

**S4 Table. Genomic localisation for c-Myb footprints in the six cell types analysed.** FDR-corrected p values, p', and normalised ratio for the distribution of c-Myb footprints at annotated genes, promoters and intergenic regions for the six cell-types analysed.

<b>CD20+ cells</b>	<b>p'</b>	<b>Normalised ratio</b>
Intergenic regions	1.00	0.95
UTRs	0.52	1.10
Exons	$1.87 \times 10^{-3}$	3.07
Introns	$8.86 \times 10^{-3}$	1.08
Promoters	1.00	0.95
<b>CD34+ cells</b>		
Intergenic regions	1.00	0.91
UTRs	0.074	1.17
Exons	$1.87 \times 10^{-3}$	3.52
Introns	1.00	0.98
Promoters	0.68	1.00
<b>GM12865 cells</b>		
Intergenic regions	1.00	0.87
UTRs	0.12	1.15
Exons	$1.67 \times 10^{-3}$	3.96
Introns	1.00	0.95
Promoters	$1.67 \times 10^{-3}$	1.04
<b>K562 cells</b>		
Intergenic regions	1.00	0.85
UTRs	0.043	1.25
Exons	$9.37 \times 10^{-4}$	3.47
Introns	1.00	0.91
Promoters	$9.37 \times 10^{-4}$	1.10
<b>NB4 cells</b>		
Intergenic regions	1.00	0.83
UTRs	0.12	1.13
Exons	$9.37 \times 10^{-4}$	3.93
Introns	1.00	0.92
Promoters	$9.37 \times 10^{-4}$	1.08
<b>Th1 cells</b>		
Intergenic regions	1.00	0.95
UTRs	$2.25 \times 10^{-3}$	1.44
Exons	$1.87 \times 10^{-3}$	2.98
Introns	0.069	1.06
Promoters	1.00	0.95