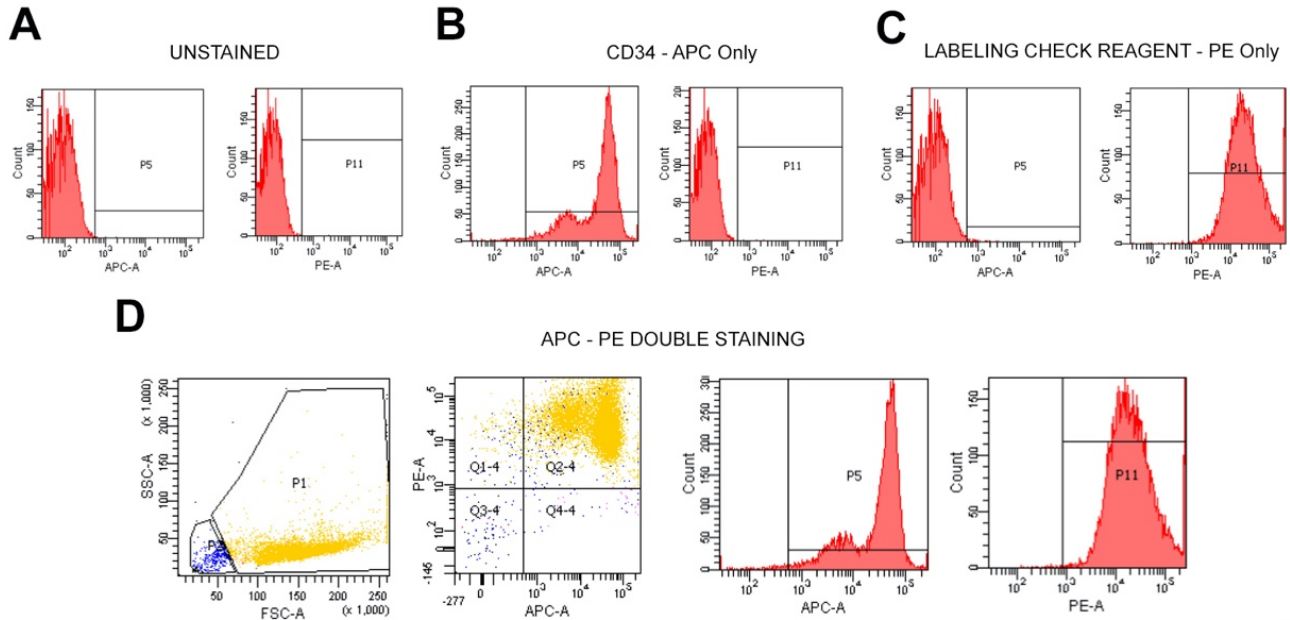


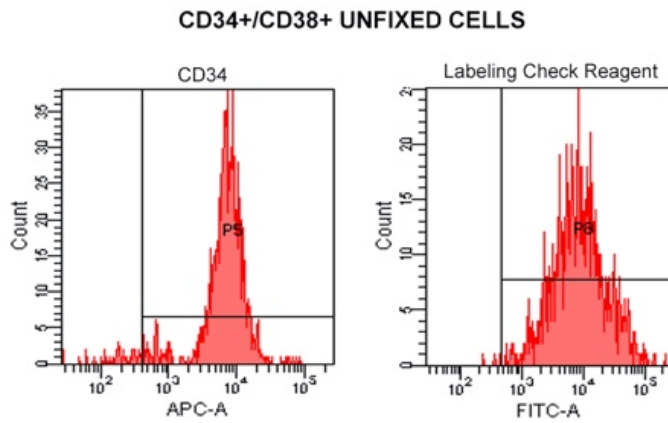
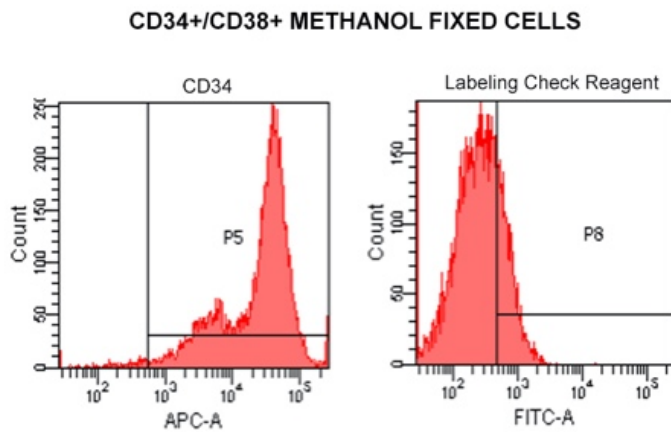
**"Genomic Analysis of hematopoietic stem cell at the Single-Cell Level: optimization of cell fixation and Whole Genome Amplification (WGA) protocol" By Carretta and Mallia et al,**

**SUPPLEMENTARY MATERIAL**

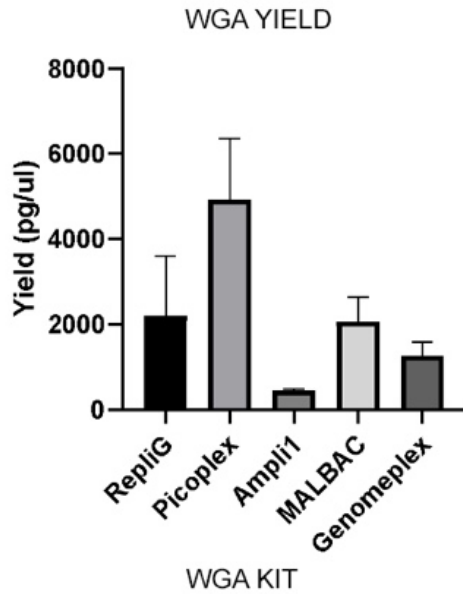
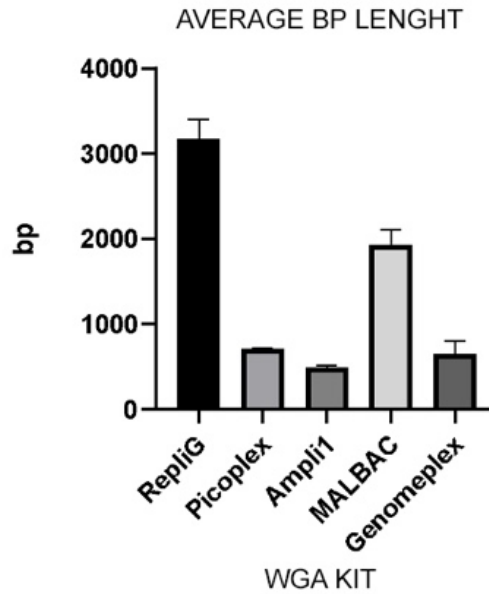


**Figure S1**

**Figure S1.** Cytofluorimetric controls referring to CD34-APC/Labeling check reagent-PE immunostaining. **(A)** Unstained control of unfixed CD34+CD38+ cells. **(B)** CD34-APC single staining performed on unfixed CD34+/CD38+ cells. **(C)** Labeling check reagent-PE single staining performed on unfixed CD34+/CD38+ cells. **(D)** CD34-APC/Labeling check reagent-PE double staining performed on unfixed CD34+CD38+ cells.

**A****B****Figure S2**

**Figure S2.** Cytofluorimetric analysis of CD34-APC/Labeling check reagent-FITC immunostaining. **(A)** Double staining performed on unfixed CD34+/CD38+ cells. **(B)** Double staining performed on 100% MetOH fixed CD34+/CD38+ cells.

**A****B****Figure S3**

**Figure S3.** Comparison of WGA yield and average fragment length of the different WGA kits. **(A)** Analysis of the WGA yield of PFA 0.5% 15' fixed K562 cells subjected to WGA with five different WGA kits (n=5 for each kit). **(B)** Analysis of the average length of the genomic fragments coming from PFA 0.5% 15' fixed K562 cells subjected to WGA with five different WGA kits (n=5 for each kit). Data are shown as mean  $\pm$  SEM.