Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:14:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525013.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_SRR10525013 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525013.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:14:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525013.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,047,145
Mapped reads	976,199 / 93.22%
Unmapped reads	70,946 / 6.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,916 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	23,216 / 2.22%
Duplication rate	1.59%
Clipped reads	978,493 / 93.44%

2.2. ACGT Content

Number/percentage of A's	13,393,649 / 23.5%
Number/percentage of C's	10,721,904 / 18.82%
Number/percentage of T's	18,184,260 / 31.91%
Number/percentage of G's	14,685,083 / 25.77%
Number/percentage of N's	566 / 0%
GC Percentage	44.59%

2.3. Coverage

Mean	0.0184

Standard Deviation	0.1949

2.4. Mapping Quality

Mean Mapping Quality	43.69

2.5. Mismatches and indels

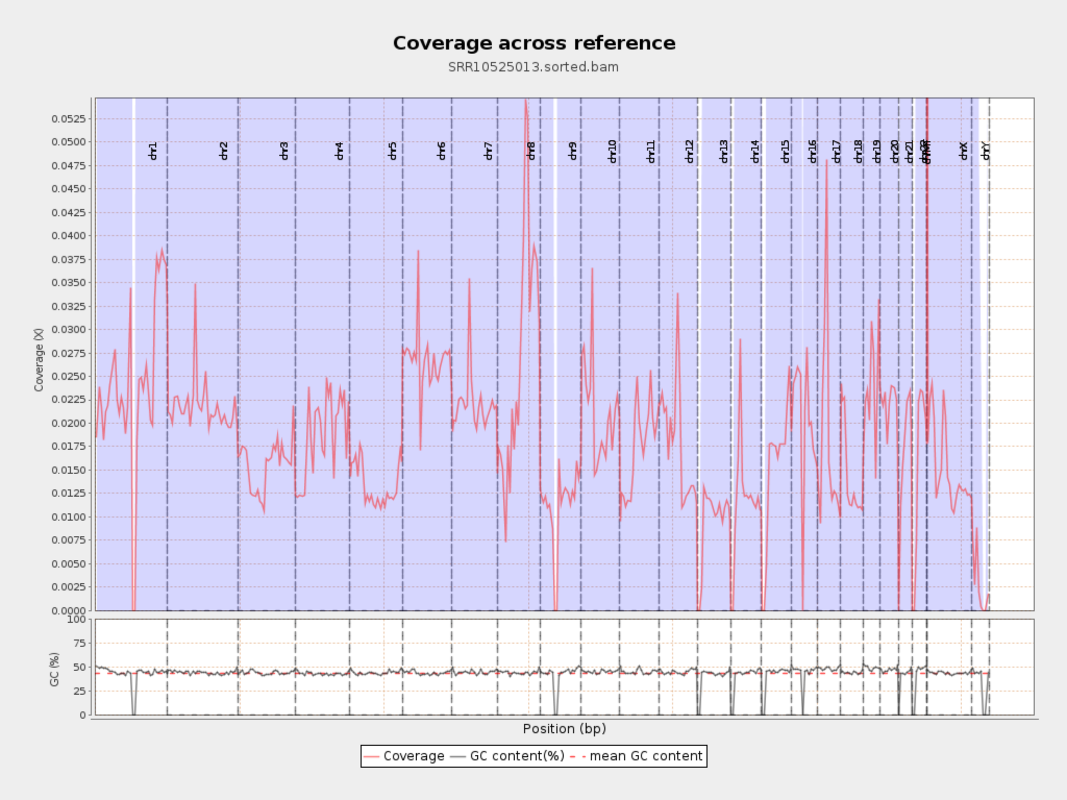
General error rate	0.49%
Mismatches	273,642
Insertions	3,062
Mapped reads with at least one insertion	0.31%
Deletions	11,005
Mapped reads with at least one deletion	1.12%
Homopolymer indels	45.6%

2.6. Chromosome stats

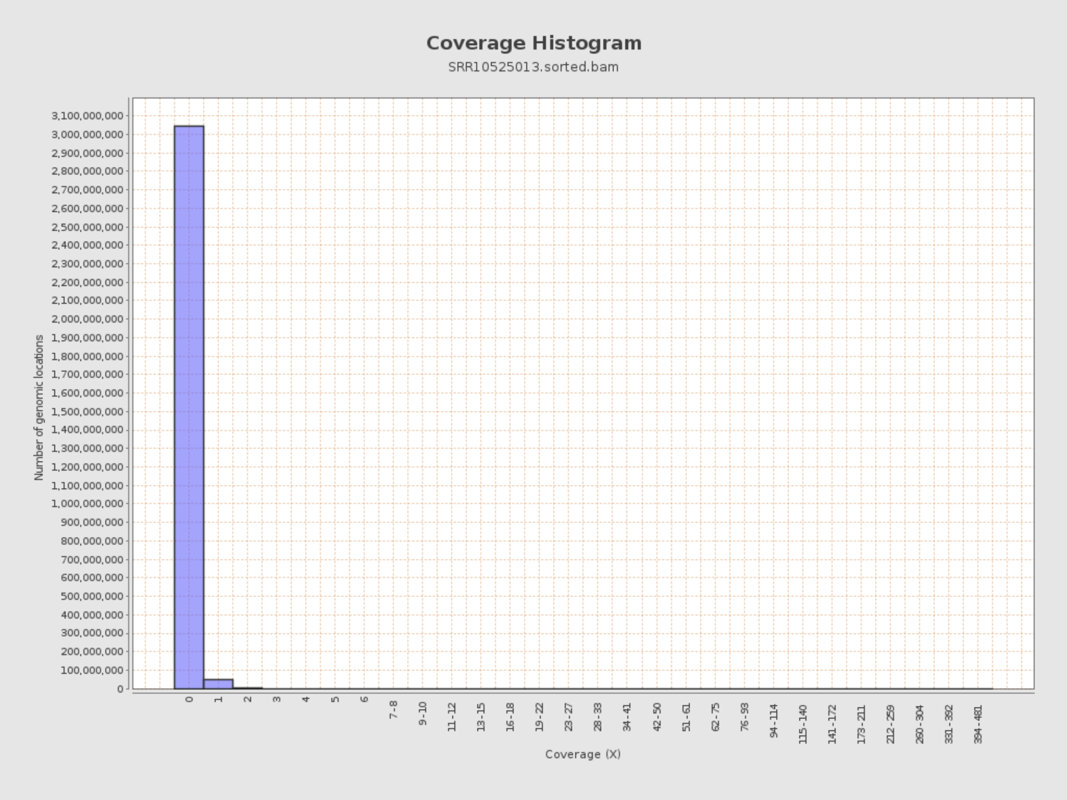
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5991573	0.024	0.3534
chr2	243199373	5296540	0.0218	0.2263
chr3	198022430	3082620	0.0156	0.133
chr4	191154276	3587824	0.0188	0.1522
chr5	180915260	2420908	0.0134	0.1246
chr6	171115067	4569561	0.0267	0.2212
chr7	159138663	3520640	0.0221	0.2543

chr8	146364022	4008877	0.0274	0.2022
chr9	141213431	1567961	0.0111	0.1466
chr10	135534747	2888385	0.0213	0.1924
chr11	135006516	2367757	0.0175	0.1777
chr12	133851895	2392492	0.0179	0.1421
chr13	115169878	1081536	0.0094	0.1017
chr14	107349540	1264009	0.0118	0.1151
chr15	102531392	1566933	0.0153	0.1359
chr16	90354753	1823047	0.0202	0.1557
chr17	81195210	1499031	0.0185	0.1807
chr18	78077248	1114791	0.0143	0.2192
chr19	59128983	1428772	0.0242	0.2369
chr20	63025520	1386353	0.022	0.1566
chr21	48129895	805753	0.0167	0.1401
chr22	51304566	784324	0.0153	0.1293
chrMT	16571	6443	0.3888	0.6868
chrX	155270560	2384171	0.0154	0.147
chrY	59373566	163701	0.0028	0.0802

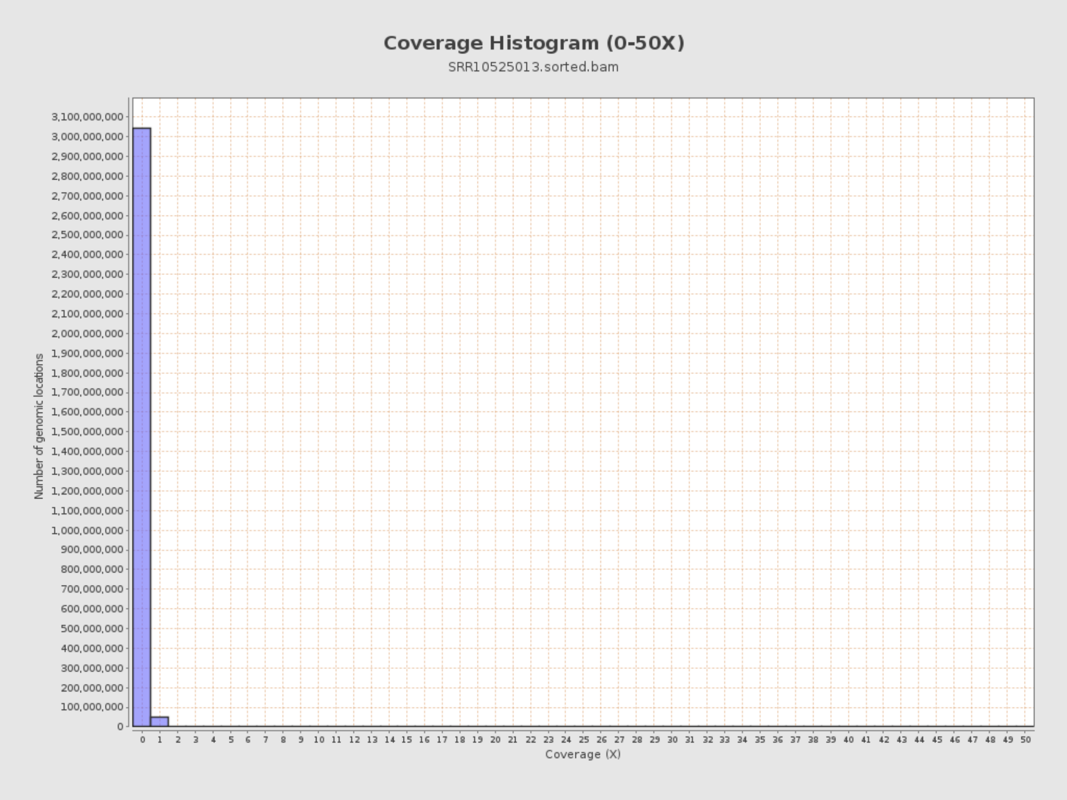
3. Results : Coverage across reference



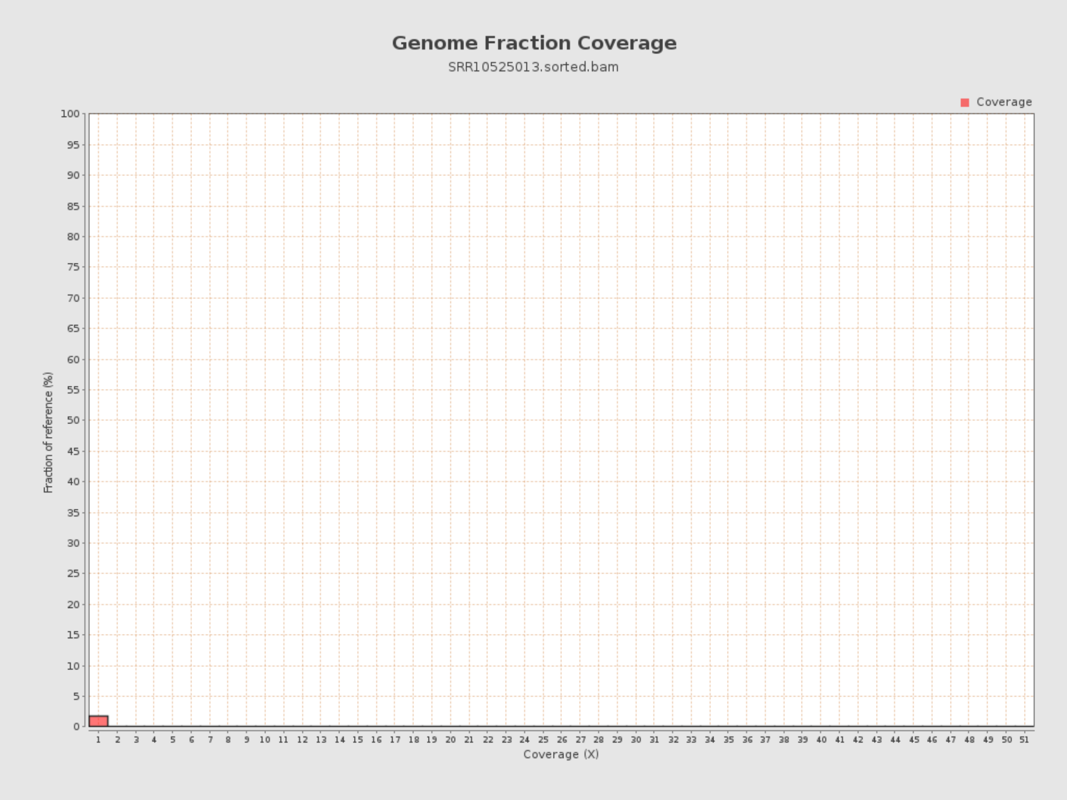
4. Results : Coverage Histogram



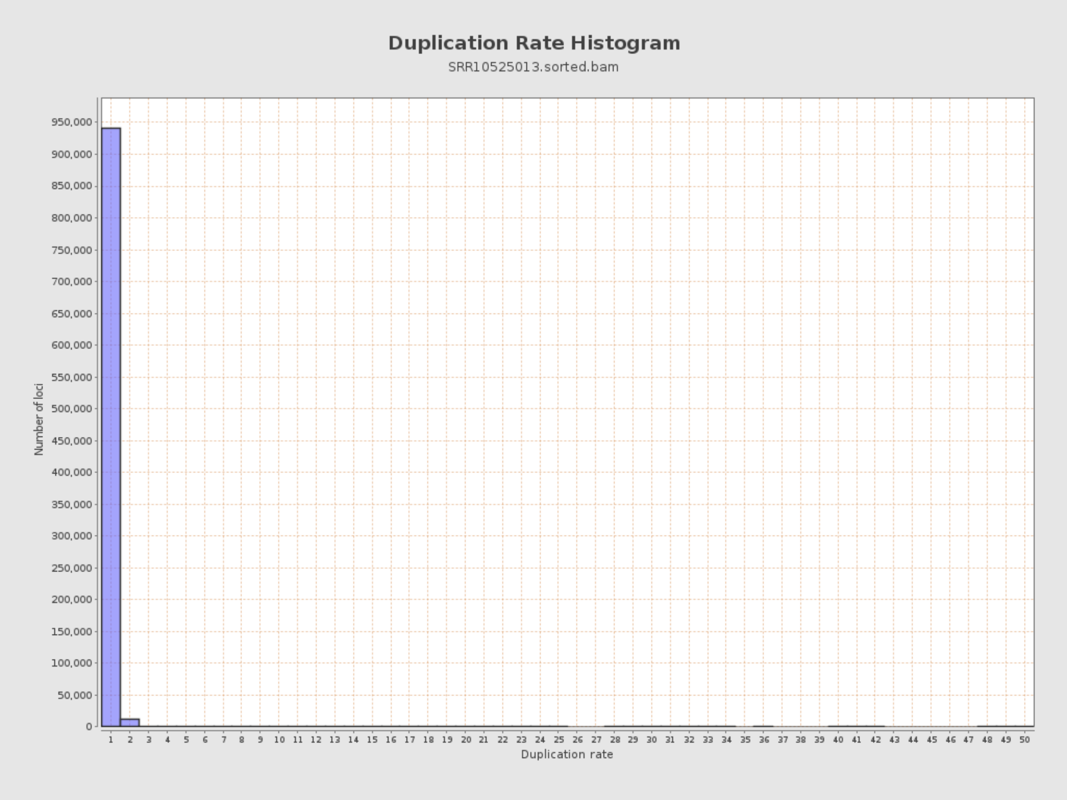
5. Results : Coverage Histogram (0-50X)



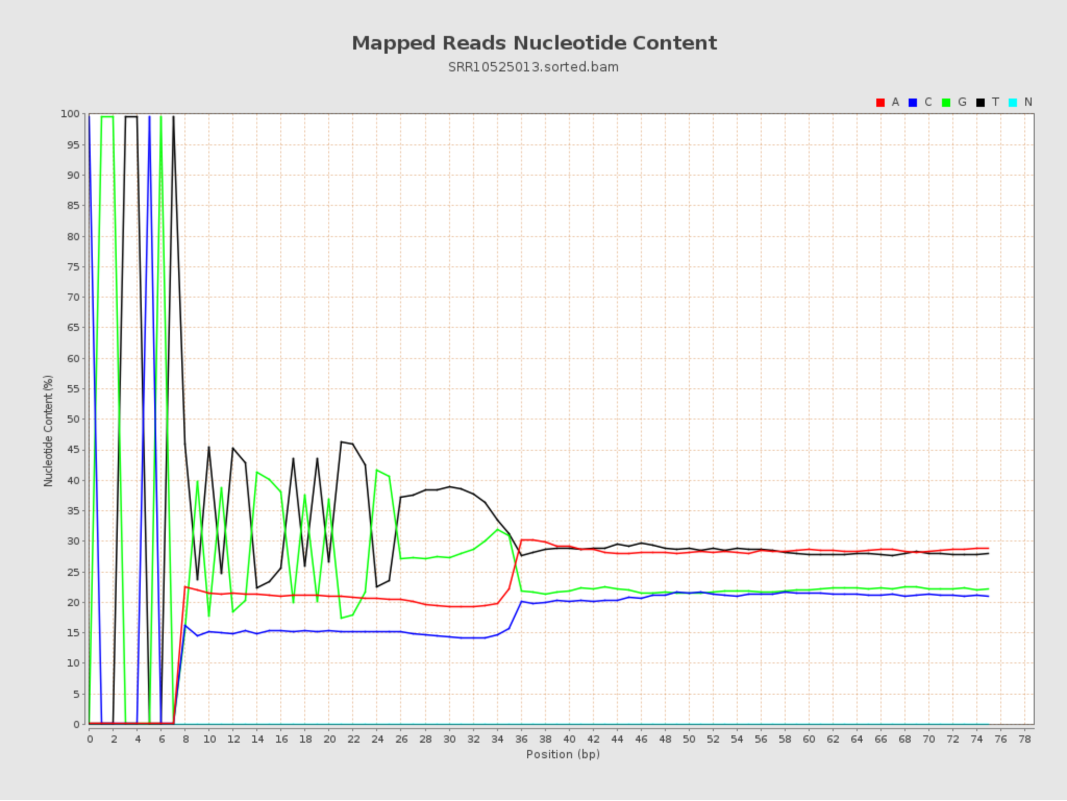
6. Results : Genome Fraction Coverage



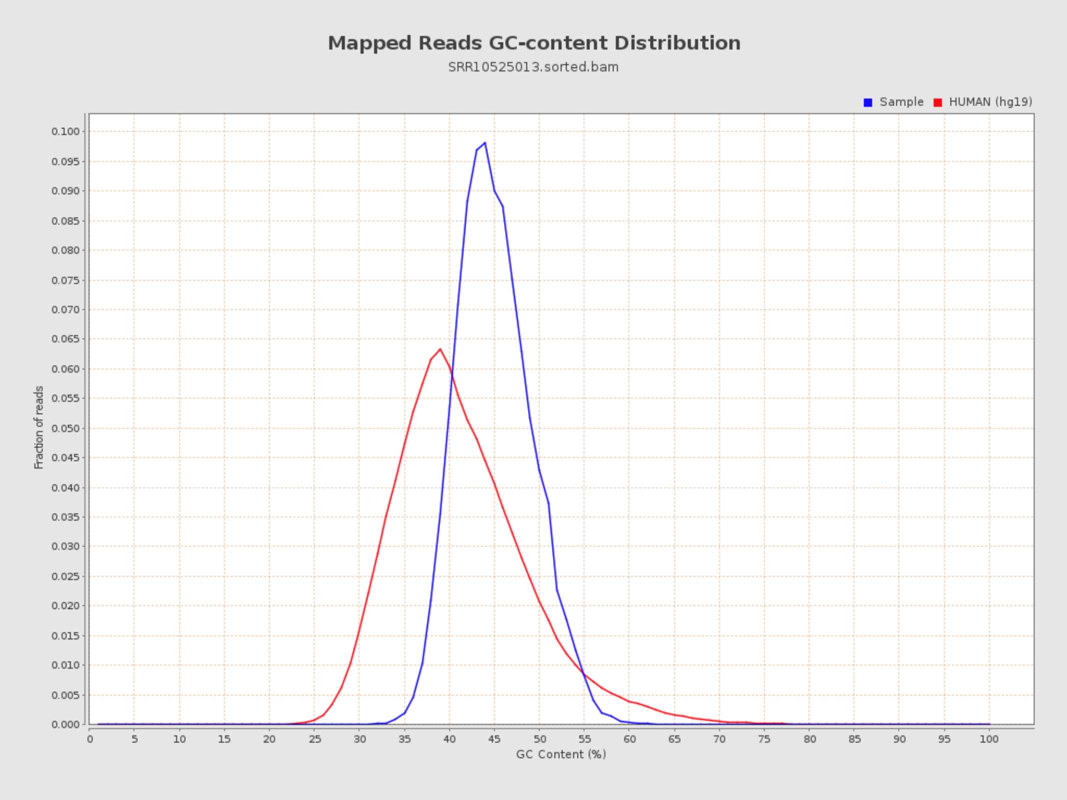
7. Results : Duplication Rate Histogram



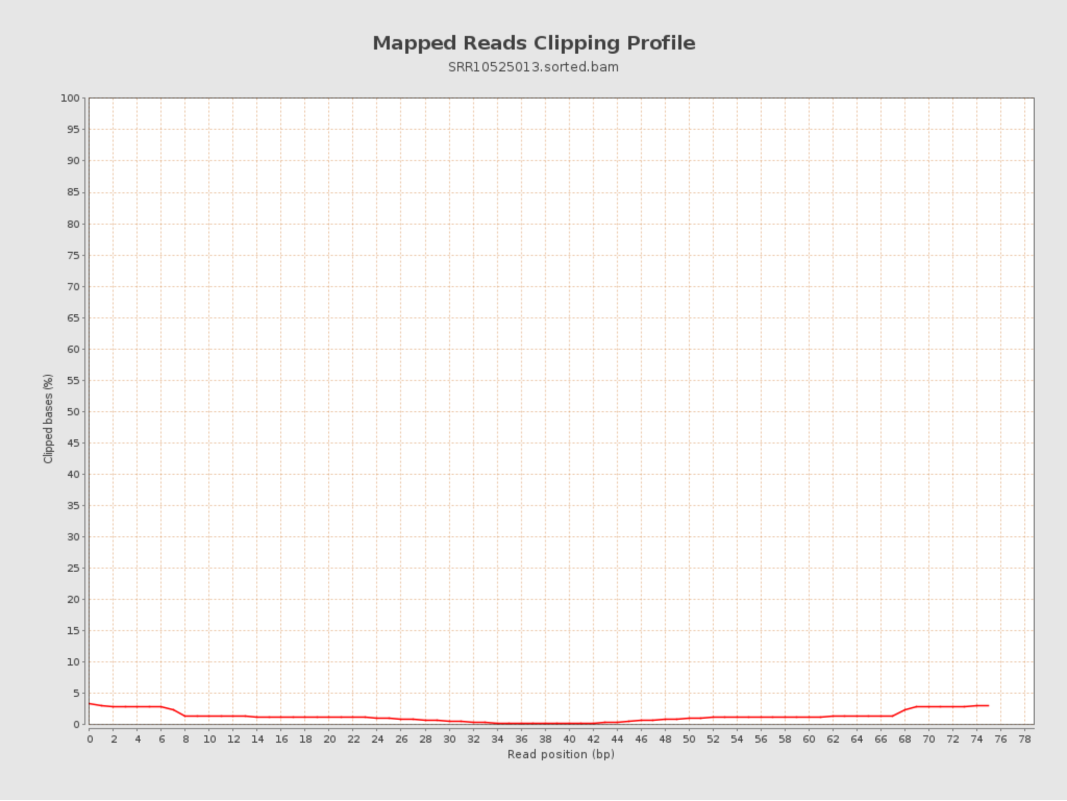
8. Results : Mapped Reads Nucleotide Content



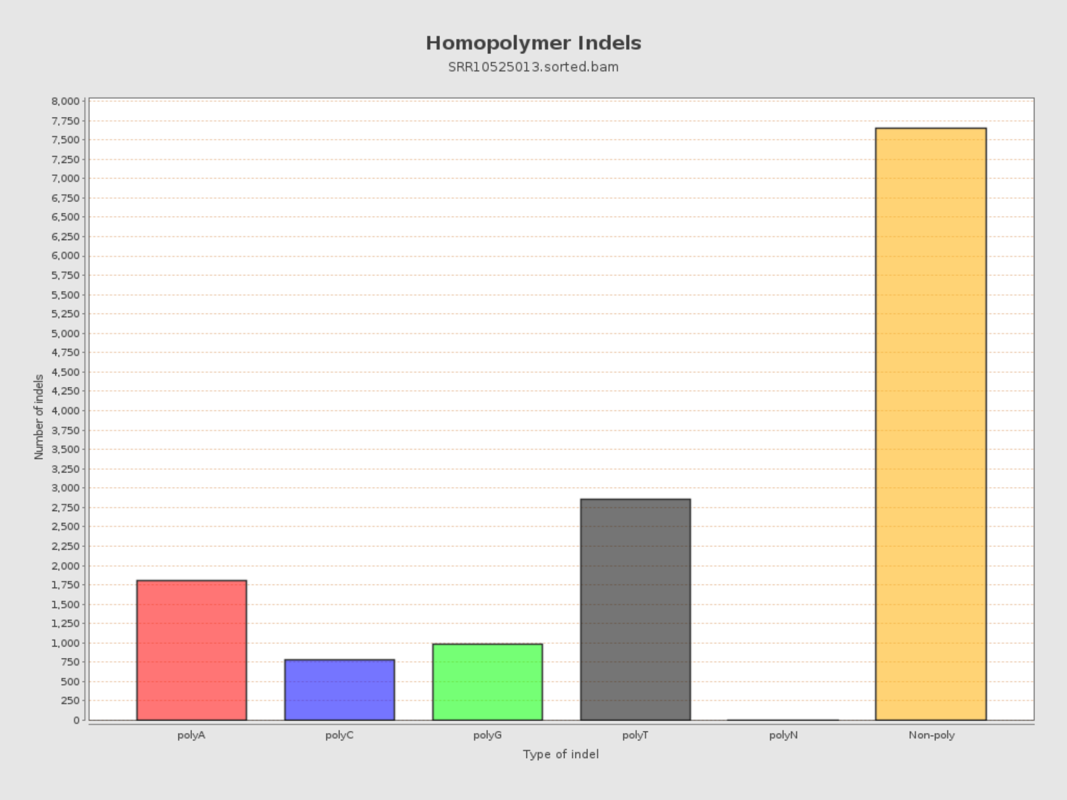
9. Results : Mapped Reads GC-content Distribution



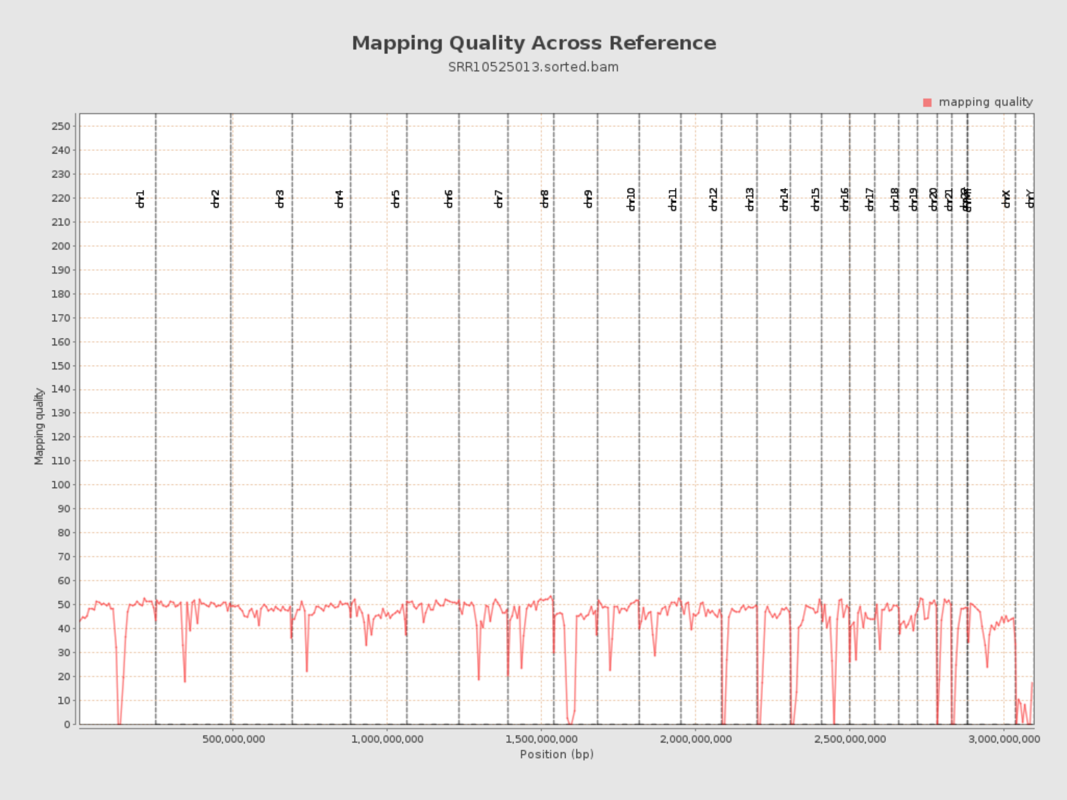
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram