Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 02:17:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506321.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_SRR1506321 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506321.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 02:17:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506321.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,796,726
Mapped reads	10,140,860 / 79.25%
Unmapped reads	2,655,866 / 20.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	137,772 / 1.08%
Read min/max/mean length	30 / 94 / 94.39
Duplicated reads (estimated)	2,154,263 / 16.83%
Duplication rate	14.79%
Clipped reads	6,508,800 / 50.86%

2.2. ACGT Content

Number/percentage of A's	212,296,939 / 26.68%
Number/percentage of C's	146,672,049 / 18.43%
Number/percentage of T's	235,775,834 / 29.63%
Number/percentage of G's	200,802,204 / 25.24%
Number/percentage of N's	175,685 / 0.02%
GC Percentage	43.67%

2.3. Coverage

Mean	0.2571

Standard Deviation	1.7278

2.4. Mapping Quality

Mean Mapping Quality	47.5

2.5. Mismatches and indels

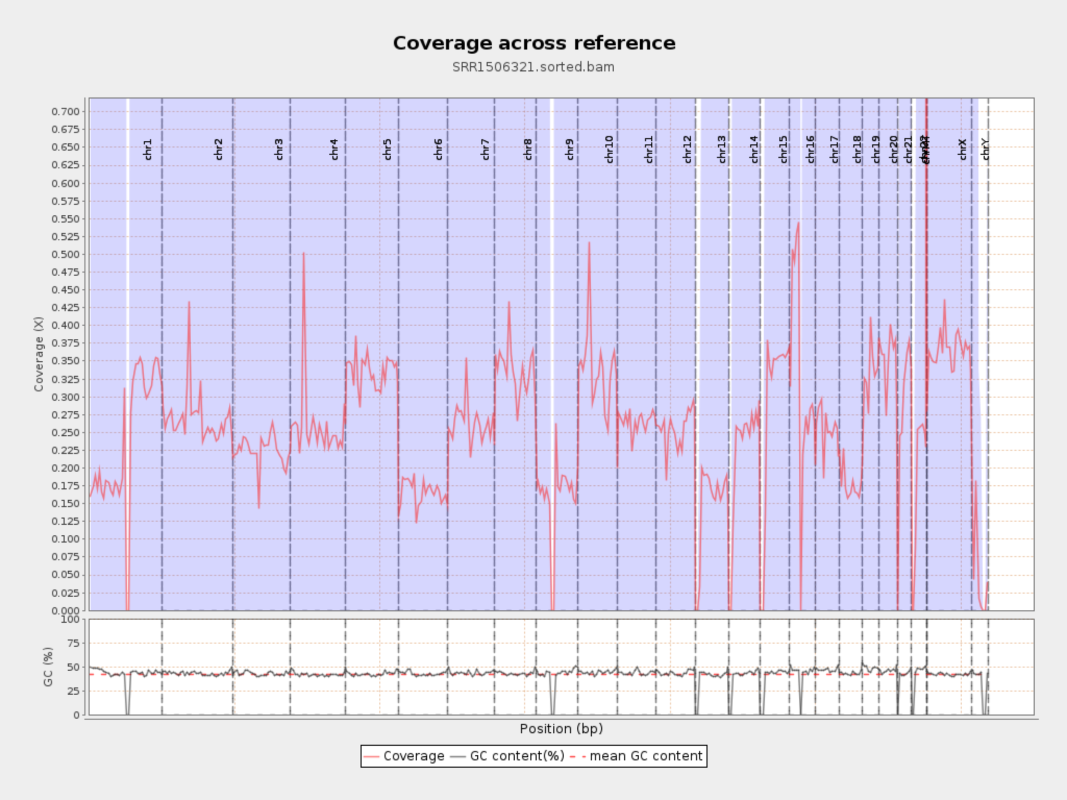
General error rate	0.78%
Mismatches	6,093,746
Insertions	63,159
Mapped reads with at least one insertion	0.61%
Deletions	166,612
Mapped reads with at least one deletion	1.61%
Homopolymer indels	43.73%

2.6. Chromosome stats

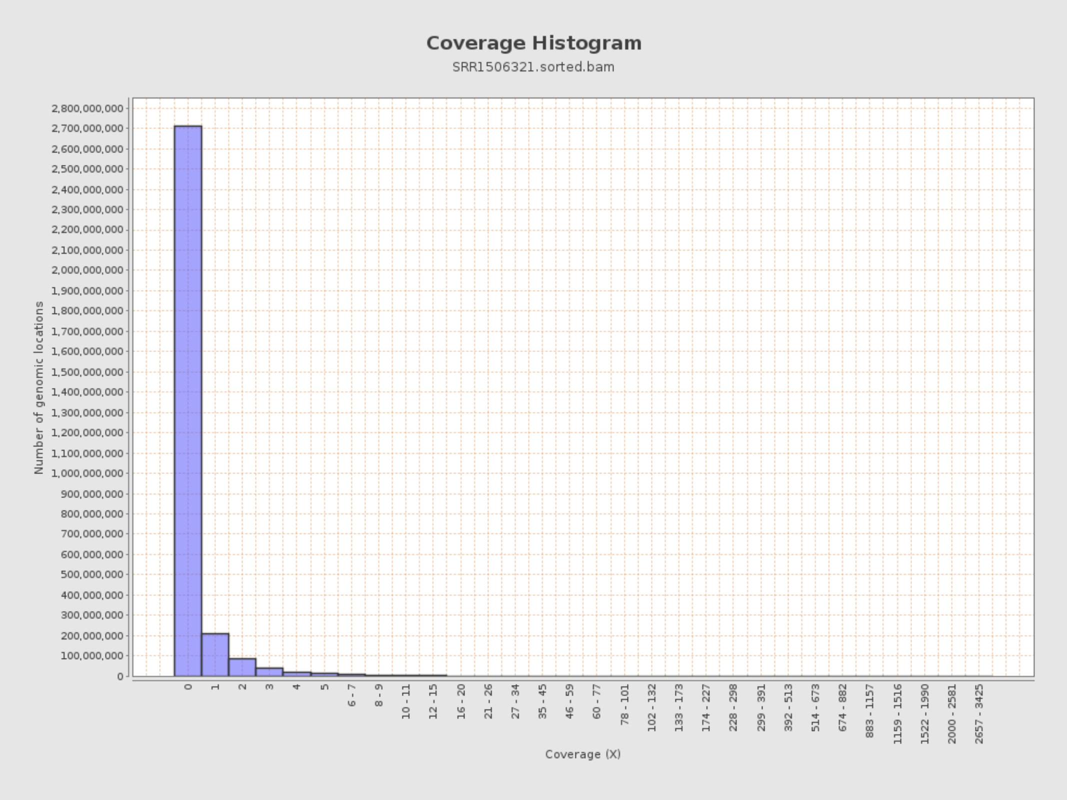
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	58796952	0.2359	2.9723
chr2	243199373	65910412	0.271	1.9698
chr3	198022430	44402442	0.2242	0.859
chr4	191154276	49396763	0.2584	1.4105
chr5	180915260	60781690	0.336	1.087
chr6	171115067	28370098	0.1658	0.8425
chr7	159138663	42033944	0.2641	2.3336

chr8	146364022	49454514	0.3379	2.3371
chr9	141213431	22136267	0.1568	1.8205
chr10	135534747	46270034	0.3414	1.9818
chr11	135006516	35710999	0.2645	1.7071
chr12	133851895	34095752	0.2547	0.9577
chr13	115169878	16975679	0.1474	0.6798
chr14	107349540	23259765	0.2167	1.1001
chr15	102531392	29554157	0.2882	1.0158
chr16	90354753	29830381	0.3301	1.3192
chr17	81195210	20711212	0.2551	1.1926
chr18	78077248	13820095	0.177	2.5788
chr19	59128983	19669626	0.3327	2.2559
chr20	63025520	22319014	0.3541	1.1989
chr21	48129895	13723114	0.2851	1.2953
chr22	51304566	9074030	0.1769	0.815
chrMT	16571	108720	6.5609	5.3908
chrX	155270560	56772543	0.3656	1.3899
chrY	59373566	2876366	0.0484	1.5816

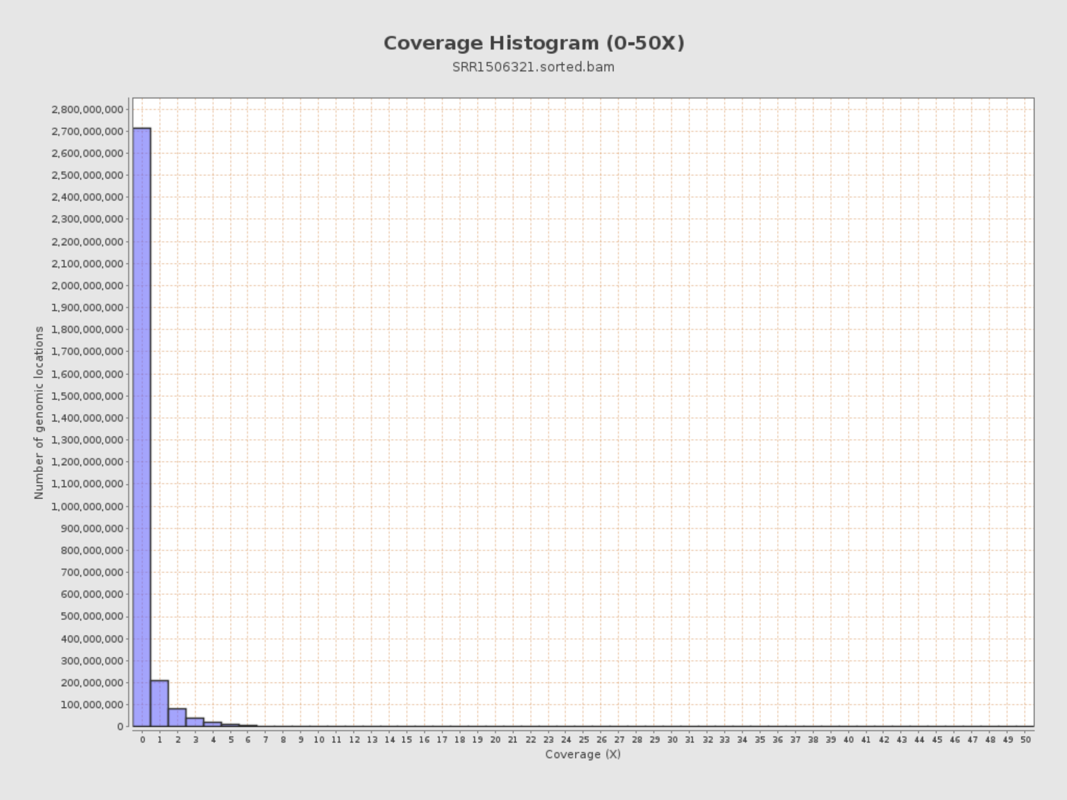
3. Results : Coverage across reference



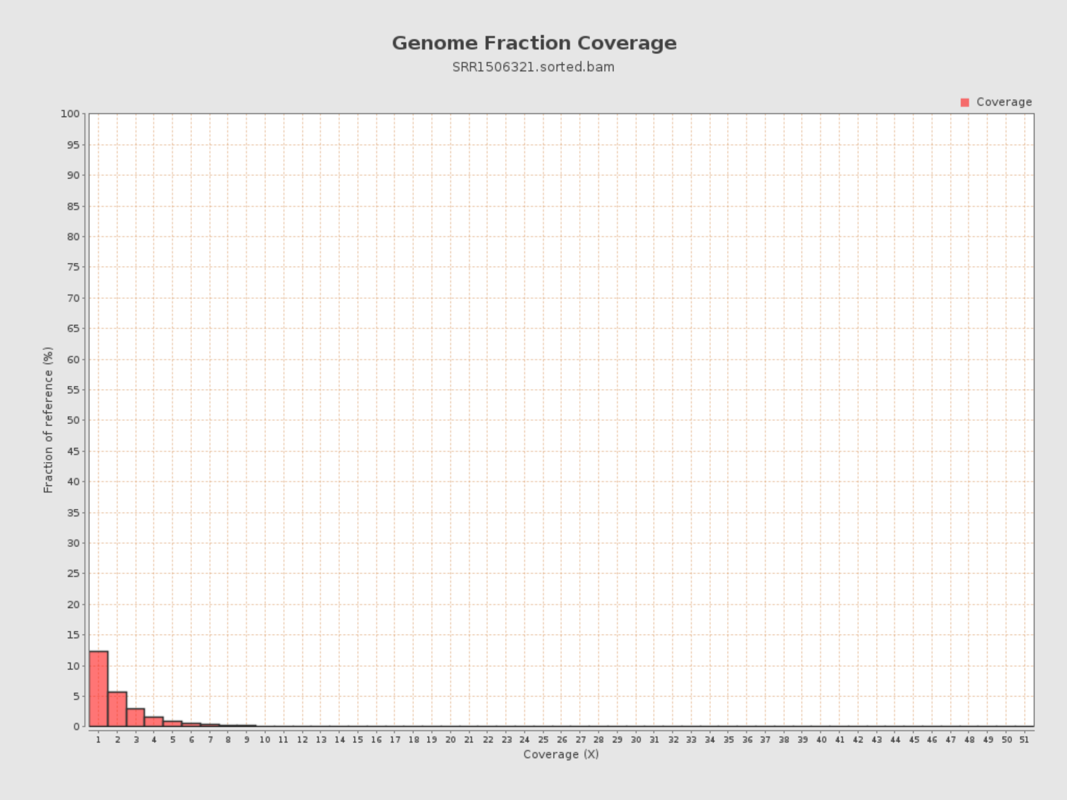
4. Results : Coverage Histogram



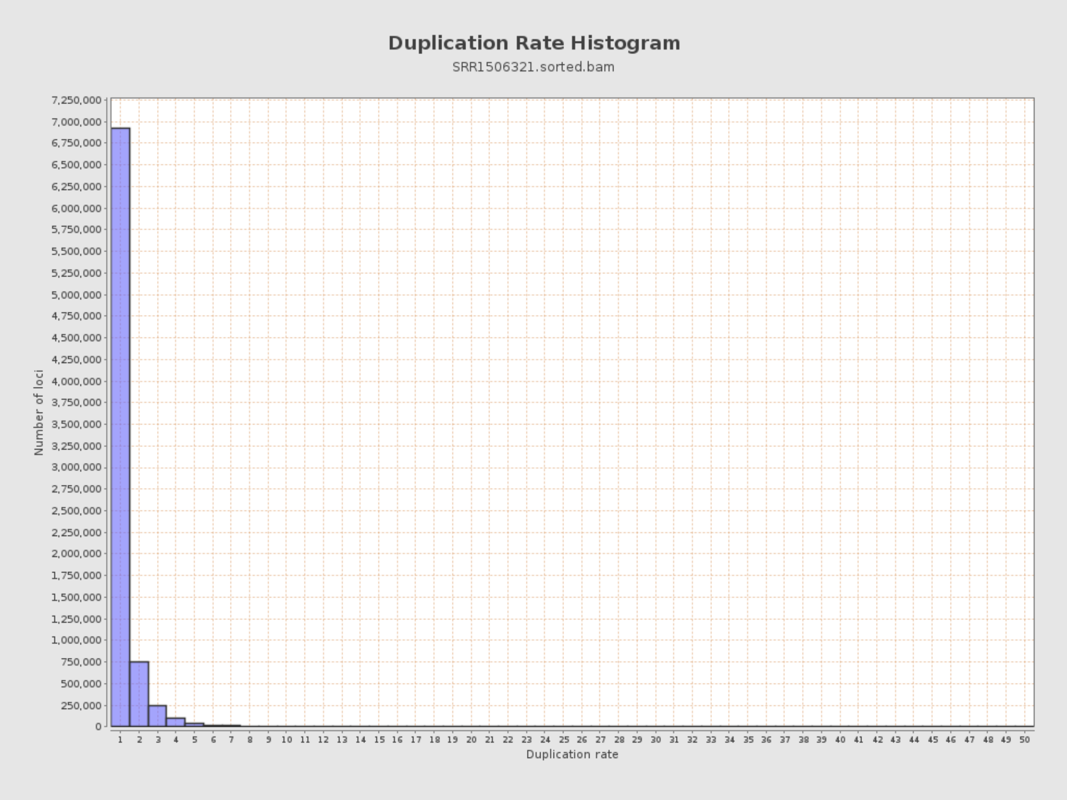
5. Results : Coverage Histogram (0-50X)



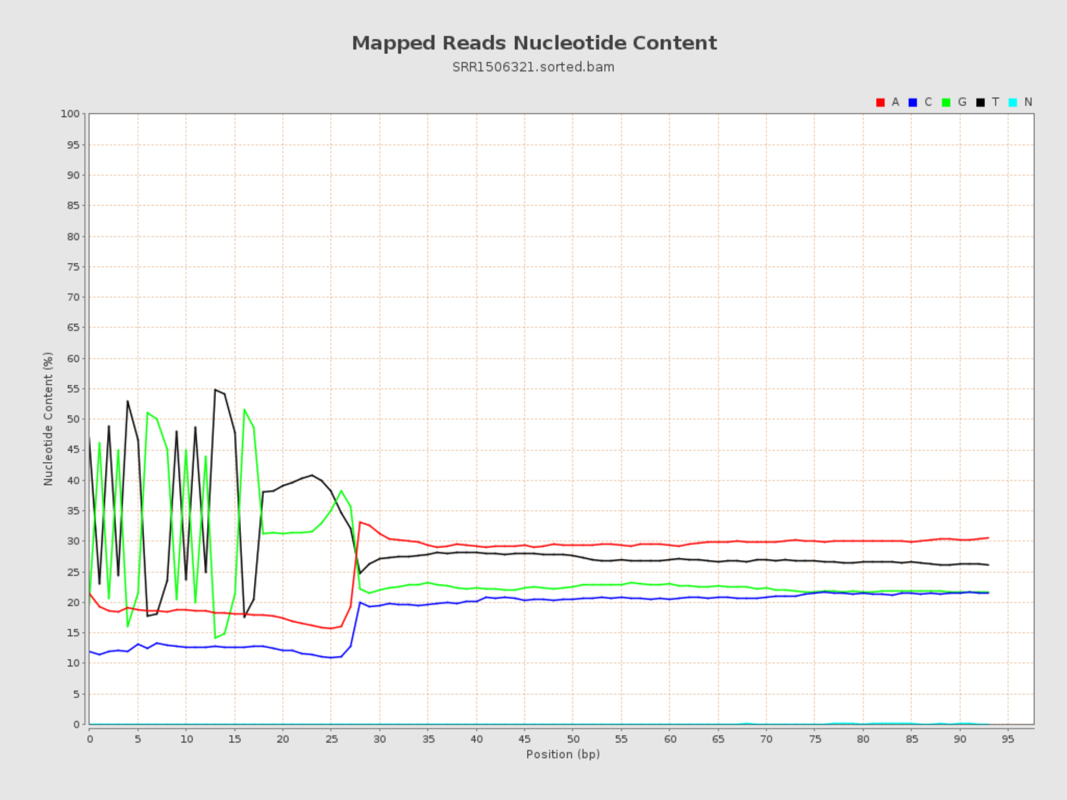
6. Results : Genome Fraction Coverage



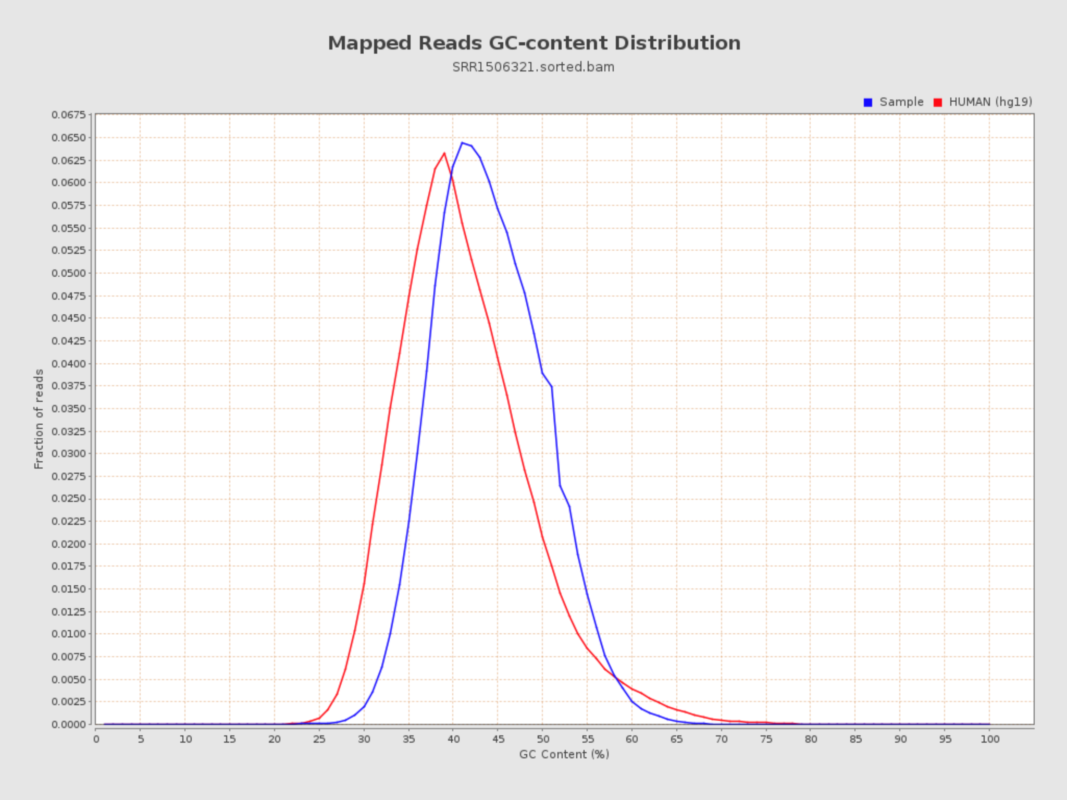
7. Results : Duplication Rate Histogram



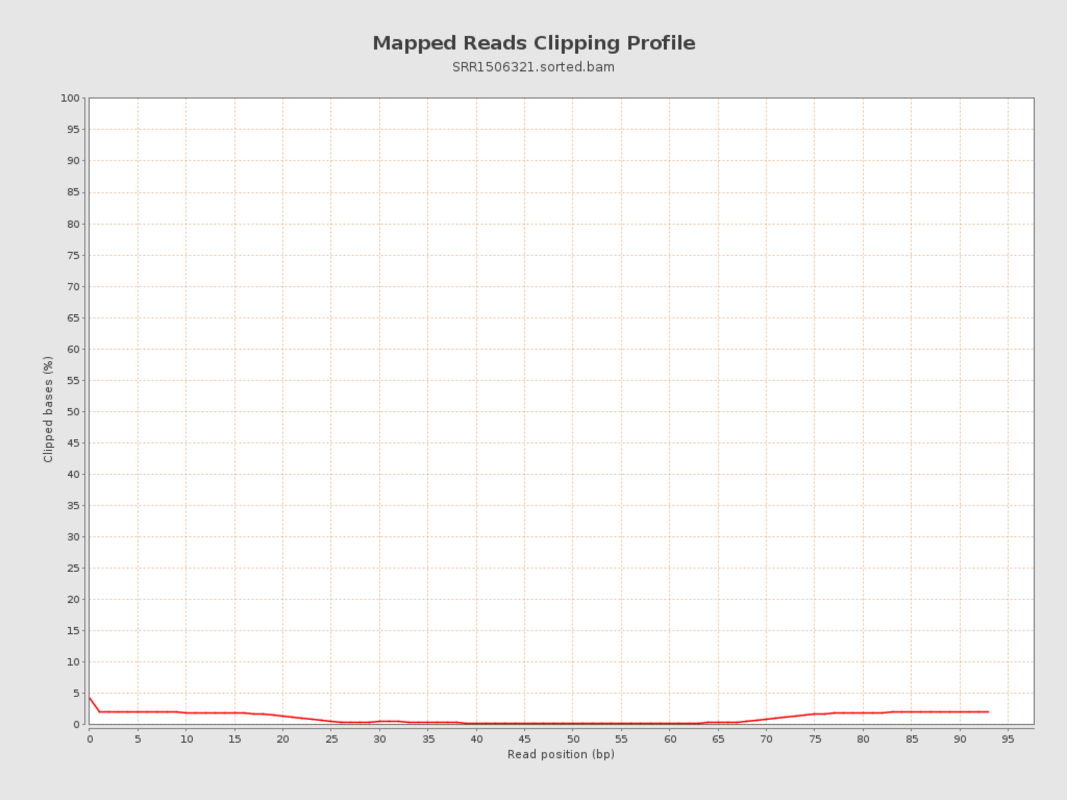
8. Results : Mapped Reads Nucleotide Content



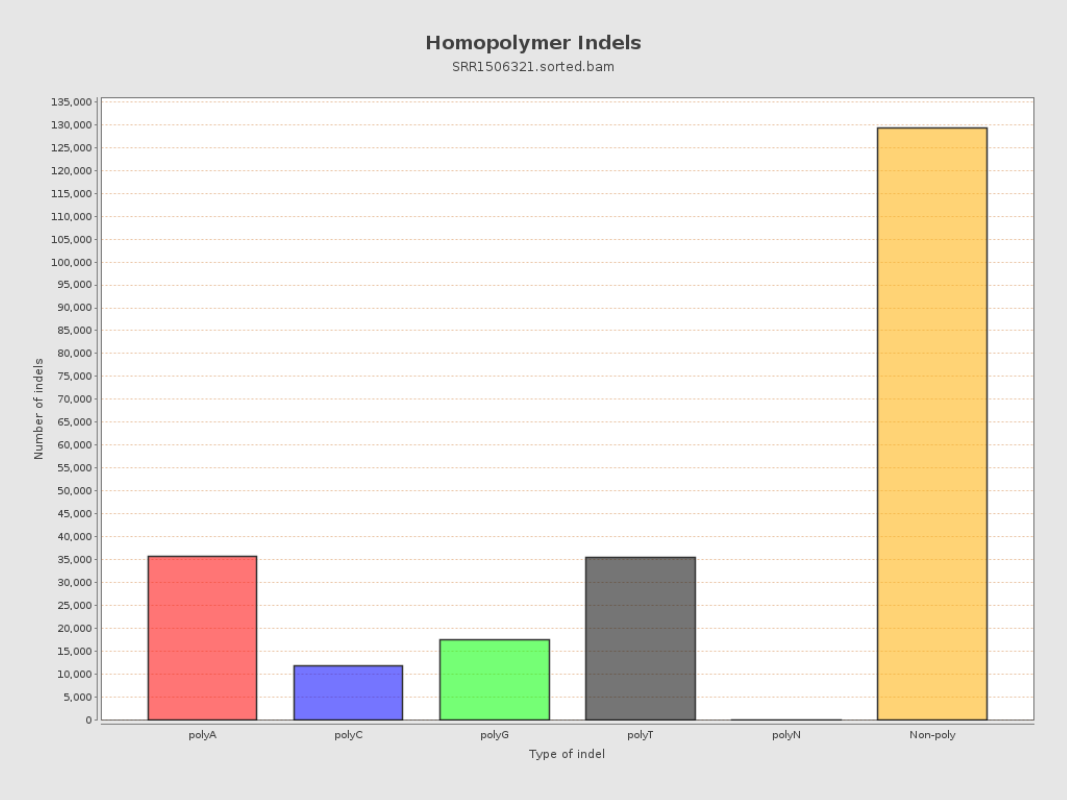
9. Results : Mapped Reads GC-content Distribution



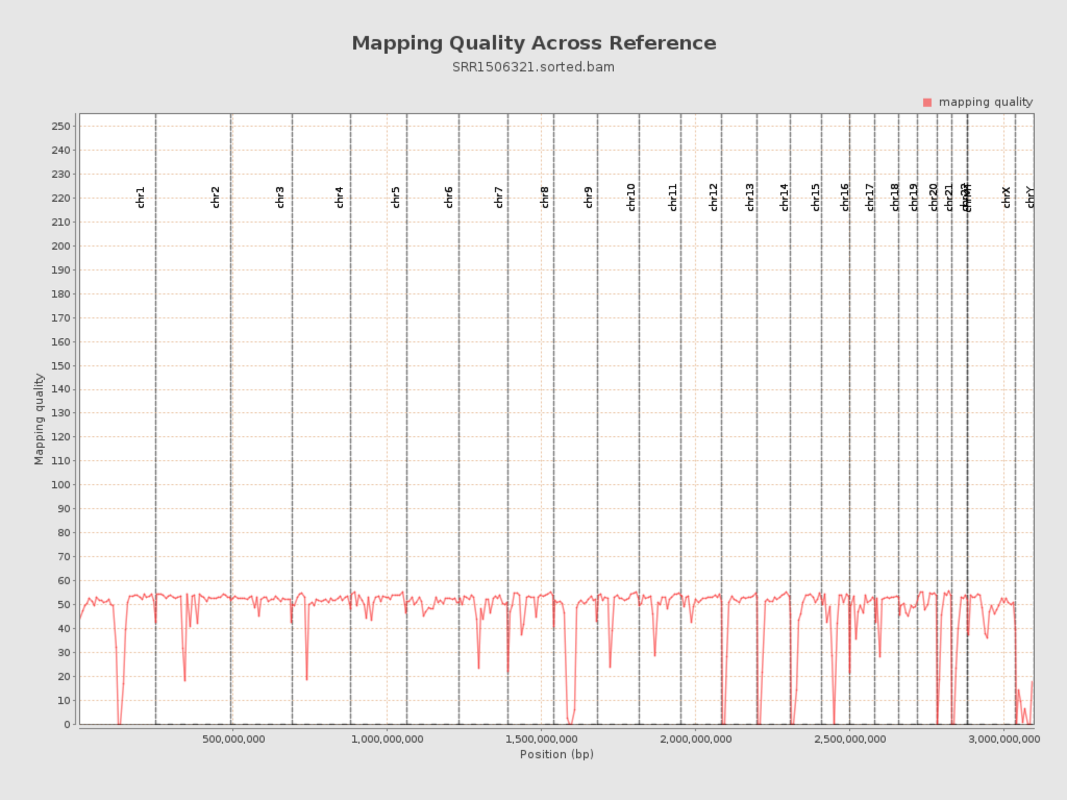
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram