Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 16:50:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751186.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_SRR8751186 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751186.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 16:50:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751186.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,001,127
Mapped reads	4,381,128 / 87.6%
Unmapped reads	619,999 / 12.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	157,554 / 3.15%
Read min/max/mean length	30 / 101 / 102.3
Duplicated reads (estimated)	141,929 / 2.84%
Duplication rate	1.69%
Clipped reads	877,524 / 17.55%

2.2. ACGT Content

Number/percentage of A's	125,866,175 / 29.29%
Number/percentage of C's	88,923,844 / 20.69%
Number/percentage of T's	126,621,996 / 29.47%
Number/percentage of G's	88,292,845 / 20.55%
Number/percentage of N's	2,378 / 0%
GC Percentage	41.24%

2.3. Coverage

Mean	0.1388

Standard Deviation	1.4229

2.4. Mapping Quality

Mean Mapping Quality	51.2

2.5. Mismatches and indels

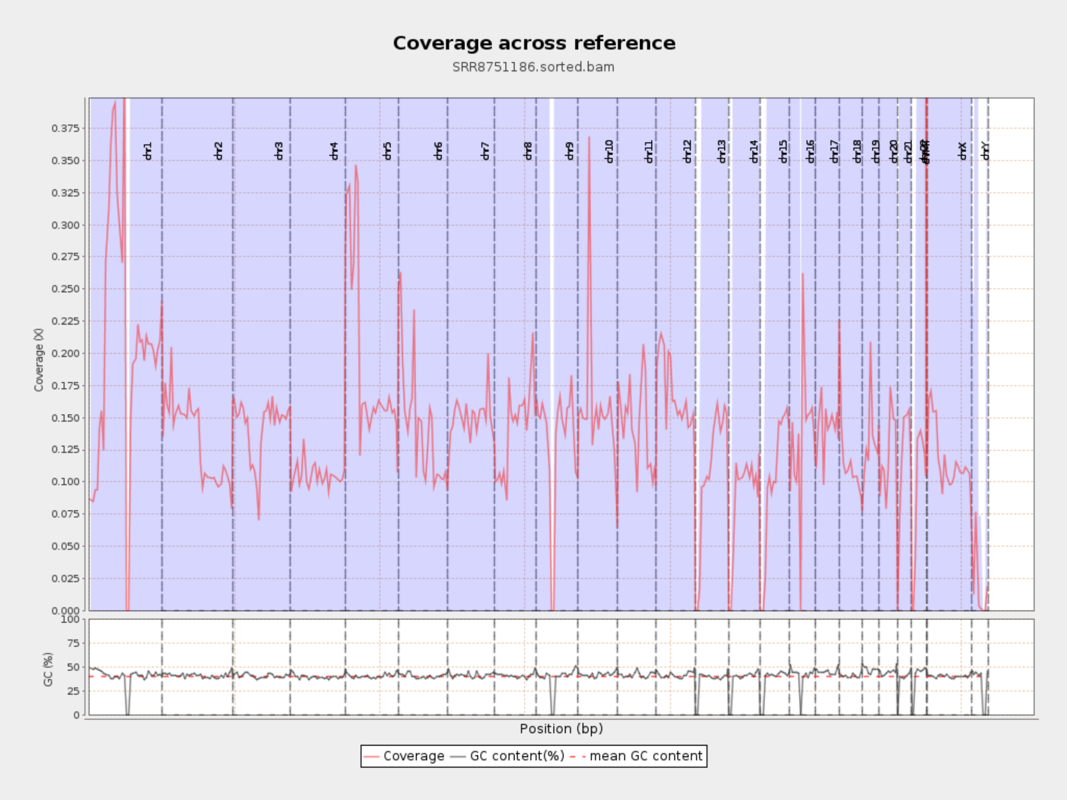
General error rate	0.42%
Mismatches	1,638,929
Insertions	108,736
Mapped reads with at least one insertion	2.43%
Deletions	58,867
Mapped reads with at least one deletion	1.32%
Homopolymer indels	48.91%

2.6. Chromosome stats

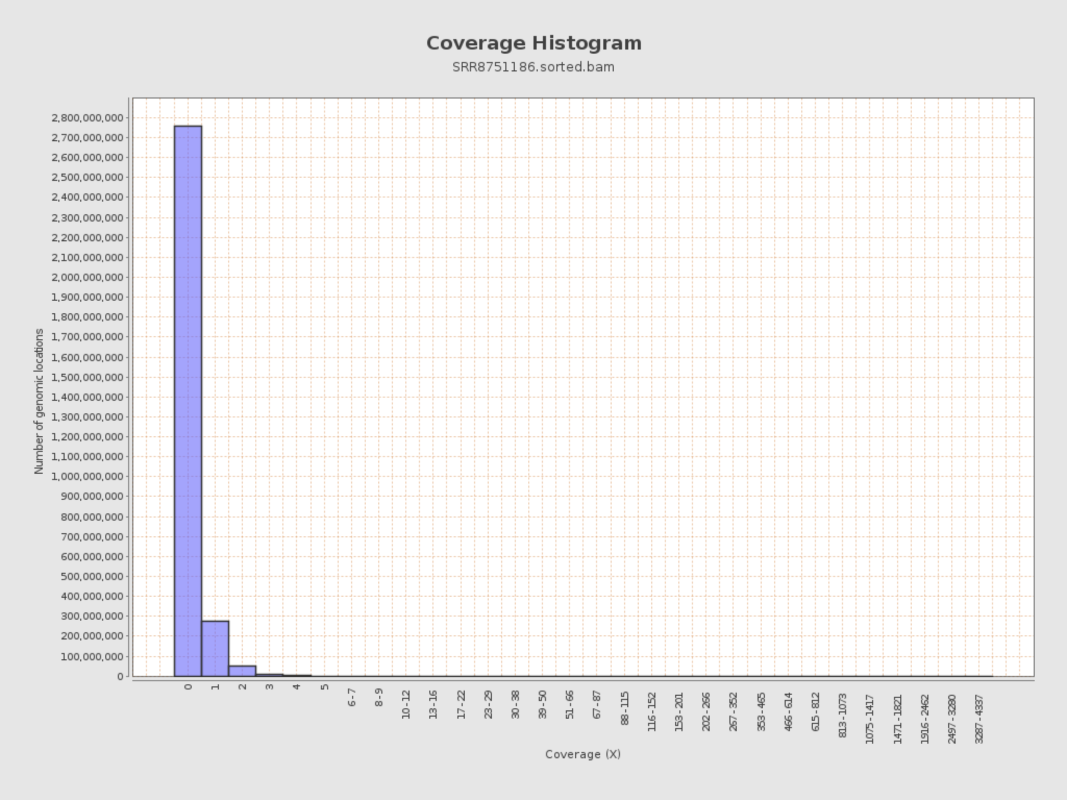
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	51917951	0.2083	4.0412
chr2	243199373	32175709	0.1323	0.5917
chr3	198022430	28246225	0.1426	0.5148
chr4	191154276	20070004	0.105	0.482
chr5	180915260	34966342	0.1933	0.5284
chr6	171115067	24643911	0.144	0.9489
chr7	159138663	24038980	0.1511	0.7922

chr8	146364022	20972291	0.1433	0.5253
chr9	141213431	18567932	0.1315	0.7234
chr10	135534747	21583387	0.1592	2.0301
chr11	135006516	19424916	0.1439	0.6934
chr12	133851895	22683185	0.1695	0.4886
chr13	115169878	12434726	0.108	0.3816
chr14	107349540	9318234	0.0868	0.3758
chr15	102531392	10231676	0.0998	0.3675
chr16	90354753	12091230	0.1338	0.9987
chr17	81195210	11508627	0.1417	0.6906
chr18	78077248	8965278	0.1148	1.3843
chr19	59128983	7834044	0.1325	2.7675
chr20	63025520	7622575	0.1209	0.4261
chr21	48129895	5563632	0.1156	0.4519
chr22	51304566	4601564	0.0897	0.3545
chrMT	16571	978213	59.0316	25.9662
chrX	155270560	18310109	0.1179	0.4714
chrY	59373566	1085228	0.0183	0.7014

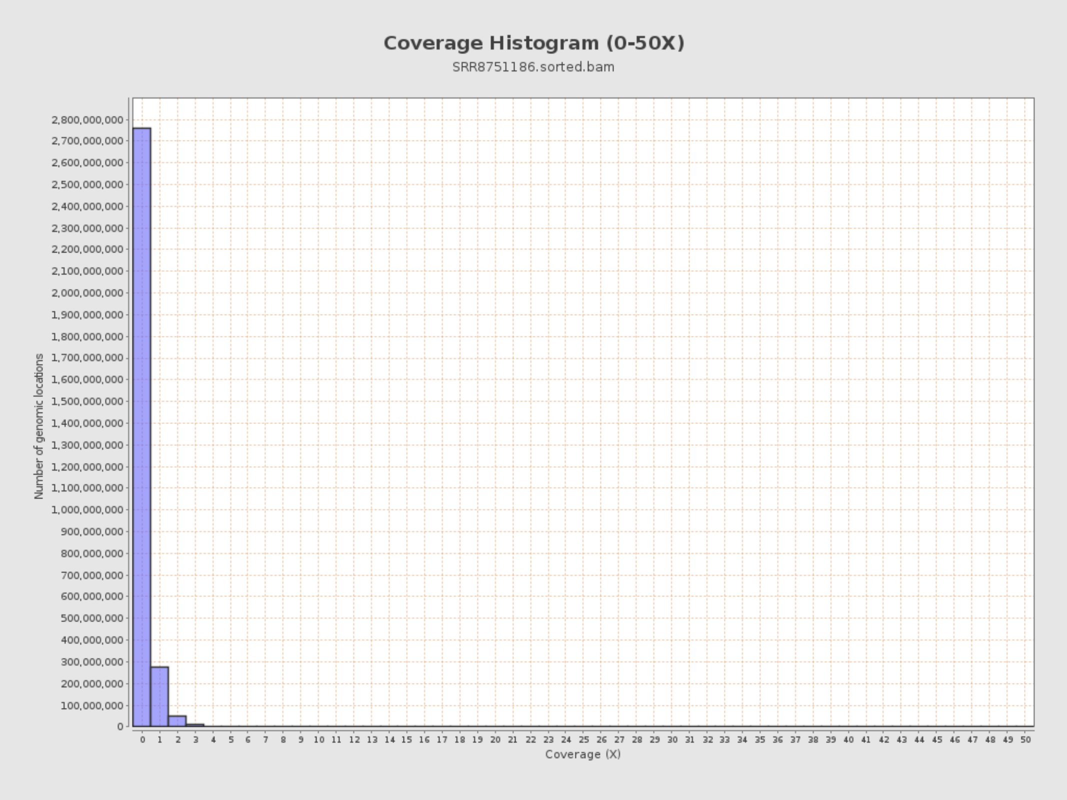
3. Results : Coverage across reference



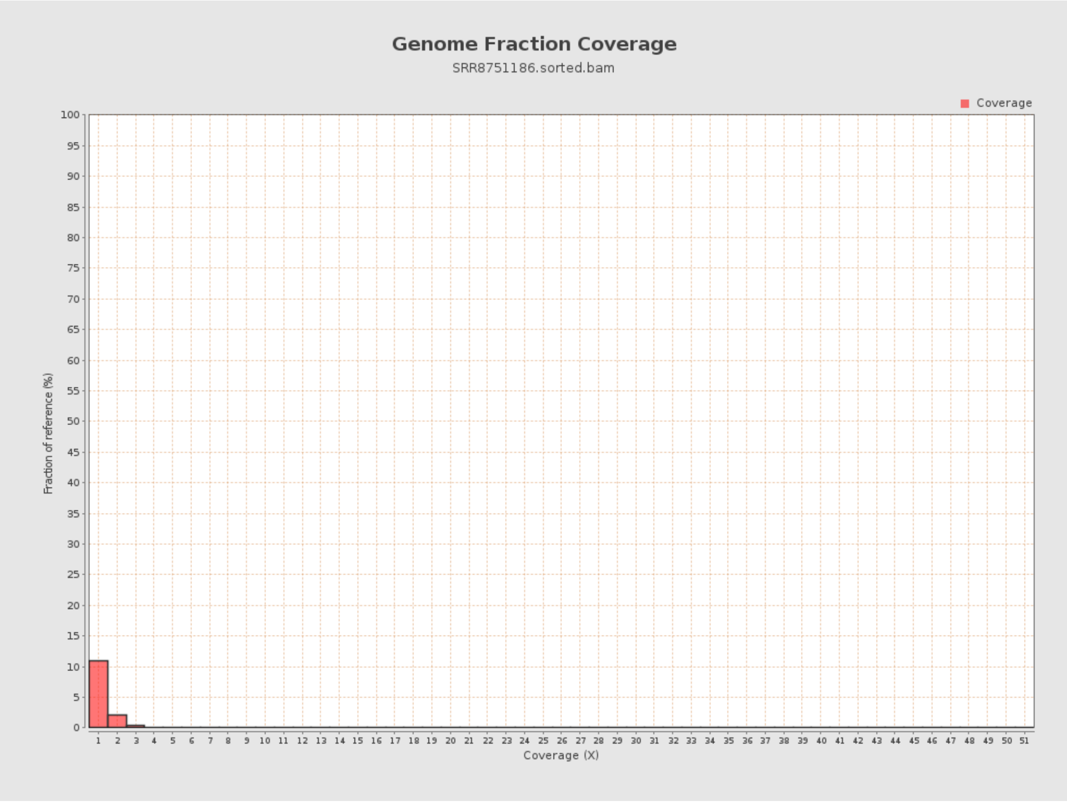
4. Results : Coverage Histogram



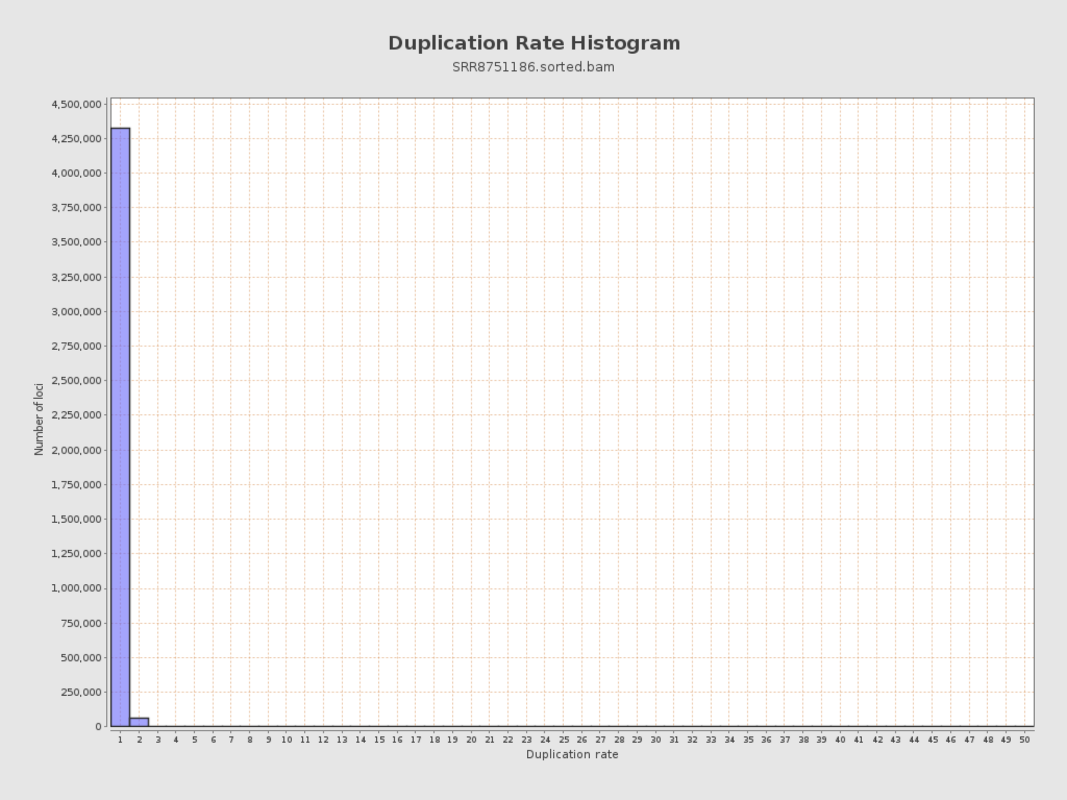
5. Results : Coverage Histogram (0-50X)



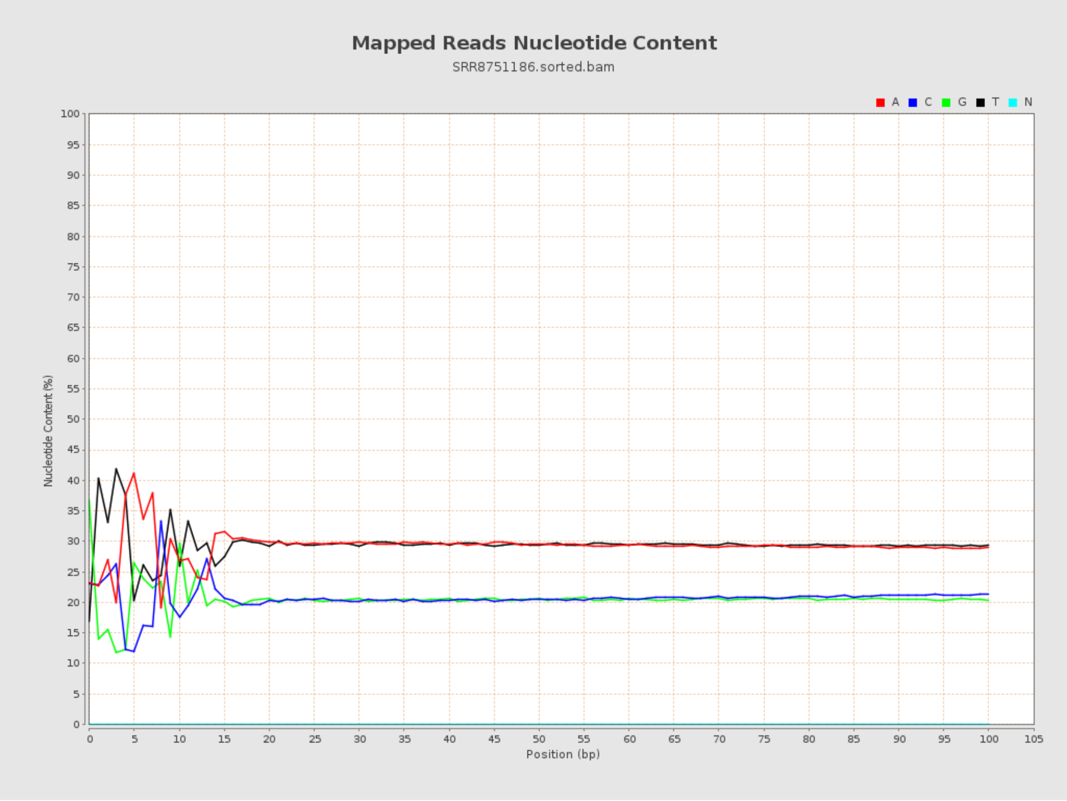
6. Results : Genome Fraction Coverage



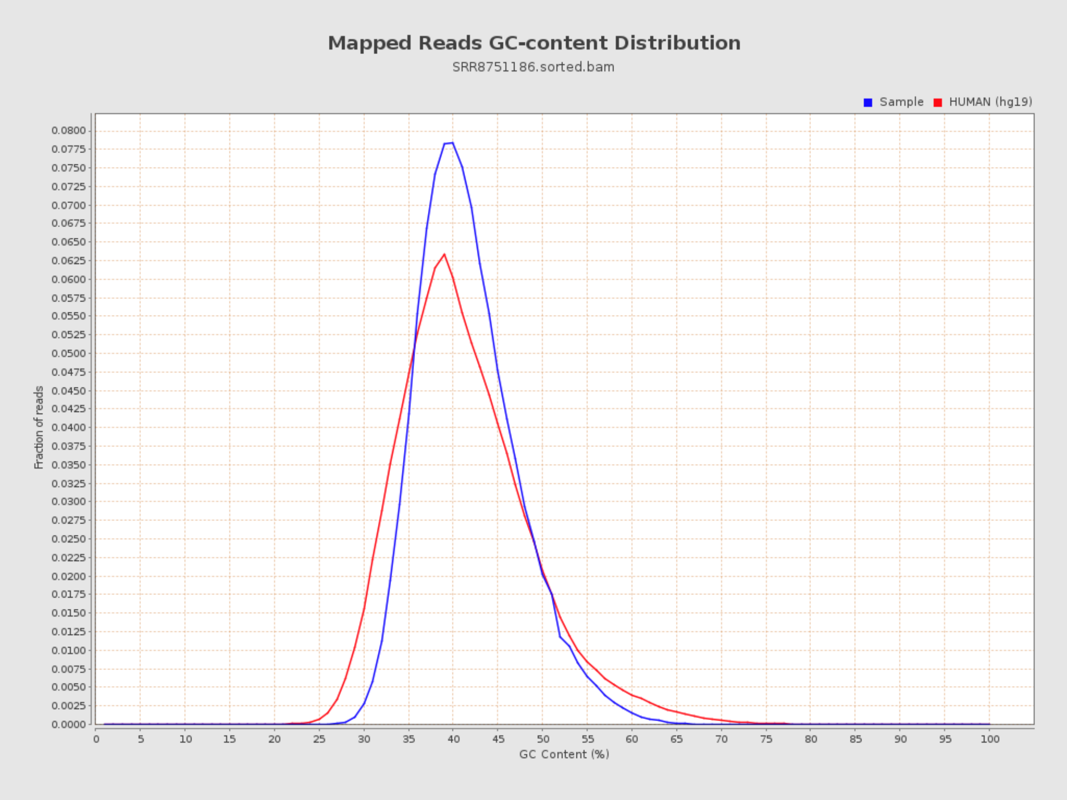
7. Results : Duplication Rate Histogram



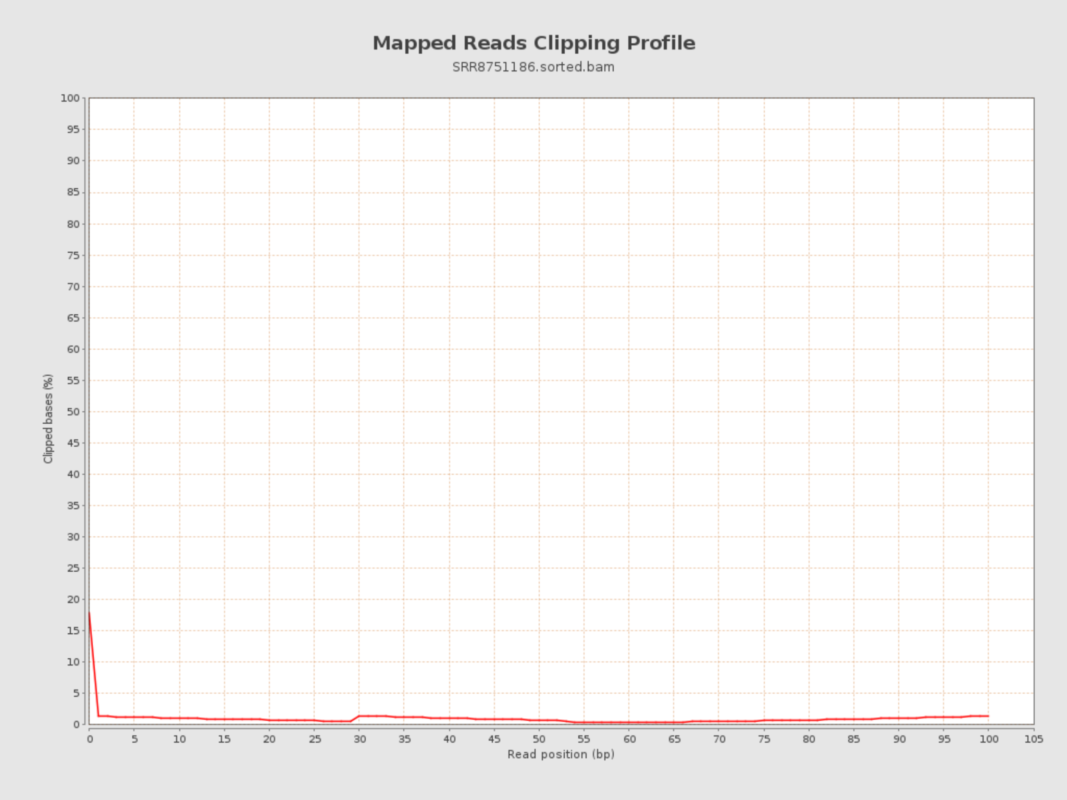
8. Results : Mapped Reads Nucleotide Content



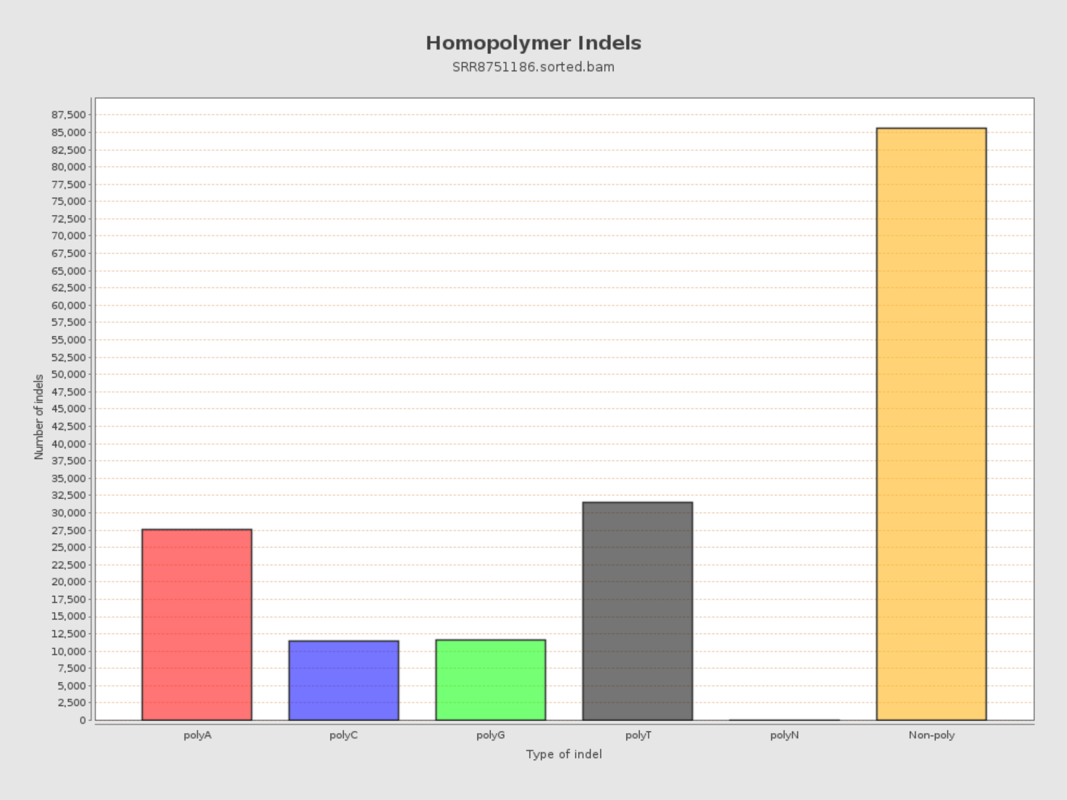
9. Results : Mapped Reads GC-content Distribution



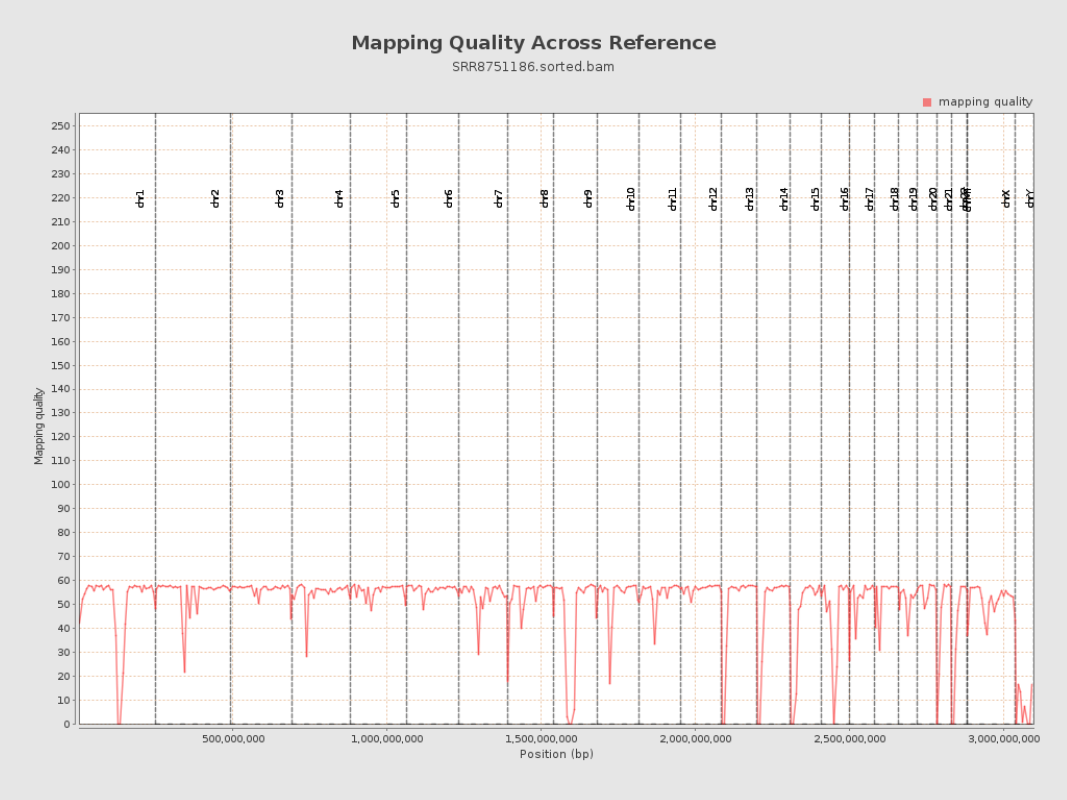
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram