Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 09:01:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240261.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_SRR6240261 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240261.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 09:01:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240261.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,679,679
Mapped reads	1,389,662 / 82.73%
Unmapped reads	290,017 / 17.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,746 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	59,923 / 3.57%
Duplication rate	3.43%
Clipped reads	890,708 / 53.03%

2.2. ACGT Content

Number/percentage of A's	23,296,454 / 27.04%
Number/percentage of C's	14,905,713 / 17.3%
Number/percentage of T's	27,408,952 / 31.81%
Number/percentage of G's	20,536,679 / 23.83%
Number/percentage of N's	19,877 / 0.02%
GC Percentage	41.13%

2.3. Coverage

Mean	0.0278

Standard Deviation	0.2786

2.4. Mapping Quality

Mean Mapping Quality	43.4

2.5. Mismatches and indels

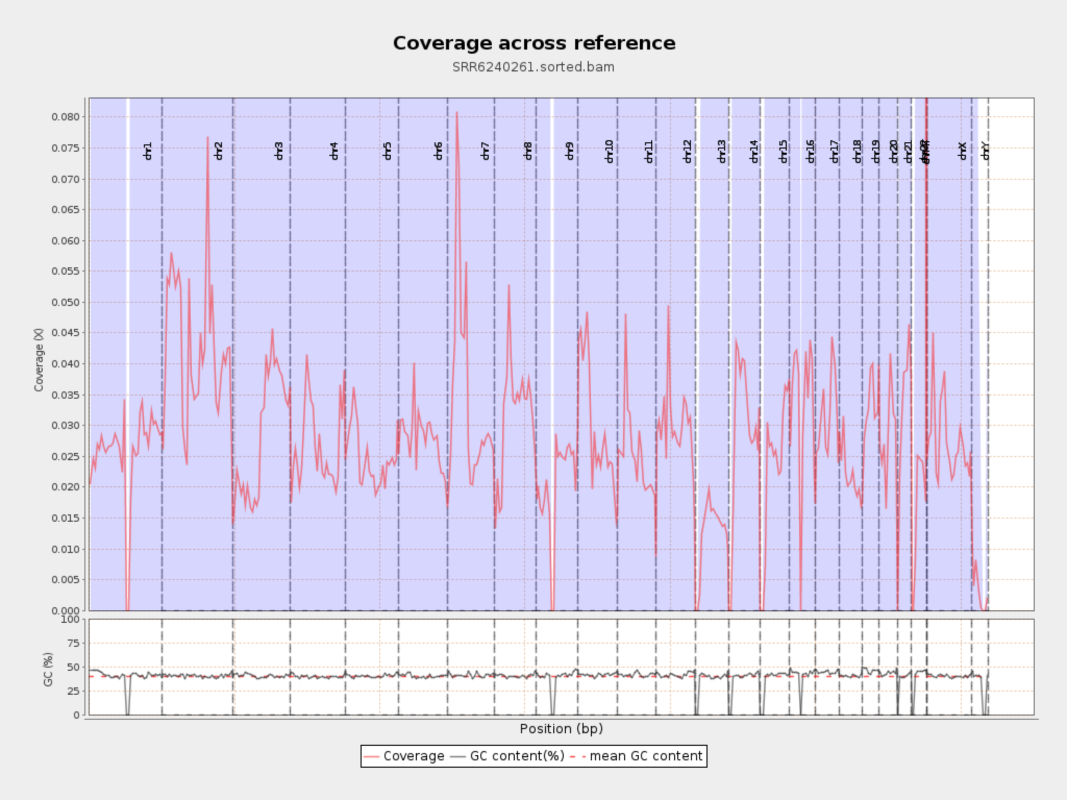
General error rate	0.96%
Mismatches	817,402
Insertions	6,364
Mapped reads with at least one insertion	0.46%
Deletions	27,589
Mapped reads with at least one deletion	1.96%
Homopolymer indels	49.21%

2.6. Chromosome stats

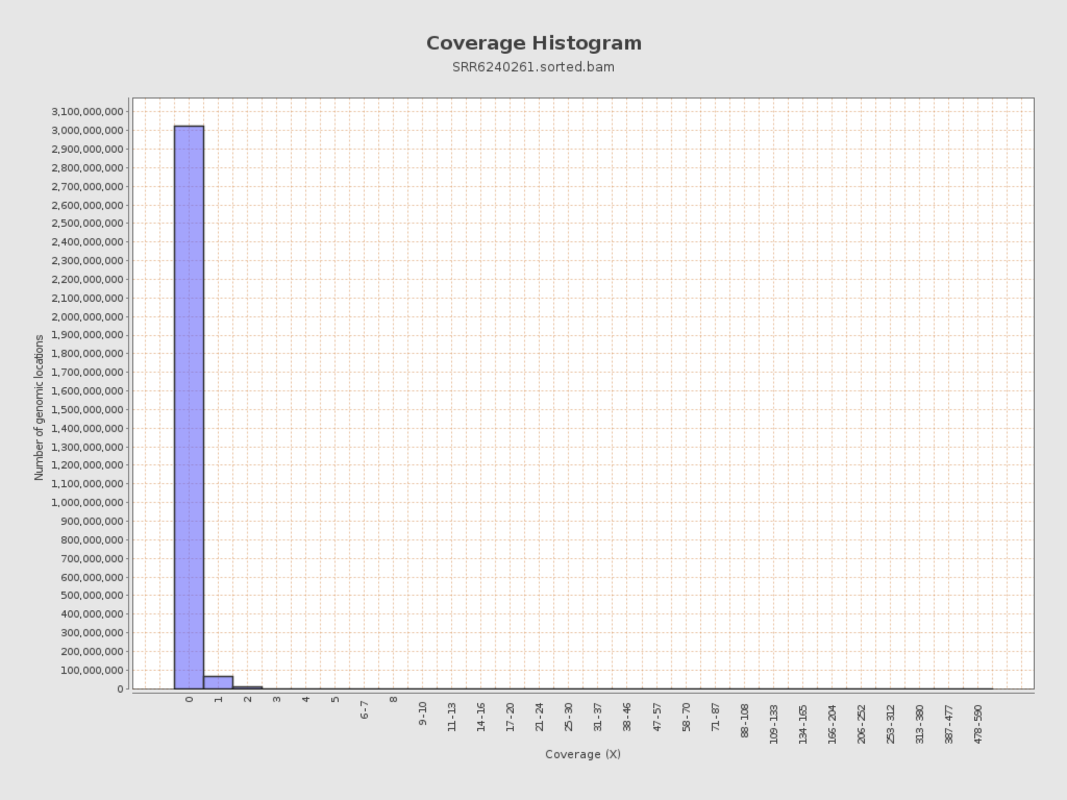
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6384402	0.0256	0.3848
chr2	243199373	10417269	0.0428	0.3612
chr3	198022430	5621765	0.0284	0.1915
chr4	191154276	5118574	0.0268	0.1946
chr5	180915260	4481672	0.0248	0.1804
chr6	171115067	4758206	0.0278	0.2359
chr7	159138663	5572730	0.035	0.5591

chr8	146364022	4653123	0.0318	0.3499
chr9	141213431	2832459	0.0201	0.2312
chr10	135534747	4125224	0.0304	0.233
chr11	135006516	3410405	0.0253	0.2295
chr12	133851895	4062431	0.0304	0.199
chr13	115169878	1448863	0.0126	0.1289
chr14	107349540	3090404	0.0288	0.2032
chr15	102531392	2368950	0.0231	0.1974
chr16	90354753	3001897	0.0332	0.2148
chr17	81195210	2563151	0.0316	0.2153
chr18	78077248	1734156	0.0222	0.3656
chr19	59128983	1945980	0.0329	0.2934
chr20	63025520	1769563	0.0281	0.1949
chr21	48129895	1556808	0.0323	0.2114
chr22	51304566	828365	0.0161	0.1406
chrMT	16571	25920	1.5642	1.7634
chrX	155270560	4260478	0.0274	0.2093
chrY	59373566	182221	0.0031	0.07

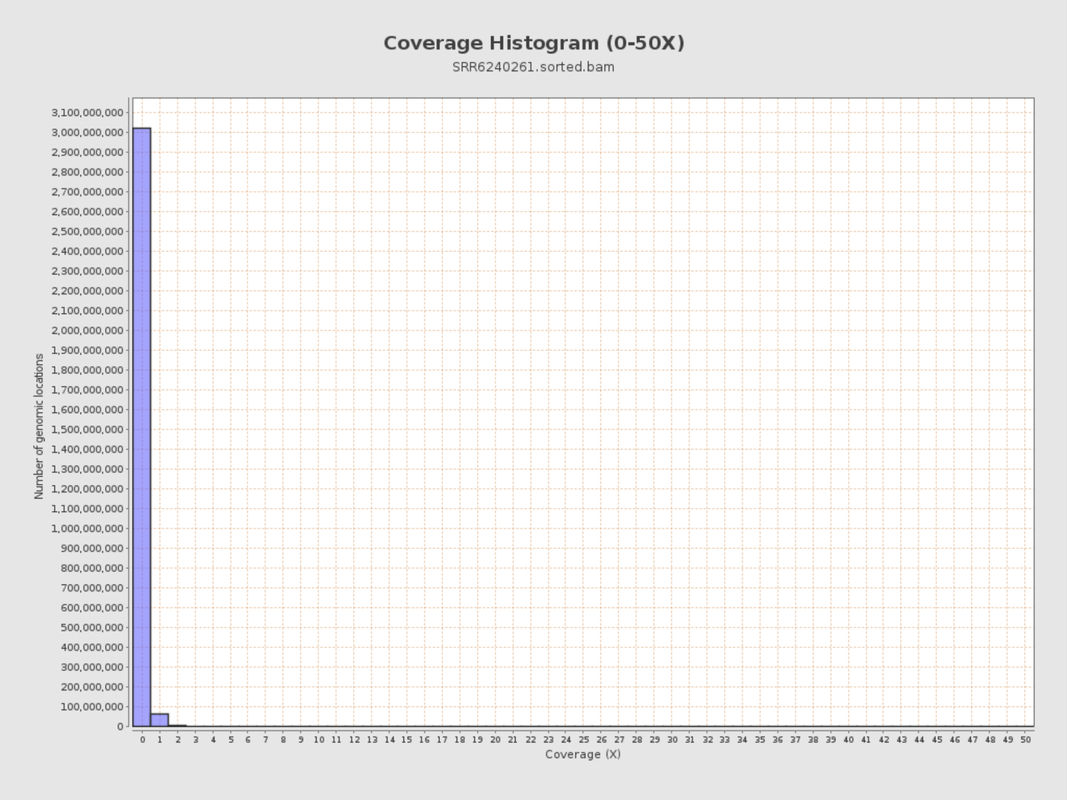
3. Results : Coverage across reference



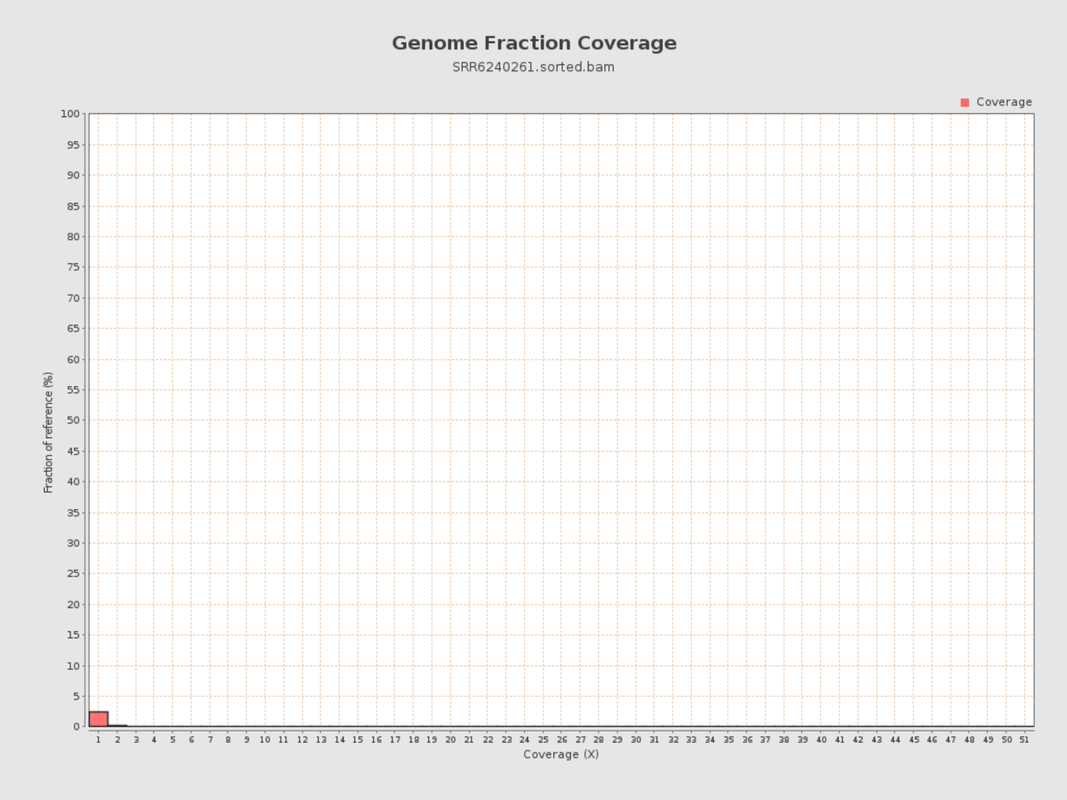
4. Results : Coverage Histogram



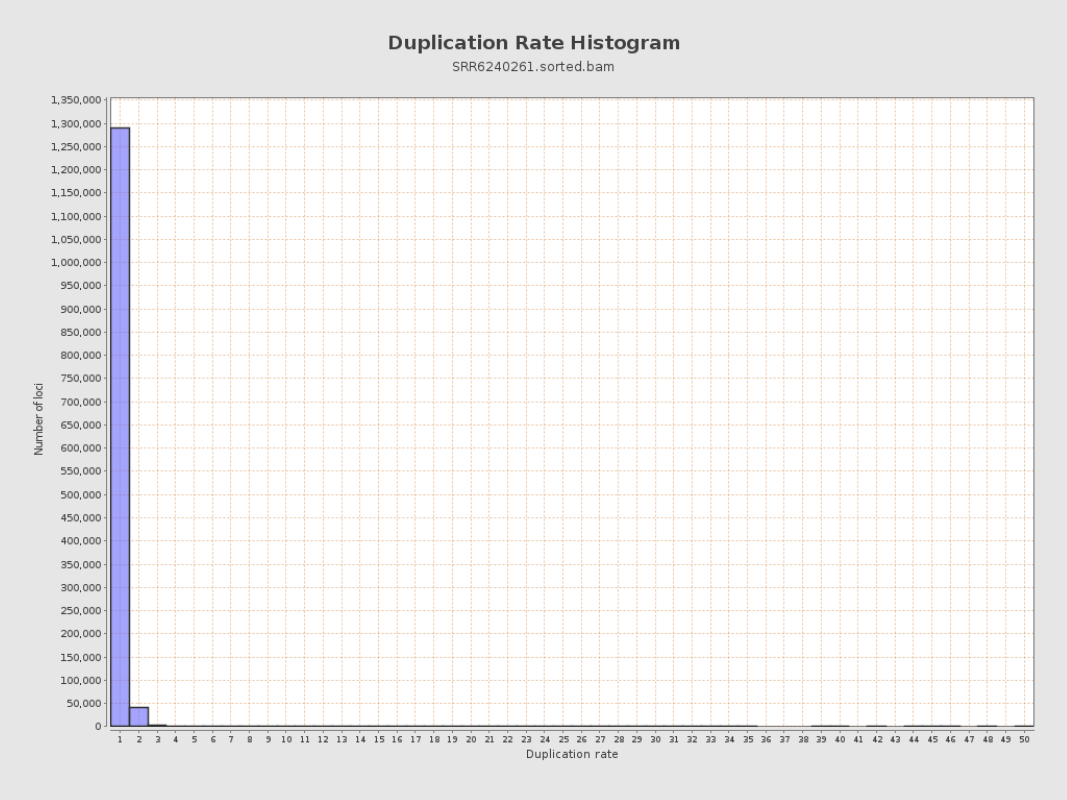
5. Results : Coverage Histogram (0-50X)



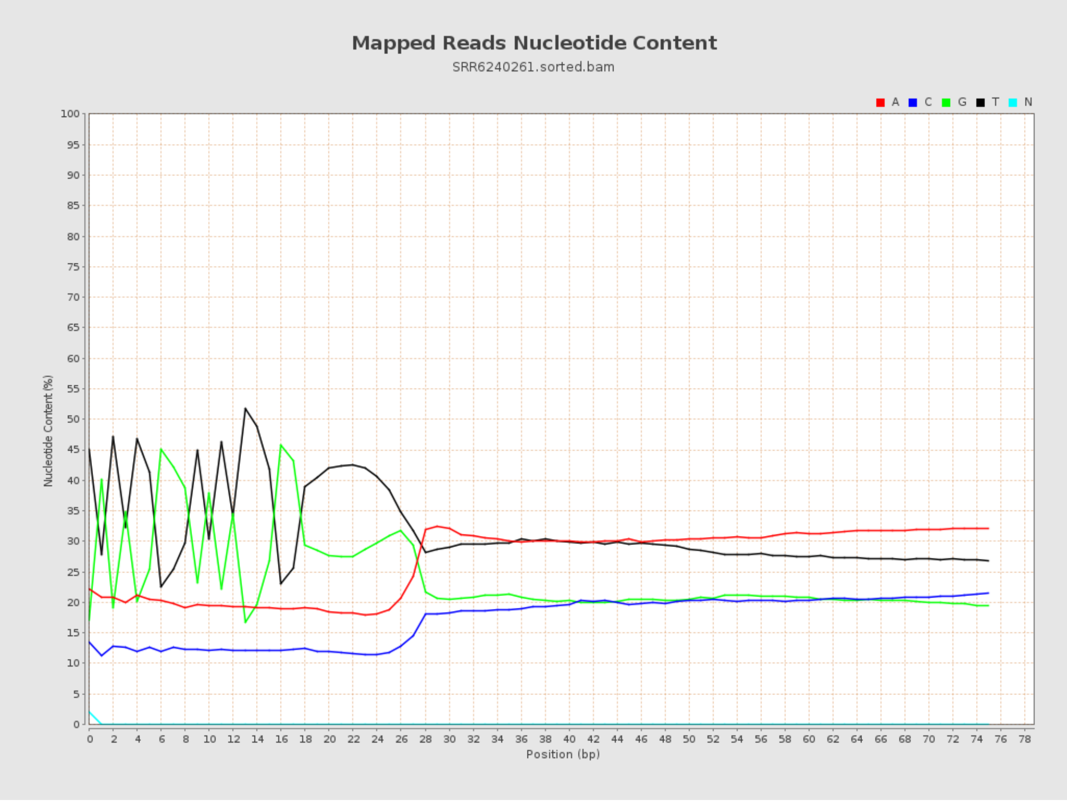
6. Results : Genome Fraction Coverage



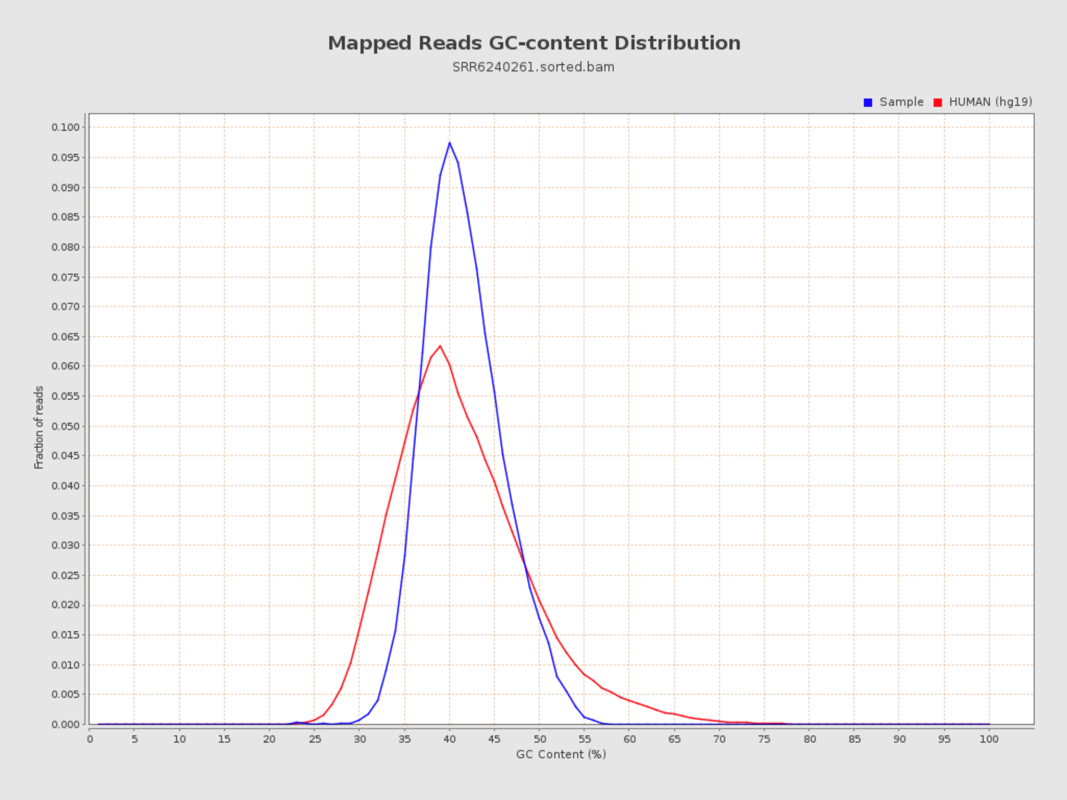
7. Results : Duplication Rate Histogram



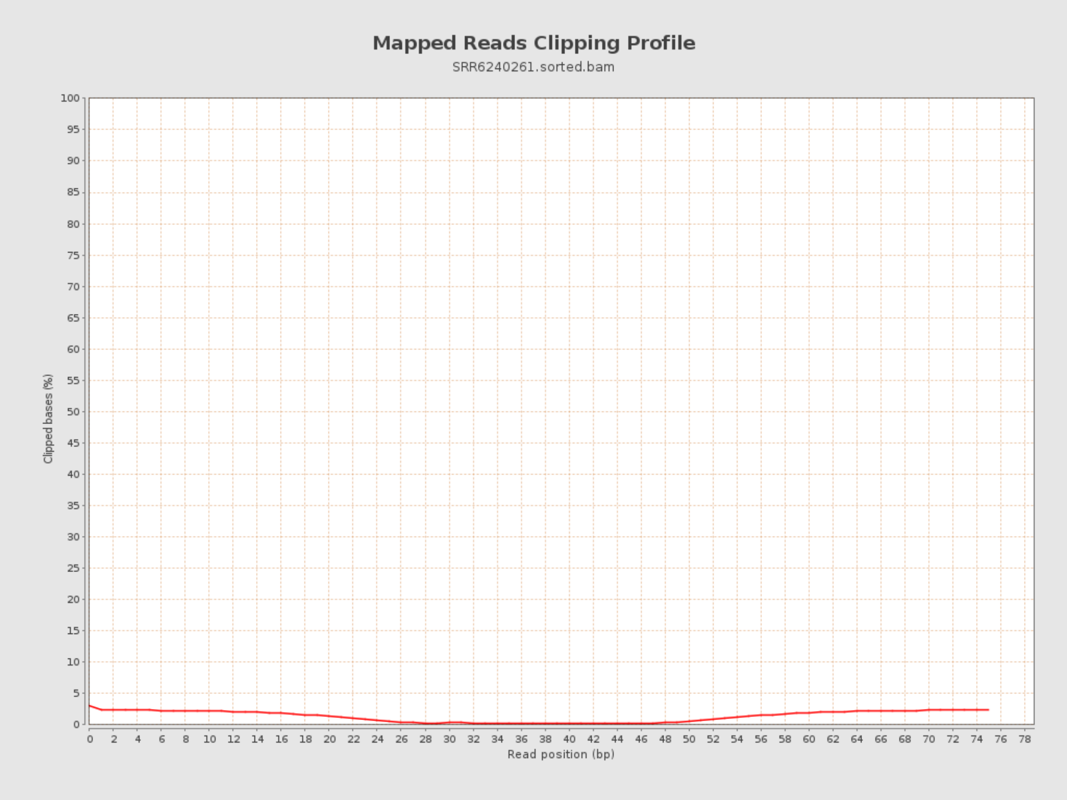
8. Results : Mapped Reads Nucleotide Content



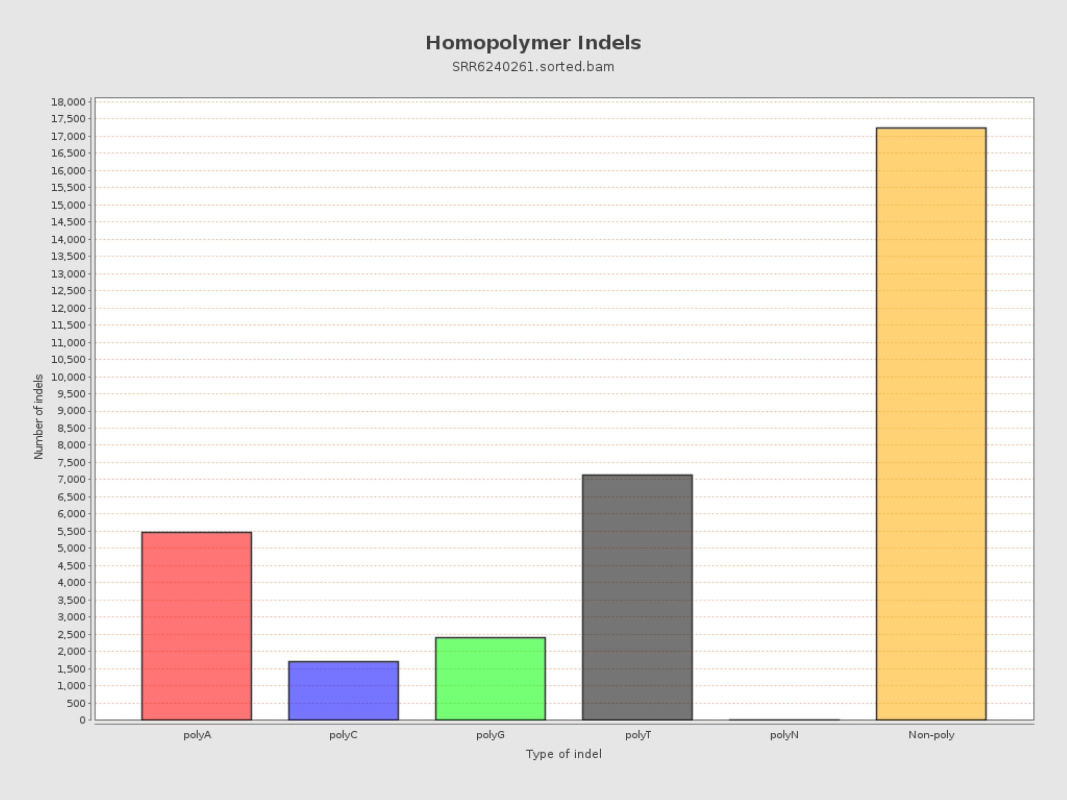
9. Results : Mapped Reads GC-content Distribution



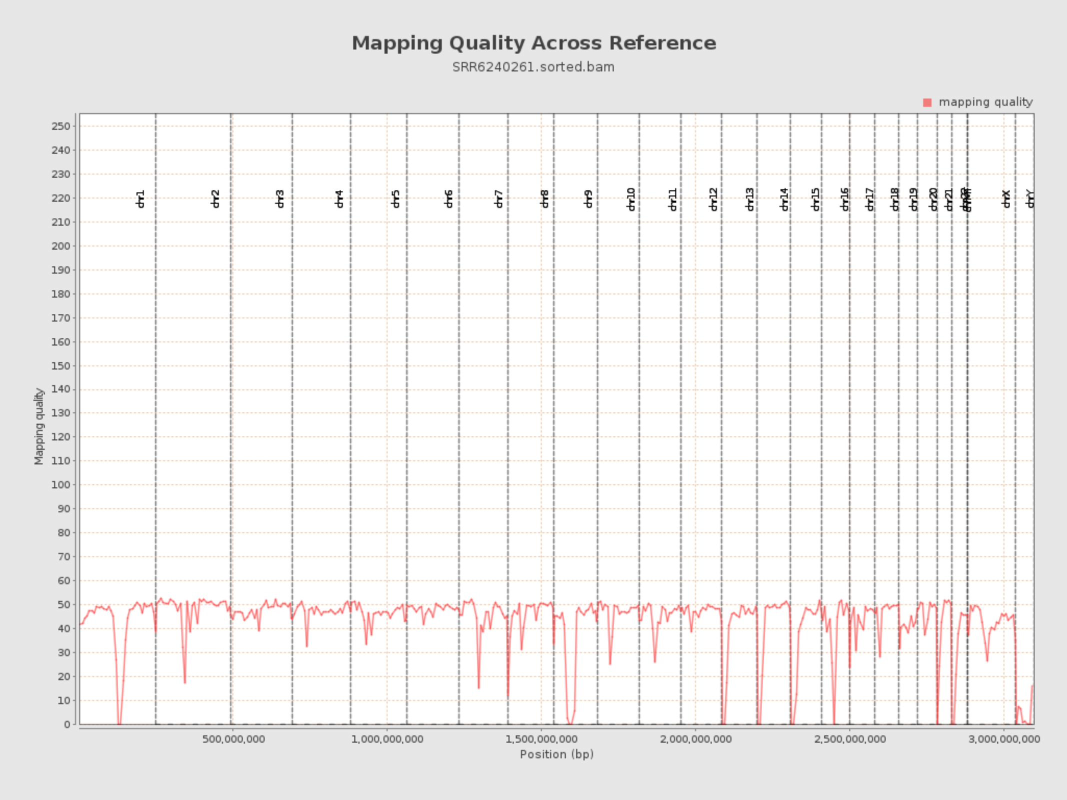
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram