Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 21:48:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505980.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_SRR1505980 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505980.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 21:48:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505980.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,222,788
Mapped reads	5,330,930 / 64.83%
Unmapped reads	2,891,858 / 35.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	290 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	540,556 / 6.57%
Duplication rate	7.41%
Clipped reads	1,162,431 / 14.14%

2.2. ACGT Content

Number/percentage of A's	71,471,390 / 29.25%
Number/percentage of C's	51,406,173 / 21.04%
Number/percentage of T's	69,631,916 / 28.5%
Number/percentage of G's	51,840,780 / 21.22%
Number/percentage of N's	1,075 / 0%
GC Percentage	42.25%

2.3. Coverage

Mean	0.0789

Standard Deviation	0.7188

2.4. Mapping Quality

Mean Mapping Quality	43.44

2.5. Mismatches and indels

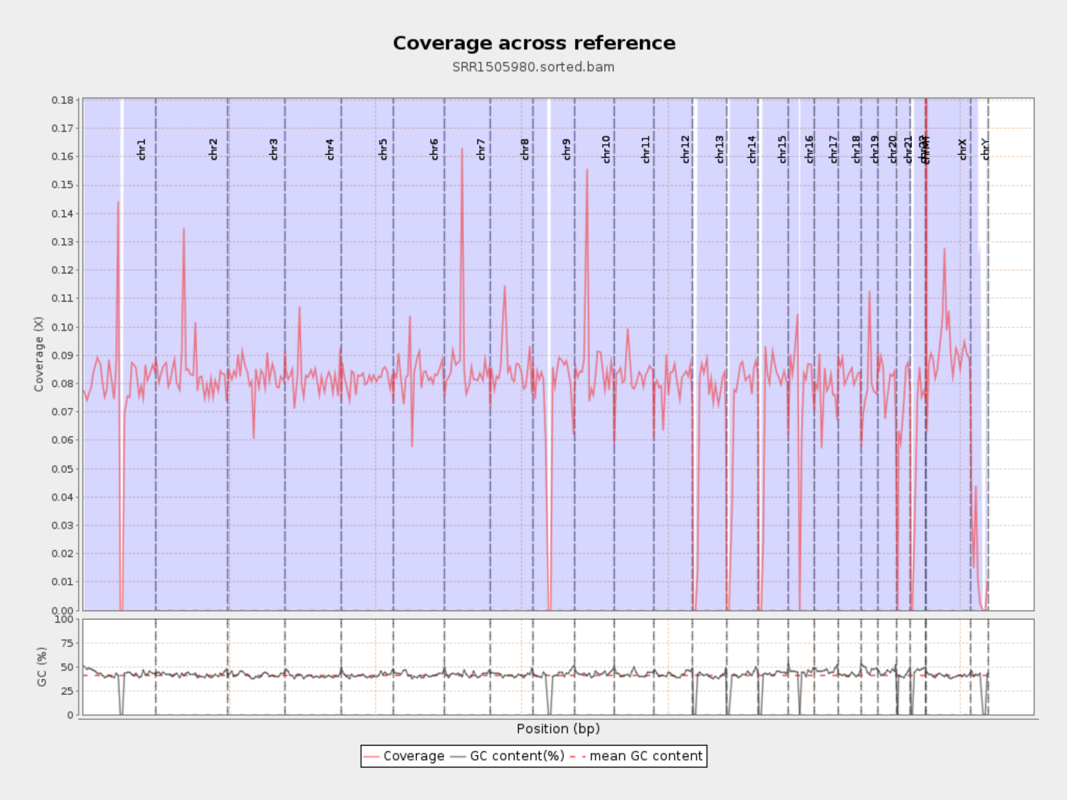
General error rate	0.5%
Mismatches	1,215,334
Insertions	10,850
Mapped reads with at least one insertion	0.2%
Deletions	31,758
Mapped reads with at least one deletion	0.59%
Homopolymer indels	42.98%

2.6. Chromosome stats

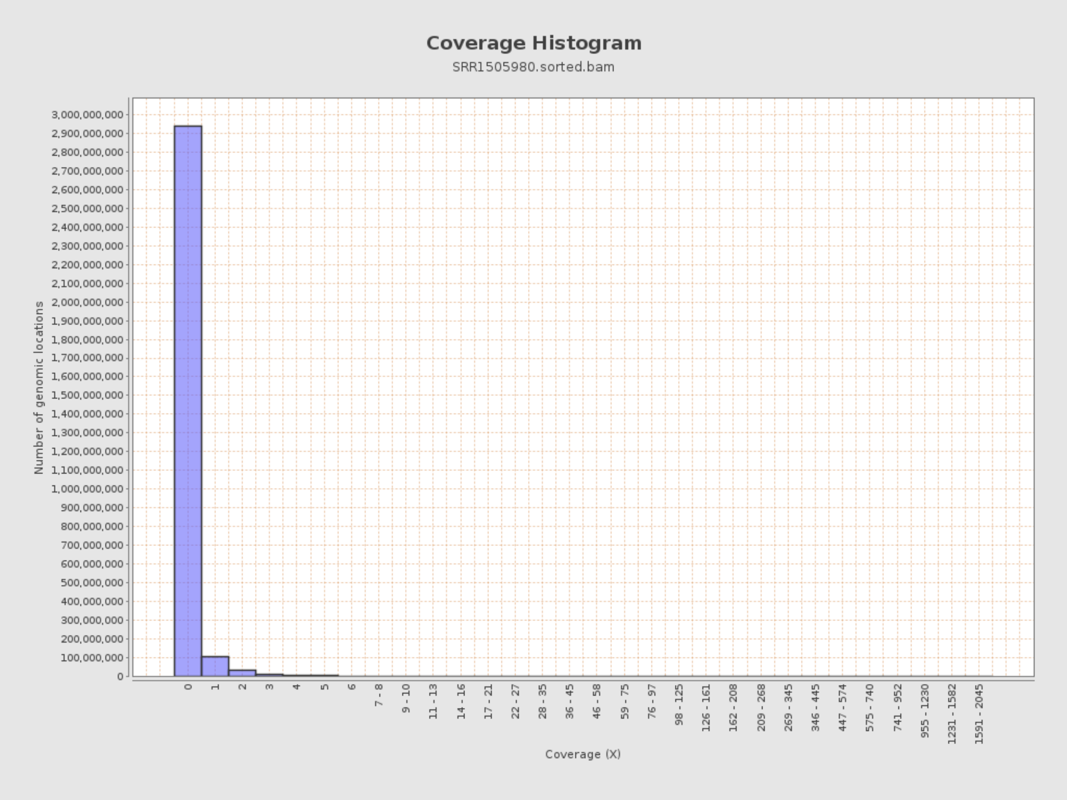
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19450851	0.078	1.4489
chr2	243199373	20484446	0.0842	0.6132
chr3	198022430	16329052	0.0825	0.4236
chr4	191154276	15740313	0.0823	0.4508
chr5	180915260	14807840	0.0818	0.4263
chr6	171115067	14252272	0.0833	0.5142
chr7	159138663	13913544	0.0874	1.0745

chr8	146364022	12571968	0.0859	0.9922
chr9	141213431	10174943	0.0721	0.5406
chr10	135534747	11820494	0.0872	0.7338
chr11	135006516	11227537	0.0832	0.639
chr12	133851895	10825582	0.0809	0.4438
chr13	115169878	7733991	0.0672	0.3769
chr14	107349540	7381617	0.0688	0.5383
chr15	102531392	6967192	0.068	0.3825
chr16	90354753	6870420	0.076	0.4455
chr17	81195210	6314695	0.0778	0.4684
chr18	78077248	6532465	0.0837	1.011
chr19	59128983	4753543	0.0804	0.9772
chr20	63025520	5094220	0.0808	0.4451
chr21	48129895	3243208	0.0674	0.4412
chr22	51304566	2781776	0.0542	0.3458
chrMT	16571	89070	5.3751	4.8258
chrX	155270560	14211337	0.0915	0.5124
chrY	59373566	822490	0.0139	0.268

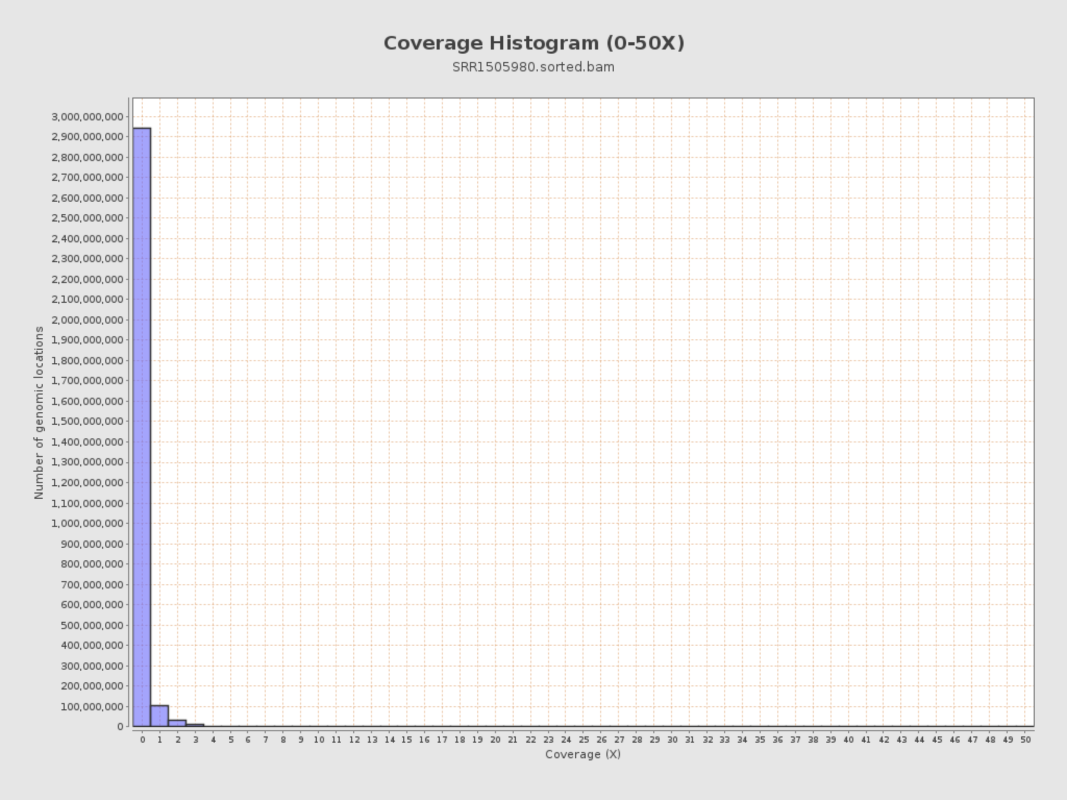
3. Results : Coverage across reference



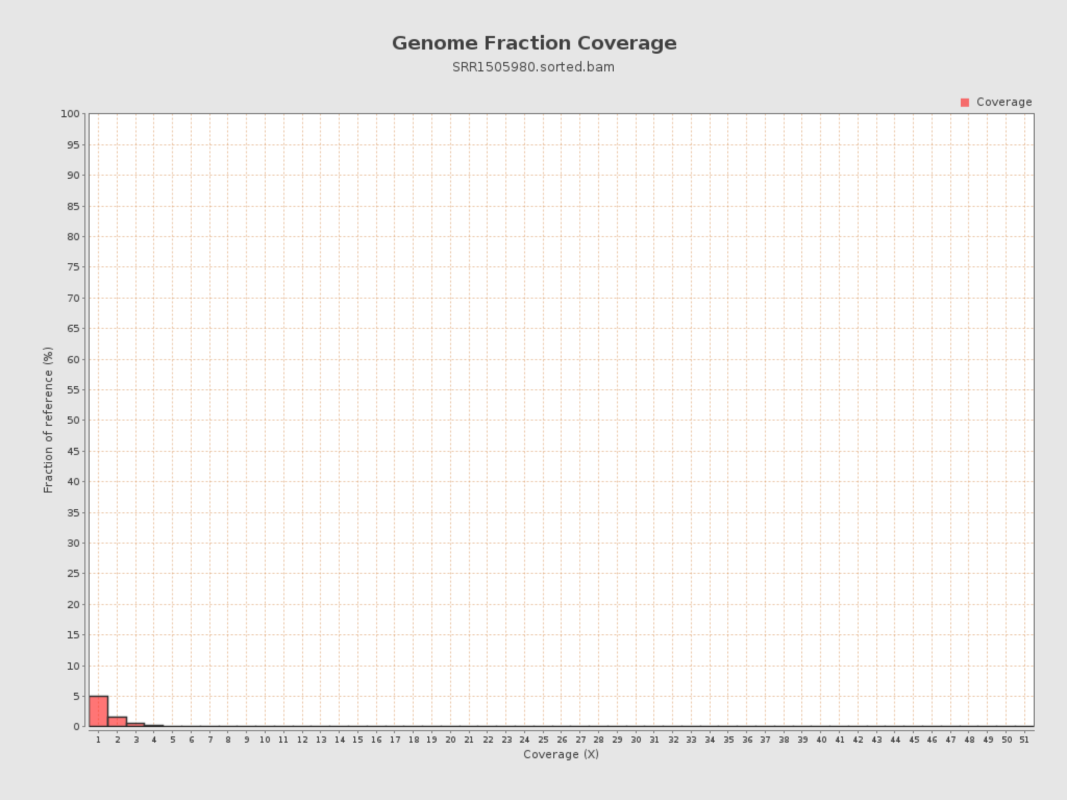
4. Results : Coverage Histogram



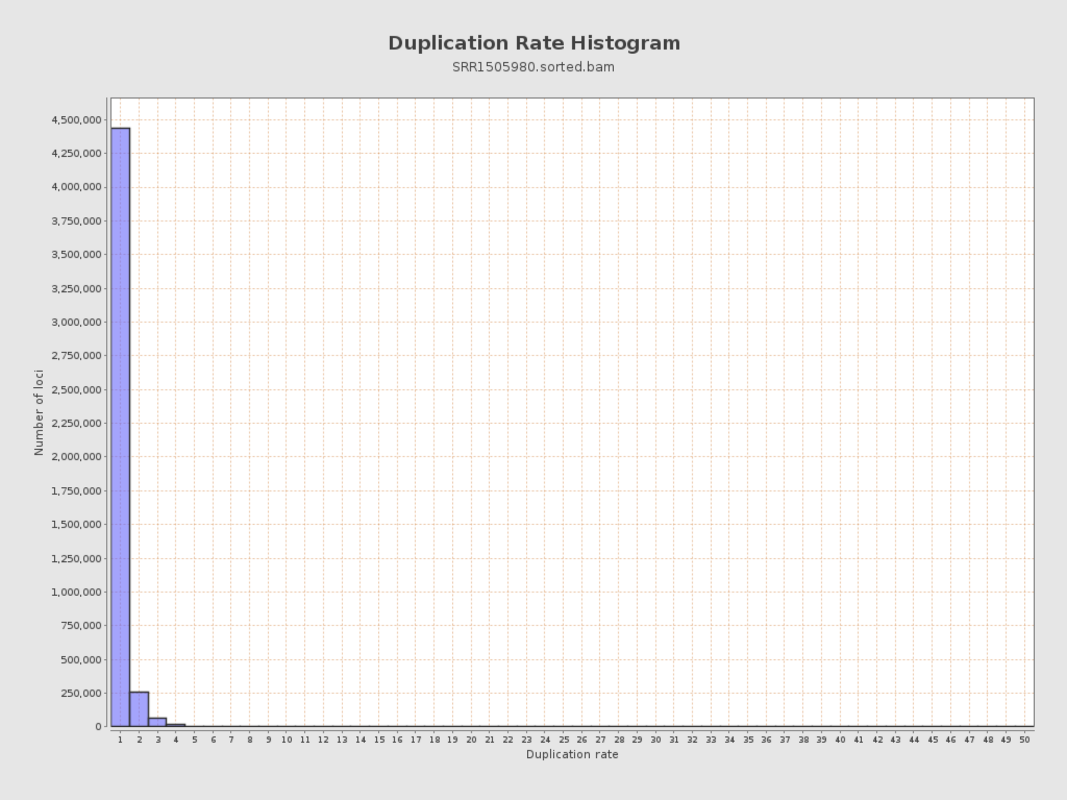
5. Results : Coverage Histogram (0-50X)



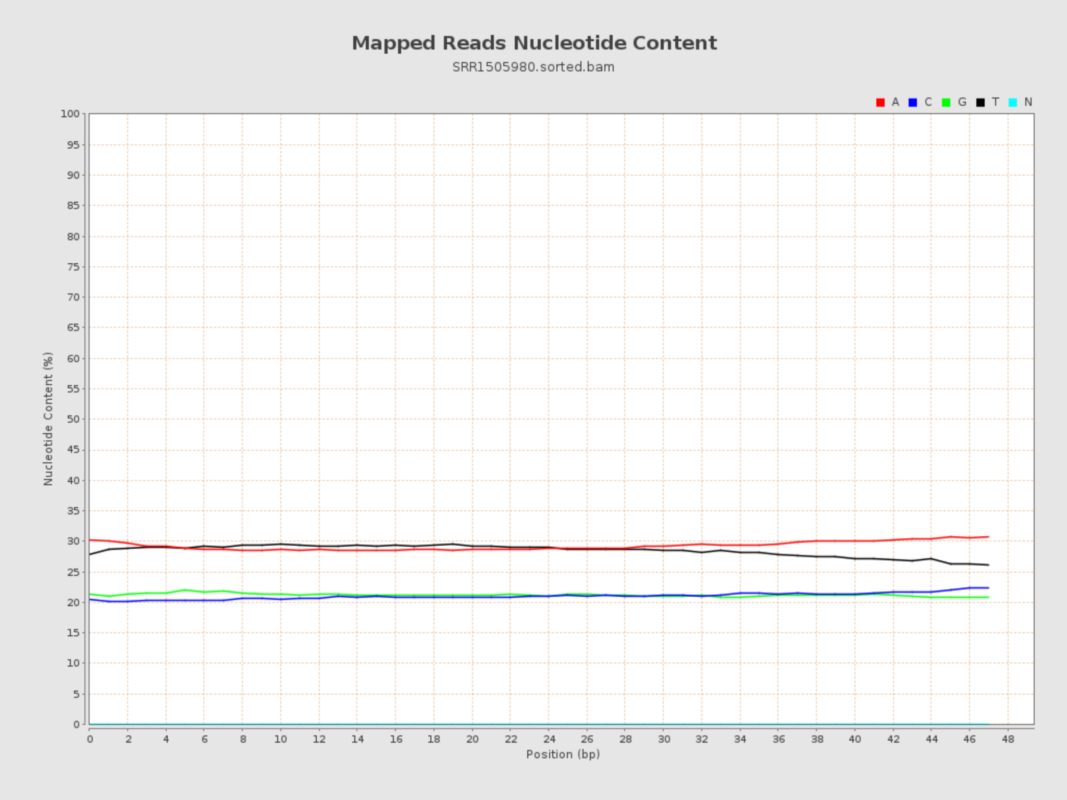
6. Results : Genome Fraction Coverage



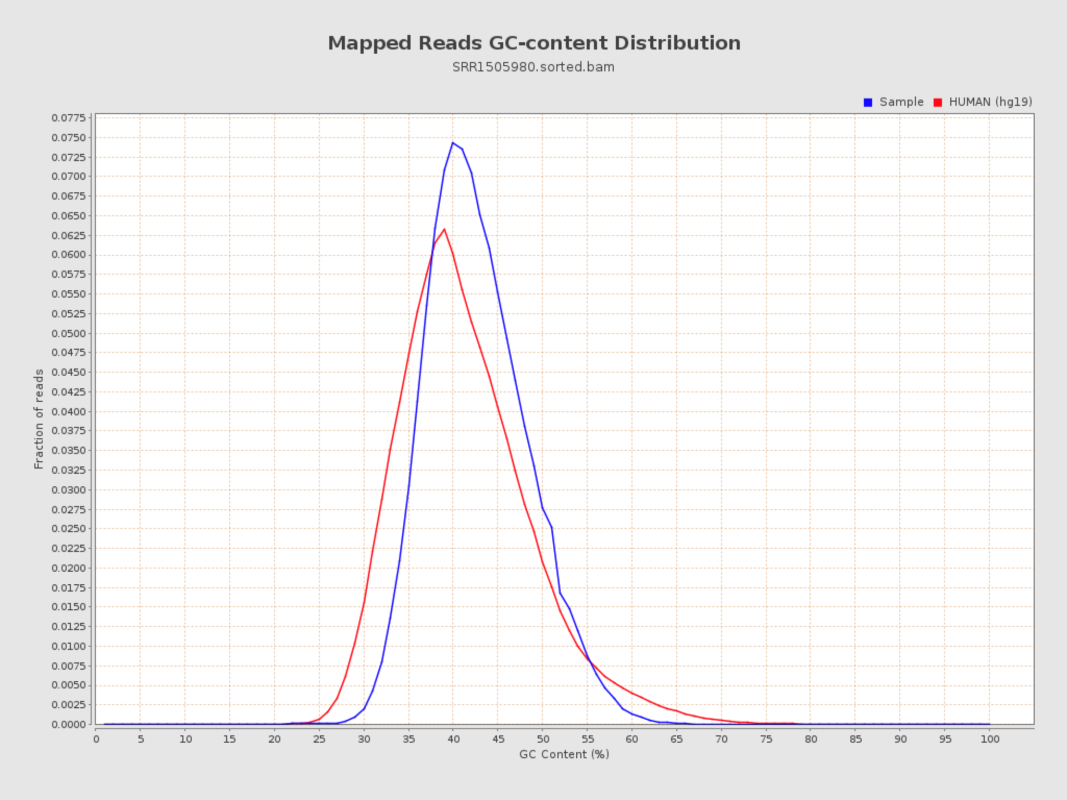
7. Results : Duplication Rate Histogram



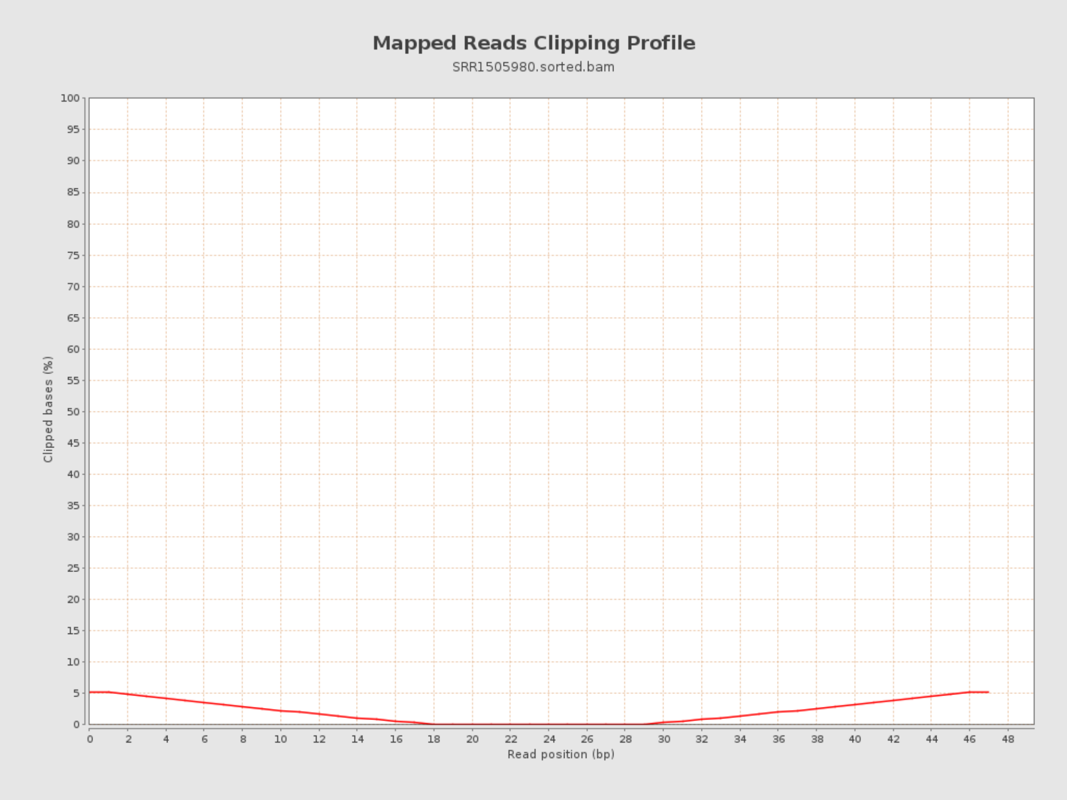
8. Results : Mapped Reads Nucleotide Content



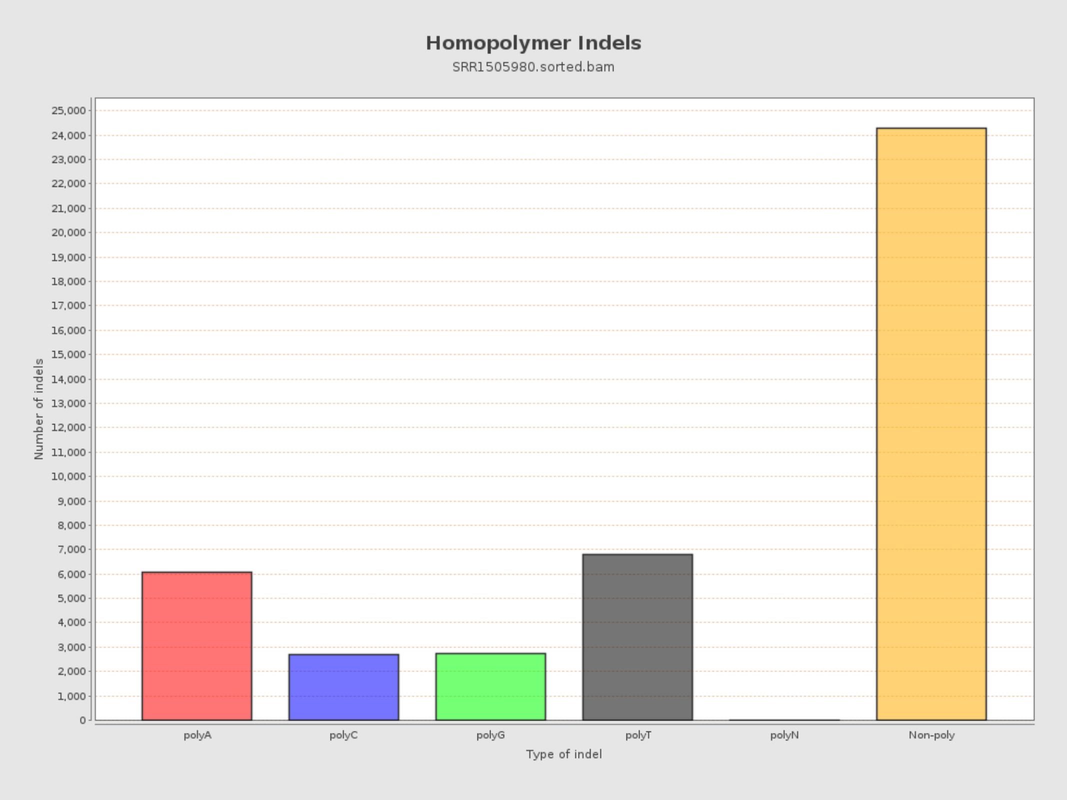
9. Results : Mapped Reads GC-content Distribution



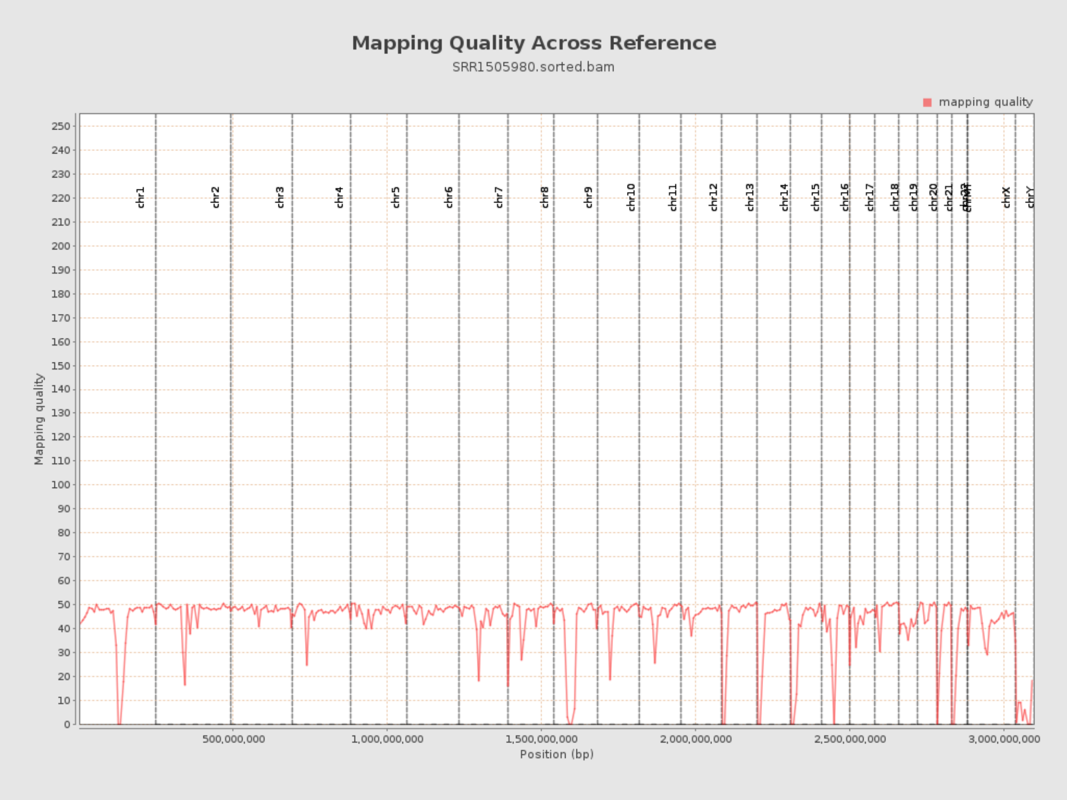
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram