

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 09:52:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237868.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_SRR6237868 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237868.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 09:52:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237868.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,589,999
Mapped reads	1,960,535 / 75.7%
Unmapped reads	629,464 / 24.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,796 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	79,946 / 3.09%
Duplication rate	3%
Clipped reads	1,158,147 / 44.72%

2.2. ACGT Content

Number/percentage of A's	34,132,529 / 27.77%
Number/percentage of C's	22,324,019 / 18.17%
Number/percentage of T's	38,987,807 / 31.72%
Number/percentage of G's	27,339,077 / 22.25%
Number/percentage of N's	110,246 / 0.09%
GC Percentage	40.41%

2.3. Coverage

Mean	0.0397

Standard Deviation	0.3828
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2.4. Mapping Quality

Mean Mapping Quality	45.69
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2.5. Mismatches and indels

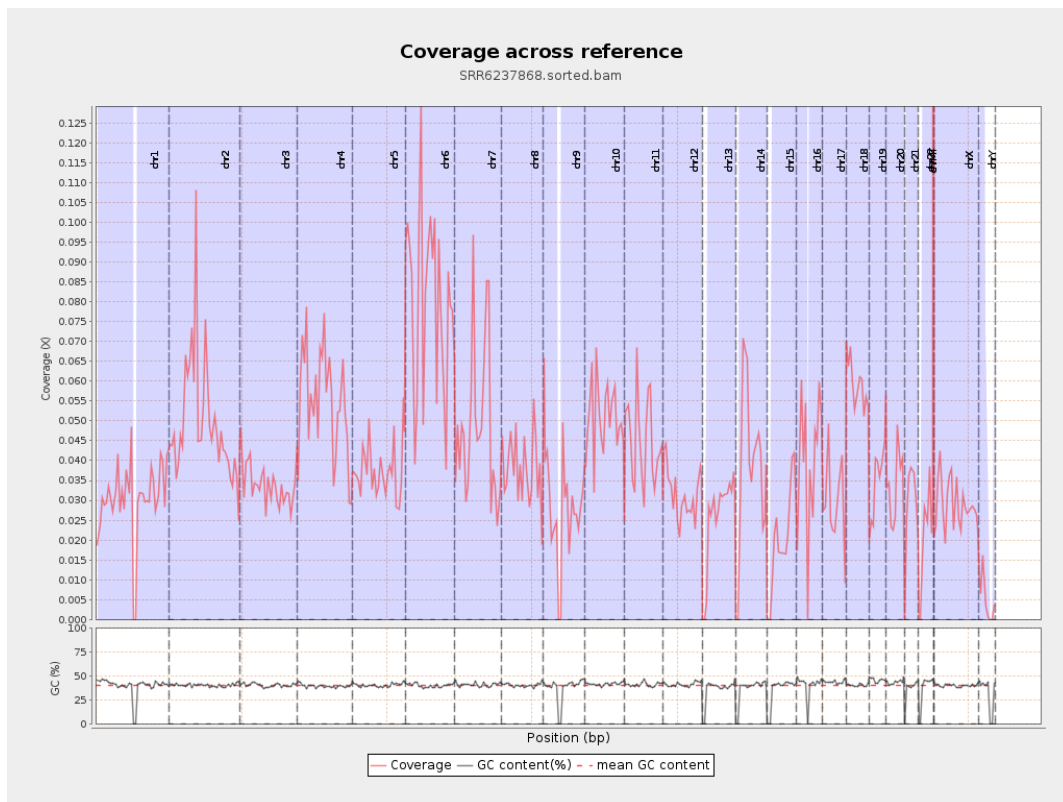
General error rate	0.81%
Mismatches	976,131
Insertions	9,946
Mapped reads with at least one insertion	0.5%
Deletions	29,682
Mapped reads with at least one deletion	1.5%
Homopolymer indels	46.48%

2.6. Chromosome stats

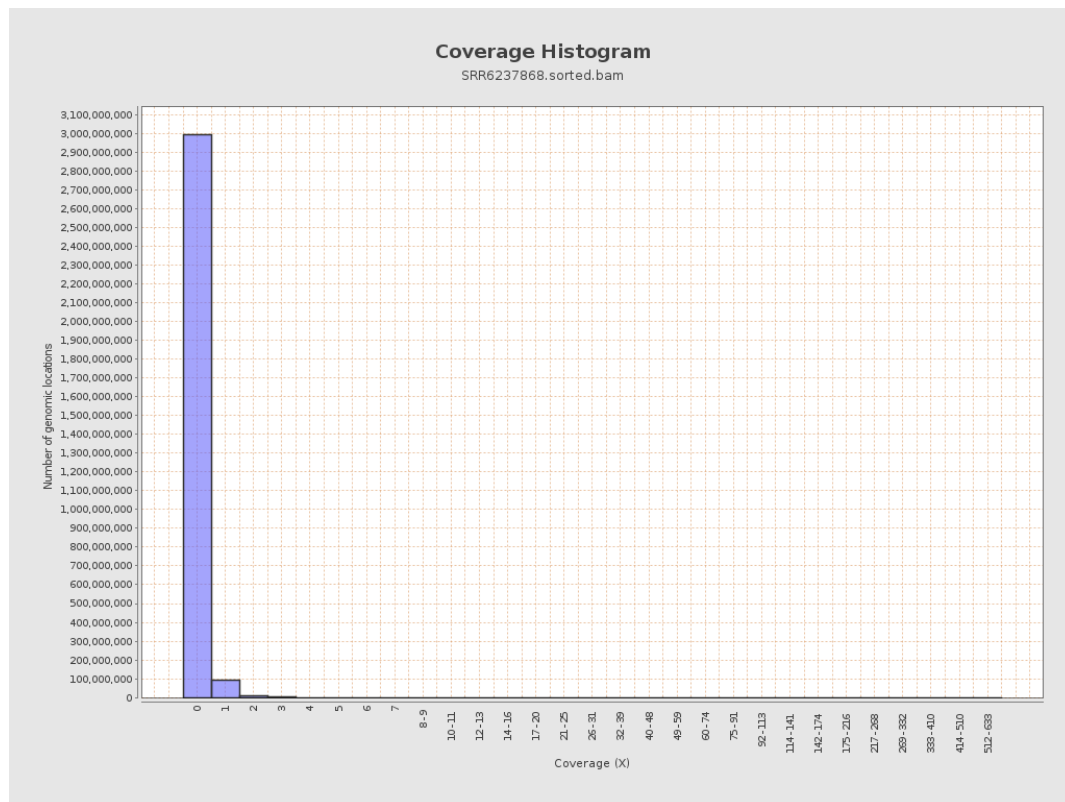
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7562622	0.0303	0.4545
chr2	243199373	12156786	0.05	0.5175
chr3	198022430	6741736	0.034	0.2098
chr4	191154276	10471127	0.0548	0.2703
chr5	180915260	6811718	0.0377	0.2202
chr6	171115067	13807853	0.0807	0.5559
chr7	159138663	7710008	0.0484	0.6824

chr8	146364022	5583843	0.0382	0.3818
chr9	141213431	3823643	0.0271	0.3752
chr10	135534747	6889847	0.0508	0.3545
chr11	135006516	6013241	0.0445	0.3824
chr12	133851895	4194486	0.0313	0.2064
chr13	115169878	2935255	0.0255	0.1778
chr14	107349540	4116569	0.0383	0.2456
chr15	102531392	2087442	0.0204	0.1613
chr16	90354753	3674639	0.0407	0.2535
chr17	81195210	2322883	0.0286	0.3157
chr18	78077248	4625652	0.0592	0.7385
chr19	59128983	2098065	0.0355	0.3523
chr20	63025520	2080846	0.033	0.2138
chr21	48129895	1392922	0.0289	0.2087
chr22	51304566	1048639	0.0204	0.1584
chrMT	16571	17758	1.0716	1.3887
chrX	155270560	4488642	0.0289	0.2604
chrY	59373566	284964	0.0048	0.1111

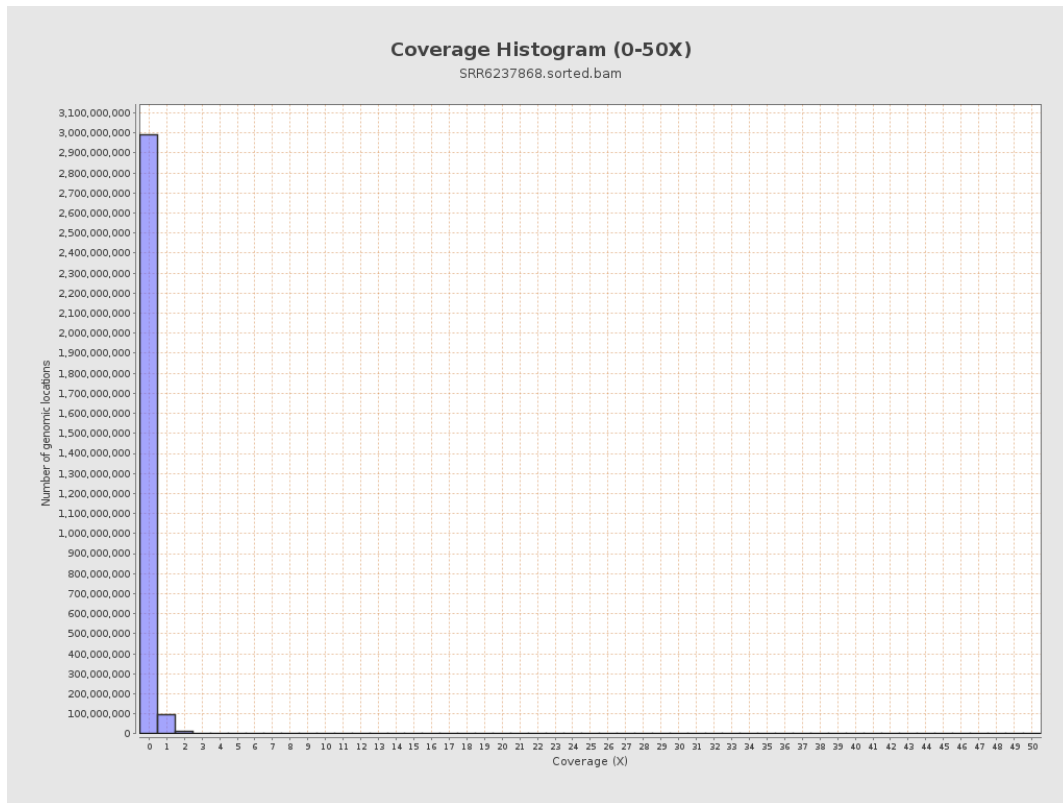
3. Results : Coverage across reference



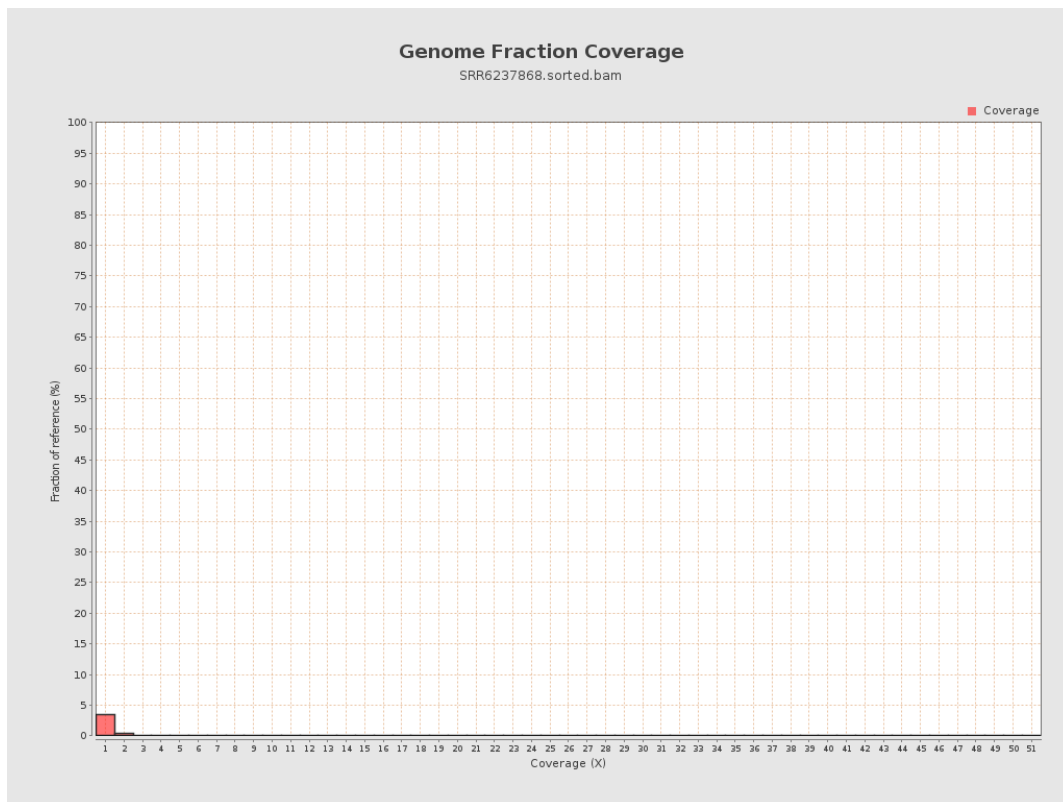
4. Results : Coverage Histogram



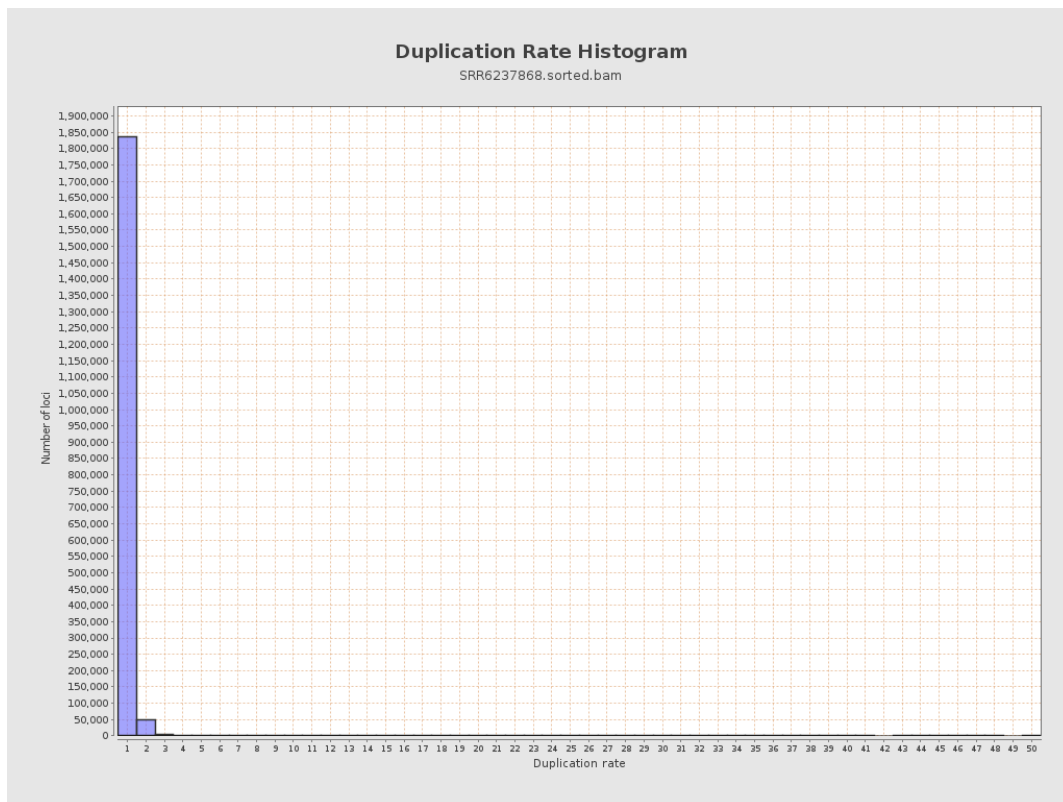
5. Results : Coverage Histogram (0-50X)



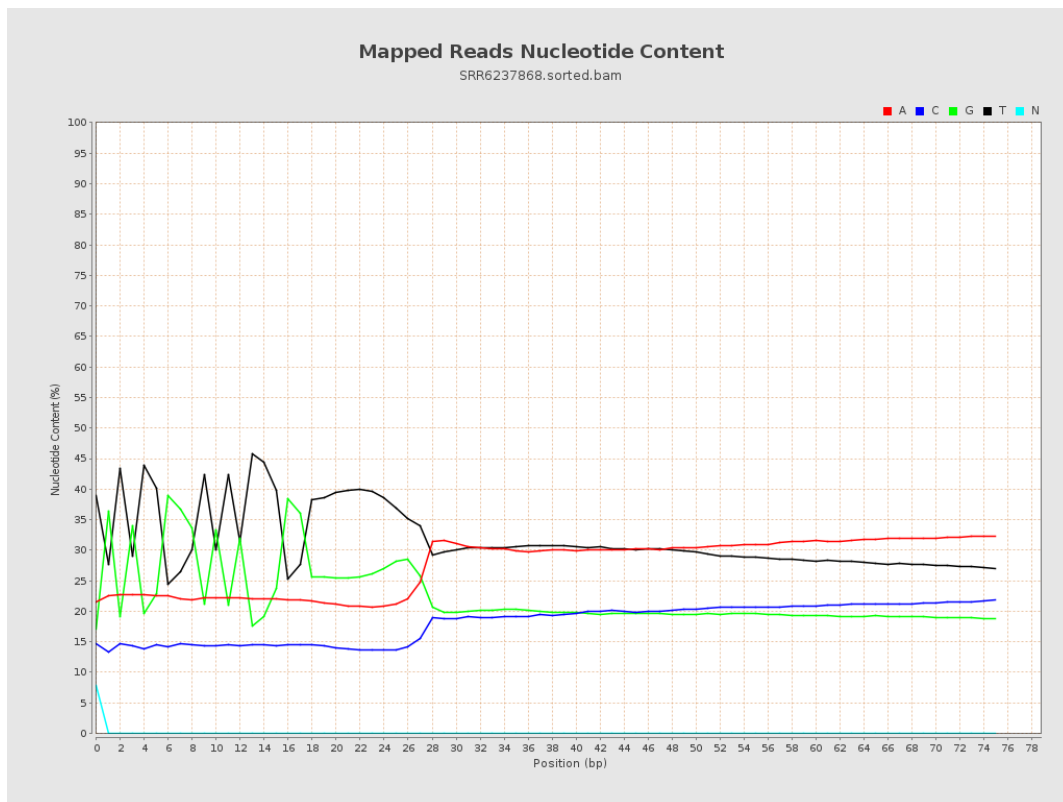
6. Results : Genome Fraction Coverage



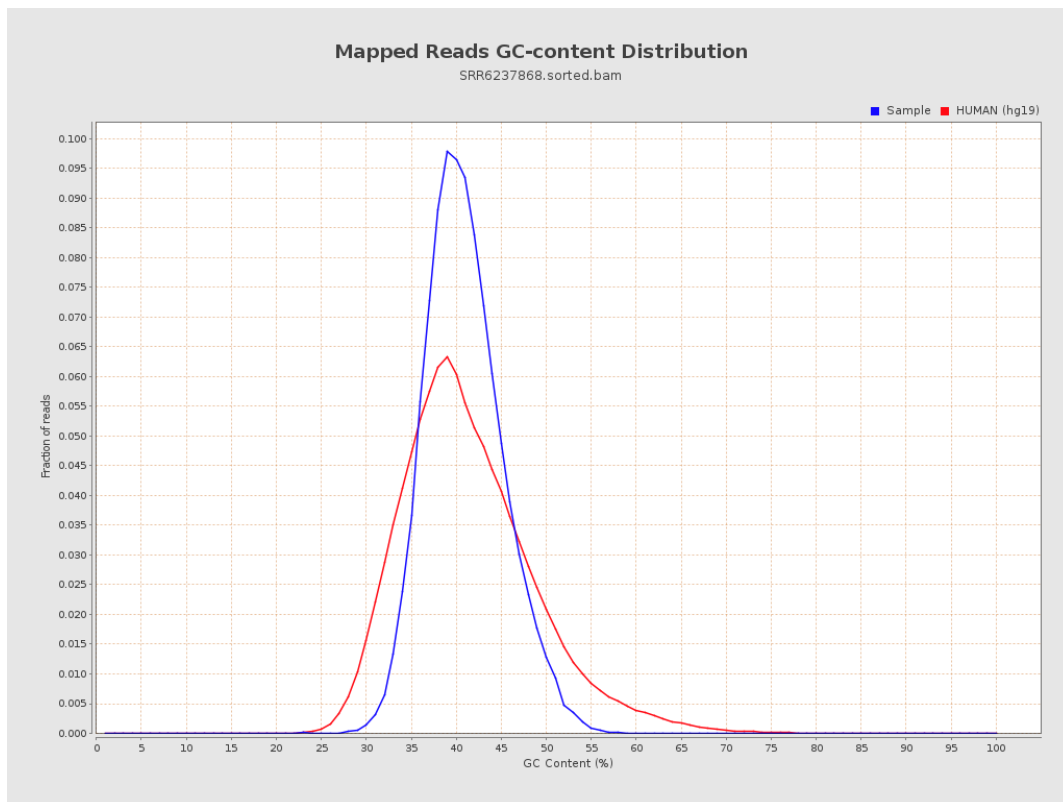
7. Results : Duplication Rate Histogram



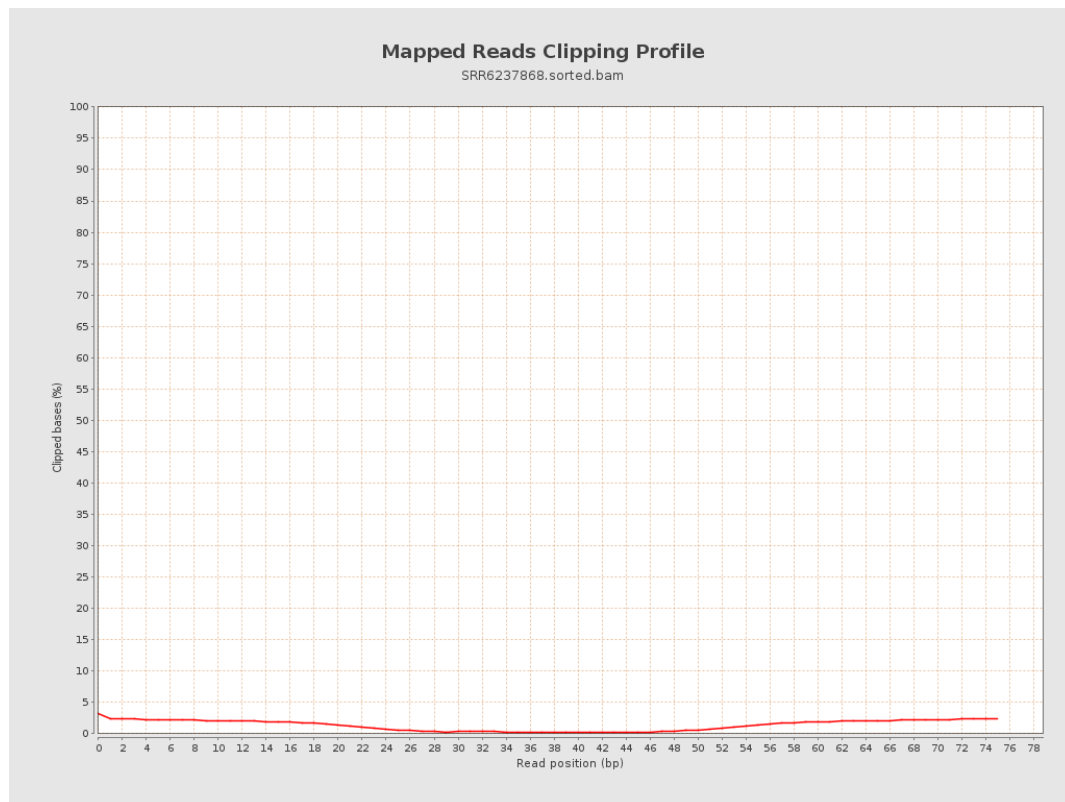
8. Results : Mapped Reads Nucleotide Content



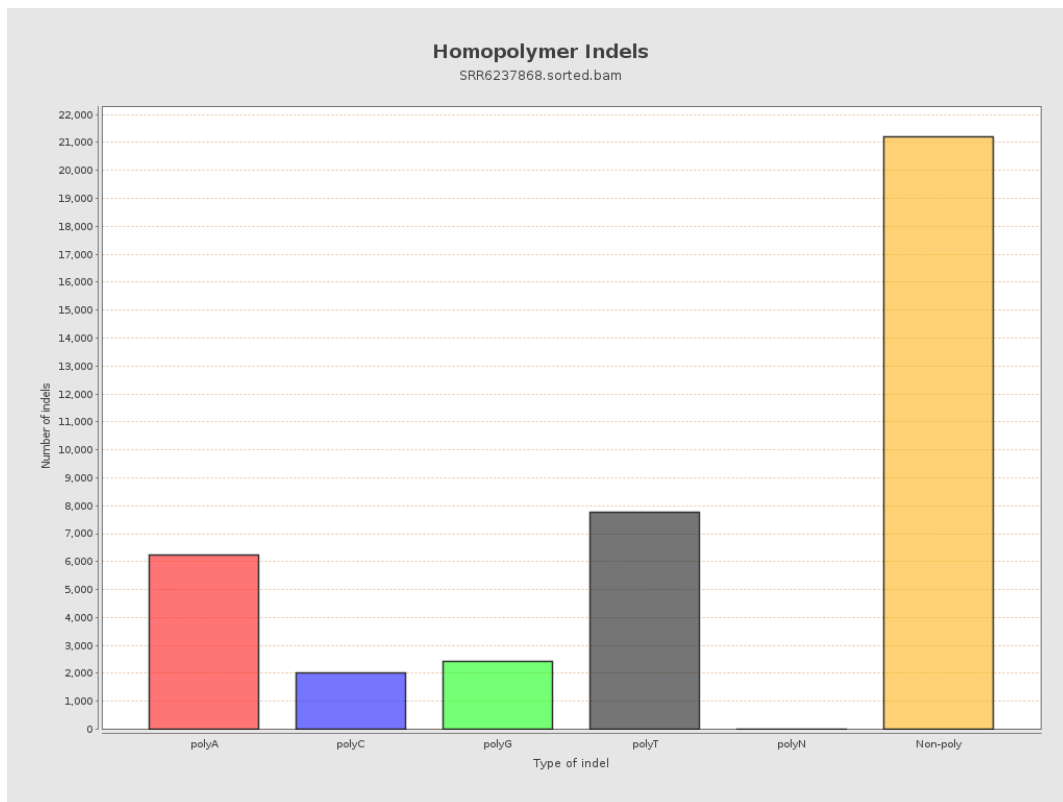
9. Results : Mapped Reads GC-content Distribution



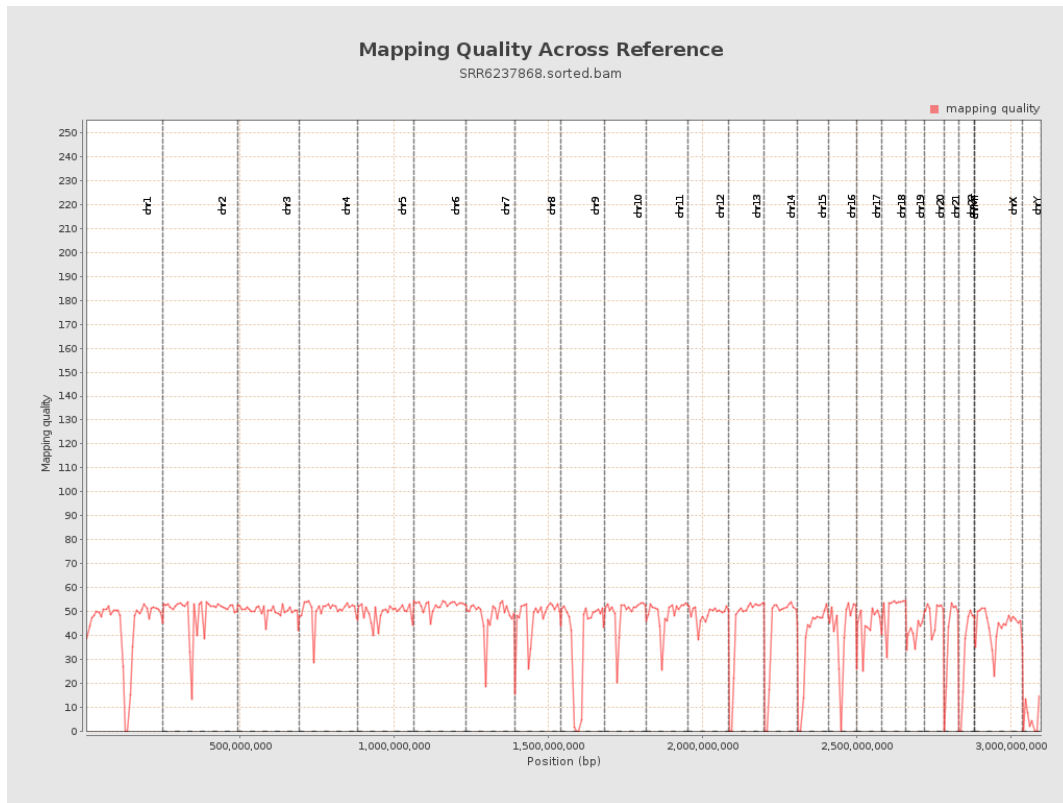
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

