

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:03:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013252.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_SRR6013252 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013252.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:03:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013252.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,716,790
Mapped reads	1,343,674 / 78.27%
Unmapped reads	373,116 / 21.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,948 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	102,695 / 5.98%
Duplication rate	6.47%
Clipped reads	744,448 / 43.36%

2.2. ACGT Content

Number/percentage of A's	22,315,401 / 25.94%
Number/percentage of C's	15,925,062 / 18.51%
Number/percentage of T's	27,261,639 / 31.68%
Number/percentage of G's	20,537,390 / 23.87%
Number/percentage of N's	1,145 / 0%
GC Percentage	42.38%

2.3. Coverage

Mean	0.0278

Standard Deviation	0.2654
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2.4. Mapping Quality

Mean Mapping Quality	45.23
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2.5. Mismatches and indels

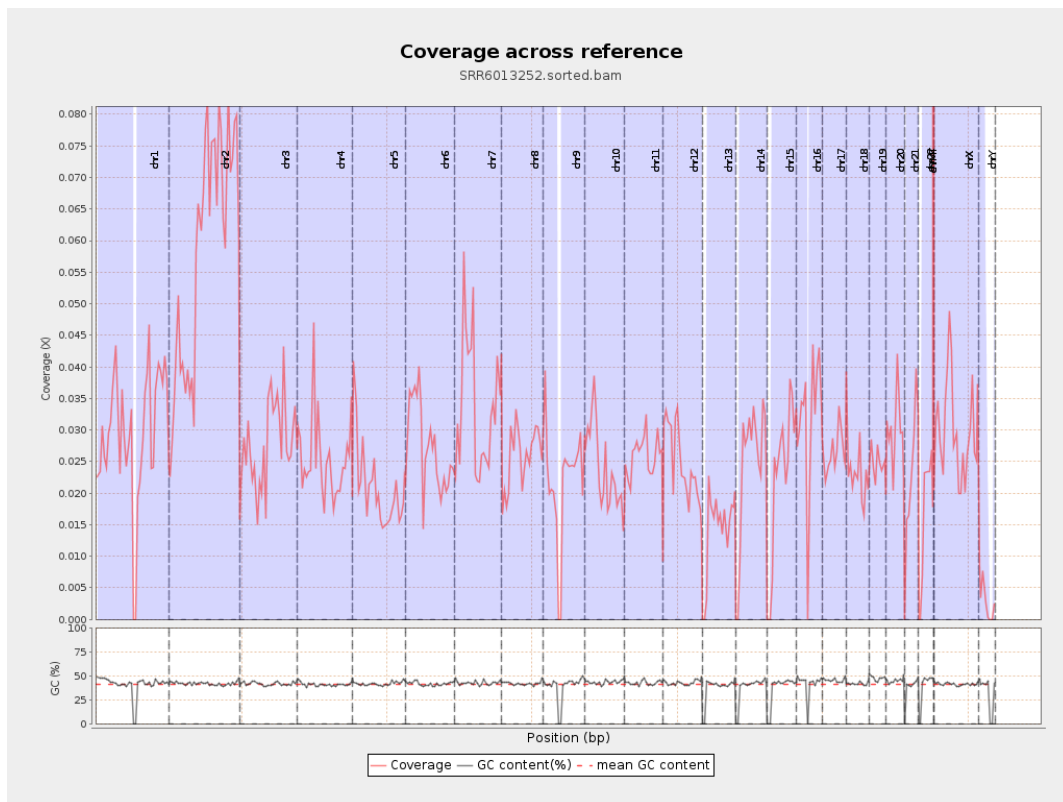
General error rate	0.78%
Mismatches	662,087
Insertions	5,320
Mapped reads with at least one insertion	0.39%
Deletions	20,946
Mapped reads with at least one deletion	1.54%
Homopolymer indels	45.94%

2.6. Chromosome stats

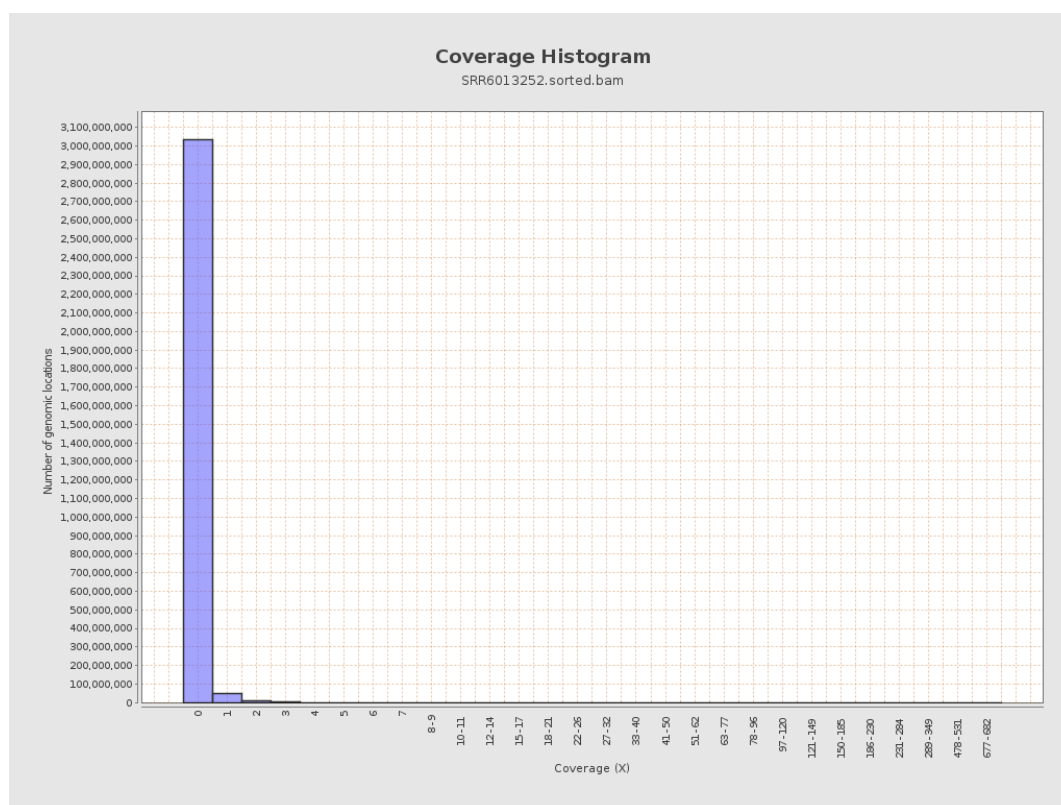
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7377144	0.0296	0.3242
chr2	243199373	14207980	0.0584	0.4321
chr3	198022430	5486646	0.0277	0.2136
chr4	191154276	4816541	0.0252	0.2068
chr5	180915260	3757420	0.0208	0.1853
chr6	171115067	4646072	0.0272	0.2407
chr7	159138663	5331266	0.0335	0.437

chr8	146364022	3778624	0.0258	0.2423
chr9	141213431	3070955	0.0217	0.2152
chr10	135534747	3267538	0.0241	0.2235
chr11	135006516	3477243	0.0258	0.2441
chr12	133851895	3332490	0.0249	0.2032
chr13	115169878	1625642	0.0141	0.1517
chr14	107349540	2616988	0.0244	0.2066
chr15	102531392	2334304	0.0228	0.1968
chr16	90354753	2863088	0.0317	0.2323
chr17	81195210	2144007	0.0264	0.2207
chr18	78077248	1804320	0.0231	0.2985
chr19	59128983	1464535	0.0248	0.2581
chr20	63025520	1884907	0.0299	0.2241
chr21	48129895	1108695	0.023	0.1984
chr22	51304566	840431	0.0164	0.1625
chrMT	16571	23836	1.4384	1.6551
chrX	155270560	4645784	0.0299	0.2439
chrY	59373566	170525	0.0029	0.0718

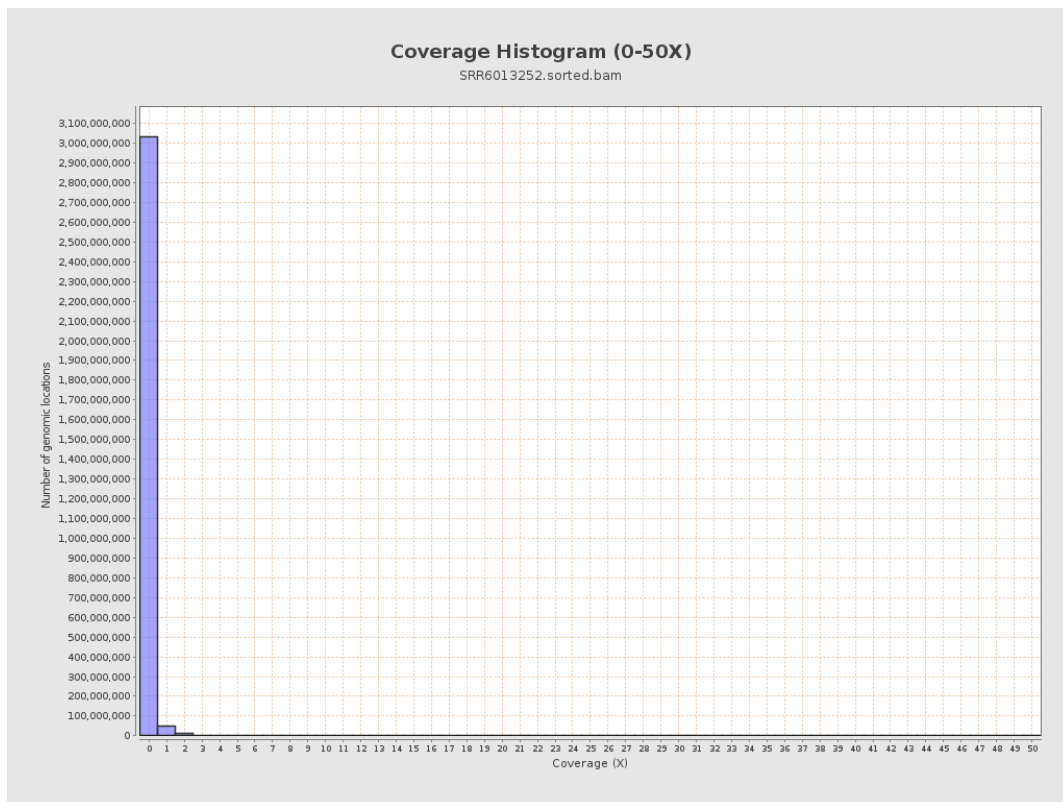
3. Results : Coverage across reference



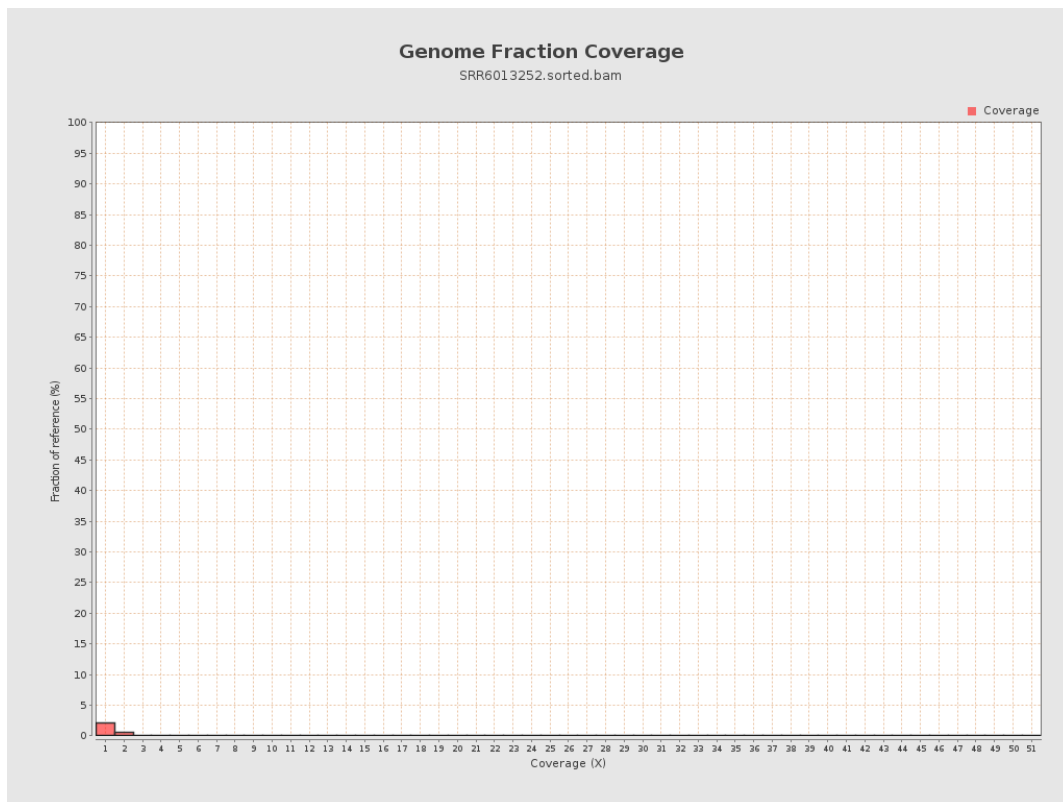
4. Results : Coverage Histogram



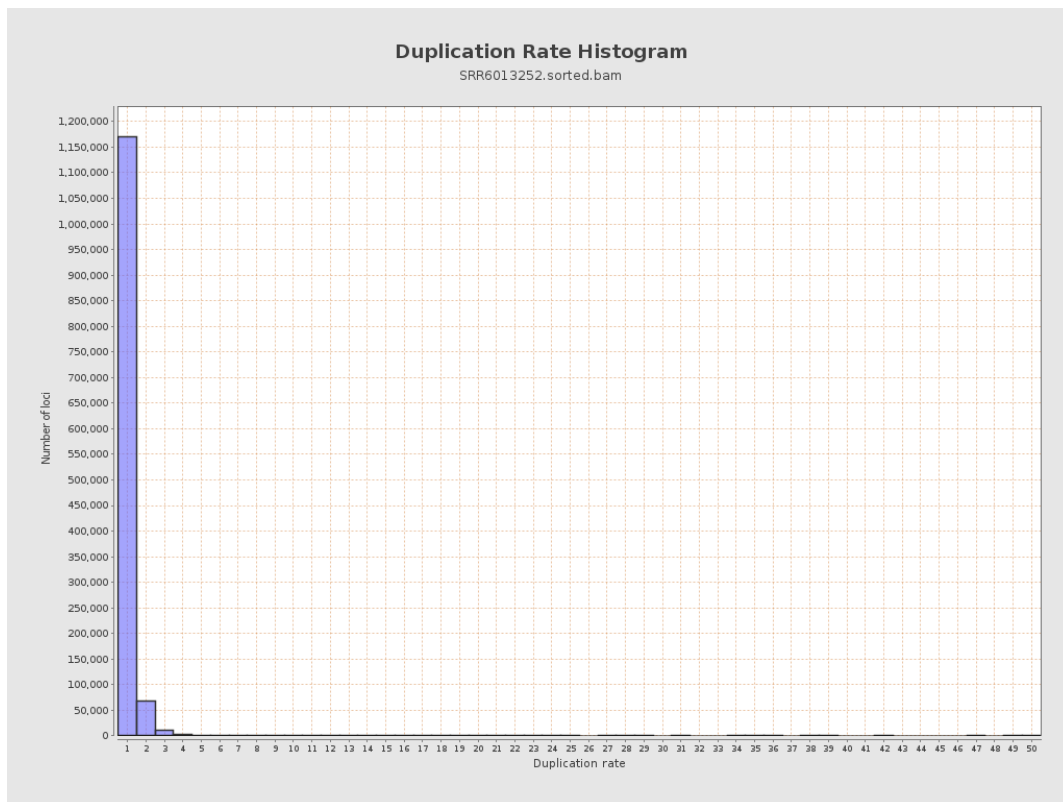
5. Results : Coverage Histogram (0-50X)



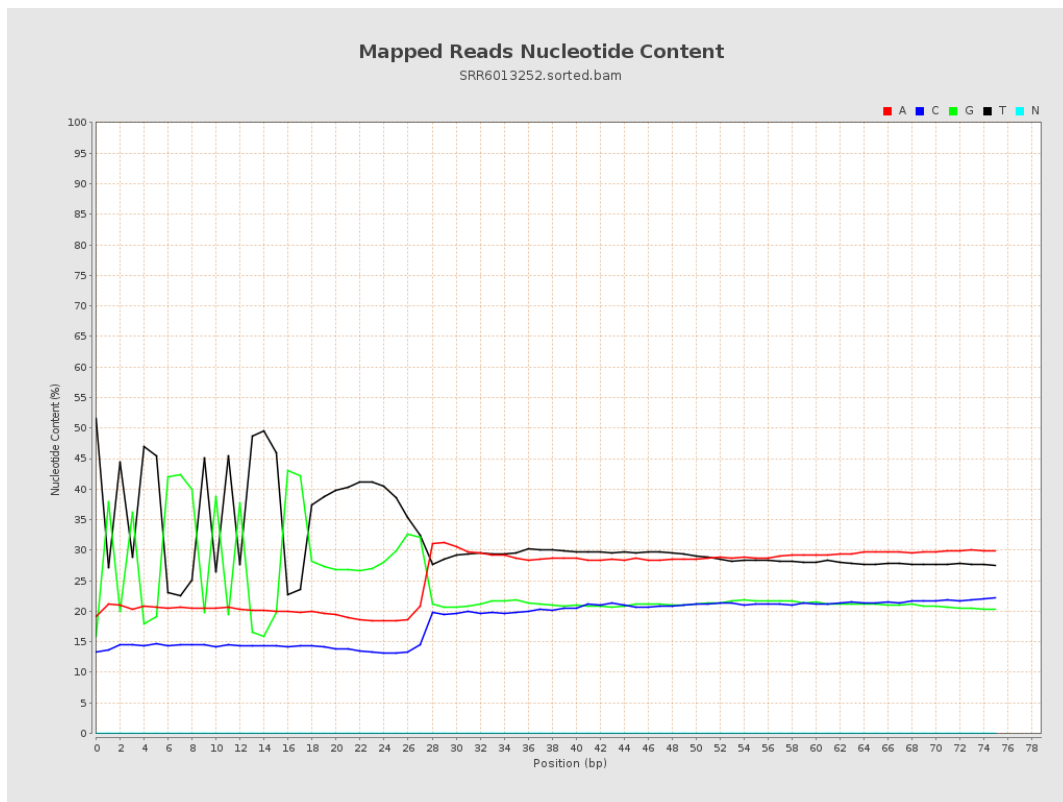
6. Results : Genome Fraction Coverage



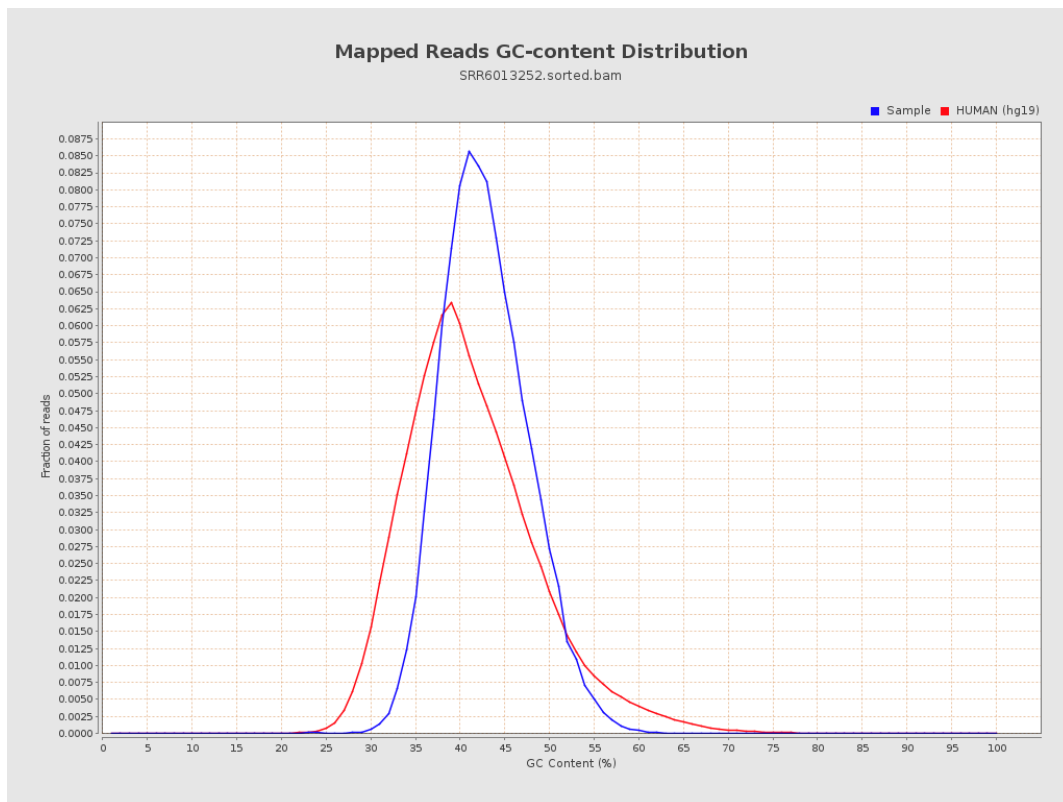
7. Results : Duplication Rate Histogram



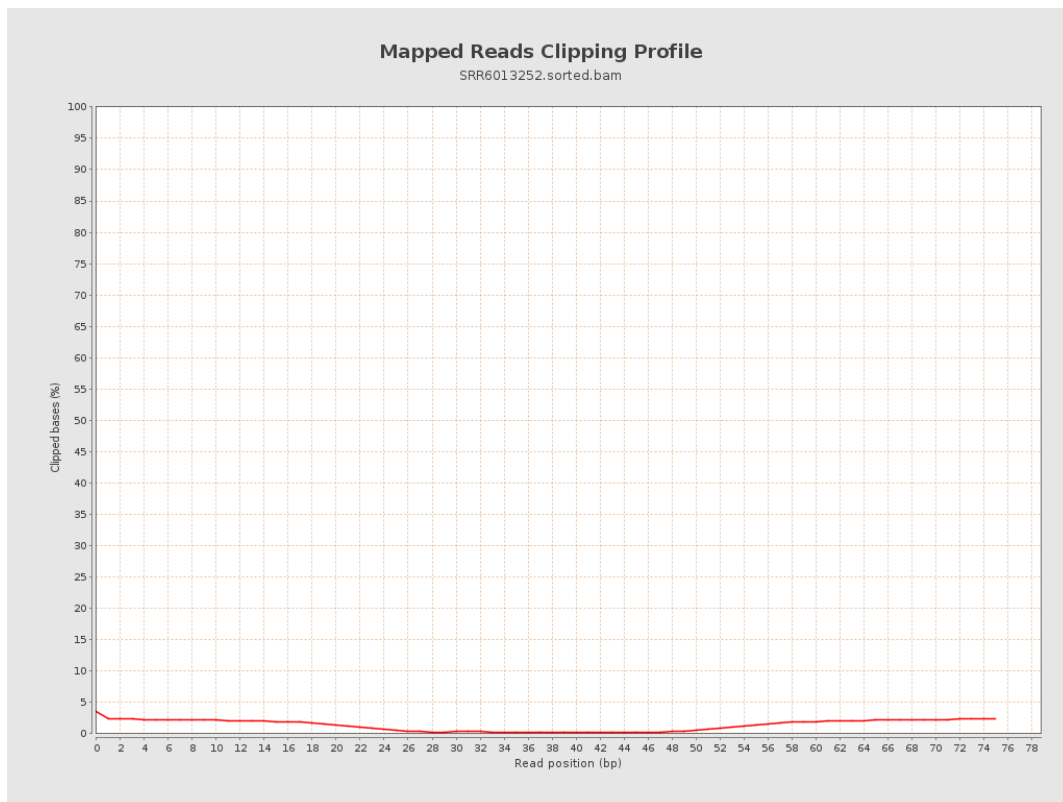
8. Results : Mapped Reads Nucleotide Content



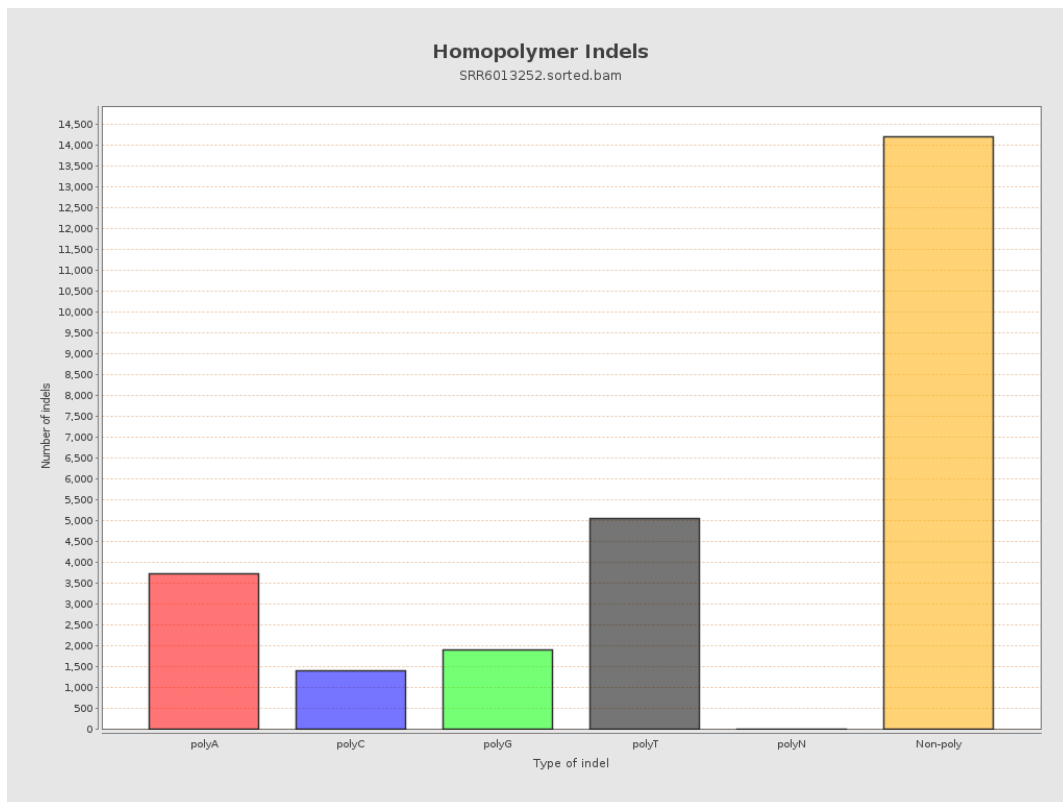
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

