Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 16:26:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751183.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_SRR8751183 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751183.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 16:26:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751183.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,444,265
Mapped reads	7,374,751 / 99.07%
Unmapped reads	69,514 / 0.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	51,002 / 0.69%
Read min/max/mean length	30 / 151 / 151.32
Duplicated reads (estimated)	1,122,980 / 15.09%
Duplication rate	14.27%
Clipped reads	3,988,686 / 53.58%

2.2. ACGT Content

Number/percentage of A's	293,810,470 / 30.19%
Number/percentage of C's	193,389,013 / 19.87%
Number/percentage of T's	292,171,555 / 30.02%
Number/percentage of G's	193,907,538 / 19.92%
Number/percentage of N's	29,741 / 0%
GC Percentage	39.79%

2.3. Coverage

Mean	0.3145

Standard Deviation	1.4582

2.4. Mapping Quality

Mean Mapping Quality	52

2.5. Mismatches and indels

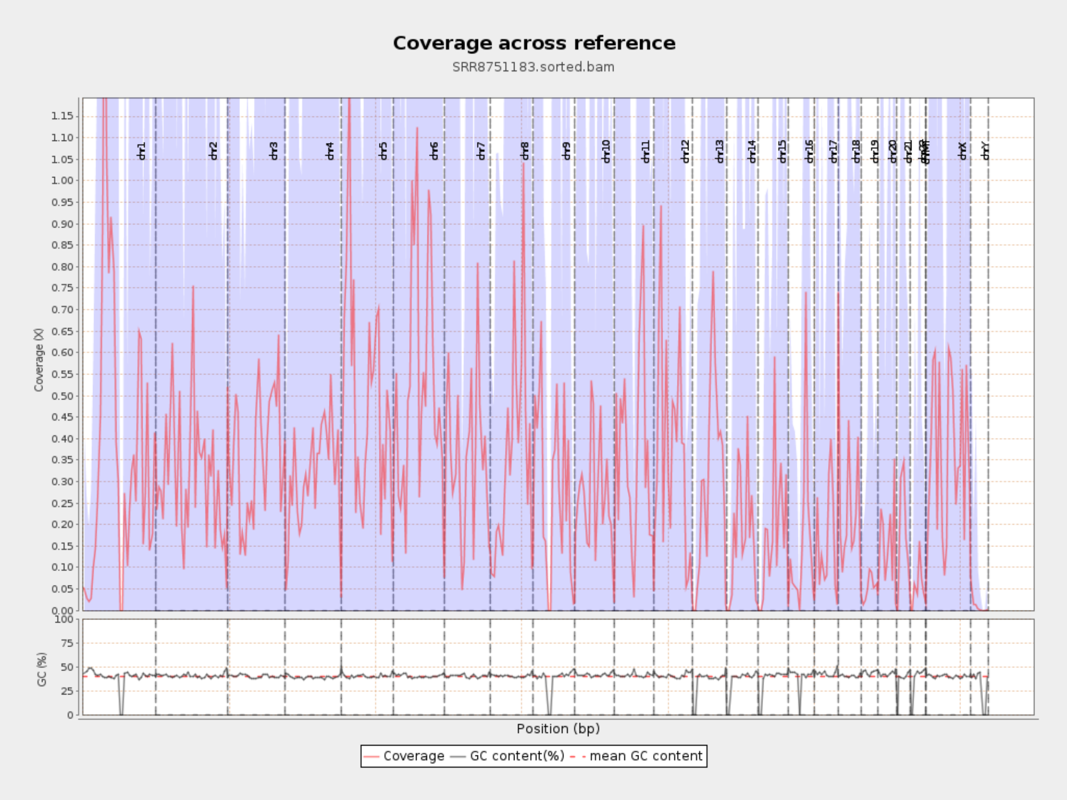
General error rate	1.7%
Mismatches	16,329,689
Insertions	108,959
Mapped reads with at least one insertion	1.45%
Deletions	181,928
Mapped reads with at least one deletion	2.39%
Homopolymer indels	41.29%

2.6. Chromosome stats

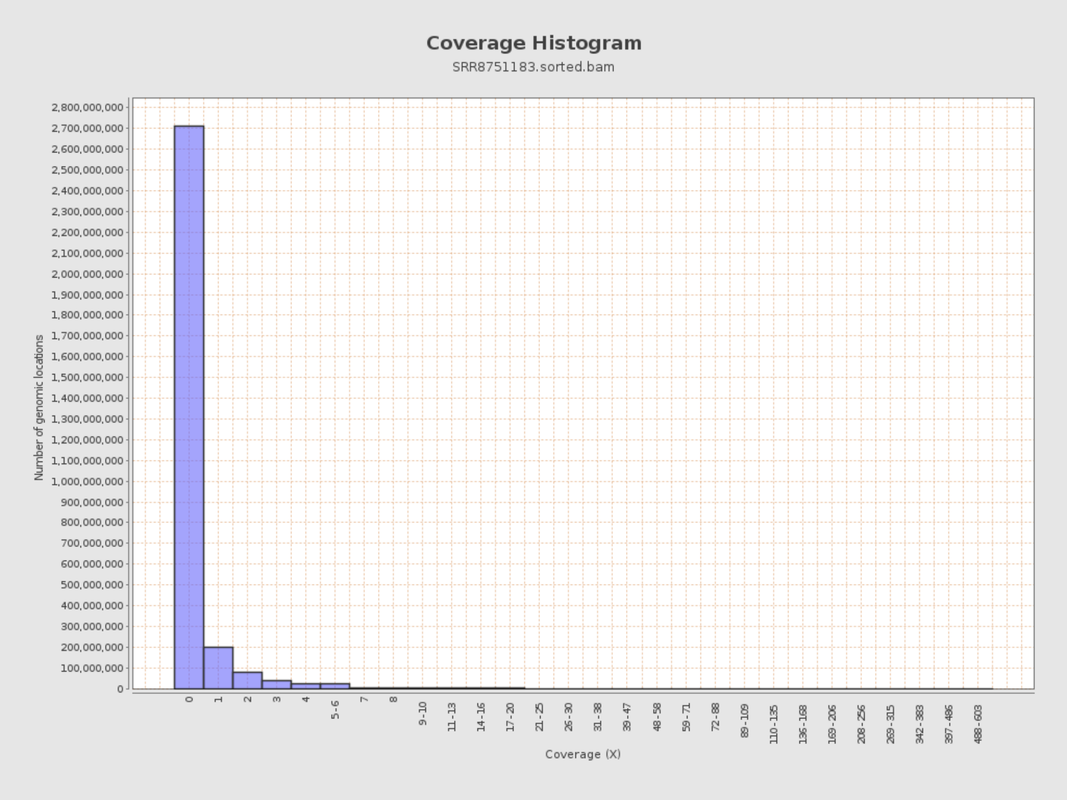
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	95937202	0.3849	1.5455
chr2	243199373	76733826	0.3155	1.3769
chr3	198022430	71650363	0.3618	1.4191
chr4	191154276	60565364	0.3168	1.433
chr5	180915260	87123932	0.4816	1.6087
chr6	171115067	90930805	0.5314	1.8479
chr7	159138663	56248440	0.3535	1.4635

chr8	146364022	53283188	0.364	2.1397
chr9	141213431	41534133	0.2941	1.3046
chr10	135534747	36826844	0.2717	1.0769
chr11	135006516	50031914	0.3706	1.6707
chr12	133851895	50311419	0.3759	1.6315
chr13	115169878	36624275	0.318	1.337
chr14	107349540	19134567	0.1782	1.0809
chr15	102531392	18962484	0.1849	1.1779
chr16	90354753	14368204	0.159	1.1906
chr17	81195210	13331653	0.1642	1.3236
chr18	78077248	18465520	0.2365	1.1341
chr19	59128983	3147153	0.0532	0.436
chr20	63025520	10407011	0.1651	1.1181
chr21	48129895	7988640	0.166	0.7775
chr22	51304566	2963725	0.0578	0.5332
chrMT	16571	783	0.0473	0.2447
chrX	155270560	56475336	0.3637	1.8277
chrY	59373566	560036	0.0094	0.2306

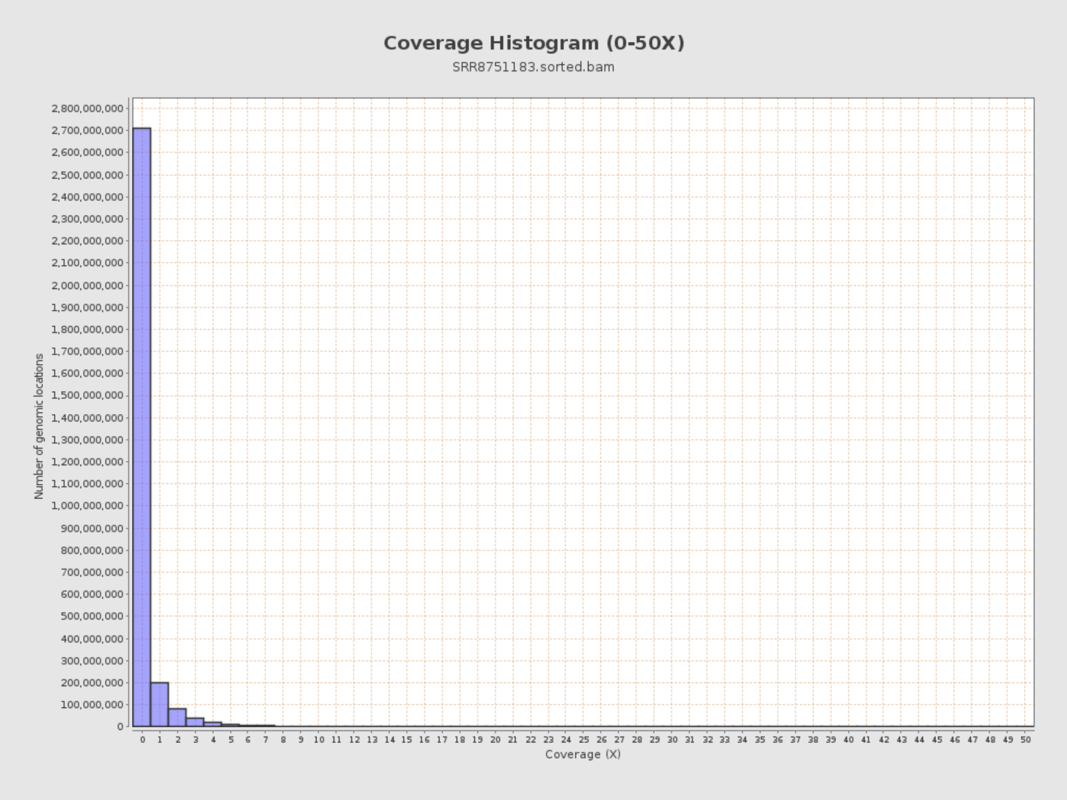
3. Results : Coverage across reference



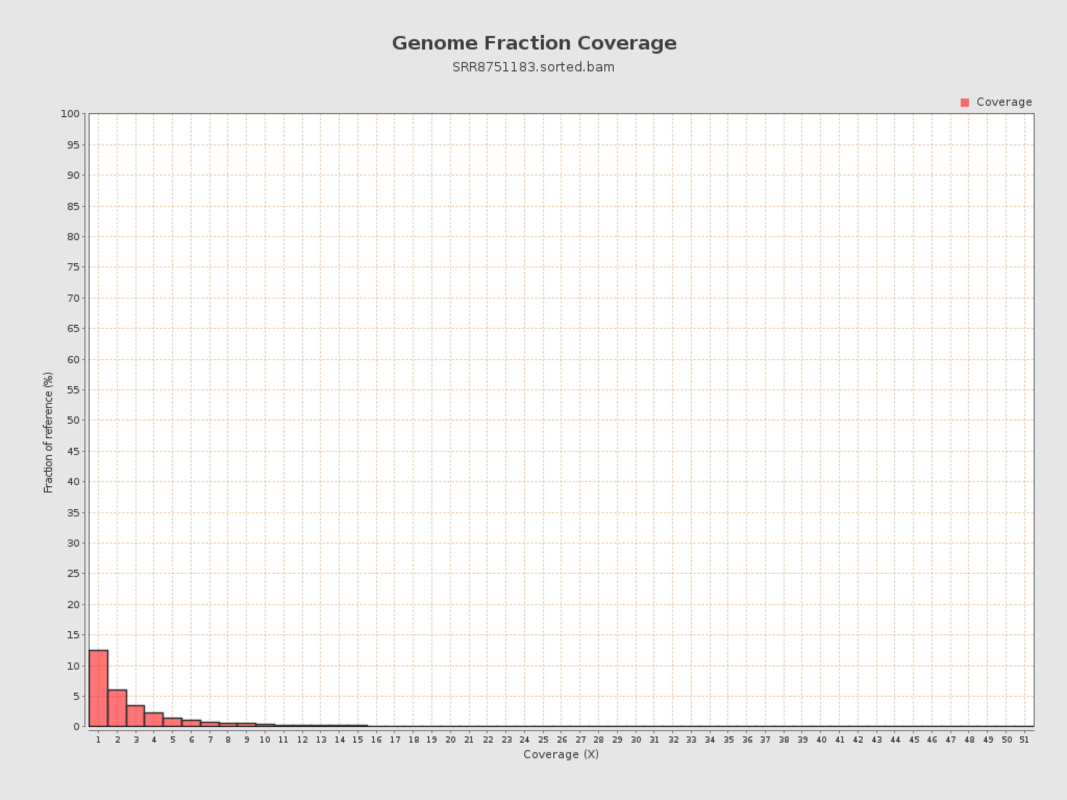
4. Results : Coverage Histogram



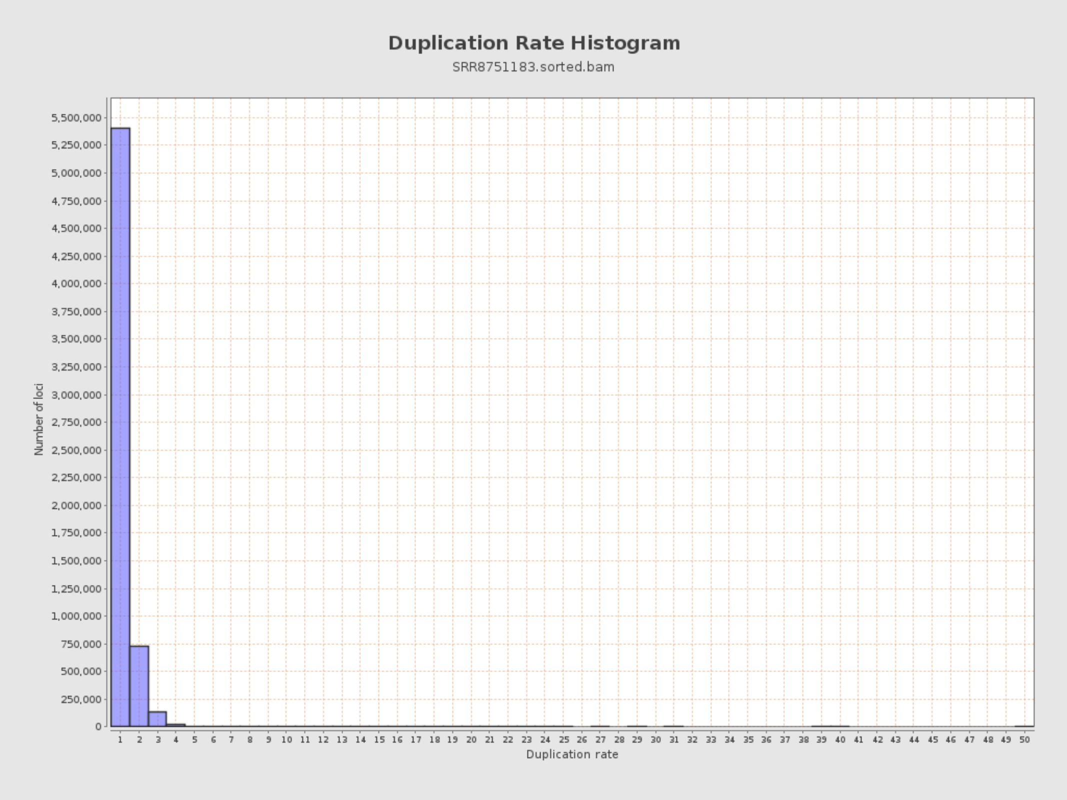
5. Results : Coverage Histogram (0-50X)



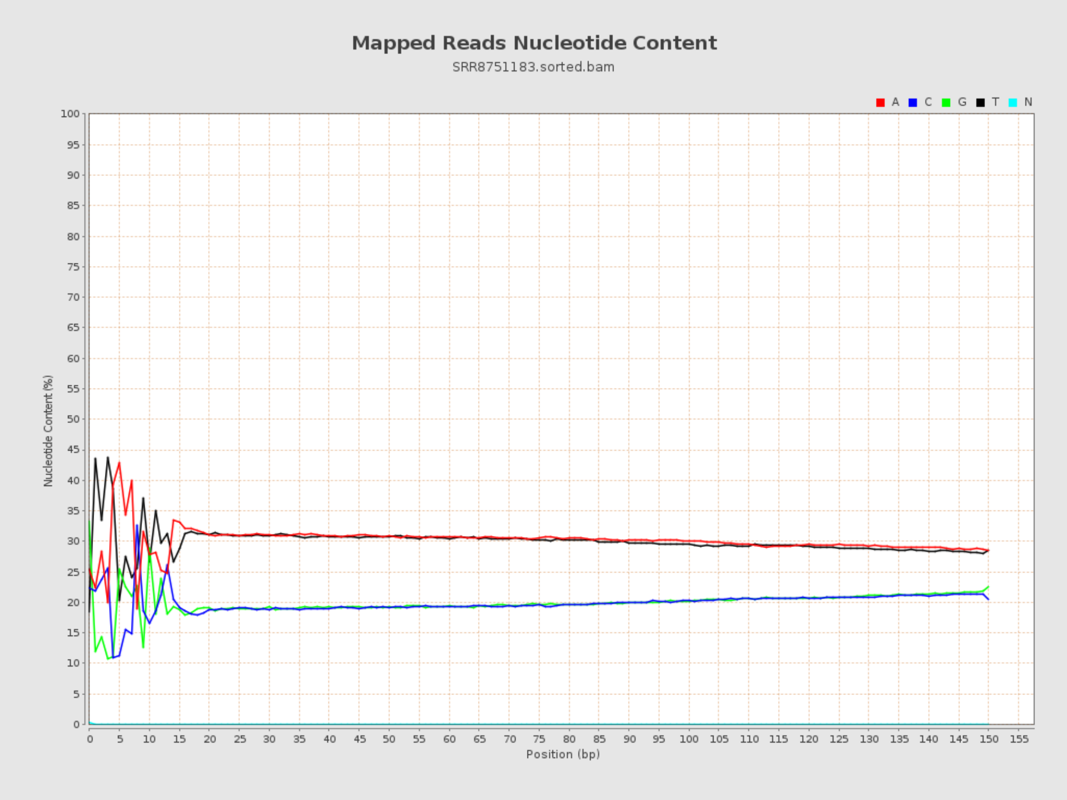
6. Results : Genome Fraction Coverage



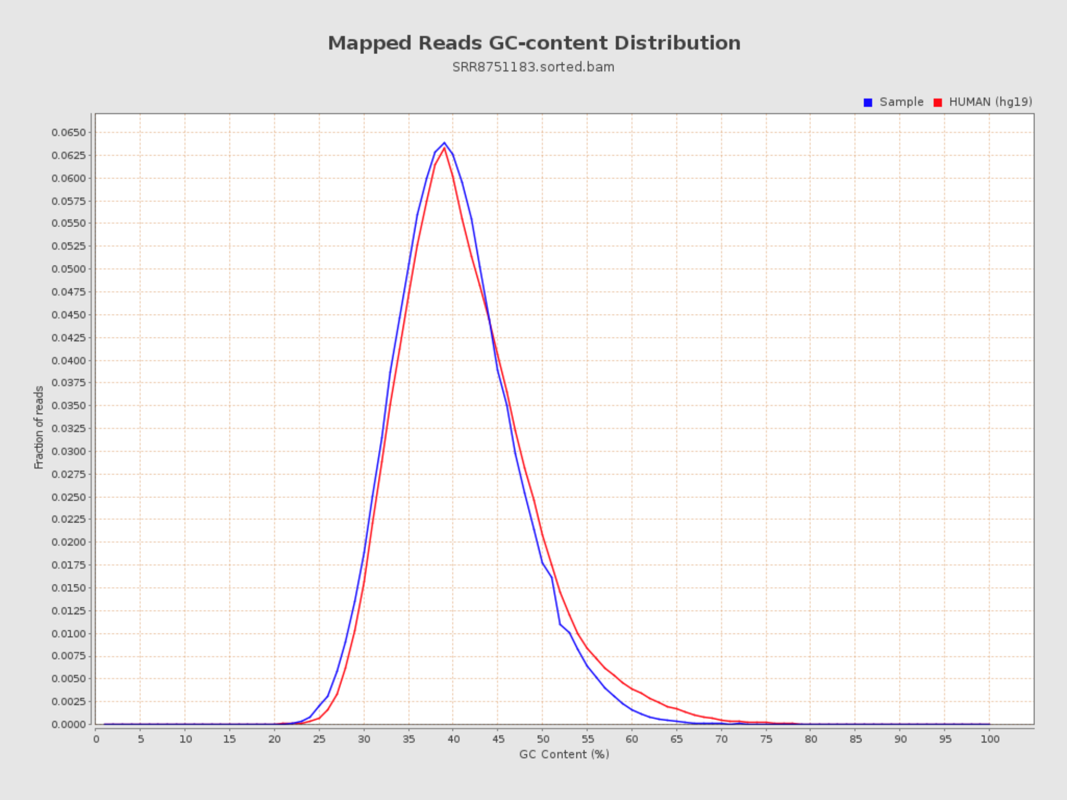
7. Results : Duplication Rate Histogram



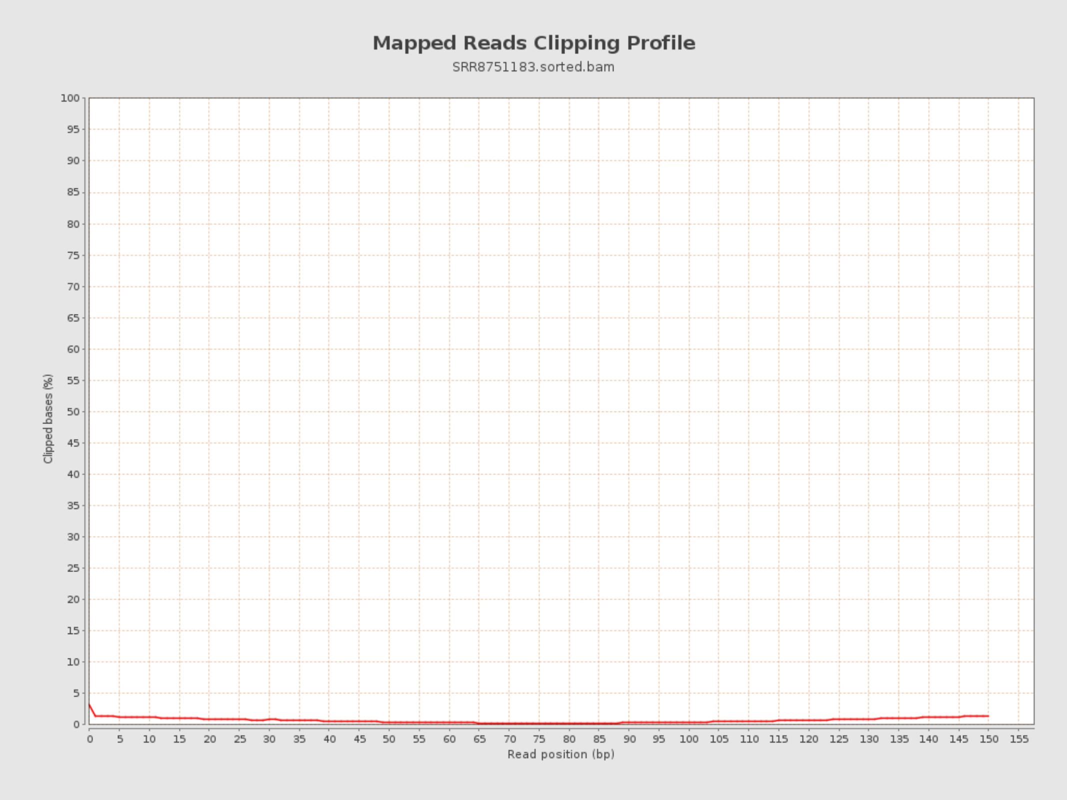
8. Results : Mapped Reads Nucleotide Content



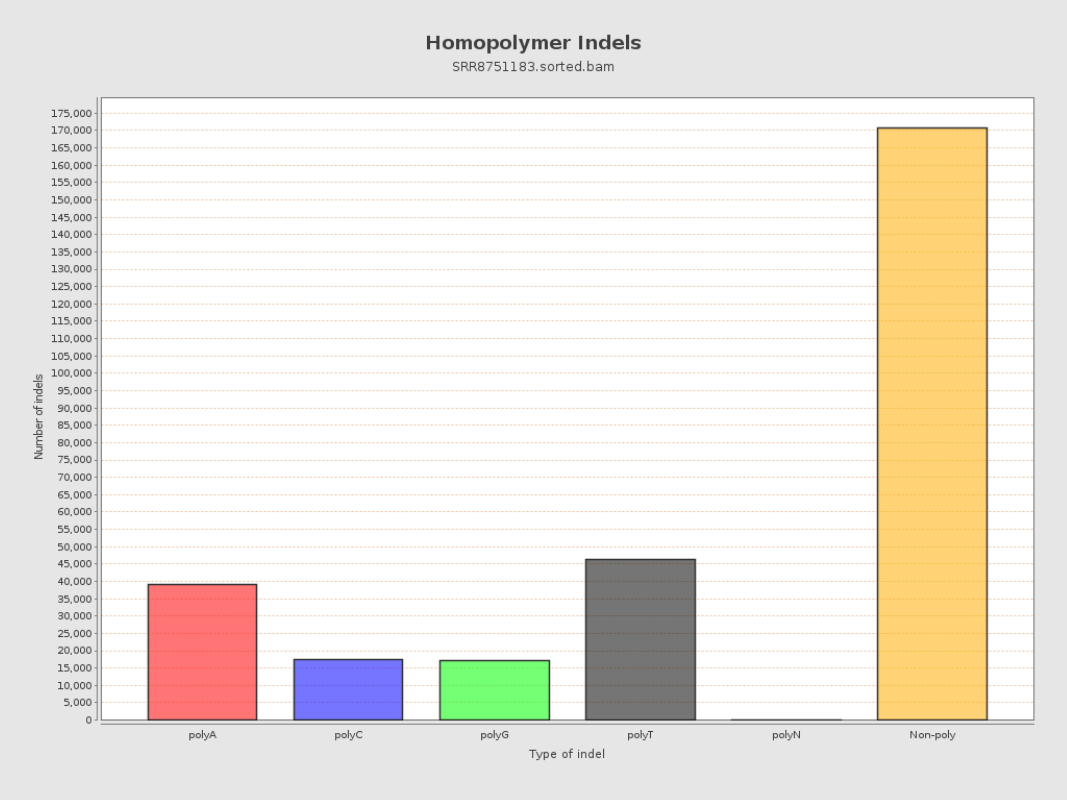
9. Results : Mapped Reads GC-content Distribution



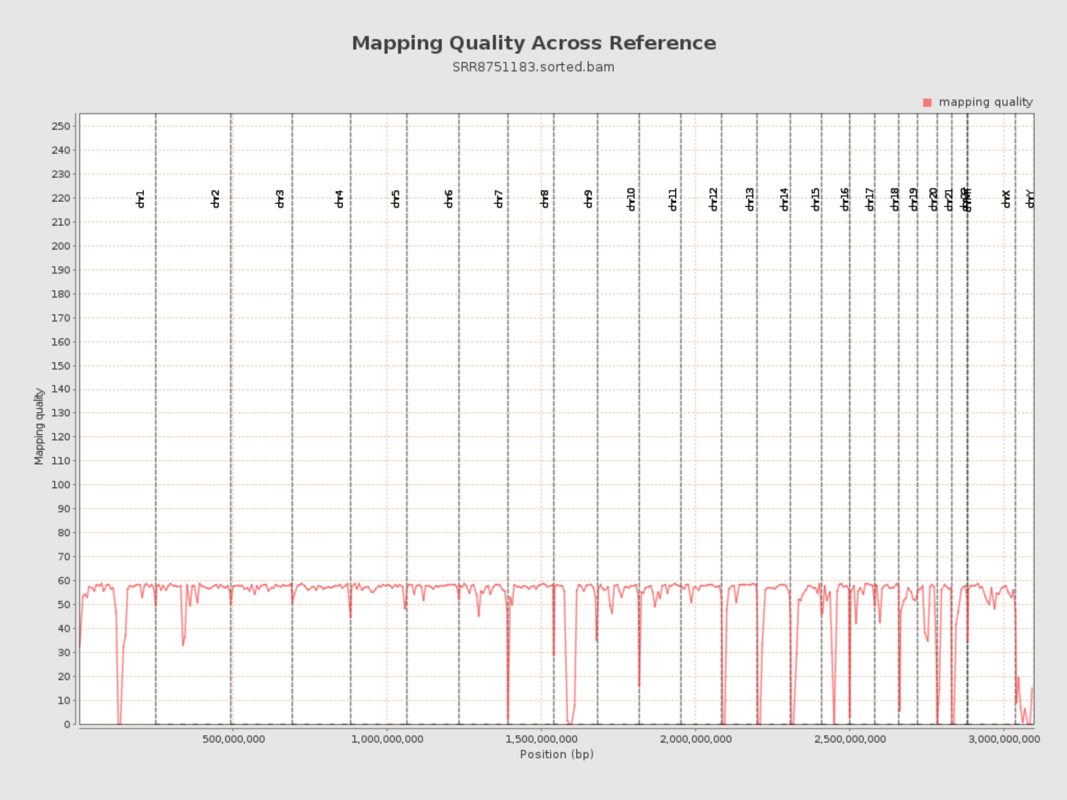
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram