

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:40:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013202.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_SRR6013202 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013202.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:40:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013202.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,261,259
Mapped reads	1,941,556 / 85.86%
Unmapped reads	319,703 / 14.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,387 / 0.5%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	116,937 / 5.17%
Duplication rate	4.97%
Clipped reads	808,491 / 35.75%

2.2. ACGT Content

Number/percentage of A's	36,025,137 / 27.56%
Number/percentage of C's	24,438,728 / 18.69%
Number/percentage of T's	41,315,731 / 31.6%
Number/percentage of G's	28,931,255 / 22.13%
Number/percentage of N's	27,647 / 0.02%
GC Percentage	40.82%

2.3. Coverage

Mean	0.0422

Standard Deviation	0.3601
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2.4. Mapping Quality

Mean Mapping Quality	44.55
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2.5. Mismatches and indels

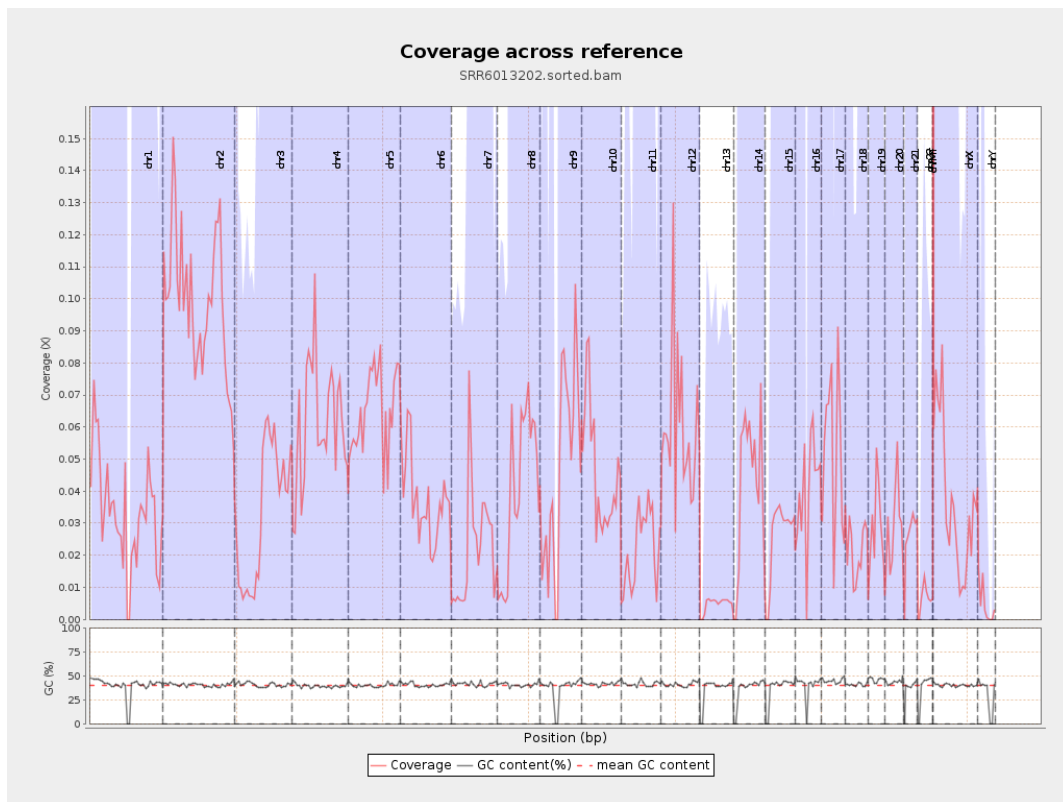
General error rate	0.79%
Mismatches	1,018,716
Insertions	9,247
Mapped reads with at least one insertion	0.47%
Deletions	29,162
Mapped reads with at least one deletion	1.49%
Homopolymer indels	47.46%

2.6. Chromosome stats

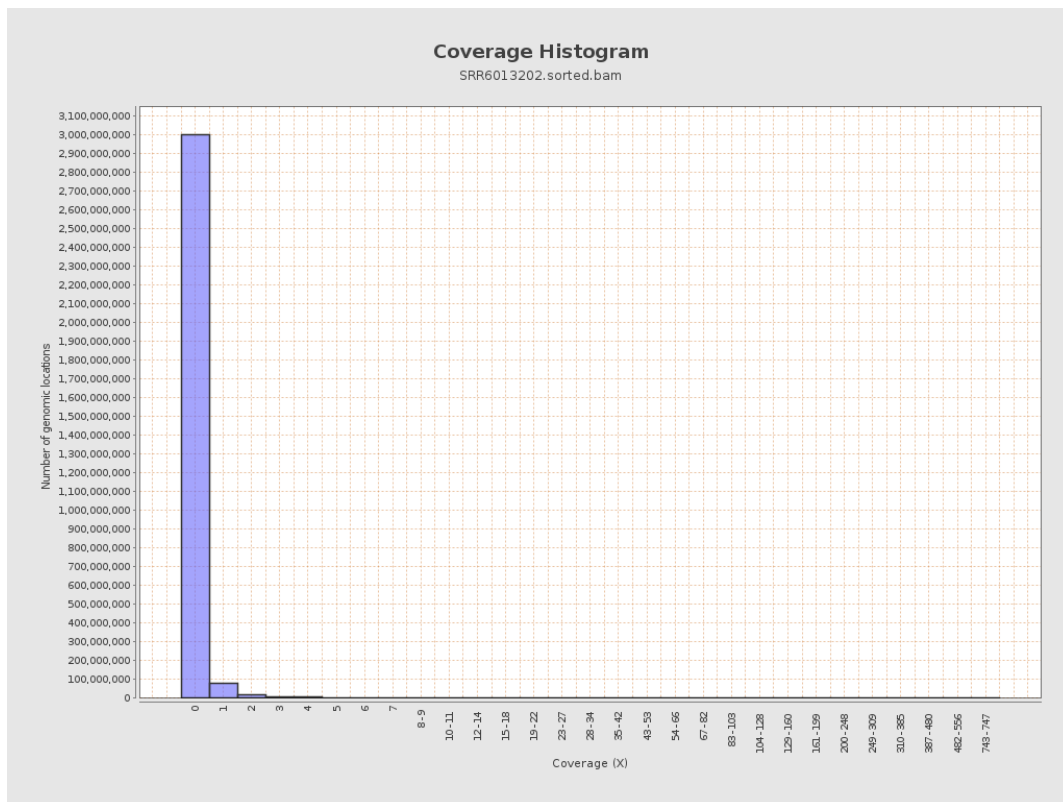
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8299879	0.0333	0.4409
chr2	243199373	24149203	0.0993	0.5685
chr3	198022430	6547595	0.0331	0.2307
chr4	191154276	11774859	0.0616	0.3334
chr5	180915260	11814837	0.0653	0.3251
chr6	171115067	6285871	0.0367	0.2711
chr7	159138663	3589412	0.0226	0.5797

chr8	146364022	5905951	0.0404	0.4243
chr9	141213431	6581488	0.0466	0.3462
chr10	135534747	6199609	0.0457	0.3891
chr11	135006516	3062987	0.0227	0.2204
chr12	133851895	7927416	0.0592	0.3174
chr13	115169878	554870	0.0048	0.0827
chr14	107349540	4678330	0.0436	0.2845
chr15	102531392	2626602	0.0256	0.2019
chr16	90354753	3618523	0.04	0.2638
chr17	81195210	4229178	0.0521	0.3619
chr18	78077248	1702582	0.0218	0.4376
chr19	59128983	1717862	0.0291	0.3803
chr20	63025520	1819043	0.0289	0.2215
chr21	48129895	1253288	0.026	0.2339
chr22	51304566	328165	0.0064	0.093
chrMT	16571	26697	1.6111	1.7119
chrX	155270560	5817891	0.0375	0.2596
chrY	59373566	277164	0.0047	0.1386

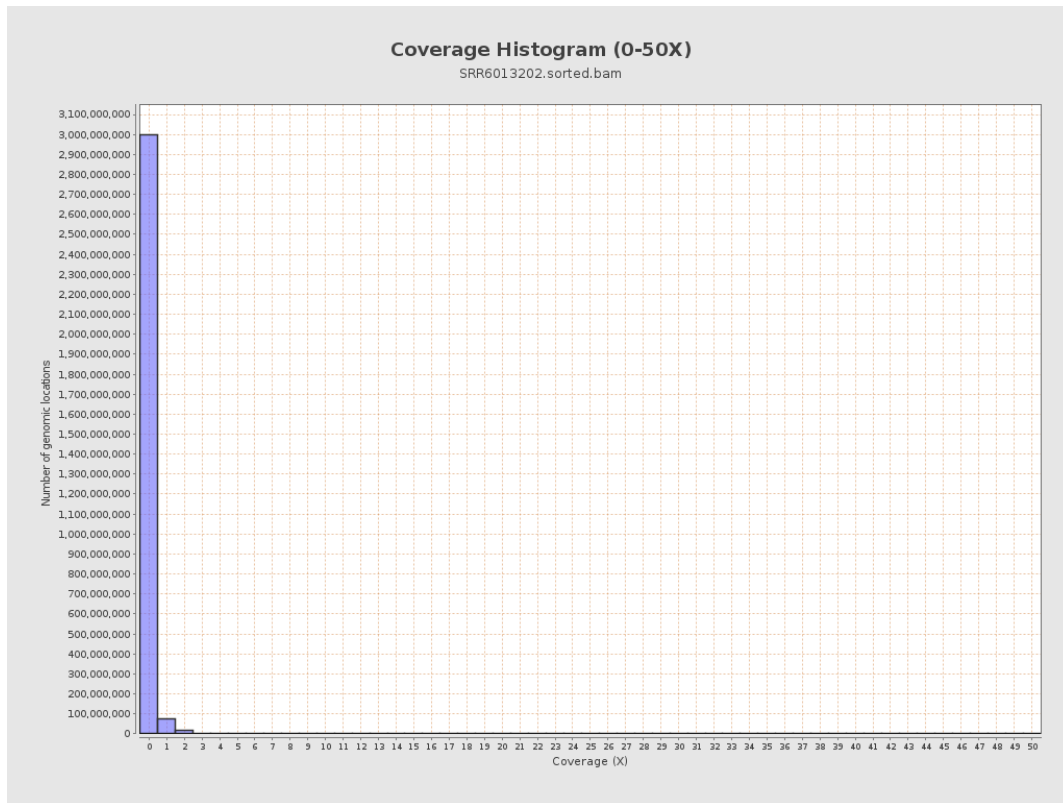
3. Results : Coverage across reference



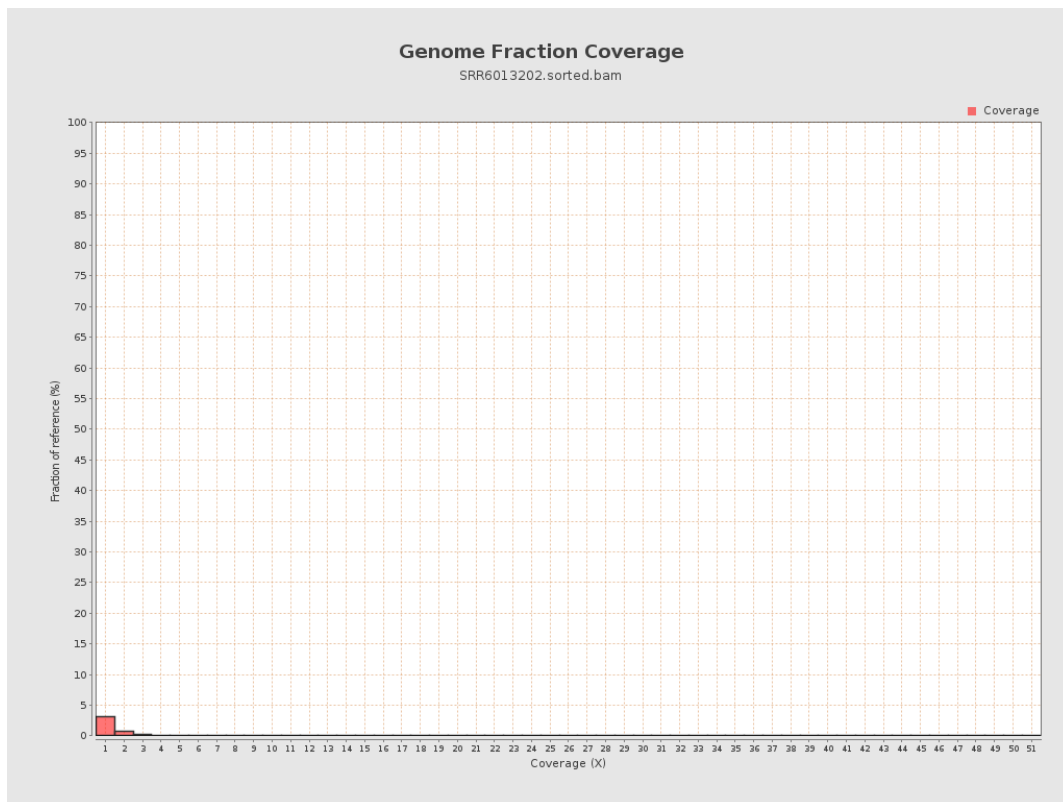
4. Results : Coverage Histogram



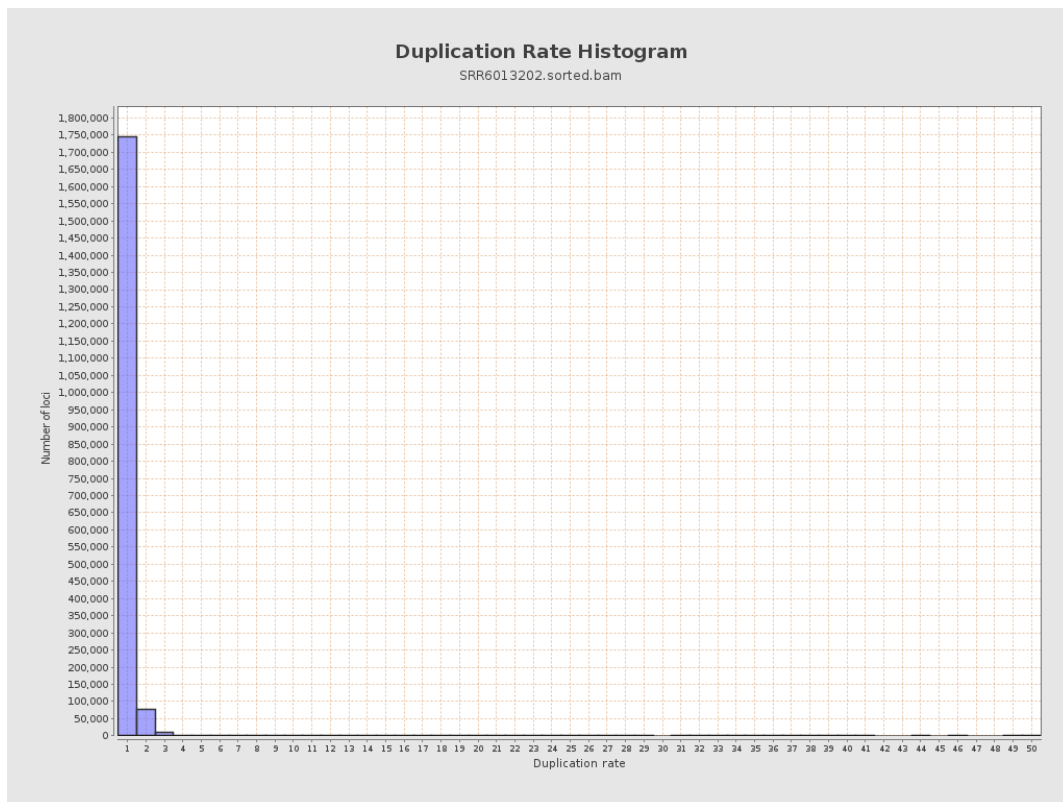
5. Results : Coverage Histogram (0-50X)



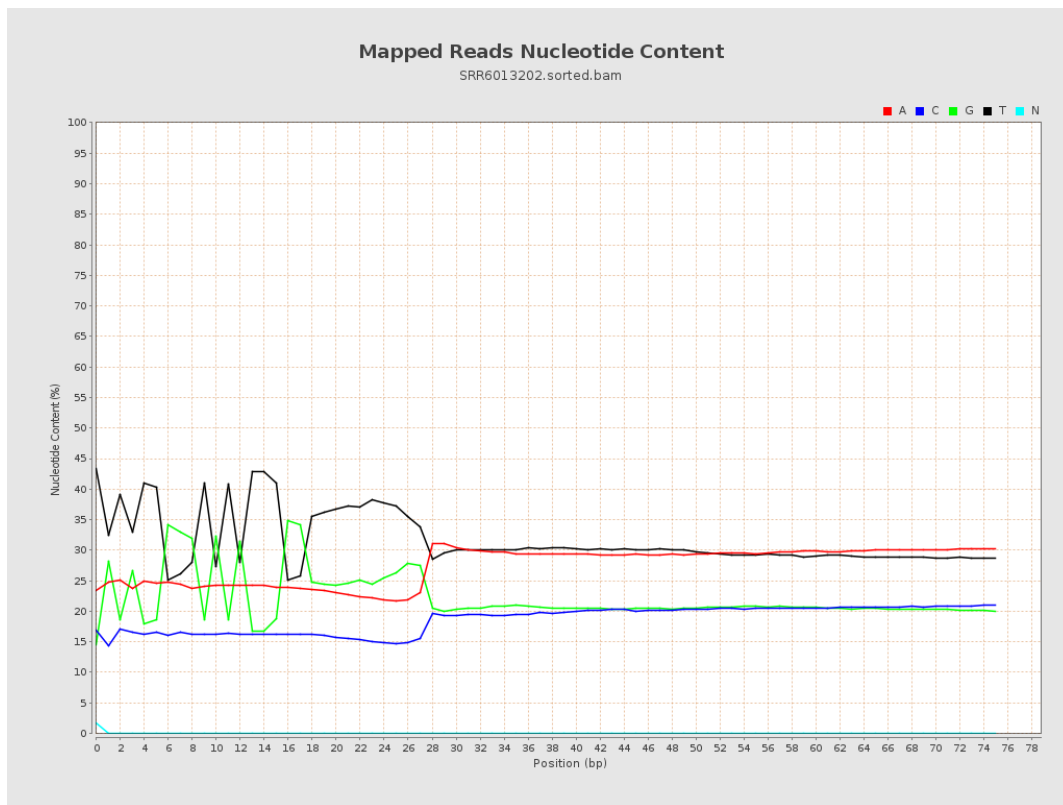
6. Results : Genome Fraction Coverage



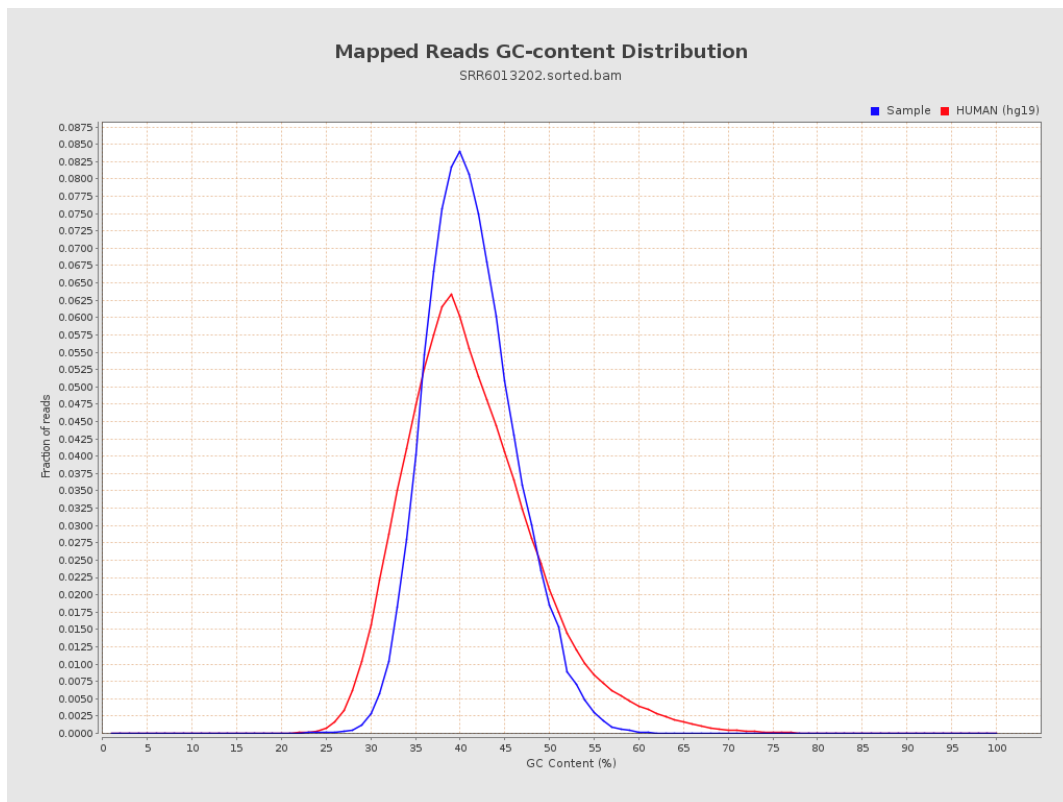
7. Results : Duplication Rate Histogram



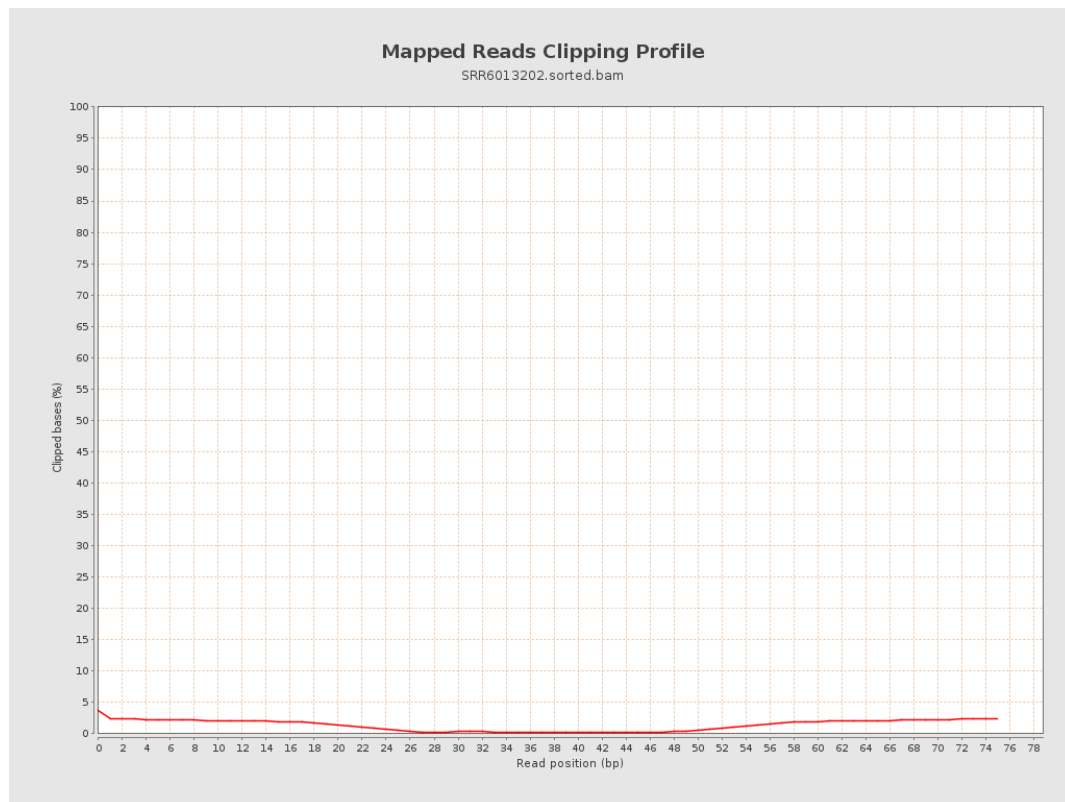
8. Results : Mapped Reads Nucleotide Content



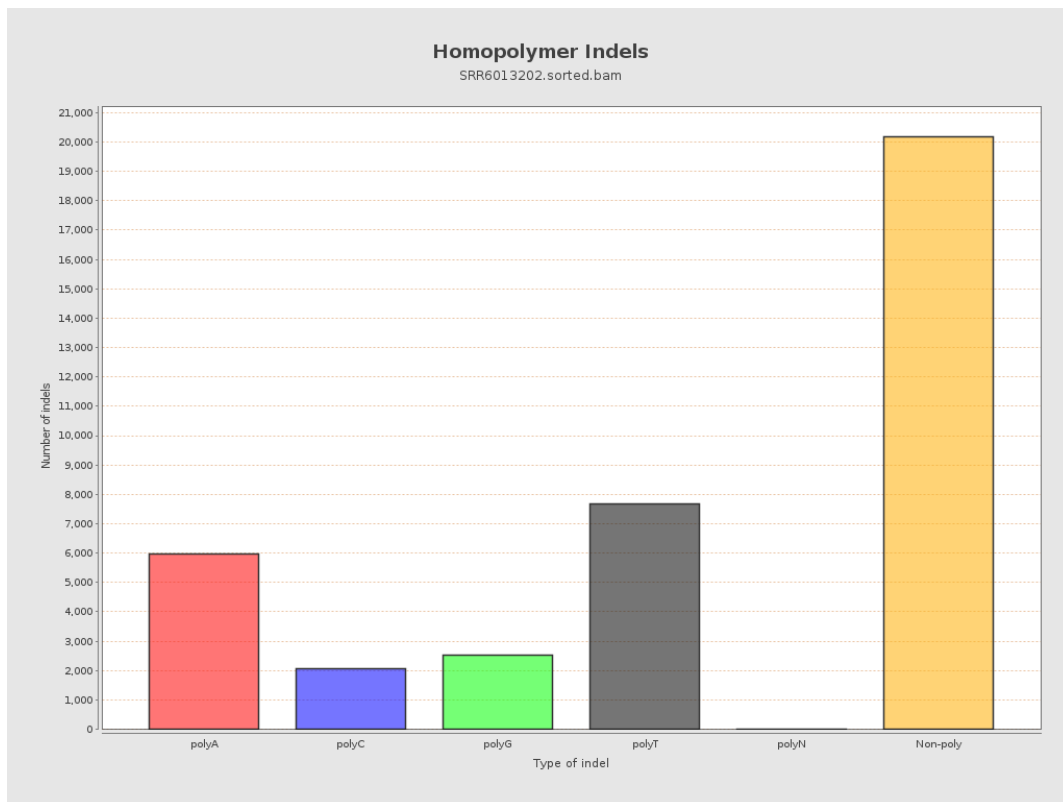
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

