Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 19:30:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6003992.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_SRR6003992 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6003992.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 19:30:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6003992.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,173,147
Mapped reads	2,247,197 / 70.82%
Unmapped reads	925,950 / 29.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,653 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	82,282 / 2.59%
Duplication rate	2.58%
Clipped reads	1,135,491 / 35.78%

2.2. ACGT Content

Number/percentage of A's	41,414,499 / 28.05%
Number/percentage of C's	25,583,548 / 17.33%
Number/percentage of T's	47,700,164 / 32.3%
Number/percentage of G's	32,947,148 / 22.31%
Number/percentage of N's	14,456 / 0.01%
GC Percentage	39.64%

2.3. Coverage

Mean	0.0477

Standard Deviation	0.4498

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Mismatches and indels

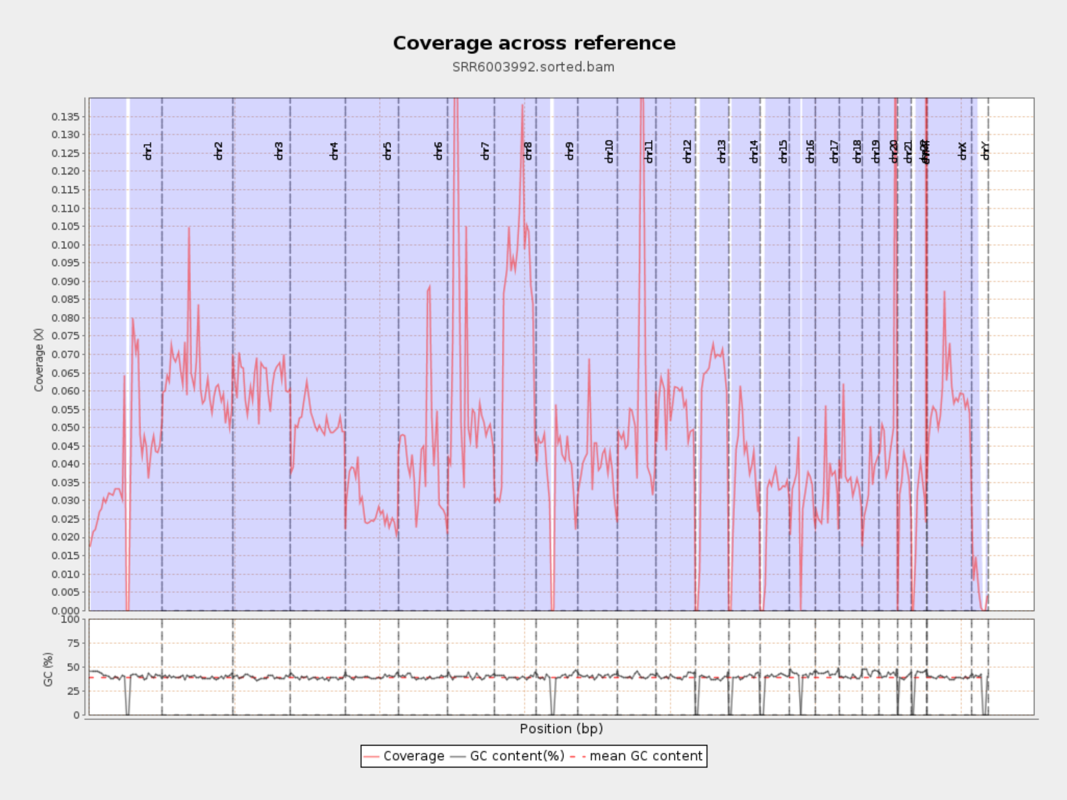
General error rate	1.09%
Mismatches	1,591,307
Insertions	13,940
Mapped reads with at least one insertion	0.61%
Deletions	38,020
Mapped reads with at least one deletion	1.67%
Homopolymer indels	46.32%

2.6. Chromosome stats

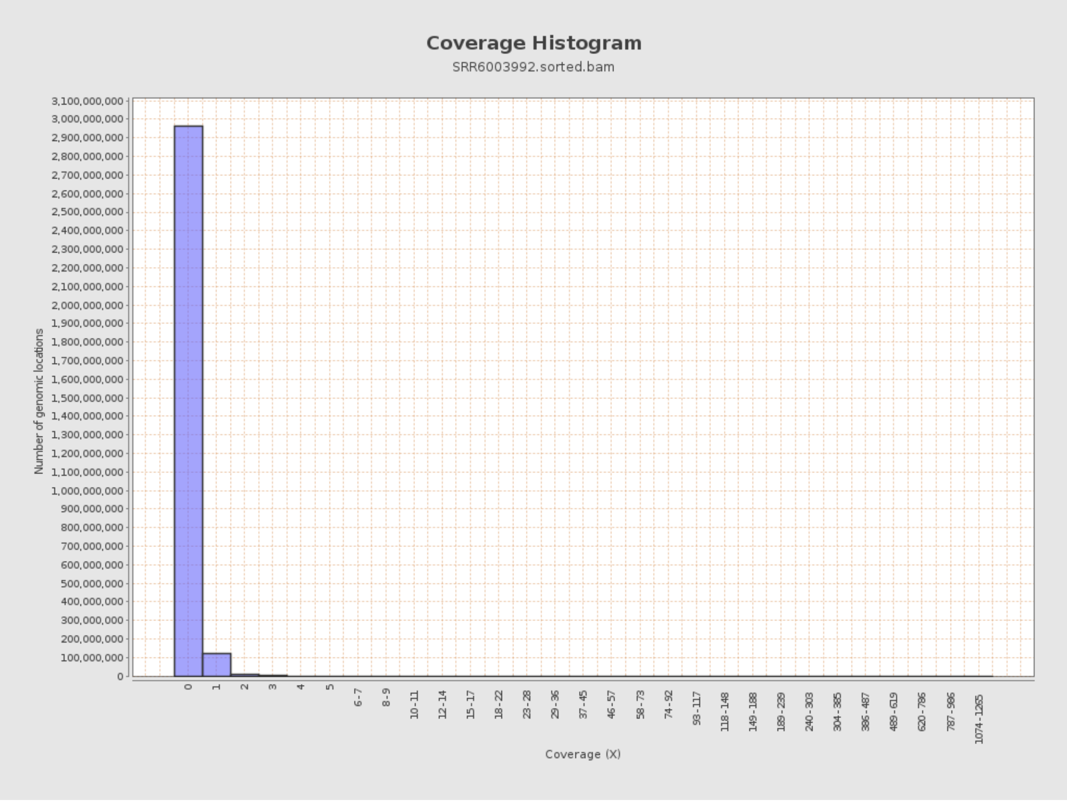
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9352516	0.0375	0.6652
chr2	243199373	15445808	0.0635	0.523
chr3	198022430	12439616	0.0628	0.2743
chr4	191154276	9691625	0.0507	0.2479
chr5	180915260	5143738	0.0284	0.191
chr6	171115067	7321605	0.0428	0.2529
chr7	159138663	10319001	0.0648	0.7732

chr8	146364022	12065811	0.0824	0.8285
chr9	141213431	5283658	0.0374	0.4244
chr10	135534747	5543253	0.0409	0.3783
chr11	135006516	7971136	0.059	0.4379
chr12	133851895	7394735	0.0552	0.2655
chr13	115169878	6389550	0.0555	0.2542
chr14	107349540	3904405	0.0364	0.2792
chr15	102531392	2839423	0.0277	0.1925
chr16	90354753	2807163	0.0311	0.2612
chr17	81195210	2676144	0.033	0.238
chr18	78077248	2925843	0.0375	0.888
chr19	59128983	2091491	0.0354	0.4185
chr20	63025520	3960589	0.0628	0.2973
chr21	48129895	1559625	0.0324	0.2321
chr22	51304566	1227376	0.0239	0.1645
chrMT	16571	77053	4.6499	3.3973
chrX	155270560	8948670	0.0576	0.318
chrY	59373566	342356	0.0058	0.1037

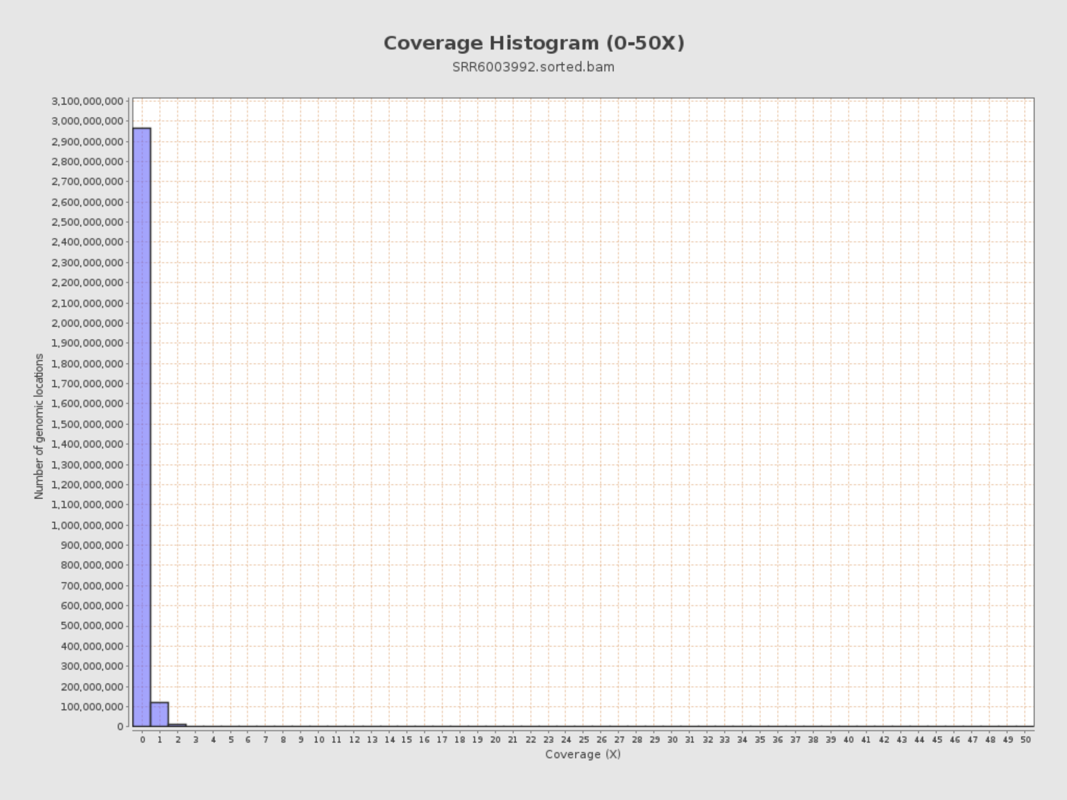
3. Results : Coverage across reference



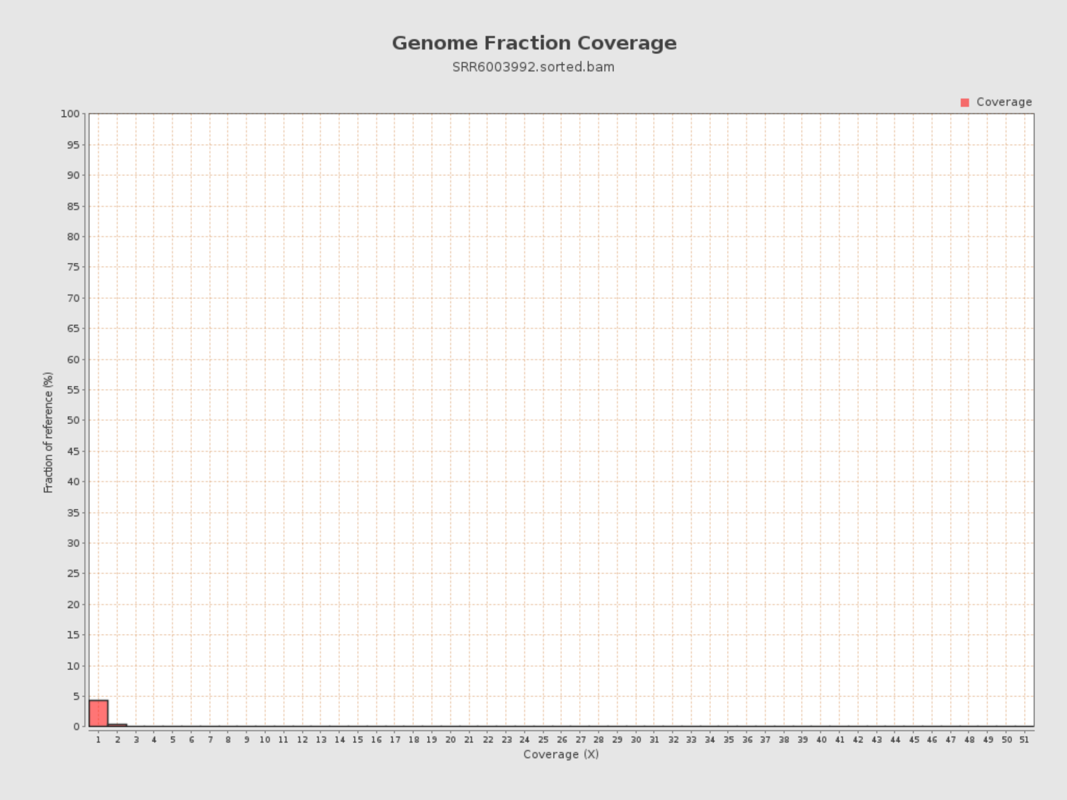
4. Results : Coverage Histogram



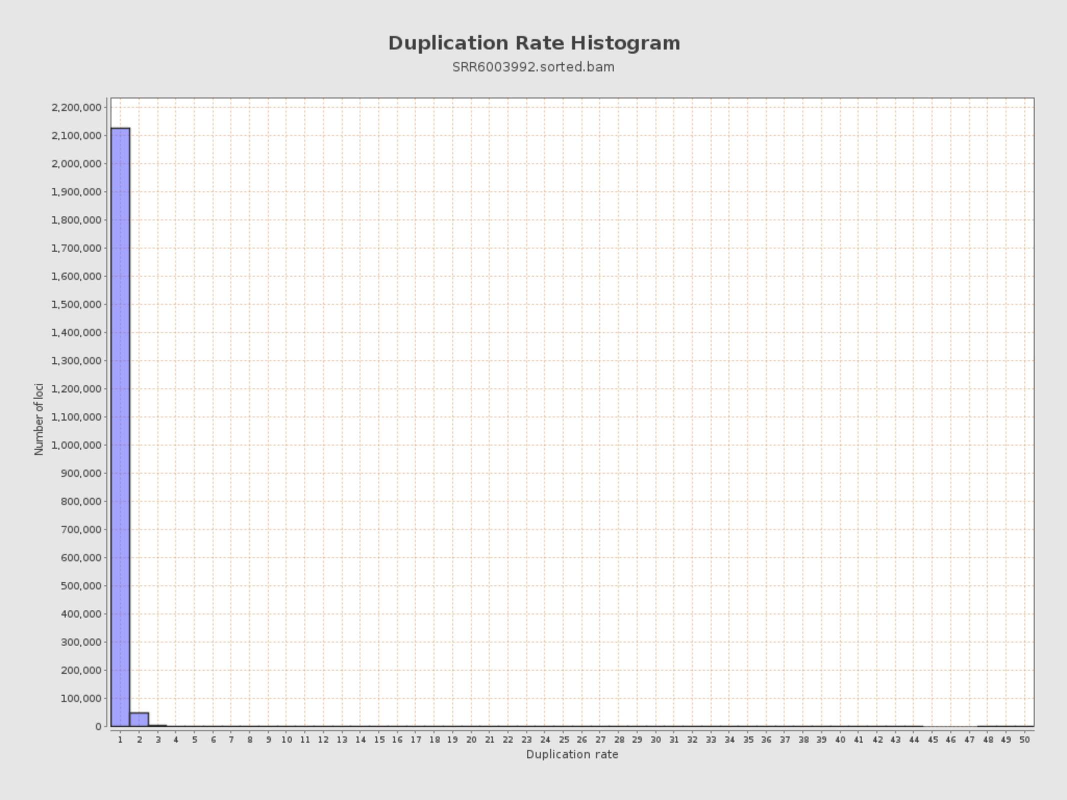
5. Results : Coverage Histogram (0-50X)



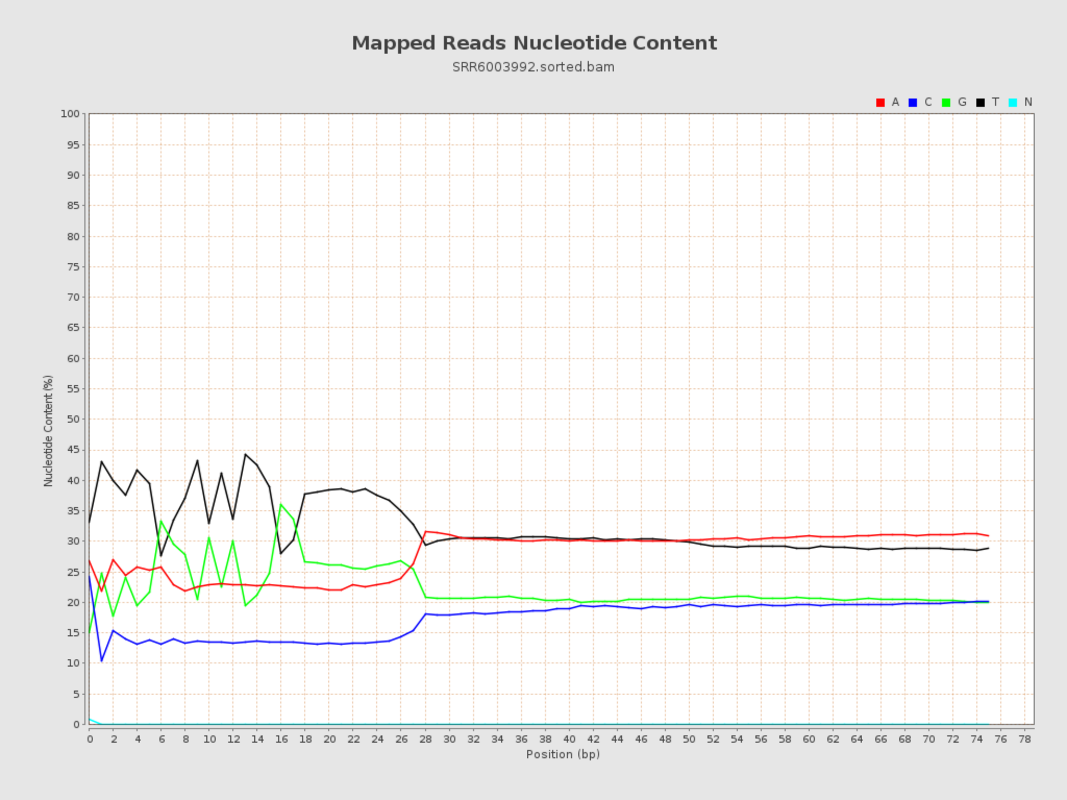
6. Results : Genome Fraction Coverage



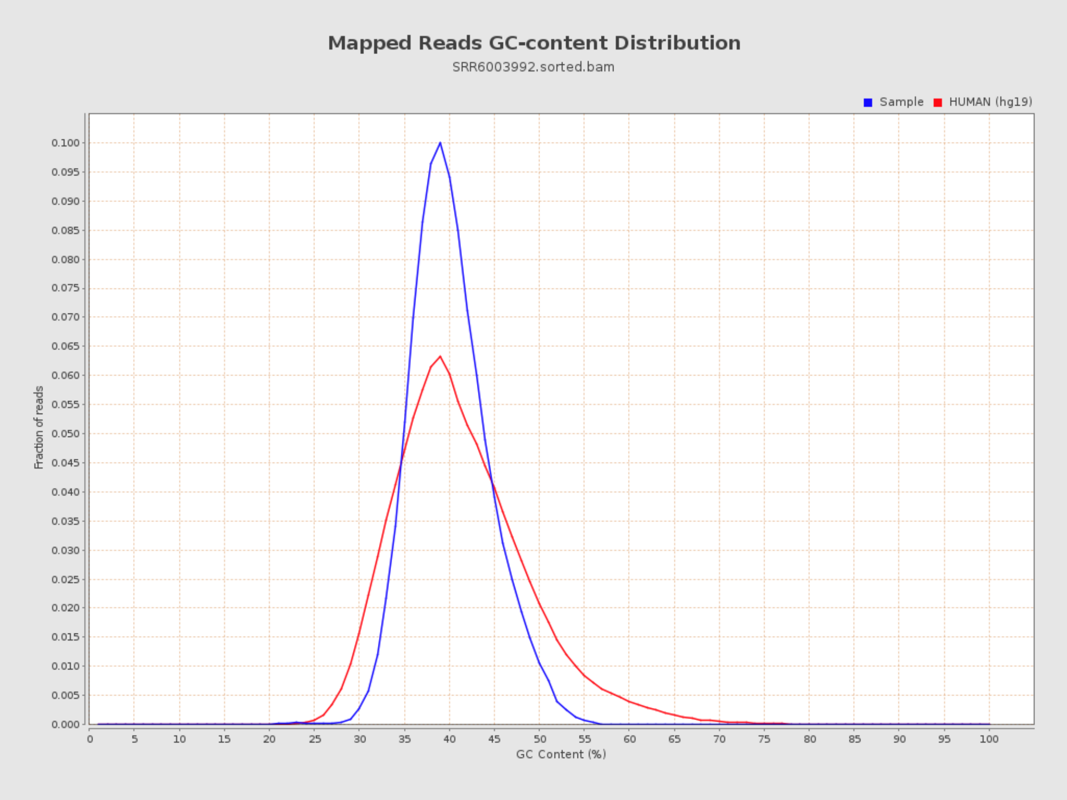
7. Results : Duplication Rate Histogram



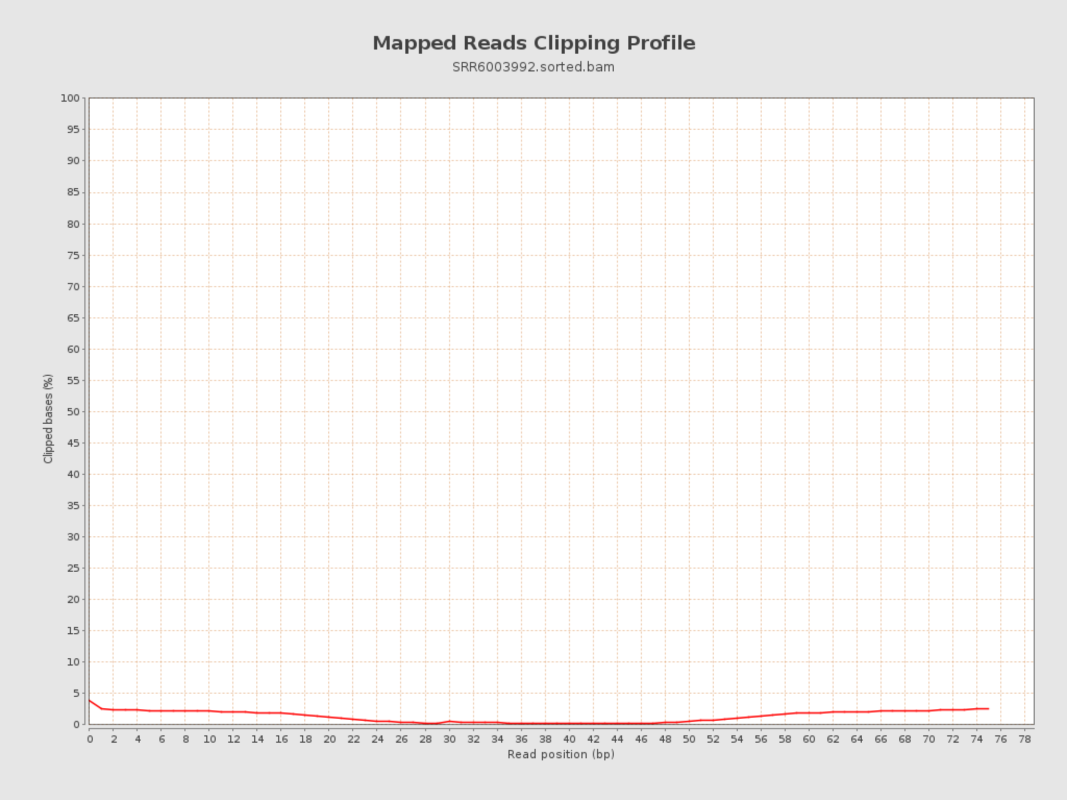
8. Results : Mapped Reads Nucleotide Content



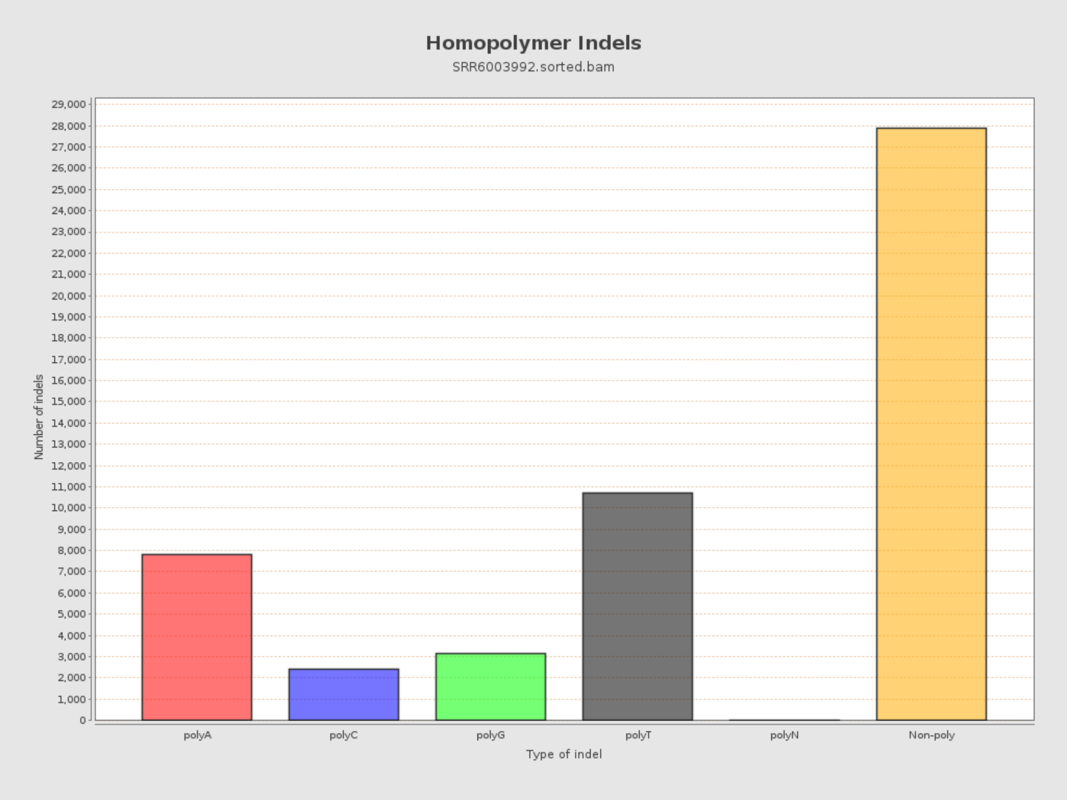
9. Results : Mapped Reads GC-content Distribution



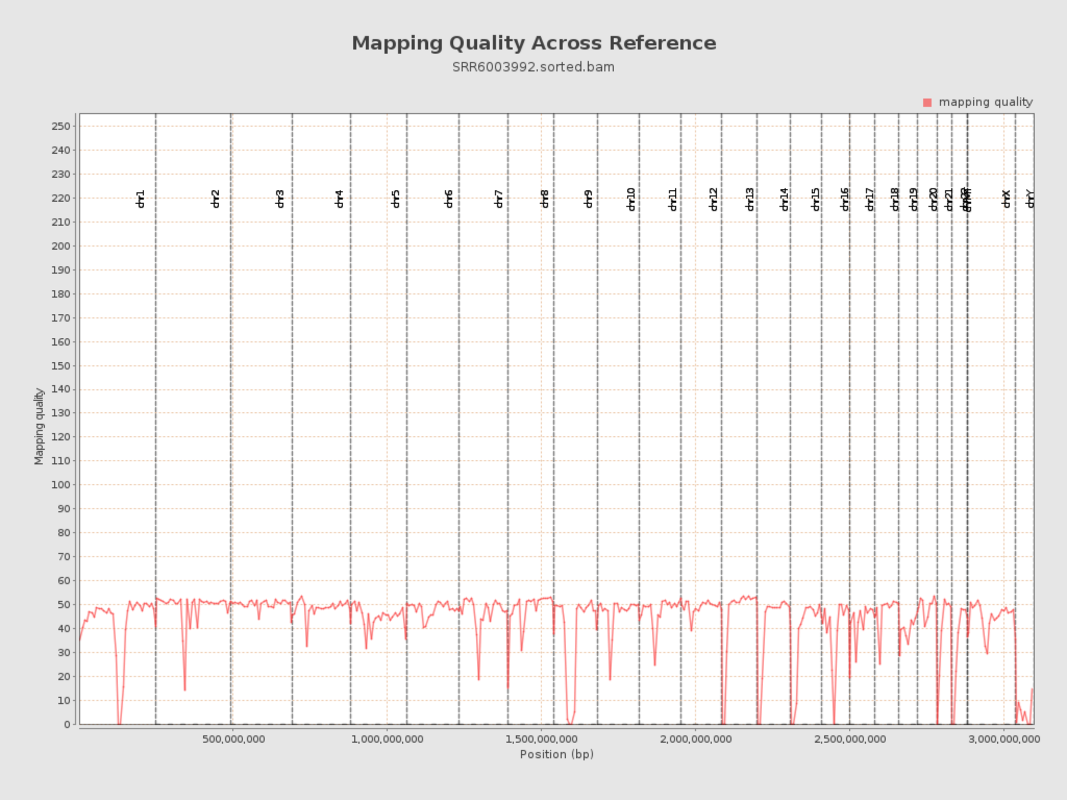
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram