

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:13:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525057.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_SRR10525057 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525057.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:13:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,152,567
Mapped reads	1,070,576 / 92.89%
Unmapped reads	81,991 / 7.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,207 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	43,438 / 3.77%
Duplication rate	3.39%
Clipped reads	1,075,137 / 93.28%

2.2. ACGT Content

Number/percentage of A's	17,047,975 / 26.41%
Number/percentage of C's	12,665,233 / 19.62%
Number/percentage of T's	19,667,799 / 30.47%
Number/percentage of G's	15,153,450 / 23.48%
Number/percentage of N's	7,547 / 0.01%
GC Percentage	43.1%

2.3. Coverage

Mean	0.0209

Standard Deviation	0.2061
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2.4. Mapping Quality

Mean Mapping Quality	46.34
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2.5. Mismatches and indels

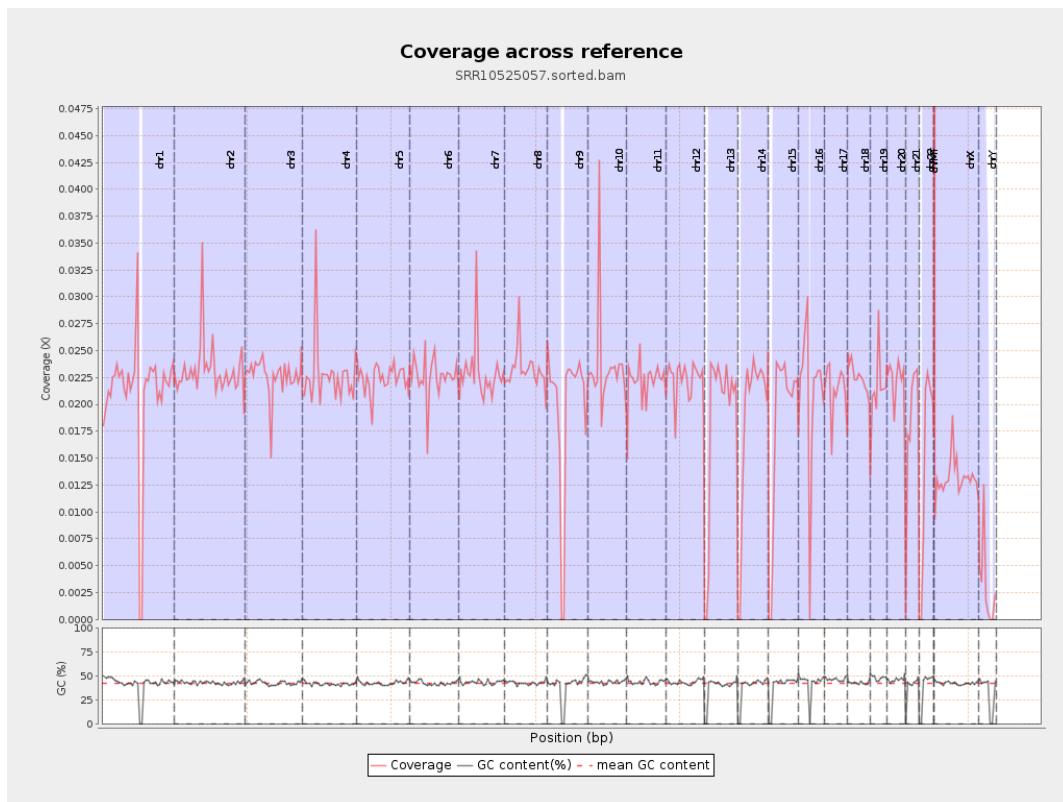
General error rate	0.48%
Mismatches	300,299
Insertions	3,948
Mapped reads with at least one insertion	0.37%
Deletions	12,965
Mapped reads with at least one deletion	1.2%
Homopolymer indels	43.59%

2.6. Chromosome stats

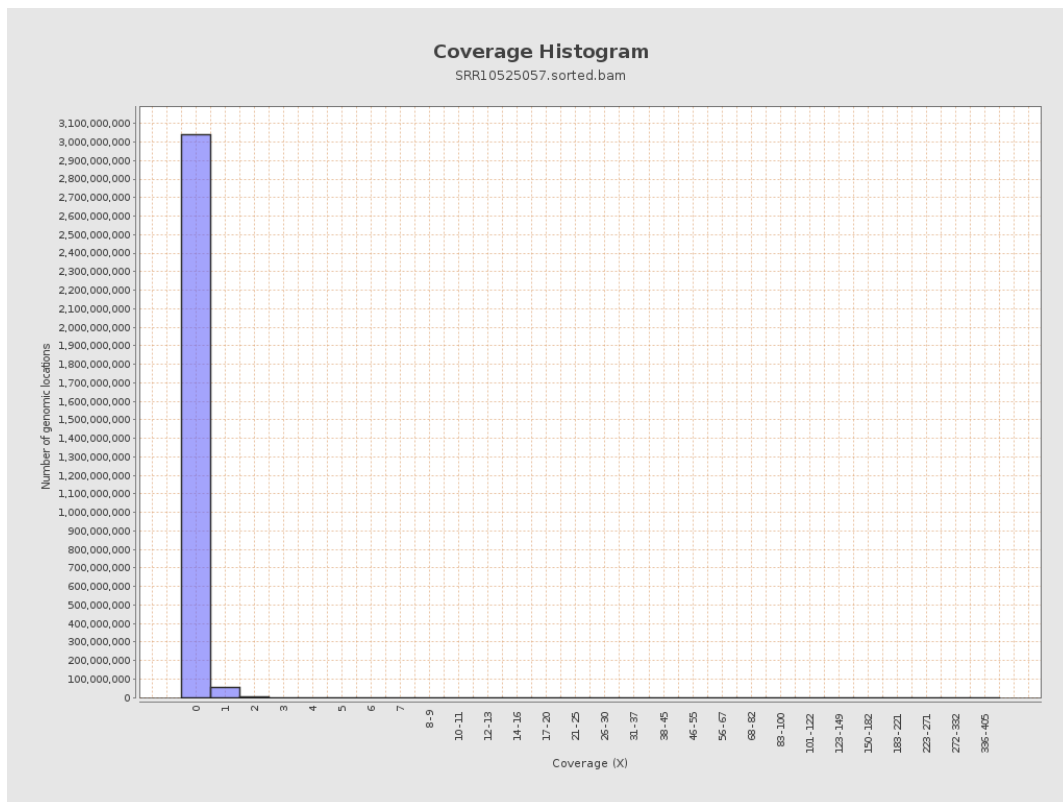
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5235372	0.021	0.3412
chr2	243199373	5632721	0.0232	0.2419
chr3	198022430	4476497	0.0226	0.1621
chr4	191154276	4335335	0.0227	0.1752
chr5	180915260	4059634	0.0224	0.1614
chr6	171115067	3863810	0.0226	0.1726
chr7	159138663	3650128	0.0229	0.2426

chr8	146364022	3402868	0.0232	0.2507
chr9	141213431	2766724	0.0196	0.1749
chr10	135534747	3177550	0.0234	0.2284
chr11	135006516	3011645	0.0223	0.1807
chr12	133851895	2990178	0.0223	0.1634
chr13	115169878	2130452	0.0185	0.1464
chr14	107349540	2008033	0.0187	0.1517
chr15	102531392	1874982	0.0183	0.1457
chr16	90354753	1881980	0.0208	0.1637
chr17	81195210	1732298	0.0213	0.1632
chr18	78077248	1759164	0.0225	0.2787
chr19	59128983	1282811	0.0217	0.2741
chr20	63025520	1392934	0.0221	0.163
chr21	48129895	884404	0.0184	0.1544
chr22	51304566	762320	0.0149	0.1302
chrMT	16571	13668	0.8248	1.1158
chrX	155270560	2052687	0.0132	0.1319
chrY	59373566	184875	0.0031	0.118

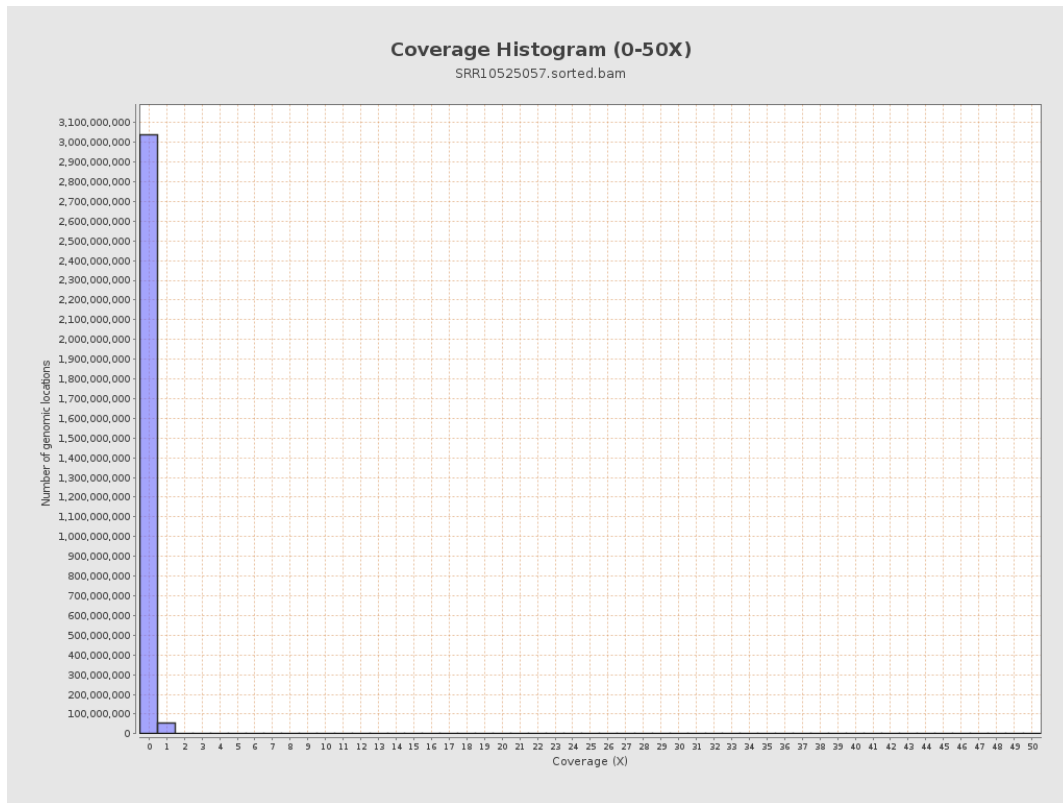
3. Results : Coverage across reference



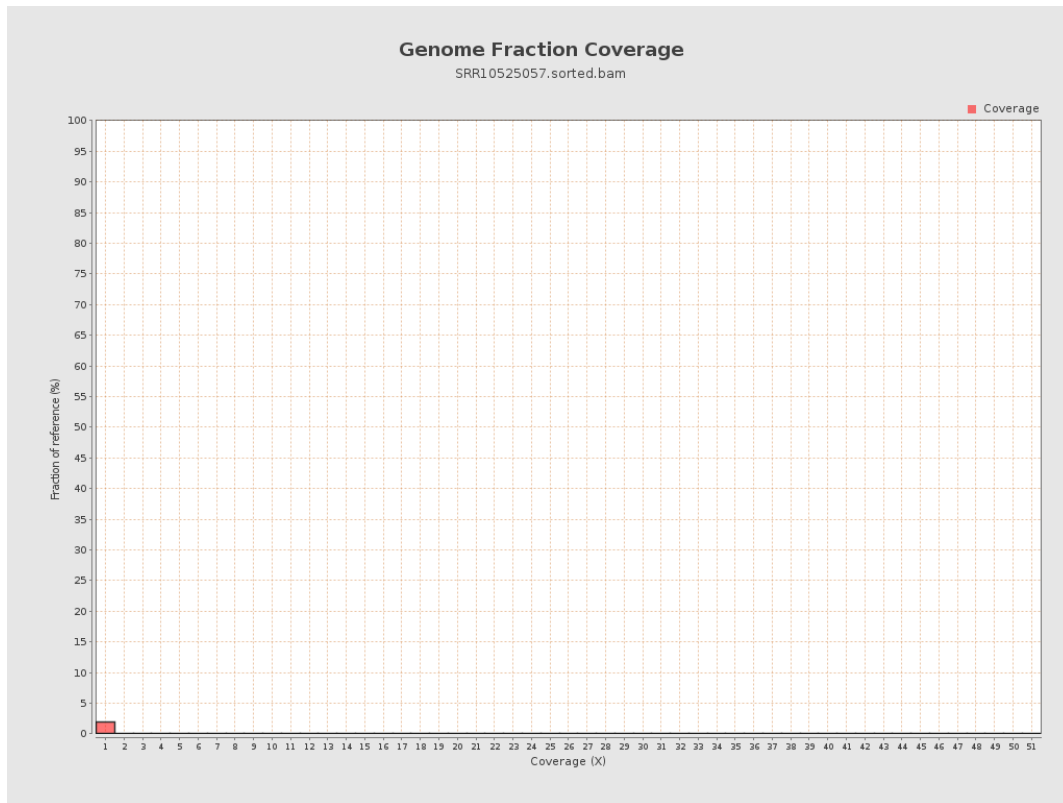
4. Results : Coverage Histogram



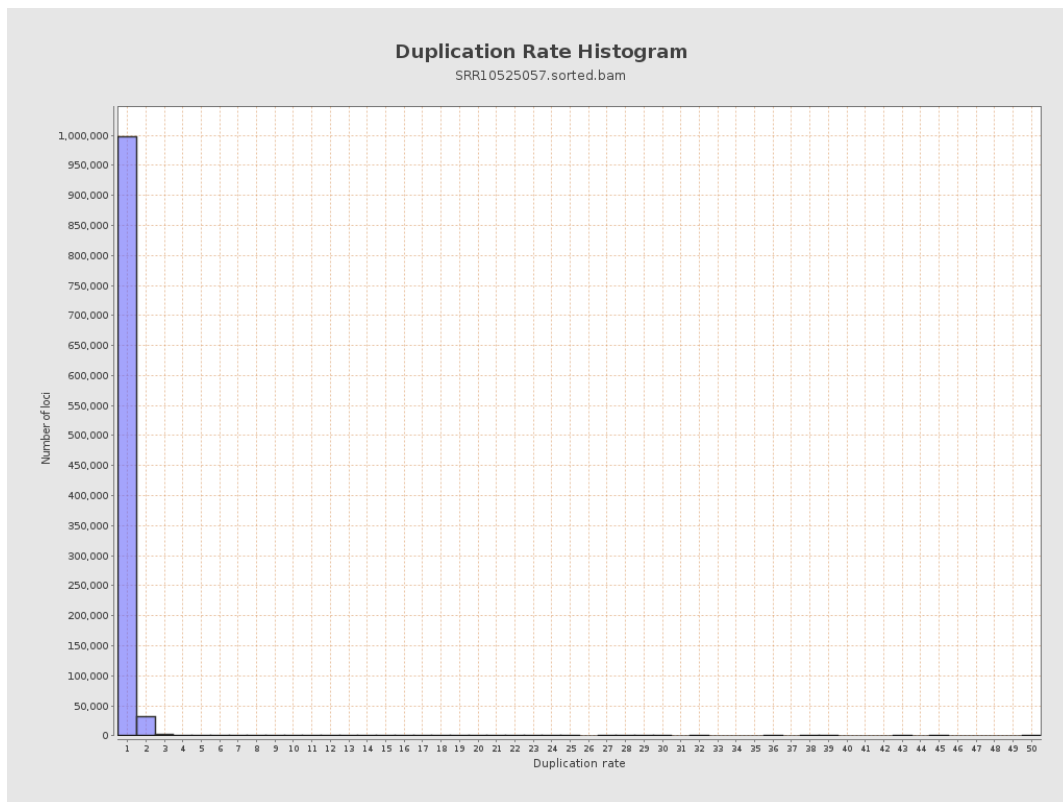
5. Results : Coverage Histogram (0-50X)



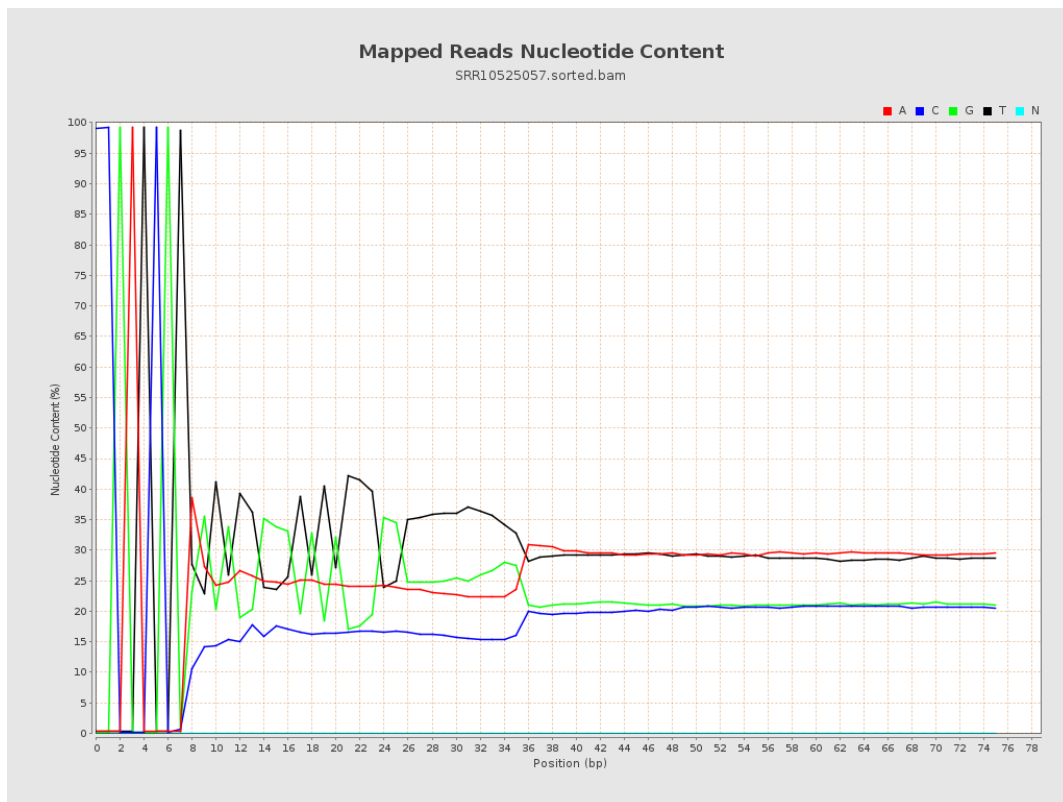
6. Results : Genome Fraction Coverage



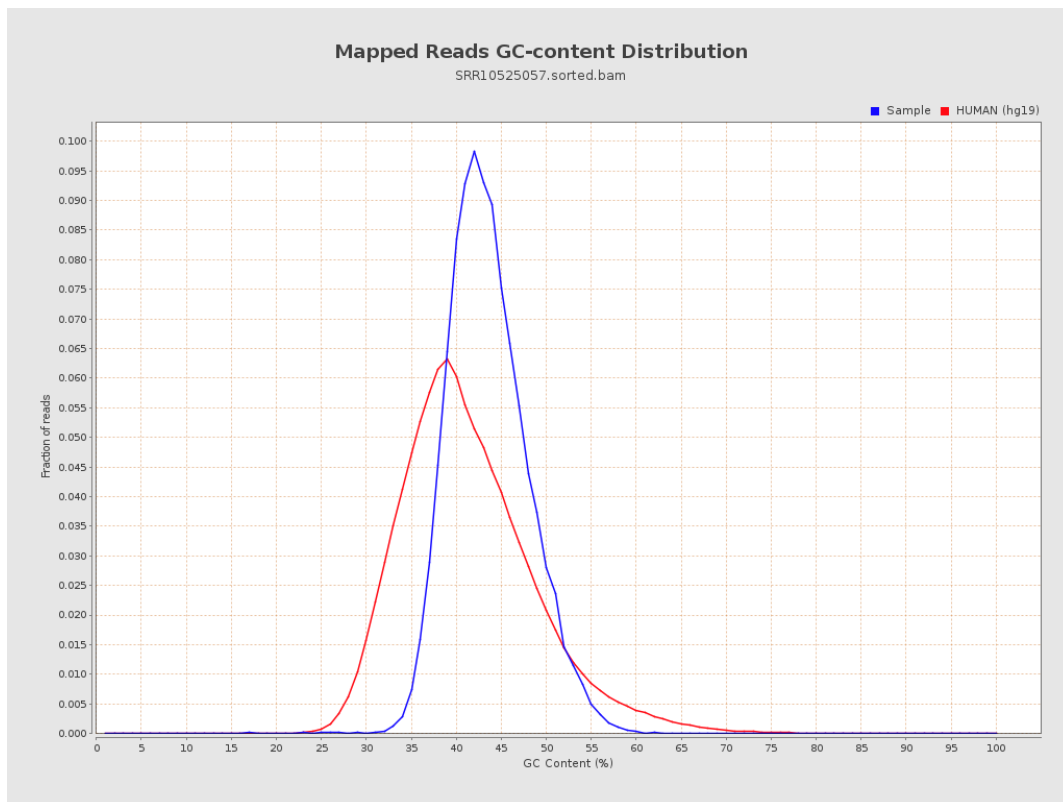
7. Results : Duplication Rate Histogram



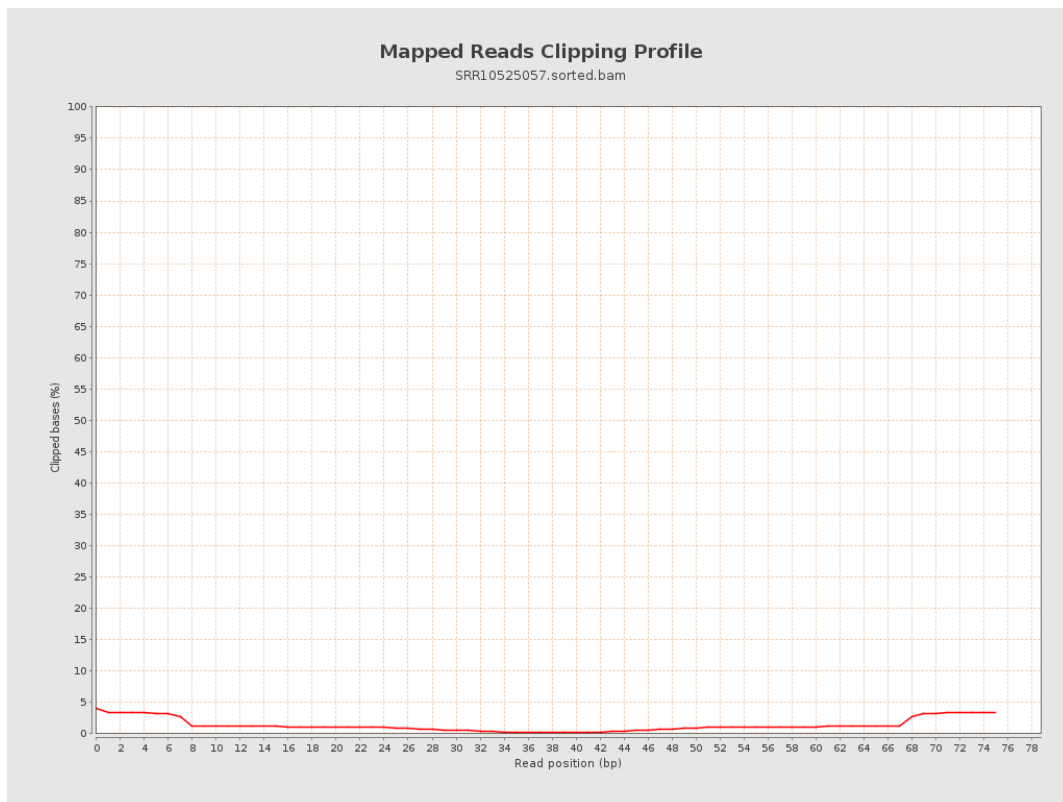
8. Results : Mapped Reads Nucleotide Content



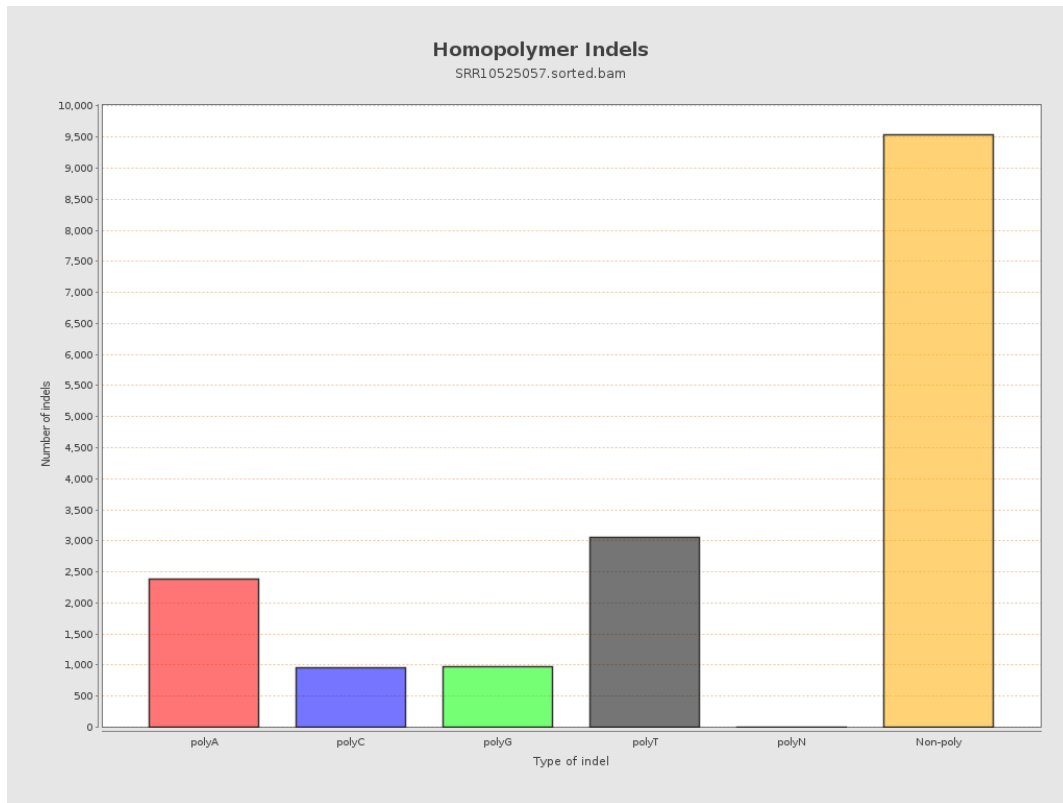
9. Results : Mapped Reads GC-content Distribution



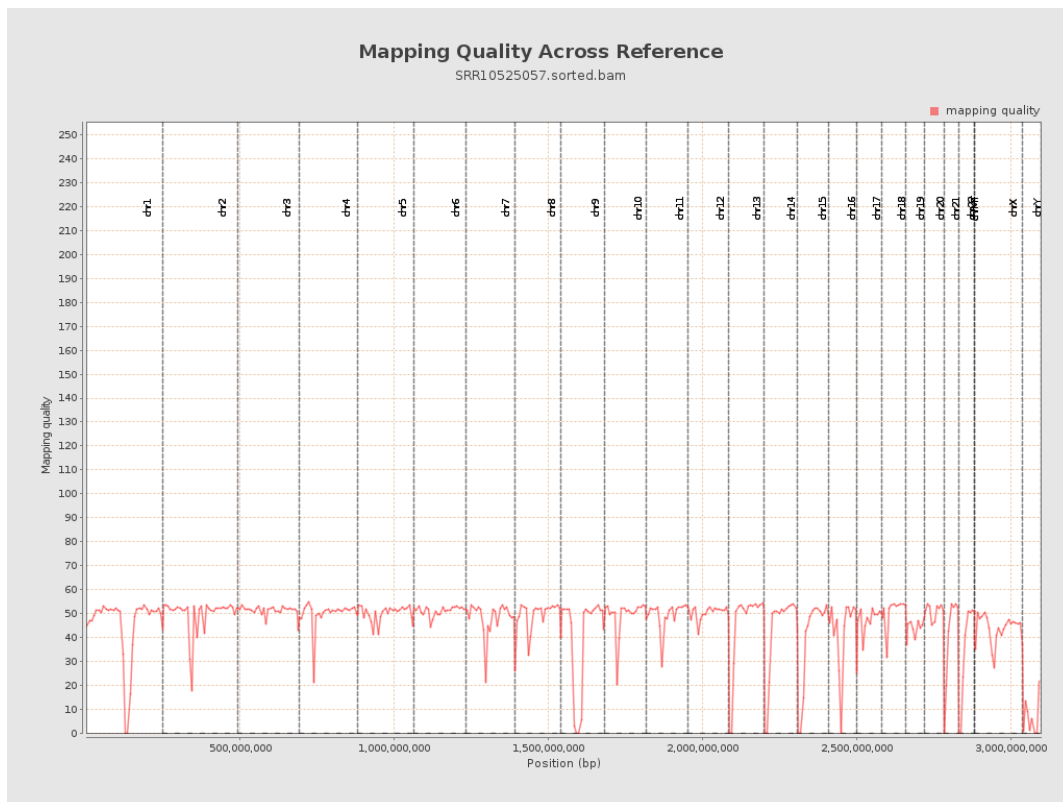
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

