

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:21:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068138.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_SRR6068138 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068138.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:21:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068138.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,591,461
Mapped reads	1,080,303 / 67.88%
Unmapped reads	511,158 / 32.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,502 / 0.53%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	240,781 / 15.13%
Duplication rate	14.06%
Clipped reads	432,496 / 27.18%

2.2. ACGT Content

Number/percentage of A's	20,395,328 / 28.03%
Number/percentage of C's	13,442,024 / 18.48%
Number/percentage of T's	23,129,423 / 31.79%
Number/percentage of G's	15,746,329 / 21.64%
Number/percentage of N's	42,592 / 0.06%
GC Percentage	40.12%

2.3. Coverage

Mean	0.0235

Standard Deviation	0.5295
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2.4. Mapping Quality

Mean Mapping Quality	46.79
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2.5. Mismatches and indels

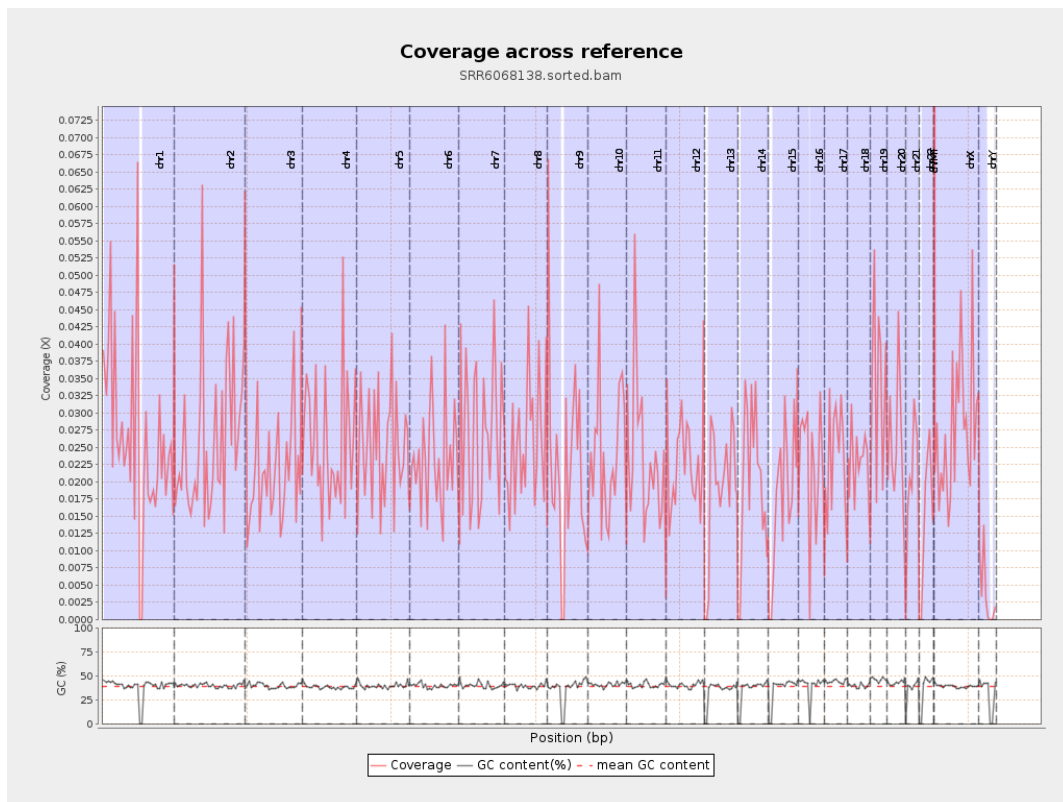
General error rate	0.87%
Mismatches	621,698
Insertions	5,739
Mapped reads with at least one insertion	0.53%
Deletions	17,023
Mapped reads with at least one deletion	1.56%
Homopolymer indels	49.14%

2.6. Chromosome stats

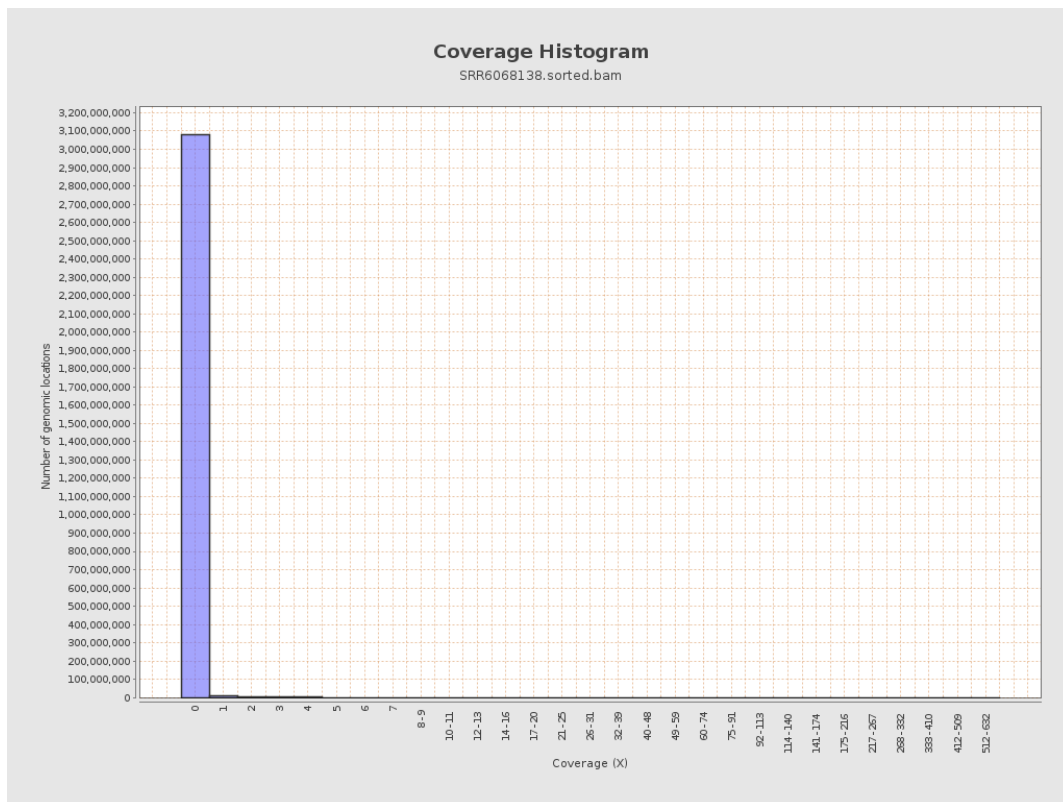
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6559400	0.0263	0.6653
chr2	243199373	6198333	0.0255	0.5588
chr3	198022430	4260068	0.0215	0.4527
chr4	191154276	4924321	0.0258	0.5678
chr5	180915260	4624515	0.0256	0.5018
chr6	171115067	3945451	0.0231	0.4896
chr7	159138663	4348908	0.0273	0.5774

chr8	146364022	3759955	0.0257	0.6144
chr9	141213431	3118956	0.0221	0.5117
chr10	135534747	3214840	0.0237	0.5101
chr11	135006516	3140966	0.0233	0.4985
chr12	133851895	3043687	0.0227	0.497
chr13	115169878	2165878	0.0188	0.4184
chr14	107349540	2108224	0.0196	0.4544
chr15	102531392	1857293	0.0181	0.5738
chr16	90354753	1982962	0.0219	0.46
chr17	81195210	1900681	0.0234	0.461
chr18	78077248	1796115	0.023	0.6235
chr19	59128983	2031758	0.0344	0.6118
chr20	63025520	1555094	0.0247	0.5064
chr21	48129895	976271	0.0203	0.4443
chr22	51304566	771776	0.015	0.3623
chrMT	16571	9478	0.572	1.9341
chrX	155270560	4265105	0.0275	0.5469
chrY	59373566	224426	0.0038	0.1693

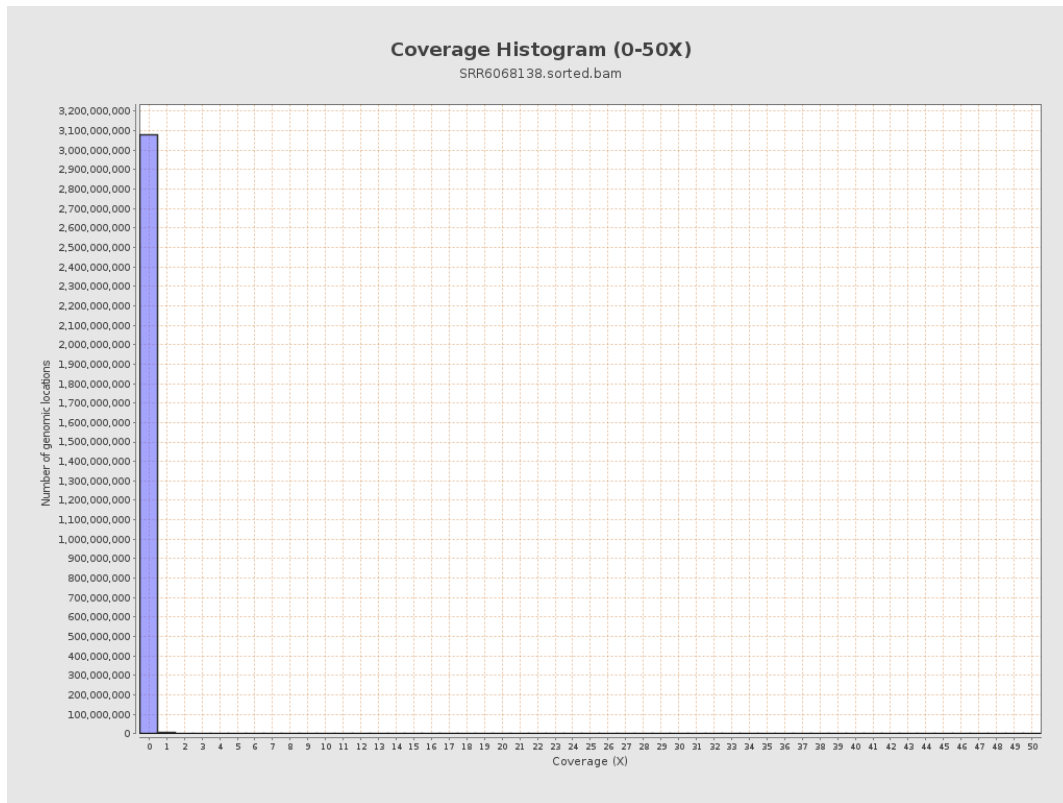
3. Results : Coverage across reference



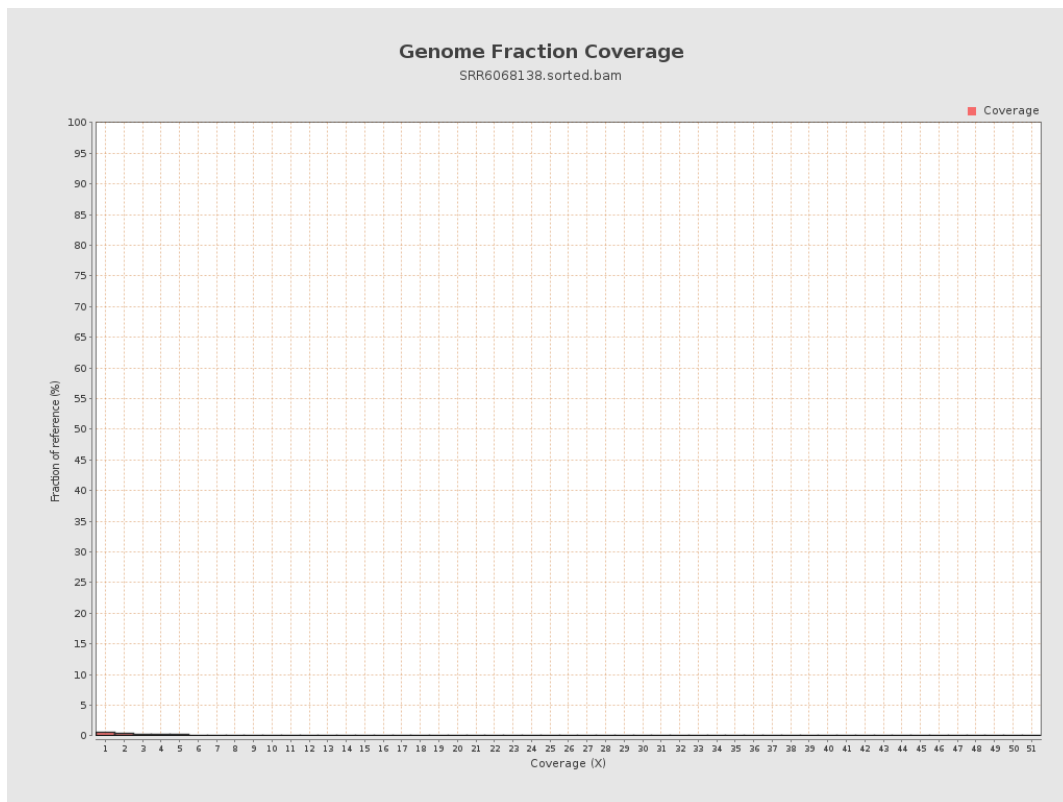
4. Results : Coverage Histogram



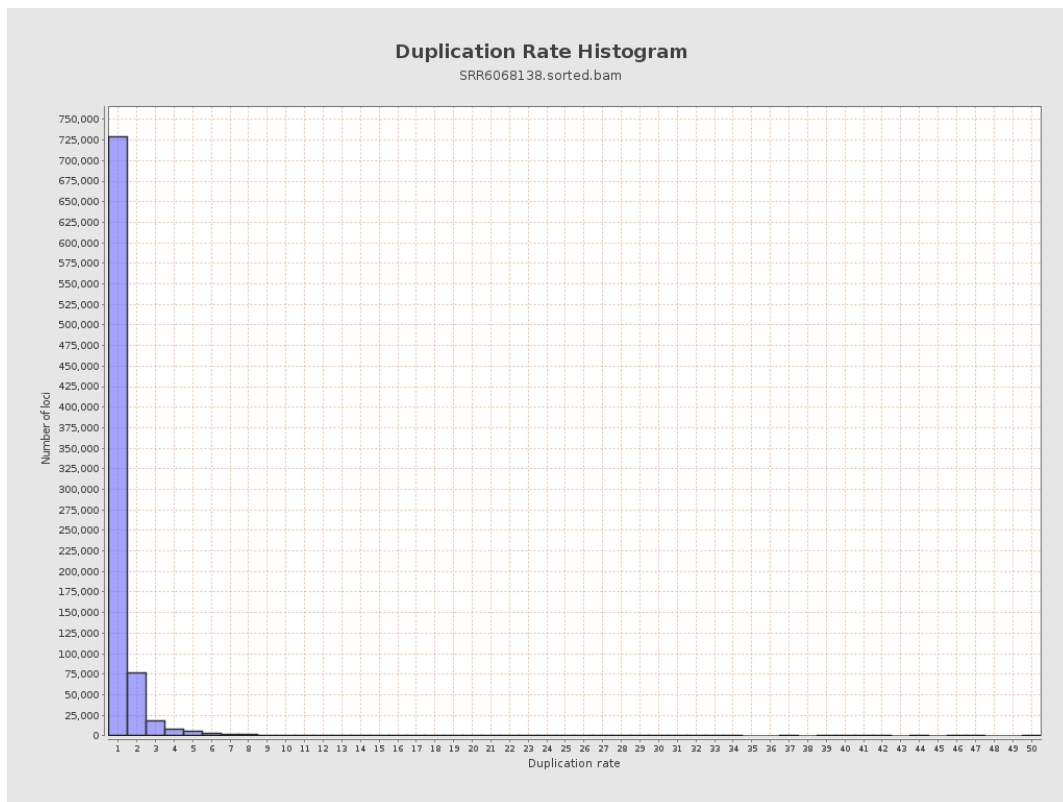
5. Results : Coverage Histogram (0-50X)



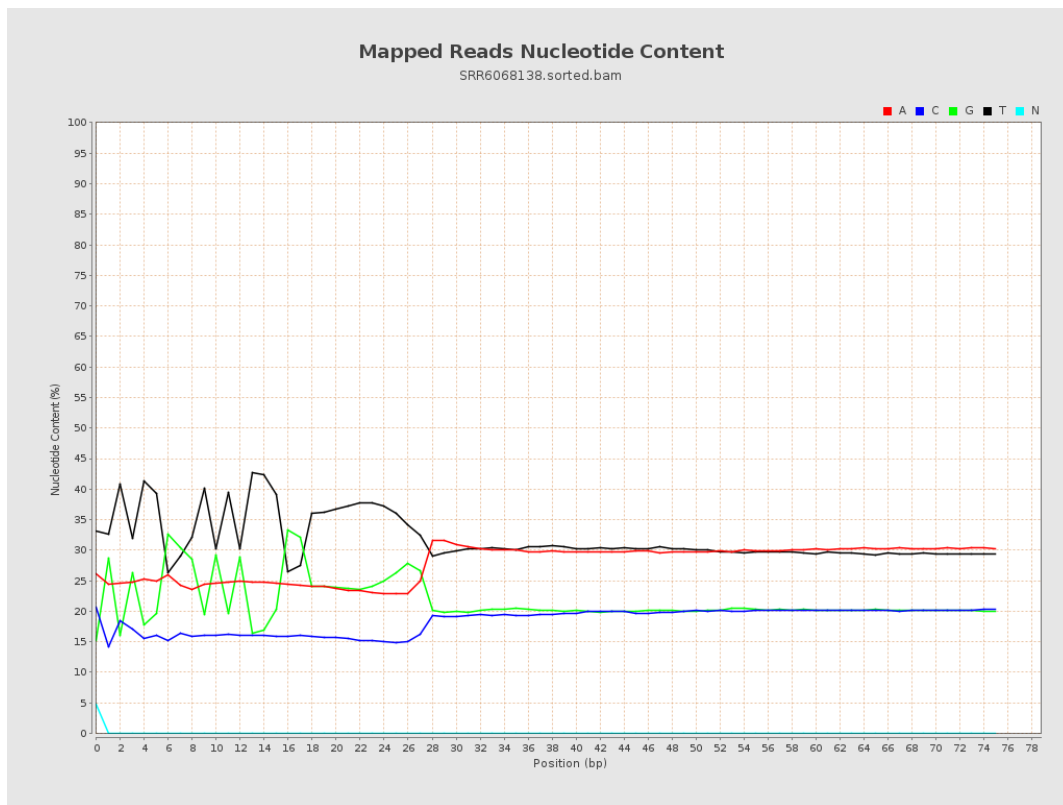
6. Results : Genome Fraction Coverage



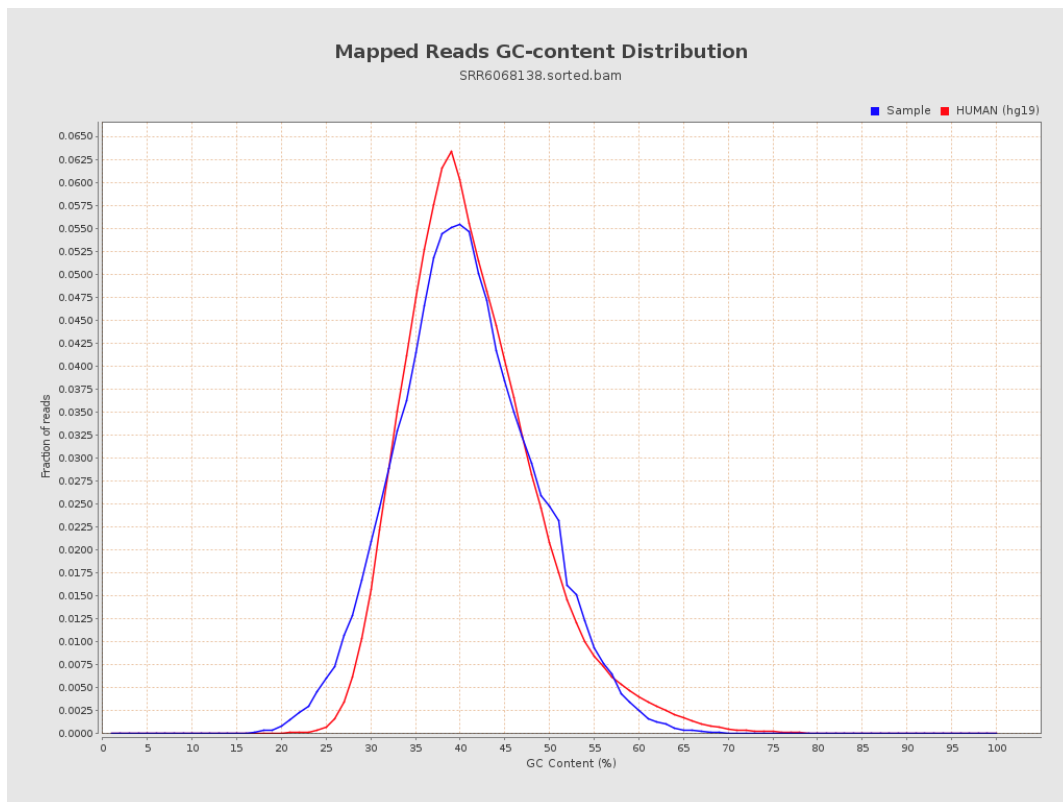
7. Results : Duplication Rate Histogram



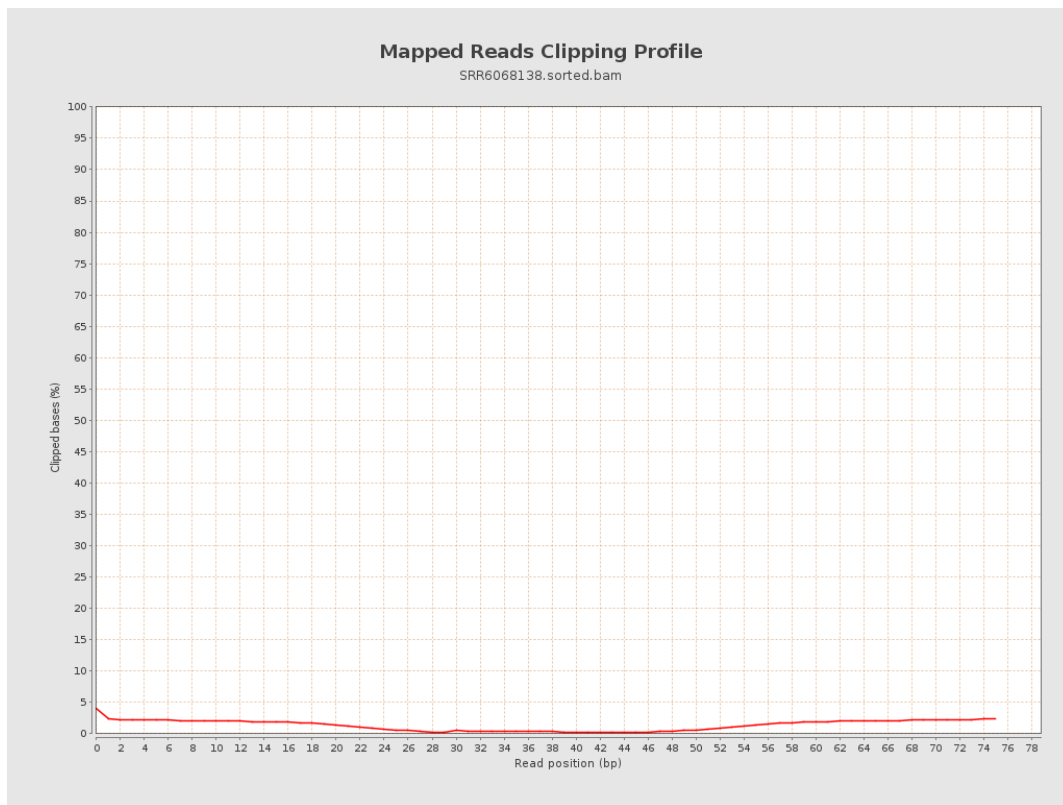
8. Results : Mapped Reads Nucleotide Content



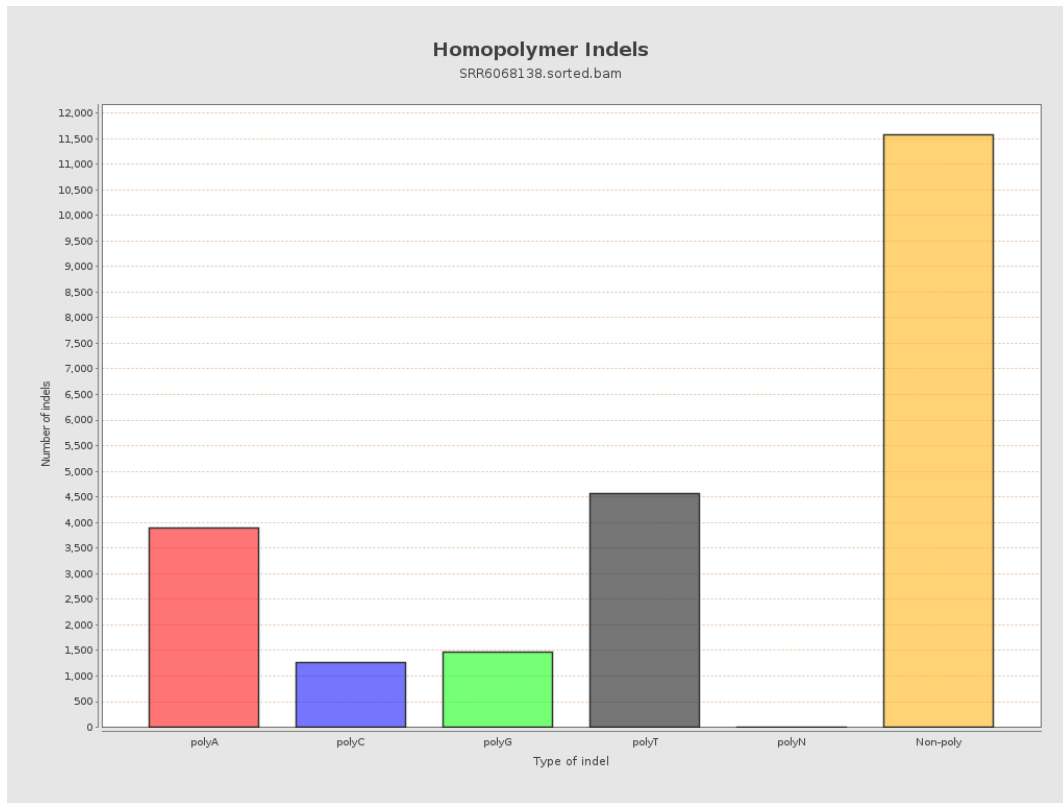
9. Results : Mapped Reads GC-content Distribution



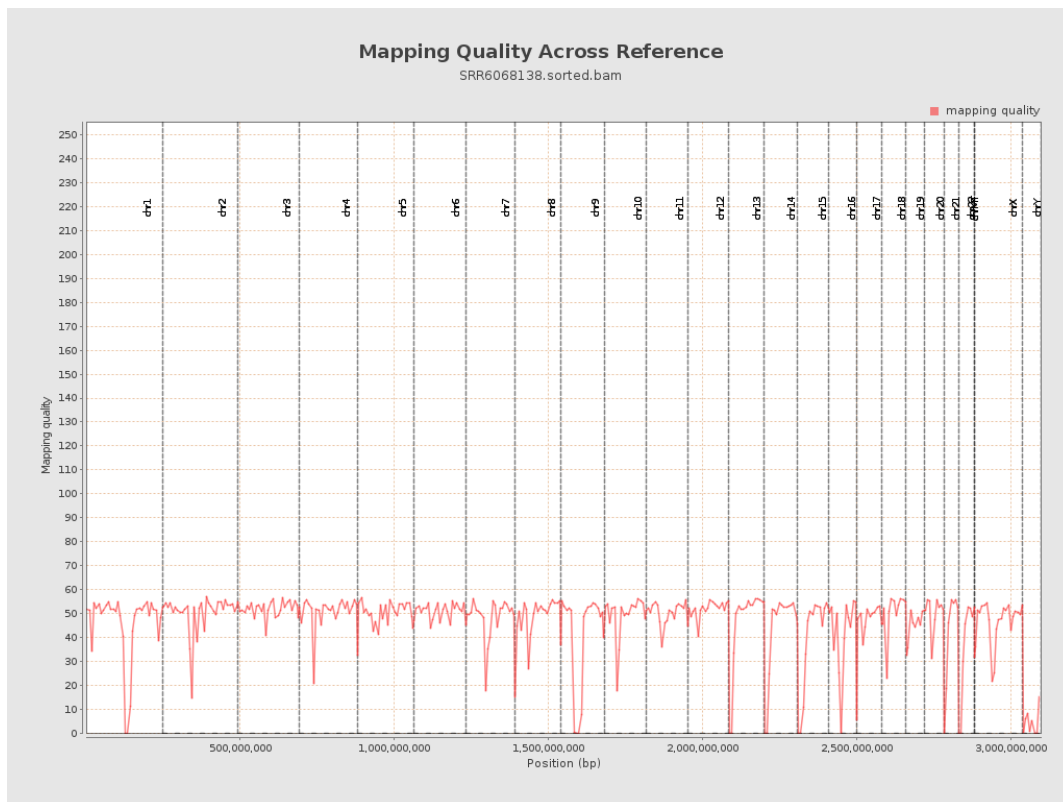
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

