Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:56:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717015.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_SRR9717015 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717015.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:56:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717015.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	745,564
Mapped reads	665,302 / 89.23%
Unmapped reads	80,262 / 10.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,199 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	11,218 / 1.5%
Duplication rate	1.28%
Clipped reads	666,248 / 89.36%

2.2. ACGT Content

Number/percentage of A's	8,782,261 / 23.33%
Number/percentage of C's	7,507,904 / 19.95%
Number/percentage of T's	12,191,724 / 32.39%
Number/percentage of G's	9,159,948 / 24.33%
Number/percentage of N's	850 / 0%
GC Percentage	44.28%

2.3. Coverage

Mean	0.0122

Standard Deviation	0.129

2.4. Mapping Quality

Mean Mapping Quality	43.73

2.5. Mismatches and indels

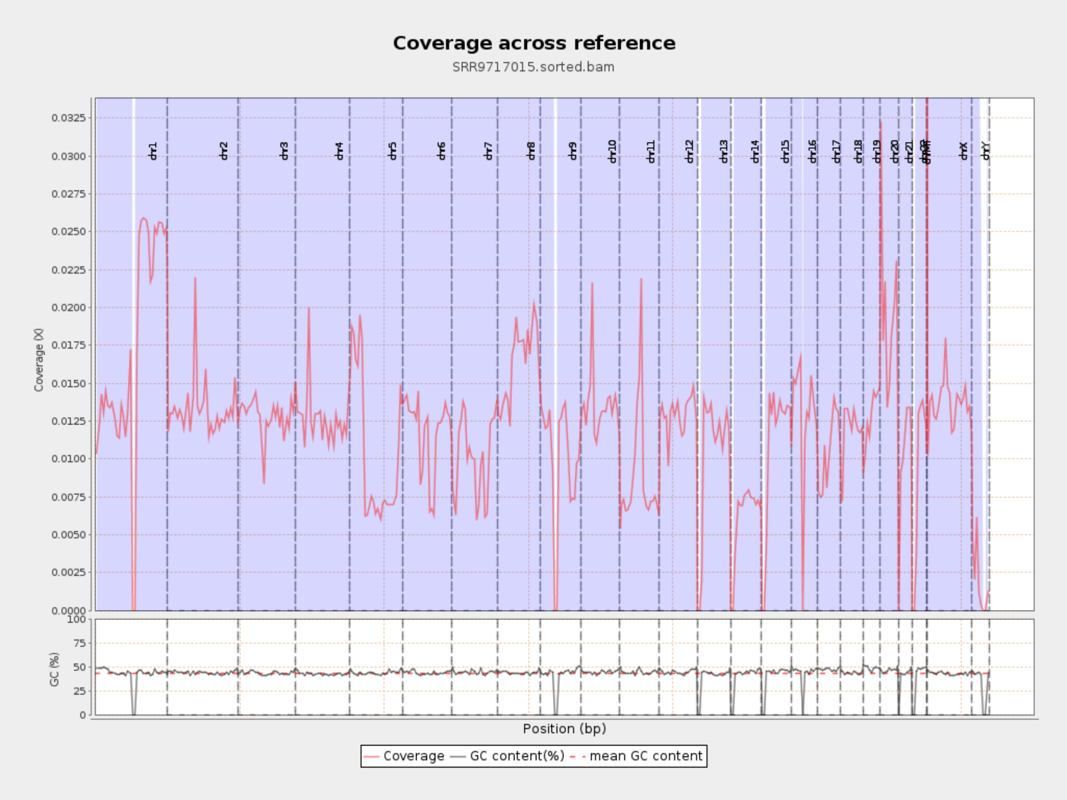
General error rate	0.51%
Mismatches	189,186
Insertions	2,599
Mapped reads with at least one insertion	0.39%
Deletions	6,096
Mapped reads with at least one deletion	0.91%
Homopolymer indels	38.21%

2.6. Chromosome stats

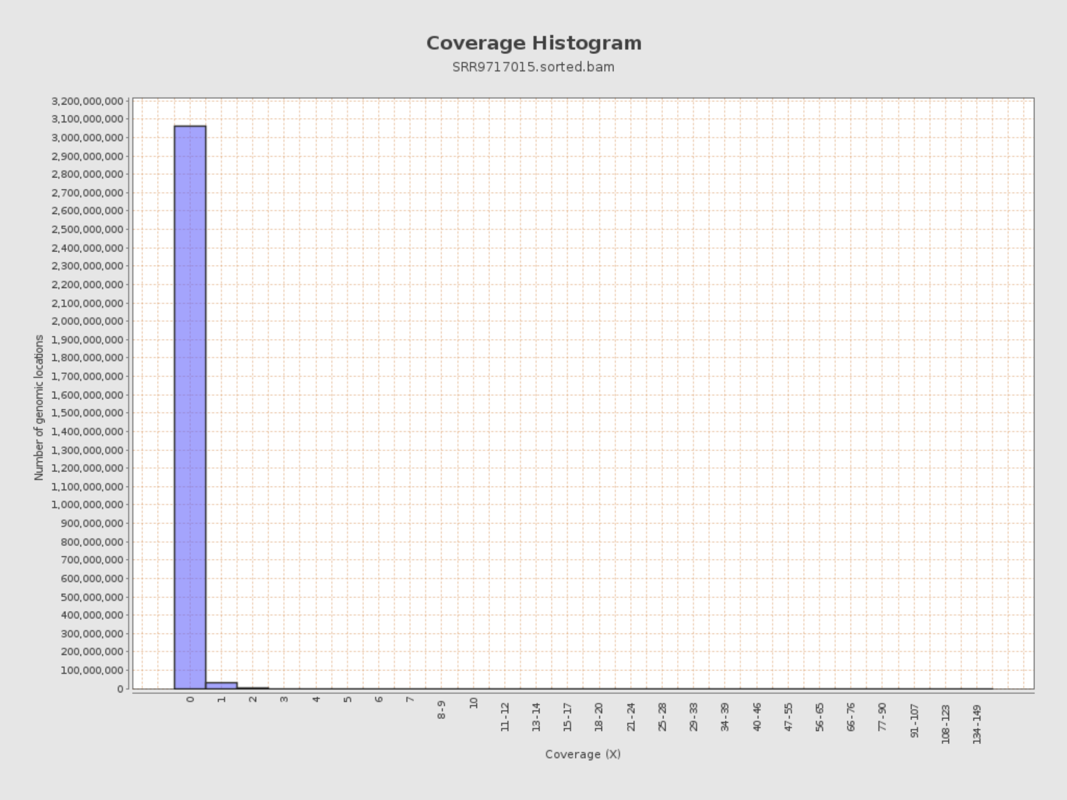
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4284610	0.0172	0.176
chr2	243199373	3236286	0.0133	0.1484
chr3	198022430	2533249	0.0128	0.1176
chr4	191154276	2434029	0.0127	0.1227
chr5	180915260	1869785	0.0103	0.1057
chr6	171115067	2009564	0.0117	0.1159
chr7	159138663	1604086	0.0101	0.1166

chr8	146364022	2403200	0.0164	0.1416
chr9	141213431	1397776	0.0099	0.1212
chr10	135534747	1845864	0.0136	0.1444
chr11	135006516	1220995	0.009	0.1192
chr12	133851895	1736071	0.013	0.1191
chr13	115169878	1188430	0.0103	0.1055
chr14	107349540	658834	0.0061	0.0862
chr15	102531392	1106420	0.0108	0.1082
chr16	90354753	1154385	0.0128	0.1229
chr17	81195210	854151	0.0105	0.1089
chr18	78077248	919441	0.0118	0.183
chr19	59128983	757475	0.0128	0.1419
chr20	63025520	1229233	0.0195	0.1474
chr21	48129895	502198	0.0104	0.1108
chr22	51304566	458187	0.0089	0.0985
chrMT	16571	1161	0.0701	0.2757
chrX	155270560	2137041	0.0138	0.1288
chrY	59373566	110465	0.0019	0.0566

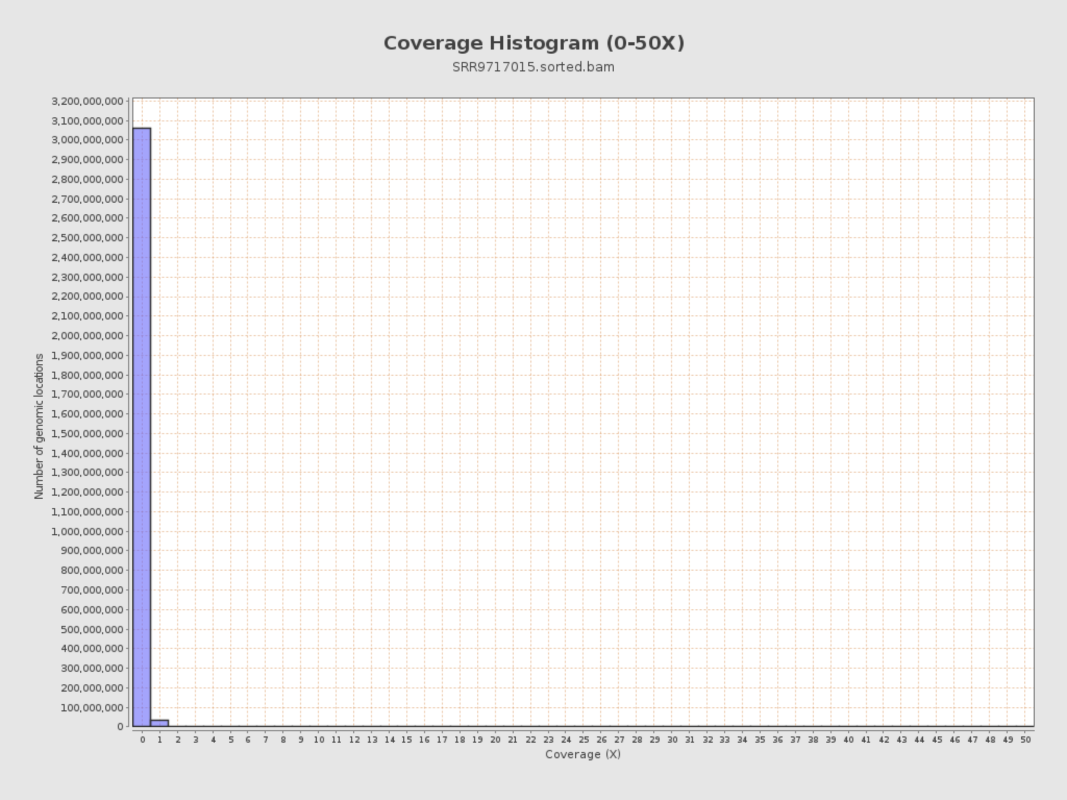
3. Results : Coverage across reference



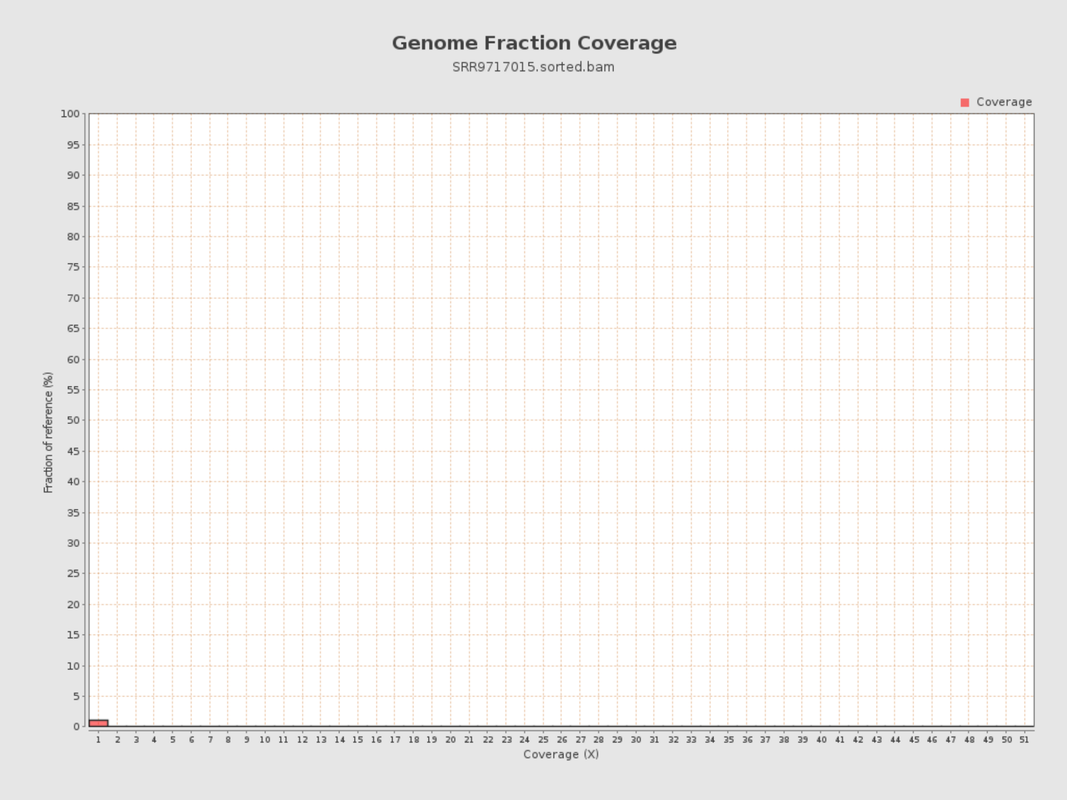
4. Results : Coverage Histogram



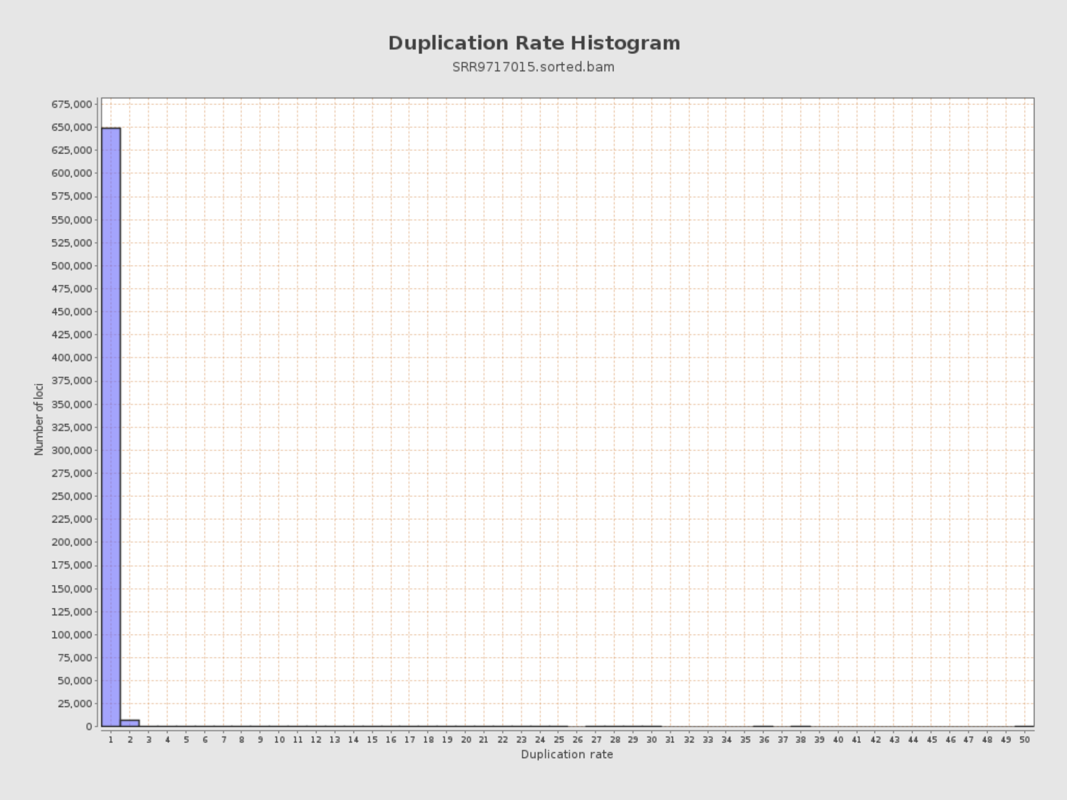
5. Results : Coverage Histogram (0-50X)



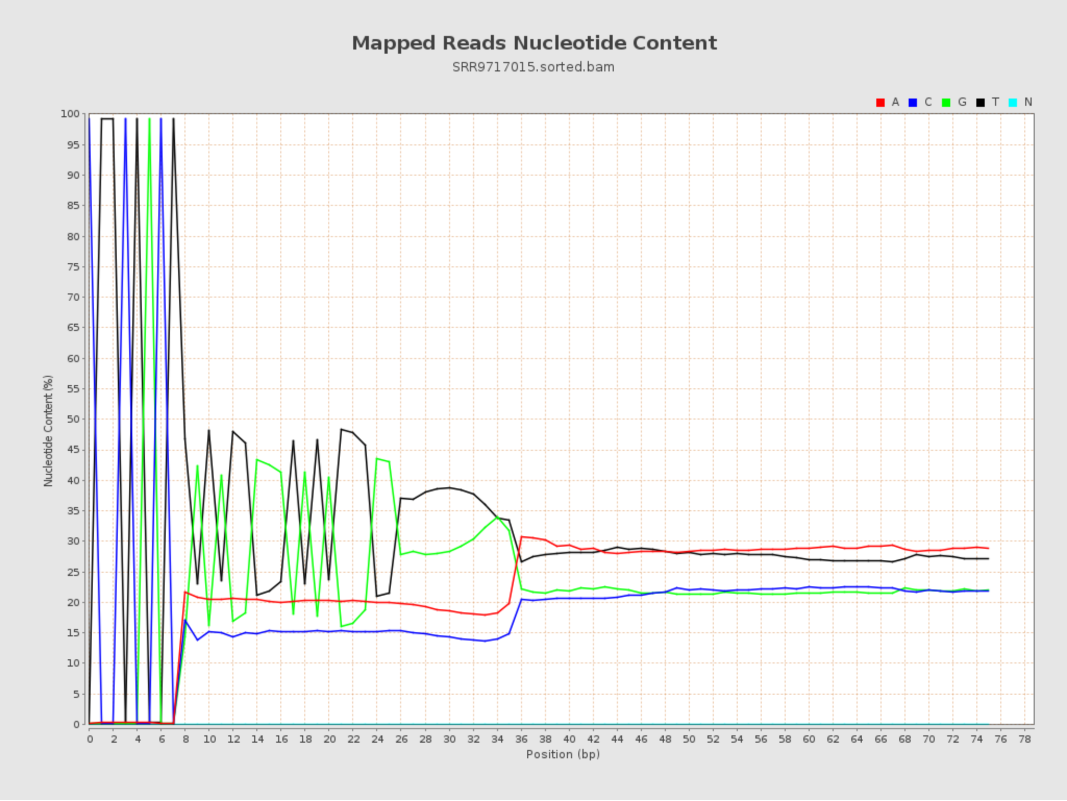
6. Results : Genome Fraction Coverage



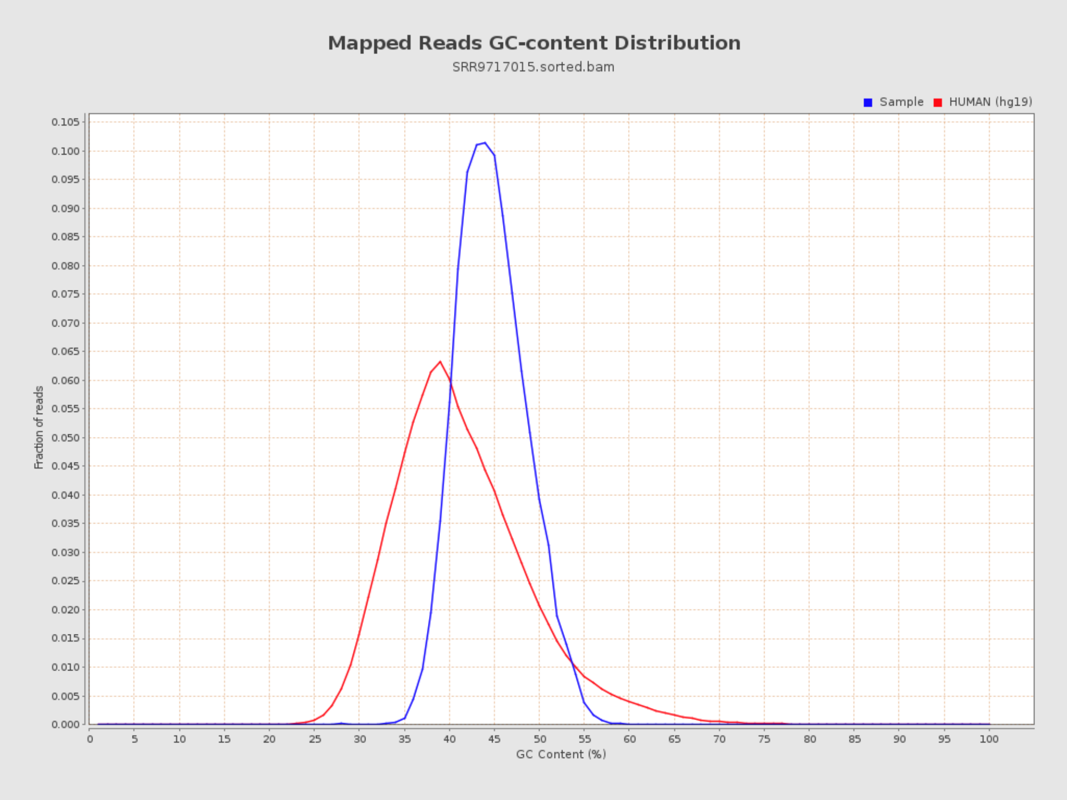
7. Results : Duplication Rate Histogram



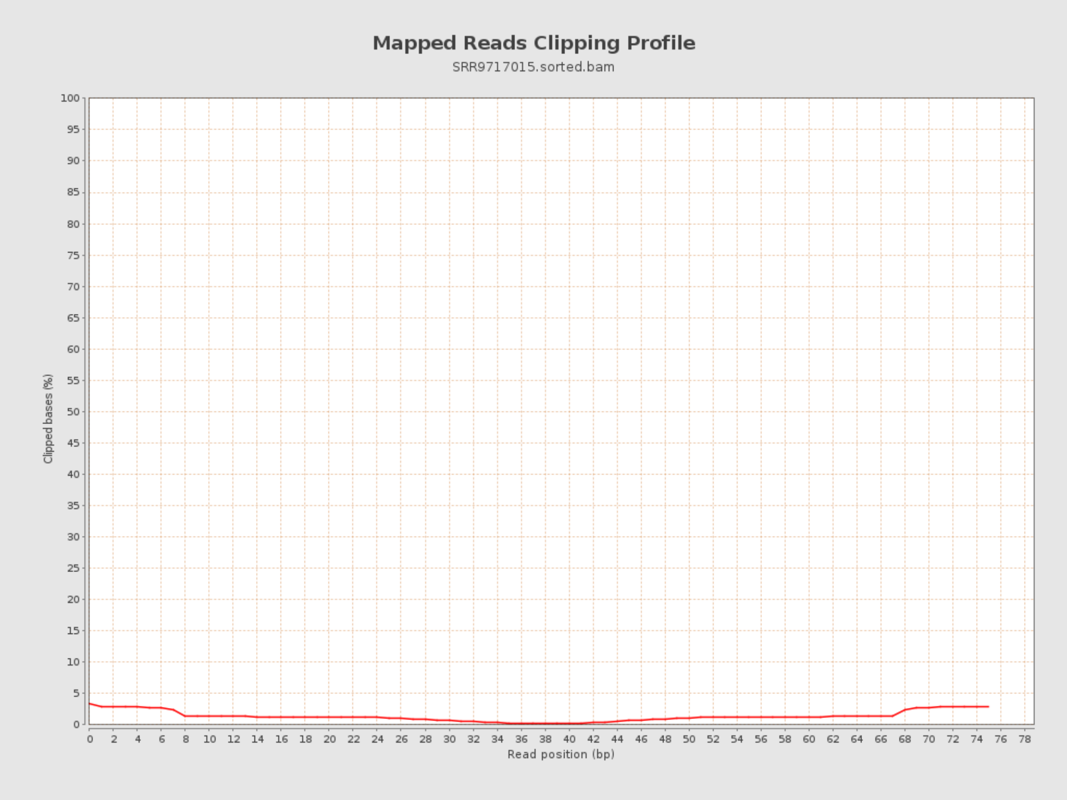
8. Results : Mapped Reads Nucleotide Content



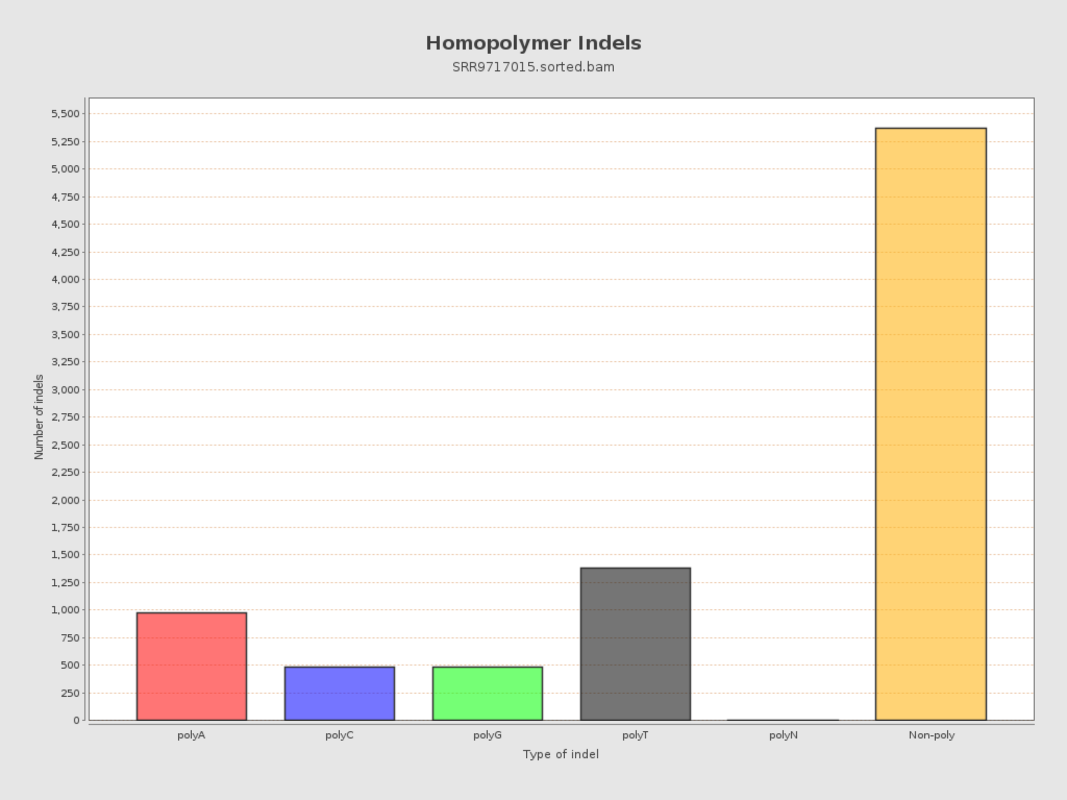
9. Results : Mapped Reads GC-content Distribution



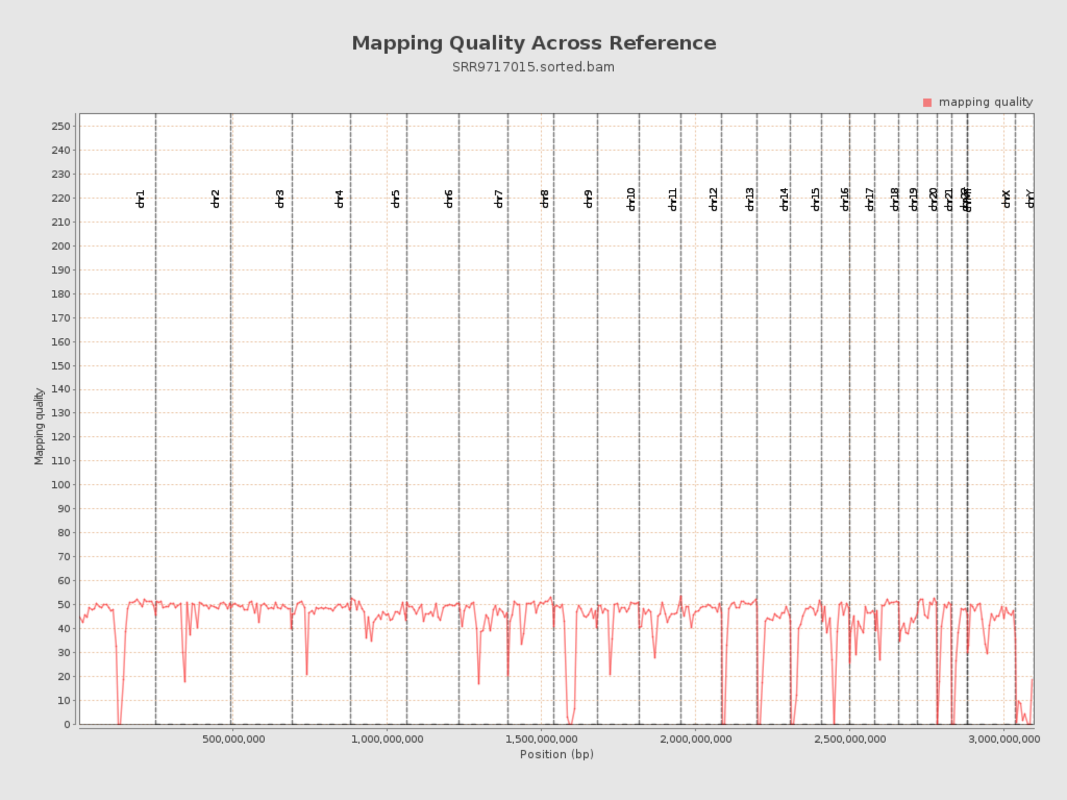
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram