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## Data Article

# Transcriptomic data of piglet blood compartments with 3' mRNA sequencing



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## ABSTRACT

This article reports transcriptomic dataset generated by rationalized sequencing of the 3' ends of messenger RNAs (3' mRNA-Seq) in porcine samples. Libraries were prepared from whole blood, plasma, serum, and exosome-enriched fractions derived from plasma and serum. This approach was applied to whole blood, with porcine globin blockers being used to minimise the impact of the large quantity of globin transcripts. In addition, serum and plasma-derived RNA were processed without globin depletion, allowing a direct assessment of transcriptome profiles from these biofluids.

Although the library preparation protocol employed was not originally designed for plasma or serum samples, we successfully produced libraries from RNA extracted from these different compartments. More unexpectedly, libraries could also be generated from exosome-enriched fractions. While expression profiles from plasma and serum fractions display distinctive characteristics compared to whole blood, a quite high proportion of genes were detected in these extracts. The resulting data provide comprehensive transcriptomic information across multiple sample types, including minimally invasive compartments, and are made available to support

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further exploration of 3' mRNA-Seq in biomedical and veterinary research.

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## Specifications Table

Subject	Biology
Specific subject area	Omics: 3' mRNA-Seq analysis of distinct blood compartments in piglets.
Type of data	Raw FASTQ files Processed raw counts matrix table (tsv format) Processed normalized counts matrix table (txt format)
Data collection	Data were collected from blood samples of four 5-week-old female piglets. RNA quality was assessed using DropSense 96 and TapeStation 4200 technologies. 3' mRNA-Sequencing libraries were prepared and sequenced on the Illumina NextSeq 2000 platform with a single-end read length of $1 \times 76$ pb. The data were preprocessed by Nextflow nf-core/rnaseq pipeline for transcriptome quantification.
Data source location	Institution: INRAE Laboratory: Toxalim, GenPhySE, PGTB Town: Toulouse, Toulouse and Bordeaux Country: France
Data accessibility	Repository name: ArrayExpress Data identification number: E-MTAB-16252 Direct URL to data: <a href="https://www.ebi.ac.uk/biostudies/ArrayExpress/studies/E-MTAB-16252">https://www.ebi.ac.uk/biostudies/ArrayExpress/studies/E-MTAB-16252</a>
Related research article	

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## 1. Value of the Data

- Different RNA extraction methods were tested on serum, plasma, and exosomes to compare yield and assess the feasibility of RNA-Seq library preparations.
- This dataset provides compartment-specific RNA expression profiles from whole blood, serum, plasma, and exosome extracts derived from serum and plasma of piglets, enabling researchers to investigate differential RNA content across distinct blood fractions with precision.
- The use of 3' mRNA sequencing technology enables streamlined transcriptomic analysis on blood collections, suitable for large cohorts.
- Researchers working on porcine models of health and disease—particularly in immunology, infectious disease, and biomarker discovery—can reuse this dataset for comparative analyses or meta-studies.
- As pigs are biologically similar to humans, particularly about physiology and immune function, this dataset could inform translational studies centered on blood-based diagnostics or RNA biomarker validation.

## 2. Background

RNA sequencing is commonly used to study gene expression in diverse biological contexts. Conventional RNA sequencing methods often require full-length transcript coverage, which can be expensive and technically challenging, particularly when working with large cohorts or biofluids with limited RNA amounts. Sequencing of the 3' ends of messenger RNAs (3' mRNA-Seq) provides a simplified alternative, enabling quantitative transcriptome analysis with reduced complexity, improved efficiency and reduced sequencing costs.

Blood and its derivatives, such as plasma and serum, are highly accessible sources of RNA for biomarker discovery and translational research. Blood sampling is also a minimally invasive procedure to collect samples from animals with limited impact on their health. However, the high abundance of globin transcripts in whole blood limits the detection of less abundant RNAs, making unbiased transcriptomic studies challenging. Globin blockers have been developed to address this issue for few model organisms [1], but their applicability across different species remains to be fully characterized.

This article presents a transcriptomic dataset generated by 3' mRNA-Seq from porcine whole blood, plasma, serum, and exosome-enriched fractions. The dataset includes transcriptomic profiles obtained with globin blockers in whole blood and without blockers in other subcompartments, providing a resource for further exploration of transcriptome analysis in minimally invasive sample types.

### 3. Data Description

This study describes the transcriptome of distinct blood compartments derived from whole blood collected from four 5-week-old female piglets, crossbred between Duroc DanBred X DanBred Hybrid lines, locally obtained from a commercial farm (GAEC Calvignac, St Vincent d'Autejac, France). The dataset includes RNA-Seq data from 20 samples representing five blood compartments: whole blood, serum, plasma, serum-derived exosomes, and plasma-derived exosomes.

#### 3.1. RNA extraction of blood compartments

From each whole blood sample, the different fractions were carefully prepared and stored according to a validated protocol. Total RNA was extracted using optimized and compartment-specific protocols as described in the *Materials and Methods* section and quality controlled. The RNA Integrity Number (RIN, which reflects quality) values of the whole blood RNA ranged from 6.6 to 8. RIN values for the other samples (plasma, serum, exosomes) could not be determined. The total RNA concentration is approximately 100 ng/ $\mu$ l for whole blood samples, as expected for library construction. Spectrophotometric analysis confirms appropriate absorbance ratio 260/230 nm and 260/280 nm (approximately 2), indicating RNA purity and integrity. For other RNA fractions, the measured concentrations fall below the confident limits of the instrument (Table 1).

#### 3.2. Compartment-specific optimization of RNA-Seq library protocol

Despite the difficulty of assessing the quality of RNA extracted from plasma, serum, and exosomes samples, several processing steps were adapted for these blood fractions.

RNA-Seq libraries were prepared using the LEXOGEN QuantSeq 3' mRNA-Seq V2 Library Prep Kit (FORWARD orientation with Unique Dual Indices), applying manufacturer's recommendations to process whole blood samples. Recommendations for low-quality and low-input RNA were applied for RNA extracted from plasma, serum, and exosome samples. Quality control metrics for the twenty 3' mRNA-Seq libraries highlight differences in fragment size, yield, and molarity specific to each sample type (Table 2).

Whole blood libraries showed the largest average fragment sizes (387–407 bp) with consistent yields between 3.25 and 4.49 ng/ $\mu$ l. The proportion of fragments in the target size (180 – 1000 bp) remained high (79–86 %). Serum and plasma libraries displayed fragment sizes in the range of 328–362 bp. Yields were variable and higher than those observed for whole blood, reaching up to 18.20 ng/ $\mu$ l in serum and 10.10 ng/ $\mu$ l in plasma. Target proportions exceeded 81 %,

**Table 1**  
Quality control metrics of RNA extracts from each sample.

Sample dataset	Animal	Sample type	Extraction method	RIN	RNA concentration (ng/μl)	260/230	260/280
1	2	SERUM	NOR_std	NA	7.11	0.25	1.56
2	6	SERUM	NOR_std	NA	19.69	0.65	1.80
3	3	SERUM	NOR_std	NA	14.23	0.36	1.78
4	4	SERUM	NOR_std	NA	11.96	0.02	1.96
5	2	PLASMA	NOR_std	NA	7.28	0.01	2.12
6	6	PLASMA	NOR_std	NA	7.37	0.08	1.66
7	3	PLASMA	NOR_std	NA	8.66	0.33	1.65
8	4	PLASMA	NOR_std	NA	7.26	0.40	1.49
9	2	SERUM	NOR_exo	NA	6.54	0.05	1.21
10	6	SERUM	NOR_exo	NA	2.06	0.07	0.73
11	3	SERUM	NOR_exo	NA	5.21	0.15	1.16
12	4	SERUM	NOR_exo	NA	5.04	0.07	1.28
13	2	PLASMA	NOR_exo	NA	5.10	0.15	1.11
14	6	PLASMA	NOR_exo	NA	3.11	0.12	1.05
15	3	PLASMA	NOR_exo	NA	2.01	0.08	0.71
16	4	PLASMA	NOR_exo	NA	2.25	0.08	0.79
17	2	WHOLE_BLOOD	PAX	8.0	85.04	1.63	2.22
18	6	WHOLE_BLOOD	PAX	6.7	94.21	1.58	2.17
19	3	WHOLE_BLOOD	PAX	6.6	92.72	1.88	2.22
20	4	WHOLE_BLOOD	PAX	7.5	102.00	1.54	2.09

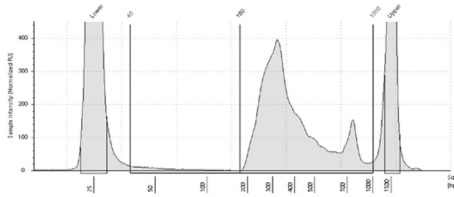
**Table 2**  
Quality metrics of libraries generated from each sample.

Sample dataset	Animal	Sample type	Extraction method	Library mean size (pb)	Library yield (ng/μl)	Library molarity (nmol/L)	Library target proportion 180–1000pb (Percentage)
1	2	SERUM	NOR_std	348	5.96	29.50	84.09
2	6	SERUM	NOR_std	336	12.20	61.40	91.31
3	3	SERUM	NOR_std	328	18.20	94.60	94.09
4	4	SERUM	NOR_std	338	10.40	52.80	91.81
5	2	PLASMA	NOR_std	341	3.46	18.00	81.19
6	6	PLASMA	NOR_std	362	9.85	47.00	91.88
7	3	PLASMA	NOR_std	343	8.09	40.80	91.03
8	4	PLASMA	NOR_std	355	10.10	48.30	92.38
9	2	SERUM	NOR_exo	290	1.87	11.00	66.81
10	6	SERUM	NOR_exo	282	1.60	9.84	67.84
11	3	SERUM	NOR_exo	293	1.73	10.00	65.06
12	4	SERUM	NOR_exo	282	1.65	9.92	60.39
13	2	PLASMA	NOR_exo	268	1.29	8.18	58.61
14	6	PLASMA	NOR_exo	265	1.17	7.57	56.14
15	3	PLASMA	NOR_exo	264	1.29	8.40	55.69
16	4	PLASMA	NOR_exo	266	1.50	9.43	61.75
17	2	WHOLE_BLOOD	PAX	404	4.49	19.60	85.89
18	6	WHOLE_BLOOD	PAX	392	3.25	14.60	82.06
19	3	WHOLE_BLOOD	PAX	387	3.82	17.20	85.86
20	4	WHOLE_BLOOD	PAX	407	3.42	14.70	79.51

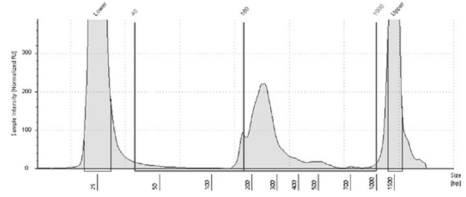
with several samples above 90 %. Exosomes libraries were shorter, with mean sizes between 264 and 293 bp. Yields were lower (1.17–1.5 ng/μl for plasma exosomes and 1.60–1.87 ng/μl for serum exosomes). Target proportions were reduced compared to other compartments, ranging from 55 % to 67 %. Overall, all libraries achieved yields above 1 ng/μl and fragment sizes  $\geq$  180 bp, meeting the requirements for downstream sequencing.

Fig. 1 illustrates representative 3' mRNA-Seq library profiles obtained from different blood compartments. Fig. 1A shows the profile generated from whole blood, characterised by longer

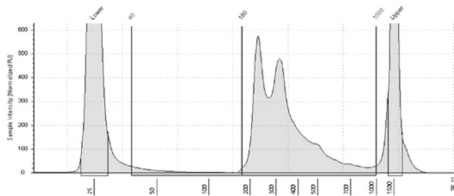
## A-Blood



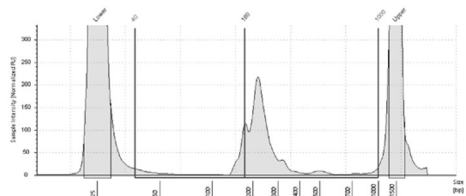
## D-Exosome Serum



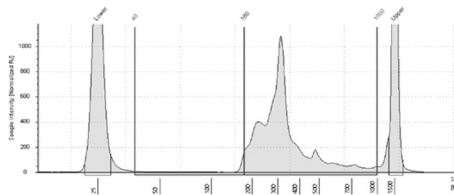
## B-Serum



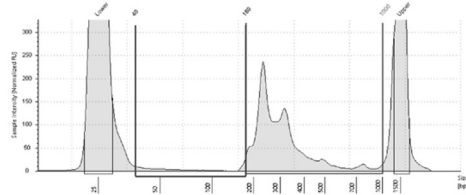
## E-Exosome Plasma



## C-Plasma



## F-Pool

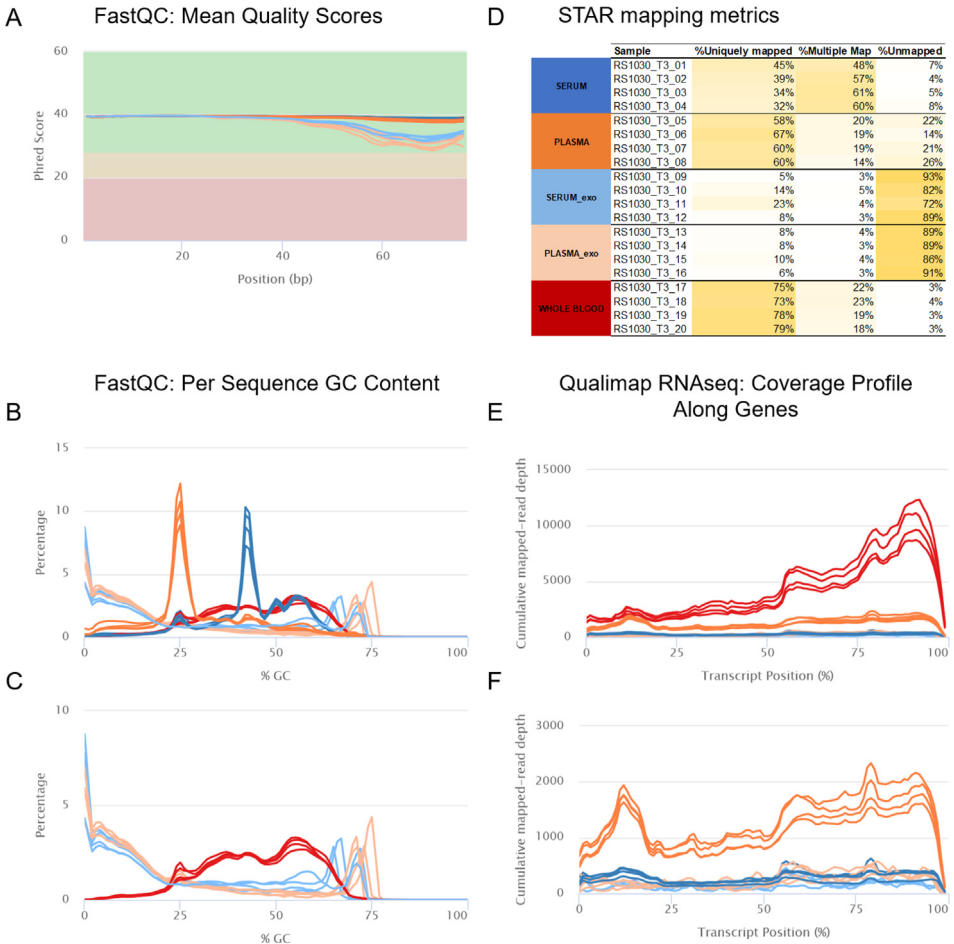


**Fig. 1.** Example of library profiles. Library profiles obtained using D1000 ScreenTape Assay on TapeStation 4200 system for (A) whole blood, (B) serum, (C) plasma, (D) exosome from serum, (E) exosome from plasma, and (F) pool of all samples.

fragment distributions with a distinct peak observed around 700 bp. Fig. 1B corresponds to serum libraries, while Fig. 1C displays plasma libraries, both presenting intermediate fragment sizes. A narrow main peak extending up to the size marker is observed, which may indicate over-amplification in some libraries. This feature is accompanied by variable and elevated concentrations ranging from 3 ng/ $\mu$ l to 18 ng/ $\mu$ l (Table 2). In serum samples, a distinct peak appears around 200 bp, which may correspond to the presence of ribosomal RNA fragments. Fig. 1D and Fig. 1E depict libraries derived from exosomes isolated from serum and plasma, respectively, which exhibit shorter fragment distributions compared to whole blood. A distinct peak appears around 180 bp, which may correspond to adapter dimers without insert fragments. Fig. 1F represents the pooled profile of all samples, summarizing the overall fragment size distribution across all compartments.

Profiles differ in shape and average insert size, reflecting the specific library fragments composition of each blood fraction. In addition, a distinct peak appearing beyond 230 bp was consistently observed across all samples, which may correspond to the fragments of interest.

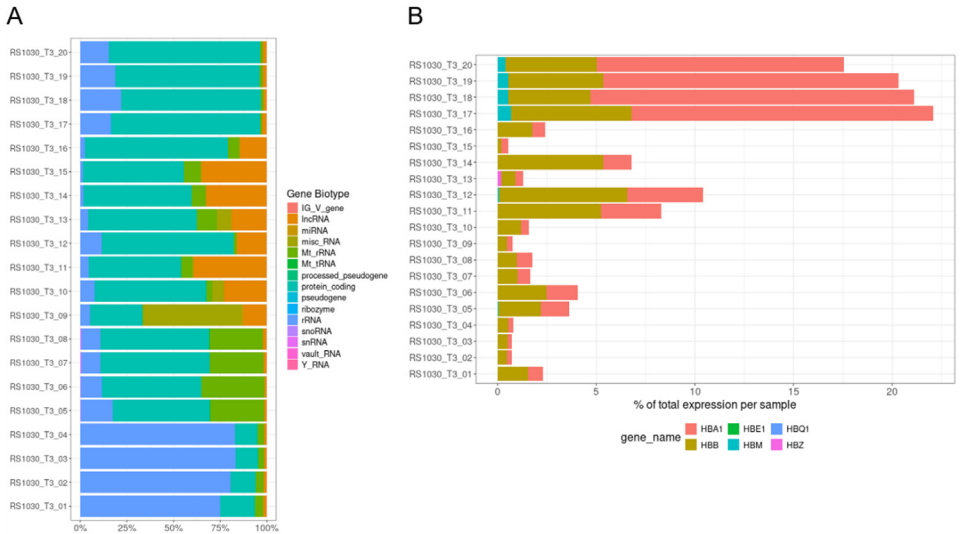
All libraries were diluted and pooled in equimolar concentrations into a single sequencing pool. Sequencing was performed on the Illumina NextSeq2000 platform using 76 cycles single-read mode. Sequencing generated between 16.4 and 25.7 million raw reads per sample.



**Fig. 2.** Metrics summary of sequences and alignments. The different blood compartments are illustrated using colors: dark red for whole blood, orange for plasma, blue for serum, light orange for plasma exosomes and light blue for serum exosomes. (A) Distribution of Phred score along the sequence position. (B) Distribution of GC content for all samples or (C) only whole blood, serum exosomes and plasma exosomes. (D) STAR mapping metrics of all samples. (E) Mapping coverage profile along genes for all samples or (F) all samples except whole blood.

### 3.3. Bioinformatic metrics of sequences and alignments

Bioinformatic pre-processing was conducted using the Nextflow *nf-core/rnaseq* pipeline to ensure the reproducibility of analyses. The sequences generated are of high quality (phred score > 30) for all samples (Fig. 2A), and we can show a slight loss of quality for exosome extracts after cycle 40 bp. GC content distributions per sequence (Figs. 2B and C) show specific patterns according to the type of compartment. Whole blood samples have a flattened Gaussian distribution between 25 % and 70 % GC. Sequences from plasma samples have a tight peak at 25 % GC, while serum samples show a peak at 45 % GC. Sequences generated from exosome extracts (from plasma or serum) show extreme values of GC content, with a majority of sequences having very low (<20 %) or high (70 %) GC content. The metrics of STAR mapping to the *Sus scrofa* reference genome are different regarding blood compartments (Fig. 2D). Sequences produced from whole blood show the best unique mapping rate (73 to 79 %). Plasma has lower unique mapping rates



**Fig. 3.** Gene biotypes proportion per sample. (A) The proportion of gene biotypes in each sample is expressed as a percentage of the total counts per gene biotype. (B) The proportion of globin transcripts in each sample is expressed as a percentage of counts per million (CPM) for each globin family gene. Samples RS1030\_T3\_01 to 04 are serum samples. Samples RS1030\_T3\_05 to 08 correspond to plasma. Samples RS1030\_T3\_09 to 12 correspond to exosomes derived from serum. Samples RS1030\_T3\_13 to 16 correspond to exosomes derived from plasma. And samples RS1030\_T3\_17 to 20 correspond to whole blood extracts.

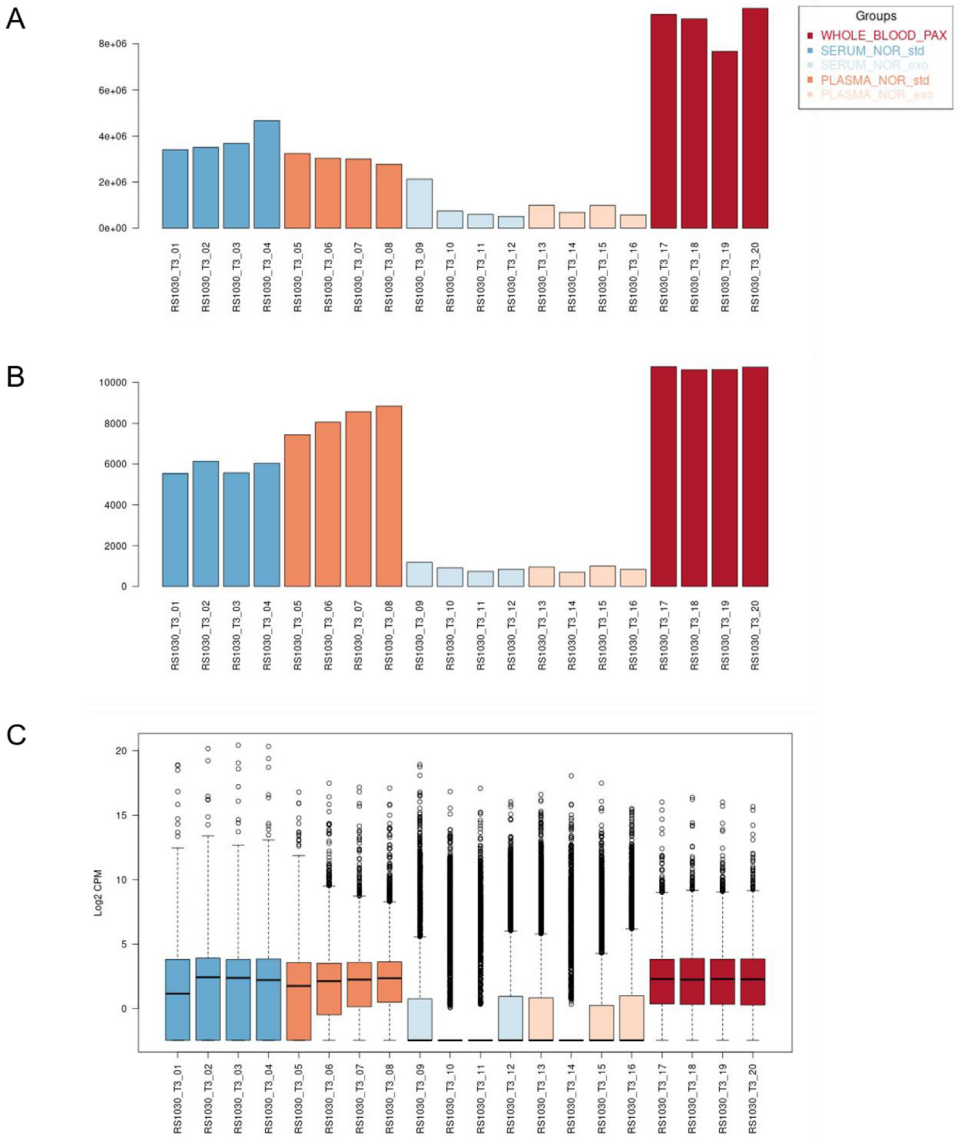
(approximately 60%), and serum has 30 to 40% unique mapping. Exosomes samples show very low mapping rates, about 10% regardless of the source (plasma or serum). The coverage profile of sequenced reads along genes shows an enrichment of reads mapping to 3' ends for whole blood samples (Fig. 2E). In other blood subcompartments, the mapping profiles do not show a marked enrichment in the 3' end region (Fig. 2F), although plasma samples do exhibit a slight bias at the 3' ends.

### 3.4. Exploration of gene expression diversity

The raw count matrix resummed by gene obtained with STAR\_salmon quantification contains 35,670 rows (genes) and 20 columns (individuals). The total of counts resummed by gene biotype for each sample are illustrated in Fig. 3A. The majority of counts (>75%) obtained for serum samples (samples RS1030\_T3\_01 to 04) correspond to ribosomal RNA (rRNA), while the remaining correspond to messenger RNA (mRNA). In contrast, plasma samples (samples 05 to 08) produced more mRNA counts, with approximately 55% of total counts. These plasma extracts also yielded 25–30% of mitochondrial ribosomal RNA (Mt rRNA) and approximately 15% rRNA. RNA extracts of exosomes derived from serum (samples 09 to 12) or plasma (samples 13 to 16) produced roughly the same proportions of gene biotypes counts: 50–60% of mRNA, 15–25% of long non-coding RNA (lncRNA), and variable proportions of rRNA and Mt rRNA. Finally, the whole blood extracts (samples 17 to 20) produced a majority of mRNA (about 75%), 20% of rRNA, and small amounts of lncRNA.

As whole blood RNA extracts are known to be very rich in globin transcripts (up to 80%), we used a globin blocking procedure to limit the proportion of globin reads in these samples in order to increase the detection of other transcripts expressed at lower levels. Fig. 3B illustrates the proportion of counts per million (CPM) corresponding to globin genes in each sample. We can see that the counts attributed to globin genes represent around 20% of CPM in whole blood

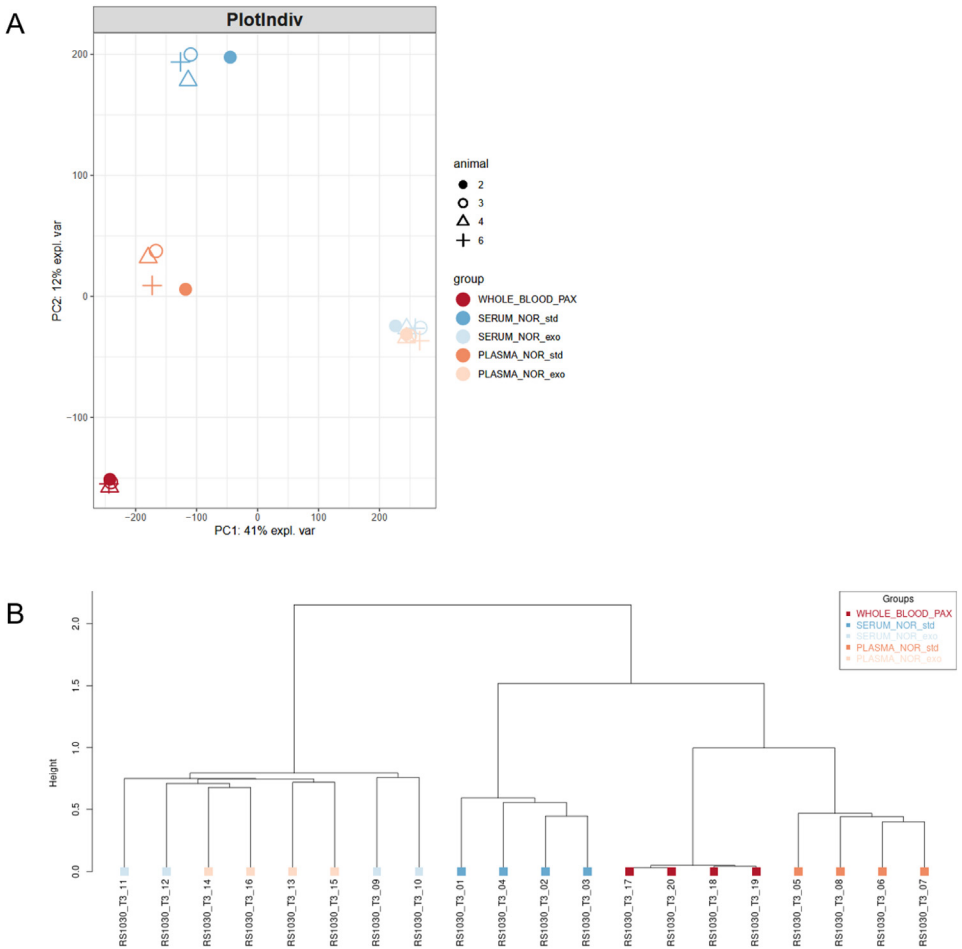




**Fig. 4.** Gene detection and expression distributions. (A) The total counts for each sample are summarized as bar charts coloured by compartment. (B) The number of genes detected with >10 counts is illustrated as coloured bar charts. (C) The global log<sub>2</sub> CPM distributions of each sample are illustrated as coloured boxplots. Legend: Serum - blue, Plasma - orange, serum-derived exosomes - light blue, plasma-derived exosomes - light orange, whole blood - dark red.

samples, with the HBA1 gene contributing the most. This proportion is in accordance with what was expected. In other extracts (serum, plasma, and exosomes), the proportion of globin genes is below 5 %, except for two serum-derived exosome samples (approximately 10 % of CPM) and one plasma-derived exosome sample (about 7 %).

Although the libraries from the five compartments were multiplexed at the same molarities, the number of reads assigned to genes varies from one compartment to another (Fig. 4A). Whole blood samples produced >8 million reads per sample, while serum and plasma extracts



**Fig. 5.** Multivariate data exploration. (A) Projection of individuals on the first two components (PC1 and PC2) of the principal component analysis performed on TMM normalized log<sub>2</sub> CPM expression values. (B) Dendrogram illustrating the hierarchical clustering of samples (Ward method) according to their gene expression correlation distance (1 - Pearson correlation coefficient).

produced, on average, 3 to 4 million reads. In contrast, exosome extracts from serum or plasma produced less than one million read counts, except for sample 09, which accounted for 2 million.

The number of genes detected per sample is contrasted regarding the compartment extracts (Fig. 4B). An average of 10,000 genes are detected in the whole blood compartment, when only 1000 genes are detectable in exosome extracts. Almost 8000 genes are measured in plasma, but 6000 are detected in serum samples.

The boxplots illustrating the global gene expression distributions (Fig. 4C) indicate a classical distribution pattern of log CPM for whole blood samples. Plasma samples exhibit a classical distribution but slightly skewed toward lower values, and serum log CPM are more skewed than plasma indicating more genes with lower counts. However, log CPM values of exosome samples are extremely skewed toward low values, with more than approximately 70 % of the distribution under a log CPM value of zero.

A principal component analysis (PCA) was performed to explore the sources of variability in normalized expression data (Fig. 5A). The first source of variability (principal component 1,

explaining 41 % of the variance) distinguishes between exosome extracts and other sample types. The second component (PC2 explaining 12 % of the total variance) separates serum from whole blood extracts. The hierarchical clustering (Fig. 5B) indicates that the plasma samples are closer to the whole blood extracts, together forming a cluster with the serum samples. This cluster is distant from a second cluster composed of the exosome extracts, with no distinction made between the source compartment (plasma or serum).

Regarding the gene expression data acquired on these five blood subcompartments, exosome-derived compartment seems to generate limited information and may require further investigation. Nevertheless, bioinformatic and statistical analyses confirm that these RNA-Seq data are suitable for investigating complex molecular mechanisms across different blood compartments using differential expression analysis.

RNA-Seq raw FASTQ and processed data are available in the ArrayExpress database (<http://www.ebi.ac.uk/arrayexpress>) under accession number E-MTAB-16252. These data can be reused by the community interested in gene expression analysis of RNA samples collected from blood and are useful to assess detectable transcripts by the 3' mRNA-Seq protocol applied to distinct blood compartments of piglets.

## 4. Experimental Design, Materials and Methods

Several tests of RNA extraction and library preparation were performed on the samples, but only the protocols actually used to produce the dataset presented are reported here.

### 4.1. Sample collection

Samples were collected from four 5-week-old crossbred female piglets (Duroc DanBred X Hybride DanBred). Animal experimentation procedures were approved by the Ethics Committee of Pharmacology-Toxicology Occitanie-Toulouse, Toxcom 310 LSV, in accordance with the European Directive on the protection of animals used for scientific purposes (2010/63/EU). The animals were acclimatized for one week in the animal facility, then euthanized by electronarcosis before exsanguination, during which blood samples were collected.

#### 4.1.1. Whole blood samples

Approximately 2.5 ml of fresh whole blood was collected from each animal in a PAXgene® RNA Blood tube (QIAGEN, Cat. No. 762,165). The tubes were then homogenised 10 times by inversion and left at room temperature for two hours. Then, they were frozen at  $-20^{\circ}\text{C}$  overnight before being stored at  $-80^{\circ}\text{C}$  until extraction.

#### 4.1.2. Plasma samples

Approximately 4 ml of fresh whole blood was collected from each animal in tubes containing EDTA anticoagulant (OZYME, Cat. No. BD367862). The tubes were homogenised 10 times by inversion and placed on melting ice until centrifugation at 2000 g for 10 min at  $4^{\circ}\text{C}$  (within two hours of collection). Four to six tubes were collected for each animal. After centrifugation, the plasma from each tube was pooled, homogenised and then divided into aliquots for future extractions.

#### 4.1.3. Serum samples

Approximately 4 ml of fresh whole blood was collected from each animal in clot activator tubes (OZYME, Cat. No. BD365904). The tubes were then homogenised 10 times by inversion and left at room temperature for 30 min before being centrifuged at 1300 g for 10 min at room temperature. Four to six tubes were collected for each animal. After centrifugation, the serum from each tube was pooled, homogenised and divided into aliquots for future extractions.

Collection information for each sample is detailed in Table 3.

**Table 3**

Samples description.

Sample dataset	Animal	Sampling date	Sample type	Collection volume (ml)	Extraction method	Extraction volume (ml)
1	2	2023/10/03	SERUM	3.6	NORGEN standard	0.2
2	6	2023/10/05	SERUM	6.6	NORGEN standard	0.2
3	3	2024/04/10	SERUM	7.3	NORGEN standard	0.2
4	4	2024/04/10	SERUM	8.5	NORGEN standard	0.2
5	2	2023/10/03	PLASMA	7.6	NORGEN standard	0.2
6	6	2023/10/05	PLASMA	7.4	NORGEN standard	0.2
7	3	2024/04/10	PLASMA	9.1	NORGEN standard	0.2
8	4	2024/04/10	PLASMA	10.6	NORGEN standard	0.2
9	2	2023/10/03	SERUM	3.6	NORGEN exosome	1
10	6	2023/10/05	SERUM	6.6	NORGEN exosome	1
11	3	2024/04/10	SERUM	7.3	NORGEN exosome	1
12	4	2024/04/10	SERUM	8.5	NORGEN exosome	1
13	2	2023/10/03	PLASMA	7.6	NORGEN exosome	1
14	6	2023/10/05	PLASMA	7.4	NORGEN exosome	1
15	3	2024/04/10	PLASMA	9.1	NORGEN exosome	1
16	4	2024/04/10	PLASMA	10.6	NORGEN exosome	1
17	2	2023/10/03	WHOLE_BLOOD	2.5	PAXGENE	2.5
18	6	2023/10/05	WHOLE_BLOOD	2.5	PAXGENE	2.5
19	3	2024/04/10	WHOLE_BLOOD	2.5	PAXGENE	2.5
20	4	2024/04/10	WHOLE_BLOOD	2.5	PAXGENE	2.5

## 4.2. RNA extraction

### 4.2.1. Whole blood RNA extraction

Total RNA was extracted using the PAXgene® Blood RNA Kit (QIAGEN, Cat. No. 762164), following the manufacturer's instructions (manual protocol).

### 4.2.2. Serum/plasma RNA extraction

Plasma and serum total RNA extractions were performed using the Plasma/Serum RNA Purification Mini Kit (NORGEN, Cat. No. 55000) following the manufacturer's instructions and using 200 µL of plasma or serum per sample.

### 4.2.3. Serum/plasma exosomes RNA extraction

Exosome purification was performed on 1 ml aliquots of plasma or serum using Plasma/Serum Exosome Purification Mini Kit (NORGEN, Cat. No. 57400), following the manufacturer's instructions. Next, 200 µL of the previously obtained exosomes were used to extract exosomal RNA using the Exosomal RNA Isolation Kit (NORGEN, Cat. No. 58000), again following the manufacturer's instructions.

**Table 4**  
Summary cDNA library preparation.

Sample Type	RNA Extraction Method	RNA Input	PCR Cycles	Protocol Library	RNA Removal
Whole Blood	PAXgene	200 ng	17	Standard input	RS-Globin Block, <i>Sus scrofa</i> Standard
Serum and Plasma	NORGEN Standard	5 µl	21	Low input / low quality	Standard
Exosome (Serum/Plasma)	NORGEN Exosome	5 µl	26	Low input / low quality	Standard

After extractions, samples were quantified using the DropSense 96 system (Trinean, Unchained Labs). RNA from whole blood samples were diluted to a concentration of 100ng/µl, while pure RNA extracts were used for other blood fractions. RNA integrity numbers (RIN) were assessed on whole blood RNA samples using RNA ScreenTape Assay on the TapeStation 4200 System (Agilent technologies, Santa Clara, USA).

Information on extraction conditions for each sample is detailed in [Table 3](#).

#### 4.3. cDNA library preparation

Library preparation was performed at the Genotoul Genomics Facility GeT-TRiX (<https://doi.org/10.15454/1.5572370921303193E12>). RNA libraries were prepared according to Lexogen's protocols using the QuantSeq 3' mRNA-Seq V2 Library Prep Kit FWD with 12-nt Unique Dual Indices (UDI) (Lexogen, Austria, Cat. No. 192.24). Multiple experiments were conducted according to the specific characteristics of blood compartments and under experimentally adapted conditions, as summarised in [Table 4](#).

For whole blood samples, RNA-Seq libraries were generated from 200 ng of total RNA, following the manufacturer's standard input protocol with the RNA Removal Solution Globin Block, *Sus scrofa* (RS-GBSs, Cat. No. 071). The first-strand cDNA was synthesized by reverse transcription with oligo-dT priming. Before second-strand synthesis, RS-GBs containing porcine globin-specific oligonucleotide mixtures were used to selectively bind globin mRNA-derived cDNA strands and prevent their extension during second-strand synthesis initiated by random priming. Double-stranded cDNA fragments were indexed with UDI and amplified with seventeen PCR cycles.

For serum, plasma, and exosome samples, libraries were prepared from 5 µl of total RNA following the manufacturer's low-input/low-quality protocol. First-strand cDNA synthesis was performed using oligo-dT priming, and the standard RNA Removal Solution was applied before second-strand synthesis, initiated by random priming. Double-stranded cDNA fragments were indexed with UDI and amplified with twenty-one PCR cycles for standard serum and plasma samples, and twenty-six PCR cycles for exosomes derived from serum or plasma.

Library yield and quality were assessed using D1000 ScreenTape Assay on TapeStation 4200 system (Agilent Technologies, Santa Clara, USA).

#### 4.4. Illumina sequencing

Libraries were multiplexed at equimolar concentrations and transferred to the INRAE PGTB sequencing facility (doi :10.15454/1.5572396583599417E12). The pool of 20 libraries was loaded into a P2 Flow Cell using NextSeq 1000/2000 XLEAP-SBS P2 Reagent kit (100 Cycles), with 10 % of PhiX spike-in to compensate for low diversity expected in serum/plasma samples. Sequencing was performed using single-end 76 bp reads on the Illumina NextSeq 2000 Sequencing System (Illumina, USA).

#### 4.5. Bioinformatic alignment and gene expression quantification

Bioinformatic treatment of sequencing data was performed by the GeT-TRIX facility (Genotoul, Genopole Toulouse Midi-Pyrénées) using the computing resources of Genotoul bioinformatics platform Toulouse Midi-Pyrenees (Bioinfo Genotoul). The analysis pipeline was executed with Nextflow v23.10.0 [2] and processed using nf-core/rnaseq v3.14.0 (<https://doi.org/10.5281/zenodo.10471647>) of the nf-core collection of workflows [3], utilizing reproducible software environments from the Bioconda [4] and Biocontainers [5] projects. Extra parameters were adapted to 3' mRNA-seq reads: `-extra_star_align_args '-alignIntronMax 1000,000 -alignIntronMin 20 -alignMatesGapMax 1000,000 -alignSjoverhangMin 8 -outFilterMismatchNmax 999 -outFilterMultimapNmax 20 -outFilterType BySjout -outFilterMismatchNoverLmax 0.1 -clip3pAdapterSeq AAAAAAAA'`. Reads were aligned to pig genome reference Sscrofa11.1 (build GCA\_000003025.6), and the quantification of reads was resumed to genes defined in Ensembl release 112 annotation. Finally, the pipeline produced a gene count matrix, which is available for statistical exploration analysis. Quality control of sequencing reads and sequence alignments was performed using FastQC and QualiMap software executed in Nextflow nf-core/rnaseq pipeline and the metrics were summarised by MultiQC tool.

#### 4.6. Bioinformatic software versions

Software versions used for bioinformatic analyses.

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Cutadapt, version 3.4  
FastQC, version 0.12.1  
Nextflow, version 23.10.0  
nf-core/rnaseq, version 3.14.0  
QualiMap, version 2.3  
RSeQC, version 5.0.2  
Salmon, version 1.10.1  
Samtools, version 1.16.1  
STAR, version 2.7.9a  
Subread, version 2.0.1  
Trim Galore, version 0.6.7

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#### 4.7. Biostatistics gene expression exploration

Biostatistics analyses were performed under R v 4.3.0 [6], edgeR [7], limma [8], and Bioconductor packages [9] as described in ArrayExpress accession E-MTAB-16252. Briefly, raw count table was filtered to eliminate undetected genes using filterByExpr function with `min.count=10`. Normalization factors were calculated using trimmed mean of M values method (TMM). Then the common, trended and tagwise negative binomial dispersions were estimated with the robust mode of estimateDisp function.

### Limitations

The library preparation protocol applied in this study is not specifically recommended or optimized for serum and plasma samples. To achieve sufficient yield for sequencing, the number of PCR cycles was increased for libraries derived from exosome samples, which may introduce amplification-related biases. Additionally, the incomplete or poor annotation of the porcine genome can result in non-standard or unconventional metrics, potentially affecting downstream data quality assessments.

## Ethics Statement

Experiments complied with the ARRIVE guidelines and were carried out in accordance with the EU Directive 2010/63/EU for animal experiments. This study was conducted on female animals only, and sex did not influence the descriptive results.

## CRedit Author Statement

**Gaëlle Payros:** Supervision, Methodology, Validation, Writing, Original draft, Formal analysis; **Kory Jason:** Bioinformatic Software; **Laure Gress:** Methodology, Validation, Writing; **Maëlle Gusmini:** Methodology, Validation; **Laurence Liaubet:** Conceptualization, Formal analysis, Writing; **Yannick Lippi:** Conceptualization, Methodology, Formal analysis, Writing.

## Declaration of Generative AI and Ai-assisted Technologies IN the Manuscript Preparation Process

During the preparation of this work the authors used DeepL (<https://www.deepl.com>) TRANSLATOR and WRITE tools as an aid in translating and rephrasing parts of the text. The authors used Microsoft Copilot software in order to help structure and summarize few paragraphs. After using these tools, the authors reviewed and edited the content as needed and take full responsibility for the content of the published article.

## Data Availability

3' mRNA sequencing of piglet blood compartments (Original data) (ArrayExpress).

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## Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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