Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:59:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240197.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_SRR6240197 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240197.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:59:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240197.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,614,601
Mapped reads	1,383,230 / 85.67%
Unmapped reads	231,371 / 14.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,968 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	60,777 / 3.76%
Duplication rate	3.45%
Clipped reads	767,703 / 47.55%

2.2. ACGT Content

Number/percentage of A's	23,854,881 / 27.03%
Number/percentage of C's	15,433,159 / 17.49%
Number/percentage of T's	28,341,373 / 32.11%
Number/percentage of G's	20,607,921 / 23.35%
Number/percentage of N's	22,188 / 0.03%
GC Percentage	40.84%

2.3. Coverage

Mean	0.0285

Standard Deviation	0.2898

2.4. Mapping Quality

Mean Mapping Quality	45

2.5. Mismatches and indels

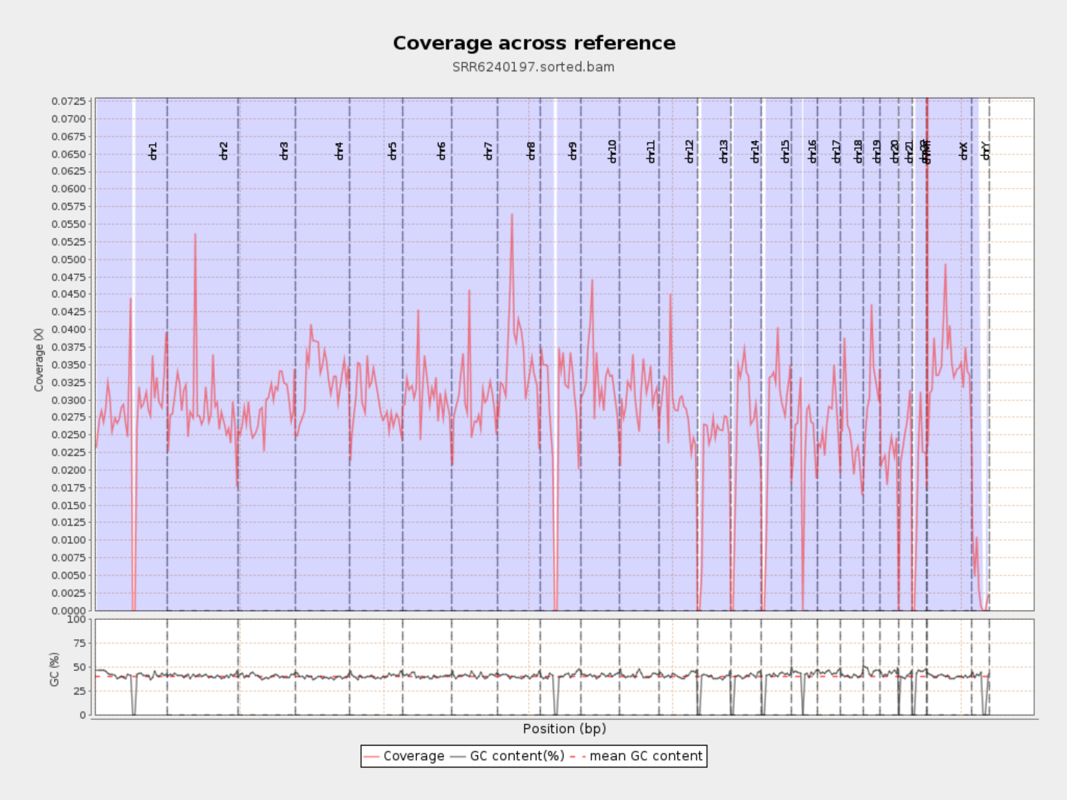
General error rate	0.85%
Mismatches	742,684
Insertions	6,284
Mapped reads with at least one insertion	0.45%
Deletions	22,271
Mapped reads with at least one deletion	1.59%
Homopolymer indels	48.39%

2.6. Chromosome stats

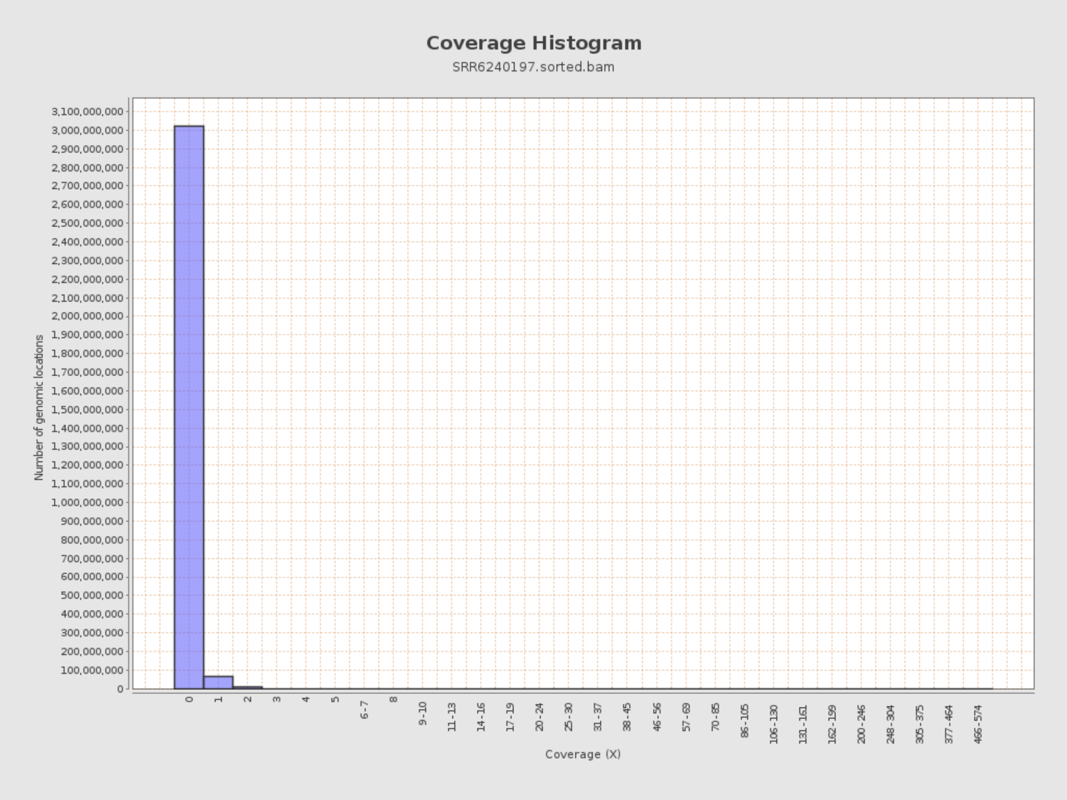
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6974577	0.028	0.4841
chr2	243199373	7046309	0.029	0.3268
chr3	198022430	5728233	0.0289	0.192
chr4	191154276	6351594	0.0332	0.2114
chr5	180915260	5343213	0.0295	0.197
chr6	171115067	5275034	0.0308	0.2468
chr7	159138663	4744118	0.0298	0.3492

chr8	146364022	5245140	0.0358	0.4038
chr9	141213431	4029837	0.0285	0.3078
chr10	135534747	4465058	0.0329	0.2617
chr11	135006516	4161405	0.0308	0.2628
chr12	133851895	3881824	0.029	0.1988
chr13	115169878	2486248	0.0216	0.1653
chr14	107349540	2729101	0.0254	0.1991
chr15	102531392	2704263	0.0264	0.193
chr16	90354753	2099495	0.0232	0.1941
chr17	81195210	2154910	0.0265	0.1986
chr18	78077248	1927015	0.0247	0.5429
chr19	59128983	1863653	0.0315	0.3277
chr20	63025520	1360021	0.0216	0.1758
chr21	48129895	1107718	0.023	0.185
chr22	51304566	880455	0.0172	0.145
chrMT	16571	52033	3.14	2.6279
chrX	155270560	5467754	0.0352	0.2415
chrY	59373566	219177	0.0037	0.0831

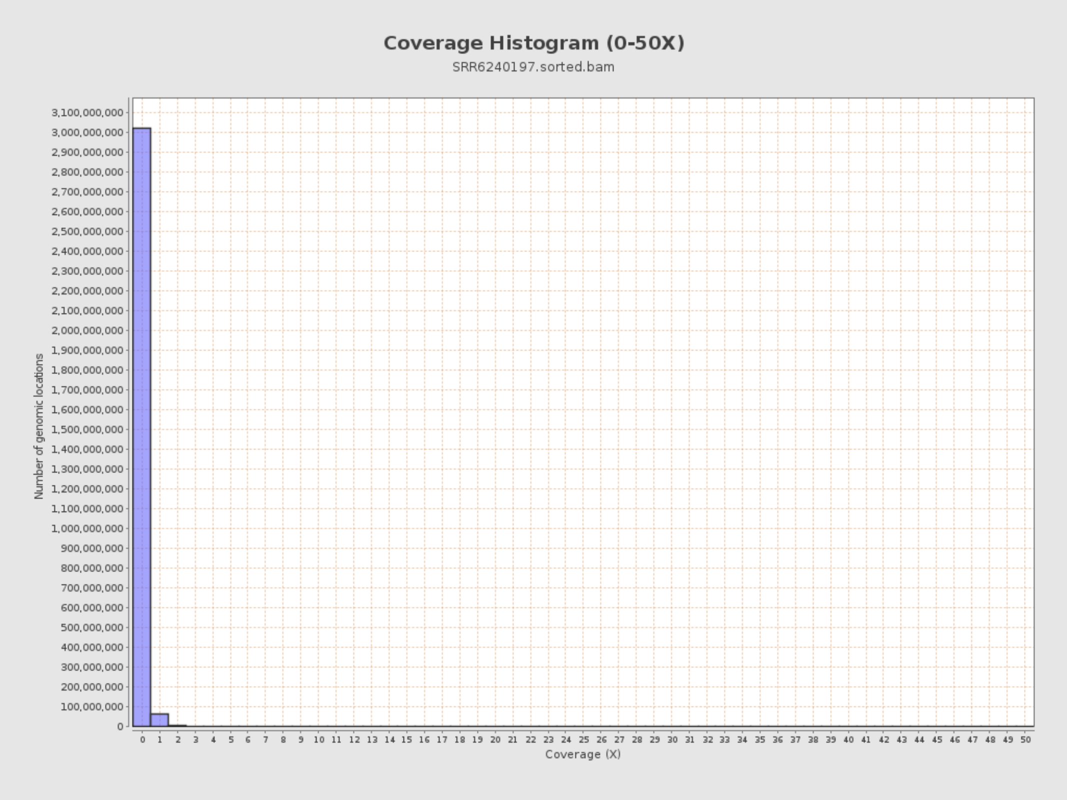
3. Results : Coverage across reference



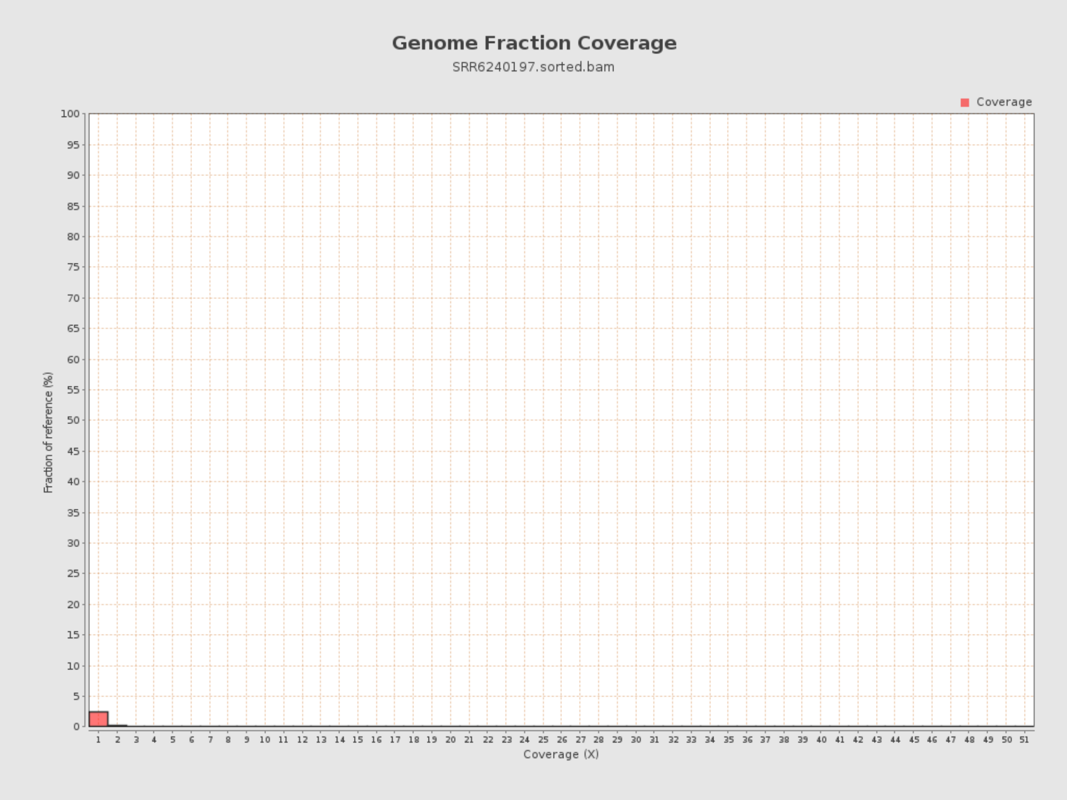
4. Results : Coverage Histogram



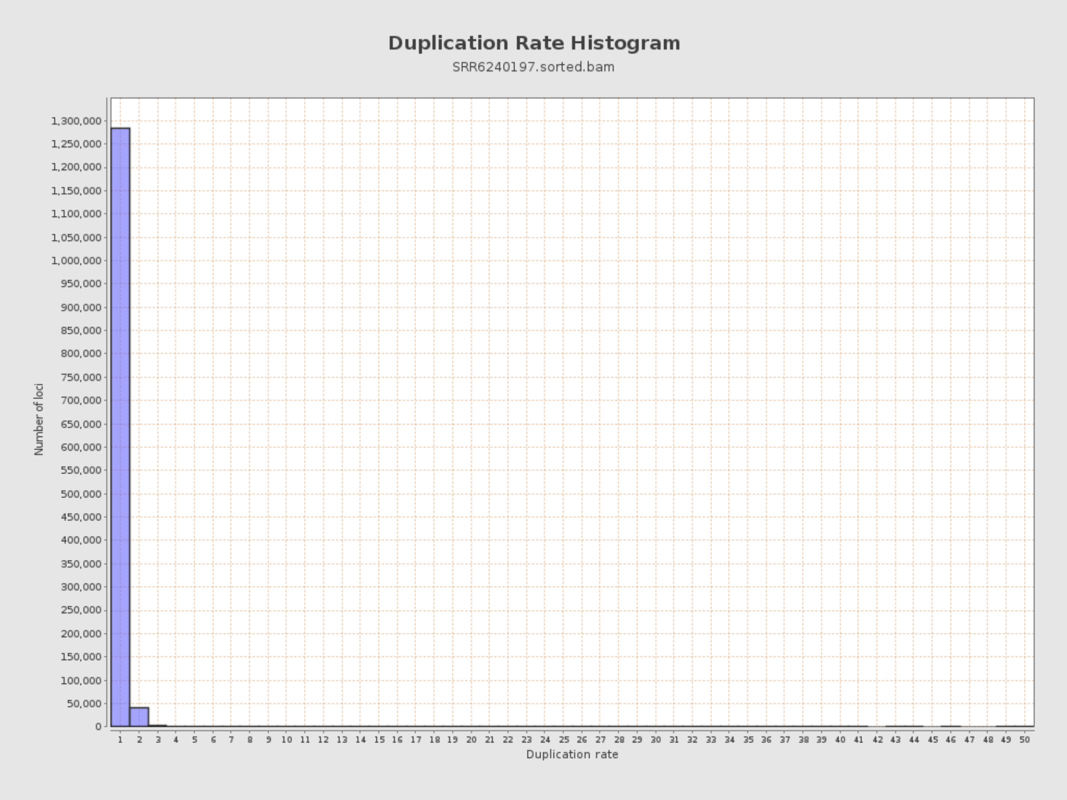
5. Results : Coverage Histogram (0-50X)



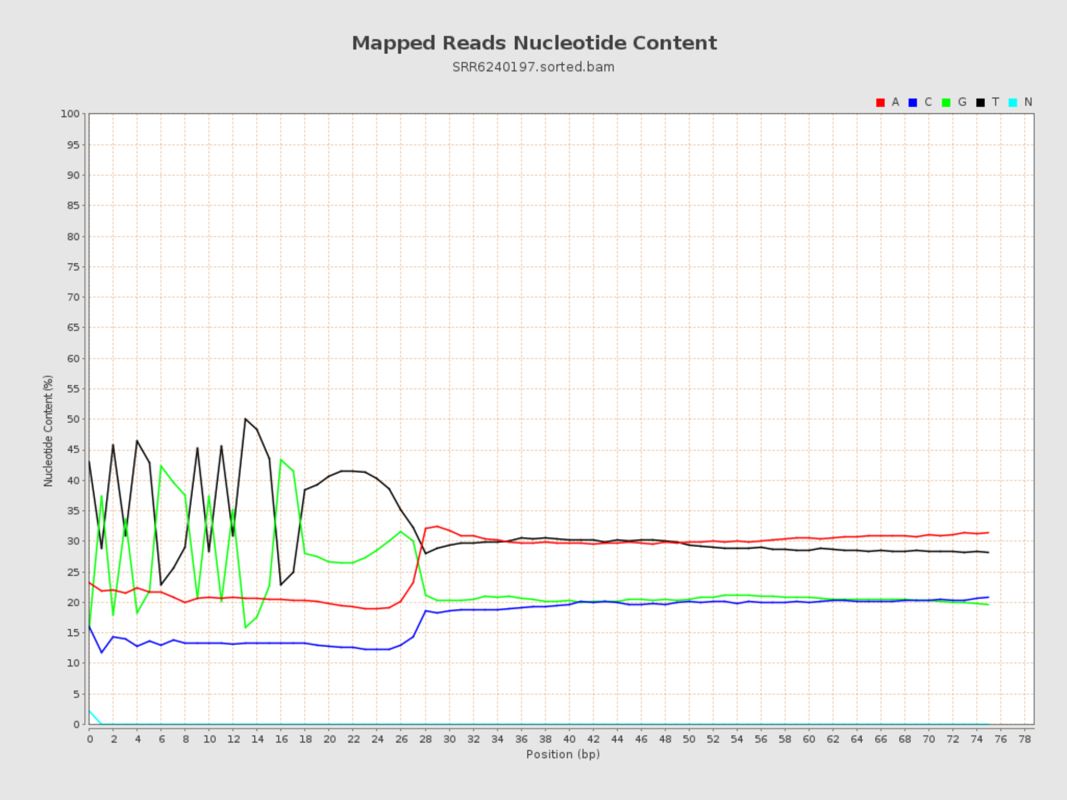
6. Results : Genome Fraction Coverage



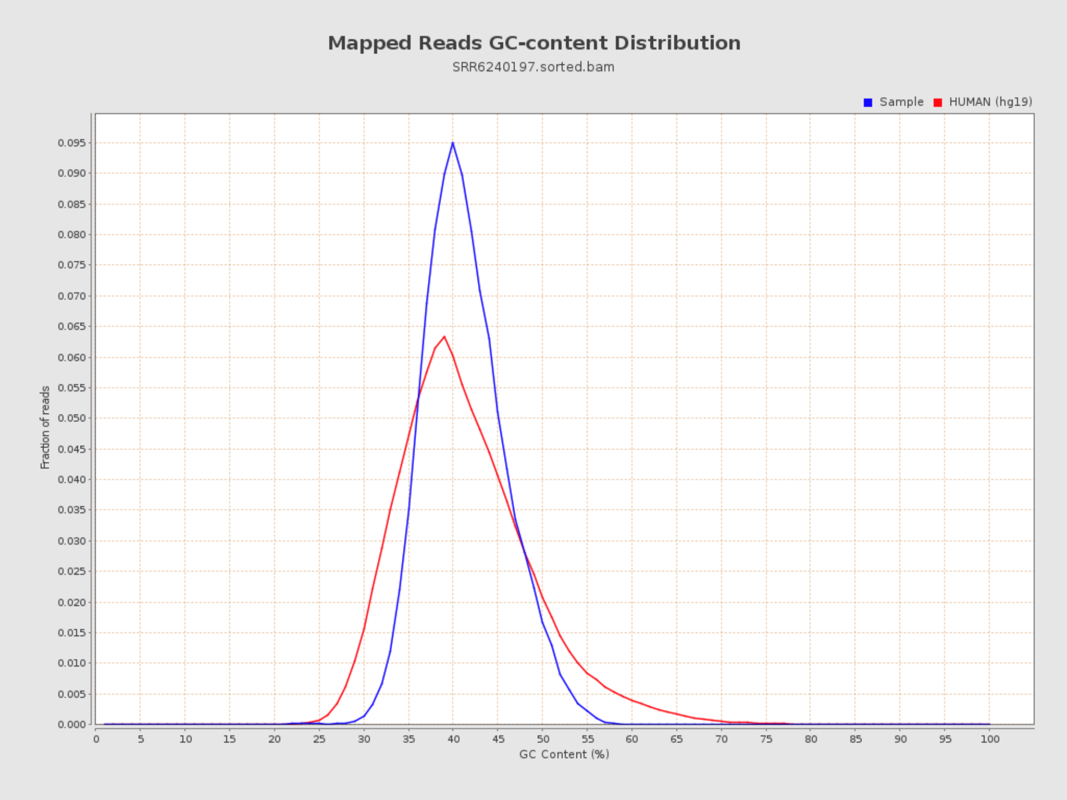
7. Results : Duplication Rate Histogram



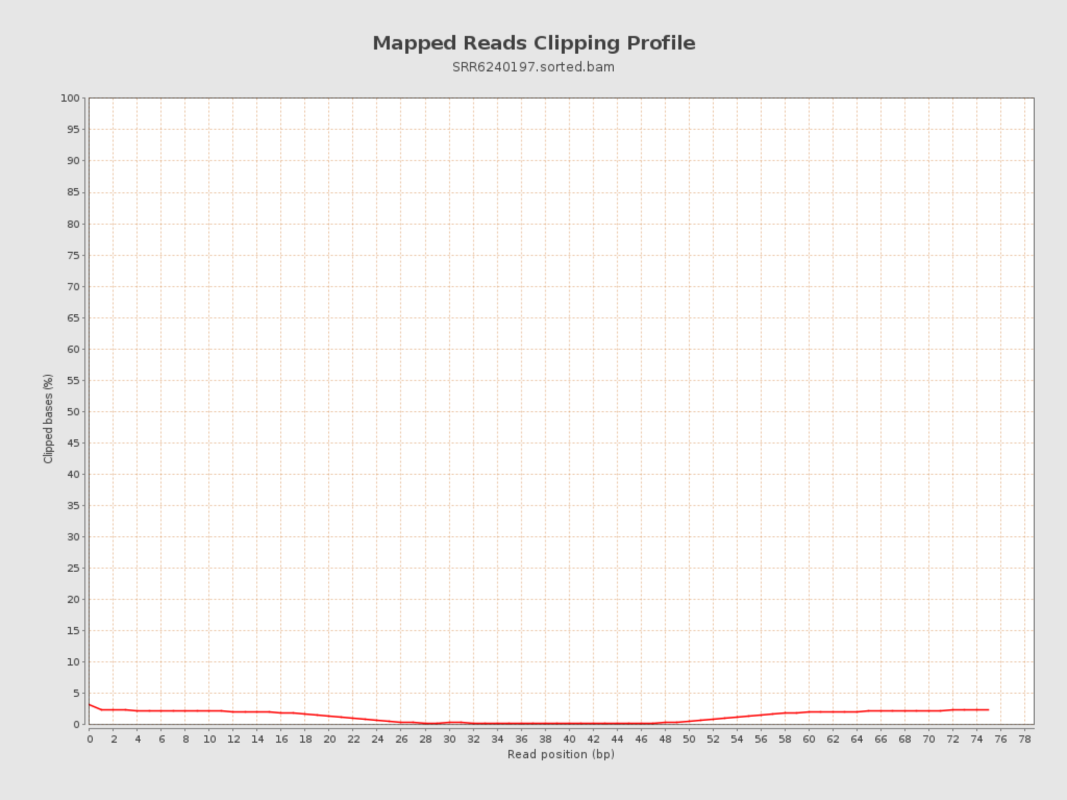
8. Results : Mapped Reads Nucleotide Content



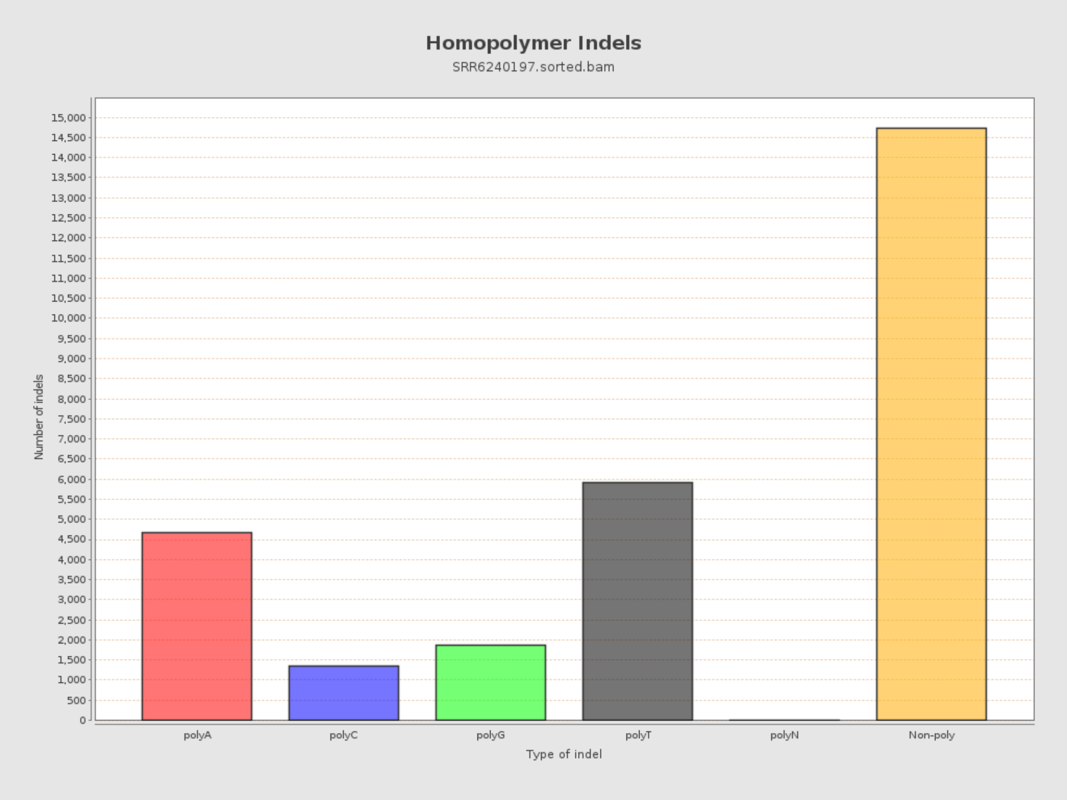
9. Results : Mapped Reads GC-content Distribution



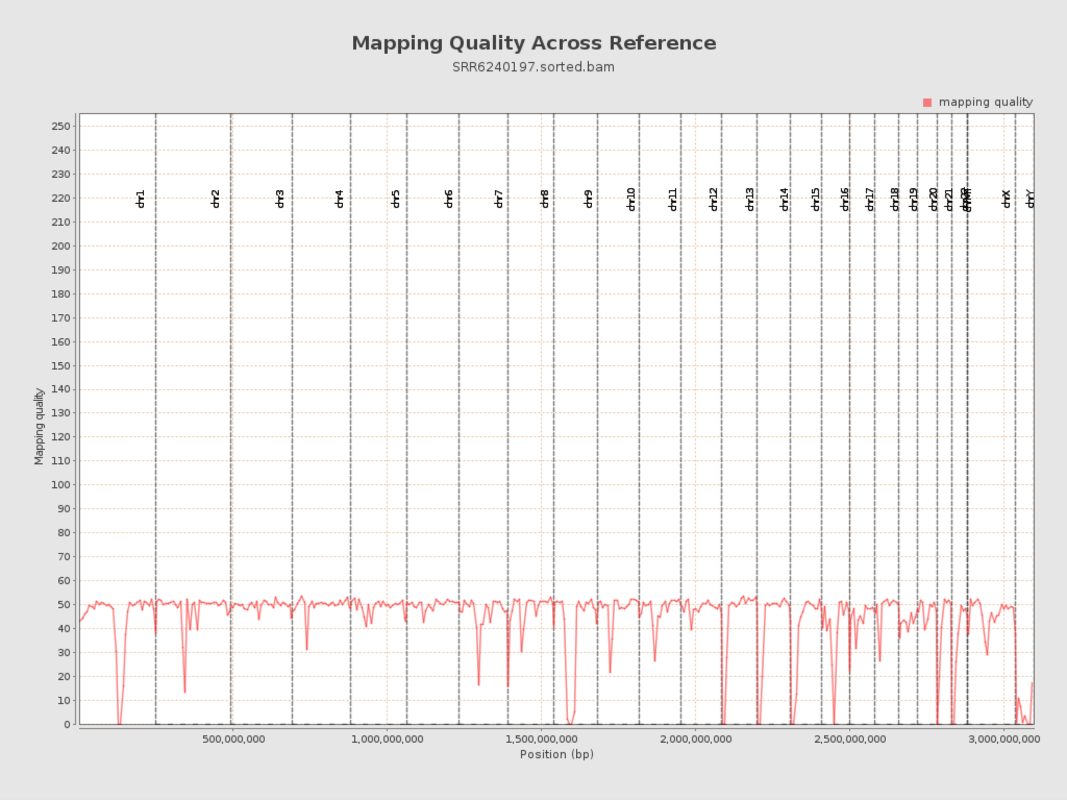
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram