Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:43:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751202.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_SRR8751202 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751202.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:43:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751202.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,753,504
Mapped reads	3,654,322 / 97.36%
Unmapped reads	99,182 / 2.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,137 / 0.8%
Read min/max/mean length	30 / 151 / 151.38
Duplicated reads (estimated)	444,463 / 11.84%
Duplication rate	9.28%
Clipped reads	590,387 / 15.73%

2.2. ACGT Content

Number/percentage of A's	152,792,848 / 28.89%
Number/percentage of C's	111,674,986 / 21.12%
Number/percentage of T's	154,170,438 / 29.15%
Number/percentage of G's	110,197,636 / 20.84%
Number/percentage of N's	15,974 / 0%
GC Percentage	41.95%

2.3. Coverage

Mean	0.1709

Standard Deviation	2.6818

2.4. Mapping Quality

Mean Mapping Quality	52.26

2.5. Mismatches and indels

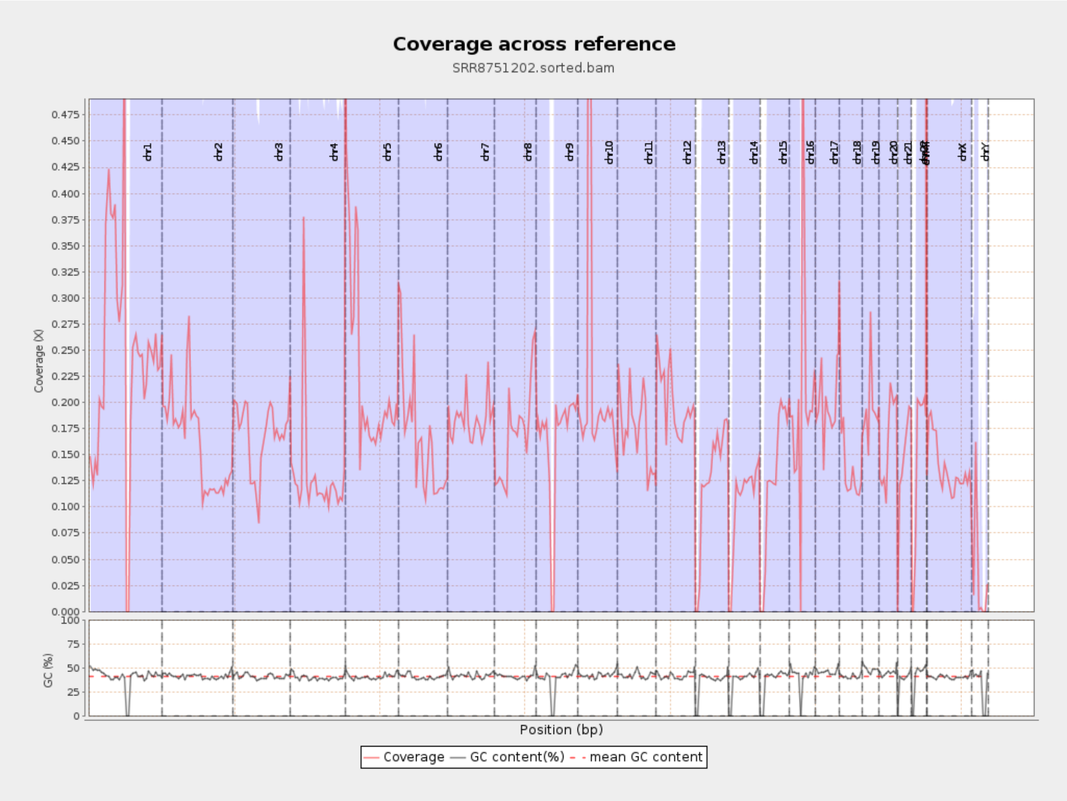
General error rate	0.77%
Mismatches	3,796,062
Insertions	73,918
Mapped reads with at least one insertion	1.88%
Deletions	75,617
Mapped reads with at least one deletion	1.96%
Homopolymer indels	41.15%

2.6. Chromosome stats

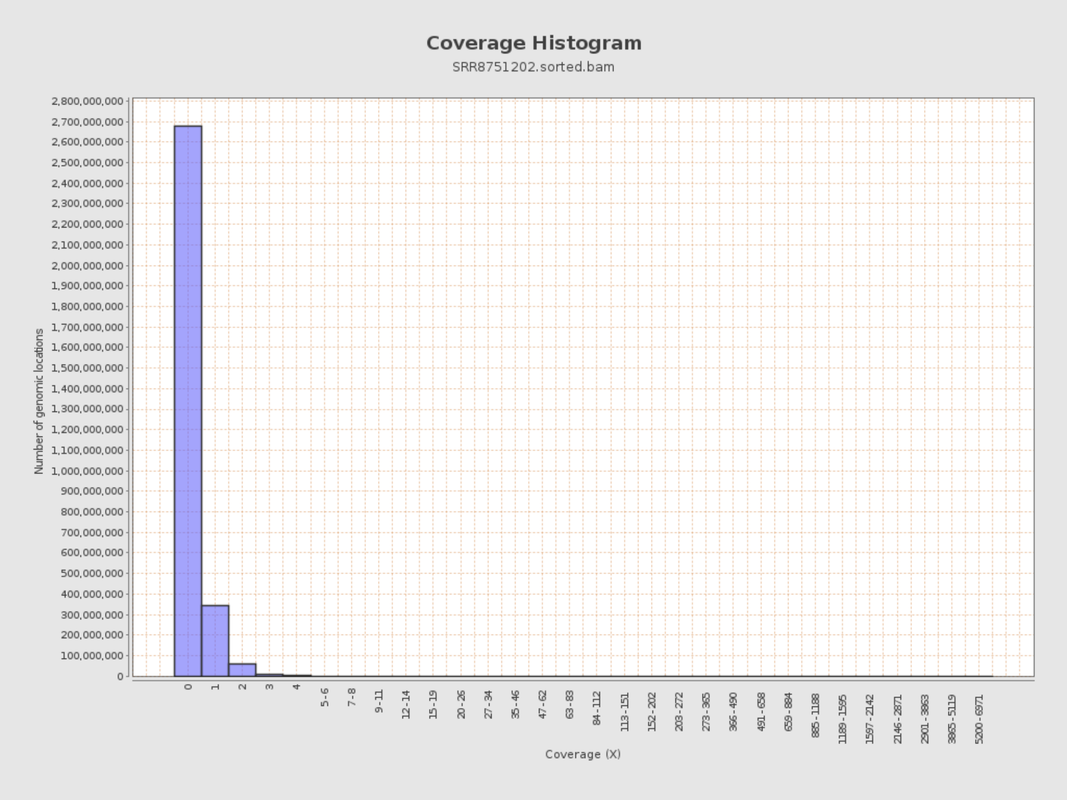
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	61445230	0.2465	6.2906
chr2	243199373	39443007	0.1622	1.0914
chr3	198022430	33246744	0.1679	0.6858
chr4	191154276	24400713	0.1276	1.7055
chr5	180915260	40463532	0.2237	0.5404
chr6	171115067	28382288	0.1659	1.1148
chr7	159138663	29197517	0.1835	1.338

chr8	146364022	25088423	0.1714	0.6263
chr9	141213431	22902327	0.1622	1.3824
chr10	135534747	30649145	0.2261	7.6199
chr11	135006516	23527820	0.1743	1.0845
chr12	133851895	26920466	0.2011	0.5563
chr13	115169878	14369162	0.1248	0.3936
chr14	107349540	11062808	0.1031	0.3742
chr15	102531392	13132081	0.1281	0.4303
chr16	90354753	18133822	0.2007	2.5918
chr17	81195210	15976870	0.1968	0.9613
chr18	78077248	10965761	0.1404	2.1481
chr19	59128983	11539815	0.1952	3.989
chr20	63025520	10237310	0.1624	0.8201
chr21	48129895	6929178	0.144	1.1789
chr22	51304566	7011955	0.1367	0.4179
chrMT	16571	941500	56.8161	12.5763
chrX	155270560	21262777	0.1369	0.5162
chrY	59373566	1846488	0.0311	2.0908

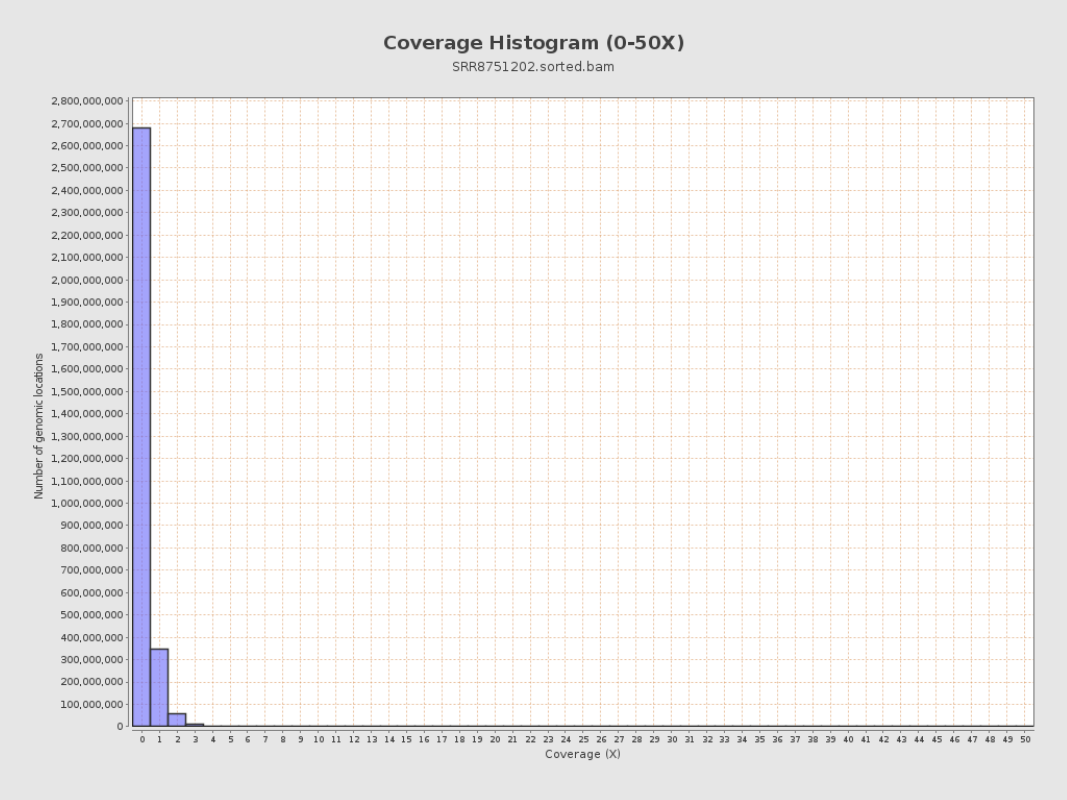
3. Results : Coverage across reference



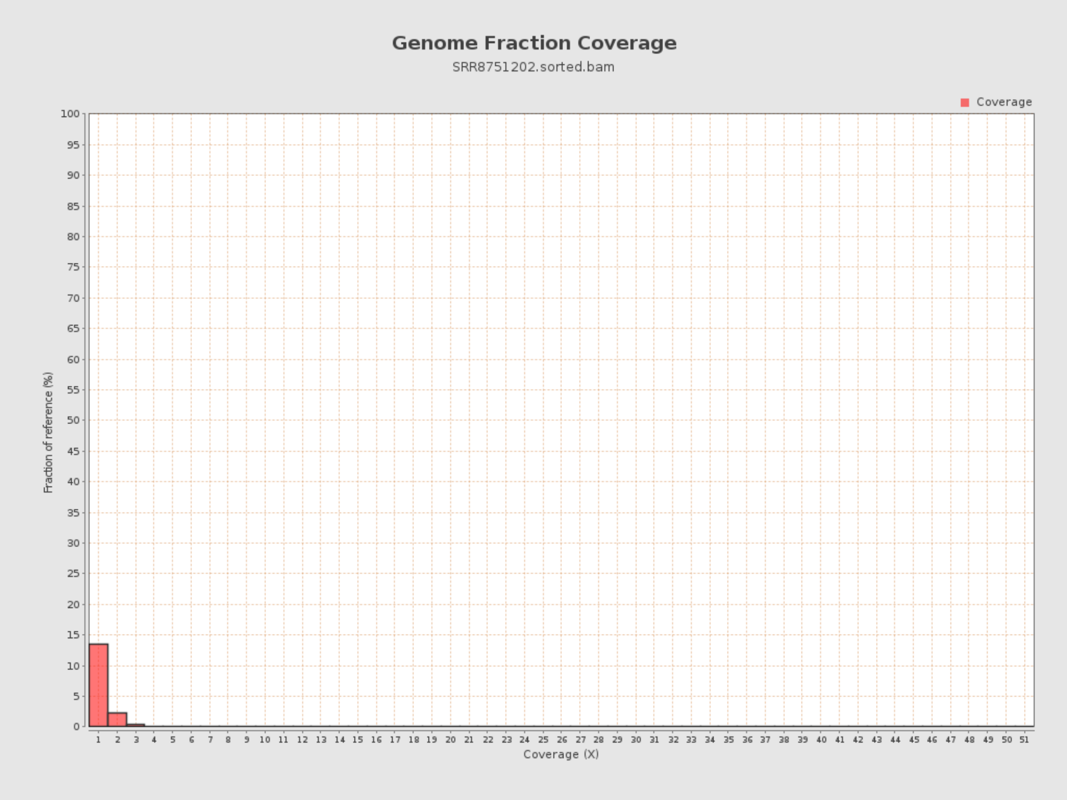
4. Results : Coverage Histogram



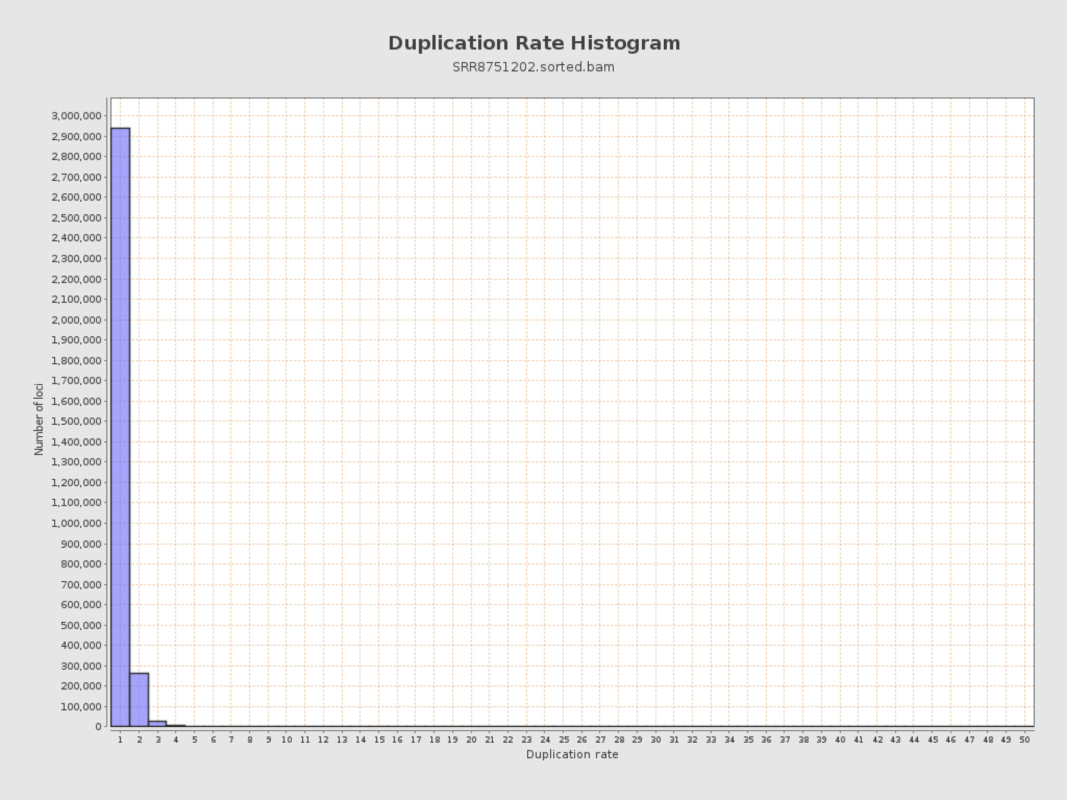
5. Results : Coverage Histogram (0-50X)



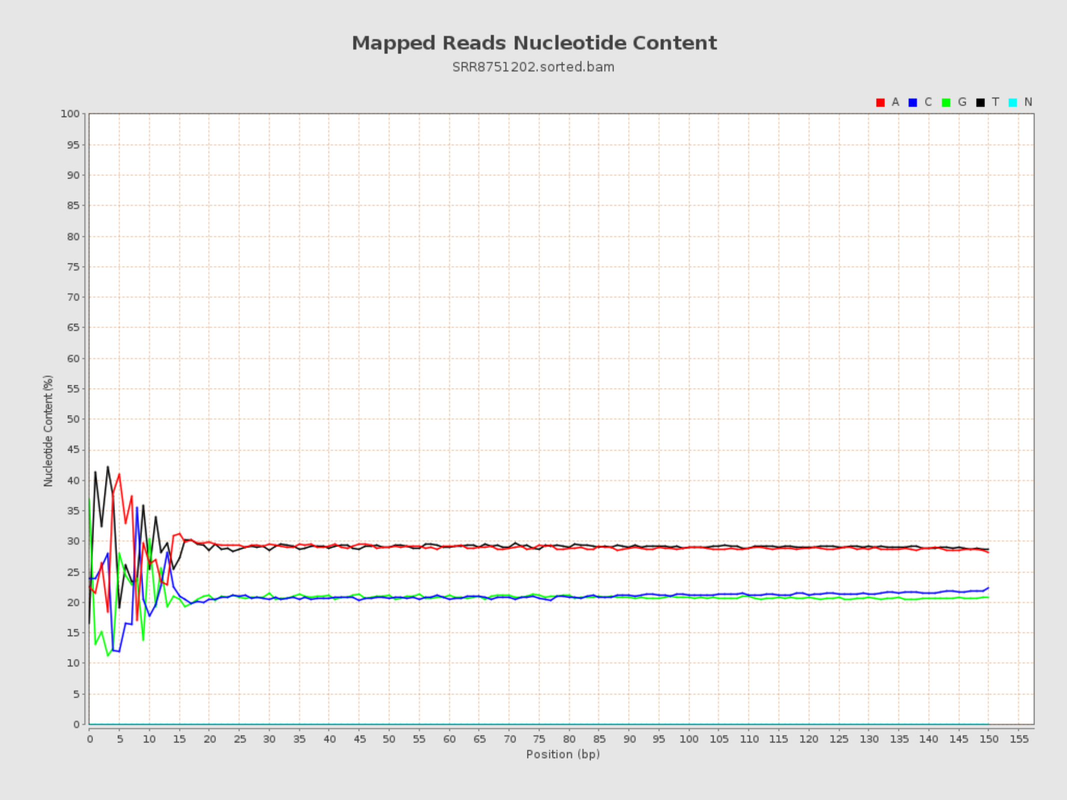
6. Results : Genome Fraction Coverage



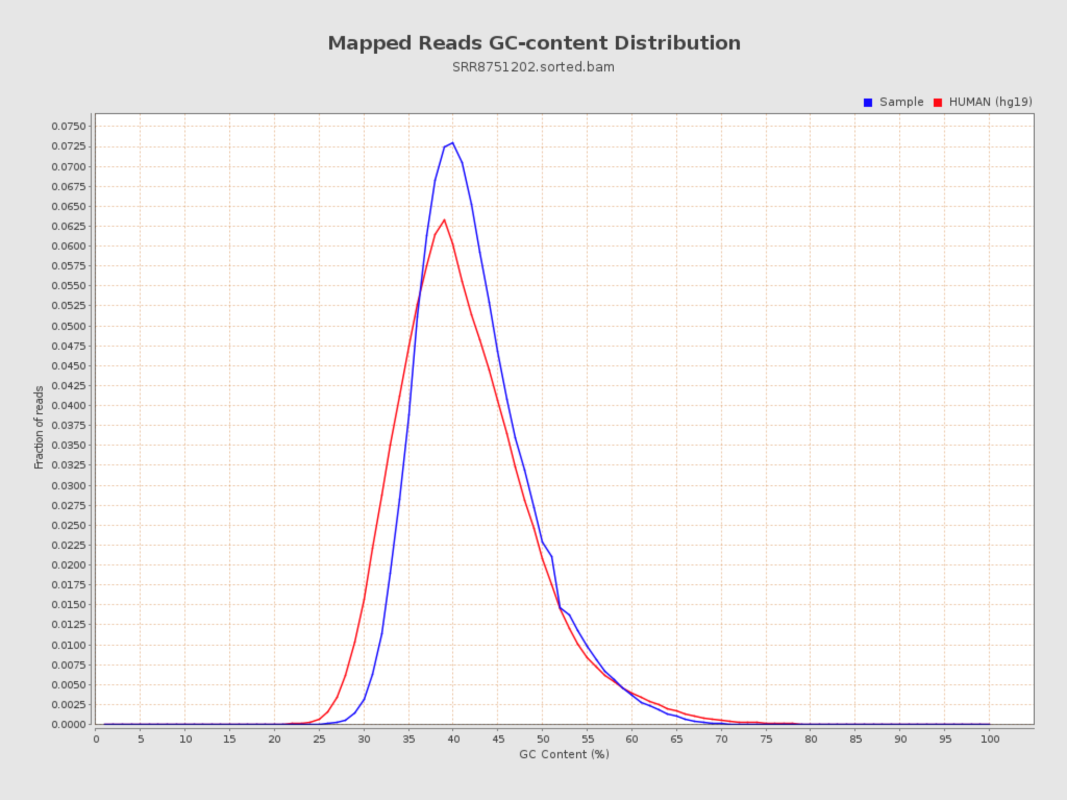
7. Results : Duplication Rate Histogram



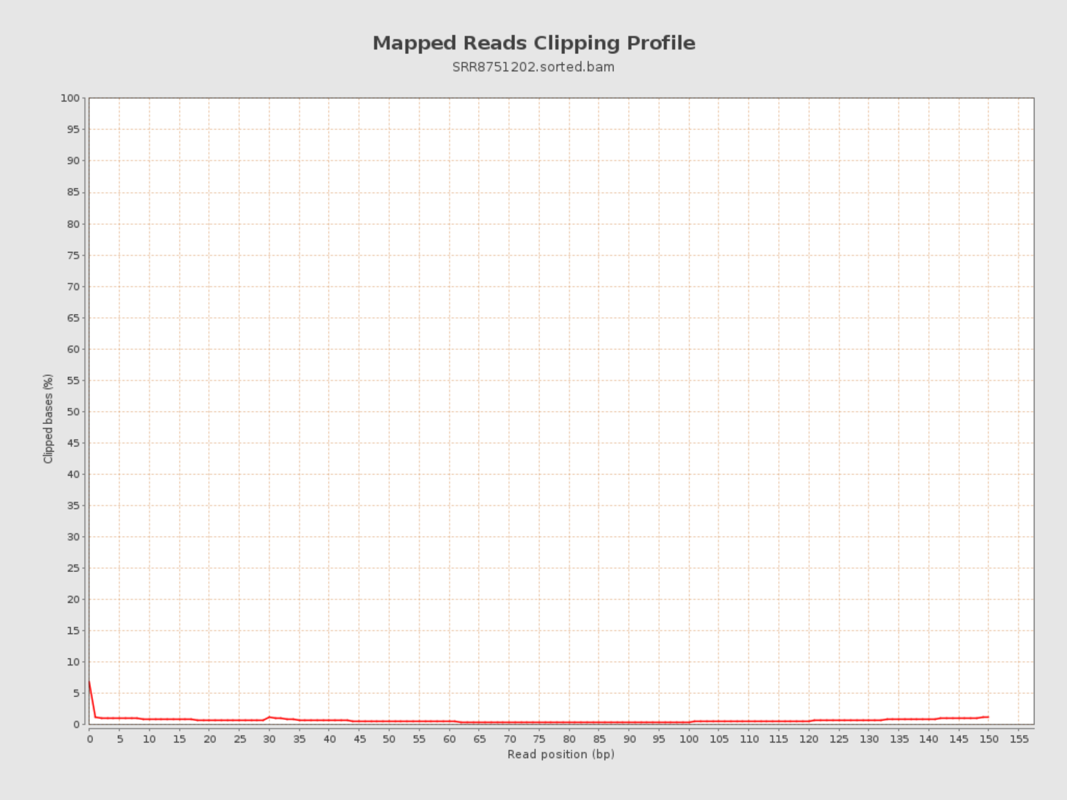
8. Results : Mapped Reads Nucleotide Content



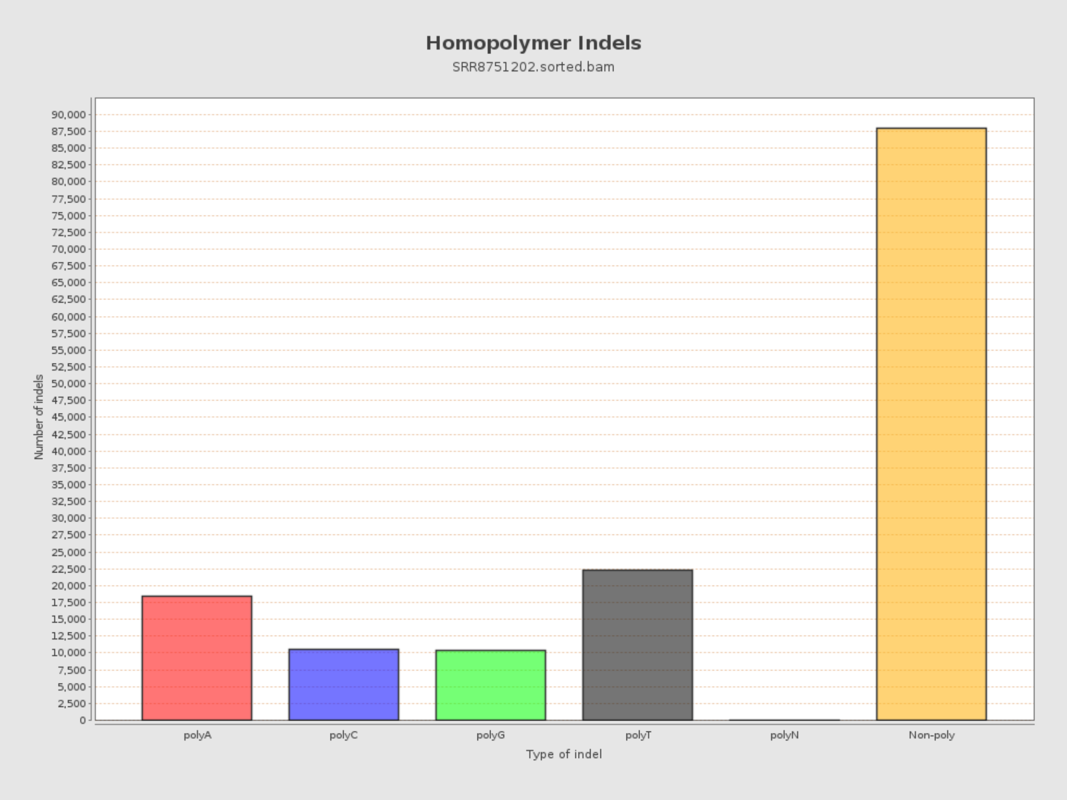
9. Results : Mapped Reads GC-content Distribution



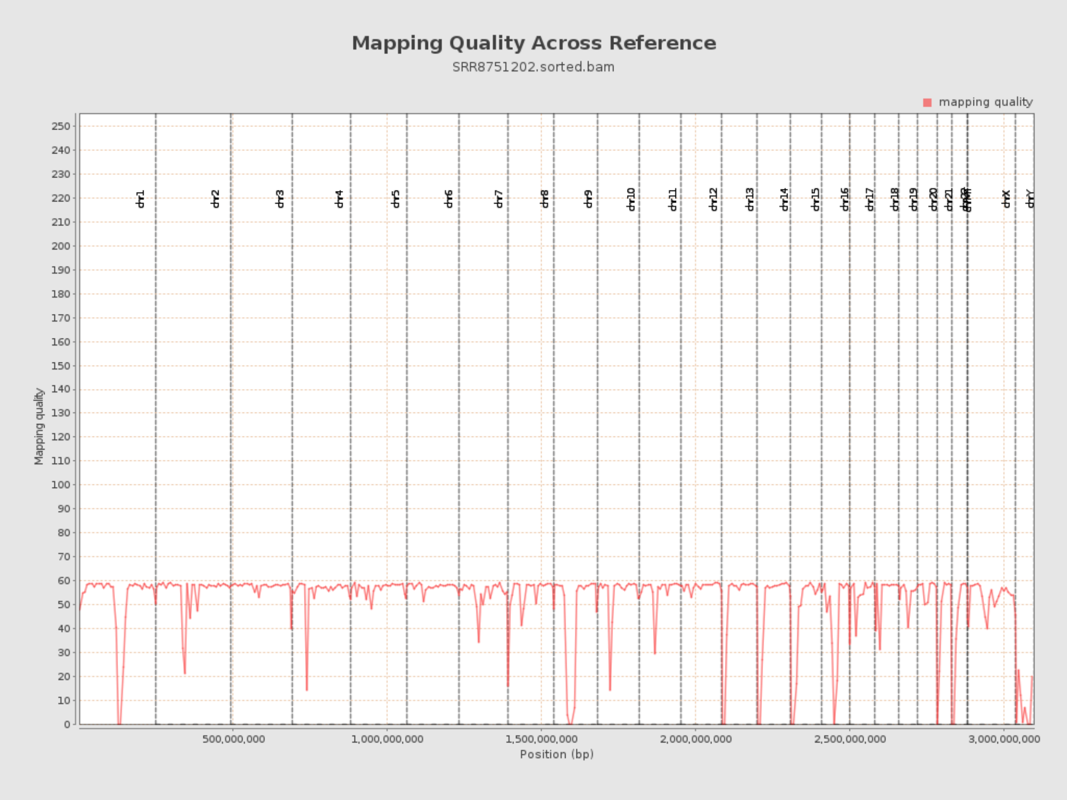
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram