

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:04:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240199.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_SRR6240199 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240199.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:04:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240199.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,609,573
Mapped reads	1,216,168 / 75.56%
Unmapped reads	393,405 / 24.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,490 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	134,884 / 8.38%
Duplication rate	9.37%
Clipped reads	856,097 / 53.19%

2.2. ACGT Content

Number/percentage of A's	20,020,114 / 27.29%
Number/percentage of C's	12,763,463 / 17.4%
Number/percentage of T's	23,981,551 / 32.69%
Number/percentage of G's	16,575,366 / 22.6%
Number/percentage of N's	16,390 / 0.02%
GC Percentage	39.99%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.2536
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2.4. Mapping Quality

Mean Mapping Quality	45.5
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2.5. Mismatches and indels

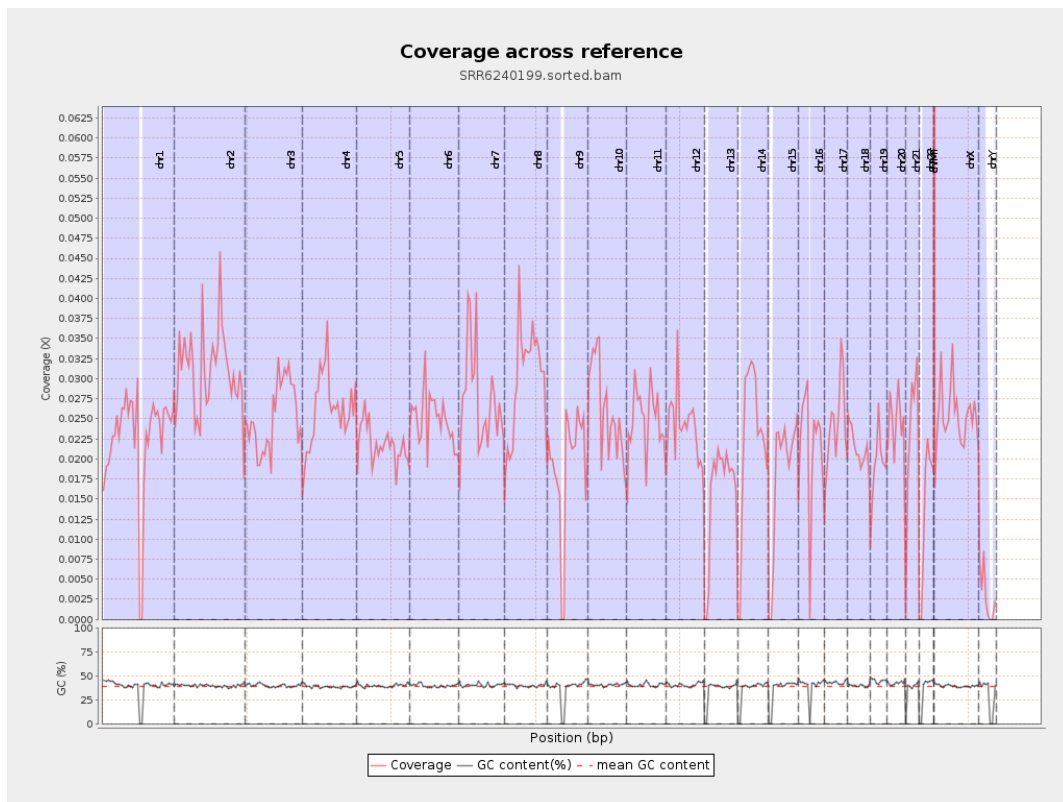
General error rate	0.99%
Mismatches	718,843
Insertions	5,113
Mapped reads with at least one insertion	0.42%
Deletions	25,468
Mapped reads with at least one deletion	2.07%
Homopolymer indels	50.64%

2.6. Chromosome stats

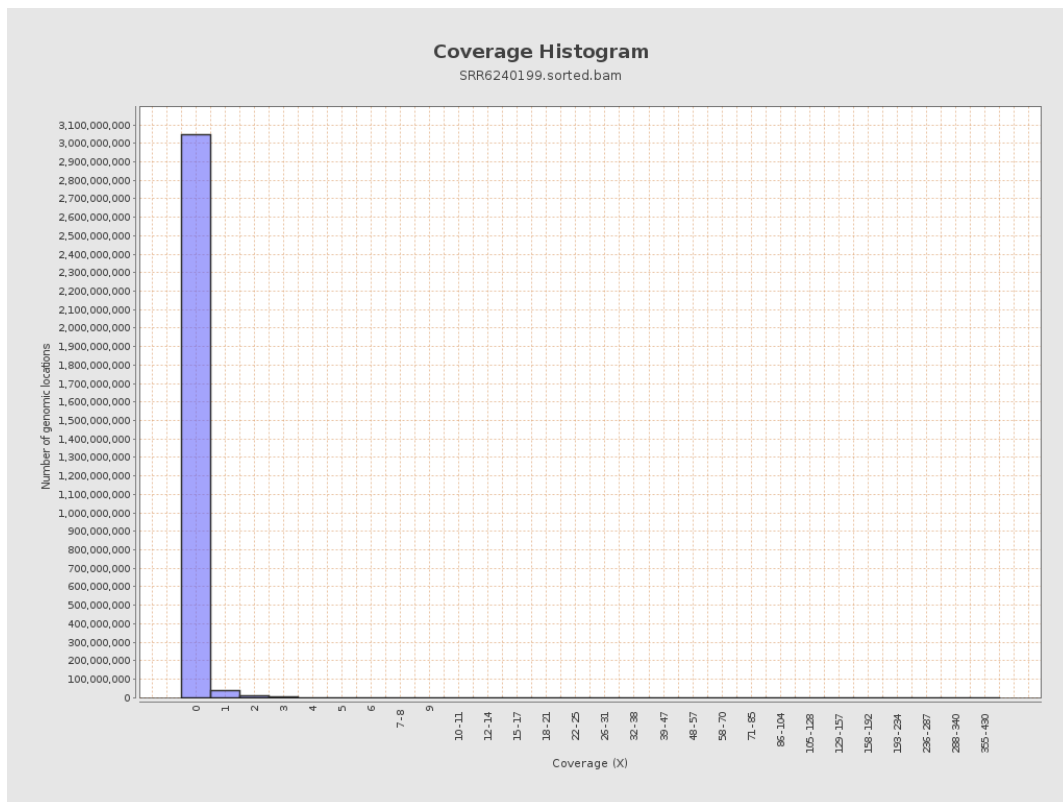
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5625993	0.0226	0.3077
chr2	243199373	7563650	0.0311	0.3035
chr3	198022430	4998231	0.0252	0.2181
chr4	191154276	4987840	0.0261	0.2284
chr5	180915260	3956026	0.0219	0.2038
chr6	171115067	4264993	0.0249	0.24
chr7	159138663	4371445	0.0275	0.3734

chr8	146364022	4415036	0.0302	0.3485
chr9	141213431	2710245	0.0192	0.2264
chr10	135534747	3535766	0.0261	0.2467
chr11	135006516	3368811	0.025	0.2533
chr12	133851895	3218302	0.024	0.2119
chr13	115169878	1809522	0.0157	0.1713
chr14	107349540	2423189	0.0226	0.2122
chr15	102531392	1853321	0.0181	0.1919
chr16	90354753	1912019	0.0212	0.2012
chr17	81195210	1991089	0.0245	0.2219
chr18	78077248	1665680	0.0213	0.3124
chr19	59128983	1162109	0.0197	0.2411
chr20	63025520	1536158	0.0244	0.2188
chr21	48129895	1121968	0.0233	0.2096
chr22	51304566	724514	0.0141	0.1586
chrMT	16571	47572	2.8708	3.7877
chrX	155270560	3966441	0.0255	0.2301
chrY	59373566	170124	0.0029	0.0769

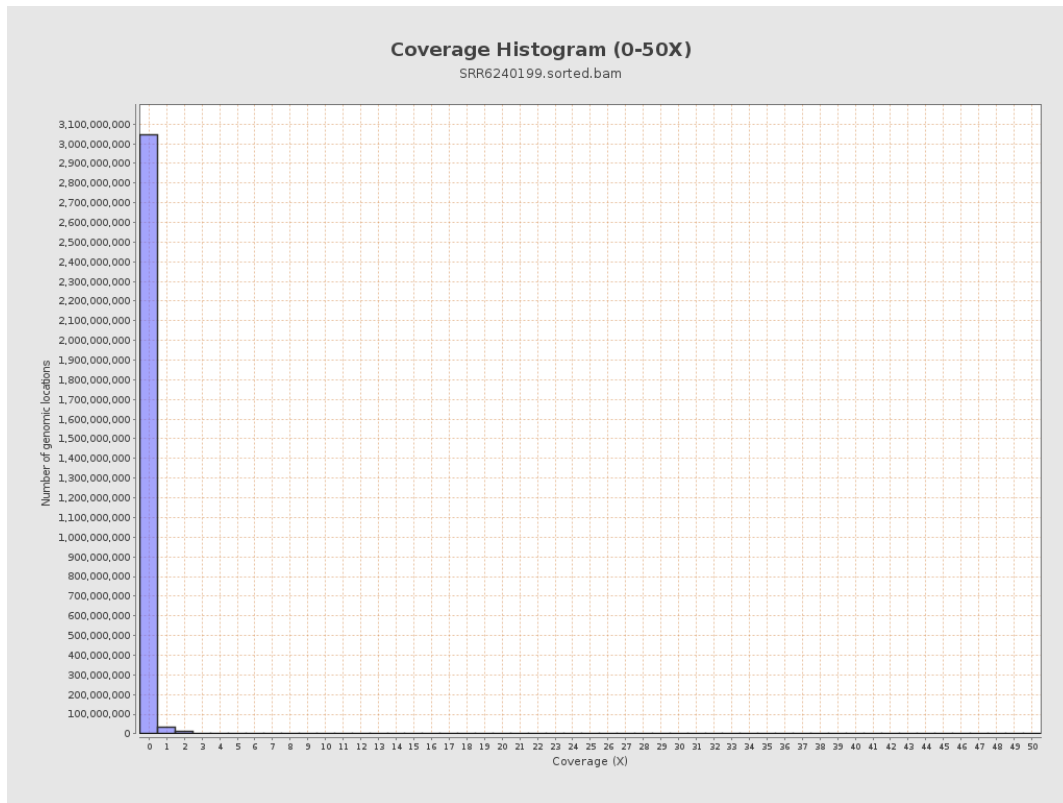
3. Results : Coverage across reference



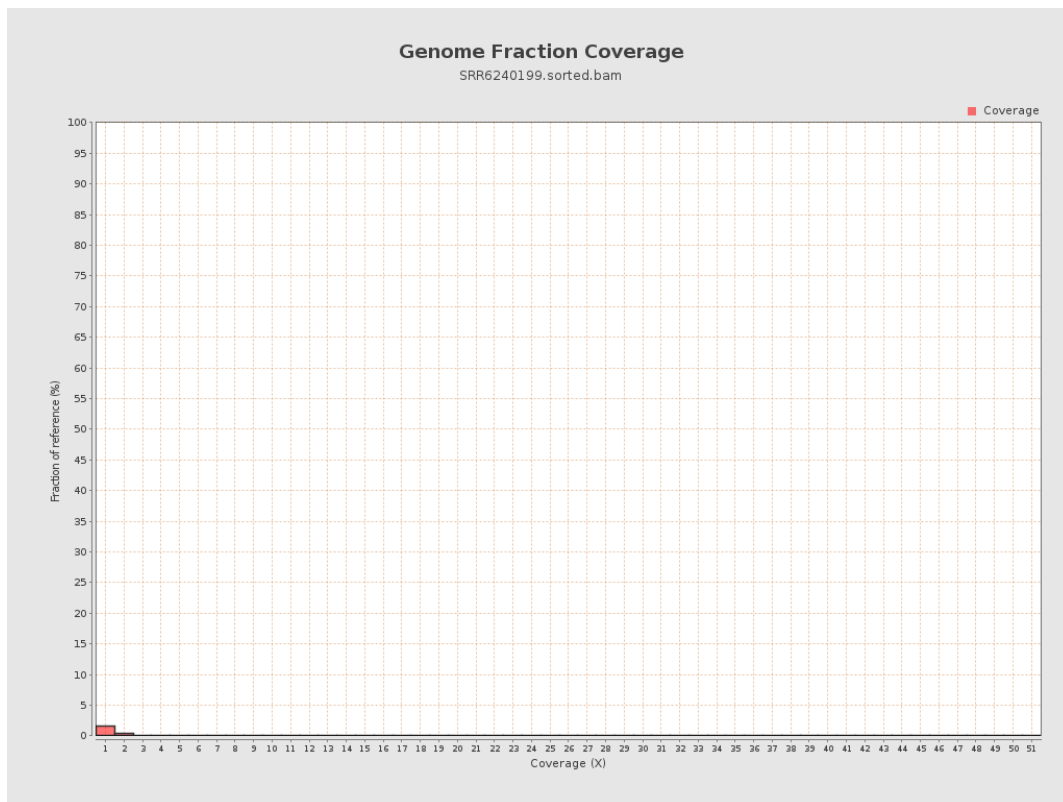
4. Results : Coverage Histogram



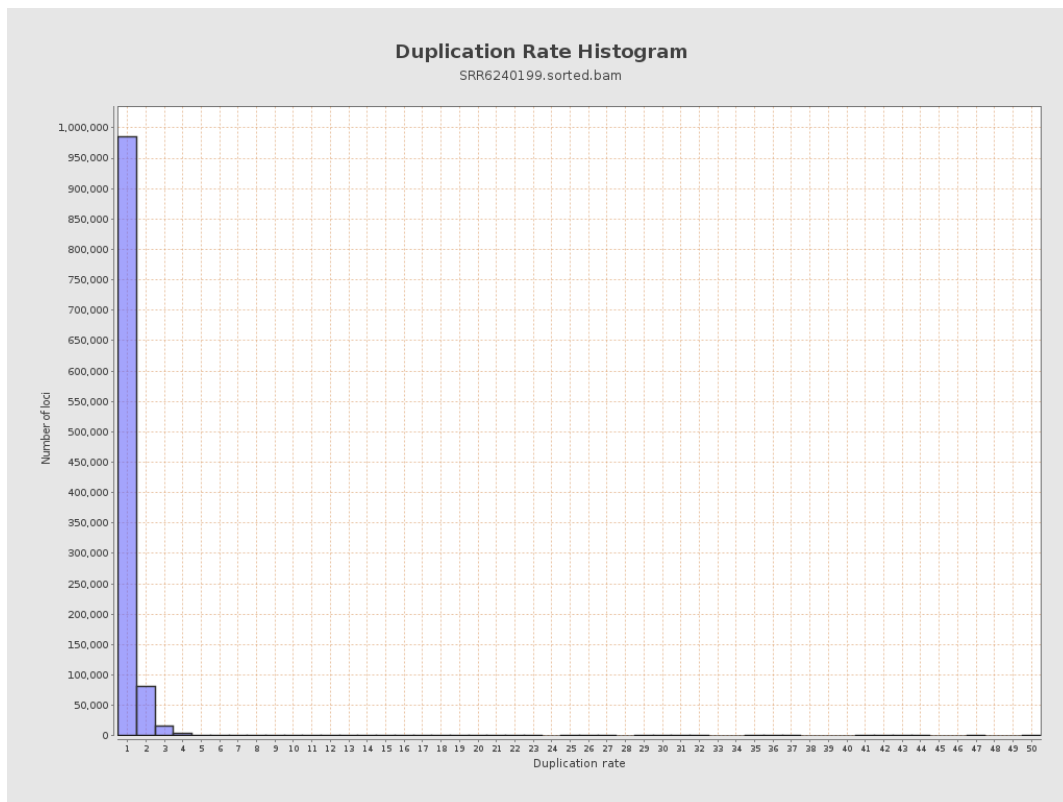
5. Results : Coverage Histogram (0-50X)



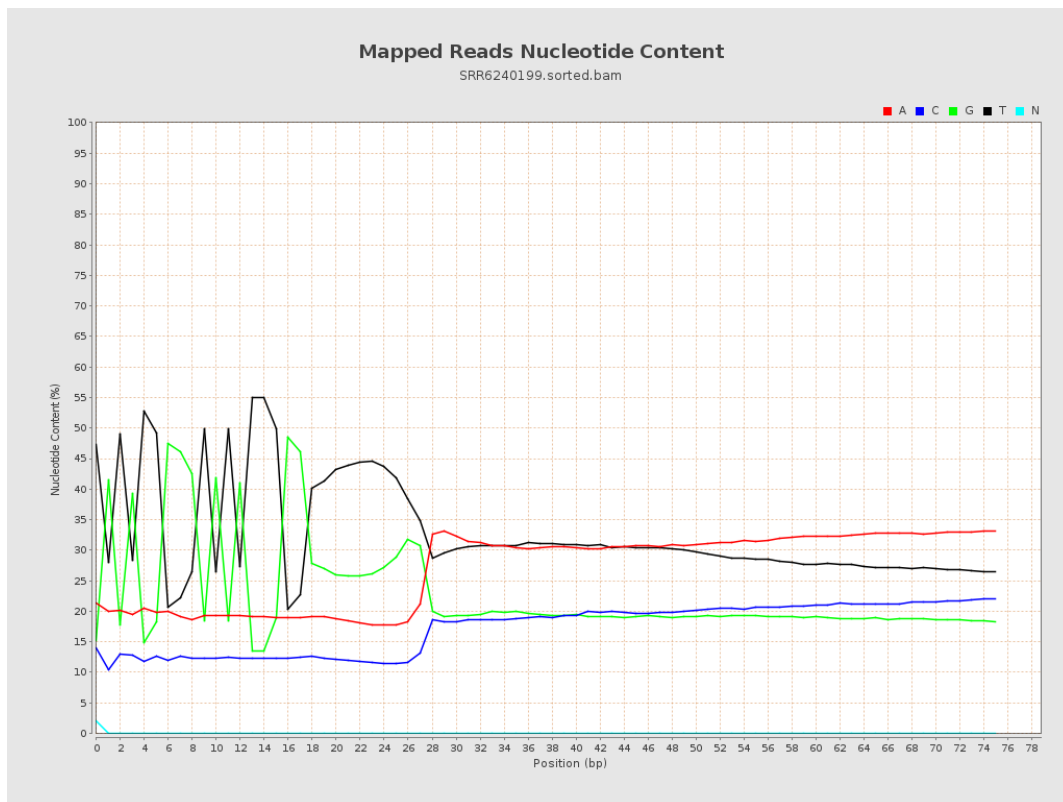
6. Results : Genome Fraction Coverage



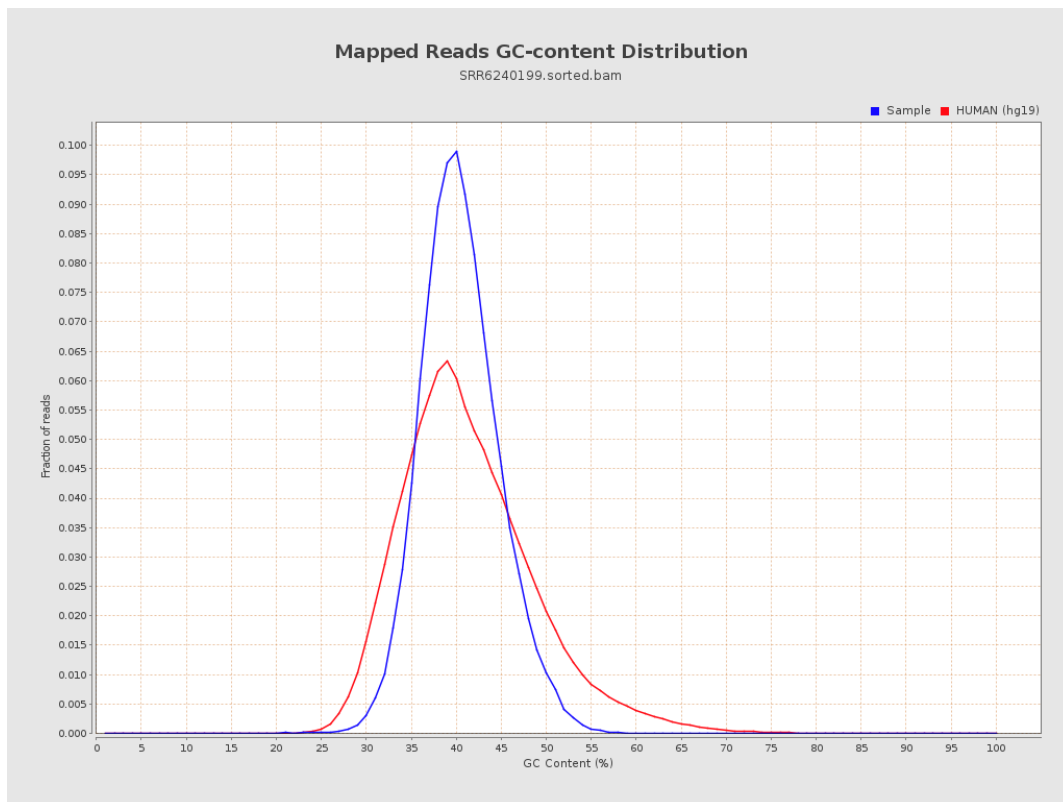
7. Results : Duplication Rate Histogram



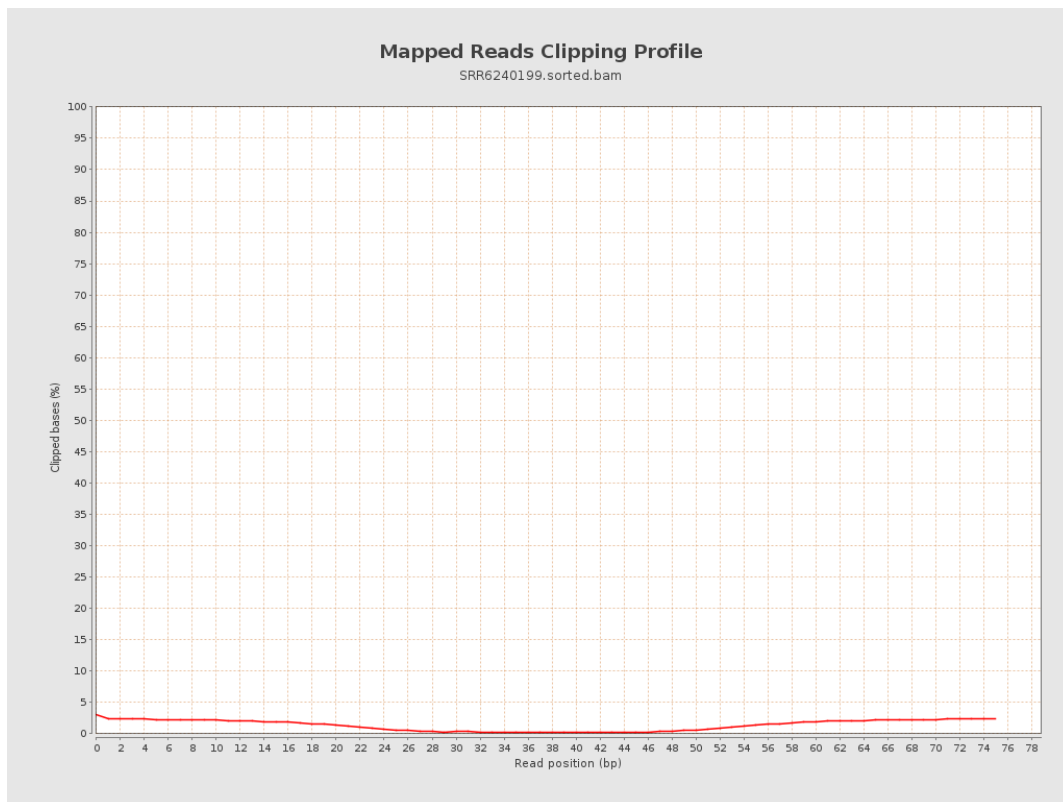
8. Results : Mapped Reads Nucleotide Content



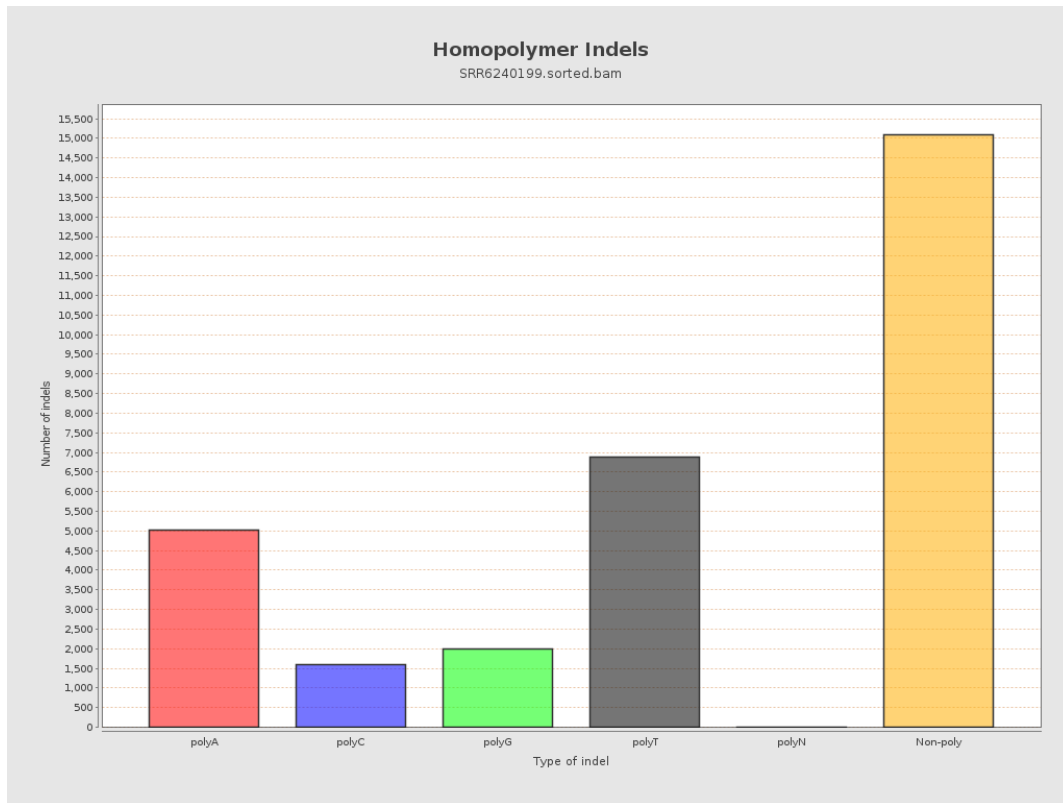
9. Results : Mapped Reads GC-content Distribution



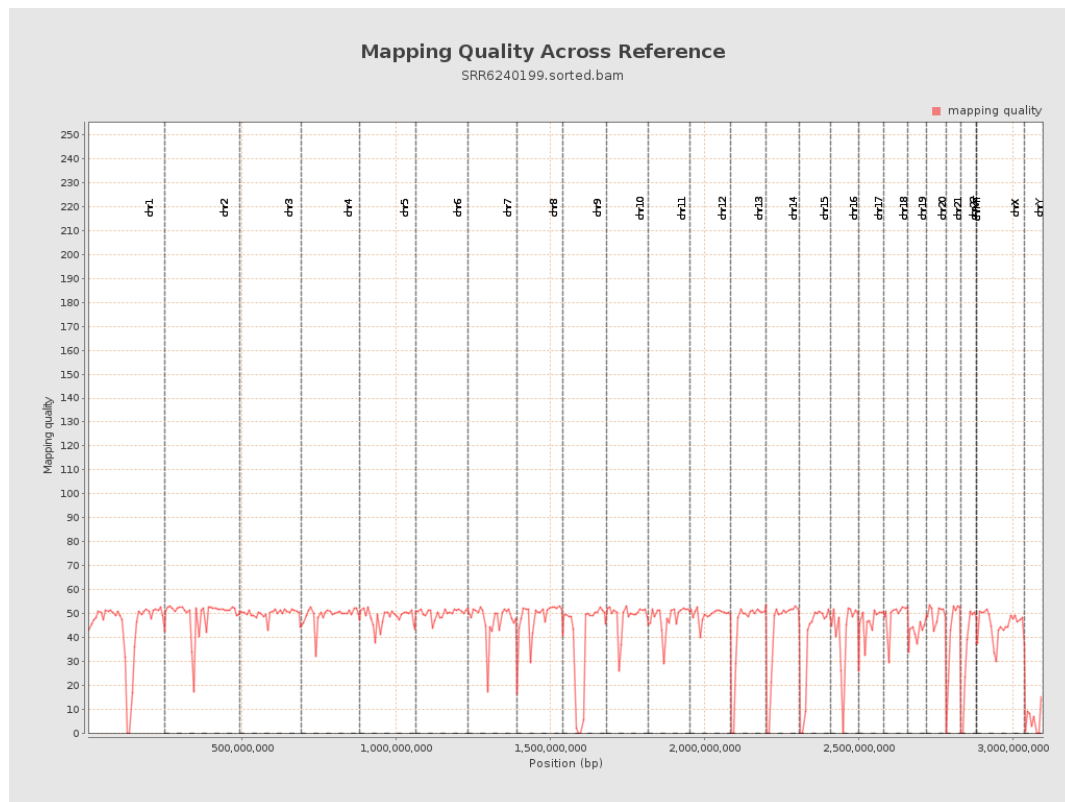
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

