Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 02:37:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085129.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_SRR3085129 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085129.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 02:37:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085129.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,885,669
Mapped reads	1,670,388 / 88.58%
Unmapped reads	215,281 / 11.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,863 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	57,378 / 3.04%
Duplication rate	2.64%
Clipped reads	772,898 / 40.99%

2.2. ACGT Content

Number/percentage of A's	30,770,563 / 27.71%
Number/percentage of C's	20,705,009 / 18.64%
Number/percentage of T's	34,640,425 / 31.19%
Number/percentage of G's	24,909,427 / 22.43%
Number/percentage of N's	24,882 / 0.02%
GC Percentage	41.08%

2.3. Coverage

Mean	0.0359

Standard Deviation	0.3176

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

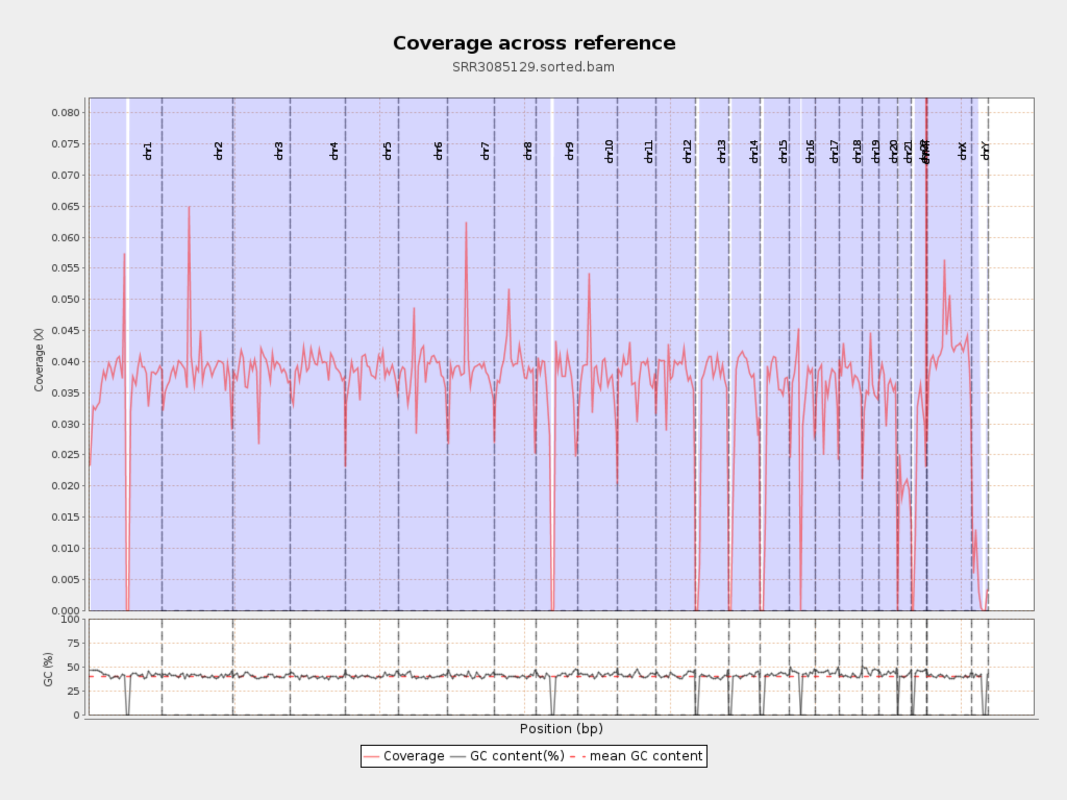
General error rate	0.89%
Mismatches	968,463
Insertions	8,725
Mapped reads with at least one insertion	0.52%
Deletions	24,251
Mapped reads with at least one deletion	1.44%
Homopolymer indels	46.88%

2.6. Chromosome stats

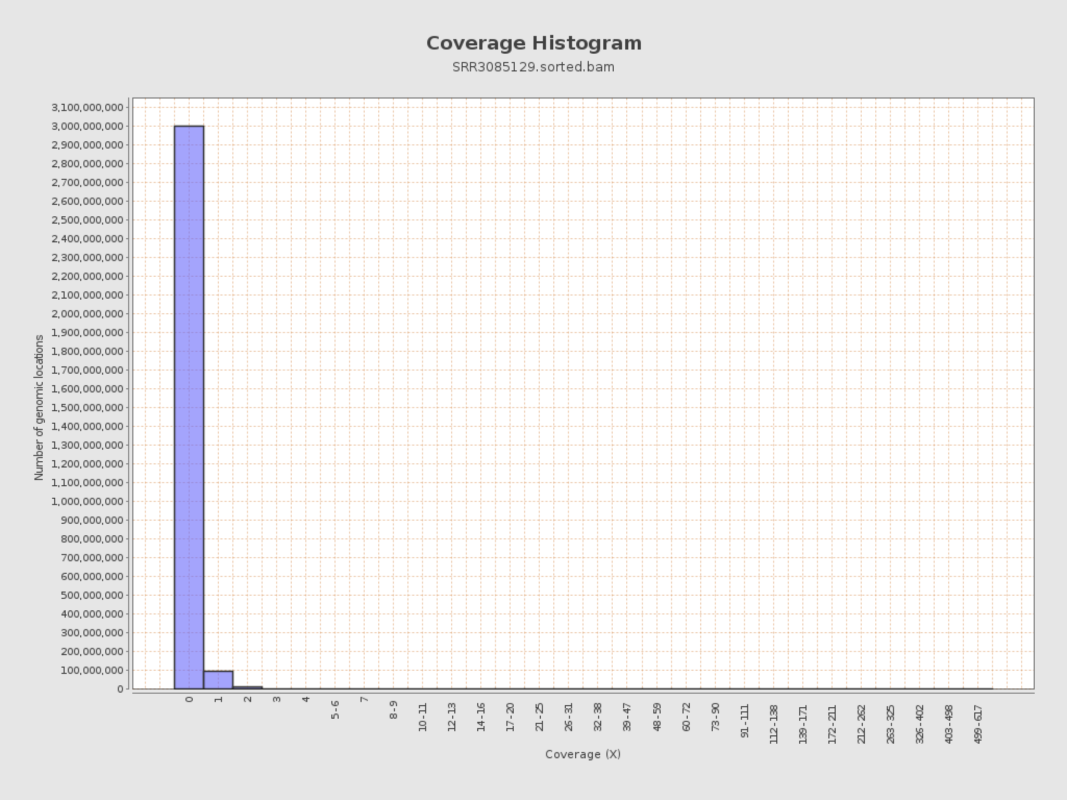
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8779052	0.0352	0.5281
chr2	243199373	9503019	0.0391	0.416
chr3	198022430	7621311	0.0385	0.2121
chr4	191154276	7453812	0.039	0.2204
chr5	180915260	6939804	0.0384	0.2138
chr6	171115067	6587239	0.0385	0.2477
chr7	159138663	6238907	0.0392	0.4281

chr8	146364022	5707183	0.039	0.4368
chr9	141213431	4696292	0.0333	0.2967
chr10	135534747	5136750	0.0379	0.2874
chr11	135006516	5106267	0.0378	0.2825
chr12	133851895	5106700	0.0382	0.2158
chr13	115169878	3691081	0.032	0.1959
chr14	107349540	3405446	0.0317	0.2048
chr15	102531392	3134143	0.0306	0.1956
chr16	90354753	2997653	0.0332	0.2156
chr17	81195210	2839521	0.035	0.2214
chr18	78077248	2997115	0.0384	0.5063
chr19	59128983	2085953	0.0353	0.4048
chr20	63025520	2229691	0.0354	0.2081
chr21	48129895	869279	0.0181	0.1566
chr22	51304566	1157023	0.0226	0.1615
chrMT	16571	4649	0.2806	0.6058
chrX	155270560	6535752	0.0421	0.245
chrY	59373566	265405	0.0045	0.0981

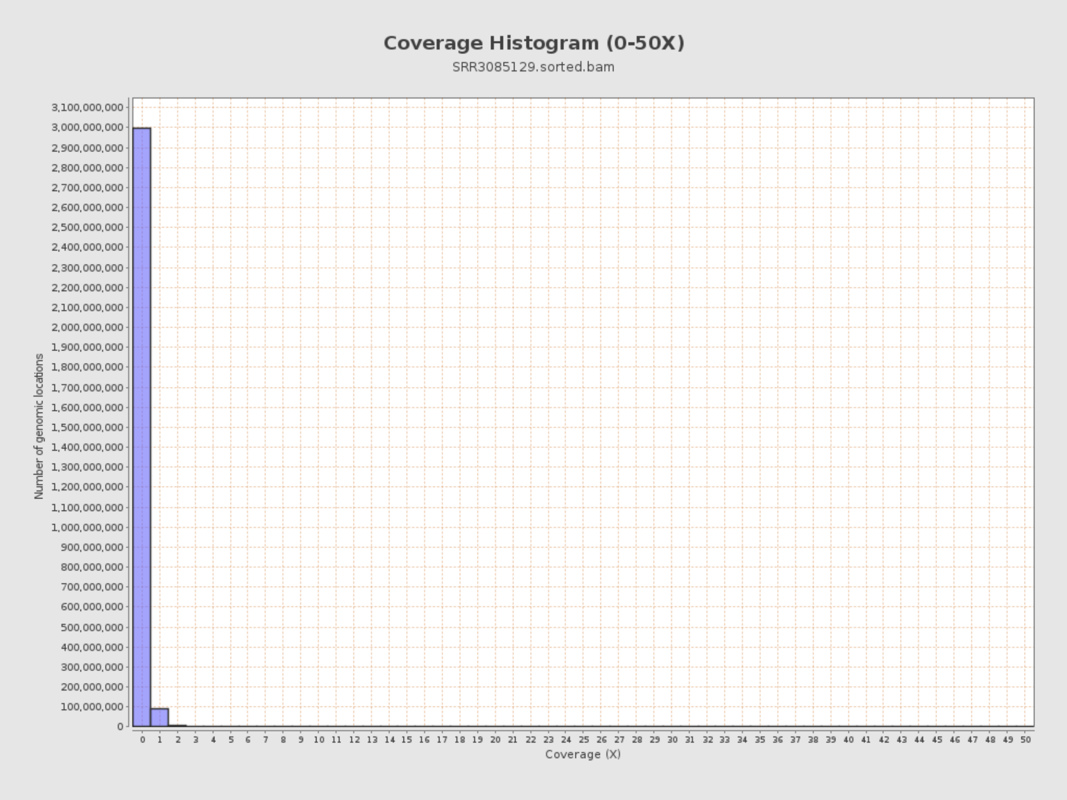
3. Results : Coverage across reference



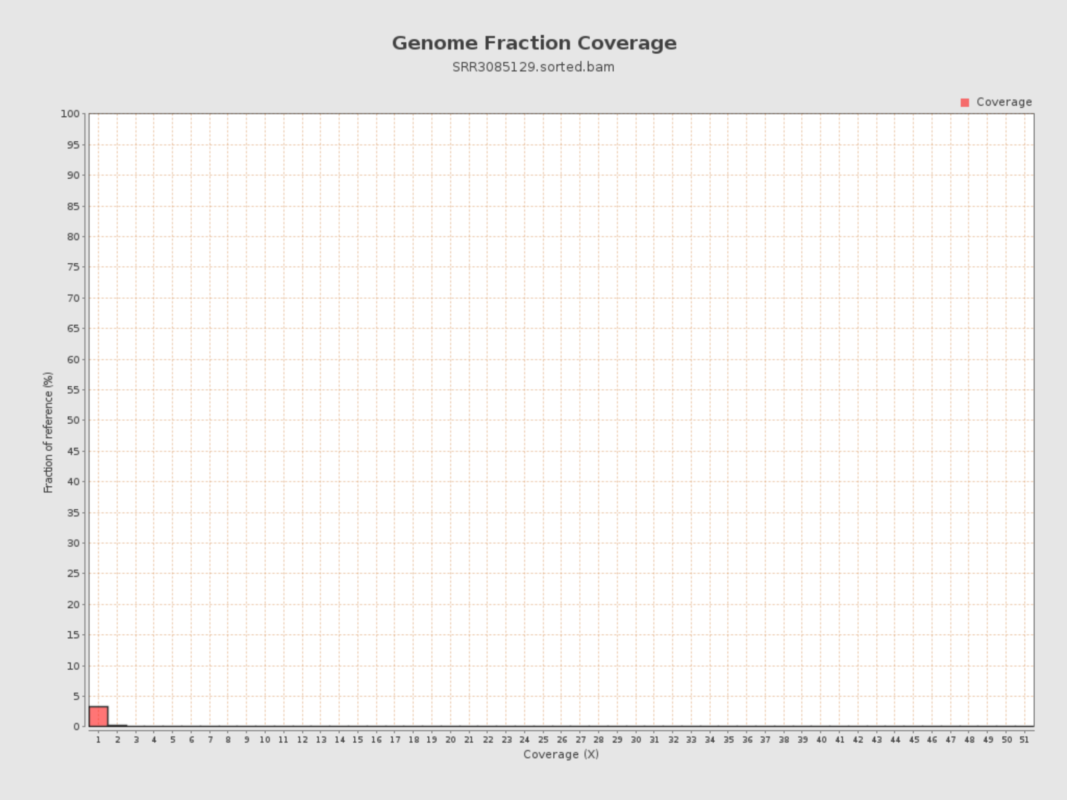
4. Results : Coverage Histogram



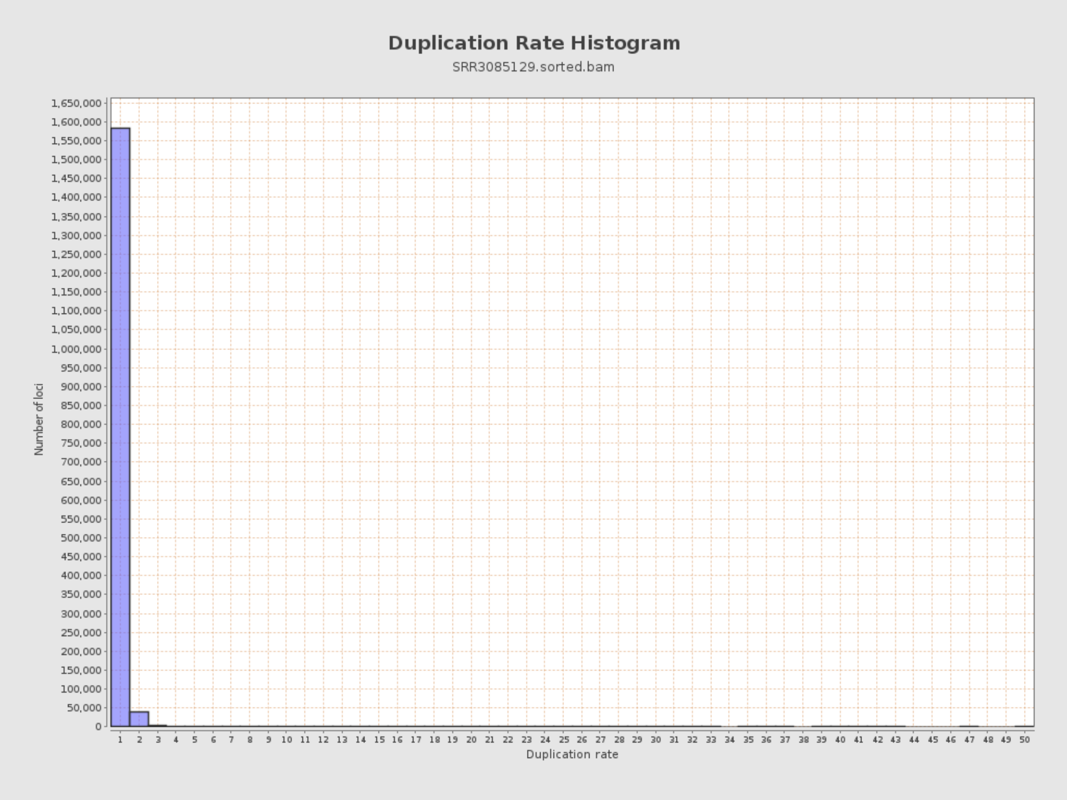
5. Results : Coverage Histogram (0-50X)



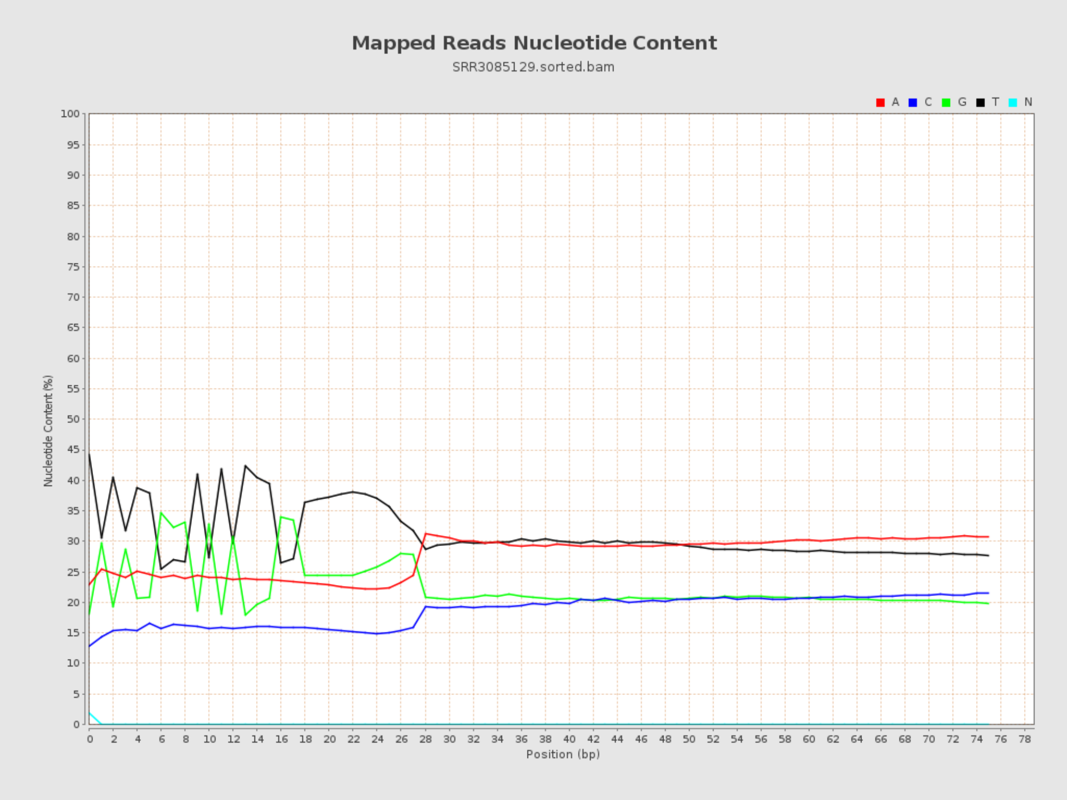
6. Results : Genome Fraction Coverage



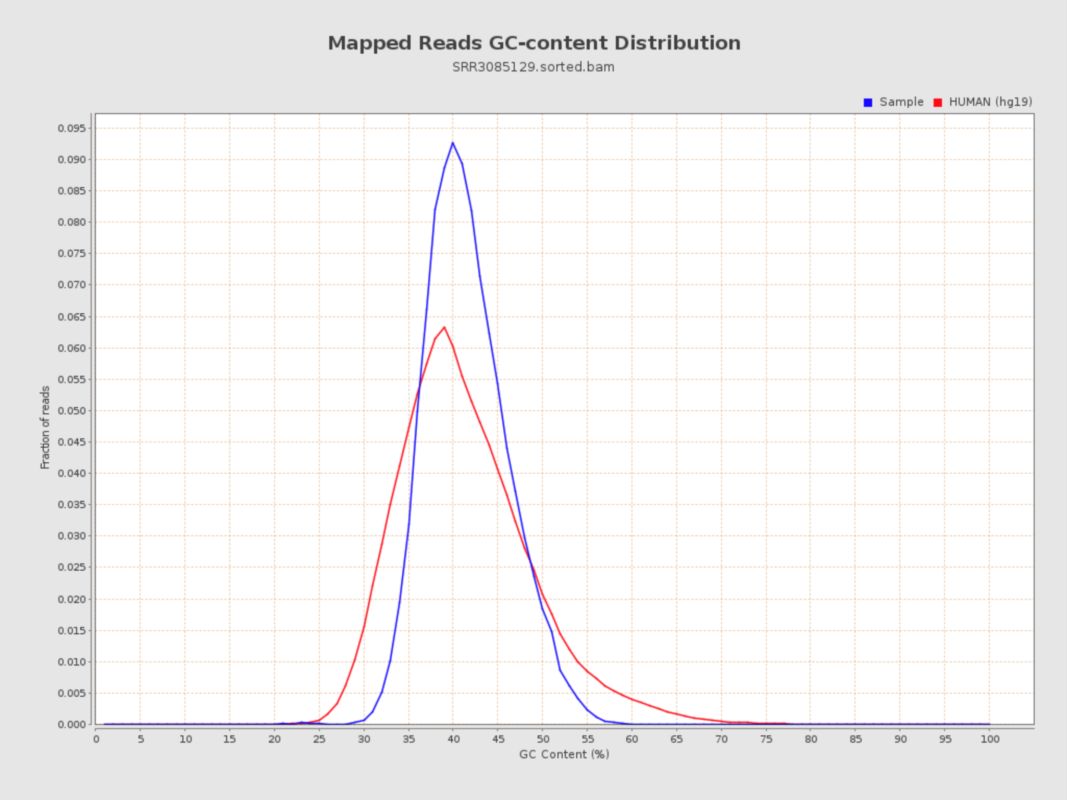
7. Results : Duplication Rate Histogram



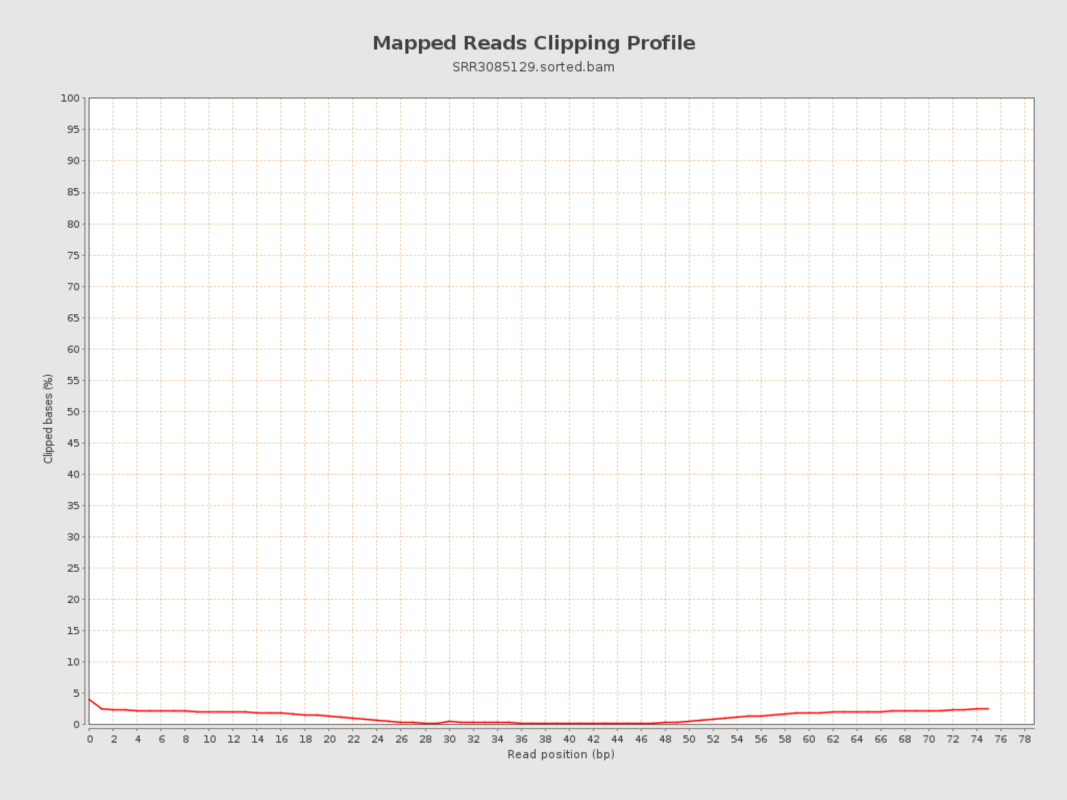
8. Results : Mapped Reads Nucleotide Content



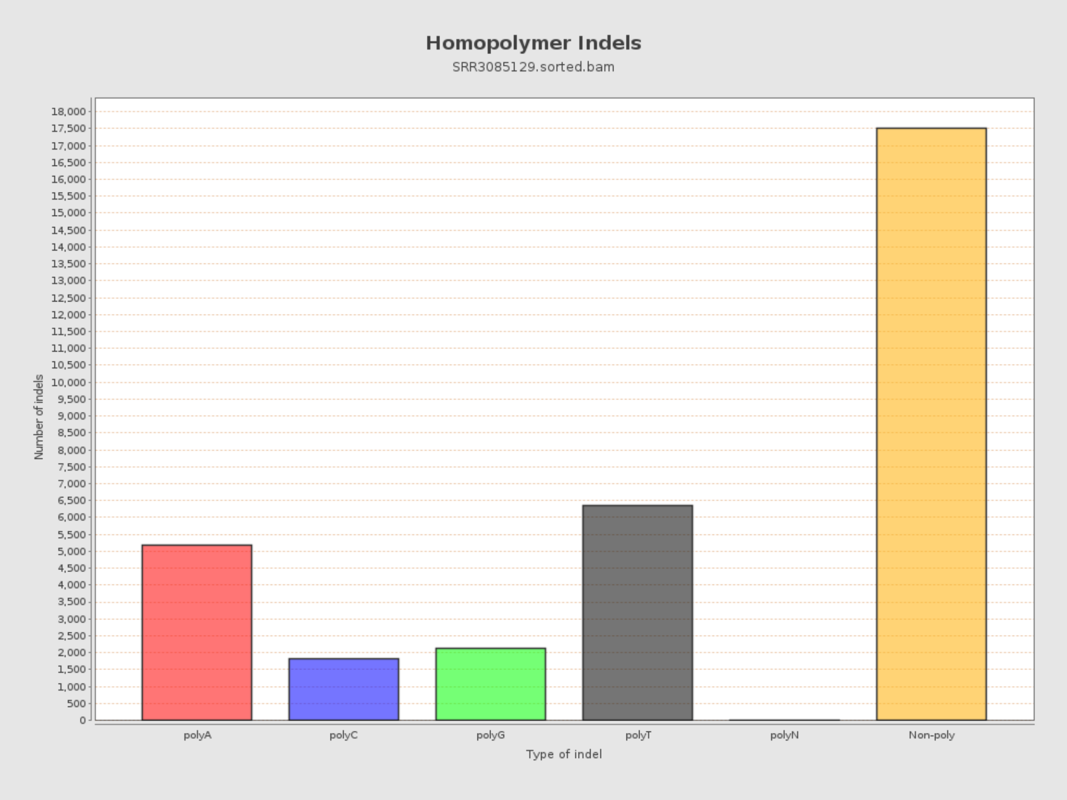
9. Results : Mapped Reads GC-content Distribution



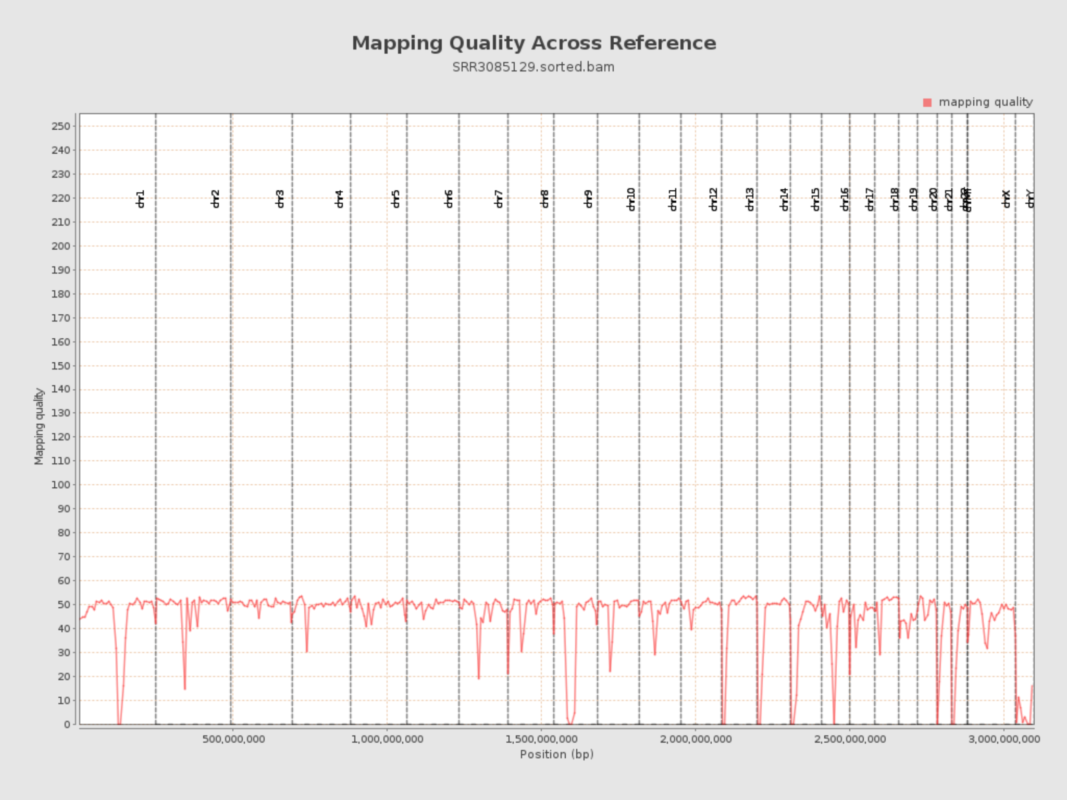
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram