

REVIEW

The potential of using blood circular RNA as liquid biopsy biomarker for human diseases

Guoxia Wen¹ , Tong Zhou² , Wanjun Gu¹ 

¹ State Key Laboratory of Bioelectronics, School of Biological Sciences and Medical Engineering, Southeast University, Nanjing 210096, China

² Department of Physiology and Cell Biology, Reno School of Medicine, University of Nevada, Reno, NV 89557, USA

✉ Correspondence: tongz@med.unr.edu (T. Zhou), wanjungu@seu.edu.cn (W. Gu)

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ABSTRACT

Circular RNA (circRNA) is a novel class of single-stranded RNAs with a closed loop structure. The majority of circRNAs are formed by a back-splicing process in pre-mRNA splicing. Their expression is dynamically regulated and shows spatiotemporal patterns among cell types, tissues and developmental stages. CircRNAs have important biological functions in many physiological processes, and their aberrant expression is implicated in many human diseases. Due to their high stability, circRNAs are becoming promising biomarkers in many human diseases, such as cardiovascular diseases, autoimmune diseases and human cancers. In this review, we focus on the translational potential of using human blood circRNAs as liquid biopsy biomarkers for human diseases. We highlight their abundant expression, essential biological functions and significant correlations to human diseases in various components of peripheral blood, including whole blood, blood cells and extracellular vesicles. In addition, we summarize the current knowledge of blood circRNA biomarkers for disease diagnosis or prognosis.

KEYWORDS peripheral blood circular RNA, liquid biopsy, human diseases, translational biomarkers

INTRODUCTION

Liquid biopsy is a biopsy that uses body liquids as the sample source to diagnose, predict the outcome of or monitor the development of human diseases (Rubis et al., 2019; Luo et al., 2020a). Compared to traditional tissue biopsy, liquid biopsy has the advantages of being noninvasive, performed in real-time and accurate (Rubis et al., 2019; Luo

et al., 2020a). It has been proven to be applicable to the management of many human diseases, including cancers (Heitzer et al., 2019; Mattox et al., 2019; Rubis et al., 2019), prenatal genetic disorders (Zhang et al., 2019a), heart diseases (Zemmour et al., 2018), schizophrenia (Chen et al., 2020b), transplant rejection (Bloom et al., 2017) and infectious diseases (Burnham et al., 2018; Hong et al., 2018; Blauwkamp et al., 2019; Han et al., 2020a). To date, most liquid biopsy studies have focused on its clinical application in human cancers (reviewed in Siravegna et al., 2017; Heitzer et al., 2019; Mattox et al., 2019; Rubis et al., 2019). For example, a cell-free DNA (cfDNA)-based liquid biopsy test that determines the mutational status of the epidermal growth factor receptor (*EGFR*) gene was used to guide the response of *EGFR* tyrosine kinase inhibitors in non-small cell lung cancer (NSCLC) patients, which was approved by the FDA in clinical practice (Kwapisz, 2017). Another FDA-approved liquid biopsy test, Epi proColon, assessed the methylation status of the *Septin9* gene in whole blood, which was used to screen colorectal cancer patients from healthy controls (Lamb and Dhillon, 2017). In addition to cfDNA (Wan et al., 2017; Cescon et al., 2020), several other analytes within circulating body fluids were investigated as liquid biopsy biomarkers, such as circulating tumor cells (CTCs) (Yu et al., 2013), extracellular vesicles (EVs) (Torrano et al., 2016), cell-free RNA (cfRNA) (Zaporozhchenko et al., 2018), circulating proteins (Surinova et al., 2015), circulating metabolites (Crutchfield et al., 2016) and platelets (Joosse and Pantel, 2015; Best et al., 2017). Among them, RNA-based liquid biopsy biomarkers have gained much more attention in recent years since they have dynamic expressions and are closely related to different disease conditions (Zaporozhchenko et al., 2018; Sole et al., 2019). Circulating noncoding RNAs, especially microRNAs (miRNAs), have shown promising potential as stable blood-based biomarkers

in liquid biopsy (Mitchell et al., 2008; Anfossi et al., 2018; Pardini et al., 2019).

Circular RNAs (circRNAs) are a group of endogenous noncoding RNA molecules (Chen, 2016, 2020; Li et al., 2018d). They were first found in plant viroids (Sanger et al., 1976) and eukaryotic cells (Hsu and Coca-Prados, 1979) in 1970s, and were recently observed to be functional (Hansen et al., 2013; Memczak et al., 2013). They are joined head to tail to generate a covalently closed loop structure through back-splicing (Vicens and Westhof, 2014; Li et al., 2018d). They lack a 5-prime cap and 3-prime poly-A tail, which is quite different from canonical linear RNAs (Vicens and Westhof, 2014; Li et al., 2018d). CircRNAs have been identified in almost all organisms across the eukaryotic tree of life (Wang et al., 2014). Some circRNAs are the predominant transcript isoform of their host genes expressed in specific tissues or cell types (Salzman et al., 2012, 2013; Rybak-Wolf et al., 2015). Furthermore, they are expressed in a tissue- (Zhou et al., 2018a), cell-type- (Salzman et al., 2013) and developmental stage-specific manner (Zhou et al., 2018a). Accumulating studies have revealed many regulatory roles and versatile cellular functions that circRNAs can perform (Li et al., 2018d; Chen, 2020). They can act as miRNA decoys (Hansen et al., 2013), RNA binding protein (RBP) sponges (Ashwal-Fluss et al., 2014; Huang et al., 2020a) and protein scaffolds (Li et al., 2015c, 2019a). Moreover, a small percentage of circRNAs can be translated into proteins (Legnini et al., 2017; Pamudurti et al., 2017; Heesch et al., 2019). Aberrant expression of circRNAs has been related to many human diseases, including cancers (Shang et al., 2019; Vo et al., 2019), neurodegenerative diseases, cardiovascular diseases (Aufiero et al., 2019) and immune diseases (Chen et al., 2019c; Zhou et al., 2019b). Due to their high stability (Enuka et al., 2015), abundant expression (Jeck et al., 2013) and high specificity (Zhou et al., 2018a), circRNAs are becoming promising biomarkers for human diseases (Zhang et al., 2018j).

Due to the importance of liquid biopsy biomarkers in precision medicine (Vargas and Harris, 2016) and the superior characteristics of circRNAs as disease biomarkers (Zhang et al., 2018j), recent studies have put great efforts into researching the use of circRNAs as liquid biopsy biomarkers for human diseases. Here, we review current progress that has been made on this topic. We focus on circRNAs in the peripheral blood, although circRNAs are abundantly expressed in other body fluids, such as saliva (Bahn et al., 2014; Ghods, 2018) and urine (Kölling et al., 2019; Lam and Lo, 2019; Vo et al., 2019). In this review, we first briefly introduce the biogenesis, function, and expression patterns of circRNAs and their close correlations to human diseases. Then, we emphasize the functional roles they may play in different blood components, including blood cells, serum, plasma, platelets and EVs in the blood. We summarize peripheral blood circRNA biomarkers that have been constructed for the management of human diseases.

Finally, we discuss future opportunities and challenges of translating blood circRNAs into clinical practice.

THE BIOGENESIS OF CIRCRNAS

CircRNAs are derived from pre-mRNAs and formed by back-splicing, in which a downstream 5-prime splice site (ss) is covalently joined with an upstream 3-prime ss (Fig. 1) (Li et al., 2018d). There are three major types of circRNAs, exonic circRNAs (ecircRNAs), exon-intron circRNAs (EI-circRNAs) and circular intronic RNAs (ciRNAs) (Fig. 1). EcircRNAs only contain exons, and most ecircRNAs are located in the cytoplasm. Two models have been proposed to explain the production of ecircRNAs (Fig. 1A) (Chen, 2016; Wu et al., 2017a; Kristensen et al., 2019; Xiao et al., 2020). The first model suggests that when the pre-mRNA is partially folded during transcription, canonical splicing will cause an “exon jump” and generate a linear RNA containing skipped exons (Starke et al., 2014; Kelly et al., 2015). A subsequent back-splicing event will turn the ‘lariat intermediate’ into a closed circular transcript (Barrett et al., 2015; Li et al., 2018d). The second model proposes that when the 5-prime ss is pulled closer to the 3-prime ss by base pairing of flanking intronic complementary sequences (Ivanov et al., 2014; Vicens and Westhof, 2014; Zhang et al., 2014; Wilusz, 2015) or specific bindings of intronic sequences to RBPs (Conn et al., 2015), a back-splicing event may occur, and a circRNA may be generated (Jeck et al., 2013). These models are supported by accumulating evidence showing that cis-acting elements (Jeck et al., 2013; Zhang et al., 2014; Yoshimoto et al., 2019) and trans-acting factors (Ashwal-Fluss et al., 2014; Conn et al., 2015; Agirre et al., 2019) play crucial regulatory roles in circRNA formation. ElcircRNAs are generated when an intron or several introns are alternatively retained in splicing (Li et al., 2015c). Therefore, ElcircRNAs are mainly considered intermediates of ecircRNAs (Li et al., 2015c). CiRNAs, which only contain introns, are produced through escape from debranching of intron lariats (Zhang et al., 2013). This process depends on a GU-rich motif near the 5-prime ss and a C-rich motif close to the branch-point site (Zhang et al., 2013). Unlike ecircRNAs, ElcircRNAs and ciRNAs are mainly located in the nucleus.

THE FUNCTION OF CIRCRNAS

With the rapid application of high-throughput RNA-sequencing (RNA-seq) technology (Stark et al., 2019) and related bioinformatics tools that identify circRNAs from RNA-seq datasets (Jeck and Sharpless, 2014; Szabo and Salzman, 2016; Li et al., 2017a; Gao and Zhao, 2018), more than one million circRNAs have been annotated in model organisms (Glažar et al., 2014; Vo et al., 2019; Cai et al., 2020; Wu et al., 2020a). However, the functional characterization of circRNAs is still at its early stage (Chen, 2016, 2020; Li et al., 2018d). Their circular conformation and the large sequence overlap with their linear mRNA counterparts have posed

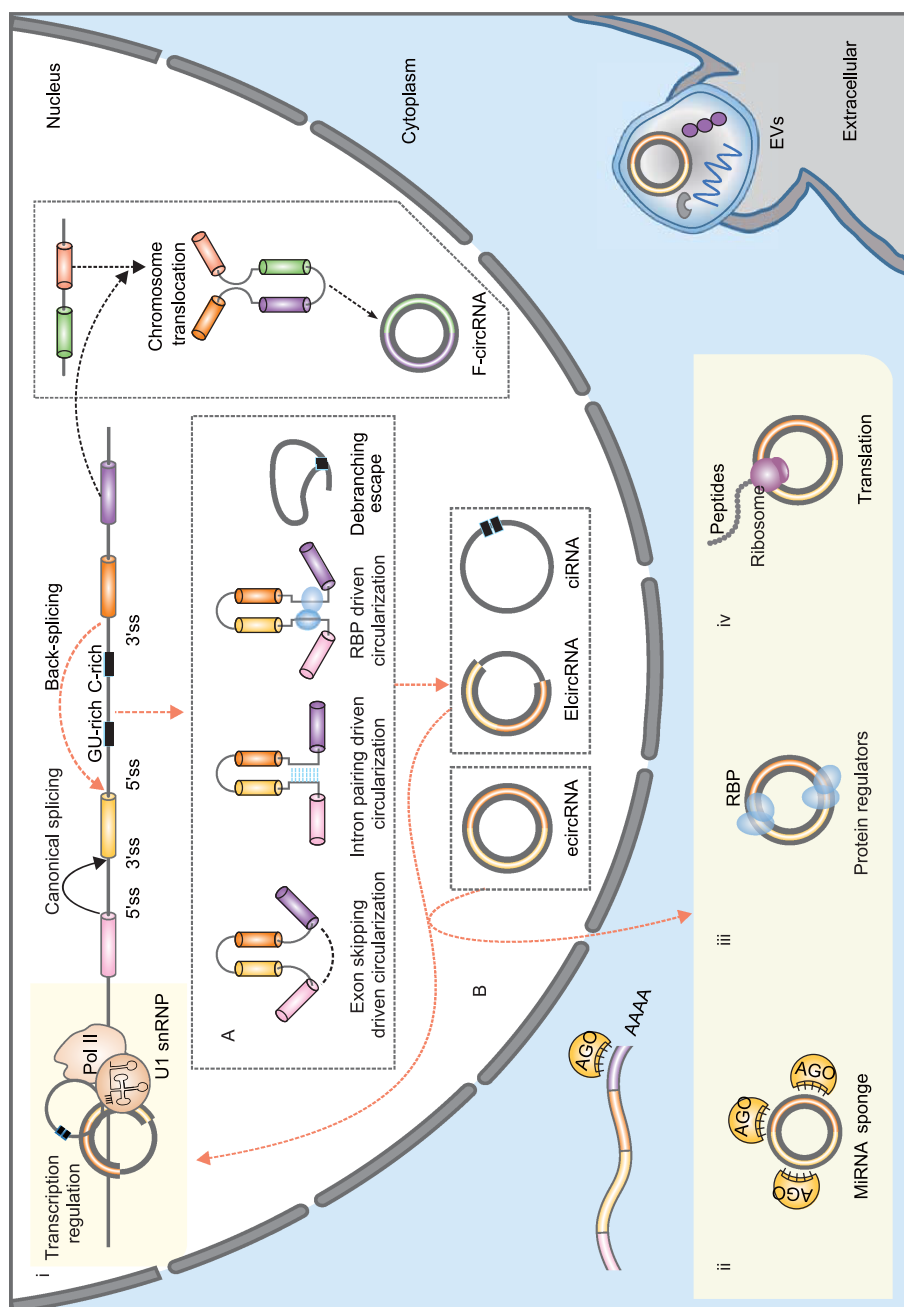


Figure 1. The biogenesis and function of circRNAs. (A) CircRNAs are formed by back-splicing of pre-mRNAs by different mechanisms, including: lariat driven circularization, intron pairing driven circularization, RBP driven circularization, and debranching escape of intron lariats. (B) CircRNAs can perform diverse biological functions. First, ElcircRNAs can interact with RNA Pol II and U1 snRNP to regulate gene transcription in the nucleus (i). Second, ecircRNAs can accumulate in the cytoplasm and act as miRNA decoys (ii), protein regulators (iii), and translation templates (iv). Third, circRNAs can be secreted into EVs by many cell types and transported to recipient cells by EVs. EV circRNAs can also act as important gene regulators.

Table 1. Cell-free circRNA biomarkers in circulating peripheral blood.

Disease	CircRNA biomarker	Source	Expression change	Cohort size	Clinical significance	AUC	Method	Reference
Breast cancer	Hsa_circ_0001785	Plasma	Up	57 breast cancer/17 HC	Associated with histological grade, TNM stage and distant metastasis; significant expression difference between pre-treatment and post-treatment.	0.784	Microarray RT-qPCR	Yin et al. (2018)
Bladder cancer	Hsa_circ_0000285	Serum	Down	97 Bladder cancer/97 HC	Associated with tumor size, differentiation, LNM, distant metastasis, TNM stage and cisplatin response.	NA	RT-qPCR	Chi et al. (2019)
CA	Hsa_circ_0003204	Plasma derived EV	Up	35 CA/32 HC	Associated with proliferation, migration and tube formation of endothelial cells.	0.770	RT-qPCR	Zhang et al. (2020b)
CAD	Hsa_circ_0005540	Plasma derived exosome	Up	108 CAD/89 HC	Associated with the Framingham Heart Study risk factors.	0.853	RNA-seq RT-qPCR	Wu et al. (2020b)
CHB	CircMTO1	Serum	Down	360 CHB/360 HC	Associated with liver fibrosis progression and prognosis.	0.914	RT-qPCR	Wang et al. (2019c)
CHD	Hsa_circ_004183 Hsa_circ_079265 Hsa_circ_105039	Plasma	Down	40 CHD/40 HC	NA	0.965	Microarray RT-qPCR	Wu et al. (2019a)
CLL	Circ-RPL15	Plasma	Up	150 CLL/65 HC	Associated with progression and outcome.	0.840	Microarray RT-qPCR	Wu et al. (2020c)
CRC	Hsa_circ_0006990	Plasma	Up	60 CRC/43 HC	Associated with TNM stage.	0.724	RT-qPCR	Li et al. (2019c)
CRC	Circ-CCDC66 Circ-ABCC1 Circ-STIL	Plasma	Down	45 CRC/61 HC	Circ-ABCC1 was associated with tumor growth and progression; significant expression difference of circ-CCDC66 between pre-treatment and post-treatment.	0.780	RT-qPCR	Lin et al. (2019)
CRC	Hsa_circ_0004771	Serum derived exosome	Up	135 CRC/45 HC	Associated with TNM stage and distant metastasis; significant expression difference between pre-treatment and post-treatment.	0.880	RT-qPCR	Pan et al. (2019)

Table 1 continued							
Disease	CircRNA biomarker	Source	Expression change	Cohort size	Clinical significance	AUC	Method Reference
CRC	Hsa_circ_0000826	Serum	Up	100 CRC/100 HC	Associated with liver metastasis.	0.778	RT-qPCR Shi et al. (2020)
CRC	Hsa_circ_0101802	Serum derived exosome	Up	221 CRC/221 HC	NA	0.854	RNA-seq RT-qPCR Xie et al. (2020c)
CRC	Hsa_circ_0082182 Hsa_circ_0000370 Hsa_circ_0035445	Plasma	Up Up Down	156 CRC/66 HC	The first two circRNAs were associated with LNM and had significant expression difference between pre-treatment and post-treatment; the third was associated with TNM stage.	0.835	Microarray RT-qPCR Ye et al. (2019)
CRC	Hsa_circ_0007534	Plasma	Up	112 CRC/46 HC	Associated with progression of clinical classification, metastatic phenotype, and differentiation.	0.780	RT-qPCR Zhang et al. (2018f)
EC	Hsa_circ_0109046 Hsa_circ_0002577	Serum derived EV	Up	10 EC/10 HC	NA	NA	RNA-seq RT-qPCR Xu et al. (2018a)
EOC	CircBNC2	Plasma	Down	83 EOC/83 benign ovarian cyst/83 HC	Associated with histological grade, serious subtype, LNM and distant metastasis.	0.923	RT-qPCR Hu et al. (2019b)
ESCC	Hsa_circ_0001946 Hsa_circ_0043603	Plasma	Down	50 ESCC/50 HC	Associated with recurrence, overall survival and disease-free survival.	0.894 0.836	Microarray RT-qPCR Fan et al. (2019)
ESCC	CircGSK3 β	Plasma	Up	86 ESCC/11 benign lesion/43 HC	Associated with recurrence, metastasis, clinical stage and outcome; significant expression difference between pre-treatment and post-treatment.	0.793	Microarray ddPCR RT-qPCR Hu et al. (2019a)
ESCC	Circ-TTC17	Plasma	Up	30 ESCC/25 HC	Associated with TNM stage, LNM and survival time.	0.820	RT-qPCR Wang et al. (2019b)
ESCC	Circ-SLC7A5	Plasma	Up	87 ESCC/53 HC	Associated with TNM stage and survival time.	0.772	Microarray RT-qPCR Wang et al. (2020c)

Table 1 continued

Disease	CircRNA biomarker	Source	Expression change	Cohort size	Clinical significance	AUC	Method	Reference
GBM	CircFOXO3 Hsa_circ_0029426 Circ-SHPRH	Plasma	Down	100 GBM/100 HC	NA	0.906-0.980	RT-qPCR	Chen et al. (2020a)
GC	Hsa_circ_0000190	Plasma	Down	104 GC/104 HC	Associated with blood carcinoembryonic antigen level.	0.600	RT-qPCR	Chen et al. (2017c)
GC	Hsa_circ_0021087 Hsa_circ_0005051	Plasma	Down	70 GC/70 HC	Associated with tumor size and TNM stage; significant expression difference of hsa_circ_0021087 between pre-treatment and post-treatment.	0.773	RT-qPCR	Han et al. (2020c)
GC	Hsa_circ_0000745	Plasma	Down	60 GC/60 HC	Associated with TNM stage.	0.683	RNA-seq RT-qPCR	Huang et al. (2017a)
GC	Hsa_circ_00001649	Serum	Down	20 GC (pre-operation vs. post-operation)	Associated with pathological differentiation; significant expression difference between pre-treatment and post-treatment.	0.834	RT-qPCR	Li et al. (2017d)
GC	Hsa_circ_0001017 Hsa_circ_0061276	Plasma	Down	121 GC/121 HC	Associated with distal metastasis, overall survival, prognosis and outcome.	0.912	Microarray RT-qPCR RT-ddPCR	Li et al. (2018c)
GC	Hsa_circ_0000467	Plasma	Up	40 GC/20 HC	Associated with TNM stage; significant expression difference between pre-treatment and post-treatment.	0.790	RT-qPCR	Lu et al. (2019a)
GC	Hsa_circ_0006848	Plasma	Down	30 GC/30 HC	Associated with differentiation and tumor size; significant expression difference between pre-treatment and post-treatment.	0.733	RT-qPCR	Lu et al. (2019b)
GC	Hsa_circ_0010882	Plasma	Up	66 GC/66 HC	Associated with tumor size and histological grade, overall survive and prognosis.	NA	RT-qPCR	Peng et al. (2020)

Table 1 continued							
Disease	CircRNA biomarker	Source	Expression change	Cohort size	Clinical significance	AUC	Method
GC	CircPSMC3	Plasma	Down	106 GC/21 HC	Associated with TNM stage, LNM and overall survival.	0.933	Microarray RT-qPCR
GC	Hsa_circ_0065149	Plasma derived exosome	Down	39 GC/41 HC	NA	0.640	RT-qPCR
GC	CircKIAA1244	Plasma	Down	62 GC/25 HC	Associated with TNM stage, LNM and overall survival.	0.748	Microarray RT-qPCR
GC	Hsa_circ_0000419	Plasma	Down	44 GC/43 HC	Associated with tumor stage, lymphatic and distal metastasis, venous and perineural invasion.	0.840	RT-qPCR
GC	Hsa_circ_0000936	Serum derived exosome	Up	32 GC/20 HC	Associated with TNM stage and prognosis; significant expression difference before and after gastrectomy.	NA	RT-qPCR
GC	Hsa_circ_0000181	Plasma	Down	102 GC/105 HC	Associated with differentiation and carcinoembryonic antigen.	0.756	RT-qPCR
Glioma	CircNF1X	Serum derived exosome	Up	69 glioma/10 HC	Associated with temozolomide response and prognosis.	0.885	RT-qPCR
HCC	Hsa_circ_0051443	Plasma derived exosome	Down	60 HCC/60 HC	Associated with progression.	0.809	Microarray RT-qPCR
HCC	Circ-ZEB1.33	Serum	Up	64 HCC/30 HC	Associated with TNM stage and prognosis.	NA	RT-qPCR
HCC	Hsa_circ_100338	Serum derived exosome	Up	39 HCC (pre-operation vs. post-operation)	Associated with metastasis, proliferation, angiogenesis and prognosis.	NA	RT-qPCR
HCC	CircSMARCA5	Plasma	Down	135 HCC/143 cirrhosis /117 hepatitis/103 HC	NA	0.938	RT-qPCR
							Li et al. (2019e)

Table 1 continued

Disease	CircRNA biomarker	Source	Expression change	Cohort size	Clinical significance	AUC	Method	Reference
HCC	Hsa_circ_0003998	Plasma	Up	100 HCC/50 hepatitis/50 HC	Significant expression difference between pre-treatment and post-treatment.	0.892	RT-qPCR	Qiao et al. (2019)
HCC	Hsa_circ_0004001 Hsa_circ_0004123 Hsa_circ_0075792	Serum	Up	21 HCC/32 HC	Associated with TNM stage and tumor size.	0.890	RT-qPCR	Sun et al. (2020b)
HCC	Circ_FOXP1	Serum	Up	30 HCC/16 HC	Associated with tumor size, microvascular invasion and advanced TNM stage and survival time.	0.932	RT-qPCR	Wang et al. (2020d)
HCC	Hsa_circ_104075	Serum	Up	101 HCC/60 HC/23 hepatitis B/26 hepatitis C/23 cirrhosis/20 LC/19 GC/30 colon cancer/21 breast cancer	Associated with TNM stage; significant expression difference between pre-treatment and post-treatment.	0.973	RT-qPCR	Zhang et al. (2018g)
HCC	Hsa_circ_0001445	Plasma	Down	104 HCC/57 cirrhosis/44 hepatitis B/52 HC	Associated with serum alpha-fetoprotein level.	0.862	RT-qPCR	Zhang et al. (2018h)
HCM	CircDNAJC6 CircTMEM56 CircMBOAT2	Serum	Down	64 HCM/53 HC	Associated with left ventricular outflow tract gradient and thickness of interventricular septum in patients with obstructive HCM.	0.819 0.756 0.738	RT-qPCR	Sonnenschein et al. (2019)
Hypertension	Hsa_circ_0005870	Plasma	Down	54 Hypertension/54 HC	NA	NA	Microarray RT-qPCR	Wu et al. (2017b)
Heart failure	Hsa_circ_0062960	Plasma	Up	30 Heart failure/30 HC	Associated with B-type natriuretic peptide serum levels.	0.838	Microarray RT-qPCR	Sun et al. (2020c)

Table 1 continued

Disease	CircRNA biomarker	Source	Expression change	Cohort size	Clinical significance	AUC	Method	Reference
IPAH	Hsa_circ_0068481	Serum	Up	82 IPAH/82 HC	Associated with heart function, 6-min walk distance, serum N-terminal pro-B-type natriuretic peptide, serum H2S, risk stratification, right heart failure, and death.	0.895	RT-qPCR	Zhang et al. (2019b)
KD	CircANRIL Hsa_circ_0123996	Serum	Down Up	56 KD/56 HC	Associated with multiple clinical laboratory factors; significant expression difference of circANRIL between pre-treatment and post-treatment.	0.624 0.747	RT-qPCR	Wu et al. (2019b)
LAC	Hsa_circ_0056616	Plasma derived exosome	Up	42 LAC with LNM/48 LAC without LNM	Associated with the level of CXCR4 protein, T stage, M stage, and TNM grade.	0.812	RT-qPCR	He et al. (2020)
LAC	Hsa_circ_0013958	Plasma	Up	30 LAC/30 HC	Associated with TNM stage and LNM.	0.794	Microarray RT-qPCR	Zhu et al. (2017)
LC	Hsa_circ_0000190	Plasma	Up	231 LC/41 HC	Associated with tumor size, histological type, stage, distant metastasis, extrathoracic metastasis, survival, prognosis, PD-L1 level and therapy response.	0.950	RNA-seq RT-qPCR RT-ddPCR	Luo et al. (2020c)
LN	Hsa_circ_002453	Plasma	Up	59 SLE (30 with LN and 29 without LN)/26 RA/32 HC	Associated with severity of renal involvement and 24-hour proteinuria.	0.906	Microarray RT-qPCR	Ouyang et al. (2018)
LUAD	Hsa_circ_0005962 Hsa_circ_0086414	Plasma	Up Down	153 LUAD/54 HC	Hsa_circ_0086414 was associated with EGFR mutations; significant expression difference of hsa_circ_0005962 between pre-treatment and post-treatment.	0.810	RT-qPCR	Liu et al. (2019b)
LUAD	Hsa_circ_002178	Serum derived exosome	Up	120 LUAD/30 HC	Associated with programmed cell death protein 1 (PD1) expression.	0.997	RT-qPCR	Wang et al. (2020b)

Table 1 continued

Disease	CircRNA biomarker	Source	Expression change	Cohort size	Clinical significance	AUC	Method	Reference
MCL	CircCDYL	Plasma	Up	18 MCL/17 HC	Associated with cell proliferation.	0.856	RT-qPCR	Mei et al. (2019)
MDD	CircDYM	Plasma	Down	60 MDD/32 HC	Associated with the scores of the 24-item Hamilton Depression Rating Scale, retardation subscale and treatment response.	0.643	RT-qPCR	Song et al. (2020)
NPC	Hsa_circ_0000285	Serum	Up	150 NPC/100 HC	Associated with tumor size, differentiation, LNM, distant metastasis, TNM stage, survival rate and radiotherapy response.	NA	RT-qPCR	Shuai et al. (2018)
NPC	Hsa_circ_0066755	Plasma	Up	86 NPC/86 HC	Associated with clinical stage.	0.904	RT-qPCR	Wang et al. (2020a)
NSCLC	CircFARSA	Plasma	Up	50 NSCLC/50 HC	NA	0.710	RNA-seq RT-qPCR	Hang et al. (2018)
NSCLC	Hsa_circ_0109320	Plasma	Up	90 NSCLC	Associated with progression-free survival and gefitinib response.	0.805	Microarray RT-qPCR	Liu et al. (2019c)
NSCLC	Hsa_circ_0002130	Serum derived exosome	Up	28 drug-resistance NSCLC/32 drug-sensitive NSCLC	Associated with osimertinib response.	0.792	RT-qPCR	Ma et al. (2020)
Osteosarcoma	Hsa_circ_0000885	Serum	Up	55 osteosarcoma/27 benign bone tumor/25 HC	Associated with clinical prognosis; significant expression difference between pre-treatment and post-treatment.	0.783	RNA-seq RT-qPCR	Zhu et al. (2019a)
PBC	Hsa_circ_402458	Plasma	Up	35 PBC/36 HC	NA	0.710	Microarray RT-qPCR	Zheng et al. (2016)
PC	Circ-LDLRAD3	Plasma	Up	31 PC/31 HC	Associated with CA19-9, N classification, venous invasion, lymphatic invasion, stage, metastasis.	0.670	RT-qPCR	Yang et al. (2017a)

Table 1 continued								
Disease	CircRNA biomarker	Source	Expression change	Cohort size	Clinical significance	AUC	Method	Reference
PDAC	Hsa_circ_0036627	Plasma derived exosome	Up	93 PDAC/20 HC	Associated with duodenal invasion, vascular invasion, T factor, TNM stage and survival rate.	NA	Microarray RT-qPCR	Li et al. (2018e)
PDAC	Circ-IARS	Plasma derived exosome	Up	20 PDAC with metastasis/20 PDAC without metastasis	Associated with tumor vessel invasion, liver metastasis, TNM stage, and prognosis.	NA	Microarray RT-qPCR	Li et al. (2018a)
PoAF	Hsa_circ_025016	Plasma	Up	769 underwent off-pump coronary artery bypass grafting/15 HC	Associated with fasting blood glucose.	0.802	Microarray RT-qPCR	Zhang et al. (2018c)
SAI	CircFUNDCl	Plasma	Up	26 AIS with SAI/42 AIS without SAI	Associated with neutrophils counts, white blood cell and neutrophil ratios.	0.661	RT-qPCR	Zuo et al. (2020)
SCC	CircFoxO3a	Serum	Down	103 SCC/30 HC	Associated with stromal invasion, LNM and prognosis.	NA	RT-qPCR	Tang et al. (2020)
SCLC	CircFLI1	Serum derived exosome	Up	61 SCLC/55 HC	Associated with tumor survival and chemotherapy response.	NA	RT-qPCR	Li et al. (2018b)
SLE	Hsa_circ_407176 Hsa_circ_001308	Plasma	Down	126 SLE/102 HC	NA	0.599 0.662	Microarray RT-qPCR	Zhang et al. (2018e)
SOC	CircSETDBI	Serum	Up	60 SOC/60 HC	Associated with clinical stage, LNM, chemotherapy response and progression-free survival.	0.830	RT-qPCR	Wang et al. (2019d)
TB	Hsa_circ_0001204 Hsa_circ_0001747	Plasma	Down	195 TB/50 pneumonia/50 LC/50 COPD/170 HC	Associated with the radiological severity scores; significant expression difference between pre-treatment and post-treatment.	0.928	RT-qPCR	Huang et al. (2018b)
TB	Hsa_circ_0001953 Hsa_circ_0009024	Plasma	Up	123 TB/103 HC	Associated with TB severity; significant expression difference between pre-treatment and post-treatment.	0.915	Microarray RT-qPCR	Huang et al. (2018a)

Table 1 continued

Disease	CircRNA biomarker	Source	Expression change	Cohort size	Clinical significance	AUC	Method	Reference
TB	Hsa_circ_051239 Hsa_circ_029965 Hsa_circ_404022	Serum	Up	131 TB/50 pneumonia/53 HC	Hsa_circRNA_051239 was associated with TB drug response.	0.992	Microarray RT-qPCR	Liu et al. (2020)
TB	Hsa_circ_103571	Plasma	Down	35 TB/32 HC	NA	0.838	Microarray RT-qPCR	Yi et al. (2018)
UCB	CircPRMT5	Serum derived exosome	Up	71 UCB/50 HC	Associated with LNM and tumor progression.	NA	RT-qPCR	Chen et al. (2018b)

Abbreviation: AIS: acute ischemic stroke; CA: cerebral atherosclerosis; CAD: coronary artery disease; CHB: chronic hepatitis B; CHD: congenital heart diseases; CLL: chronic lymphocytic leukemia; COPD: chronic obstructive pulmonary disease; CRC: colorectal cancer; ddPCR: droplet digital PCR; EC: endometrial cancer; EOC: epithelial ovarian cancer; ESSC: esophageal squamous cell cancer; EV: extracellular vesicle; GBM: glioblastoma; GC: gastric cancer; HC: healthy control; HCC: hepatocellular carcinoma; HCM: hypertrophic cardiomyopathy; IPAH: idiopathic pulmonary arterial hypertension; KD: Kawasaki disease; LAC: lung adenocarcinoma; LC: lung cancer; LN: lymph node metastasis; LUAD: lung adenocarcinoma; MCL: mantle cell lymphoma; MDD: major depressive disorder; NA: not applicable; RT-qPCR: reverse transcription and quantitative PCR; NPC: nasopharyngeal carcinoma; NSCLC: non-small cell lung cancer; PBC: primary biliary cholangitis; PC: pancreatic cancer; PDAC: pancreatic ductal adenocarcinoma; PoAF: postoperative atrial fibrillation; SAI: stroke associated infection; SCC: squamous cervical cancer; SCLC: small cell lung cancer; SLE: systemic lupus erythematosus; SOC: serous ovarian cancer; TB: tuberculosis; TNM: tumor node metastasis; UCB: urothelial carcinoma of the bladder..

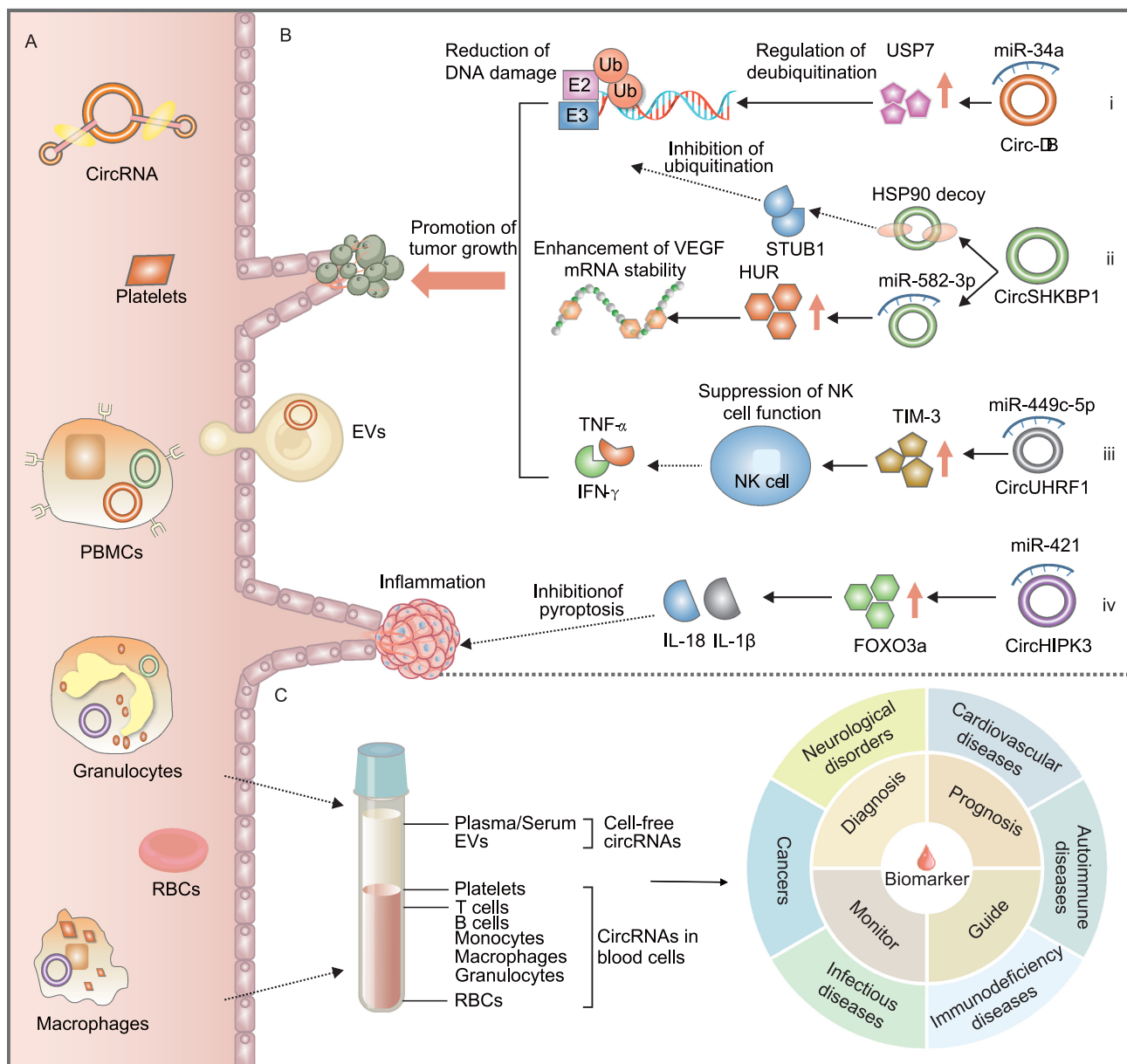


Figure 2. Peripheral blood circRNAs are implicated in human diseases and can be used as potential disease biomarkers in liquid biopsy. (A) Peripheral blood circRNAs are abundantly expressed and can be reliably detected in cell-free circulating blood components (such as exosomes, EVs, plasma, and serum) and blood cells (including PBMCs, macrophages, RBCs, and platelets). (B) Some exosomal circRNAs, such as *circ-DB* (i), *circSHKBP1* (ii), and *circUHRF1* (iii), are important regulators in oncogenic pathways, while some circRNAs in exosomes, such as *circHIPK3* (iv), play key roles in the release of inflammatory cytokines. (C) Peripheral blood circRNAs, both cell-free circRNAs and intracellular circRNAs in blood cells, have potential clinical applications as liquid biopsy biomarkers in many human diseases, such as the diagnosis, prognosis and treatment guidance of many human diseases, including autoimmune diseases, cancers, cardiovascular diseases, immuno-deficiency diseases, infectious diseases, and neurodegenerative diseases.

substantial challenges in investigating the functions of circRNAs (Li et al., 2018d). Based on our current knowledge, circRNAs have diverse functions as miRNA decoys, protein

regulators and translation templates (Fig. 1B, see (Chen, 2016, 2020; Li et al., 2018d) for excellent reviews).

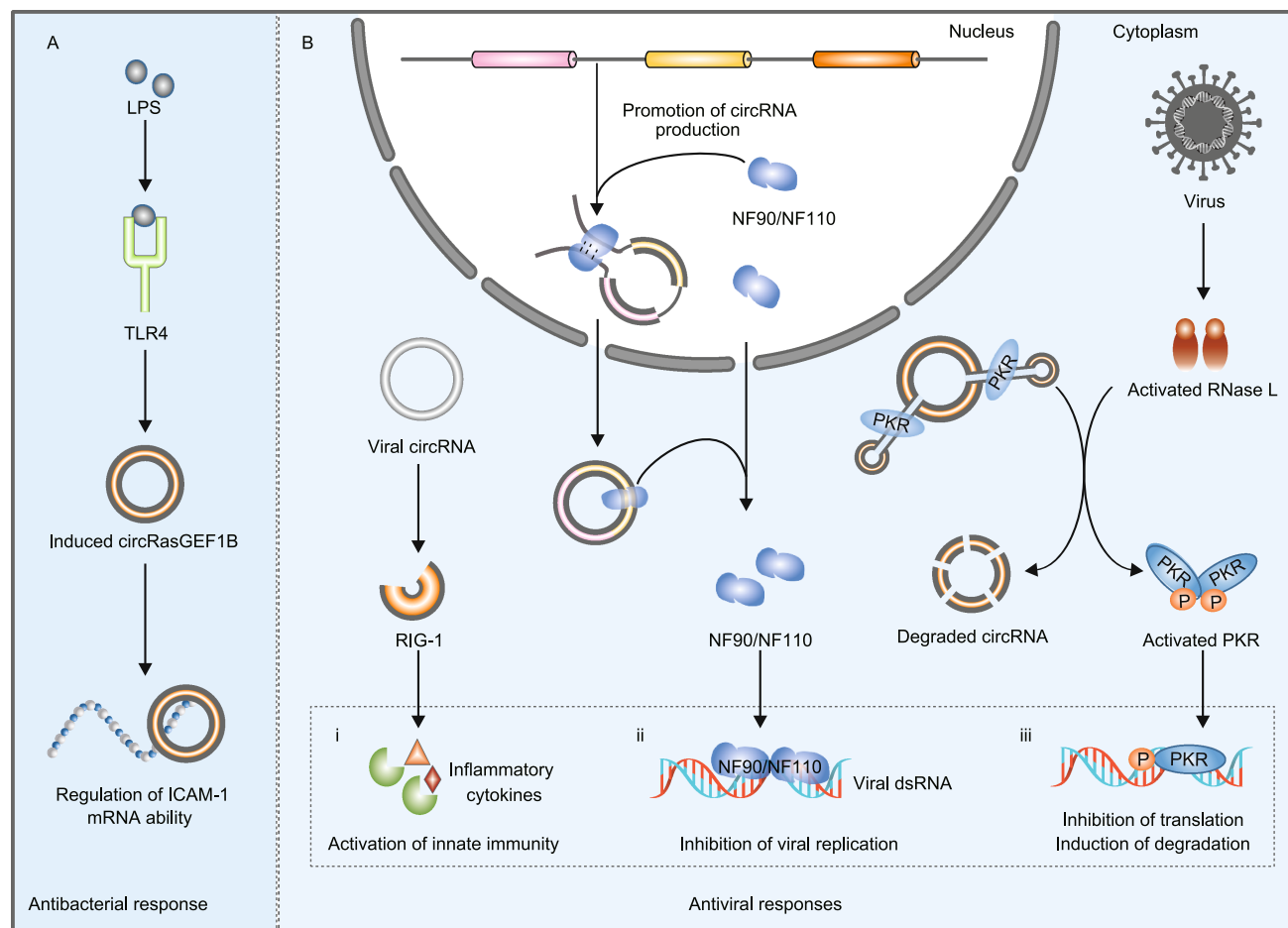


Figure 3. CircRNAs are actively involved in host immune responses to exogenous pathogens. (A) *CircRasGEF1B*, a circRNA induced by *LPS*, can protect cells from bacterial infection by regulating the expression of *ICAM-1* mRNA in the *TLR4/LPS* pathway. (B) Exogenous circRNAs released by viruses can be recognized by *RIG-I*, thus activating the host innate immunity to viruses (i). Moreover, *NF90/NF110* not only promotes circRNA production in the nucleus but also interacts with mature host circRNAs to form circRNP complexes in the cytoplasm. Upon viral infection, *NF90/NF110* can be released from circRNP complexes and bind viral mRNAs to inhibit viral replication (ii). In addition, circRNAs can form RNA duplexes and act as inhibitors of *PKR* under normal conditions. When a virus invades the cells of its host, *RNase L* is activated to efficiently degrade circRNAs, and *PKR* is released and activated to initiate the early cellular innate immune response (iii).

MiRNA decoys

The most well-known function of circRNAs is that they can act as a sponge to inhibit the function of miRNAs and indirectly regulate the expression of miRNA target genes at the posttranscriptional level (Fig. 1B) (Hansen et al., 2013; Memczak et al., 2013; Weng et al., 2017). For example, *Cdr1as* can compete with mRNAs by binding *miR-7* through miRNA response elements (MREs) (Hansen et al., 2013). A follow-up *in vivo* experiment that knocked down the *Cdr1as* locus in the mouse genome confirmed the importance of the *Cdr1as* and *miR-7* interaction in normal brain function (Piwecka et al., 2017). Although it may not be a common

phenomenon for most circRNAs (Guo et al., 2014), several abundant circRNAs also function as miRNA sponges, including *circASAP1* (Hu et al., 2019c), *circBIRC6* (Yu et al., 2017), *circHIPK2* (Huang et al., 2017b), *circHIPK3* (Zheng et al., 2016) and *circSry* (Hansen et al., 2013).

Protein regulators

In addition to miRNAs, circRNAs can interact with proteins or protein complexes to regulate protein expression and function (Fig. 1B) (Huang et al., 2020a). First, circRNAs can bind to some RBPs and act as RBP sponges. *CircMbl*, a circRNA originating from the second exon of the splicing factor

Table 2. CircRNA biomarkers in blood cells or whole blood.

Disease	CircRNA biomarker	Source	Expression change	Cohort size	Clinical significance	AUC	Method	Reference
AIS	Circ-DLGAP4	PBMC	Down	170 AIS /170 HC	Associated with Health Stroke Scale score and levels of C-reactive protein, TNF- α , IL-6, IL-8, IL-22.	0.816	RT-qPCR	Zhu et al. (2019b)
ALS	Hsa_circ_0023919 Hsa_circ_0063411 Hsa_circ_0088036	Leukocyte	Down Up Up	60 ALS/15 HC	Hsa_circ_0063411 was associated with the disease duration and survival time.	0.950	Microarray RT-qPCR	Dolinar et al. (2019)
AML	Hsa_circ_0004277	Mononuclear cell	Down	115 AML/12 HC	Associated with progressive stage.	0.957	Microarray RT-qPCR	Li et al. (2017c)
CAD	CircZNF609	Leukocyte	Down	330 CAD/209 HC	Associated with inflammatory processes.	0.761	RT-qPCR	Liang et al. (2020)
CAD	Hsa_circ_0001879 Hsa_circ_0004104	PBM	Up	436 CAD/297 HC	Hsa_circ_0001879 was associated with body mass index (BMI), systolic blood pressure, diastolic blood pressure and Gensini score; hsa_circ_0004104 was associated with high-density lipoprotein cholesterol.	0.703 0.700	Microarray RT-qPCR	Wang et al. (2019a)
CAD	Hsa_circ_0124644	Whole blood	Up	179 CAD/157 HC	Associated with severity.	0.769	Microarray RT-qPCR	Zhao et al. (2017a)
CAP	Hsa_circ_0018429 Hsa_circ_0026579 Hsa_circ_0099188 Hsa_circ_0012535	Whole blood	Up	36 CAP/36 HC	NA	0.878	Microarray RT-qPCR	Zhao et al. (2019)
CML	Hsa_circ_100053	PBMC	Up	150 CML/100 HC	Associated with clinical stage, BCR/ABL mutant status, imatinib response and prognosis.	NA	RNA-seq RT-qPCR	Ping et al. (2019)
CSCC	Hsa_circ_0101996 Hsa_circ_0101119	Whole blood	Up	87 CSCC/55 HC	NA	0.964	RT-qPCR	Wang et al. (2017a)
EH	Hsa_circ_0037911	Whole blood	Up	100 EH/100 HC	Associated with gender, smoking, drinking and serum creatinine.	0.627	Microarray RT-qPCR	Bao et al. (2018)
EH	Hsa_circ_0037909	Whole blood	Up	48 EH/48 HC	Associated with serum creatinine and low-density lipoprotein.	0.682	RT-qPCR	Bao et al. (2019)
EH	Hsa_circ_0014243	Whole blood	Up	89 EH/89 HC	Associated with age, high-density lipoprotein level and glucose level.	0.732	RT-qPCR	Zheng et al. (2019)

Table 2 continued

Disease	CircRNA biomarker	Source	Expression change	Cohort size	Clinical significance	AUC	Method	Reference
EH	Hsa_circ_91025	Whole blood	Up	96 EH/96 HC	Associated with high-density lipoprotein, BMI, diastolic blood pressure and systolic blood pressure.	0.620	RT-qPCR	Zheng et al. (2020)
GC	Hsa_circ_0001821	Whole blood	Down	30 GC/30 HC	NA	0.872	RT-qPCR	Kong et al. (2019)
HCC	Hsa_circ_0000798	PBMC	Up	72 HCC/30 HC	Associated with tumor size, cirrhosis and overall survival.	0.703	RNA-seq RT-qPCR	Lei et al. (2019)
HT	Hsa_circ_0089172	PBMC	Up	35 HT/35 HC	Associated with the serum level of the thyroid peroxidase antibody.	0.715	RNA-seq RT-qPCR	Xiong et al. (2019)
IA	Hsa_circ_0021001	Whole blood	Down	223 IA/131 HC	Associated with aneurysm rupture, Hunt, Hess level, timing of surgery, disease-free survival and overall survival.	0.870	RT-qPCR	Teng et al. (2017)
MI	MICRA	Whole blood	Down	642 Acute MI/86 HC	Associated with the risk of left ventricular dysfunction.	NA	Microarray RT-qPCR	Vausort et al. (2016)
MS	Hsa_circ_0005402 Hsa_circ_0035560	Leucocyte	Down	45 MS/26 HC	NA	0.899 0.706	Microarray RT-qPCR	Iparraguirre et al. (2017)
NSCLC	Hsa_circ_0102533	Whole blood	Up	41 NSCLC/26 HC	Associated with tumor type, TNM stage, LNM and distant metastasis.	0.774	Microarray RT-qPCR	Zhou et al. (2018b)
OA	Hsa_circ_0032131	Whole blood	Up	25 OA/25 HC	Associated with the pathological process.	0.846	Microarray RT-qPCR	Wang et al. (2019f)
KBD / OA	Hsa_circ_0020014	Whole blood	Down	25 KBD/25 OA	Associated with early diagnosis of OA and KBD.	0.642	Microarray RT-qPCR	Wang et al. (2020e)
PE	Hsa_circ_0004904 Hsa_circ_0001855	Whole blood	Up	35 PE/35 HC	Associated with serum pregnancy-associated plasma protein A level.	0.611 0.621	Microarray RT-qPCR	Jiang et al. (2018)
PE	Hsa_circ_101222	Blood corpuscle	Up	41 PE/41 HC	NA	0.706	Microarray RT-qPCR	Zhang et al. (2016)
PMOP	Hsa_circ_0001275	PBMC	Up	58 PMOP/41 HC	Associated with T-score.	0.759	Microarray RT-qPCR	Zhao et al. (2018a)
RA	Hsa_circ_0044235	Whole blood	Down	77 RA/31 SLE/50 HC	NA	0.779	RT-qPCR	Luo et al. (2018)

Table 2 continued

Disease	CircRNA biomarker	Source	Expression change	Cohort size	Clinical significance	AUC	Method	Reference
RA	Hsa_circ_104871 Hsa_circ_003524 Hsa_circ_101873 Hsa_circ_103047	PBMC	Up	35 RA/30 HC	NA	0.833 0.683 0.676 0.671	Microarray RT-qPCR	Ouyang et al. (2017)
RA	Hsa_circ_0000396 Hsa_circ_0130438	PBMC	Down	32 RA/20 HC	NA	0.809 0.774	RNA-seq RT-qPCR	Yang et al. (2019)
SLE	Hsa_circ_0000479	PBMC	Up	97 SLE/50 RA/ 89 HC	Associated with albumin level, urine protein, IgG, leukocytes, hemoglobin and ESR.	0.731	RNA-seq RT-qPCR	Guo et al. (2019)
SLE	Hsa_circ_0057762 Hsa_circ_0003090	Whole blood	Up	24 SLE/24 HC	Hsa_circ_0057762 was associated with the SLEDAI-2K score.	0.804 0.848	Microarray RT-qPCR	Li et al. (2019b)
SLE	Hsa_circ_0044235 Hsa_circ_0068367	PBMC	Down	79 SLE/30 RA/ 62 HC	Hsa_circ_0044235 was associated with the numbers of monocytes and autoantibodies.	0.873 0.768	Microarray RT-qPCR	Luo et al. (2019)
SLE	CircPTPN22	PBMC	Down	53 SLE/40 HC	Associated with SLE activity index scores.	0.918	RNA-seq RT-qPCR	Miao et al. (2019)
SLE	Hsa_circ_407176 Hsa_circ_001308	PBMC	Down	126 SLE/102 HC	NA	0.806 0.722	Microarray RT-qPCR	Zhang et al. (2018e)
SLE	Hsa_circ_0012919	CD4 ⁺ T cell	Up	28 SLE/18 HC	Associated with clinical and lab features.	–	Microarray RT-qPCR	Zhang et al. (2018a)
Schizophrenia	Hsa_circ_104597	PBMC	Down	102 Schizophrenia/ 103 HC	Significant expression difference between pre-treatment and post-treatment.	0.885	Microarray RT-qPCR	Yao et al. (2019)
T2DM	CircANKRD36	Leucocyte	Up	43 T2DM/45 HC	Associated with glucose, glycosylated hemoglobin and interleukin.	NA	RNA-seq RT-qPCR	Fang et al. (2018)
T2DM	Hsa_circ_0054633	Whole blood	Up	90 T2DM/83 Pre-diabetes/ 86 HC	NA	0.751	Microarray RT-qPCR	Zhao et al. (2017b)
TB	Hsa_circ_103017 Hsa_circ_059914 Hsa_circ_101128	PBMC	Up	31 TB/30 HC	Hsa_circ_101128 was associated with the level of let-7a.	0.870 0.821 0.817	Microarray RT-qPCR	Fu et al. (2019)

Table 2 continued

Disease	CircRNA biomarker	Source	Expression change	Cohort size	Clinical significance	AUC	Method	Reference
TB	Hsa_circ_0043497 Hsa_circ_0001204	Monocyte	Up	101 TB/88 HC	Significant expression difference between pre-treatment and post-treatment.	0.860 0.848	Microarray RT-qPCR	Huang et al., (2017c)
TB	Hsa_circ_001937	PBMC	Up	178 TB/40 PE/ 40 COPD/40 LC/133 HC	Associated with radiological scores; significant expression difference between pre-treatment and post-treatment.	0.873	Microarray RT-qPCR	Huang et al., (2018c)
TB	Hsa_circ_0001380	PBMC	Down	32 TB/31 HC	NA	0.950	RT-qPCR	Luo et al. (2020b)
TB	Hsa_circ_0000414 Hsa_circ_0000681 Hsa_circ_0002113 Hsa_circ_0002362 Hsa_circ_0002908 Hsa_circ_0008797 Hsa_circ_0063179	PBMC	Up	12 TB/13 HC	NA	0.946	RNA-seq Microarray RT-qPCR	Qian et al. (2018)
TB	Hsa_circ_0005836	PBMC	Down	49 TB/45 HC	NA	NA	RNA-seq RT-qPCR	(Zhuang et al., 2017)

Abbreviation: AIS: acute ischemic stroke; ALS: amyotrophic lateral sclerosis; AML: acute myeloid leukemia; CAD: coronary artery disease; CAP: community-acquired pneumonia; CML: chronic myeloid leukemia; COPD: chronic obstructive pulmonary disease; CSCC: cervical squamous cell carcinoma; EH: essential hypertension; GC: gastric cancer; HC: healthy control; HCC: hepatocellular carcinoma; HT: Hashimoto's thyroiditis; IA: intracranial aneurysm; KBD: Kashin-Beck disease; MI: myocardial infarction; MS: multiple sclerosis; NA: not applicable; NSCLC: non-small cell lung cancer; OA: osteoarthritis; PBMC: peripheral blood mononuclear cell; PE: pre-eclampsia; PMOP: postmenopausal osteoporosis; RA: rheumatoid arthritis; SLE: systemic lupus erythematosus; T2DM: type 2 diabetes mellitus; TB: tuberculosis..

muscleblind (*MBL*), is the first circRNA that was discovered to function as an RBP sponge (Ashwal-Fluss et al., 2014). It was observed that both the circular exon and the flanking introns of *circMbl* contain many *MBL* binding sites that can be specifically bound by *MBL* (Ashwal-Fluss et al., 2014). Therefore, increased expression of *MBL* can promote back-splicing of *circMbl* and lead to decreased expression of canonical linear *MBL* transcripts. At the same time, *circMbl* can sequester *MBL* in the cytoplasm and prevent it from performing splicing functions (Ashwal-Fluss et al., 2014). Several other circRNAs, such as *circAmotl1* (Yang et al., 2017b), *circANRIL* (Holdt et al., 2016), *circPABPN1* (Abdelmohsen et al., 2017), *circPOLR2A* (Li et al., 2017e) and *circDHX34* (Li et al., 2017e), can function as protein decoys as well. Second, circRNAs can form a complex with other RNAs and proteins to perform functions. For example, some intron-containing circRNAs, such as *circEIF3J* and *circBPTF*, can interact with U1 snRNP to form an RNA-protein complex, which further interacts with RNA polymerase II (*Pol II*) at the promoter region of their parental genes and enhances their transcription (Zhang et al., 2013; Li et al., 2015c). Similarly, some ciRNAs, such as *ci-ankrd52*, can also associate with *Pol II* as well (Zhang et al., 2013; Li et al., 2015c). They can also regulate the expression of their parental gene by modulating the elongation of *Pol II* (Zhang et al., 2013; Li et al., 2015c). Many circRNAs, rather than a specific circRNA, can interact with *NF90/NF110* as a group to form circRNP complexes in the cytoplasm, which may function as a reservoir of *NF90/NF110* (Li et al., 2017e). Upon viral invasion, *NF90/NF110* could be released from circRNP complexes and bind to viral mRNAs to perform its antiviral functions (Li et al., 2017e). Third, the interaction of circRNAs with proteins can facilitate or block the function of their binding proteins. For instance, increased expression of *circFoxo3* in the cytoplasm may arrest the anti-senescent protein *ID1*, transcription factor *E2F1*, anti-stress proteins *FAK* and *HIF1 α* and prevent the nuclear translocation of these transcription factors and their function, thus leading to increased cellular senescence (Du et al., 2017). *CircFoxo3* can also form a tertiary circRNA-protein complex with cyclin-dependent kinase 2 (*CDK2*) and cyclin-dependent kinase inhibitor 1 (*p21*), which facilitates the inhibition of *CDK2* by *p21*, thus blocking cell cycle progression (Du et al., 2016a). Moreover, *circFoxo3* can bind to *Mdm2* and *p53* in a breast cancer cell line, which leads to tumor cell apoptosis (Du et al., 2016b).

Translation

Some circRNAs with an internal ribosome entry site (IRES), such as *circMbl* (Pamudurti et al., 2017) and *circZNF609* (Legnini et al., 2017), can share the start codon of their host genes and be translated in a cap-independent manner. The translation initiation of circRNAs may be promoted by N⁶-methyladenosine (m⁶A) modification of circRNAs (Yang et al., 2017c). In the human heart, 40 circRNAs were

observed to be associated with ribosomes and thus may be translated (Heesch et al., 2019). Some of them, including *circSLC8A1*, *circMYBPC3* and *circRYR2*, are heart-specific circRNAs (Heesch et al., 2019). The translation of these circRNAs may be related to the physiological roles of the human heart. Further functional analysis observed that some circRNA-encoded proteins can exert agonist or antagonist effects on cancer progression. For example, *PINT87aa* (Zhang et al., 2018d) and *AKT3-A74aa* (Xia et al., 2019), two peptides encoded by circRNAs, can interact with signal factors and inhibit glioblastoma tumorigenicity in glioblastoma. However, *circGprc5a*-secreted peptides can promote bladder oncogenesis and metastasis through its binding to *Gprc5a* (Gu et al., 2018).

CIRC RNA EXPRESSION AND ITS IMPLICATION IN DISEASES

Given the important functions that circRNAs can perform, their expression may provide significant clues in understanding the underlying mechanisms of biological processes and disease states. Previous studies have observed that circRNAs are widely expressed in all tissues (Zhou et al., 2018a; Ji et al., 2019; Wu et al., 2020a) and cell types (Salzman et al., 2013) of nearly all species across the eukaryotic tree of life (Wang et al., 2014). Specifically, circRNAs are enriched in brain samples (Westholm et al., 2014; Rybak-Wolf et al., 2015; Szabo et al., 2015; Venø et al., 2015) and human blood samples (Memczak et al., 2015), including peripheral blood mononuclear cells (PBMCs) (Qian et al., 2018), erythrocytes (Alhasan et al., 2016), platelets (Alhasan et al., 2016) and exosomes (Li et al., 2015b). Furthermore, circRNAs are expressed in tissue- (Guo et al., 2014; Szabo et al., 2015; Zhou et al., 2018a) or cell-type- (Salzman et al., 2013) specific and age-dependent manner (Rybak-Wolf et al., 2015; Szabo et al., 2015; You et al., 2015; Zhou et al., 2018a). Using the rat *BodyMap* dataset, we observed tissue-specific circRNA expression in all 11 rat tissues, which may be closely related to the physiological functions of those tissues (Zhou et al., 2018a). The dynamic expression of circRNAs across time has also been correlated with neuronal differentiation (Rybak-Wolf et al., 2015), neural development (Szabo et al., 2015; You et al., 2015), human terminal B cell differentiation (Agirre et al., 2019) and spermatogenesis (Zhou et al., 2018a).

The spatiotemporal expression of circRNAs is mediated by the balance between circRNA generation and circRNA turnover, which can be regulated at both the transcriptional and posttranscriptional levels (Li et al., 2018d; Chen, 2020). On the one hand, the production of circRNAs can be regulated by intronic complement sequences (ICSs) (Jeck et al., 2013; Liang and Wilusz, 2014; Zhang et al., 2014), cis-splicing elements (Ashwal-Fluss et al., 2014; Starke et al., 2014; Wang and Wang, 2015) and trans-acting splicing

factors (Ashwal-Fluss et al., 2014; Conn et al., 2015; Kramer et al., 2015; Khan et al., 2016; Aktaş et al., 2017; Errichelli et al., 2017; Fei et al., 2017; Li et al., 2017e). On the other hand, the degradation of circRNAs can be affiliated by miRNA-initiated AGO2 cleavage (Kleaveland et al., 2018) and nuclease-mediated cleavage, including RNase L endonuclease (Liu et al., 2019a), RNase P/MRP endonuclease complex (Park et al., 2019) and G3BP1 endonuclease (Fischer et al., 2020). Dysregulation of circRNA generation or turnover may lead to aberrant circRNA expression in cells or tissues, which may be related to many human diseases (Chen et al., 2016). *Cdr1as*, one of the most studied circRNAs, harbors more than 70 binding sites for *miR-7*, and its overexpression strongly inhibits the activity of the tumor suppressor *miR-7* (Hansen et al., 2013). Accumulating evidence has demonstrated its significant increase in colorectal cancer samples, which can inhibit *miR-7* function and activate *EGFR* and *RAF1* oncogenes (Weng et al., 2017). Moreover, the dysregulation of the *miR-7/Cdr1as* axis is involved in some other diseases, such as Alzheimer's diseases (Lukiw, 2013), diabetes (Xu et al., 2015) and cardiometabolic diseases (Geng et al., 2016). Furthermore, the loss of the *Cdr1as* locus causes miRNA deregulation and affects synaptic transmission in knockout mice (Piwecka et al., 2017). In addition to *Cdr1as*, other circRNAs are also implicated in many different human diseases, including cancers (Zhang et al., 2018j; Chen et al., 2019b; Smid et al., 2019; Su et al., 2019; Vo et al., 2019), cardiovascular diseases (Zhang et al., 2018j; Aufiero et al., 2019), neurodevelopment and neurodegenerative diseases (Kumar et al., 2017; Zhang et al., 2018j; Dube et al., 2019; Chen et al., 2020d; Hanan et al., 2020) and immune diseases (Chen et al., 2019c; Zhou et al., 2019b).

CIRC RNAs ARE PROMISING BIOMARKERS FOR HUMAN DISEASES

In general, biomarkers are physiological indexes or biological molecules that can be objectively measured and can indicate either a normal or a pathogenic state (Lesko and Atkinson, 2001). Technological advances in genomics, transcriptomics, proteomics and metabolomics have led to the discovery and validation of many biomarkers that are pushing personalized medicine forward (Chen et al., 2012; Karczewski and Snyder, 2018; Ahadi et al., 2020). A good biomarker with clinical significance must meet the criteria of analytical validity, clinical validity and clinical utility (Byron et al., 2016). As a novel type of noncoding RNA, circRNA has several distinct advantages over canonical linear RNAs as a disease biomarker (Zhang et al., 2018j). First, circRNA is more stable than linear RNAs because it has a closed loop structure without 5-prime and 3-prime ends (Enuka et al., 2015; Li et al., 2015b). In the *MCF10A* human mammary epithelial cell line, Enuka et al. observed at least 2.5 times longer half-lives of circRNAs compared to linear RNAs,

including mRNAs and miRNAs (Enuka et al., 2015). Second, circRNAs are abundantly expressed in many tissue samples. For example, brain samples express more than 10,000 circRNAs in the rat *BodyMap* dataset (Zhou et al., 2018a). In some cases, the expression values of circRNAs are much higher than their linear counterparts (Westholm et al., 2014; Rybak-Wolf et al., 2015; You et al., 2015; Liang et al., 2017). Third, circRNAs are expressed in a tissue-specific (Salzman et al., 2013; Guo et al., 2014; Szabo et al., 2015; Zhou et al., 2018a) and developmental stage-specific manner (Rybak-Wolf et al., 2015; Szabo et al., 2015; You et al., 2015; Zhou et al., 2018a). Importantly, the tissue specificity of circRNA is higher than that of mRNA of its host gene (Guo et al., 2014; Zhou et al., 2018a). These features suggest that circRNAs may have better analytical validity (Zhang et al., 2018j), including analytical specificity, robustness, reproducibility and repeatability (Byron et al., 2016), when used as biomarker molecules. In a recent study, Maass et al. investigated circRNA expression in 20 clinically relevant tissue samples, which underscored the feasibility of using circRNAs as potential disease biomarkers (Maass et al., 2017).

To date, many circRNAs have been identified as biomarkers for human diseases (Zhang et al., 2018j), especially human cancers (Li et al., 2015a; Meng et al., 2017; Su et al., 2019; Sheng et al., 2020). For example, *Cdr1as* has been revealed as a prognostic biomarker in colorectal cancer patients (Weng et al., 2017). In a training cohort comprising 153 primary colorectal cancer tissues and 44 matched normal mucosae, significantly increased *Cdr1as* expression was observed in colorectal cancer tissues, and its overexpression was associated with poor patient survival. The prognostic power of *Cdr1as* was further validated in an independent validation cohort comprising 165 colorectal cancer patients (Weng et al., 2017). A four-circRNA signature, consisting of *hsa_circ_101308*, *hsa_circ_104423*, *hsa_circ_104916* and *hsa_circ_100269*, has been constructed that can predict the early recurrence of stage III gastric cancer (GC) patients after surgery (Zhang et al., 2017). Moreover, Vo et al. constructed a comprehensive catalog of circRNAs in human cancer tissues in a systematic analysis of more than 2,000 cancer samples (Vo et al., 2019). They identified two circRNAs, *circ-AURKA* and *circ-AMACR*, as potential diagnostic biomarkers for neuroendocrine prostate cancer (Vo et al., 2019). Although these circRNA biomarkers are potentially useful in cancer management, most of them are derived from tissue samples (Li et al., 2015a; Meng et al., 2017; Su et al., 2019; Sheng et al., 2020). To improve biomarker accessibility, especially for biomarkers of cancer screening and diagnosis, circRNA biomarkers in body fluids are ideal for clinical application (Anfossi et al., 2018). Hence, the authors further investigated and validated the reliability of detecting circRNA biomarkers in urine samples of prostate cancer patients (Vo et al., 2019), which suggests that circRNA in urine samples is a promising strategy for prostate cancer screening.

BLOOD CIRC RNAs AND LIQUID BIOPSY BIOMARKERS

Liquid biopsy has been a revolutionary tool in disease management, supporting the diagnosis, prognosis and treatment guidance of human diseases (Heitzer et al., 2019; Mattox et al., 2019; Rubis et al., 2019; Luo et al., 2020a). In comparison to urine, saliva or cerebrospinal fluid, peripheral blood has been used as the major body fluid in liquid biopsy (Rubis et al., 2019; Luo et al., 2020a). In the circulating blood, aberrantly expressed RNAs or fusion transcripts in different blood components have been associated with human cancers (Byron et al., 2016; Zaporozhchenko et al., 2018; Sole et al., 2019) and infectious diseases (Byron et al., 2016; Correia et al., 2017). These RNA biomarkers include cfRNAs in plasma or serum (Mitchell et al., 2008; Fehlmann et al., 2020), exosome-derived RNAs (Maas et al., 2017), EV-incorporated cfRNAs (Maas et al., 2017) and RNA transcripts in tumor-educated platelets (Best et al., 2017, 2018). These cell-free or EV-incorporated RNA biomarkers represent the changes in expression that occur in abnormal cells, such as dysregulated genes in cancer cells (Byron et al., 2016; Rubis et al., 2019; Luo et al., 2020a). Other than cfRNAs, gene expression profiles of PBMCs or whole blood have been proven to be good indicators of many human diseases (Chaussabel and Baldwin, 2014; Chaussabel, 2015), since they can assess the immune status (Chaussabel, 2015). Unlike the expression of cfRNAs in serum, plasma or EVs, RNA expression levels in PBMCs or whole blood are measures of the host response to exogenous pathogens or autoantigens (Schnell et al., 2018; Shaked, 2019). Several whole blood or PBMC gene expression signatures have been developed for cancer management, including the early diagnosis of colorectal cancer (Marshall et al., 2010; Ciarloni et al., 2015, 2016) and lung cancer (Showe et al., 2009; Kossenkov et al., 2018), the prognosis of adult acute myeloid leukemia (Bullinger et al., 2004; Valk et al., 2004) and prostate cancer patients (Ross et al., 2012), and the monitoring of renal cell carcinoma relapse (Giraldo et al., 2017). Moreover, whole blood or PBMC RNA signatures have been widely investigated as liquid biopsy diagnostic tools for infectious diseases (Ramilo and Mejias, 2017), such as discriminating influenza from other respiratory viral infections (Zaas et al., 2009), differentiating viral and bacterial infections (Tsalik et al., 2016), diagnosing septic patients (Sweeney et al., 2018; Gunsolus et al., 2019; Mayhew et al., 2020), and discriminating active tuberculosis (TB) patients from patients with latent TB or other lung diseases (Bloom et al., 2013; Anderson et al., 2014; Qian et al., 2016; Zak et al., 2016; Sambarey et al., 2017; MacLean et al., 2019; Warsinske et al., 2019; Esmail et al., 2020; Gupta et al., 2020). In addition, the transcriptome of blood cells has been implicated in assessing the likelihood of developing obstructive coronary artery disease in symptomatic nondiabetic patients (Vargas et al., 2013) and

predicting antibody-mediated kidney allograft rejection in kidney transplant patients (Loon et al., 2019).

With regard to RNA molecules, both protein-coding mRNAs (Byron et al., 2016; Sole et al., 2019) and several classes of noncoding RNAs (Byron et al., 2016; Anfossi et al., 2018; Pardini et al., 2019; Sole et al., 2019) have been used as blood disease biomarkers. In comparison to mRNAs or long noncoding RNAs, small noncoding RNAs, such as miRNAs (Mitchell et al., 2008; Max et al., 2018; Fehlmann et al., 2020) and noncanonical small RNAs (Fritz et al., 2016; Pardini et al., 2019), have the advantage of high stability in the circulating blood (Mitchell et al., 2008; Anfossi et al., 2018). This superiority is especially important when translating RNA biomarkers into clinical practice (Byron et al., 2016; Anfossi et al., 2018), since fast mRNA degradation in blood sample processing may affect the performance of mRNA biomarkers (Dvinge et al., 2014). Given the high stability of circRNAs, great efforts and substantial progress have been made to investigate the possibility of using circRNA biomarkers in liquid biopsy in recent years.

Next, we summarize circRNAs in the peripheral blood, their correlations with human diseases and their potential application in liquid biopsy as disease biomarkers (Fig. 2). We classified blood circRNAs into blood cell-free circRNAs and circRNAs in blood cells since they have distinct biological meanings in the context of human diseases. Blood cell-free circRNAs, including circulating cell-free circRNAs in plasma, serum and blood EVs, are secreted from different tissue cells into the blood. Therefore, cell-free circRNAs have corresponding tissue origins, and cell-free circRNA biomarkers represent their clinical significance in the original tissue (Li et al., 2019d, 2020). On the other hand, blood cell circRNAs consist of circRNAs in various blood cells, such as monocytes, erythrocytes, neutrophils and platelets. CircRNAs in mixtures of different blood cells, such as circRNAs in lymphocytes, PBMCs and whole blood, are classified in this group as well. The circRNA expression profiles of peripheral blood cells or a mixture of blood cells are important indicators of the host's immune status (Chaussabel, 2015), which may undergo dynamic changes during acute events such as viral infections (Chen et al., 2018a; Rose et al., 2019; Zhou et al., 2019a). Hence, circRNA biomarkers in blood cells, PBMCs or whole blood represent the specific immune response of an individual to different physiological aspects.

Cell-free circRNAs in peripheral blood

Mounting evidence has demonstrated abundant circRNA expression in blood plasma (Maass et al., 2017; Yi et al., 2018; Smid et al., 2019) and serum (Gu et al., 2017; Maass et al., 2017; Sonnenschein et al., 2019; Sun et al., 2020b) (Fig. 2A). In the circulating blood, EVs, including exosomes and microvesicles, are important blood components that have great diagnostic and prognostic value (Revenfeld et al., 2014). Li et al. investigated circRNA expression in *MHCC-*

LM3 liver cancer cells and cell-derived exosomes and found at least 2-fold circRNA enrichment in exosomes compared to producer cells (Li et al., 2015b). They further found that the expression level of exosomal circRNAs is largely the same after serum incubation at room temperature for up to 24 h (Li et al., 2015b). Using the extracellular vesicle long RNA (exLR) sequencing method, the same group explored the expression profiles of circRNAs in 352 plasma EV samples (Li et al., 2019d). They found 137,196 circRNA candidates that were expressed in normal plasma EV samples, and the circular to linear ratio was significantly higher in EVs than in PBMCs (Li et al., 2019d). A recent study also isolated platelet-derived EVs and demonstrated the selective release of platelet-specific circRNAs in exosomes and microvesicles (Preußner et al., 2018). Based on these data, a database of blood exosomal circRNAs, exoRBase, has been developed to facilitate the development of circRNA signatures in blood exosomes (Li et al., 2017b). In addition, two previous studies have observed that the majority of circulating cell-free miRNAs were associated with AGO2 protein complexes rather than with vesicles in blood plasma (Arroyo et al., 2011; Turchinovich et al., 2011). Like cell-free miRNAs, blood cell-free circRNAs may bind to several RNA-binding proteins or protein complexes as well (Huang et al., 2020a). Therefore, some cell-free circRNAs may not be associated with blood EVs. In a pilot study of circRNA expression profiles in 348 primary breast cancer tissue samples, Smid et al. found that *circCNOT2* is a prognostic biomarker of aromatase inhibitor therapy in advanced breast cancer patients (Smid et al., 2019). To investigate the possibility of using *circCNOT2* as a noninvasive biomarker, they further amplified *circCNOT2* in plasma samples of four breast cancer patients and found variable *circCNOT2* expression in all plasma samples (Smid et al., 2019). All these results suggest that cell-free circRNAs in peripheral blood are stable, enriched and detectable.

Blood EVs can be secreted from cells of many different biological systems and can be circulated to recipient cells through the bloodstream (Revenfeld et al., 2014; Lasda and Parker, 2016). Therefore, blood cell-free circRNAs can perform vital roles in many biological processes, such as cancer cell proliferation, cancer metastasis, drug resistance, hemostasis and inflammation (Fig. 2B) (Wang et al., 2019e; Cui et al., 2020; Li et al., 2020; Shang et al., 2020; Xu et al., 2020b). For example, *circ-deubiquitination* (*circ-DB*) in adipose-secreted exosomes was found to regulate deubiquitination via the suppression of *miR-34a* and the activation of deubiquitination-related *USP7* in plasma samples of hepatocellular carcinoma (HCC) patients, which could reduce DNA damage and promote HCC cell growth (Zhang et al., 2018b). Exosomal *circSHKBP1* was found to promote the progression of GC by regulating the *miR-582-3p/HUR/VEGF* pathway and suppressing *HSP90* degradation (Xie et al., 2020a). *CircUHRF1* in plasma exosomes can inhibit the functions of natural killer cells by upregulating the expression of *TIM-3* via *miR-449c-5p* degradation and drive resistance to anti-*PD1* immunotherapy in HCC patients (Zhang et al.,

2020a). Moreover, exosomal *circHIPK3* can prevent ischemic muscle injury by downregulating *miR-421* expression, increasing *FOXO3a* expression, inhibiting pyroptosis and releasing *IL-1 β* and *IL-18* (Yan et al., 2020).

Given the biological functions that blood cell-free circRNAs can perform (Wang et al., 2019e; Cui et al., 2020; Li et al., 2020) and their implications in many human diseases, cell-free circRNAs in the peripheral blood have great potential as liquid biopsy biomarkers of human diseases (Fig. 2C) (Anfossi et al., 2018; Zaporozhchenko et al., 2018; Zhang et al., 2018j). To date, many blood cell-free circRNAs have been introduced for cancer management, including early cancer diagnosis, cancer prognosis and prediction of cancer treatment (Preußner et al., 2018; Aufiero et al., 2019; Fraipont et al., 2019; Lu et al., 2019c; Pardini et al., 2019; Sole et al., 2019; Su et al., 2019; Wang et al., 2019e; Beltrán-García et al., 2020; Cui et al., 2020; Li et al., 2020). In a recent study, Luo et al. measured the expression levels of two circRNAs in plasma samples of 231 lung cancer patients and 41 healthy controls using reverse transcription droplet digital PCR (RT-ddPCR) (Luo et al., 2020c). They identified *hsa_circ_0000190* as a circRNA biomarker in human blood plasma that can predict the survival outcomes of lung cancer patients (Luo et al., 2020c). Furthermore, the increased expression of plasma *hsa_circ_0000190* was also correlated with poor response to systemic therapy and immunotherapy in lung cancer patients (Luo et al., 2020c). Similarly, Li et al. investigated the clinical relevance of serum exosomal *circFLI1* in lung cancer patients in a cohort of 61 small cell lung cancer (SCLC) patients and 55 normal subjects. They found that serum exosomal *circFLI1* levels were significantly higher in SCLC patients, especially in SCLC patients with distant metastasis (Li et al., 2018b). Notably, they observed that SCLC patients with lower exosomal *circFLI1* expression levels experienced longer disease remissions, indicating its prognostic power in SCLC. The authors also suggested that serum exosomal *circFLI1* may be used as a biomarker that can monitor the clinical response to chemotherapy in SCLC patients (Li et al., 2018b). By analyzing blood plasma samples of 62 GC patients and 25 healthy controls, Tang et al. proposed a novel circulating diagnostic biomarker of GC, plasma exosomal *circKIAA124*, that was correlated with clinical TNM stage, lymphatic metastasis and overall survival time of GC patients (Tang et al., 2018). In addition to the aberrant expression of blood cell-free circRNAs, the presence of some fusion circRNAs (f-circRNAs) in the peripheral blood has also been used as a liquid biopsy biomarker. Guarnerio et al. found that f-circRNAs could be produced from cancer-associated chromosomal translocations in cancer cells (Fig. 1), and f-circRNAs could promote cellular transformation, cell viability and resistance upon therapy (Guarnerio et al., 2016). In a systematic analysis of f-circRNAs in localized prostate cancer tissues, Chen et al. observed more f-circRNAs in tumors with worse prognosis (Chen et al., 2019b). Due to the lack of recurrence of these f-circRNAs, the authors suggested that f-circRNAs are good

biomarker candidates (Chen et al., 2019b). In NSCLC patients, Tan et al. found that *F-circEA*, an f-circRNA originating from the *EML4-ALK* fusion gene, was exclusively expressed in the plasma of patients with the *EML4-ALK* fusion (Tan et al., 2018). Therefore, plasma *F-circEA* may serve as a liquid biopsy biomarker to diagnose NSCLC patients with *EML4-ALK* translocation and guide targeted therapy for NSCLC patients in this subgroup (Tan et al., 2018). More cell-free circRNA biomarkers in the blood are summarized in Table 1.

CircRNAs in blood cells and whole blood

CircRNA expression in blood cells and whole blood, a major source of liquid biopsy samples, has been extensively investigated (Fig. 2A). In a pilot study, Memczak et al. detected thousands of circRNAs in peripheral whole blood samples using RNA-seq (Memczak et al., 2015). They found that the expression levels of these blood circRNAs were comparable to those in circRNA-rich cerebellar tissue (Memczak et al., 2015). In separate blood cell populations, circRNAs were observed to be enriched approximately 100-fold in platelets and anucleate erythrocytes relative to nucleated tissues, such as lung, brain and colon (Alhasan et al., 2016). Gaffo et al. investigated circRNA expression in T cells, B cells and monocytes of healthy subjects and found abundant circRNA expression in these mature blood cells (Gaffo et al., 2019). We also explored the expression landscape of circRNAs in PBMCs and found that the expression level of circRNAs in PBMCs, together with that in platelets, red blood cells (RBCs) and whole blood, is high enough to be detected (Qian et al., 2018). All these results suggest that whole blood (Memczak et al., 2015; Qian et al., 2018), PBMCs (Qian et al., 2018), and several blood cells, including neutrophils (Maass et al., 2017), T cells (Gaffo et al., 2019), B cells (Gaffo et al., 2019), monocytes (Gaffo et al., 2019), RBCs (Alhasan et al., 2016; Qian et al., 2018) and platelets (Maass et al., 2017; Qian et al., 2018; Gaffo et al., 2019), are reliable clinical samples for circRNA profiling in liquid biopsy.

Accumulating evidence has suggested that circRNAs play crucial roles in the immune response and its regulation (Fig. 3) (Chen et al., 2017b, 2019c; Xu et al., 2018b, 2020a; Yang et al., 2018; Zhou et al., 2019b; Awan et al., 2020). First, circRNAs are important regulators of blood cell biogenesis, differentiation and activation (Chen et al., 2019c; Zhou et al., 2019b; Xu et al., 2020a). In a comprehensive study of circRNA expression in hematopoietic progenitors, differentiated lymphoid and myeloid cells, Nicolet et al. observed a cell-type specific pattern of circRNA expression profiles in blood cells, and the type and number of circRNAs increased upon hematopoietic maturation (Nicolet et al., 2018). Moreover, Holdt et al. found that *circANRIL* can bind to *PES1* to impede the generation of pre-rRNA and ribosomes, resulting in the biogenesis of macrophages by *p53* activation (Holdt et al., 2016). Second, circRNAs are actively involved in antiviral immune responses (Fig. 3B) (Cadena

and Hur, 2017; Awan et al., 2020). For example, Chen et al. showed that exogenous circRNAs released by viruses can be recognized by the pattern recognition receptor *RIG-I* of host cells, which activates host innate immunity (Chen et al., 2017a). In their subsequent work, the authors showed that m⁶A RNA modification of human circRNAs inhibits innate immunity, while unmodified circRNAs and K63-polyubiquitin can activate *RIG-I* and innate immune response (Chen et al., 2019a). Li et al. found that two immune factors, *NF90/NF110*, not only promote circRNA production in the nucleus but also bind to mature host circRNAs to form circRNP complexes in the cytoplasm. Upon viral infection, circRNP complexes in the cytoplasm can release *NF90/NF110*, which binds viral mRNAs to inhibit viral replication (Li et al., 2017e). Moreover, Liu et al. presented that circRNAs can form RNA duplexes and act as inhibitors of innate immunity-related protein kinase (*PKR*) under normal conditions (Liu et al., 2019a). Upon poly(I:C) treatment or viral infection, RNase L is activated to efficiently degrade circRNAs, and *PKR* is thus released from circRNA inhibition to initiate the early cellular innate immune response (Liu et al., 2019a). Third, circRNAs are closely associated with the antibacterial immune response as well. Ng et al. characterized circRNAs induced by lipopolysaccharide (*LPS*) and identified *circRasGEF1B* as a conserved positive regulator of the *LPS* response (Ng et al., 2016). Their functional analysis revealed that *circRasGEF1B* can induce the expression of *ICAM-1* in the *TLR4/LPS* pathway, which activates pathogen recognition and the inflammatory response upon microbial infection (Fig. 3A) (Ng et al., 2016).

The important functions of circRNAs in blood cells suggest that the dysregulation of circRNA expression in blood cells is likely to contribute to the occurrence and progression of immune-related diseases, including autoimmune diseases, infectious diseases and cardiovascular diseases (Chen et al., 2019c; Gaffo et al., 2019; Zhou et al., 2019b; Xie et al., 2020b; Xu et al., 2020a). For instance, we determined that the expression level of PBMC circRNAs is higher in TB patients than healthy controls, and five immune-related pathways were upregulated upon *Mycobacterium tuberculosis* infection, including “cytokine-cytokine receptor interactions”, “chemokine signaling pathways”, and “neurotrophic signaling pathways” (Qian et al., 2018). Similarly, Huang et al. identified 13 upregulated and 24 downregulated circRNAs in PBMCs of TB patients (Huang et al., 2018c). Among them, *hsa_circRNA_001937* is likely to participate in the inflammatory response by targeting *miR-26b* and modulating the *NF-κB* pathway (Huang et al., 2018c). In addition, Zhang et al. investigated the roles that circRNAs play in early human immunodeficiency virus (HIV) infection (EHI), especially in regulating HIV replication (Zhang et al., 2018i). EHI represents a stage where viral replication increases to a peak level and intense antiviral immune response and immune injury occur (Powers et al., 2011; Richey and Halperin, 2013). The authors characterized the expression profiles of circRNAs, mRNAs and miRNAs in PBMCs of EHI

patients and constructed a circRNA-associated competing endogenous network in EHI patients. They revealed 67 differentially expressed circRNAs, such as *CCNK*, *CDKN1A* and *IL-15*, that are potentially involved in HIV replication by regulating the expression of genes in the immune response, inflammatory response and defense response to the virus (Zhang et al., 2018i). Regarding autoimmune diseases, Liu et al. detected a global reduction in circRNAs and activation of RNase L in PBMCs of systemic lupus erythematosus (SLE) patients (Liu et al., 2019a). They further found that *circPOLR2A* overexpression can lead to reduced *PKR* activation, *EIF2 α* phosphorylation and type I IFN-induced gene suppression. This highlights the link between circRNAs and innate immunity regulation and provides the potential for circRNA manipulation in SLE treatment (Liu et al., 2019a). In addition to the above examples, the abnormal expression of blood circRNAs is related to several other diseases, such as the immune response to Ebola virus (Wang et al., 2017b) and hepatitis C virus (Jost et al., 2018), rheumatoid arthritis (RA) (Yang et al., 2019), type 2 diabetes mellitus (T2DM) (Fang et al., 2018), heart failure (Han et al., 2020b) and adenosine deaminase deficiency (Maass et al., 2017).

With increasing knowledge of blood cell circRNAs and their function, many circRNAs in blood cells or whole blood have been proposed as liquid biopsy biomarkers for human diseases (Fig. 2C) (Aufiero et al., 2019; Beltrán-García et al., 2020; Kumar et al., 2017; Ravnik-Glavač and Glavač, 2020; Sun et al., 2020a). For instance, we developed a PBMC circRNA-based molecular signature that discriminates active TB patients from healthy controls in our previous study (Qian et al., 2018). The classification power of this PBMC circRNA signature was further validated in an independent cohort with an area under the receiver operating characteristic curve (AUC) of 0.946 (Qian et al., 2018). In another study, Huang et al. found that the expression of *hsa_circ_001937* in PBMCs was significantly higher in TB patients than in pneumonia, chronic obstructive pulmonary disease (COPD) and lung cancer patients (Huang et al., 2018c). In a cohort consisting of 115 TB, 40 pneumonia, 40 COPD, and 40 lung cancer patients and 90 healthy control subjects, *hsa_circ_001937* had good discriminative power with an AUC of 0.873. After anti-TB treatment, the expression level of *hsa_circ_001937* was significantly decreased compared to that of healthy controls. These results suggest that PBMC *hsa_circ_001937* may be a TB diagnostic biomarker (Huang et al., 2018c). Furthermore, Lei et al. found an upregulation of *circ_0000798* expression in PBMCs of HCC patients, which was associated with poor overall survival (Lei et al., 2019). In a cohort of 72 HCC patients and 30 healthy control subjects, *circ_0000798* expression could distinguish HCC patients from healthy controls with an AUC of up to 0.703. The authors suggested that PBMC *circ_0000798* has potential as a blood biomarker for HCC diagnosis and prognosis (Lei et al., 2019). In addition, Li et al. measured circRNA expression changes between children with SLE and healthy children and investigated the significance of blood

circRNAs in SLE diagnosis (Li et al., 2019b). They identified and validated the diagnostic power of two circRNAs in whole blood, *hsa_circ_0057762* and *hsa_circ_0003090*, that can differentiate children with SLE from healthy controls (Li et al., 2019b). Zhao et al. also identified and validated *hsa_circ_0054633* in peripheral whole blood as a sensitive and specific diagnostic biomarker for prediabetes and T2DM (Zhao et al., 2017b). In addition to the above examples, the potential of using blood circRNAs as disease biomarkers has been explored for many other human diseases, such as coronary artery disease (Zhao et al., 2017a; Wang et al., 2019a; Liang et al., 2020), community-acquired pneumonia (Zhao et al., 2019), and schizophrenia (Yao et al., 2019). A list of current proposed potential blood circRNA biomarkers is listed in Table 2.

CONCLUSIONS AND FUTURE PERSPECTIVES

The high stability, abundance and spatiotemporal specific expression of blood circRNAs make them ideal biomarkers for liquid biopsy. In the past several years, many studies have shown that blood circRNAs, both cell-free blood circRNAs and circRNAs in blood cells, have great potential as biomarkers of many human diseases in liquid biopsy. A biomarker with broad clinical application must have demonstrated analytical validity, clinical validity and clinical utility (Byron et al., 2016). Therefore, several issues need to be considered and investigated before peripheral blood circRNA biomarkers can be translated into clinical practice. First, a blood circRNA-based gene test should prove its analytical validity within clinically relevant conditions. Although substantial advances have been made in the past several years (Szabo and Salzman, 2016; Kristensen et al., 2019), the methods to discover and profile circRNAs are far from optimal. Future studies need to test the analytical performance of different circRNA profiling methods in clinical blood samples, such as RNA-seq, circRNA microarray, reverse transcription quantitative PCR (RT-qPCR) and RT-ddPCR (Kristensen et al., 2019). In estimating analytical sensitivity and specificity, reference standards that can be specifically applied in circRNA discovery and profiling are needed (Hardwick et al., 2017). Furthermore, the procedure to discover and validate blood circRNA biomarkers needs to be standardized, including blood collection and preservation, circRNA extraction, library construction, and computational analysis (Byron et al., 2016; Anfossi et al., 2018). With the use of a standardized procedure, future studies need to estimate the technical robustness and reproducibility of the proposed biomarkers within and between laboratories. Second, the blood circRNA biomarkers identified in current studies (Tables 1 and 2) are only preliminary biomarker signatures for human diseases. The designed experiments in most studies are case-control studies of samples with well-defined phenotypes, and the sample size is relatively small. To test their clinical validity, more clinical samples are required to validate their sensitivity and specificity in a larger

cohort, especially their performance in discriminating patients with similar clinical phenotypes. Moreover, their performance in diagnosing the disease or predicting the disease outcome also needs to be tested in a prospective cohort in a clinical practice setting. Finally, further studies are needed to test and validate the usefulness of these biomarkers in clinical practice, such as their ability to inform clinical decisions and improve outcomes. Although many challenges and problems need to be solved, the promising potential of translating blood circRNA biomarkers into the clinic brings us new and inspiring options for liquid biopsy.

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ABBREVIATIONS

AUC, area under the receiver operating characteristic curve; CDK2, cyclin-dependent kinase 2; cfDNA, cell-free DNA; cfRNA, cell-free RNA; circ-DB, circ-deubiquitination; circRNA, circular RNA; ciRNA, circular intronic RNA; COPD, chronic obstructive pulmonary disease; CTC, circulating tumor cells; ecircRNA, exonic circular RNA; EGFR, epidermal growth factor receptor; EHI, early human immunodeficiency virus infection; ElcircRNA, exon-intron circular RNA; EV, extracellular vesicle; exLR, extracellular vesicle long RNA; f-circRNA, fusion circRNA; GC, gastric cancer; HCC, hepatocellular carcinoma; HIV, human immunodeficiency virus; ICS, intronic complement sequence; IRES, internal ribosome entry site; LPS, lipopolysaccharide; m6A, N6-methyladenosine; MBL, muscleblind; miRNA, microRNA; MRE, microRNA response element; NSCLC, non-small cell lung cancer; p21, cyclin-dependent kinase inhibitor 1; PBMC, peripheral blood mononuclear cell; PKR, protein kinase; Pol II, polymerase II; RA, rheumatoid arthritis; RBC, red blood cell; RBP, RNA binding protein; RNA-seq, RNA-sequencing; RT-ddPCR, reverse transcription droplet digital PCR; RT-qPCR, reverse transcription and quantitative PCR; SCLC, small cell lung cancer; SLE, systemic lupus erythematosus; ss, splice site; T2DM, type 2 diabetes mellitus; TB, tuberculosis.

COMPLIANCE WITH ETHICS GUIDELINES

Guoxia Wen, Tong Zhou and Wanjun Gu declare that they have no conflict of interest. This article does not contain any studies with human or animal subjects performed by the any of the authors.

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REFERENCES

- Abdelmohsen K, Panda AC, Munk R, Grammatikakis I, Dudekula DB, De S, Kim J, Noh J, Kim K, Martindale JL et al (2017) Identification of HuR target circular RNAs uncovers suppression of PABPN1 translation by CircPABPN1. *RNA Biol* 14:361–369
- Agirre X, Meydan C, Jiang Y, Garate L, Doane AS, Li Z, Verma A, Paiva B, Martín-Subero JI, Elemento O et al (2019) Long non-coding RNAs discriminate the stages and gene regulatory states of human humoral immune response. *Nat Commun* 10:821
- Ahadi S, Zhou W, Rose S, Sailani RM, Contrepas K, Avina M, Ashland M, Brunet A, Snyder M (2020) Personal aging markers and ageotypes revealed by deep longitudinal profiling. *Nat Med* 26:83–90
- Aktaş T, İlk İ, Maticzka D, Bhardwaj V, Rodrigues C, Mittler G, Manke T, Backofen R, Akhtar A (2017) DHX9 suppresses RNA processing defects originating from the Alu invasion of the human genome. *Nature* 544:115–119
- Alhasan AA, Izuogu OG, Al-Balool HH, Steyn JS, Evans A, Colzani M, Ghevaert C, Mountford JC, Marenah L, Elliott DJ et al (2016) Circular RNA enrichment in platelets is a signature of transcriptome degradation. *Blood* 127:e1–e11
- Anderson ST, Kaforou M, Brent AJ, Wright VJ, Banwell CM, Chagaluka G, Crampin AC, Dockrell HM, French N, Hamilton MS et al (2014) Diagnosis of childhood tuberculosis and host RNA expression in Africa. *N Engl J Med* 370:1712–1723
- Anfossi S, Babayan A, Pantel K, Calin GA (2018) Clinical utility of circulating non-coding RNAs—an update. *Nat Rev Clin Oncol* 15:541–563
- Arroyo JD, Chevillet JR, Kroh EM, Ruf IK, Pritchard CC, Gibson DF, Mitchell PS, Bennett CF, Pogosova-Agadjanyan EL, Stirewalt DL et al (2011) Argonaute2 complexes carry a population of circulating microRNAs independent of vesicles in human plasma. *Proc Natl Acad Sci USA* 108:5003–5008
- Ashwal-Fluss R, Meyer M, Pamudurti NR, Ivanov A, Bartok O, Hanan M, Evtantal N, Memczak S, Rajewsky N, Kadener S (2014) CircRNA biogenesis competes with pre-mRNA splicing. *Mol Cell* 56:55–66
- Aufiero S, Reckman YJ, Pinto YM, Creemers EE (2019) Circular RNAs open a new chapter in cardiovascular biology. *Nat Rev Cardiol* 16:503–514
- Awan FM, Yang BB, Naz A, Hanif A, Ikram A, Obaid A, Malik A, Janjua HA, Ali A, Sharif S (2020) The emerging role and significance of circular RNAs in viral infections and antiviral immune responses: possible implication as theranostic agents. *RNA Biol*. <https://doi.org/10.1080/15476286.2020.1790198>
- Bahn JH, Zhang Q, Li F, Chan TM, Lin X, Kim Y, Wong DTW, Xiao X (2014) The landscape of microRNA, piwi-interacting RNA, and circular RNA in human saliva. *Clin Chem* 61:221–230
- Bao X, He X, Zheng S, Sun J, Luo Y, Tan R, Zhao J, Zhong F, Zhang L (2019) Up-regulation of circular RNA hsa_circ_0037909 promotes essential hypertension. *J Clin Lab Anal* 33:e22853
- Bao X, Zheng S, Mao S, Gu T, Liu S, Sun J, Zhang L (2018) A potential risk factor of essential hypertension in case-control study: circular RNA hsa_circ_0037911. *Biochem Biophys Res Commun* 498:789–794

- Barrett SP, Wang PL, Salzman J (2015) Circular RNA biogenesis can proceed through an exon-containing lariat precursor. *eLife* 4: e07540
- Beltrán-García J, Osca-Verdegal R, Nacher-Sendra E, Pallardó FV, García-Giménez JL (2020) Circular RNAs in sepsis: biogenesis, function, and clinical significance. *Cells* 9:1544
- Best MG, Vancura A, Wurdinger T (2017) Platelet RNA as a circulating biomarker trove for cancer diagnostics. *J Thromb Haemost* 15:1295–1306
- Best MG, Wesseling P, Wurdinger T (2018) Tumor-educated platelets as a noninvasive biomarker source for cancer detection and progression monitoring. *Cancer Res* 78:3407–3412
- Blauwkamp TA, Thair S, Rosen MJ, Blair L, Lindner MS, Vilfan ID, Kawli T, Christians FC, Venkatasubrahmanyam S, Wall GD et al (2019) Analytical and clinical validation of a microbial cell-free DNA sequencing test for infectious disease. *Nat Microbiol* 4:663–674
- Bloom CI, Graham CM, Berry MP, Rozakeas F, Redford PS, Wang Y, Xu Z, Wilkinson KA, Wilkinson RJ, Kendrick Y et al (2013) Transcriptional blood signatures distinguish pulmonary tuberculosis, pulmonary sarcoidosis, pneumonias and lung cancers. *PLoS ONE* 8:e70630
- Bloom RD, Bromberg JS, Poggio ED, Bunnapradist S, Langone AJ, Sood P, Matas AJ, Mehta S, Mannon RB, Sharfuddin A et al (2017) Cell-free DNA and active rejection in kidney allografts. *J Am Soc Nephrol* 28:2221–2232
- Bullinger L, Döhner K, Bair E, Fröhling S, Schlenk RF, Tibshirani R, Döhner H, Pollack JR (2004) Use of gene-expression profiling to identify prognostic subclasses in adult acute myeloid leukemia. *N Engl J Med* 350:1605–1616
- Burnham P, Dadhania D, Heyang M, Chen F, Westblade LF, Suthanthiran M, Lee J, Vlamincik I (2018) Urinary cell-free DNA is a versatile analyte for monitoring infections of the urinary tract. *Nat Commun* 9:2412
- Byron SA, Keuren-Jensen KR, Engelthaler DM, Carpten JD, Craig DW (2016) Translating RNA sequencing into clinical diagnostics: opportunities and challenges. *Nat Rev Genet* 17:257–271
- Cadena C, Hur S (2017) Antiviral immunity and circular RNA: no end in sight. *Mol Cell* 67:163–164
- Cai Z, Fan Y, Zhang Z, Lu C, Zhu Z, Jiang T, Shan T, Peng Y (2020) VirusCircBase: a database of virus circular RNAs. *Brief Bioinform*. <https://doi.org/10.1093/bib/bbaa052>
- Cescon DW, Bratman SV, Chan SM, Siu LL (2020) Circulating tumor DNA and liquid biopsy in oncology. *Nat Cancer* 1:276–290
- Chaussabel D (2015) Assessment of immune status using blood transcriptomics and potential implications for global health. *Semin Immunol* 27:58–66
- Chaussabel D, Baldwin N (2014) Democratizing systems immunology with modular transcriptional repertoire analyses. *Nat Rev Immunol* 14:271–280
- Chen A, Zhong L, Ju K, Lu T, Lv J, Cao H (2020) Plasmatic circRNA predicting the occurrence of human glioblastoma. *Cancer Manag Res* 12:2917–2923
- Chen GY, Chen R, Ahmad S, Verma R, Kasturi S, Amaya L, Broughton JP, Kim J, Cadena C, Pulendran B et al (2019) N⁶-methyladenosine modification controls circular RNA immunity. *Mol Cell* 76:96–109.e109
- Chen GY, Kim MV, Chen X, Batista PJ, Aoyama S, Wilusz JE, Iwasaki A, Chang HY (2017) Sensing self and foreign circular RNAs by intron identity. *Mol Cell* 67:228–238
- Chen GY, Satpathy AT, Chang HY (2017) Gene regulation in the immune system by long noncoding RNAs. *Nat Immunol* 18:962–972
- Chen J, Zang Z, Braun U, Schwarz K, Harneit A, Kremer T, Ma R, Schweiger J, Moessnang C, Geiger L et al (2020) Association of a reproducible epigenetic risk profile for schizophrenia with brain methylation and function. *JAMA Psychiatry* 77(6):628–636
- Chen L-L (2016) The biogenesis and emerging roles of circular RNAs. *Nat Rev Mol Cell Biol* 17:205–211
- Chen L-L (2020) The expanding regulatory mechanisms and cellular functions of circular RNAs. *Nat Rev Mol Cell Biol* 21:1–16
- Chen R, Mias GI, Li-Pook-Than J, Jiang L, Lam H, Chen R, Miriami E, Karczewski KJ, Hariharan M, Dewey FE et al (2012) Personal omics profiling reveals dynamic molecular and medical phenotypes. *Cell* 148:1293–1307
- Chen R, Xia L, Tu K, Duan M, Kukurba K, Li-Pook-Than J, Xie D, Snyder M (2018) Longitudinal personal DNA methylome dynamics in a human with a chronic condition. *Nat Med* 24:1930–1939
- Chen S, Huang V, Xu X, Livingstone J, Soares F, Jeon J, Zeng Y, Hua J, Petricca J, Guo H et al (2019) Widespread and functional RNA circularization in localized prostate cancer. *Cell* 176:831–843.e822
- Chen S, Li T, Zhao Q, Xiao B, Guo J (2017) Using circular RNA hsa_circ_0000190 as a new biomarker in the diagnosis of gastric cancer. *Clin Chim Acta* 466:167–171
- Chen W, Quan Y, Fan S, Wang H, Liang J, Huang L, Chen L, Liu Q, He P, Ye Y (2020) Exosome-transmitted circular RNA hsa_circ_0051443 suppresses hepatocellular carcinoma progression. *Cancer Lett* 475:119–128
- Chen X, Chen RX, Wei WS, Li YH, Feng ZH, Tan L, Chen JW, Yuan GJ, Chen SL, Guo SJ et al (2018) PRMT5 circular RNA promotes metastasis of urothelial carcinoma of the bladder through sponging miR-30c to induce epithelial–mesenchymal transition. *Clin Cancer Res* 24:6319–6330
- Chen X, Yang T, Wang W, Xi W, Zhang T, Li Q, Yang A, Wang T (2019) Circular RNAs in immune responses and immune diseases. *Theranostics* 9:588–607
- Chen Y, Li C, Tan C, Liu X (2016) Circular RNAs: a new frontier in the study of human diseases. *J Med Genet* 53:359–365
- Chen Y-J, Chen C-Y, Mai T-L, Chuang C-F, Chen Y-C, Gupta SK, Yen L, Wang Y-D, Chuang T-J (2020) Genome-wide, integrative analysis of circular RNA dysregulation and the corresponding circular RNA–microRNA–mRNA regulatory axes in autism. *Genome Res* 30:375–391
- Chi BJ, Zhao DM, Liu L, Yin XZ, Wang FF, Bi S, Gui SL, Zhou SB, Qin WB, Wu DM et al (2019) Downregulation of hsa_circ_0000285 serves as a prognostic biomarker for bladder cancer and is involved in cisplatin resistance. *Neoplasma* 66:197–202
- Ciarloni L, Ehrensberger S, Imaizumi N, Monnier-Benoit S, Nichita C, Myung S-J, Kim J, Song S, Kim T, van der Weg B et al (2016) Development and clinical validation of a blood test based on

- 29-gene expression for early detection of colorectal cancer. *Clin Cancer Res* 22:4604–4611
- Ciarloni L, Hosseini S, Monnier-Benoit S, Imaizumi N, Dorta G, Ruegg C, and Group O.b.o.t (2015) Discovery of a 29-gene panel in peripheral blood mononuclear cells for the detection of colorectal cancer and adenomas using high throughput real-time PCR. *PLoS ONE* 10:e0123904
- Conn SJ, Pillman KA, Toubia J, Conn VM, Salmanidis M, Phillips CA, Roslan S, Schreiber AW, Gregory PA, Goodall GJ (2015) The RNA binding protein quaking regulates formation of circRNAs. *Cell* 160:1125–1134
- Correia CN, Nalpas NC, McLoughlin KE, Browne JA, Gordon SV, MacHugh DE, Shaughnessy RG (2017) Circulating microRNAs as potential biomarkers of infectious disease. *Front Immunol* 8:118
- Crutchfield CA, Thomas SN, Sokoll LJ, Chan DW (2016) Advances in mass spectrometry-based clinical biomarker discovery. *Clin Proteomics* 13:1
- Cui C, Yang J, Li X, Liu D, Fu L, Wang X (2020) Functions and mechanisms of circular RNAs in cancer radiotherapy and chemotherapy resistance. *Mol Cancer* 19:58
- de Fraipont F, Gazzeri S, Cho WC, Eymin B (2019) Circular RNAs and RNA splice variants as biomarkers for prognosis and therapeutic response in the liquid biopsies of lung cancer patients. *Front Genet* 10:390
- Ding C, Yi X, Wu X, Bu X, Wang D, Wu Z, Zhang G, Gu J, Kang D (2020) Exosome-mediated transfer of circRNA CircNFIX enhances temozolomide resistance in glioma. *Cancer Lett* 479:1–12
- Dolinar A, Koritnik B, Glavac D, Ravnik-Glavac M (2019) Circular RNAs as potential blood biomarkers in amyotrophic lateral sclerosis. *Mol Neurobiol* 56:8052–8062
- Du WW, Fang L, Yang W, Wu N, Awan FM, Yang Z, Yang BB (2016) Induction of tumor apoptosis through a circular RNA enhancing Foxo3 activity. *Cell Death Differ* 24:357–370
- Du WW, Yang W, Chen Y, Wu Z-K, Foster FS, Yang Z, Li X, Yang BB (2017) Foxo3 circular RNA promotes cardiac senescence by modulating multiple factors associated with stress and senescence responses. *Eur Heart J* 38:1402–1412
- Du WW, Yang W, Liu E, Yang Z, Dhaliwal P, Yang BB (2016) Foxo3 circular RNA retards cell cycle progression via forming ternary complexes with p21 and CDK2. *Nucleic Acids Res* 44:2846–2858
- Dube U, Del-Aguila JL, Li Z, Budde JP, Jiang S, Hsu S, Ibanez L, Fernandez M, Farias F, Norton J et al (2019) An atlas of cortical circular RNA expression in Alzheimer disease brains demonstrates clinical and pathological associations. *Nat Neurosci* 22:1–10
- Dvinge H, Ries RE, Ilagan JO, Stirewalt DL, Meshinchi S, Bradley RK (2014) Sample processing obscures cancer-specific alterations in leukemic transcriptomes. *Proc Natl Acad Sci USA* 111:16802–16807
- Enuka Y, Lauriola M, Feldman ME, Sas-Chen A, Ulitsky I, Yarden Y (2015) Circular RNAs are long-lived and display only minimal early alterations in response to a growth factor. *Nucleic Acids Res* 44:1370–1383
- Errichelli L, Modigliani S, Laneve P, Colantoni A, Legnini I, Caputo D, Rosa A, Santis R, Scarfò R, Peruzzi G et al (2017) FUS affects circular RNA expression in murine embryonic stem cell-derived motor neurons. *Nat Commun* 8:14741
- Esmail H, Cobelens F, Goletti D (2020) Transcriptional biomarkers for predicting development of tuberculosis: progress and clinical considerations. *Eur Respir J* 55:1901957
- Fan L, Cao Q, Liu J, Zhang J, Li B (2019) Circular RNA profiling and its potential for esophageal squamous cell cancer diagnosis and prognosis. *Mol Cancer* 18:16
- Fang Y, Wang X, Li W, Han J, Jin J, Su F, Zhang J, Huang W, Xiao F, Pan Q et al (2018) Screening of circular RNAs and validation of circANKRD36 associated with inflammation in patients with type 2 diabetes mellitus. *Int J Mol Med* 42:1865–1874
- Fehlmann T, Kahraman M, Ludwig N, Backes C, Galata V, Keller V, Geffers L, Mercaldo N, Hornung D, Weis T et al (2020) Evaluating the use of circulating microRNA profiles for lung cancer detection in symptomatic patients. *JAMA Oncol* 6(5):714–723
- Fei T, Chen Y, Xiao T, Li W, Cato L, Zhang P, Cotter MB, Bowden M, Lis RT, Zhao SG et al (2017) Genome-wide CRISPR screen identifies HNRNPL as a prostate cancer dependency regulating RNA splicing. *Proc Natl Acad Sci USA* 114:E5207–E5215
- Fischer JW, Busa VF, Shao Y, Leung AKL (2020) Structure-mediated RNA decay by UPF1 and G3BP1. *Mol Cell* 78:70–84.e76
- Fritz JV, Heintz-Buschart A, Ghosal A, Wampach L, Etheridge A, Galas D, Wilmes P (2016) Sources and functions of extracellular small RNAs in human circulation. *Annu Rev Nutr* 36:301–336
- Fu Y, Wang J, Qiao J, Yi Z (2019) Signature of circular RNAs in peripheral blood mononuclear cells from patients with active tuberculosis. *J Cell Mol Med* 23:1917–1925
- Gaffo E, Boldrin E, Molin A, Bresolin S, Bonizzato A, Trentin L, Frasson C, Debatin K-M, Meyer LH, te Kronnie et al (2019) Circular RNA differential expression in blood cell populations and exploration of circRNA deregulation in pediatric acute lymphoblastic leukemia. *Sci Rep* 9:14670
- Gao Y, Zhao F (2018) Computational strategies for exploring circular RNAs. *Trends Genet*. <https://doi.org/10.1016/j.tig.2017.12.016>
- Geng H-H, Li R, Su Y-M, Xiao J, Pan M, Cai X-X, Ji X-P (2016) The circular RNA Cdr1as promotes myocardial infarction by mediating the regulation of miR-7a on its target genes expression. *PLoS ONE* 11:e0151753
- Ghods F (2018) Circular RNA in saliva. *Adv Exp Med Biol* 1087:131–139
- Giraldo NA, Becht E, Vano Y, Petitprez F, Lacroix L, Validire P, Sanchez-Salas R, Ingels A, Oudard S, Moatti A et al (2017) Tumor-infiltrating and peripheral blood T-cell immunophenotypes predict early relapse in localized clear cell renal cell carcinoma. *Clin Cancer Res* 23:4416–4428
- Glažar P, Papavasiliou P, Rajewsky N (2014) circBase: a database for circular RNAs. *RNA* 20:1666–1670
- Gong Y, Mao J, Wu D, Wang X, Li L, Zhu L, Song R (2018) Circ-ZEB1.33 promotes the proliferation of human HCC by sponging miR-200a-3p and upregulating CDK6. *Cancer Cell Int* 18:116
- Gu C, Zhou N, Wang Z, Li G, Kou Y, Yu S, Feng Y, Chen L, Yang J, Tian F (2018) circGprc5a promoted bladder oncogenesis and metastasis through Gprc5a-targeting peptide. *Mol Ther Nucleic Acids* 13:633–641

- Gu Y, Ke G, Wang L, Zhou E, Zhu K, Wei Y (2017) Altered expression profile of circular RNAs in the serum of patients with diabetic retinopathy revealed by microarray. *Ophthalmic Res* 58:176–184
- Guarnerio J, Bezzi M, Jeong J, Paffenholz SV, Berry K, Naldini MM, Lo-Coco F, Tay Y, Beck AH, Pandolfi P (2016) Oncogenic role of fusion-circRNAs derived from cancer-associated chromosomal translocations. *Cell* 165:289–302
- Gunsolus IL, Sweeney TE, Liesenfeld O, Ledebore NA (2019) Diagnosing and managing sepsis by probing the host response to infection: advances, opportunities, and challenges. *J Clin Microbiol* 57:e00425-e1419
- Guo JU, Agarwal V, Guo H, Bartel DP (2014) Expanded identification and characterization of mammalian circular RNAs. *Genome Biol* 15:409
- Guo G, Wang H, Ye L, Shi X, Yan K, Lin K, Huang Q, Li B, Lin Q, Zhu L et al (2019) Hsa_circ_0000479 as a novel diagnostic biomarker of systemic lupus erythematosus. *Front Immunol* 10:2281
- Gupta RK, Turner CT, Venturini C, Esmail H, Rangaka MX, Copas A, Lipman M, Abubakar I, Noursadeghi M, Gupta RK et al (2020) Concise whole blood transcriptional signatures for incipient tuberculosis: a systematic review and patient-level pooled meta-analysis. *Lancet Respir Med* 8:395–406
- Han D, Li R, Shi J, Tan P, Zhang R, Li J (2020a) Liquid biopsy for infectious diseases: a focus on microbial cell-free DNA sequencing. *Theranostics* 10:5501–5513
- Han J, Zhang L, Hu L, Yu H, Xu F, Yang B, Zhang R, Zhang Y, An Y (2020b) Circular RNA-expression profiling reveals a potential role of hsa_circ_0097435 in heart failure via sponging multiple microRNAs. *Front Genet* 11:212
- Han L, Zhang X, Wang A, Ji Y, Cao X, Qin Q, Yu T, Yin L, Huang H (2020c) A dual-circular RNA signature as a non-invasive diagnostic biomarker for gastric cancer. *Front Oncol* 10:184
- Hanan M, Simchovitz A, Yayan N, Vaknine S, Cohen-Fultheim R, Karmon M, Madrer N, Rohlich TM, Maman M, Bennett ER et al (2020) A Parkinson's disease circRNAs resource reveals a link between circSLC8A1 and oxidative stress. *EMBO Mol Med* 12(9): e11942
- Hang D, Zhou J, Qin N, Zhou W, Ma H, Jin G, Hu Z, Dai J, Shen H (2018) A novel plasma circular RNA circFARSA is a potential biomarker for non-small cell lung cancer. *Cancer Med* 7:2783–2791
- Hansen TB, Jensen TI, Clausen BH, Bramsen JB, Finsen B, Damgaard CK, Kjems J (2013) Natural RNA circles function as efficient microRNA sponges. *Nature* 495:384–388
- Hardwick SA, Deveson IW, Mercer TR (2017) Reference standards for next-generation sequencing. *Nat Rev Genet* 18(8):473–484
- He F, Zhong X, Lin Z, Lin J, Qiu M, Li X, Hu Z (2020) Plasma exo-hsa_circRNA_0056616: A potential biomarker for lymph node metastasis in lung adenocarcinoma. *J Cancer* 11:4037–4046
- Heitzer E, Haque IS, Roberts CES, Speicher MR (2019) Current and future perspectives of liquid biopsies in genomics-driven oncology. *Nat Rev Genet* 20:71–88
- Holdt LM, Stahnger A, Sass K, Pichler G, Kulak NA, Wilfert W, Kohlmaier A, Herbst A, Northoff BH, Nicolaou A et al (2016) Circular non-coding RNA ANRIL modulates ribosomal RNA maturation and atherosclerosis in humans. *Nat Commun* 7:12429
- Hong DK, Blauwkamp TA, Kertesz M, Bercovici S, Truong C, Banaei N (2018) Liquid biopsy for infectious diseases: sequencing of cell-free plasma to detect pathogen DNA in patients with invasive fungal disease. *Diagn Microbiol Infect Dis* 92(3):210–213
- Hsu M-T, Coca-Prados M (1979) Electron microscopic evidence for the circular form of RNA in the cytoplasm of eukaryotic cells. *Nature* 280:339–340
- Hu X, Wu D, He X, Zhao H, He Z, Lin J, Wang K, Wang W, Pan Z, Lin H et al (2019) circGSK3 β promotes metastasis in esophageal squamous cell carcinoma by augmenting beta-catenin signaling. *Mol Cancer* 18:160
- Hu Y, Zhu Y, Zhang W, Lang J, Ning L (2019) Utility of plasma circBNC2 as a diagnostic biomarker in epithelial ovarian cancer. *Onco Targets Ther* 12:9715–9723
- Hu ZQ, Zhou SL, Li J, Zhou ZJ, Wang PC, Xin HY, Mao L, Luo CB, Yu SY, Huang XW et al (2019) Circular RNA sequencing identifies circASAP1 as a key regulator in hepatocellular carcinoma metastasis. *Hepatology*. <https://doi.org/10.1002/hep.31068>
- Huang M, He YR, Liang LC, Huang Q, Zhu ZQ (2017a) Circular RNA hsa_circ_0000745 may serve as a diagnostic marker for gastric cancer. *World J Gastroenterol* 23:6330–6338
- Huang R, Zhang Y, Han B, Bai Y, Zhou R, Gan G, Chao J, Hu G, Yao H (2017b) Circular RNA HIPK2 regulates astrocyte activation via cooperation of autophagy and ER stress by targeting MIR124-2HG. *Autophagy* 13:1722–1741
- Huang Z, Su R, Deng Z, Xu J, Peng Y, Luo Q, Li J (2017c) Identification of differentially expressed circular RNAs in human monocyte derived macrophages response to *Mycobacterium tuberculosis* infection. *Sci Rep* 7:13673
- Huang Z, Su R, Qing C, Peng Y, Luo Q, Li J (2018a) Plasma circular RNAs hsa_circ_0001953 and hsa_circ_0009024 as diagnostic biomarkers for active tuberculosis. *Front Microbiol* 9:2010
- Huang Z, Su R, Yao F, Peng Y, Luo Q, Li J (2018b) Circulating circular RNAs hsa_circ_0001204 and hsa_circ_0001747 act as diagnostic biomarkers for active tuberculosis detection. *Int J Clin Exp Pathol* 11:586–594
- Huang Z-K, Yao F-Y, Xu J-Q, Deng Z, Su R-G, Peng Y-P, Luo Q, Li J-M (2018c) Microarray expression profile of circular RNAs in peripheral blood mononuclear cells from active tuberculosis patients. *Cell Physiol Biochem* 45:1230–1240
- Huang A, Zheng H, Wu Z, Chen M, Huang Y (2020a) Circular RNA–protein interactions: functions, mechanisms, and identification. *Theranostics* 10:3503–3517
- Huang XY, Huang ZL, Huang J, Xu B, Huang XY, Xu YH, Zhou J, Tang ZY (2020b) Exosomal circRNA-100338 promotes hepatocellular carcinoma metastasis via enhancing invasiveness and angiogenesis. *J Exp Clin Cancer Res* 39:20
- Iparraguirre L, Muñoz-Culla M, Prada-Luengo I, Castillo-Triviño T, Olascoaga J, Otaegui D (2017) Circular RNA profiling reveals that circular RNAs from ANXA2 can be used as new biomarkers for multiple sclerosis. *Hum Mol Genet* 26:3564–3572
- Ivanov A, Memczak S, Wyler E, Torti F, Porath HT, Orejuela MR, Piechotta M, Levanon EY, Landthaler M, Dieterich C et al (2014) Analysis of intron sequences reveals hallmarks of circular RNA biogenesis in animals. *Cell Rep* 10:170–177
- Jeck WR, Sharpless NE (2014) Detecting and characterizing circular RNAs. *Nat Biotechnol* 32:453–461

- Jeck WR, Sorrentino JA, Wang K, Slevin MK, Burd CE, Liu J, Marzluff WF, Sharpless NE (2013) Circular RNAs are abundant, conserved, and associated with ALU repeats. *RNA* 19:141–157
- Ji P, Wu W, Chen S, Zheng Y, Zhou L, Zhang J, Cheng H, Yan J, Zhang S, Yang P et al (2019) Expanded expression landscape and prioritization of circular RNAs in mammals. *Cell Rep* 26:3444–3460.e3445
- Jiang M, Lash GE, Zhao X, Long Y, Guo C, Yang H (2018) CircRNA-0004904, circRNA-0001855, and PAPP-A: potential novel biomarkers for the prediction of preeclampsia. *Cell Physiol Biochem* 46:2576–2586
- Joesse SA, Pantel K (2015) Tumor-educated platelets as liquid biopsy in cancer patients. *Cancer Cell* 28:552–554
- Jost I, Shalamova LA, Gerresheim GK, Niepmann M, Bindereif A, Rossbach O (2018) Functional sequestration of microRNA-122 from Hepatitis C Virus by circular RNA sponges. *RNA Biol* 15(8):1–8
- Karczewski KJ, Snyder MP (2018) Integrative omics for health and disease. *Nat Rev Genet* 19:299–310
- Kelly S, Greenman C, Cook PR, Papantonis A (2015) Exon skipping is correlated with exon circularization. *J Mol Biol* 427:2414–2417
- Khan M, Reckman YJ, Aufiero S, van den Hoogenhof M, van der Made I, Beqqali A, Koolbergen DR, Rasmussen TB, van der Velden J, Creemers EE et al (2016) RBM20 regulates circular RNA production from the Titin gene. *Circ Res* 119:996–1003
- Kleaveland B, Shi CY, Stefano J, Bartel DP (2018) A network of noncoding regulatory RNAs acts in the mammalian brain. *Cell* 174(2):350–362
- Kölling M, Haddad G, Wegmann U, Kistler A, Bosakova A, Seeger H, Hübel K, Haller H, Mueller T, Wüthrich RP et al (2019) Circular RNAs in urine of kidney transplant patients with acute T cell-mediated allograft rejection. *Clin Chem* 65:1287–1294
- Kong S, Yang Q, Tang C, Wang T, Shen X, Ju S (2019) Identification of hsa_circ_0001821 as a novel diagnostic biomarker in gastric cancer via comprehensive circular RNA profiling. *Front Genet* 10:878
- Kossenkov AV, Qureshi R, Dawany NB, Wickramasinghe J, Liu Q, Majumdar SR, Chang C, Widura S, Kumar T, Horng W-H et al (2018) A gene expression classifier from whole blood distinguishes benign from malignant lung nodules detected by low-dose CT. *Cancer Res* 79:263–273
- Kramer MC, Liang D, Tatomer DC, Gold B, March ZM, Cherry S, Wilusz JE (2015) Combinatorial control of *Drosophila* circular RNA expression by intronic repeats, hnRNPs, and SR proteins. *Genes Dev* 29(20):2168–2182
- Kristensen LS, Andersen MS, Stagsted LVW, Ebbesen KK, Hansen TB, Kjems J (2019) The biogenesis, biology and characterization of circular RNAs. *Nat Rev Genet* 20:1–17
- Kumar L, Shamsuzzama HR, Haque R, Baghel T, Nazir A (2017) Circular RNAs: the emerging class of non-coding RNAs and their potential role in human neurodegenerative diseases. *Mol Neurobiol* 54:7224–7234
- Kwapisz D (2017) The first liquid biopsy test approved. Is it a new era of mutation testing for non-small cell lung cancer? *Ann Transl Med* 5:46
- Lam WKJ, Lo YMD (2019) Circular RNAs as urinary biomarkers. *Clin Chem* 65:1196–1198
- Lamb YN, Dhillon S (2017) Epi proColon® 2.0 CE: a blood-based screening test for colorectal cancer. *Mol Diagn Ther* 21:225–232
- Lasda E, Parker R (2016) Circular RNAs co-precipitate with extracellular vesicles: a possible mechanism for circRNA clearance. *PLoS ONE* 11:e0148407
- Legnini I, Timoteo GD, Rossi F, Morlando M, Briganti F, Sthandier O, Fatica A, Santini T, Andronache A, Wade M et al (2017) Circ-ZNF609 is a circular RNA that can be translated and functions in myogenesis. *Mol Cell* 66:22–37
- Lei B, Zhou J, Xuan X, Tian Z, Zhang M, Gao W, Lin Y, Ni B, Pang H, Fan W (2019) Circular RNA expression profiles of peripheral blood mononuclear cells in hepatocellular carcinoma patients by sequence analysis. *Cancer Med* 8:1423–1433
- Lesko LJ, Atkinson AJ (2001) Use of biomarkers and surrogate endpoints in drug development and regulatory decision making: criteria, validation, strategies. *Annu Rev Pharmacol Toxicol* 41:347–366
- Li P, Chen S, Chen H, Mo X, Li T, Shao Y, Xiao B, Guo J (2015a) Using circular RNA as a novel type of biomarker in the screening of gastric cancer. *Clin Chim Acta* 444:132–136
- Li Y, Zheng Q, Bao C, Li S, Guo W, Zhao J, Chen D, Gu J, He X, Huang S (2015b) Circular RNA is enriched and stable in exosomes: a promising biomarker for cancer diagnosis. *Cell Res* 25:981–984
- Li Z, Huang C, Bao C, Chen L, Lin M, Wang X, Zhong G, Yu B, Hu W, Dai L et al (2015c) Exon-intron circular RNAs regulate transcription in the nucleus. *Nat Struct Mol Biol* 22:256–264
- Li M, Xie X, Zhou J, Sheng M, Yin X, Ko E-A, Zhou T, Gu W (2017a) Quantifying circular RNA expression from RNA-seq data using model-based framework. *Bioinformatics* 33(14):2131–2139
- Li S, Li Y, Chen B, Zhao J, Yu S, Tang Y, Zheng Q, Li Y, Wang P, He X et al (2017b) exoRBase: a database of circRNA, lncRNA and mRNA in human blood exosomes. *Nucleic Acids Res* 46:D106–D112
- Li W, Zhong C, Jiao J, Li P, Cui B, Ji C, Ma D (2017c) Characterization of hsa_circ_0004277 as a new biomarker for acute myeloid leukemia via circular RNA profile and bioinformatics analysis. *Int J Mol Sci* 18(3):597
- Li WH, Song YC, Zhang H, Zhou ZJ, Xie X, Zeng QN, Guo K, Wang T, Xia P, Chang DM (2017d) Decreased expression of hsa_circ_00001649 in gastric cancer and its clinical significance. *Dis Markers* 2017:4587698
- Li X, Liu C-X, Xue W, Zhang Y, Jiang S, Yin Q-F, Wei J, Yao R-W, Yang L, Chen L-L (2017e) Coordinated circRNA biogenesis and function with NF90/NF110 in viral infection. *Mol Cell* 67:214–227.e217
- Li J, Li Z, Jiang P, Peng M, Zhang X, Chen K, Liu H, Bi H, Liu X, Li X (2018a) Circular RNA IARS (circ-IARS) secreted by pancreatic cancer cells and located within exosomes regulates endothelial monolayer permeability to promote tumor metastasis. *J Exp Clin Cancer Res* 37:177
- Li L, Li W, Chen N, Zhao H, Xu G, Zhao Y, Pan X, Zhang X, Zhou L, Yu D et al (2018b) FLI1 exonic circular RNAs as a novel oncogenic driver to promote tumor metastasis in small cell lung cancer. *Clin Cancer Res* 25:1302–1317
- Li T, Shao Y, Fu L, Xie Y, Zhu L, Sun W, Yu R, Xiao B, Guo J (2018c) Plasma circular RNA profiling of patients with gastric cancer and their droplet digital RT-PCR detection. *J Mol Med (Berl)* 96:85–96
- Li X, Yang L, Chen L-L (2018d) The biogenesis, functions, and challenges of circular RNAs. *Mol Cell* 71:428–442

- Li Z, Yanfang W, Li J, Jiang P, Peng T, Chen K, Zhao X, Zhang Y, Zhen P, Zhu J et al (2018e) Tumor-released exosomal circular RNA PDE8A promotes invasive growth via the miR-338/MACC1/MET pathway in pancreatic cancer. *Cancer Lett* 432:237–250
- Li Q, Wang Y, Wu S, Zhou Z, Ding X, Shi R, Thorne RF, Zhang XD, Hu W, Wu M (2019a) CircACC1 regulates assembly and activation of AMPK complex under metabolic stress. *Cell Metab* 30:157–173
- Li S, Zhang J, Tan X, Deng J, Li Y, Piao Y, Li C, Yang W, Mo W, Sun J et al (2019b) Microarray expression profile of circular RNAs and mRNAs in children with systemic lupus erythematosus. *Clin Rheumatol* 38:1339–1350
- Li XN, Wang ZJ, Ye CX, Zhao BC, Huang XX, Yang L (2019c) Circular RNA circVAPA is up-regulated and exerts oncogenic properties by sponging miR-101 in colorectal cancer. *Biomed Pharmacother* 112:108611
- Li Y, Zhao J, Yu S, Wang Z, He X, Su Y, Guo T, Sheng H, Chen J, Zheng Q et al (2019d) Extracellular vesicles long RNA sequencing reveals abundant mRNA, circRNA, and lncRNA in human blood as potential biomarkers for cancer diagnosis. *Clin Chem* 65:798–808
- Li Z, Zhou Y, Yang G, He S, Qiu X, Zhang L, Deng Q, Zheng F (2019e) Using circular RNA SMARCA5 as a potential novel biomarker for hepatocellular carcinoma. *Clin Chim Acta* 492:37–44
- Li Z, Zhu X, Huang S (2020) Extracellular vesicle long non-coding RNAs and circular RNAs: biology, functions and applications in cancer. *Cancer Lett* 489:111–120
- Liang D, Wilusz JE (2014) Short intronic repeat sequences facilitate circular RNA production. *Genes Dev* 28:2233–2247
- Liang D, Tatomer DC, Luo Z, Wu H, Yang L, Chen L-L, Cherry S, Wilusz JE (2017) The output of protein-coding genes shifts to circular RNAs when the pre-mRNA processing machinery is limiting. *Mol Cell* 68:940–954.e943
- Liang B, Li M, Deng Q, Wang C, Rong J, He S, Xiang Y, Zheng F (2020) CircRNA ZNF609 in peripheral blood leukocytes acts as a protective factor and a potential biomarker for coronary artery disease. *Ann Transl Med* 8:741
- Lin J, Cai D, Li W, Yu T, Mao H, Jiang S, Xiao B (2019) Plasma circular RNA panel acts as a novel diagnostic biomarker for colorectal cancer. *Clin Biochem* 74:60–68
- Liu C-X, Li X, Nan F, Jiang S, Gao X, Guo S-K, Xue W, Cui Y, Dong K, Ding H et al (2019a) Structure and degradation of circular RNAs regulate PKR activation in innate immunity. *Cell* 177(4):865–880
- Liu XX, Yang YE, Liu X, Zhang MY, Li R, Yin YH, Qu YQ (2019b) A two-circular RNA signature as a noninvasive diagnostic biomarker for lung adenocarcinoma. *J Transl Med* 17:50
- Liu YT, Han XH, Xing PY, Hu XS, Hao XZ, Wang Y, Li JL, Zhang ZS, Yang ZH, Shi YK (2019c) Circular RNA profiling identified as a biomarker for predicting the efficacy of Gefitinib therapy for non-small cell lung cancer. *J Thorac Dis* 11:1779–1787
- Liu H, Lu G, Wang W, Jiang X, Gu S, Wang J, Yan X, He F, Wang J (2020) A panel of circRNAs in the serum serves as biomarkers for *Mycobacterium tuberculosis* Infection. *Front Microbiol* 11:1215
- Loon EV, Gazut S, Yazdani S, Lerut E, de Loor H, Coemans M, Noël L-H, Thorrez L, Lommel LV, Schuit F et al (2019) Development and validation of a peripheral blood mRNA assay for the assessment of antibody-mediated kidney allograft rejection: a multicentre, prospective study. *EBioMedicine* 46:463–472
- Lu J, Zhang PY, Xie JW, Wang JB, Lin JX, Chen QY, Cao LL, Huang CM, Li P, Zheng CH (2019a) hsa_circ_0000467 promotes cancer progression and serves as a diagnostic and prognostic biomarker for gastric cancer. *J Clin Lab Anal* 33:e22726
- Lu J, Zhang PY, Xie JW, Wang JB, Lin JX, Chen QY, Cao LL, Li P, Zheng CH, Huang CM (2019b) Circular RNA hsa_circ_0006848 related to ribosomal protein L6 acts as a novel biomarker for early gastric cancer. *Dis Markers* 2019:3863458
- Lu X, Song M, Wang F (2019c) Circulating circular RNAs as biomarkers of cancer. *Non-coding RNA Investig* 3:8
- Lukiw WJ (2013) Circular RNA (circRNA) in Alzheimer's disease (AD). *Front Genet* 4:307
- Luo Q, Zhang L, Li X, Fu B, Deng Z, Qing C, Su R, Xu J, Guo Y, Huang Z et al (2018) Identification of circular RNAs hsa_circ_0044235 in peripheral blood as novel biomarkers for rheumatoid arthritis. *Clin Exp Immunol* 194:118–124
- Luo Q, Zhang L, Li X, Fu B, Guo Y, Huang Z, Li J (2019) Identification of circular RNAs hsa_circ_0044235 and hsa_circ_0068367 as novel biomarkers for systemic lupus erythematosus. *Int J Mol Med* 44:1462–1472
- Luo H, Zhao Q, Wei W, Zheng L, Yi S, Li G, Wang W, Sheng H, Pu H, Mo H et al (2020a) Circulating tumor DNA methylation profiles enable early diagnosis, prognosis prediction, and screening for colorectal cancer. *Sci Transl Med* 12:eaax7533
- Luo HL, Peng Y, Luo H, Zhang JA, Liu GB, Xu H, Huang GX, Sun YF, Huang J, Zheng BY et al (2020b) Circular RNA hsa_circ_0001380 in peripheral blood as a potential diagnostic biomarker for active pulmonary tuberculosis. *Mol Med Rep* 21:1890–1896
- Luo Y-H, Yang Y-P, Chien C-S, Yarmishyn AA, Ishola AA, Chien Y, Chen Y-M, Huang T-W, Lee K-Y, Huang W-C et al (2020c) Plasma level of circular RNA hsa_circ_0000190 correlates with tumor progression and poor treatment response in advanced lung cancers. *Cancers* 12:1740
- Ma J, Qi G, Li L (2020) A novel serum exosomes-based biomarker hsa_circ_0002130 facilitates osimertinib-resistance in non-small cell lung cancer by sponging miR-498. *Onco Targets Ther* 13:5293–5307
- Maas SLN, Breakefield XO, Weaver AM (2017) Extracellular vesicles: unique intercellular delivery vehicles. *Trends Cell Biol* 27:172–188
- Maass PG, Glažar P, Memczak S, Dittmar G, Hollfinger I, Schreyer L, Sauer AV, Toka O, Aiuti A, Luft FC et al (2017) A map of human circular RNAs in clinically relevant tissues. *J Mol Med (Berl)* 95:1179–1189
- MacLean E, Broger T, Yerlikaya S, Fernandez-Carballo BL, Pai M, Denking CM (2019) A systematic review of biomarkers to detect active tuberculosis. *Nat Microbiol* 4:748–758
- Marshall K, Mohr S, Khettabi F, Nossova N, Chao S, Bao W, Ma J, Li XJ, Liew CC (2010) A blood-based biomarker panel for stratifying current risk for colorectal cancer. *Int J Cancer* 126:1177–1186
- Mattox AK, Bettgowda C, Zhou S, Papadopoulos N, Kinzler KW, Vogelstein B (2019) Applications of liquid biopsies for cancer. *Sci Transl Med* 11:eaay1984

- Max KEA, Bertram K, Akat K, Bogardus KA, Li J, Morozov P, Ben-Dov IZ, Li X, Weiss ZR, Azizian A et al (2018) Human plasma and serum extracellular small RNA reference profiles and their clinical utility. *Proc Natl Acad Sci USA* 115:201714397
- Mayhew MB, Buturovic L, Luethy R, Midic U, Moore AR, Roque JA, Shaller BD, Asuni T, Rawling D, Remmel M et al (2020) A generalizable 29-mRNA neural-network classifier for acute bacterial and viral infections. *Nat Commun* 11:1177
- Mei M, Wang Y, Wang Q, Liu Y, Song W, Zhang M (2019) CircCDYL serves as a new biomarker in Mantle cell lymphoma and promotes cell proliferation. *Cancer Manag Res* 11:10215–10221
- Memczak S, Jens M, Elefsinioti A, Torti F, Krueger J, Rybak A, Maier L, Mackowiak SD, Gregersen LH, Munschauer M et al (2013) Circular RNAs are a large class of animal RNAs with regulatory potency. *Nature* 495:333–338
- Memczak S, Papavasileiou P, Peters O, Rajewsky N (2015) Identification and characterization of circular RNAs as a new class of putative biomarkers in human blood. *PLoS ONE* 10: e0141214
- Meng S, Zhou H, Feng Z, Xu Z, Tang Y, Li P, Wu M (2017) CircRNA: functions and properties of a novel potential biomarker for cancer. *Mol Cancer* 16:94
- Miao Q, Zhong Z, Jiang Z, Lin Y, Ni B, Yang W, Tang J (2019) RNA-seq of circular RNAs identified circPTPN22 as a potential new activity indicator in systemic lupus erythematosus. *Lupus* 28:520–528
- Mitchell PS, Parkin RK, Kroh EM, Fritz BR, Wyman SK, Pogosova-Agadjanyan EL, Peterson A, Noteboom J, O'Briant KC, Allen A et al (2008) Circulating microRNAs as stable blood-based markers for cancer detection. *Proc Natl Acad Sci USA* 105:10513–10518
- Ng WL, Marinov GK, Liao ES, Lam YL, Lim Y-Y, Ea C-K (2016) Inducible RasGEF1B circular RNA is a positive regulator of ICAM-1 in the TLR4/LPS pathway. *RNA Biol* 13:861–871
- Nicolet BP, Engels S, Agliarolo F, van den Akker E, von Lindern M, Wolters MC (2018) Circular RNA expression in human hematopoietic cells is widespread and cell-type specific. *Nucleic Acids Res* 46:8168–8180
- Ouyang Q, Huang Q, Jiang Z, Zhao J, Shi GP, Yang M (2018) Using plasma circRNA_002453 as a novel biomarker in the diagnosis of lupus nephritis. *Mol Immunol* 101:531–538
- Ouyang Q, Wu J, Jiang Z, Zhao J, Wang R, Lou A, Zhu D, Shi GP, Yang M (2017) Microarray expression profile of circular RNAs in peripheral blood mononuclear cells from rheumatoid arthritis patients. *Cell Physiol Biochem* 42:651–659
- Pamudurti NR, Bartok O, Jens M, Ashwal-Fluss R, Stottmeister C, Ruhe L, Hanan M, Wyler E, Perez-Hernandez D, Ramberger E et al (2017) Translation of circRNAs. *Mol Cell* 66:9–21
- Pan B, Qin J, Liu X, He B, Wang X, Pan Y, Sun H, Xu T, Xu M, Chen X et al (2019) Identification of serum exosomal hsa-circ-0004771 as a novel diagnostic biomarker of colorectal cancer. *Front Genet* 10:1096
- Pardini B, Sabo A, Birolo G, Calin G (2019) Noncoding RNAs in extracellular fluids as cancer biomarkers: the new frontier of liquid biopsies. *Cancers* 11:1170
- Park O, Ha H, Lee Y, Boo S, Kwon D, Song H, Kim Y (2019) Endoribonucleolytic cleavage of m⁶A-containing RNAs by RNase P/MRP complex. *Mol Cell* 74(3):494–507
- Peng YK, Pu K, Su HX, Zhang J, Zheng Y, Ji R, Guo QH, Wang YP, Guan QL, Zhou YN (2020) Circular RNA hsa_circ_0010882 promotes the progression of gastric cancer via regulation of the PI3K/Akt/mTOR signaling pathway. *Eur Rev Med Pharmacol Sci* 24:1142–1151
- Ping L, Jian-Jun C, Chu-Shu L, Guang-Hua L, Ming Z (2019) High circ_100053 predicts a poor outcome for chronic myeloid leukemia and is involved in imatinib resistance. *Oncol Res*. <https://doi.org/10.3727/096504018x15412701483326>
- Piwecka M, Glazar P, Hernandez-Miranda LR, Memczak S, Wolf SA, Rybak-Wolf A, Filipchuk A, Klironomos F, Cerda Jara CA, Fenske P et al (2017) Loss of a mammalian circular RNA locus causes miRNA deregulation and affects brain function. *Science* 357: eaam8526
- Powers KA, Ghani AC, Miller WC, Hoffman IF, Pettifor AE, Kamanga G, Martinson FE, Cohen MS (2011) The role of acute and early HIV infection in the spread of HIV and implications for transmission prevention strategies in Lilongwe, Malawi: a modelling study. *Lancet* 378:256–268
- Preußner C, Hung L-H, Schneider T, Schreiner S, Hardt M, Moebus A, Santoso S, Bindereif A (2018) Selective release of circRNAs in platelet-derived extracellular vesicles. *J Extracell Vesicles* 7:1424473
- Qian Z, Liu H, Li M, Shi J, Li N, Zhang Y, Zhang X, Lv J, Xie X, Bai Y et al (2018) Potential diagnostic power of blood circular RNA expression in active pulmonary tuberculosis. *EBioMedicine* 27:18–26
- Qian Z, Lv J, Kelly GT, Wang H, Zhang X, Gu W, Yin X, Wang T, Zhou T (2016) Expression of nuclear factor, erythroid 2-like 2-mediated genes differentiates tuberculosis. *Tuberculosis* 99:56–62
- Qiao GL, Chen L, Jiang WH, Yang C, Yang CM, Song LN, Chen Y, Yan HL, Ma LJ (2019) Hsa_circ_0003998 may be used as a new biomarker for the diagnosis and prognosis of hepatocellular carcinoma. *Onco Targets Ther* 12:5849–5860
- Ramilo O, Mejias A (2017) Host transcriptomics for diagnosis of infectious diseases: one step closer to clinical application. *Eur Respir J* 49:1700993
- Ravnik-Glavač M, Glavač D (2020) Circulating RNAs as potential biomarkers in amyotrophic lateral sclerosis. *Int J Mol Sci* 21:1714
- Revenfeld ALS, Bæk R, Nielsen MH, Stensballe A, Varming K, Jørgensen M (2014) Diagnostic and prognostic potential of extracellular vesicles in peripheral blood. *Clin Ther* 36:830–846
- Richey LE, Halperin J (2013) Acute human immunodeficiency virus infection. *Am J Med Sci* 345:136–142
- Rong D, Lu C, Zhang B, Fu K, Zhao S, Tang W, Cao H (2019) CircPSMC3 suppresses the proliferation and metastasis of gastric cancer by acting as a competitive endogenous RNA through sponging miR-296-5p. *Mol Cancer* 18:25
- Rose S, Contrepas K, Moneghetti KJ, Zhou W, Mishra T, Mataraso S, Dagan-Rosenfeld O, Ganz AB, Dunn J, Hornburg D et al (2019) A longitudinal big data approach for precision health. *Nat Med* 25:792–804

- Ross RW, Galsky MD, Scher HI, Magidson J, Wassmann K, Lee G-S, Katz L, Subudhi SK, Anand A, Fleisher M et al (2012) A whole-blood RNA transcript-based prognostic model in men with castration-resistant prostate cancer: a prospective study. *Lancet Oncol* 13:1105–1113
- Rubis G, Krishnan S, Bebawy M (2019) Liquid biopsies in cancer diagnosis, monitoring, and prognosis. *Trends Pharmacol Sci* 40:172–186
- Rybak-Wolf A, Stottmeister C, Glažar P, Jens M, Pino N, Giusti S, Hanan M, Behm M, Bartok O, Ashwal-Fluss R et al (2015) Circular RNAs in the mammalian brain are highly abundant, conserved, and dynamically expressed. *Mol Cell* 58:870–885
- Salzman J, Chen RE, Olsen MN, Wang PL, Brown PO (2013) Cell-type specific features of circular RNA expression. *PLoS Genet* 9(9):e1003777
- Salzman J, Gawad C, Wang P, Lacayo N, Brown PO (2012) Circular RNAs are the predominant transcript isoform from hundreds of human genes in diverse cell types. *PLoS ONE*. <https://doi.org/10.1371/journal.pone.0030733>
- Sambarey A, Devaprasad A, Mohan A, Ahmed A, Nayak S, Swaminathan S, D'Souza G, Jesuraj A, Dhar C, Babu S et al (2017) Unbiased identification of blood-based biomarkers for pulmonary tuberculosis by modeling and mining molecular interaction networks. *EBioMedicine* 15:112–126
- Sanger HL, Klotz G, Riesner D, Gross HJ, Kleinschmidt AK (1976) Viroids are single-stranded covalently closed circular RNA molecules existing as highly base-paired rod-like structures. *Proc Natl Acad Sci USA* 73:3852–3856
- Schnell A, Schmidl C, Herr W, Siska PJ (2018) The peripheral and intratumoral immune cell landscape in cancer patients: a proxy for tumor biology and a tool for outcome prediction. *Biomedicines* 6:25
- Shaked Y (2019) The pro-tumorigenic host response to cancer therapies. *Nat Rev Cancer* 19:667–685
- Shang A, Gu C, Wang W, Wang X, Sun J, Zeng B, Chen C, Chang W, Ping Y, Ji P et al (2020) Exosomal circPACRGL promotes progression of colorectal cancer via the miR-142-3p/miR-506-3p-TGF- β 1 axis. *Mol Cancer* 19:117
- Shang Q, Yang Z, Jia R, Ge S (2019) The novel roles of circRNAs in human cancer. *Mol Cancer* 18:6
- Shao Y, Tao X, Lu R, Zhang H, Ge J, Xiao B, Ye G, Guo J (2020) Hsa_circ_0065149 is an indicator for early gastric cancer screening and prognosis prediction. *Pathol Oncol Res* 26:1475–1482
- Sheng R, Li X, Wang Z, Wang X (2020) Circular RNAs and their emerging roles as diagnostic and prognostic biomarkers in ovarian cancer. *Cancer Lett* 473:139–147
- Shi L, Tao C, Tang Y, Xia Y, Li X, Wang X (2020) Hypoxia-induced hsa_circ_0000826 is linked to liver metastasis of colorectal cancer. *J Clin Lab Anal* 34(9):e23405
- Showe MK, Vachani A, Kossenkova AV, Yousef M, Nichols C, Nikonova EV, Chang C, Kucharczuk J, Tran B, Wakeam E et al (2009) Gene expression profiles in peripheral blood mononuclear cells can distinguish patients with non-small cell lung cancer from patients with nonmalignant lung disease. *Cancer Res* 69:9202–9210
- Shuai M, Hong J, Huang D, Zhang X, Tian Y (2018) Upregulation of circRNA_0000285 serves as a prognostic biomarker for nasopharyngeal carcinoma and is involved in radiosensitivity. *Oncol Lett* 16:6495–6501
- Siravegna G, Marsoni S, Siena S, Bardelli A (2017) Integrating liquid biopsies into the management of cancer. *Nat Rev Clin Oncol* 14:531–548
- Smid M, Wiltling SM, Uhr K, Rodríguez-González GF, de Weerd V, van der Smitten WJC, van der Vlugt-Daane M, van Galen A, Nik-Zainal S, Butler A et al (2019) The circular RNome of primary breast cancer. *Genome Res* 29:356–366
- Sole C, Arnaiz E, Manterola L, Otaegui D, Lawrie CH (2019) The circulating transcriptome as a source of cancer liquid biopsy biomarkers. *Semin Cancer Biol* 58:100–108
- Song R, Bai Y, Li X, Zhu J, Zhang H, Shi Y, Li K, Wang B, Zhang H, Yang Y et al (2020) Plasma circular RNA DYM related to major depressive disorder and rapid antidepressant effect treated by visual cortical repetitive transcranial magnetic stimulation. *J Affect Disord* 274:486–493
- Sonnenschein K, Wilczek A, de Gonzalo-Calvo D, Pfanne A, Derda A, Zwadlo C, Bavendiek U, Bauersachs J, Fiedler J, Thum T (2019) Serum circular RNAs act as blood-based biomarkers for hypertrophic obstructive cardiomyopathy. *Sci Rep* 9:20350
- Stark R, Grzelak M, Hadfield J (2019) RNA sequencing: the teenage years. *Nat Rev Genet* 20:1–26
- Starke S, Jost I, Rossbach O, Schneider T, Schreiner S, Hung L-H, Bindereif A (2014) Exon circularization requires canonical splice signals. *Cell Rep* 10:103–111
- Su M, Xiao Y, Ma J, Tang Y, Tian B, Zhang Y, Li X, Wu Z, Yang D, Zhou Y et al (2019) Circular RNAs in cancer: emerging functions in hallmarks, stemness, resistance and roles as potential biomarkers. *Mol Cancer* 18:90
- Sun J-Y, Shi Y, Cai X-Y, Liu J (2020) Potential diagnostic and therapeutic value of circular RNAs in cardiovascular diseases. *Cell Signal* 71:109604
- Sun X-H, Wang Y-T, Li G-F, Zhang N, Fan L (2020) Serum-derived three-circRNA signature as a diagnostic biomarker for hepatocellular carcinoma. *Cancer Cell Int* 20:226
- Sun Y, Jiang X, Lv Y, Liang X, Zhao B, Bian W, Zhang D, Jiang J, Zhang C (2020) Circular RNA expression profiles in plasma from patients with heart failure related to platelet activity. *Biomolecules* 10(2):187
- Surinova S, Radová L, Choi M, Srovnal J, Brenner H, Vitek O, Hajdúch M, Aebbersold R (2015) Non-invasive prognostic protein biomarker signatures associated with colorectal cancer. *EMBO Mol Med* 7:1153–1165
- Sweeney TE, Perumal TM, Henao R, Nichols M, Howrylak JA, Choi AM, Bermejo-Martin JFF, Almansa R, Tamayo E, Davenport EE et al (2018) A community approach to mortality prediction in sepsis via gene expression analysis. *Nat Commun* 9:694
- Szabo L, Morey R, Palpant NJ, Wang PL, Afari N, Jiang C, Parast MM, Murry CE, Laurent LC, Salzman J (2015) Statistically based splicing detection reveals neural enrichment and tissue-specific induction of circular RNA during human fetal development. *Genome Biol* 16:126
- Szabo L, Salzman J (2016) Detecting circular RNAs: bioinformatic and experimental challenges. *Nat Rev Genet* 17:679–692

- Tan S, Gou Q, Pu W, Guo C, Yang Y, Wu K, Liu Y, Liu L, Wei Y-Q, Peng Y (2018) Circular RNA F-circEA produced from EML4-ALK fusion gene as a novel liquid biopsy biomarker for non-small cell lung cancer. *Cell Res* 28:693–695
- Tang W, Fu K, Sun H, Rong D, Wang H, Cao H (2018) CircRNA microarray profiling identifies a novel circulating biomarker for detection of gastric cancer. *Mol Cancer* 17:137
- Tang X, Liu S, Ding Y, Guo C, Guo J, Hua K, Qiu J (2020) Serum circular FoxO3a serves as a novel prognostic biomarker in squamous cervical cancer. *Cancer Manag Res* 12:2531–2540
- Tao X, Shao Y, Lu R, Ye Q, Xiao B, Ye G, Guo J (2020) Clinical significance of hsa_circ_0000419 in gastric cancer screening and prognosis estimation. *Pathol Res Pract* 216:152763
- Teng L, Chen Y, Chen H, He X, Wang J, Peng Y, Duan H, Li H, Lin D, Shao B (2017) Circular RNA hsa_circ_0021001 in peripheral blood: a potential novel biomarker in the screening of intracranial aneurysm. *Oncotarget* 8:107125–107133
- Torrano V, Royo F, Peinado H, Loizaga-Iriarte A, Unda M, Falcón-Perez JM, Carracedo A (2016) Vesicle-MaNiA: extracellular vesicles in liquid biopsy and cancer. *Curr Opin Pharmacol* 29:47–53
- Tsalik EL, Henao R, Nichols M, Burke T, Ko ER, McClain MT, Hudson LL, Mazur A, Freeman DH, Veldman T et al (2016) Host gene expression classifiers diagnose acute respiratory illness etiology. *Sci Transl Med* 8:322ra311
- Turchinovich A, Weiz L, Langheinz A, Burwinkel B (2011) Characterization of extracellular circulating microRNA. *Nucleic Acids Res* 39:7223–7233
- Valk PJM, Verhaak RGW, Beijen MA, Erpelinck CAJ, van Doorn-Khosrovani SBW, Boer JM, Beverloo HB, Moorhouse MJ, van der Spek PJ, Löwenberg B et al (2004) Prognostically useful gene-expression profiles in acute myeloid leukemia. *N Engl J Med* 350:1617–1628
- van Heesch S, Witte F, Schneider-Lunitz V, Schulz JF, Adami E, Faber AB, Kirchner M, Maatz H, Blachut S, Sandmann C-L et al (2019) The translational landscape of the human heart. *Cell* 178(1):242–260
- Vargas AJ, Harris CC (2016) Biomarker development in the precision medicine era: lung cancer as a case study. *Nat Rev Cancer* 16:525–537
- Vargas J, Lima JA, Kraus WE, Douglas PS, Rosenberg S (2013) Use of the Corus® CAD gene expression test for assessment of obstructive coronary artery disease likelihood in symptomatic non-diabetic patients. *PLoS Curr.* <https://doi.org/10.1371/currents.eogt.0f04f6081905998fa92b99593478aeab>
- Vausort M, Salgado-Somoza A, Zhang L, Leszek P, Scholz M, Teren A, Burkhardt R, Thiery J, Wagner DR, Devaux Y (2016) Myocardial infarction-associated circular RNA predicting left ventricular dysfunction. *J Am Coll Cardiol* 68:1247–1248
- Venø MT, Hansen TB, Venø ST, Clausen BH, Grebing M, Finsen B, Holm IE, Kjems J (2015) Spatio-temporal regulation of circular RNA expression during porcine embryonic brain development. *Genome Biol* 16:245
- Vicens Q, Westhof E (2014) Biogenesis of circular RNAs. *Cell* 159:13–14
- Vo JN, Cieslik M, Zhang Y, Shukla S, Xiao L, Zhang Y, Wu Y-M, Dhanasekaran SM, Engelke CG, Cao X et al (2019) The landscape of circular RNA in cancer. *Cell* 176:869–881.e813
- Wan JCM, Massie C, Garcia-Corbacho J, Mouliere F, Brenton JD, Caldas C, Pacey S, Baird R, Rosenfeld N (2017) Liquid biopsies come of age: towards implementation of circulating tumour DNA. *Nat Rev Cancer* 17:223–238
- Wang Y, Wang Z (2015) Efficient backsplicing produces translatable circular mRNAs. *RNA* 21:172–179
- Wang PL, Bao Y, Yee M-C, Barrett SP, Hogan GJ, Olsen MN, Dinneny JR, Brown PO, Salzman J (2014) Circular RNA is expressed across the eukaryotic tree of life. *PLoS ONE* 9(6):e90859
- Wang YM, Huang LM, Li DR, Shao JH, Xiong SL, Wang CM, Lu SM (2017a) Hsa_circ_0101996 combined with hsa_circ_0101119 in peripheral whole blood can serve as the potential biomarkers for human cervical squamous cell carcinoma. *Int J Clin Exp Pathol* 10:11924–11931
- Wang Z-Y, Guo Z-D, Li J-M, Zhao Z-Z, Fu Y-Y, Zhang C-M, Zhang Y, Liu L-N, Qian J, Liu L-N (2017b) Genome-wide search for competing endogenous RNAs responsible for the effects induced by Ebola virus replication and transcription using a trVLP system. *Front Cell Infect Microbiol* 7:479
- Wang L, Shen C, Wang Y, Zou T, Zhu H, Lu X, Li L, Yang B, Chen J, Chen S et al (2019a) Identification of circular RNA hsa_circ_0001879 and hsa_circ_0004104 as novel biomarkers for coronary artery disease. *Atherosclerosis* 286:88–96
- Wang Q, Zhang Q, Sun H, Tang W, Yang L, Xu Z, Liu Z, Jin H, Cao X (2019b) Circ-TTC17 promotes proliferation and migration of esophageal squamous cell carcinoma. *Dig Dis Sci* 64:751–758
- Wang W, Dong R, Guo Y, He J, Shao C, Yi P, Yu F, Gu D, Zheng J (2019c) CircMTO1 inhibits liver fibrosis via regulation of miR-17-5p and Smad7. *J Cell Mol Med* 23:5486–5496
- Wang W, Wang J, Zhang X, Liu G (2019d) Serum circSETDB1 is a promising biomarker for predicting response to platinum-taxane-combined chemotherapy and relapse in high-grade serous ovarian cancer. *Onco Targets Ther* 12:7451–7457
- Wang Y, Liu J, Ma J, Sun T, Zhou Q, Wang W, Wang G, Wu P, Wang H, Jiang L et al (2019e) Exosomal circRNAs: biogenesis, effect and application in human diseases. *Mol Cancer* 18:116
- Wang Y, Wu C, Zhang F, Zhang Y, Ren Z, Lammi MJ, Guo X (2019f) Screening for differentially expressed circular RNAs in the cartilage of osteoarthritis patients for their diagnostic value. *Genet Test Mol Biomark* 23:706–716
- Wang J, Kong J, Nie Z, Chen D, Qiang J, Gao W, Chen X (2020a) Circular RNA hsa_circ_0066755 as an oncogene via sponging miR-651 and as a promising diagnostic biomarker for nasopharyngeal carcinoma. *Int J Med Sci* 17:1499–1507
- Wang J, Zhao X, Wang Y, Ren F, Sun D, Yan Y, Kong X, Bu J, Liu M, Xu S (2020b) CircRNA-002178 act as a ceRNA to promote PDL1/PD1 expression in lung adenocarcinoma. *Cell Death Dis* 11:32
- Wang Q, Liu H, Liu Z, Yang L, Zhou J, Cao X, Sun H (2020c) Circ-SLC7A5, a potential prognostic circulating biomarker for detection of ESCC. *Cancer Genet* 240:33–39
- Wang W, Li Y, Li X, Liu B, Han S, Li X, Zhang B, Li J, Sun S (2020d) Circular RNA circ-FOXP1 induced by SOX9 promotes

- hepatocellular carcinoma progression via sponging miR-875-3p and miR-421. *Biomed Pharmacother* 121:109517
- Wang Y, Wu C, Zhang Y, Yang Y, Ren Z, Lammi MJ, Guo X (2020e) Screening for differentially expressed circRNA between Kashin-Beck disease and osteoarthritis patients based on circRNA chips. *Clin Chim Acta* 501:92–101
- Warsinske H, Vashisht R, Khatri P (2019) Host-response-based gene signatures for tuberculosis diagnosis: a systematic comparison of 16 signatures. *PLoS Med* 16:e1002786
- Weng W, Wei Q, Toden S, Yoshida K, Nagasaka T, Fujiwara T, Cai S, Qin H, Ma Y, Goel A (2017) Circular RNA ciRS-7—a promising prognostic biomarker and a potential therapeutic target in colorectal cancer. *Clin Cancer Res* 23:3918–3928
- Westholm JO, Miura P, Olson S, Shenker S, Joseph B, Sanfilippo P, Celniker SE, Graveley BR, Lai EC (2014) Genome-wide analysis of *Drosophila* circular RNAs reveals their structural and sequence properties and age-dependent neural accumulation. *Cell Rep* 9:1966–1980
- Wilusz JE (2015) Repetitive elements regulate circular RNA biogenesis. *Mob Genet Elem* 5:39–45
- Wu H, Yang L, Chen L-L (2017a) The diversity of long noncoding RNAs and their generation. *Trends Genet* 33:540–552
- Wu N, Jin L, Cai J (2017b) Profiling and bioinformatics analyses reveal differential circular RNA expression in hypertensive patients. *Clin Exp Hypertens* 39:454–459
- Wu J, Li J, Liu H, Yin J, Zhang M, Yu Z, Miao H (2019a) Circulating plasma circular RNAs as novel diagnostic biomarkers for congenital heart disease in children. *J Clin Lab Anal* 33:e22998
- Wu J, Zhou Q, Niu Y, Chen J, Zhu Y, Ye S, Xi Y, Wang F, Qiu H, Bu S (2019b) Aberrant expression of serum circANRIL and hsa_circ_0123996 in children with Kawasaki disease. *J Clin Lab Anal* 33:e22874
- Wu W, Ji P, Zhao F (2020a) CircAtlas: an integrated resource of one million highly accurate circular RNAs from 1070 vertebrate transcriptomes. *Genome Biol* 21:101
- Wu WP, Pan YH, Cai MY, Cen JM, Chen C, Zheng L, Liu X, Xiong XD (2020b) Plasma-derived exosomal circular RNA hsa_circ_0005540 as a novel diagnostic biomarker for coronary artery disease. *Dis Markers* 2020:3178642
- Wu Z, Sun H, Liu W, Zhu H, Fu J, Yang C, Fan L, Wang L, Liu Y, Xu W et al (2020c) Circ-RPL15: a plasma circular RNA as novel oncogenic driver to promote progression of chronic lymphocytic leukemia. *Leukemia* 34:919–923
- Xia X, Li X, Li F, Wu X, Zhang M, Zhou H, Huang N, Yang X, Xiao F, Liu D et al (2019) A novel tumor suppressor protein encoded by circular AKT3 RNA inhibits glioblastoma tumorigenicity by competing with active phosphoinositide-dependent Kinase-1. *Mol Cancer* 18:131
- Xiao M-S, Ai Y, Wilusz JE (2020) Biogenesis and functions of circular RNAs come into focus. *Trends Cell Biol* 30(3):226–240
- Xie M, Yu T, Jing X, Ma L, Fan Y, Yang F, Ma P, Jiang H, Wu X, Shu Y et al (2020a) Exosomal circSHKBP1 promotes gastric cancer progression via regulating the miR-582-3p/HUR/VEGF axis and suppressing HSP90 degradation. *Mol Cancer* 19:112
- Xie R, Zhang Y, Zhang J, Li J, Zhou X (2020b) The role of circular RNAs in immune-related diseases. *Front Immunol* 11:545
- Xie Y, Li J, Li P, Li N, Zhang Y, Binang H, Zhao Y, Duan W, Chen Y, Wang Y et al (2020c) RNA-Seq profiling of serum exosomal circular RNAs reveals circ-PNN as a potential biomarker for human colorectal cancer. *Front Oncol* 10:982
- Xiong S, Peng H, Ding X, Wang X, Wang L, Wu C, Wang S, Xu H, Liu Y (2019) Circular RNA expression profiling and the potential role of hsa_circ_0089172 in Hashimoto's thyroiditis via sponging miR125a-3p. *Mol Ther Nucleic Acids* 17:38–48
- Xu H, Guo S, Li W, Yu P (2015) The circular RNA Cdr1as, via miR-7 and its targets, regulates insulin transcription and secretion in islet cells. *Sci Rep* 5:12453
- Xu H, Gong Z, Shen Y, Fang Y, Zhong S (2018a) Circular RNA expression in extracellular vesicles isolated from serum of patients with endometrial cancer. *Epigenomics* 10:187–197
- Xu Z, Li P, Fan L, Wu M (2018b) The potential role of circRNA in tumor immunity regulation and immunotherapy. *Front Immunol* 9:9
- Xu M, Xie F, Tang X, Wang T, Wang S (2020a) Insights into the role of circular RNA in macrophage activation and fibrosis disease. *Pharmacol Res* 156:104777
- Xu Y, Leng K, Yao Y, Kang P, Liao G, Han Y, Shi G, Ji D, Huang P, Zheng W et al (2020b) A novel circular RNA, circ-CCAC1, contributes to CCA progression, induces angiogenesis, and disrupts vascular endothelial barriers. *Hepatology*. <https://doi.org/10.1002/hep.31493>
- Yan B, Zhang Y, Liang C, Liu B, Ding F, Wang Y, Zhu B, Zhao R, Yu X-Y, Li Y (2020) Stem cell-derived exosomes prevent pyroptosis and repair ischemic muscle injury through a novel exosome/circHIPK3/FOXO3a pathway. *Theranostics* 10:6728–6742
- Yang F, Liu DY, Guo JT, Ge N, Zhu P, Liu X, Wang S, Wang GX, Sun SY (2017a) Circular RNA circ-LDLRAD3 as a biomarker in diagnosis of pancreatic cancer. *World J Gastroenterol* 23:8345–8354
- Yang Q, Du WW, Wu N, Yang W, Awan F, Fang L, Ma J, Li X, Zeng Y, Yang Z et al (2017b) A circular RNA promotes tumorigenesis by inducing c-myc nuclear translocation. *Cell Death Differ* 24(9):1609–1620
- Yang Y, Fan X, Mao M, Song X, Wu P, Zhang Y, Jin Y, Yang Y, Chen L, Wang Y et al (2017c) Extensive translation of circular RNAs driven by N⁶-methyladenosine. *Cell Res* 27:626–641
- Yang L, Fu J, Zhou Y (2018) Circular RNAs and their emerging roles in immune regulation. *Front Immunol* 9:2977
- Yang X, Li J, Wu Y, Ni B, Zhang B (2019) Aberrant dysregulated circular RNAs in the peripheral blood mononuclear cells of patients with rheumatoid arthritis revealed by RNA sequencing: novel diagnostic markers for RA. *Scand J Clin Lab Invest* 79:551–559
- Yao G, Niu W, Zhu X, He M, Kong L, Chen S, Zhang L, Cheng Z (2019) hsa_circRNA_104597: a novel potential diagnostic and therapeutic biomarker for schizophrenia. *Biomark Med* 13:331–340
- Ye DX, Wang SS, Huang Y, Chi P (2019) A 3-circular RNA signature as a noninvasive biomarker for diagnosis of colorectal cancer. *Cancer Cell Int* 19:276
- Yi Z, Gao K, Li R, Fu Y (2018) Dysregulated circRNAs in plasma from active tuberculosis patients. *J Cell Mol Med* 22:4076–4084

- Yin WB, Yan MG, Fang X, Guo JJ, Xiong W, Zhang RP (2018) Circulating circular RNA hsa_circ_0001785 acts as a diagnostic biomarker for breast cancer detection. *Clin Chim Acta* 487:363–368
- Yoshimoto R, Rahimi K, Hansen T, Kjems J, Mayeda A (2019) Biosynthesis of circular RNA ciRS-7/CDR1as is mediated by mammalian-wide interspersed repeats (MIRs). *Biorxiv* 411231
- You X, Vlatkovic I, Babic A, Will T, Epstein I, Tushev G, Akbalik G, Wang M, Glock C, Quedenau C (2015) Neural circular RNAs are derived from synaptic genes and regulated by development and plasticity. *Nat Neurosci* 18:603–610
- Yu C-Y, Li T-C, Wu Y-Y, Yeh C-H, Chiang W, Chuang C-Y, Kuo H-C (2017) The circular RNA circBIRC6 participates in the molecular circuitry controlling human pluripotency. *Nat Commun* 8:1149
- Yu M, Bardia A, Wittner BS, Stott SL, Smas ME, Ting DT, Isakoff SJ, Ciciliano JC, Wells MN, Shah AM et al (2013) Circulating breast tumor cells exhibit dynamic changes in epithelial and mesenchymal composition. *Science* 339:580–584
- Zaas AK, Chen M, Varkey J, Veldman T, Hero AO, Lucas J, Huang Y, Turner R, Gilbert A, Lambkin-Williams R et al (2009) Gene expression signatures diagnose Influenza and other symptomatic respiratory viral infections in humans. *Cell Host Microbe* 6:207–217
- Zak DE, Penn-Nicholson A, Scriba TJ, Thompson E, Suliman S, Amon LM, Mahomed H, Erasmus M, Whatney W, Hussey GD et al (2016) A blood RNA signature for tuberculosis disease risk: a prospective cohort study. *Lancet* 387:2312–2322
- Zaporozhchenko IA, Ponomaryova AA, Rykova EY, Laktionov PP (2018) The potential of circulating cell-free RNA as a cancer biomarker: challenges and opportunities. *Expert Rev Mol Diagn* 18:133–145
- Zemmour H, Planer D, Magenheimer J, Moss J, Neiman D, Gilon D, Korach A, Glaser B, Shemer R, Landesberg G et al (2018) Non-invasive detection of human cardiomyocyte death using methylation patterns of circulating DNA. *Nat Commun* 9:1443
- Zhang Y, Zhang XO, Chen T, Xiang JF, Yin QF, Xing YH, Zhu S, Yang L, Chen LL (2013) Circular intronic long noncoding RNAs. *Mol Cell* 51:792–806
- Zhang X-O, Wang H-B, Zhang Y, Lu X, Chen L-L, Yang L (2014) Complementary sequence-mediated exon circularization. *Cell* 159:134–147
- Zhang YG, Yang HL, Long Y, Li WL (2016) Circular RNA in blood corpuscles combined with plasma protein factor for early prediction of pre-eclampsia. *BJOG* 123:2113–2118
- Zhang Y, Li J, Yu J, Liu H, Shen Z, Ye G, Mou T, Qi X, Li G (2017) Circular RNAs signature predicts the early recurrence of stage III gastric cancer after radical surgery. *Oncotarget* 8:22936–22943
- Zhang C, Wang X, Chen Y, Wu Z, Zhang C, Shi W (2018a) The down-regulation of hsa_circ_0012919, the sponge for miR-125a-3p, contributes to DNA methylation of CD11a and CD70 in CD4 (+) T cells of systemic lupus erythematosus. *Clin Sci (Lond)* 132:2285–2298
- Zhang H, Deng T, Ge S, Liu Y, Bai M, Zhu K, Fan Q, Li J, Ning T, Tian F et al (2018b) Exosome circRNA secreted from adipocytes promotes the growth of hepatocellular carcinoma by targeting deubiquitination-related USP7. *Oncogene* 38:2844–2859
- Zhang J, Xu Y, Xu S, Liu Y, Yu L, Li Z, Xue X, Wang H (2018c) Plasma circular RNAs, hsa_circRNA_025016, predict postoperative atrial fibrillation after isolated off-pump coronary artery bypass grafting. *J Am Heart Assoc* 7:e006642
- Zhang M, Zhao K, Xu X, Yang Y, Yan S, Wei P, Liu H, Xu J, Xiao F, Zhou H et al (2018d) A peptide encoded by circular form of LINC-PINT suppresses oncogenic transcriptional elongation in glioblastoma. *Nat Commun* 9:4475
- Zhang MY, Wang JB, Zhu ZW, Li LJ, Liu RS, Yang XK, Leng RX, Li XM, Pan HF, Ye DQ (2018e) Differentially expressed circular RNAs in systemic lupus erythematosus and their clinical significance. *Biomed Pharmacother* 107:1720–1727
- Zhang W, Yang S, Liu Y, Wang Y, Lin T, Li Y, Zhang R (2018f) Hsa_circ_0007534 as a blood-based marker for the diagnosis of colorectal cancer and its prognostic value. *Int J Clin Exp Pathol* 11:1399–1406
- Zhang X, Xu Y, Qian Z, Zheng W, Wu Q, Chen Y, Zhu G, Liu Y, Bian Z, Xu W et al (2018g) CircRNA_104075 stimulates YAP-dependent tumorigenesis through the regulation of HNF4a and may serve as a diagnostic marker in hepatocellular carcinoma. *Cell Death Dis* 9:1091
- Zhang X, Zhou H, Jing W, Luo P, Qiu S, Liu X, Zhu M, Liang C, Yu M, Tu J (2018h) The circular RNA hsa_circ_0001445 regulates the proliferation and migration of hepatocellular carcinoma and may serve as a diagnostic biomarker. *Dis Markers* 2018:3073467
- Zhang Y, Zhang H, An M, Zhao B, Ding H, Zhang Z, He Y, Shang H, Han X (2018i) Crosstalk in competing endogenous RNA networks reveals new circular RNAs involved in the pathogenesis of early HIV infection. *J Transl Med* 16:332
- Zhang Z, Yang T, Xiao J (2018j) Circular RNAs: promising biomarkers for human diseases. *EBioMedicine* 34:267–274
- Zhang J, Li J, Saucier JB, Feng Y, Jiang Y, Sinson J, McCombs AK, Schmitt ES, Peacock S, Chen S et al (2019a) Non-invasive prenatal sequencing for multiple Mendelian monogenic disorders using circulating cell-free fetal DNA. *Nat Med* 25:1–9
- Zhang Y, Chen Y, Yao H, Lie Z, Chen G, Tan H, Zhou Y (2019b) Elevated serum circ_0068481 levels as a potential diagnostic and prognostic indicator in idiopathic pulmonary arterial hypertension. *Pulm Circ* 9:2045894019888416
- Zhang P-F, Gao C, Huang X-Y, Lu J-C, Guo X-J, Shi G-M, Cai J-B, Ke A-W (2020a) Cancer cell-derived exosomal circUHRF1 induces natural killer cell exhaustion and may cause resistance to anti-PD1 therapy in hepatocellular carcinoma. *Mol Cancer* 19:110
- Zhang S, Song G, Yuan J, Qiao S, Xu S, Si Z, Yang Y, Xu X, Wang A (2020b) Circular RNA circ_0003204 inhibits proliferation, migration and tube formation of endothelial cell in atherosclerosis via miR-370-3p/TGFBetaR2/phosph-SMAD3 axis. *J Biomed Sci* 27:11
- Zhao Z, Li X, Gao C, Jian D, Hao P, Rao L, Li M (2017a) Peripheral blood circular RNA hsa_circ_0124644 can be used as a diagnostic biomarker of coronary artery disease. *Sci Rep* 7:39918
- Zhao Z, Li X, Jian D, Hao P, Rao L, Li M (2017b) Hsa_circ_0054633 in peripheral blood can be used as a diagnostic biomarker of pre-diabetes and type 2 diabetes mellitus. *Acta Diabetol* 54:237–245
- Zhao K, Zhao Q, Guo Z, Chen Z, Hu Y, Su J, Chen L, He Z, Cai X, Chen M et al (2018a) Hsa_circ_0001275: a potential novel

- diagnostic biomarker for postmenopausal osteoporosis. *Cell Physiol Biochem* 46:2508–2516
- Zhao Q, Chen S, Li T, Xiao B, Zhang X (2018b) Clinical values of circular RNA 0000181 in the screening of gastric cancer. *J Clin Lab Anal* 32:e22333
- Zhao T, Zheng Y, Hao D, Jin X, Luo Q, Guo Y, Li D, Xi W, Xu Y, Chen Y et al (2019) Blood circRNAs as biomarkers for the diagnosis of community-acquired pneumonia. *J Cell Biochem* 120:16483–16494
- Zheng Q, Bao C, Guo W, Li S, Chen J, Chen B, Luo Y, Lyu D, Li Y, Shi G et al (2016) Circular RNA profiling reveals an abundant circHIPK3 that regulates cell growth by sponging multiple miRNAs. *Nat Commun* 7:11215
- Zheng S, Gu T, Bao X, Sun J, Zhao J, Zhang T, Zhang L (2019) Circular RNA hsa_circ_0014243 may serve as a diagnostic biomarker for essential hypertension. *Exp Ther Med* 17:1728–1736
- Zheng S, He X, Sun J, Li Q, Zhang T, Zhang L (2020) The up-regulated hsa-circRNA9102-5 may be a risk factor for essential hypertension. *J Clin Lab Anal*. <https://doi.org/10.1002/jcla.23339>
- Zhou T, Xie X, Li M, Shi J, Zhou JJ, Knox KS, Wang T, Chen Q, Gu W (2018a) Rat BodyMap transcriptomes reveal unique circular RNA features across tissue types and developmental stages. *RNA* 24:1443–1456
- Zhou X, Liu HY, Wang WY, Zhao H, Wang T (2018b) Hsa_circ_0102533 serves as a blood-based biomarker for non-small-cell lung cancer diagnosis and regulates apoptosis in vitro. *Int J Clin Exp Pathol* 11:4395–4404
- Zhou W, Sailani RM, Contrepois K, Zhou Y, Ahadi S, Leopold SR, Zhang MJ, Rao V, Avina M, Mishra T et al (2019a) Longitudinal multi-omics of host-microbe dynamics in prediabetes. *Nature* 569:663–671
- Zhou Z, Sun B, Huang S, Zhao L (2019b) Roles of circular RNAs in immune regulation and autoimmune diseases. *Cell Death Dis* 10:503
- Zhu X, Wang X, Wei S, Chen Y, Chen Y, Fan X, Han S, Wu G (2017) hsa_circ_0013958: a circular RNA and potential novel biomarker for lung adenocarcinoma. *FEBS J* 284:2170–2182
- Zhu K, Niu L, Wang J, Wang Y, Zhou J, Wang F, Cheng Y, Zhang Q, Li H (2019a) Circular RNA hsa_circ_0000885 levels are increased in tissue and serum samples from patients with osteosarcoma. *Med Sci Monit* 25:1499–1505
- Zhu X, Ding J, Wang B, Wang J, Xu M (2019b) Circular RNA DLGAP4 is down-regulated and negatively correlates with severity, inflammatory cytokine expression and pro-inflammatory gene miR-143 expression in acute ischemic stroke patients. *Int J Clin Exp Pathol* 12:941–948
- Zhuang Z-G, Zhang J-A, Luo H-L, Liu G-B, Lu Y-B, Ge N-H, Zheng B-Y, Li RX, Chen C, Wang X et al (2017) The circular RNA of peripheral blood mononuclear cells: Hsa_circ_0005836 as a new diagnostic biomarker and therapeutic target of active pulmonary tuberculosis. *Mol Immunol* 90:264–272
- Zuo L, Li C, Zu J, Yao H, Yan F (2020) Circular RNA FUNDC1 improves prediction of stroke associated infection in acute ischemic stroke patients with high risk. *Biosci Rep*. <https://doi.org/10.1042/BSR20200902>