

# Low numbers of pre-leukemic fusion genes are frequently present in umbilical cord blood without affecting DNA damage response

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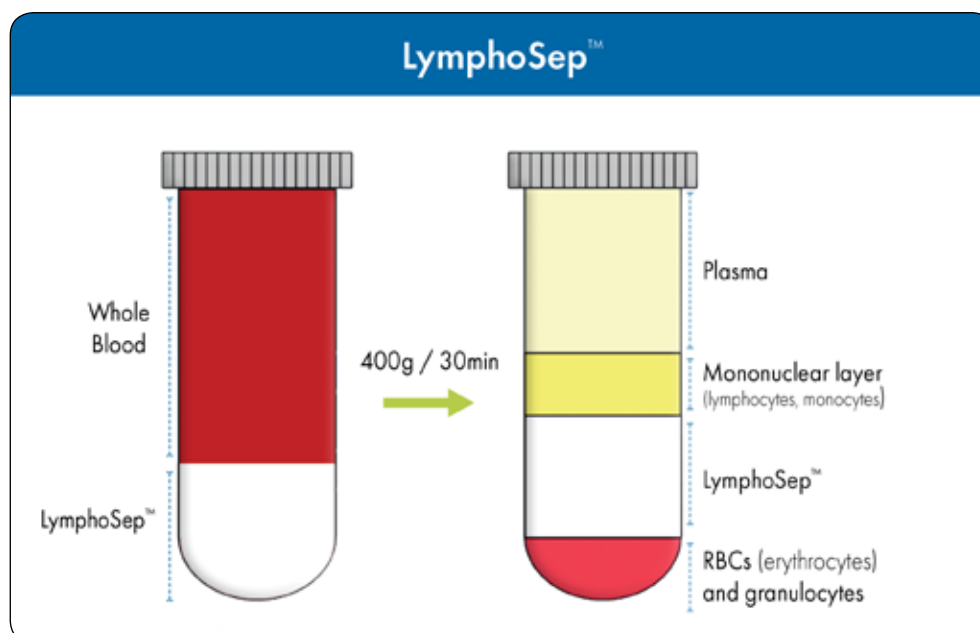
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### Introduction

It is widely accepted that many childhood leukemias may originate during embryonic/fetal development from hematopoietic stem/progenitor cells (HSPC) with pre-leukemic fusion genes (PFG). However, the data on PFG incidence in newborns remains contradictory. To gain a better understanding of the prenatal origins of leukemia, a study was conducted to screen for the presence of the most frequent PFGs associated with pediatric B-cell acute lymphoblastic leukemia (B-ALL). Umbilical cord blood from newborns was collected and MNCs with high yield and viability were isolated using LymphoSep™ separation media from MP Bio.

### Overview

- **Keyword:** Pre-leukemic fusion genes, stem cells, DNA damage response, apoptosis, acute lymphoblastic leukemia (ALL)
- **Aim of the study:** To better understand the prenatal origin of pediatric B-cell acute lymphoblastic leukemia (ALL)
- **Application:** RT-qPCR
- **Sample name:** Mononuclear cells (MNC) from umbilical cord blood (UCB)
- **Material:** LymphoSep™ - Lymphocyte Separation Medium (SKU 0916922) from MP Bio



**Figure 1.**

Isolation of mononuclear cells from whole blood using LymphoSep™ density separation medium.

# CASE STUDY

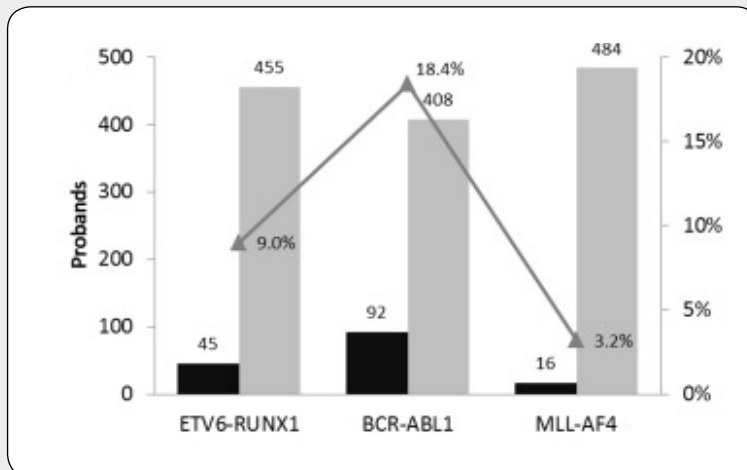
## Protocol and Parameters

1. 80 - 100 mL of umbilical cord blood was collected from 300 newborns.
2. MNC were isolated from UCB within 24 hours from birth using LymphoSep™.
3. Number of cells was assessed using autohematology analyzer.
4. Isolated UCB MNC pellets, (~10<sup>7</sup> MNC), were then frozen and stored in liquid nitrogen before analysis.

## Conclusion

- LymphoSep™ was used in the initial stages of this study to isolate mononuclear cells from umbilical cord blood obtained from newborns.

The researchers were able to demonstrate that low numbers of PFGs do not correlate with impaired DNA damage response in HSPC or lymphocytes. However, high PFG copy numbers arising during specific time frames within the hematopoietic stem cell hierarchy may serve as an important prognostic tool for assessing the potential for ALL.



**Figure 2.**

The number of probands tested for PFG in 500 primary RT-qPCR runs. The incidence of PFG positive probands is displayed as a percentage.

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