Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:20:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819057.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_SRR1819057 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819057.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:20:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	990,235
Mapped reads	902,219 / 91.11%
Unmapped reads	88,016 / 8.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,795 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	17,047 / 1.72%
Duplication rate	1.45%
Clipped reads	904,140 / 91.31%

2.2. ACGT Content

Number/percentage of A's	12,566,510 / 24.48%
Number/percentage of C's	10,789,591 / 21.02%
Number/percentage of T's	15,252,721 / 29.71%
Number/percentage of G's	12,723,813 / 24.79%
Number/percentage of N's	1,062 / 0%
GC Percentage	45.81%

2.3. Coverage

Mean	0.0166

Standard Deviation	0.1558

2.4. Mapping Quality

Mean Mapping Quality	43.96

2.5. Mismatches and indels

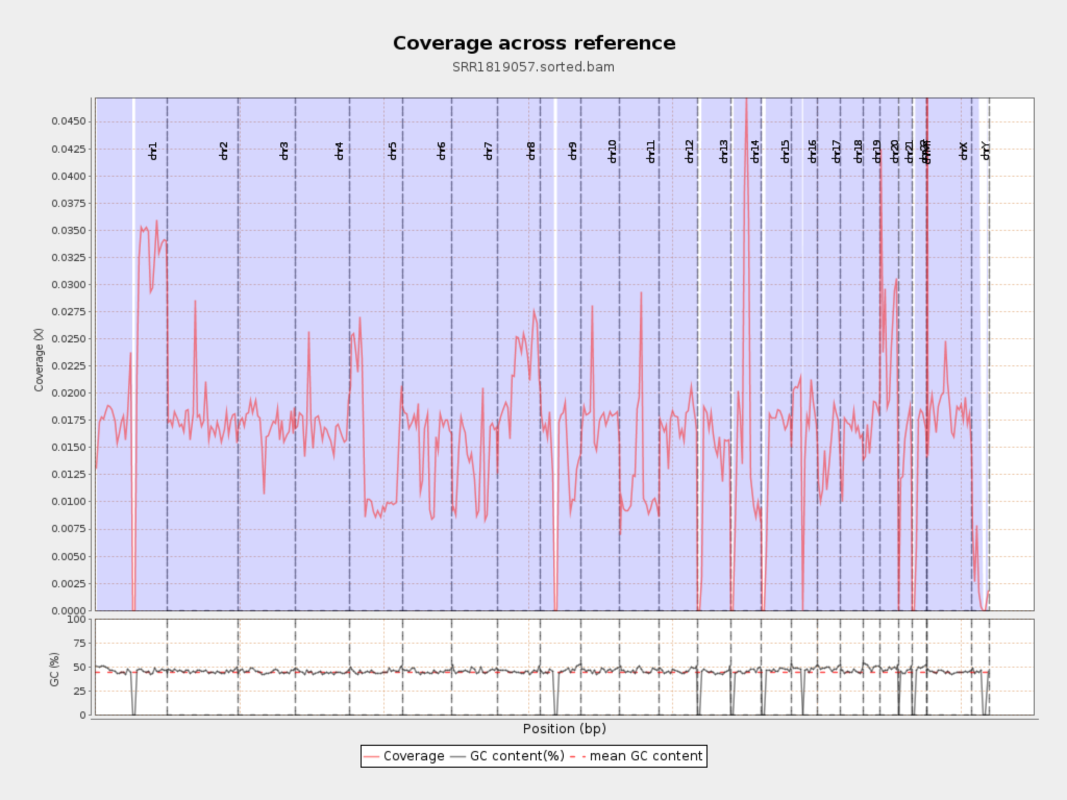
General error rate	0.51%
Mismatches	254,885
Insertions	3,344
Mapped reads with at least one insertion	0.37%
Deletions	8,047
Mapped reads with at least one deletion	0.89%
Homopolymer indels	40.9%

2.6. Chromosome stats

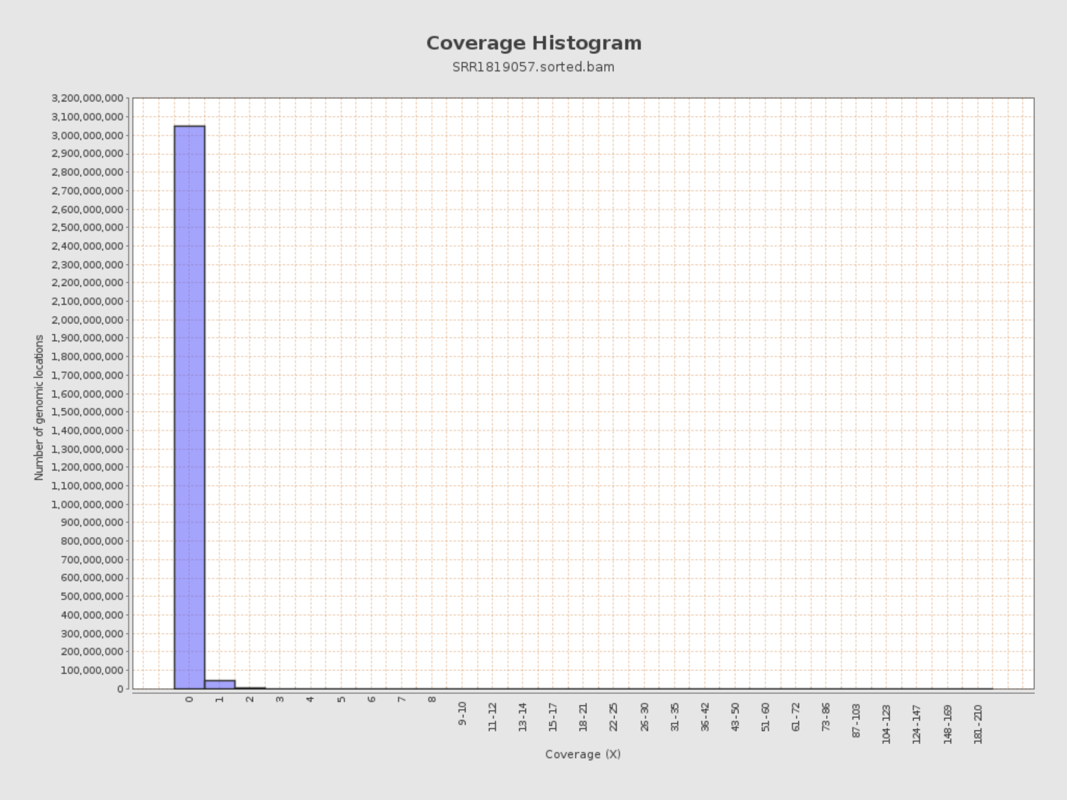
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5767209	0.0231	0.2215
chr2	243199373	4291365	0.0176	0.1747
chr3	198022430	3367454	0.017	0.1372
chr4	191154276	3240830	0.017	0.1429
chr5	180915260	2561605	0.0142	0.1261
chr6	171115067	2674414	0.0156	0.1366
chr7	159138663	2182878	0.0137	0.1377

chr8	146364022	3224182	0.022	0.1656
chr9	141213431	1897950	0.0134	0.1527
chr10	135534747	2452236	0.0181	0.169
chr11	135006516	1637023	0.0121	0.1367
chr12	133851895	2318124	0.0173	0.1395
chr13	115169878	1535389	0.0133	0.1205
chr14	107349540	1788310	0.0167	0.1448
chr15	102531392	1466839	0.0143	0.1258
chr16	90354753	1543356	0.0171	0.1441
chr17	81195210	1162392	0.0143	0.1279
chr18	78077248	1252075	0.016	0.2429
chr19	59128983	1002935	0.017	0.1681
chr20	63025520	1662495	0.0264	0.174
chr21	48129895	664291	0.0138	0.1308
chr22	51304566	622682	0.0121	0.1155
chrMT	16571	2364	0.1427	0.379
chrX	155270560	2879946	0.0185	0.1549
chrY	59373566	148890	0.0025	0.0652

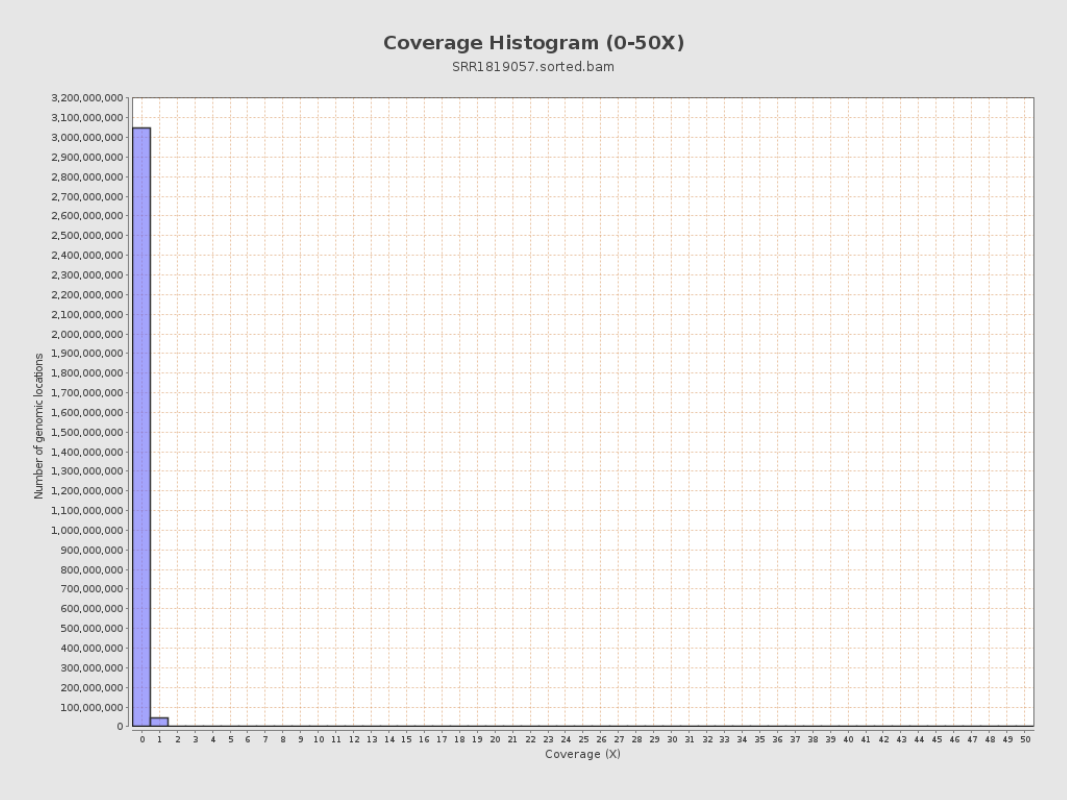
3. Results : Coverage across reference



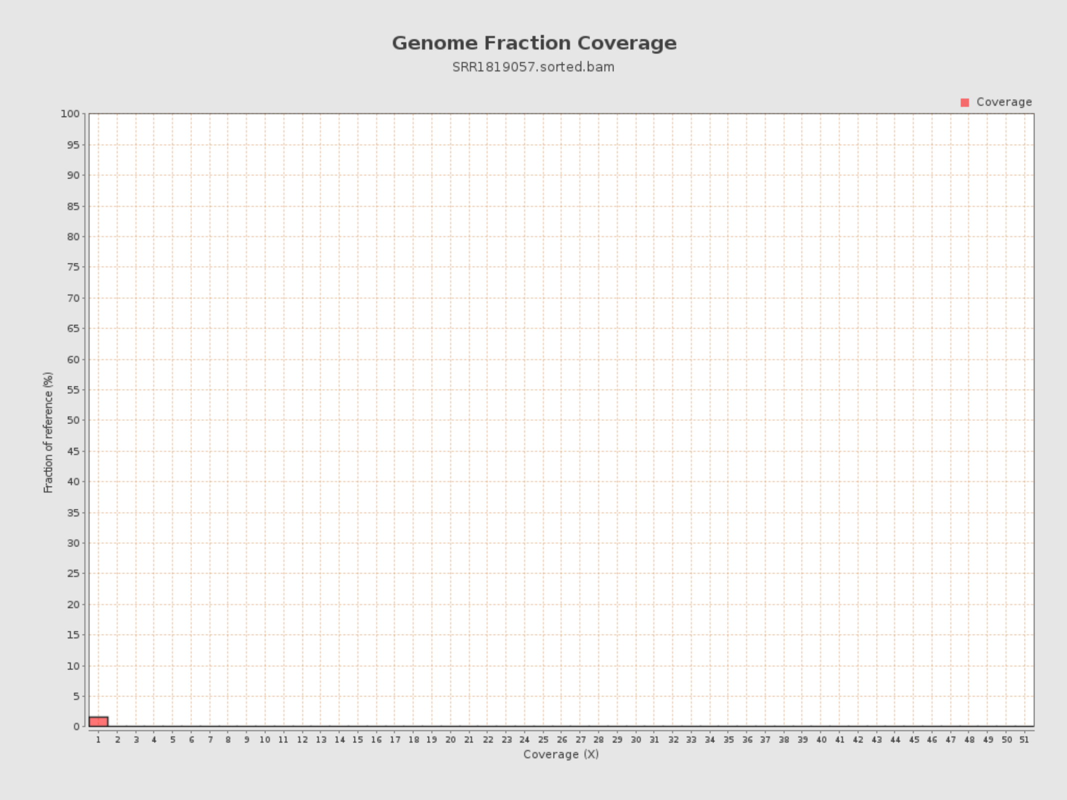
4. Results : Coverage Histogram



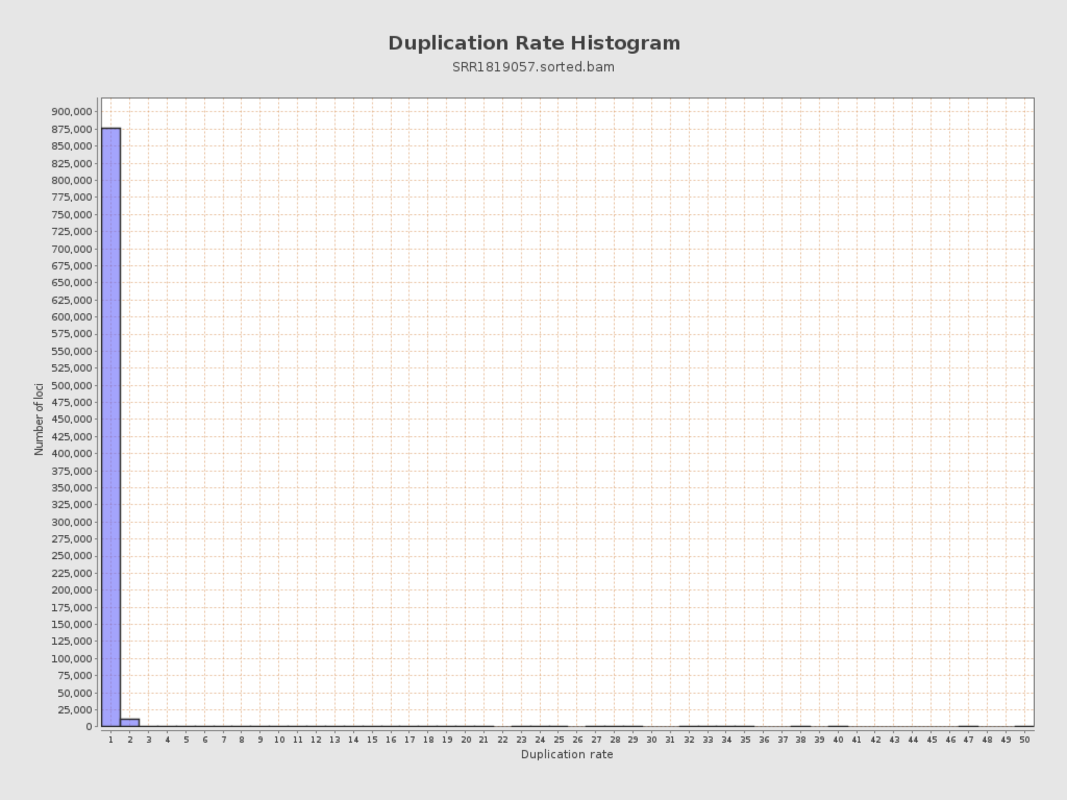
5. Results : Coverage Histogram (0-50X)



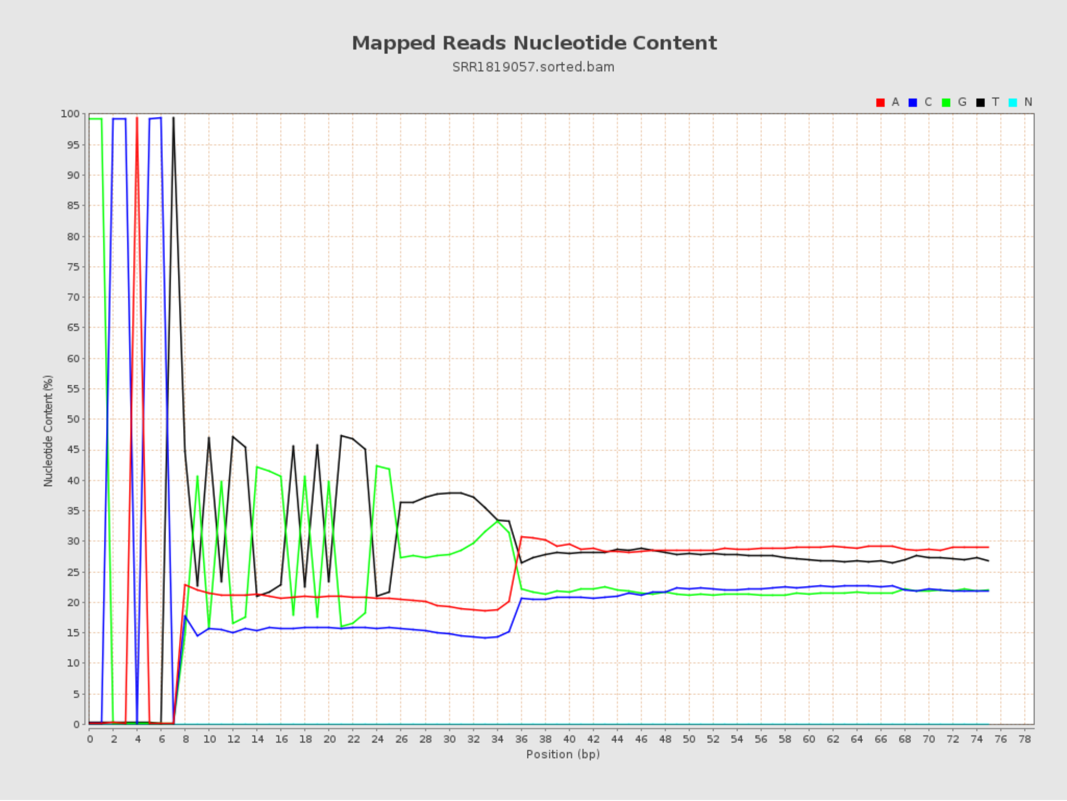
6. Results : Genome Fraction Coverage



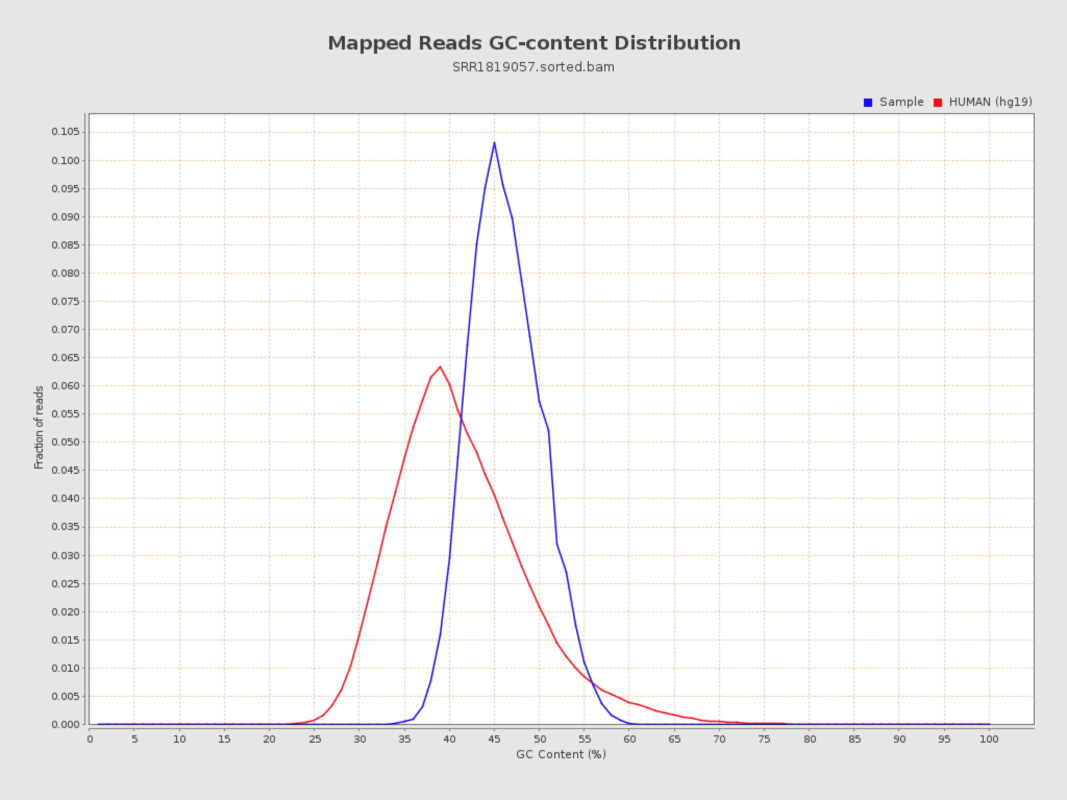
7. Results : Duplication Rate Histogram



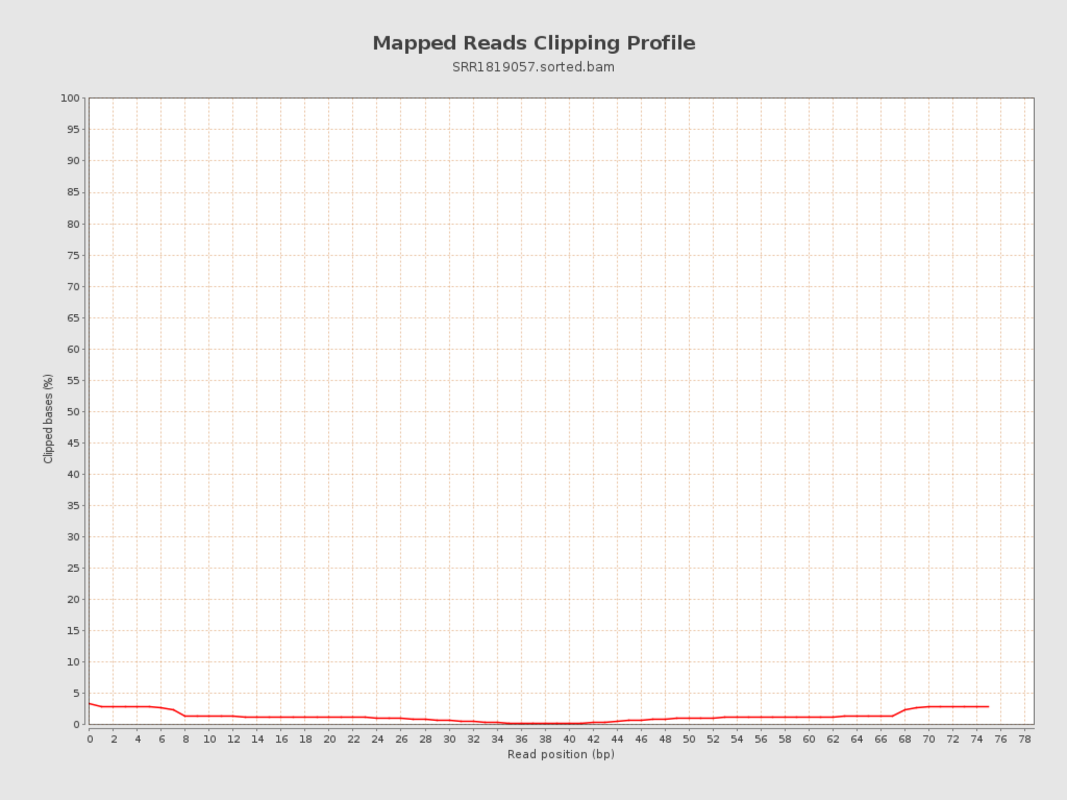
8. Results : Mapped Reads Nucleotide Content



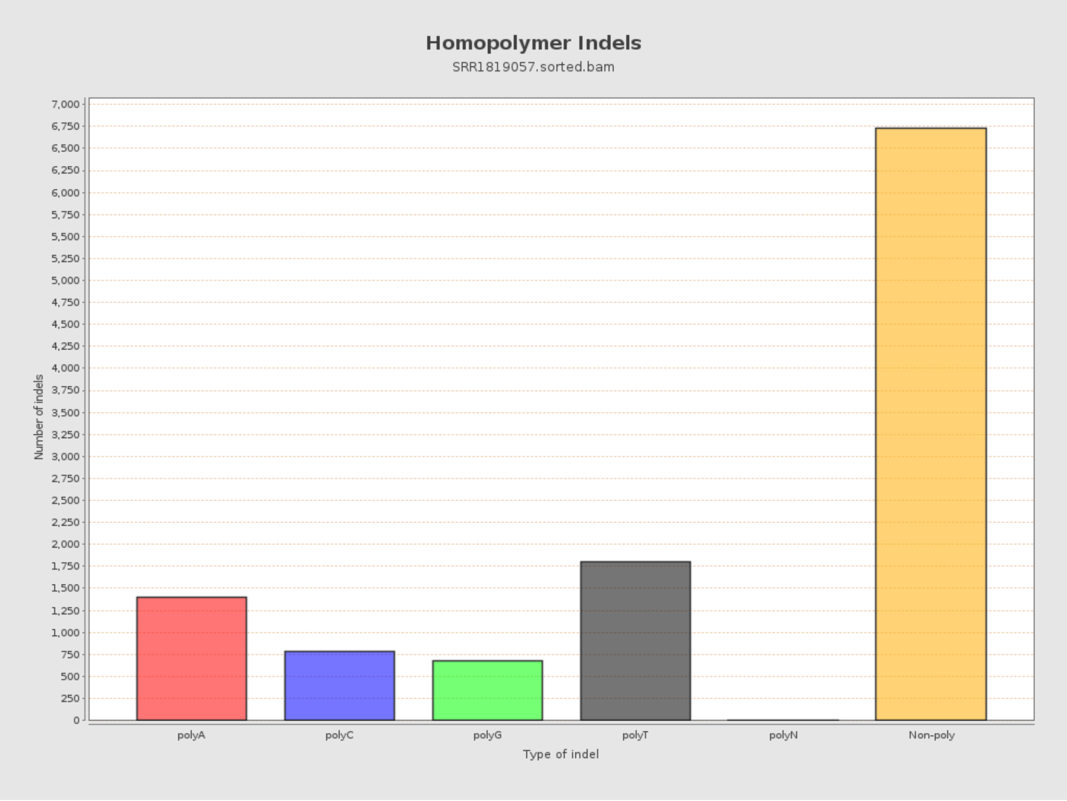
9. Results : Mapped Reads GC-content Distribution



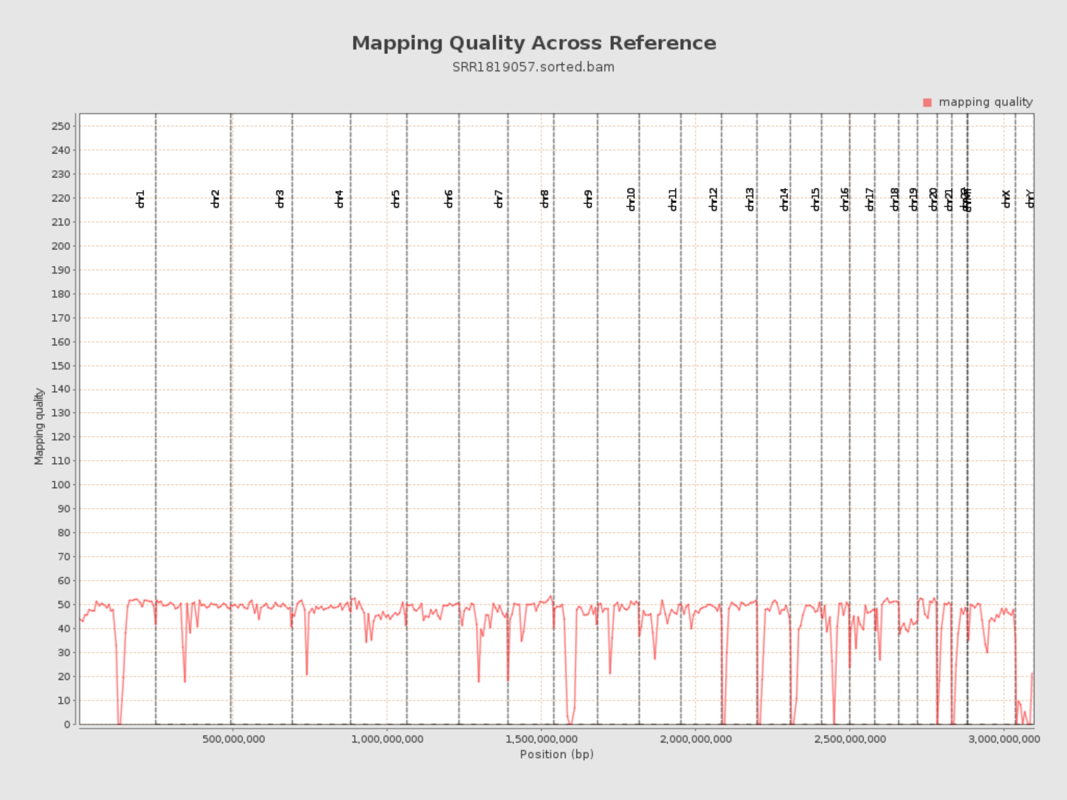
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram