

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:07:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240241.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_SRR6240241 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240241.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:07:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240241.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,422,137
Mapped reads	1,727,250 / 71.31%
Unmapped reads	694,887 / 28.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,553 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	310,755 / 12.83%
Duplication rate	13.48%
Clipped reads	1,033,948 / 42.69%

2.2. ACGT Content

Number/percentage of A's	29,020,673 / 26.61%
Number/percentage of C's	20,004,195 / 18.34%
Number/percentage of T's	34,762,102 / 31.88%
Number/percentage of G's	25,253,524 / 23.16%
Number/percentage of N's	8,524 / 0.01%
GC Percentage	41.5%

2.3. Coverage

Mean	0.0352

Standard Deviation	0.3899
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2.4. Mapping Quality

Mean Mapping Quality	45.53
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2.5. Mismatches and indels

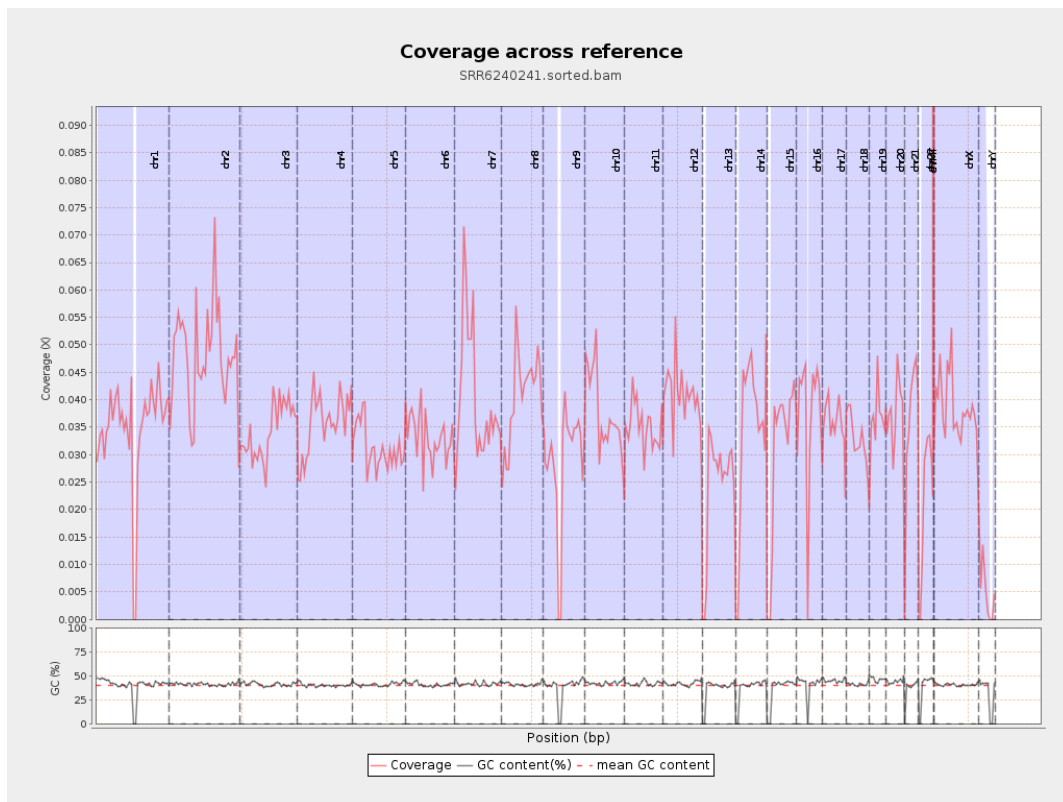
General error rate	0.89%
Mismatches	959,217
Insertions	7,409
Mapped reads with at least one insertion	0.43%
Deletions	28,916
Mapped reads with at least one deletion	1.66%
Homopolymer indels	47.53%

2.6. Chromosome stats

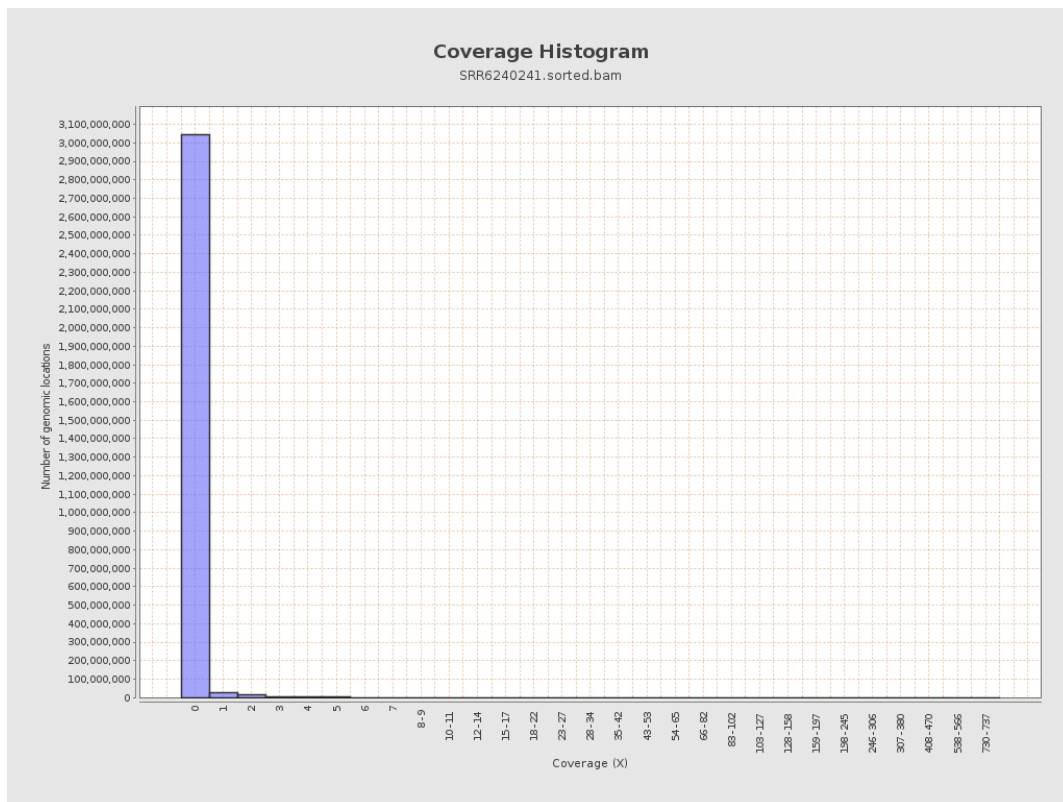
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8662444	0.0348	0.4877
chr2	243199373	11635589	0.0478	0.5305
chr3	198022430	6788850	0.0343	0.3277
chr4	191154276	6815289	0.0357	0.3392
chr5	180915260	5635129	0.0311	0.3086
chr6	171115067	5657838	0.0331	0.356
chr7	159138663	6459268	0.0406	0.5097

chr8	146364022	5963289	0.0407	0.4194
chr9	141213431	4030019	0.0285	0.3338
chr10	135534747	5131748	0.0379	0.3782
chr11	135006516	4736209	0.0351	0.3888
chr12	133851895	5480028	0.0409	0.3625
chr13	115169878	2779921	0.0241	0.2784
chr14	107349540	3648570	0.034	0.3481
chr15	102531392	3157092	0.0308	0.3405
chr16	90354753	3390007	0.0375	0.3412
chr17	81195210	2892752	0.0356	0.3479
chr18	78077248	2586573	0.0331	0.4713
chr19	59128983	2174654	0.0368	0.4182
chr20	63025520	2336554	0.0371	0.3486
chr21	48129895	1735441	0.0361	0.3349
chr22	51304566	1096399	0.0214	0.256
chrMT	16571	20094	1.2126	1.8162
chrX	155270560	5981393	0.0385	0.3684
chrY	59373566	303839	0.0051	0.1196

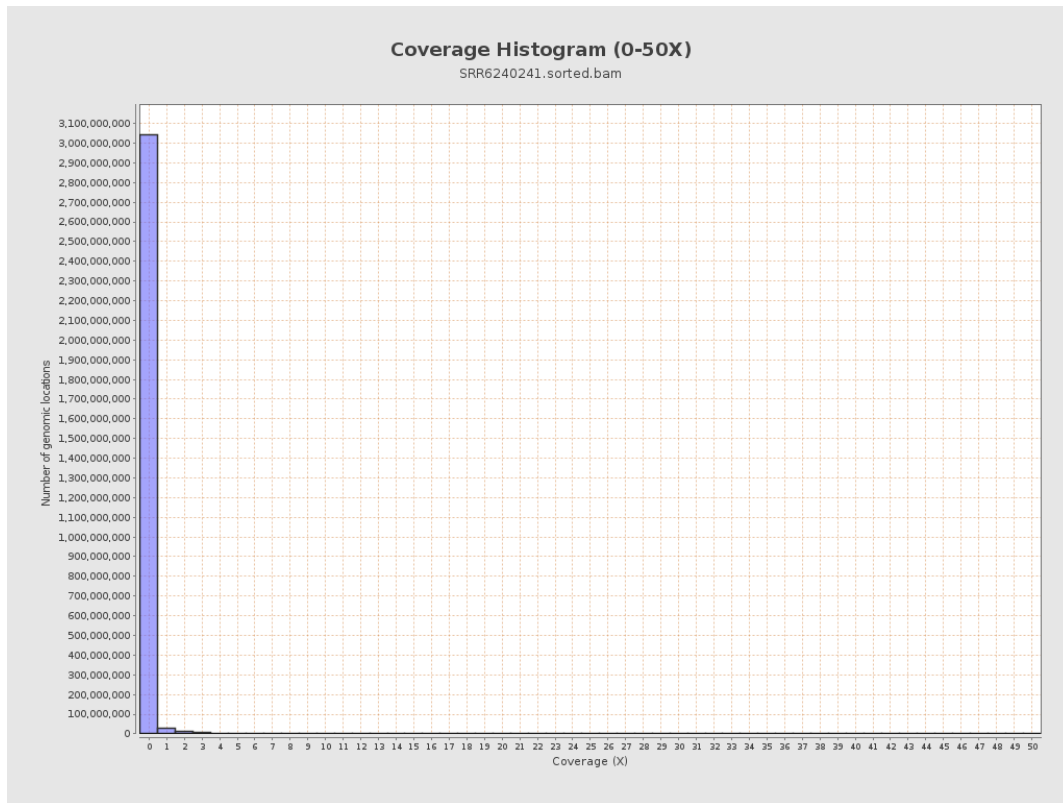
3. Results : Coverage across reference



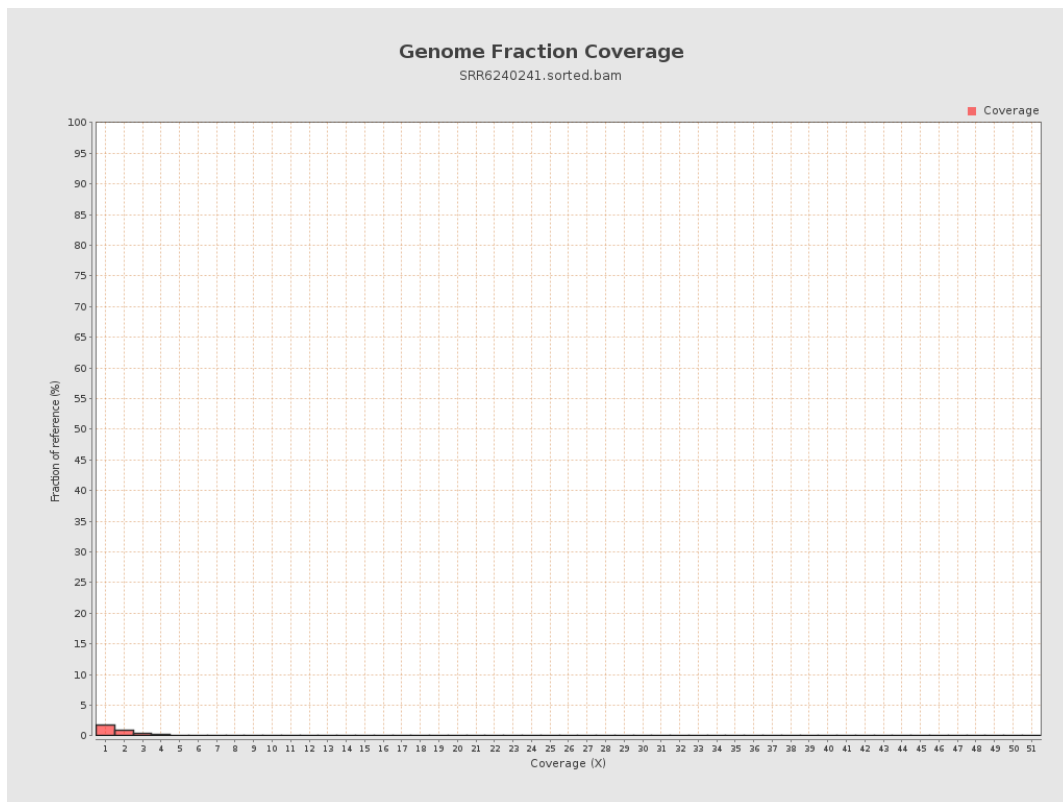
4. Results : Coverage Histogram



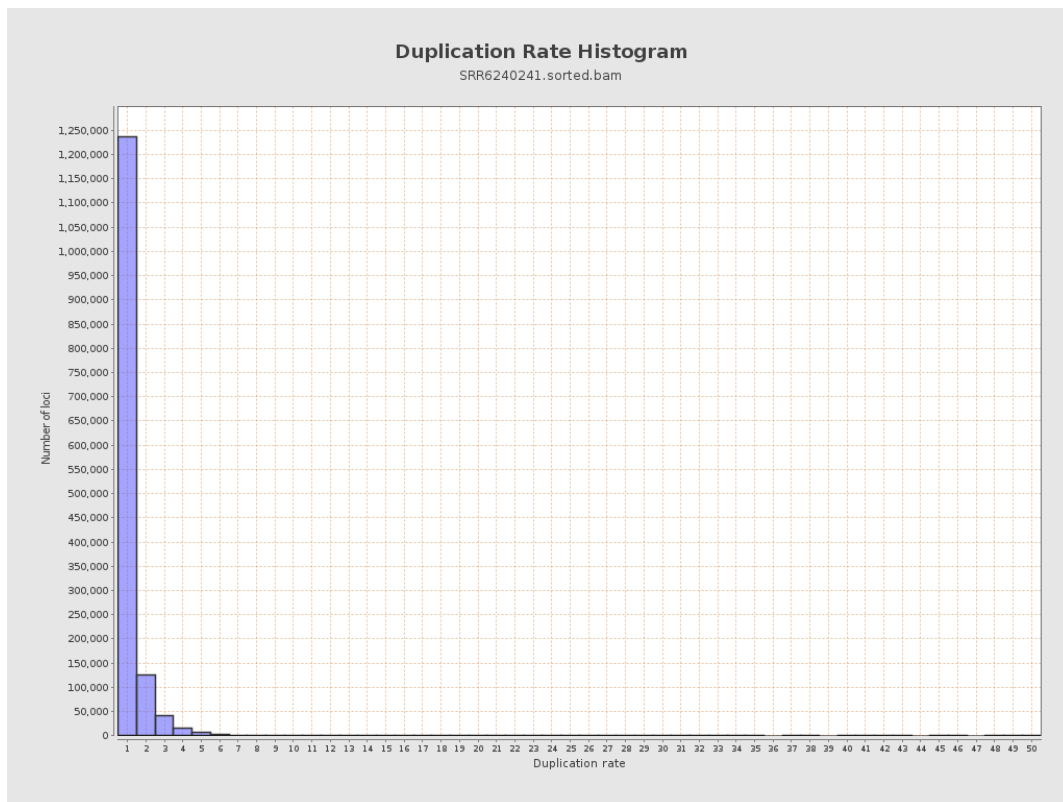
5. Results : Coverage Histogram (0-50X)



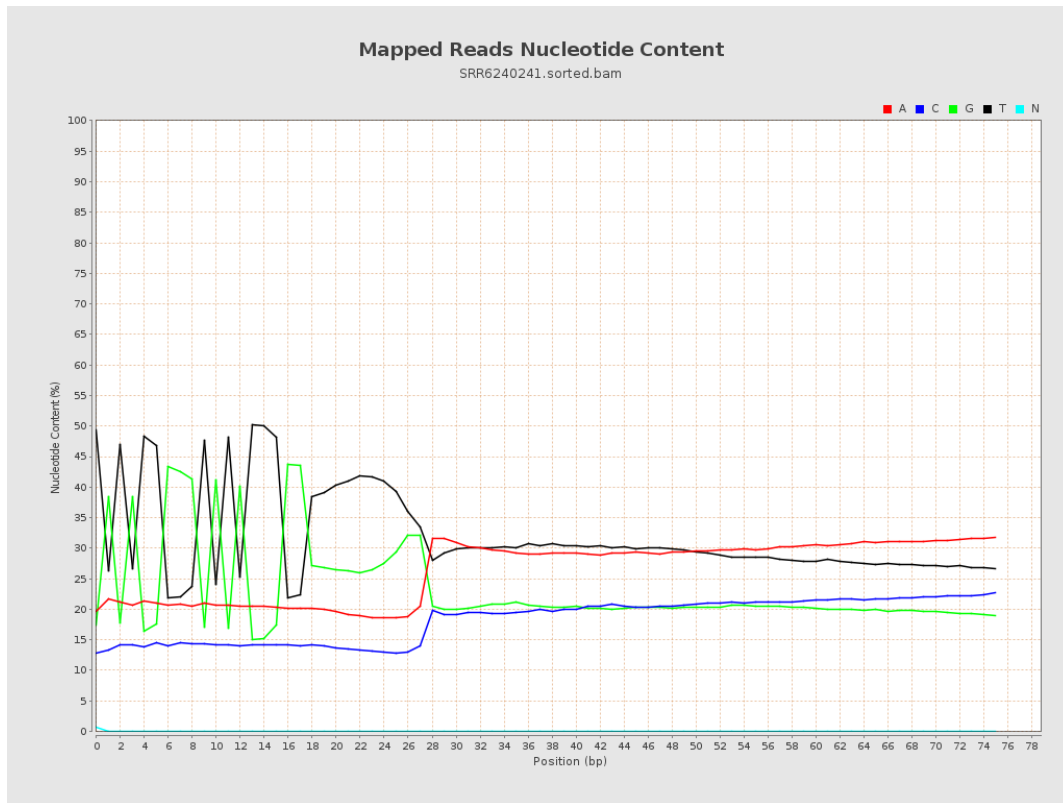
6. Results : Genome Fraction Coverage



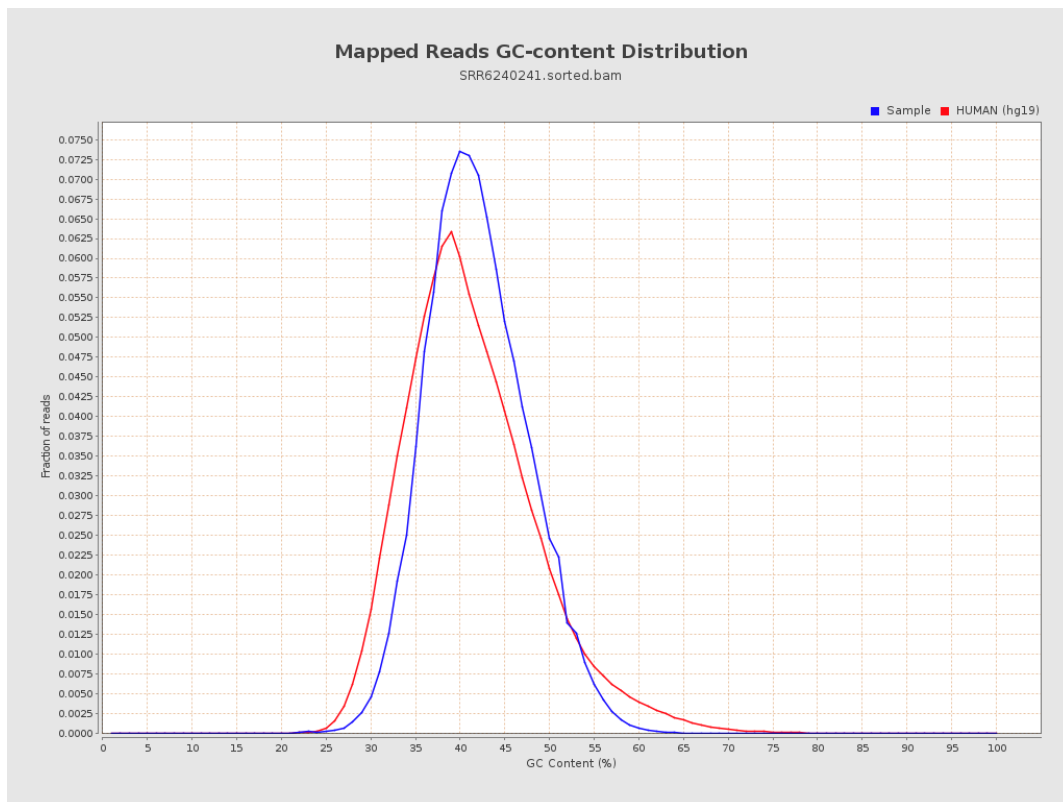
7. Results : Duplication Rate Histogram



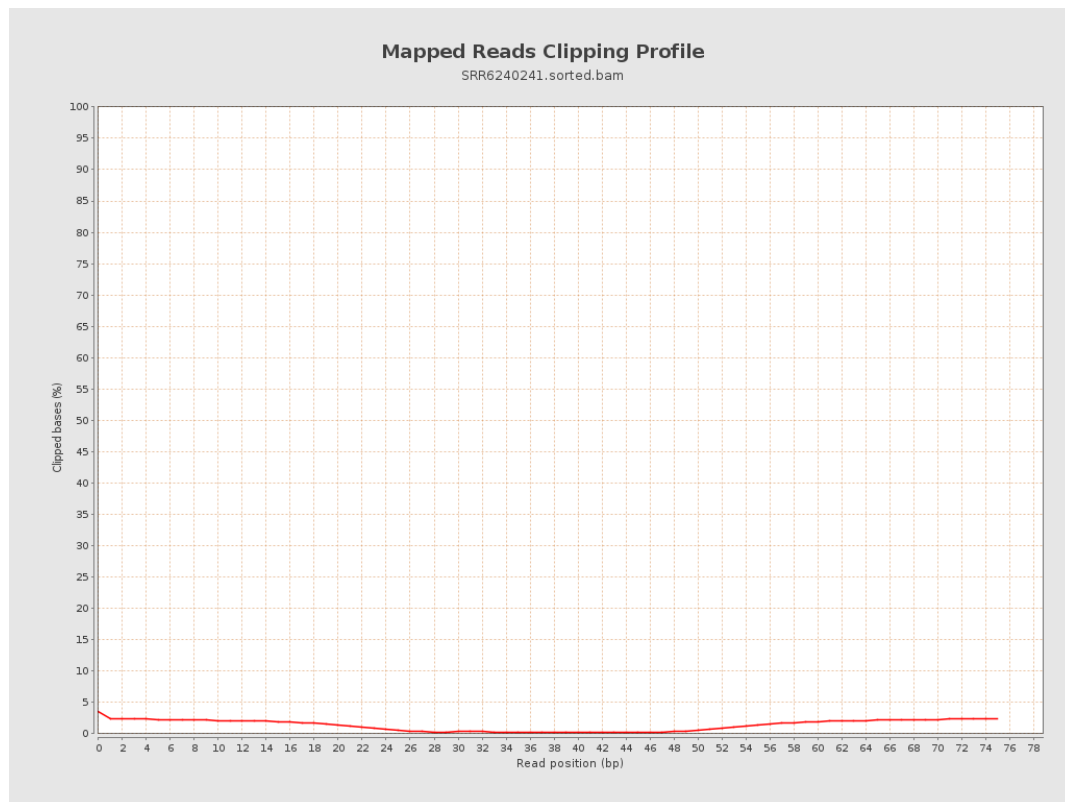
8. Results : Mapped Reads Nucleotide Content



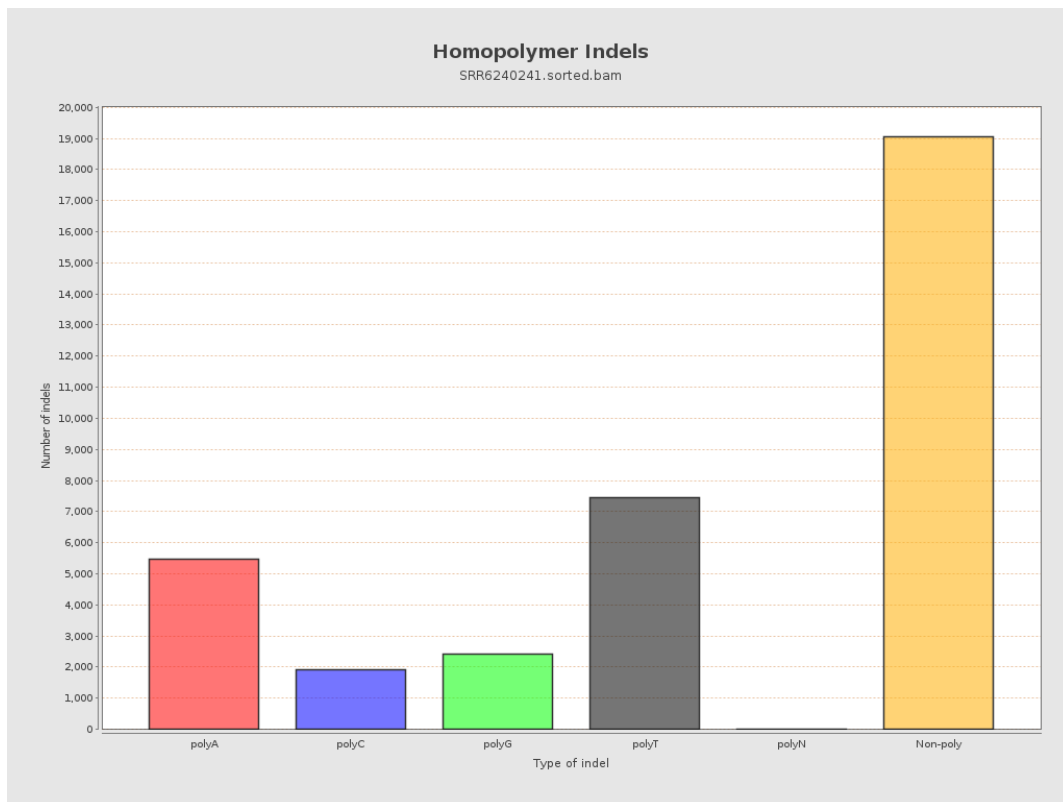
9. Results : Mapped Reads GC-content Distribution



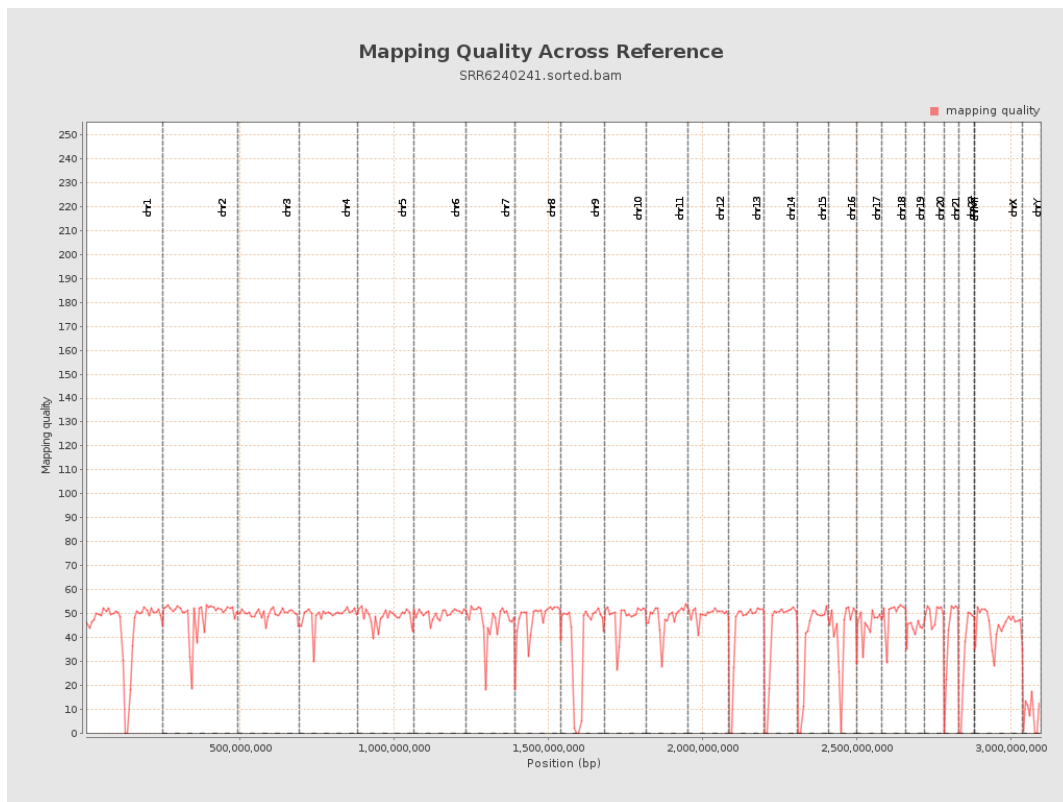
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

