

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:26:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004127.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_SRR6004127 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004127.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:26:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004127.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,826,202
Mapped reads	3,916,368 / 81.15%
Unmapped reads	909,834 / 18.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,471 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	202,971 / 4.21%
Duplication rate	3.82%
Clipped reads	1,623,691 / 33.64%

2.2. ACGT Content

Number/percentage of A's	74,623,597 / 28.17%
Number/percentage of C's	48,215,212 / 18.2%
Number/percentage of T's	84,811,664 / 32.01%
Number/percentage of G's	57,237,164 / 21.61%
Number/percentage of N's	28,517 / 0.01%
GC Percentage	39.81%

2.3. Coverage

Mean	0.0856

Standard Deviation	0.7572
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2.4. Mapping Quality

Mean Mapping Quality	45.38
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2.5. Mismatches and indels

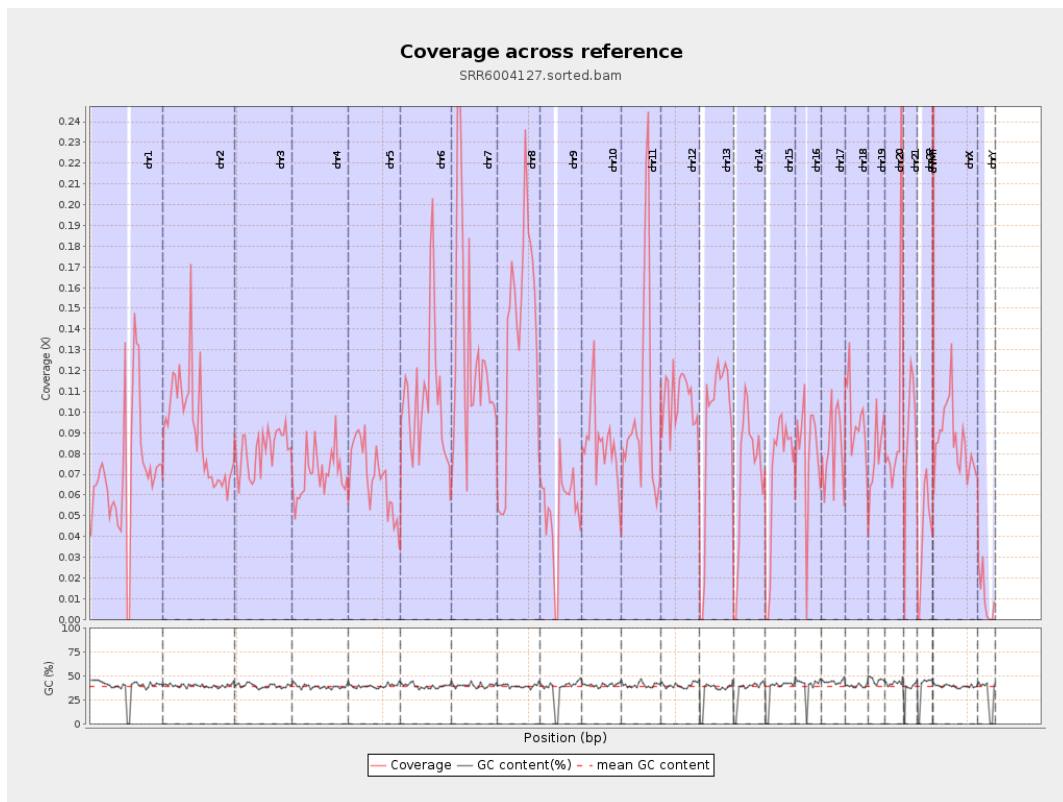
General error rate	0.97%
Mismatches	2,526,626
Insertions	23,464
Mapped reads with at least one insertion	0.59%
Deletions	73,477
Mapped reads with at least one deletion	1.85%
Homopolymer indels	46.74%

2.6. Chromosome stats

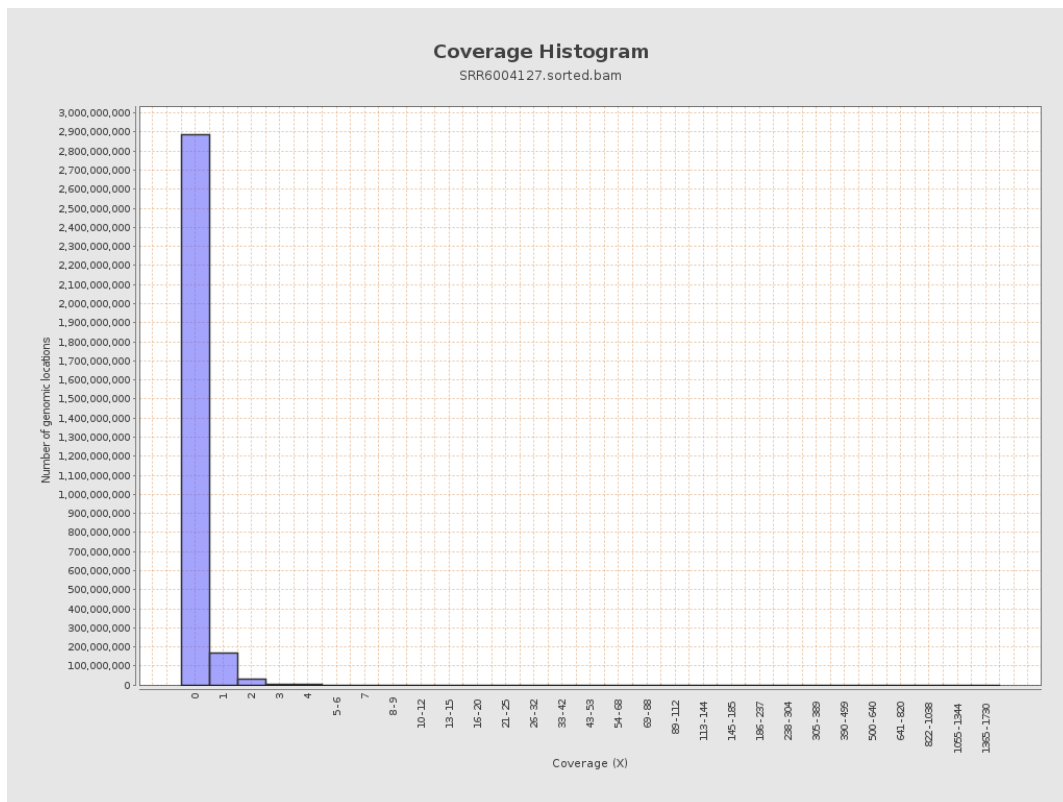
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17574997	0.0705	1.4096
chr2	243199373	21938689	0.0902	0.8654
chr3	198022430	16207557	0.0818	0.348
chr4	191154276	13474616	0.0705	0.346
chr5	180915260	12393354	0.0685	0.3258
chr6	171115067	18133438	0.106	0.5061
chr7	159138663	20352974	0.1279	1.2798

chr8	146364022	19921820	0.1361	1.1956
chr9	141213431	7394675	0.0524	0.6015
chr10	135534747	11529817	0.0851	0.6529
chr11	135006516	13451889	0.0996	0.6057
chr12	133851895	14034882	0.1049	0.4022
chr13	115169878	10664567	0.0926	0.3636
chr14	107349540	7715840	0.0719	0.3933
chr15	102531392	7050215	0.0688	0.3252
chr16	90354753	7197598	0.0797	0.4462
chr17	81195210	6683185	0.0823	0.4219
chr18	78077248	7565906	0.0969	1.3956
chr19	59128983	4724376	0.0799	0.9451
chr20	63025520	6622049	0.1051	0.4454
chr21	48129895	4192164	0.0871	0.3974
chr22	51304566	2127762	0.0415	0.2416
chrMT	16571	109891	6.6315	4.7757
chrX	155270560	13346997	0.086	0.4345
chrY	59373566	630709	0.0106	0.2045

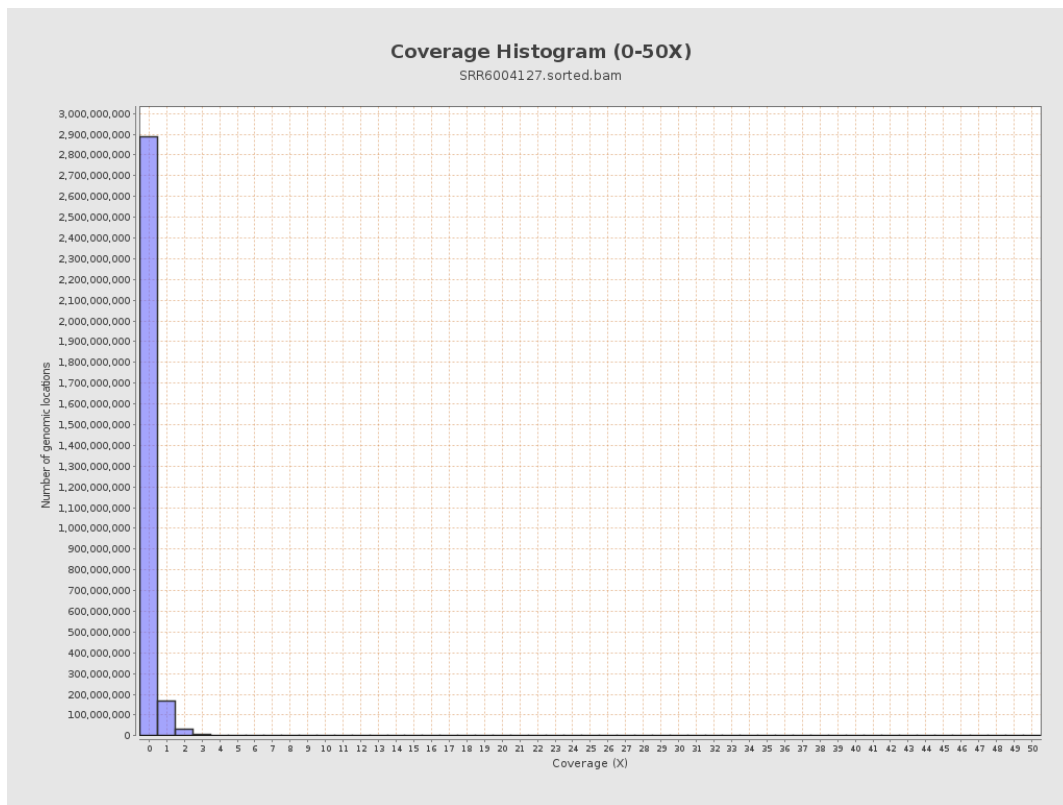
3. Results : Coverage across reference



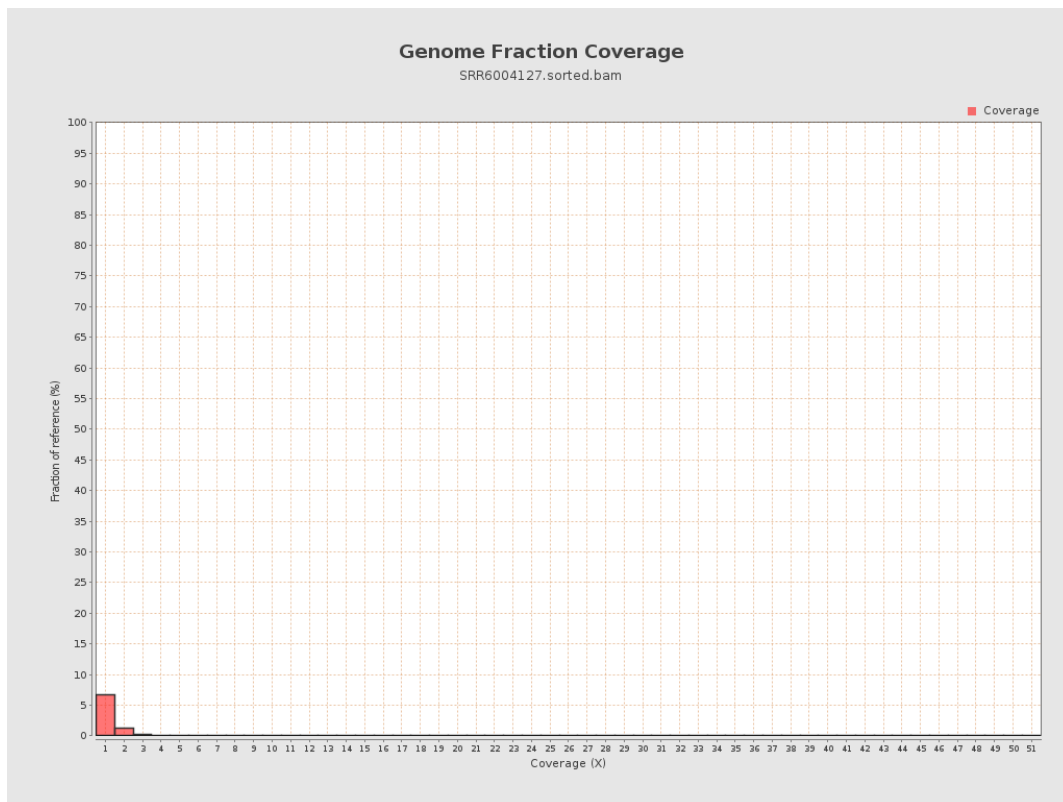
4. Results : Coverage Histogram



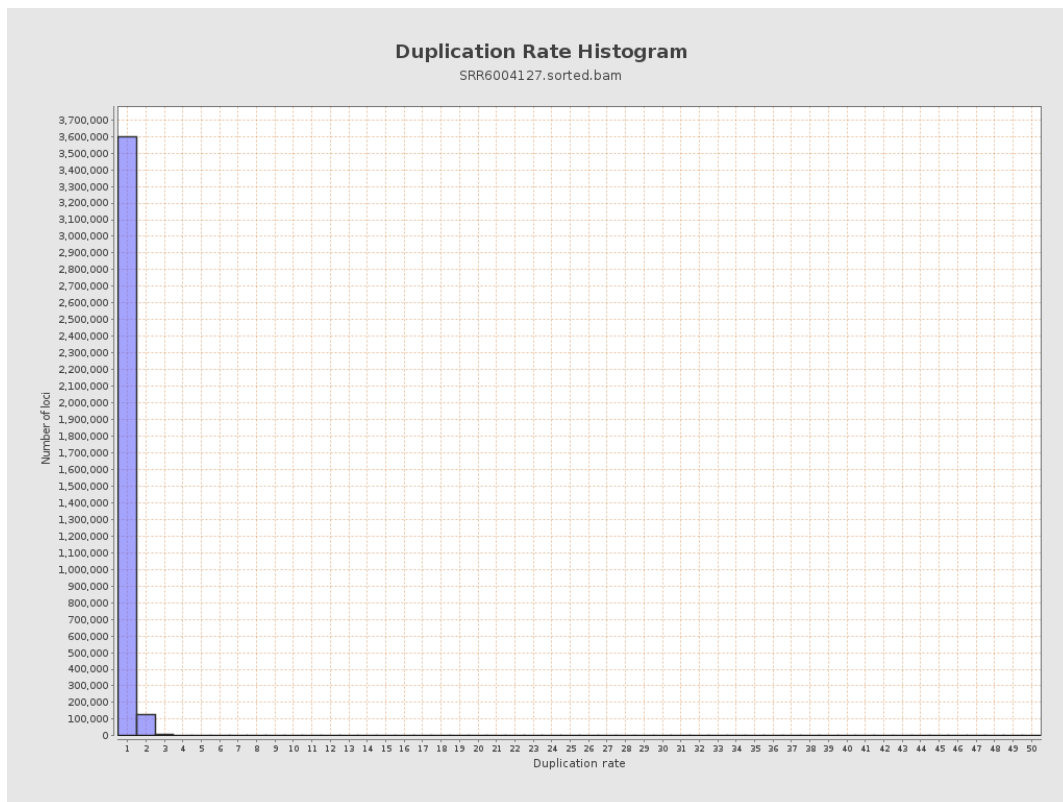
5. Results : Coverage Histogram (0-50X)



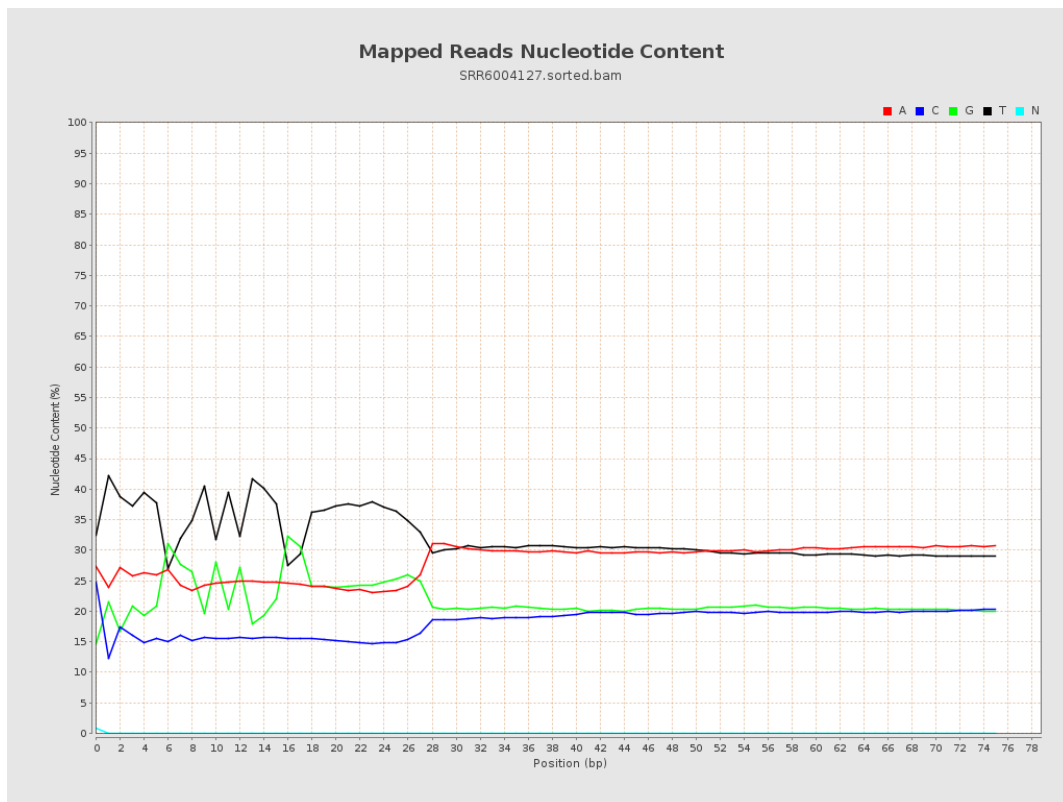
6. Results : Genome Fraction Coverage



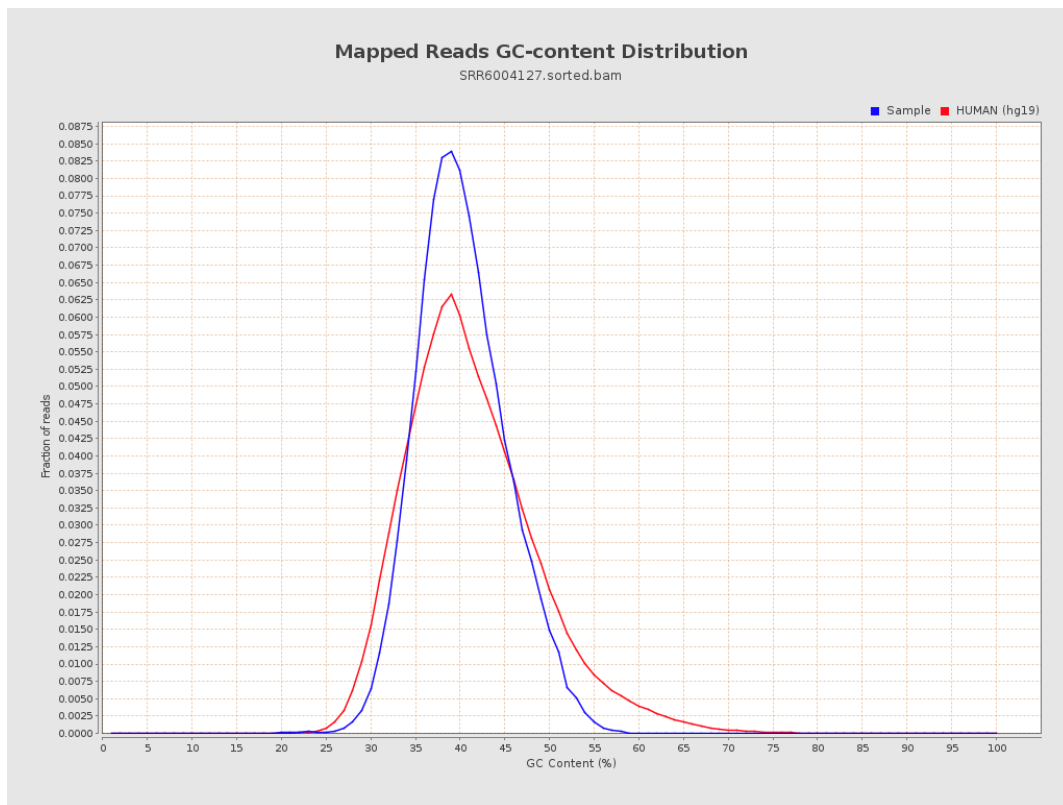
7. Results : Duplication Rate Histogram



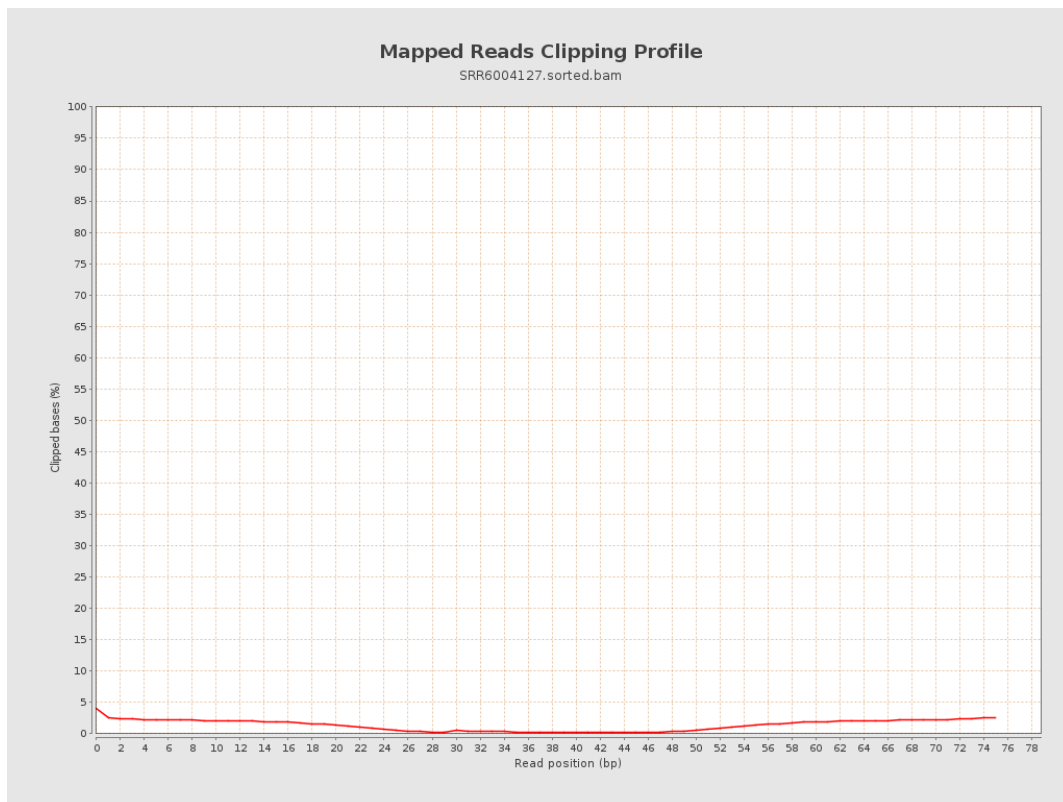
8. Results : Mapped Reads Nucleotide Content



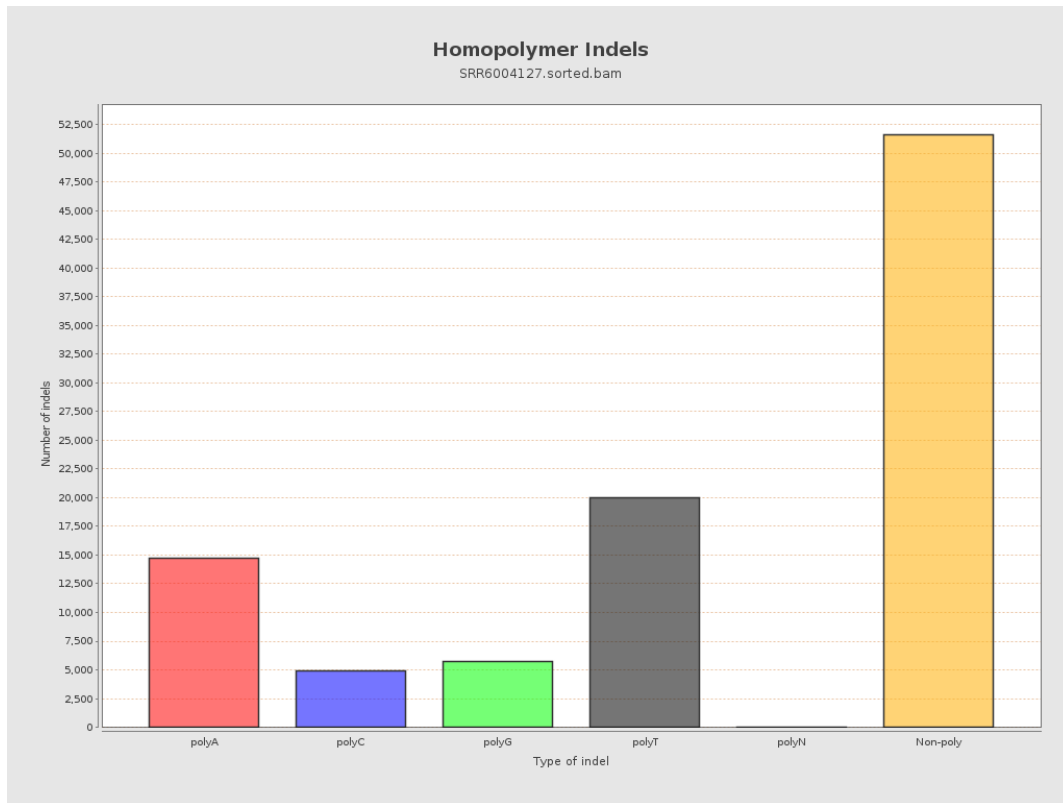
9. Results : Mapped Reads GC-content Distribution



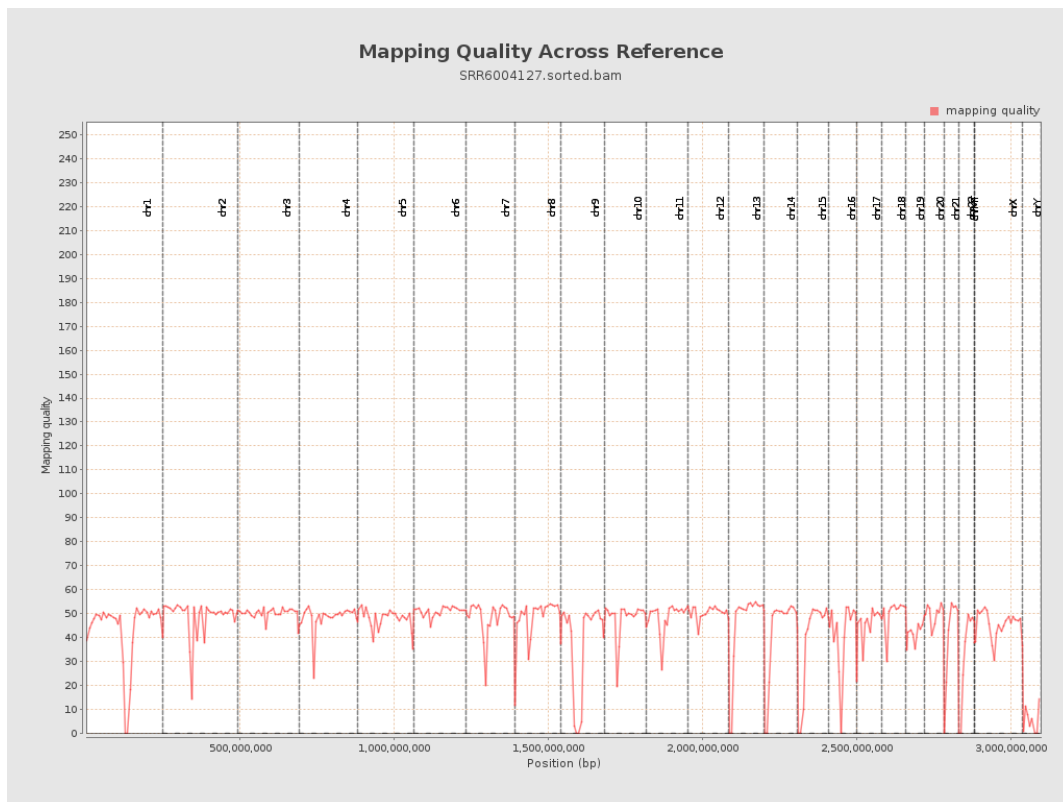
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

