# Supplementary File 1 for:

## Genome-scale DNA methylome and transcriptome profiling of human neutrophils

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## Supplementary Figures S1 – S10.

## Supplementary Tables S1.

## Supplementary Figures

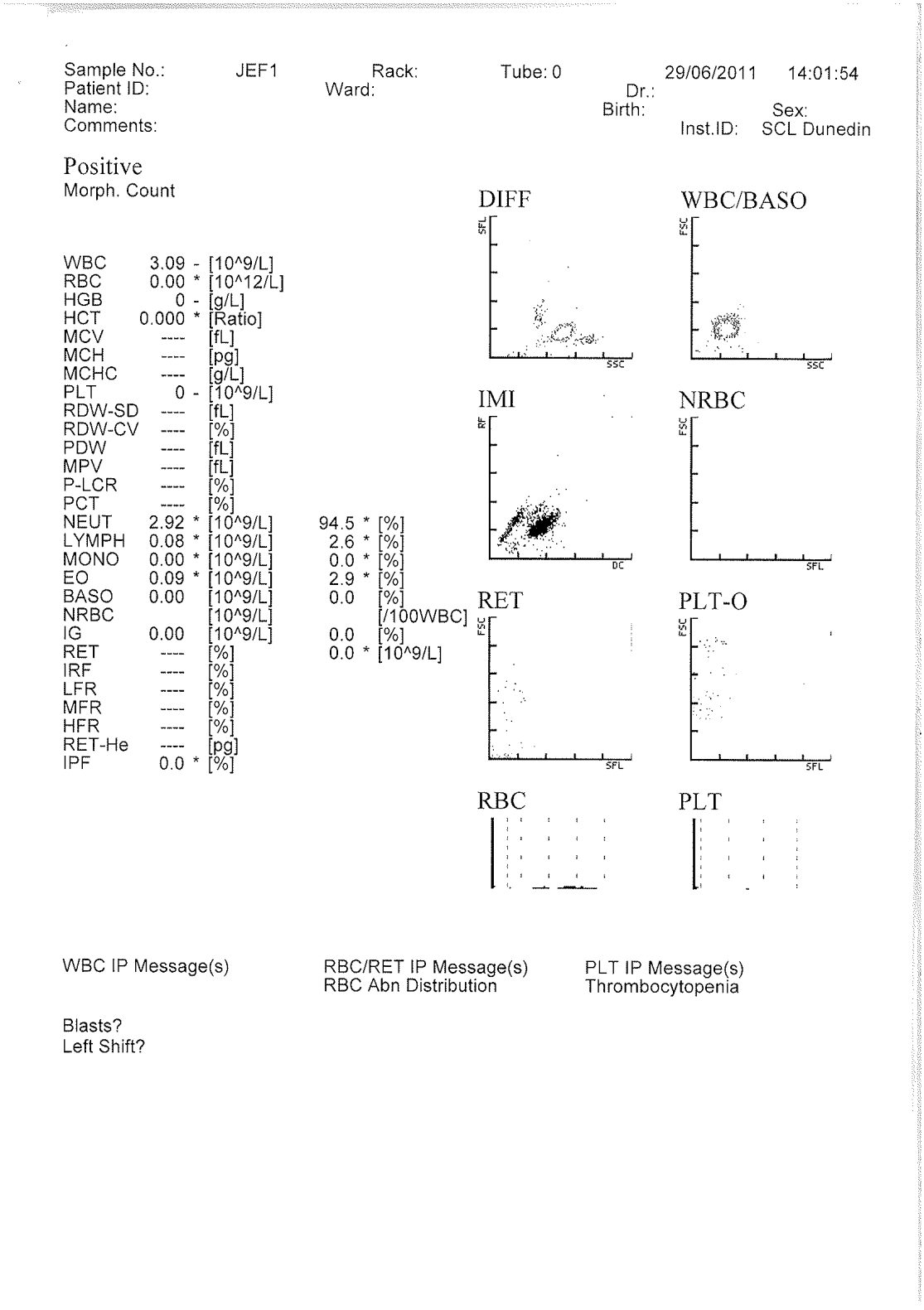



**Fig. S1: Whole blood cell count of X9010 sample before enrichment as a representative example.** 200 µL of peripheral blood was used to count the cells in XE2100 Haematology Analyser. NEUT represents neutrophils. The percentage of neutrophils was 37.2% in peripheral blood before enrichment.

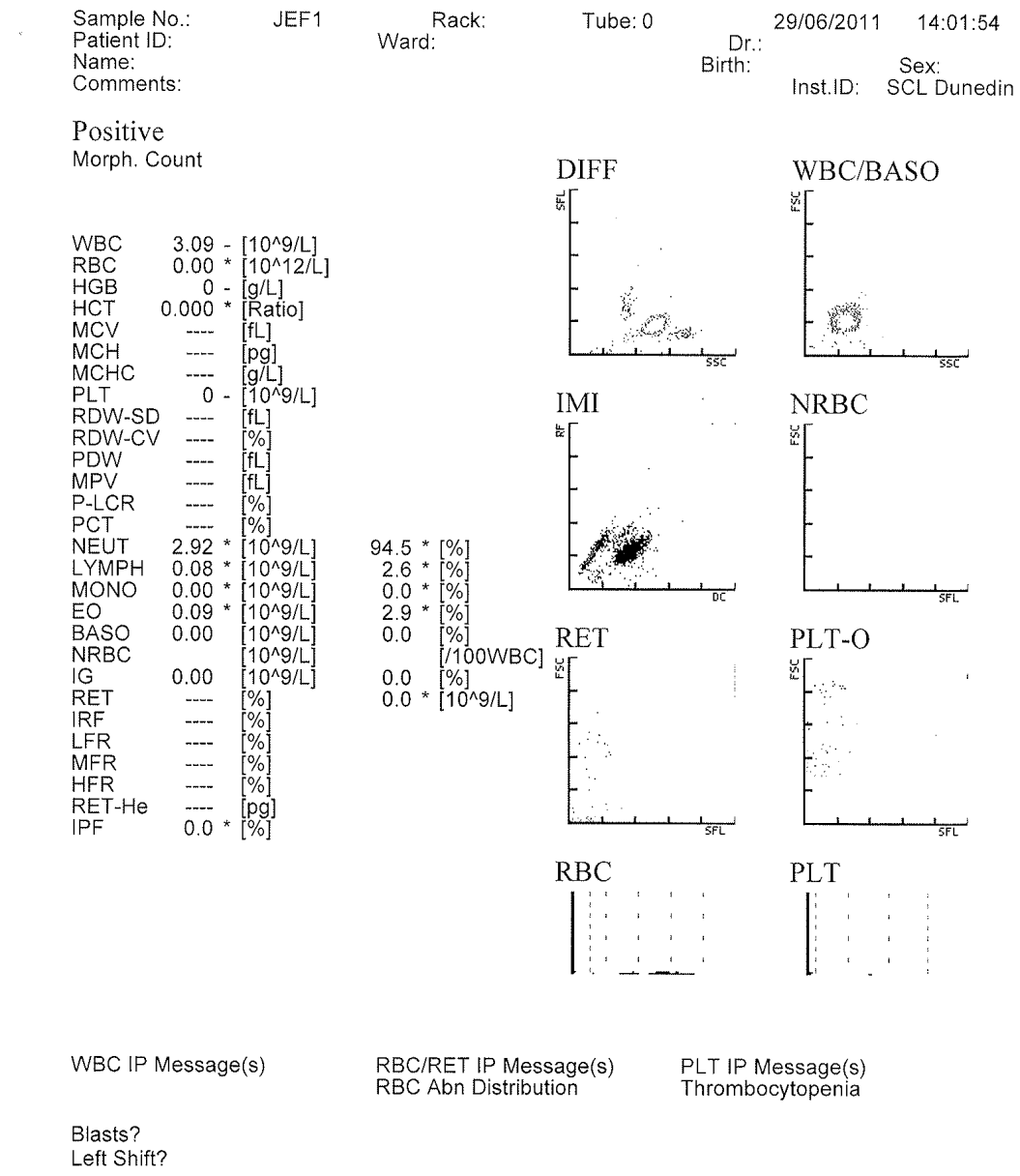



**Fig. S2: Whole blood cell count of X9010 sample after enrichment as a representative example.** 200 µL of peripheral blood was used to count the cells in XE2100 Haematology Analyser. NEUT represents neutrophils. The percentage of neutrophils was 94.2% in peripheral blood after enrichment.

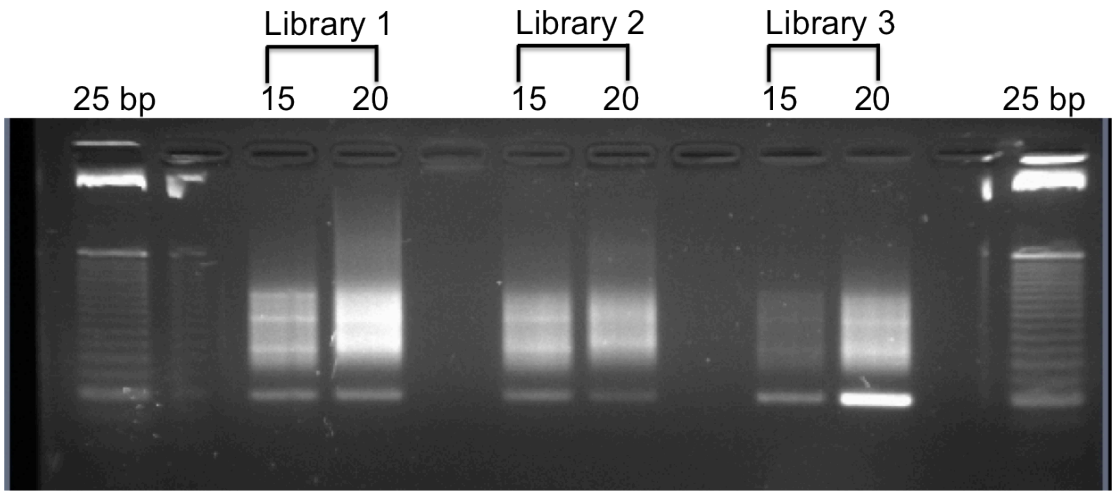



**Fig. S3: Example of three successful RRBS libraries prepared following the described protocol in the manuscript.** Three different RRBS libraries (X9012, X9014 and X9016) were amplified after bisulfite conversion with 15 and 20 PCR cycles and electrophoresed in 3% nusieve gel for 90 minutes (50 volts). Ladder: 25 bp (Invitrogen).

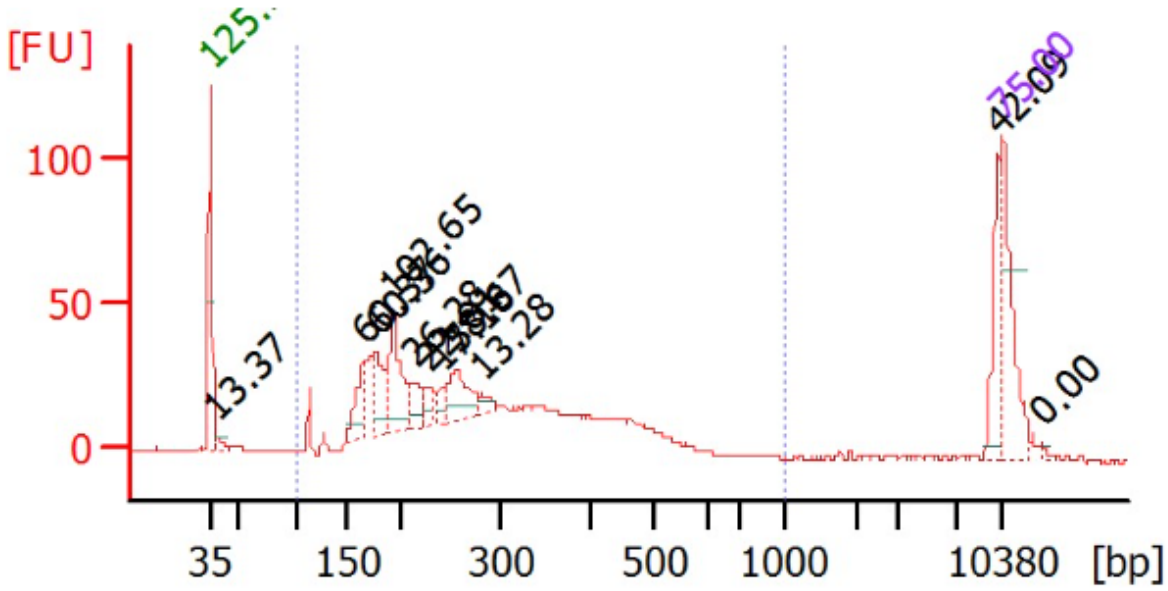



**Fig. S4: A representative bioanalyzer electropherogram of a sequenced RRBS library.** The prepared RRBS library was run on an Agilent 2100 Bioanalyzer using the high sensitivity DNA kit to determine the quality of the samples. The electropherogram displays a plot of fragment size in the x-axis (bp) versus fluorescence intensity (fluorescence units, FU) in y-axis. Peaks at 35 bp and 10380 bp represent lower and upper markers. The 150- 330 bp peaks represent the RRBS library (size after ligation of the adaptor, this corresponds to the actual size of 40-220 bp DNA fragments).

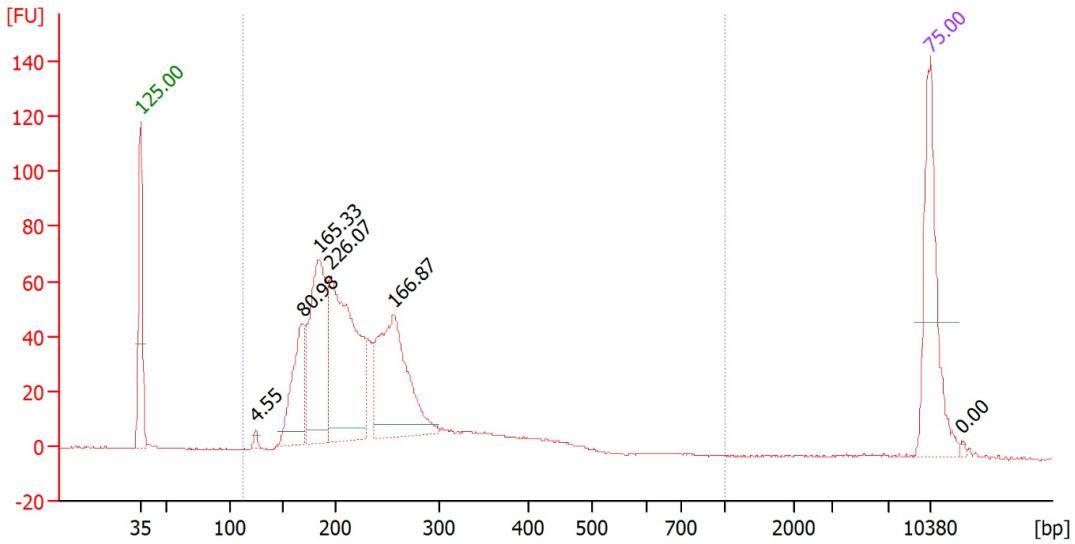
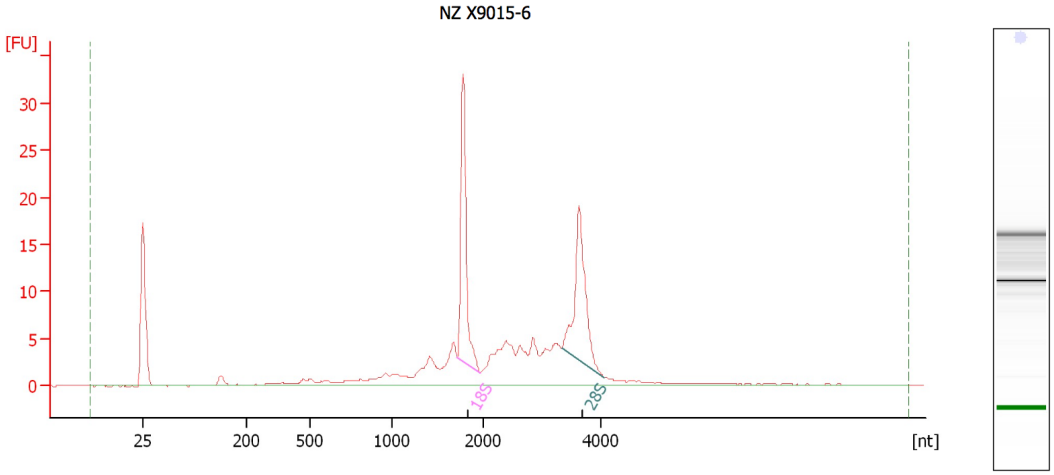



**Fig. S5: A representative bioanalyzer electropherogram of a sequenced RRBS library.** The prepared RRBS library was run on an Agilent 2100 Bioanalyzer using the high sensitivity DNA kit to determine the quality of the samples. The electropherogram displays a plot of fragment size in the x-axis (bp) versus fluorescence intensity (fluorescence units, FU) in y-axis. Peaks at 35 bp and 10380 bp represent lower and upper markers. The 150- 330 bp peaks represent the RRBS library (size after ligation of the adaptor, this corresponds to the actual size of 40-220 bp DNA fragments).



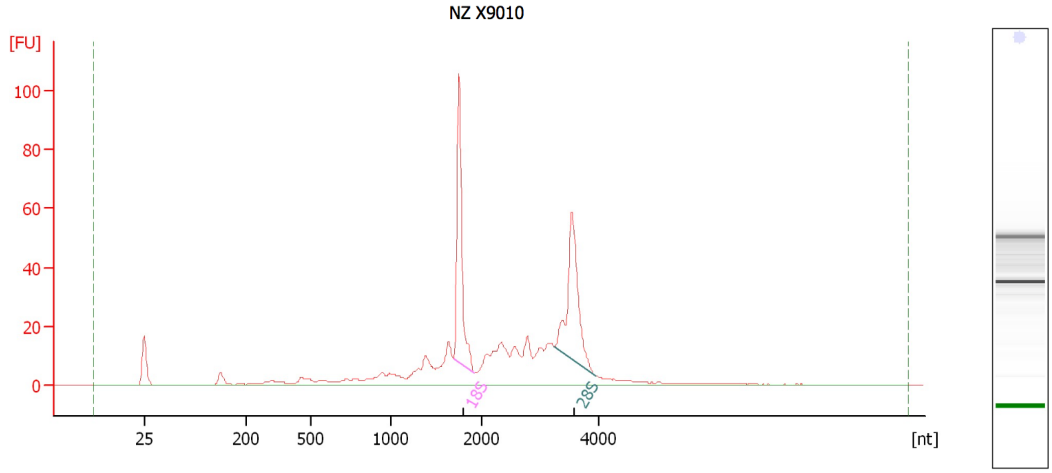

**Overall Results for sample 4 : NZ X9015-6**

| | | | |
|---|---|---|---|
| RNA Area: | 147.5 | RNA Integrity Number (RIN): | 7.9 (B.02.08) |
| RNA Concentration: | 58 ng/µl | Result Flagging Color: | |
| rRNA Ratio [28s / 18s]: | 1.0 | Result Flagging Label: | RIN: 7.90 |

**Fragment table for sample 4 : NZ X9015-6**

| Name | Start Size [nt] | End Size [nt] | Area | % of total Area |
|---|---|---|---|---|
| 18S | 1,716 | 1,960 | 25.7 | 17.4 |
| 28S | 3,321 | 4,047 | 24.7 | 16.7 |

**Fig. S6: Bioanalyzer electropherogram of X9015 RNA-Seq library.** The prepared RRBS library was run on an Agilent 2100 Bioanalyzer using the high sensitivity RNA nano kit (from Agilent) to determine the quality of the samples. The electropherogram displays a plot of fragment size in the x-axis (nt) versus fluorescence intensity (fluorescence units, FU) in y-axis. RNA Integrity Number (RIN) is shown below in the figure. Further, RNA concentration, and ratio of different RNA submits are shown.



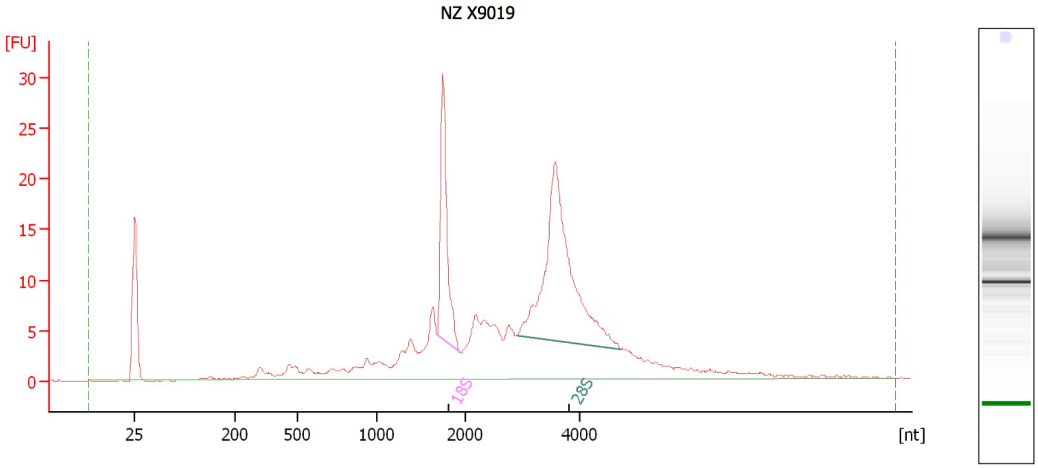

**Overall Results for sample 7 : NZ X9010**

| | | | |
|---|---|---|---|
| RNA Area: | 462.3 | RNA Integrity Number (RIN): | 7.8 (B.02.08) |
| RNA Concentration: | 183 ng/µl | Result Flagging Color: | |
| rRNA Ratio [28s / 18s]: | 0.9 | Result Flagging Label: | RIN: 7.80 |

**Fragment table for sample 7 : NZ X9010**

| Name | Start Size [nt] | End Size [nt] | Area | % of total Area |
|---|---|---|---|---|
| 18S | 1,686 | 1,922 | 85.0 | 18.4 |
| 28S | 3,240 | 3,956 | 75.3 | 16.3 |

**Fig. S7: Bioanalyzer electropherogram of X9010 RNA-Seq library.** The prepared RRBS library was run on an Agilent 2100 Bioanalyzer using the high sensitivity RNA nano kit (from Agilent) to determine the quality of the samples. The electropherogram displays a plot of fragment size in the x-axis (nt) versus fluorescence intensity (fluorescence units, FU) in y-axis. RNA Integrity Number (RIN) is shown below in the figure. Further, RNA concentration, and ratio of different RNA submits are shown.



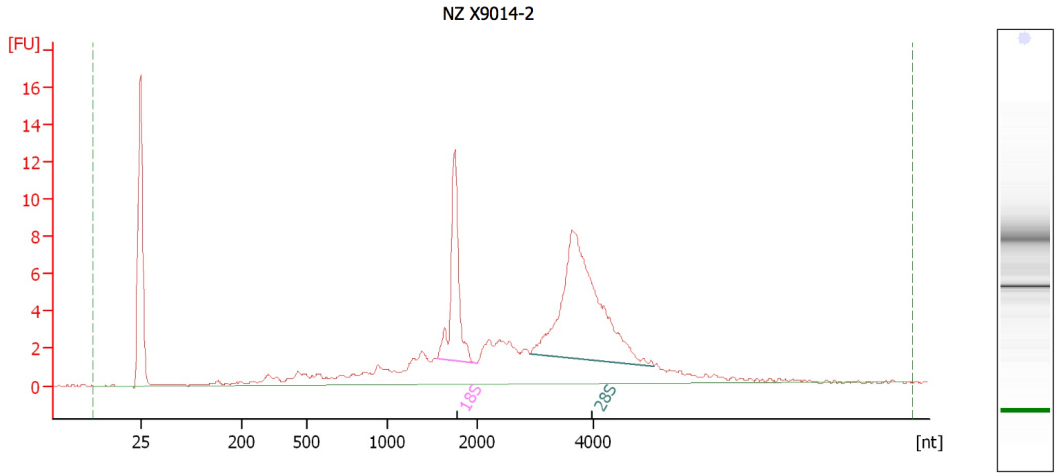

**Overall Results for sample 10 : NZ X9019**

| | | | |
|---|---|---|---|
| RNA Area: | 258.9 | RNA Integrity Number (RIN): | 8.2 (B.02.08) |
| RNA Concentration: | 103 ng/µl | Result Flagging Color: | |
| rRNA Ratio [28s / 18s]: | 2.4 | Result Flagging Label: | RIN: 8.20 |

**Fragment table for sample 10 : NZ X9019**

| Name | Start Size [nt] | End Size [nt] | Area | % of total Area |
|---|---|---|---|---|
| 18S | 1,678 | 1,944 | 27.9 | 10.8 |
| 28S | 2,893 | 4,723 | 66.6 | 25.7 |

**Fig. S8: Bioanalyzer electropherogram of X9019 RNA-Seq library.** The prepared RRBS library was run on an Agilent 2100 Bioanalyzer using the high sensitivity RNA nano kit (from Agilent) to determine the quality of the samples. The electropherogram displays a plot of fragment size in the x-axis (nt) versus fluorescence intensity (fluorescence units, FU) in y-axis. RNA Integrity Number (RIN) is shown below in the figure. Further, RNA concentration, and ratio of different RNA submits are shown.




**Overall Results for sample 9 : NZ X9014-2**

| | | | |
|---|---|---|---|
| RNA Area: | 118.8 | RNA Integrity Number (RIN): | 8.9 (B.02.08) |
| RNA Concentration: | 47 ng/µl | Result Flagging Color: | |
| rRNA Ratio [28s / 18s]: | 2.5 | Result Flagging Label: | RIN: 8.90 |

**Fragment table for sample 9 : NZ X9014-2**

| Name | Start Size [nt] | End Size [nt] | Area | % of total Area |
|---|---|---|---|---|
| 18S | 1,552 | 2,001 | 14.3 | 12.0 |
| 28S | 2,892 | 5,029 | 35.1 | 29.6 |

**Fig. S9: Bioanalyzer electropherogram of X9014 RNA-Seq library.** The prepared RRBS library was run on an Agilent 2100 Bioanalyzer using the high sensitivity RNA nano kit (from Agilent) to determine the quality of the samples. The electropherogram displays a plot of fragment size in the x-axis (nt) versus fluorescence intensity (fluorescence units, FU) in y-axis. RNA Integrity Number (RIN) is shown below in the figure. Further, RNA concentration, and ratio of different RNA submits are shown.

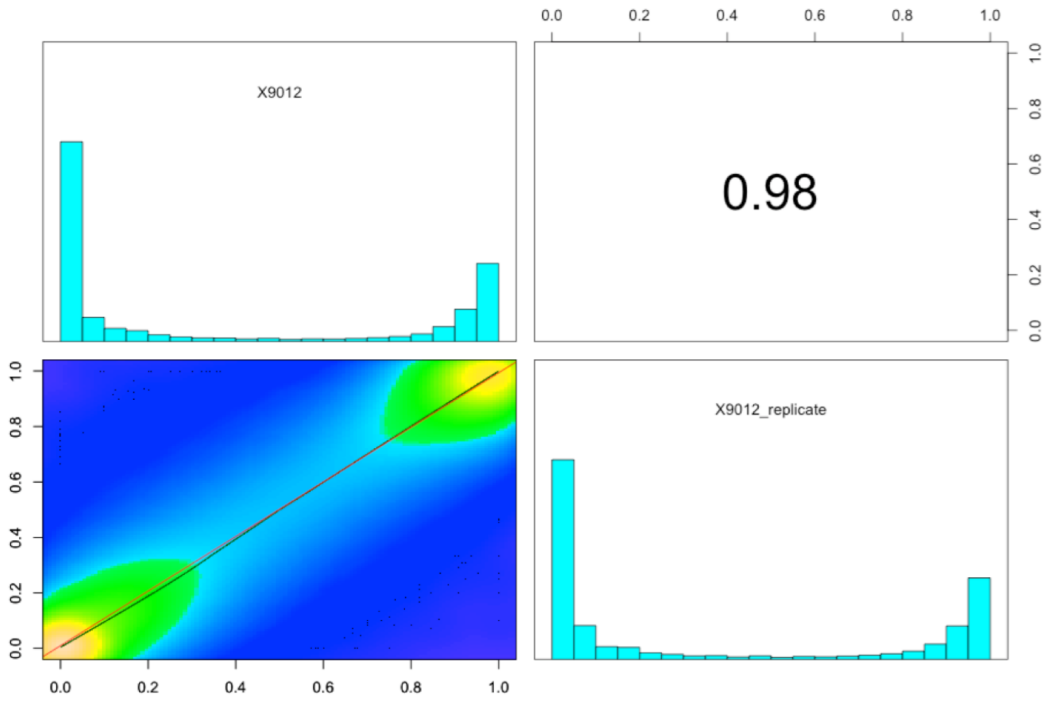



**Fig. S10: Scatter plots of CpG methylation for sample X9012 and X9012_replicate.** Lower left is the scatter plot of CpG methylation values for each sample. The number on upper right denotes pair-wise CpG base Pearson's correlation score for X9012 and X9012_replicate samples. The histograms show the frequency of CpG methylation in these two samples. The X and Y axis scales of the scatter plot in lower left was modified to 0.0-1.0 by methylKit program, instead of 0-100 percent methylation as shown in Figure 6.4. In this plot 0.0 represents complete unmethylation (0%) and 1.0 represents complete methylation (100%).

## Supplementary Tables

**Table S1. Neutrophil isolation percentages and DNA concentrations of the sequenced samples**

| Sample ID | Neutrophil isolation (%) | Amount of DNA ($\mu$g) | 260/280 ratio on Nanodrop |
|---|---|---|---|
| X9015 | 96.0 | 38.5 | 1.81 |
| X9006 | 96.5 | 27.4 | 1.83 |
| X9010 | 94.7 | 43.0 | 1.87 |
| X9007 | 97.0 | 26.5 | 1.89 |
| X9017 | 94.0 | 49.2 | 1.87 |
| X9019 | 96.0 | 34.5 | 1.87 |
| X9020 | 97.1 | 40.9 | 1.88 |
| X9014 | 92.0 | 20.6 | 1.89 |
| X9016 | 96.5 | 66.2 | 1.86 |
| X9018 | 90.0 | 50.0 | 1.87 |
| X9012 | 95.5 | 68.0 | 1.87 |
| X9021 | 97.4 | 50.0 | 1.88 |