Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:31:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240038.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_SRR6240038 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240038.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:31:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240038.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,926,768
Mapped reads	1,488,466 / 77.25%
Unmapped reads	438,302 / 22.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,377 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	276,103 / 14.33%
Duplication rate	14.4%
Clipped reads	1,015,789 / 52.72%

2.2. ACGT Content

Number/percentage of A's	24,058,406 / 26.58%
Number/percentage of C's	15,827,803 / 17.49%
Number/percentage of T's	29,441,741 / 32.53%
Number/percentage of G's	21,135,455 / 23.35%
Number/percentage of N's	55,466 / 0.06%
GC Percentage	40.83%

2.3. Coverage

Mean	0.0293

Standard Deviation	0.3371

2.4. Mapping Quality

Mean Mapping Quality	44.31

2.5. Mismatches and indels

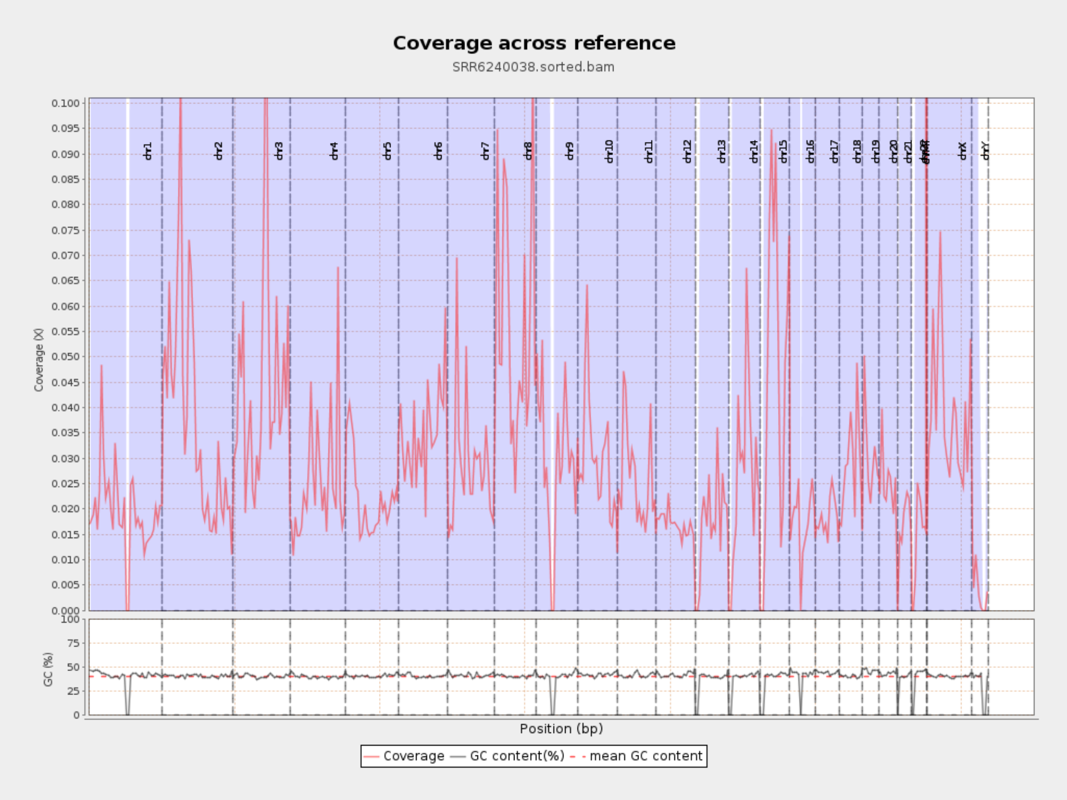
General error rate	0.95%
Mismatches	847,720
Insertions	5,928
Mapped reads with at least one insertion	0.4%
Deletions	29,400
Mapped reads with at least one deletion	1.95%
Homopolymer indels	45.6%

2.6. Chromosome stats

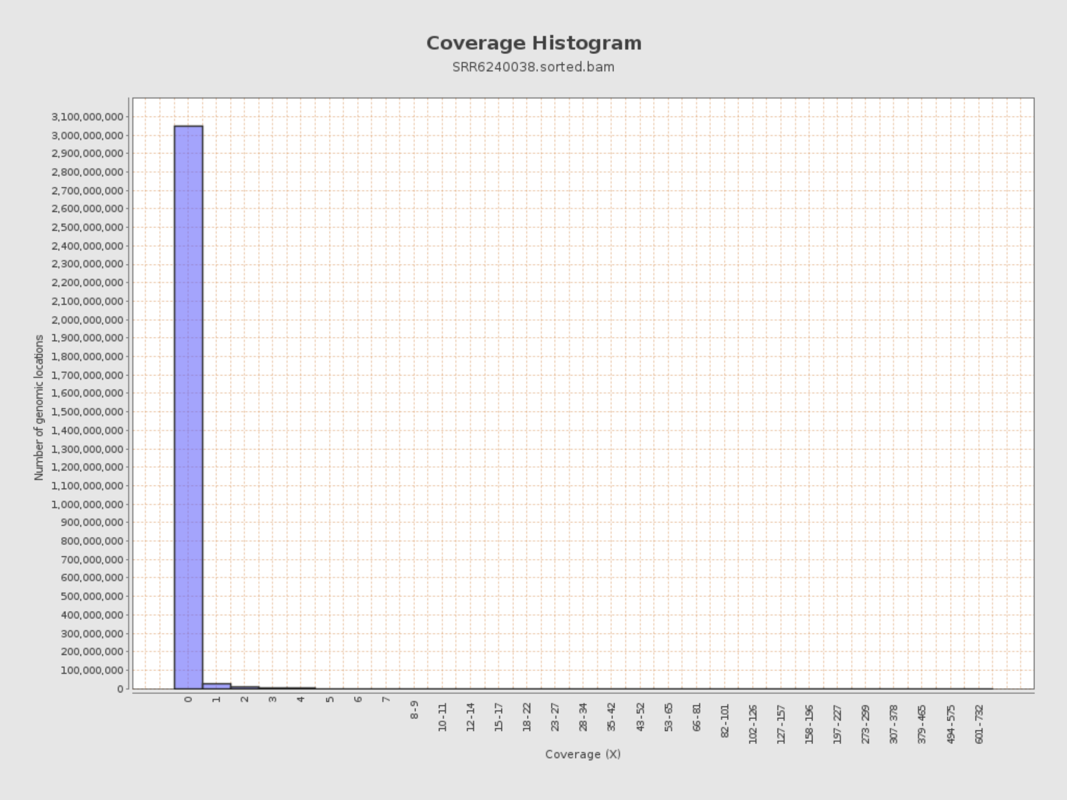
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4841155	0.0194	0.273
chr2	243199373	9132072	0.0375	0.4348
chr3	198022430	8773744	0.0443	0.351
chr4	191154276	4846005	0.0254	0.2676
chr5	180915260	4023351	0.0222	0.2455
chr6	171115067	6036258	0.0353	0.374
chr7	159138663	4633105	0.0291	0.4917

chr8	146364022	8158069	0.0557	0.5848
chr9	141213431	4015841	0.0284	0.3036
chr10	135534747	4123296	0.0304	0.317
chr11	135006516	3500108	0.0259	0.2984
chr12	133851895	2257957	0.0169	0.2144
chr13	115169878	1976500	0.0172	0.2208
chr14	107349540	2878584	0.0268	0.2831
chr15	102531392	4742529	0.0463	0.3661
chr16	90354753	1594724	0.0176	0.2174
chr17	81195210	1487319	0.0183	0.2251
chr18	78077248	2276959	0.0292	0.3617
chr19	59128983	1796280	0.0304	0.3093
chr20	63025520	1591695	0.0253	0.2645
chr21	48129895	796192	0.0165	0.2074
chr22	51304566	696672	0.0136	0.185
chrMT	16571	136455	8.2346	7.7806
chrX	155270560	6019653	0.0388	0.3336
chrY	59373566	234234	0.0039	0.1064

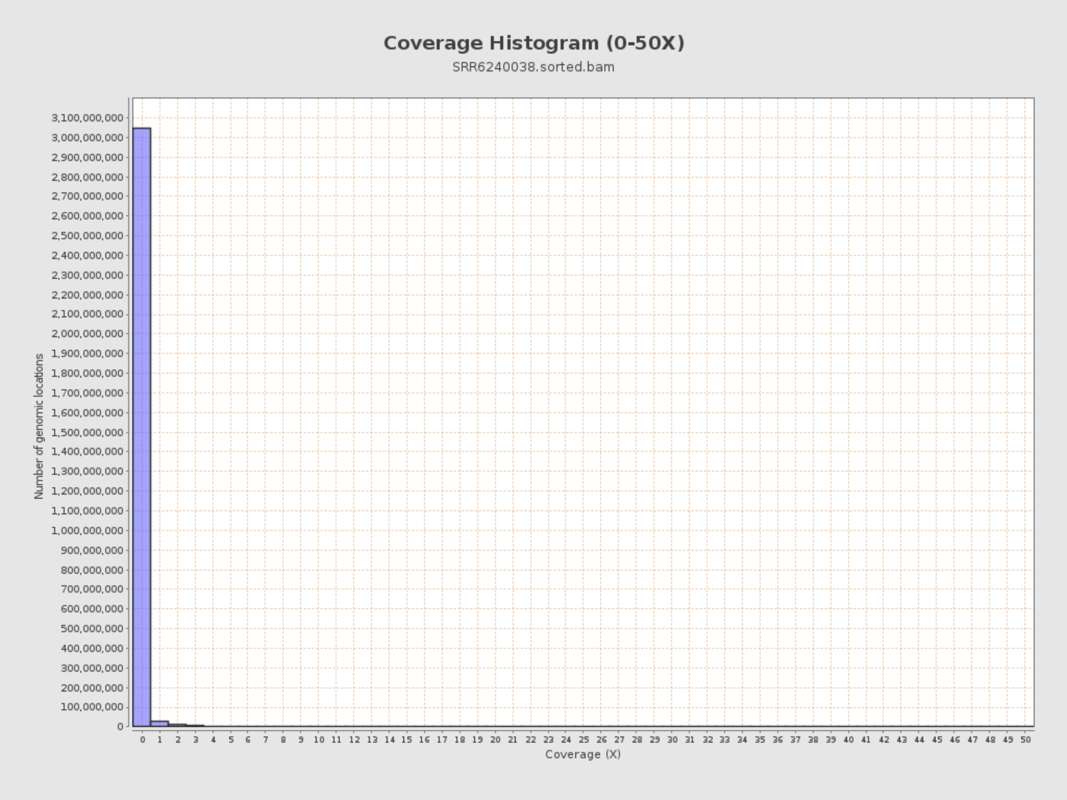
3. Results : Coverage across reference



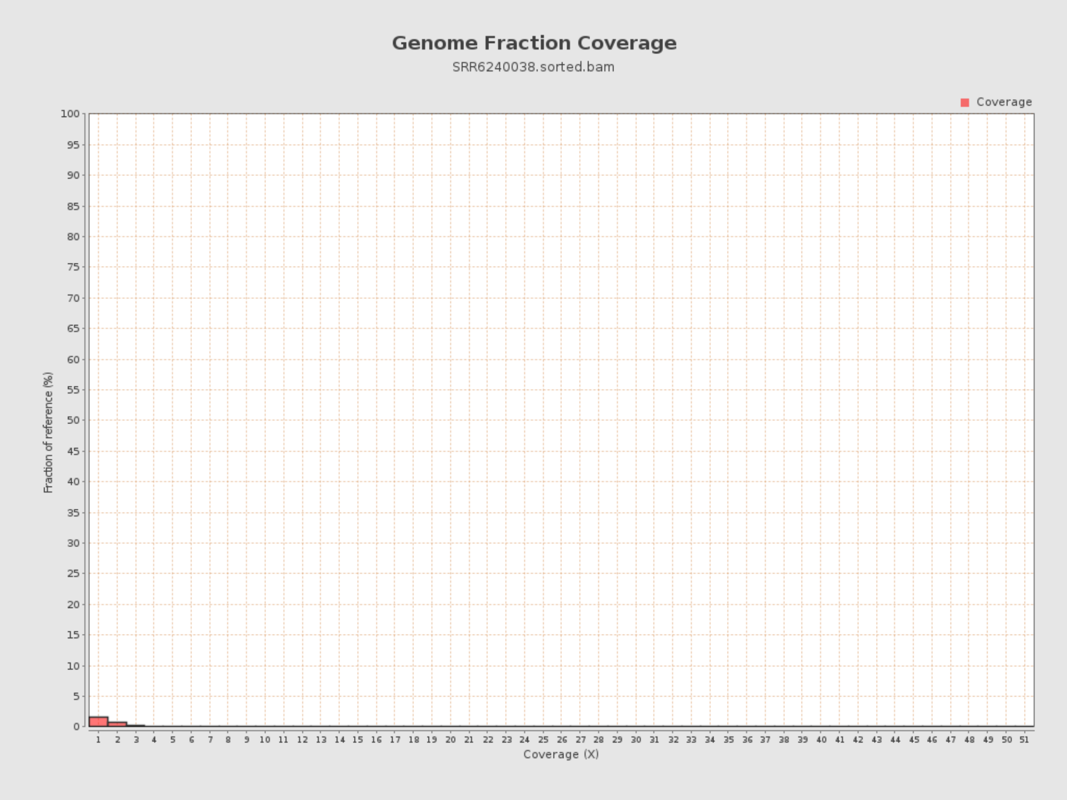
4. Results : Coverage Histogram



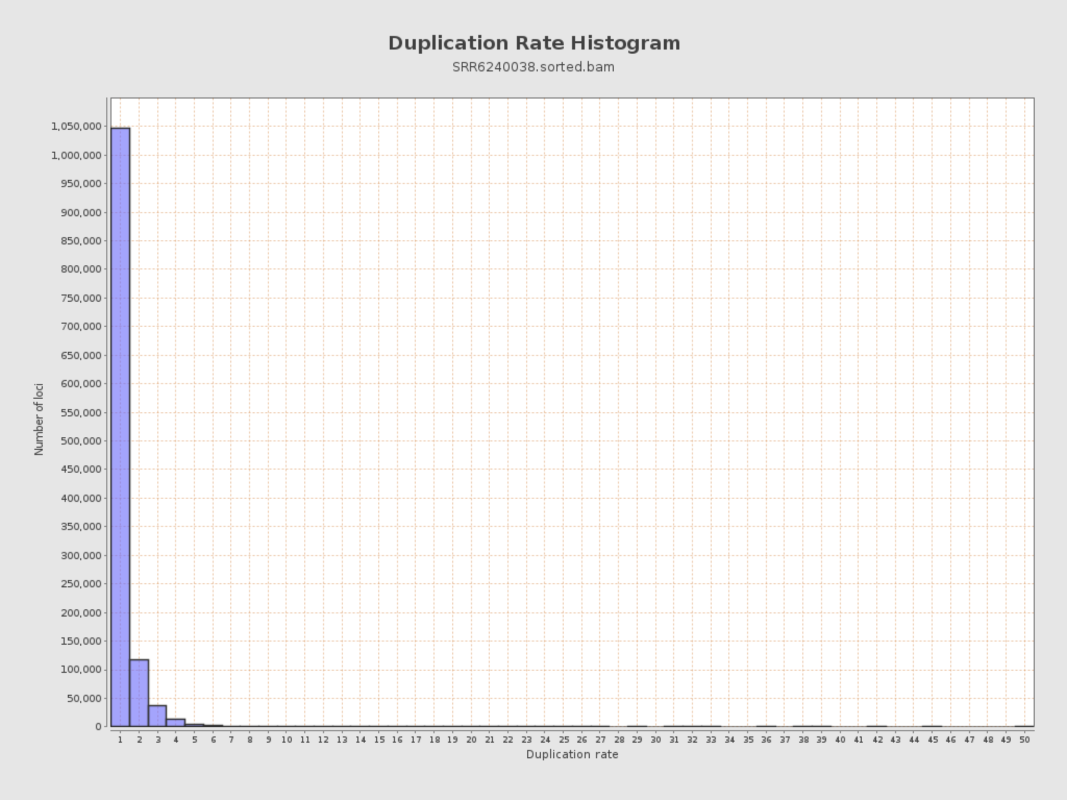
5. Results : Coverage Histogram (0-50X)



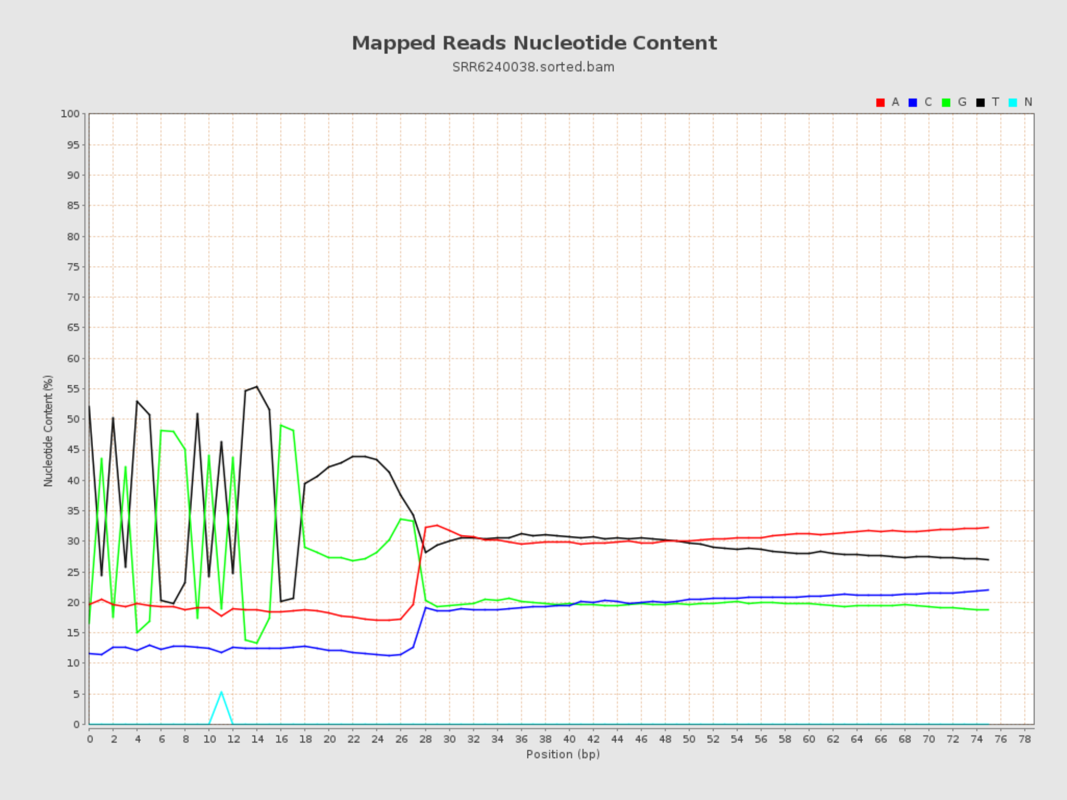
6. Results : Genome Fraction Coverage



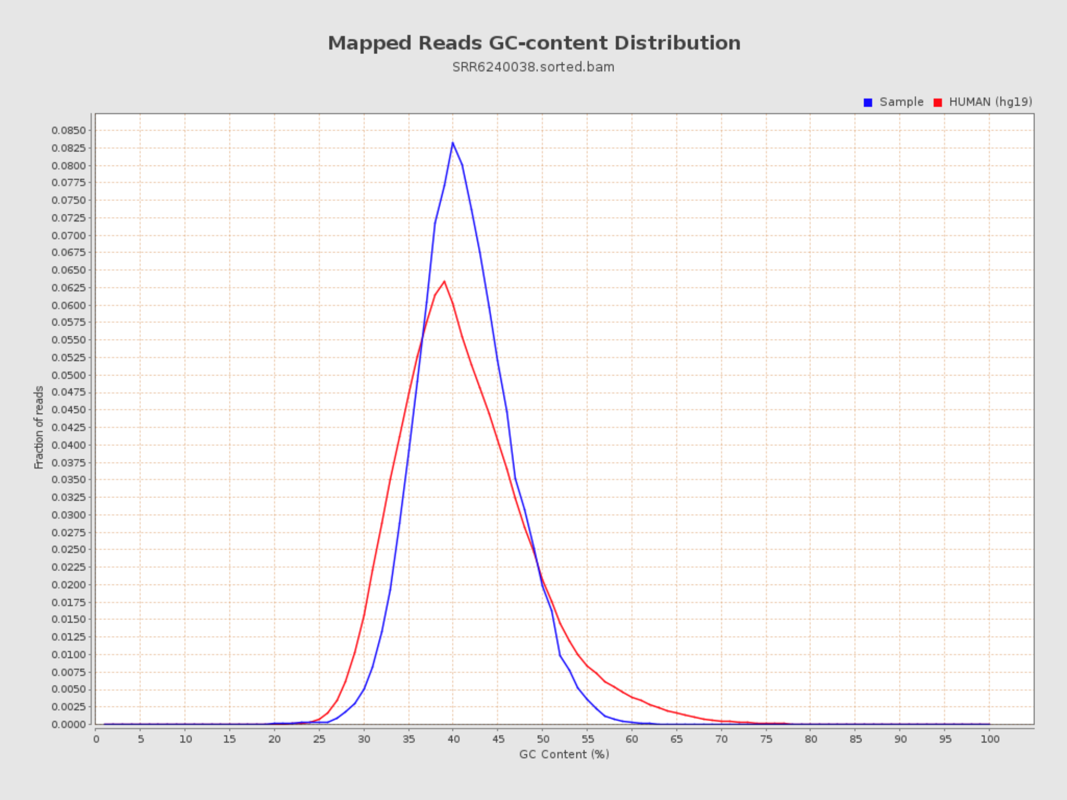
7. Results : Duplication Rate Histogram



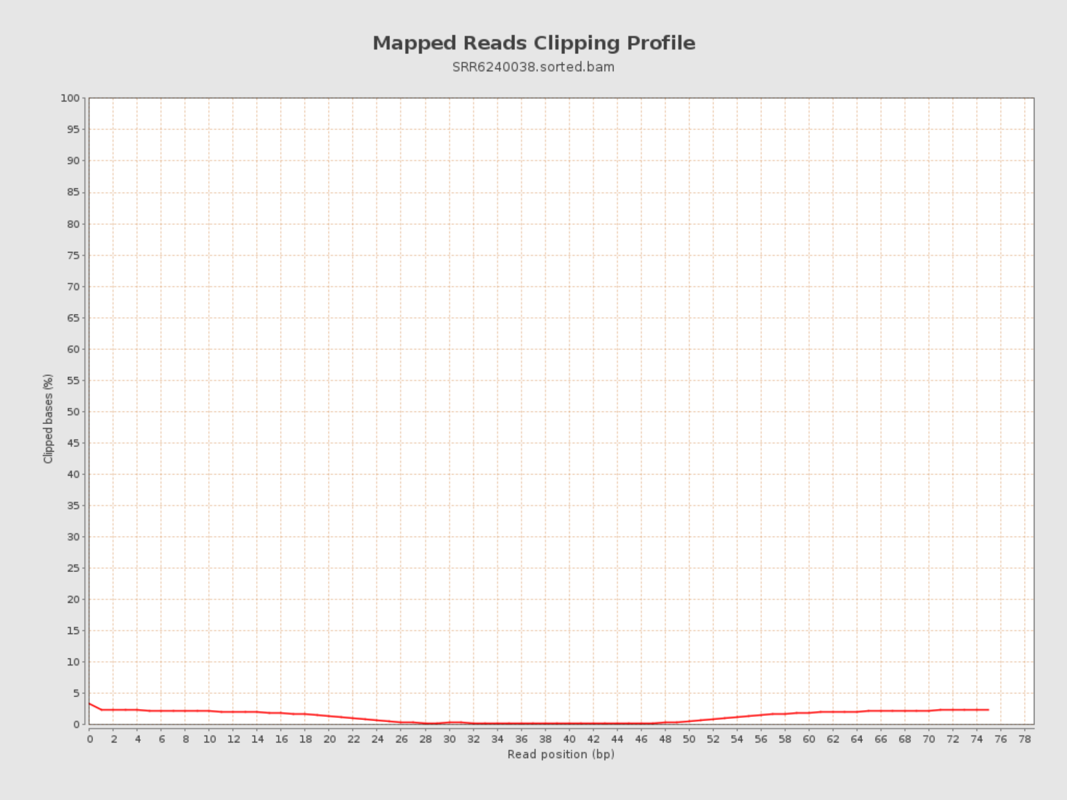
8. Results : Mapped Reads Nucleotide Content



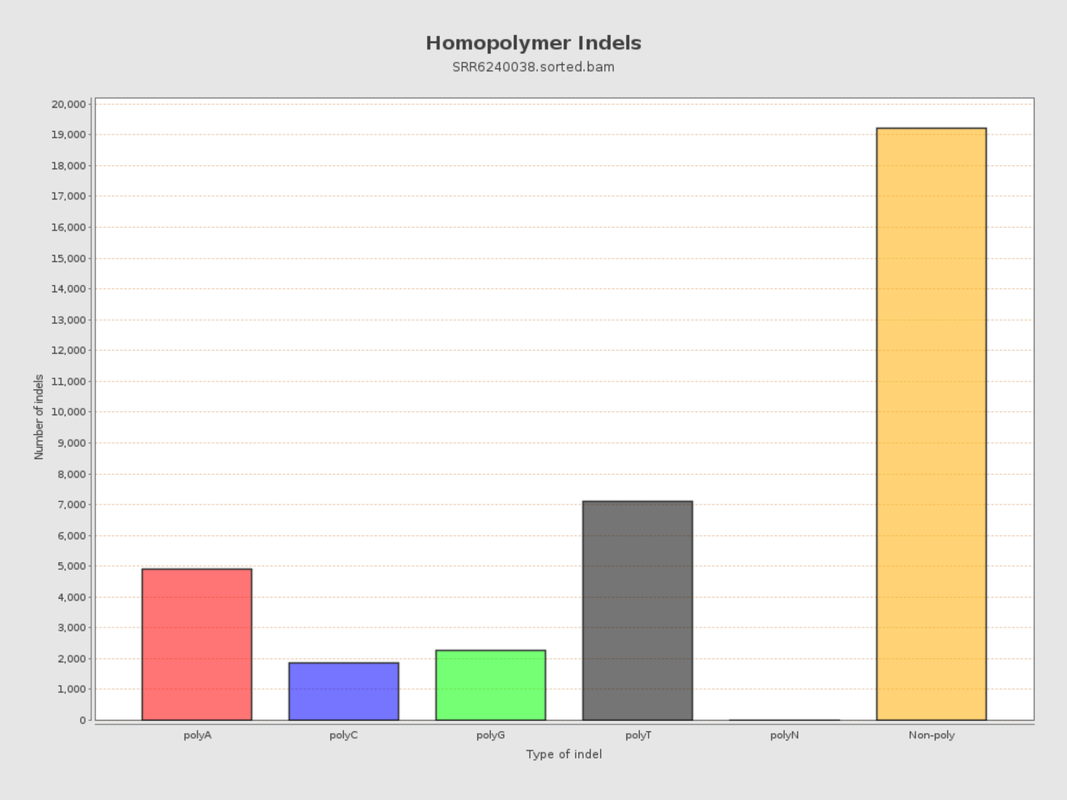
9. Results : Mapped Reads GC-content Distribution



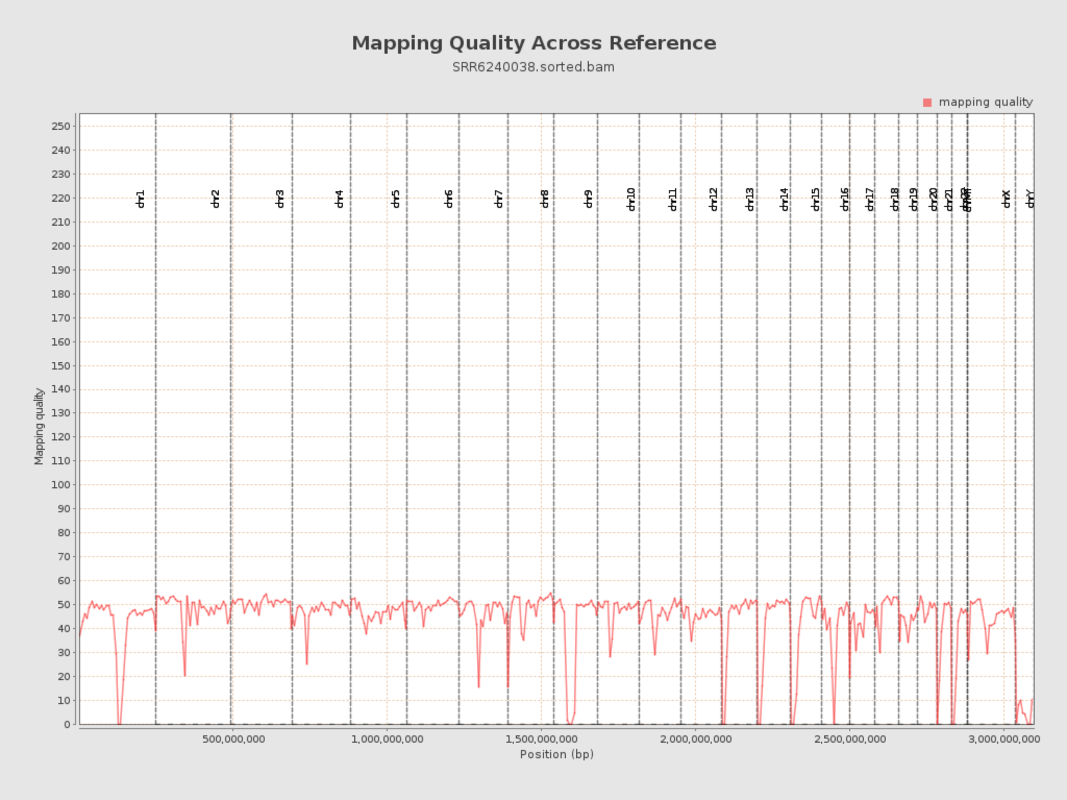
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram