Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 01:08:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085107.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_SRR3085107 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085107.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 01:08:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085107.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,705,491
Mapped reads	3,104,976 / 83.79%
Unmapped reads	600,515 / 16.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,446 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	138,886 / 3.75%
Duplication rate	3.43%
Clipped reads	2,178,688 / 58.8%

2.2. ACGT Content

Number/percentage of A's	53,269,704 / 28.65%
Number/percentage of C's	38,288,363 / 20.59%
Number/percentage of T's	52,689,290 / 28.34%
Number/percentage of G's	41,677,621 / 22.42%
Number/percentage of N's	4,014 / 0%
GC Percentage	43.01%

2.3. Coverage

Mean	0.0601

Standard Deviation	0.4672

2.4. Mapping Quality

Mean Mapping Quality	42.57

2.5. Mismatches and indels

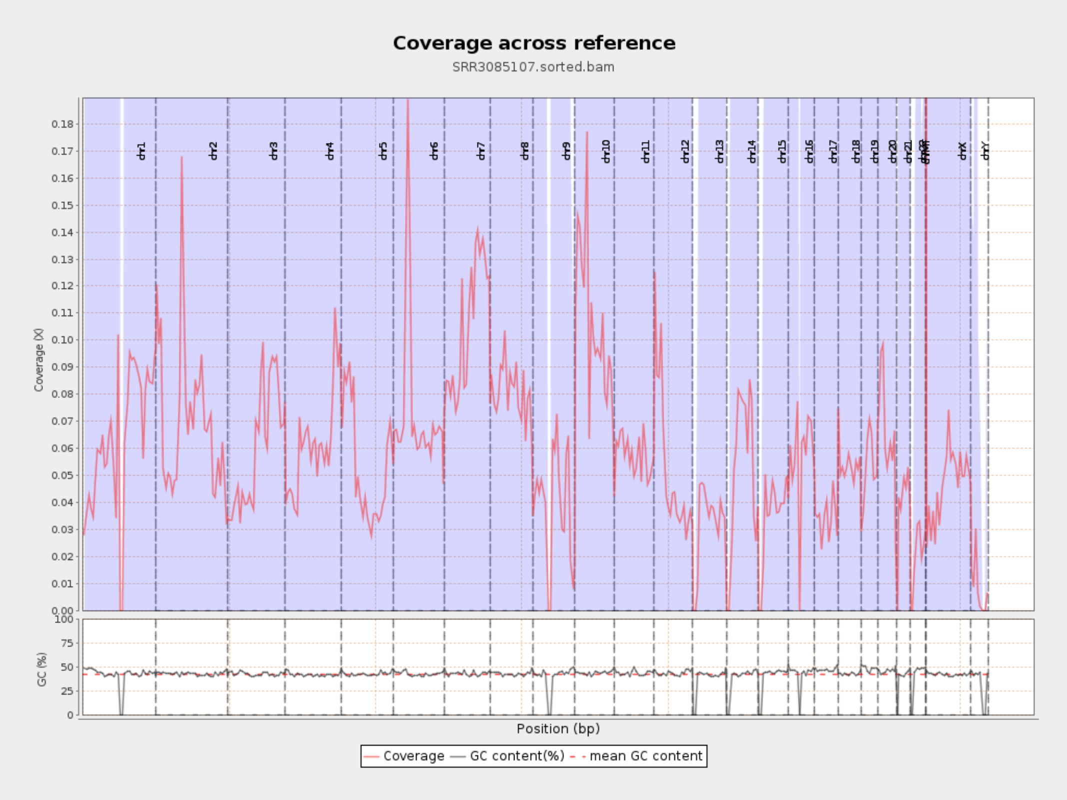
General error rate	0.86%
Mismatches	1,576,660
Insertions	13,792
Mapped reads with at least one insertion	0.44%
Deletions	37,216
Mapped reads with at least one deletion	1.19%
Homopolymer indels	44.21%

2.6. Chromosome stats

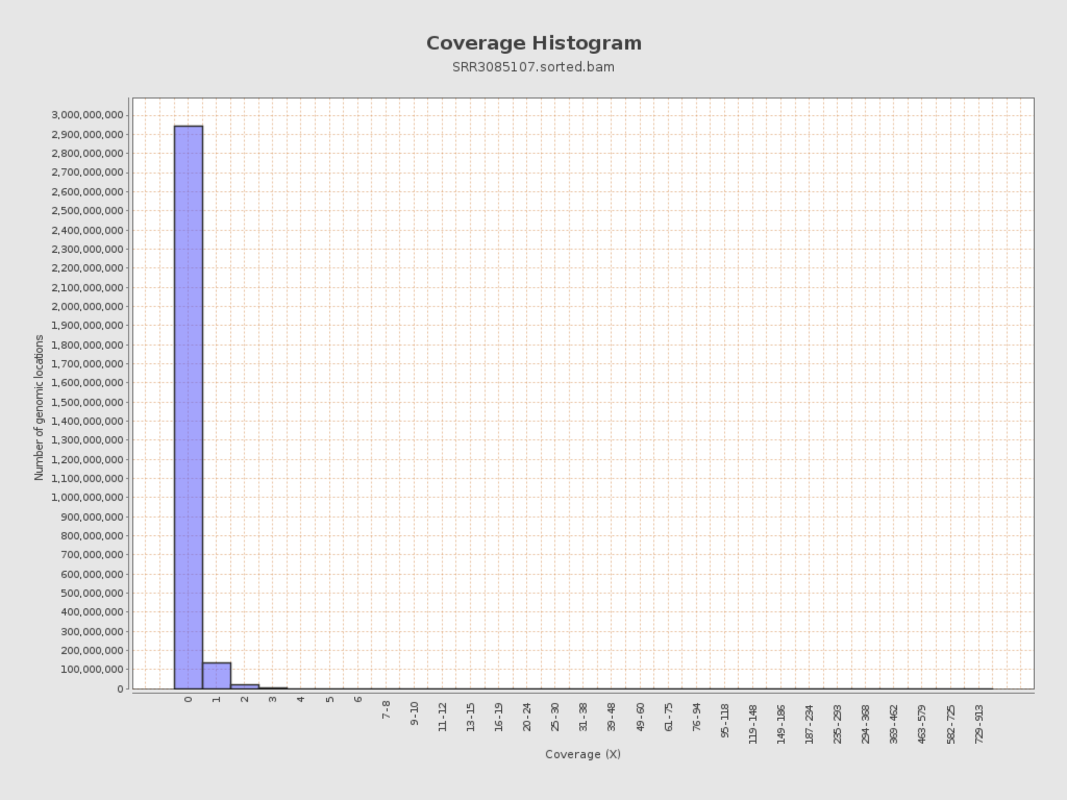
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15710158	0.063	0.6916
chr2	243199373	17253895	0.0709	0.5796
chr3	198022430	11877079	0.06	0.3081
chr4	191154276	11801021	0.0617	0.3191
chr5	180915260	9557567	0.0528	0.2666
chr6	171115067	12994938	0.0759	0.4633
chr7	159138663	16832687	0.1058	0.6159

chr8	146364022	11871721	0.0811	0.6408
chr9	141213431	5624410	0.0398	0.4337
chr10	135534747	14440221	0.1065	0.8413
chr11	135006516	7761791	0.0575	0.3757
chr12	133851895	7084655	0.0529	0.2764
chr13	115169878	3686194	0.032	0.2026
chr14	107349540	5735972	0.0534	0.3027
chr15	102531392	3472624	0.0339	0.2112
chr16	90354753	5050914	0.0559	0.3259
chr17	81195210	2809836	0.0346	0.2473
chr18	78077248	4182964	0.0536	0.6989
chr19	59128983	3201674	0.0541	0.4911
chr20	63025520	4290600	0.0681	0.3146
chr21	48129895	1944367	0.0404	0.2789
chr22	51304566	1017723	0.0198	0.16
chrMT	16571	6295	0.3799	0.7111
chrX	155270560	7289732	0.0469	0.2992
chrY	59373566	489196	0.0082	0.1862

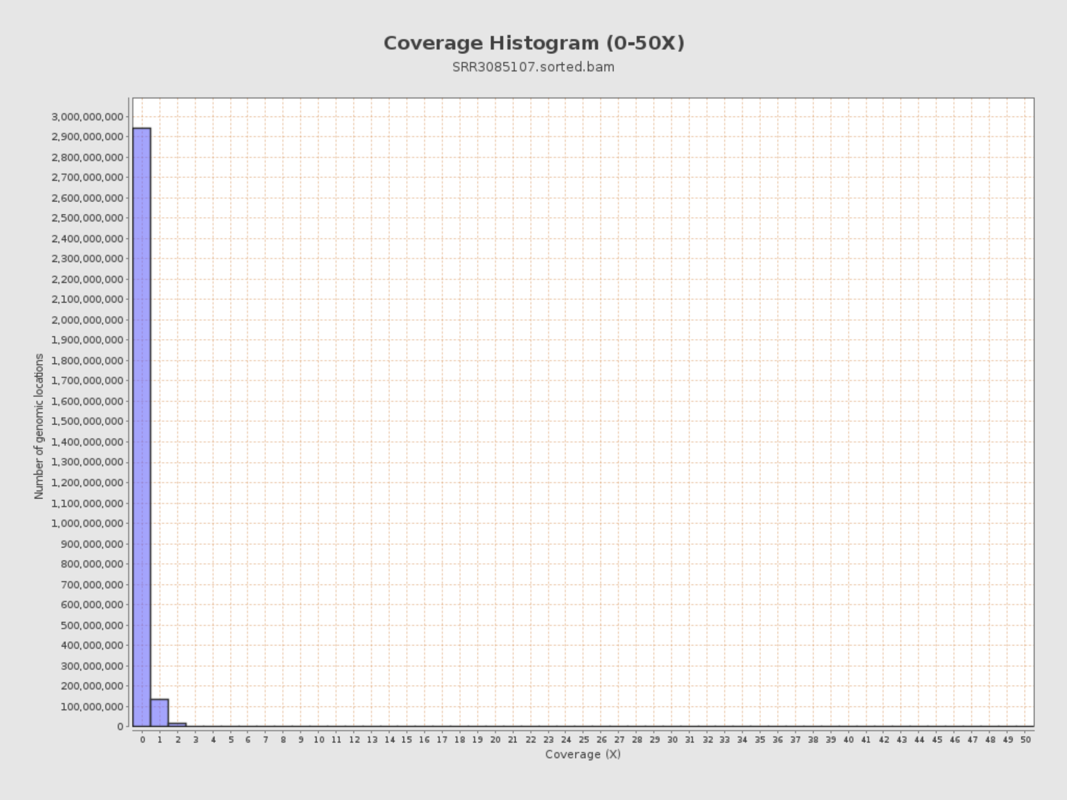
3. Results : Coverage across reference



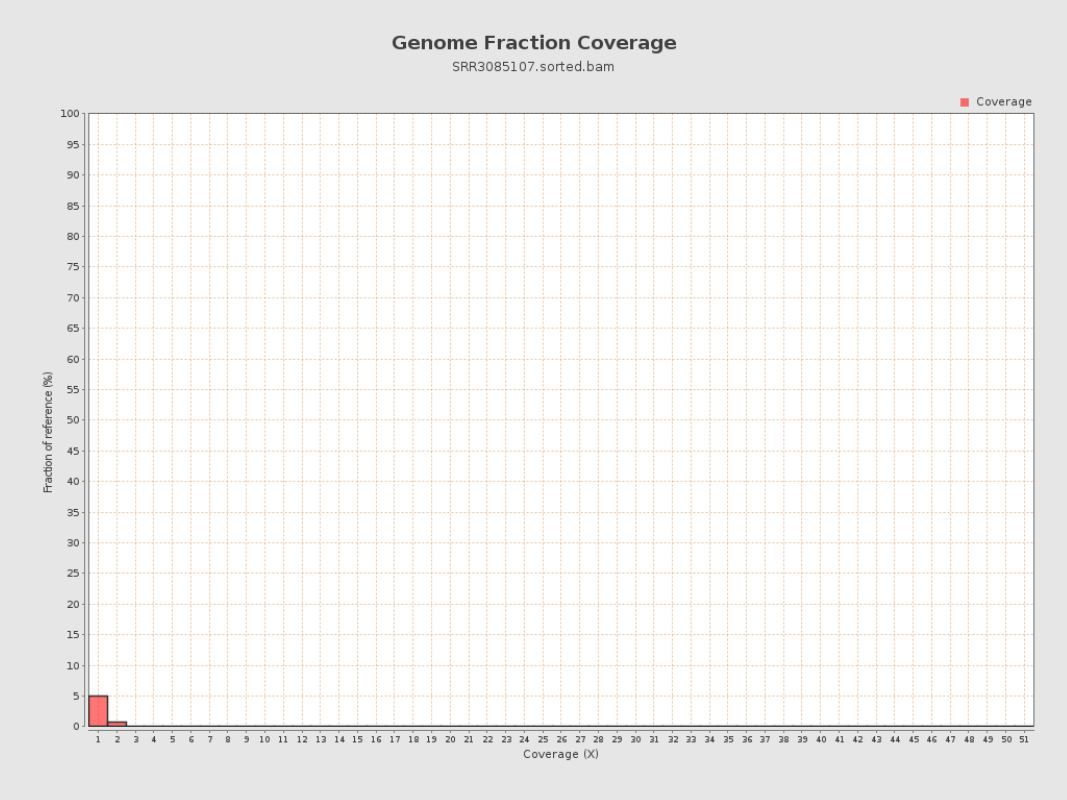
4. Results : Coverage Histogram



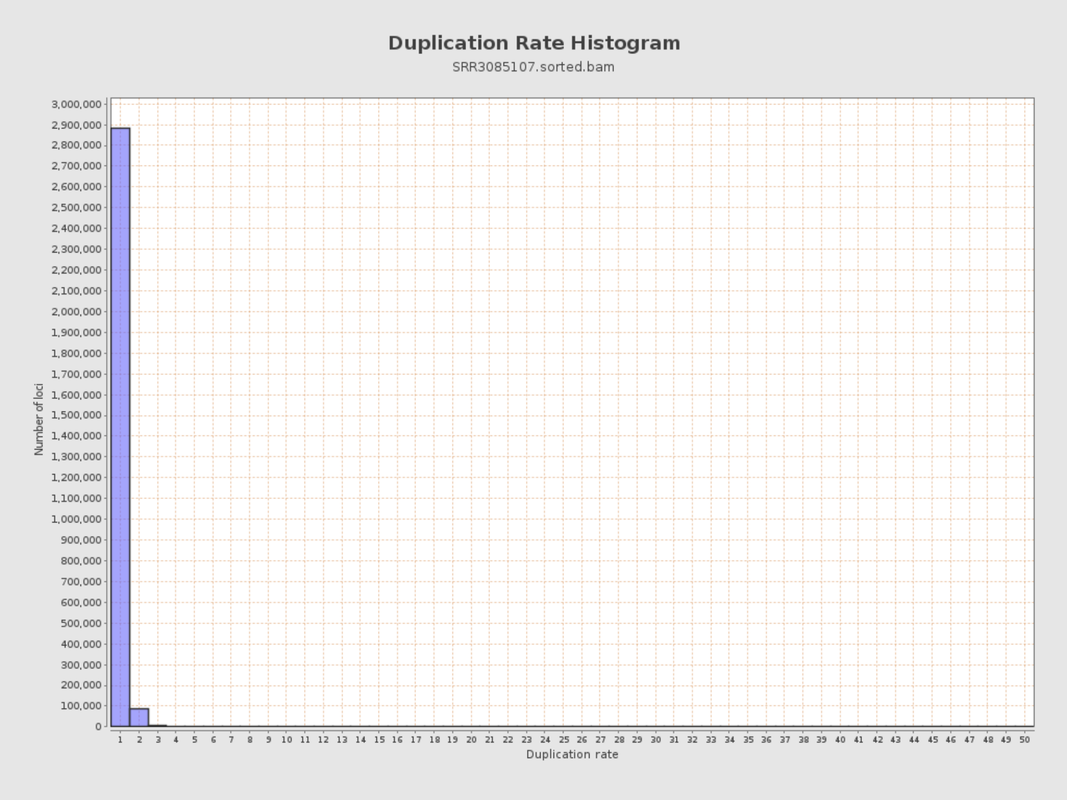
5. Results : Coverage Histogram (0-50X)



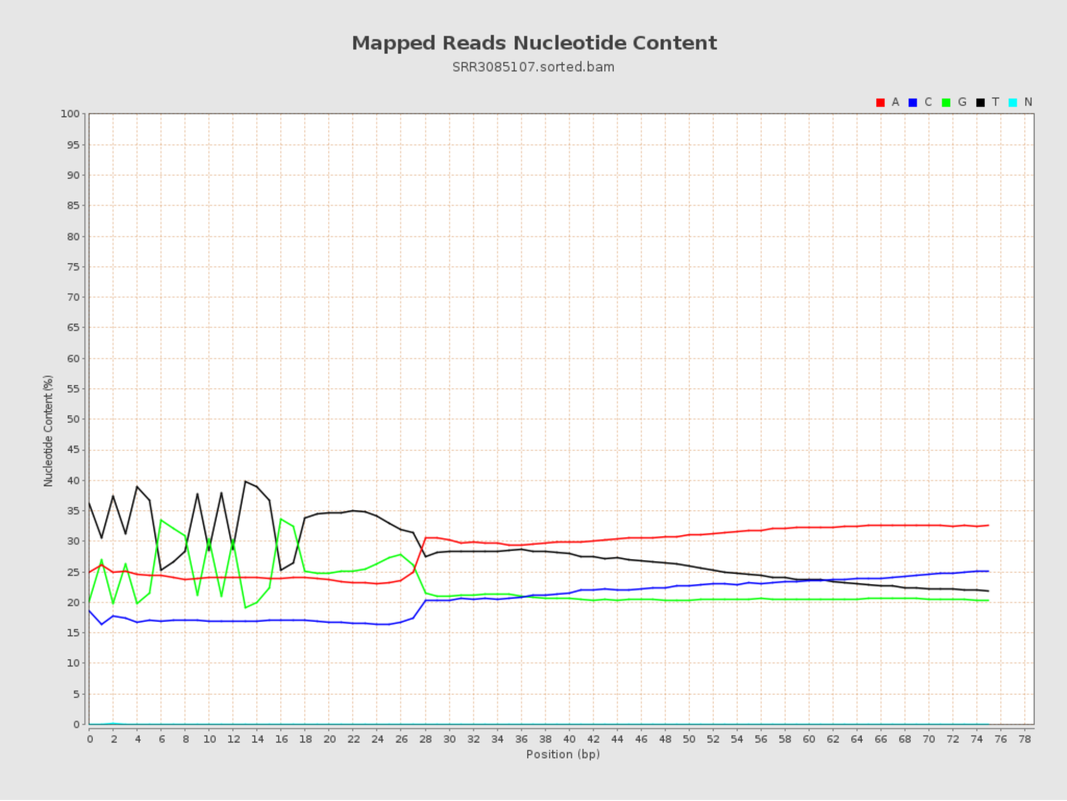
6. Results : Genome Fraction Coverage



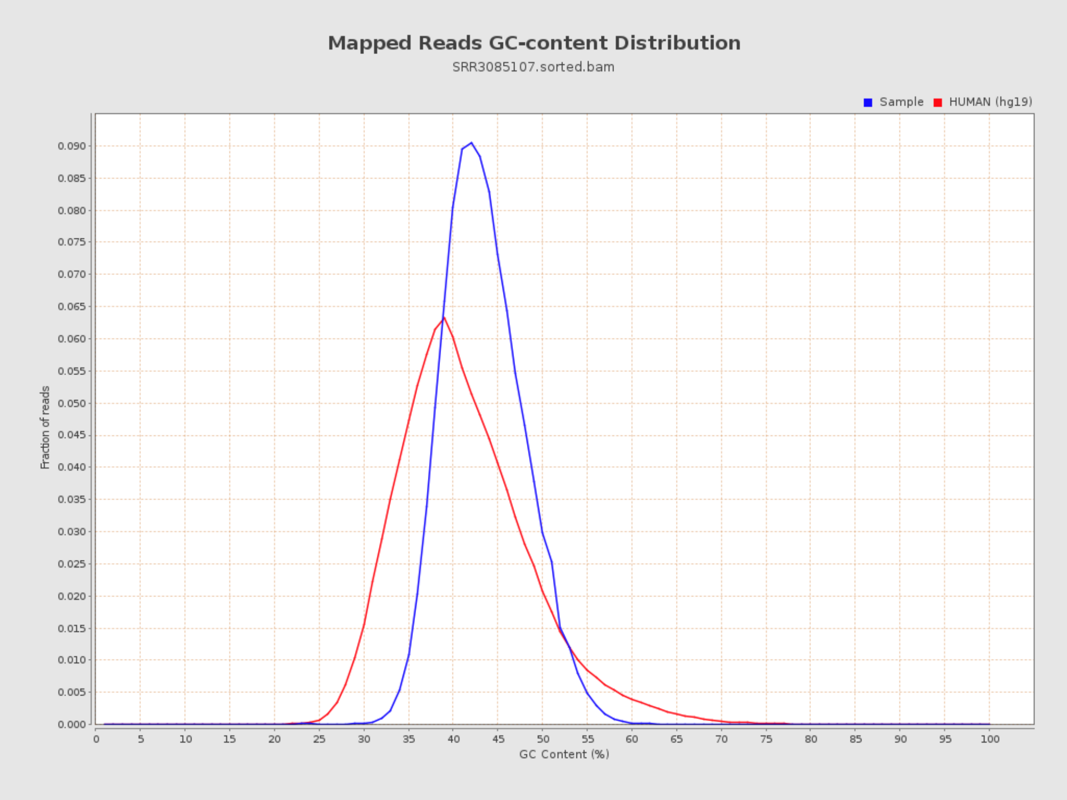
7. Results : Duplication Rate Histogram



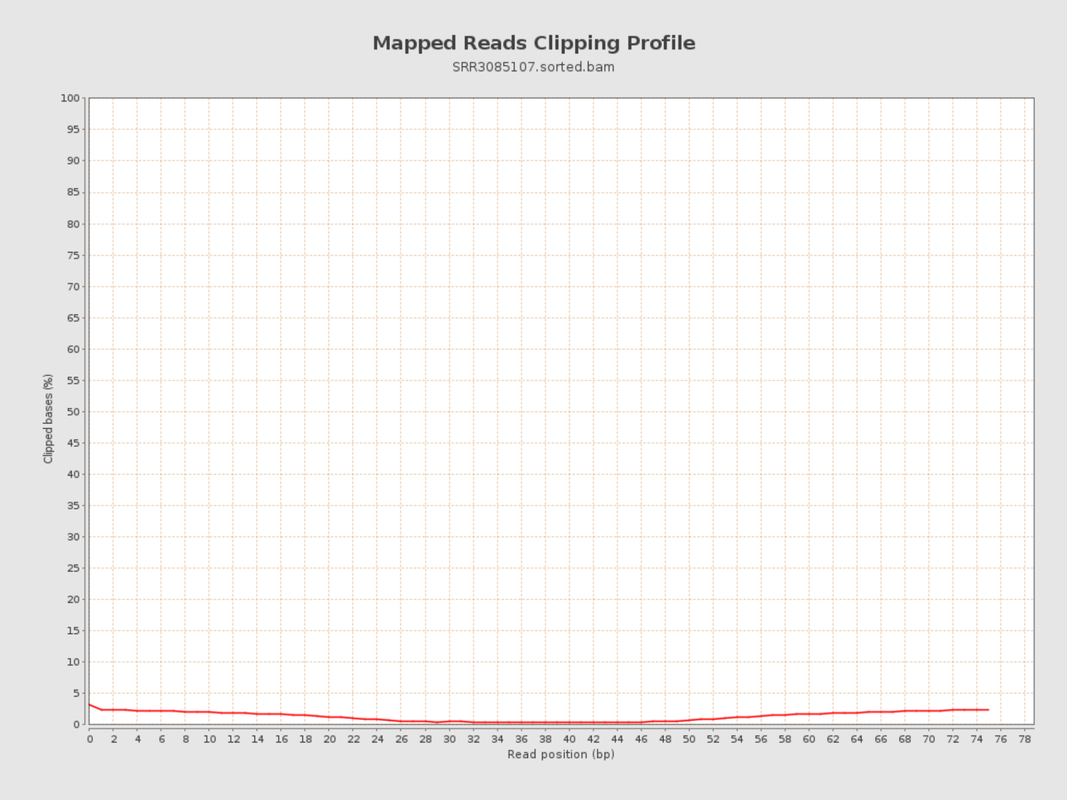
8. Results : Mapped Reads Nucleotide Content



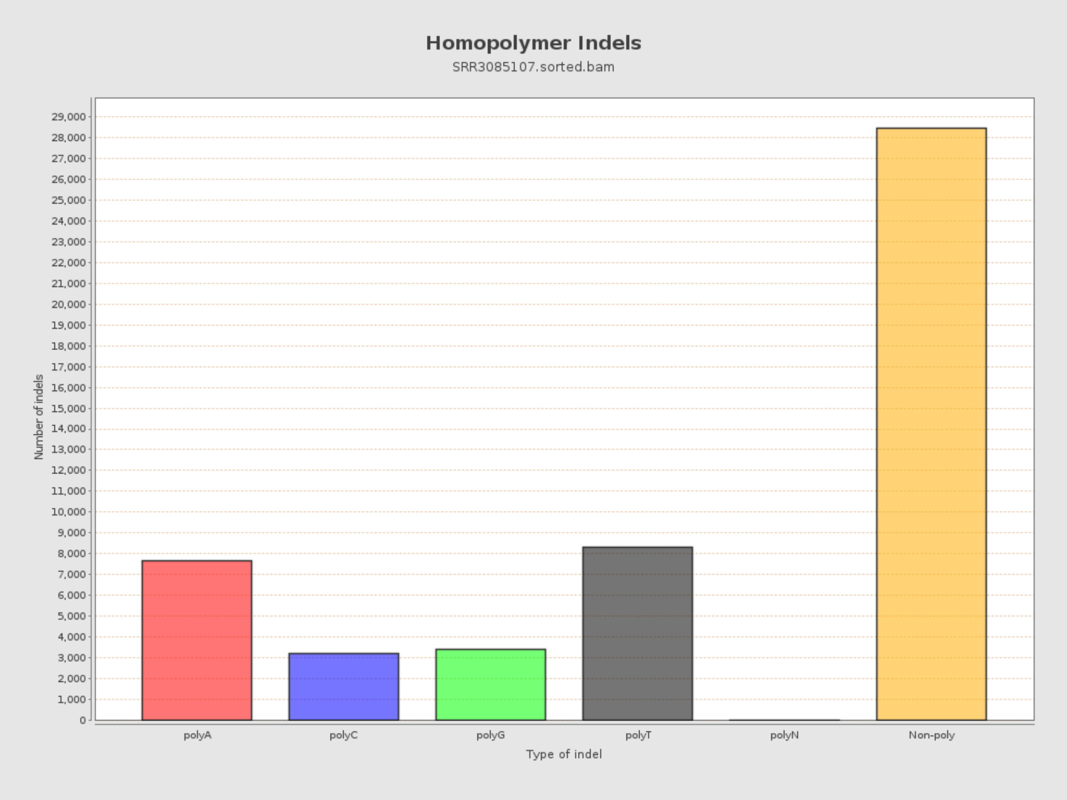
9. Results : Mapped Reads GC-content Distribution



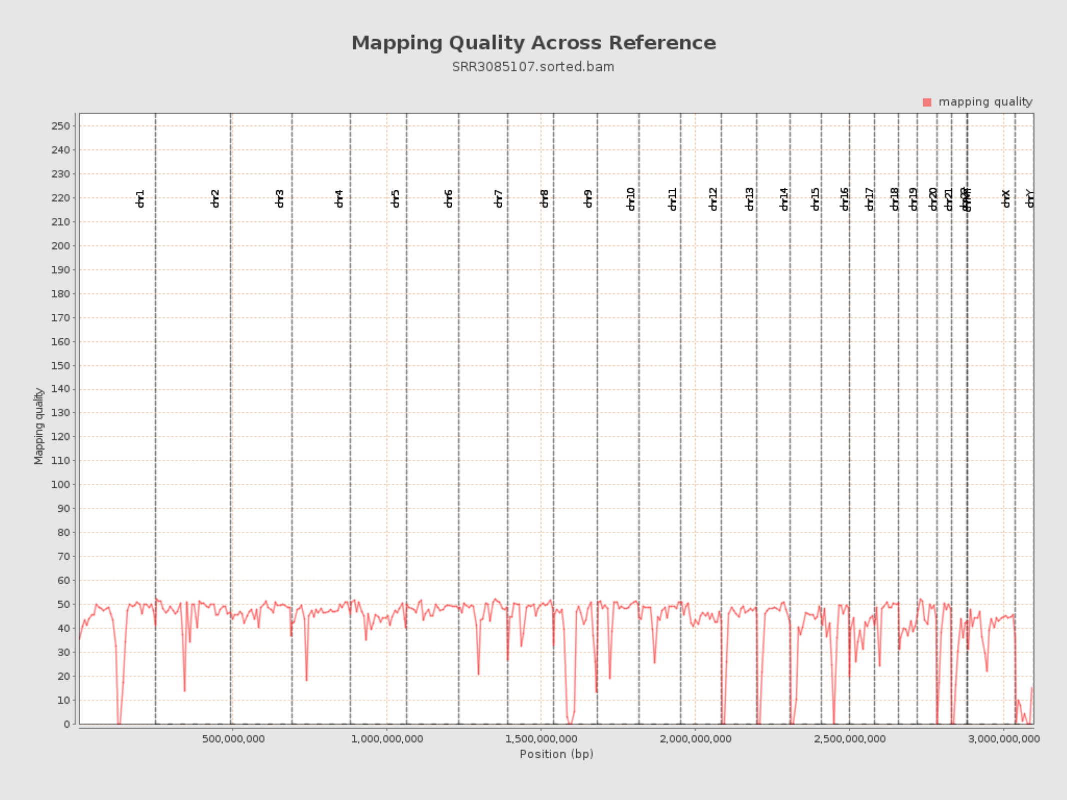
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram