Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:55:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525248.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_SRR10525248 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525248.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:55:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525248.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,444,781
Mapped reads	1,333,241 / 92.28%
Unmapped reads	111,540 / 7.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,189 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	38,471 / 2.66%
Duplication rate	1.99%
Clipped reads	1,333,964 / 92.33%

2.2. ACGT Content

Number/percentage of A's	19,901,109 / 25.6%
Number/percentage of C's	13,830,701 / 17.79%
Number/percentage of T's	24,493,095 / 31.51%
Number/percentage of G's	19,515,230 / 25.1%
Number/percentage of N's	1,392 / 0%
GC Percentage	42.89%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.2406

2.4. Mapping Quality

Mean Mapping Quality	44.46

2.5. Mismatches and indels

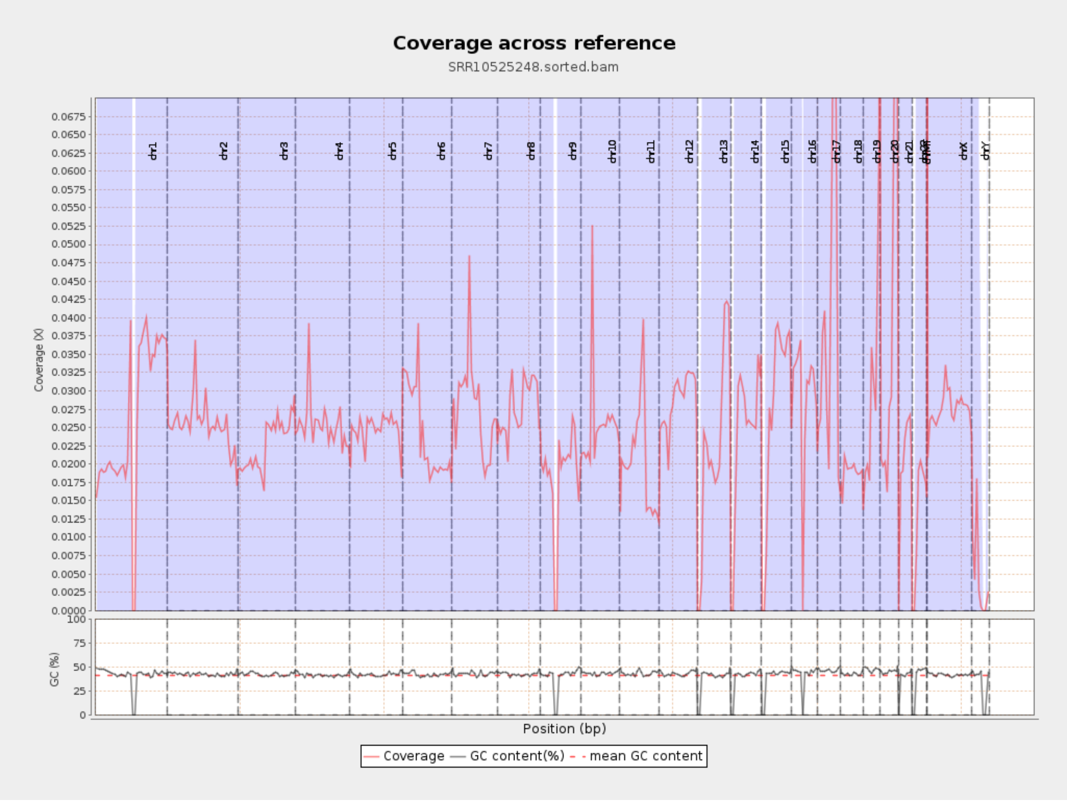
General error rate	0.51%
Mismatches	383,446
Insertions	6,222
Mapped reads with at least one insertion	0.46%
Deletions	14,627
Mapped reads with at least one deletion	1.09%
Homopolymer indels	40.74%

2.6. Chromosome stats

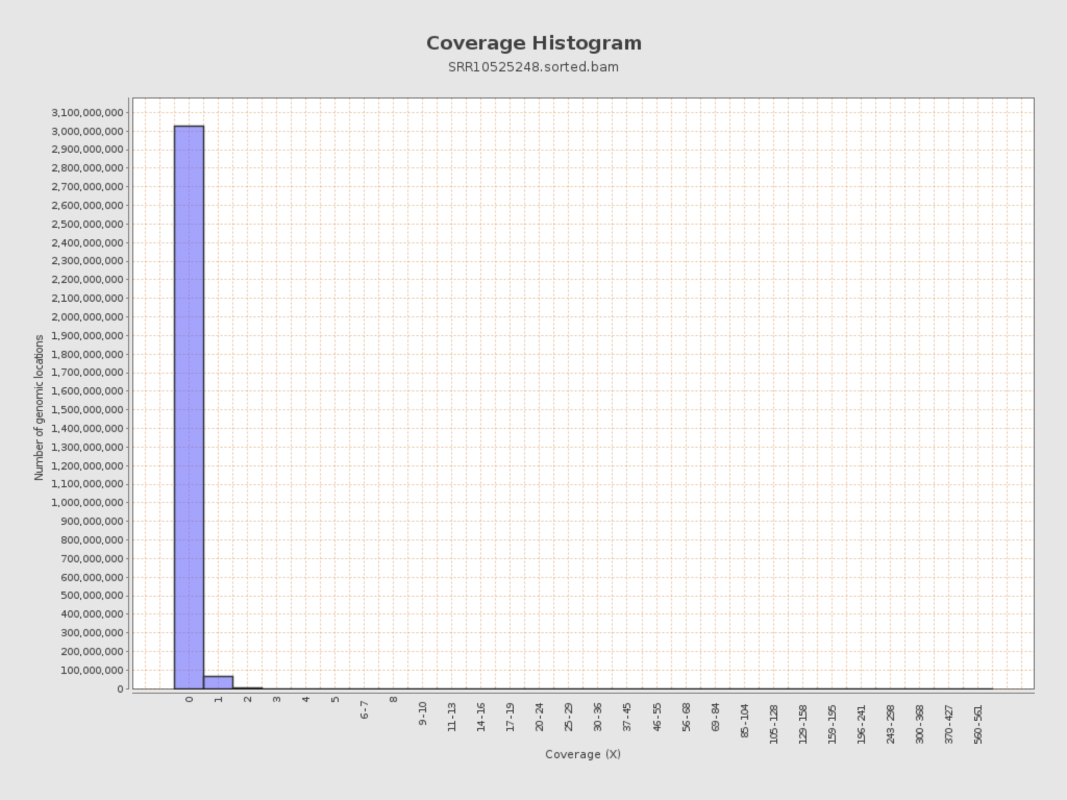
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6448702	0.0259	0.3822
chr2	243199373	6183972	0.0254	0.2953
chr3	198022430	4472330	0.0226	0.1627
chr4	191154276	4857151	0.0254	0.1876
chr5	180915260	4500884	0.0249	0.1671
chr6	171115067	4152681	0.0243	0.1977
chr7	159138663	4420516	0.0278	0.3413

chr8	146364022	4092568	0.028	0.3012
chr9	141213431	2570025	0.0182	0.1769
chr10	135534747	3452285	0.0255	0.2656
chr11	135006516	2781918	0.0206	0.1885
chr12	133851895	3831964	0.0286	0.182
chr13	115169878	2572669	0.0223	0.1599
chr14	107349540	2587864	0.0241	0.1679
chr15	102531392	2816349	0.0275	0.1776
chr16	90354753	2595105	0.0287	0.1937
chr17	81195210	3318574	0.0409	0.2251
chr18	78077248	1473833	0.0189	0.299
chr19	59128983	1890886	0.032	0.3255
chr20	63025520	2512499	0.0399	0.2193
chr21	48129895	989361	0.0206	0.1723
chr22	51304566	679486	0.0132	0.1226
chrMT	16571	4090	0.2468	0.5226
chrX	155270560	4291554	0.0276	0.1897
chrY	59373566	267525	0.0045	0.1802

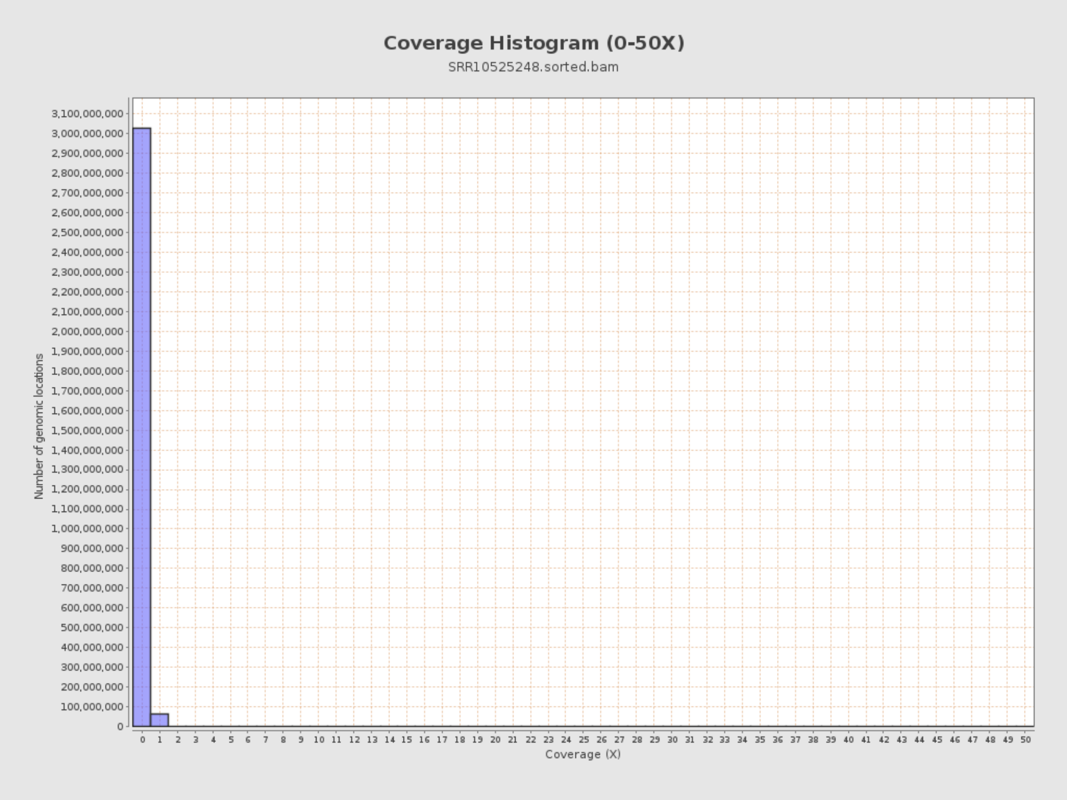
3. Results : Coverage across reference



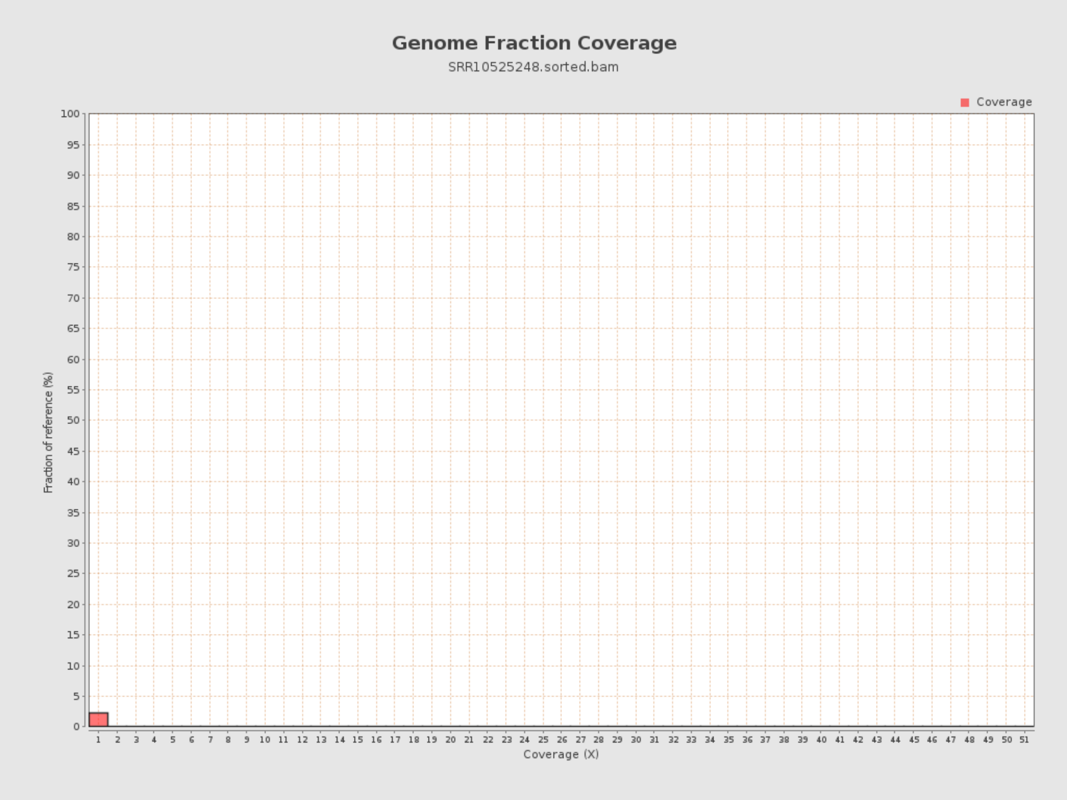
4. Results : Coverage Histogram



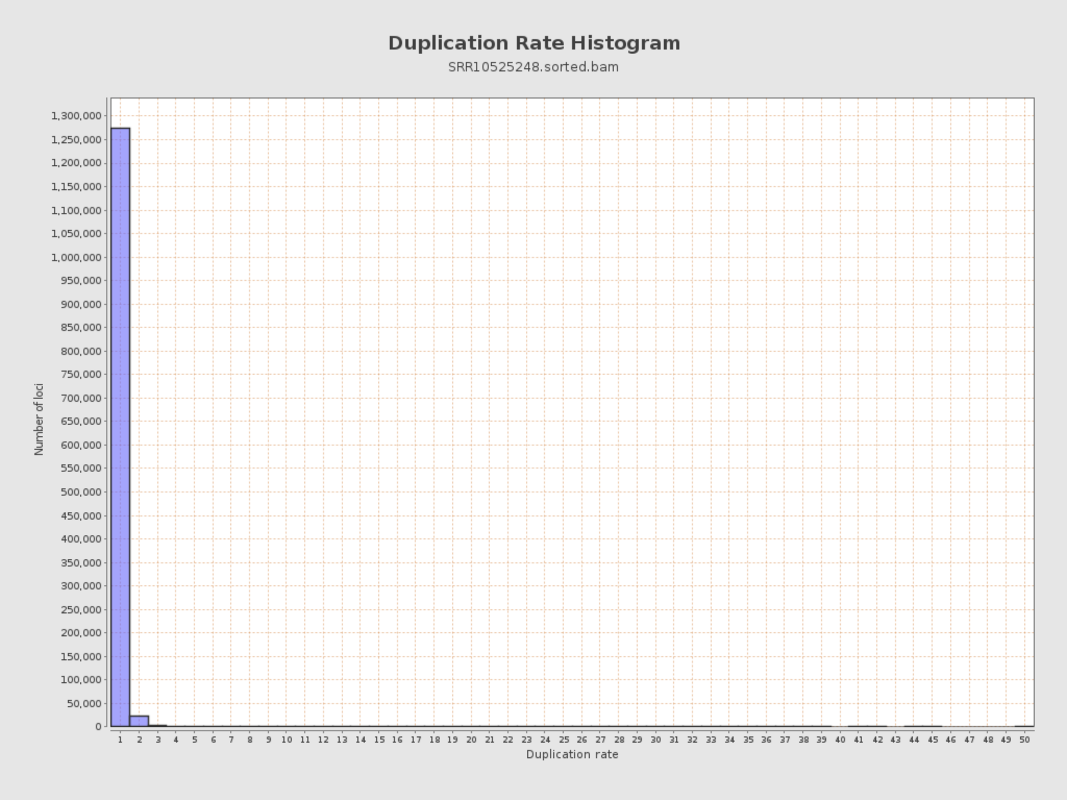
5. Results : Coverage Histogram (0-50X)



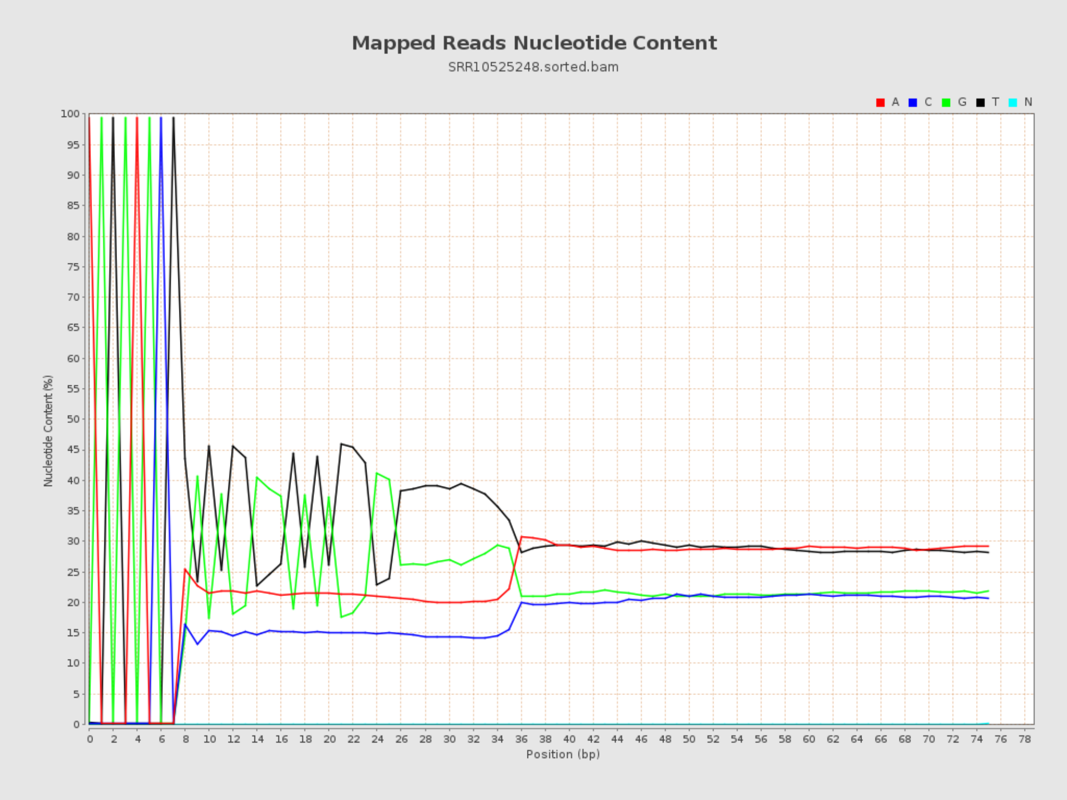
6. Results : Genome Fraction Coverage



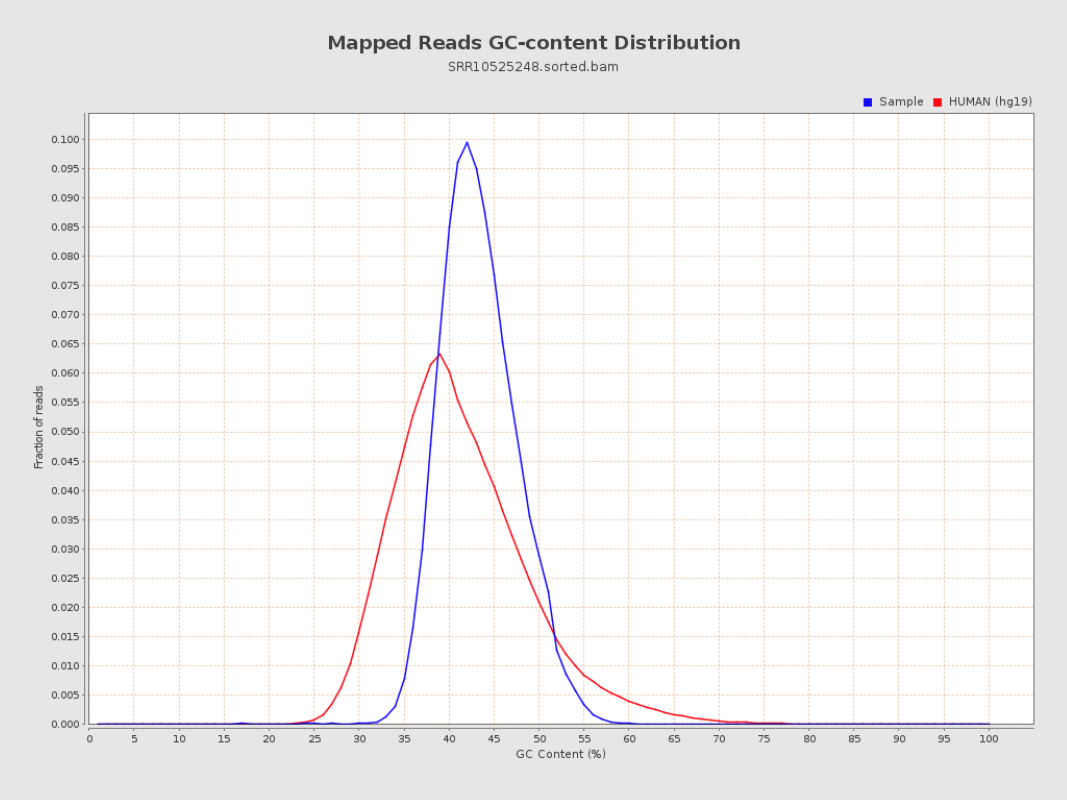
7. Results : Duplication Rate Histogram



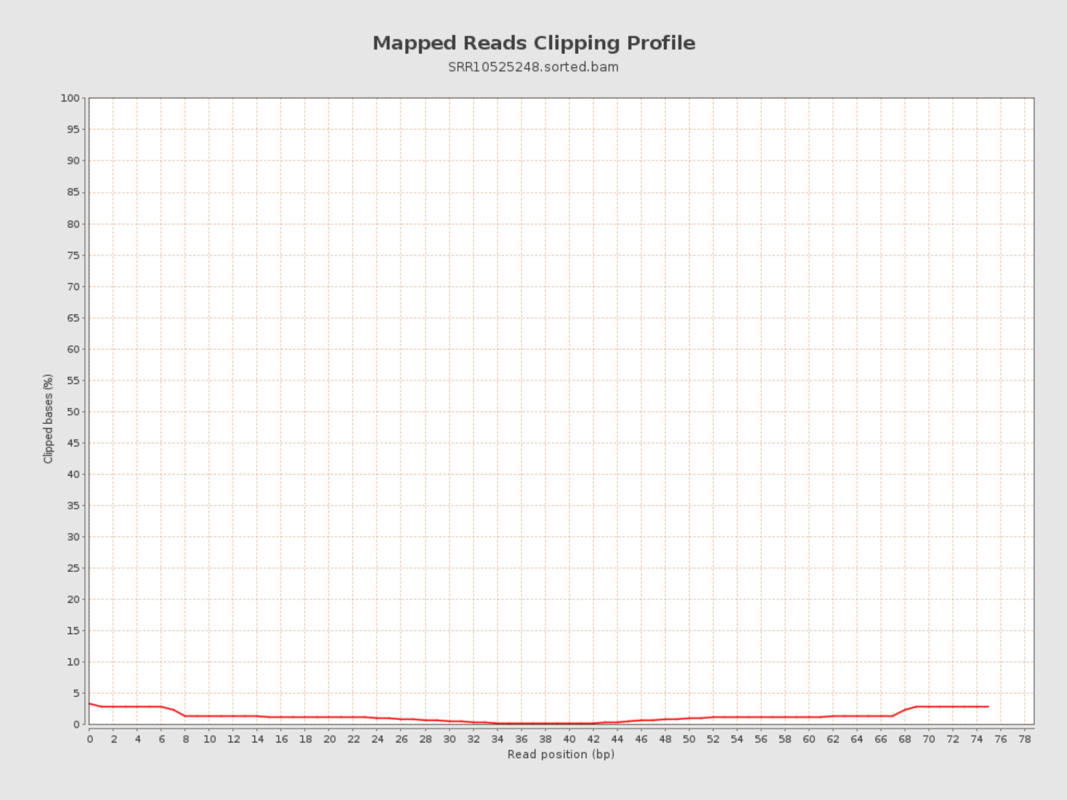
8. Results : Mapped Reads Nucleotide Content



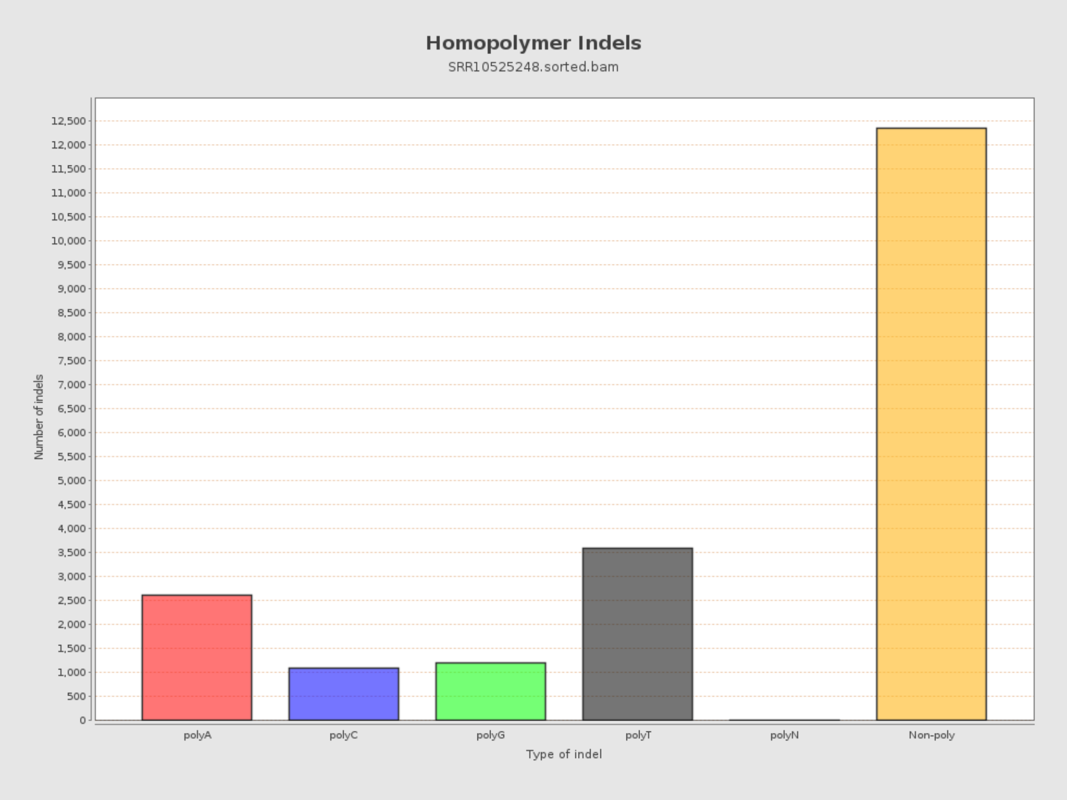
9. Results : Mapped Reads GC-content Distribution



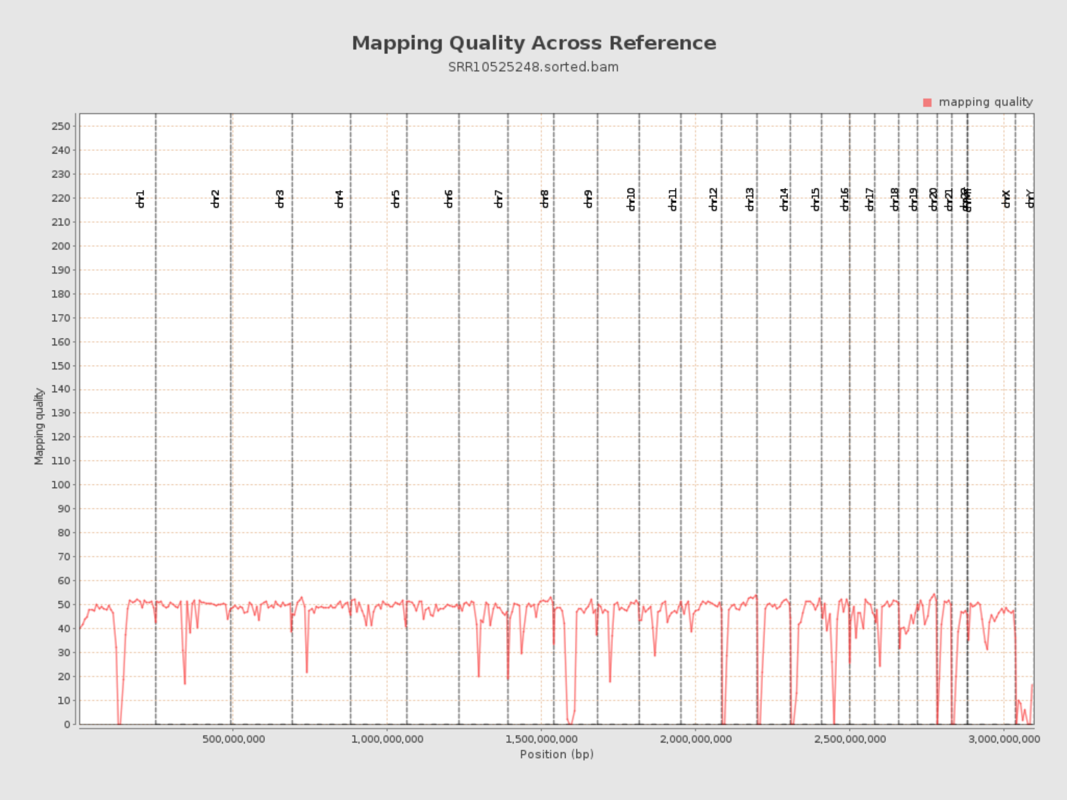
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram