Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 21:57:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085017.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_SRR3085017 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085017.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 21:57:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085017.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,262,130
Mapped reads	2,034,969 / 89.96%
Unmapped reads	227,161 / 10.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,693 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	68,200 / 3.01%
Duplication rate	2.74%
Clipped reads	938,412 / 41.48%

2.2. ACGT Content

Number/percentage of A's	38,237,749 / 28.22%
Number/percentage of C's	25,723,643 / 18.98%
Number/percentage of T's	41,973,829 / 30.97%
Number/percentage of G's	29,559,210 / 21.81%
Number/percentage of N's	14,976 / 0.01%
GC Percentage	40.8%

2.3. Coverage

Mean	0.0438

Standard Deviation	0.3239

2.4. Mapping Quality

Mean Mapping Quality	45.65

2.5. Mismatches and indels

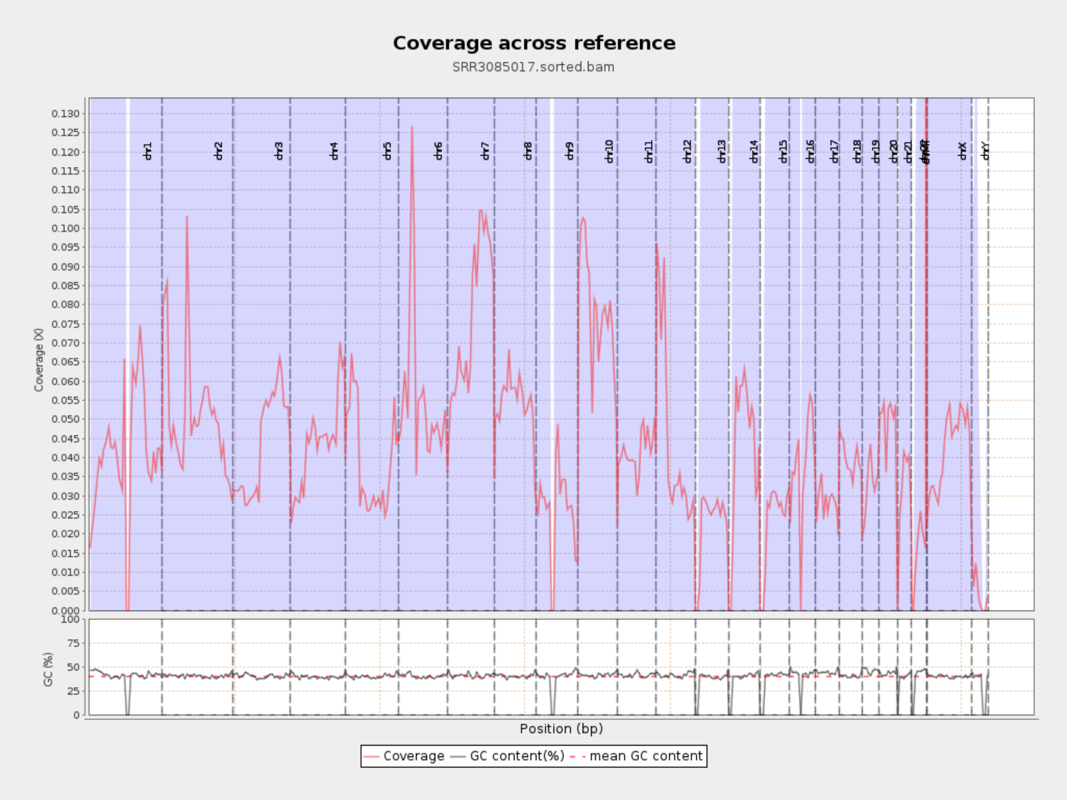
General error rate	0.87%
Mismatches	1,165,984
Insertions	9,391
Mapped reads with at least one insertion	0.46%
Deletions	27,092
Mapped reads with at least one deletion	1.32%
Homopolymer indels	46.84%

2.6. Chromosome stats

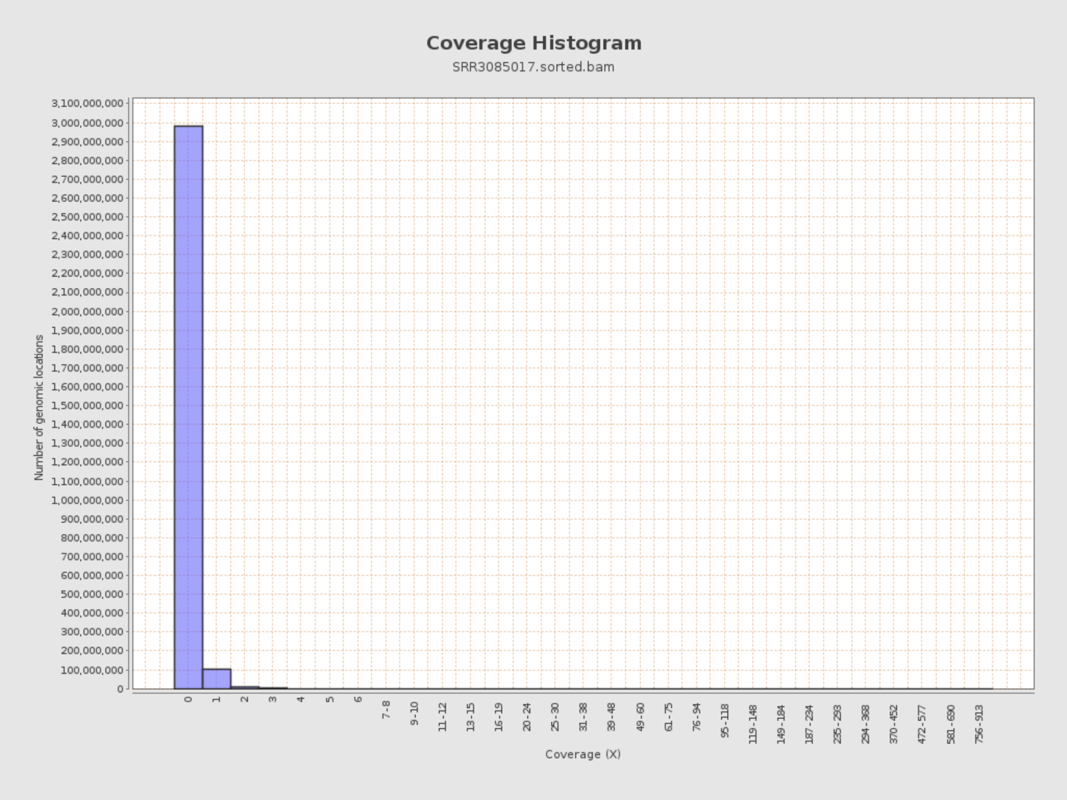
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10291785	0.0413	0.4473
chr2	243199373	12700304	0.0522	0.38
chr3	198022430	8620600	0.0435	0.2385
chr4	191154276	8411821	0.044	0.2389
chr5	180915260	7037777	0.0389	0.222
chr6	171115067	9647388	0.0564	0.3252
chr7	159138663	12316163	0.0774	0.3934

chr8	146364022	8019616	0.0548	0.6011
chr9	141213431	3744908	0.0265	0.254
chr10	135534747	10786995	0.0796	0.4456
chr11	135006516	5575209	0.0413	0.3016
chr12	133851895	5974692	0.0446	0.2412
chr13	115169878	2568660	0.0223	0.1668
chr14	107349540	4570109	0.0426	0.2365
chr15	102531392	2355407	0.023	0.1775
chr16	90354753	3465977	0.0384	0.2294
chr17	81195210	2268437	0.0279	0.2126
chr18	78077248	3116751	0.0399	0.3982
chr19	59128983	1960999	0.0332	0.3205
chr20	63025520	3108204	0.0493	0.253
chr21	48129895	1497581	0.0311	0.2039
chr22	51304566	744206	0.0145	0.1323
chrMT	16571	17003	1.0261	1.3736
chrX	155270560	6496936	0.0418	0.248
chrY	59373566	258035	0.0043	0.0855

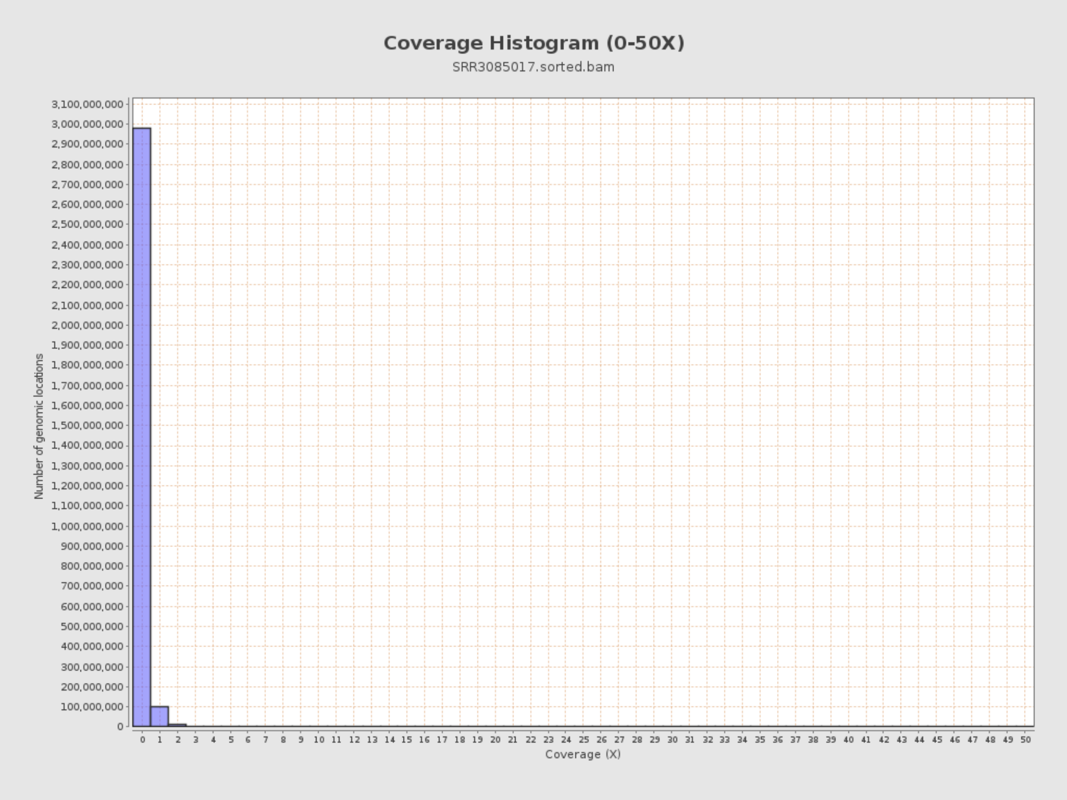
3. Results : Coverage across reference



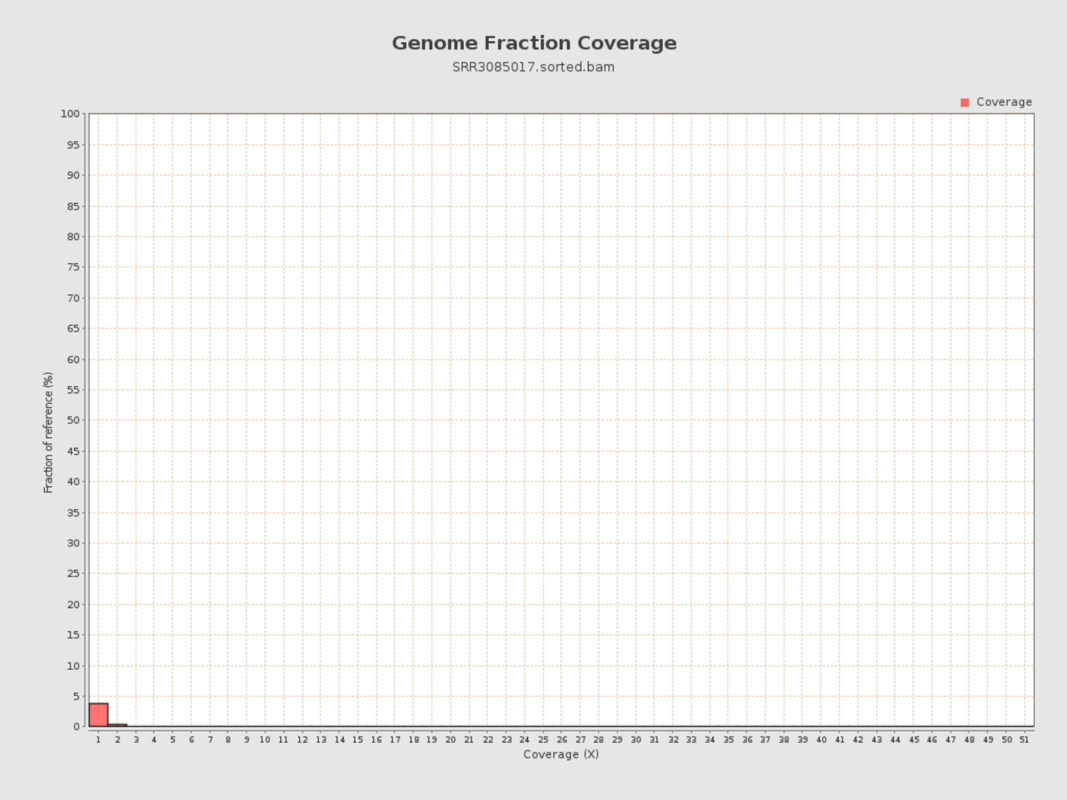
4. Results : Coverage Histogram



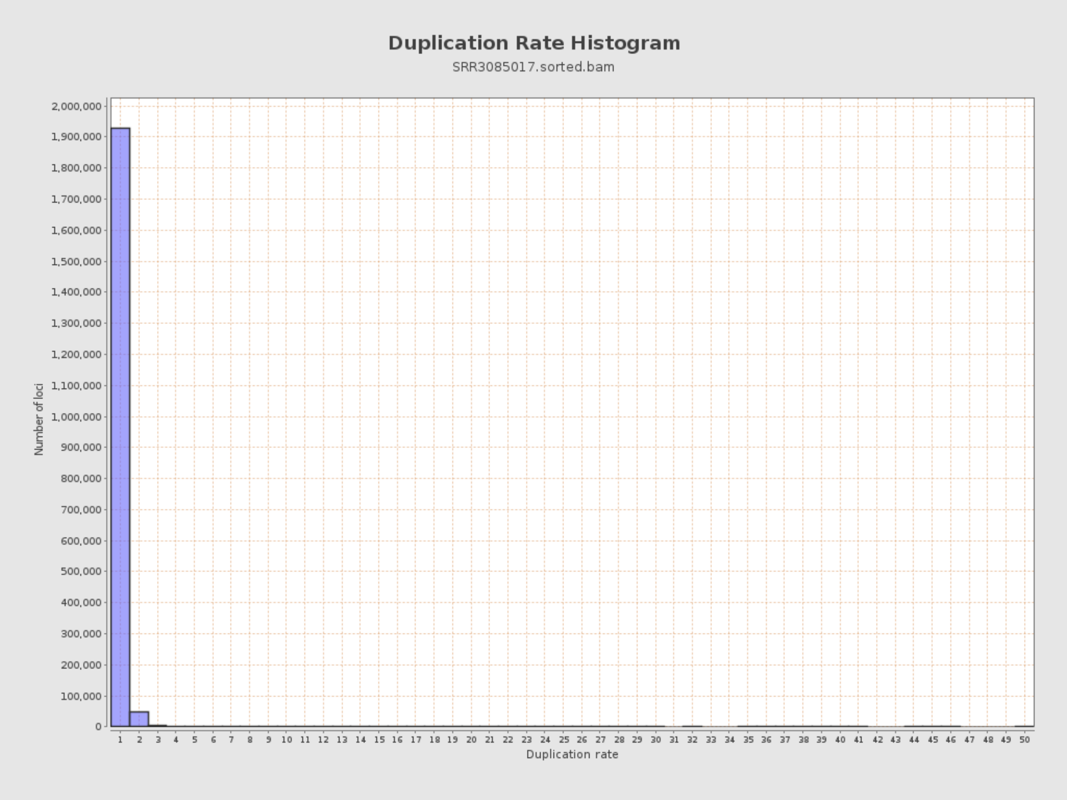
5. Results : Coverage Histogram (0-50X)



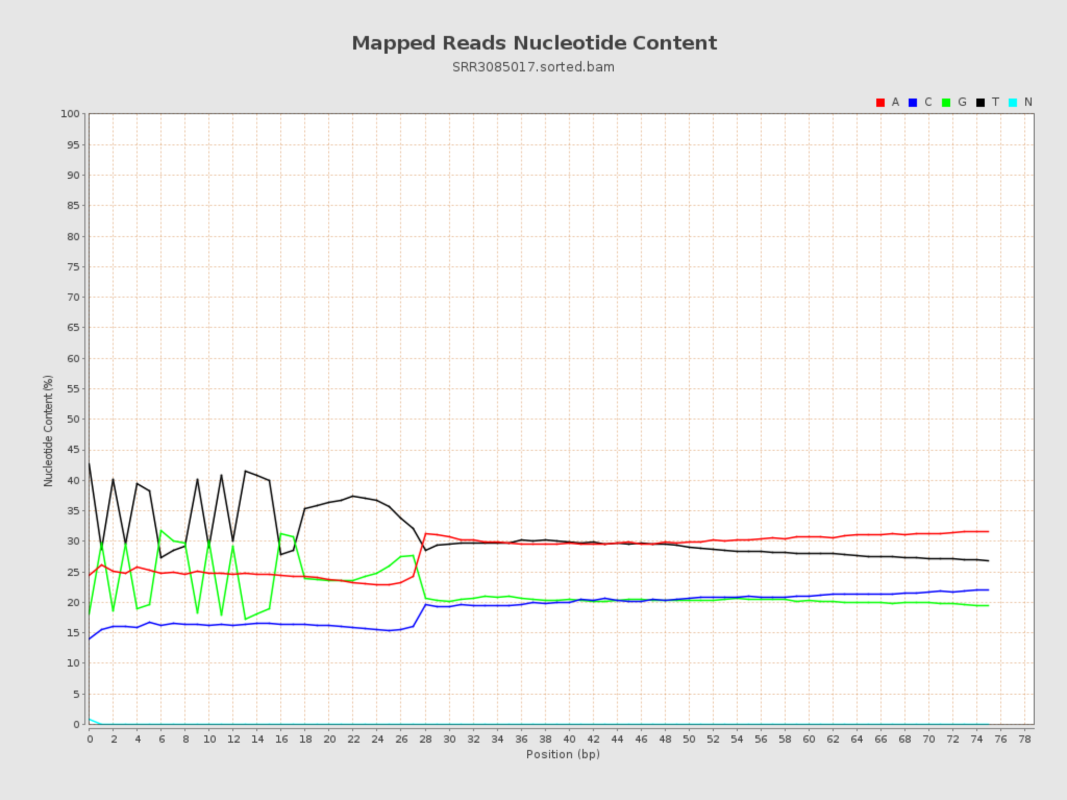
6. Results : Genome Fraction Coverage



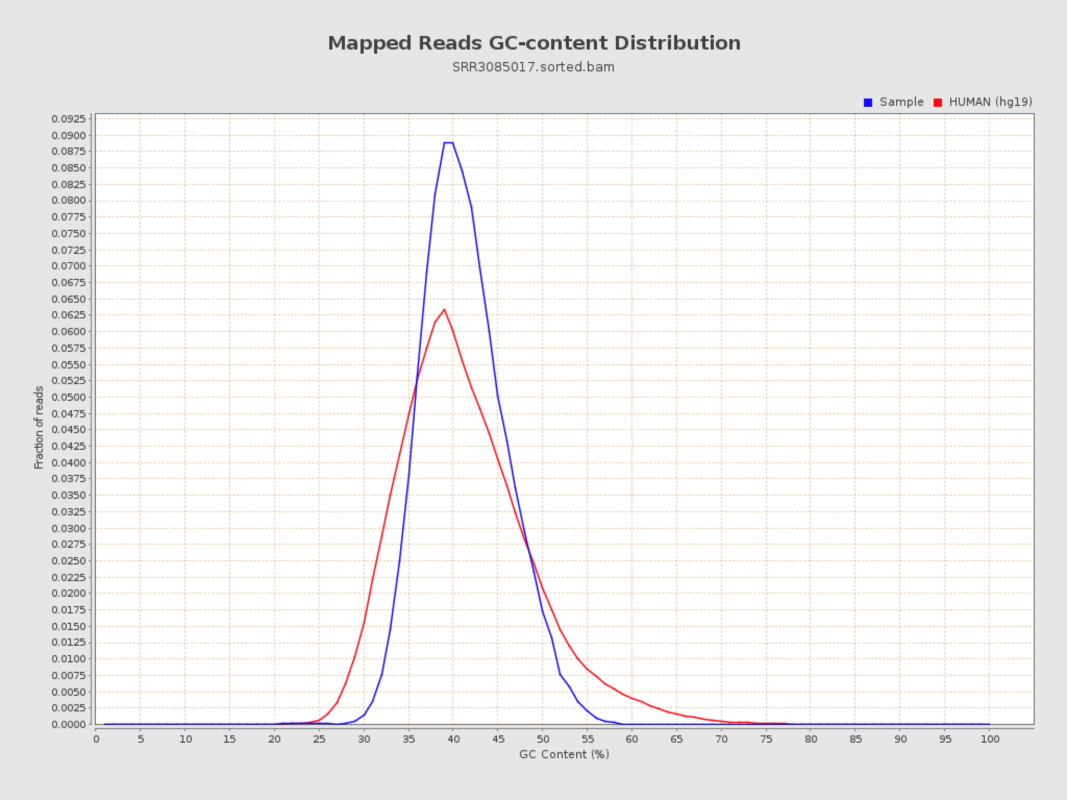
7. Results : Duplication Rate Histogram



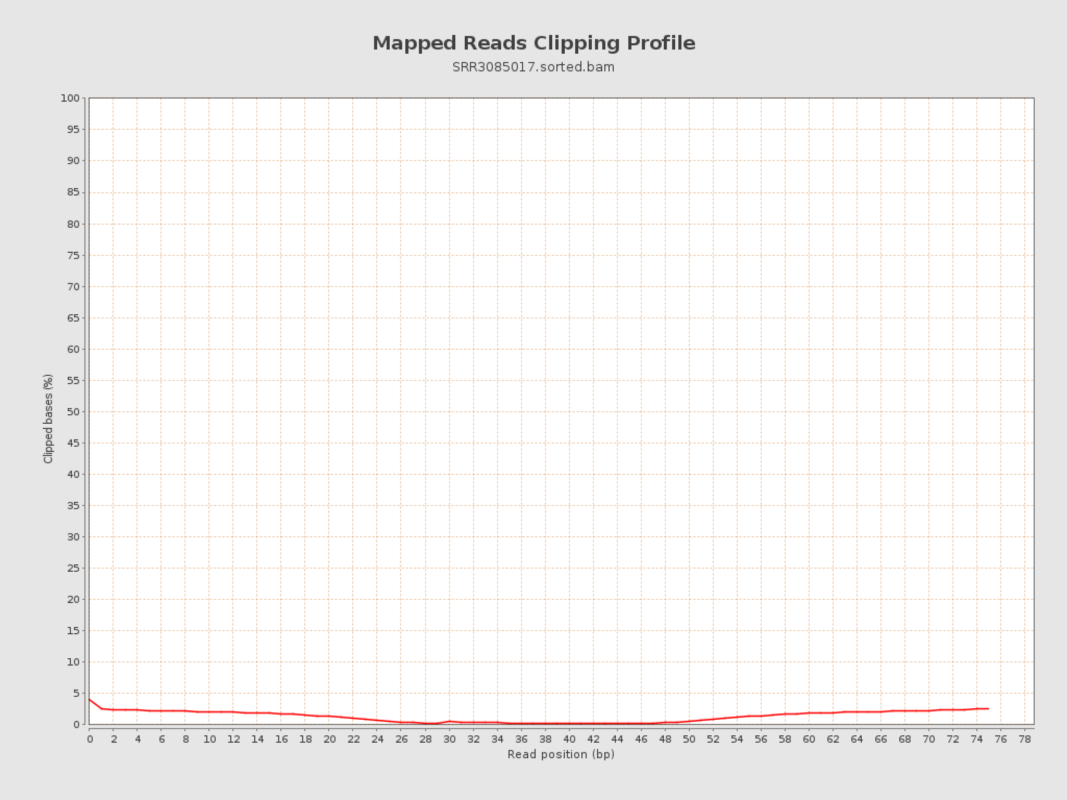
8. Results : Mapped Reads Nucleotide Content



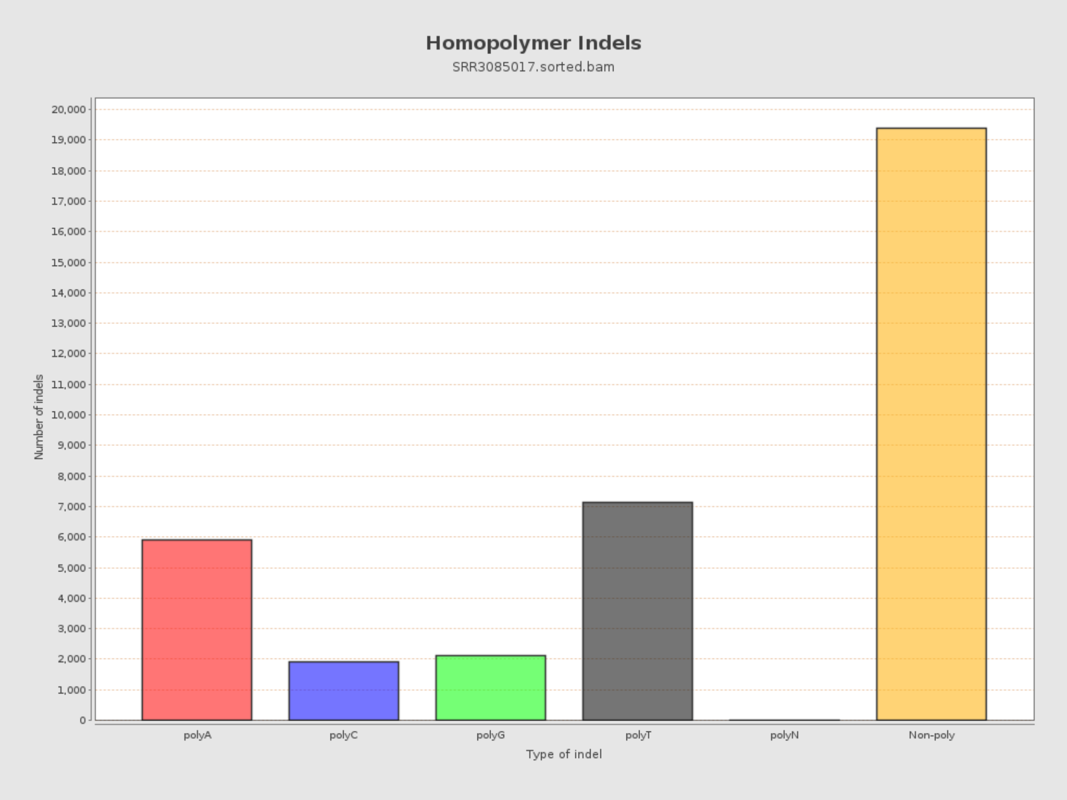
9. Results : Mapped Reads GC-content Distribution



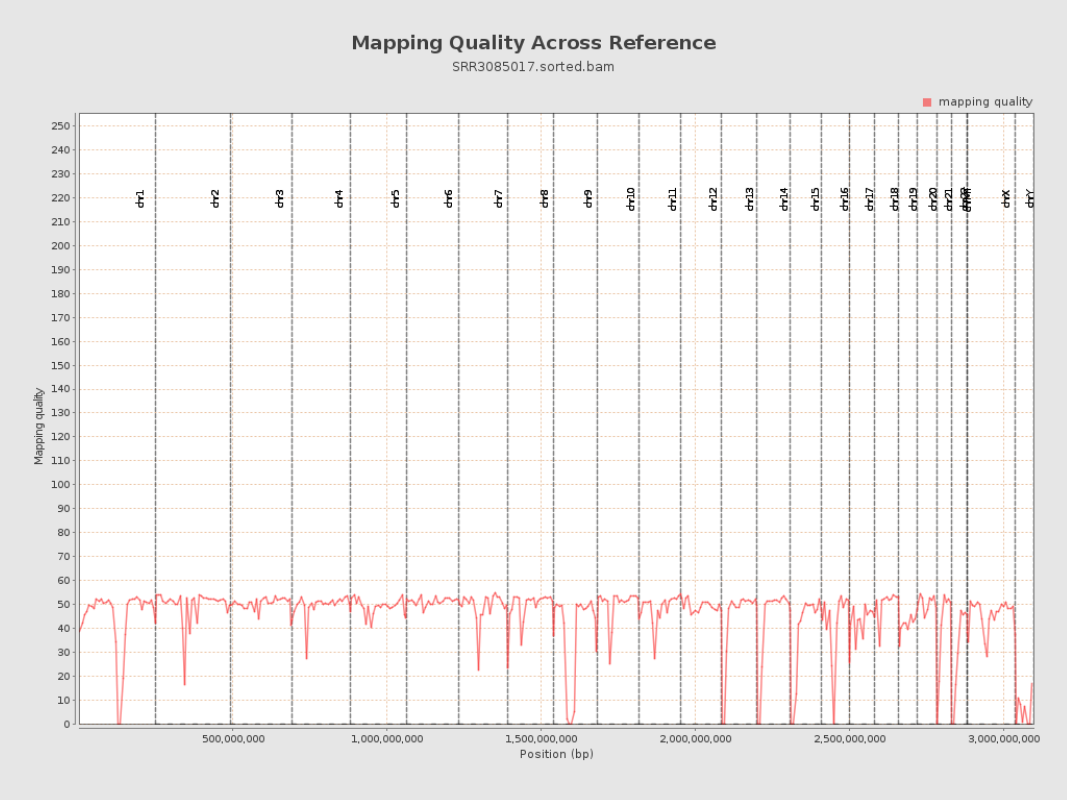
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram