Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:26:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525037.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_SRR10525037 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525037.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:26:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525037.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	849,151
Mapped reads	776,697 / 91.47%
Unmapped reads	72,454 / 8.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,465 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	40,422 / 4.76%
Duplication rate	4.15%
Clipped reads	778,492 / 91.68%

2.2. ACGT Content

Number/percentage of A's	10,578,095 / 24.01%
Number/percentage of C's	8,147,453 / 18.49%
Number/percentage of T's	14,283,185 / 32.41%
Number/percentage of G's	11,056,067 / 25.09%
Number/percentage of N's	389 / 0%
GC Percentage	43.58%

2.3. Coverage

Mean	0.0142

Standard Deviation	0.1652

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Mismatches and indels

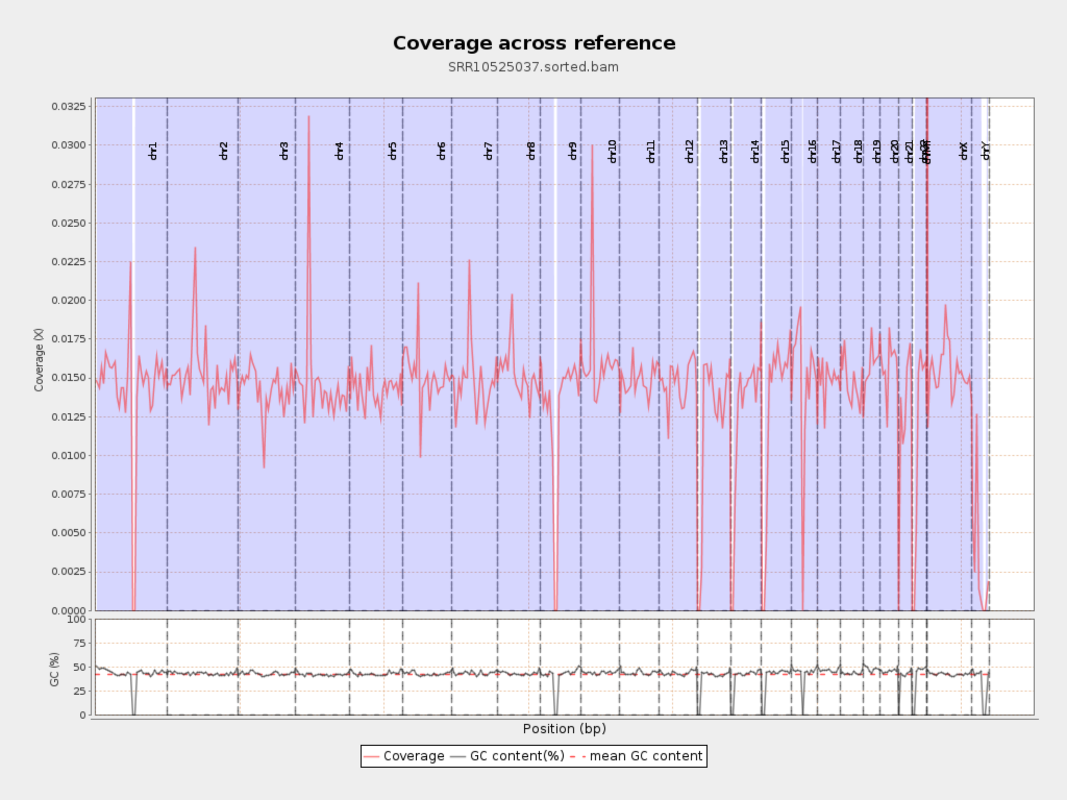
General error rate	0.53%
Mismatches	226,121
Insertions	3,264
Mapped reads with at least one insertion	0.42%
Deletions	9,337
Mapped reads with at least one deletion	1.19%
Homopolymer indels	42.7%

2.6. Chromosome stats

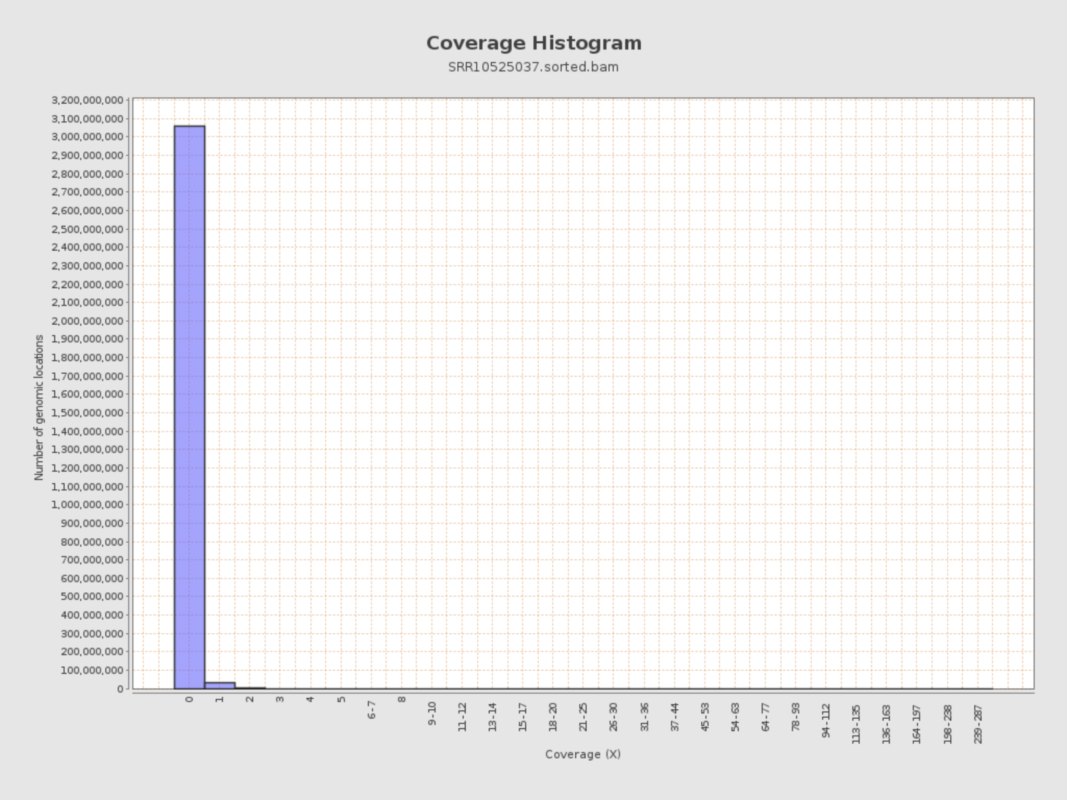
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3546768	0.0142	0.2372
chr2	243199373	3726887	0.0153	0.2045
chr3	198022430	2819631	0.0142	0.1338
chr4	191154276	2827863	0.0148	0.1624
chr5	180915260	2602900	0.0144	0.1339
chr6	171115067	2592226	0.0151	0.1529
chr7	159138663	2360404	0.0148	0.1718

chr8	146364022	2237047	0.0153	0.1759
chr9	141213431	1801570	0.0128	0.1415
chr10	135534747	2200047	0.0162	0.1974
chr11	135006516	2006680	0.0149	0.1587
chr12	133851895	1969279	0.0147	0.1367
chr13	115169878	1377700	0.012	0.1221
chr14	107349540	1323937	0.0123	0.1266
chr15	102531392	1322355	0.0129	0.1285
chr16	90354753	1315224	0.0146	0.1381
chr17	81195210	1215924	0.015	0.1474
chr18	78077248	1142721	0.0146	0.2057
chr19	59128983	938016	0.0159	0.1747
chr20	63025520	993840	0.0158	0.1457
chr21	48129895	610162	0.0127	0.1498
chr22	51304566	562316	0.011	0.1161
chrMT	16571	8204	0.4951	0.8313
chrX	155270560	2400268	0.0155	0.1471
chrY	59373566	178826	0.003	0.1305

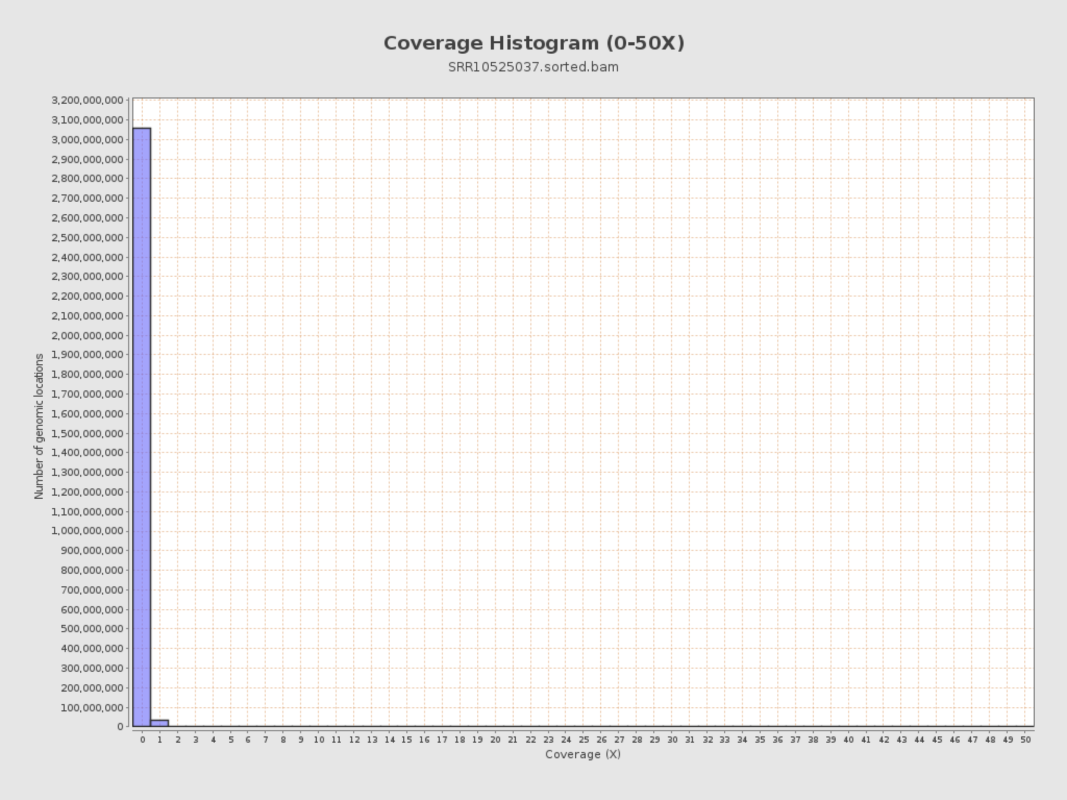
3. Results : Coverage across reference



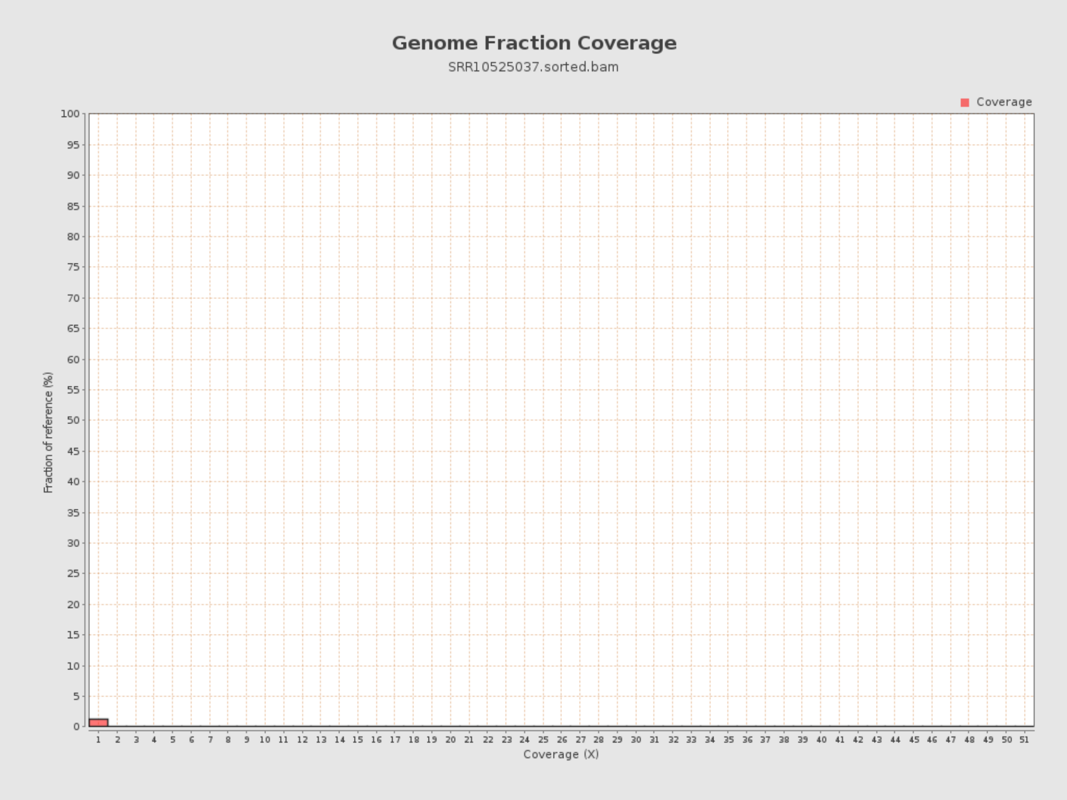
4. Results : Coverage Histogram



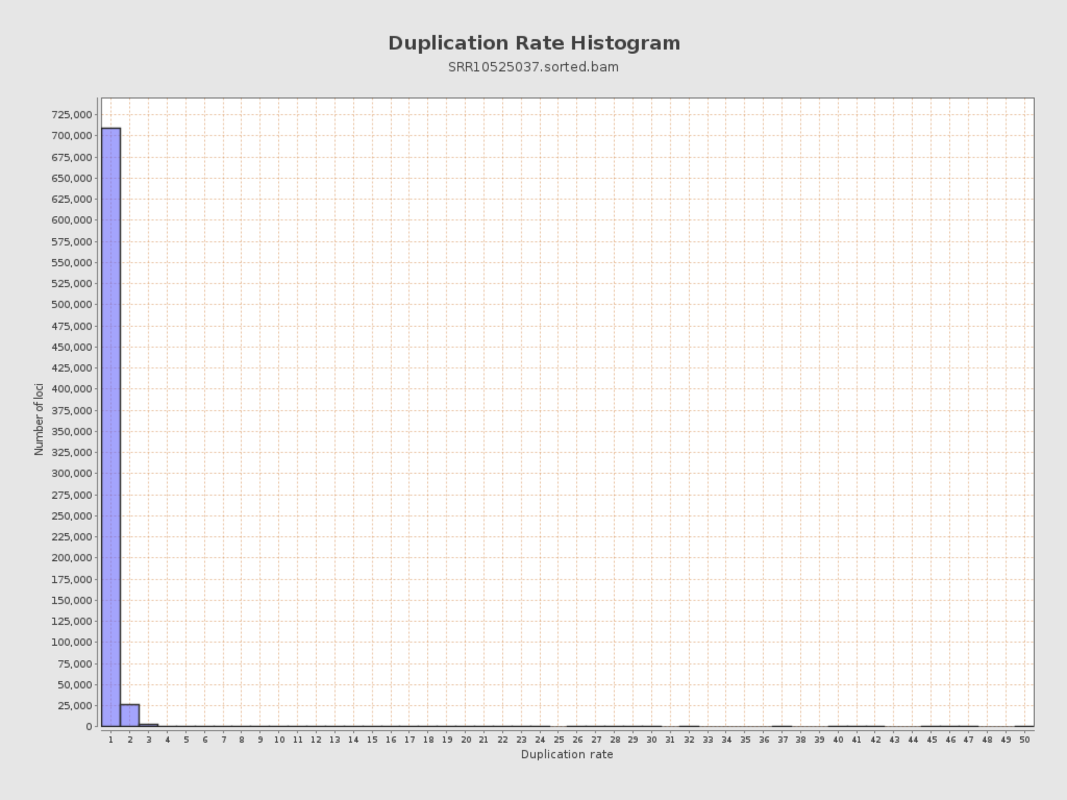
5. Results : Coverage Histogram (0-50X)



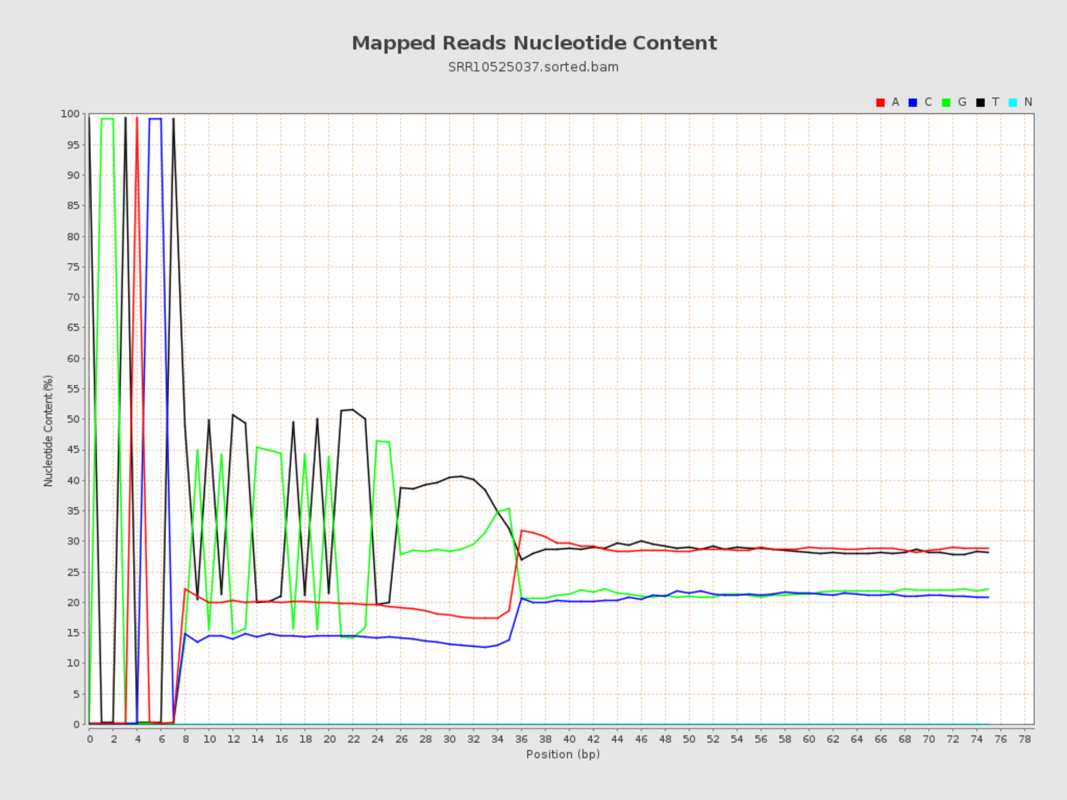
6. Results : Genome Fraction Coverage



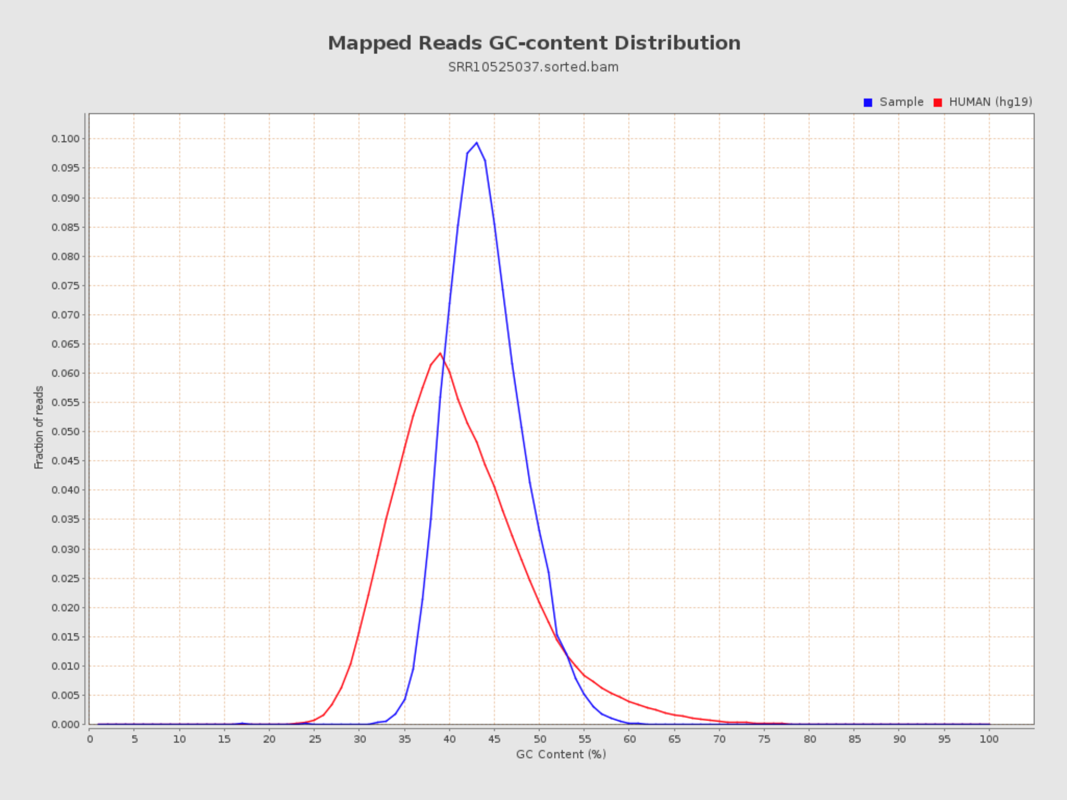
7. Results : Duplication Rate Histogram



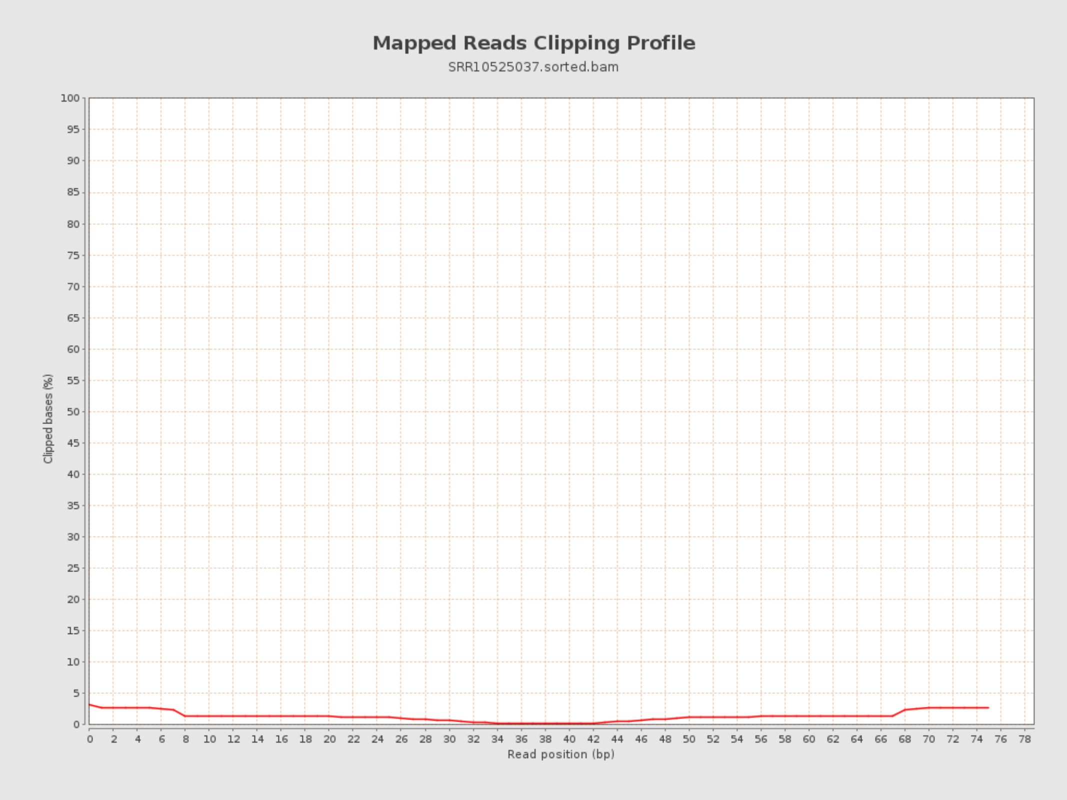
8. Results : Mapped Reads Nucleotide Content



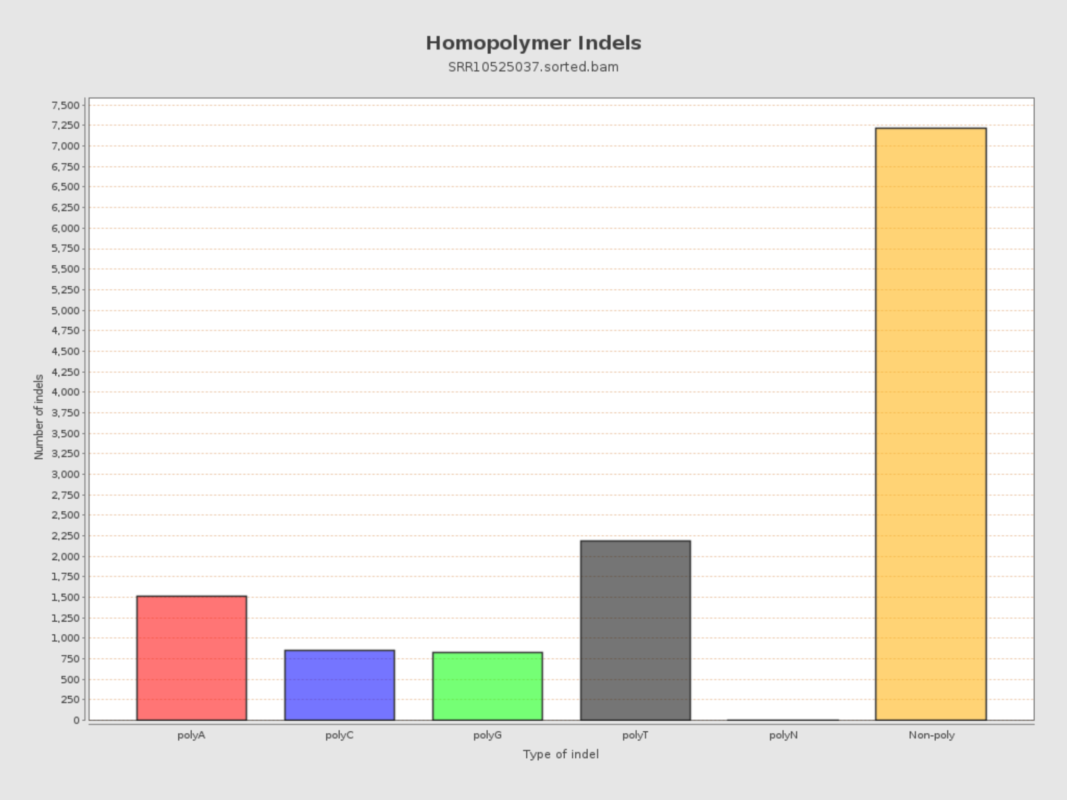
9. Results : Mapped Reads GC-content Distribution



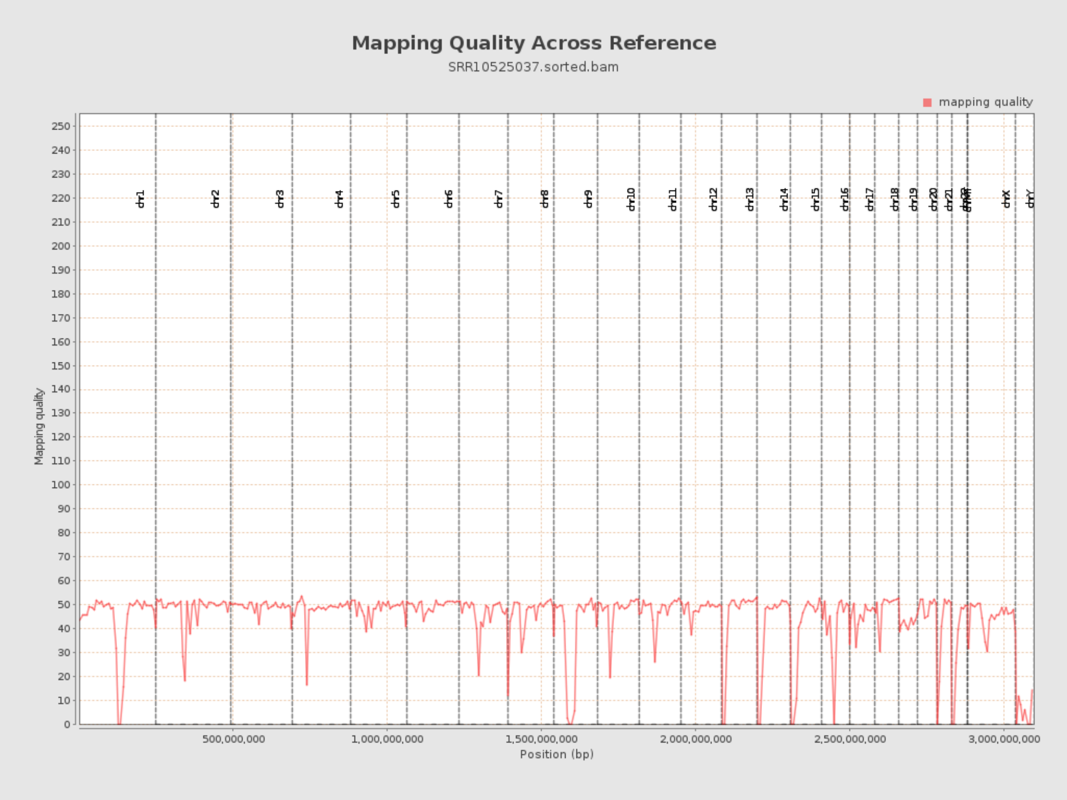
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram