Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:55:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013332.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_SRR6013332 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013332.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:55:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013332.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,818,379
Mapped reads	1,314,242 / 72.28%
Unmapped reads	504,137 / 27.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,355 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	86,928 / 4.78%
Duplication rate	5.66%
Clipped reads	969,126 / 53.3%

2.2. ACGT Content

Number/percentage of A's	20,754,921 / 26.78%
Number/percentage of C's	12,519,147 / 16.15%
Number/percentage of T's	25,213,162 / 32.53%
Number/percentage of G's	19,009,126 / 24.52%
Number/percentage of N's	14,301 / 0.02%
GC Percentage	40.68%

2.3. Coverage

Mean	0.025

Standard Deviation	0.2082

2.4. Mapping Quality

Mean Mapping Quality	45.61

2.5. Mismatches and indels

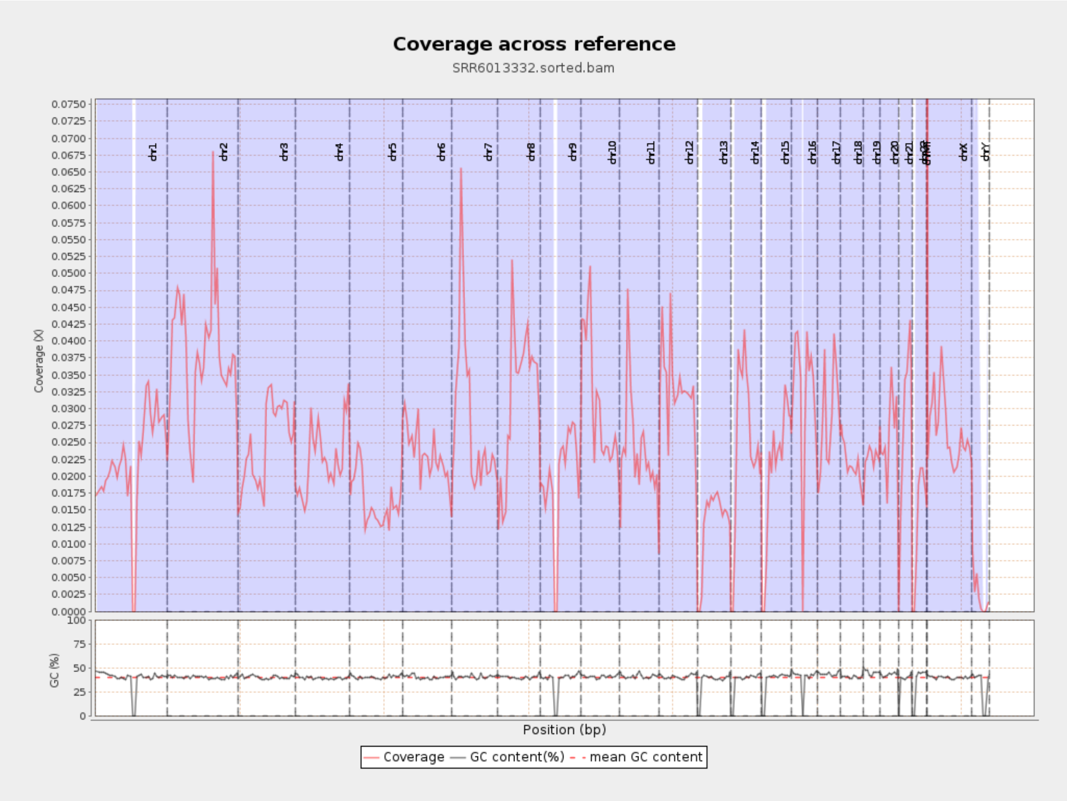
General error rate	0.95%
Mismatches	728,758
Insertions	4,627
Mapped reads with at least one insertion	0.35%
Deletions	19,850
Mapped reads with at least one deletion	1.5%
Homopolymer indels	48.35%

2.6. Chromosome stats

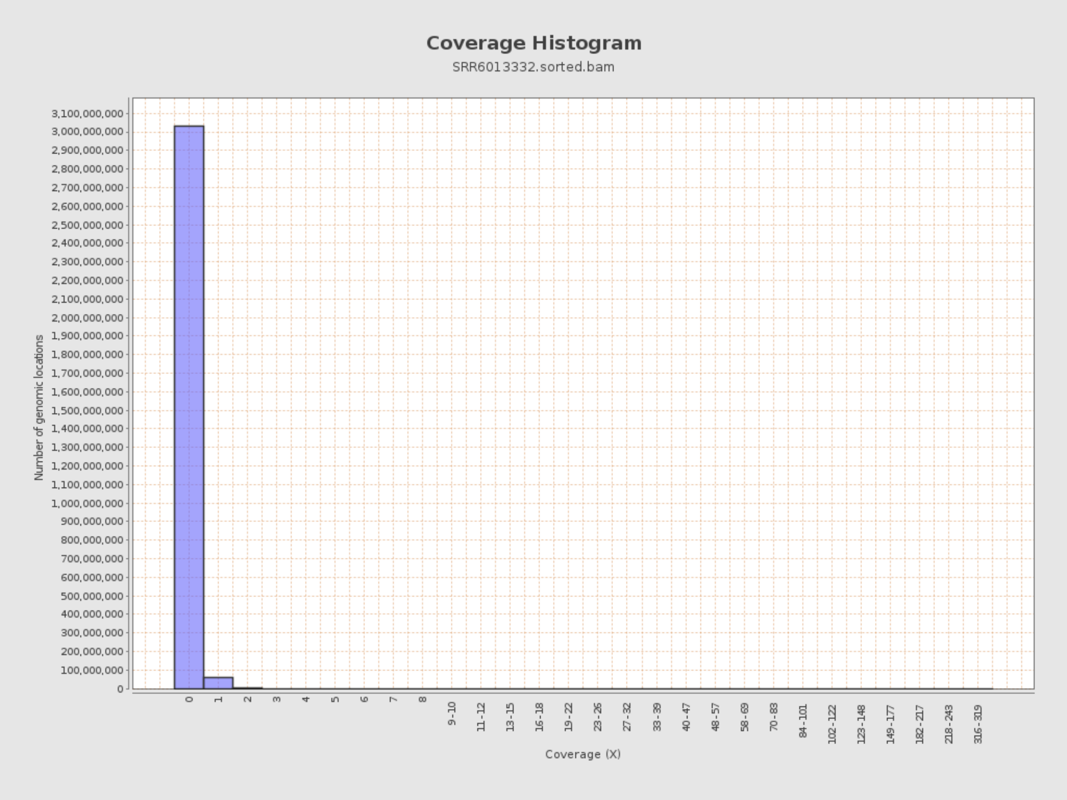
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5552438	0.0223	0.2308
chr2	243199373	9358727	0.0385	0.2758
chr3	198022430	4913357	0.0248	0.1806
chr4	191154276	4323369	0.0226	0.178
chr5	180915260	2967729	0.0164	0.1499
chr6	171115067	4001765	0.0234	0.1979
chr7	159138663	4557829	0.0286	0.2959

chr8	146364022	4713795	0.0322	0.2501
chr9	141213431	2760917	0.0196	0.1814
chr10	135534747	4169781	0.0308	0.214
chr11	135006516	3252919	0.0241	0.192
chr12	133851895	4428756	0.0331	0.2081
chr13	115169878	1492080	0.013	0.1291
chr14	107349540	2667181	0.0248	0.1827
chr15	102531392	2127434	0.0207	0.1723
chr16	90354753	2854819	0.0316	0.2085
chr17	81195210	2334669	0.0288	0.204
chr18	78077248	1706668	0.0219	0.2422
chr19	59128983	1347815	0.0228	0.2029
chr20	63025520	1640003	0.026	0.1894
chr21	48129895	1349515	0.028	0.1959
chr22	51304566	698653	0.0136	0.1323
chrMT	16571	21141	1.2758	1.7292
chrX	155270560	4160209	0.0268	0.1983
chrY	59373566	141169	0.0024	0.0569

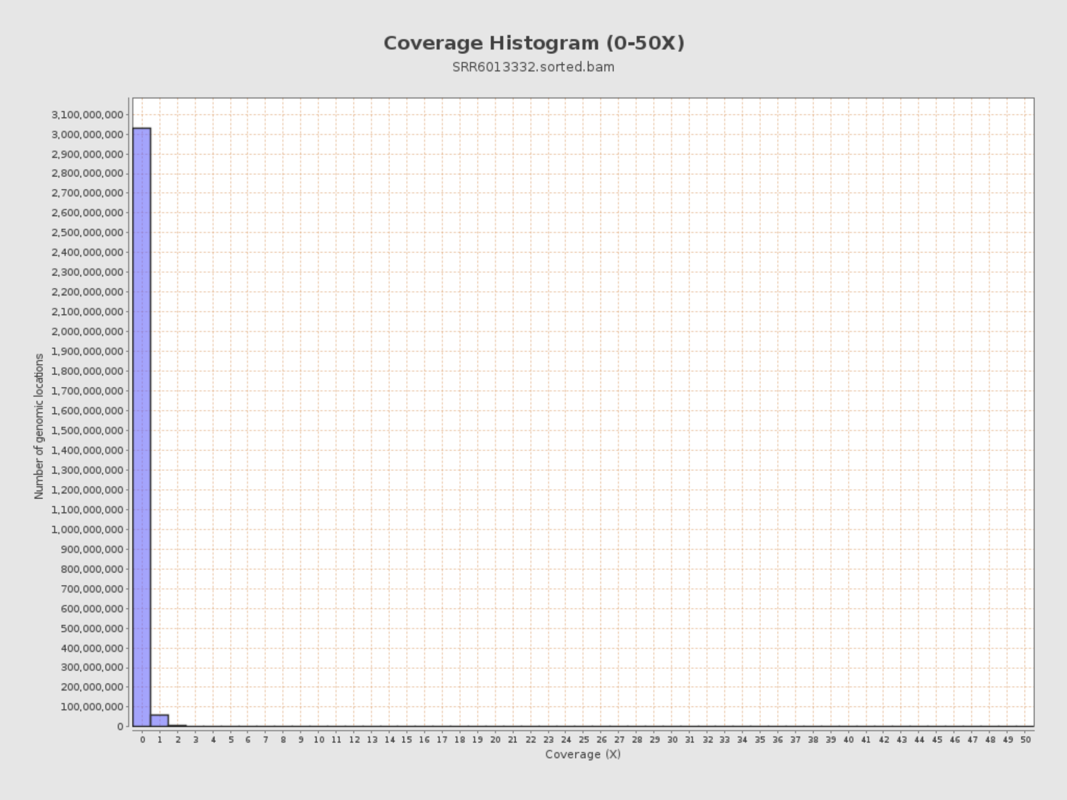
3. Results : Coverage across reference



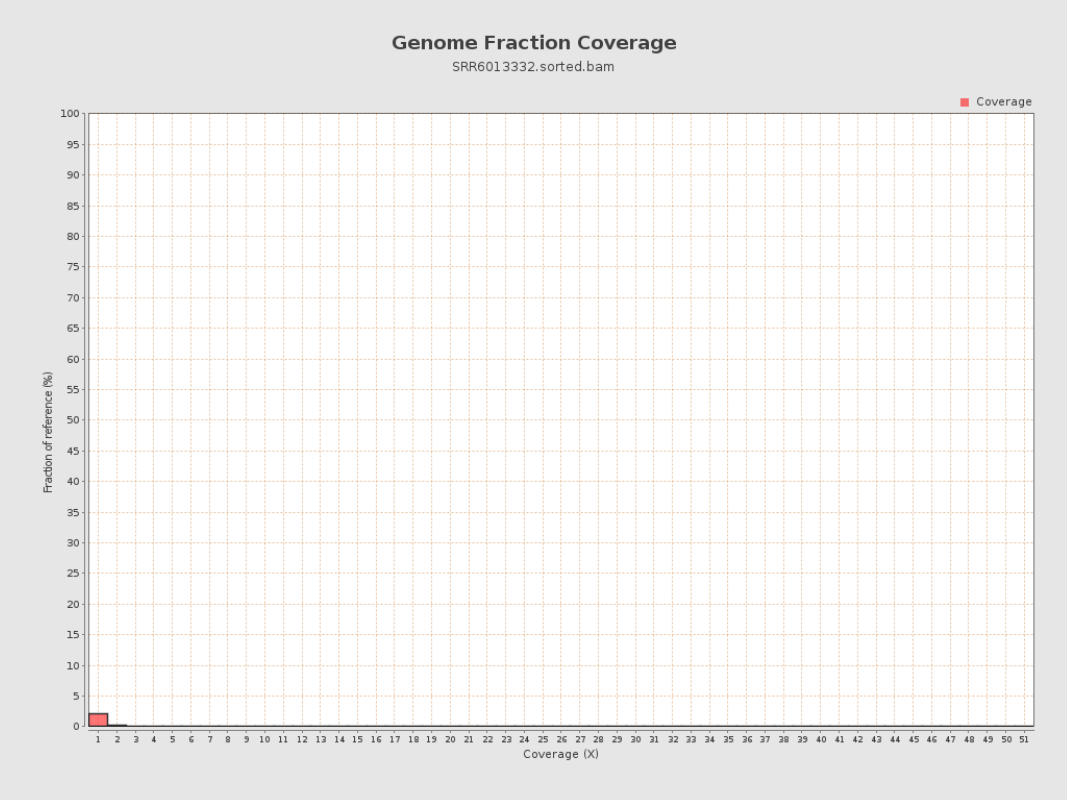
4. Results : Coverage Histogram



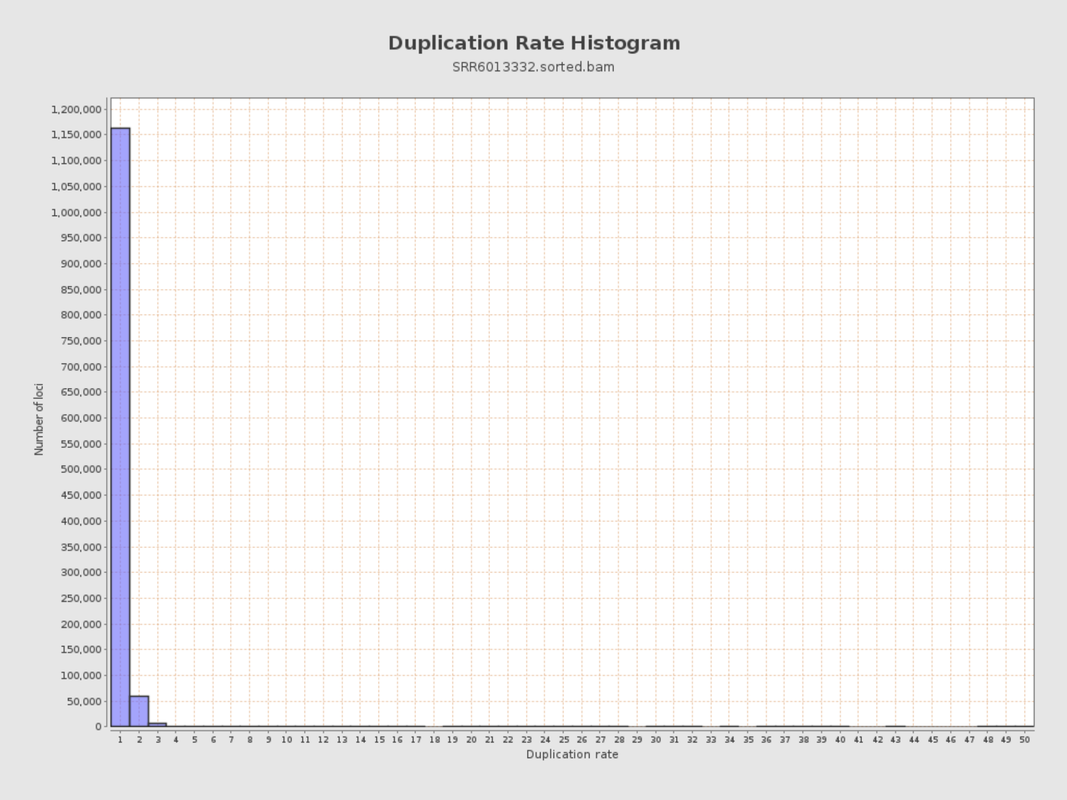
5. Results : Coverage Histogram (0-50X)



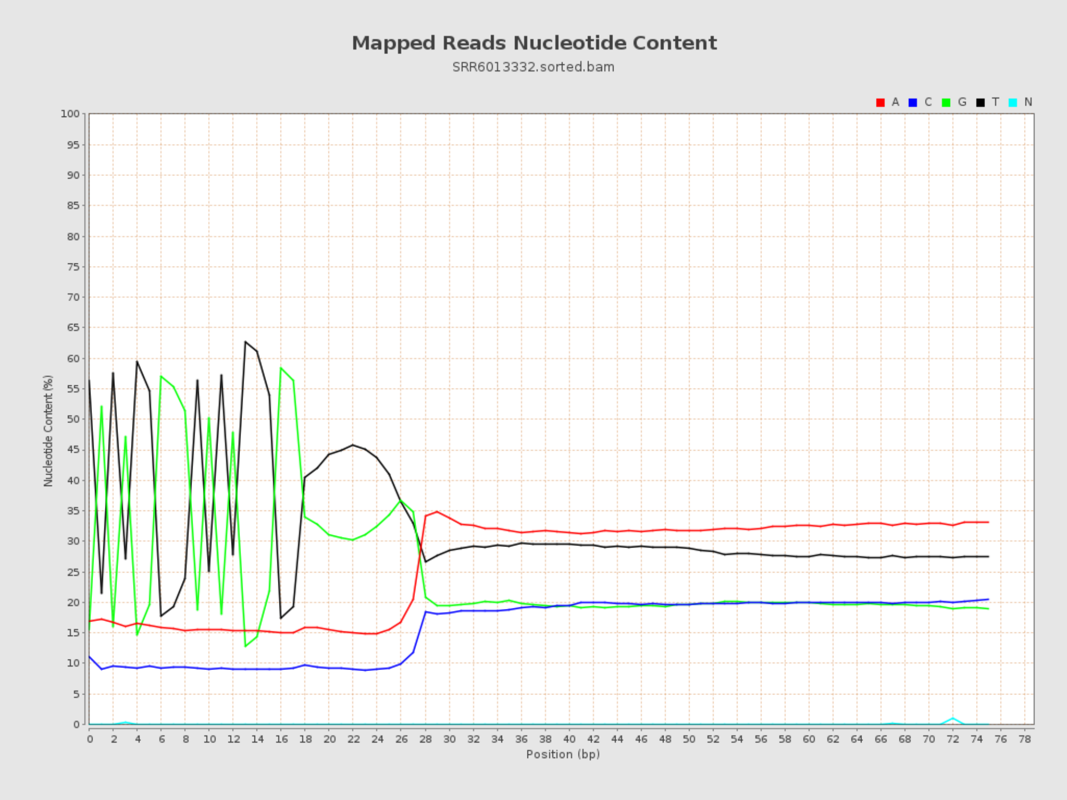
6. Results : Genome Fraction Coverage



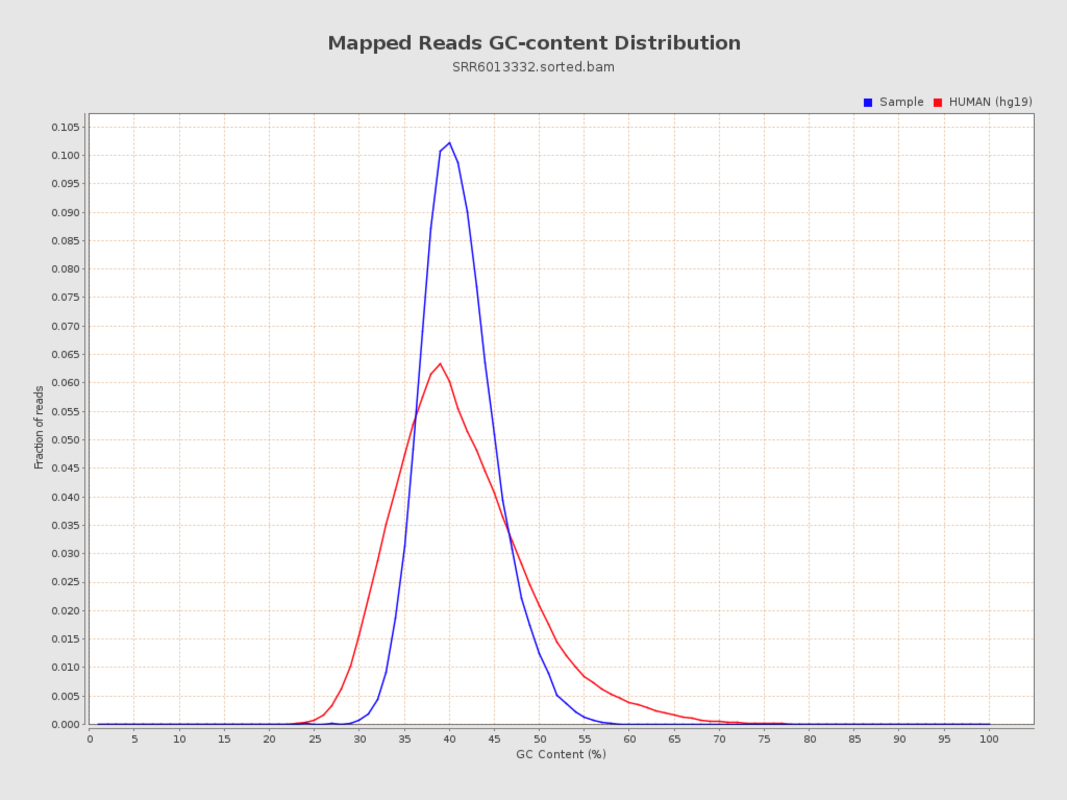
7. Results : Duplication Rate Histogram



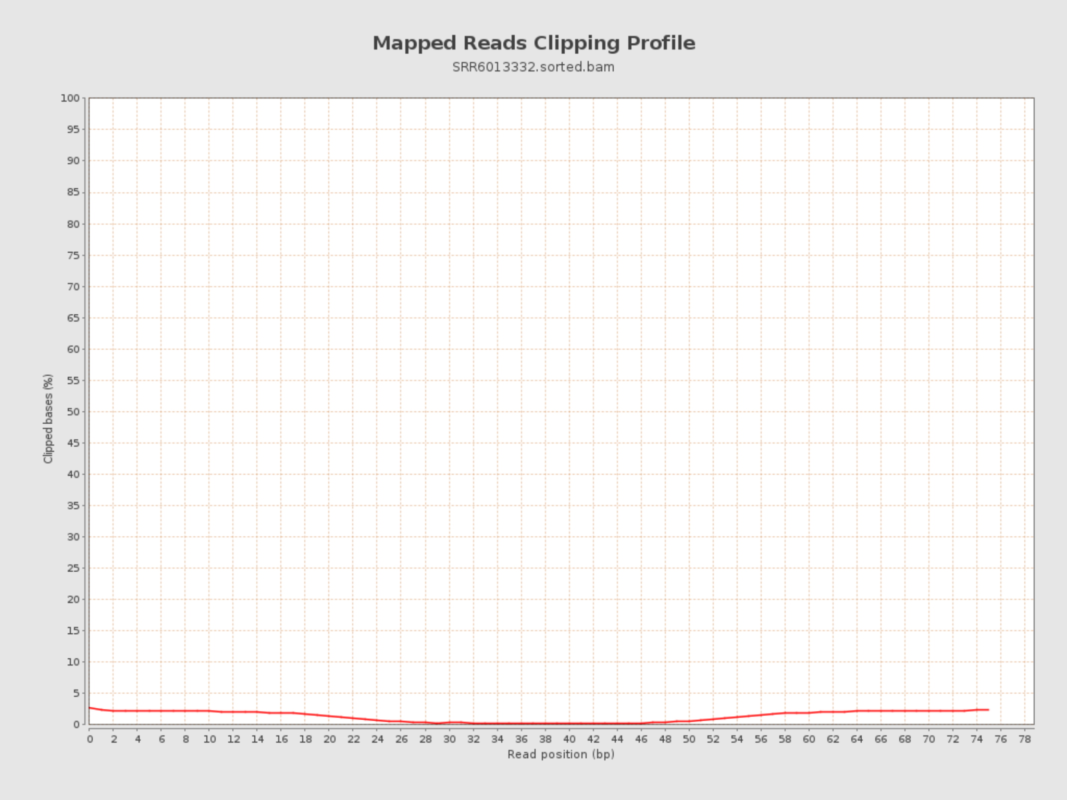
8. Results : Mapped Reads Nucleotide Content



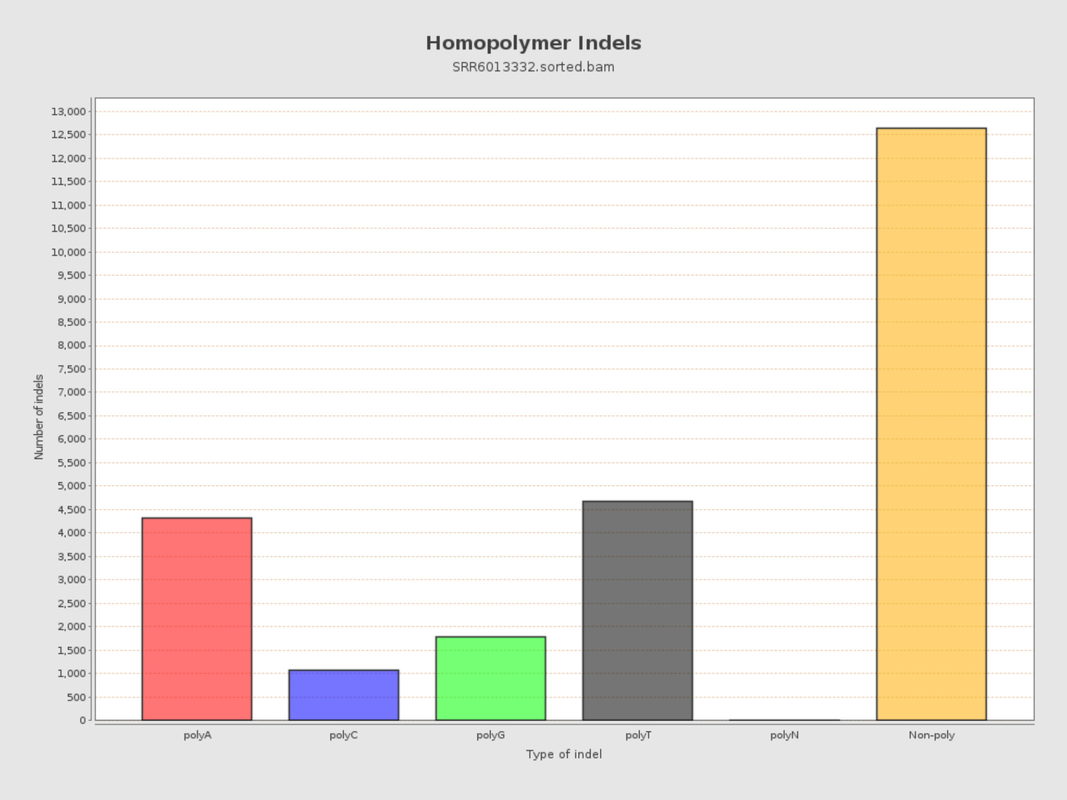
9. Results : Mapped Reads GC-content Distribution



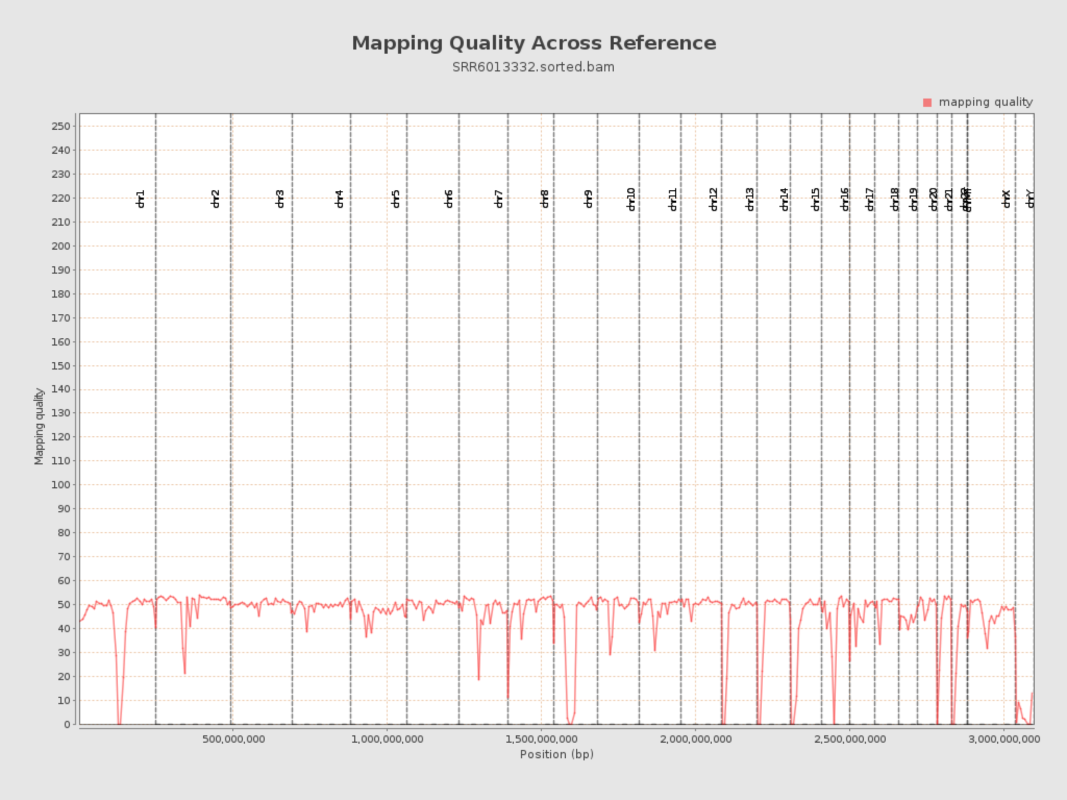
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram