

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:44:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013184.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_SRR6013184 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013184.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:44:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013184.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,809,757
Mapped reads	1,356,440 / 74.95%
Unmapped reads	453,317 / 25.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,006 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	190,561 / 10.53%
Duplication rate	10.17%
Clipped reads	975,206 / 53.89%

2.2. ACGT Content

Number/percentage of A's	22,781,821 / 28.28%
Number/percentage of C's	13,019,519 / 16.16%
Number/percentage of T's	25,595,107 / 31.77%
Number/percentage of G's	19,134,891 / 23.75%
Number/percentage of N's	26,960 / 0.03%
GC Percentage	39.91%

2.3. Coverage

Mean	0.026

Standard Deviation	0.2561
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2.4. Mapping Quality

Mean Mapping Quality	45.65
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2.5. Mismatches and indels

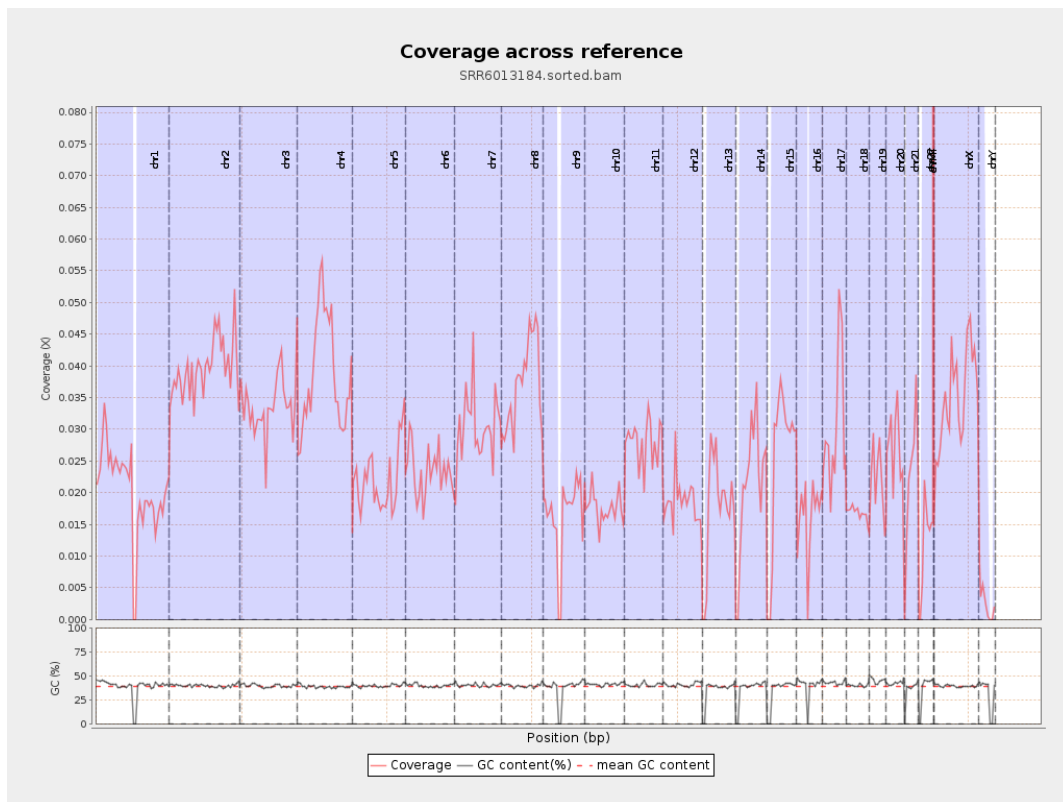
General error rate	1.04%
Mismatches	828,713
Insertions	5,037
Mapped reads with at least one insertion	0.37%
Deletions	19,752
Mapped reads with at least one deletion	1.44%
Homopolymer indels	50.56%

2.6. Chromosome stats

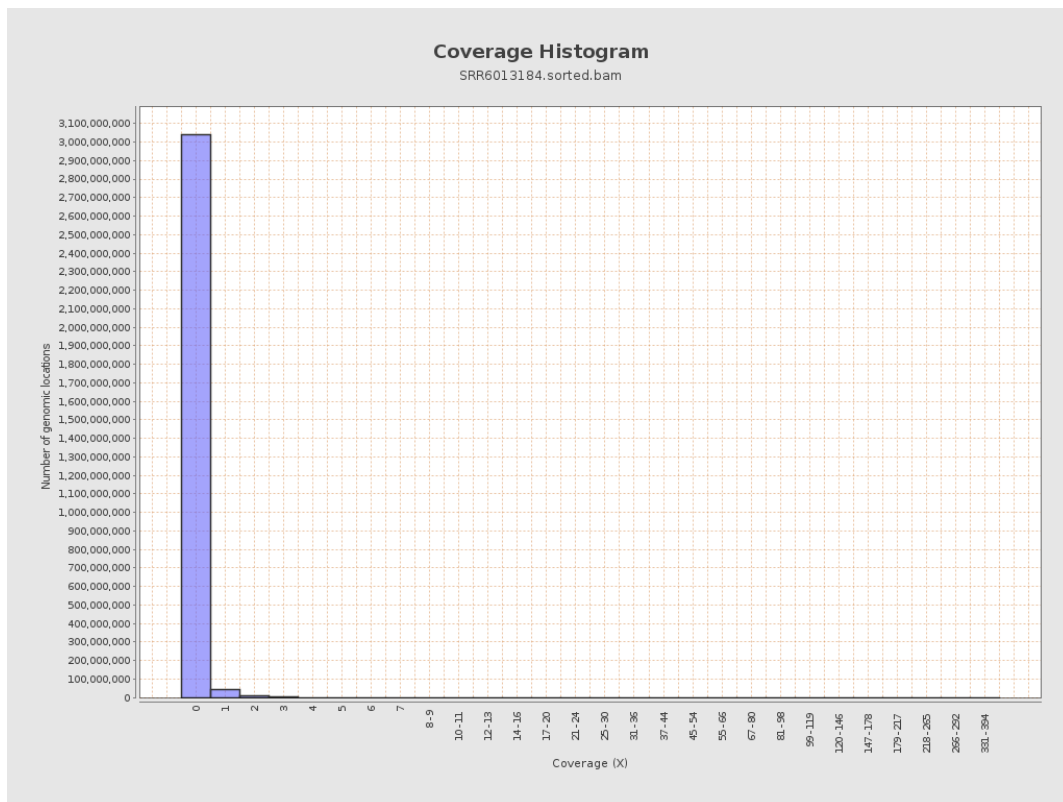
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5096196	0.0204	0.2582
chr2	243199373	9678221	0.0398	0.3031
chr3	198022430	6672124	0.0337	0.2581
chr4	191154276	7435494	0.0389	0.2948
chr5	180915260	3963840	0.0219	0.2082
chr6	171115067	3980395	0.0233	0.2235
chr7	159138663	4852098	0.0305	0.3828

chr8	146364022	5453497	0.0373	0.3471
chr9	141213431	2305722	0.0163	0.1946
chr10	135534747	2396830	0.0177	0.1943
chr11	135006516	3757226	0.0278	0.2405
chr12	133851895	2483410	0.0186	0.1885
chr13	115169878	2017000	0.0175	0.1845
chr14	107349540	2271285	0.0212	0.205
chr15	102531392	2630251	0.0257	0.2335
chr16	90354753	1464789	0.0162	0.2001
chr17	81195210	2427629	0.0299	0.2495
chr18	78077248	1316074	0.0169	0.2454
chr19	59128983	1302017	0.022	0.2259
chr20	63025520	1679902	0.0267	0.2357
chr21	48129895	1085591	0.0226	0.2115
chr22	51304566	589889	0.0115	0.1517
chrMT	16571	197041	11.8907	12.0807
chrX	155270560	5381745	0.0347	0.2706
chrY	59373566	152281	0.0026	0.065

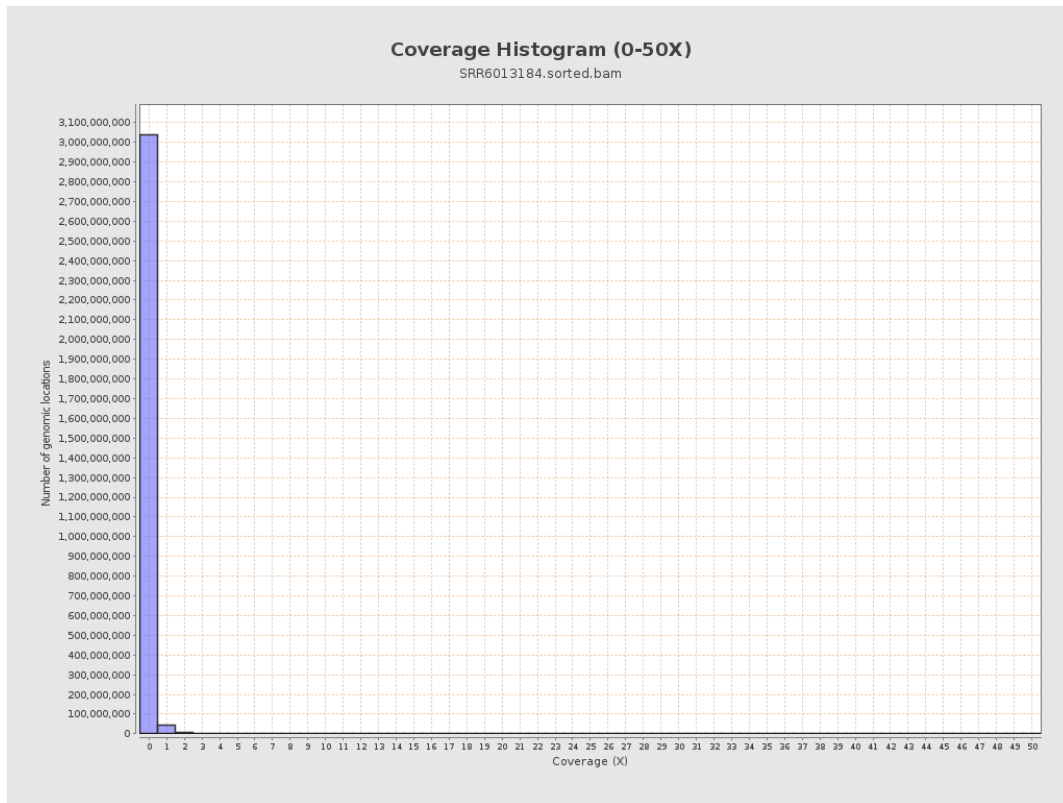
3. Results : Coverage across reference



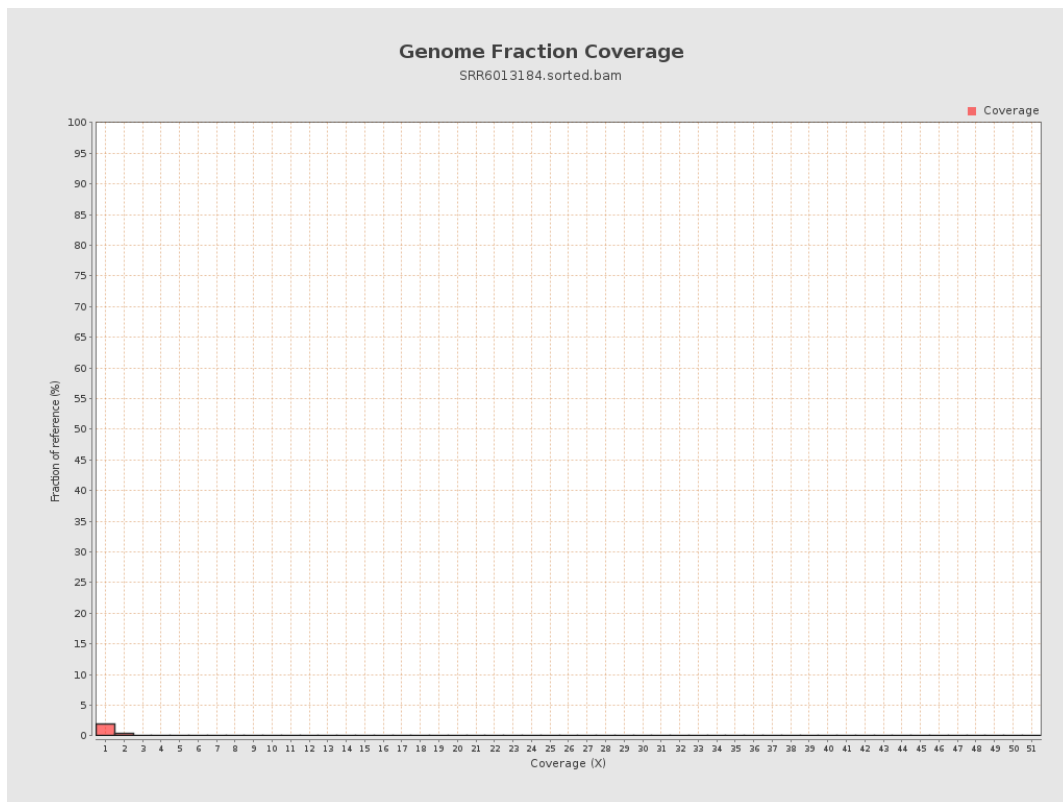
4. Results : Coverage Histogram



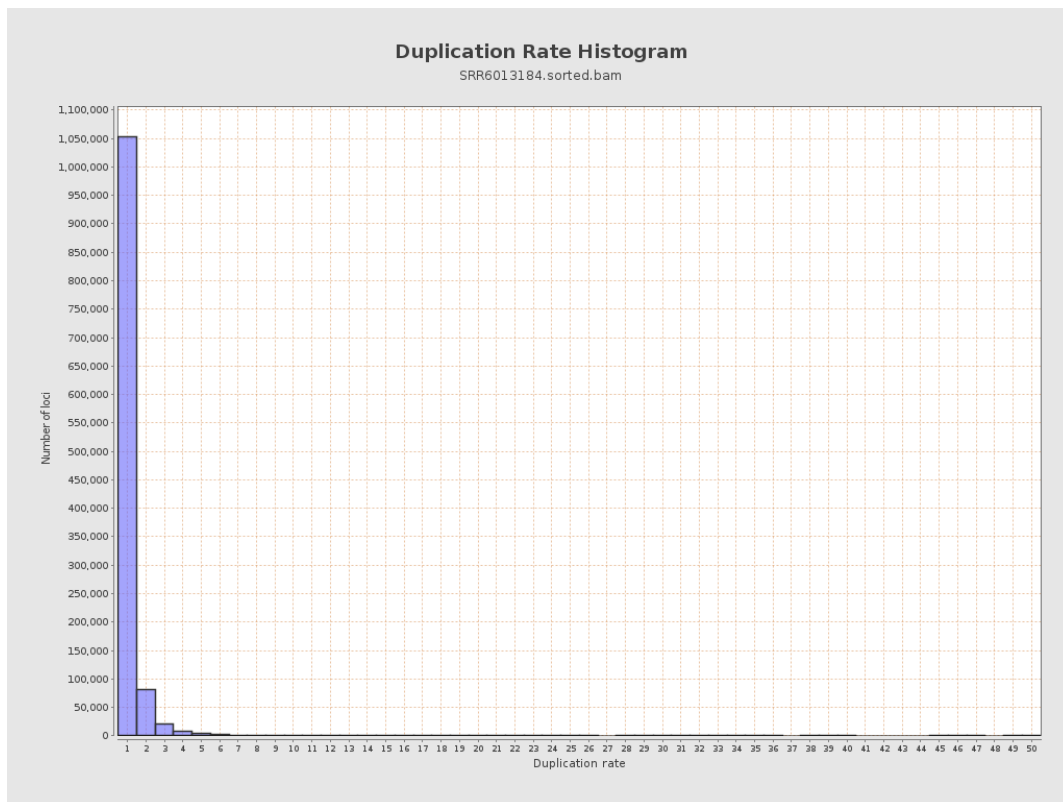
5. Results : Coverage Histogram (0-50X)



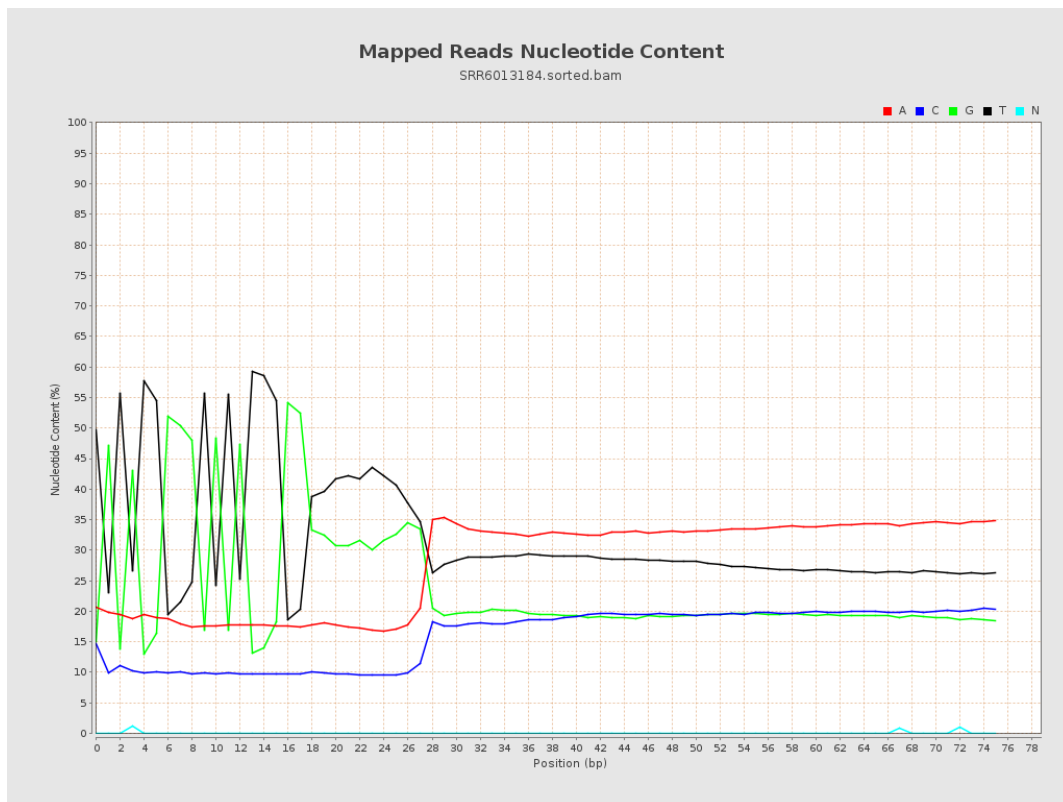
6. Results : Genome Fraction Coverage



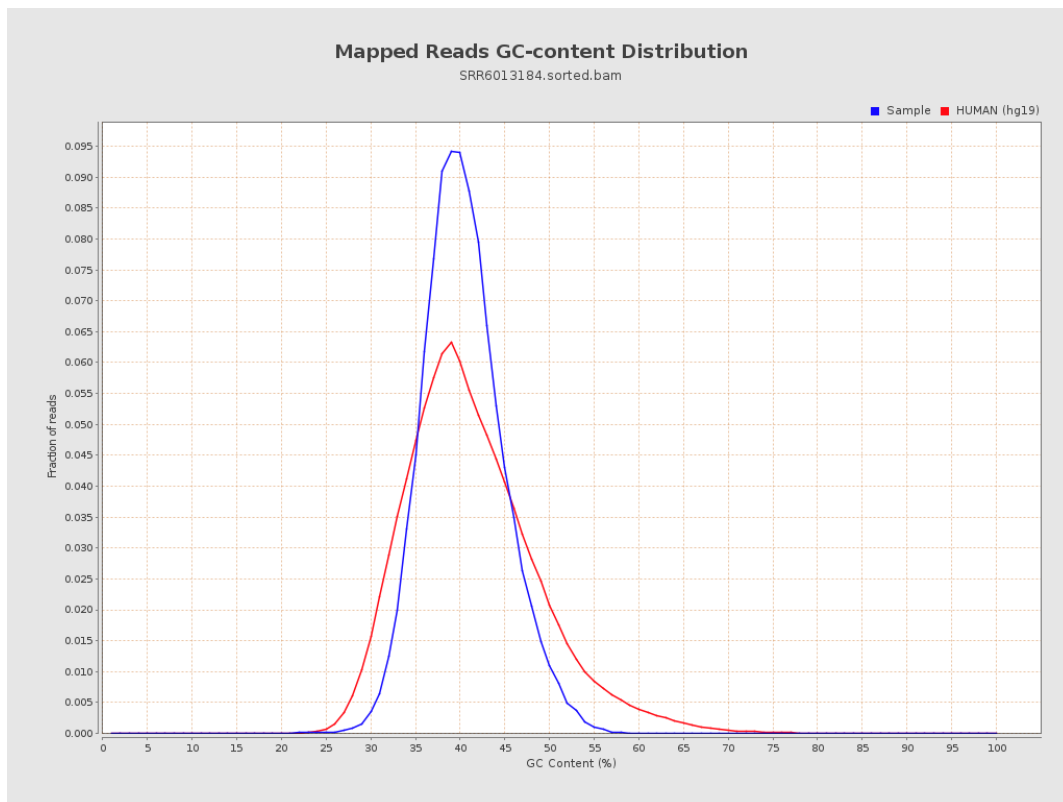
7. Results : Duplication Rate Histogram



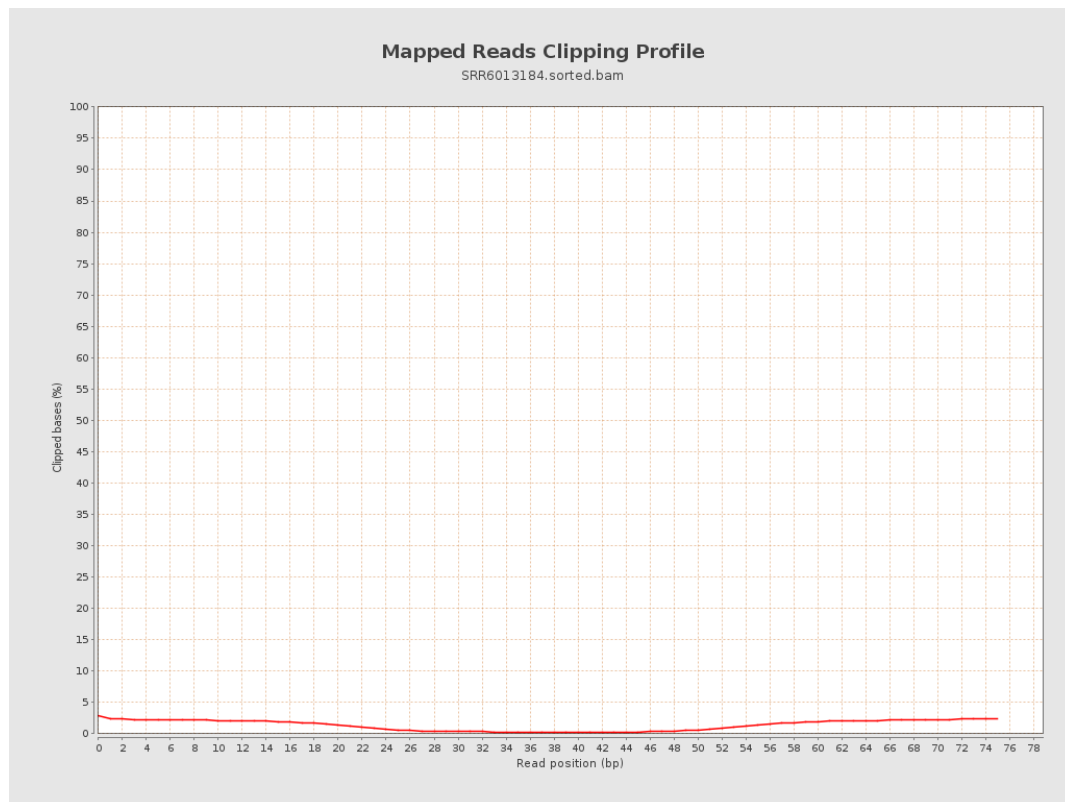
8. Results : Mapped Reads Nucleotide Content



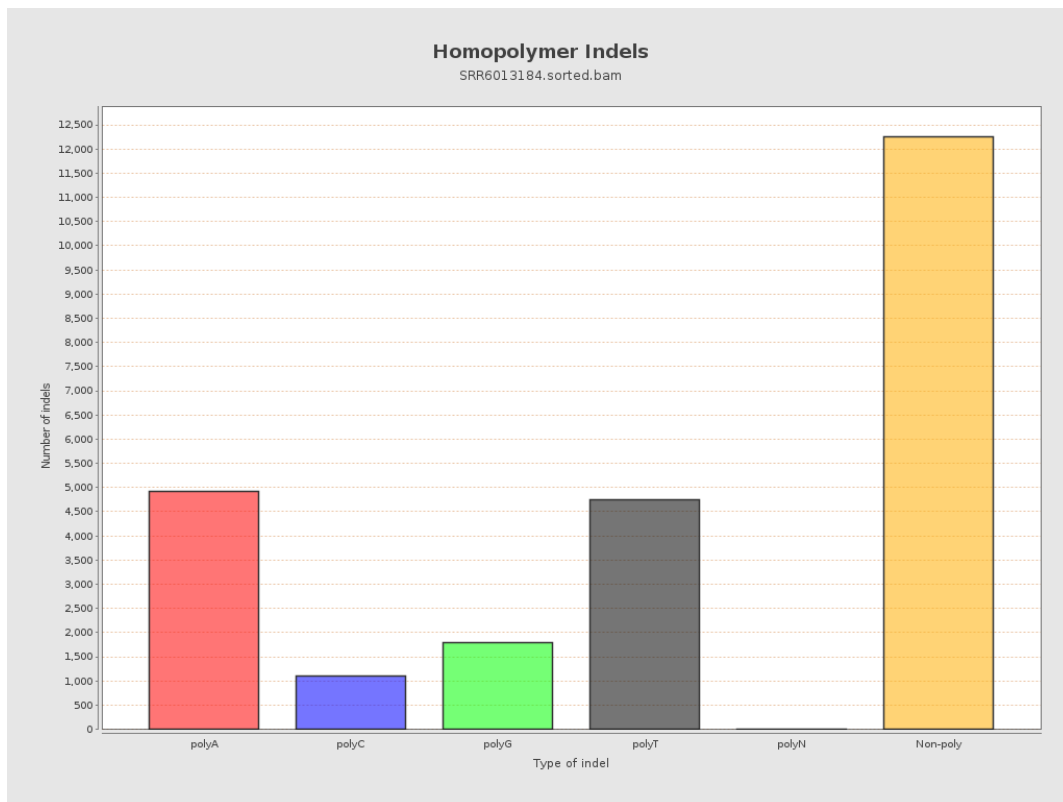
9. Results : Mapped Reads GC-content Distribution



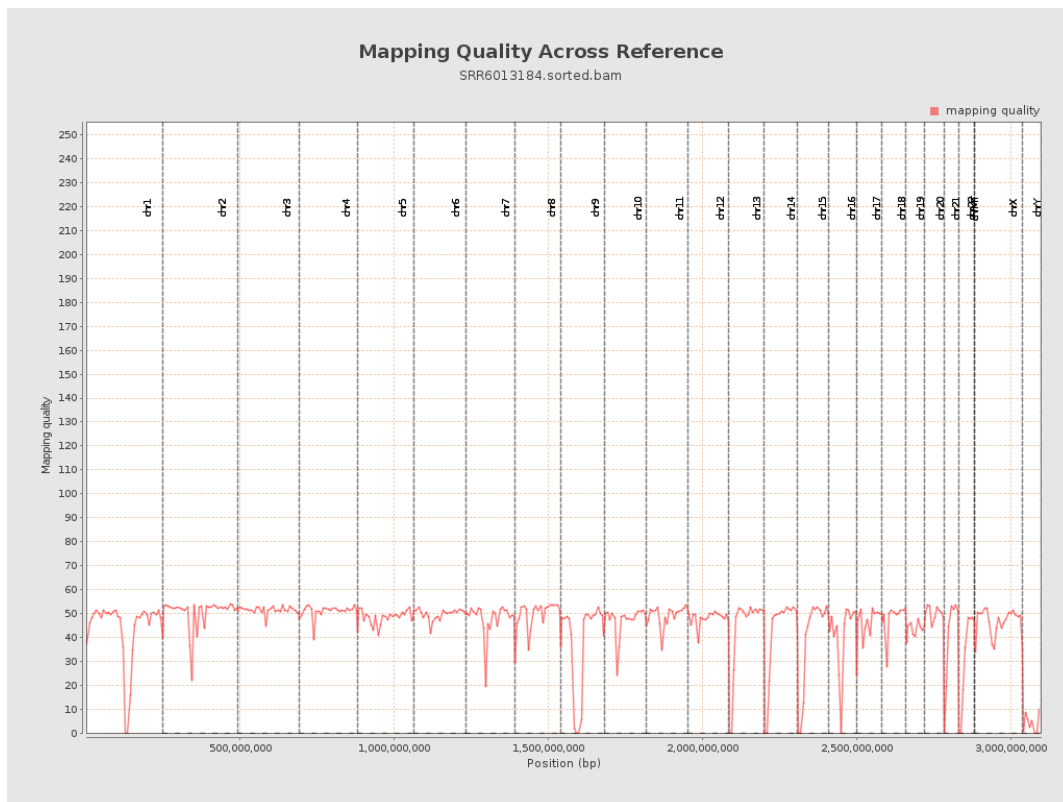
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

