Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:15:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240075.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_SRR6240075 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240075.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:15:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240075.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,593,823
Mapped reads	1,204,205 / 75.55%
Unmapped reads	389,618 / 24.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,218 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	146,405 / 9.19%
Duplication rate	9.76%
Clipped reads	683,874 / 42.91%

2.2. ACGT Content

Number/percentage of A's	20,851,857 / 27.24%
Number/percentage of C's	13,720,953 / 17.93%
Number/percentage of T's	24,484,807 / 31.99%
Number/percentage of G's	17,430,306 / 22.77%
Number/percentage of N's	50,952 / 0.07%
GC Percentage	40.7%

2.3. Coverage

Mean	0.0247

Standard Deviation	0.2829

2.4. Mapping Quality

Mean Mapping Quality	45.87

2.5. Mismatches and indels

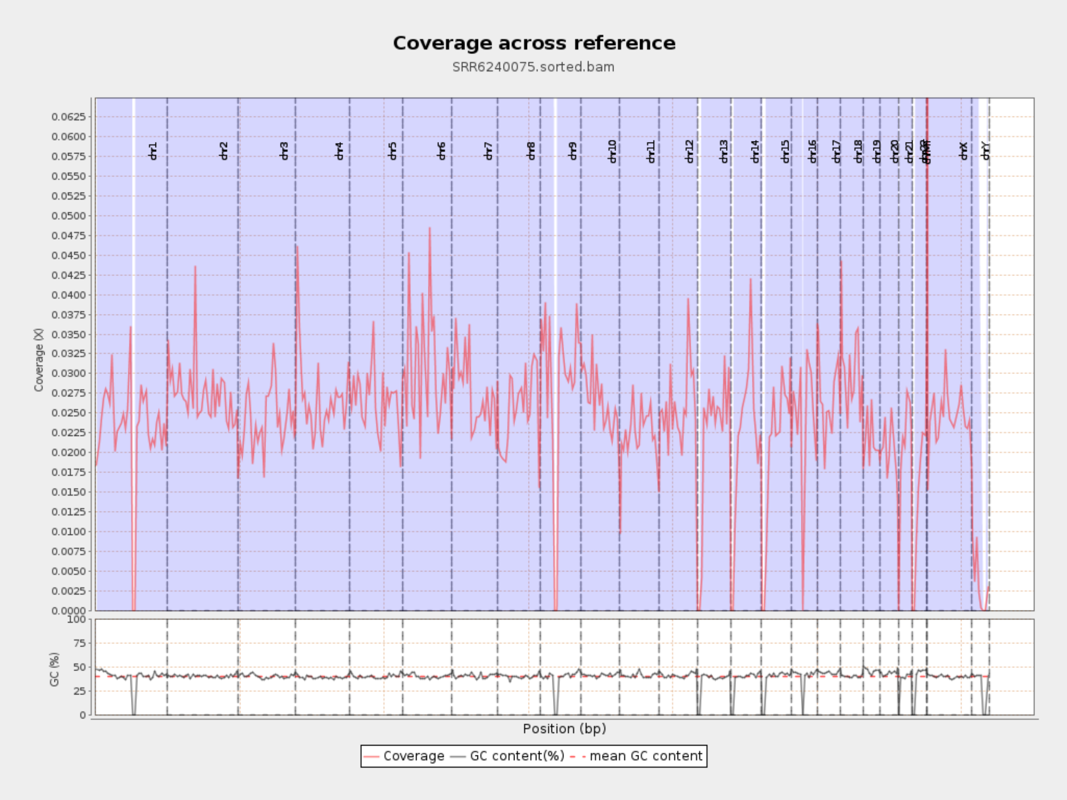
General error rate	0.86%
Mismatches	648,389
Insertions	5,366
Mapped reads with at least one insertion	0.44%
Deletions	17,505
Mapped reads with at least one deletion	1.44%
Homopolymer indels	48.08%

2.6. Chromosome stats

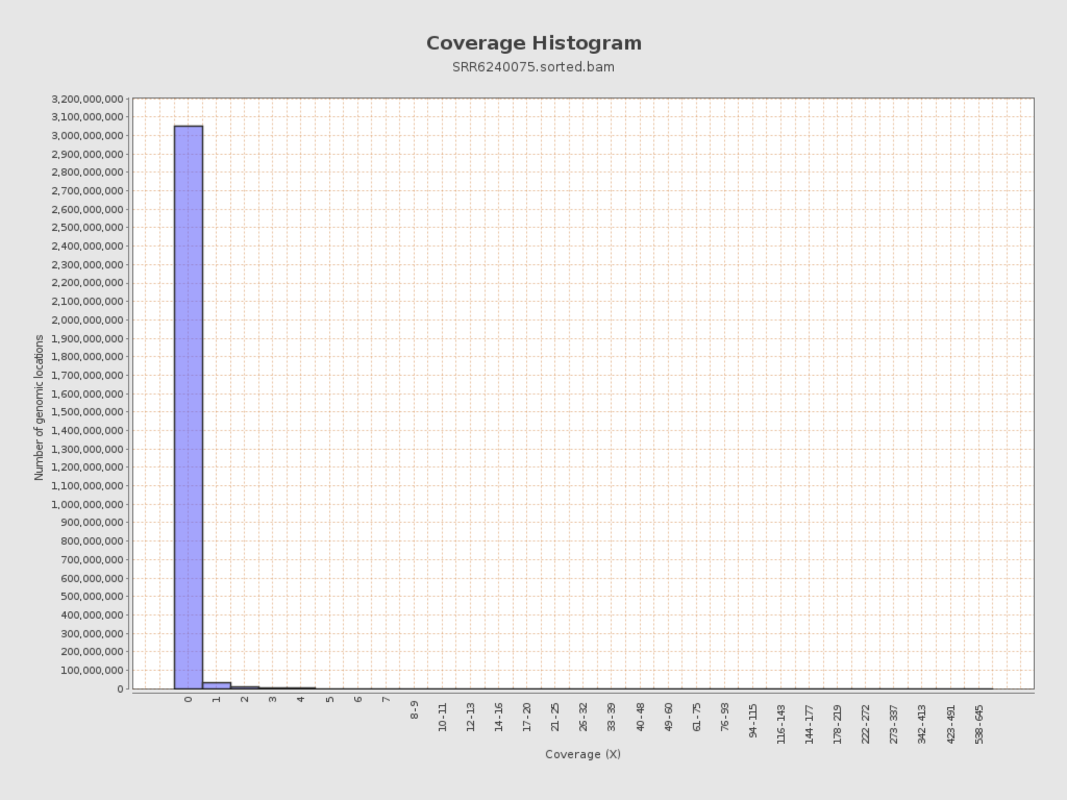
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5723668	0.023	0.3327
chr2	243199373	6696299	0.0275	0.3291
chr3	198022430	4808878	0.0243	0.2382
chr4	191154276	5097111	0.0267	0.2568
chr5	180915260	4819598	0.0266	0.2502
chr6	171115067	5273550	0.0308	0.2863
chr7	159138663	4379411	0.0275	0.2921

chr8	146364022	3707633	0.0253	0.4471
chr9	141213431	4019429	0.0285	0.2872
chr10	135534747	3575161	0.0264	0.2753
chr11	135006516	3057327	0.0226	0.2523
chr12	133851895	3418412	0.0255	0.2493
chr13	115169878	2508442	0.0218	0.2272
chr14	107349540	2331797	0.0217	0.2334
chr15	102531392	2084528	0.0203	0.2272
chr16	90354753	2140417	0.0237	0.2401
chr17	81195210	2183501	0.0269	0.2543
chr18	78077248	2375044	0.0304	0.4138
chr19	59128983	1282315	0.0217	0.2815
chr20	63025520	1279429	0.0203	0.2189
chr21	48129895	1002294	0.0208	0.2236
chr22	51304566	759028	0.0148	0.1824
chrMT	16571	14158	0.8544	1.4423
chrX	155270560	3838941	0.0247	0.2496
chrY	59373566	192398	0.0032	0.0845

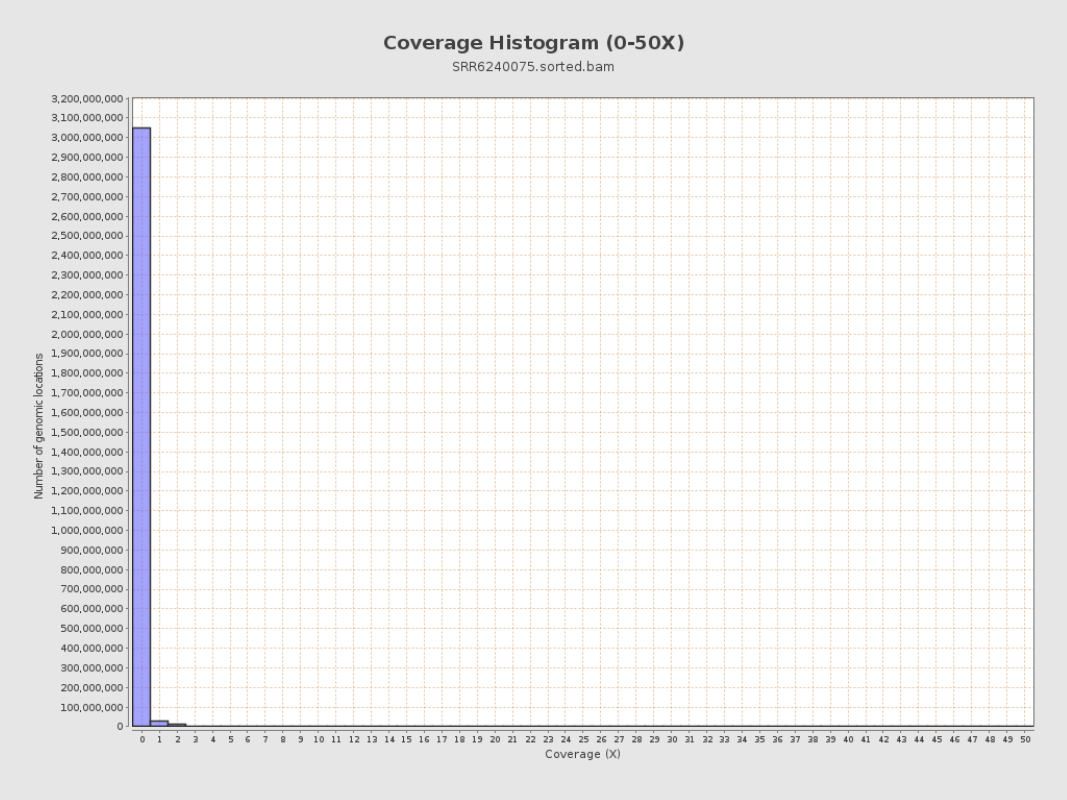
3. Results : Coverage across reference



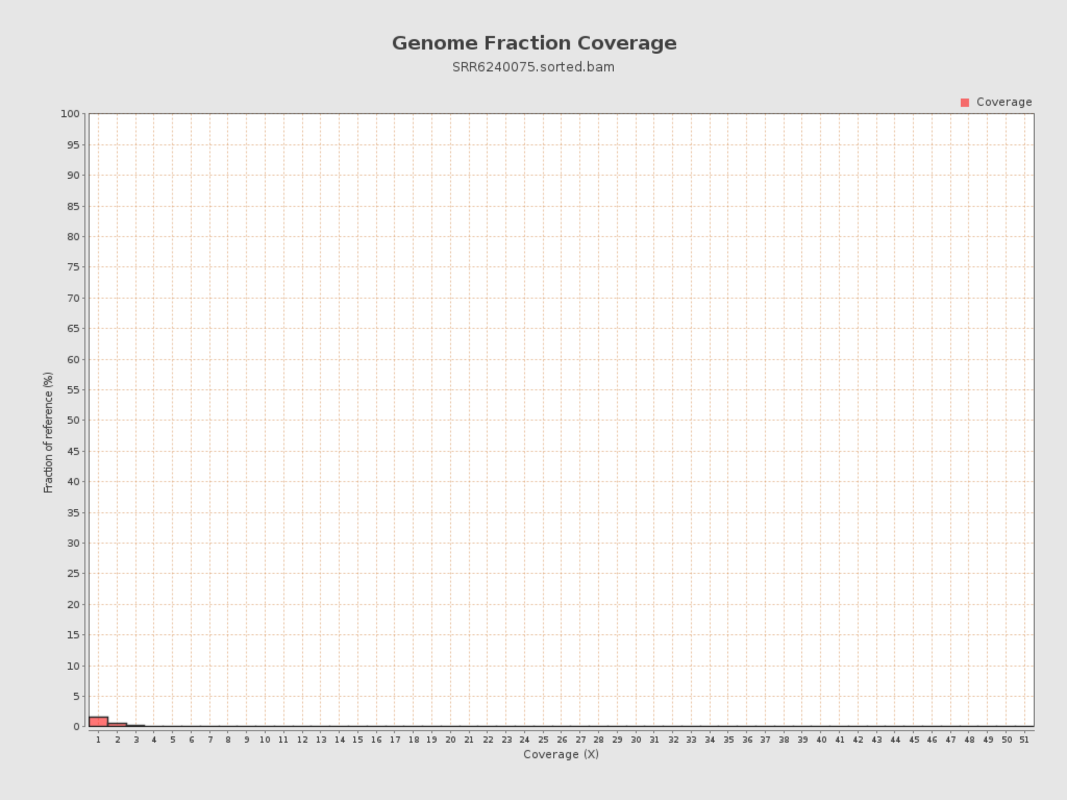
4. Results : Coverage Histogram



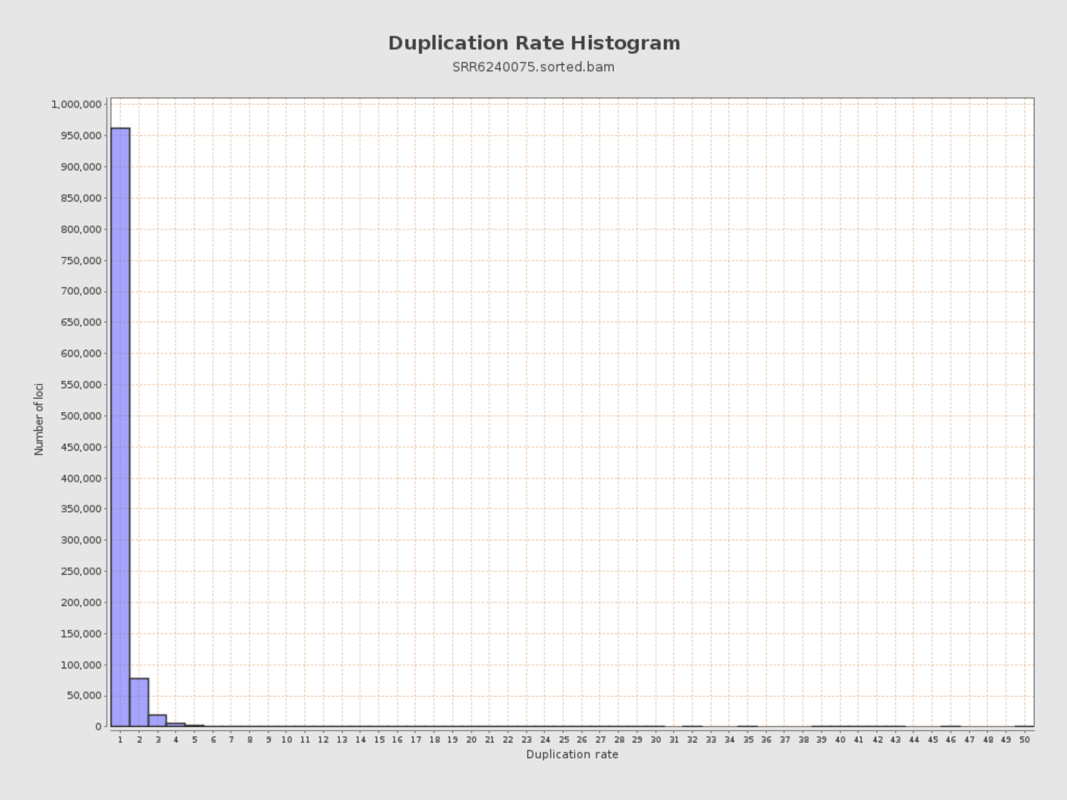
5. Results : Coverage Histogram (0-50X)



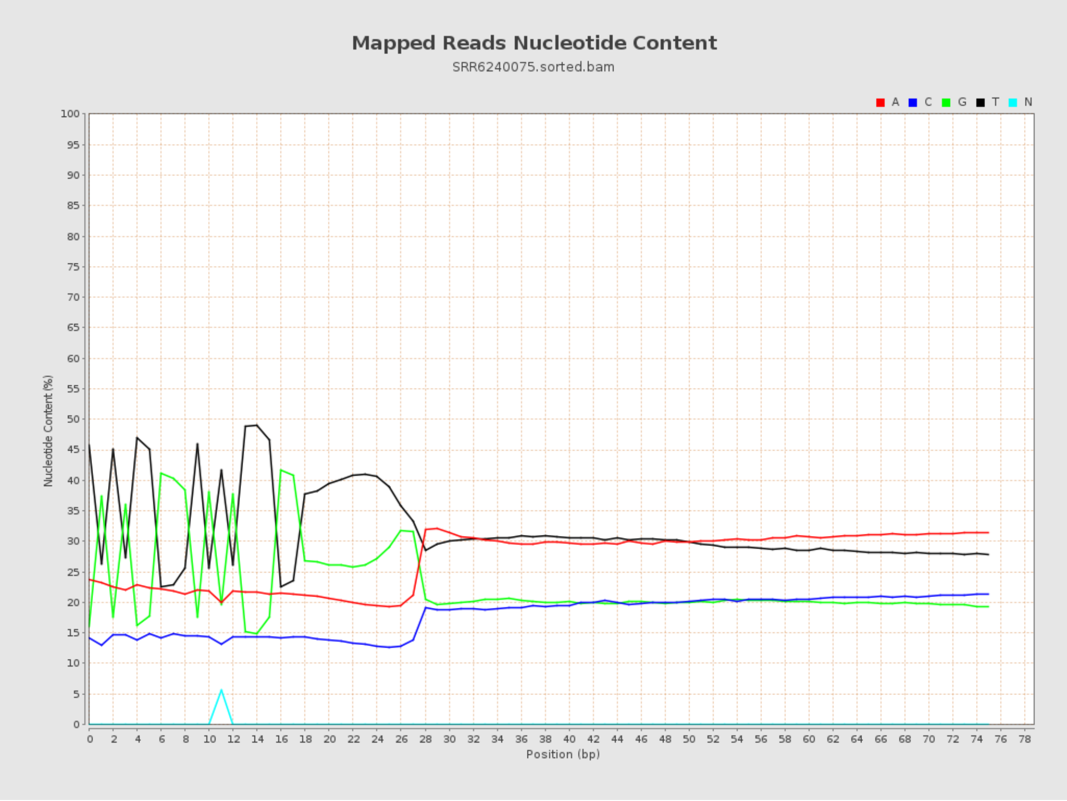
6. Results : Genome Fraction Coverage



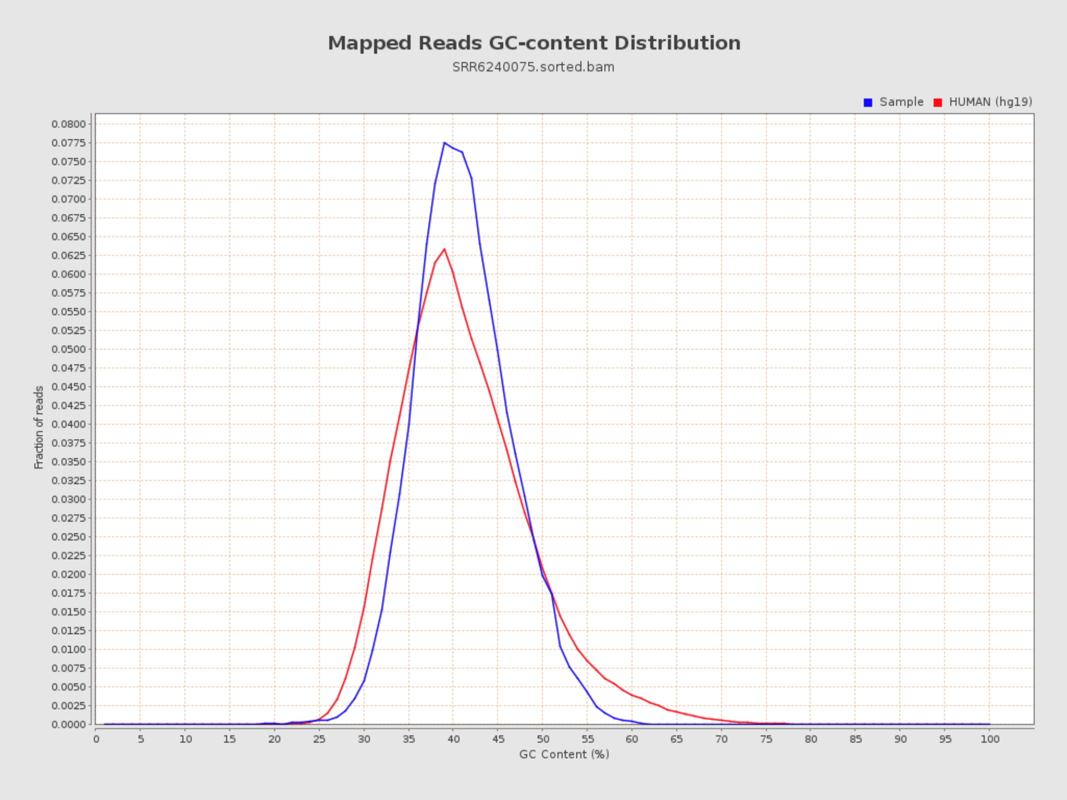
7. Results : Duplication Rate Histogram



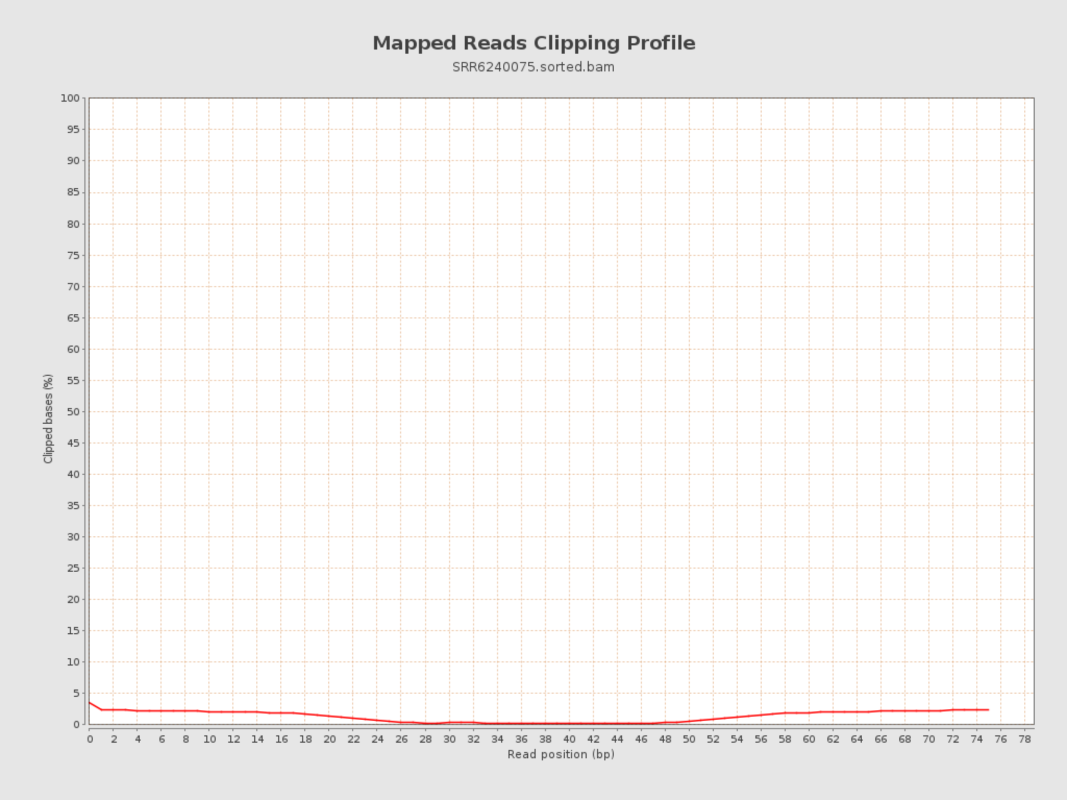
8. Results : Mapped Reads Nucleotide Content



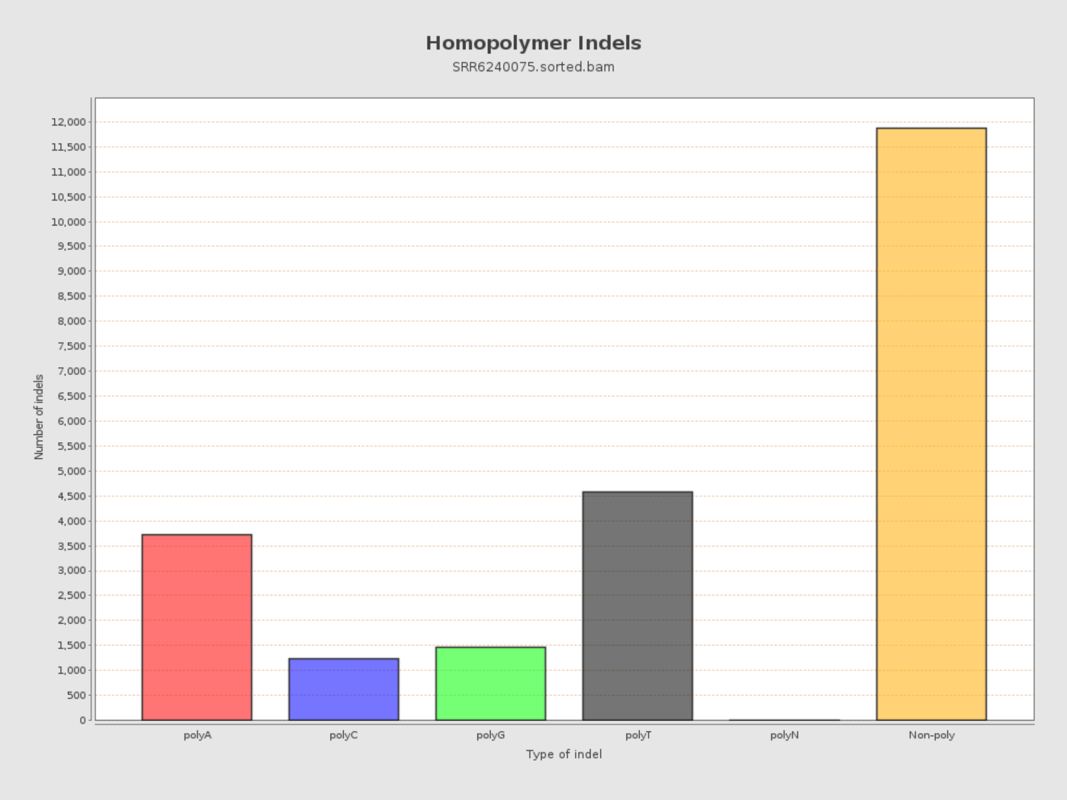
9. Results : Mapped Reads GC-content Distribution



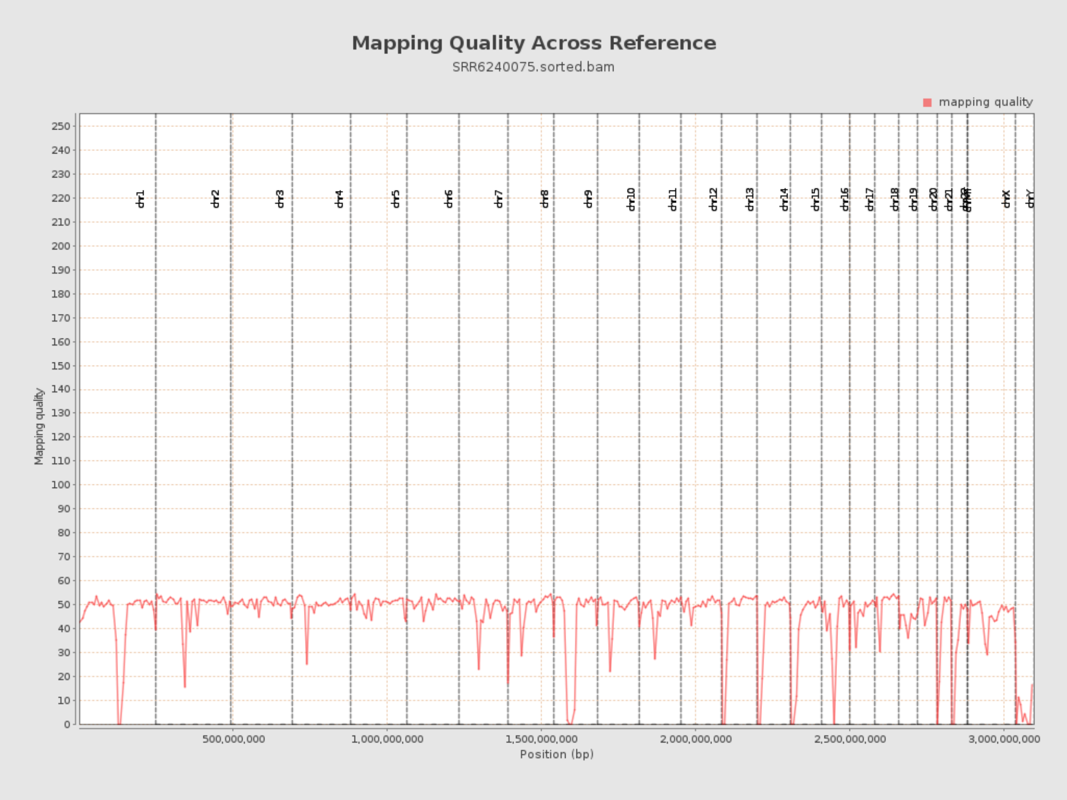
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram