Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 10:04:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818780.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	`/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1818780 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818780.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 10:04:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818780.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	718,670
Mapped reads	689,618 / 95.96%
Unmapped reads	29,052 / 4.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,953 / 0.83%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	234,673 / 32.65%
Duplication rate	30.42%
Clipped reads	691,368 / 96.2%

2.2. ACGT Content

Number/percentage of A's	13,222,665 / 28.31%
Number/percentage of C's	10,693,341 / 22.9%
Number/percentage of T's	13,513,606 / 28.94%
Number/percentage of G's	9,270,162 / 19.85%
Number/percentage of N's	3,032 / 0.01%
GC Percentage	42.75%

2.3. Coverage

Mean	0.0151

Standard Deviation	0.2348

2.4. Mapping Quality

Mean Mapping Quality	47.94

2.5. Mismatches and indels

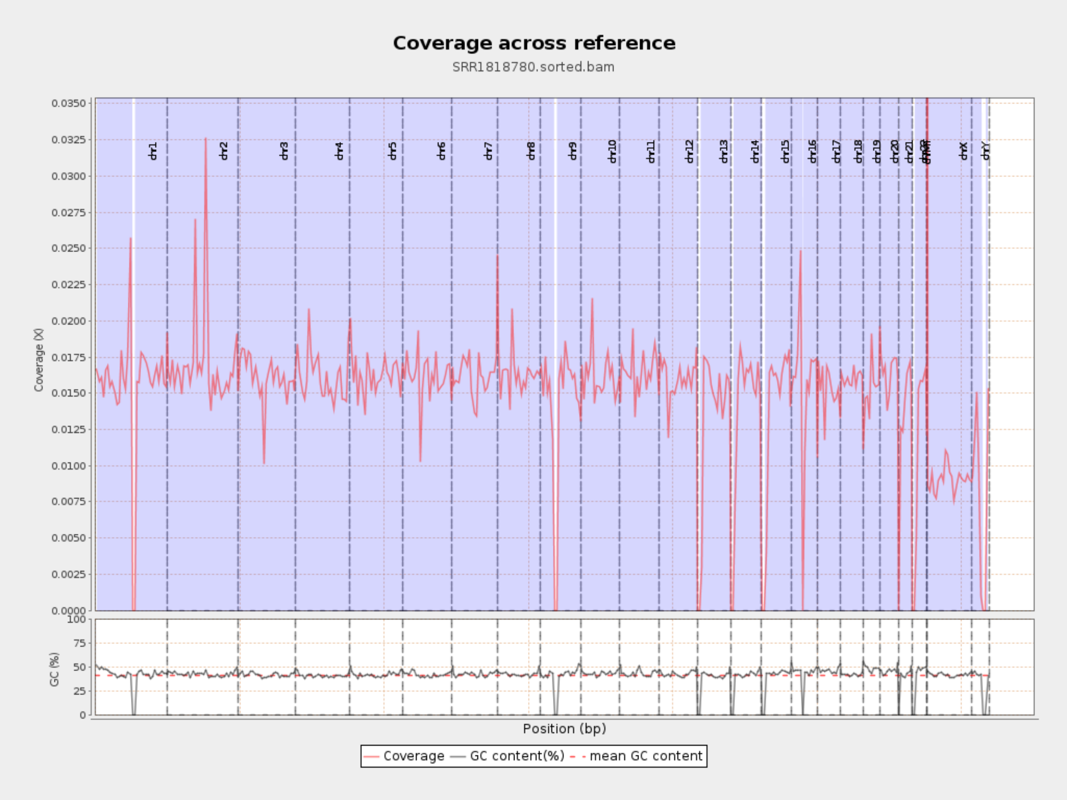
General error rate	0.55%
Mismatches	245,689
Insertions	5,876
Mapped reads with at least one insertion	0.84%
Deletions	12,031
Mapped reads with at least one deletion	1.72%
Homopolymer indels	41.78%

2.6. Chromosome stats

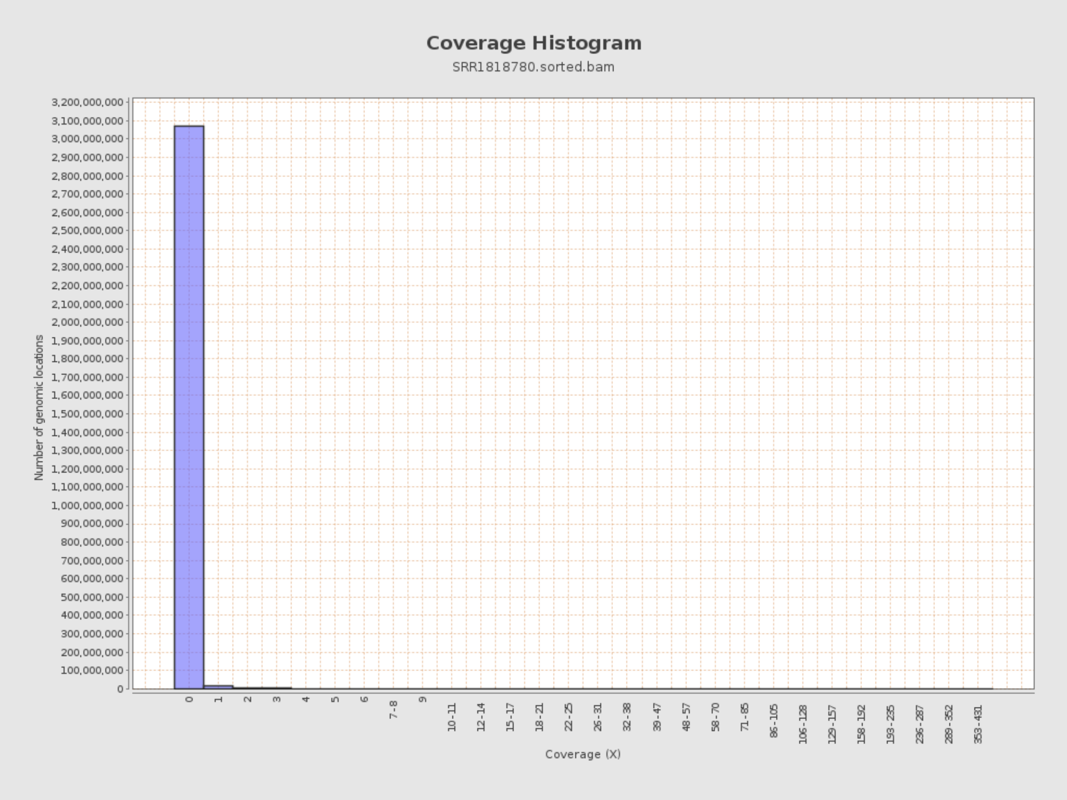
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3851595	0.0155	0.2943
chr2	243199373	4151837	0.0171	0.3609
chr3	198022430	3183076	0.0161	0.196
chr4	191154276	3084933	0.0161	0.2186
chr5	180915260	2929488	0.0162	0.2016
chr6	171115067	2763375	0.0161	0.2071
chr7	159138663	2578056	0.0162	0.2172

chr8	146364022	2398007	0.0164	0.2111
chr9	141213431	1991091	0.0141	0.1975
chr10	135534747	2206514	0.0163	0.2464
chr11	135006516	2228583	0.0165	0.2134
chr12	133851895	2138808	0.016	0.2046
chr13	115169878	1498487	0.013	0.176
chr14	107349540	1450390	0.0135	0.1909
chr15	102531392	1355511	0.0132	0.1795
chr16	90354753	1383711	0.0153	0.2576
chr17	81195210	1240401	0.0153	0.1985
chr18	78077248	1253826	0.0161	0.241
chr19	59128983	913930	0.0155	0.2731
chr20	63025520	1033275	0.0164	0.2091
chr21	48129895	641784	0.0133	0.1877
chr22	51304566	557836	0.0109	0.1705
chrMT	16571	20296	1.2248	1.83
chrX	155270560	1410445	0.0091	0.1546
chrY	59373566	456897	0.0077	0.3605

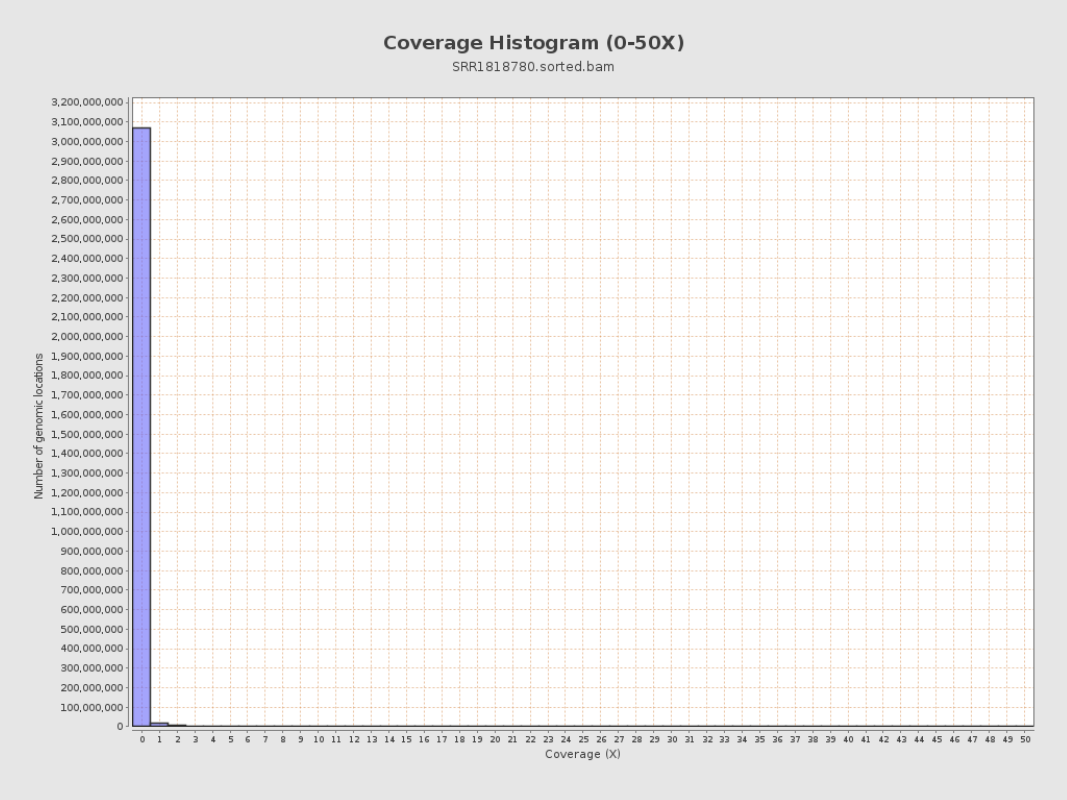
3. Results : Coverage across reference



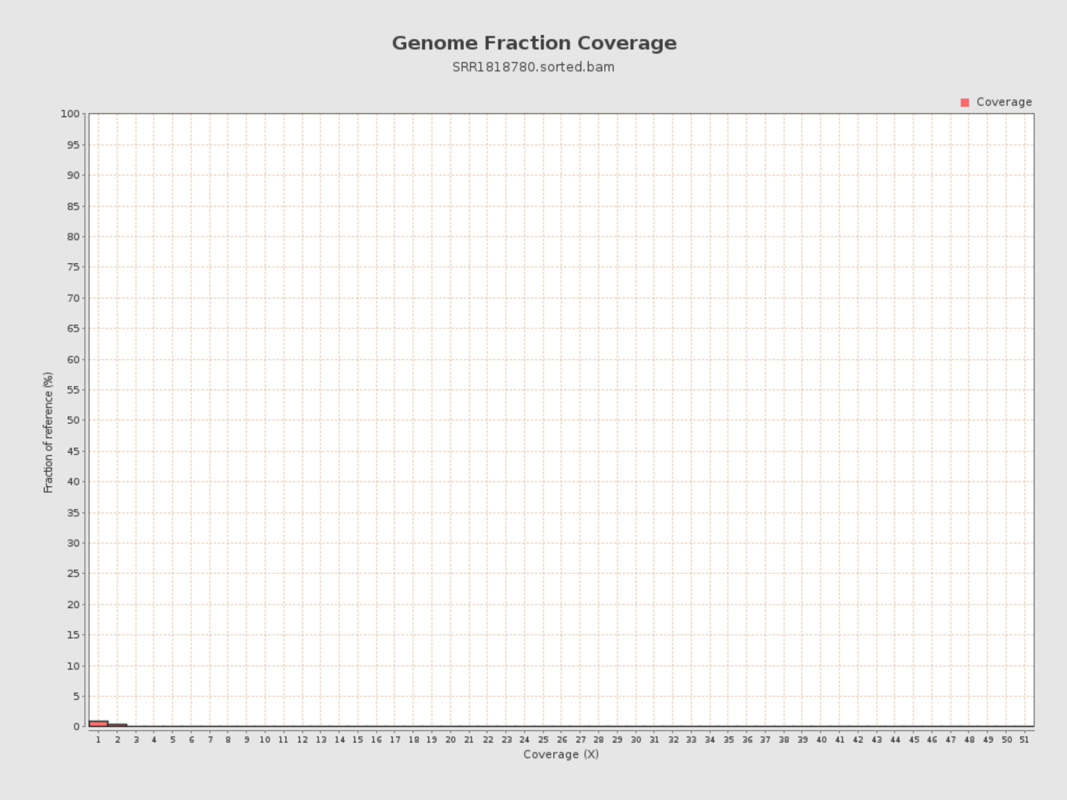
4. Results : Coverage Histogram



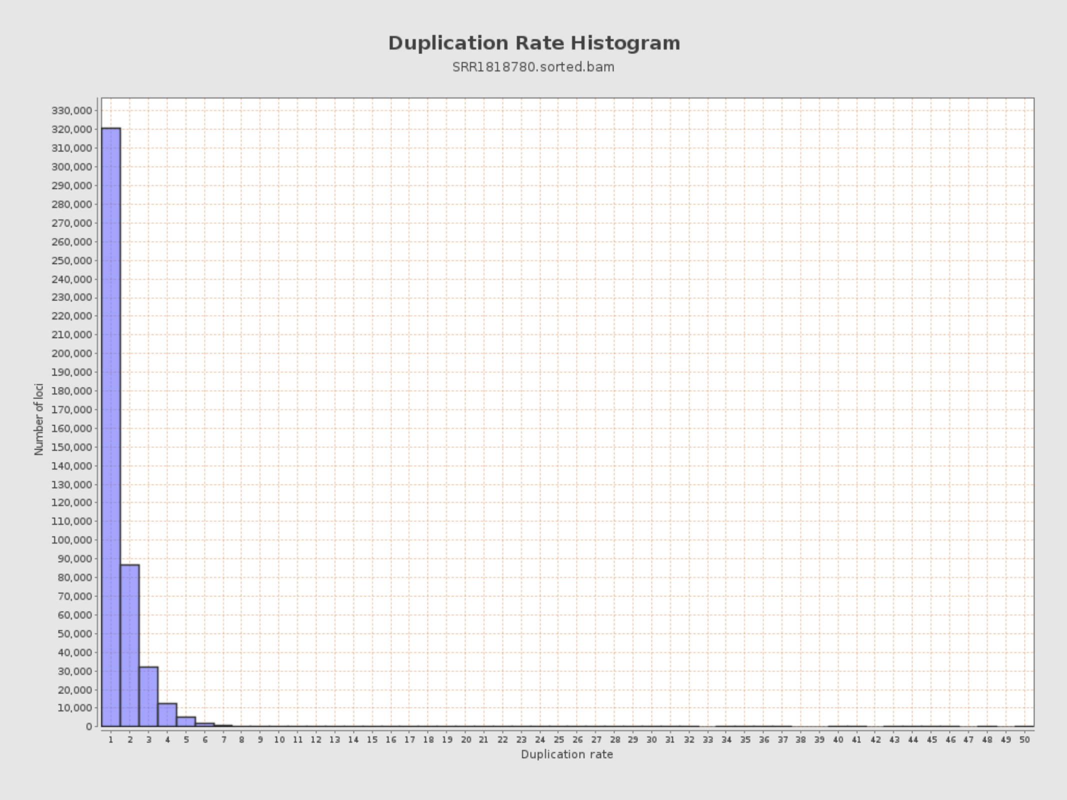
5. Results : Coverage Histogram (0-50X)



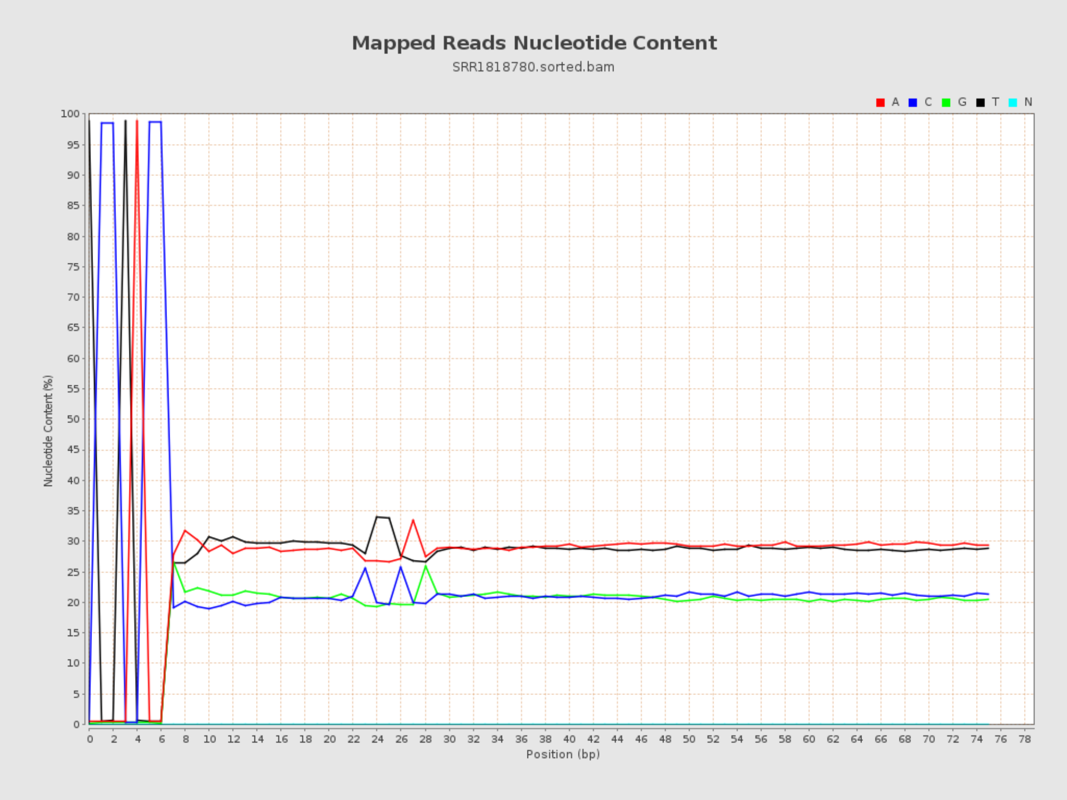
6. Results : Genome Fraction Coverage



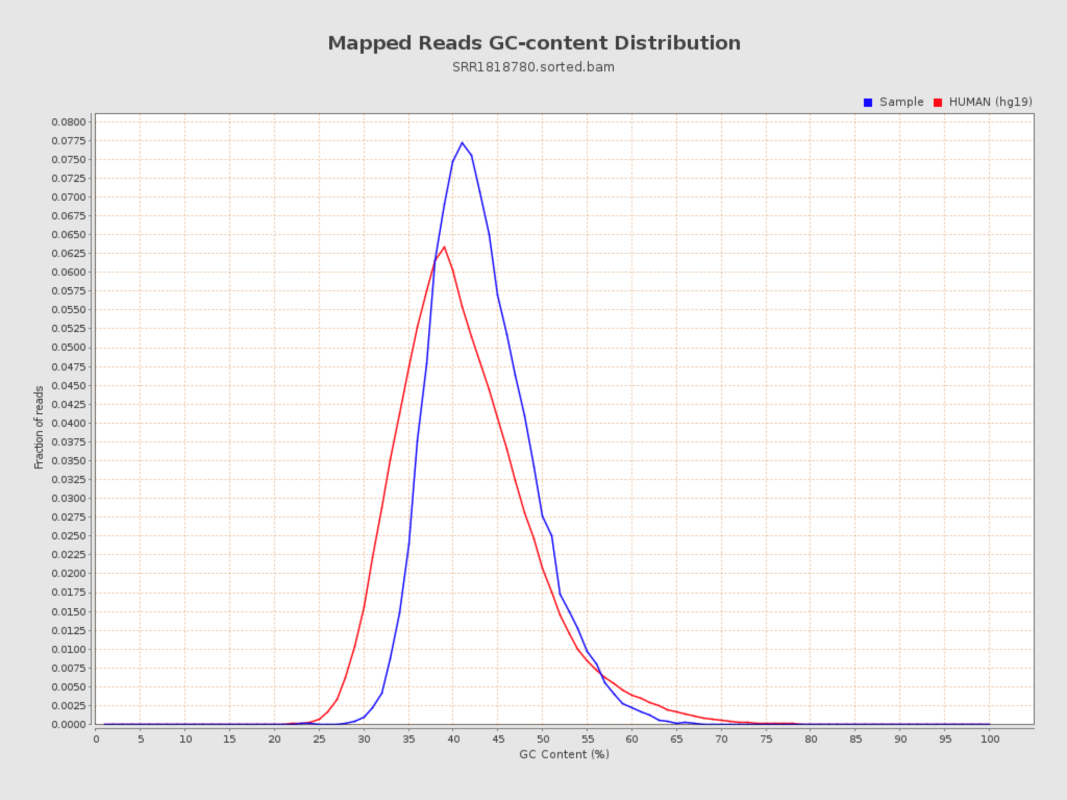
7. Results : Duplication Rate Histogram



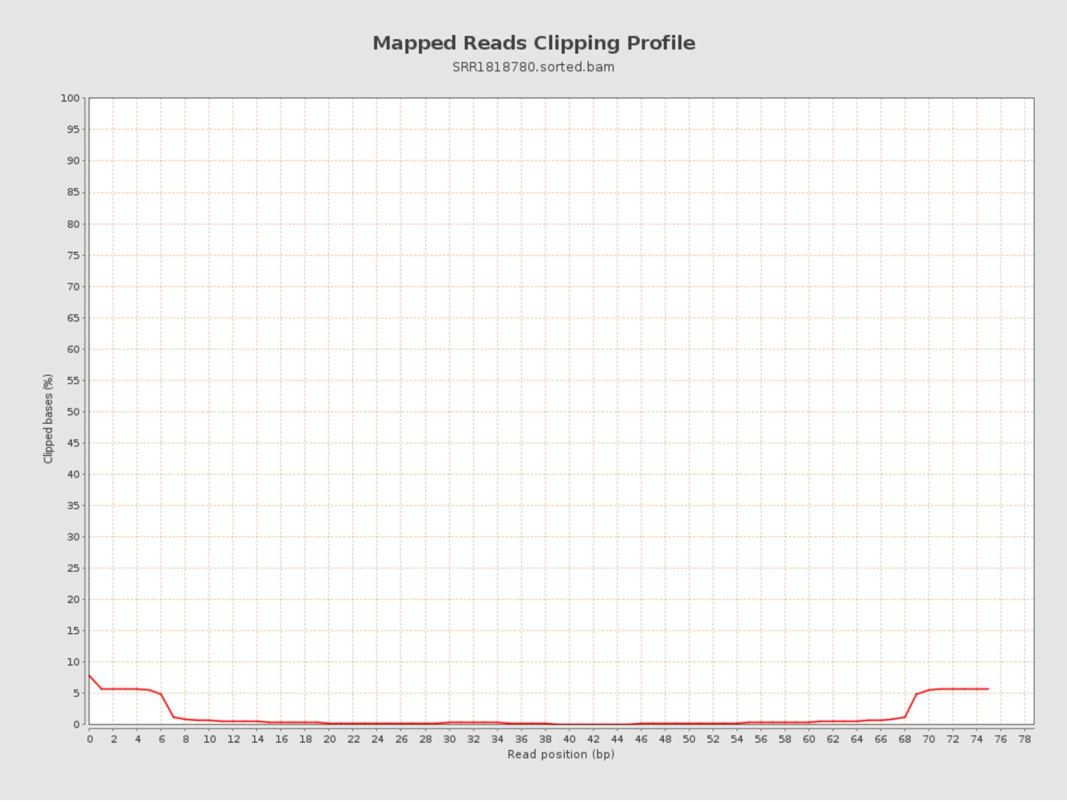
8. Results : Mapped Reads Nucleotide Content



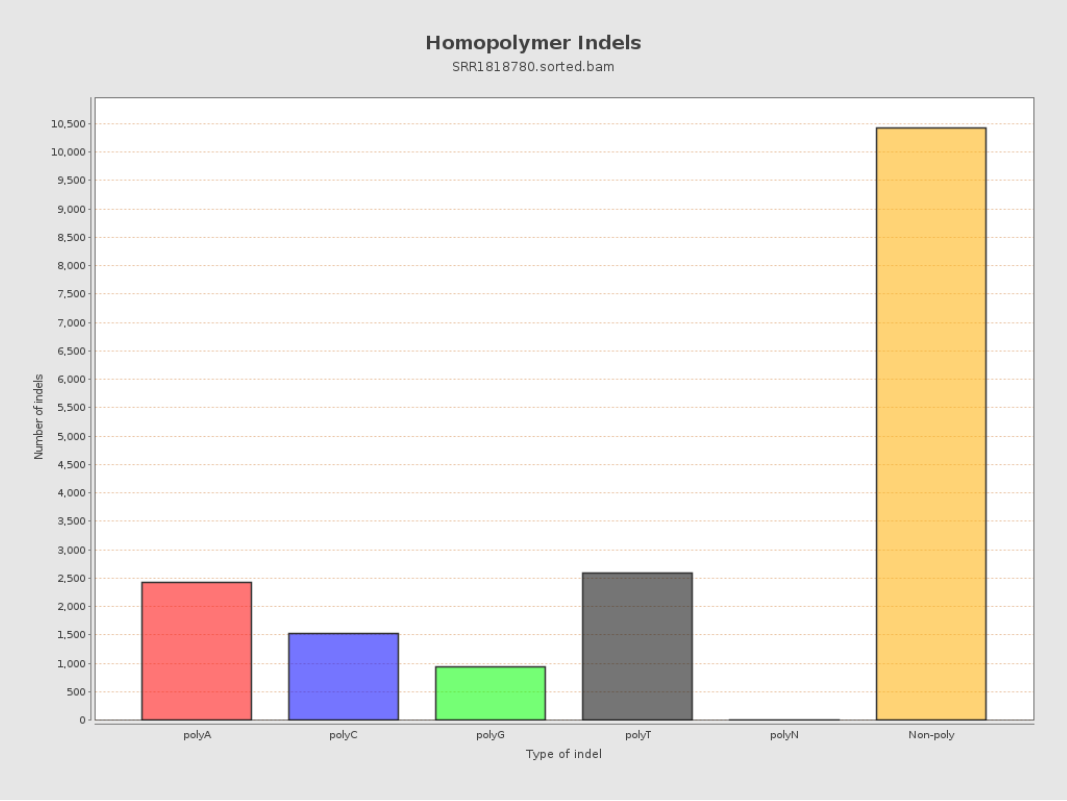
9. Results : Mapped Reads GC-content Distribution



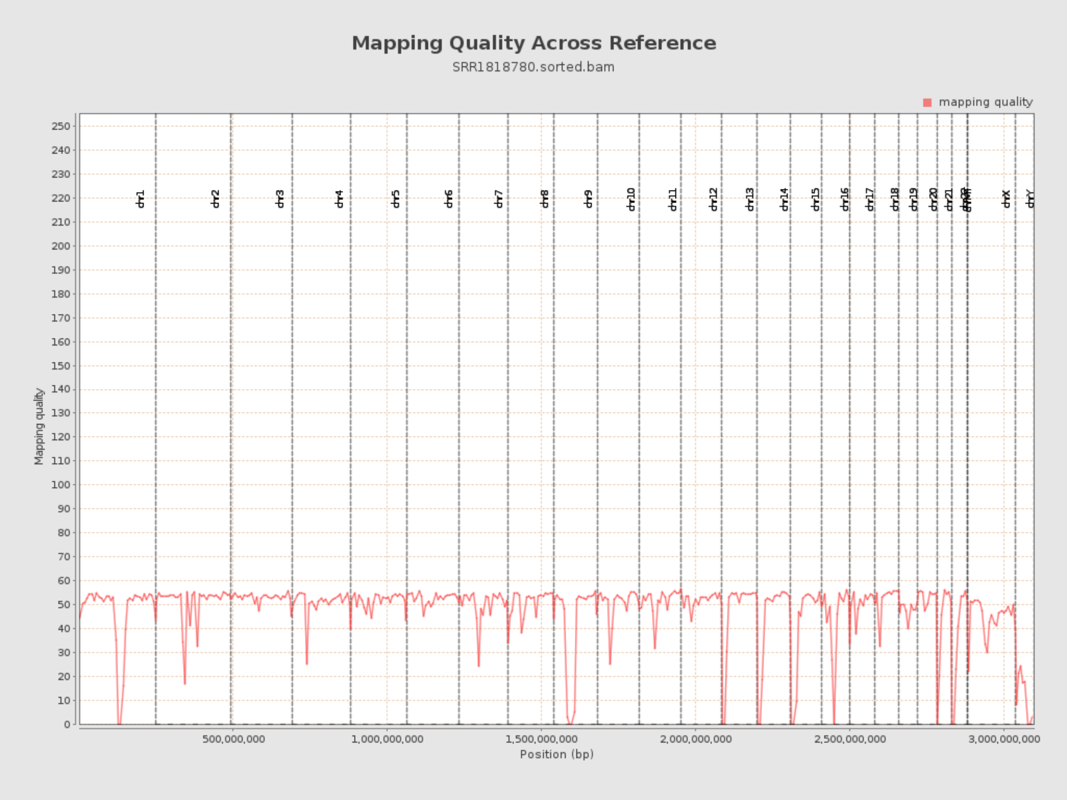
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram