Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:35:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230400.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_SRR6230400 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230400.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:35:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230400.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	294,171
Mapped reads	265,996 / 90.42%
Unmapped reads	28,175 / 9.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,958 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	5,397 / 1.83%
Duplication rate	1.78%
Clipped reads	107,838 / 36.66%

2.2. ACGT Content

Number/percentage of A's	5,273,443 / 29.23%
Number/percentage of C's	3,305,230 / 18.32%
Number/percentage of T's	5,735,112 / 31.79%
Number/percentage of G's	3,717,367 / 20.6%
Number/percentage of N's	10,307 / 0.06%
GC Percentage	38.92%

2.3. Coverage

Mean	0.0058

Standard Deviation	0.0907

2.4. Mapping Quality

Mean Mapping Quality	47.46

2.5. Mismatches and indels

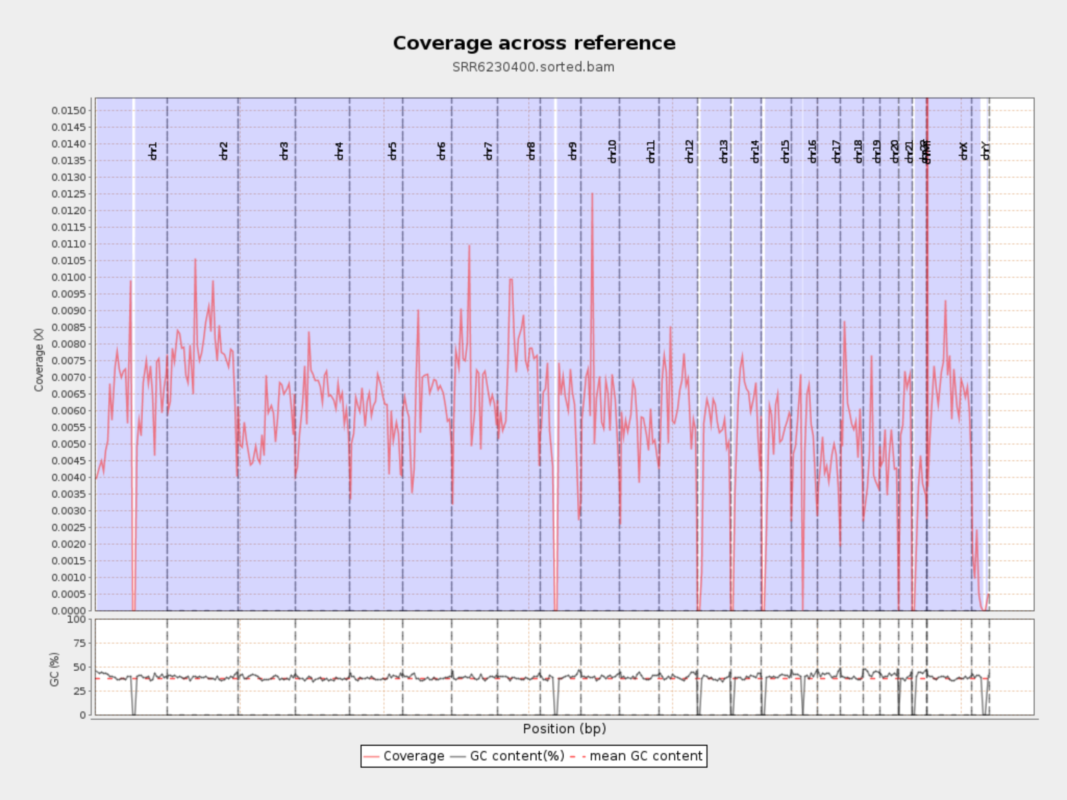
General error rate	0.91%
Mismatches	161,262
Insertions	1,514
Mapped reads with at least one insertion	0.56%
Deletions	5,155
Mapped reads with at least one deletion	1.92%
Homopolymer indels	46.24%

2.6. Chromosome stats

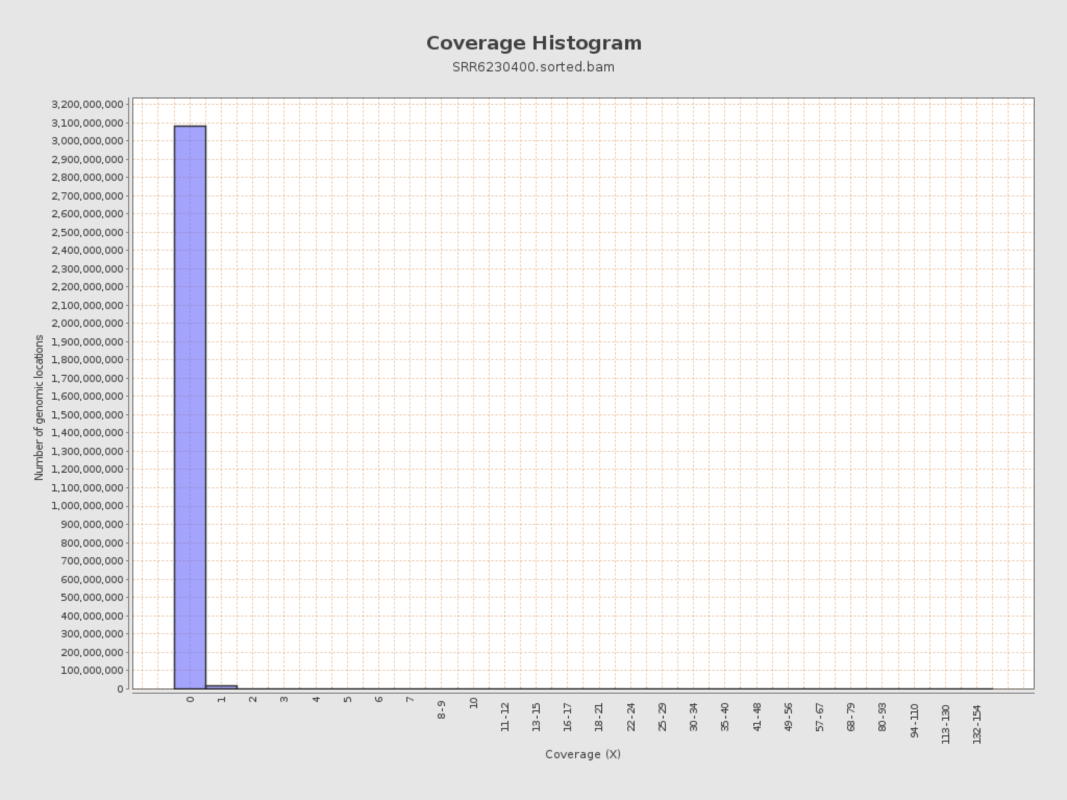
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1474205	0.0059	0.1193
chr2	243199373	1889537	0.0078	0.0991
chr3	198022430	1104567	0.0056	0.0775
chr4	191154276	1214929	0.0064	0.0836
chr5	180915260	1056580	0.0058	0.0791
chr6	171115067	1078312	0.0063	0.0849
chr7	159138663	1092616	0.0069	0.1068

chr8	146364022	1084150	0.0074	0.1308
chr9	141213431	755168	0.0053	0.0868
chr10	135534747	877968	0.0065	0.0964
chr11	135006516	735024	0.0054	0.0831
chr12	133851895	847297	0.0063	0.0826
chr13	115169878	544179	0.0047	0.0709
chr14	107349540	575448	0.0054	0.0767
chr15	102531392	473072	0.0046	0.0699
chr16	90354753	437169	0.0048	0.0741
chr17	81195210	345079	0.0042	0.0687
chr18	78077248	451949	0.0058	0.1224
chr19	59128983	256488	0.0043	0.0878
chr20	63025520	280117	0.0044	0.0692
chr21	48129895	268305	0.0056	0.0789
chr22	51304566	141173	0.0028	0.0539
chrMT	16571	1830	0.1104	0.3467
chrX	155270560	1021621	0.0066	0.0852
chrY	59373566	43358	0.0007	0.0317

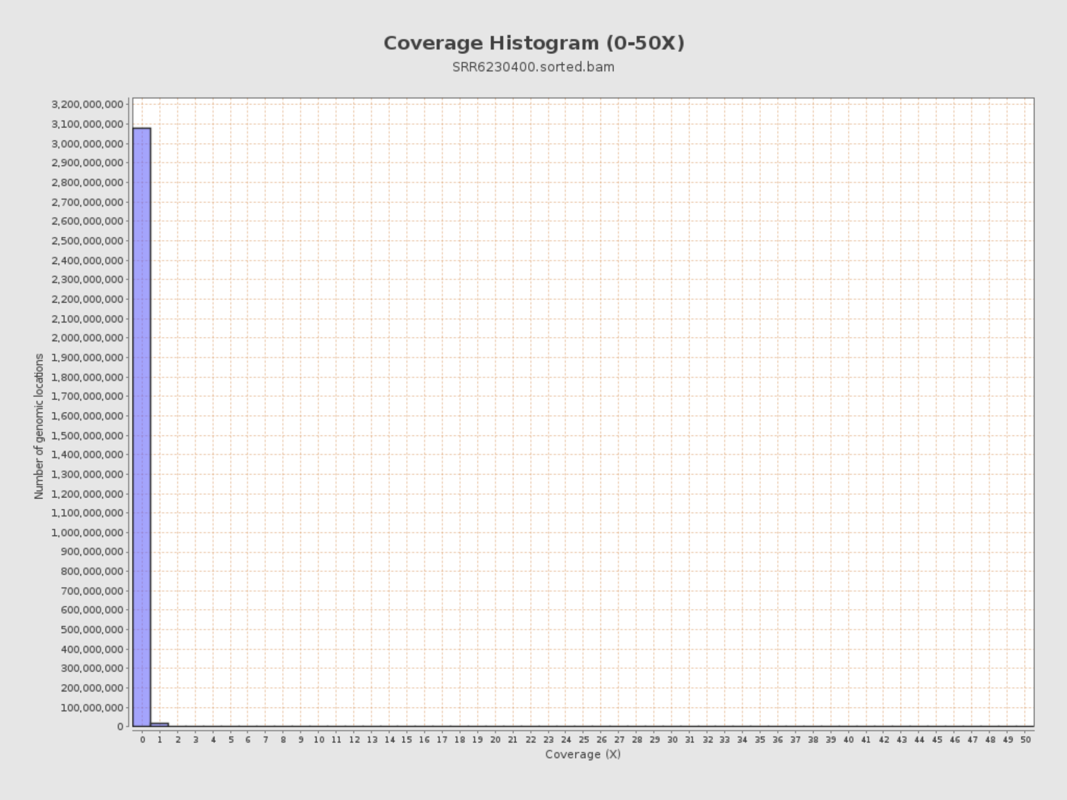
3. Results : Coverage across reference



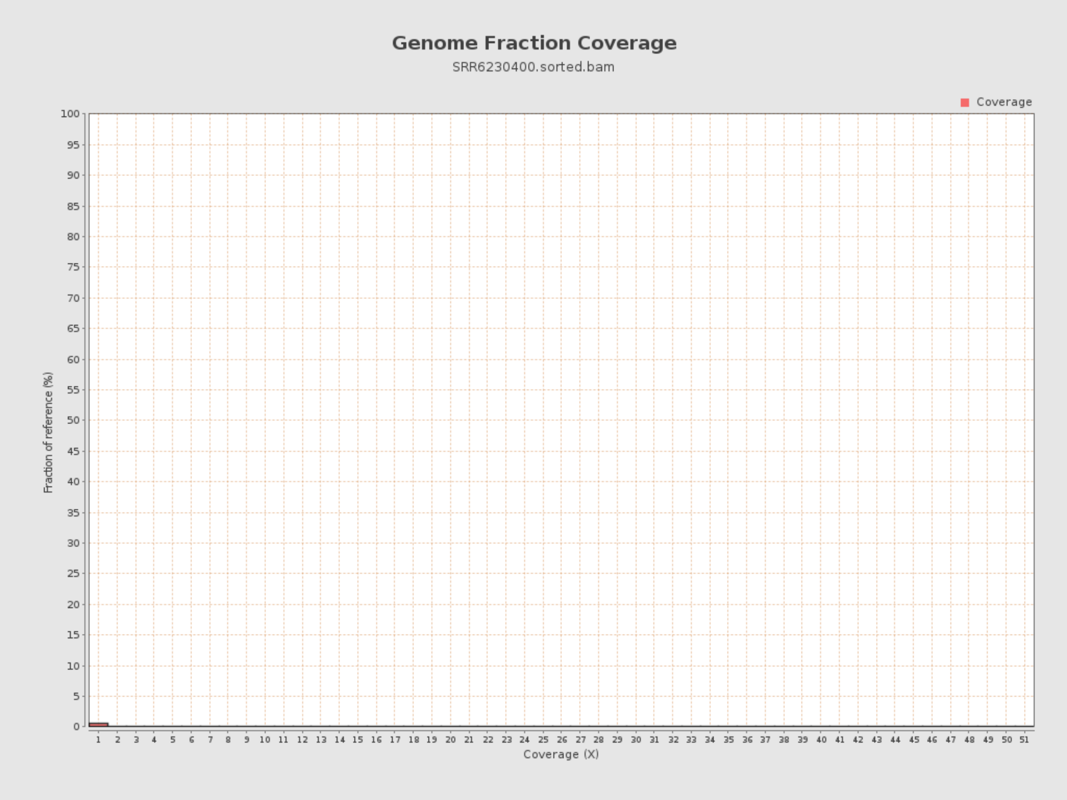
4. Results : Coverage Histogram



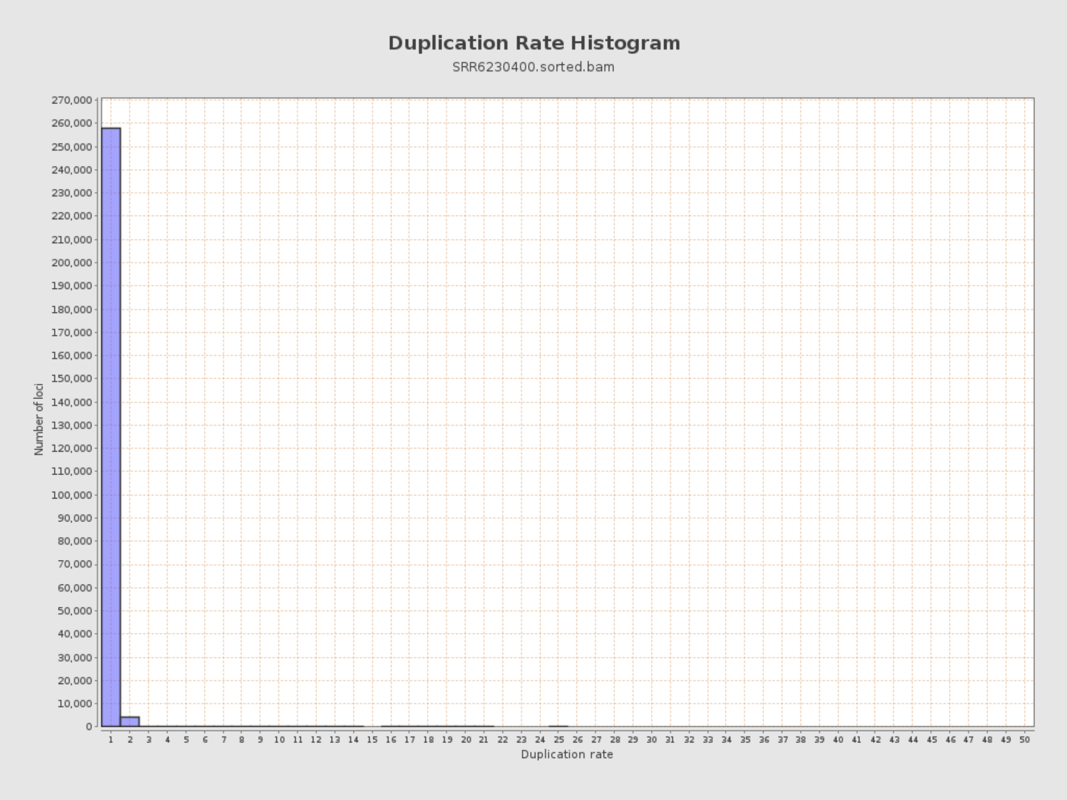
5. Results : Coverage Histogram (0-50X)



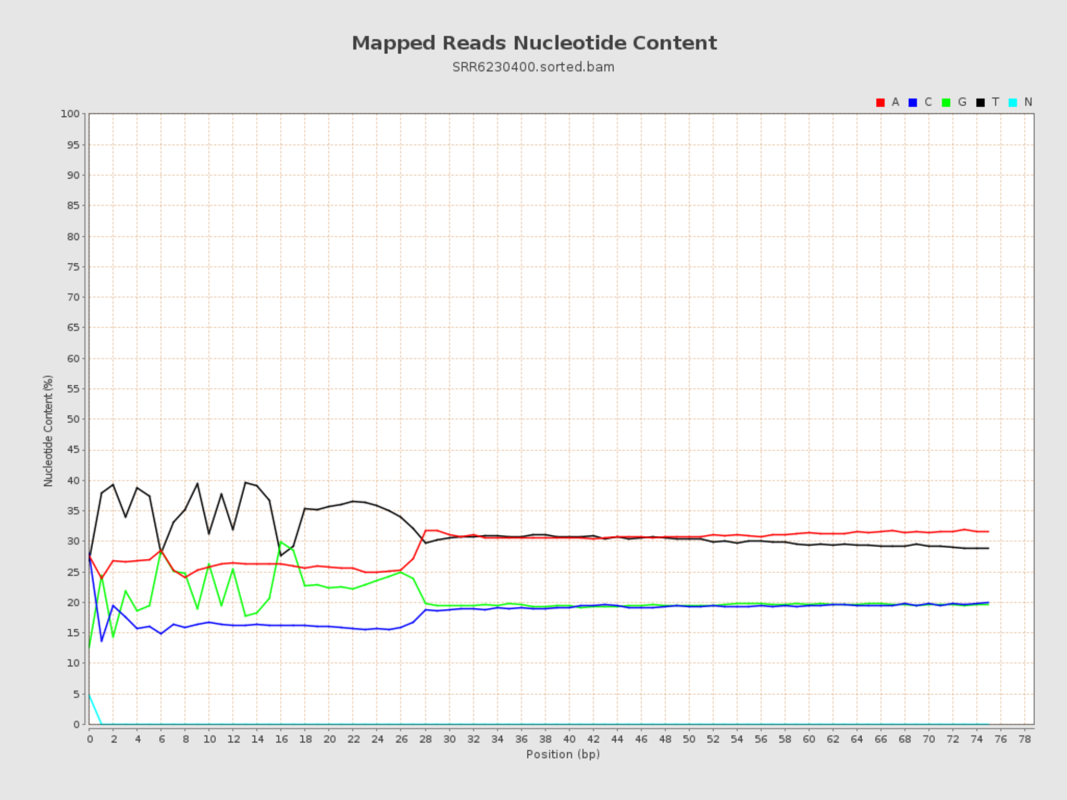
6. Results : Genome Fraction Coverage



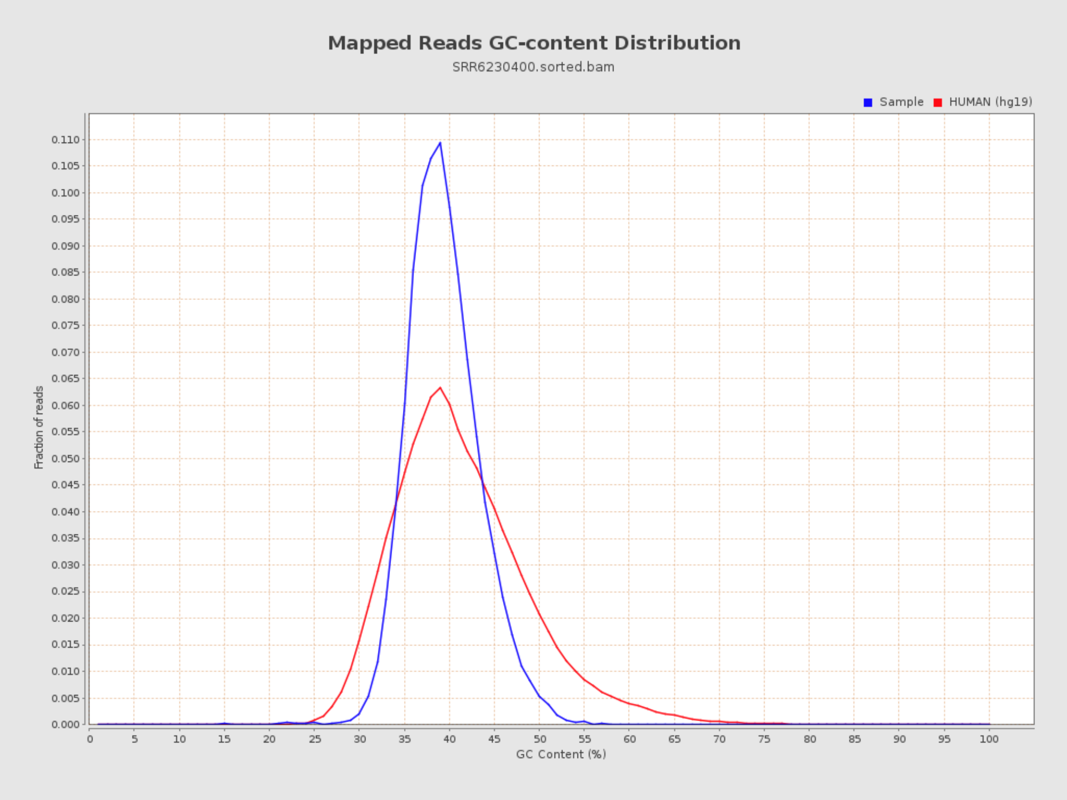
7. Results : Duplication Rate Histogram



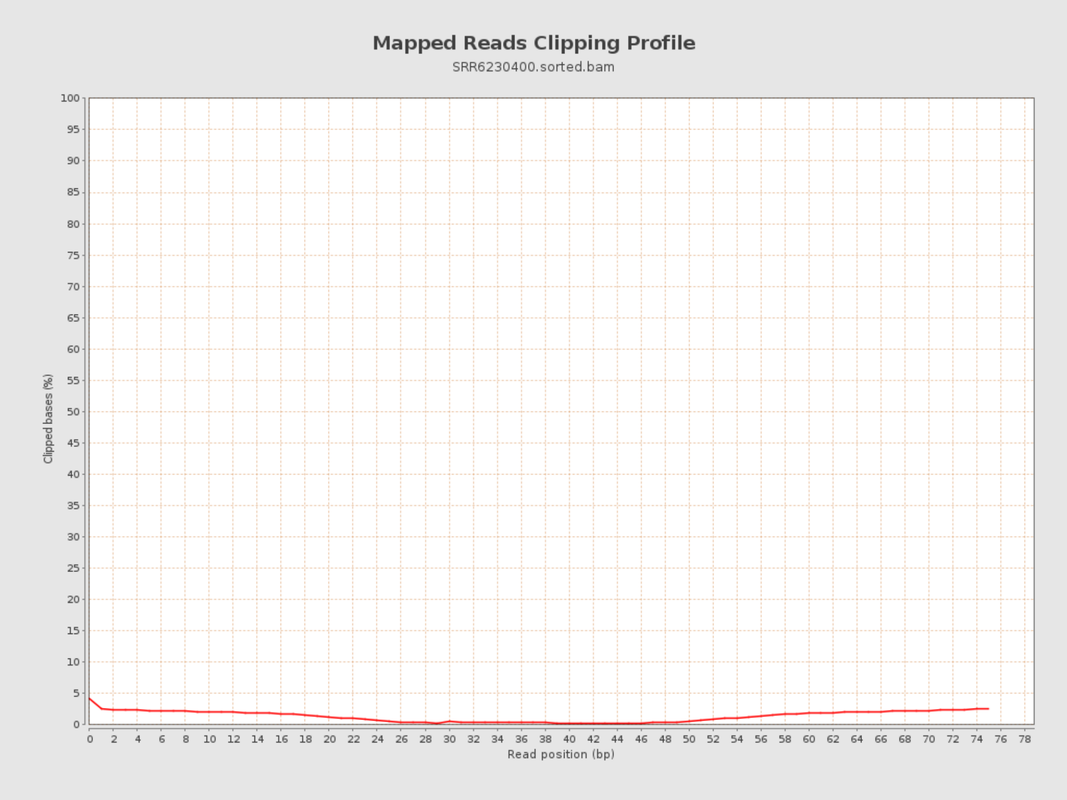
8. Results : Mapped Reads Nucleotide Content



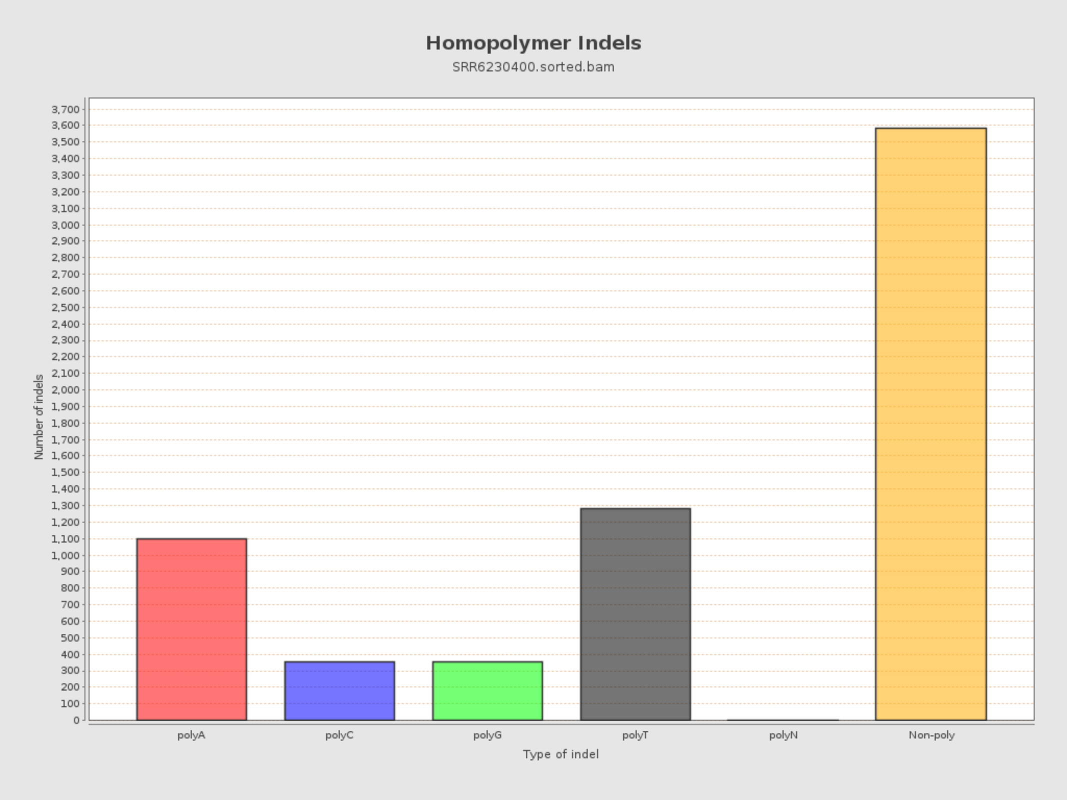
9. Results : Mapped Reads GC-content Distribution



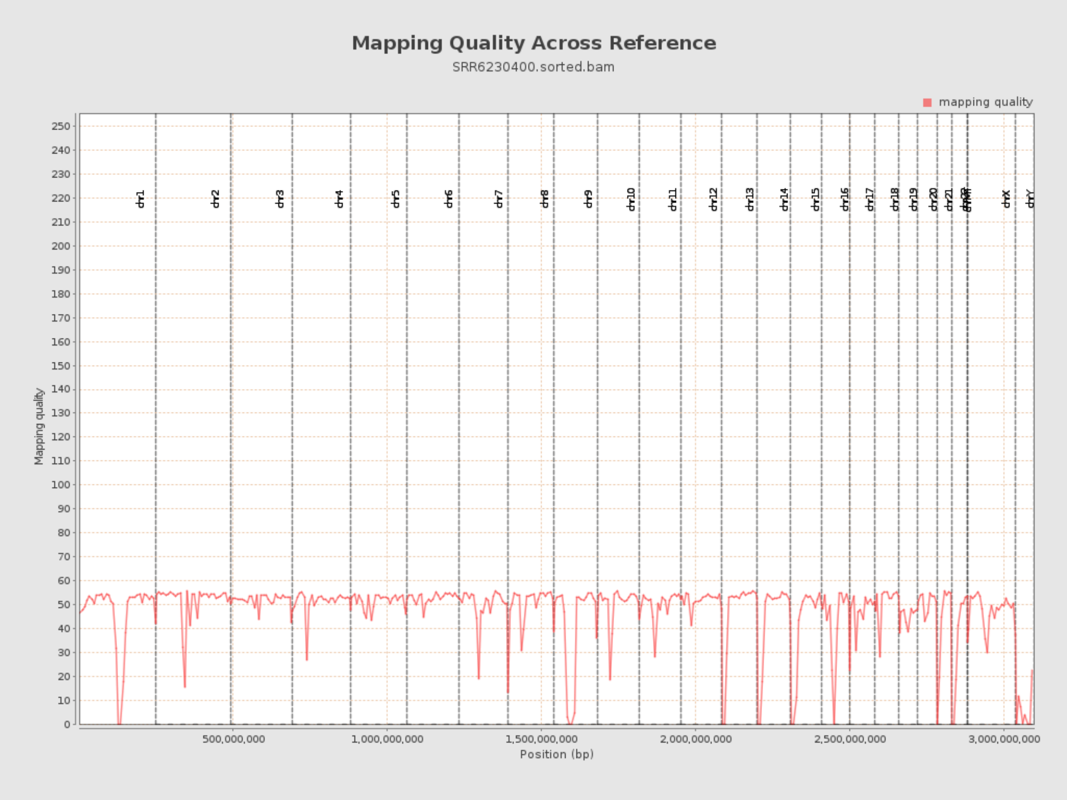
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram