297	4.7809	1.5667	0.5414	2.36E-06	1.0253	2.1081	**1.03**
CTSC	0	14	414	143	18721	4.4271	1.11E-05	14	414	129	18307	4.7990	1.5705	0.5599	4.82E-06	1.0106	2.1304	**1.01**
IL18	0	29	399	354	18510	3.8004	9.89E-09	29	399	325	18111	4.0503	1.4012	0.3925	2.74E-09	1.0087	1.7938	**1.01**
AIF1	0	16	412	170	18694	4.2705	4.20E-06	16	412	154	18282	4.6103	1.5305	0.5239	1.72E-06	1.0066	2.0543	**1.01**
SYK	0	75	353	1123	17741	3.3565	2.07E-16	75	353	1048	17388	3.5251	1.2627	0.2569	1.98E-17	1.0059	1.5196	**1.01**
LCK	1	73	355	1098	17766	3.3272	6.98E-16	73	355	1025	17411	3.4930	1.2536	0.2596	7.31E-17	0.9940	1.5132	**0.99**
LYN	0	72	356	1091	17773	3.2947	1.64E-15	72	356	1019	17417	3.4569	1.2432	0.2610	1.83E-16	0.9822	1.5043	**0.98**
LYZ	0	21	407	245	18619	3.9212	5.63E-07	21	407	224	18212	4.1950	1.4363	0.4579	2.06E-07	0.9784	1.8942	**0.98**
A2M	0	37	391	497	18367	3.4971	1.01E-09	37	391	460	17976	3.6979	1.3105	0.3496	2.51E-10	0.9609	1.6600	**0.96**

GeneSymbol	Gold list	degreeE	n-degreeE	degree	N-degree	oddsratio	pValue	n11	n12	n21	n22	ratioR	ln(ratioR)	Sig0,05(ln(R))	pValueR	minLNR	maxLNR	w_i (rang)
MAFB	0	9	419	85	18779	4.7455	0.000241	9	419	76	18360	5.1890	1.6485	0.6973	1.31E-04	0.9511	2.3458	**0.95**
TLR3	0	24	404	304	18560	3.6269	3.56E-07	24	404	280	18156	3.8521	1.3512	0.4283	1.31E-07	0.9229	1.7795	**0.92**
FCGR2B	0	22	406	276	18588	3.6494	9.46E-07	22	406	254	18182	3.8789	1.3581	0.4465	3.73E-07	0.9116	1.8046	**0.91**
S100A10	0	14	414	165	18699	3.8323	4.81E-05	14	414	151	18285	4.0949	1.4122	0.5560	2.49E-05	0.8562	1.9682	**0.86**
CEBPD	0	14	414	168	18696	3.7633	5.77E-05	14	414	154	18282	4.0145	1.3924	0.5556	3.04E-05	0.8368	1.9480	**0.84**
TGFBI	0	12	416	139	18725	3.8859	0.000142	12	416	127	18309	4.1586	1.4276	0.5996	7.92E-05	0.8280	2.0272	**0.83**
CD44	0	26	402	367	18497	3.2597	8.04E-07	26	402	341	18095	3.4320	1.2361	0.4108	3.31E-07	0.8253	1.6468	**0.83**
CXCL8	0	27	401	389	18475	3.1978	7.16E-07	27	401	362	18074	3.3617	1.2154	0.4033	2.95E-07	0.8122	1.6187	**0.81**
ANXA2	0	30	398	452	18412	3.0704	4.18E-07	30	398	422	18014	3.2176	1.1717	0.3834	1.69E-07	0.7884	1.5551	**0.79**
IL2	1	22	406	314	18550	3.2012	6.71E-06	22	406	292	18144	3.3670	1.2170	0.4443	3.22E-06	0.7727	1.6613	**0.77**
TNF	1	35	393	556	18308	2.9325	1.48E-07	35	393	521	17915	3.0623	1.1224	0.3565	5.72E-08	0.7659	1.4789	**0.77**
HAVCR2	0	20	408	281	18583	3.2417	1.42E-05	20	408	261	18175	3.4135	1.2307	0.4651	7.12E-06	0.7656	1.6958	**0.77**
SLAMF1	0	17	411	232	18632	3.3218	4.41E-05	17	411	215	18221	3.5054	1.2572	0.5033	2.38E-05	0.7539	1.7604	**0.75**
IL4	0	17	411	235	18629	3.2789	5.13E-05	17	411	218	18218	3.4566	1.2432	0.5030	2.80E-05	0.7402	1.7462	**0.74**
JUN	1	106	322	2169	16695	2.5338	5.08E-14	106	322	2063	16373	2.6126	0.9642	0.2242	1.19E-14	0.7400	1.1884	**0.74**
ADAM9	0	15	413	201	18663	3.3723	0.000102	15	413	186	18250	3.5636	1.2736	0.5349	5.77E-05	0.7387	1.8085	**0.74**
IL12B	0	26	402	402	18462	2.9703	3.89E-06	26	402	376	18060	3.1065	1.1367	0.4095	1.85E-06	0.7272	1.5462	**0.73**
ITGAL	1	31	397	499	18365	2.8738	1.01E-06	31	397	468	17968	2.9980	1.1013	0.3768	4.48E-07	0.7245	1.4781	**0.72**
HLA-F	0	16	412	221	18643	3.2760	8.40E-05	16	412	205	18231	3.4537	1.2423	0.5179	4.75E-05	0.7244	1.7602	**0.72**
THBD	0	22	406	329	18535	3.0528	1.33E-05	22	406	307	18129	3.1999	1.1662	0.4435	6.81E-06	0.7227	1.6098	**0.72**
PYCARD	0	16	412	222	18642	3.2611	8.83E-05	16	412	206	18230	3.4367	1.2374	0.5178	5.02E-05	0.7196	1.7552	**0.72**
CMTM7	0	4	424	34	18830	5.2248	0.00972	4	424	30	18406	5.7881	1.7575	1.0466	7.07E-03	0.7110	2.8041	**0.71**
LGALS3	0	28	400	453	18411	2.8450	3.74E-06	28	400	425	18011	2.9665	1.0908	0.3950	1.80E-06	0.6958	1.4857	**0.70**
CFD	0	21	407	320	18544	2.9900	2.71E-05	21	407	299	18137	3.1298	1.1442	0.4531	1.46E-05	0.6910	1.5973	**0.69**
ACTN4	0	30	398	496	18368	2.7914	2.53E-06	30	398	466	17970	2.9067	1.0705	0.3823	1.20E-06	0.6882	1.4527	**0.69**
CXCL10	0	24	404	379	18485	2.8974	1.27E-05	24	404	355	18081	3.0257	1.1104	0.4249	6.61E-06	0.6855	1.5353	**0.69**
HSD17B10	0	25	403	401	18463	2.8562	1.08E-05	25	403	376	18060	2.9796	1.0952	0.4166	5.58E-06	0.6785	1.5118	**0.68**
ARRB2	0	54	374	1019	17845	2.5285	2.15E-08	54	374	965	17471	2.6140	0.9647	0.2926	6.51E-09	0.6721	1.2573	**0.67**
TLR7	0	11	417	144	18720	3.4293	0.000699	11	417	133	18303	3.6302	1.2920	0.6223	4.53E-04	0.6698	1.9143	**0.67**
CSK	0	32	396	549	18315	2.6958	2.45E-06	32	396	517	17919	2.8008	1.0335	0.3706	1.17E-06	0.6628	1.4041	**0.66**
ITCH	0	38	390	678	18186	2.6135	7.52E-07	38	390	640	17796	2.7093	1.0004	0.3423	4.33E-07	0.6581	1.3426	**0.66**
TIMP1	0	17	411	254	18610	3.0305	0.000125	17	411	237	18199	3.1762	1.1588	0.5016	7.42E-05	0.6572	1.6604	**0.66**
FYN	0	68	360	1375	17489	2.4025	3.71E-09	68	360	1307	17129	2.4755	0.9105	0.2652	1.21E-09	0.6453	1.1757	**0.65**
LAT	0	18	410	276	18588	2.9567	0.000108	18	410	258	18178	3.0933	1.1324	0.4876	6.42E-05	0.6448	1.6201	**0.64**
CD2AP	0	32	396	560	18304	2.6413	5.00E-06	32	396	528	17908	2.7407	1.0119	0.3704	1.79E-06	0.6415	1.3823	**0.64**
CD274	0	19	409	301	18563	2.8649	0.000105	19	409	282	18154	2.9906	1.0988	0.4747	6.28E-05	0.6241	1.5735	**0.62**
UBA2	0	23	405	385	18479	2.7258	4.54E-05	23	405	362	18074	2.8354	1.0457	0.4327	2.60E-05	0.6130	1.4785	**0.61**
GAPDH	0	35	393	642	18222	2.5278	3.59E-06	35	393	607	17829	2.6159	0.9654	0.3550	2.01E-06	0.6104	1.3204	**0.61**
STAT4	0	12	416	171	18693	3.1533	0.00082	12	416	159	18277	3.3159	1.2017	0.5945	5.46E-04	0.6072	1.7963	**0.61**
FCGR3A	0	9	419	119	18745	3.3835	0.002235	9	419	110	18326	3.5785	1.2777	0.6861	1.57E-03	0.5917	1.9638	**0.59**
VIM	0	46	382	914	17950	2.3649	8.54E-07	46	382	868	17568	2.4372	0.8950	0.3134	4.92E-07	0.5816	1.2083	**0.58**
SP100	0	27	401	487	18377	2.5408	4.31E-05	27	401	460	17976	2.6312	0.9712	0.4005	3.20E-05	0.5708	1.3717	**0.57**
LGALS1	0	26	402	466	18398	2.5535	5.77E-05	26	402	440	17996	2.6453	0.9765	0.4077	2.55E-05	0.5689	1.3842	**0.57**
PRDM1	0	11	417	159	18705	3.1033	0.001487	11	417	148	18288	3.2596	1.1847	0.6199	1.03E-03	0.5647	1.8046	**0.56**

GeneSymbol	Gold list	degreeE	n-degreeE	degree	N-degree	oddsratio	pValue	n11	n12	n21	n22	ratioR	ln(ratioR)	Sig0,05(ln(R))	pValueR	minLNR	maxLNR	w_i (rang)
CFP	0	7	421	87	18777	3.5886	0.004924	7	421	80	18356	3.8151	1.3416	0.7781	3.62E-03	0.5635	2.1196	**0.56**
SUMO2	0	33	395	632	18232	2.4101	1.94E-05	33	395	599	17837	2.4878	0.9154	0.3643	8.79E-06	0.5511	1.2797	**0.55**
P4HB	0	20	408	344	18520	2.6391	0.000198	20	408	324	18112	2.7403	1.0117	0.4620	1.25E-04	0.5497	1.4737	**0.55**
CSF2RA	0	9	419	124	18740	3.2462	0.002897	9	419	115	18321	3.4220	1.2331	0.6849	2.09E-03	0.5482	1.9181	**0.55**
NMI	0	19	409	327	18537	2.6334	0.000287	19	409	308	18128	2.7342	1.0095	0.4735	1.85E-04	0.5360	1.4829	**0.54**
CD3G	1	9	419	126	18738	3.1943	0.003202	9	419	117	18319	3.3631	1.2158	0.6845	2.33E-03	0.5313	1.9004	**0.53**
PF4	0	19	409	329	18535	2.6171	0.000308	19	409	310	18126	2.7163	1.0029	0.4734	2.00E-04	0.5296	1.4763	**0.53**
EEF1B2	0	25	403	464	18400	2.4600	0.000119	25	403	439	17997	2.5431	0.9373	0.4148	8.48E-05	0.5225	1.3522	**0.52**
TNFSF13	0	10	418	147	18717	3.0461	0.002698	10	418	137	18299	3.1954	1.1648	0.6490	1.96E-03	0.5158	1.8139	**0.52**
CD9	0	11	417	169	18695	2.9181	0.002336	11	417	158	18278	3.0516	1.1189	0.6186	1.69E-03	0.5003	1.7375	**0.50**
CIITA	0	13	415	214	18650	2.7300	0.001746	13	415	201	18235	2.8419	1.0480	0.5691	1.25E-03	0.4789	1.6171	**0.48**
SDHA	0	18	410	323	18541	2.5201	0.000654	18	410	305	18131	2.6098	0.9631	0.4853	4.49E-04	0.4778	1.4484	**0.48**
MYC	1	67	361	1573	17291	2.0401	1.03E-06	67	361	1506	16930	2.0864	0.7402	0.2660	5.06E-07	0.4742	1.0062	**0.47**
YWHAG	0	44	384	962	17902	2.1323	2.11E-05	44	384	918	17518	2.1866	0.7869	0.3189	1.02E-05	0.4680	1.1058	**0.47**
SELL	0	13	415	218	18646	2.6793	0.002037	13	415	205	18231	2.7858	1.0281	0.5688	1.48E-03	0.4594	1.5969	**0.46**
HLA-DOB	0	9	419	135	18729	2.9800	0.004898	9	419	126	18310	3.1214	1.1415	0.6828	3.71E-03	0.4587	1.8243	**0.46**
NFE2	0	11	417	176	18688	2.8010	0.003136	11	417	165	18271	2.9210	1.0754	0.6178	2.33E-03	0.4576	1.6931	**0.46**
HIF1A	0	38	390	816	18048	2.1551	6.48E-05	38	390	778	17658	2.2115	0.7982	0.3407	3.06E-05	0.4575	1.1389	**0.46**
HLA-DRB1	0	15	413	263	18601	2.5687	0.001449	15	413	248	18188	2.6636	0.9834	0.5300	1.04E-03	0.4534	1.5135	**0.45**
ATF3	0	16	412	288	18576	2.5049	0.001321	16	412	272	18164	2.5934	0.9568	0.5134	9.47E-04	0.4434	1.4702	**0.44**
HSPA9	0	38	390	829	18035	2.1197	7.38E-05	38	390	791	17645	2.1735	0.7809	0.3406	3.85E-05	0.4404	1.1215	**0.44**
C1QBP	0	31	397	652	18212	2.1811	0.000167	31	397	621	17815	2.2401	0.8110	0.3741	1.26E-04	0.4369	1.1851	**0.44**
IER3	0	7	421	99	18765	3.1516	0.009366	7	421	92	18344	3.3153	1.2016	0.7740	7.34E-03	0.4275	1.9756	**0.43**
DUSP1	0	15	413	278	18586	2.4282	0.00374	15	413	263	18173	2.5096	0.9241	0.5292	1.80E-03	0.3949	1.4533	**0.39**
CST3	0	12	416	210	18654	2.5624	0.004129	12	416	198	18238	2.6571	0.9810	0.5905	3.16E-03	0.3905	1.5715	**0.39**
HSPB1	0	31	397	688	18176	2.0629	0.000417	31	397	657	17779	2.1131	0.7529	0.3737	3.32E-04	0.3792	1.1265	**0.38**
S100A8	0	13	415	238	18626	2.4515	0.004154	13	415	225	18211	2.5354	0.9343	0.5673	3.19E-03	0.3670	1.5016	**0.37**
MITF	0	12	416	215	18649	2.5021	0.004923	12	416	203	18233	2.5909	0.9559	0.5901	3.81E-03	0.3657	1.5460	**0.37**
CFB	0	14	414	263	18601	2.3917	0.005634	14	414	249	18187	2.4700	0.9082	0.5469	2.85E-03	0.3613	1.4552	**0.36**
CARD9	0	15	413	288	18576	2.3426	0.004368	15	413	273	18163	2.4164	0.8864	0.5287	3.81E-03	0.3577	1.4151	**0.36**
PKM	0	25	403	544	18320	2.0891	0.001225	25	403	519	17917	2.1416	0.7662	0.4132	1.02E-03	0.3530	1.1794	**0.35**
PTK2B	0	44	384	1069	17795	1.9074	0.000207	44	384	1025	17411	1.9464	0.6711	0.3182	1.23E-04	0.3529	0.9893	**0.35**
TUBB	0	46	382	1127	17737	1.8952	0.000194	46	382	1081	17355	1.9333	0.6644	0.3120	1.13E-04	0.3524	0.9763	**0.35**
CFL2	0	8	420	128	18736	2.7881	0.01102	8	420	120	18316	2.9073	1.0707	0.7218	8.85E-03	0.3489	1.7924	**0.35**
ATXN1	0	26	402	579	18285	2.0425	0.001677	26	402	553	17883	2.0915	0.7427	0.4055	9.41E-04	0.3372	1.1481	**0.34**
HK3	0	7	421	109	18755	2.8609	0.014874	7	421	102	18334	2.9886	1.0982	0.7714	1.21E-02	0.3268	1.8695	**0.33**
LTA	1	12	416	227	18637	2.3683	0.011867	12	416	215	18221	2.4447	0.8980	0.5892	5.85E-03	0.3088	1.4872	**0.31**
ANXA1	0	15	413	302	18562	2.2323	0.005783	15	413	287	18149	2.2967	0.8358	0.5280	4.87E-03	0.3078	1.3639	**0.31**
TKT	0	14	414	278	18586	2.2608	0.007248	14	414	264	18172	2.3277	0.8492	0.5461	6.28E-03	0.3030	1.3953	**0.30**
CDCA7L	0	5	423	70	18794	3.1736	0.025535	5	423	65	18371	3.3408	1.2092	0.9139	2.13E-02	0.2953	2.1231	**0.30**
WIPF1	0	11	417	206	18658	2.3892	0.00937	11	417	195	18241	2.4676	0.9073	0.6149	7.58E-03	0.2924	1.5221	**0.29**
TLR9	0	8	420	136	18728	2.6230	0.01515	8	420	128	18308	2.7244	1.0059	0.7204	1.25E-02	0.2855	1.7263	**0.29**
PACSIN1	0	18	410	392	18472	2.0688	0.005839	18	410	374	18062	2.1202	0.7562	0.4829	5.02E-03	0.2734	1.2391	**0.27**
GSN	0	18	410	394	18470	2.0581	0.006047	18	410	376	18060	2.1087	0.7508	0.4828	5.18E-03	0.2680	1.2336	**0.27**

GeneSymbol	Gold list	degreeE	n-degreeE	degree	N-degree	oddsratio	pValue	n11	n12	n21	n22	ratioR	ln(ratioR)	Sig0,05(ln(R))	pValueR	minLNR	maxLNR	w_i (rang)
CD244	0	8	420	139	18725	2.5659	0.016955	8	420	131	18305	2.6616	0.9827	0.7199	1.41E-02	0.2628	1.7026	**0.26**
MDH2	0	11	417	212	18652	2.3208	0.017861	11	417	201	18235	2.3931	0.8768	0.6144	9.29E-03	0.2624	1.4911	**0.26**
IL12A	0	12	416	238	18626	2.2575	0.013808	12	416	226	18210	2.3243	0.8477	0.5885	1.25E-02	0.2592	1.4362	**0.26**
CEBPA	0	19	409	436	18428	1.9635	0.008759	19	409	417	18019	2.0074	0.7018	0.4700	7.91E-03	0.2318	1.1718	**0.23**
BAG6	0	27	401	677	18187	1.8088	0.005735	27	401	650	17786	1.8424	0.6165	0.3974	5.17E-03	0.2191	1.0139	**0.22**
GNL3	0	15	413	329	18535	2.0462	0.013992	15	413	314	18122	2.0961	0.7449	0.5270	1.28E-02	0.2179	1.2718	**0.22**
LCN2	0	7	421	123	18741	2.5334	0.025998	7	421	116	18320	2.6259	0.9692	0.7684	2.22E-02	0.2008	1.7377	**0.20**
CD84	0	15	413	335	18529	2.0089	0.015185	15	413	320	18116	2.0561	0.7257	0.5267	1.37E-02	0.1989	1.2524	**0.20**
FOXP3	0	24	404	603	18261	1.7990	0.012008	24	404	579	17857	1.8321	0.6109	0.4200	7.64E-03	0.1910	1.0309	**0.19**
SLC44A1	0	3	425	36	18828	3.6918	0.055053	3	425	33	18403	3.9365	1.3728	1.1840	4.77E-02	0.1888	2.5568	**0.19**
TERF2	0	19	409	457	18407	1.8711	0.016306	19	409	438	17998	1.9089	0.6517	0.4695	1.03E-02	0.1822	1.1213	**0.18**
FLOT1	0	11	417	230	18634	2.1371	0.023492	11	417	219	18217	2.1943	0.7904	0.6131	2.12E-02	0.1773	1.4035	**0.18**
CD79B	0	13	415	286	18578	2.0348	0.025714	13	415	273	18163	2.0841	0.7391	0.5646	1.54E-02	0.1745	1.3038	**0.17**
CSNK2B	0	25	403	644	18220	1.7551	0.010604	25	403	619	17817	1.7856	0.5853	0.4118	9.66E-03	0.1736	0.9971	**0.17**
ADIPOQ	0	11	417	231	18633	2.1278	0.023923	11	417	220	18216	2.1842	0.7858	0.6130	2.16E-02	0.1728	1.3988	**0.17**
PRRC2A	0	10	418	205	18659	2.1775	0.029972	10	418	195	18241	2.2379	0.8100	0.6426	2.78E-02	0.1674	1.4525	**0.17**
ITGA6	0	11	417	242	18622	2.0299	0.029533	11	417	231	18205	2.0789	0.7366	0.6123	2.65E-02	0.1243	1.3490	**0.12**
TES	0	15	413	363	18501	1.8511	0.03135	15	413	348	18088	1.8878	0.6407	0.5258	2.95E-02	0.1149	1.1665	**0.11**
MAT2B	0	5	423	84	18780	2.6427	0.047979	5	423	79	18357	2.7467	1.0140	0.9081	4.22E-02	0.1059	1.9221	**0.11**
KLKB1	0	14	414	338	18526	1.8535	0.040688	14	414	324	18112	1.8904	0.6421	0.5436	2.64E-02	0.0984	1.1857	**0.10**
SPIB	0	7	421	136	18728	2.2896	0.040484	7	421	129	18307	2.3596	0.8627	0.7662	3.56E-02	0.0965	1.6290	**0.10**
EIF4A2	0	12	416	279	18585	1.9215	0.040478	12	416	267	18169	1.9629	0.6795	0.5863	3.80E-02	0.0933	1.2658	**0.09**
JDP2	0	9	419	192	18672	2.0889	0.046566	9	419	183	18253	2.1425	0.7666	0.6758	4.34E-02	0.0908	1.4424	**0.09**
VBP1	0	14	414	341	18523	1.8369	0.041616	14	414	327	18109	1.8727	0.6327	0.5435	3.98E-02	0.0892	1.1763	**0.09**
HBA1	0	7	421	137	18727	2.2728	0.041778	7	421	130	18306	2.3413	0.8550	0.7661	3.68E-02	0.0889	1.6211	**0.09**
MSH2	0	17	411	439	18425	1.7360	0.034968	17	411	422	18014	1.7657	0.5742	0.4945	3.27E-02	0.0797	1.0686	**0.08**
VAV3	0	32	396	947	17917	1.5289	0.03323	32	396	915	17521	1.5474	0.4430	0.3662	2.44E-02	0.0768	0.8092	**0.08**
MAPKAPK3	0	10	418	226	18638	1.9729	0.043263	10	418	216	18220	2.0180	0.7070	0.6411	3.94E-02	0.0660	1.3481	**0.07**
ERH	0	11	417	257	18607	1.9099	0.054336	11	417	246	18190	1.9505	0.6732	0.6115	5.18E-02	0.0617	1.2847	**0.06**
GMPS	0	10	418	227	18637	1.9641	0.04409	10	418	217	18219	2.0086	0.7024	0.6410	4.02E-02	0.0614	1.3434	**0.06**
IPO4	0	11	417	259	18605	1.8949	0.05542	11	417	248	18188	1.9346	0.6651	0.6114	5.27E-02	0.0536	1.2765	**0.05**
HSD3B7	0	17	411	452	18412	1.6849	0.053737	17	411	435	18001	1.7116	0.5433	0.4942	3.72E-02	0.0491	1.0375	**0.05**
HMGN1	0	9	419	200	18664	2.0045	0.053047	9	419	191	18245	2.0518	0.7236	0.6752	4.92E-02	0.0484	1.3988	**0.05**
PTCD3	0	7	421	143	18721	2.1768	0.050108	7	421	136	18300	2.2373	0.8097	0.7652	4.47E-02	0.0445	1.5750	**0.04**
LEF1	0	15	413	389	18475	1.7249	0.056716	15	413	374	18062	1.7540	0.5676	0.5251	5.48E-02	0.0425	1.0927	**0.04**
IGF1R	0	26	402	765	18099	1.5302	0.047164	26	402	739	17697	1.5488	0.4439	0.4033	4.57E-02	0.0406	0.8473	**0.04**
TUBB4B	0	19	409	523	18341	1.6291	0.052078	19	409	504	17932	1.6528	0.5085	0.4683	5.03E-02	0.0402	0.9768	**0.04**
TXK	0	10	418	232	18632	1.9213	0.072064	10	418	222	18214	1.9628	0.6795	0.6407	4.43E-02	0.0388	1.3201	**0.04**
XBP1	1	7	421	144	18720	2.1615	0.051591	7	421	137	18299	2.2209	0.8024	0.7651	4.61E-02	0.0373	1.5675	**0.04**
TALDO1	0	9	419	204	18660	1.9648	0.056846	9	419	195	18241	2.0093	0.7027	0.6749	5.27E-02	0.0279	1.3776	**0.03**
HAT1	0	14	414	362	18502	1.7284	0.051373	14	414	348	18088	1.7577	0.5697	0.5429	4.81E-02	0.0268	1.1126	**0.03**
NCF1	0	11	417	271	18593	1.8098	0.063567	11	417	260	18176	1.8441	0.6174	0.6108	5.99E-02	0.0066	1.2282	**0.01**
ITPR1	0	10	418	240	18624	1.8565	0.07681	10	418	230	18206	1.8937	0.6438	0.6402	7.38E-02	0.0036	1.2840	**0.00**
ATP6V1G2	0	0	428	261	18603	0.0000	0.004927	0	428	261	18175	0.0000	**-4.6052**	19.6006	5.06E-03	-24.2058	14.9954	**0.00**

GeneSymbol	Gold list	degreeE	n-degreeE	degree	N-degree	oddsratio	pValue	n11	n12	n21	n22	ratioR	ln(ratioR)	Sig0,05(ln(R))	pValueR	minLNR	maxLNR	w_i (rang)
PTGER4	0	6	422	124	18740	2.1488	0.069815	6	422	118	18318	2.2072	0.7962	0.8253	6.34E-02	-0.0290	1.6215	**0.00**
HGF	0	15	413	414	18450	1.6186	0.093305	15	413	399	18037	1.6418	0.5019	0.5245	6.60E-02	-0.0226	1.0264	**0.00**
THAP9	0	1	427	3	18861	14.7237	0.085838	1	427	2	18434	21.5855	3.0725	2.3925	6.65E-02	0.6800	5.4650	**0.00**
ANXA3	0	5	423	96	18768	2.3109	0.074246	5	423	91	18345	2.3829	0.8725	0.9046	6.74E-02	-0.0321	1.7771	**0.00**
HSPA14	0	5	423	96	18768	2.3109	0.074246	5	423	91	18345	2.3829	0.8725	0.9046	6.74E-02	-0.0321	1.7771	**0.00**
APIP	0	6	422	127	18737	2.0977	0.07609	6	422	121	18315	2.1521	0.7711	0.8248	6.95E-02	-0.0537	1.5959	**0.00**
HMGB1	0	14	414	373	18491	1.6764	0.077118	14	414	359	18077	1.7028	0.5381	0.5426	7.47E-02	-0.0045	1.0807	**0.00**
CXCR2	0	8	420	190	18674	1.8721	0.086213	8	420	182	18254	1.9104	0.6525	0.7142	8.11E-02	-0.0616	1.3667	**0.00**
SYNCRIP	0	22	406	661	18203	1.4922	0.083405	22	406	639	17797	1.5092	0.4182	0.4362	8.15E-02	-0.0180	0.8543	**0.00**
ITGB7	0	8	420	192	18672	1.8524	0.089142	8	420	184	18252	1.8894	0.6416	0.7140	8.38E-02	-0.0725	1.3556	**0.00**
RARA	0	19	409	568	18296	1.4964	0.114509	19	409	549	17887	1.5135	0.4210	0.4676	8.51E-02	-0.0466	0.8887	**0.00**
DYNLL1	0	17	411	490	18374	1.5510	0.090239	17	411	473	17963	1.5708	0.4579	0.4935	8.77E-02	-0.0355	0.9514	**0.00**
CYB5R3	0	7	421	154	18710	2.0201	0.09453	7	421	147	18289	2.0687	0.7317	0.7639	9.06E-02	-0.0321	1.4956	**0.00**
DNAJC1	0	5	423	106	18758	2.0918	0.10103	5	423	101	18335	2.1458	0.7682	0.9023	9.36E-02	-0.1341	1.6704	**0.00**
LAMP1	0	7	421	157	18707	1.9812	0.098233	7	421	150	18286	2.0270	0.7115	0.7635	9.39E-02	-0.0521	1.4750	**0.00**
DST	0	10	418	264	18600	1.6855	0.141043	10	418	254	18182	1.7125	0.5438	0.6390	9.56E-02	-0.0952	1.1828	**0.00**
APEX1	0	13	415	352	18512	1.6474	0.101433	13	415	339	18097	1.6723	0.5201	0.5622	9.90E-02	-0.0421	1.0823	**0.00**
NFKBIL1	0	3	425	49	18815	2.7104	0.108357	3	425	46	18390	2.8220	1.0410	1.1701	9.96E-02	-0.1291	2.2110	**0.00**
AP4B1	0	3	425	49	18815	2.7104	0.108357	3	425	46	18390	2.8220	1.0410	1.1701	9.96E-02	-0.1291	2.2110	**0.00**
MKNK1	0	13	415	355	18509	1.6332	0.103085	13	415	342	18094	1.6573	0.5112	0.5621	1.00E-01	-0.0509	1.0733	**0.00**
SIRPA	0	9	419	219	18645	1.8287	0.104878	9	419	210	18226	1.8642	0.6282	0.6738	1.02E-01	-0.0456	1.3020	**0.00**
TNXB	0	9	419	219	18645	1.8287	0.104878	9	419	210	18226	1.8642	0.6282	0.6738	1.02E-01	-0.0456	1.3020	**0.00**
PCYOX1	0	2	426	24	18840	3.6854	0.112662	2	426	22	18414	3.9296	1.3711	1.4474	1.02E-01	-0.0763	2.8185	**0.00**
HSD17B4	0	9	419	220	18644	1.8203	0.10568	9	419	211	18225	1.8553	0.6234	0.6738	1.03E-01	-0.0503	1.2972	**0.00**
NAE1	0	7	421	164	18700	1.8959	0.108279	7	421	157	18279	1.9358	0.6657	0.7628	1.03E-01	-0.0971	1.4285	**0.00**
ENOPH1	0	3	425	50	18814	2.6561	0.113071	3	425	47	18389	2.7618	1.0195	1.1693	1.04E-01	-0.1498	2.1888	**0.00**
BCL11A	0	4	424	83	18781	2.1347	0.127959	4	424	79	18357	2.1921	0.7894	1.0079	1.20E-01	-0.2185	1.7973	**0.00**
AP1B1	0	9	419	245	18619	1.6324	0.19039	9	419	236	18200	1.6565	0.5107	0.6723	1.30E-01	-0.1616	1.1830	**0.00**
FCN1	0	6	422	136	18728	1.9579	0.137617	6	422	130	18306	2.0021	0.6992	0.8234	1.33E-01	-0.1243	1.5226	**0.00**
ATM	1	17	411	522	18342	1.4534	0.13661	17	411	505	17931	1.4687	0.3911	0.4930	1.34E-01	-0.1018	0.8841	**0.00**
FDPS	1	6	422	137	18727	1.9435	0.139168	6	422	131	18305	1.9867	0.6915	0.8233	1.35E-01	-0.1318	1.5148	**0.00**
JAML	0	6	422	139	18725	1.9153	0.14243	6	422	133	18303	1.9566	0.6763	0.8230	1.38E-01	-0.1467	1.4994	**0.00**
MAT2A	0	6	422	139	18725	1.9153	0.14243	6	422	133	18303	1.9566	0.6763	0.8230	1.38E-01	-0.1467	1.4994	**0.00**
CDC16	1	5	423	426	18438	0.5116	0.18168	5	423	421	18015	0.5058	-0.6620	0.8861	1.39E-01	-1.5481	0.2241	**0.00**
CCNG1	0	10	418	271	18593	1.6414	0.146392	10	418	261	18175	1.6659	0.5164	0.6387	1.43E-01	-0.1223	1.1550	**0.00**
IFNG	0	8	420	202	18662	1.7597	0.147718	8	420	194	18242	1.7911	0.5884	0.7133	1.44E-01	-0.1249	1.3017	**0.00**
SNRNP70	0	15	413	453	18411	1.4761	0.149886	15	413	438	17998	1.4924	0.4071	0.5237	1.47E-01	-0.1166	0.9307	**0.00**
SORCS3	0	2	426	30	18834	2.9474	0.15801	2	426	28	18408	3.0865	1.1303	1.4344	1.48E-01	-0.3042	2.5647	**0.00**
CD2BP2	0	10	418	279	18585	1.5936	0.15431	10	418	269	18167	1.6157	0.4859	0.6383	1.50E-01	-0.1524	1.1242	**0.00**
GLMN	0	6	422	147	18717	1.8103	0.15751	6	422	141	18295	1.8448	0.6178	0.8220	1.52E-01	-0.2043	1.4398	**0.00**
CTSW	0	2	426	31	18833	2.8522	0.16587	2	426	29	18407	2.9799	1.0952	1.4328	1.56E-01	-0.3375	2.5280	**0.00**
TRAM2	0	2	426	32	18832	2.7629	0.173796	2	426	30	18406	2.8804	1.0614	1.4313	1.64E-01	-0.3698	2.4927	**0.00**
CHI3L1	0	3	425	62	18802	2.1406	0.17495	3	425	59	18377	2.1986	0.7924	1.1622	1.66E-01	-0.3698	1.9545	**0.00**
CTPS1	0	11	417	314	18550	1.5584	0.177518	11	417	303	18133	1.5786	0.4629	0.6091	1.75E-01	-0.1462	1.0720	**0.00**

GeneSymbol	Gold list	degreeE	n-degreeE	degree	N-degree	oddsratio	pValue	n11	n12	n21	n22	ratioR	ln(ratioR)	Sig0,05(ln(R))	pValueR	minLNR	maxLNR	w_i (rang)
RBBP7	0	20	408	645	18219	1.3846	0.177582	20	408	625	17811	1.3969	0.3414	0.4558	1.76E-01	-0.1144	0.7972	**0.00**
GNG5	0	8	420	226	18638	1.5708	0.182961	8	420	218	18218	1.5918	0.4711	0.7117	1.78E-01	-0.2406	1.1829	**0.00**
RPL19	0	11	417	319	18545	1.5335	0.181407	11	417	308	18128	1.5526	0.4463	0.6089	1.78E-01	-0.1626	1.0553	**0.00**
KLRC1	0	0	428	105	18759	0.0000	0.178658	0	428	105	18331	0.0000	-4.6052	19.6012	1.80E-01	-24.2063	14.9960	**0.00**
STX7	0	2	426	245	18619	0.3568	0.186016	2	426	243	18193	0.3515	-1.0175	1.3915	1.88E-01	-2.4090	0.3740	**0.00**
EFHD2	0	3	425	66	18798	2.0105	0.19734	3	425	63	18373	2.0586	0.7269	1.1604	1.89E-01	-0.4335	1.8873	**0.00**
QSOX1	0	5	423	119	18745	1.8620	0.203356	5	423	114	18322	1.8998	0.6470	0.8999	1.99E-01	-0.2529	1.5468	**0.00**
TMBIM6	0	7	421	185	18679	1.6788	0.207268	7	421	178	18258	1.7055	0.5397	0.7609	2.04E-01	-0.2212	1.3006	**0.00**
TIMP2	0	5	423	125	18739	1.7720	0.21658	5	423	120	18316	1.8042	0.5956	0.8989	2.11E-01	-0.3033	1.4946	**0.00**
TCF4	0	15	413	489	18375	1.3648	0.220931	15	413	474	17962	1.3763	0.3266	0.5230	2.18E-01	-0.1964	0.8497	**0.00**
MAP4K3	0	9	419	274	18590	1.4573	0.302515	9	419	265	18171	1.4729	0.3940	0.6710	2.22E-01	-0.2770	1.0650	**0.00**
NIFK	0	9	419	274	18590	1.4573	0.302515	9	419	265	18171	1.4729	0.3940	0.6710	2.22E-01	-0.2770	1.0650	**0.00**
GCM1	0	7	421	199	18665	1.5595	0.229827	7	421	192	18244	1.5799	0.4637	0.7598	2.25E-01	-0.2962	1.2235	**0.00**
IL17RA	0	5	423	137	18727	1.6158	0.249191	5	423	132	18304	1.6391	0.5002	0.8973	2.43E-01	-0.3971	1.3975	**0.00**
CCR3	0	2	426	213	18651	0.4111	0.247863	2	426	211	18225	0.4055	-0.8782	1.3924	2.48E-01	-2.2706	0.5141	**0.00**
TEP1	0	3	425	76	18788	1.7450	0.255829	3	425	73	18363	1.7756	0.5798	1.1568	2.48E-01	-0.5770	1.7366	**0.00**
CCT5	0	17	411	566	18298	1.3372	0.250739	17	411	549	17887	1.3476	0.3057	0.4923	2.48E-01	-0.1866	0.7981	**0.00**
BAP1	0	8	420	233	18631	1.5231	0.262924	8	420	225	18211	1.5417	0.4393	0.7114	2.60E-01	-0.2720	1.1507	**0.00**
SYNGR2	0	0	428	85	18779	0.0000	0.268213	0	428	85	18351	0.0000	-4.6052	19.6014	2.69E-01	-24.2066	14.9962	**0.00**
ADRA2A	0	1	427	151	18713	0.2902	0.268758	1	427	150	18286	0.2855	-1.2191	1.9592	2.69E-01	-3.1783	0.7401	**0.00**
IFI30	0	0	428	87	18777	0.0000	0.269343	0	428	87	18349	0.0000	-4.6052	19.6014	2.71E-01	-24.2065	14.9962	**0.00**
LAG3	0	2	426	45	18819	1.9634	0.280121	2	426	43	18393	2.0082	0.7022	1.4177	2.72E-01	-0.7155	2.1199	**0.00**
F5	0	1	427	157	18707	0.2790	0.271342	1	427	156	18280	0.2744	-1.2573	1.9589	2.73E-01	-3.2162	0.7016	**0.00**
RABGAP1L	0	1	427	163	18701	0.2687	0.276318	1	427	162	18274	0.2642	-1.2940	1.9587	2.79E-01	-3.2527	0.6647	**0.00**
DSTN	0	8	420	248	18616	1.4298	0.284411	8	420	240	18196	1.4441	0.3744	0.7106	2.80E-01	-0.3362	1.0850	**0.00**
G6PD	0	6	422	165	18699	1.6113	0.284906	6	422	159	18277	1.6344	0.4973	0.8202	2.82E-01	-0.3228	1.3175	**0.00**
CABIN1	0	4	424	97	18767	1.8252	0.289698	4	424	93	18343	1.8607	0.6263	1.0043	2.86E-01	-0.3780	1.6306	**0.00**
PLA2G7	0	2	426	47	18817	1.8796	0.296615	2	426	45	18391	1.9187	0.6569	1.4163	2.89E-01	-0.7594	2.0731	**0.00**
LGALSL	0	2	426	47	18817	1.8796	0.296615	2	426	45	18391	1.9187	0.6569	1.4163	2.89E-01	-0.7594	2.0731	**0.00**
COTL1	0	4	424	103	18761	1.7184	0.304033	4	424	99	18337	1.7474	0.5638	1.0030	3.00E-01	-0.4392	1.5669	**0.00**
ACAT1	0	6	422	185	18679	1.4356	0.323402	6	422	179	18257	1.4502	0.3785	0.8185	3.19E-01	-0.4400	1.1971	**0.00**
ANG	0	4	424	110	18754	1.6084	0.324101	4	424	106	18330	1.6314	0.4955	1.0018	3.19E-01	-0.5062	1.4973	**0.00**
EHHADH	0	4	424	111	18753	1.5938	0.327224	4	424	107	18329	1.6160	0.4861	1.0016	3.23E-01	-0.5154	1.4877	**0.00**
ISG20	0	4	424	111	18753	1.5938	0.327224	4	424	107	18329	1.6160	0.4861	1.0016	3.23E-01	-0.5154	1.4877	**0.00**
BORCS8	0	1	427	17	18847	2.5964	0.332364	1	427	16	18420	2.6961	0.9955	2.0131	3.23E-01	-1.0176	3.0087	**0.00**
PEBP1	0	9	419	296	18568	1.3474	0.328525	9	419	287	18149	1.3583	0.3136	0.6702	3.25E-01	-0.3566	0.9838	**0.00**
DYNLT1	0	9	419	299	18565	1.3337	0.429965	9	419	290	18146	1.3440	0.3031	0.6701	3.30E-01	-0.3670	0.9732	**0.00**
NDUFA4	0	4	424	302	18562	0.5798	0.428657	4	424	298	18138	0.5742	-0.5375	0.9900	3.32E-01	-1.5275	0.4525	**0.00**
PDCD1	0	4	424	115	18749	1.5381	0.340274	4	424	111	18325	1.5575	0.4495	1.0009	3.36E-01	-0.5515	1.4504	**0.00**
SIRT5	0	2	426	53	18811	1.6663	0.345644	2	426	51	18385	1.6924	0.5321	1.4127	3.39E-01	-0.8807	1.9448	**0.00**
DUSP6	0	7	421	224	18640	1.3836	0.36434	7	421	217	18219	1.3960	0.3407	0.7583	3.61E-01	-0.4176	1.0991	**0.00**
PKHD1	0	2	426	56	18808	1.5768	0.369756	2	426	54	18382	1.5982	0.4751	1.4112	3.64E-01	-0.9362	1.8863	**0.00**
SMIM20	0	1	427	20	18844	2.2066	0.375863	1	427	19	18417	2.2701	0.8242	2.0037	3.68E-01	-1.1795	2.8279	**0.00**
DAG1	0	11	417	366	18498	1.3332	0.37255	11	417	355	18081	1.3435	0.3027	0.6076	3.71E-01	-0.3049	0.9103	**0.00**

GeneSymbol	Gold list	degreeE	n-degreeE	degree	N-degree	oddsratio	pValue	n11	n12	n21	n22	ratioR	ln(ratioR)	Sig0,05(ln(R))	pValueR	minLNR	maxLNR	w_i (rang)
ADORA2B	0	2	426	57	18807	1.5490	0.377717	2	426	55	18381	1.5690	0.4568	1.4108	3.72E-01	-0.9540	1.8676	**0.00**
RPF1	0	1	427	127	18737	0.3455	0.536339	1	427	126	18310	0.3403	-1.0489	1.9604	3.76E-01	-3.0093	0.9115	**0.00**
ARHGAP9	0	1	427	127	18737	0.3455	0.536339	1	427	126	18310	0.3403	-1.0489	1.9604	3.76E-01	-3.0093	0.9115	**0.00**
NDUFB5	0	8	420	257	18607	1.3791	0.39417	8	420	249	18187	1.3912	0.3374	0.7102	3.92E-01	-0.3728	1.0476	**0.00**
RTN4	0	8	420	259	18605	1.3683	0.396113	8	420	251	18185	1.3800	0.3293	0.7101	3.94E-01	-0.3808	1.0394	**0.00**
NACA	0	8	420	262	18602	1.3524	0.399296	8	420	254	18182	1.3635	0.3173	0.7100	3.97E-01	-0.3926	1.0273	**0.00**
RHBDL1	0	0	428	62	18802	0.0000	0.649615	0	428	62	18374	0.0000	-4.6052	19.6018	4.07E-01	-24.2070	14.9966	**0.00**
OSBPL7	0	0	428	63	18801	0.0000	0.406791	0	428	63	18373	0.0000	-4.6052	19.6018	4.07E-01	-24.2070	14.9966	**0.00**
FCHO2	0	0	428	66	18798	0.0000	0.407379	0	428	66	18370	0.0000	-4.6052	19.6017	4.08E-01	-24.2069	14.9965	**0.00**
TRIM31	0	0	428	66	18798	0.0000	0.407379	0	428	66	18370	0.0000	-4.6052	19.6017	4.08E-01	-24.2069	14.9965	**0.00**
PIGO	0	0	428	68	18796	0.0000	0.408586	0	428	68	18368	0.0000	-4.6052	19.6017	4.10E-01	-24.2068	14.9965	**0.00**
TRIM40	0	0	428	68	18796	0.0000	0.408586	0	428	68	18368	0.0000	-4.6052	19.6017	4.10E-01	-24.2068	14.9965	**0.00**
APOM	0	0	428	76	18788	0.0000	0.419136	0	428	76	18360	0.0000	-4.6052	19.6015	4.22E-01	-24.2067	14.9964	**0.00**
USP11	0	9	419	301	18563	1.3247	0.431401	9	419	292	18144	1.3347	0.2962	0.6700	4.30E-01	-0.3738	0.9662	**0.00**
NR2F6	0	5	423	167	18697	1.3234	0.437009	5	423	162	18274	1.3334	0.2952	0.8943	4.34E-01	-0.5991	1.1895	**0.00**
CXXC5	0	1	427	25	18839	1.7648	0.442168	1	427	24	18412	1.7966	0.5915	1.9932	4.37E-01	-1.4017	2.5847	**0.00**
ZMYM6	0	3	425	83	18781	1.5973	0.442668	3	425	80	18356	1.6196	0.4884	1.1548	4.39E-01	-0.6664	1.6432	**0.00**
MRPS18B	0	3	425	85	18779	1.5595	0.448451	3	425	82	18354	1.5800	0.4637	1.1543	4.45E-01	-0.6906	1.6180	**0.00**
SHTN1	0	3	425	85	18779	1.5595	0.448451	3	425	82	18354	1.5800	0.4637	1.1543	4.45E-01	-0.6906	1.6180	**0.00**
NEDD4L	0	14	414	504	18360	1.2319	0.446892	14	414	490	17946	1.2385	0.2220	0.5399	4.45E-01	-0.3180	0.7619	**0.00**
KIF2C	0	14	414	511	18353	1.2145	0.451168	14	414	497	17939	1.2206	0.2075	0.5398	4.49E-01	-0.3323	0.7473	**0.00**
KLF4	0	6	422	201	18663	1.3202	0.470598	6	422	195	18241	1.3300	0.2927	0.8174	4.68E-01	-0.5248	1.1101	**0.00**
STK40	0	3	425	94	18770	1.4095	0.477773	3	425	91	18345	1.4230	0.3598	1.1523	4.75E-01	-0.7925	1.5121	**0.00**
KBTBD8	0	1	427	29	18835	1.5210	0.490113	1	427	28	18408	1.5396	0.4380	1.9874	4.86E-01	-1.5494	2.4255	**0.00**
PDE4A	0	3	425	99	18765	1.3380	0.495869	3	425	96	18340	1.3485	0.3064	1.1513	4.93E-01	-0.8449	1.4577	**0.00**
PDE2A	0	3	425	100	18764	1.3245	0.499604	3	425	97	18339	1.3346	0.2961	1.1511	4.97E-01	-0.8551	1.4472	**0.00**
GDI2	0	7	421	244	18620	1.2688	0.512573	7	421	237	18199	1.2768	0.2521	0.7573	5.11E-01	-0.5052	1.0095	**0.00**
ACTL6A	0	12	416	443	18421	1.1995	0.517119	12	416	431	18005	1.2050	0.1948	0.5816	5.16E-01	-0.3868	0.7764	**0.00**
CDCA2	0	3	425	105	18759	1.2611	0.518739	3	425	102	18334	1.2688	0.2459	1.1503	5.16E-01	-0.9044	1.3962	**0.00**
PHF12	0	3	425	105	18759	1.2611	0.518739	3	425	102	18334	1.2688	0.2459	1.1503	5.16E-01	-0.9044	1.3962	**0.00**
BCCIP	0	3	425	106	18758	1.2491	0.522643	3	425	103	18333	1.2564	0.2362	1.1501	5.20E-01	-0.9140	1.3863	**0.00**
KIR3DL3	0	1	427	32	18832	1.3782	0.523354	1	427	31	18405	1.3904	0.3368	1.9841	5.21E-01	-1.6473	2.3209	**0.00**
SNRPD3	0	12	416	450	18414	1.1804	0.522109	12	416	438	17998	1.1853	0.1784	0.5815	5.21E-01	-0.4030	0.7599	**0.00**
PABPC4	0	12	416	454	18410	1.1697	0.525364	12	416	442	17994	1.1743	0.1692	0.5814	5.24E-01	-0.4122	0.7506	**0.00**
SULT1A1	0	1	427	112	18752	0.3921	0.523909	1	427	111	18325	0.3866	-0.9248	1.9615	5.24E-01	-2.8862	1.0367	**0.00**
MZB1	0	1	427	36	18828	1.2248	0.564337	1	427	35	18401	1.2312	0.2161	1.9805	5.63E-01	-1.7644	2.1966	**0.00**
SORCS1	0	1	427	36	18828	1.2248	0.564337	1	427	35	18401	1.2312	0.2161	1.9805	5.63E-01	-1.7644	2.1966	**0.00**
RBM34	0	8	420	304	18560	1.1629	0.695322	8	420	296	18140	1.1673	0.1632	0.7085	5.63E-01	-0.5452	0.8717	**0.00**
RHOQ	0	10	418	567	18297	0.7720	0.563978	10	418	557	17879	0.7679	-0.2511	0.6325	5.65E-01	-0.8837	0.3814	**0.00**
KMT2C	0	4	424	143	18721	1.2351	0.571088	4	424	139	18297	1.2418	0.2246	0.9975	5.69E-01	-0.7729	1.2221	**0.00**
NEU1	0	1	427	38	18826	1.1602	0.58349	1	427	37	18399	1.1646	0.1609	1.9790	5.82E-01	-1.8181	2.1399	**0.00**
CDKN2D	0	2	426	159	18705	0.5523	0.590322	2	426	157	18279	0.5466	-0.5859	1.3946	5.91E-01	-1.9805	0.8087	**0.00**
COL21A1	0	1	427	41	18823	1.0752	0.610655	1	427	40	18396	1.0770	0.0835	1.9771	6.10E-01	-1.8936	2.0605	**0.00**
SRSF9	0	11	417	429	18435	1.1336	0.622843	11	417	418	18018	1.1371	0.1372	0.6062	6.22E-01	-0.4690	0.7435	**0.00**

GeneSymbol	Gold list	degreeE	n-degreeE	degree	N-degree	oddsratio	pValue	n11	n12	n21	n22	ratioR	ln(ratioR)	Sig0,05(ln(R))	pValueR	minLNR	maxLNR	w_i (rang)
KAT6B	0	5	423	191	18673	1.1556	0.626667	5	423	186	18250	1.1598	0.1568	0.8926	6.26E-01	-0.7358	1.0494	**0.00**
SORL1	0	5	423	192	18672	1.1495	0.628315	5	423	187	18249	1.1535	0.1515	0.8925	6.27E-01	-0.7411	1.0440	**0.00**
MEX3A	0	0	428	45	18819	0.0000	0.627545	0	428	45	18391	0.0000	-4.6052	19.6024	6.28E-01	-24.2076	14.9972	**0.00**
PPP1R3B	0	0	428	45	18819	0.0000	0.627545	0	428	45	18391	0.0000	-4.6052	19.6024	6.28E-01	-24.2076	14.9972	**0.00**
WLS	0	0	428	48	18816	0.0000	0.628575	0	428	48	18388	0.0000	-4.6052	19.6023	6.29E-01	-24.2074	14.9971	**0.00**
ZBTB20	0	0	428	48	18816	0.0000	0.628575	0	428	48	18388	0.0000	-4.6052	19.6023	6.29E-01	-24.2074	14.9971	**0.00**
FKBP11	0	0	428	49	18815	0.0000	0.62925	0	428	49	18387	0.0000	-4.6052	19.6022	6.30E-01	-24.2074	14.9971	**0.00**
DNASE2	0	0	428	51	18813	0.0000	0.631053	0	428	51	18385	0.0000	-4.6052	19.6022	6.32E-01	-24.2073	14.9970	**0.00**
SLC31A2	0	0	428	52	18812	0.0000	0.632167	0	428	52	18384	0.0000	-4.6052	19.6021	6.34E-01	-24.2073	14.9969	**0.00**
RGS2	0	3	425	196	18668	0.6723	0.80579	3	425	193	18243	0.6672	-0.3898	1.1426	6.34E-01	-1.5323	0.7528	**0.00**
GPT2	0	0	428	54	18810	0.0000	0.634787	0	428	54	18382	0.0000	-4.6052	19.6020	6.37E-01	-24.2072	14.9969	**0.00**
TFAP2D	0	0	428	56	18808	0.0000	0.637887	0	428	56	18380	0.0000	-4.6052	19.6020	6.40E-01	-24.2072	14.9968	**0.00**
CRISP1	0	0	428	57	18807	0.0000	0.639603	0	428	57	18379	0.0000	-4.6052	19.6020	6.42E-01	-24.2071	14.9968	**0.00**
LGMN	0	0	428	61	18803	0.0000	0.647438	0	428	61	18375	0.0000	-4.6052	19.6018	6.50E-01	-24.2070	14.9967	**0.00**
RRP7A	0	2	426	63	18801	1.4011	0.656593	2	426	61	18375	1.4142	0.3536	1.4083	6.55E-01	-1.0547	1.7620	**0.00**
AVEN	0	2	426	64	18800	1.3791	0.659054	2	426	62	18374	1.3913	0.3374	1.4080	6.58E-01	-1.0706	1.7454	**0.00**
RNF130	0	2	426	67	18797	1.3171	0.666783	2	426	65	18371	1.3269	0.2904	1.4070	6.65E-01	-1.1166	1.6973	**0.00**
SOAT1	0	4	424	245	18619	0.7169	0.665985	4	424	241	18195	0.7122	-0.3254	0.9916	6.66E-01	-1.3170	0.6662	**0.00**
HSPA4	0	16	412	635	18229	1.1148	0.683284	16	412	619	17817	1.1178	0.1203	0.5057	6.83E-01	-0.3854	0.6259	**0.00**
SH3GLB2	0	7	421	284	18580	1.0878	0.839318	7	421	277	18159	1.0900	0.0953	0.7558	6.91E-01	-0.6605	0.8511	**0.00**
JCHAIN	0	2	426	78	18786	1.1307	0.698264	2	426	76	18360	1.1342	0.1347	1.4039	6.98E-01	-1.2692	1.5386	**0.00**
PAIP2	0	2	426	78	18786	1.1307	0.698264	2	426	76	18360	1.1342	0.1347	1.4039	6.98E-01	-1.2692	1.5386	**0.00**
TSPAN17	0	2	426	79	18785	1.1164	0.701283	2	426	77	18359	1.1194	0.1217	1.4037	7.01E-01	-1.2820	1.5254	**0.00**
LMO2	0	8	420	315	18549	1.1216	0.701292	8	420	307	18129	1.1248	0.1265	0.7081	7.01E-01	-0.5817	0.8346	**0.00**
HADH	0	2	426	80	18784	1.1023	0.704316	2	426	78	18358	1.1050	0.1088	1.4035	7.04E-01	-1.2946	1.5123	**0.00**
ABT1	0	2	426	81	18783	1.0887	0.707363	2	426	79	18357	1.0909	0.0962	1.4032	7.07E-01	-1.3071	1.4994	**0.00**
NDEL1	0	6	422	342	18522	0.7700	0.711796	6	422	336	18100	0.7659	-0.2537	0.8124	7.12E-01	-1.0661	0.5587	**0.00**
GPN3	0	2	426	86	18778	1.0251	0.722723	2	426	84	18352	1.0257	0.0351	1.4022	7.23E-01	-1.3671	1.4373	**0.00**
RSRC1	0	1	427	87	18777	0.5055	1	1	427	86	18350	0.4997	-0.6739	1.9640	7.26E-01	-2.6380	1.2901	**0.00**
RIDA	0	1	427	87	18777	0.5055	1	1	427	86	18350	0.4997	-0.6739	1.9640	7.26E-01	-2.6380	1.2901	**0.00**
SPSB2	0	1	427	91	18773	0.4831	0.725819	1	427	90	18346	0.4774	-0.7187	1.9635	7.26E-01	-2.6822	1.2448	**0.00**
NUDT3	0	1	427	97	18767	0.4531	0.727898	1	427	96	18340	0.4474	-0.7822	1.9629	7.29E-01	-2.7450	1.1807	**0.00**
TPD52	0	3	425	119	18745	1.1119	0.753511	3	425	116	18320	1.1148	0.1176	1.1483	7.53E-01	-1.0307	1.2659	**0.00**
TRMT5	0	3	425	122	18742	1.0844	0.758063	3	425	119	18317	1.0865	0.0921	1.1480	7.58E-01	-1.0558	1.2401	**0.00**
CA2	0	3	425	125	18739	1.0582	0.762809	3	425	122	18314	1.0596	0.0673	1.1476	7.63E-01	-1.0803	1.2149	**0.00**
PPM1E	0	2	426	136	18728	0.6465	0.772833	2	426	134	18302	0.6412	-0.4289	1.3961	7.73E-01	-1.8250	0.9672	**0.00**
CNTN3	0	2	426	137	18727	0.6418	0.772974	2	426	135	18301	0.6364	-0.4363	1.3960	7.73E-01	-1.8323	0.9598	**0.00**
BMS1	0	3	425	176	18688	0.7495	0.801507	3	425	173	18263	0.7452	-0.2808	1.1436	8.01E-01	-1.4244	0.8628	**0.00**
SEC31A	0	3	425	175	18689	0.7538	1	3	425	172	18264	0.7495	-0.2750	1.1436	8.01E-01	-1.4186	0.8686	**0.00**
ITPR3	0	3	425	183	18681	0.7206	0.801971	3	425	180	18256	0.7159	-0.3203	1.1432	8.02E-01	-1.4635	0.8229	**0.00**
CDK5R1	0	3	425	192	18672	0.6865	0.804235	3	425	189	18247	0.6815	-0.3689	1.1427	8.05E-01	-1.5116	0.7738	**0.00**
ZNF106	0	5	423	214	18650	1.0301	0.817743	5	423	209	18227	1.0309	0.0400	0.8913	8.18E-01	-0.8513	0.9314	**0.00**
SNRPA1	0	7	421	304	18560	1.0151	0.846733	7	421	297	18139	1.0155	0.0252	0.7552	8.47E-01	-0.7300	0.7803	**0.00**
TK1	0	8	420	398	18466	0.8838	0.865337	8	420	390	18046	0.8814	-0.1150	0.7063	8.65E-01	-0.8213	0.5913	**0.00**

GeneSymbol	Gold list	degreeE	n-degreeE	degree	N-degree	oddsratio	pValue	n11	n12	n21	n22	ratioR	ln(ratioR)	Sig0,05(ln(R))	pValueR	minLNR	maxLNR	w_i (rang)
PHGDH	0	10	418	421	18443	1.0480	0.867772	10	418	411	18025	1.0492	0.0575	0.6344	8.68E-01	-0.5769	0.6920	**0.00**
SDCBP	0	12	416	530	18334	0.9979	1	12	416	518	17918	0.9978	0.0078	0.5803	1.00E+00	-0.5725	0.5881	**0.00**
PPP2CB	0	8	420	383	18481	0.9191	1	8	420	375	18061	0.9174	-0.0754	0.7065	1.00E+00	-0.7819	0.6312	**0.00**
EIF2S3	0	6	422	286	18578	0.9236	1	6	422	280	18156	0.9219	-0.0705	0.8138	1.00E+00	-0.8843	0.7433	**0.00**
DAZAP2	0	5	423	226	18638	0.9748	1	5	423	221	18215	0.9742	-0.0159	0.8908	1.00E+00	-0.9066	0.8749	**0.00**
GLRX3	0	5	423	230	18634	0.9577	1	5	423	225	18211	0.9567	-0.0339	0.8906	1.00E+00	-0.9244	0.8567	**0.00**
CBX6	0	5	423	235	18629	0.9370	1	5	423	230	18206	0.9357	-0.0559	0.8904	1.00E+00	-0.9463	0.8345	**0.00**
STOM	0	5	423	242	18622	0.9096	1	5	423	237	18199	0.9077	-0.0859	0.8901	1.00E+00	-0.9760	0.8042	**0.00**
CAPN2	0	4	424	181	18683	0.9738	1	4	424	177	18259	0.9732	-0.0170	0.9945	1.00E+00	-1.0114	0.9775	**0.00**
AP3D1	1	4	424	182	18682	0.9684	1	4	424	178	18258	0.9677	-0.0226	0.9944	1.00E+00	-1.0170	0.9718	**0.00**
ATP6AP2	0	4	424	187	18677	0.9422	1	4	424	183	18253	0.9410	-0.0503	0.9941	1.00E+00	-1.0444	0.9438	**0.00**
ZBTB32	0	3	425	133	18731	0.9941	1	3	425	130	18306	0.9940	0.0040	1.1468	1.00E+00	-1.1428	1.1508	**0.00**
CRTC3	1	3	425	134	18730	0.9867	1	3	425	131	18305	0.9863	-0.0037	1.1467	1.00E+00	-1.1503	1.1430	**0.00**
PGRMC1	0	3	425	143	18721	0.9241	1	3	425	140	18296	0.9225	-0.0699	1.1458	1.00E+00	-1.2157	1.0759	**0.00**
PRIM1	0	3	425	146	18718	0.9050	1	3	425	143	18293	0.9030	-0.0910	1.1456	1.00E+00	-1.2366	1.0546	**0.00**
IGHA1	0	3	425	146	18718	0.9050	1	3	425	143	18293	0.9030	-0.0910	1.1456	1.00E+00	-1.2366	1.0546	**0.00**
GUCY1B1	0	3	425	149	18715	0.8866	1	3	425	146	18290	0.8843	-0.1117	1.1454	1.00E+00	-1.2571	1.0336	**0.00**
IPCEF1	0	3	425	155	18709	0.8520	1	3	425	152	18284	0.8491	-0.1519	1.1449	1.00E+00	-1.2968	0.9930	**0.00**
MRPL50	0	3	425	159	18705	0.8304	1	3	425	156	18280	0.8271	-0.1778	1.1446	1.00E+00	-1.3224	0.9669	**0.00**
PCK2	0	2	426	91	18773	0.9685	1	2	426	89	18347	0.9678	-0.0224	1.4013	1.00E+00	-1.4237	1.3789	**0.00**
TRMT112	0	2	426	96	18768	0.9178	1	2	426	94	18342	0.9161	-0.0768	1.4005	1.00E+00	-1.4773	1.3237	**0.00**
SLC7A5	0	2	426	100	18764	0.8809	1	2	426	98	18338	0.8785	-0.1182	1.3999	1.00E+00	-1.5181	1.2817	**0.00**
LPAR6	0	2	426	105	18759	0.8388	1	2	426	103	18333	0.8356	-0.1677	1.3992	1.00E+00	-1.5669	1.2315	**0.00**
PPA2	0	2	426	110	18754	0.8004	1	2	426	108	18328	0.7967	-0.2148	1.3986	1.00E+00	-1.6133	1.1838	**0.00**
ARPC5L	0	2	426	112	18752	0.7860	1	2	426	110	18326	0.7822	-0.2330	1.3984	1.00E+00	-1.6313	1.1654	**0.00**
UAP1	0	2	426	112	18752	0.7860	1	2	426	110	18326	0.7822	-0.2330	1.3984	1.00E+00	-1.6313	1.1654	**0.00**
SOX5	0	2	426	125	18739	0.7038	1	2	426	123	18313	0.6990	-0.3439	1.3970	1.00E+00	-1.7409	1.0531	**0.00**
LXN	0	1	427	43	18821	1.0251	1	1	427	42	18394	1.0256	0.0350	1.9759	1.00E+00	-1.9409	2.0109	**0.00**
CDC42EP3	0	1	427	45	18819	0.9794	1	1	427	44	18392	0.9789	-0.0111	1.9749	1.00E+00	-1.9860	1.9637	**0.00**
PRR3	0	1	427	47	18817	0.9376	1	1	427	46	18390	0.9363	-0.0552	1.9739	1.00E+00	-2.0291	1.9187	**0.00**
MACROD1	0	1	427	50	18814	0.8812	1	1	427	49	18387	0.8788	-0.1179	1.9726	1.00E+00	-2.0905	1.8547	**0.00**
PLBD1	0	1	427	50	18814	0.8812	1	1	427	49	18387	0.8788	-0.1179	1.9726	1.00E+00	-2.0905	1.8547	**0.00**
PLA2G16	0	1	427	54	18810	0.8158	1	1	427	53	18383	0.8123	-0.1957	1.9711	1.00E+00	-2.1668	1.7754	**0.00**
STARD7	0	1	427	57	18807	0.7727	1	1	427	56	18380	0.7687	-0.2502	1.9701	1.00E+00	-2.2203	1.7199	**0.00**
TBC1D2B	0	1	427	60	18804	0.7340	1	1	427	59	18377	0.7294	-0.3019	1.9692	1.00E+00	-2.2711	1.6674	**0.00**
CPD	0	1	427	66	18798	0.6670	1	1	427	65	18371	0.6619	-0.3976	1.9677	1.00E+00	-2.3654	1.5701	**0.00**
GPANK1	0	1	427	66	18798	0.6670	1	1	427	65	18371	0.6619	-0.3976	1.9677	1.00E+00	-2.3654	1.5701	**0.00**
RASGEF1B	0	1	427	71	18793	0.6199	1	1	427	70	18366	0.6145	-0.4709	1.9666	1.00E+00	-2.4375	1.4958	**0.00**
YPEL5	0	1	427	71	18793	0.6199	1	1	427	70	18366	0.6145	-0.4709	1.9666	1.00E+00	-2.4375	1.4958	**0.00**
GLIPR2	0	1	427	72	18792	0.6112	1	1	427	71	18365	0.6058	-0.4849	1.9664	1.00E+00	-2.4513	1.4815	**0.00**
ABHD16A	0	1	427	75	18789	0.5867	1	1	427	74	18362	0.5811	-0.5257	1.9659	1.00E+00	-2.4916	1.4401	**0.00**
NCOA7	0	1	427	79	18785	0.5569	1	1	427	78	18358	0.5512	-0.5777	1.9652	1.00E+00	-2.5429	1.3875	**0.00**
ALAS2	0	1	427	81	18783	0.5431	1	1	427	80	18356	0.5374	-0.6027	1.9649	1.00E+00	-2.5675	1.3622	**0.00**
MTMR9	0	1	427	83	18781	0.5299	1	1	427	82	18354	0.5242	-0.6270	1.9646	1.00E+00	-2.5916	1.3376	**0.00**

GeneSymbol	Gold list	degreeE	n-degreeE	degree	N-degree	oddsratio	pValue	n11	n12	n21	n22	ratioR	ln(ratioR)	Sig0,05(ln(R))	pValueR	minLNR	maxLNR	w_i (rang)
MXD4	0	1	427	83	18781	0.5299	1	1	427	82	18354	0.5242	-0.6270	1.9646	1.00E+00	-2.5916	1.3376	**0.00**
NAT1	0	0	428	37	18827	0.0000	1	0	428	37	18399	0.0000	-4.6052	19.6029	1.00E+00	-24.2081	14.9977	**0.00**
RADX	0	0	428	36	18828	0.0000	1	0	428	36	18400	0.0000	-4.6052	19.6030	1.00E+00	-24.2081	14.9978	**0.00**
PNPLA1	0	0	428	35	18829	0.0000	1	0	428	35	18401	0.0000	-4.6052	19.6030	1.00E+00	-24.2082	14.9979	**0.00**
CC2D1B	0	0	428	31	18833	0.0000	1	0	428	31	18405	0.0000	-4.6052	19.6034	1.00E+00	-24.2086	14.9982	**0.00**
NRN1	0	0	428	30	18834	0.0000	1	0	428	30	18406	0.0000	-4.6052	19.6035	1.00E+00	-24.2087	14.9983	**0.00**
CYP27A1	0	0	428	29	18835	0.0000	1	0	428	29	18407	0.0000	-4.6052	19.6036	1.00E+00	-24.2088	14.9984	**0.00**
C1orf21	0	0	428	28	18836	0.0000	1	0	428	28	18408	0.0000	-4.6052	19.6037	1.00E+00	-24.2089	14.9986	**0.00**
HNMT	0	0	428	28	18836	0.0000	1	0	428	28	18408	0.0000	-4.6052	19.6037	1.00E+00	-24.2089	14.9986	**0.00**
ADGRE3	0	0	428	28	18836	0.0000	1	0	428	28	18408	0.0000	-4.6052	19.6037	1.00E+00	-24.2089	14.9986	**0.00**
TRIM45	0	0	428	25	18839	0.0000	1	0	428	25	18411	0.0000	-4.6052	19.6042	1.00E+00	-24.2093	14.9990	**0.00**
TSPAN13	0	0	428	25	18839	0.0000	1	0	428	25	18411	0.0000	-4.6052	19.6042	1.00E+00	-24.2093	14.9990	**0.00**
SFTA2	0	0	428	24	18840	0.0000	1	0	428	24	18412	0.0000	-4.6052	19.6043	1.00E+00	-24.2095	14.9991	**0.00**
BBIP1	0	0	428	23	18841	0.0000	1	0	428	23	18413	0.0000	-4.6052	19.6045	1.00E+00	-24.2097	14.9993	**0.00**
C12orf57	0	0	428	18	18846	0.0000	1	0	428	18	18418	0.0000	-4.6052	19.6057	1.00E+00	-24.2108	15.0005	**0.00**
SLC35F2	0	0	428	16	18848	0.0000	1	0	428	16	18420	0.0000	-4.6052	19.6064	1.00E+00	-24.2115	15.0012	**0.00**
RHNO1	0	0	428	16	18848	0.0000	1	0	428	16	18420	0.0000	-4.6052	19.6064	1.00E+00	-24.2115	15.0012	**0.00**
NRSN1	0	0	428	15	18849	0.0000	1	0	428	15	18421	0.0000	-4.6052	19.6068	1.00E+00	-24.2119	15.0016	**0.00**
SELENOH	0	0	428	15	18849	0.0000	1	0	428	15	18421	0.0000	-4.6052	19.6068	1.00E+00	-24.2119	15.0016	**0.00**
SLC4A10	0	0	428	15	18849	0.0000	1	0	428	15	18421	0.0000	-4.6052	19.6068	1.00E+00	-24.2119	15.0016	**0.00**
LY6G5B	0	0	428	13	18851	0.0000	1	0	428	13	18423	0.0000	-4.6052	19.6078	1.00E+00	-24.2129	15.0026	**0.00**
ELOVL5	0	0	428	13	18851	0.0000	1	0	428	13	18423	0.0000	-4.6052	19.6078	1.00E+00	-24.2129	15.0026	**0.00**
DEXI	0	0	428	12	18852	0.0000	1	0	428	12	18424	0.0000	-4.6052	19.6084	1.00E+00	-24.2136	15.0032	**0.00**
B3GNT5	0	0	428	11	18853	0.0000	1	0	428	11	18425	0.0000	-4.6052	19.6091	1.00E+00	-24.2143	15.0040	**0.00**
SLC40A1	0	0	428	11	18853	0.0000	1	0	428	11	18425	0.0000	-4.6052	19.6091	1.00E+00	-24.2143	15.0040	**0.00**
NRSN2	0	0	428	10	18854	0.0000	1	0	428	10	18426	0.0000	-4.6052	19.6100	1.00E+00	-24.2152	15.0049	**0.00**
SLC46A2	0	0	428	10	18854	0.0000	1	0	428	10	18426	0.0000	-4.6052	19.6100	1.00E+00	-24.2152	15.0049	**0.00**
C6orf47	0	0	428	10	18854	0.0000	1	0	428	10	18426	0.0000	-4.6052	19.6100	1.00E+00	-24.2152	15.0049	**0.00**
LRRC25	0	0	428	10	18854	0.0000	1	0	428	10	18426	0.0000	-4.6052	19.6100	1.00E+00	-24.2152	15.0049	**0.00**
MIEN1	0	0	428	10	18854	0.0000	1	0	428	10	18426	0.0000	-4.6052	19.6100	1.00E+00	-24.2152	15.0049	**0.00**
FAM53B	0	0	428	8	18856	0.0000	1	0	428	8	18428	0.0000	-4.6052	19.6125	1.00E+00	-24.2176	15.0073	**0.00**
LY6G5C	0	0	428	7	18857	0.0000	1	0	428	7	18429	0.0000	-4.6052	19.6142	1.00E+00	-24.2194	15.0090	**0.00**
WDFY4	0	0	428	6	18858	0.0000	1	0	428	6	18430	0.0000	-4.6052	19.6165	1.00E+00	-24.2217	15.0114	**0.00**
SNX10	0	0	428	6	18858	0.0000	1	0	428	6	18430	0.0000	-4.6052	19.6165	1.00E+00	-24.2217	15.0114	**0.00**
MOSPD1	0	0	428	5	18859	0.0000	1	0	428	5	18431	0.0000	-4.6052	19.6198	1.00E+00	-24.2250	15.0146	**0.00**
PARP8	0	0	428	5	18859	0.0000	1	0	428	5	18431	0.0000	-4.6052	19.6198	1.00E+00	-24.2250	15.0146	**0.00**
TMEM134	0	0	428	4	18860	0.0000	1	0	428	4	18432	0.0000	-4.6052	19.6247	1.00E+00	-24.2298	15.0195	**0.00**
SLC44A4	0	0	428	3	18861	0.0000	1	0	428	3	18433	0.0000	-4.6052	19.6328	1.00E+00	-24.2379	15.0276	**0.00**
DEFB107A	0	0	428	2	18862	0.0000	1	0	428	2	18434	0.0000	-4.6052	19.6489	1.00E+00	-24.2541	15.0438	**0.00**

Таблица S13.

Функциии генов из каталога, имеющих наибольшую значимость (вес) w_i в сети белок-белковых взаимодействий.

Gene Symbol	w_i (rang)	Назвние гена	Функции гена по данным RefSeq
SLC7A7	1.77	solute carrier family 7 member 7	The protein encoded by this gene is the light subunit of a cationic amino acid transporter. This sodium-independent transporter is formed when the light subunit encoded by this gene dimerizes with the heavy subunit transporter protein SLC3A2. This transporter is found in epithelial cell membranes where it transfers cationic and large neutral amino acids from the cell to the extracellular space. Defects in this gene are a cause of lysinuric protein intolerance (LPI). Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jul 2011]
TYROBP	1.47	TYRO protein tyrosine kinase binding protein	This gene encodes a transmembrane signaling polypeptide which contains an **immunoreceptor** tyrosine-based activation motif (ITAM) in its cytoplasmic domain. The encoded protein may associate with the killer-cell inhibitory receptor (KIR) family of membrane glycoproteins and may act as an activating signal transduction element. This protein may bind zeta-chain (TCR) associated protein kinase 70kDa (ZAP-70) and spleen tyrosine kinase (SYK) and play a role in signal transduction, bone modeling, brain myelination, and **inflammation**. Mutations within this gene have been associated with polycystic lipomembranous osteodysplasia with sclerosing leukoencephalopathy (PLOSL), also known as Nasu-Hakola disease. Its putative receptor, triggering receptor expressed on myeloid cells 2 (TREM2), also causes PLOSL. Multiple alternative transcript variants encoding distinct isoforms have been identified for this gene. [provided by RefSeq, Mar 2010]
CD79A	1.45	CD79a molecule	The B lymphocyte antigen receptor is a multimeric complex that includes the **antigen-specific component, surface immunoglobulin (Ig)**. Surface Ig non-covalently associates with two other proteins, Ig-alpha and Ig-beta, which are necessary for expression and function of the B-cell antigen receptor. This gene encodes the Ig-alpha protein of the B-cell antigen component. Alternatively spliced transcript variants encoding different isoforms have been described. [provided by RefSeq, Jul 2008]
MS4A1	1.39	membrane spanning 4-domains A1	This gene encodes a member of the membrane-spanning 4A gene family. Members of this nascent protein family are characterized by common structural features and similar intron/exon splice boundaries and display unique expression patterns among hematopoietic cells and nonlymphoid tissues. This gene encodes a B-lymphocyte surface molecule which **plays a role in the development and differentiation of B-cells into plasma cells**. This family member is localized to 11q12, among a cluster of family members. Alternative splicing of this gene results in two transcript variants which encode the same protein. [provided by RefSeq, Jul 2008]
CTSS	1.36	cathepsin S	The protein encoded by this gene, a member of the peptidase C1 family, is a lysosomal cysteine proteinase that **may participate in the degradation of antigenic proteins to peptides for presentation on MHC class II molecules.** The encoded protein can function as an elastase over a broad pH range in alveolar macrophages. Alternatively spliced transcript variants encoding distinct isoforms have been found for this gene. [provided by RefSeq, Dec 2010]
CD3E	1.34	CD3e molecule	The protein encoded by this gene is the CD3-epsilon polypeptide, which together with CD3-gamma, -delta and -zeta, and the T-cell receptor alpha/beta and gamma/delta heterodimers, forms the T-cell receptor-CD3 complex. This complex plays an important role in **coupling antigen recognition to several intracellular signal-transduction pathways**. The genes encoding the epsilon, gamma and delta polypeptides are located in the same cluster on chromosome 11. The epsilon polypeptide plays an essential role in **T-cell development**. **Defects in this gene cause immunodeficiency.** This gene has also been linked to a susceptibility to type I diabetes in women. [provided by RefSeq, Jul 2008]
C1QA	1.29	complement C1q A chain	This gene encodes the A-chain polypeptide of serum complement subcomponent C1q, which associates with C1r and C1s to yield the first **component of the serum complement system**. C1q deficiency is associated with lupus erythematosus and glomerulonephritis. C1q is composed of 18 polypeptide chains which include 6 A-chains, 6 B-chains, and 6 C-chains. Each chain contains an N-terminal collagen-like region and a C-terminal C1q globular domain. Alternate splicing results in multiple transcript variants. [provided by RefSeq, Nov 2016]
TLR8	1.26	toll like receptor 8	The protein encoded by this gene is **a member of the Toll-like receptor (TLR) family which plays a fundamental role in pathogen recognition and activation of innate immunity**. TLRs are highly conserved from Drosophila to humans and share structural and functional similarities. They recognize pathogen-associated molecular patterns (PAMPs) that are expressed on infectious agents, and mediate the production of cytokines necessary for the development of effective immunity. The various TLRs exhibit different patterns of expression. This gene is predominantly expressed in lung and peripheral blood leukocytes, and lies in close proximity to another family member, TLR7, on chromosome X. [provided by RefSeq, Jul 2008]
IL2RA	1.25	interleukin 2 receptor subunit alpha	The interleukin 2 (IL2) receptor alpha (IL2RA) and beta (IL2RB) chains, together with the common gamma chain (IL2RG), constitute the **high-affinity IL2 receptor**. Homodimeric alpha chains (IL2RA) result in low-affinity receptor, while homodimeric beta (IL2RB) chains

Gene Symbol	w_i (rang)	Назвние гена	Функции гена по данным RefSeq
			produce a medium-affinity receptor. Normally an integral-membrane protein, soluble IL2RA has been isolated and determined to result from extracellular proteolyisis. Alternately-spliced IL2RA mRNAs have been isolated, but the significance of each is presently unknown. Mutations in this gene are associated with interleukin 2 receptor alpha deficiency.[provided by RefSeq, Nov 2009]
CD2	1.24	CD2 molecule	The protein encoded by this gene is **a surface antigen** found on all peripheral blood T-cells. The encoded protein interacts with LFA3 (CD58) on antigen presenting cells **to optimize immune recognition**. A locus control region (LCR) has been found in the 3' flanking sequence of this gene. [provided by RefSeq, Jun 2016]
FGL2	1.24	fibrinogen like 2	The protein encoded by this gene is a secreted protein that is similar to the beta- and gamma-chains of fibrinogen. The carboxyl-terminus of the encoded protein consists of the fibrinogen-related domains (FRED). The encoded protein forms a tetrameric complex which is stabilized by interchain disulfide bonds. This protein may **play a role in physiologic functions at mucosal sites**. [provided by RefSeq, Jul 2008]
IL6R	1.21	interleukin 6 receptor	This gene encodes **a subunit of the interleukin 6 (IL6) receptor complex**. Interleukin 6 is a potent pleiotropic cytokine that regulates cell growth and differentiation and plays an **important role in the immune response**. The IL6 receptor is a protein complex consisting of this protein and interleukin 6 signal transducer (IL6ST/GP130/IL6-beta), a receptor subunit also shared by many other cytokines. Dysregulated production of IL6 and this receptor are implicated in the pathogenesis of many diseases, such as multiple myeloma, autoimmune diseases and prostate cancer. Alternatively spliced transcript variants encoding distinct isoforms have been reported. A pseudogene of this gene is found on chromosome 9.[provided by RefSeq, May 2011]
CD63	1.21	CD63 molecule	The protein encoded by this gene is a member of the transmembrane 4 superfamily, also known as the tetraspanin family. Most of these members are cell-surface proteins that are characterized by the presence of four hydrophobic domains. The proteins mediate signal transduction events that play a role in the regulation of cell development, activation, growth and motility. The encoded protein is a **cell surface glycoprotein that is known to complex with integrins**. **It may function as a blood platelet activation marker**. Deficiency of this protein is associated with Hermansky-Pudlak syndrome. Also this gene has been associated with tumor progression. Alternative splicing results in multiple transcript variants encoding different protein isoforms. [provided by RefSeq, Apr 2012]
TNFRSF1B	1.20	TNF receptor superfamily member 1B	The protein encoded by this gene is **a member of the TNF-receptor superfamily**. This protein and TNF-receptor 1 form a heterocomplex that mediates the recruitment of two anti-apoptotic proteins, c-IAP1 and c-IAP2, which possess E3 ubiquitin ligase activity. The function of IAPs in TNF-receptor signalling is unknown, however, c-IAP1 is thought to potentiate TNF-induced apoptosis by the ubiquitination and degradation of TNF-receptor-associated factor 2, which mediates anti-apoptotic signals. Knockout studies in mice also suggest a role of this protein in protecting neurons from apoptosis by stimulating antioxidative pathways. [provided by RefSeq, Jul 2008]

Таблица S14.

Обучающее множество генов (21)

Gene	KEGG PATHWAY: bta05166	Experiment
AP3D1	0	1
ATF2	1	1
ATM	1	0
BOLA-DQA1	0	1
BOLA-DRB3	1	1
CD3E	1	0
CD3G	1	0
CDC16	1	0
CRTC3	1	0
FDPS	1	1
IL2	1	0
IL2RA	1	0
IL6	1	0
ITGAL	1	0
JUN	1	0
LCK	1	0
LOC616942	1	0
LTA	1	0
MYC	1	0
TNF	1	1
XBP1	1	0
Сумма	19	6

Таблица S15.

Ранги генов согласно критериям 1-7 и итоговый ранг (суммарный балл).

Ensembl Gene ID (human)	Gene Symbol (Homo sapiens)	Gene Symbol (Bos taurus)	Gene is in Golden list - 1, not - 0	Evidence	**Крите-рий 1.** GWAS-1, not GWAS-0	**Крите-рий 2.** Has associated allele-1, not has-0	**Крите-рий 3.** Knockout -1, not -0	**Крите-рий 4.** Has PPI with virus-1, not has -0	**Крите-рий 5.** Has overepresented GO term-1, not has -0	**Крите-рий 6.** Has overepresented Pathway-1, not has -0	**Крите-рий 7.** Rang in the PPI network	**Суммарный балл**
ENSG00000232810	*TNF*	*TNF*	1	GWAS Knockout Expr_Articles Alleles	1	1	1	0	1	1	0.77	**5.77**
ENSG00000231389	*HLA-DPA1*	*BOLA-DQA1*	1	GWAS Alleles	1	1	0	0	1	1	1.05	**5.05**
ENSG00000196126	*HLA-DRB1*	*BOLA-DRB3*	1	GWAS Alleles	1	1	0	0	1	1	0.45	**4.45**
ENSG00000115966	*ATF2*	*ATF2*	1	PPI	0	0	0	1	1	1	1.11	**4.11**
ENSG00000227507	*LTB*	*LTB*	0	GWAS	1	0	0	0	1	1	1.03	**4.03**
ENSG00000163131	*CTSS*	*CTSS*	0	Expr_Chip	0	0	0	0	1	1	1.36	**3.36**
ENSG00000198851	*CD3E*	*CD3E*	1	Expr_Chip	0	0	0	0	1	1	1.34	**3.34**
ENSG00000226979	*LTA*	*LTA*	1	GWAS	1	0	0	0	1	1	0.31	**3.31**
ENSG00000173372	*C1QA*	*C1QA*	0	Expr_Chip	0	0	0	0	1	1	1.29	**3.29**
ENSG00000134460	*IL2RA*	*IL2RA*	1	Expr_Articles	0	0	0	0	1	1	1.25	**3.25**
ENSG00000116824	*CD2*	*CD2*	0	Expr_Chip	0	0	0	0	1	1	1.24	**3.24**
ENSG00000160712	*IL6R*	*IL6R*	0	Expr_Chip	0	0	0	0	1	1	1.21	**3.21**
ENSG00000028137	*TNFRSF1B*	*TNFRSF1B*	0	Expr_Articles	0	0	0	0	1	1	1.20	**3.20**
ENSG00000163599	*CTLA4*	*CTLA4*	0	Expr_Articles	0	0	0	0	1	1	1.18	**3.18**
ENSG00000204435	*CSNK2B*	*CSNK2B*	0	GWAS	1	0	0	0	1	1	0.17	**3.17**
ENSG00000136634	*IL10*	*IL10*	0	Expr_Articles	0	0	0	0	1	1	1.15	**3.15**
ENSG00000043462	*LCP2*	*LCP2*	0	Expr_Chip	0	0	0	0	1	1	1.12	**3.12**
ENSG00000110876	*SELPLG*	*SELPLG*	0	Expr_Chip	0	0	0	0	1	1	1.12	**3.12**
ENSG00000136244	*IL6*	*IL6*	1	Expr_Articles	0	0	0	0	1	1	1.10	**3.10**
ENSG00000159189	*C1QC*	*C1QC*	0	Expr_Chip	0	0	0	0	1	1	1.09	**3.09**

Ensembl Gene ID (human)	Gene Symbol (Homo sapiens)	Gene Symbol (Bos taurus)	Gene is in Golden list - 1, not - 0	Evidence	**Крите-рий 1.** GWAS-1, not GWAS-0	**Крите-рий 2.** Has associated allele-1, not has-0	**Крите-рий 3.** Knockout -1, not -0	**Крите-рий 4.** Has PPI with virus-1, not has -0	**Крите-рий 5.** Has overepresented GO term-1, not has -0	**Крите-рий 6.** Has overepresented Pathway-1, not has -0	**Крите-рий 7.** Rang in the PPI network	**Суммарный балл**
ENSG00000177455	*CD19*	*CD19*	0	Expr_Chip	0	0	0	0	1	1	1.07	**3.07**
ENSG00000125538	*IL1B*	*IL1B*	0	Expr_Chip	0	0	0	0	1	1	1.03	**3.03**
ENSG00000150782	*IL18*	*IL18*	0	Expr_Chip	0	0	0	0	1	1	1.01	**3.01**
ENSG00000165025	*SYK*	*SYK*	0	Expr_Articles Expr_Chip	0	0	0	0	1	1	1.01	**3.01**
ENSG00000019991	*HGF*	*HGF*	0	GWAS	1	0	0	0	1	1	0.00	**3.00**
ENSG00000182866	*LCK*	*LCK*	1	Expr_Chip	0	0	0	0	1	1	0.99	**2.99**
ENSG00000254087	*LYN*	*LYN*	0	Expr_Chip	0	0	0	0	1	1	0.98	**2.98**
ENSG00000164342	*TLR3*	*TLR3*	0	Expr_Articles	0	0	0	0	1	1	0.92	**2.92**
ENSG00000026508	*CD44*	*CD44*	0	Expr_Chip	0	0	0	0	1	1	0.83	**2.83**
ENSG00000169429	*CXCL8*	*CXCL8*	0	Expr_Chip	0	0	0	0	1	1	0.81	**2.81**
ENSG00000109471	*IL2*	*IL2*	1	Expr_Articles	0	0	0	0	1	1	0.77	**2.77**
ENSG00000117090	*SLAMF1*	*SLAMF1*	0	Expr_Chip	0	0	0	0	1	1	0.75	**2.75**
ENSG00000113520	*IL4*	*IL4*	0	Expr_Articles	0	0	0	0	1	1	0.74	**2.74**
ENSG00000177606	*JUN*	*JUN*	1	Expr_Chip	0	0	0	0	1	1	0.74	**2.74**
ENSG00000113302	*IL12B*	*IL12B*	0	Expr_Articles	0	0	0	0	1	1	0.73	**2.73**
ENSG00000005844	*ITGAL*	*ITGAL*	1	Expr_Chip	0	0	0	0	1	1	0.72	**2.72**
ENSG00000103490	*PYCARD*	*PYCARD*	0	Expr_Chip	0	0	0	0	1	1	0.72	**2.72**
ENSG00000197766	*CFD*	*CFD*	0	Expr_Chip	0	0	0	0	1	1	0.69	**2.69**
ENSG00000169245	*CXCL10*	*CXCL10*	0	Expr_Chip	0	0	0	0	1	1	0.69	**2.69**
ENSG00000196664	*TLR7*	*TLR7*	0	Expr_Articles	0	0	0	0	1	1	0.67	**2.67**
ENSG00000010810	*FYN*	*FYN*	0	Expr_Chip	0	0	0	0	1	1	0.65	**2.65**
ENSG00000213658	*LAT*	*LAT*	0	Expr_Chip	0	0	0	0	1	1	0.64	**2.64**

Ensembl Gene ID (human)	Gene Symbol (Homo sapiens)	Gene Symbol (Bos taurus)	Gene is in Golden list - 1, not - 0	Evidence	**Критерий 1.** GWAS-1, not GWAS-0	**Критерий 2.** Has associated allele-1, not has-0	**Критерий 3.** Knockout -1, not -0	**Критерий 4.** Has PPI with virus-1, not has -0	**Критерий 5.** Has overepresented GO term-1, not has -0	**Критерий 6.** Has overepresented Pathway-1, not has -0	**Критерий 7.** Rang in the PPI network	**Суммарный балл**
ENSG00000198087	*CD2AP*	*CD2AP*	0	GWAS	1	0	0	0	1	0	0.64	**2.64**
ENSG00000138378	*STAT4*	*STAT4*	0	Expr_Chip	0	0	0	0	1	1	0.61	**2.61**
ENSG00000160654	*CD3G*	*CD3G*	1	Expr_Chip	0	0	0	0	1	1	0.53	**2.53**
ENSG00000163737	*PF4*	*PF4*	0	Expr_Chip	0	0	0	0	1	1	0.53	**2.53**
ENSG00000161955	*TNFSF13*	*TNFSF13*	0	Expr_Chip	0	0	0	0	1	1	0.52	**2.52**
ENSG00000011600	*TYROBP*	*TYROBP*	0	Expr_Chip	0	0	0	0	1	0	1.47	**2.47**
ENSG00000188404	*SELL*	*SELL*	0	Expr_Chip	0	0	0	0	1	1	0.46	**2.46**
ENSG00000105369	*CD79A*	*CD79A*	0	Expr_Articles	0	0	0	0	1	0	1.45	**2.45**
ENSG00000113013	*HSPA9*	*HSPA9*	0	Expr_Chip	0	0	0	0	1	1	0.44	**2.44**
ENSG00000108561	*C1QBP*	*C1QBP*	0	Expr_Chip	0	0	0	0	1	1	0.44	**2.44**
ENSG00000156738	*MS4A1*	*MS4A1*	0	Expr_Chip	0	0	0	0	0	1	1.39	**2.39**
ENSG00000243649	*CFB*	*CFB*	0	Expr_Chip	0	0	0	0	1	1	0.36	**2.36**
ENSG00000187796	*CARD9*	*CARD9*	0	Expr_Chip	0	0	0	0	1	1	0.36	**2.36**
ENSG00000239732	*TLR9*	*TLR9*	0	Expr_Articles	0	0	0	0	1	1	0.29	**2.29**
ENSG00000122223	*CD244*	*CD244*	0	Expr_Chip	0	0	0	0	1	1	0.26	**2.26**
ENSG00000168811	*IL12A*	*IL12A*	0	Expr_Articles	0	0	0	0	1	1	0.26	**2.26**
ENSG00000101916	*TLR8*	*TLR8*	0	Expr_Articles	0	0	0	0	1	0	1.26	**2.26**
ENSG00000066294	*CD84*	*CD84*	0	Expr_Chip	0	0	0	0	1	1	0.20	**2.20**
ENSG00000049768	*FOXP3*	*FOXP3*	0	Expr_Articles	0	0	0	0	1	1	0.19	**2.19**
ENSG00000235568	*NFAM1*	*NFAM1*	0	Expr_Chip	0	0	0	0	1	0	1.18	**2.18**
ENSG00000137312	*FLOT1*	*FLOT1*	0	GWAS	1	0	0	0	1	0	0.18	**2.18**
ENSG00000091409	*ITGA6*	*ITGA6*	0	Expr_Chip	0	0	0	0	1	1	0.12	**2.12**

Ensembl Gene ID (human)	Gene Symbol (Homo sapiens)	Gene Symbol (Bos taurus)	Gene is in Golden list - 1, not - 0	Evidence	**Критерий 1.** GWAS-1, not GWAS-0	**Критерий 2.** Has associated allele-1, not has-0	**Критерий 3.** Knockout -1, not -0	**Критерий 4.** Has PPI with virus-1, not has -0	**Критерий 5.** Has overepresented GO term-1, not has -0	**Критерий 6.** Has overepresented Pathway-1, not has -0	**Критерий 7.** Rang in the PPI network	**Суммарный балл**
ENSG00000134215	*VAV3*	*VAV3*	0	Expr_Chip	0	0	0	0	1	1	0.08	**2.08**
ENSG00000109861	*CTSC*	*CTSC*	0	Expr_Chip	0	0	0	0	1	0	1.01	**2.01**
ENSG00000204472	*AIF1*	*AIF1*	0	Expr_Chip	0	0	0	0	1	0	1.01	**2.01**
ENSG00000065000	*AP3D1*	*AP3D1*	1	PPI	0	0	0	1	1	0	0.00	**2.00**
ENSG00000213760	*ATP6V1G2*	*ATP6V1G2*	0	GWAS	1	0	0	0	0	1	0.00	**2.00**
ENSG00000183625	*CCR3*	*CCR3*	0	Expr_Chip	0	0	0	0	1	1	0.00	**2.00**
ENSG00000160752	*FDPS*	*FDPS*	1	PPI	0	0	0	1	0	1	0.00	**2.00**
ENSG00000111537	*IFNG*	*IFNG*	0	Expr_Articles	0	0	0	0	1	1	0.00	**2.00**
ENSG00000185896	*LAMP1*	*LAMP1*	0	Expr_Chip	0	0	0	0	1	1	0.00	**2.00**
ENSG00000204498	*NFKBIL1*	*NFKBIL1*	0	GWAS	1	0	0	0	1	0	0.00	**2.00**
ENSG00000188389	*PDCD1*	*PDCD1*	0	Expr_Articles	0	0	0	0	1	1	0.00	**2.00**
ENSG00000168477	*TNXB*	*TNXB*	0	GWAS	1	0	0	0	1	0	0.00	**2.00**
ENSG00000204616	*TRIM31*	*TRIM31*	0	GWAS	1	0	0	0	1	0	0.00	**2.00**
ENSG00000181722	*ZBTB20*	*ZBTB20*	0	GWAS	1	0	0	0	1	0	0.00	**2.00**
ENSG00000090382	*LYZ*	*LYZ2*	0	Expr_Chip	0	0	0	0	1	0	0.98	**1.98**
ENSG00000175899	*A2M*	*A2M*	0	Expr_Chip	0	0	0	0	1	0	0.96	**1.96**
ENSG00000204103	*MAFB*	*MAFB*	0	Expr_Chip	0	0	0	0	1	0	0.95	**1.95**
ENSG00000072694	*FCGR2B*	*FCGR2B*	0	Expr_Chip	0	0	0	0	0	1	0.91	**1.91**
ENSG00000197747	*S100A10*	*S100A10*	0	Expr_Chip	0	0	0	0	1	0	0.86	**1.86**
ENSG00000182718	*ANXA2*	*ANXA2*	0	Expr_Chip	0	0	0	0	1	0	0.79	**1.79**
ENSG00000155465	*SLC7A7*	*SLC7A7*	0	Expr_Chip	0	0	0	0	0	0	1.77	**1.77**
ENSG00000168615	*ADAM9*	*ADAM9*	0	Expr_Chip	0	0	0	0	1	0	0.74	**1.74**

Ensembl Gene ID (human)	Gene Symbol (Homo sapiens)	Gene Symbol (Bos taurus)	Gene is in Golden list - 1, not - 0	Evidence	**Критерий 1.** GWAS-1, not GWAS-0	**Критерий 2.** Has associated allele-1, not has-0	**Критерий 3.** Knockout -1, not -0	**Критерий 4.** Has PPI with virus-1, not has -0	**Критерий 5.** Has overepresented GO term-1, not has -0	**Критерий 6.** Has overepresented Pathway-1, not has -0	**Критерий 7.** Rang in the PPI network	**Суммарный балл**
ENSG00000204642	*HLA-F*	*LOC616942*	1	GWAS	1	0	0	0	0	0	0.72	**1.72**
ENSG00000178726	*THBD*	*THBD*	0	Expr_Chip	0	0	0	0	0	1	0.72	**1.72**
ENSG00000153551	*CMTM7*	*CMTM7*	0	Expr_Chip	0	0	0	0	1	0	0.71	**1.71**
ENSG00000131981	*LGALS3*	*LGALS3*	0	Expr_Chip	0	0	0	0	1	0	0.70	**1.70**
ENSG00000130402	*ACTN4*	*ACTN4*	0	Expr_Chip	0	0	0	0	1	0	0.69	**1.69**
ENSG00000141480	*ARRB2*	*ARRB2*	0	Expr_Chip	0	0	0	0	1	0	0.67	**1.67**
ENSG00000103653	*CSK*	*CSK*	0	Expr_Chip	0	0	0	0	1	0	0.66	**1.66**
ENSG00000078747	*ITCH*	*ITCH*	0	Expr_Chip	0	0	0	0	1	0	0.66	**1.66**
ENSG00000102265	*TIMP1*	*TIMP1*	0	Expr_Chip	0	0	0	0	1	0	0.66	**1.66**
ENSG00000120217	*CD274*	*CD274*	0	Expr_Articles	0	0	0	0	1	0	0.62	**1.62**
ENSG00000111640	*GAPDH*	*GAPDH*	0	Expr_Chip	0	0	0	0	1	0	0.61	**1.61**
ENSG00000203747	*FCGR3A*	*FCGR3A*	0	Expr_Chip	0	0	0	0	0	1	0.59	**1.59**
ENSG00000067066	*SP100*	*SP100*	0	Expr_Chip	0	0	0	0	0	1	0.57	**1.57**
ENSG00000100097	*LGALS1*	*LGALS1*	0	Expr_Chip	0	0	0	0	1	0	0.57	**1.57**
ENSG00000057657	*PRDM1*	*PRDM1*	0	Expr_Chip	0	0	0	0	1	0	0.56	**1.56**
ENSG00000126759	*CFP*	*CFP*	0	Expr_Chip	0	0	0	0	0	1	0.56	**1.56**
ENSG00000198223	*CSF2RA*	*CSF2RA*	0	Expr_Chip	0	0	0	0	0	1	0.55	**1.55**
ENSG00000123609	*NMI*	*NMI*	0	Expr_Chip	0	0	0	0	1	0	0.54	**1.54**
ENSG00000010278	*CD9*	*CD9*	0	Expr_Chip	0	0	0	0	0	1	0.50	**1.50**
ENSG00000179583	*CIITA*	*CIITA*	0	Expr_Chip	0	0	0	0	0	1	0.48	**1.48**
ENSG00000136997	*MYC*	*MYC*	1	Expr_Articles	0	0	0	0	1	0	0.47	**1.47**
ENSG00000100644	*HIF1A*	*HIF1A*	0	Expr_Chip	0	0	0	0	1	0	0.46	**1.46**

Ensembl Gene ID (human)	Gene Symbol (Homo sapiens)	Gene Symbol (Bos taurus)	Gene is in Golden list - 1, not - 0	Evidence	**Критерий 1.** GWAS-1, not GWAS-0	**Критерий 2.** Has associated allele-1, not has-0	**Критерий 3.** Knockout -1, not -0	**Критерий 4.** Has PPI with virus-1, not has -0	**Критерий 5.** Has overepresented GO term-1, not has -0	**Критерий 6.** Has overepresented Pathway-1, not has -0	**Критерий 7.** Rang in the PPI network	**Суммарный балл**
ENSG00000137331	*IER3*	*IER3*	0	GWAS	1	0	0	0	0	0	0.43	**1.43**
ENSG00000106211	*HSPB1*	*HSPB1*	0	Expr_Chip	0	0	0	0	1	0	0.38	**1.38**
ENSG00000143546	*S100A8*	*S100A8*	0	Expr_Chip	0	0	0	0	1	0	0.37	**1.37**
ENSG00000187098	*MITF*	*MITF*	0	Expr_Chip	0	0	0	0	1	0	0.37	**1.37**
ENSG00000120899	*PTK2B*	*PTK2B*	0	Expr_Chip	0	0	0	0	1	0	0.35	**1.35**
ENSG00000196230	*TUBB*	*TUBB*	0	GWAS	1	0	0	0	0	0	0.35	**1.35**
ENSG00000165410	*CFL2*	*CFL2*	0	Expr_Chip	0	0	0	0	0	1	0.35	**1.35**
ENSG00000135046	*ANXA1*	*ANXA1*	0	Expr_Chip	0	0	0	0	1	0	0.31	**1.31**
ENSG00000127951	*FGL2*	*FGL2*	0	Expr_Chip	0	0	0	0	0	0	1.24	**1.24**
ENSG00000245848	*CEBPA*	*CEBPA*	0	Expr_Chip	0	0	0	0	1	0	0.23	**1.23**
ENSG00000204463	*BAG6*	*BAG6*	0	GWAS	1	0	0	0	0	0	0.22	**1.22**
ENSG00000135404	*CD63*	*CD63*	0	Expr_Chip	0	0	0	0	0	0	1.21	**1.21**
ENSG00000007312	*CD79B*	*CD79B*	0	Expr_Chip	0	0	0	0	1	0	0.17	**1.17**
ENSG00000181092	*ADIPOQ*	*ADIPOQ*	0	Expr_Chip	0	0	0	0	1	0	0.17	**1.17**
ENSG00000204469	*PRRC2A*	*PRRC2A*	0	GWAS	1	0	0	0	0	0	0.17	**1.17**
ENSG00000164344	*KLKB1*	*KLKB1*	0	Expr_Chip	0	0	0	0	1	0	0.10	**1.10**
ENSG00000269404	*SPIB*	*SPIB*	0	Expr_Chip	0	0	0	0	1	0	0.10	**1.10**
ENSG00000206172	*HBA1*	*HBA*	0	Expr_Chip	0	0	0	0	0	1	0.09	**1.09**
ENSG00000095002	*MSH2*	*MSH2*	0	Expr_Chip	0	0	0	0	1	0	0.08	**1.08**
ENSG00000153064	*BANK1*	*BANK1*	0	Expr_Chip	0	0	0	0	0	0	1.07	**1.07**
ENSG00000114738	*MAPKAPK3*	*MAPKAPK3*	0	Expr_Chip	0	0	0	0	1	0	0.07	**1.07**
ENSG00000196154	*S100A4*	*S100A4*	0	Expr_Chip	0	0	0	0	0	0	1.06	**1.06**

Ensembl Gene ID (human)	Gene Symbol (Homo sapiens)	Gene Symbol (Bos taurus)	Gene is in Golden list - 1, not - 0	Evidence	**Критерий 1.** GWAS-1, not GWAS-0	**Критерий 2.** Has associated allele-1, not has-0	**Критерий 3.** Knockout -1, not -0	**Критерий 4.** Has PPI with virus-1, not has -0	**Критерий 5.** Has overepresented GO term-1, not has -0	**Критерий 6.** Has overepresented Pathway-1, not has -0	**Критерий 7.** Rang in the PPI network	**Суммарный балл**
ENSG00000169413	*RNASE6*	*RNASE6*	0	Expr_Chip	0	0	0	0	0	0	1.05	**1.05**
ENSG00000205581	*HMGN1*	*HMGN1*	0	Expr_Chip	0	0	0	0	0	1	0.05	**1.05**
ENSG00000138795	*LEF1*	*LEF1*	0	Expr_Chip	0	0	0	0	1	0	0.04	**1.04**
ENSG00000140443	*IGF1R*	*IGF1R*	0	Expr_Chip	0	0	0	0	1	0	0.04	**1.04**
ENSG00000074966	*TXK*	*TXK*	0	Expr_Chip	0	0	0	0	1	0	0.04	**1.04**
ENSG00000100219	*XBP1*	*XBP1*	1	Expr_Chip	0	0	0	0	1	0	0.04	**1.04**
ENSG00000158517	*NCF1*	*NCF1*	0	Expr_Chip	0	0	0	0	0	1	0.01	**1.01**
ENSG00000204427	*ABHD16A*	*ABHD16A*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000146109	*ABT1*	*ABT1*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000136518	*ACTL6A*	*ACTL6A*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000164393	*ADGRF2*	*ADGRF2*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000170425	*ADORA2B*	*ADORA2B*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000150594	*ADRA2A*	*ADRA2A*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000158578	*ALAS2*	*ALAS2*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000214274	*ANG*	*ANG*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000138772	*ANXA3*	*ANXA3*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000134262	*AP4B1*	*AP4B1*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000204444	*APOM*	*APOM*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000149311	*ATM*	*ATM*	1	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000130770	*ATP5IF1*	*ATPIF1*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000163930	*BAP1*	*BAP1*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000204439	*C6orf47*	*C23H6orf47*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**

Ensembl Gene ID (human)	Gene Symbol (Homo sapiens)	Gene Symbol (Bos taurus)	Gene is in Golden list - 1, not - 0	Evidence	**Критерий 1.** GWAS-1, not GWAS-0	**Критерий 2.** Has associated allele-1, not has-0	**Критерий 3.** Knockout -1, not -0	**Критерий 4.** Has PPI with virus-1, not has -0	**Критерий 5.** Has overepresented GO term-1, not has -0	**Критерий 6.** Has overepresented Pathway-1, not has -0	**Критерий 7.** Rang in the PPI network	**Суммарный балл**
ENSG00000150753	*CCT5*	*CCT5*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000066294	*CD84*	*CD96*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000184661	*CDCA2*	*CDCA2*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000176749	*CDK5R1*	*CDK5R1*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000133048	*CHI3L1*	*CHI3L1*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000113805	*CNTN3*	*CNTN3*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000124749	*COL21A1*	*COL21A1*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000124812	*CRISP1*	*CRISP1*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000140577	*CRTC3*	*CRTC3*	1	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000172543	*CTSW*	*CTSW*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000180871	*CXCR2*	*CXCR2*	0	Expr_Chip	0	0	0	0	0	1	0.00	**1.00**
ENSG00000173402	*DAG1*	*DAG1*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000186572	*DEFB107A*	*DEFB7*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000136770	*DNAJC1*	*DNAJC1*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000105612	*DNASE2*	*DNASE2*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000198734	*F5*	*F5*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000160211	*G6PD*	*G6PD*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000137270	*GCM1*	*GCM1*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000122694	*GLIPR2*	*GLIPR2*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000174842	*GLMN*	*GLMN*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000204438	*GPANK1*	*GPANK1*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000176998	*HCG4*	*LOC784787*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**

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ENSG00000189403	*HMGB1*	*HMGB1*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000150540	*HNMT*	*HNMT*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000172183	*ISG20*	*ISG20*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000139626	*ITGB7*	*ITGB7*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000136826	*KLF4*	*KLF4*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000089692	*LAG3*	*LAG3*	0	Expr_Articles	0	0	0	0	1	0	0.00	**1.00**
ENSG00000240053	*LY6G5B*	*LY6G5B*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000204428	*LY6G5C*	*LY6G5C*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000011566	*MAP4K3*	*MAP4K3*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000141741	*MIEN1*	*MIEN1*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000170476	*MZB1*	*MZB1*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000204386	*NEU1*	*NEU1*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000152954	*NRSN1*	*NRSN1*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000186642	*PDE2A*	*PDE2A*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000170927	*PKHD1*	*PKHD1*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000146070	*PLA2G7*	*PLA2G7*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000180316	*PNPLA1*	*PNPLA1*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000104695	*PPP2CB*	*PPP2CB*	0	Expr_Chip	0	0	0	0	0	1	0.00	**1.00**
ENSG00000204576	*PRR3*	*PRR3*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000171522	*PTGER4*	*PTGER4*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000147231	*RADX*	*CYB5R1*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000131759	*RARA*	*RARA*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**

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ENSG00000137575	*SDCBP*	*SDCBP*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000196260	*SFTA2*	*SFTA2*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000198053	*SIRPA*	*SIRPA*	0	Expr_Chip	0	0	0	0	0	1	0.00	**1.00**
ENSG00000138449	*SLC40A1*	*SLC40A1*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000204385	*SLC44A4*	*SLC44A4*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000119457	*SLC46A2*	*SLC46A2*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000086300	*SNX10*	*SNX10*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000137642	*SORL1*	*SORL1*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000111786	*SRSF9*	*SRSF9*	0	Expr_Chip	0	0	0	0	0	1	0.00	**1.00**
ENSG00000084090	*STARD7*	*STARD7*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000148175	*STOM*	*STOM*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000079950	*STX7*	*STX7*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000135316	*SYNCRIP*	*SYNCRIP*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000196628	*TCF4*	*TCF4*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000008197	*TFAP2D*	*TFAP2D*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000035862	*TIMP2*	*TIMP2*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000139644	*TMBIM6*	*TMBIM6*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000076554	*TPD52*	*TPD52*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**
ENSG00000065308	*TRAM2*	*TRAM2*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000204614	*TRIM40*	*TRIM40*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000134253	*TRIM45*	*TRIM45*	0	GWAS	1	0	0	0	0	0	0.00	**1.00**
ENSG00000134744	*TUT4*	*ZCCHC11*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**

Ensembl Gene ID (human)	Gene Symbol (Homo sapiens)	Gene Symbol (Bos taurus)	Gene is in Golden list - 1, not - 0	Evidence	**Крите-рий 1**. GWAS-1, not GWAS-0	**Крите-рий 2**. Has associated allele-1, not has-0	**Крите-рий 3**. Knockout -1, not -0	**Крите-рий 4.** Has PPI with virus-1, not has -0	**Крите-рий 5.** Has overepresented GO term-1, not has -0	**Крите-рий 6.** Has overepresented Pathway-1, not has -0	**Крите-рий 7**. Rang in the PPI network	**Суммарный балл**
ENSG00000116729	*WLS*	*WLS*	0	Expr_Chip	0	0	0	0	1	0	0.00	**1.00**