Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:14:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524881.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_SRR10524881 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524881.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:14:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524881.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,494,836
Mapped reads	1,384,851 / 92.64%
Unmapped reads	109,985 / 7.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,275 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	49,449 / 3.31%
Duplication rate	2.6%
Clipped reads	1,386,703 / 92.77%

2.2. ACGT Content

Number/percentage of A's	21,012,944 / 25.94%
Number/percentage of C's	15,628,567 / 19.29%
Number/percentage of T's	25,473,329 / 31.44%
Number/percentage of G's	18,891,708 / 23.32%
Number/percentage of N's	10,875 / 0.01%
GC Percentage	42.61%

2.3. Coverage

Mean	0.0262

Standard Deviation	0.2701

2.4. Mapping Quality

Mean Mapping Quality	46.21

2.5. Mismatches and indels

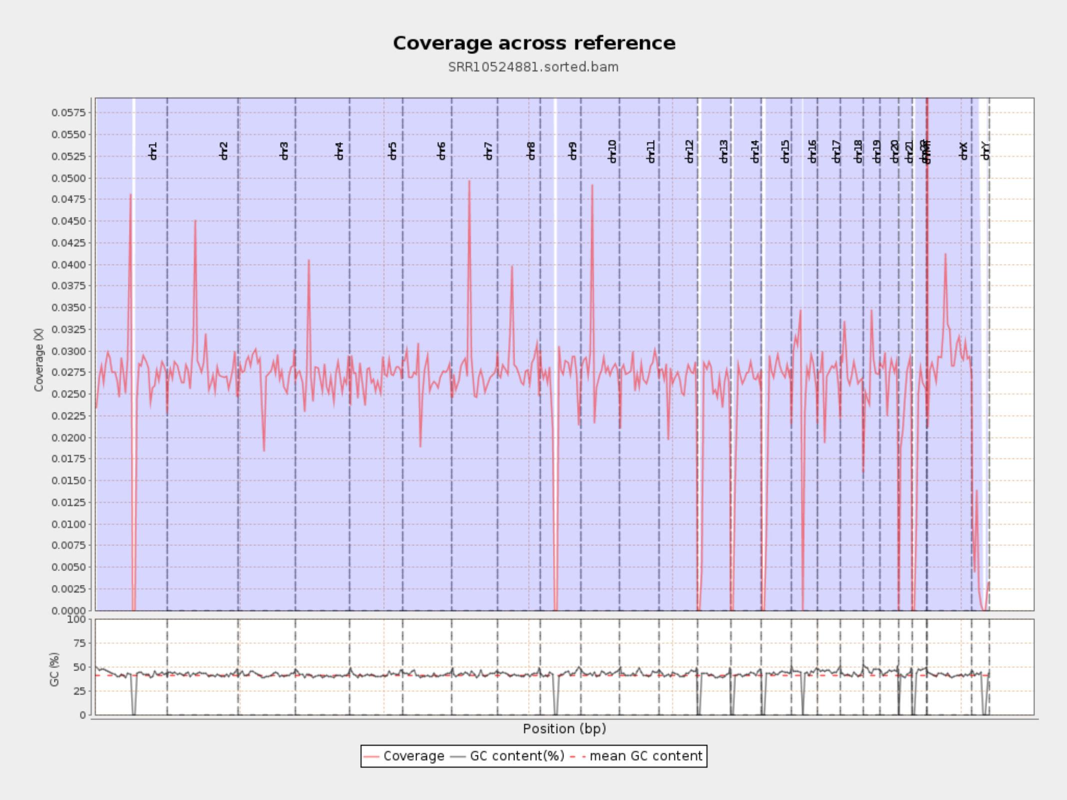
General error rate	0.5%
Mismatches	390,233
Insertions	6,145
Mapped reads with at least one insertion	0.44%
Deletions	15,007
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.79%

2.6. Chromosome stats

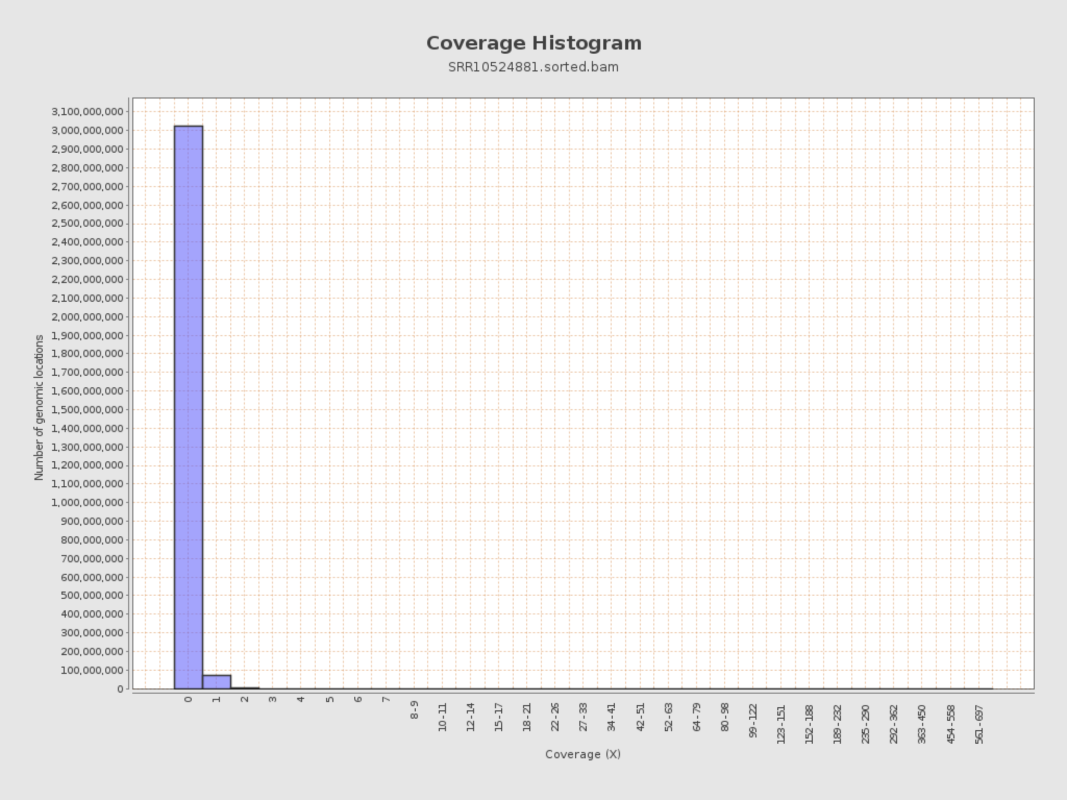
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6540058	0.0262	0.5337
chr2	243199373	6827960	0.0281	0.2821
chr3	198022430	5431579	0.0274	0.1783
chr4	191154276	5198638	0.0272	0.193
chr5	180915260	4912336	0.0272	0.1778
chr6	171115067	4628630	0.027	0.1876
chr7	159138663	4468619	0.0281	0.3675

chr8	146364022	4170439	0.0285	0.2601
chr9	141213431	3427032	0.0243	0.234
chr10	135534747	3901908	0.0288	0.2546
chr11	135006516	3724998	0.0276	0.2461
chr12	133851895	3572790	0.0267	0.1798
chr13	115169878	2551216	0.0222	0.159
chr14	107349540	2455543	0.0229	0.1704
chr15	102531392	2315221	0.0226	0.1609
chr16	90354753	2346838	0.026	0.1893
chr17	81195210	2173998	0.0268	0.1912
chr18	78077248	2178914	0.0279	0.4499
chr19	59128983	1591858	0.0269	0.3432
chr20	63025520	1721749	0.0273	0.1812
chr21	48129895	1062729	0.0221	0.1743
chr22	51304566	935737	0.0182	0.1441
chrMT	16571	14680	0.8859	1.1239
chrX	155270560	4646457	0.0299	0.2097
chrY	59373566	241025	0.0041	0.1098

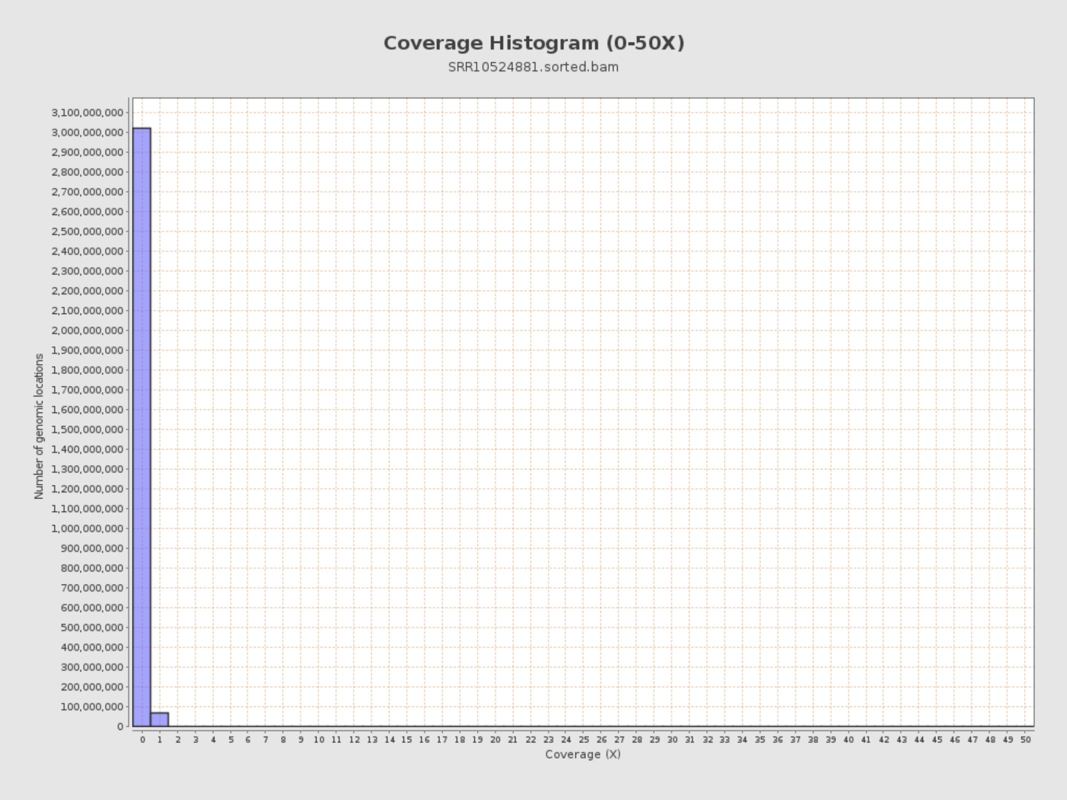
3. Results : Coverage across reference



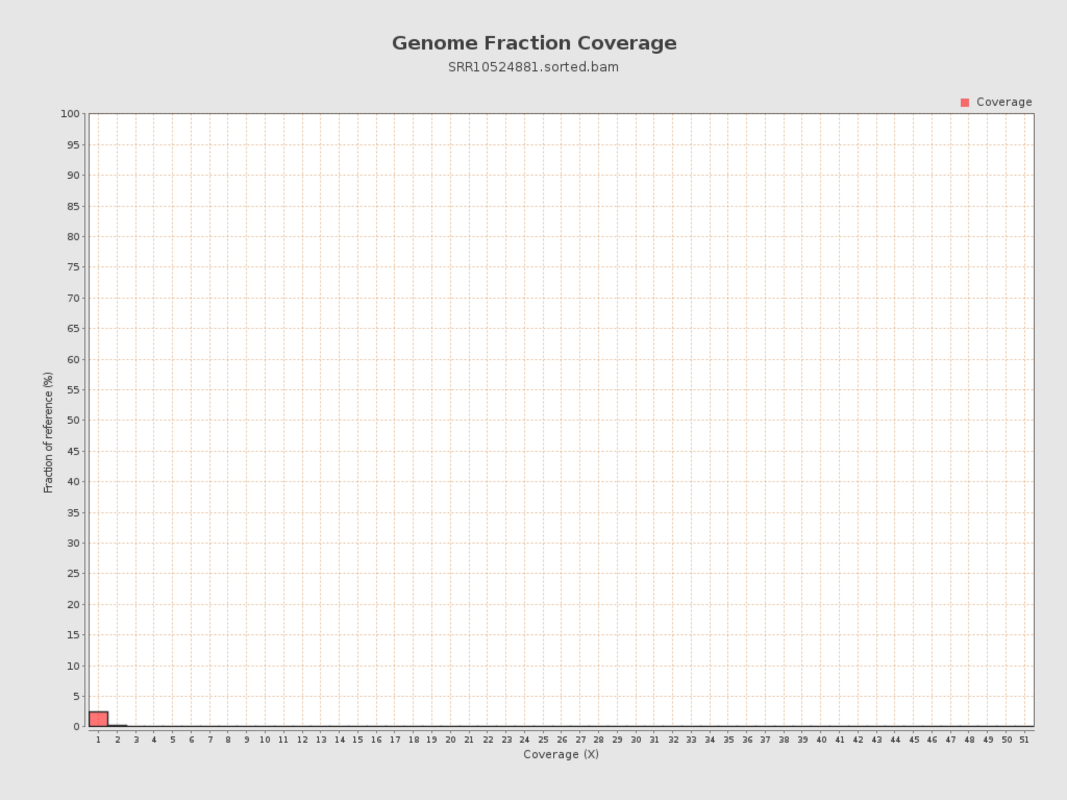
4. Results : Coverage Histogram



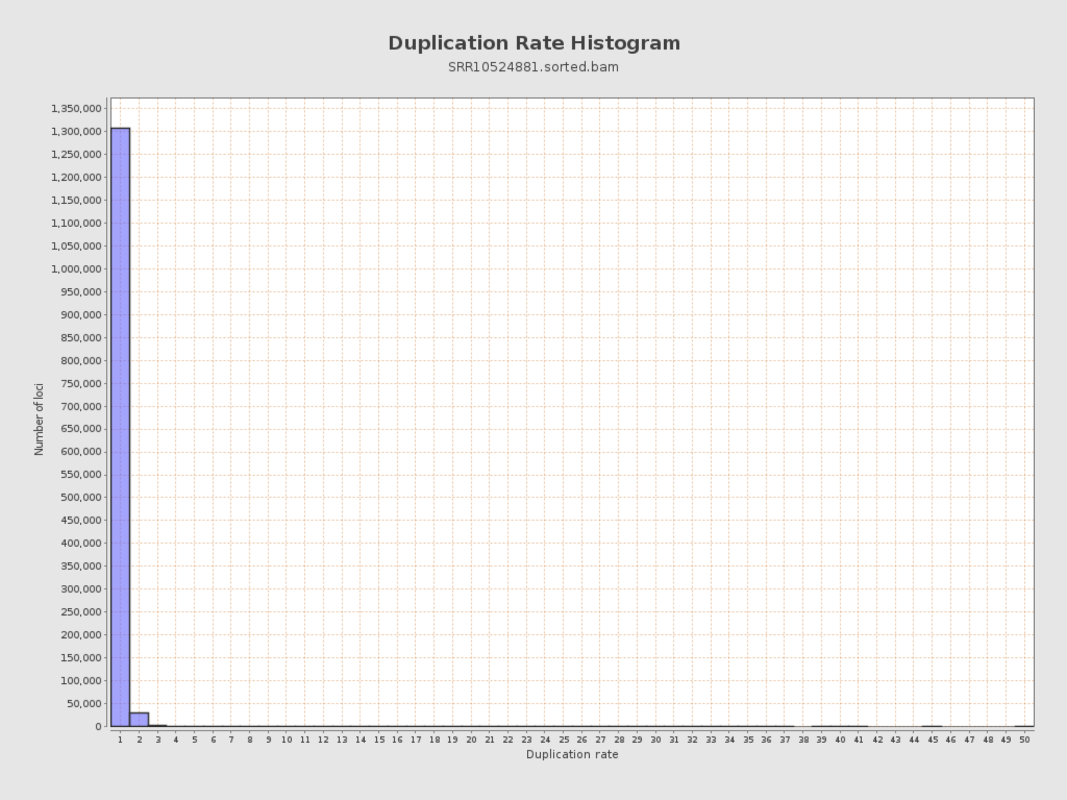
5. Results : Coverage Histogram (0-50X)



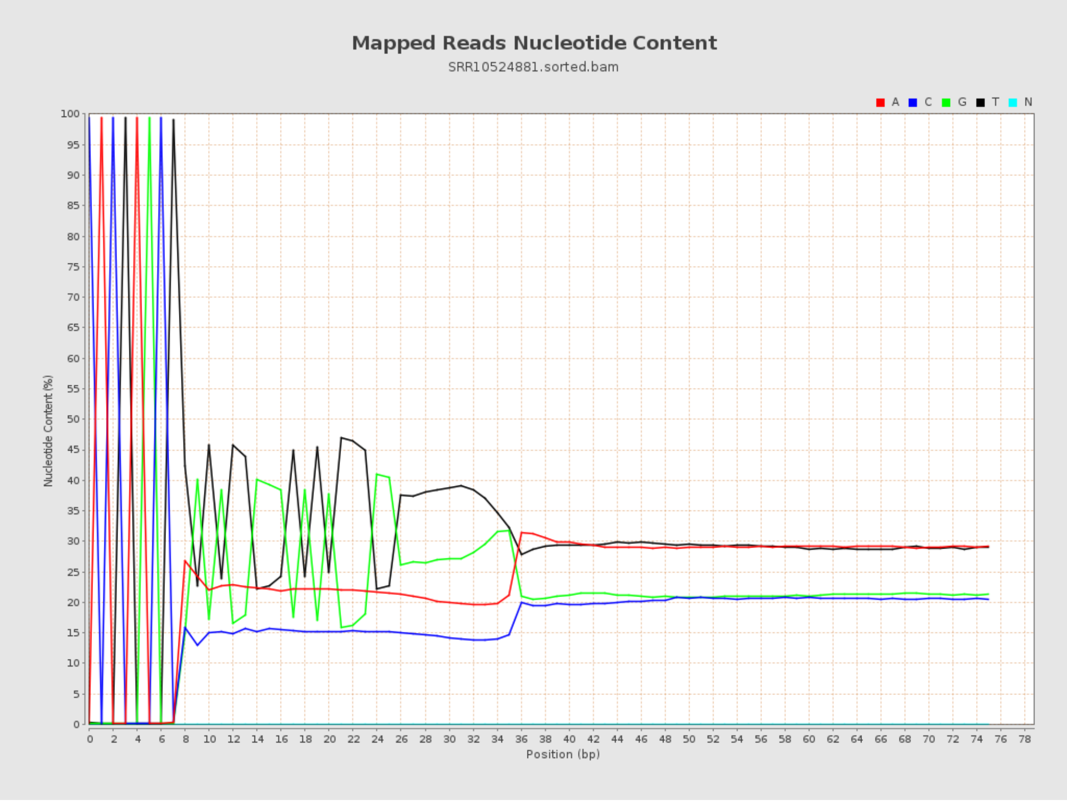
6. Results : Genome Fraction Coverage



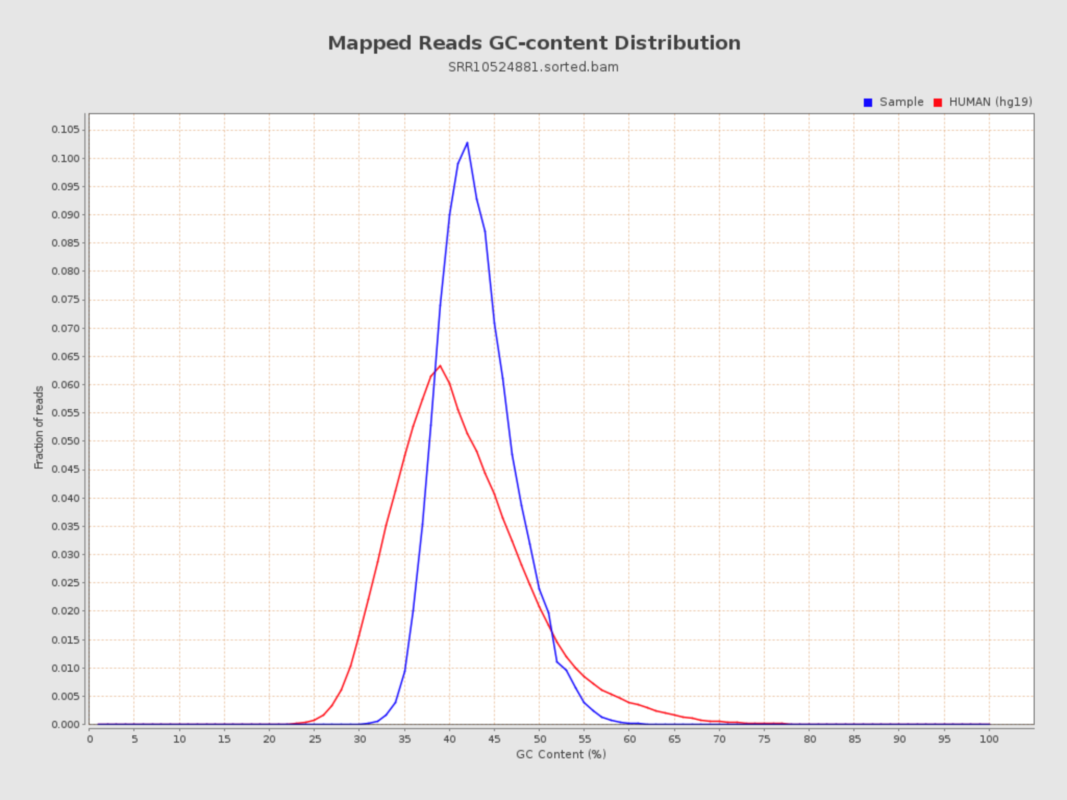
7. Results : Duplication Rate Histogram



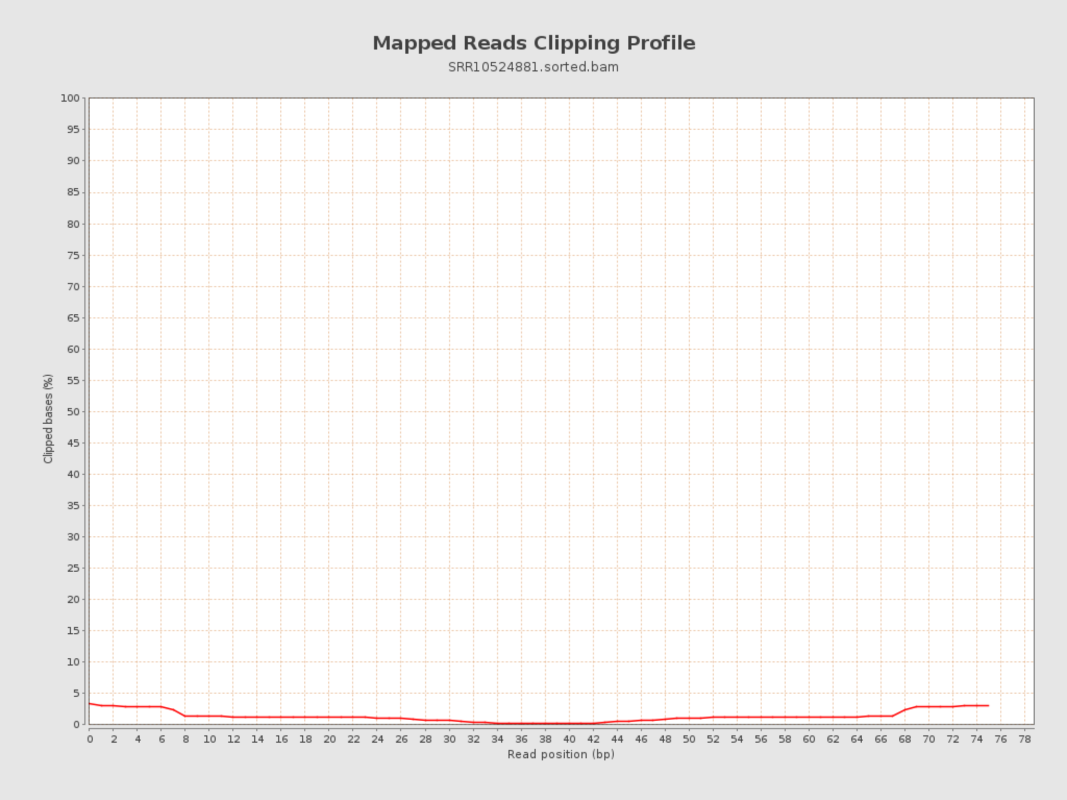
8. Results : Mapped Reads Nucleotide Content



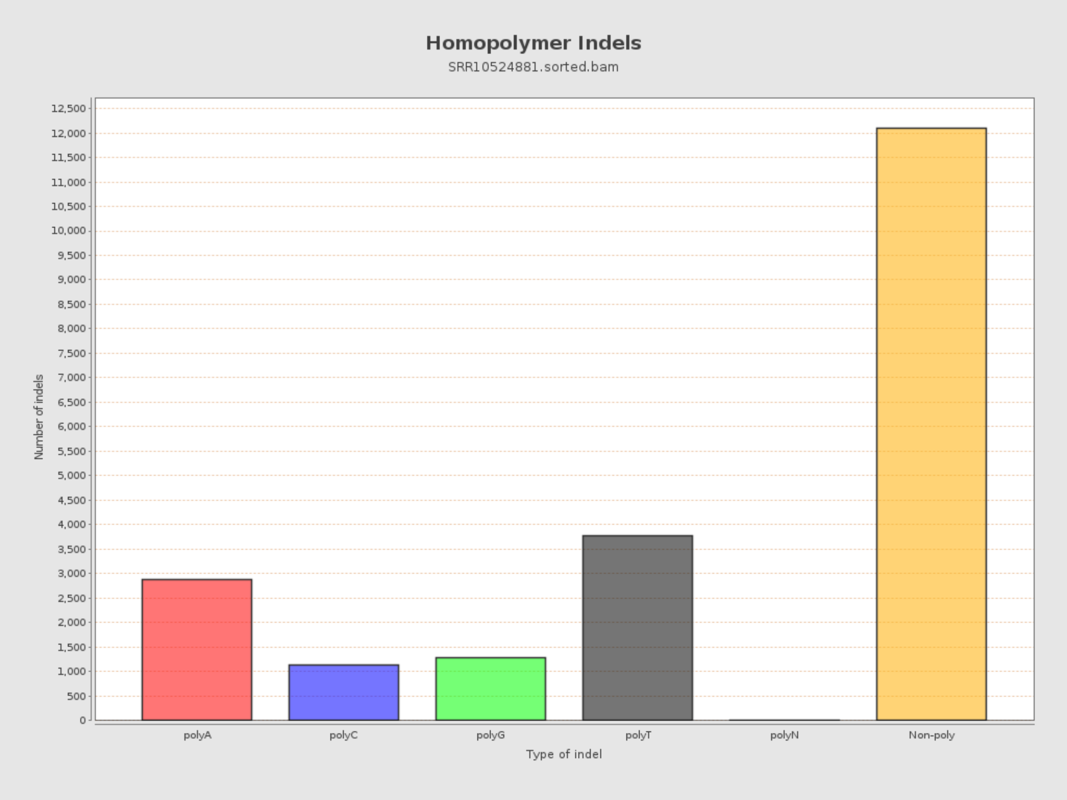
9. Results : Mapped Reads GC-content Distribution



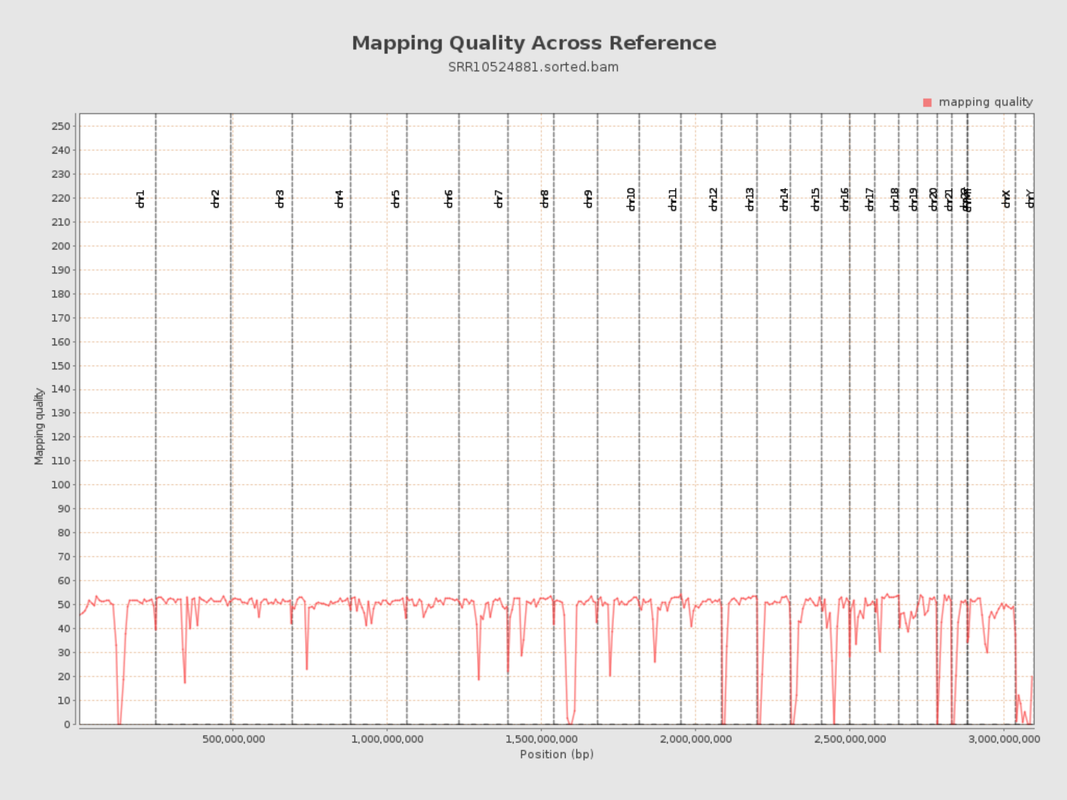
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram