Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 18:50:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751198.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_SRR8751198 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751198.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 18:50:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751198.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,969,864
Mapped reads	5,928,805 / 99.31%
Unmapped reads	41,059 / 0.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	135,261 / 2.27%
Read min/max/mean length	30 / 151 / 152.2
Duplicated reads (estimated)	849,533 / 14.23%
Duplication rate	14.01%
Clipped reads	1,121,937 / 18.79%

2.2. ACGT Content

Number/percentage of A's	246,938,120 / 28.41%
Number/percentage of C's	187,541,491 / 21.57%
Number/percentage of T's	248,108,109 / 28.54%
Number/percentage of G's	186,665,816 / 21.47%
Number/percentage of N's	7,961 / 0%
GC Percentage	43.05%

2.3. Coverage

Mean	0.2809

Standard Deviation	0.8212

2.4. Mapping Quality

Mean Mapping Quality	52.91

2.5. Mismatches and indels

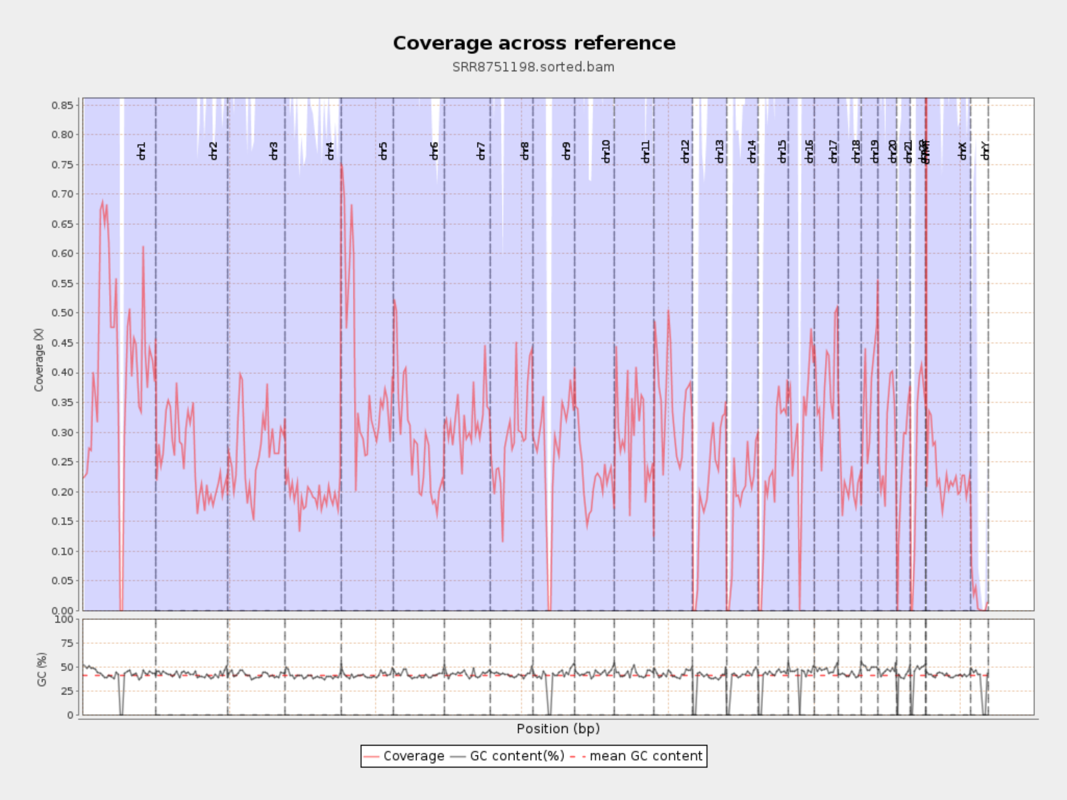
General error rate	0.74%
Mismatches	6,228,361
Insertions	107,270
Mapped reads with at least one insertion	1.77%
Deletions	99,860
Mapped reads with at least one deletion	1.64%
Homopolymer indels	48.24%

2.6. Chromosome stats

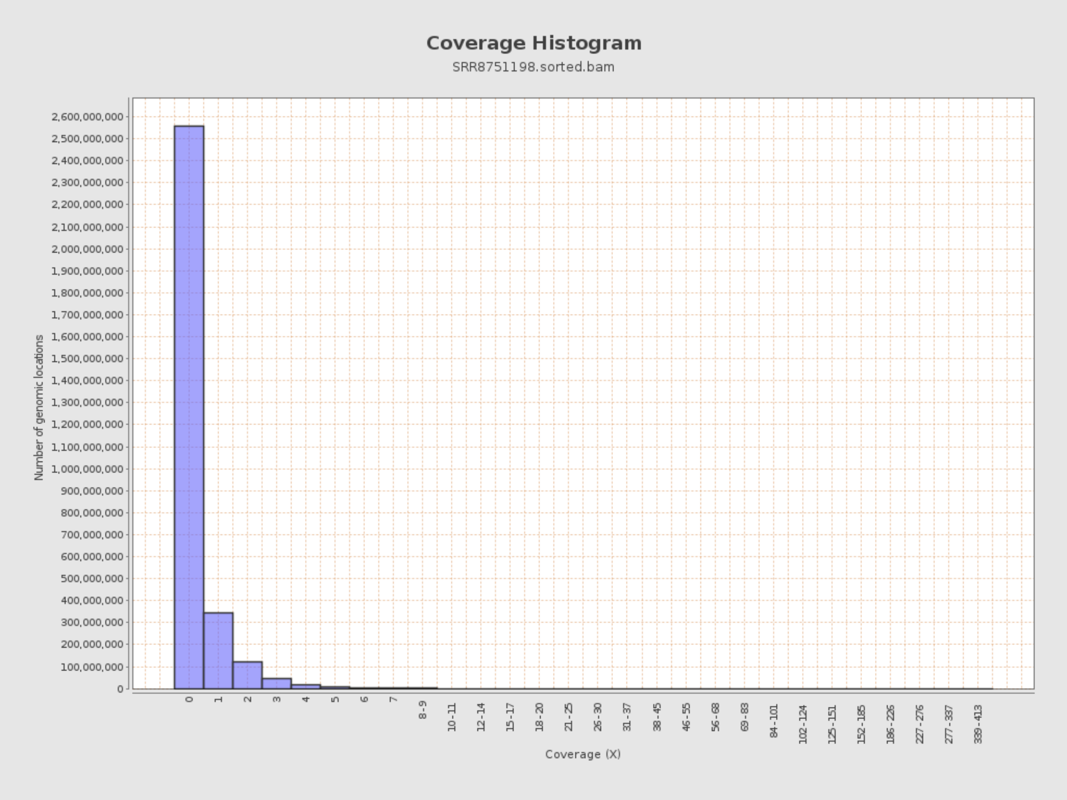
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	102734891	0.4122	1.0619
chr2	243199373	61434663	0.2526	0.8089
chr3	198022430	53199627	0.2687	0.7199
chr4	191154276	36715039	0.1921	0.6056
chr5	180915260	71823298	0.397	0.9638
chr6	171115067	47864398	0.2797	0.8115
chr7	159138663	50587832	0.3179	0.8163

chr8	146364022	42910179	0.2932	0.9288
chr9	141213431	38216344	0.2706	0.7543
chr10	135534747	30830292	0.2275	0.702
chr11	135006516	40221726	0.2979	0.7692
chr12	133851895	47637018	0.3559	0.8639
chr13	115169878	24352971	0.2115	0.6995
chr14	107349540	19803239	0.1845	0.6463
chr15	102531392	23274420	0.227	0.6937
chr16	90354753	27714582	0.3067	0.9139
chr17	81195210	30962958	0.3813	1.0304
chr18	78077248	16855260	0.2159	0.7064
chr19	59128983	21764235	0.3681	0.9126
chr20	63025520	18441959	0.2926	0.7718
chr21	48129895	11584941	0.2407	0.719
chr22	51304566	13226689	0.2578	0.7354
chrMT	16571	810093	48.8862	23.96
chrX	155270560	35515303	0.2287	0.6628
chrY	59373566	1038118	0.0175	0.3977

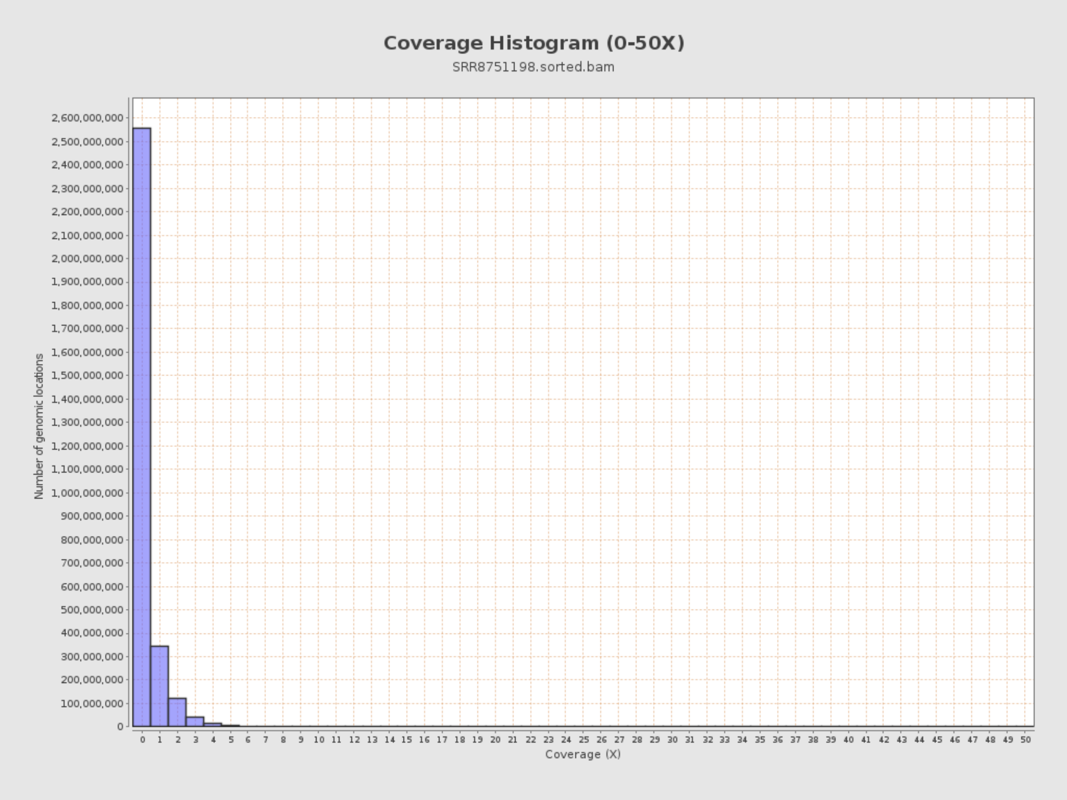
3. Results : Coverage across reference



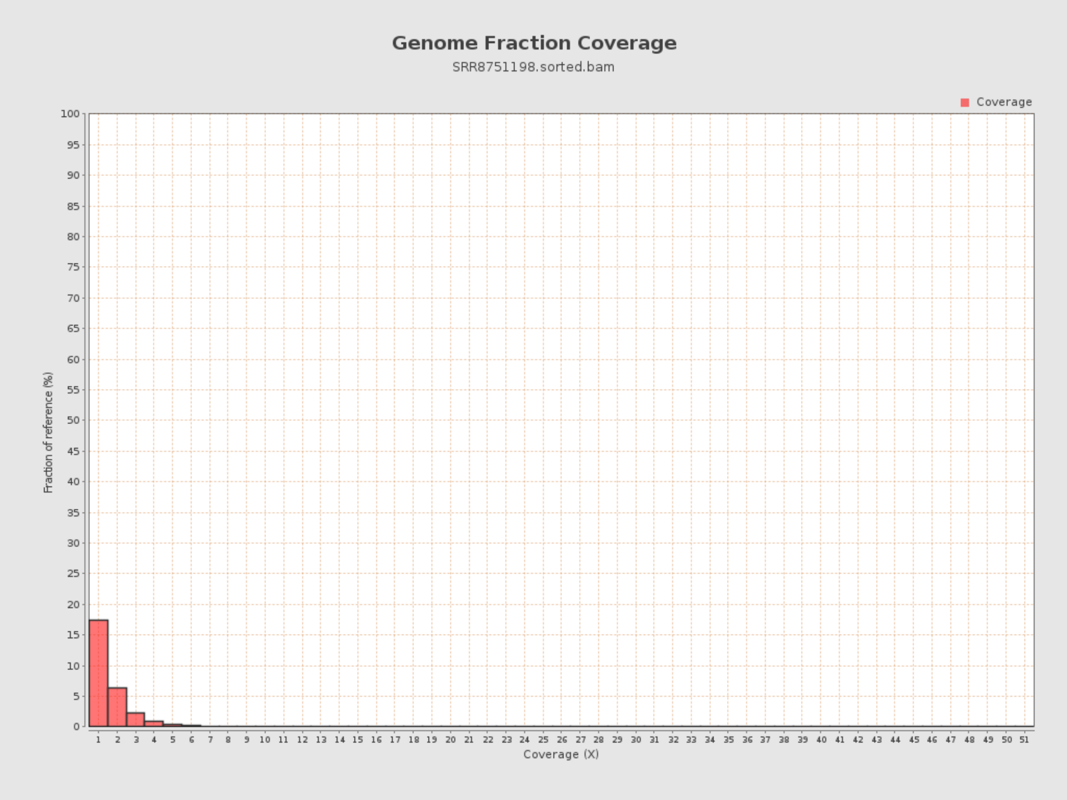
4. Results : Coverage Histogram



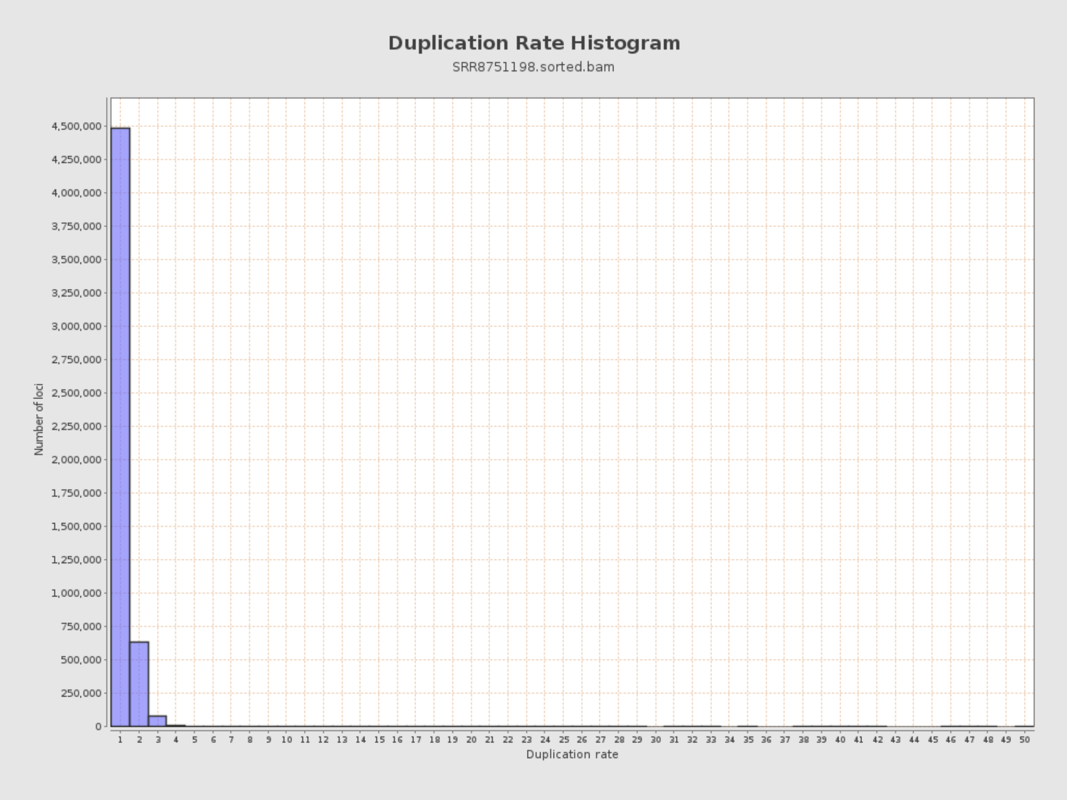
5. Results : Coverage Histogram (0-50X)



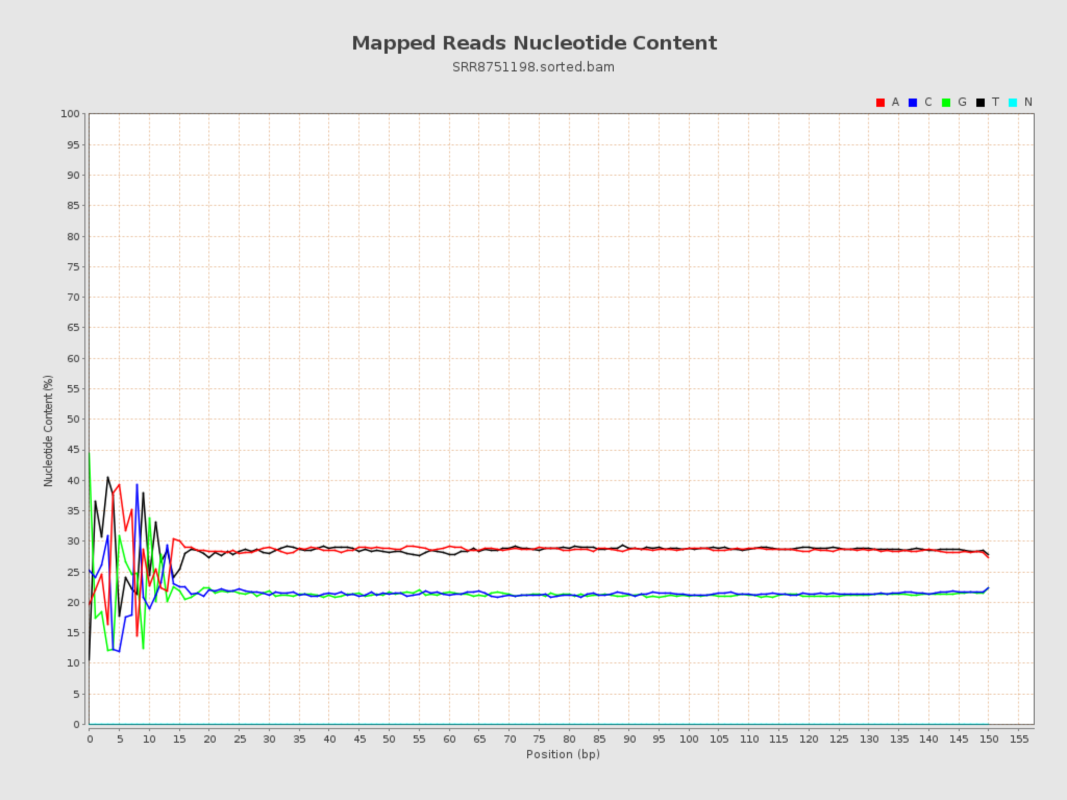
6. Results : Genome Fraction Coverage



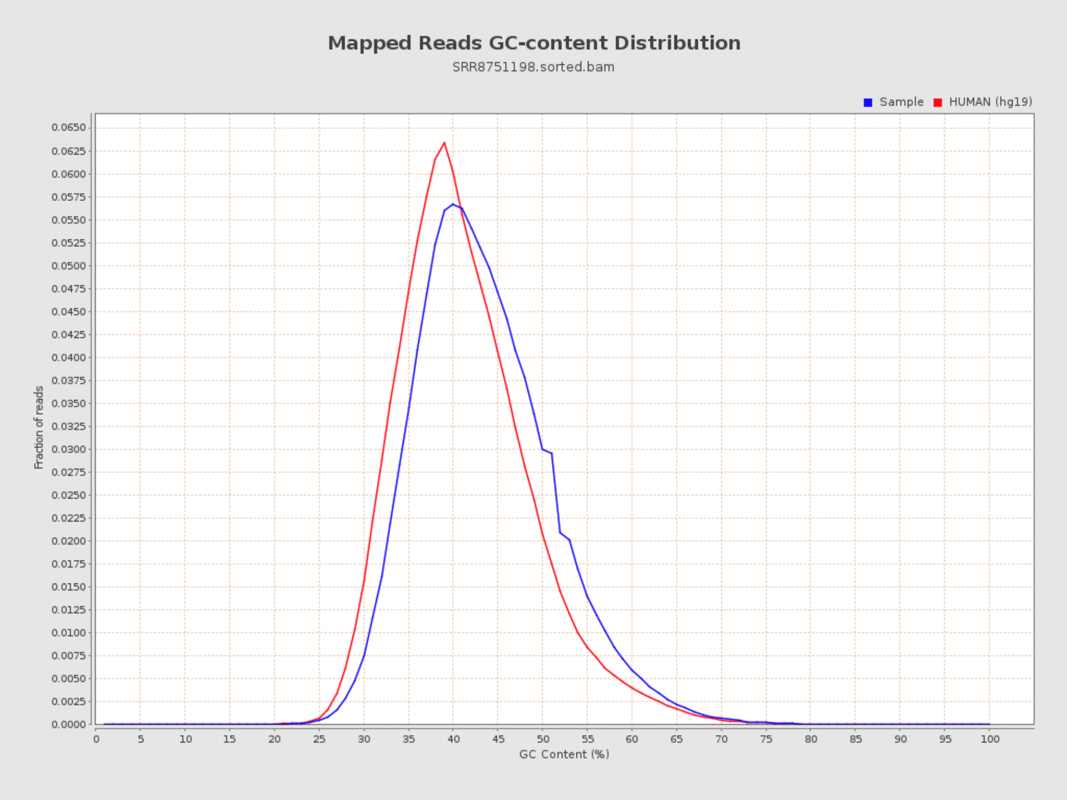
7. Results : Duplication Rate Histogram



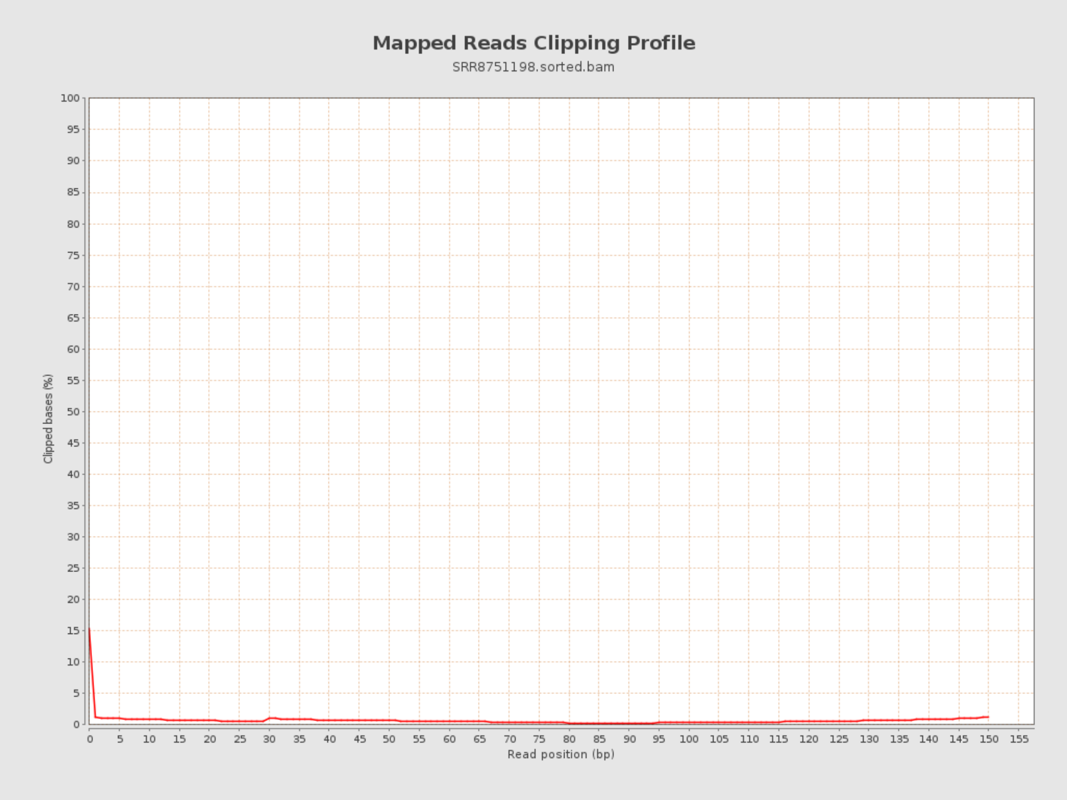
8. Results : Mapped Reads Nucleotide Content



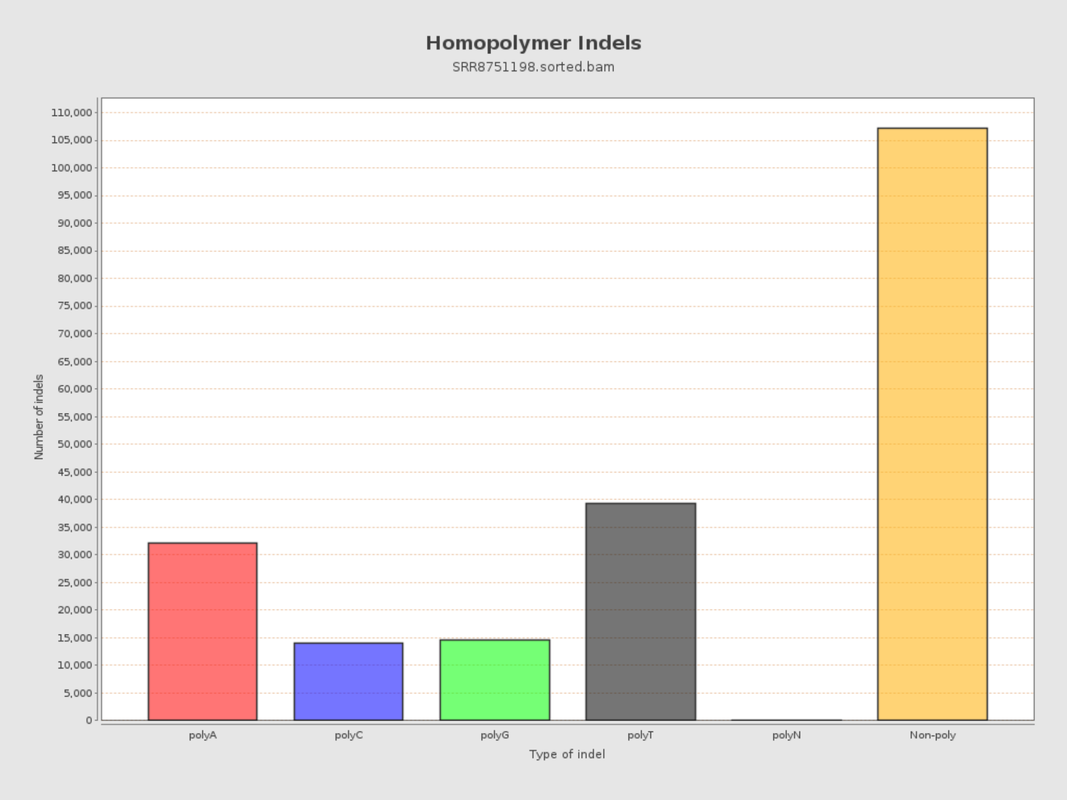
9. Results : Mapped Reads GC-content Distribution



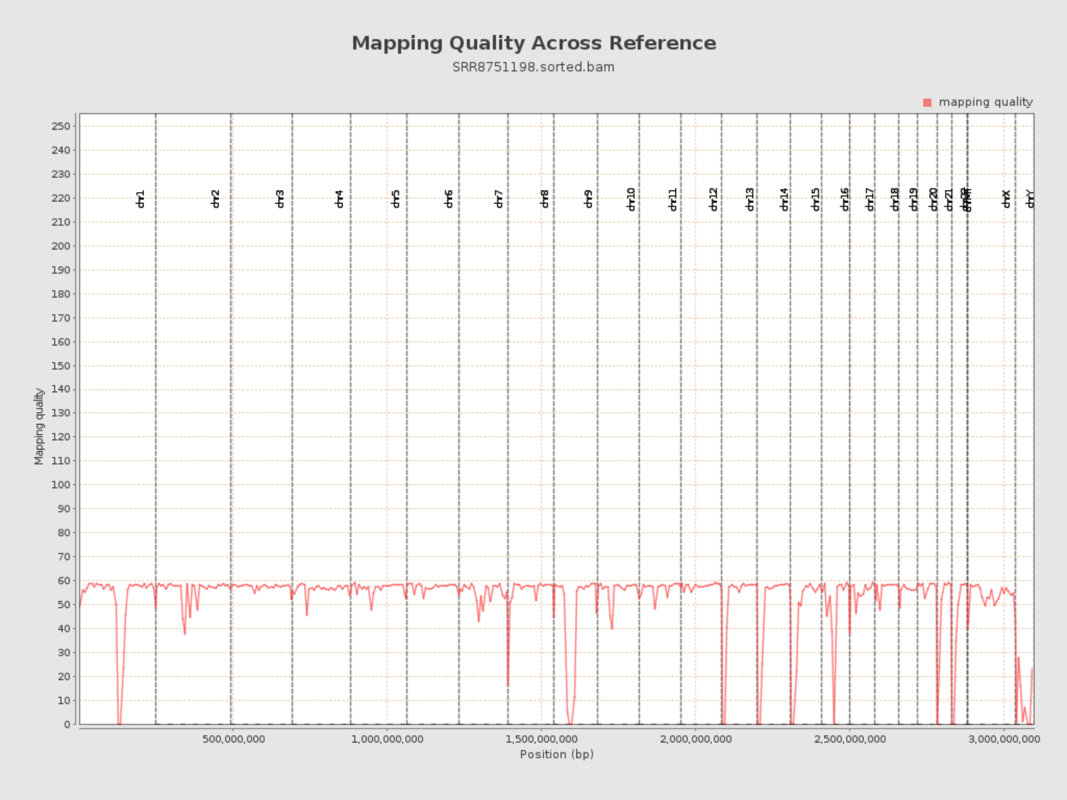
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram