

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:49:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238249.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_SRR6238249 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238249.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:49:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238249.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,902,818
Mapped reads	2,591,942 / 89.29%
Unmapped reads	310,876 / 10.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,924 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	101,194 / 3.49%
Duplication rate	2.94%
Clipped reads	1,398,027 / 48.16%

2.2. ACGT Content

Number/percentage of A's	46,620,252 / 27.74%
Number/percentage of C's	32,714,424 / 19.47%
Number/percentage of T's	50,939,205 / 30.31%
Number/percentage of G's	37,741,531 / 22.46%
Number/percentage of N's	39,630 / 0.02%
GC Percentage	41.92%

2.3. Coverage

Mean	0.0543

Standard Deviation	0.4288
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2.4. Mapping Quality

Mean Mapping Quality	43.69
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2.5. Mismatches and indels

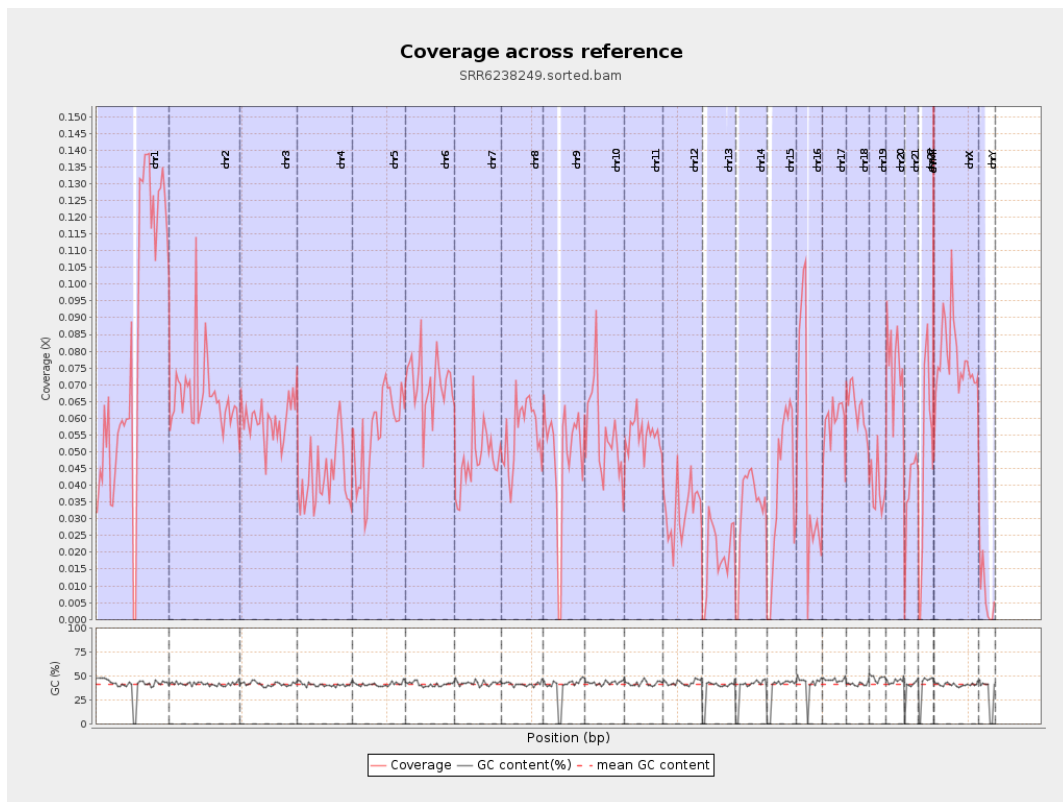
General error rate	0.9%
Mismatches	1,494,315
Insertions	13,086
Mapped reads with at least one insertion	0.5%
Deletions	52,003
Mapped reads with at least one deletion	1.98%
Homopolymer indels	44.68%

2.6. Chromosome stats

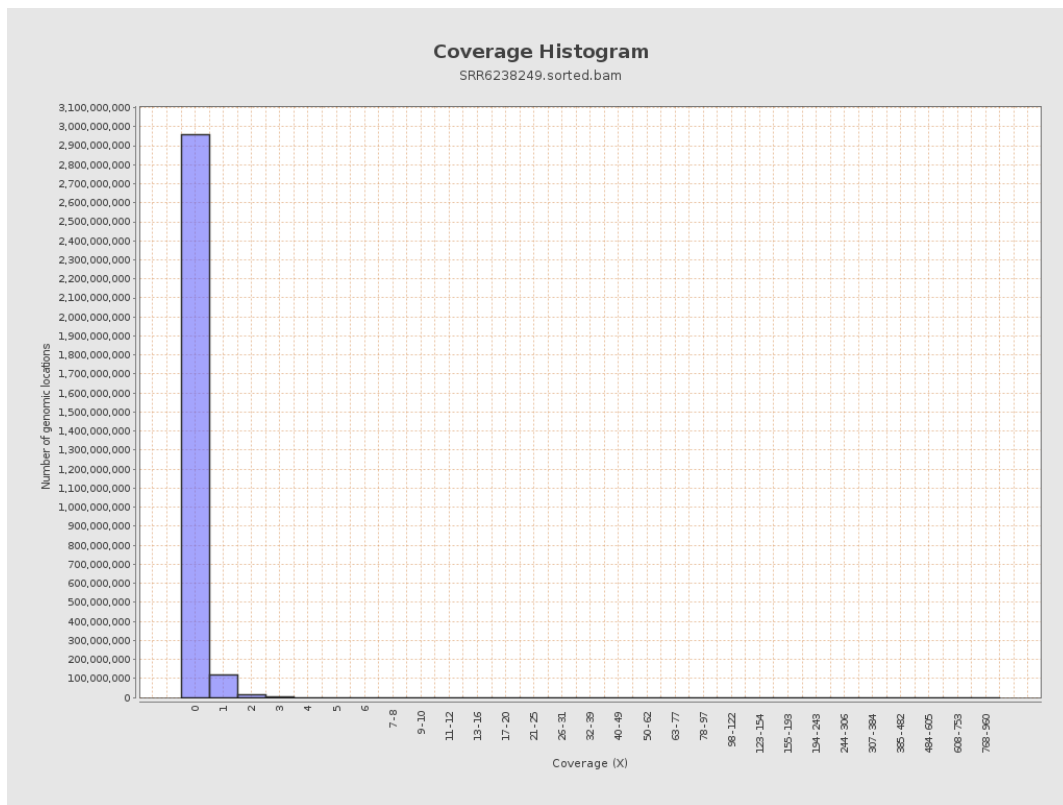
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20231740	0.0812	0.712
chr2	243199373	16235059	0.0668	0.6338
chr3	198022430	11733412	0.0593	0.2837
chr4	191154276	8050214	0.0421	0.2515
chr5	180915260	10134829	0.056	0.2739
chr6	171115067	12080527	0.0706	0.4378
chr7	159138663	7603876	0.0478	0.5036

chr8	146364022	8159176	0.0557	0.5467
chr9	141213431	6823758	0.0483	0.3765
chr10	135534747	7512644	0.0554	0.4268
chr11	135006516	7404327	0.0548	0.3917
chr12	133851895	4381046	0.0327	0.2141
chr13	115169878	2215924	0.0192	0.1631
chr14	107349540	3568901	0.0332	0.23
chr15	102531392	3957900	0.0386	0.2393
chr16	90354753	4506860	0.0499	0.2929
chr17	81195210	4755607	0.0586	0.3172
chr18	78077248	4941265	0.0633	0.5978
chr19	59128983	2333465	0.0395	0.5851
chr20	63025520	4793701	0.0761	0.3221
chr21	48129895	1863564	0.0387	0.2428
chr22	51304566	2448225	0.0477	0.2553
chrMT	16571	3725	0.2248	0.5003
chrX	155270560	11963137	0.077	0.3722
chrY	59373566	437821	0.0074	0.1503

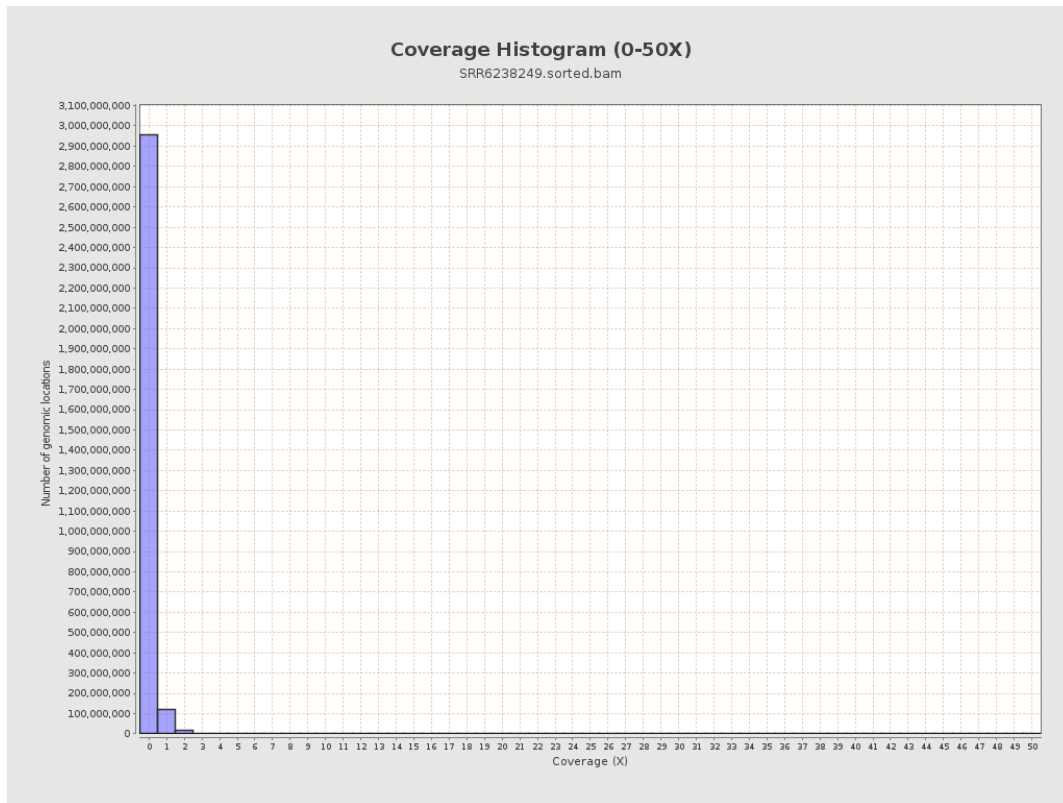
3. Results : Coverage across reference



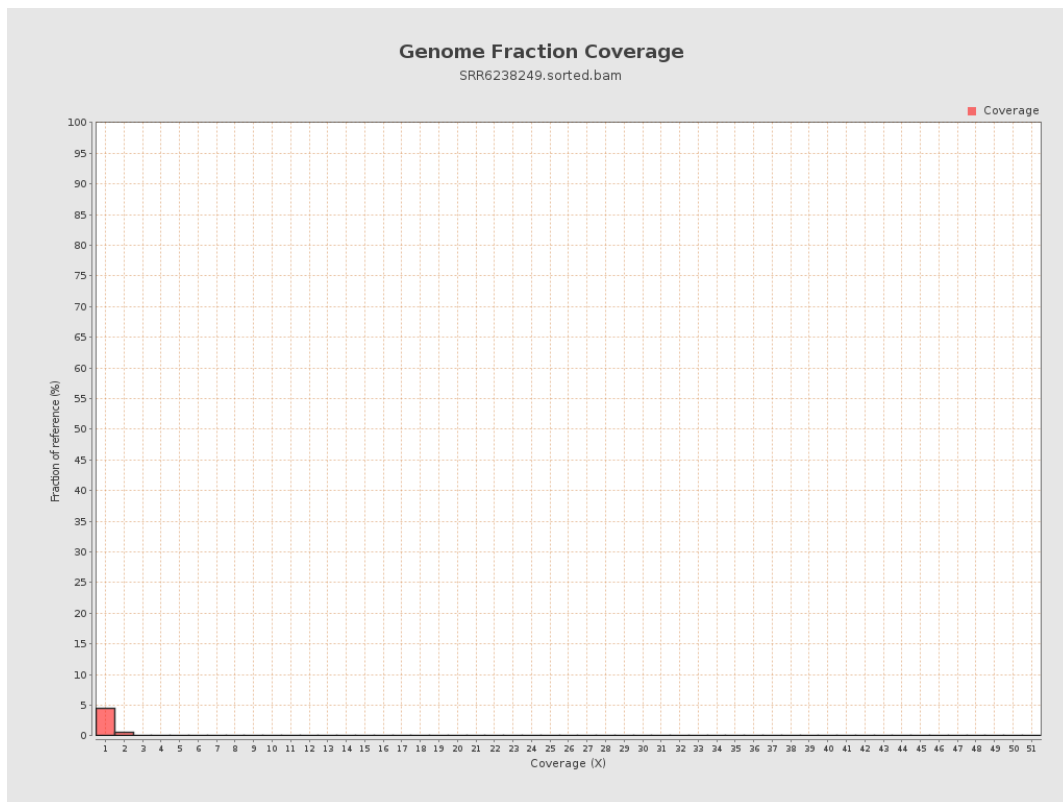
4. Results : Coverage Histogram



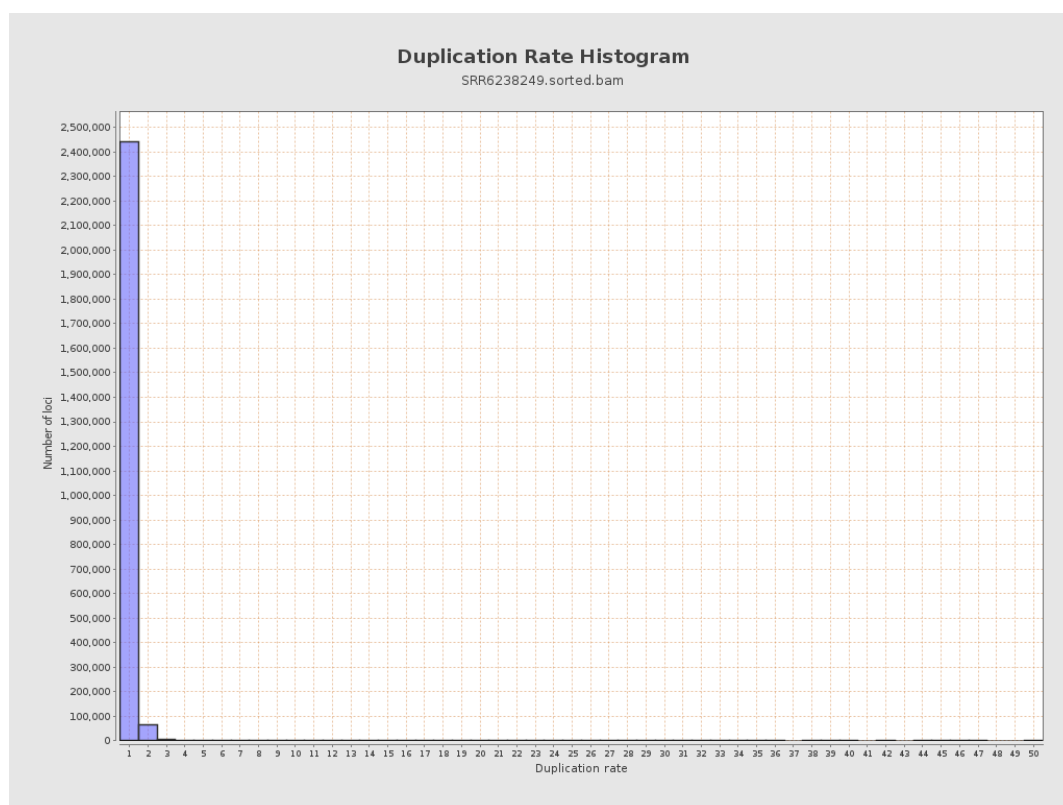
5. Results : Coverage Histogram (0-50X)



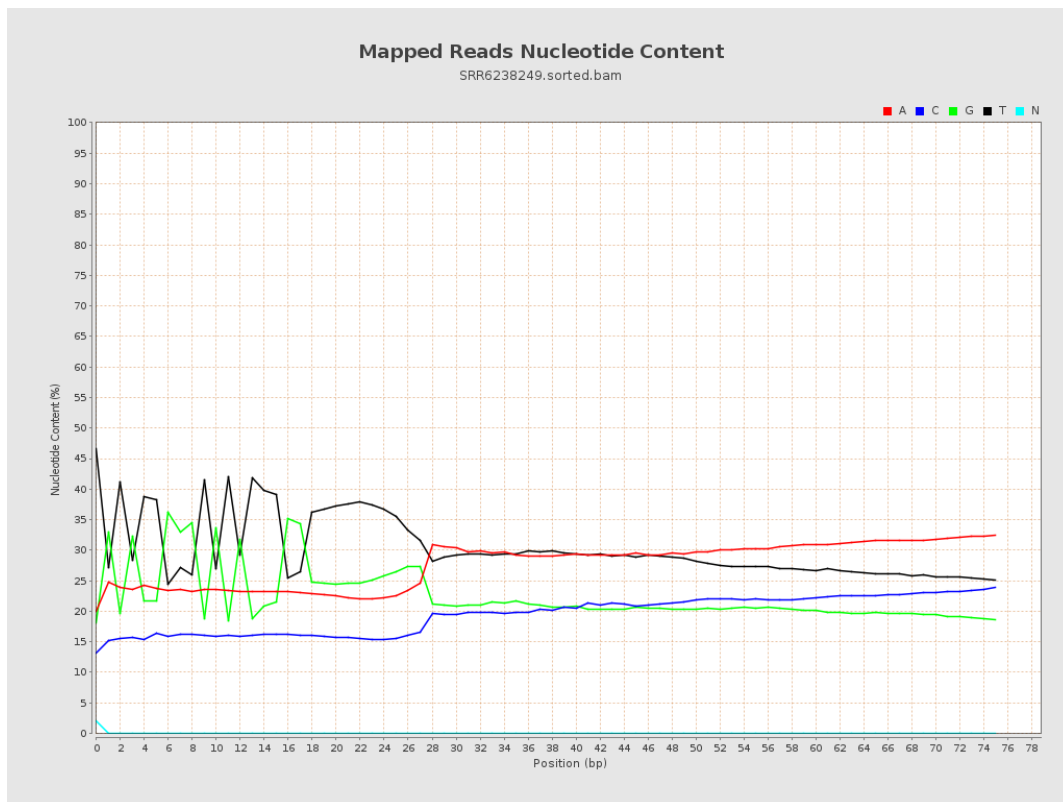
6. Results : Genome Fraction Coverage



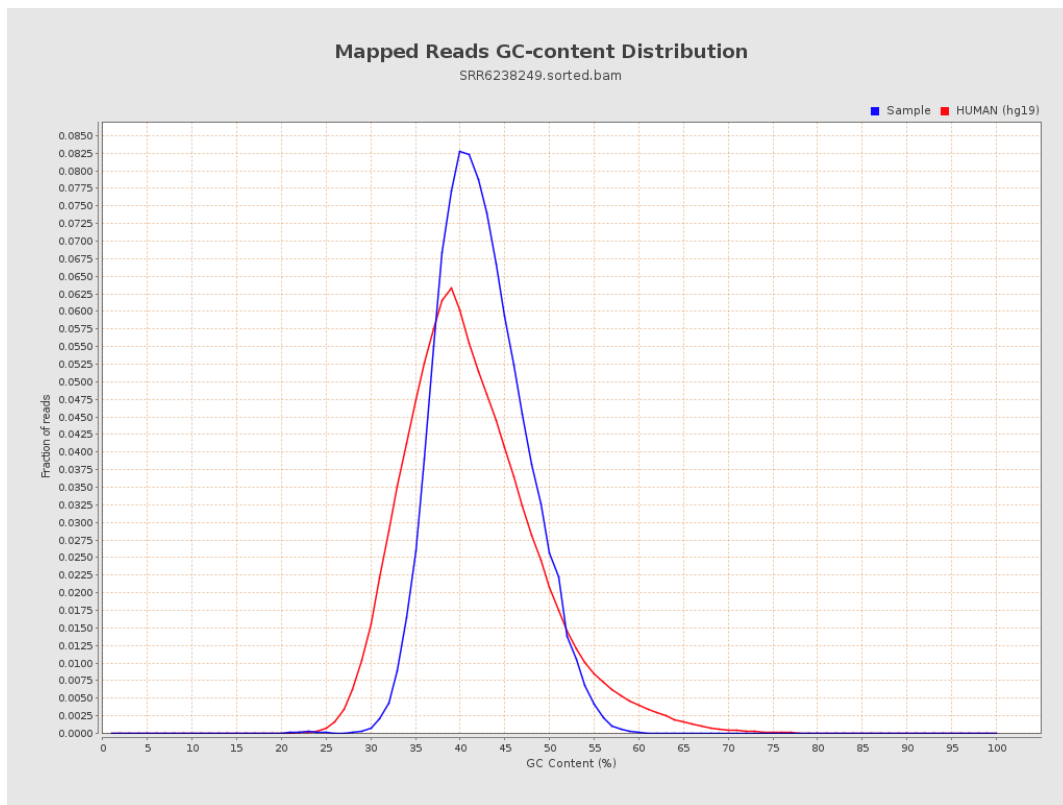
7. Results : Duplication Rate Histogram



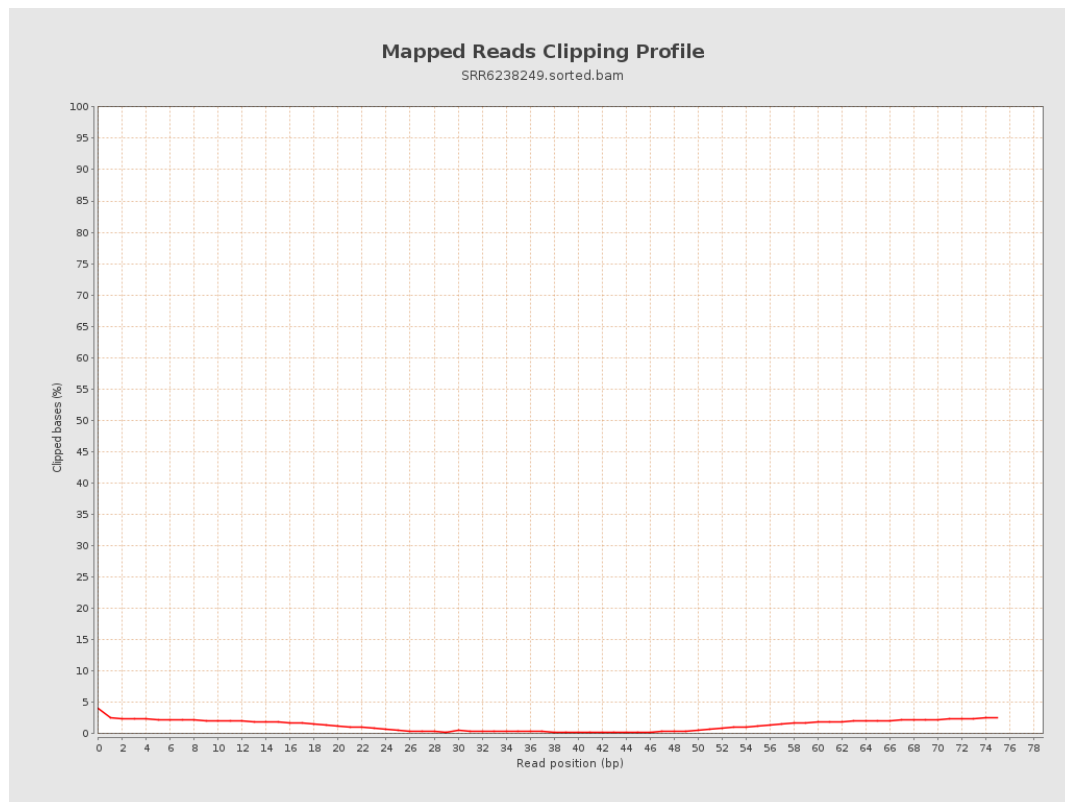
8. Results : Mapped Reads Nucleotide Content



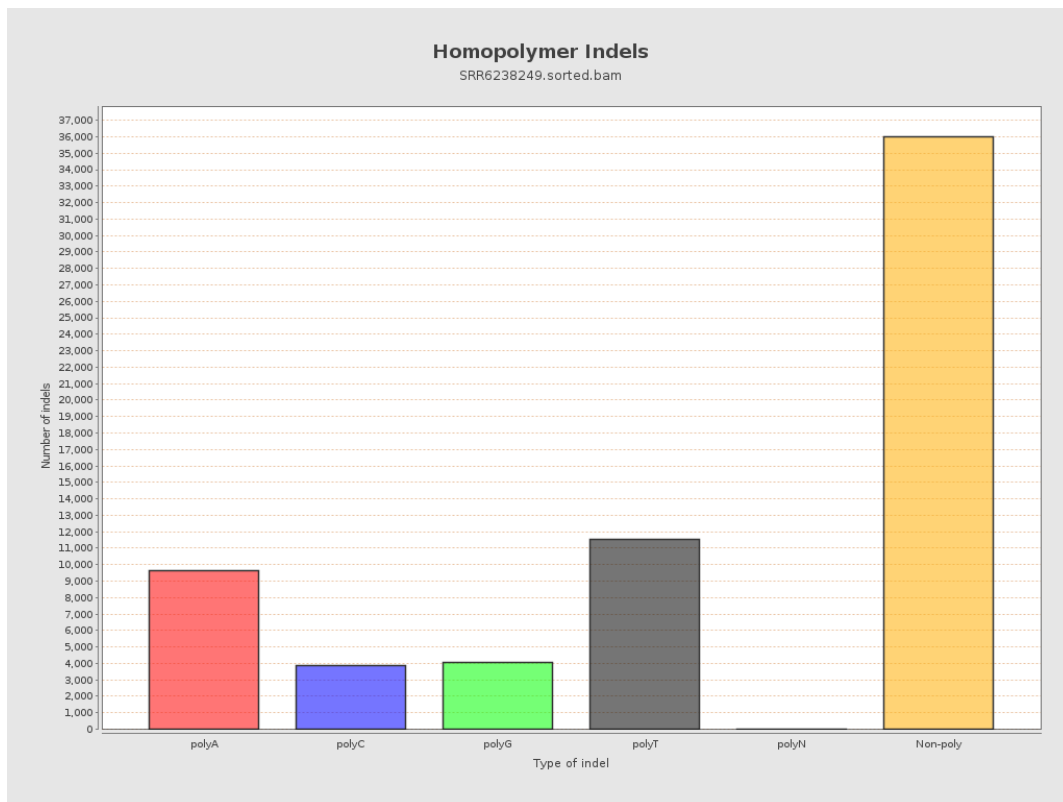
9. Results : Mapped Reads GC-content Distribution



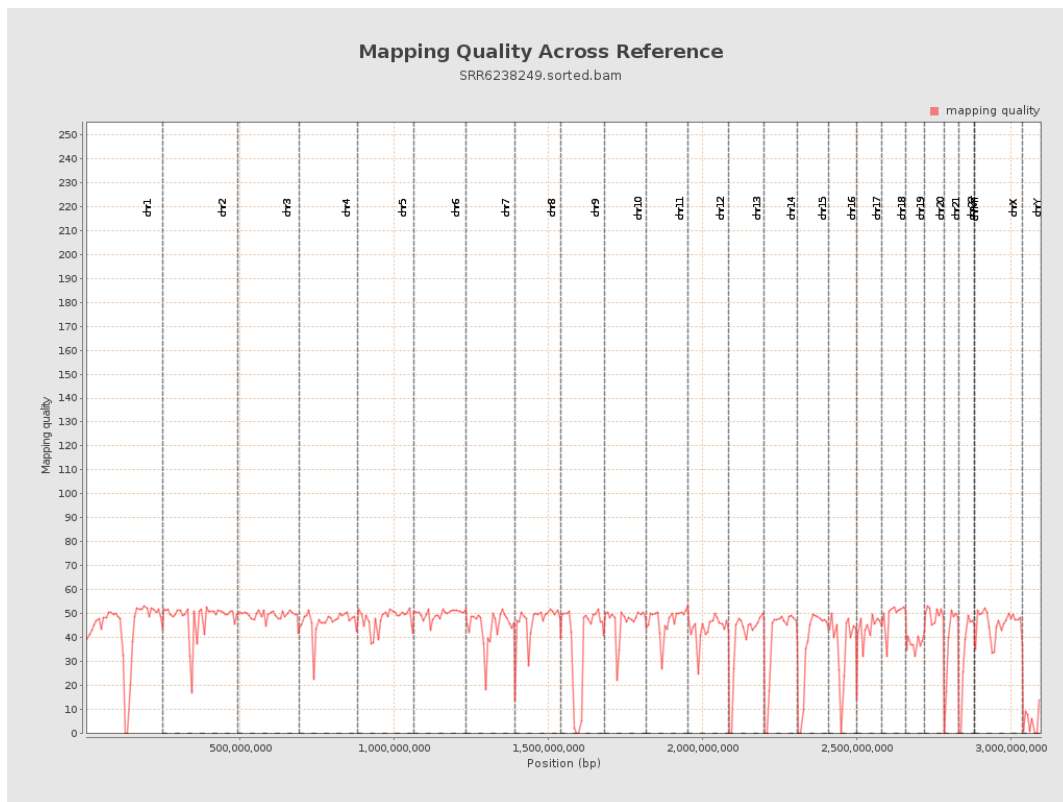
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

