Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 04:06:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524917.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_SRR10524917 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524917.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 04:05:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524917.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,161,181
Mapped reads	1,081,309 / 93.12%
Unmapped reads	79,872 / 6.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,521 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	53,705 / 4.63%
Duplication rate	4.06%
Clipped reads	1,082,730 / 93.24%

2.2. ACGT Content

Number/percentage of A's	15,948,823 / 25.24%
Number/percentage of C's	11,460,840 / 18.14%
Number/percentage of T's	19,635,412 / 31.07%
Number/percentage of G's	16,145,035 / 25.55%
Number/percentage of N's	493 / 0%
GC Percentage	43.69%

2.3. Coverage

Mean	0.0204

Standard Deviation	0.1949

2.4. Mapping Quality

Mean Mapping Quality	44.51

2.5. Mismatches and indels

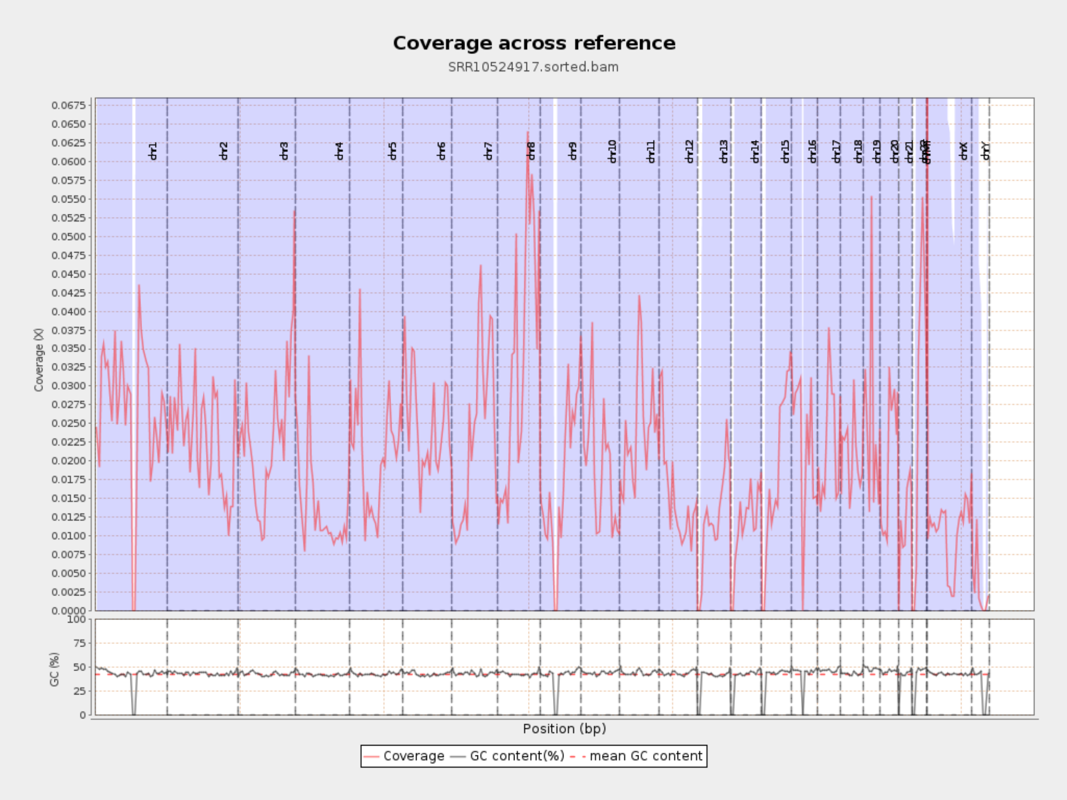
General error rate	0.5%
Mismatches	309,549
Insertions	4,085
Mapped reads with at least one insertion	0.38%
Deletions	12,264
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.61%

2.6. Chromosome stats

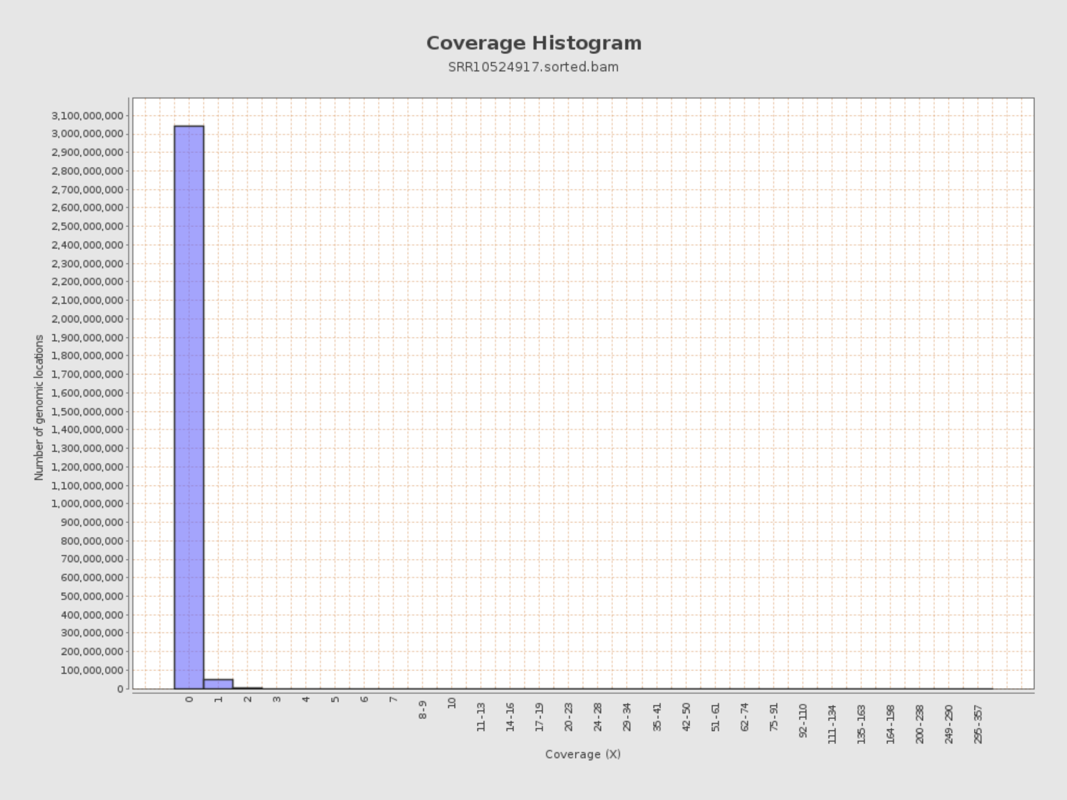
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6735127	0.027	0.2905
chr2	243199373	5616209	0.0231	0.2419
chr3	198022430	4562899	0.023	0.1689
chr4	191154276	2663393	0.0139	0.1595
chr5	180915260	3812243	0.0211	0.1615
chr6	171115067	4265506	0.0249	0.181
chr7	159138663	3701040	0.0233	0.2094

chr8	146364022	5012851	0.0342	0.2798
chr9	141213431	2363890	0.0167	0.1594
chr10	135534747	2703915	0.0199	0.2158
chr11	135006516	3312265	0.0245	0.1871
chr12	133851895	2055793	0.0154	0.1403
chr13	115169878	1402892	0.0122	0.1227
chr14	107349540	1200366	0.0112	0.1205
chr15	102531392	1845085	0.018	0.1494
chr16	90354753	2004066	0.0222	0.1706
chr17	81195210	1786910	0.022	0.1707
chr18	78077248	1609471	0.0206	0.2326
chr19	59128983	1479321	0.025	0.2303
chr20	63025520	1261892	0.02	0.1643
chr21	48129895	579605	0.012	0.1428
chr22	51304566	1432286	0.0279	0.1894
chrMT	16571	6730	0.4061	0.696
chrX	155270560	1621544	0.0104	0.1216
chrY	59373566	175853	0.003	0.1246

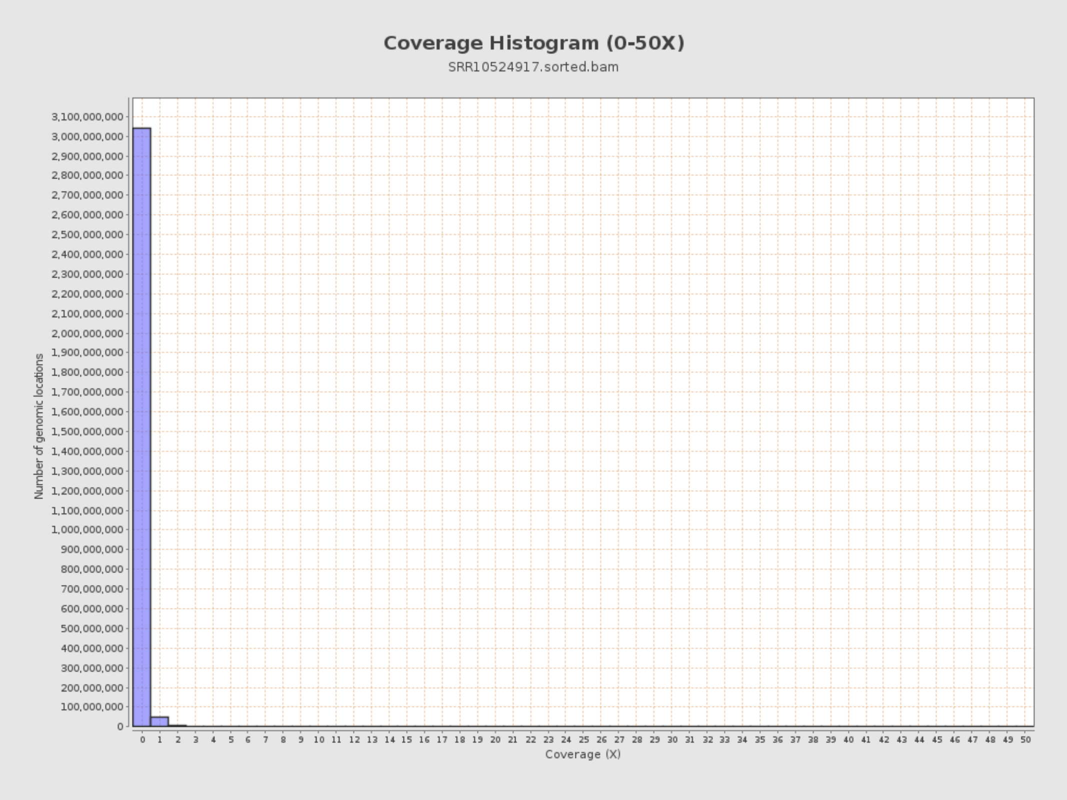
3. Results : Coverage across reference



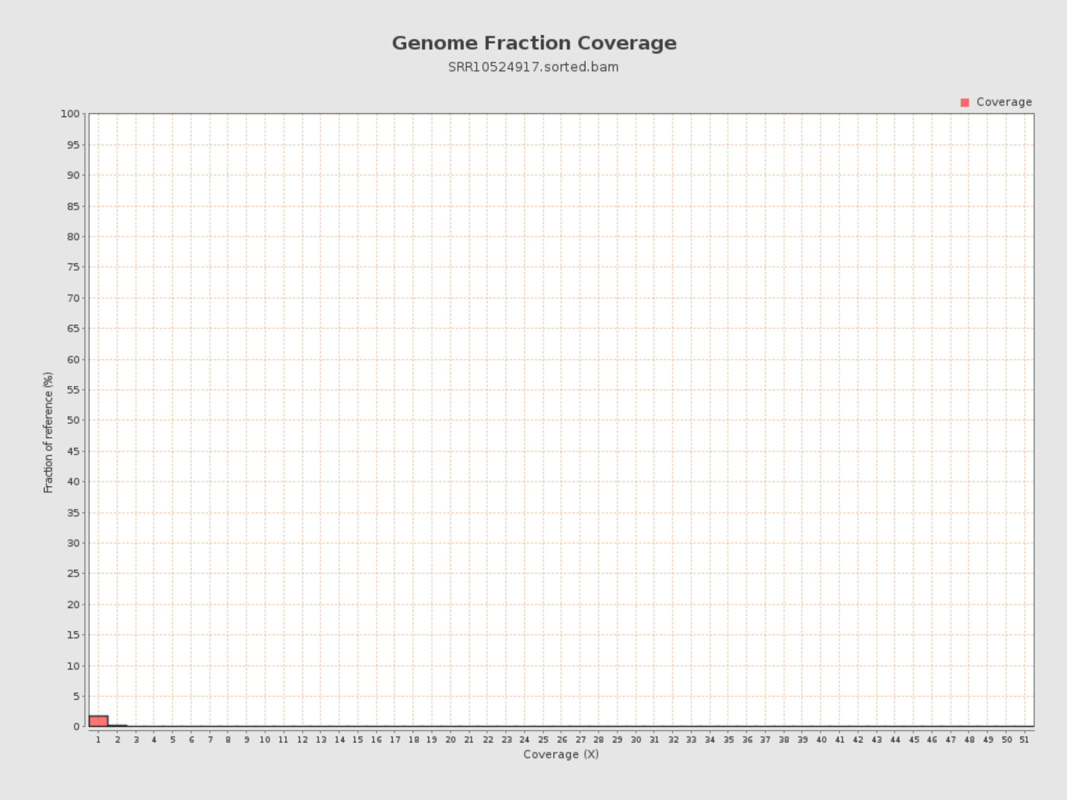
4. Results : Coverage Histogram



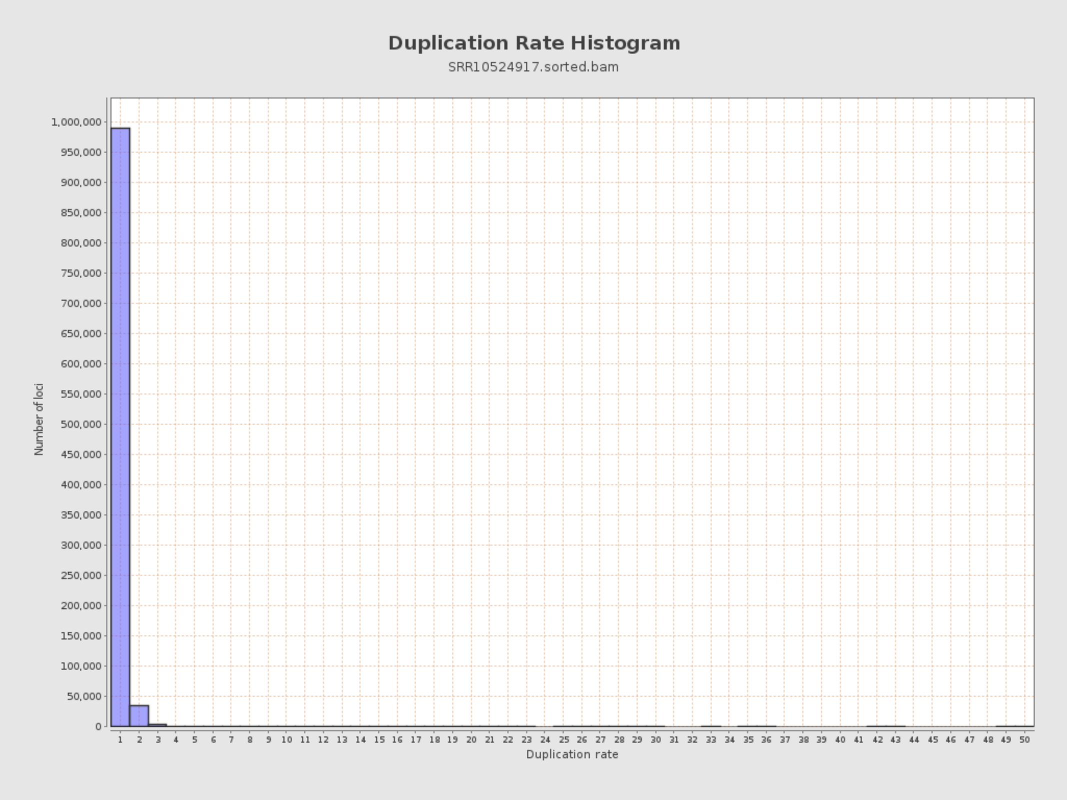
5. Results : Coverage Histogram (0-50X)



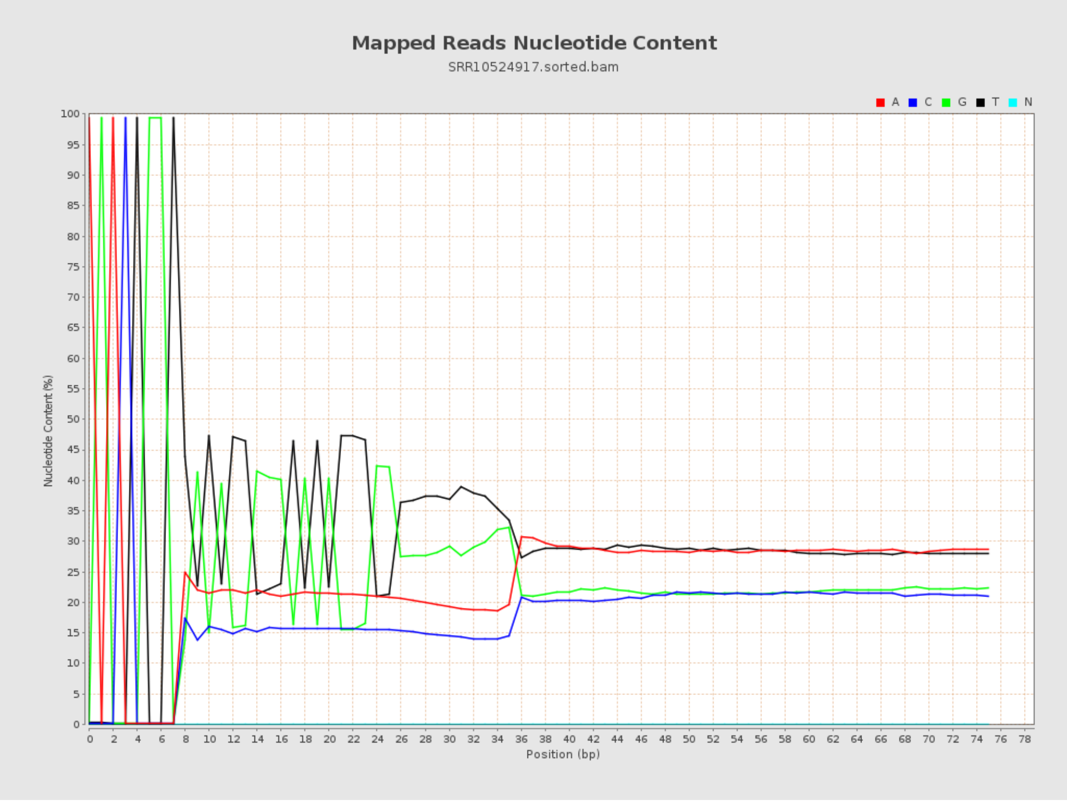
6. Results : Genome Fraction Coverage



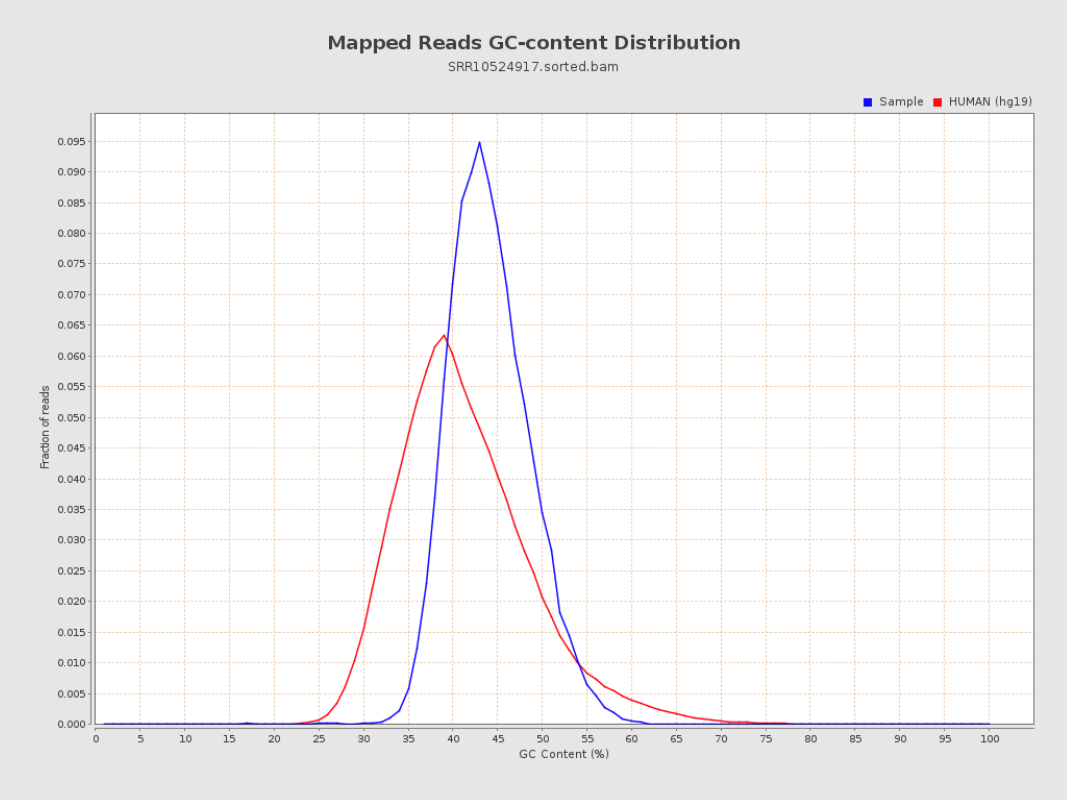
7. Results : Duplication Rate Histogram



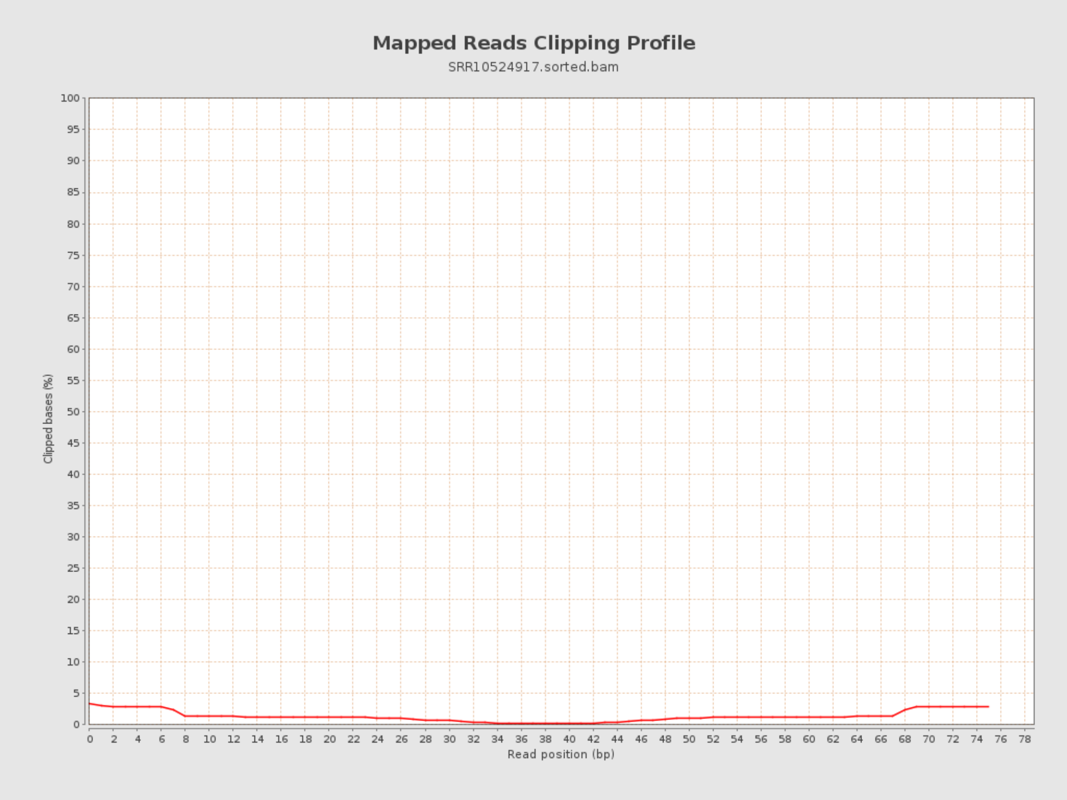
8. Results : Mapped Reads Nucleotide Content



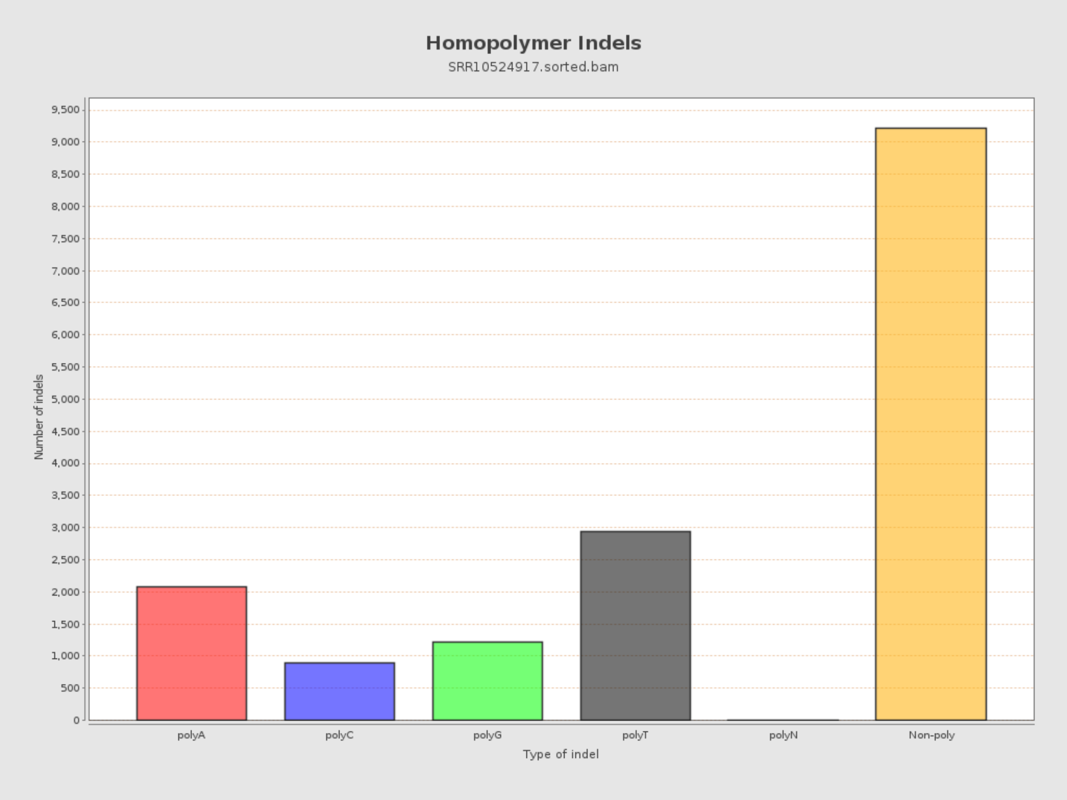
9. Results : Mapped Reads GC-content Distribution



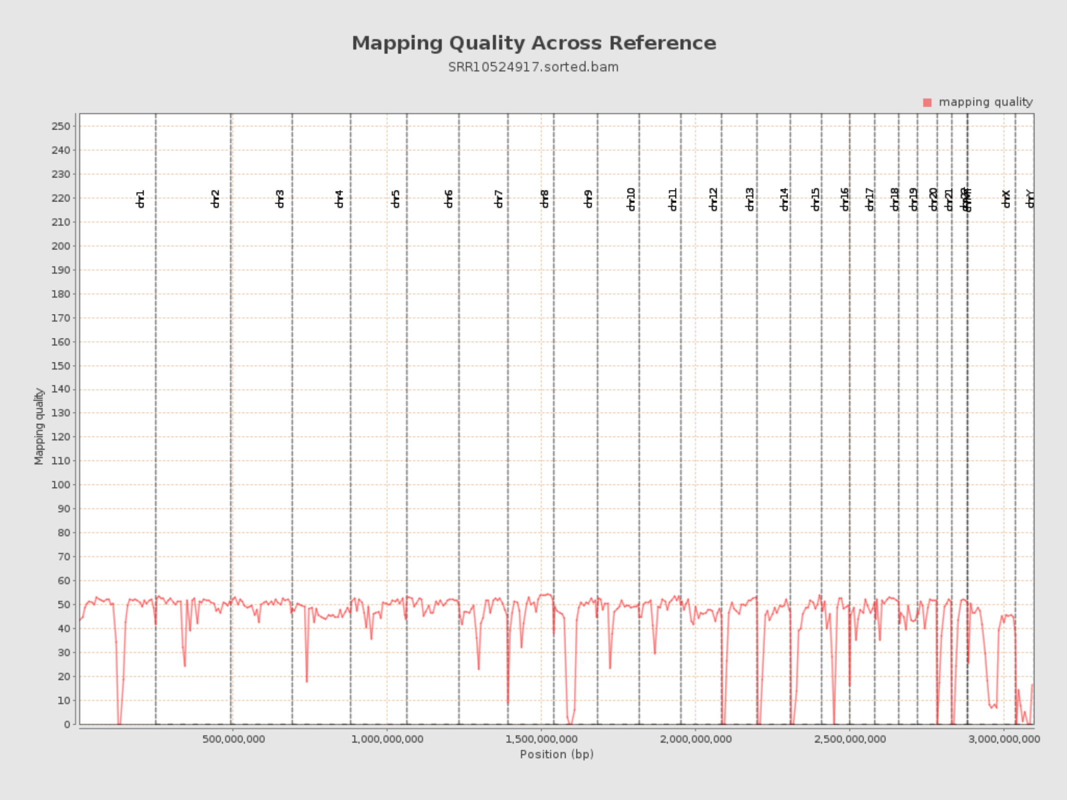
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram