Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:00:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240027.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_SRR6240027 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240027.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:00:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240027.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,308,775
Mapped reads	993,181 / 75.89%
Unmapped reads	315,594 / 24.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,571 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	139,754 / 10.68%
Duplication rate	10.66%
Clipped reads	486,862 / 37.2%

2.2. ACGT Content

Number/percentage of A's	17,884,272 / 27.56%
Number/percentage of C's	11,539,343 / 17.78%
Number/percentage of T's	21,320,866 / 32.86%
Number/percentage of G's	14,140,433 / 21.79%
Number/percentage of N's	5,797 / 0.01%
GC Percentage	39.57%

2.3. Coverage

Mean	0.021

Standard Deviation	0.2881

2.4. Mapping Quality

Mean Mapping Quality	46.73

2.5. Mismatches and indels

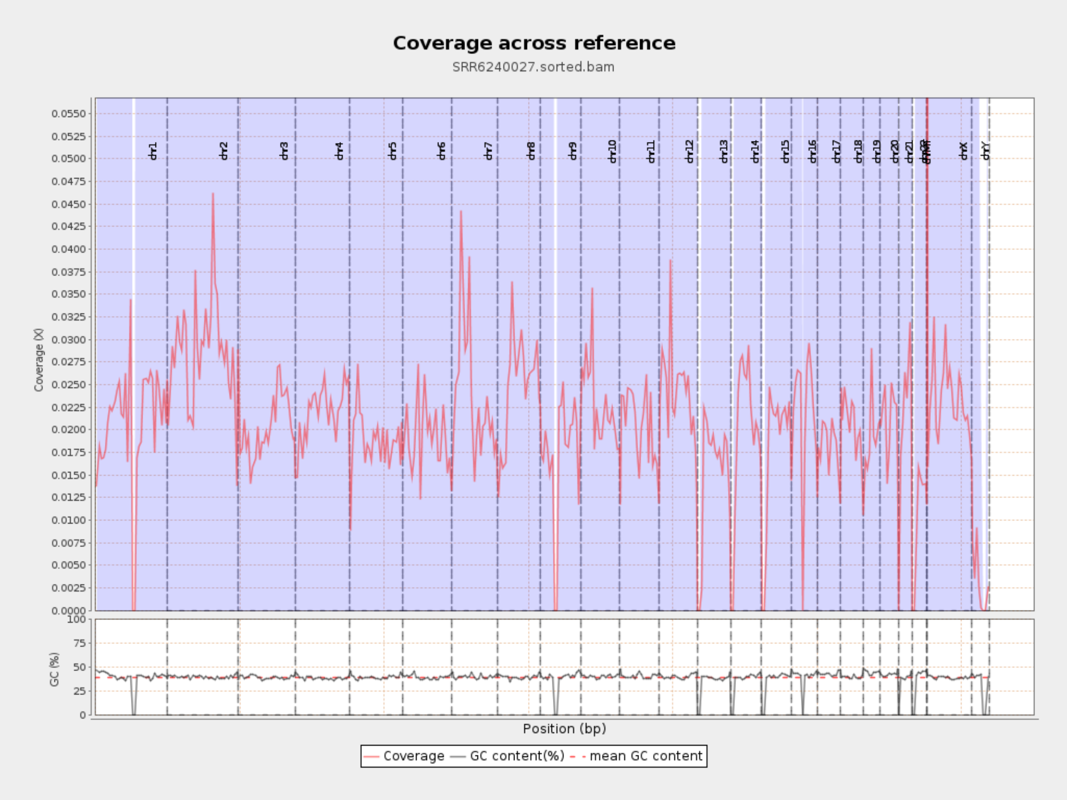
General error rate	0.86%
Mismatches	551,982
Insertions	4,752
Mapped reads with at least one insertion	0.47%
Deletions	17,931
Mapped reads with at least one deletion	1.79%
Homopolymer indels	49.28%

2.6. Chromosome stats

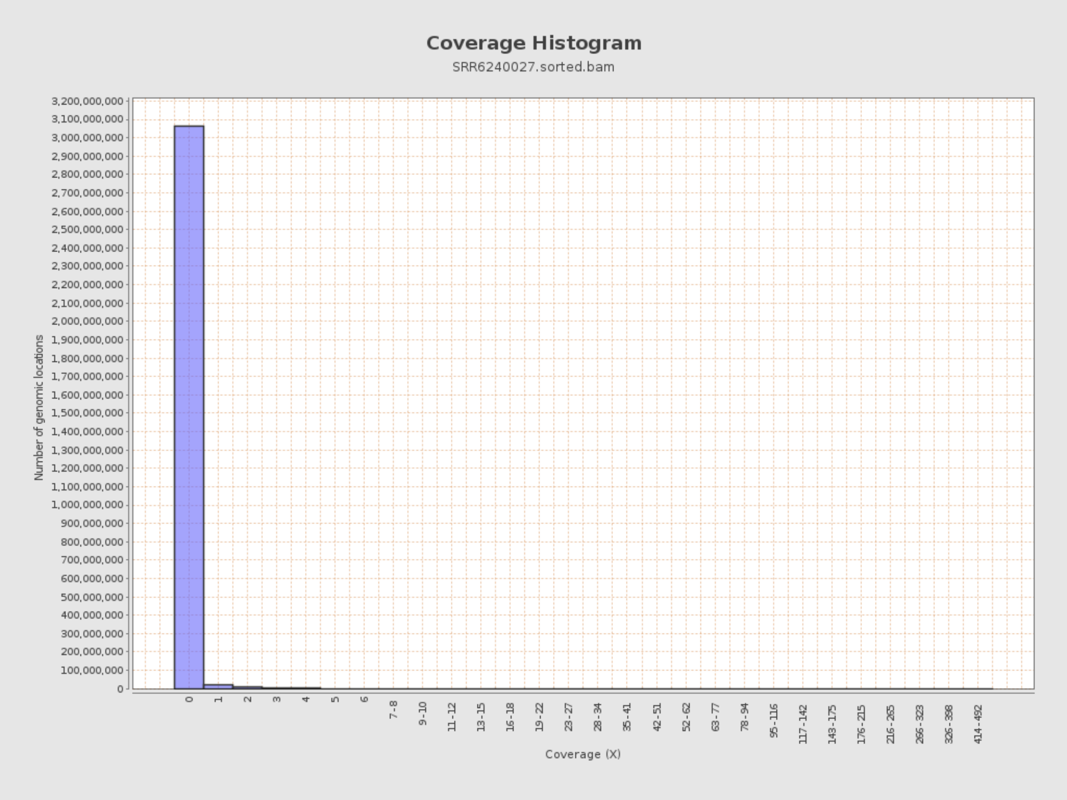
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5148016	0.0207	0.3937
chr2	243199373	7010428	0.0288	0.3384
chr3	198022430	4040726	0.0204	0.2452
chr4	191154276	4198956	0.022	0.2539
chr5	180915260	3436699	0.019	0.235
chr6	171115067	3308436	0.0193	0.2491
chr7	159138663	3848496	0.0242	0.3656

chr8	146364022	3662196	0.025	0.3976
chr9	141213431	2431795	0.0172	0.253
chr10	135534747	3123445	0.023	0.296
chr11	135006516	2775707	0.0206	0.2609
chr12	133851895	3289848	0.0246	0.2683
chr13	115169878	1737292	0.0151	0.2072
chr14	107349540	2123204	0.0198	0.2425
chr15	102531392	1825885	0.0178	0.2254
chr16	90354753	1953159	0.0216	0.2495
chr17	81195210	1489028	0.0183	0.2282
chr18	78077248	1619025	0.0207	0.3569
chr19	59128983	1134194	0.0192	0.2939
chr20	63025520	1337668	0.0212	0.2502
chr21	48129895	1050523	0.0218	0.2539
chr22	51304566	534987	0.0104	0.1633
chrMT	16571	10318	0.6227	1.2585
chrX	155270560	3652505	0.0235	0.2691
chrY	59373566	179509	0.003	0.0856

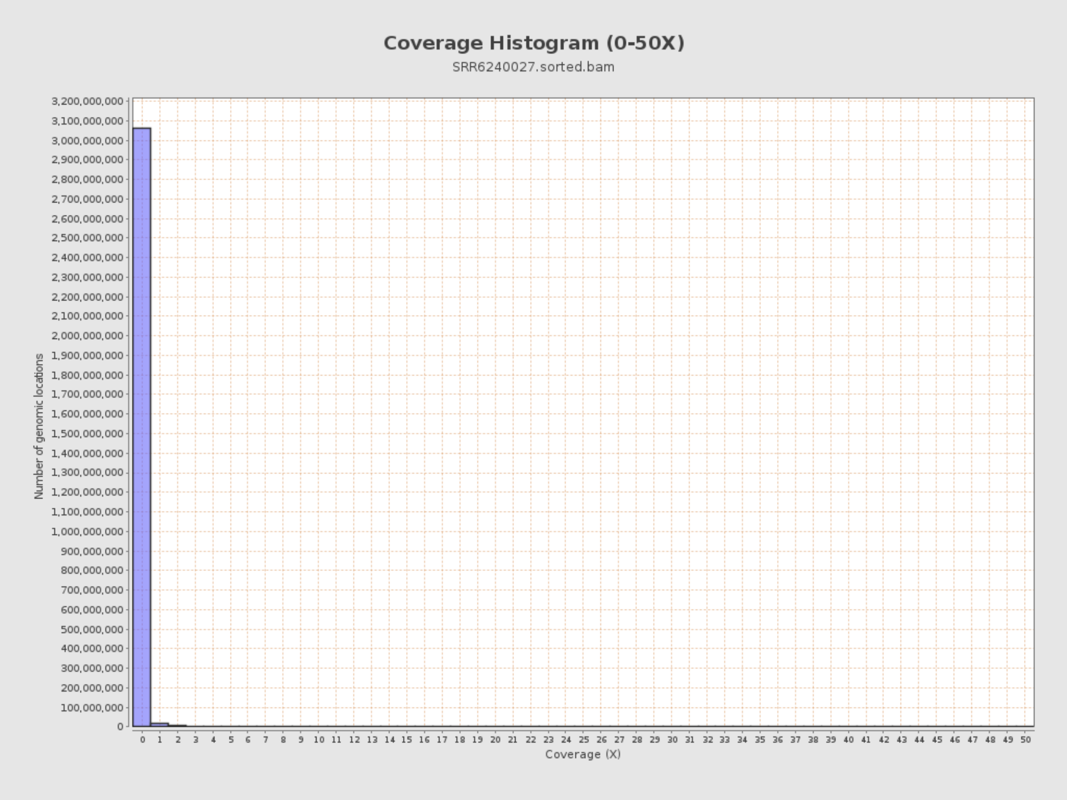
3. Results : Coverage across reference



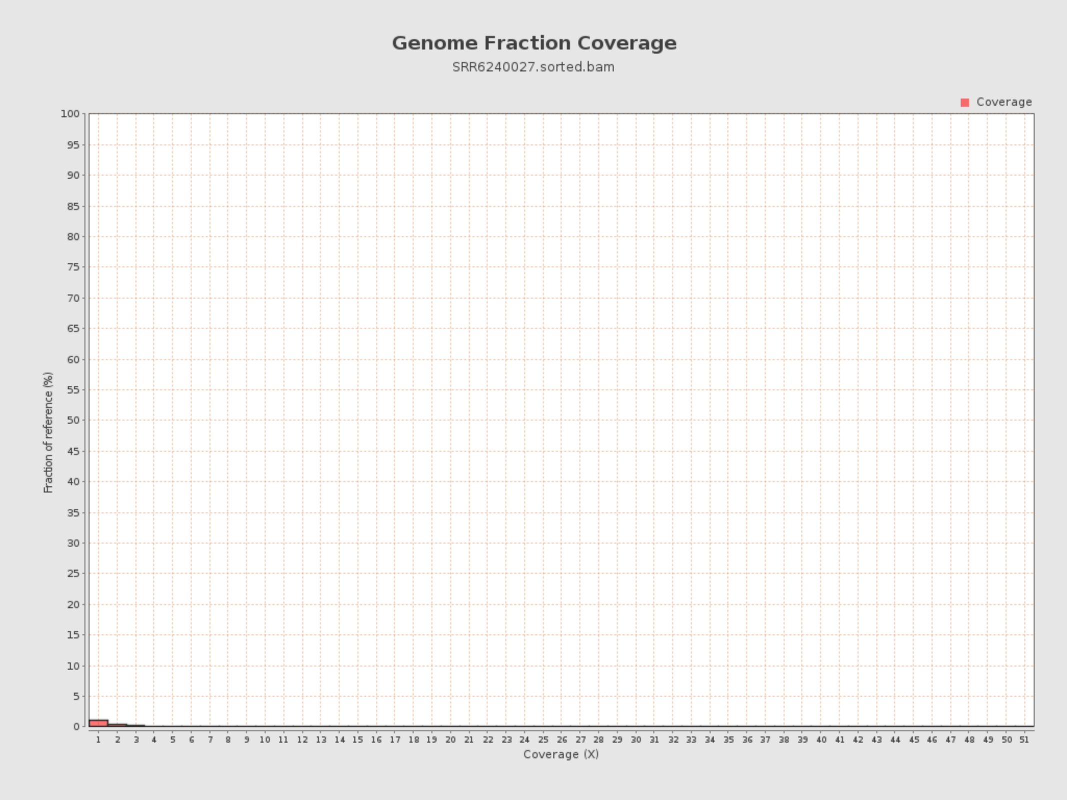
4. Results : Coverage Histogram



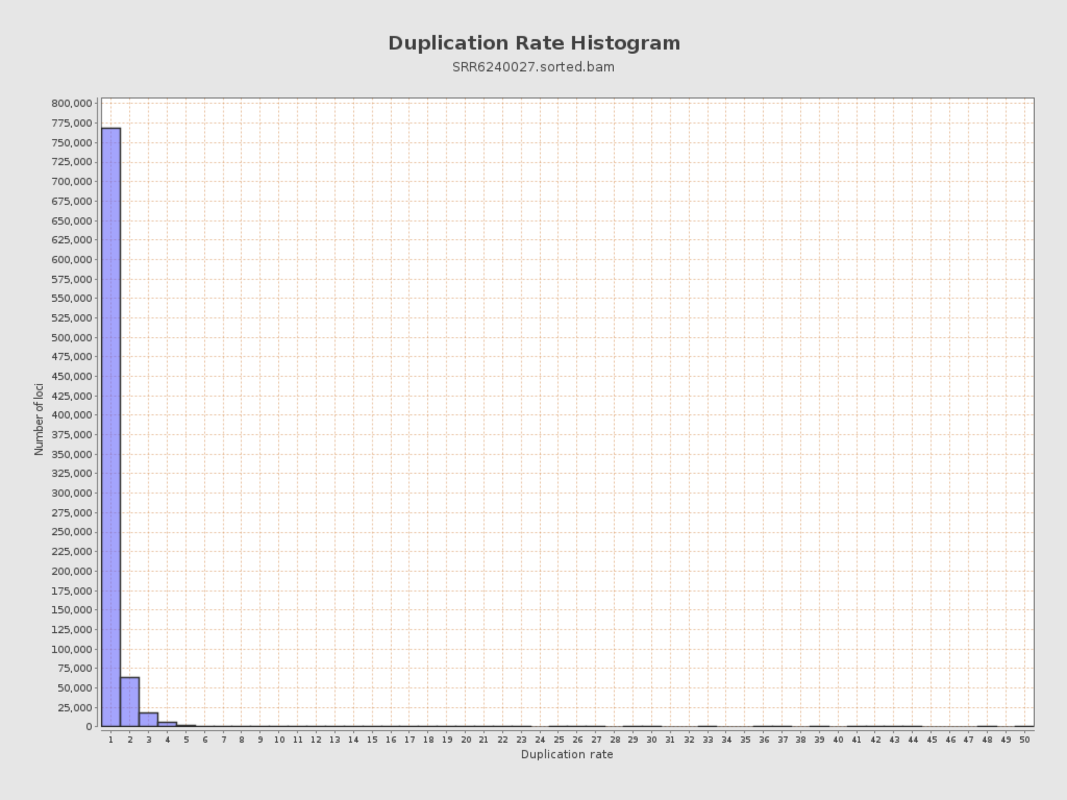
5. Results : Coverage Histogram (0-50X)



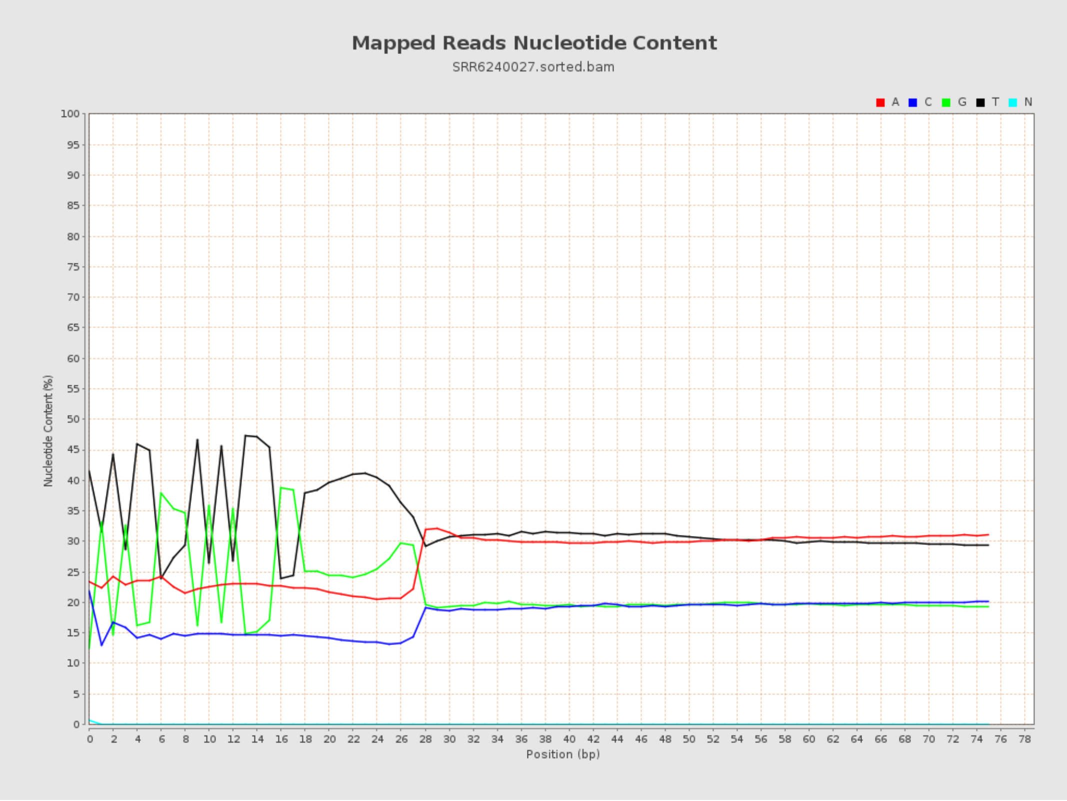
6. Results : Genome Fraction Coverage



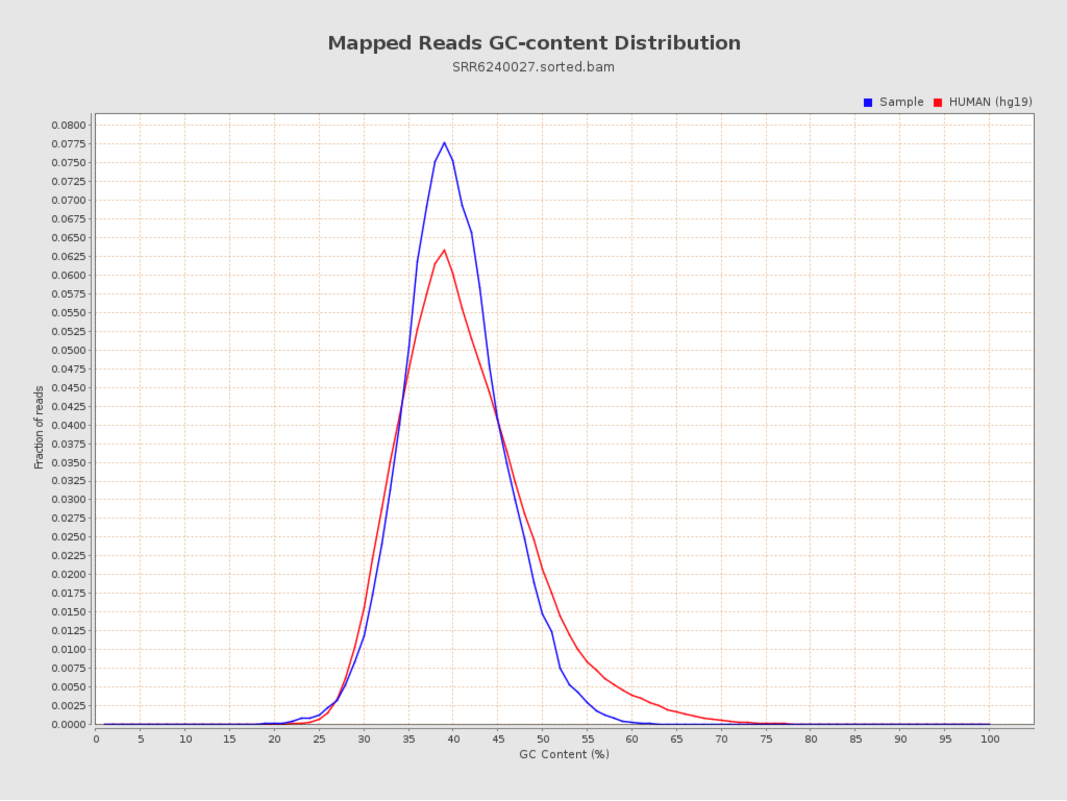
7. Results : Duplication Rate Histogram



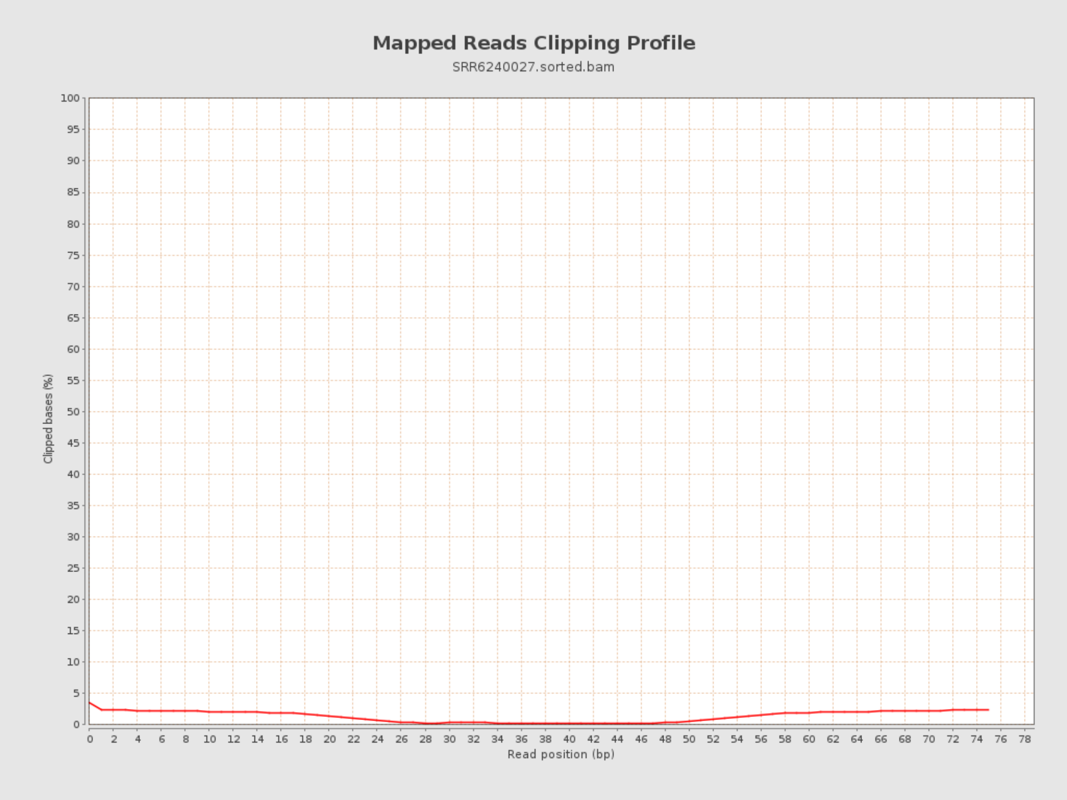
8. Results : Mapped Reads Nucleotide Content



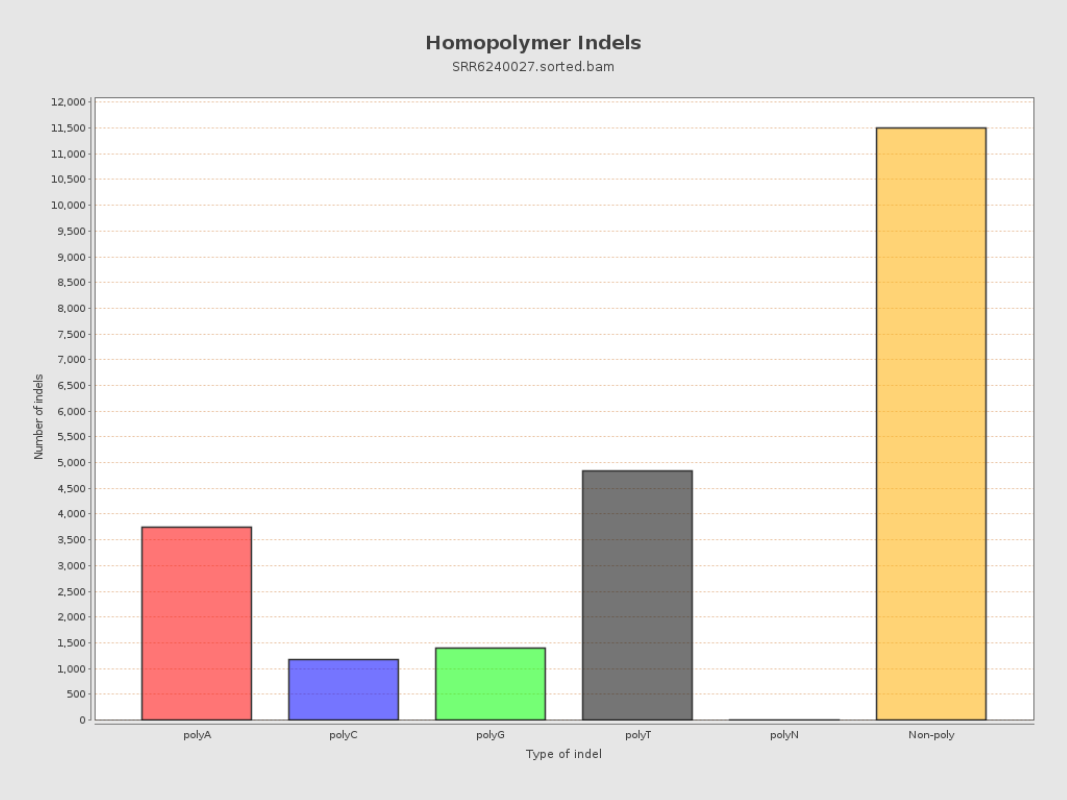
9. Results : Mapped Reads GC-content Distribution



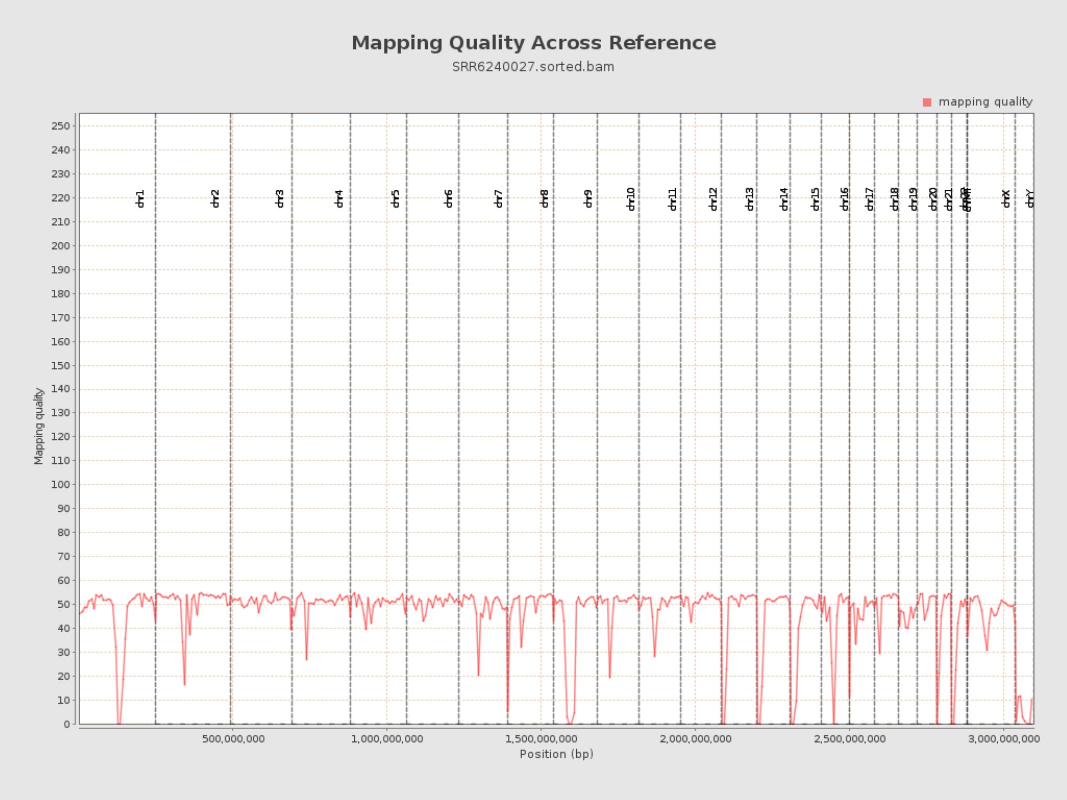
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram