Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:09:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525087.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_SRR10525087 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525087.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:09:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525087.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,236,243
Mapped reads	1,128,190 / 91.26%
Unmapped reads	108,053 / 8.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,282 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	49,506 / 4%
Duplication rate	3.58%
Clipped reads	1,131,198 / 91.5%

2.2. ACGT Content

Number/percentage of A's	16,359,628 / 24.87%
Number/percentage of C's	11,705,126 / 17.79%
Number/percentage of T's	20,599,306 / 31.31%
Number/percentage of G's	17,120,206 / 26.02%
Number/percentage of N's	6,966 / 0.01%
GC Percentage	43.81%

2.3. Coverage

Mean	0.0213

Standard Deviation	0.2089

2.4. Mapping Quality

Mean Mapping Quality	45.91

2.5. Mismatches and indels

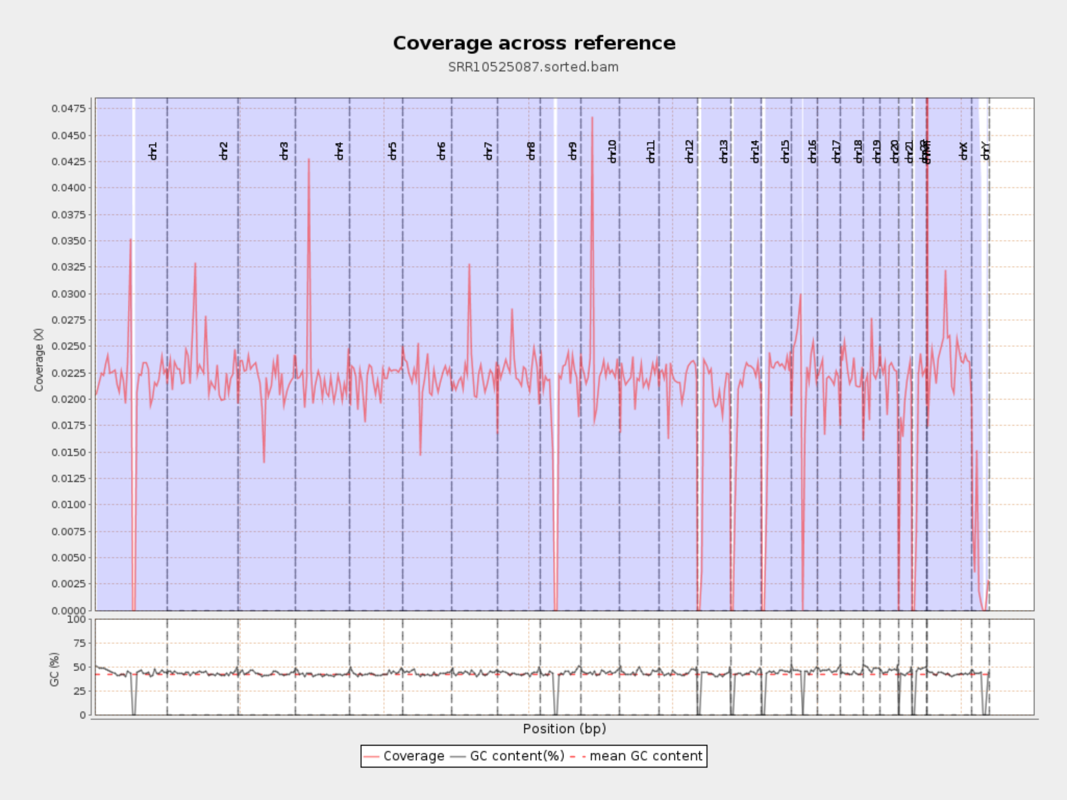
General error rate	0.49%
Mismatches	313,566
Insertions	3,969
Mapped reads with at least one insertion	0.35%
Deletions	12,773
Mapped reads with at least one deletion	1.12%
Homopolymer indels	44.23%

2.6. Chromosome stats

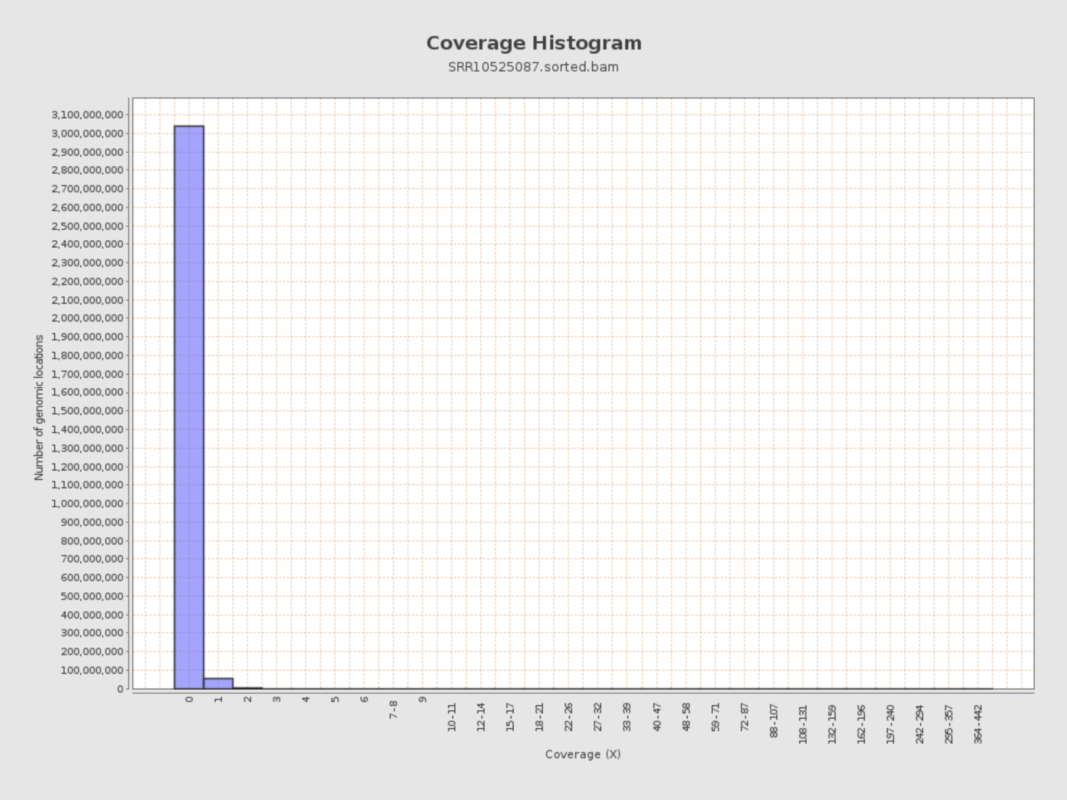
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5266016	0.0211	0.3505
chr2	243199373	5565710	0.0229	0.2511
chr3	198022430	4318554	0.0218	0.1611
chr4	191154276	4274409	0.0224	0.1844
chr5	180915260	3974502	0.022	0.1609
chr6	171115067	3777958	0.0221	0.1707
chr7	159138663	3575766	0.0225	0.2435

chr8	146364022	3342701	0.0228	0.2058
chr9	141213431	2755708	0.0195	0.1769
chr10	135534747	3193789	0.0236	0.2437
chr11	135006516	2976786	0.022	0.1815
chr12	133851895	2947560	0.022	0.1633
chr13	115169878	2049015	0.0178	0.1455
chr14	107349540	2006683	0.0187	0.1517
chr15	102531392	1946989	0.019	0.1528
chr16	90354753	1956834	0.0217	0.1696
chr17	81195210	1750906	0.0216	0.1637
chr18	78077248	1772658	0.0227	0.2718
chr19	59128983	1314009	0.0222	0.2475
chr20	63025520	1407167	0.0223	0.1665
chr21	48129895	880197	0.0183	0.1662
chr22	51304566	807916	0.0157	0.1382
chrMT	16571	4517	0.2726	0.5939
chrX	155270560	3716408	0.0239	0.1828
chrY	59373566	229501	0.0039	0.1312

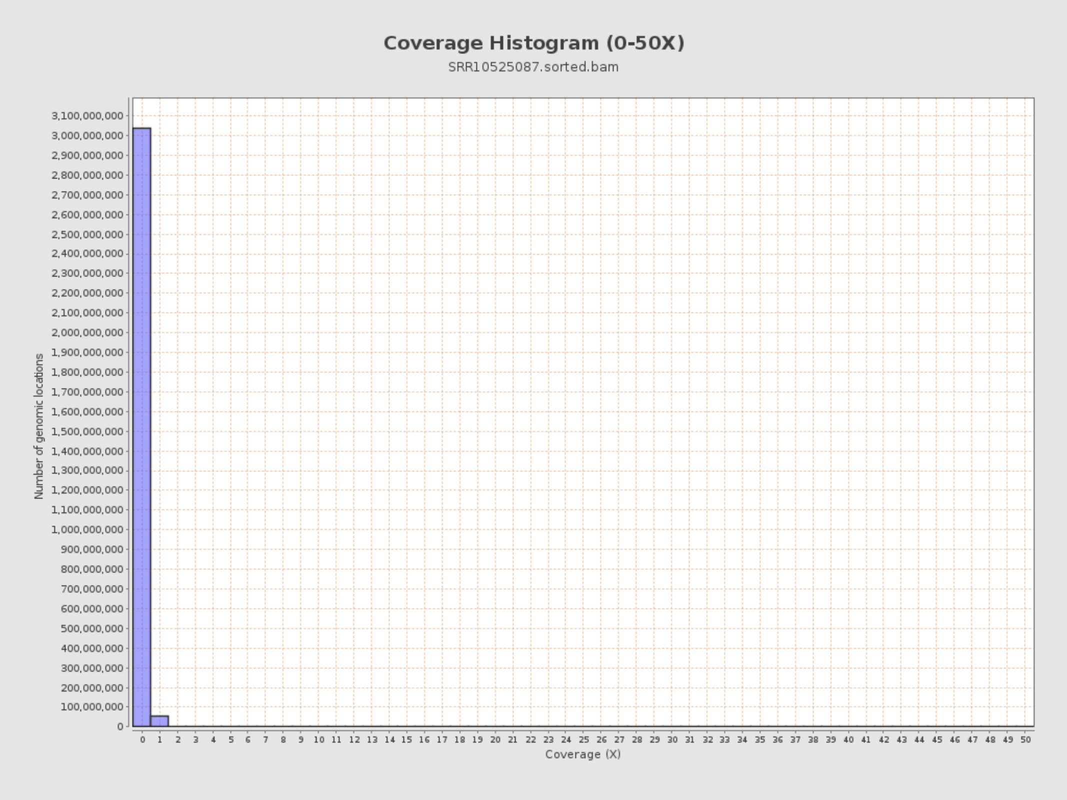
3. Results : Coverage across reference



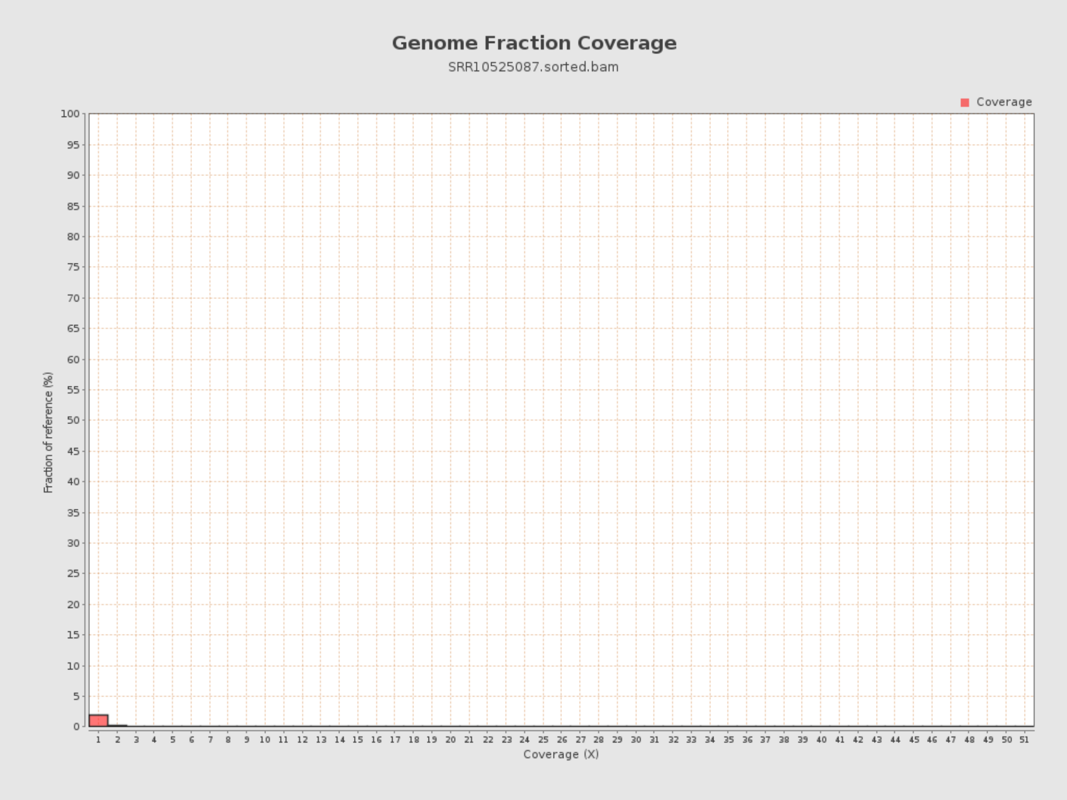
4. Results : Coverage Histogram



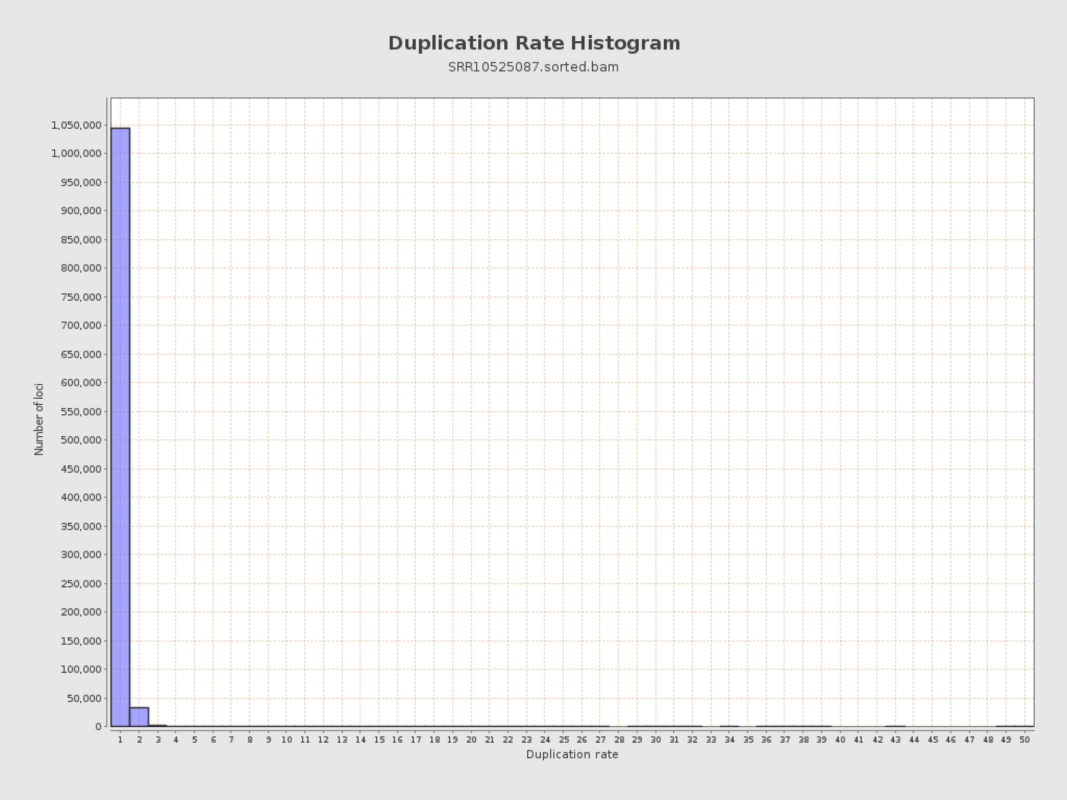
5. Results : Coverage Histogram (0-50X)



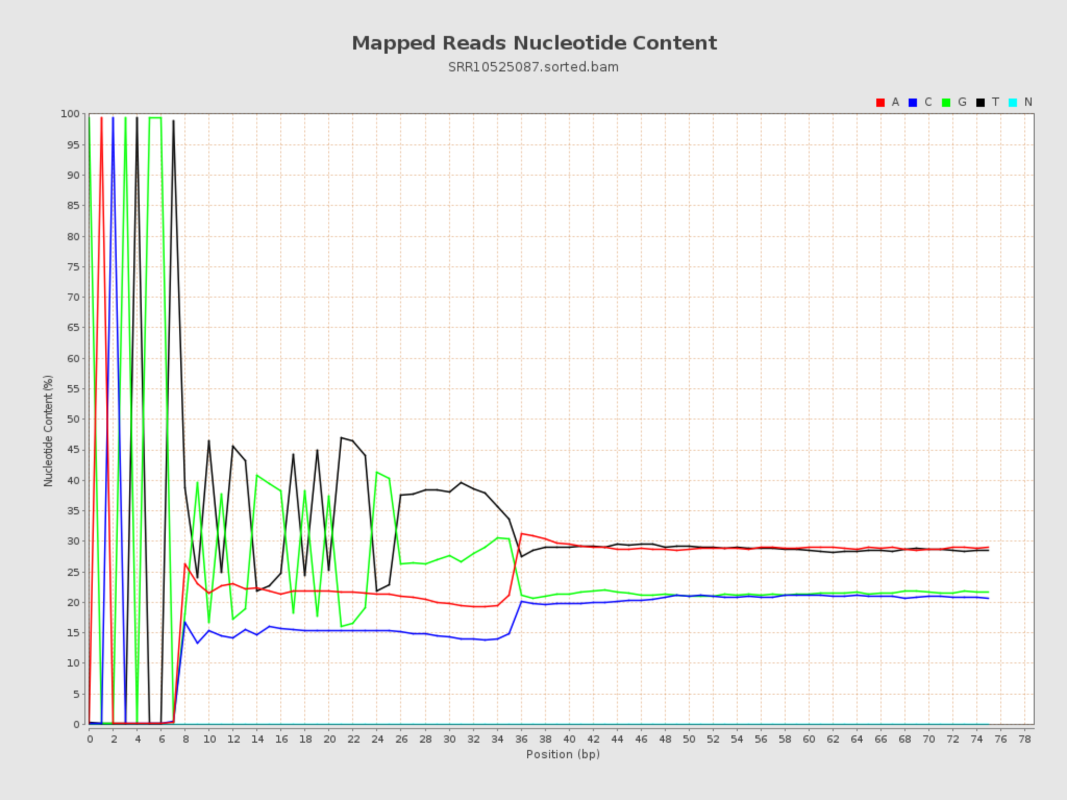
6. Results : Genome Fraction Coverage



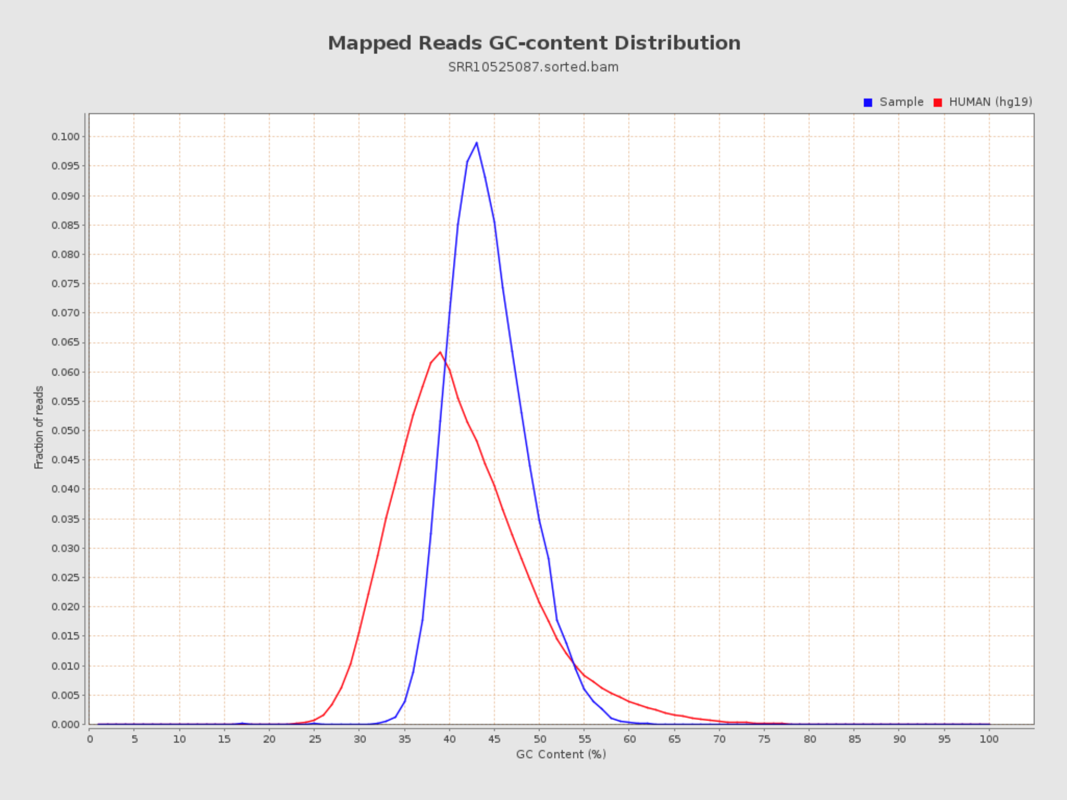
7. Results : Duplication Rate Histogram



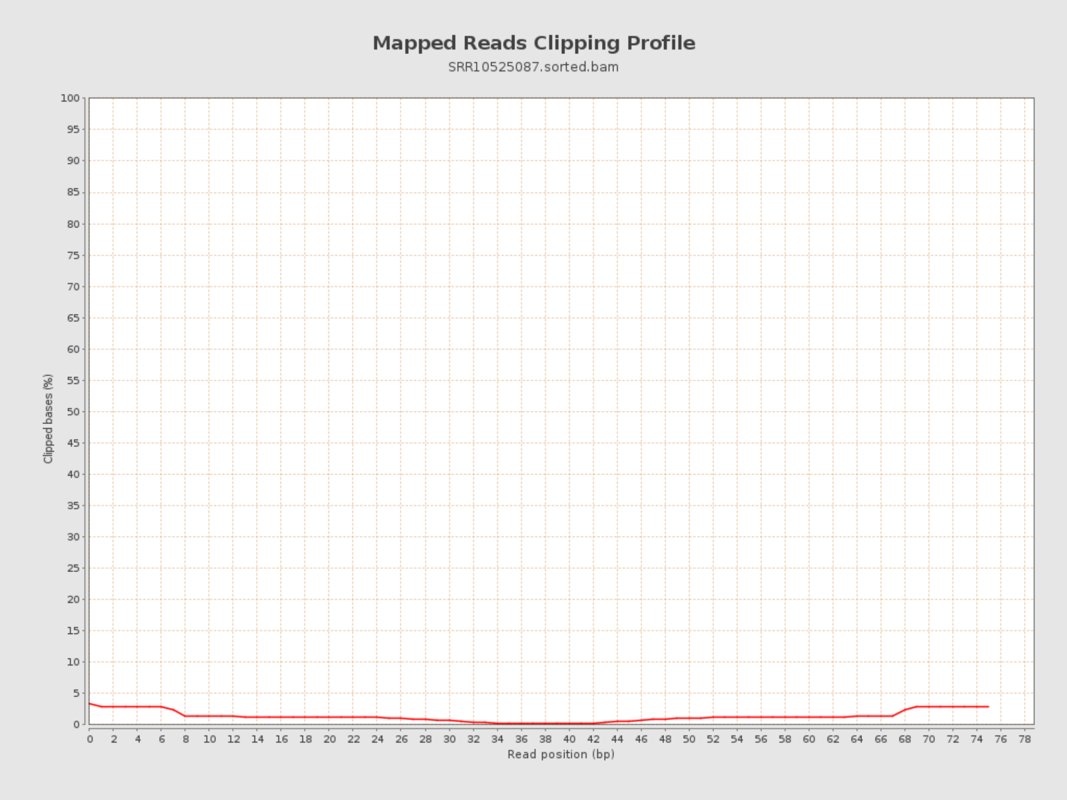
8. Results : Mapped Reads Nucleotide Content



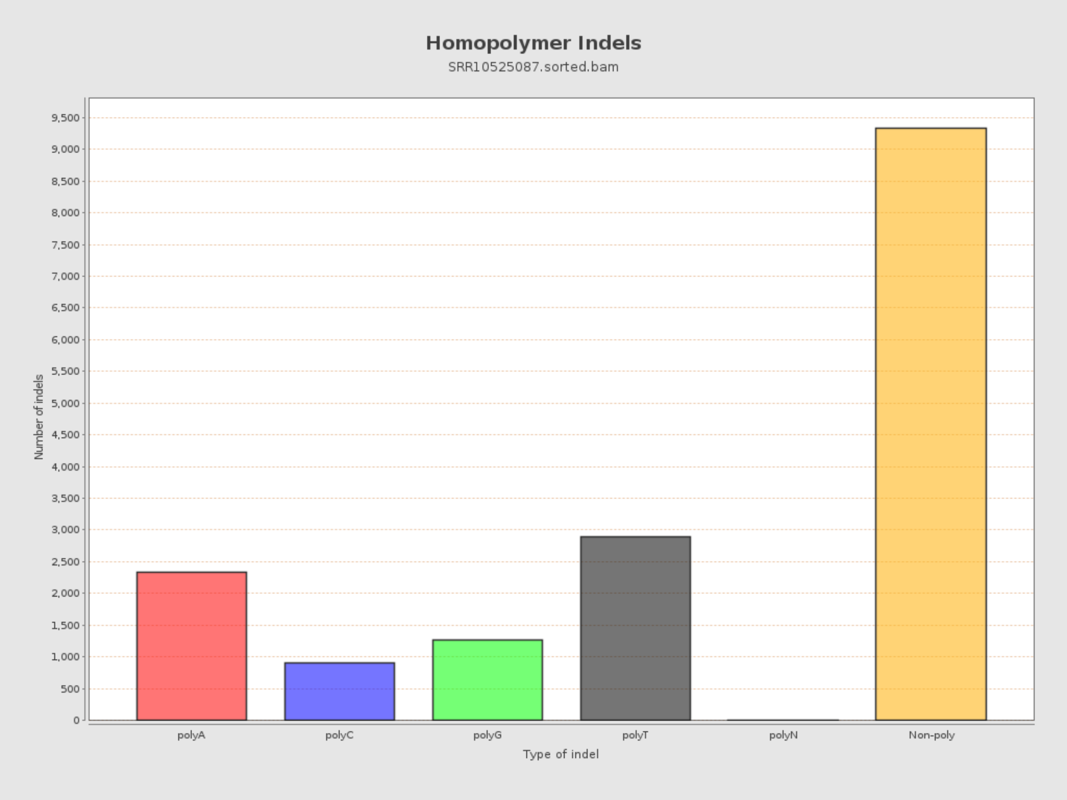
9. Results : Mapped Reads GC-content Distribution



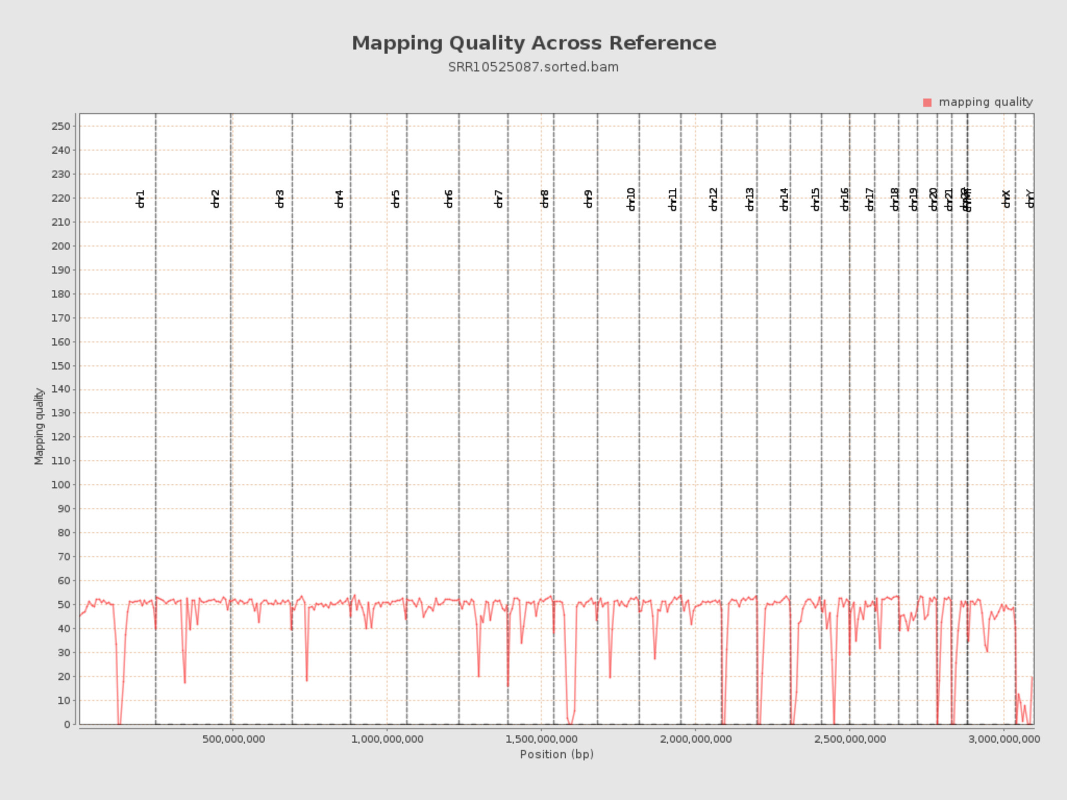
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram