Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 20:05:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505916.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_SRR1505916 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505916.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 20:05:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505916.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,015,067
Mapped reads	4,953,289 / 70.61%
Unmapped reads	2,061,778 / 29.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	266 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	236,799 / 3.38%
Duplication rate	3.64%
Clipped reads	977,582 / 13.94%

2.2. ACGT Content

Number/percentage of A's	67,664,462 / 29.68%
Number/percentage of C's	46,360,770 / 20.33%
Number/percentage of T's	66,869,326 / 29.33%
Number/percentage of G's	47,114,849 / 20.66%
Number/percentage of N's	701 / 0%
GC Percentage	41%

2.3. Coverage

Mean	0.0737

Standard Deviation	0.5972

2.4. Mapping Quality

Mean Mapping Quality	43.59

2.5. Mismatches and indels

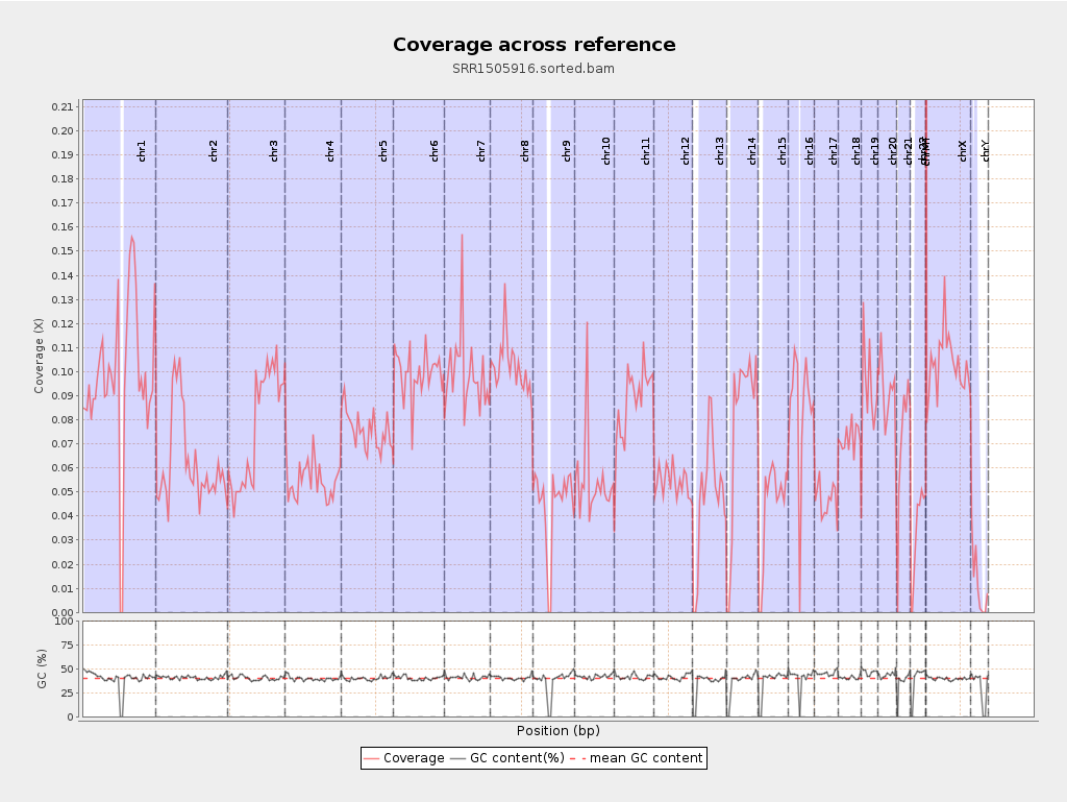
General error rate	0.51%
Mismatches	1,148,396
Insertions	10,352
Mapped reads with at least one insertion	0.21%
Deletions	34,004
Mapped reads with at least one deletion	0.68%
Homopolymer indels	45.97%

2.6. Chromosome stats

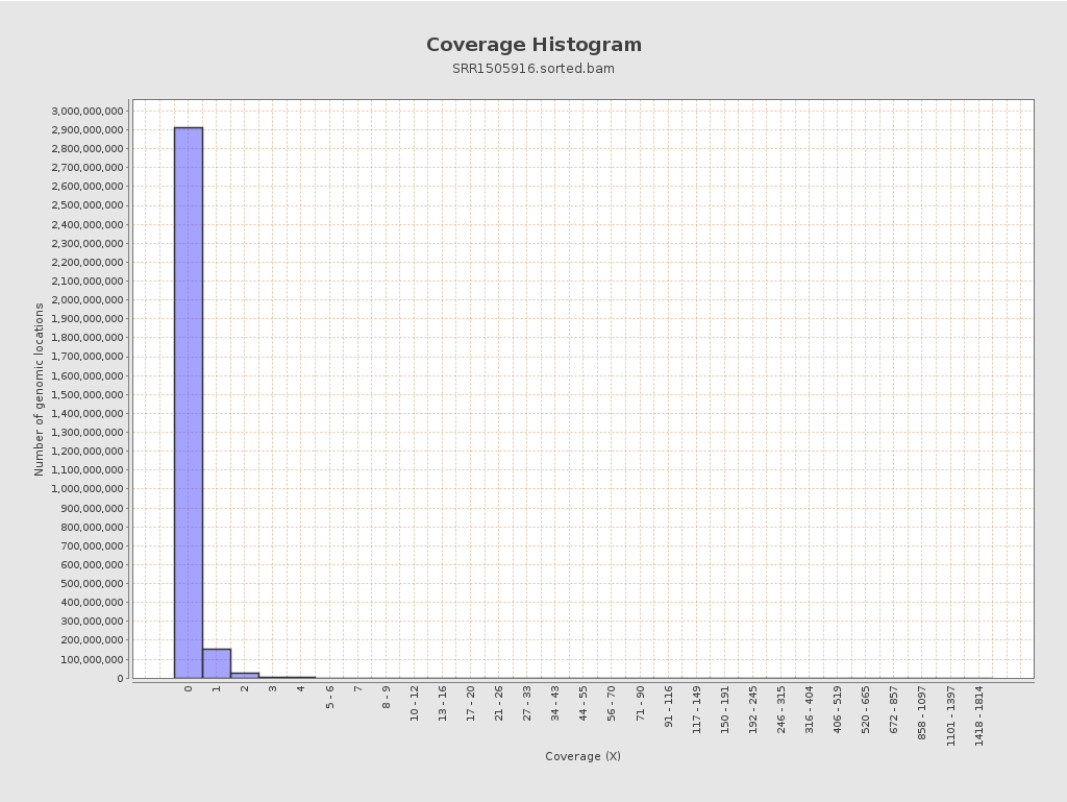
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24542327	0.0985	1.2769
chr2	243199373	15120489	0.0622	0.4202
chr3	198022430	15032319	0.0759	0.3301
chr4	191154276	10510862	0.055	0.2825
chr5	180915260	13642485	0.0754	0.333
chr6	171115067	17001681	0.0994	0.4714
chr7	159138663	15744785	0.0989	0.9349

chr8	146364022	14871791	0.1016	0.8181
chr9	141213431	6324809	0.0448	0.3666
chr10	135534747	7315260	0.054	0.6289
chr11	135006516	11922218	0.0883	0.5395
chr12	133851895	7266949	0.0543	0.2963
chr13	115169878	5581437	0.0485	0.2582
chr14	107349540	8573170	0.0799	0.5828
chr15	102531392	4440554	0.0433	0.2446
chr16	90354753	7550252	0.0836	0.4034
chr17	81195210	3818535	0.047	0.3012
chr18	78077248	5655968	0.0724	0.6564
chr19	59128983	5558934	0.094	0.8545
chr20	63025520	5785261	0.0918	0.3655
chr21	48129895	3417958	0.071	0.3388
chr22	51304566	1698146	0.0331	0.2139
chrMT	16571	13163	0.7943	1.1489
chrX	155270560	15989516	0.103	0.4436
chrY	59373566	678457	0.0114	0.1521

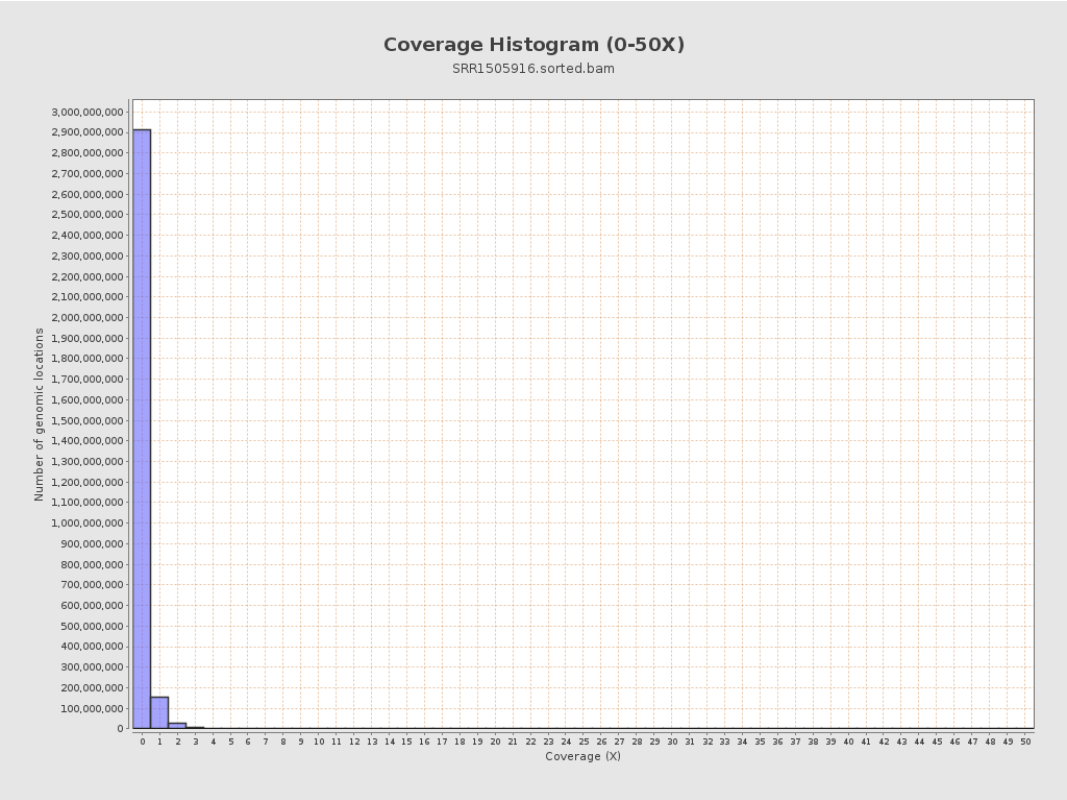
3. Results : Coverage across reference



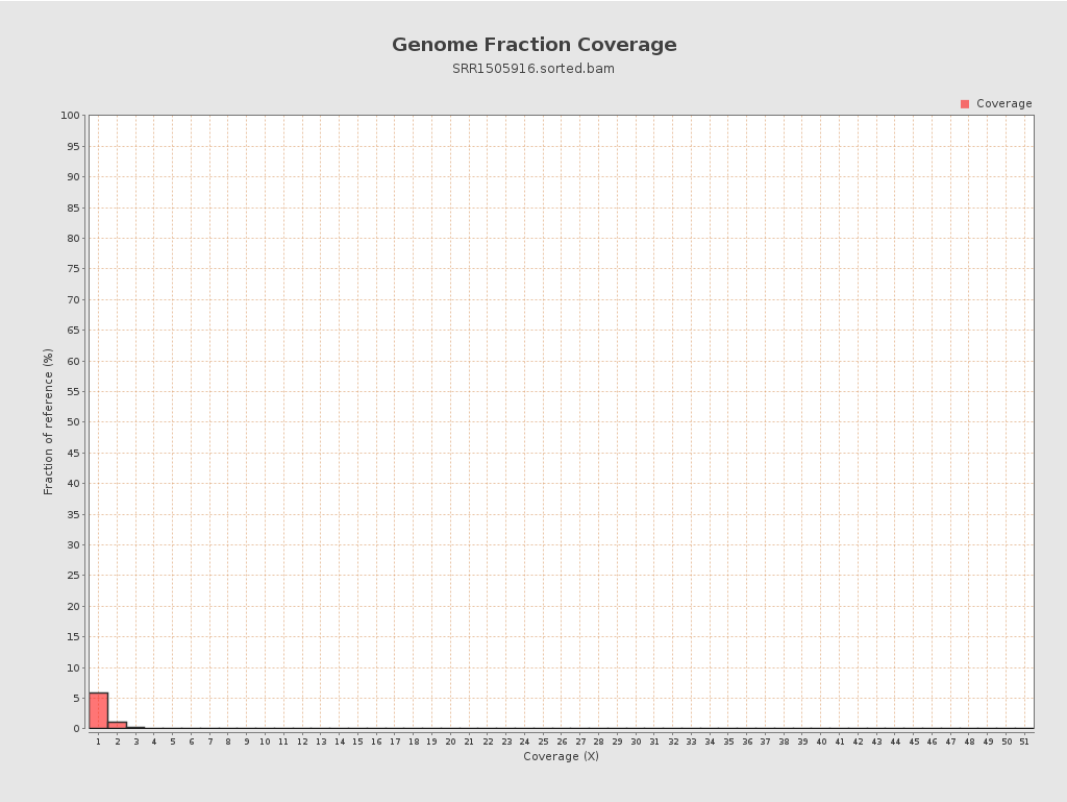
4. Results : Coverage Histogram



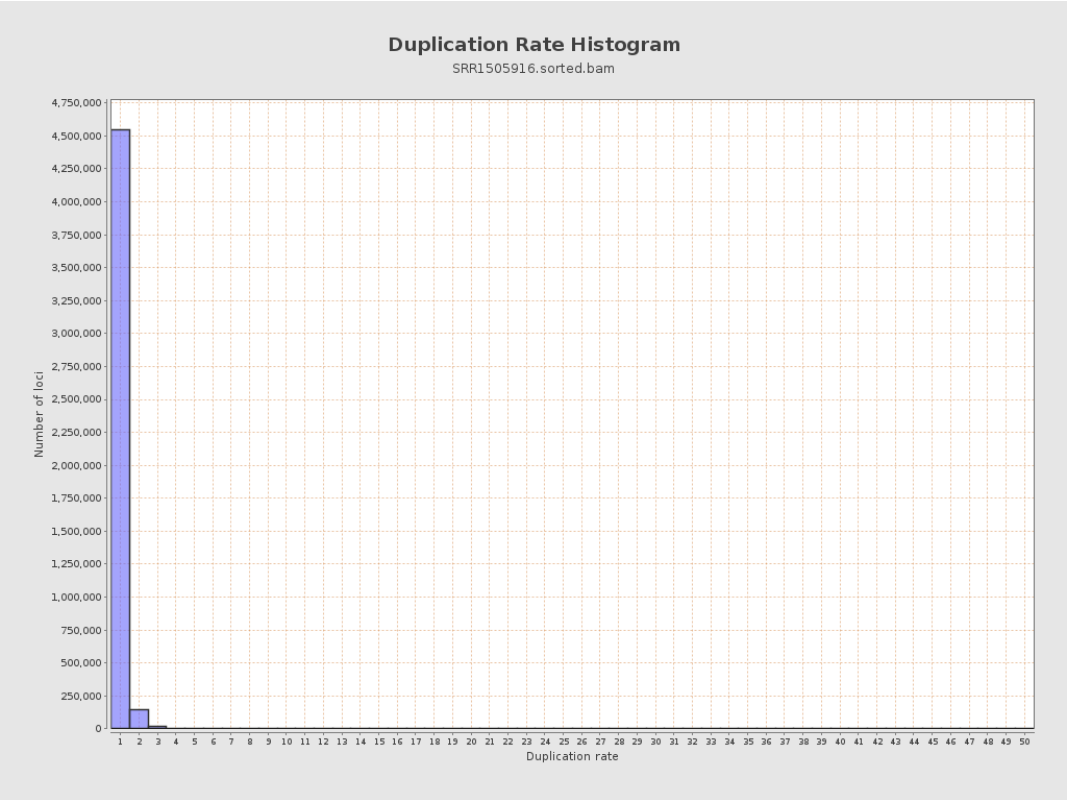
5. Results : Coverage Histogram (0-50X)



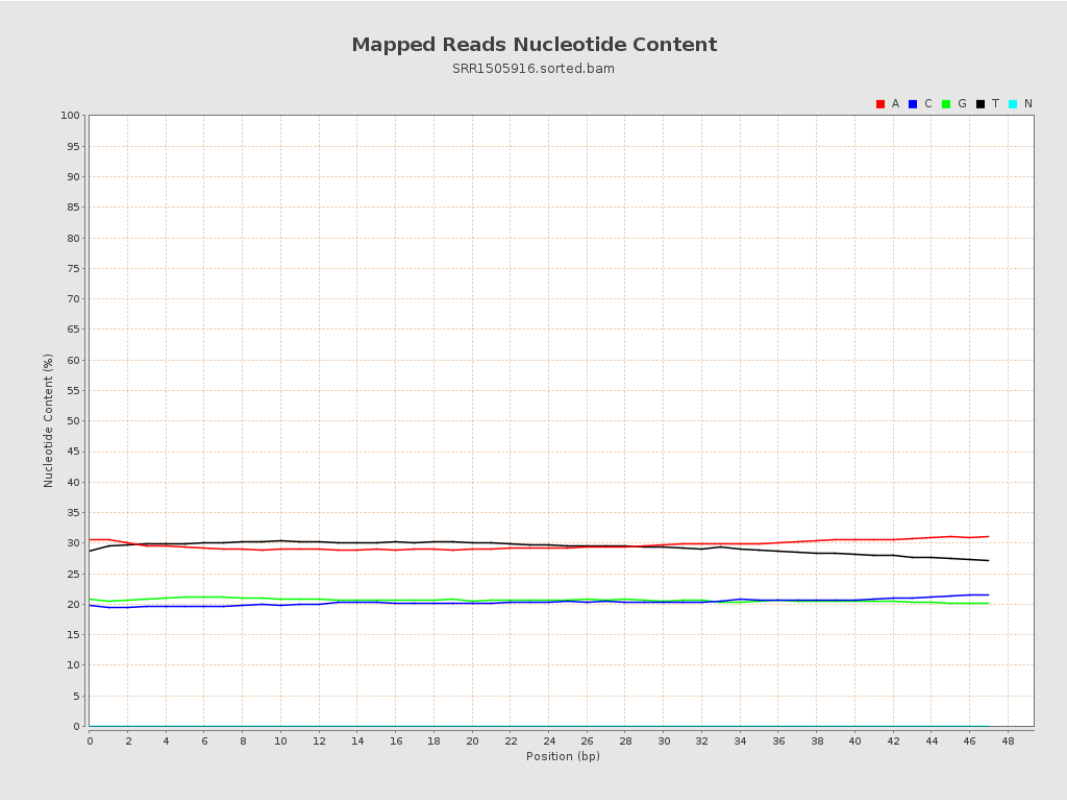
6. Results : Genome Fraction Coverage



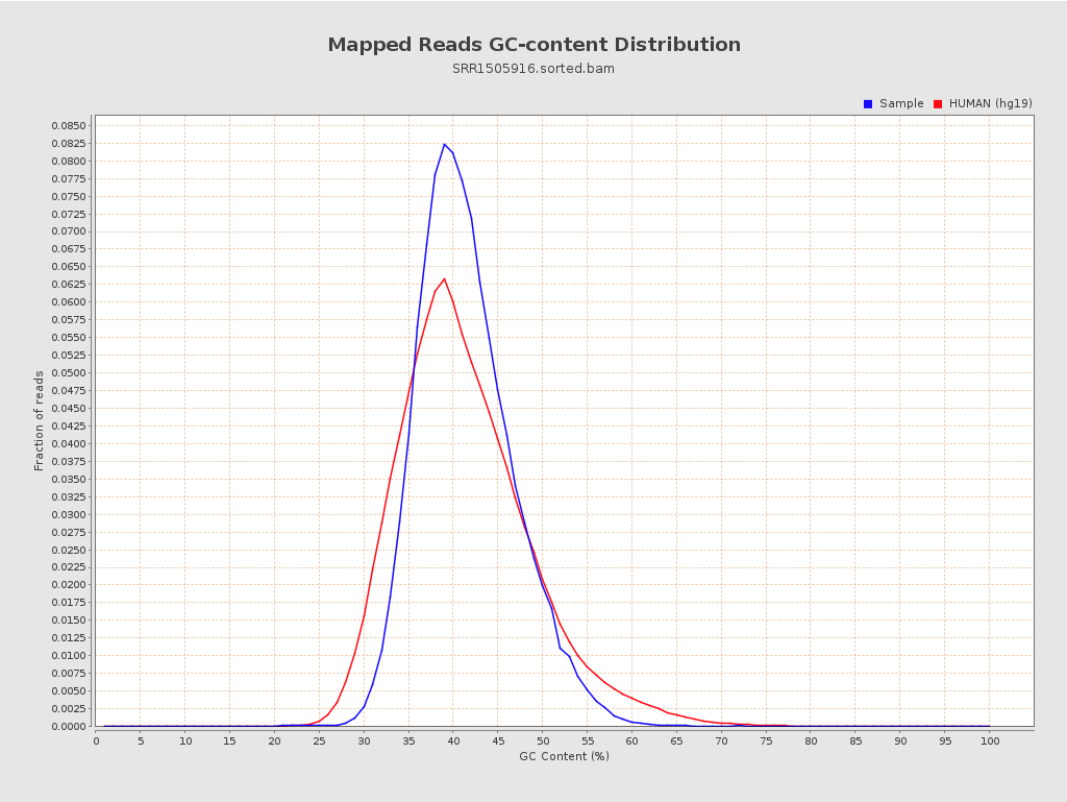
7. Results : Duplication Rate Histogram



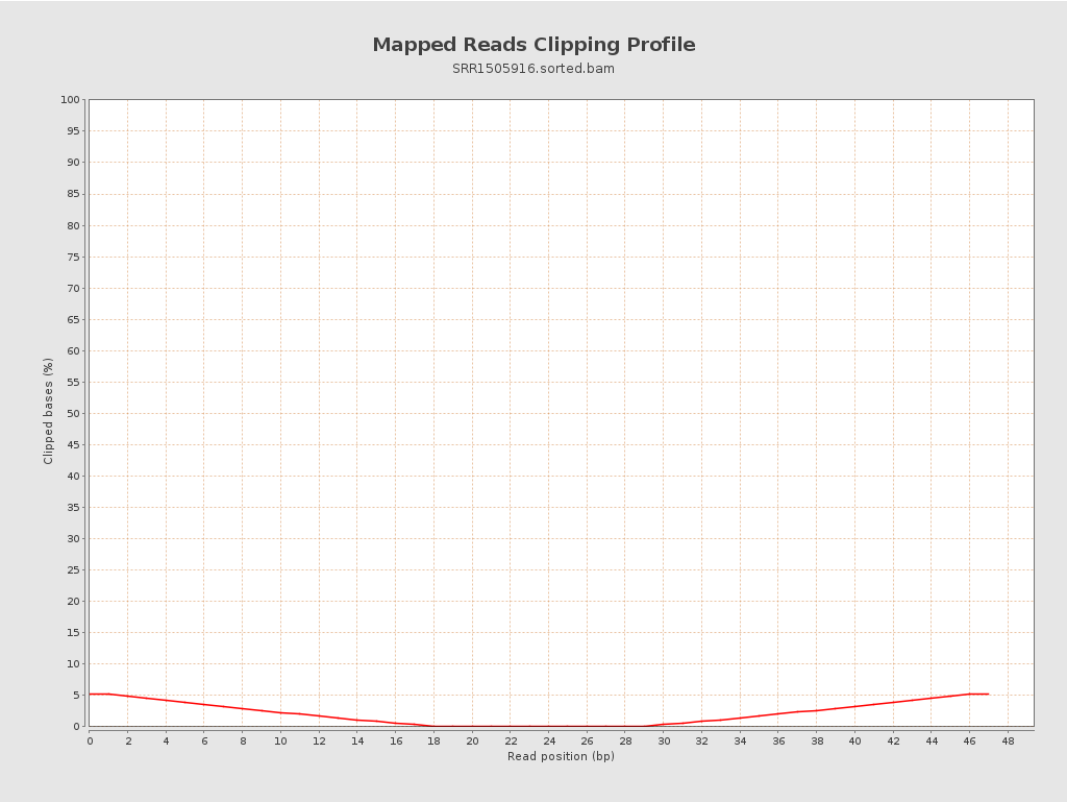
8. Results : Mapped Reads Nucleotide Content



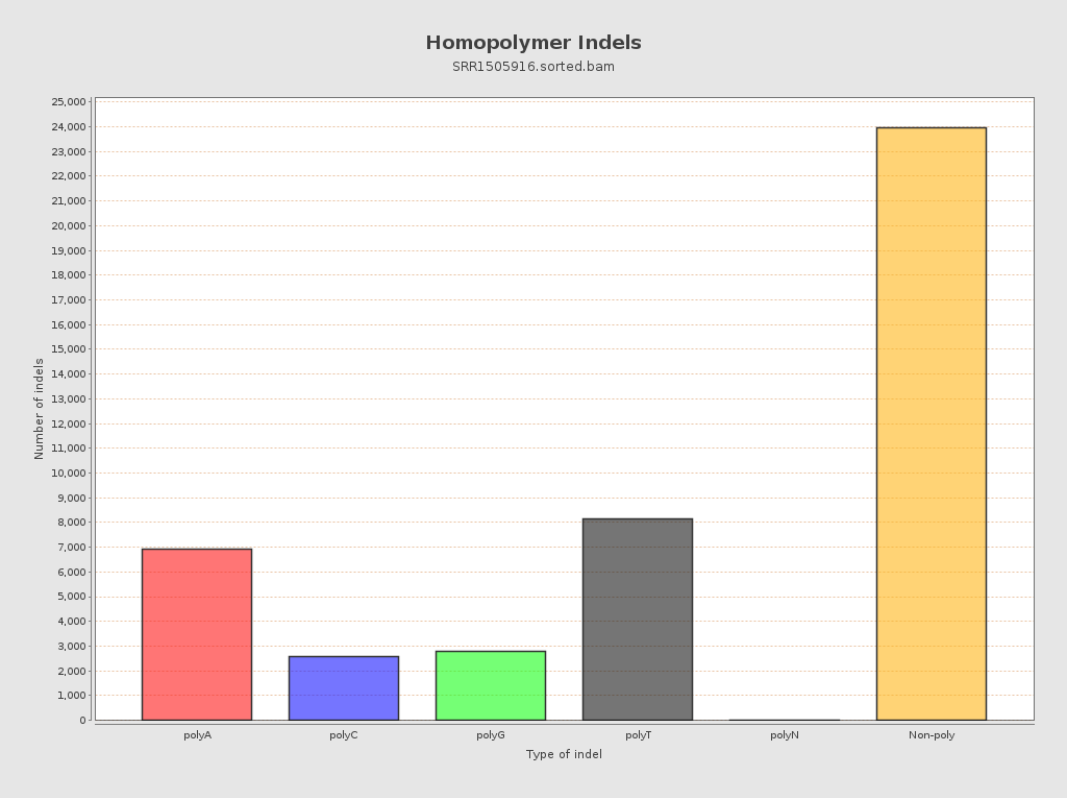
9. Results : Mapped Reads GC-content Distribution



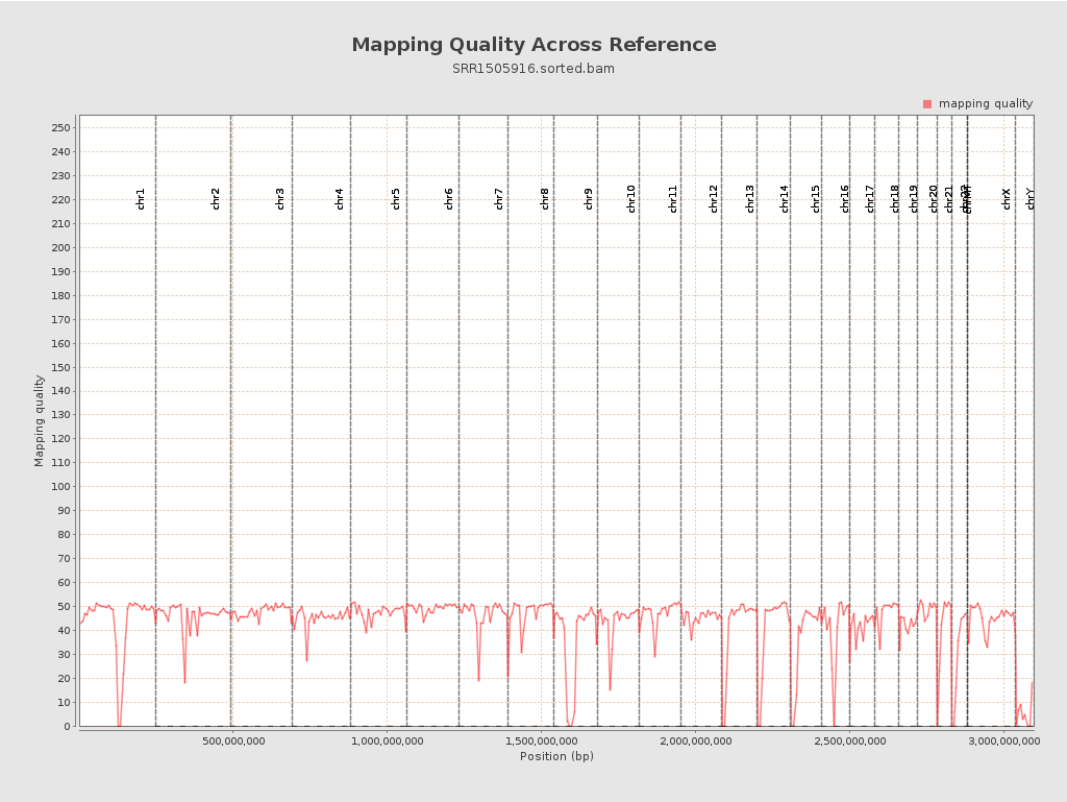
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram