Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 11:36:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084387.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_SRR3084387 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084387.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 11:36:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084387.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,838,353
Mapped reads	1,688,289 / 91.84%
Unmapped reads	150,064 / 8.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,120 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	51,398 / 2.8%
Duplication rate	2.44%
Clipped reads	743,009 / 40.42%

2.2. ACGT Content

Number/percentage of A's	31,465,404 / 27.84%
Number/percentage of C's	21,170,282 / 18.73%
Number/percentage of T's	35,195,127 / 31.14%
Number/percentage of G's	25,037,789 / 22.15%
Number/percentage of N's	145,732 / 0.13%
GC Percentage	40.89%

2.3. Coverage

Mean	0.0365

Standard Deviation	0.3004

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

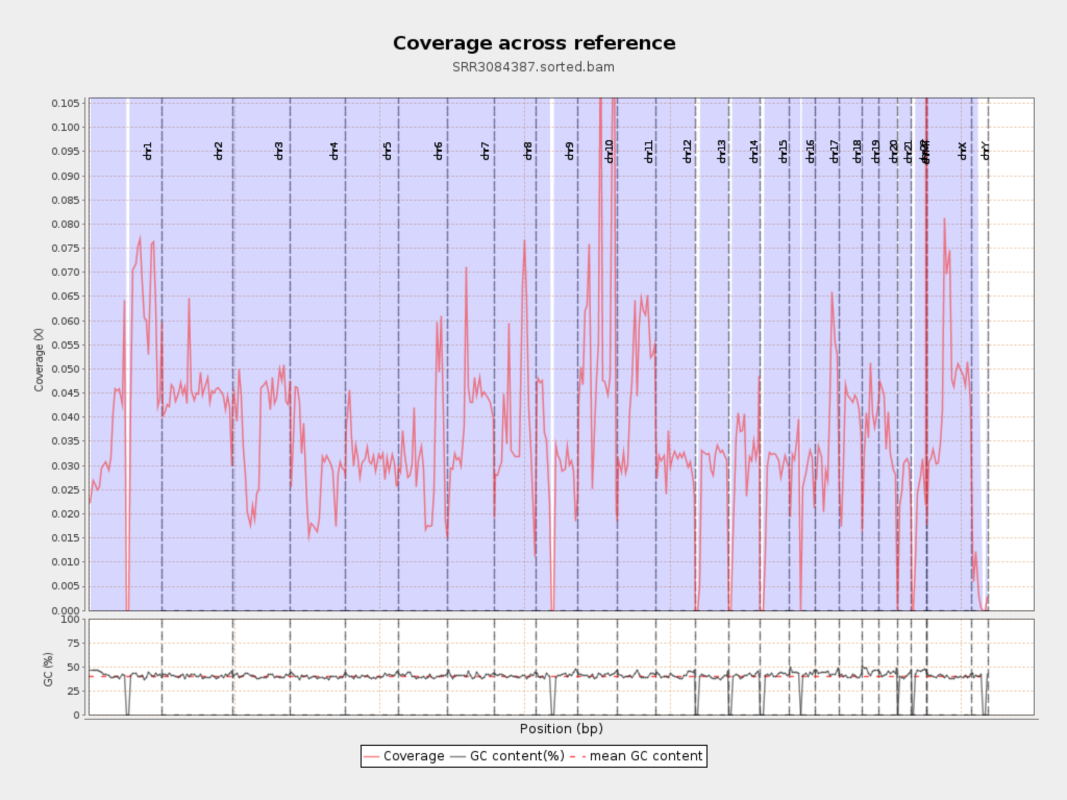
General error rate	0.99%
Mismatches	1,106,265
Insertions	7,982
Mapped reads with at least one insertion	0.47%
Deletions	23,234
Mapped reads with at least one deletion	1.36%
Homopolymer indels	46.74%

2.6. Chromosome stats

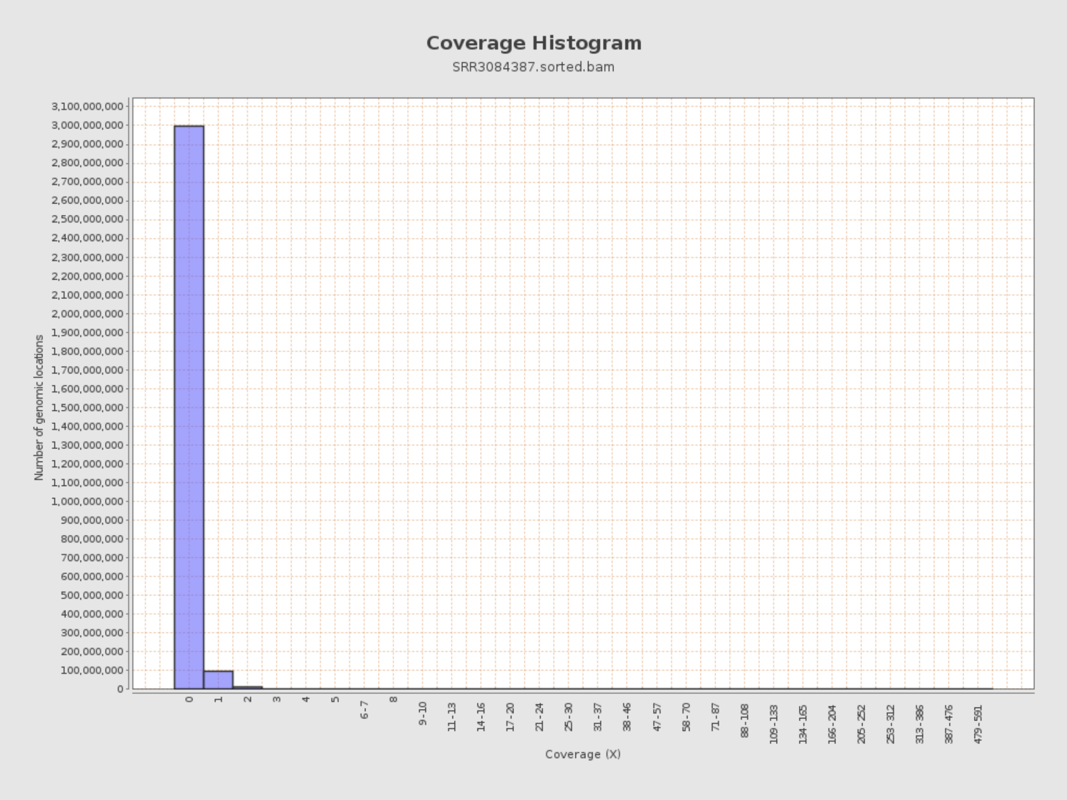
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11266389	0.0452	0.5389
chr2	243199373	10948336	0.045	0.3175
chr3	198022430	7674086	0.0388	0.222
chr4	191154276	5460433	0.0286	0.192
chr5	180915260	5754242	0.0318	0.1937
chr6	171115067	5392524	0.0315	0.216
chr7	159138663	6490397	0.0408	0.4452

chr8	146364022	5669338	0.0387	0.279
chr9	141213431	4209278	0.0298	0.2433
chr10	135534747	8156296	0.0602	0.4563
chr11	135006516	6428683	0.0476	0.284
chr12	133851895	4109955	0.0307	0.1921
chr13	115169878	3035220	0.0264	0.1759
chr14	107349540	3096692	0.0288	0.1901
chr15	102531392	2579321	0.0252	0.18
chr16	90354753	2494917	0.0276	0.2017
chr17	81195210	3150901	0.0388	0.2254
chr18	78077248	3010885	0.0386	0.4001
chr19	59128983	2313438	0.0391	0.3628
chr20	63025520	2280908	0.0362	0.21
chr21	48129895	1177456	0.0245	0.1789
chr22	51304566	955133	0.0186	0.1478
chrMT	16571	10069	0.6076	0.818
chrX	155270560	7137254	0.046	0.2585
chrY	59373566	252725	0.0043	0.0961

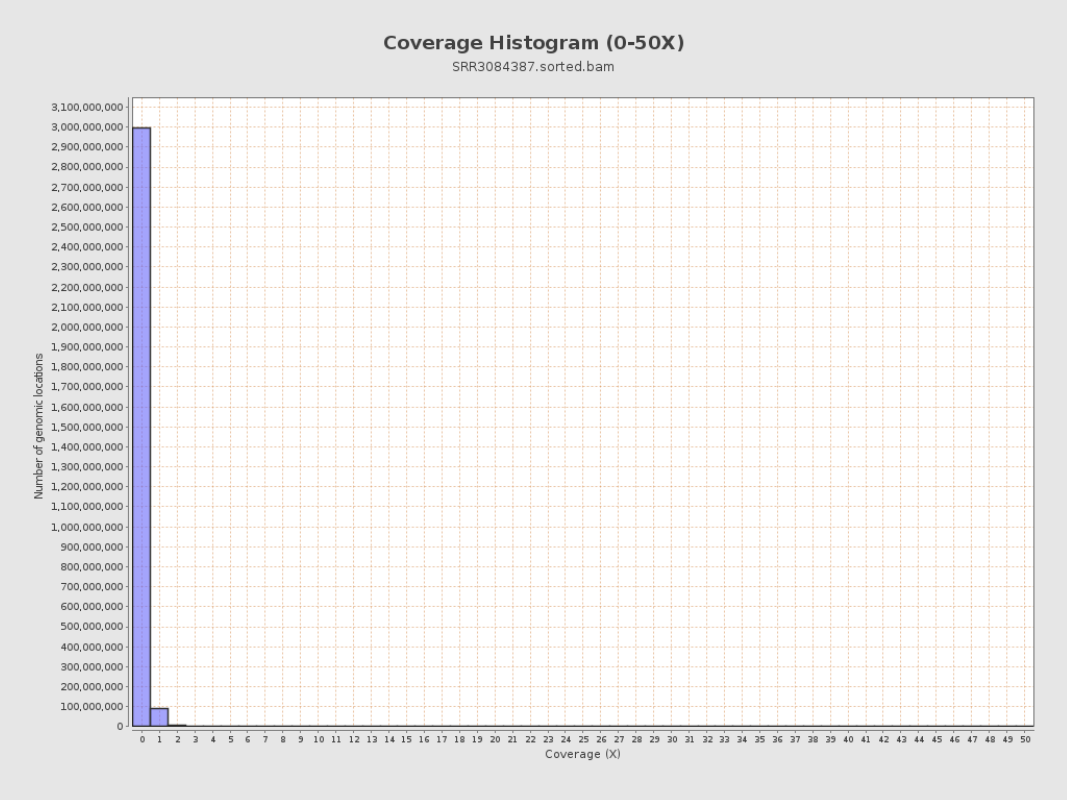
3. Results : Coverage across reference



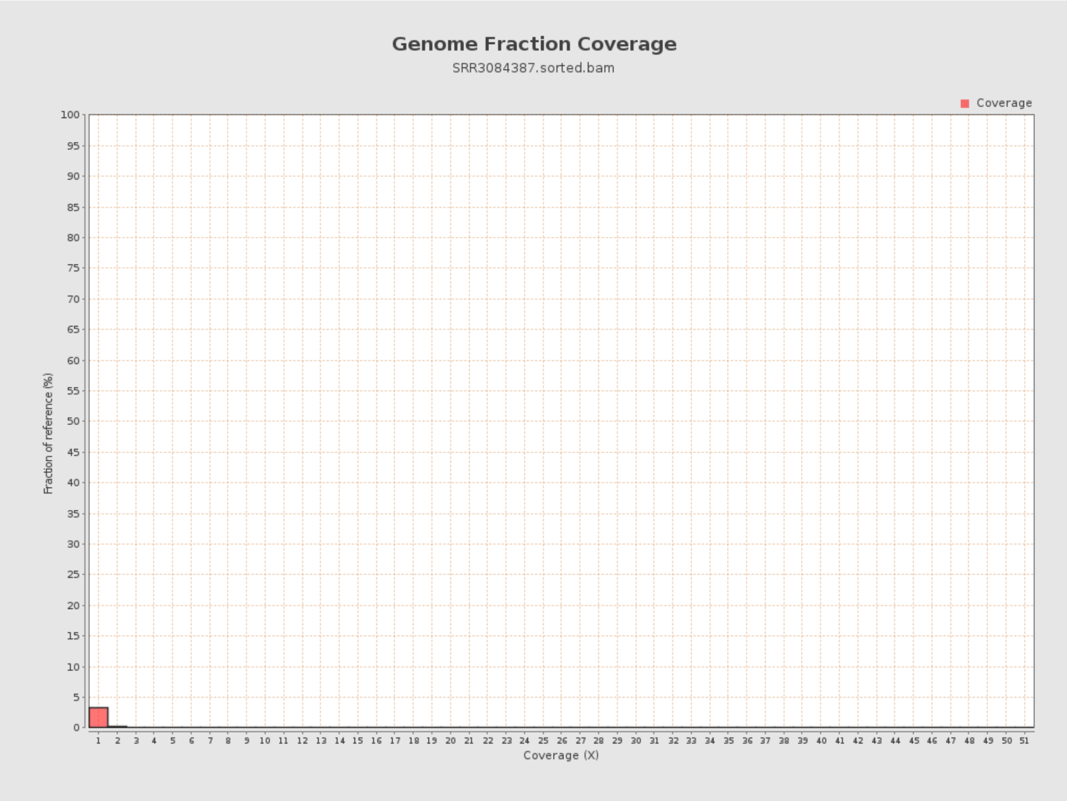
4. Results : Coverage Histogram



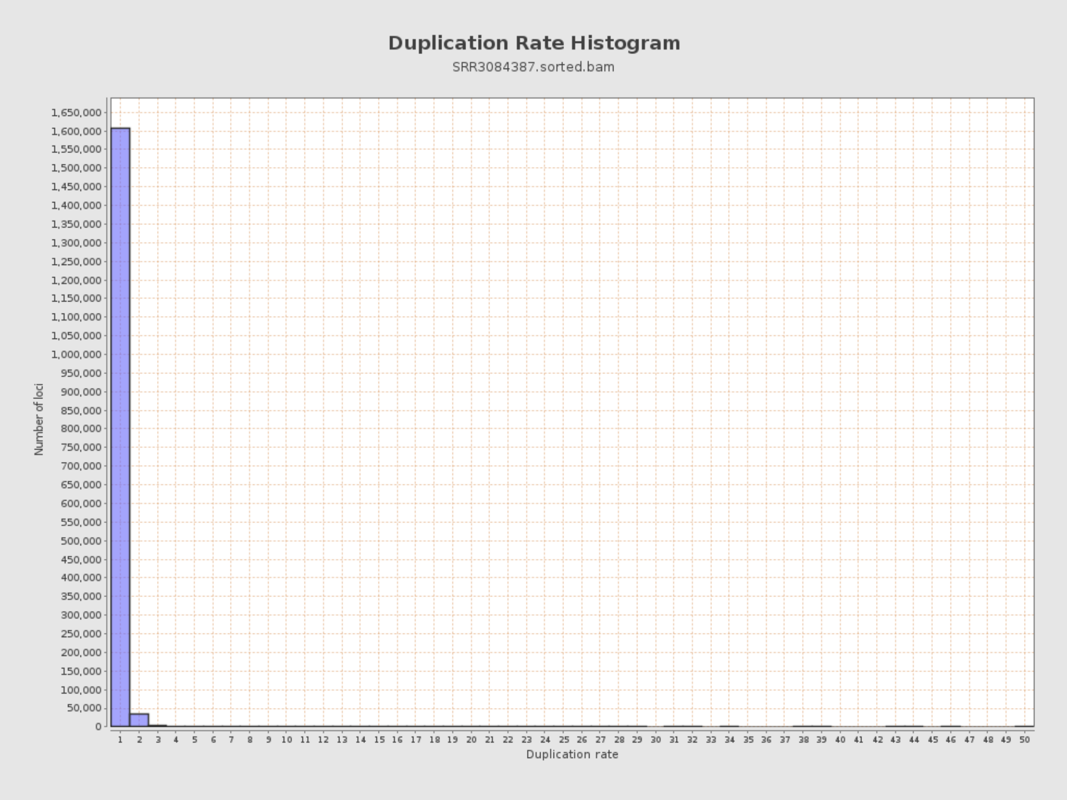
5. Results : Coverage Histogram (0-50X)



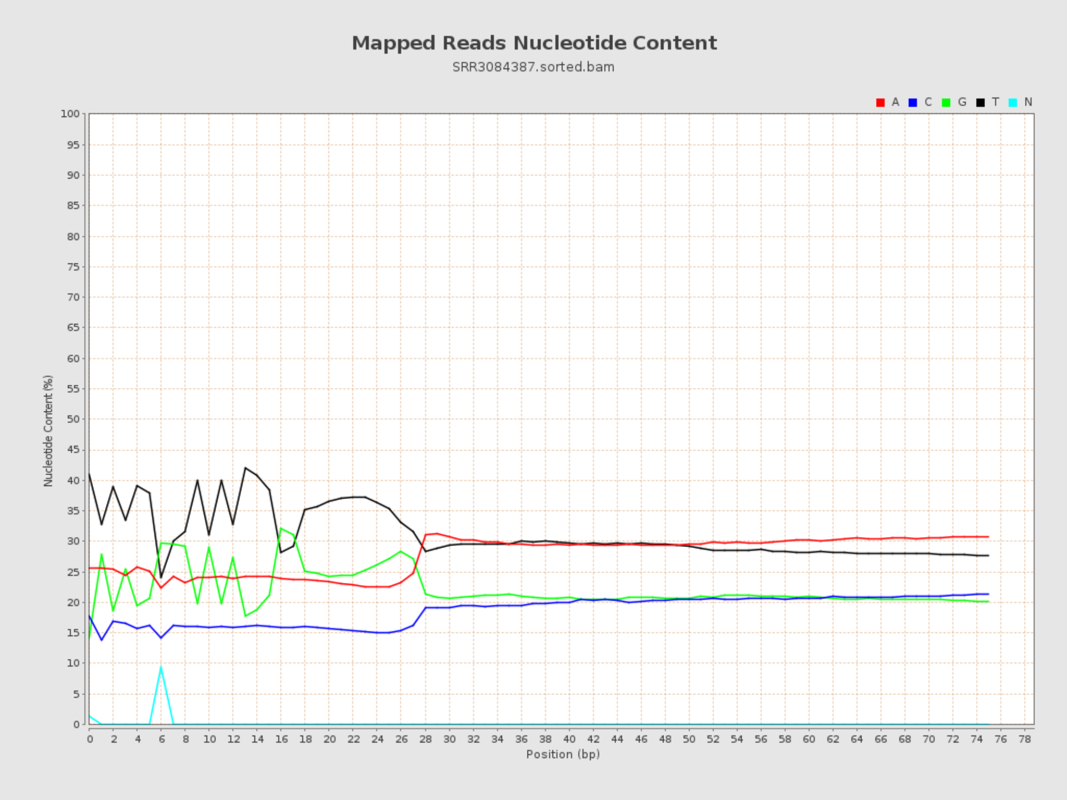
6. Results : Genome Fraction Coverage



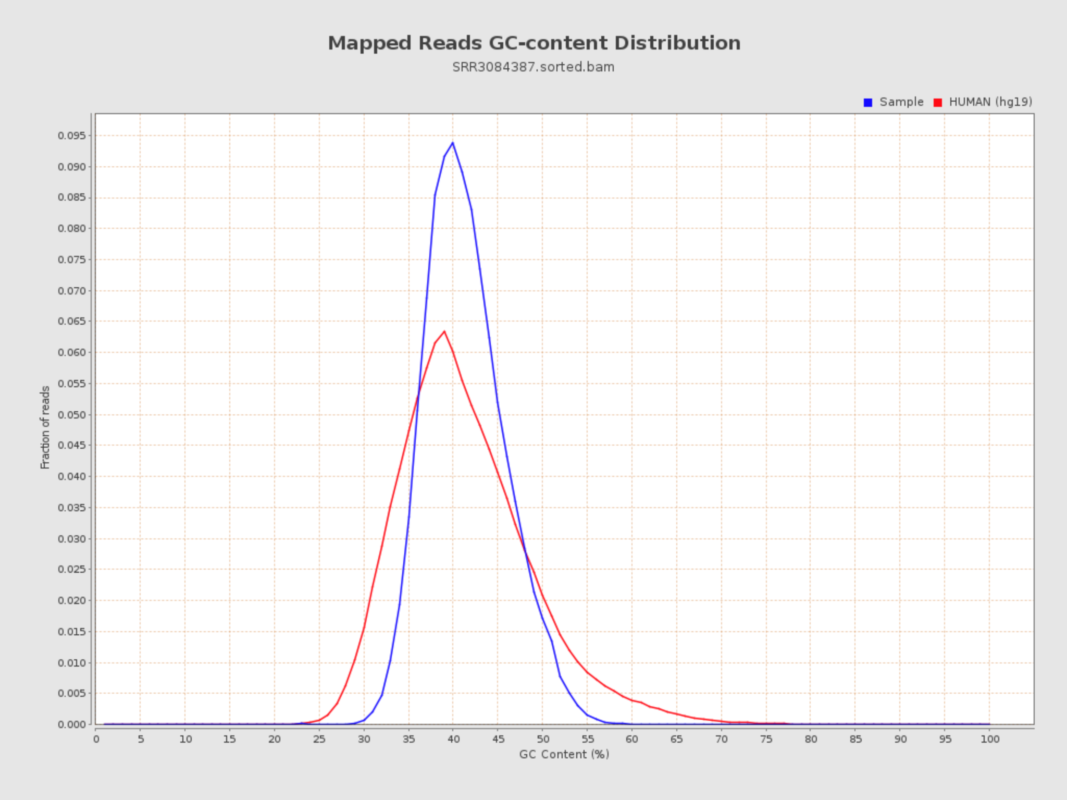
7. Results : Duplication Rate Histogram



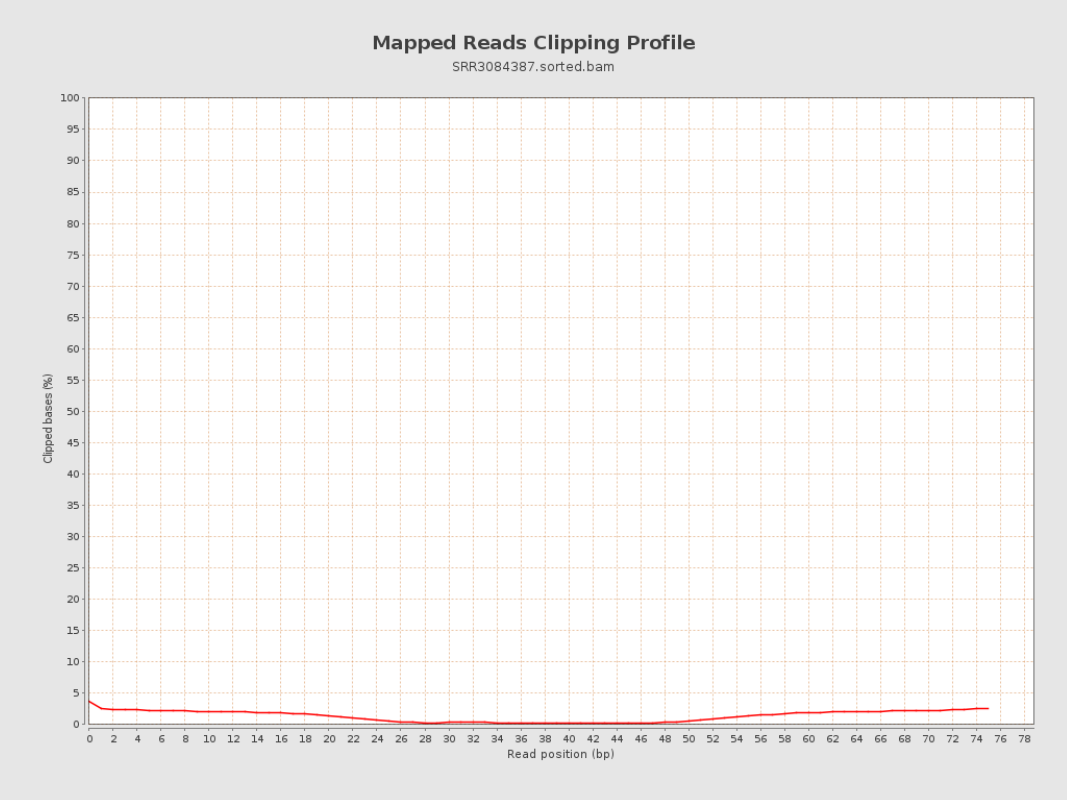
8. Results : Mapped Reads Nucleotide Content



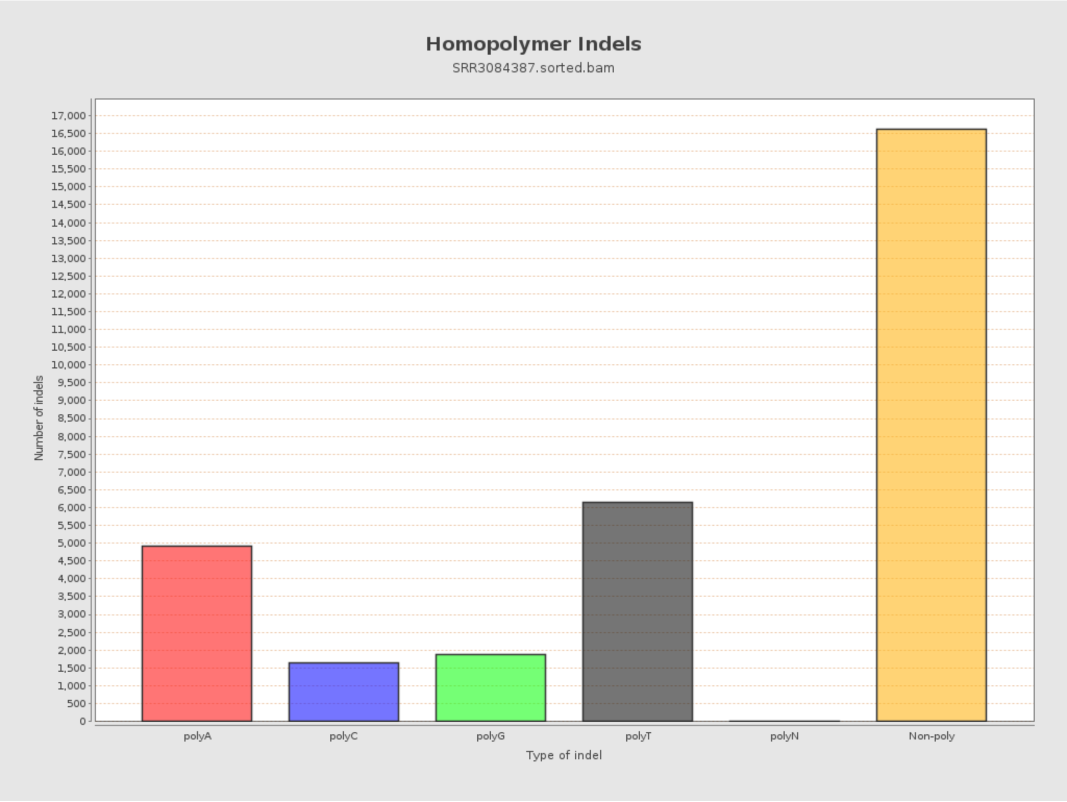
9. Results : Mapped Reads GC-content Distribution



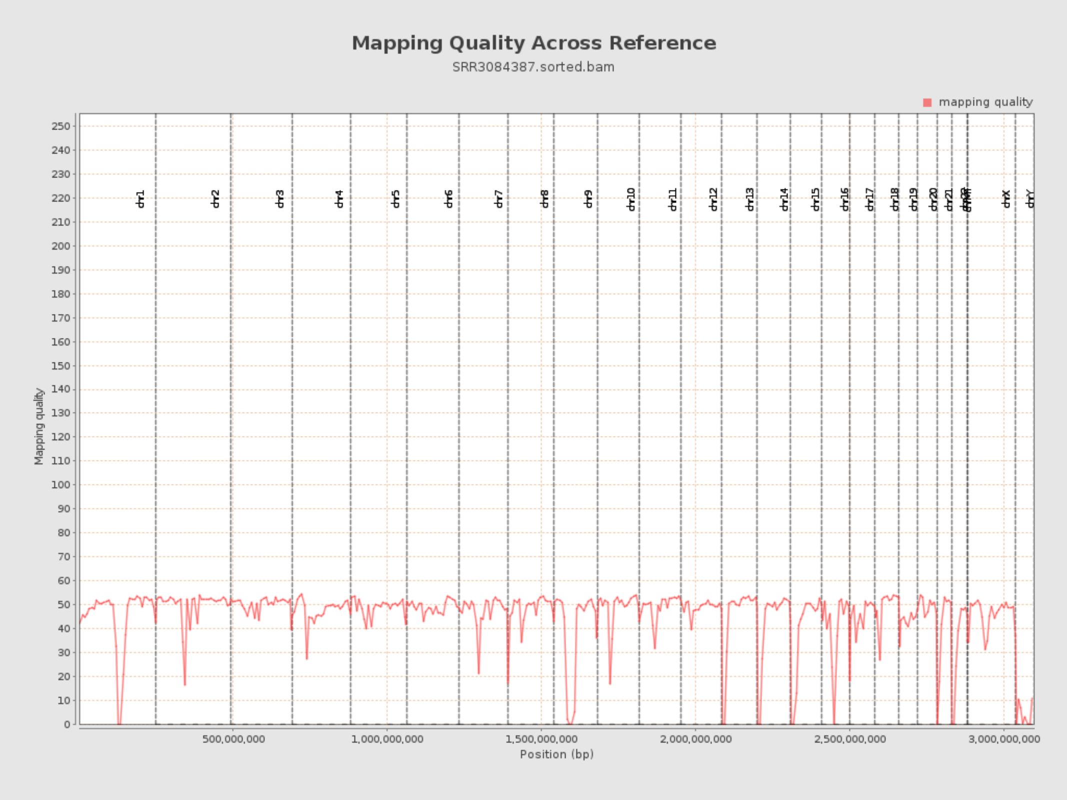
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram