Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 13:01:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524620.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_SRR10524620 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524620.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 13:01:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524620.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,828,900
Mapped reads	1,699,946 / 92.95%
Unmapped reads	128,954 / 7.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,875 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	80,901 / 4.42%
Duplication rate	3.7%
Clipped reads	1,699,200 / 92.91%

2.2. ACGT Content

Number/percentage of A's	25,235,778 / 25.52%
Number/percentage of C's	19,002,191 / 19.22%
Number/percentage of T's	31,187,305 / 31.54%
Number/percentage of G's	23,456,859 / 23.72%
Number/percentage of N's	611 / 0%
GC Percentage	42.94%

2.3. Coverage

Mean	0.032

Standard Deviation	0.2804

2.4. Mapping Quality

Mean Mapping Quality	45.29

2.5. Mismatches and indels

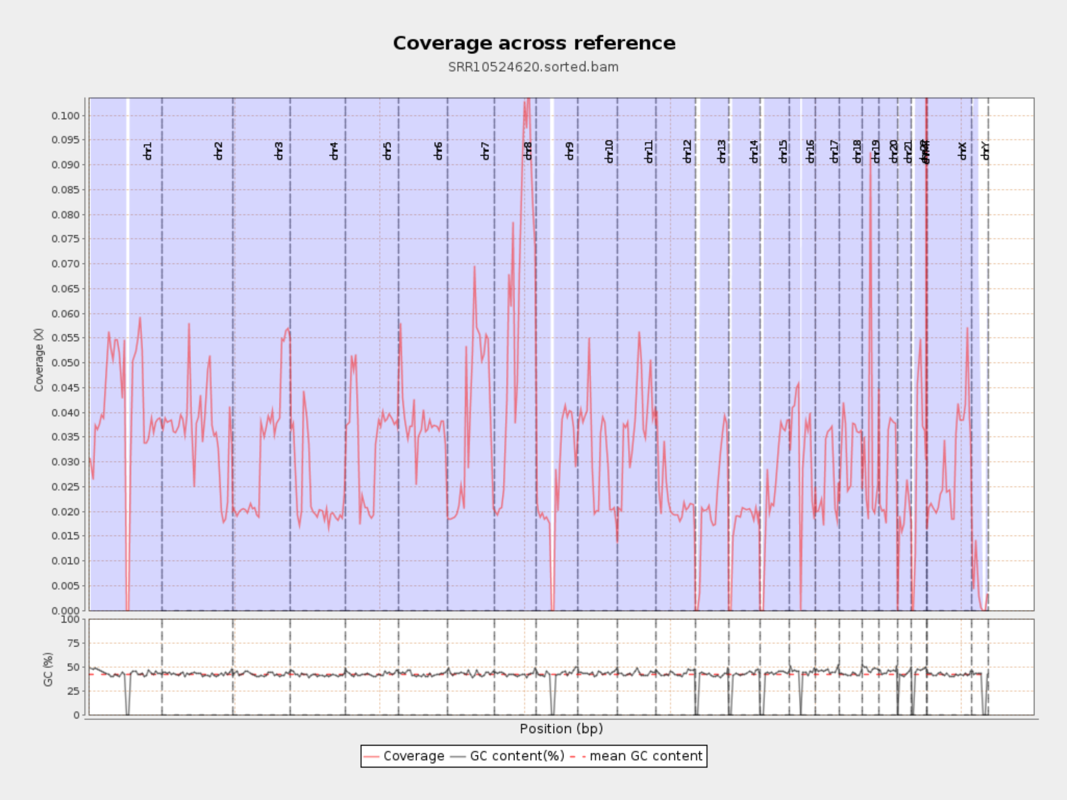
General error rate	0.49%
Mismatches	471,440
Insertions	5,934
Mapped reads with at least one insertion	0.35%
Deletions	18,949
Mapped reads with at least one deletion	1.11%
Homopolymer indels	44.56%

2.6. Chromosome stats

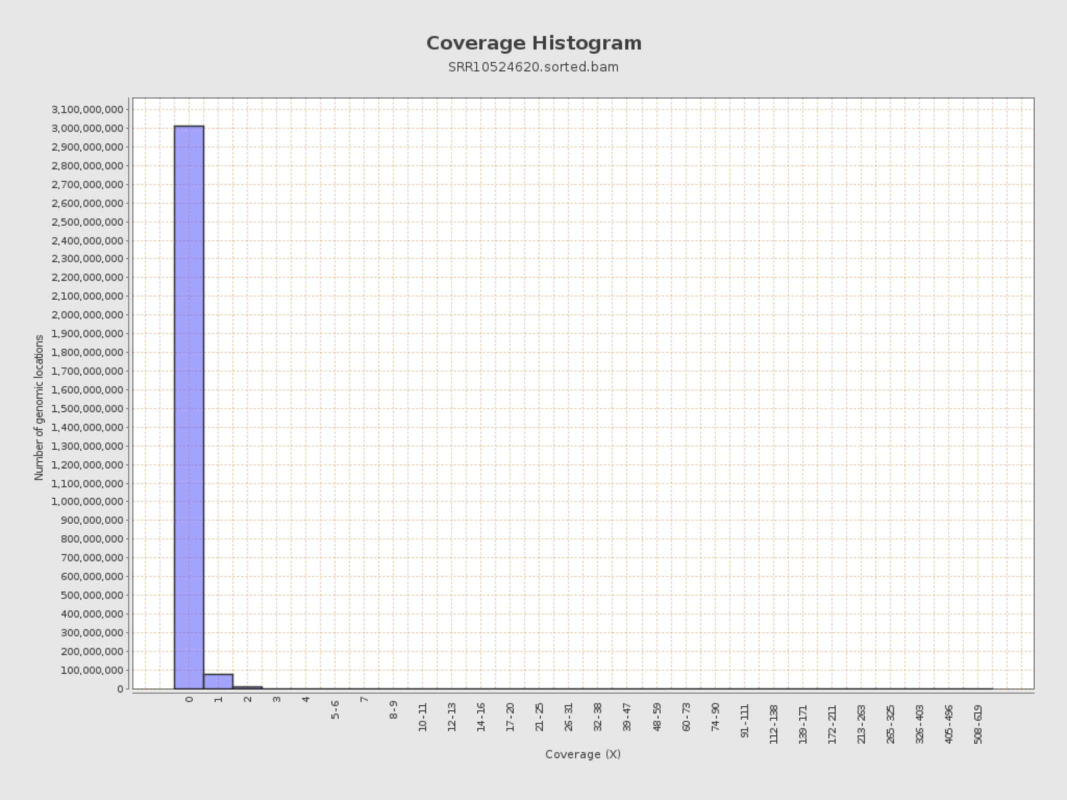
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10162197	0.0408	0.4882
chr2	243199373	8844990	0.0364	0.3338
chr3	198022430	6378656	0.0322	0.2021
chr4	191154276	4482260	0.0234	0.1929
chr5	180915260	6182978	0.0342	0.2072
chr6	171115067	6491892	0.0379	0.2323
chr7	159138663	6077282	0.0382	0.3678

chr8	146364022	8867812	0.0606	0.3656
chr9	141213431	3603623	0.0255	0.2398
chr10	135534747	4259657	0.0314	0.2752
chr11	135006516	5078254	0.0376	0.2812
chr12	133851895	3020025	0.0226	0.1755
chr13	115169878	2447046	0.0212	0.166
chr14	107349540	1811958	0.0169	0.1526
chr15	102531392	2543672	0.0248	0.1838
chr16	90354753	2929587	0.0324	0.2128
chr17	81195210	2137385	0.0263	0.1871
chr18	78077248	2647384	0.0339	0.4043
chr19	59128983	1975992	0.0334	0.3529
chr20	63025520	1825123	0.029	0.1953
chr21	48129895	867335	0.018	0.1659
chr22	51304566	1497454	0.0292	0.1901
chrMT	16571	5362	0.3236	0.653
chrX	155270560	4541757	0.0293	0.2192
chrY	59373566	235069	0.004	0.1148

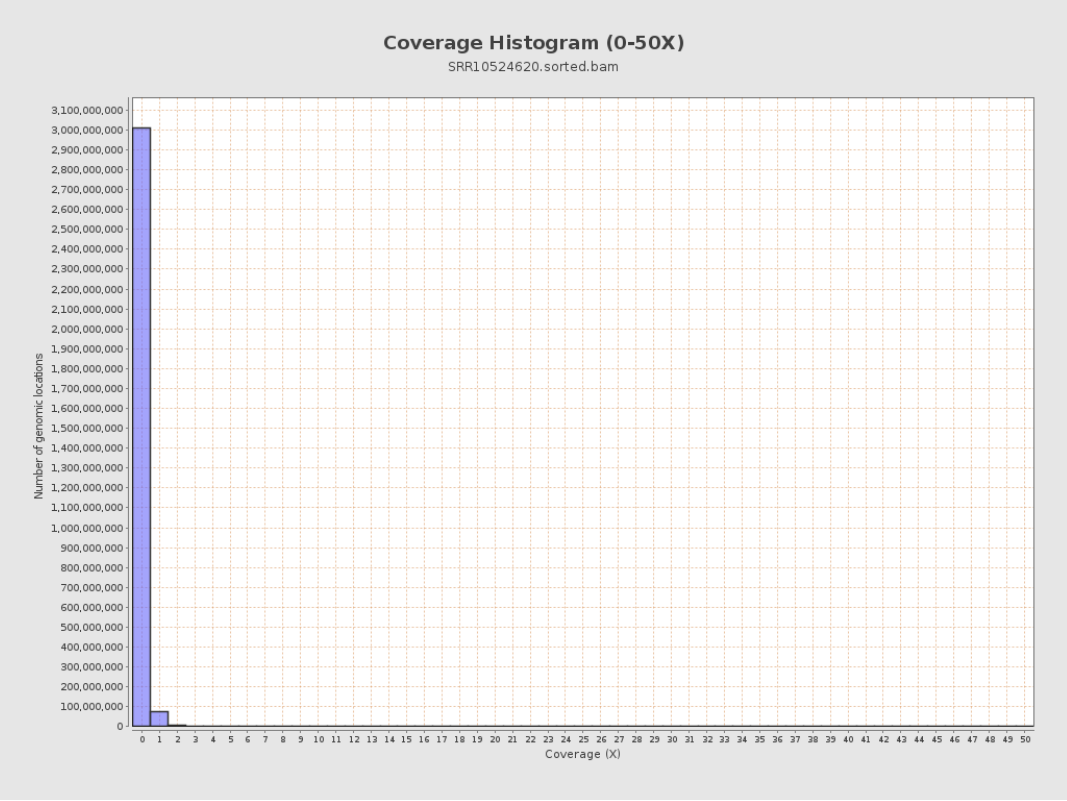
3. Results : Coverage across reference



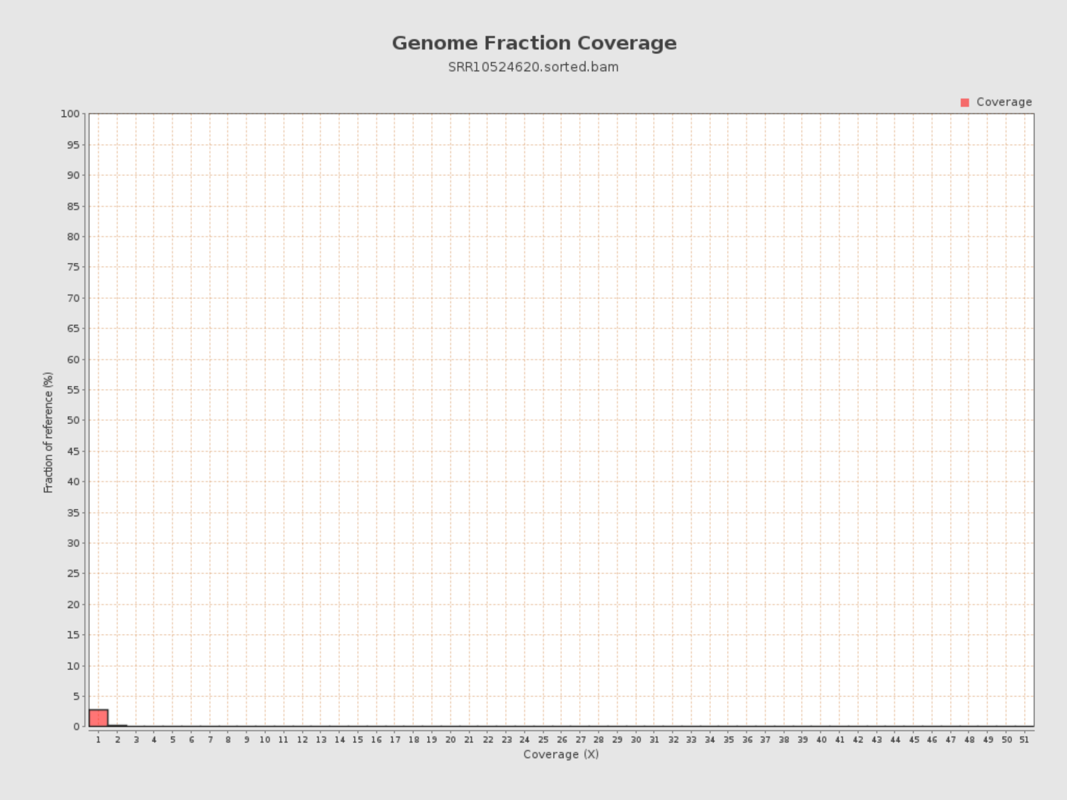
4. Results : Coverage Histogram



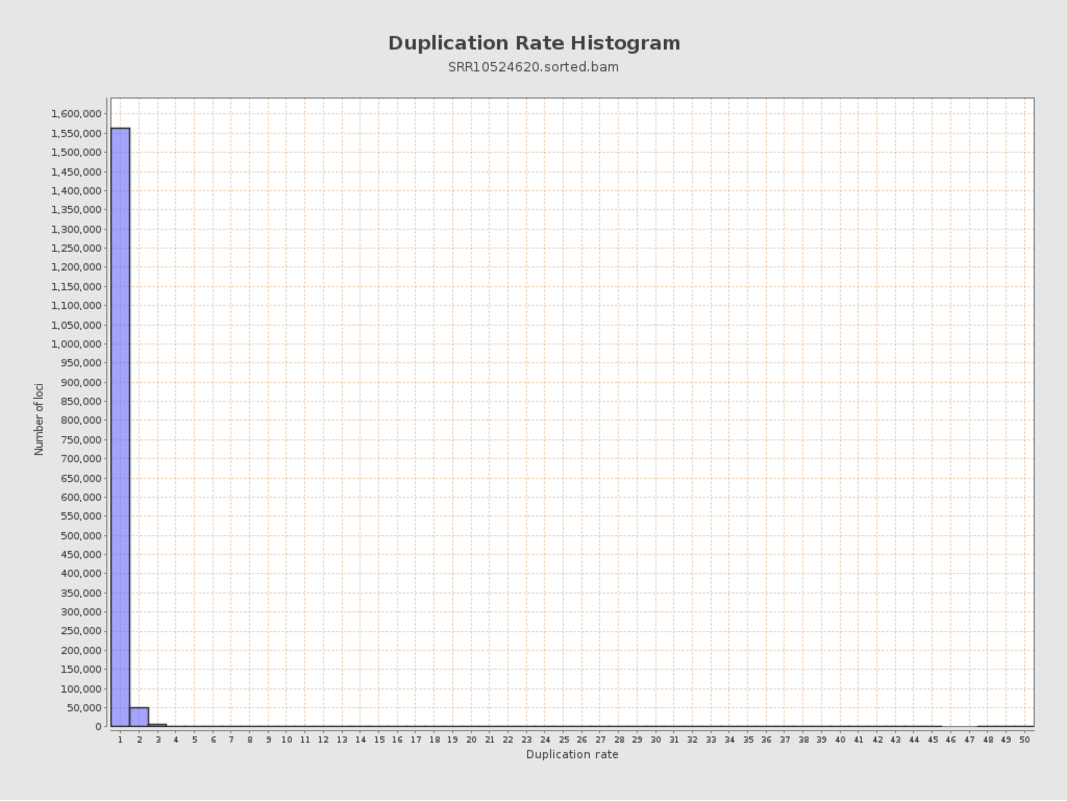
5. Results : Coverage Histogram (0-50X)



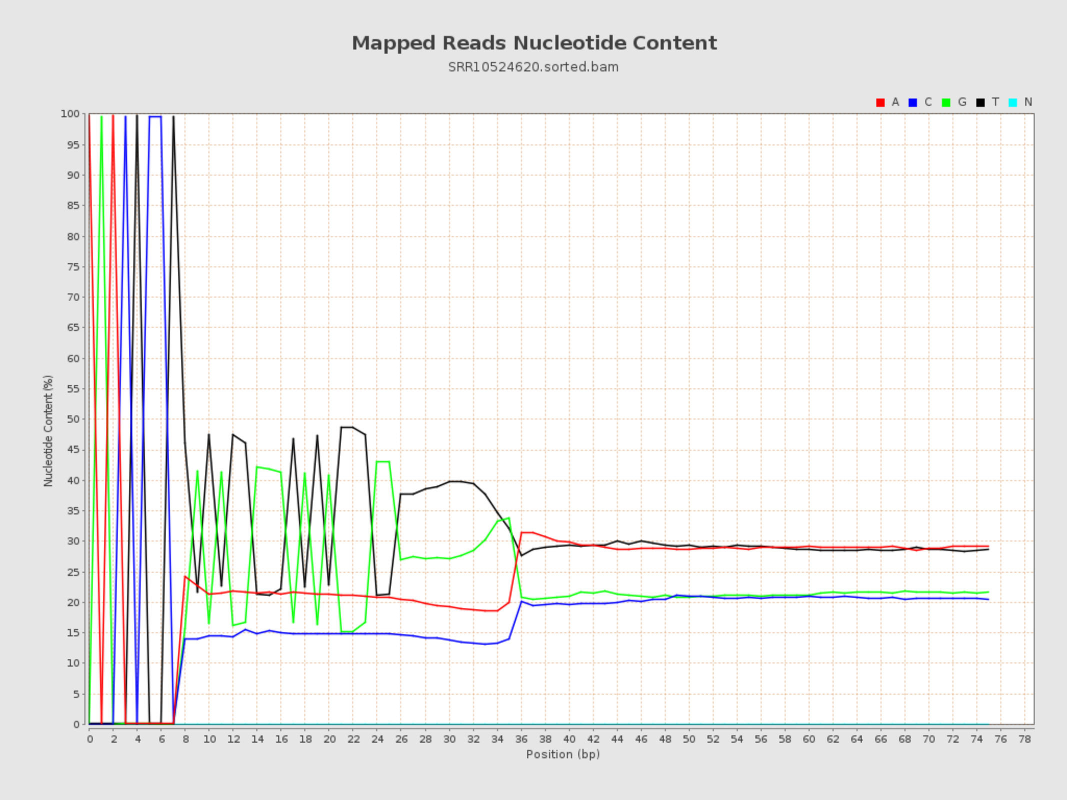
6. Results : Genome Fraction Coverage



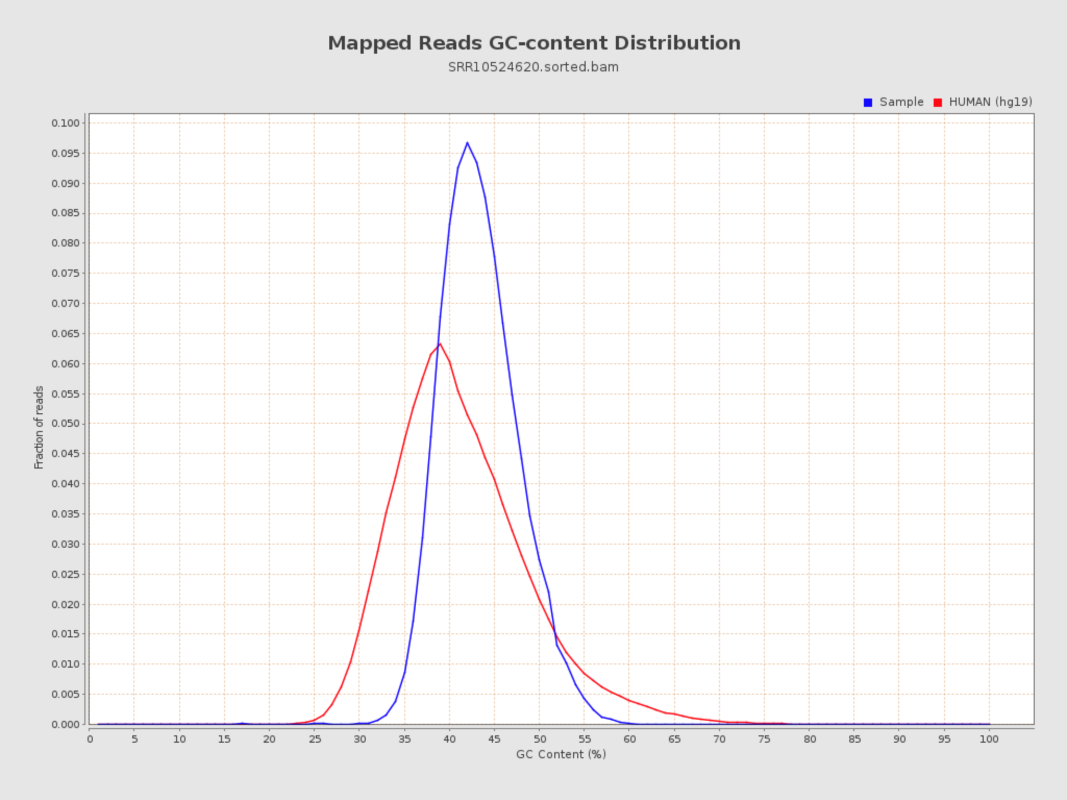
7. Results : Duplication Rate Histogram



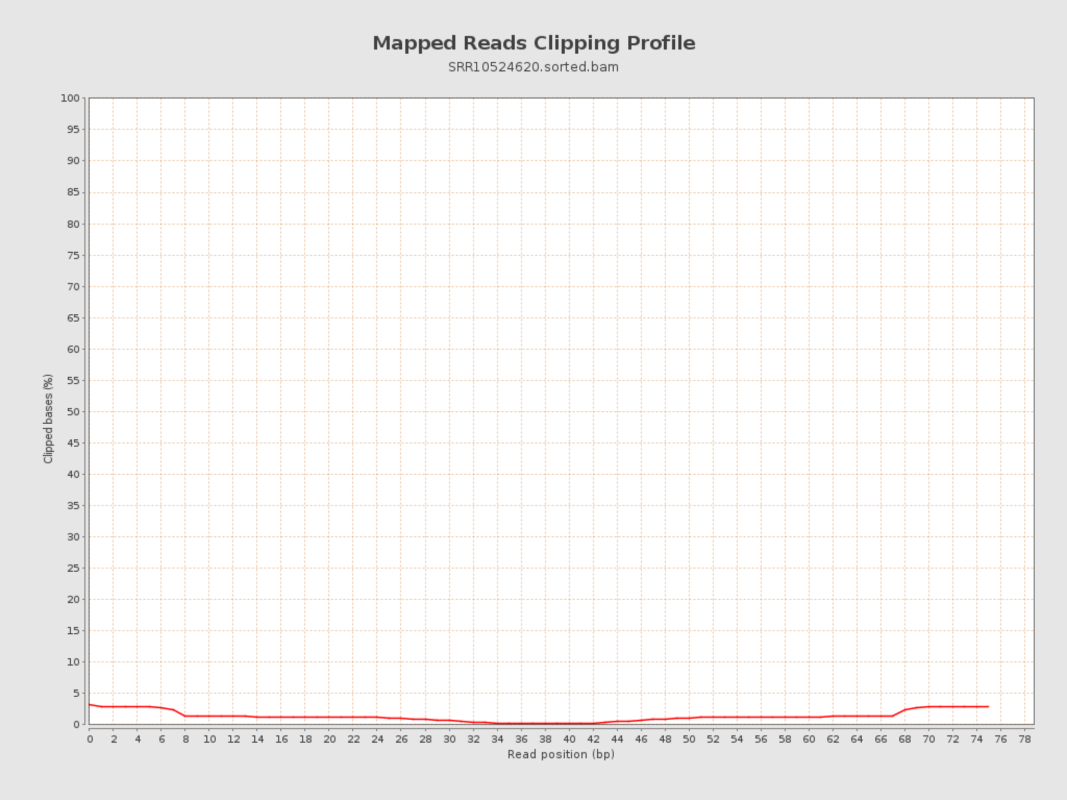
8. Results : Mapped Reads Nucleotide Content



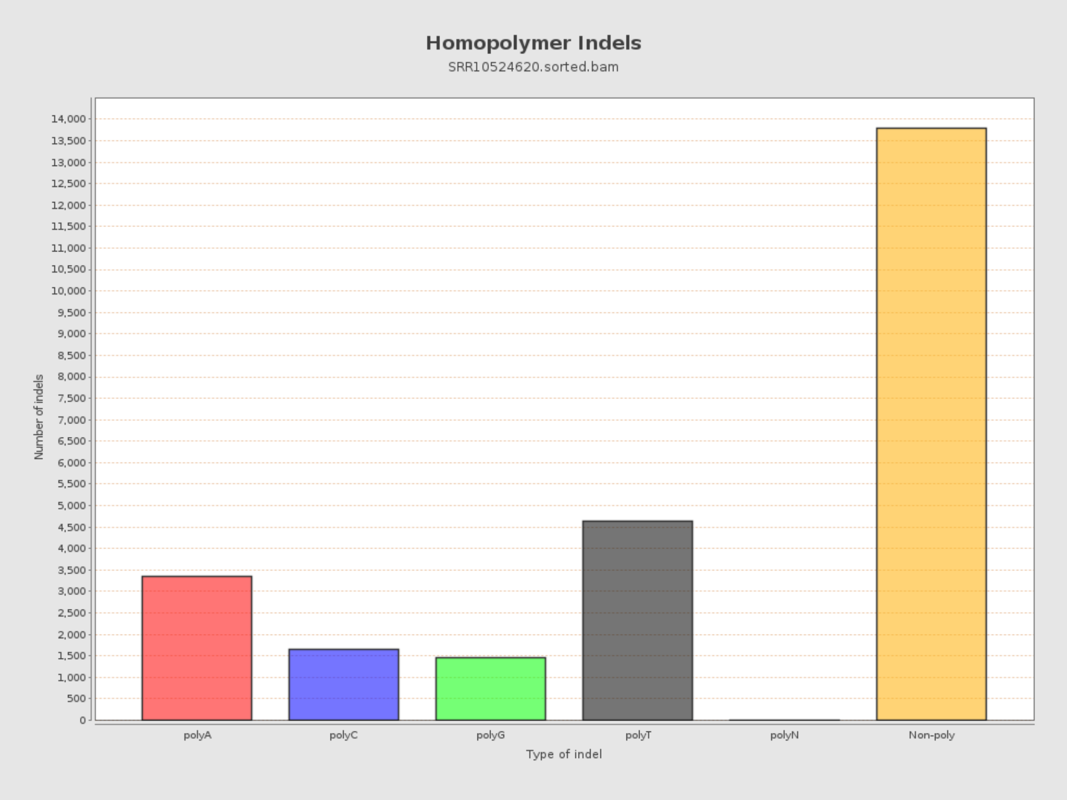
9. Results : Mapped Reads GC-content Distribution



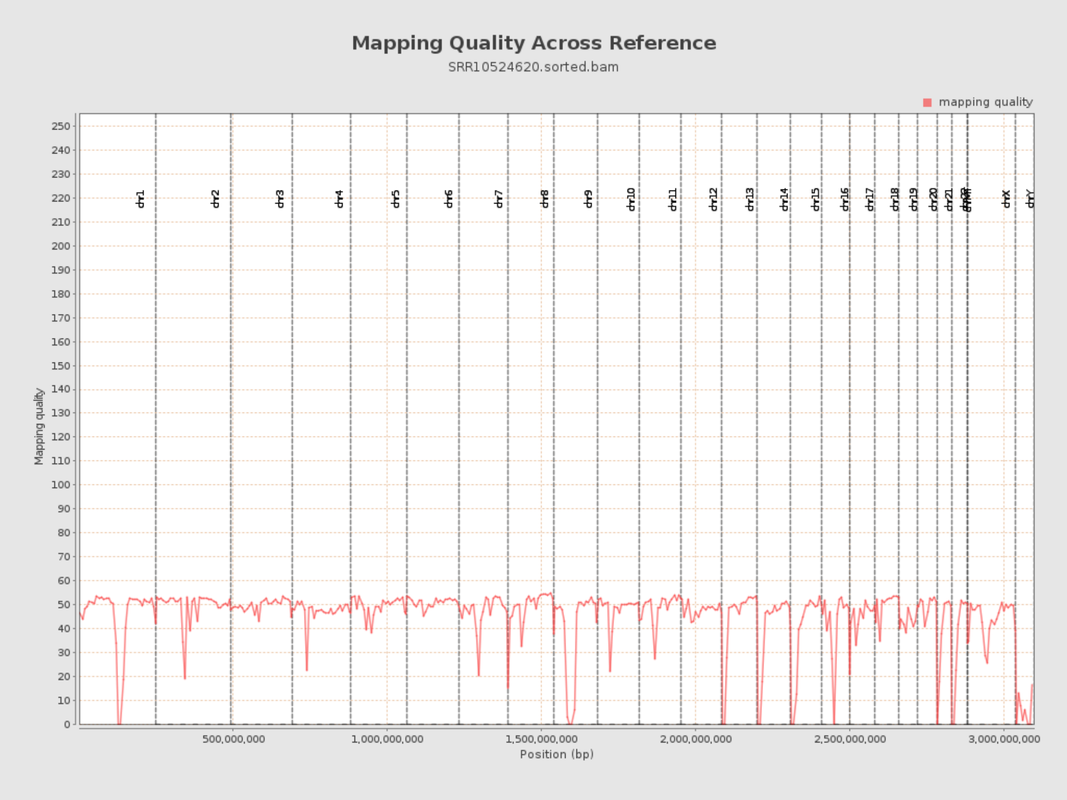
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram