

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 21:41:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236123.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_SRR6236123 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236123.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 21:41:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236123.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,511,964
Mapped reads	1,280,536 / 84.69%
Unmapped reads	231,428 / 15.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,023 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	73,389 / 4.85%
Duplication rate	4.65%
Clipped reads	640,551 / 42.37%

2.2. ACGT Content

Number/percentage of A's	22,705,120 / 27.21%
Number/percentage of C's	14,784,439 / 17.72%
Number/percentage of T's	27,154,611 / 32.54%
Number/percentage of G's	18,768,675 / 22.49%
Number/percentage of N's	41,255 / 0.05%
GC Percentage	40.21%

2.3. Coverage

Mean	0.027

Standard Deviation	0.2969
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2.4. Mapping Quality

Mean Mapping Quality	44.22
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2.5. Mismatches and indels

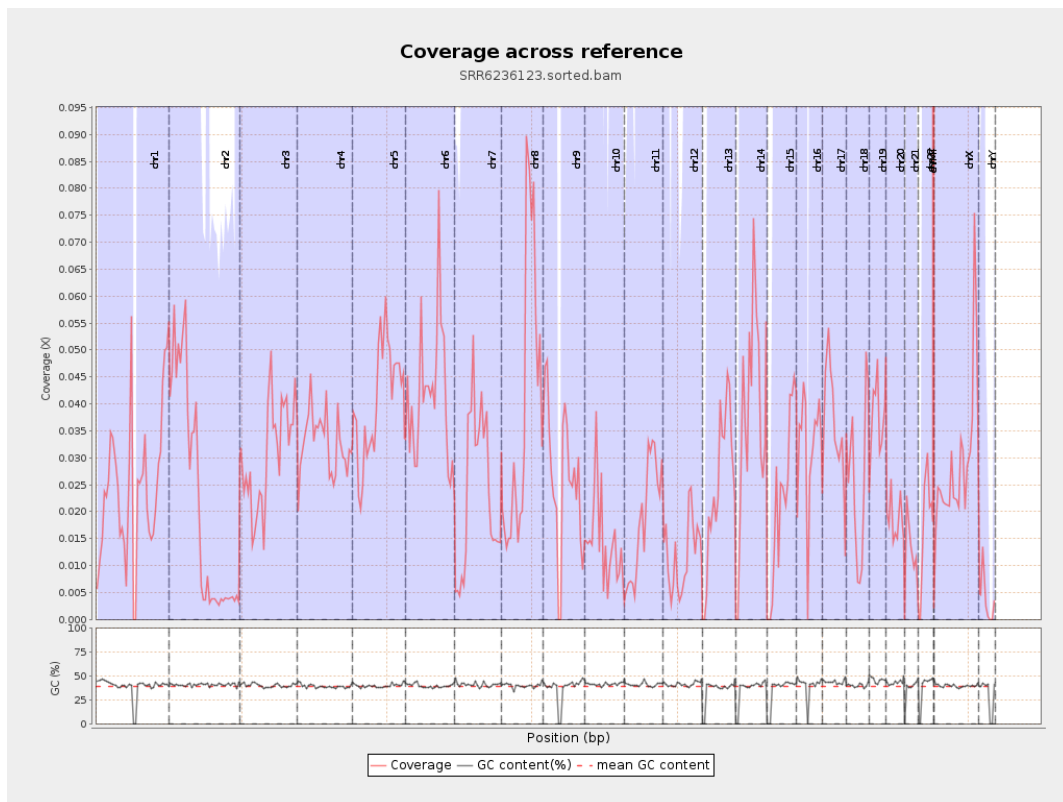
General error rate	0.85%
Mismatches	696,154
Insertions	6,132
Mapped reads with at least one insertion	0.48%
Deletions	23,351
Mapped reads with at least one deletion	1.8%
Homopolymer indels	46.79%

2.6. Chromosome stats

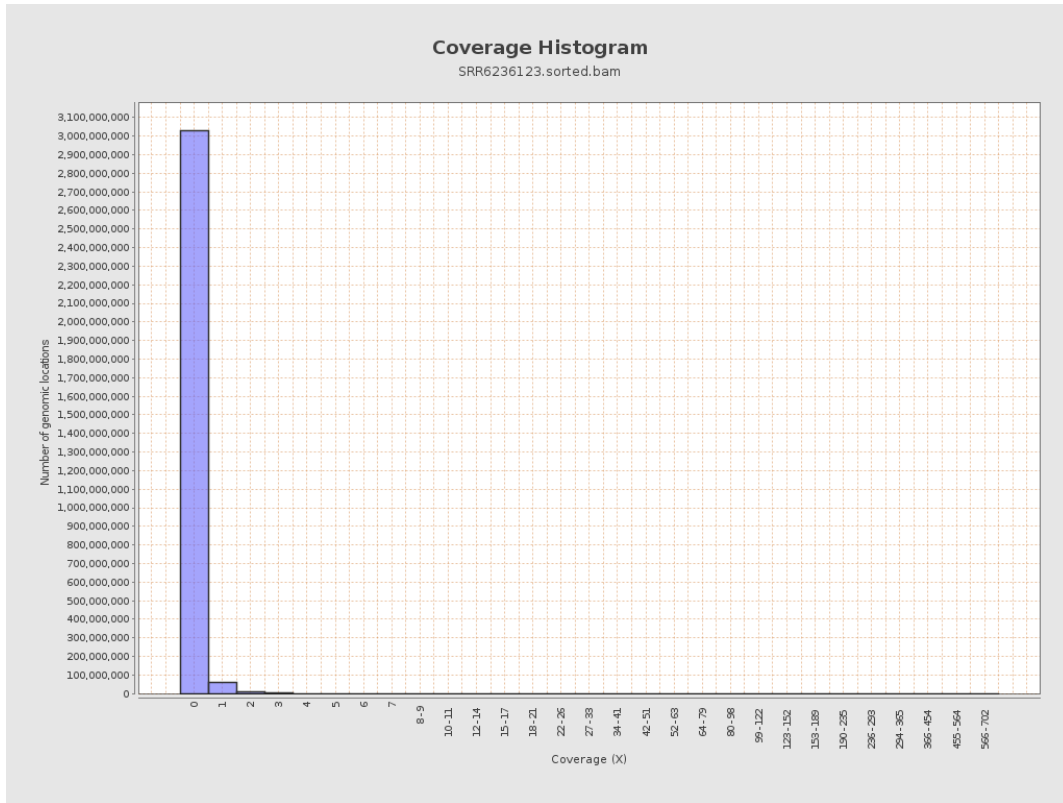
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6055082	0.0243	0.5398
chr2	243199373	5149866	0.0212	0.2863
chr3	198022430	6023396	0.0304	0.2031
chr4	191154276	6254989	0.0327	0.2421
chr5	180915260	7340375	0.0406	0.237
chr6	171115067	7056100	0.0412	0.2976
chr7	159138663	3725554	0.0234	0.314

chr8	146364022	5635154	0.0385	0.4857
chr9	141213431	3674533	0.026	0.2622
chr10	135534747	1951463	0.0144	0.2408
chr11	135006516	2506935	0.0186	0.1994
chr12	133851895	1617719	0.0121	0.1337
chr13	115169878	2831880	0.0246	0.1831
chr14	107349540	3910872	0.0364	0.2324
chr15	102531392	2286604	0.0223	0.1786
chr16	90354753	2899950	0.0321	0.2198
chr17	81195210	2908594	0.0358	0.2684
chr18	78077248	1975136	0.0253	0.4178
chr19	59128983	2256631	0.0382	0.4163
chr20	63025520	1168322	0.0185	0.1649
chr21	48129895	600213	0.0125	0.1558
chr22	51304566	887059	0.0173	0.151
chrMT	16571	101720	6.1384	4.6121
chrX	155270560	4463862	0.0287	0.2092
chrY	59373566	212743	0.0036	0.1236

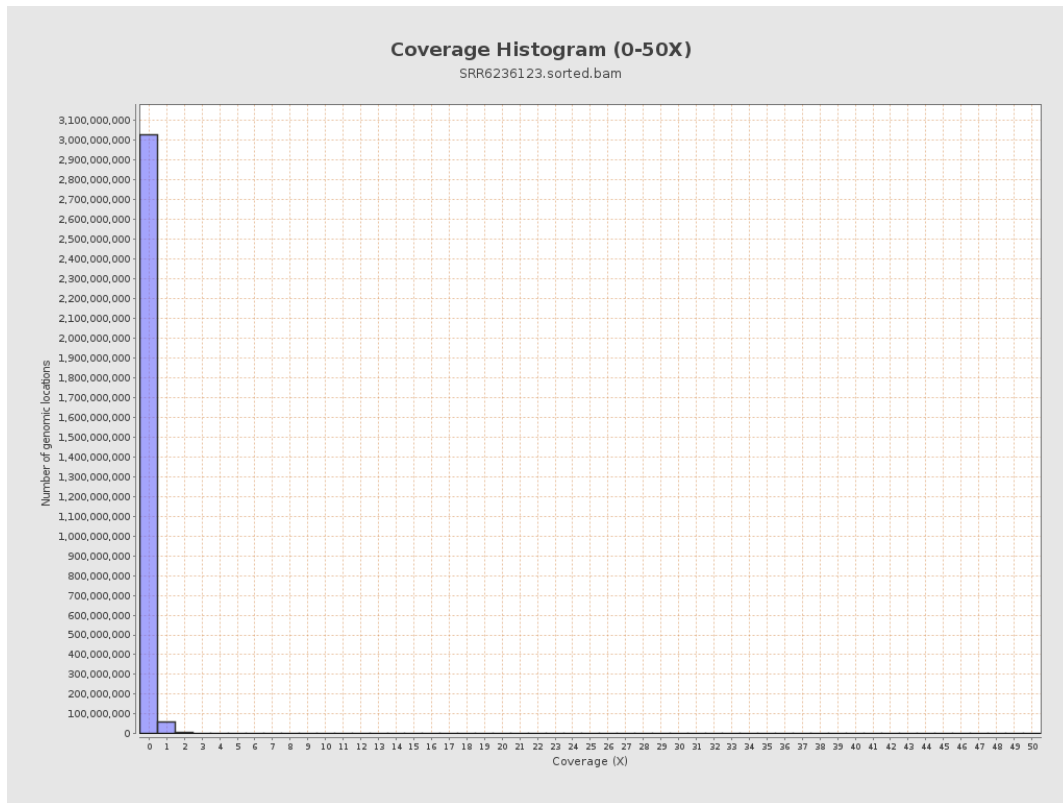
3. Results : Coverage across reference



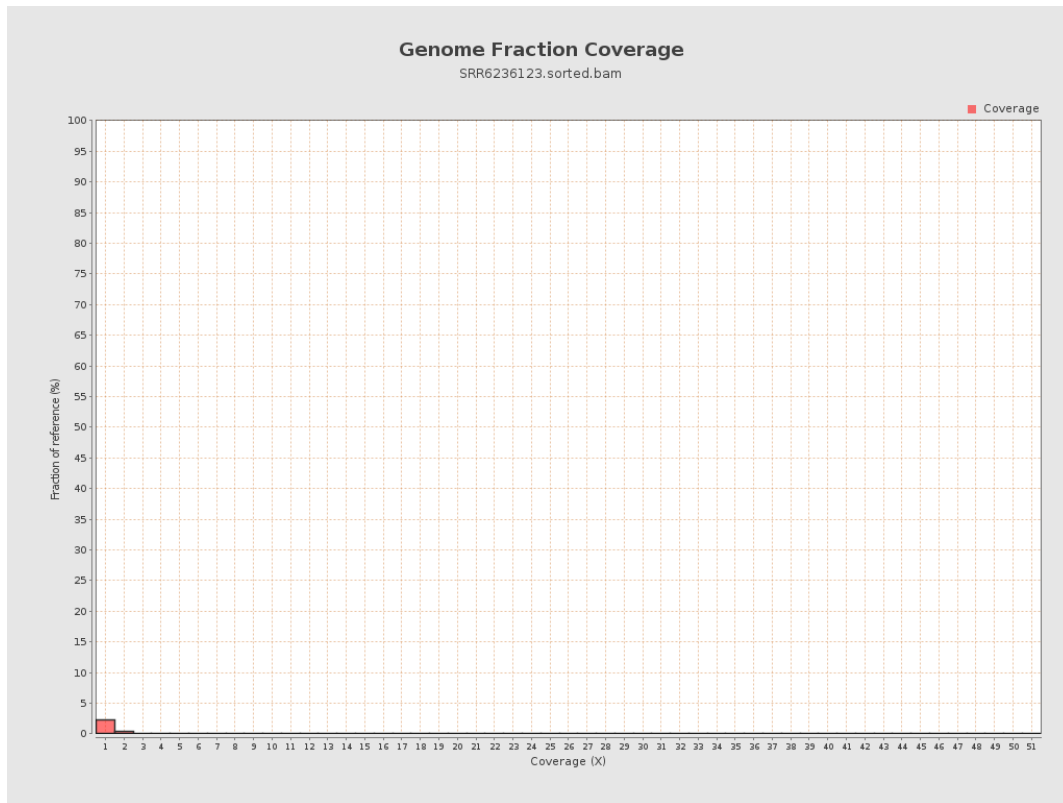
4. Results : Coverage Histogram



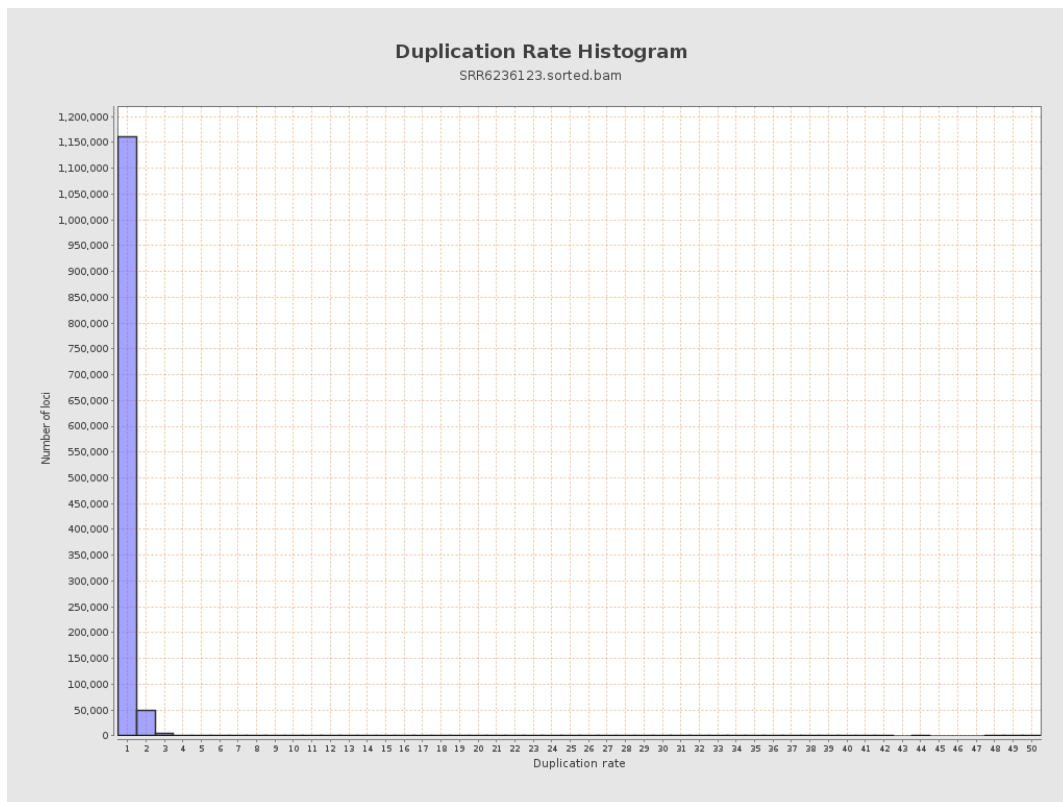
5. Results : Coverage Histogram (0-50X)



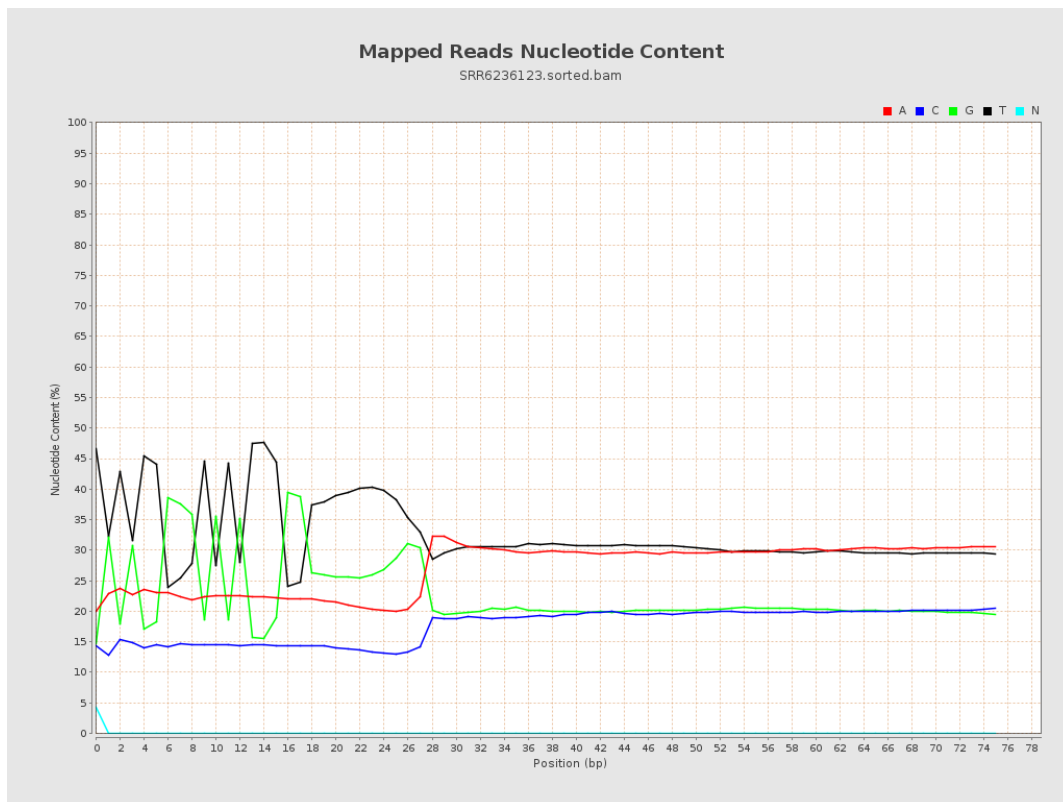
6. Results : Genome Fraction Coverage



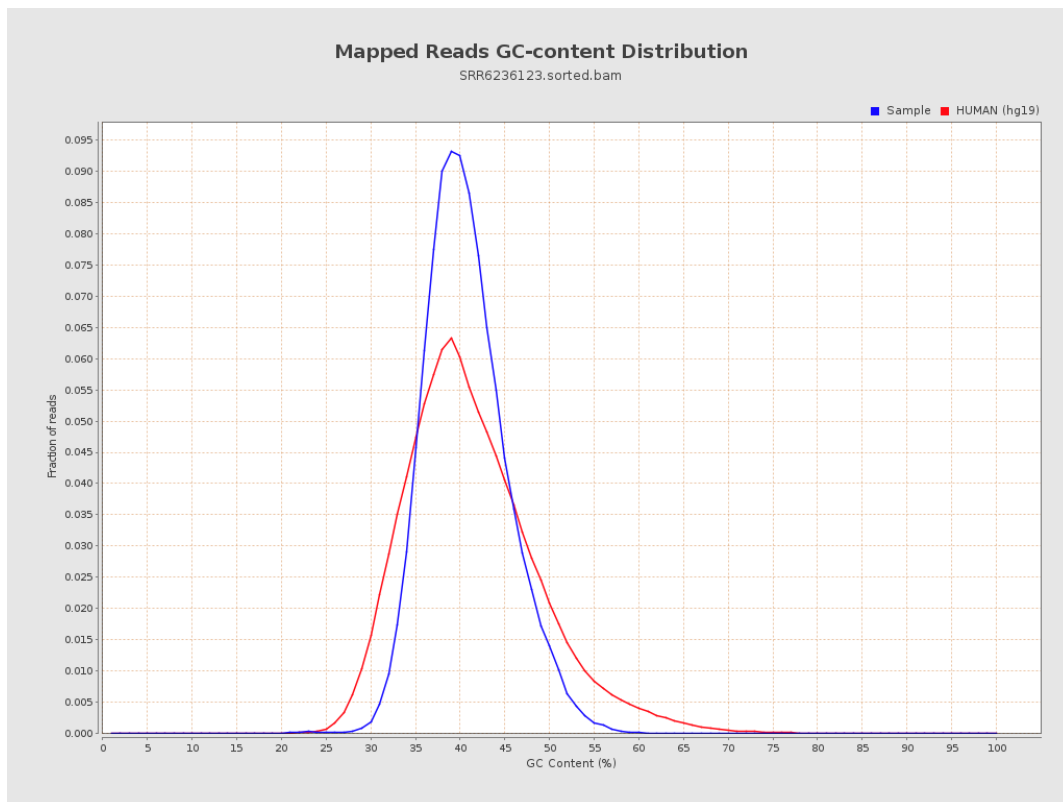
7. Results : Duplication Rate Histogram



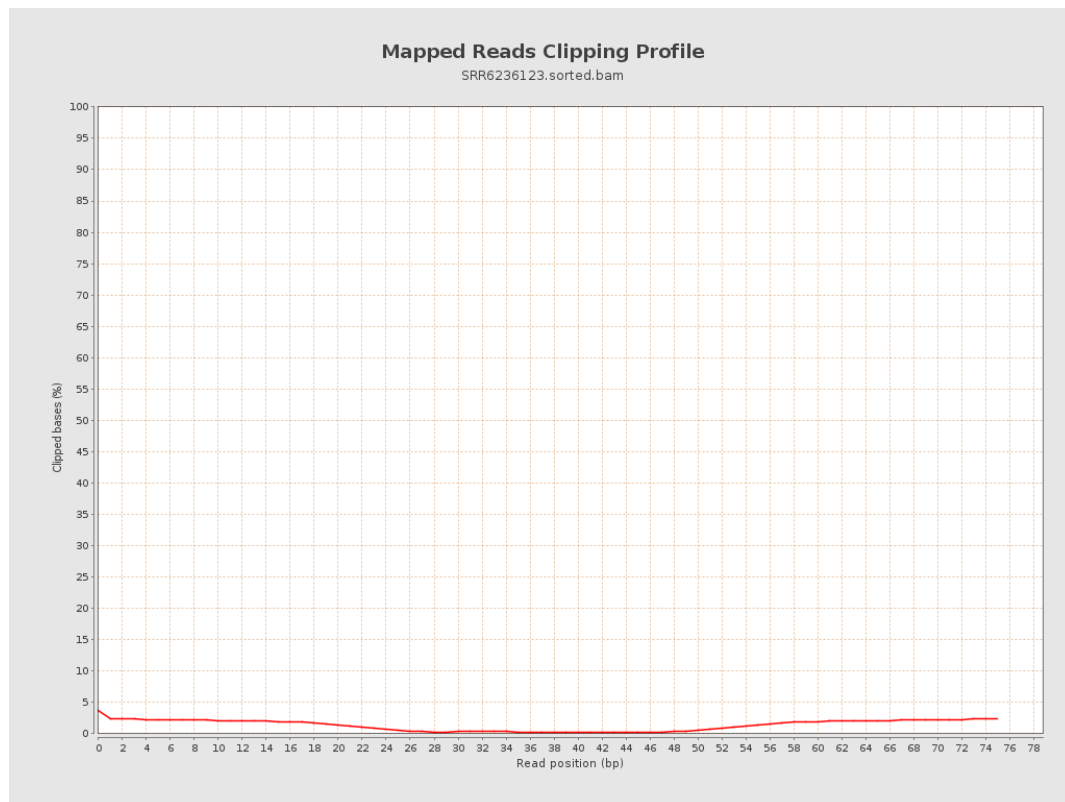
8. Results : Mapped Reads Nucleotide Content



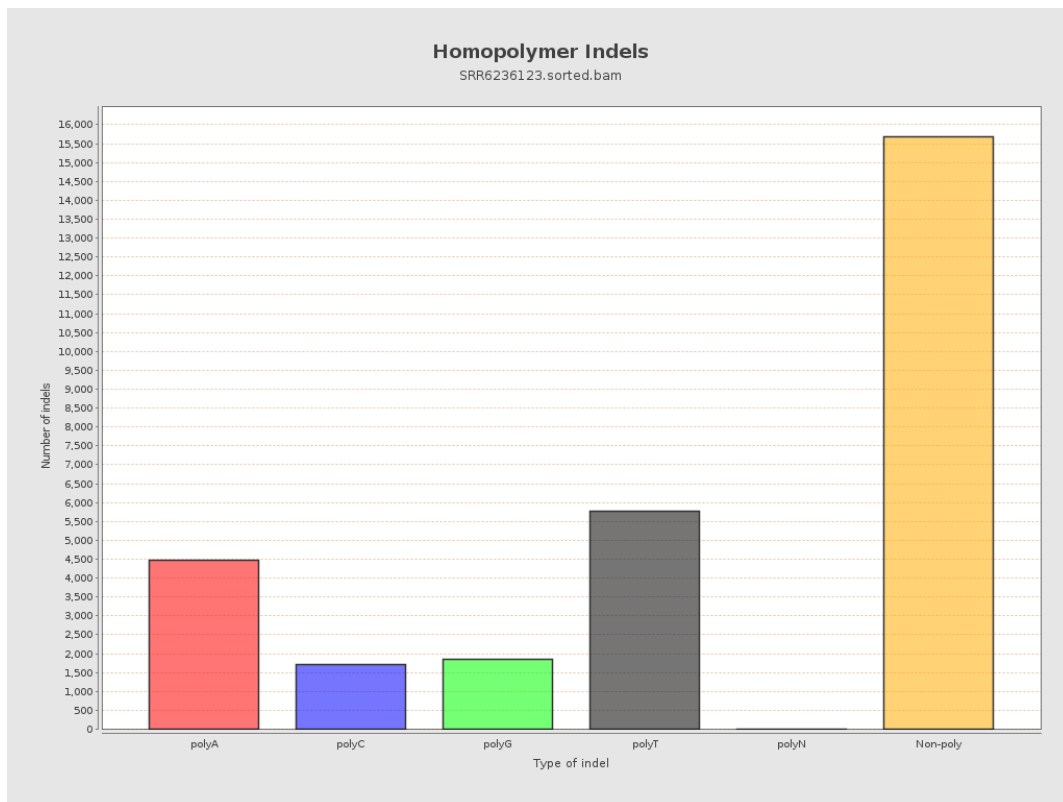
9. Results : Mapped Reads GC-content Distribution



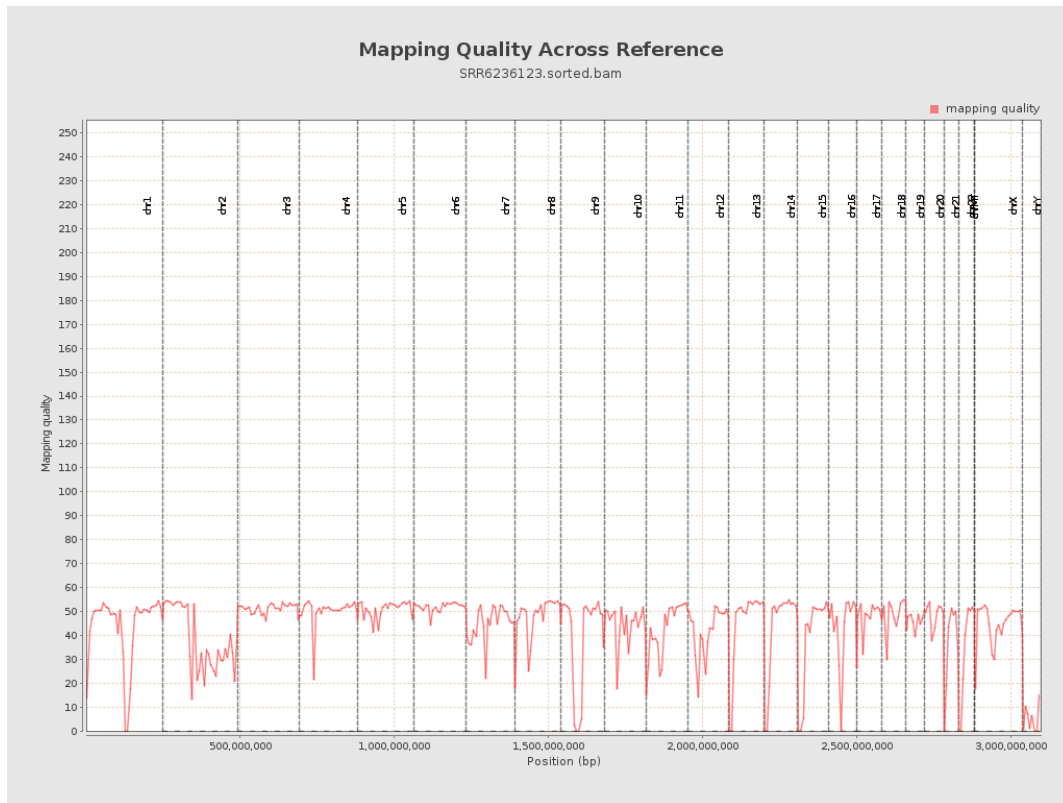
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

