Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:49:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230405.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_SRR6230405 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230405.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:49:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230405.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,186,540
Mapped reads	1,925,947 / 88.08%
Unmapped reads	260,593 / 11.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,626 / 0.9%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	215,544 / 9.86%
Duplication rate	8.81%
Clipped reads	898,912 / 41.11%

2.2. ACGT Content

Number/percentage of A's	35,724,269 / 28.05%
Number/percentage of C's	22,990,274 / 18.05%
Number/percentage of T's	41,006,361 / 32.19%
Number/percentage of G's	27,595,212 / 21.67%
Number/percentage of N's	53,919 / 0.04%
GC Percentage	39.72%

2.3. Coverage

Mean	0.0412

Standard Deviation	0.3721

2.4. Mapping Quality

Mean Mapping Quality	41.57

2.5. Mismatches and indels

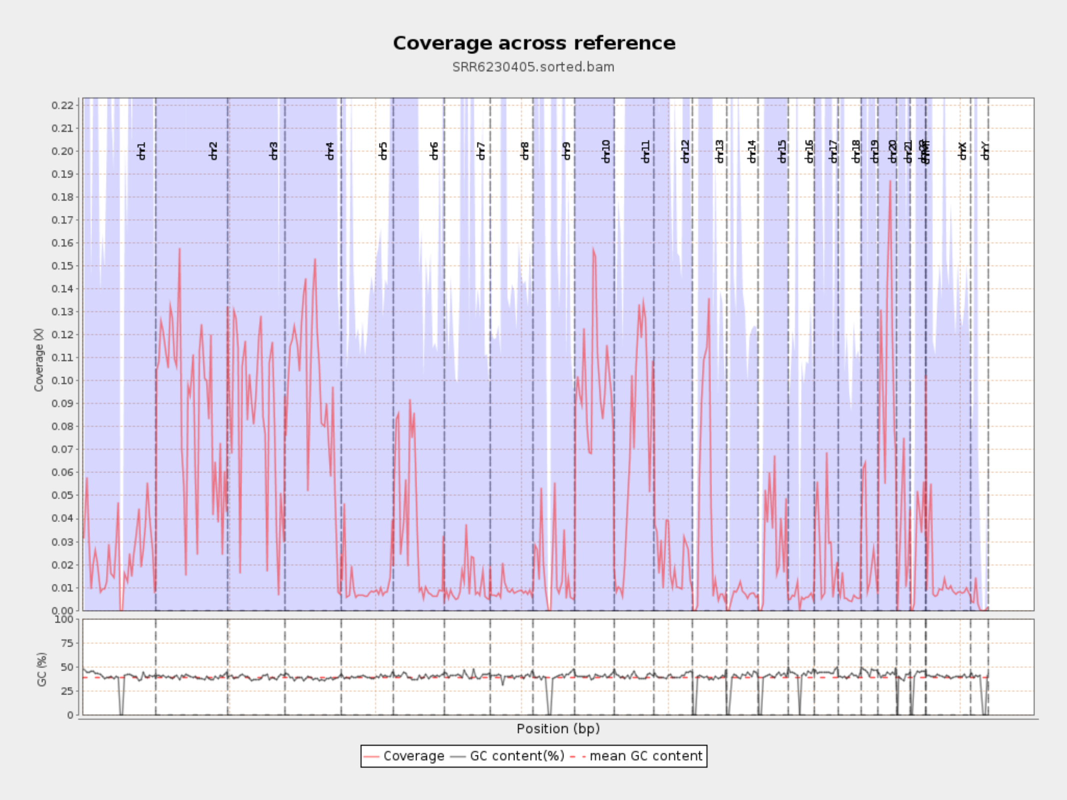
General error rate	0.84%
Mismatches	1,046,588
Insertions	10,302
Mapped reads with at least one insertion	0.53%
Deletions	36,080
Mapped reads with at least one deletion	1.85%
Homopolymer indels	46.62%

2.6. Chromosome stats

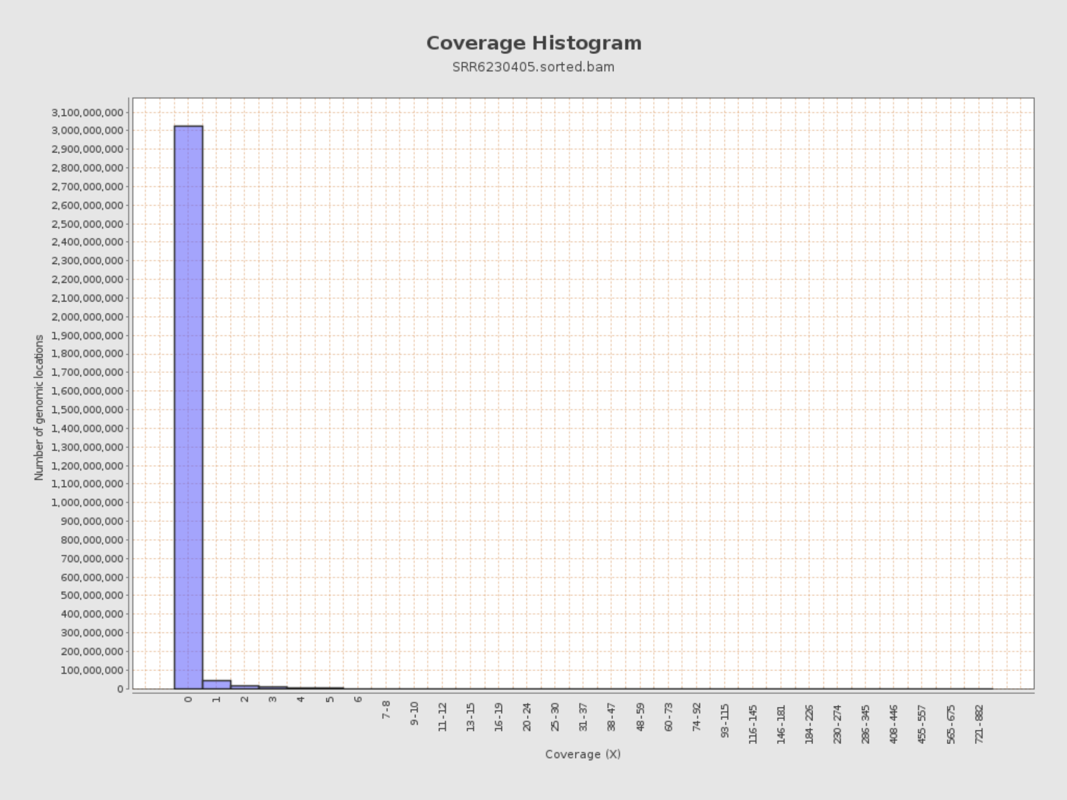
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5852689	0.0235	0.2523
chr2	243199373	21581635	0.0887	0.5624
chr3	198022430	16684368	0.0843	0.4679
chr4	191154276	18349513	0.096	0.5197
chr5	180915260	2106598	0.0116	0.1643
chr6	171115067	5684107	0.0332	0.3903
chr7	159138663	1761601	0.0111	0.1746

chr8	146364022	1259199	0.0086	0.514
chr9	141213431	2560550	0.0181	0.2804
chr10	135534747	13627228	0.1005	0.5811
chr11	135006516	9525701	0.0706	0.4337
chr12	133851895	2946253	0.022	0.2459
chr13	115169878	4683511	0.0407	0.3281
chr14	107349540	721840	0.0067	0.1487
chr15	102531392	3113823	0.0304	0.2861
chr16	90354753	533954	0.0059	0.1226
chr17	81195210	2313989	0.0285	0.2616
chr18	78077248	525129	0.0067	0.2757
chr19	59128983	1685618	0.0285	0.2703
chr20	63025520	6850167	0.1087	0.5358
chr21	48129895	1422241	0.0296	0.2958
chr22	51304566	1524312	0.0297	0.2651
chrMT	16571	1696	0.1023	0.3919
chrX	155270560	1917362	0.0123	0.1712
chrY	59373566	196573	0.0033	0.1682

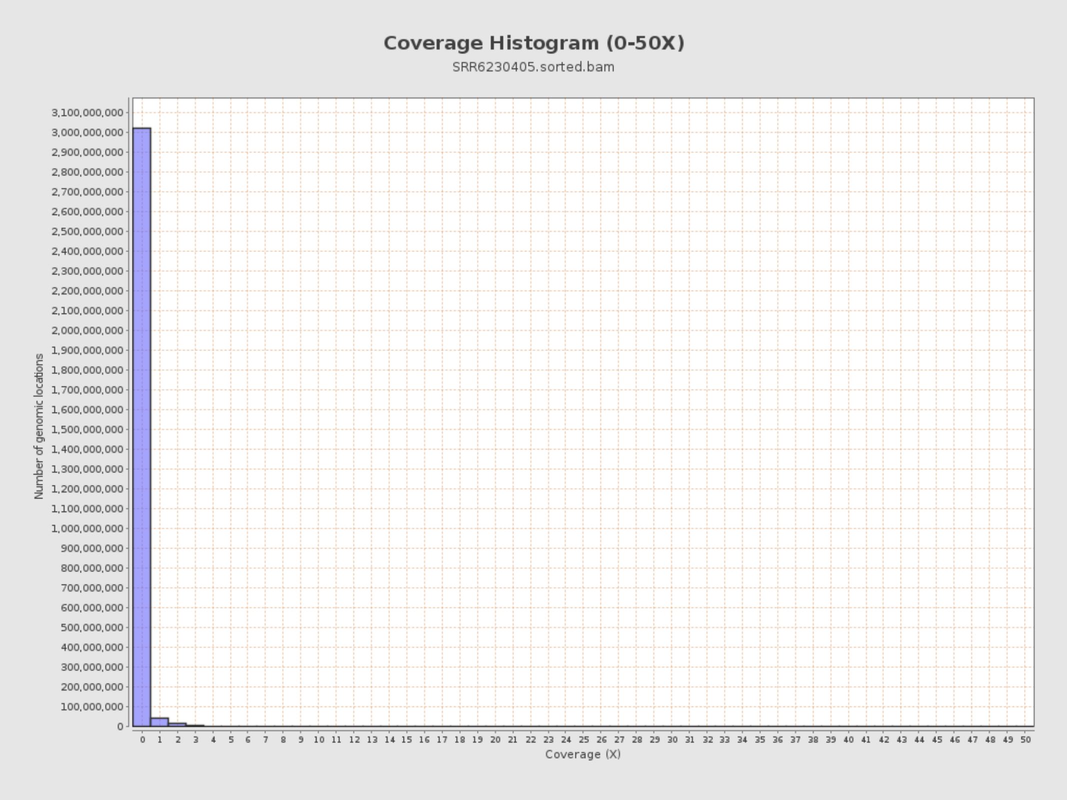
3. Results : Coverage across reference



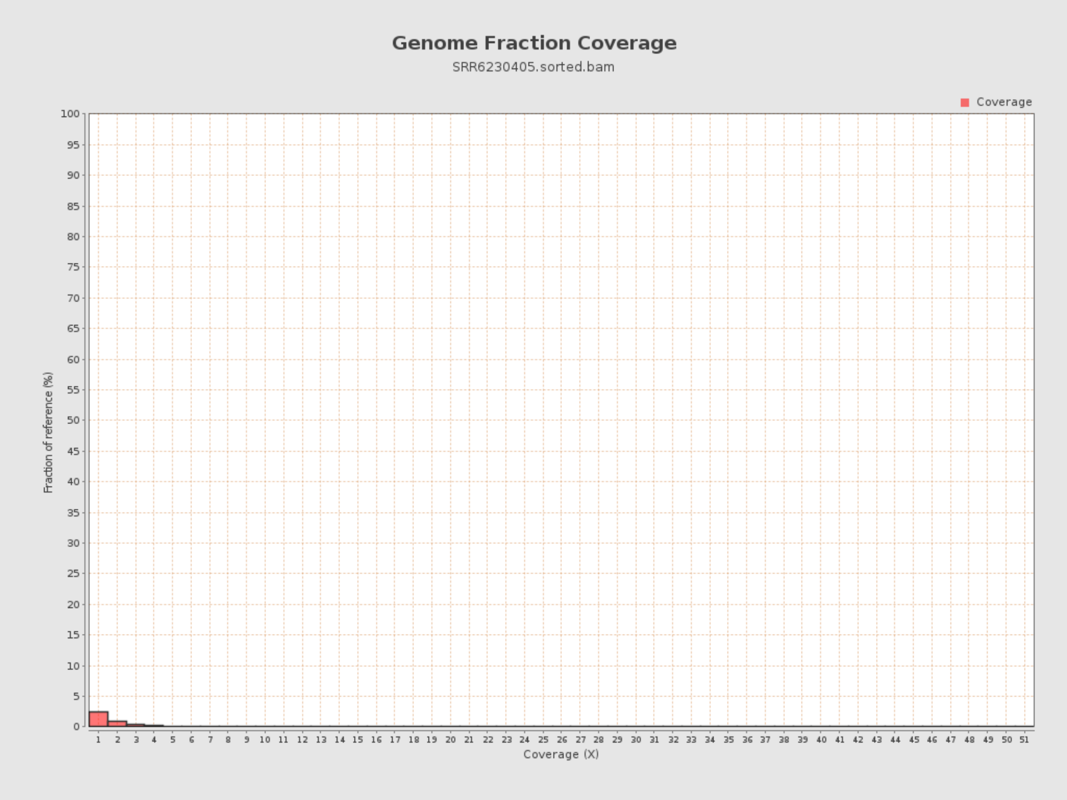
4. Results : Coverage Histogram



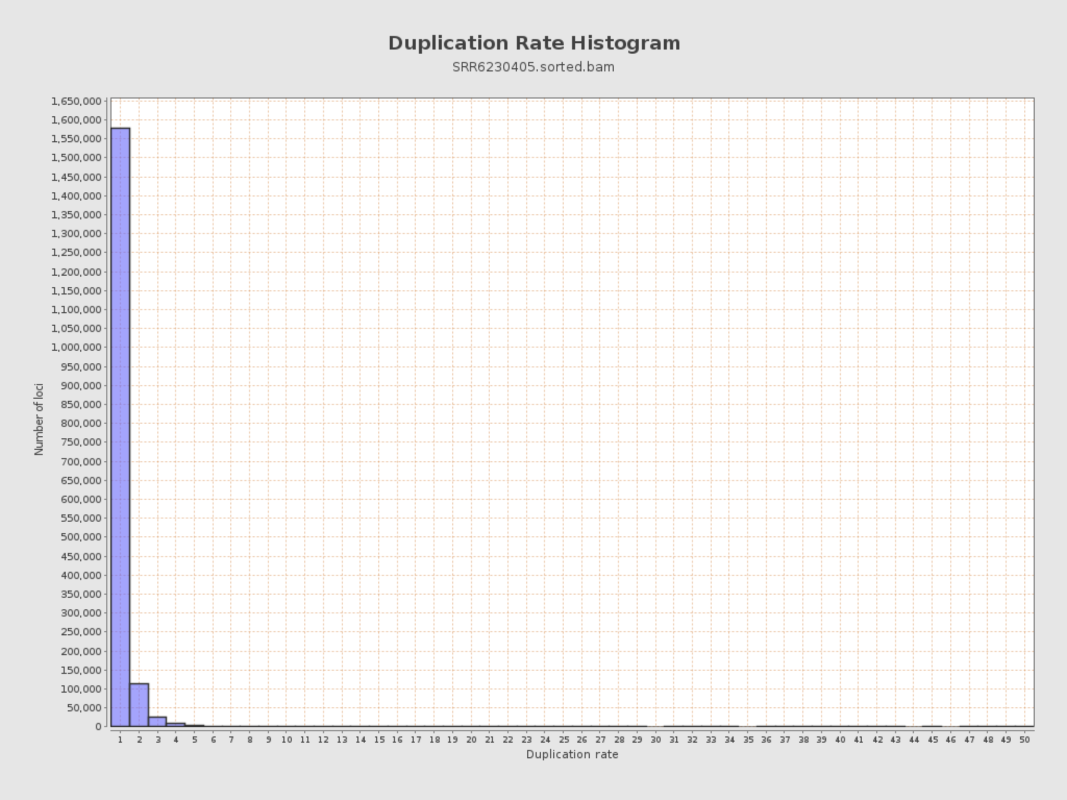
5. Results : Coverage Histogram (0-50X)



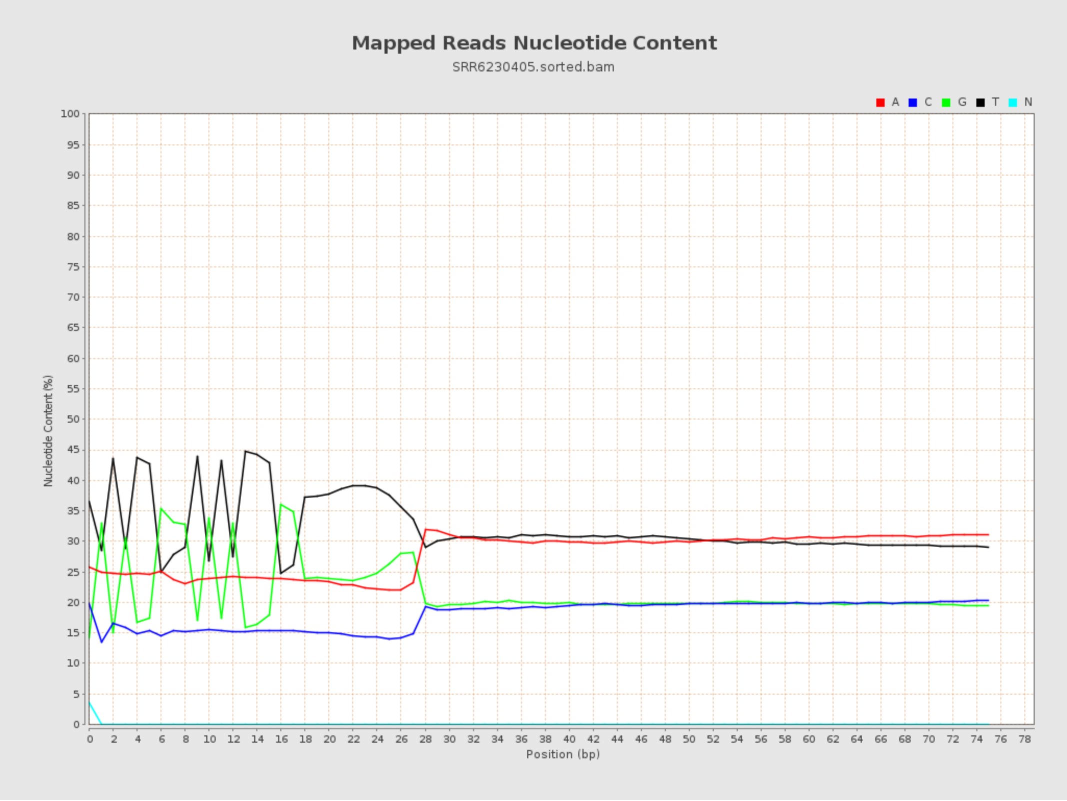
6. Results : Genome Fraction Coverage



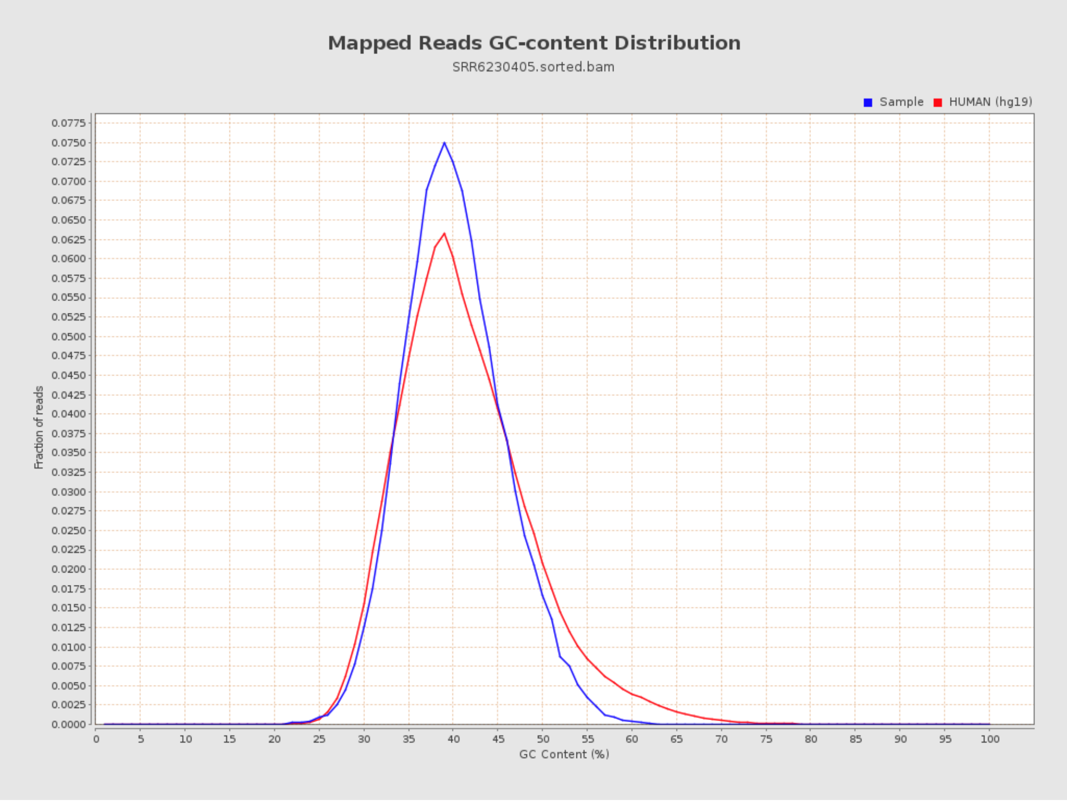
7. Results : Duplication Rate Histogram



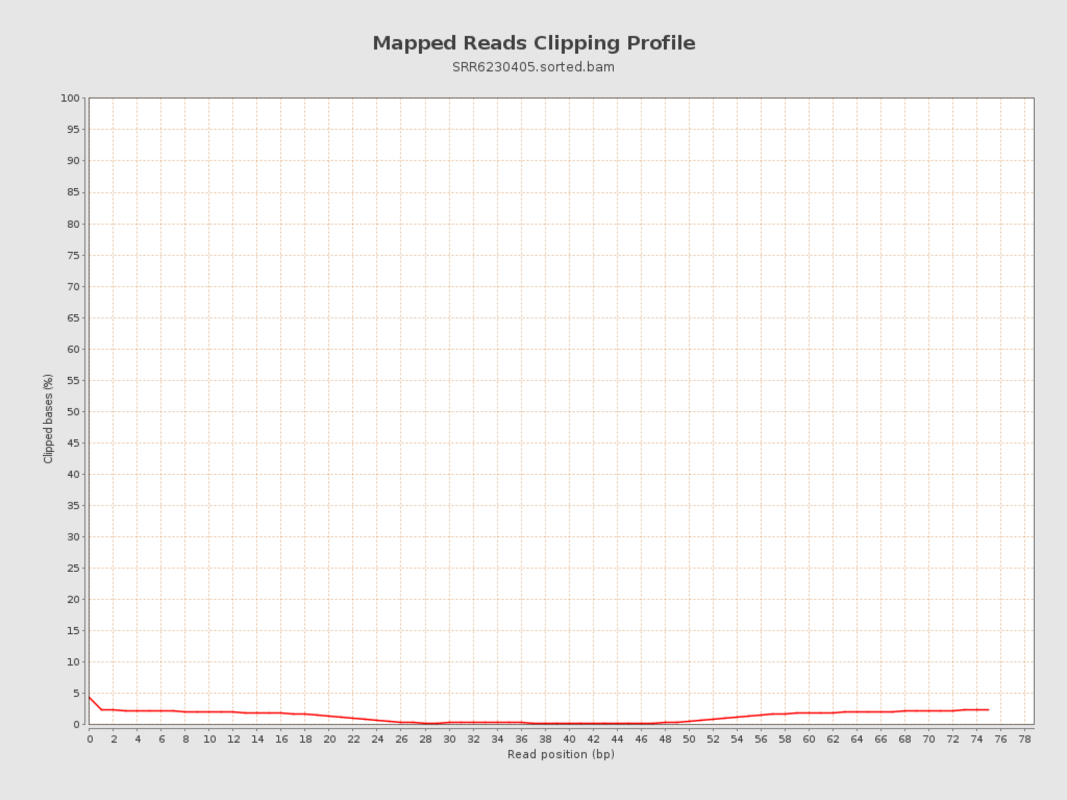
8. Results : Mapped Reads Nucleotide Content



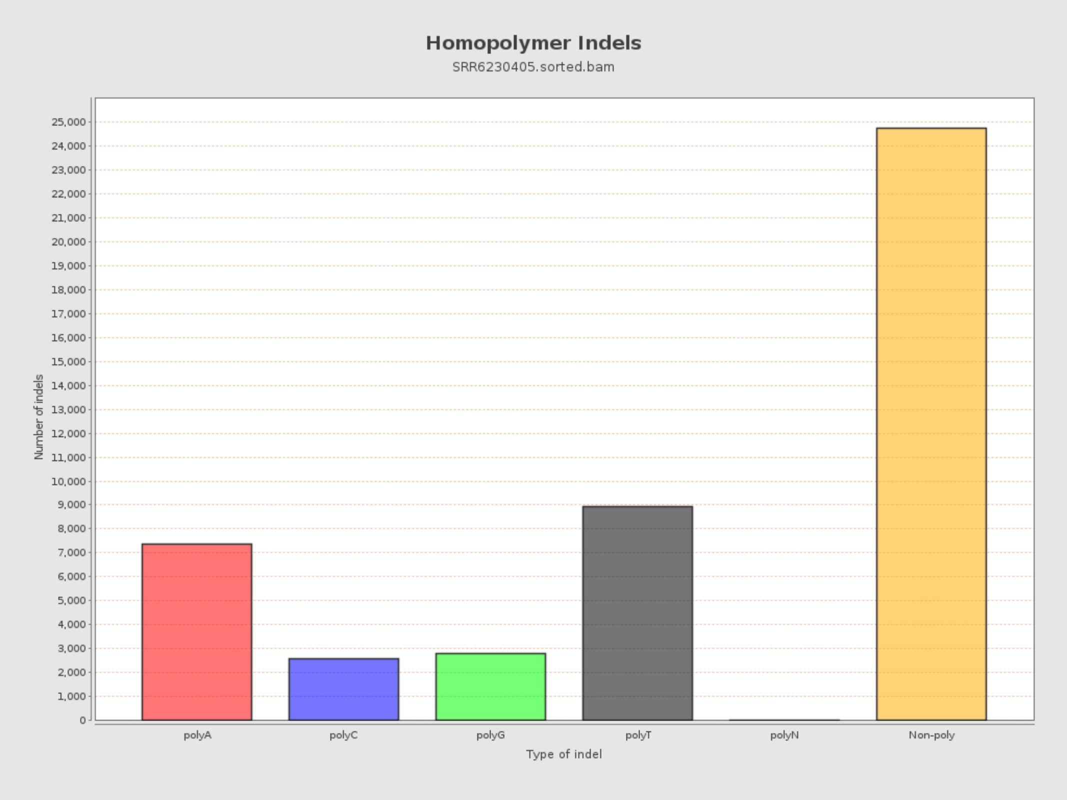
9. Results : Mapped Reads GC-content Distribution



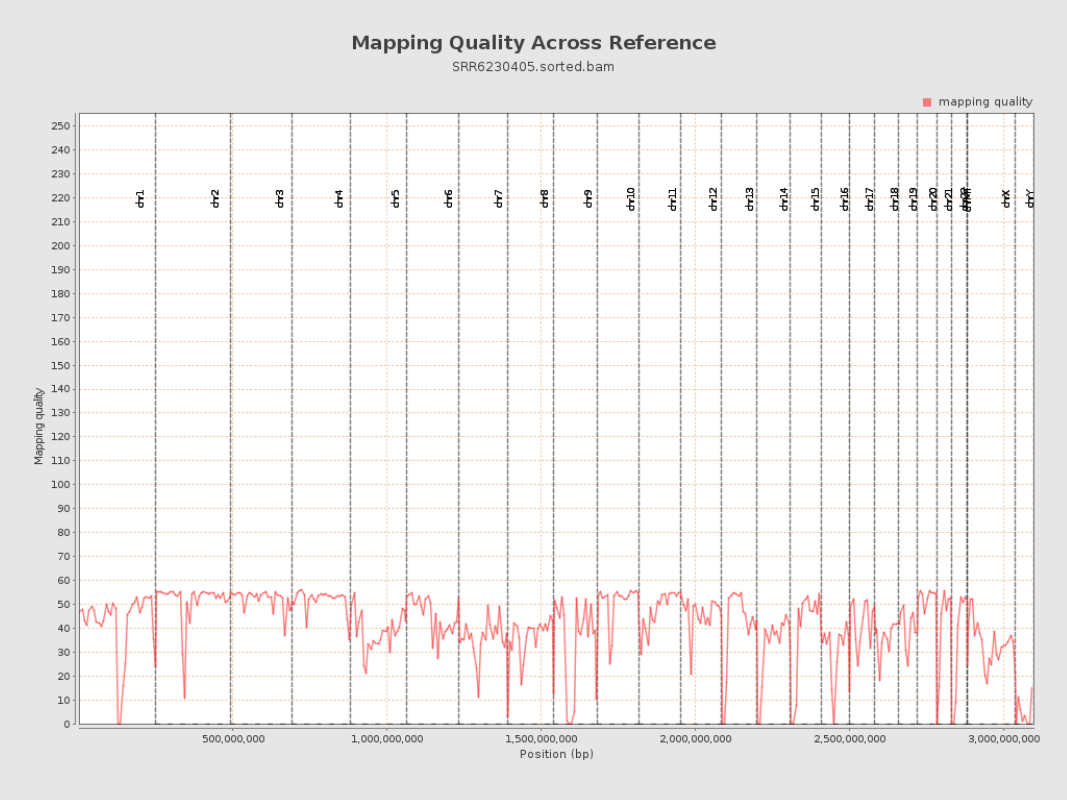
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram