Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 23:09:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506012.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_SRR1506012 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506012.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 23:09:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506012.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,195,582
Mapped reads	5,620,656 / 68.58%
Unmapped reads	2,574,926 / 31.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	276 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	490,121 / 5.98%
Duplication rate	6.38%
Clipped reads	676,587 / 8.26%

2.2. ACGT Content

Number/percentage of A's	78,863,116 / 29.94%
Number/percentage of C's	51,676,920 / 19.62%
Number/percentage of T's	79,367,408 / 30.13%
Number/percentage of G's	52,595,858 / 19.97%
Number/percentage of N's	879,180 / 0.33%
GC Percentage	39.59%

2.3. Coverage

Mean	0.0851

Standard Deviation	0.7787

2.4. Mapping Quality

Mean Mapping Quality	44.7

2.5. Mismatches and indels

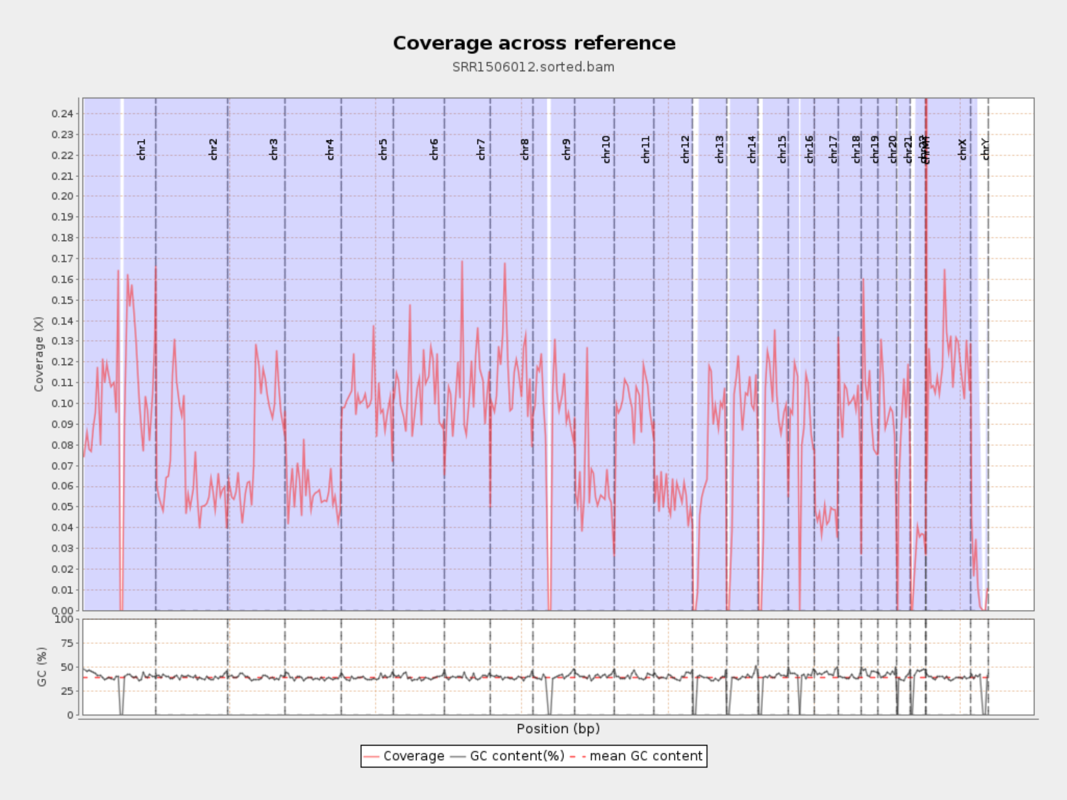
General error rate	0.8%
Mismatches	2,086,650
Insertions	12,353
Mapped reads with at least one insertion	0.22%
Deletions	41,191
Mapped reads with at least one deletion	0.73%
Homopolymer indels	47.11%

2.6. Chromosome stats

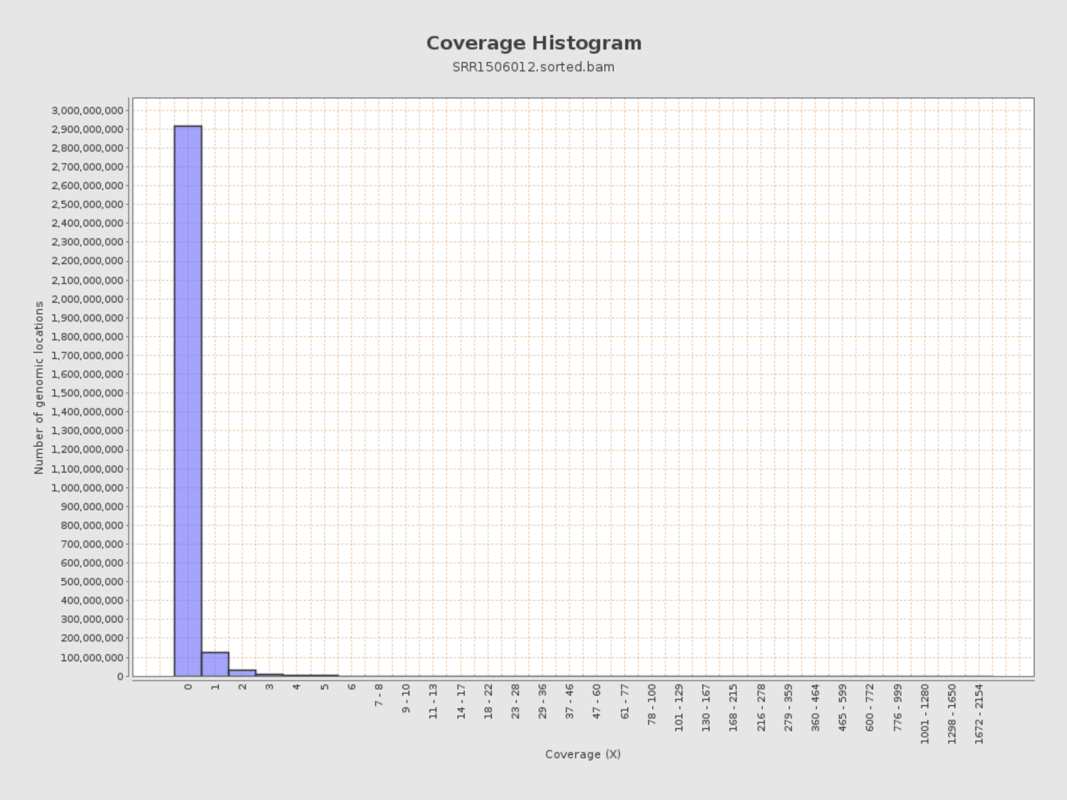
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25482983	0.1022	1.501
chr2	243199373	16089626	0.0662	0.5395
chr3	198022430	16444513	0.083	0.4039
chr4	191154276	10984677	0.0575	0.3331
chr5	180915260	18227917	0.1008	0.4495
chr6	171115067	18228764	0.1065	0.6042
chr7	159138663	17116033	0.1076	1.0982

chr8	146364022	16658145	0.1138	1.2336
chr9	141213431	12997043	0.092	0.5847
chr10	135534747	8040767	0.0593	0.7267
chr11	135006516	13428024	0.0995	0.6435
chr12	133851895	7322716	0.0547	0.3756
chr13	115169878	8260549	0.0717	0.368
chr14	107349540	9373108	0.0873	1.386
chr15	102531392	8729629	0.0851	0.3998
chr16	90354753	7869727	0.0871	0.4924
chr17	81195210	3667968	0.0452	0.3433
chr18	78077248	7878002	0.1009	1.0312
chr19	59128983	5903555	0.0998	0.94
chr20	63025520	6142336	0.0975	0.4573
chr21	48129895	3995909	0.083	0.4323
chr22	51304566	1345501	0.0262	0.2181
chrMT	16571	142266	8.5852	5.9332
chrX	155270560	18306832	0.1179	0.5537
chrY	59373566	803510	0.0135	0.1991

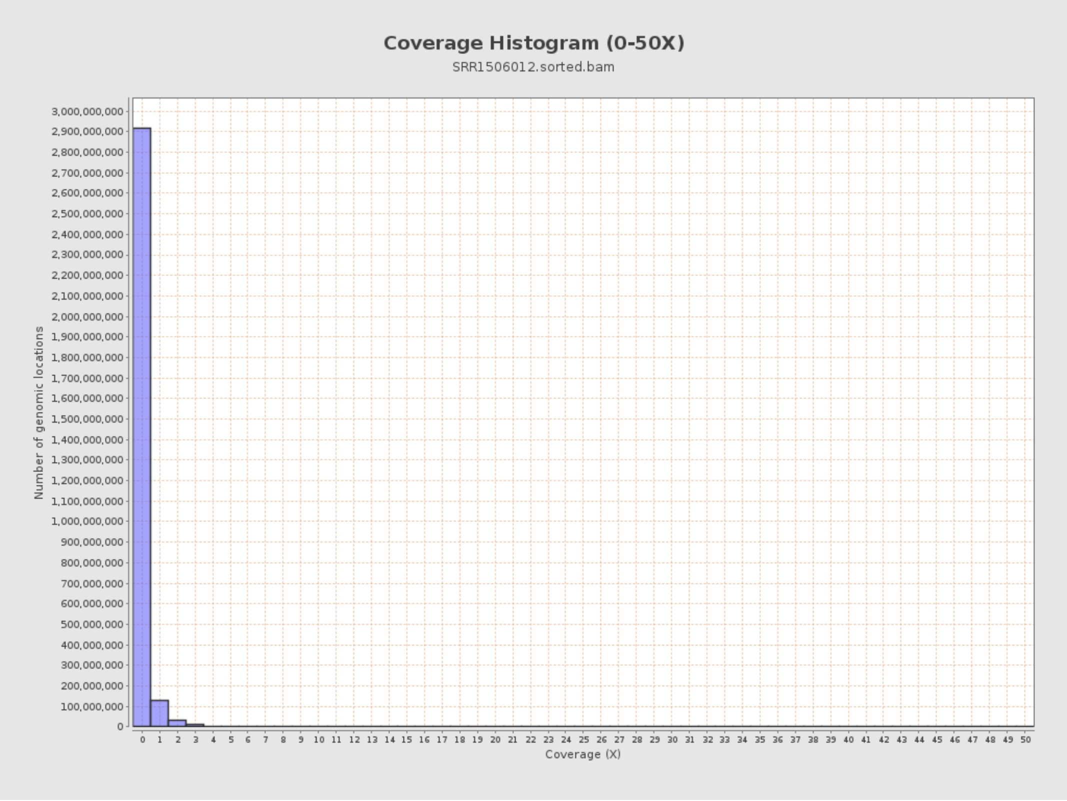
3. Results : Coverage across reference



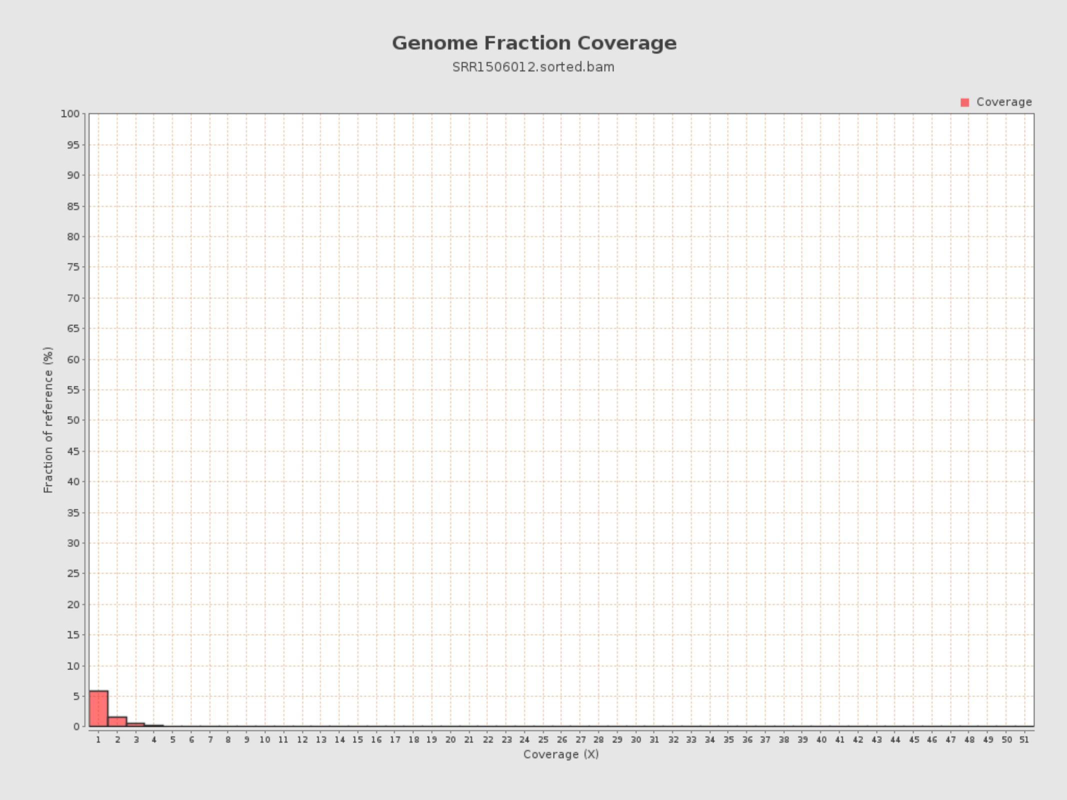
4. Results : Coverage Histogram



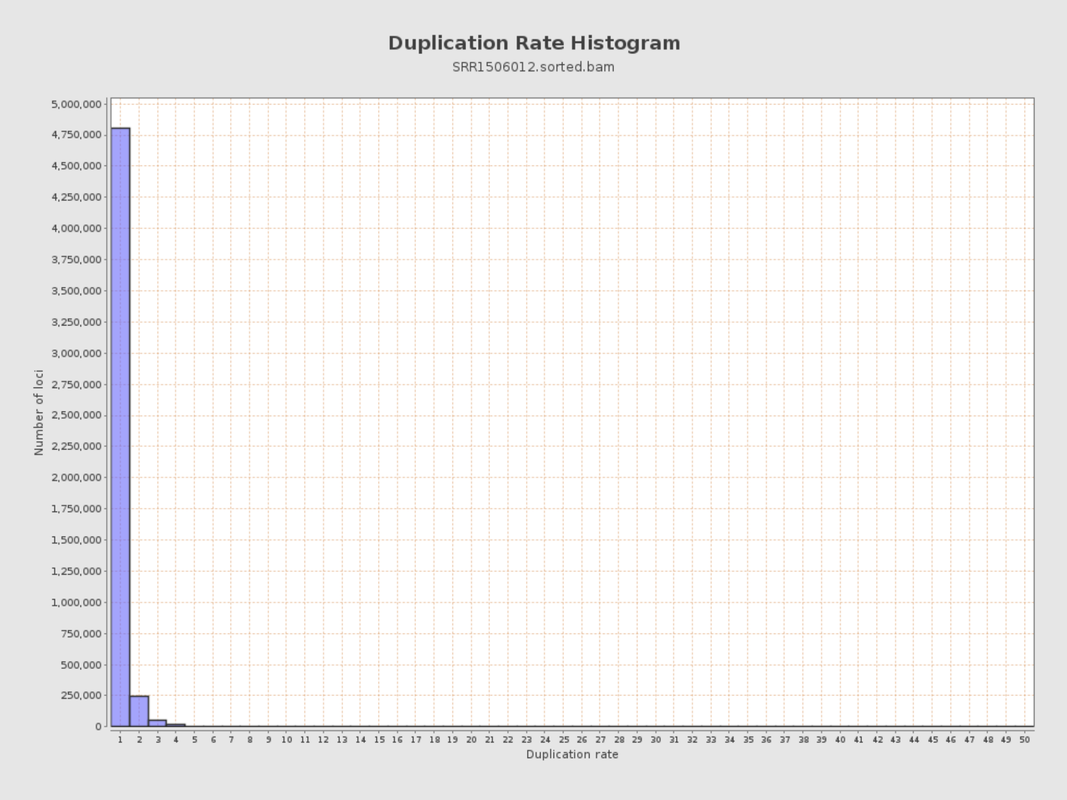
5. Results : Coverage Histogram (0-50X)



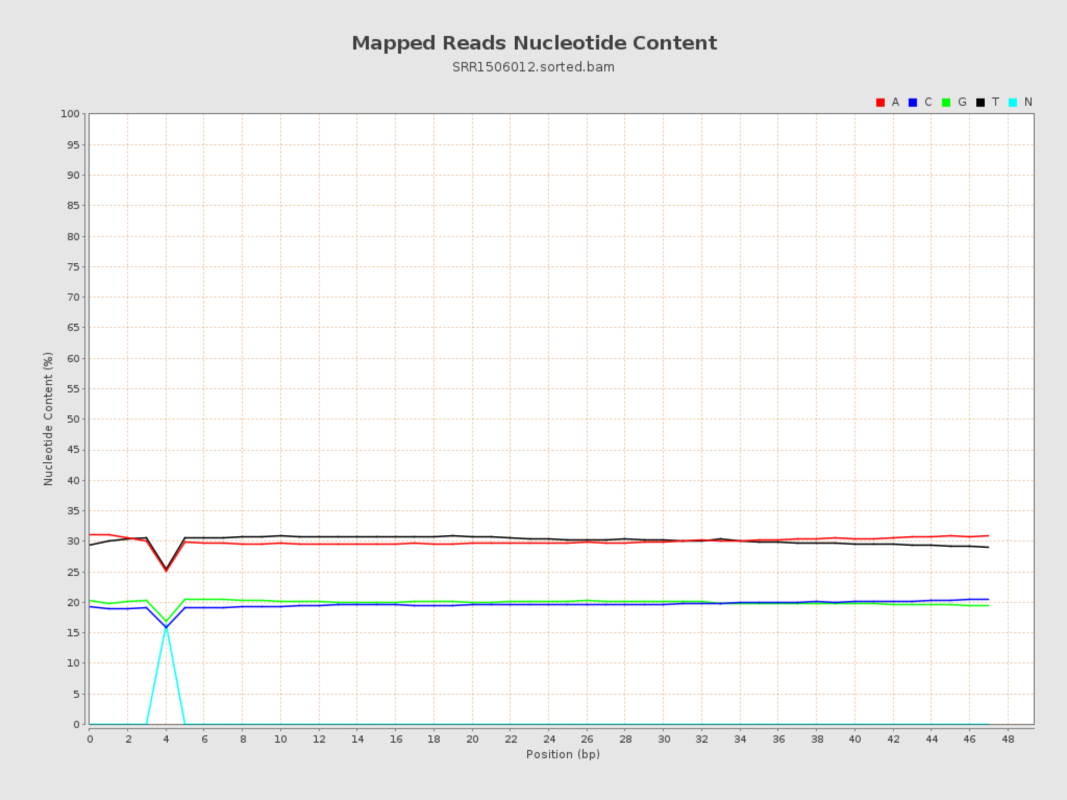
6. Results : Genome Fraction Coverage



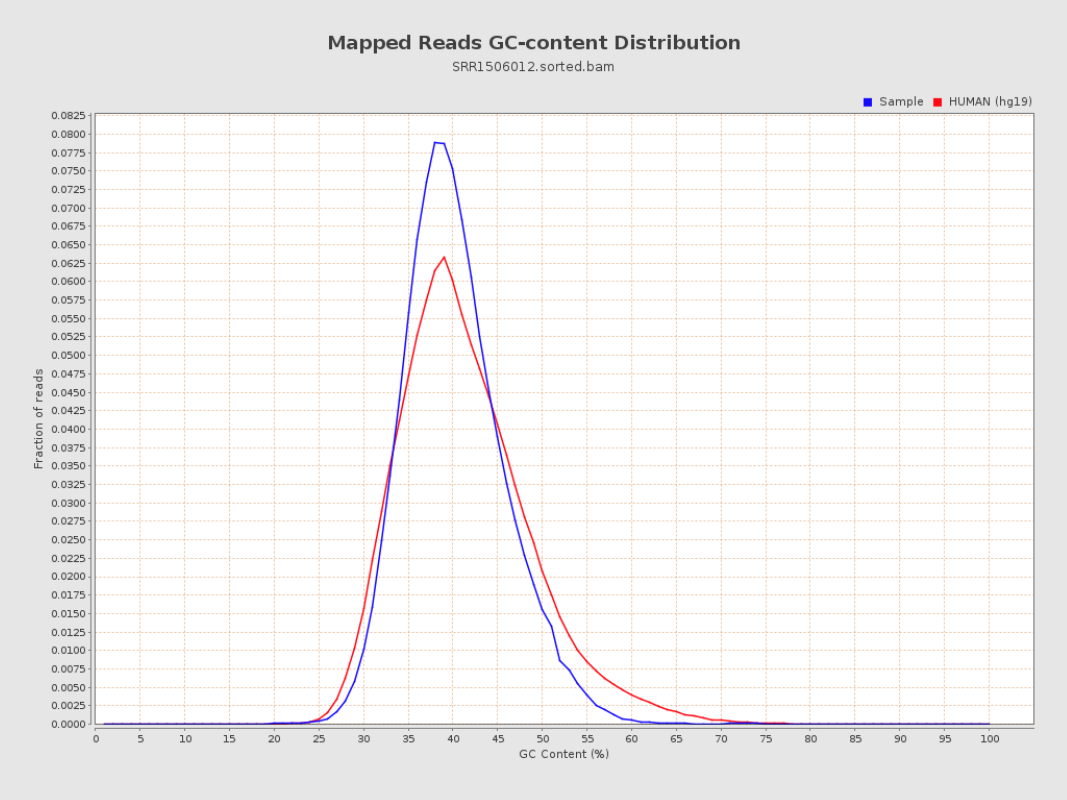
7. Results : Duplication Rate Histogram



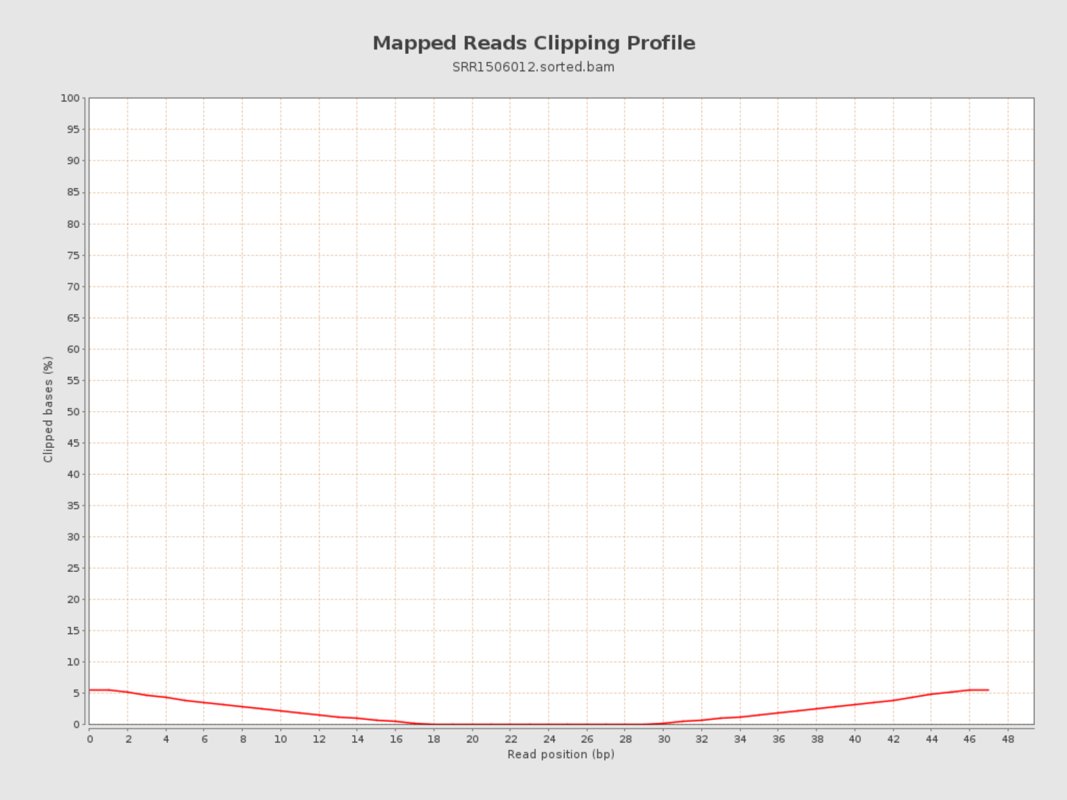
8. Results : Mapped Reads Nucleotide Content



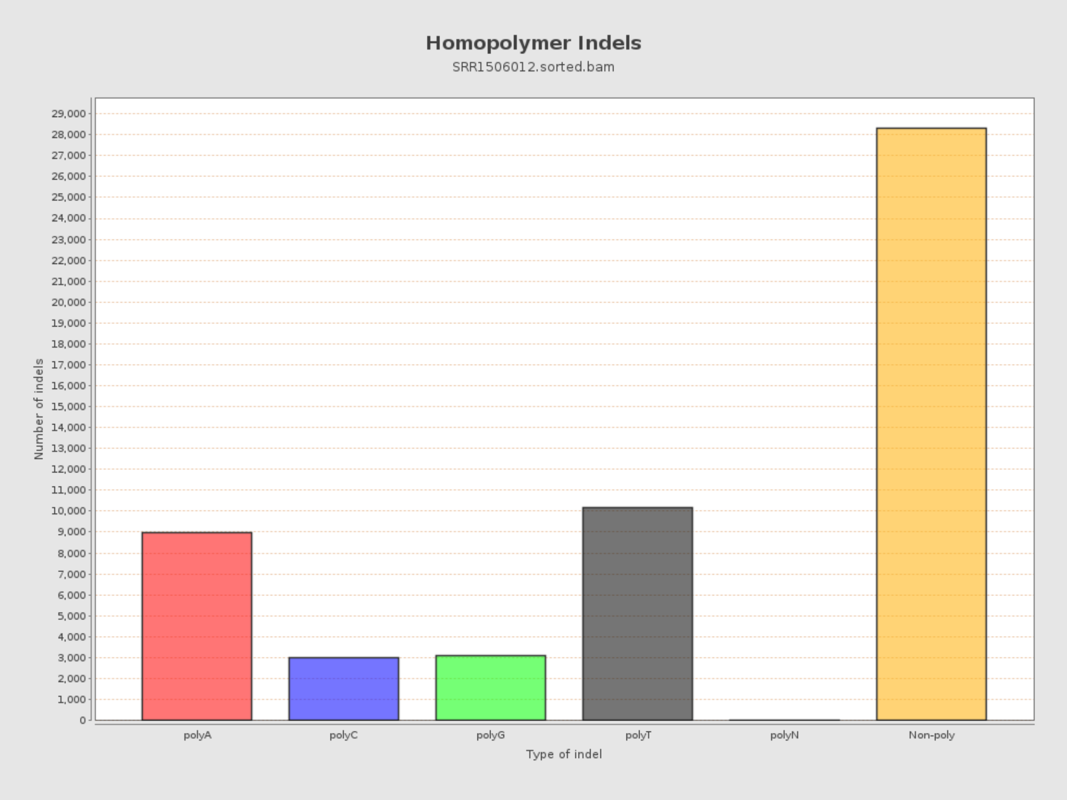
9. Results : Mapped Reads GC-content Distribution



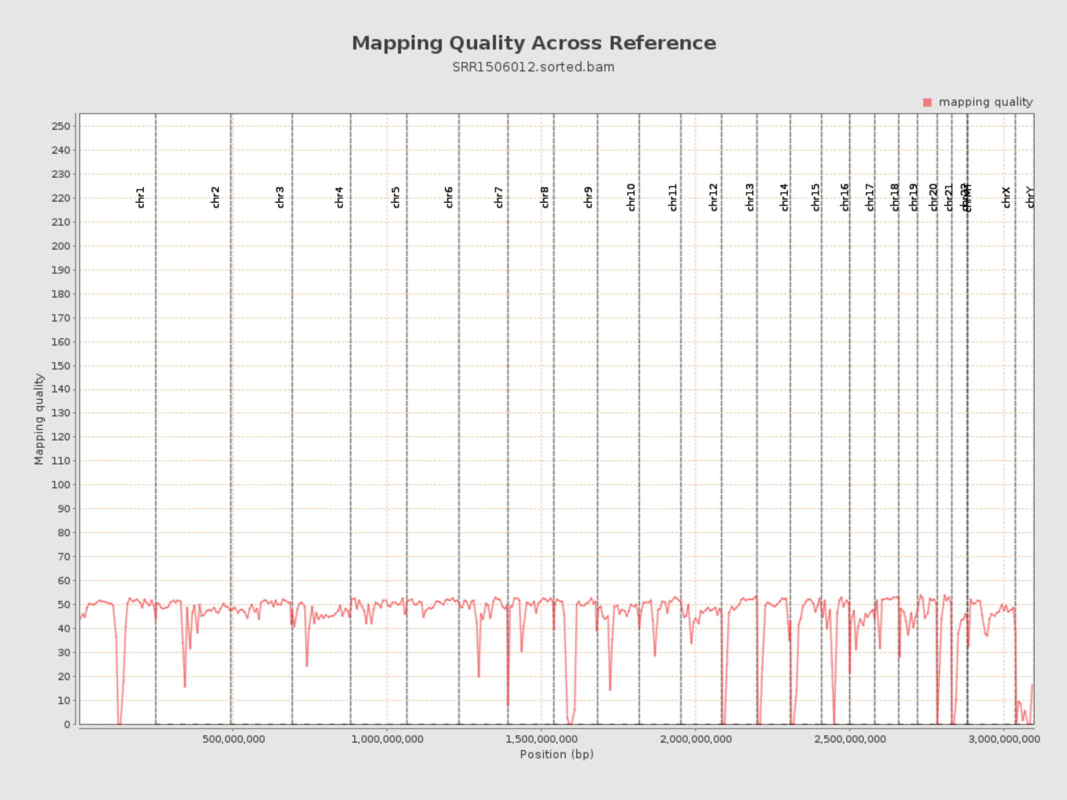
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram