Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:03:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008757.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_SRR6008757 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008757.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:03:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008757.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,141,052
Mapped reads	1,957,527 / 91.43%
Unmapped reads	183,525 / 8.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,683 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	76,480 / 3.57%
Duplication rate	2.4%
Clipped reads	883,403 / 41.26%

2.2. ACGT Content

Number/percentage of A's	34,202,997 / 26.45%
Number/percentage of C's	24,810,882 / 19.19%
Number/percentage of T's	39,657,824 / 30.67%
Number/percentage of G's	30,450,105 / 23.55%
Number/percentage of N's	199,696 / 0.15%
GC Percentage	42.73%

2.3. Coverage

Mean	0.0418

Standard Deviation	0.4712

2.4. Mapping Quality

Mean Mapping Quality	43.54

2.5. Mismatches and indels

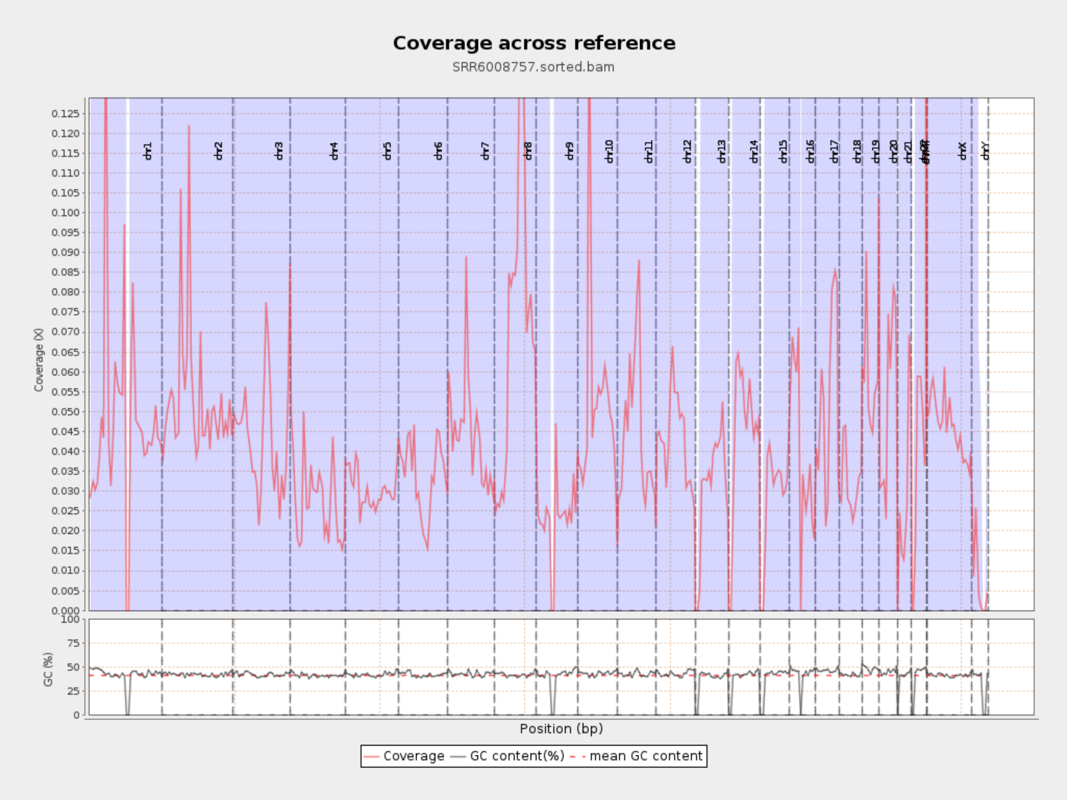
General error rate	0.88%
Mismatches	1,112,500
Insertions	9,887
Mapped reads with at least one insertion	0.5%
Deletions	36,404
Mapped reads with at least one deletion	1.84%
Homopolymer indels	44.67%

2.6. Chromosome stats

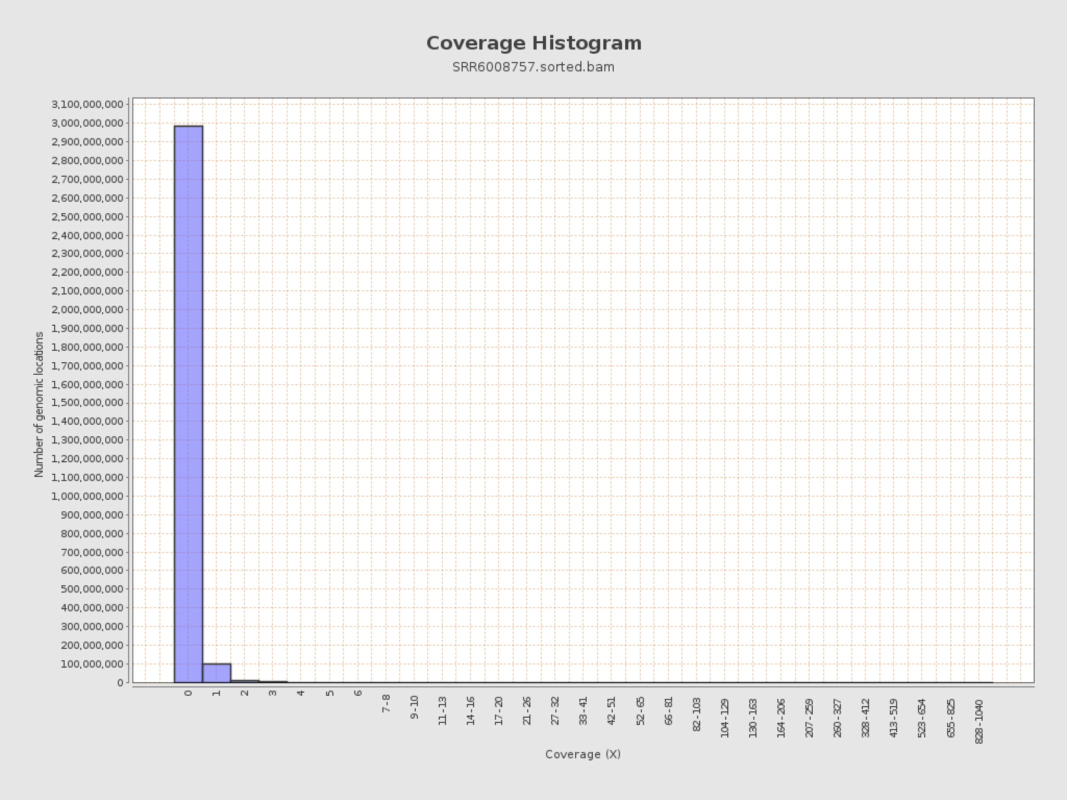
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11861195	0.0476	0.8759
chr2	243199373	13056411	0.0537	0.5855
chr3	198022430	8580531	0.0433	0.3207
chr4	191154276	5229350	0.0274	0.219
chr5	180915260	5491365	0.0304	0.1945
chr6	171115067	5786535	0.0338	0.241
chr7	159138663	7091281	0.0446	0.6057

chr8	146364022	10480804	0.0716	0.4384
chr9	141213431	3232057	0.0229	0.3365
chr10	135534747	7104198	0.0524	0.9536
chr11	135006516	6066691	0.0449	0.3794
chr12	133851895	5837793	0.0436	0.2342
chr13	115169878	3560466	0.0309	0.1943
chr14	107349540	4765212	0.0444	0.2456
chr15	102531392	2933199	0.0286	0.1876
chr16	90354753	3604779	0.0399	0.3697
chr17	81195210	4364501	0.0538	0.3524
chr18	78077248	2483633	0.0318	0.6135
chr19	59128983	3503468	0.0593	0.5864
chr20	63025520	3324643	0.0528	0.2675
chr21	48129895	1424411	0.0296	0.2201
chr22	51304566	1787770	0.0348	0.2091
chrMT	16571	164434	9.923	5.4486
chrX	155270560	7199215	0.0464	0.2769
chrY	59373566	452469	0.0076	0.2516

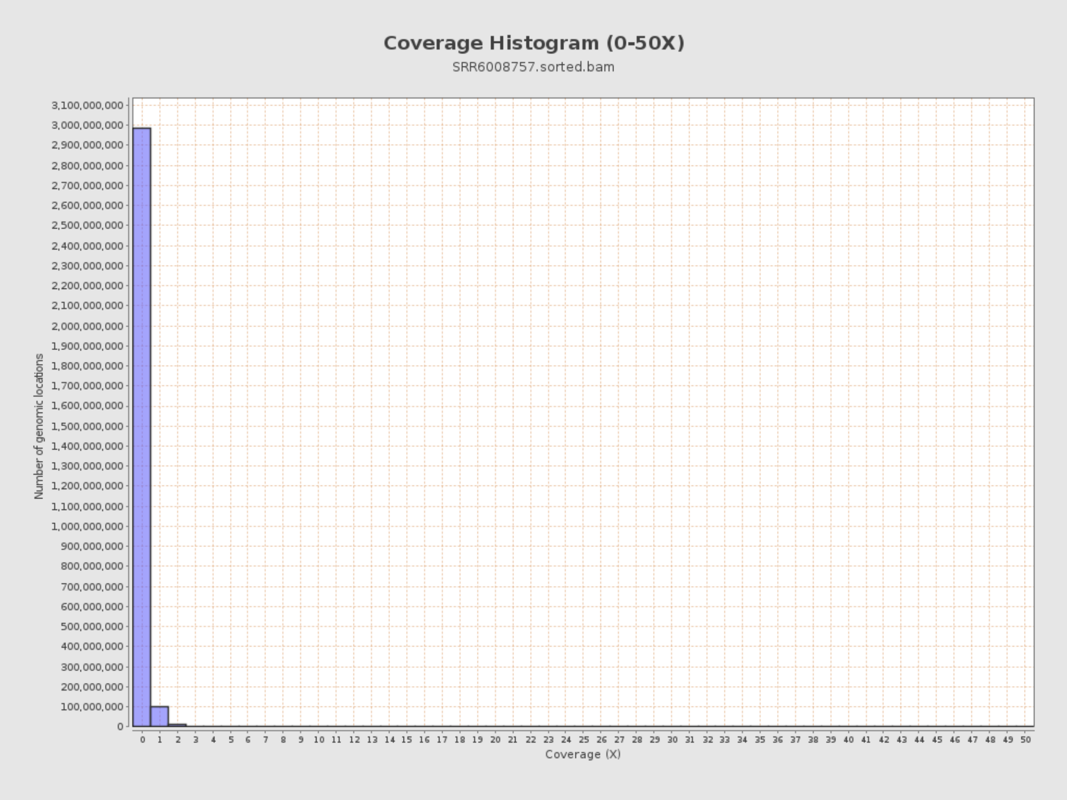
3. Results : Coverage across reference



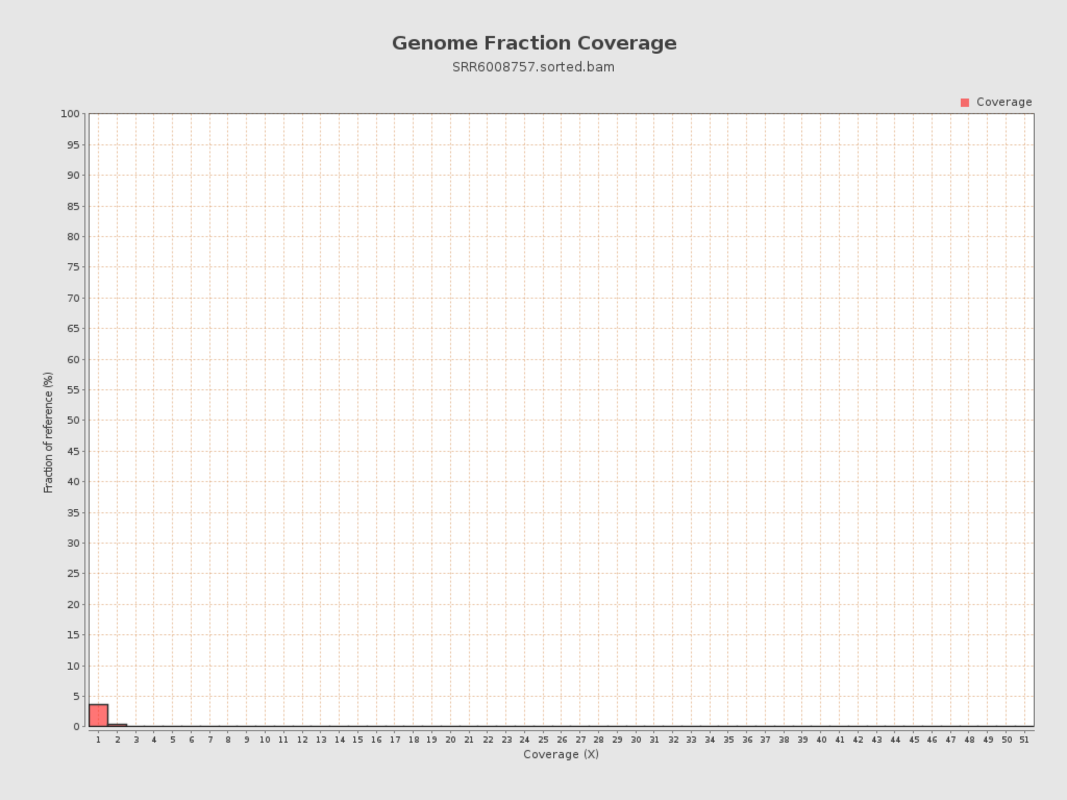
4. Results : Coverage Histogram



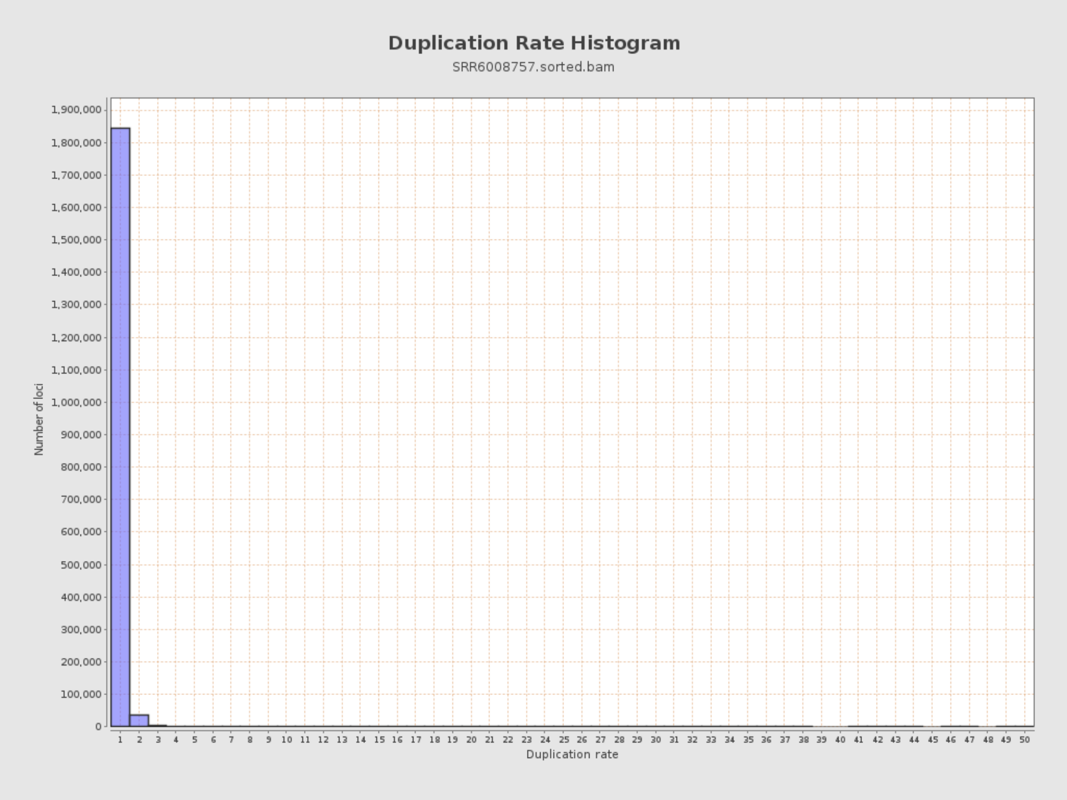
5. Results : Coverage Histogram (0-50X)



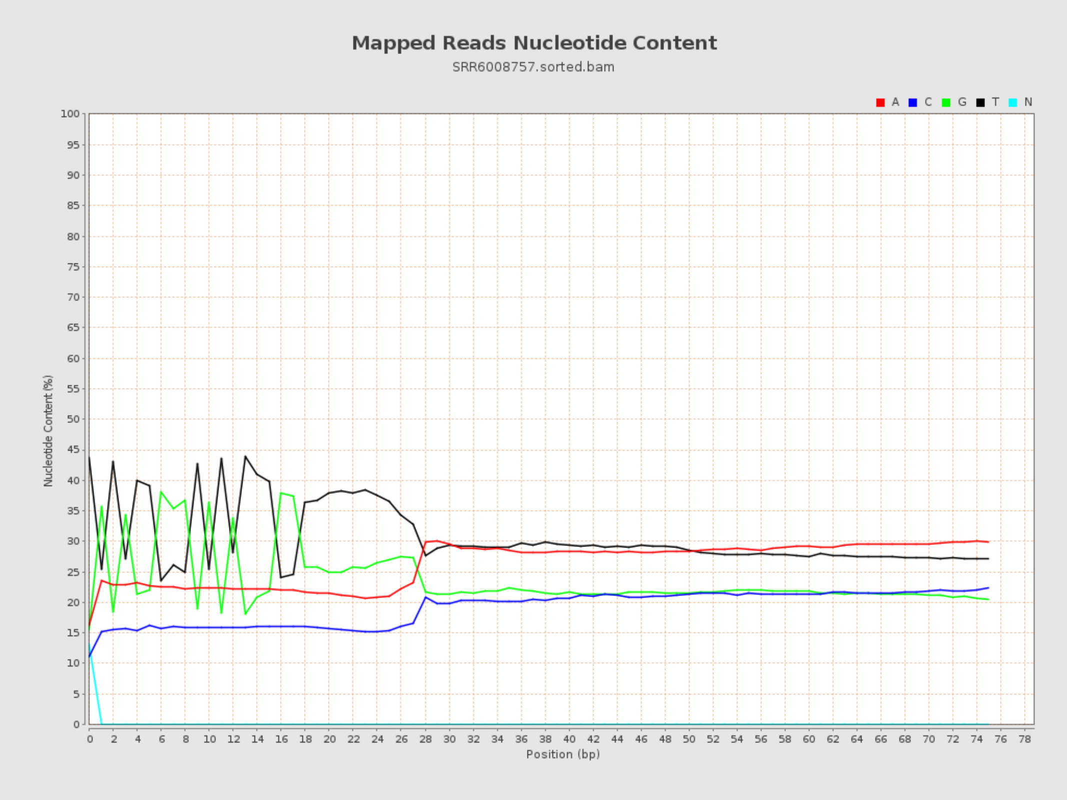
6. Results : Genome Fraction Coverage



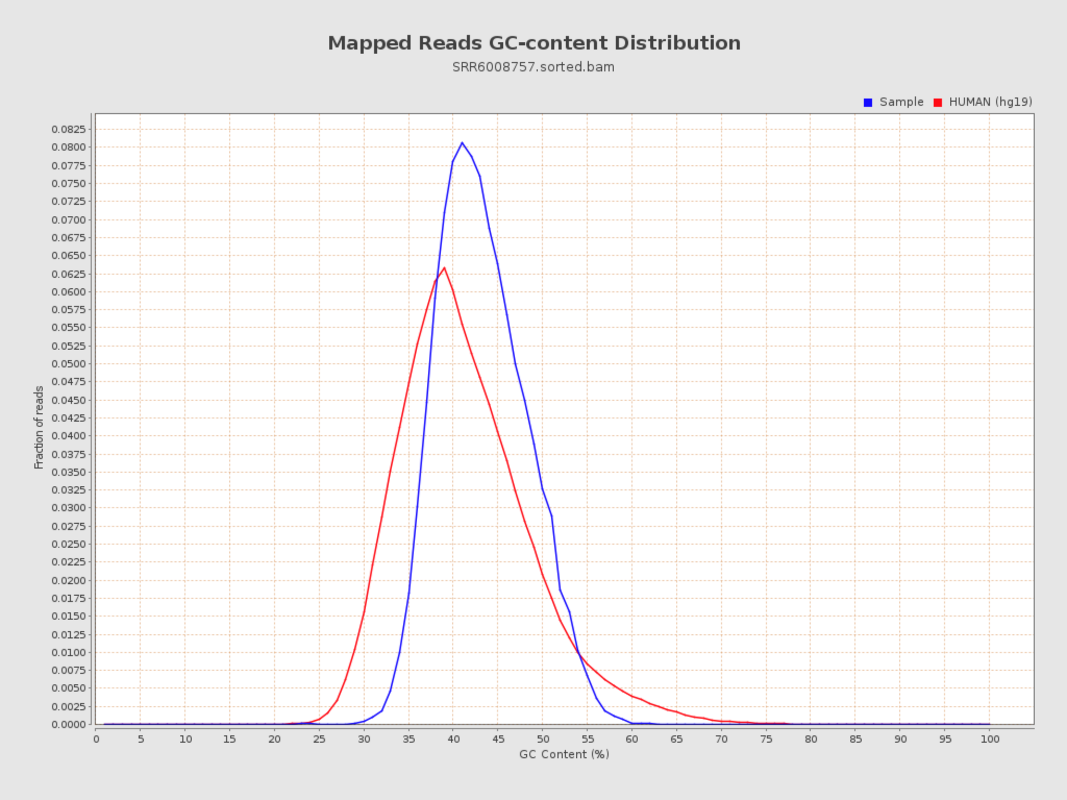
7. Results : Duplication Rate Histogram



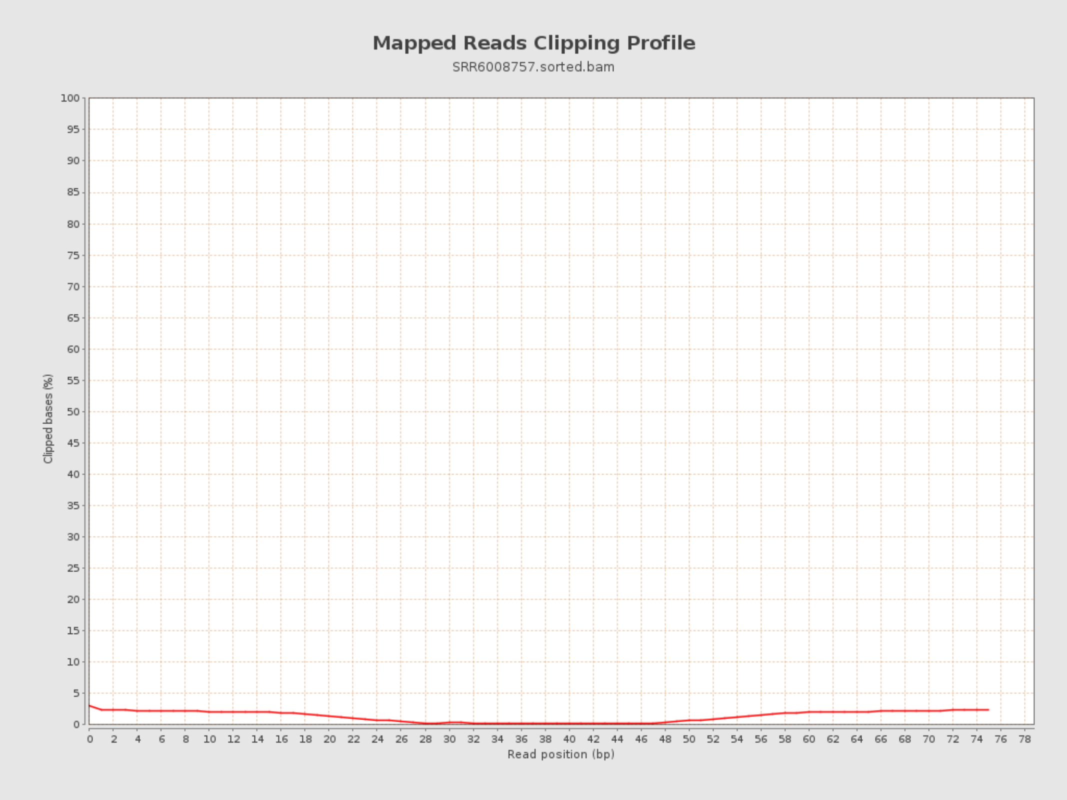
8. Results : Mapped Reads Nucleotide Content



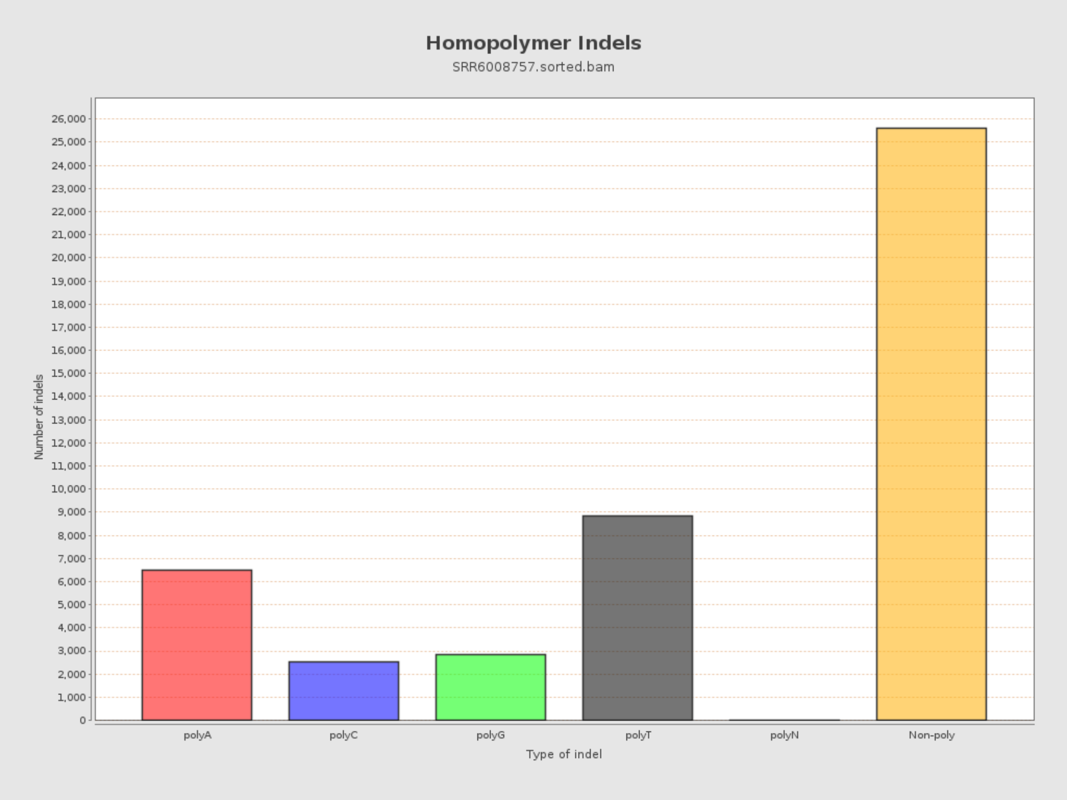
9. Results : Mapped Reads GC-content Distribution



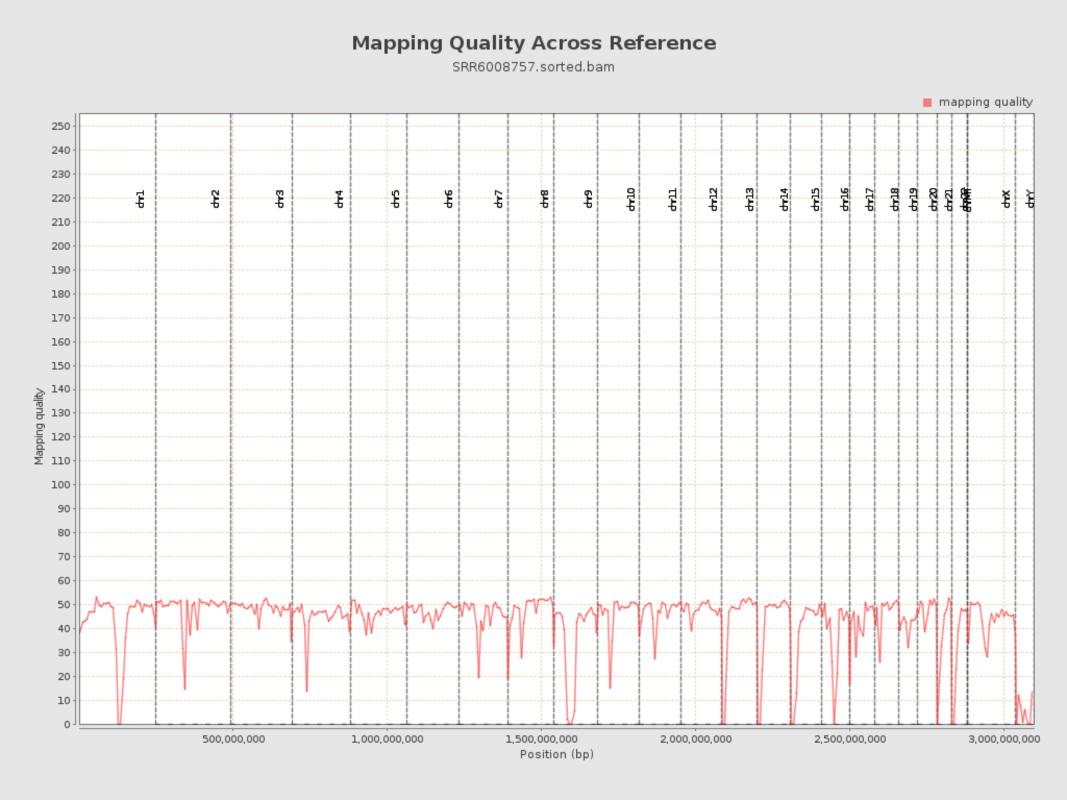
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram