Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:09:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751234.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_SRR8751234 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751234.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:09:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751234.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,720,145
Mapped reads	4,076,872 / 86.37%
Unmapped reads	643,273 / 13.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	150,713 / 3.19%
Read min/max/mean length	30 / 101 / 102.32
Duplicated reads (estimated)	112,435 / 2.38%
Duplication rate	1.51%
Clipped reads	811,439 / 17.19%

2.2. ACGT Content

Number/percentage of A's	117,194,217 / 29.3%
Number/percentage of C's	82,594,721 / 20.65%
Number/percentage of T's	117,885,329 / 29.47%
Number/percentage of G's	82,296,631 / 20.58%
Number/percentage of N's	2,176 / 0%
GC Percentage	41.23%

2.3. Coverage

Mean	0.1292

Standard Deviation	1.2102

2.4. Mapping Quality

Mean Mapping Quality	51.22

2.5. Mismatches and indels

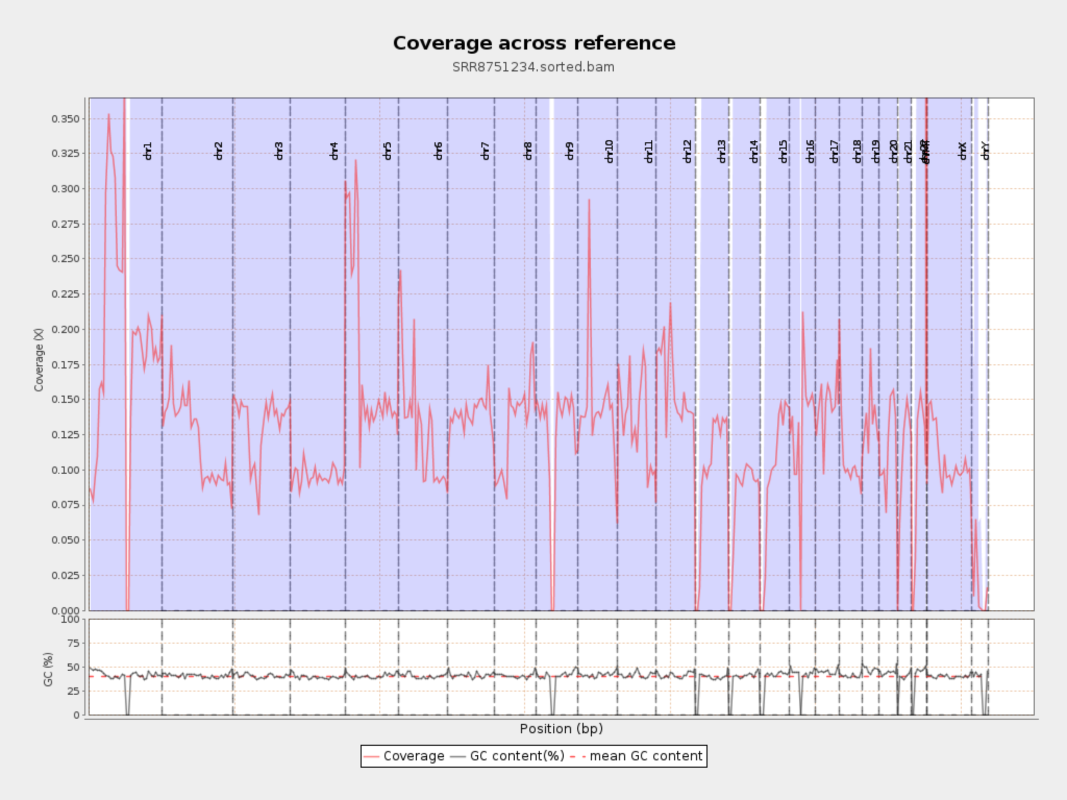
General error rate	0.43%
Mismatches	1,509,686
Insertions	156,060
Mapped reads with at least one insertion	3.72%
Deletions	56,914
Mapped reads with at least one deletion	1.37%
Homopolymer indels	51.35%

2.6. Chromosome stats

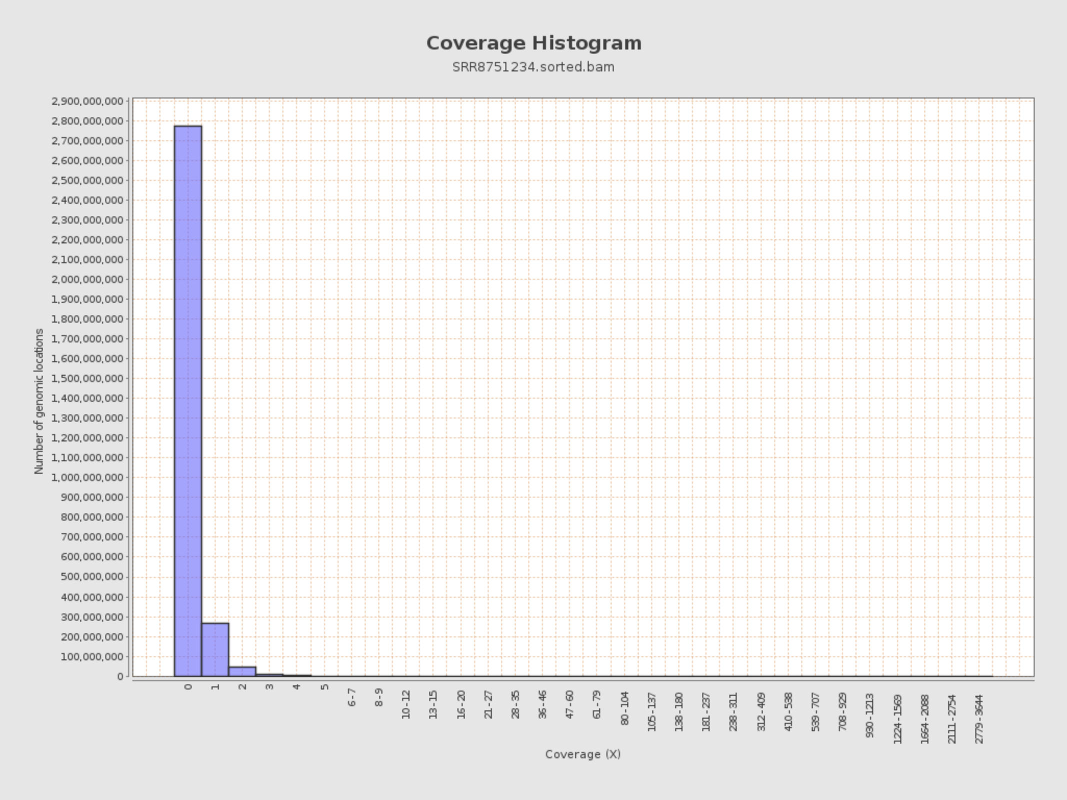
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	48048534	0.1928	3.4437
chr2	243199373	29521183	0.1214	0.5271
chr3	198022430	26135168	0.132	0.4467
chr4	191154276	18203779	0.0952	0.4271
chr5	180915260	31993586	0.1768	0.485
chr6	171115067	22419860	0.131	0.8319
chr7	159138663	22366374	0.1405	0.7118

chr8	146364022	19414087	0.1326	0.4865
chr9	141213431	17436500	0.1235	0.6355
chr10	135534747	19728554	0.1456	1.6041
chr11	135006516	18289162	0.1355	0.6024
chr12	133851895	21420712	0.16	0.463
chr13	115169878	11409677	0.0991	0.3585
chr14	107349540	8505270	0.0792	0.3377
chr15	102531392	9876913	0.0963	0.3534
chr16	90354753	11682578	0.1293	0.7931
chr17	81195210	11813412	0.1455	0.6152
chr18	78077248	8346931	0.1069	1.2031
chr19	59128983	8047569	0.1361	2.36
chr20	63025520	7309228	0.116	0.403
chr21	48129895	5081039	0.1056	0.4108
chr22	51304566	4869641	0.0949	0.3577
chrMT	16571	665257	40.1459	13.3161
chrX	155270560	16611858	0.107	0.4227
chrY	59373566	898435	0.0151	0.5985

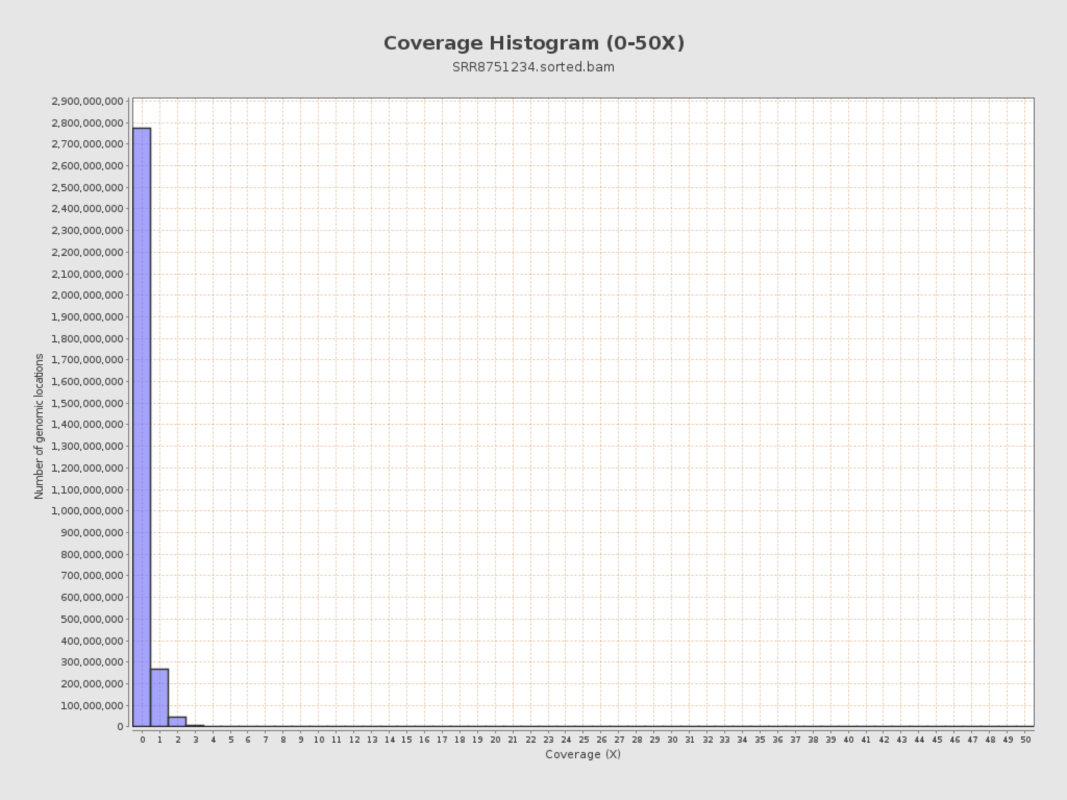
3. Results : Coverage across reference



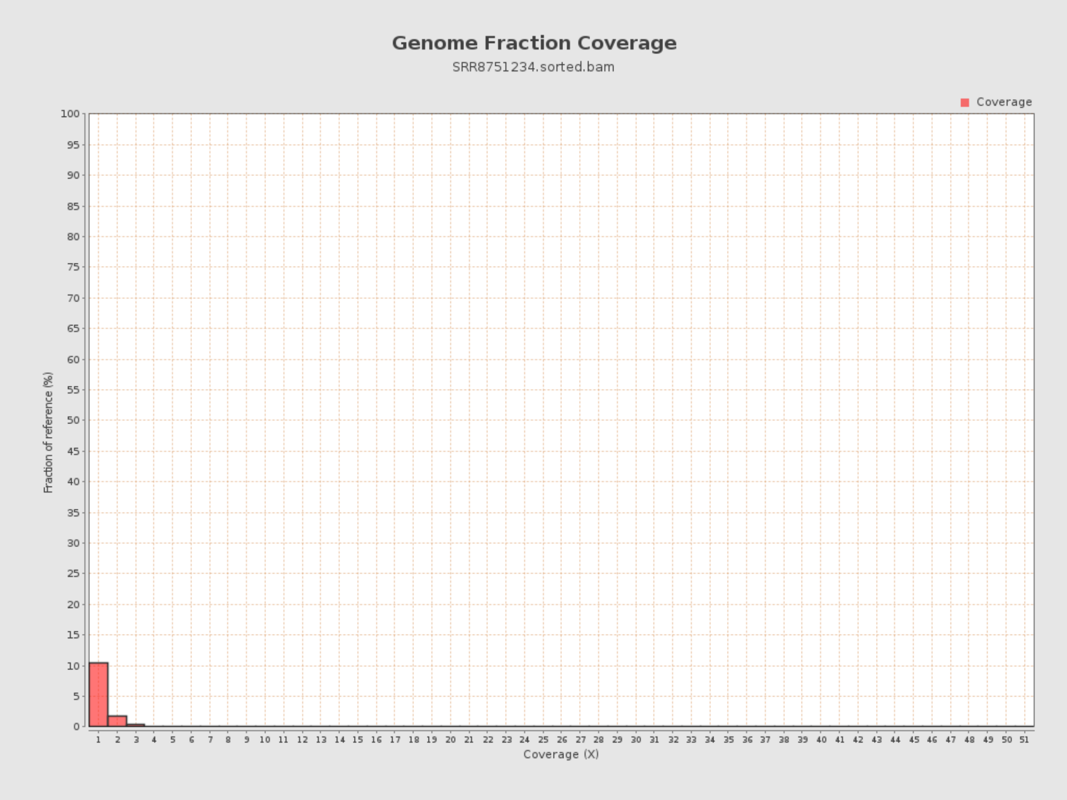
4. Results : Coverage Histogram



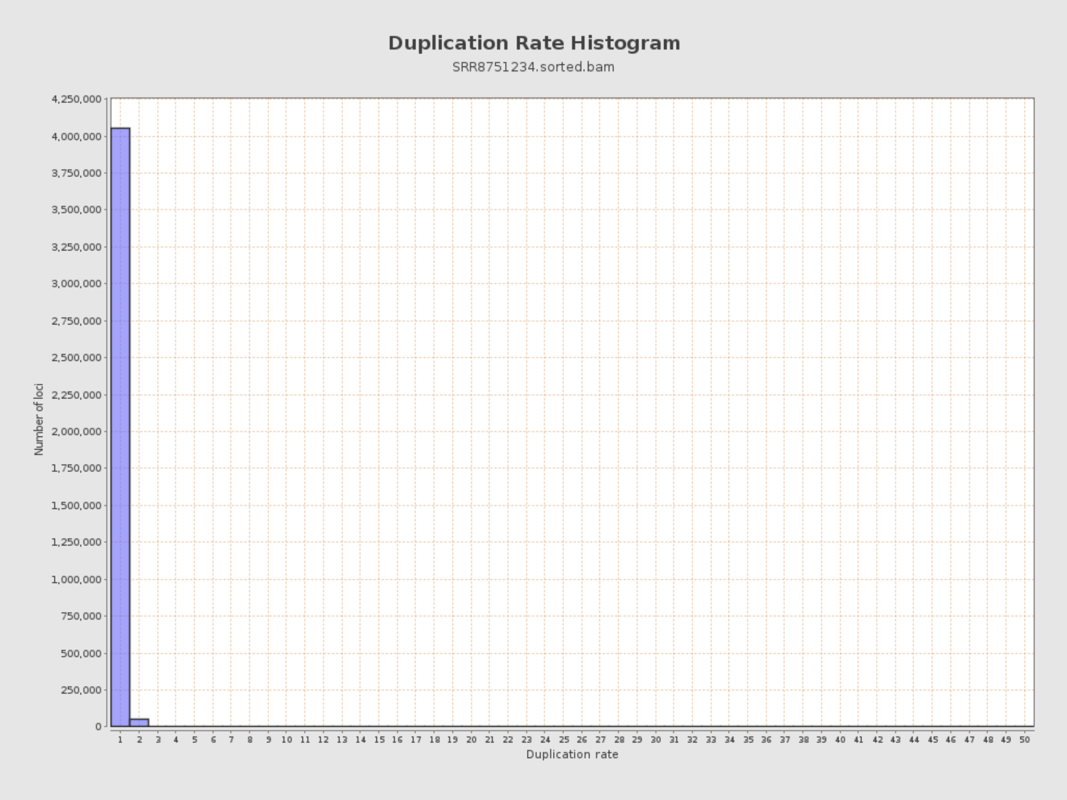
5. Results : Coverage Histogram (0-50X)



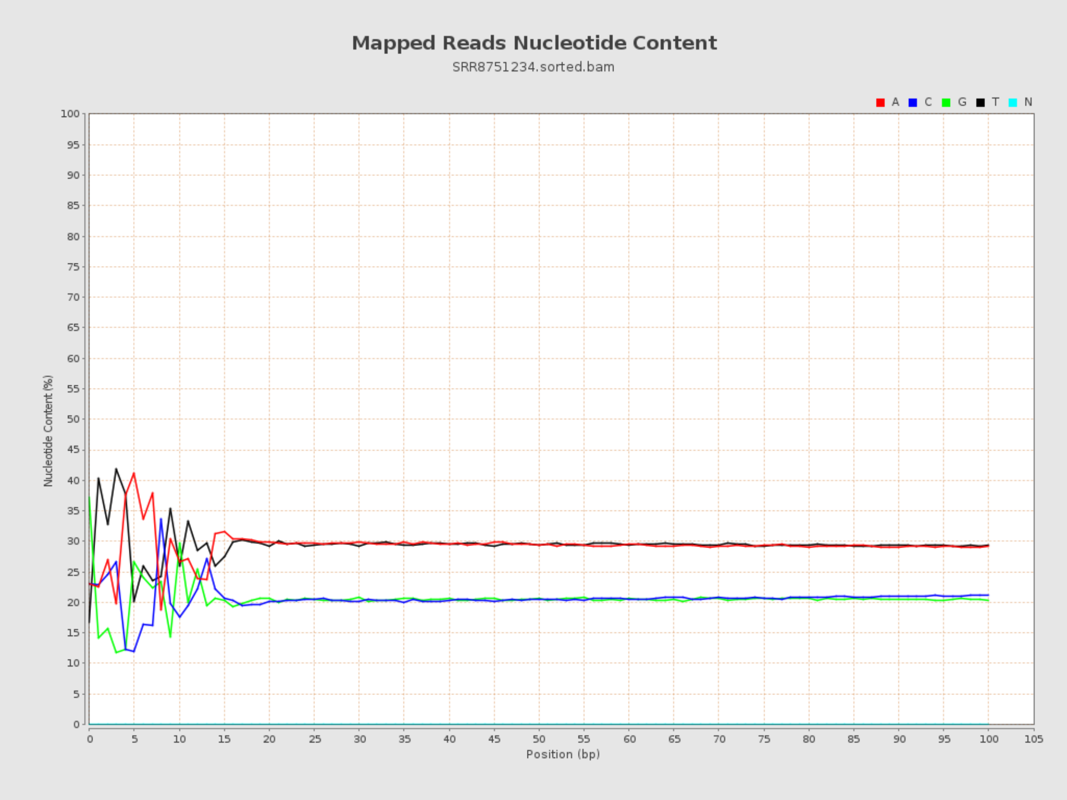
6. Results : Genome Fraction Coverage



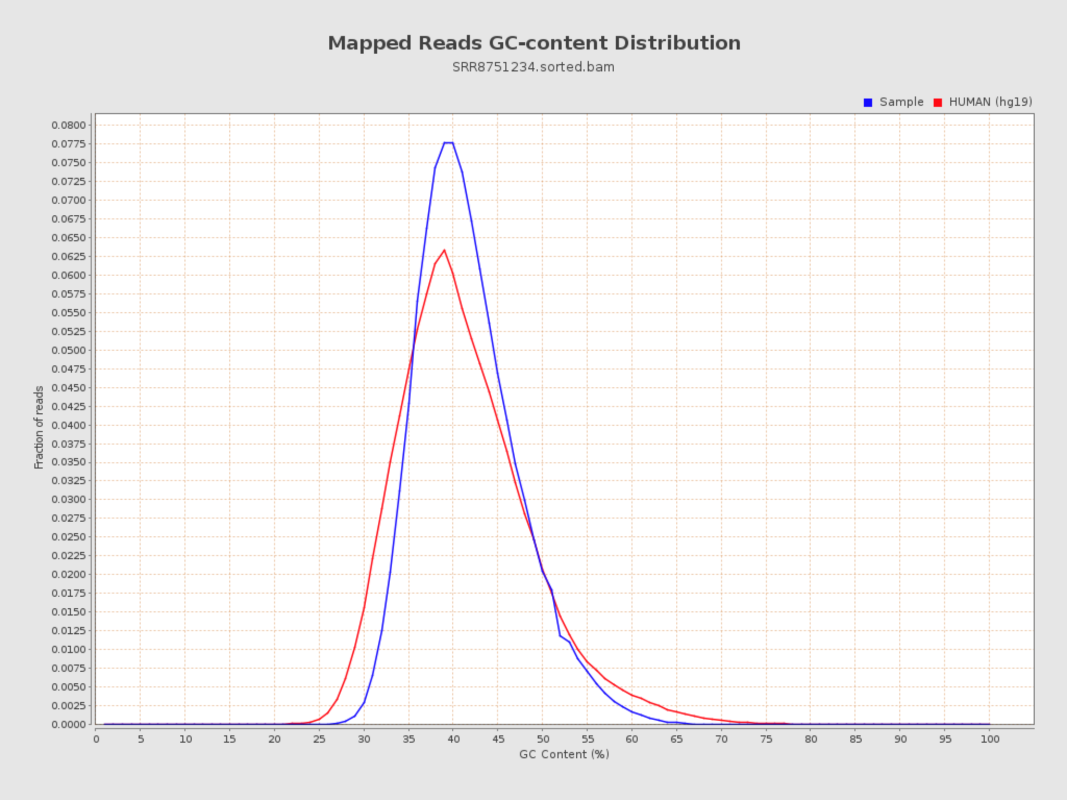
7. Results : Duplication Rate Histogram



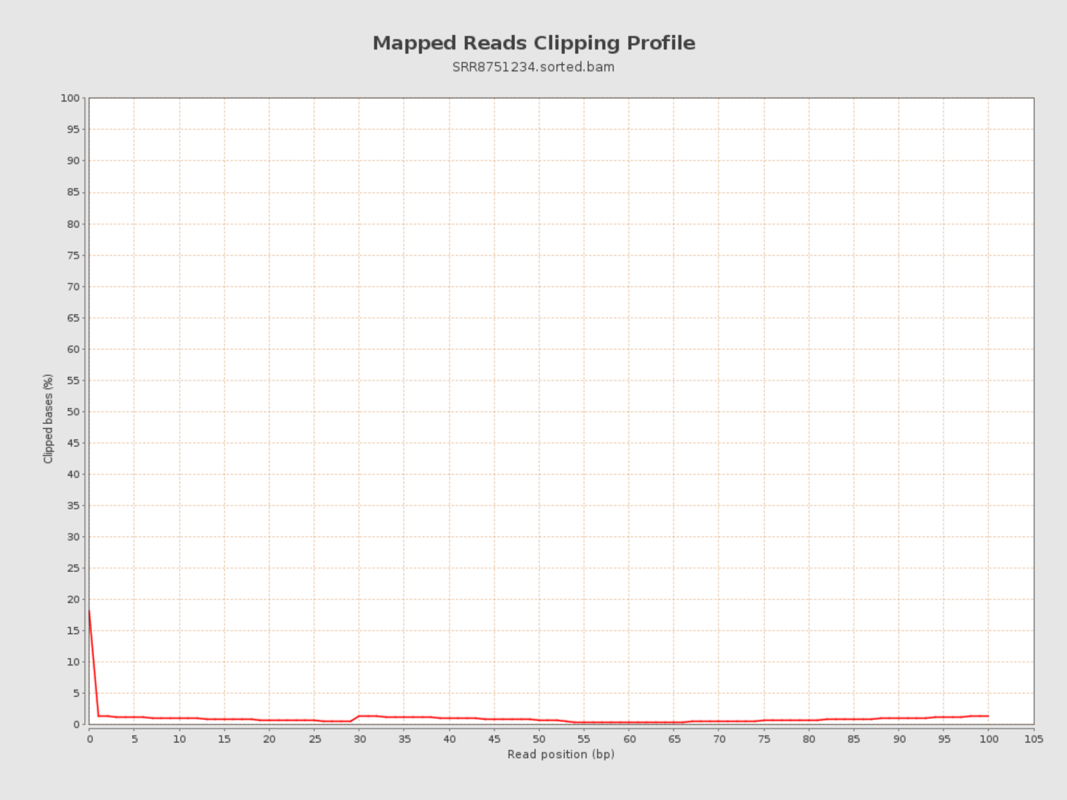
8. Results : Mapped Reads Nucleotide Content



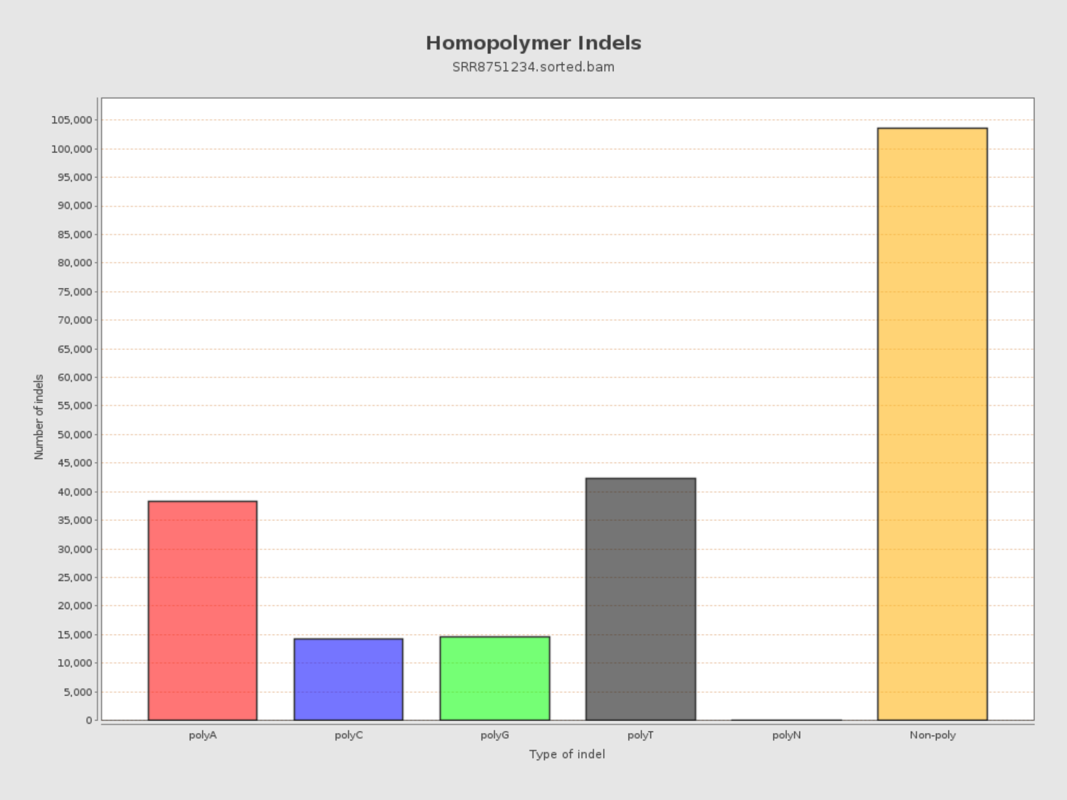
9. Results : Mapped Reads GC-content Distribution



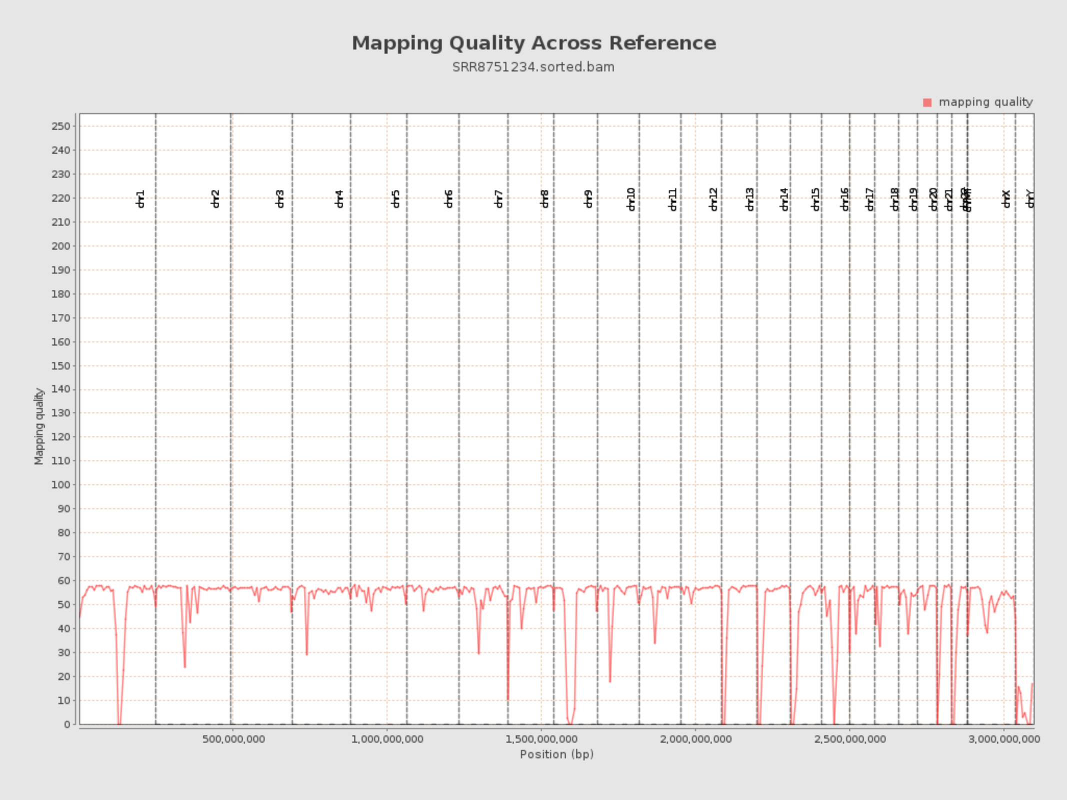
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram