Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 22:00:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505982.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_SRR1505982 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505982.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 22:00:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505982.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,706,033
Mapped reads	6,561,915 / 75.37%
Unmapped reads	2,144,118 / 24.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	224 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	515,852 / 5.93%
Duplication rate	5.71%
Clipped reads	886,869 / 10.19%

2.2. ACGT Content

Number/percentage of A's	92,208,710 / 30.1%
Number/percentage of C's	61,618,432 / 20.12%
Number/percentage of T's	90,090,806 / 29.41%
Number/percentage of G's	62,375,952 / 20.36%
Number/percentage of N's	1,328 / 0%
GC Percentage	40.48%

2.3. Coverage

Mean	0.099

Standard Deviation	0.8842

2.4. Mapping Quality

Mean Mapping Quality	45.41

2.5. Mismatches and indels

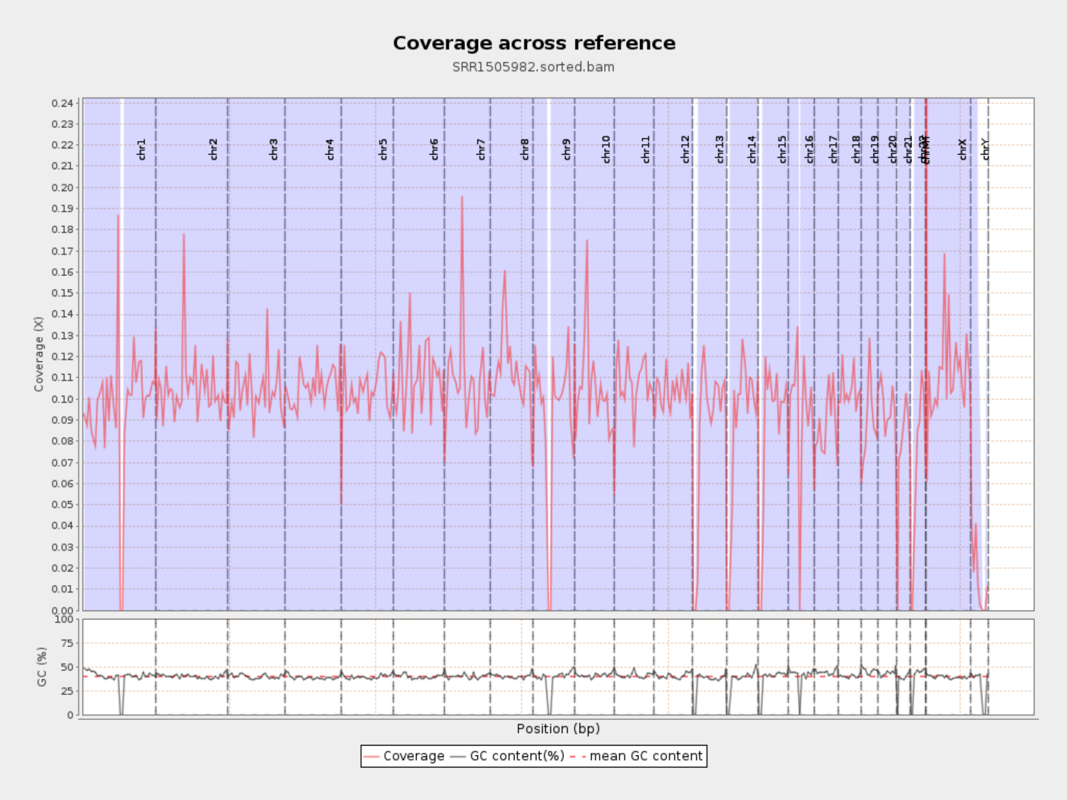
General error rate	0.47%
Mismatches	1,415,629
Insertions	13,542
Mapped reads with at least one insertion	0.21%
Deletions	41,180
Mapped reads with at least one deletion	0.63%
Homopolymer indels	46.61%

2.6. Chromosome stats

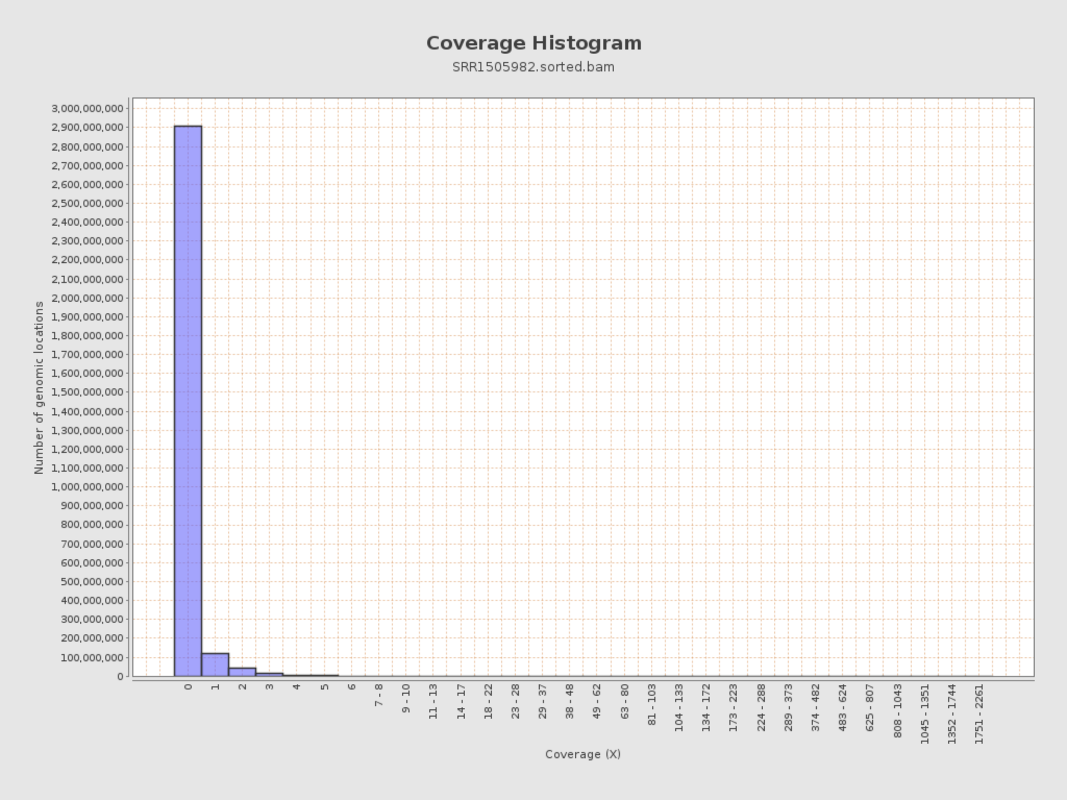
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23941780	0.0961	1.688
chr2	243199373	25629546	0.1054	0.7482
chr3	198022430	20564258	0.1038	0.4908
chr4	191154276	20333056	0.1064	0.4934
chr5	180915260	18965348	0.1048	0.4914
chr6	171115067	18810836	0.1099	0.7359
chr7	159138663	17256836	0.1084	1.158

chr8	146364022	16580564	0.1133	1.3408
chr9	141213431	13066096	0.0925	0.6728
chr10	135534747	14100052	0.104	0.8542
chr11	135006516	14493876	0.1074	0.7737
chr12	133851895	13822629	0.1033	0.5156
chr13	115169878	9790599	0.085	0.4296
chr14	107349540	9309500	0.0867	1.0198
chr15	102531392	8637364	0.0842	0.427
chr16	90354753	8254485	0.0914	0.5128
chr17	81195210	7254327	0.0893	0.5063
chr18	78077248	8137226	0.1042	1.5161
chr19	59128983	5353028	0.0905	1.1799
chr20	63025520	6099181	0.0968	0.4876
chr21	48129895	3711894	0.0771	0.4686
chr22	51304566	3441813	0.0671	0.3769
chrMT	16571	667374	40.2736	23.53
chrX	155270560	17255601	0.1111	0.6055
chrY	59373566	873874	0.0147	0.2299

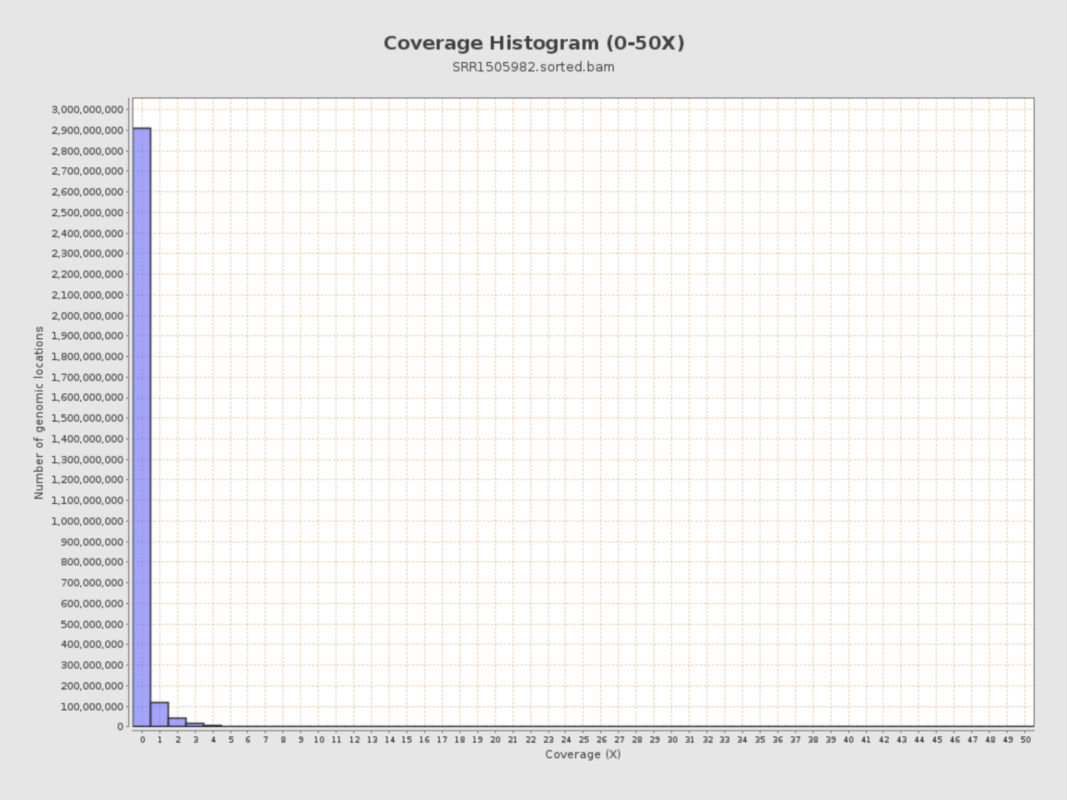
3. Results : Coverage across reference



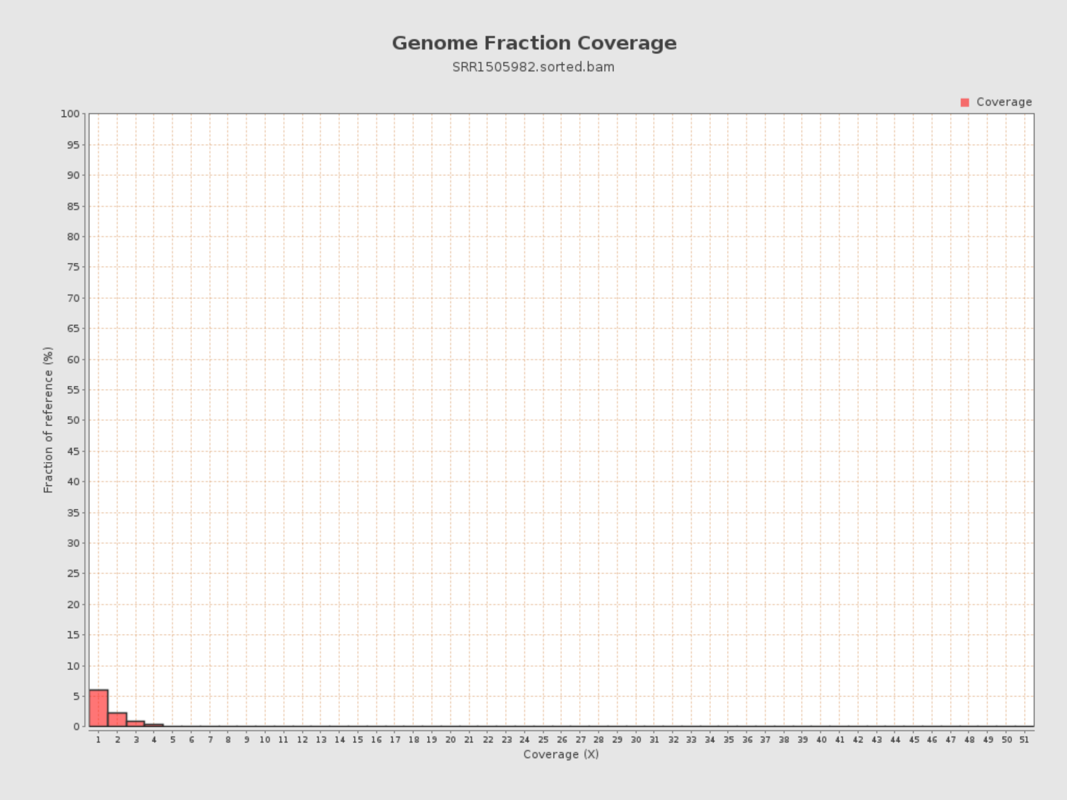
4. Results : Coverage Histogram



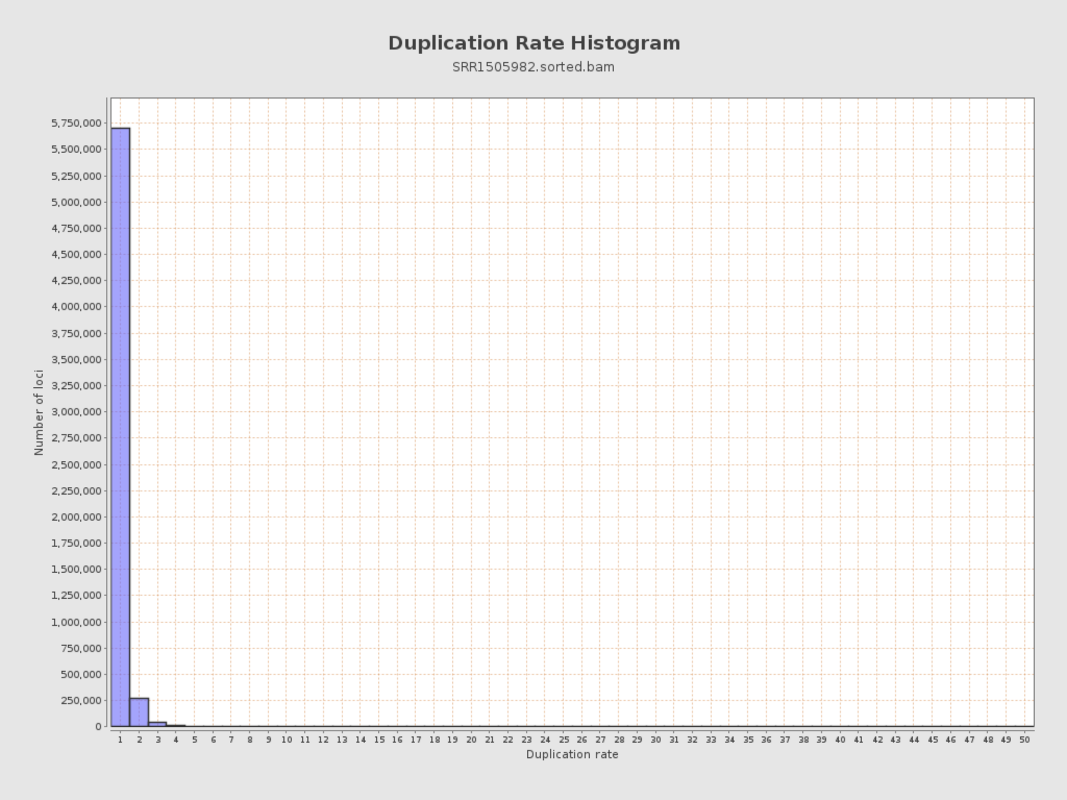
5. Results : Coverage Histogram (0-50X)



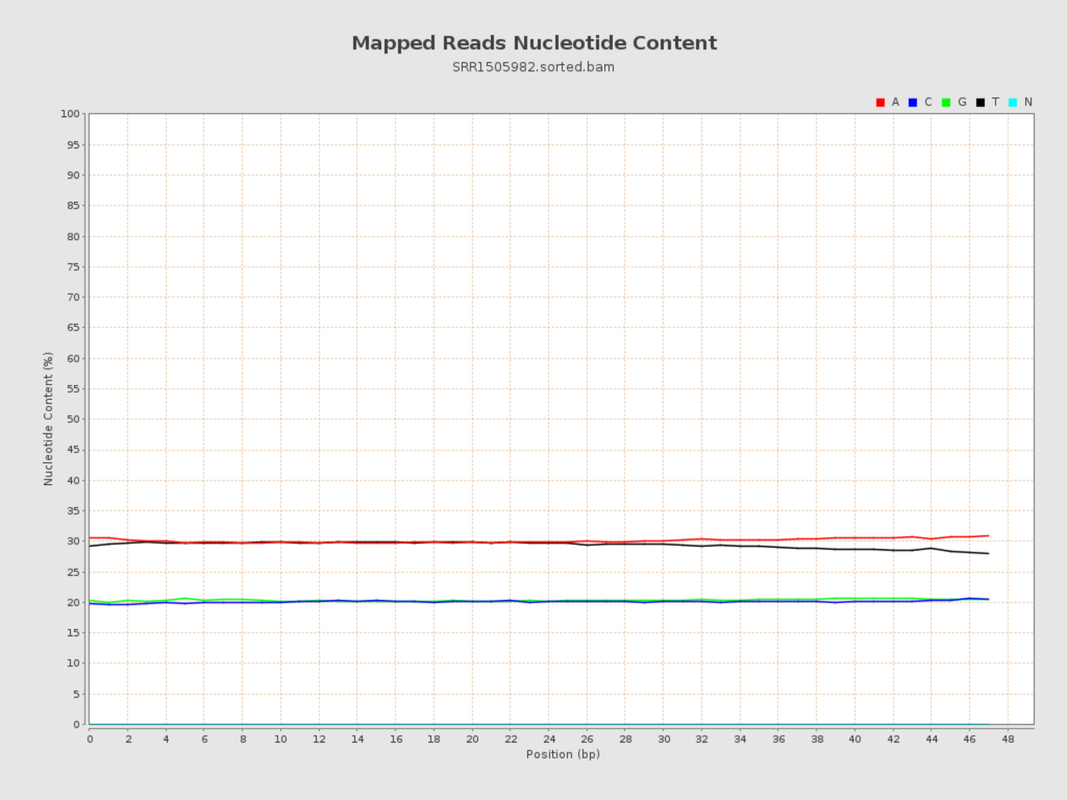
6. Results : Genome Fraction Coverage



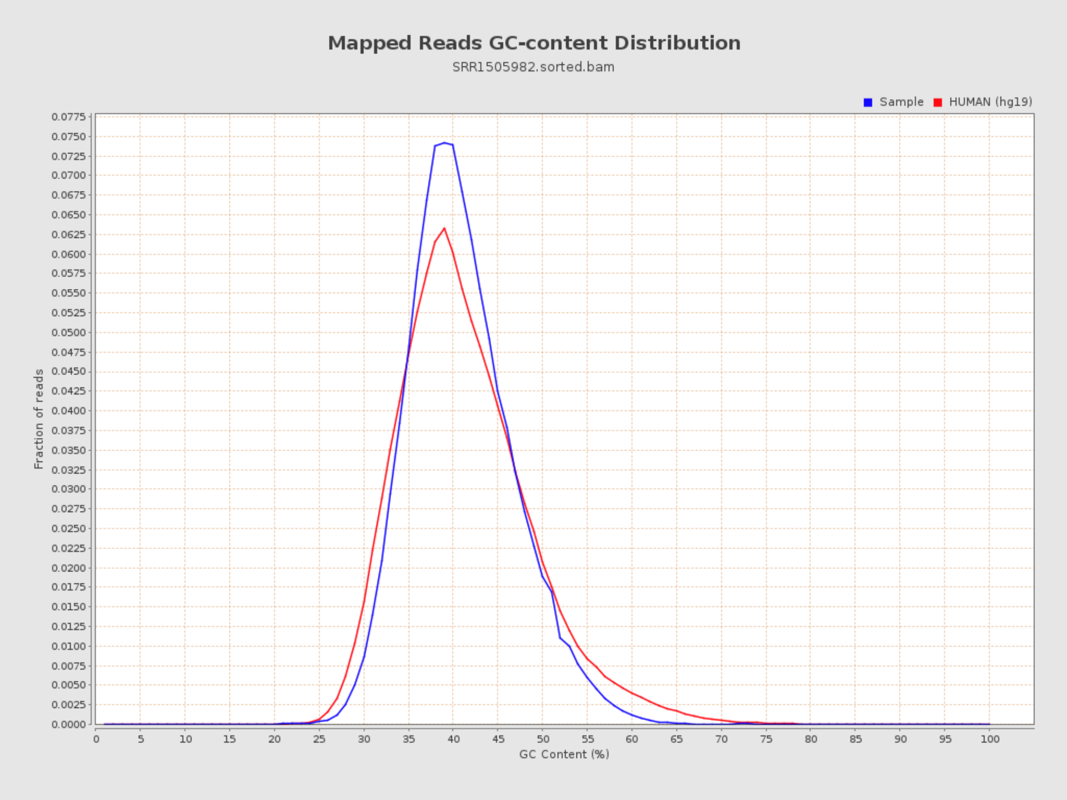
7. Results : Duplication Rate Histogram



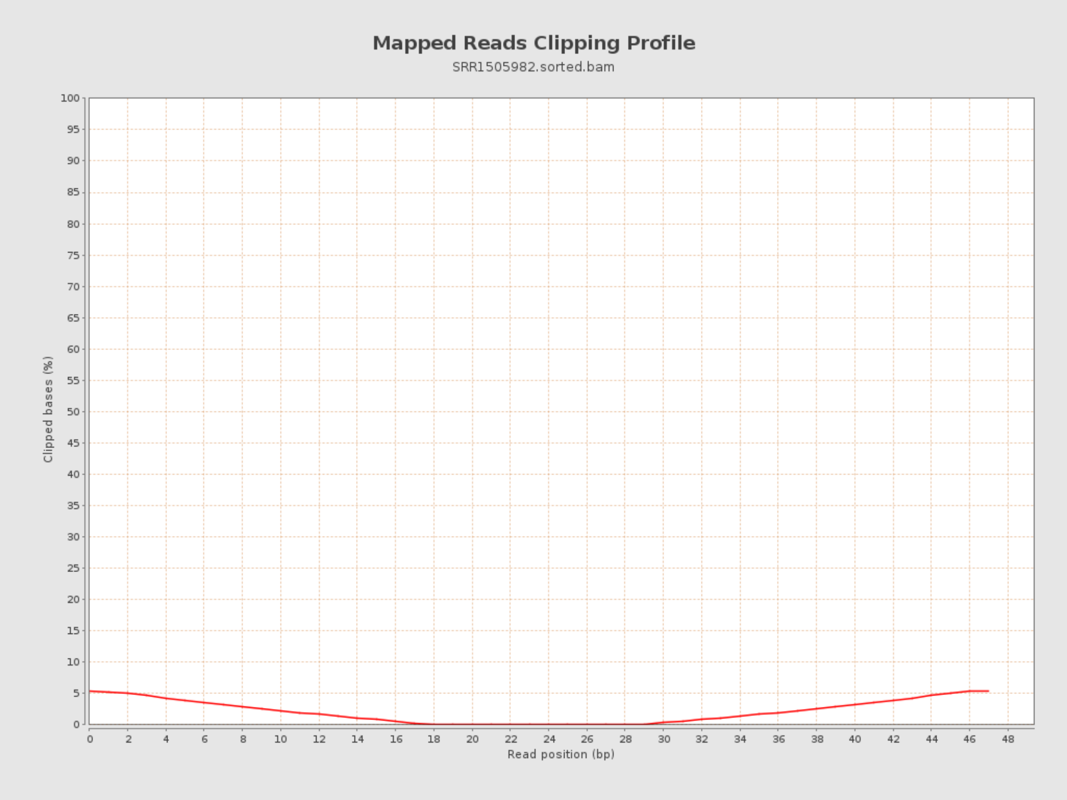
8. Results : Mapped Reads Nucleotide Content



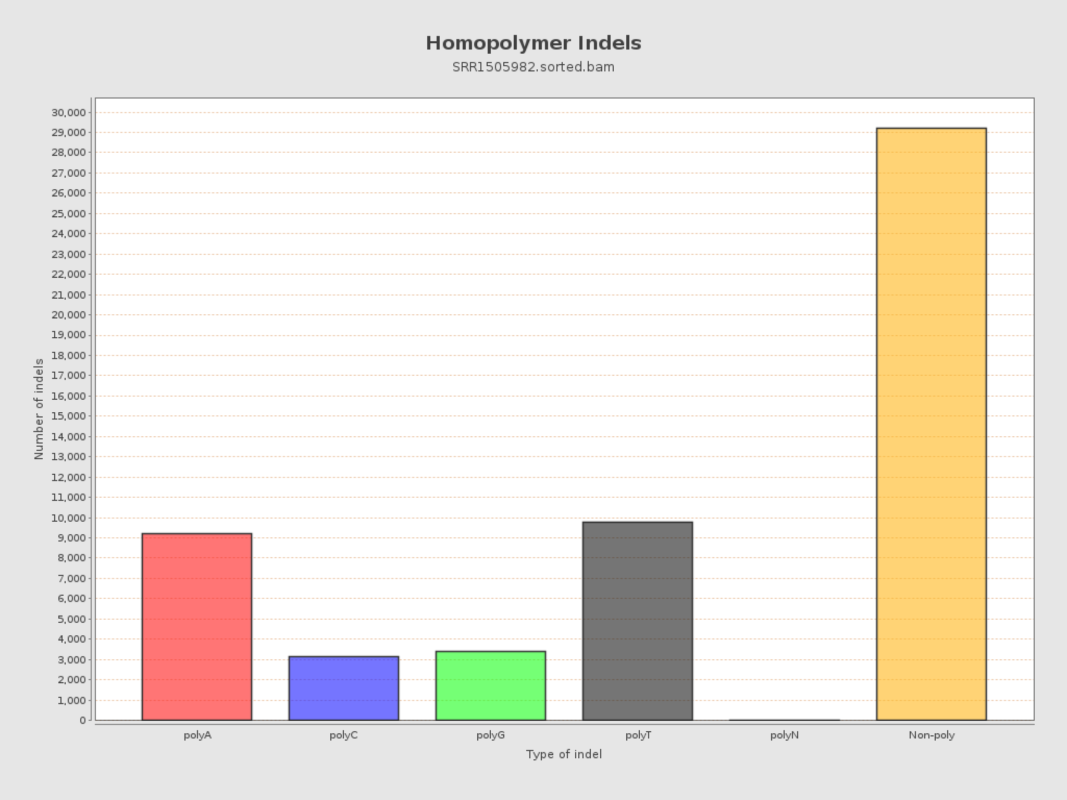
9. Results : Mapped Reads GC-content Distribution



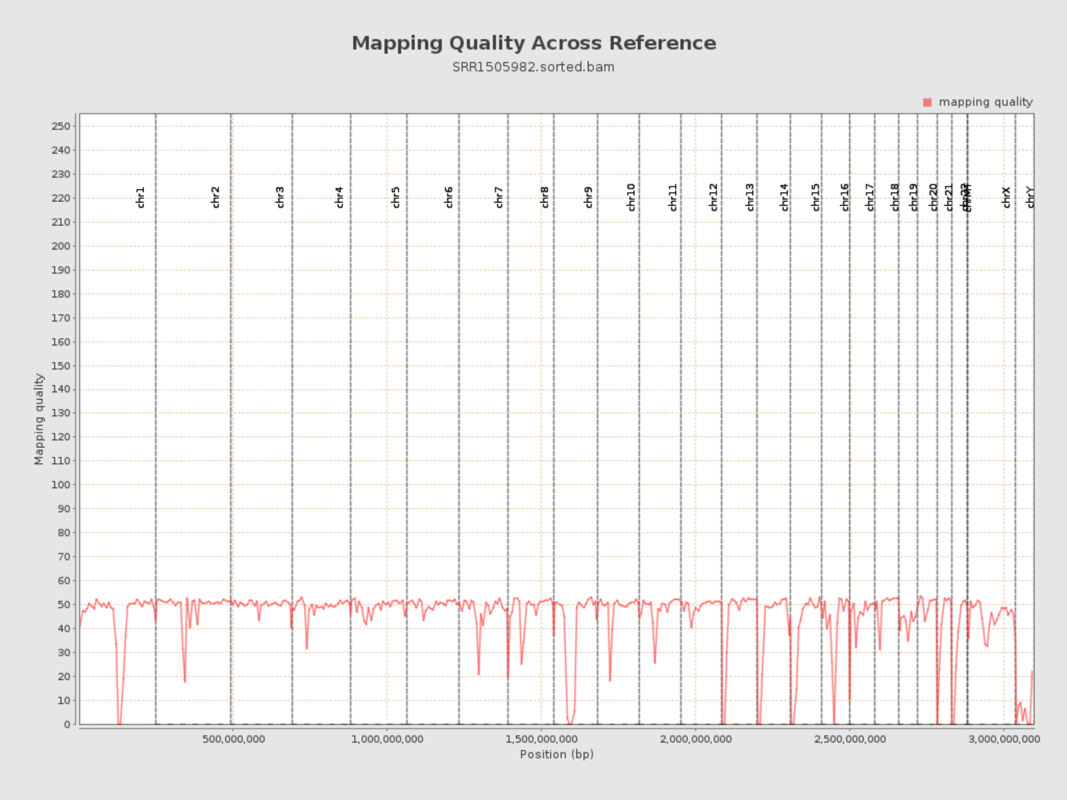
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram