Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 20:33:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505922.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_SRR1505922 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505922.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 20:33:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505922.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,895,980
Mapped reads	4,366,786 / 74.06%
Unmapped reads	1,529,194 / 25.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	246 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	187,936 / 3.19%
Duplication rate	3.23%
Clipped reads	766,676 / 13%

2.2. ACGT Content

Number/percentage of A's	59,791,614 / 29.59%
Number/percentage of C's	41,433,327 / 20.51%
Number/percentage of T's	59,046,647 / 29.22%
Number/percentage of G's	41,788,879 / 20.68%
Number/percentage of N's	648 / 0%
GC Percentage	41.19%

2.3. Coverage

Mean	0.0653

Standard Deviation	0.5389

2.4. Mapping Quality

Mean Mapping Quality	44

2.5. Mismatches and indels

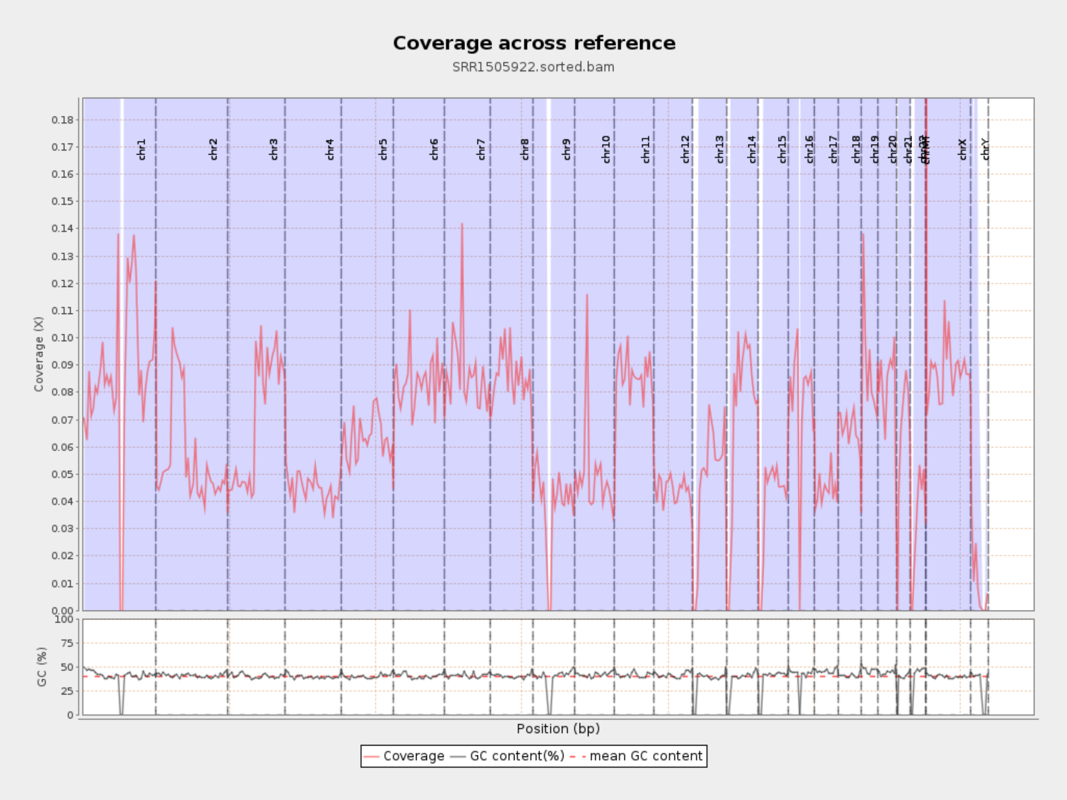
General error rate	0.5%
Mismatches	997,177
Insertions	9,106
Mapped reads with at least one insertion	0.21%
Deletions	29,566
Mapped reads with at least one deletion	0.68%
Homopolymer indels	45.58%

2.6. Chromosome stats

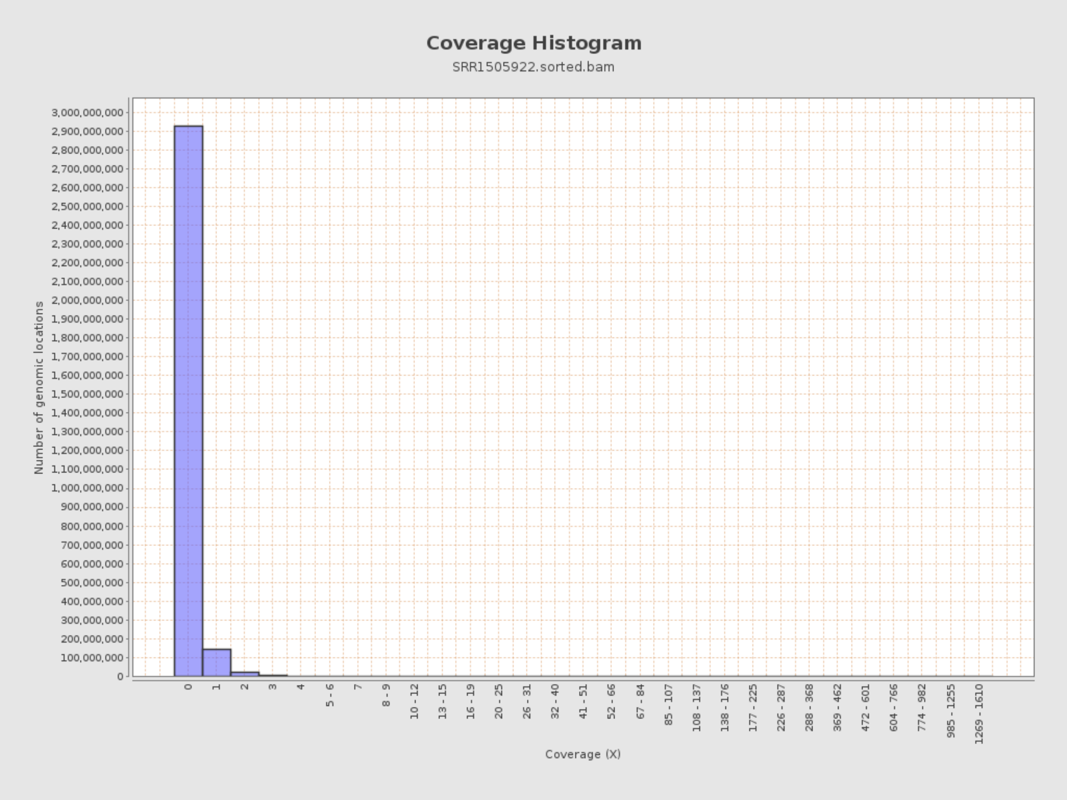
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21471456	0.0861	1.1244
chr2	243199373	13739914	0.0565	0.3969
chr3	198022430	13694973	0.0692	0.3127
chr4	191154276	8579134	0.0449	0.2517
chr5	180915260	11459848	0.0633	0.2968
chr6	171115067	14450103	0.0844	0.4519
chr7	159138663	13857955	0.0871	0.885

chr8	146364022	12589950	0.086	0.6809
chr9	141213431	5521616	0.0391	0.3213
chr10	135534747	6675567	0.0493	0.6457
chr11	135006516	11552601	0.0856	0.4839
chr12	133851895	5941769	0.0444	0.2593
chr13	115169878	5620731	0.0488	0.254
chr14	107349540	7834896	0.073	0.3967
chr15	102531392	3983535	0.0389	0.2262
chr16	90354753	6780550	0.075	0.3908
chr17	81195210	3606618	0.0444	0.2809
chr18	78077248	5241789	0.0671	0.5757
chr19	59128983	5230209	0.0885	0.8549
chr20	63025520	5257719	0.0834	0.3414
chr21	48129895	3065236	0.0637	0.3149
chr22	51304566	1661626	0.0324	0.2116
chrMT	16571	9803	0.5916	0.9616
chrX	155270560	13694534	0.0882	0.3856
chrY	59373566	579976	0.0098	0.1557

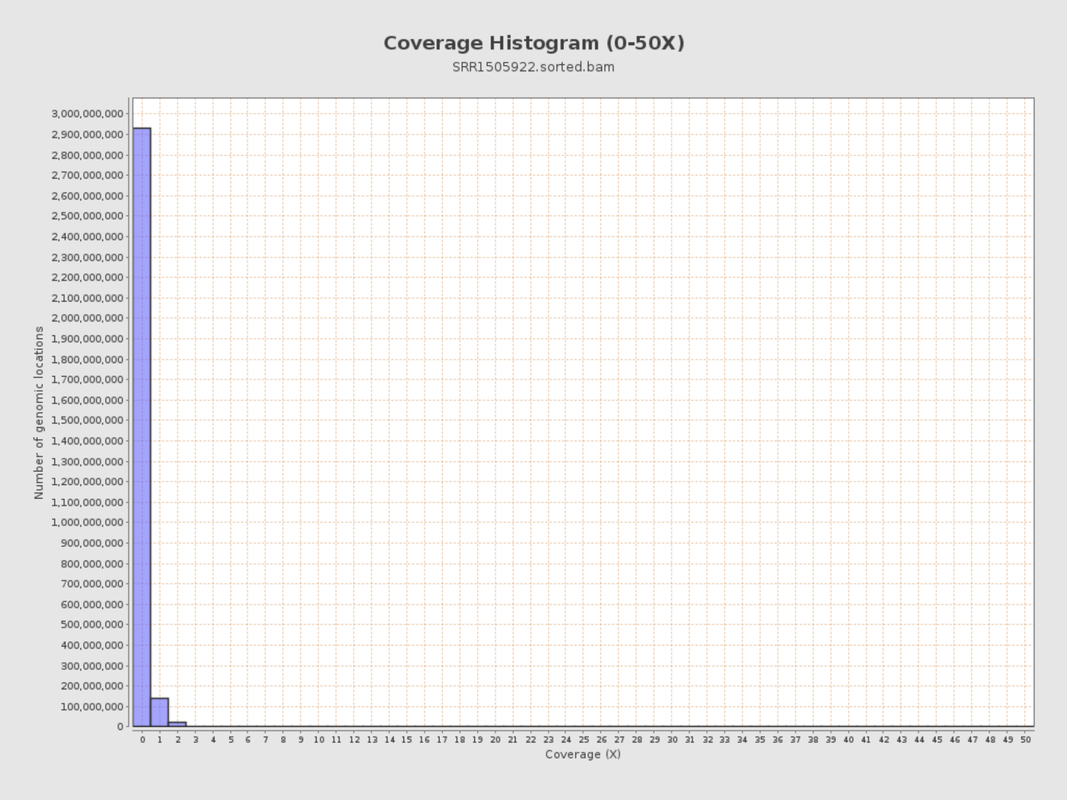
3. Results : Coverage across reference



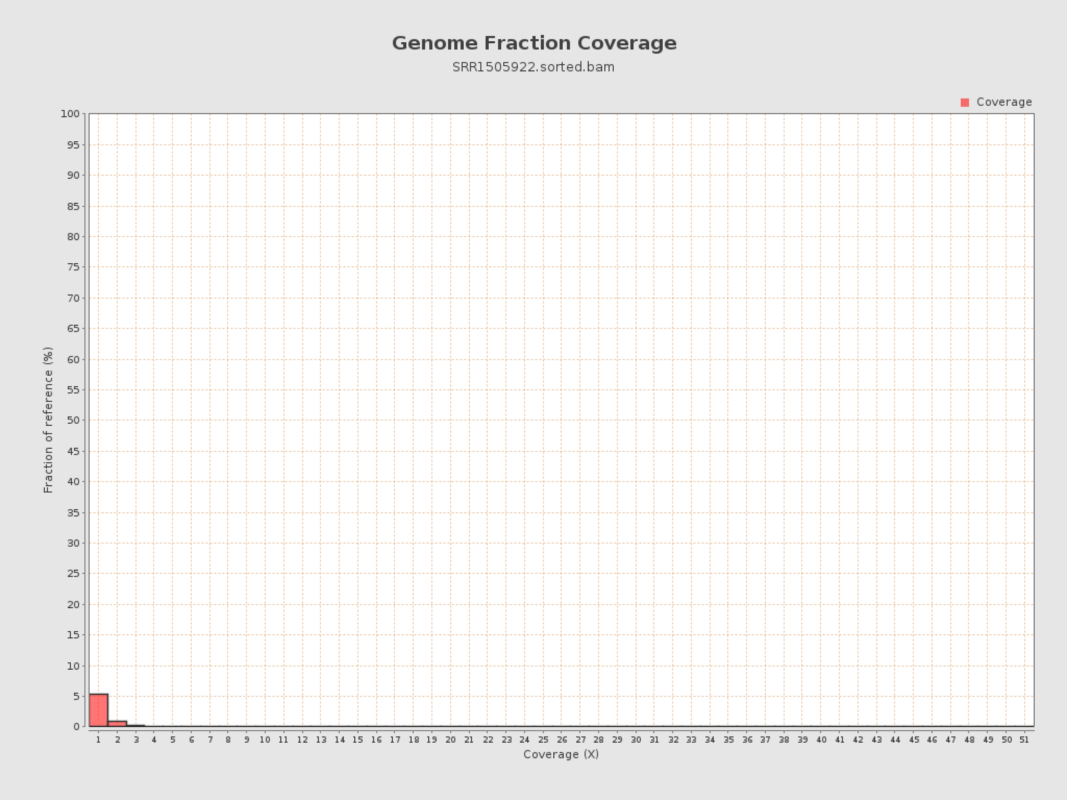
4. Results : Coverage Histogram



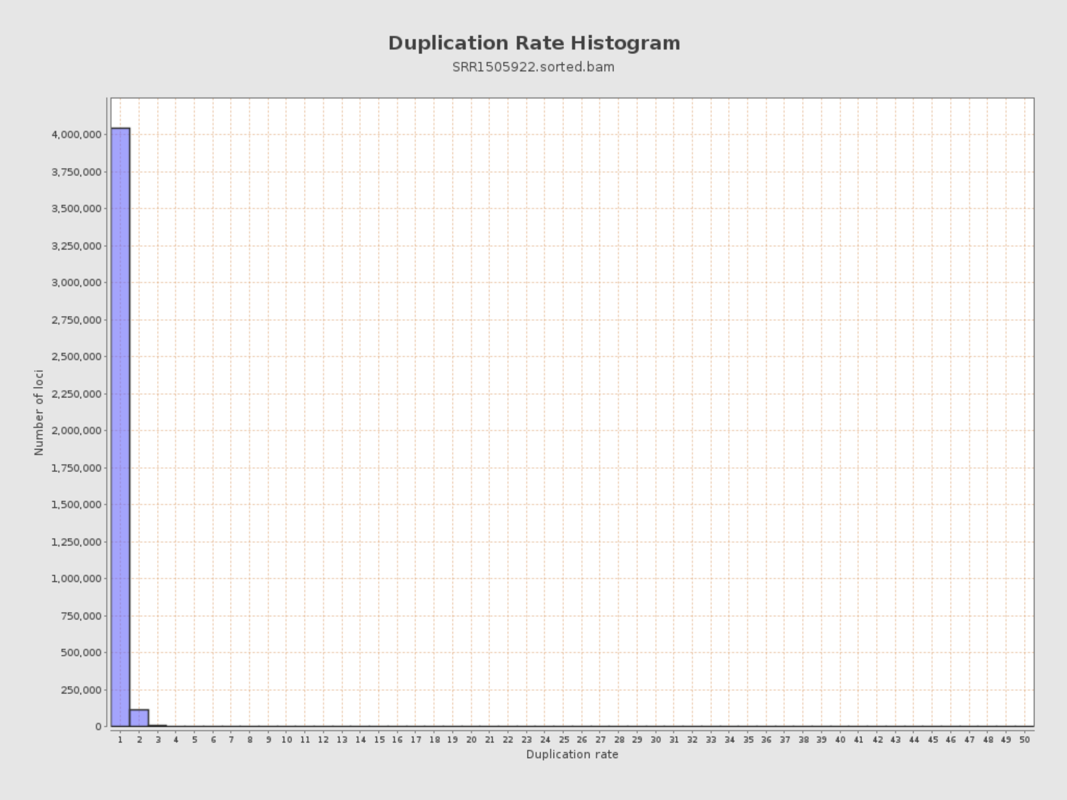
5. Results : Coverage Histogram (0-50X)



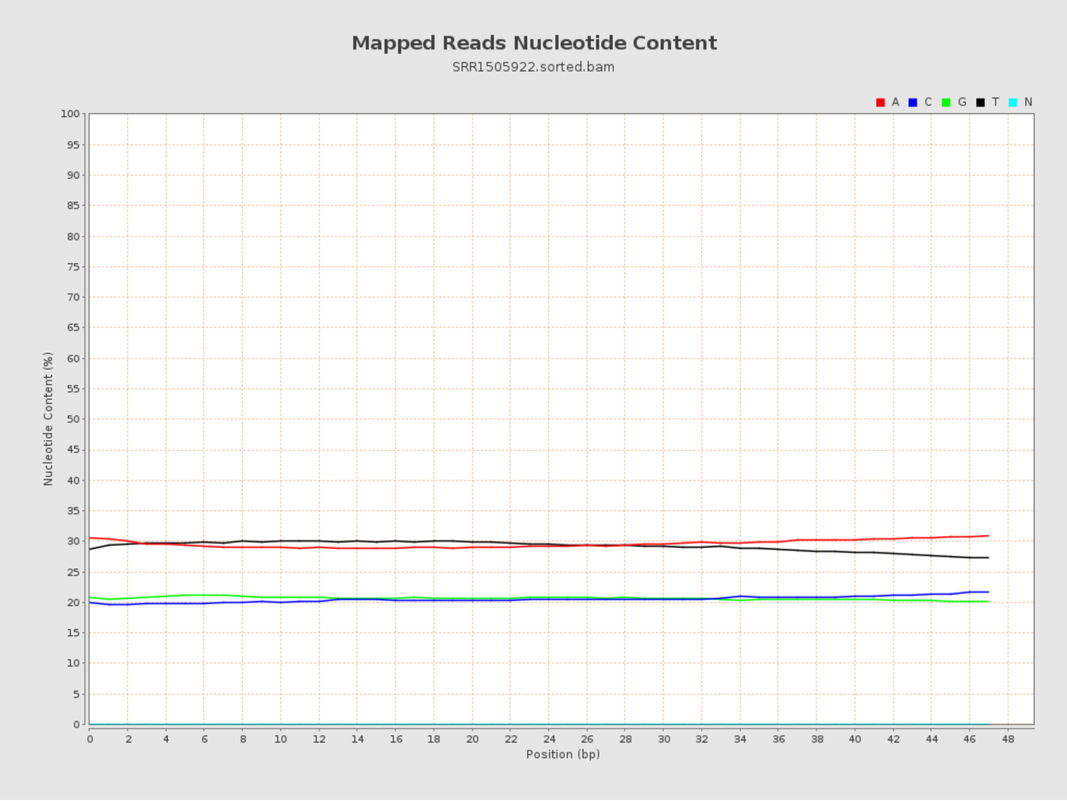
6. Results : Genome Fraction Coverage



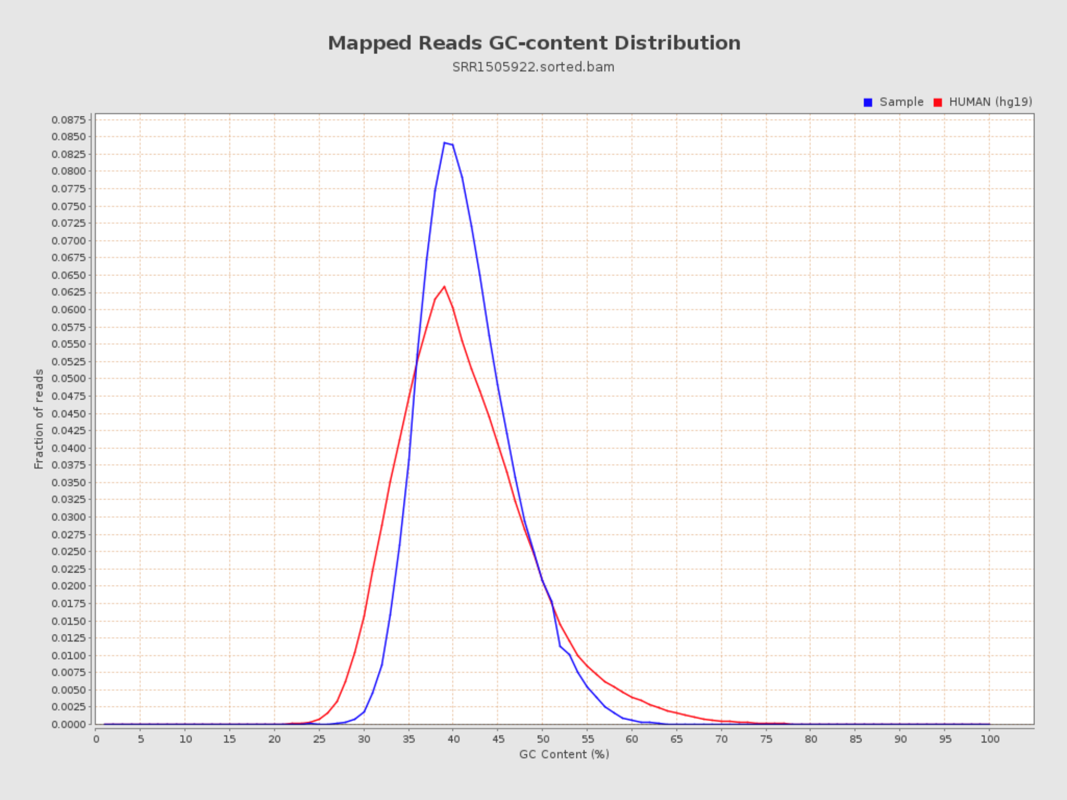
7. Results : Duplication Rate Histogram



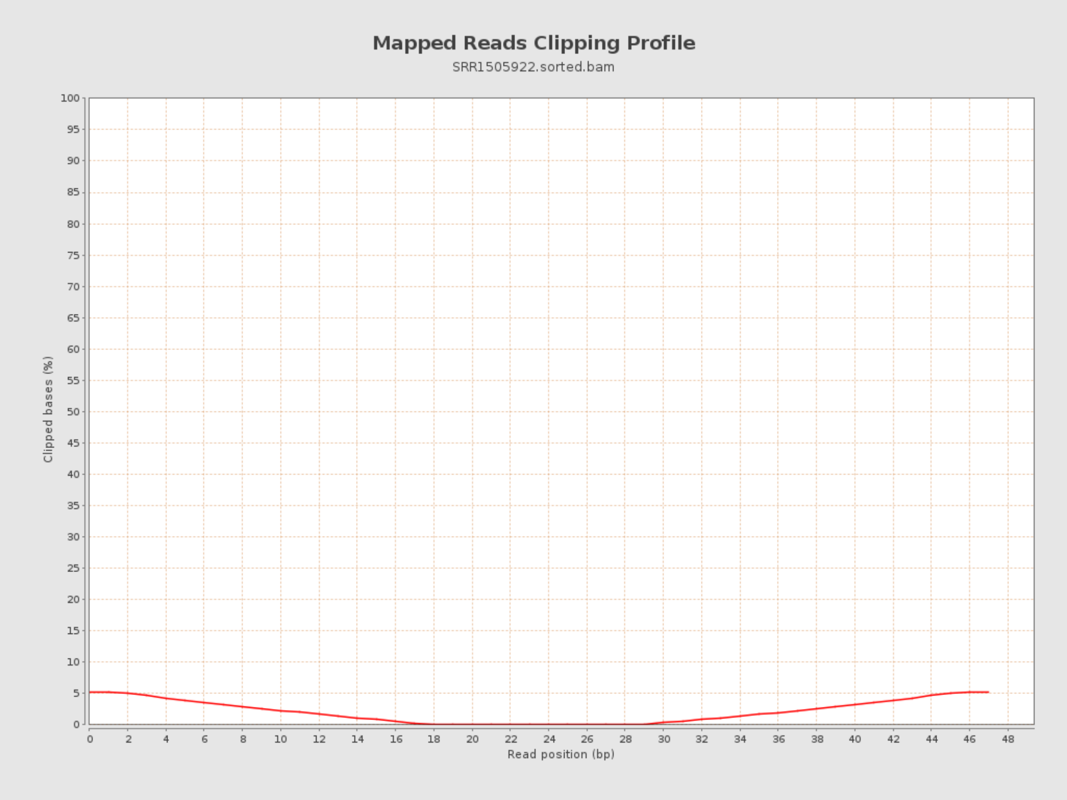
8. Results : Mapped Reads Nucleotide Content



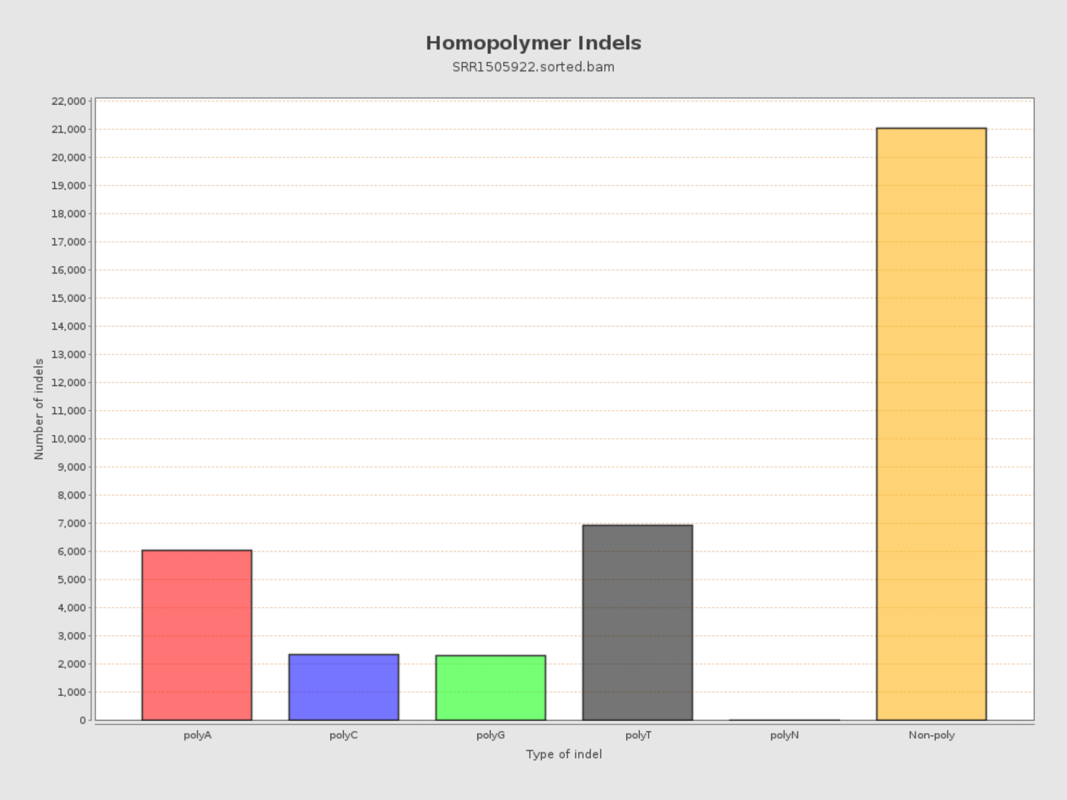
9. Results : Mapped Reads GC-content Distribution



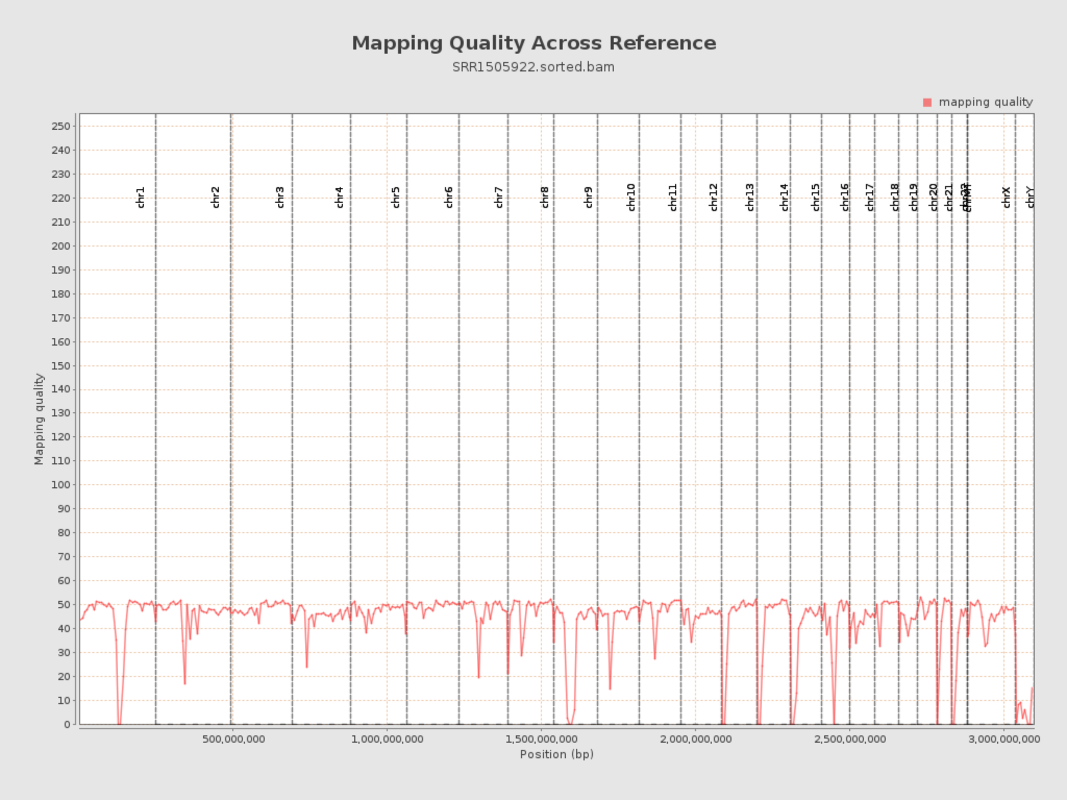
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram