

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:11:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234136.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_SRR6234136 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234136.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:11:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234136.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,546,437
Mapped reads	1,557,624 / 61.17%
Unmapped reads	988,813 / 38.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,440 / 0.25%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	113,486 / 4.46%
Duplication rate	5.97%
Clipped reads	1,110,461 / 43.61%

2.2. ACGT Content

Number/percentage of A's	24,505,684 / 26.13%
Number/percentage of C's	17,004,328 / 18.13%
Number/percentage of T's	29,474,111 / 31.42%
Number/percentage of G's	22,792,491 / 24.3%
Number/percentage of N's	20,908 / 0.02%
GC Percentage	42.43%

2.3. Coverage

Mean	0.0303

Standard Deviation	0.2909
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2.4. Mapping Quality

Mean Mapping Quality	42.49
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2.5. Mismatches and indels

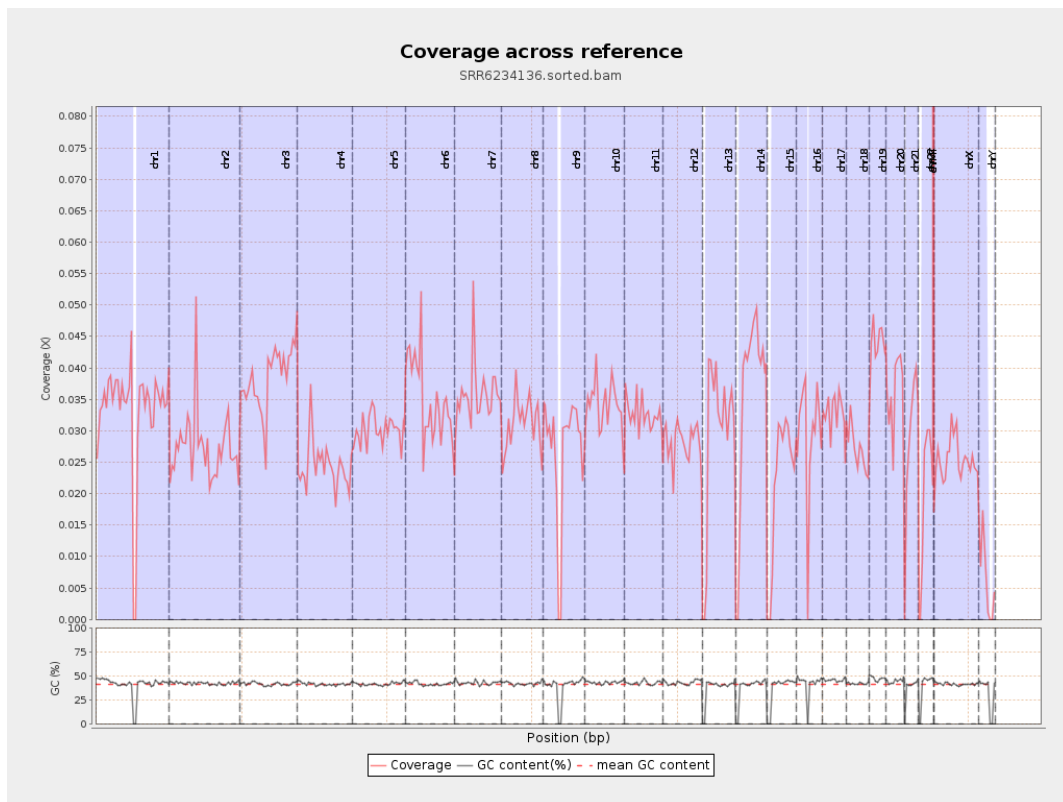
General error rate	0.97%
Mismatches	898,555
Insertions	8,171
Mapped reads with at least one insertion	0.52%
Deletions	37,527
Mapped reads with at least one deletion	2.37%
Homopolymer indels	46.27%

2.6. Chromosome stats

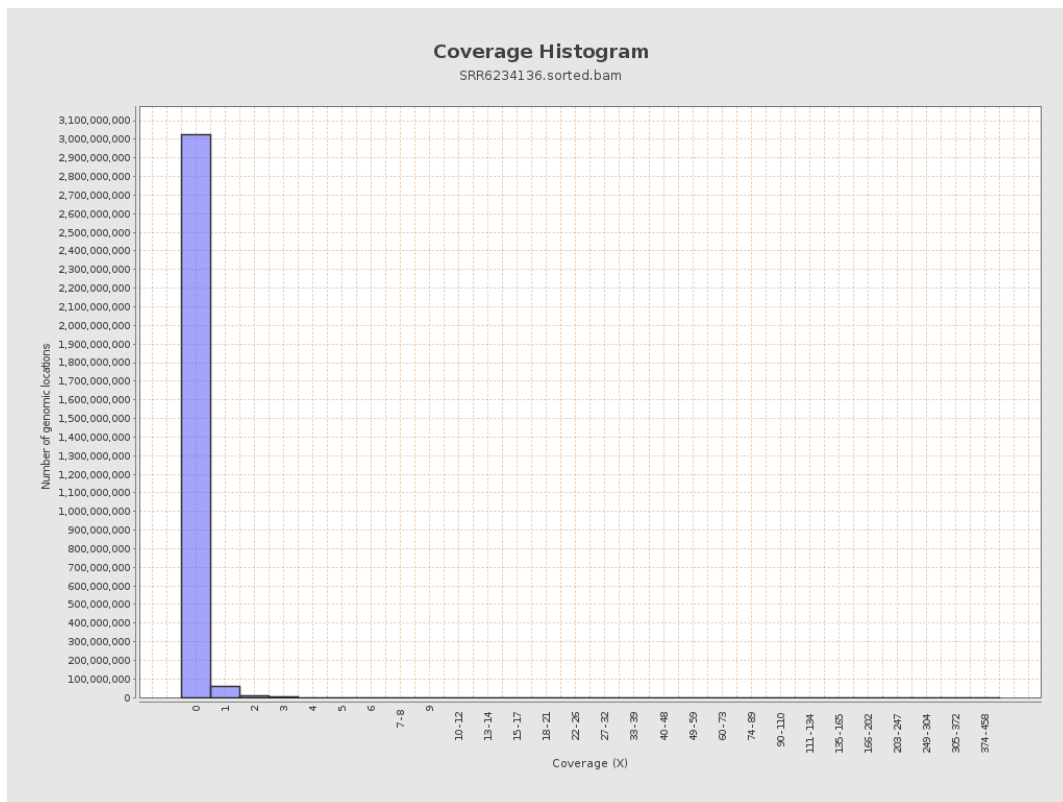
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8246253	0.0331	0.4028
chr2	243199373	6651498	0.0273	0.3293
chr3	198022430	7559383	0.0382	0.2479
chr4	191154276	4638991	0.0243	0.2117
chr5	180915260	5445134	0.0301	0.2243
chr6	171115067	5989353	0.035	0.2985
chr7	159138663	5729872	0.036	0.452

chr8	146364022	4543485	0.031	0.3123
chr9	141213431	3764730	0.0267	0.2647
chr10	135534747	4641027	0.0342	0.2682
chr11	135006516	4373122	0.0324	0.3077
chr12	133851895	3775531	0.0282	0.213
chr13	115169878	3370228	0.0293	0.2458
chr14	107349540	3835741	0.0357	0.2583
chr15	102531392	2268694	0.0221	0.1985
chr16	90354753	2665871	0.0295	0.2384
chr17	81195210	2650029	0.0326	0.2509
chr18	78077248	2129859	0.0273	0.3956
chr19	59128983	2599648	0.044	0.3583
chr20	63025520	2240456	0.0355	0.2519
chr21	48129895	1394888	0.029	0.2201
chr22	51304566	992620	0.0193	0.1735
chrMT	16571	68045	4.1063	4.6616
chrX	155270560	3924122	0.0253	0.2165
chrY	59373566	365550	0.0062	0.1084

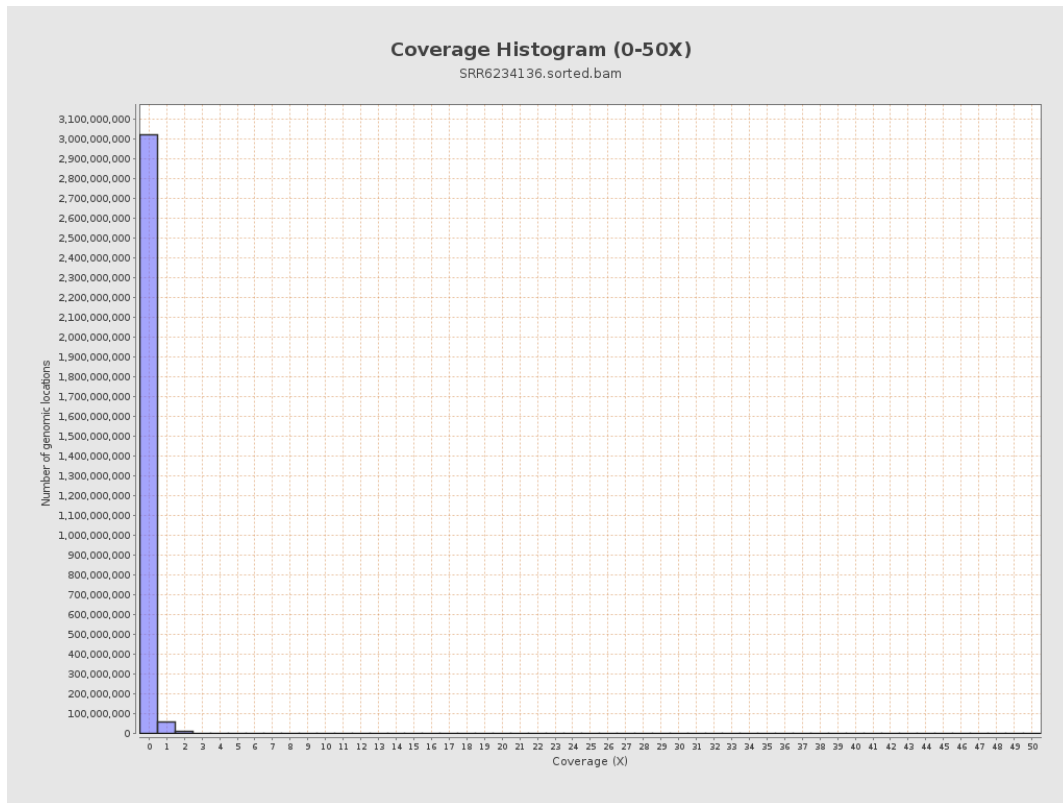
3. Results : Coverage across reference



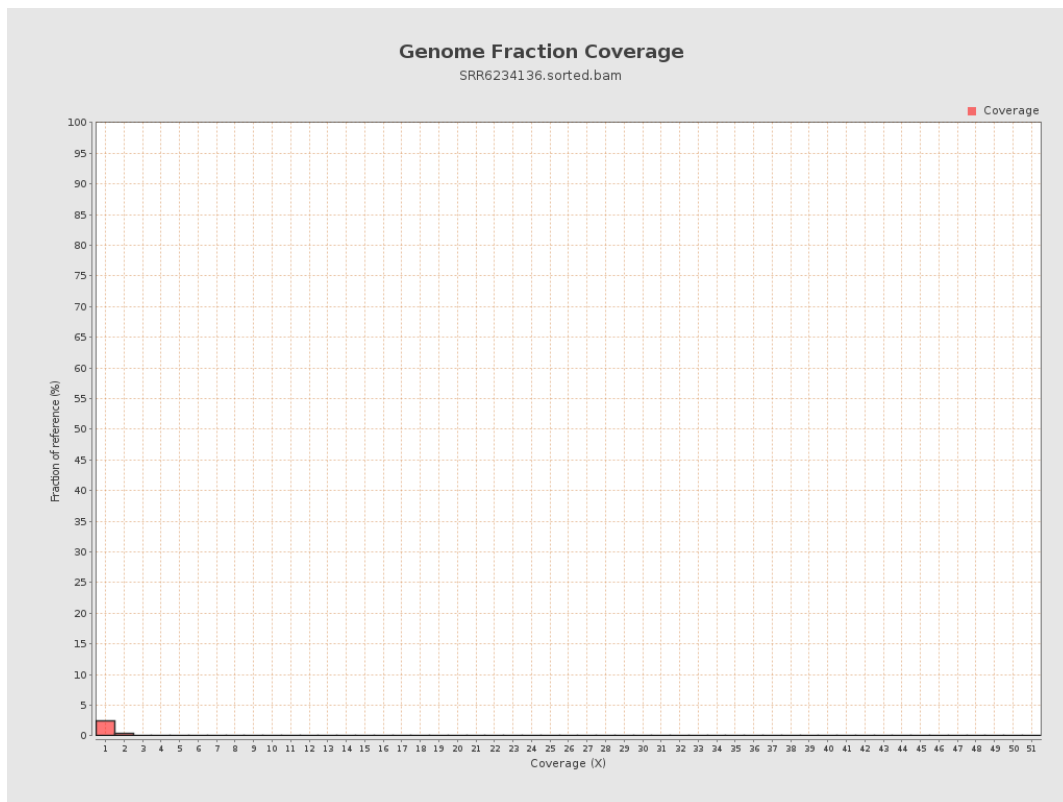
4. Results : Coverage Histogram



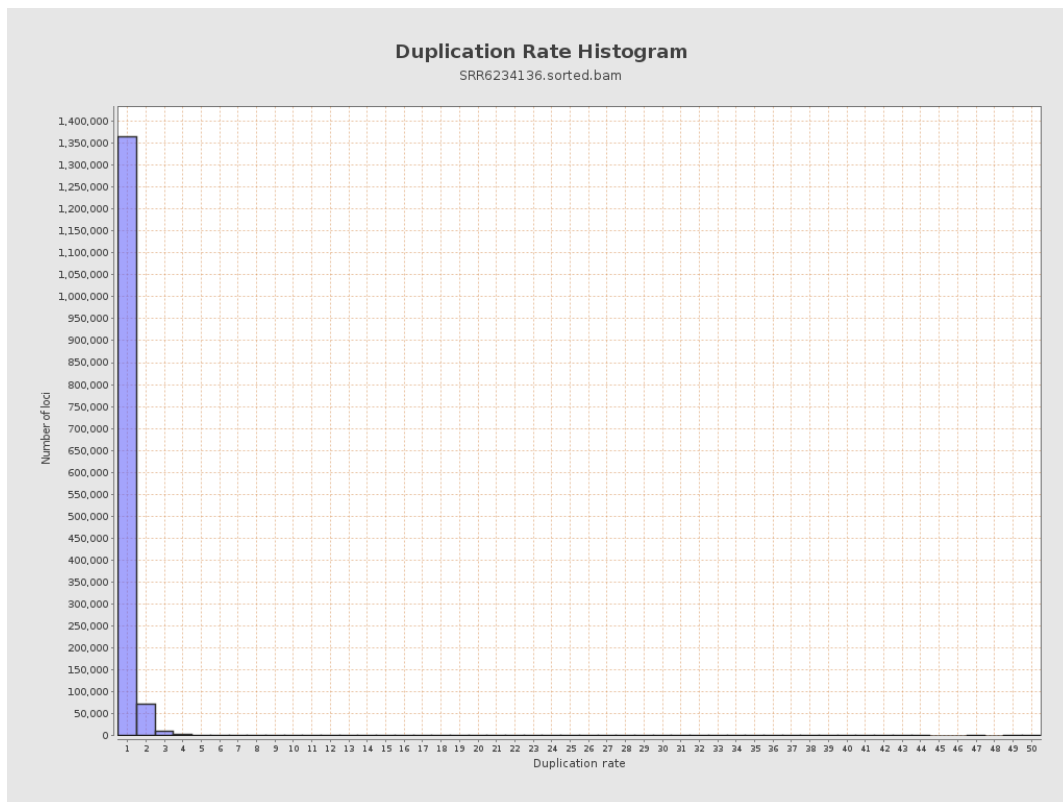
5. Results : Coverage Histogram (0-50X)



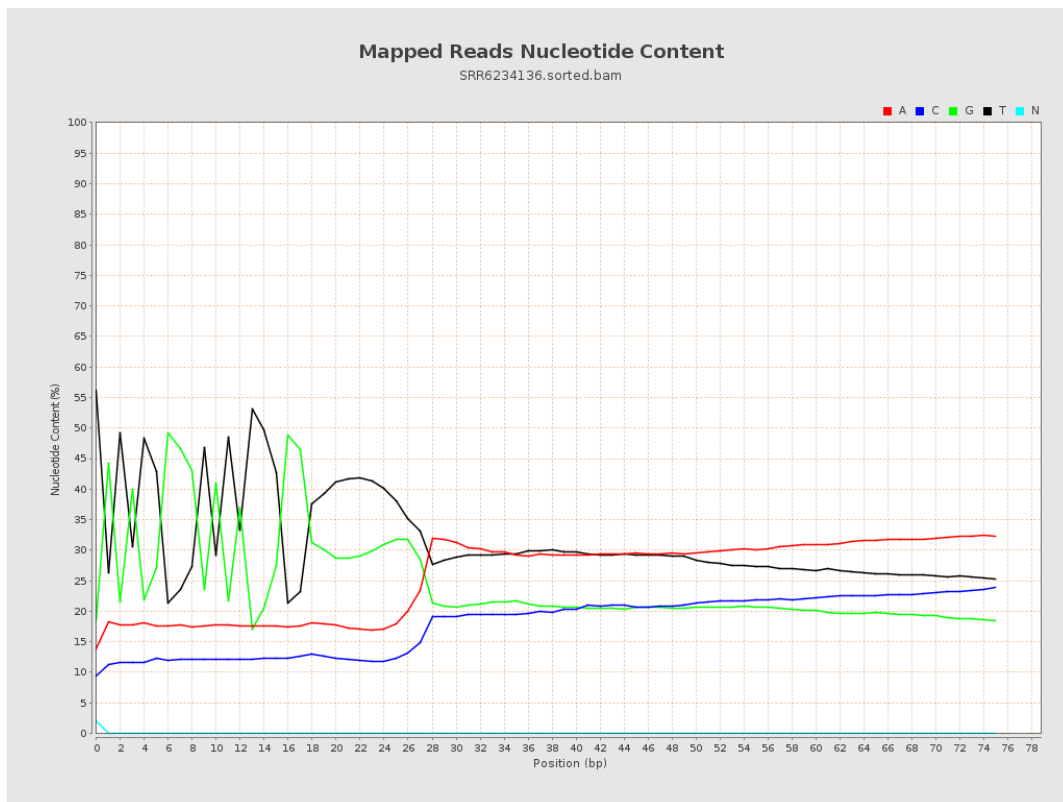
6. Results : Genome Fraction Coverage



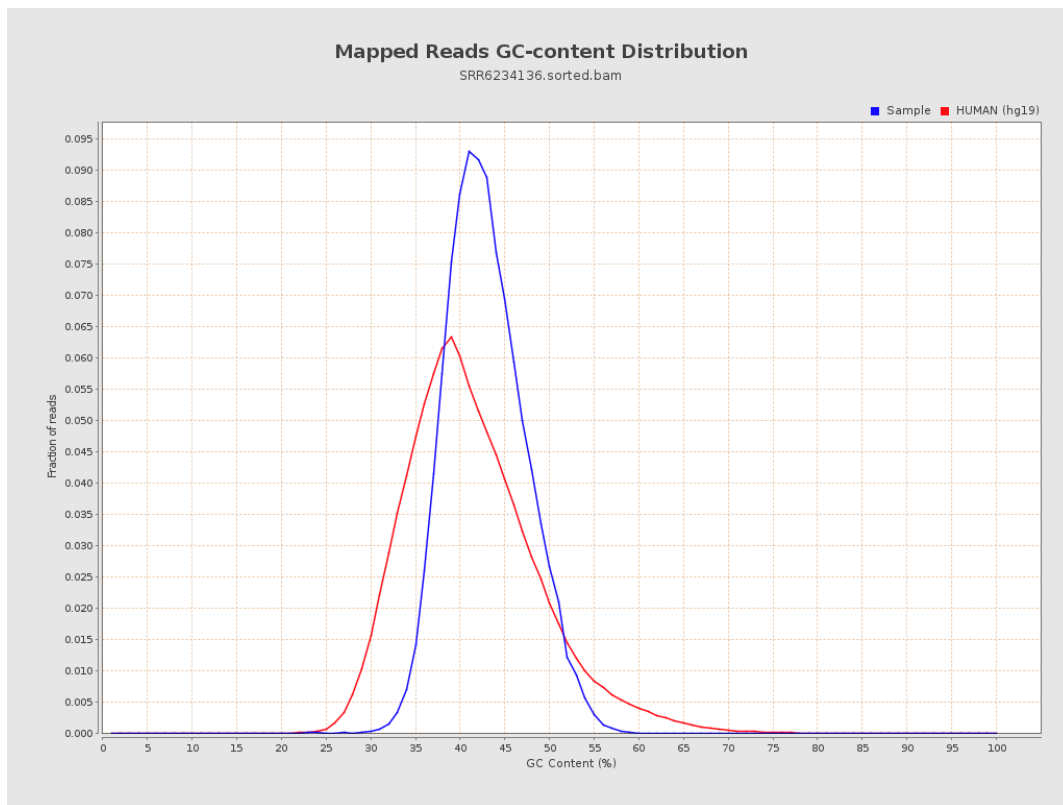
7. Results : Duplication Rate Histogram



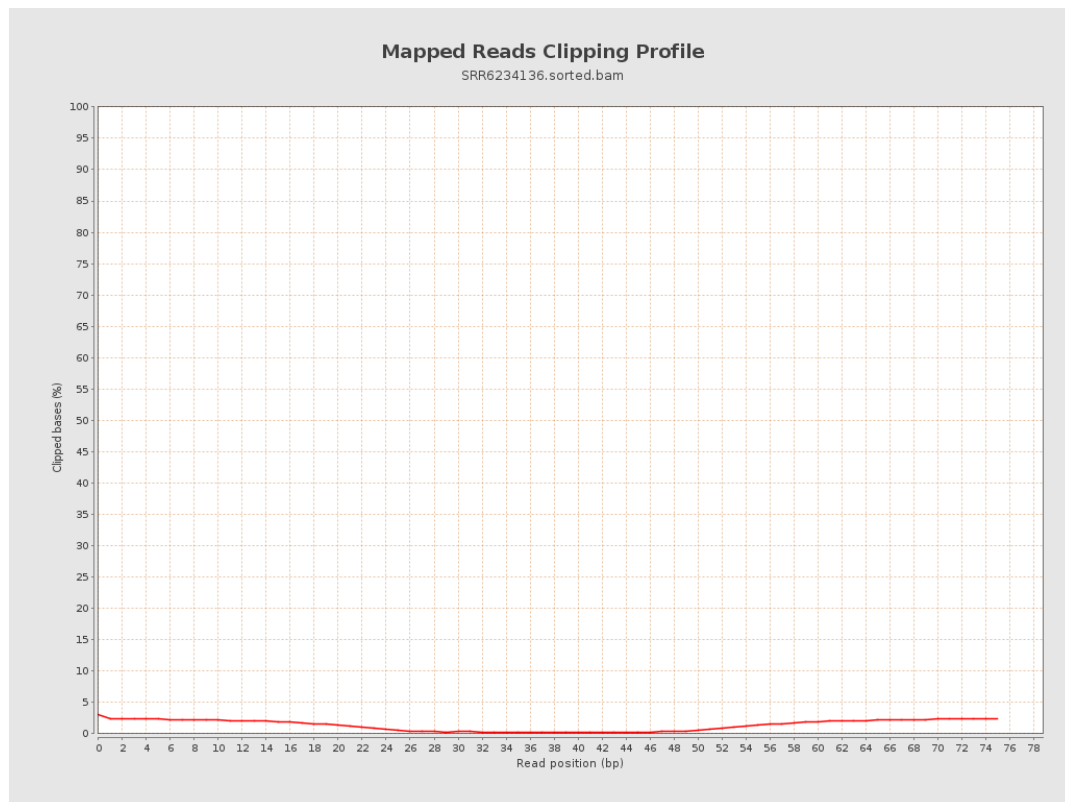
8. Results : Mapped Reads Nucleotide Content



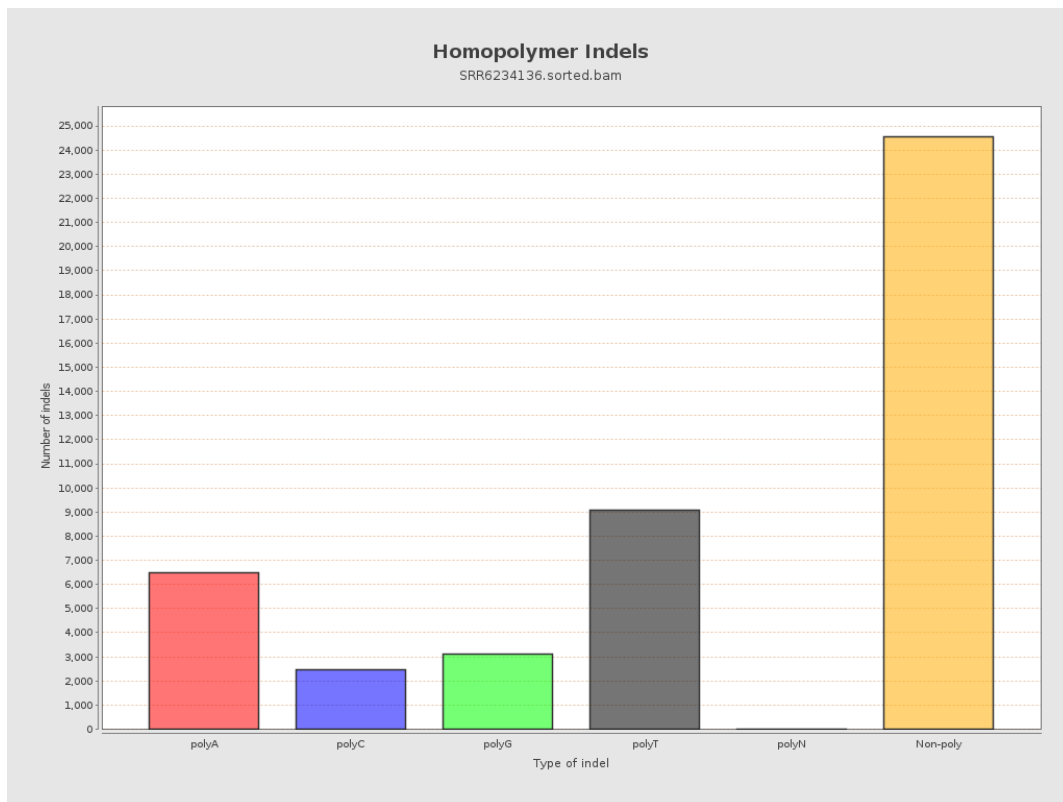
9. Results : Mapped Reads GC-content Distribution



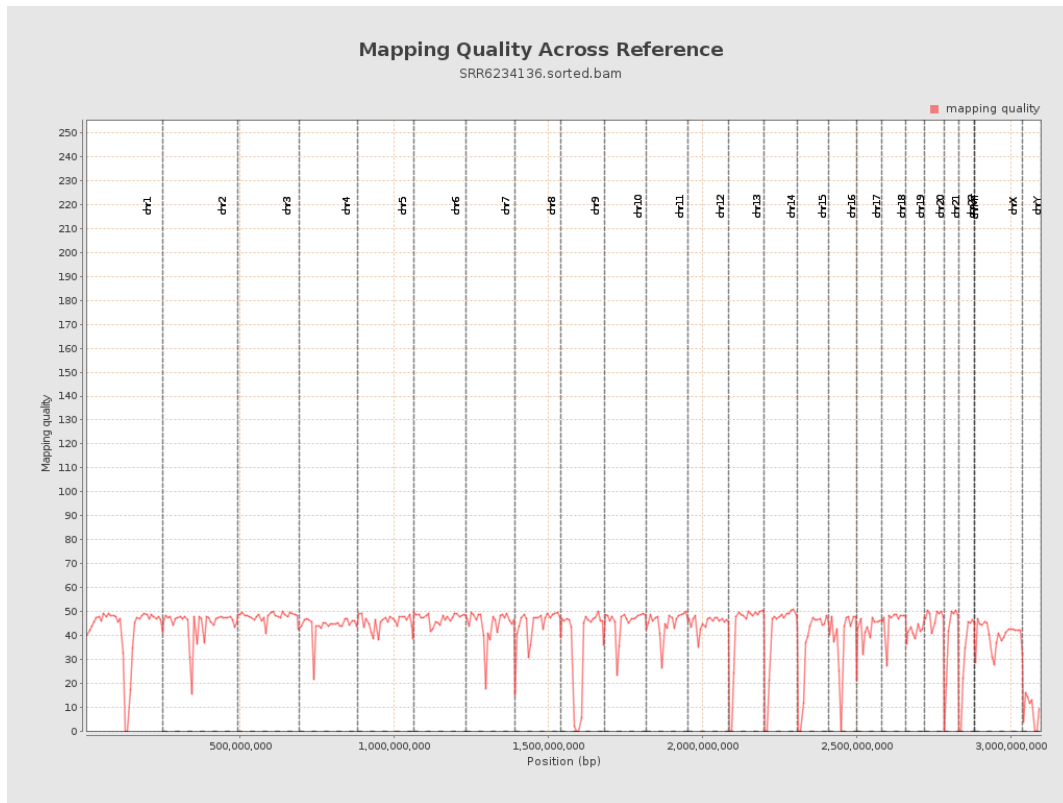
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

