Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 02:41:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085130.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_SRR3085130 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085130.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 02:41:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085130.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,741,271
Mapped reads	1,552,719 / 89.17%
Unmapped reads	188,552 / 10.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,942 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	55,278 / 3.17%
Duplication rate	2.73%
Clipped reads	696,652 / 40.01%

2.2. ACGT Content

Number/percentage of A's	29,222,076 / 28.18%
Number/percentage of C's	19,208,583 / 18.52%
Number/percentage of T's	32,501,529 / 31.34%
Number/percentage of G's	22,756,355 / 21.94%
Number/percentage of N's	20,929 / 0.02%
GC Percentage	40.46%

2.3. Coverage

Mean	0.0335

Standard Deviation	0.3161

2.4. Mapping Quality

Mean Mapping Quality	45.98

2.5. Mismatches and indels

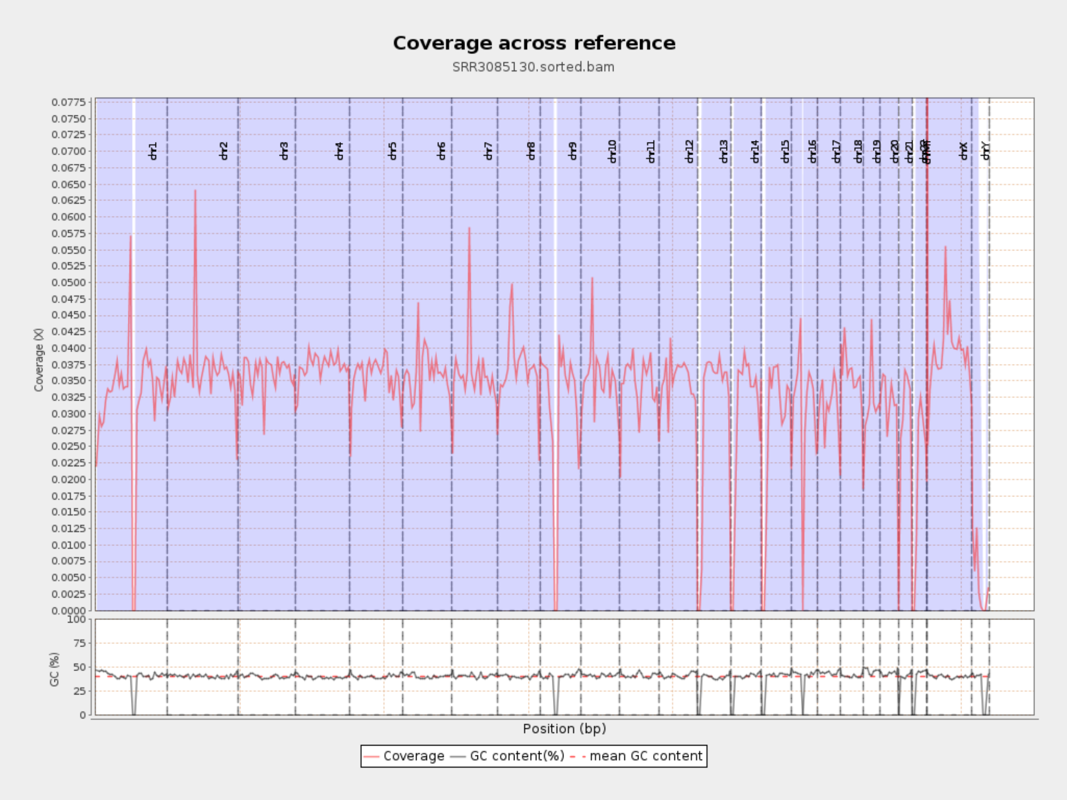
General error rate	0.89%
Mismatches	906,209
Insertions	8,204
Mapped reads with at least one insertion	0.52%
Deletions	22,821
Mapped reads with at least one deletion	1.45%
Homopolymer indels	46.91%

2.6. Chromosome stats

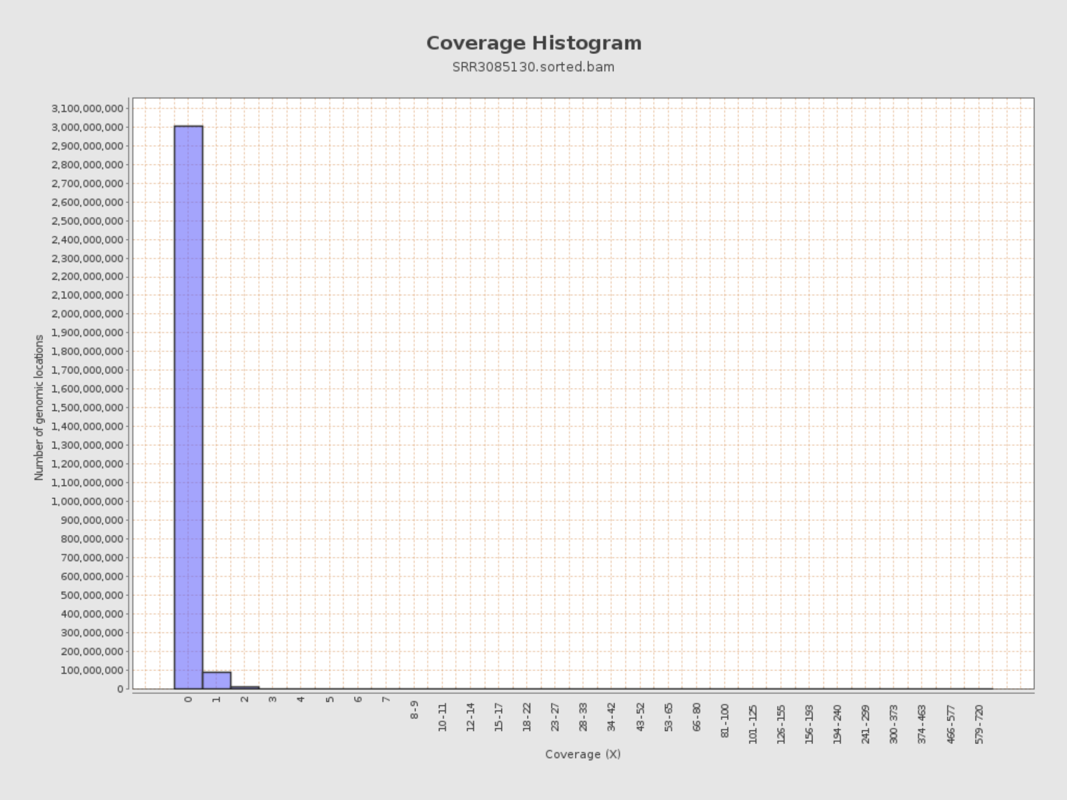
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8051574	0.0323	0.5524
chr2	243199373	8904738	0.0366	0.372
chr3	198022430	7148957	0.0361	0.2055
chr4	191154276	7098268	0.0371	0.213
chr5	180915260	6494651	0.0359	0.2057
chr6	171115067	6155480	0.036	0.2387
chr7	159138663	5747506	0.0361	0.4064

chr8	146364022	5421708	0.037	0.4863
chr9	141213431	4359181	0.0309	0.2887
chr10	135534747	4806144	0.0355	0.283
chr11	135006516	4701025	0.0348	0.2693
chr12	133851895	4680968	0.035	0.2058
chr13	115169878	3466795	0.0301	0.1881
chr14	107349540	3131105	0.0292	0.1958
chr15	102531392	2833208	0.0276	0.1817
chr16	90354753	2726875	0.0302	0.207
chr17	81195210	2524407	0.0311	0.2058
chr18	78077248	2824234	0.0362	0.5115
chr19	59128983	1873951	0.0317	0.4512
chr20	63025520	1991800	0.0316	0.1968
chr21	48129895	1370161	0.0285	0.191
chr22	51304566	1023640	0.02	0.151
chrMT	16571	5955	0.3594	0.6678
chrX	155270560	6141979	0.0396	0.2393
chrY	59373566	262108	0.0044	0.0971

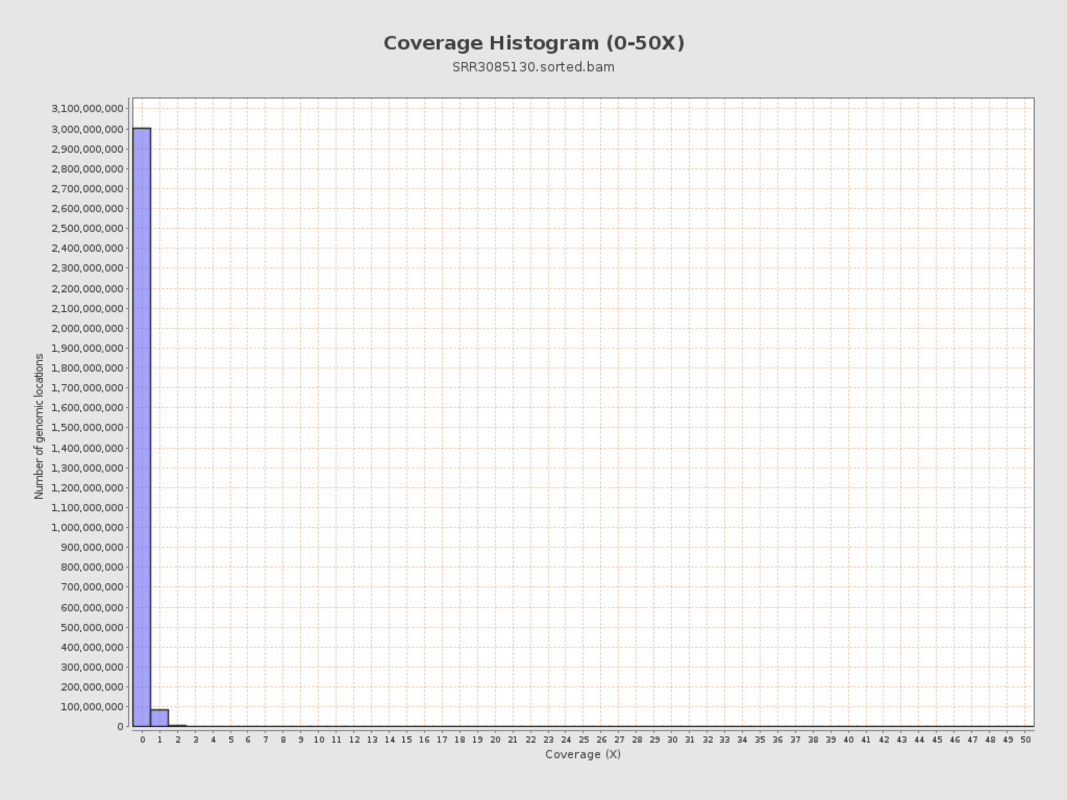
3. Results : Coverage across reference



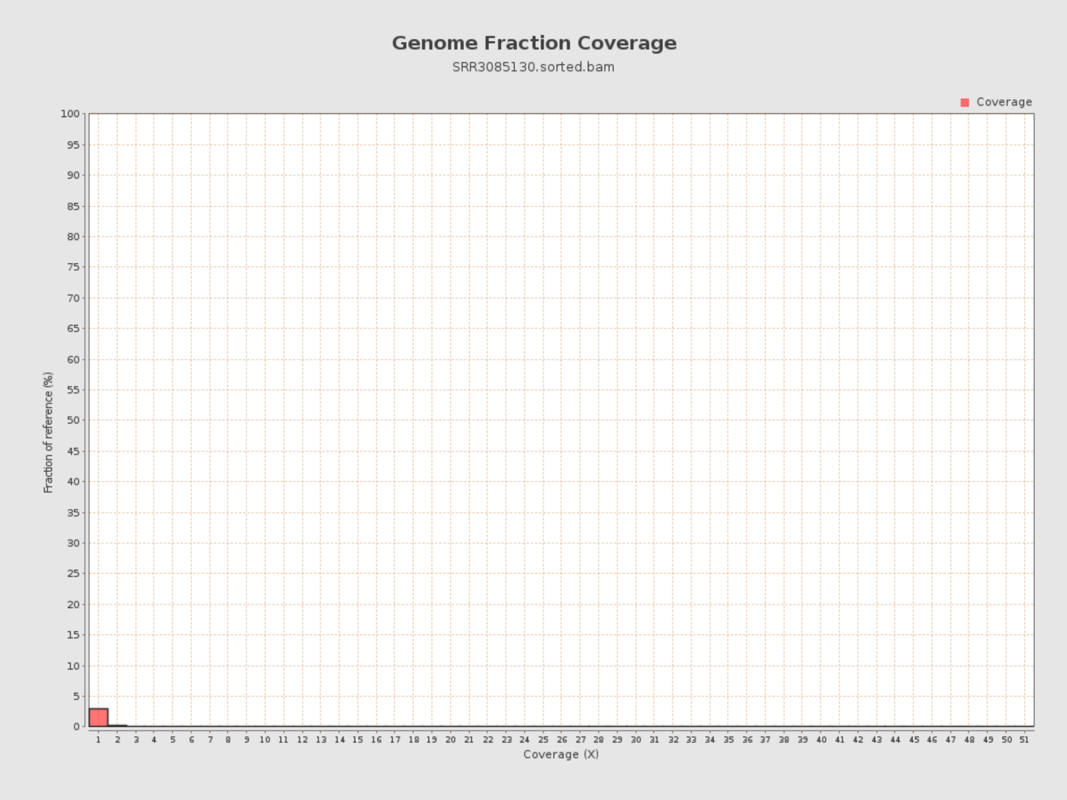
4. Results : Coverage Histogram



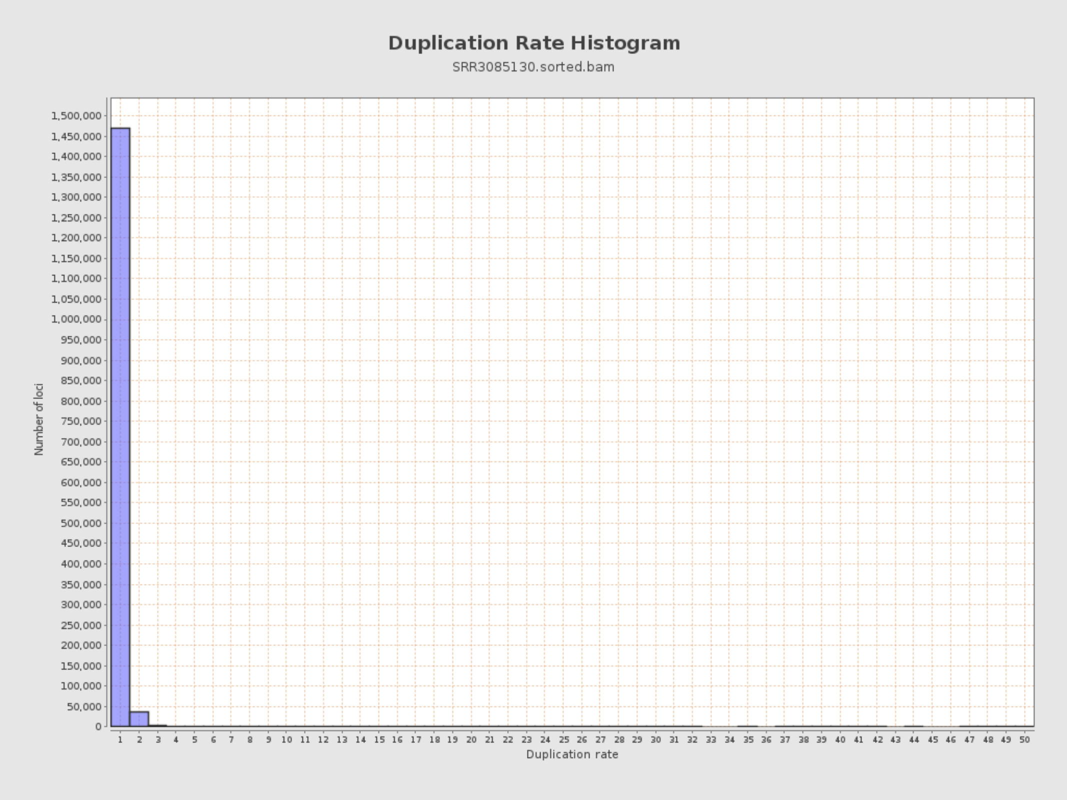
5. Results : Coverage Histogram (0-50X)



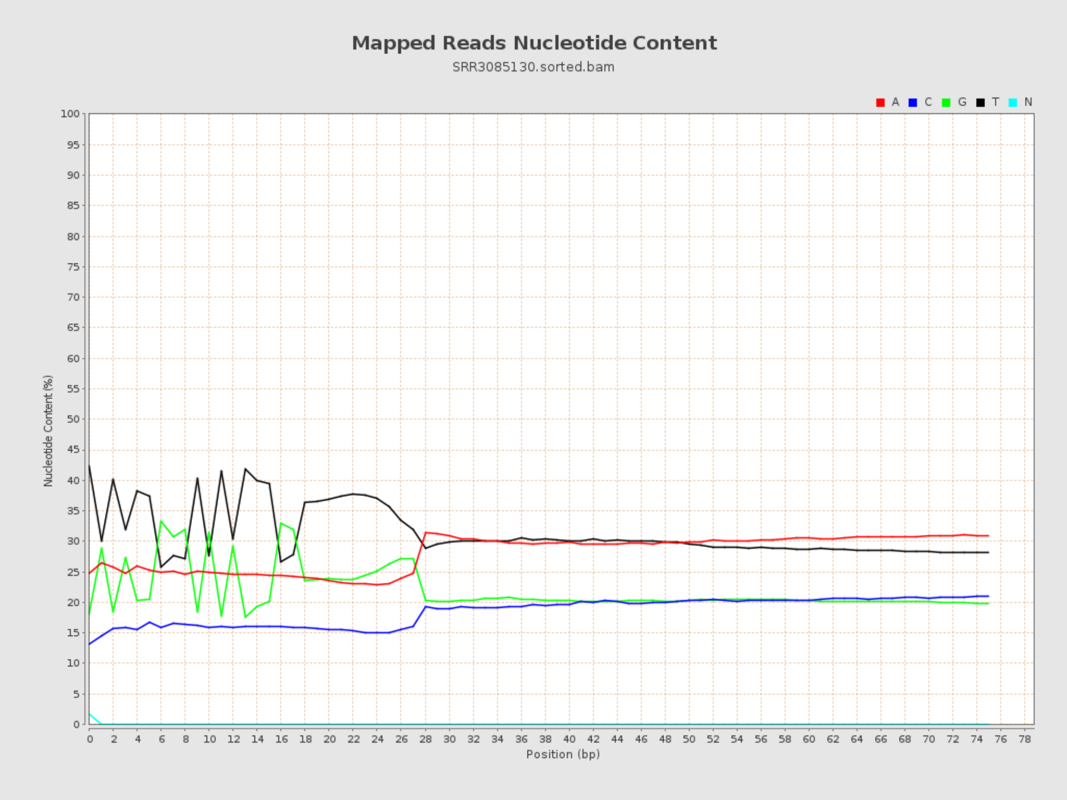
6. Results : Genome Fraction Coverage



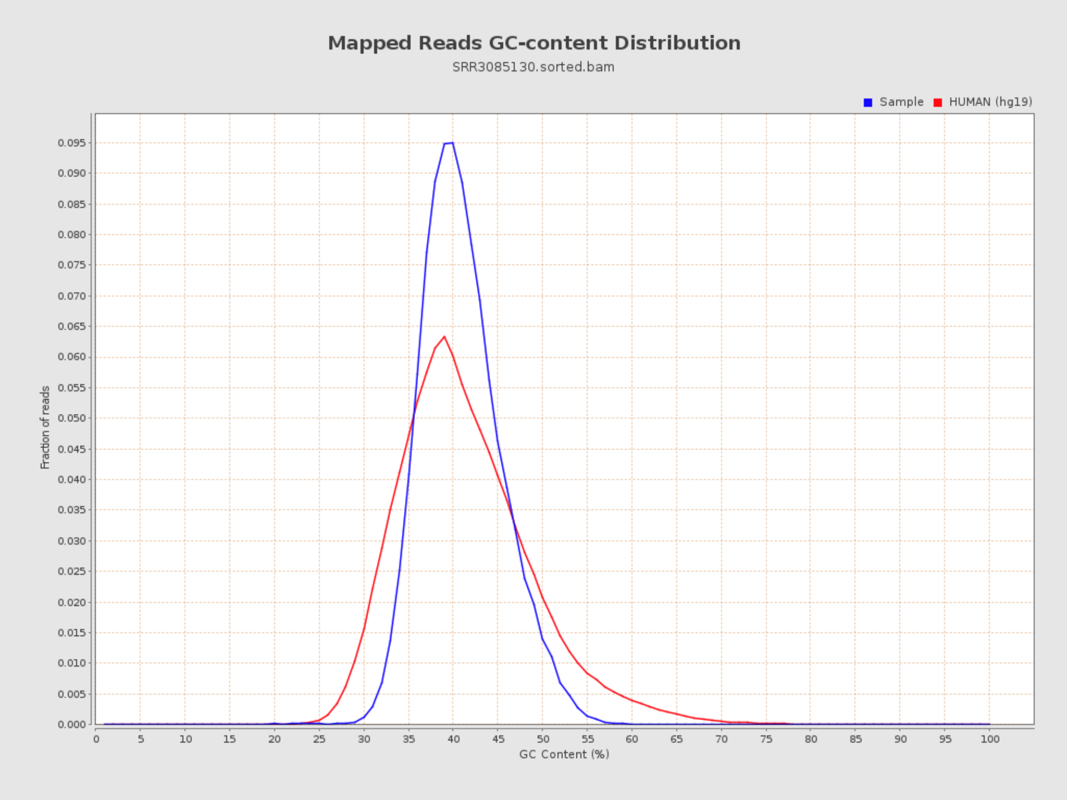
7. Results : Duplication Rate Histogram



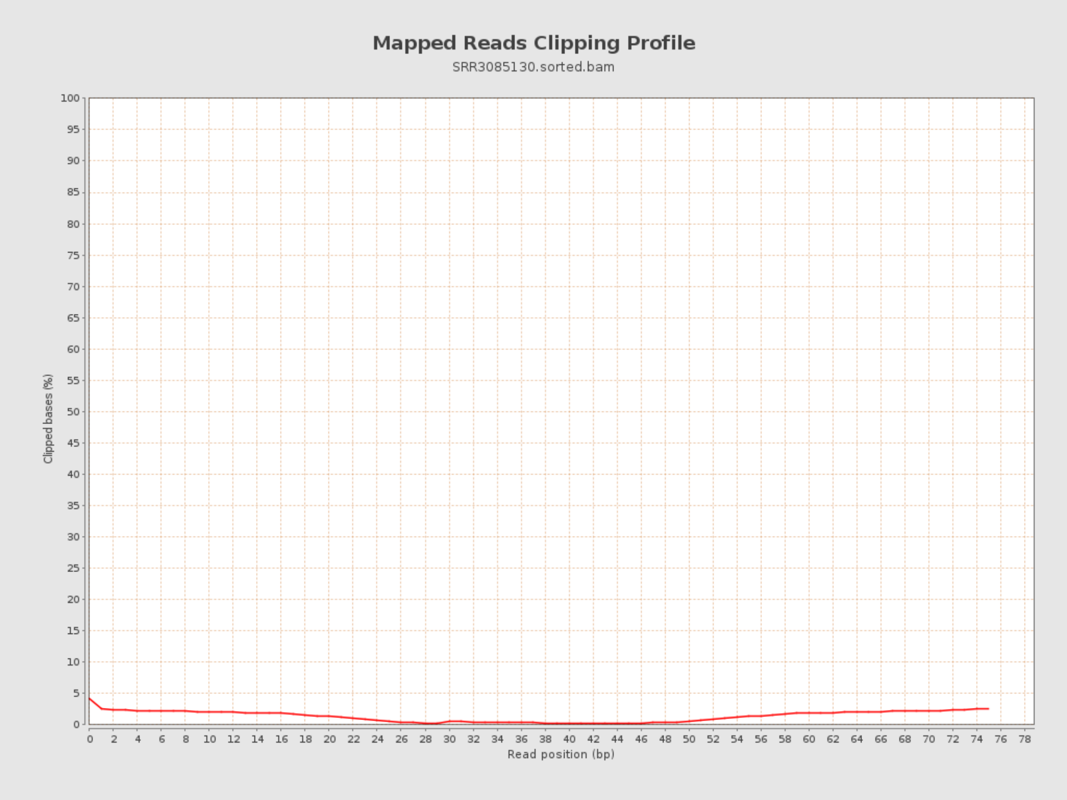
8. Results : Mapped Reads Nucleotide Content



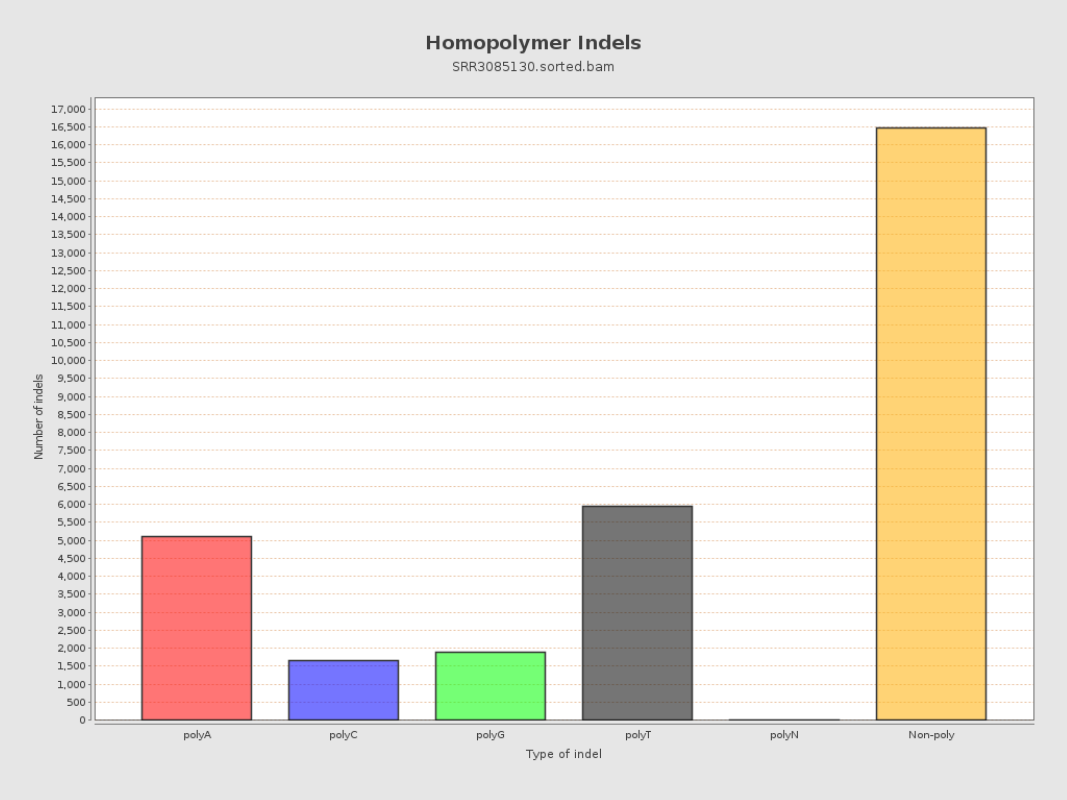
9. Results : Mapped Reads GC-content Distribution



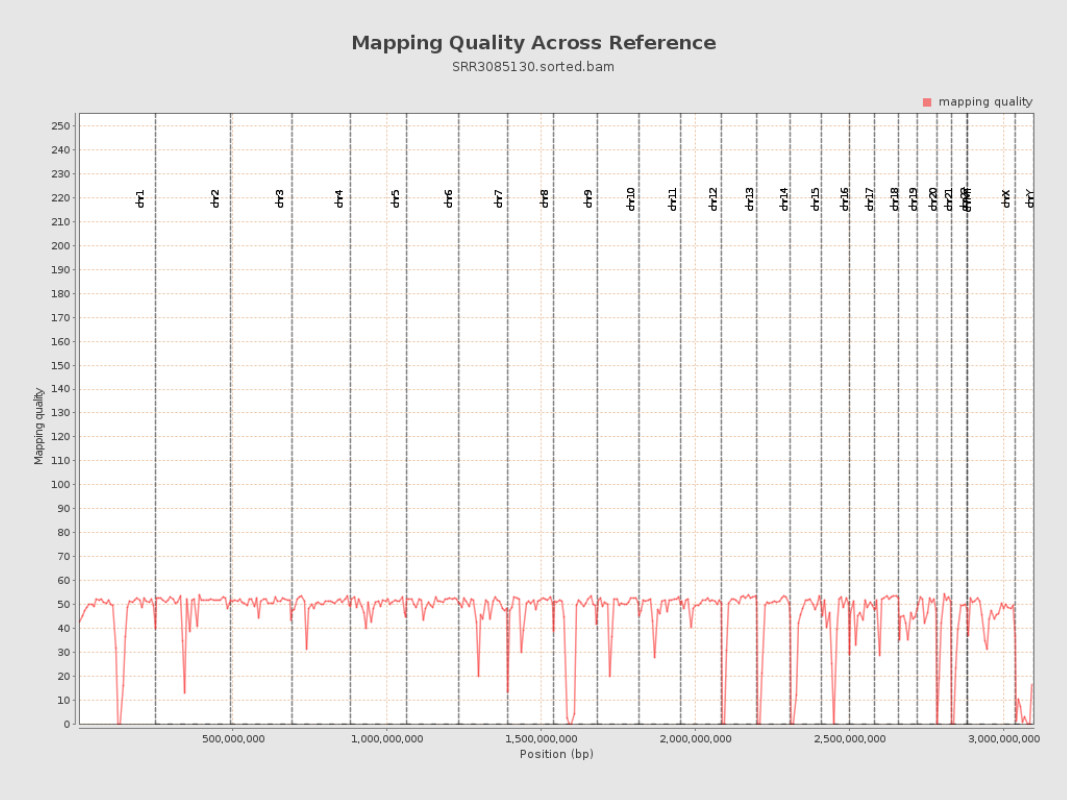
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram