

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 19:30:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238518.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_SRR6238518 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238518.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 19:30:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238518.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,566,354
Mapped reads	5,000,143 / 89.83%
Unmapped reads	566,211 / 10.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,474 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	1,377,811 / 24.75%
Duplication rate	19.38%
Clipped reads	3,111,809 / 55.9%

2.2. ACGT Content

Number/percentage of A's	74,575,775 / 24.07%
Number/percentage of C's	55,463,363 / 17.9%
Number/percentage of T's	103,882,408 / 33.54%
Number/percentage of G's	75,828,895 / 24.48%
Number/percentage of N's	20,959 / 0.01%
GC Percentage	42.38%

2.3. Coverage

Mean	0.1001

Standard Deviation	1.6419
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2.4. Mapping Quality

Mean Mapping Quality	42.34
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2.5. Mismatches and indels

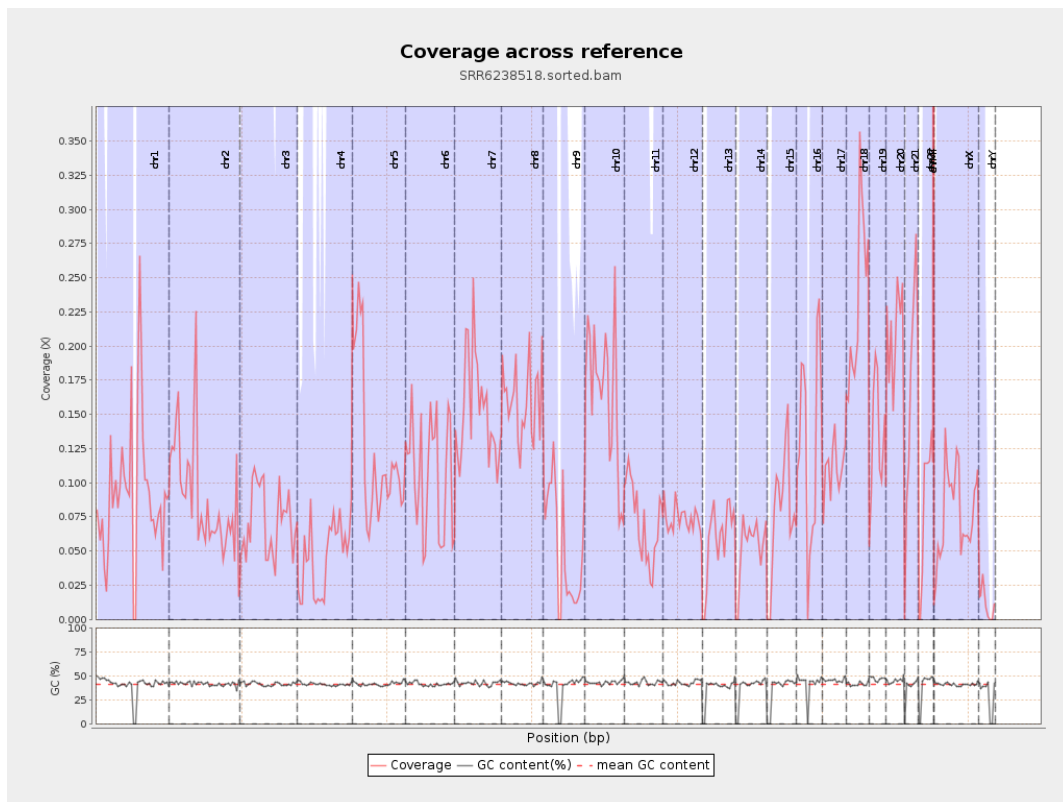
General error rate	0.62%
Mismatches	1,891,865
Insertions	20,714
Mapped reads with at least one insertion	0.41%
Deletions	91,129
Mapped reads with at least one deletion	1.8%
Homopolymer indels	40.64%

2.6. Chromosome stats

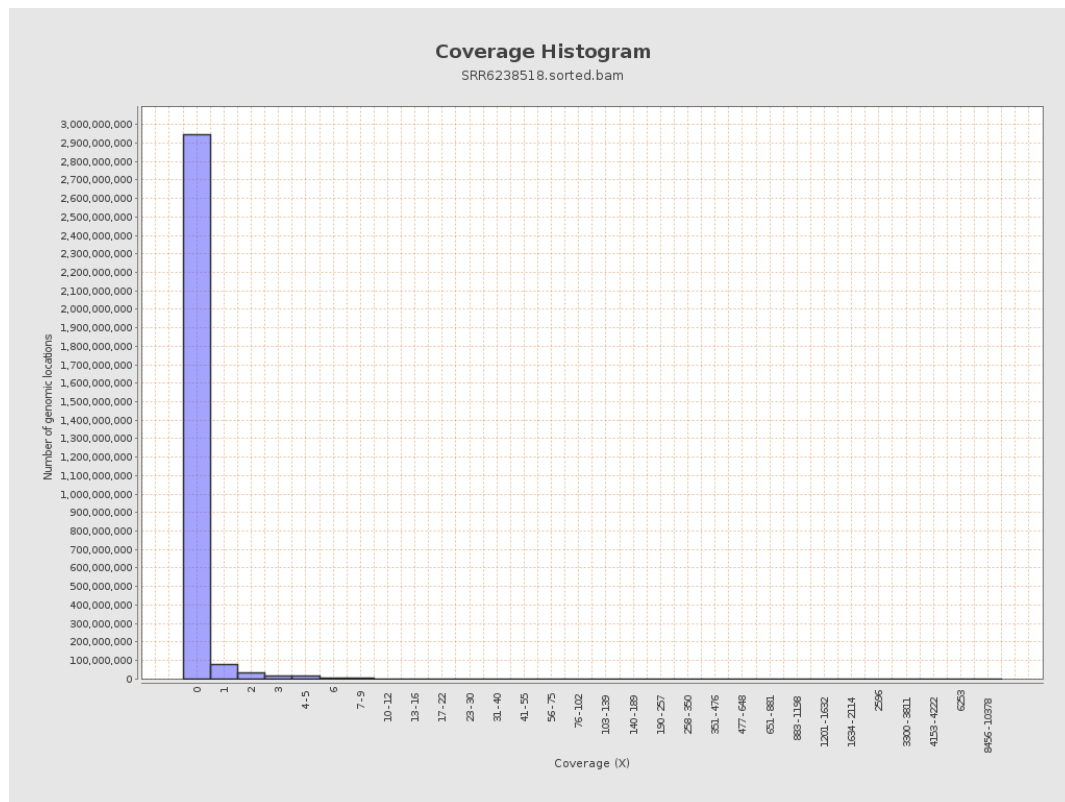
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22397182	0.0899	1.6636
chr2	243199373	22006589	0.0905	4.5603
chr3	198022430	14082670	0.0711	0.5375
chr4	191154276	8713356	0.0456	0.4163
chr5	180915260	22101781	0.1222	0.6871
chr6	171115067	18400036	0.1075	1.4362
chr7	159138663	24399464	0.1533	1.8281

chr8	146364022	23367701	0.1597	1.04
chr9	141213431	7050522	0.0499	0.8051
chr10	135534747	22303642	0.1646	0.8982
chr11	135006516	9623639	0.0713	0.5763
chr12	133851895	9877986	0.0738	0.543
chr13	115169878	6667669	0.0579	0.8533
chr14	107349540	5562434	0.0518	0.4657
chr15	102531392	7958644	0.0776	0.9054
chr16	90354753	11908110	0.1318	0.8138
chr17	81195210	8958364	0.1103	0.6332
chr18	78077248	18465777	0.2365	2.6829
chr19	59128983	8079728	0.1366	1.1103
chr20	63025520	13104604	0.2079	0.9044
chr21	48129895	7961999	0.1654	0.8364
chr22	51304566	4231342	0.0825	0.5475
chrMT	16571	25208	1.5212	2.2209
chrX	155270560	12023387	0.0774	0.5764
chrY	59373566	652297	0.011	0.5339

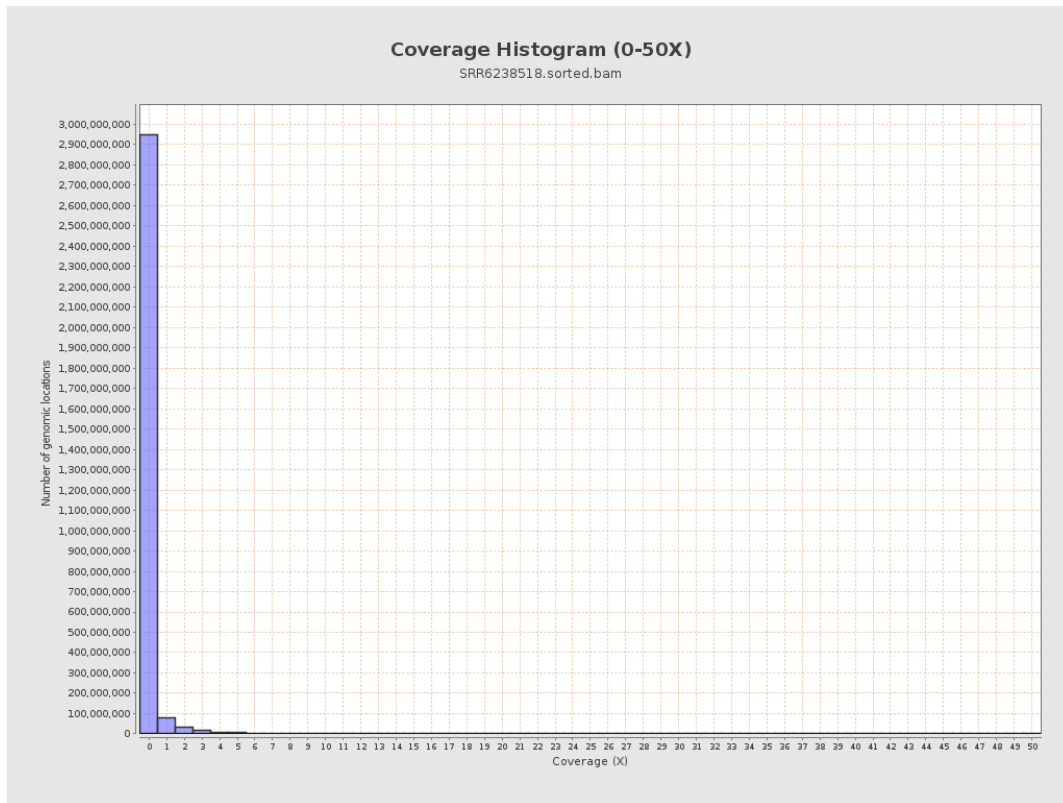
3. Results : Coverage across reference



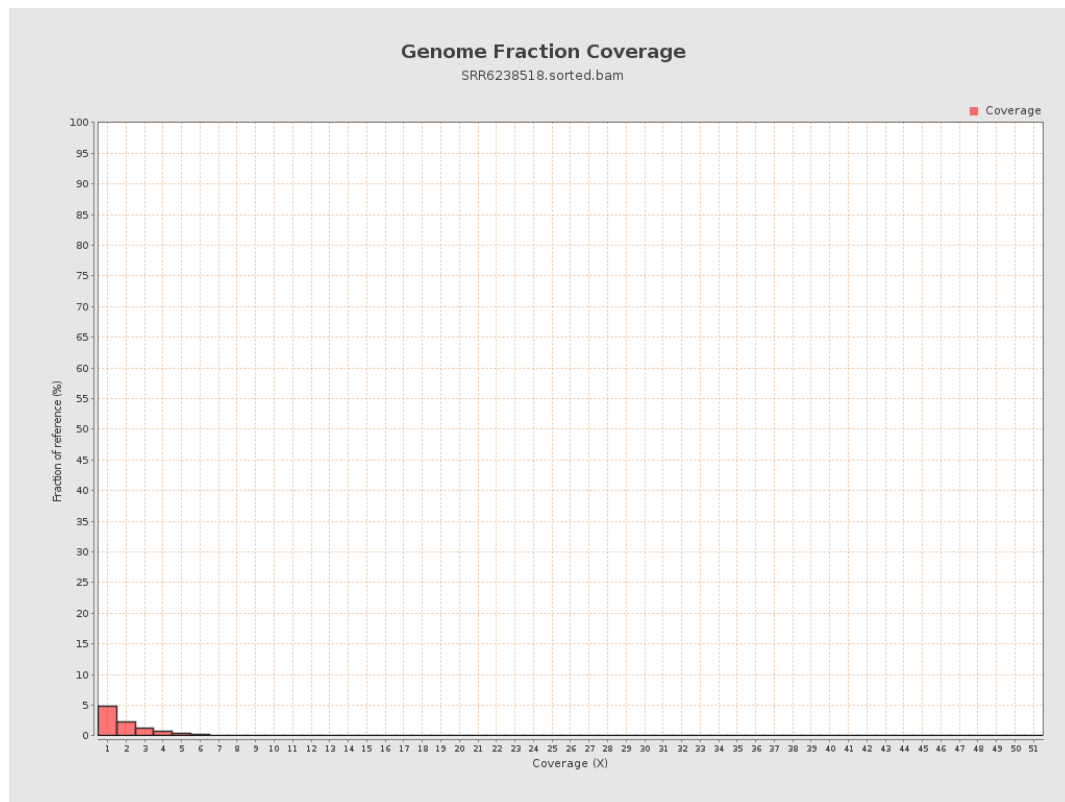
4. Results : Coverage Histogram



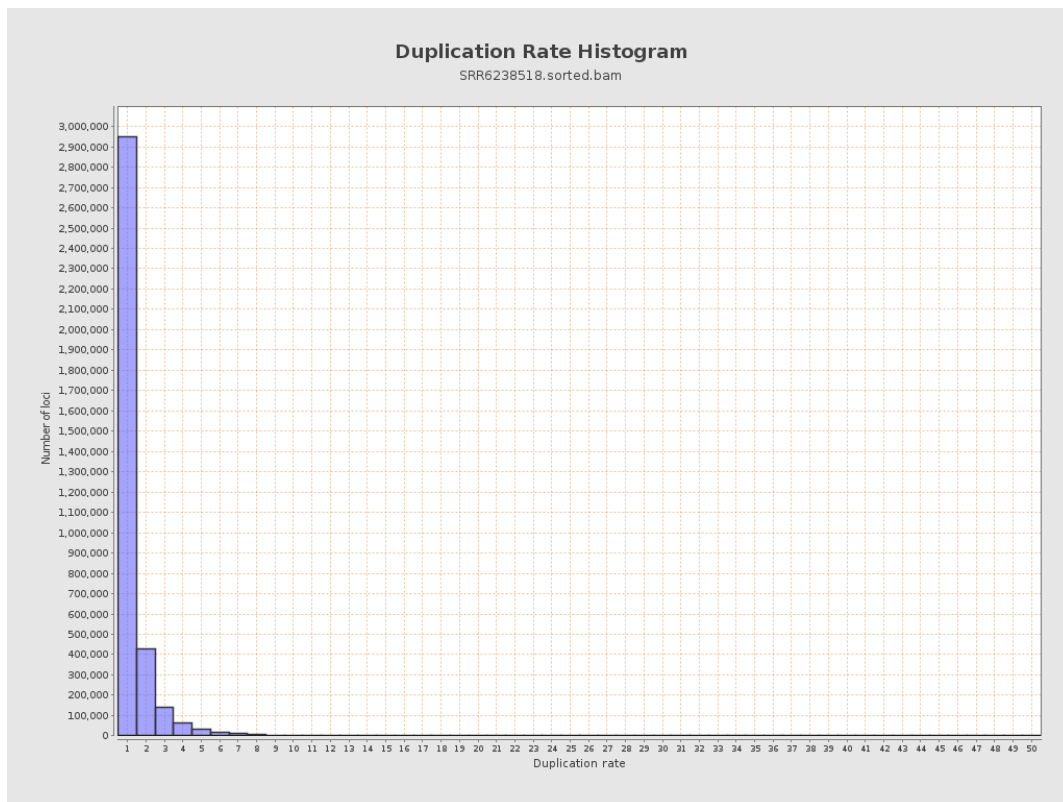
5. Results : Coverage Histogram (0-50X)



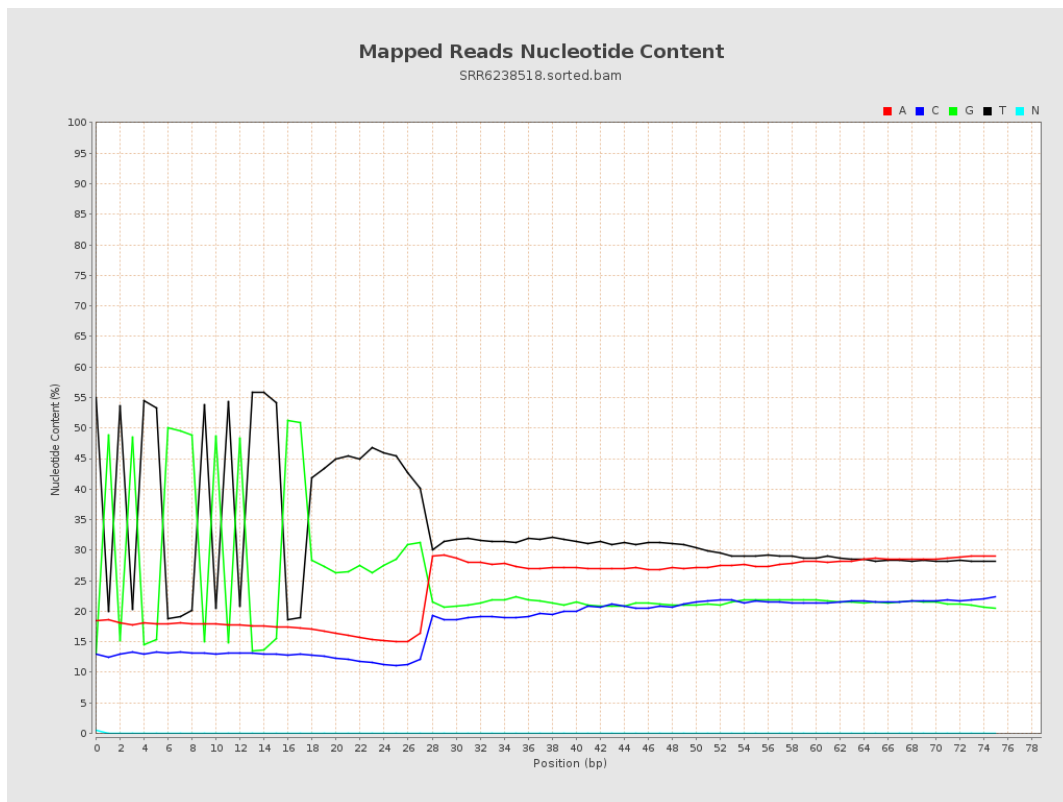
6. Results : Genome Fraction Coverage



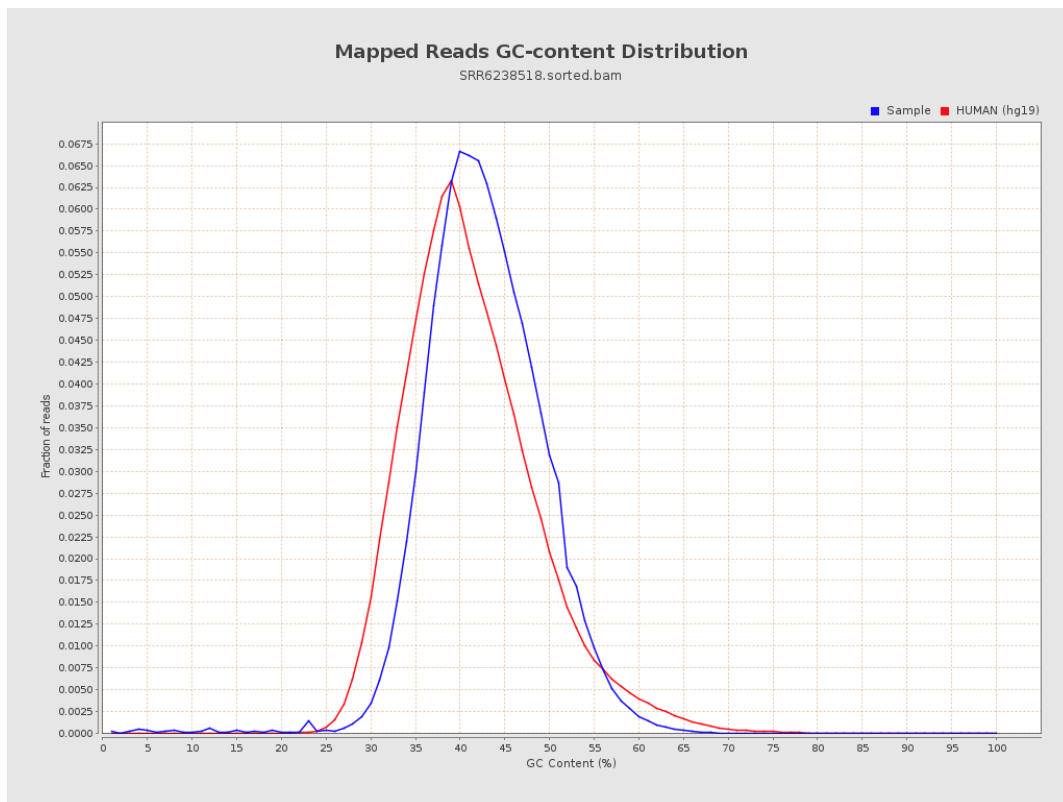
7. Results : Duplication Rate Histogram



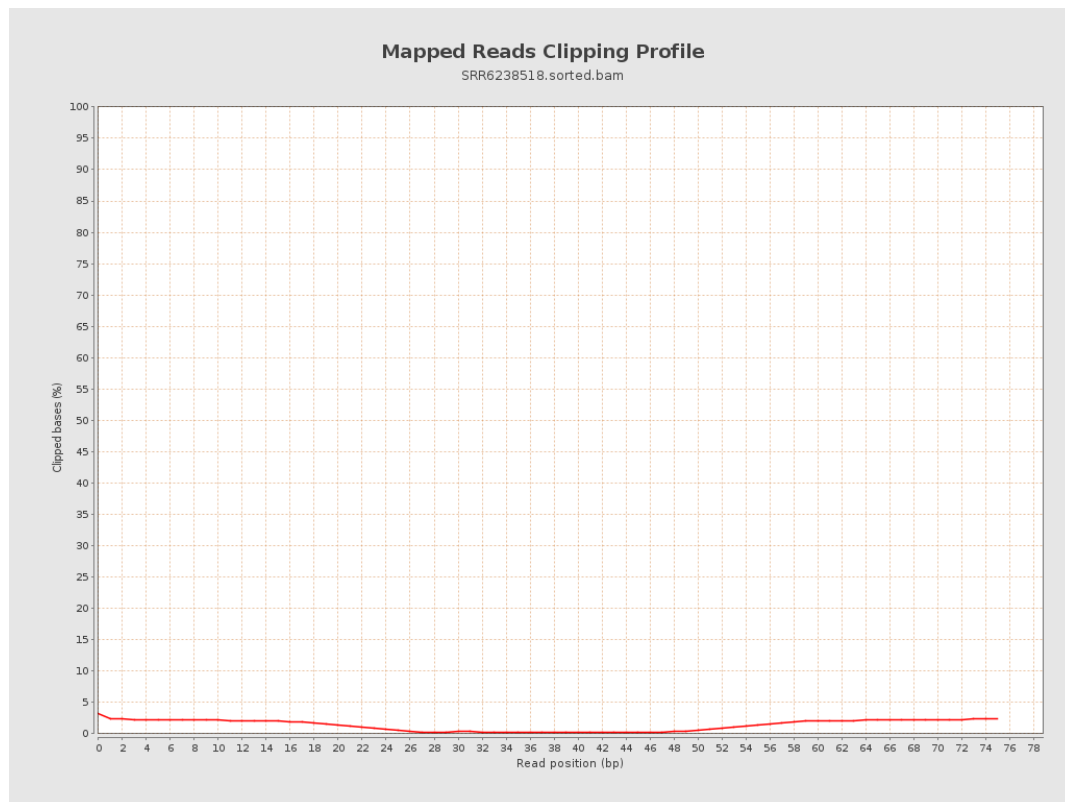
8. Results : Mapped Reads Nucleotide Content



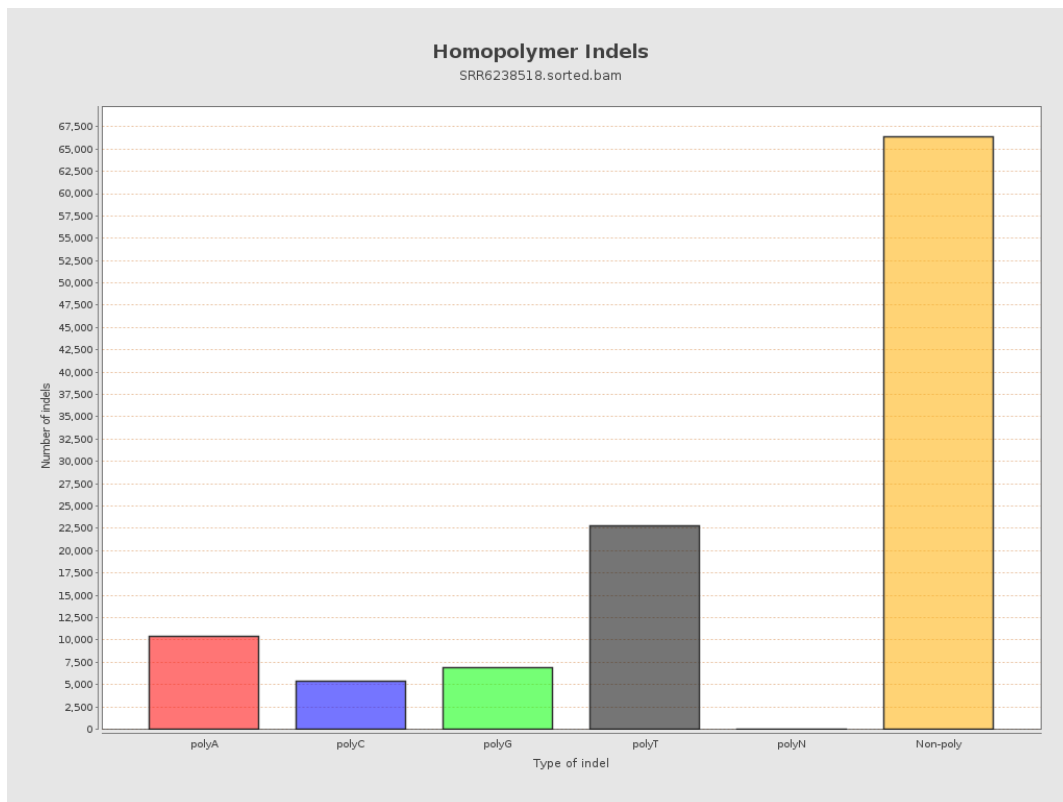
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

