

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 12:44:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234057.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_SRR6234057 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234057.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 12:44:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,497,640
Mapped reads	4,180,777 / 92.95%
Unmapped reads	316,863 / 7.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,968 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	397,024 / 8.83%
Duplication rate	7.53%
Clipped reads	2,551,022 / 56.72%

2.2. ACGT Content

Number/percentage of A's	64,363,235 / 24.63%
Number/percentage of C's	47,232,861 / 18.07%
Number/percentage of T's	85,060,852 / 32.55%
Number/percentage of G's	64,678,108 / 24.75%
Number/percentage of N's	23,337 / 0.01%
GC Percentage	42.82%

2.3. Coverage

Mean	0.0845

Standard Deviation	0.9094
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2.4. Mapping Quality

Mean Mapping Quality	42.06
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2.5. Mismatches and indels

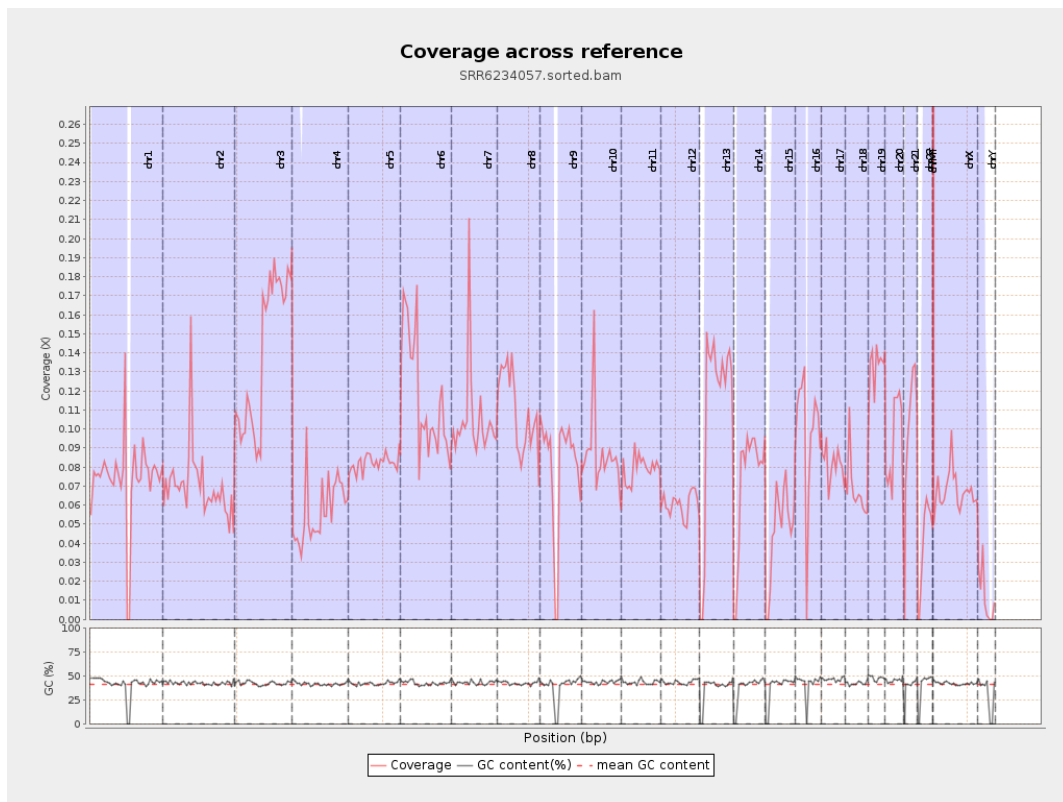
General error rate	0.68%
Mismatches	1,730,072
Insertions	20,722
Mapped reads with at least one insertion	0.49%
Deletions	73,474
Mapped reads with at least one deletion	1.74%
Homopolymer indels	43.23%

2.6. Chromosome stats

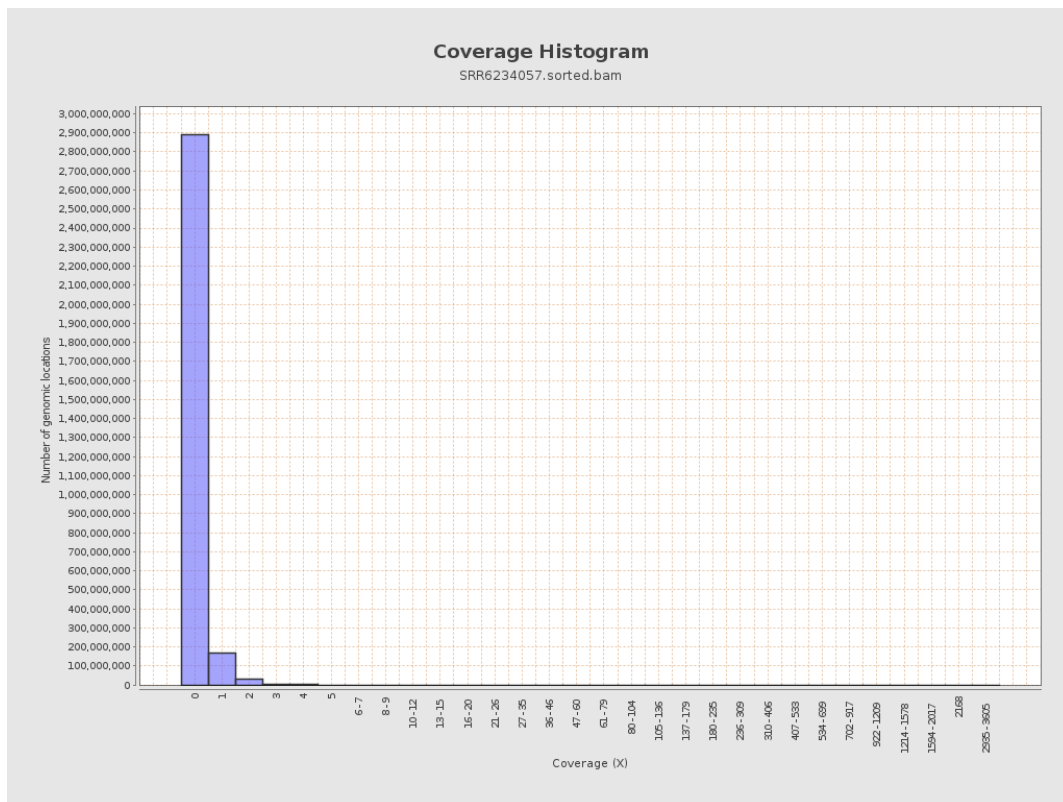
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18363969	0.0737	1.5459
chr2	243199373	17119519	0.0704	1.7163
chr3	198022430	27442875	0.1386	0.4718
chr4	191154276	10939121	0.0572	0.3633
chr5	180915260	14898238	0.0823	0.3672
chr6	171115067	20053035	0.1172	0.8534
chr7	159138663	16730226	0.1051	1.4601

chr8	146364022	15884020	0.1085	0.7141
chr9	141213431	11341168	0.0803	0.6209
chr10	135534747	11757804	0.0868	0.7608
chr11	135006516	10612047	0.0786	0.5787
chr12	133851895	8160533	0.061	0.3278
chr13	115169878	12917141	0.1122	0.491
chr14	107349540	7869608	0.0733	0.4381
chr15	102531392	4680231	0.0456	0.3549
chr16	90354753	8738479	0.0967	0.4868
chr17	81195210	6662238	0.0821	0.4241
chr18	78077248	5350947	0.0685	1.5883
chr19	59128983	7860881	0.1329	1.0465
chr20	63025520	5884356	0.0934	0.4428
chr21	48129895	4800186	0.0997	0.434
chr22	51304566	2071521	0.0404	0.2447
chrMT	16571	142366	8.5913	8.682
chrX	155270560	10492982	0.0676	0.4398
chrY	59373566	708826	0.0119	0.2978

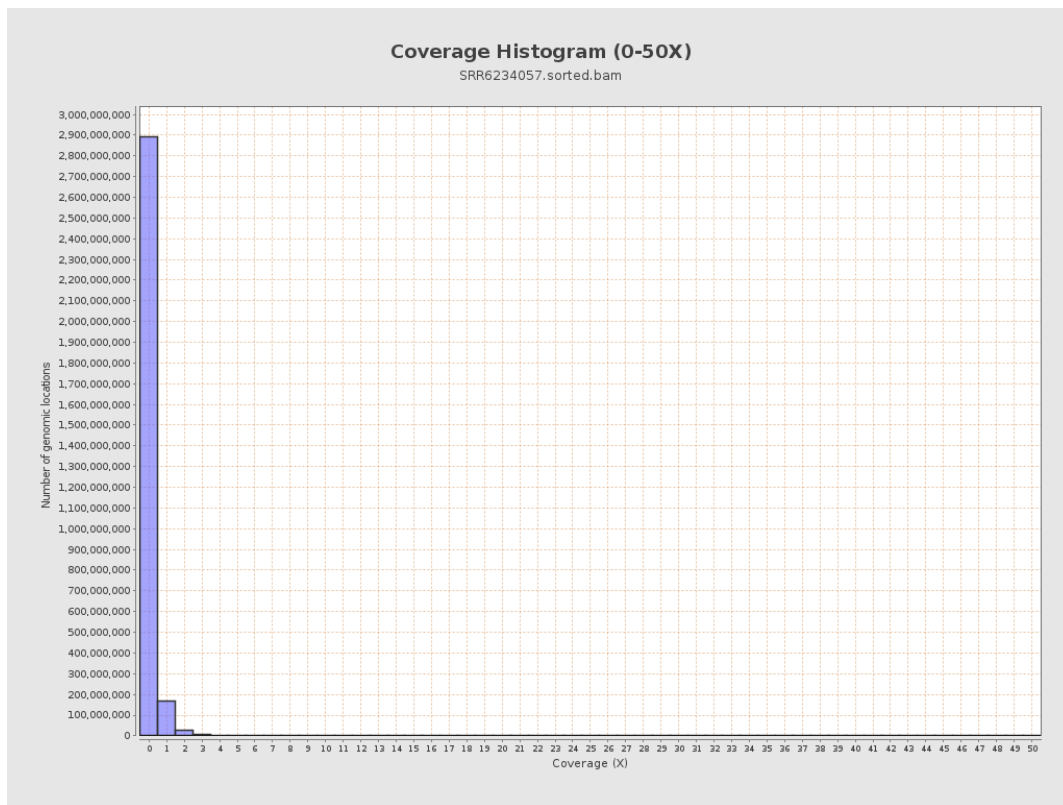
3. Results : Coverage across reference



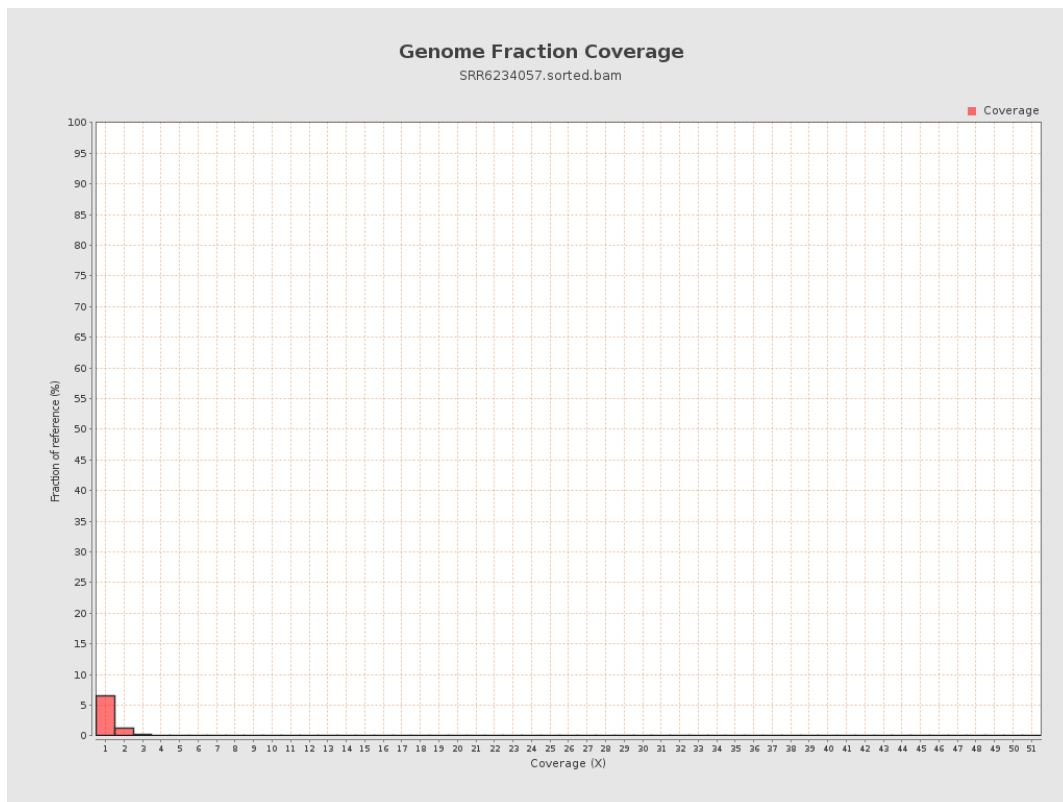
4. Results : Coverage Histogram



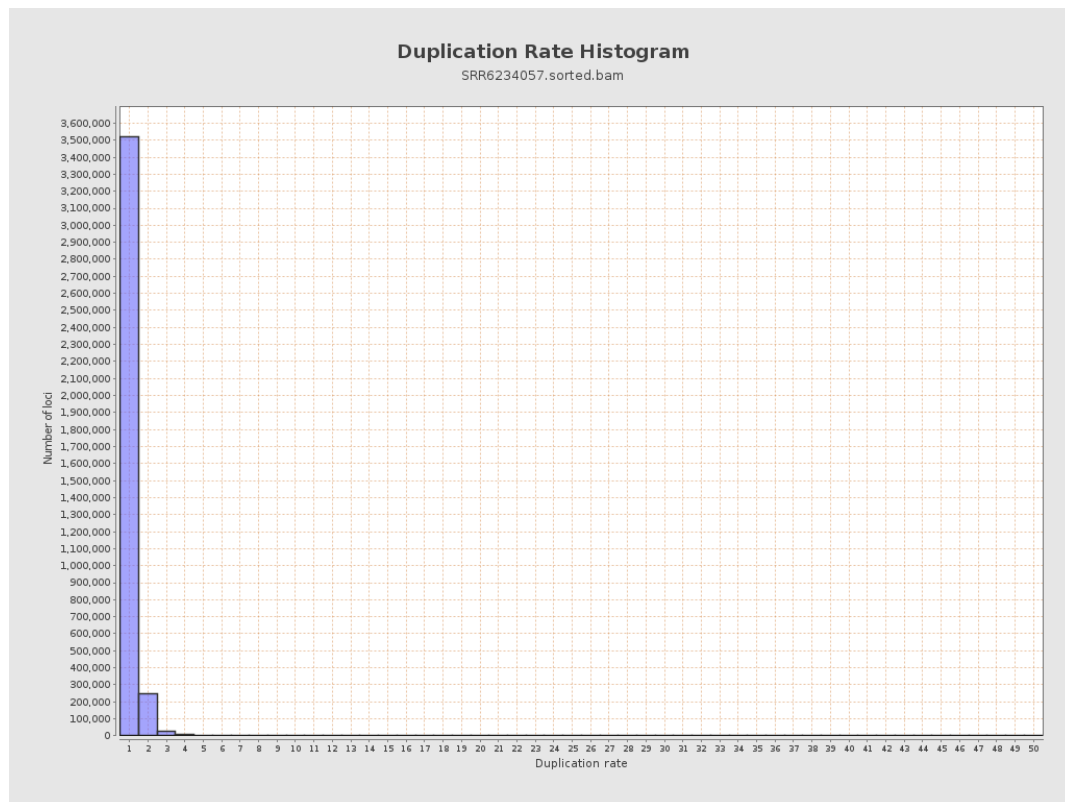
5. Results : Coverage Histogram (0-50X)



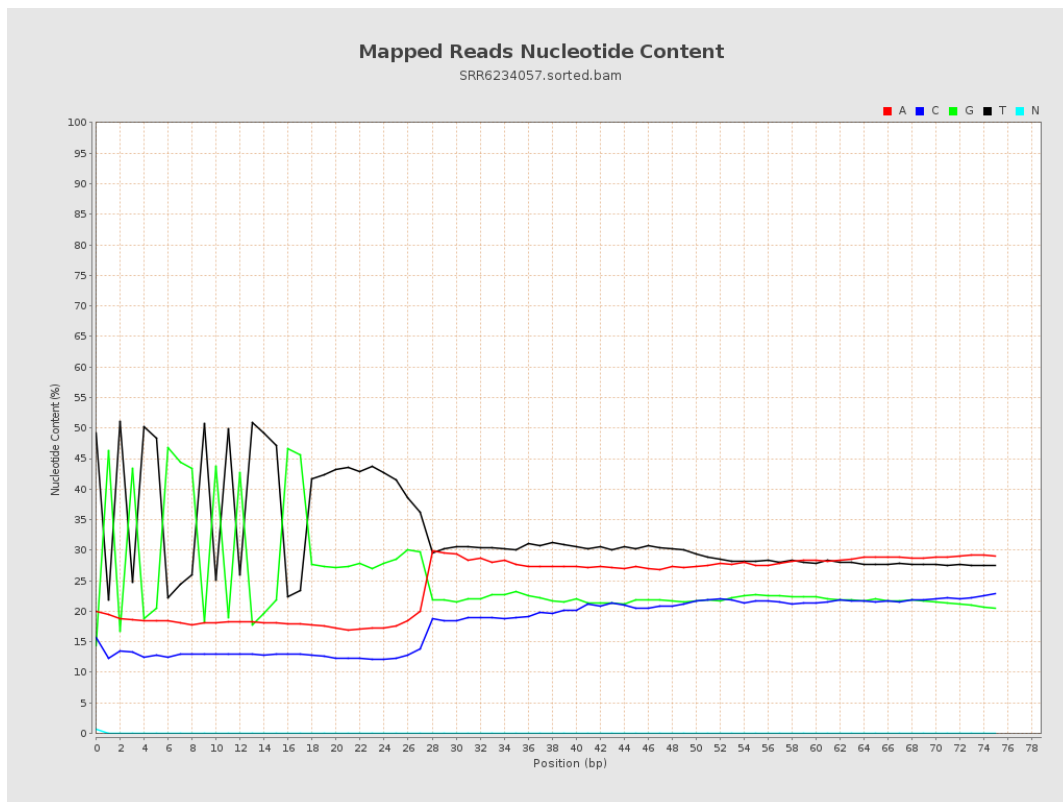
6. Results : Genome Fraction Coverage



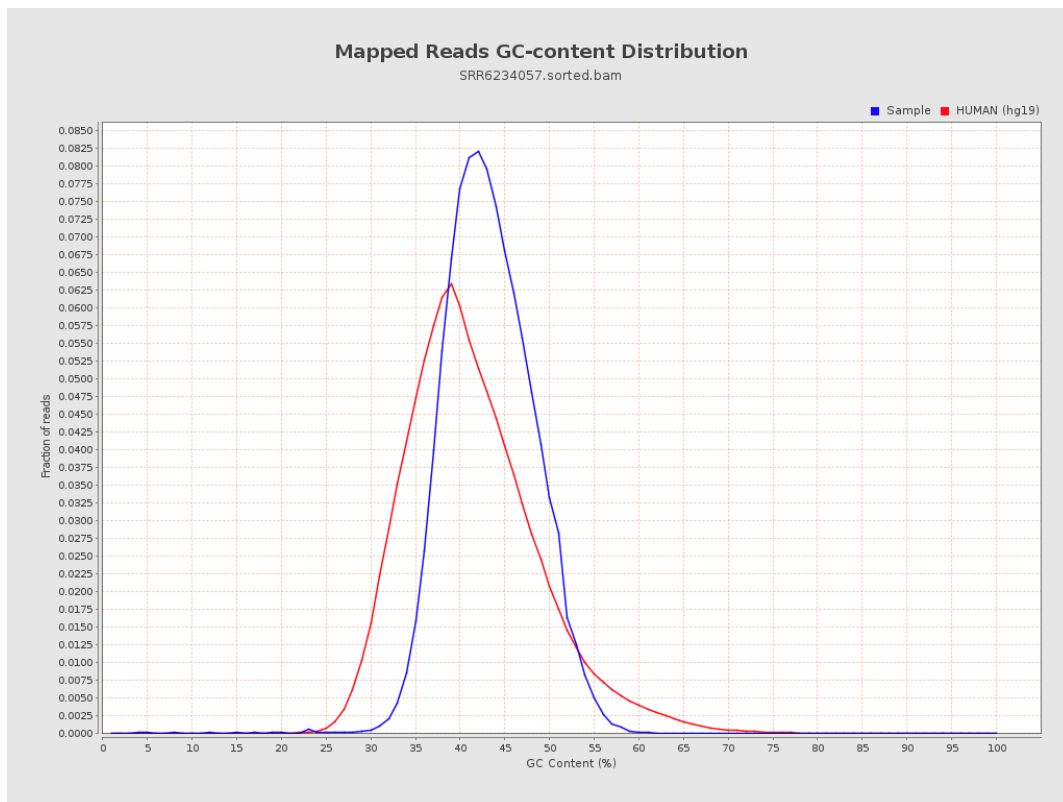
7. Results : Duplication Rate Histogram



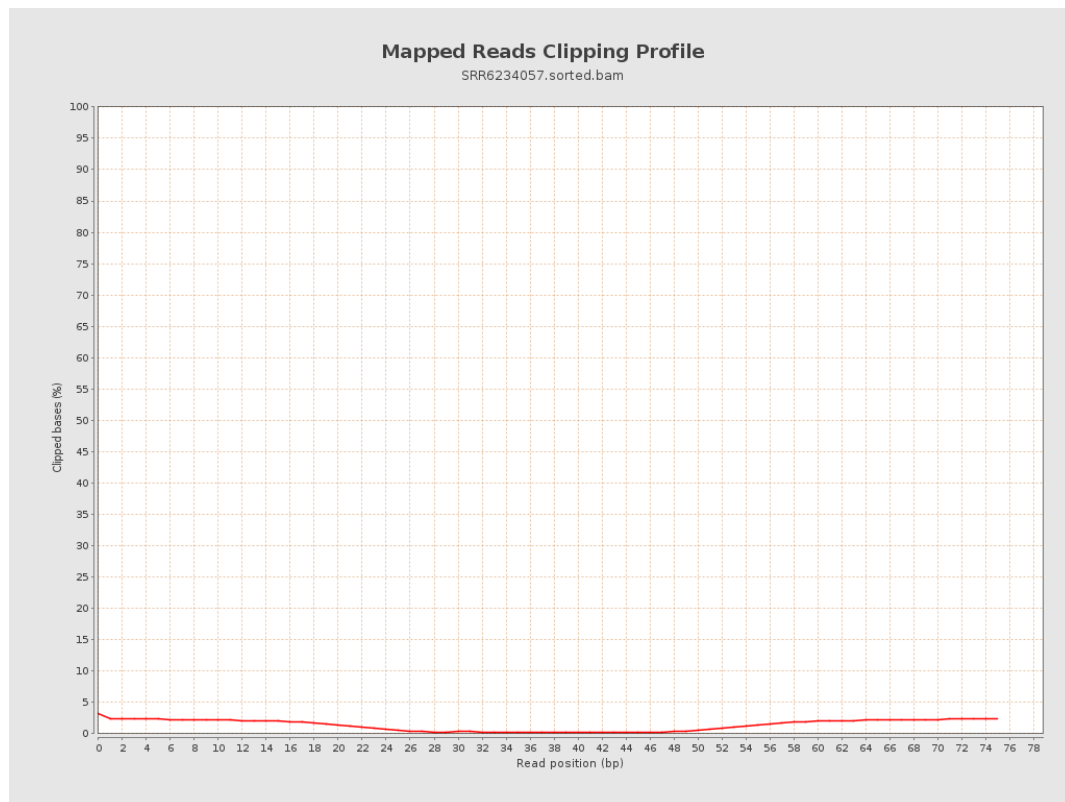
8. Results : Mapped Reads Nucleotide Content



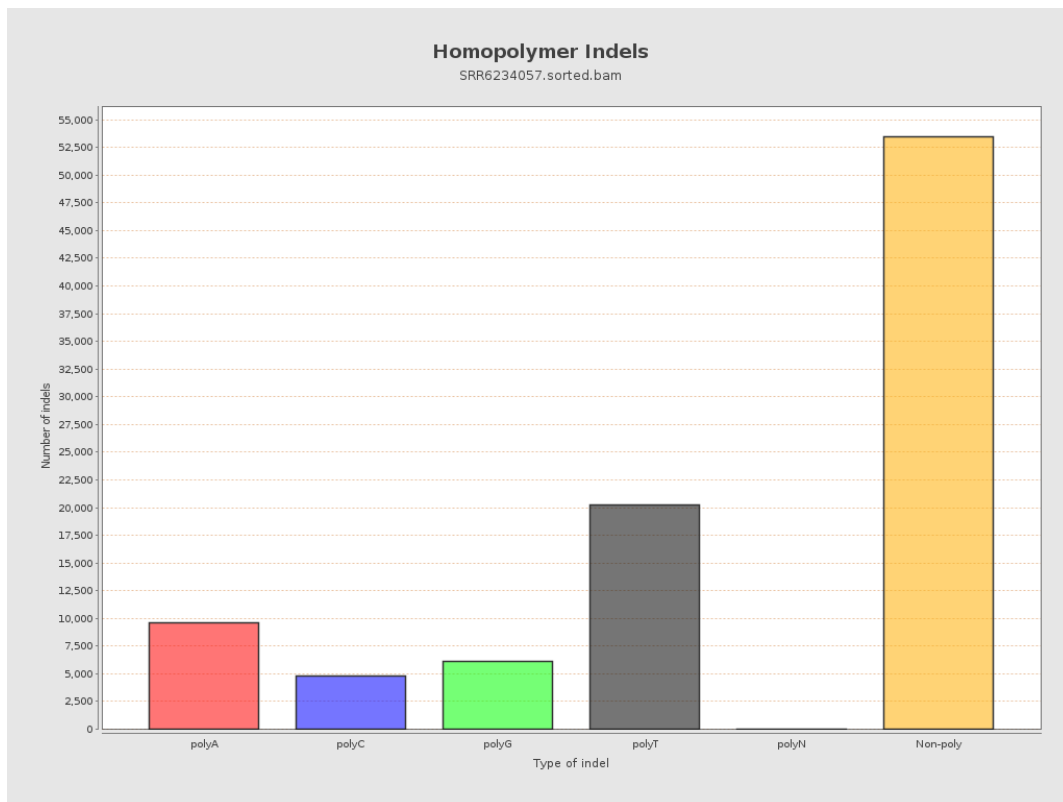
9. Results : Mapped Reads GC-content Distribution



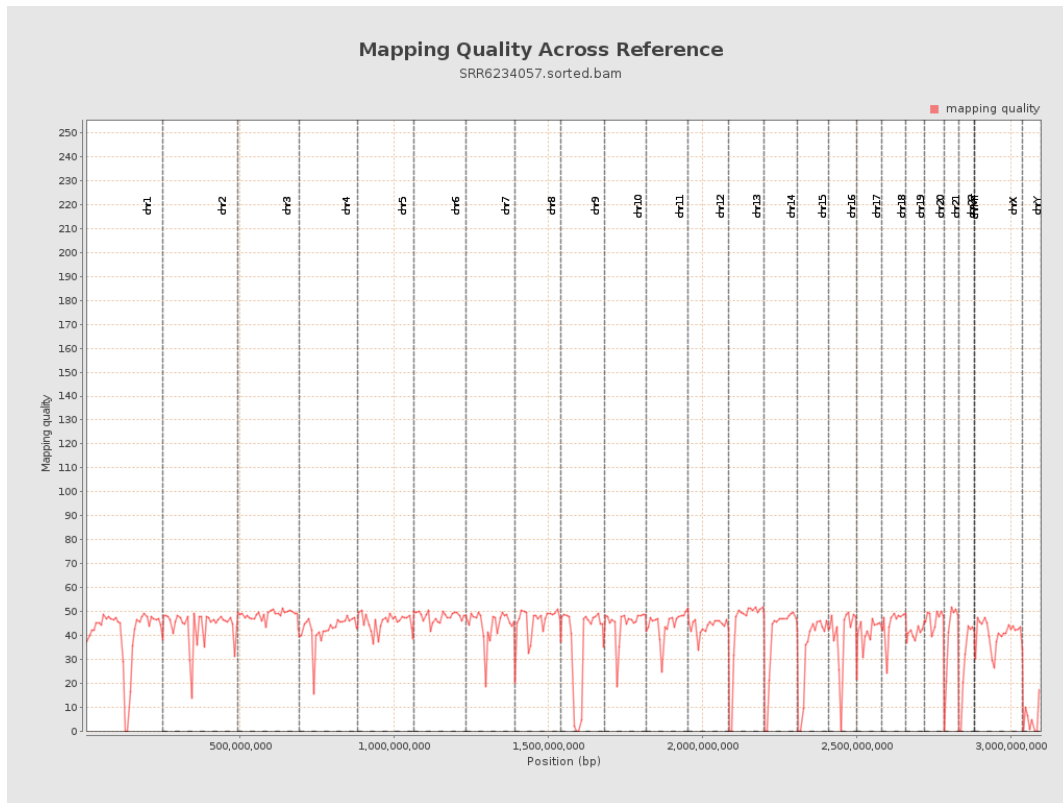
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

