Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 21:08:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505956.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_SRR1505956 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505956.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 21:08:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505956.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,434,164
Mapped reads	10,123,027 / 81.41%
Unmapped reads	2,311,137 / 18.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	415 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	540,683 / 4.35%
Duplication rate	3.51%
Clipped reads	1,101,736 / 8.86%

2.2. ACGT Content

Number/percentage of A's	144,489,841 / 30.4%
Number/percentage of C's	93,945,641 / 19.77%
Number/percentage of T's	141,578,836 / 29.79%
Number/percentage of G's	95,222,163 / 20.04%
Number/percentage of N's	1,551 / 0%
GC Percentage	39.8%

2.3. Coverage

Mean	0.1535

Standard Deviation	1.4487

2.4. Mapping Quality

Mean Mapping Quality	46.22

2.5. Mismatches and indels

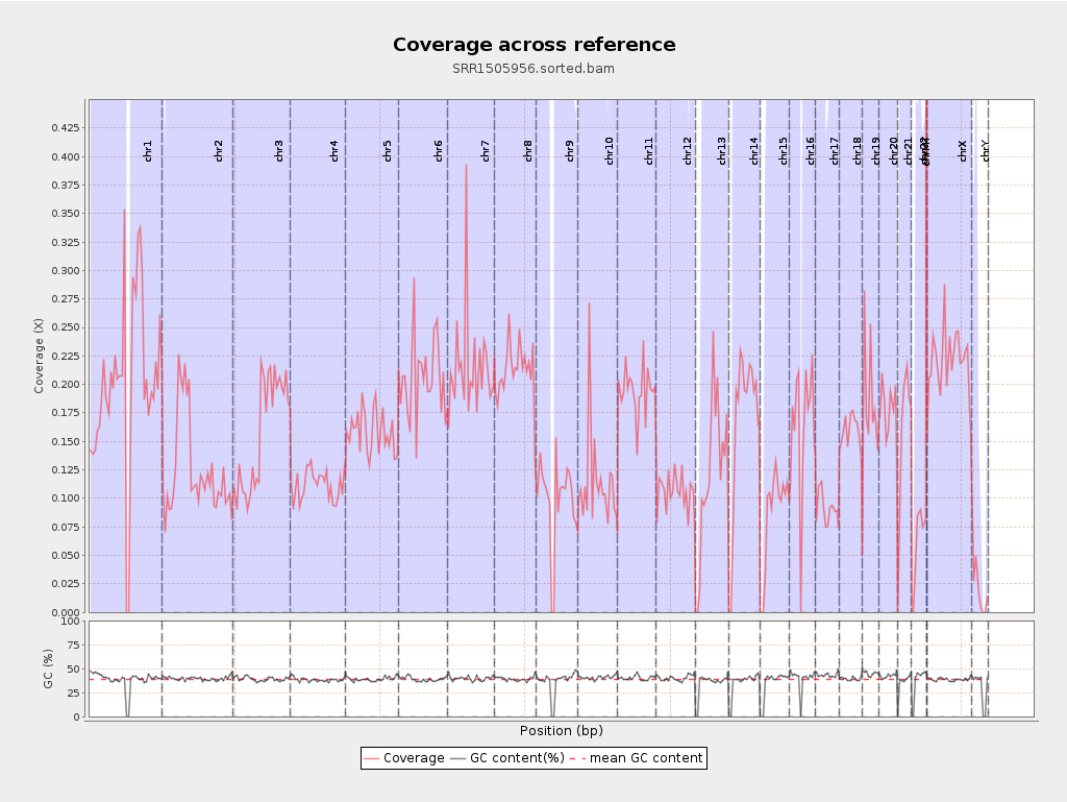
General error rate	0.46%
Mismatches	2,164,959
Insertions	20,523
Mapped reads with at least one insertion	0.2%
Deletions	73,714
Mapped reads with at least one deletion	0.73%
Homopolymer indels	48.61%

2.6. Chromosome stats

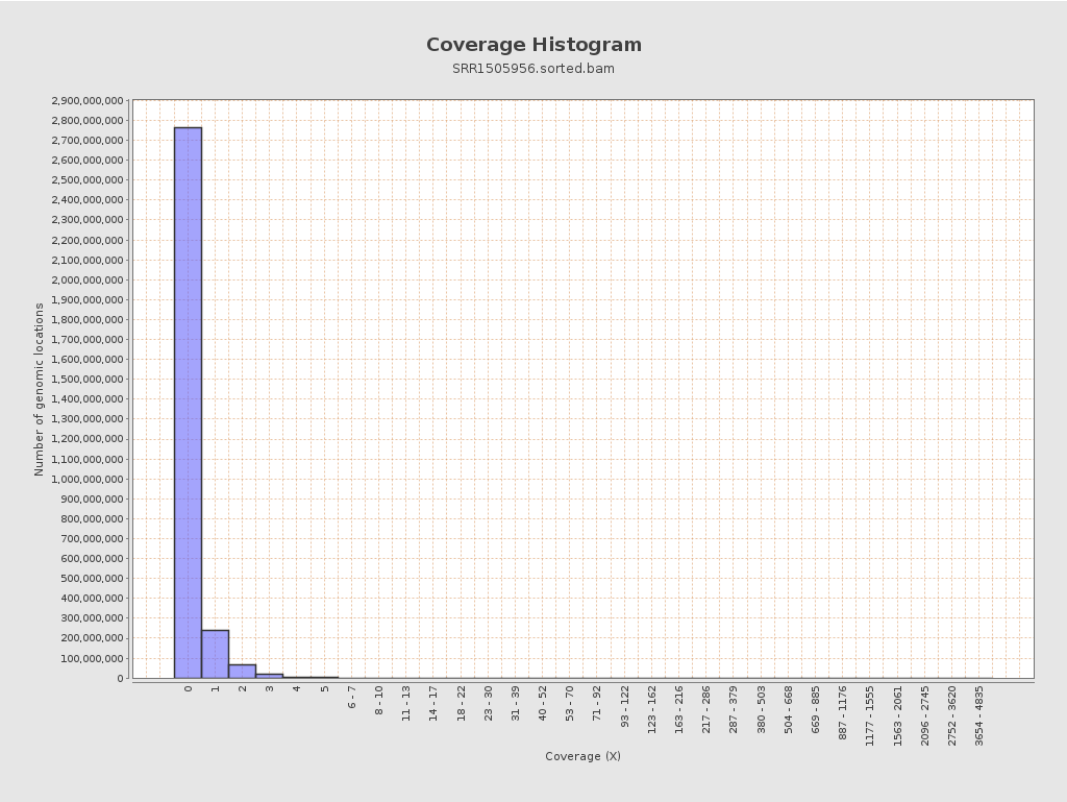
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	50358740	0.202	3.3242
chr2	243199373	30352393	0.1248	0.8839
chr3	198022430	31040896	0.1568	0.5561
chr4	191154276	21346080	0.1117	0.4431
chr5	180915260	28560020	0.1579	0.5446
chr6	171115067	35140257	0.2054	1.1208
chr7	159138663	34358843	0.2159	2.792

chr8	146364022	30970475	0.2116	1.9596
chr9	141213431	13937379	0.0987	0.76
chr10	135534747	15457369	0.114	1.4069
chr11	135006516	25933498	0.1921	1.2404
chr12	133851895	14108884	0.1054	0.5157
chr13	115169878	14080379	0.1223	0.4514
chr14	107349540	17862591	0.1664	0.5786
chr15	102531392	8876966	0.0866	0.3773
chr16	90354753	14875006	0.1646	0.6953
chr17	81195210	7325757	0.0902	0.5684
chr18	78077248	12533842	0.1605	1.7124
chr19	59128983	10929793	0.1848	2.0305
chr20	63025520	11288831	0.1791	0.5687
chr21	48129895	7558315	0.157	0.5983
chr22	51304566	3012105	0.0587	0.3258
chrMT	16571	31934	1.9271	1.8405
chrX	155270560	34161052	0.22	0.8754
chrY	59373566	1239497	0.0209	0.2498

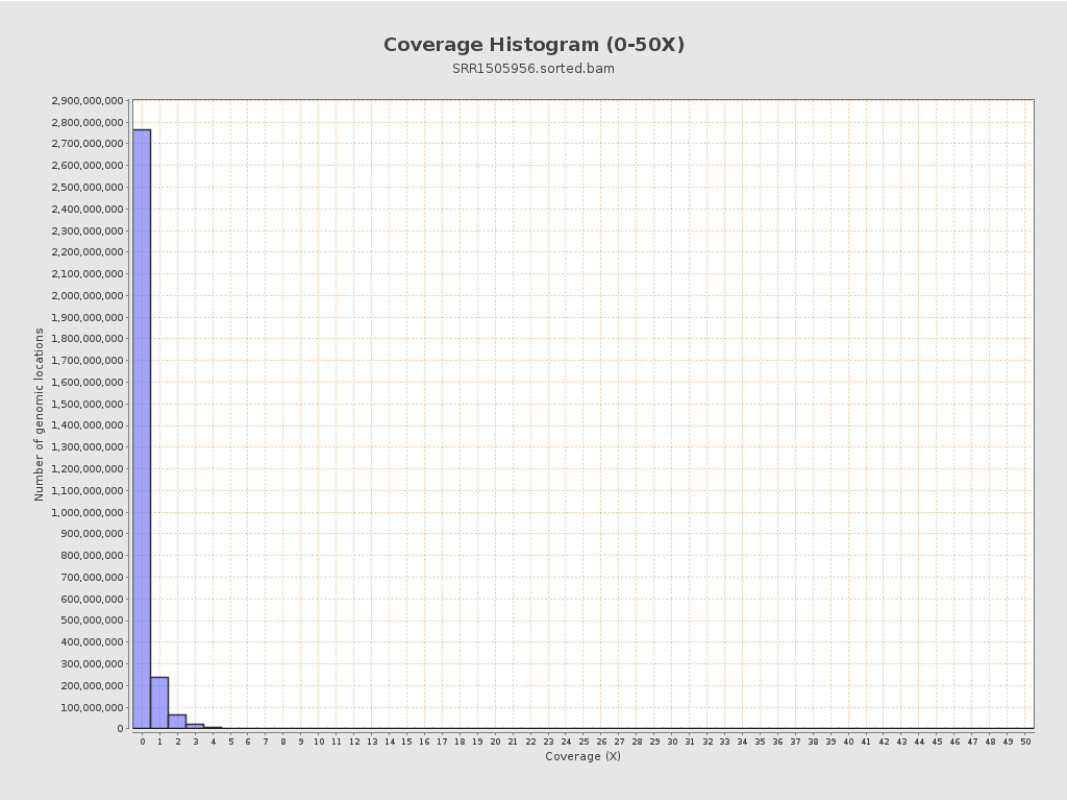
3. Results : Coverage across reference



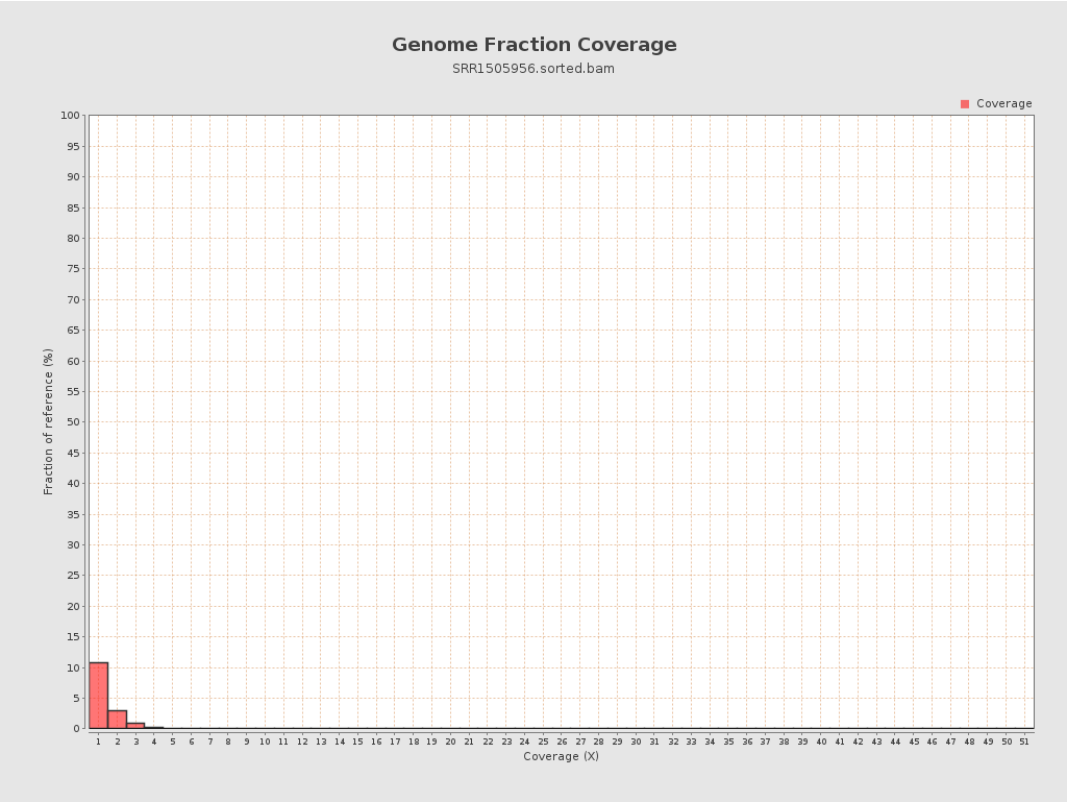
4. Results : Coverage Histogram



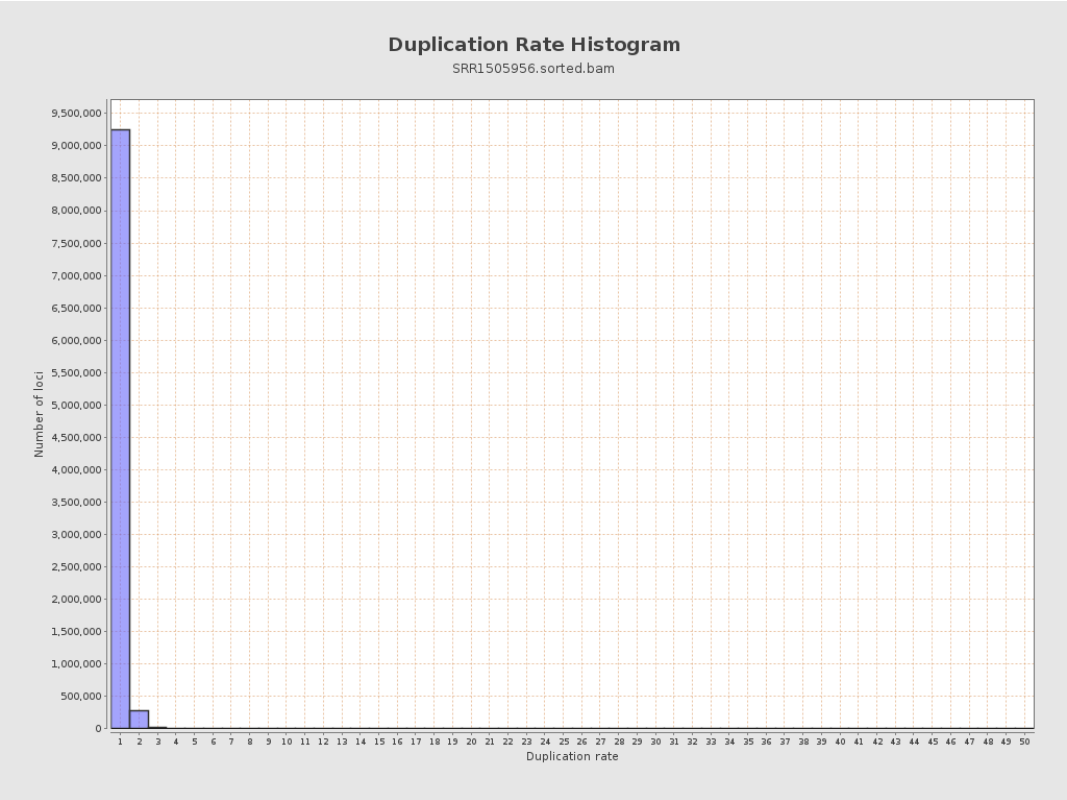
5. Results : Coverage Histogram (0-50X)



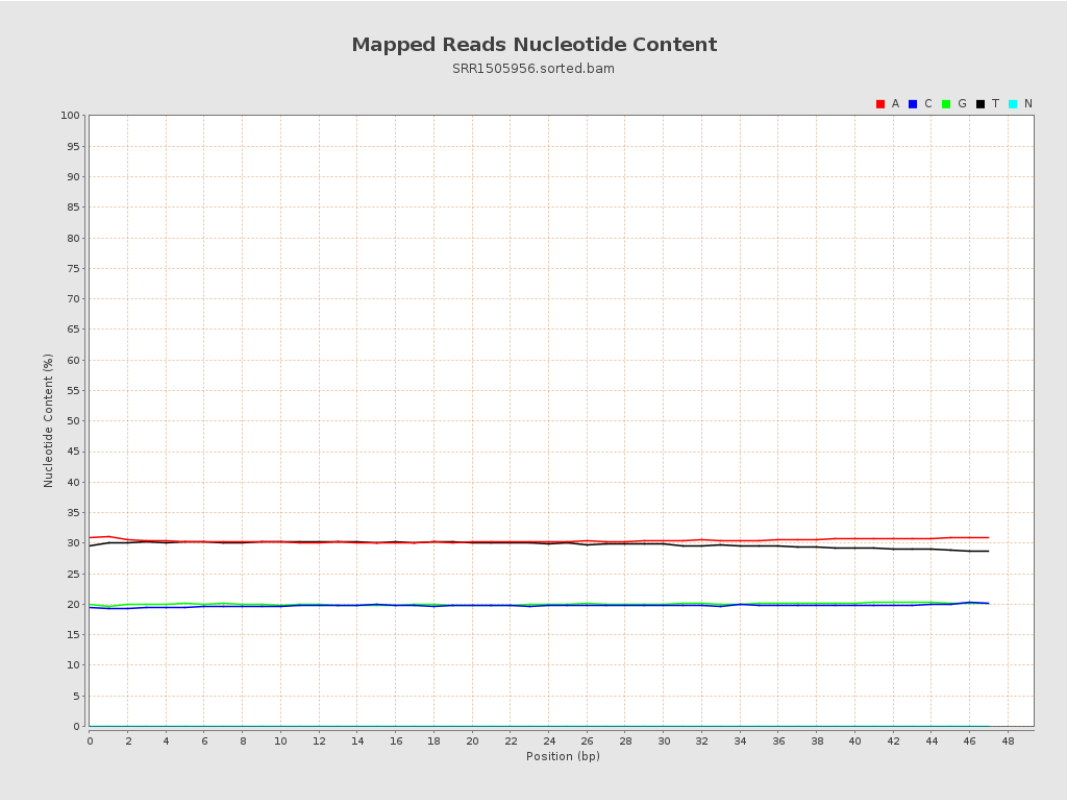
6. Results : Genome Fraction Coverage



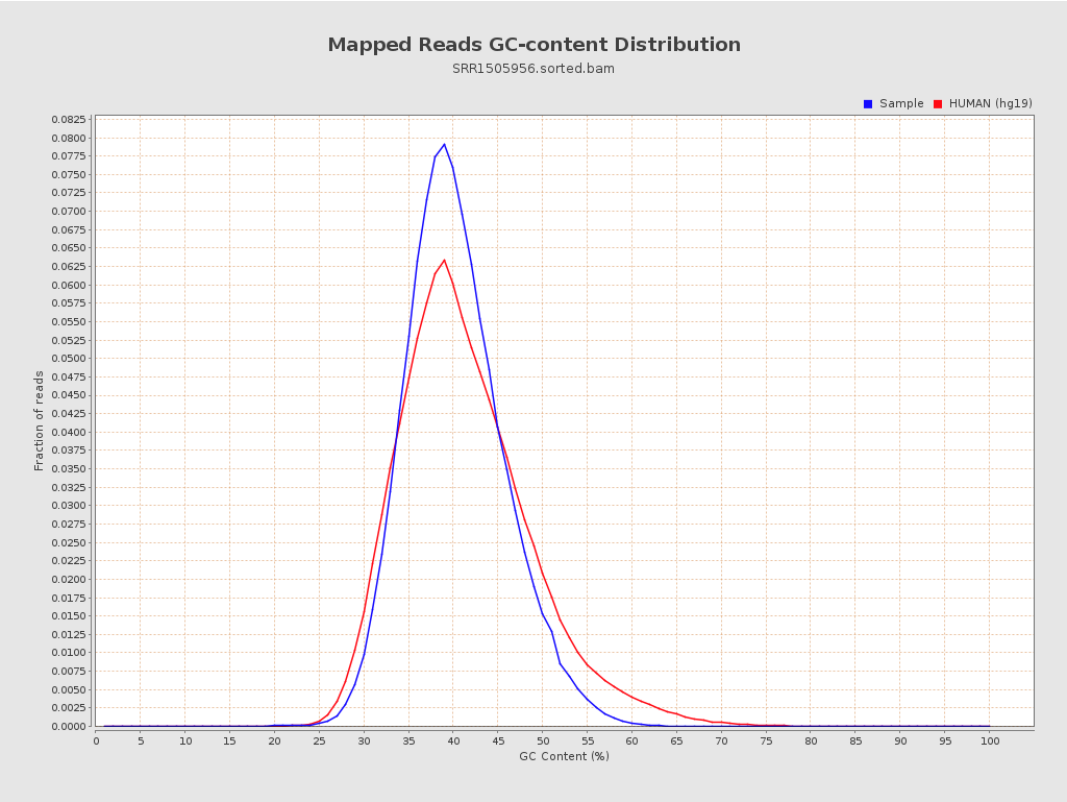
7. Results : Duplication Rate Histogram



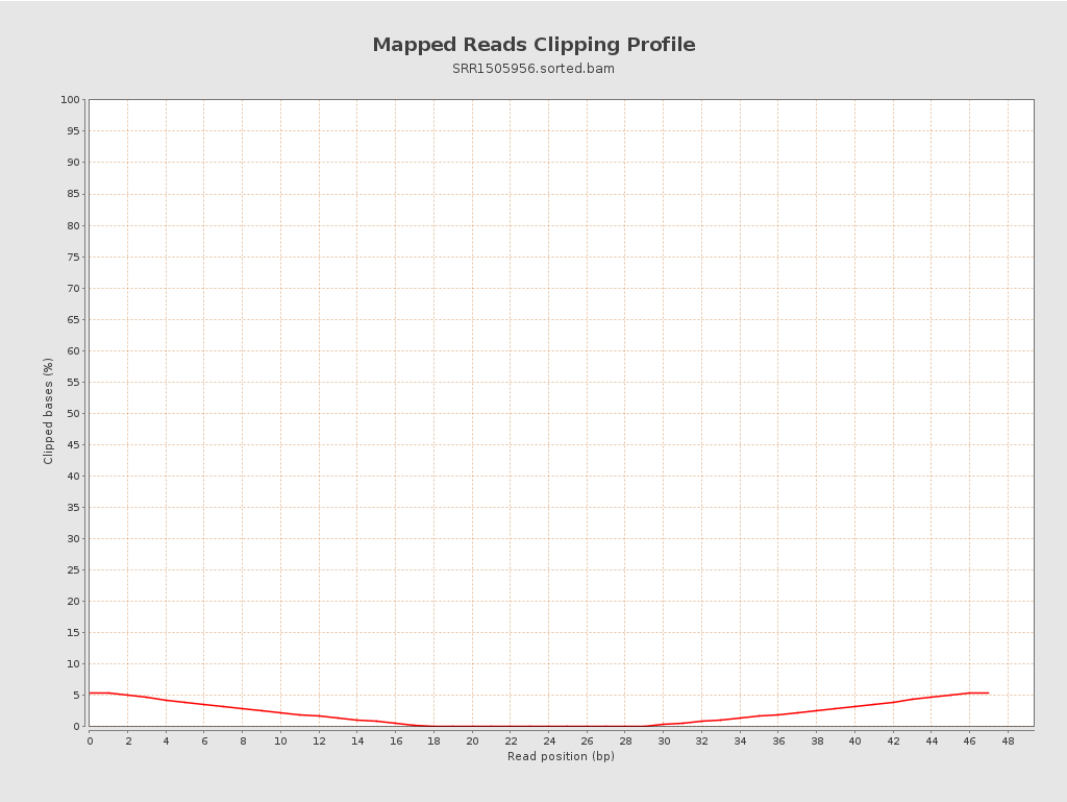
8. Results : Mapped Reads Nucleotide Content



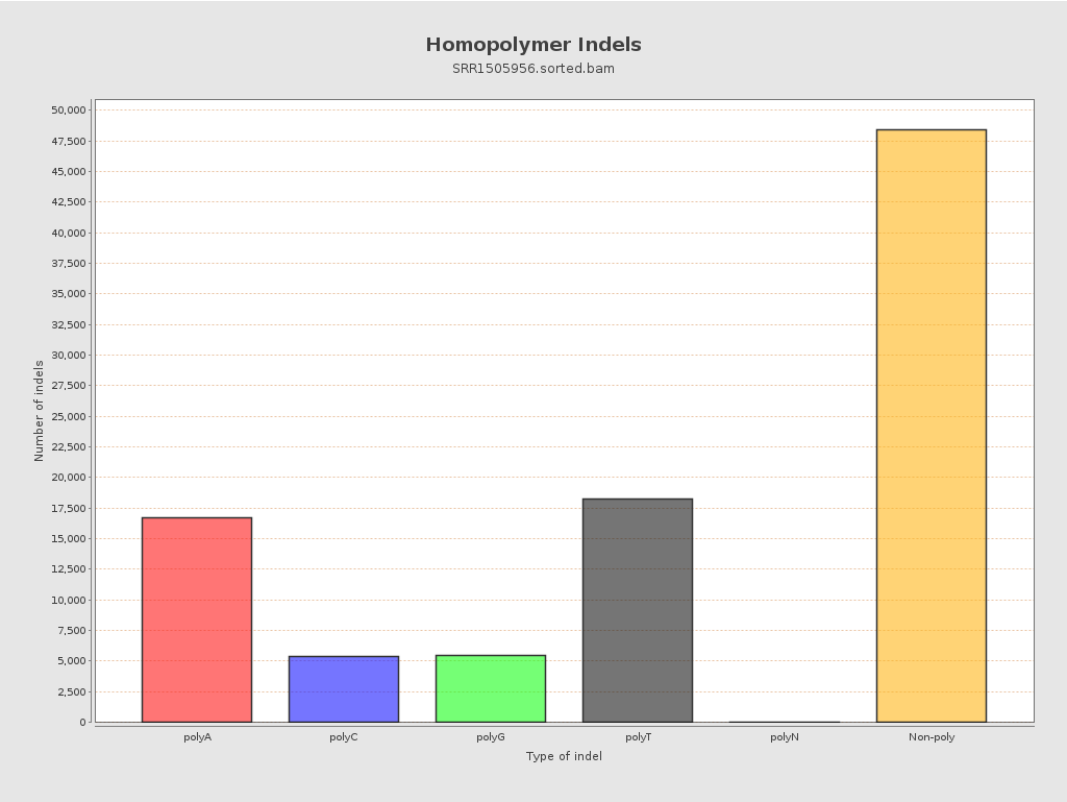
9. Results : Mapped Reads GC-content Distribution



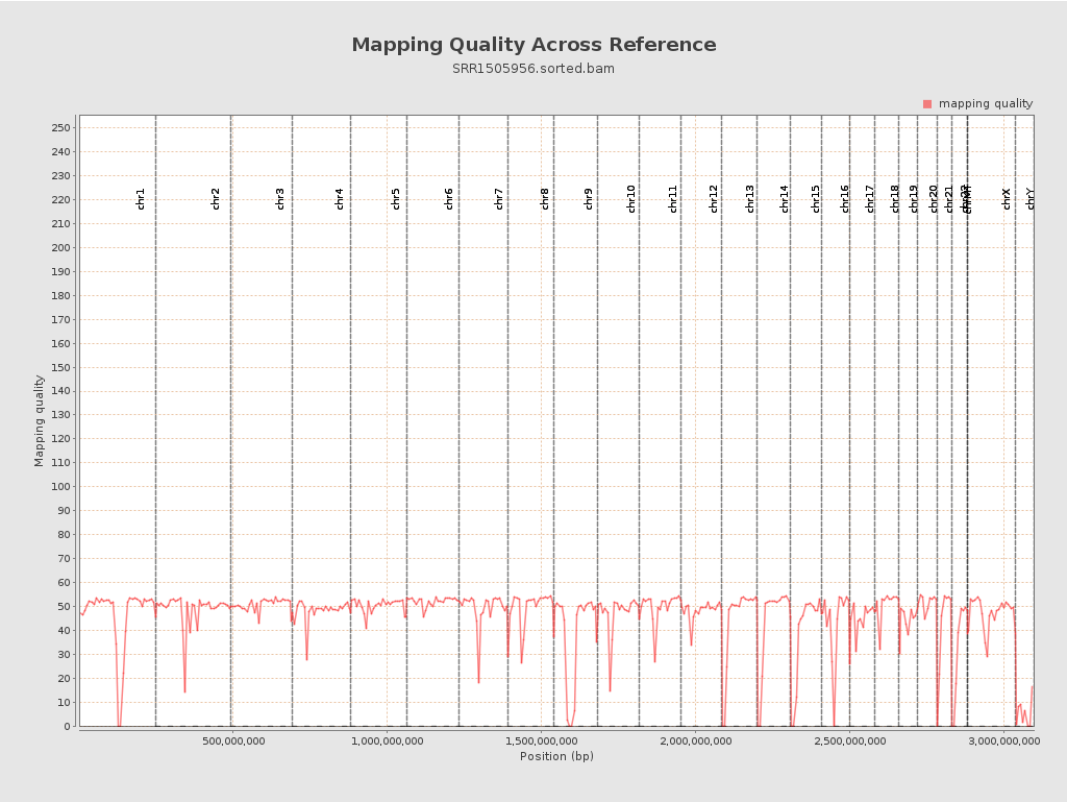
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram