

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:23:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240206.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_SRR6240206 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240206.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:23:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240206.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,654,599
Mapped reads	1,376,881 / 83.22%
Unmapped reads	277,718 / 16.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,741 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	74,850 / 4.52%
Duplication rate	4.5%
Clipped reads	861,694 / 52.08%

2.2. ACGT Content

Number/percentage of A's	23,253,224 / 27.12%
Number/percentage of C's	14,979,650 / 17.47%
Number/percentage of T's	27,761,811 / 32.38%
Number/percentage of G's	19,733,110 / 23.01%
Number/percentage of N's	20,831 / 0.02%
GC Percentage	40.48%

2.3. Coverage

Mean	0.0277

Standard Deviation	0.268
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2.4. Mapping Quality

Mean Mapping Quality	45.22
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2.5. Mismatches and indels

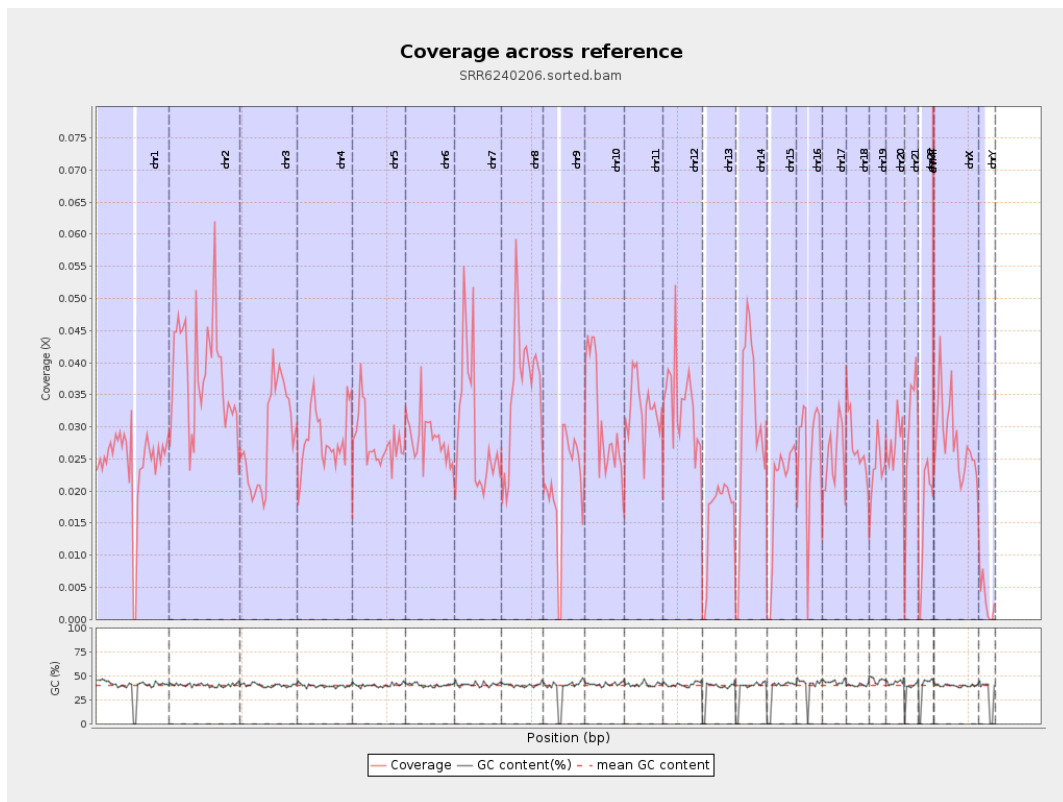
General error rate	0.91%
Mismatches	768,568
Insertions	5,912
Mapped reads with at least one insertion	0.43%
Deletions	27,608
Mapped reads with at least one deletion	1.98%
Homopolymer indels	49.35%

2.6. Chromosome stats

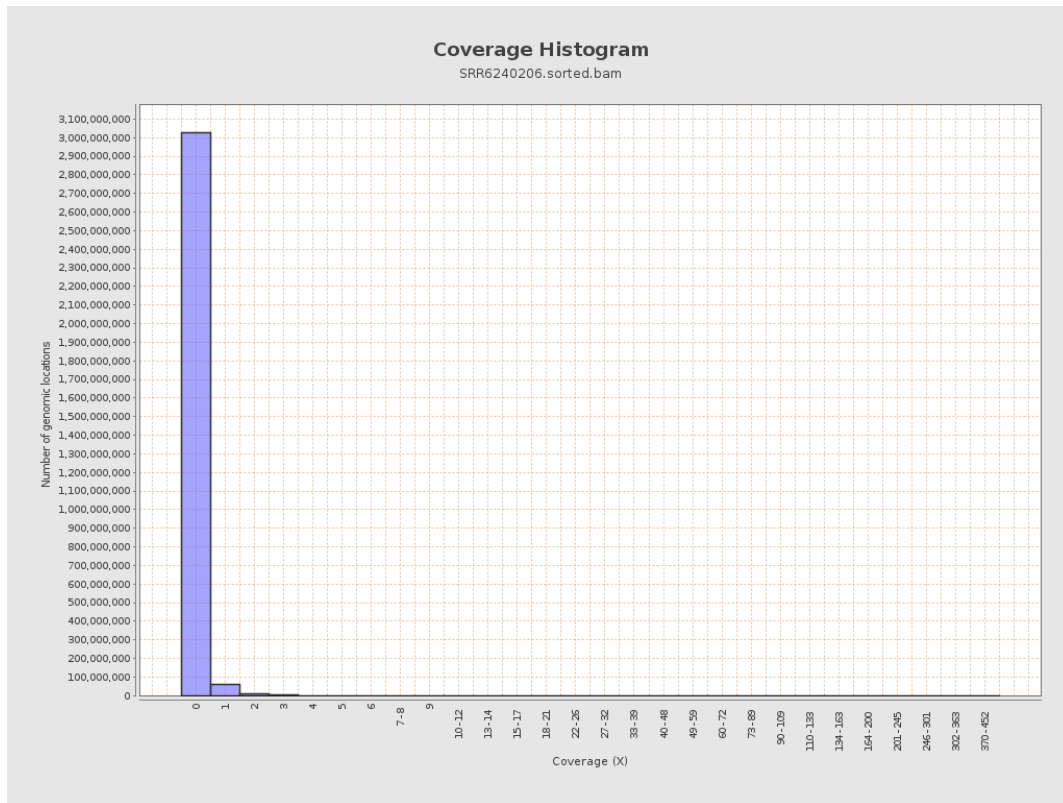
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6076930	0.0244	0.3545
chr2	243199373	9291106	0.0382	0.3335
chr3	198022430	5614668	0.0284	0.196
chr4	191154276	5386978	0.0282	0.203
chr5	180915260	5019566	0.0277	0.1959
chr6	171115067	4809780	0.0281	0.2349
chr7	159138663	4718686	0.0297	0.4601

chr8	146364022	5278839	0.0361	0.3571
chr9	141213431	2946104	0.0209	0.2364
chr10	135534747	4222294	0.0312	0.248
chr11	135006516	4409331	0.0327	0.2907
chr12	133851895	4499573	0.0336	0.2158
chr13	115169878	1838167	0.016	0.1494
chr14	107349540	3245476	0.0302	0.2122
chr15	102531392	2040137	0.0199	0.1782
chr16	90354753	2373981	0.0263	0.1936
chr17	81195210	2037186	0.0251	0.2057
chr18	78077248	2111804	0.027	0.376
chr19	59128983	1413727	0.0239	0.2693
chr20	63025520	1719647	0.0273	0.1953
chr21	48129895	1433377	0.0298	0.2069
chr22	51304566	805500	0.0157	0.1432
chrMT	16571	22413	1.3525	1.6487
chrX	155270560	4300882	0.0277	0.2134
chrY	59373566	180347	0.003	0.0714

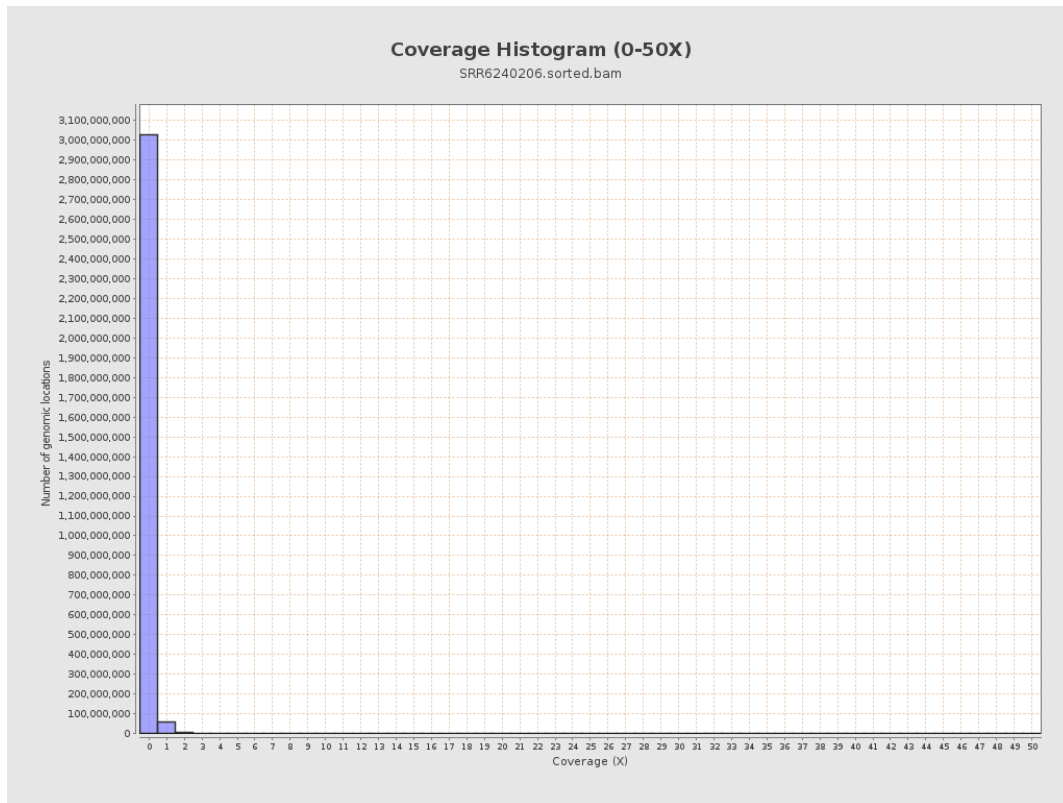
3. Results : Coverage across reference



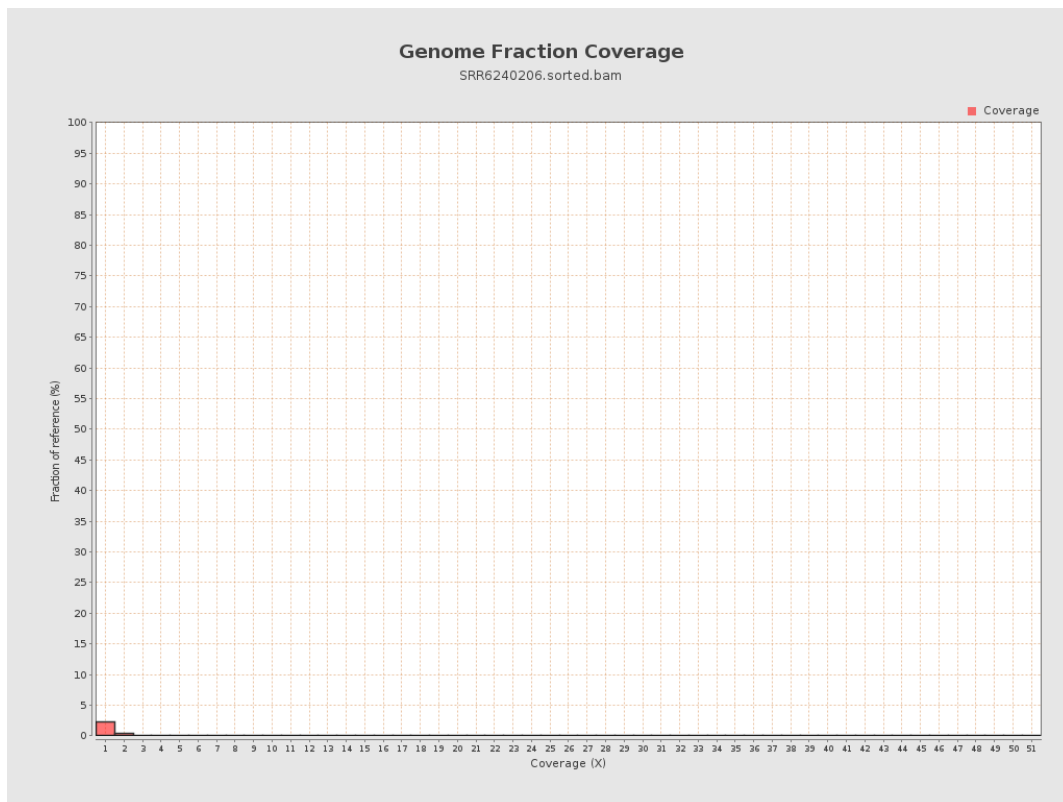
4. Results : Coverage Histogram



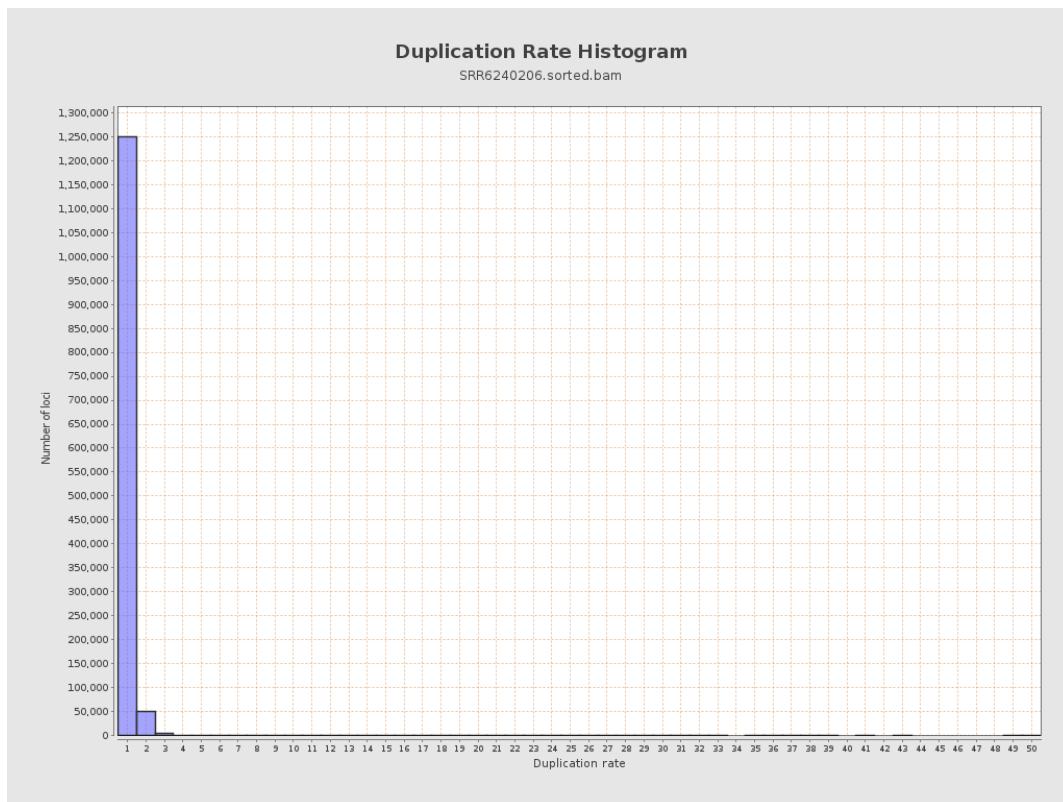
5. Results : Coverage Histogram (0-50X)



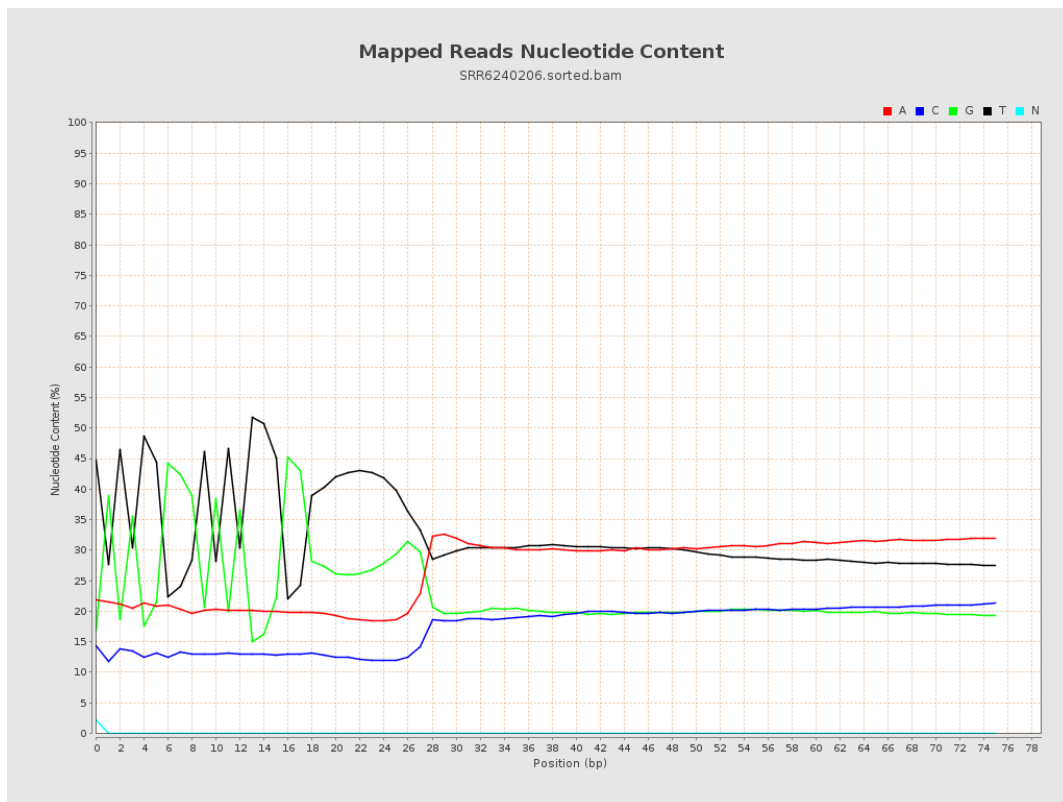
6. Results : Genome Fraction Coverage



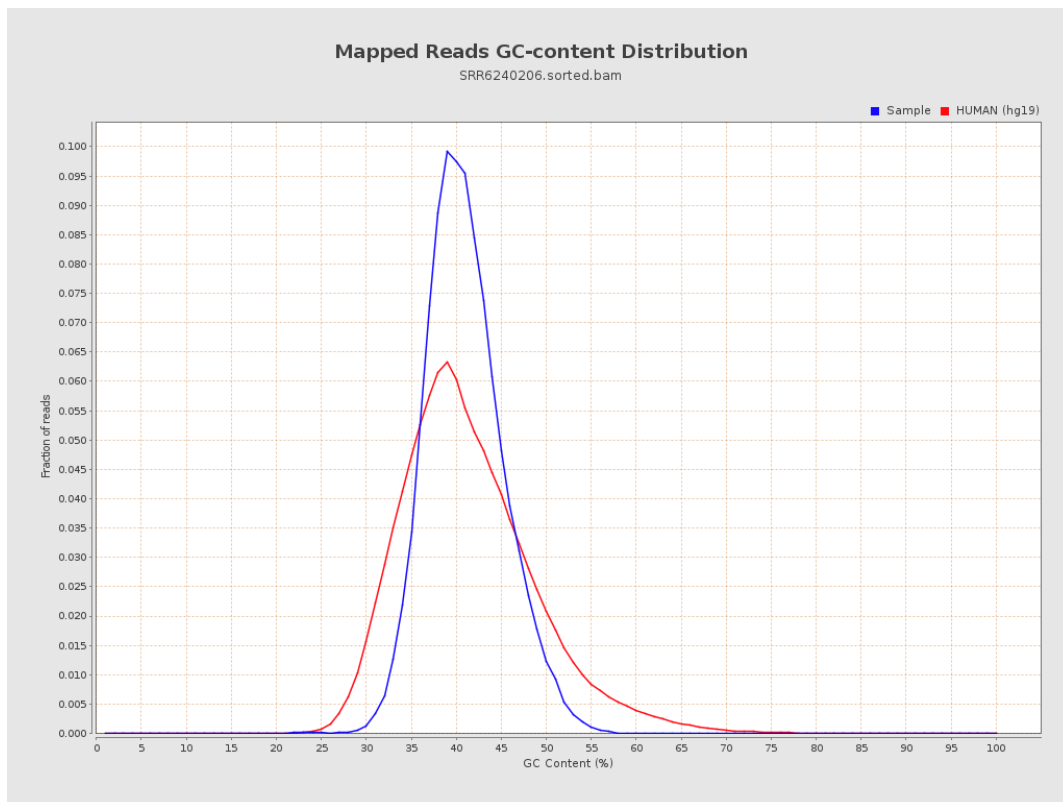
7. Results : Duplication Rate Histogram



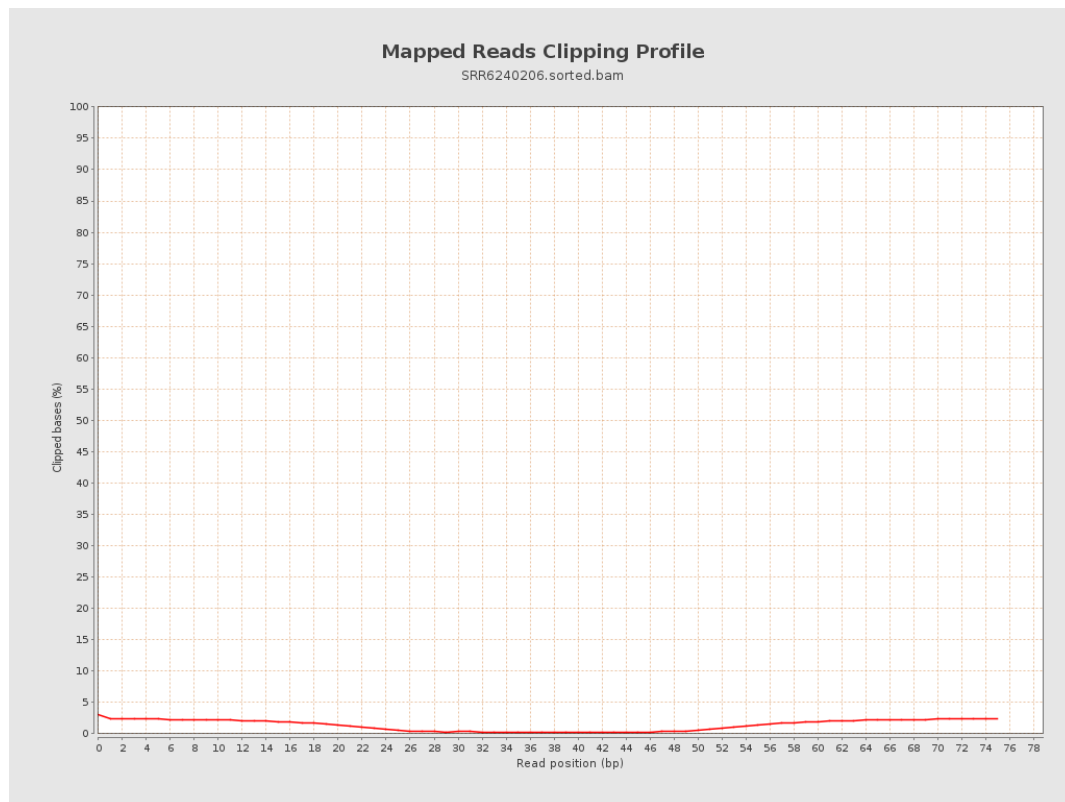
8. Results : Mapped Reads Nucleotide Content



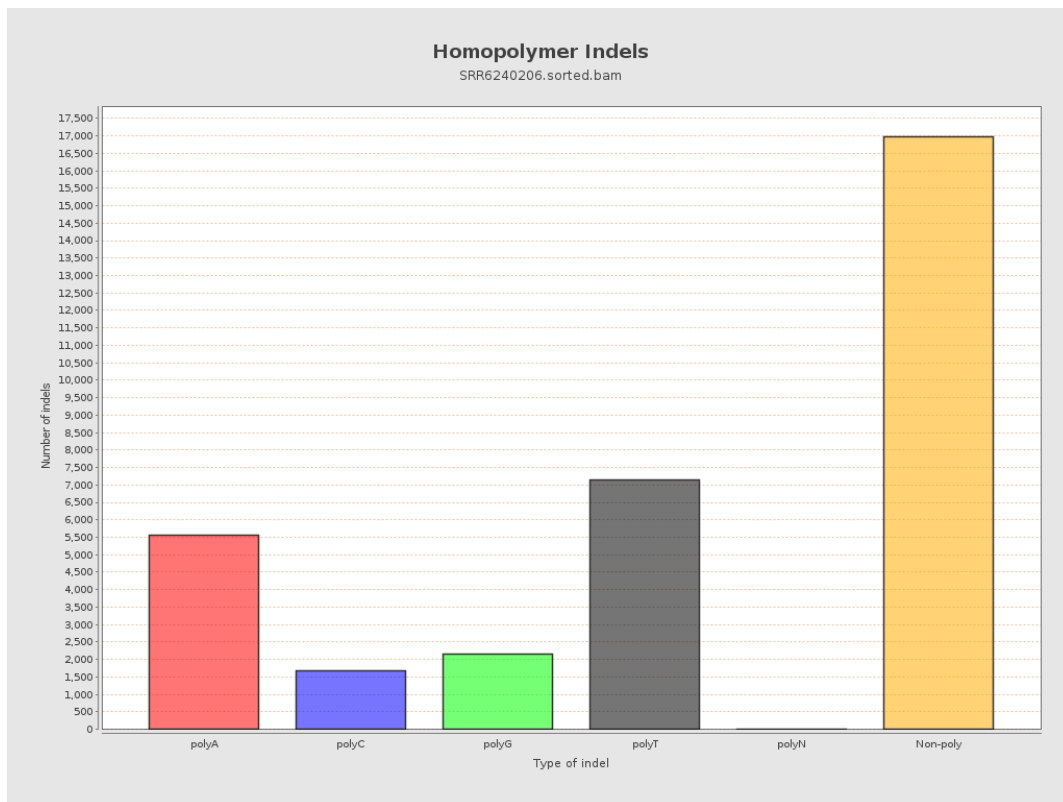
9. Results : Mapped Reads GC-content Distribution



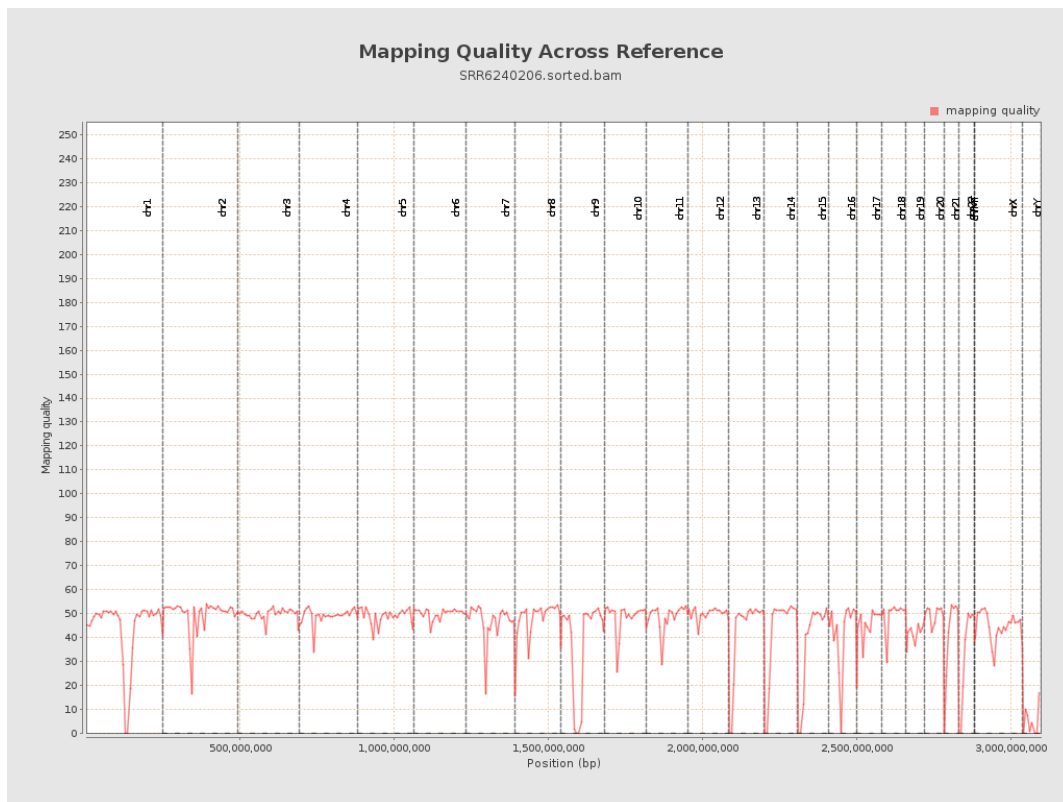
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

