Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:00:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525167.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_SRR10525167 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525167.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:00:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525167.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,183,570
Mapped reads	1,075,711 / 90.89%
Unmapped reads	107,859 / 9.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,196 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	27,689 / 2.34%
Duplication rate	1.85%
Clipped reads	1,075,524 / 90.87%

2.2. ACGT Content

Number/percentage of A's	15,642,471 / 24.41%
Number/percentage of C's	11,701,472 / 18.26%
Number/percentage of T's	20,685,175 / 32.28%
Number/percentage of G's	16,049,138 / 25.05%
Number/percentage of N's	1,547 / 0%
GC Percentage	43.31%

2.3. Coverage

Mean	0.0207

Standard Deviation	0.2136

2.4. Mapping Quality

Mean Mapping Quality	45.05

2.5. Mismatches and indels

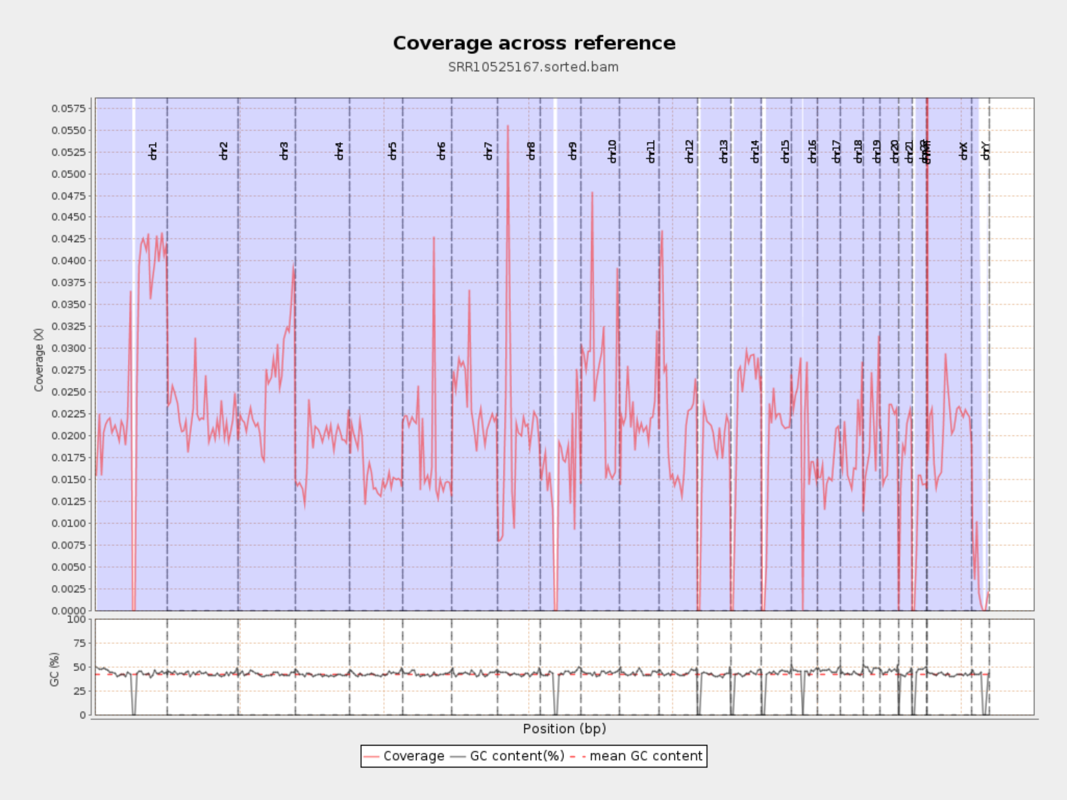
General error rate	0.52%
Mismatches	324,595
Insertions	4,716
Mapped reads with at least one insertion	0.44%
Deletions	12,711
Mapped reads with at least one deletion	1.17%
Homopolymer indels	42.23%

2.6. Chromosome stats

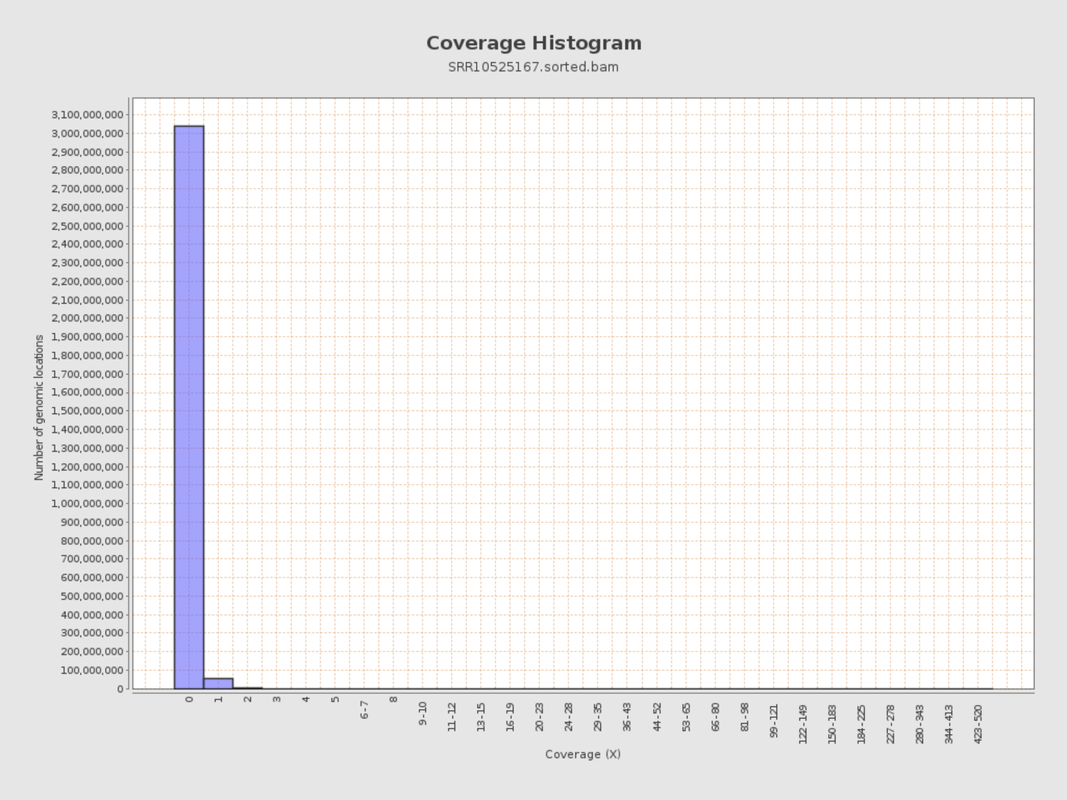
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6996782	0.0281	0.3952
chr2	243199373	5389015	0.0222	0.2659
chr3	198022430	5067487	0.0256	0.171
chr4	191154276	3635659	0.019	0.1512
chr5	180915260	2907904	0.0161	0.1335
chr6	171115067	3217121	0.0188	0.1624
chr7	159138663	3828679	0.0241	0.2849

chr8	146364022	3007971	0.0206	0.1841
chr9	141213431	2176447	0.0154	0.1549
chr10	135534747	3605880	0.0266	0.2419
chr11	135006516	3009708	0.0223	0.1837
chr12	133851895	2966397	0.0222	0.1586
chr13	115169878	2045255	0.0178	0.1412
chr14	107349540	2468509	0.023	0.1631
chr15	102531392	1818042	0.0177	0.1423
chr16	90354753	1815382	0.0201	0.1641
chr17	81195210	1334412	0.0164	0.1394
chr18	78077248	1427076	0.0183	0.2893
chr19	59128983	1211667	0.0205	0.2688
chr20	63025520	1237285	0.0196	0.1502
chr21	48129895	844954	0.0176	0.1451
chr22	51304566	540133	0.0105	0.1077
chrMT	16571	65721	3.966	2.8222
chrX	155270560	3295377	0.0212	0.1633
chrY	59373566	187852	0.0032	0.0904

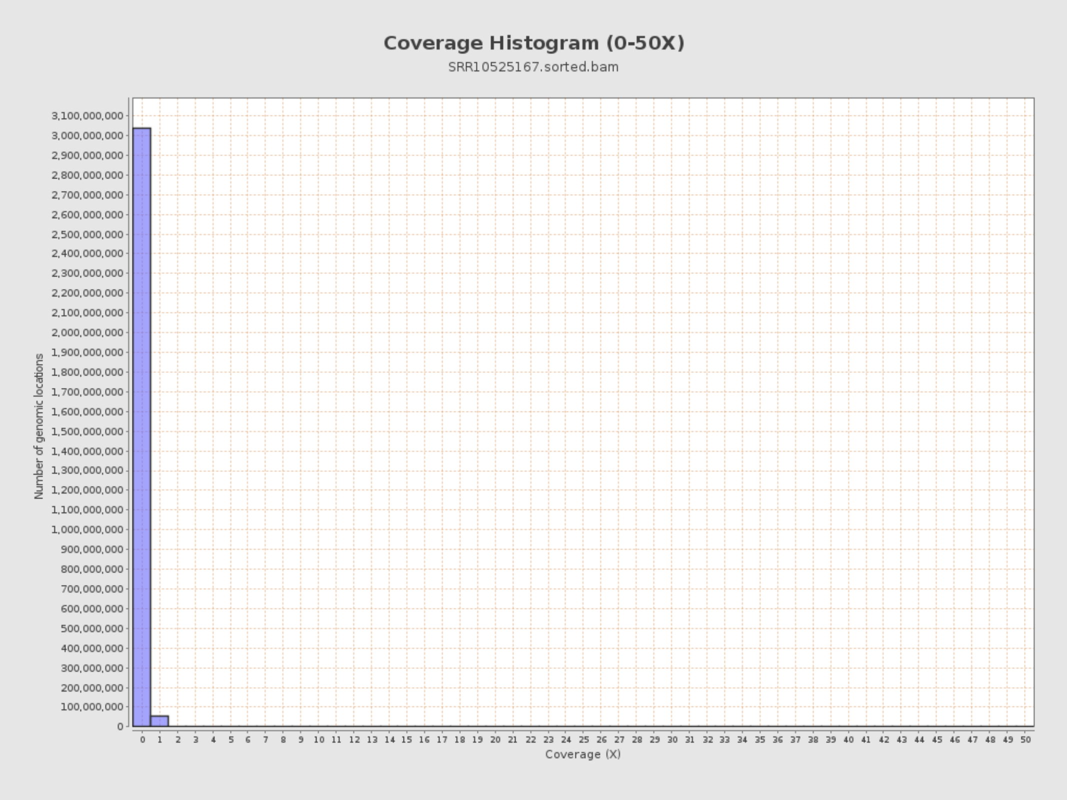
3. Results : Coverage across reference



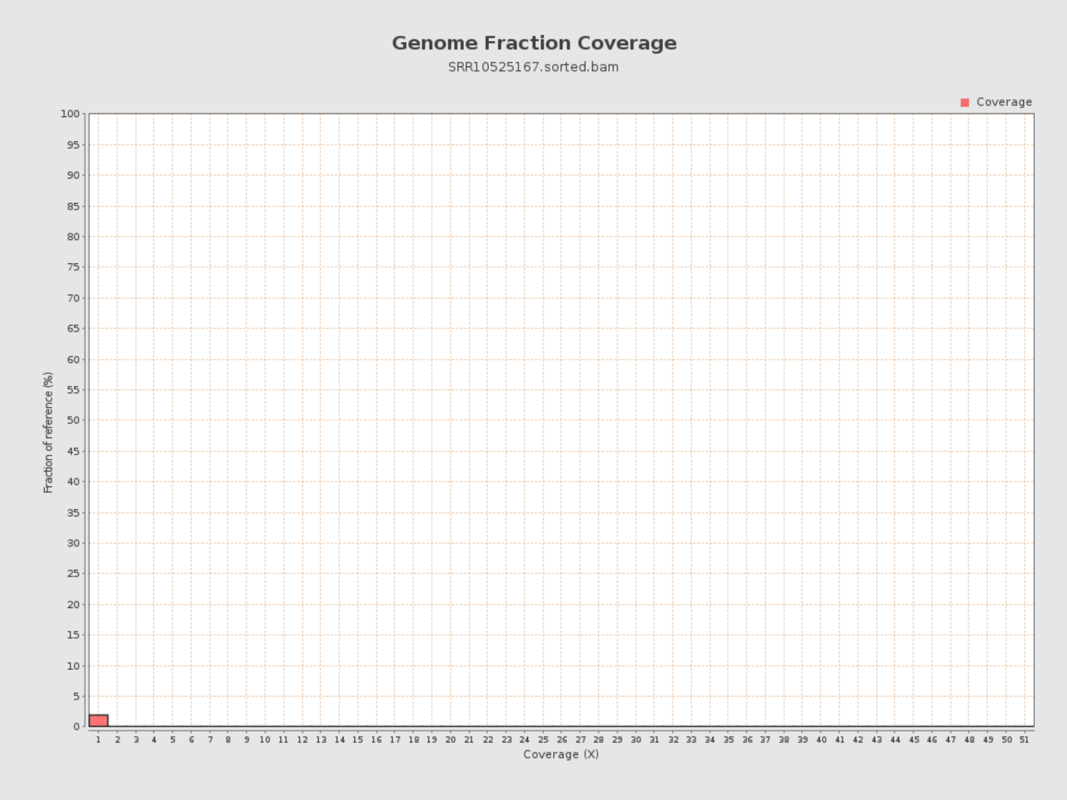
4. Results : Coverage Histogram



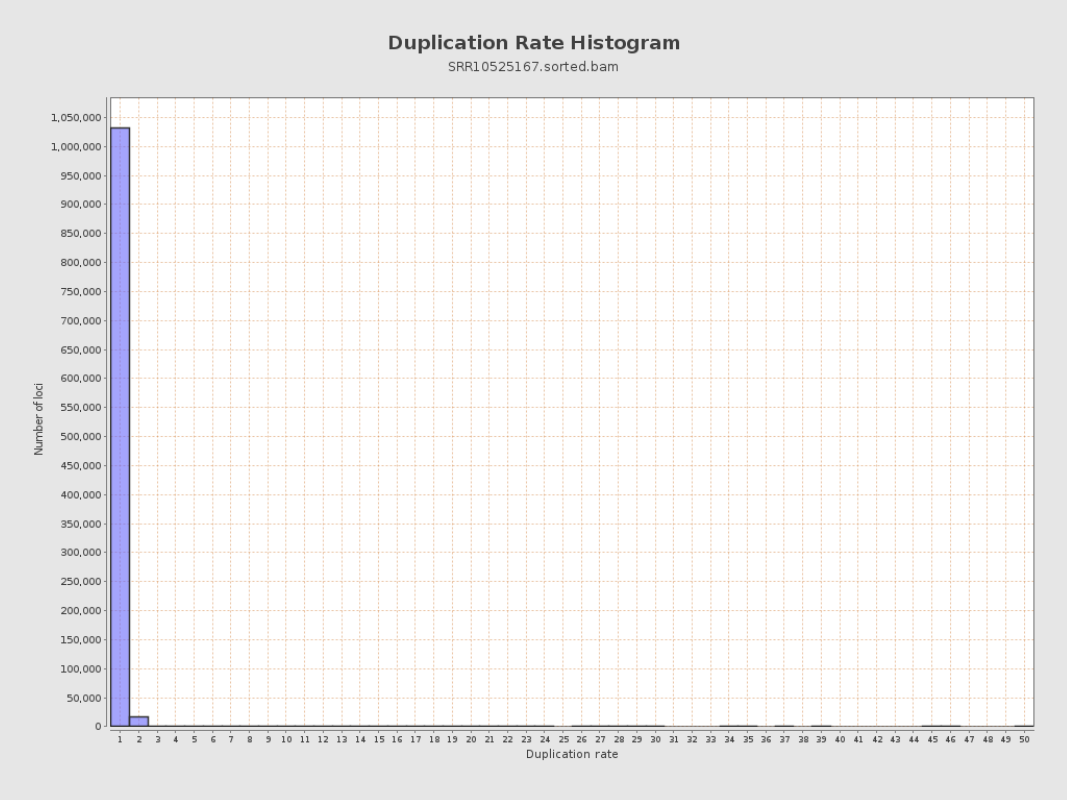
5. Results : Coverage Histogram (0-50X)



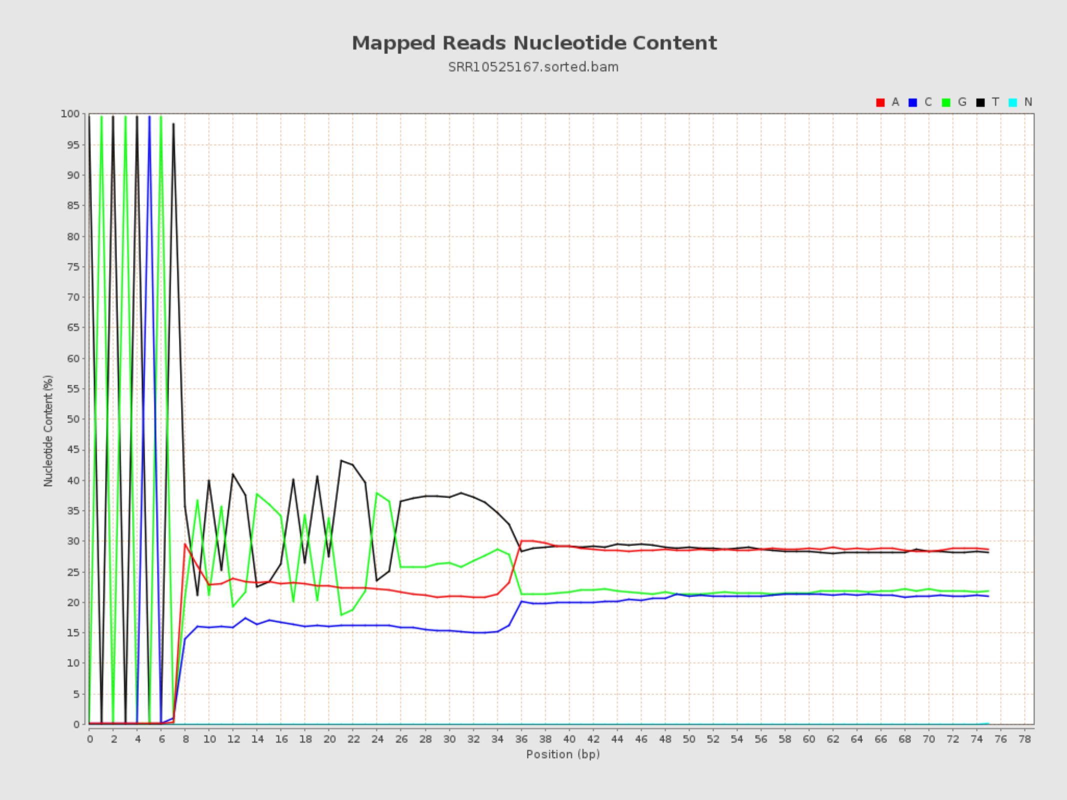
6. Results : Genome Fraction Coverage



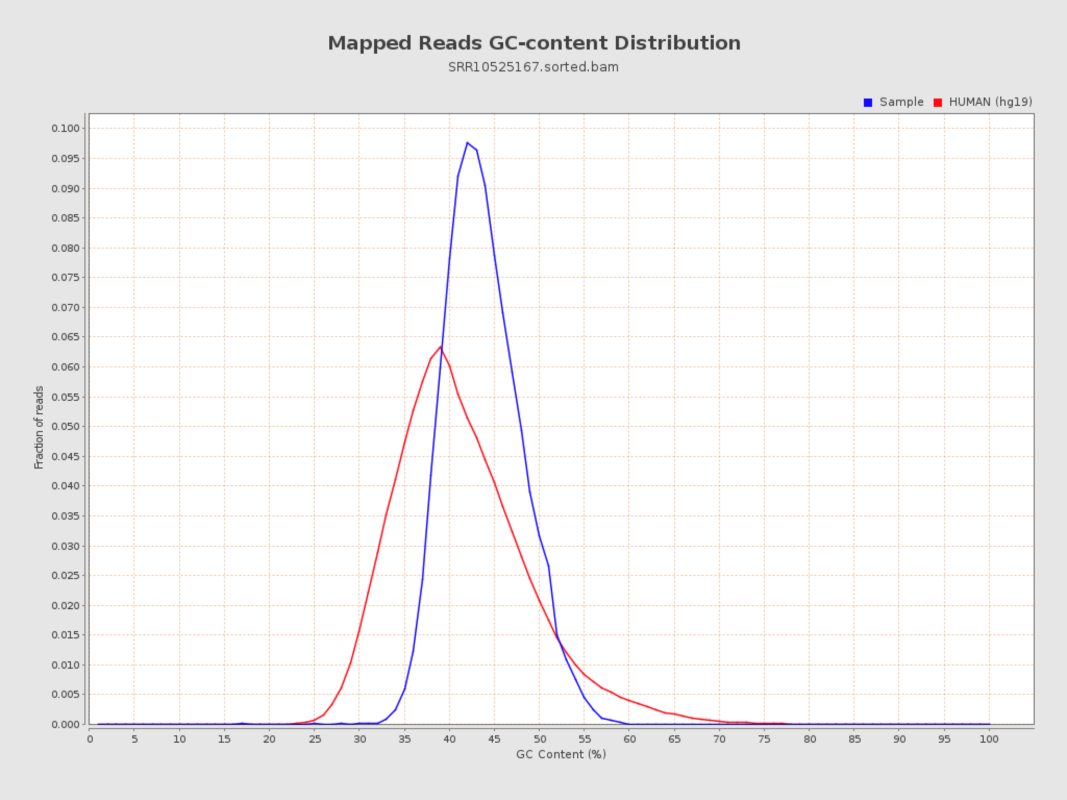
7. Results : Duplication Rate Histogram



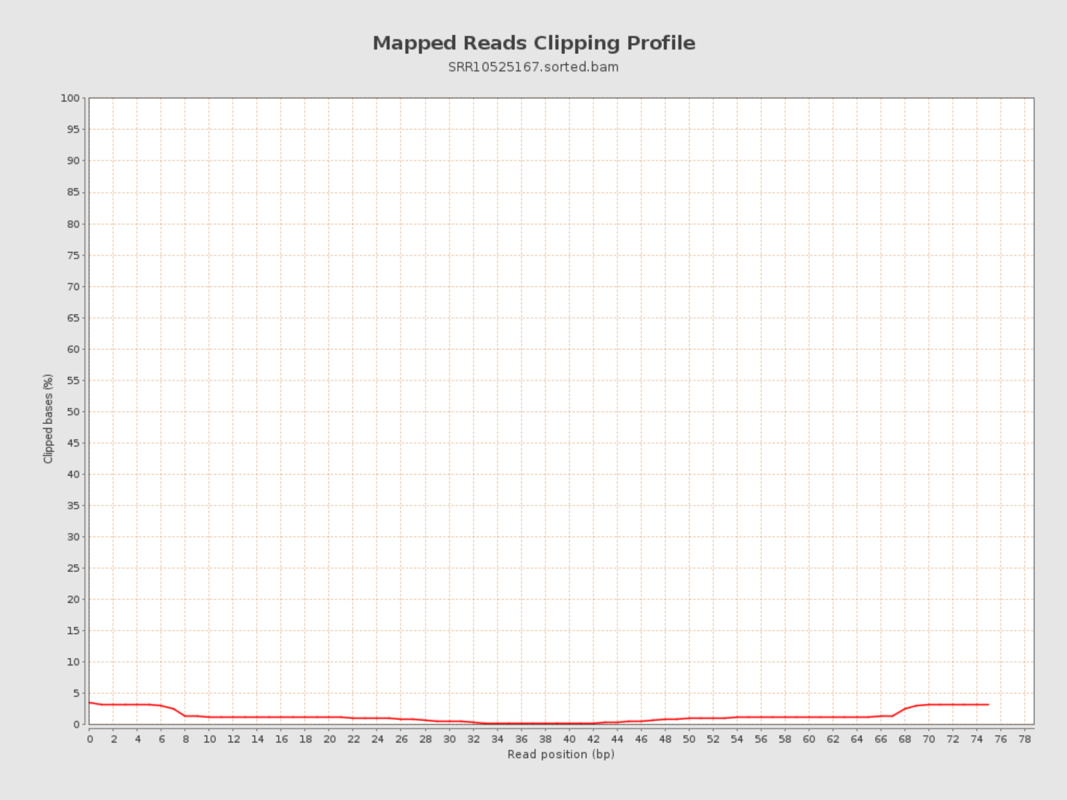
8. Results : Mapped Reads Nucleotide Content



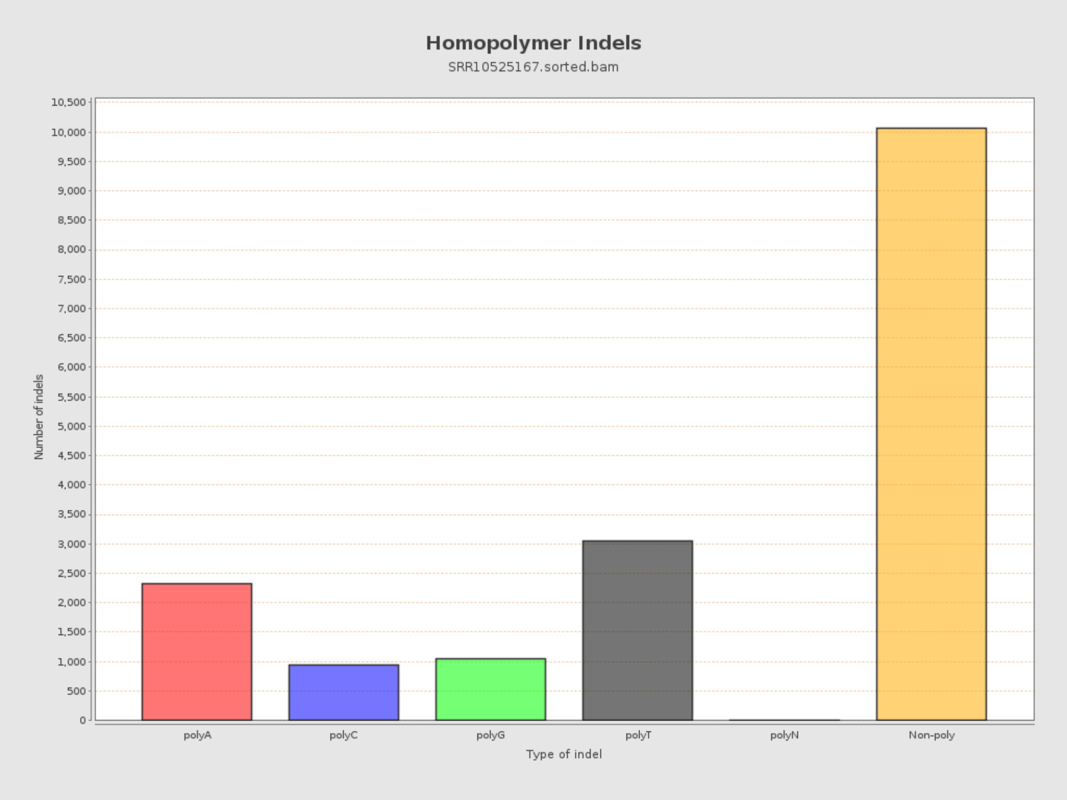
9. Results : Mapped Reads GC-content Distribution



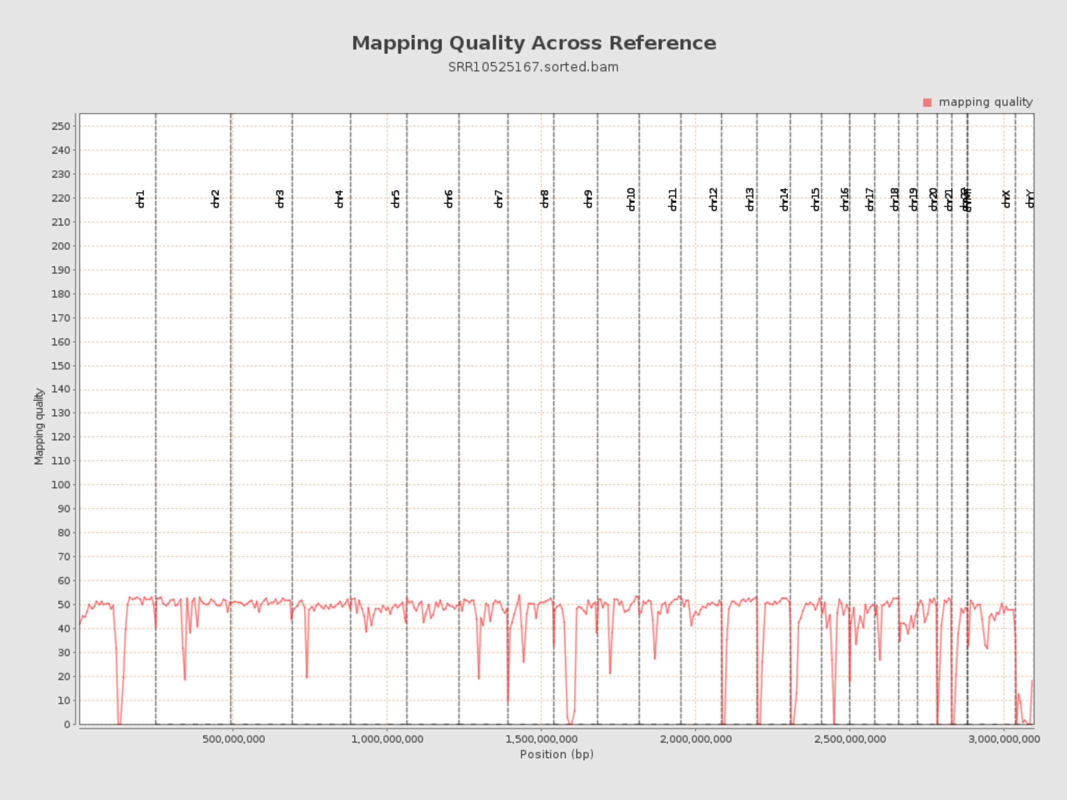
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram