Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:31:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240059.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_SRR6240059 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240059.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:31:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240059.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,414,805
Mapped reads	1,075,076 / 75.99%
Unmapped reads	339,729 / 24.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,524 / 0.67%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	114,097 / 8.06%
Duplication rate	8.57%
Clipped reads	492,116 / 34.78%

2.2. ACGT Content

Number/percentage of A's	20,154,360 / 28.17%
Number/percentage of C's	13,169,601 / 18.41%
Number/percentage of T's	22,983,137 / 32.13%
Number/percentage of G's	15,221,118 / 21.28%
Number/percentage of N's	6,699 / 0.01%
GC Percentage	39.69%

2.3. Coverage

Mean	0.0231

Standard Deviation	0.29

2.4. Mapping Quality

Mean Mapping Quality	47.02

2.5. Mismatches and indels

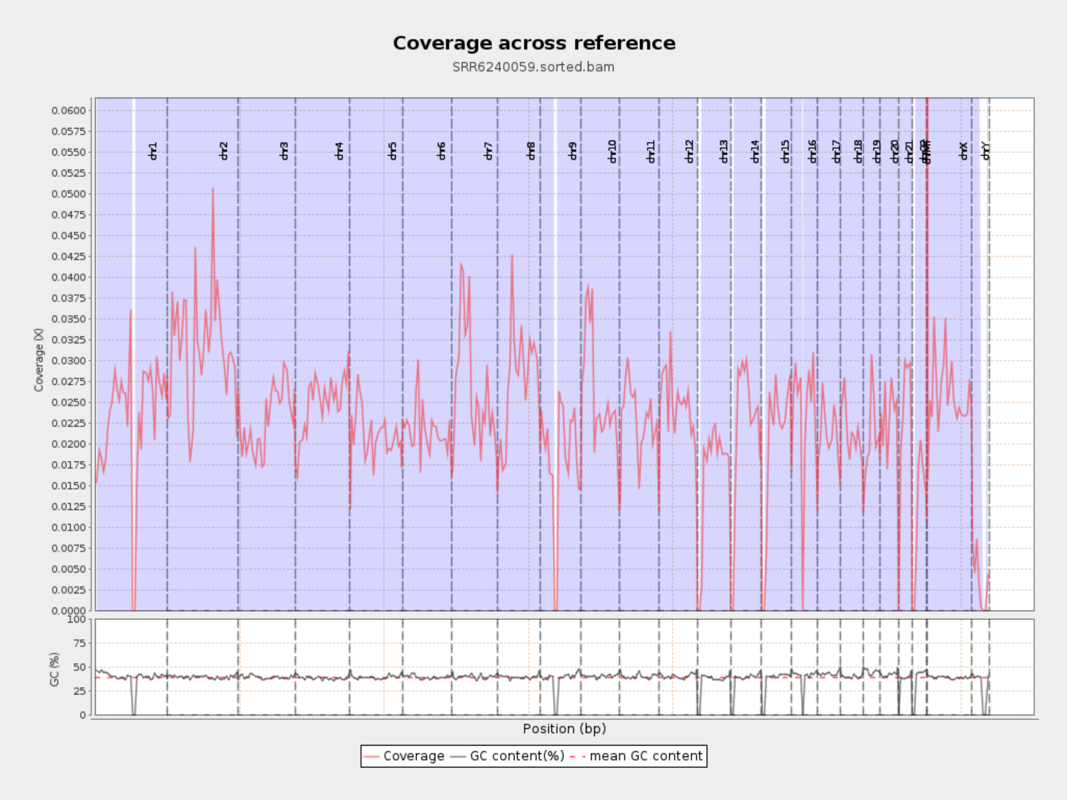
General error rate	0.87%
Mismatches	610,048
Insertions	5,150
Mapped reads with at least one insertion	0.48%
Deletions	21,487
Mapped reads with at least one deletion	1.97%
Homopolymer indels	48.54%

2.6. Chromosome stats

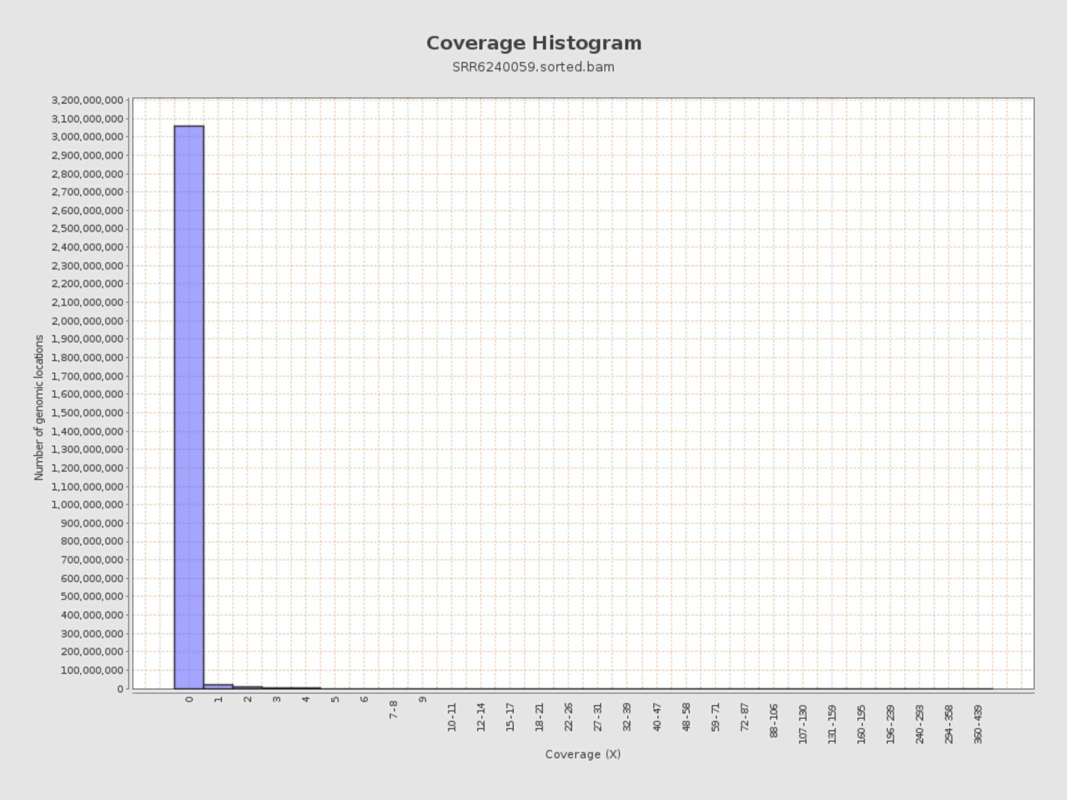
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5727569	0.023	0.4123
chr2	243199373	7739120	0.0318	0.3336
chr3	198022430	4529787	0.0229	0.2449
chr4	191154276	4739213	0.0248	0.2604
chr5	180915260	3845789	0.0213	0.2346
chr6	171115067	3707570	0.0217	0.254
chr7	159138663	4248703	0.0267	0.3511

chr8	146364022	4066875	0.0278	0.3789
chr9	141213431	2606613	0.0185	0.2516
chr10	135534747	3526711	0.026	0.2965
chr11	135006516	3115725	0.0231	0.2782
chr12	133851895	3326119	0.0248	0.2573
chr13	115169878	1869411	0.0162	0.2073
chr14	107349540	2328720	0.0217	0.2427
chr15	102531392	2031814	0.0198	0.2284
chr16	90354753	2079788	0.023	0.2435
chr17	81195210	1728583	0.0213	0.2582
chr18	78077248	1680069	0.0215	0.3829
chr19	59128983	1242460	0.021	0.2972
chr20	63025520	1448941	0.023	0.2471
chr21	48129895	1125483	0.0234	0.2518
chr22	51304566	616656	0.012	0.1674
chrMT	16571	8664	0.5228	1.0186
chrX	155270560	4025849	0.0259	0.2713
chrY	59373566	206294	0.0035	0.0887

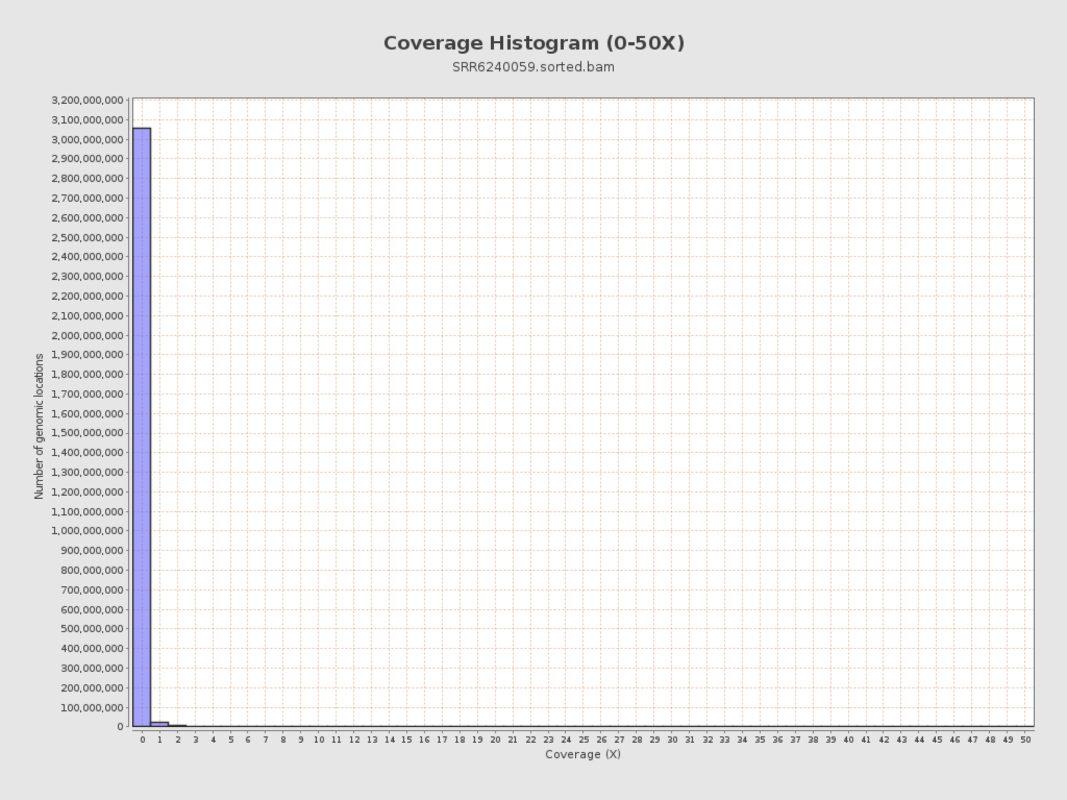
3. Results : Coverage across reference



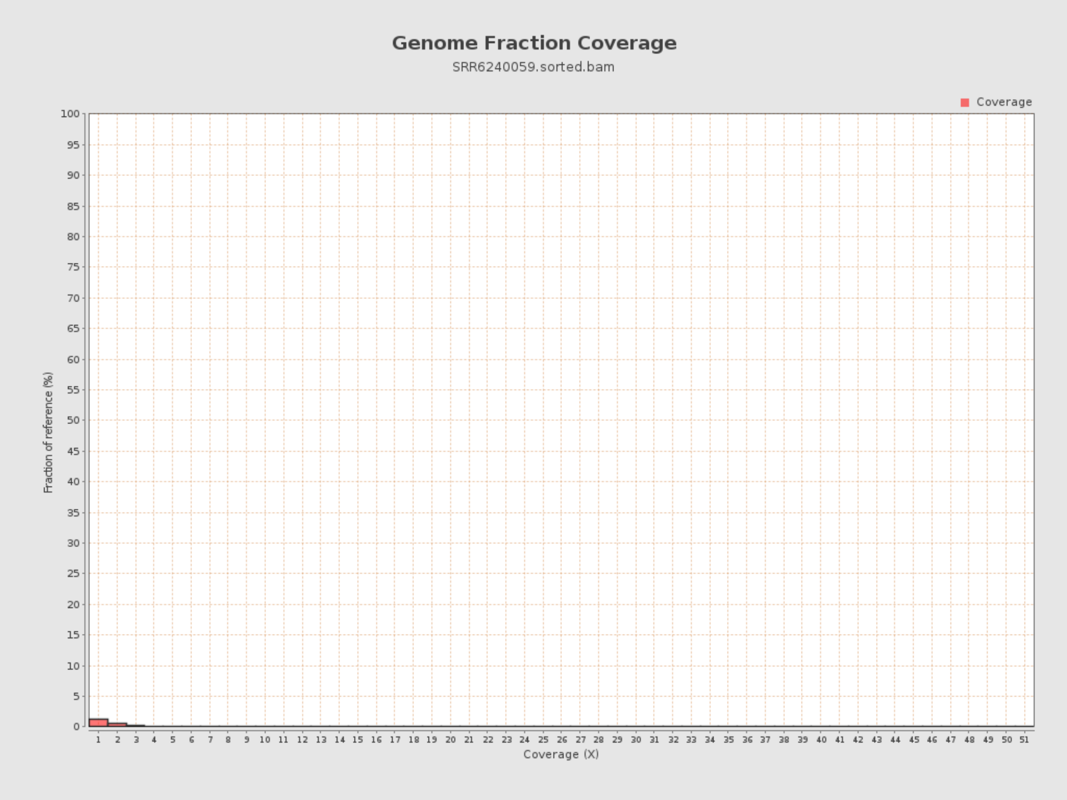
4. Results : Coverage Histogram



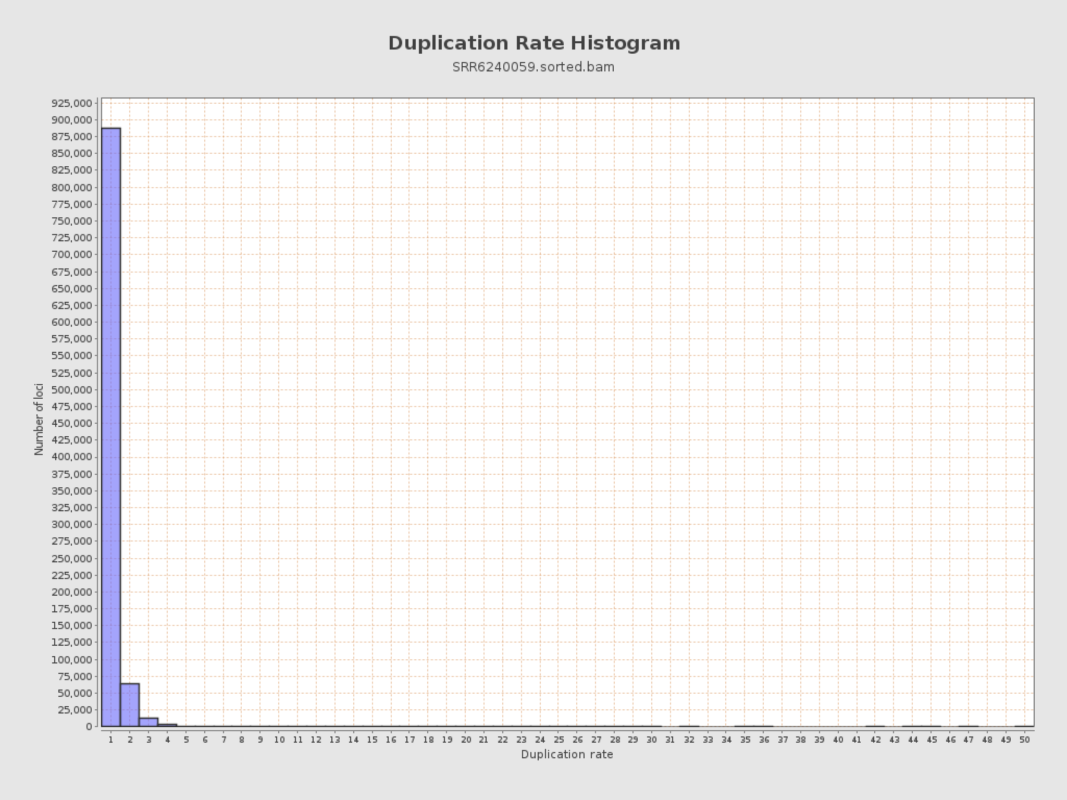
5. Results : Coverage Histogram (0-50X)



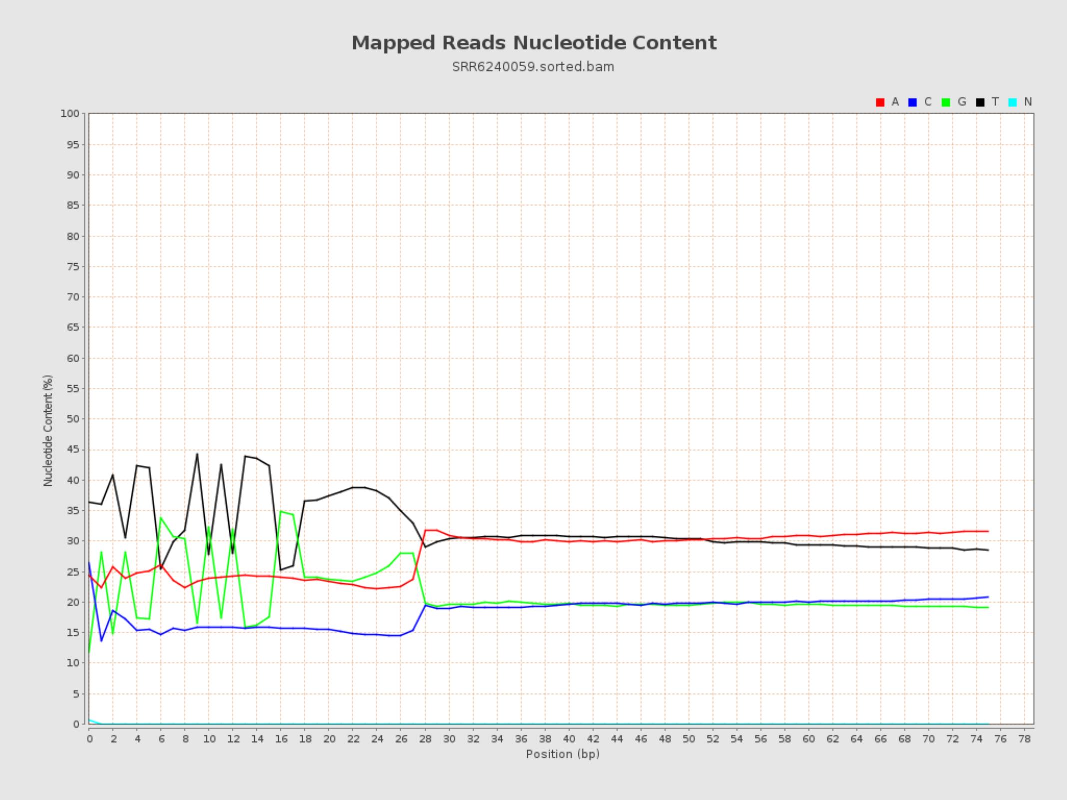
6. Results : Genome Fraction Coverage



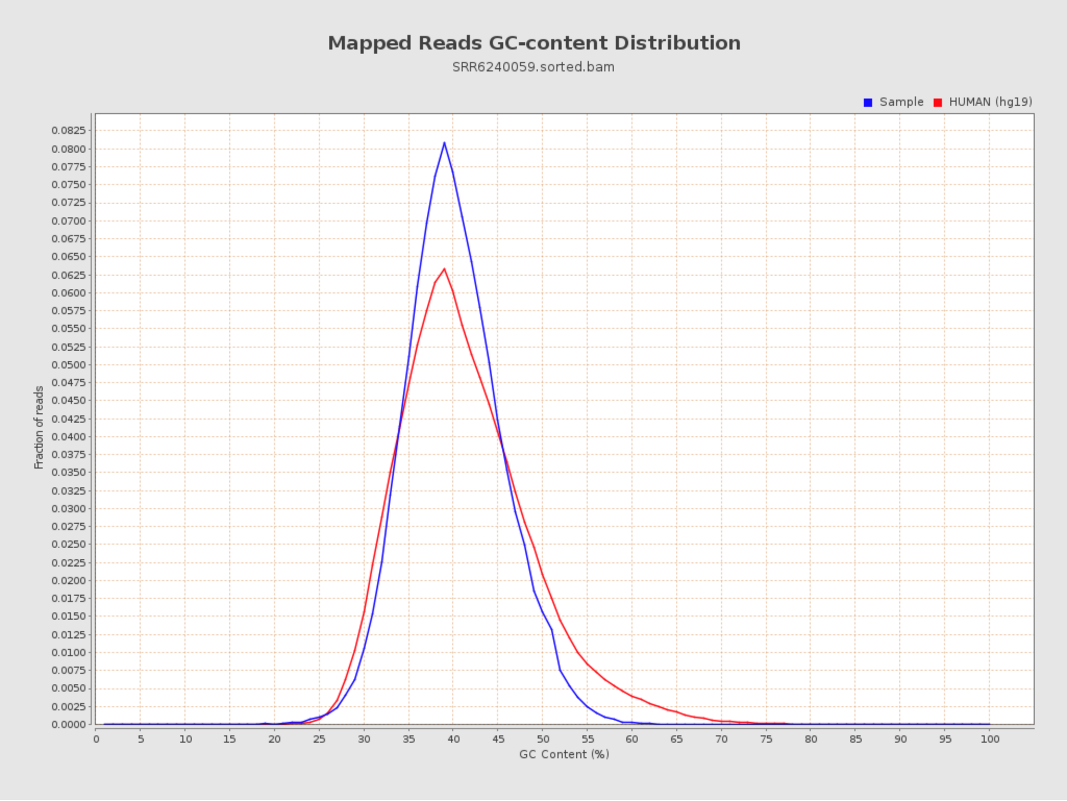
7. Results : Duplication Rate Histogram



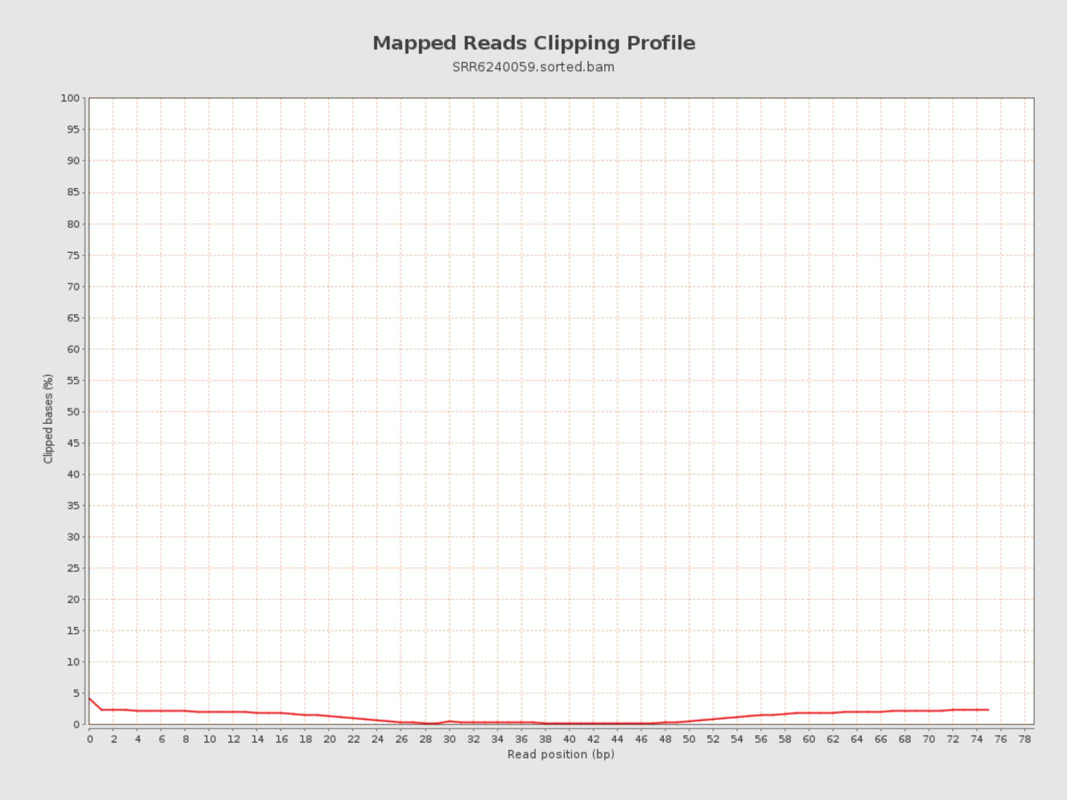
8. Results : Mapped Reads Nucleotide Content



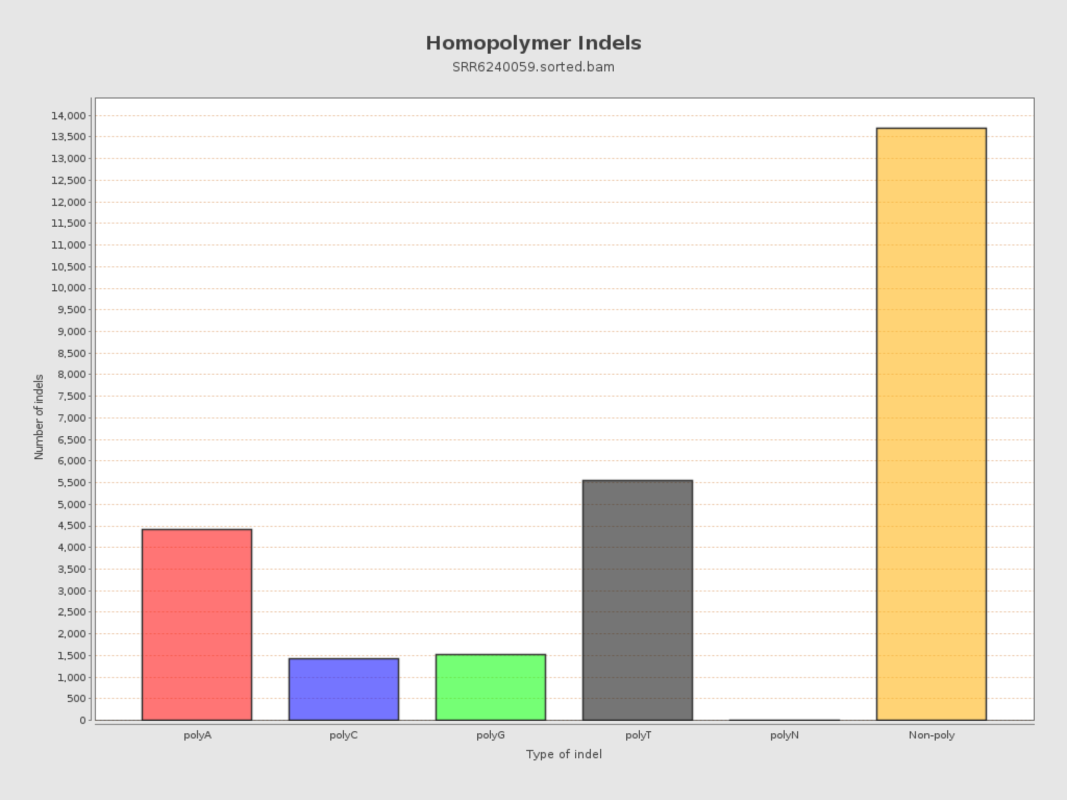
9. Results : Mapped Reads GC-content Distribution



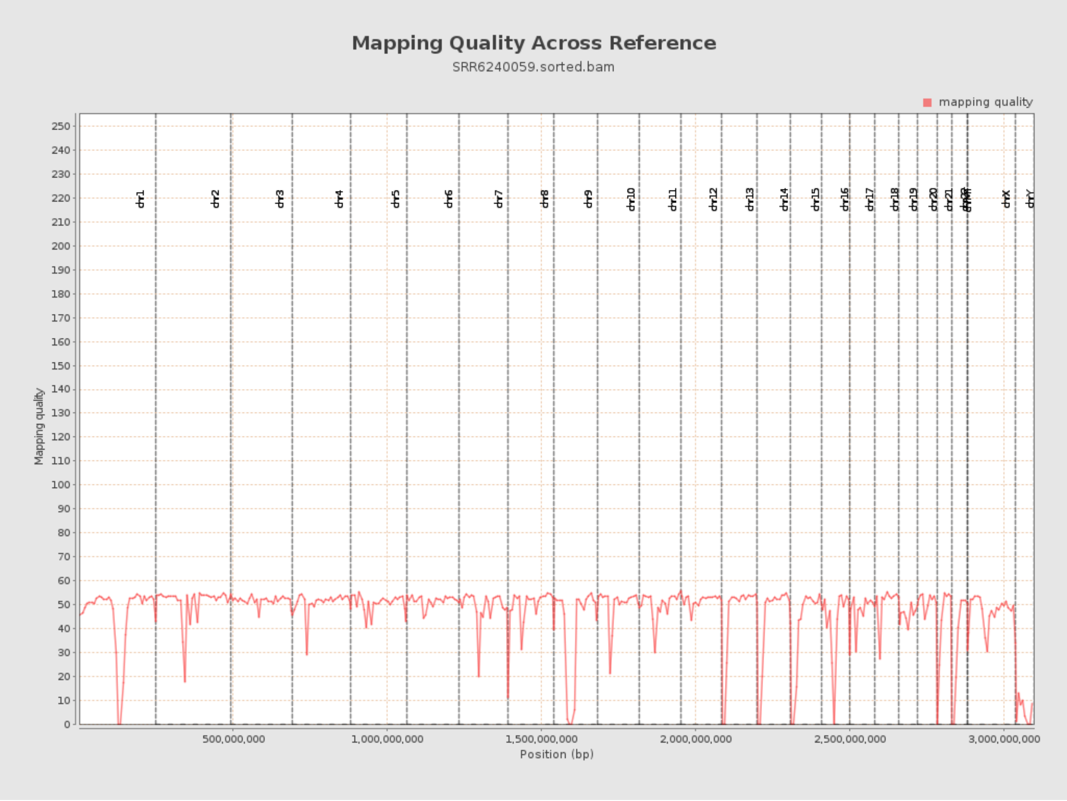
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram