

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:19:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524315.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_SRR10524315 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524315.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:19:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524315.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,151,655
Mapped reads	1,912,350 / 88.88%
Unmapped reads	239,305 / 11.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,161 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	64,671 / 3.01%
Duplication rate	2.19%
Clipped reads	1,917,180 / 89.1%

2.2. ACGT Content

Number/percentage of A's	26,740,948 / 24.75%
Number/percentage of C's	20,002,442 / 18.52%
Number/percentage of T's	35,065,056 / 32.46%
Number/percentage of G's	26,199,254 / 24.25%
Number/percentage of N's	15,665 / 0.01%
GC Percentage	42.77%

2.3. Coverage

Mean	0.0349

Standard Deviation	0.3395
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2.4. Mapping Quality

Mean Mapping Quality	42.3
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2.5. Mismatches and indels

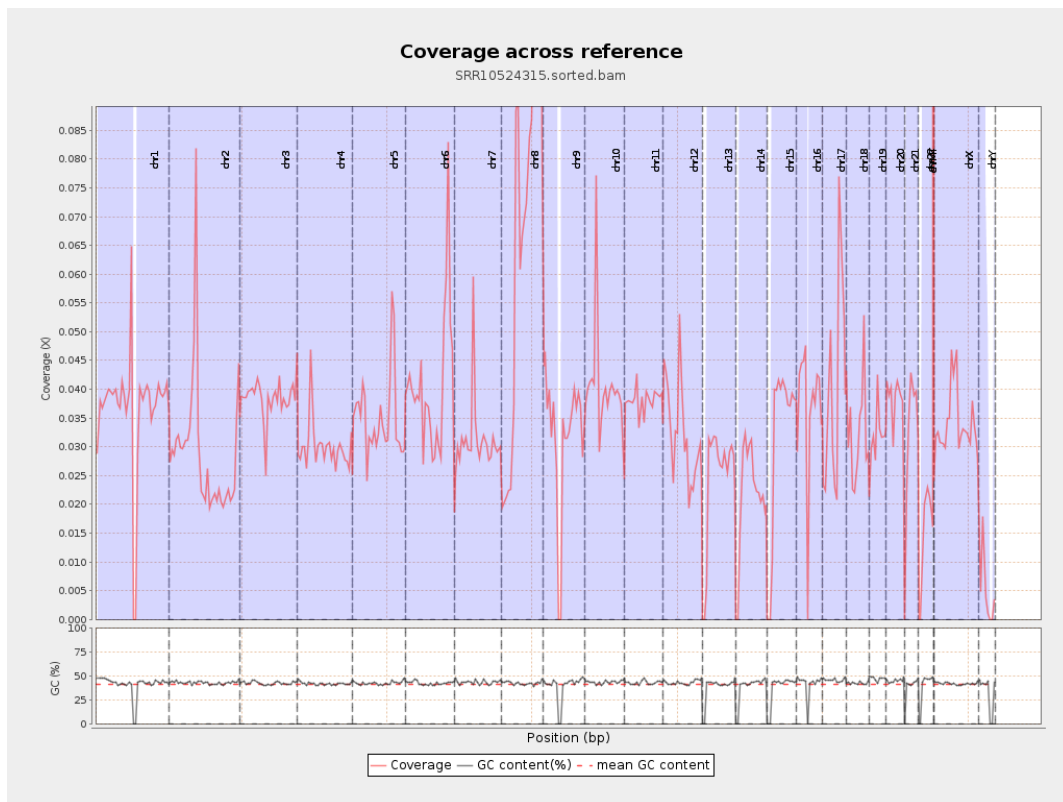
General error rate	0.55%
Mismatches	579,893
Insertions	7,359
Mapped reads with at least one insertion	0.38%
Deletions	17,550
Mapped reads with at least one deletion	0.91%
Homopolymer indels	41.33%

2.6. Chromosome stats

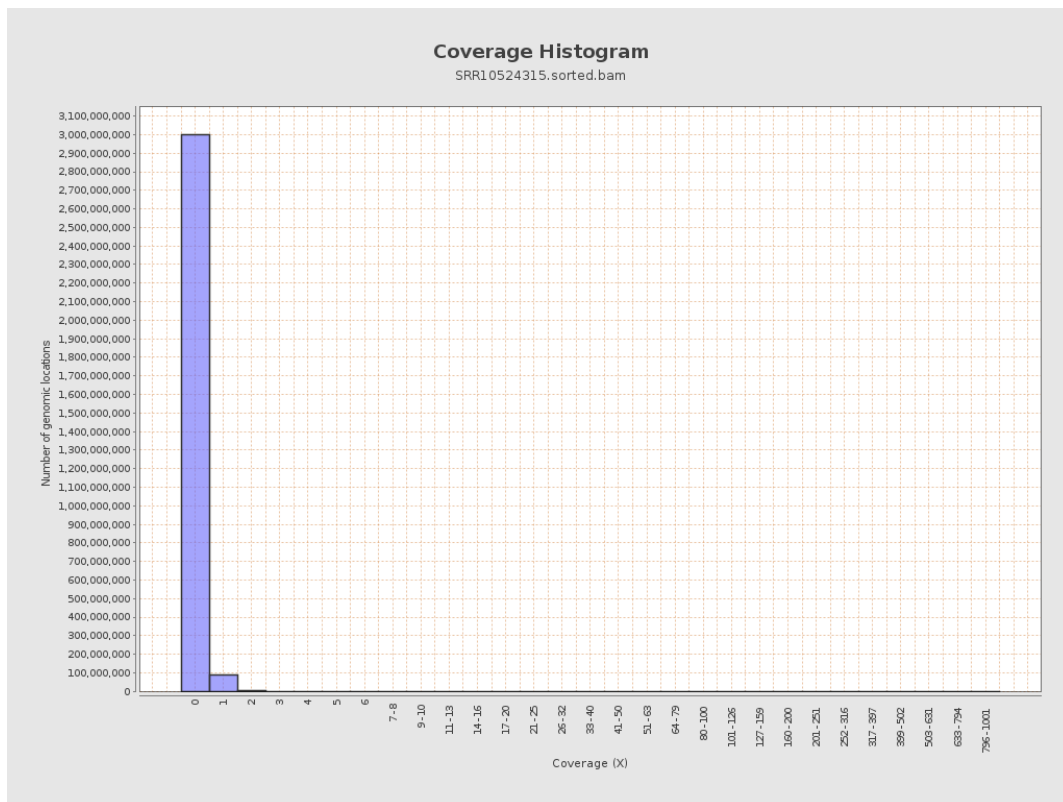
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9110634	0.0366	0.6765
chr2	243199373	7018099	0.0289	0.4164
chr3	198022430	7578831	0.0383	0.2173
chr4	191154276	5718776	0.0299	0.2098
chr5	180915260	6366190	0.0352	0.2068
chr6	171115067	6911075	0.0404	0.2473
chr7	159138663	5002961	0.0314	0.4296

chr8	146364022	11167886	0.0763	0.3982
chr9	141213431	4469851	0.0317	0.2539
chr10	135534747	5486005	0.0405	0.3704
chr11	135006516	5109174	0.0378	0.27
chr12	133851895	4321826	0.0323	0.2011
chr13	115169878	2791049	0.0242	0.1711
chr14	107349540	2316915	0.0216	0.1783
chr15	102531392	3246822	0.0317	0.2019
chr16	90354753	3335255	0.0369	0.2394
chr17	81195210	3250064	0.04	0.2442
chr18	78077248	2560154	0.0328	0.4735
chr19	59128983	1900277	0.0321	0.4594
chr20	63025520	2383378	0.0378	0.2195
chr21	48129895	1537610	0.0319	0.2093
chr22	51304566	749172	0.0146	0.134
chrMT	16571	138191	8.3393	5.118
chrX	155270560	5274394	0.034	0.24
chrY	59373566	306526	0.0052	0.14

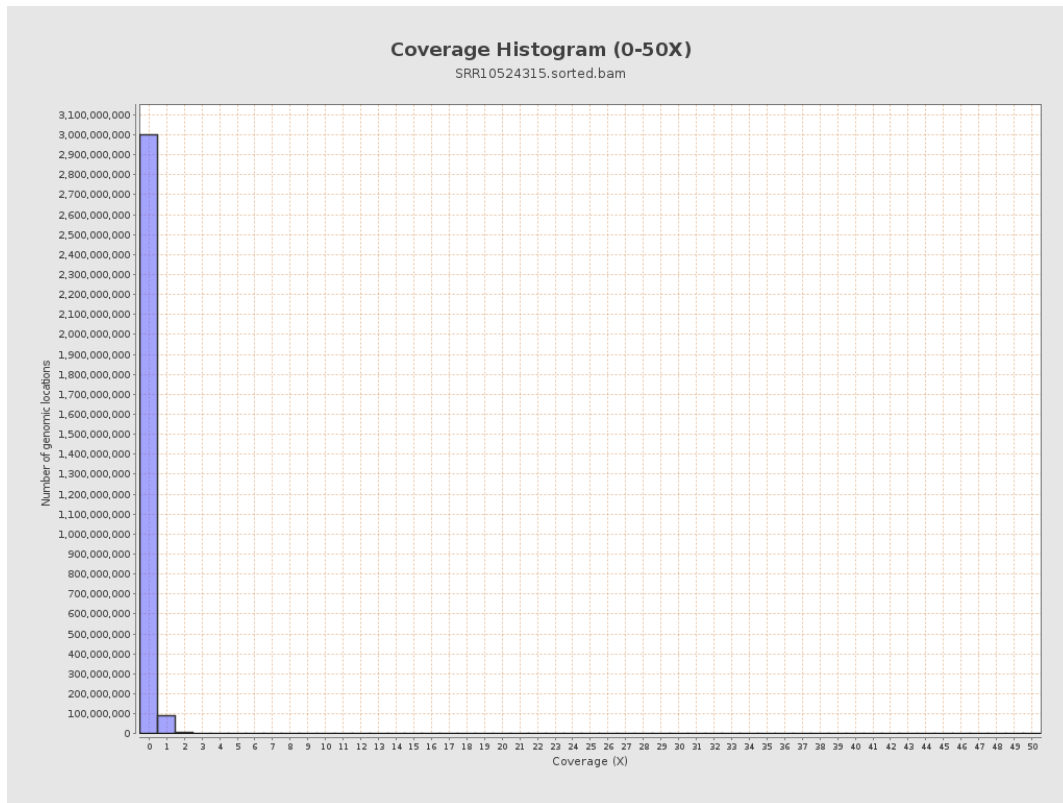
3. Results : Coverage across reference



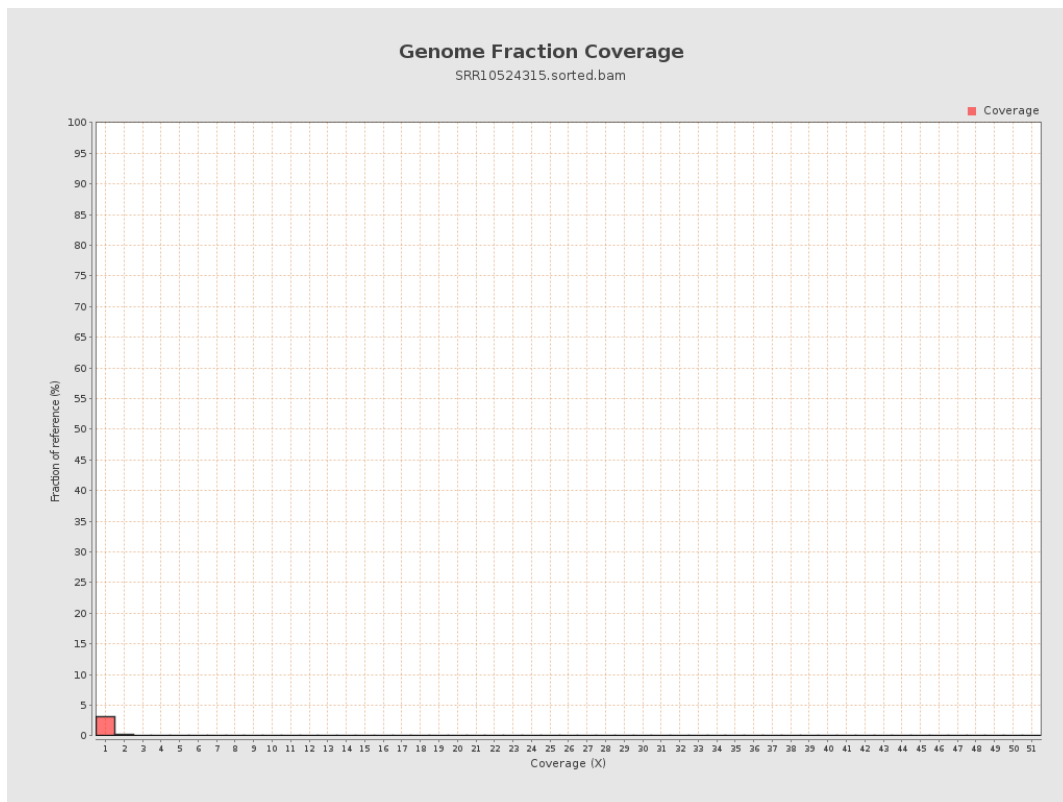
4. Results : Coverage Histogram



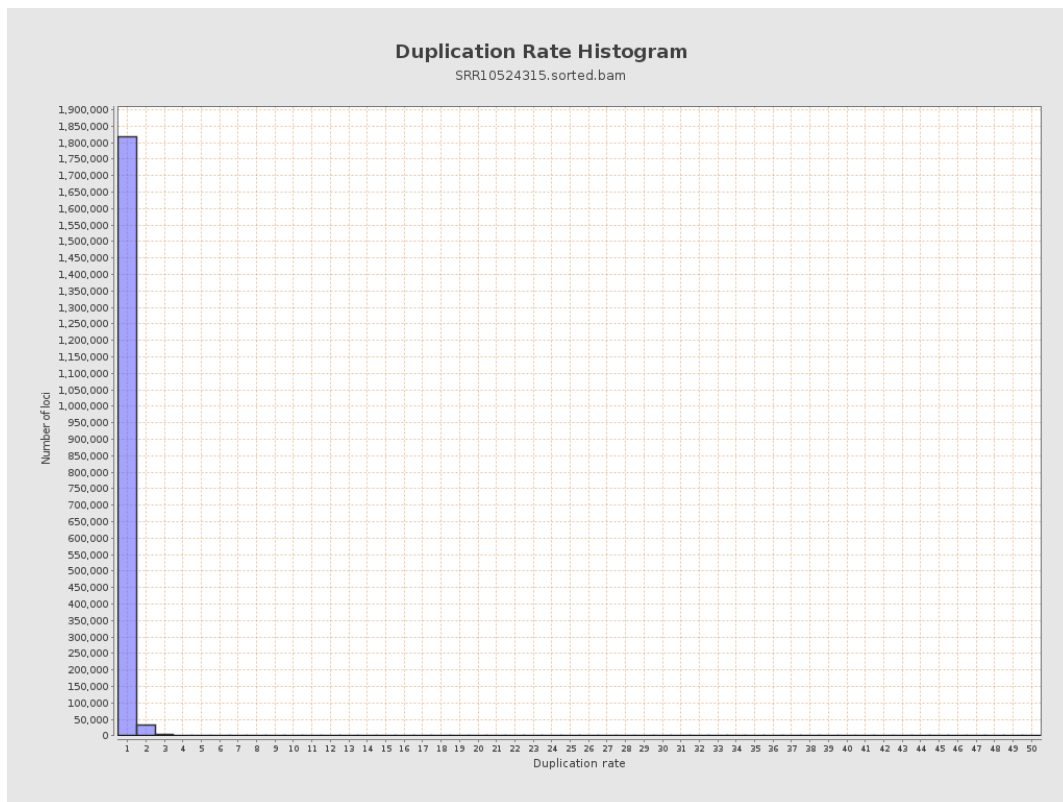
5. Results : Coverage Histogram (0-50X)



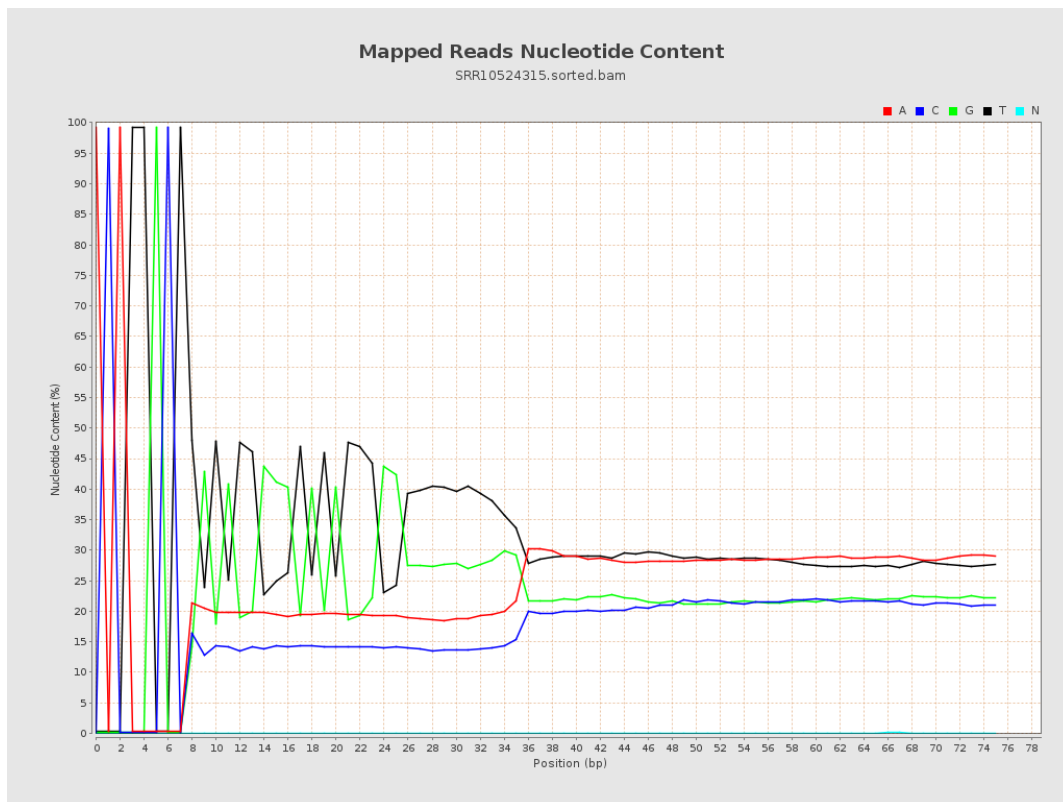
6. Results : Genome Fraction Coverage



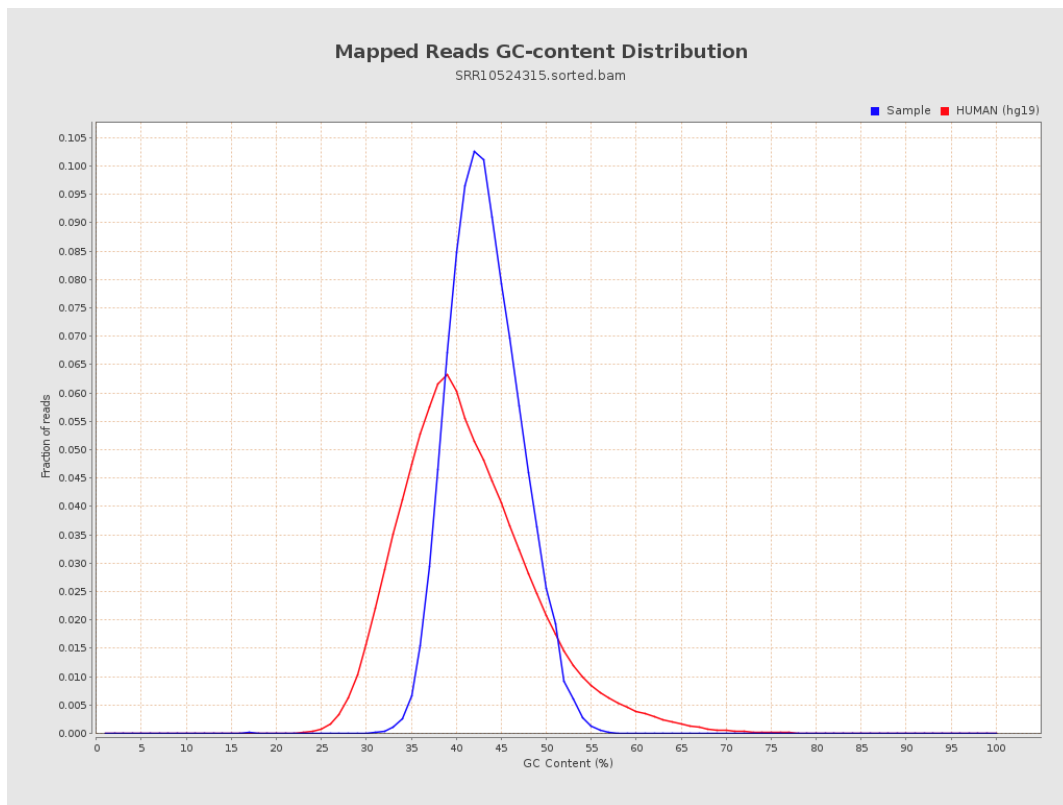
7. Results : Duplication Rate Histogram



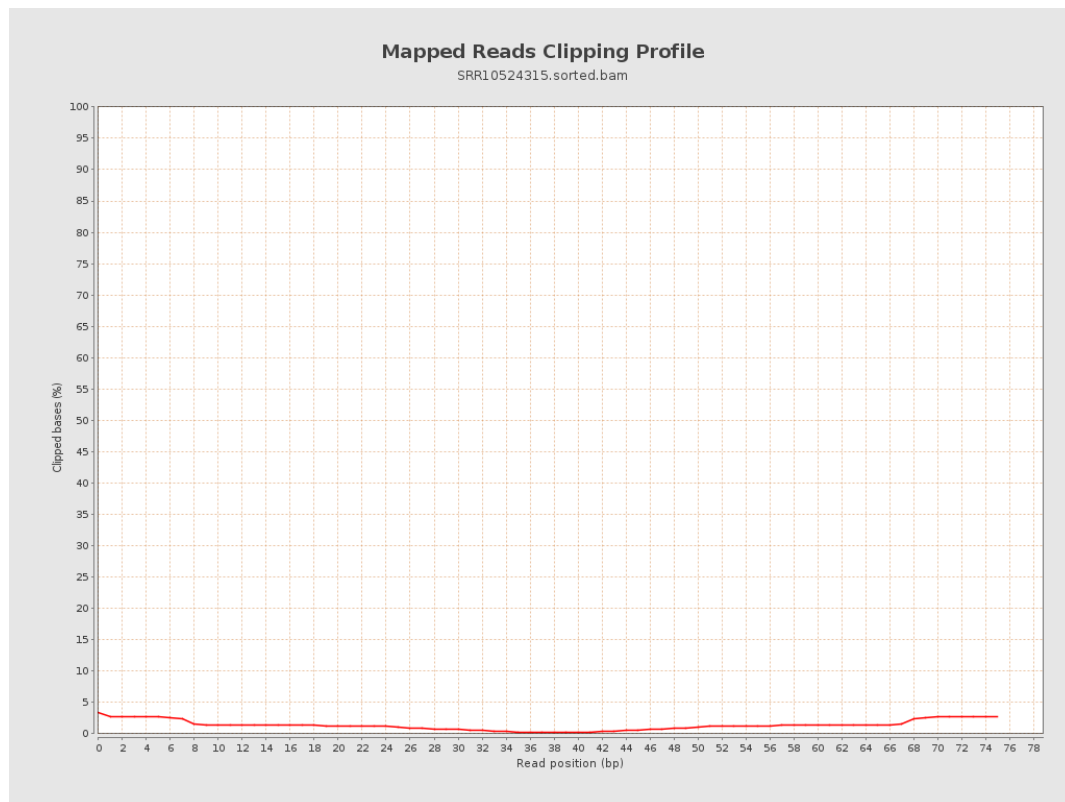
8. Results : Mapped Reads Nucleotide Content



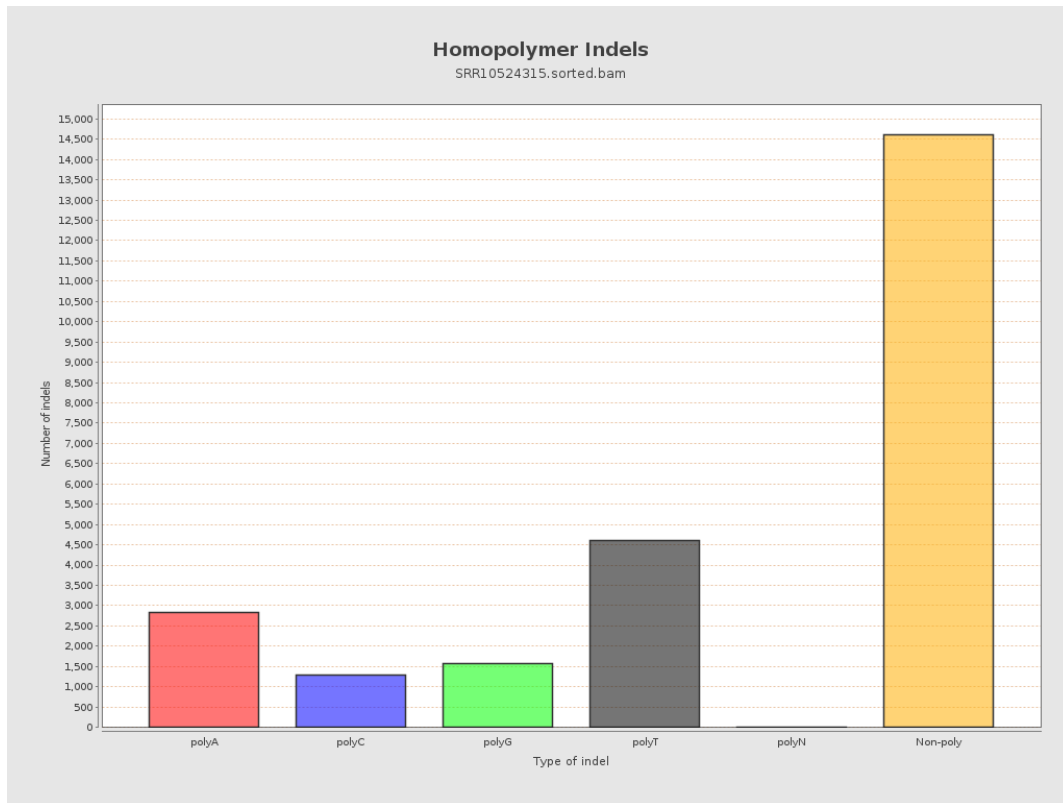
9. Results : Mapped Reads GC-content Distribution



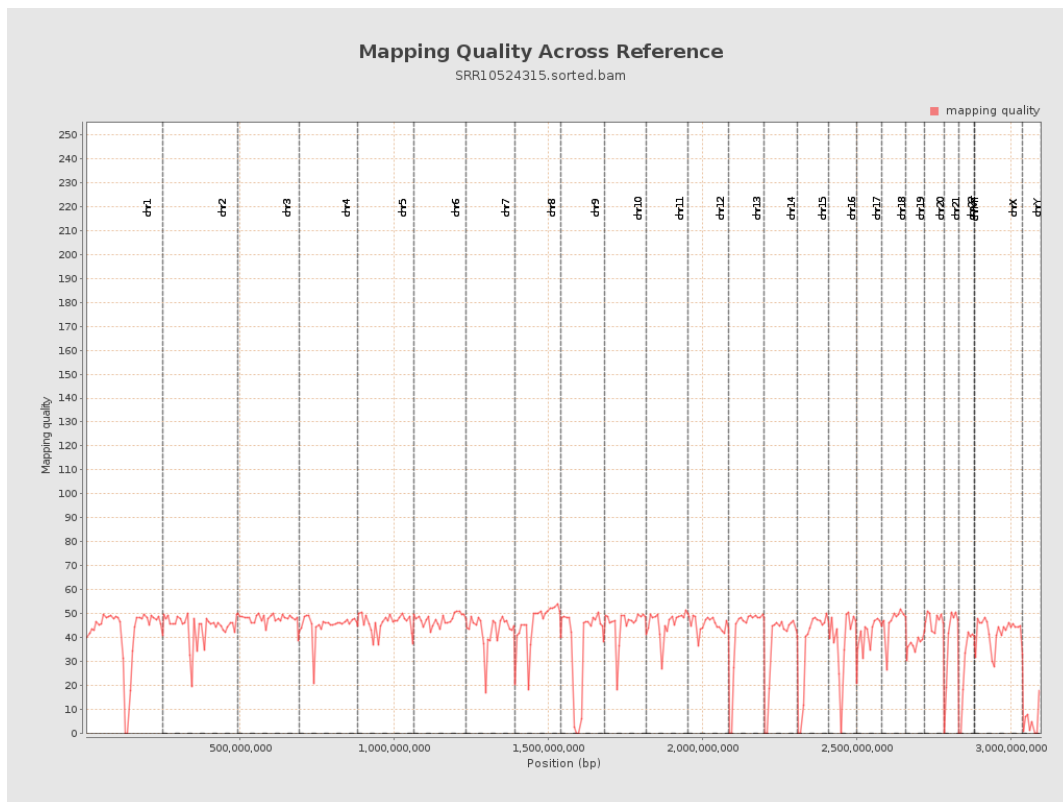
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

