Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/17 17:43:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153401.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_SRR1153401 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153401.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 17 17:43:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153401.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	391,345,290
Mapped reads	377,546,960 / 96.47%
Unmapped reads	13,798,330 / 3.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	489,079 / 0.12%
Read min/max/mean length	30 / 100 / 100.05
Duplicated reads (estimated)	142,744,235 / 36.48%
Duplication rate	36.12%
Clipped reads	179,872,150 / 45.96%

2.2. ACGT Content

Number/percentage of A's	8,640,315,743 / 26.91%
Number/percentage of C's	7,466,183,812 / 23.26%
Number/percentage of T's	8,862,227,787 / 27.6%
Number/percentage of G's	7,074,807,616 / 22.04%
Number/percentage of N's	61,051,021 / 0.19%
GC Percentage	45.29%

2.3. Coverage

Mean	10.3733

Standard Deviation	74.6122

2.4. Mapping Quality

Mean Mapping Quality	50.22

2.5. Mismatches and indels

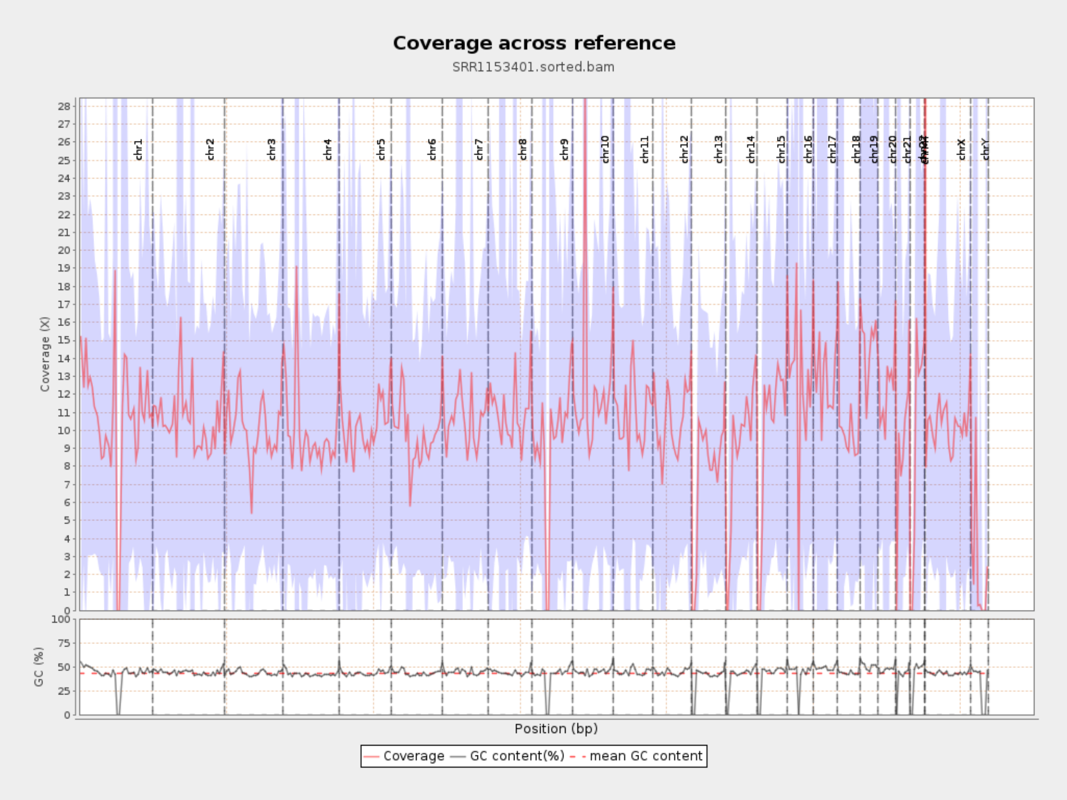
General error rate	0.8%
Mismatches	247,966,819
Insertions	2,834,739
Mapped reads with at least one insertion	0.73%
Deletions	3,367,995
Mapped reads with at least one deletion	0.87%
Homopolymer indels	39.59%

2.6. Chromosome stats

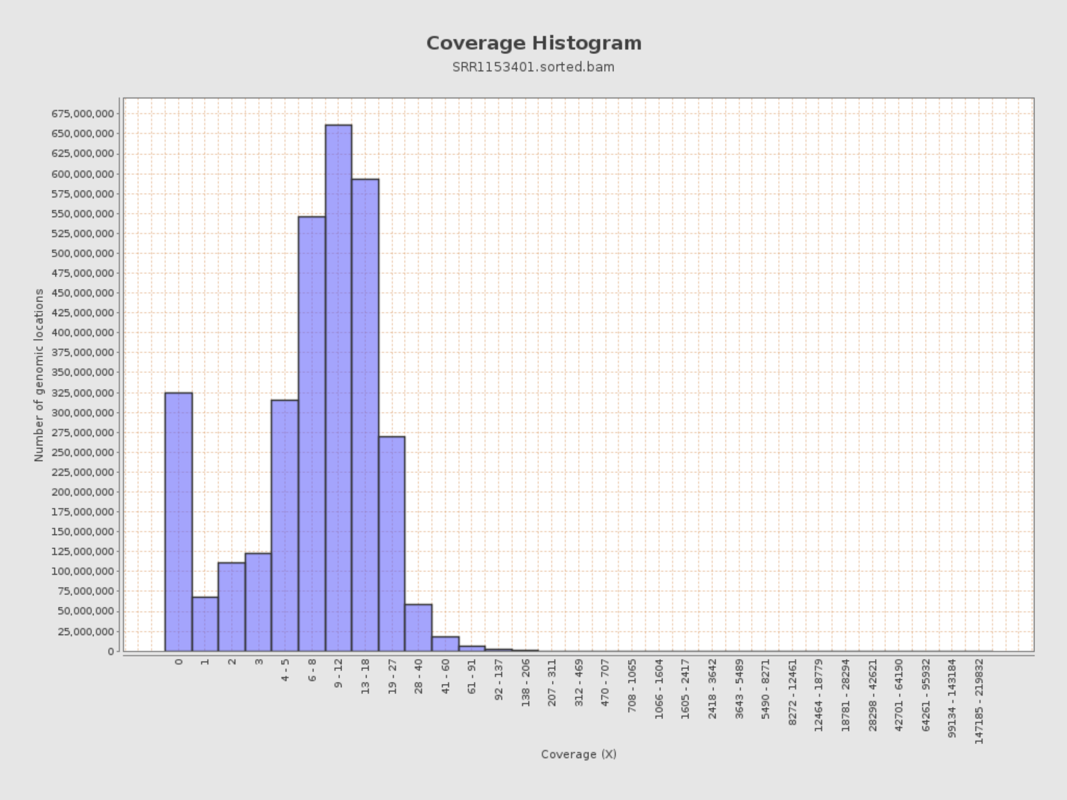
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2697073612	10.8207	189.938
chr2	243199373	2600266233	10.6919	52.5914
chr3	198022430	2001003827	10.1049	19.3959
chr4	191154276	1887162886	9.8725	53.1998
chr5	180915260	1875928259	10.3691	11.3842
chr6	171115067	1660814580	9.7058	23.306
chr7	159138663	1710788179	10.7503	66.1685

chr8	146364022	1608475849	10.9896	38.6183
chr9	141213431	1321058775	9.3551	46.9084
chr10	135534747	1656046874	12.2186	138.0869
chr11	135006516	1503500526	11.1365	31.6006
chr12	133851895	1410481844	10.5376	10.6613
chr13	115169878	879737159	7.6386	7.1499
chr14	107349540	956597775	8.9111	11.9596
chr15	102531392	1001491217	9.7677	9.9912
chr16	90354753	1157415031	12.8097	54.0691
chr17	81195210	1050788683	12.9415	35.8772
chr18	78077248	790333462	10.1225	104.2883
chr19	59128983	876389974	14.8217	124.5678
chr20	63025520	770896932	12.2315	20.4192
chr21	48129895	454498916	9.4432	44.0306
chr22	51304566	509395682	9.9289	13.686
chrMT	16571	5408009	326.3538	96.414
chrX	155270560	1589169856	10.2348	19.3286
chrY	59373566	137757866	2.3202	92.9139

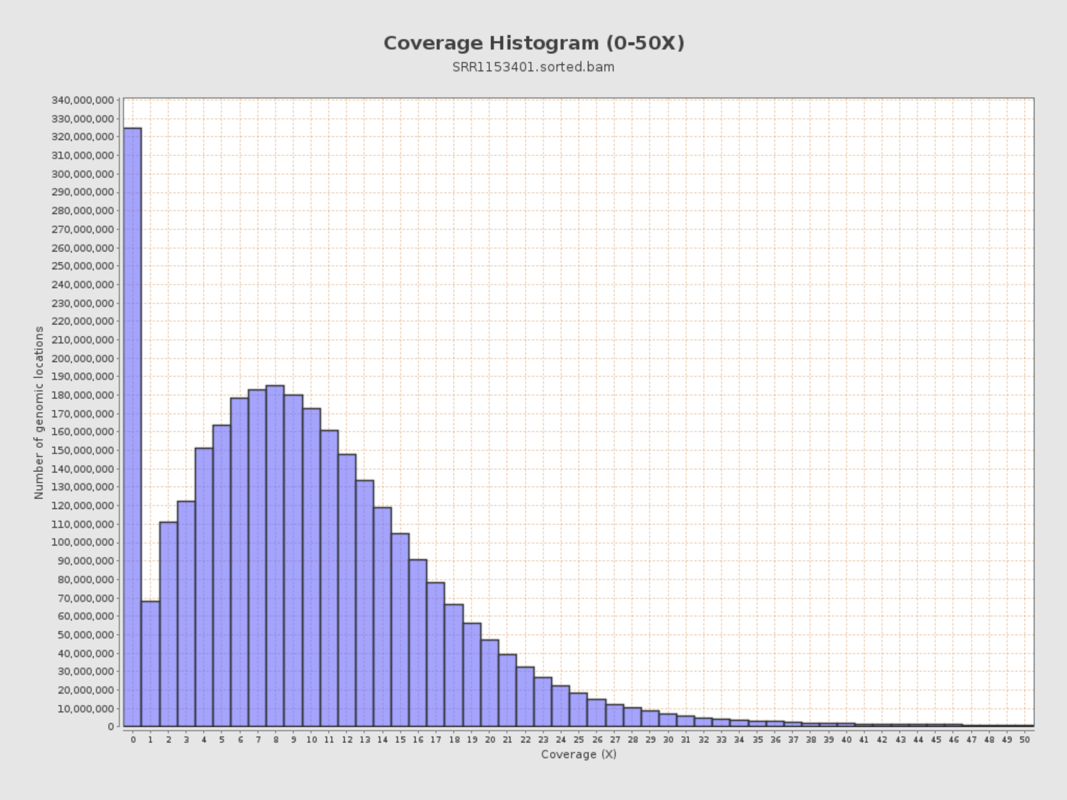
3. Results : Coverage across reference



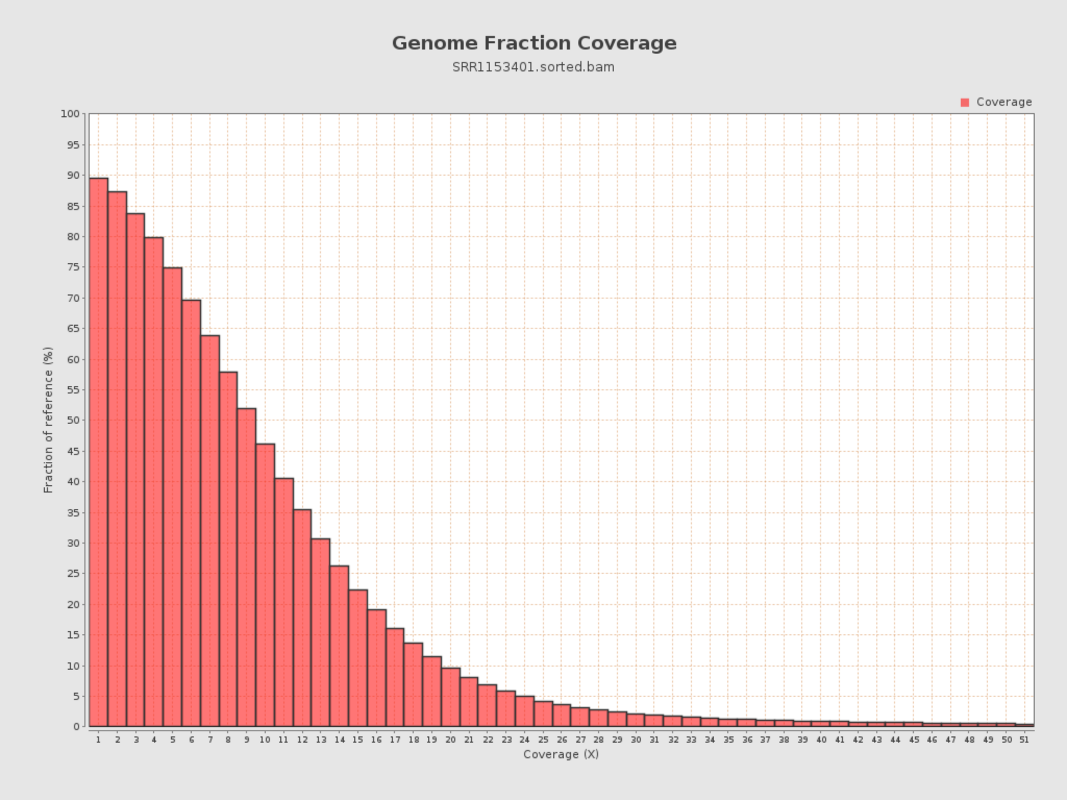
4. Results : Coverage Histogram



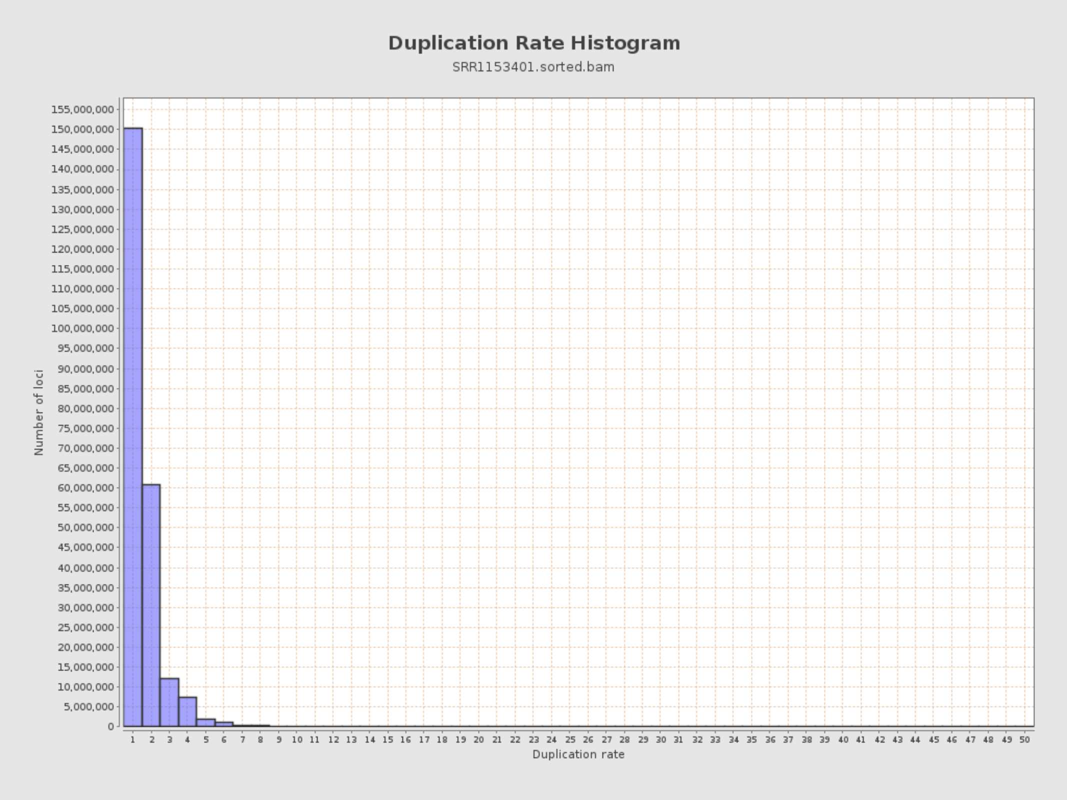
5. Results : Coverage Histogram (0-50X)



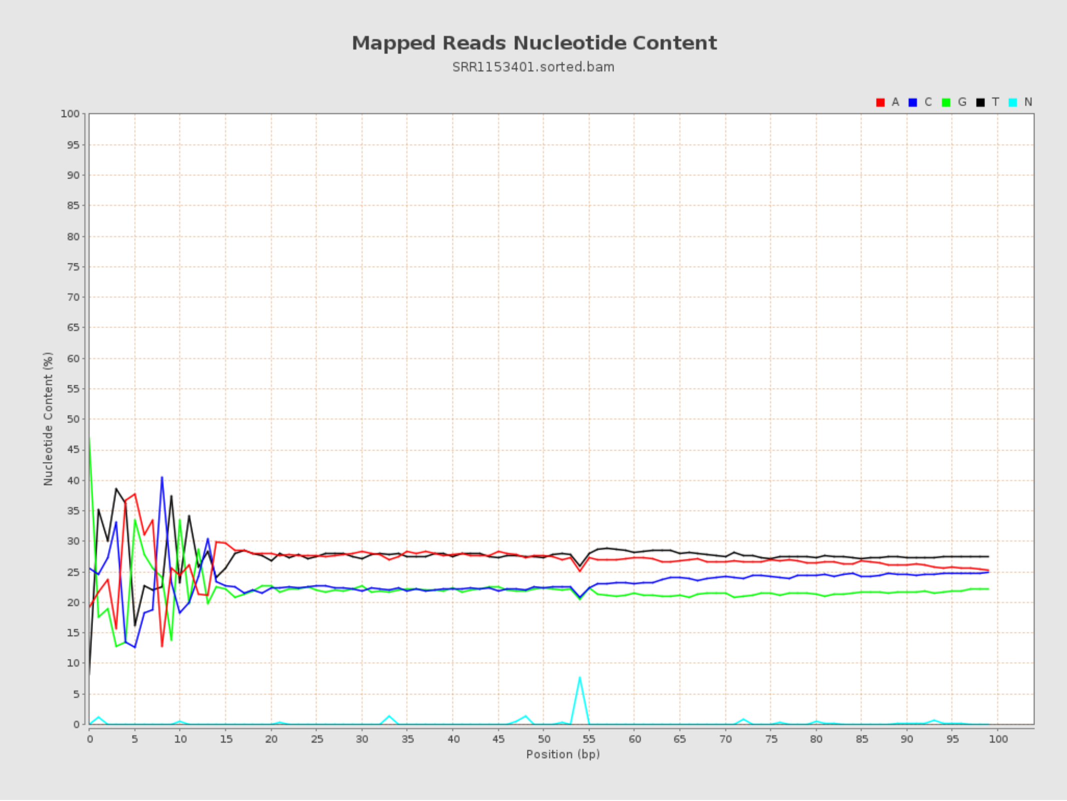
6. Results : Genome Fraction Coverage



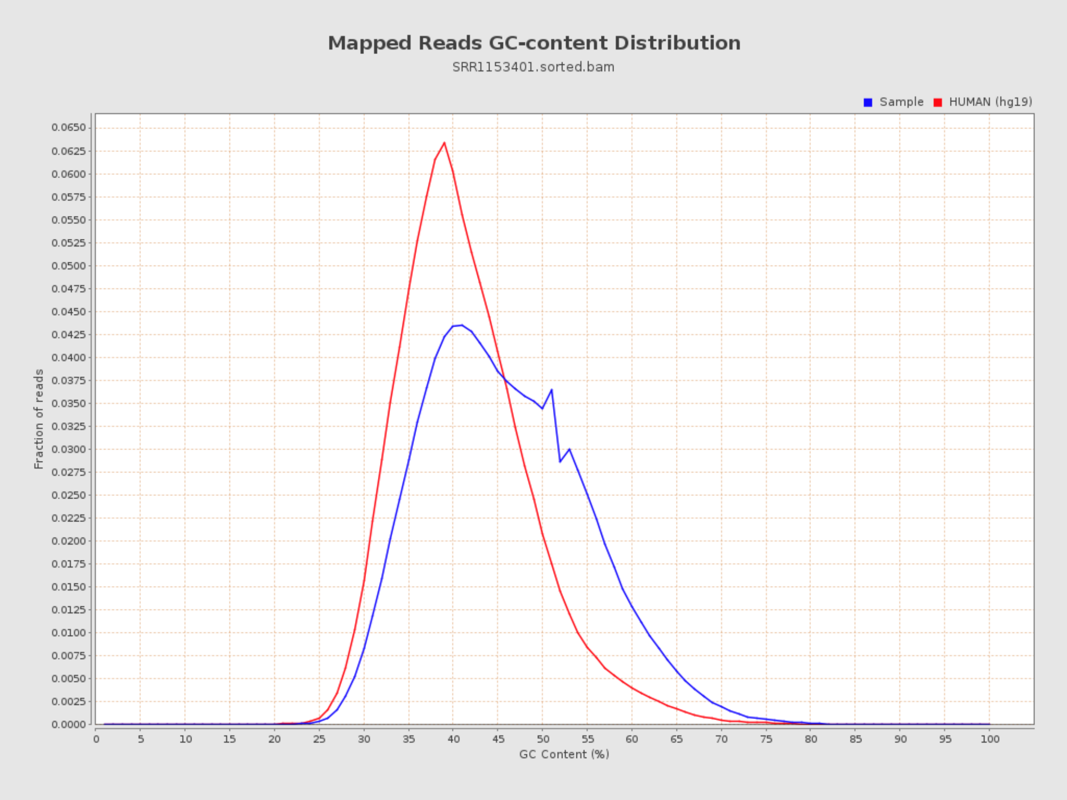
7. Results : Duplication Rate Histogram



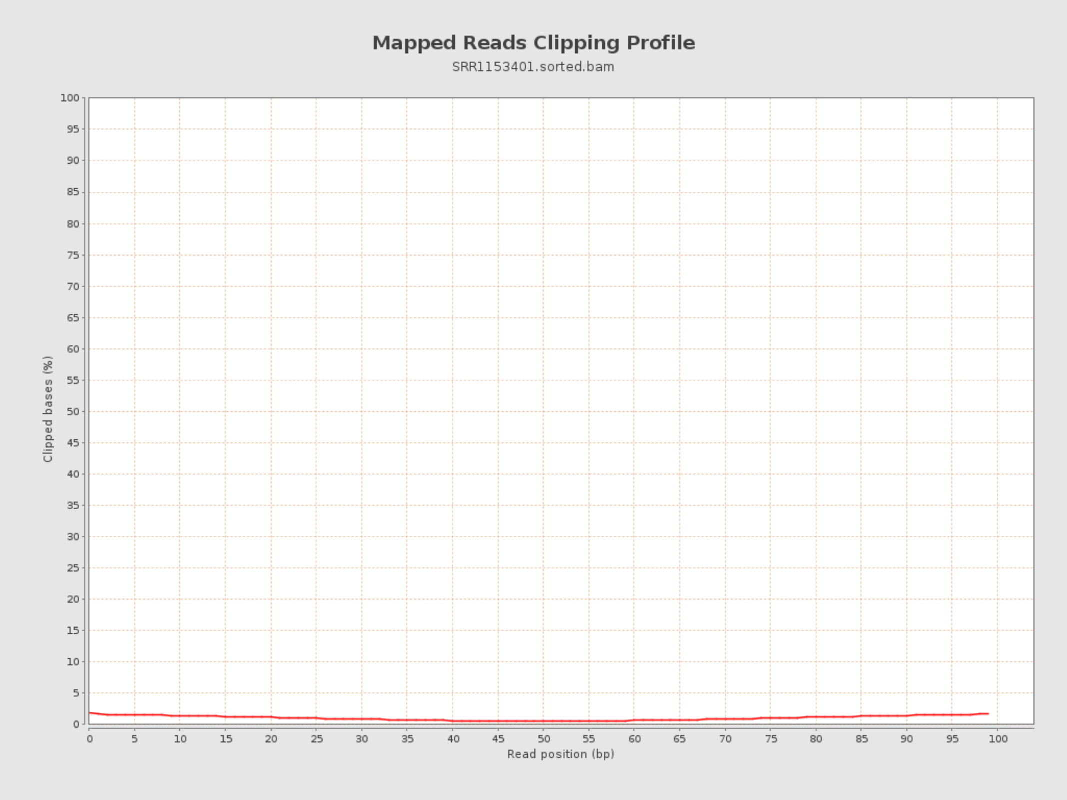
8. Results : Mapped Reads Nucleotide Content



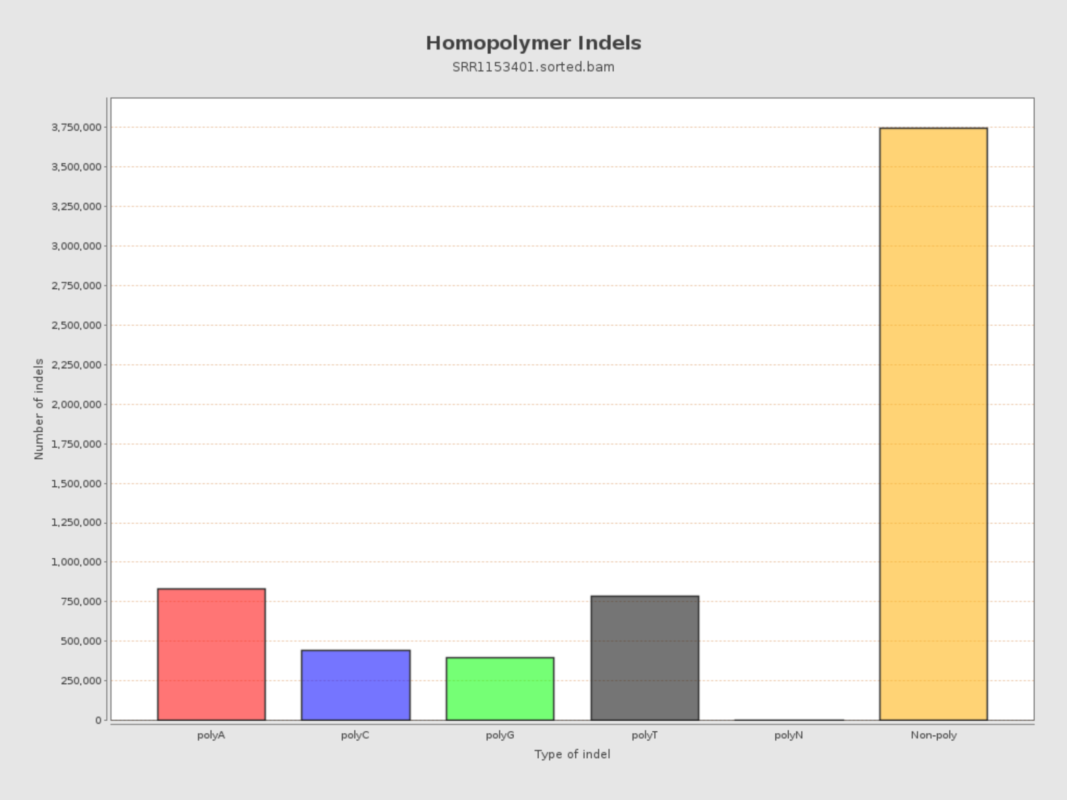
9. Results : Mapped Reads GC-content Distribution



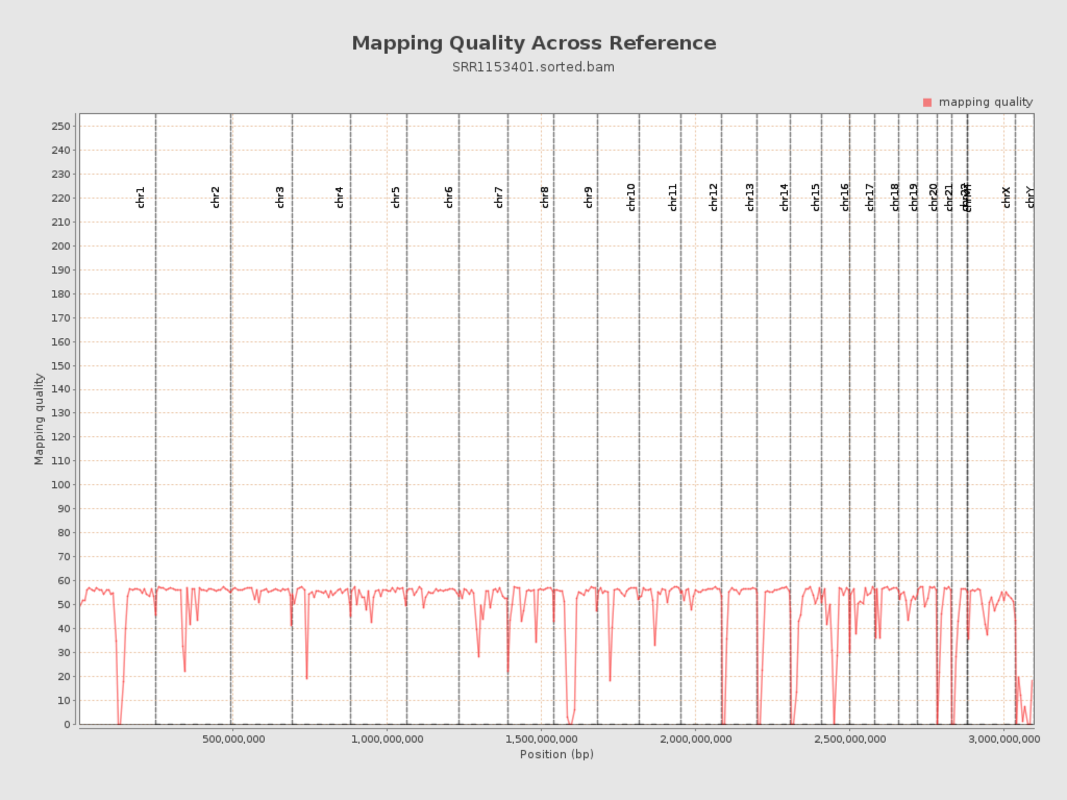
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram