Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 11:30:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084383.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_SRR3084383 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084383.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 11:30:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084383.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,401,588
Mapped reads	1,266,012 / 90.33%
Unmapped reads	135,576 / 9.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,533 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	33,614 / 2.4%
Duplication rate	2.21%
Clipped reads	465,488 / 33.21%

2.2. ACGT Content

Number/percentage of A's	25,185,749 / 29.01%
Number/percentage of C's	15,962,625 / 18.38%
Number/percentage of T's	27,583,373 / 31.77%
Number/percentage of G's	17,981,493 / 20.71%
Number/percentage of N's	113,335 / 0.13%
GC Percentage	39.09%

2.3. Coverage

Mean	0.0281

Standard Deviation	0.2405

2.4. Mapping Quality

Mean Mapping Quality	47

2.5. Mismatches and indels

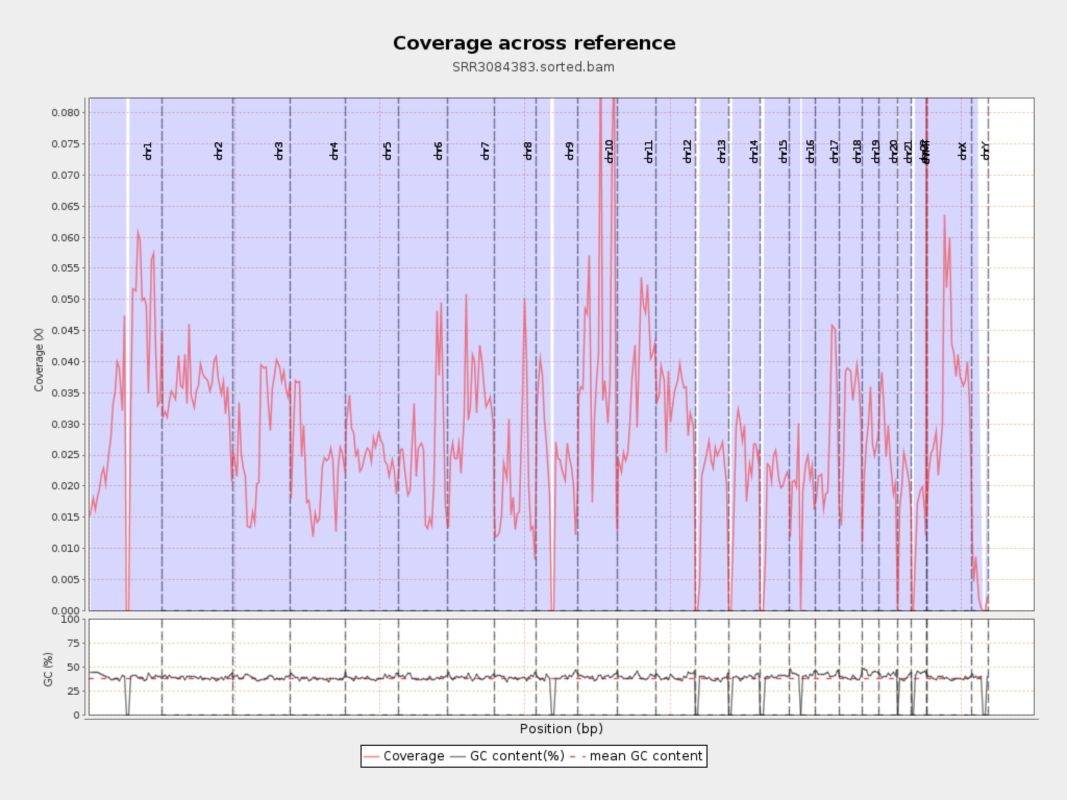
General error rate	1.01%
Mismatches	862,636
Insertions	6,314
Mapped reads with at least one insertion	0.49%
Deletions	18,585
Mapped reads with at least one deletion	1.45%
Homopolymer indels	48.17%

2.6. Chromosome stats

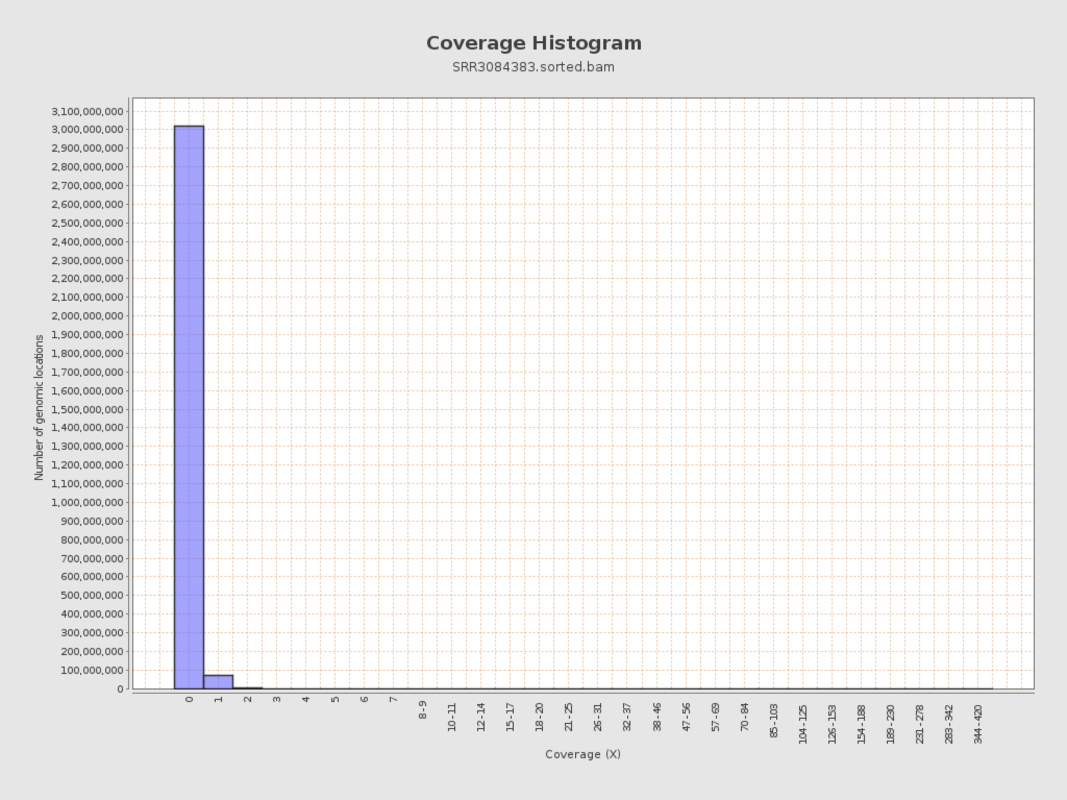
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8540947	0.0343	0.4102
chr2	243199373	8682264	0.0357	0.2472
chr3	198022430	5751893	0.029	0.1895
chr4	191154276	4400349	0.023	0.1681
chr5	180915260	4632269	0.0256	0.1728
chr6	171115067	4290461	0.0251	0.1816
chr7	159138663	5143715	0.0323	0.3209

chr8	146364022	2973316	0.0203	0.2778
chr9	141213431	3272914	0.0232	0.1914
chr10	135534747	6080834	0.0449	0.3486
chr11	135006516	4929535	0.0365	0.2411
chr12	133851895	4545447	0.034	0.1996
chr13	115169878	2315378	0.0201	0.1523
chr14	107349540	2351900	0.0219	0.1623
chr15	102531392	1845659	0.018	0.1442
chr16	90354753	1766748	0.0196	0.1612
chr17	81195210	2207936	0.0272	0.1854
chr18	78077248	2517465	0.0322	0.3065
chr19	59128983	1593017	0.0269	0.2705
chr20	63025520	1689598	0.0268	0.1782
chr21	48129895	892698	0.0185	0.1498
chr22	51304566	649053	0.0127	0.1201
chrMT	16571	2796	0.1687	0.4635
chrX	155270560	5595113	0.036	0.2179
chrY	59373566	187385	0.0032	0.0794

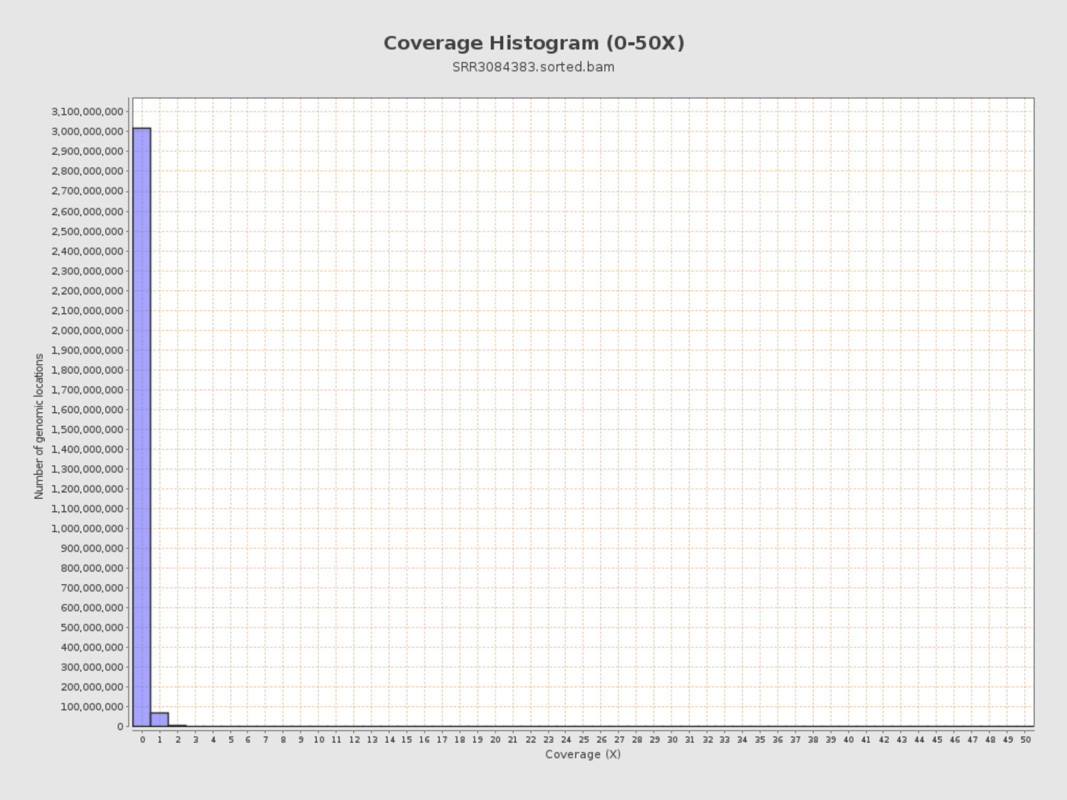
3. Results : Coverage across reference



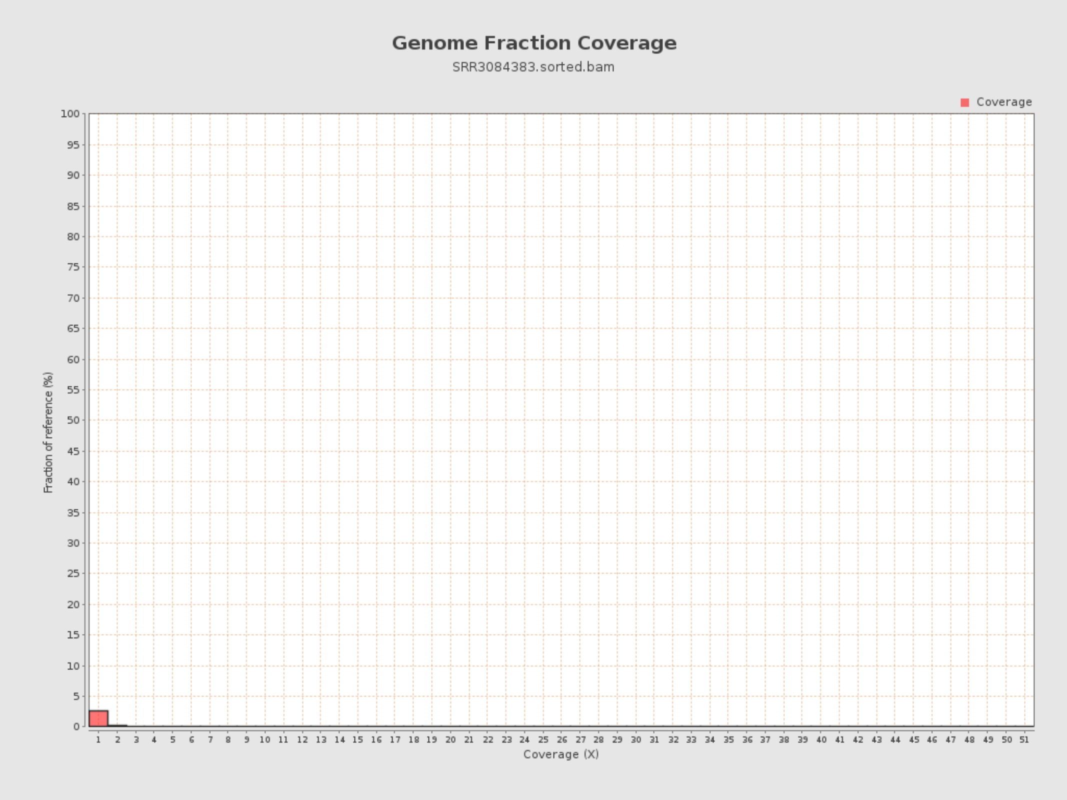
4. Results : Coverage Histogram



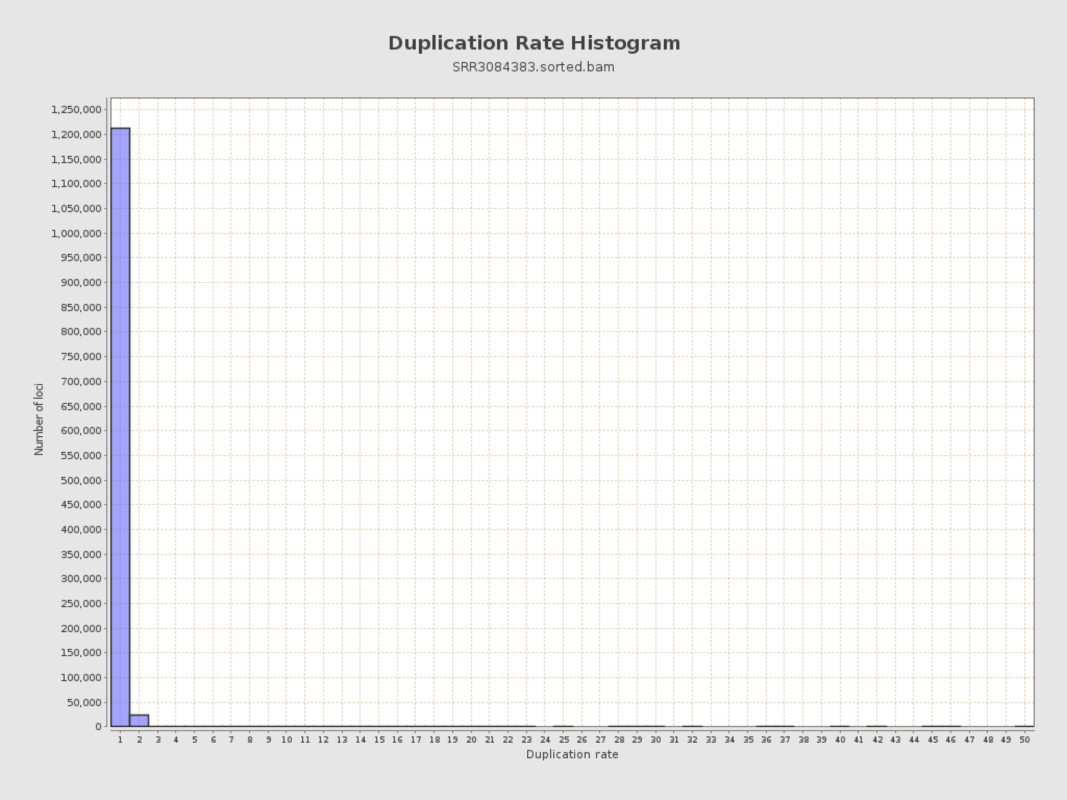
5. Results : Coverage Histogram (0-50X)



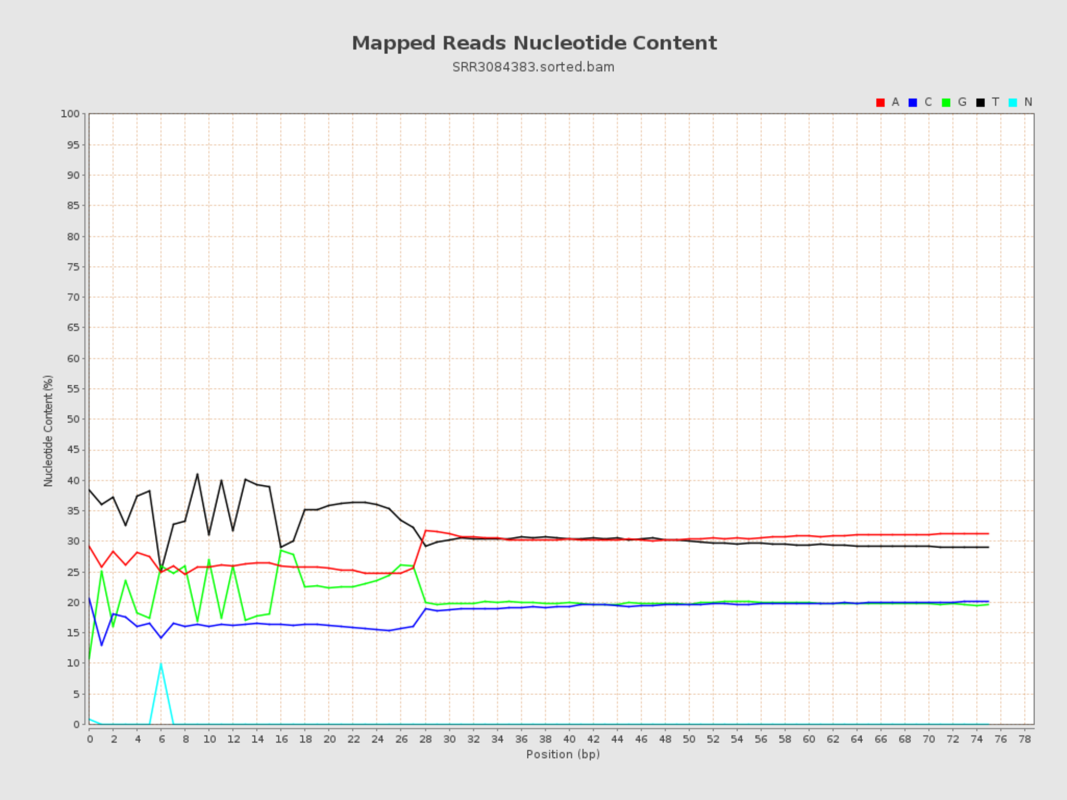
6. Results : Genome Fraction Coverage



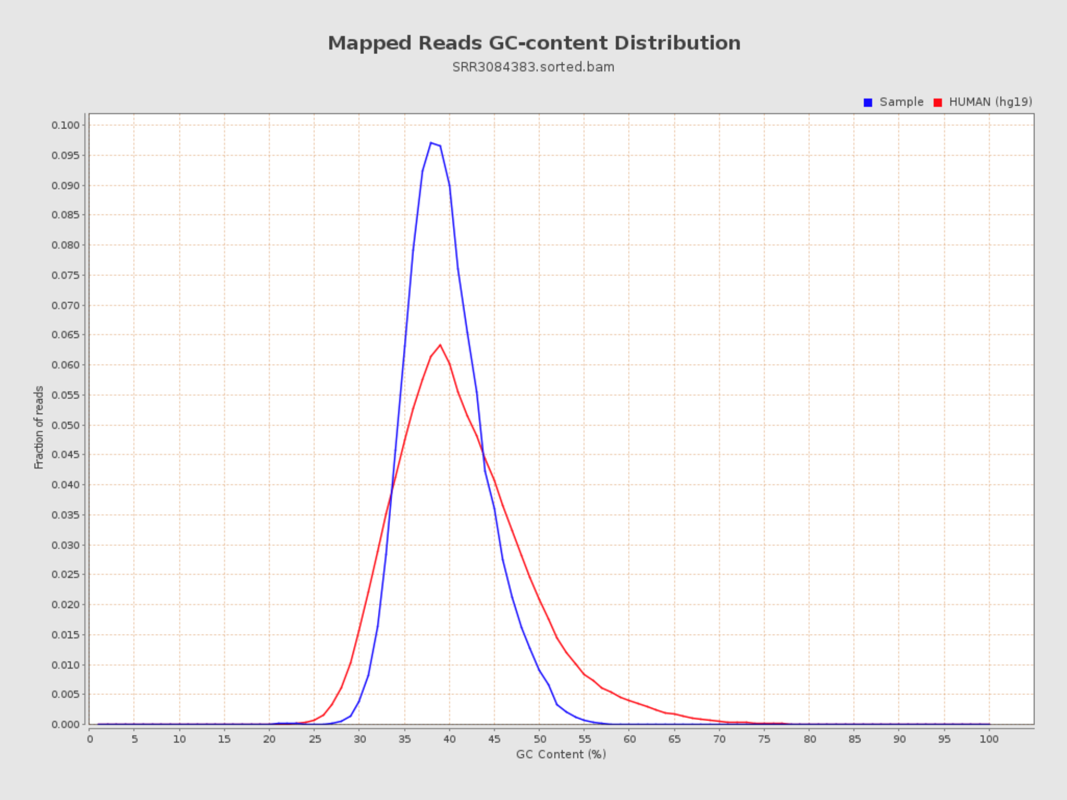
7. Results : Duplication Rate Histogram



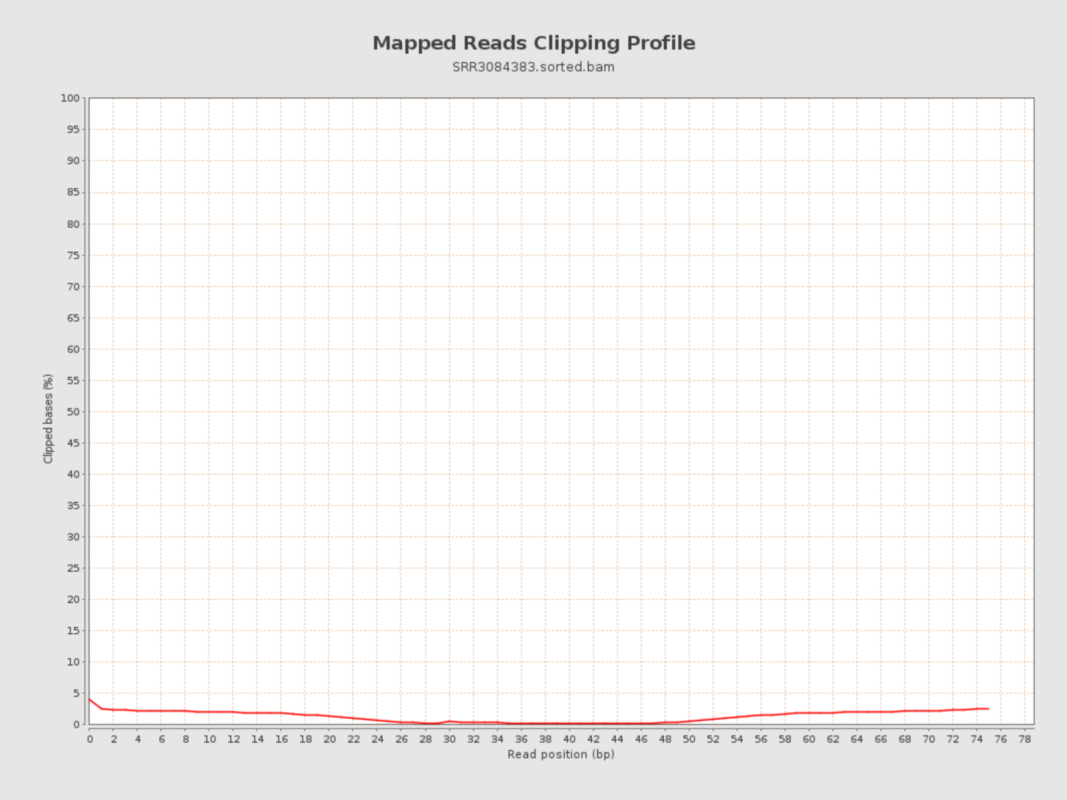
8. Results : Mapped Reads Nucleotide Content



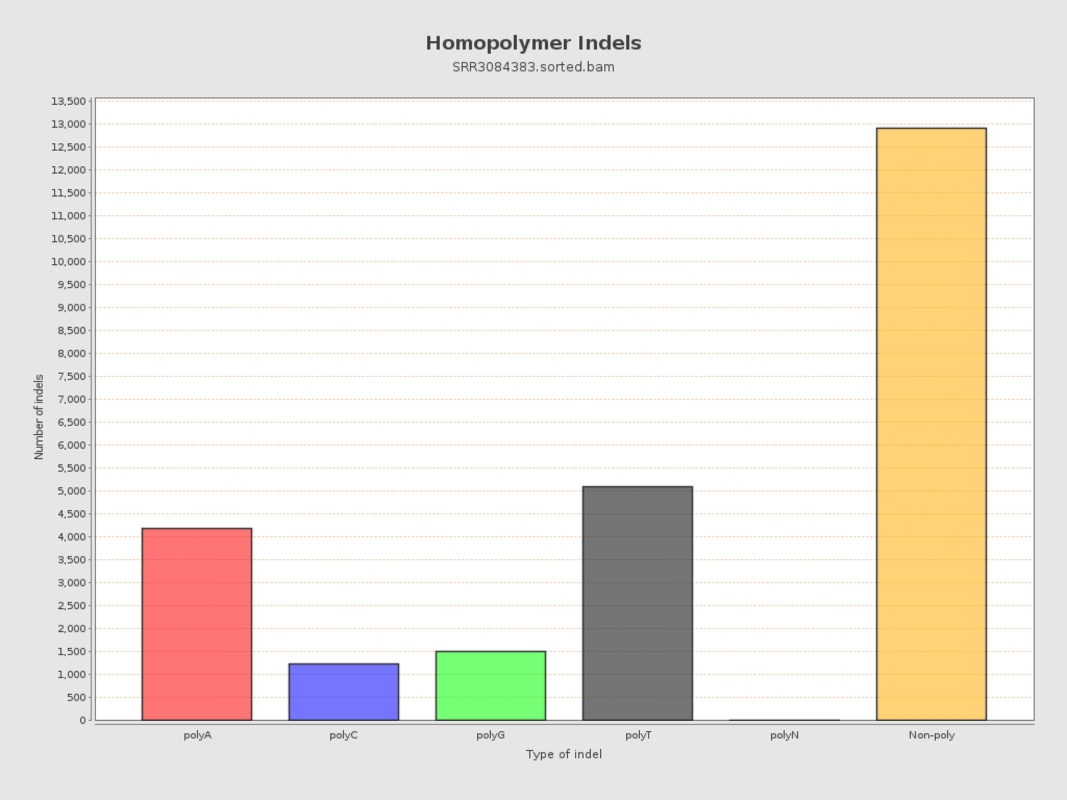
9. Results : Mapped Reads GC-content Distribution



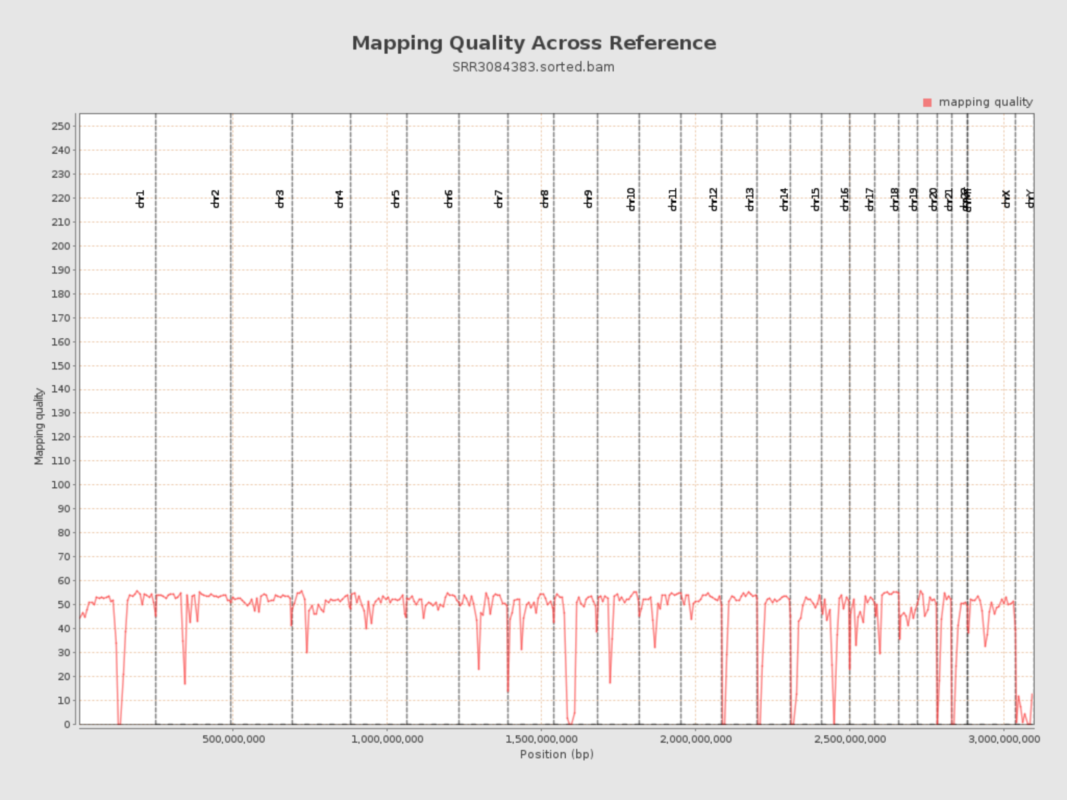
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram