Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:52:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230406.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_SRR6230406 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230406.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:52:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230406.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,079,398
Mapped reads	1,174,964 / 56.51%
Unmapped reads	904,434 / 43.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,312 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	307,576 / 14.79%
Duplication rate	14.04%
Clipped reads	672,491 / 32.34%

2.2. ACGT Content

Number/percentage of A's	20,641,605 / 27.69%
Number/percentage of C's	13,740,317 / 18.43%
Number/percentage of T's	23,659,854 / 31.74%
Number/percentage of G's	16,439,192 / 22.06%
Number/percentage of N's	54,135 / 0.07%
GC Percentage	40.49%

2.3. Coverage

Mean	0.0241

Standard Deviation	0.5213

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Mismatches and indels

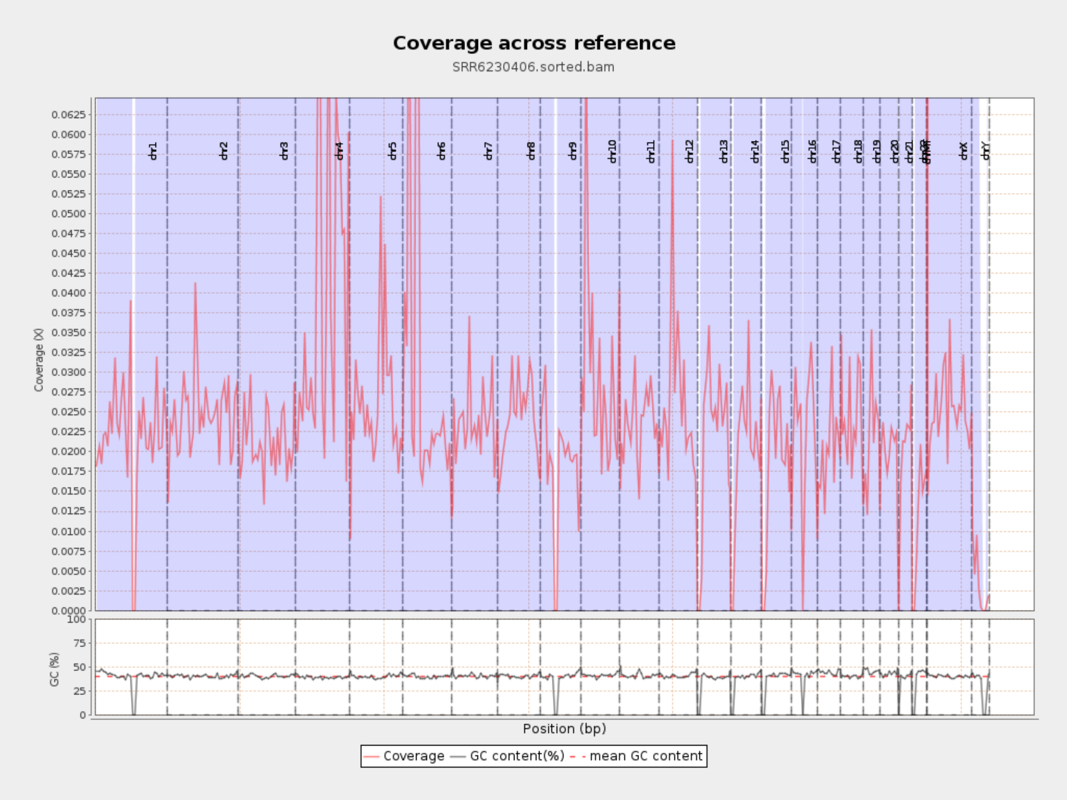
General error rate	0.99%
Mismatches	727,347
Insertions	5,585
Mapped reads with at least one insertion	0.47%
Deletions	19,424
Mapped reads with at least one deletion	1.64%
Homopolymer indels	46.53%

2.6. Chromosome stats

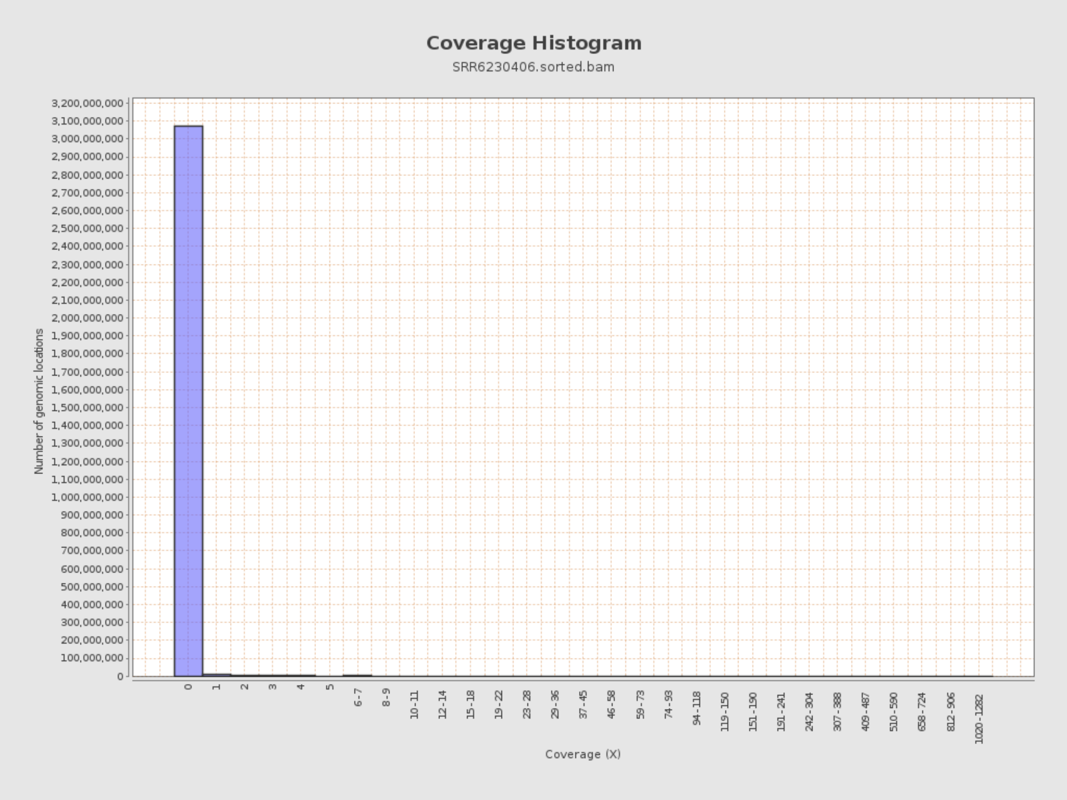
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5504298	0.0221	0.5585
chr2	243199373	6045779	0.0249	0.628
chr3	198022430	4192736	0.0212	0.4251
chr4	191154276	7575628	0.0396	0.5988
chr5	180915260	4823653	0.0267	0.4733
chr6	171115067	5350939	0.0313	0.5756
chr7	159138663	3778260	0.0237	0.4782

chr8	146364022	3571150	0.0244	0.4963
chr9	141213431	2584952	0.0183	0.3936
chr10	135534747	4065307	0.03	0.5151
chr11	135006516	3199364	0.0237	0.445
chr12	133851895	3525845	0.0263	0.4827
chr13	115169878	2492189	0.0216	0.4773
chr14	107349540	2114448	0.0197	0.7232
chr15	102531392	1894868	0.0185	0.8235
chr16	90354753	2003287	0.0222	0.4346
chr17	81195210	1632973	0.0201	0.4133
chr18	78077248	1914659	0.0245	0.4939
chr19	59128983	1302402	0.022	0.4245
chr20	63025520	1279881	0.0203	0.3934
chr21	48129895	952007	0.0198	0.3932
chr22	51304566	599259	0.0117	0.278
chrMT	16571	25199	1.5207	3.9584
chrX	155270560	3940069	0.0254	0.5191
chrY	59373566	197403	0.0033	0.1783

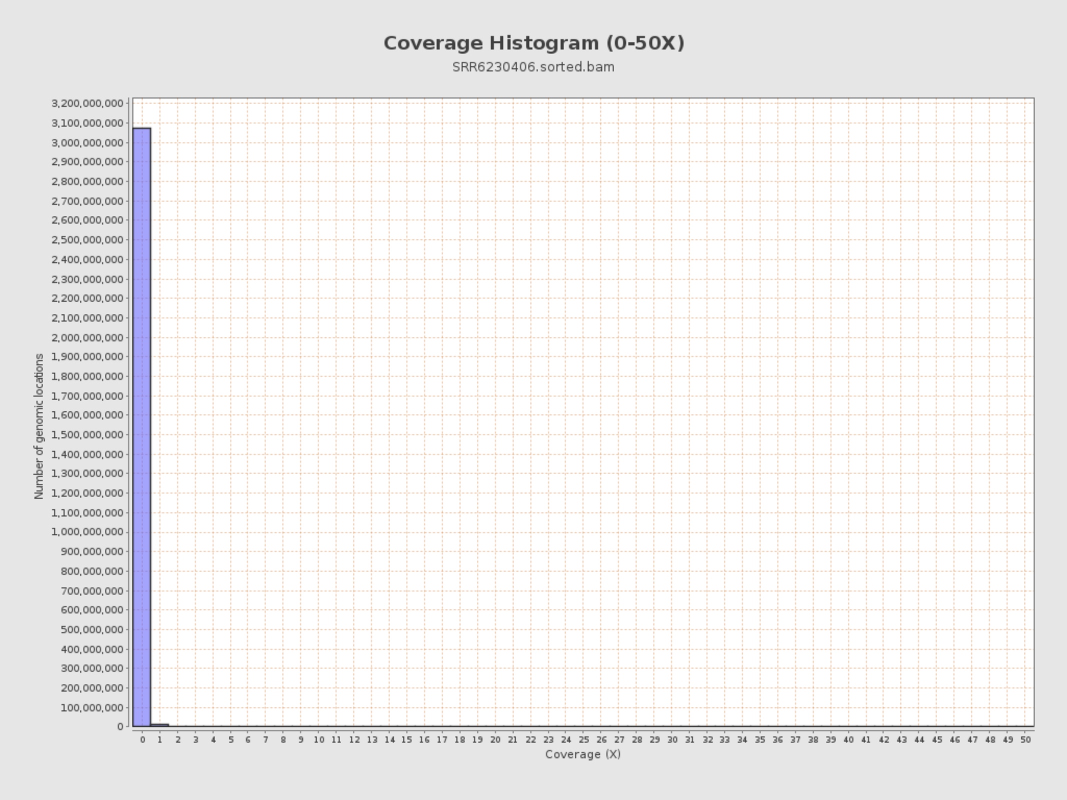
3. Results : Coverage across reference



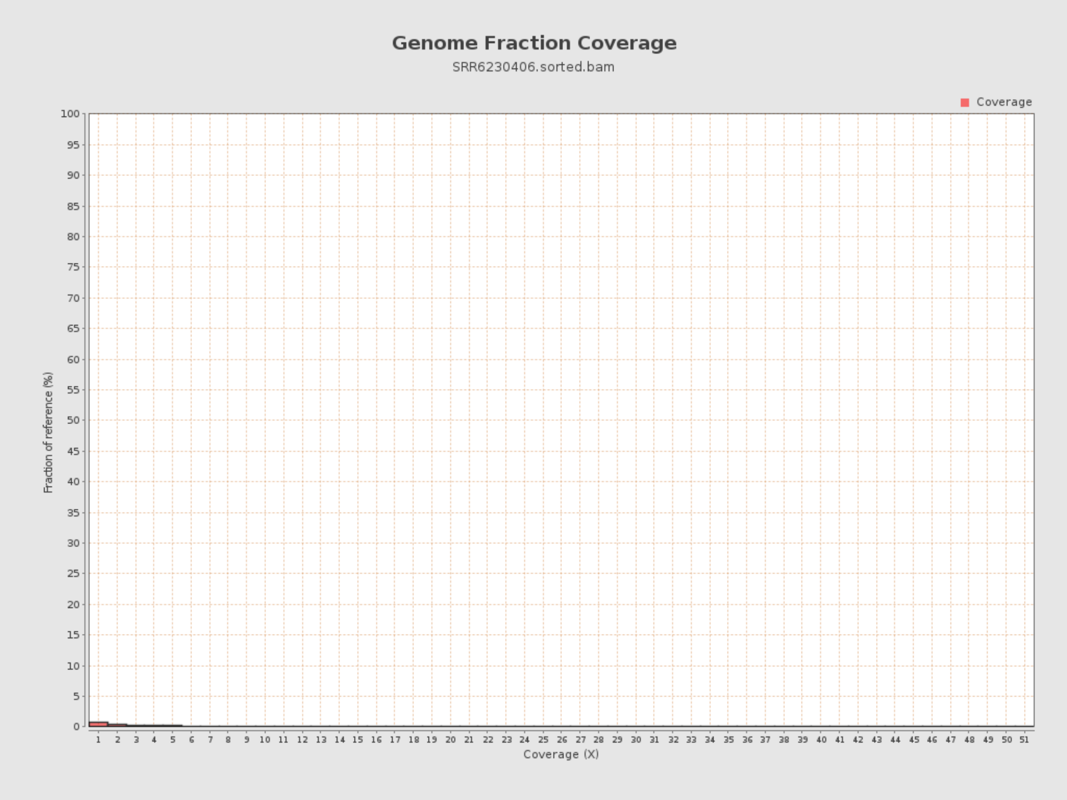
4. Results : Coverage Histogram



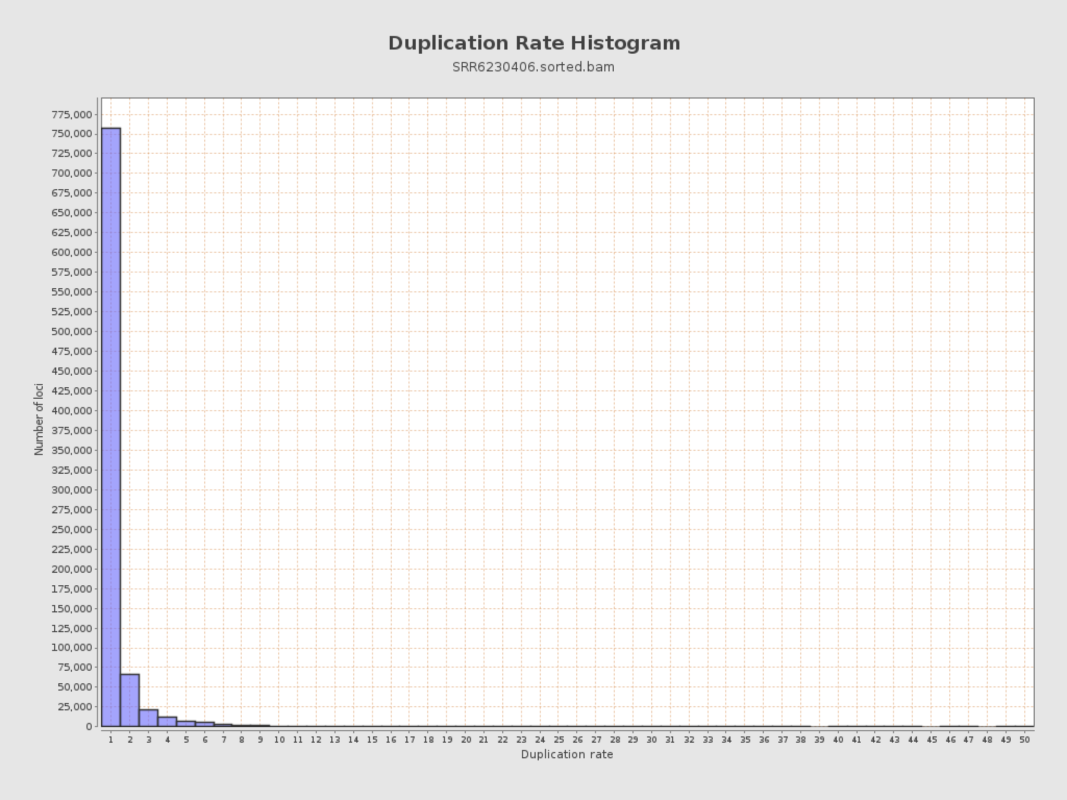
5. Results : Coverage Histogram (0-50X)



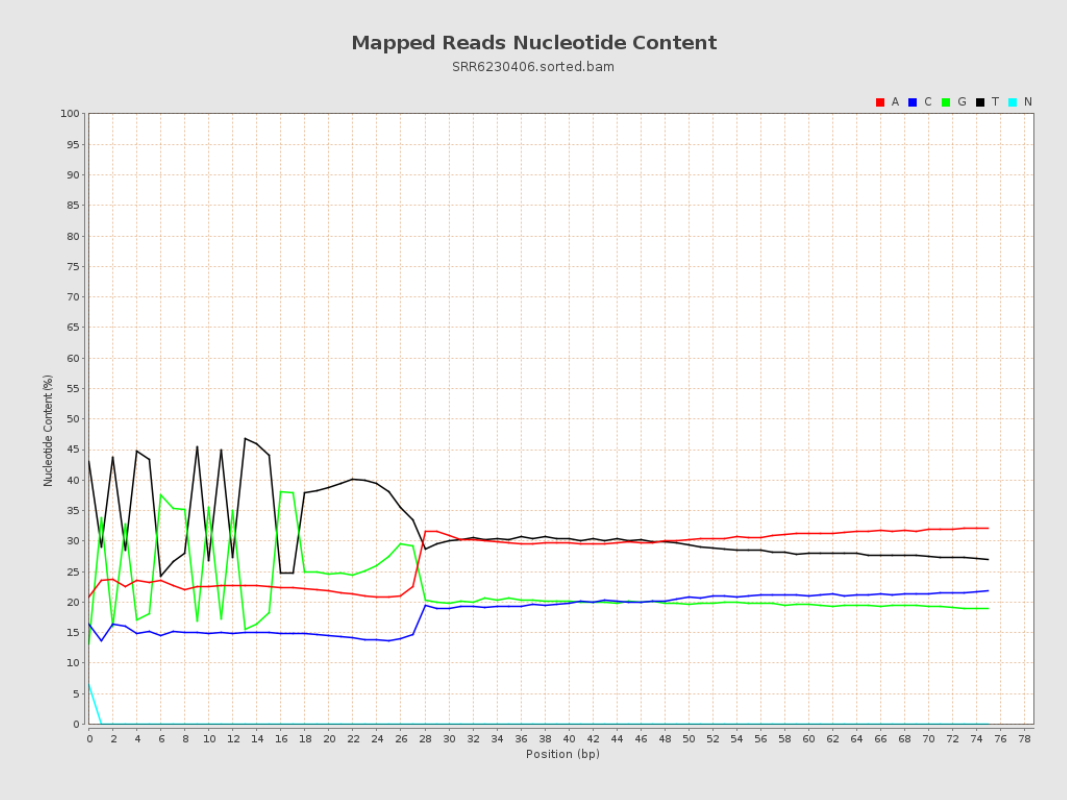
6. Results : Genome Fraction Coverage



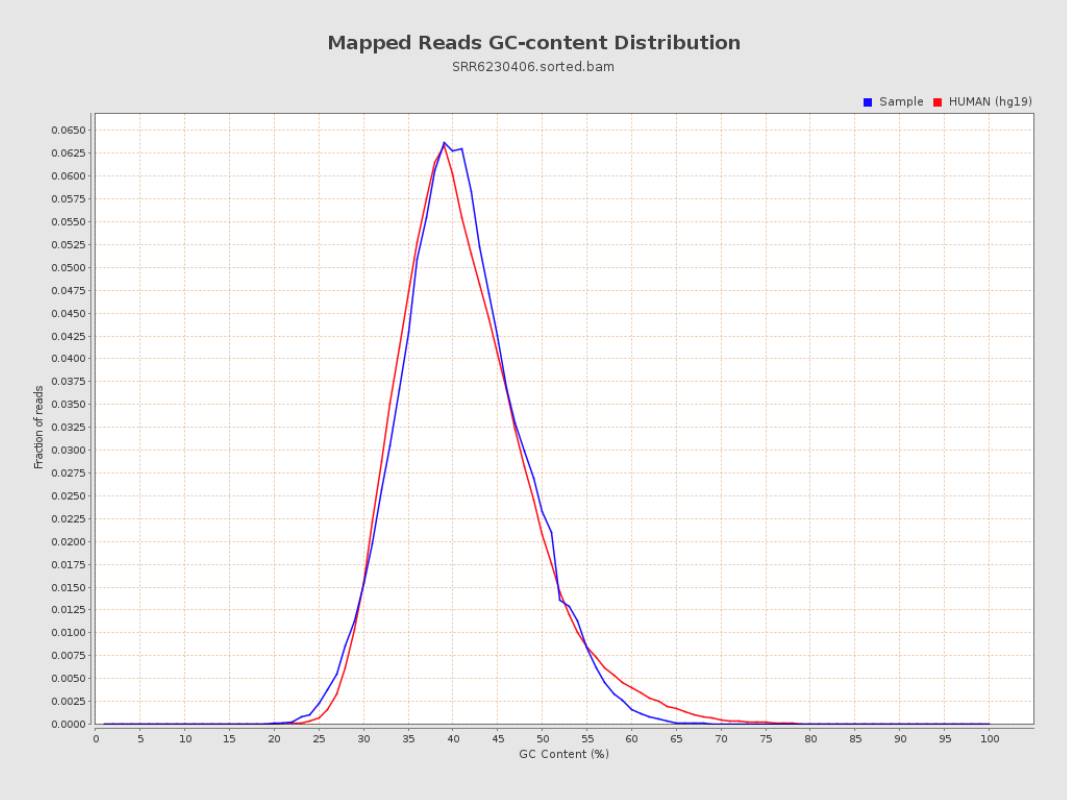
7. Results : Duplication Rate Histogram



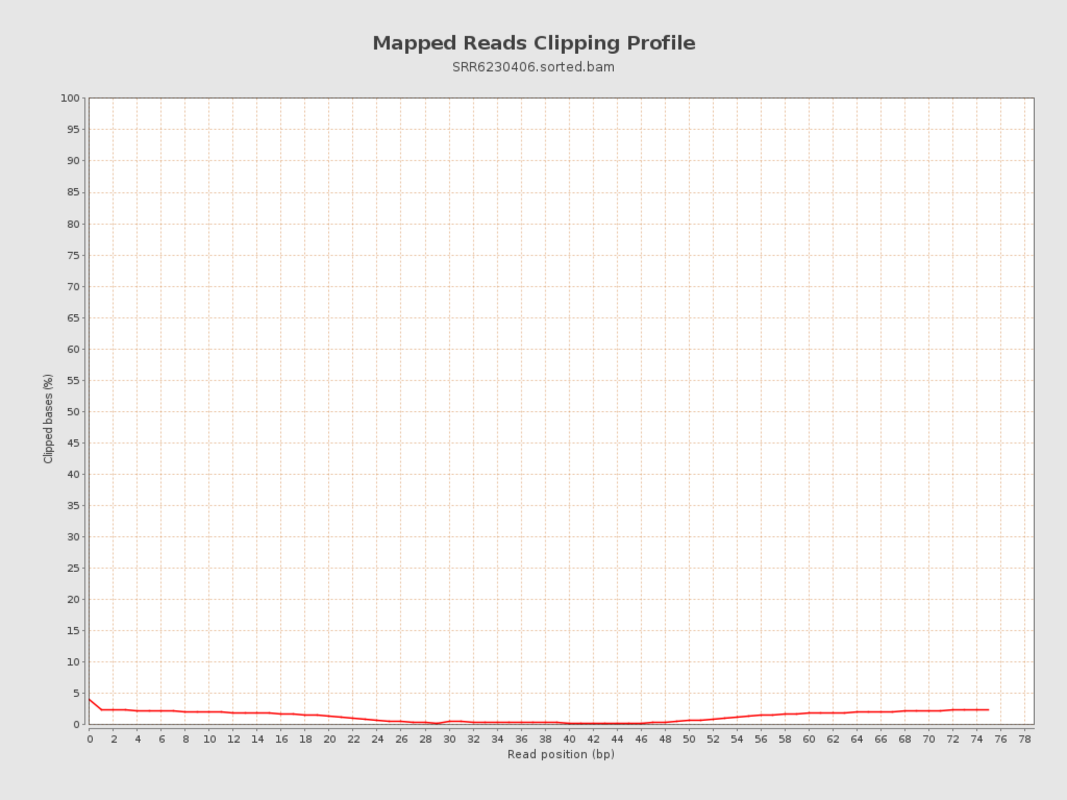
8. Results : Mapped Reads Nucleotide Content



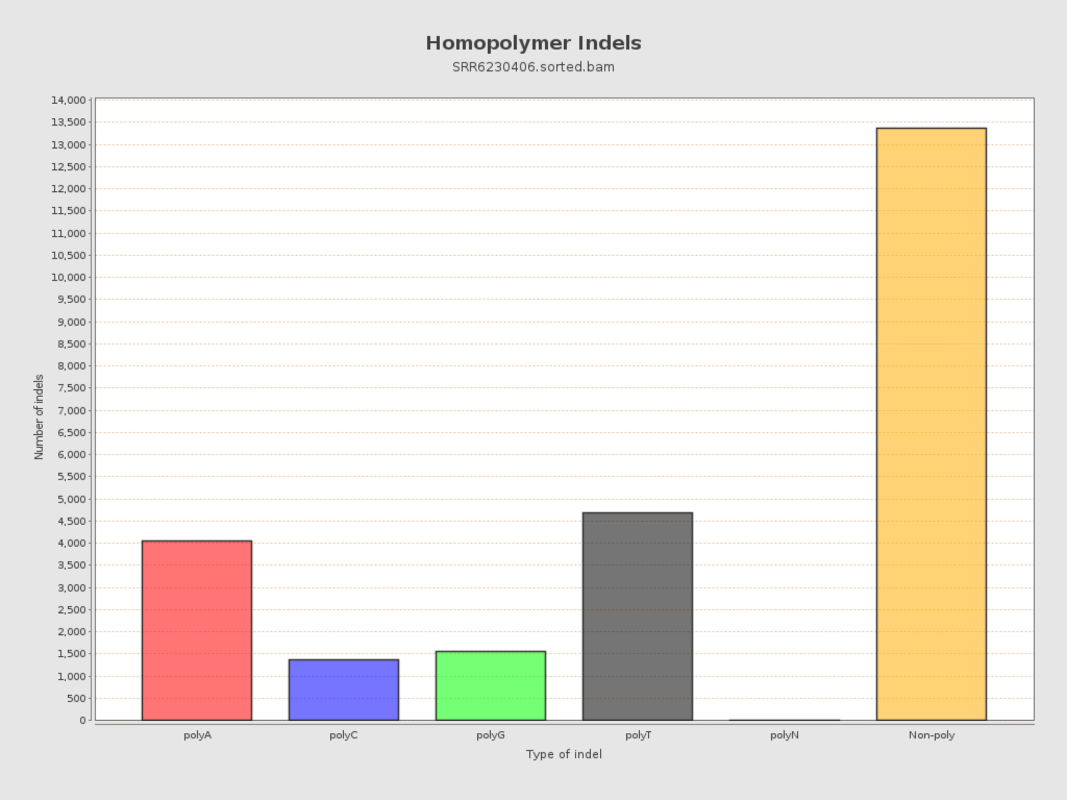
9. Results : Mapped Reads GC-content Distribution



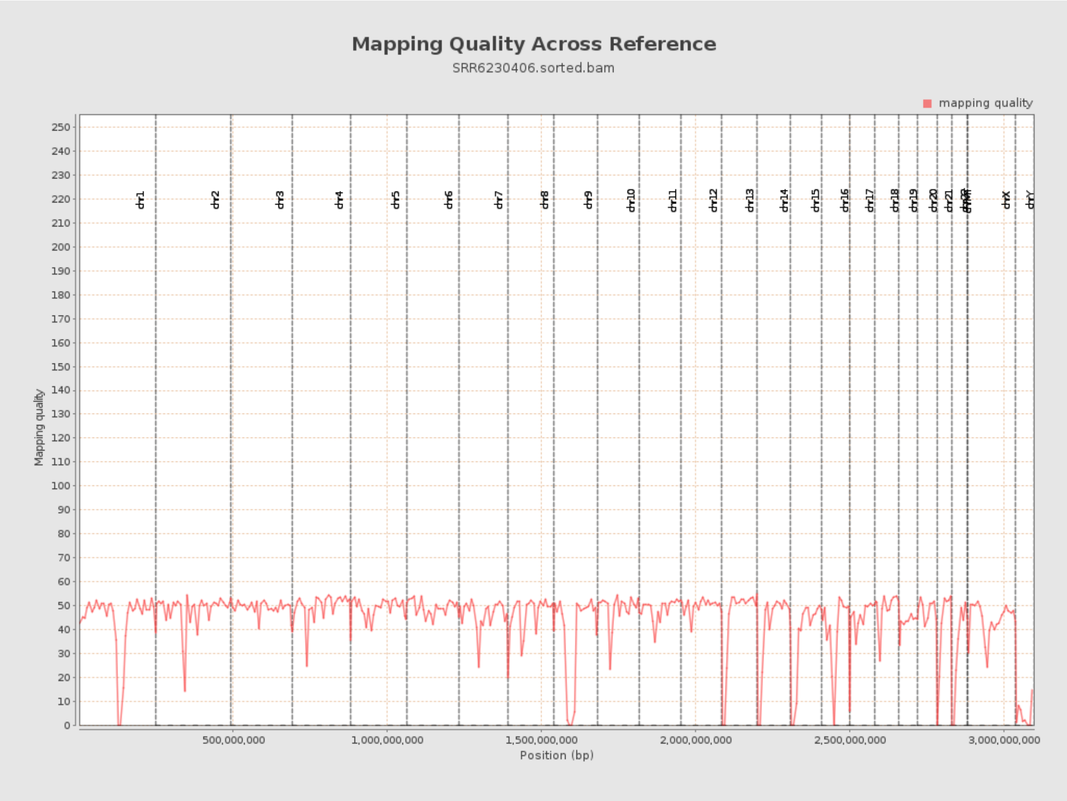
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram