

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 09:26:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237859.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_SRR6237859 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237859.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 09:26:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237859.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,583,431
Mapped reads	2,259,007 / 87.44%
Unmapped reads	324,424 / 12.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,906 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	72,514 / 2.81%
Duplication rate	2.33%
Clipped reads	1,139,803 / 44.12%

2.2. ACGT Content

Number/percentage of A's	41,659,569 / 28.44%
Number/percentage of C's	26,590,717 / 18.16%
Number/percentage of T's	45,896,881 / 31.34%
Number/percentage of G's	32,177,426 / 21.97%
Number/percentage of N's	131,980 / 0.09%
GC Percentage	40.13%

2.3. Coverage

Mean	0.0473

Standard Deviation	0.3897
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2.4. Mapping Quality

Mean Mapping Quality	45.45
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2.5. Mismatches and indels

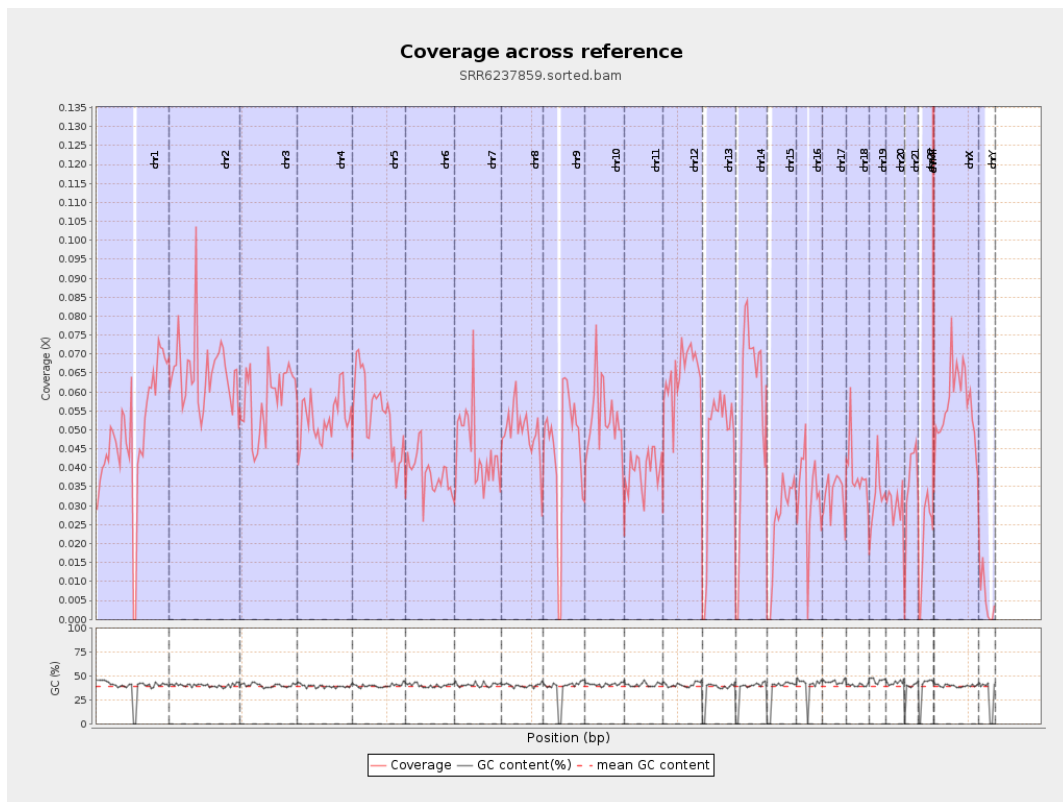
General error rate	0.75%
Mismatches	1,076,317
Insertions	11,966
Mapped reads with at least one insertion	0.53%
Deletions	32,369
Mapped reads with at least one deletion	1.42%
Homopolymer indels	48.21%

2.6. Chromosome stats

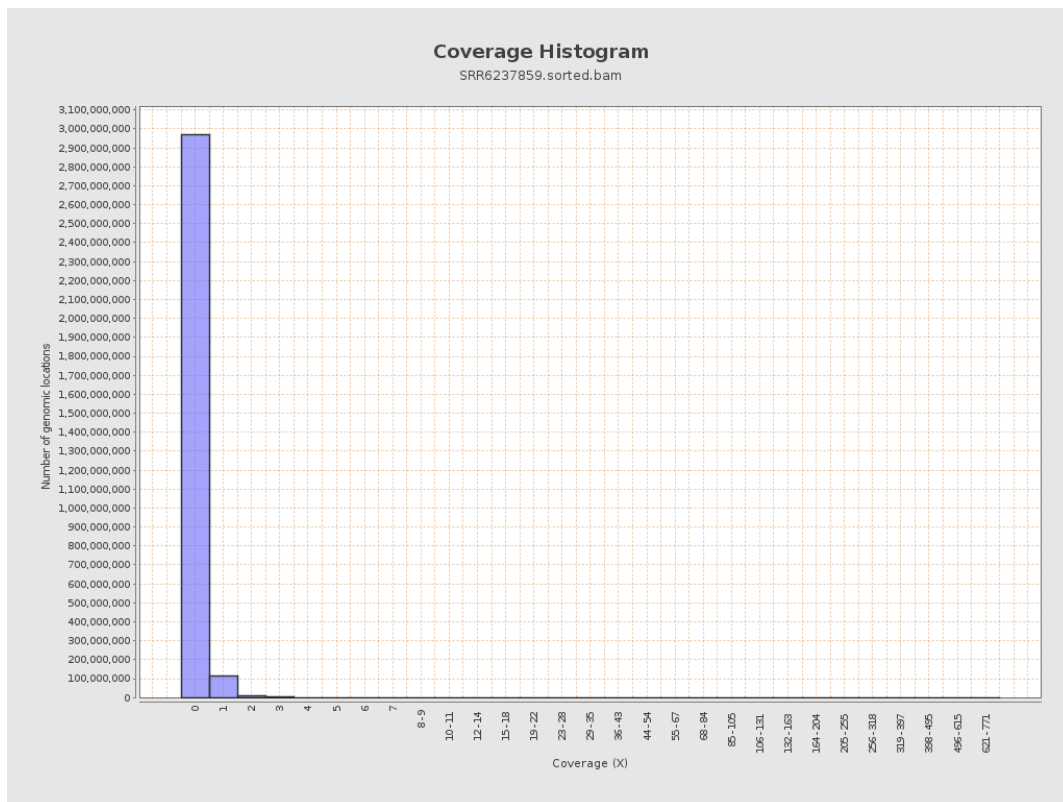
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12227374	0.0491	0.5512
chr2	243199373	15869668	0.0653	0.4872
chr3	198022430	11547889	0.0583	0.2667
chr4	191154276	10139193	0.053	0.2664
chr5	180915260	9886996	0.0546	0.2611
chr6	171115067	6537742	0.0382	0.2522
chr7	159138663	7144665	0.0449	0.5467

chr8	146364022	7249314	0.0495	0.5452
chr9	141213431	6429139	0.0455	0.4357
chr10	135534747	7203632	0.0531	0.3853
chr11	135006516	5310155	0.0393	0.359
chr12	133851895	8666482	0.0647	0.2923
chr13	115169878	5187240	0.045	0.2314
chr14	107349540	6057807	0.0564	0.328
chr15	102531392	2611388	0.0255	0.1756
chr16	90354753	2970986	0.0329	0.255
chr17	81195210	2660164	0.0328	0.2445
chr18	78077248	3043298	0.039	0.824
chr19	59128983	1937806	0.0328	0.4169
chr20	63025520	1895146	0.0301	0.2083
chr21	48129895	1707528	0.0355	0.2373
chr22	51304566	1066018	0.0208	0.156
chrMT	16571	51644	3.1165	2.5884
chrX	155270560	8777907	0.0565	0.3187
chrY	59373566	331074	0.0056	0.1172

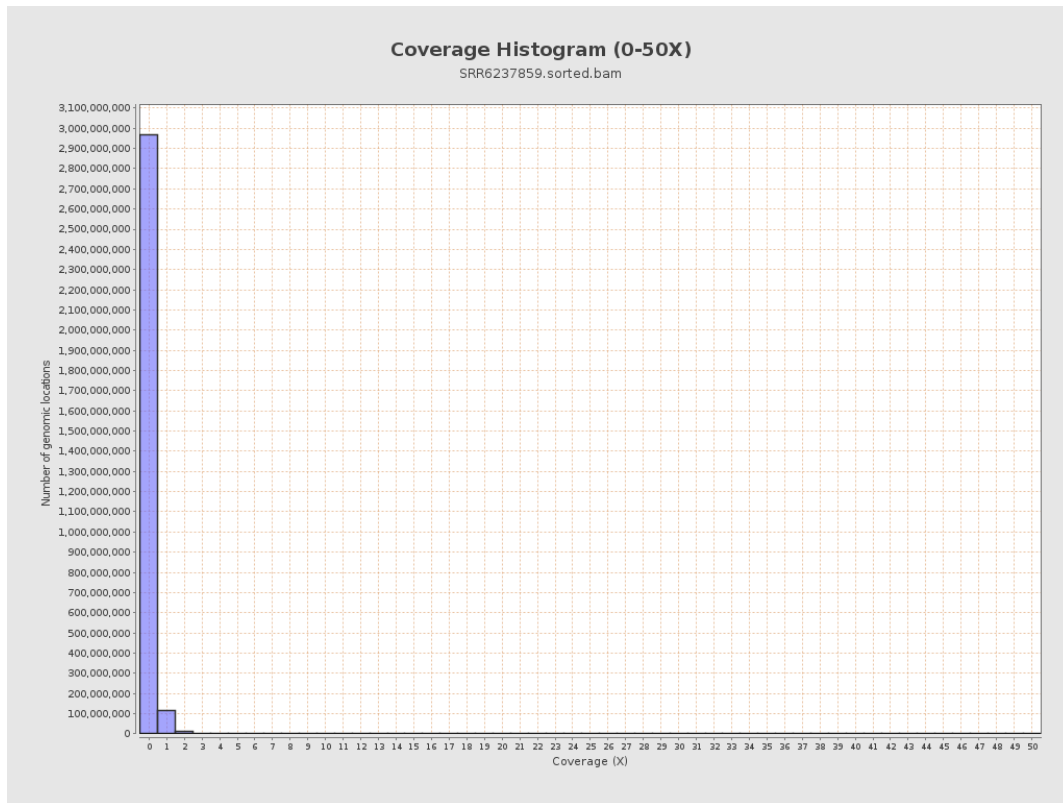
3. Results : Coverage across reference



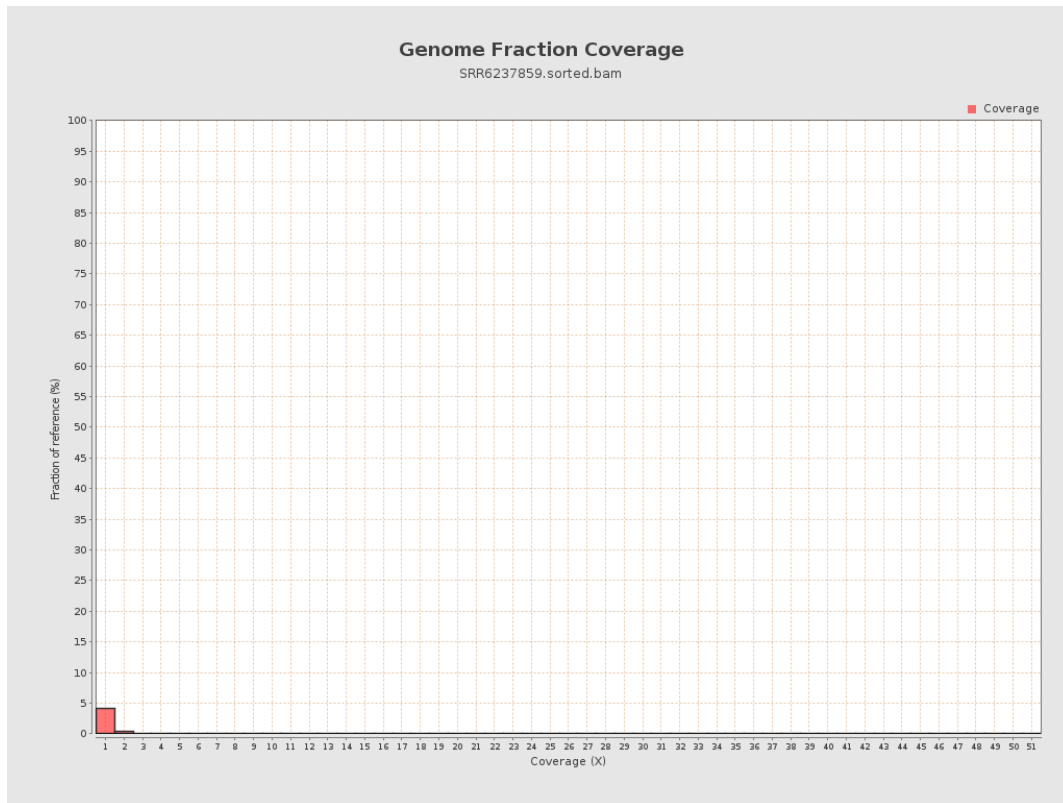
4. Results : Coverage Histogram



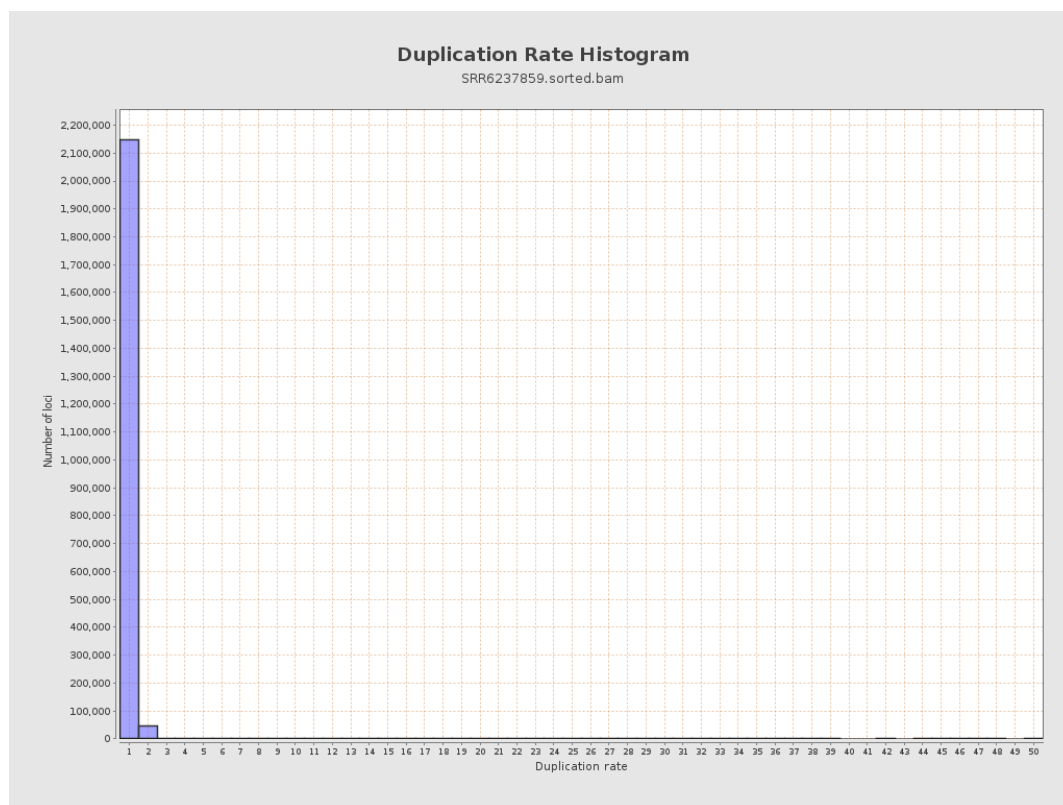
5. Results : Coverage Histogram (0-50X)



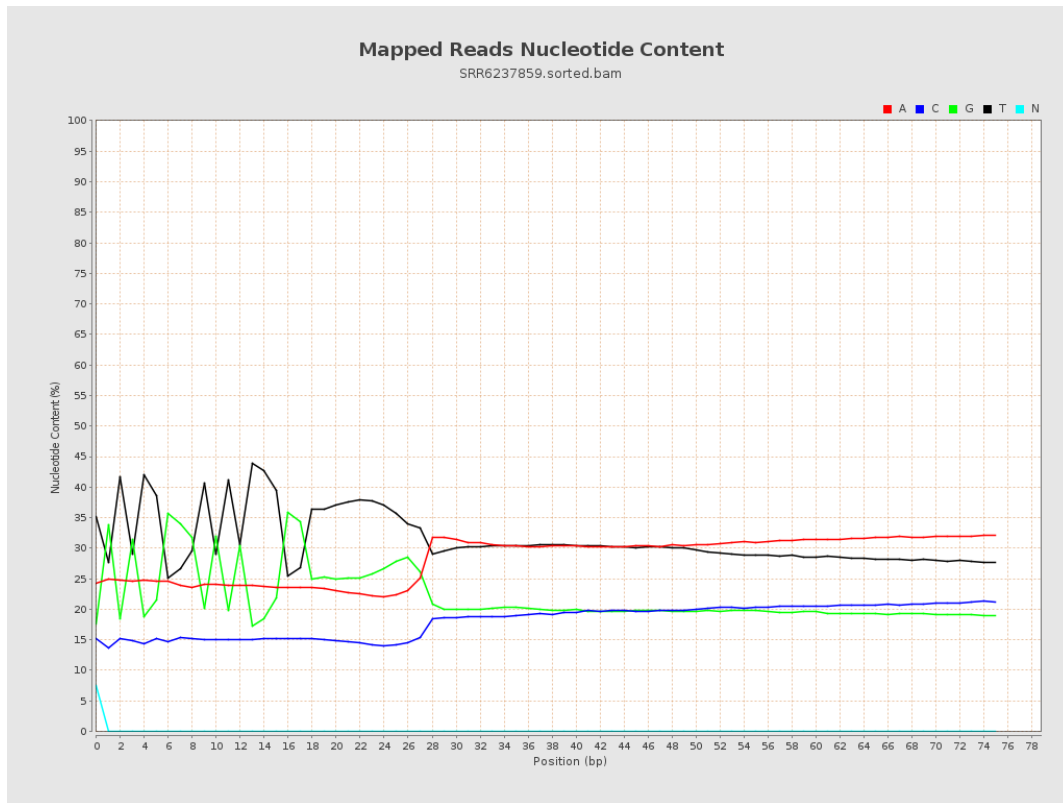
6. Results : Genome Fraction Coverage



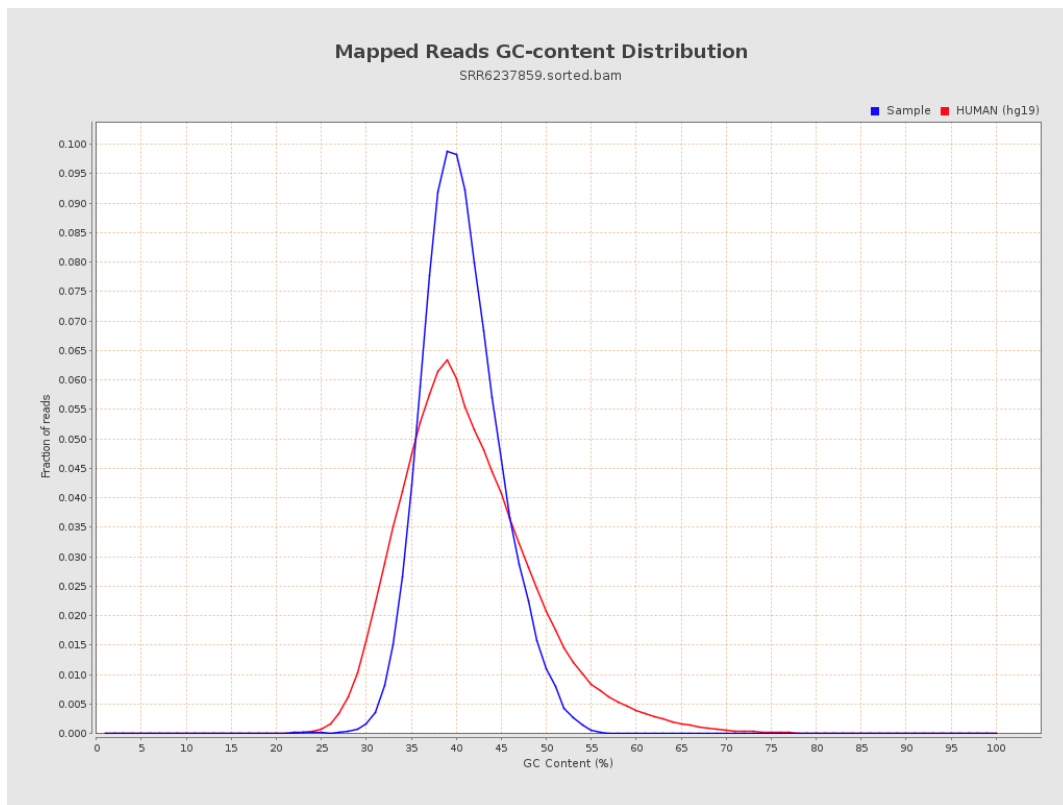
7. Results : Duplication Rate Histogram



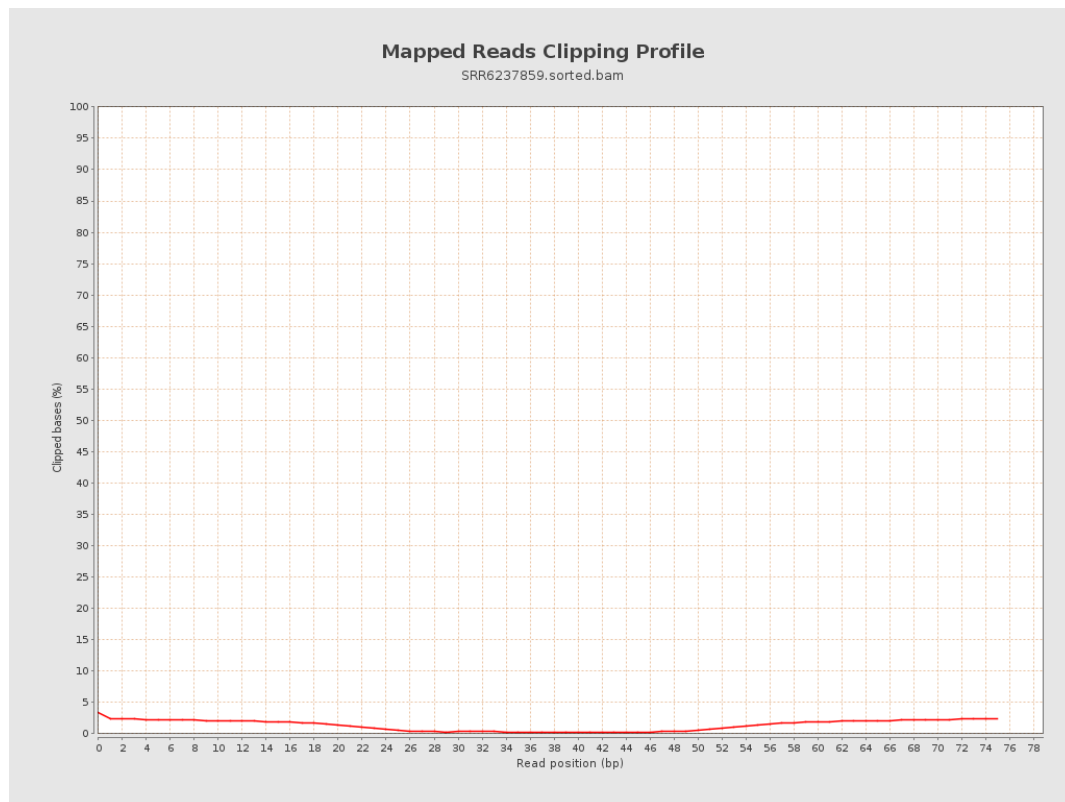
8. Results : Mapped Reads Nucleotide Content



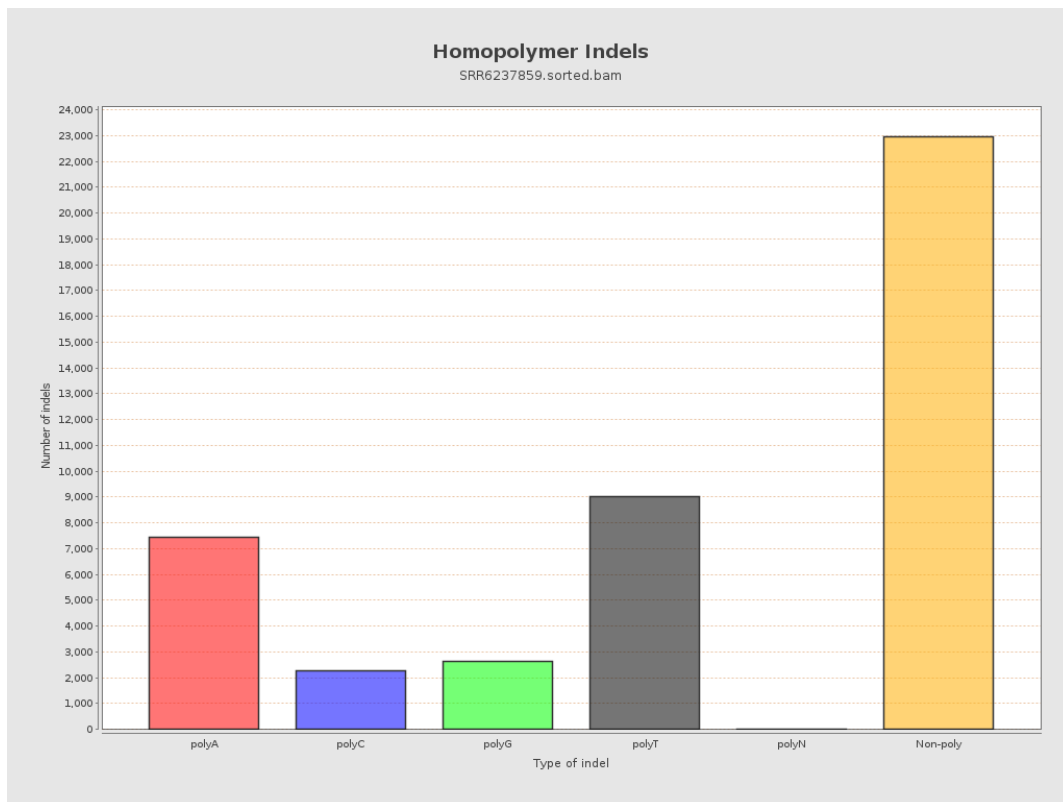
9. Results : Mapped Reads GC-content Distribution



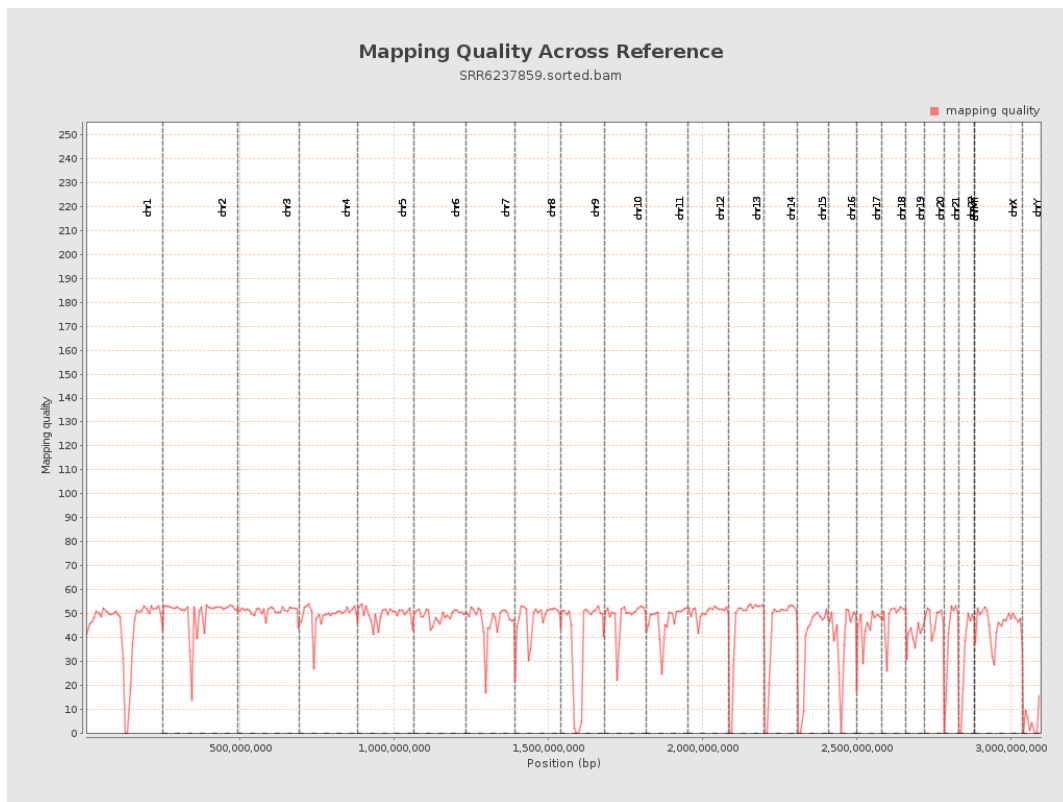
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

