

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 09:32:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240273.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_SRR6240273 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240273.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 09:32:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240273.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,062,042
Mapped reads	1,613,203 / 78.23%
Unmapped reads	448,839 / 21.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,791 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	231,379 / 11.22%
Duplication rate	10.74%
Clipped reads	889,936 / 43.16%

2.2. ACGT Content

Number/percentage of A's	28,901,460 / 27.99%
Number/percentage of C's	18,699,168 / 18.11%
Number/percentage of T's	32,920,431 / 31.88%
Number/percentage of G's	22,717,134 / 22%
Number/percentage of N's	26,822 / 0.03%
GC Percentage	40.11%

2.3. Coverage

Mean	0.0334

Standard Deviation	0.3918
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2.4. Mapping Quality

Mean Mapping Quality	46.03
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2.5. Mismatches and indels

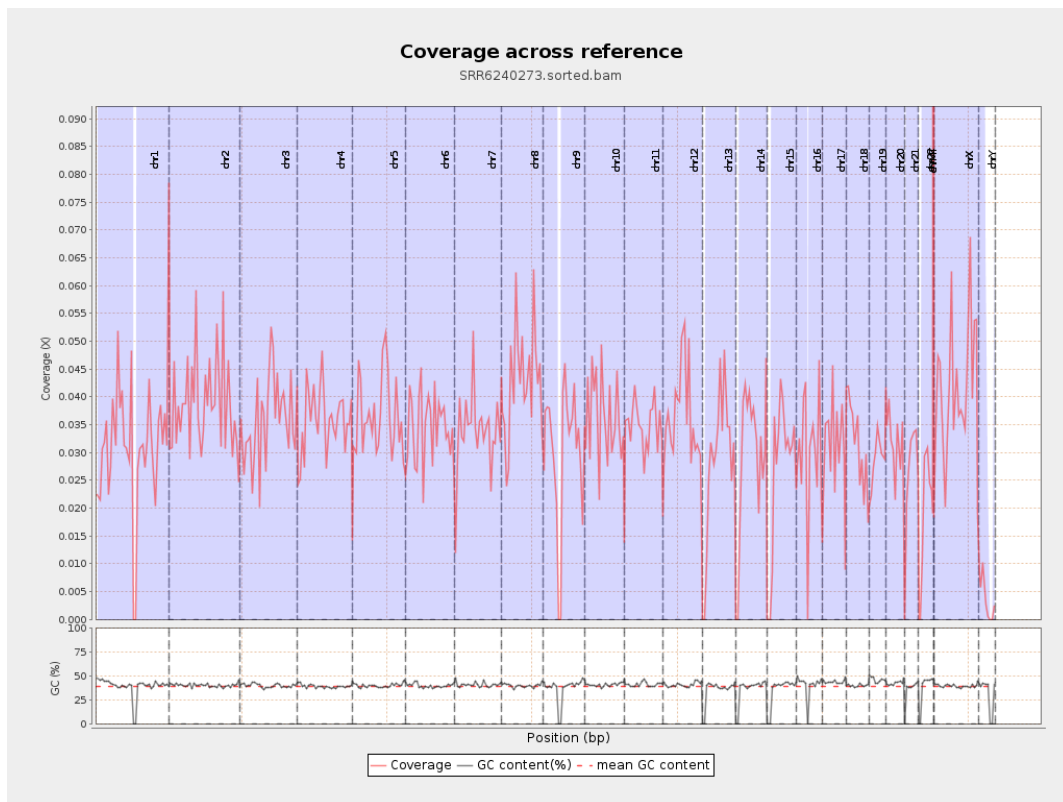
General error rate	0.79%
Mismatches	803,018
Insertions	7,364
Mapped reads with at least one insertion	0.45%
Deletions	22,898
Mapped reads with at least one deletion	1.4%
Homopolymer indels	48.17%

2.6. Chromosome stats

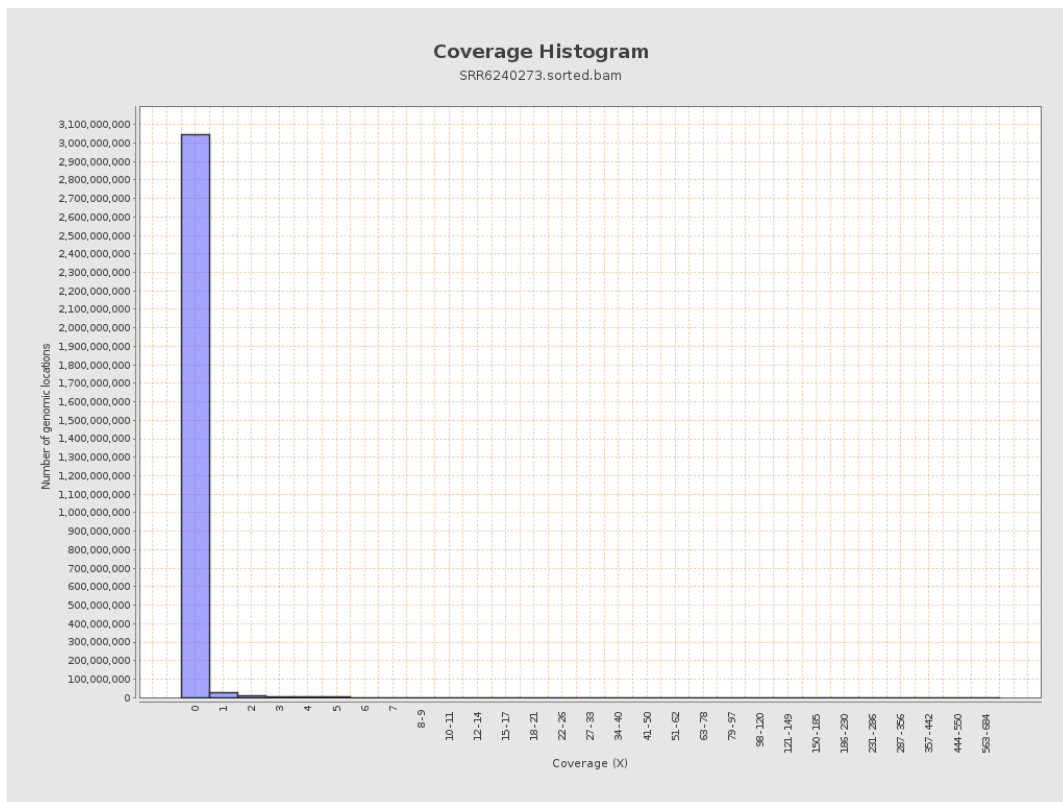
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7705734	0.0309	0.5314
chr2	243199373	9456414	0.0389	0.4634
chr3	198022430	7053807	0.0356	0.3321
chr4	191154276	6871763	0.0359	0.3386
chr5	180915260	6584895	0.0364	0.3335
chr6	171115067	5859133	0.0342	0.3662
chr7	159138663	5412555	0.034	0.445

chr8	146364022	6265445	0.0428	0.5493
chr9	141213431	4270456	0.0302	0.3645
chr10	135534747	4955973	0.0366	0.393
chr11	135006516	4671977	0.0346	0.3793
chr12	133851895	4873981	0.0364	0.3352
chr13	115169878	3267248	0.0284	0.2999
chr14	107349540	3081941	0.0287	0.3208
chr15	102531392	2767362	0.027	0.3275
chr16	90354753	2683053	0.0297	0.3
chr17	81195210	2517618	0.031	0.3118
chr18	78077248	2466558	0.0316	0.5449
chr19	59128983	1734617	0.0293	0.4161
chr20	63025520	1977747	0.0314	0.3111
chr21	48129895	1275048	0.0265	0.281
chr22	51304566	961133	0.0187	0.2273
chrMT	16571	12708	0.7669	1.4253
chrX	155270560	6367924	0.041	0.3665
chrY	59373566	207825	0.0035	0.0915

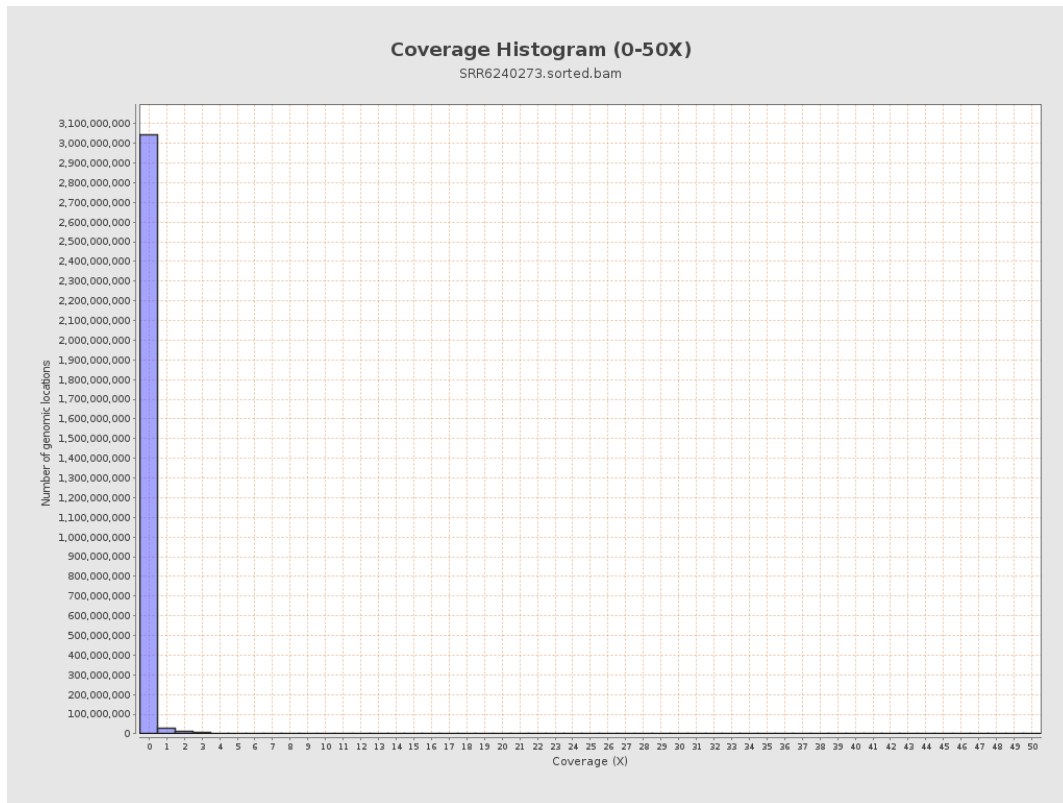
3. Results : Coverage across reference



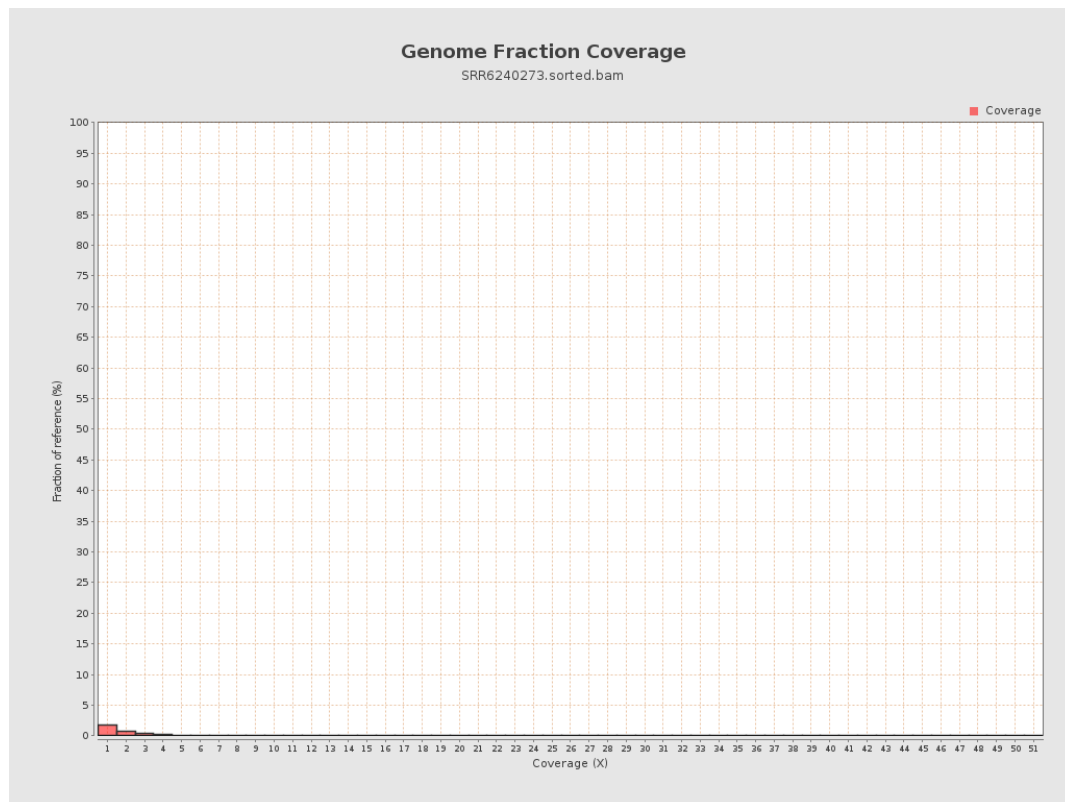
4. Results : Coverage Histogram



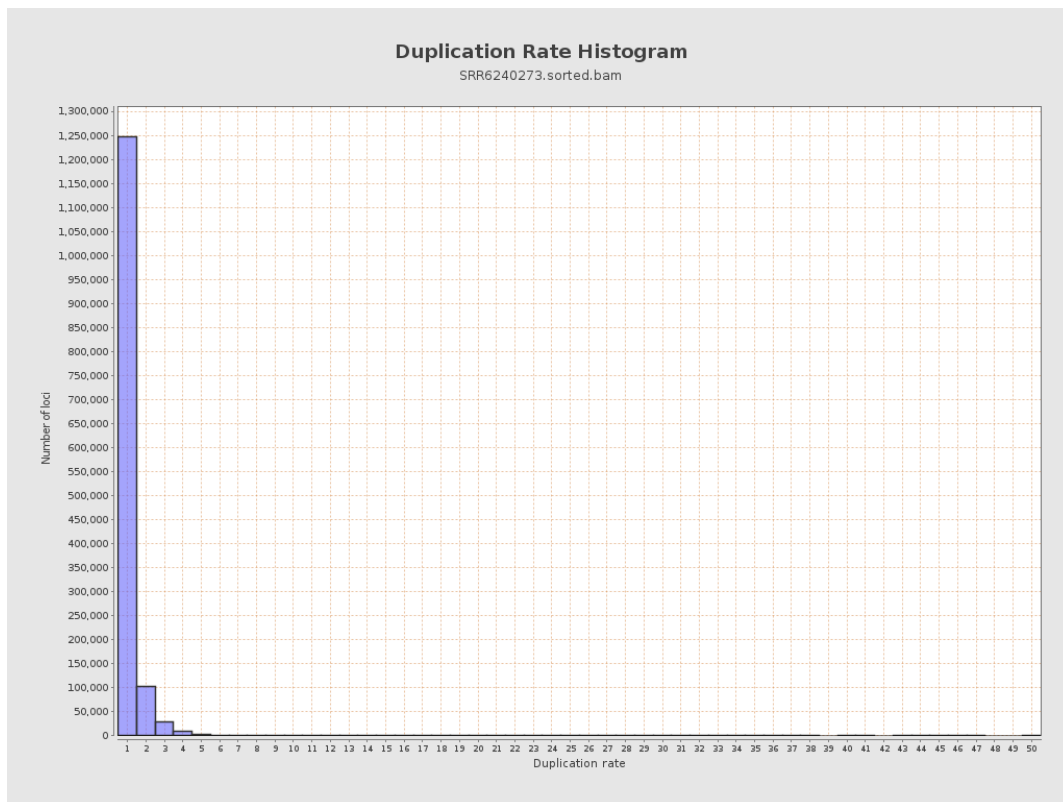
5. Results : Coverage Histogram (0-50X)



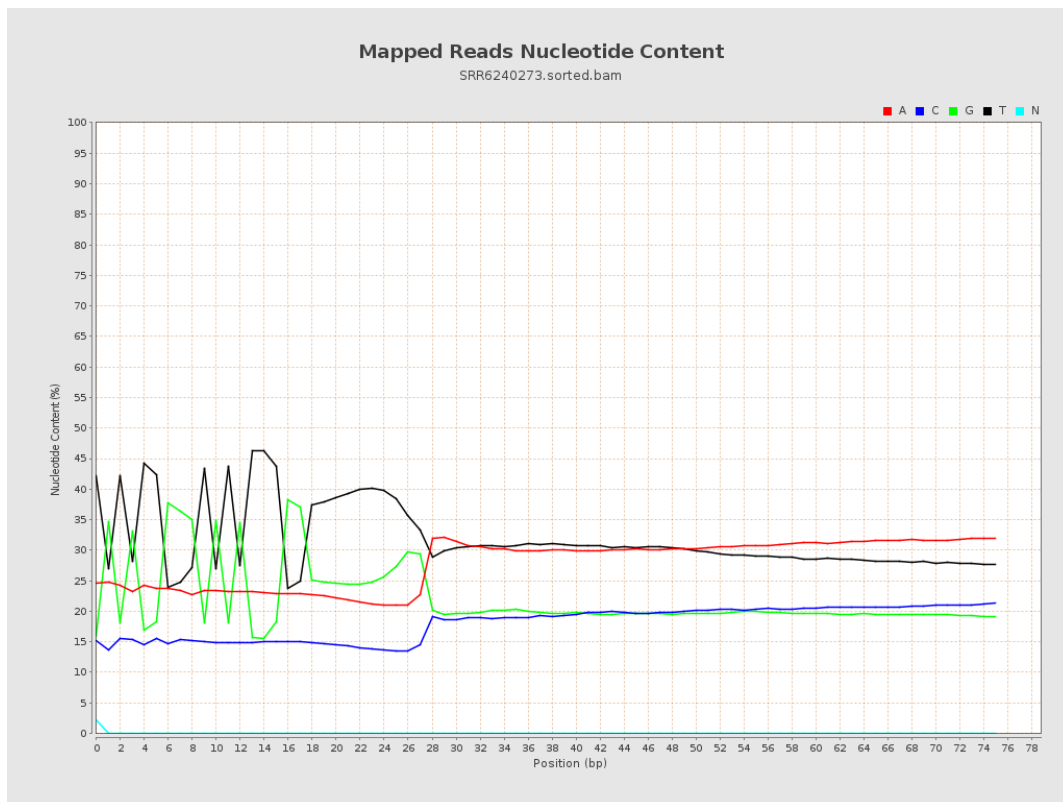
6. Results : Genome Fraction Coverage



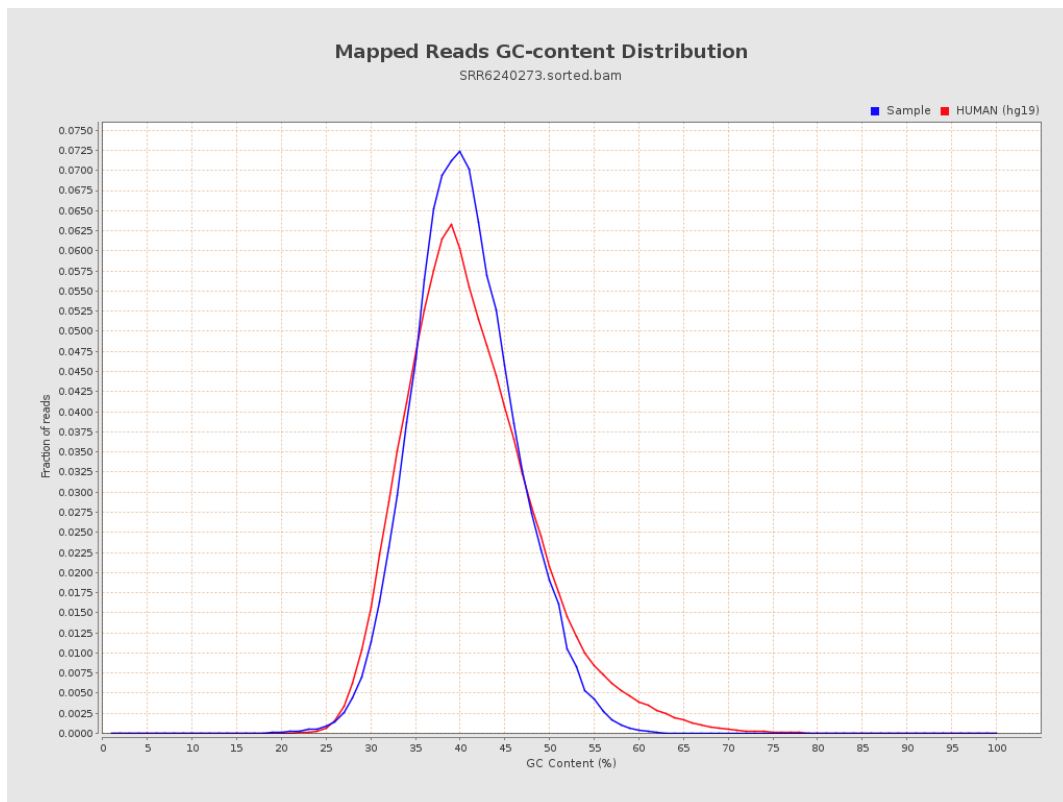
7. Results : Duplication Rate Histogram



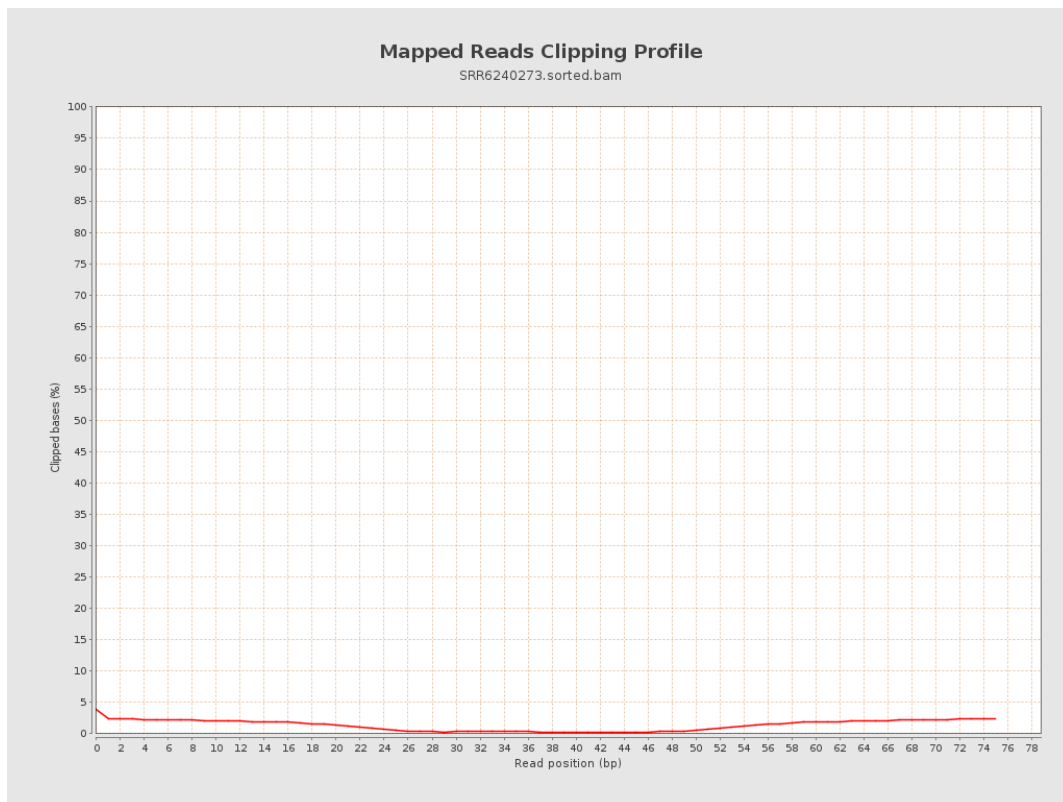
8. Results : Mapped Reads Nucleotide Content



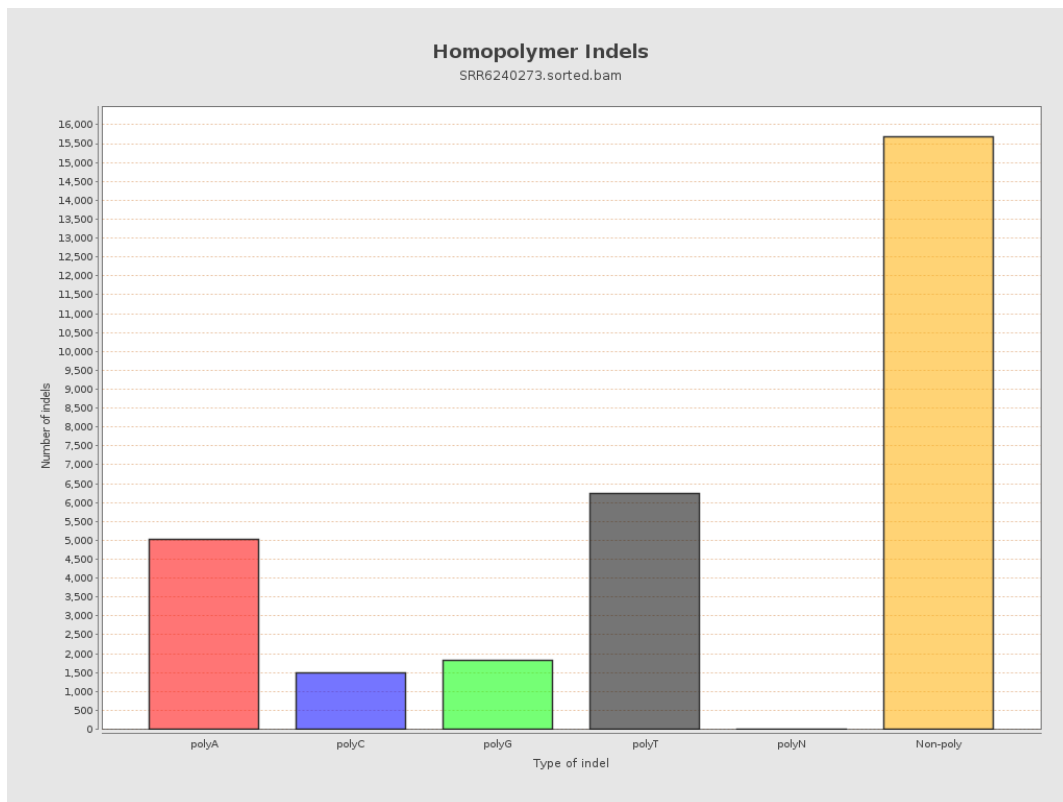
9. Results : Mapped Reads GC-content Distribution



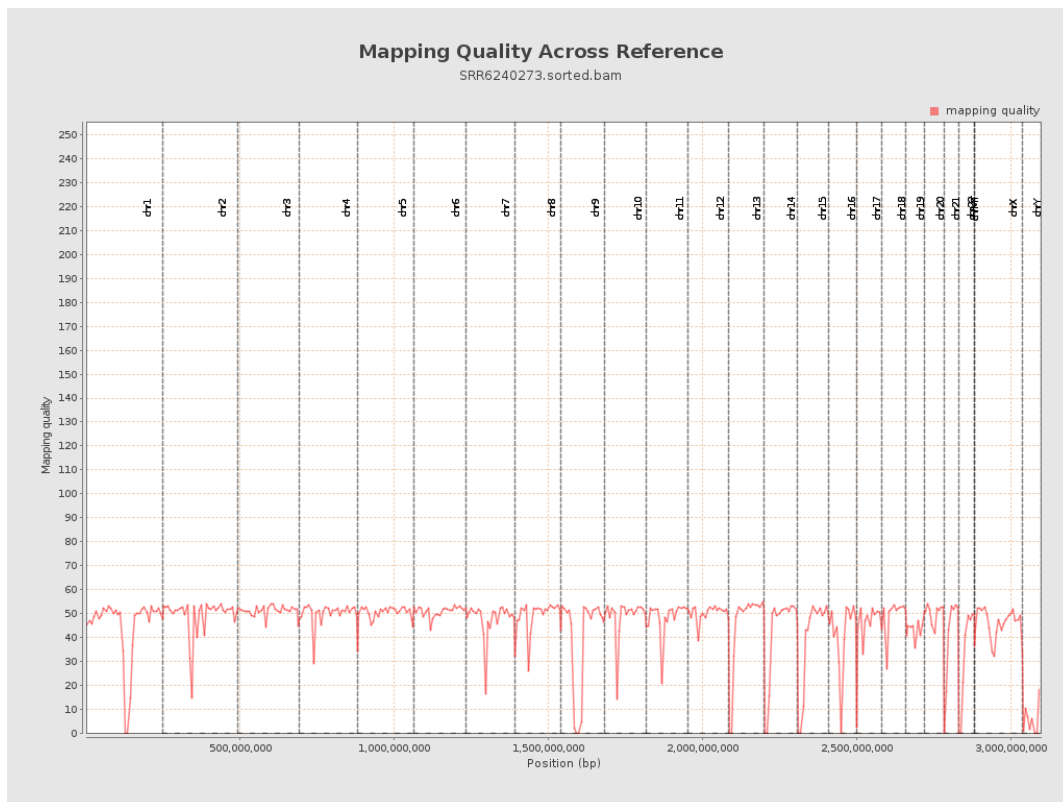
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

