Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 14:56:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751170.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_SRR8751170 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751170.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 14:56:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751170.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,871,480
Mapped reads	7,822,051 / 99.37%
Unmapped reads	49,429 / 0.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	68,627 / 0.87%
Read min/max/mean length	30 / 151 / 151.42
Duplicated reads (estimated)	1,274,809 / 16.2%
Duplication rate	14.92%
Clipped reads	4,348,640 / 55.25%

2.2. ACGT Content

Number/percentage of A's	309,698,284 / 30.1%
Number/percentage of C's	205,112,935 / 19.94%
Number/percentage of T's	310,020,522 / 30.13%
Number/percentage of G's	203,984,549 / 19.83%
Number/percentage of N's	30,588 / 0%
GC Percentage	39.76%

2.3. Coverage

Mean	0.3325

Standard Deviation	1.8025

2.4. Mapping Quality

Mean Mapping Quality	51.6

2.5. Mismatches and indels

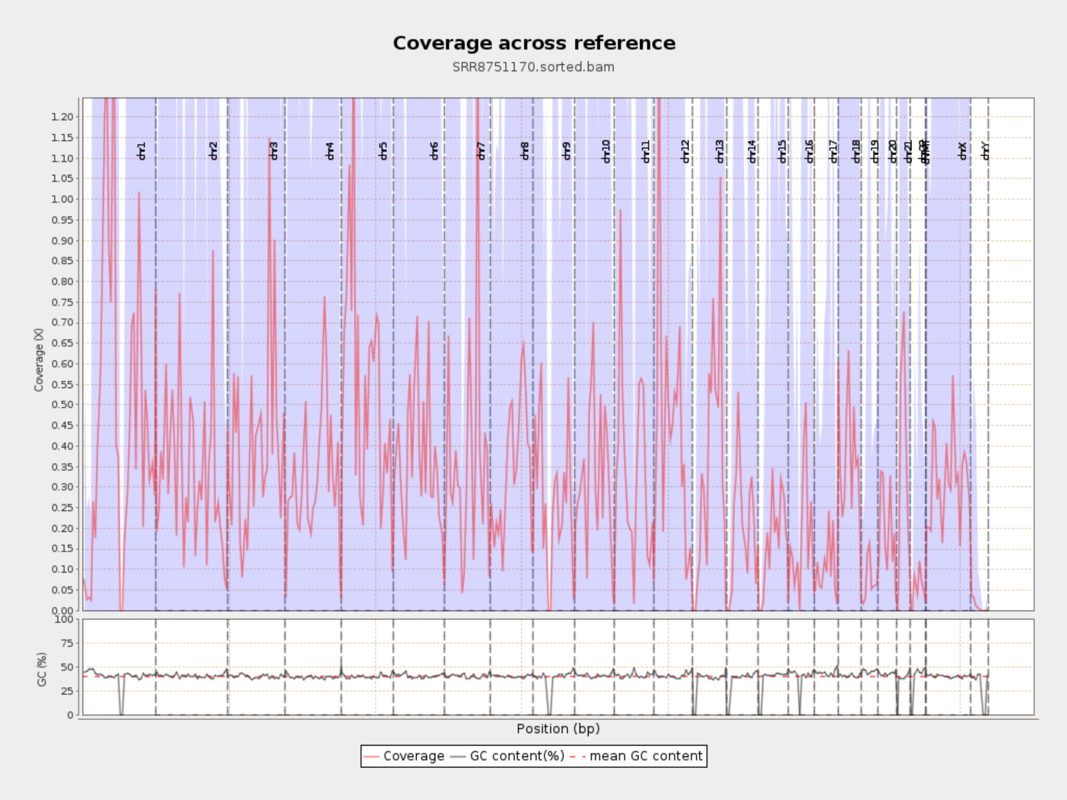
General error rate	1.68%
Mismatches	17,050,602
Insertions	116,866
Mapped reads with at least one insertion	1.47%
Deletions	194,261
Mapped reads with at least one deletion	2.41%
Homopolymer indels	41.02%

2.6. Chromosome stats

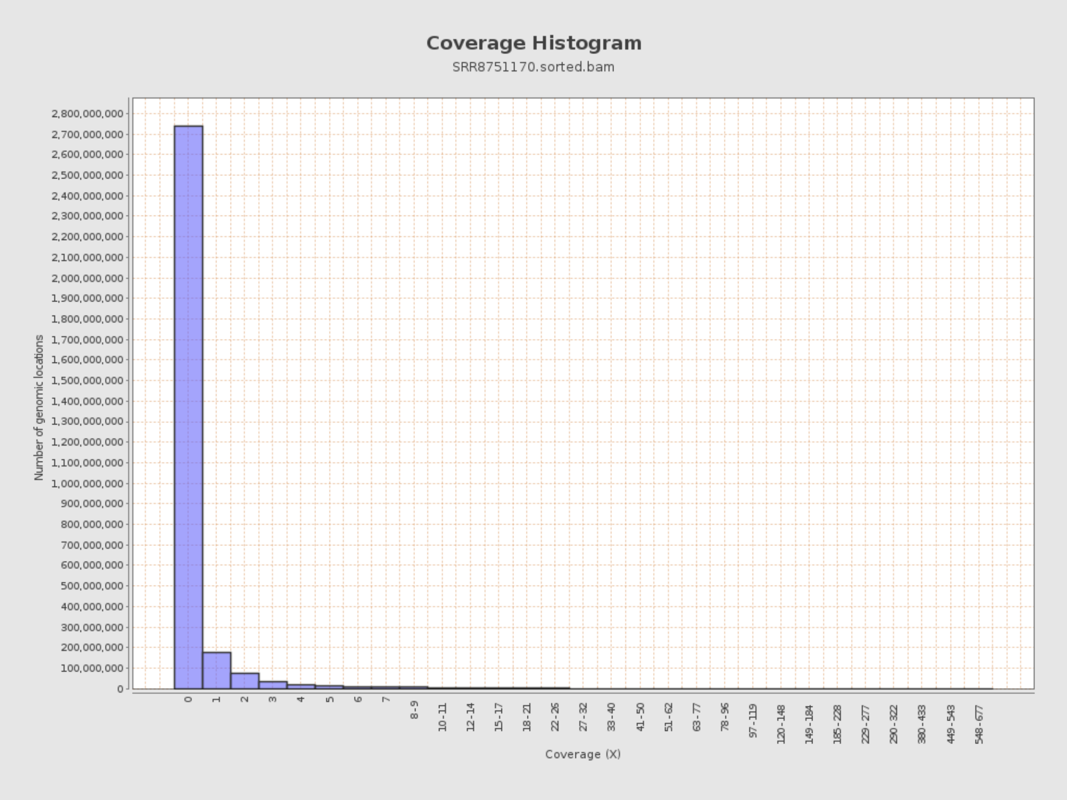
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	120999992	0.4855	1.9391
chr2	243199373	80736086	0.332	2.1631
chr3	198022430	80547728	0.4068	2.059
chr4	191154276	62976338	0.3295	1.8881
chr5	180915260	99025767	0.5474	2.0838
chr6	171115067	63886295	0.3734	1.6734
chr7	159138663	58627128	0.3684	2.1022

chr8	146364022	51152383	0.3495	1.5533
chr9	141213431	39281933	0.2782	1.3071
chr10	135534747	45865458	0.3384	1.6915
chr11	135006516	46183607	0.3421	2.2384
chr12	133851895	59442603	0.4441	2.3356
chr13	115169878	41912966	0.3639	2.4905
chr14	107349540	22339483	0.2081	1.3117
chr15	102531392	16967603	0.1655	1.0631
chr16	90354753	16028665	0.1774	1.2847
chr17	81195210	8557954	0.1054	0.6638
chr18	78077248	29404230	0.3766	1.7064
chr19	59128983	4358605	0.0737	0.6762
chr20	63025520	12871176	0.2042	0.988
chr21	48129895	15850951	0.3293	1.6838
chr22	51304566	2885769	0.0562	0.445
chrMT	16571	1110	0.067	0.2796
chrX	155270560	48666577	0.3134	1.5929
chrY	59373566	596998	0.0101	0.2703

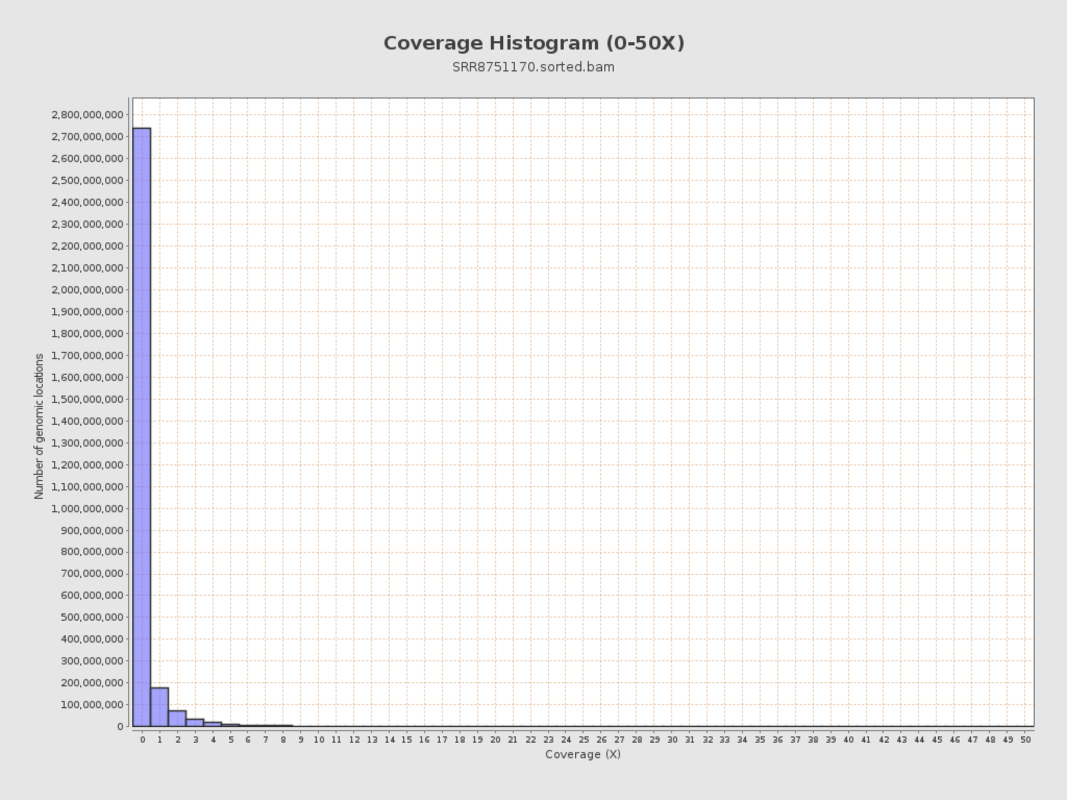
3. Results : Coverage across reference



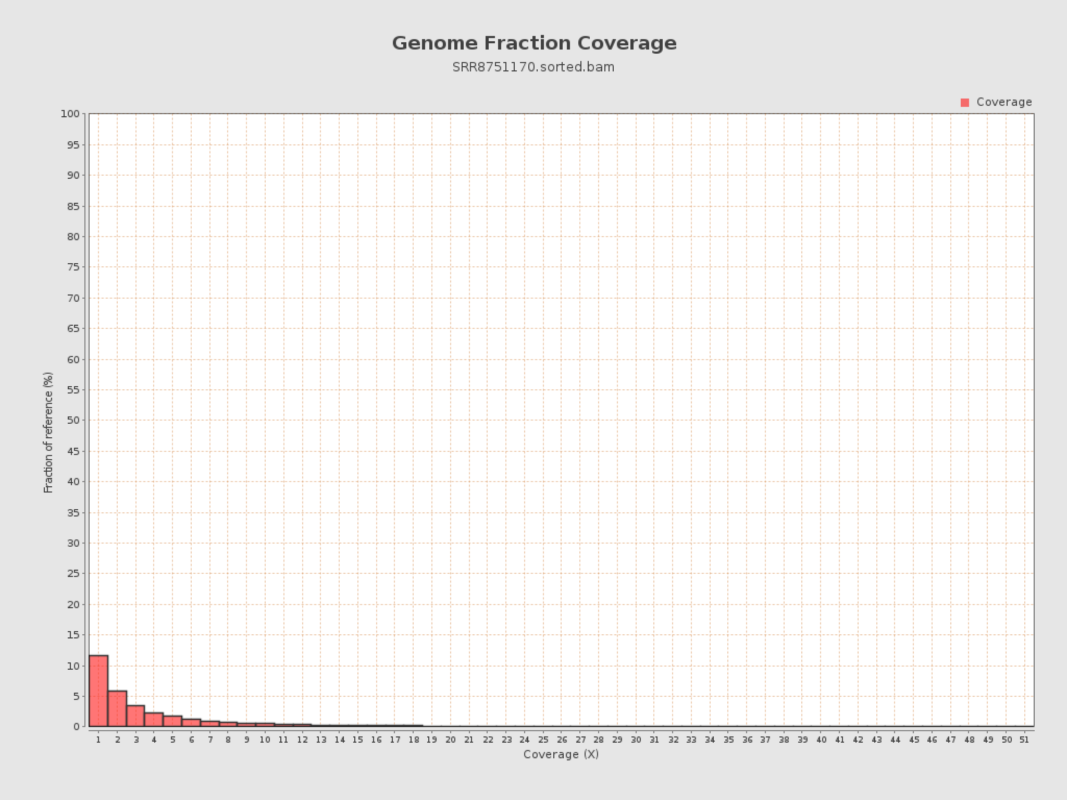
4. Results : Coverage Histogram



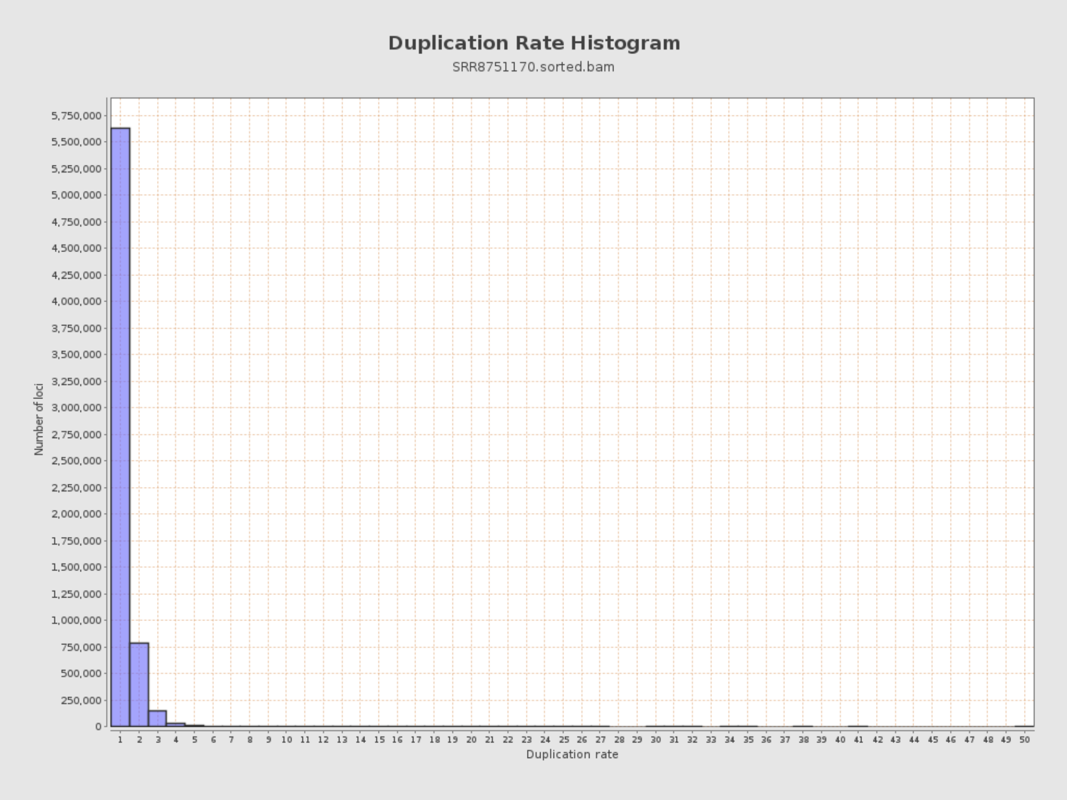
5. Results : Coverage Histogram (0-50X)



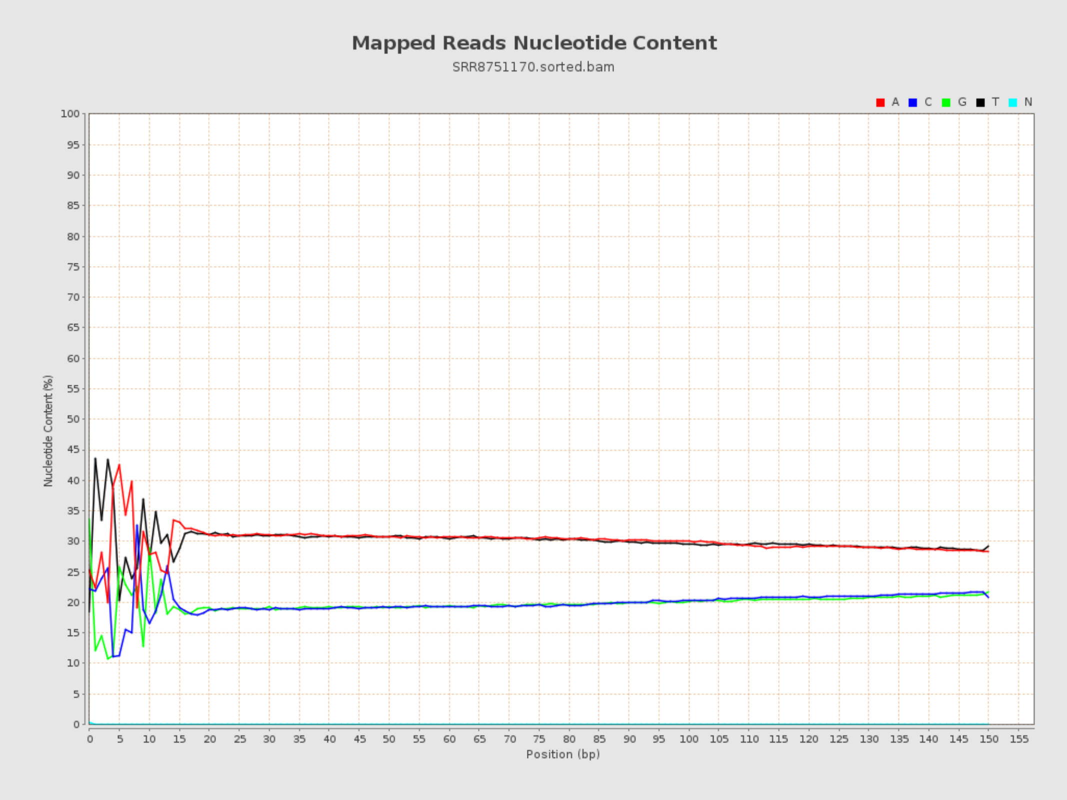
6. Results : Genome Fraction Coverage



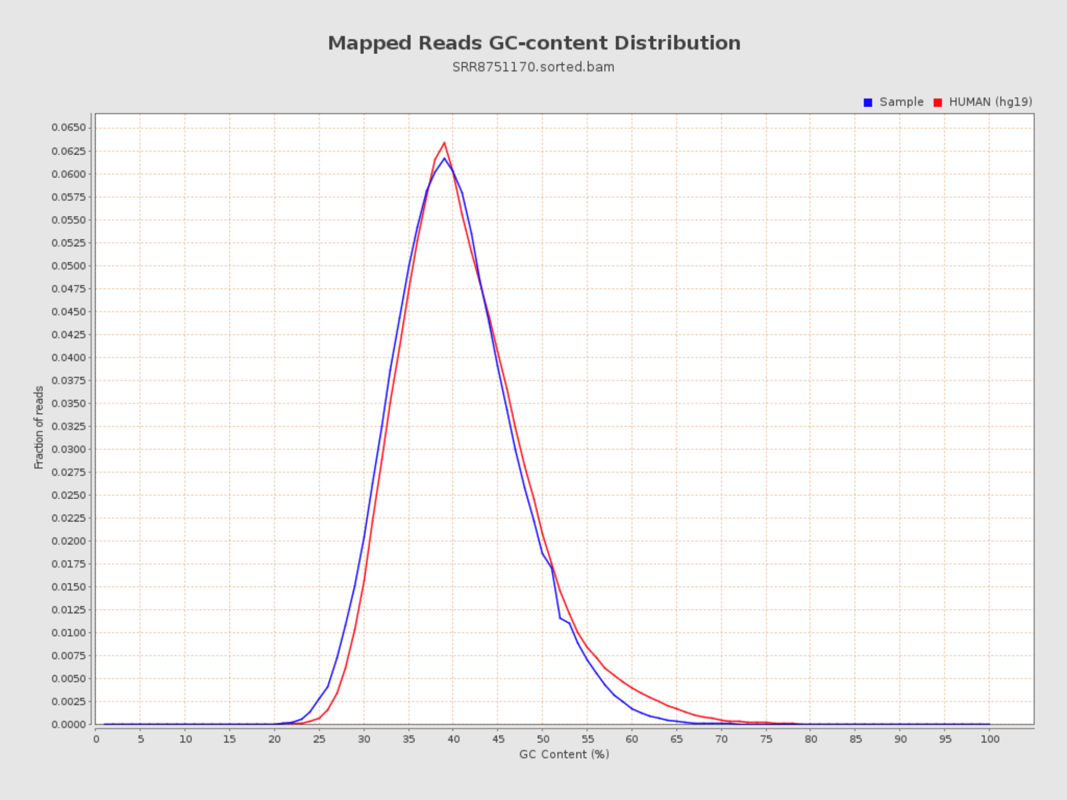
7. Results : Duplication Rate Histogram



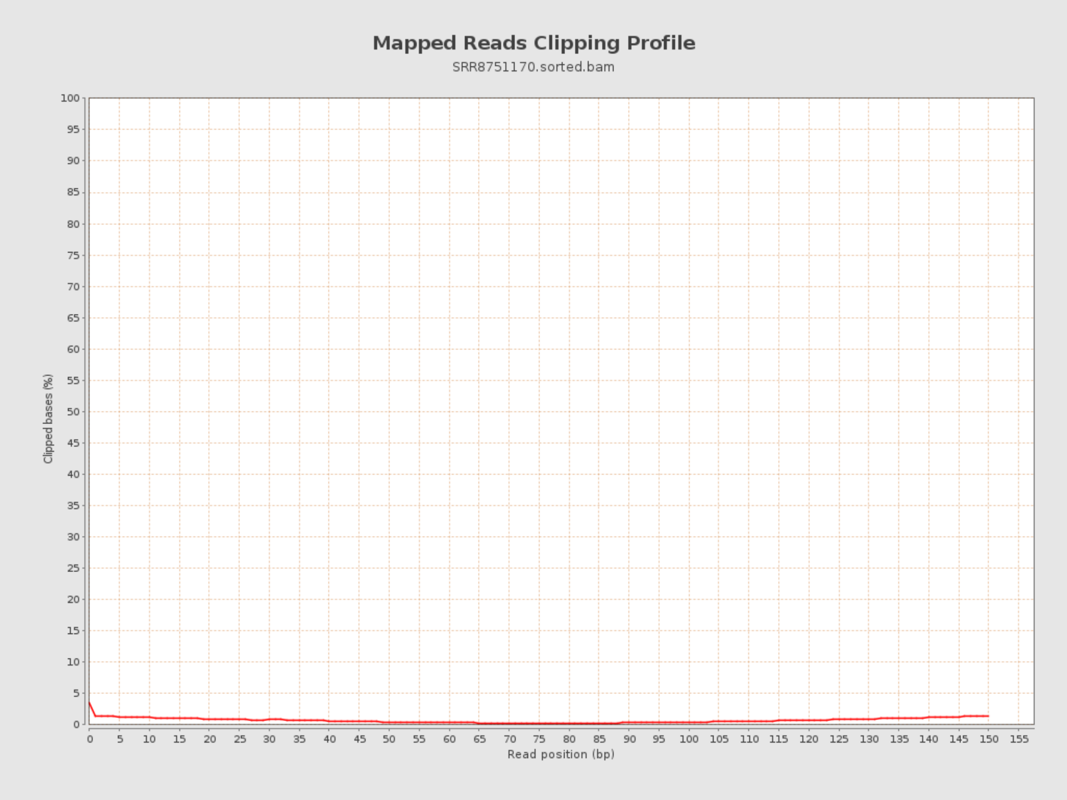
8. Results : Mapped Reads Nucleotide Content



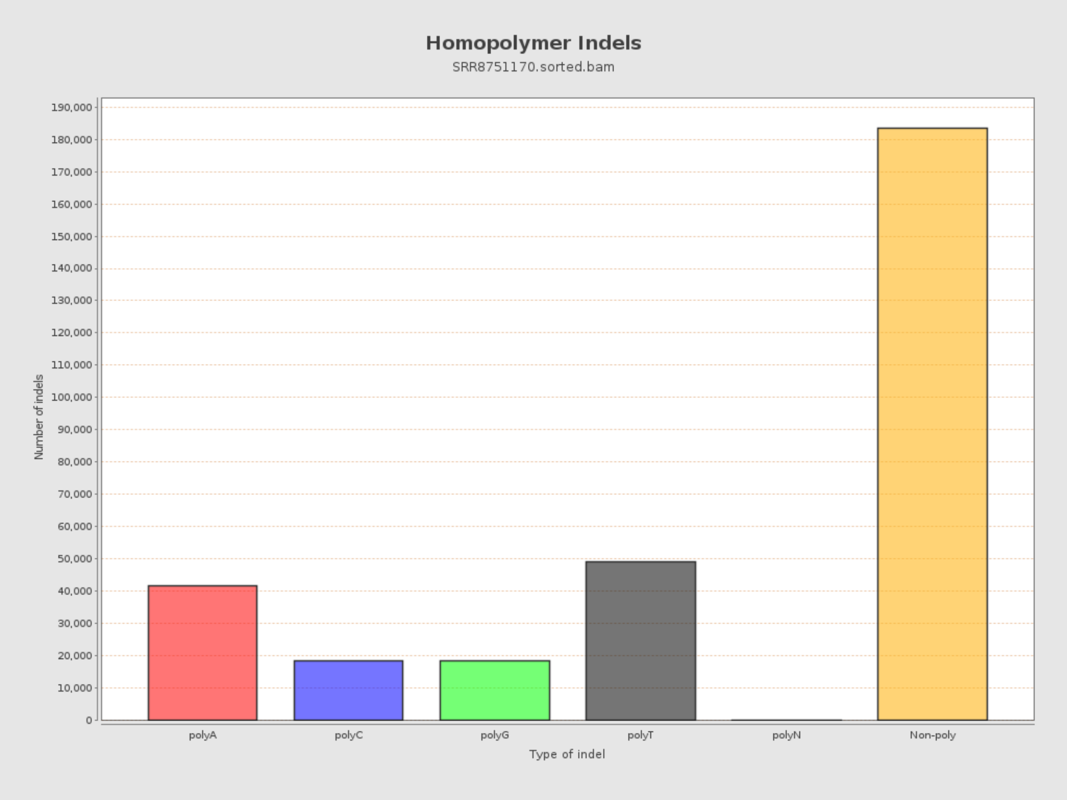
9. Results : Mapped Reads GC-content Distribution



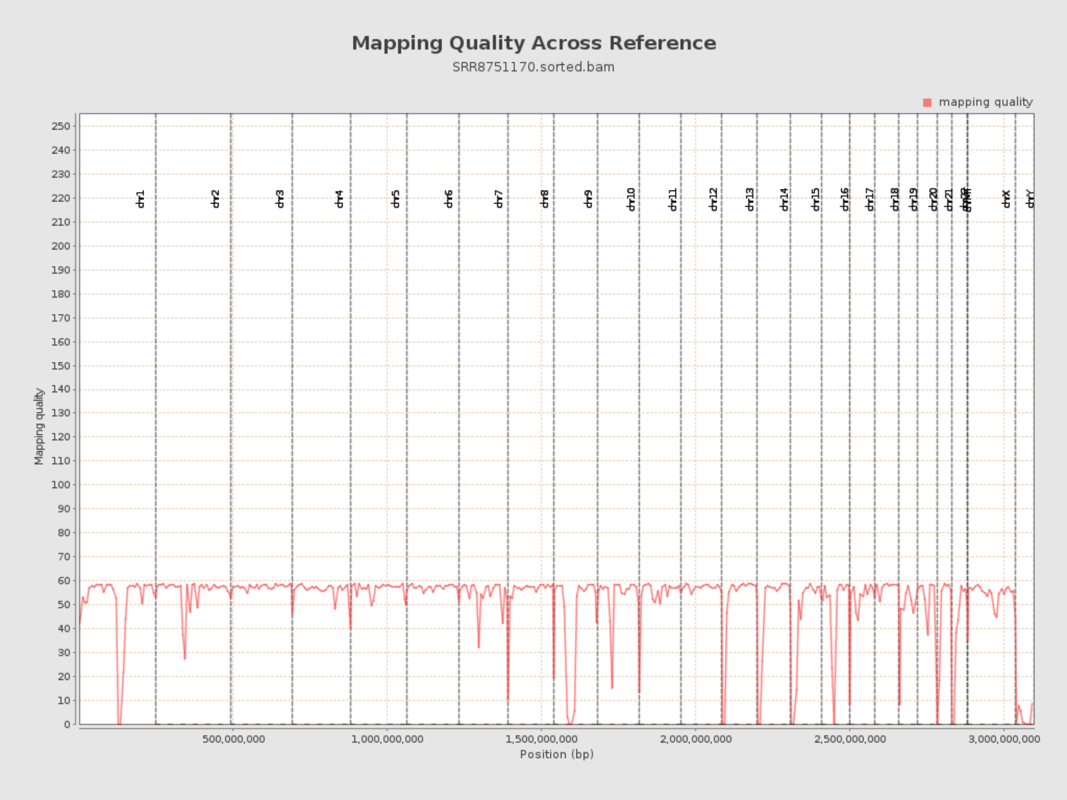
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram