

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:39:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240019.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_SRR6240019 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240019.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:39:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240019.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,879,110
Mapped reads	1,491,419 / 79.37%
Unmapped reads	387,691 / 20.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,269 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	210,305 / 11.19%
Duplication rate	11.25%
Clipped reads	931,882 / 49.59%

2.2. ACGT Content

Number/percentage of A's	25,356,649 / 27.29%
Number/percentage of C's	16,384,298 / 17.63%
Number/percentage of T's	30,154,222 / 32.45%
Number/percentage of G's	20,974,381 / 22.57%
Number/percentage of N's	61,450 / 0.07%
GC Percentage	40.2%

2.3. Coverage

Mean	0.03

Standard Deviation	0.3152
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2.4. Mapping Quality

Mean Mapping Quality	45.6
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2.5. Mismatches and indels

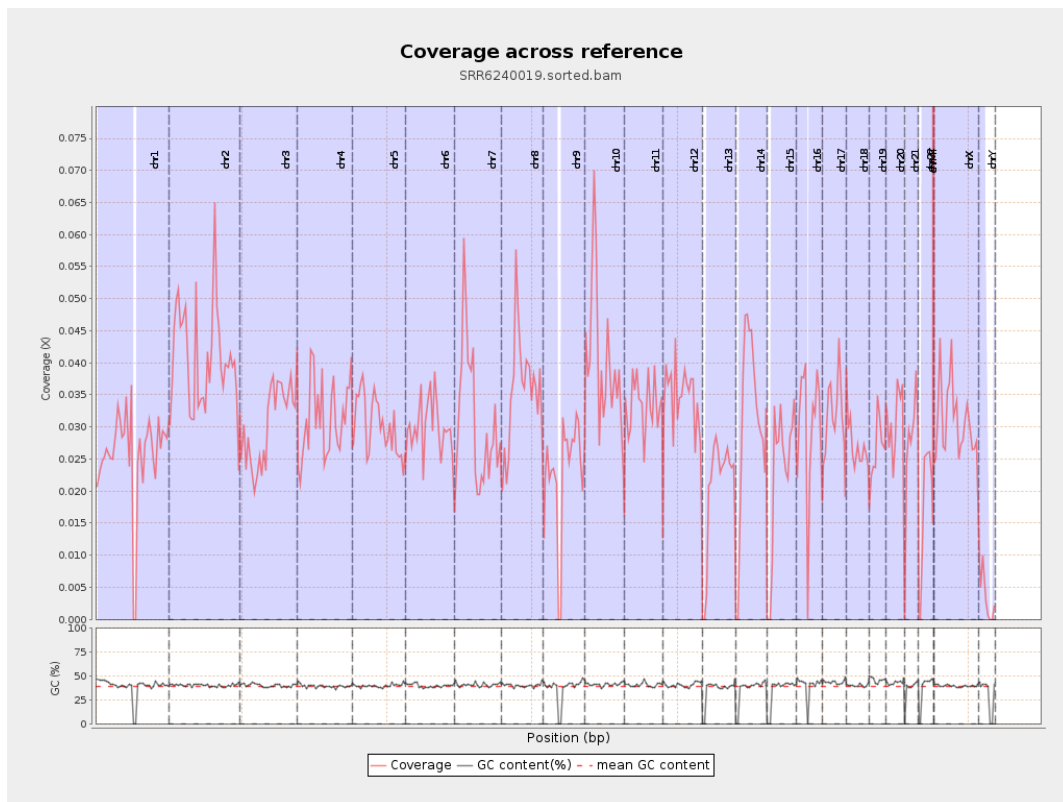
General error rate	0.95%
Mismatches	870,379
Insertions	6,512
Mapped reads with at least one insertion	0.43%
Deletions	25,969
Mapped reads with at least one deletion	1.72%
Homopolymer indels	48.54%

2.6. Chromosome stats

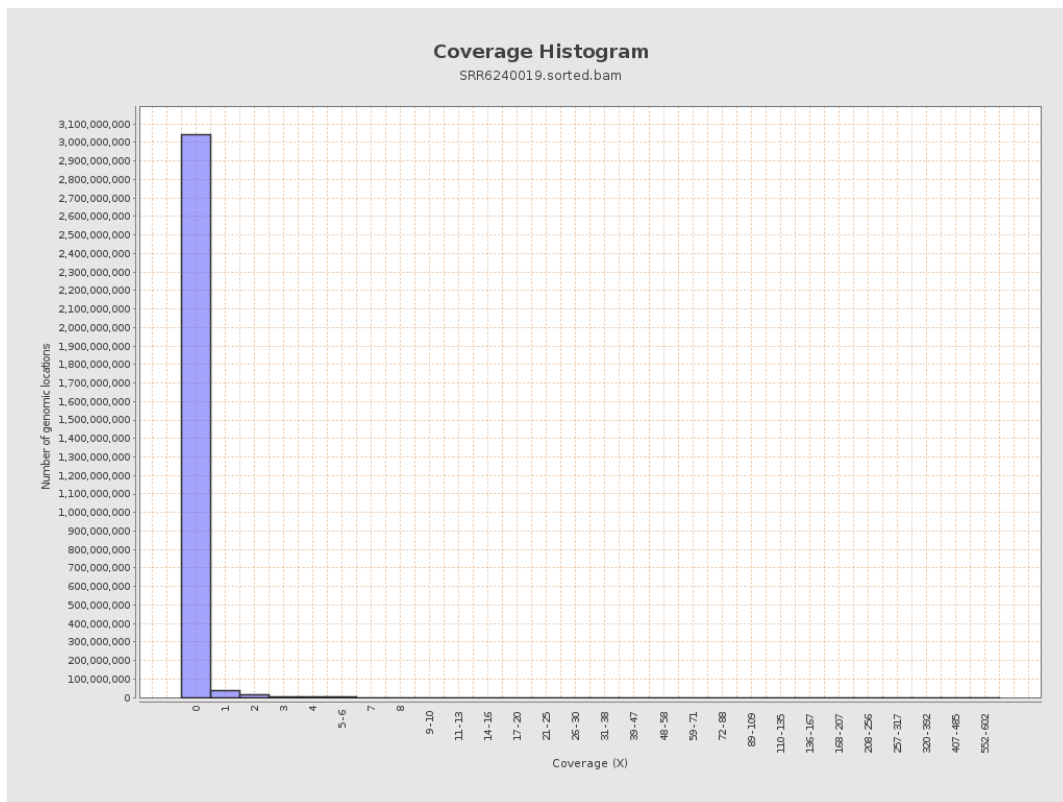
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6433168	0.0258	0.4135
chr2	243199373	9874359	0.0406	0.3992
chr3	198022430	6005719	0.0303	0.2614
chr4	191154276	5979371	0.0313	0.272
chr5	180915260	5486595	0.0303	0.2635
chr6	171115067	5120210	0.0299	0.2852
chr7	159138663	4954696	0.0311	0.3738

chr8	146364022	5204530	0.0356	0.455
chr9	141213431	3245191	0.023	0.2673
chr10	135534747	5500138	0.0406	0.3348
chr11	135006516	4474276	0.0331	0.3122
chr12	133851895	4612883	0.0345	0.2826
chr13	115169878	2341953	0.0203	0.2132
chr14	107349540	3303947	0.0308	0.2702
chr15	102531392	2367049	0.0231	0.2303
chr16	90354753	2705420	0.0299	0.2598
chr17	81195210	2544331	0.0313	0.2723
chr18	78077248	2115988	0.0271	0.3894
chr19	59128983	1596780	0.027	0.3218
chr20	63025520	1910622	0.0303	0.2636
chr21	48129895	1316231	0.0273	0.2569
chr22	51304566	884365	0.0172	0.1904
chrMT	16571	23111	1.3947	1.9211
chrX	155270560	4769338	0.0307	0.2744
chrY	59373566	204737	0.0034	0.0893

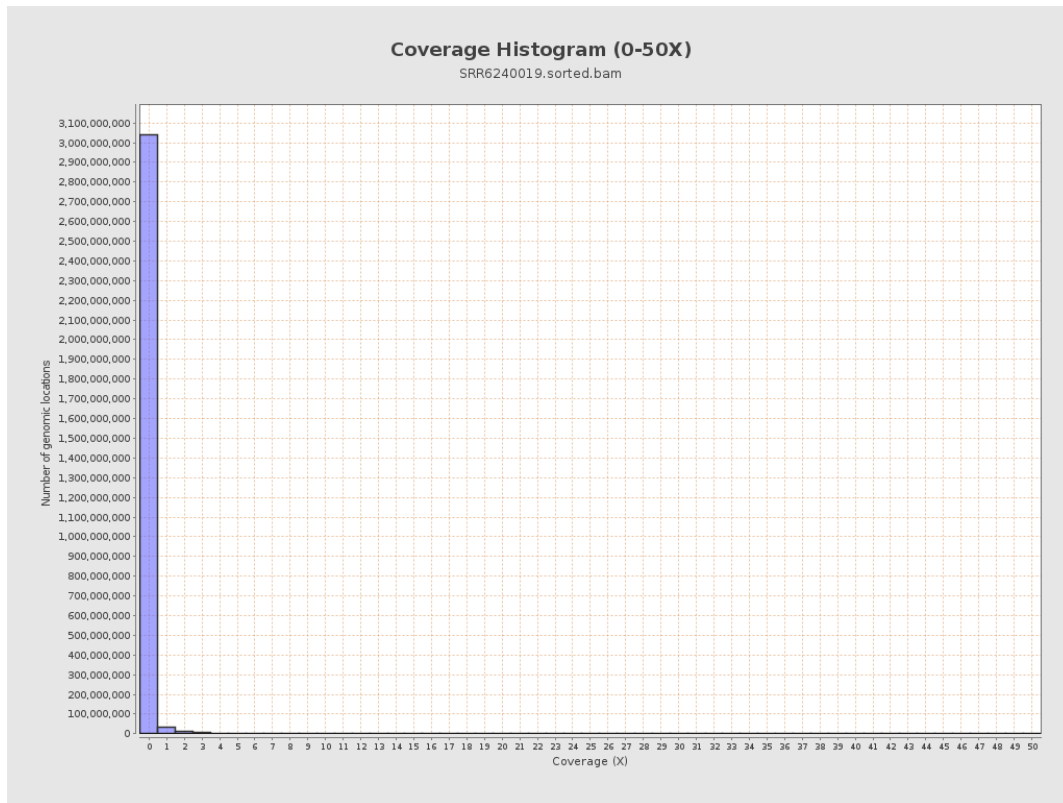
3. Results : Coverage across reference



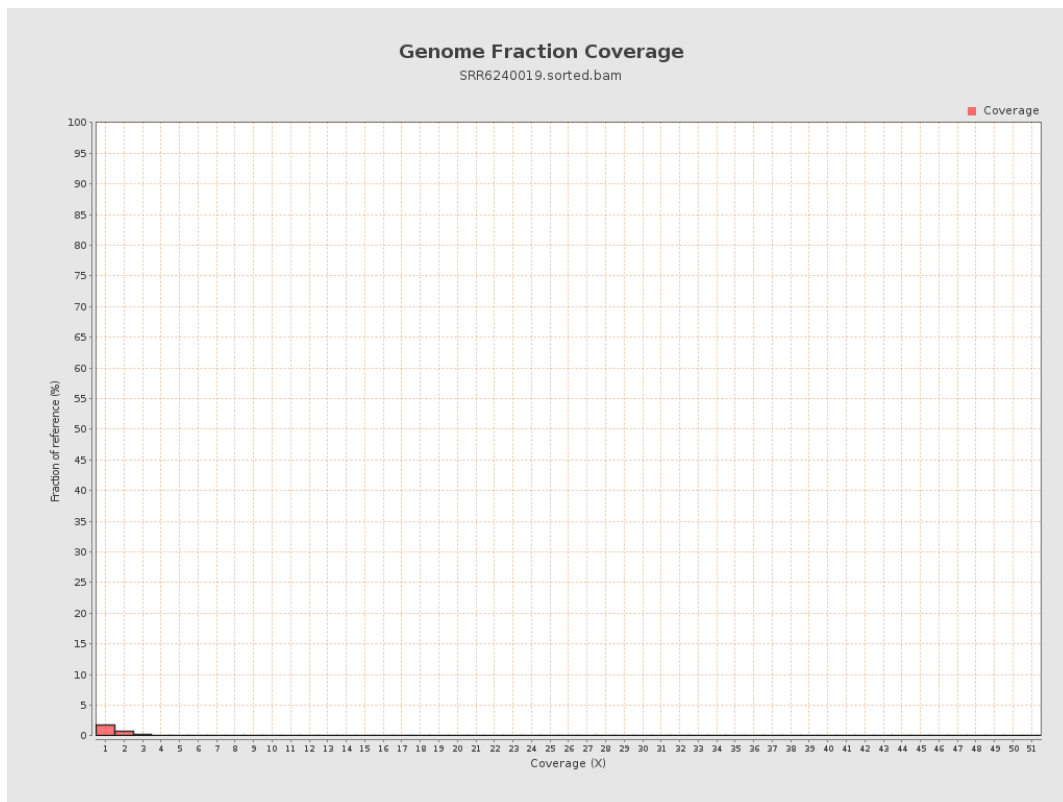
4. Results : Coverage Histogram



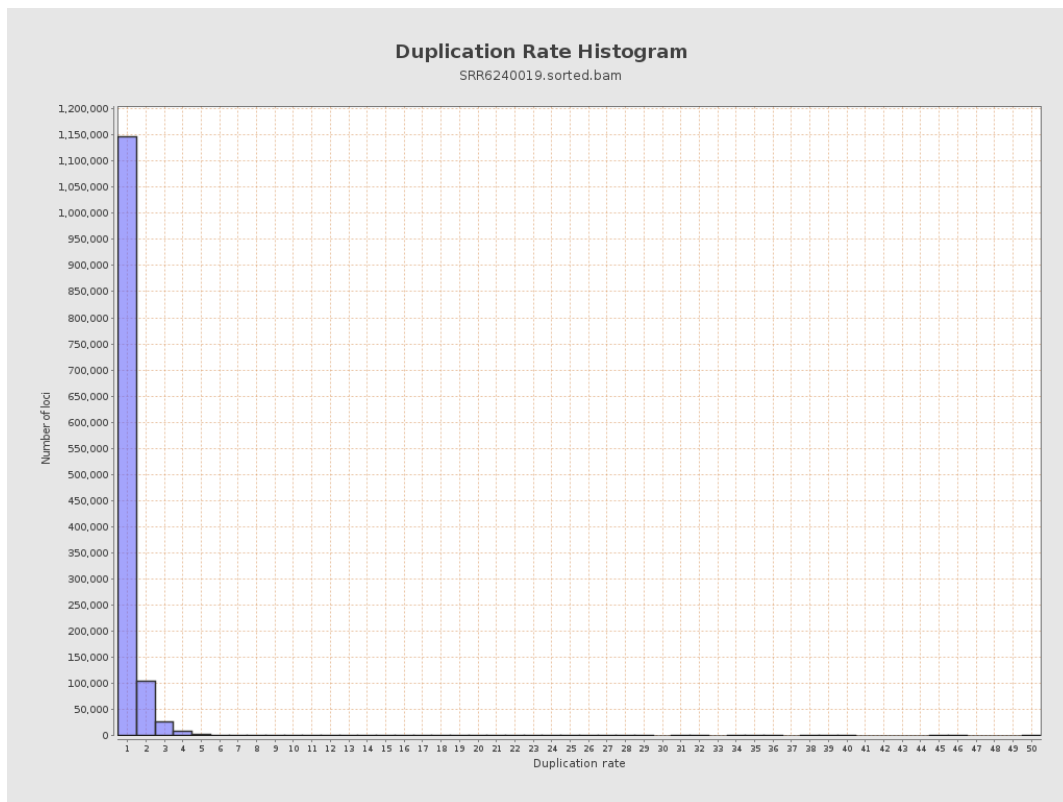
5. Results : Coverage Histogram (0-50X)



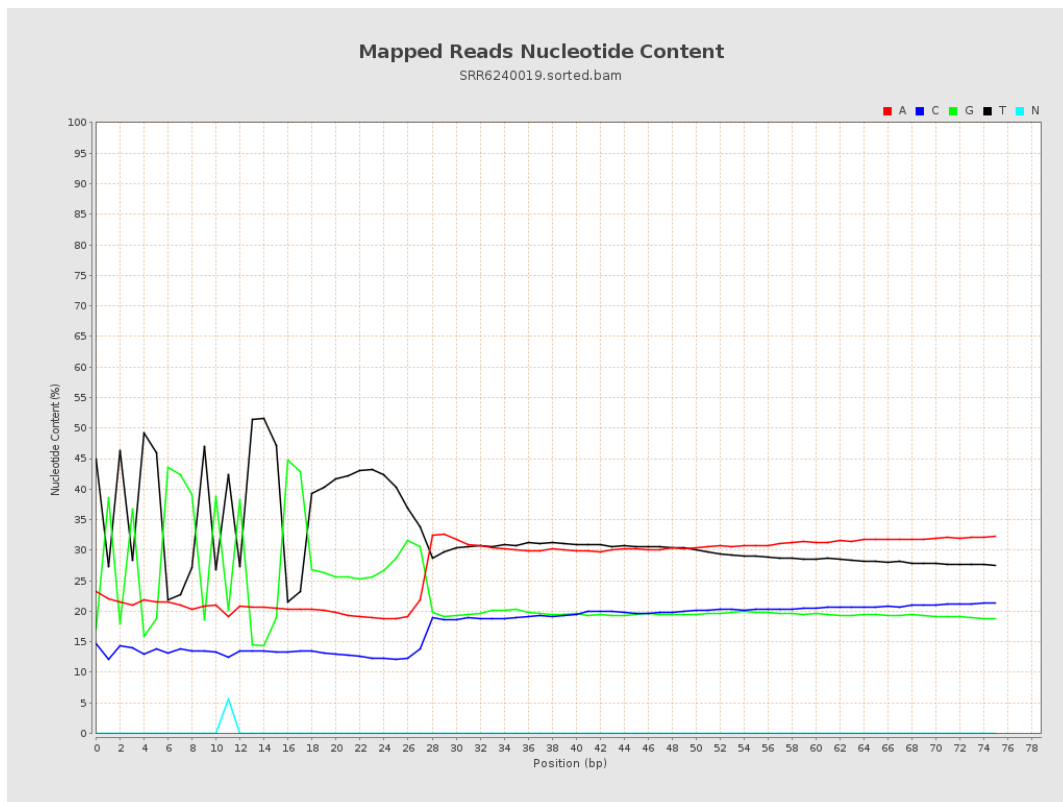
6. Results : Genome Fraction Coverage



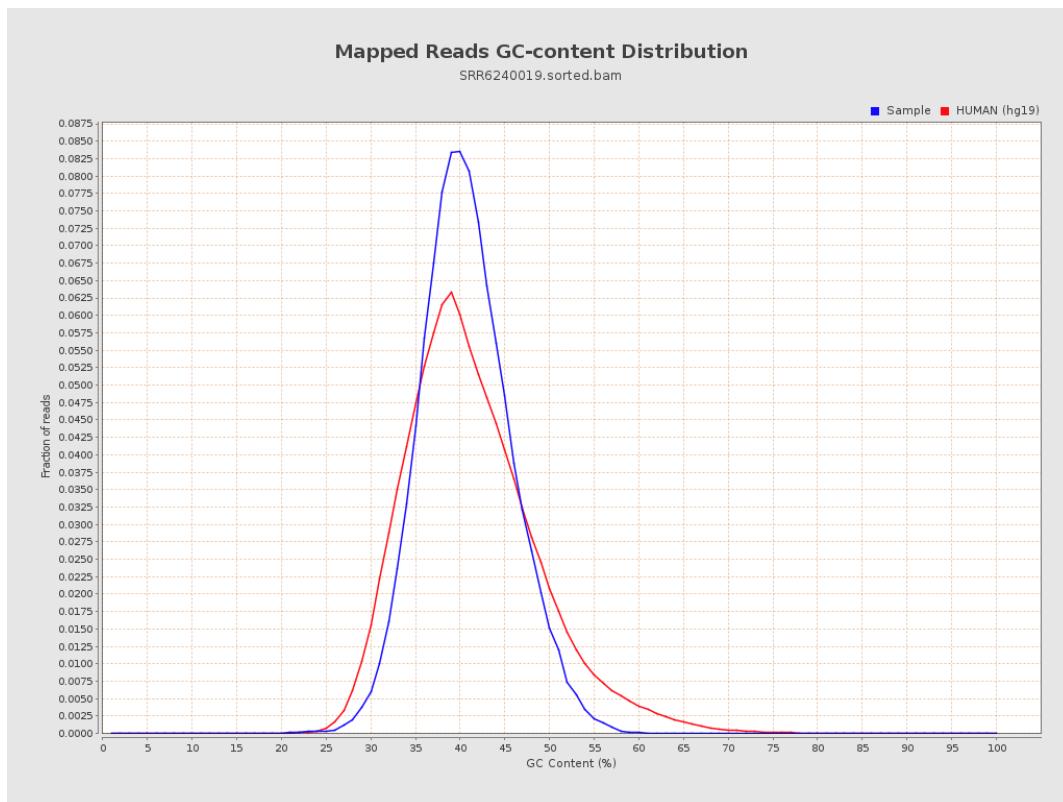
7. Results : Duplication Rate Histogram



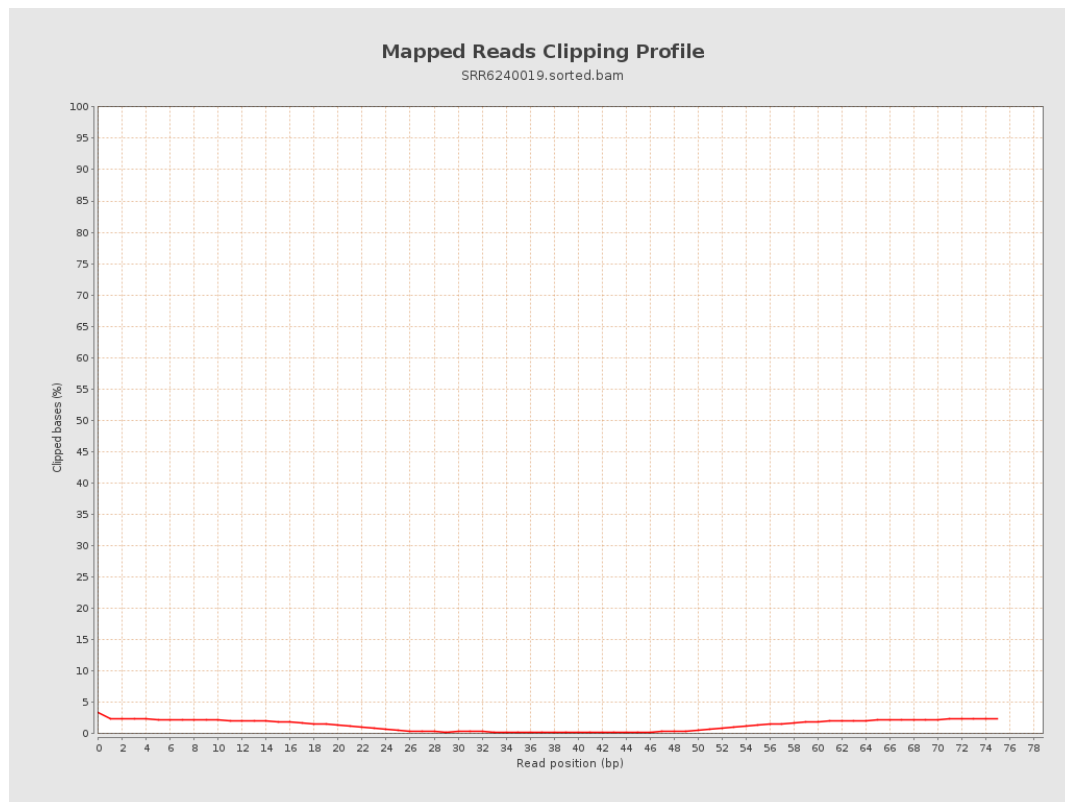
8. Results : Mapped Reads Nucleotide Content



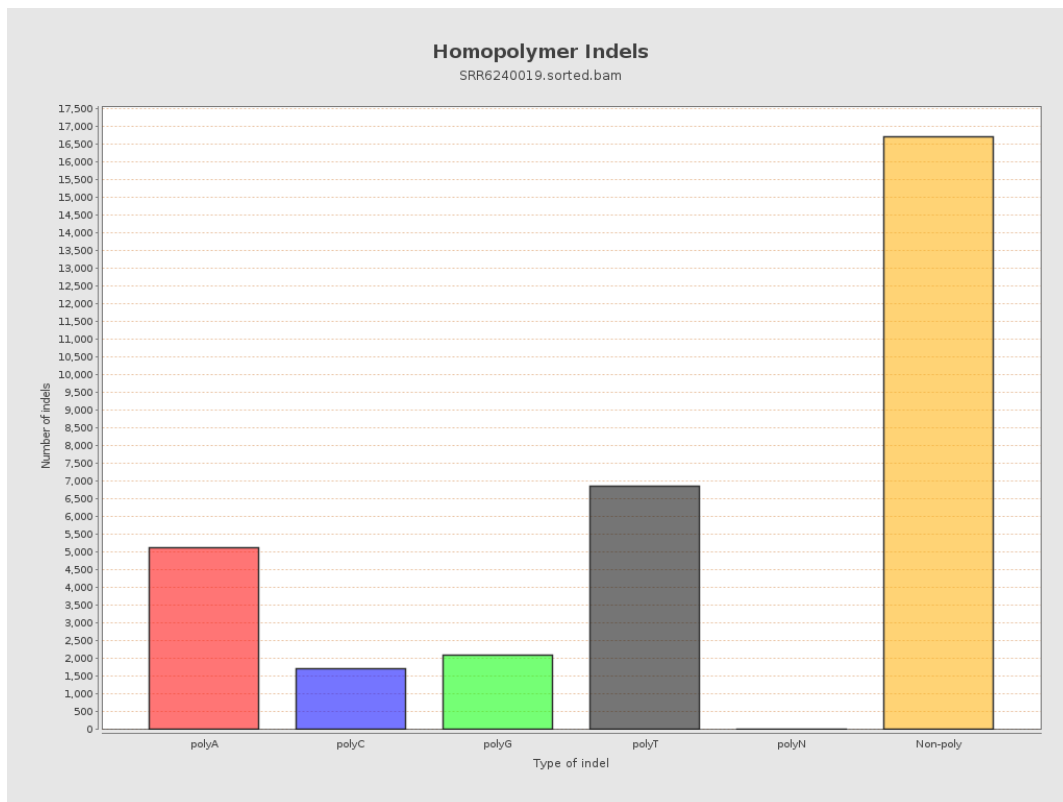
9. Results : Mapped Reads GC-content Distribution



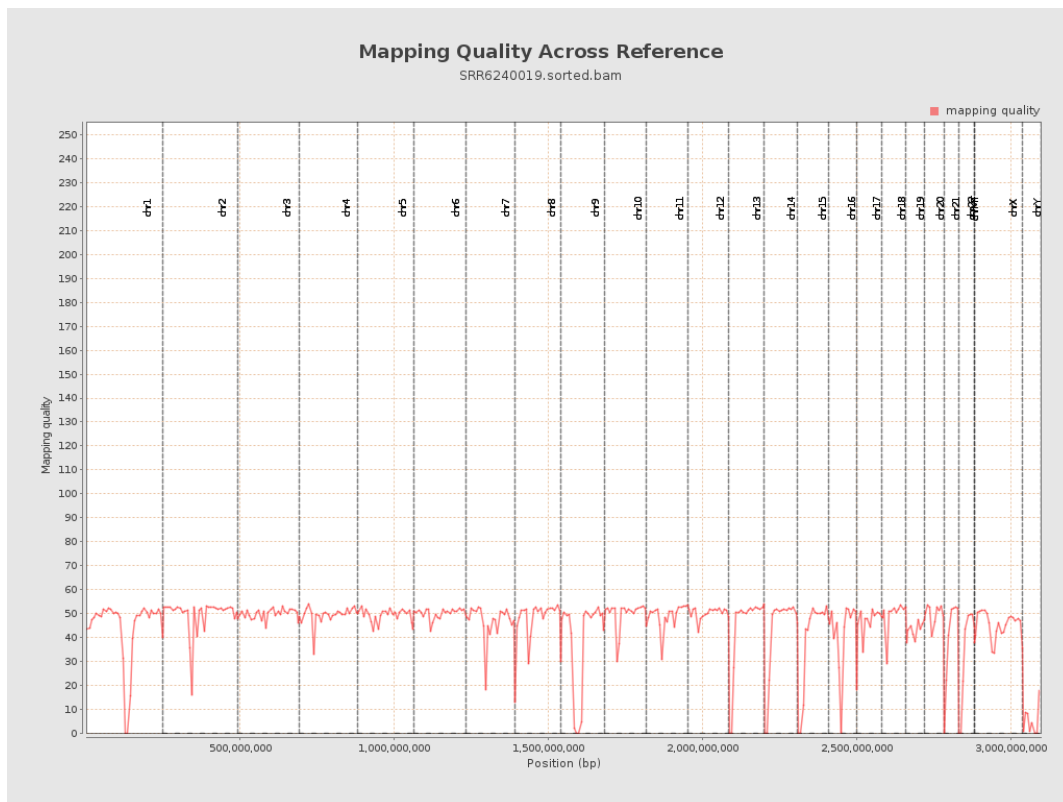
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

