Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 17:29:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234124.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_SRR6234124 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234124.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 17:29:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234124.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,299,814
Mapped reads	3,883,422 / 90.32%
Unmapped reads	416,392 / 9.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,755 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	1,114,177 / 25.91%
Duplication rate	11.83%
Clipped reads	1,290,484 / 30.01%

2.2. ACGT Content

Number/percentage of A's	64,319,337 / 23.89%
Number/percentage of C's	44,616,713 / 16.57%
Number/percentage of T's	68,801,190 / 25.55%
Number/percentage of G's	91,449,339 / 33.97%
Number/percentage of N's	57,906 / 0.02%
GC Percentage	50.54%

2.3. Coverage

Mean	0.087

Standard Deviation	84.5897

2.4. Mapping Quality

Mean Mapping Quality	37.2

2.5. Mismatches and indels

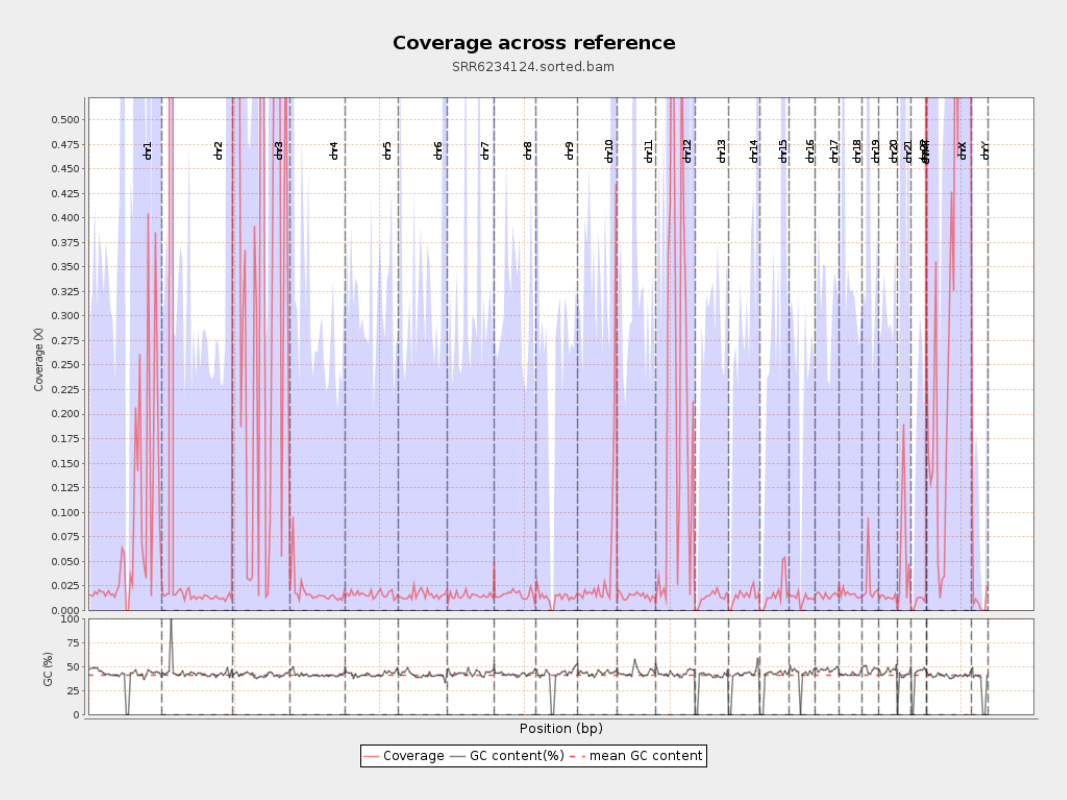
General error rate	0.51%
Mismatches	1,341,540
Insertions	14,120
Mapped reads with at least one insertion	0.36%
Deletions	45,615
Mapped reads with at least one deletion	1.16%
Homopolymer indels	48.35%

2.6. Chromosome stats

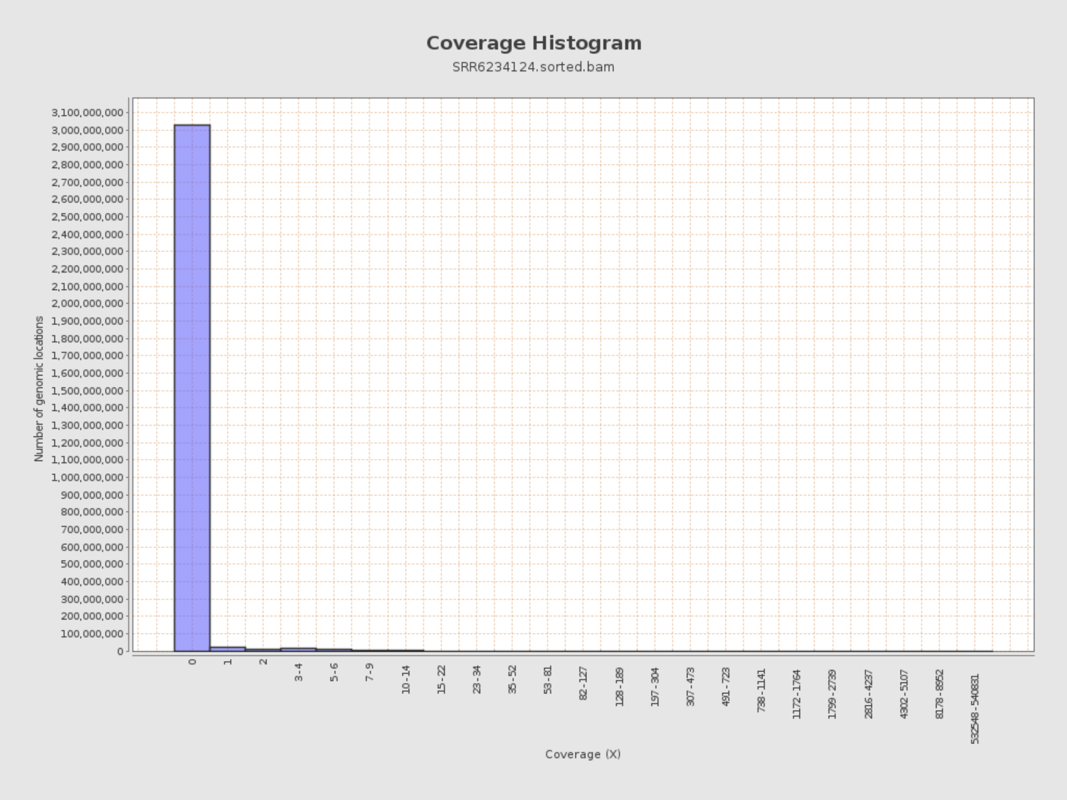
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19061849	0.0765	0.723
chr2	243199373	45379031	0.1866	301.786
chr3	198022430	72518941	0.3662	1.6227
chr4	191154276	3623040	0.019	0.3246
chr5	180915260	2957715	0.0163	0.3026
chr6	171115067	2677592	0.0156	0.4226
chr7	159138663	2359038	0.0148	0.3227

chr8	146364022	2347295	0.016	0.3039
chr9	141213431	1815849	0.0129	0.2635
chr10	135534747	6244089	0.0461	0.568
chr11	135006516	1988631	0.0147	0.4553
chr12	133851895	30392322	0.2271	1.2998
chr13	115169878	1502681	0.013	0.2666
chr14	107349540	1516296	0.0141	0.4226
chr15	102531392	1792183	0.0175	0.4445
chr16	90354753	1086844	0.012	0.2471
chr17	81195210	1219912	0.015	0.3038
chr18	78077248	1306376	0.0167	0.3723
chr19	59128983	1584137	0.0268	0.3985
chr20	63025520	850838	0.0135	0.2929
chr21	48129895	2874656	0.0597	0.6354
chr22	51304566	427784	0.0083	0.2037
chrMT	16571	85768	5.1758	5.2557
chrX	155270560	62749918	0.4041	1.6974
chrY	59373566	953642	0.0161	0.2601

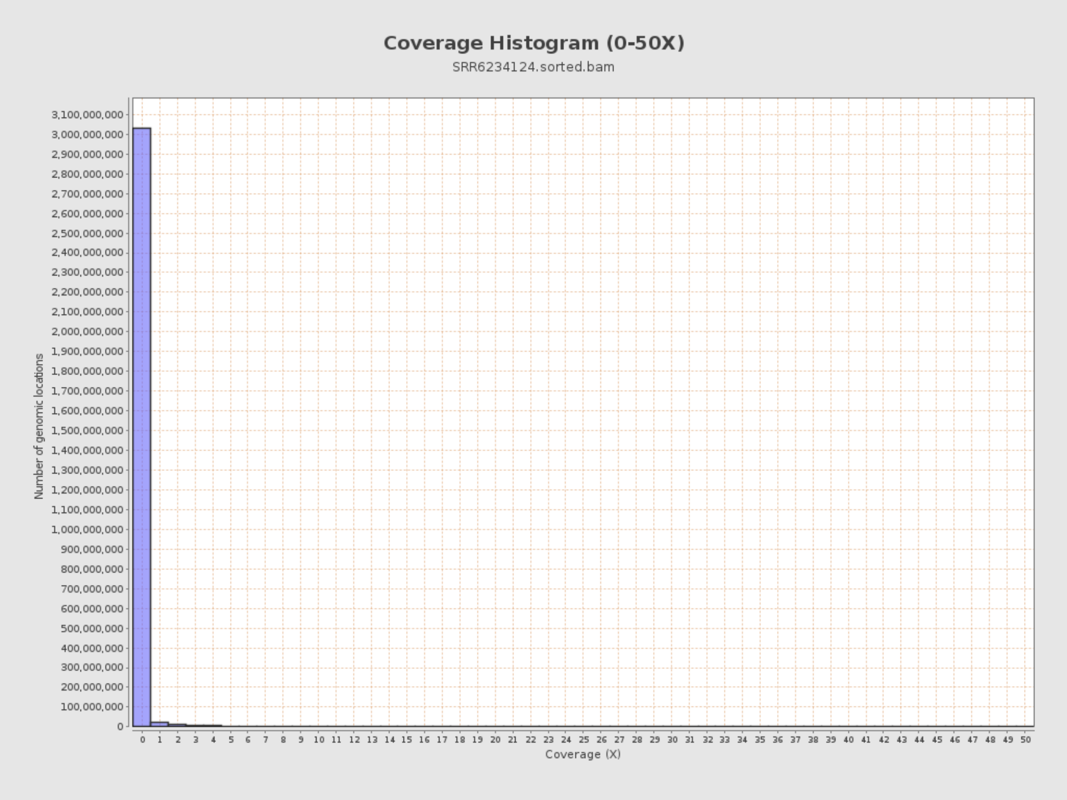
3. Results : Coverage across reference



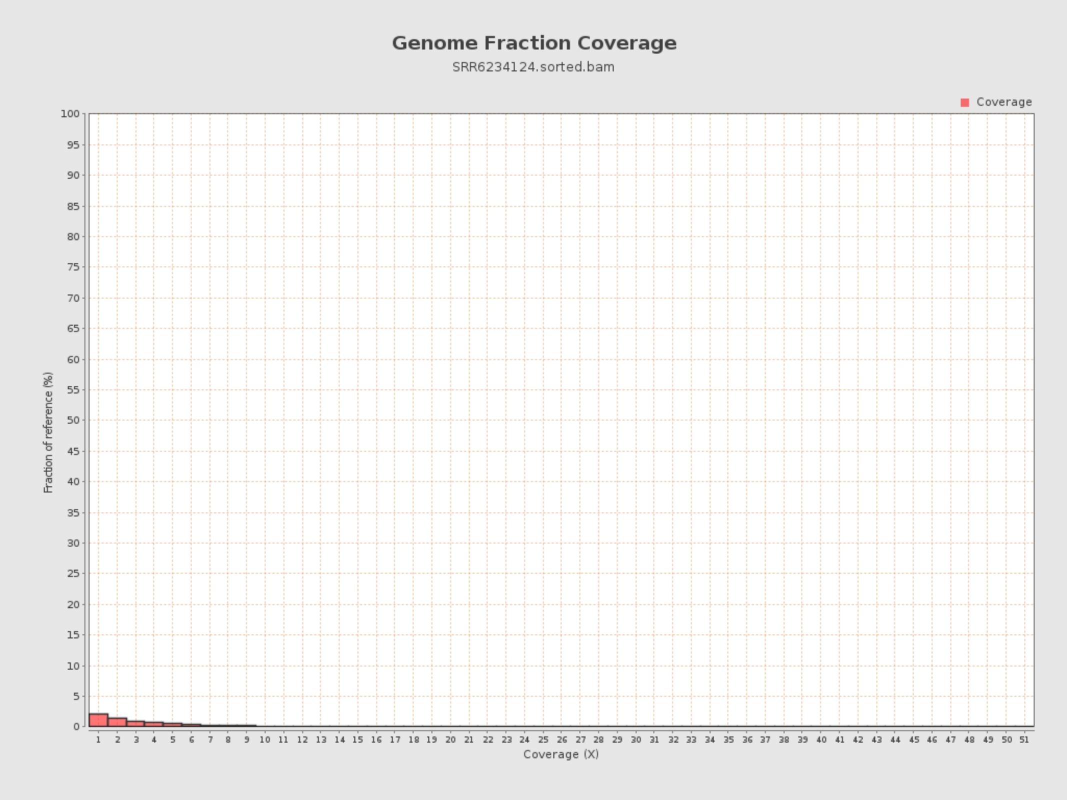
4. Results : Coverage Histogram



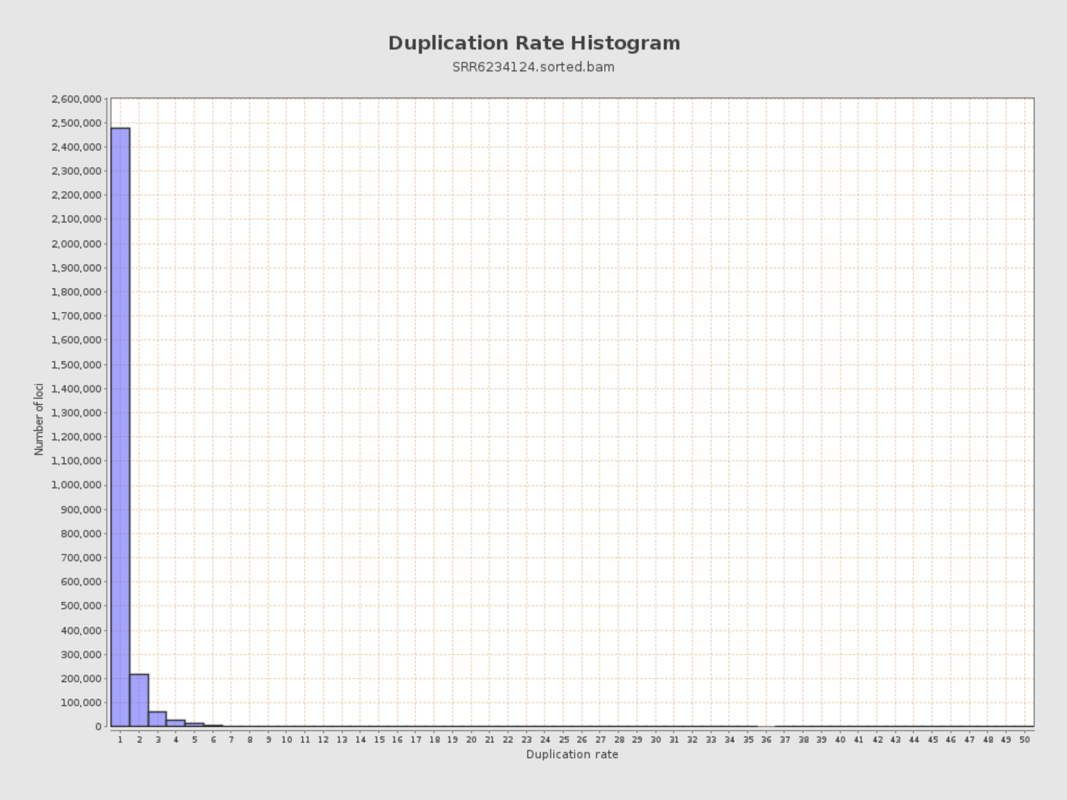
5. Results : Coverage Histogram (0-50X)



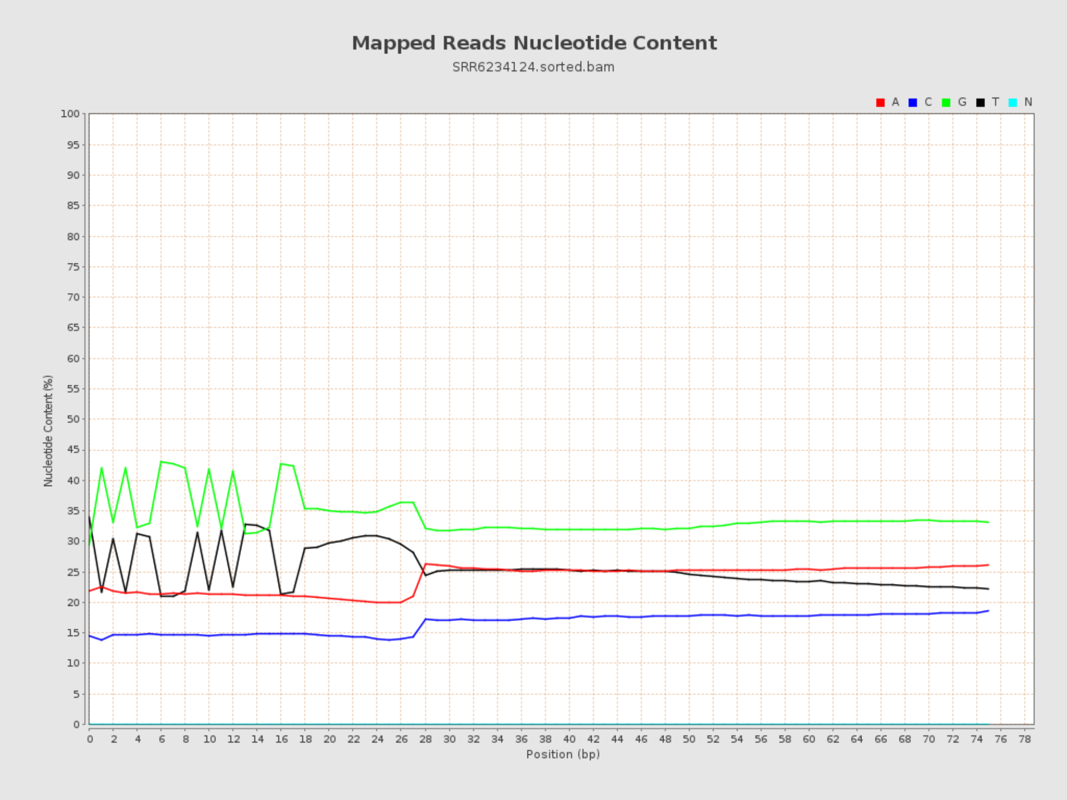
6. Results : Genome Fraction Coverage



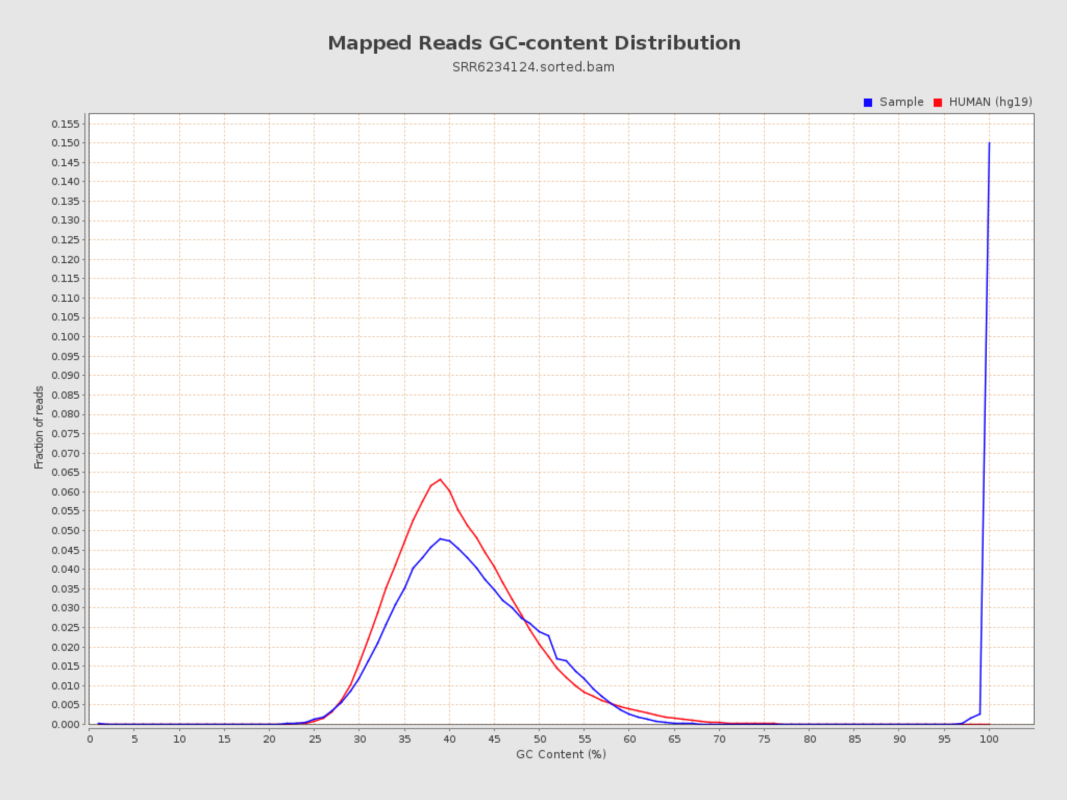
7. Results : Duplication Rate Histogram



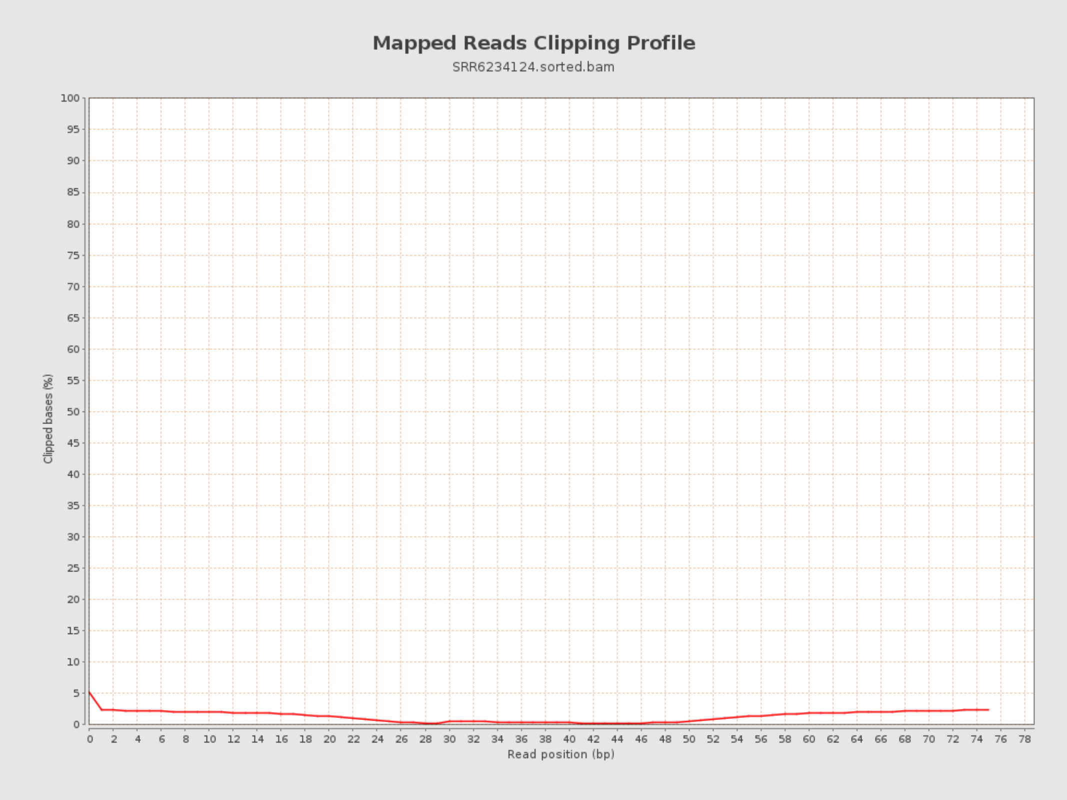
8. Results : Mapped Reads Nucleotide Content



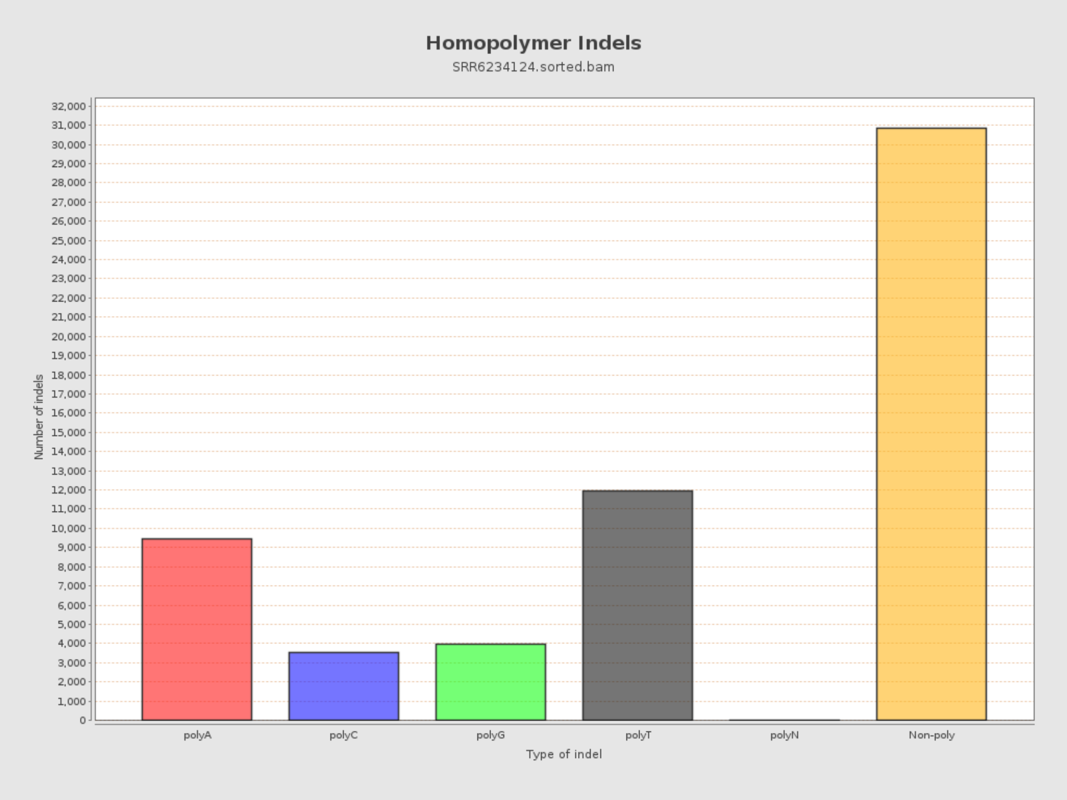
9. Results : Mapped Reads GC-content Distribution



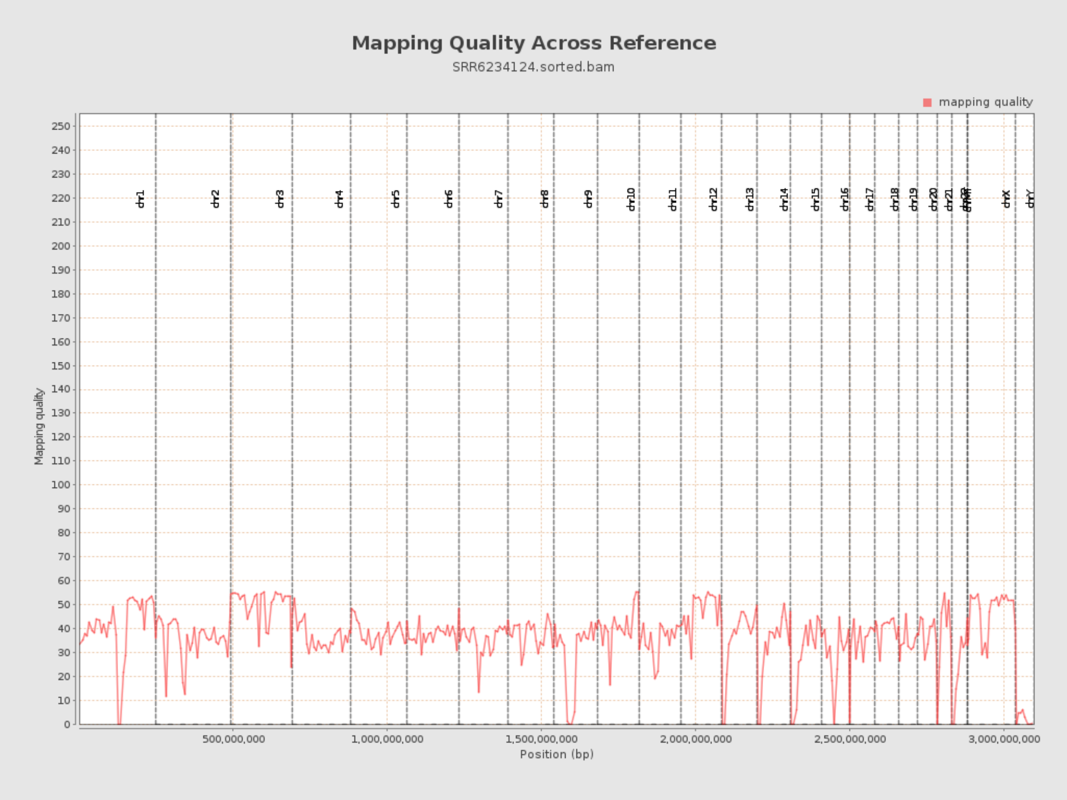
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram