Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 19:55:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013290.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_SRR6013290 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013290.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 19:55:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013290.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,367,782
Mapped reads	2,142,715 / 90.49%
Unmapped reads	225,067 / 9.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,629 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	86,704 / 3.66%
Duplication rate	2.88%
Clipped reads	891,696 / 37.66%

2.2. ACGT Content

Number/percentage of A's	40,650,451 / 28.27%
Number/percentage of C's	26,016,913 / 18.09%
Number/percentage of T's	46,057,107 / 32.03%
Number/percentage of G's	31,070,213 / 21.61%
Number/percentage of N's	2,051 / 0%
GC Percentage	39.7%

2.3. Coverage

Mean	0.0465

Standard Deviation	0.4813

2.4. Mapping Quality

Mean Mapping Quality	46.31

2.5. Mismatches and indels

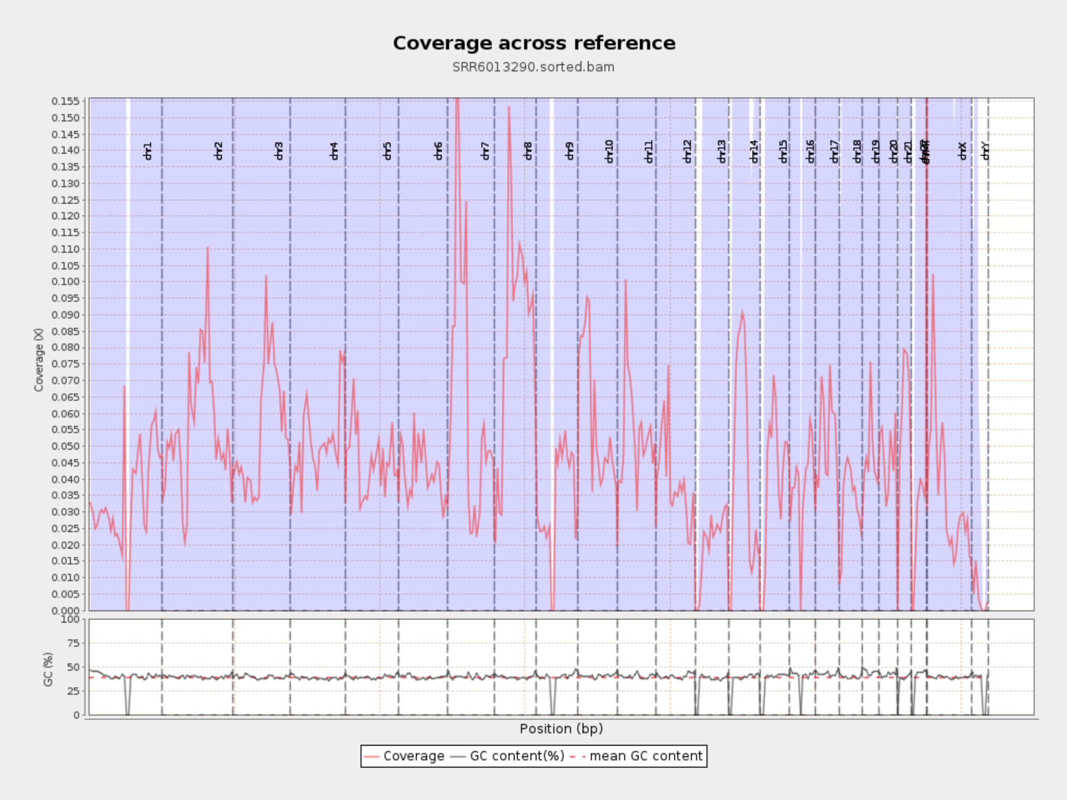
General error rate	0.72%
Mismatches	1,021,291
Insertions	10,348
Mapped reads with at least one insertion	0.48%
Deletions	39,383
Mapped reads with at least one deletion	1.82%
Homopolymer indels	46.54%

2.6. Chromosome stats

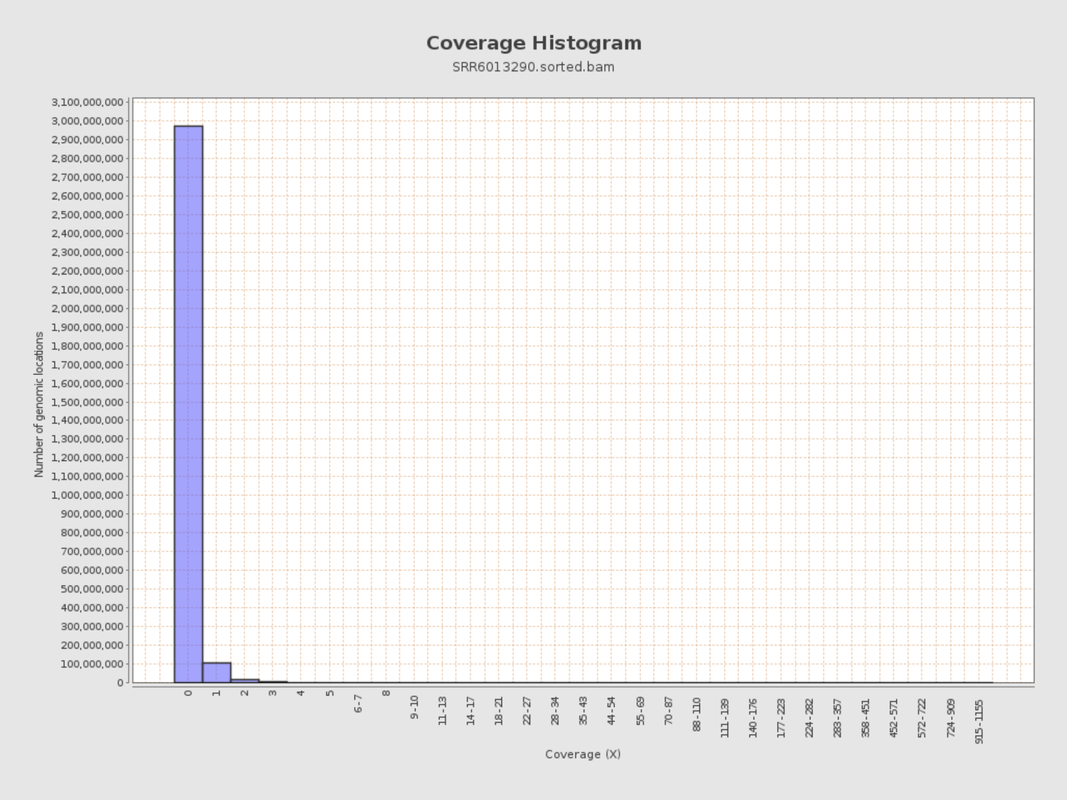
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8468693	0.034	0.9088
chr2	243199373	13517522	0.0556	0.4269
chr3	198022430	10936886	0.0552	0.2657
chr4	191154276	9766231	0.0511	0.2683
chr5	180915260	8277501	0.0458	0.245
chr6	171115067	7192844	0.042	0.362
chr7	159138663	10563276	0.0664	1.0557

chr8	146364022	12546546	0.0857	0.5613
chr9	141213431	4730433	0.0335	0.348
chr10	135534747	8102334	0.0598	0.4407
chr11	135006516	7272584	0.0539	0.4066
chr12	133851895	5291094	0.0395	0.2335
chr13	115169878	2325420	0.0202	0.1606
chr14	107349540	4737863	0.0441	0.2548
chr15	102531392	4118419	0.0402	0.234
chr16	90354753	3465570	0.0384	0.2485
chr17	81195210	4233521	0.0521	0.3786
chr18	78077248	2594010	0.0332	0.6881
chr19	59128983	2791803	0.0472	0.5608
chr20	63025520	2936131	0.0466	0.2509
chr21	48129895	2778669	0.0577	0.2896
chr22	51304566	1332108	0.026	0.1793
chrMT	16571	3234	0.1952	0.4608
chrX	155270560	5623024	0.0362	0.2516
chrY	59373566	259444	0.0044	0.1248

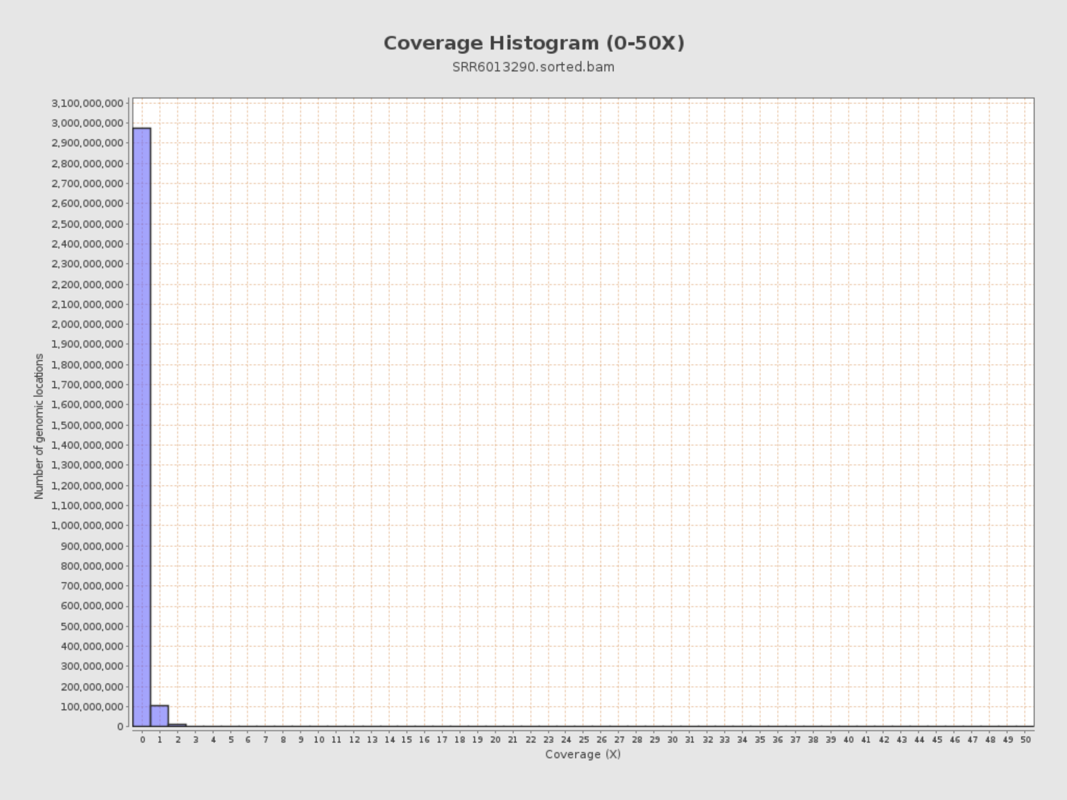
3. Results : Coverage across reference



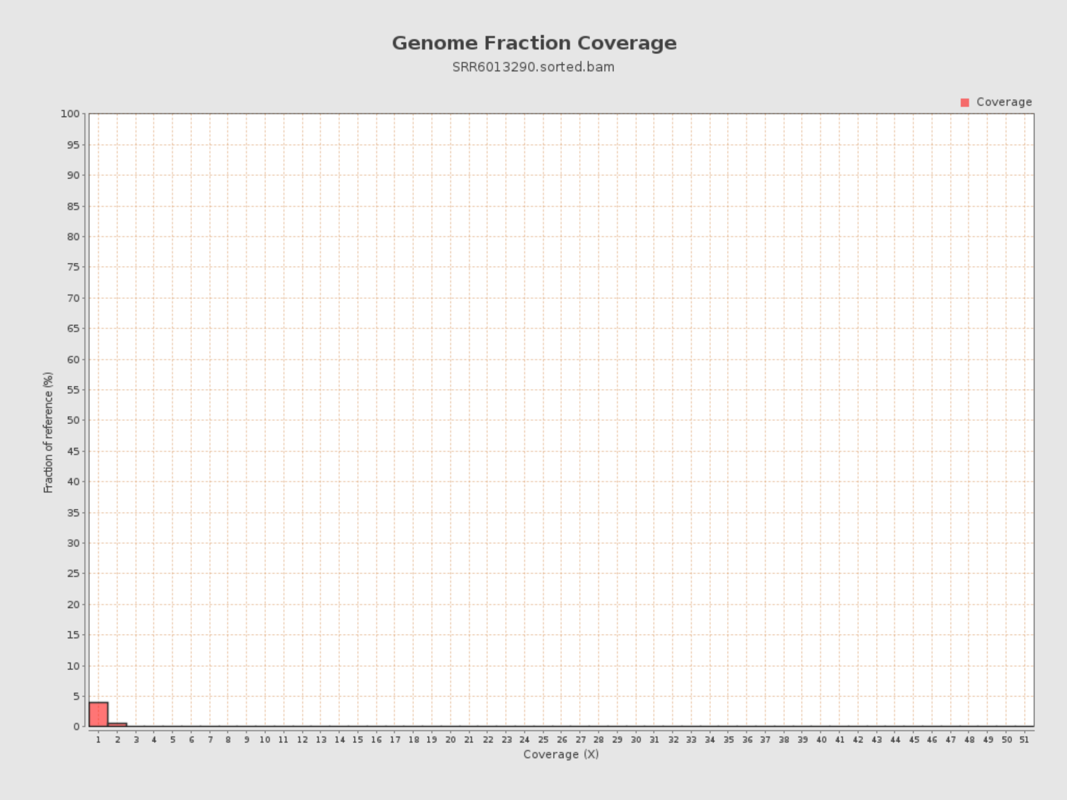
4. Results : Coverage Histogram



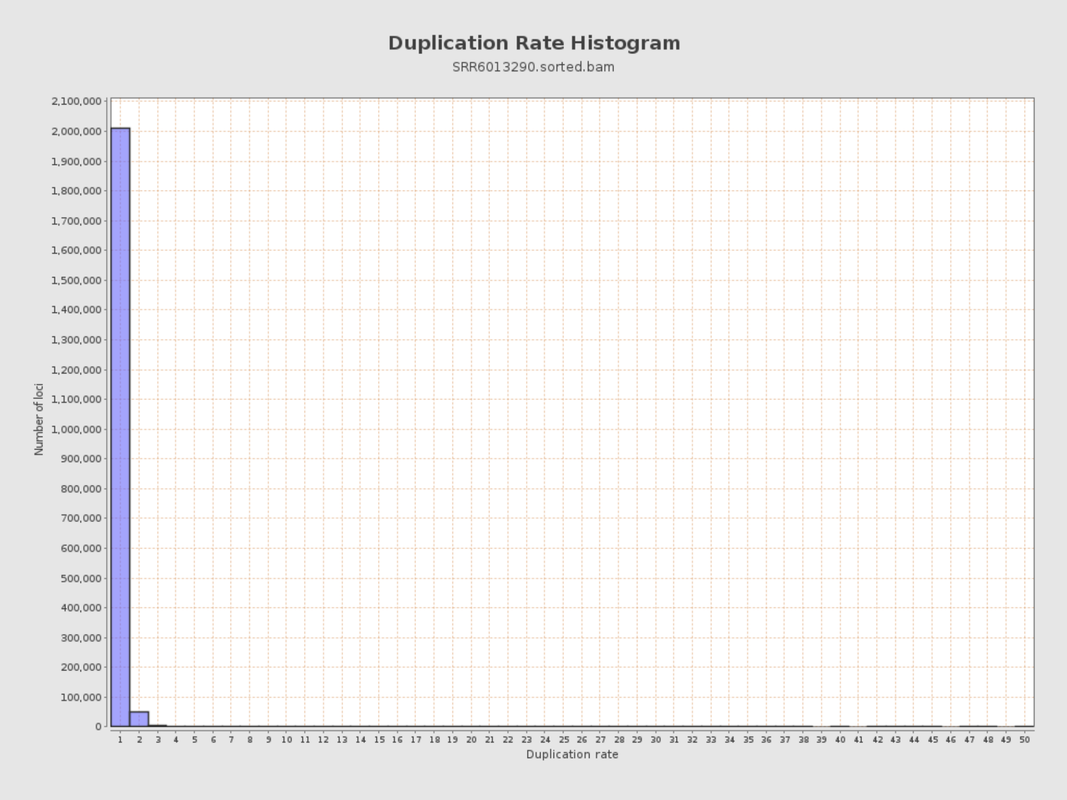
5. Results : Coverage Histogram (0-50X)



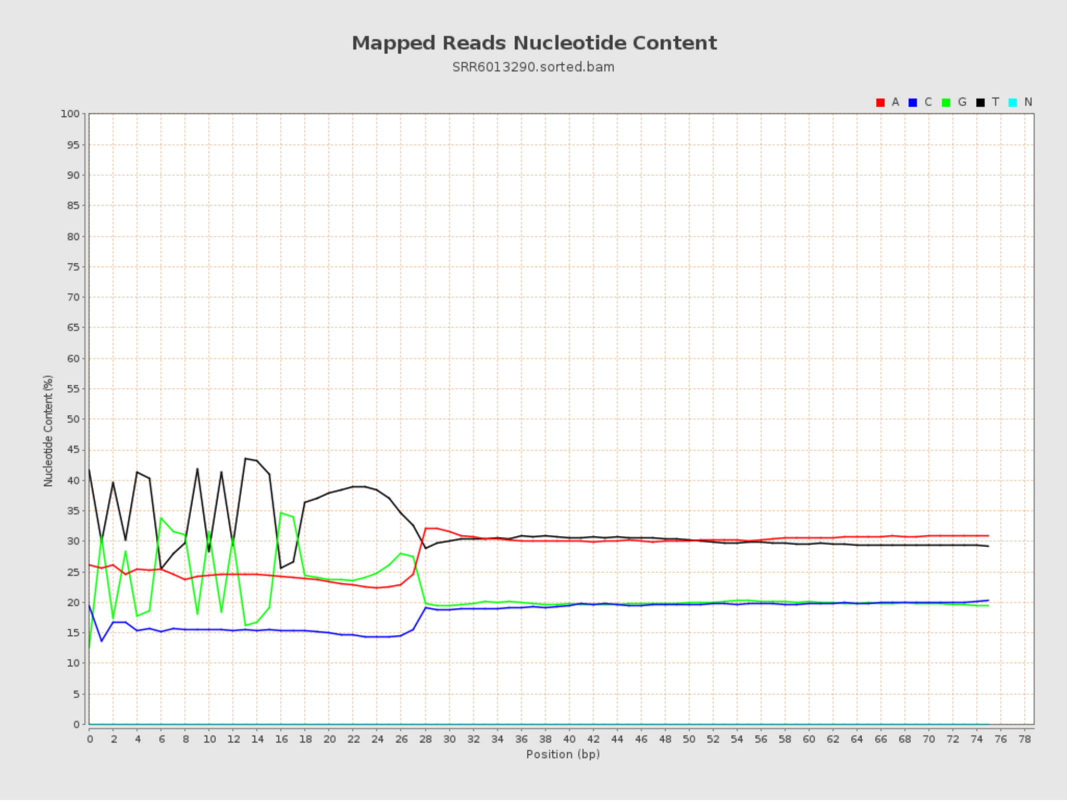
6. Results : Genome Fraction Coverage



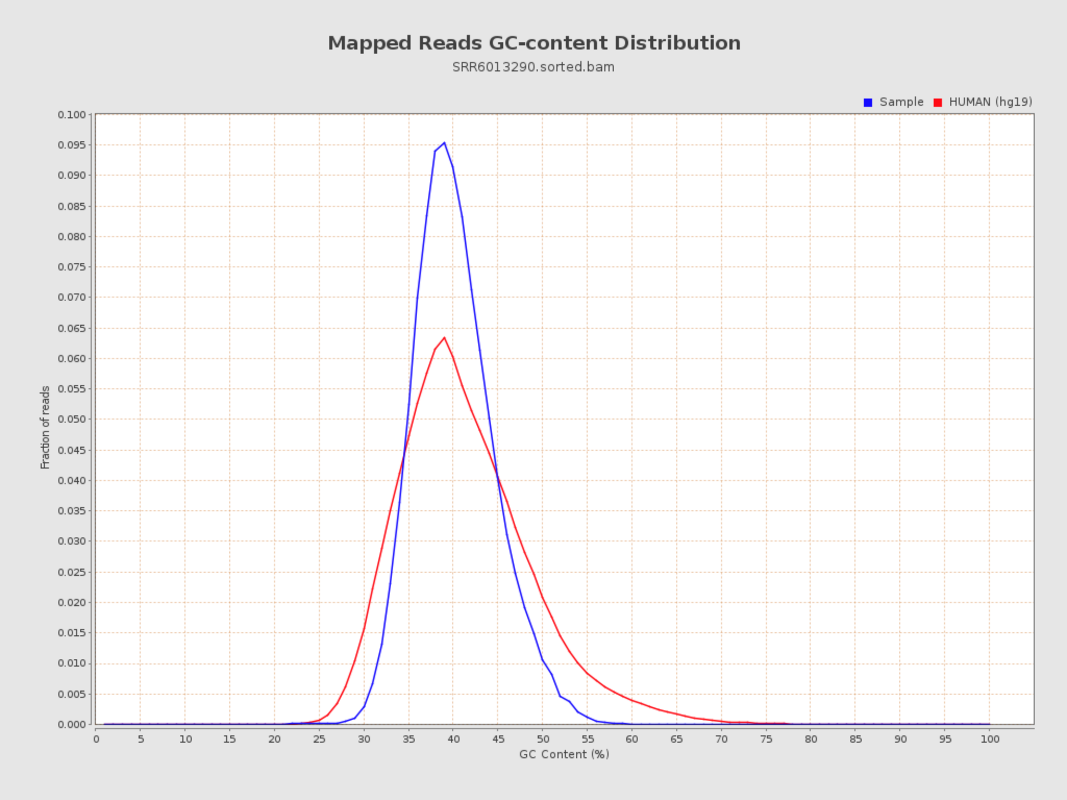
7. Results : Duplication Rate Histogram



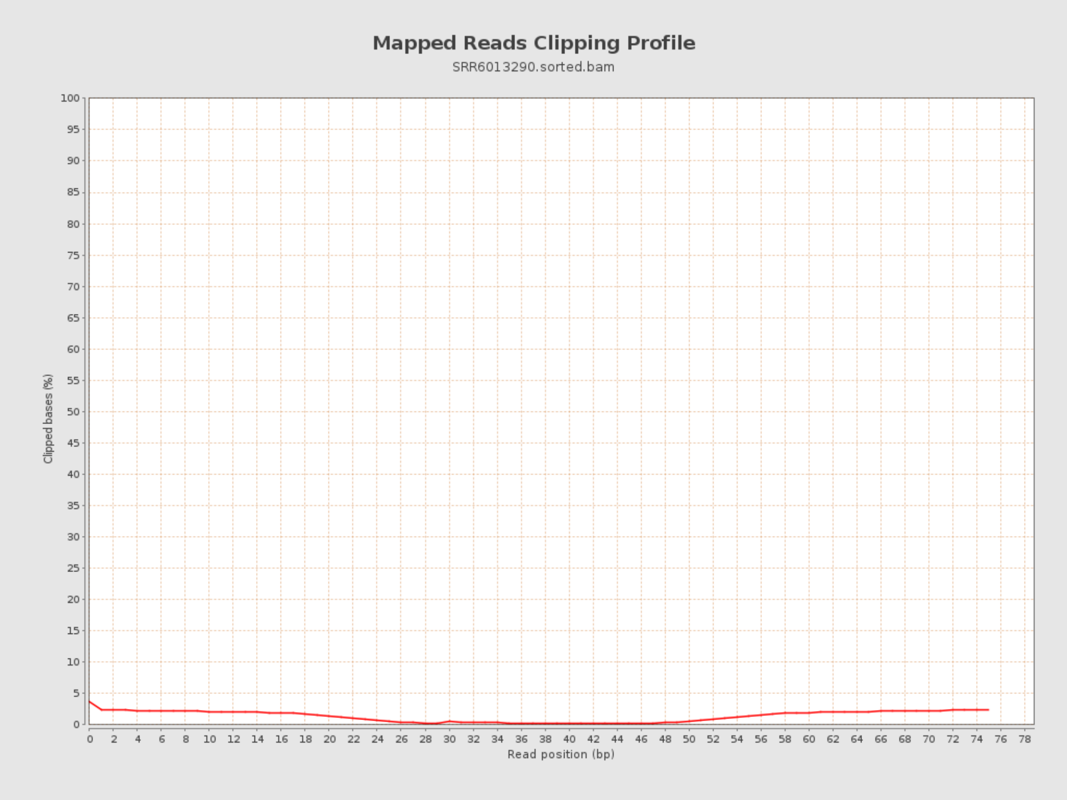
8. Results : Mapped Reads Nucleotide Content



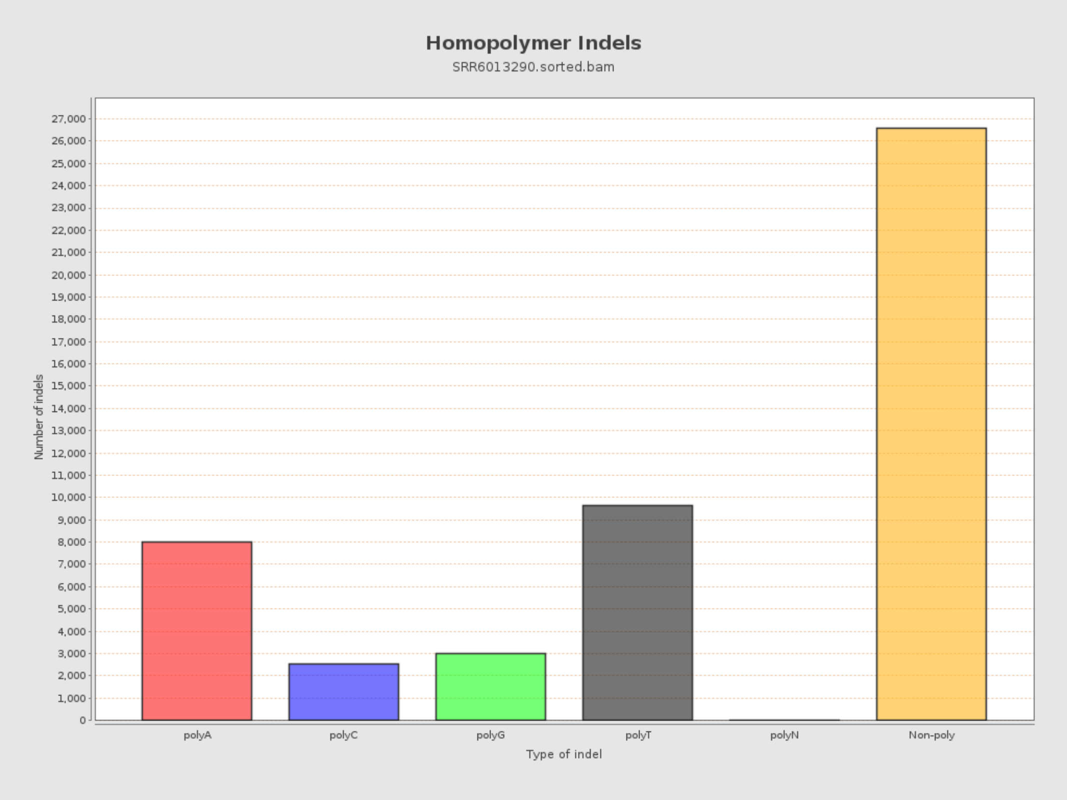
9. Results : Mapped Reads GC-content Distribution



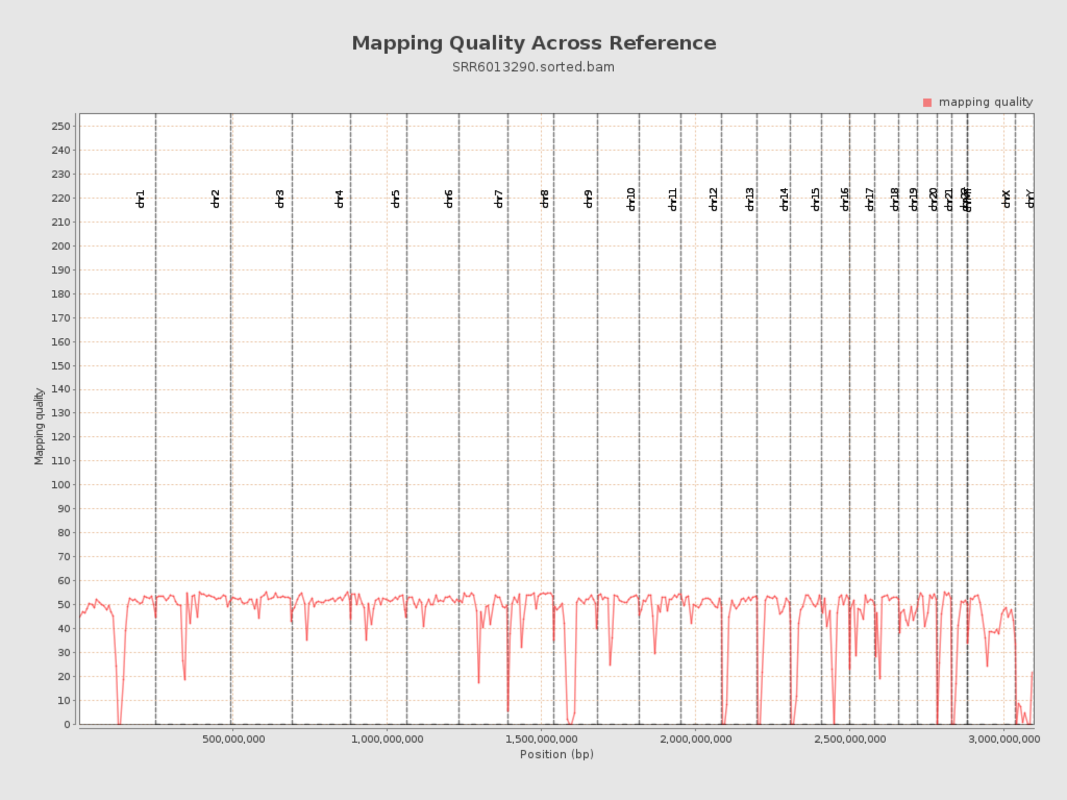
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram