

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 20:50:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004015.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_SRR6004015 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004015.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 20:50:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004015.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,005,535
Mapped reads	1,831,658 / 91.33%
Unmapped reads	173,877 / 8.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,164 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	75,377 / 3.76%
Duplication rate	3.41%
Clipped reads	765,928 / 38.19%

2.2. ACGT Content

Number/percentage of A's	34,971,759 / 28.28%
Number/percentage of C's	23,049,907 / 18.64%
Number/percentage of T's	39,034,023 / 31.57%
Number/percentage of G's	26,570,762 / 21.49%
Number/percentage of N's	21,861 / 0.02%
GC Percentage	40.13%

2.3. Coverage

Mean	0.04

Standard Deviation	0.3142
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2.4. Mapping Quality

Mean Mapping Quality	46.68
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2.5. Mismatches and indels

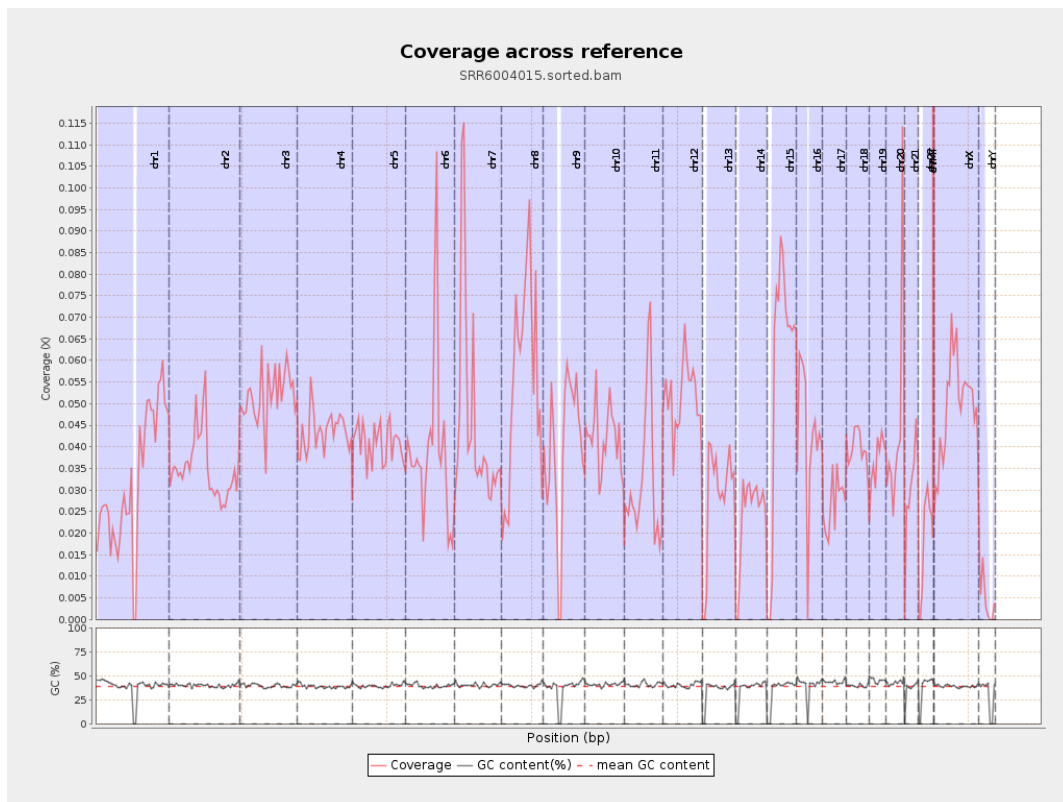
General error rate	0.85%
Mismatches	1,038,968
Insertions	8,889
Mapped reads with at least one insertion	0.48%
Deletions	28,813
Mapped reads with at least one deletion	1.55%
Homopolymer indels	47.2%

2.6. Chromosome stats

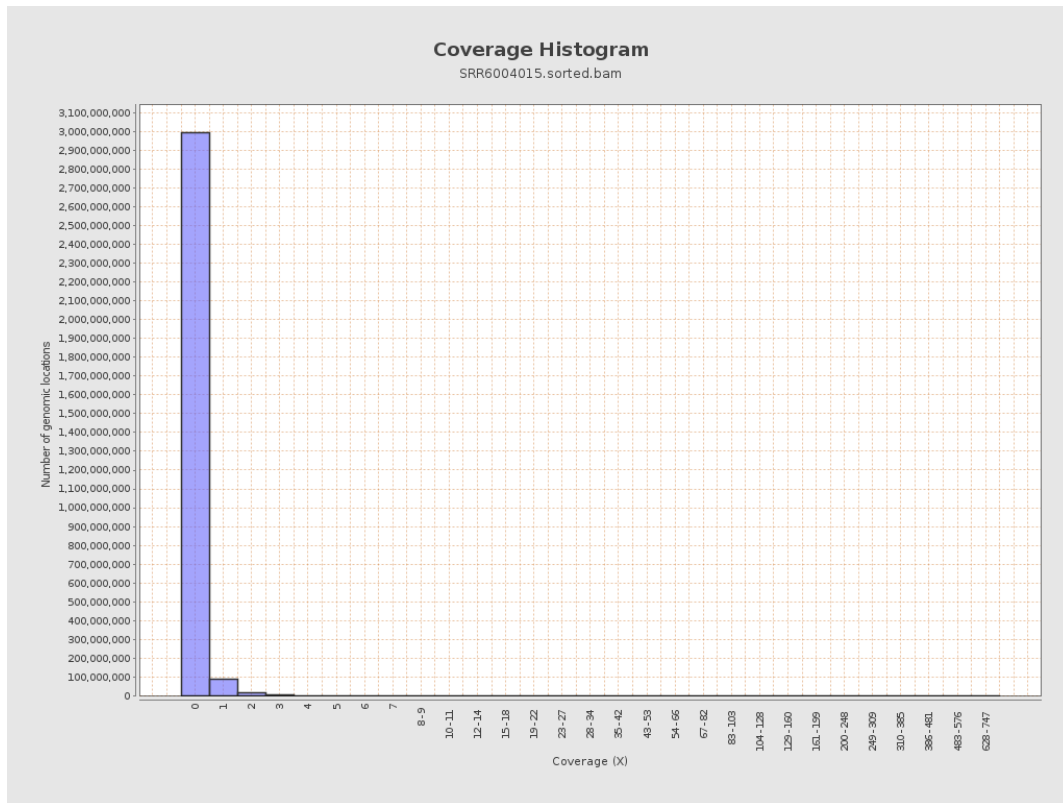
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8035426	0.0322	0.3864
chr2	243199373	8542256	0.0351	0.3249
chr3	198022430	10285508	0.0519	0.2662
chr4	191154276	8291169	0.0434	0.2598
chr5	180915260	7427005	0.0411	0.2368
chr6	171115067	6697397	0.0391	0.2442
chr7	159138663	7369154	0.0463	0.5145

chr8	146364022	8017528	0.0548	0.5213
chr9	141213431	5571498	0.0395	0.2968
chr10	135534747	5712103	0.0421	0.3248
chr11	135006516	4427781	0.0328	0.241
chr12	133851895	6902295	0.0516	0.2698
chr13	115169878	3267295	0.0284	0.2021
chr14	107349540	2568795	0.0239	0.1926
chr15	102531392	5956713	0.0581	0.2847
chr16	90354753	3928973	0.0435	0.2545
chr17	81195210	2197358	0.0271	0.1969
chr18	78077248	3095487	0.0396	0.4548
chr19	59128983	2184957	0.037	0.3181
chr20	63025520	2913393	0.0462	0.2581
chr21	48129895	1454903	0.0302	0.2249
chr22	51304566	926278	0.0181	0.1527
chrMT	16571	32263	1.947	2.0441
chrX	155270560	7618098	0.0491	0.2773
chrY	59373566	275573	0.0046	0.1145

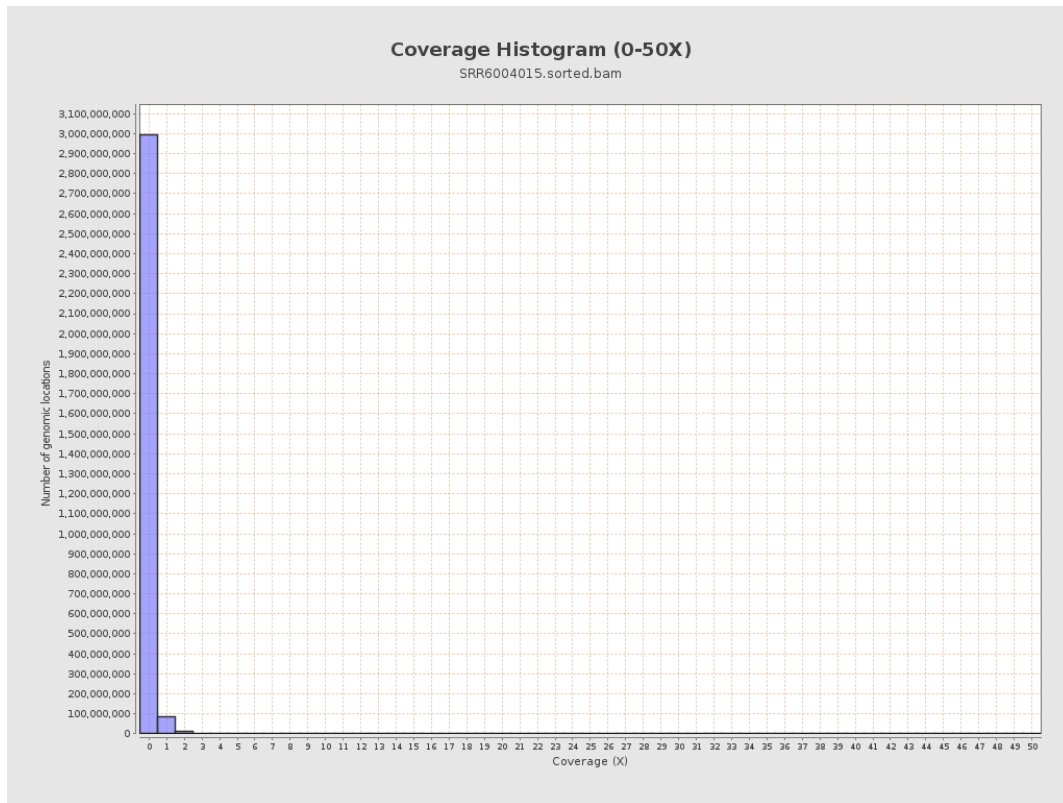
3. Results : Coverage across reference



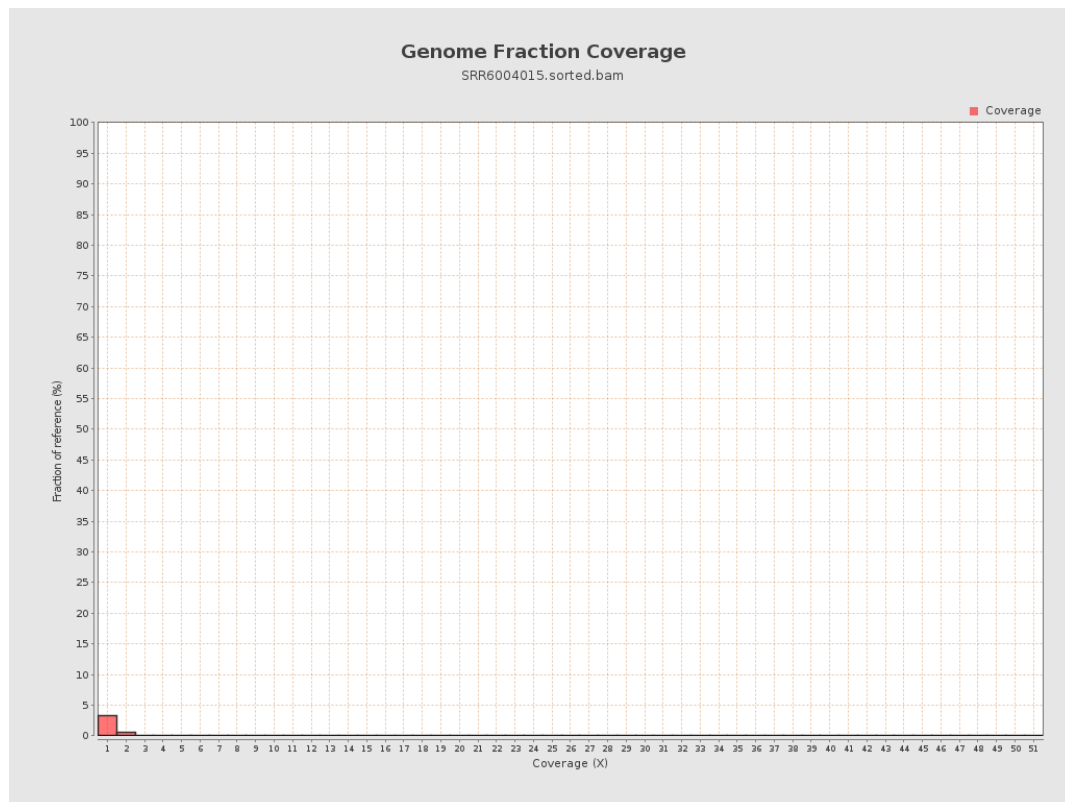
4. Results : Coverage Histogram



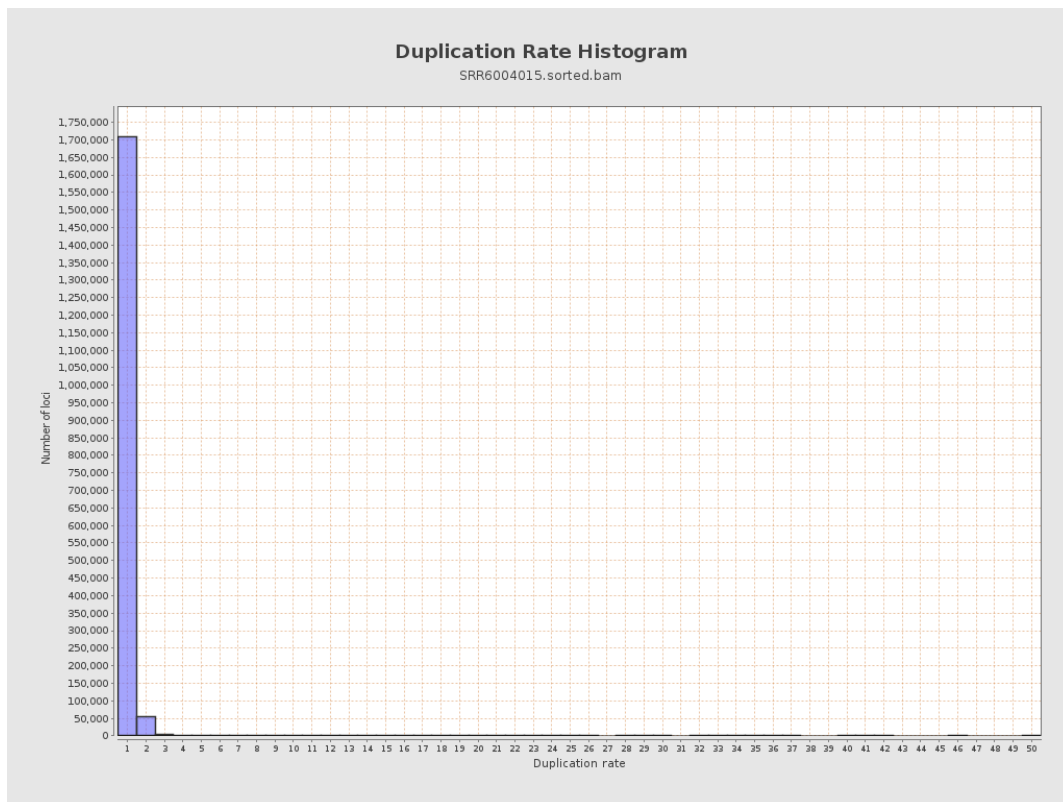
5. Results : Coverage Histogram (0-50X)



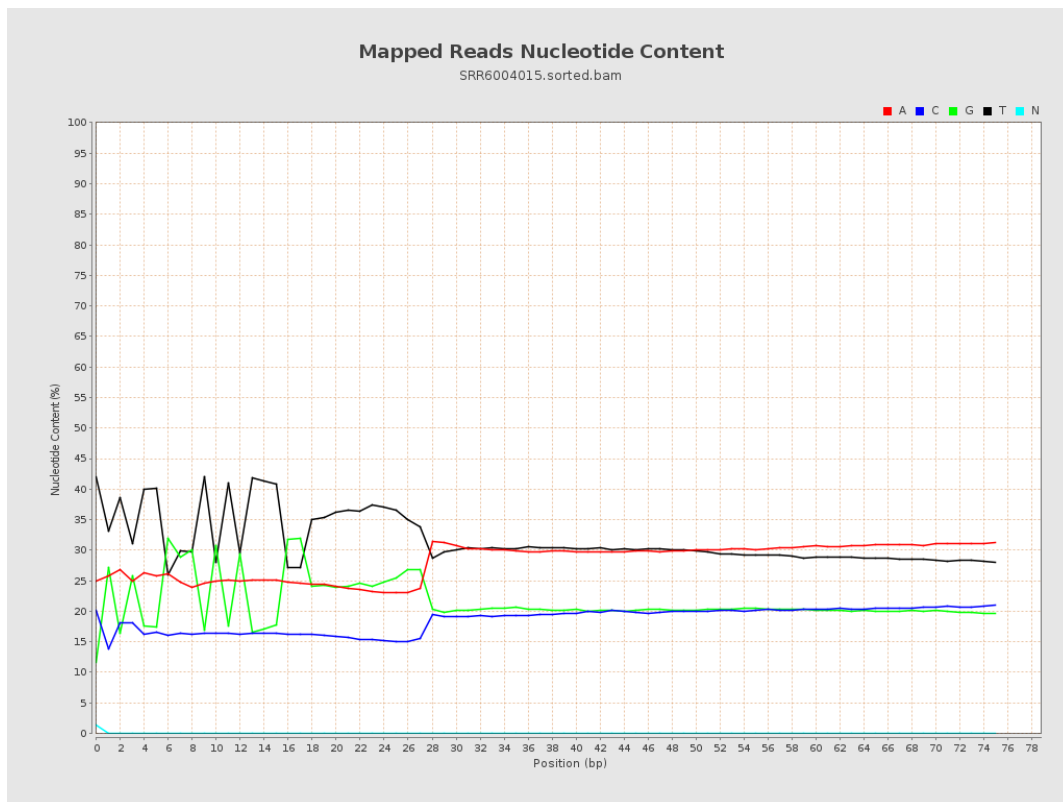
6. Results : Genome Fraction Coverage



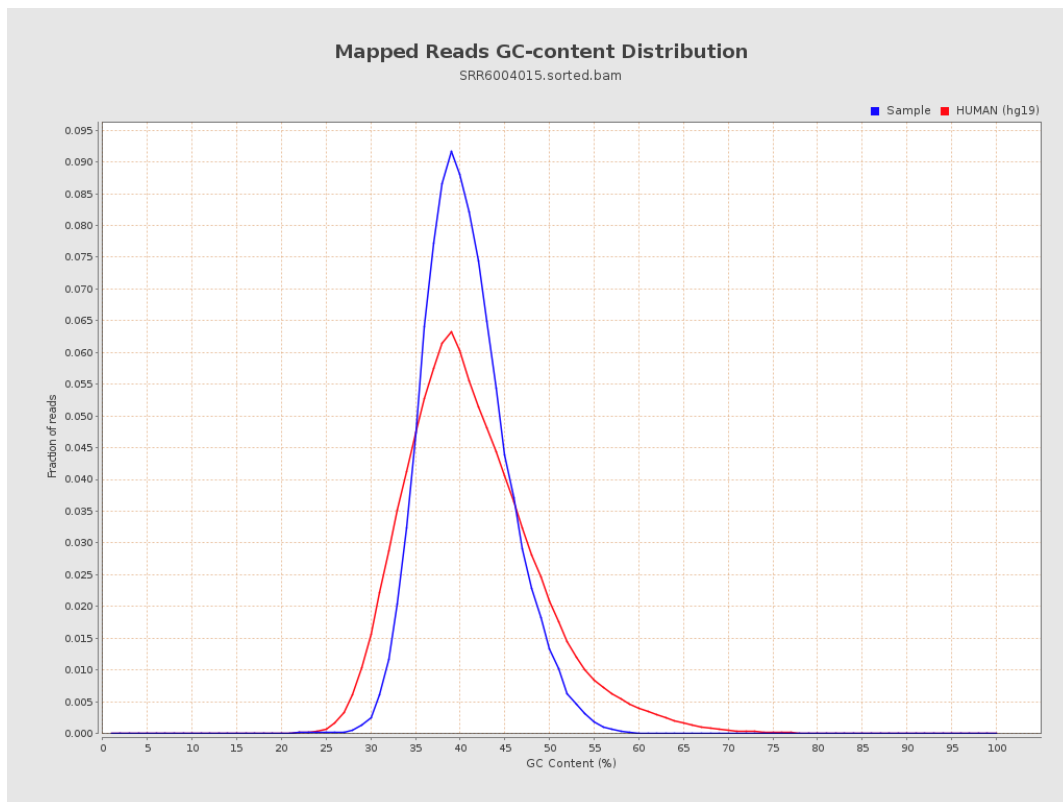
7. Results : Duplication Rate Histogram



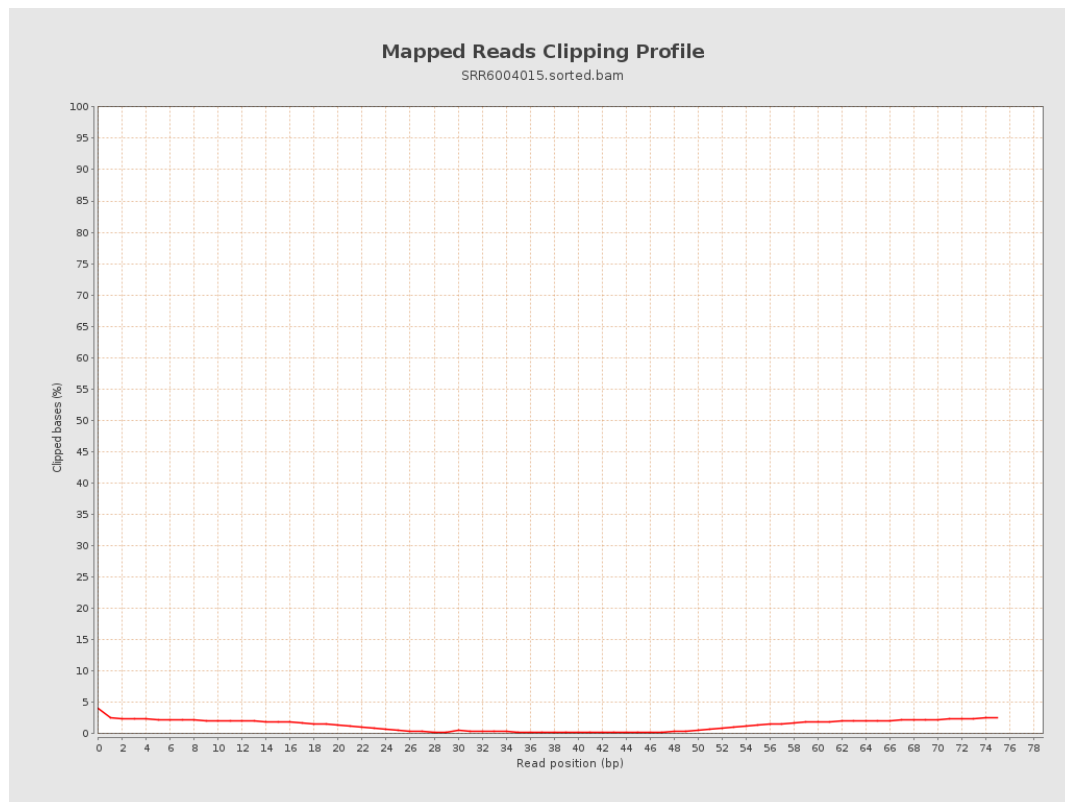
8. Results : Mapped Reads Nucleotide Content



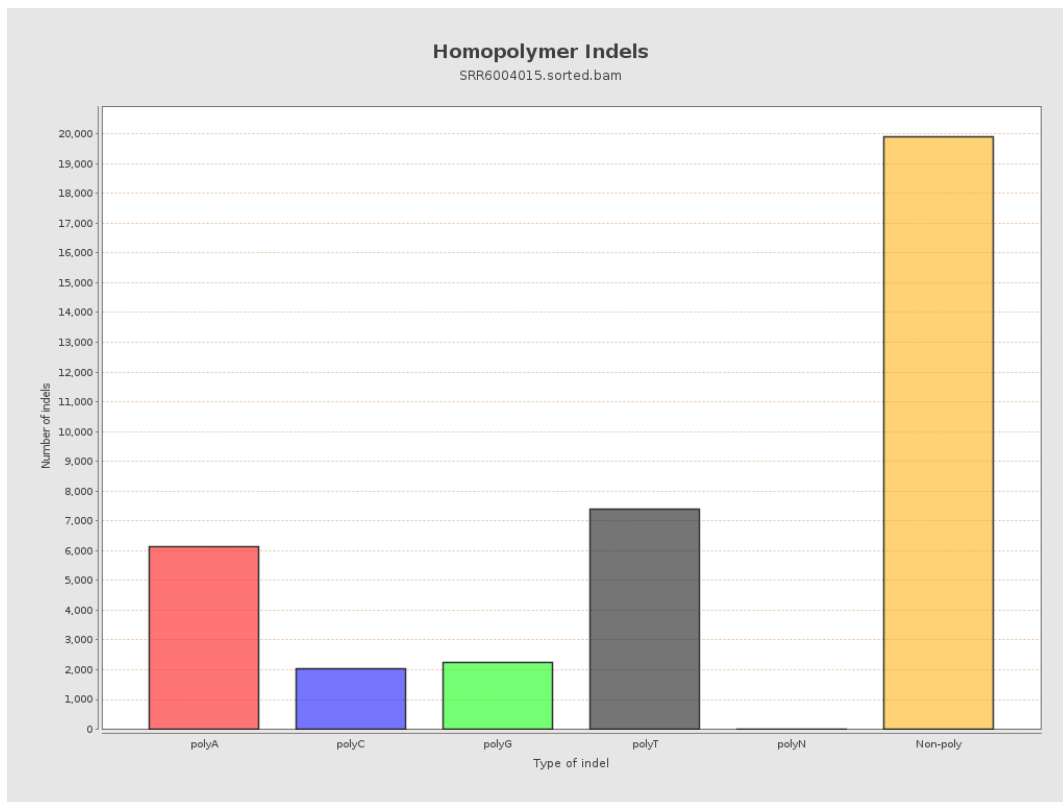
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

