Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 15:45:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751177.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_SRR8751177 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751177.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 15:45:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751177.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,550,290
Mapped reads	4,416,507 / 79.57%
Unmapped reads	1,133,783 / 20.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	251,581 / 4.53%
Read min/max/mean length	30 / 101 / 102.87
Duplicated reads (estimated)	173,569 / 3.13%
Duplication rate	1.86%
Clipped reads	1,137,954 / 20.5%

2.2. ACGT Content

Number/percentage of A's	128,693,459 / 29.77%
Number/percentage of C's	87,452,831 / 20.23%
Number/percentage of T's	129,361,535 / 29.93%
Number/percentage of G's	86,755,720 / 20.07%
Number/percentage of N's	3,109 / 0%
GC Percentage	40.3%

2.3. Coverage

Mean	0.1397

Standard Deviation	1.7823

2.4. Mapping Quality

Mean Mapping Quality	50.87

2.5. Mismatches and indels

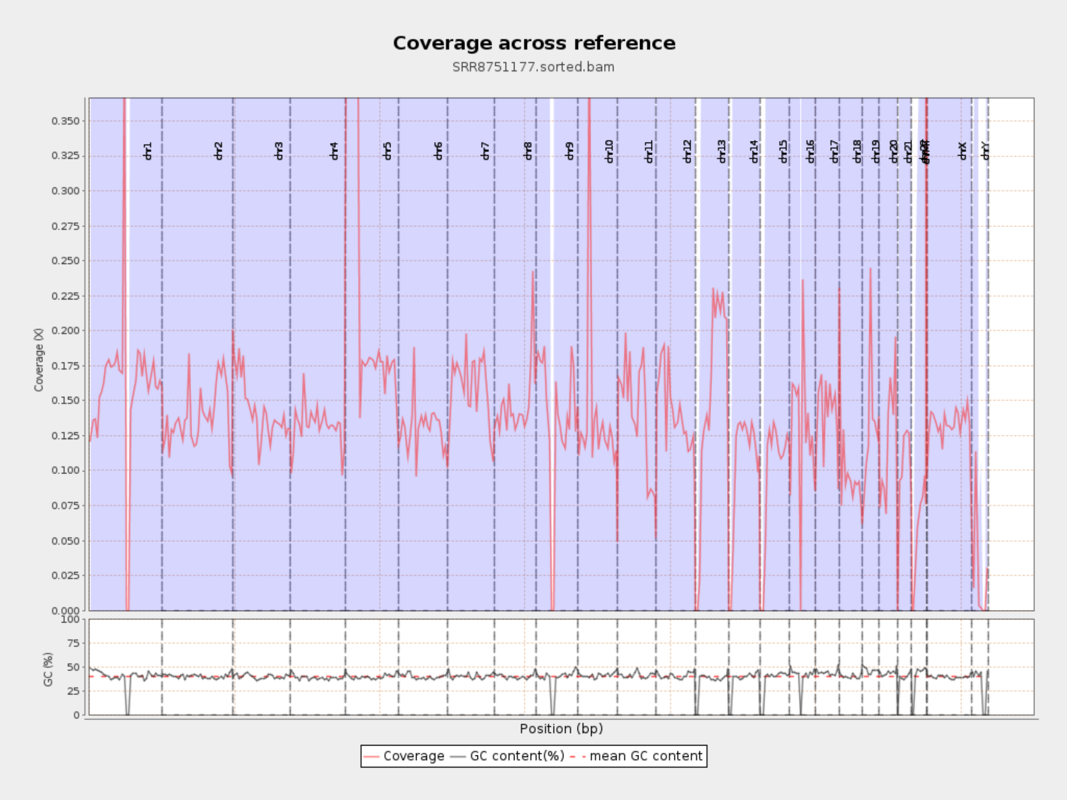
General error rate	0.5%
Mismatches	1,757,480
Insertions	278,400
Mapped reads with at least one insertion	6.06%
Deletions	68,700
Mapped reads with at least one deletion	1.52%
Homopolymer indels	52.19%

2.6. Chromosome stats

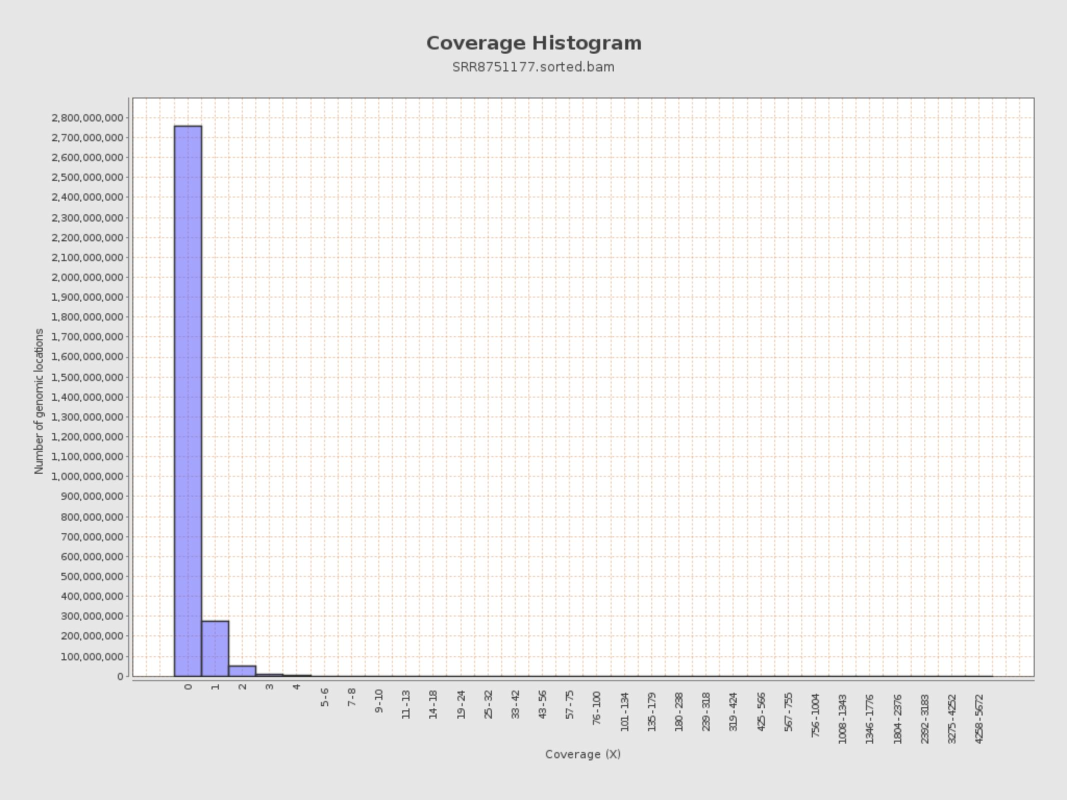
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	40141449	0.161	5.1705
chr2	243199373	33776075	0.1389	0.7173
chr3	198022430	28417022	0.1435	0.598
chr4	191154276	25220344	0.1319	0.5666
chr5	180915260	44211951	0.2444	0.6063
chr6	171115067	22347366	0.1306	0.7653
chr7	159138663	25573601	0.1607	0.9899

chr8	146364022	21623427	0.1477	1.1376
chr9	141213431	19178620	0.1358	0.9041
chr10	135534747	18963309	0.1399	2.4744
chr11	135006516	18947632	0.1403	0.6865
chr12	133851895	19174329	0.1433	0.4589
chr13	115169878	17460650	0.1516	0.4608
chr14	107349540	11113862	0.1035	0.4174
chr15	102531392	10007541	0.0976	0.3638
chr16	90354753	11762304	0.1302	0.9725
chr17	81195210	11415143	0.1406	0.7098
chr18	78077248	7681512	0.0984	1.9681
chr19	59128983	7793202	0.1318	3.5156
chr20	63025520	7670073	0.1217	0.4389
chr21	48129895	4821697	0.1002	0.4622
chr22	51304566	2808763	0.0547	0.2755
chrMT	16571	236994	14.3017	8.1655
chrX	155270560	20606523	0.1327	0.5033
chrY	59373566	1467652	0.0247	1.1093

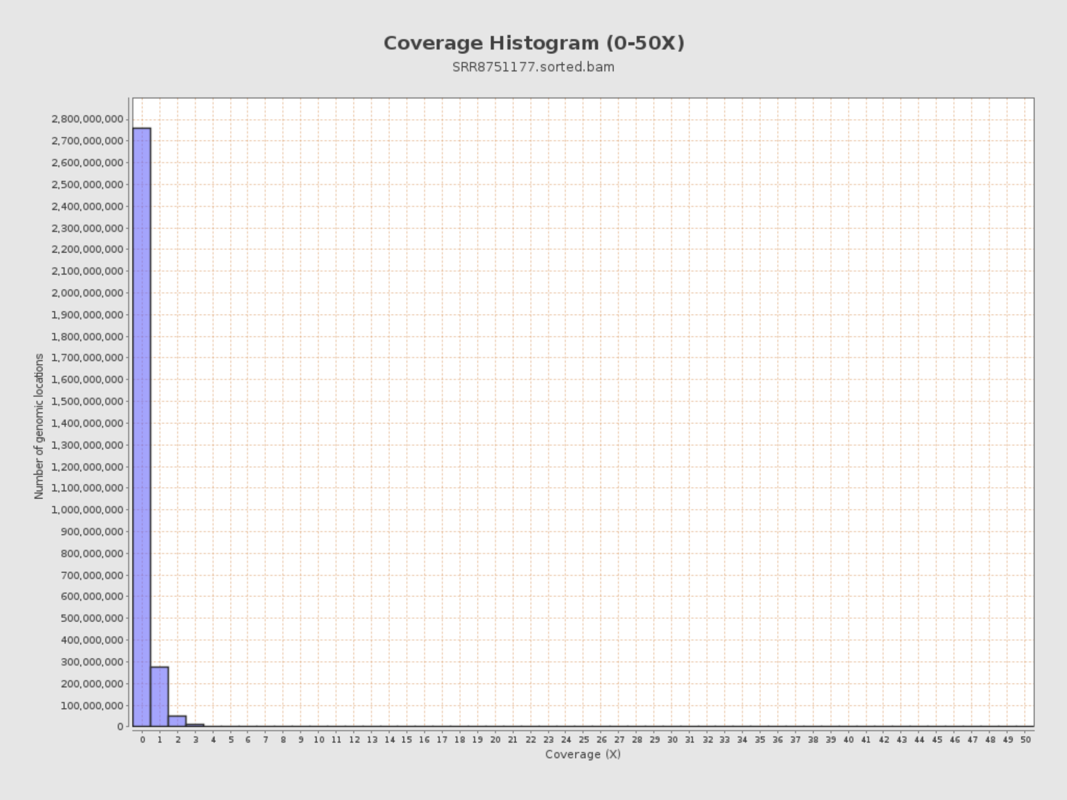
3. Results : Coverage across reference



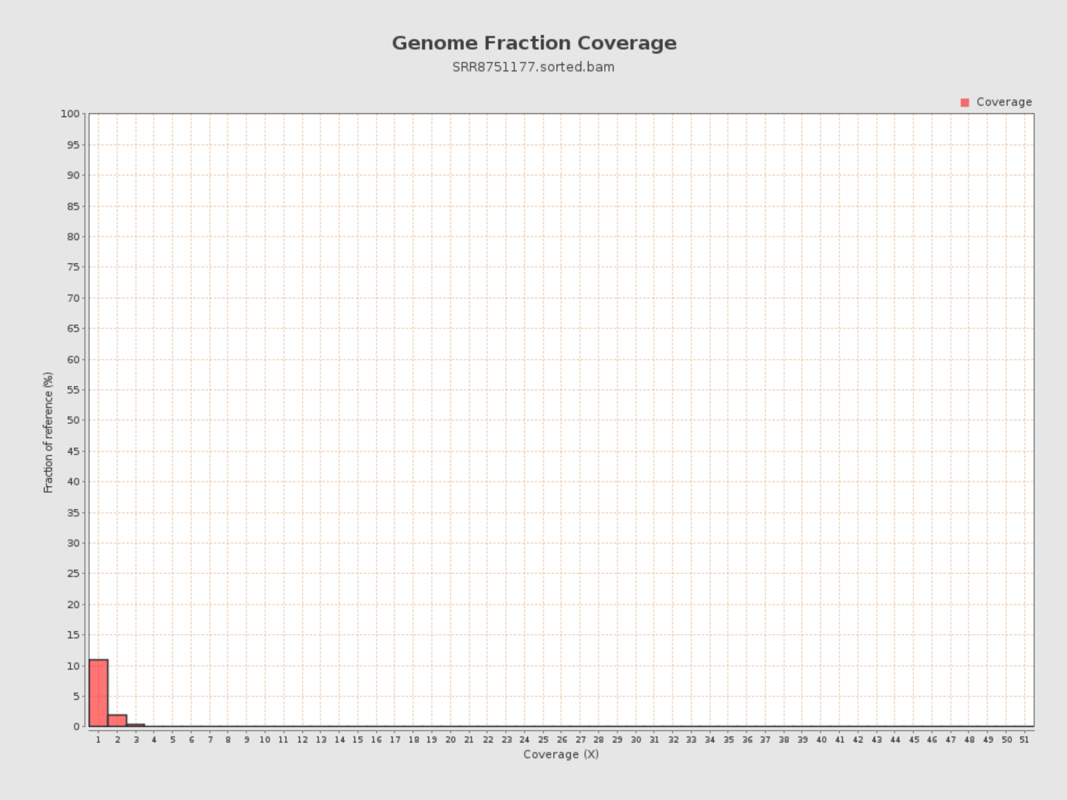
4. Results : Coverage Histogram



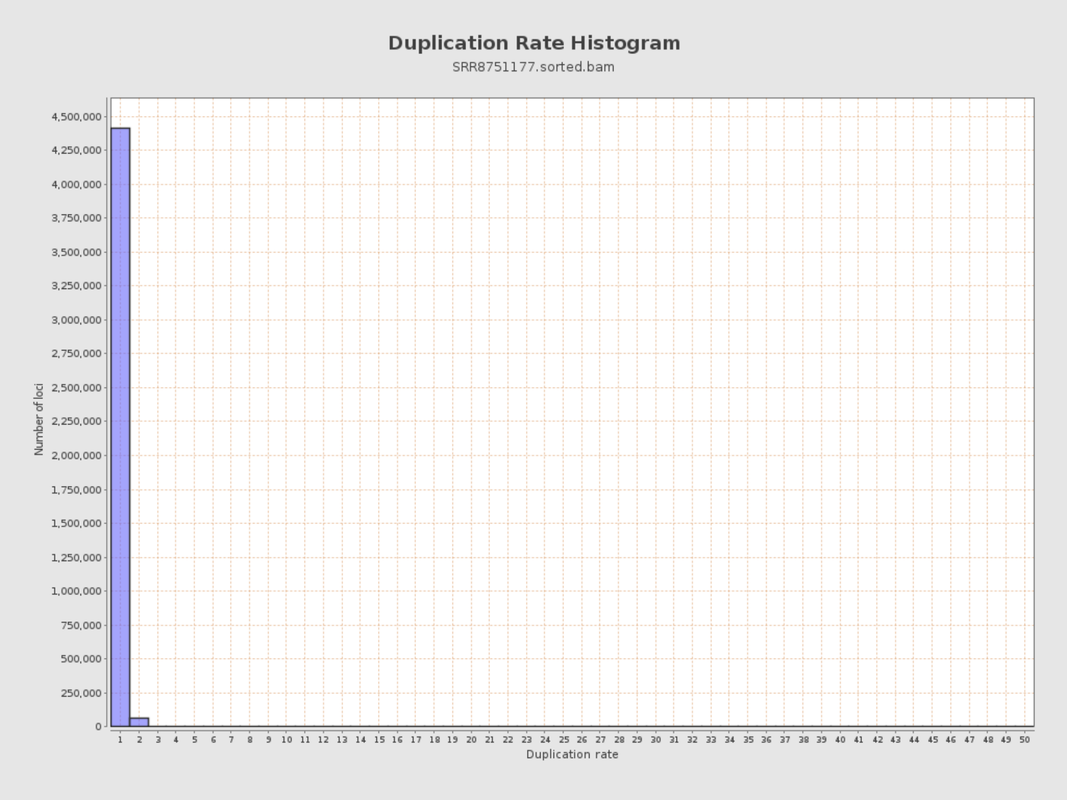
5. Results : Coverage Histogram (0-50X)



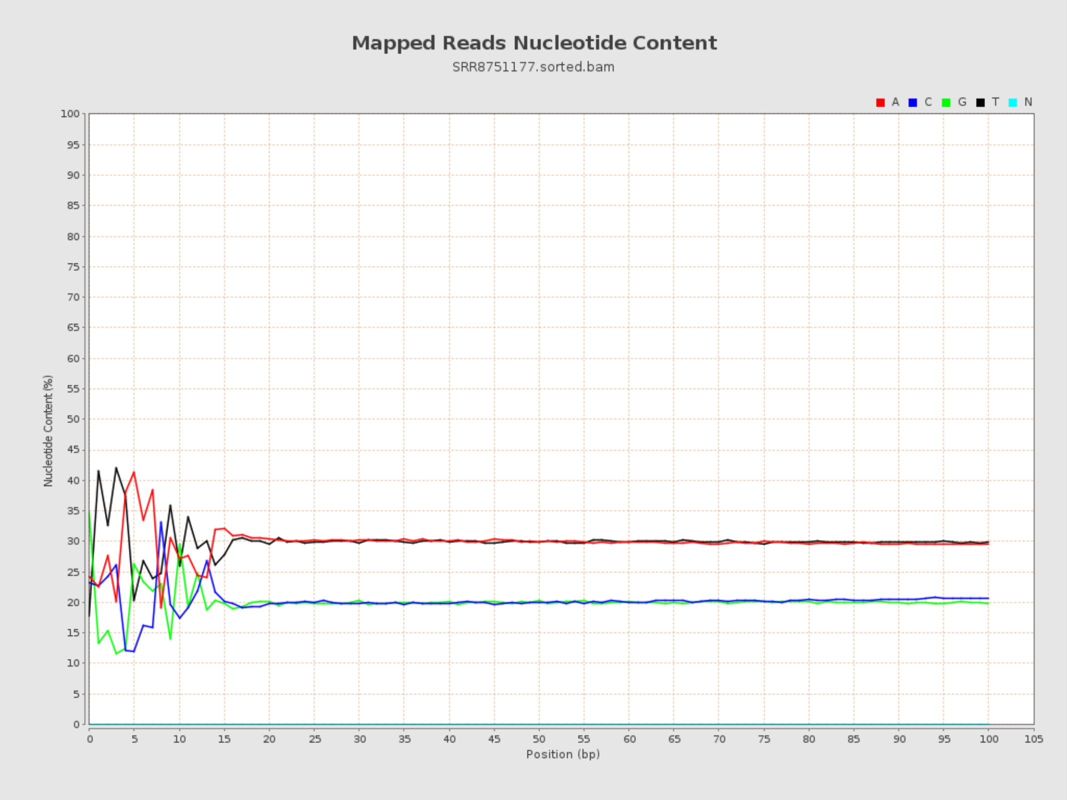
6. Results : Genome Fraction Coverage



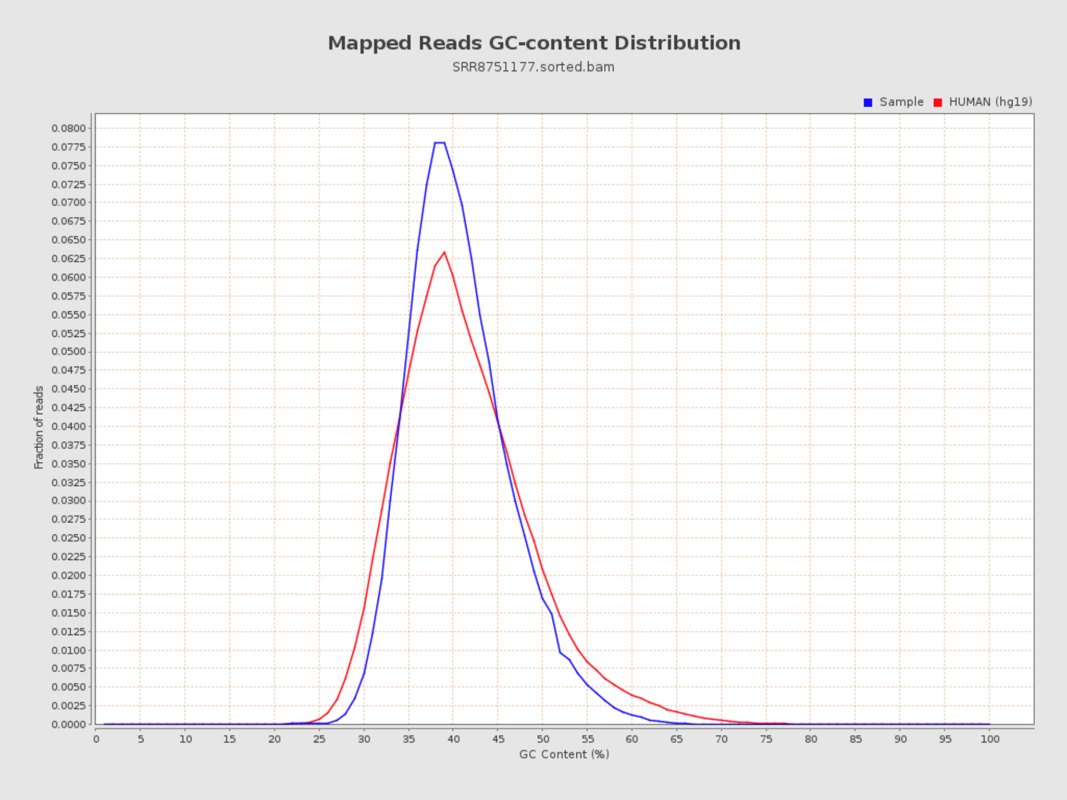
7. Results : Duplication Rate Histogram



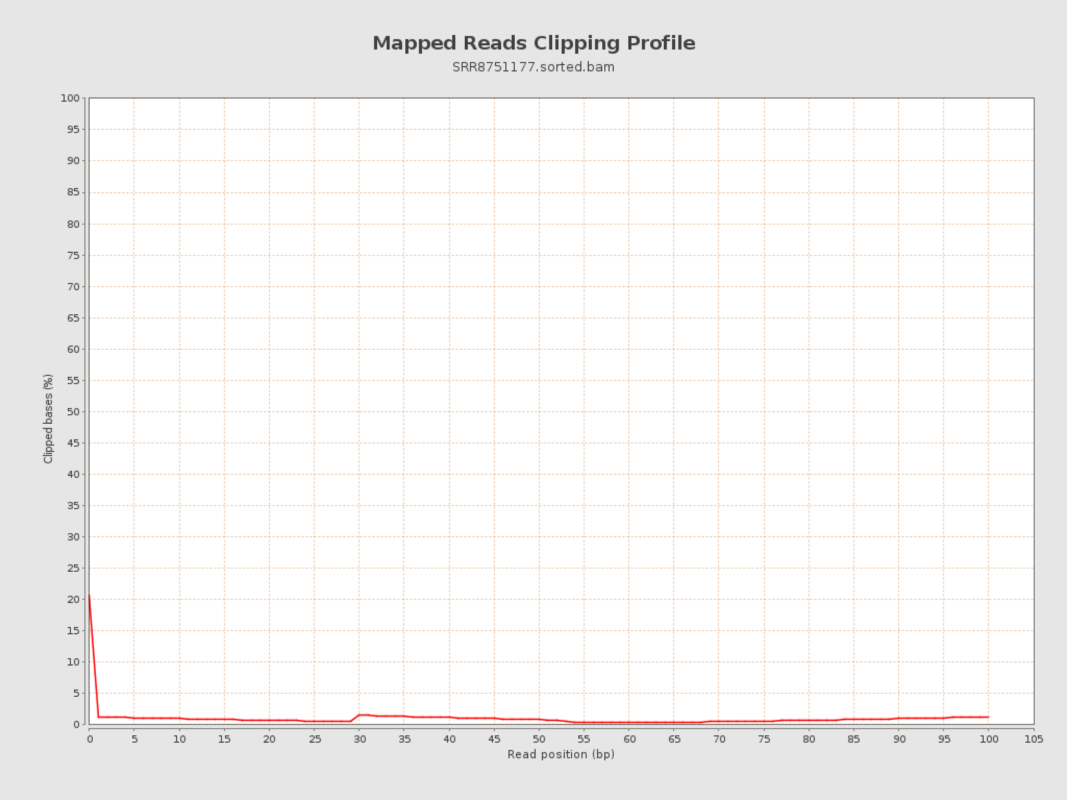
8. Results : Mapped Reads Nucleotide Content



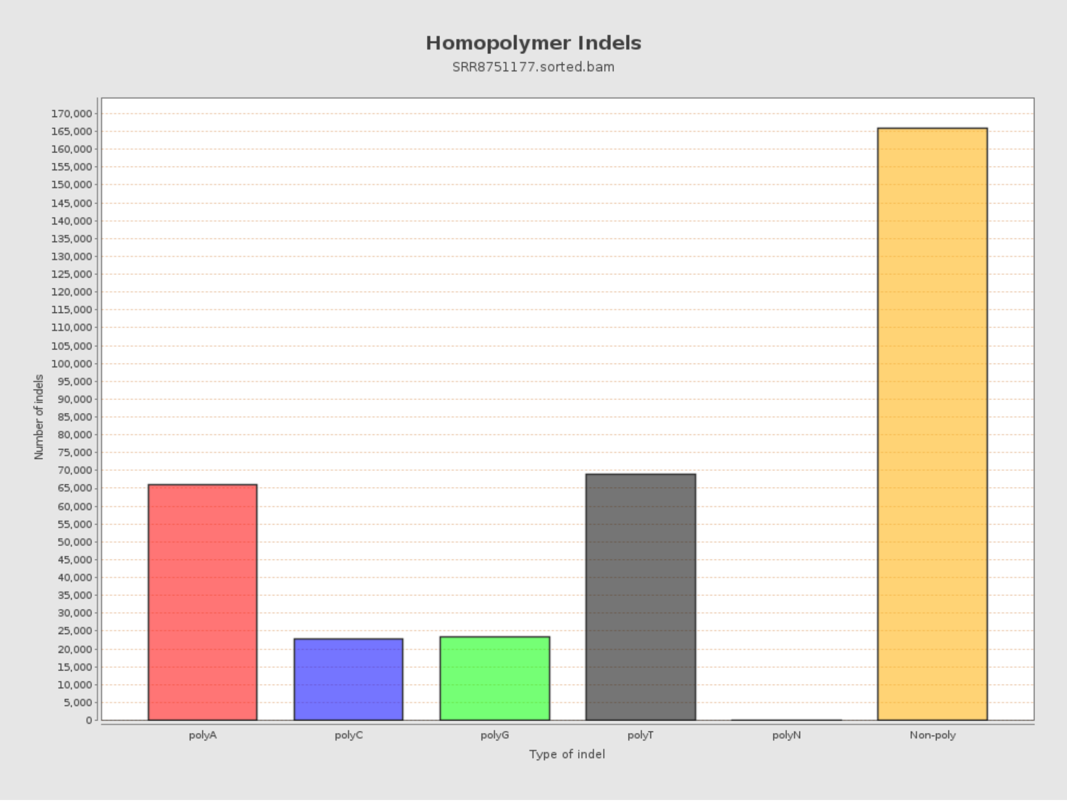
9. Results : Mapped Reads GC-content Distribution



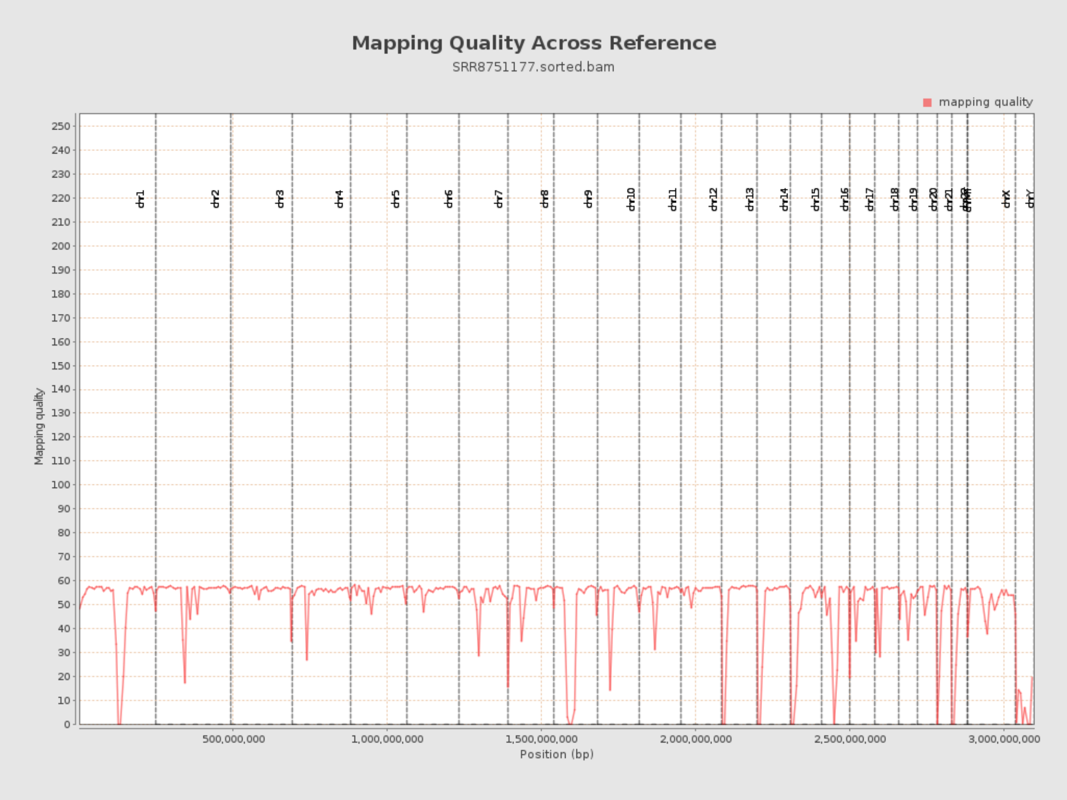
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram