Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:32:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240249.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_SRR6240249 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240249.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:32:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240249.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,274,593
Mapped reads	2,755,936 / 84.16%
Unmapped reads	518,657 / 15.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,520 / 0.96%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	433,445 / 13.24%
Duplication rate	10.66%
Clipped reads	1,217,800 / 37.19%

2.2. ACGT Content

Number/percentage of A's	53,435,544 / 28.8%
Number/percentage of C's	34,485,909 / 18.59%
Number/percentage of T's	58,777,890 / 31.68%
Number/percentage of G's	38,793,017 / 20.91%
Number/percentage of N's	18,190 / 0.01%
GC Percentage	39.5%

2.3. Coverage

Mean	0.0599

Standard Deviation	0.7795

2.4. Mapping Quality

Mean Mapping Quality	46.96

2.5. Mismatches and indels

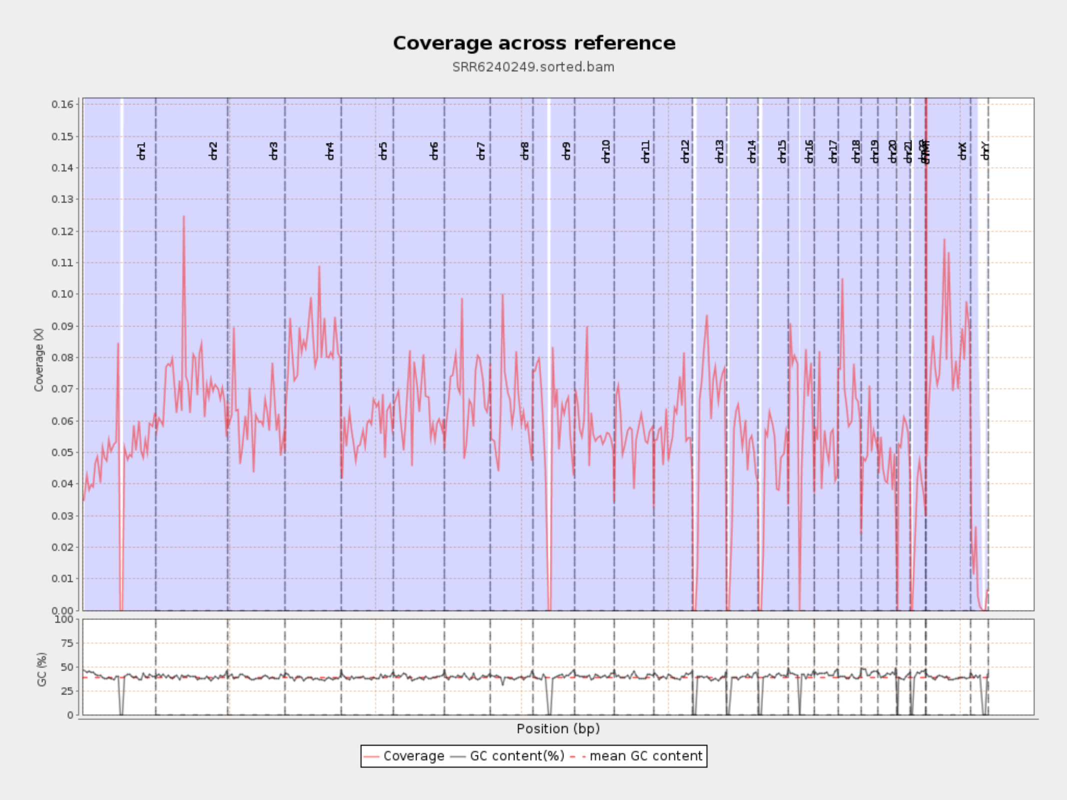
General error rate	0.79%
Mismatches	1,437,071
Insertions	13,618
Mapped reads with at least one insertion	0.49%
Deletions	39,353
Mapped reads with at least one deletion	1.41%
Homopolymer indels	48.05%

2.6. Chromosome stats

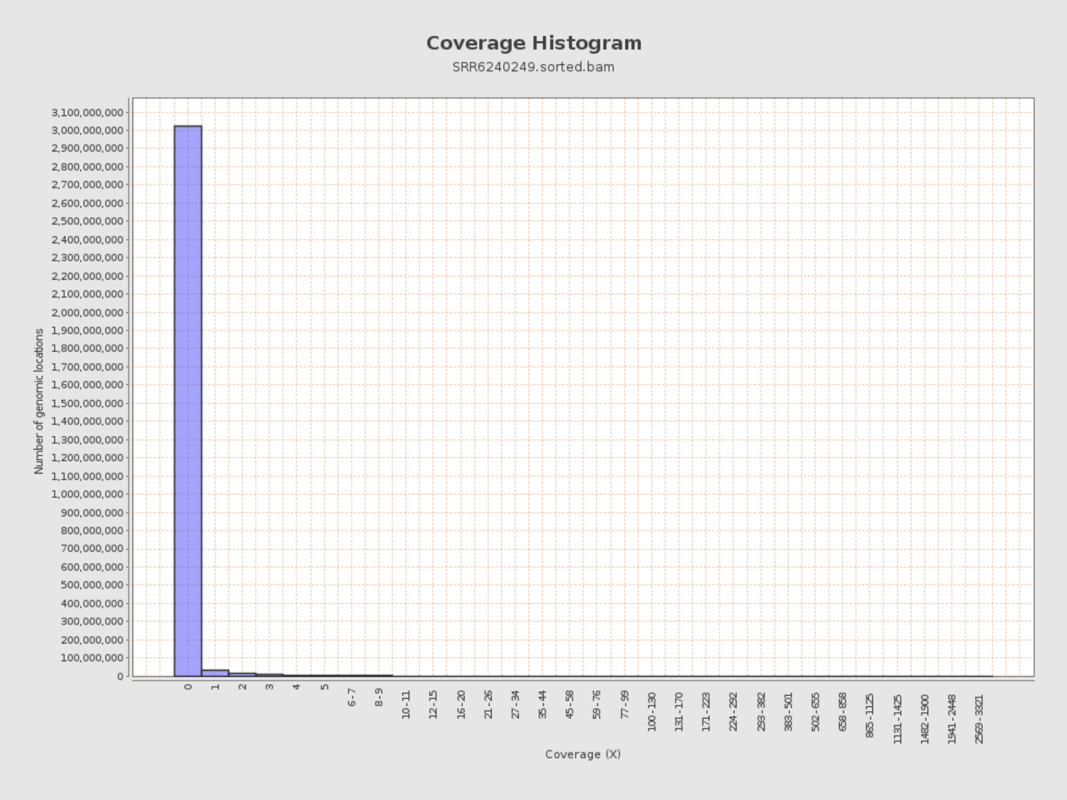
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11881461	0.0477	0.918
chr2	243199373	17468347	0.0718	0.764
chr3	198022430	12053502	0.0609	0.5064
chr4	191154276	16018770	0.0838	0.6167
chr5	180915260	10403192	0.0575	0.4962
chr6	171115067	11028789	0.0645	0.5726
chr7	159138663	10961095	0.0689	0.7568

chr8	146364022	9159858	0.0626	2.0131
chr9	141213431	8131902	0.0576	0.7322
chr10	135534747	7908357	0.0583	0.5794
chr11	135006516	7612523	0.0564	0.5886
chr12	133851895	7807890	0.0583	0.5062
chr13	115169878	7108376	0.0617	0.5185
chr14	107349540	4916007	0.0458	0.4918
chr15	102531392	4323919	0.0422	0.4112
chr16	90354753	5739267	0.0635	0.5519
chr17	81195210	4352421	0.0536	0.4949
chr18	78077248	5564364	0.0713	1.4861
chr19	59128983	3088917	0.0522	0.6902
chr20	63025520	2831315	0.0449	0.4629
chr21	48129895	2390387	0.0497	0.481
chr22	51304566	1479614	0.0288	0.3225
chrMT	16571	47255	2.8517	3.5885
chrX	155270560	12794848	0.0824	0.6346
chrY	59373566	506074	0.0085	0.2164

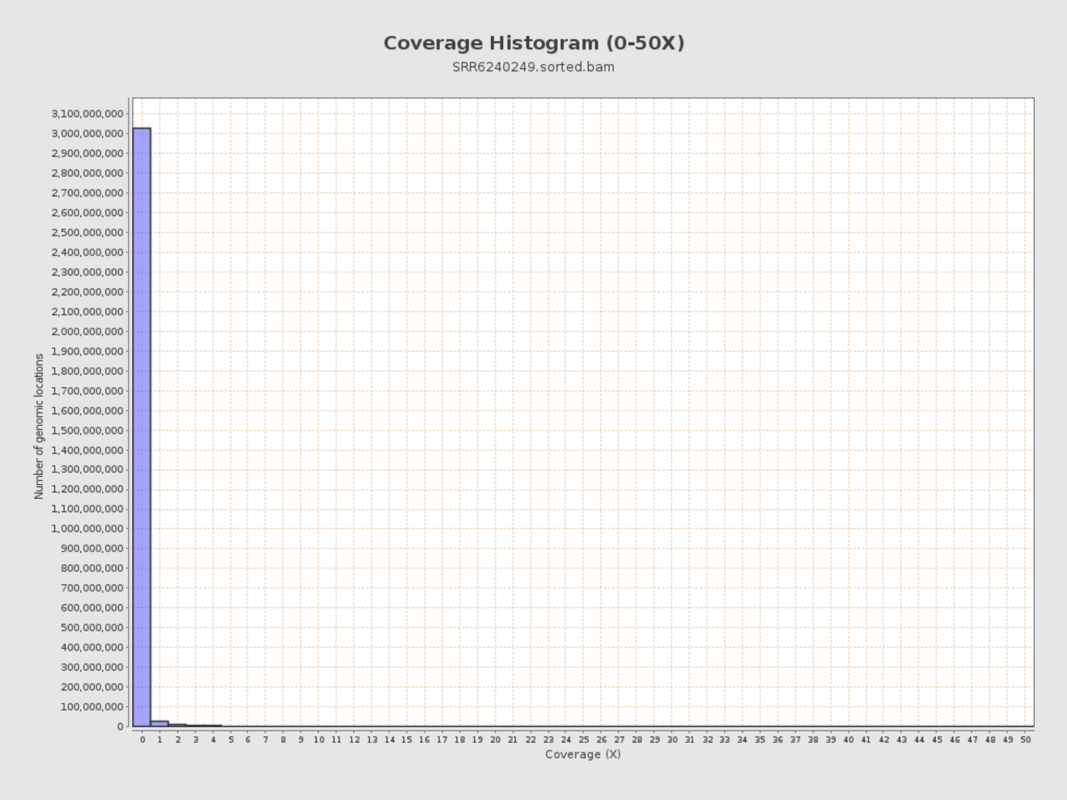
3. Results : Coverage across reference



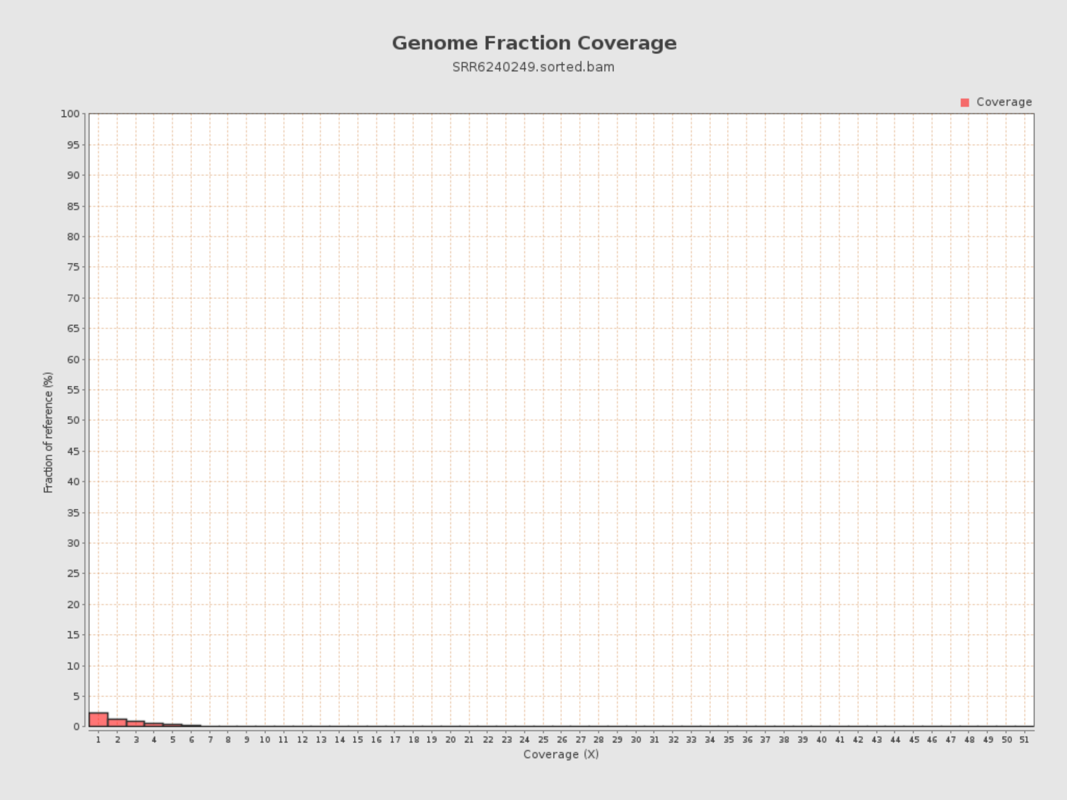
4. Results : Coverage Histogram



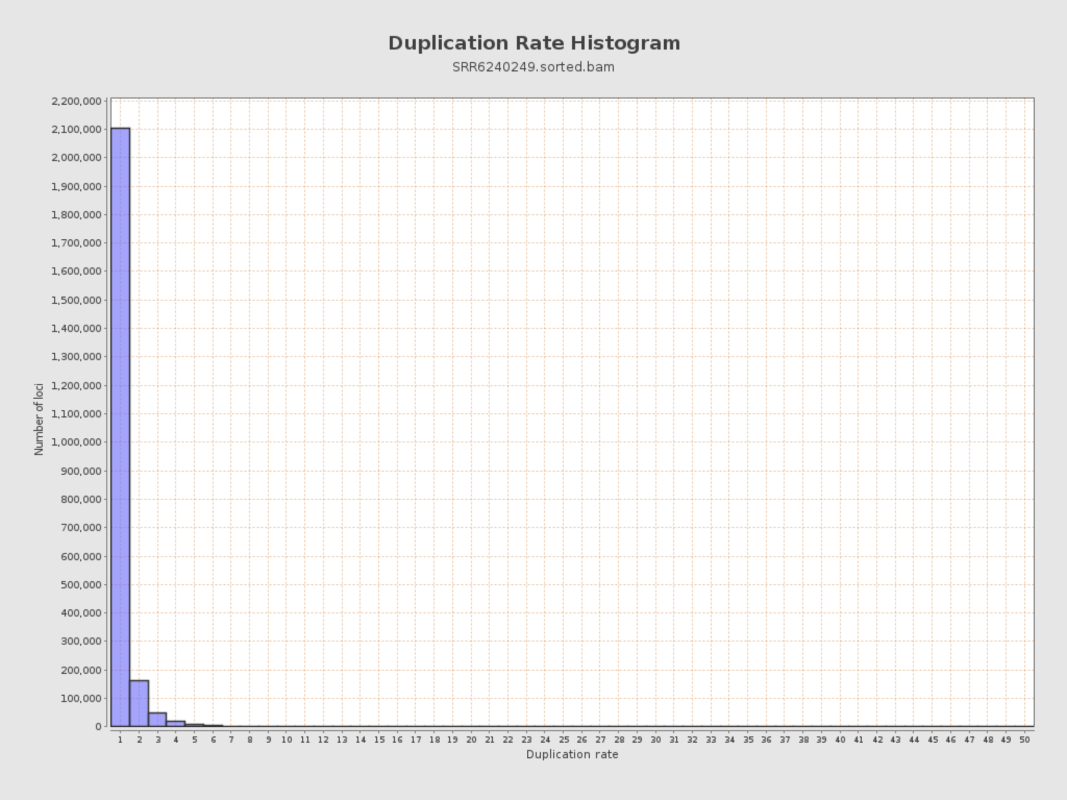
5. Results : Coverage Histogram (0-50X)



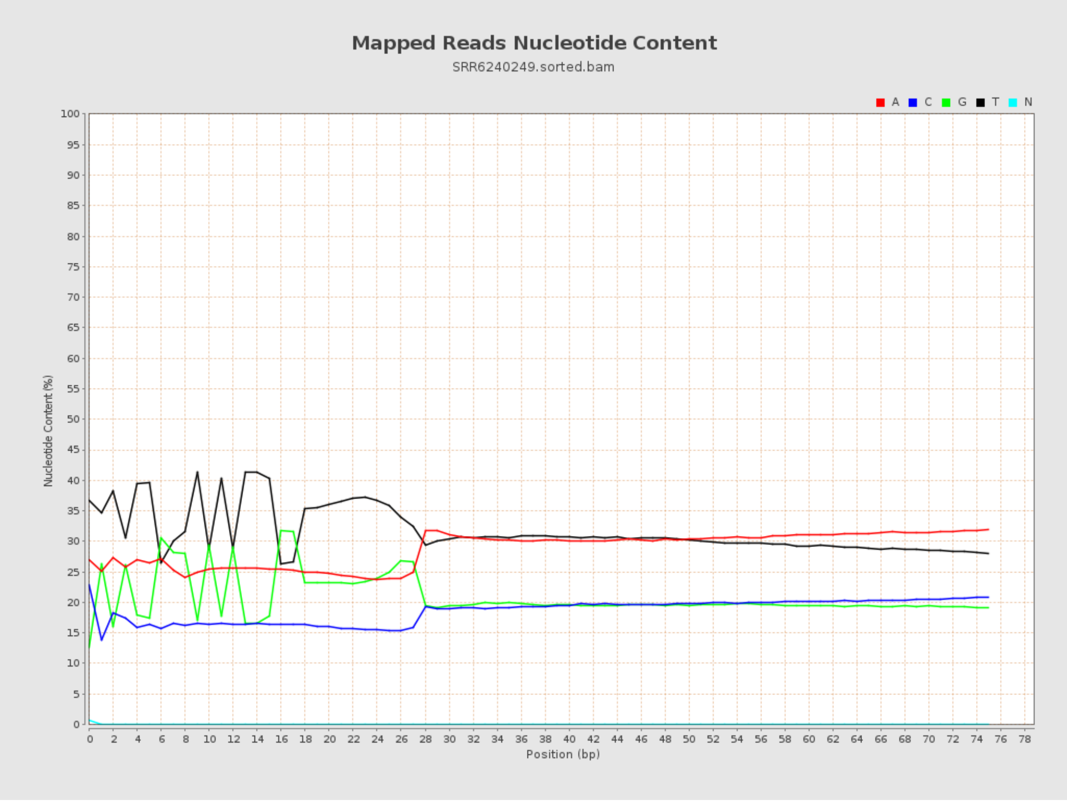
6. Results : Genome Fraction Coverage



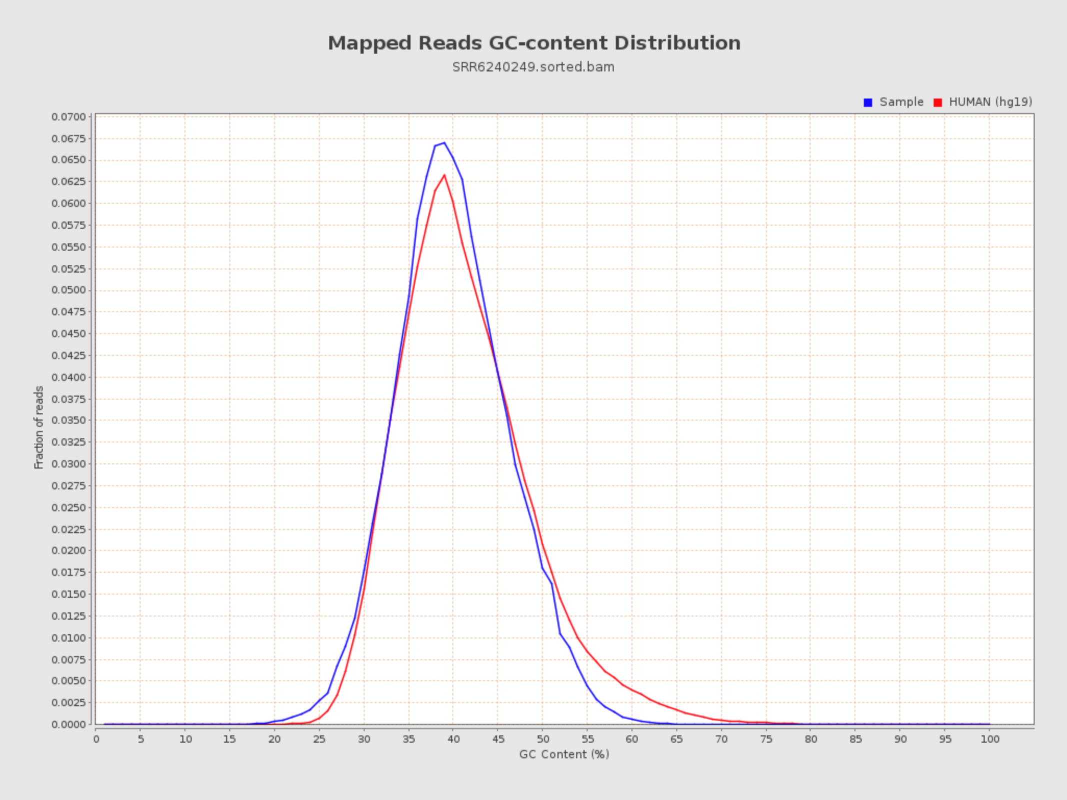
7. Results : Duplication Rate Histogram



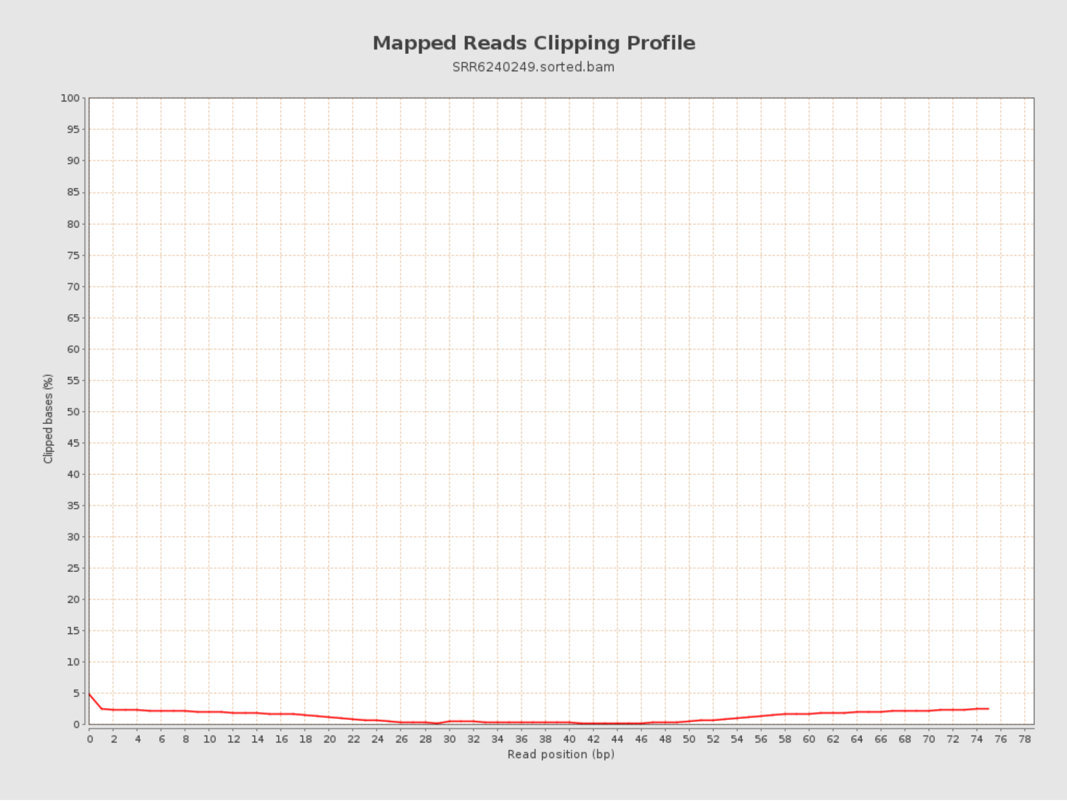
8. Results : Mapped Reads Nucleotide Content



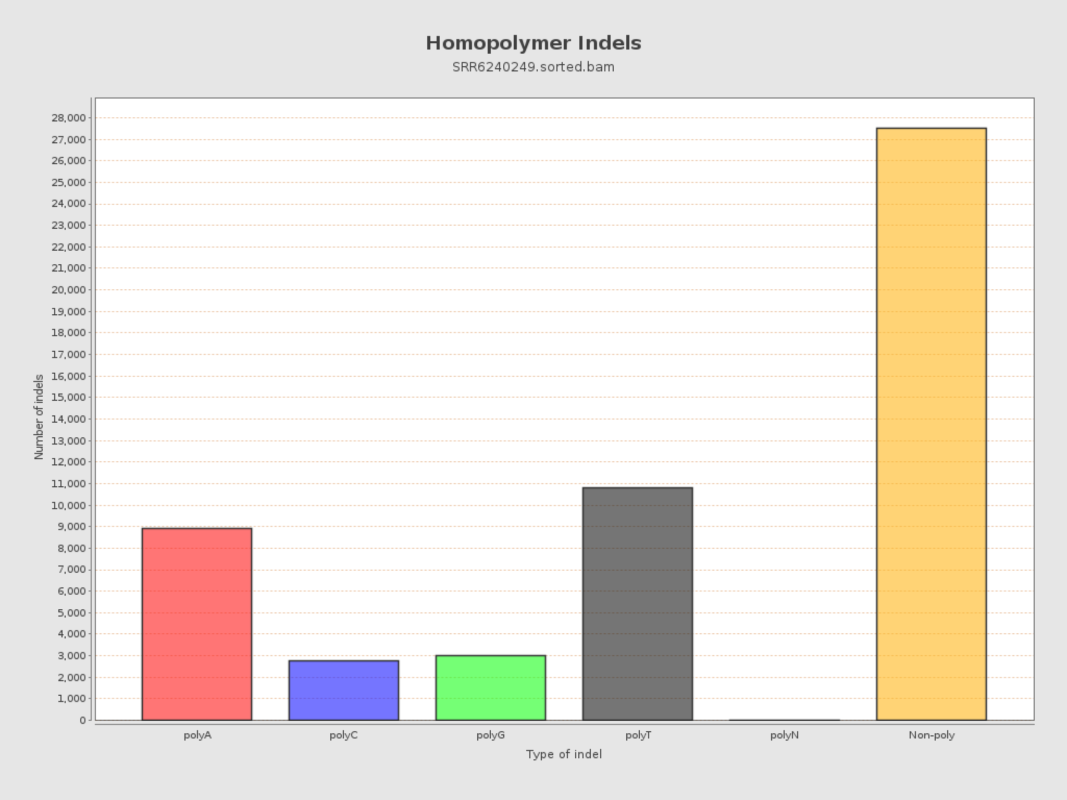
9. Results : Mapped Reads GC-content Distribution



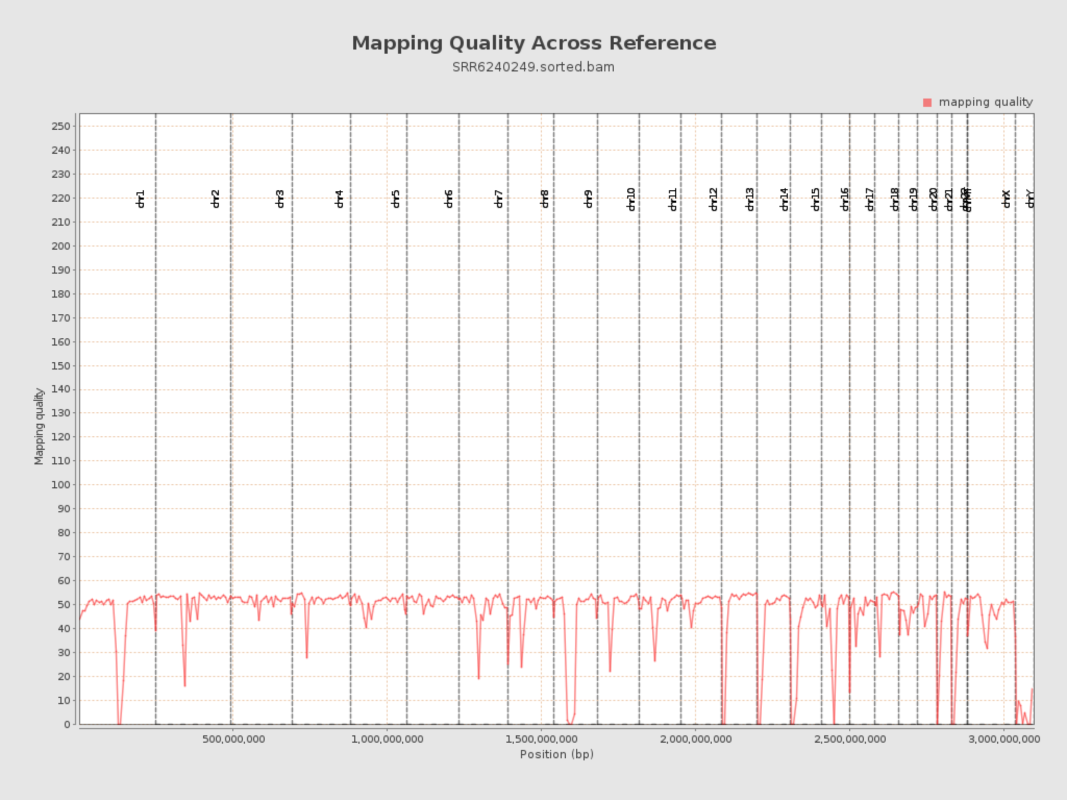
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram