Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:18:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751224.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_SRR8751224 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751224.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:18:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751224.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,469,273
Mapped reads	5,224,000 / 95.52%
Unmapped reads	245,273 / 4.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	168,168 / 3.07%
Read min/max/mean length	30 / 101 / 102.28
Duplicated reads (estimated)	159,799 / 2.92%
Duplication rate	1.67%
Clipped reads	924,099 / 16.9%

2.2. ACGT Content

Number/percentage of A's	149,646,148 / 29.11%
Number/percentage of C's	107,500,564 / 20.91%
Number/percentage of T's	150,141,197 / 29.21%
Number/percentage of G's	106,732,807 / 20.76%
Number/percentage of N's	2,768 / 0%
GC Percentage	41.68%

2.3. Coverage

Mean	0.1661

Standard Deviation	1.6407

2.4. Mapping Quality

Mean Mapping Quality	51.16

2.5. Mismatches and indels

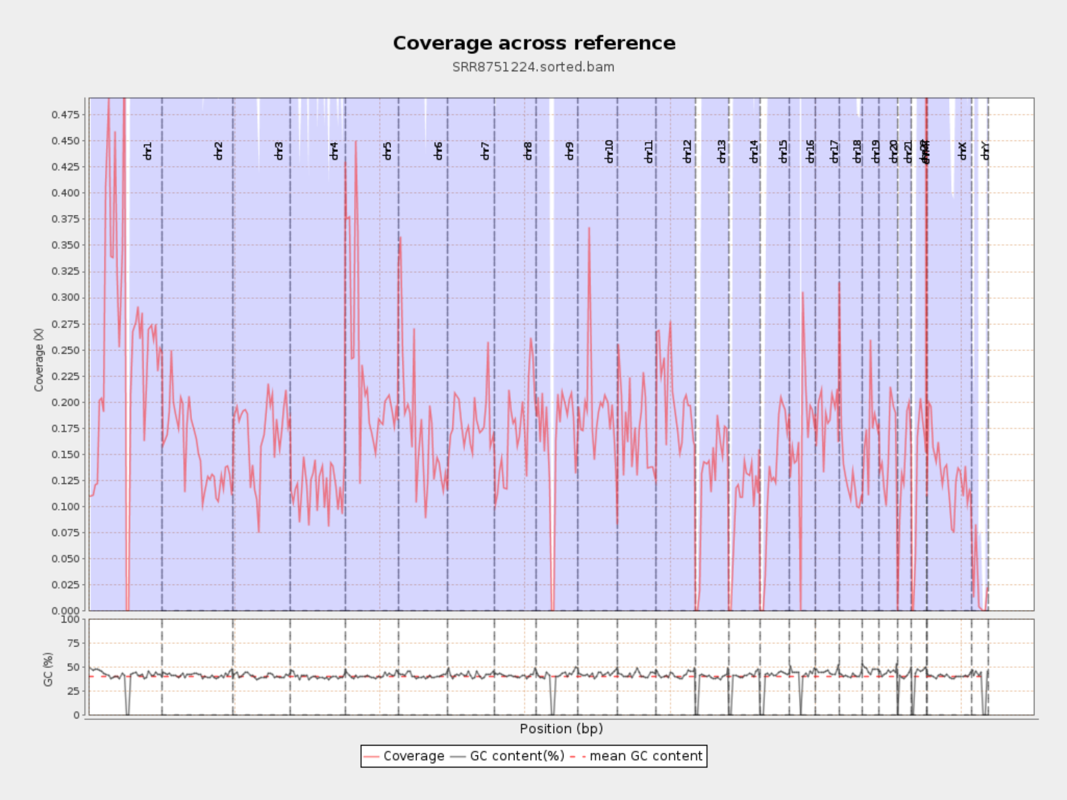
General error rate	0.4%
Mismatches	1,895,263
Insertions	118,918
Mapped reads with at least one insertion	2.23%
Deletions	68,234
Mapped reads with at least one deletion	1.28%
Homopolymer indels	48.02%

2.6. Chromosome stats

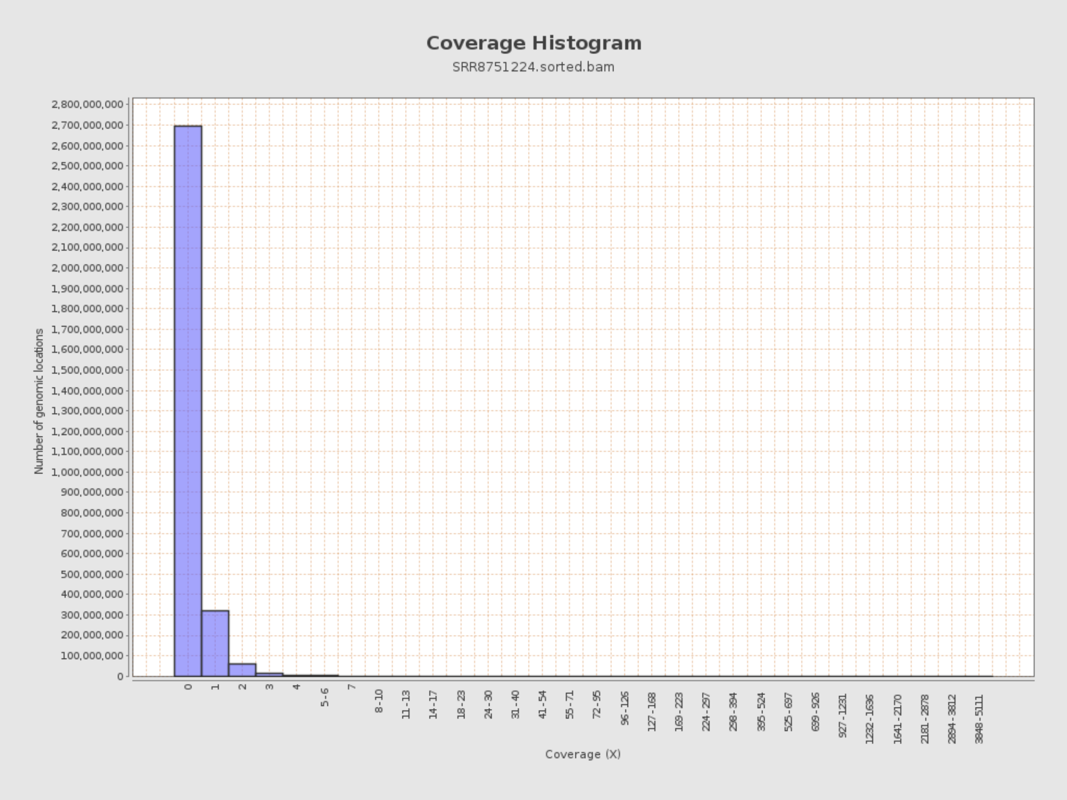
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	63066857	0.253	4.8101
chr2	243199373	37469348	0.1541	0.6139
chr3	198022430	33618564	0.1698	0.5088
chr4	191154276	22338174	0.1169	0.4901
chr5	180915260	40996844	0.2266	0.5647
chr6	171115067	29668690	0.1734	1.0868
chr7	159138663	28826057	0.1811	0.7884

chr8	146364022	25022971	0.171	0.6
chr9	141213431	22937570	0.1624	0.7665
chr10	135534747	26119942	0.1927	1.9543
chr11	135006516	23142377	0.1714	0.7925
chr12	133851895	27711600	0.207	0.5368
chr13	115169878	14388194	0.1249	0.4113
chr14	107349540	10923302	0.1018	0.3928
chr15	102531392	12939513	0.1262	0.4151
chr16	90354753	15031254	0.1664	1.083
chr17	81195210	15085095	0.1858	0.8114
chr18	78077248	10326292	0.1323	1.5441
chr19	59128983	10232171	0.173	3.4667
chr20	63025520	9634495	0.1529	0.4717
chr21	48129895	6443654	0.1339	0.4813
chr22	51304566	6234684	0.1215	0.4191
chrMT	16571	523747	31.6062	15.1036
chrX	155270560	20344566	0.131	0.4972
chrY	59373566	1148861	0.0193	0.754

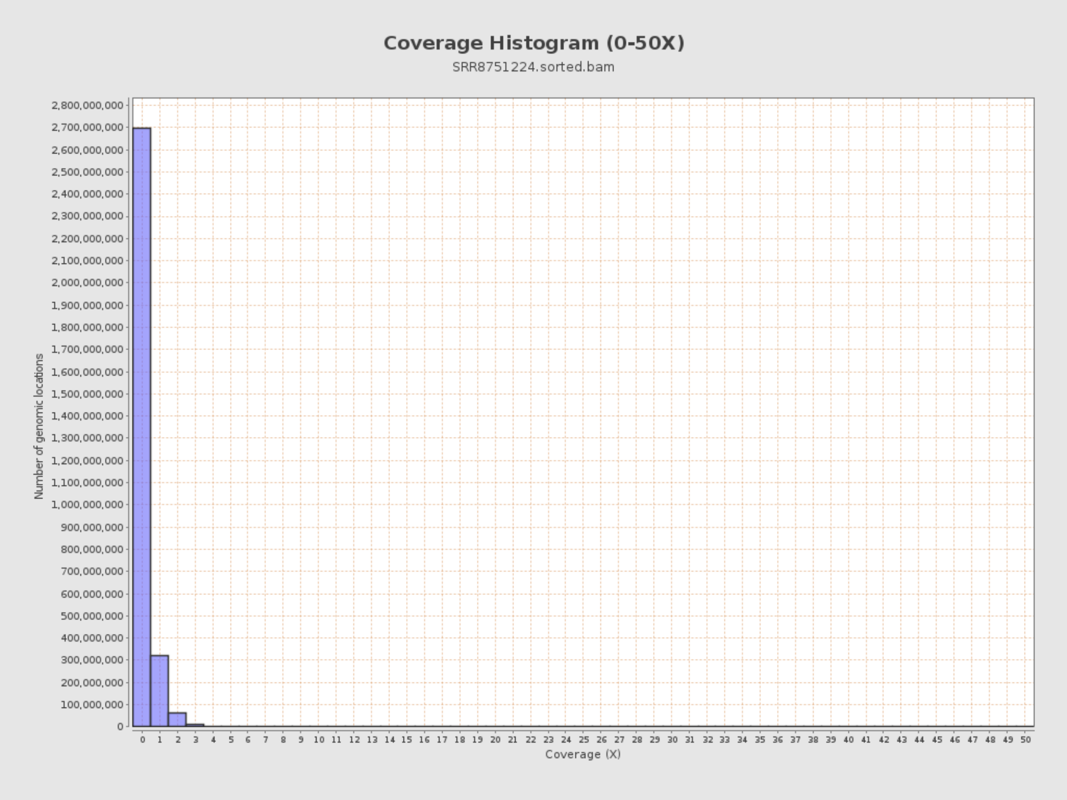
3. Results : Coverage across reference



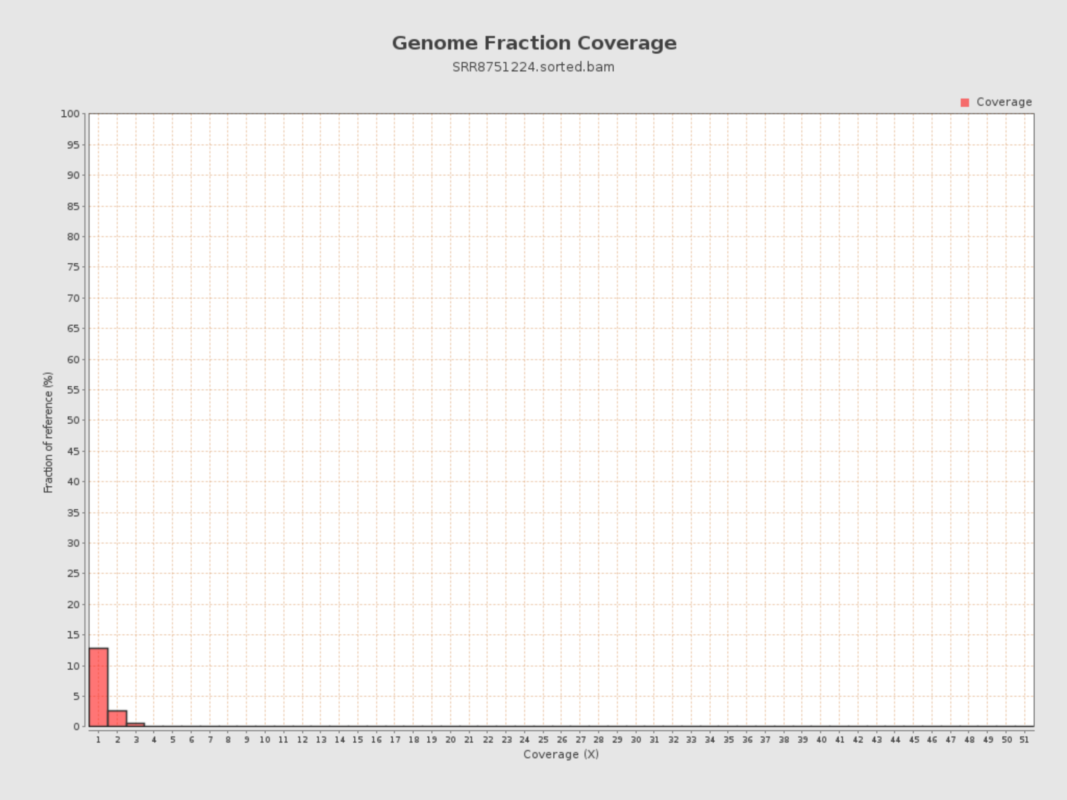
4. Results : Coverage Histogram



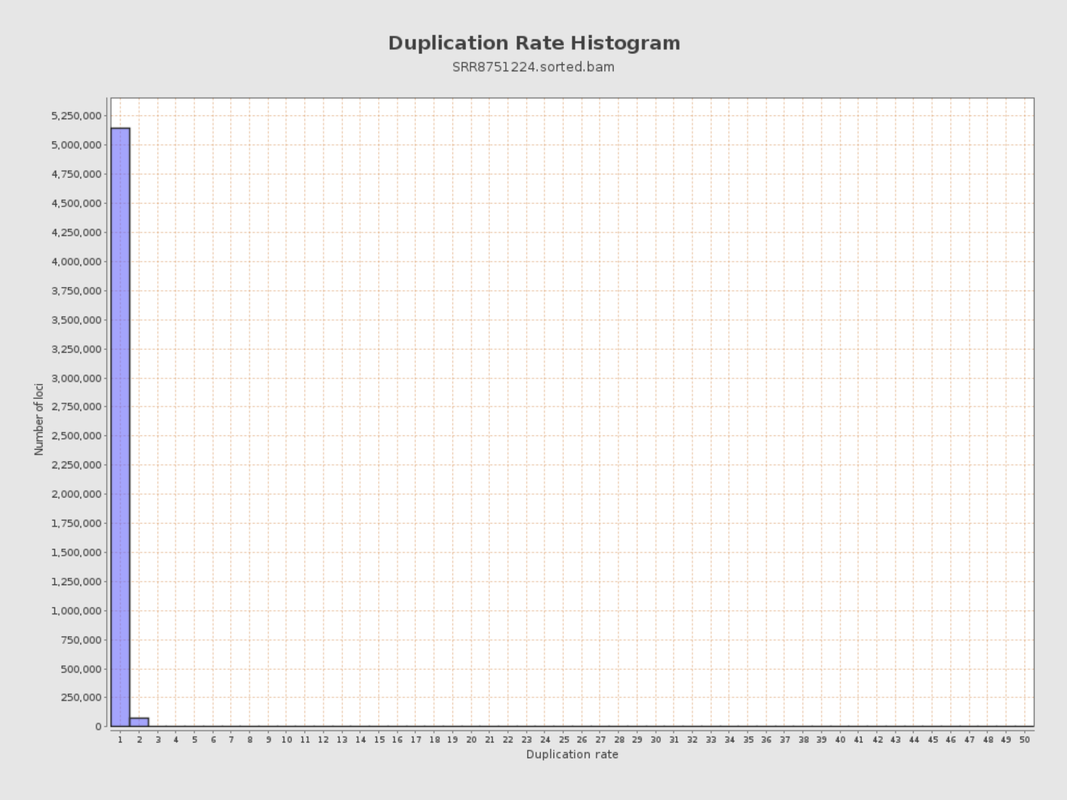
5. Results : Coverage Histogram (0-50X)



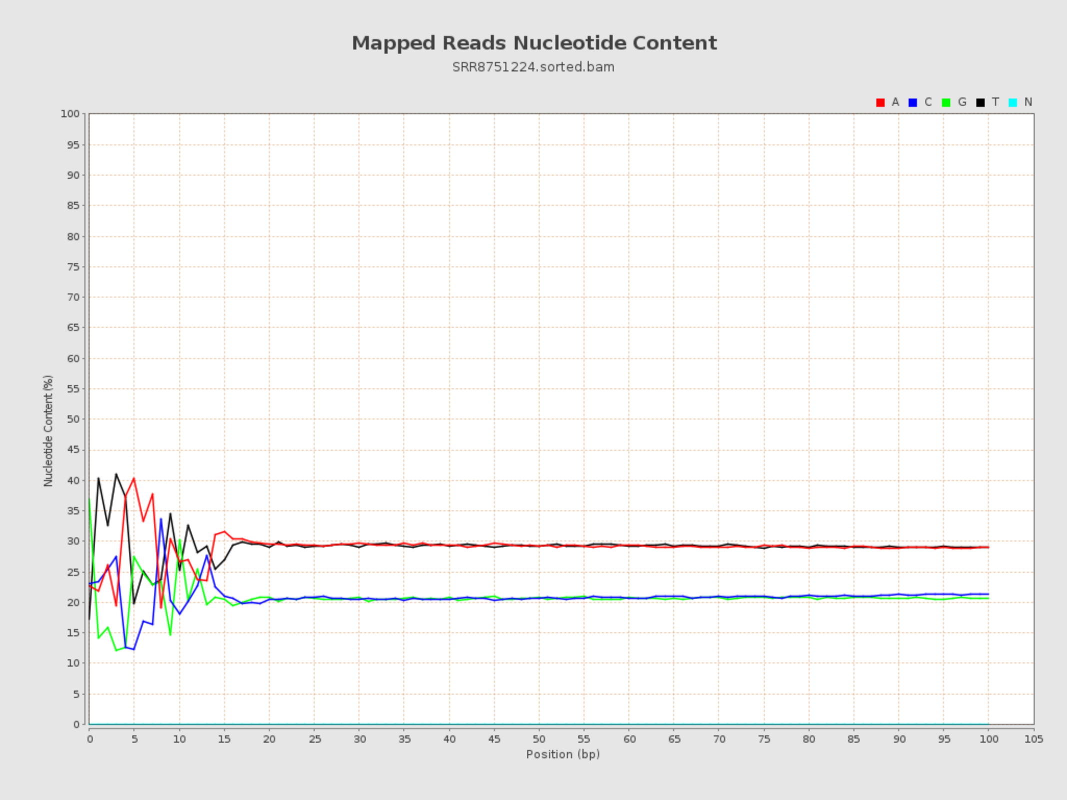
6. Results : Genome Fraction Coverage



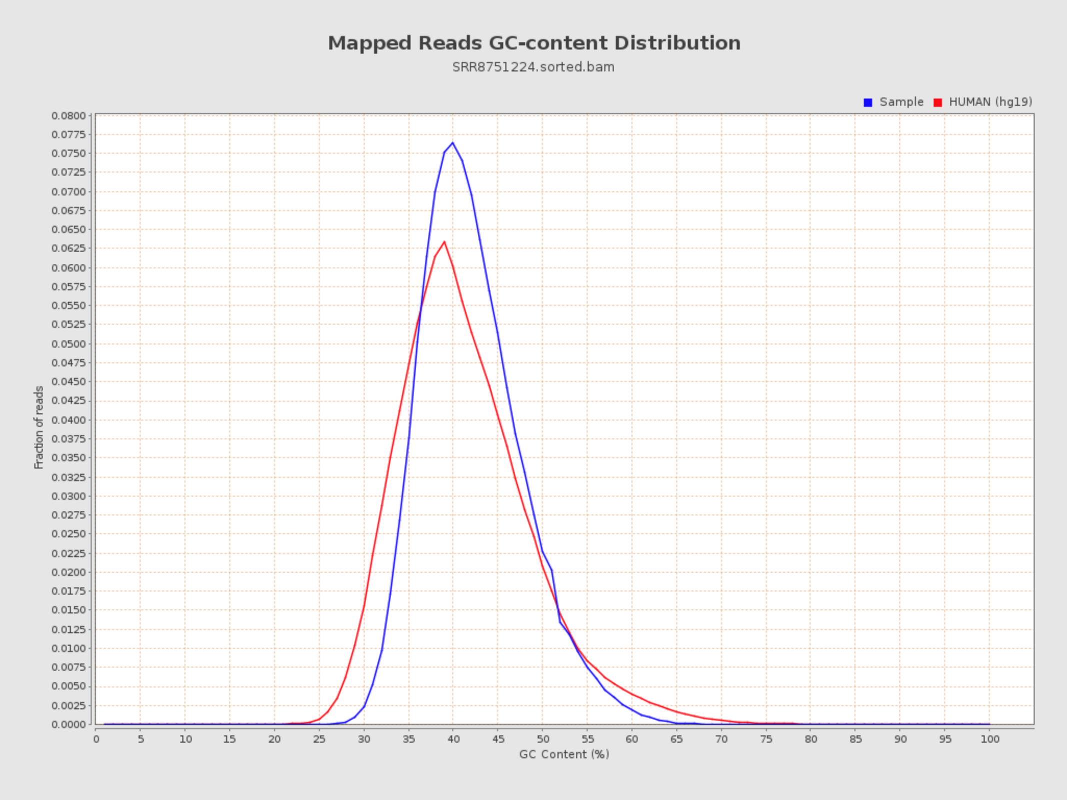
7. Results : Duplication Rate Histogram



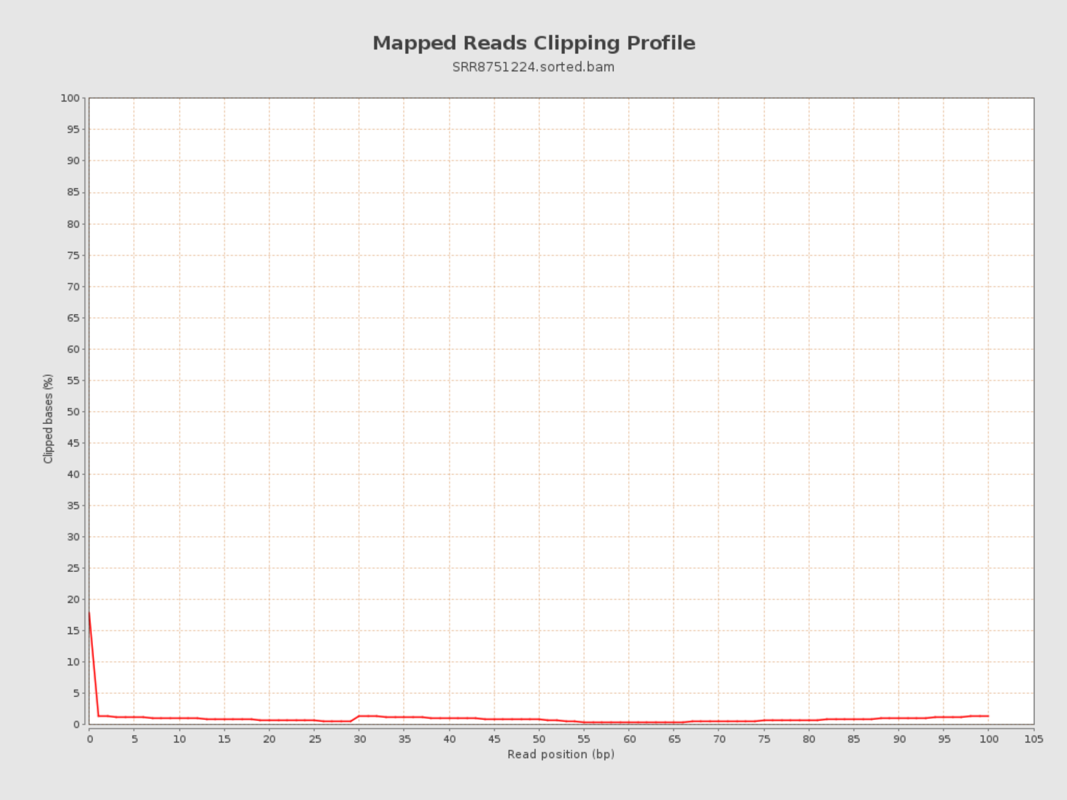
8. Results : Mapped Reads Nucleotide Content



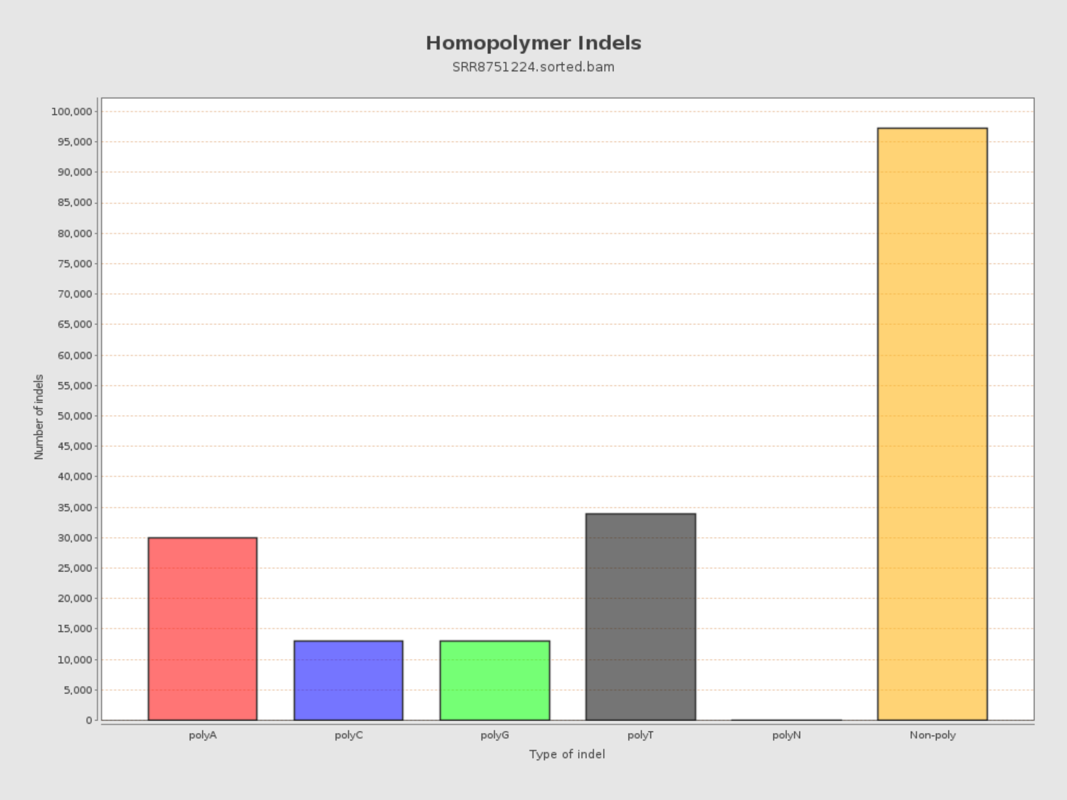
9. Results : Mapped Reads GC-content Distribution



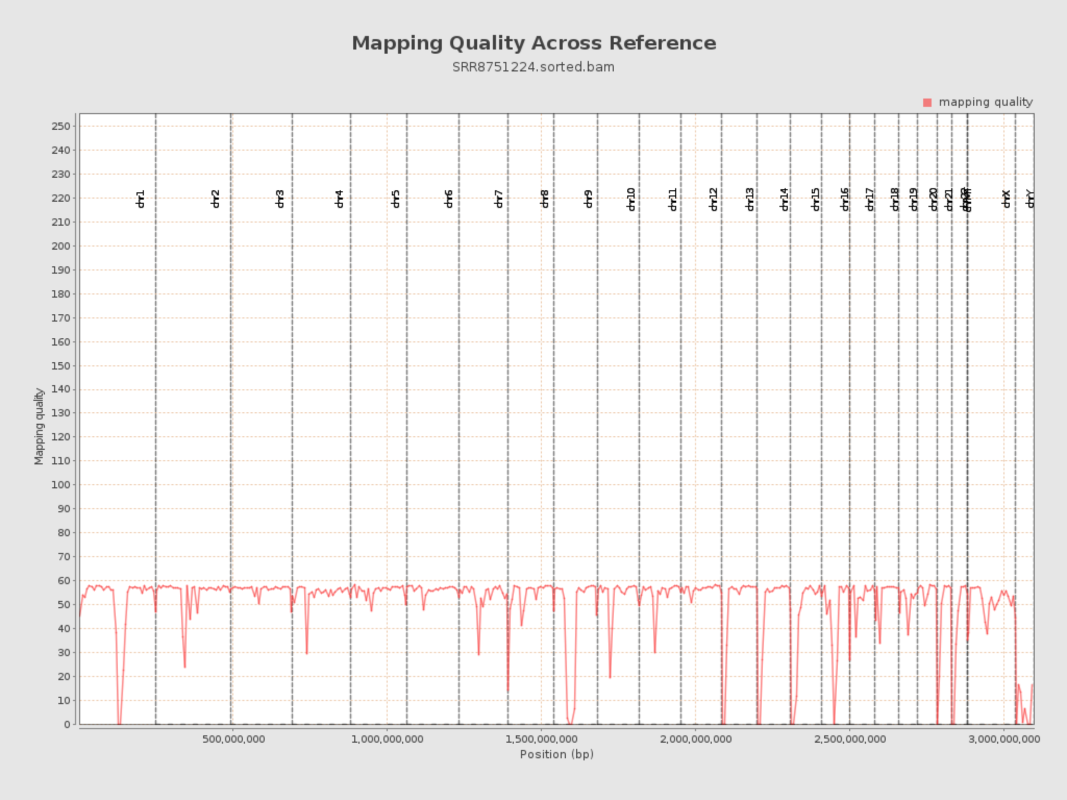
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram