Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:58:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240026.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_SRR6240026 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240026.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:58:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240026.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,411,273
Mapped reads	1,868,304 / 77.48%
Unmapped reads	542,969 / 22.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,959 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	264,583 / 10.97%
Duplication rate	10.5%
Clipped reads	845,886 / 35.08%

2.2. ACGT Content

Number/percentage of A's	35,454,270 / 28.44%
Number/percentage of C's	22,549,353 / 18.09%
Number/percentage of T's	40,437,227 / 32.44%
Number/percentage of G's	26,202,171 / 21.02%
Number/percentage of N's	12,420 / 0.01%
GC Percentage	39.11%

2.3. Coverage

Mean	0.0403

Standard Deviation	0.5294

2.4. Mapping Quality

Mean Mapping Quality	46.89

2.5. Mismatches and indels

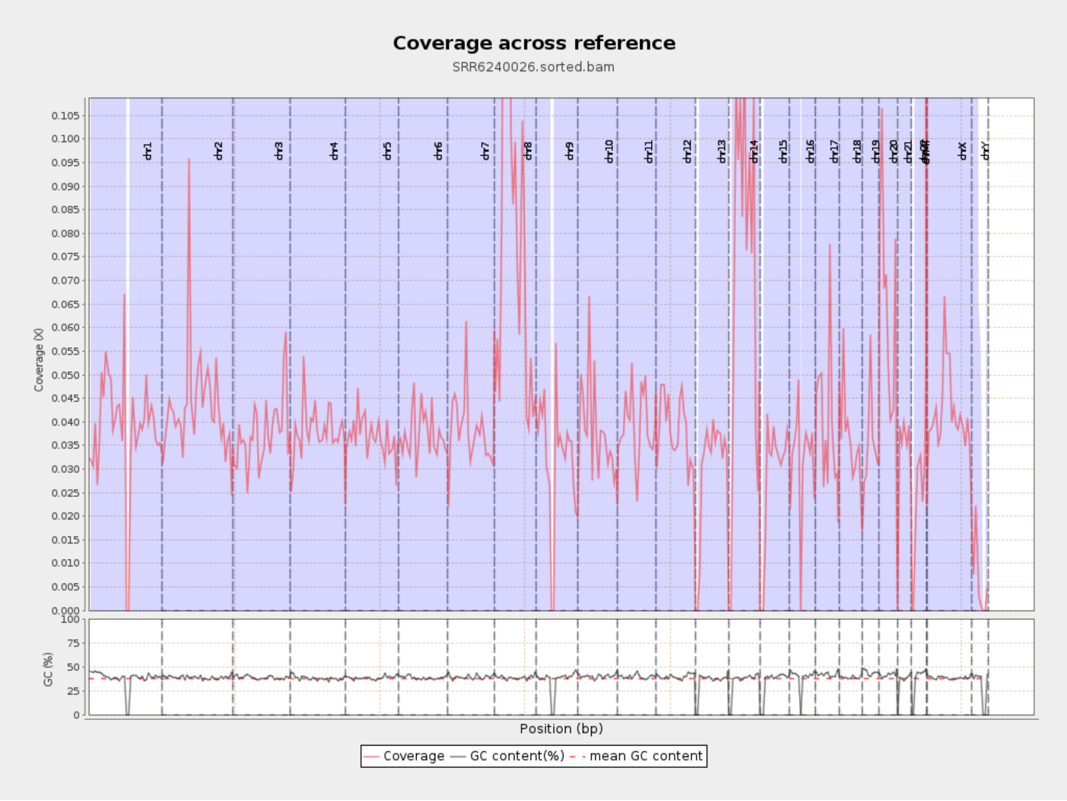
General error rate	0.83%
Mismatches	1,018,892
Insertions	9,485
Mapped reads with at least one insertion	0.5%
Deletions	29,676
Mapped reads with at least one deletion	1.57%
Homopolymer indels	48.14%

2.6. Chromosome stats

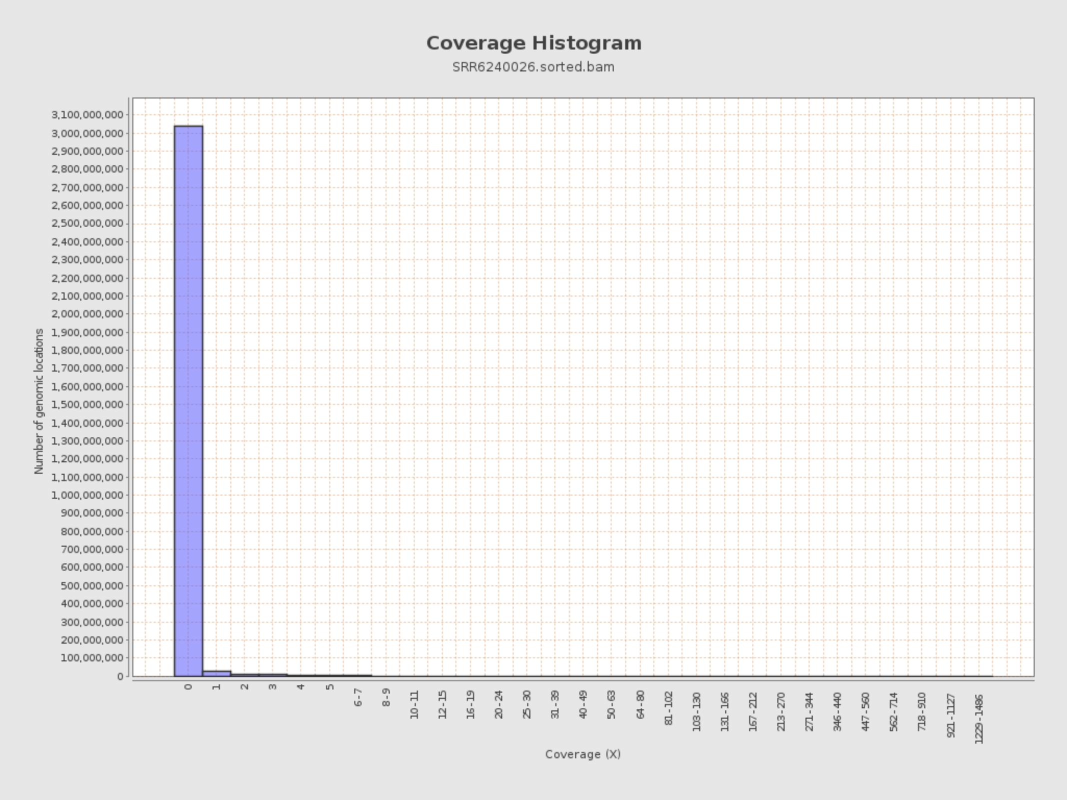
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9606149	0.0385	0.8563
chr2	243199373	10572917	0.0435	0.5662
chr3	198022430	7485393	0.0378	0.3636
chr4	191154276	7292034	0.0381	0.3753
chr5	180915260	6633525	0.0367	0.3602
chr6	171115067	6394522	0.0374	0.3772
chr7	159138663	6084415	0.0382	0.4676

chr8	146364022	11801187	0.0806	1.0565
chr9	141213431	4557836	0.0323	0.4768
chr10	135534747	5168234	0.0381	0.4424
chr11	135006516	5253444	0.0389	0.4885
chr12	133851895	5091554	0.038	0.3693
chr13	115169878	3384770	0.0294	0.3229
chr14	107349540	7679411	0.0715	0.514
chr15	102531392	2920676	0.0285	0.3082
chr16	90354753	2880310	0.0319	0.3443
chr17	81195210	3231433	0.0398	0.3838
chr18	78077248	2882076	0.0369	0.867
chr19	59128983	2088735	0.0353	0.5194
chr20	63025520	4090963	0.0649	0.4793
chr21	48129895	1586849	0.033	0.3453
chr22	51304566	1136715	0.0222	0.2588
chrMT	16571	94609	5.7093	6.0039
chrX	155270560	6426011	0.0414	0.3958
chrY	59373566	363233	0.0061	0.1734

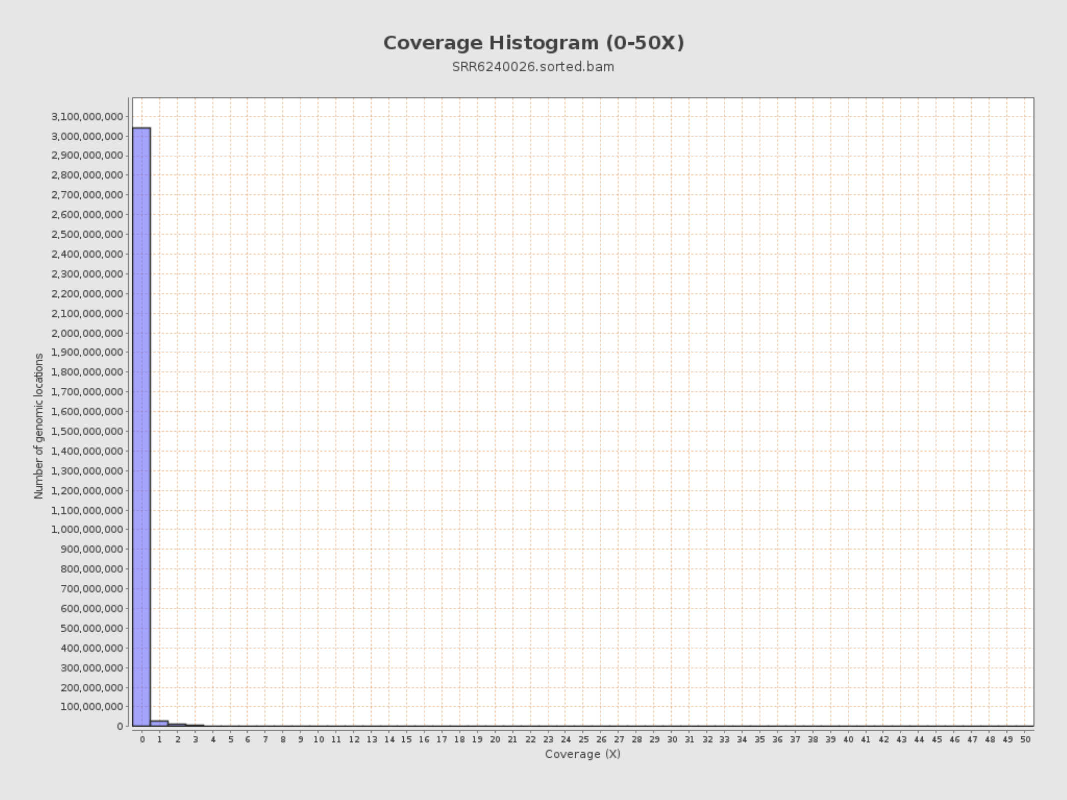
3. Results : Coverage across reference



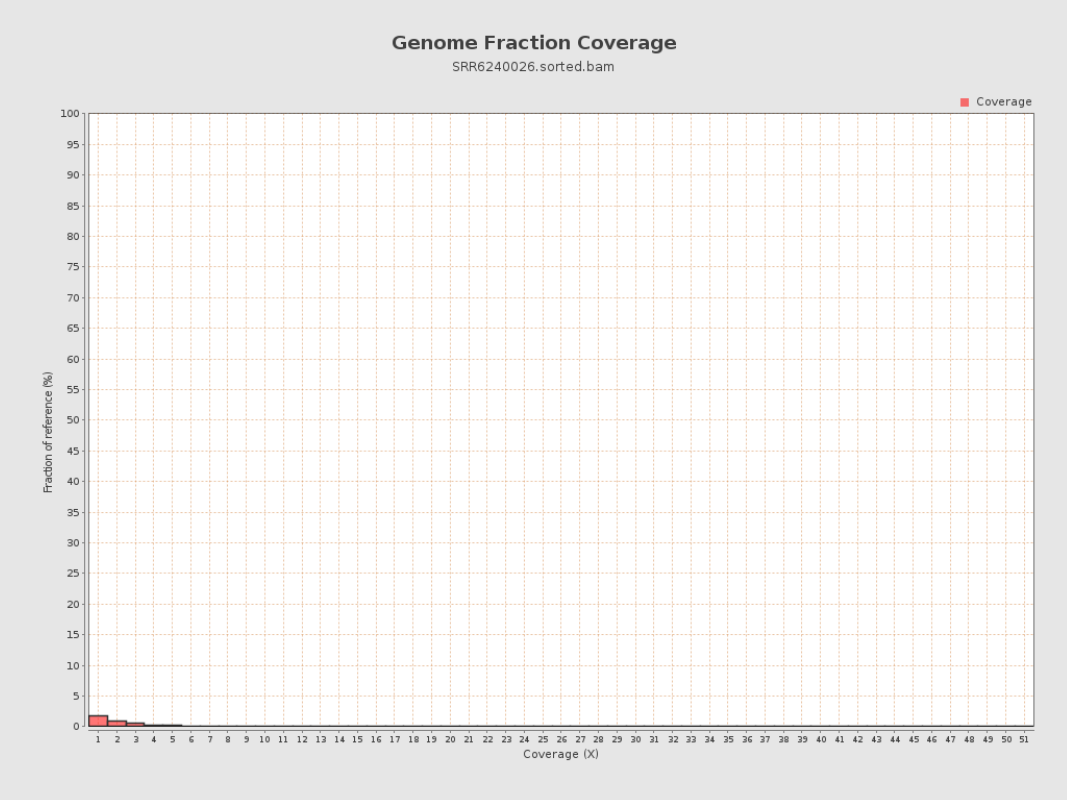
4. Results : Coverage Histogram



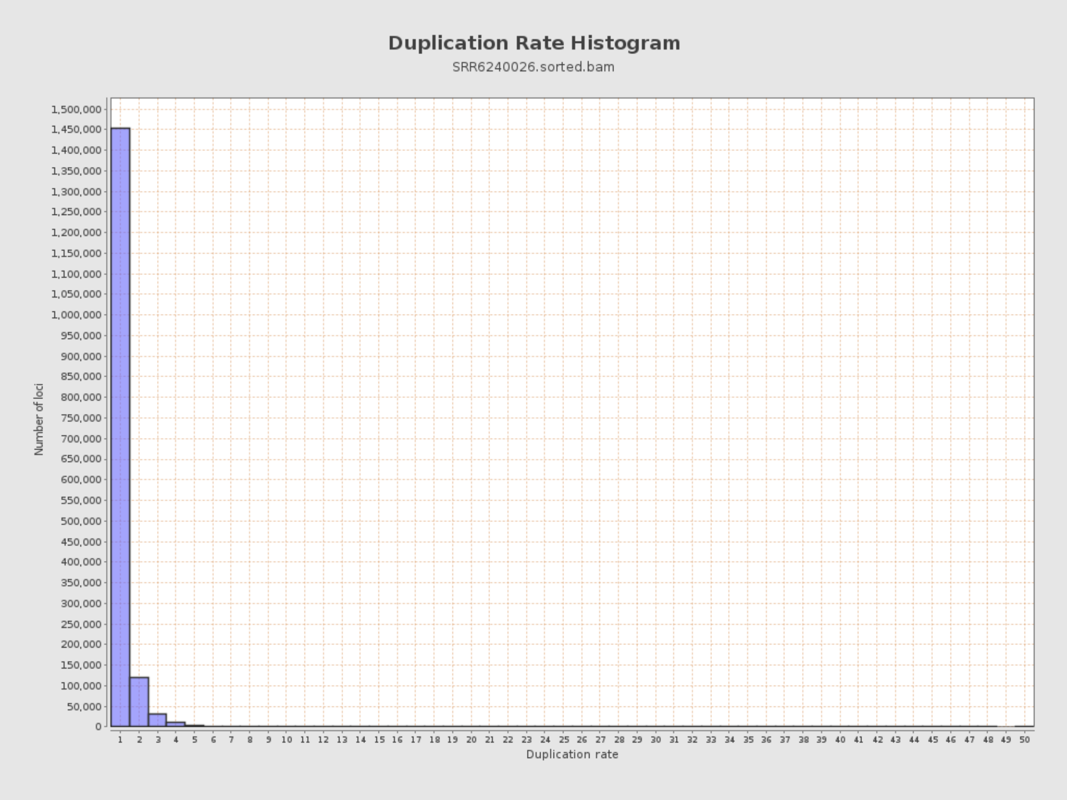
5. Results : Coverage Histogram (0-50X)



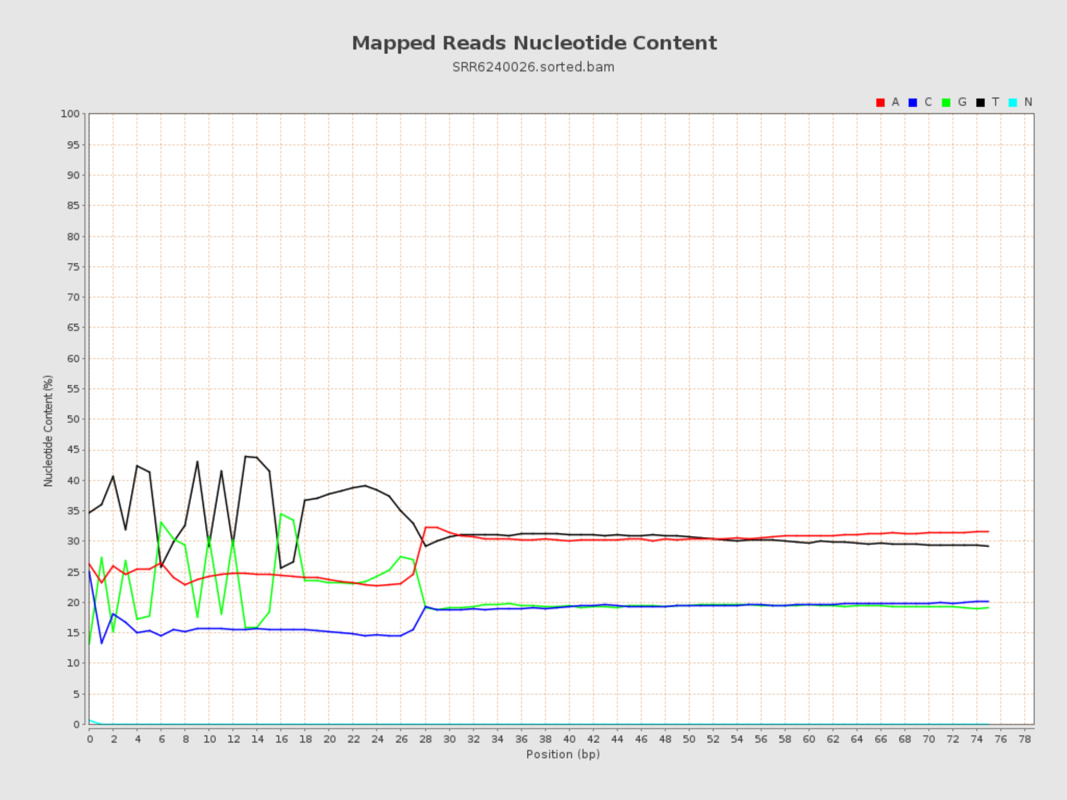
6. Results : Genome Fraction Coverage



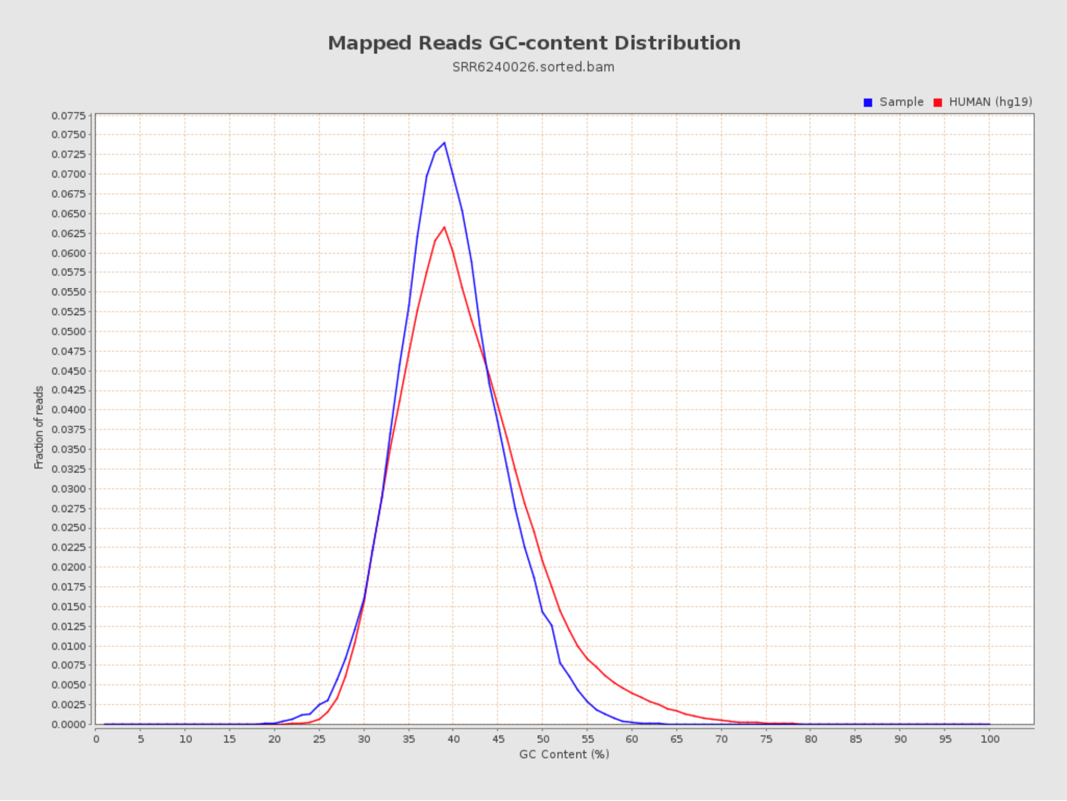
7. Results : Duplication Rate Histogram



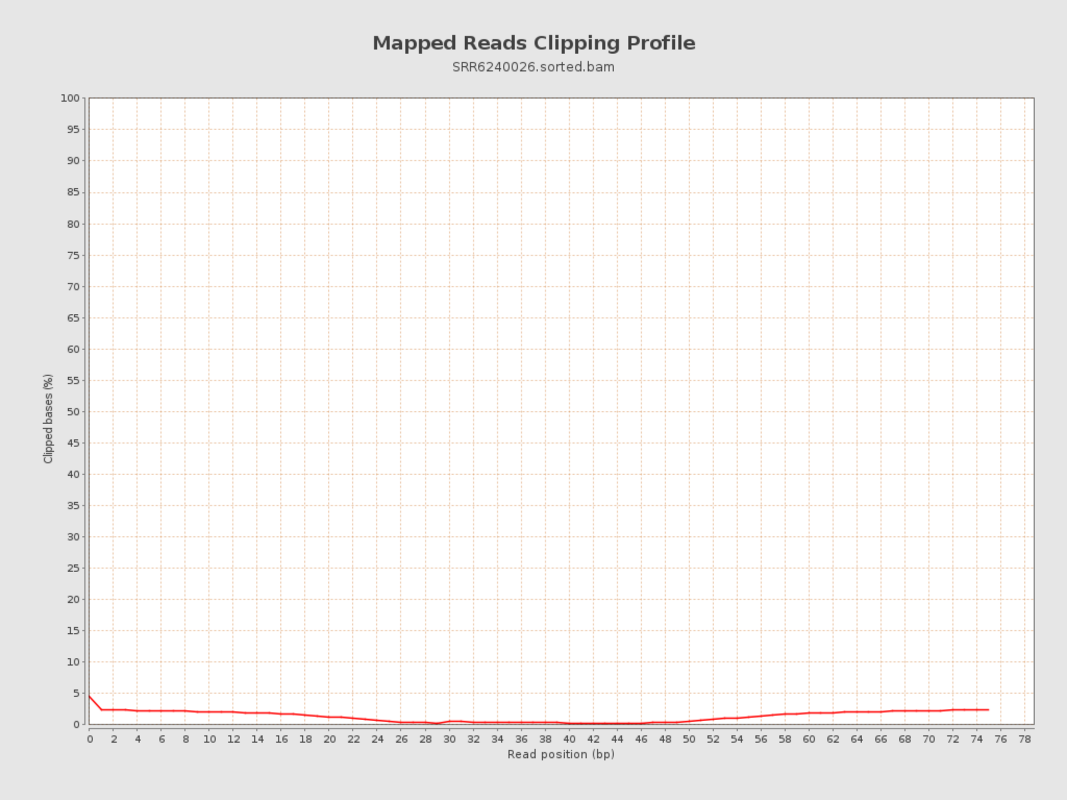
8. Results : Mapped Reads Nucleotide Content



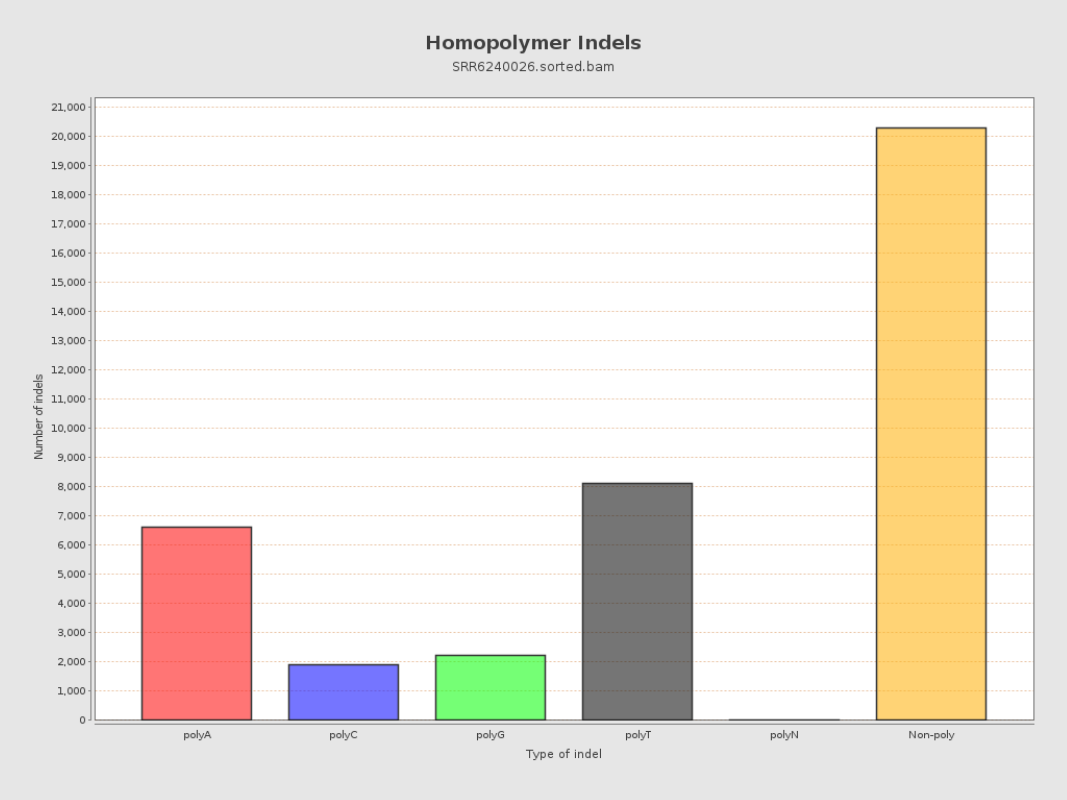
9. Results : Mapped Reads GC-content Distribution



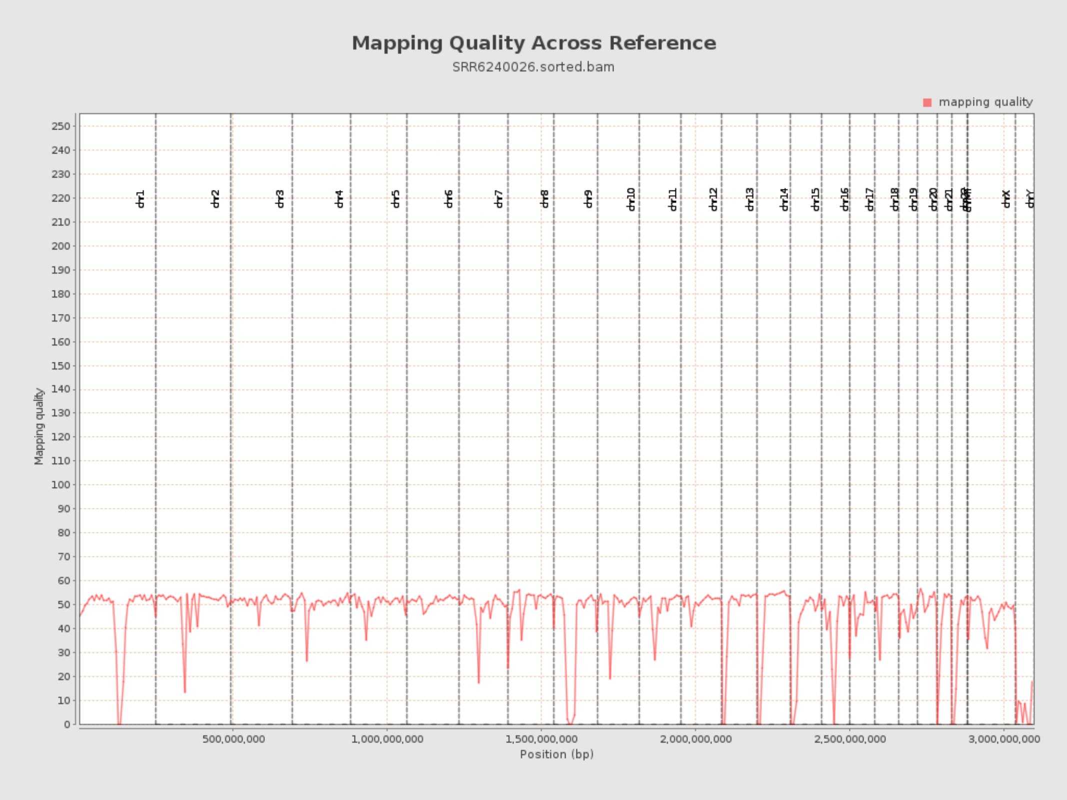
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram