

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 02:01:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004107.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_SRR6004107 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004107.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 02:01:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004107.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,942,124
Mapped reads	2,144,858 / 72.9%
Unmapped reads	797,266 / 27.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,405 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	139,797 / 4.75%
Duplication rate	5.33%
Clipped reads	1,256,788 / 42.72%

2.2. ACGT Content

Number/percentage of A's	35,351,462 / 25.86%
Number/percentage of C's	24,396,353 / 17.85%
Number/percentage of T's	44,807,547 / 32.78%
Number/percentage of G's	32,124,298 / 23.5%
Number/percentage of N's	17,040 / 0.01%
GC Percentage	41.35%

2.3. Coverage

Mean	0.0442

Standard Deviation	0.4024
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2.4. Mapping Quality

Mean Mapping Quality	44.54
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2.5. Mismatches and indels

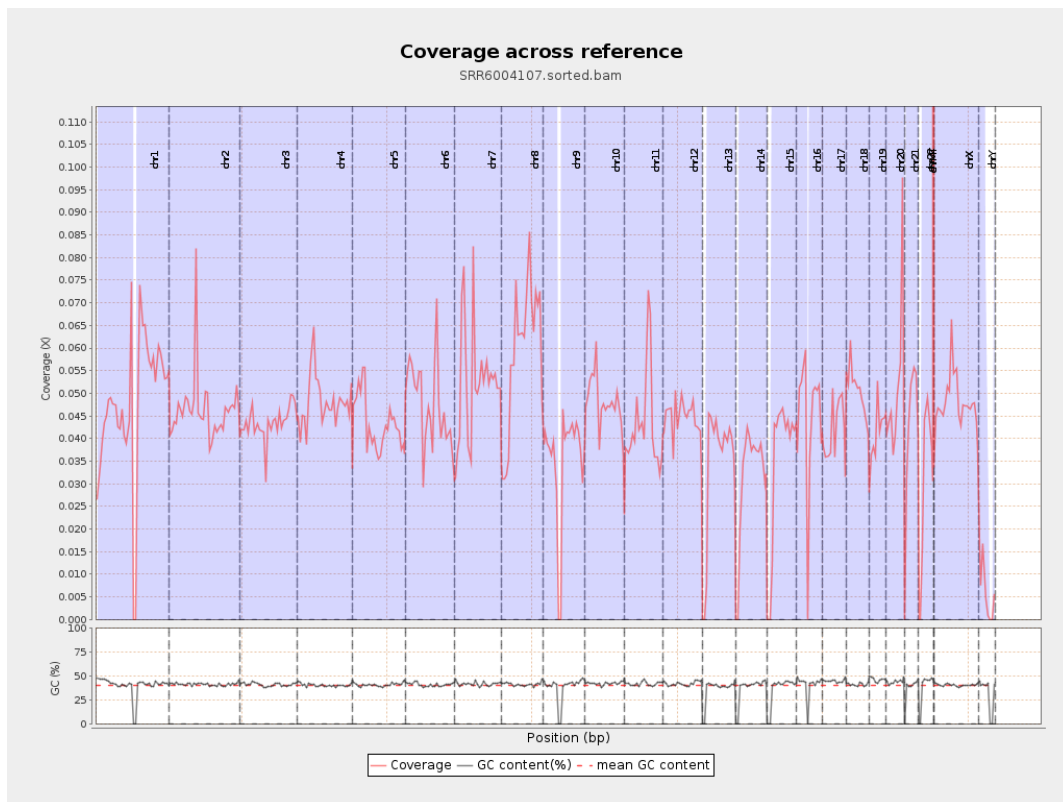
General error rate	1.08%
Mismatches	1,463,623
Insertions	11,800
Mapped reads with at least one insertion	0.54%
Deletions	49,668
Mapped reads with at least one deletion	2.28%
Homopolymer indels	47.83%

2.6. Chromosome stats

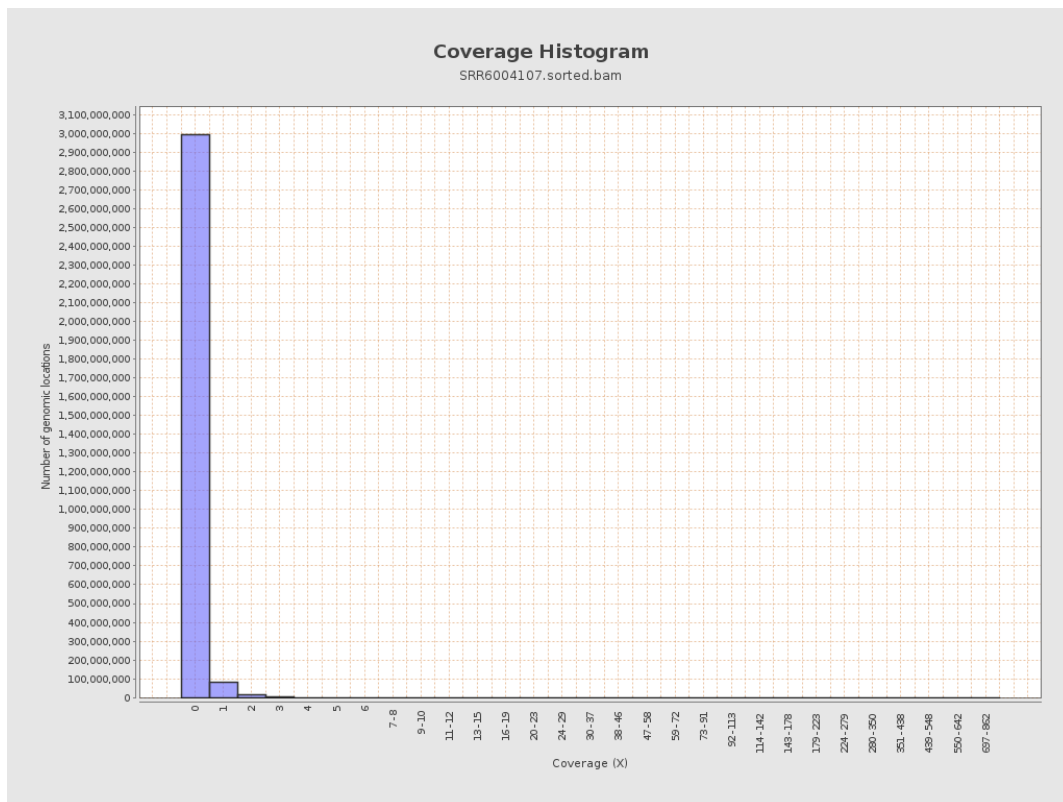
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11891742	0.0477	0.6465
chr2	243199373	11280425	0.0464	0.5385
chr3	198022430	8615577	0.0435	0.2605
chr4	191154276	9165587	0.0479	0.2841
chr5	180915260	7831801	0.0433	0.2608
chr6	171115067	8108171	0.0474	0.3093
chr7	159138663	8459022	0.0532	0.6563

chr8	146364022	8647693	0.0591	0.4465
chr9	141213431	4932761	0.0349	0.3715
chr10	135534747	6530526	0.0482	0.3335
chr11	135006516	5853470	0.0434	0.3692
chr12	133851895	5978359	0.0447	0.2683
chr13	115169878	3925933	0.0341	0.2303
chr14	107349540	3360237	0.0313	0.2497
chr15	102531392	3589435	0.035	0.2416
chr16	90354753	4052958	0.0449	0.285
chr17	81195210	3377261	0.0416	0.2769
chr18	78077248	3960366	0.0507	0.6794
chr19	59128983	2449075	0.0414	0.4302
chr20	63025520	3273582	0.0519	0.3016
chr21	48129895	2033042	0.0422	0.2734
chr22	51304566	1539324	0.03	0.2139
chrMT	16571	123361	7.4444	5.6174
chrX	155270560	7441218	0.0479	0.3119
chrY	59373566	357064	0.006	0.1224

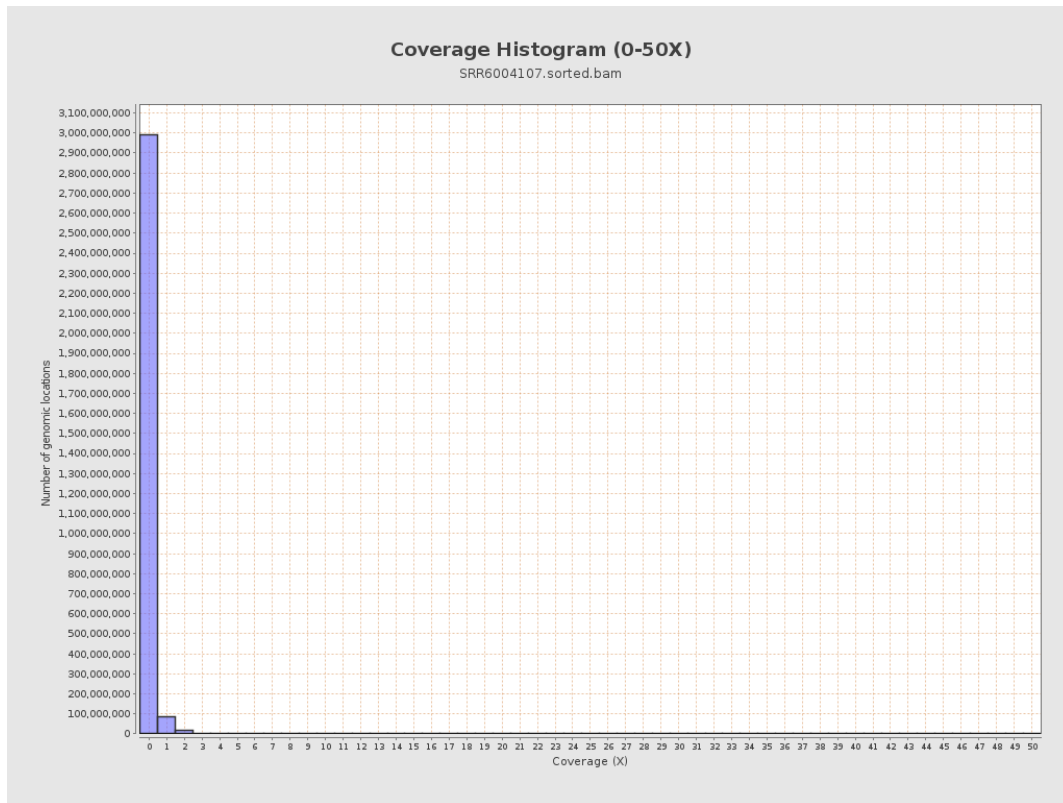
3. Results : Coverage across reference



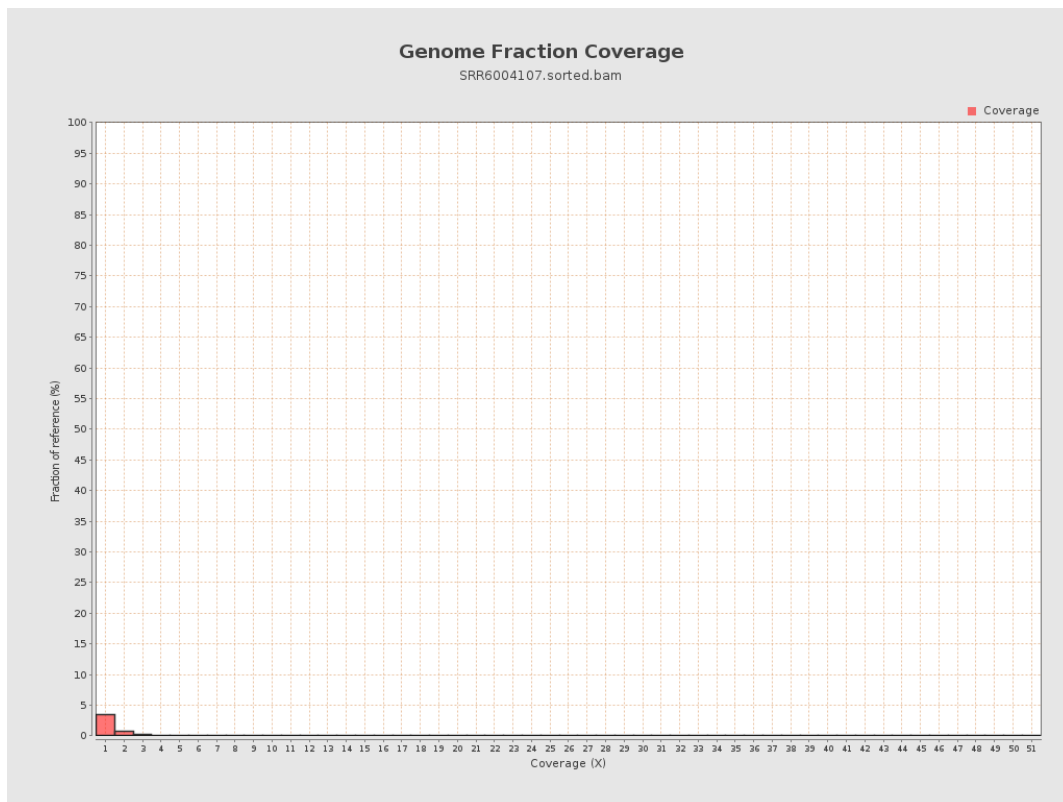
4. Results : Coverage Histogram



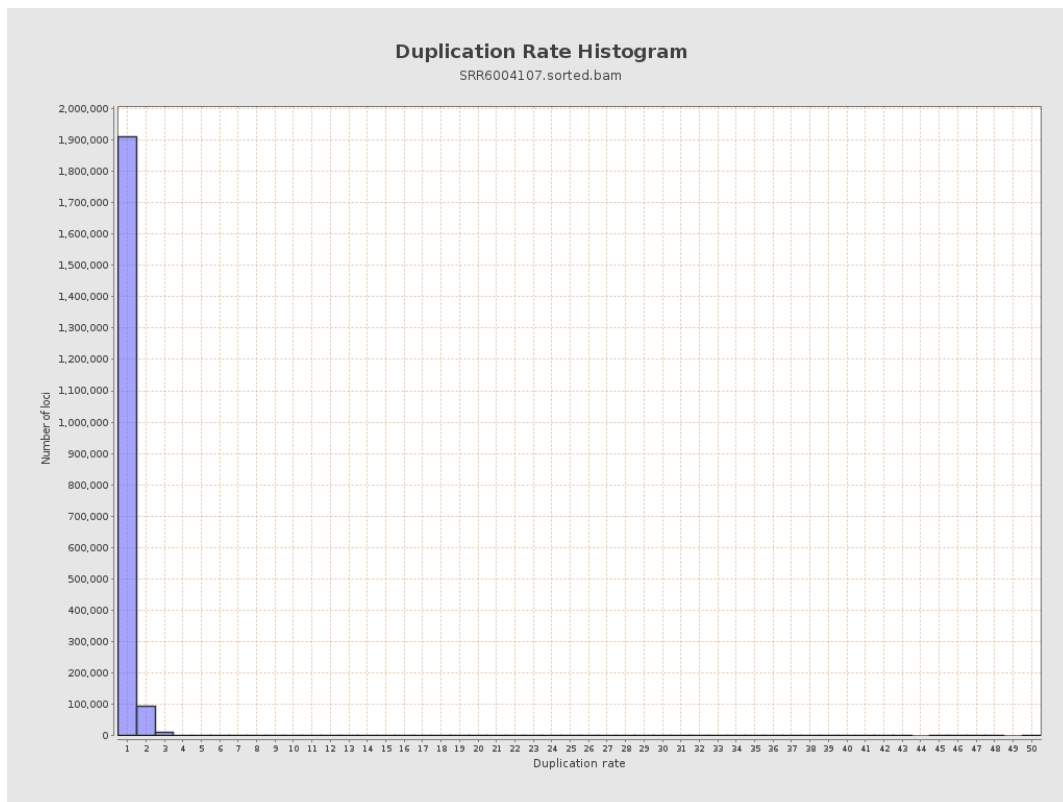
5. Results : Coverage Histogram (0-50X)



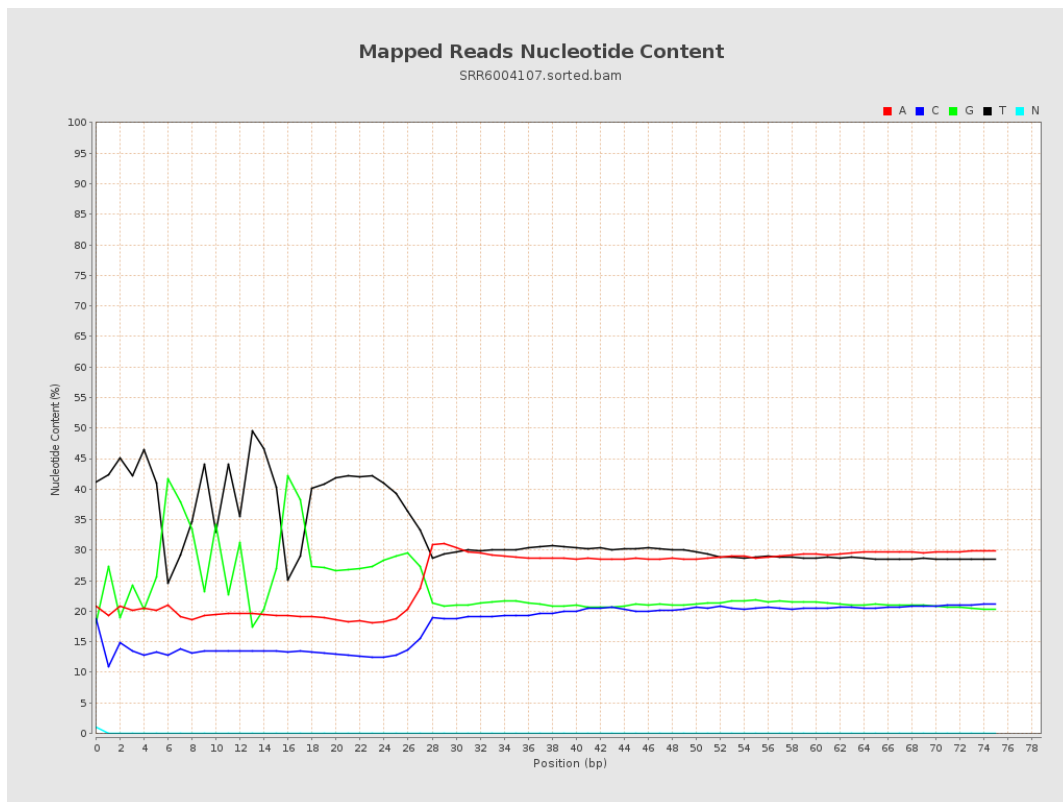
6. Results : Genome Fraction Coverage



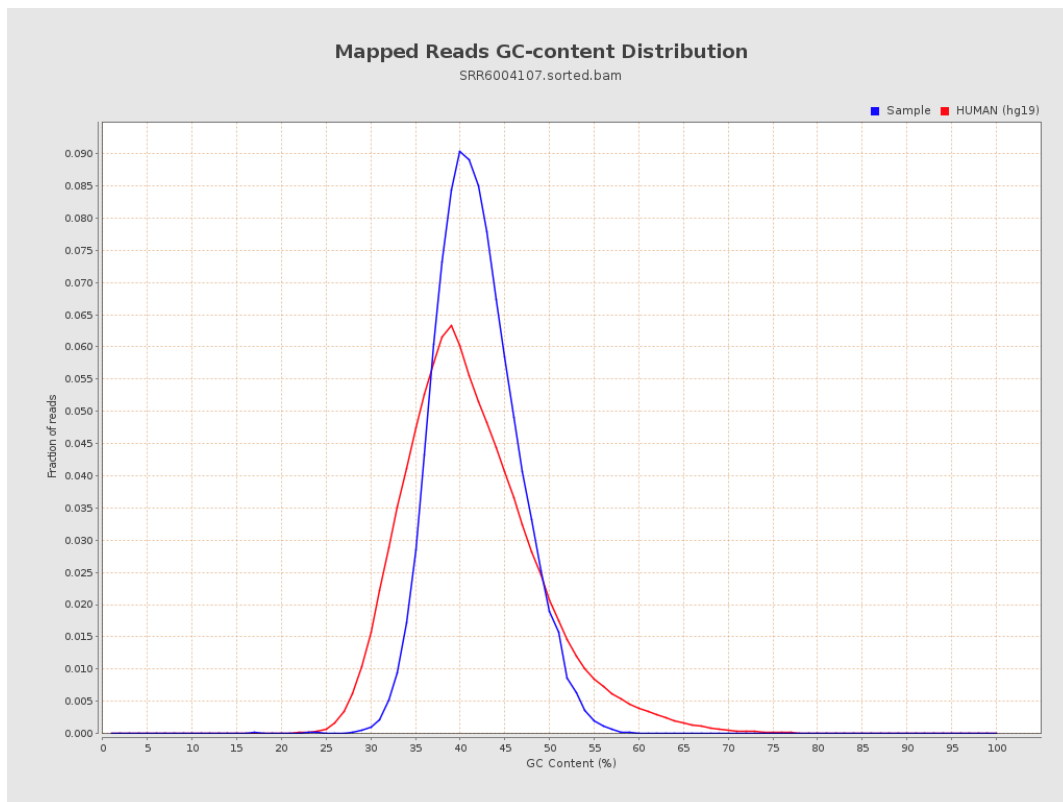
7. Results : Duplication Rate Histogram



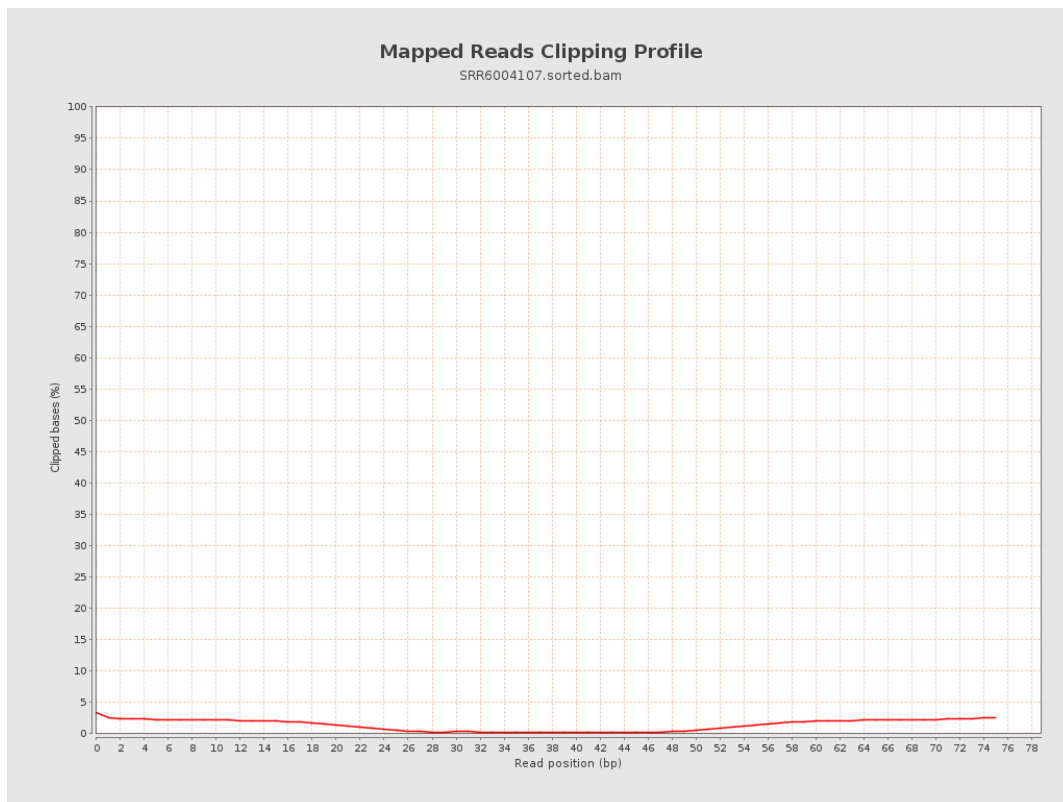
8. Results : Mapped Reads Nucleotide Content



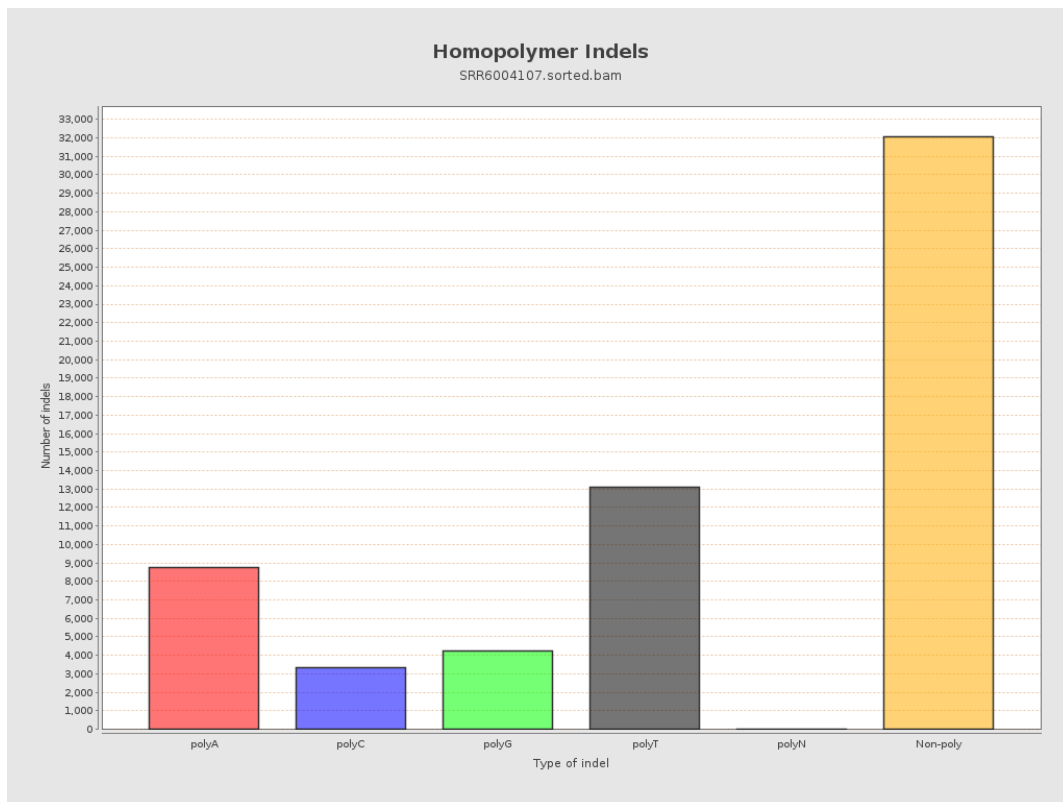
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

