Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:22:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004126.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_SRR6004126 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004126.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:22:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004126.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,692,452
Mapped reads	2,150,657 / 79.88%
Unmapped reads	541,795 / 20.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,873 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	98,839 / 3.67%
Duplication rate	3.13%
Clipped reads	1,040,004 / 38.63%

2.2. ACGT Content

Number/percentage of A's	38,729,812 / 27.22%
Number/percentage of C's	25,863,848 / 18.18%
Number/percentage of T's	45,191,334 / 31.76%
Number/percentage of G's	32,496,232 / 22.84%
Number/percentage of N's	14,908 / 0.01%
GC Percentage	41.01%

2.3. Coverage

Mean	0.046

Standard Deviation	0.5955

2.4. Mapping Quality

Mean Mapping Quality	42.25

2.5. Mismatches and indels

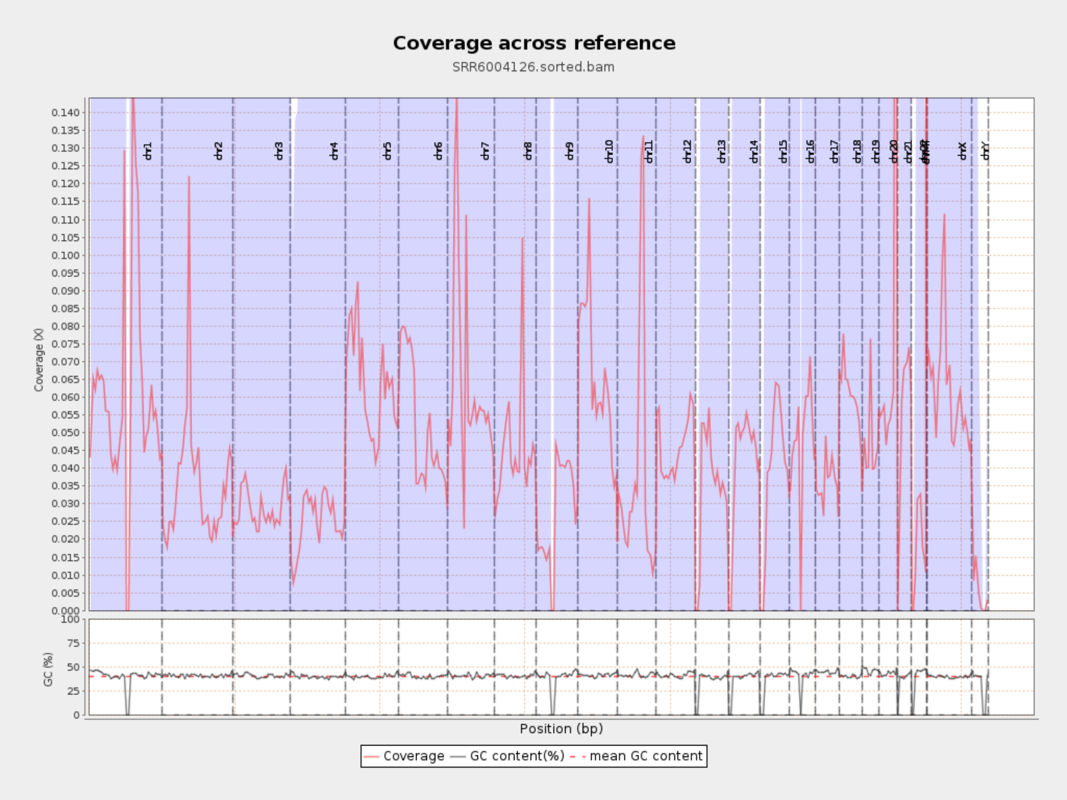
General error rate	1.04%
Mismatches	1,456,925
Insertions	13,506
Mapped reads with at least one insertion	0.62%
Deletions	40,524
Mapped reads with at least one deletion	1.86%
Homopolymer indels	46.69%

2.6. Chromosome stats

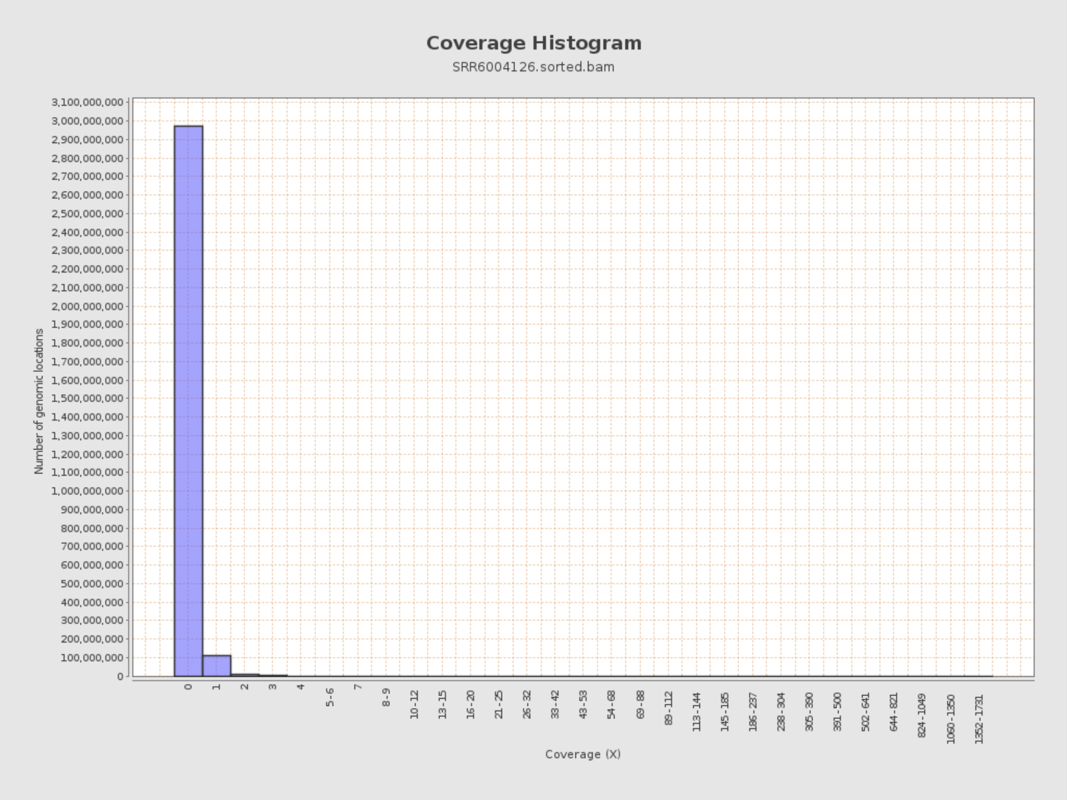
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15135086	0.0607	1.4846
chr2	243199373	8643656	0.0355	0.6605
chr3	198022430	5706748	0.0288	0.1982
chr4	191154276	4743272	0.0248	0.1875
chr5	180915260	11553693	0.0639	0.2862
chr6	171115067	8962121	0.0524	0.3421
chr7	159138663	10456029	0.0657	0.8702

chr8	146364022	6547772	0.0447	0.4592
chr9	141213431	3893408	0.0276	0.3847
chr10	135534747	9012854	0.0665	0.51
chr11	135006516	5280478	0.0391	0.3102
chr12	133851895	6172455	0.0461	0.2456
chr13	115169878	3955599	0.0343	0.2036
chr14	107349540	4410693	0.0411	0.244
chr15	102531392	3997646	0.039	0.2329
chr16	90354753	4334928	0.048	0.2834
chr17	81195210	2928172	0.0361	0.2351
chr18	78077248	4813487	0.0617	0.7666
chr19	59128983	2779411	0.047	0.9487
chr20	63025520	5364073	0.0851	0.3647
chr21	48129895	2607349	0.0542	0.2679
chr22	51304566	839465	0.0164	0.1401
chrMT	16571	36534	2.2047	2.1113
chrX	155270560	9810599	0.0632	0.3767
chrY	59373566	379014	0.0064	0.1256

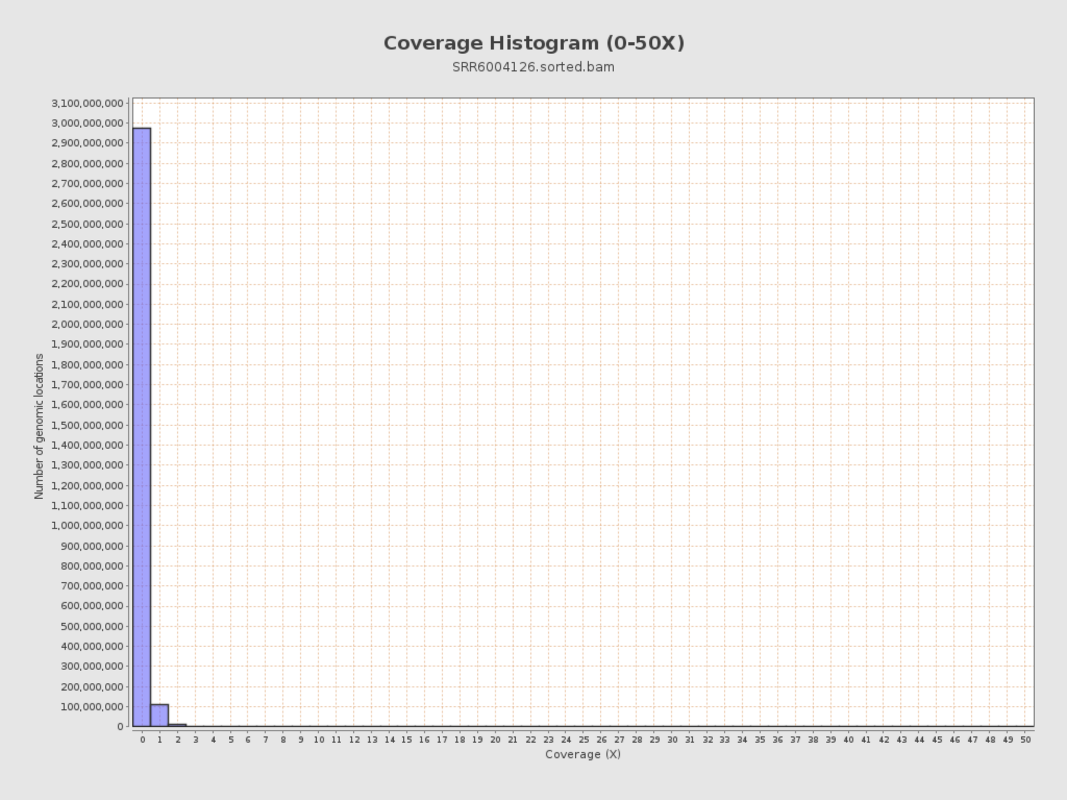
3. Results : Coverage across reference



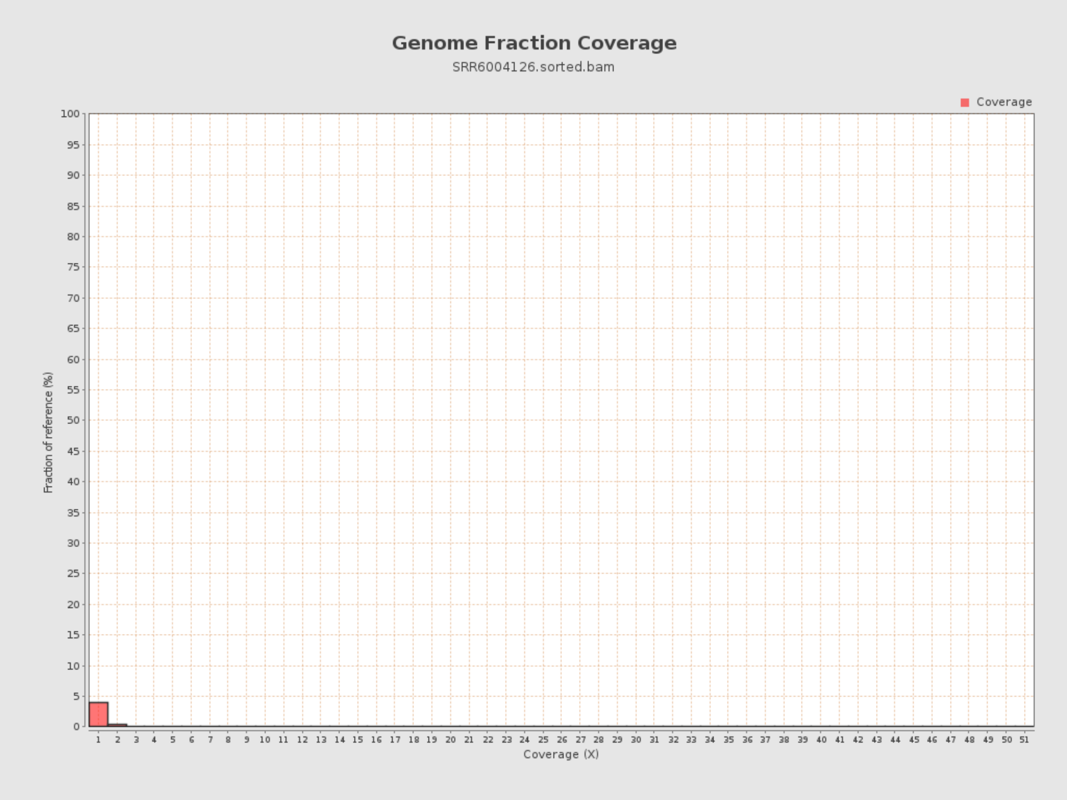
4. Results : Coverage Histogram



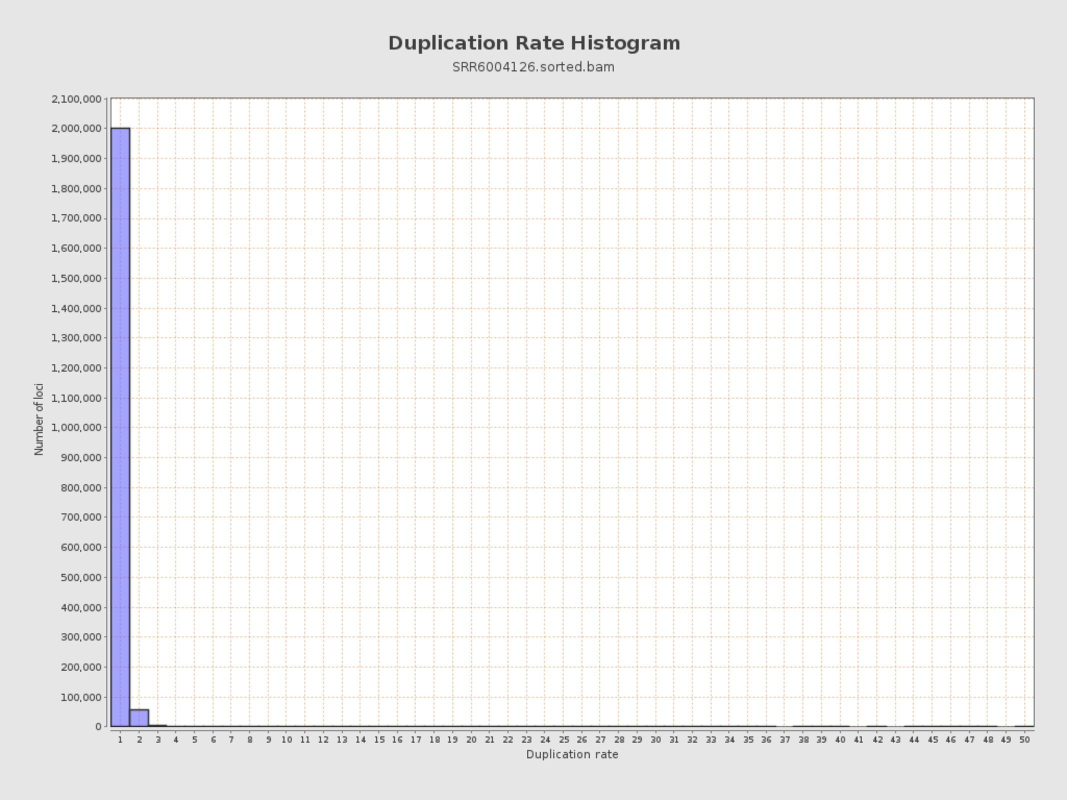
5. Results : Coverage Histogram (0-50X)



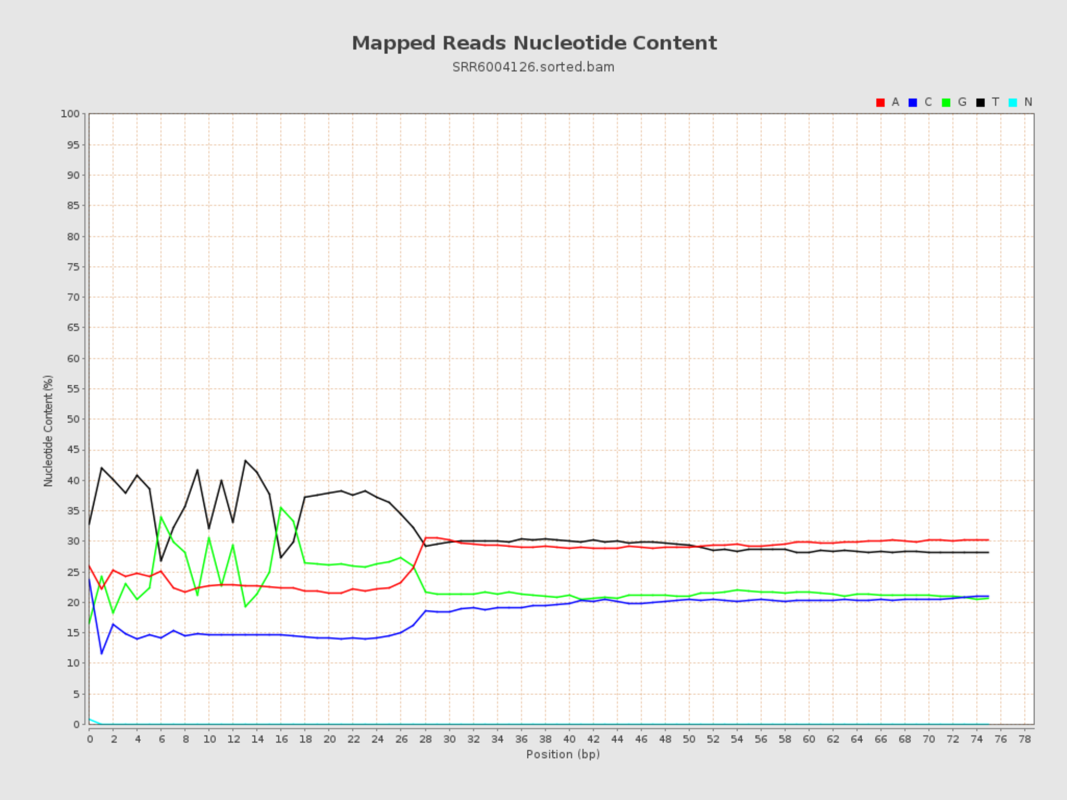
6. Results : Genome Fraction Coverage



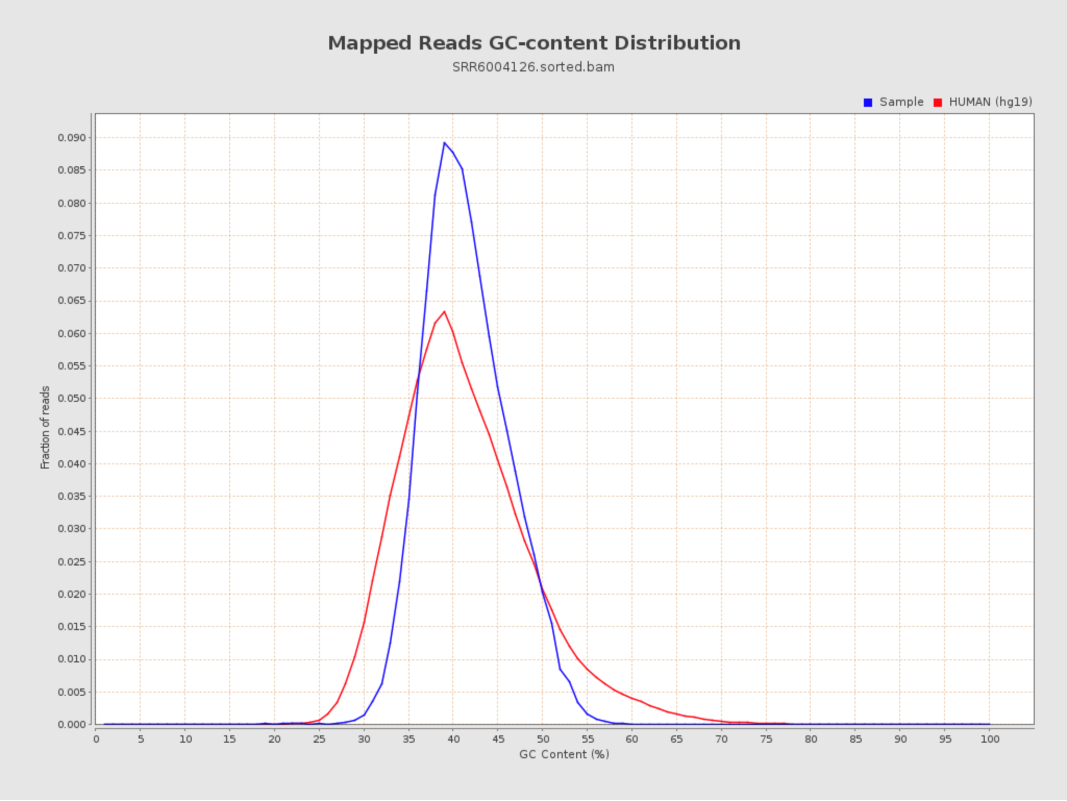
7. Results : Duplication Rate Histogram



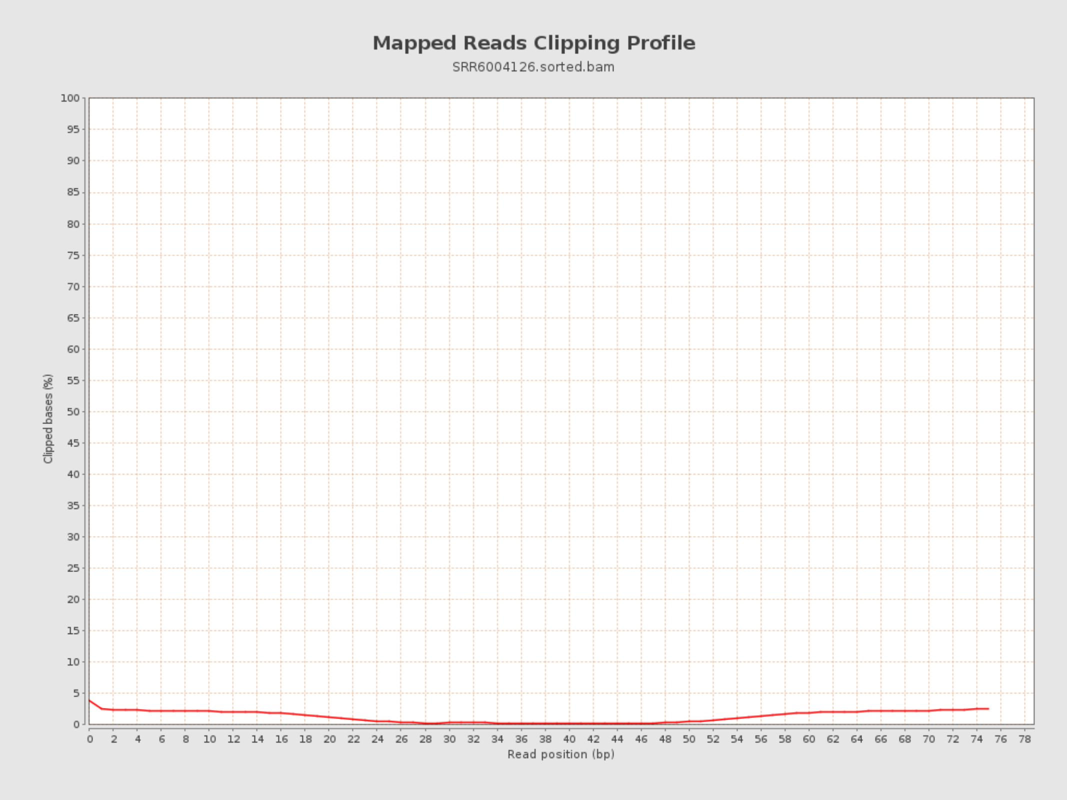
8. Results : Mapped Reads Nucleotide Content



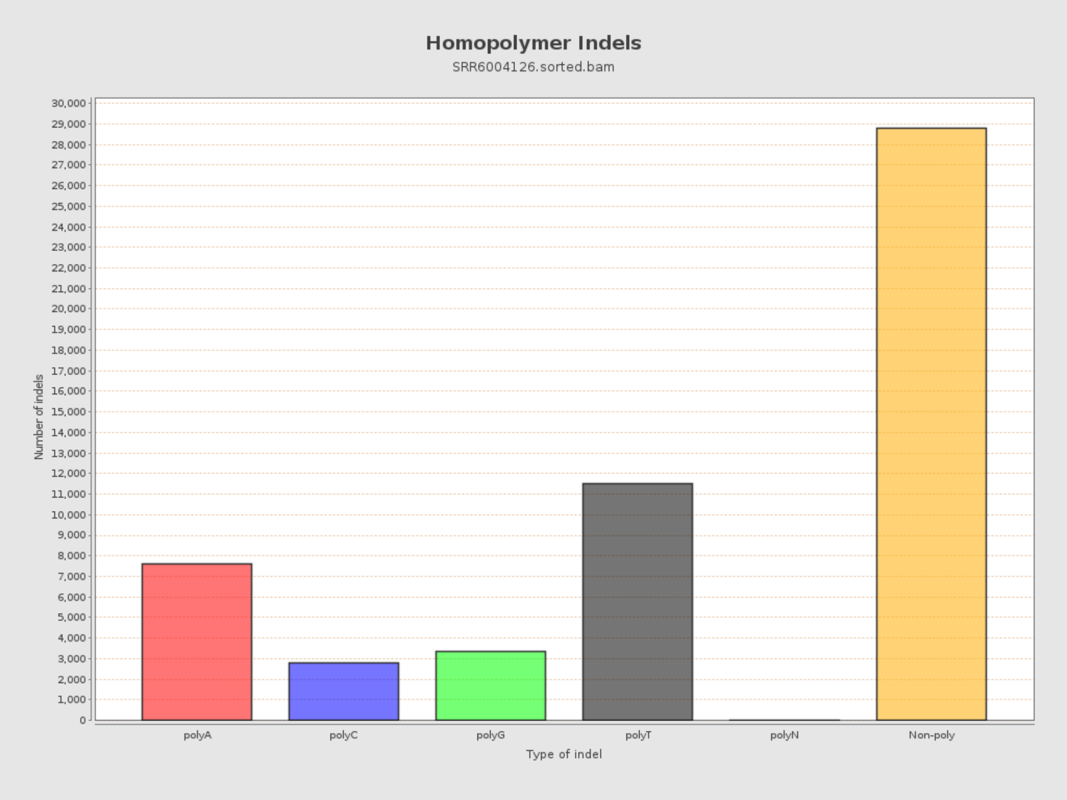
9. Results : Mapped Reads GC-content Distribution



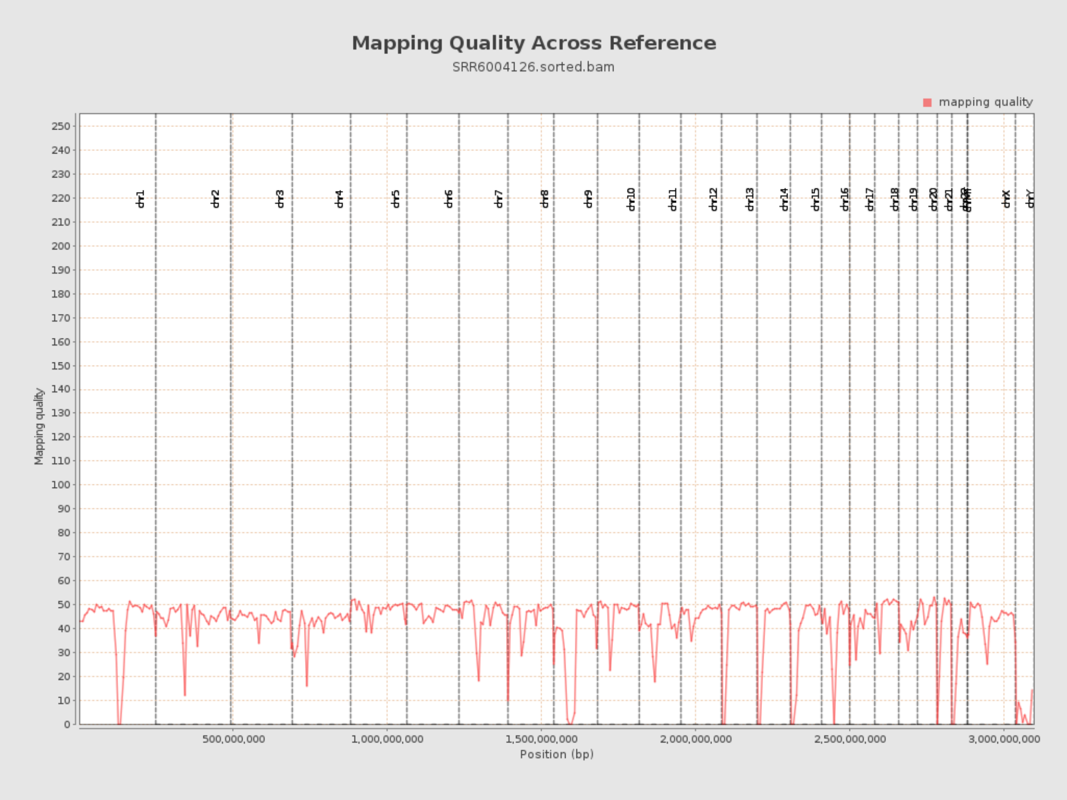
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram