

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:16:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068136.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_SRR6068136 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068136.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:16:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068136.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,650,762
Mapped reads	1,158,025 / 70.15%
Unmapped reads	492,737 / 29.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,739 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	267,373 / 16.2%
Duplication rate	13.88%
Clipped reads	509,445 / 30.86%

2.2. ACGT Content

Number/percentage of A's	21,373,712 / 27.83%
Number/percentage of C's	13,755,713 / 17.91%
Number/percentage of T's	24,880,413 / 32.39%
Number/percentage of G's	16,719,714 / 21.77%
Number/percentage of N's	82,616 / 0.11%
GC Percentage	39.68%

2.3. Coverage

Mean	0.0248

Standard Deviation	0.5098
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2.4. Mapping Quality

Mean Mapping Quality	46.6
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2.5. Mismatches and indels

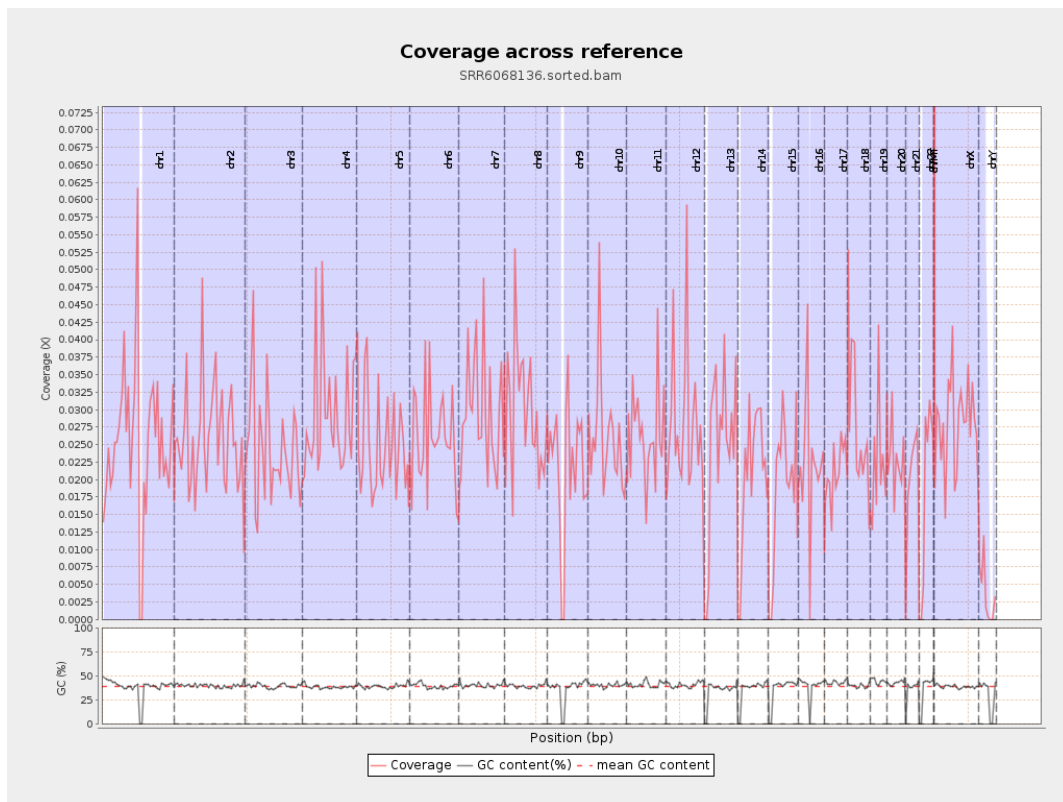
General error rate	0.91%
Mismatches	689,967
Insertions	6,171
Mapped reads with at least one insertion	0.53%
Deletions	17,380
Mapped reads with at least one deletion	1.48%
Homopolymer indels	48.05%

2.6. Chromosome stats

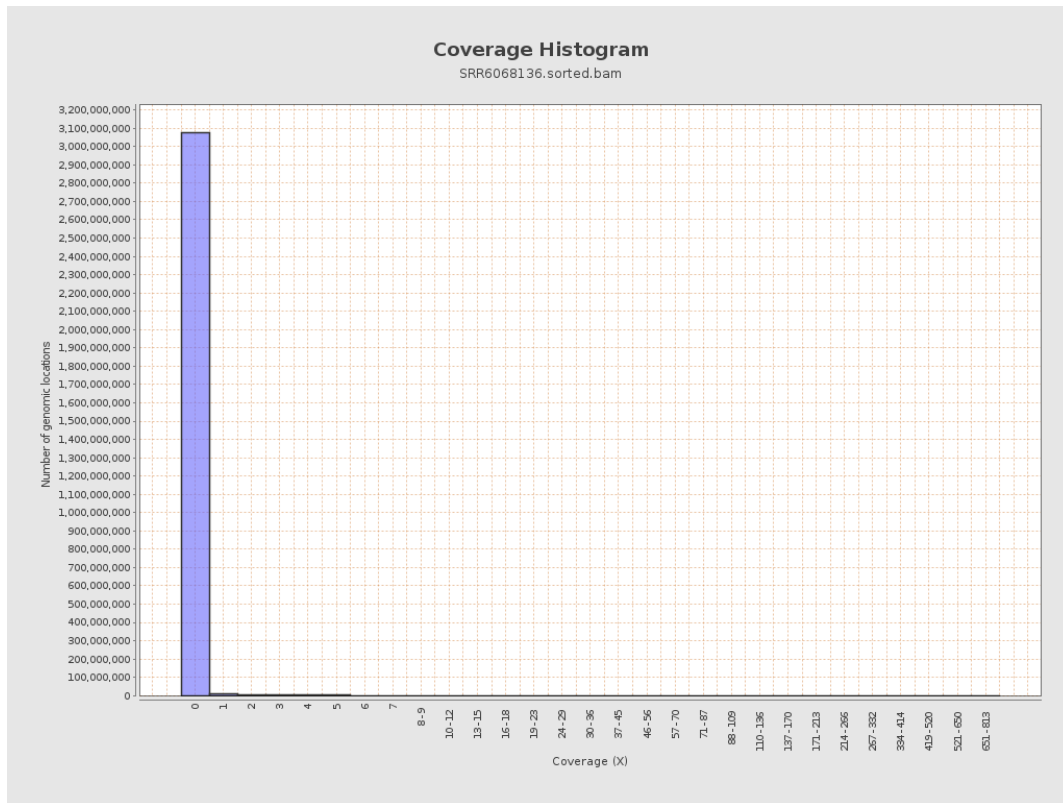
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6261889	0.0251	0.7719
chr2	243199373	6243401	0.0257	0.4942
chr3	198022430	4809548	0.0243	0.4355
chr4	191154276	5538395	0.029	0.4915
chr5	180915260	4433831	0.0245	0.4334
chr6	171115067	4448239	0.026	0.4768
chr7	159138663	4722579	0.0297	0.5508

chr8	146364022	4380118	0.0299	0.5675
chr9	141213431	3066590	0.0217	0.465
chr10	135534747	3554325	0.0262	0.515
chr11	135006516	3578201	0.0265	0.4701
chr12	133851895	3718424	0.0278	0.4751
chr13	115169878	2842583	0.0247	0.4388
chr14	107349540	2198648	0.0205	0.4094
chr15	102531392	1944594	0.019	0.427
chr16	90354753	1981074	0.0219	0.4263
chr17	81195210	1714024	0.0211	0.3911
chr18	78077248	2124173	0.0272	0.7663
chr19	59128983	1334017	0.0226	0.6079
chr20	63025520	1439506	0.0228	0.4247
chr21	48129895	974815	0.0203	0.3831
chr22	51304566	947627	0.0185	0.36
chrMT	16571	20950	1.2643	2.6162
chrX	155270560	4350608	0.028	0.4823
chrY	59373566	213587	0.0036	0.1428

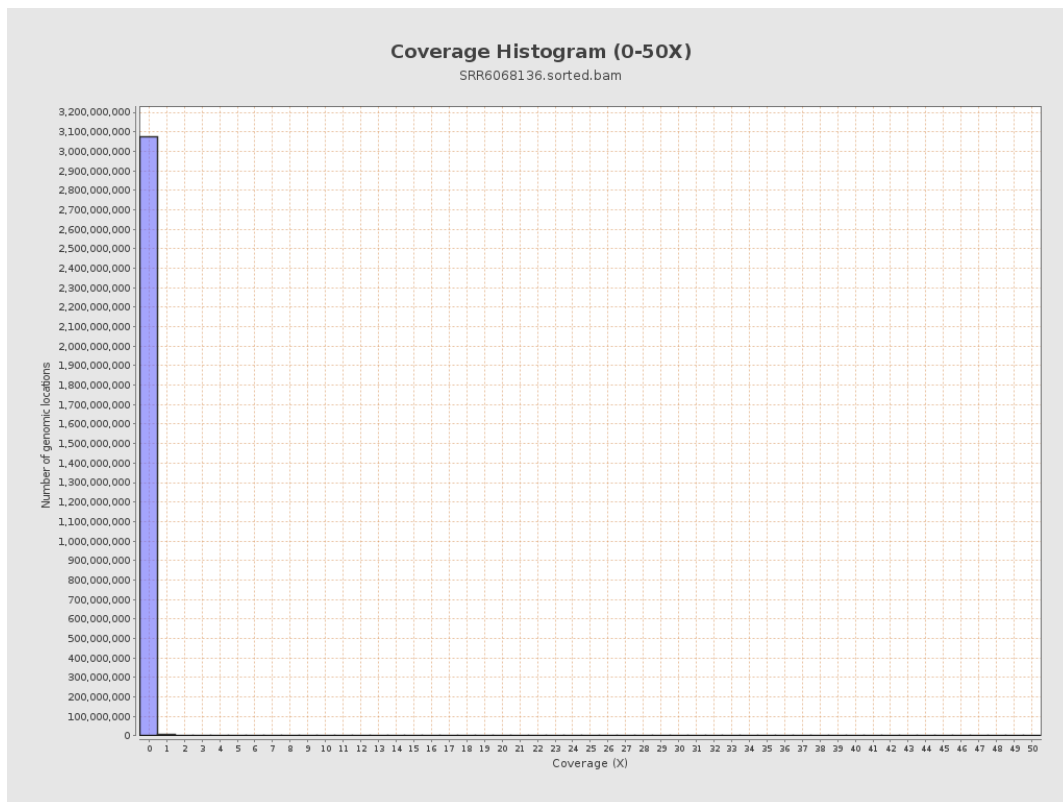
3. Results : Coverage across reference



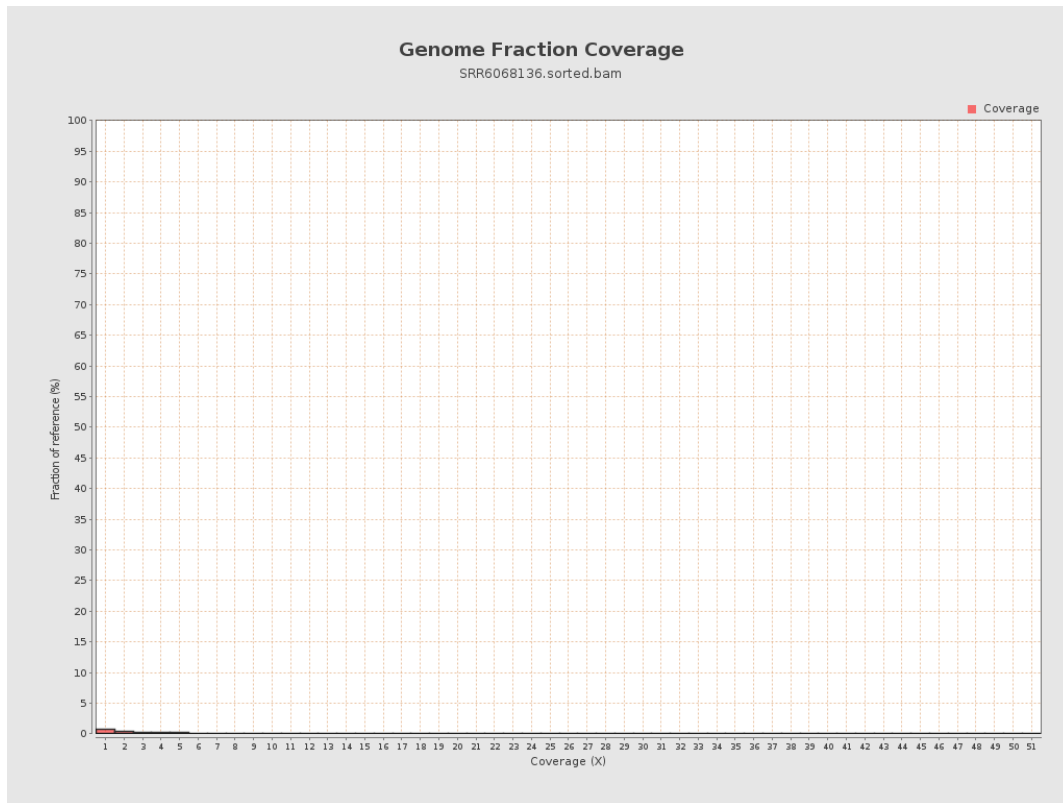
4. Results : Coverage Histogram



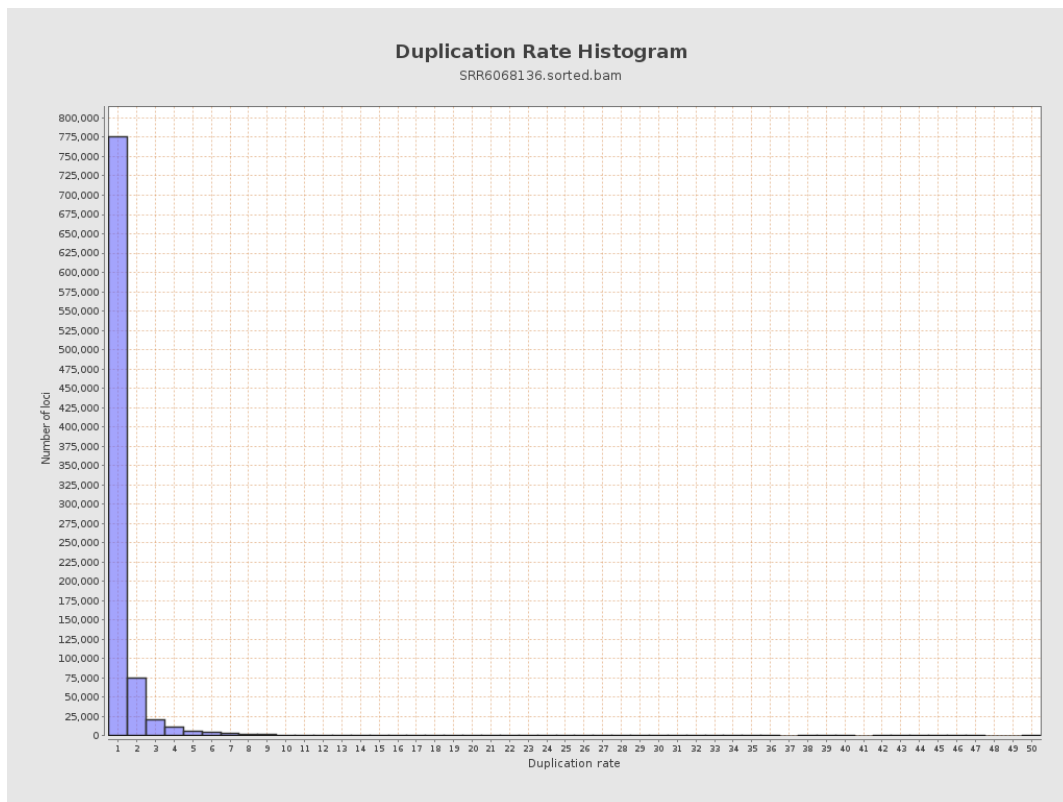
5. Results : Coverage Histogram (0-50X)



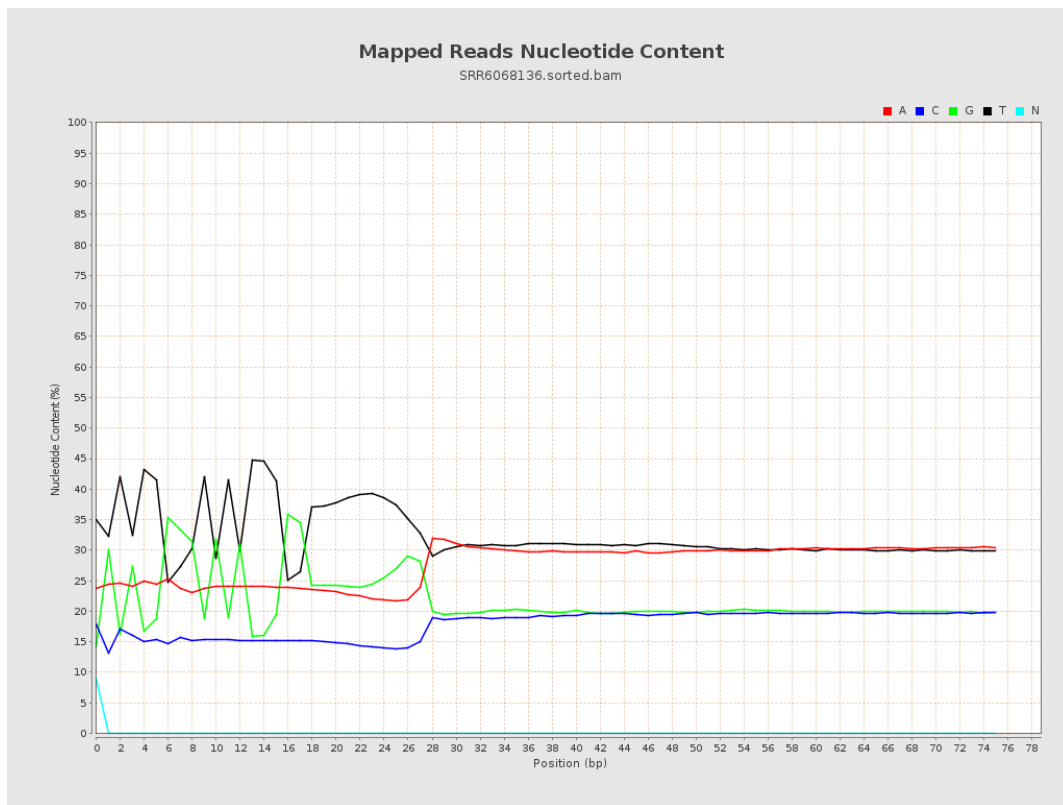
6. Results : Genome Fraction Coverage



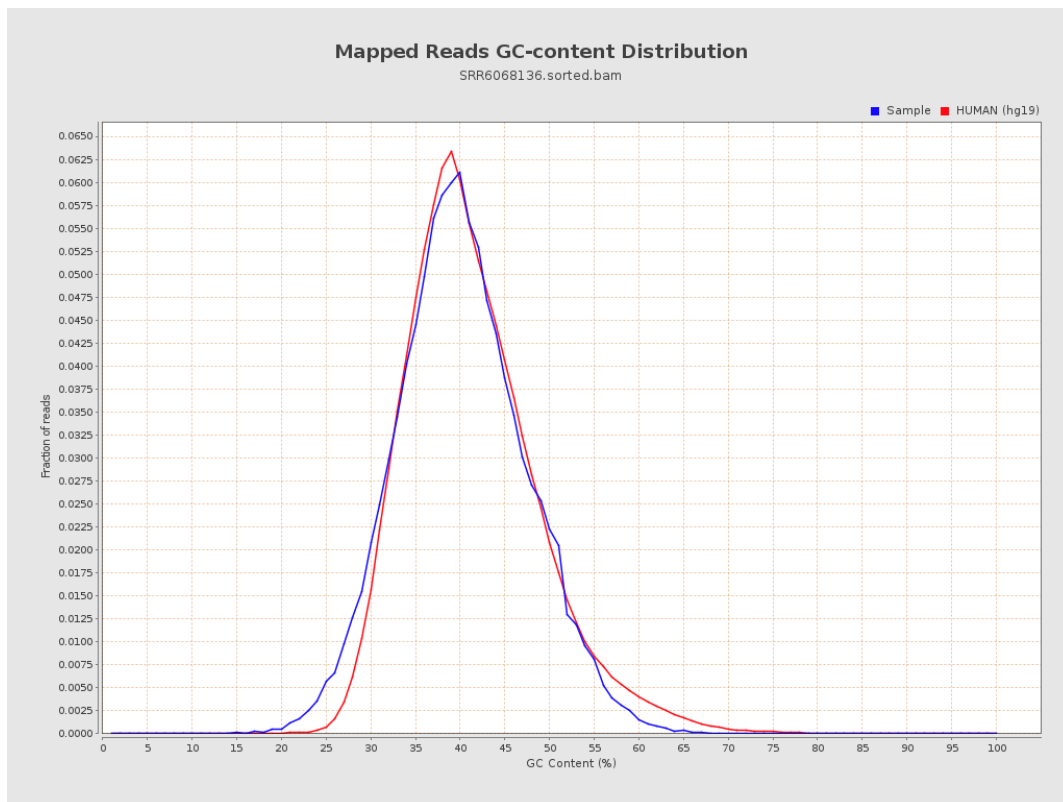
7. Results : Duplication Rate Histogram



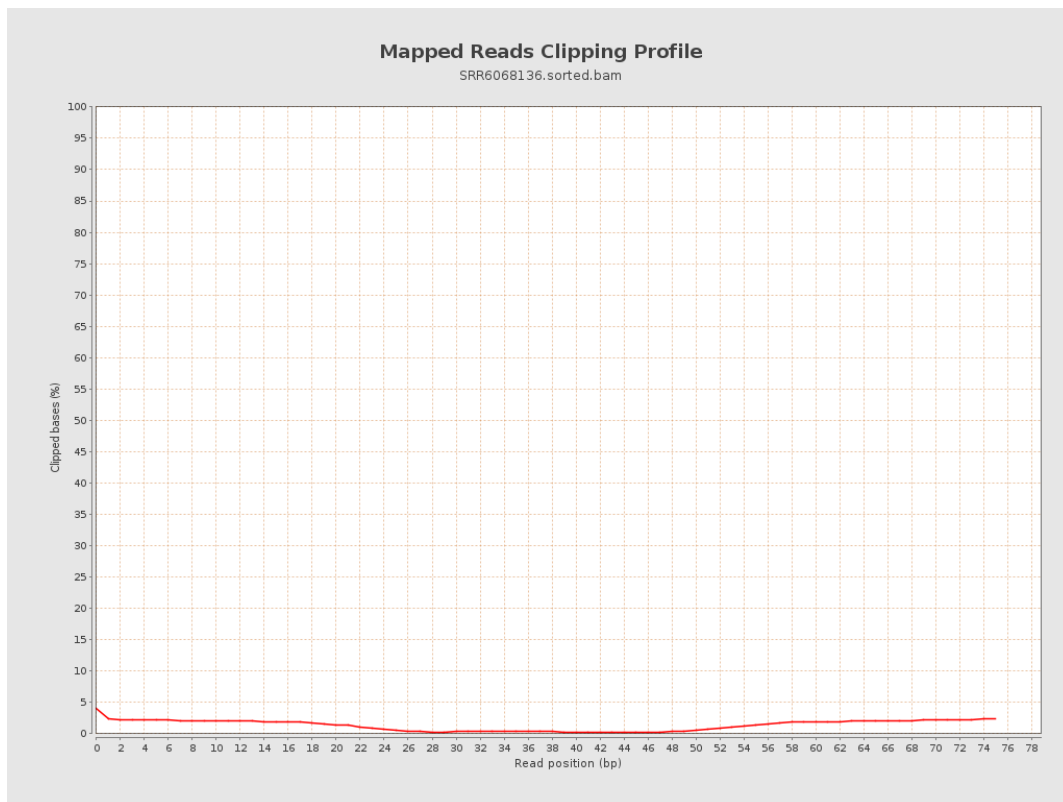
8. Results : Mapped Reads Nucleotide Content



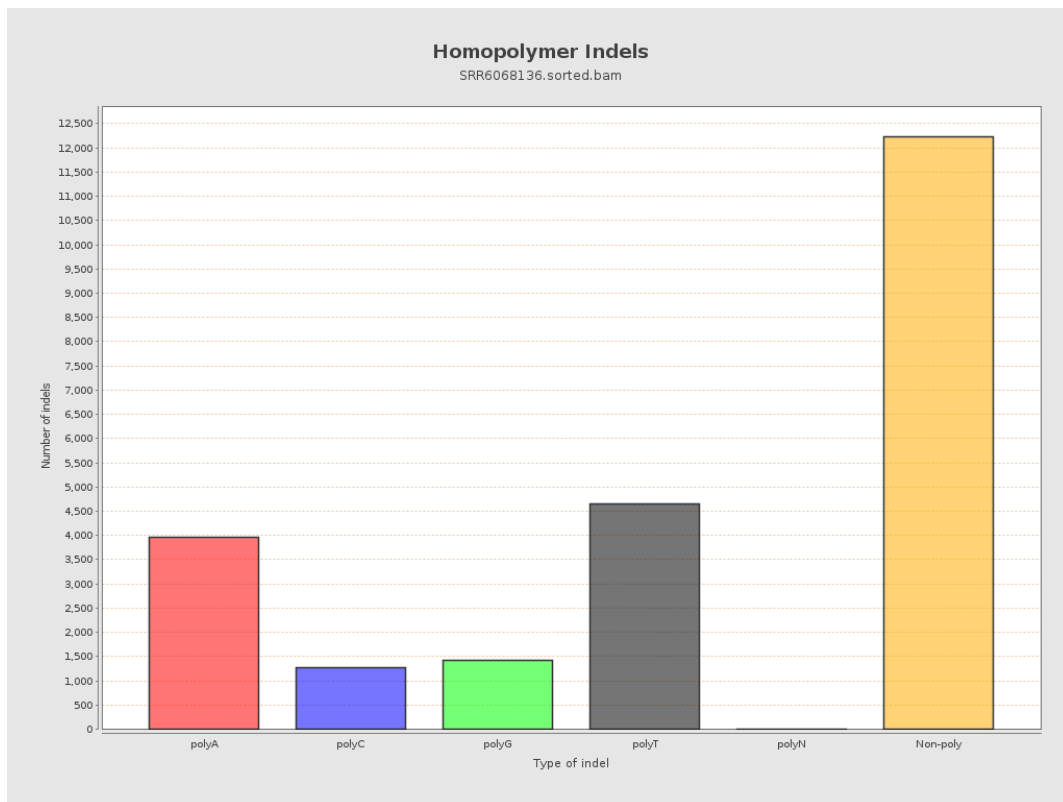
9. Results : Mapped Reads GC-content Distribution



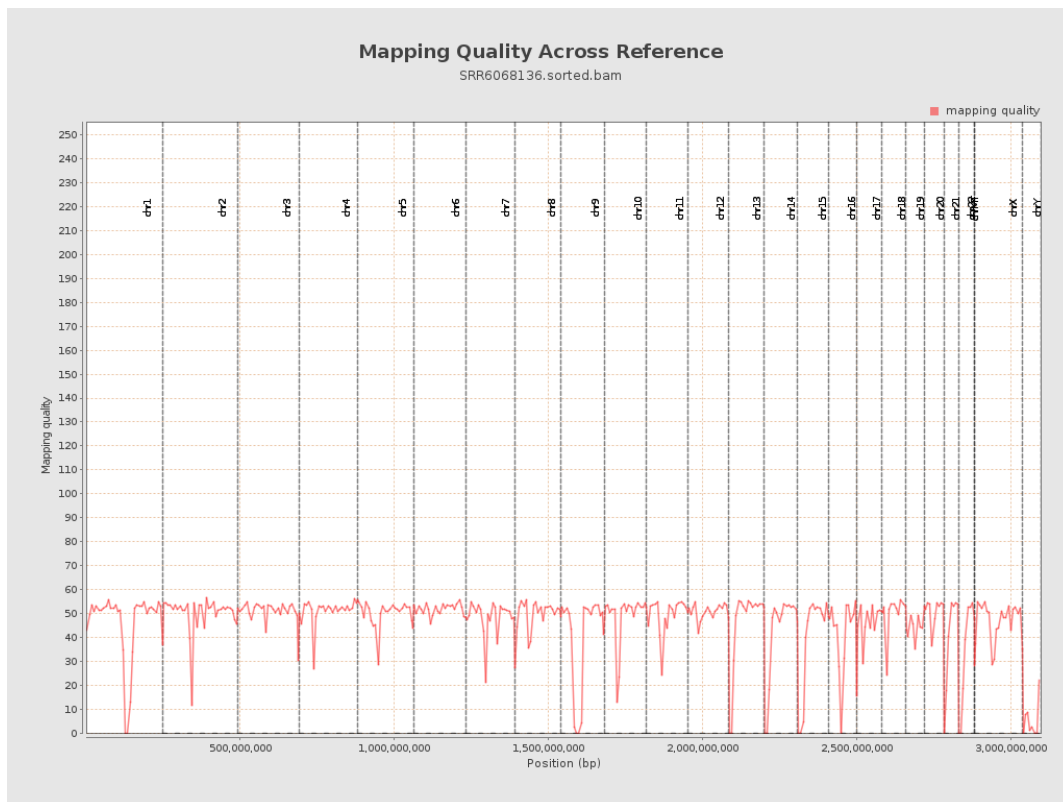
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

