Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 21:14:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505957.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_SRR1505957 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505957.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 21:14:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505957.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,630,871
Mapped reads	3,969,229 / 70.49%
Unmapped reads	1,661,642 / 29.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	182 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	167,568 / 2.98%
Duplication rate	3.11%
Clipped reads	691,229 / 12.28%

2.2. ACGT Content

Number/percentage of A's	54,188,113 / 29.5%
Number/percentage of C's	37,856,900 / 20.61%
Number/percentage of T's	53,512,871 / 29.14%
Number/percentage of G's	38,108,680 / 20.75%
Number/percentage of N's	548 / 0%
GC Percentage	41.36%

2.3. Coverage

Mean	0.0593

Standard Deviation	0.5662

2.4. Mapping Quality

Mean Mapping Quality	43.93

2.5. Mismatches and indels

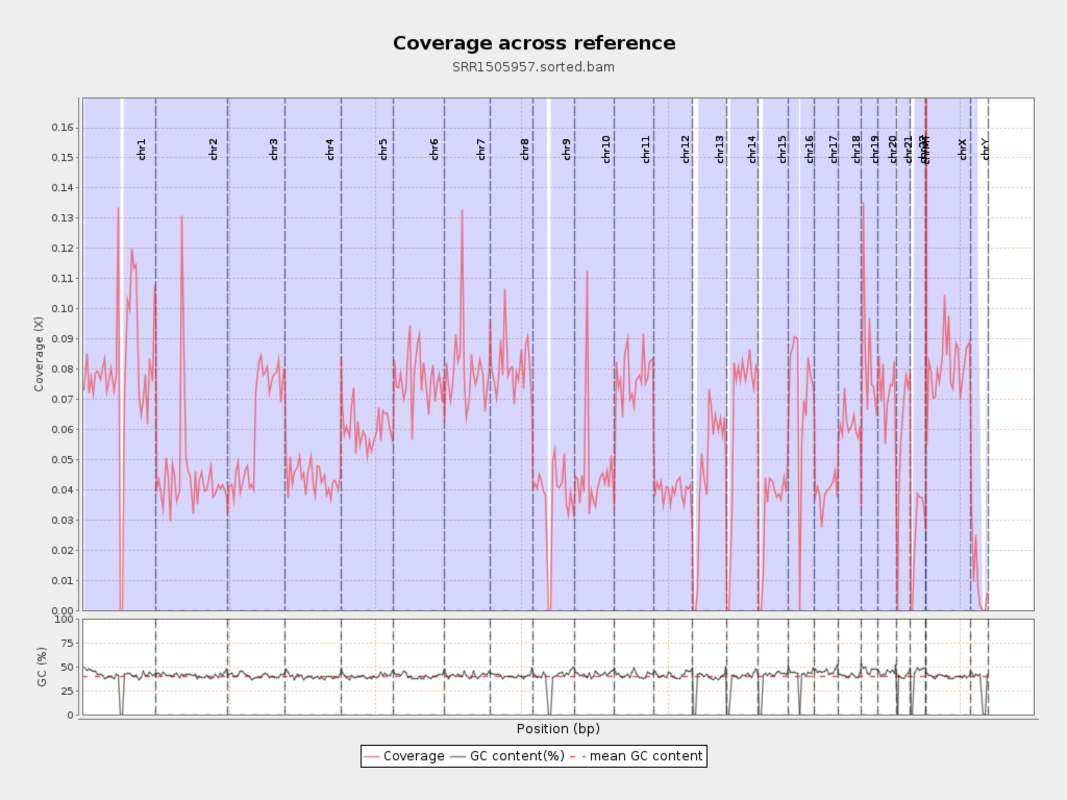
General error rate	0.5%
Mismatches	899,260
Insertions	7,907
Mapped reads with at least one insertion	0.2%
Deletions	26,911
Mapped reads with at least one deletion	0.68%
Homopolymer indels	46.49%

2.6. Chromosome stats

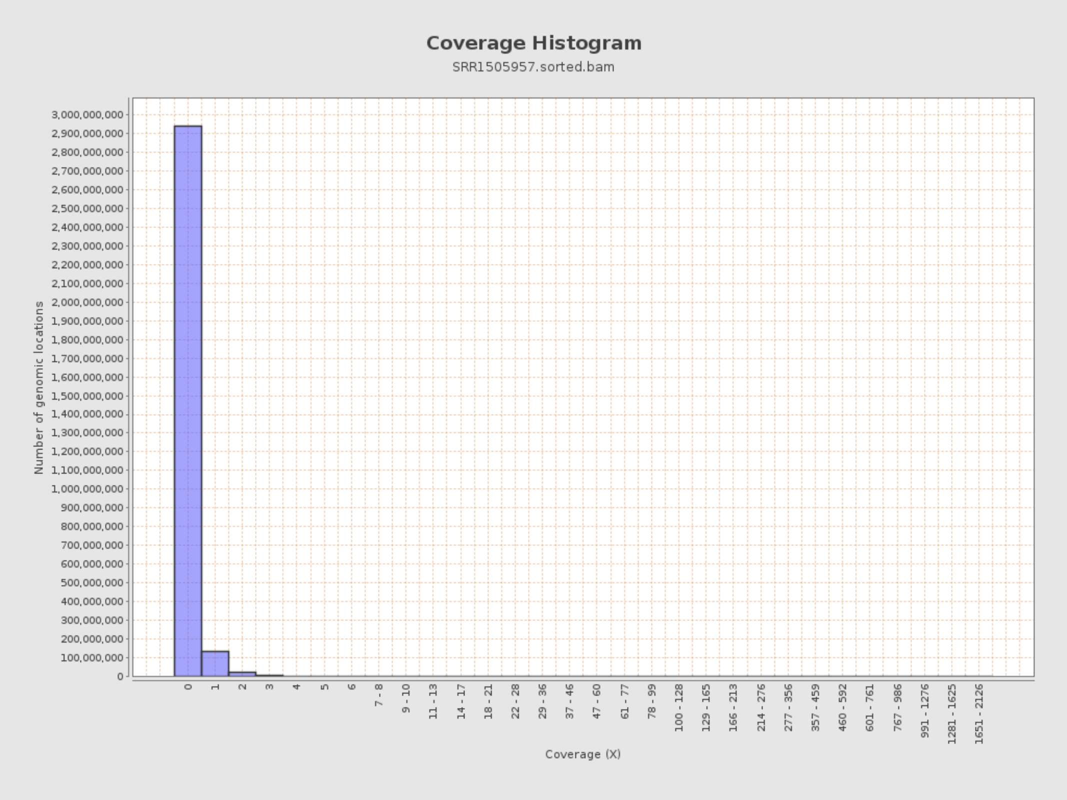
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19713665	0.0791	1.3751
chr2	243199373	11126319	0.0457	0.3875
chr3	198022430	12043107	0.0608	0.2877
chr4	191154276	8387178	0.0439	0.2442
chr5	180915260	10914733	0.0603	0.2875
chr6	171115067	13160600	0.0769	0.37
chr7	159138663	12654540	0.0795	0.793

chr8	146364022	11776391	0.0805	0.7139
chr9	141213431	5226183	0.037	0.3182
chr10	135534747	6146437	0.0453	0.5813
chr11	135006516	10352165	0.0767	0.472
chr12	133851895	5282161	0.0395	0.2413
chr13	115169878	5445901	0.0473	0.2467
chr14	107349540	7088365	0.066	0.3322
chr15	102531392	3348249	0.0327	0.2061
chr16	90354753	6342148	0.0702	0.375
chr17	81195210	3186811	0.0392	0.2584
chr18	78077248	4817651	0.0617	0.5743
chr19	59128983	4870597	0.0824	0.8558
chr20	63025520	4562882	0.0724	0.313
chr21	48129895	2825954	0.0587	0.2958
chr22	51304566	1342346	0.0262	0.1867
chrMT	16571	7923	0.4781	0.8795
chrX	155270560	12533972	0.0807	0.3686
chrY	59373566	548675	0.0092	0.1398

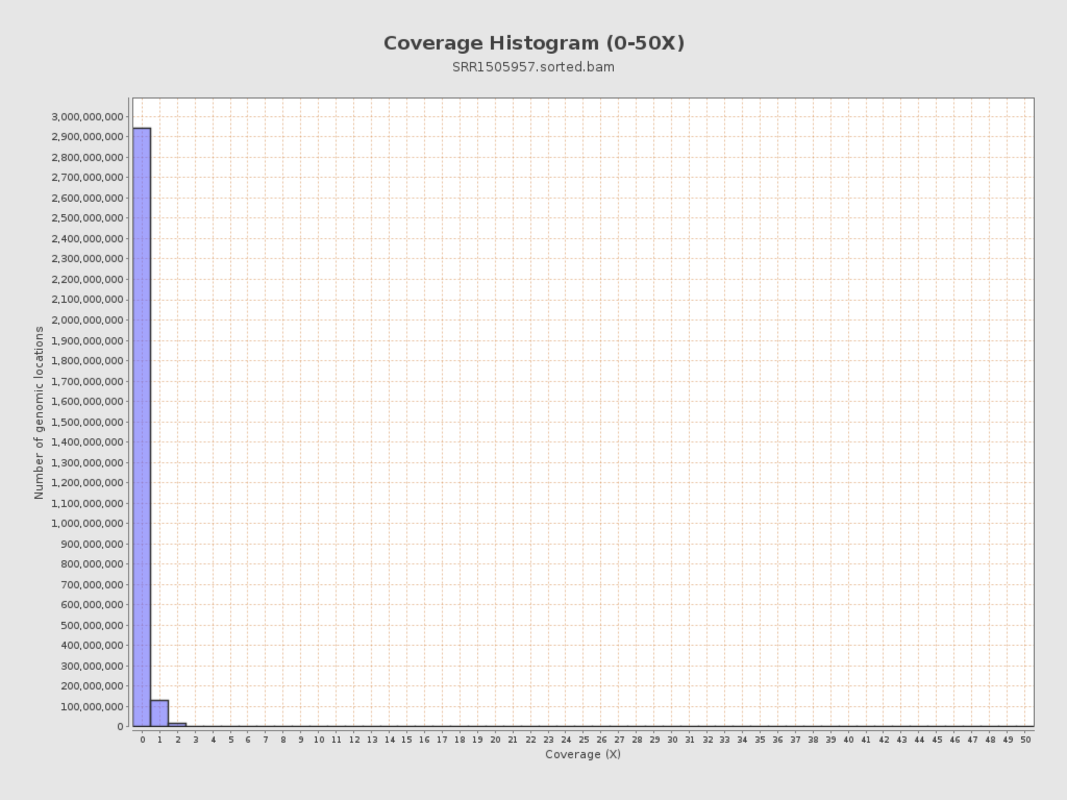
3. Results : Coverage across reference



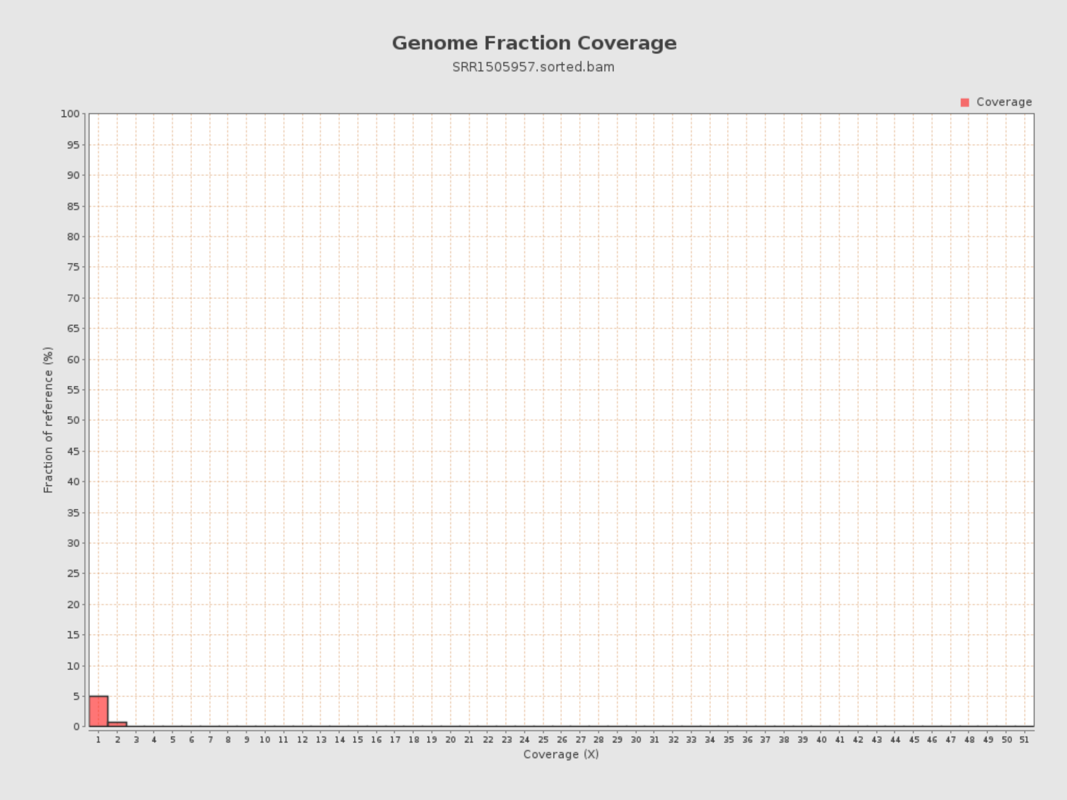
4. Results : Coverage Histogram



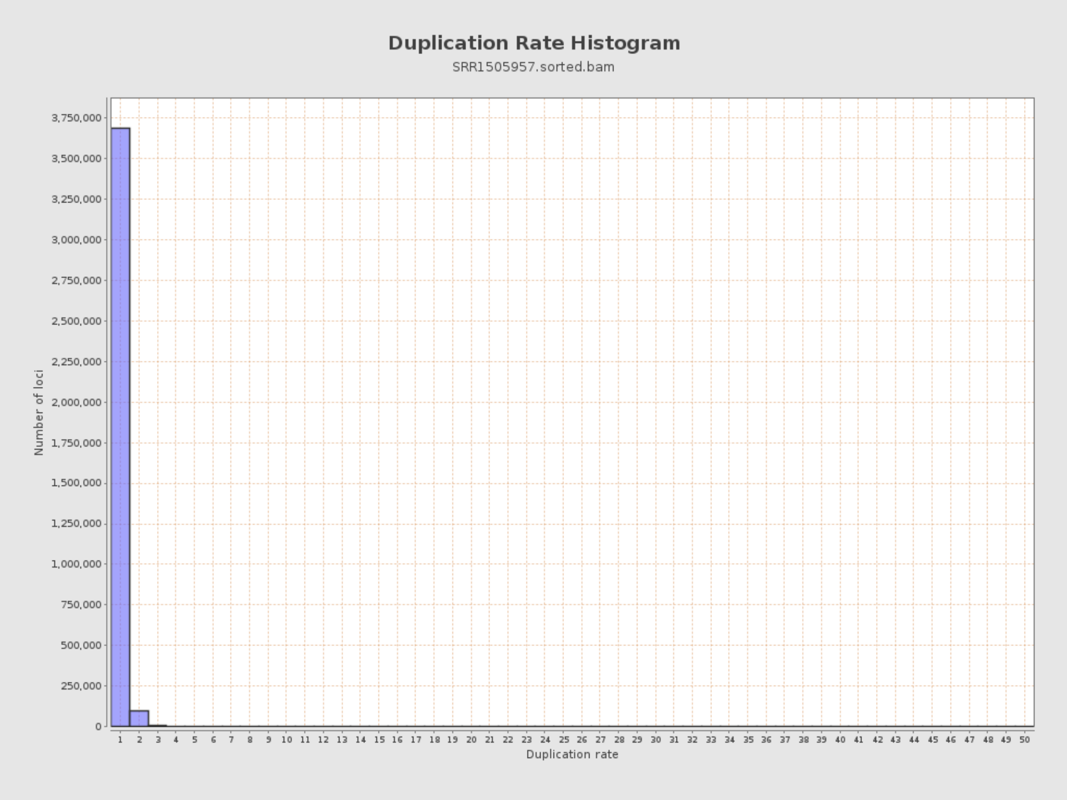
5. Results : Coverage Histogram (0-50X)



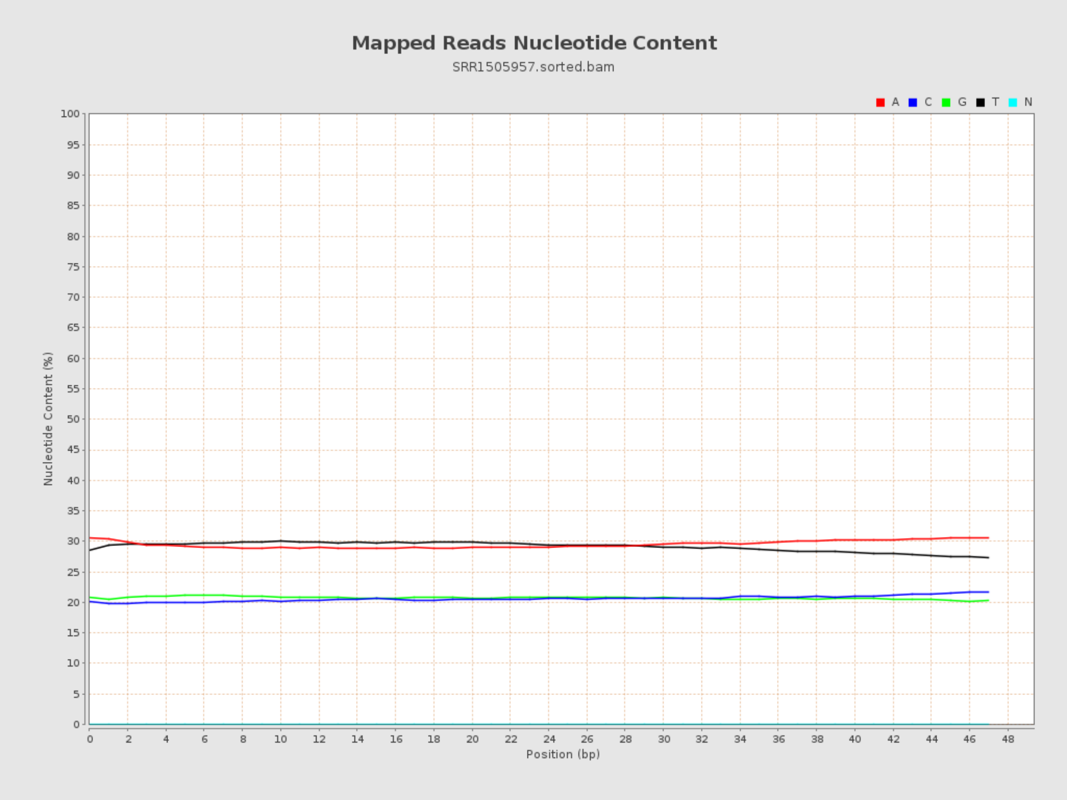
6. Results : Genome Fraction Coverage



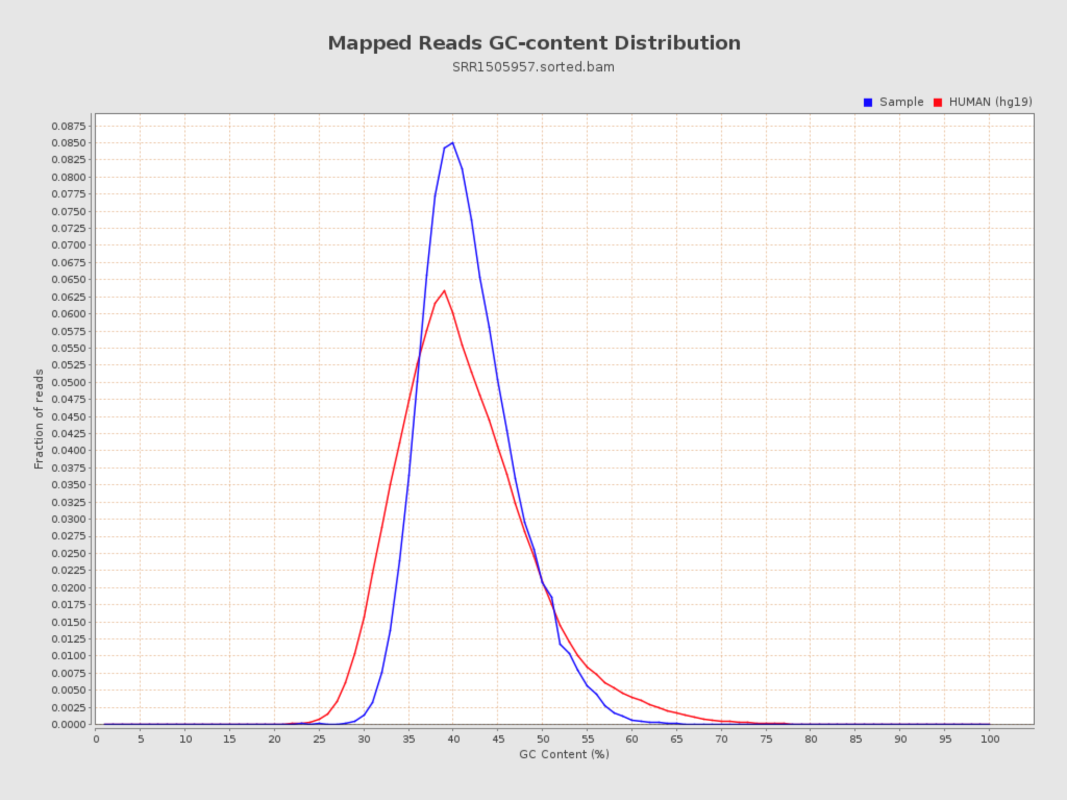
7. Results : Duplication Rate Histogram



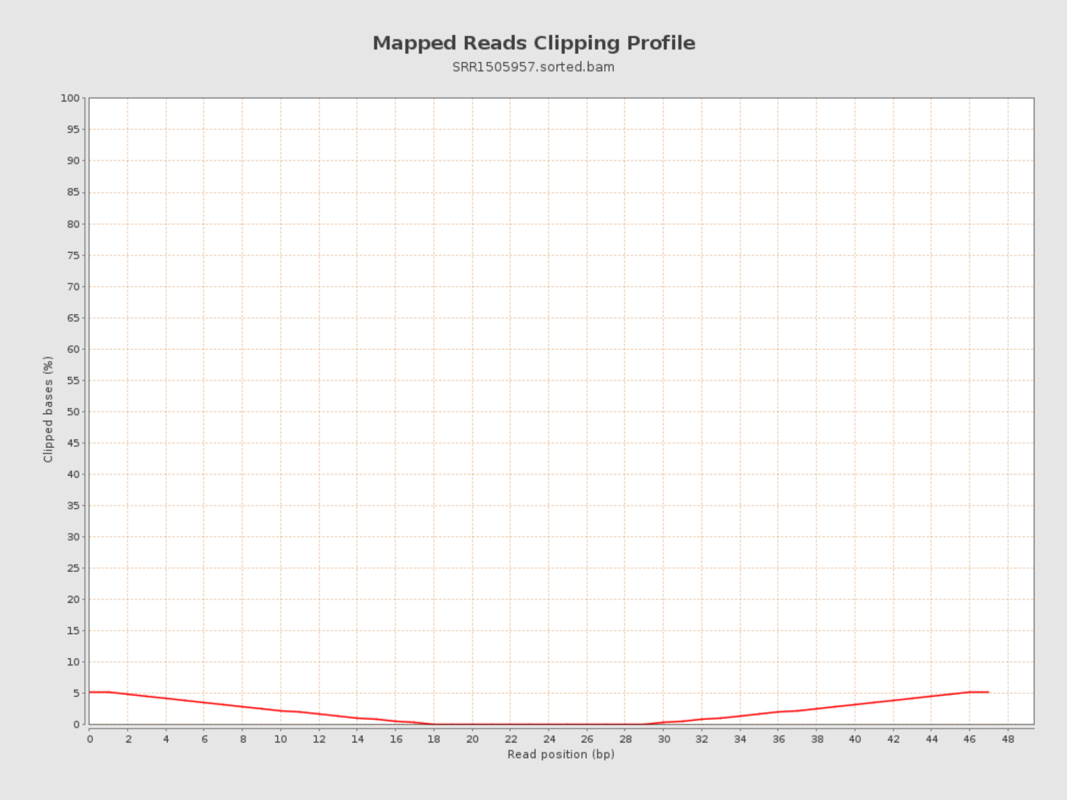
8. Results : Mapped Reads Nucleotide Content



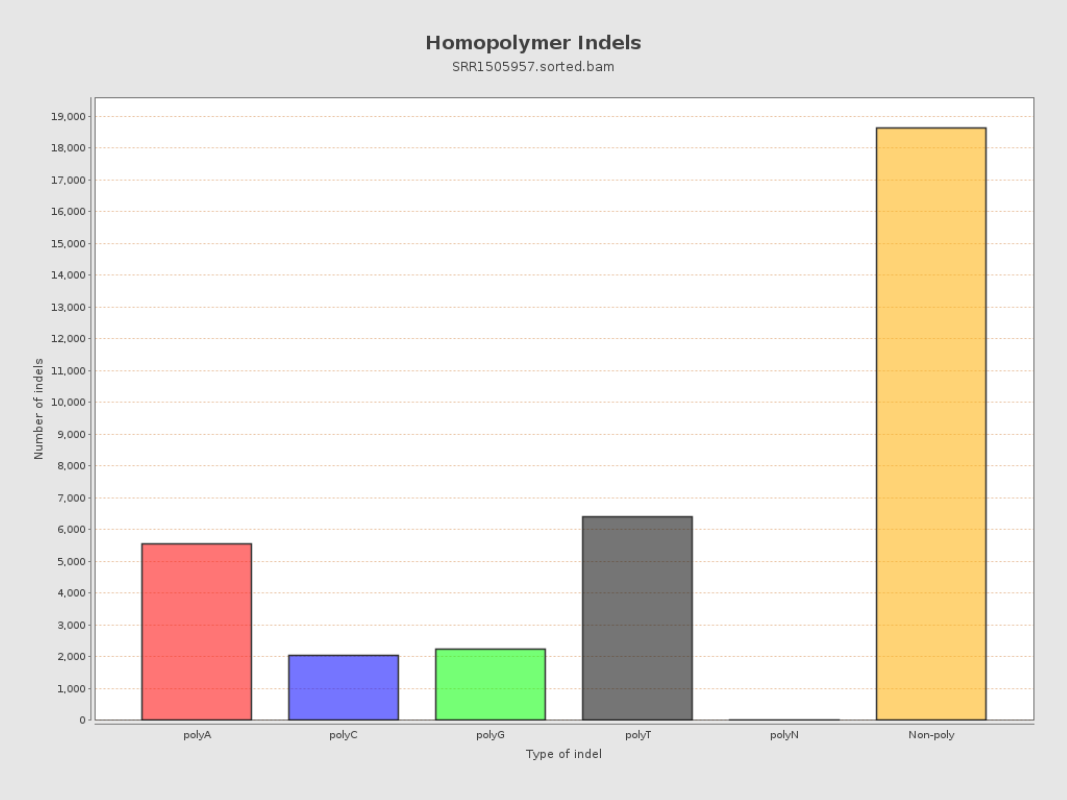
9. Results : Mapped Reads GC-content Distribution



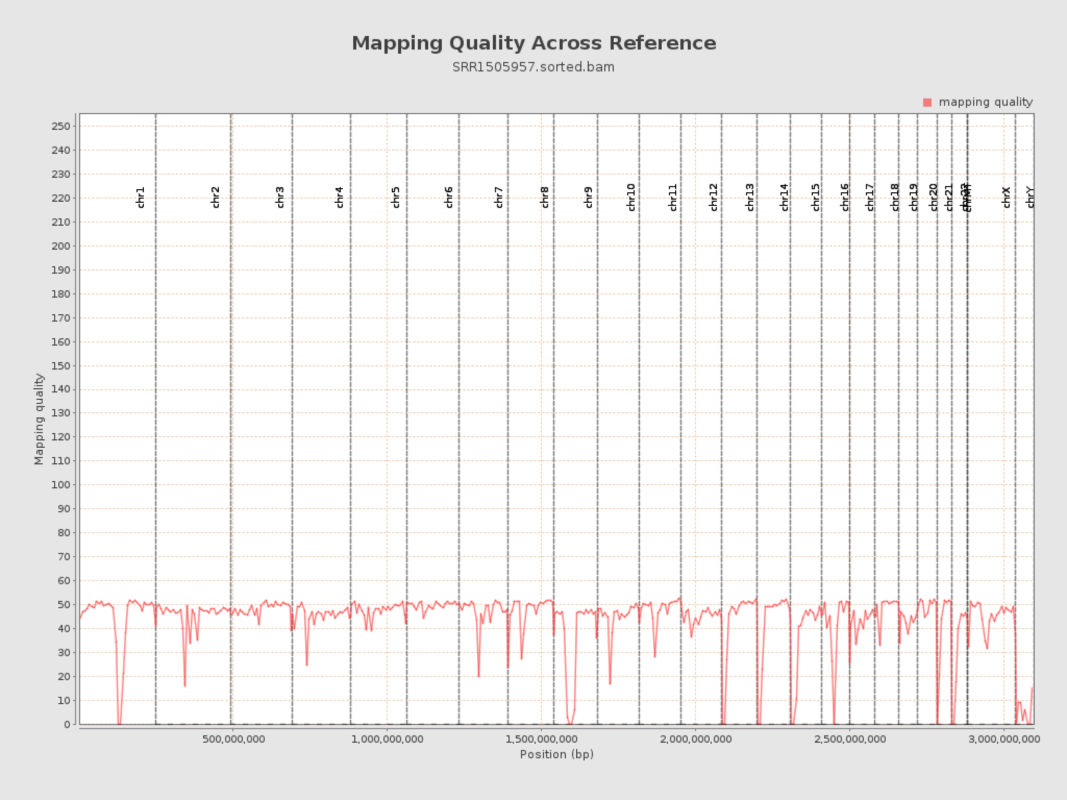
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram