Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 02:02:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085117.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_SRR3085117 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085117.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 02:02:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085117.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,095,554
Mapped reads	842,737 / 76.92%
Unmapped reads	252,817 / 23.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,366 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	12,011 / 1.1%
Duplication rate	1.17%
Clipped reads	280,665 / 25.62%

2.2. ACGT Content

Number/percentage of A's	18,237,861 / 31.27%
Number/percentage of C's	10,516,015 / 18.03%
Number/percentage of T's	16,919,175 / 29.01%
Number/percentage of G's	12,651,776 / 21.69%
Number/percentage of N's	1,482 / 0%
GC Percentage	39.72%

2.3. Coverage

Mean	0.0188

Standard Deviation	0.1665

2.4. Mapping Quality

Mean Mapping Quality	48.77

2.5. Mismatches and indels

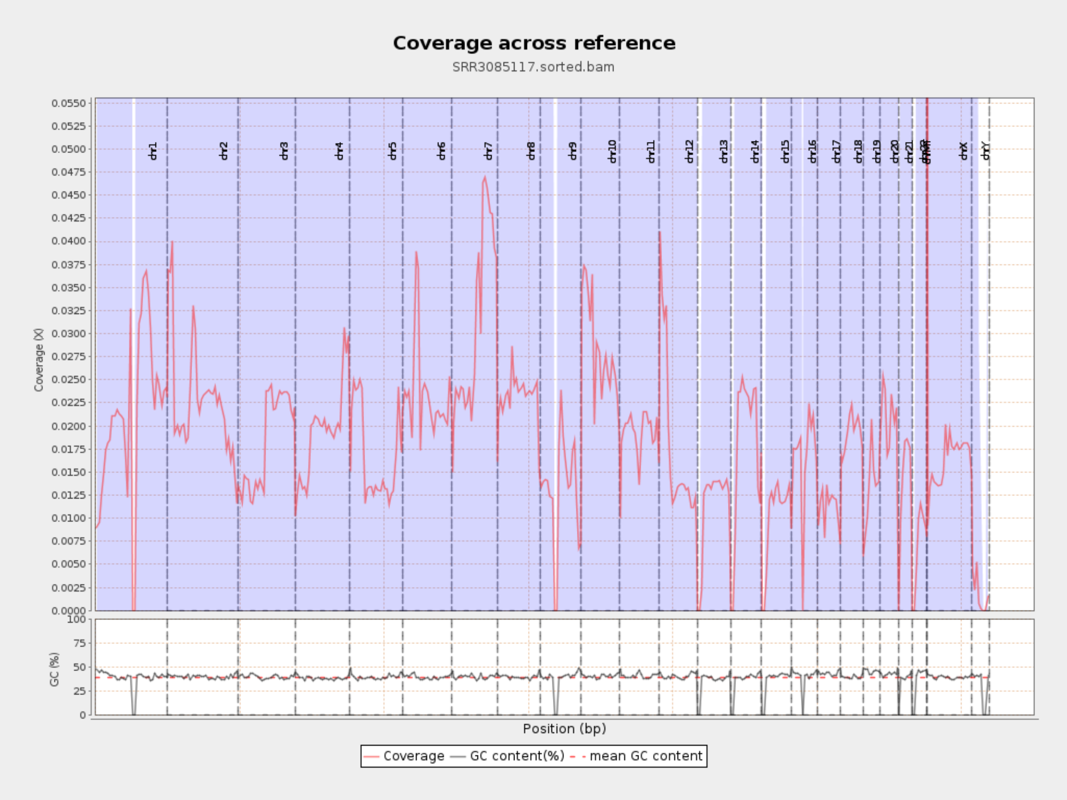
General error rate	0.88%
Mismatches	507,868
Insertions	3,703
Mapped reads with at least one insertion	0.44%
Deletions	9,793
Mapped reads with at least one deletion	1.15%
Homopolymer indels	46%

2.6. Chromosome stats

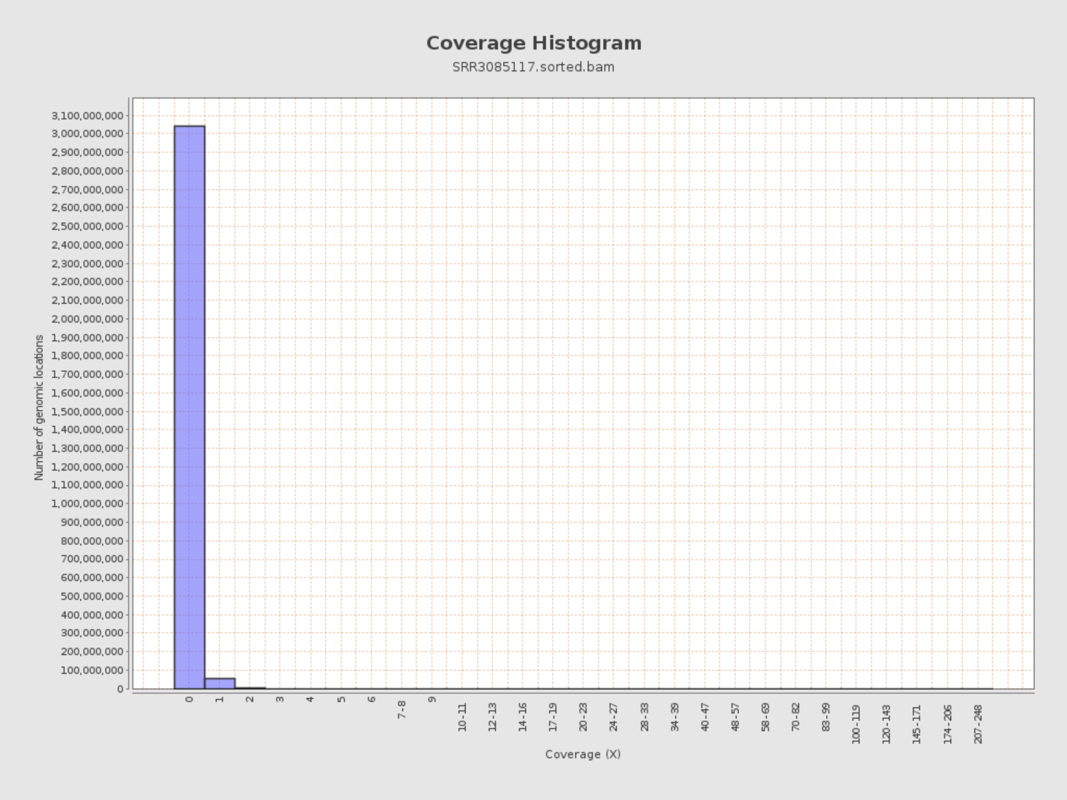
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5295819	0.0212	0.2517
chr2	243199373	5560426	0.0229	0.1776
chr3	198022430	3618260	0.0183	0.1388
chr4	191154276	3720454	0.0195	0.1429
chr5	180915260	3033880	0.0168	0.1322
chr6	171115067	4037424	0.0236	0.181
chr7	159138663	4997019	0.0314	0.1992

chr8	146364022	3421087	0.0234	0.2119
chr9	141213431	1866312	0.0132	0.1314
chr10	135534747	3861254	0.0285	0.2132
chr11	135006516	2588345	0.0192	0.1665
chr12	133851895	2422778	0.0181	0.1382
chr13	115169878	1296018	0.0113	0.1077
chr14	107349540	1913851	0.0178	0.1372
chr15	102531392	1034732	0.0101	0.1019
chr16	90354753	1469363	0.0163	0.1358
chr17	81195210	907222	0.0112	0.1135
chr18	78077248	1516614	0.0194	0.2162
chr19	59128983	799849	0.0135	0.1665
chr20	63025520	1302755	0.0207	0.1477
chr21	48129895	676026	0.014	0.1242
chr22	51304566	367132	0.0072	0.0859
chrMT	16571	7402	0.4467	0.675
chrX	155270560	2528928	0.0163	0.1364
chrY	59373566	99344	0.0017	0.0485

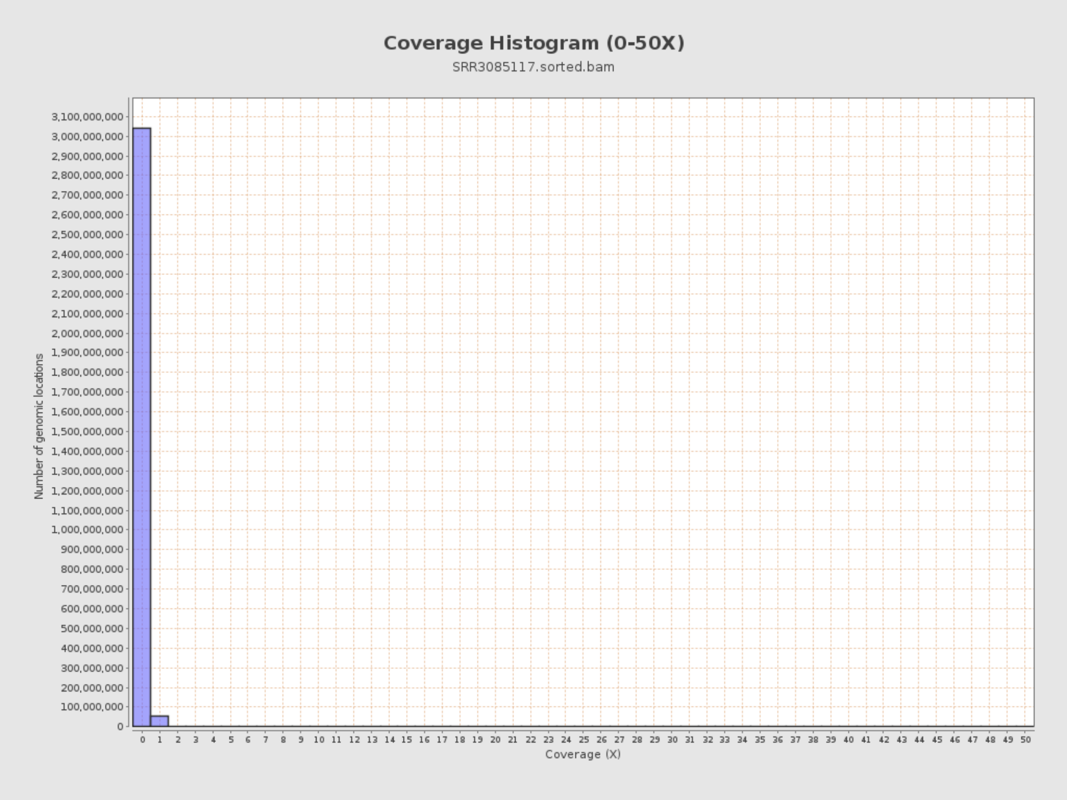
3. Results : Coverage across reference



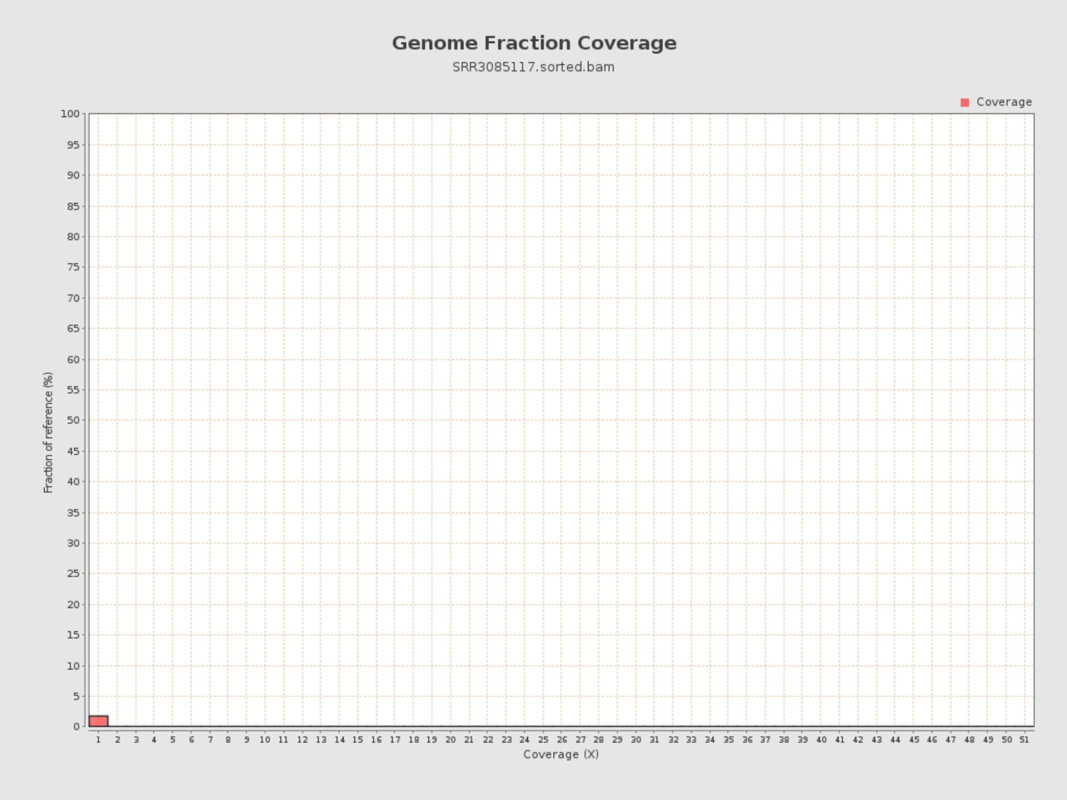
4. Results : Coverage Histogram



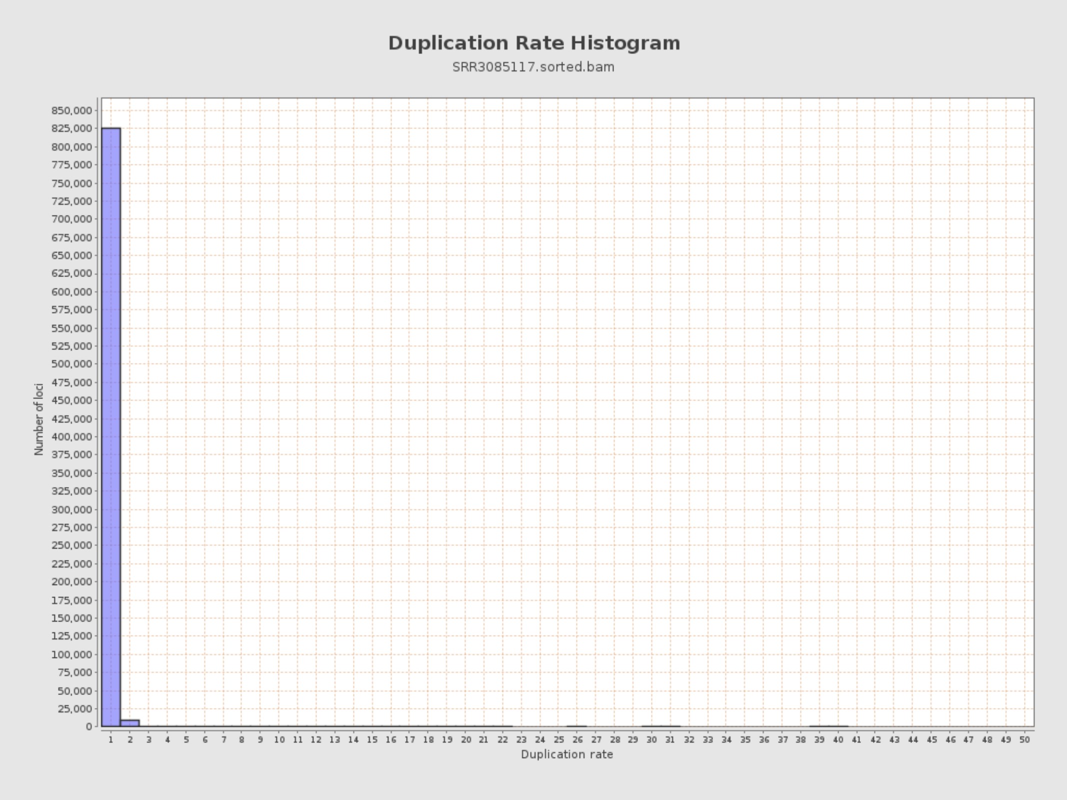
5. Results : Coverage Histogram (0-50X)



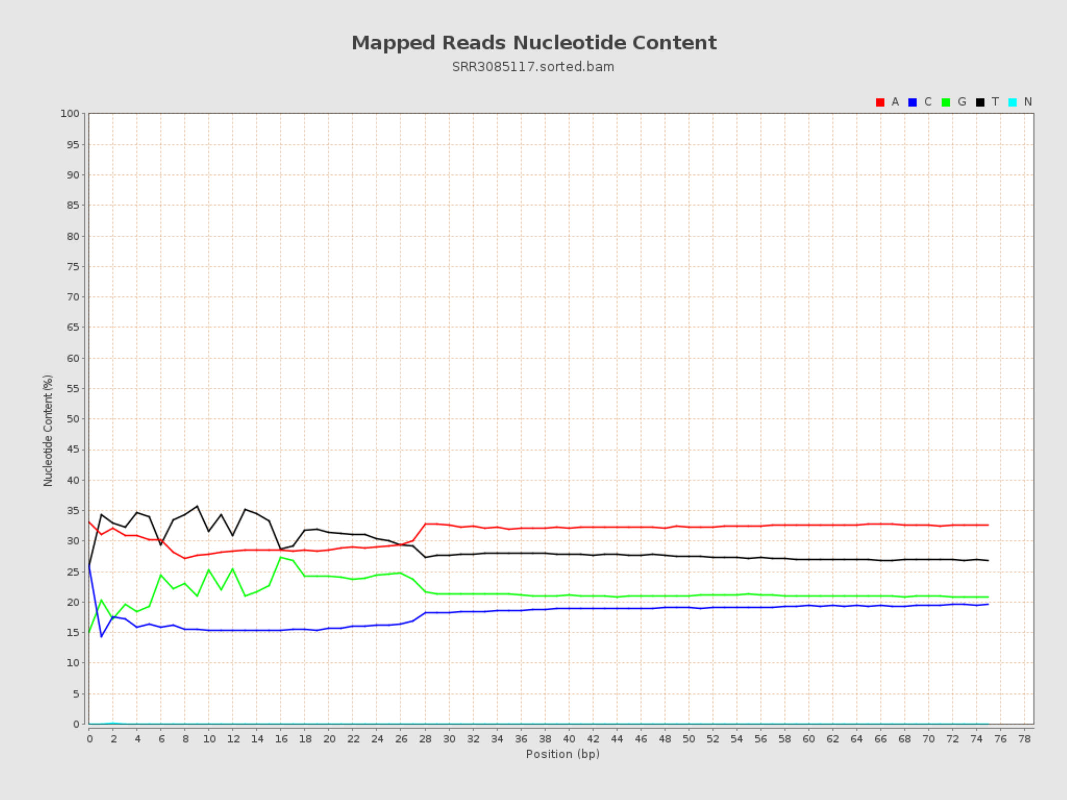
6. Results : Genome Fraction Coverage



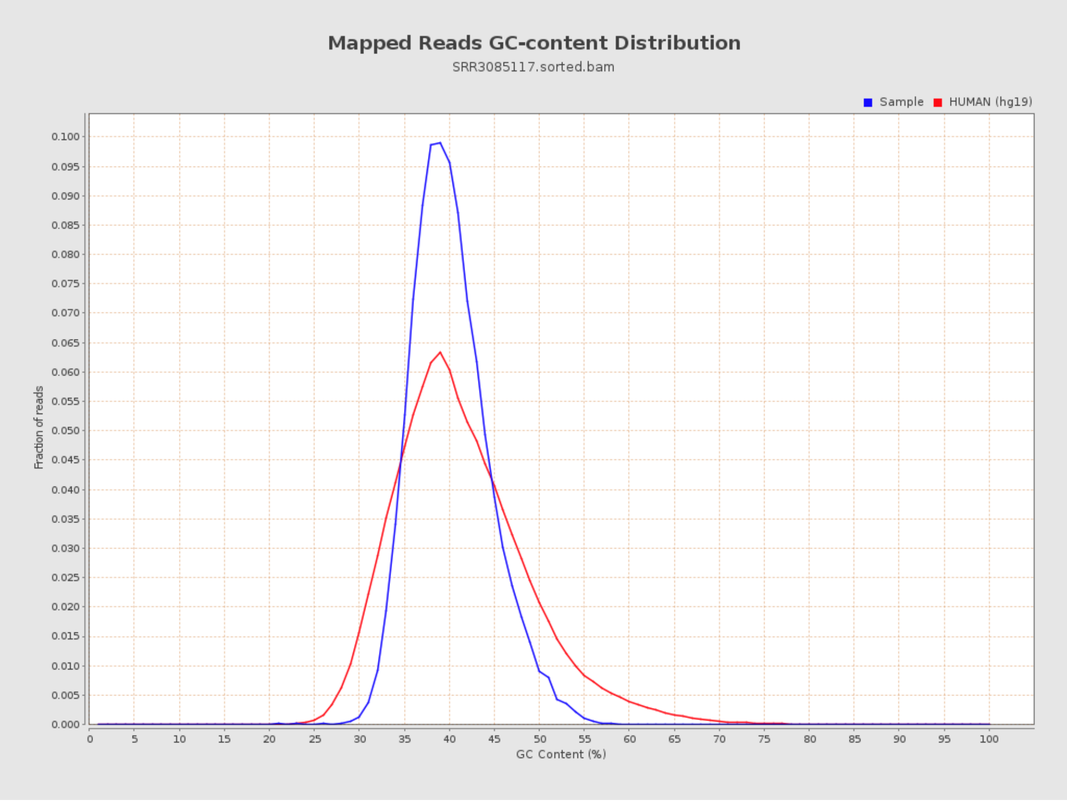
7. Results : Duplication Rate Histogram



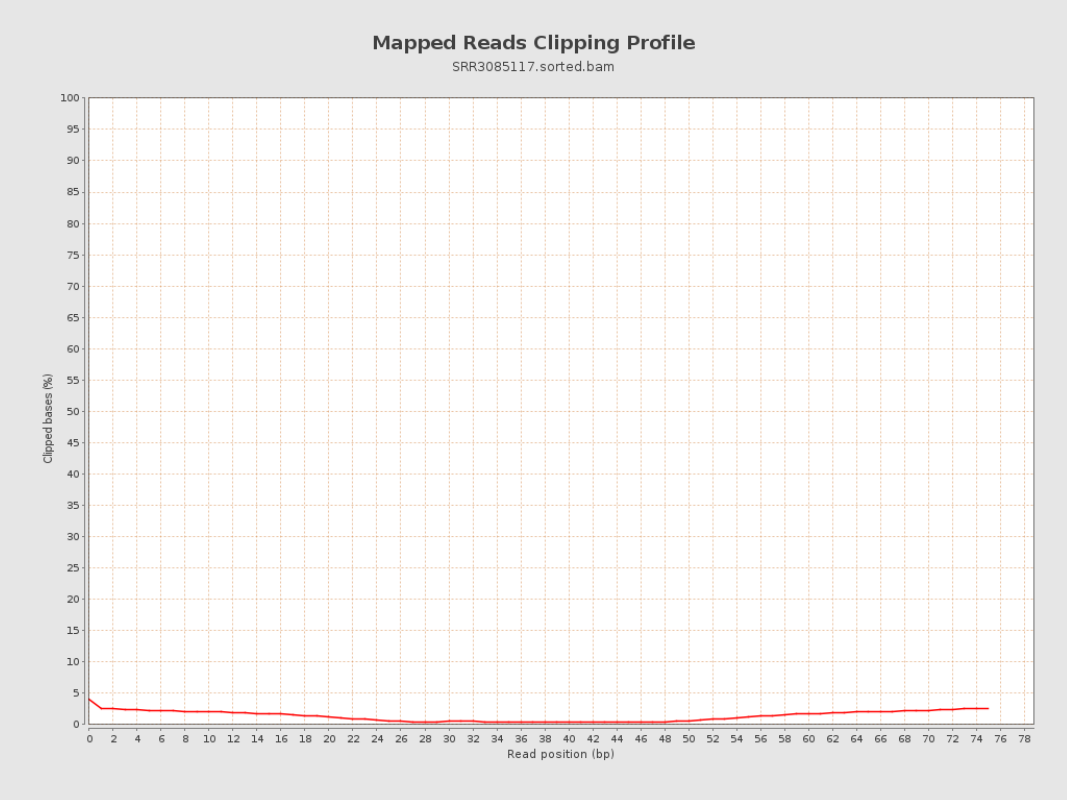
8. Results : Mapped Reads Nucleotide Content



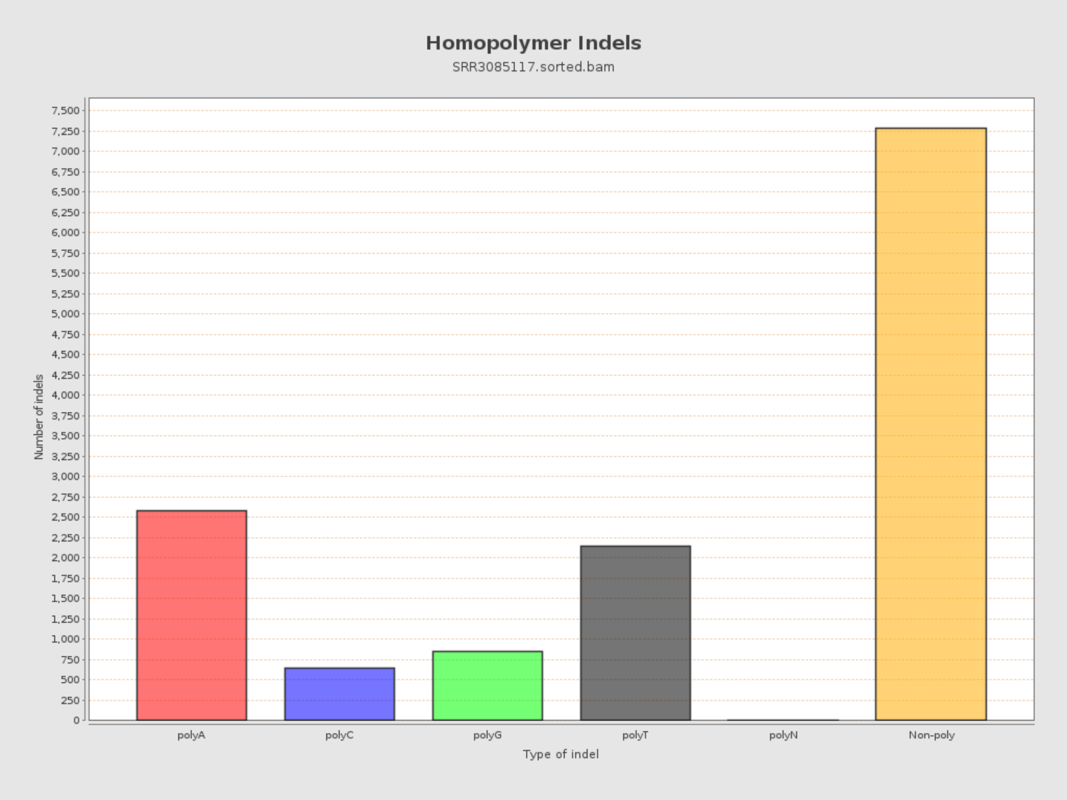
9. Results : Mapped Reads GC-content Distribution



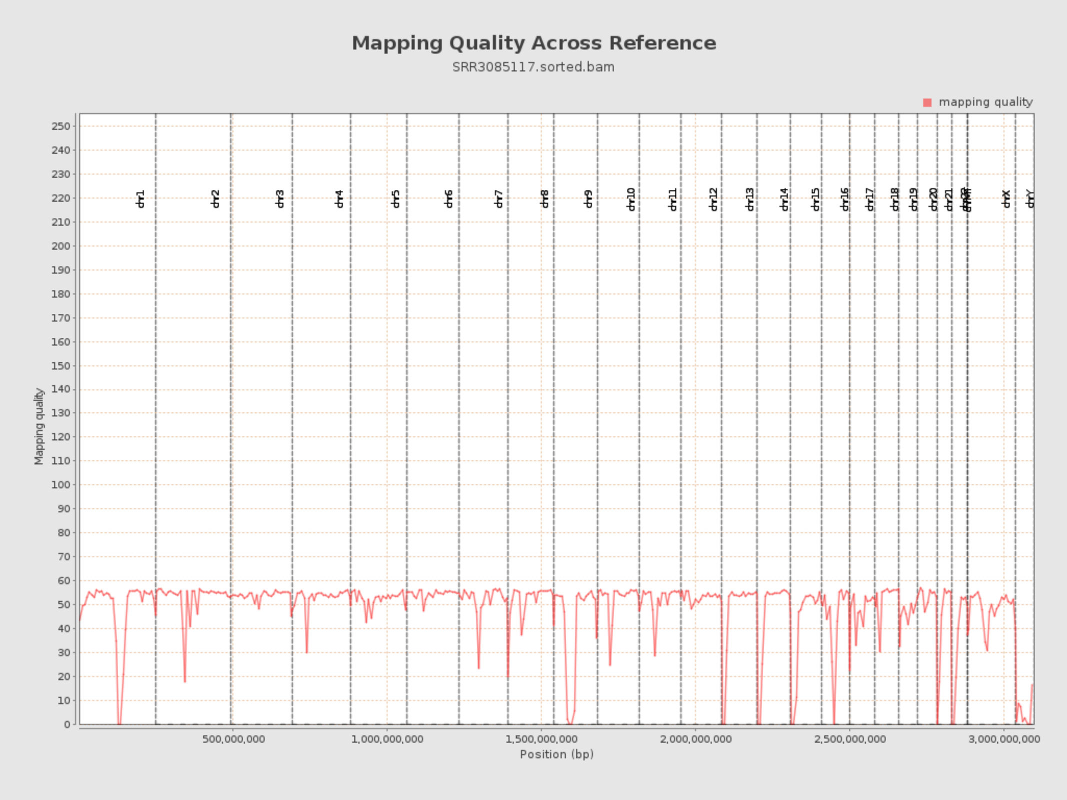
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram