Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 00:28:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506105.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_SRR1506105 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506105.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 00:28:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506105.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,883,100
Mapped reads	7,730,030 / 87.02%
Unmapped reads	1,153,070 / 12.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	147,582 / 1.66%
Read min/max/mean length	30 / 94 / 94.6
Duplicated reads (estimated)	1,633,883 / 18.39%
Duplication rate	13.14%
Clipped reads	4,167,046 / 46.91%

2.2. ACGT Content

Number/percentage of A's	169,886,535 / 27.08%
Number/percentage of C's	119,482,325 / 19.04%
Number/percentage of T's	190,297,243 / 30.33%
Number/percentage of G's	147,611,671 / 23.53%
Number/percentage of N's	109,288 / 0.02%
GC Percentage	42.57%

2.3. Coverage

Mean	0.2028

Standard Deviation	1.7994

2.4. Mapping Quality

Mean Mapping Quality	48.25

2.5. Mismatches and indels

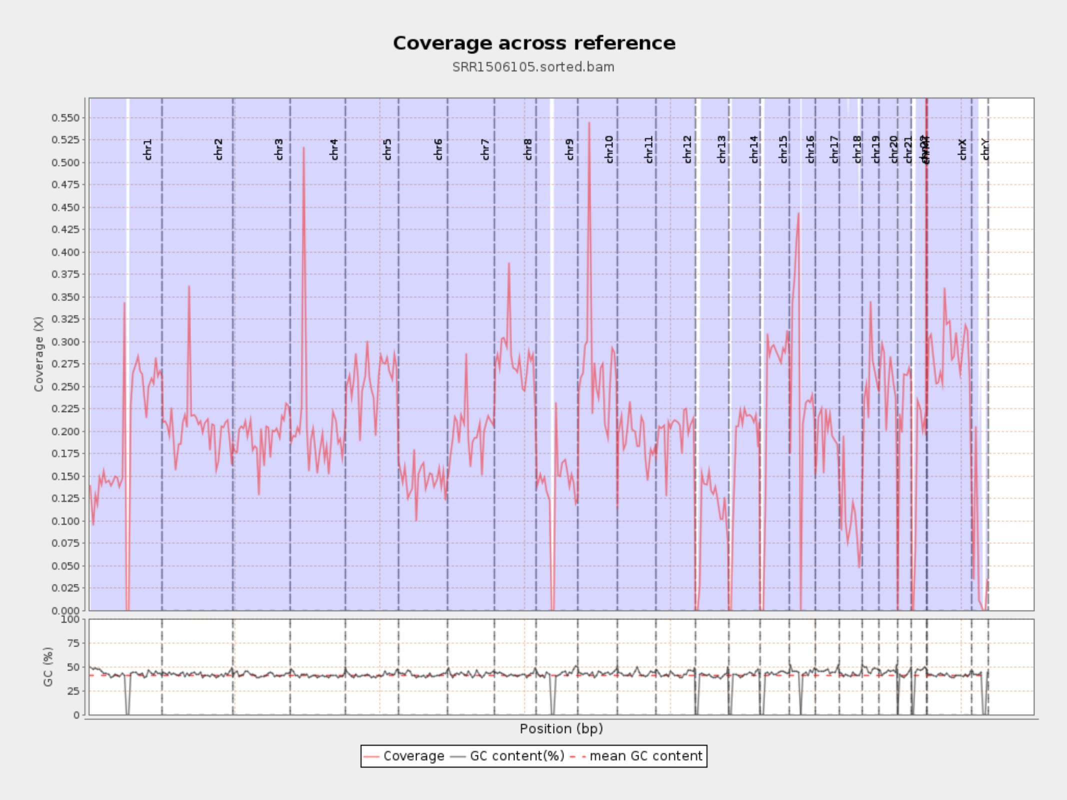
General error rate	0.79%
Mismatches	4,841,677
Insertions	55,166
Mapped reads with at least one insertion	0.7%
Deletions	144,587
Mapped reads with at least one deletion	1.84%
Homopolymer indels	43.47%

2.6. Chromosome stats

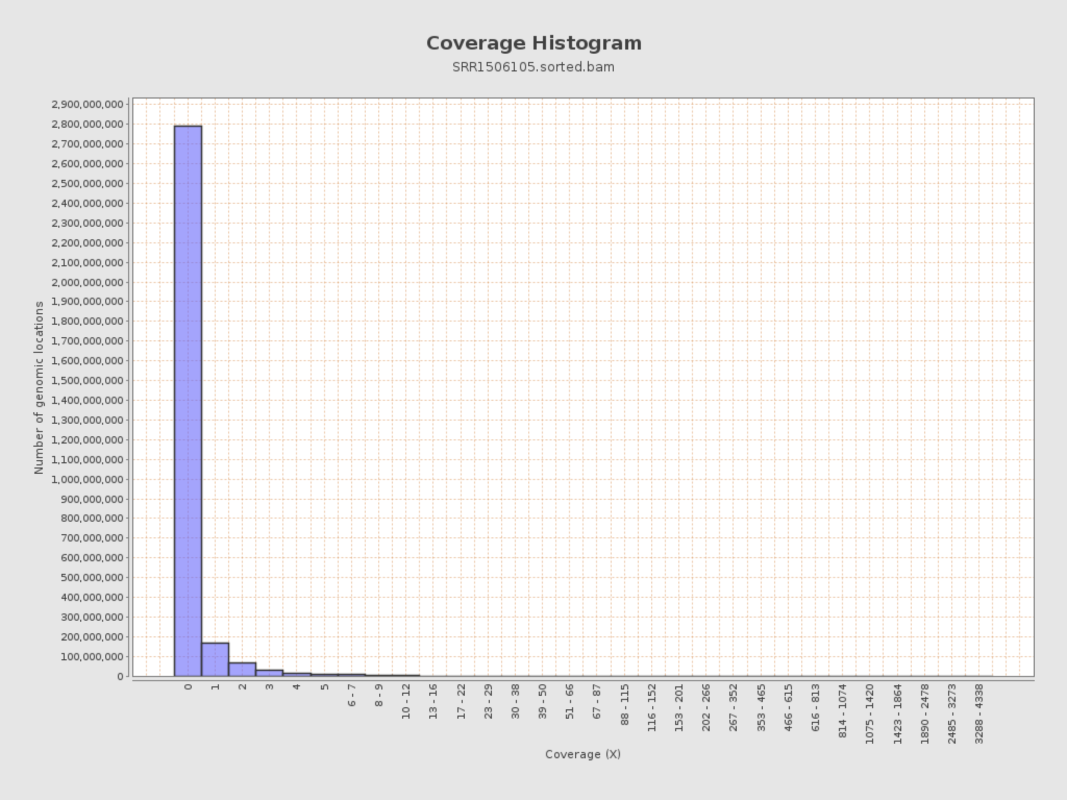
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	47101512	0.189	3.9139
chr2	243199373	49953656	0.2054	1.6496
chr3	198022430	38699725	0.1954	0.8043
chr4	191154276	38643230	0.2022	1.5006
chr5	180915260	46711070	0.2582	0.9287
chr6	171115067	24988003	0.146	0.8596
chr7	159138663	31797174	0.1998	1.6913

chr8	146364022	41128034	0.281	1.9605
chr9	141213431	18962594	0.1343	1.5485
chr10	135534747	37193087	0.2744	2.3396
chr11	135006516	25701863	0.1904	1.4993
chr12	133851895	26754635	0.1999	0.8553
chr13	115169878	12267467	0.1065	0.5737
chr14	107349540	19014997	0.1771	0.9388
chr15	102531392	24341526	0.2374	0.9051
chr16	90354753	23622624	0.2614	1.2555
chr17	81195210	15914251	0.196	1.061
chr18	78077248	7985294	0.1023	3.0298
chr19	59128983	15185051	0.2568	2.6349
chr20	63025520	16070706	0.255	1.0425
chr21	48129895	10661371	0.2215	1.343
chr22	51304566	7687380	0.1498	0.8355
chrMT	16571	32845	1.9821	2.6775
chrX	155270560	44544329	0.2869	1.22
chrY	59373566	2715312	0.0457	1.8055

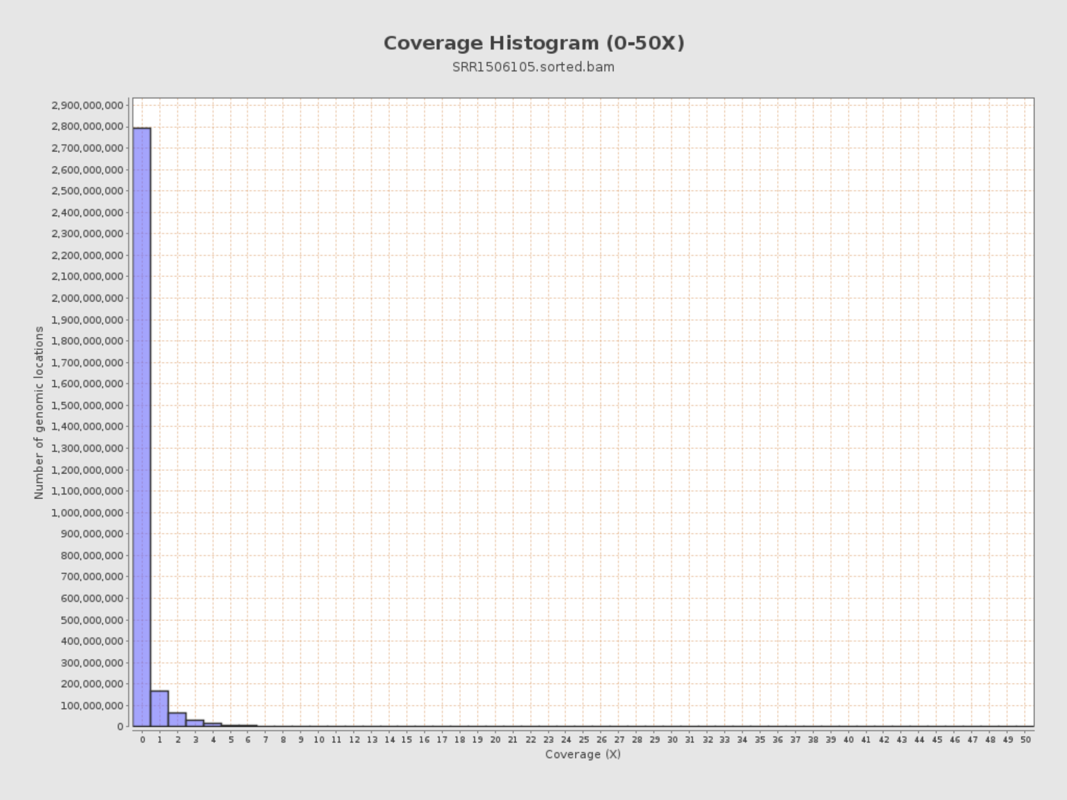
3. Results : Coverage across reference



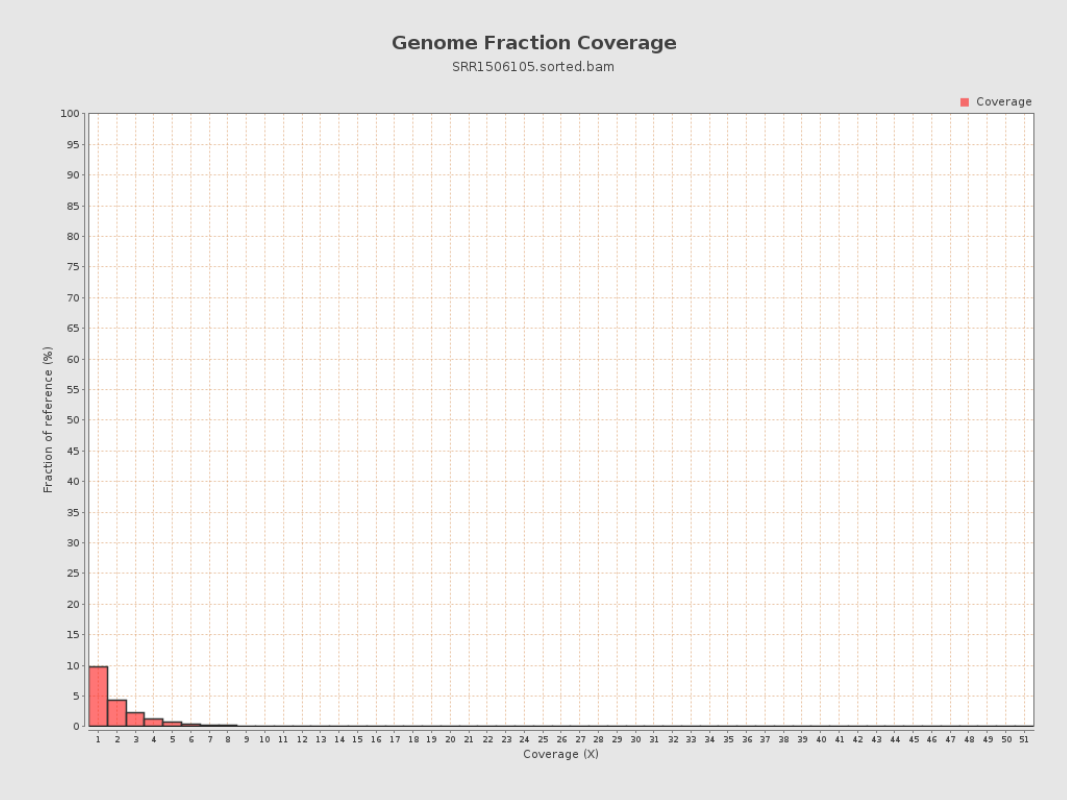
4. Results : Coverage Histogram



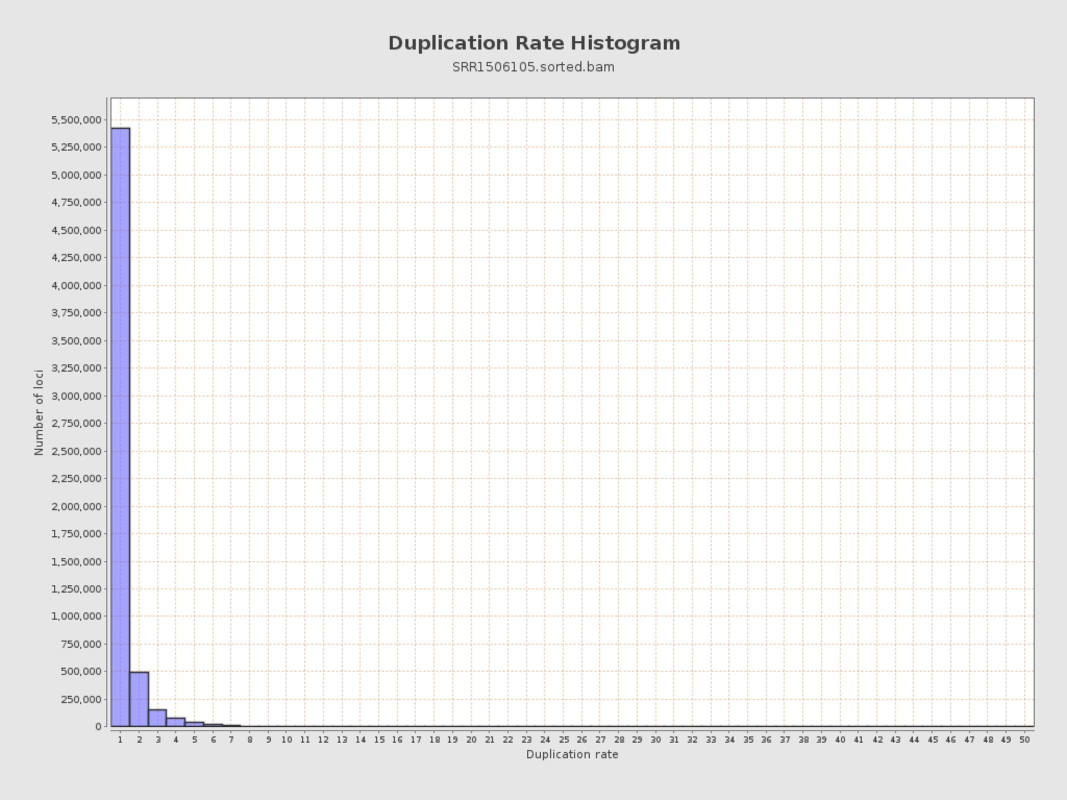
5. Results : Coverage Histogram (0-50X)



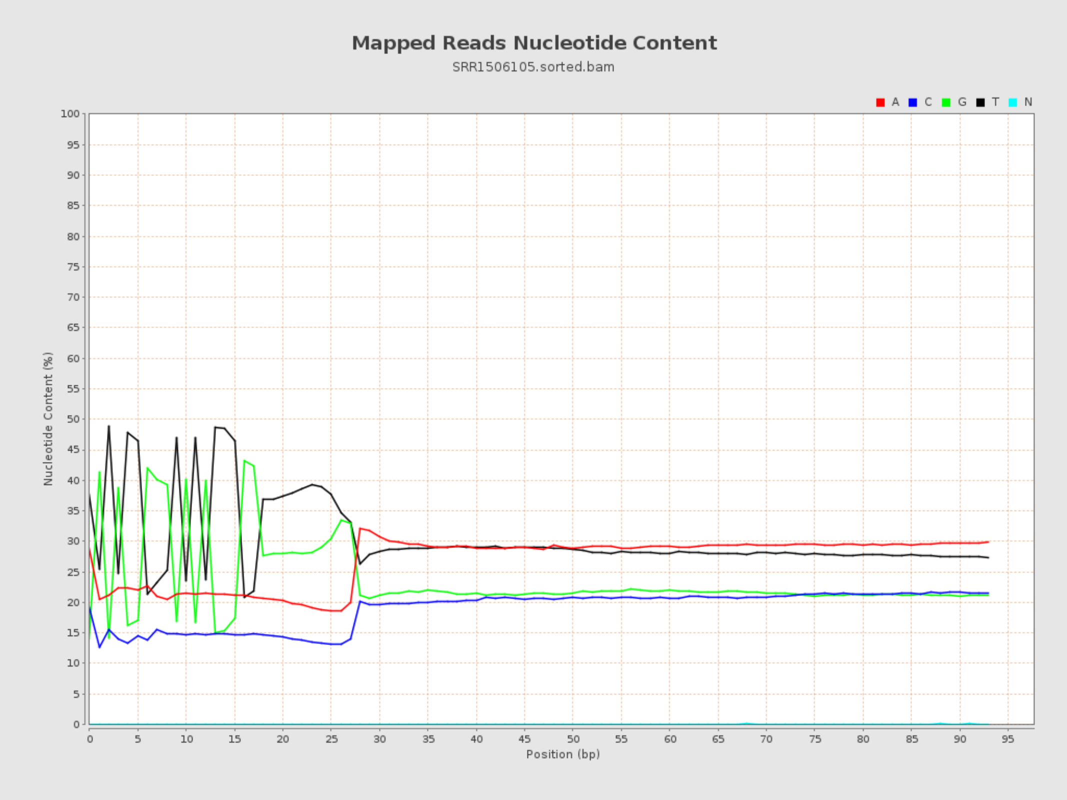
6. Results : Genome Fraction Coverage



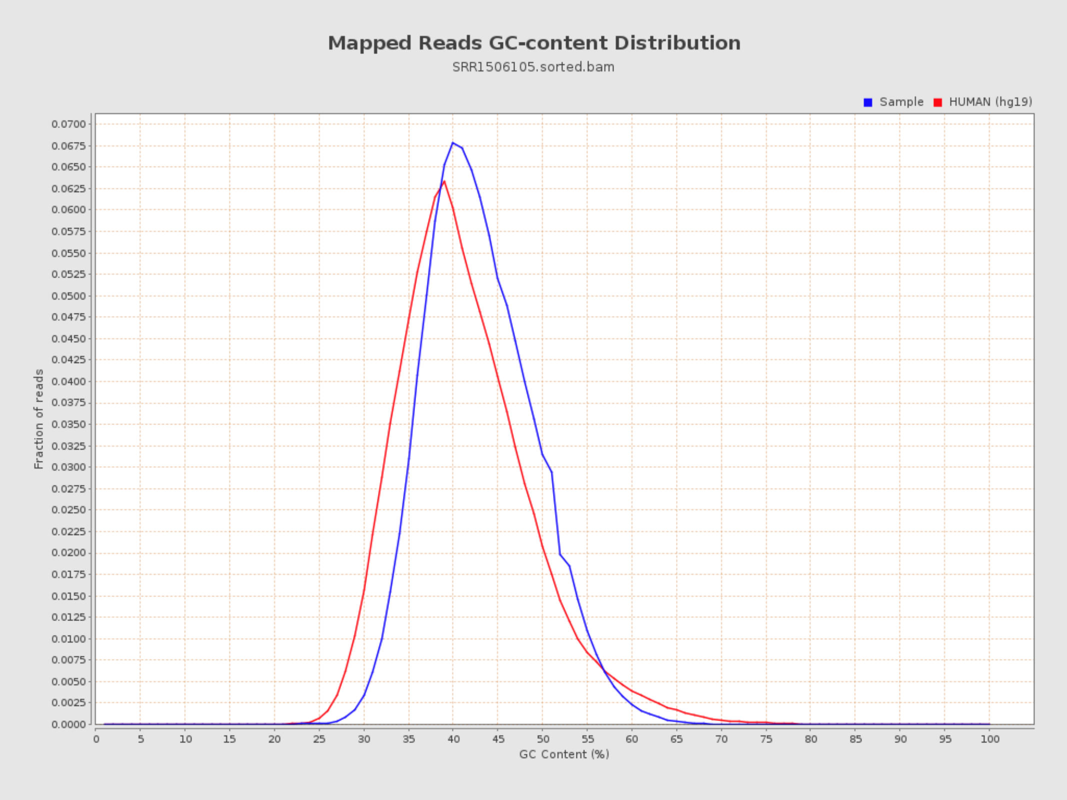
7. Results : Duplication Rate Histogram



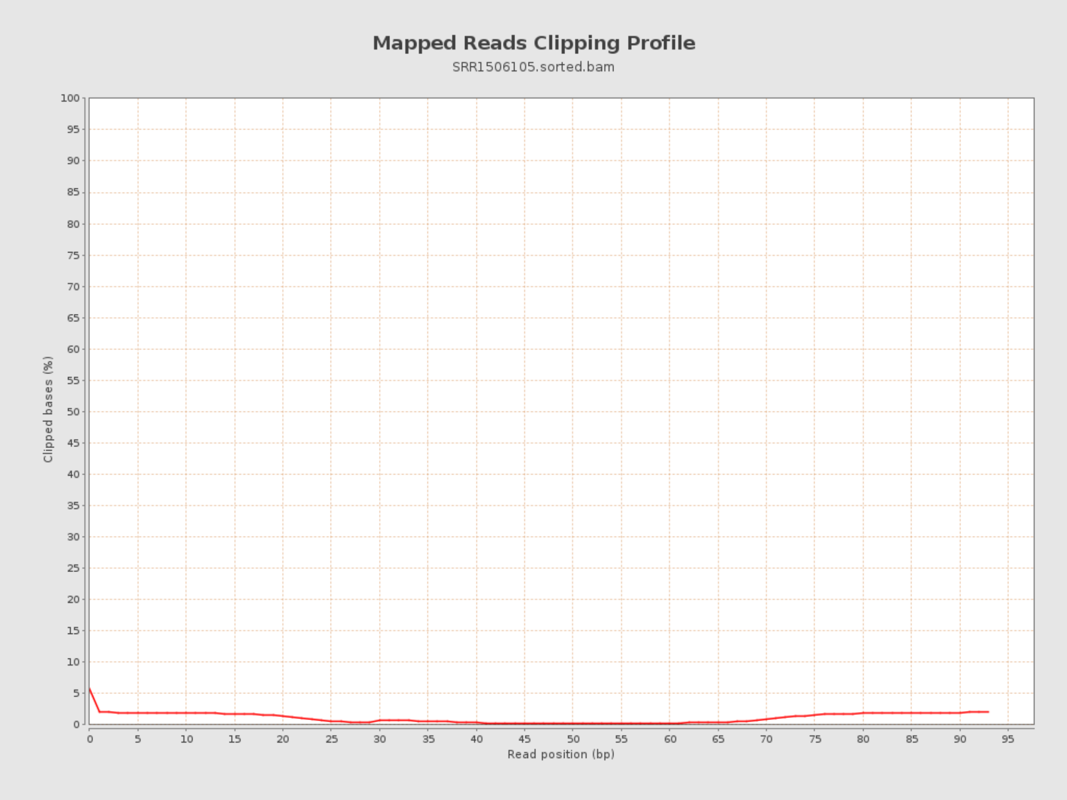
8. Results : Mapped Reads Nucleotide Content



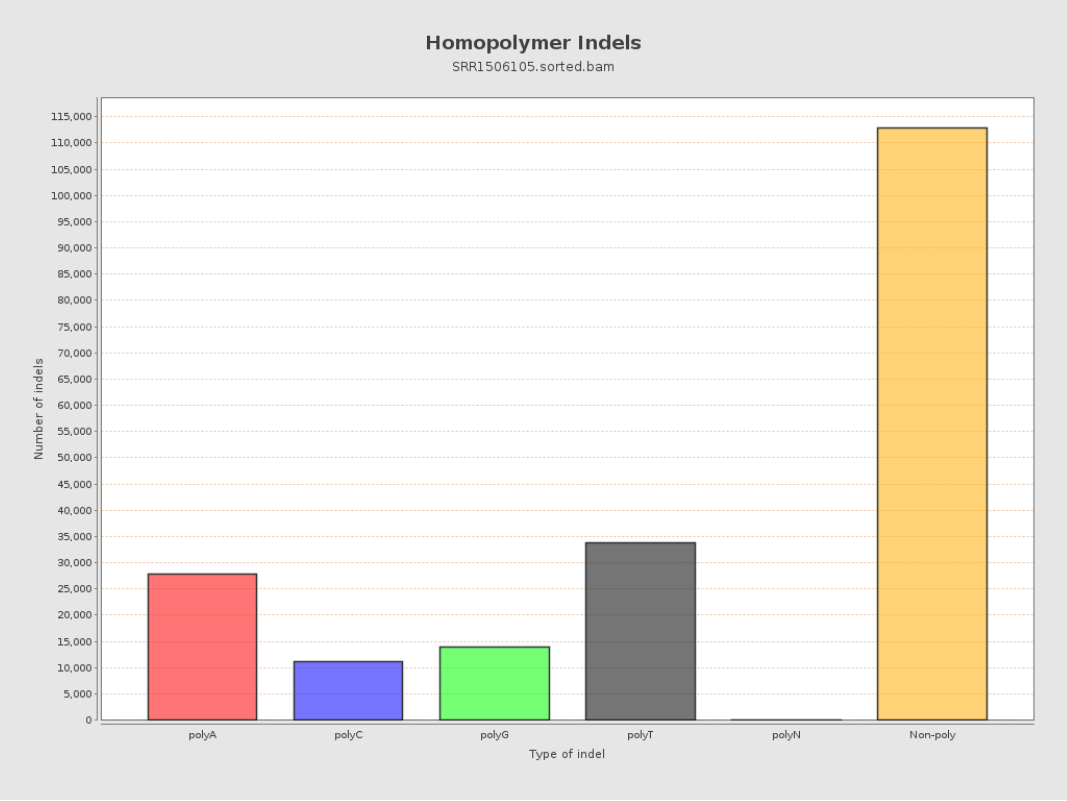
9. Results : Mapped Reads GC-content Distribution



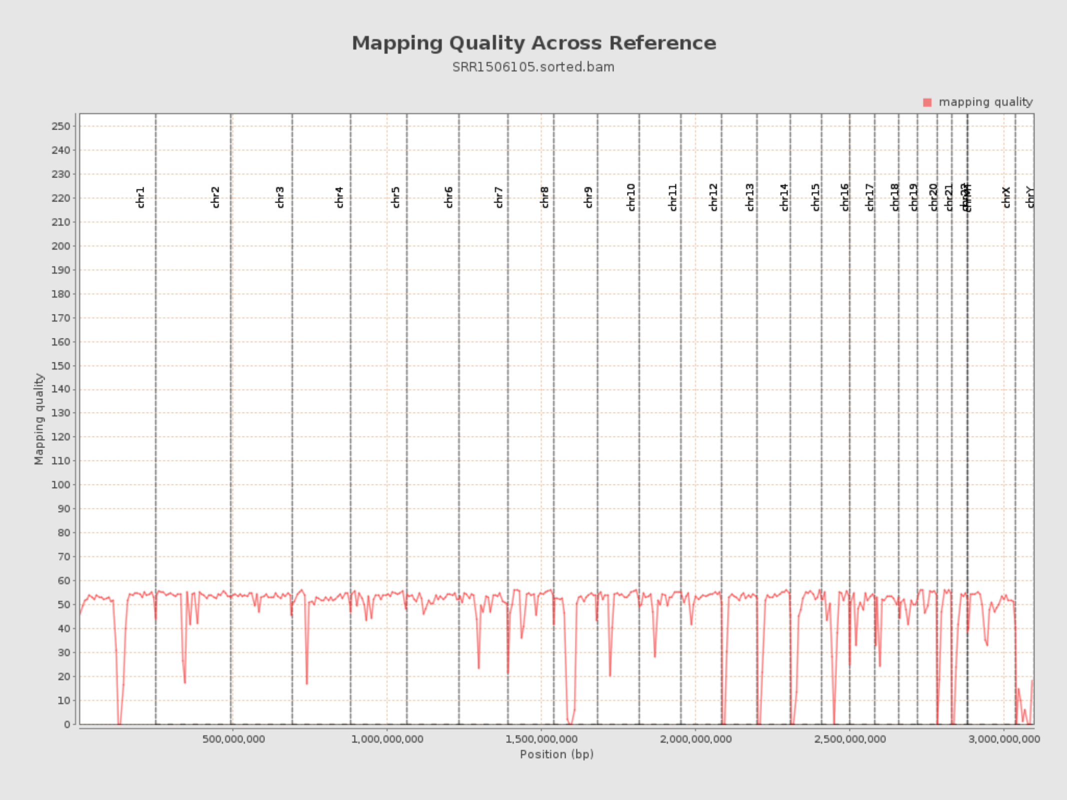
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram