Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 03:25:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524912.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_SRR10524912 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524912.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 03:25:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524912.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,594,033
Mapped reads	1,478,540 / 92.75%
Unmapped reads	115,493 / 7.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,290 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	76,736 / 4.81%
Duplication rate	4.05%
Clipped reads	1,482,221 / 92.99%

2.2. ACGT Content

Number/percentage of A's	21,177,953 / 24.56%
Number/percentage of C's	16,162,641 / 18.75%
Number/percentage of T's	27,769,468 / 32.21%
Number/percentage of G's	21,103,860 / 24.48%
Number/percentage of N's	630 / 0%
GC Percentage	43.23%

2.3. Coverage

Mean	0.0279

Standard Deviation	0.2655

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Mismatches and indels

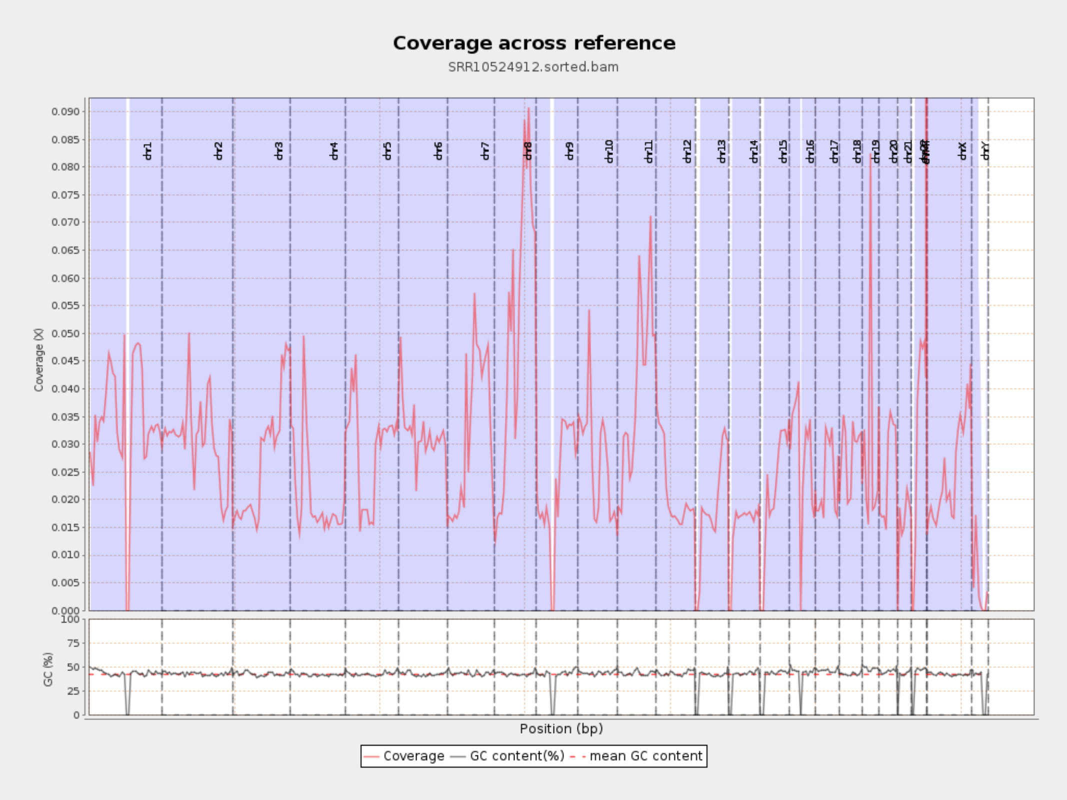
General error rate	0.51%
Mismatches	431,727
Insertions	5,198
Mapped reads with at least one insertion	0.35%
Deletions	17,174
Mapped reads with at least one deletion	1.15%
Homopolymer indels	42.92%

2.6. Chromosome stats

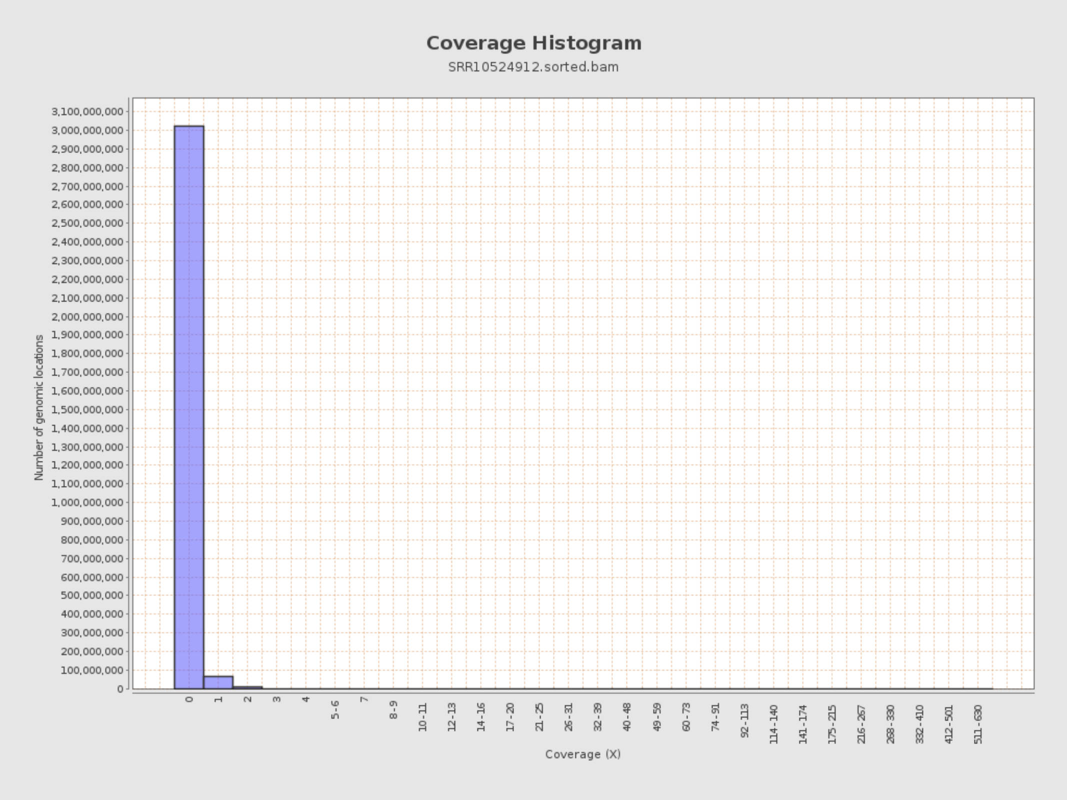
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8456550	0.0339	0.4865
chr2	243199373	7563953	0.0311	0.3141
chr3	198022430	5383713	0.0272	0.1837
chr4	191154276	3899922	0.0204	0.2011
chr5	180915260	5257163	0.0291	0.1903
chr6	171115067	5508736	0.0322	0.2125
chr7	159138663	5174728	0.0325	0.321

chr8	146364022	7455151	0.0509	0.3572
chr9	141213431	3140070	0.0222	0.2127
chr10	135534747	3714553	0.0274	0.2762
chr11	135006516	5415359	0.0401	0.2557
chr12	133851895	2868888	0.0214	0.1693
chr13	115169878	2082870	0.0181	0.1499
chr14	107349540	1592959	0.0148	0.142
chr15	102531392	2187596	0.0213	0.164
chr16	90354753	2539027	0.0281	0.1954
chr17	81195210	1932873	0.0238	0.1791
chr18	78077248	2247794	0.0288	0.3412
chr19	59128983	1760096	0.0298	0.3311
chr20	63025520	1605096	0.0255	0.1827
chr21	48129895	772384	0.016	0.173
chr22	51304566	1586249	0.0309	0.1985
chrMT	16571	8787	0.5303	0.8627
chrX	155270560	3834575	0.0247	0.1901
chrY	59373566	254111	0.0043	0.1576

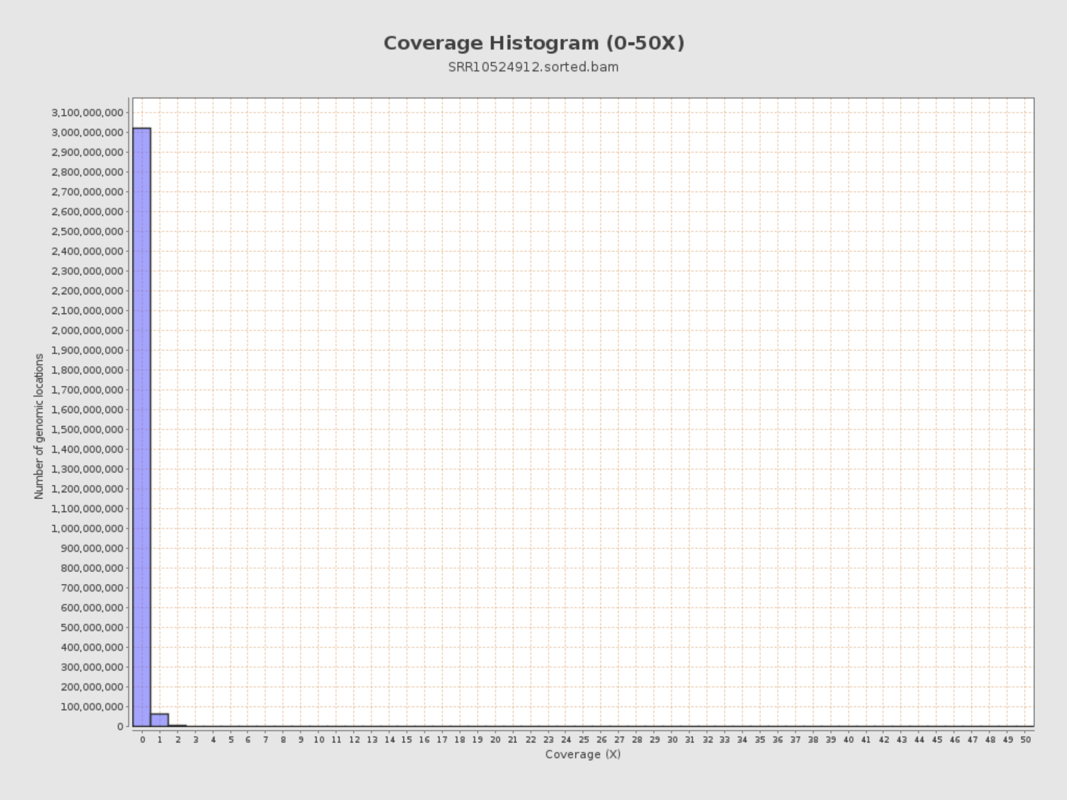
3. Results : Coverage across reference



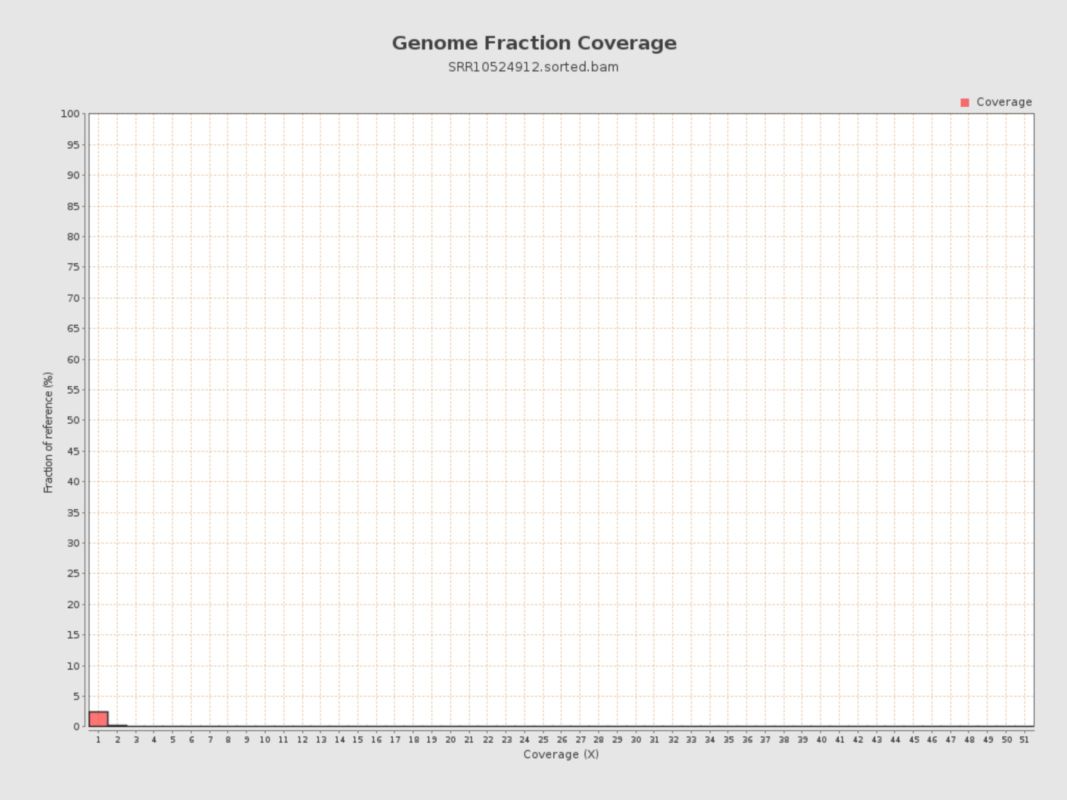
4. Results : Coverage Histogram



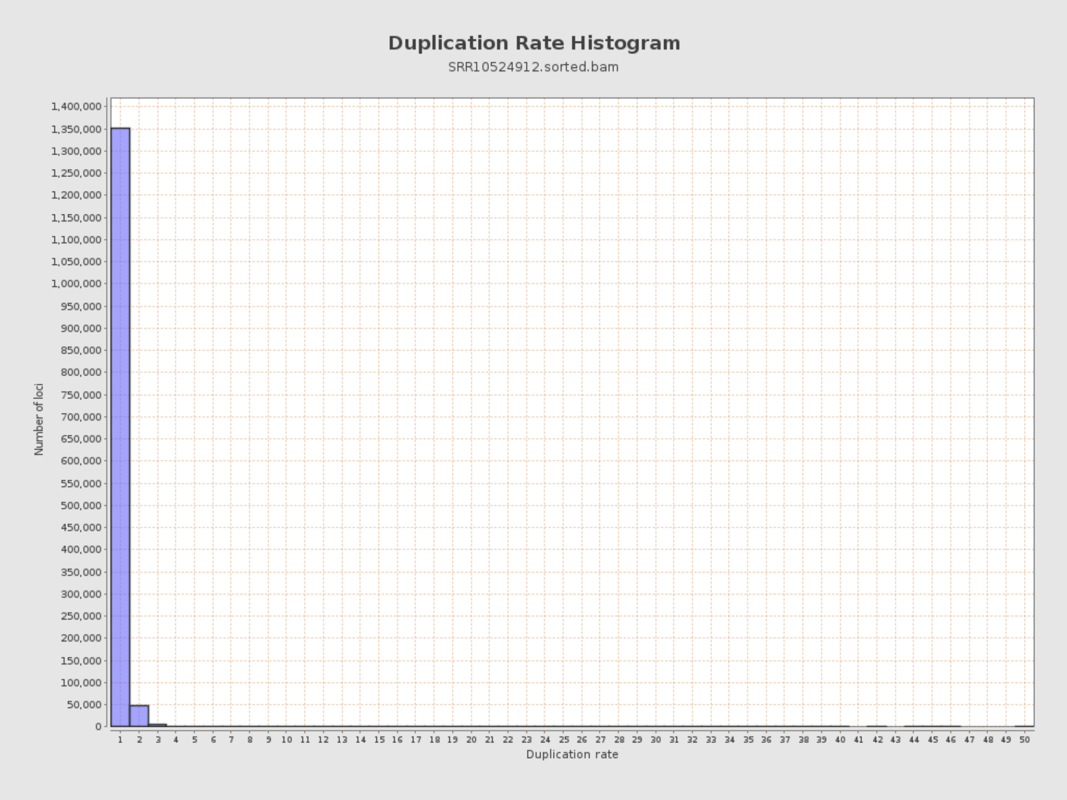
5. Results : Coverage Histogram (0-50X)



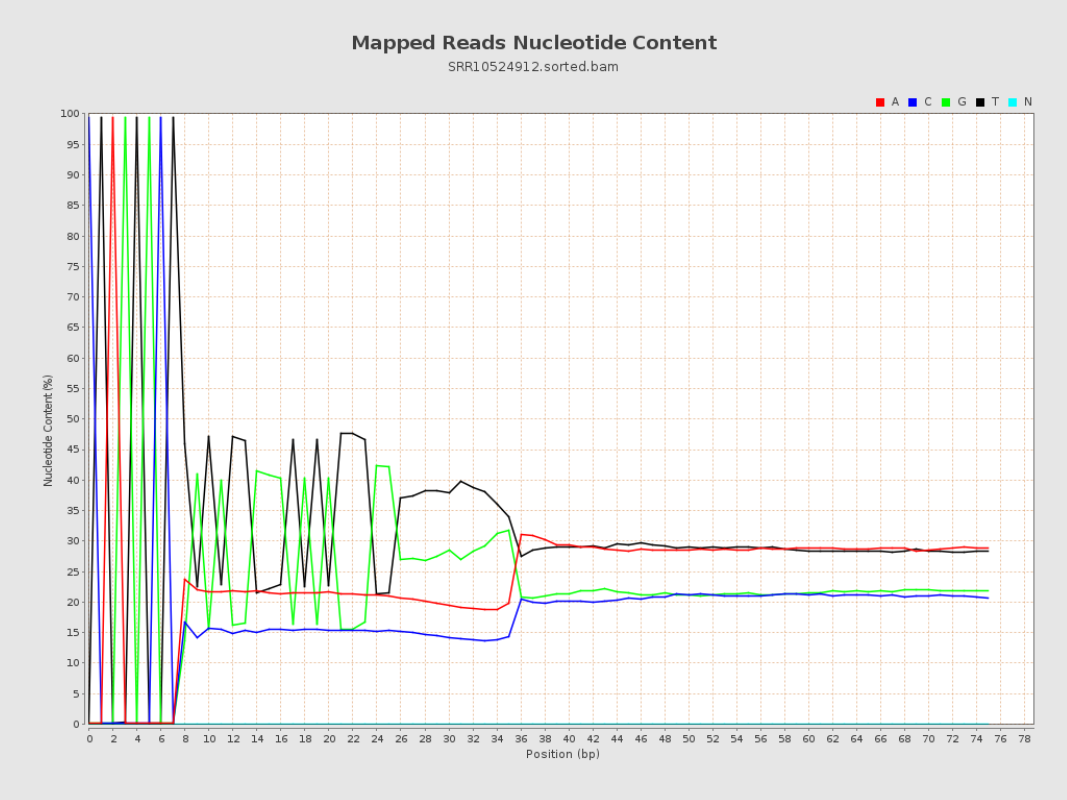
6. Results : Genome Fraction Coverage



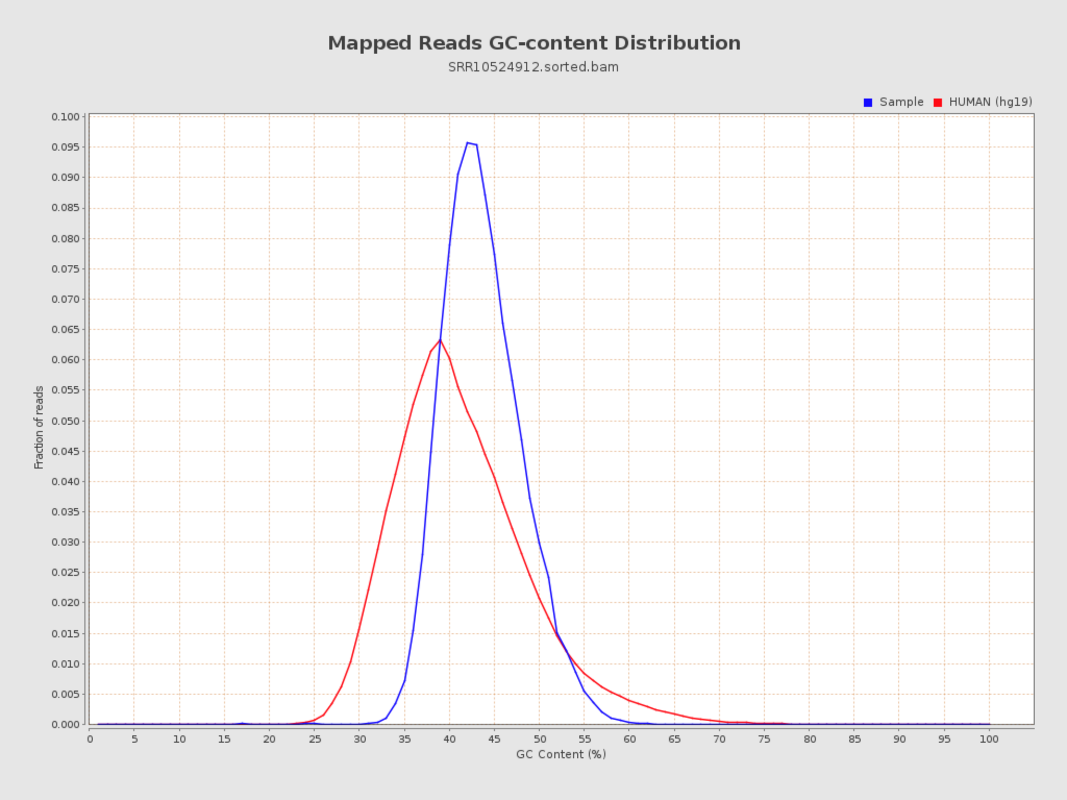
7. Results : Duplication Rate Histogram



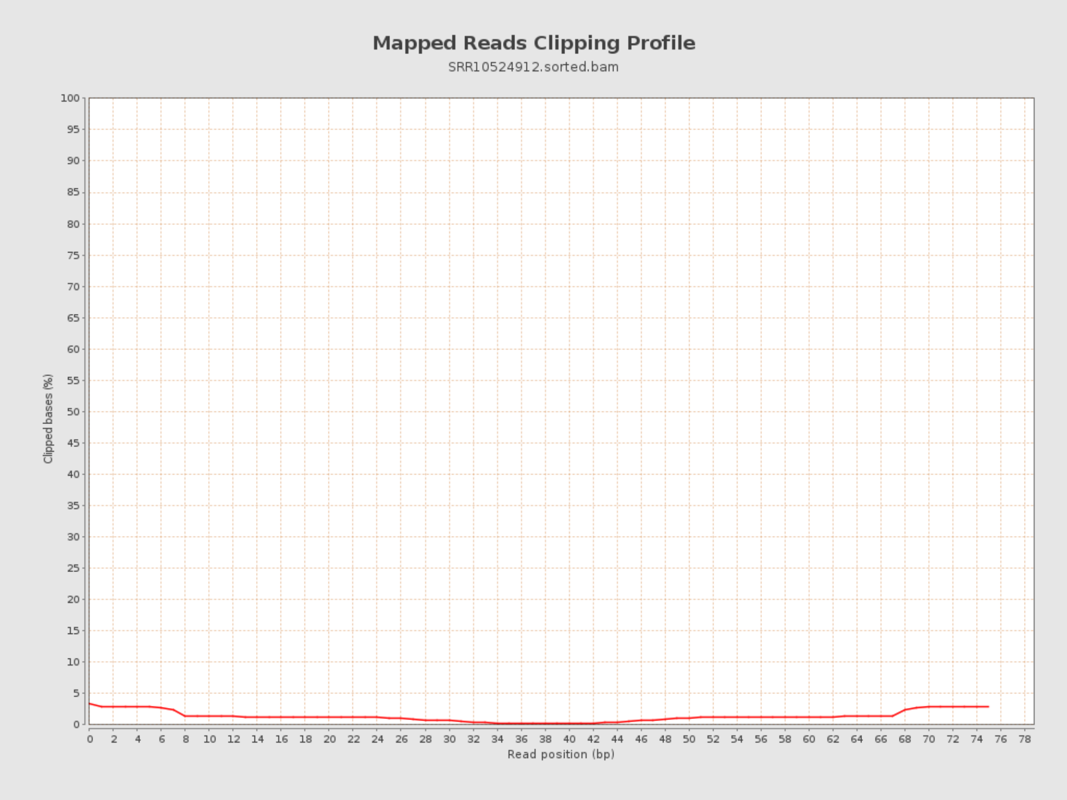
8. Results : Mapped Reads Nucleotide Content



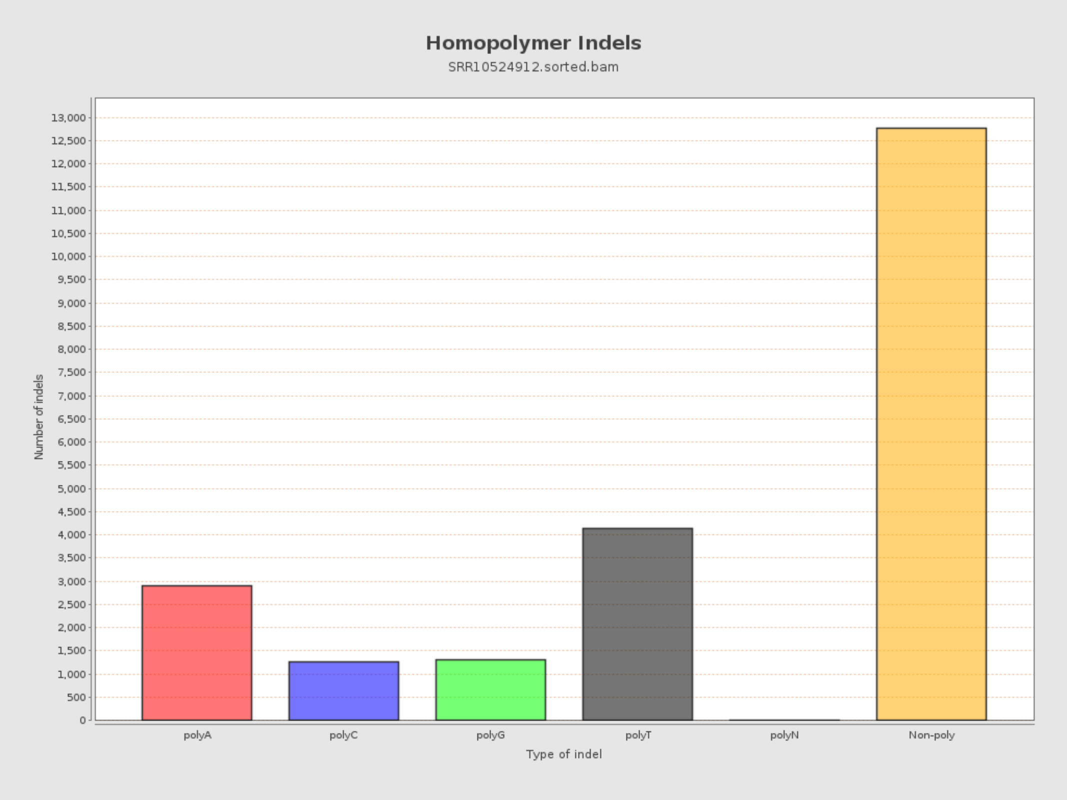
9. Results : Mapped Reads GC-content Distribution



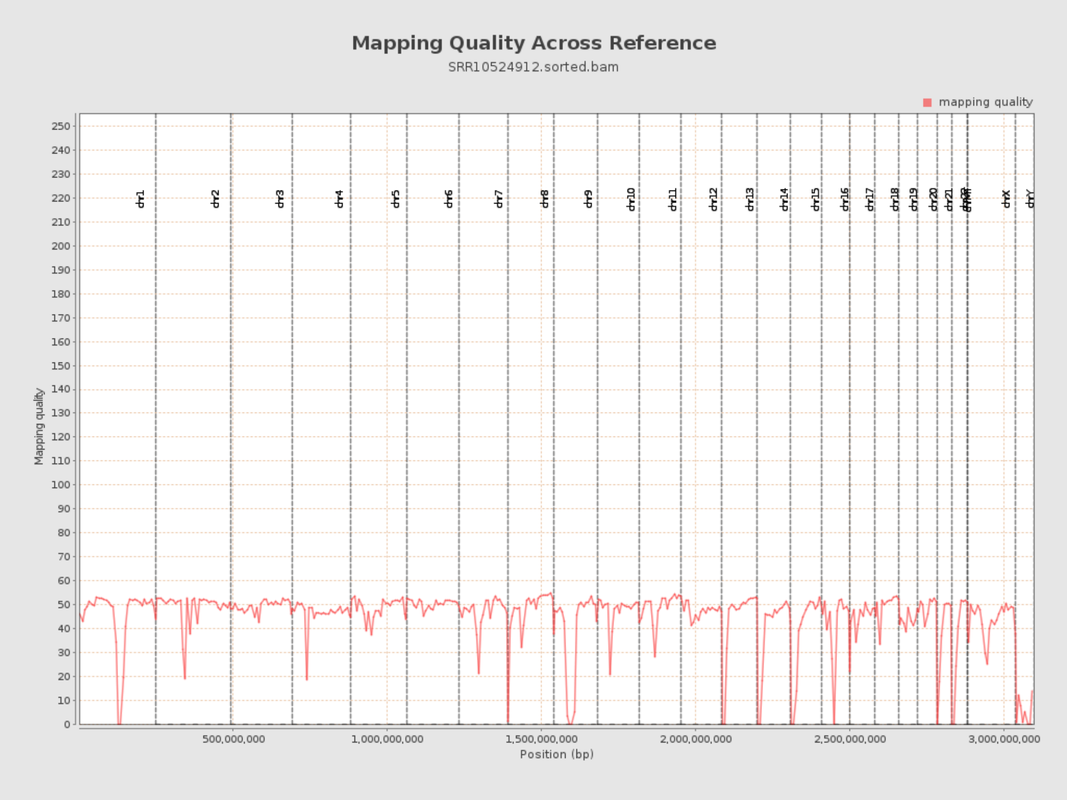
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram