Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:17:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751228.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_SRR8751228 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751228.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:17:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751228.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,189,429
Mapped reads	3,950,879 / 94.31%
Unmapped reads	238,550 / 5.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	144,149 / 3.44%
Read min/max/mean length	30 / 101 / 102.43
Duplicated reads (estimated)	95,972 / 2.29%
Duplication rate	1.43%
Clipped reads	744,356 / 17.77%

2.2. ACGT Content

Number/percentage of A's	112,773,956 / 28.99%
Number/percentage of C's	81,715,392 / 21.01%
Number/percentage of T's	113,388,730 / 29.15%
Number/percentage of G's	81,090,879 / 20.85%
Number/percentage of N's	2,196 / 0%
GC Percentage	41.86%

2.3. Coverage

Mean	0.1257

Standard Deviation	0.9729

2.4. Mapping Quality

Mean Mapping Quality	51.35

2.5. Mismatches and indels

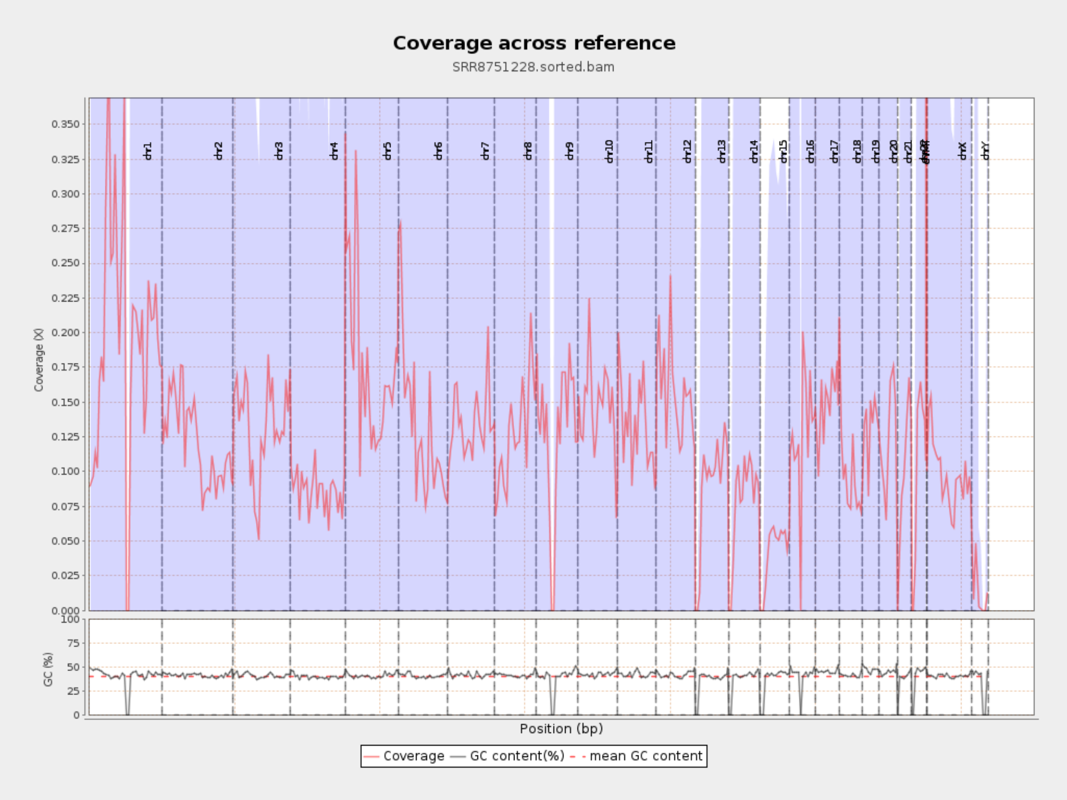
General error rate	0.38%
Mismatches	1,339,210
Insertions	104,697
Mapped reads with at least one insertion	2.59%
Deletions	52,276
Mapped reads with at least one deletion	1.3%
Homopolymer indels	49.05%

2.6. Chromosome stats

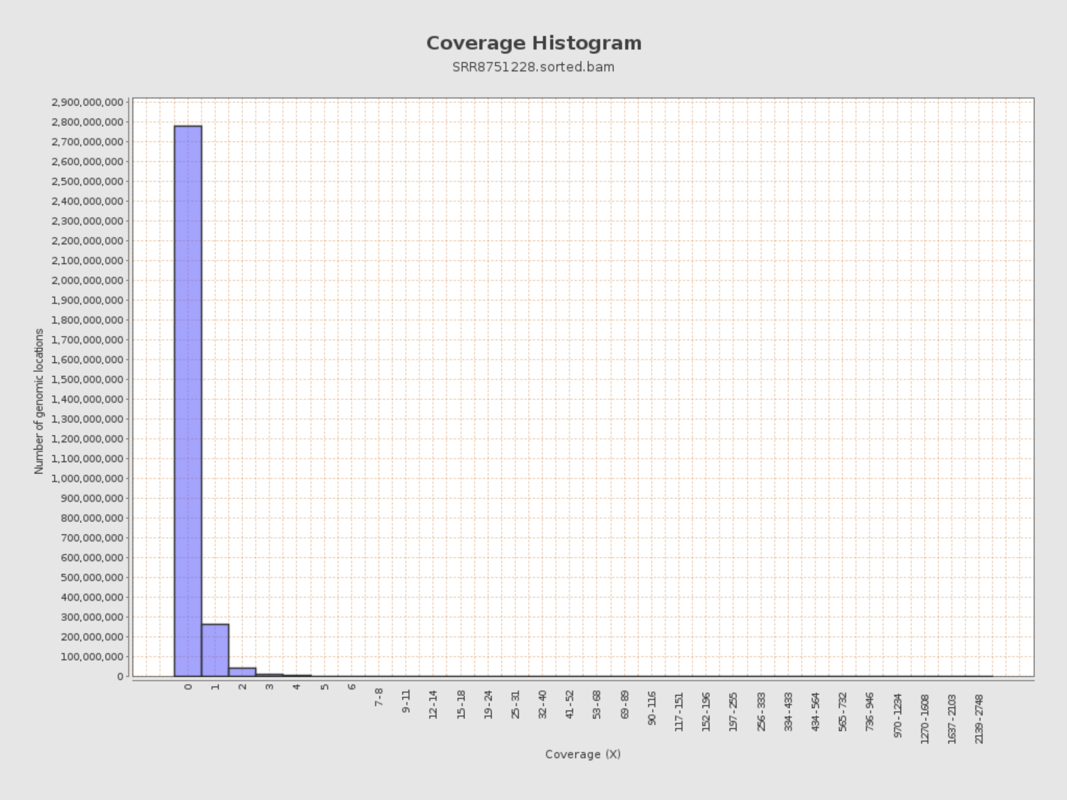
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	48883528	0.1961	2.6194
chr2	243199373	29550635	0.1215	0.4667
chr3	198022430	25987951	0.1312	0.4313
chr4	191154276	16414392	0.0859	0.3711
chr5	180915260	31582165	0.1746	0.4844
chr6	171115067	22708123	0.1327	0.6679
chr7	159138663	21473687	0.1349	0.5606

chr8	146364022	18686363	0.1277	0.4663
chr9	141213431	17668258	0.1251	0.5216
chr10	135534747	19950054	0.1472	1.1982
chr11	135006516	18121826	0.1342	0.5457
chr12	133851895	21246312	0.1587	0.4575
chr13	115169878	10228773	0.0888	0.3386
chr14	107349540	8418469	0.0784	0.3305
chr15	102531392	4358839	0.0425	0.2308
chr16	90354753	11371537	0.1259	0.6975
chr17	81195210	12030654	0.1482	0.5622
chr18	78077248	7651500	0.098	0.9212
chr19	59128983	7772297	0.1314	1.8955
chr20	63025520	7626928	0.121	0.4053
chr21	48129895	4793503	0.0996	0.3817
chr22	51304566	5082647	0.0991	0.3634
chrMT	16571	1497687	90.38	37.0344
chrX	155270560	15246896	0.0982	0.3939
chrY	59373566	734268	0.0124	0.4658

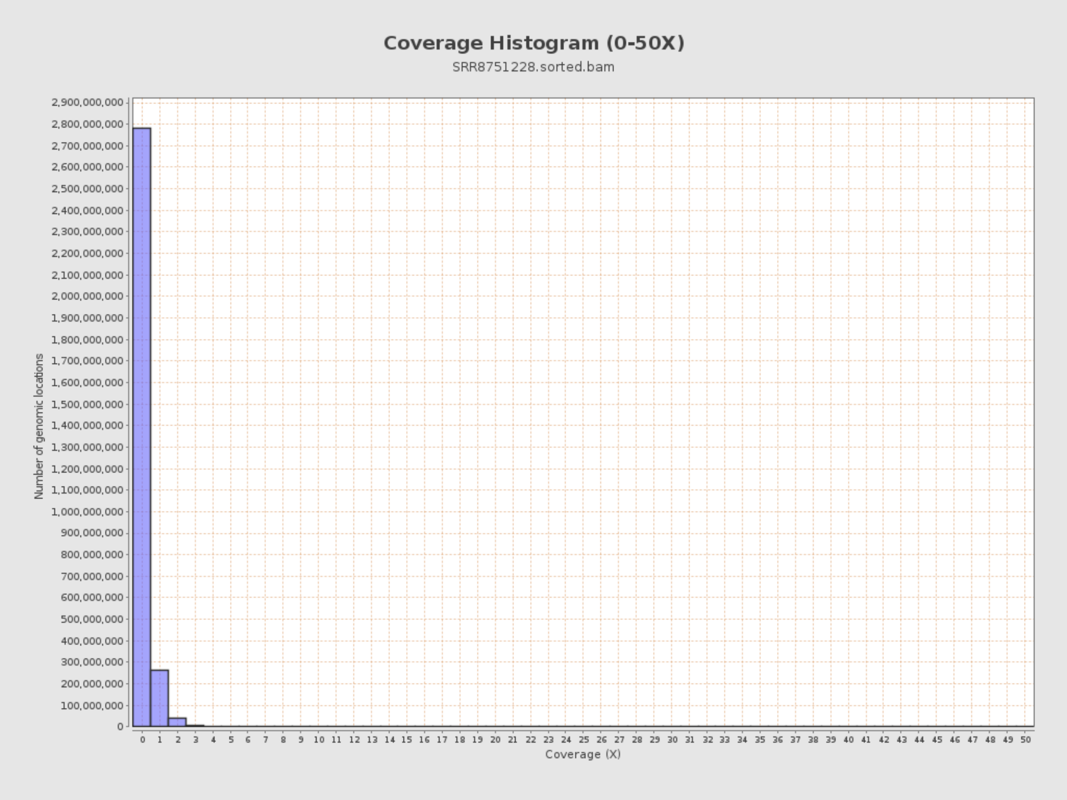
3. Results : Coverage across reference



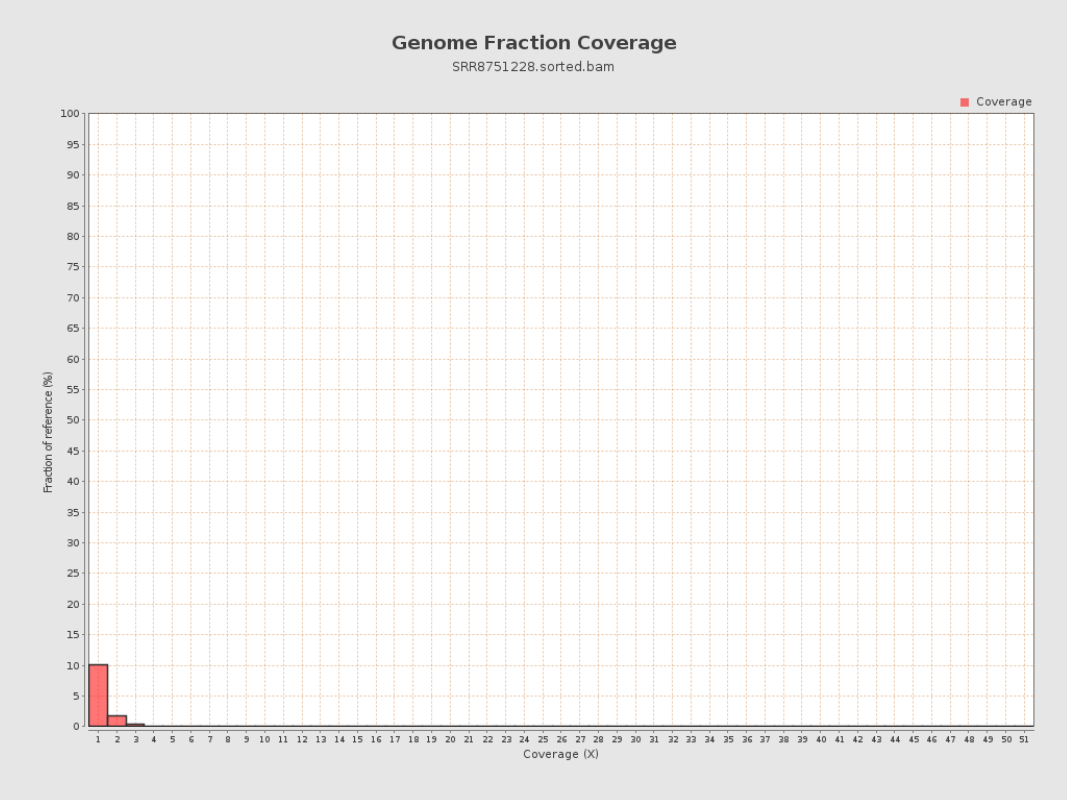
4. Results : Coverage Histogram



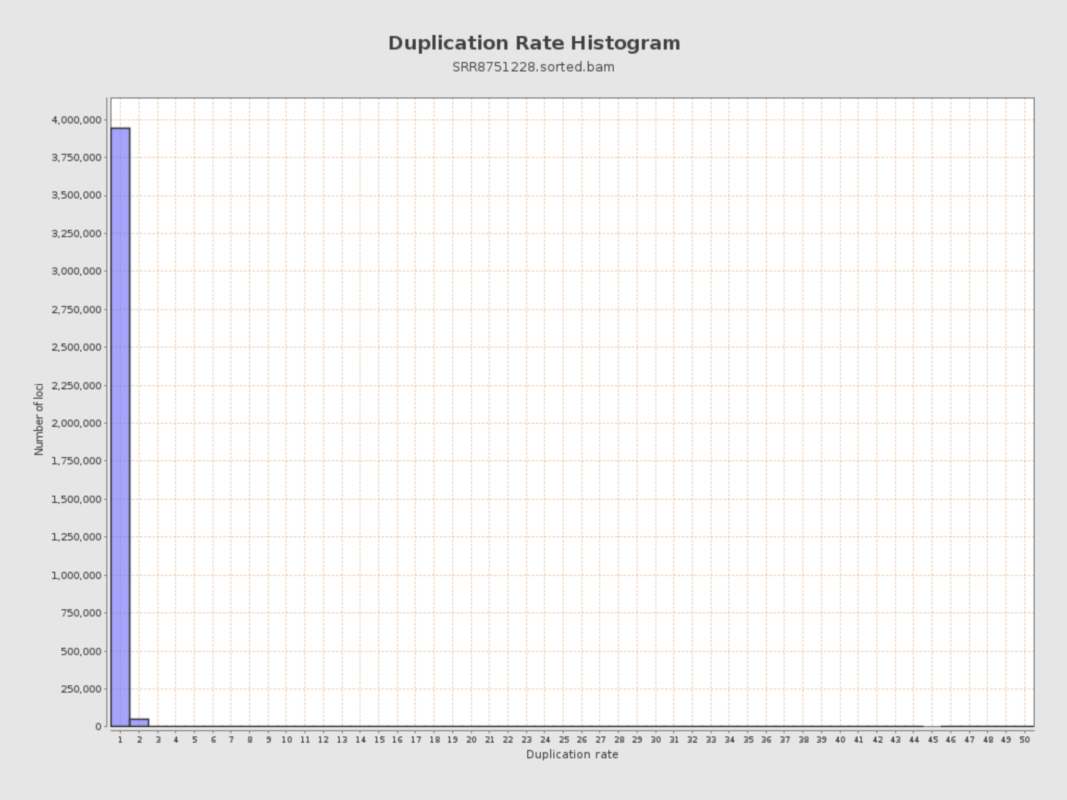
5. Results : Coverage Histogram (0-50X)



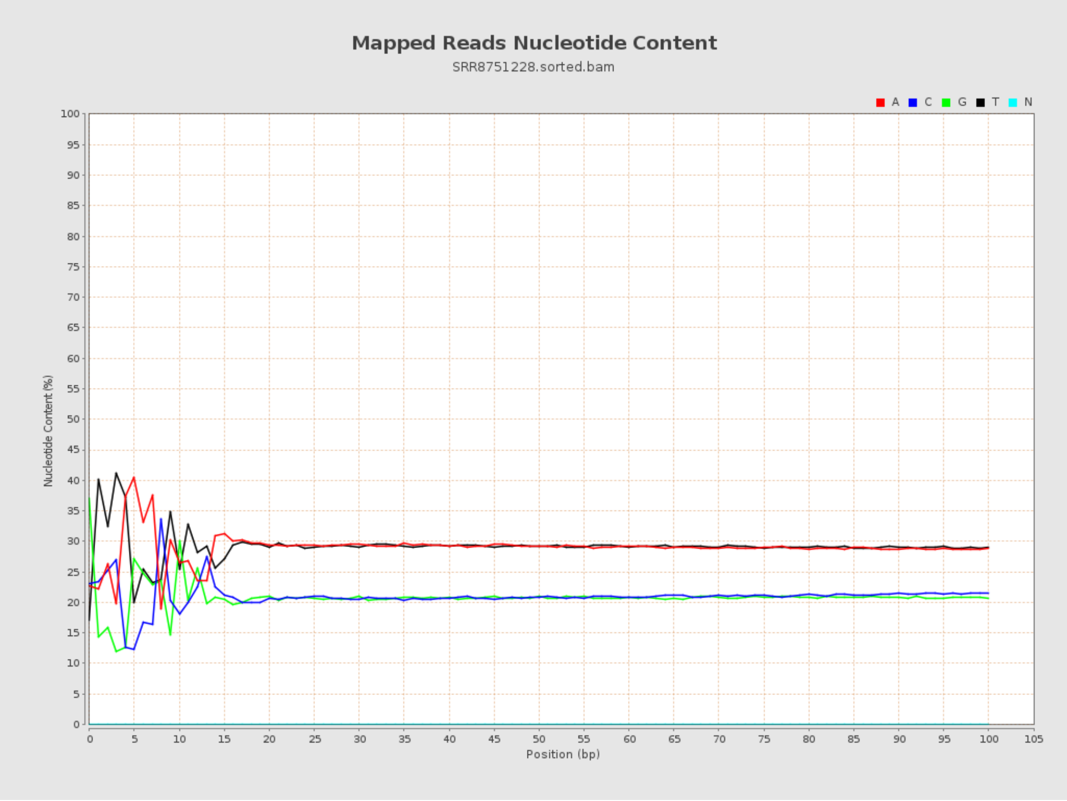
6. Results : Genome Fraction Coverage



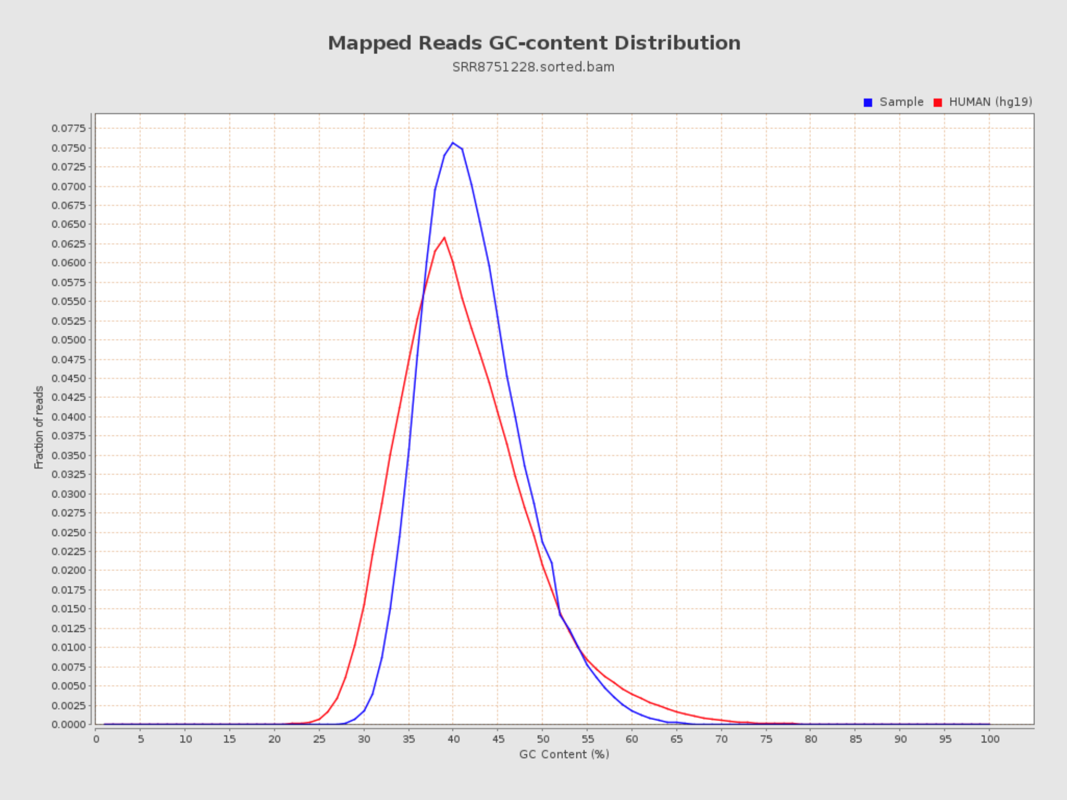
7. Results : Duplication Rate Histogram



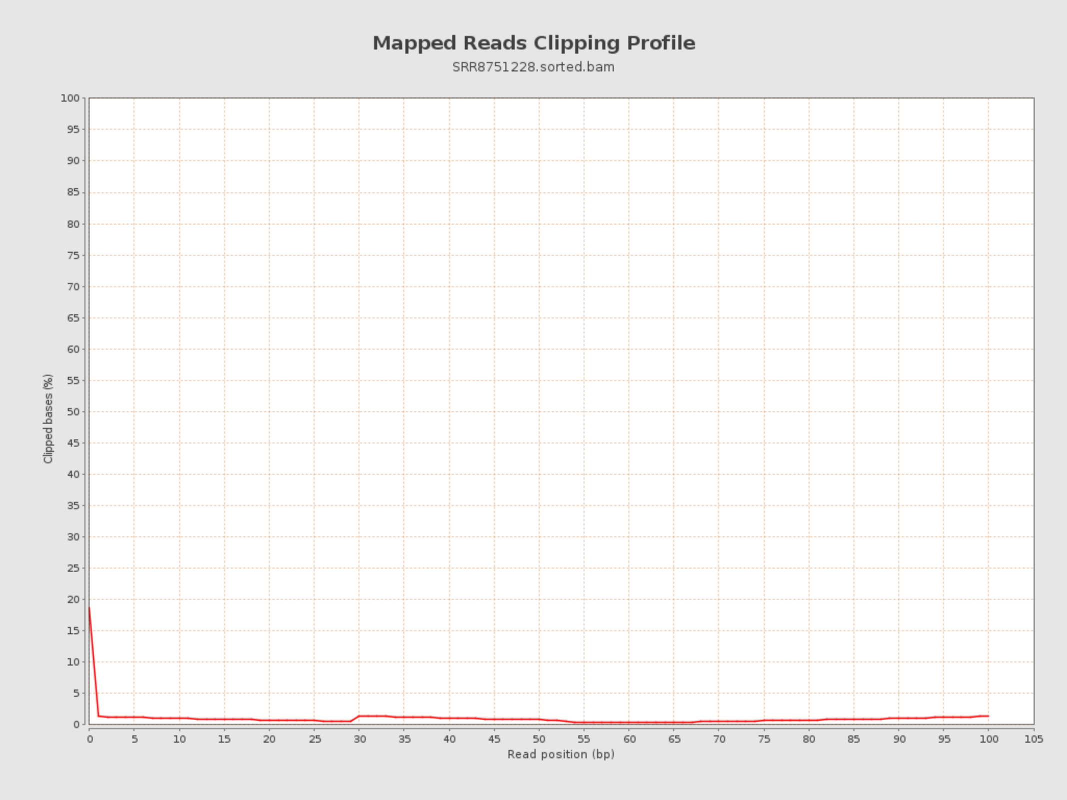
8. Results : Mapped Reads Nucleotide Content



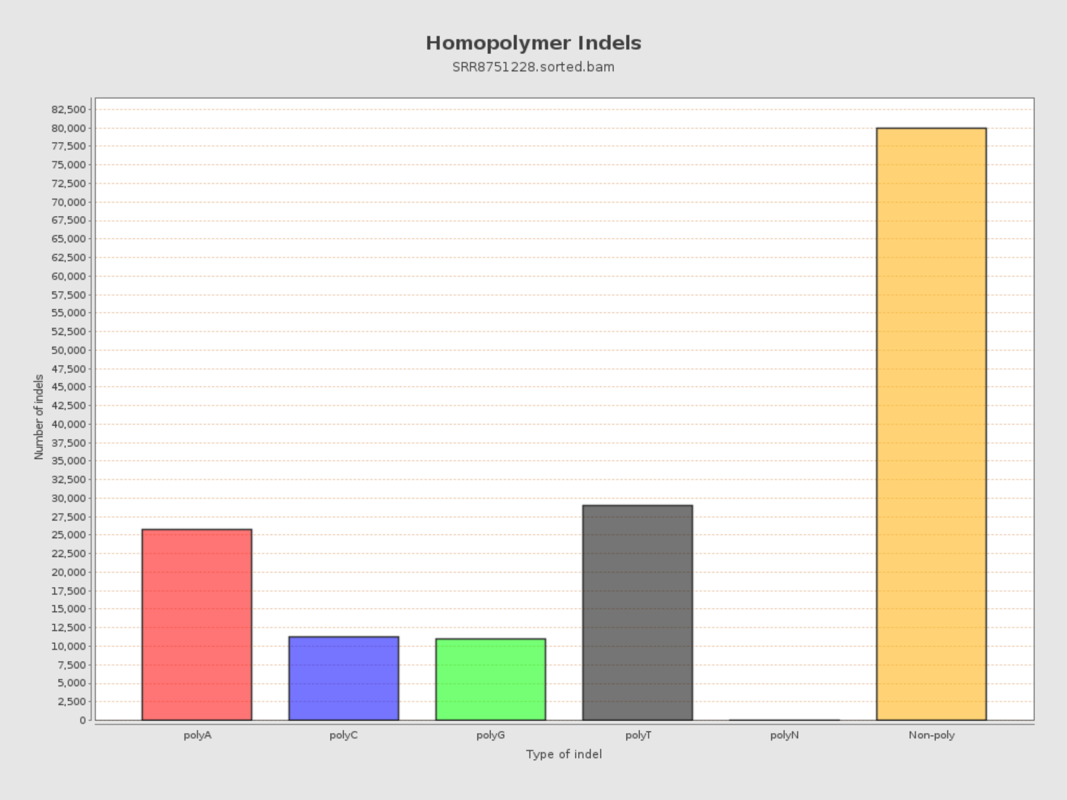
9. Results : Mapped Reads GC-content Distribution



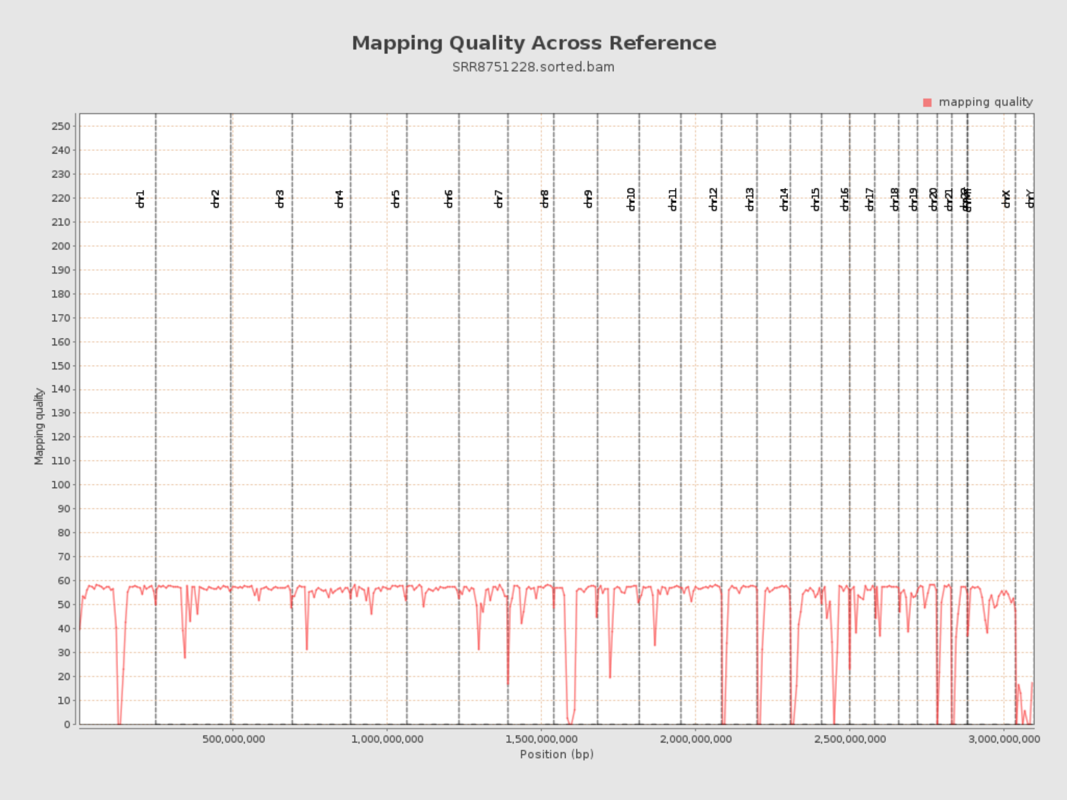
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram