Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:38:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548981.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_SRR1548981 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548981.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:38:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548981.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,224,172
Mapped reads	4,435,479 / 43.38%
Unmapped reads	5,788,693 / 56.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	122,878 / 1.2%
Duplication rate	2.14%
Clipped reads	447,859 / 4.38%

2.2. ACGT Content

Number/percentage of A's	52,929,627 / 30.24%
Number/percentage of C's	34,455,266 / 19.69%
Number/percentage of T's	53,171,939 / 30.38%
Number/percentage of G's	34,449,348 / 19.68%
Number/percentage of N's	9,262 / 0.01%
GC Percentage	39.37%

2.3. Coverage

Mean	0.0565
Standard Deviation	0.3849

2.4. Mapping Quality

Mean Mapping Quality	42.87

2.5. Mismatches and indels

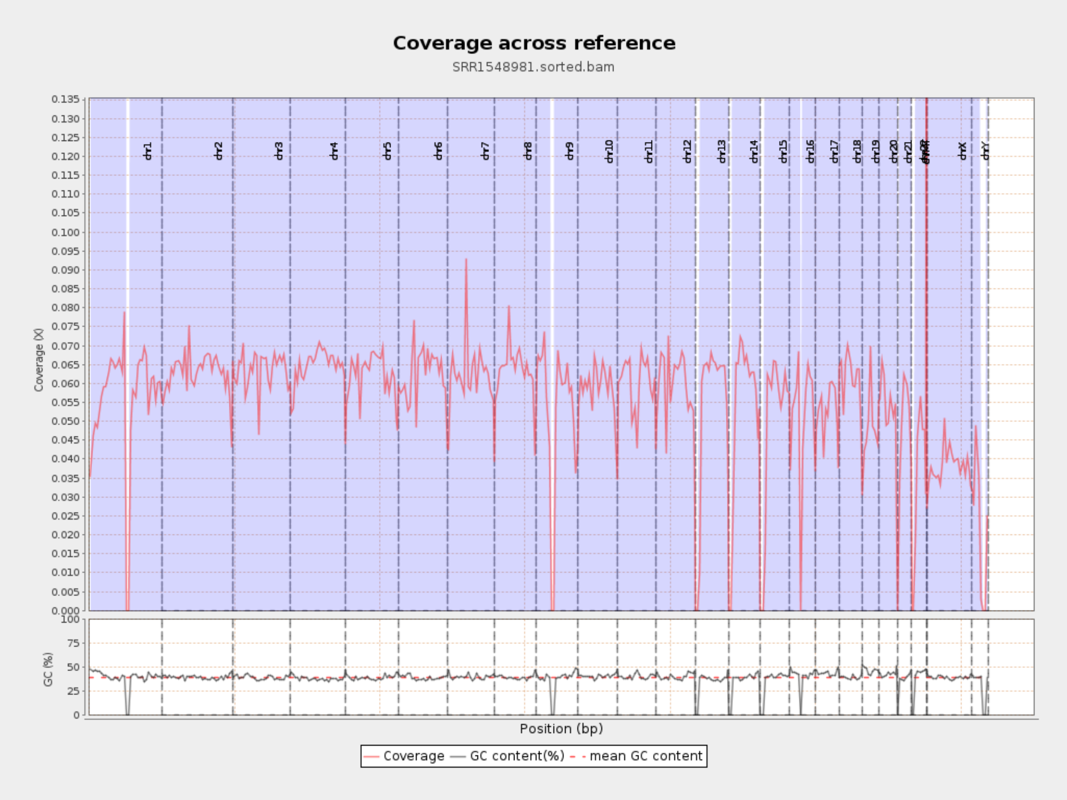
General error rate	0.31%
Mismatches	536,514
Insertions	7,695
Mapped reads with at least one insertion	0.17%
Deletions	18,162
Mapped reads with at least one deletion	0.41%
Homopolymer indels	45.25%

2.6. Chromosome stats

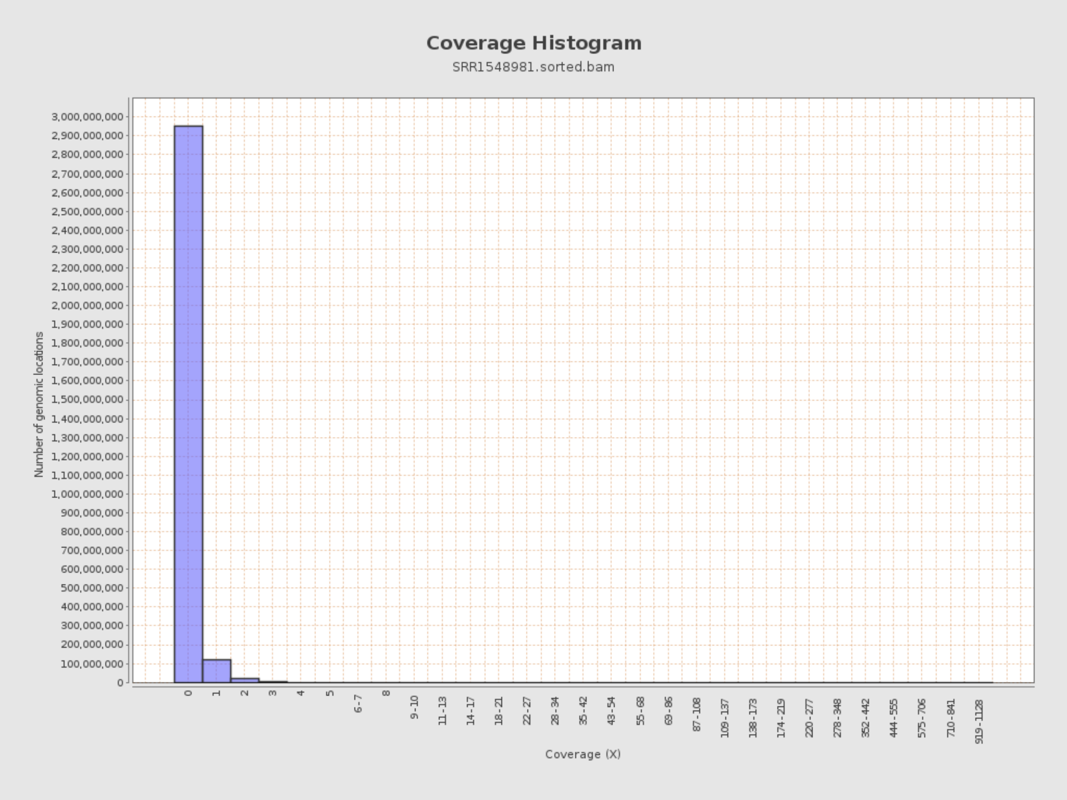
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13920888	0.0559	0.6285
chr2	243199373	15342069	0.0631	0.3574
chr3	198022430	12583905	0.0635	0.2963
chr4	191154276	12385249	0.0648	0.3035
chr5	180915260	11308026	0.0625	0.2951
chr6	171115067	10700938	0.0625	0.3299
chr7	159138663	10046049	0.0631	0.5666
chr8	146364022	9291009	0.0635	0.6347

chr9	141213431	7447984	0.0527	0.3179
chr10	135534747	8052115	0.0594	0.3183
chr11	135006516	8113958	0.0601	0.332
chr12	133851895	8015663	0.0599	0.2933
chr13	115169878	6090700	0.0529	0.2704
chr14	107349540	5651130	0.0526	0.2935
chr15	102531392	4968257	0.0485	0.2583
chr16	90354753	4613108	0.0511	0.2706
chr17	81195210	4254436	0.0524	0.2761
chr18	78077248	4828954	0.0618	0.4682
chr19	59128983	2889887	0.0489	0.5265
chr20	63025520	3405649	0.054	0.2784
chr21	48129895	2210162	0.0459	0.2671
chr22	51304566	1737335	0.0339	0.2721
chrMT	16571	6249	0.3771	0.7092
chrX	155270560	5929334	0.0382	0.2519
chrY	59373566	1244859	0.021	0.1943

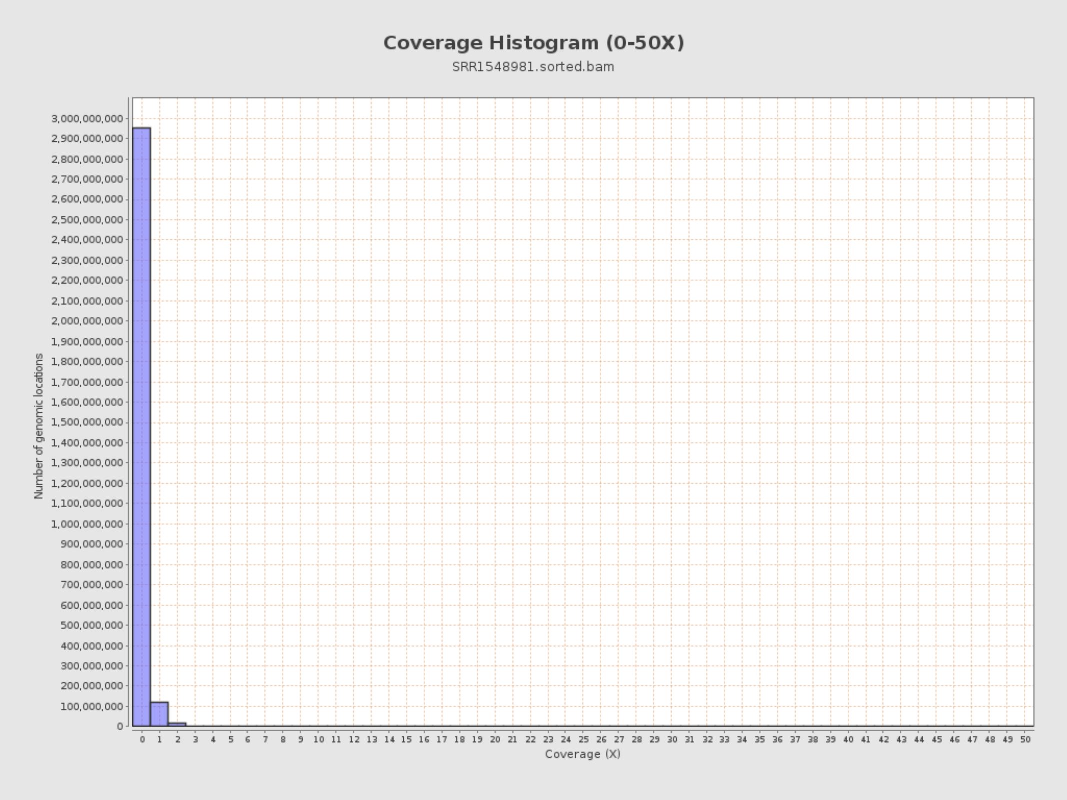
3. Results : Coverage across reference



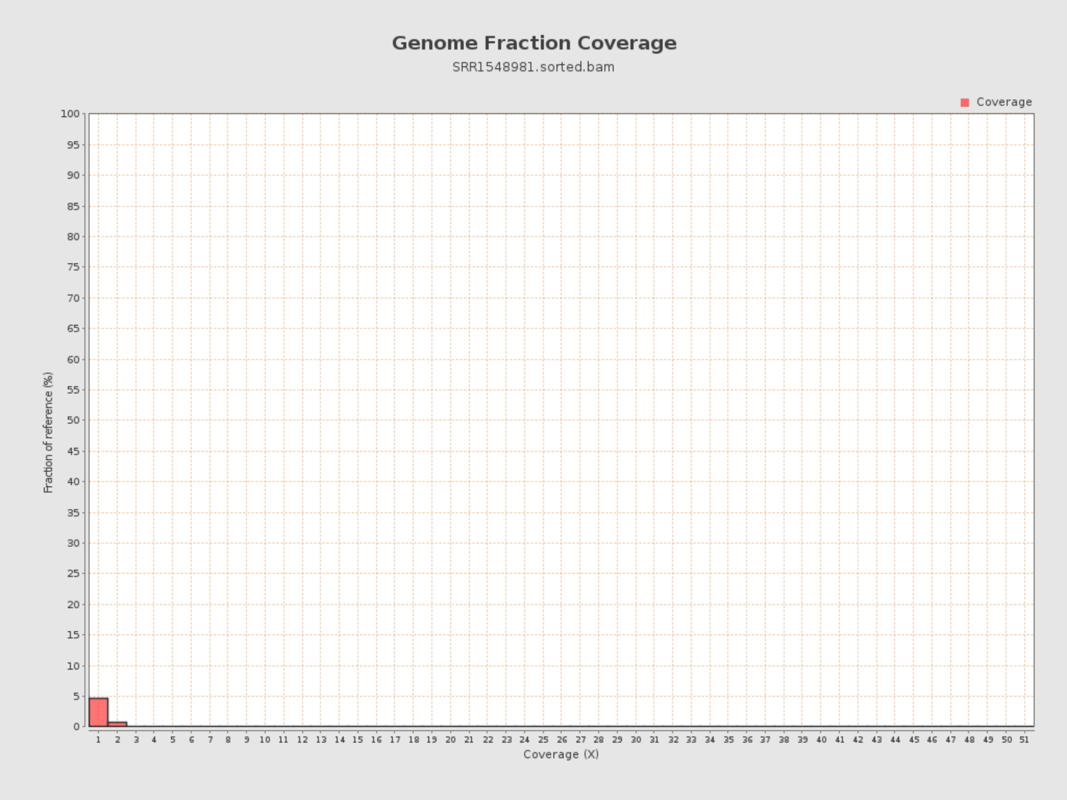
4. Results : Coverage Histogram



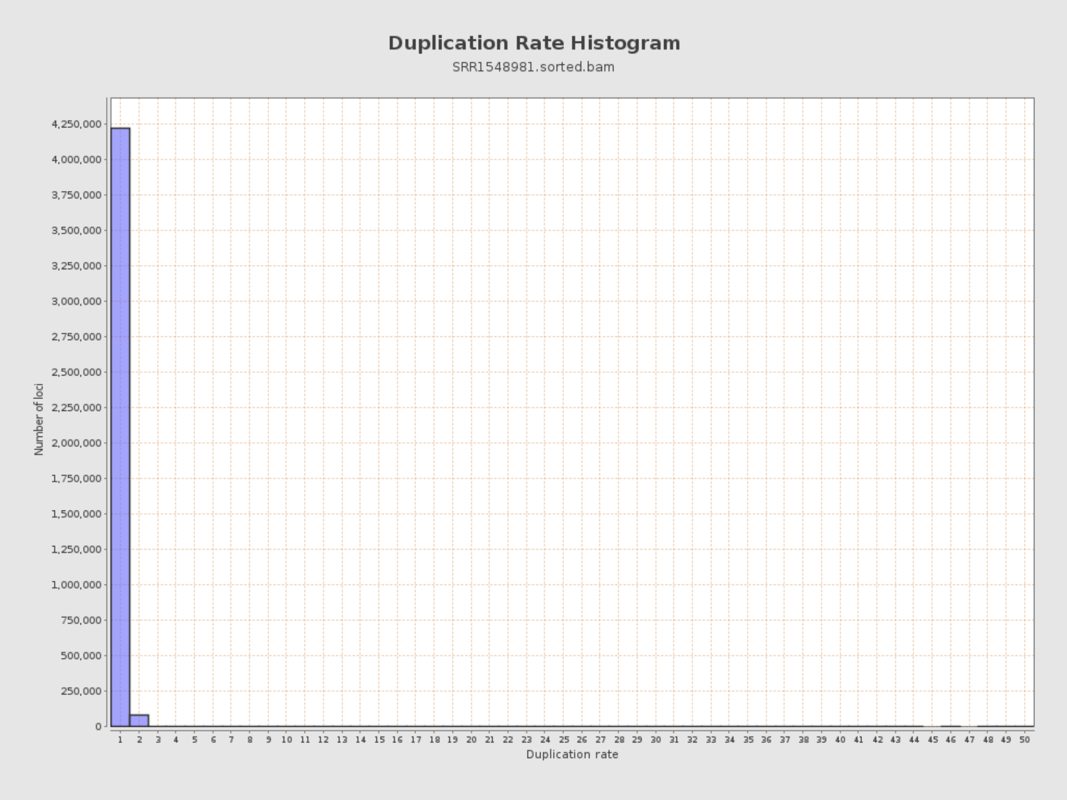
5. Results : Coverage Histogram (0-50X)



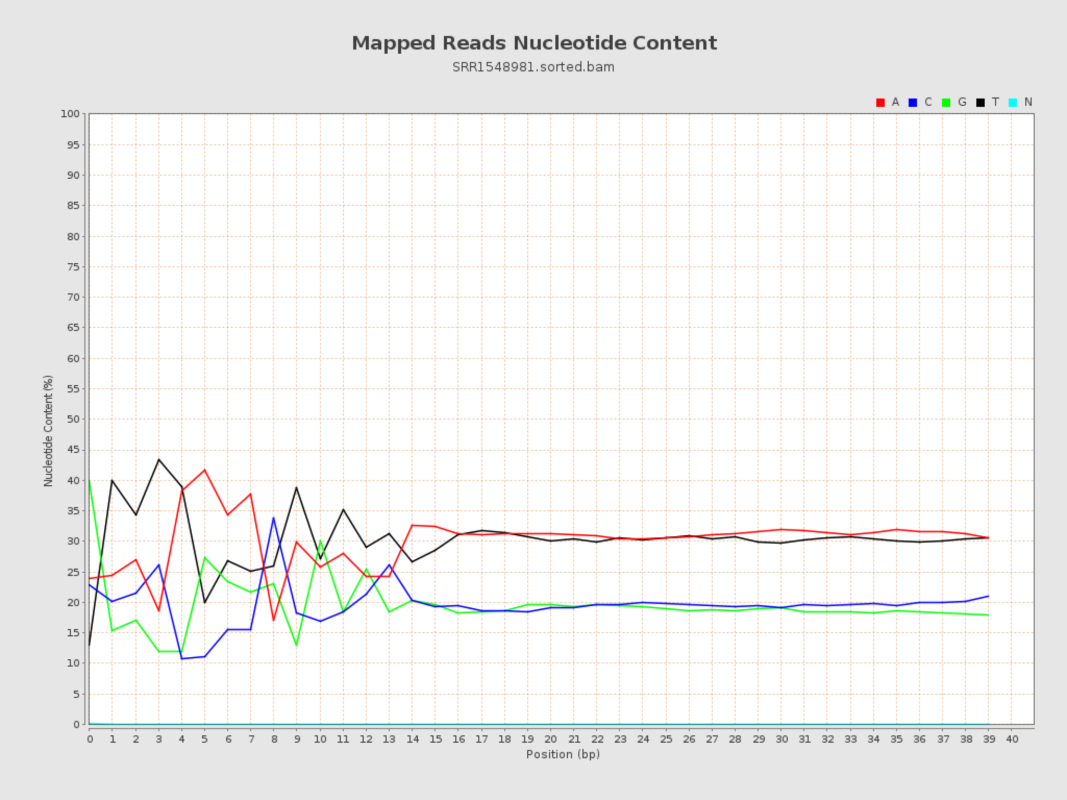
6. Results : Genome Fraction Coverage



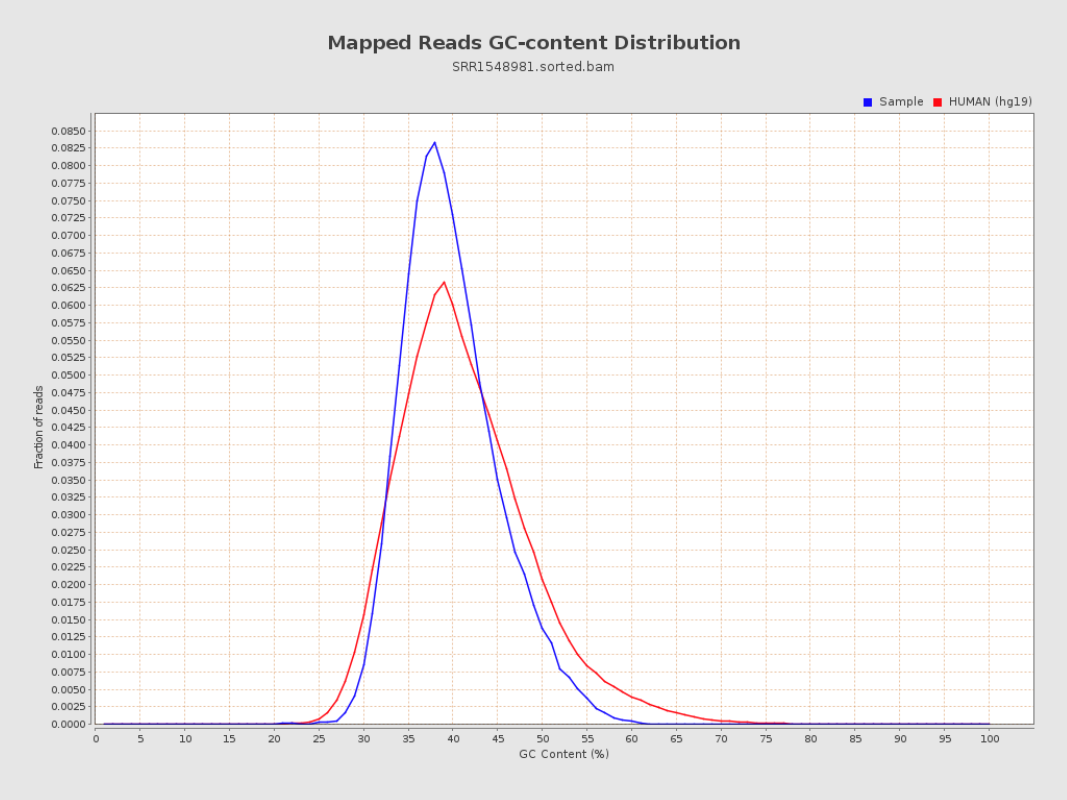
7. Results : Duplication Rate Histogram



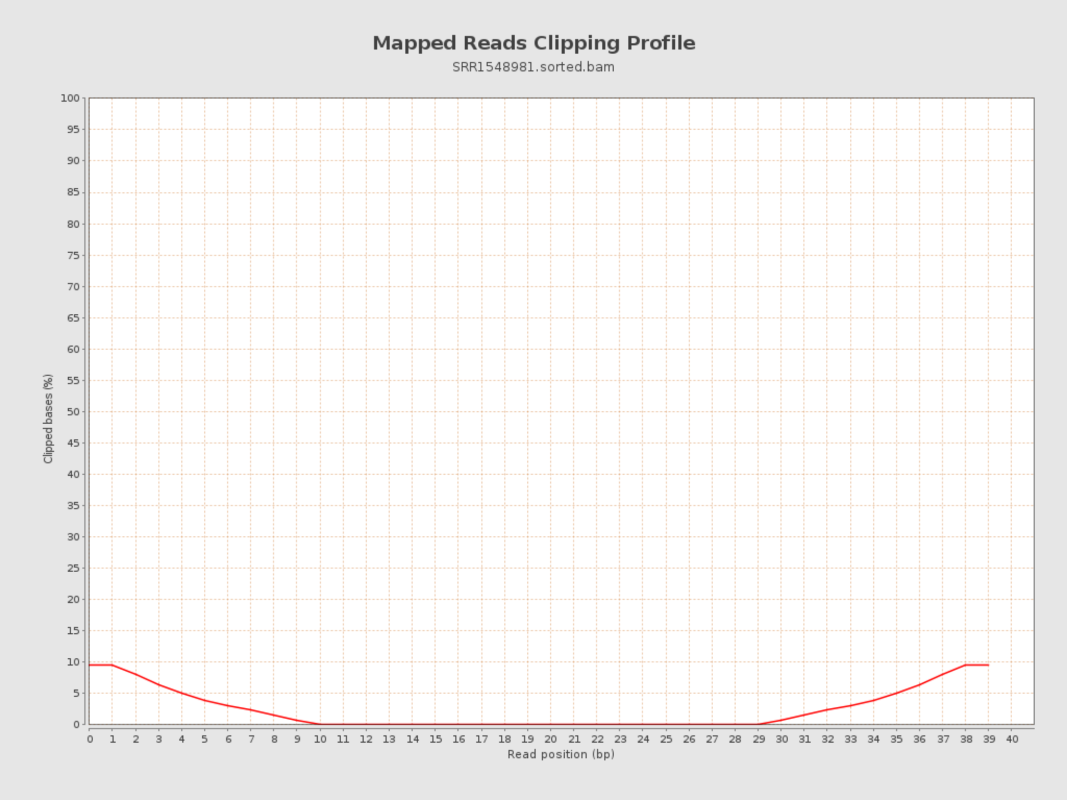
8. Results : Mapped Reads Nucleotide Content



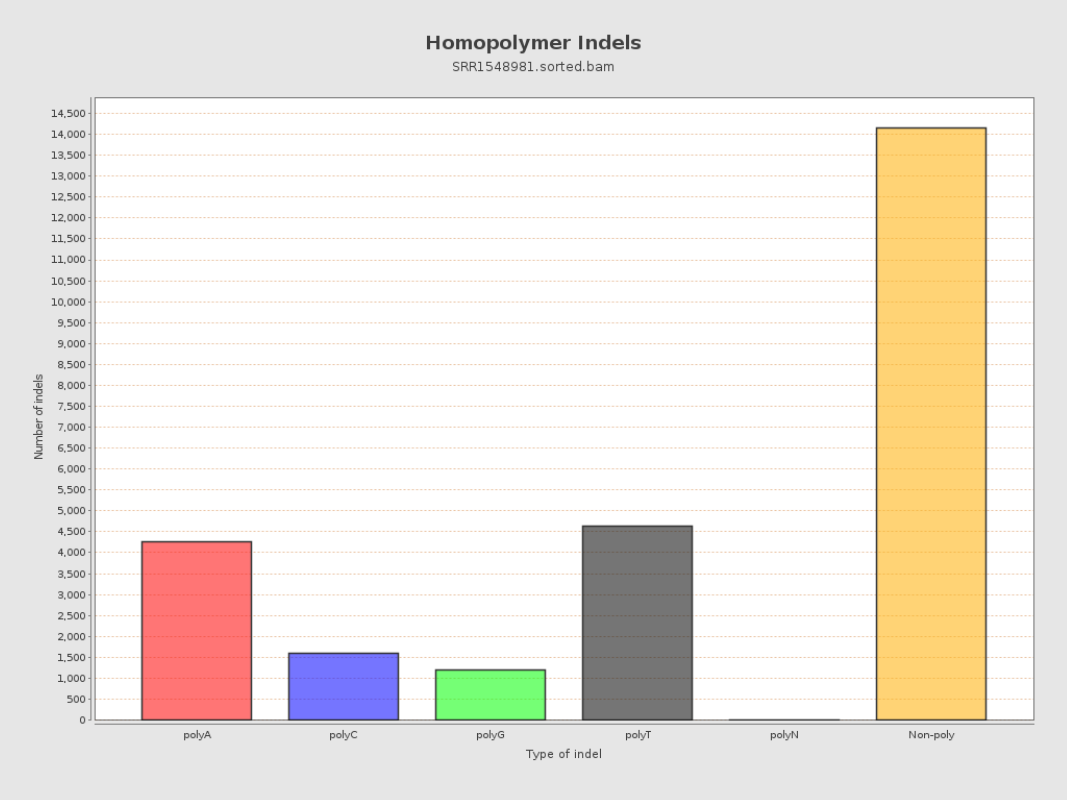
9. Results : Mapped Reads GC-content Distribution



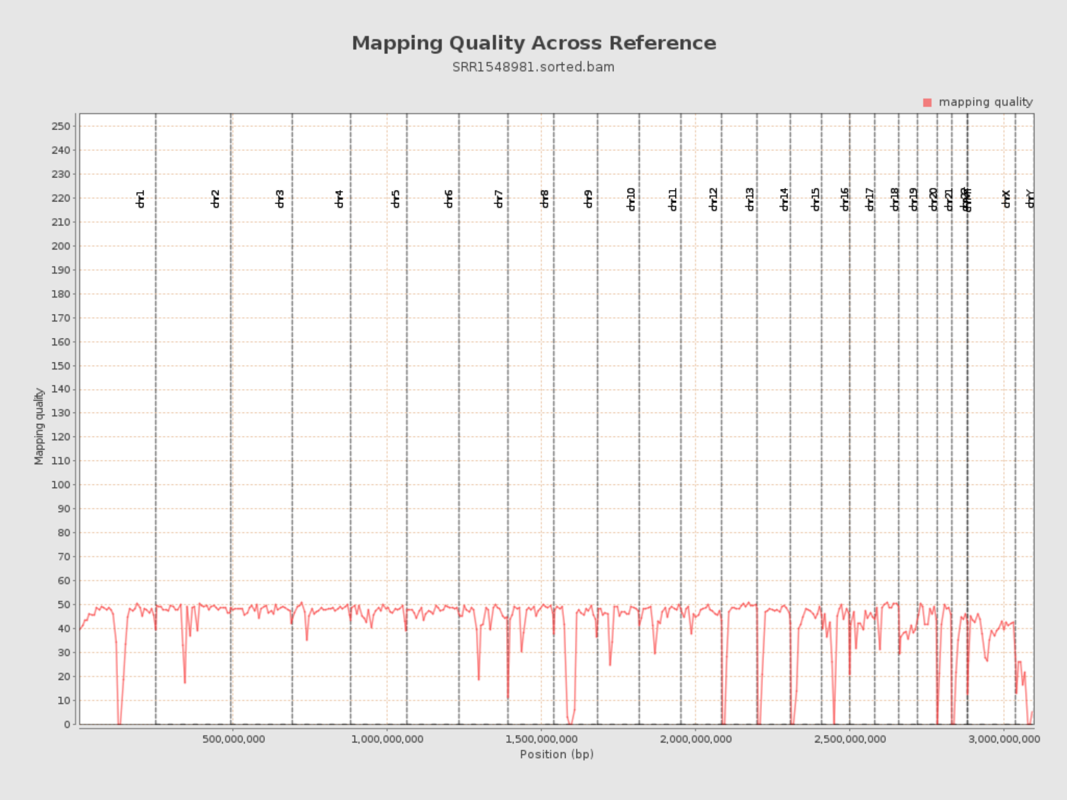
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram