Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:13:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751200.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_SRR8751200 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751200.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:13:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751200.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,519,300
Mapped reads	7,392,962 / 98.32%
Unmapped reads	126,338 / 1.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	100,647 / 1.34%
Read min/max/mean length	30 / 151 / 151.69
Duplicated reads (estimated)	1,078,978 / 14.35%
Duplication rate	14.14%
Clipped reads	1,503,174 / 19.99%

2.2. ACGT Content

Number/percentage of A's	296,707,845 / 27.63%
Number/percentage of C's	240,404,544 / 22.39%
Number/percentage of T's	299,574,459 / 27.9%
Number/percentage of G's	237,021,849 / 22.07%
Number/percentage of N's	10,254 / 0%
GC Percentage	44.46%

2.3. Coverage

Mean	0.3469

Standard Deviation	1.3108

2.4. Mapping Quality

Mean Mapping Quality	52.76

2.5. Mismatches and indels

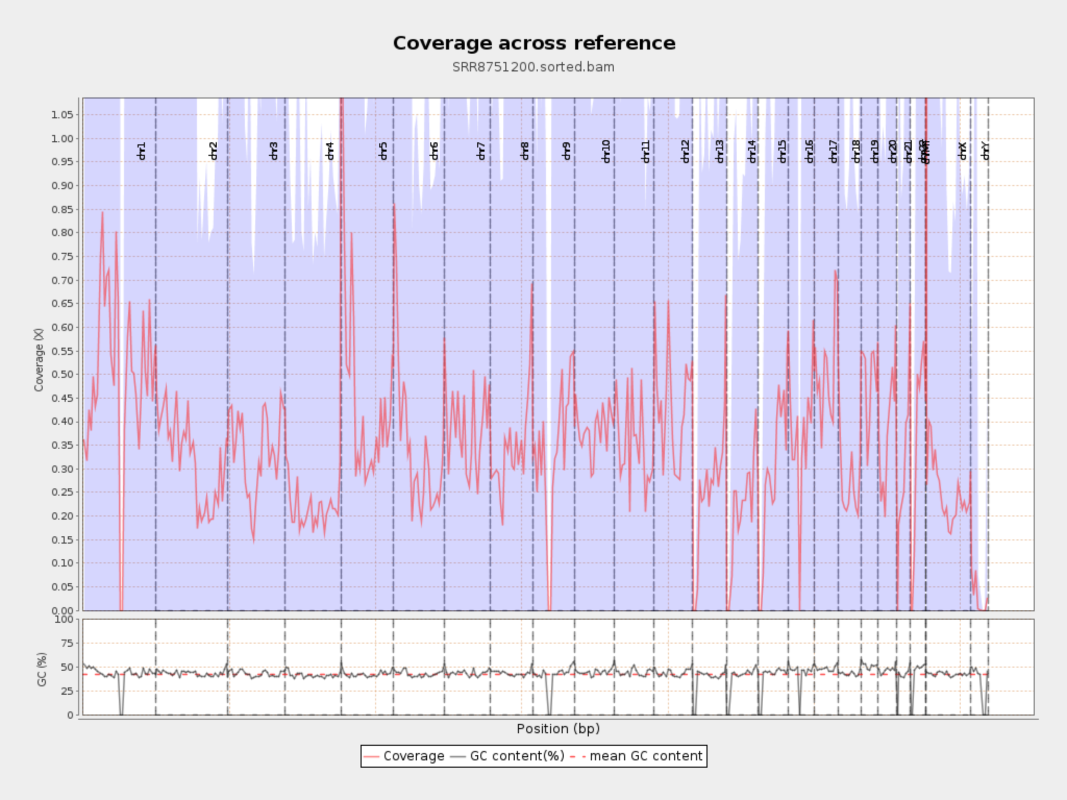
General error rate	0.77%
Mismatches	7,958,502
Insertions	132,068
Mapped reads with at least one insertion	1.74%
Deletions	125,627
Mapped reads with at least one deletion	1.66%
Homopolymer indels	47.36%

2.6. Chromosome stats

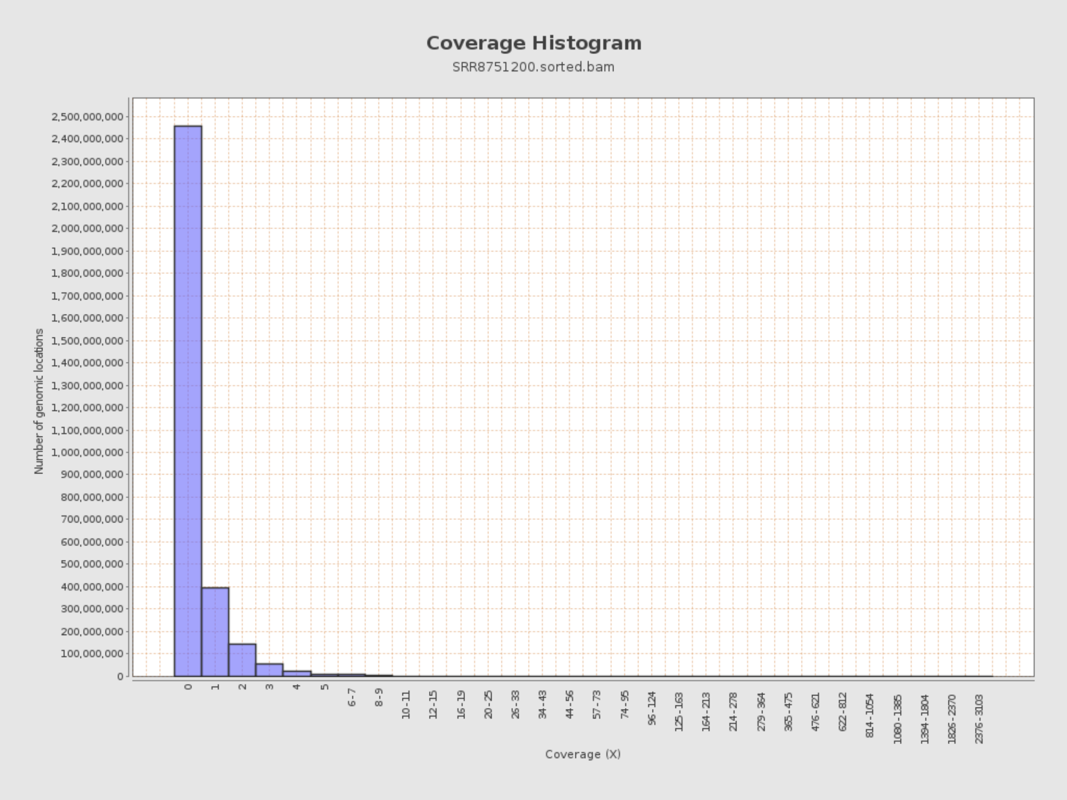
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	125807710	0.5047	2.9263
chr2	243199373	77401587	0.3183	1.0261
chr3	198022430	66908298	0.3379	0.8369
chr4	191154276	41734896	0.2183	0.6906
chr5	180915260	83273188	0.4603	1.0362
chr6	171115067	58356160	0.341	1.073
chr7	159138663	61573955	0.3869	1.0178

chr8	146364022	50935753	0.348	0.871
chr9	141213431	47159969	0.334	0.979
chr10	135534747	51957325	0.3834	1.4812
chr11	135006516	47587550	0.3525	1.0821
chr12	133851895	58409662	0.4364	1.002
chr13	115169878	28771548	0.2498	0.7246
chr14	107349540	23026144	0.2145	0.6858
chr15	102531392	28637413	0.2793	0.7979
chr16	90354753	33976790	0.376	0.9188
chr17	81195210	40793218	0.5024	1.2866
chr18	78077248	20895604	0.2676	1.1852
chr19	59128983	28536149	0.4826	2.0123
chr20	63025520	23291088	0.3696	0.9077
chr21	48129895	14473404	0.3007	0.9101
chr22	51304566	17877165	0.3485	0.9023
chrMT	16571	1981146	119.555	57.7867
chrX	155270560	39063818	0.2516	0.7523
chrY	59373566	1612552	0.0272	0.7149

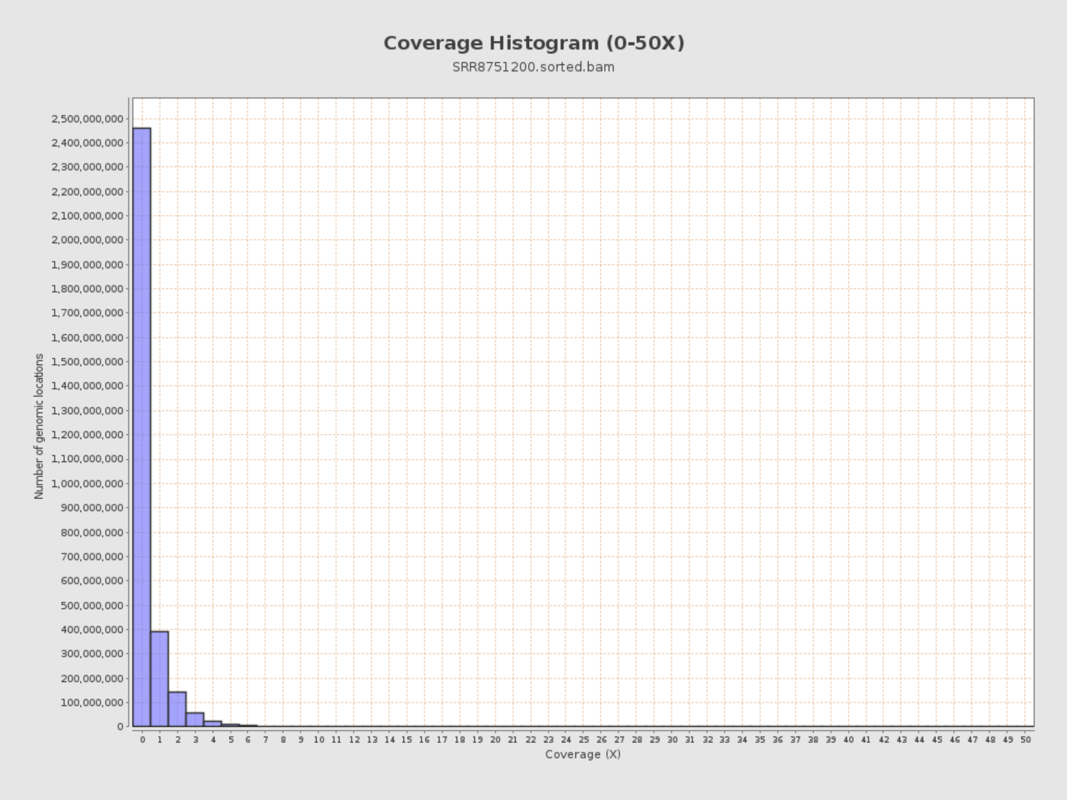
3. Results : Coverage across reference



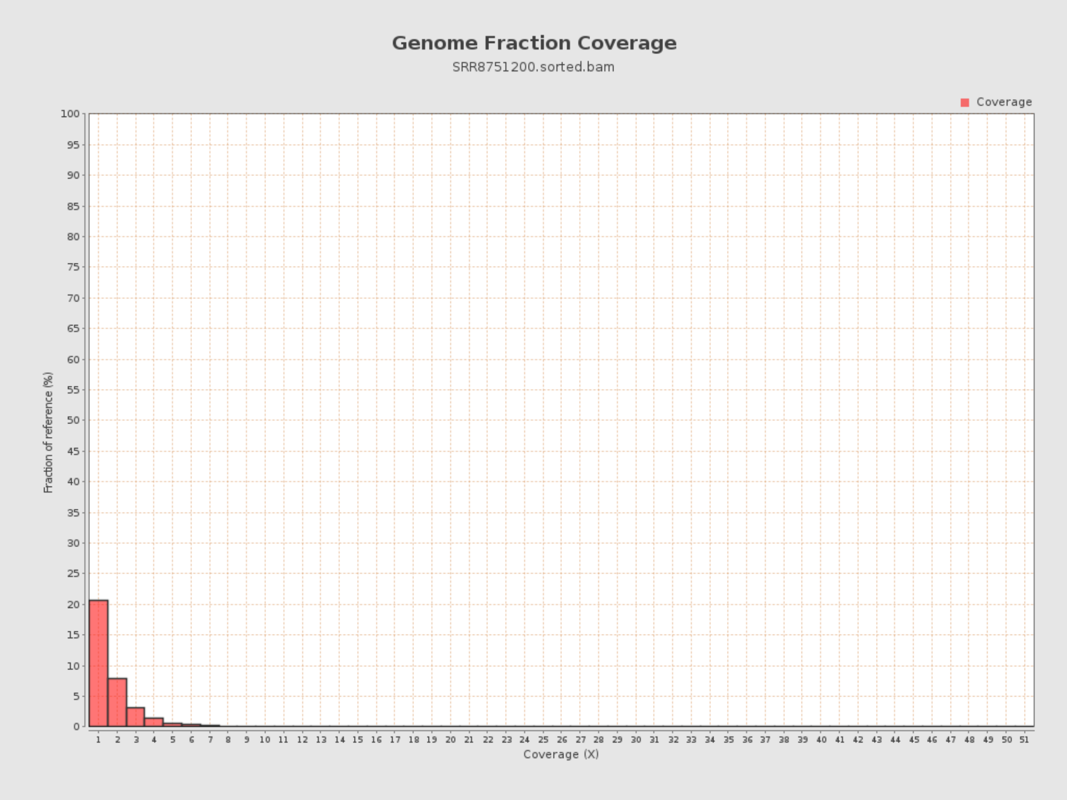
4. Results : Coverage Histogram



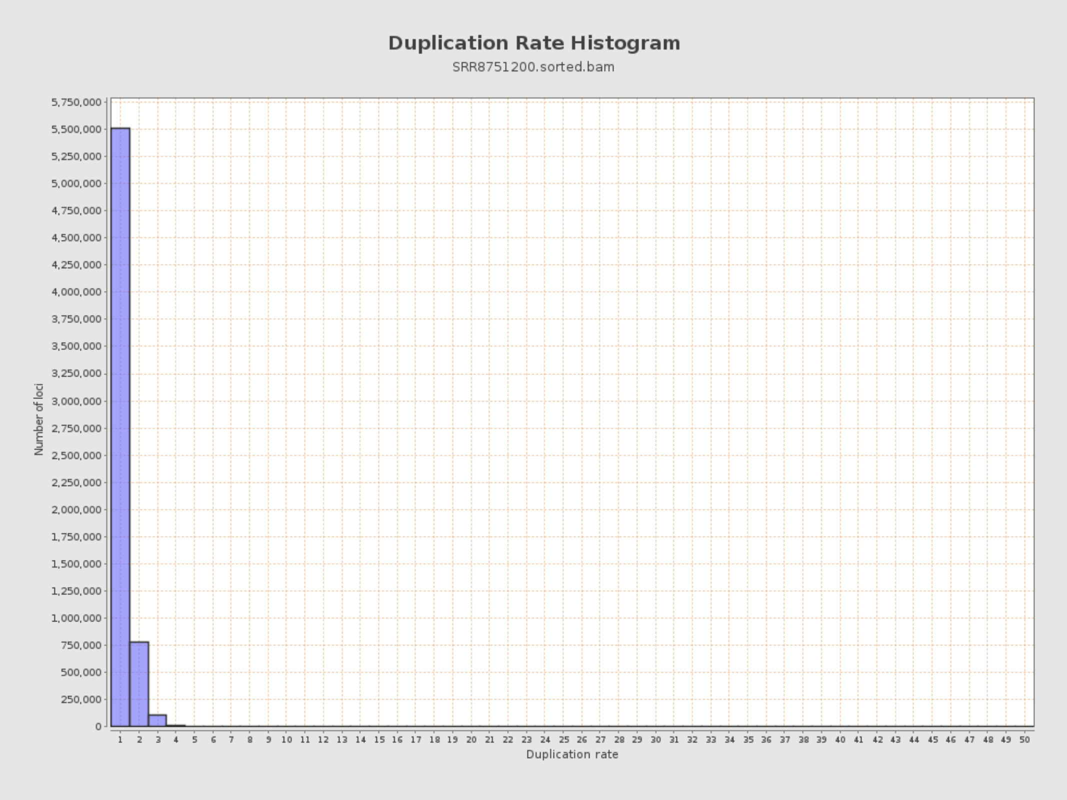
5. Results : Coverage Histogram (0-50X)



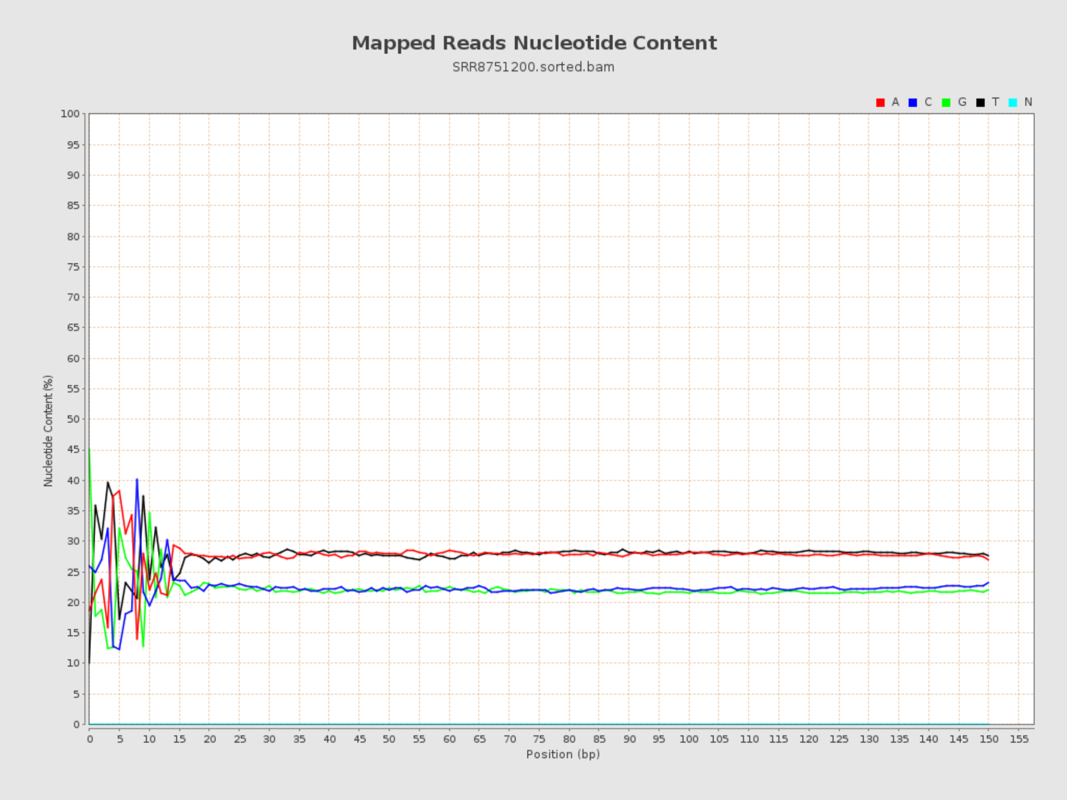
6. Results : Genome Fraction Coverage



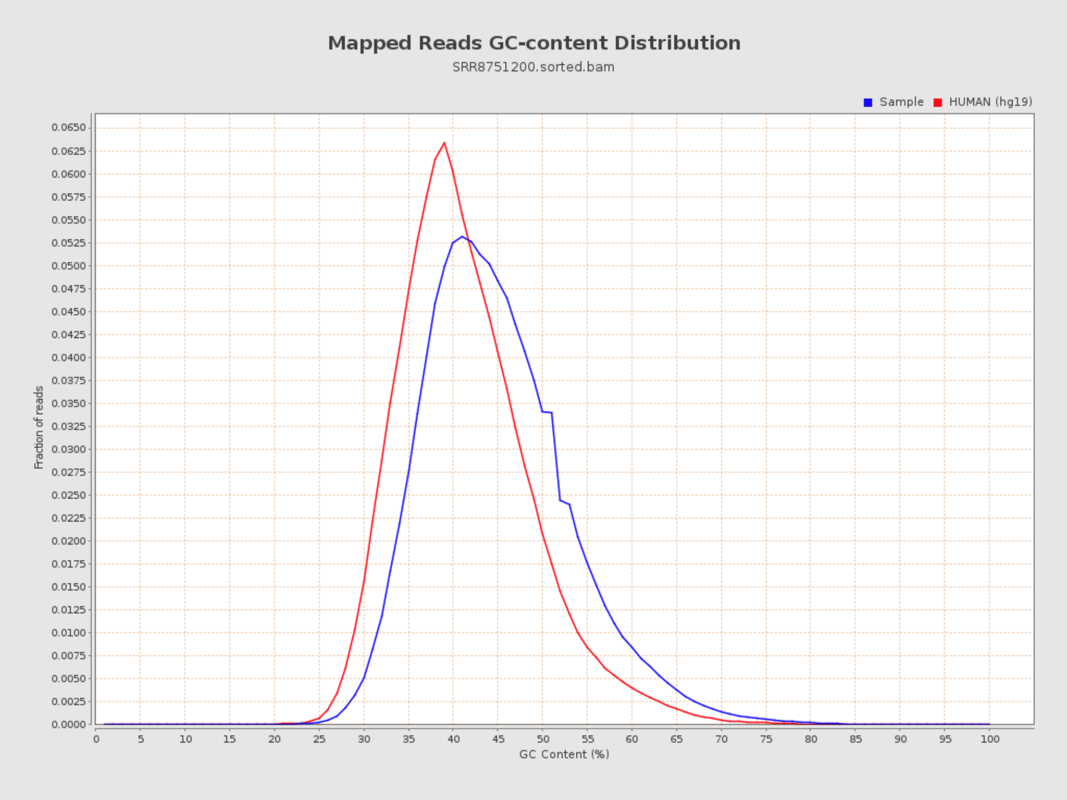
7. Results : Duplication Rate Histogram



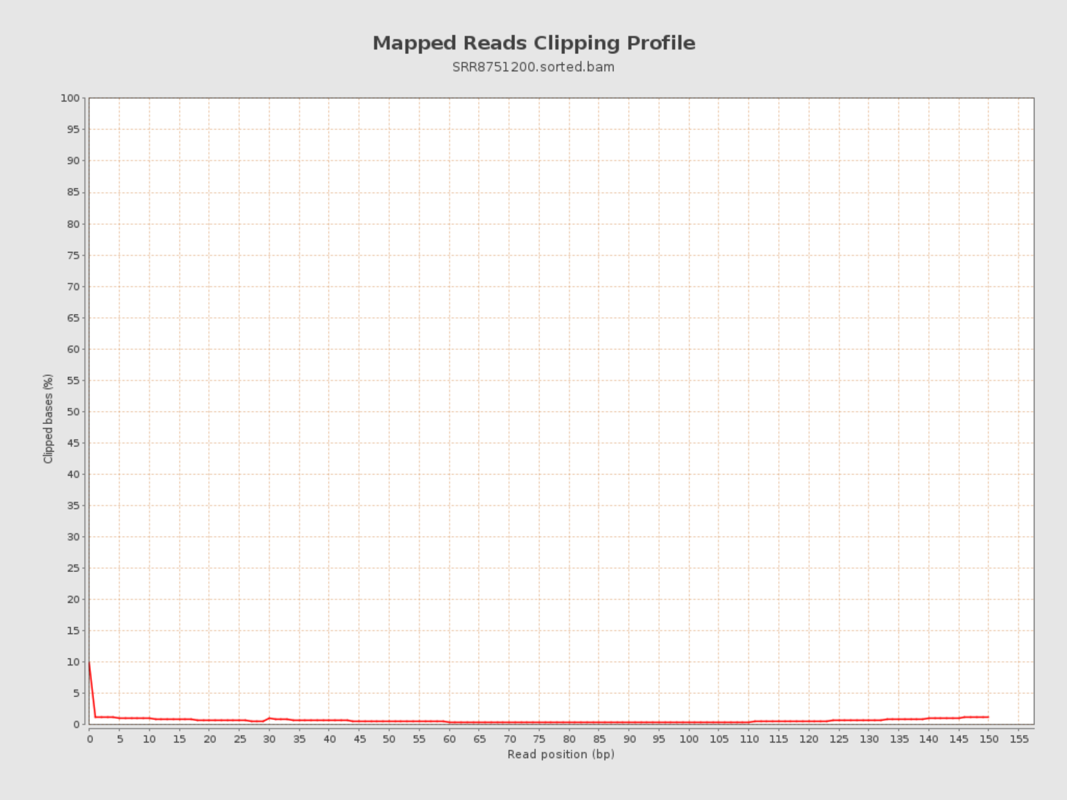
8. Results : Mapped Reads Nucleotide Content



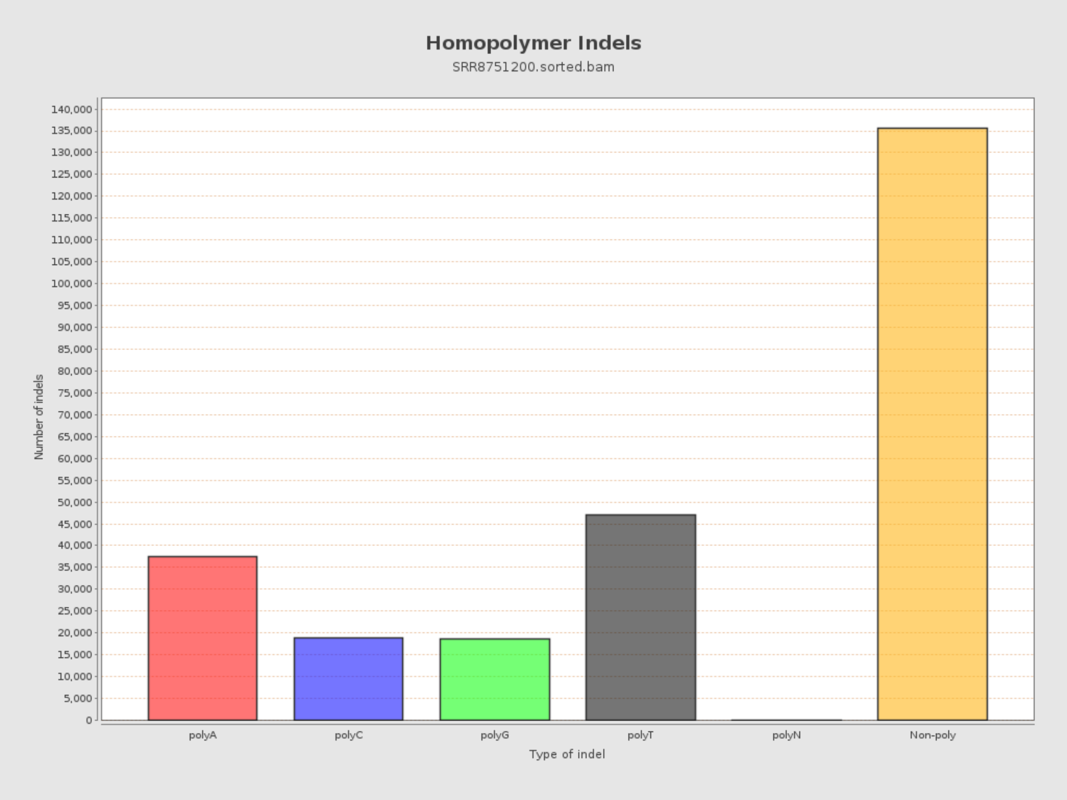
9. Results : Mapped Reads GC-content Distribution



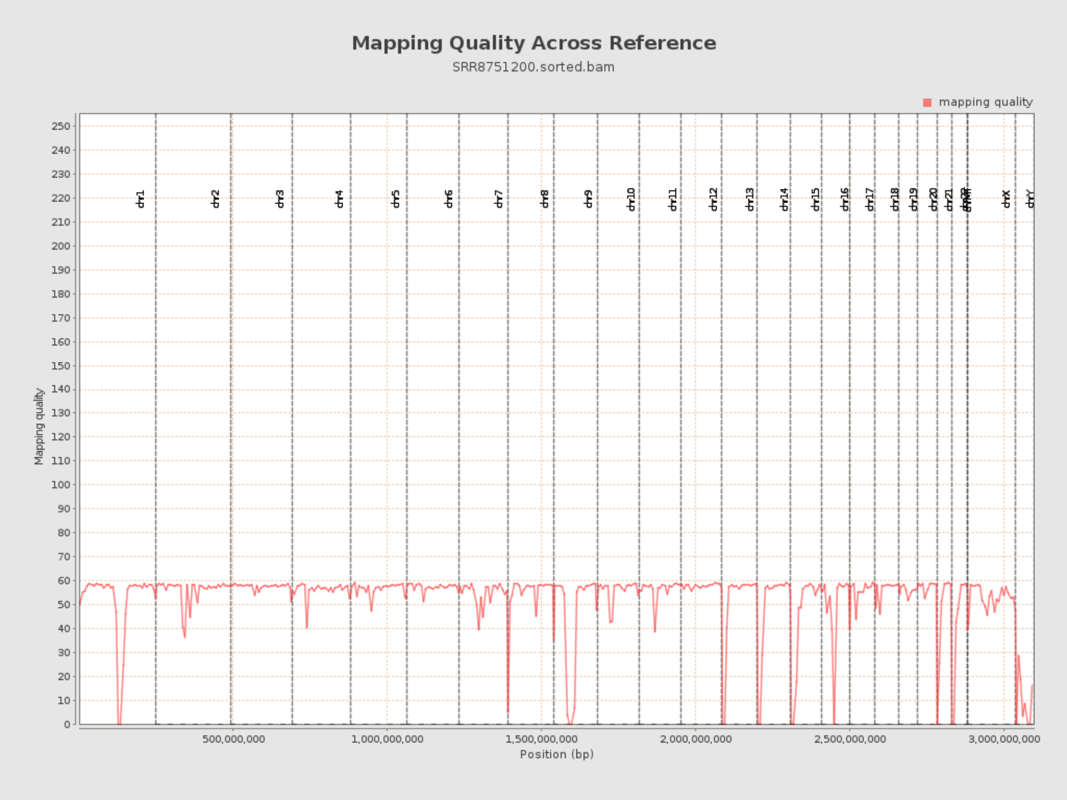
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram