

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:32:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237290.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_SRR6237290 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237290.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:32:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237290.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,074,468
Mapped reads	2,665,274 / 86.69%
Unmapped reads	409,194 / 13.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,534 / 0.7%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	243,416 / 7.92%
Duplication rate	6.71%
Clipped reads	1,103,903 / 35.91%

2.2. ACGT Content

Number/percentage of A's	50,602,145 / 28.09%
Number/percentage of C's	33,465,833 / 18.58%
Number/percentage of T's	56,707,199 / 31.48%
Number/percentage of G's	39,333,289 / 21.84%
Number/percentage of N's	2,939 / 0%
GC Percentage	40.42%

2.3. Coverage

Mean	0.0582

Standard Deviation	0.723
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2.4. Mapping Quality

Mean Mapping Quality	45.14
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2.5. Mismatches and indels

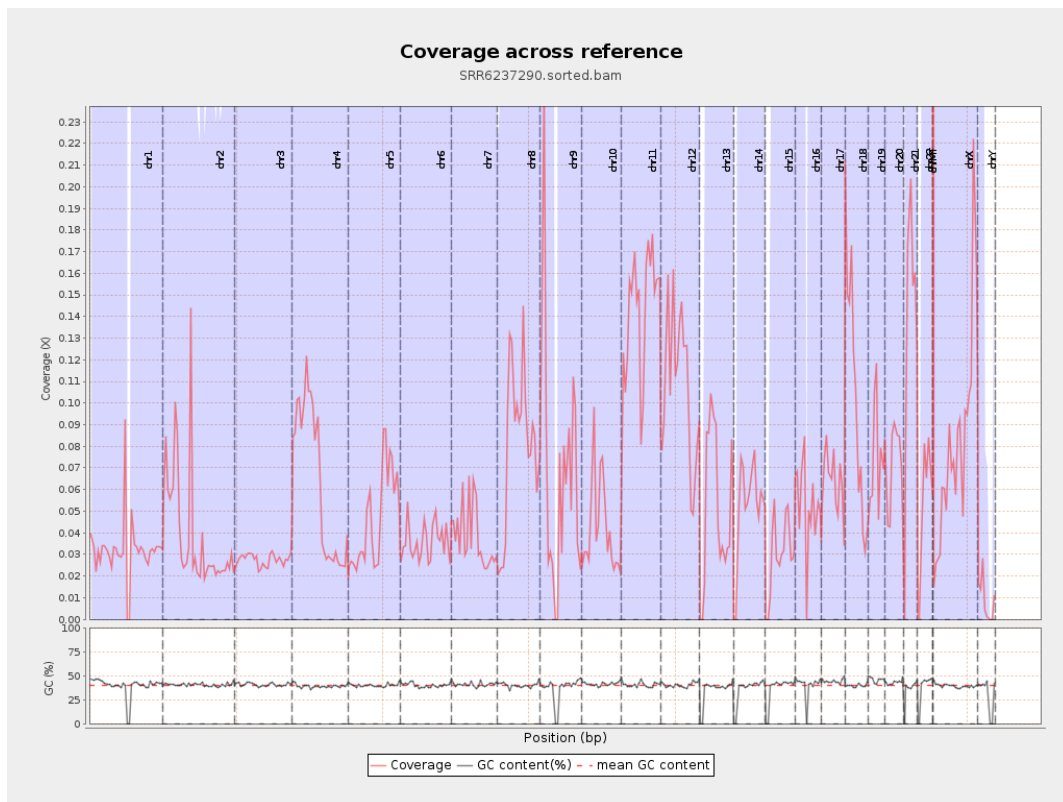
General error rate	0.82%
Mismatches	1,453,009
Insertions	14,503
Mapped reads with at least one insertion	0.54%
Deletions	44,059
Mapped reads with at least one deletion	1.63%
Homopolymer indels	47.59%

2.6. Chromosome stats

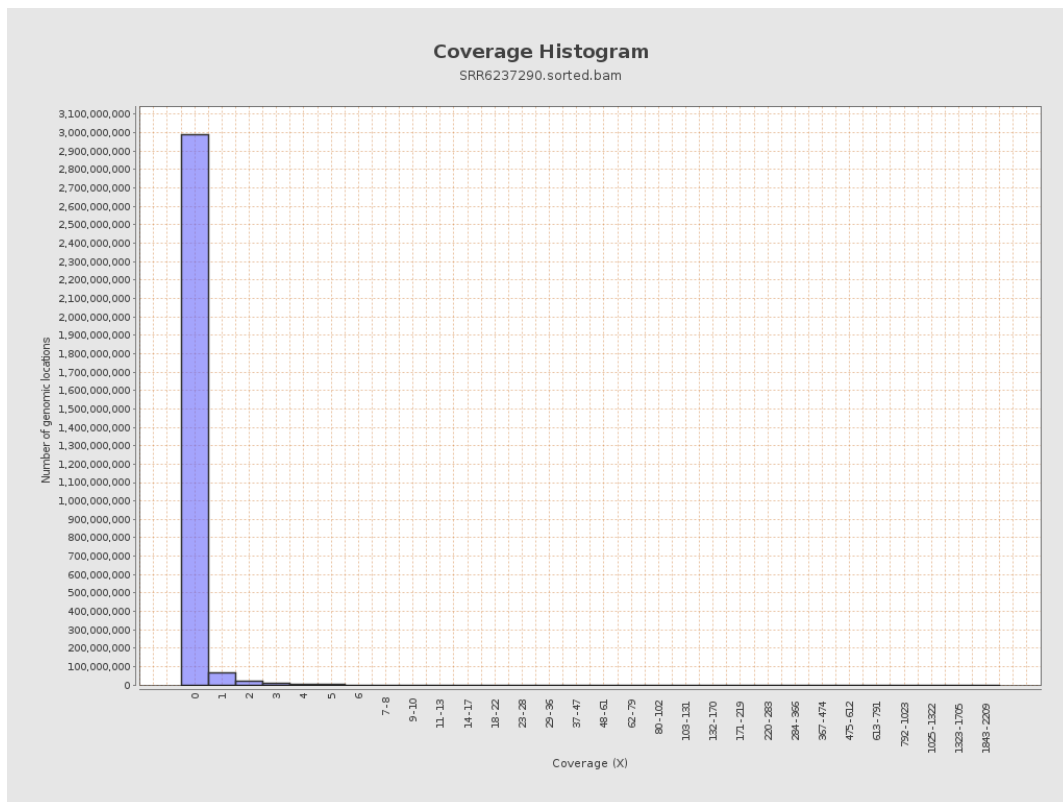
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7934463	0.0318	1.2333
chr2	243199373	9652535	0.0397	0.9269
chr3	198022430	5470172	0.0276	0.2479
chr4	191154276	12138422	0.0635	0.4211
chr5	180915260	8256799	0.0456	0.3307
chr6	171115067	6102047	0.0357	0.311
chr7	159138663	6025680	0.0379	0.504

chr8	146364022	11866048	0.0811	1.5346
chr9	141213431	9589859	0.0679	0.7321
chr10	135534747	5712557	0.0421	0.5662
chr11	135006516	19172394	0.142	0.9422
chr12	133851895	14364575	0.1073	0.5169
chr13	115169878	6010131	0.0522	0.3519
chr14	107349540	5681185	0.0529	0.3748
chr15	102531392	3038336	0.0296	0.2712
chr16	90354753	4692752	0.0519	0.3929
chr17	81195210	5235764	0.0645	0.5161
chr18	78077248	7920029	0.1014	1.107
chr19	59128983	4415721	0.0747	0.7773
chr20	63025520	4451913	0.0706	0.4363
chr21	48129895	6575277	0.1366	0.6094
chr22	51304566	2708097	0.0528	0.3435
chrMT	16571	153012	9.2337	6.4061
chrX	155270560	12481835	0.0804	0.5096
chrY	59373566	538916	0.0091	0.2179

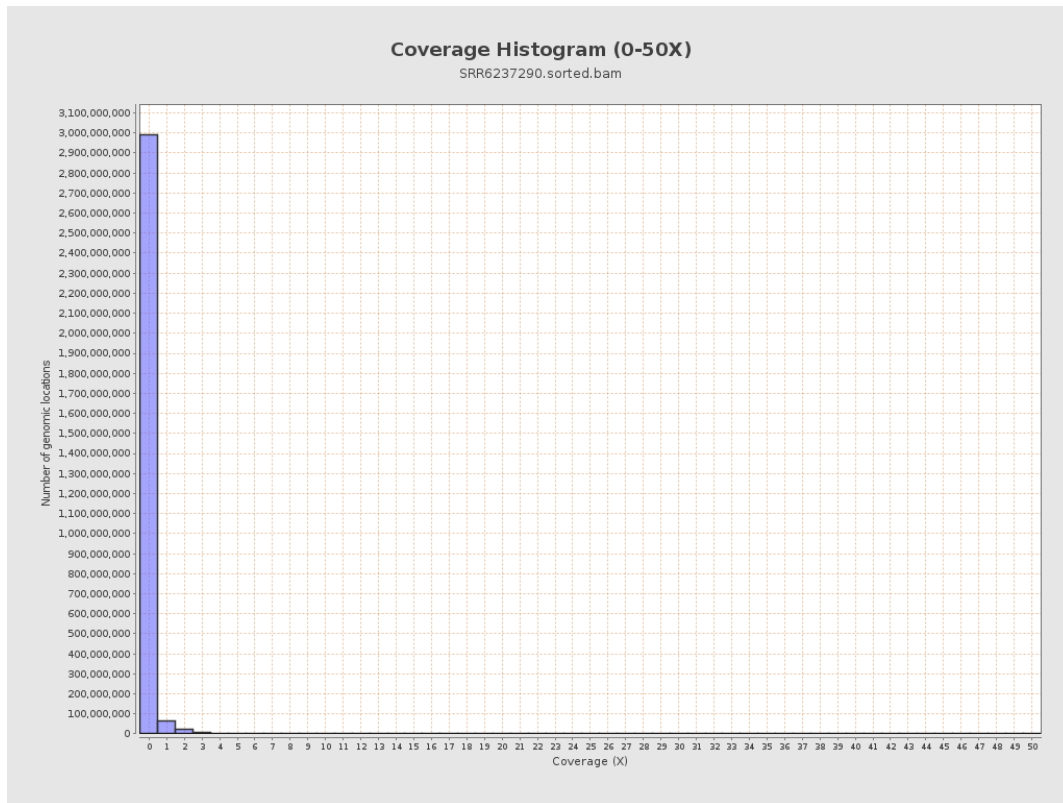
3. Results : Coverage across reference



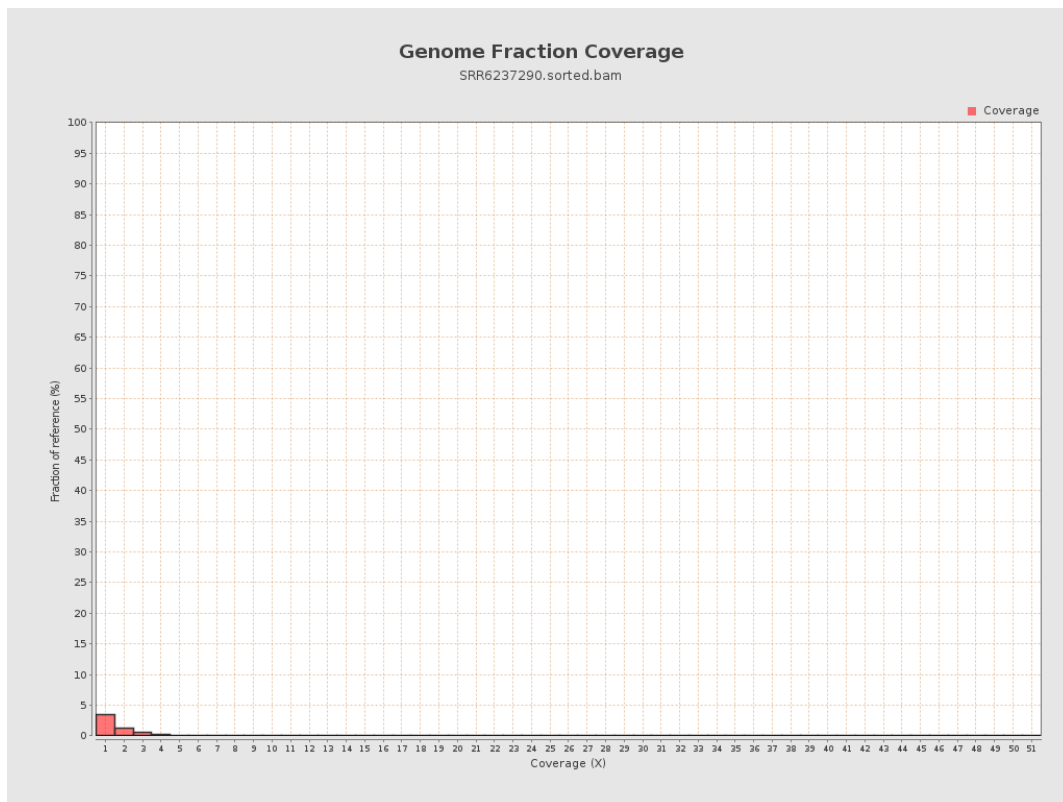
4. Results : Coverage Histogram



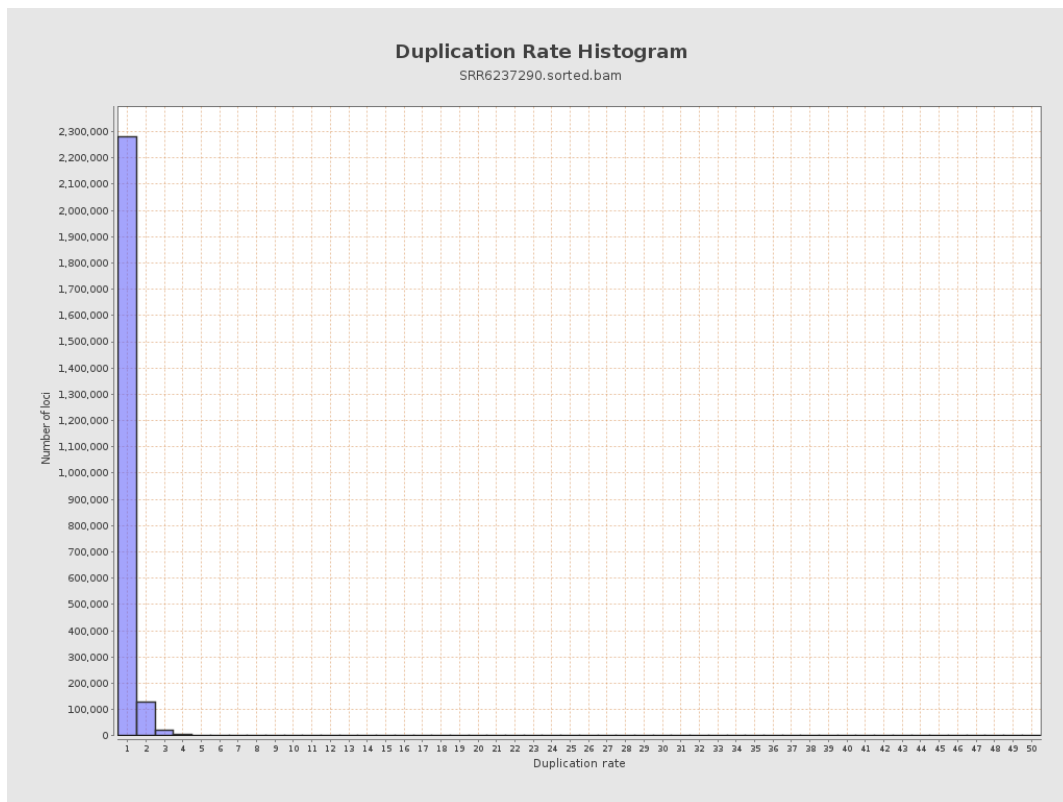
5. Results : Coverage Histogram (0-50X)



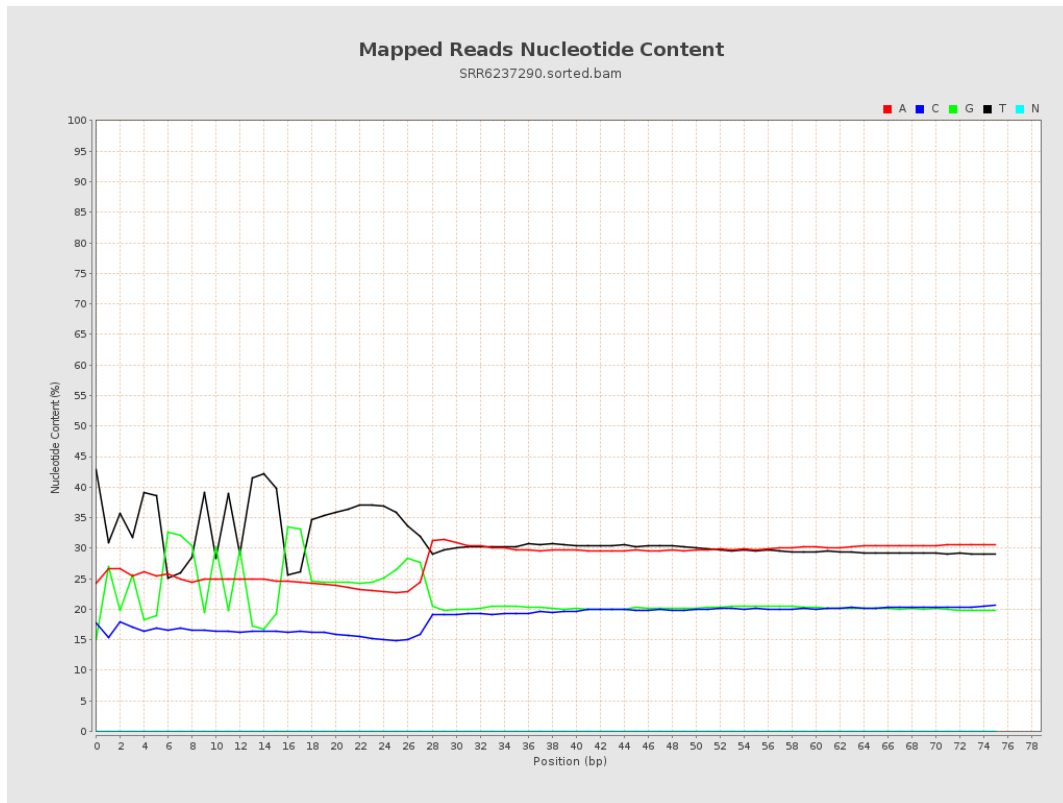
6. Results : Genome Fraction Coverage



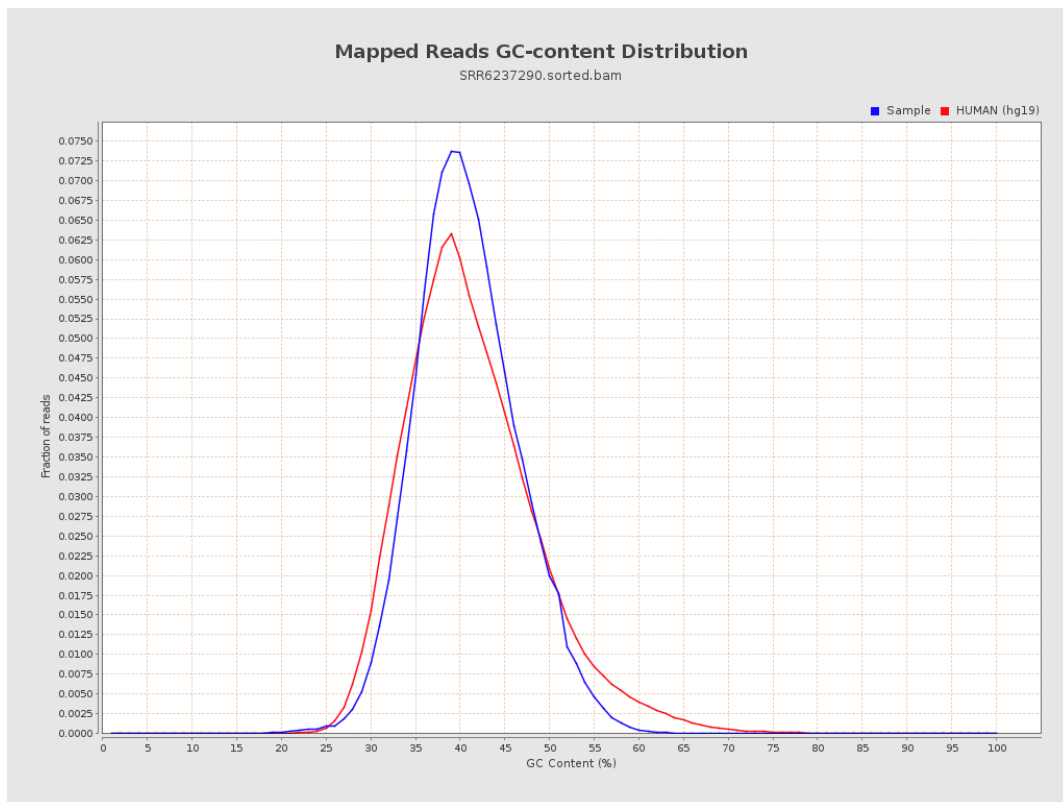
7. Results : Duplication Rate Histogram



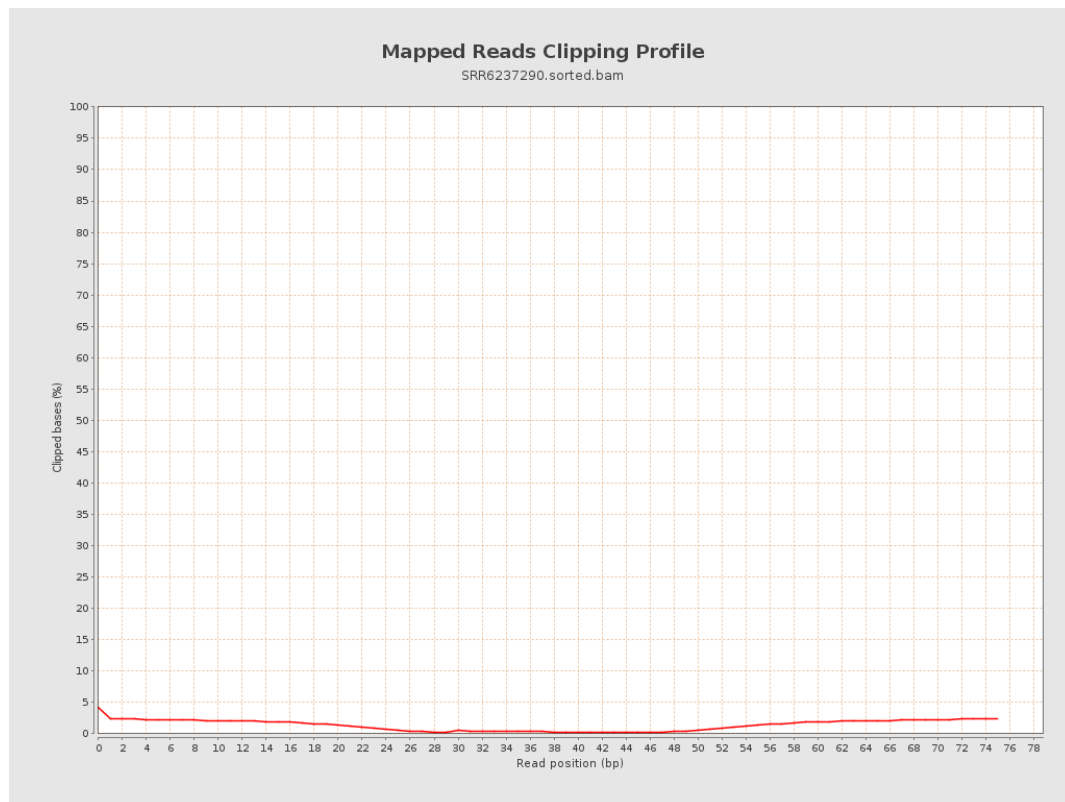
8. Results : Mapped Reads Nucleotide Content



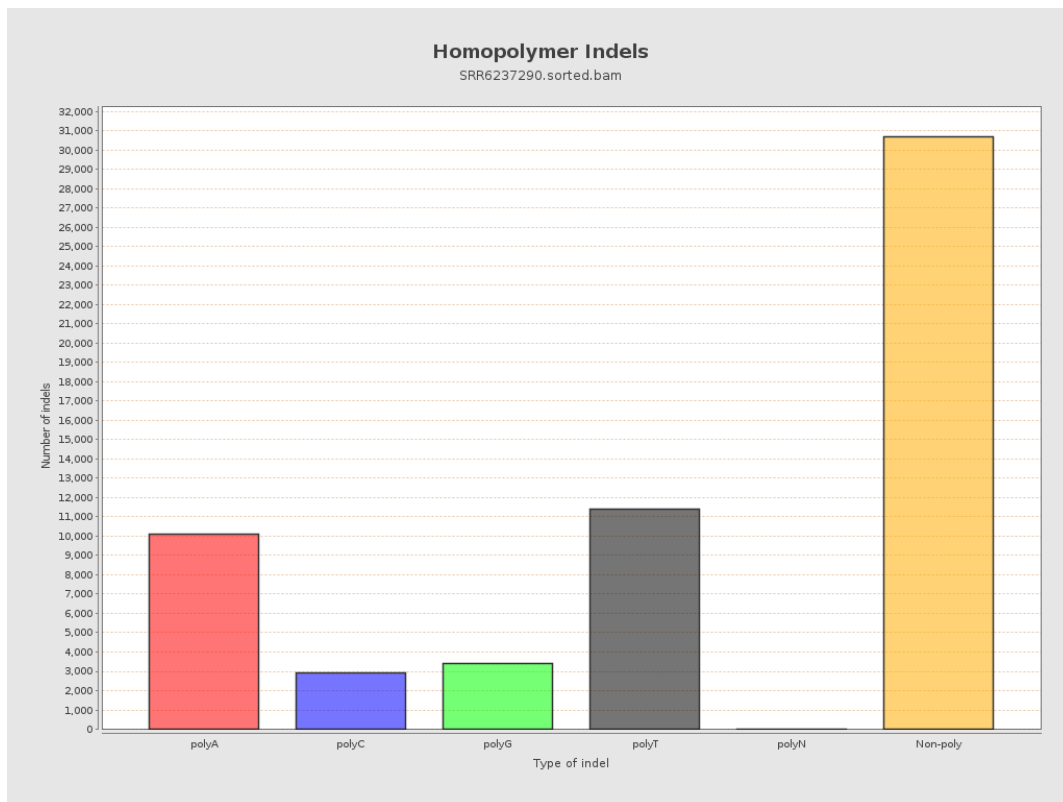
9. Results : Mapped Reads GC-content Distribution



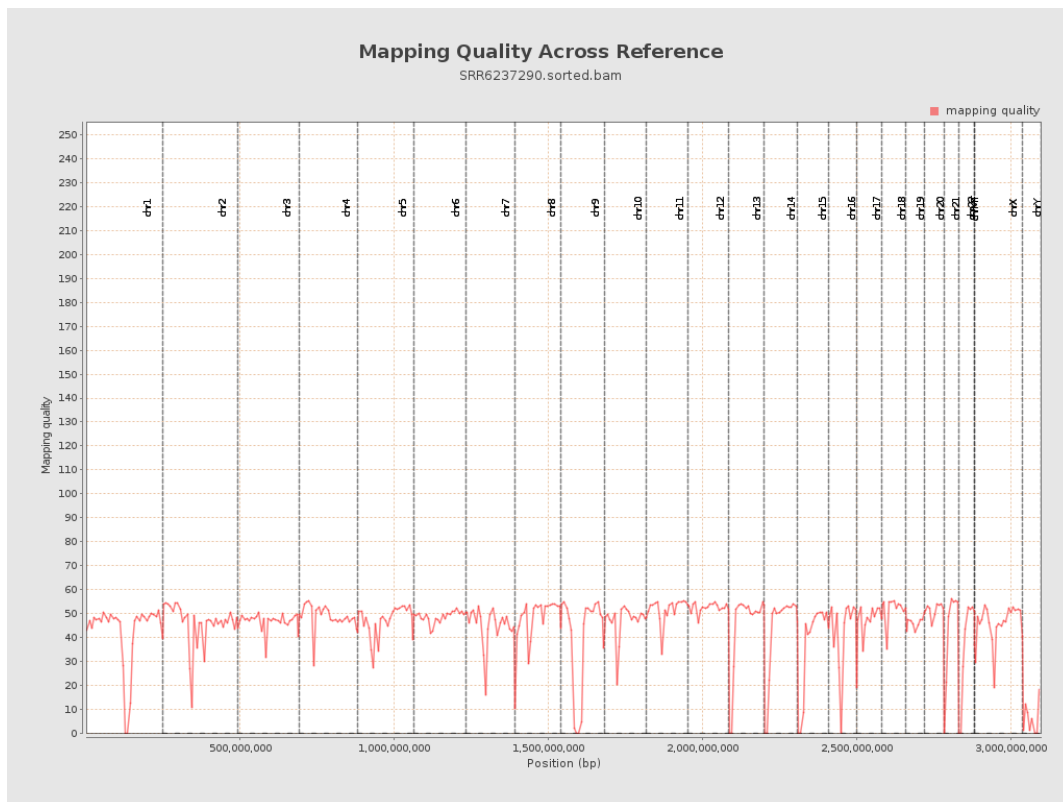
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

