Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 11:33:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524580.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_SRR10524580 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524580.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 11:33:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524580.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,446,521
Mapped reads	1,223,104 / 84.55%
Unmapped reads	223,417 / 15.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,219 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	187,391 / 12.95%
Duplication rate	10.93%
Clipped reads	1,227,097 / 84.83%

2.2. ACGT Content

Number/percentage of A's	15,801,875 / 23.36%
Number/percentage of C's	12,946,093 / 19.13%
Number/percentage of T's	22,744,911 / 33.62%
Number/percentage of G's	16,165,379 / 23.89%
Number/percentage of N's	1,039 / 0%
GC Percentage	43.03%

2.3. Coverage

Mean	0.0219

Standard Deviation	0.2735

2.4. Mapping Quality

Mean Mapping Quality	43.44

2.5. Mismatches and indels

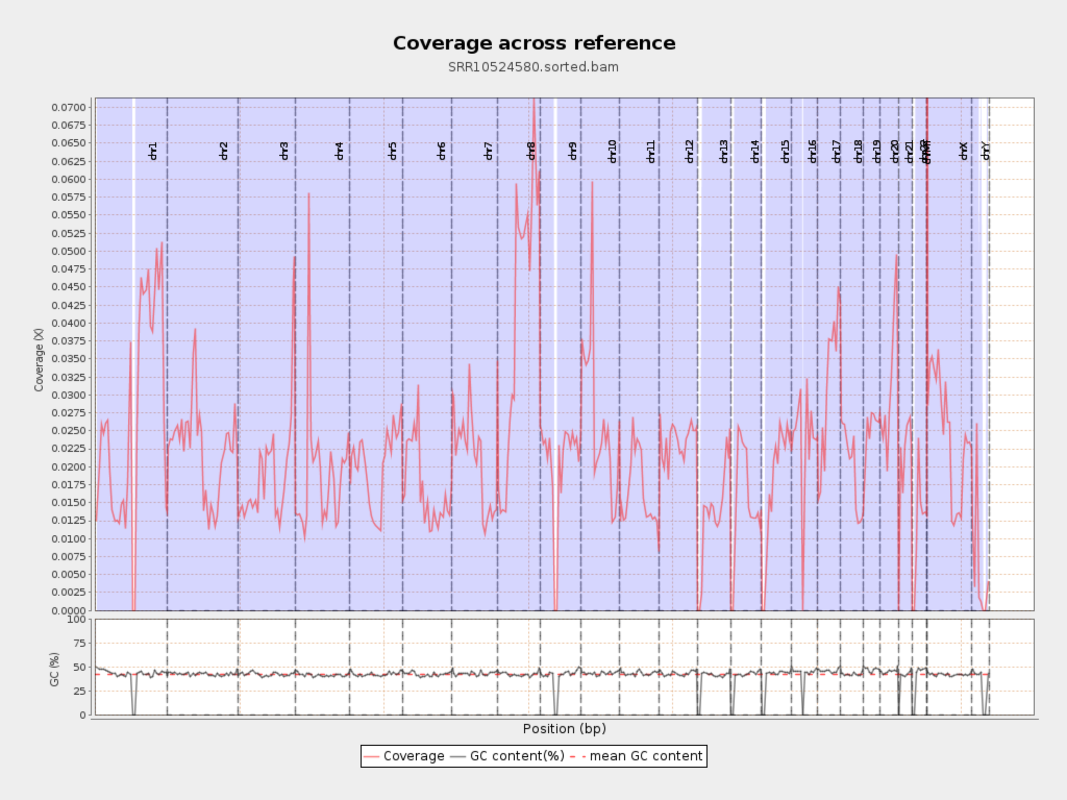
General error rate	0.62%
Mismatches	407,601
Insertions	4,570
Mapped reads with at least one insertion	0.37%
Deletions	15,654
Mapped reads with at least one deletion	1.27%
Homopolymer indels	41.57%

2.6. Chromosome stats

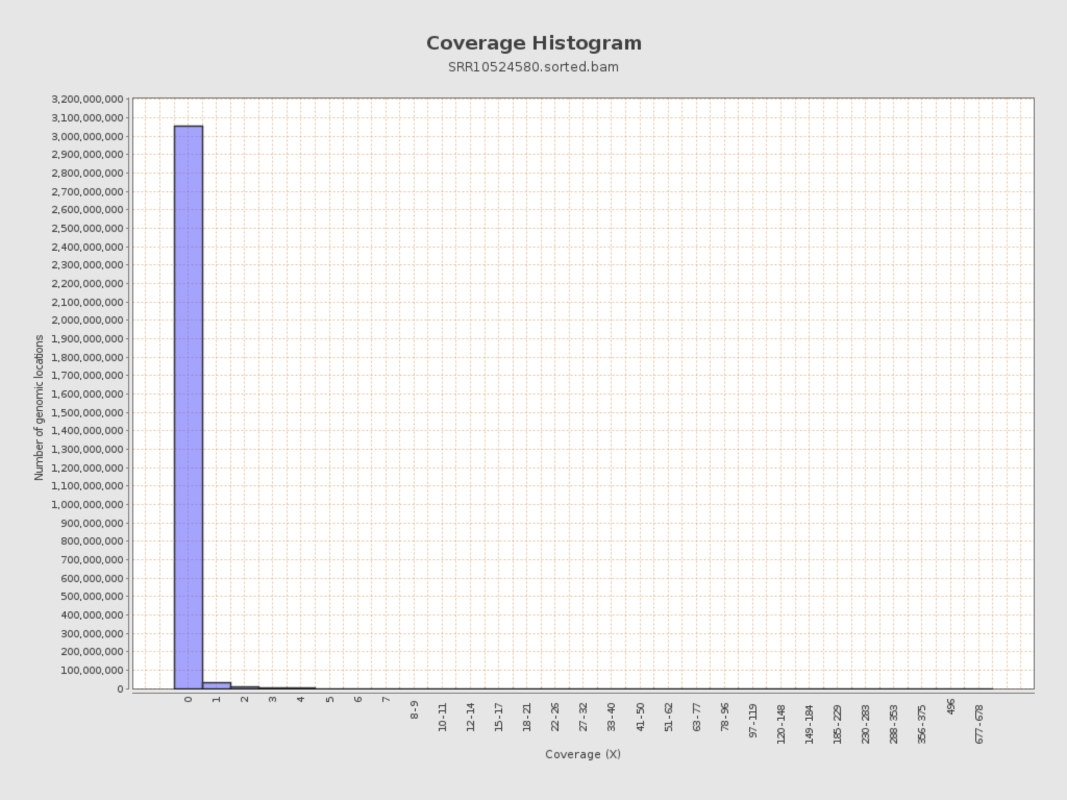
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6667174	0.0267	0.3533
chr2	243199373	5473504	0.0225	0.3929
chr3	198022430	3726891	0.0188	0.203
chr4	191154276	3587393	0.0188	0.2667
chr5	180915260	3646797	0.0202	0.2087
chr6	171115067	2911447	0.017	0.2141
chr7	159138663	3347217	0.021	0.2671

chr8	146364022	6015801	0.0411	0.3284
chr9	141213431	2838895	0.0201	0.2326
chr10	135534747	3669425	0.0271	0.3648
chr11	135006516	2266848	0.0168	0.2419
chr12	133851895	3158531	0.0236	0.2286
chr13	115169878	1524106	0.0132	0.1685
chr14	107349540	1619534	0.0151	0.1813
chr15	102531392	1801330	0.0176	0.1951
chr16	90354753	2095938	0.0232	0.2386
chr17	81195210	2527895	0.0311	0.2747
chr18	78077248	1550972	0.0199	0.3435
chr19	59128983	1477875	0.025	0.2847
chr20	63025520	1997217	0.0317	0.2766
chr21	48129895	1004613	0.0209	0.2536
chr22	51304566	604145	0.0118	0.1572
chrMT	16571	5249	0.3168	0.8211
chrX	155270560	3820746	0.0246	0.2369
chrY	59373566	346223	0.0058	0.2505

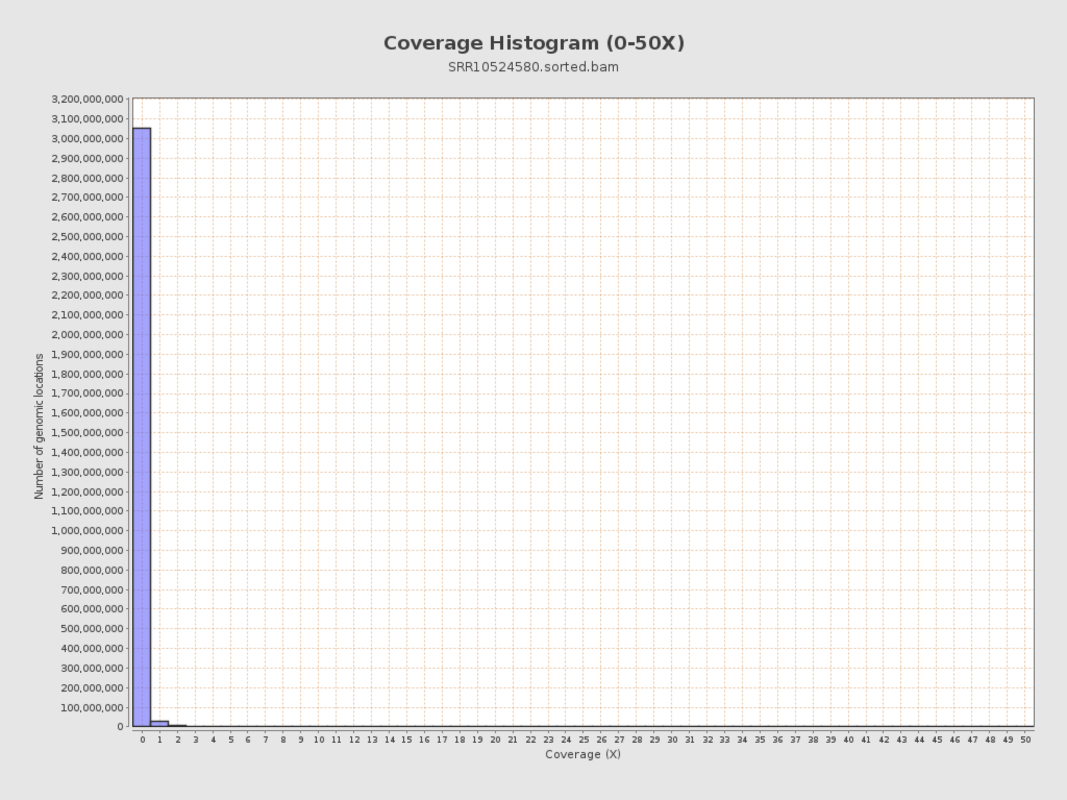
3. Results : Coverage across reference



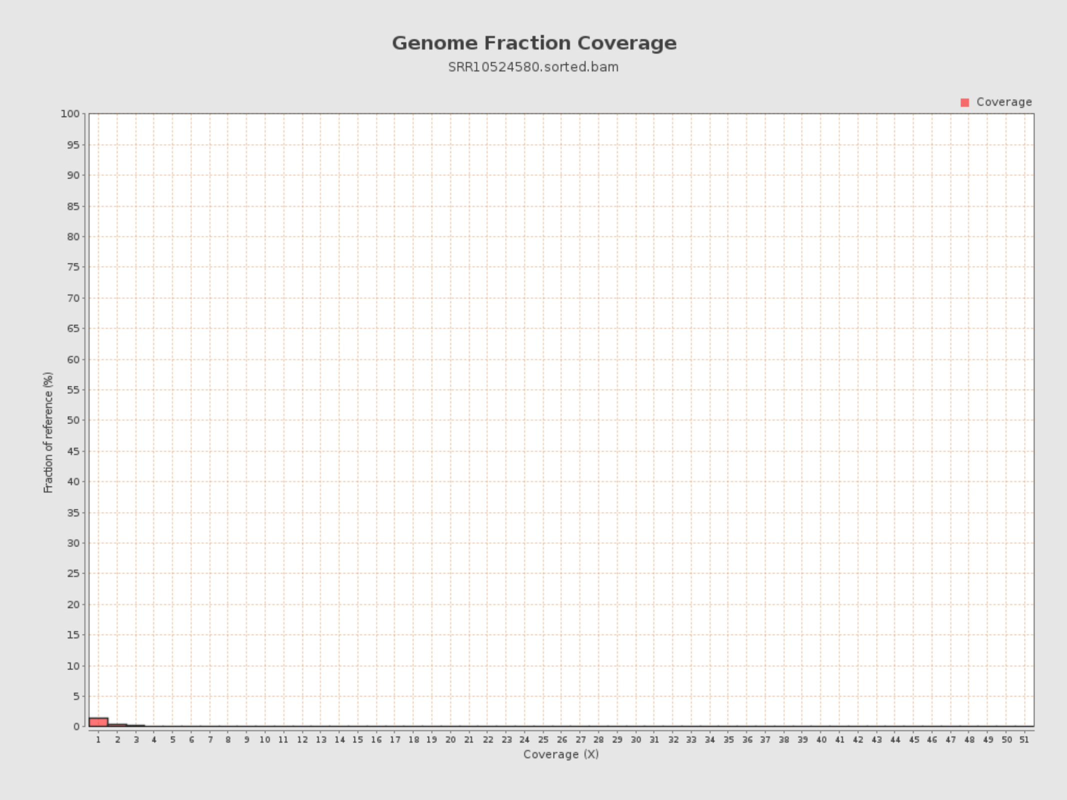
4. Results : Coverage Histogram



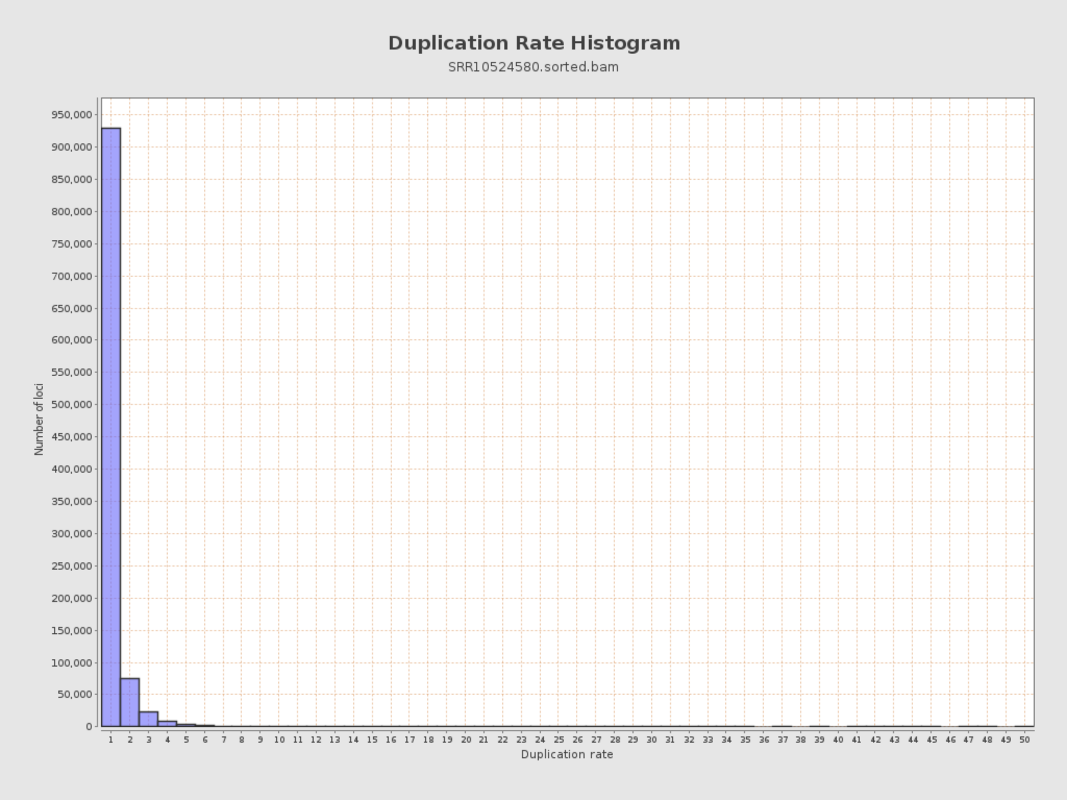
5. Results : Coverage Histogram (0-50X)



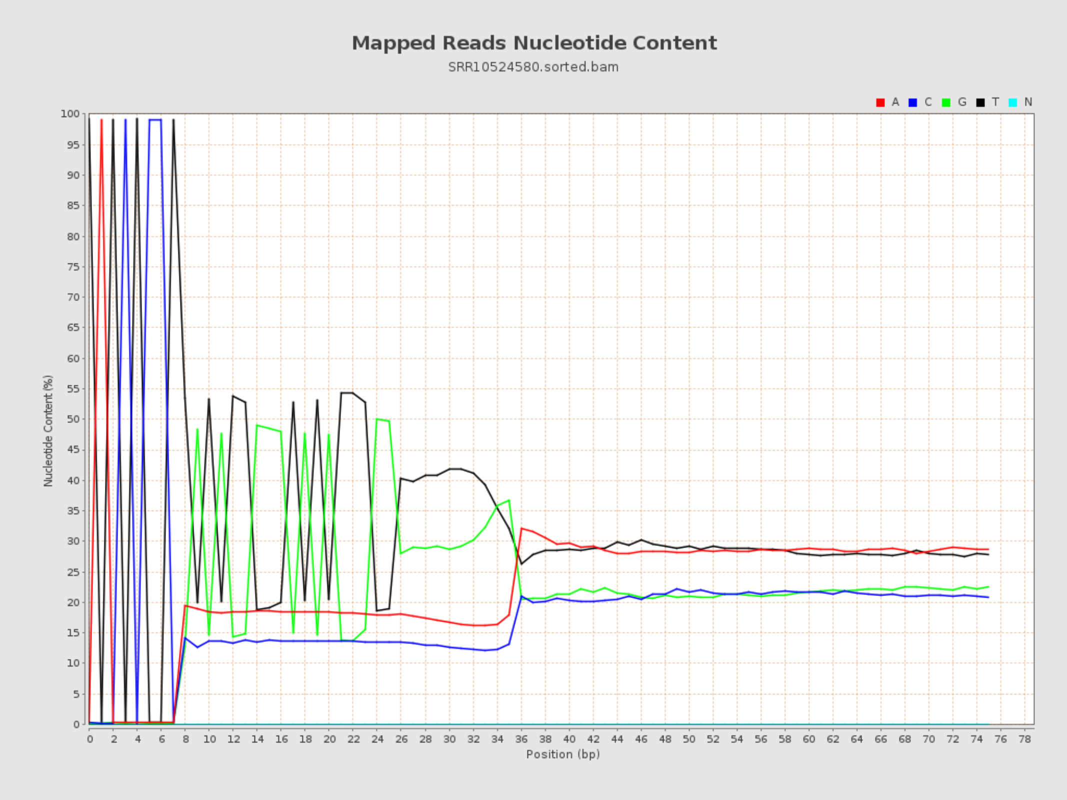
6. Results : Genome Fraction Coverage



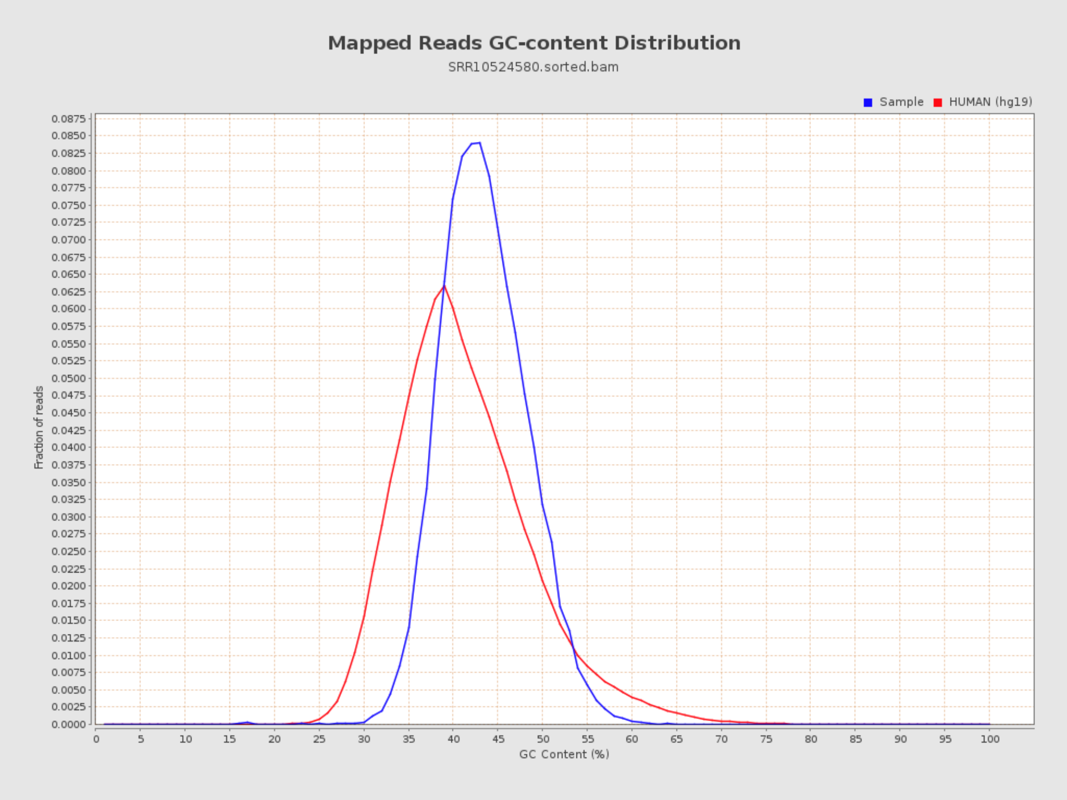
7. Results : Duplication Rate Histogram



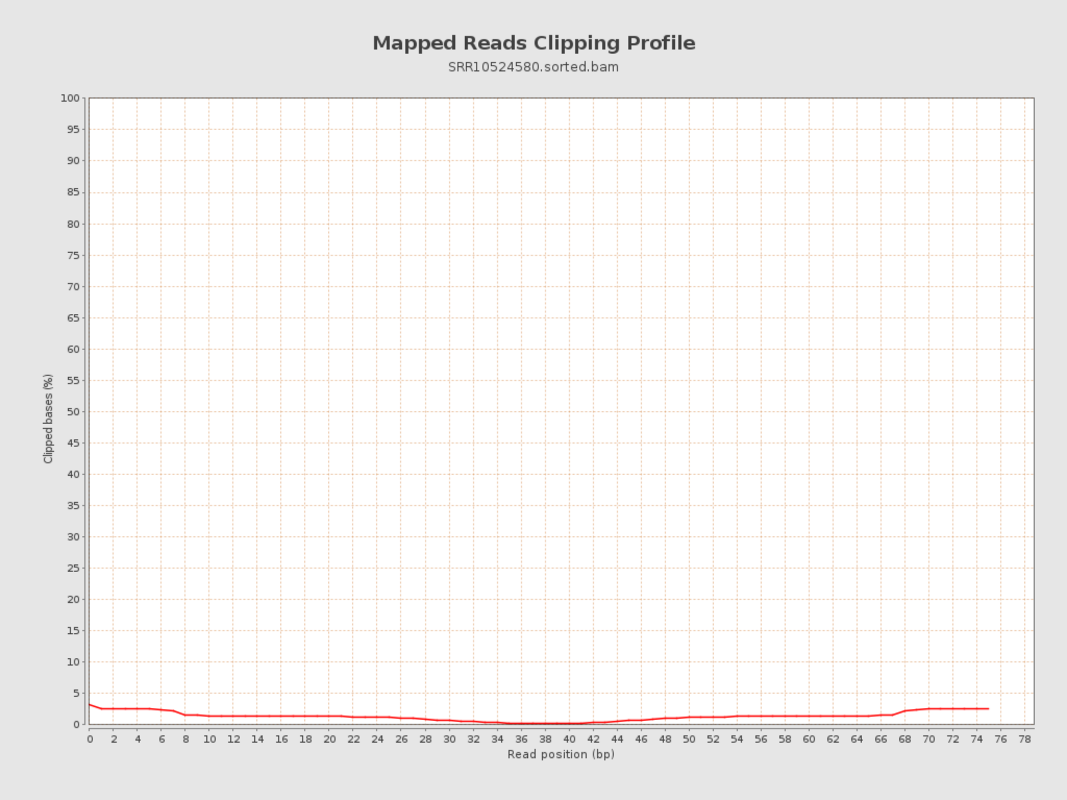
8. Results : Mapped Reads Nucleotide Content



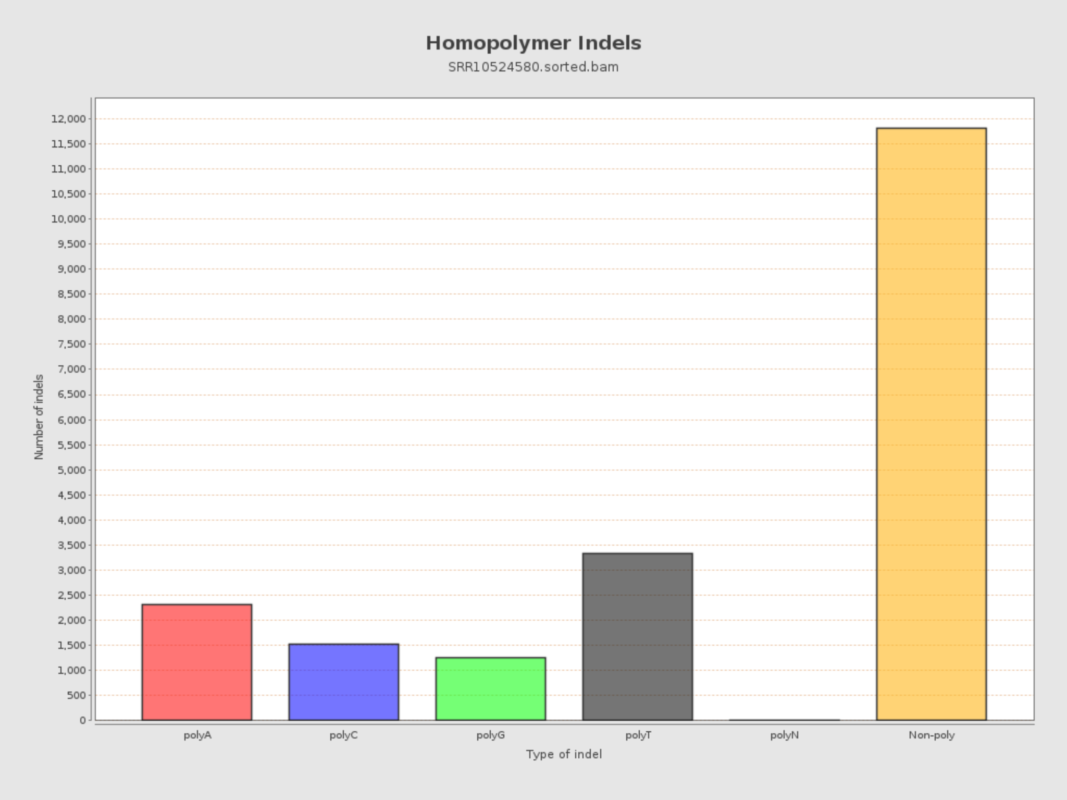
9. Results : Mapped Reads GC-content Distribution



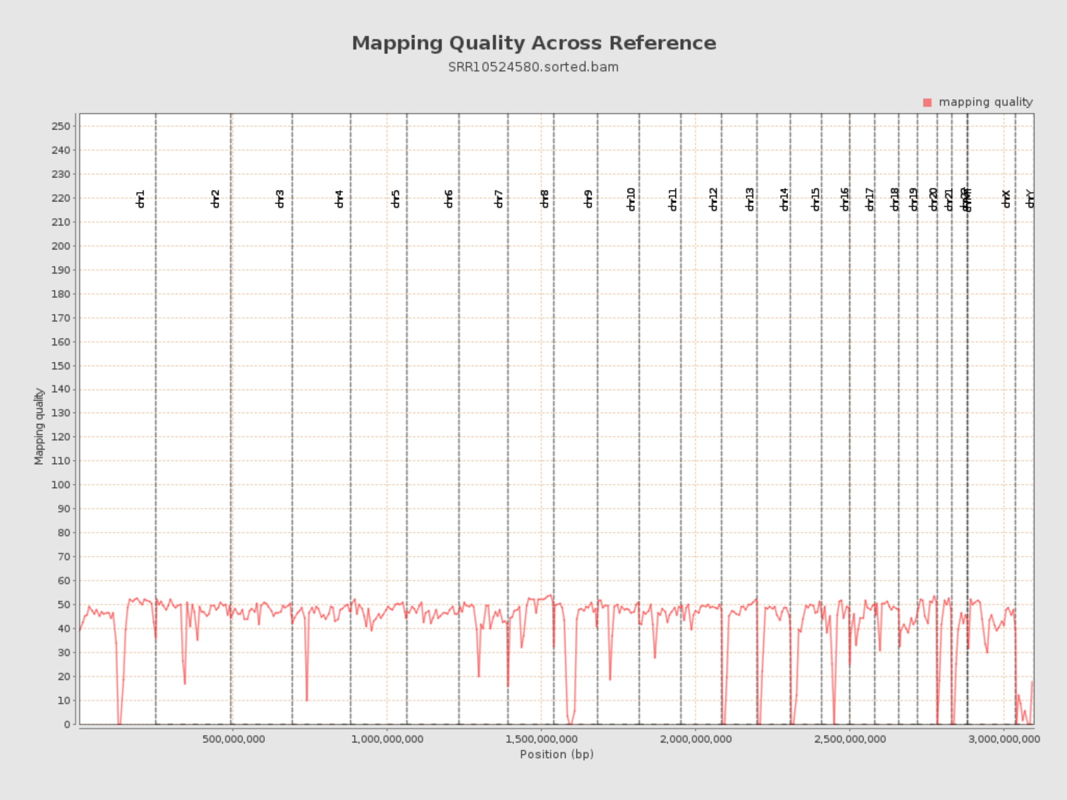
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram