Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:06:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013336.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_SRR6013336 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013336.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:06:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013336.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,876,358
Mapped reads	1,581,434 / 84.28%
Unmapped reads	294,924 / 15.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,372 / 1.03%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	202,409 / 10.79%
Duplication rate	9.88%
Clipped reads	893,791 / 47.63%

2.2. ACGT Content

Number/percentage of A's	27,401,736 / 27.07%
Number/percentage of C's	19,007,711 / 18.78%
Number/percentage of T's	31,690,376 / 31.31%
Number/percentage of G's	23,113,346 / 22.83%
Number/percentage of N's	12,097 / 0.01%
GC Percentage	41.61%

2.3. Coverage

Mean	0.0327

Standard Deviation	0.3665

2.4. Mapping Quality

Mean Mapping Quality	41.1

2.5. Mismatches and indels

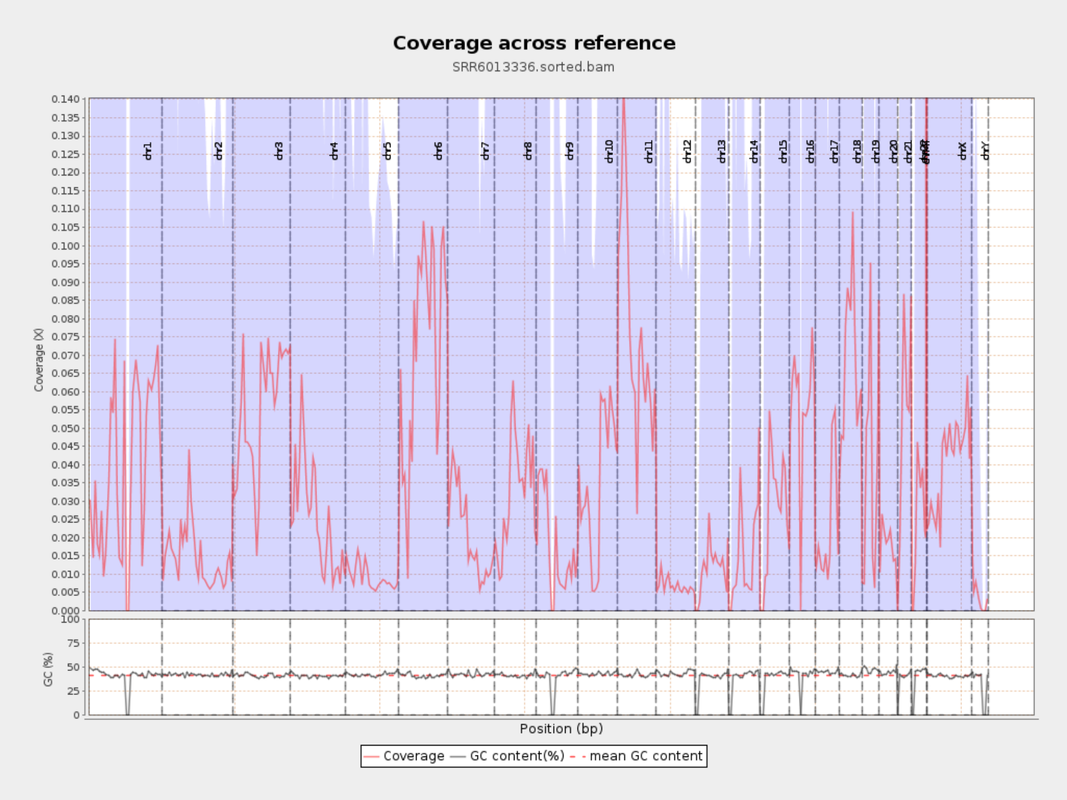
General error rate	0.84%
Mismatches	843,189
Insertions	6,402
Mapped reads with at least one insertion	0.4%
Deletions	36,051
Mapped reads with at least one deletion	2.25%
Homopolymer indels	44.02%

2.6. Chromosome stats

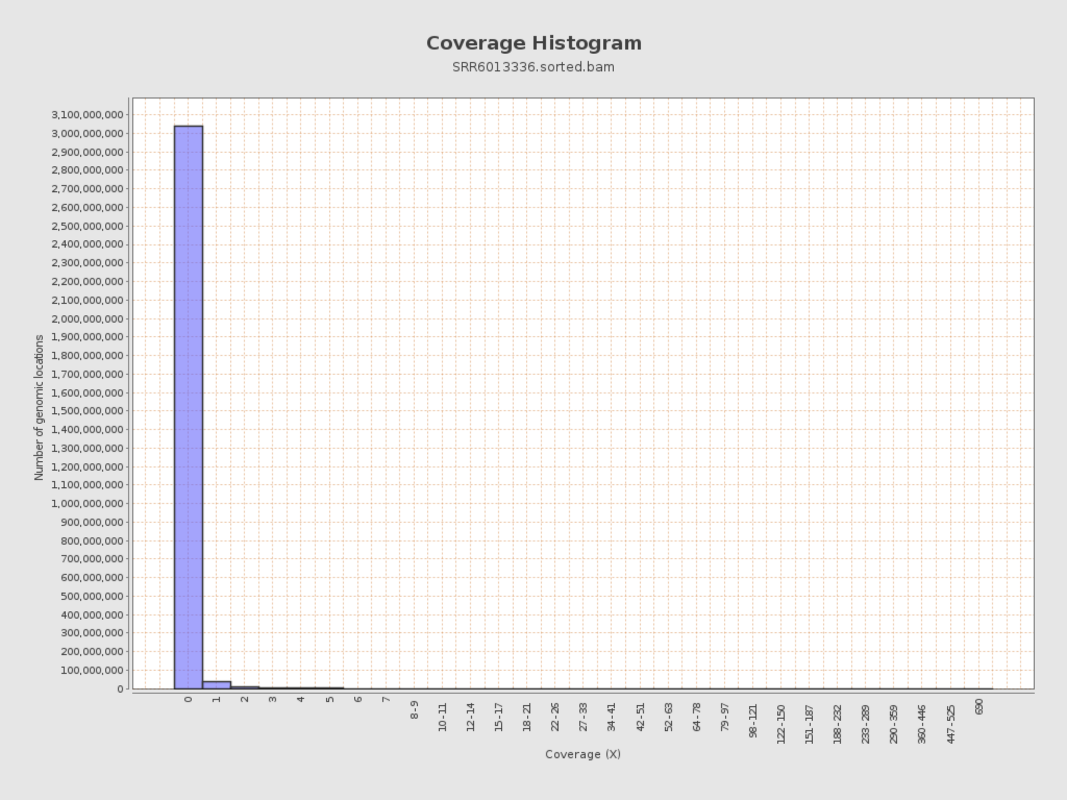
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9839802	0.0395	0.5309
chr2	243199373	3567163	0.0147	0.4049
chr3	198022430	10852926	0.0548	0.3784
chr4	191154276	4843120	0.0253	0.2484
chr5	180915260	1642625	0.0091	0.1341
chr6	171115067	12343167	0.0721	0.5869
chr7	159138663	3329875	0.0209	0.2975

chr8	146364022	4871398	0.0333	0.3289
chr9	141213431	2460871	0.0174	0.2754
chr10	135534747	4777688	0.0353	0.3338
chr11	135006516	10303221	0.0763	0.55
chr12	133851895	902422	0.0067	0.1175
chr13	115169878	1300387	0.0113	0.1571
chr14	107349540	1558516	0.0145	0.198
chr15	102531392	2789924	0.0272	0.2631
chr16	90354753	5078982	0.0562	0.3933
chr17	81195210	1773693	0.0218	0.2626
chr18	78077248	5342952	0.0684	0.5453
chr19	59128983	2345592	0.0397	0.5057
chr20	63025520	1145410	0.0182	0.2025
chr21	48129895	2470763	0.0513	0.3738
chr22	51304566	1229087	0.024	0.2462
chrMT	16571	14829	0.8949	1.3205
chrX	155270560	6276937	0.0404	0.3462
chrY	59373566	225293	0.0038	0.0875

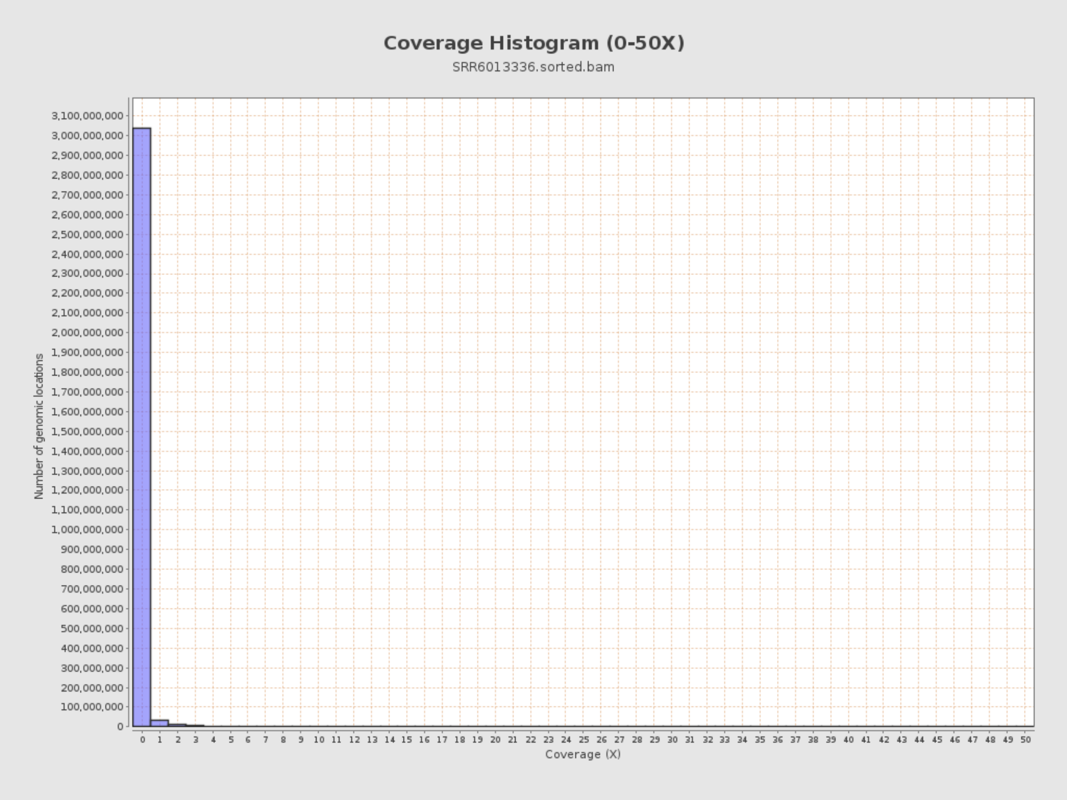
3. Results : Coverage across reference



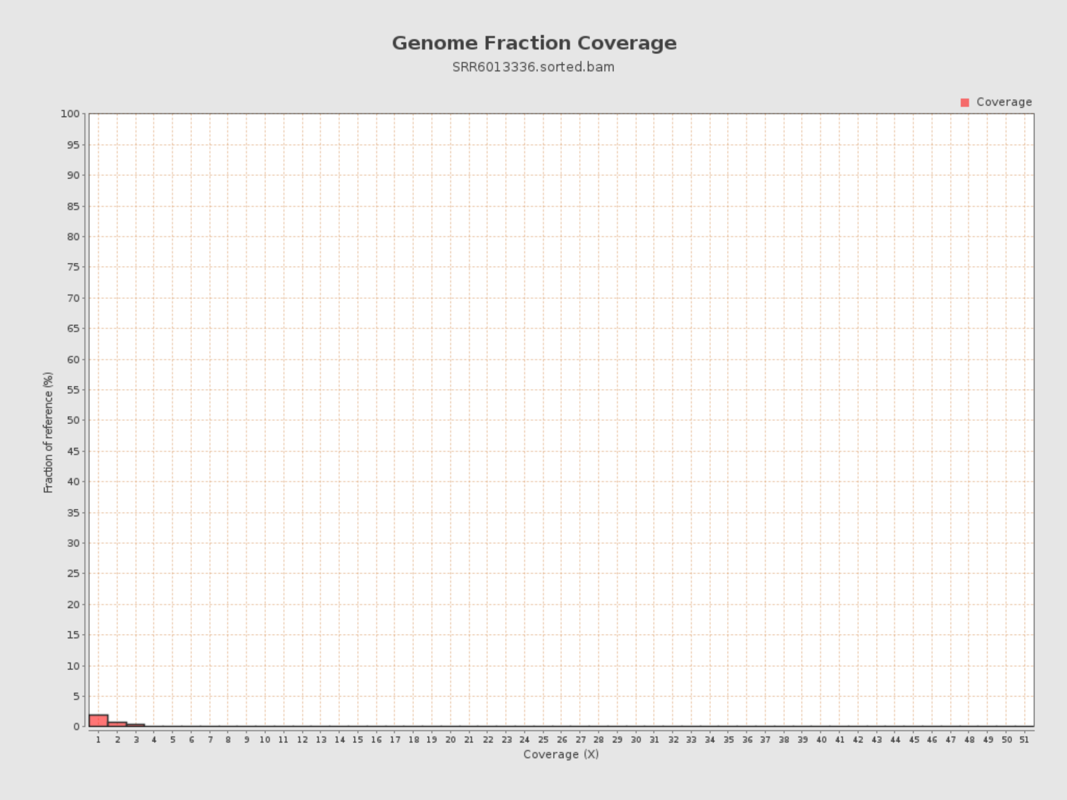
4. Results : Coverage Histogram



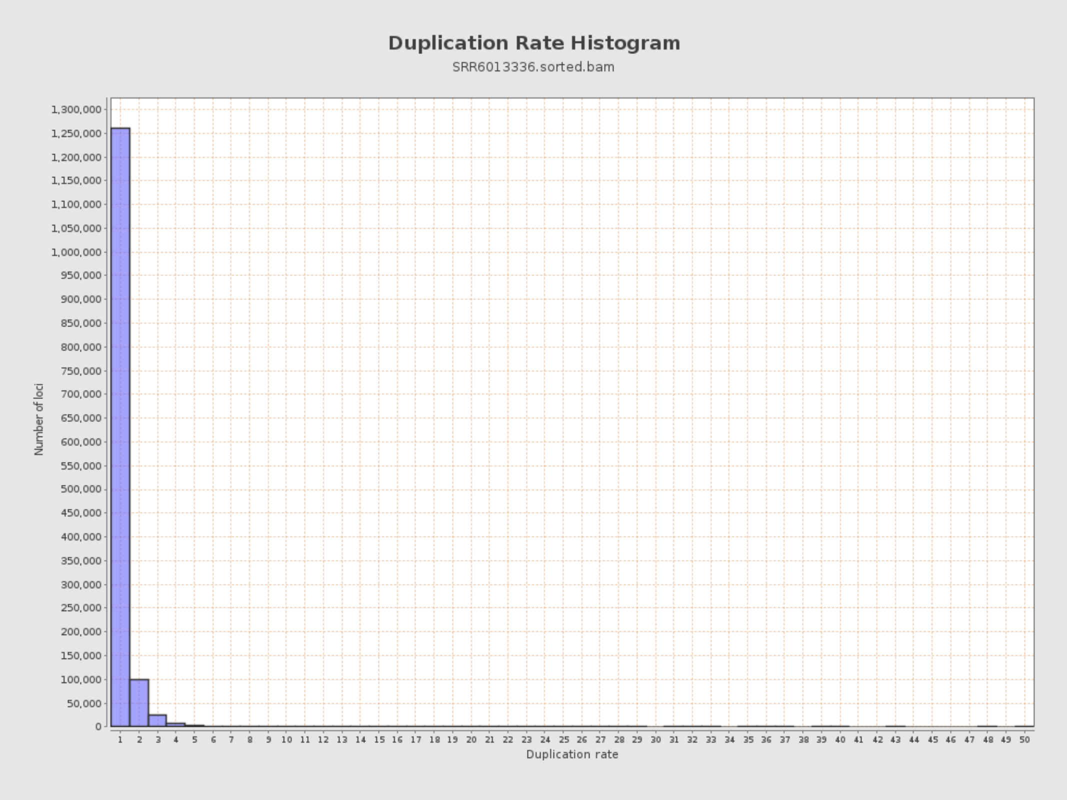
5. Results : Coverage Histogram (0-50X)



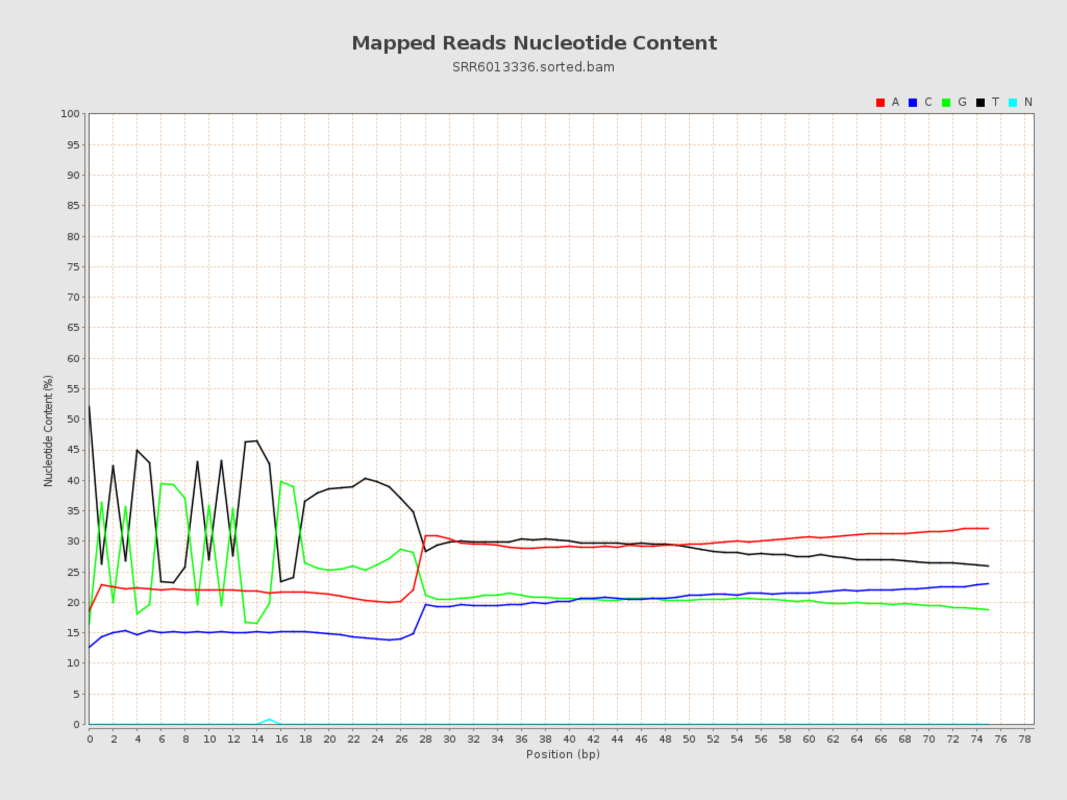
6. Results : Genome Fraction Coverage



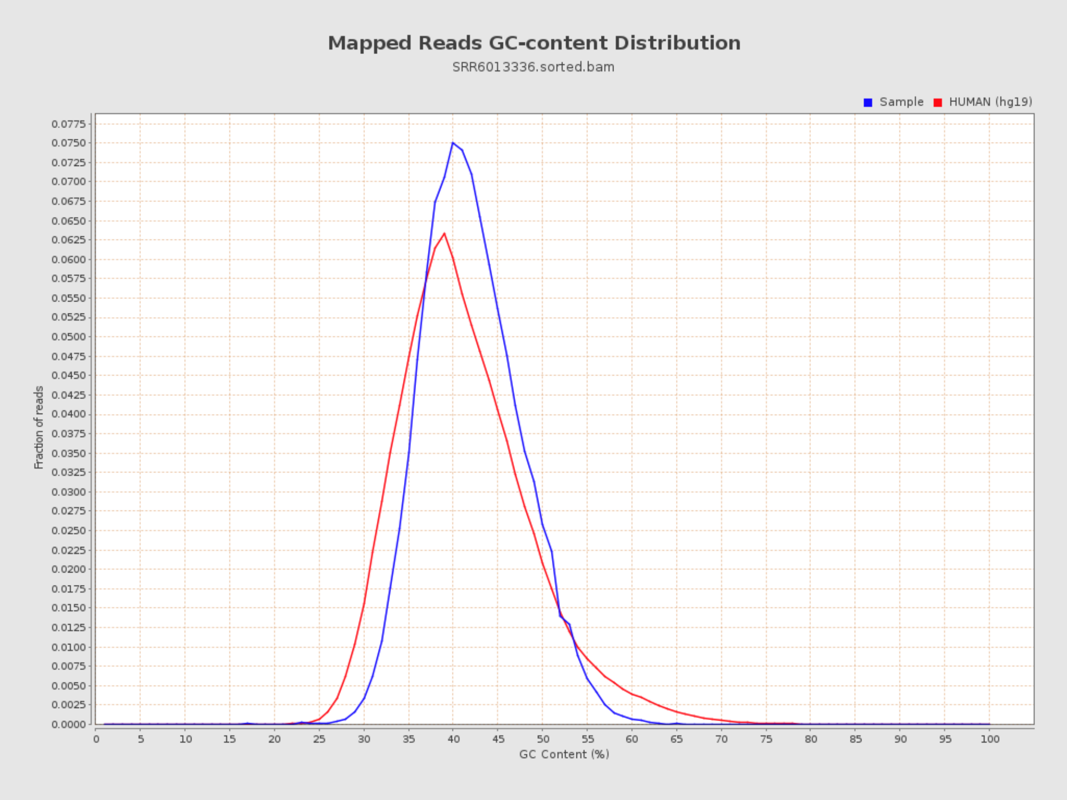
7. Results : Duplication Rate Histogram



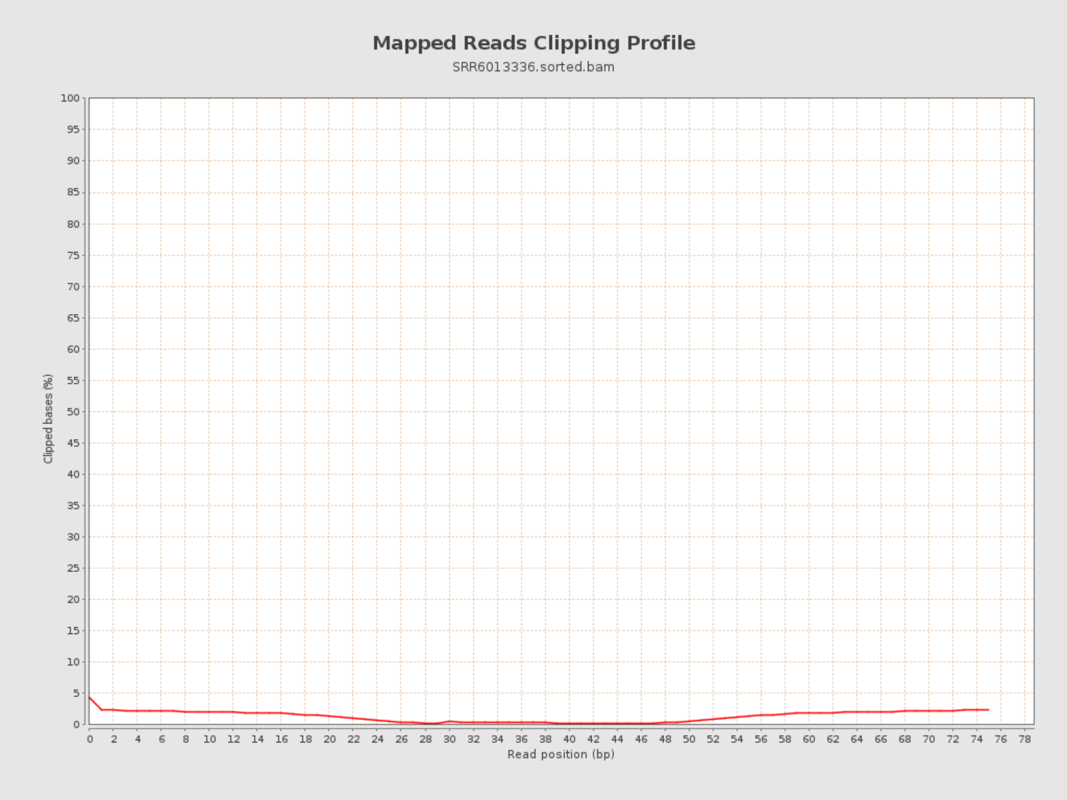
8. Results : Mapped Reads Nucleotide Content



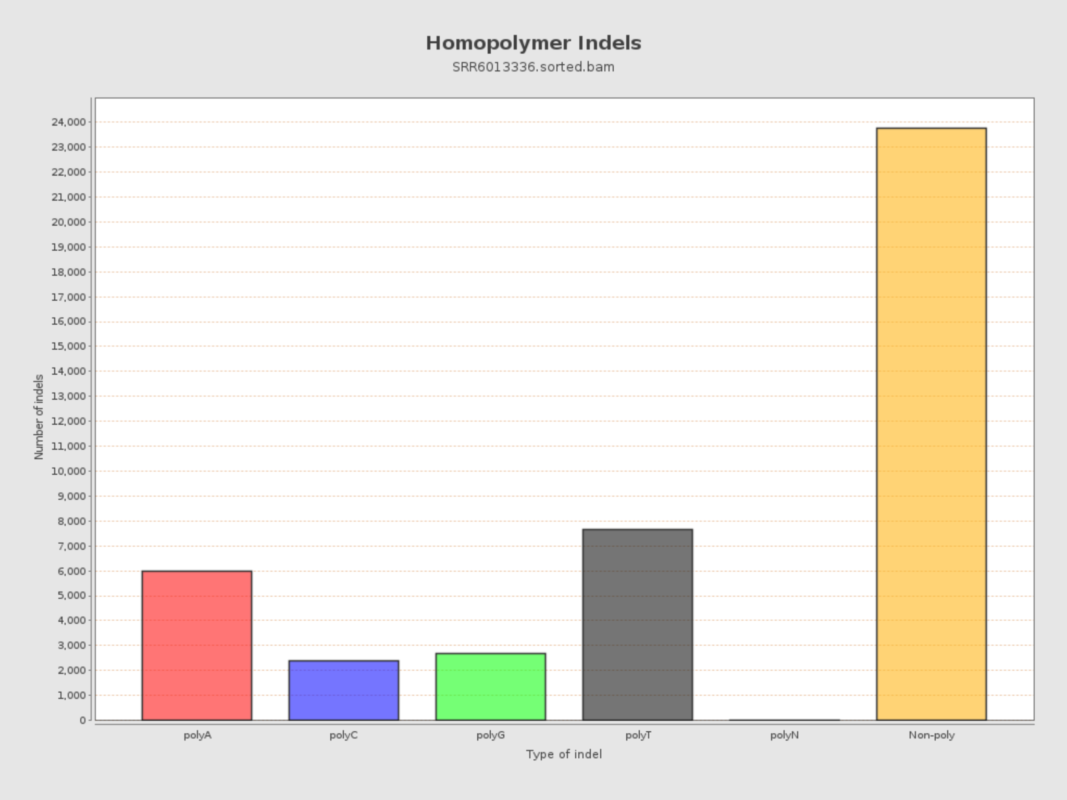
9. Results : Mapped Reads GC-content Distribution



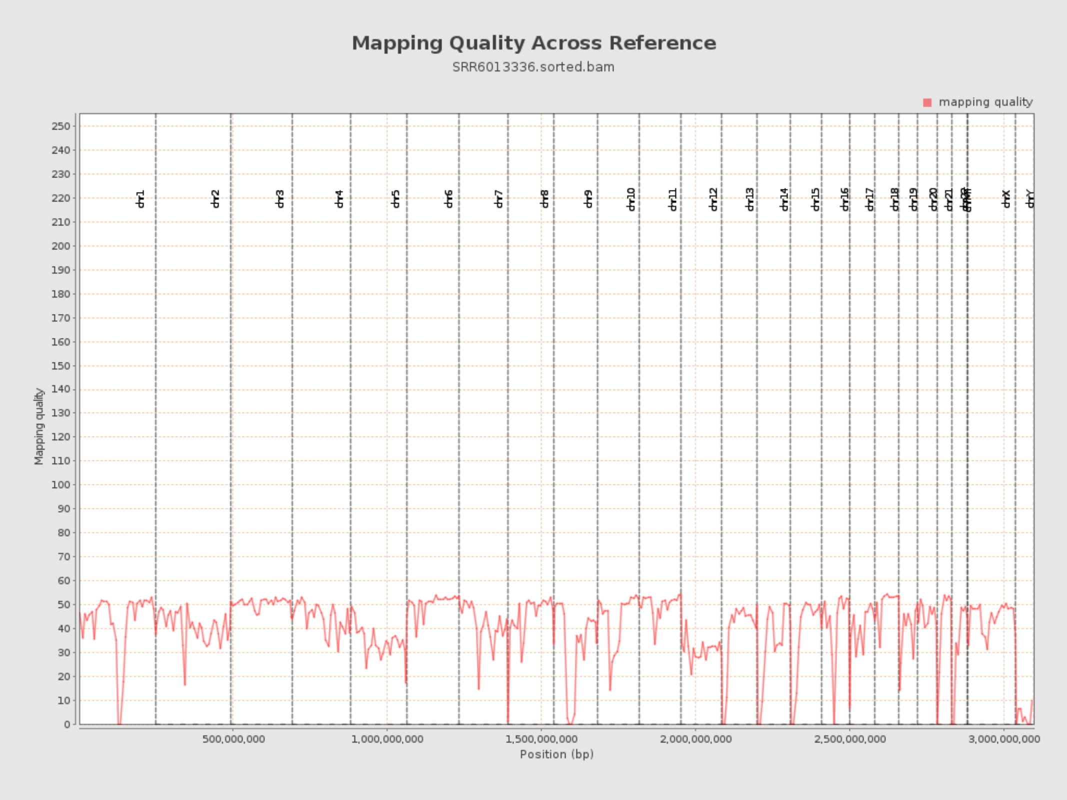
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram