Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:08:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085054.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_SRR3085054 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085054.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:08:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085054.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,193,961
Mapped reads	1,939,446 / 88.4%
Unmapped reads	254,515 / 11.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,631 / 1.67%
Read min/max/mean length	30 / 76 / 76.58
Duplicated reads (estimated)	70,938 / 3.23%
Duplication rate	1.9%
Clipped reads	957,064 / 43.62%

2.2. ACGT Content

Number/percentage of A's	37,840,569 / 29.28%
Number/percentage of C's	24,782,559 / 19.18%
Number/percentage of T's	38,187,338 / 29.55%
Number/percentage of G's	28,400,454 / 21.98%
Number/percentage of N's	13,132 / 0.01%
GC Percentage	41.16%

2.3. Coverage

Mean	0.0418

Standard Deviation	0.5888

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Mismatches and indels

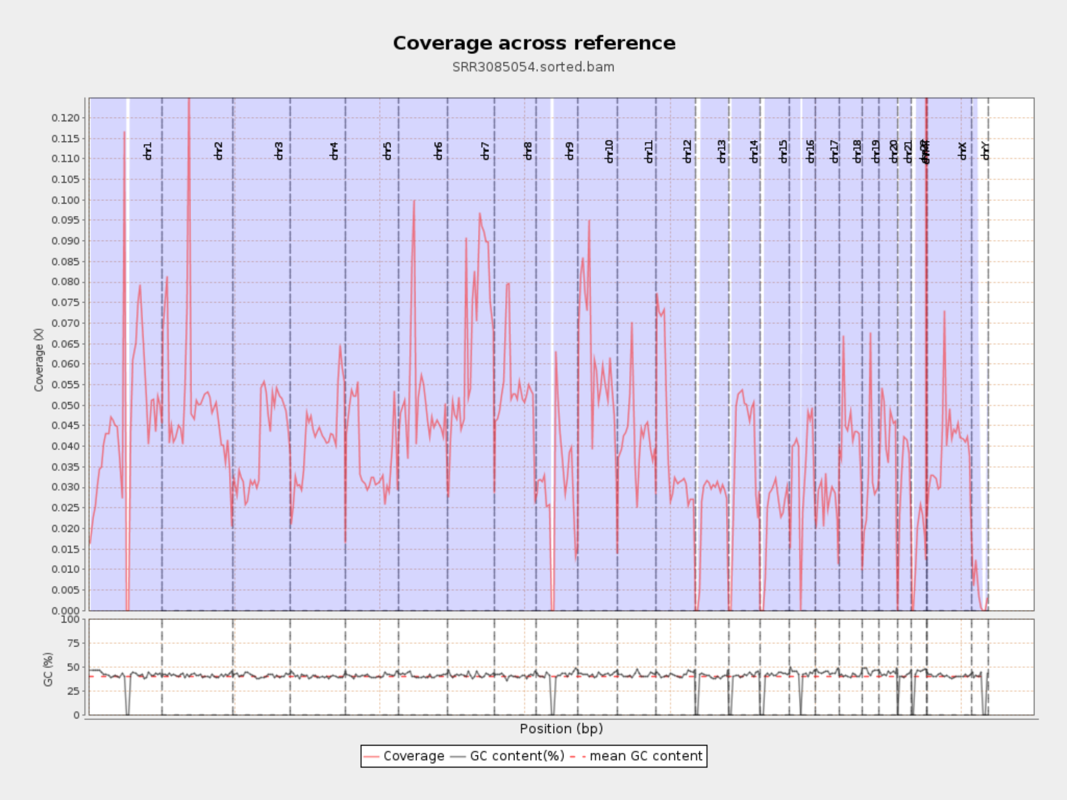
General error rate	0.96%
Mismatches	1,220,208
Insertions	10,857
Mapped reads with at least one insertion	0.55%
Deletions	23,416
Mapped reads with at least one deletion	1.2%
Homopolymer indels	42.7%

2.6. Chromosome stats

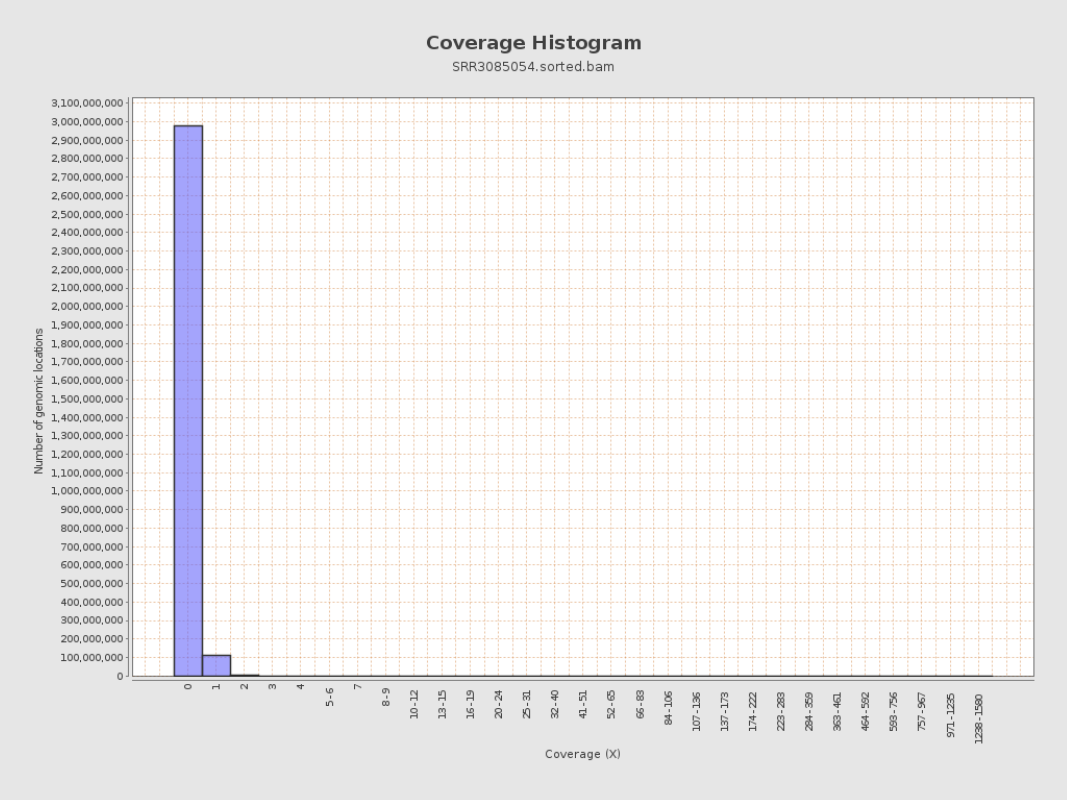
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11323447	0.0454	1.2594
chr2	243199373	12568420	0.0517	0.641
chr3	198022430	8080325	0.0408	0.2162
chr4	191154276	8038148	0.0421	0.2309
chr5	180915260	6824228	0.0377	0.2125
chr6	171115067	8792354	0.0514	0.4701
chr7	159138663	10643927	0.0669	0.5746

chr8	146364022	7847527	0.0536	0.9914
chr9	141213431	4319982	0.0306	0.5229
chr10	135534747	8423226	0.0621	0.5337
chr11	135006516	5632417	0.0417	0.6762
chr12	133851895	5466424	0.0408	0.231
chr13	115169878	2824713	0.0245	0.1625
chr14	107349540	4104304	0.0382	0.2577
chr15	102531392	2269620	0.0221	0.1611
chr16	90354753	3150888	0.0349	0.2774
chr17	81195210	2119345	0.0261	0.2799
chr18	78077248	3481561	0.0446	0.9844
chr19	59128983	1887424	0.0319	0.8415
chr20	63025520	2746554	0.0436	0.236
chr21	48129895	1485846	0.0309	0.2176
chr22	51304566	773552	0.0151	0.1271
chrMT	16571	26610	1.6058	1.6468
chrX	155270560	6177028	0.0398	0.3485
chrY	59373566	252870	0.0043	0.0951

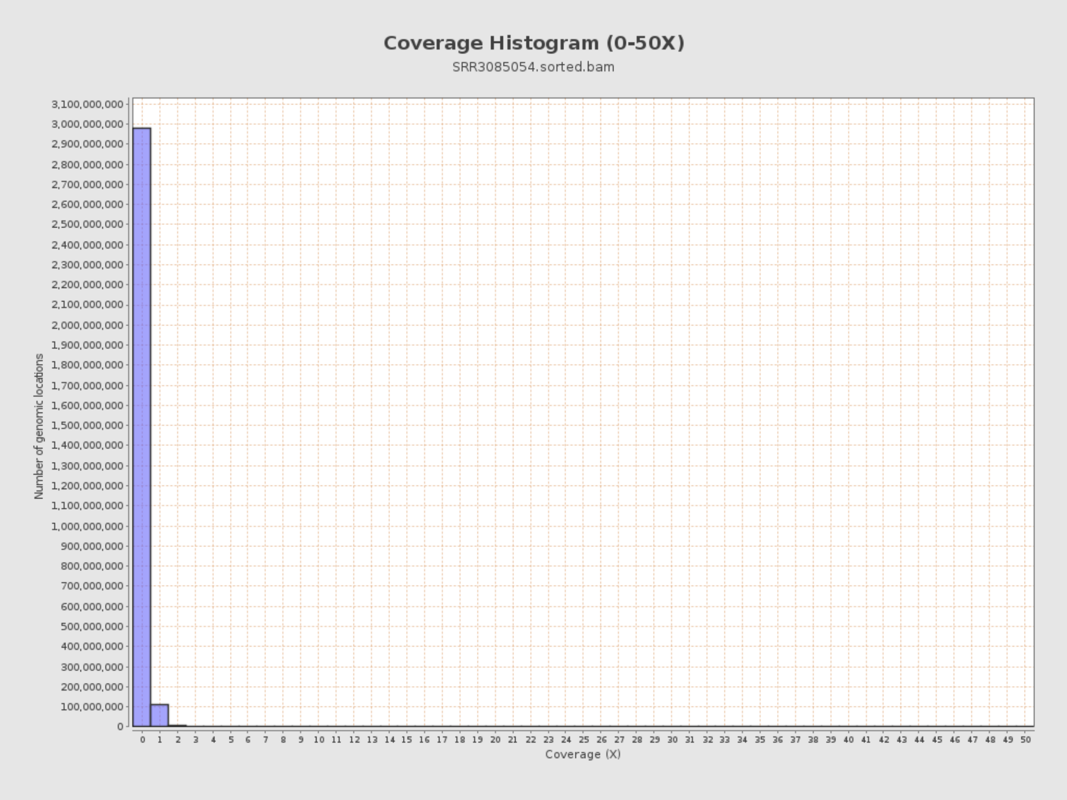
3. Results : Coverage across reference



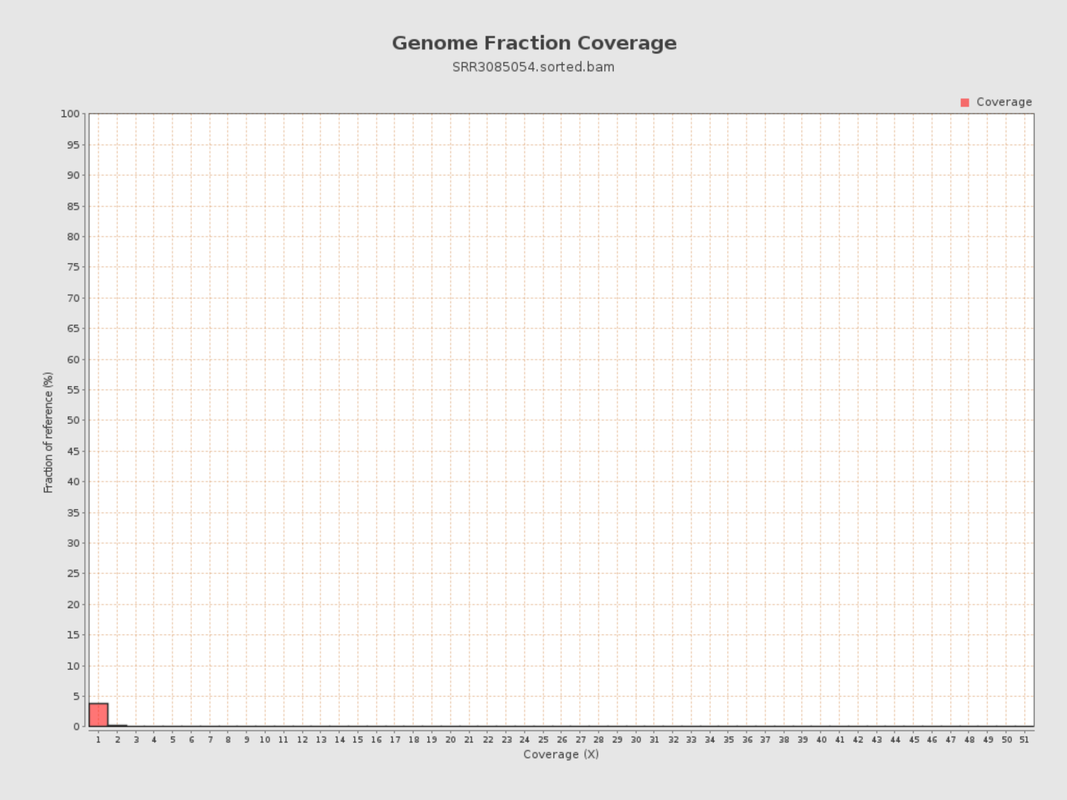
4. Results : Coverage Histogram



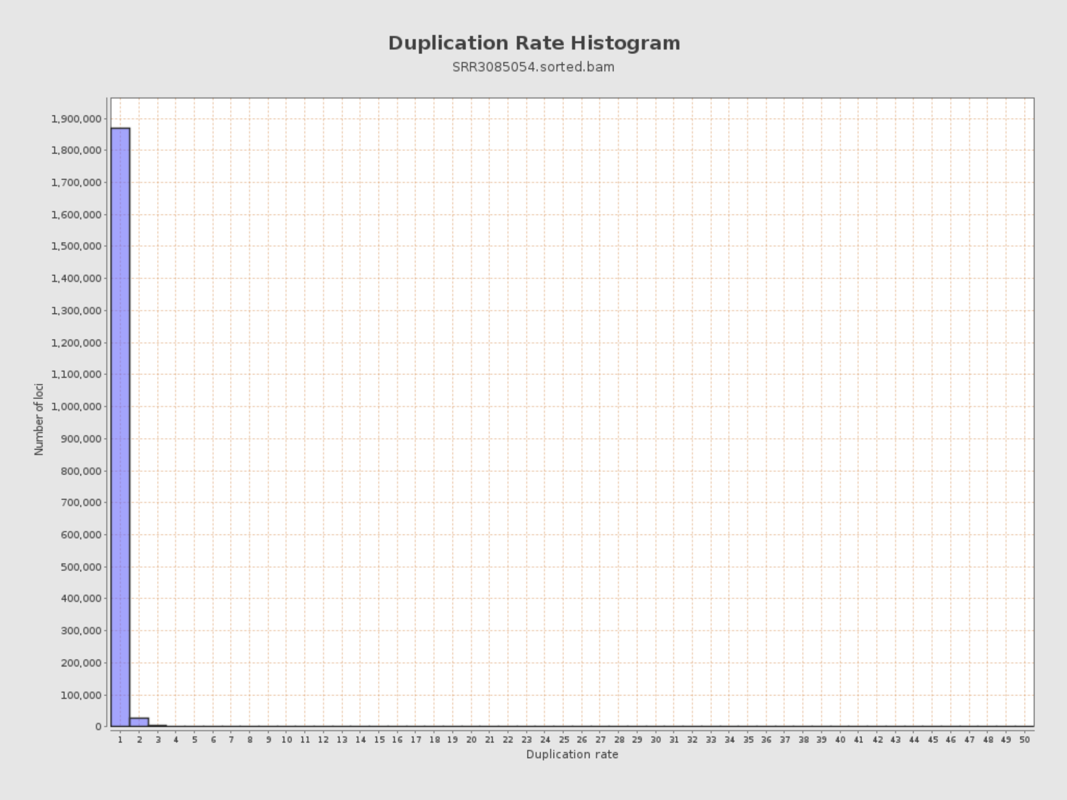
5. Results : Coverage Histogram (0-50X)



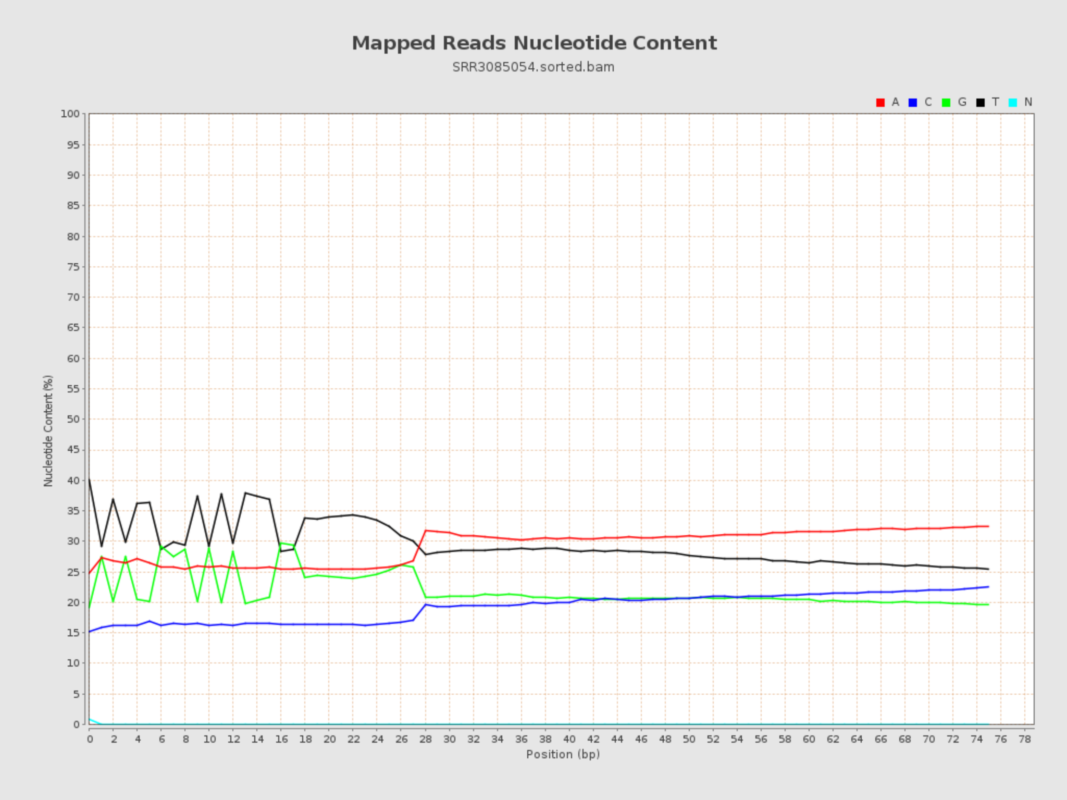
6. Results : Genome Fraction Coverage



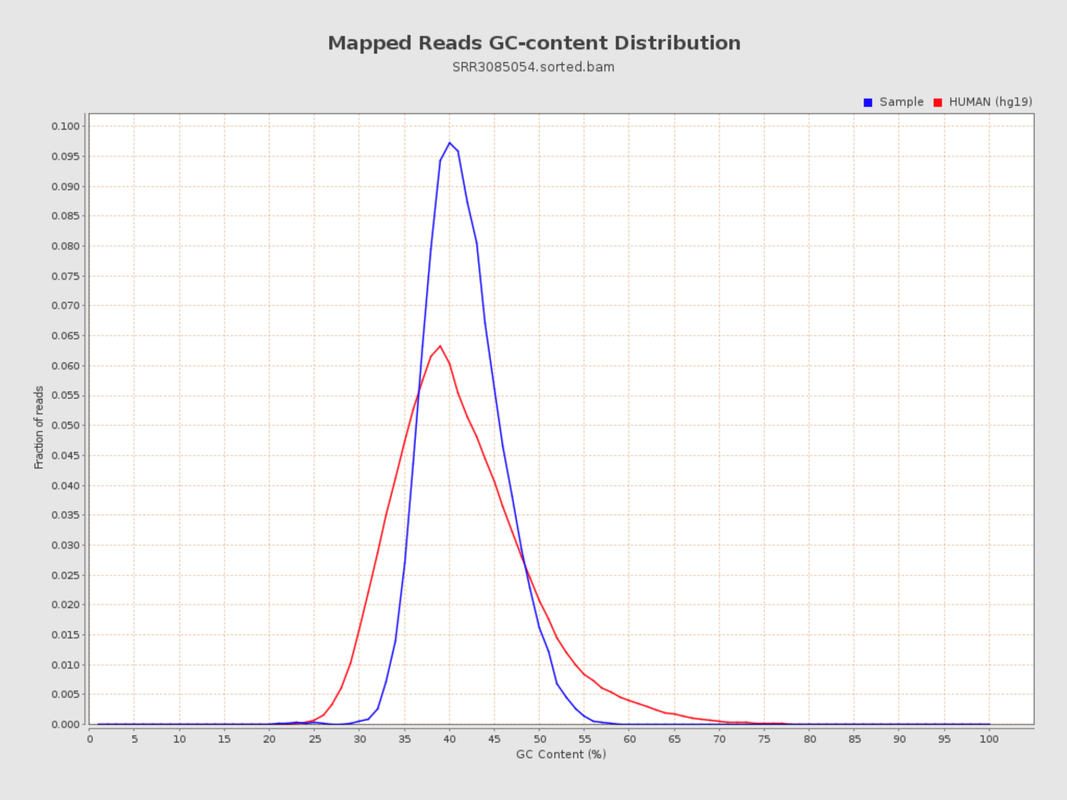
7. Results : Duplication Rate Histogram



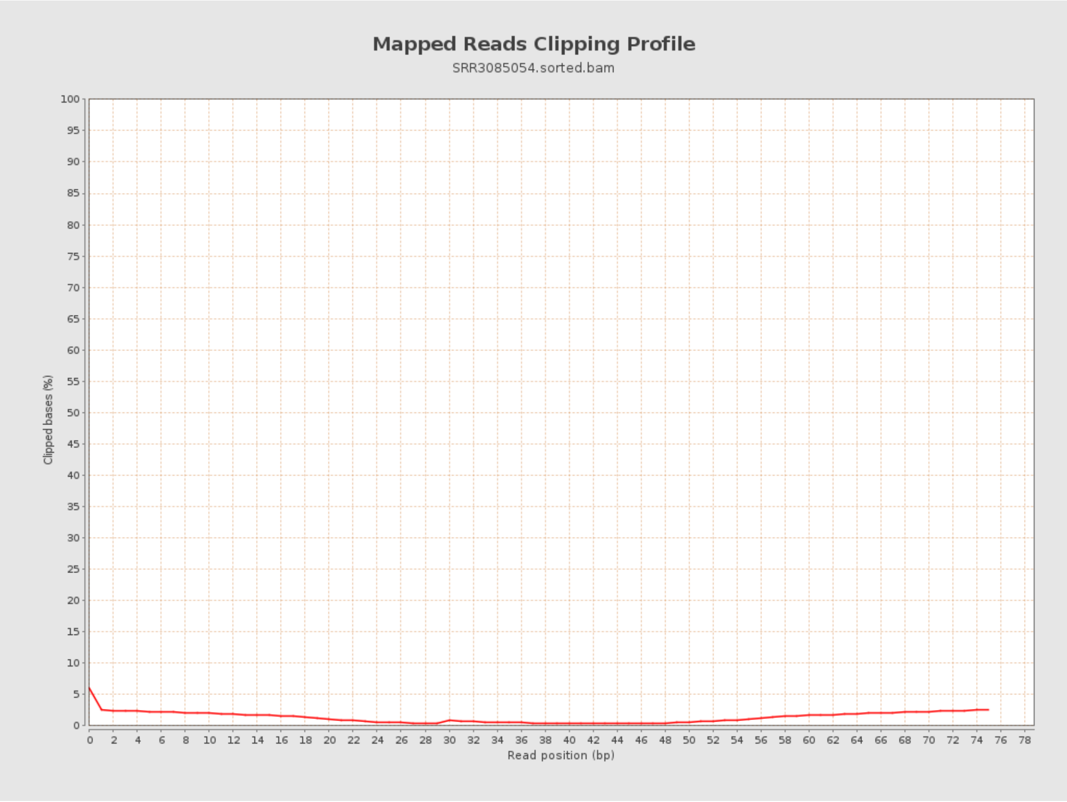
8. Results : Mapped Reads Nucleotide Content



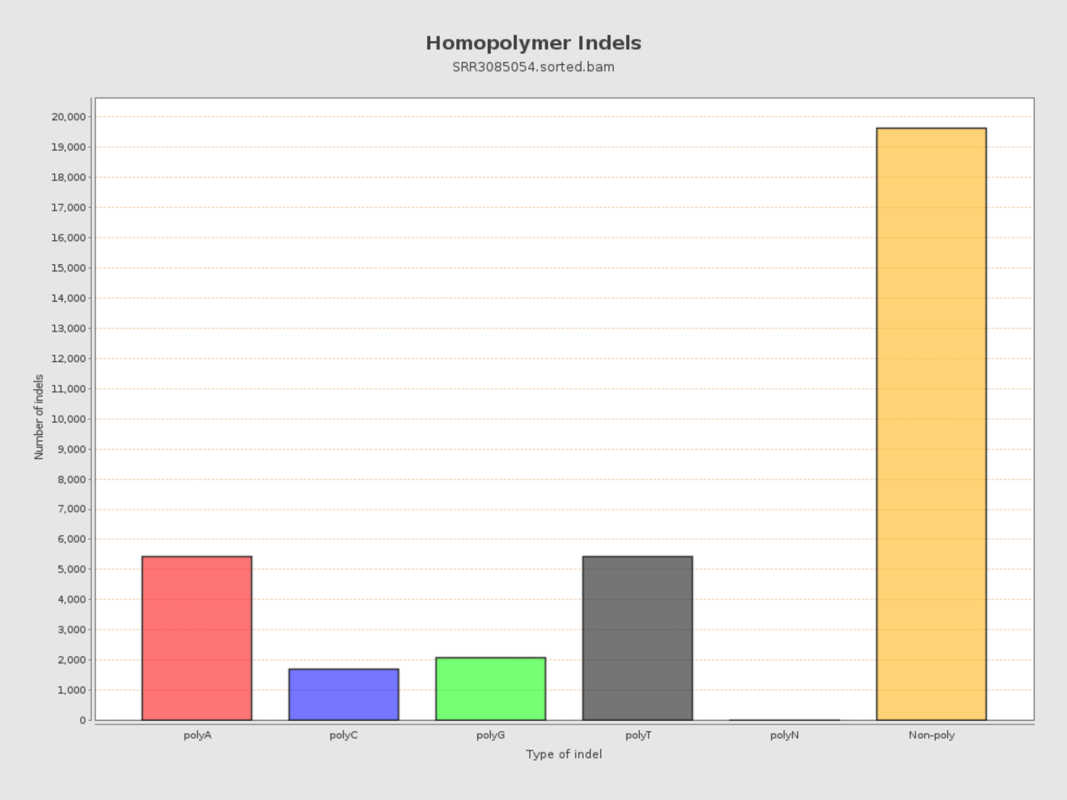
9. Results : Mapped Reads GC-content Distribution



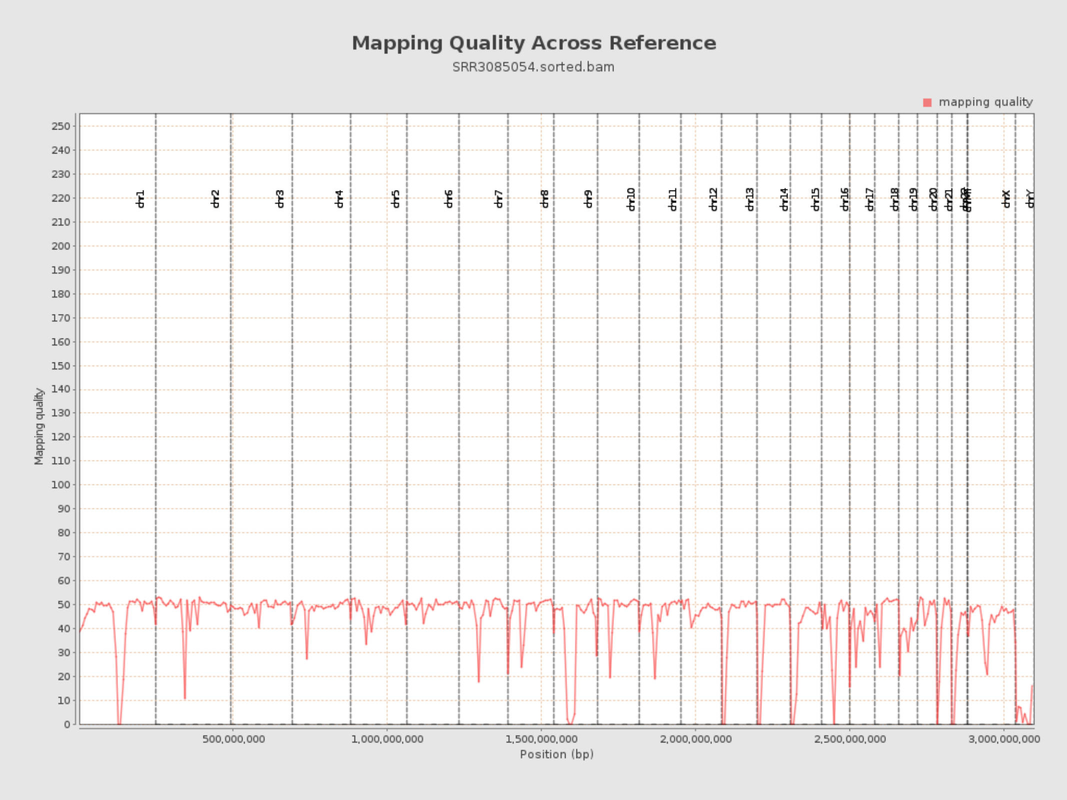
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram