Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:53:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240024.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_SRR6240024 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240024.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:53:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240024.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,666,838
Mapped reads	1,346,266 / 80.77%
Unmapped reads	320,572 / 19.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,142 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	129,701 / 7.78%
Duplication rate	8.08%
Clipped reads	819,266 / 49.15%

2.2. ACGT Content

Number/percentage of A's	22,943,311 / 27.22%
Number/percentage of C's	14,965,410 / 17.76%
Number/percentage of T's	27,208,924 / 32.29%
Number/percentage of G's	19,097,704 / 22.66%
Number/percentage of N's	59,362 / 0.07%
GC Percentage	40.42%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.2728

2.4. Mapping Quality

Mean Mapping Quality	45.89

2.5. Mismatches and indels

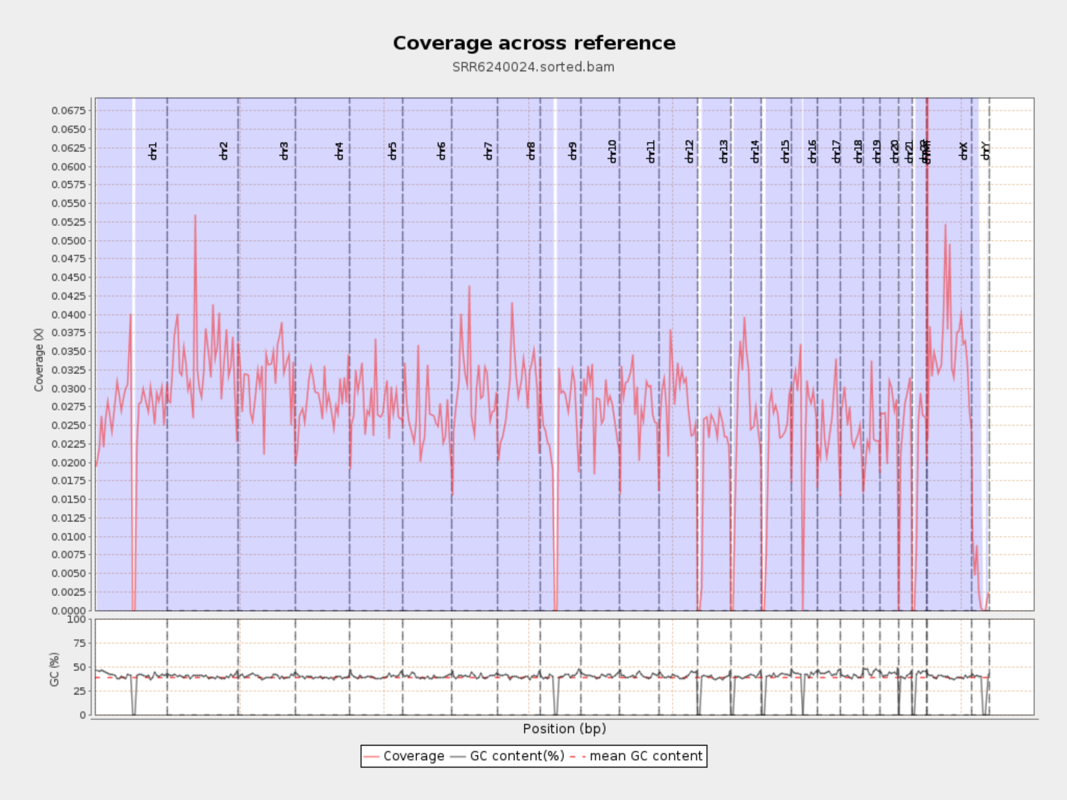
General error rate	0.94%
Mismatches	783,472
Insertions	5,994
Mapped reads with at least one insertion	0.44%
Deletions	23,092
Mapped reads with at least one deletion	1.7%
Homopolymer indels	48.8%

2.6. Chromosome stats

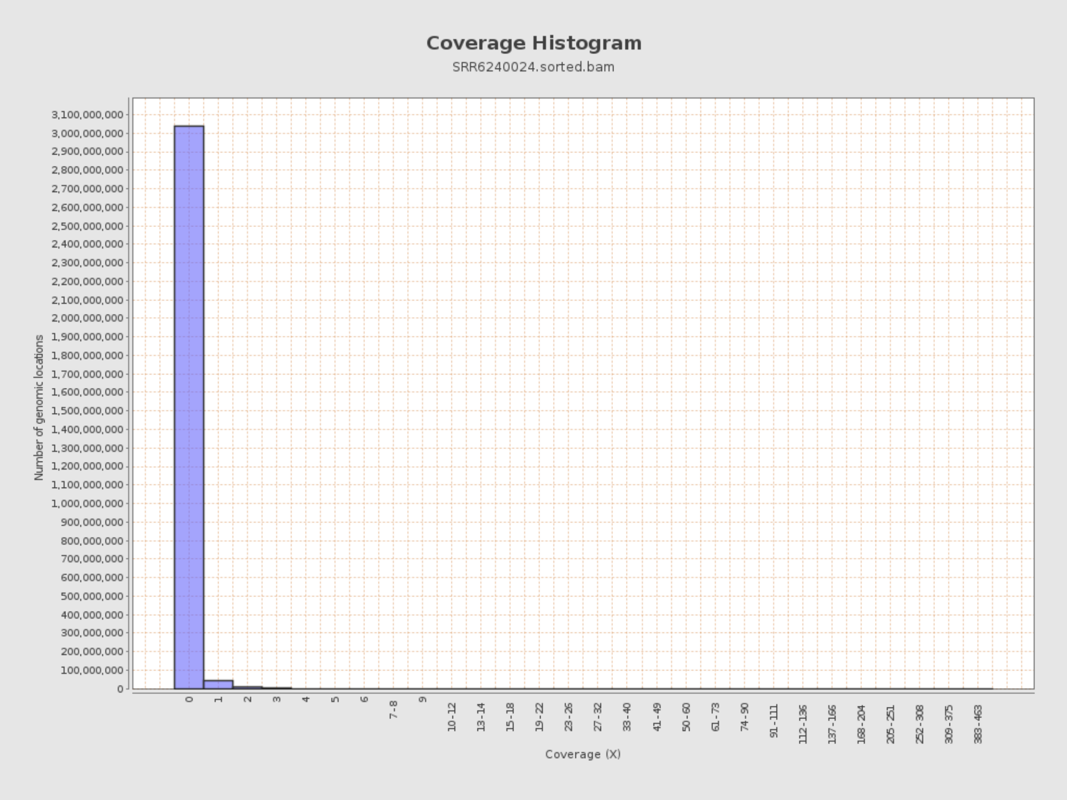
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6461394	0.0259	0.3724
chr2	243199373	8191002	0.0337	0.3471
chr3	198022430	6277643	0.0317	0.2382
chr4	191154276	5414129	0.0283	0.2296
chr5	180915260	5081040	0.0281	0.2251
chr6	171115067	4444788	0.026	0.2396
chr7	159138663	4779299	0.03	0.331

chr8	146364022	4370074	0.0299	0.3623
chr9	141213431	3354348	0.0238	0.2611
chr10	135534747	3751738	0.0277	0.2532
chr11	135006516	3839111	0.0284	0.2575
chr12	133851895	3855614	0.0288	0.2267
chr13	115169878	2364506	0.0205	0.1927
chr14	107349540	2693403	0.0251	0.2156
chr15	102531392	2192317	0.0214	0.2002
chr16	90354753	2347225	0.026	0.2206
chr17	81195210	2002298	0.0247	0.2157
chr18	78077248	1953336	0.025	0.3655
chr19	59128983	1376297	0.0233	0.2734
chr20	63025520	1678266	0.0266	0.2196
chr21	48129895	1150730	0.0239	0.2105
chr22	51304566	935205	0.0182	0.176
chrMT	16571	28818	1.7391	2.219
chrX	155270560	5575317	0.0359	0.2753
chrY	59373566	196402	0.0033	0.0784

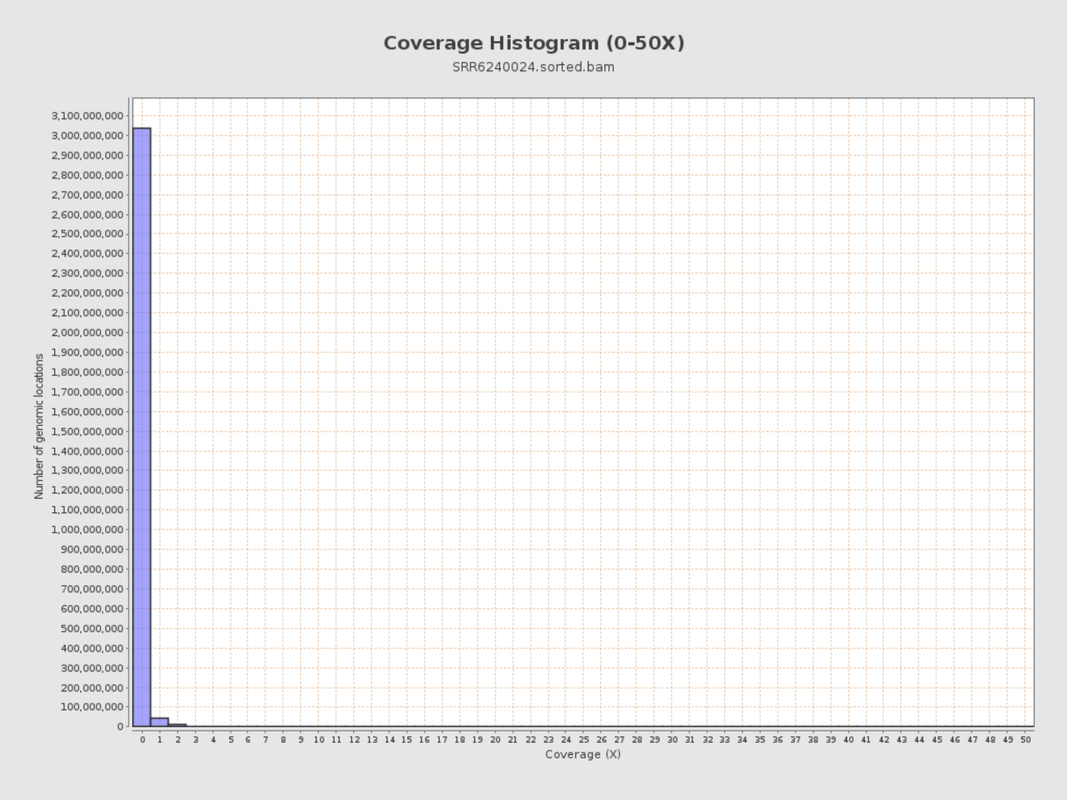
3. Results : Coverage across reference



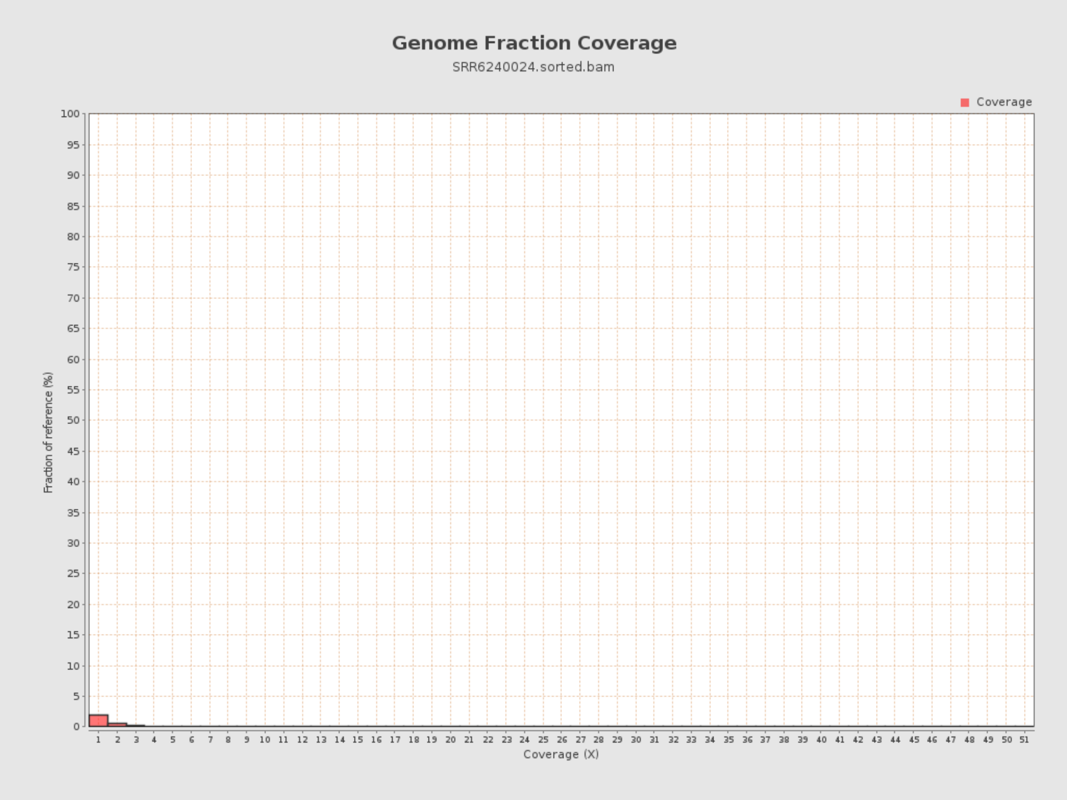
4. Results : Coverage Histogram



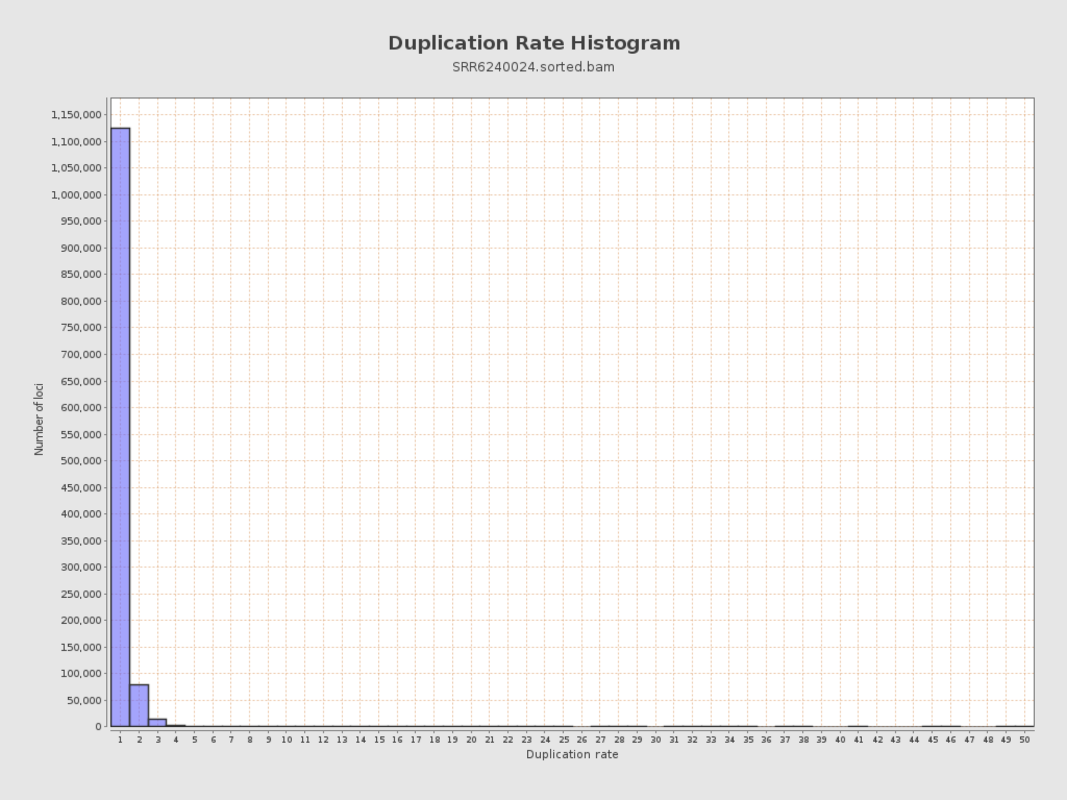
5. Results : Coverage Histogram (0-50X)



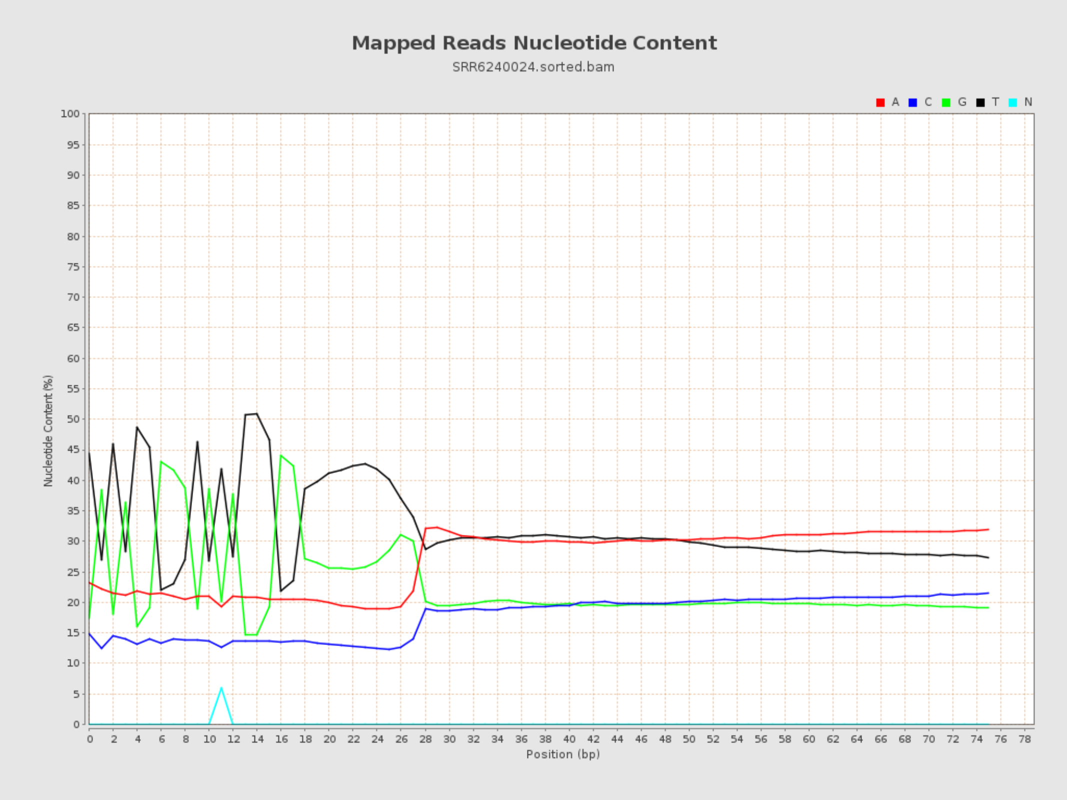
6. Results : Genome Fraction Coverage



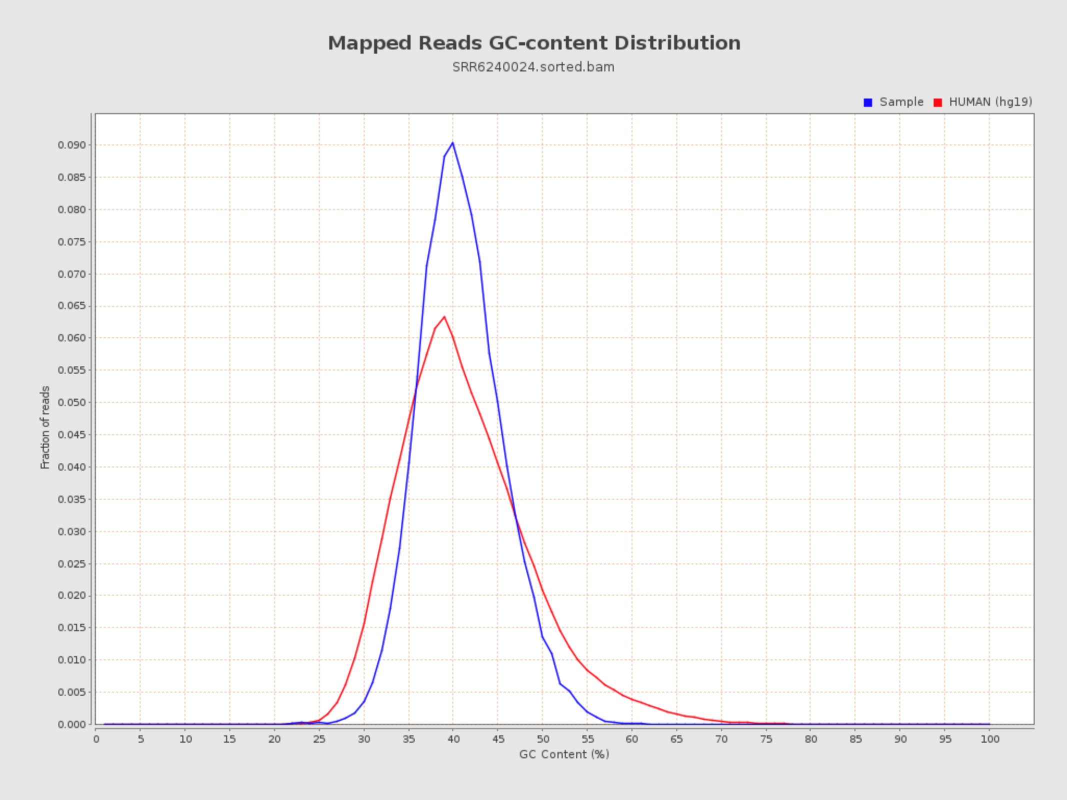
7. Results : Duplication Rate Histogram



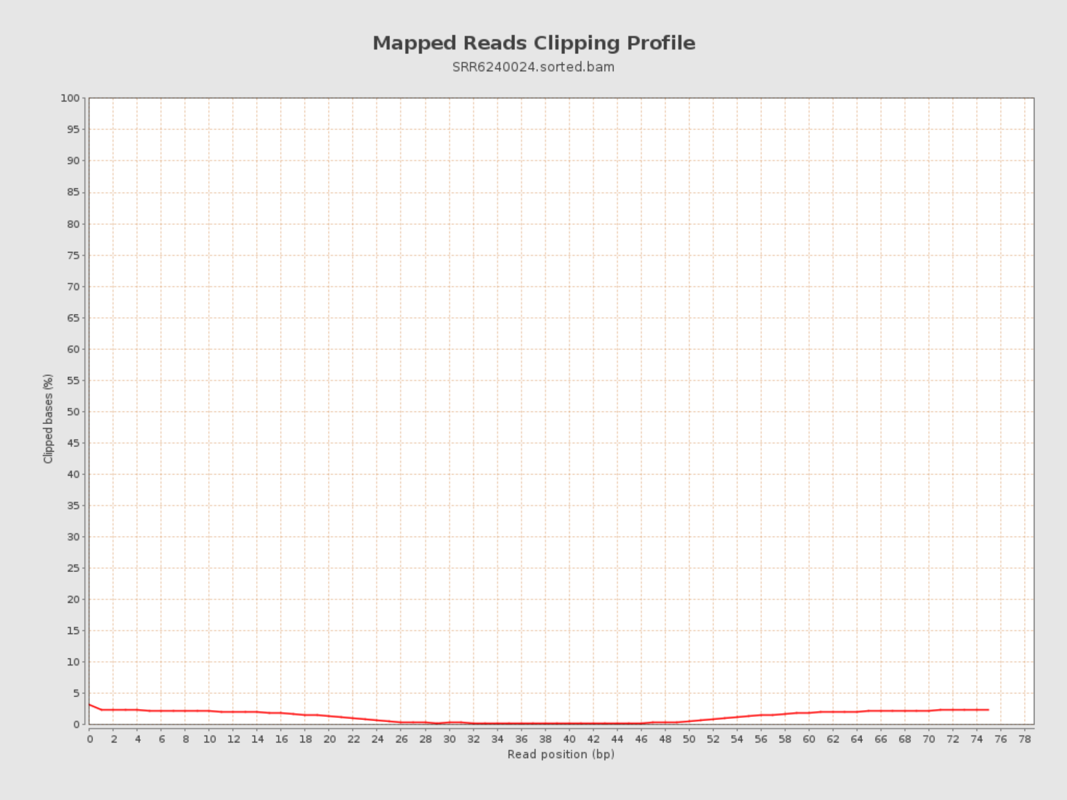
8. Results : Mapped Reads Nucleotide Content



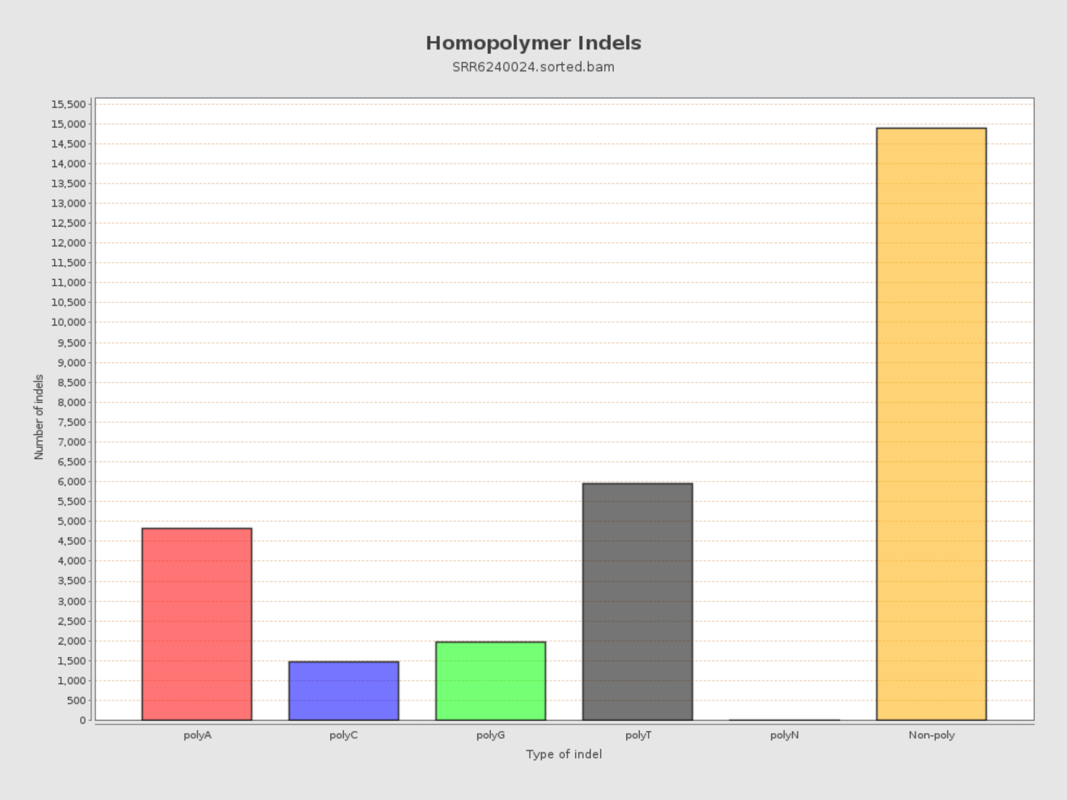
9. Results : Mapped Reads GC-content Distribution



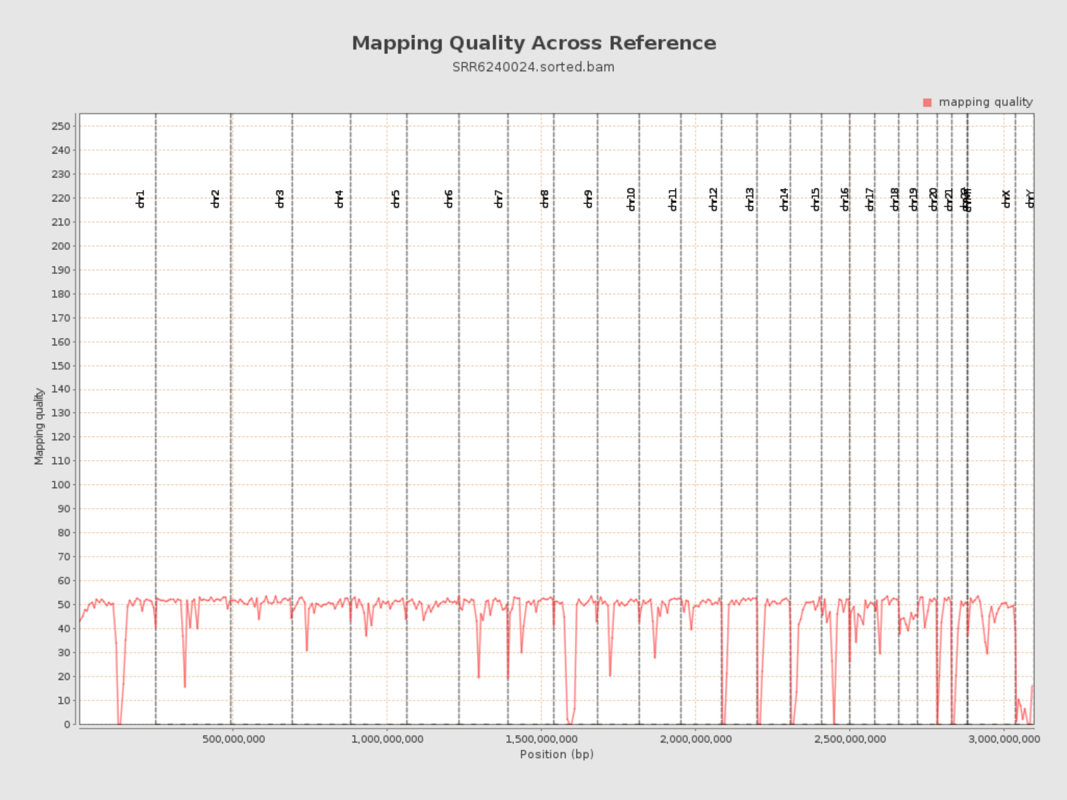
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram