

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:24:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013236.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_SRR6013236 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013236.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:24:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013236.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,854,656
Mapped reads	1,614,873 / 87.07%
Unmapped reads	239,783 / 12.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,318 / 1.2%
Read min/max/mean length	30 / 76 / 76.42
Duplicated reads (estimated)	195,779 / 10.56%
Duplication rate	9.27%
Clipped reads	805,041 / 43.41%

2.2. ACGT Content

Number/percentage of A's	28,754,031 / 27.14%
Number/percentage of C's	20,224,347 / 19.09%
Number/percentage of T's	32,889,796 / 31.05%
Number/percentage of G's	24,049,378 / 22.7%
Number/percentage of N's	12,508 / 0.01%
GC Percentage	41.8%

2.3. Coverage

Mean	0.0342

Standard Deviation	0.3889
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2.4. Mapping Quality

Mean Mapping Quality	42.95
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2.5. Mismatches and indels

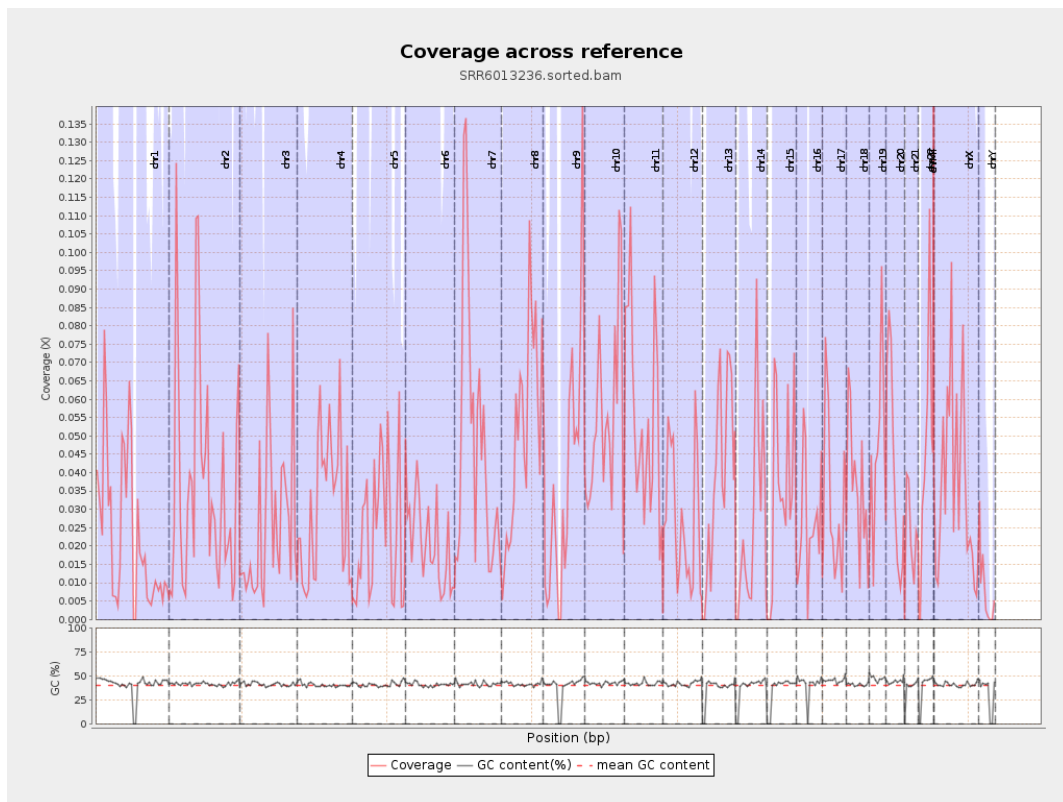
General error rate	0.76%
Mismatches	790,515
Insertions	6,792
Mapped reads with at least one insertion	0.42%
Deletions	24,668
Mapped reads with at least one deletion	1.51%
Homopolymer indels	45.39%

2.6. Chromosome stats

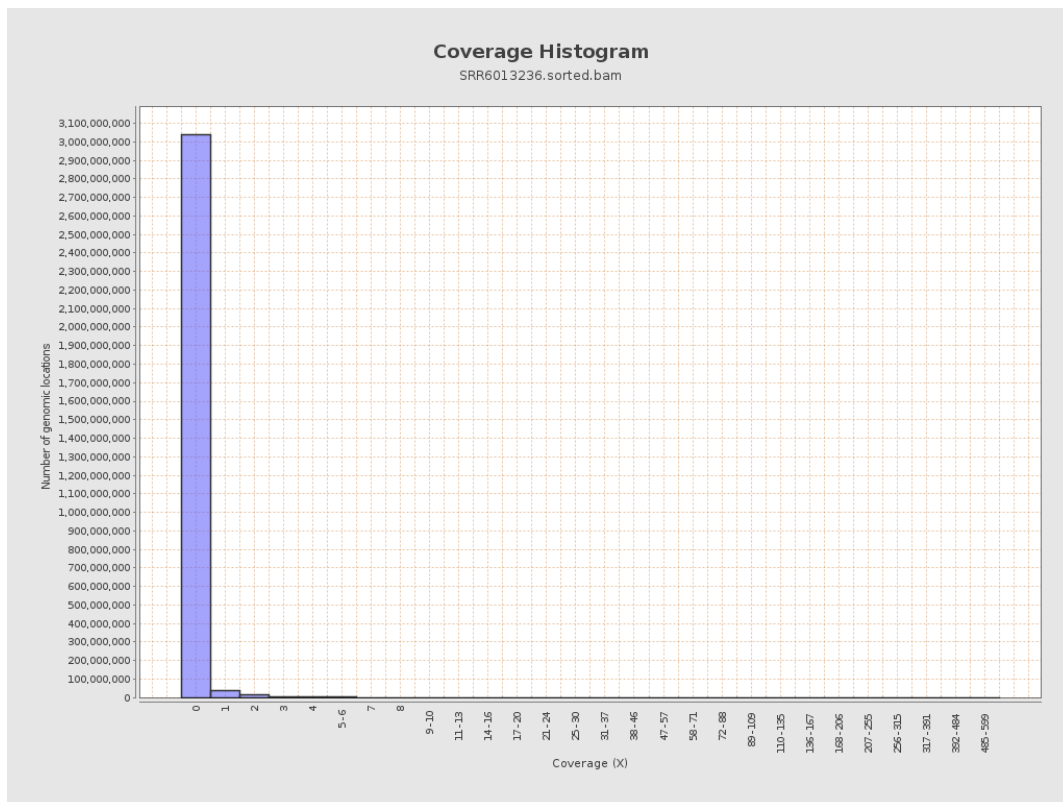
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5700343	0.0229	0.561
chr2	243199373	9026393	0.0371	0.5112
chr3	198022430	4988153	0.0252	0.2546
chr4	191154276	5830949	0.0305	0.2906
chr5	180915260	4356730	0.0241	0.2497
chr6	171115067	3662212	0.0214	0.2493
chr7	159138663	7624548	0.0479	0.4735

chr8	146364022	7432348	0.0508	0.409
chr9	141213431	5245805	0.0371	0.36
chr10	135534747	7466875	0.0551	0.4648
chr11	135006516	7260504	0.0538	0.4329
chr12	133851895	3558573	0.0266	0.2678
chr13	115169878	4539805	0.0394	0.3257
chr14	107349540	2800675	0.0261	0.284
chr15	102531392	3672938	0.0358	0.3109
chr16	90354753	2443666	0.027	0.2701
chr17	81195210	2557839	0.0315	0.3436
chr18	78077248	2847737	0.0365	0.6294
chr19	59128983	2694514	0.0456	0.4889
chr20	63025520	2633231	0.0418	0.3541
chr21	48129895	1125937	0.0234	0.2542
chr22	51304566	2342911	0.0457	0.3516
chrMT	16571	3573	0.2156	0.5921
chrX	155270560	5708228	0.0368	0.3689
chrY	59373566	448558	0.0076	0.1694

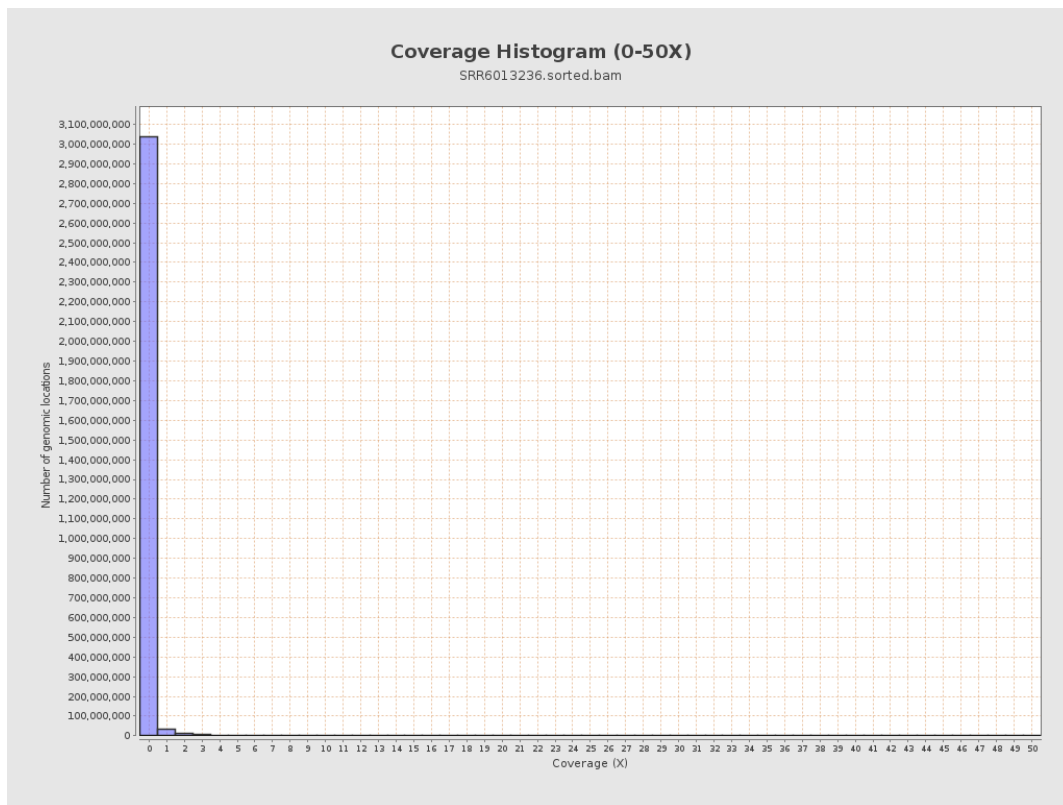
3. Results : Coverage across reference



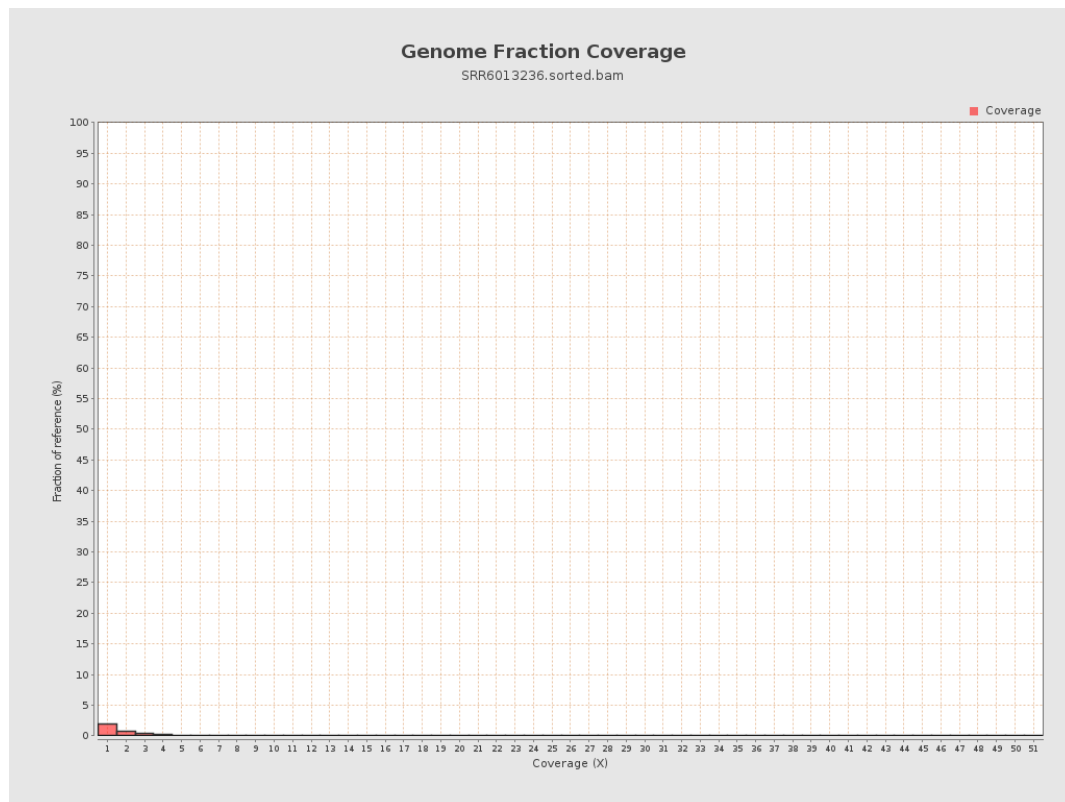
4. Results : Coverage Histogram



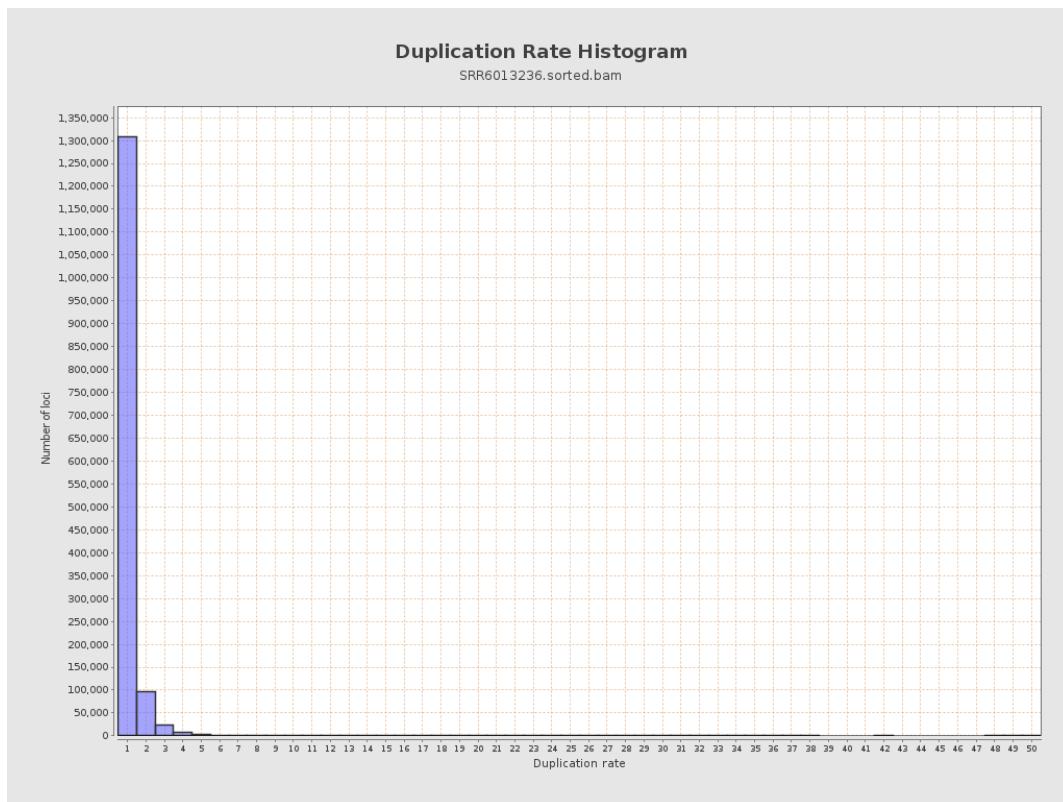
5. Results : Coverage Histogram (0-50X)



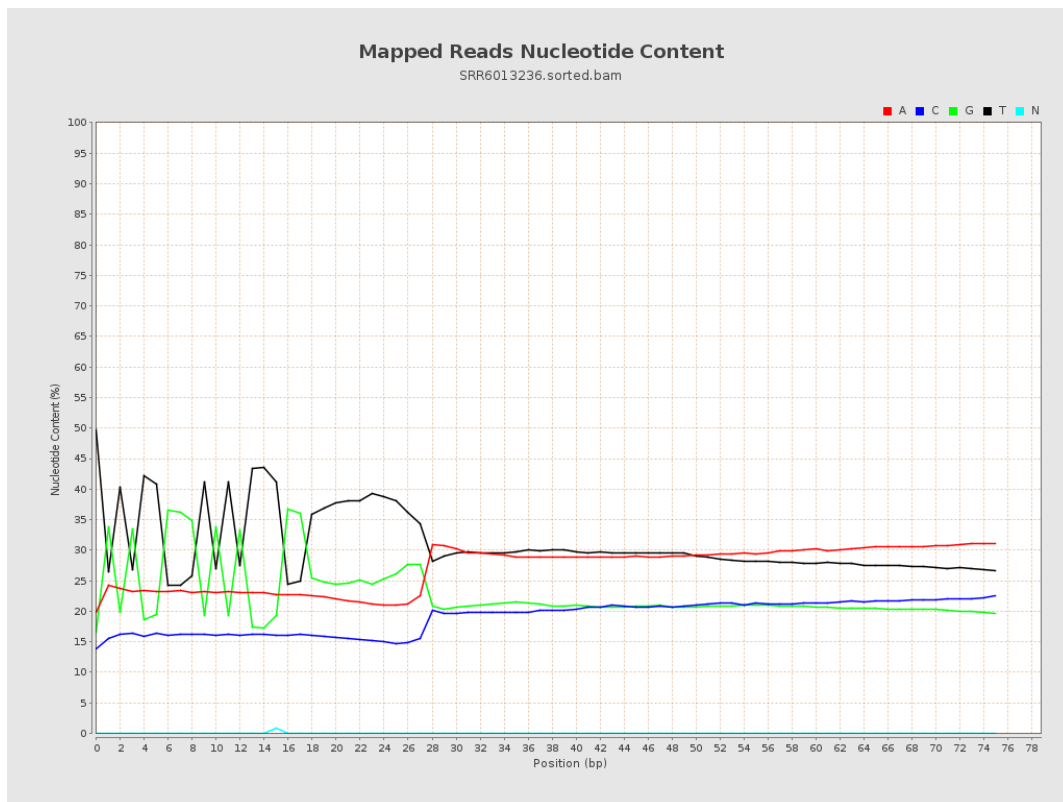
6. Results : Genome Fraction Coverage



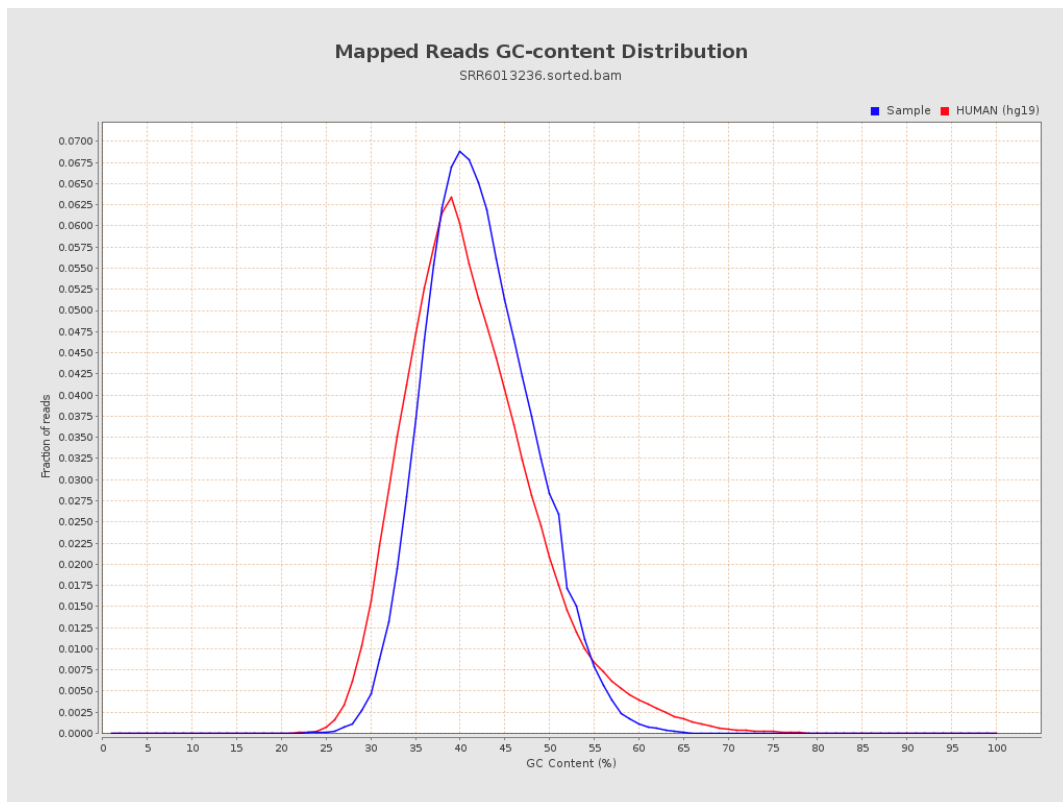
7. Results : Duplication Rate Histogram



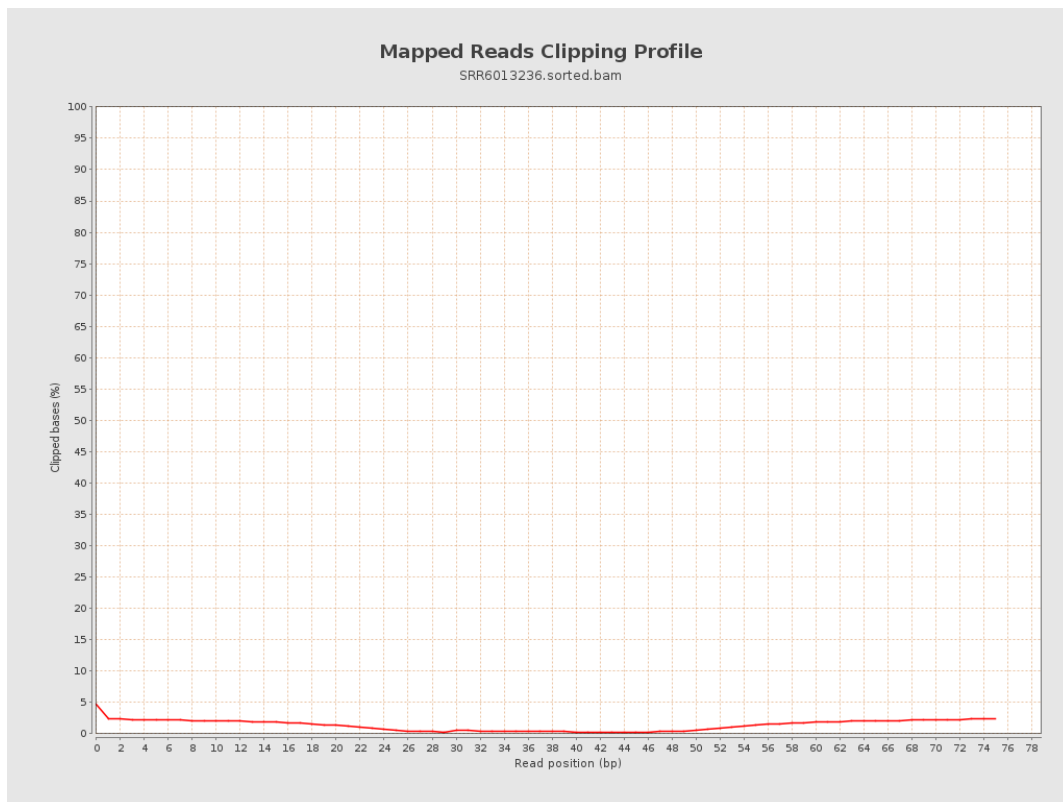
8. Results : Mapped Reads Nucleotide Content



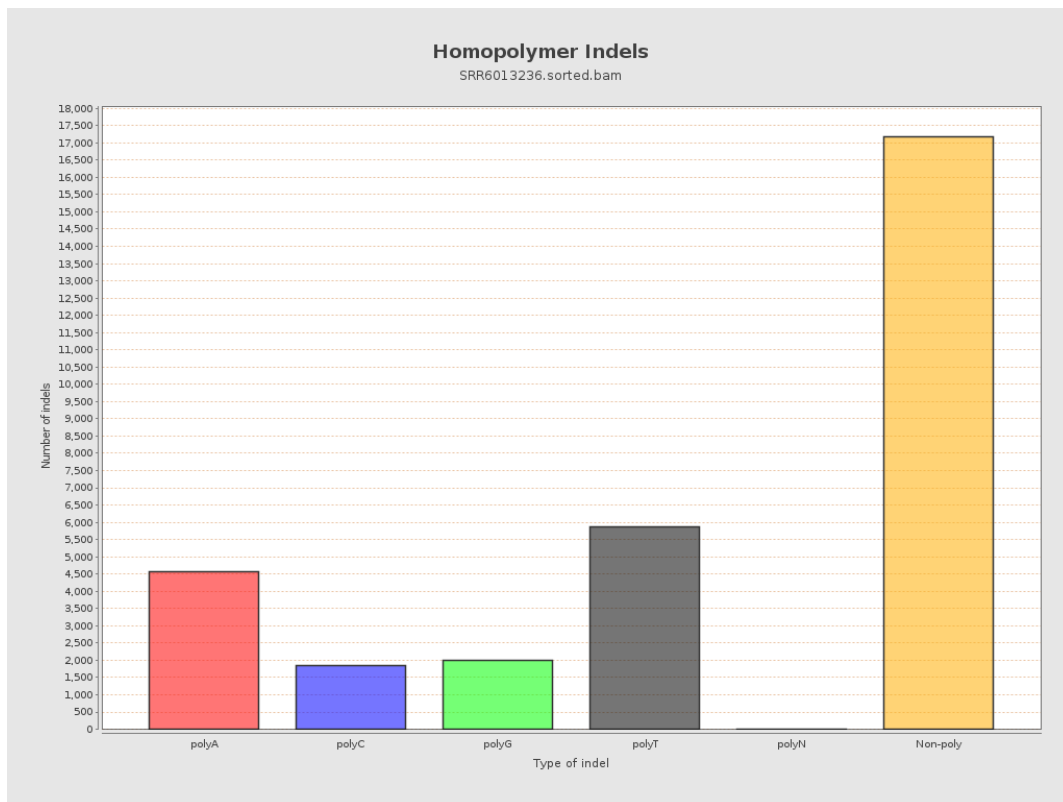
9. Results : Mapped Reads GC-content Distribution



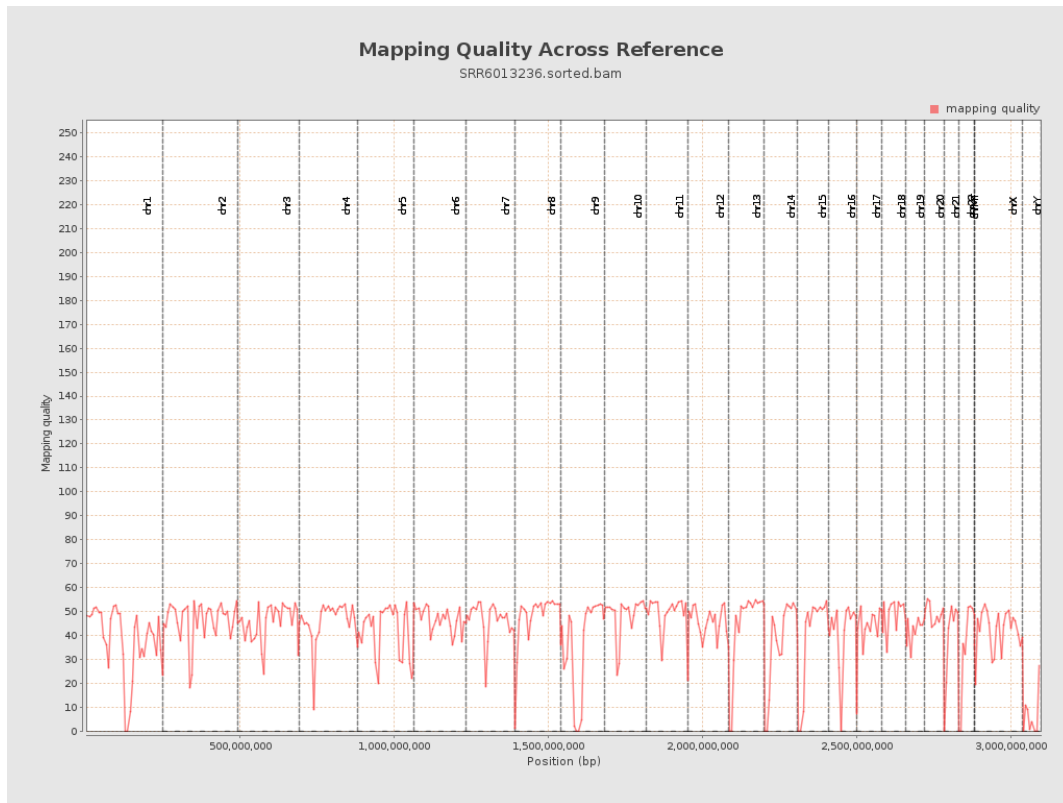
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

