Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 15:42:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153374.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_SRR1153374 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153374.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 15:42:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153374.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	37,877,850
Mapped reads	37,645,531 / 99.39%
Unmapped reads	232,319 / 0.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	225,811 / 0.6%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	21,408,149 / 56.52%
Duplication rate	44%
Clipped reads	15,499,826 / 40.92%

2.2. ACGT Content

Number/percentage of A's	891,275,763 / 26.72%
Number/percentage of C's	780,854,258 / 23.41%
Number/percentage of T's	916,628,473 / 27.48%
Number/percentage of G's	745,915,589 / 22.36%
Number/percentage of N's	942,435 / 0.03%
GC Percentage	45.77%

2.3. Coverage

Mean	1.0777

Standard Deviation	13.12

2.4. Mapping Quality

Mean Mapping Quality	49.88

2.5. Mismatches and indels

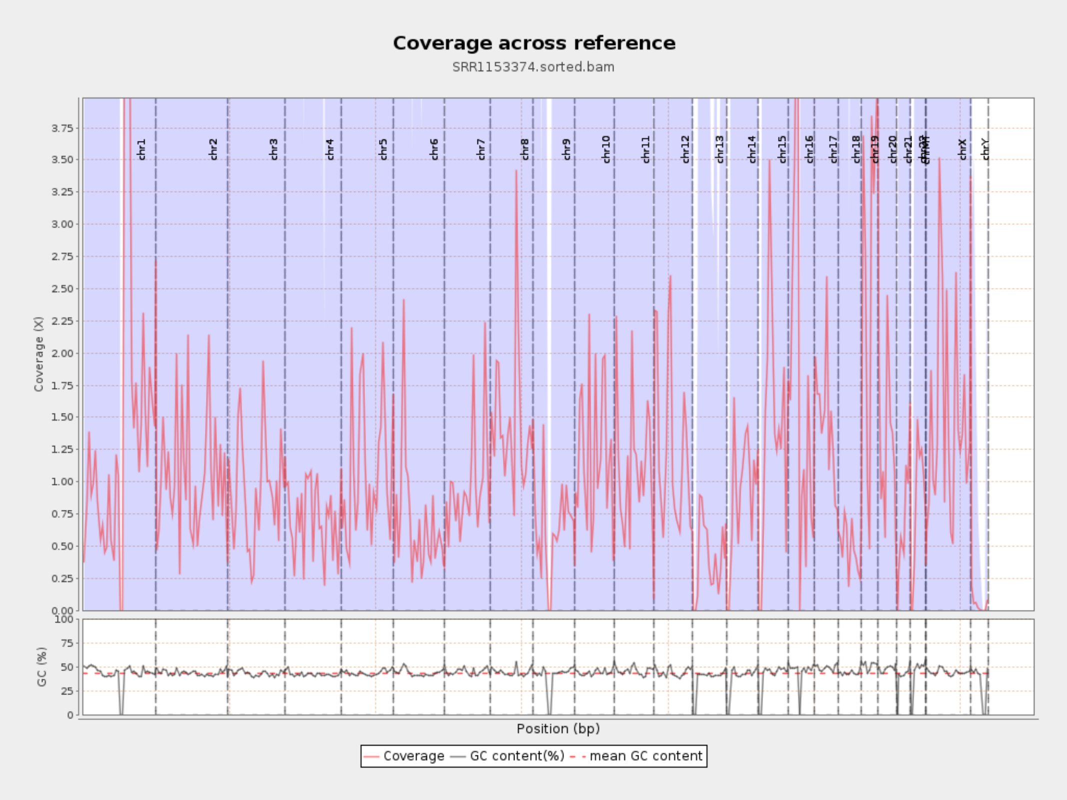
General error rate	0.23%
Mismatches	7,337,308
Insertions	337,212
Mapped reads with at least one insertion	0.89%
Deletions	265,326
Mapped reads with at least one deletion	0.7%
Homopolymer indels	49.07%

2.6. Chromosome stats

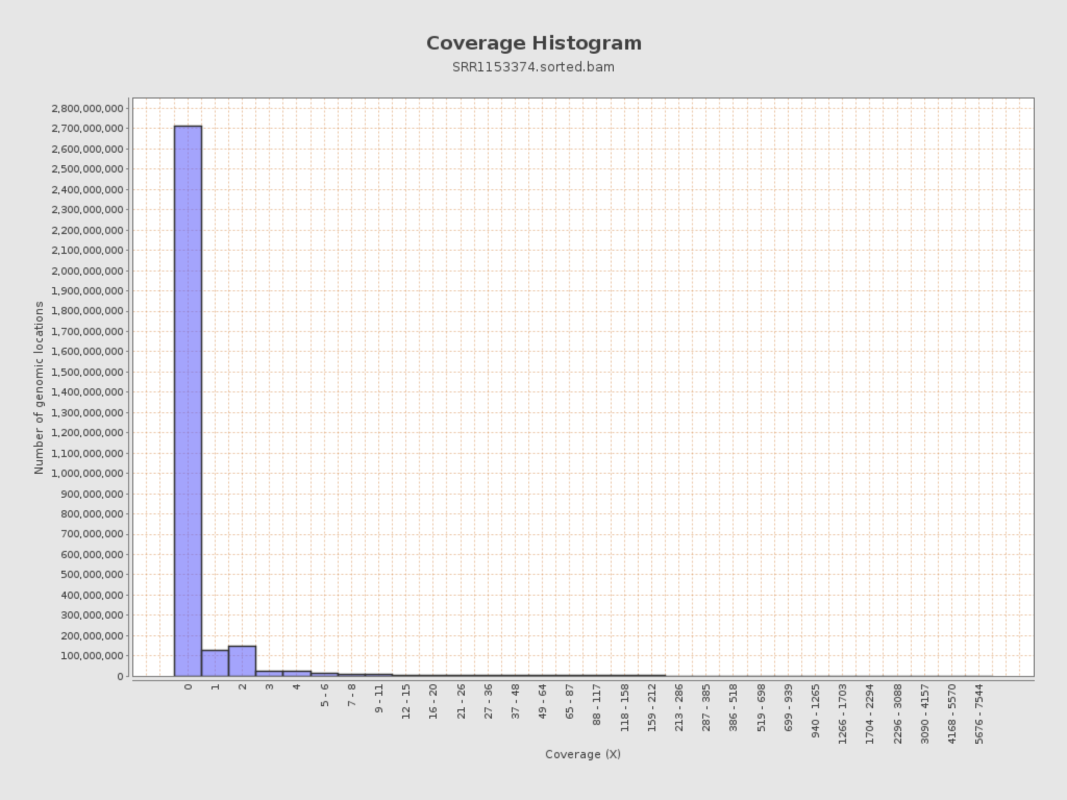
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	349524722	1.4023	15.5935
chr2	243199373	256596151	1.0551	11.6479
chr3	198022430	184699430	0.9327	10.5241
chr4	191154276	135509924	0.7089	8.5342
chr5	180915260	198547179	1.0975	12.0957
chr6	171115067	114881995	0.6714	8.5835
chr7	159138663	153593825	0.9652	11.4513

chr8	146364022	214401318	1.4648	18.0146
chr9	141213431	87950954	0.6228	7.9415
chr10	135534747	168087803	1.2402	13.3473
chr11	135006516	152126806	1.1268	11.5499
chr12	133851895	172501494	1.2887	14.0015
chr13	115169878	46541356	0.4041	6.2223
chr14	107349540	96827152	0.902	9.9092
chr15	102531392	139234375	1.358	13.9566
chr16	90354753	152917411	1.6924	26.794
chr17	81195210	123024429	1.5152	13.3588
chr18	78077248	38210493	0.4894	6.1846
chr19	59128983	157027602	2.6557	24.2419
chr20	63025520	81449728	1.2923	14.0193
chr21	48129895	34506670	0.7169	9.1008
chr22	51304566	42780879	0.8339	10.1539
chrMT	16571	5877	0.3547	2.0773
chrX	155270560	232465927	1.4972	16.8627
chrY	59373566	2737004	0.0461	2.0665

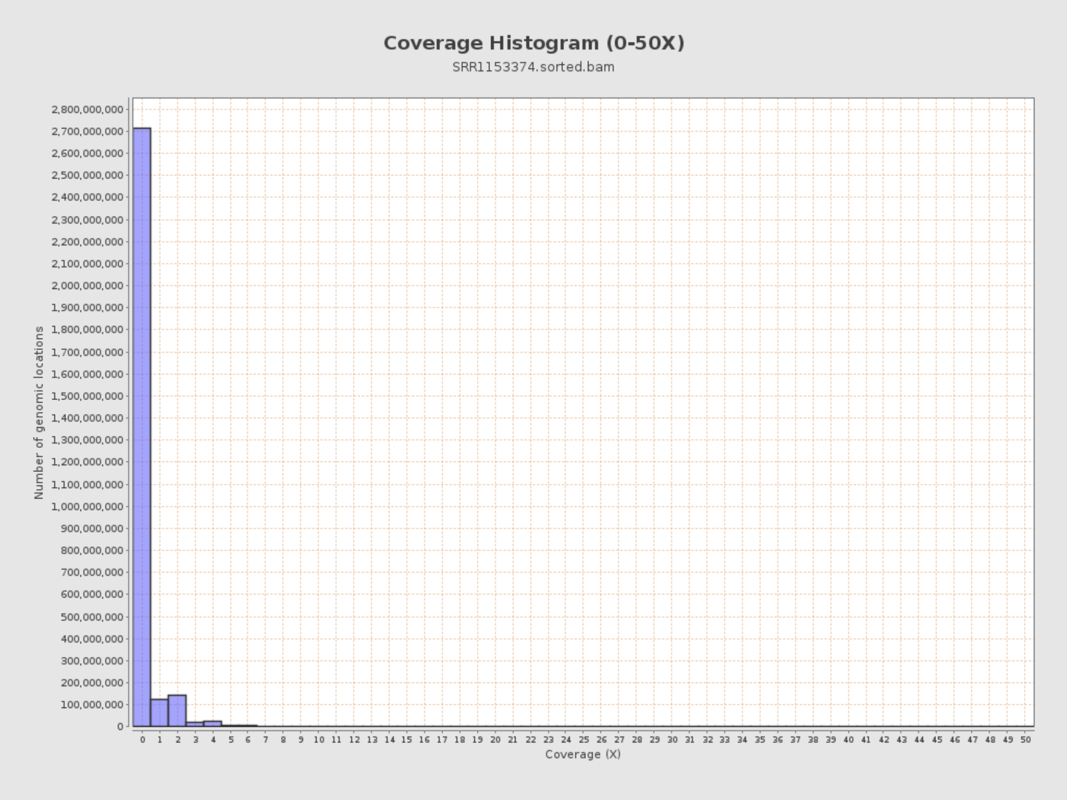
3. Results : Coverage across reference



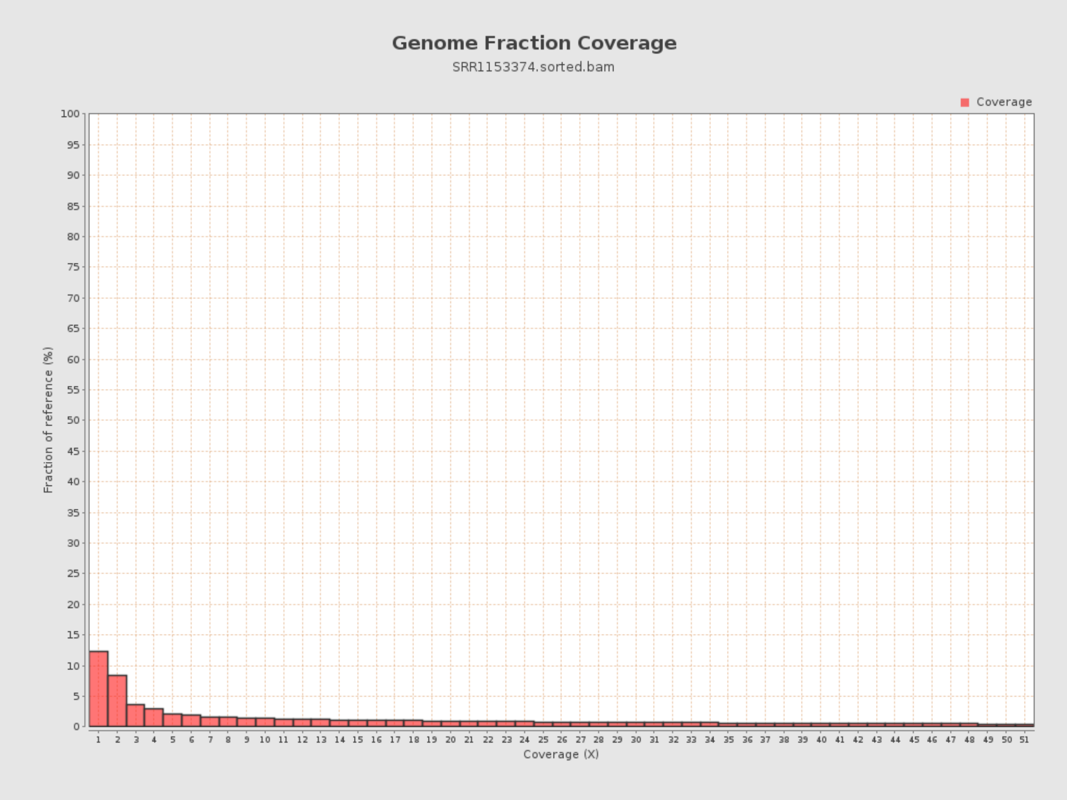
4. Results : Coverage Histogram



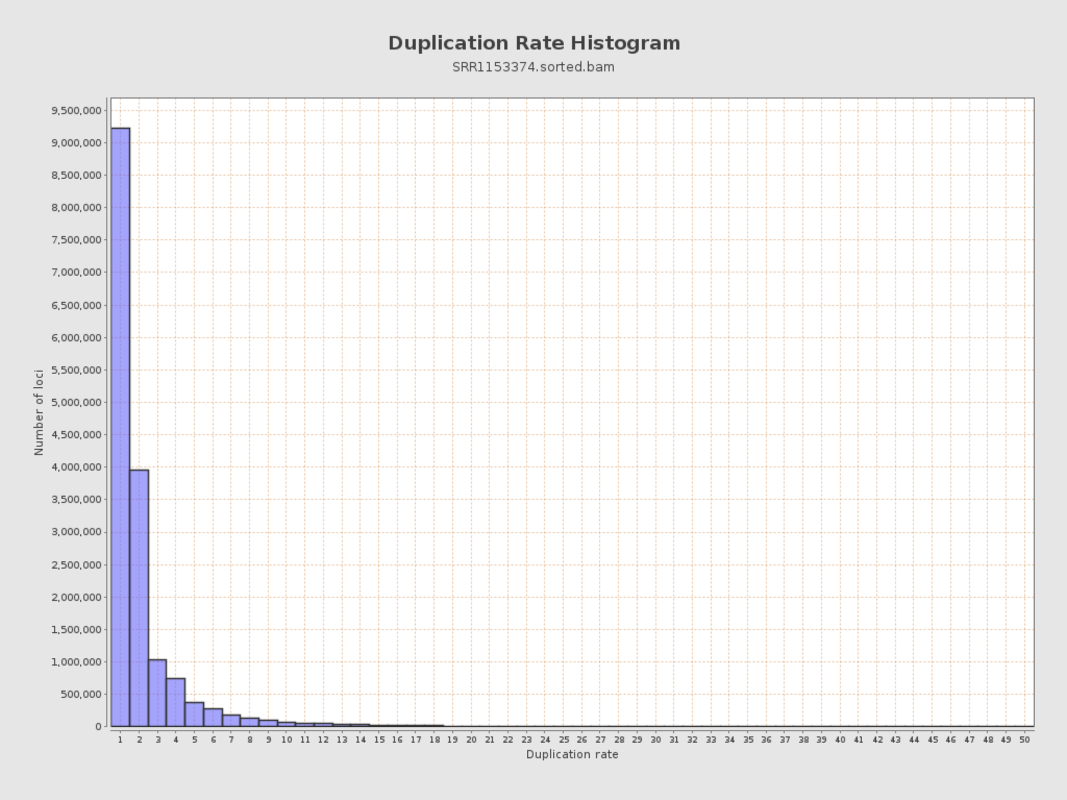
5. Results : Coverage Histogram (0-50X)



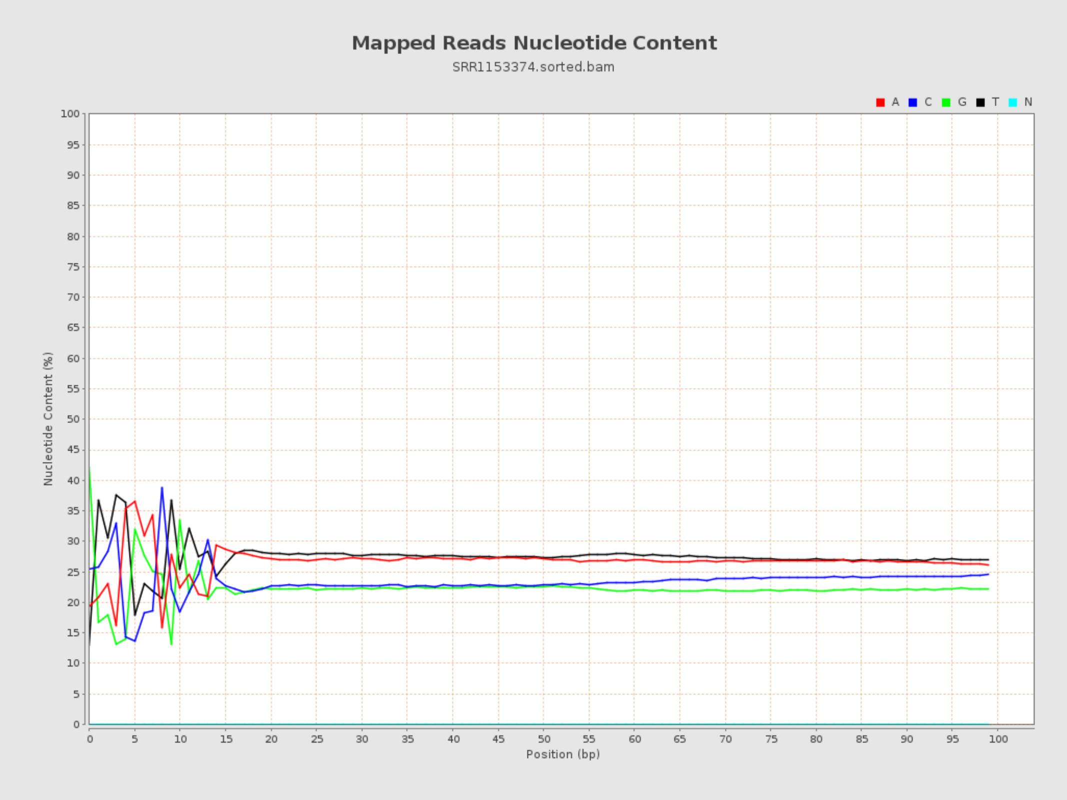
6. Results : Genome Fraction Coverage



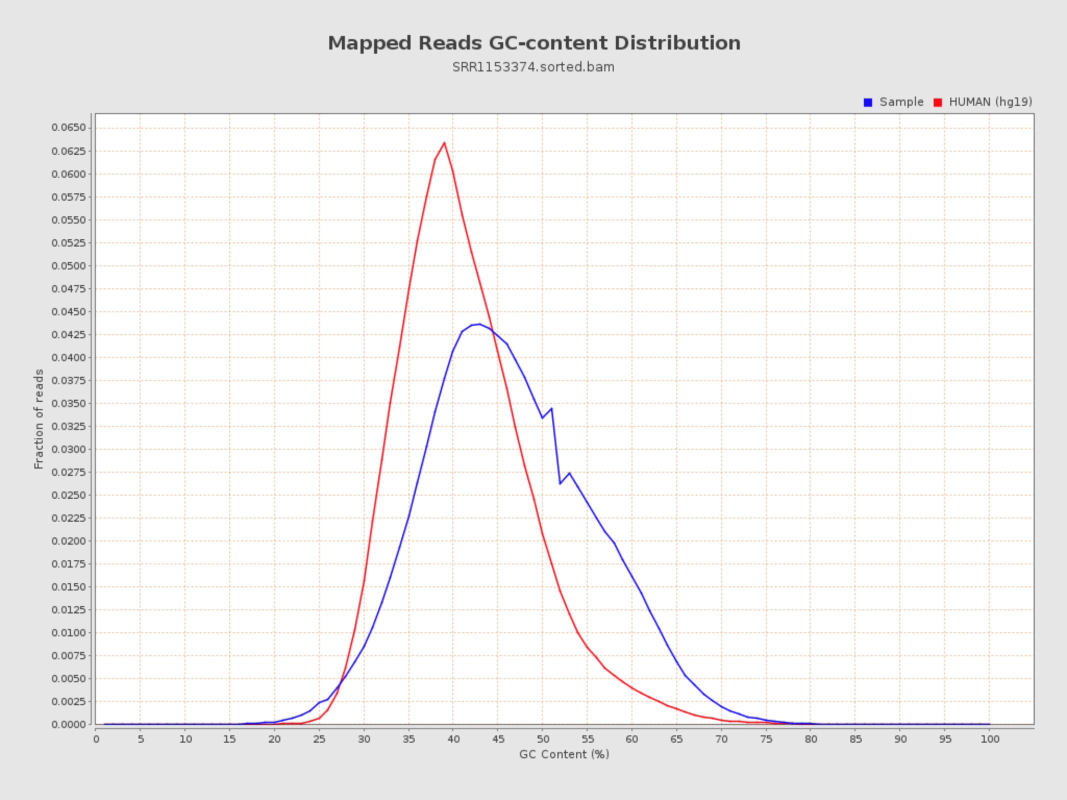
7. Results : Duplication Rate Histogram



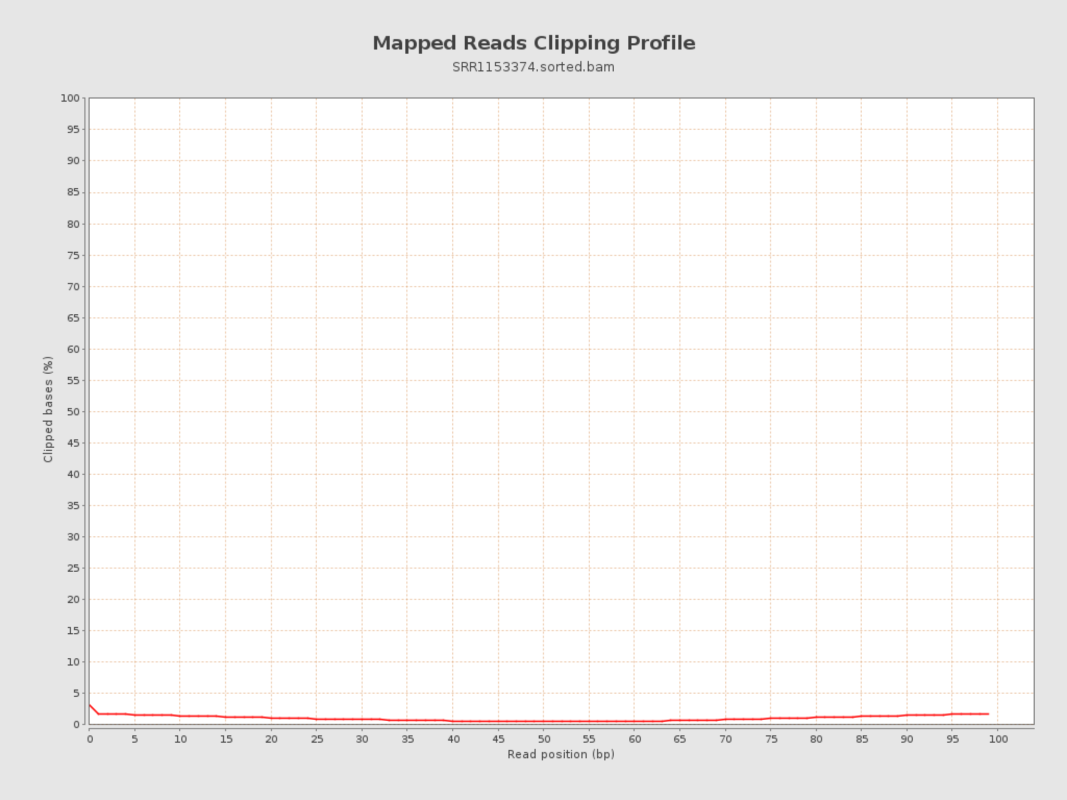
8. Results : Mapped Reads Nucleotide Content



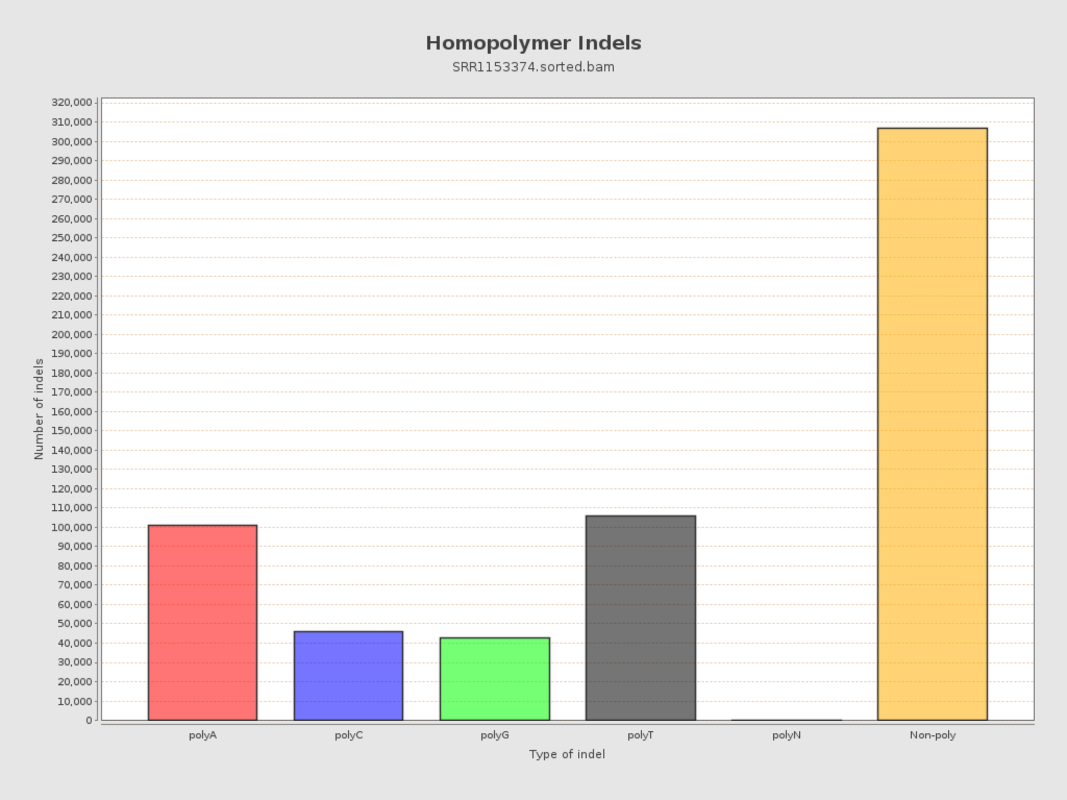
9. Results : Mapped Reads GC-content Distribution



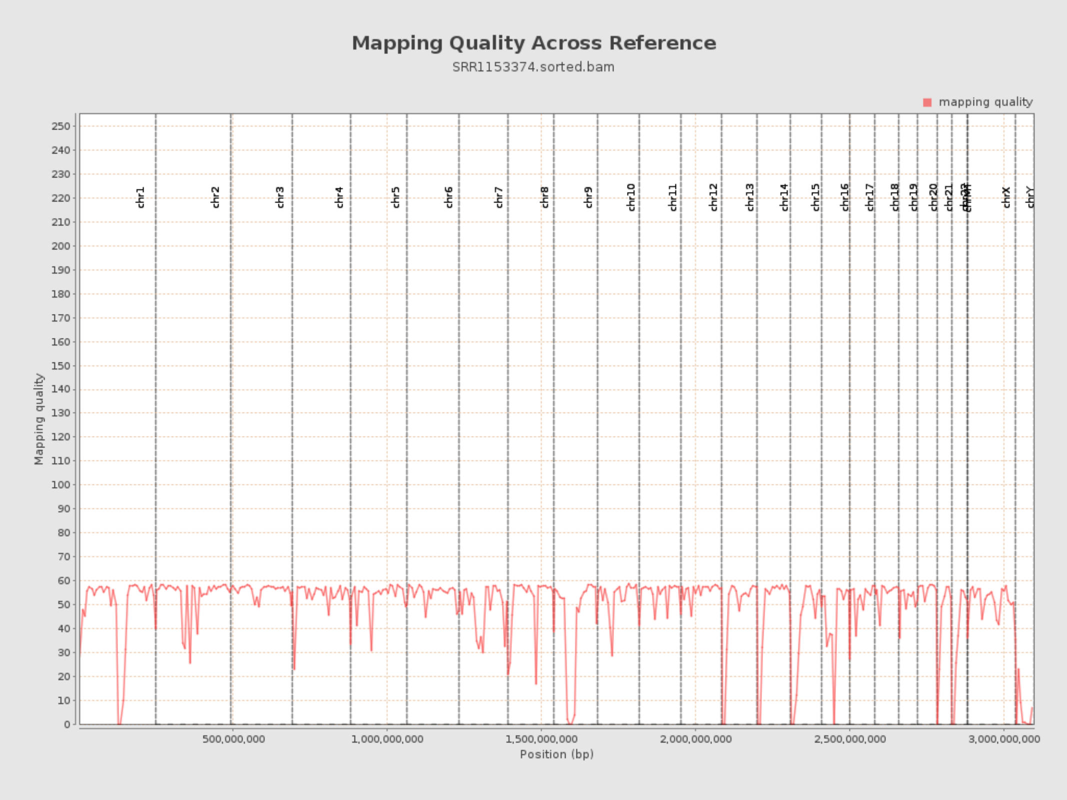
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram