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Identification Hub Genes of Consensus Molecular Subtype Correlation with Immune Infiltration and Predict Prognosis in Gastric Cancer

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Abstract

Gastric Cancer (GC) has a great fatality rate, meanwhile, there is still a lack of available biomarkers for prognosis. The goal of the research was to discover key and novel potential biomarkers for GC. We screened for the expression of significantly altered genes based on survival rates from two consensus molecular subtypes (CMS) of GC. Subsequently, functional enrichment analysis showed these genes involved in many cancers. And we picked 6 hub genes that could both secreted in the tumor microenvironment and expression enhanced in immune cells. Then, Kaplan Meier survival and expression detected in the tumor pathological stage were utilized to clarify the prognostic of these 6 hub genes. The results indicated that OGN, CHRDL2, C2orf40, THBS4, CHRDL1, and ANGPTL1, respectively, were significantly associated with poor OS in GC patients. And their expression increased with cancer advanced. Moreover, immune infiltration analysis displayed that those hub genes expression positively with M2 macrophage, CD8⁺ T Cell, most immune inhibitors, and majority

immunostimulators. In summary, our results suggested that OGN, CHRDL2, C2orf40, THBS4, CHRDL1, and ANGPTL1 were all potential biomarkers for GC prognosis and might also be potential therapeutic targets for GC.

Keywords Gastric Cancer, Prognosis, Immune Infiltration, OGN, CHRDL2

Introduction

Gastric Cancer (GC) is one of the most common malignant tumors, and its mortality ranks fourth among all malignant tumors in the world[1]. According to the global cancer statistics (2020), there were over one million new cases of GC and with a mortality rate of 7.7% of the total cancer deaths[1]. Due to the lack of effective biomarkers, most patients with GC are diagnosed at an advanced stage and distant metastasis often occurs at this stage, leading to a poor prognosis. The 5-year overall survival rate of GC is about 20%–30% in most parts of the world[2]. The earlier the effective intervention for GC patients, the more beneficial to improve their survival rate. Therefore, it is necessary to identify the key prognostic biomarkers in early time for GC therapy.

Immune checkpoint blockade (ICB) has been brought new hope for many cancers treatment. While ICB does not valid in most cases, including GC[3], and thus more research is required to drive the field forward. Immune-related cells in the tumor microenvironment (TME) also indispensable for the development, progression, and prognosis of GC. Despite CD8⁺T cells are considered to be an anti-tumor component in the TME[4], studies on the relationship between CD8⁺T cells and prognosis in GC yielded in divergence[5, 6]. Programmed cell death protein 1 (PD-1) is an important immune checkpoint molecule in CD8⁺ T cell and its upregulation disturbs the anti-

tumor function of CD8⁺ T cell[7]. PD-1+CD8⁺ T cell infiltration was significantly increased in patients with GC[6]. While PD-1 blockade combined with immune modulators, such as TGF- β 1 inhibitor, might take patients more benefits than targeted PD-1 alone [6]. And it was also reported that some subsets of CD8⁺T, such as CXCR5+CD8⁺T[8], but not CD8⁺T itself connected with better overall survival (OS) in patients with GC. Therefore, it is important to find out the key molecules that regulate immune modulators in TME or/and co-express molecular in CD8⁺T that mediated its function.

Besides, the latest studies have proved that macrophages, mostly M2 polarized macrophages, have a vital role in the GC advance[9, 10]. Infiltration of M2 macrophage might be a worthwhile biomarker for GC prognosis[11]. Targeting M2 macrophages may be a promising therapeutic strategy, therefore, it is valuable that uncover M2-related molecules.

Here, we picked out those genes that were significantly associated with the survival of GC patients. And selected hub genes, OGN, CHRDL2, C2orf40, THBS4, CHRDL1, and ANGPTL1, which secreted into TME and enhanced in immune cells. After validated their expression value for GC diagnosis, we performed immune infiltration analysis of these 6 hub genes. Our study might provide novel biomarkers for GC advance, and potential targets that combined using with ICB to improve GC therapy.

Results

Identification of robust genes associated with GC survival

The COMSUC web server[12] was used to find out the hub genes significantly

correlated with the survival of GC patients. we firstly clustered GC samples into two consensus molecular subtypes (CMS) by multiple methods, including K-means, hierarchical clustering (Hclust), non-negative matrix factorization (NMF) (Figure. 1a-b). And we found that CMS1 had lower survival than CMS2 (Figure. 1c). 52 genes prominently up-regulated expression in CMS1 compare to CMS2 (Figure. 1d). These genes may act independently or work in concert for GC survival.

Functional enrichment analysis of survival-related CMS genes

To identify the notably enriched pathway and biological process of survival-related CMS genes, we explored in Metascape website [13] and found those genes related to many processes of cancer (Figure. 2a). And the most relative pathway was early gastric cancer (Figure. 2a). Then we analyzed the sub-network of those CMS1 genes in TCGA RNAseq of STAD, most of them had some connections in each other (Figure. 2b). According to those results, we speculated whether those genes were regulated by some common transcription factors (TFs). After performing TF enrichment in Knock TF (<http://www.licpathway.net/KnockTF/index.html>), more than ten TFs predicted may regulate over 73% of genes of these selected 52 genes (Table 1). The top 4 TFs were TFAP4, TP53, CREB1, and PTEN, respectively (Figure. 2c), and they all have been reported to promote the progression of GC [14-17]. Furthermore, we explored the characteristics of the 52 genes in the GeneCards (<https://www.genecards.org/>) and the Human Protein Atlas (<https://www.proteinatlas.org/>). As shown in Table 2, 10 genes could be transcribed into secreted proteins, 22 genes enriched in immune cells and only 7 genes own both characters (Fig. 2d).

Survival outcomes in selected genes

To verify whether the selected 7 genes (OGN, CHRDL2, C2orf40, THBS4, CHRDL1, ANGPTL1, SLIT2) were correlated with worse overall survival (OS) in GC patients, survival analysis was performed in Kaplan Meier plotter [18]. On account of many articles that have been shown that SLIT2 was over-expression in gastric cancer and might be an independent risk factor for GC [19, 20], we did not explore it further in this paper. The Kaplan Meier plotter results showed that the up-regulated expression of OGN, CHRDL2, C2orf40, THBS4, CHRDL1, and ANGPTL1, respectively, was correlated with poorer OS in GC patients (Fig. 3a-f). Among them, OGN and CHRDL2 were firstly reported in GC that their expression was related to OS of GC patients. To further confirm the correlation of 6 genes expression with tumor progression in GC, expression in different stages was executed in GEPIA[21]. The analyzed results indicated that the expression of OGN, CHRDL2, C2orf40, THBS4, CHRDL1, and ANGPTL1 was gradually increased in the GC stage (Fig. 4a-f). These results revealed these 6 hub genes were significantly related to the aggravation and survival of GC.

Immune cell infiltration analysis

To investigate the relationship between the expression of these hub genes (OGN, CHRDL2, C2orf40, THBS4, CHRDL1, and ANGPTL1) and immune infiltration, the TIMER website[22] was used to analyze the correlation between these hub genes and multiple immune cells. The results indicated that the expression of these hub genes was significantly positively correlated with CD8⁺ T Cell, CD4⁺ T Cell, macrophage, neutrophil, dendritic cell (Fig. 5). Next, we further analyzed the correlations of

macrophage subtypes infiltration with these hub genes in GC. The results exhibited these 6 hub genes had no significant link in M1-related markers with their expression, but exhibited remarkable connection in M2 and TAMs (Fig. 6).

Correlation analysis between hub genes and immune markers

To better understand the immune function of these hub genes, we explored the relationship between their expression and immune markers in TISIDB[23]. Tumor immunology analysis exhibited that the expression of these 6 genes was positively correlated with most immunoinhibitors (Fig. 7a) and majority immunostimulators (Fig. 8a). Furthermore, we check out the striking different genes verified again in GEPIA, like CSF1R and Cxcl12, and got similar results (Fig. 7b-g, 8b-g). In the end, we search data found that OGN, C2orf40, CHRDL2, THBS4, CHRDL1, and ANGPTL1 had different immune subtypes in GC (Fig. 9a-f) and their expression was divergent in various molecular subtypes (Fig. 10a-f). In summary, these results implied that these 6 hub genes might potentially govern the conscription and awakening of immune cells in GC.

Discussion

Chemotherapy, radiotherapy, surgery, immunotherapy, and targeted therapy are effective in the progression of GC in appropriate indications. While the limited OS that no more than 30% in most countries, there are still need specific biomarkers to guide rational using drugs, especially for ICB treatment.

OGN is a member of the small leucine-rich proteoglycan (SLRP) family and its function may vary from different tumors. It was reported that OGN was upregulated in

meningioma, and function as a tumor promoter by inhibiting NF2 expression and triggering mTOR signaling [24]. There was, however, also experimental evidence that OGN expression reduced in multiple cancers and its expression levels positively with survival rates[25, 26]. For example, OGN inhibited cell proliferation, invasion, and epithelial to mesenchymal transition through EGFR/Akt pathway in colorectal cancers [27]. Besides, OGN, as one of the biologically active elements of the vascular extracellular matrix, could be tested in plasma/serum and acted as a biomarker in disease [28, 29]. For instance, serum OGN was an independent risk predictor for patients with chronic kidney disease [28]. OGN also could adjust immune response via mediating immune cell infiltration in cancer, such as OGN expression positively associated with CD8⁺ T cells recruitment/infiltration by inhibited HIF-1 α / VEGF pathway in colorectal cancer[26]. The role of OGN in GC has not been reported so far. Our study showed that OGN could be a new useful prognostic biomarker and immune regulator for GC.

CHRD2, an antagonist of bone morphogenic proteins (BMPs), worked as an oncogene in colorectal cancer [30] and osteosarcoma [31]. CHRD2 was firstly discovered in 2003 named as BNF-1 (breast tumor novel factor 1) and found its overexpression in breast, lung, and colon tumors detected by PCR in a small sample[32]. While the report of CHRD2 in the tumor is very limited. Here, we first pointed out that CHRD2 expression increased in the GC process and its high expression was associated with poor prognosis in GC patients. As a secreted protein, we found its expression associated with immune cell infiltration, especially for M2 macrophage, and immune inhibit

molecular markers. Therefore, CHRDL2 might be a novel target of GC therapy.

C2orf40 encodes a protein called esophageal cancer-related gene-4 (ECRG4), which is down-regulated by hypermethylation of its promoter in diverse types of tumors, including hepatocellular carcinoma [33], gastric cancer [34], breast cancer [35]. According to current reports, c2orf40 might as a potential tumor suppressor gene in tumors. However, our results exhibited that high ECRG4 expression was remarkably associated with poorer outcomes (HR=1.95, log-rank $P=6.7e-10$), and its expression showing a state of gradual increase in GC advance. The opposite result may be on account of different levels of evidence or cohort studies [34, 36]. The deep reasons yet to be further validated. It has been reported that ECRG4 interacted with TLR4 [34]. And TLR4/PI3K/Akt signaling was a vital way to promote M2 polarization of macrophages [10]. It also needs to verify whether ECRG4 is involved in the development of GC by modifying the M2 polarization of macrophages through TLR4. THBS4 belongs to the thrombospondin protein family, which is a kind of adhesive glycoproteins that mediate cell-to-cell and cell-to-matrix interactions. As a secreted extracellular matrix protein, THBS4 has been reported mediated angiogenesis responding to TGF- β signaling [37]. THBS4 in favor of an oncogene in colorectal cancer [38], prostate cancer [39], and hepatocellular carcinoma [40]. Compared to normal tissues, THBS4 expression at a higher level in those cancers. In colorectal cancer, THBS4 secretion induced by TGF β /PDGFR β pathways and promoted adhesion, migration, and proliferation of colorectal cancer [38]. And THBS4 might as a potential therapeutic target in prostate cancer, inhibited expression of THBS4 could impede the

PI3K/Akt signaling and disturb the cancer stem cell (CSC)-like properties[39]. THBS4 might as a biomarker for diffuse-type gastric adenocarcinomas[41], and a potential indicator for risk assessment and prognosis prediction of GC according to its polymorphisms [42] and bioinformatics analysis [43]. Our study found that the expression of THBS4 is notable increased following the advanced procession of GC. Moreover, THBS4 expression is associated with TGF β in GC. TGF β / PDGFR β pathways might also facilitate THBS4 secretion to promoting GC. THBS4 also positively correlated with others immunoinhibitors and majority immunostimulators. The important role of THBS4 in GC needs more evidence to confirm.

CHRD1, a paralog of CHRD2, only two papers reported in GC. One paper reported that its overexpression correlated with poor prognosis in GC[44]. Another reported low expression of CHRD1, as an antagonist of bone morphogenetic protein 4 (BMF4), might promote GC cell proliferation and migration by BMP receptor II [44]. However, our results revealed that high expression of CHRD1 with poor OS and its expression associated with tumor stages, immune cell infiltration, immunoinhibitors, and immunostimulators.

Many papers showed ANGPTL1 acted as a tumor suppressor by inhibiting angiogenesis, cancer metastasis, cancer stemness, and repressing sorafenib resistance in treatment[45, 46]. while its role in GC still not clear [47]. Our results revealed that ANGPTL1 might be a potential target in GC, according to its high expression related to poor OS and gradually increased with tumor stages as well as the feasible relationship with immune cells and biomarkers in TME.

Conclusions

Here, we searched a series of databases to find out the most relevant molecular that their expression closely related to the survival of GC. And functional enrichment analysis of survival-related CMS genes was performed. These genes are involved in many cancers, including GC, and cancer processes, such as angiogenesis. Then, we picked 6 genes that could be secreted in the TME and enhanced in immune cells. Further survival analysis demonstrated that high expression of OGN, CHRDL2, C2orf40, THBS4, CHRDL1, and ANGPTL1, respectively, was significantly associated with poor OS in GC patients. OGN and CHRDL2 were the firstly reported in GC. Moreover, the expression of these 6 genes prominently increased with the tumor pathological stage. In addition, we investigated the pathways of those hub genes by enrichment analysis. Ultimately, immune infiltration analysis displayed that those hub genes expression positively with CD8⁺ T Cell, M2 macrophage, most immunoinhibitors, and majority immunostimulators. These processes are closely relative to tumor growth and metastasis. Therefore, high expression of 6 hub genes alone or synergistically resulted in a poor prognosis in GC patients. More experiments are still needed to verify these findings.

Abbreviations

GC: Gastric Cancer; ICB: Immune checkpoint blockade; TME: tumor microenvironment; OS: overall survival; CMS: consensus molecular subtypes; TFs: transcription factors; SLRP: small leucine-rich proteoglycan; BMPs: bone

morphogenic proteins; BNF-1: breast tumor novel factor 1; ECRG4: esophageal cancer-related gene-4; CSC: cancer stem cell.

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Authors' contributions

Mei Ma, Bin Yu, and Xin Yu performed the experimental design and data analysis. Mei Ma wrote the manuscript. Jianping Xiong supervised the study. All authors read and approved the final manuscript.

Data availability

All data generated or analyzed during this study are included in this article.

Compliance with ethical standards

Conflict of interests The authors have no conflicts of interest to disclose.

Ethics approval The study was approved by the Ethics Committee of The First Affiliated Hospital of Nanchang University.

Consent to participate Not applicable.

Consent for publication Not applicable.

Code availability Not applicable.

Materials and Methods

COMSUC

COMSUC[12] (<http://comsuc.bioinformai.tech/home>) is used to identify Consensus Molecular Subtypes (CMS) by integrating multiple clustering results based on multiple platforms, multiple omics data, and multiple methods. In this study, we integrated clustering results of GC data from TCGA into two groups by three algorithms based on K-means, hierarchical clustering (Hclust), non-negative matrix factorization (NMF).

Metascape

Metascape[13] (<http://metascape.org/gp/index.html#/main/step1>) is a web server designed to provide an extensive gene list annotation and analysis resource for users. Enrichment analysis was the essential part of Metascape. Here, we analyzed the prominent changed genes of CMS1 for enrichment analysis by custom analysis.

Kaplan–Meier Plotter

Kaplan–Meier plotter[18] (<http://kmplot.com/analysis/>) is a platform utilized to discover and validate the survival biomarkers of four cancers, including gastric cancer. To analyze the prognostic value of OGN, CHRDL2, C2orf40, THBS4, CHRDL1, and ANGPTL1, the cohorts were divided into high- and low- groups through their expression. In this study, the overall survival of 6 hub genes was compared in GC. And the hazard ratios (HRs, with 95% confidence intervals) and log-rank P-values (< 0.05 as significant difference) were counted.

GEPiA

Gene Expression Profiling Interactive Analysis[21] (GEPiA, <http://gepia.cancer->

pku.cn/) uses a standard processing approach to examine genes expression by RNA sequencing data for 8,587 normal samples and 9,736 tumors from GTEx and TCGA projects. Here, GEPIA was used to investigate the six hub genes expression correlation for GC tumor stages from TCGA data. In addition, we valued the correlation between the expression of CSF1R/CXCL12 and six hub genes base on GEPIA.

TIMER

TIMER[22] (<https://cistrome.shinyapps.io/timer/>) is a web tool used to investigate immune cell infiltration in diverse cancers, including GC. It provides data to evaluate the associations between expression levels of selected genes and infiltrating immune cells, such as B cells, CD4⁺ T cells, CD8⁺ T cells, neutrophils, macrophages, and dendritic cells. In our study, we estimated the correlation of expression of OGN, CHRDL2, C2orf40, THBS4, CHRDL1, and ANGPTL1 with immune cell infiltration.

TISIDB

TISIDB[23] (<http://cis.hku.hk/TISIDB/index.php>) is an online web for assessing tumor-related gene and immune system interaction. In our study, we used TISIDB to find out the correlation between the expression of six hub genes and the abundance of immunomodulators. And distribution of six hub genes expression across immune and molecular subtypes in GC. The correlations between six hub genes and the immune system were measured by Spearman's test.

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Figures and Figure legends

Fig. 1 Identification of robust genes associated with GC survival.

a Network of GC CMS by K-means, hierarchical clustering (Hclust), non-negative matrix factorization (NMF). **b** Heatmap of GC by two groups of CMS across three clustering methods. **c** Kaplan-Meier survival analysis showed CMS1 had poor survival. **d** Identification of key modules that prominent change in CMS1 vs. CMS2.

Fig. 2 Functional enrichment analysis of survival-related CMS genes.

a Gene ontology (GO) enrichment analysis of CMS selected genes in Metascape. **b** PPI network of CMS selected genes in GENEMANIA database. **c** Venn diagram showed the number of those selected 52 genes regulated by TFAP4, TP53, CREB1, PTEN predicted in Knock TF. **d** Venn diagram displayed genes that encode secreted proteins and enriched in immune cells.

Fig. 3 Overall survival analysis of six hub genes in GC patients.

Survival curves for high and low expression of OGN, CHRDL2, C2orf40, THBS4, CHRDL1, and ANGPTL1 in GC based on the Kaplan–Meier plotter database.

Fig. 4 Relationships between mRNA levels of six hub genes and tumor stages.

mRNA expression of OGN, CHRDL2, C2orf40, THBS4, CHRDL1, and ANGPTL1 was significantly correlated with tumor stages based on GEPIA.

Fig.5 Correlations of six hub genes with immune cell infiltration level in GC. OGN, CHRDL2, C2orf40, THBS4, CHRDL1, and ANGPTL1 all had significant positive correlations with infiltrating levels of CD8+ T Cell, CD4+ T Cell, macrophage, neutrophil, dendritic cell in GC.

Fig. 6 Expression of six hub genes correlated with TAM polarization in the TME of GC. Scatterplots outline the relationship between the expression of six hub genes and various gene markers of TAMs (a), M1 macrophages (b), and M2 macrophages (c) by TIMER.

Fig. 7 Relations between the abundance of tumor-infiltrating immunoinhibitors and expression of six hub genes.

a Heatmap exhibited six hub genes that were positively correlated with most immunoinhibitors base on TISIDB. **b** CSF1R had linked with six hub genes base on GEPIA.

Fig. 8 Tumor immunology analysis exhibited the expression of six hub genes' relationship with immunostimulators base on TISIDB (a) and GEPIA (b-g).

Fig. 9 Associations between expression of six hub genes and immune subtypes in GC.

OGN (a), CHRDL2 (b), C2orf40 (c), THBS4 (d), CHRDL1(e) and ANGPTL1 (f) investigated in TISIDB. C1: wound healing; C2: IFN- γ dominant; C3: inflammatory; C4: lymphocyte depleted; C5: immunologically quiet; C6: TGF- β dominant.

Fig. 10 Correlations between expression of six hub genes and molecular subtypes in GC.

OGN (a), CHRDL2 (b), C2orf40 (c), THBS4 (d), CHRDL1(e) and ANGPTL1 (f) analyzed in TISIDB. CIN: chromosomal unstable; EBV: Epstein–Barr virus–positive; GS: genomically stable; HM-SNV: hypermutated with elevated single nucleotide variation; HM-indel: hypermutated enriched for insertion/deletion.

Tables

Table 1. Selected 52 genes with CMS1-related significant change performed TF enrichment in Knock TF.

TFs	Genes regulated by relative TFs
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TFAP4	LDB3 KIAA0408 SLITRK5 SORCS1 VIPR2 SYNMPRUNE2 ACTG2 GNAO1RGMA HSPB7 CASQ2 DES MYH11 BOC SYNPO2 MYOC GRIK5 CHRM2PGM5 LMOD1SMYD1THBS4 CADM3 CHRDL2 SCRG1 FOXP2 SCN7A ATP1A2 HAND2PDZRN4 TCEAL2 HSPB6 PLIN4 CNKSR2 RNF150CYP1B1 SFRP1 CNN1 CHRDL1 OGN C7 SLIT2 PLN MEOX2C2orf40 ANGPTL1 PLP1 CNTN1 KCNMA1 PCDH10
TP53	MEOX2 SLITRK5 PLP1 KIAA0408 CYP1B1 CHRDL1 FOXP2 CASQ2 PCDH10 HAND2RGMA HSPB6 MYH11 CNN1 CNTN1 SFRP1 KCNMA1 OGN SCN7A MYOC ATP1A2 SCRG1 HSPB7 ACTG2 SMYD1DES LDB3 CHRDL2 GNAO1THBS4 GRIK5 CHRM2SLIT2 ANGPTL1 CNKSR2 CADM3 BOC C2orf40SYNPO2 LMOD1 PGM5 RNF150PLN VIPR2 PLIN4 TCEAL2 PDZRN4 SORCS1
CREB1	CASQ2 SMYD1CHRM2PGM5 TCEAL2 MEOX2PLP1 C7 KIAA0408 SYNPO2 DES KCNMA1 LDB3 PLIN4 MYOC GNAO1SCRG1 FOXP2 SLIT2 SCN7A CYP1B1 ANGPTL1 PCDH10 ATP1A2 PRUNE2 SLITRK5 CNN1 CNTN1 ACTG2 LMOD1C2orf40 PLN CADM3 SORCS1 OGN THBS4 CHRDL2 RGMA HSPB7 SFRP1 CHRDL1 GRIK5 HAND2HSPB6 PDZRN4 CNKSR2
PTEN	KIAA0408 PCDH10 CHRDL1 GNAO1CNTN1 SLITRK5 SLIT2 SMYD1SYNM SCRG1 BOC GRIK5 HSPB6

	LMOD1LDB3	MEOX2TCEAL2	CNN1	C2orf40	ANGPTL1	
	SCN7A	CYP1B1	PLP1	HAND2	PLIN4	THBS4 CASQ2 C7
	CADM3	RGMA	CHRM2	PDZRN4	SFRP1	OGN PGM5
	RNF150	SORCS1	HSPB7	SYNPO2	VIPR2	DES PLN
	ACTG2	CHRD12	CNKSR2	ATP1A2		
GATA2	CHRD11	ACTG2	CNN1	SFRP1	KIAA0408	SCRG1 PLIN4
	CASQ2	HAND2	PLP1	ATP1A2	SYNM	GRIK5 CADM3
	THBS4	MYH11	SLIT2	MYOC	ANGPTL1	SCN7A KCNMA1
	RNF150	GNAO1	LMOD1	PCDH10	MEOX2	CHRM2TCEAL2
	CHRD12	LDB3	OGN	PRUNE2	RGMA	CNKSR2
	CYP1B1	HSPB7	FOXP2	SMYD1	PLN	PDZRN4
	SLITRK5	SYNPO2	PGM5	HSPB6	DES	
TP63	CYP1B1	PLN	SLITRK5	OGN	SCN7A	KCNMA1
	C2orf40	GNAO1	PCDH10	CNKSR2	FOXP2	LMOD1
	MYH11	SLIT2	PGM5	C7	HSPB6	LDB3 ANGPTL1 SFRP1
	CNTN1	SORCS1	HAND2	CNN1	SYNM	PDZRN4
	CHRM2	PLIN4	MEOX2	KIAA0408	THBS4	TCEAL2
	ACTG2	PLP1	HSPB7	VIPR2	CHRD11	SCRG1 PRUNE2
	GRIK5	BOC	RNF150	CHRD12		
FOXMI	CNKSR2	KCNMA1	SORCS1	PLP1	ATP1A2	
	KIAA0408	CASQ2	CYP1B1	HSPB7	PRUNE2	ACTG2
	HAND2	TCEAL2	DES	SCRG1	CHRD12	PLIN4 GRIK5
	C7	MEOX2	LDB3	SMYD1	SFRP1	CNN1 MYOC SLIT2
	OGN	MYH11	SCN7A	CADM3	PDZRN4	RNF150
	LMOD1	PCDH10	RGMA	CNTN1	C2orf40	PGM5 SYNM

	BOC	HSPB6	ANGPTL1				
FOXP1	CYP1B1	CNN1	SORCS1	PLN	LMOD1	HSPB6	CHRD12
	C2orf40	MEOX2	TCEAL2	PGM5	PDZRN4	ANGPTL1	
	CHRM2	RGMA	RNF150	DES	PLP1	HSPB7	SCN7A C7
	PLIN4	VIPR2	CNKSR2	CHRD1	CASQ2	HAND2	
	SLITRK5	SFRP1	OGN	CADM3	PRUNE2	CNTN1	
	KIAA0408	MYOC	LDB3	SYNM	KCNMA1	SLIT2	GRIK5
	GNAO1	SYNPO2					
NR2F2	HSPB7	GNAO1	DES	KCNMA1	TCEAL2	CNTN1	
	SORCS1	CHRD12	CYP1B1	SCRG1	SMYD1	PLP1	
	SFRP1	MYH11	LDB3	CNN1	C2orf40	CHRM2	ACTG2 BOC
	PRUNE2	PCDH10	SLIT2	CADM3	MYOC	OGN	
	RGMA	THBS4	PDZRN4	CNKSR2	PLIN4	HAND2	
	KIAA0408	CHRD1	GRIK5	SLITRK5	MEOX2	C7	PGM5
	SYNM	ATP1A2					
POSTN	KIAA0408	ANGPTL1	CNN1	CHRM2	C7	CASQ2	FOXP2
	OGN	ATP1A2	GNAO1	KCNMA1	SYNPO2	THBS4	
	HAND2	CADM3	LMOD1	CHRD1	PLP1	ACTG2	DES
	CNTN1	VIPR2	GRIK5	C2orf40	SCN7A	RGMA	SLIT2
	RNF150	HSPB7	SFRP1	CNKSR2	LDB3	MYH11	PLN
	SLITRK5	CHRD12	MEOX2	SYNM			

Table 2. Characteristics of the 52 genes that can be transcribed into secreted proteins or enriched in immune cells.

Characters	Selected genes
Secreted	C7 THBS4 CHRDL1 SFRP1 SLIT2 CHRDL2 SCRG1 OGN C2orf40 ANGPTL1
Immune cell- enriched	OGN CHRDL1 PLP1 VIPR2 CHRDL2 PGM5 BOC SORCS1 THBS4 GRIK5 CASQ2 PLIN4 TCEAL2 C2orf40 PLN ANGPTL1 SLIT2 GNAO1 SCN7A NBLA00301 MEOX2 CHRM2 CNKSR2