

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 22:15:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004042.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_SRR6004042 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004042.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 22:15:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004042.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,913,310
Mapped reads	1,758,224 / 91.89%
Unmapped reads	155,086 / 8.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,496 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	52,935 / 2.77%
Duplication rate	1.92%
Clipped reads	792,576 / 41.42%

2.2. ACGT Content

Number/percentage of A's	33,619,114 / 28.71%
Number/percentage of C's	21,578,154 / 18.43%
Number/percentage of T's	36,291,338 / 31%
Number/percentage of G's	25,569,891 / 21.84%
Number/percentage of N's	25,480 / 0.02%
GC Percentage	40.27%

2.3. Coverage

Mean	0.0378

Standard Deviation	0.3921
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2.4. Mapping Quality

Mean Mapping Quality	45.09
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2.5. Mismatches and indels

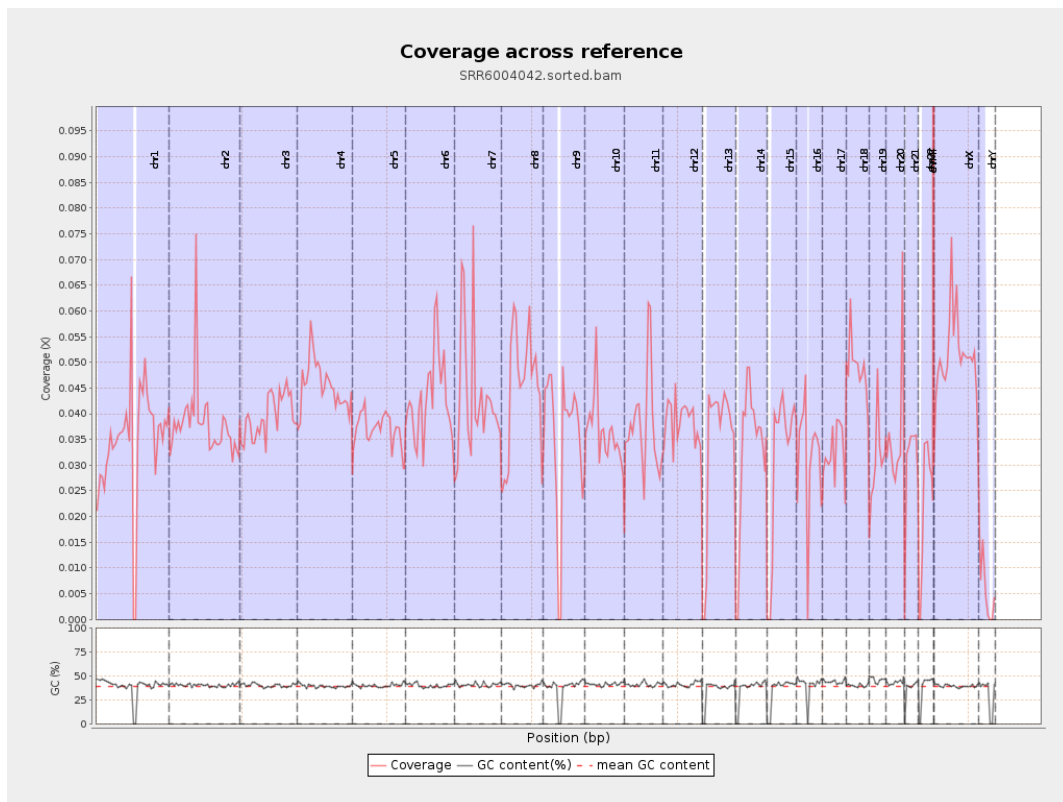
General error rate	0.79%
Mismatches	909,179
Insertions	8,794
Mapped reads with at least one insertion	0.5%
Deletions	30,149
Mapped reads with at least one deletion	1.69%
Homopolymer indels	45.58%

2.6. Chromosome stats

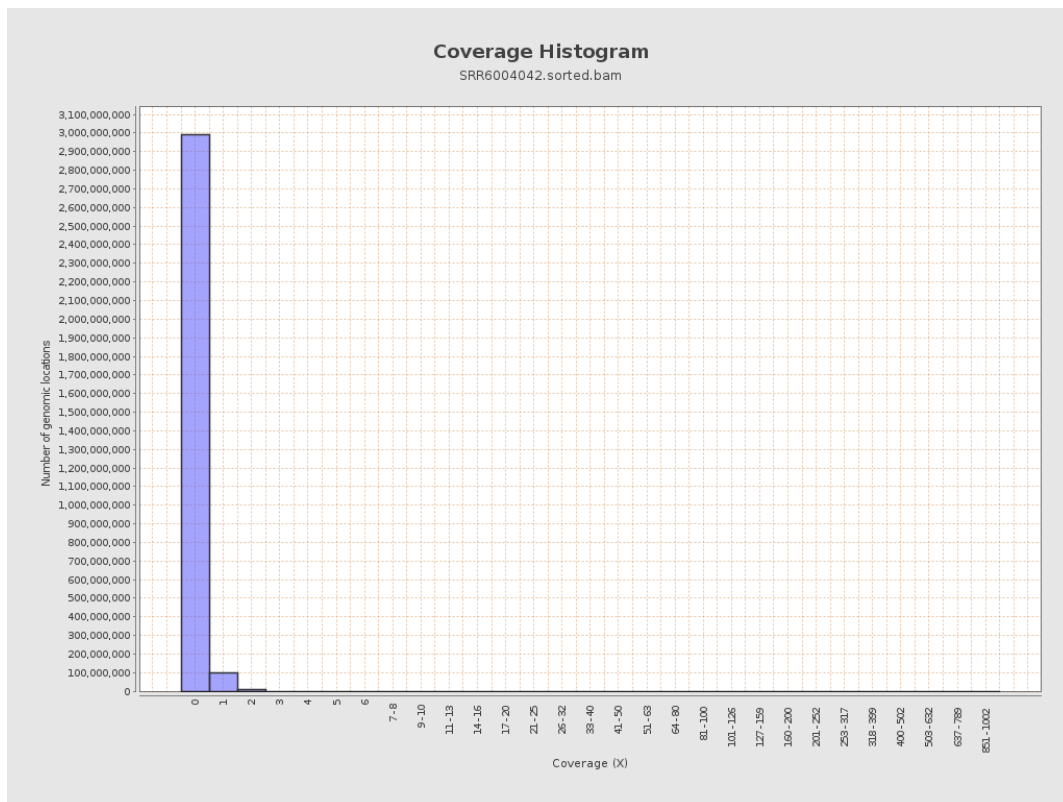
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8665170	0.0348	0.6826
chr2	243199373	9252154	0.038	0.4154
chr3	198022430	7835377	0.0396	0.2145
chr4	191154276	8675421	0.0454	0.2497
chr5	180915260	6696437	0.037	0.2128
chr6	171115067	7342173	0.0429	0.2441
chr7	159138663	6992783	0.0439	0.5772

chr8	146364022	6516011	0.0445	0.6507
chr9	141213431	5008721	0.0355	0.3924
chr10	135534747	4952879	0.0365	0.296
chr11	135006516	5068813	0.0375	0.3918
chr12	133851895	5116488	0.0382	0.2203
chr13	115169878	3898611	0.0339	0.198
chr14	107349540	3523416	0.0328	0.23
chr15	102531392	3210807	0.0313	0.2112
chr16	90354753	2865124	0.0317	0.2297
chr17	81195210	2633396	0.0324	0.2369
chr18	78077248	3841596	0.0492	0.7547
chr19	59128983	1858053	0.0314	0.4699
chr20	63025520	2312211	0.0367	0.2284
chr21	48129895	1465187	0.0304	0.2219
chr22	51304566	1124733	0.0219	0.1581
chrMT	16571	9272	0.5595	0.9251
chrX	155270560	7936021	0.0511	0.2892
chrY	59373566	335297	0.0056	0.1131

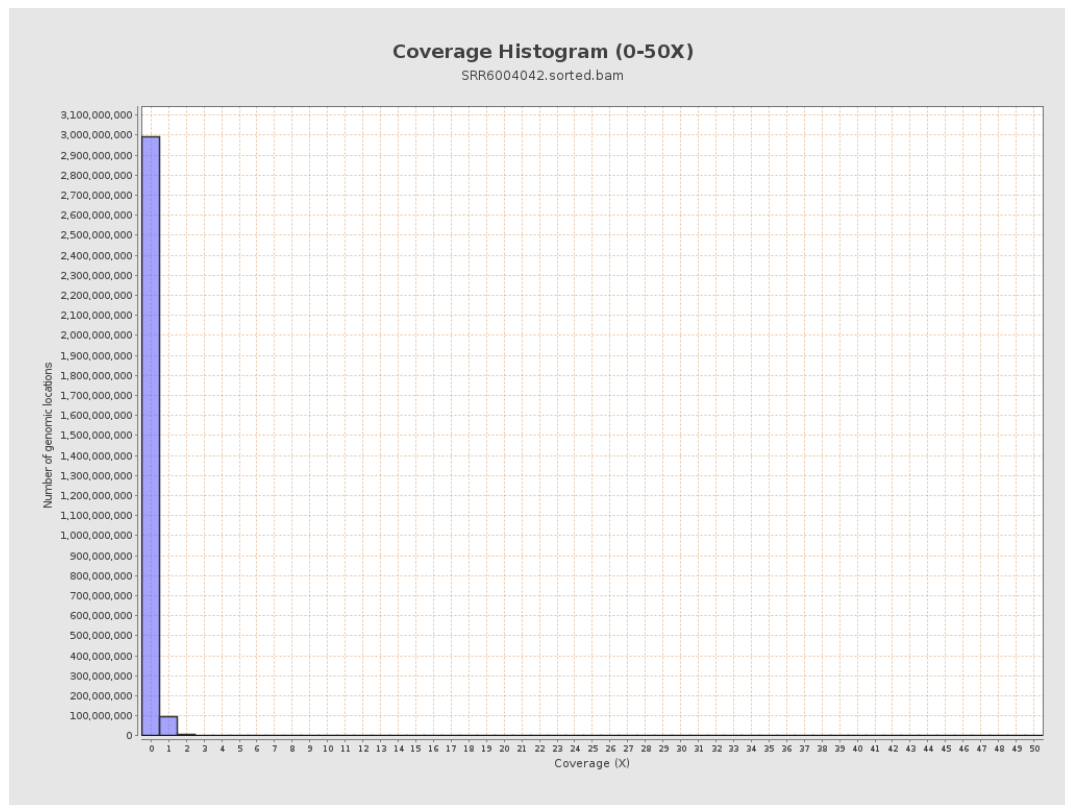
3. Results : Coverage across reference



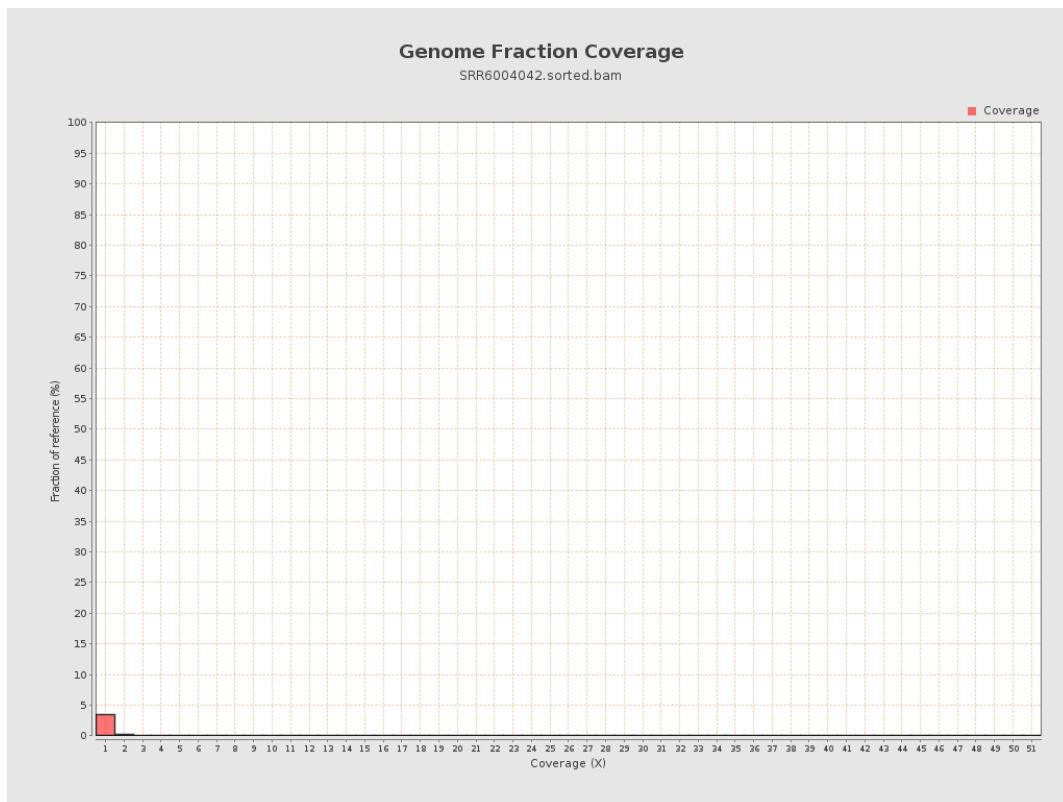
4. Results : Coverage Histogram



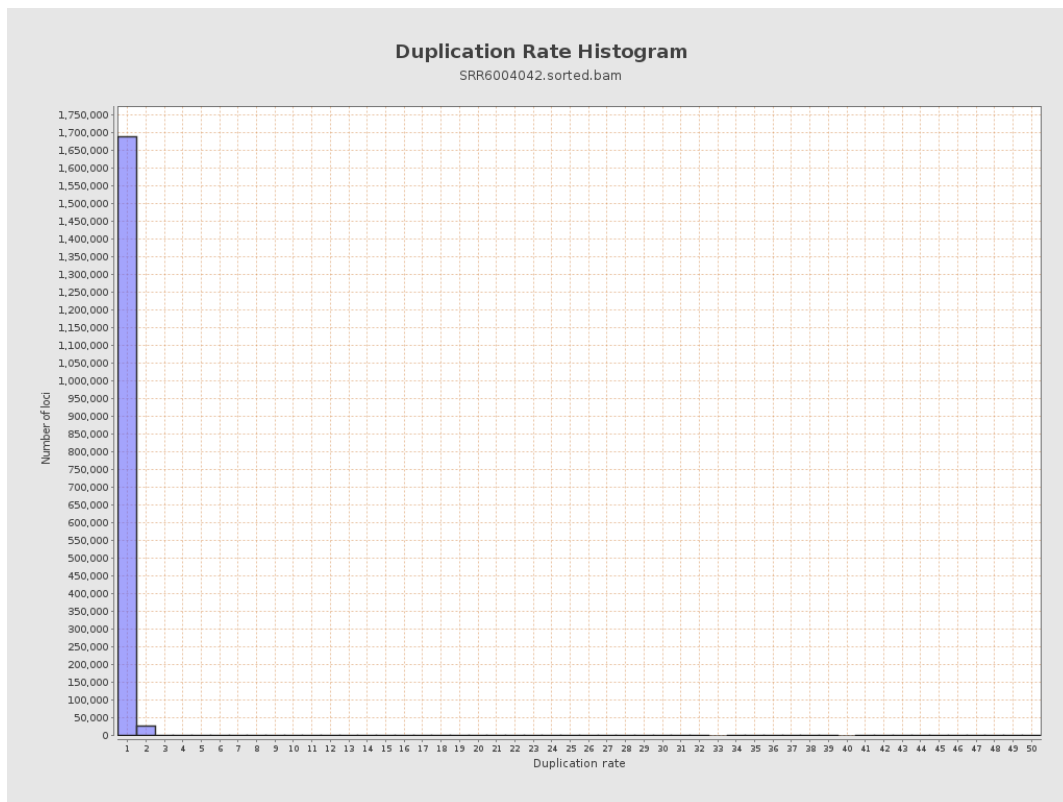
5. Results : Coverage Histogram (0-50X)



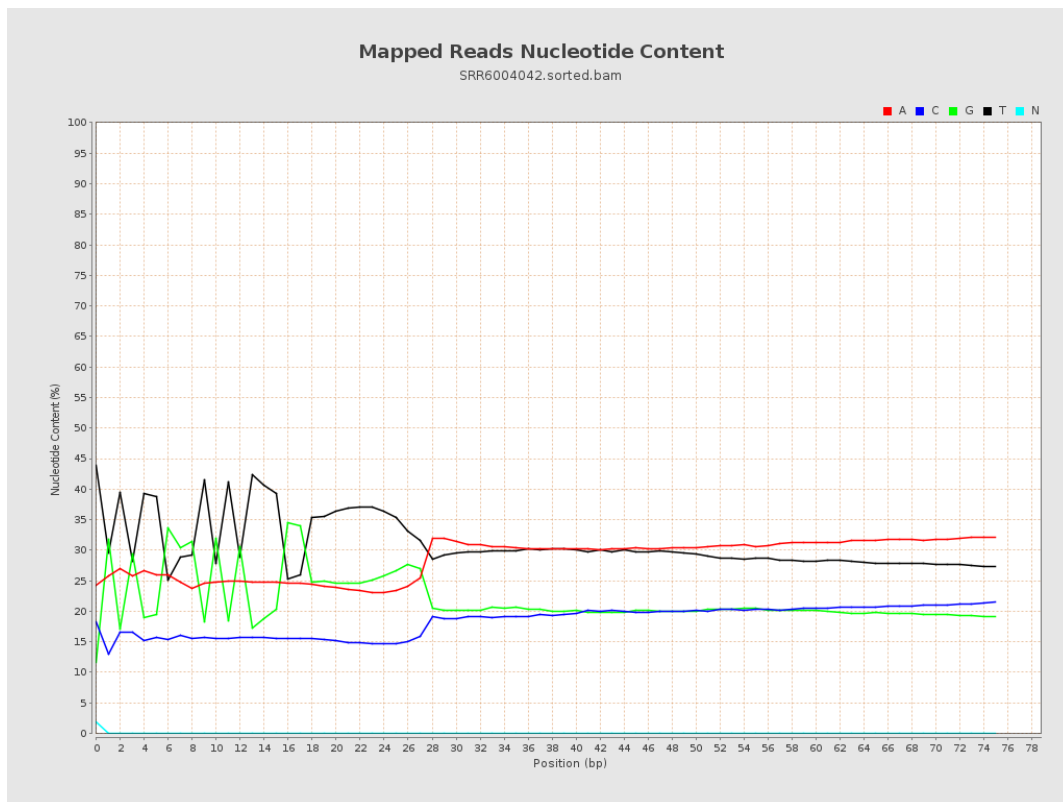
6. Results : Genome Fraction Coverage



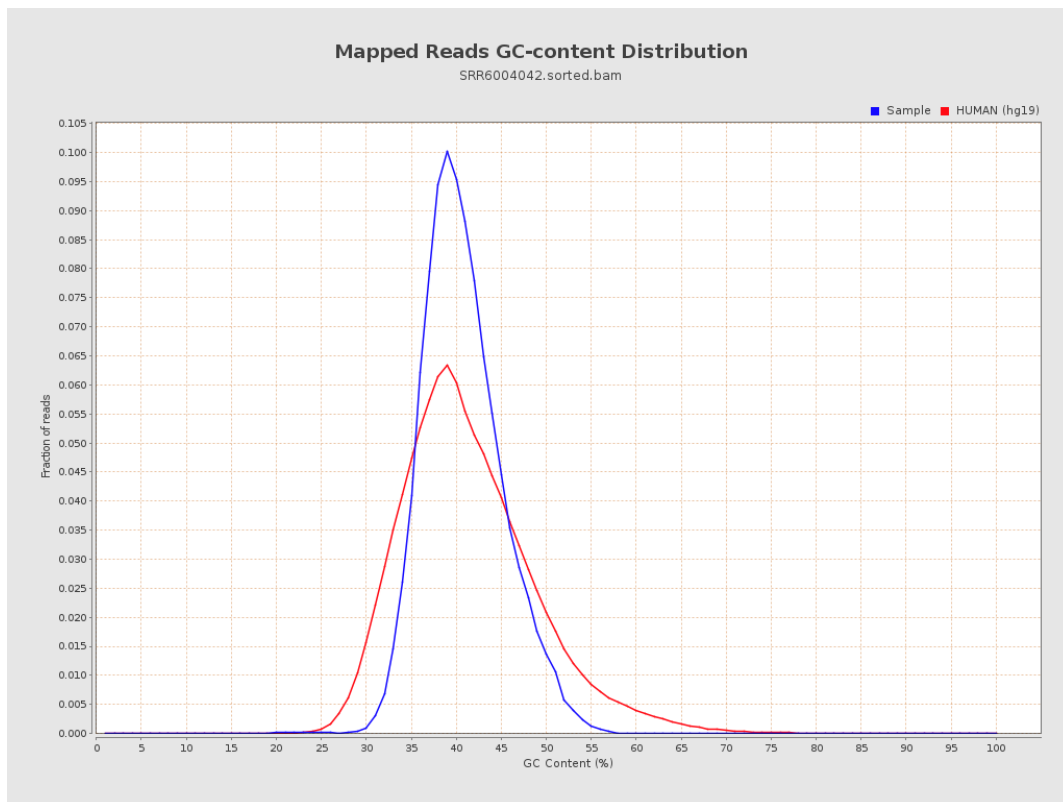
7. Results : Duplication Rate Histogram



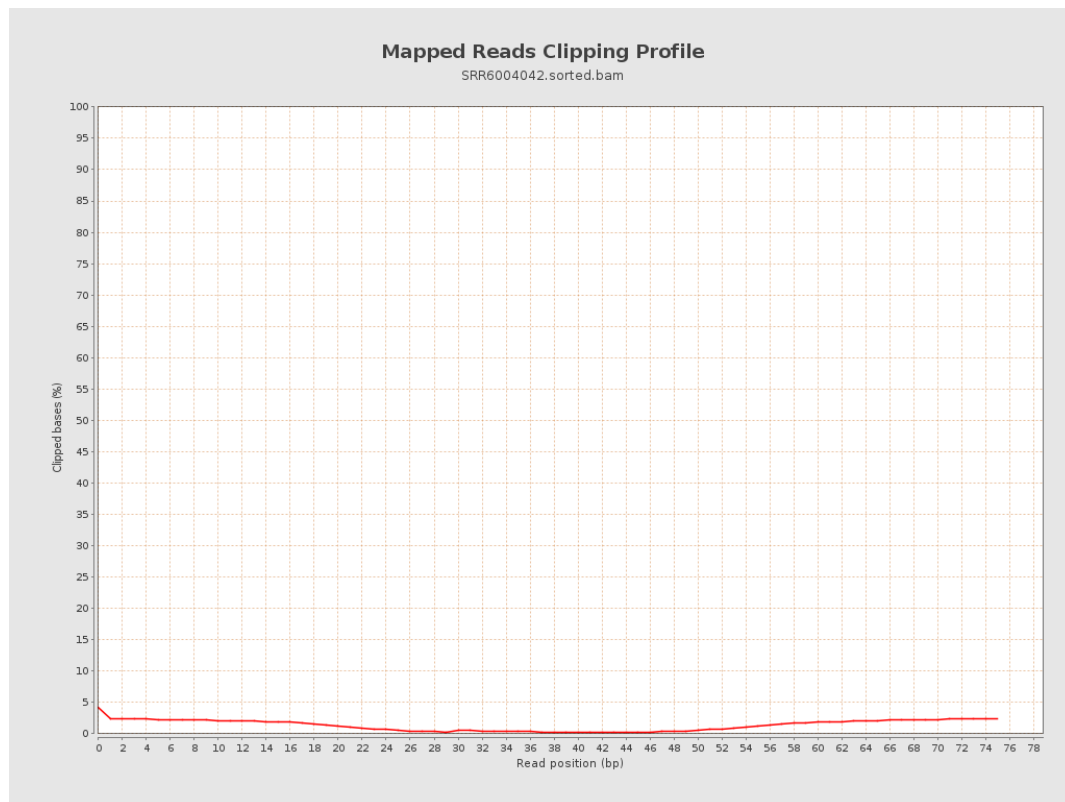
8. Results : Mapped Reads Nucleotide Content



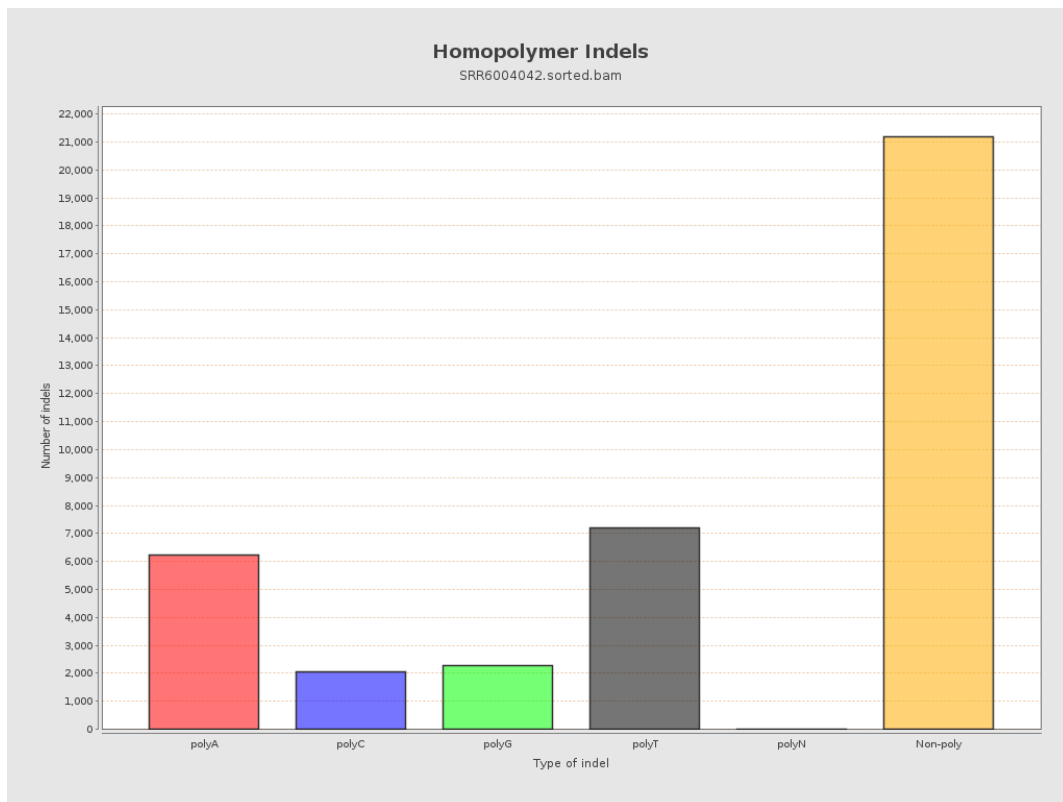
9. Results : Mapped Reads GC-content Distribution



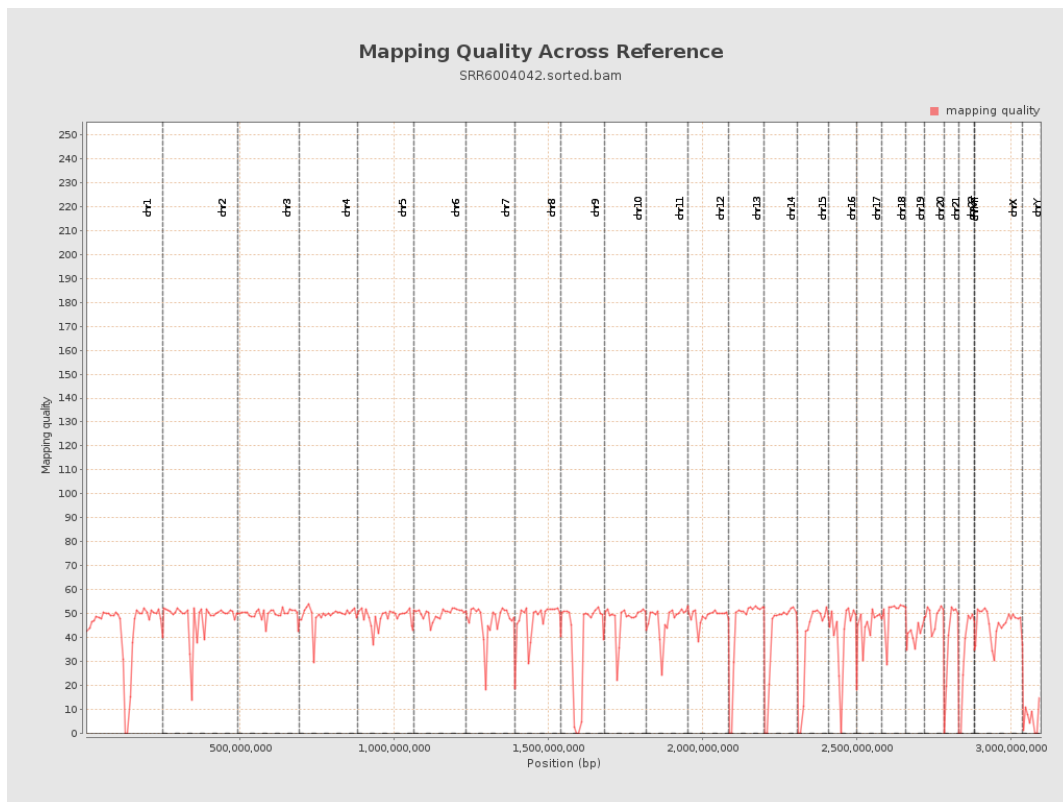
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

