

## **Transcriptome profiling identifies differentially expressed genes in systemic lupus erythematosus specific induced pluripotent stem cells from urine.**

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### **Abstract**

**In clinical practice, it is difficult to monitor the repeating relapse in patients who have been suffering from systemic lupus erythematosus (SLE). The underlying etiology remains largely unknown. In order to understand the pathogenesis of SLE, the renal tubular cells-derived iPSCs were successfully obtained from urine of SLE patients. Here, with the purpose of identifying differentially expressed genes, high-throughput Illumina sequencing technology were analyzed the mRNA expression in SLE-iPSCs group and control-iPSCs group. Within the 4,254 genes, which were differentiated at least two-fold between the SLE-iPSCs and control-iPSCs, 2,856 genes were up-regulated and 1,398 down-regulated. These differentially expressed genes were involved in 9 cellular components, 9 molecular functions, 8 biological processes and 6 pathways with p-value  $\leq 0.05$ . The clusters of "cellular process", "intracellular" and "binding" represented the largest group in Process Ontology, Component Ontology, Function Ontology, respectively. Most differentially expressed genes involved in Function of binding, which were reported to be relevant with RNA transcription in SLE. Moreover, alternative splicing events and gene structure refinements of SLE-iPSCs group were greater than those of control-iPSCs group. Occurrence and development of SLE may be related to the excessive alternative spliced genes and events of alternative splicing. Using large cohorts of patient samples with long-term clinical follow-up data deserves for further investigation and research. Thus, it could assess the usefulness of the pathogenesis of SLE.**

**Keywords:** Systemic lupus erythematosus-induced pluripotent stem cells (SLE- iPSCs), RNA sequence, Differentially expressed genes.

*Accepted on April 17, 2016*

### **Introduction**

Systemic lupus erythematosus (SLE) is the prototype of complex autoimmune disease characterized by the production of autoantibodies which results in widespread immunologic abnormalities and immune complex formation [1]. The patients can present variable manifestations and the nature courses are alternately remissions and relapses. Till now, although a lot of related researches have been undertaken [2], SLE patients still have no effective cures, whose treatments are often based upon long-term broad-spectrum immune suppressive regimes in the current therapeutic management. It has also become a major public health problem. Therefore, a rational approach for therapeutic design requires a detailed understanding of disease pathogenesis, and systematic characterization of the molecular and cellular basis of signaling abnormalities within the immune system and their relationship to regulation of gene expression remain critical for understanding [3].

The possibility of reprogramming somatic cells to induced pluripotent stem cells (iPSCs) offers an opportunity to generate pluripotent patient-specific cell lines, which can be conducive to studying pathogenesis of model human diseases [4]. Also, these iPSCs lines are powerful tools for drug discovery and the development of cellular transplantation therapies [4]. Generation of iPSCs from urine, fibroblasts and keratinocytes of disease patients has been reported [5-8]. To study SLE pathogenesis, renal tubular cells derived iPSCs were successfully established from urine of SLE patients [9]. In this study, high-throughput Illumina sequencing technology was utilized to further study the model cells of SLE-iPSCs.

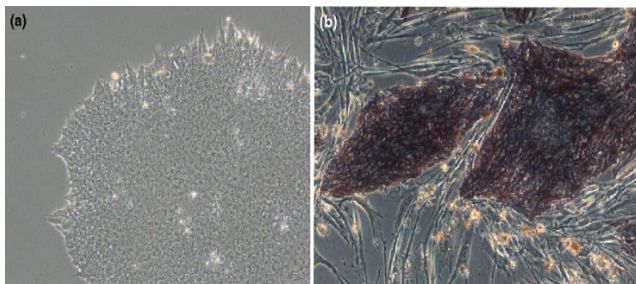
Recently, the high-throughput Illumina Genome Analyzer provides a powerful approach to identify differentially expressed genes for the given cell, tissue and organism [10-12]. It can increase transcript sensitivity and identify novel transcripts, single nucleotide polymorphisms as well as splicing events [13]. Sequencing technology is developing rapidly, which results in the discovery of new disease genes.

Actually, numerous chromosomal loci may harbor susceptibility genes [14,15]. By using the high-throughput Illumina sequencing platform, this study detects the mRNA expression in SLE-iPSCs group and control-iPSCs group, analyzes the two groups of differentially expressed genes and then identifies novel transcripts and splicing events. Further studies of gene regulation at transcriptional levels could help us to determine the pathogenesis of SLE comprehensively and accurately.

## Materials and Methods

### Materials

All the studies and other procedures were approved by the ethics committee of the Shenzhen People's Hospital (Shenzhen, China) or the Guangzhou Institutes of Biomedicine and Health (Guangzhou, China). One patient, at the age of 39, was diagnosed as active SLE with SLEDAI>8. Moreover, one subject, age and sex matched, was recruited as healthy controls. To generate human iPSCs clone, renal tubular cells from urine of SLE patients were reprogrammed. Furthermore, SLE-iPSCs clone and control-iPSCs clone were identified [9]. Morphology was identified as well [9] (Figure 1). All of the samples were collected and immediately frozen in liquid nitrogen and stored at - 80°C.



**Figure 1.** Morphological characteristics appeared at days 6-7 post-transduction. **a** The SLE-iPSCs were picked at day 19, Matrigel 10 $\times$ ; **b** Alkaline phosphatase (AP)-positive SLE-iPSCs were imaged using light microscope, feeder 10X.

### RNA extraction, cDNA library construction and sequencing

The SLE-iPSCs and Control-iPSCs were utilized for RNA extraction, and total RNA of iPSCs was extracted as described previously [16]. The individual RNA samples were quantified and examined spectrophotometrically for protein contamination (A260/A280 ratio) and reagent contamination (A260/A230 ratio), which were prior to library construction.

The cDNA library was carried out at the Beijing Genomics Institute (BGI, Shenzhen, Guangdong, China) by using the Illumina manufacturer's instructions. The main reagents and supplies were the Illumina Gene Expression Sample Prep Kit and the Solexa Sequencing Chip (flowcell), and the main instruments were the Illumina Cluster Station and the Illumina HiSeq™ 2000 System. In a nutshell, it is to extract the total RNA from samples. mRNA is enriched by utilizing the oligo

(dT) magnetic beads and removing rRNA from the total RNA with kit. Through the fragmentation buffer, the mRNA is fragmented into short fragments (about 200~700 bp). Then, the first-strand cDNA is synthesized by random hexamer-primer using the mRNA fragments as templates. Buffer, dNTPs, RNase H and DNA polymerase I are added to synthesize the second strand cDNA. The double strand cDNA is purified with QiaQuick PCR extraction kit. Finally, sequencing adapters are ligated to the fragments. The fragments are purified by agarose gel electrophoresis and enriched by PCR amplification. The library products are ready for sequencing analysis via Illumina HiSeq™ 2000.

### Bioinformatics analysis of sequencing data

Primary sequencing data produced by Illumina HiSeq™ 2000, called raw reads, is subjected to quality control (QC). To determine whether a resequencing step is necessary, the QC of alignment will be performed. Raw reads were filtered to remove reads with adapters, unknown bases of more than 10% and low quality reads (which are defined as reads having more than 50% bases with quality value  $\leq 10$ ). After filtering, the remaining reads, which are called "clean reads", will be aligned to the reference sequences with SOAP2 [17]. Then, QC of alignment is performed again. The alignment data is utilized to calculate the distribution of reads on reference genes and perform coverage analysis. If alignment results pass QC, we will proceed with downstream analysis including gene expression, gene structure refinement, alternative splicing, novel transcript prediction and SNP detection.

### Gene expression analysis

Results of gene expression contain gene expression levels and differential expression analysis. The levels of gene expression were measured as numbers of reads per kilobase of exon model in a gene per million mapped reads (RPKM), which can be directly utilized to compare the differences of gene expression among the samples.

According to Differentially Expressed Genes (DEGs), we utilize 'FDR(false discovery rate)  $\leq 0.001$  [18] and the absolute value of  $\log_2$ -Ratio  $\geq 1$ ' as the thresholds to judge the significance of DEGs. Then, more stringent criteria with smaller FDR and bigger fold change value can be applied to identify DEGs. These Differentially Expressed Genes were annotated in Gene Ontology (GO) and KEGG pathway analysis.

GO enrichment analysis maps all DEGs to GO terms in the database (<http://www.geneontology.org/>), calculating gene numbers for each term. Beyond that, the calculated p-value goes through Bonferroni Correction [19], taking corrected p-value  $\leq 0.05$  as a threshold. GO terms fulfilling this condition are defined as significantly enriched GO terms in DEGs. This analysis can recognize the main biological functions exercised by DEGs.

## Result

### High-throughput sequencing and reads mapping

In order to identify SLE-related genes, transcript profiling of iPSCs was performed using RNA-Seq. Clean reads are mapped to genome sequence by using SOAP2 aligner.

Through mapping of reads to entire genome sequence, a total of 26,749,056 and 26,855,414 high-quality reads were obtained for the SLE-iPSCs and the control-iPSCs, respectively (Table 1). After discarding the low quality tags, 2,407,415,040 and 2,416,987,260 tags remained in the SLE-iPSCs and control-

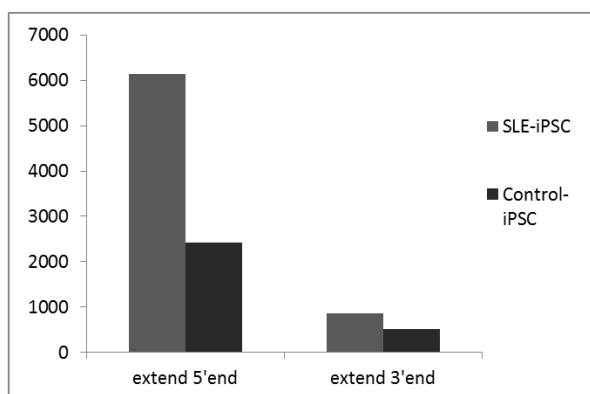
iPSCs, respectively. 23,488,075 (87.81%) and 23,928,072 (89.10%) reads were mapped to the whole genome, 16,513,998 (61.74%) and 15,718,886 (58.53%) reads were perfect match in the SLE-iPSCs and control-iPSCs, respectively. 795,112 reads were expressed exclusively in the SLE-iPSCs, which were possibly related to the SLE development. Further analysis revealed that 21,382,507 unique tags (79.94%) and 21,937,249 (81.69%) were exclusively matched in the SLE-iPSCs and control-iPSCs, respectively. These data indicate that approximately 80% of the transcripts are expressed in the SLE-iPSCs and control-iPSCs (Table 1).

**Table 1.** The SLE-iPSC and control-iPSC reads were mapped to the human Genome.

Map Genome	to	Total Reads	Total BasePairs	Total Mapped Reads	perfect match	<=5bp mismatch	unique match	multi-position match	Total Unmapped Reads
SLE- iPSC		26749056	2407415040	23488075	16513998	6974077	21382507	2105568	3260981
(%)		100.00	100.00	87.81	61.74	26.07	79.94	7.87	12.19
Control- iPSC		26855414	2416987260	23928072	15718886	8209186	21937249	1990823	2927342
(%)		100.00	100.00	89.10	58.53	30.57	81.69	7.41	10.90

### Gene structure refinement

Mapping to genome allows for potential discovery of novel exons and novel 5' and 3' ends. This can increase sensitivity and specificity due to recognition of potential reads through transcripts from neighboring genes. Transcripts were assembled with reads by Cufflinkss [20]. Through comparing assembled transcripts and gene annotation from reference sequences, it's possible to find assembled transcripts that can extend 5' or 3' end of gene annotation, and therefore refine gene structure. 6,985 and 2,935 gene structures were refined in the SLE-iPSCs and control-iPSCs, respectively. Gene structure refinements in the SLE-iPSCs were apparently higher than those in the control-iPSCs (Figure 2).



**Figure 2** Number extend 5' or 3' end of Gene structure refinement between SLE- iPSC and control-iPSC.

Novel transcript regions were also detected using Cufflinkss. As a novel transcript, an assembled transcript must meet three

requirements. This means that the transcript must be at least 200 bp away from annotated gene, the transcript is of length over 180 bp and the sequencing depth is no less than 2. In our experiment, 792 and 973 novel transcribed regions were found in the SLE-iPSCs and control-iPSCs, respectively.

### Alternative splicing analysis

To generate a mature mRNA, the introns must be removed and exons joined together in the process of pre-mRNA splicing [21]. Many pre-mRNAs in humans and other metazoans undergo the process of alternative splicing (AS) where multiple mRNA isoforms are produced from a single gene locus. In order to detect gene junctions, we perform an "intact" alignment using SOAPsplice to map complete reads to the reference genome. The remaining reads, initially unmapped reads (IUM reads), are mapped with the spliced alignment algorithm. We mainly detect four kinds of alternative spliced events, exon skipping, intron retention, alternative 5' splice site and alternative 3' splice site (Figures 3 and 4). Our results indicate that SLE-iPSCs have a higher rate of alternative splicing, compared with the control-iPSCs (Figure 4). And alternatively spliced genes of SLE-iPSCs are significantly higher than those of control-iPSCs (Figure 3). Disruption of normal splicing or splicing misregulation has been observed in a large number of diseases, which has been reviewed extensively [22-24]. The results clearly show that different organisms have different levels of alternative splicing, as well as alternatively spliced genes. Occurrence and development of SLE may be related to the excessive alternatively spliced genes and events of alternative splicing.

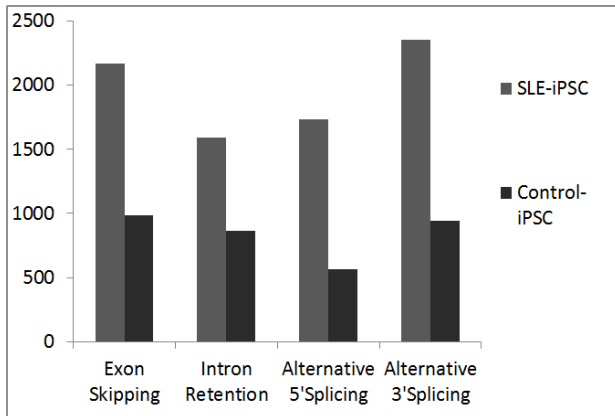


Figure 3. Genes of Alternative Splicing in SLE-iPSC and control-iPSC.

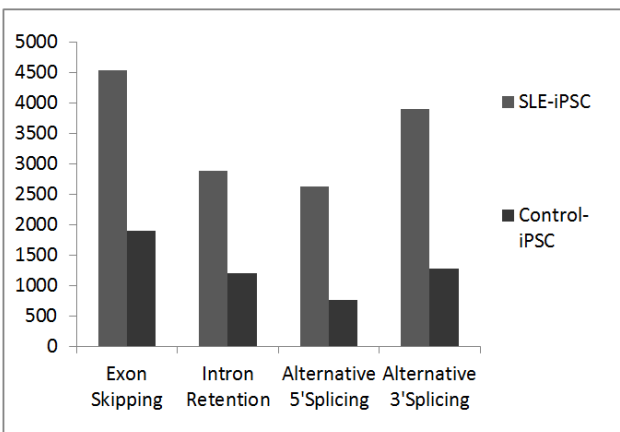


Figure 4. Events of Alternative Splicing in SLE-iPSC and control-iPSC.

### Global analysis of gene expression

One of the primary goals of transcriptome sequencing is to compare gene expression levels in different genotypes. We estimated the expression levels of genes between the SLE-iPSCs and the control-iPSCs. The expressed levels are measured in “reads per kilobase of exon model per million mapped reads” (RPKM), and the expression level of one gene is the sum of the RPKM values of its isoforms [25]. A total of 18,142 annotated genes were detected with RPKM>0. Using the P-value ≤ 0.05 and FDR ≤ 0.001 as threshold value, 4,254 genes were detected at least two-fold difference between the SLE-iPSCs and control-iPSCs (Figure 5). 2,856 genes and 1,398 genes represent a higher and lower abundance of more than two fold than those of control-iPSCs, respectively. The blue dots representing differentially expressed genes are less than two-fold between the two libraries, which are arbitrarily designated as “no difference in expression”. We observe that parts of the dots are on the axis. Red dots of Y-axis indicate that genes only express in SLE-iPSCs, and green dots of X-axis only express in control-iPSCs. The differentially expressed genes with ten-fold or greater are shown in Tables 2 and 3. We find that most differential expressed genes are

involved in binding, ion binding, GTPase regulator activity, nucleoside- triphosphatase regulator activity of Function Ontology (Table 3) and so on.

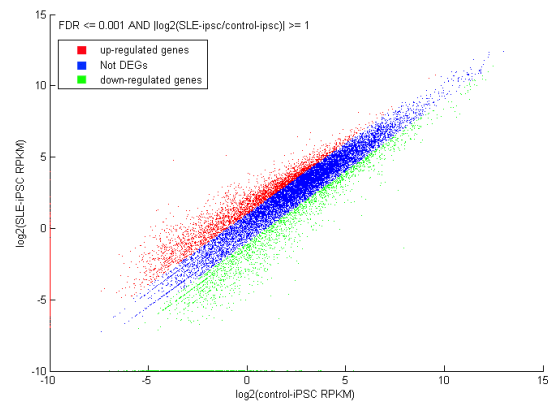


Figure 5. Comparison of gene expression levels between the SLE-iPSC and control-iPSC.

Table 2. Up-regulated of the differential expressed genes with ten-fold or greater.

Gene ID	Description	Log2ratio	GO Function
7503	X (inactive)-specific transcript (non-protein coding)	13.92469	-
647135	SLIT-ROBO Rho GTPase activating protein 2 pseudogene 2	13.37934	binding; enzyme activator activity
400680	hypothetical LOC400680	12.16684	-
728739	programmed cell death 2 pseudogene	11.70369	metal ion binding
391322	D-dopachrome tautomerase-like	11.67755	binding; carboxy-lyase activity; intramolecular oxidoreductase activity
8577	transmembrane protein with EGF-like and two follistatin-like domains 1	11.37174	-
128486	fat storage-inducing transmembrane protein 2	11.08058	-
343171	olfactory receptor, family 2, subfamily W, member 3	11.05965	G-protein coupled receptor activity
645455	centrosomal protein 170kDa pseudogene 1	11.04503	-
3043	hemoglobin, beta	10.84645	iron ion binding; protein binding
27023	forkhead box B1	10.82734	sequence-specific DNA binding RNA polymerase II transcription factor activity
168620	basic helix-loop-helix family, member a15	10.74333	nucleic acid binding; identical protein binding

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285598	ADP-ribosylation factor-like 10	10.73247	nucleotide binding	83869	testis-specific transcript, Y-linked 14	-12.454	-
85439	stonin 2	10.58868	binding	8284	lysine (K)-specific demethylase 5D	-12.052	nucleic acid binding; oxidoreductase activity; transition metal ion binding
5456	POU class 3 homeobox 4	10.427	nucleic acid binding transcription factor activity; sequence-specific DNA binding; structure-specific DNA binding	246126	chromosome Y open reading frame 15A	-12.0162	-
3188	heterogeneous nuclear ribonucleoprotein H2 (H')	10.34543	poly-pyrimidine tract binding	6736	sex determining region Y	-12.0071	nucleic acid binding transcription factor activity; nucleic acid binding; transcription regulator activity
642968	family with sequence similarity 163, member B	10.31501	-	9506	P antigen family, member 4	-11.254	-
80108	zinc finger protein 2 homolog	10.31064	nucleic acid binding transcription factor activity; nucleic acid binding; transition metal ion binding	64595	testis-specific transcript, Y-linked 15	-11.253	sequence-specific DNA binding
339535	hypothetical LOC339535	10.13272	-	728640	family with sequence similarity 133, member B pseudogene	-10.9706	-
56134	protocadherin alpha subfamily C, 2	10.12553	signal transducer activity; metal ion binding	9087	thymosin beta 4, Y-linked	-10.9171	cytoskeletal protein binding
2949	glutathione transferase mu 5	10.09299	transferase activity	729609	hypothetical LOC729609	-10.9048	binding
10887	prokineticin receptor 1	10.06696	neuropeptide receptor activity	8287	ubiquitin specific peptidase 9, Y-linked	-10.6199	endopeptidase activity; thiolester hydrolase activity; small conjugating protein-specific protease activity; SMAD binding
27091	calcium channel, voltage-dependent, gamma subunit 5	10.04713	calcium channel activity	130367	sphingosine-1-phosphate phosphatase 2	-10.456	phosphatase activity

**Table 3.** Down-regulated of the differential expressed genes with ten-fold or greater.

Gene ID	Description	Log2ratio	GO Function
9086	eukaryotic translation initiation factor 1A, Y-linked	-15.3561	translation factor activity, nucleic acid binding
8653	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	-13.7175	nucleic acid binding; RNA helicase activity; ATPase activity, coupled
55410	non-protein coding RNA 185	-13.6707	-
84663	chromosome Y open reading frame 15B	-13.5977	-
22829	neuroligin 4, Y-linked	-12.719	binding; identical protein binding;
5616	protein kinase, Y-linked	-12.7115	cyclic nucleotide-dependent protein kinase activity;
256536	transcription elongation regulator 1-like	-12.603	binding
1419	crystallin, gamma B	-10.4233	structural molecule activity
93408	myosin, light chain 10, regulatory	-10.266	metal ion binding
7404	ubiquitously transcribed tetra-tricopeptide repeat gene, Y-linked	-10.2028	oxidoreductase activity; cation binding
56891	lectin, galactoside-binding, soluble, 14	-10.1905	carboxylesterase activity; hydrolase activity; carbohydrate binding
26212	olfactory receptor, family 2, subfamily B, member 6	-10.1134	G-protein coupled receptor activity
100128124	hypothetical LOC100128124	-10.1112	-
376693	ribosomal protein S10 pseudogene 7	-10.0133	structural molecule activity; binding

**Table 4.** The classification of differentially expressed genes in different category based on function ontology.

Accession	Gene Ontology term	Numbers of DEG involved in term	Numbers of DEG involved in ontology	Cluster frequency	Corrected P-value
GO:0005488	binding	2825	3274	86.30%	2.28E-08
GO:0043167	ion binding	997	3274	30.50%	5.76E-13
GO:0043169	cation binding	986	3274	30.10%	5.43E-13
GO:0046872	metal ion binding	808	3274	24.70%	2.27E-12
GO:0046914	transition metal ion binding	552	3274	16.90%	5.15E-06
GO:0030695	GTPase regulator activity	117	3274	3.60%	0.00012
GO:0060589	nucleoside-triphosphatase regulator activity	118	3274	3.60%	9.65E-05
GO:0005085	guanyl-nucleotide exchange factor activity	36	3274	1.10%	0.02771
GO:0005088	Ras guanyl-nucleotide exchange factor activity	36	3274	1.10%	0.0159

### Gene ontology functional enrichment analysis of differentially expressed genes (DEGs)

Gene Ontology (GO) is an international standardized gene functional classification system, which offers a dynamic update and a strictly defined concept to comprehensively describe the properties of genes and their products in any organism.

Using the P-value  $\leq 0.05$  as the threshold value, 4,254 differentially expressed genes were categorized into 30 functional groups (Tables 4-6), which included 9 molecular functions (Table 4), 9 cellular components (Table 5) and 8 biological processes (Table 6).

According to biological process, 3,067 differentially expressed genes were involved in biological process. The genes involved in cellular process (2264) [GO: 0009987] were enriched more significantly than other seven biological processes. The next representative terms were metabolic process (macromolecule metabolic process, cellular macromolecule metabolic process, cellular protein metabolic process) (Table 6). According to

cellular component, 3,350 differentially expressed genes were involved in cellular component. The most representative GO term was intracellular (GO: 0005622), the next representative GO term was organelle (GO: 0043226), which was carried out at the intracellular level and results in the biosynthesis of constituent macromolecules, assembly, arrangement of constituent parts, or disassembly of an intracellular component (Table 5). The significantly enriched transcripts on the Function Ontology were 2,825 DEGs, which associated with the GO term of binding [GO: 0005488], the differentially expressed genes were also involved in ion binding, cation binding, metal ion binding, transition metal ion binding. The remaining of differentially expressed genes was categorized into regulator activity (GTPase regulator activity, nucleoside-triphosphatase regulator activity) and exchange factor activity (guanyl-nucleotide exchange factor activity, Ras guanyl-nucleotide exchange factor activity). Alessandra B and Pernis reported that deregulation of Rho GTPase-mediated pathways might play a role in the pathogenesis of SLE [26].

**Table 5.** The classification of differential expressed genes in different category based on component ontology.

Accession	Gene Ontology term	Numbers of DEG involved in term	Numbers of DEG involved in ontology	Cluster frequency	Corrected P-value
GO:0005622	intracellular	2510	3350	74.90%	0.00016
GO:0044424	intracellular part	2497	3350	74.50%	0.00013
GO:0043226	organelle	2140	3350	63.90%	0.00358
GO:0043229	intracellular organelle	2115	3350	63.10%	0.01626
GO:0044422	organelle part	1056	3350	31.50%	0.01696
GO:0005634	nucleus	461	3350	13.80%	0.03414
GO:0044428	nuclear part	449	3350	13.40%	0.03634
GO:0005840	ribosome	61	3350	1.80%	0.03914

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GO:0005840	ribosomal subunit	58	3350	1.70%	0.00816
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**Table 6.** The classification of differential expressed genes in different category based on process ontology.

Accession	Gene Ontology term	Numbers of DEG involved in term	Numbers of DEG involved in ontology	Cluster frequency	Corrected P-value
GO:0009987	cellular process	2264	3067	73.80%	0.00099
GO:0043170	macromolecule metabolic process	1154	3067	37.60%	0.01762
GO:0044260	cellular macromolecule metabolic process	1005	3067	32.80%	3.27E-05
GO:0007275	multicellular organismal development	661	3067	21.60%	0.02366
GO:0044267	cellular protein metabolic process	568	3067	18.50%	8.92E-05
GO:0007155	cell adhesion	143	3067	4.70%	0.00025
GO:0022610	biological adhesion	143	3067	4.70%	0.00025
GO:0016337	cell-cell adhesion	94	3067	3.10%	3.27E-05

**Pathway enrichment analysis for DEGs**

Genes usually interact with each other in certain biological functions. The Kyoto Encyclopedia of Genes and Genomes (KEGG) Pathway database contains a record of all known networks of molecular interactions in cells and the variants of these pathways that are specific to particular organisms [27]. Pathway enrichment analysis helps us to understand what biological functions the genes have and how these genes interact with each other. In this study, the KEGG database can be used to analyze the potential involvement of differentially expressed genes.

Pathways with Q-value  $\leq 0.05$  were significantly enriched in differentially expressed genes. The differentially expressed genes were categorized into six pathways. The most representative pathway is purine metabolism, and then 4.42% of differentially expressed genes were involved in pathways in cancer (Table 7). Purinergic signaling not only regulated numerous organ systems, but also involved in embryonic development, injury and pain [28]. Moreover, there is evidence that purinergic receptors play a role in the regulation of behaviours and immunity [29]. Our result shows most significant difference of expressed genes in SLE-iPSCs involve in purine metabolism.

**Table 7.** Pathway enrichment analysis for DEGs.

Pathway ID	Pathway	Cluster frequency	P-value	Q-value
ko00230	Purine metabolism	9.27%	0.000848	0.033532
ko05200	Pathways in cancer	4.42%	0.00021	0.016019
ko05222	Small cell lung cancer	1.48%	0.000173	0.016019
ko03010	Ribosome	1.42%	7.07E-05	0.016019

ko04350	TGF-beta pathway	signaling	1.40%	0.000879	0.033532
ko05220	Chronic myeloid leukemia		1.34%	0.000286	0.016353

**Discussion**

During the past few years, new NGS technologies have been developed with applications in complete genome sequencing, metagenomic sequencing, Chip-Seq, small RNA sequencing, transcriptome profiling, and others. Yukinori Okada et al [30] uses genome-wide association studies (GWAS) to discovery of susceptibility genes of SLE. And Graham, Deborah S Cunninghame [31] indicates that GWAS has been shown to be a powerful way of identifying novel susceptibility genes in SLE.

Our study provides the first comprehensive insight into the transcriptome of SLE- iPSCs using Illumina HiSeq™ 2000, as a powerful next generation RNA sequencing platform. We calculated the number of differentially expressed genes between SLE- iPSCs and control-iPSCs based on RPKM. 4,254 genes were considered to be significant difference, classified using Gene Ontology (GO) and KEGG Pathway. The clusters of “cellular process”, “intracellular” and “binding” represented the largest group in Process Ontology, Component Ontology and Function Ontology, respectively. Most differentially expressed genes involved in Function of binding (Tables 2 and 3), such as up-regulated hemoglobin, forkhead box B1, basic helix-loop-helix family and down- regulated eukaryotic translation initiation factor 1A, transcription elongation regulator 1-like and so on. Most of them were reported to be relevant with RNA transcription in SLE [32]. Bhatnagar et al. [33] showed that human Hemoglobin (Hb) was demonstrated in the sera of systemic lupus erythematosus (SLE). In addition, heterogeneous nuclear ribonucleoprotein H2 was significant difference in the study, which was consistent with our previous results [34]. Siapka et al. also



demonstrated that hnRNP had a predominant nuclear localization and exerted multiple functions, including regulation of alternative splicing, transport of mRNA and regulation of translation [35].

Alternative splicing has recently emerged as a major mechanism for expanding and regulating the repertoire of gene functions [36]. Alternatively spliced proteins are involved in many biological processes like apoptosis [37]. The effects of these polymorphisms on splicing efficiency are believed to contribute significantly to disease severity and susceptibility [38]. Most alternative splicing events affect the coding sequence, subsequently amino acid sequence. Recently, a number of observations indicate physiological or pathological significance of alternative splicing and its role in the genetic background of diseases [39], such as immune diseases [40]. About one third of AS events result in splice variants containing premature termination codon, or leading to nonsense-mediated decay of the RNA product [41]. Many disease-associated mutations also affect pre-mRNA alternative splicing, usually causing inappropriate exon skipping [42]. Our result indicates that four types of exon skipping, intron retention, alternative 5' splice site and alternative 3' splice site in SLE-iPSCs are higher than those in control-iPSCs. Exon skipping in SLE-iPSCs is the biggest difference among the four types of alternatives. Studies have shown that up to 50% of point mutations responsible for genetic diseases in humans cause aberrant splicing [43,44]. The most common phenotype of point mutations that affect splicing, however, is exon skipping [43,45]. A family-based analysis of Caucasian and Chinese populations shows a significant association between the major alleles of a three alternative splicing CR2 and lupus susceptibility [46]. KB Douglas et al. also confirm the association of these three CR2 variants, and identify two additional CR2 variants significantly associated with SLE susceptibility. Therefore, aberrant exon skipping is closely related to the pathogenesis of SLE, and as the most common phenotype of alternatives because it is not usually amenable to correction.

## Conclusion

The high-throughput Illumina sequencing technology is a powerful approach to identification of differentially expressed genes. We used the Illumina sequencing technology to detect the mRNAs expression in SLE-iPSCs group and control-iPSCs group; 4,254 genes were detected at least two-fold difference between the SLE-iPSCs and control-iPSCs, 2,856 genes were up-regulated and 1,398 down-regulated. Some differentially expressed genes only express in SLE-iPSCs or control-iPSCs. The 4,254 differentially expressed genes were annotated in Gene Ontology (GO) and KEGG pathway analysis. We found that the DEGs involved in 9 cellular components, 9 molecular functions, 8 biological processes and 6 pathways with  $p$ -value  $\leq 0.05$ . The clusters of "cellular process", "intracellular" and "binding" represented the largest group in Process Ontology, Component Ontology, Function Ontology, respectively. Most differentially expressed genes involved in Function of binding,

which were reported to be relevant with RNA transcription in SLE. Moreover, we also proceeded with other downstream analysis including gene structure refinement, alternative splicing and novel transcript prediction. Alternative splicing events and gene structure refinement of SLE-iPSCs group were greater than those of control-iPSCs group. The results clearly showed that different organisms had different levels of alternative splicing, as well as alternatively spliced genes. Occurrence and development of SLE may be related to the excessive alternatively spliced genes and events of alternative splicing. In the future, further investigation is necessary for using large cohorts of patient samples with long-term clinical follow-up data, to assess the usefulness of the pathogenesis of SLE.

## Acknowledgments

We thank the patients and healthy volunteers who participated in this study.

## Conflict of Interest

No financial relationship exists between any of the authors and any commercial interest with a vested interest in the outcome of the study.

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