Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 01:11:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506124.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_SRR1506124 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506124.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 01:10:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506124.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,624,038
Mapped reads	9,393,155 / 74.41%
Unmapped reads	3,230,883 / 25.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	122,317 / 0.97%
Read min/max/mean length	30 / 94 / 94.35
Duplicated reads (estimated)	1,761,803 / 13.96%
Duplication rate	12.41%
Clipped reads	4,947,346 / 39.19%

2.2. ACGT Content

Number/percentage of A's	210,115,790 / 27.5%
Number/percentage of C's	145,852,642 / 19.09%
Number/percentage of T's	218,345,814 / 28.58%
Number/percentage of G's	189,586,874 / 24.81%
Number/percentage of N's	127,335 / 0.02%
GC Percentage	43.9%

2.3. Coverage

Mean	0.2469

Standard Deviation	1.5764

2.4. Mapping Quality

Mean Mapping Quality	48.21

2.5. Mismatches and indels

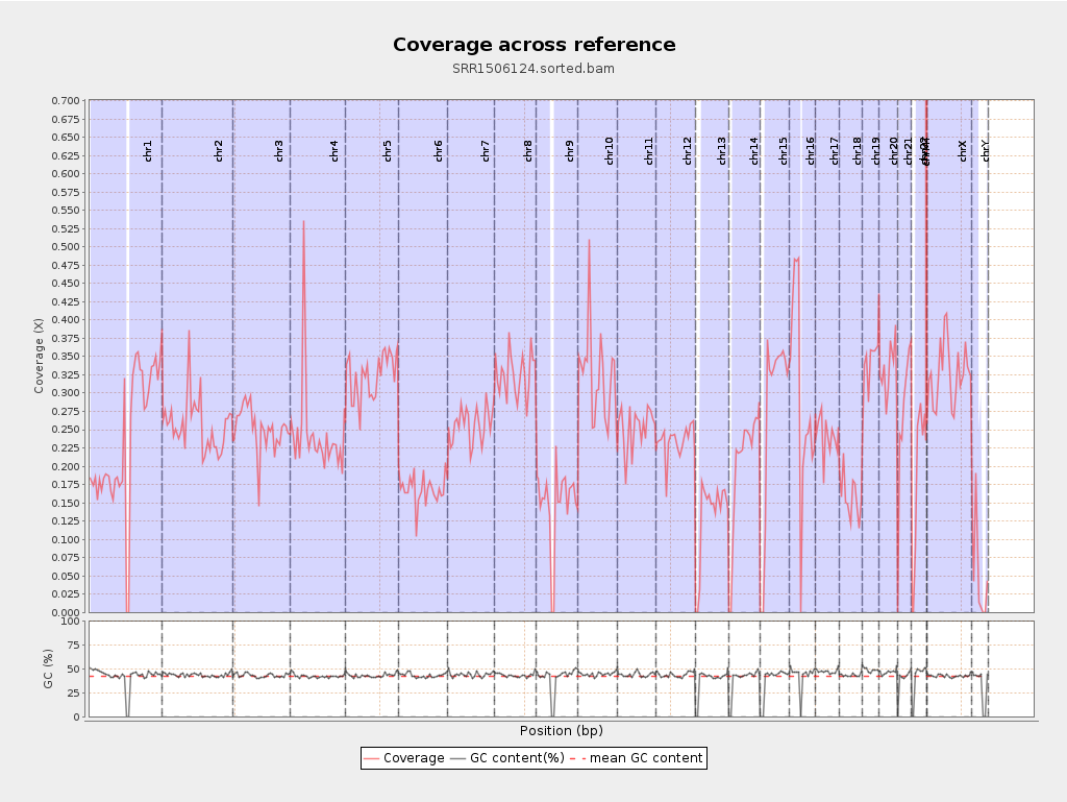
General error rate	0.79%
Mismatches	5,867,114
Insertions	61,764
Mapped reads with at least one insertion	0.64%
Deletions	152,394
Mapped reads with at least one deletion	1.59%
Homopolymer indels	43.27%

2.6. Chromosome stats

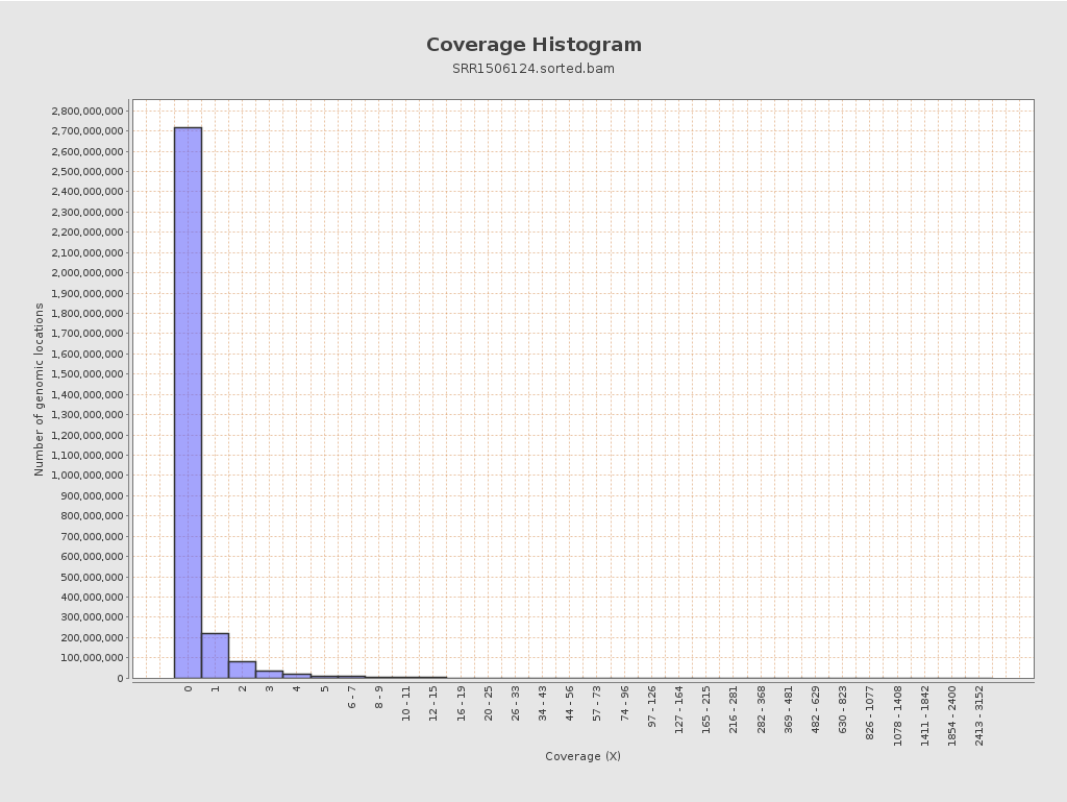
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	58493935	0.2347	2.929
chr2	243199373	62438979	0.2567	1.7167
chr3	198022430	49701112	0.251	0.9073
chr4	191154276	46205966	0.2417	1.4668
chr5	180915260	58476898	0.3232	1.0601
chr6	171115067	28902880	0.1689	0.8392
chr7	159138663	40807459	0.2564	1.5507

chr8	146364022	47710883	0.326	1.822
chr9	141213431	20782466	0.1472	1.5786
chr10	135534747	43946417	0.3242	2.029
chr11	135006516	33877363	0.2509	1.3883
chr12	133851895	31335082	0.2341	0.894
chr13	115169878	15162738	0.1317	0.6378
chr14	107349540	21519766	0.2005	0.9379
chr15	102531392	28530626	0.2783	0.9896
chr16	90354753	26967717	0.2985	1.2879
chr17	81195210	19527808	0.2405	1.0888
chr18	78077248	12371452	0.1585	2.2617
chr19	59128983	20292552	0.3432	2.1522
chr20	63025520	20854424	0.3309	1.1868
chr21	48129895	13197770	0.2742	1.3994
chr22	51304566	9330448	0.1819	0.8428
chrMT	16571	556780	33.5997	20.1976
chrX	155270560	50526409	0.3254	1.1919
chrY	59373566	2825665	0.0476	1.6187

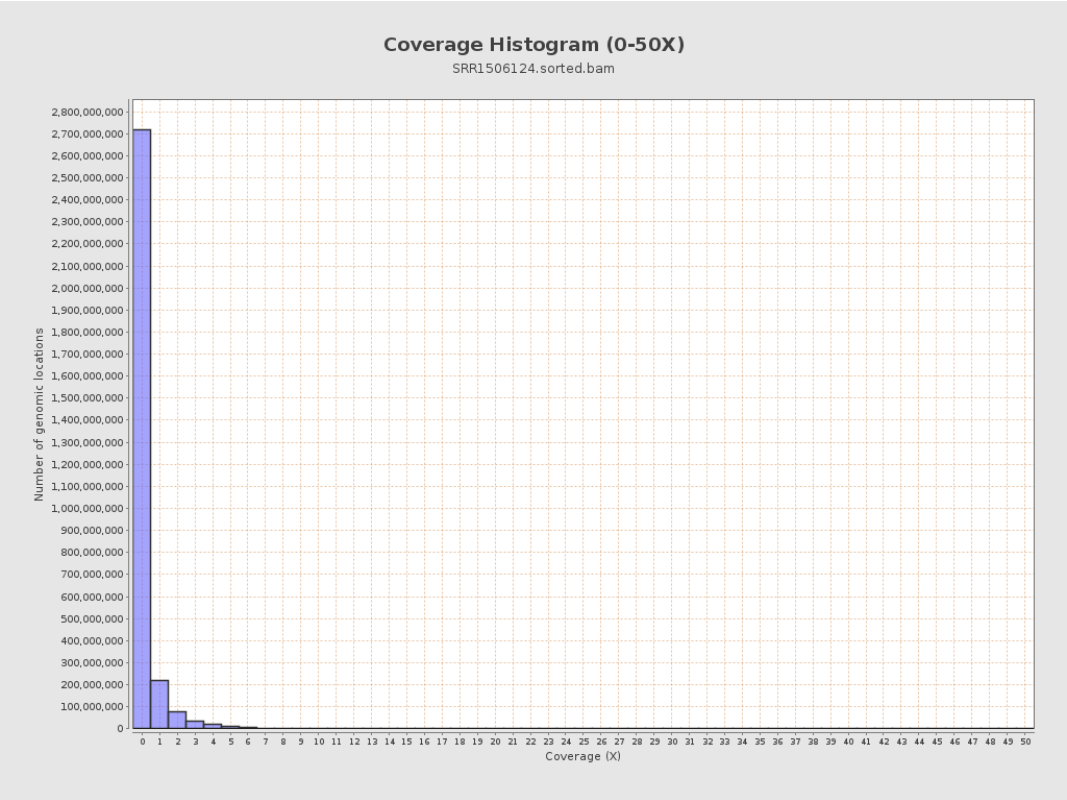
3. Results : Coverage across reference



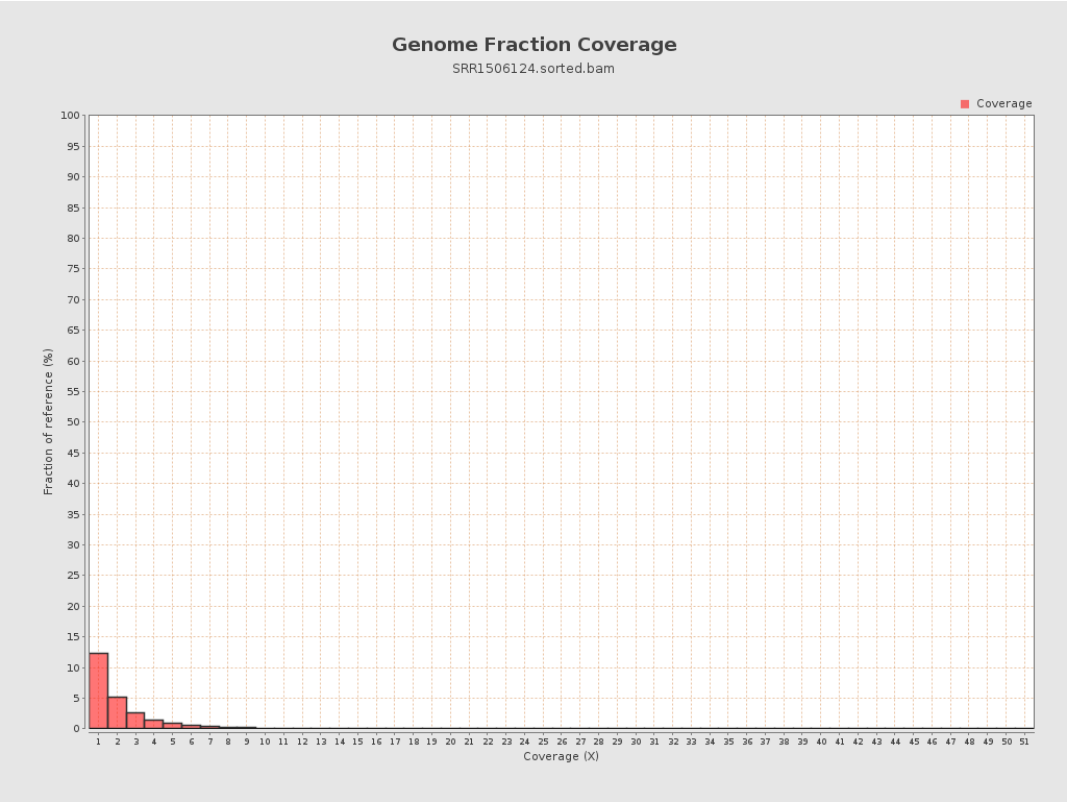
4. Results : Coverage Histogram



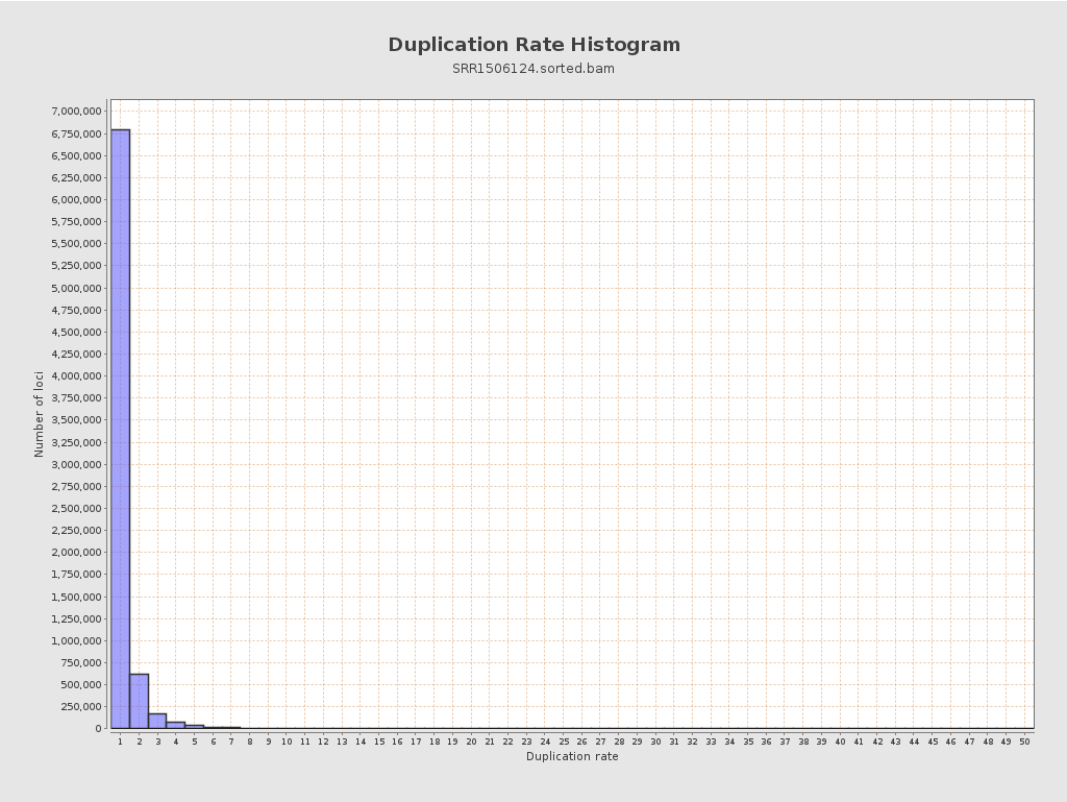
5. Results : Coverage Histogram (0-50X)



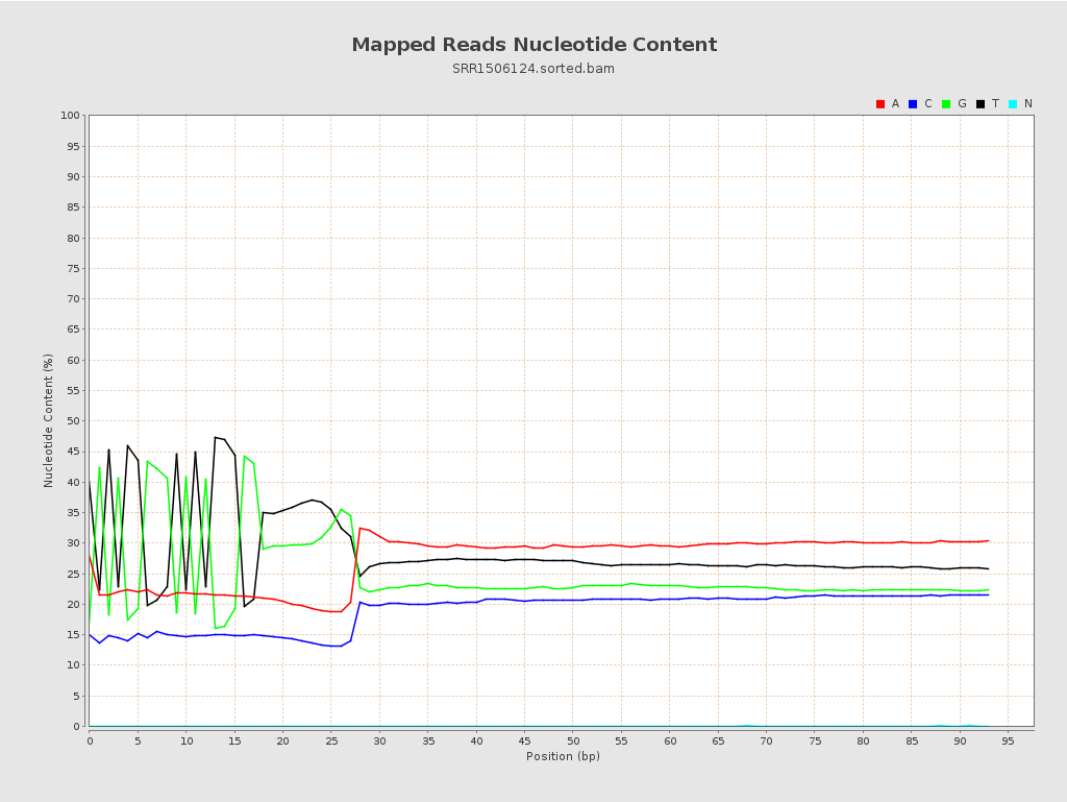
6. Results : Genome Fraction Coverage



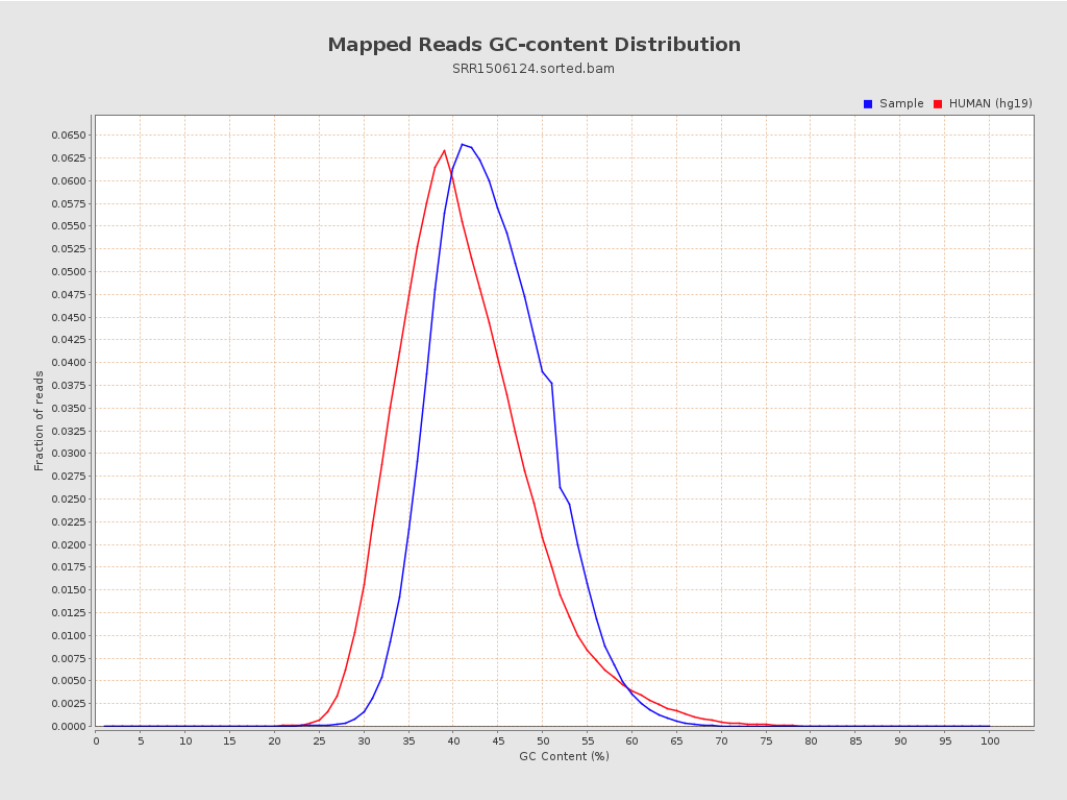
7. Results : Duplication Rate Histogram



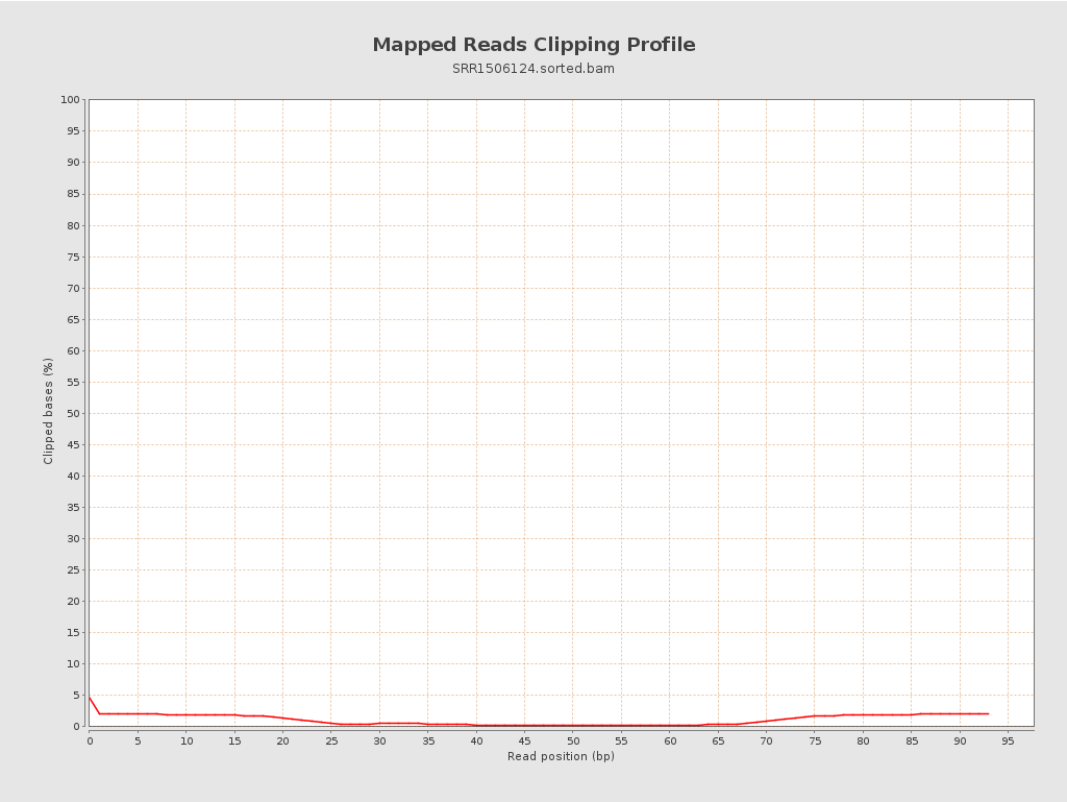
8. Results : Mapped Reads Nucleotide Content



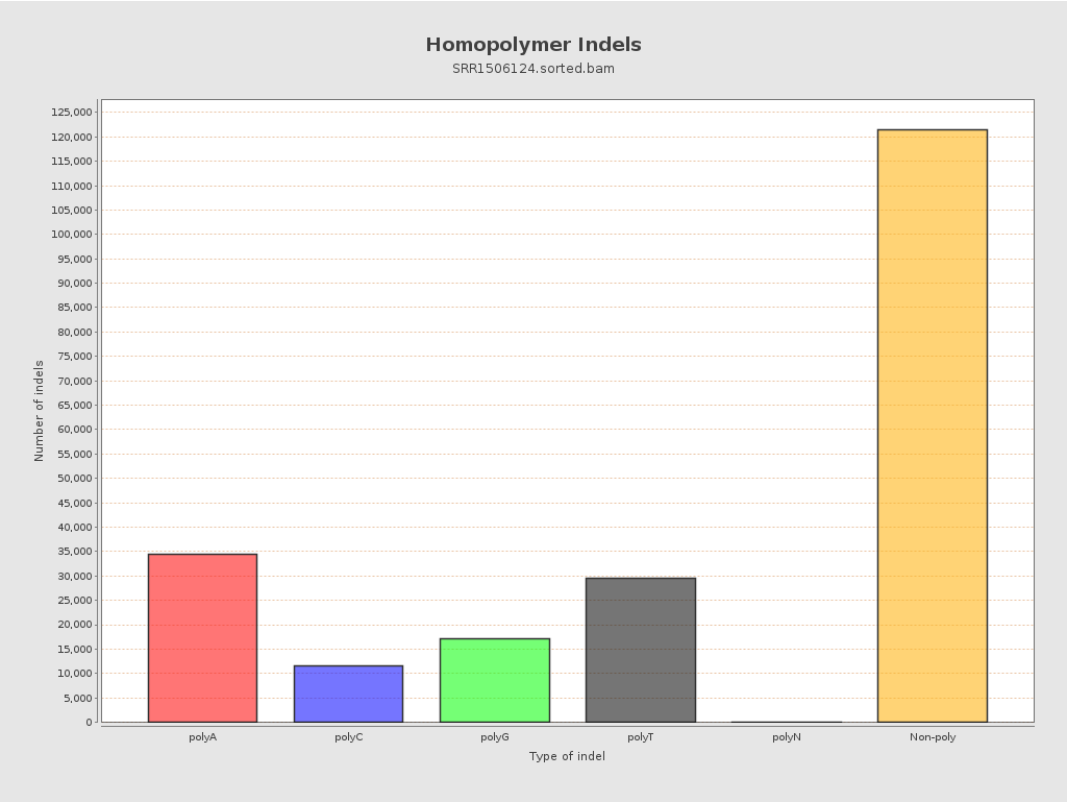
9. Results : Mapped Reads GC-content Distribution



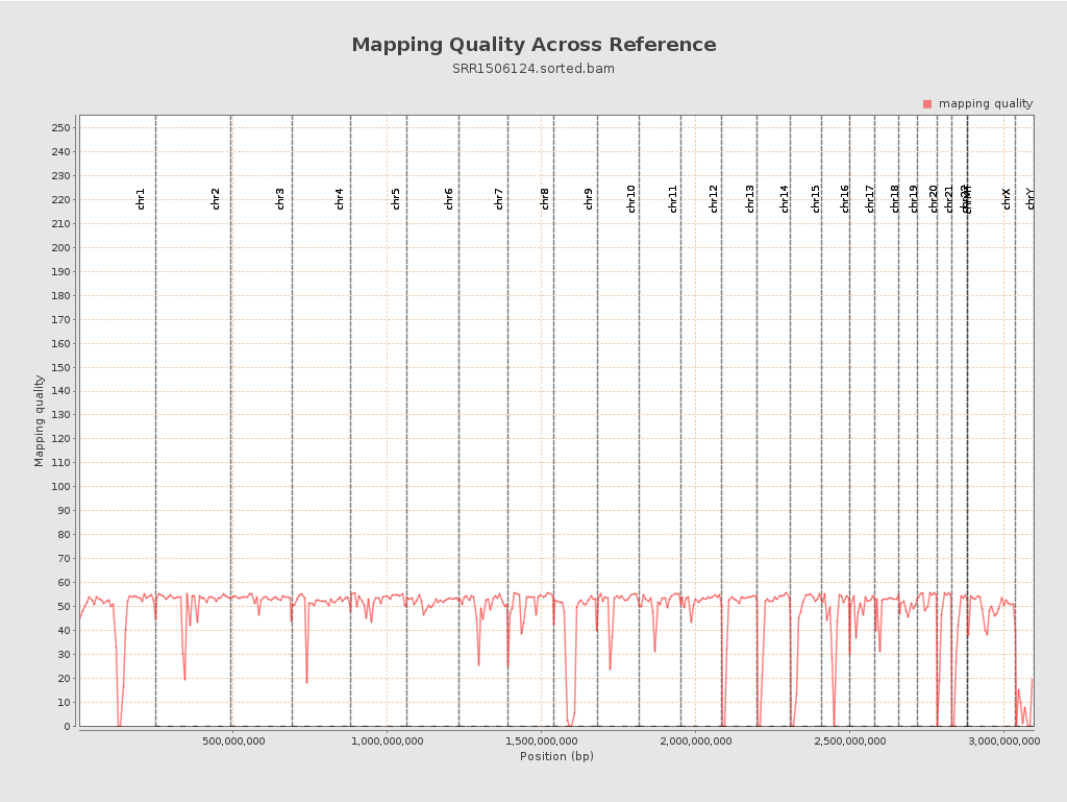
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram