Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 03:20:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717059.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_SRR9717059 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717059.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 03:20:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717059.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	402,147
Mapped reads	368,590 / 91.66%
Unmapped reads	33,557 / 8.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,332 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	6,910 / 1.72%
Duplication rate	1.34%
Clipped reads	369,545 / 91.89%

2.2. ACGT Content

Number/percentage of A's	5,125,307 / 24.34%
Number/percentage of C's	3,672,169 / 17.44%
Number/percentage of T's	6,698,418 / 31.81%
Number/percentage of G's	5,561,024 / 26.41%
Number/percentage of N's	442 / 0%
GC Percentage	43.85%

2.3. Coverage

Mean	0.0068

Standard Deviation	0.0985

2.4. Mapping Quality

Mean Mapping Quality	44.54

2.5. Mismatches and indels

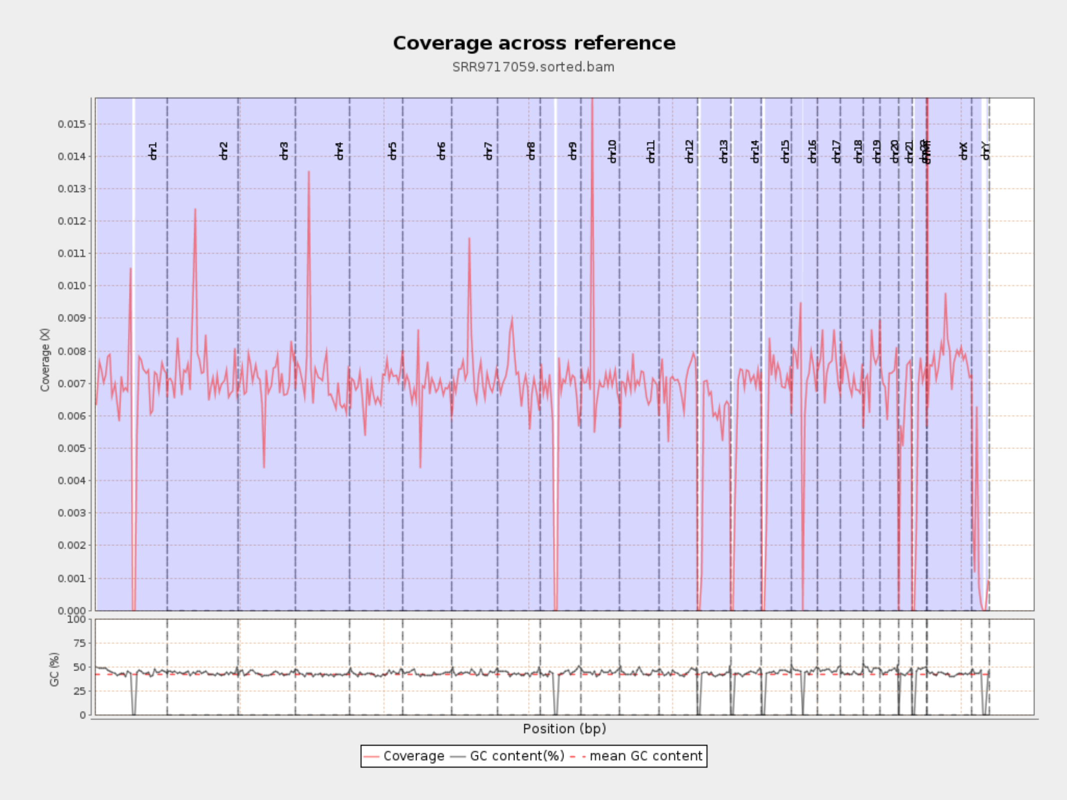
General error rate	0.52%
Mismatches	106,938
Insertions	1,329
Mapped reads with at least one insertion	0.36%
Deletions	3,592
Mapped reads with at least one deletion	0.97%
Homopolymer indels	44.52%

2.6. Chromosome stats

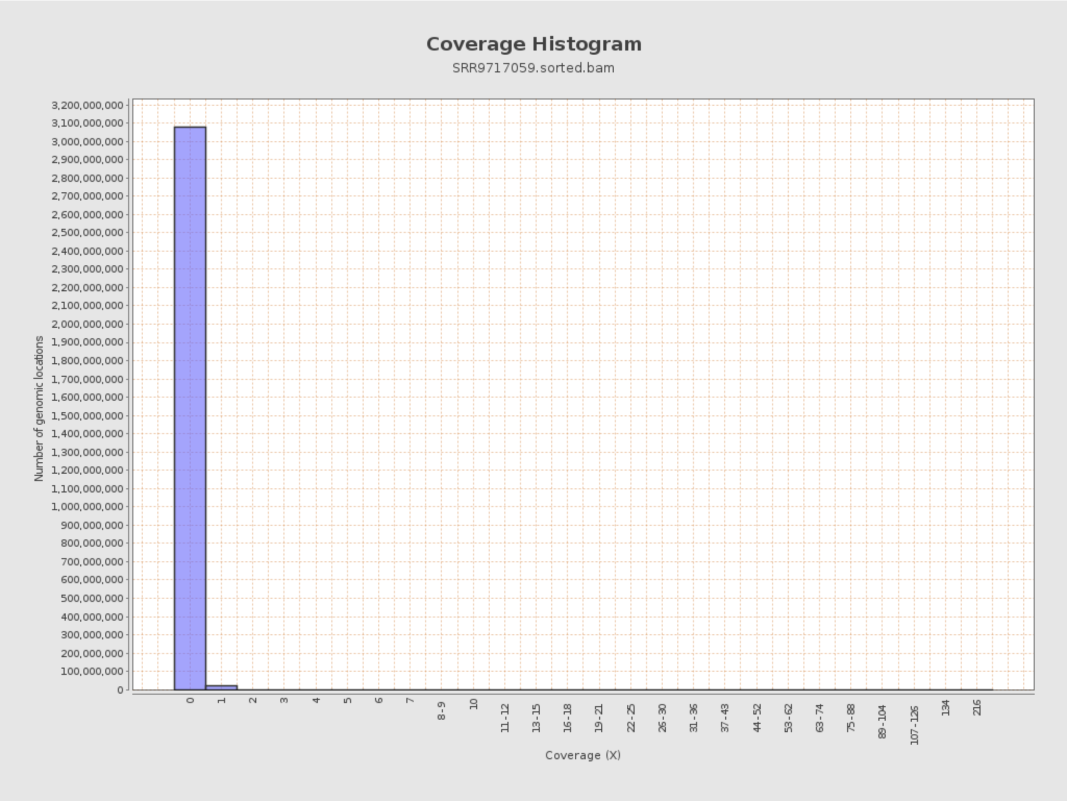
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1671156	0.0067	0.1251
chr2	243199373	1812488	0.0075	0.1289
chr3	198022430	1405040	0.0071	0.0871
chr4	191154276	1382896	0.0072	0.0924
chr5	180915260	1255997	0.0069	0.0858
chr6	171115067	1179218	0.0069	0.0883
chr7	159138663	1170489	0.0074	0.1059

chr8	146364022	1043730	0.0071	0.1111
chr9	141213431	872104	0.0062	0.0875
chr10	135534747	1008965	0.0074	0.1096
chr11	135006516	940214	0.007	0.0917
chr12	133851895	942630	0.007	0.0863
chr13	115169878	607469	0.0053	0.0746
chr14	107349540	646003	0.006	0.0808
chr15	102531392	610409	0.006	0.0797
chr16	90354753	617626	0.0068	0.088
chr17	81195210	614425	0.0076	0.0915
chr18	78077248	555353	0.0071	0.1134
chr19	59128983	440837	0.0075	0.1089
chr20	63025520	445826	0.0071	0.0874
chr21	48129895	286243	0.0059	0.0845
chr22	51304566	258289	0.005	0.0733
chrMT	16571	3857	0.2328	0.496
chrX	155270560	1204761	0.0078	0.0939
chrY	59373566	87326	0.0015	0.069

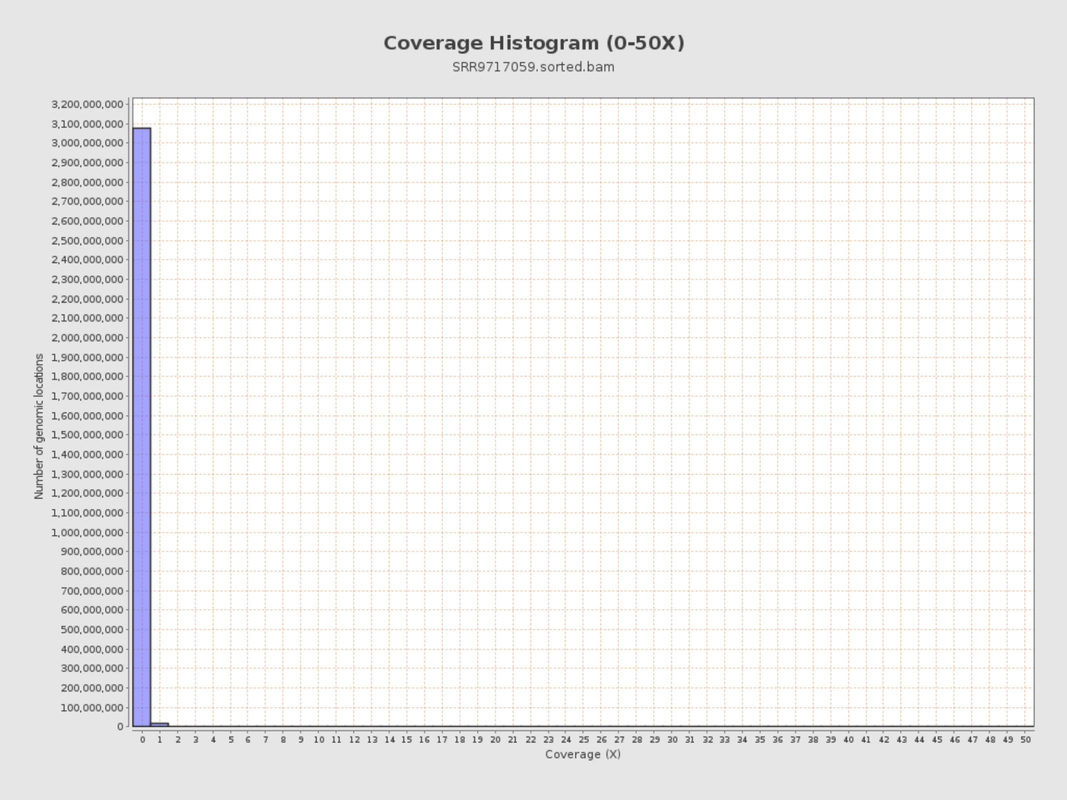
3. Results : Coverage across reference



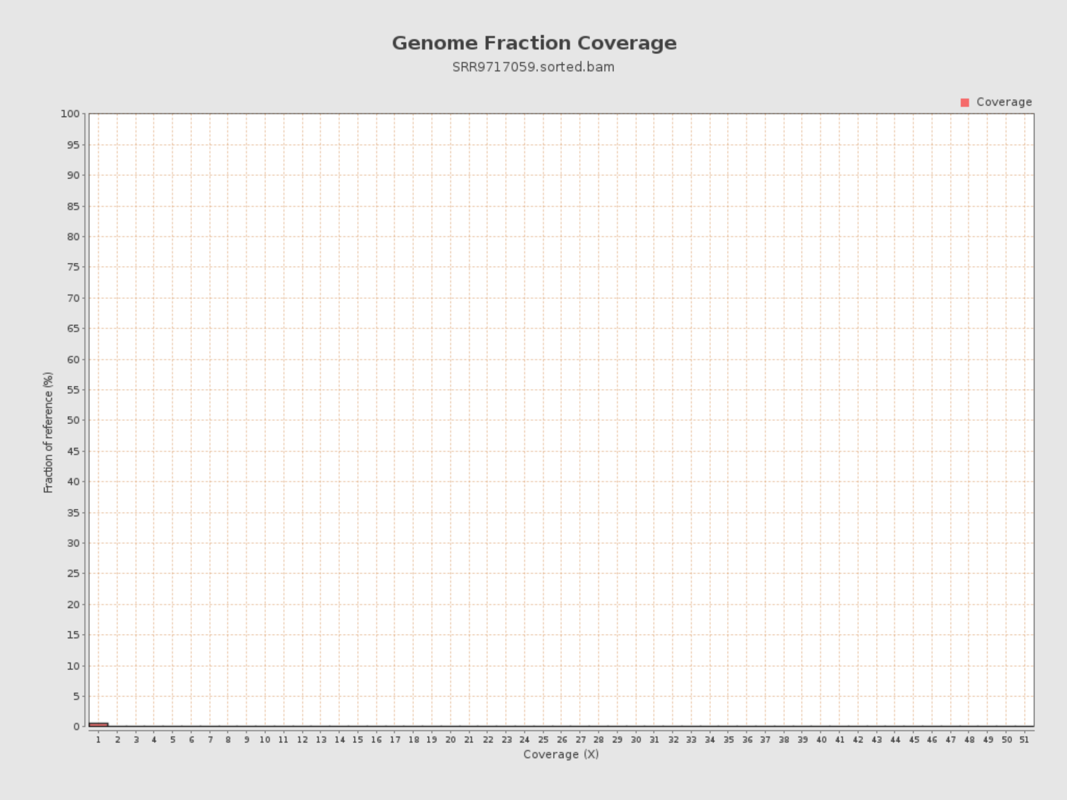
4. Results : Coverage Histogram



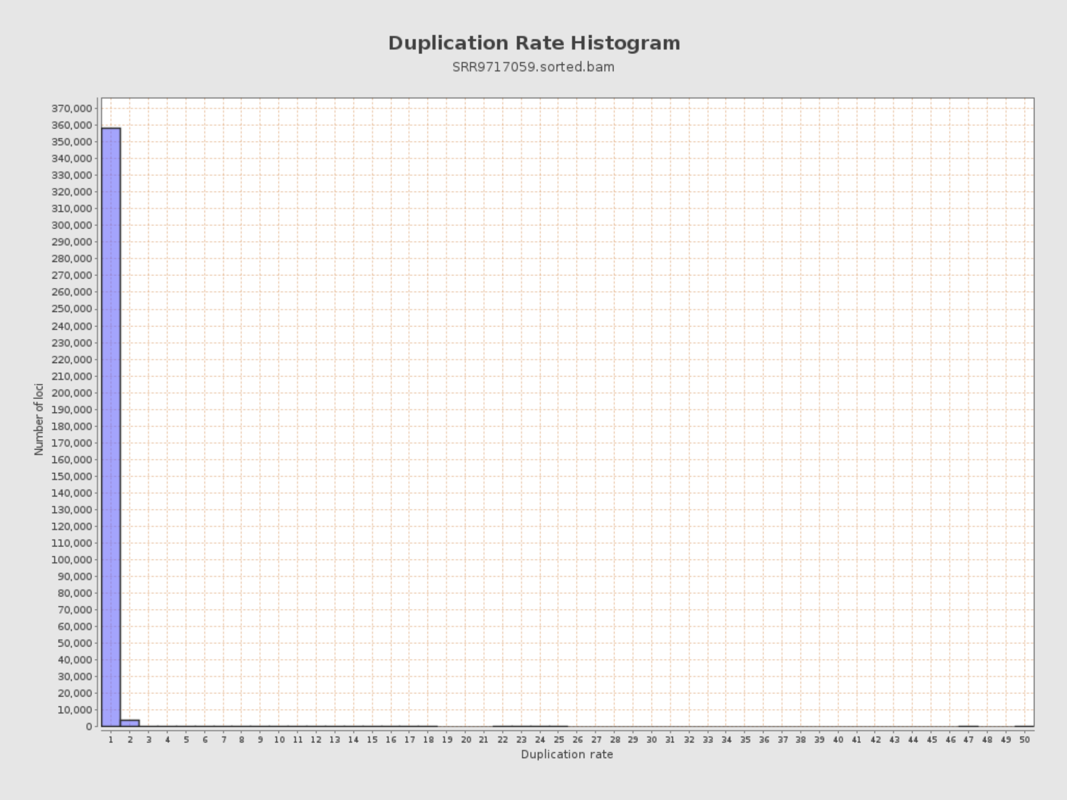
5. Results : Coverage Histogram (0-50X)



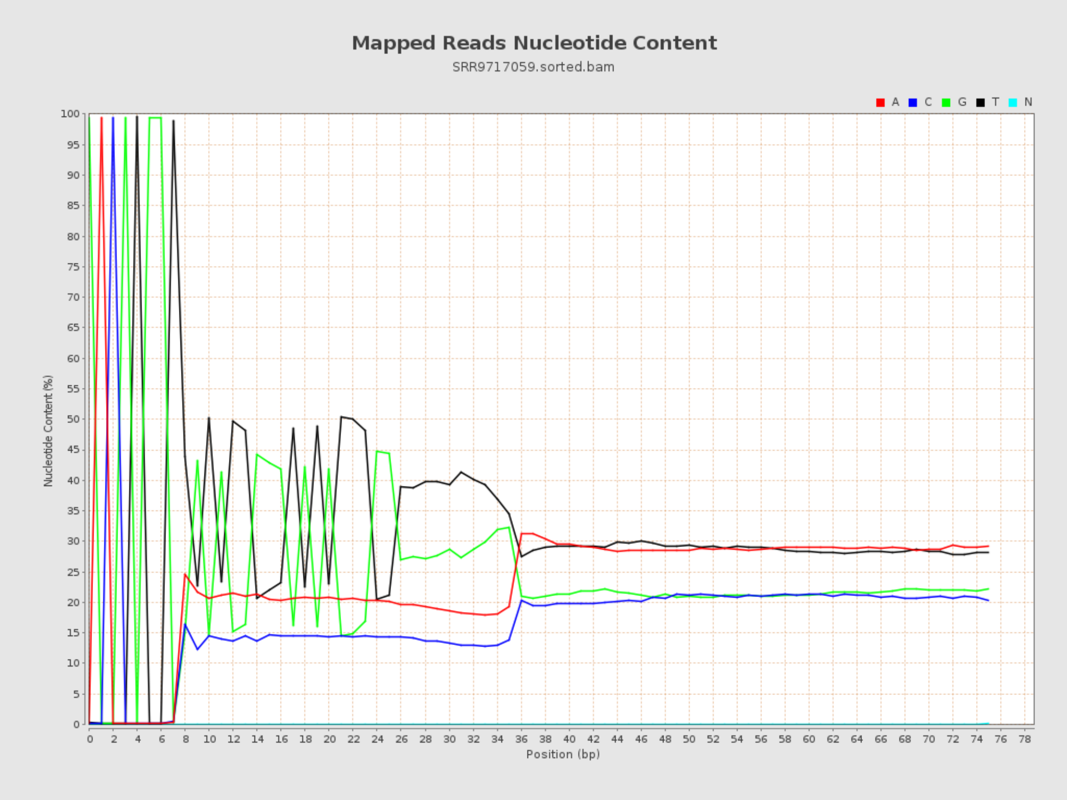
6. Results : Genome Fraction Coverage



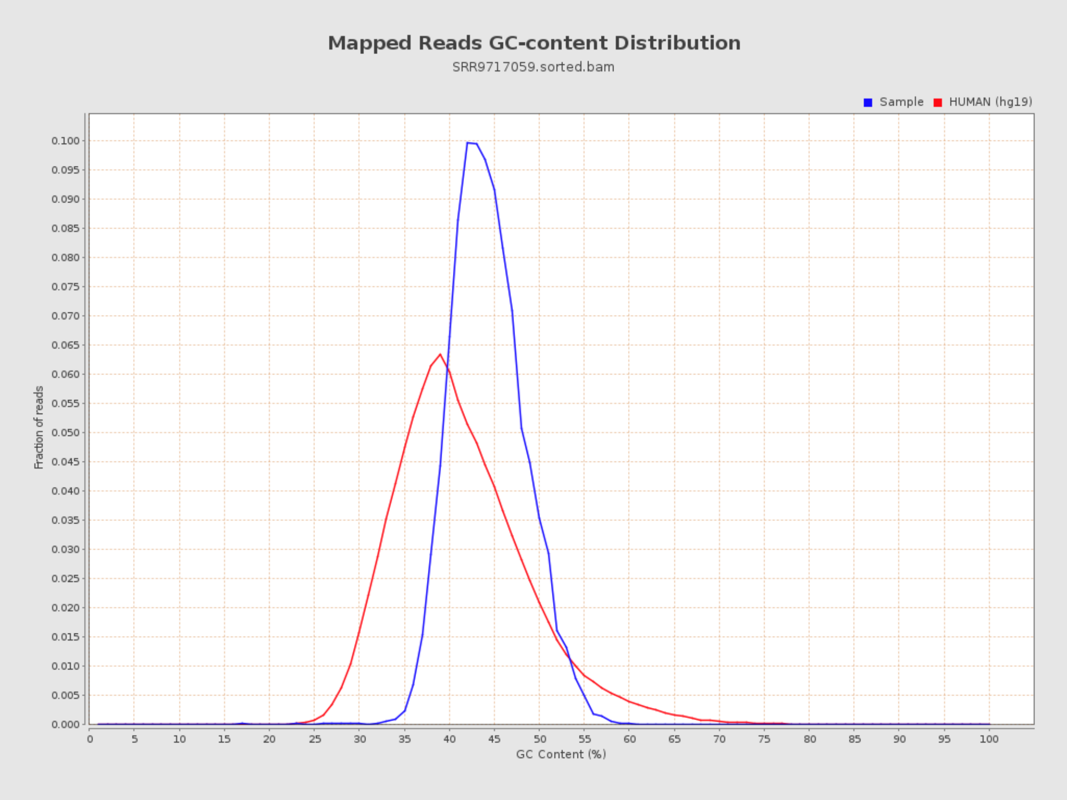
7. Results : Duplication Rate Histogram



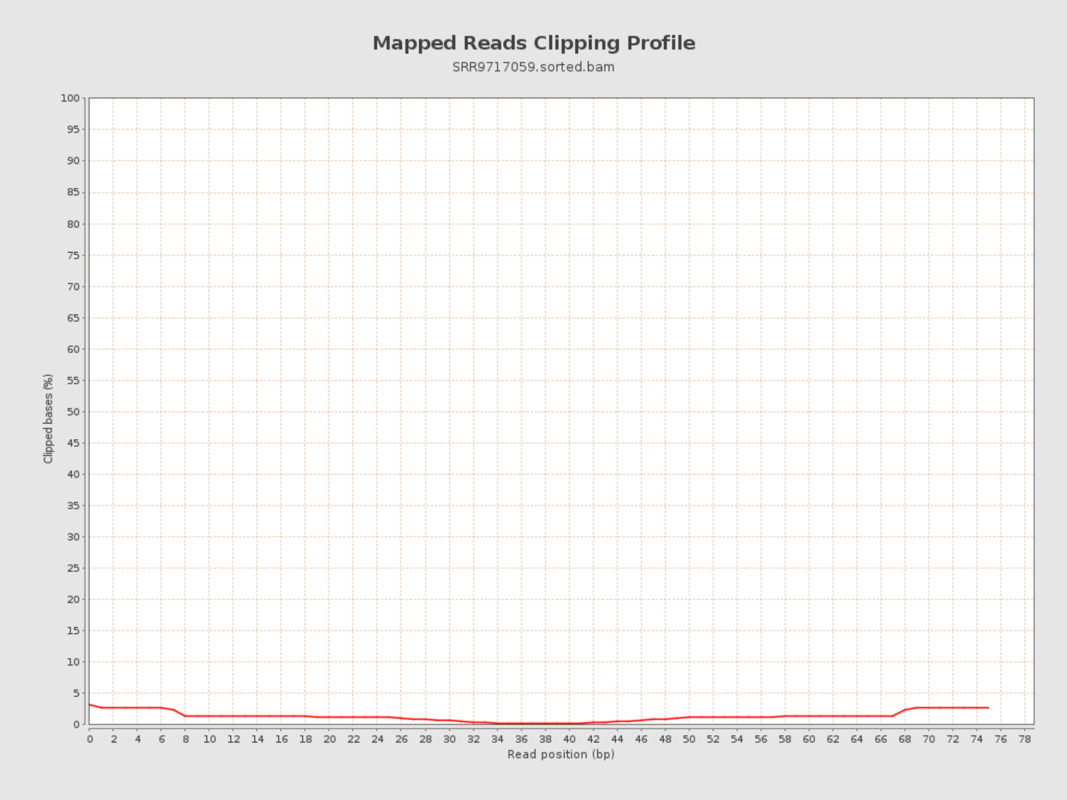
8. Results : Mapped Reads Nucleotide Content



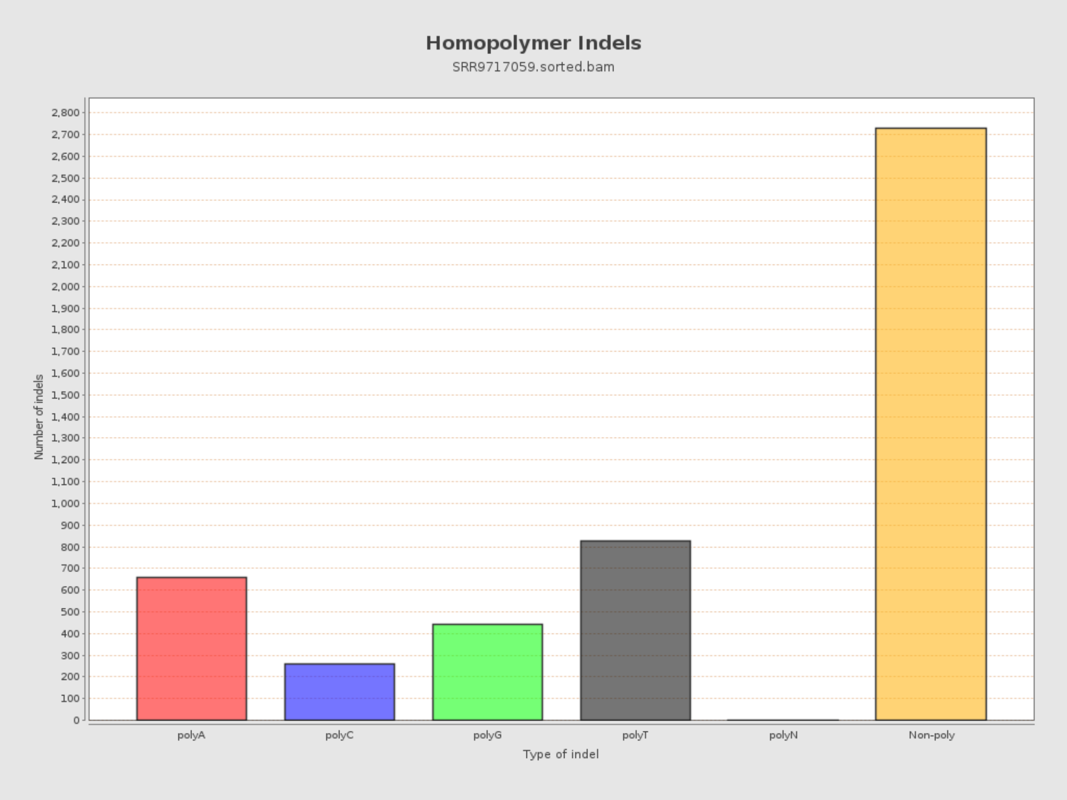
9. Results : Mapped Reads GC-content Distribution



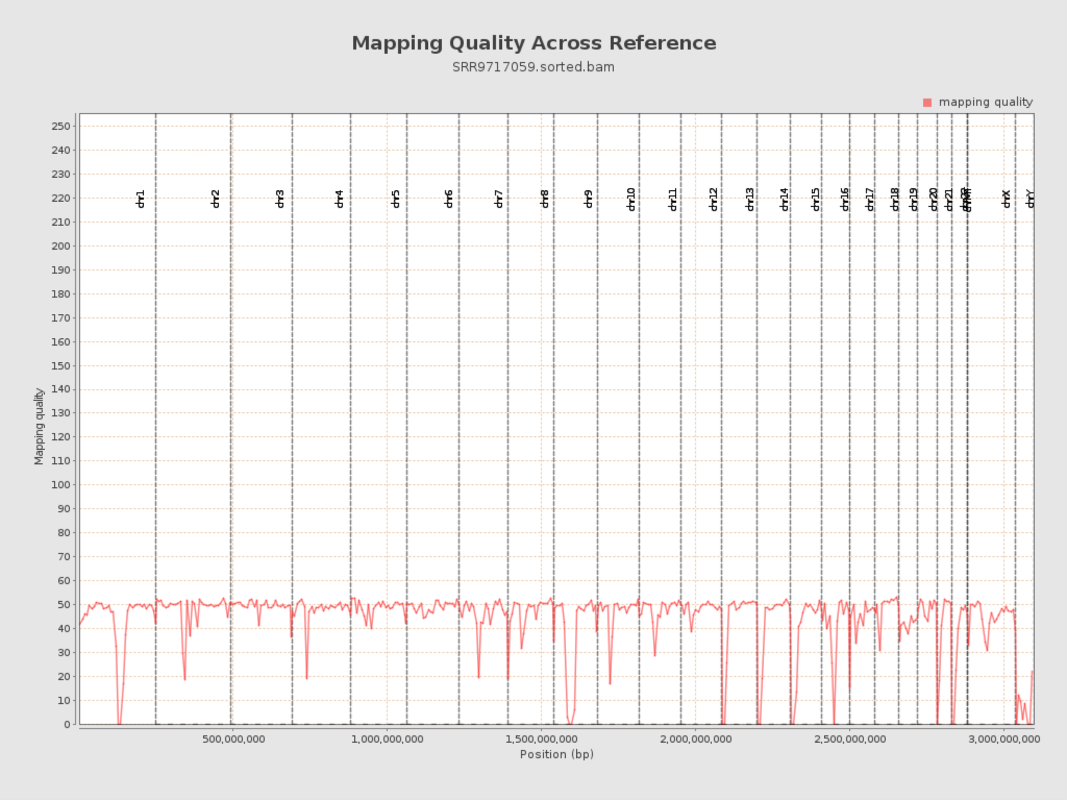
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram