Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 02:40:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506324.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_SRR1506324 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506324.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 02:40:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506324.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,408,233
Mapped reads	4,555,665 / 84.24%
Unmapped reads	852,568 / 15.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	88,619 / 1.64%
Read min/max/mean length	30 / 94 / 94.59
Duplicated reads (estimated)	828,630 / 15.32%
Duplication rate	12.45%
Clipped reads	2,878,962 / 53.23%

2.2. ACGT Content

Number/percentage of A's	100,999,670 / 28.29%
Number/percentage of C's	64,930,389 / 18.18%
Number/percentage of T's	101,608,873 / 28.46%
Number/percentage of G's	89,448,426 / 25.05%
Number/percentage of N's	80,408 / 0.02%
GC Percentage	43.24%

2.3. Coverage

Mean	0.1154

Standard Deviation	0.8345

2.4. Mapping Quality

Mean Mapping Quality	47.5

2.5. Mismatches and indels

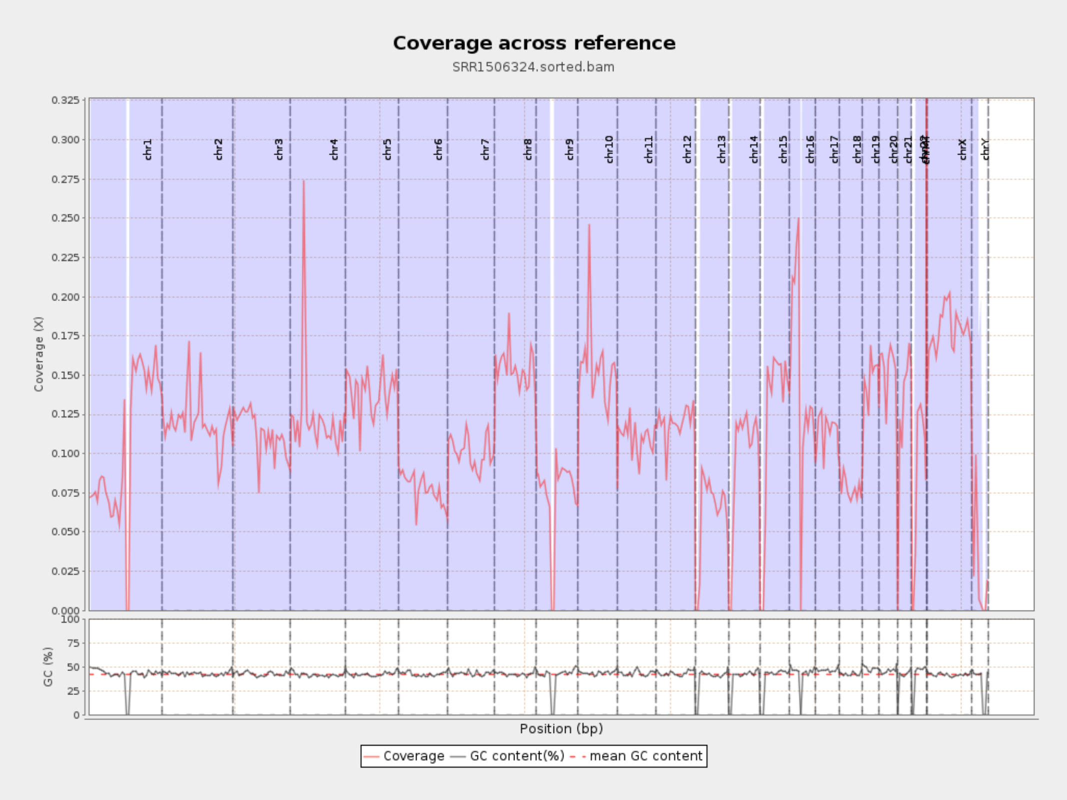
General error rate	0.74%
Mismatches	2,570,802
Insertions	31,887
Mapped reads with at least one insertion	0.68%
Deletions	77,282
Mapped reads with at least one deletion	1.66%
Homopolymer indels	43.92%

2.6. Chromosome stats

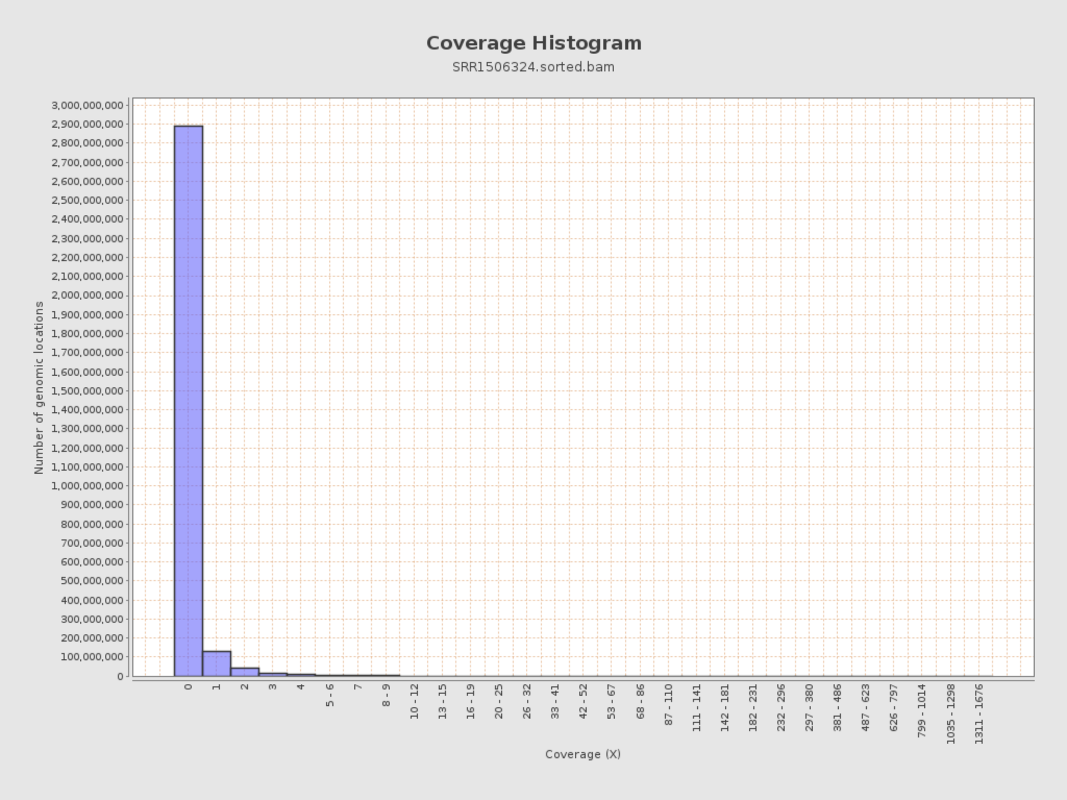
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26102738	0.1047	1.2414
chr2	243199373	29257174	0.1203	0.8868
chr3	198022430	22391547	0.1131	0.5463
chr4	191154276	23374578	0.1223	0.8637
chr5	180915260	25166814	0.1391	0.6187
chr6	171115067	13312127	0.0778	0.4756
chr7	159138663	16080147	0.101	0.7334

chr8	146364022	22644526	0.1547	1.3335
chr9	141213431	10451364	0.074	0.6779
chr10	135534747	21085872	0.1556	1.1612
chr11	135006516	14811276	0.1097	0.7548
chr12	133851895	15957330	0.1192	0.5794
chr13	115169878	7109019	0.0617	0.4026
chr14	107349540	10388913	0.0968	0.5514
chr15	102531392	12552415	0.1224	0.5897
chr16	90354753	13326609	0.1475	0.7945
chr17	81195210	9319678	0.1148	0.6316
chr18	78077248	6093994	0.0781	1.1059
chr19	59128983	8603032	0.1455	0.9911
chr20	63025520	9646325	0.1531	0.6933
chr21	48129895	6138261	0.1275	0.8705
chr22	51304566	4249587	0.0828	0.4912
chrMT	16571	12247	0.7391	1.8963
chrX	155270560	27664936	0.1782	0.7641
chrY	59373566	1484301	0.025	0.9416

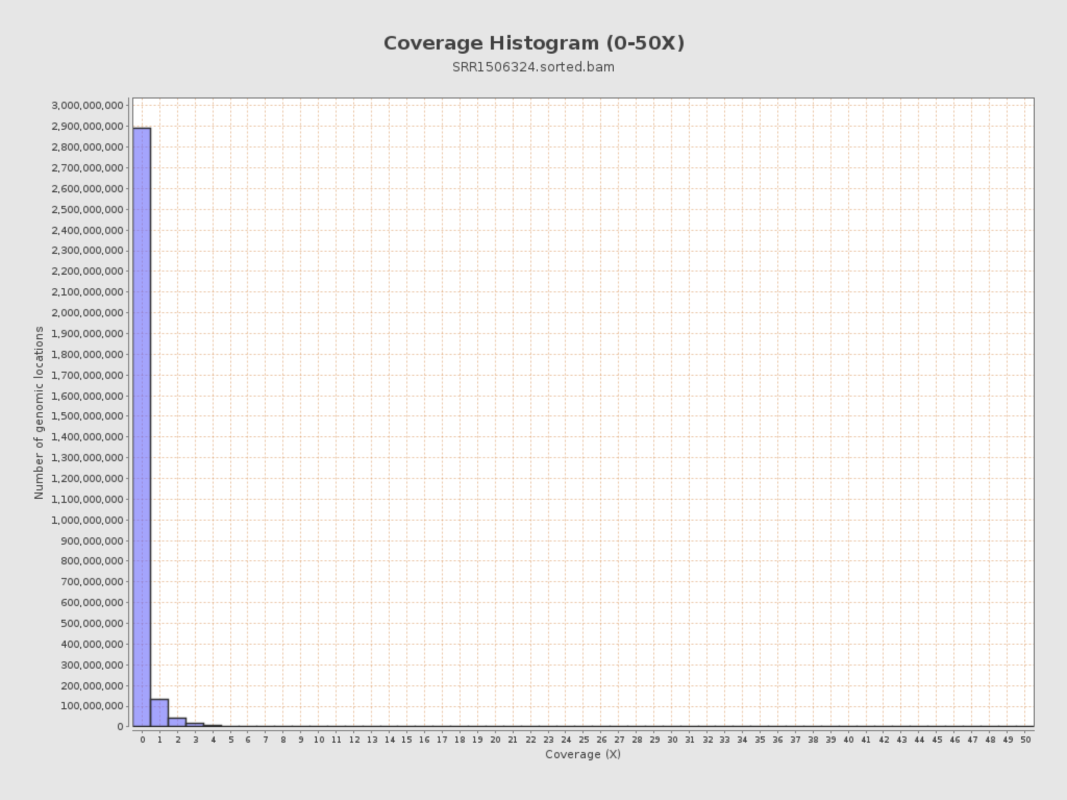
3. Results : Coverage across reference



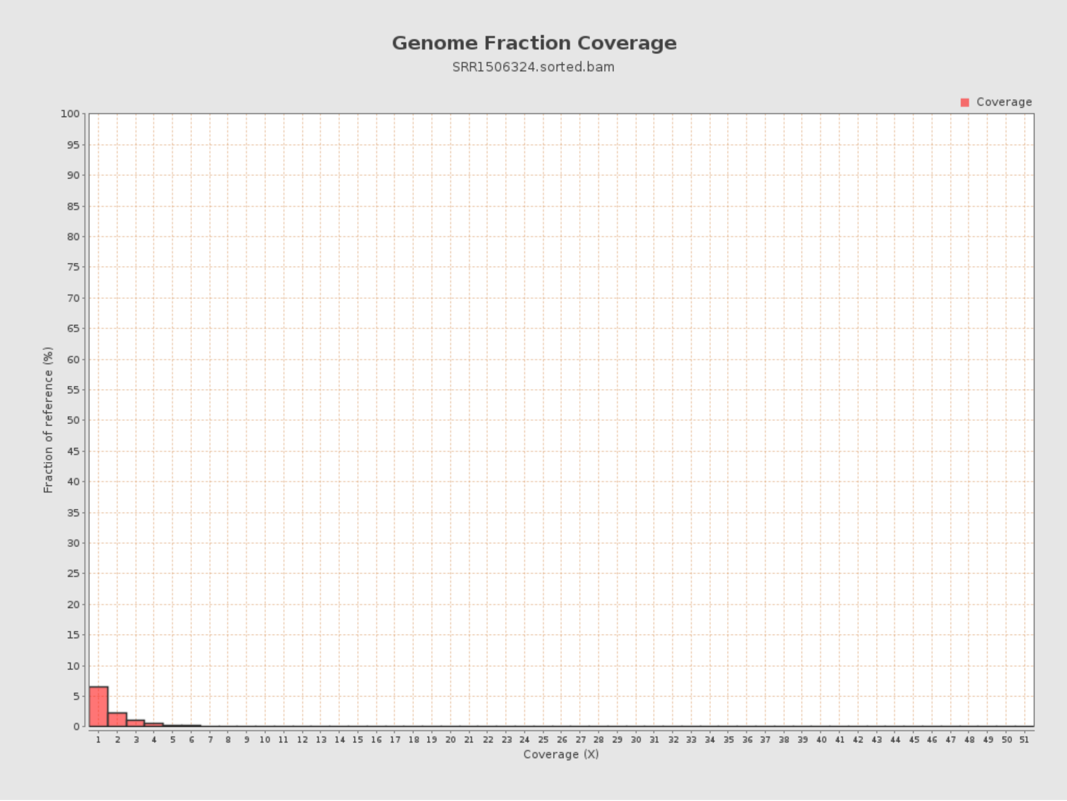
4. Results : Coverage Histogram



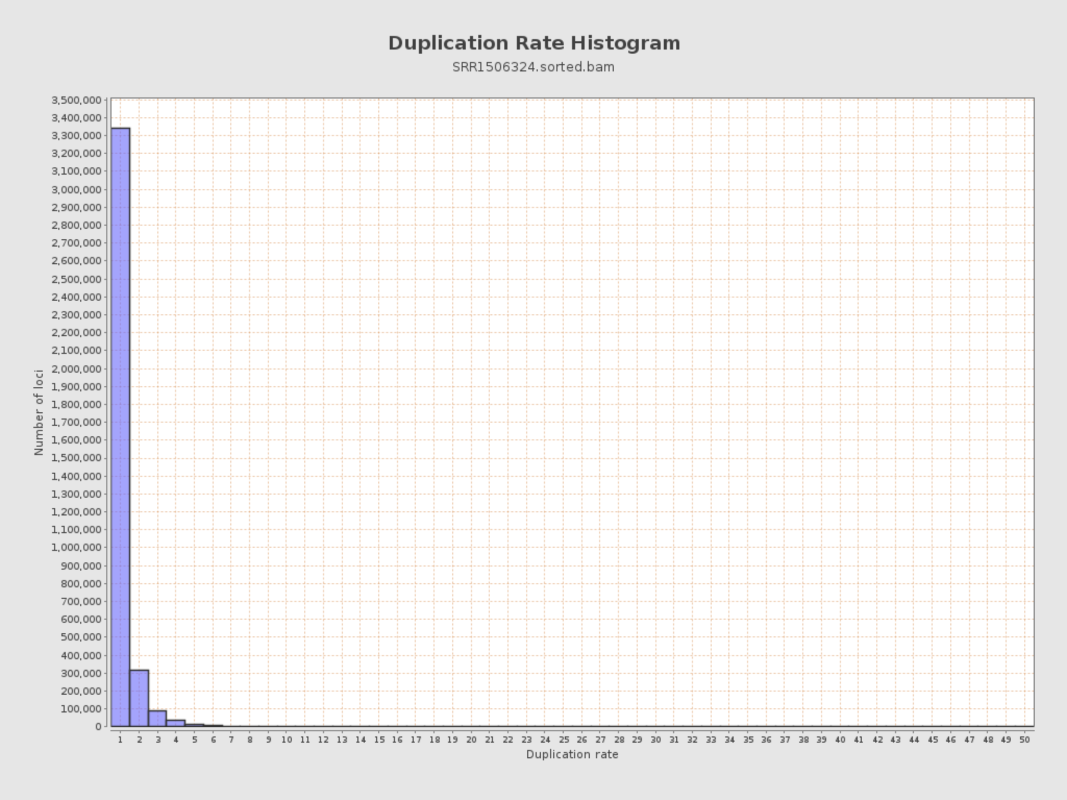
5. Results : Coverage Histogram (0-50X)



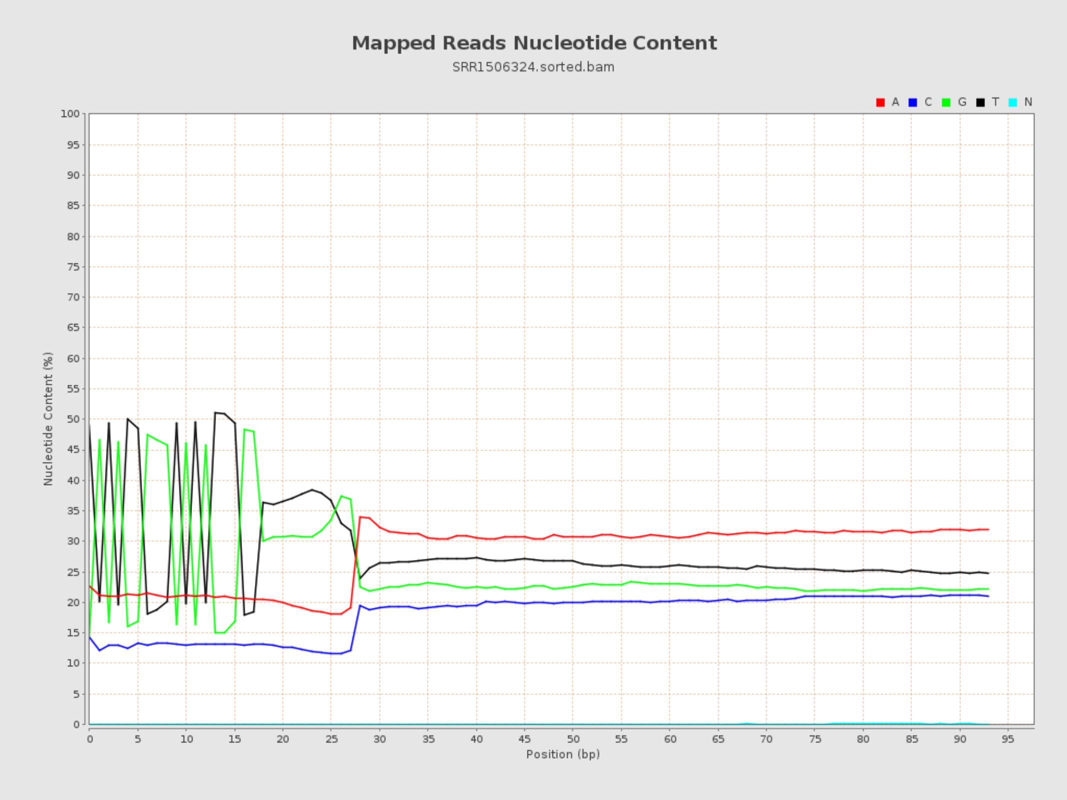
6. Results : Genome Fraction Coverage



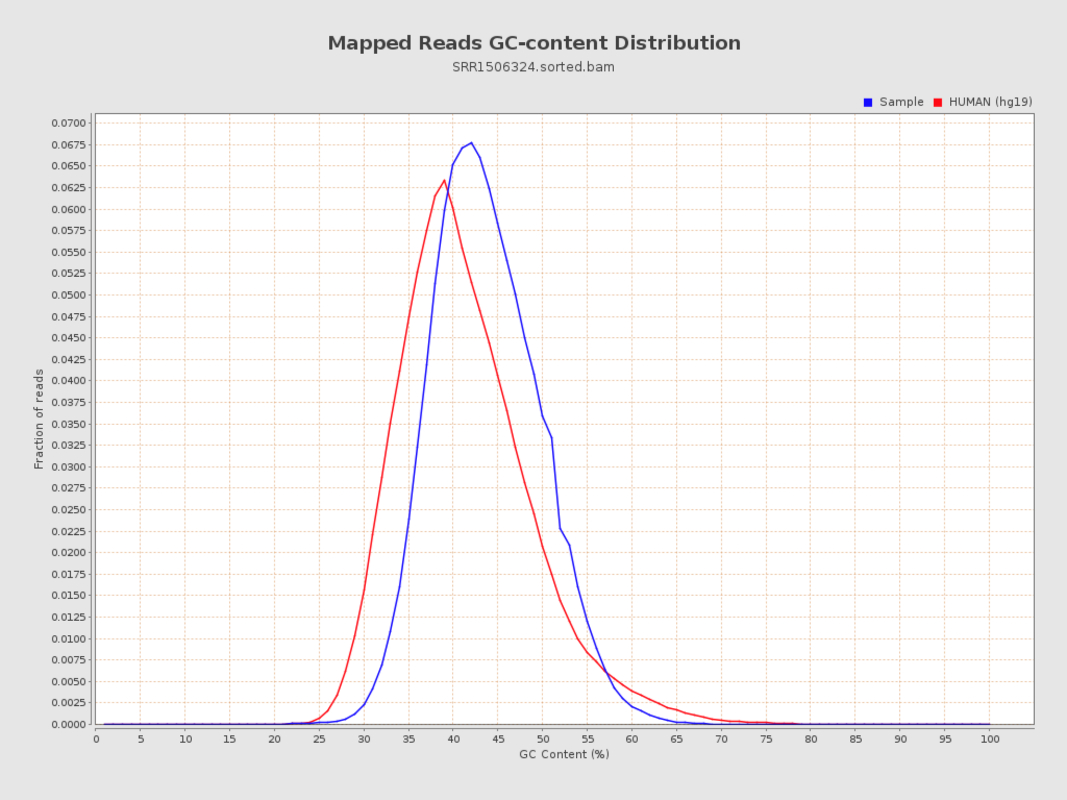
7. Results : Duplication Rate Histogram



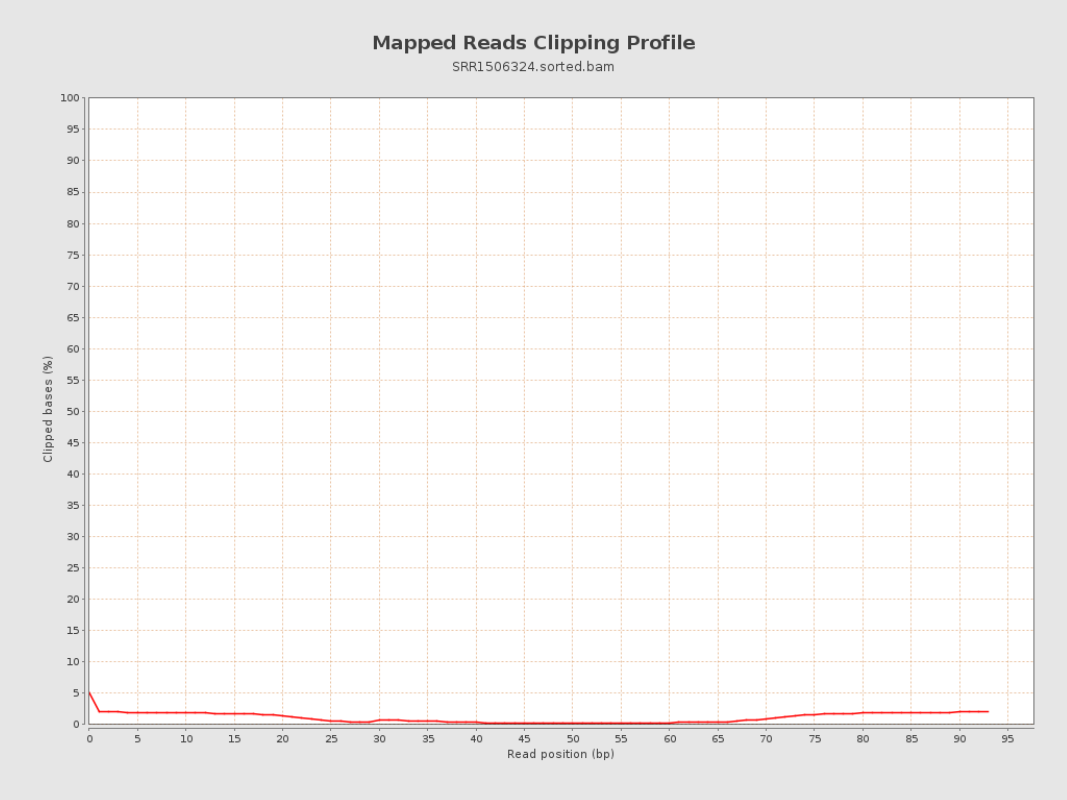
8. Results : Mapped Reads Nucleotide Content



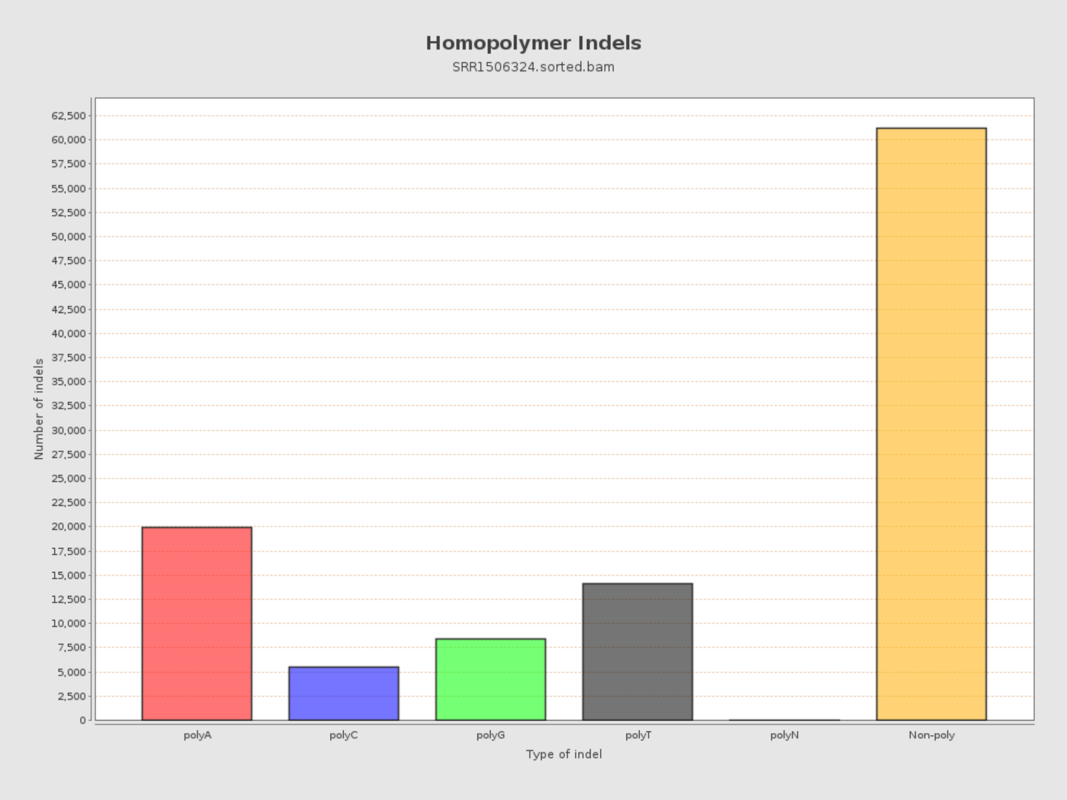
9. Results : Mapped Reads GC-content Distribution



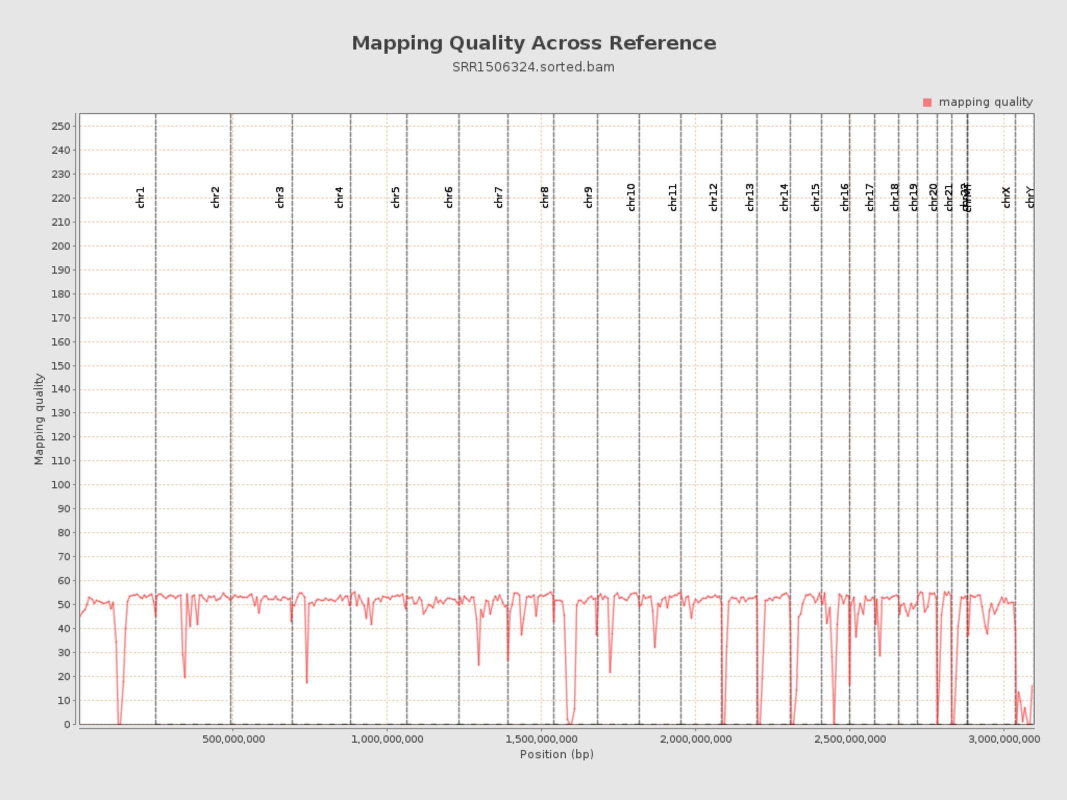
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram