Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 16:43:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751185.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_SRR8751185 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751185.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 16:43:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751185.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,282,207
Mapped reads	4,884,518 / 92.47%
Unmapped reads	397,689 / 7.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	171,493 / 3.25%
Read min/max/mean length	30 / 101 / 102.34
Duplicated reads (estimated)	133,591 / 2.53%
Duplication rate	1.64%
Clipped reads	945,902 / 17.91%

2.2. ACGT Content

Number/percentage of A's	138,261,381 / 28.85%
Number/percentage of C's	101,530,777 / 21.18%
Number/percentage of T's	139,154,847 / 29.03%
Number/percentage of G's	100,340,215 / 20.94%
Number/percentage of N's	2,498 / 0%
GC Percentage	42.12%

2.3. Coverage

Mean	0.1549

Standard Deviation	1.225

2.4. Mapping Quality

Mean Mapping Quality	51.26

2.5. Mismatches and indels

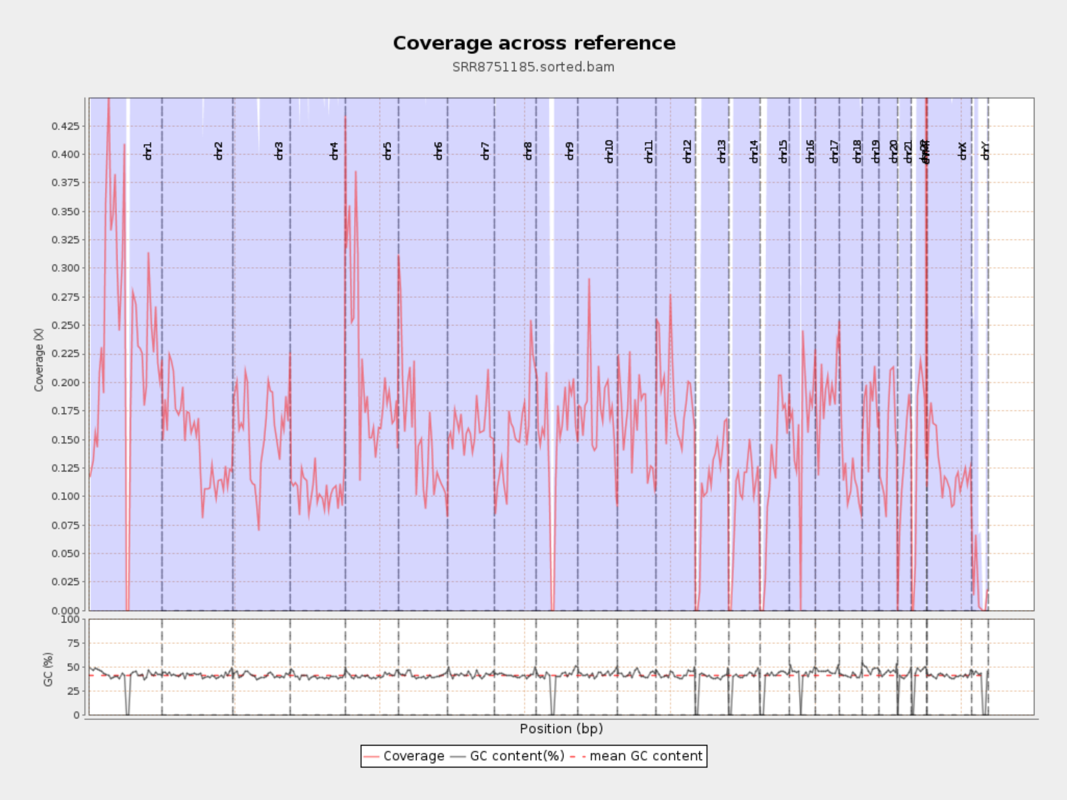
General error rate	0.4%
Mismatches	1,698,942
Insertions	150,644
Mapped reads with at least one insertion	3.01%
Deletions	66,669
Mapped reads with at least one deletion	1.34%
Homopolymer indels	49.97%

2.6. Chromosome stats

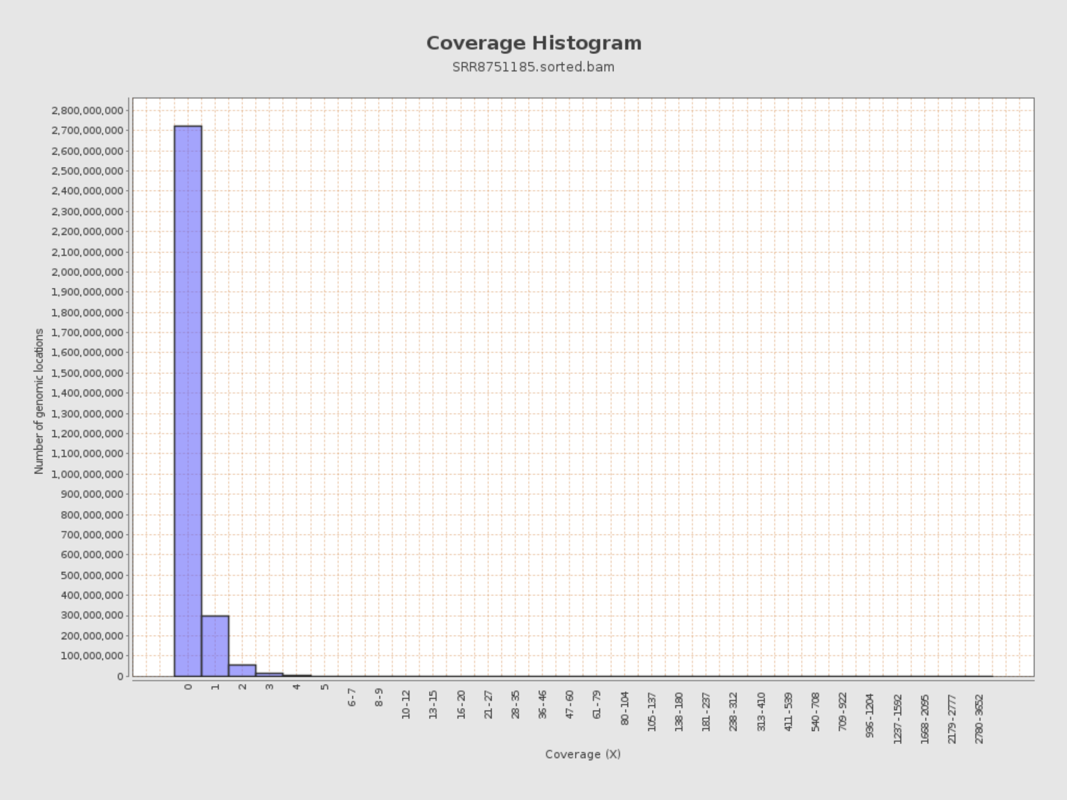
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	59068502	0.237	3.4321
chr2	243199373	35656651	0.1466	0.5403
chr3	198022430	31290610	0.158	0.4923
chr4	191154276	20079353	0.105	0.4317
chr5	180915260	37497261	0.2073	0.5422
chr6	171115067	26159025	0.1529	0.809
chr7	159138663	25555184	0.1606	0.6867

chr8	146364022	22690744	0.155	0.5527
chr9	141213431	20765219	0.147	0.6107
chr10	135534747	23888169	0.1763	1.5664
chr11	135006516	22093108	0.1636	0.6542
chr12	133851895	25760954	0.1925	0.519
chr13	115169878	12555111	0.109	0.3861
chr14	107349540	10453923	0.0974	0.3783
chr15	102531392	12457670	0.1215	0.4107
chr16	90354753	14565881	0.1612	0.8451
chr17	81195210	15450485	0.1903	0.701
chr18	78077248	9511187	0.1218	1.1484
chr19	59128983	10582913	0.179	2.4196
chr20	63025520	9251369	0.1468	0.4577
chr21	48129895	5938002	0.1234	0.4439
chr22	51304566	6760846	0.1318	0.4377
chrMT	16571	1157966	69.8791	27.5847
chrX	155270560	19239661	0.1239	0.457
chrY	59373566	1004471	0.0169	0.6341

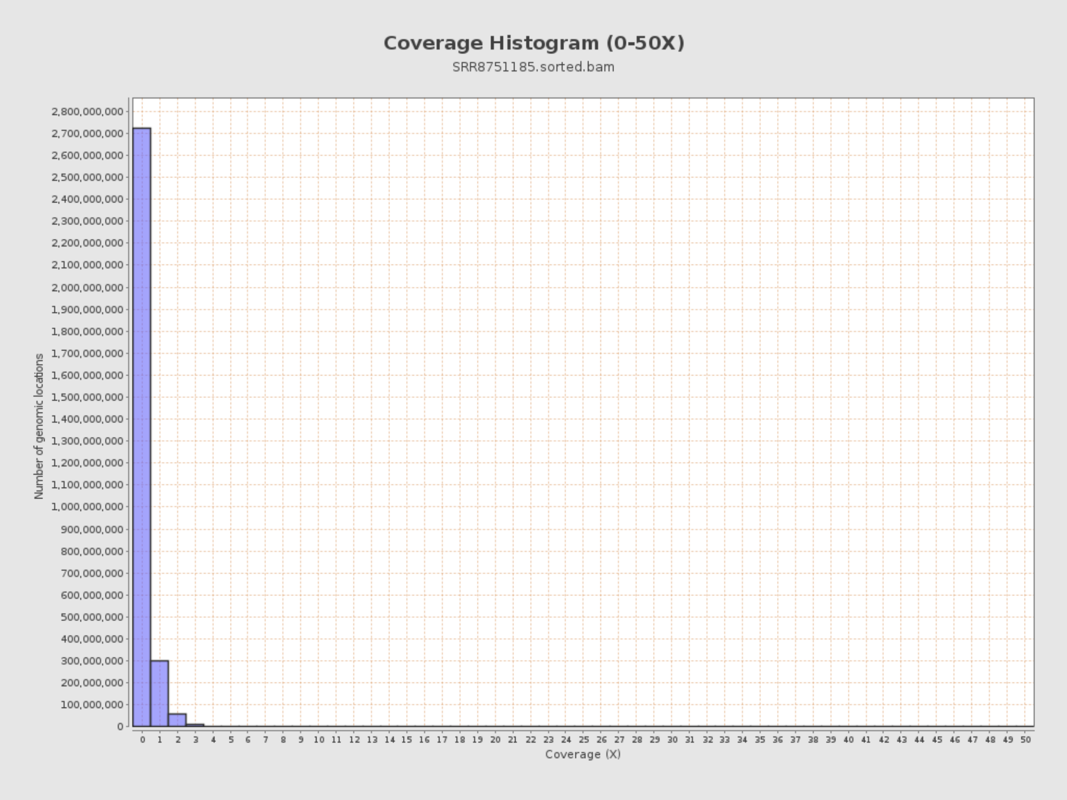
3. Results : Coverage across reference



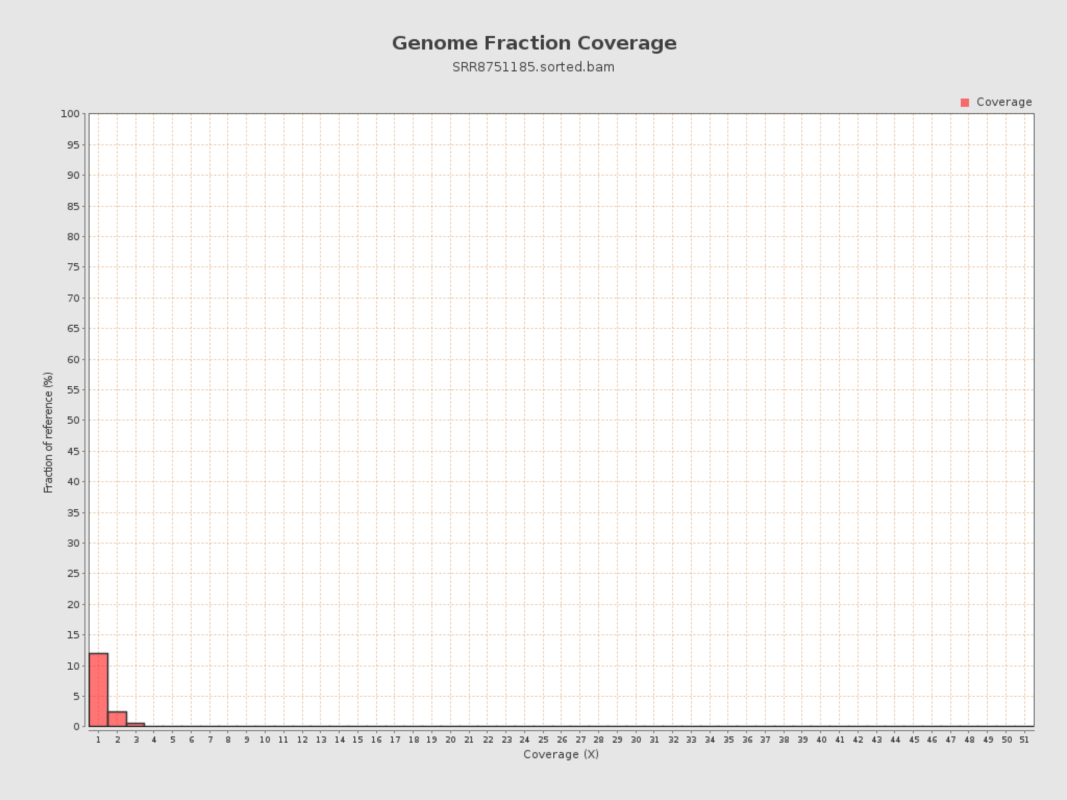
4. Results : Coverage Histogram



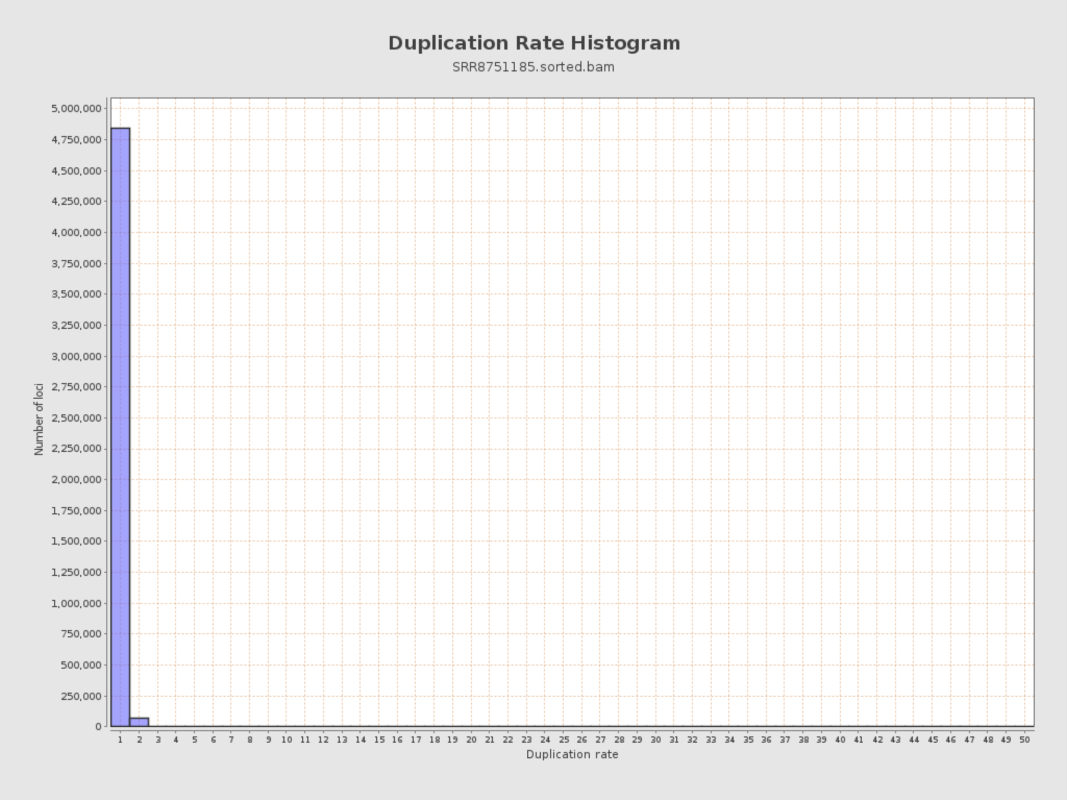
5. Results : Coverage Histogram (0-50X)



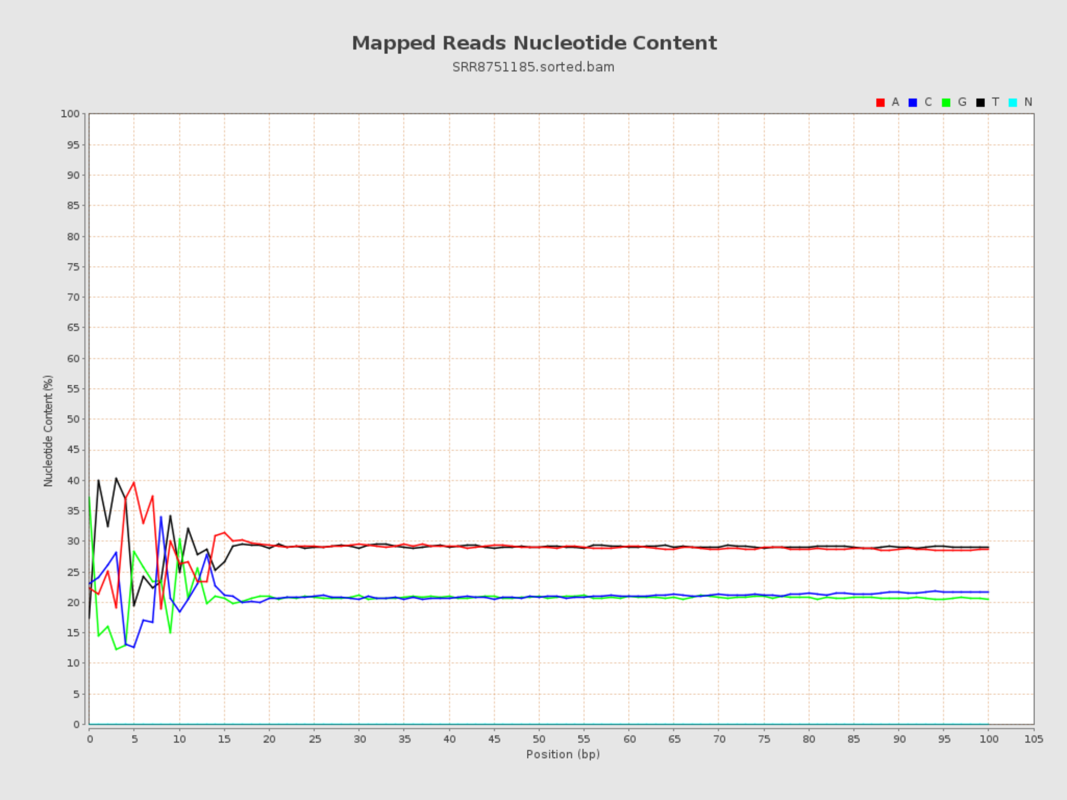
6. Results : Genome Fraction Coverage



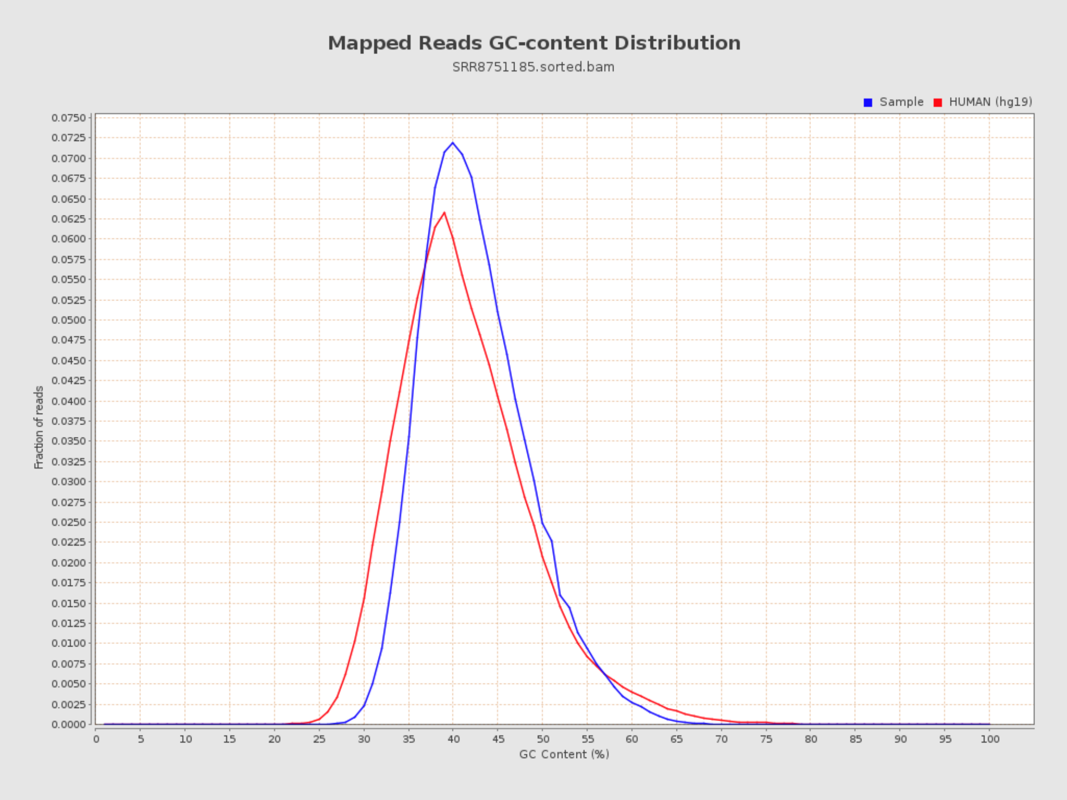
7. Results : Duplication Rate Histogram



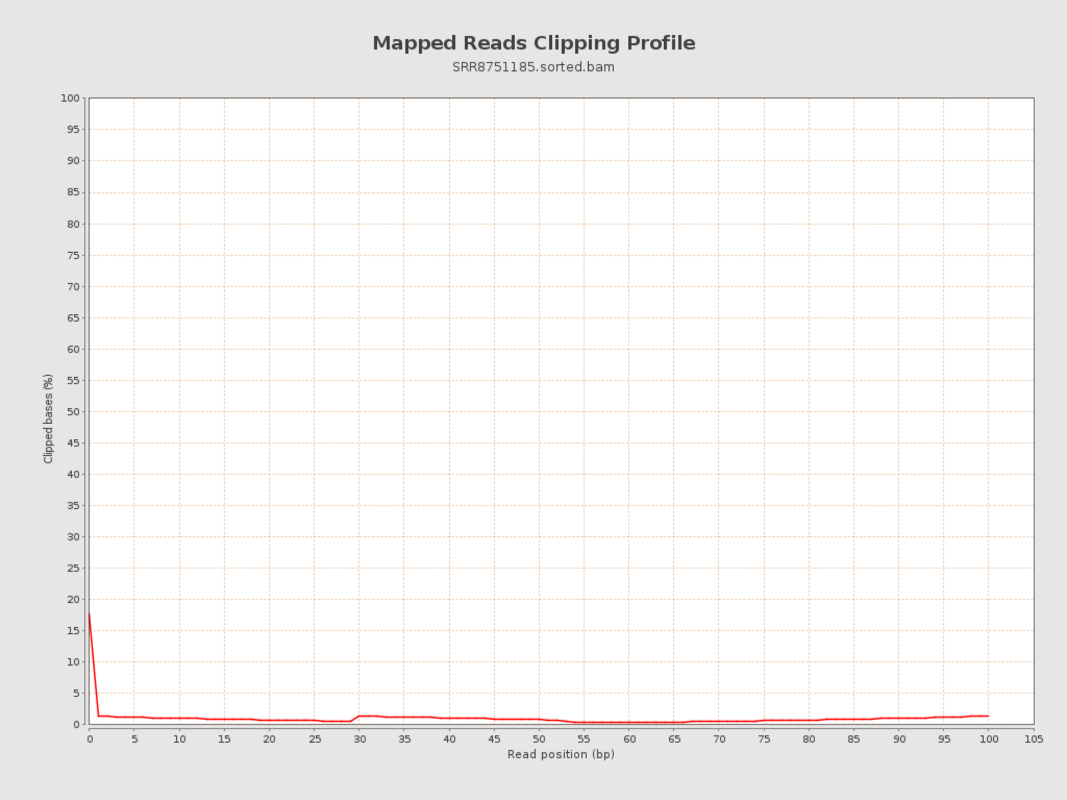
8. Results : Mapped Reads Nucleotide Content



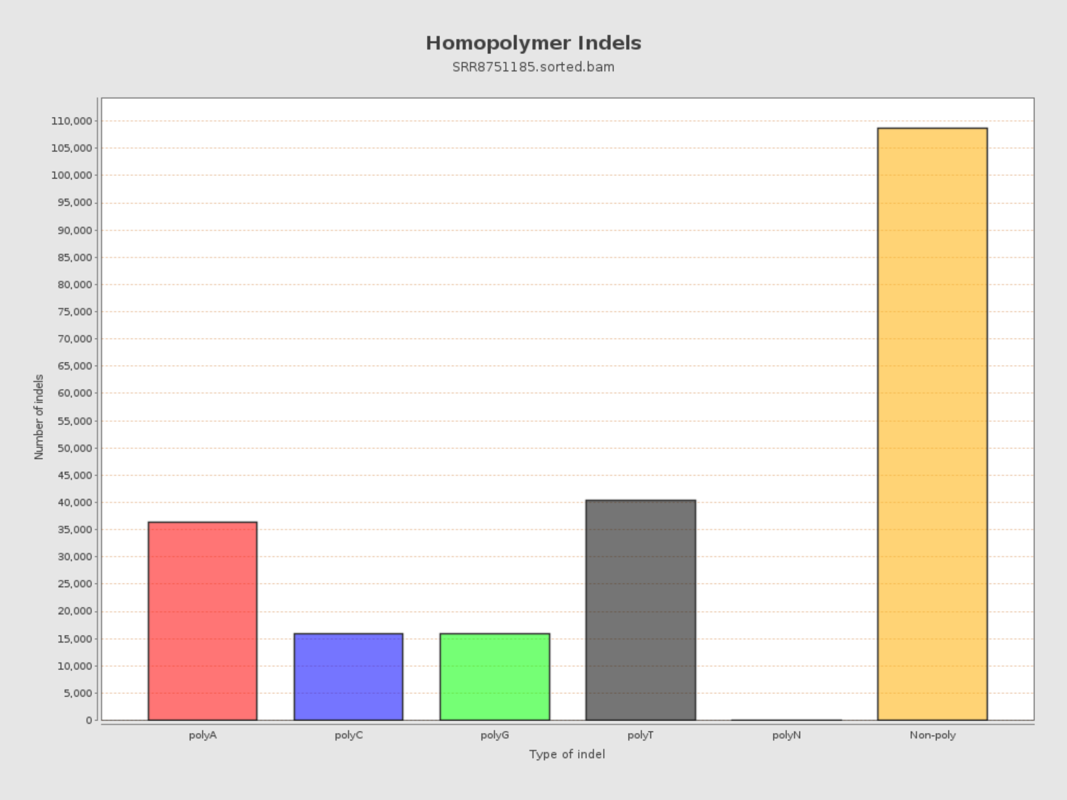
9. Results : Mapped Reads GC-content Distribution



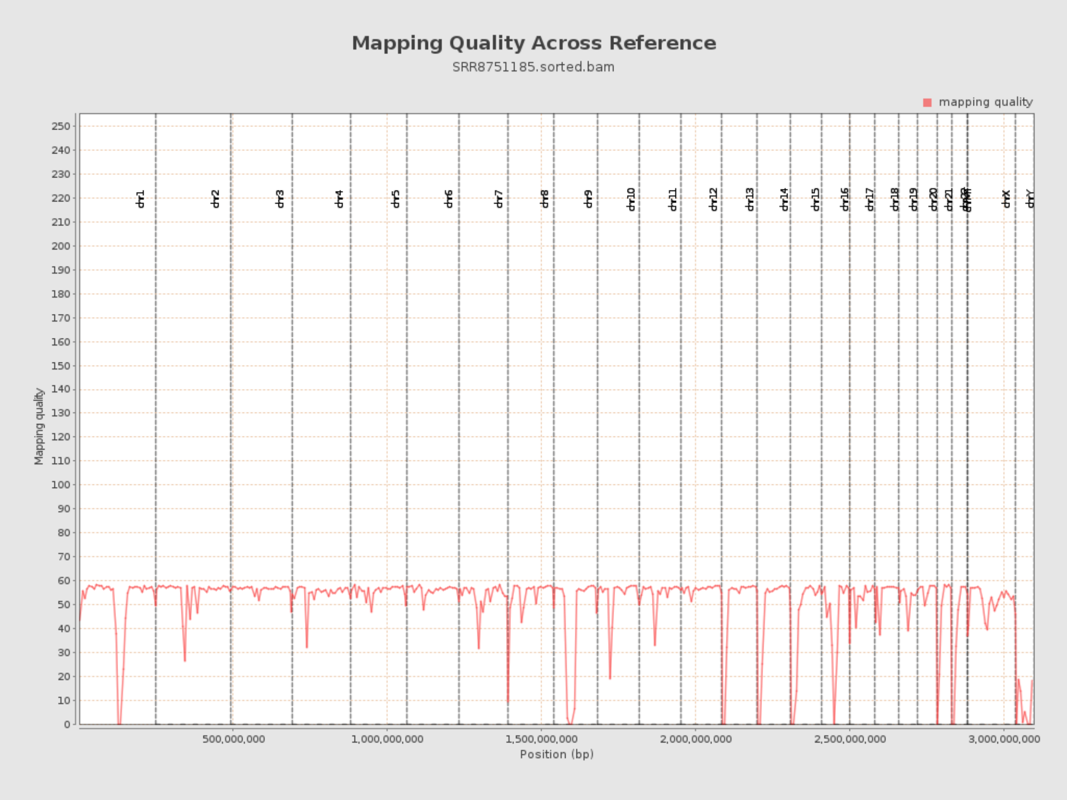
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram