Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:33:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525136.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_SRR10525136 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525136.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:33:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525136.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	646,840
Mapped reads	553,843 / 85.62%
Unmapped reads	92,997 / 14.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,095 / 2.33%
Read min/max/mean length	30 / 101 / 101.86
Duplicated reads (estimated)	10,917 / 1.69%
Duplication rate	1.2%
Clipped reads	568,009 / 87.81%

2.2. ACGT Content

Number/percentage of A's	11,018,143 / 26.15%
Number/percentage of C's	8,235,382 / 19.54%
Number/percentage of T's	12,923,311 / 30.67%
Number/percentage of G's	9,962,992 / 23.64%
Number/percentage of N's	1,617 / 0%
GC Percentage	43.18%

2.3. Coverage

Mean	0.0136

Standard Deviation	0.1655

2.4. Mapping Quality

Mean Mapping Quality	45.25

2.5. Mismatches and indels

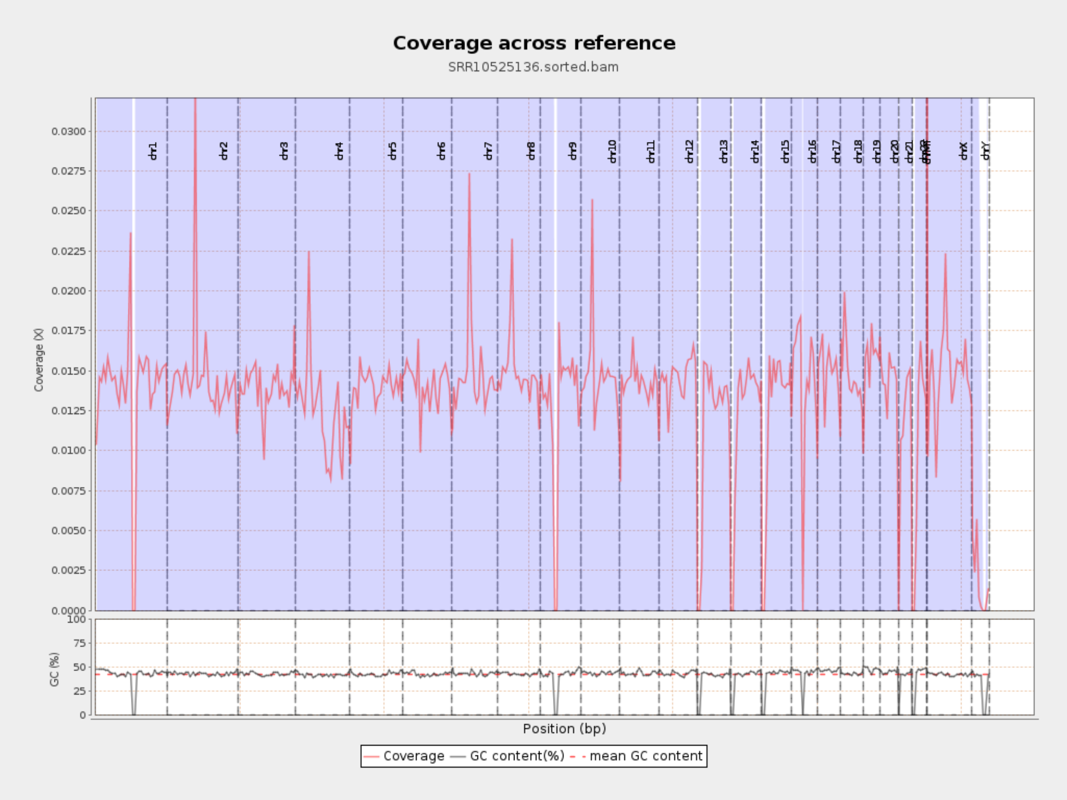
General error rate	0.79%
Mismatches	325,674
Insertions	3,934
Mapped reads with at least one insertion	0.7%
Deletions	9,843
Mapped reads with at least one deletion	1.75%
Homopolymer indels	42.54%

2.6. Chromosome stats

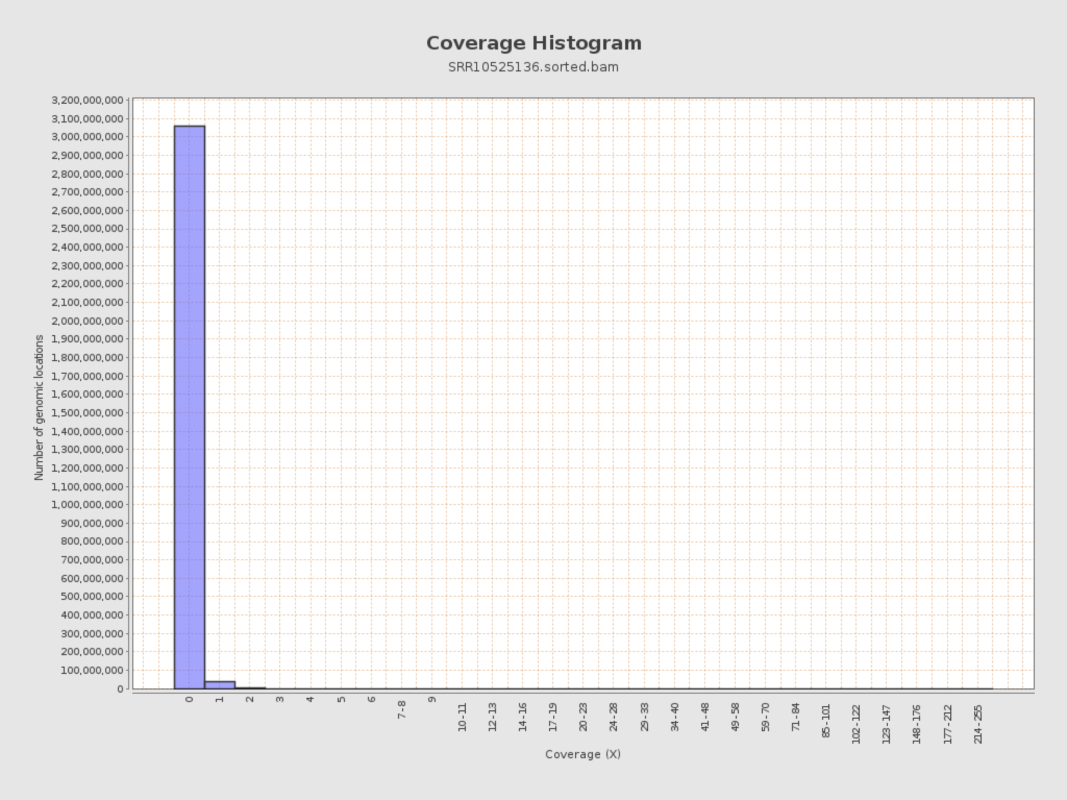
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3444119	0.0138	0.2136
chr2	243199373	3554822	0.0146	0.2352
chr3	198022430	2751246	0.0139	0.1227
chr4	191154276	2399814	0.0126	0.1228
chr5	180915260	2553258	0.0141	0.1244
chr6	171115067	2417974	0.0141	0.1315
chr7	159138663	2363465	0.0149	0.2337

chr8	146364022	2198196	0.015	0.2123
chr9	141213431	1801115	0.0128	0.1616
chr10	135534747	2004925	0.0148	0.1663
chr11	135006516	1923199	0.0142	0.166
chr12	133851895	1945891	0.0145	0.1258
chr13	115169878	1327921	0.0115	0.1116
chr14	107349540	1282709	0.0119	0.122
chr15	102531392	1227615	0.012	0.1133
chr16	90354753	1264415	0.014	0.1281
chr17	81195210	1214202	0.015	0.1401
chr18	78077248	1155147	0.0148	0.2379
chr19	59128983	935132	0.0158	0.1948
chr20	63025520	899326	0.0143	0.1261
chr21	48129895	551953	0.0115	0.1151
chr22	51304566	515555	0.01	0.104
chrMT	16571	890	0.0537	0.2307
chrX	155270560	2320421	0.0149	0.1466
chrY	59373566	105040	0.0018	0.0572

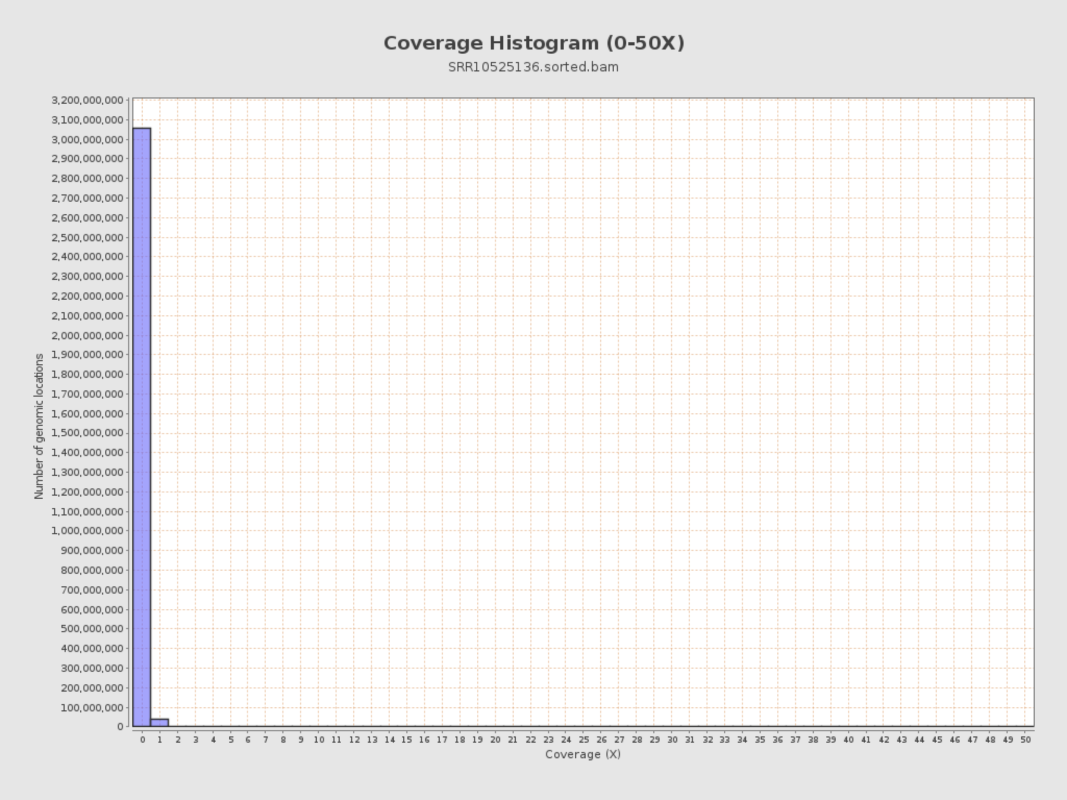
3. Results : Coverage across reference



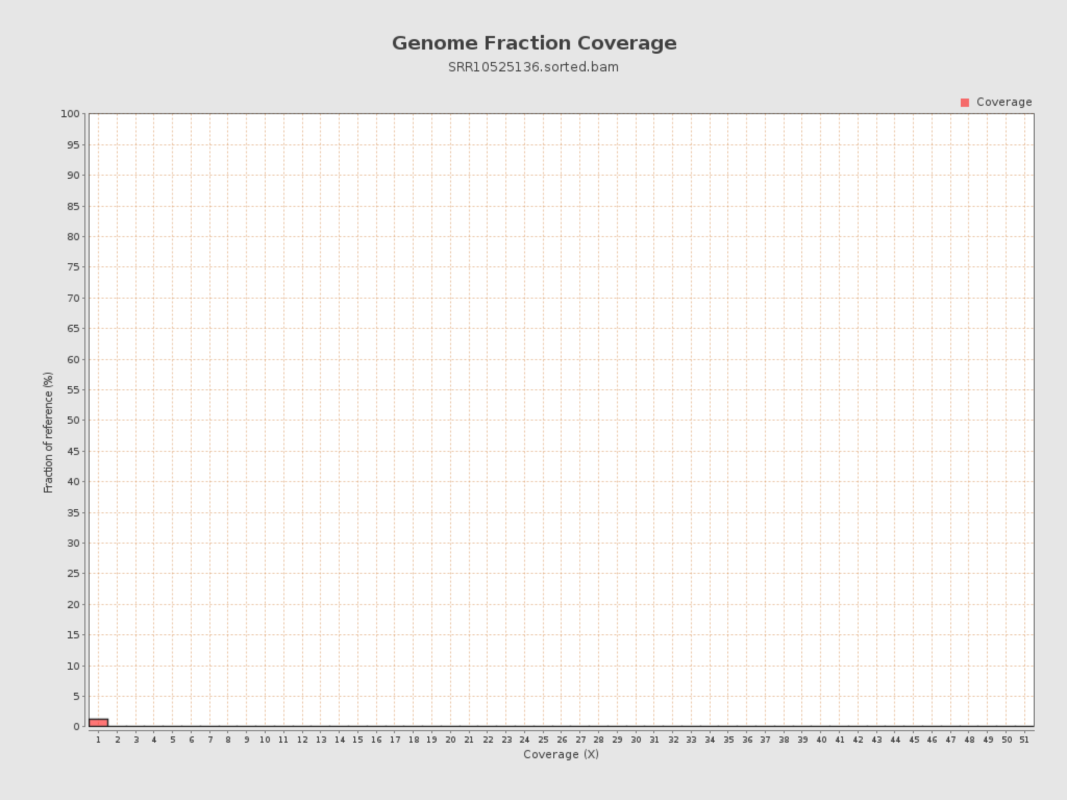
4. Results : Coverage Histogram



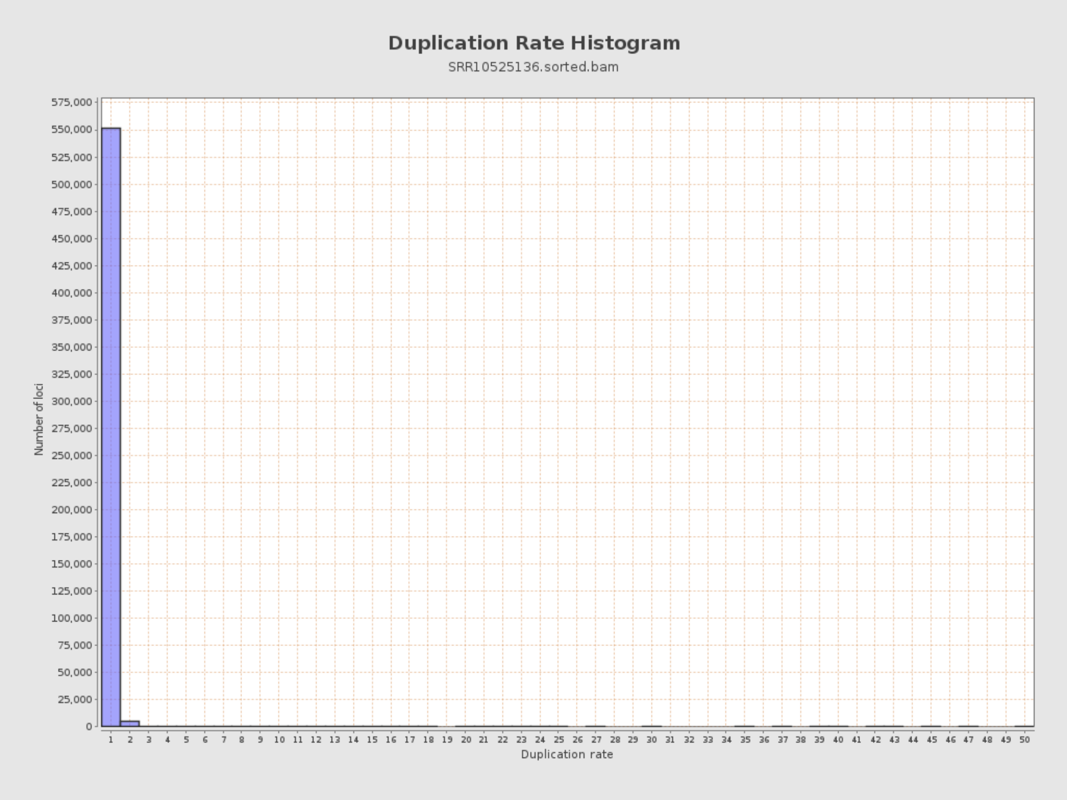
5. Results : Coverage Histogram (0-50X)



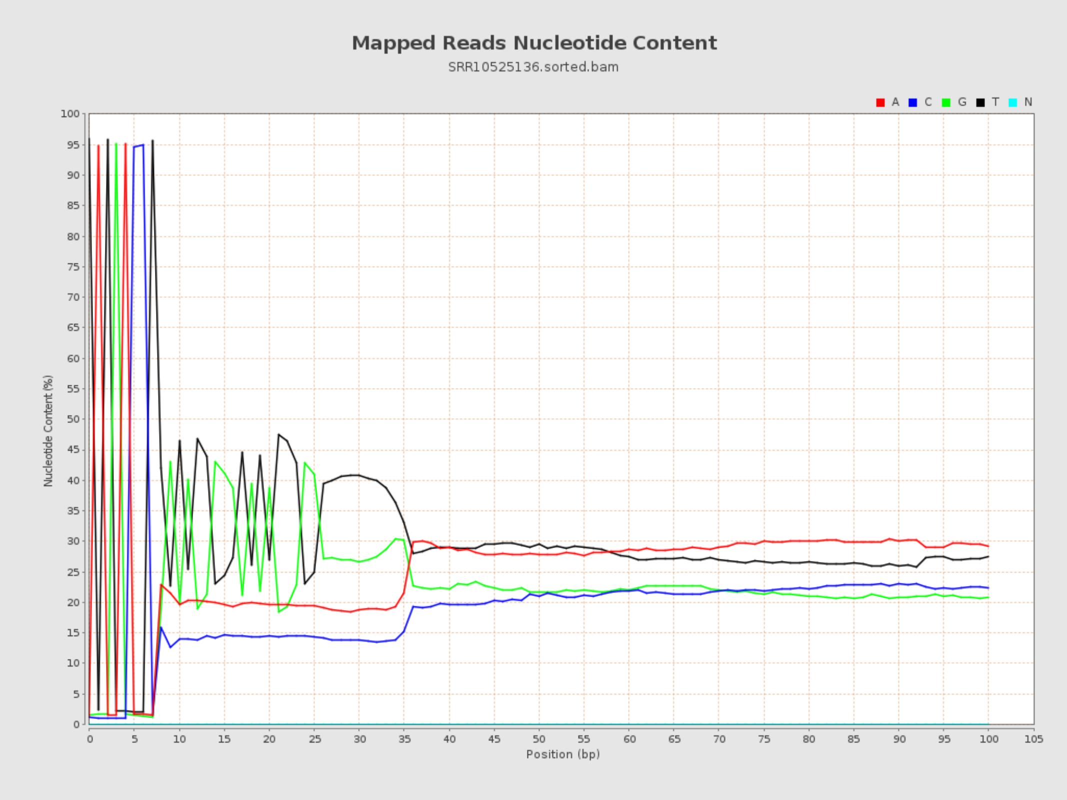
6. Results : Genome Fraction Coverage



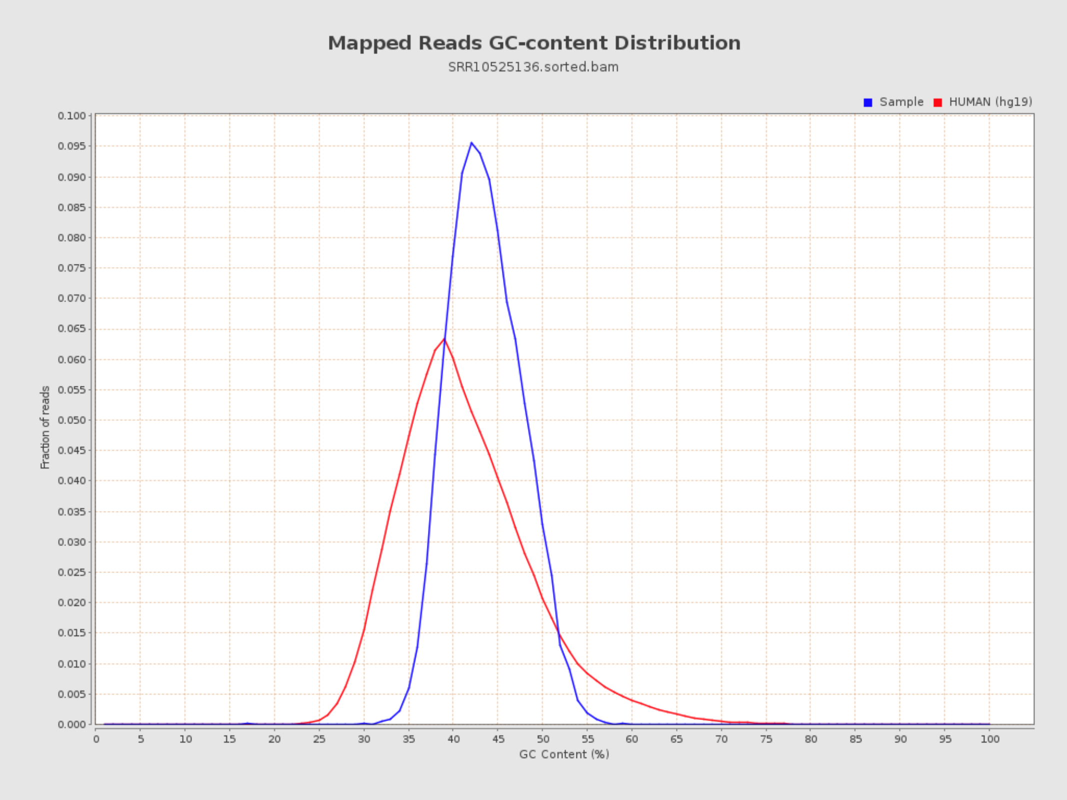
7. Results : Duplication Rate Histogram



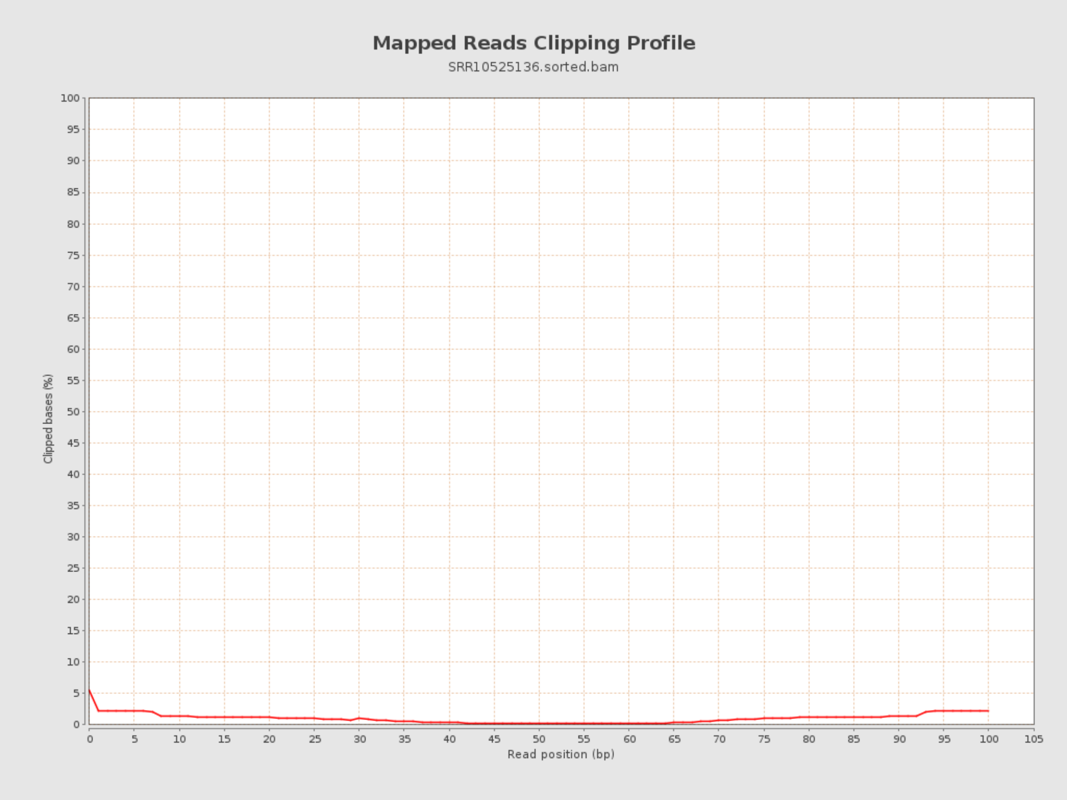
8. Results : Mapped Reads Nucleotide Content



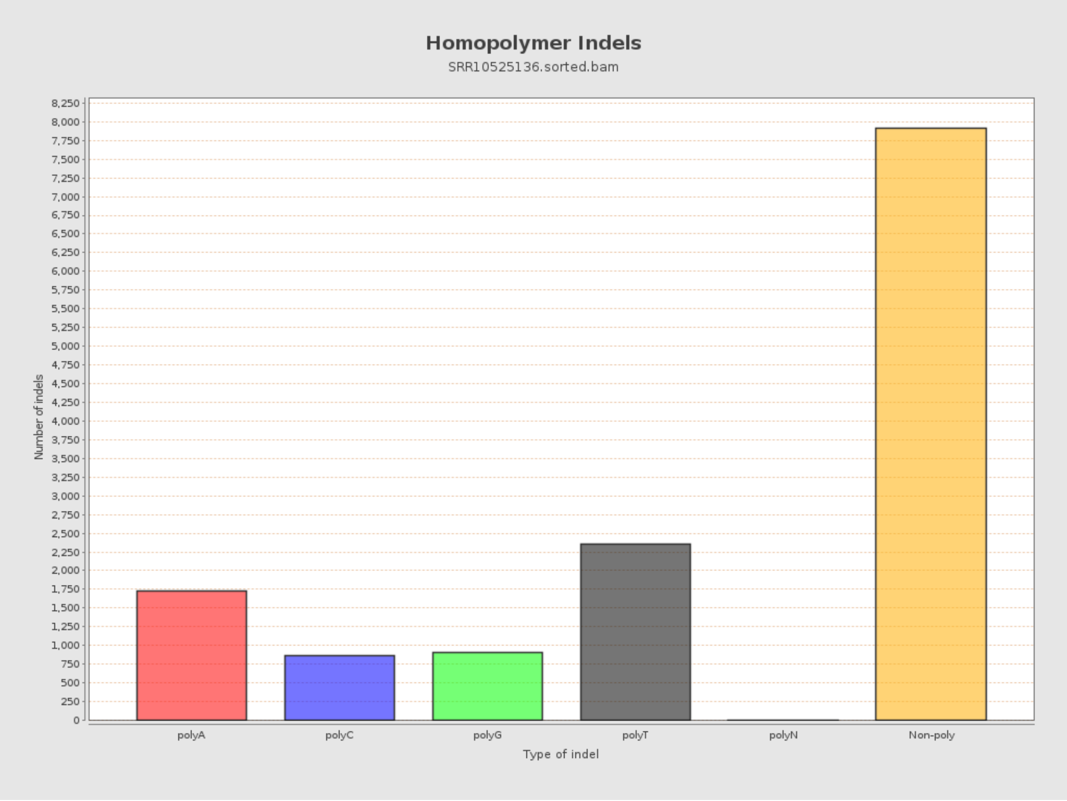
9. Results : Mapped Reads GC-content Distribution



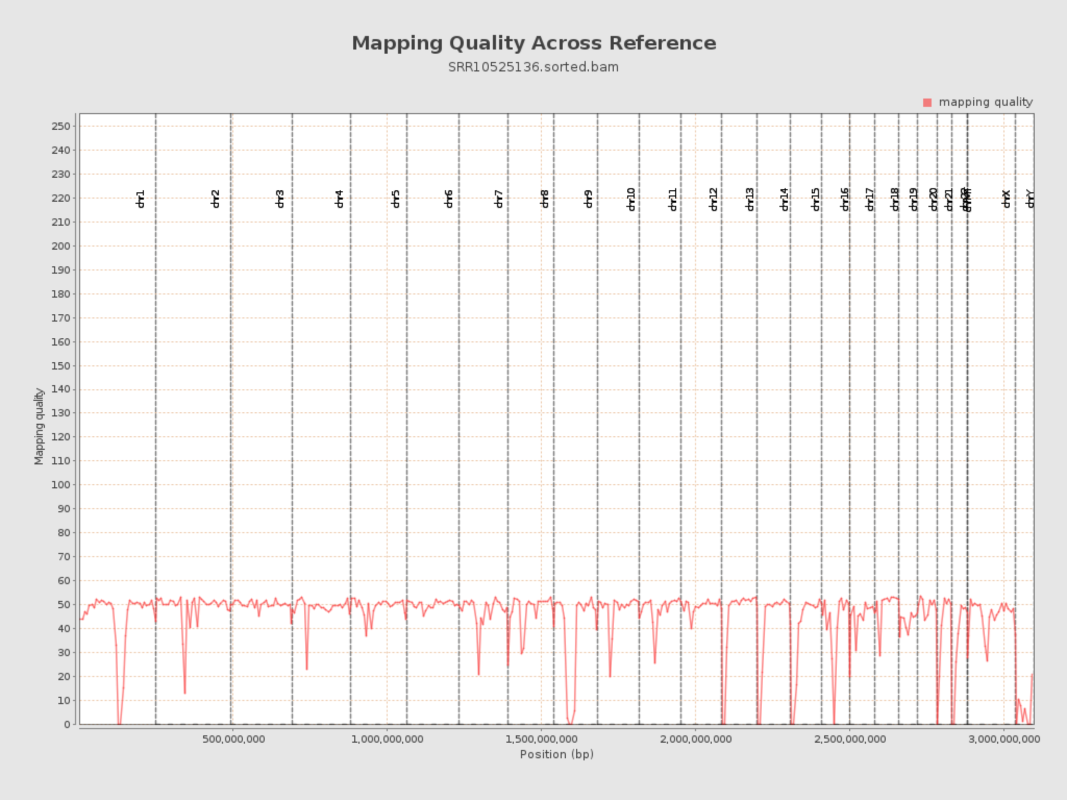
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram