Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 17:22:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751188.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_SRR8751188 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751188.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 17:22:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751188.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,468,408
Mapped reads	4,962,665 / 90.75%
Unmapped reads	505,743 / 9.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	180,857 / 3.31%
Read min/max/mean length	30 / 101 / 102.37
Duplicated reads (estimated)	164,573 / 3.01%
Duplication rate	1.86%
Clipped reads	955,098 / 17.47%

2.2. ACGT Content

Number/percentage of A's	142,238,846 / 29.17%
Number/percentage of C's	101,904,617 / 20.9%
Number/percentage of T's	142,879,081 / 29.3%
Number/percentage of G's	100,605,029 / 20.63%
Number/percentage of N's	2,633 / 0%
GC Percentage	41.53%

2.3. Coverage

Mean	0.1576

Standard Deviation	1.5389

2.4. Mapping Quality

Mean Mapping Quality	51.15

2.5. Mismatches and indels

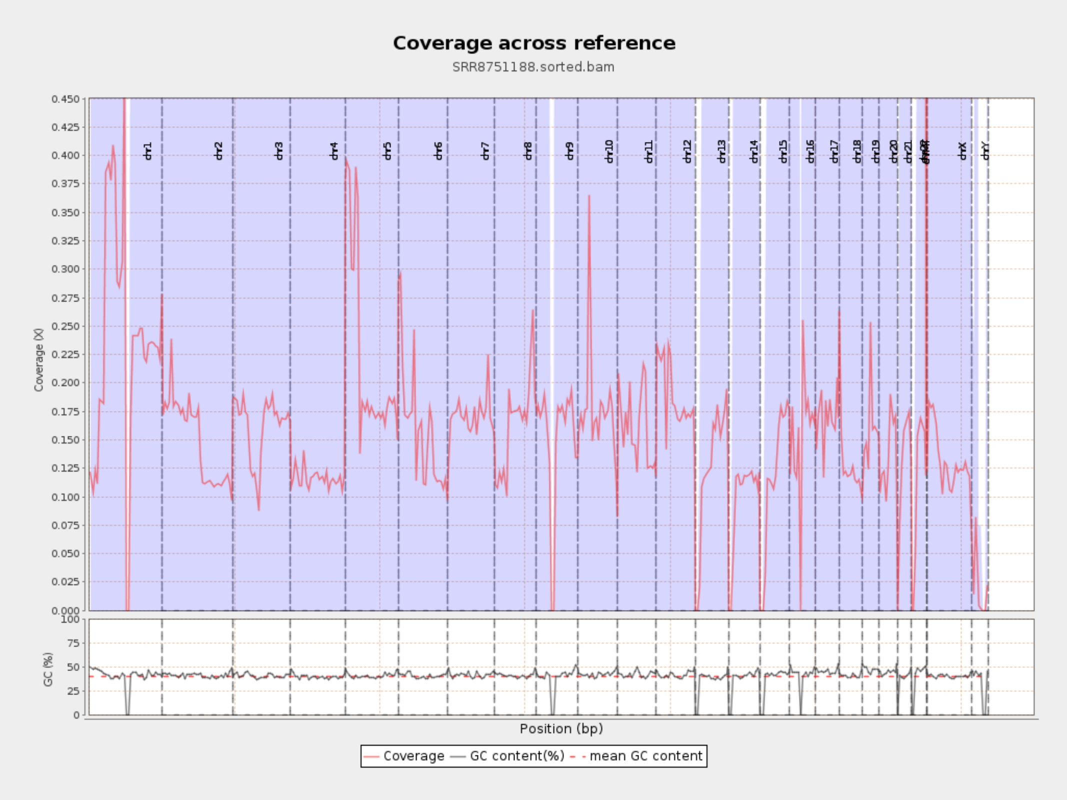
General error rate	0.41%
Mismatches	1,813,765
Insertions	122,870
Mapped reads with at least one insertion	2.42%
Deletions	66,810
Mapped reads with at least one deletion	1.32%
Homopolymer indels	48.43%

2.6. Chromosome stats

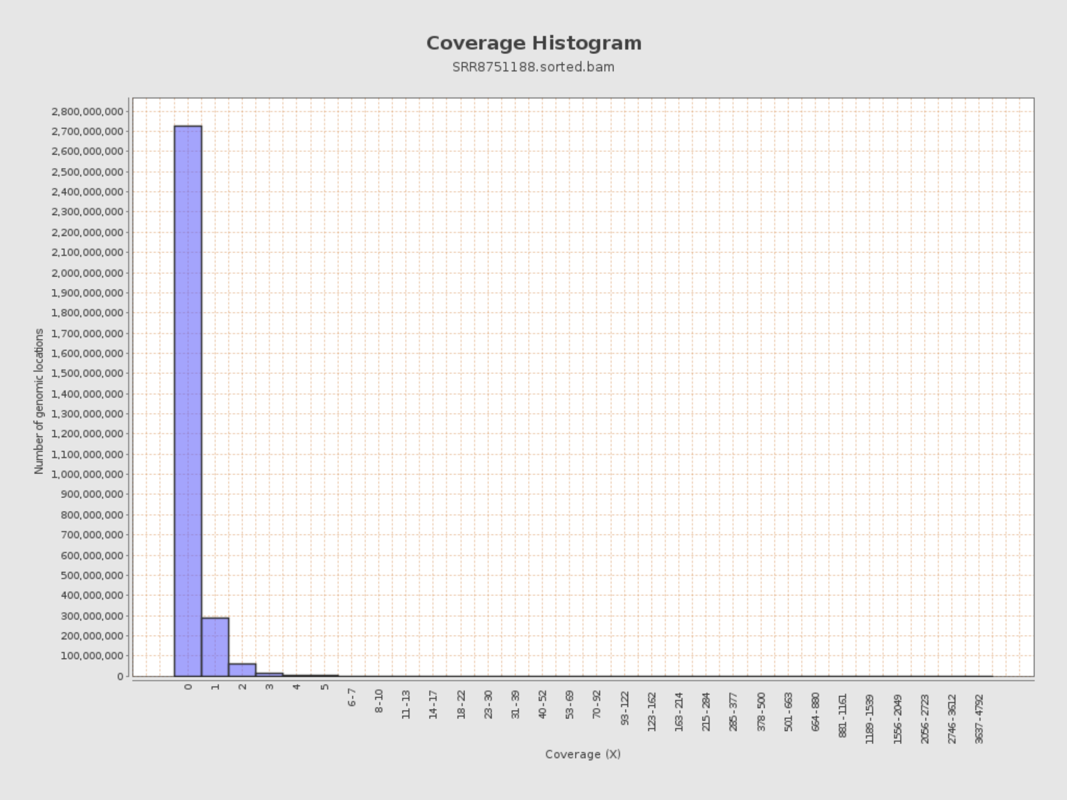
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	58966217	0.2366	4.443
chr2	243199373	36272647	0.1491	0.6047
chr3	198022430	32150666	0.1624	0.5333
chr4	191154276	22233590	0.1163	0.494
chr5	180915260	40029810	0.2213	0.5788
chr6	171115067	27286466	0.1595	0.9206
chr7	159138663	27393376	0.1721	0.8231

chr8	146364022	24109144	0.1647	0.6398
chr9	141213431	21380651	0.1514	0.6852
chr10	135534747	24163634	0.1783	1.9546
chr11	135006516	21724918	0.1609	0.7512
chr12	133851895	25383828	0.1896	0.5326
chr13	115169878	14267113	0.1239	0.4245
chr14	107349540	10337495	0.0963	0.3947
chr15	102531392	11875178	0.1158	0.4104
chr16	90354753	13774035	0.1524	0.9379
chr17	81195210	13715919	0.1689	0.7318
chr18	78077248	9984176	0.1279	1.4014
chr19	59128983	9447449	0.1598	3.1648
chr20	63025520	8623876	0.1368	0.4612
chr21	48129895	6128578	0.1273	0.4864
chr22	51304566	5591143	0.109	0.4078
chrMT	16571	1263454	76.2449	31.4916
chrX	155270560	20499723	0.132	0.5047
chrY	59373566	1173904	0.0198	0.7577

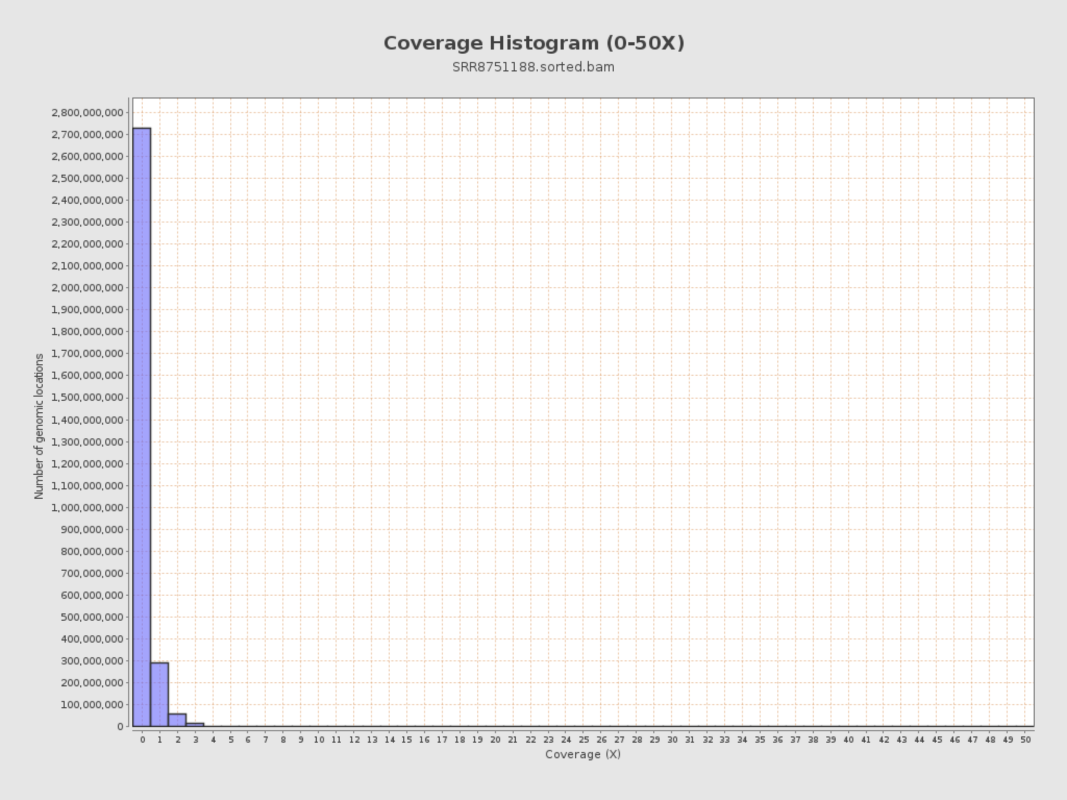
3. Results : Coverage across reference



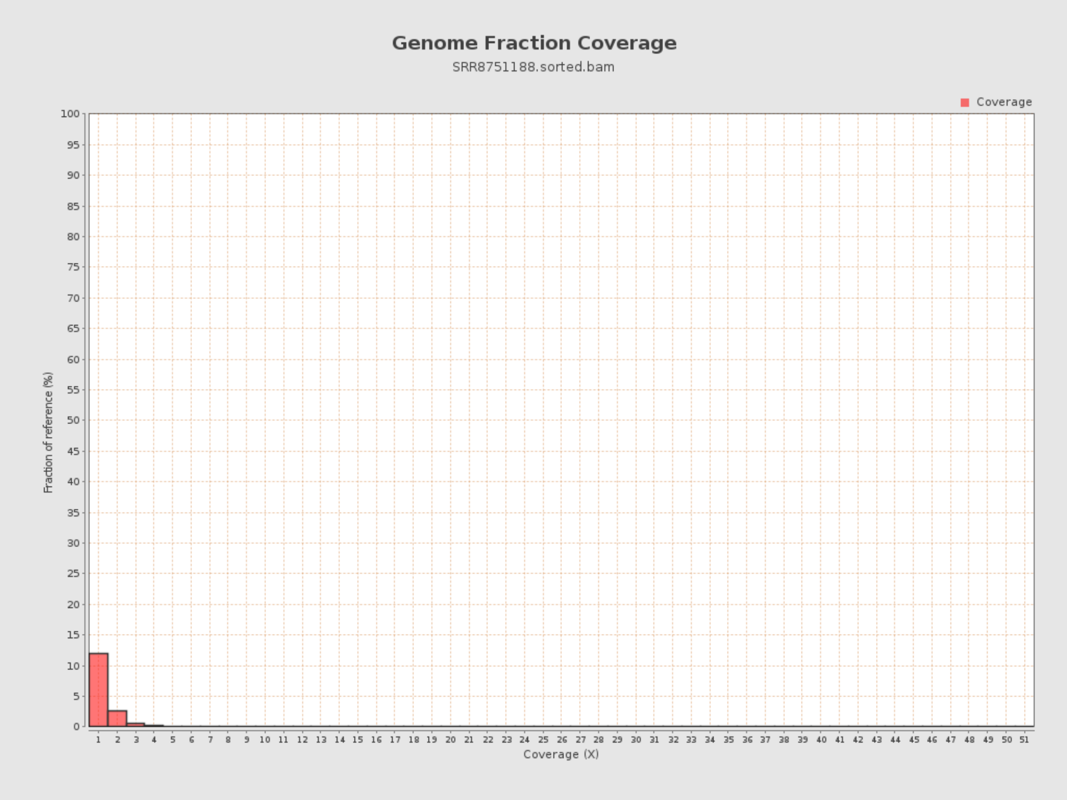
4. Results : Coverage Histogram



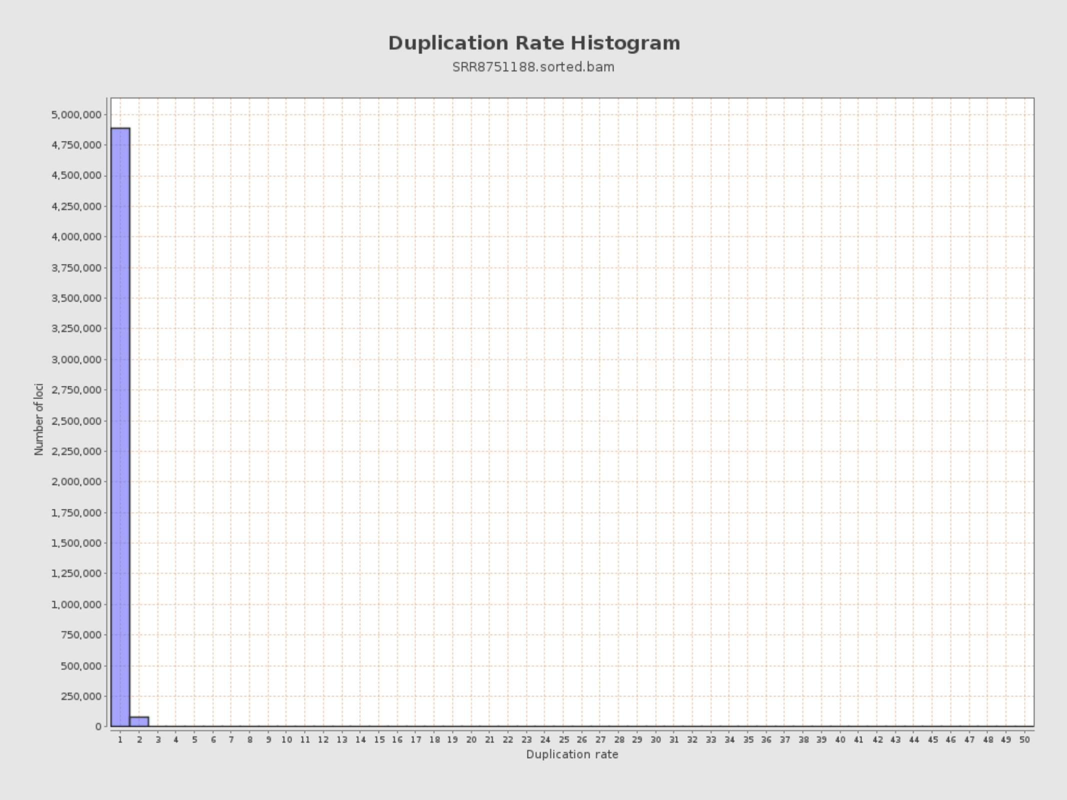
5. Results : Coverage Histogram (0-50X)



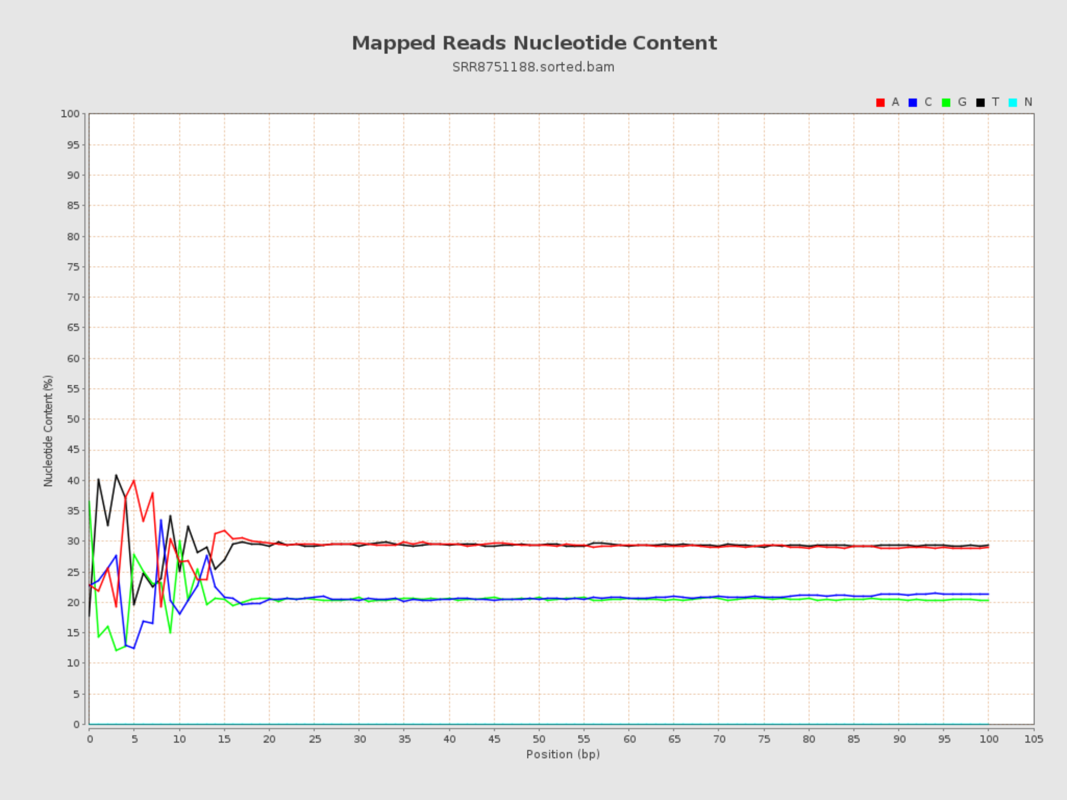
6. Results : Genome Fraction Coverage



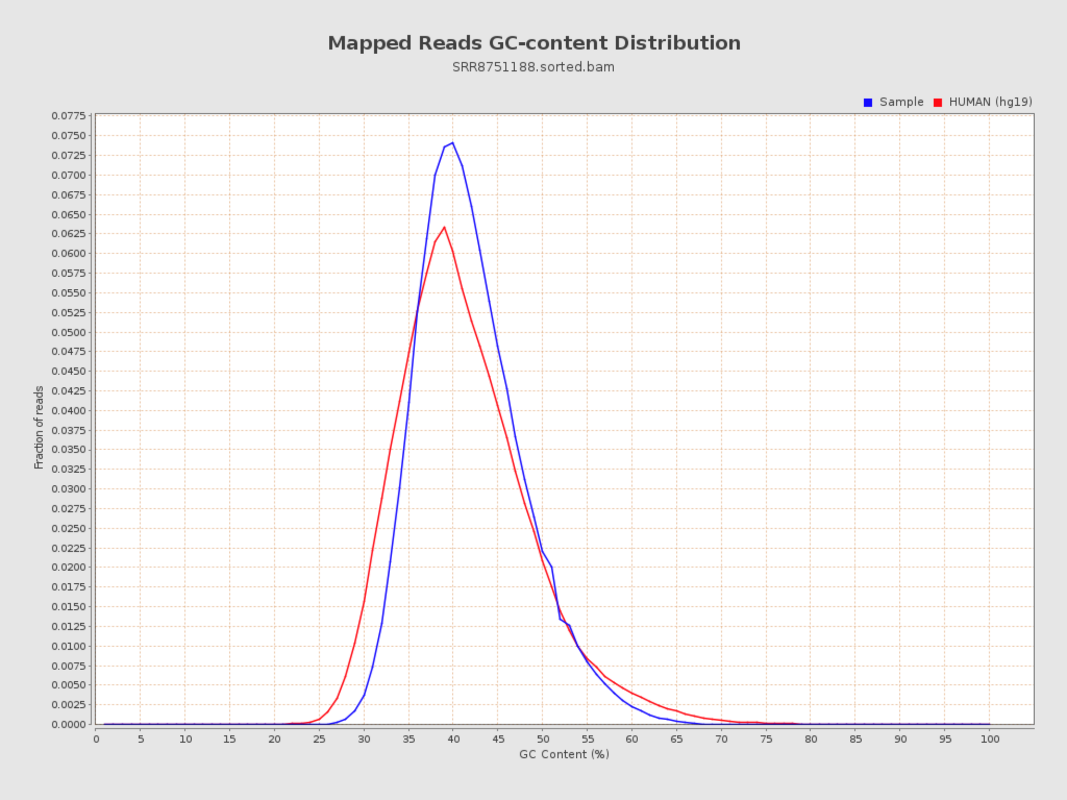
7. Results : Duplication Rate Histogram



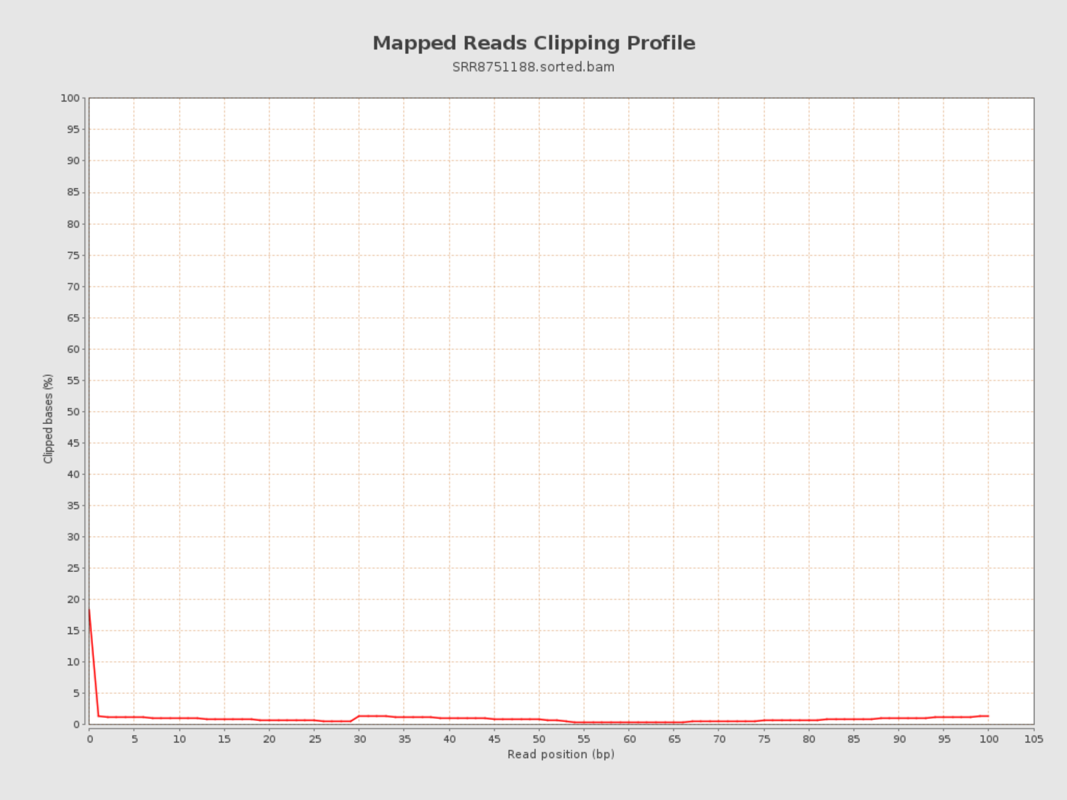
8. Results : Mapped Reads Nucleotide Content



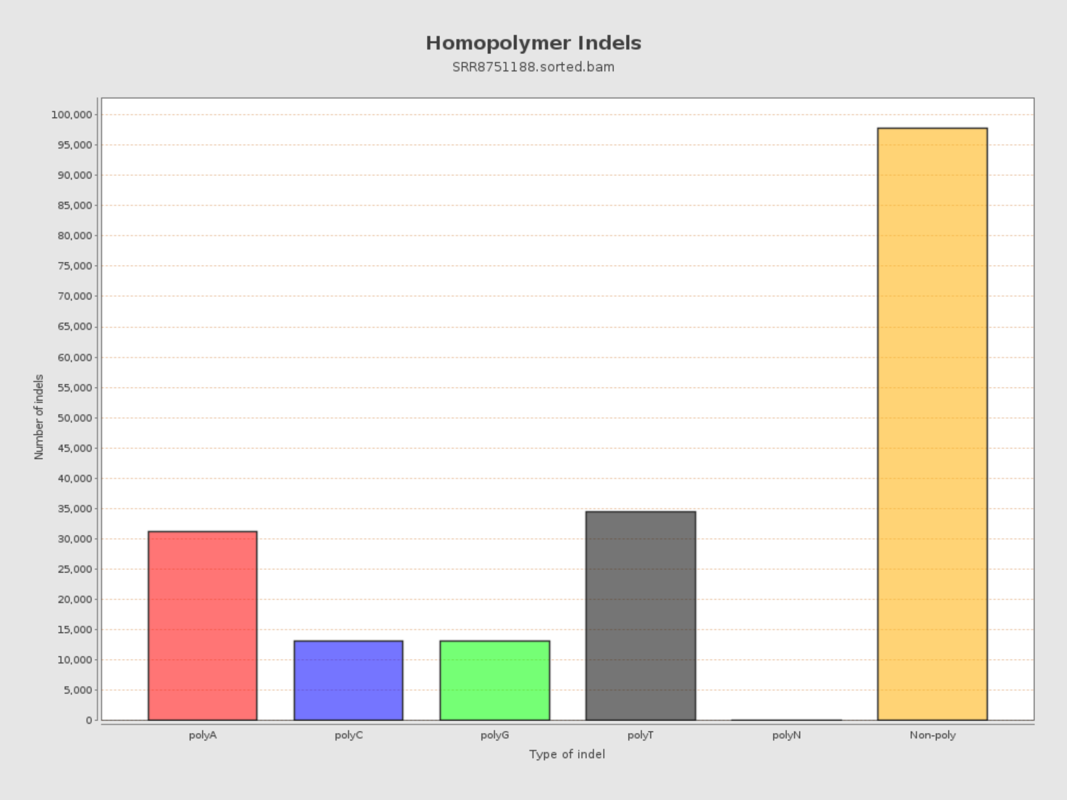
9. Results : Mapped Reads GC-content Distribution



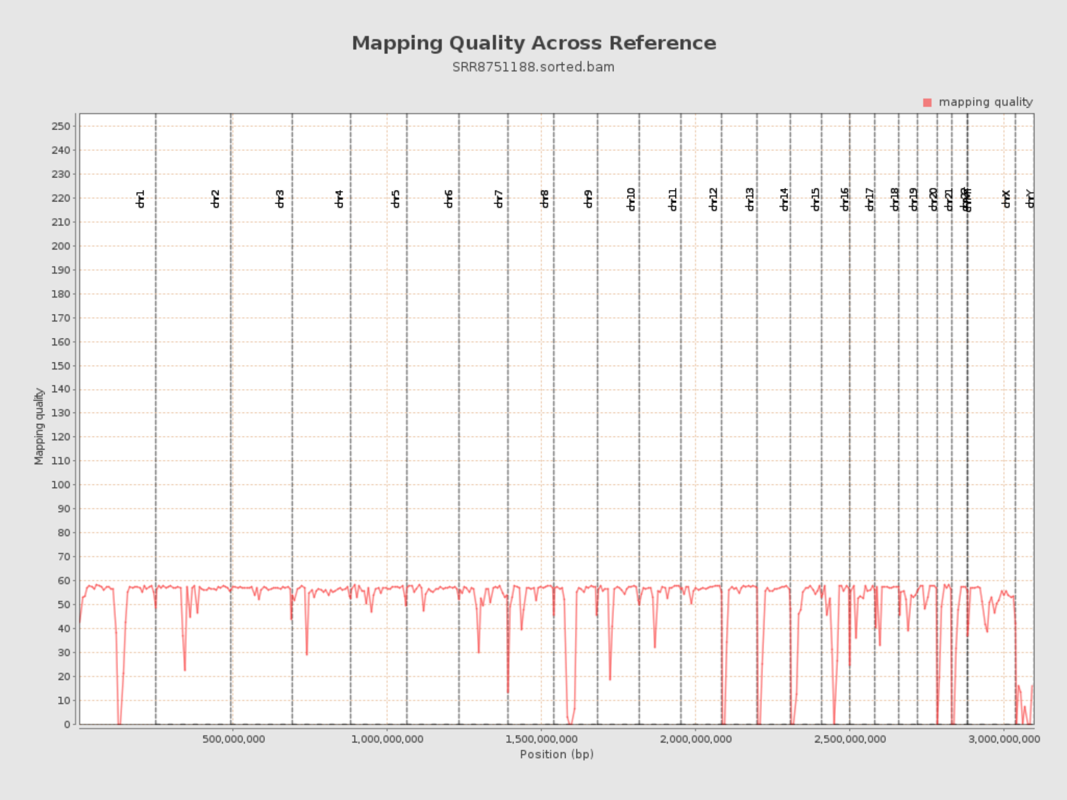
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram