

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:56:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013249.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_SRR6013249 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013249.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:56:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013249.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,467,663
Mapped reads	338,814 / 23.09%
Unmapped reads	1,128,849 / 76.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,347 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	14,644 / 1%
Duplication rate	3.66%
Clipped reads	195,698 / 13.33%

2.2. ACGT Content

Number/percentage of A's	6,015,925 / 28.16%
Number/percentage of C's	3,678,644 / 17.22%
Number/percentage of T's	7,080,575 / 33.14%
Number/percentage of G's	4,586,842 / 21.47%
Number/percentage of N's	4,382 / 0.02%
GC Percentage	38.68%

2.3. Coverage

Mean	0.0069

Standard Deviation	0.1218
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2.4. Mapping Quality

Mean Mapping Quality	44.35
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2.5. Mismatches and indels

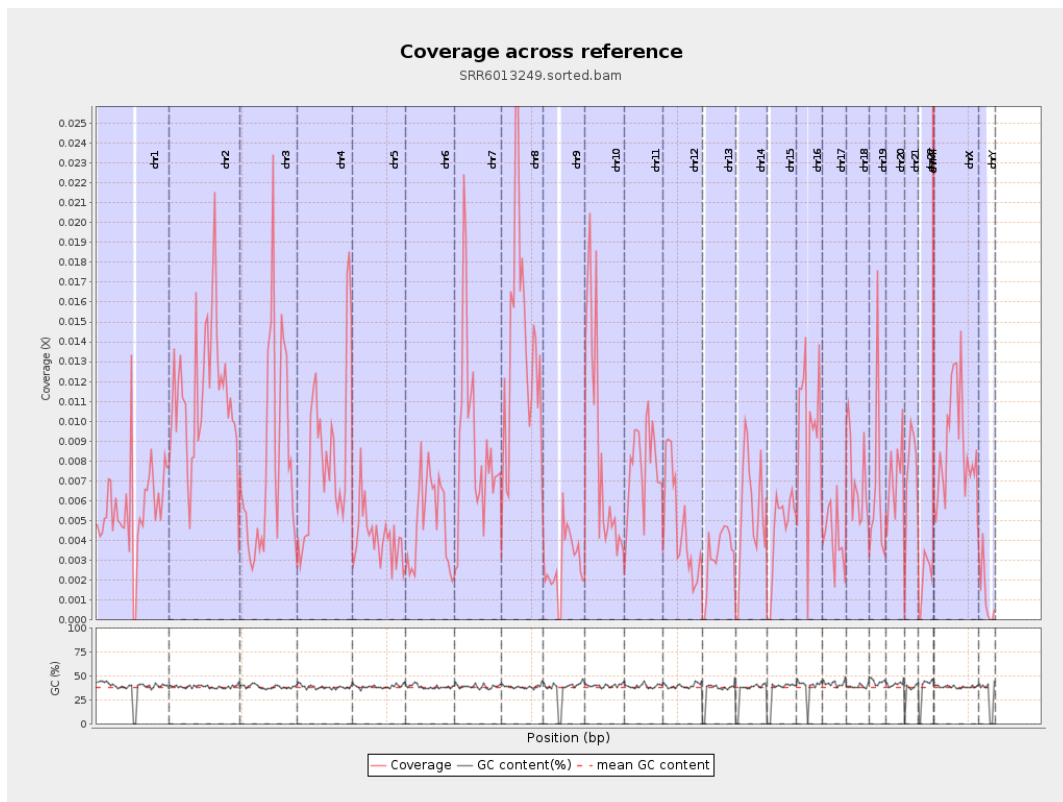
General error rate	1.11%
Mismatches	235,010
Insertions	1,736
Mapped reads with at least one insertion	0.5%
Deletions	14,256
Mapped reads with at least one deletion	4.09%
Homopolymer indels	41.74%

2.6. Chromosome stats

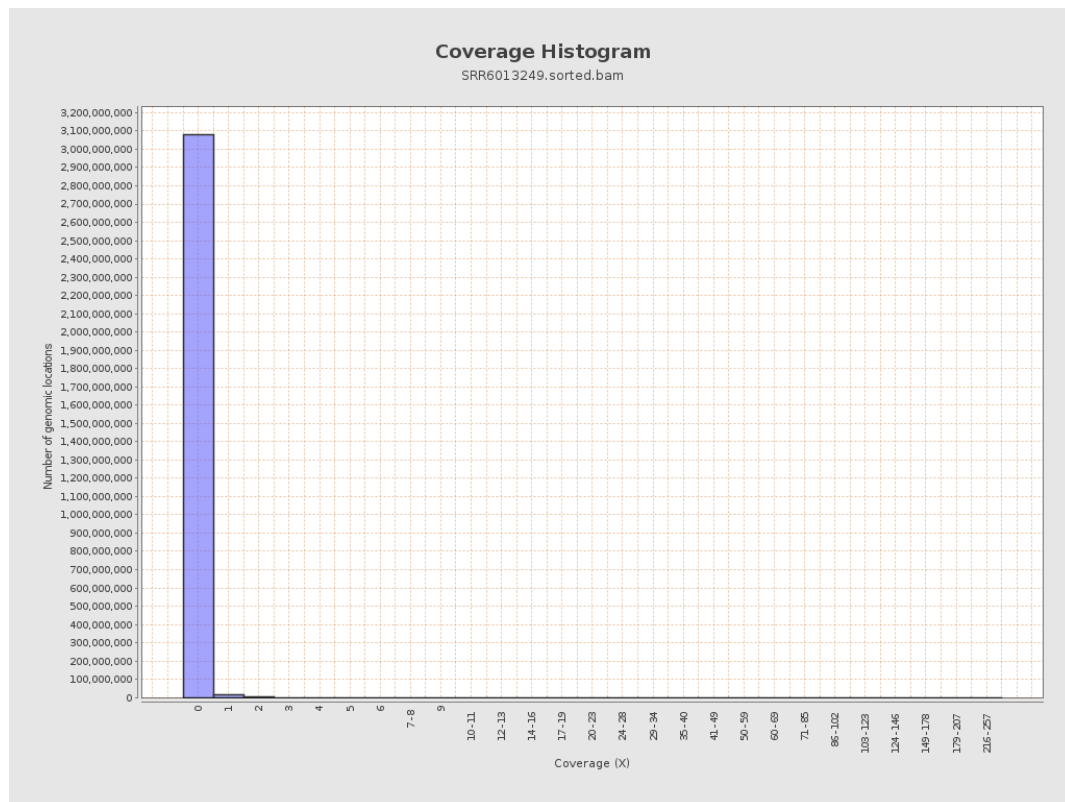
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1396296	0.0056	0.2251
chr2	243199373	2762922	0.0114	0.1603
chr3	198022430	1516596	0.0077	0.1003
chr4	191154276	1584104	0.0083	0.106
chr5	180915260	755956	0.0042	0.0727
chr6	171115067	836891	0.0049	0.0917
chr7	159138663	1426257	0.009	0.1311

chr8	146364022	2017713	0.0138	0.1641
chr9	141213431	396425	0.0028	0.0693
chr10	135534747	1147126	0.0085	0.1193
chr11	135006516	1045163	0.0077	0.1032
chr12	133851895	617932	0.0046	0.0771
chr13	115169878	369692	0.0032	0.0662
chr14	107349540	586019	0.0055	0.0848
chr15	102531392	461818	0.0045	0.0753
chr16	90354753	867143	0.0096	0.1132
chr17	81195210	328634	0.004	0.0738
chr18	78077248	553007	0.0071	0.1217
chr19	59128983	389380	0.0066	0.1437
chr20	63025520	449794	0.0071	0.0966
chr21	48129895	352556	0.0073	0.0979
chr22	51304566	107267	0.0021	0.0502
chrMT	16571	3680	0.2221	0.5286
chrX	155270560	1349601	0.0087	0.1083
chrY	59373566	69589	0.0012	0.0475

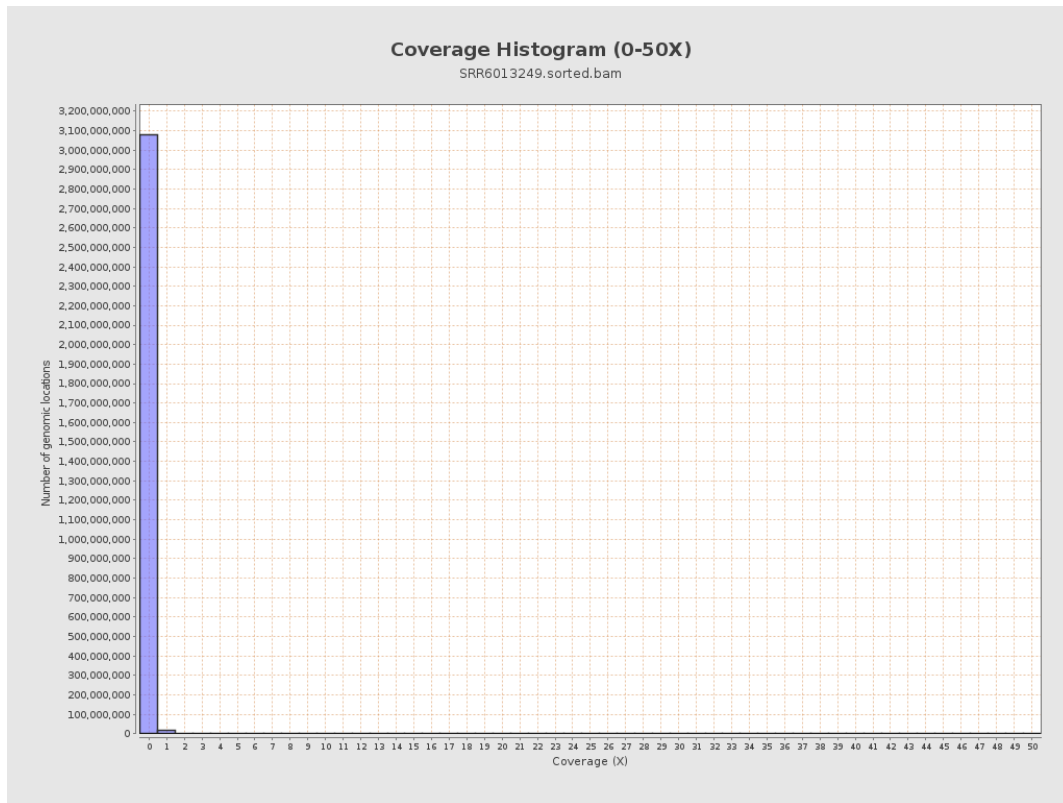
3. Results : Coverage across reference



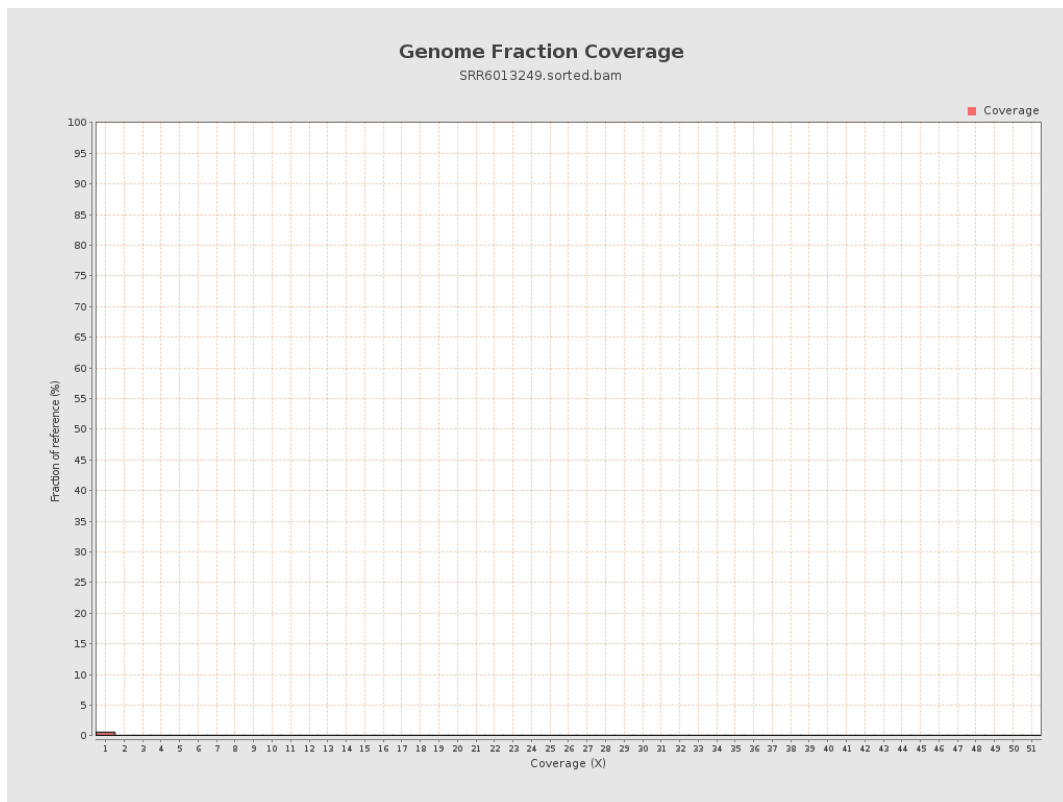
4. Results : Coverage Histogram



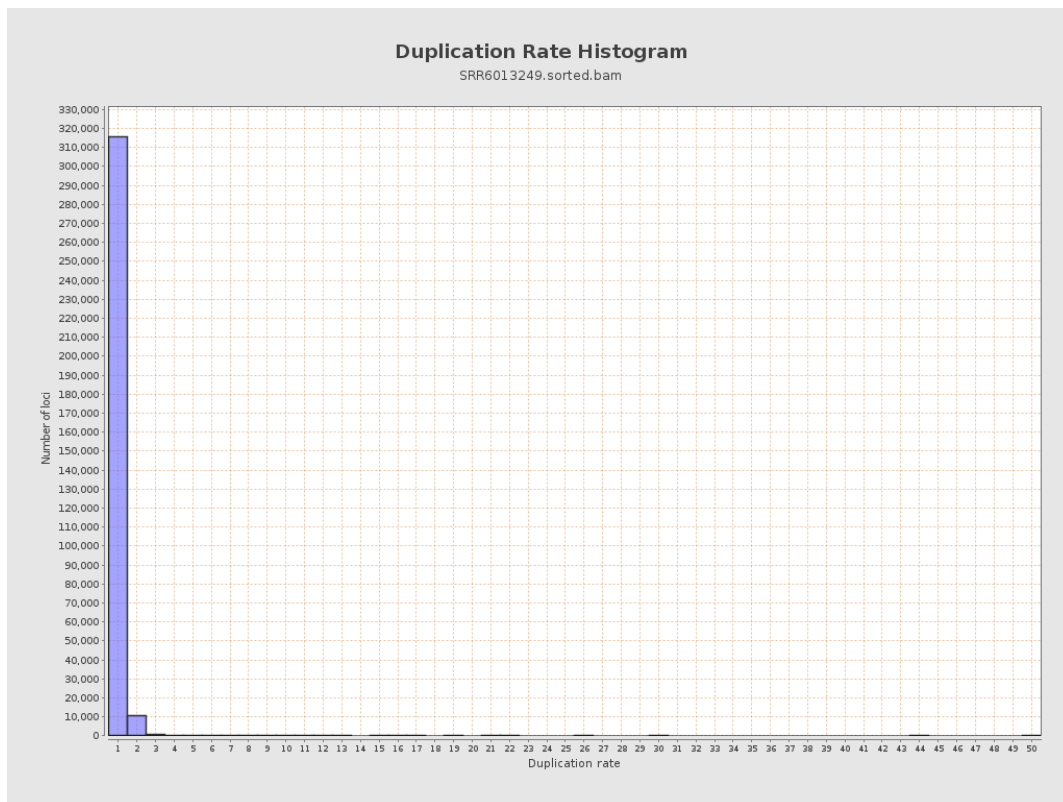
5. Results : Coverage Histogram (0-50X)



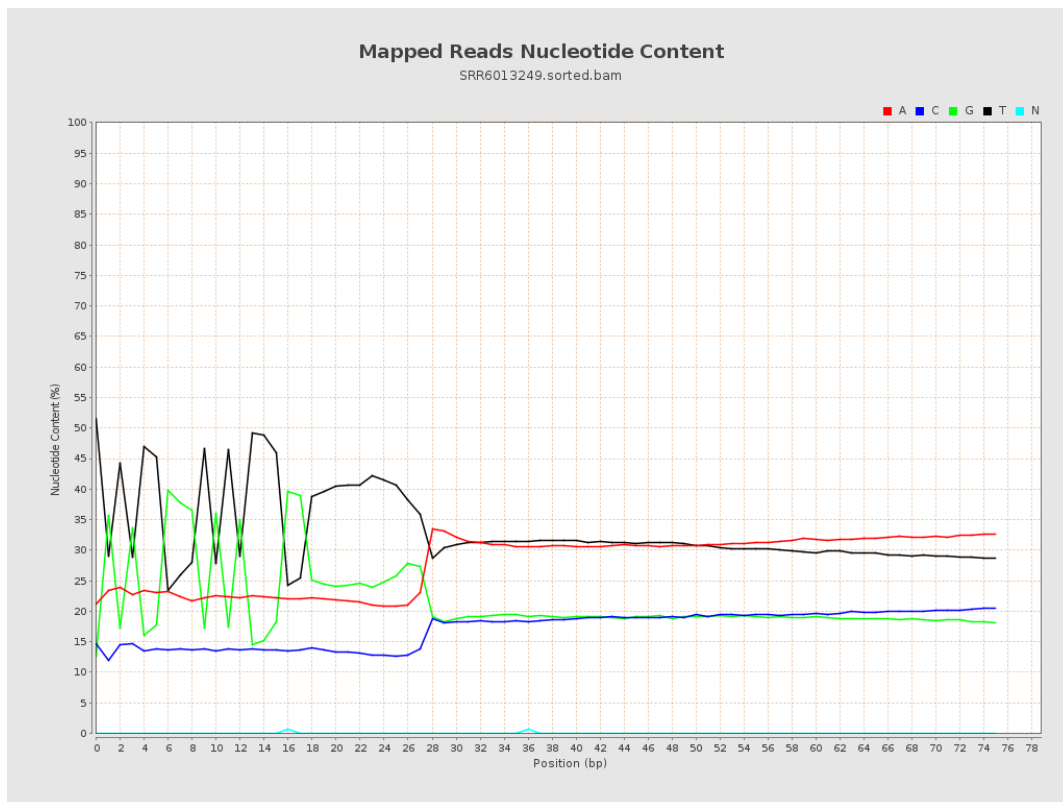
6. Results : Genome Fraction Coverage



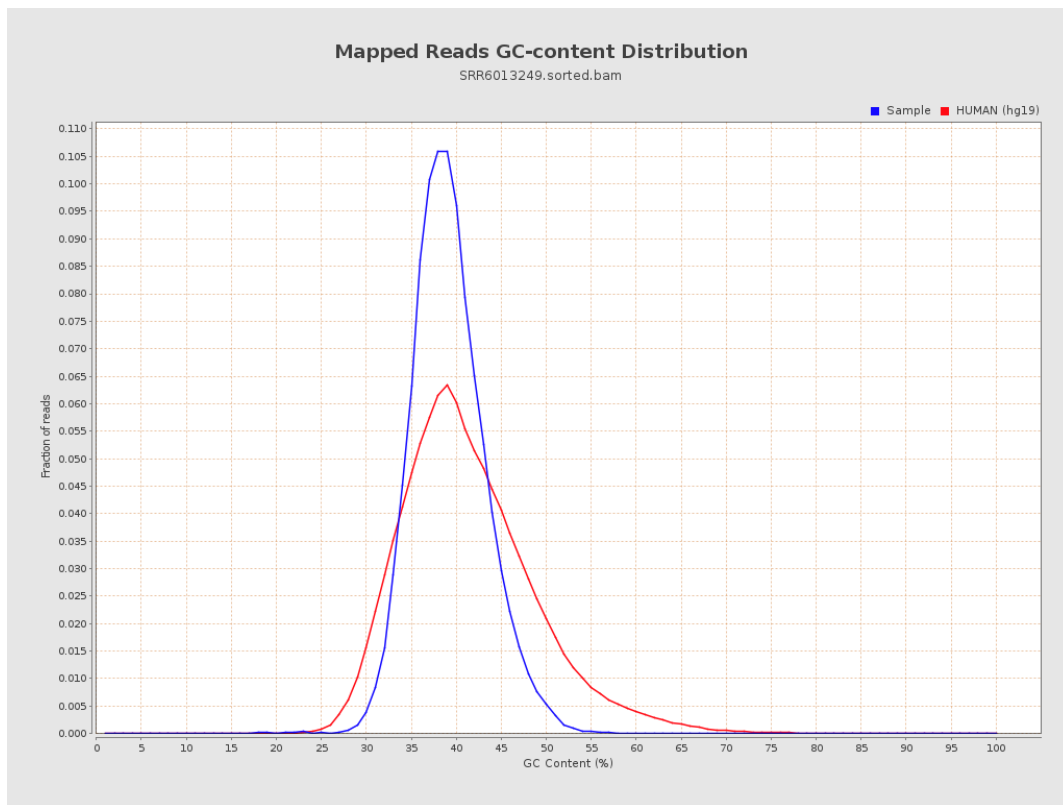
7. Results : Duplication Rate Histogram



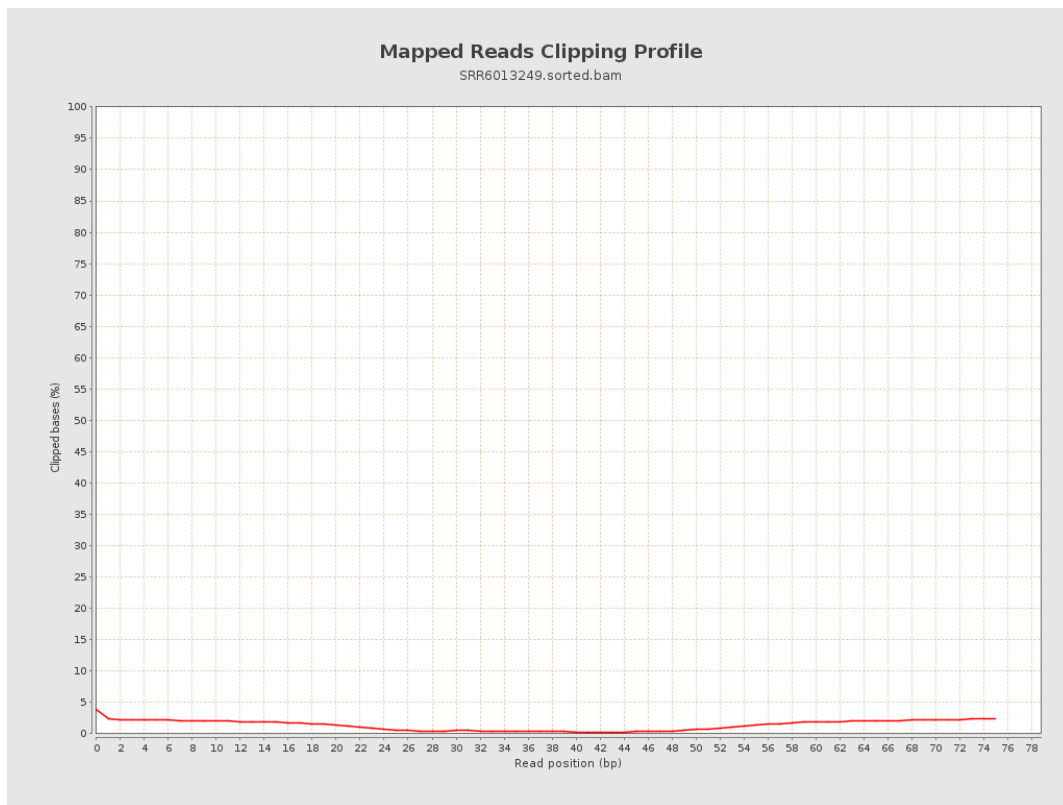
8. Results : Mapped Reads Nucleotide Content



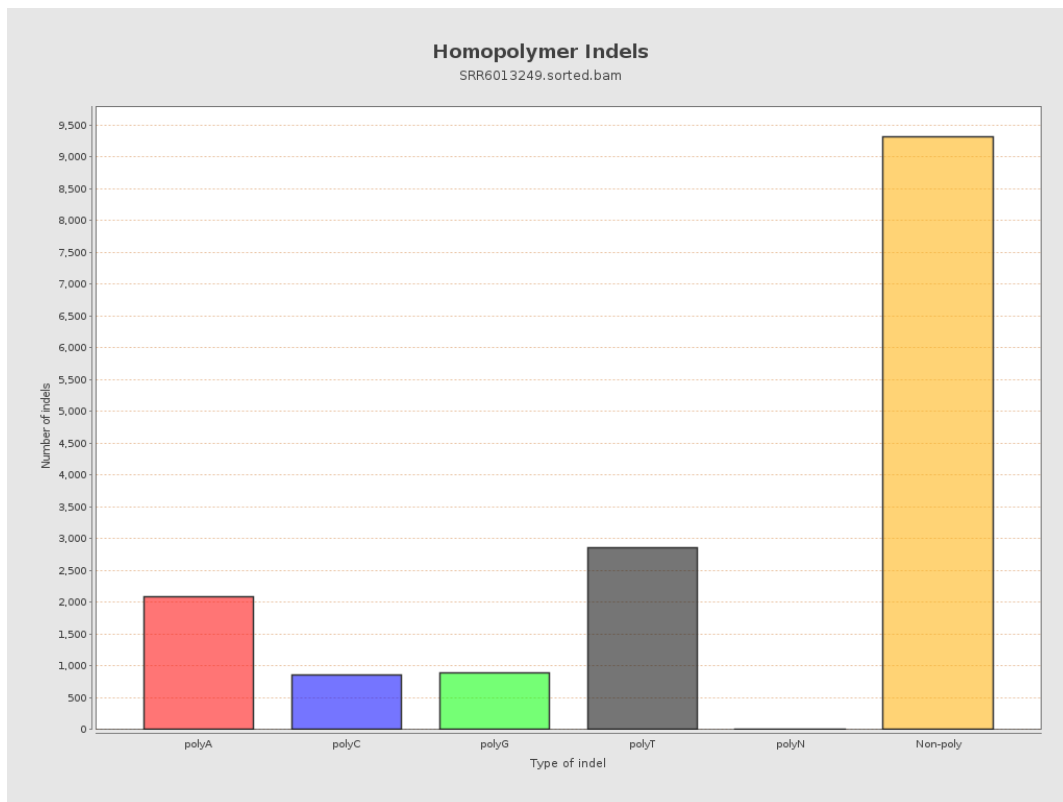
9. Results : Mapped Reads GC-content Distribution



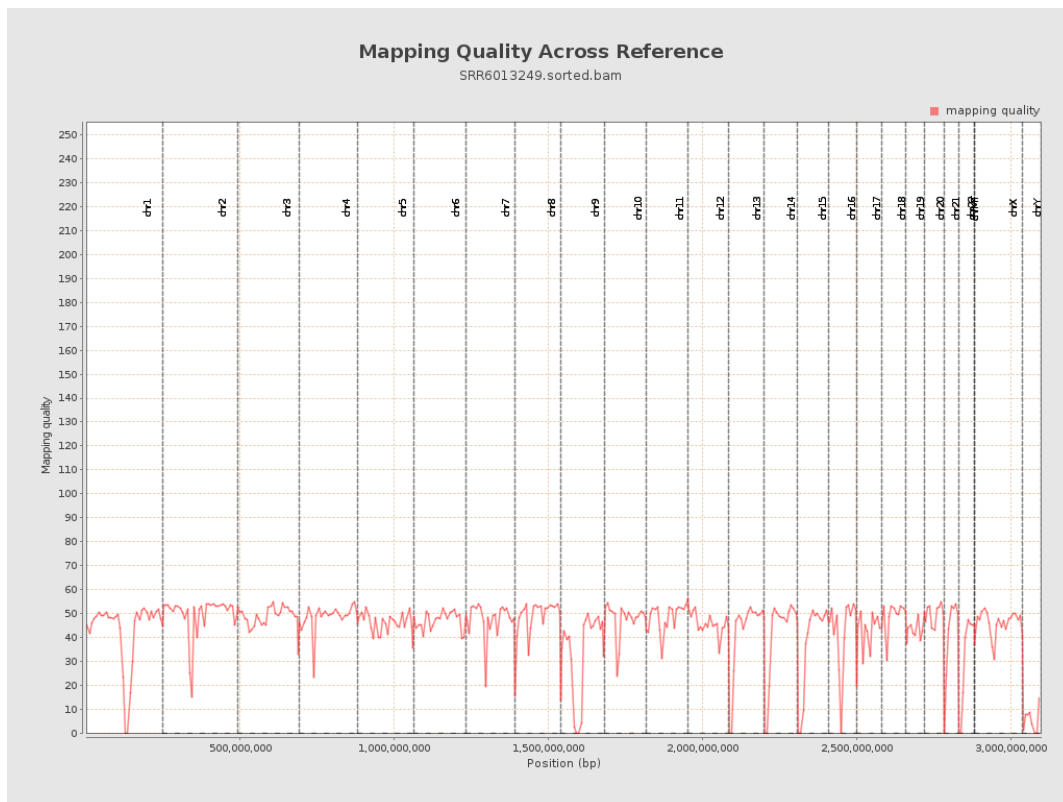
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

