Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/17 08:50:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153398.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_SRR1153398 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153398.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 17 08:50:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153398.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	49,028,572
Mapped reads	48,434,634 / 98.79%
Unmapped reads	593,938 / 1.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	386,746 / 0.79%
Read min/max/mean length	30 / 100 / 100.32
Duplicated reads (estimated)	22,161,582 / 45.2%
Duplication rate	32.73%
Clipped reads	10,481,568 / 21.38%

2.2. ACGT Content

Number/percentage of A's	1,215,394,501 / 26.65%
Number/percentage of C's	1,063,317,556 / 23.32%
Number/percentage of T's	1,241,701,414 / 27.23%
Number/percentage of G's	1,038,192,474 / 22.76%
Number/percentage of N's	1,900,053 / 0.04%
GC Percentage	46.08%

2.3. Coverage

Mean	1.4735

Standard Deviation	12.2783

2.4. Mapping Quality

Mean Mapping Quality	50.11

2.5. Mismatches and indels

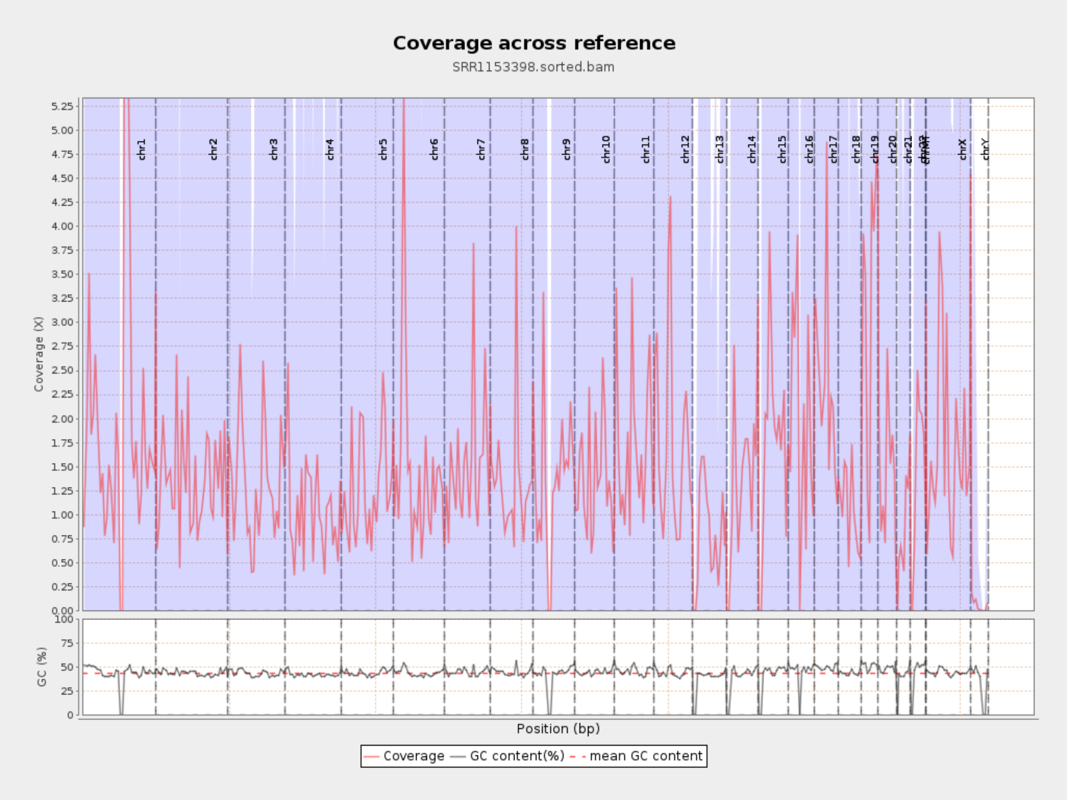
General error rate	0.33%
Mismatches	14,349,749
Insertions	505,199
Mapped reads with at least one insertion	1.03%
Deletions	421,045
Mapped reads with at least one deletion	0.86%
Homopolymer indels	49.39%

2.6. Chromosome stats

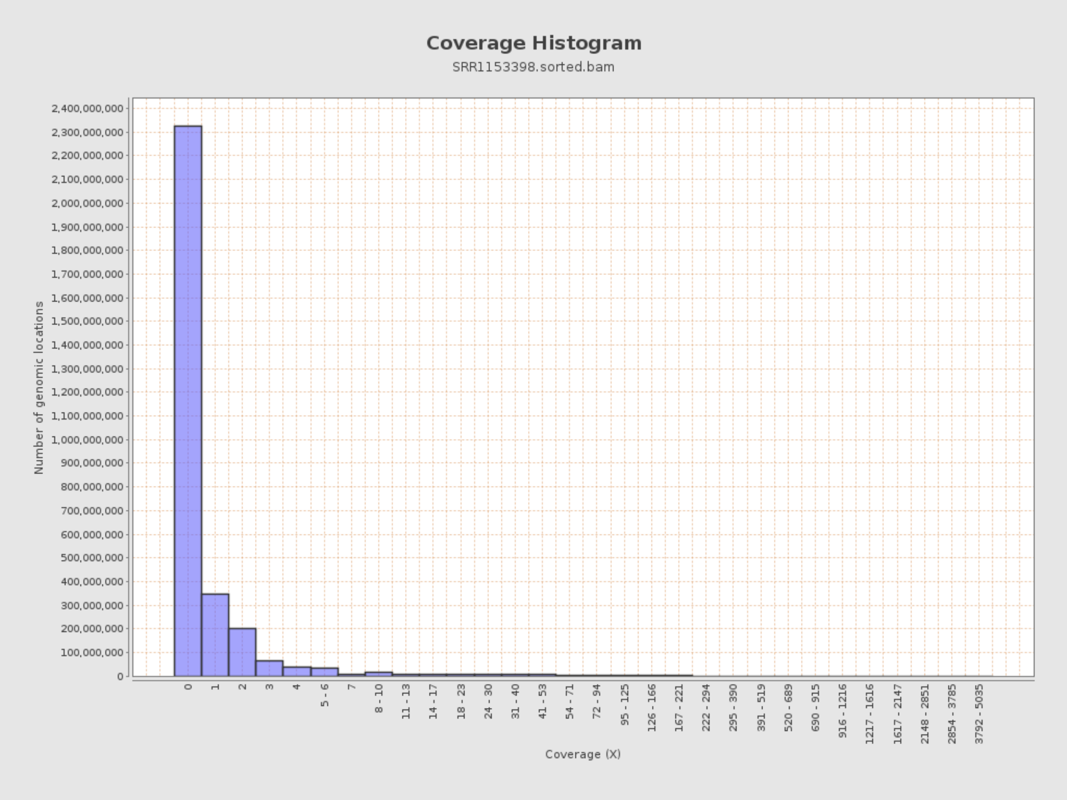
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	475571842	1.908	16.4952
chr2	243199373	333757661	1.3724	10.5043
chr3	198022430	263994773	1.3332	10.1614
chr4	191154276	204231955	1.0684	9.0933
chr5	180915260	231994485	1.2823	10.6197
chr6	171115067	249131248	1.4559	11.6209
chr7	159138663	240629266	1.5121	12.4419

chr8	146364022	195721266	1.3372	15.4767
chr9	141213431	188478756	1.3347	10.9124
chr10	135534747	189252681	1.3963	9.9912
chr11	135006516	232779156	1.7242	12.0993
chr12	133851895	242291202	1.8101	14.2083
chr13	115169878	90989773	0.79	6.858
chr14	107349540	139898646	1.3032	10.1784
chr15	102531392	171740828	1.675	13.3153
chr16	90354753	170947127	1.892	14.451
chr17	81195210	195655209	2.4097	15.5349
chr18	78077248	83768647	1.0729	8.5558
chr19	59128983	186855542	3.1601	18.8365
chr20	63025520	91536605	1.4524	11.0654
chr21	48129895	41856566	0.8697	7.8113
chr22	51304566	72592908	1.4149	11.7145
chrMT	16571	53484	3.2276	7.7385
chrX	155270560	264383669	1.7027	15.4317
chrY	59373566	3291192	0.0554	2.3047

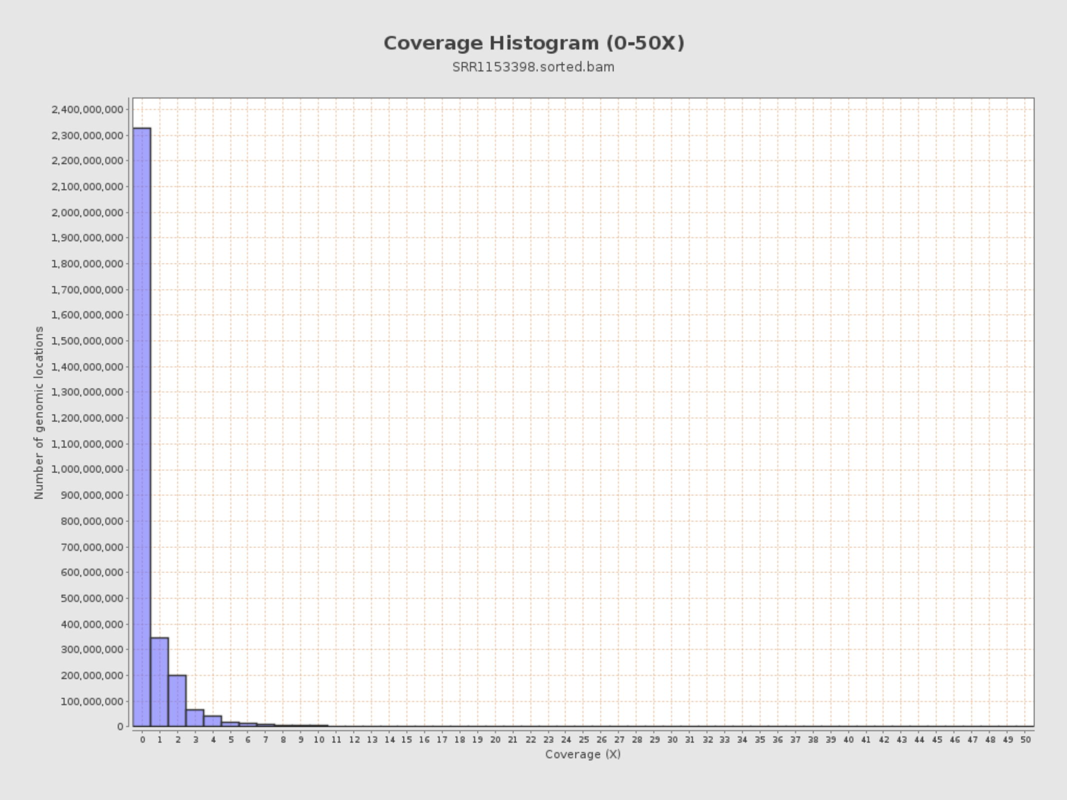
3. Results : Coverage across reference



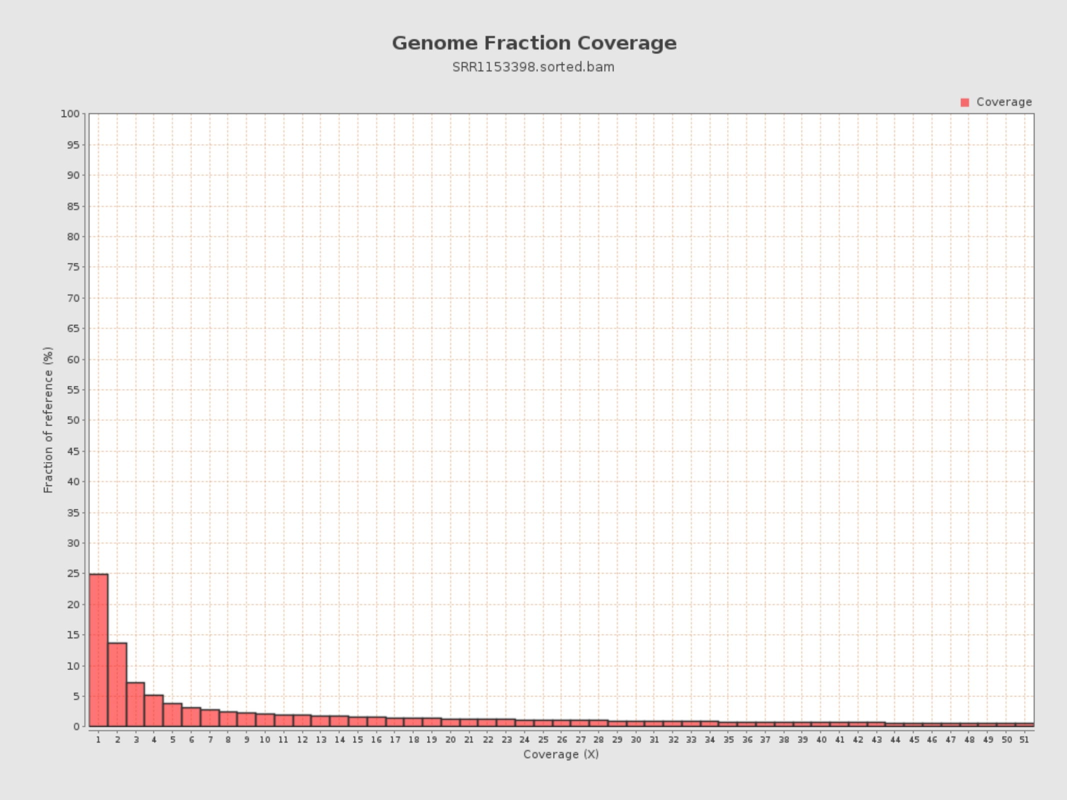
4. Results : Coverage Histogram



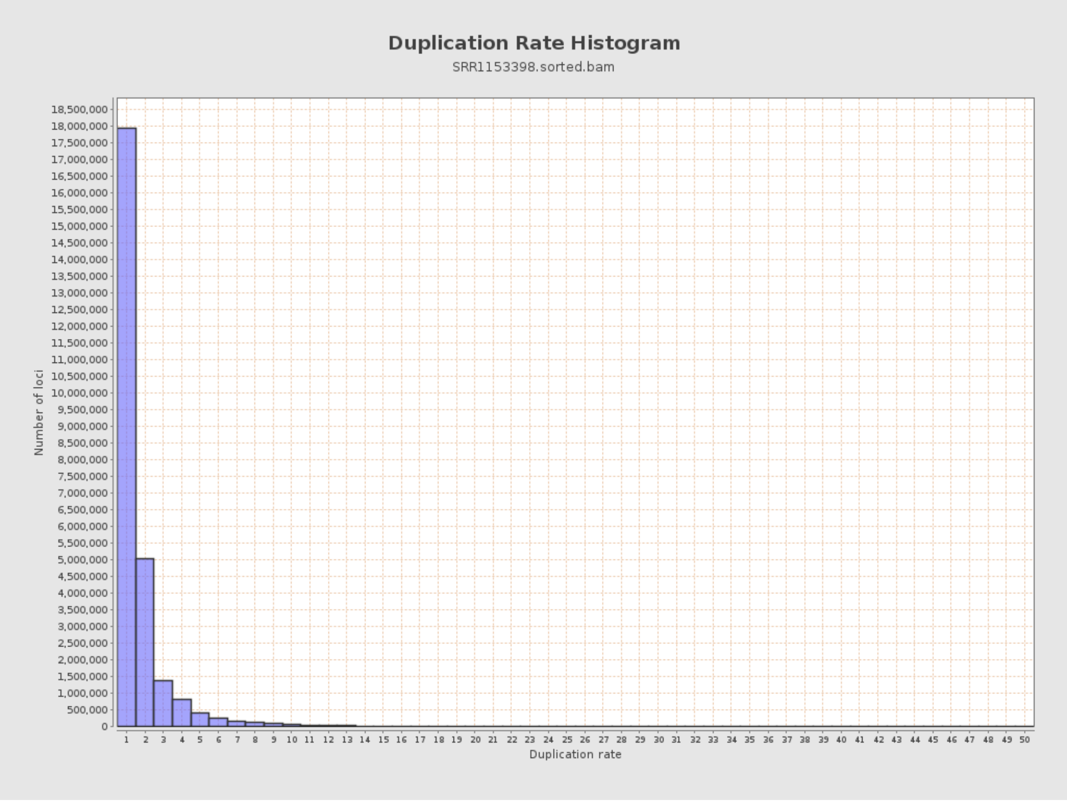
5. Results : Coverage Histogram (0-50X)



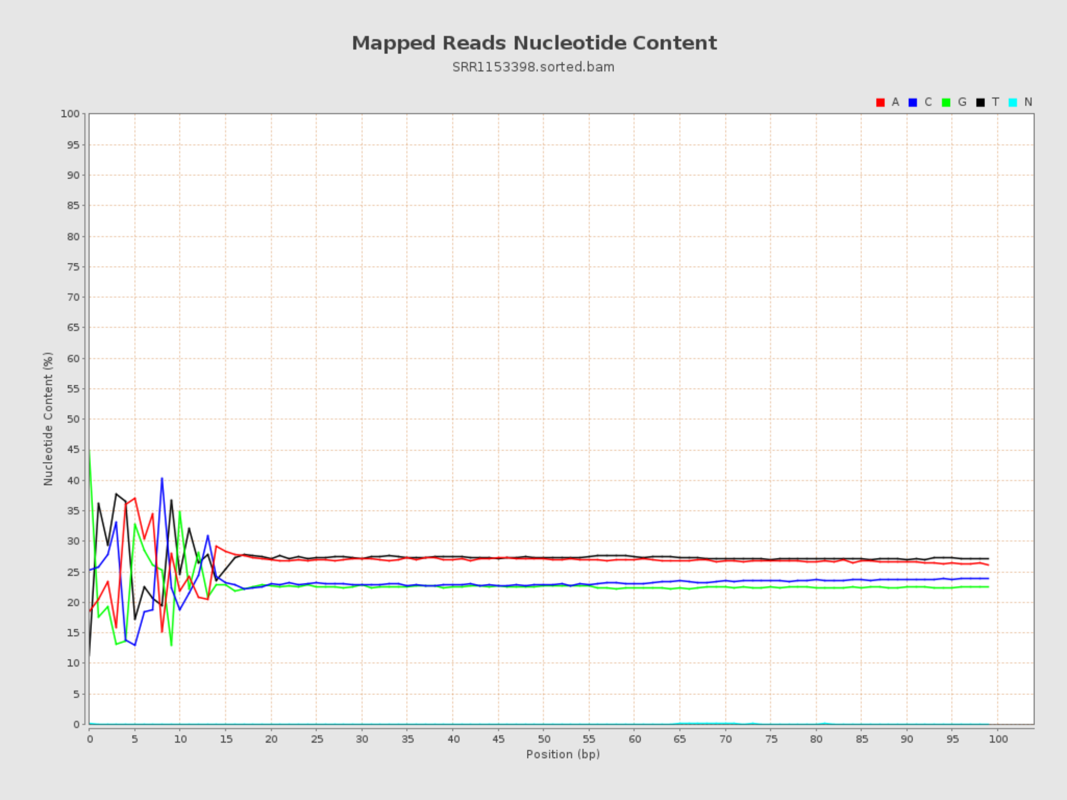
6. Results : Genome Fraction Coverage



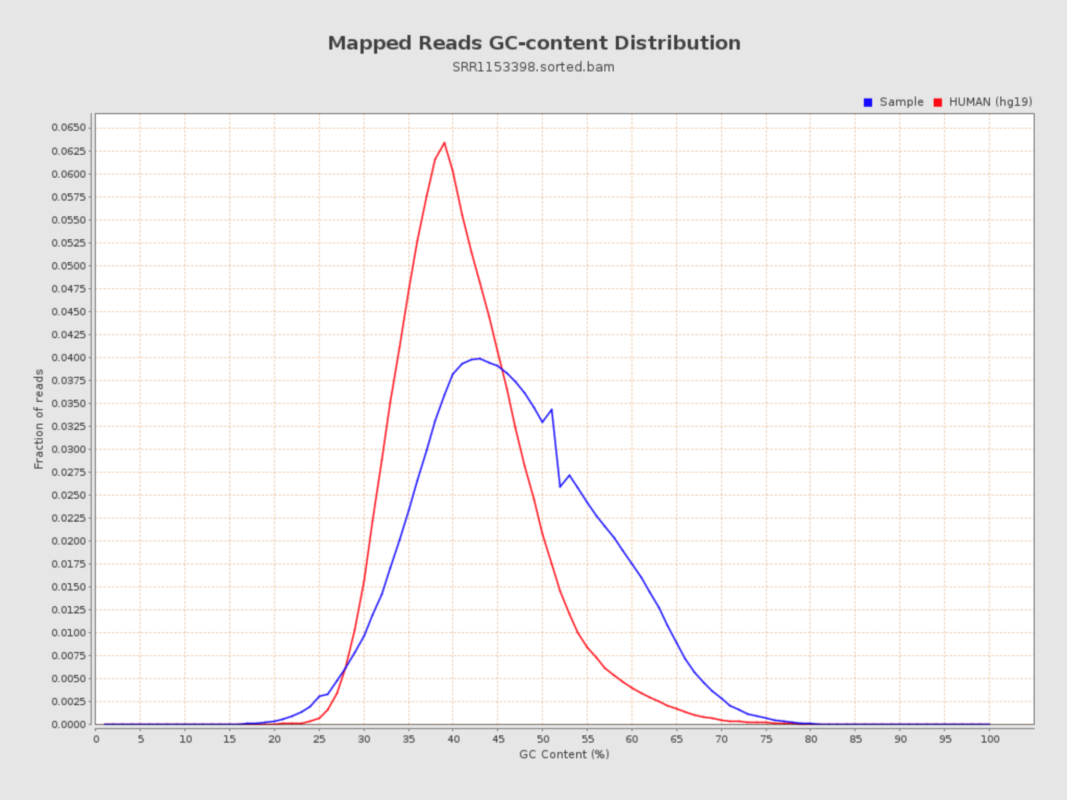
7. Results : Duplication Rate Histogram



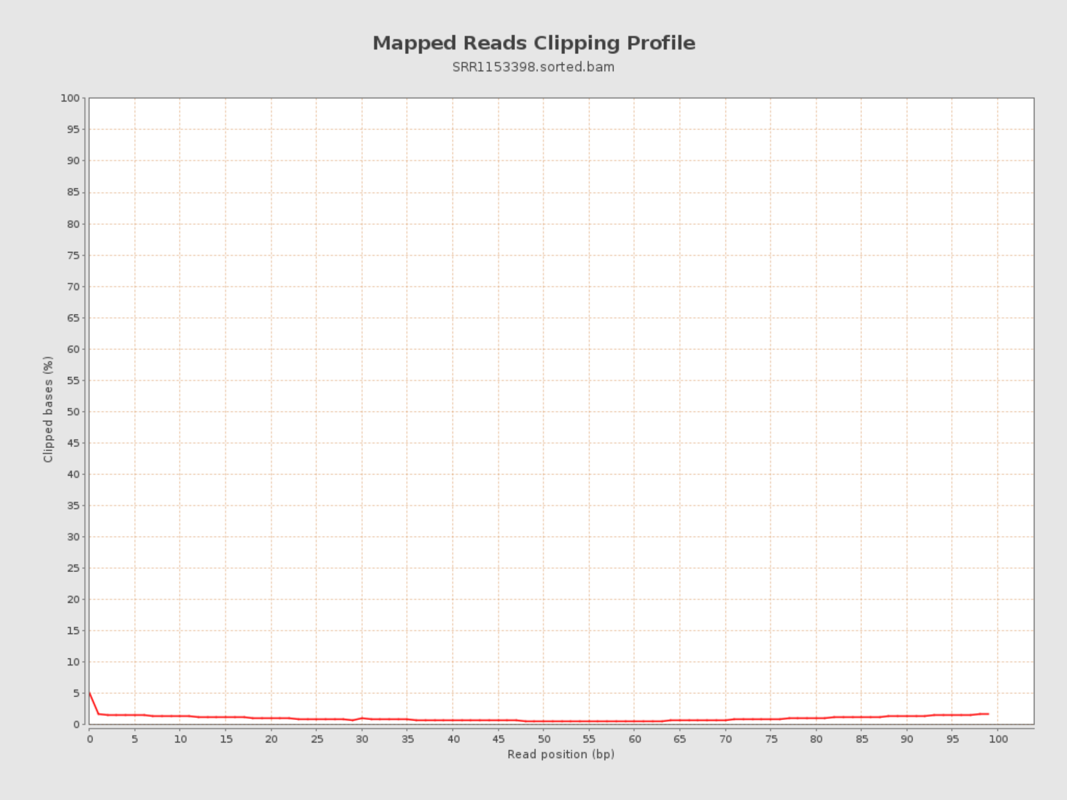
8. Results : Mapped Reads Nucleotide Content



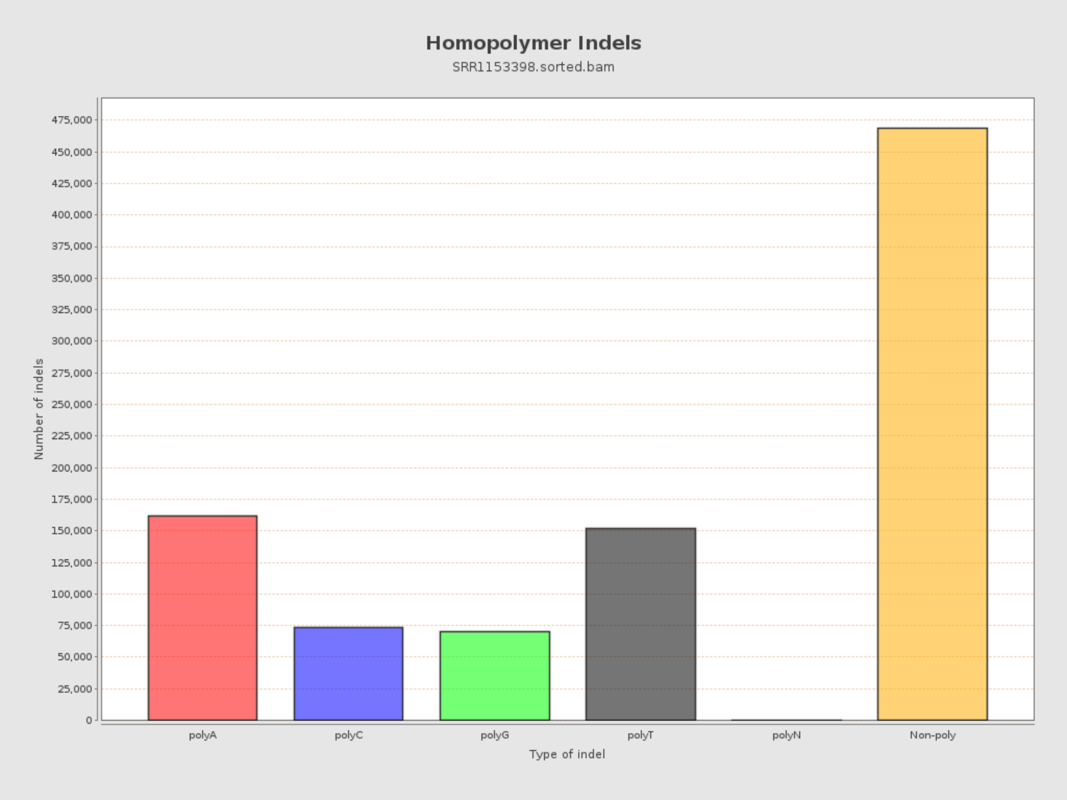
9. Results : Mapped Reads GC-content Distribution



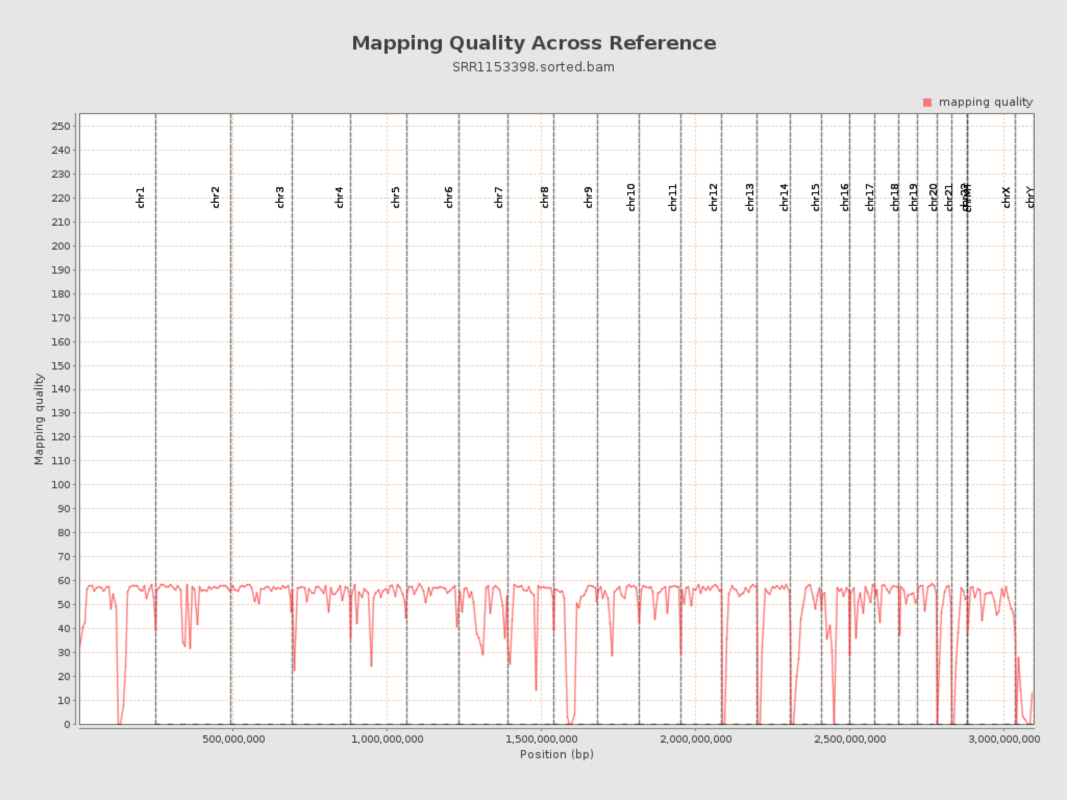
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram