Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:36:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004130.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_SRR6004130 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004130.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:36:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004130.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,019,048
Mapped reads	1,672,922 / 82.86%
Unmapped reads	346,126 / 17.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,371 / 1.01%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	110,721 / 5.48%
Duplication rate	5.39%
Clipped reads	842,379 / 41.72%

2.2. ACGT Content

Number/percentage of A's	31,016,021 / 28.18%
Number/percentage of C's	20,605,808 / 18.72%
Number/percentage of T's	34,481,175 / 31.33%
Number/percentage of G's	23,948,451 / 21.76%
Number/percentage of N's	7,725 / 0.01%
GC Percentage	40.48%

2.3. Coverage

Mean	0.0356

Standard Deviation	0.3375

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

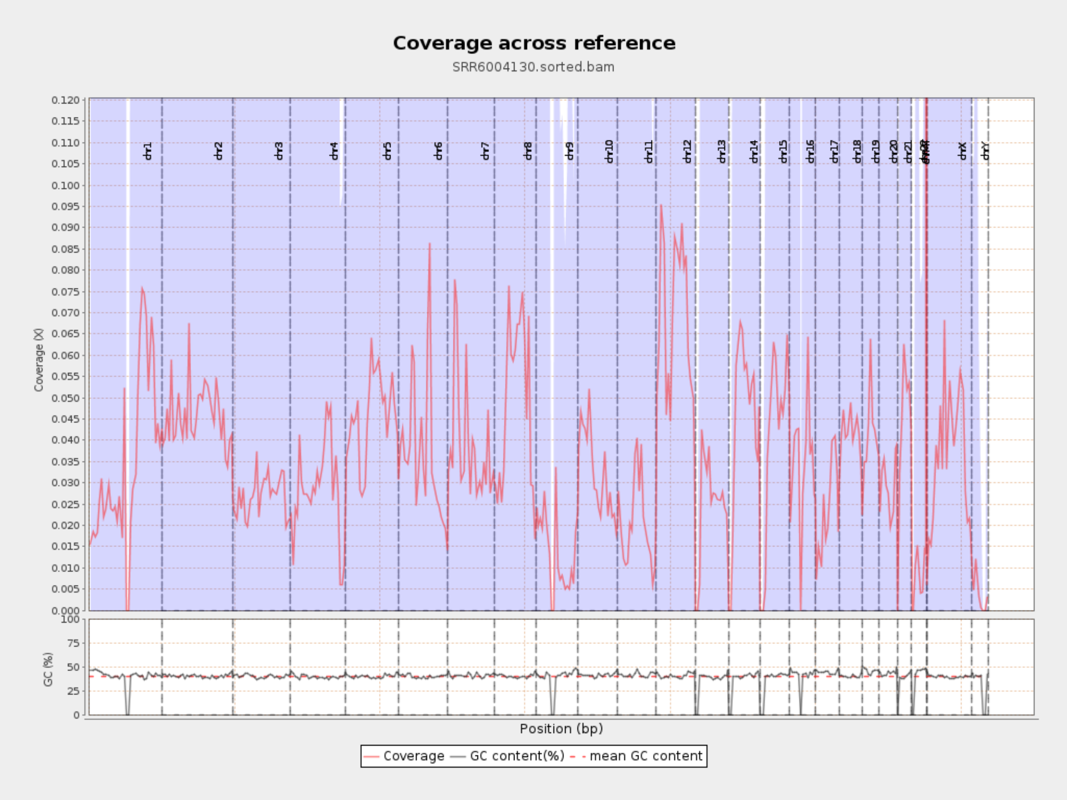
General error rate	0.92%
Mismatches	1,004,088
Insertions	7,907
Mapped reads with at least one insertion	0.47%
Deletions	26,383
Mapped reads with at least one deletion	1.56%
Homopolymer indels	46.62%

2.6. Chromosome stats

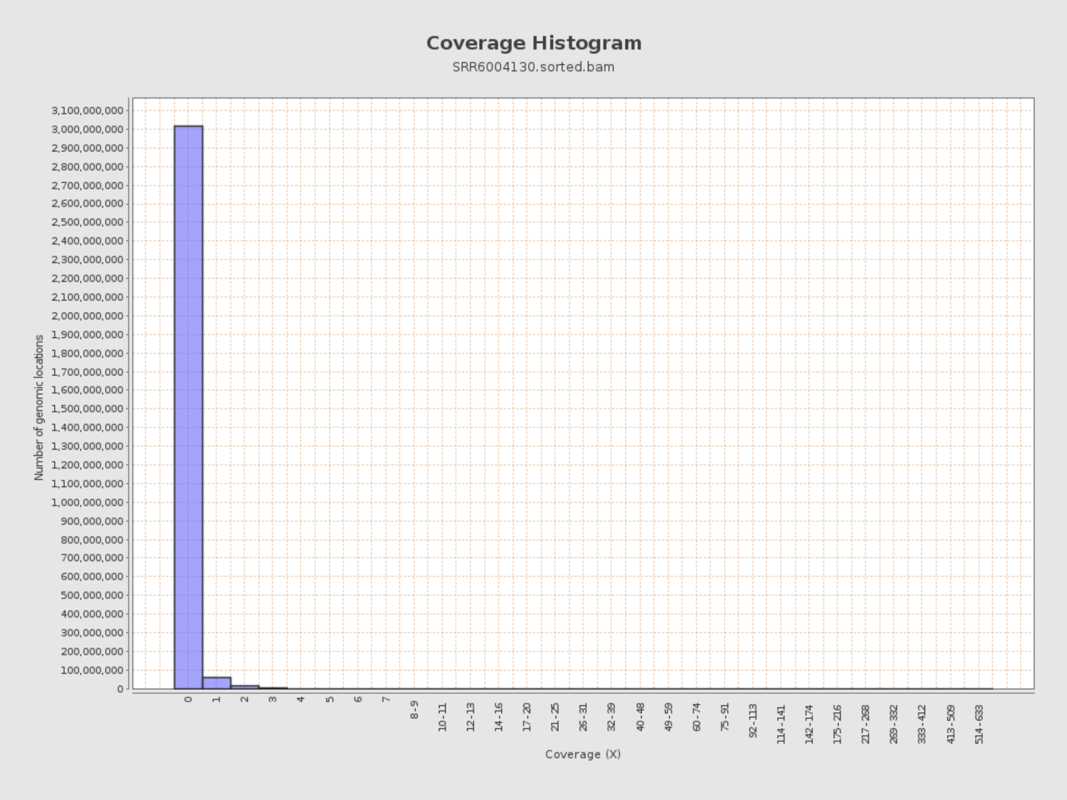
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8713663	0.035	0.5758
chr2	243199373	11184463	0.046	0.4098
chr3	198022430	5374033	0.0271	0.2102
chr4	191154276	5417428	0.0283	0.223
chr5	180915260	8360648	0.0462	0.2838
chr6	171115067	6402271	0.0374	0.2817
chr7	159138663	6301212	0.0396	0.4228

chr8	146364022	7149607	0.0488	0.4339
chr9	141213431	1846191	0.0131	0.2568
chr10	135534747	4421436	0.0326	0.3093
chr11	135006516	2772265	0.0205	0.2227
chr12	133851895	9238706	0.069	0.3468
chr13	115169878	2848769	0.0247	0.2068
chr14	107349540	4841981	0.0451	0.2863
chr15	102531392	4146159	0.0404	0.2645
chr16	90354753	3143980	0.0348	0.2588
chr17	81195210	1906661	0.0235	0.1994
chr18	78077248	3277266	0.042	0.5302
chr19	59128983	2474117	0.0418	0.408
chr20	63025520	1852255	0.0294	0.2283
chr21	48129895	2103597	0.0437	0.2786
chr22	51304566	410487	0.008	0.1094
chrMT	16571	42145	2.5433	2.4585
chrX	155270560	5648132	0.0364	0.2661
chrY	59373566	224102	0.0038	0.088

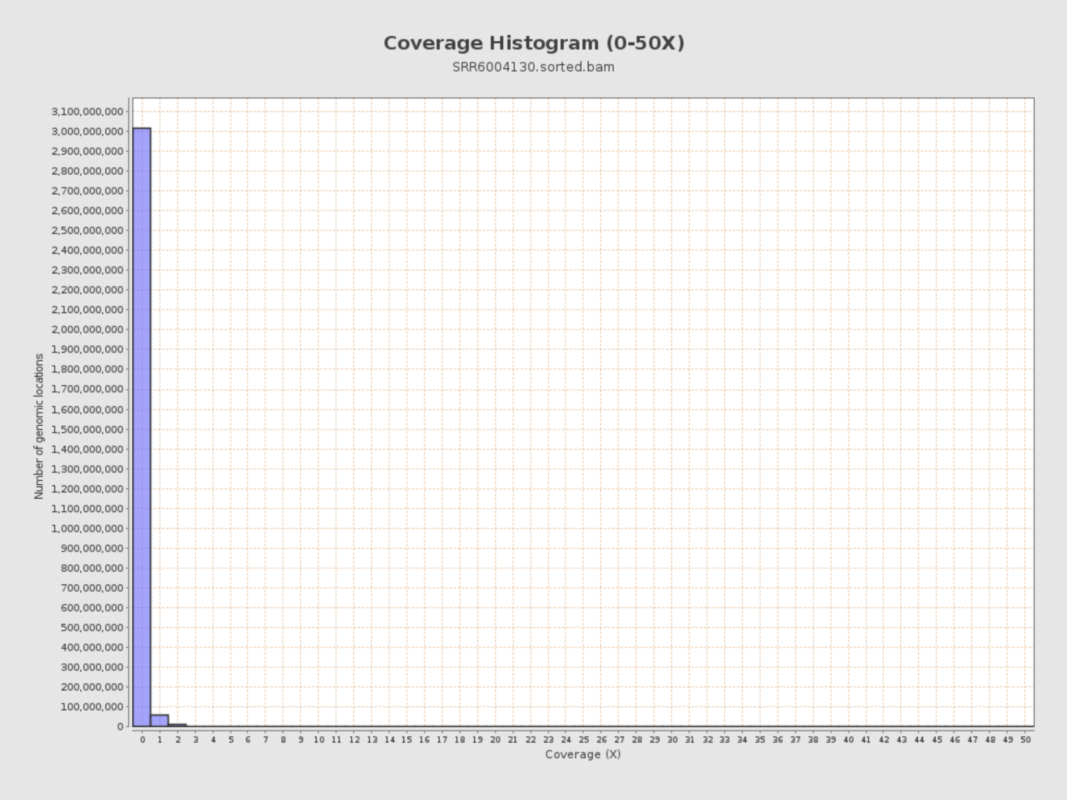
3. Results : Coverage across reference



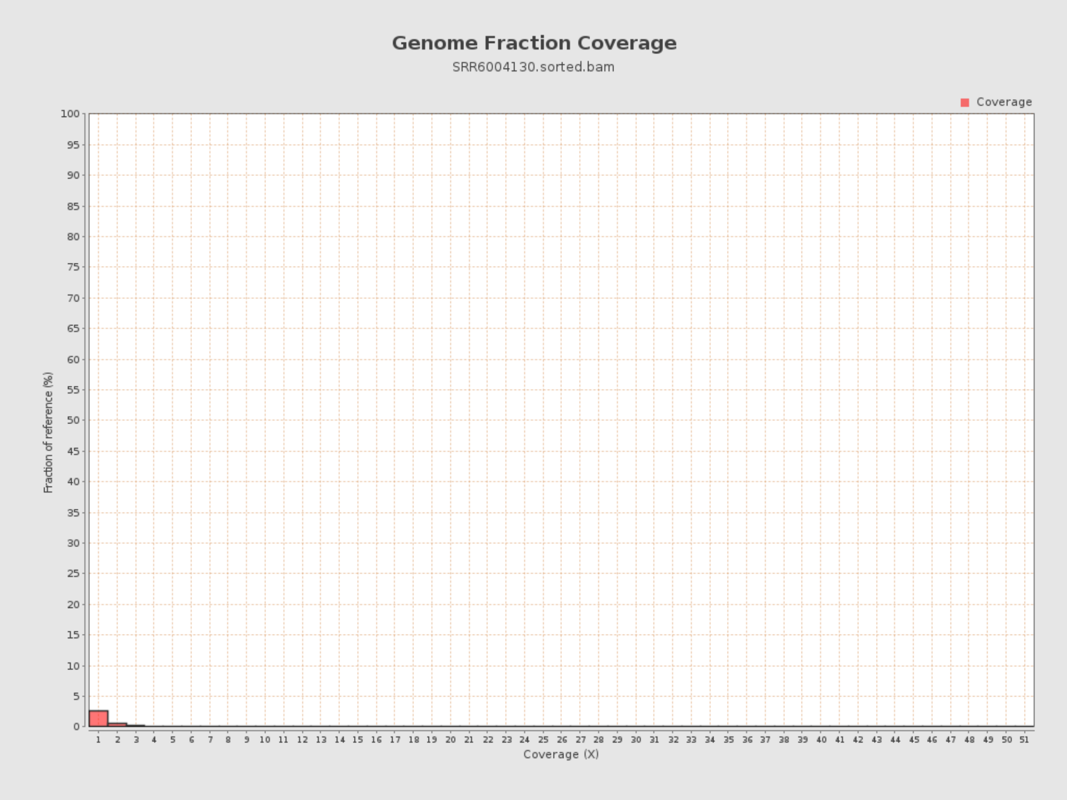
4. Results : Coverage Histogram



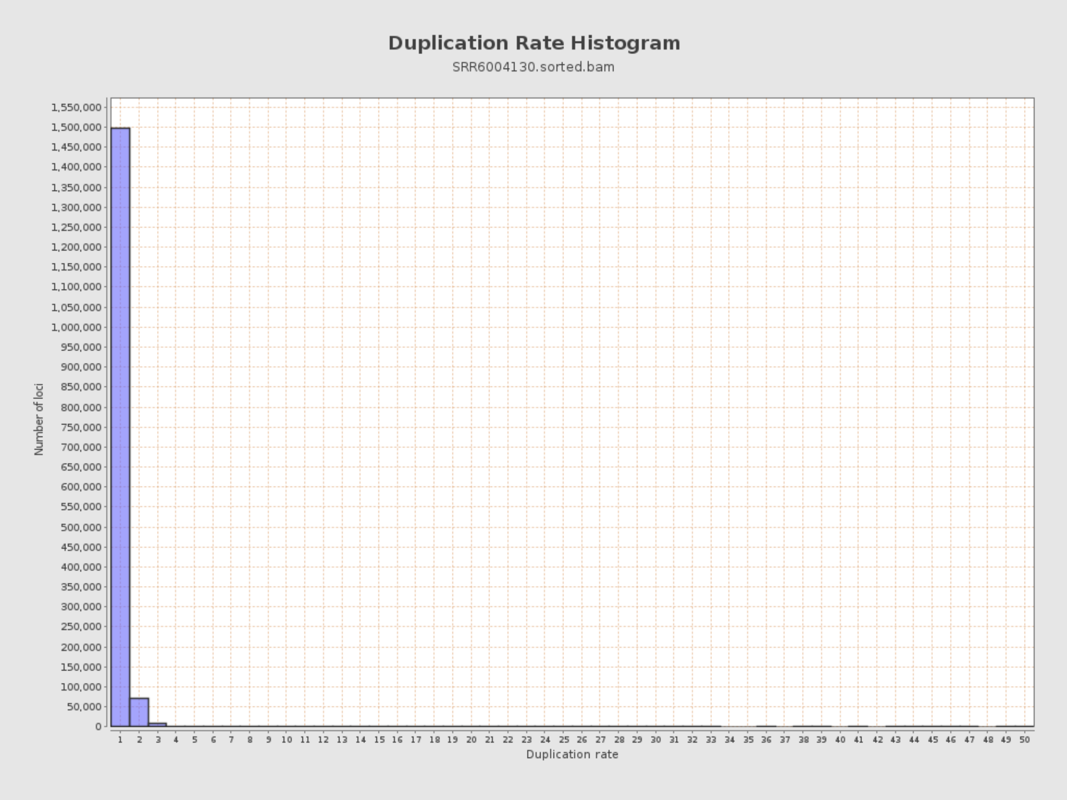
5. Results : Coverage Histogram (0-50X)



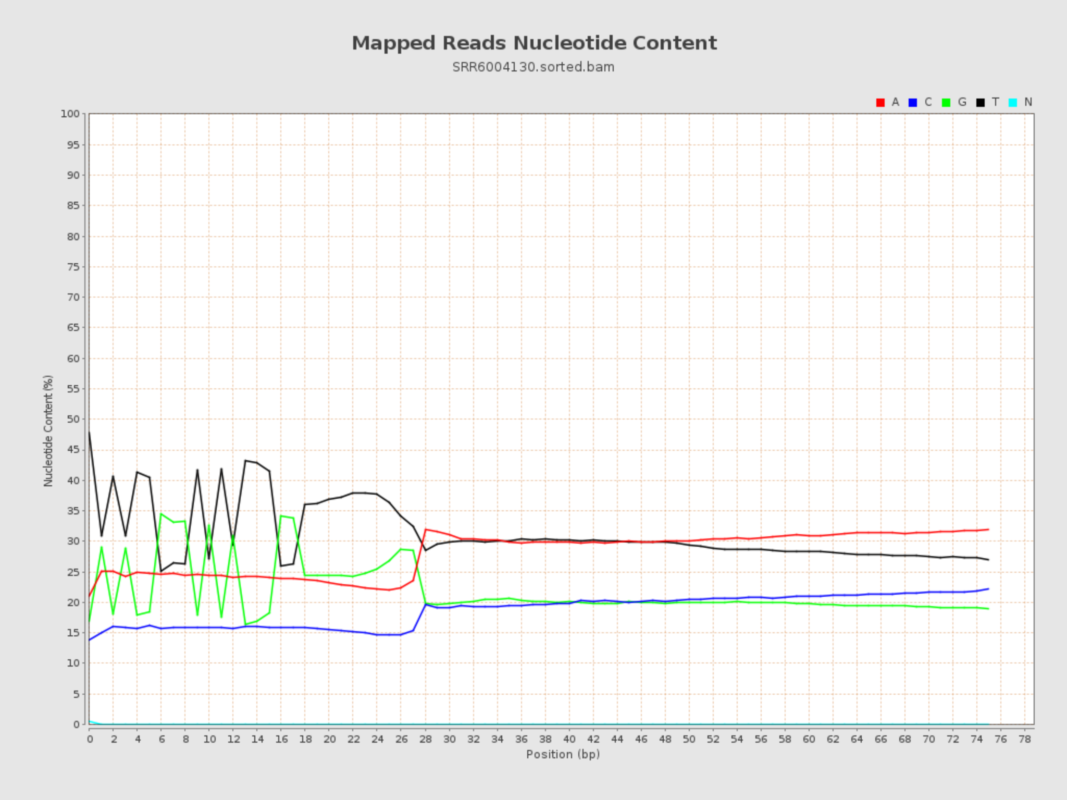
6. Results : Genome Fraction Coverage



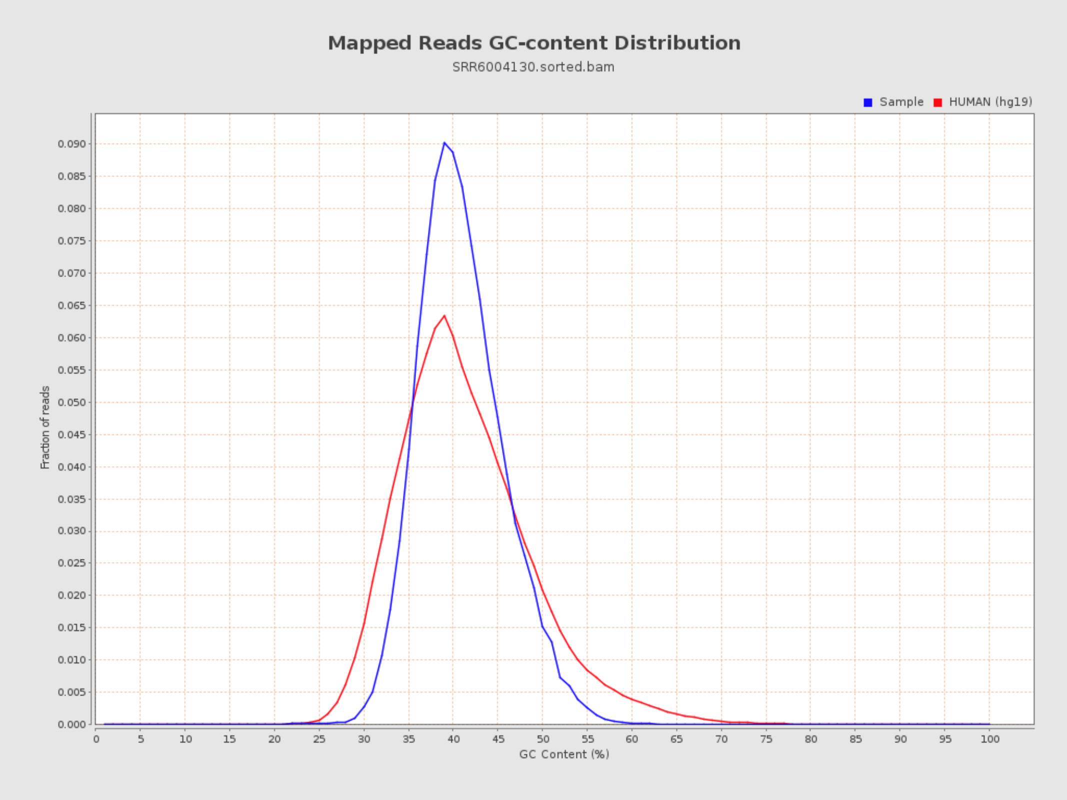
7. Results : Duplication Rate Histogram



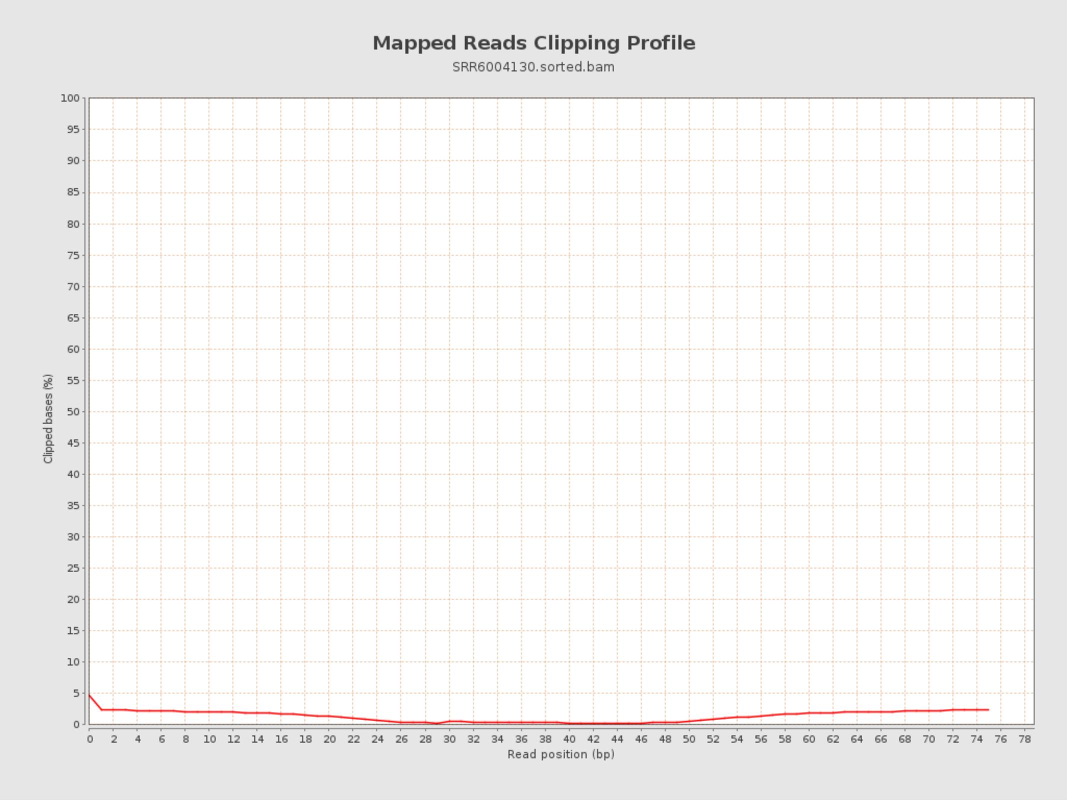
8. Results : Mapped Reads Nucleotide Content



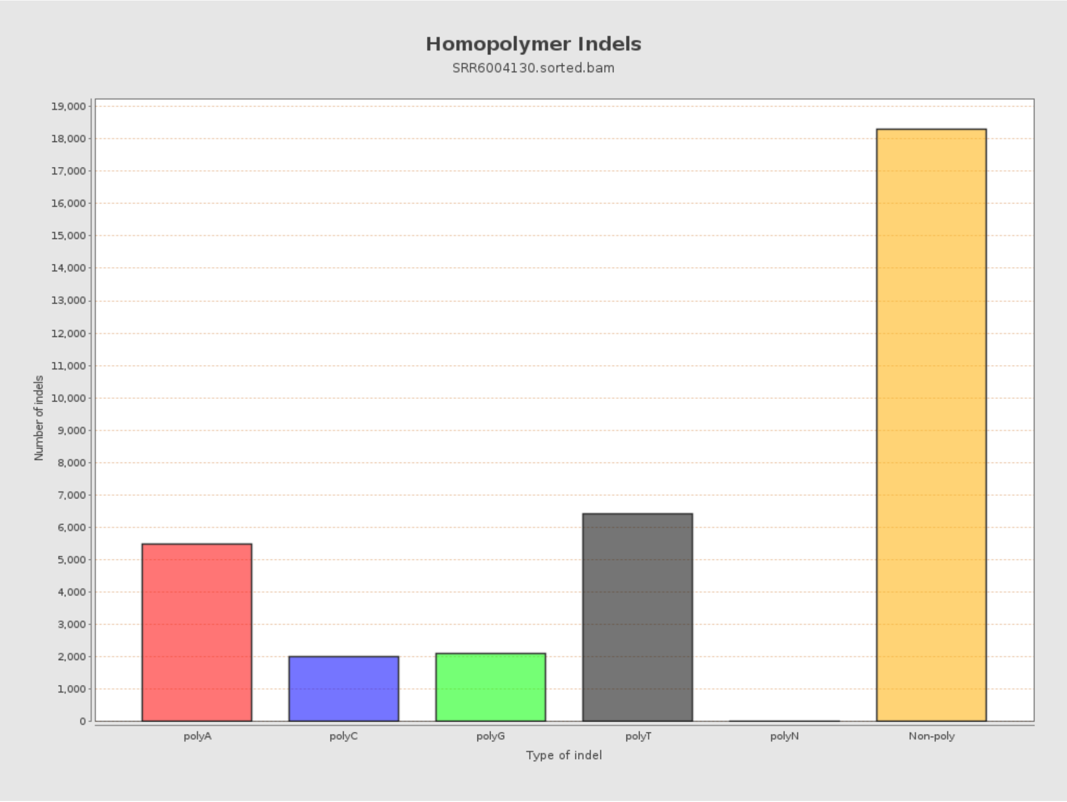
9. Results : Mapped Reads GC-content Distribution



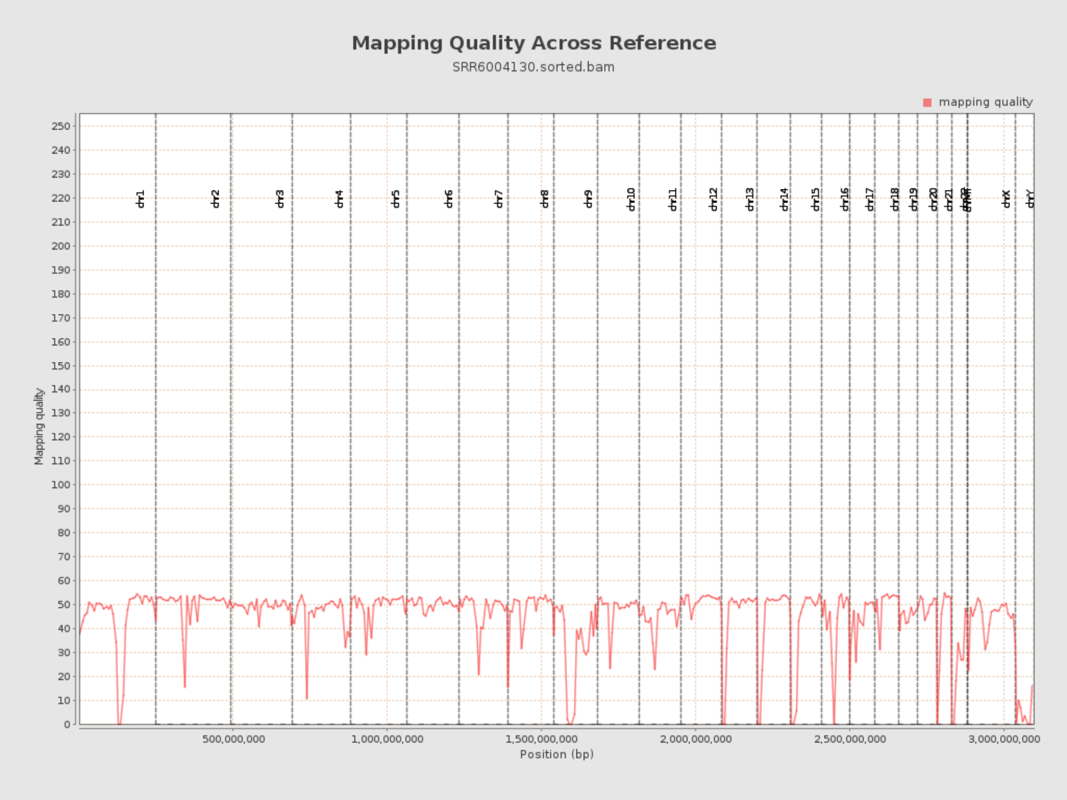
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram