Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:11:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525088.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_SRR10525088 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525088.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:11:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525088.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	517,270
Mapped reads	378,300 / 73.13%
Unmapped reads	138,970 / 26.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,386 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	9,621 / 1.86%
Duplication rate	2.15%
Clipped reads	378,689 / 73.21%

2.2. ACGT Content

Number/percentage of A's	5,394,286 / 24.62%
Number/percentage of C's	4,036,439 / 18.42%
Number/percentage of T's	7,106,037 / 32.44%
Number/percentage of G's	5,368,482 / 24.5%
Number/percentage of N's	2,503 / 0.01%
GC Percentage	42.93%

2.3. Coverage

Mean	0.0071

Standard Deviation	0.0981

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

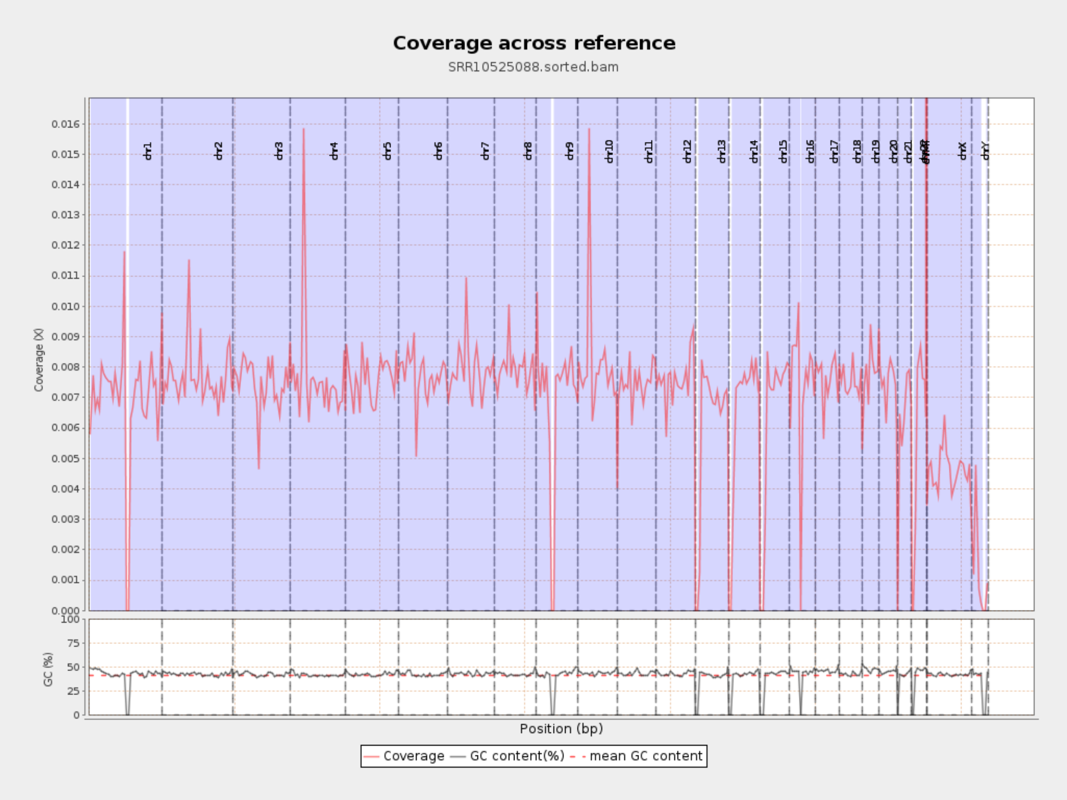
General error rate	0.48%
Mismatches	102,847
Insertions	1,447
Mapped reads with at least one insertion	0.38%
Deletions	3,895
Mapped reads with at least one deletion	1.02%
Homopolymer indels	43.35%

2.6. Chromosome stats

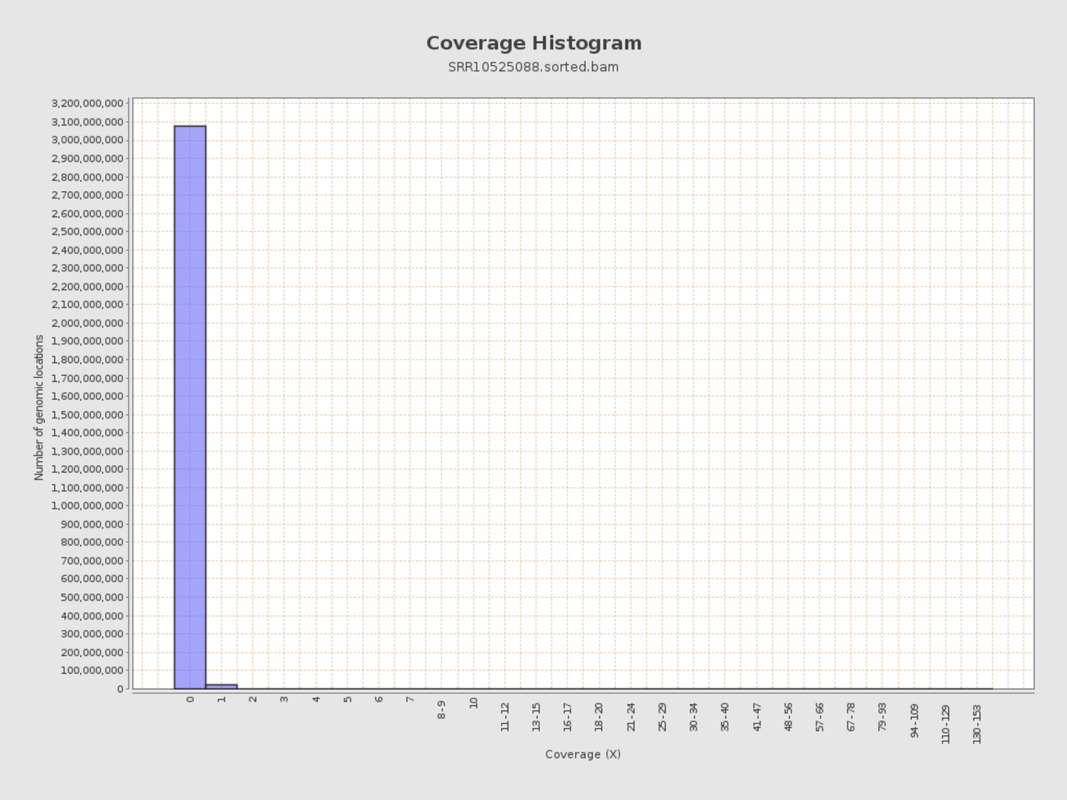
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1718533	0.0069	0.1268
chr2	243199373	1873753	0.0077	0.1152
chr3	198022430	1479010	0.0075	0.0901
chr4	191154276	1458433	0.0076	0.0971
chr5	180915260	1379301	0.0076	0.0906
chr6	171115067	1322349	0.0077	0.0938
chr7	159138663	1259496	0.0079	0.1077

chr8	146364022	1156448	0.0079	0.1037
chr9	141213431	958545	0.0068	0.092
chr10	135534747	1096590	0.0081	0.1132
chr11	135006516	1003618	0.0074	0.0933
chr12	133851895	1012530	0.0076	0.0909
chr13	115169878	691541	0.006	0.081
chr14	107349540	682373	0.0064	0.0832
chr15	102531392	644486	0.0063	0.083
chr16	90354753	667012	0.0074	0.0913
chr17	81195210	612613	0.0075	0.0919
chr18	78077248	590279	0.0076	0.1134
chr19	59128983	465109	0.0079	0.1071
chr20	63025520	470795	0.0075	0.0908
chr21	48129895	294664	0.0061	0.0884
chr22	51304566	280033	0.0055	0.0767
chrMT	16571	10076	0.6081	0.9088
chrX	155270560	715468	0.0046	0.0734
chrY	59373566	71010	0.0012	0.0517

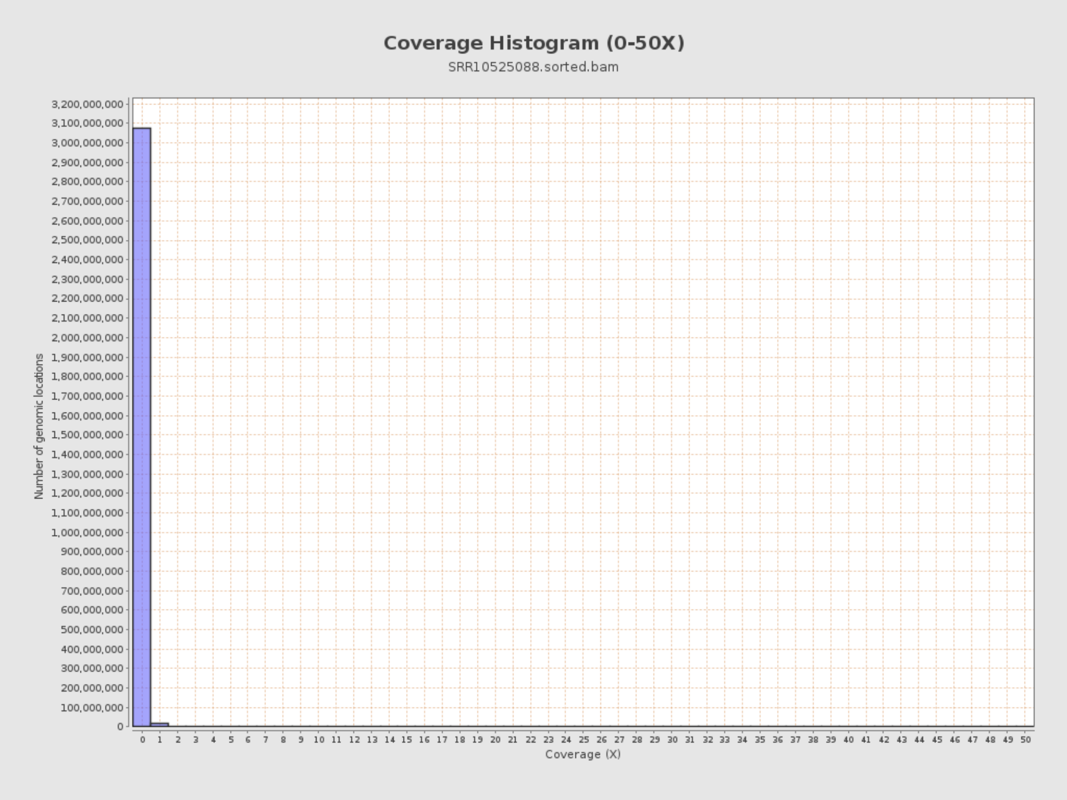
3. Results : Coverage across reference



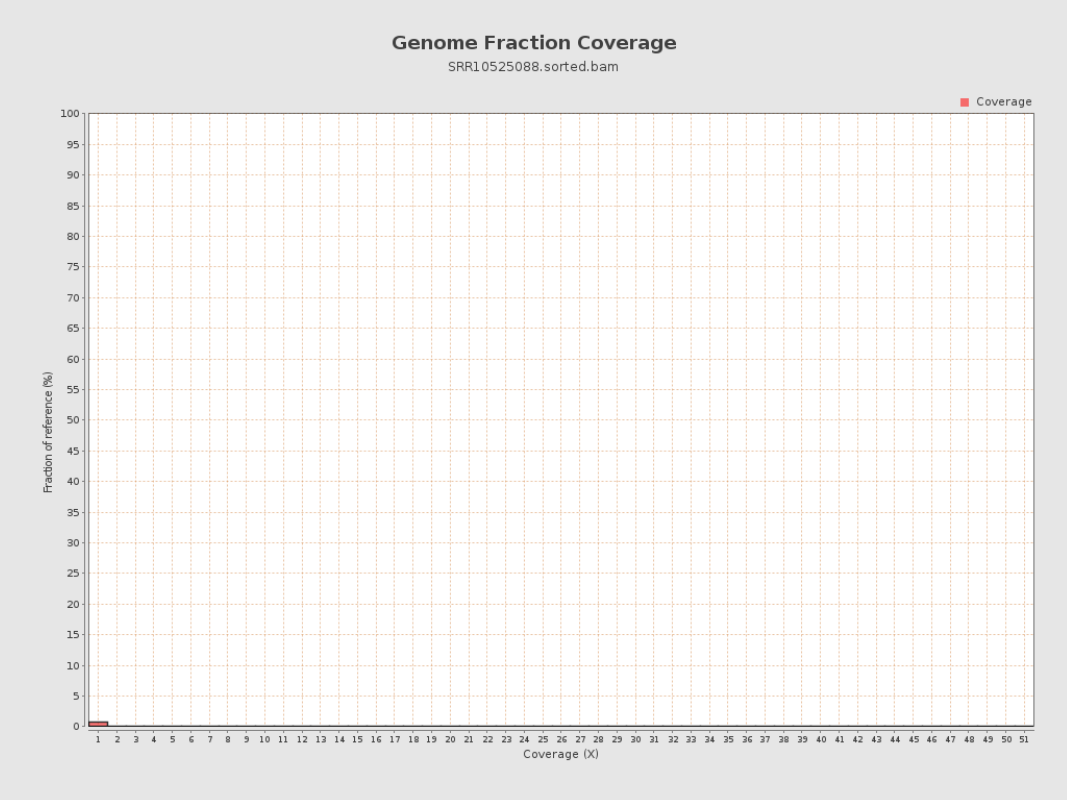
4. Results : Coverage Histogram



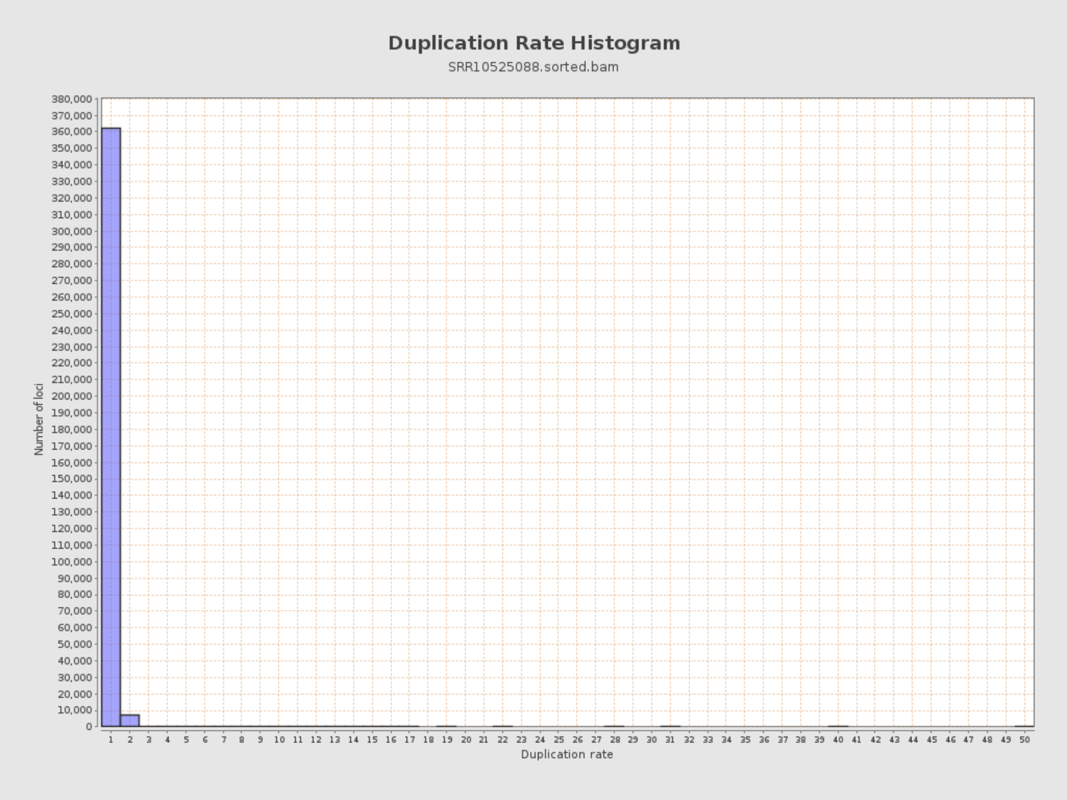
5. Results : Coverage Histogram (0-50X)



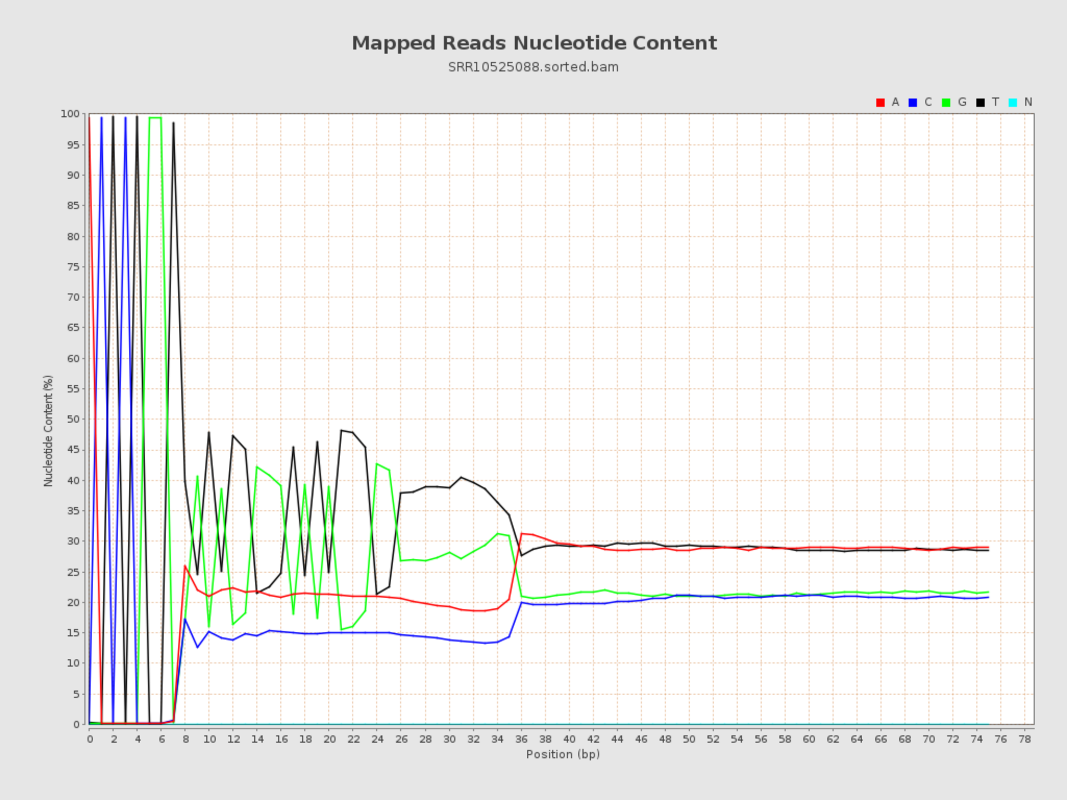
6. Results : Genome Fraction Coverage



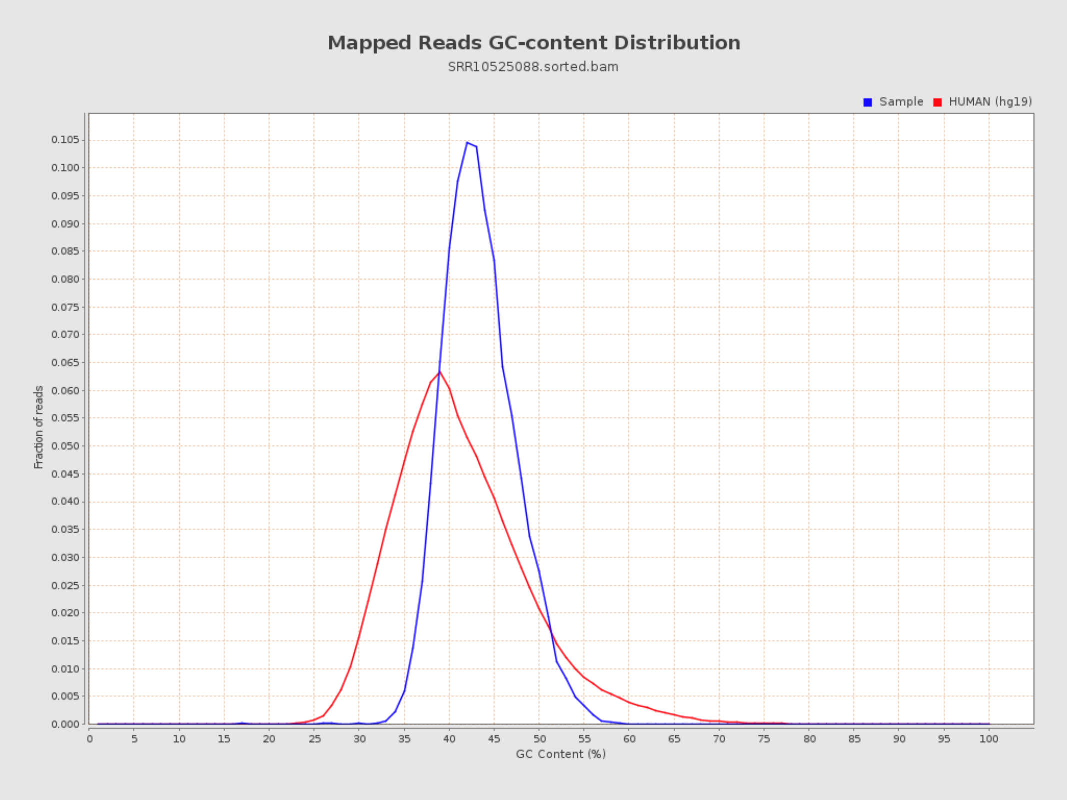
7. Results : Duplication Rate Histogram



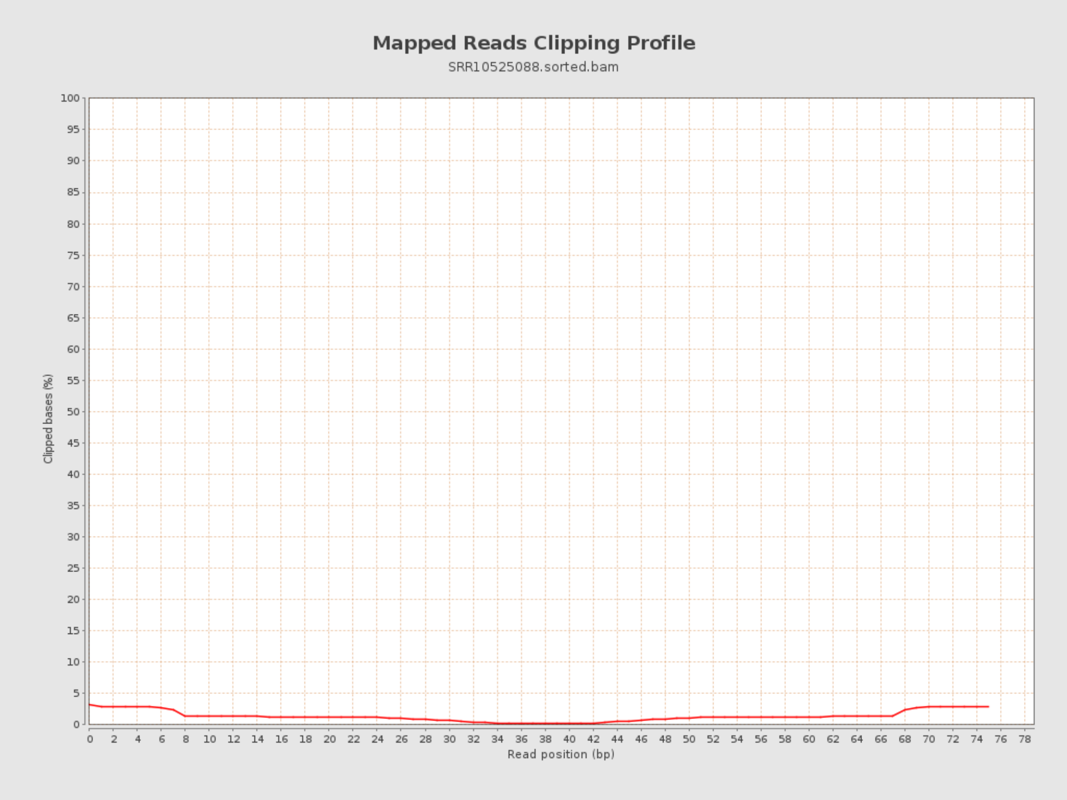
8. Results : Mapped Reads Nucleotide Content



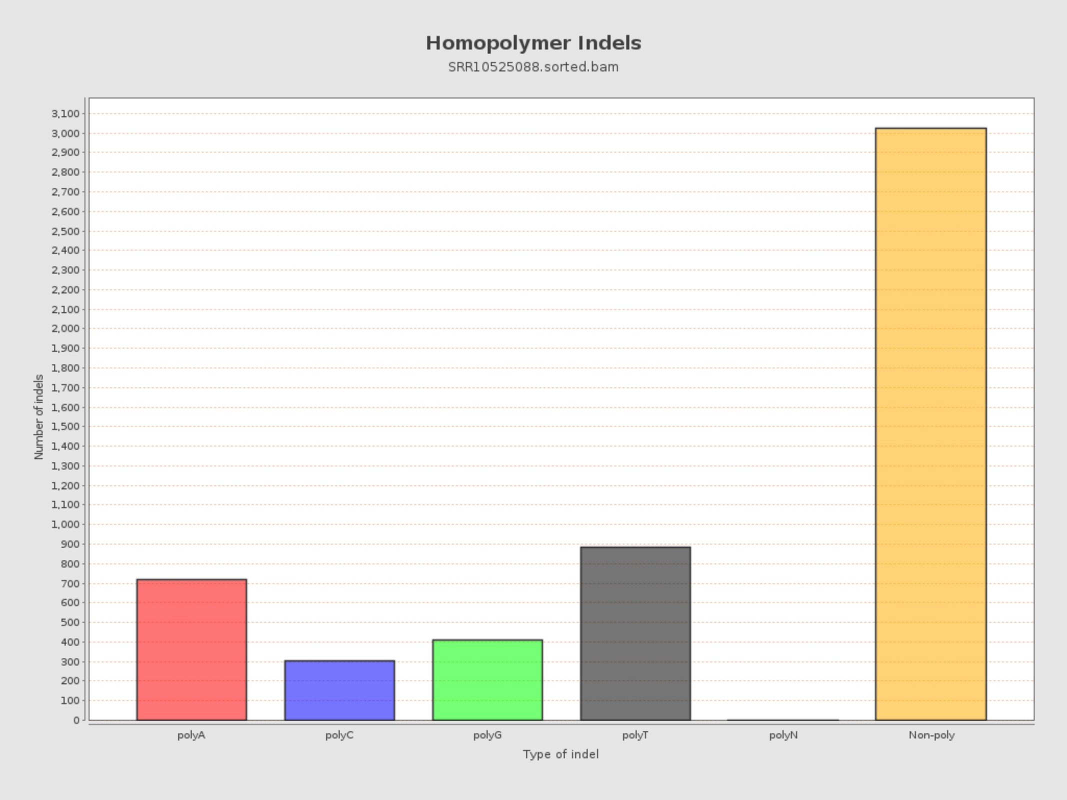
9. Results : Mapped Reads GC-content Distribution



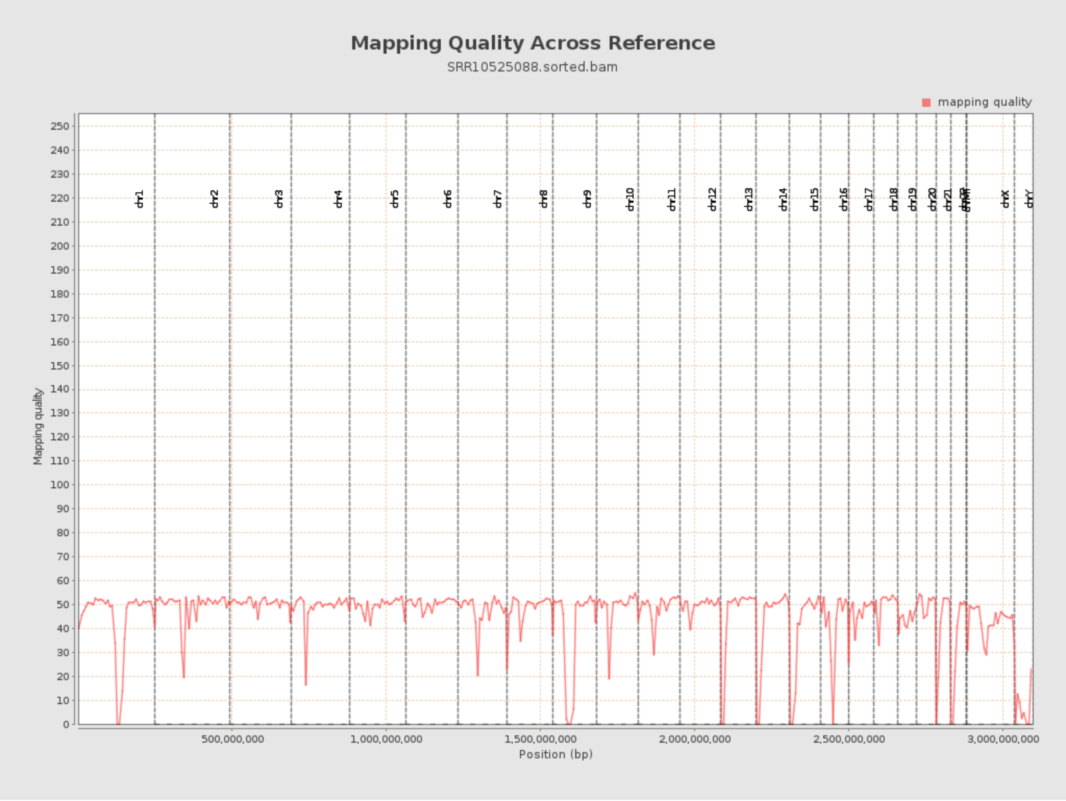
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram