Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:58:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751233.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_SRR8751233 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751233.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:58:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751233.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,585,809
Mapped reads	9,540,115 / 99.52%
Unmapped reads	45,694 / 0.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	64,728 / 0.68%
Read min/max/mean length	30 / 151 / 151.32
Duplicated reads (estimated)	1,762,979 / 18.39%
Duplication rate	16.7%
Clipped reads	5,626,181 / 58.69%

2.2. ACGT Content

Number/percentage of A's	373,598,496 / 30.16%
Number/percentage of C's	248,521,855 / 20.06%
Number/percentage of T's	376,123,405 / 30.36%
Number/percentage of G's	240,452,995 / 19.41%
Number/percentage of N's	37,572 / 0%
GC Percentage	39.47%

2.3. Coverage

Mean	0.4003

Standard Deviation	2.2541

2.4. Mapping Quality

Mean Mapping Quality	51.57

2.5. Mismatches and indels

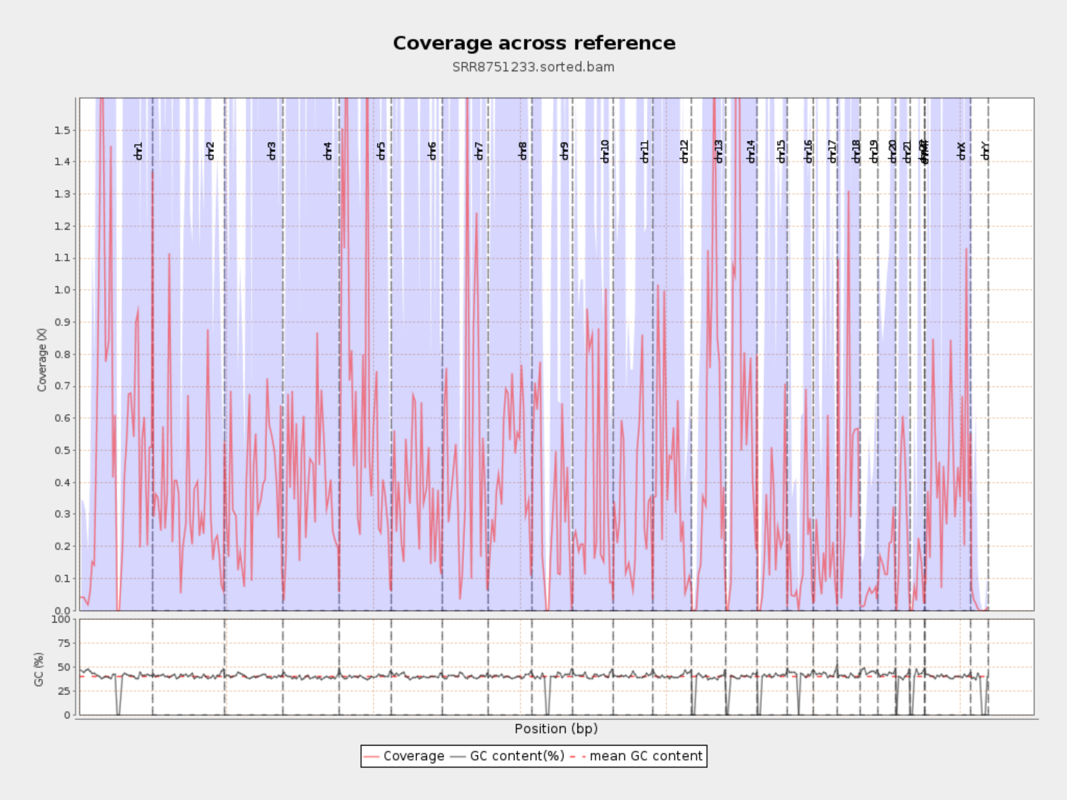
General error rate	1.59%
Mismatches	19,511,503
Insertions	136,918
Mapped reads with at least one insertion	1.41%
Deletions	226,580
Mapped reads with at least one deletion	2.3%
Homopolymer indels	40.93%

2.6. Chromosome stats

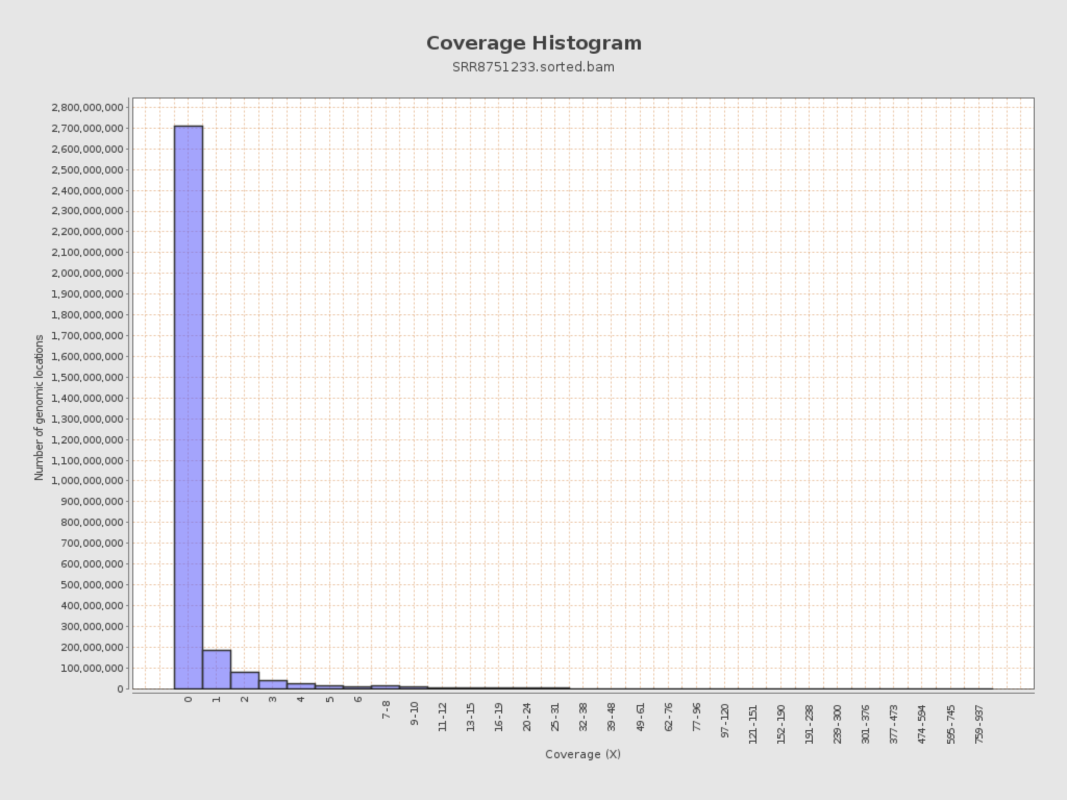
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	135423670	0.5433	2.2706
chr2	243199373	82150805	0.3378	1.9421
chr3	198022430	75242383	0.38	1.8928
chr4	191154276	78626576	0.4113	2.0769
chr5	180915260	117564852	0.6498	4.2464
chr6	171115067	62166495	0.3633	1.7857
chr7	159138663	80388649	0.5051	2.787

chr8	146364022	68049502	0.4649	1.9544
chr9	141213431	44548529	0.3155	1.7276
chr10	135534747	52772736	0.3894	2.7921
chr11	135006516	43737442	0.324	1.6186
chr12	133851895	55535437	0.4149	1.9812
chr13	115169878	61150180	0.531	2.8452
chr14	107349540	84948492	0.7913	3.1187
chr15	102531392	25017130	0.244	1.5236
chr16	90354753	14354336	0.1589	0.9825
chr17	81195210	13638827	0.168	1.1681
chr18	78077248	40516140	0.5189	2.2623
chr19	59128983	2659061	0.045	0.3711
chr20	63025520	10713185	0.17	1.3011
chr21	48129895	14665252	0.3047	1.8704
chr22	51304566	3946080	0.0769	0.784
chrMT	16571	1732	0.1045	0.3731
chrX	155270560	70382101	0.4533	2.2982
chrY	59373566	911633	0.0154	0.314

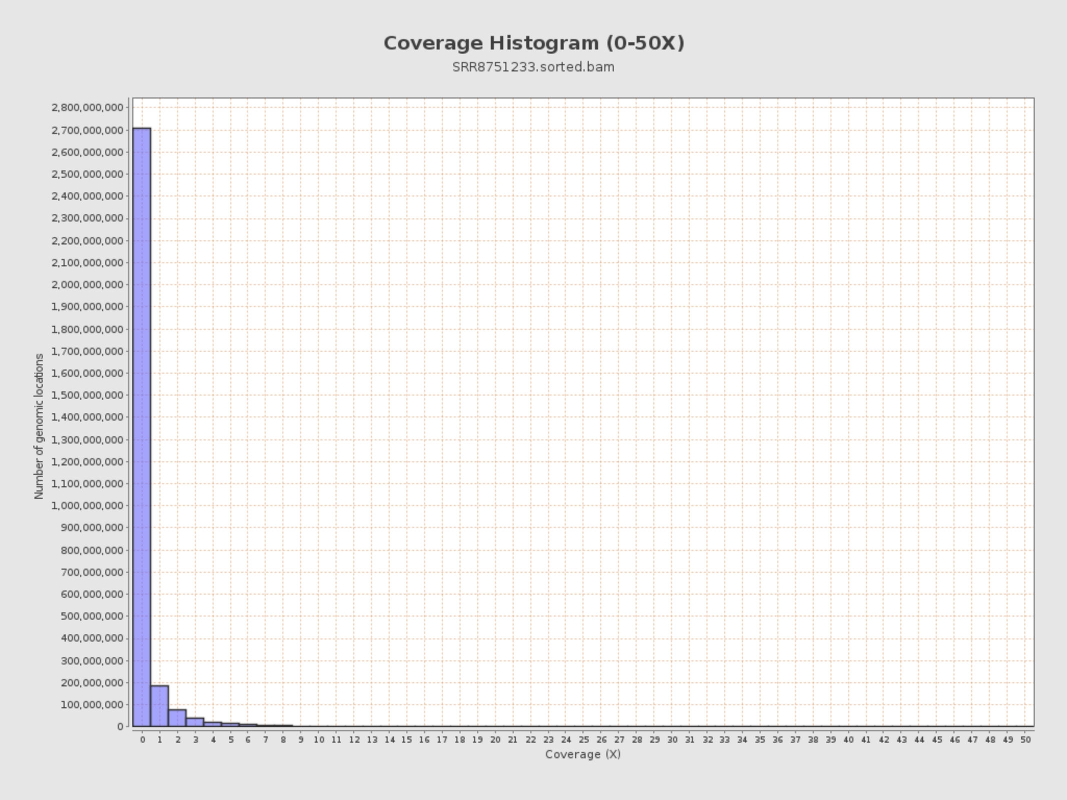
3. Results : Coverage across reference



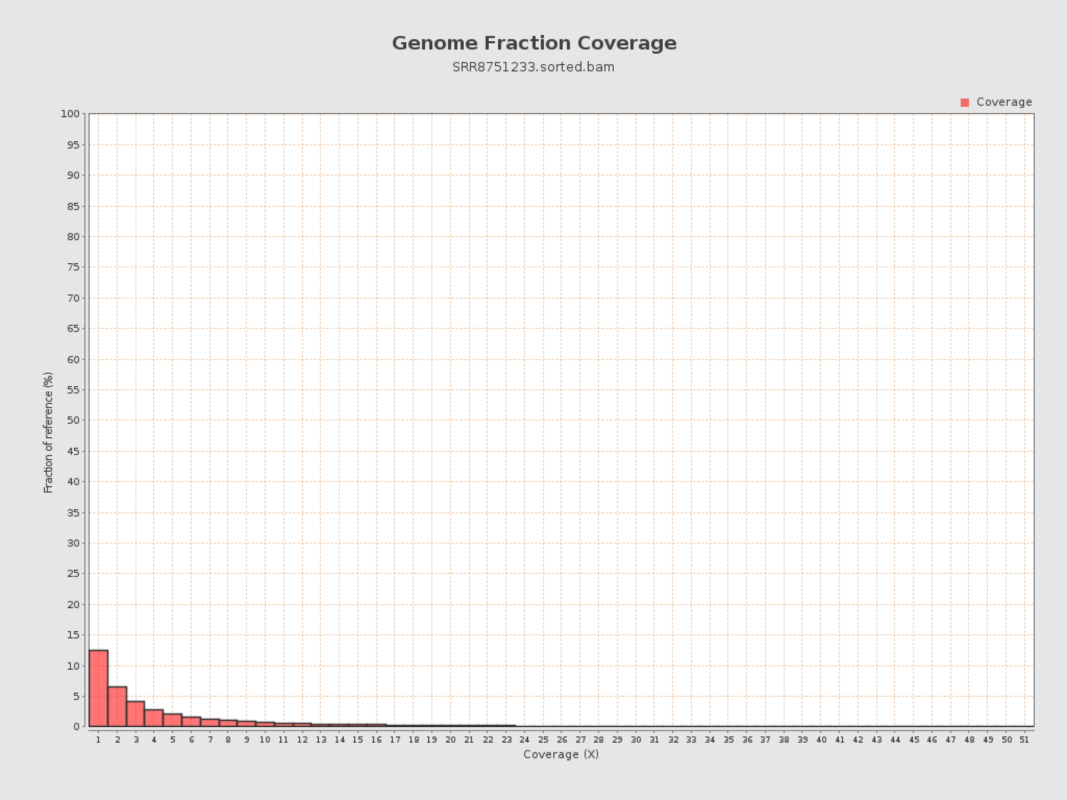
4. Results : Coverage Histogram



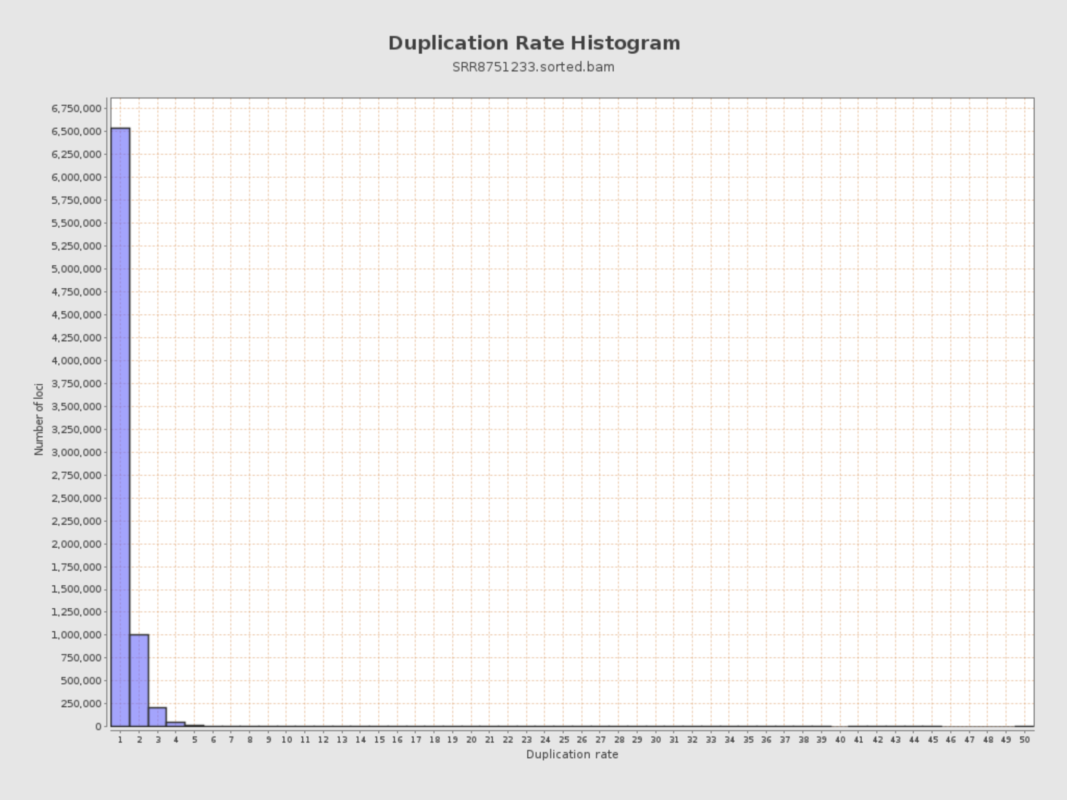
5. Results : Coverage Histogram (0-50X)



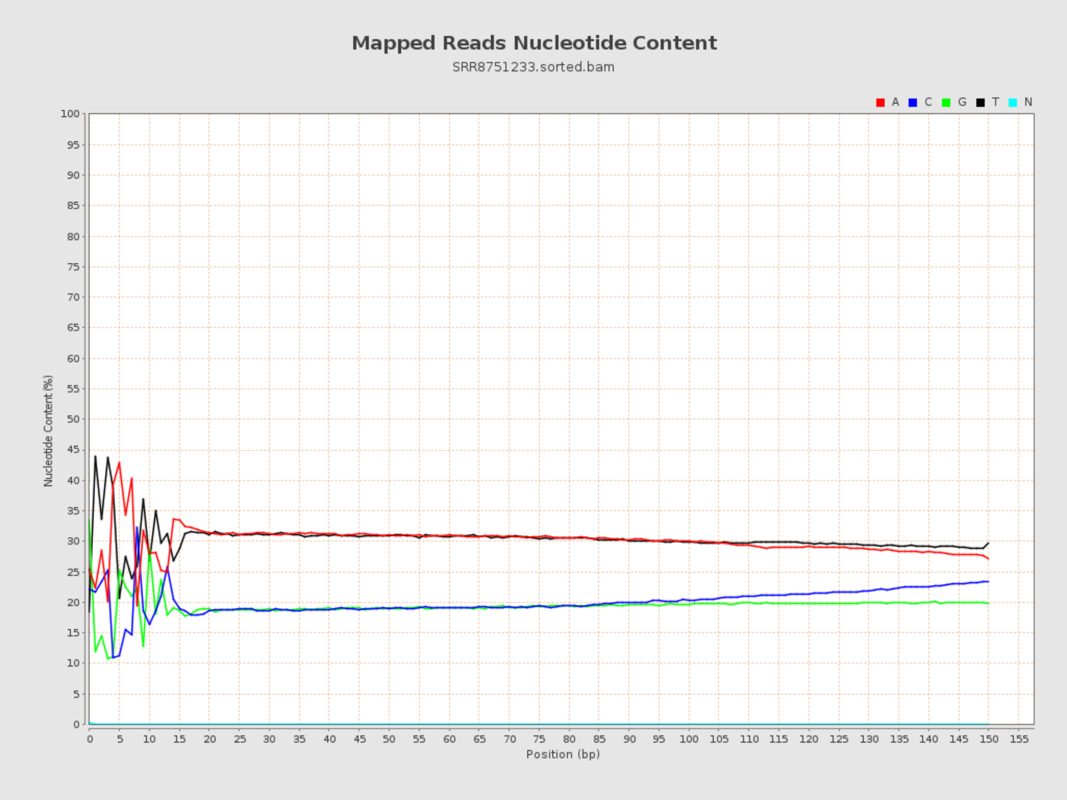
6. Results : Genome Fraction Coverage



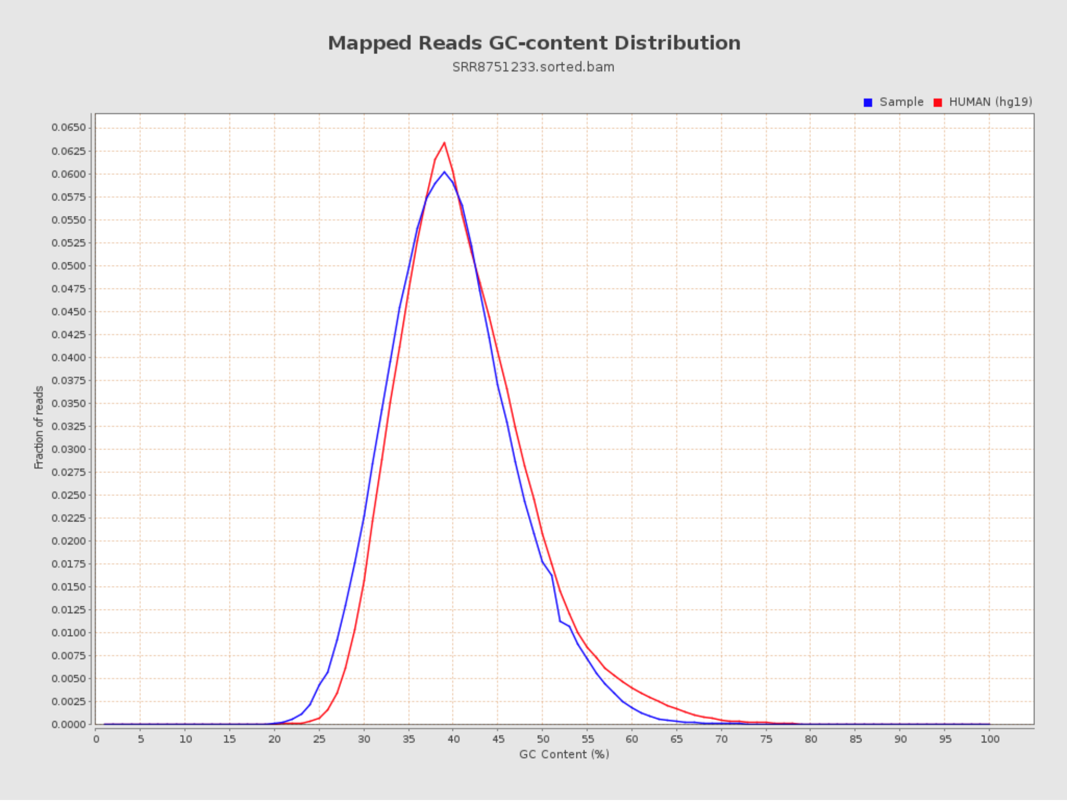
7. Results : Duplication Rate Histogram



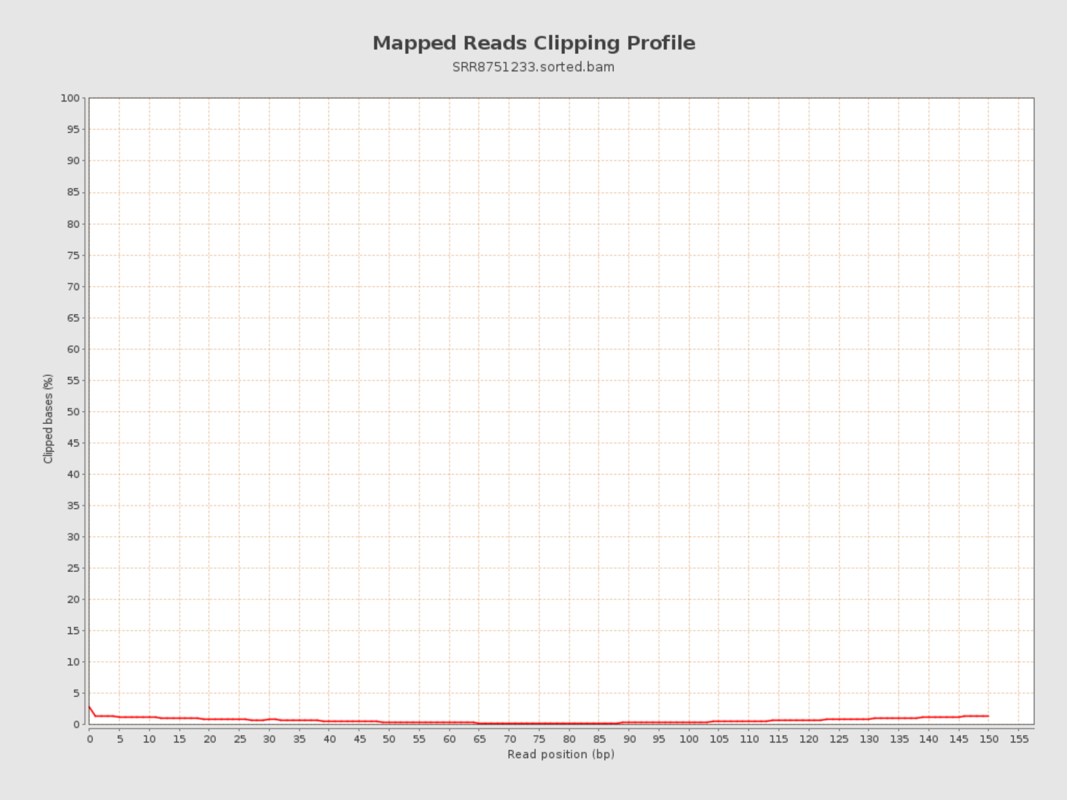
8. Results : Mapped Reads Nucleotide Content



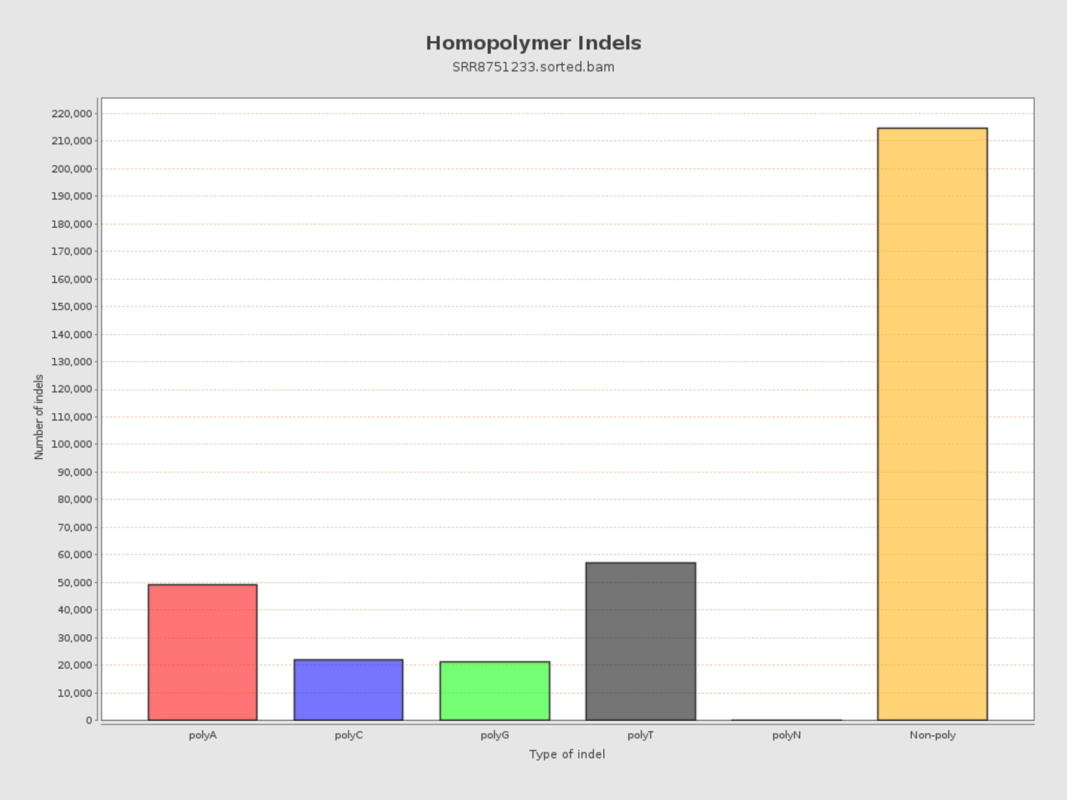
9. Results : Mapped Reads GC-content Distribution



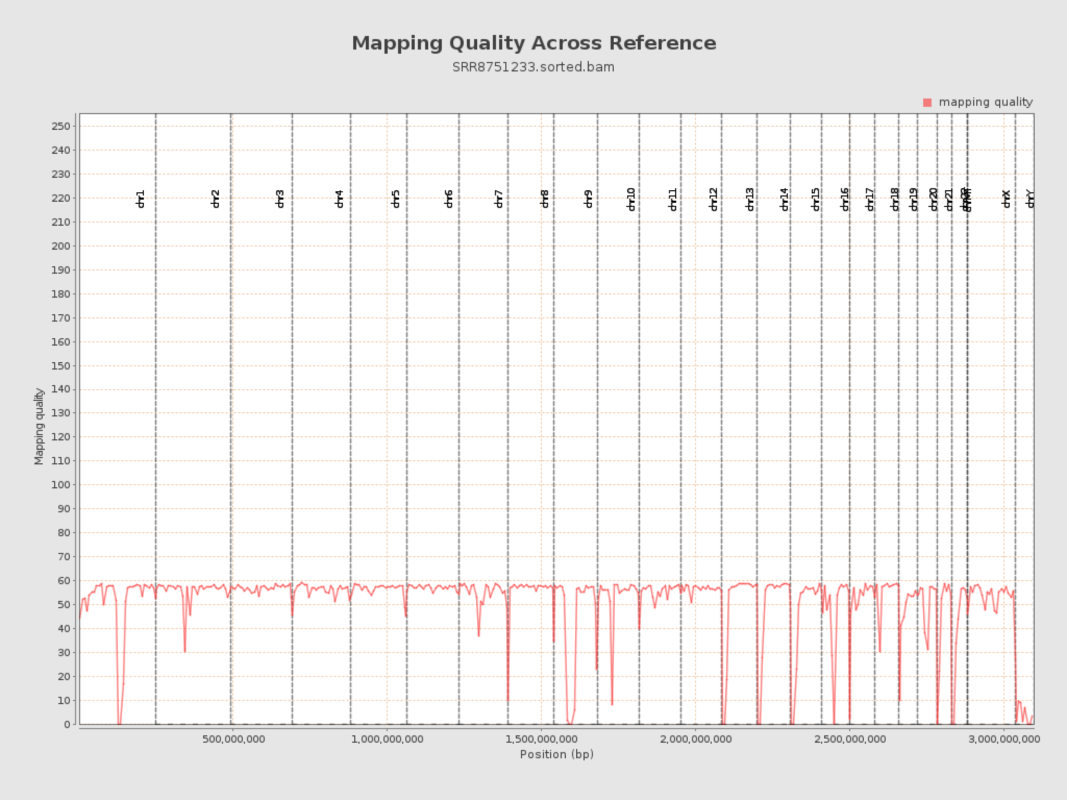
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram