Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:21:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004161.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_SRR6004161 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004161.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:21:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004161.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,738,626
Mapped reads	2,342,885 / 85.55%
Unmapped reads	395,741 / 14.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,874 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	99,603 / 3.64%
Duplication rate	3.12%
Clipped reads	934,412 / 34.12%

2.2. ACGT Content

Number/percentage of A's	43,835,564 / 27.43%
Number/percentage of C's	30,567,848 / 19.13%
Number/percentage of T's	50,142,951 / 31.38%
Number/percentage of G's	35,233,247 / 22.05%
Number/percentage of N's	21,597 / 0.01%
GC Percentage	41.18%

2.3. Coverage

Mean	0.0516

Standard Deviation	0.4669

2.4. Mapping Quality

Mean Mapping Quality	45.23

2.5. Mismatches and indels

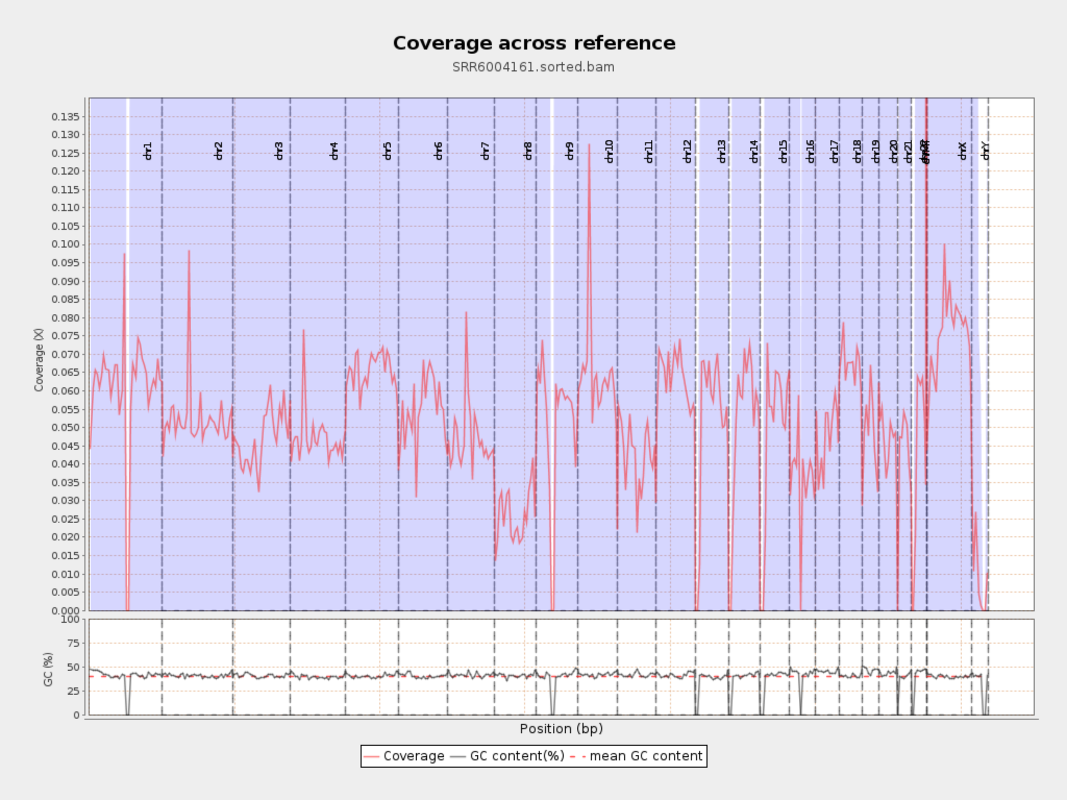
General error rate	0.99%
Mismatches	1,555,371
Insertions	14,058
Mapped reads with at least one insertion	0.59%
Deletions	45,443
Mapped reads with at least one deletion	1.92%
Homopolymer indels	46.1%

2.6. Chromosome stats

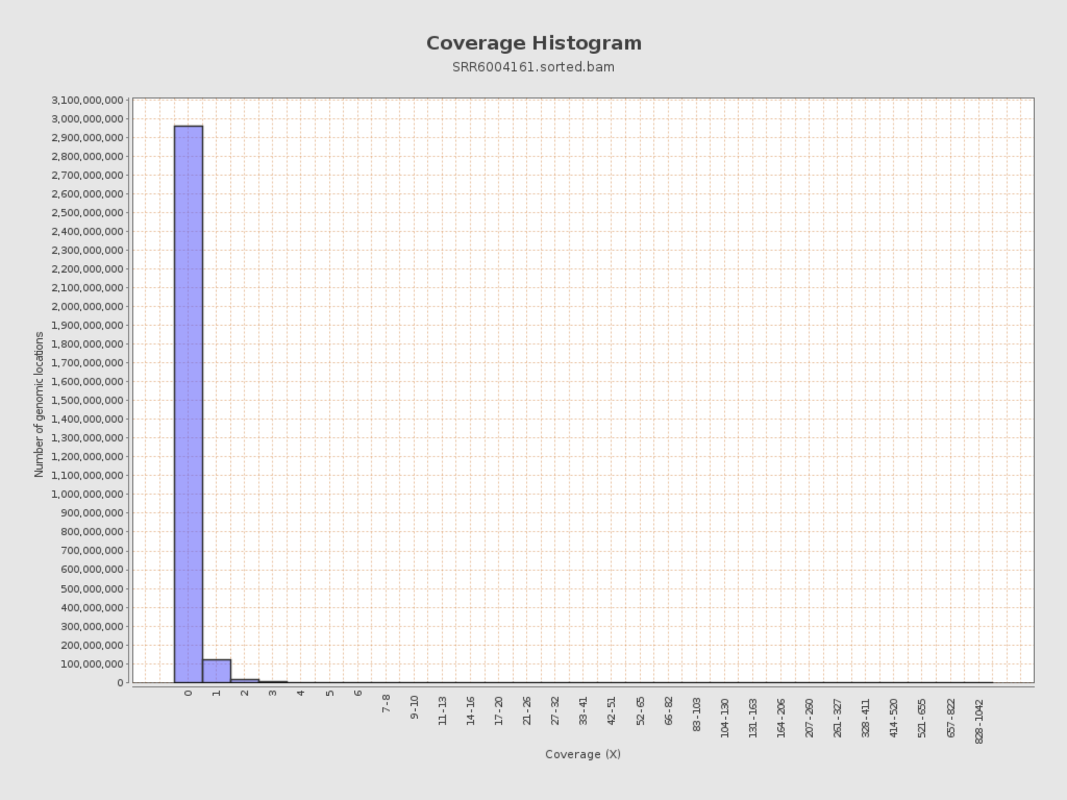
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15072771	0.0605	0.9143
chr2	243199373	12728657	0.0523	0.542
chr3	198022430	9311716	0.047	0.2575
chr4	191154276	8953328	0.0468	0.2868
chr5	180915260	11890884	0.0657	0.2933
chr6	171115067	9380466	0.0548	0.3125
chr7	159138663	7566445	0.0475	0.532

chr8	146364022	3787664	0.0259	0.4062
chr9	141213431	7203499	0.051	0.451
chr10	135534747	8856867	0.0653	0.59
chr11	135006516	5676724	0.042	0.3565
chr12	133851895	8530090	0.0637	0.2954
chr13	115169878	5840489	0.0507	0.2544
chr14	107349540	5481827	0.0511	0.2921
chr15	102531392	4908773	0.0479	0.25
chr16	90354753	3252231	0.036	0.304
chr17	81195210	3883168	0.0478	0.2667
chr18	78077248	5303300	0.0679	0.9364
chr19	59128983	2946420	0.0498	0.5948
chr20	63025520	2921826	0.0464	0.2609
chr21	48129895	2005007	0.0417	0.2802
chr22	51304566	2083157	0.0406	0.2296
chrMT	16571	39290	2.371	1.9887
chrX	155270560	11718236	0.0755	0.3511
chrY	59373566	535893	0.009	0.2168

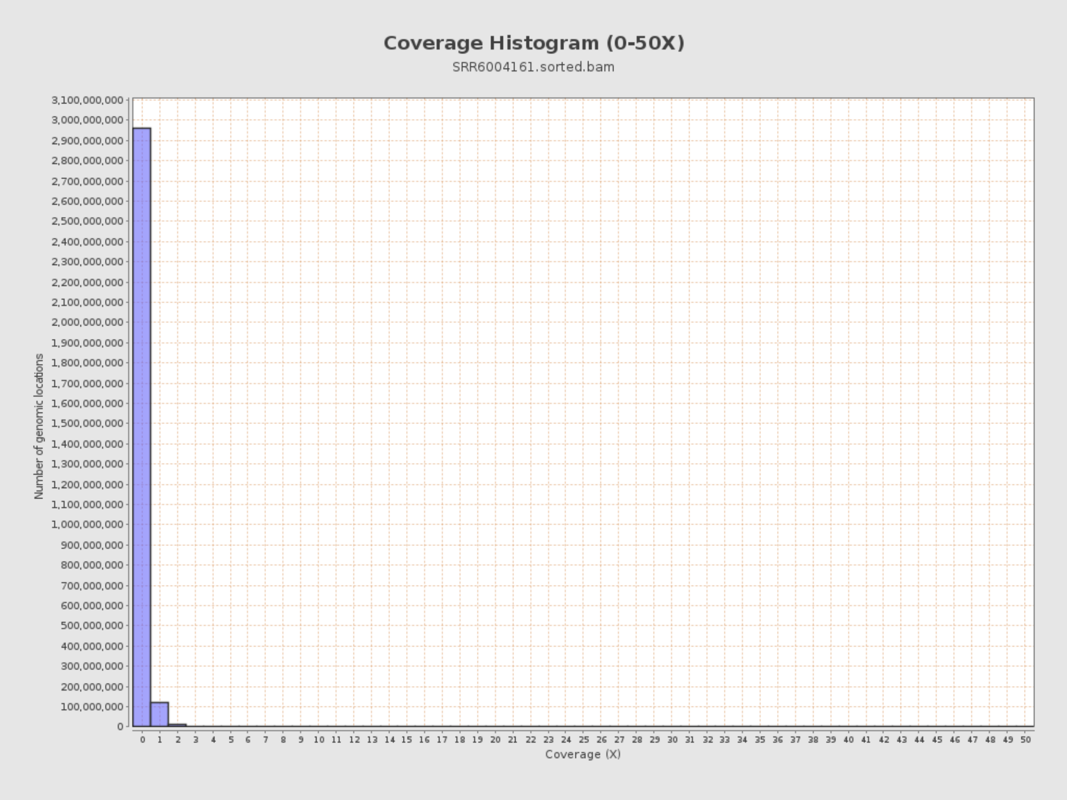
3. Results : Coverage across reference



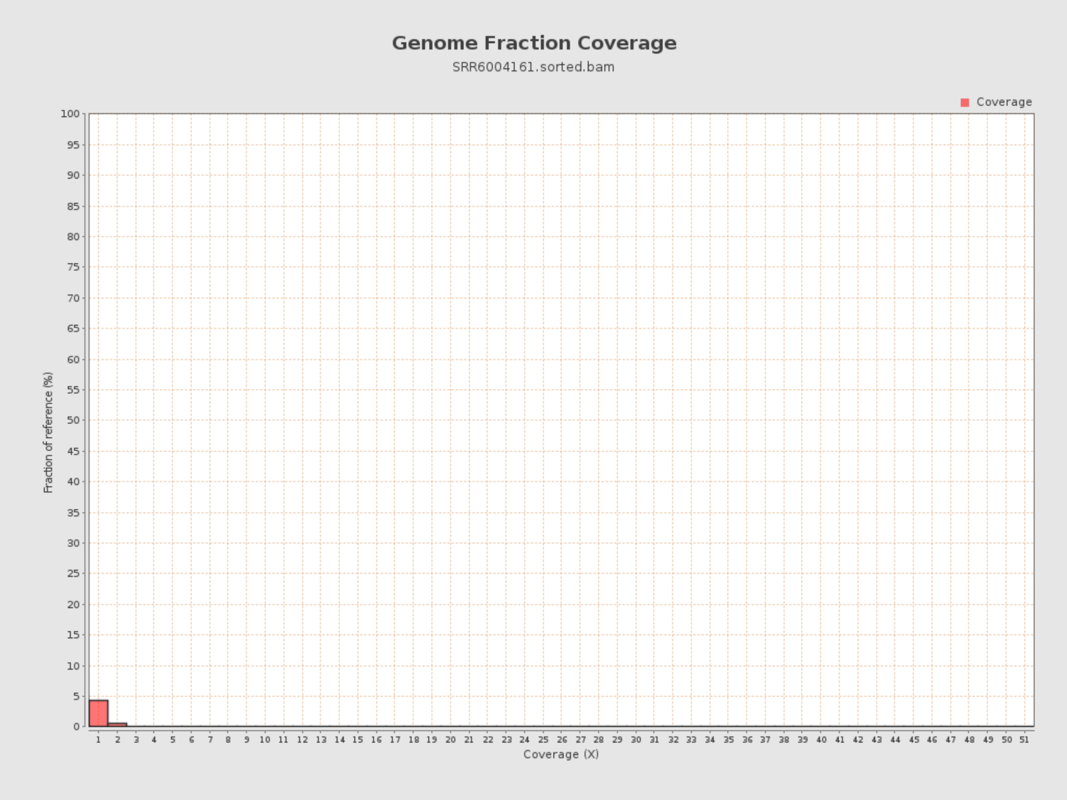
4. Results : Coverage Histogram



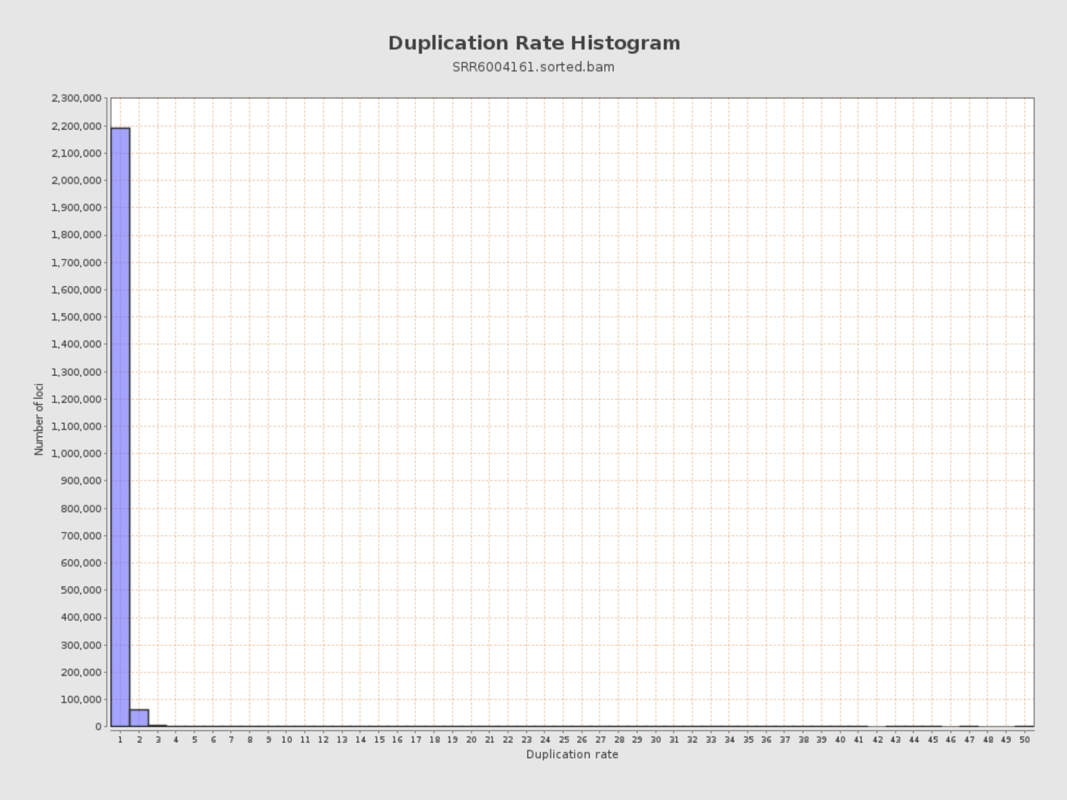
5. Results : Coverage Histogram (0-50X)



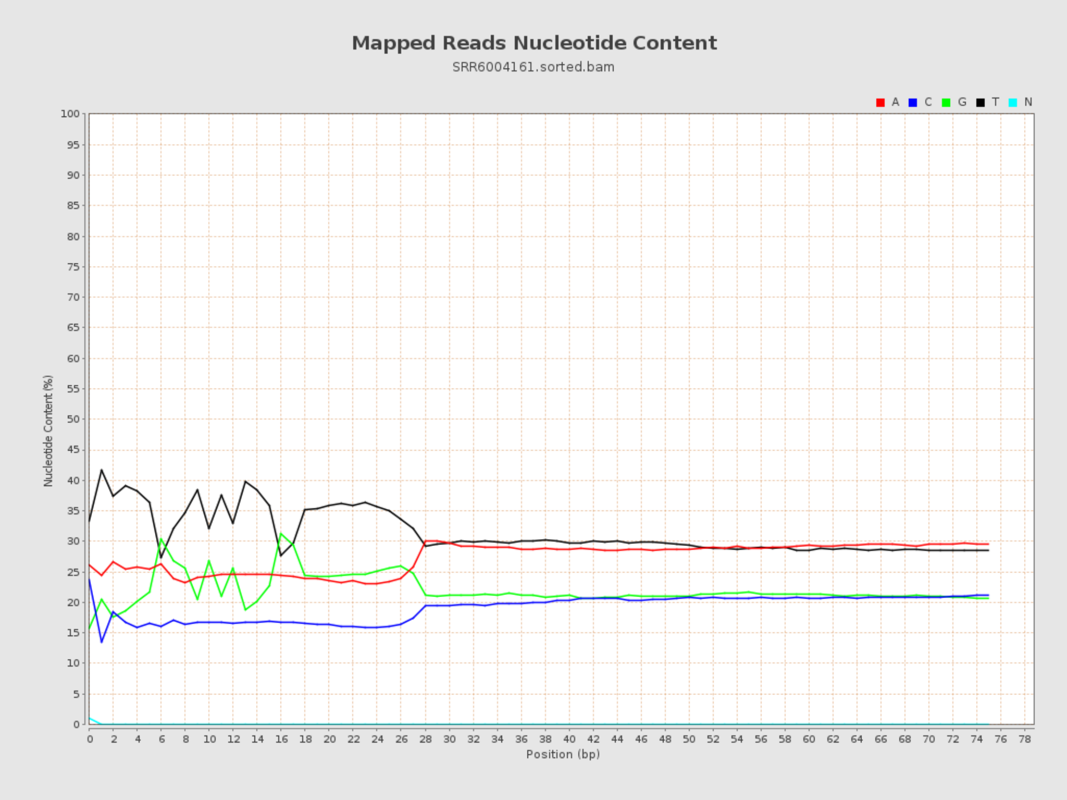
6. Results : Genome Fraction Coverage



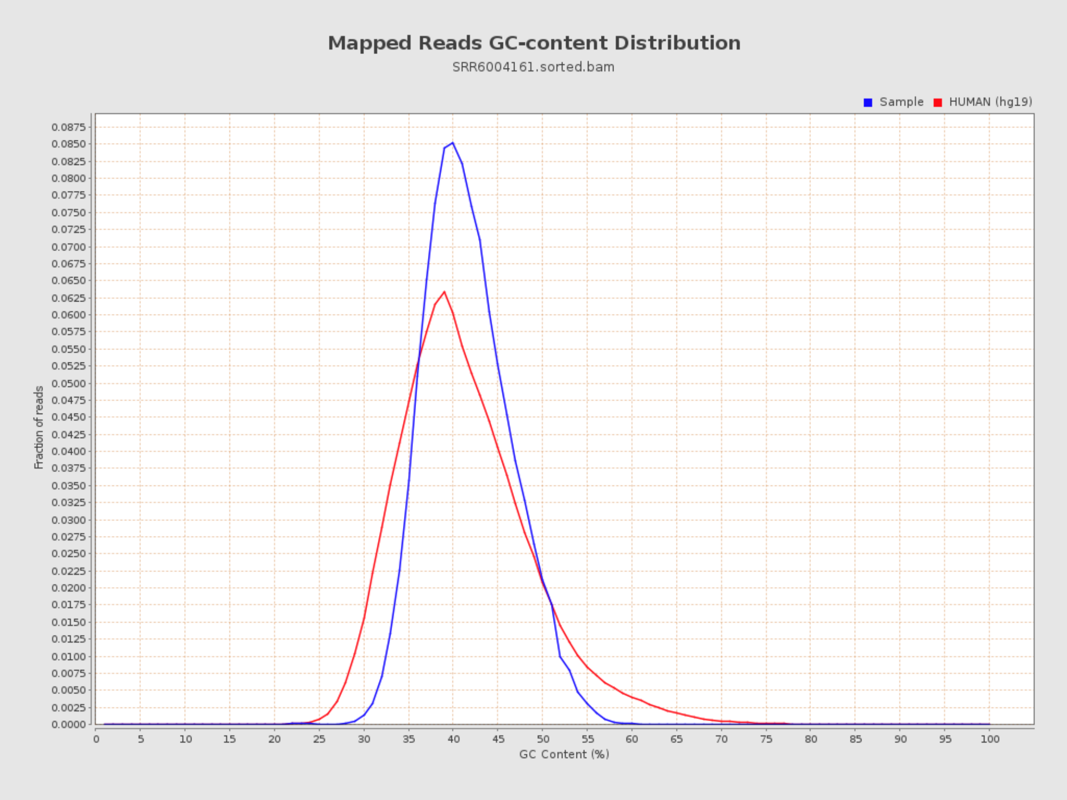
7. Results : Duplication Rate Histogram



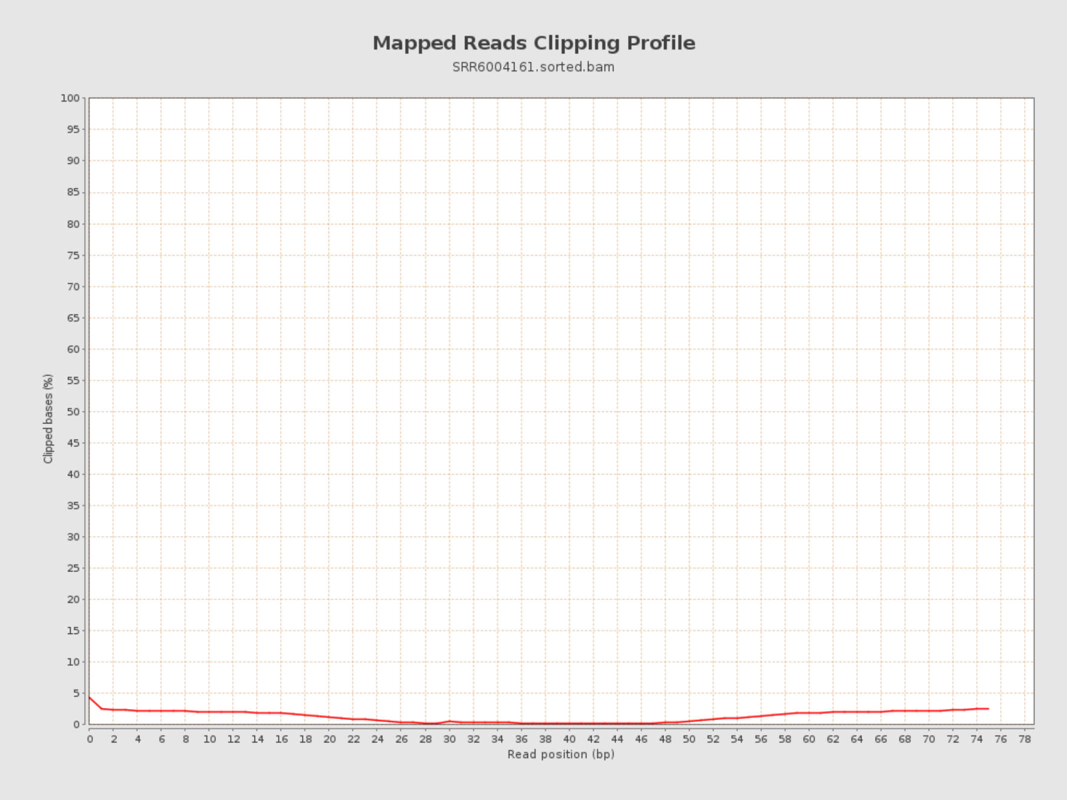
8. Results : Mapped Reads Nucleotide Content



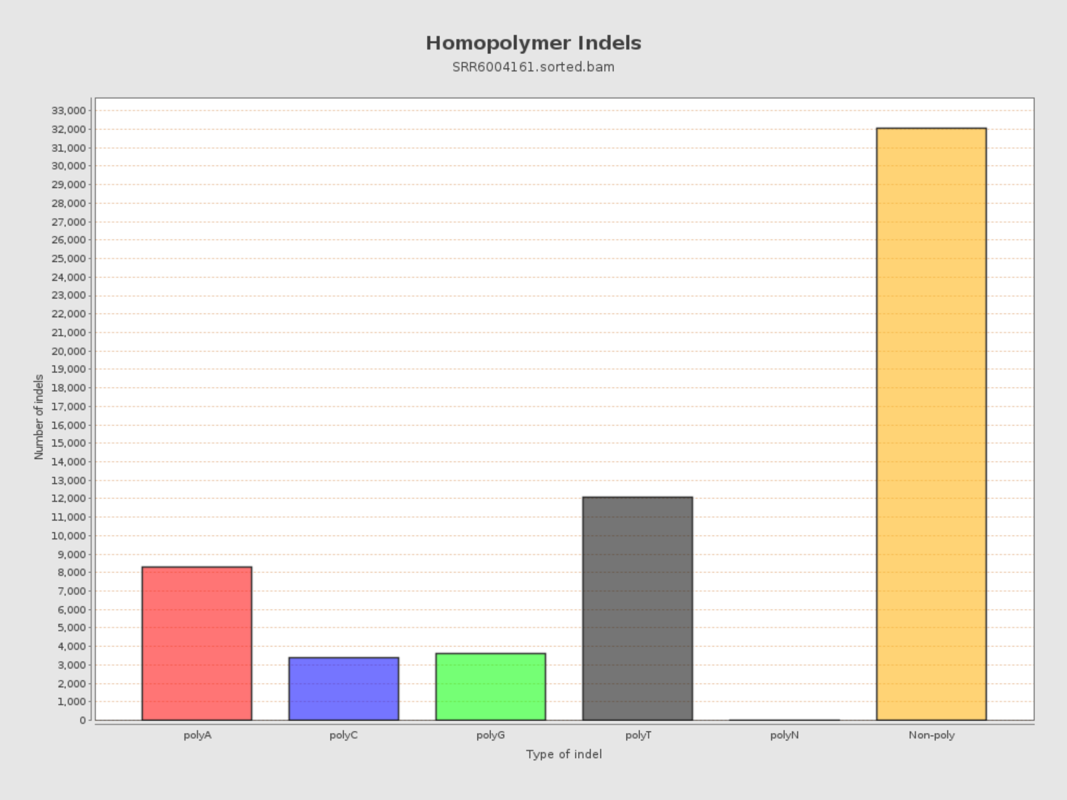
9. Results : Mapped Reads GC-content Distribution



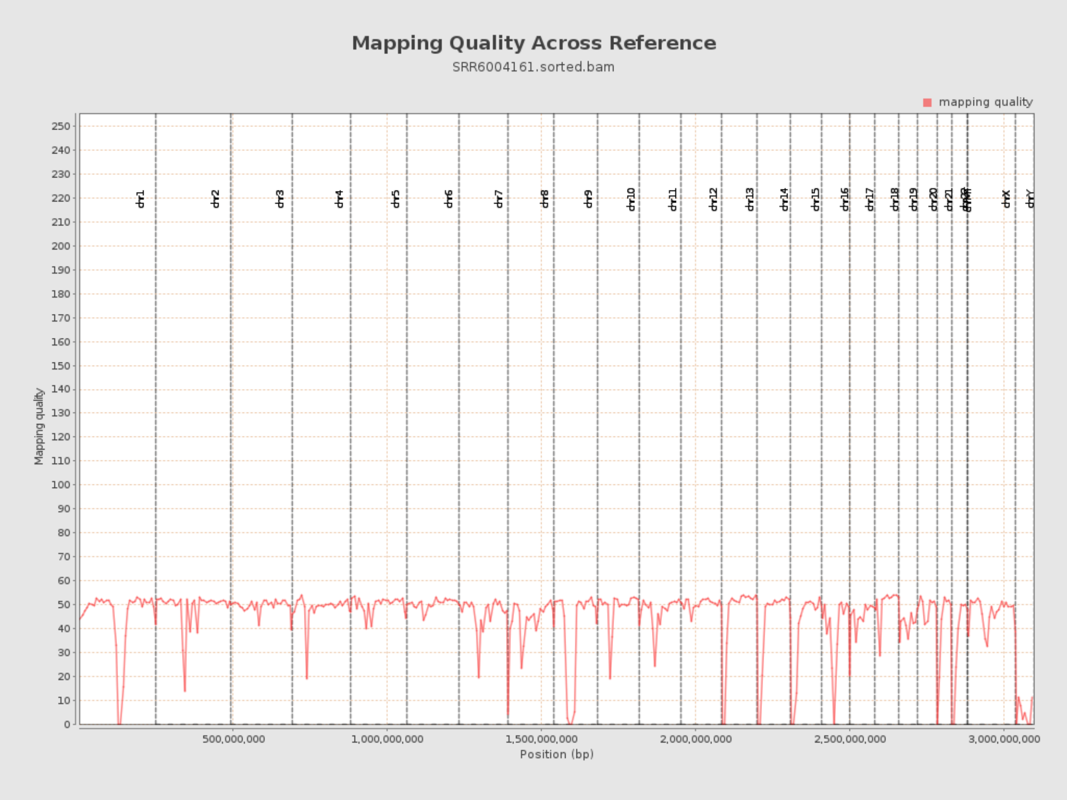
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram