Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 13:45:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084787.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_SRR3084787 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084787.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 13:45:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084787.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,726,713
Mapped reads	1,532,646 / 88.76%
Unmapped reads	194,067 / 11.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,745 / 1.26%
Read min/max/mean length	30 / 76 / 76.44
Duplicated reads (estimated)	57,862 / 3.35%
Duplication rate	2.17%
Clipped reads	719,393 / 41.66%

2.2. ACGT Content

Number/percentage of A's	28,858,406 / 28.32%
Number/percentage of C's	19,239,220 / 18.88%
Number/percentage of T's	30,707,629 / 30.13%
Number/percentage of G's	23,069,465 / 22.64%
Number/percentage of N's	25,820 / 0.03%
GC Percentage	41.52%

2.3. Coverage

Mean	0.0329

Standard Deviation	0.4574

2.4. Mapping Quality

Mean Mapping Quality	43.21

2.5. Mismatches and indels

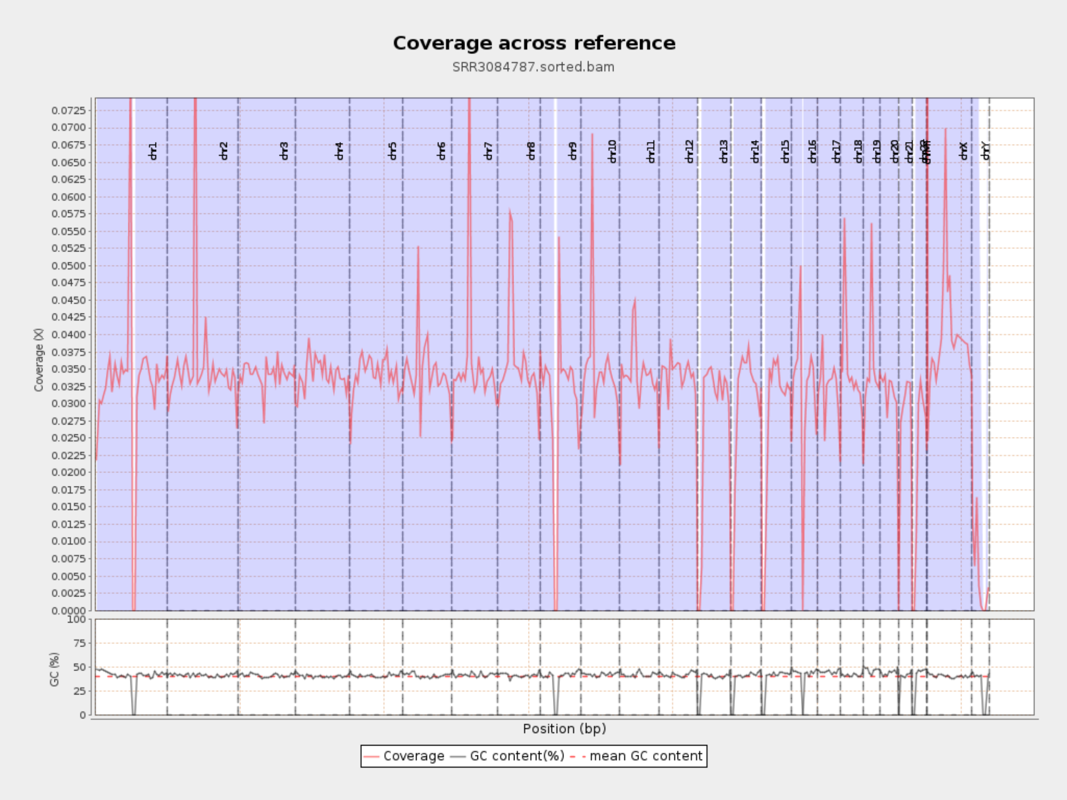
General error rate	0.88%
Mismatches	878,092
Insertions	9,037
Mapped reads with at least one insertion	0.58%
Deletions	20,757
Mapped reads with at least one deletion	1.34%
Homopolymer indels	43.99%

2.6. Chromosome stats

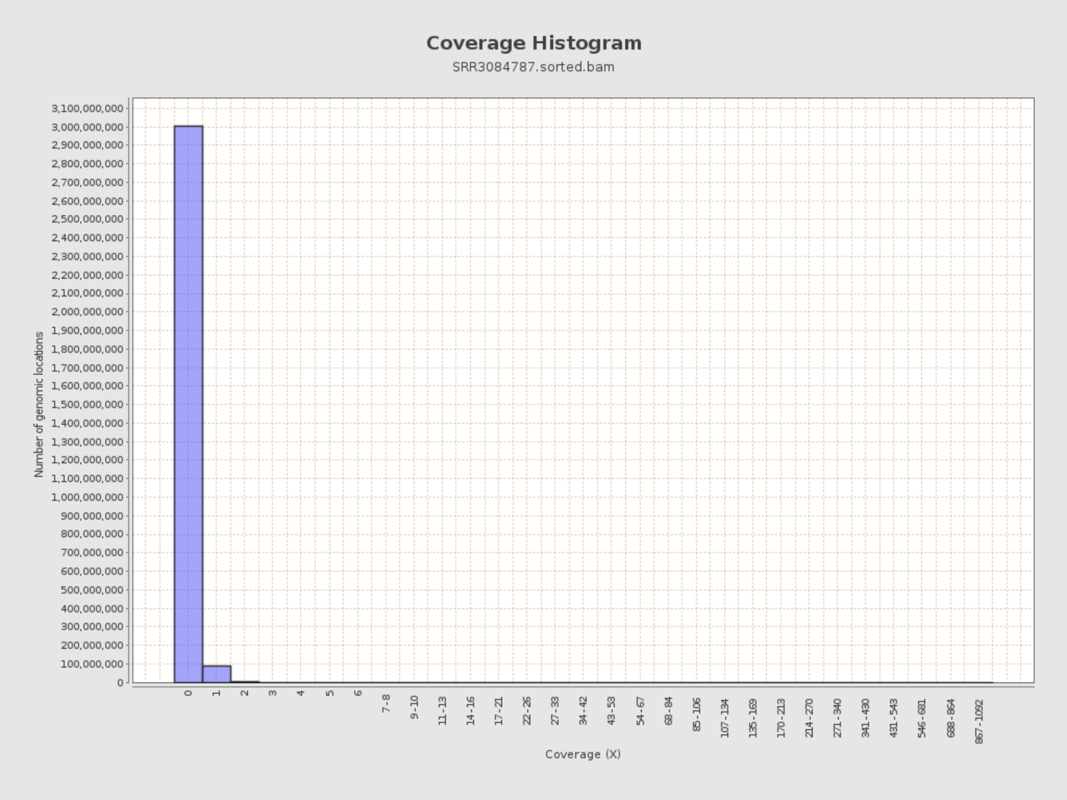
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8179620	0.0328	0.9547
chr2	243199373	8723290	0.0359	0.5122
chr3	198022430	6776097	0.0342	0.1974
chr4	191154276	6531710	0.0342	0.2118
chr5	180915260	6213752	0.0343	0.2018
chr6	171115067	5915597	0.0346	0.2769
chr7	159138663	5734942	0.036	0.649

chr8	146364022	5285941	0.0361	0.6802
chr9	141213431	4280985	0.0303	0.402
chr10	135534747	4777340	0.0352	0.3973
chr11	135006516	4660911	0.0345	0.3756
chr12	133851895	4570614	0.0341	0.2052
chr13	115169878	3156476	0.0274	0.1756
chr14	107349540	3078587	0.0287	0.2116
chr15	102531392	2819588	0.0275	0.1885
chr16	90354753	2816944	0.0312	0.2395
chr17	81195210	2615513	0.0322	0.2376
chr18	78077248	2763492	0.0354	0.7807
chr19	59128983	2104111	0.0356	0.6884
chr20	63025520	1977588	0.0314	0.1982
chr21	48129895	1320000	0.0274	0.1918
chr22	51304566	1079735	0.021	0.1516
chrMT	16571	13718	0.8278	0.9985
chrX	155270560	6235520	0.0402	0.279
chrY	59373566	302980	0.0051	0.1395

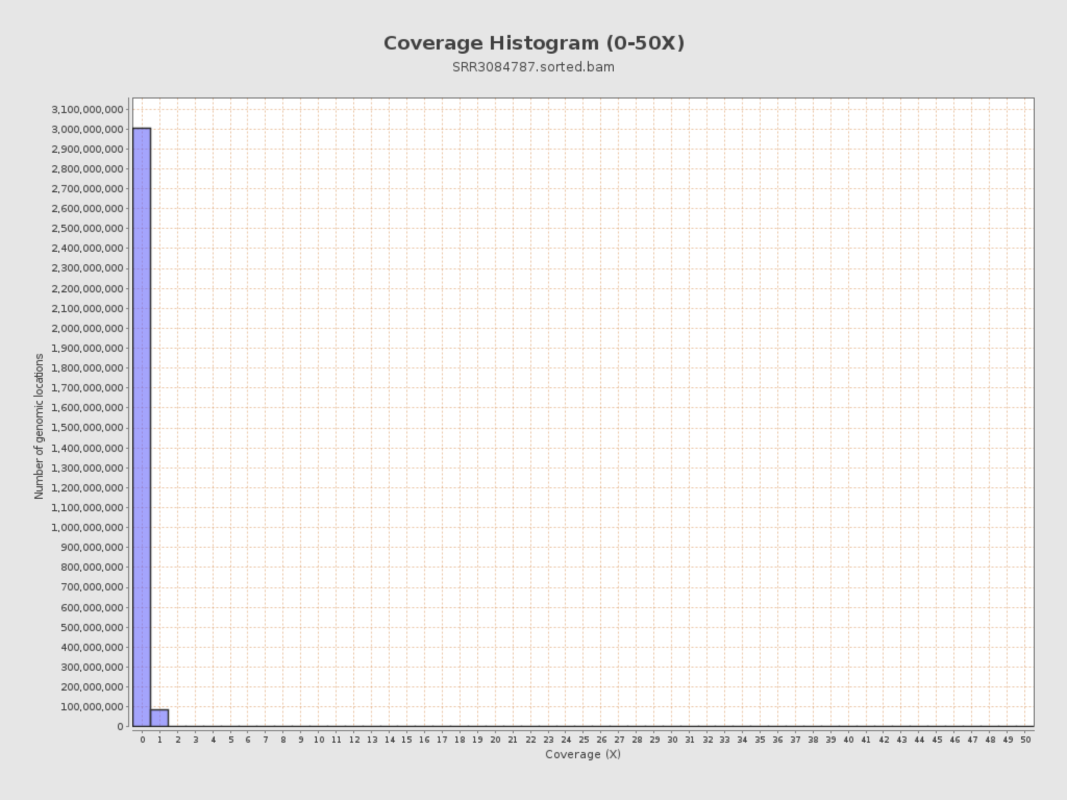
3. Results : Coverage across reference



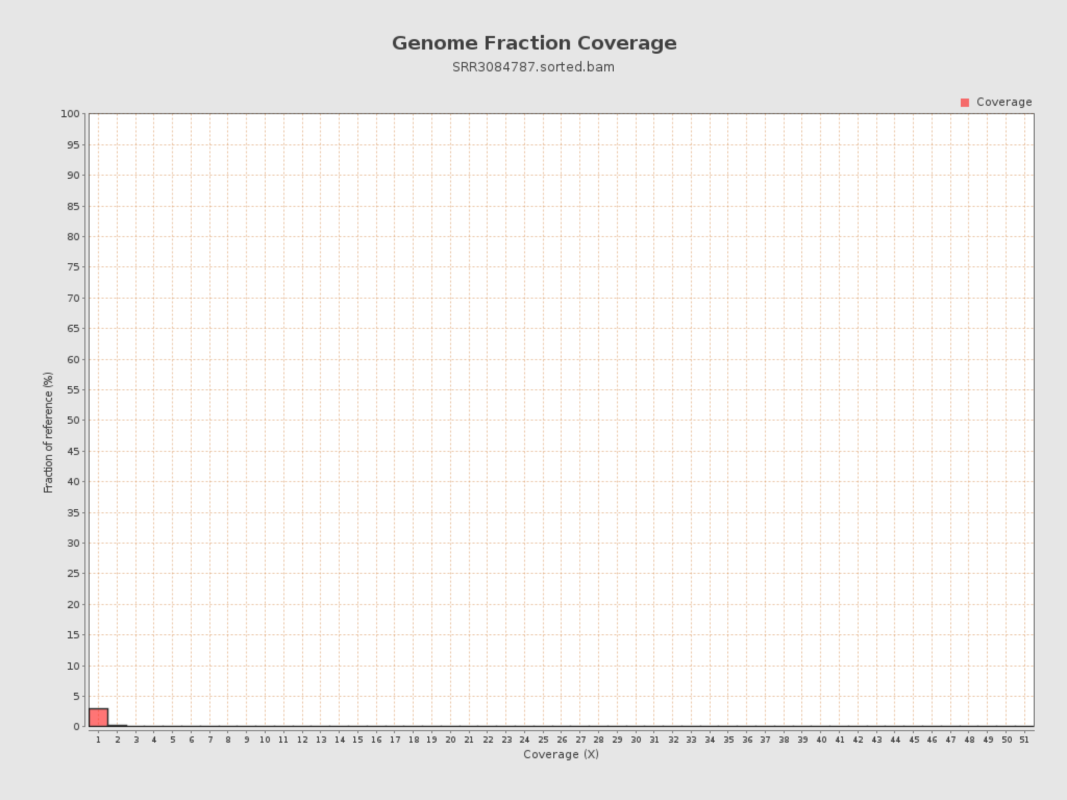
4. Results : Coverage Histogram



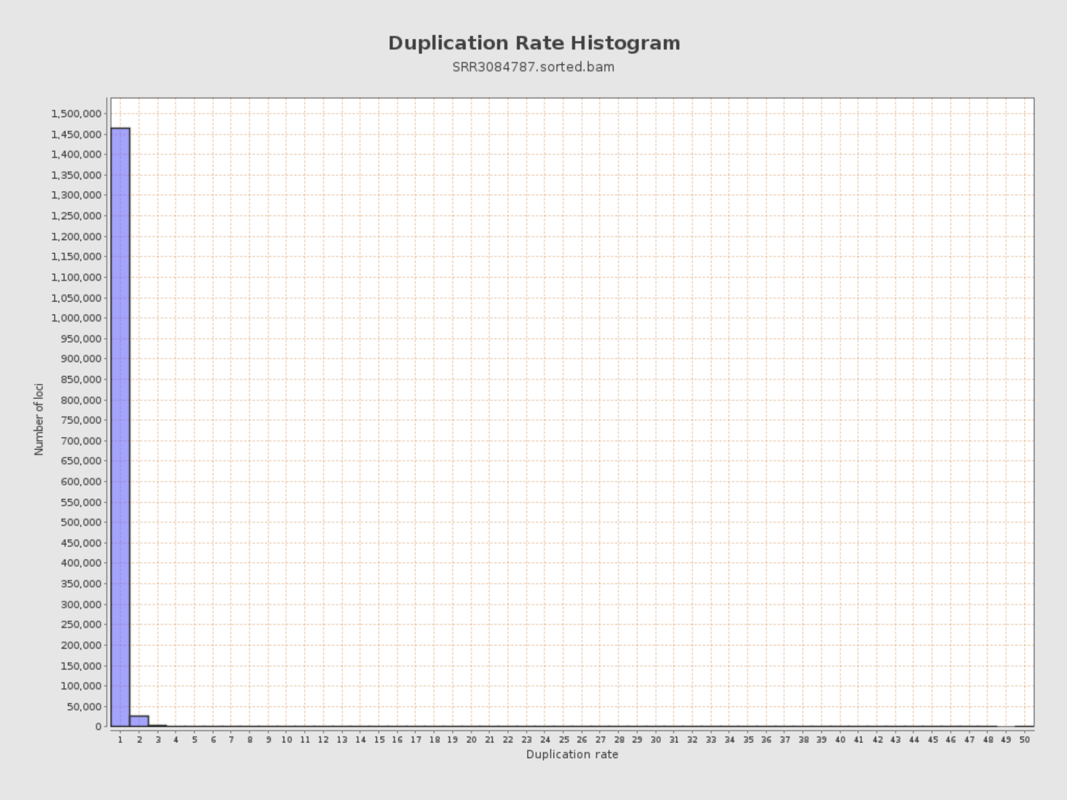
5. Results : Coverage Histogram (0-50X)



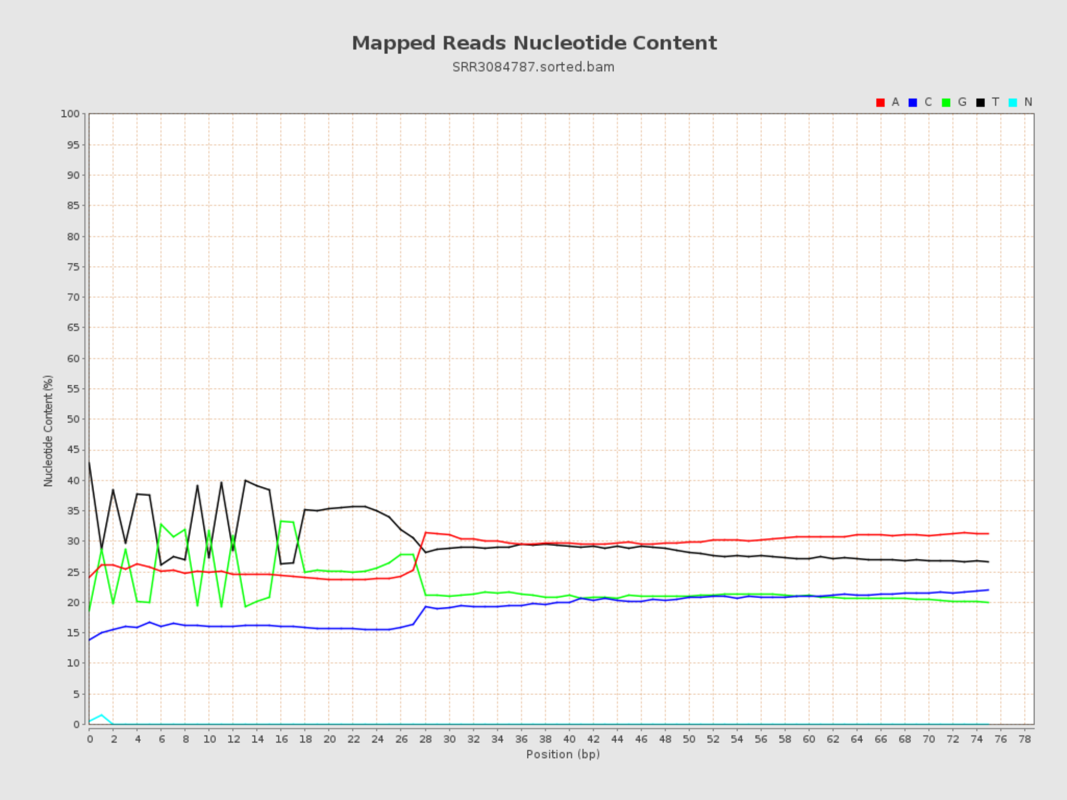
6. Results : Genome Fraction Coverage



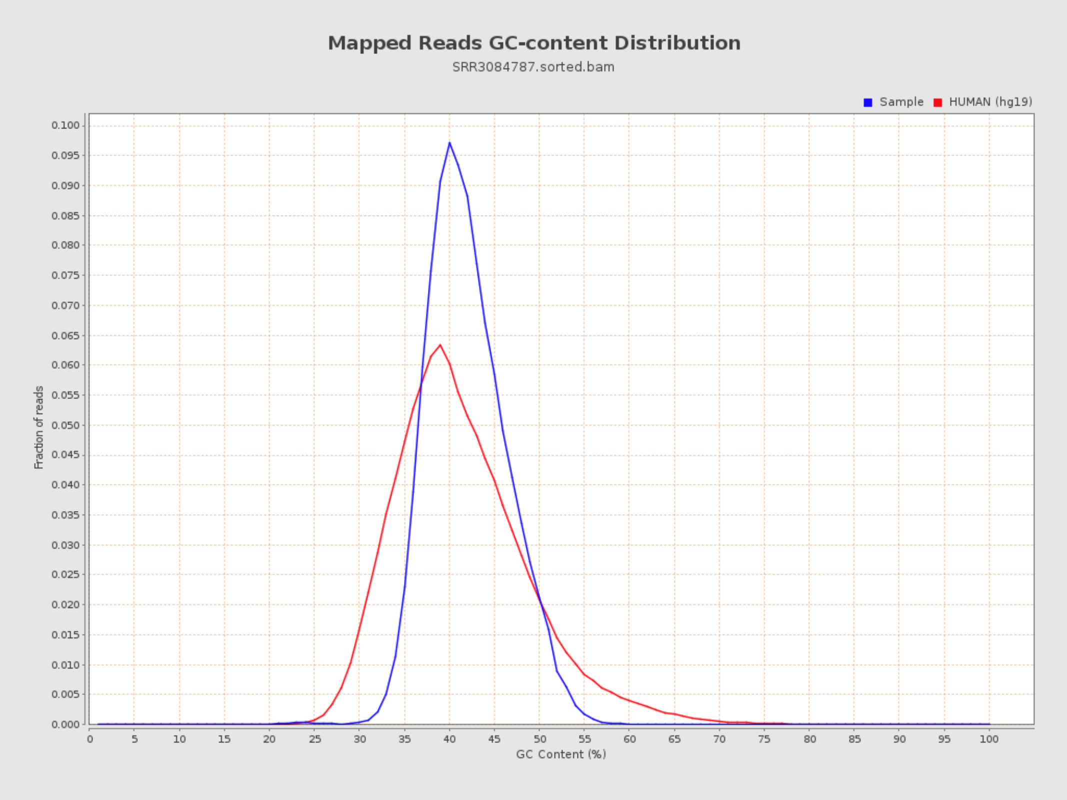
7. Results : Duplication Rate Histogram



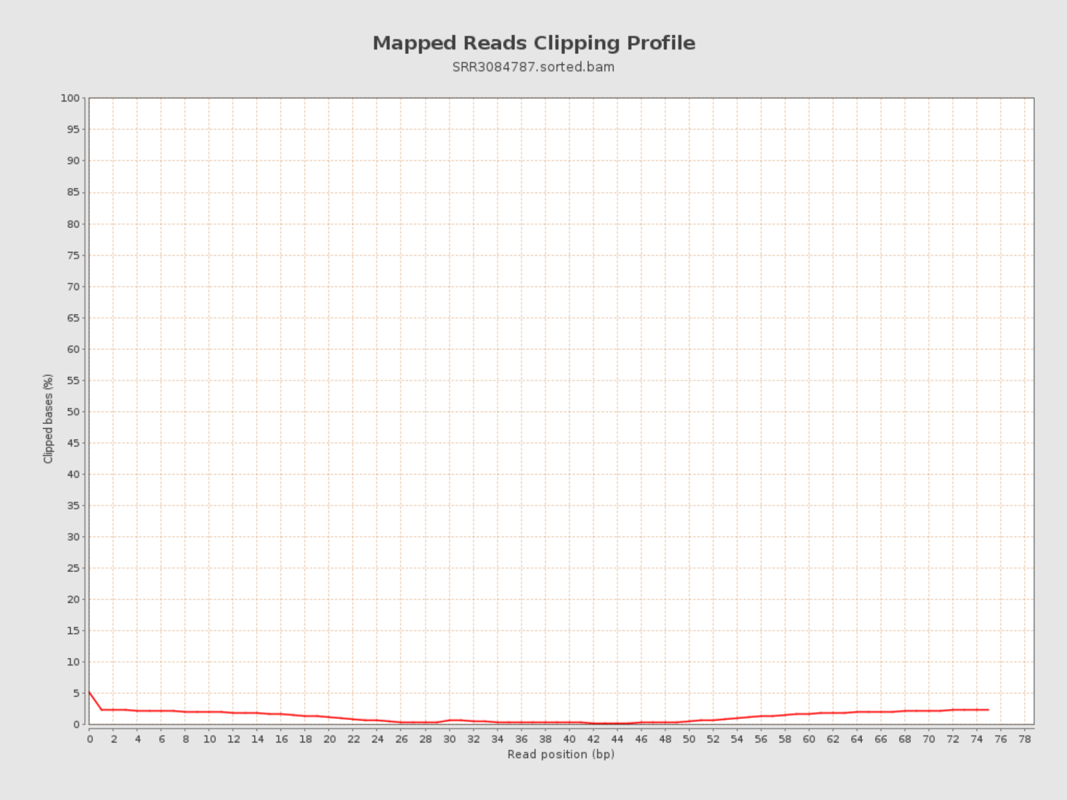
8. Results : Mapped Reads Nucleotide Content



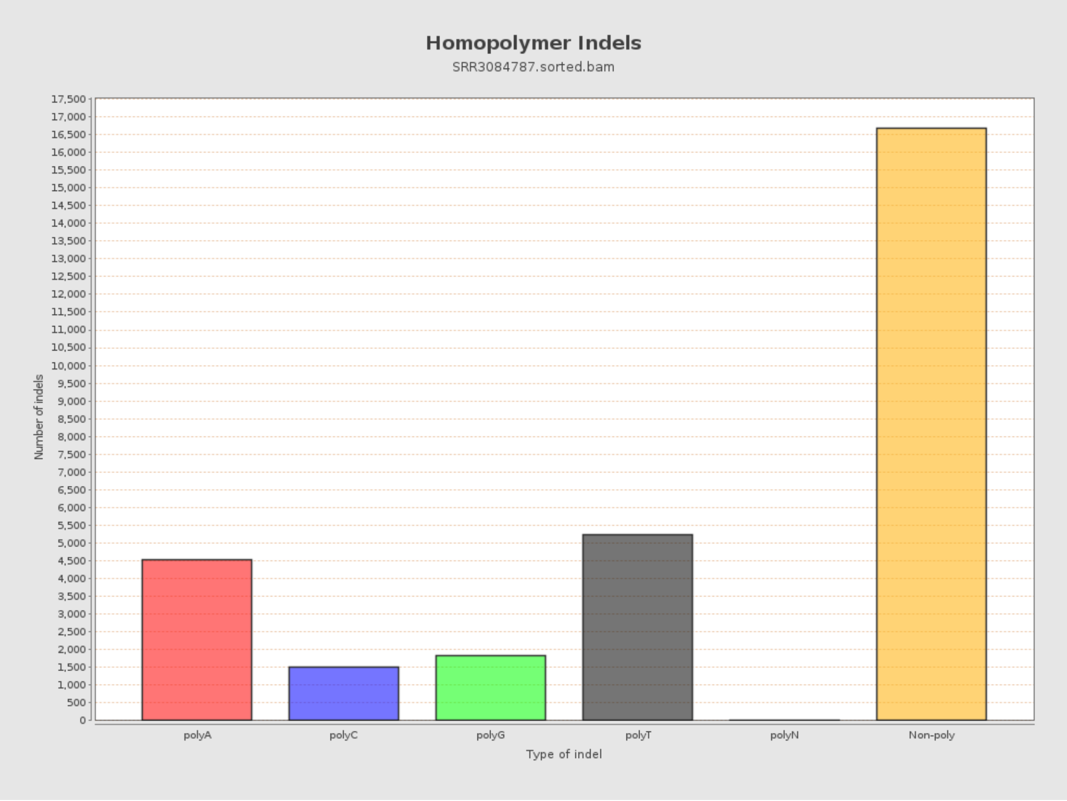
9. Results : Mapped Reads GC-content Distribution



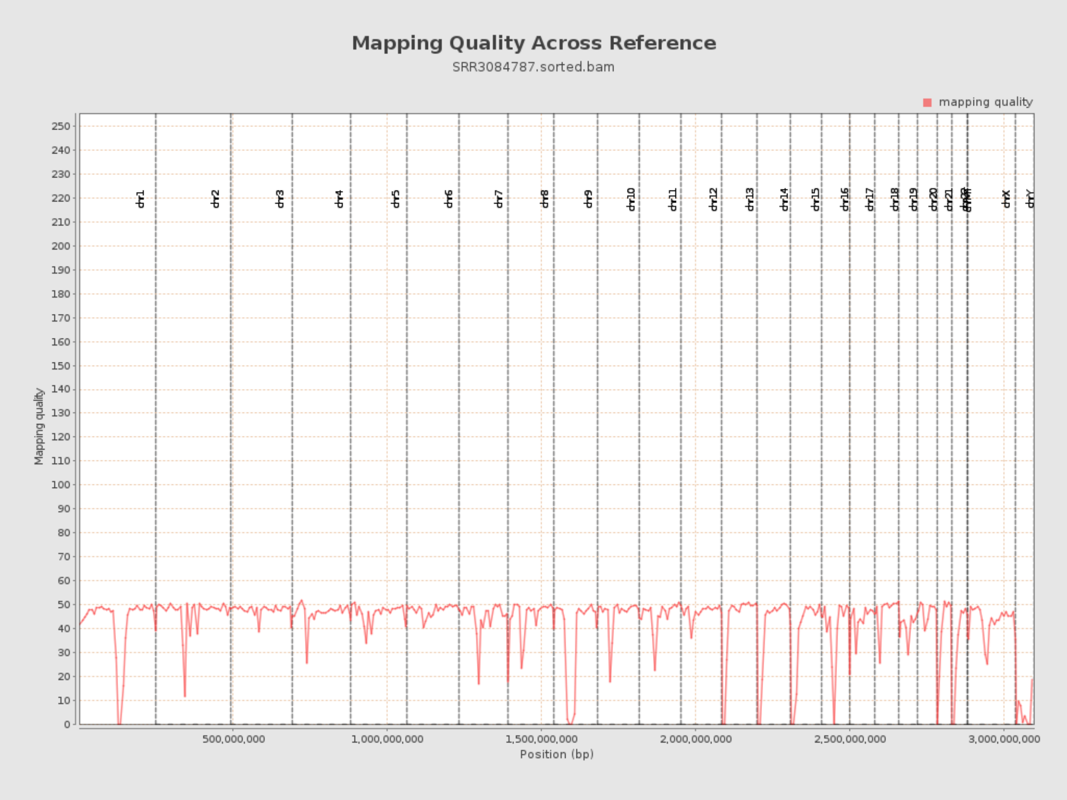
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram