Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:39:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525217.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_SRR10525217 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525217.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:39:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525217.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	808,671
Mapped reads	732,699 / 90.61%
Unmapped reads	75,972 / 9.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,934 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	16,068 / 1.99%
Duplication rate	1.57%
Clipped reads	733,024 / 90.65%

2.2. ACGT Content

Number/percentage of A's	11,952,540 / 26.87%
Number/percentage of C's	8,771,794 / 19.72%
Number/percentage of T's	13,715,778 / 30.83%
Number/percentage of G's	10,044,583 / 22.58%
Number/percentage of N's	1,015 / 0%
GC Percentage	42.3%

2.3. Coverage

Mean	0.0144

Standard Deviation	0.1685

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

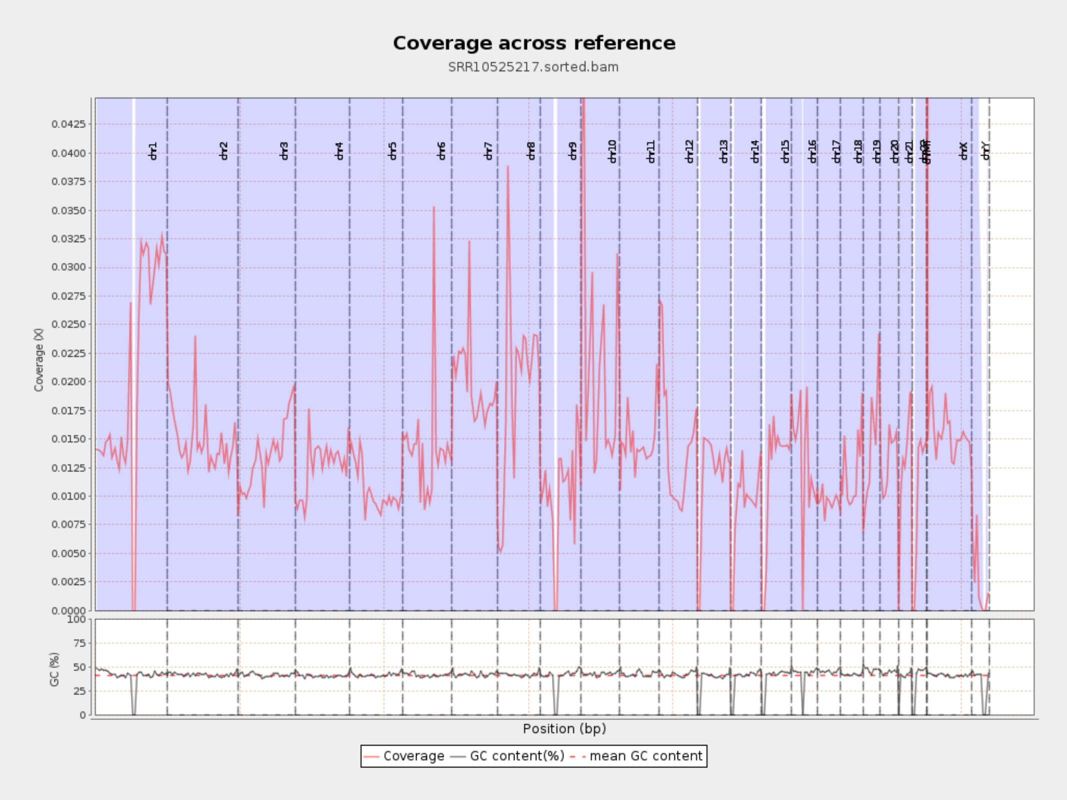
General error rate	0.51%
Mismatches	221,348
Insertions	3,214
Mapped reads with at least one insertion	0.44%
Deletions	9,647
Mapped reads with at least one deletion	1.31%
Homopolymer indels	41.73%

2.6. Chromosome stats

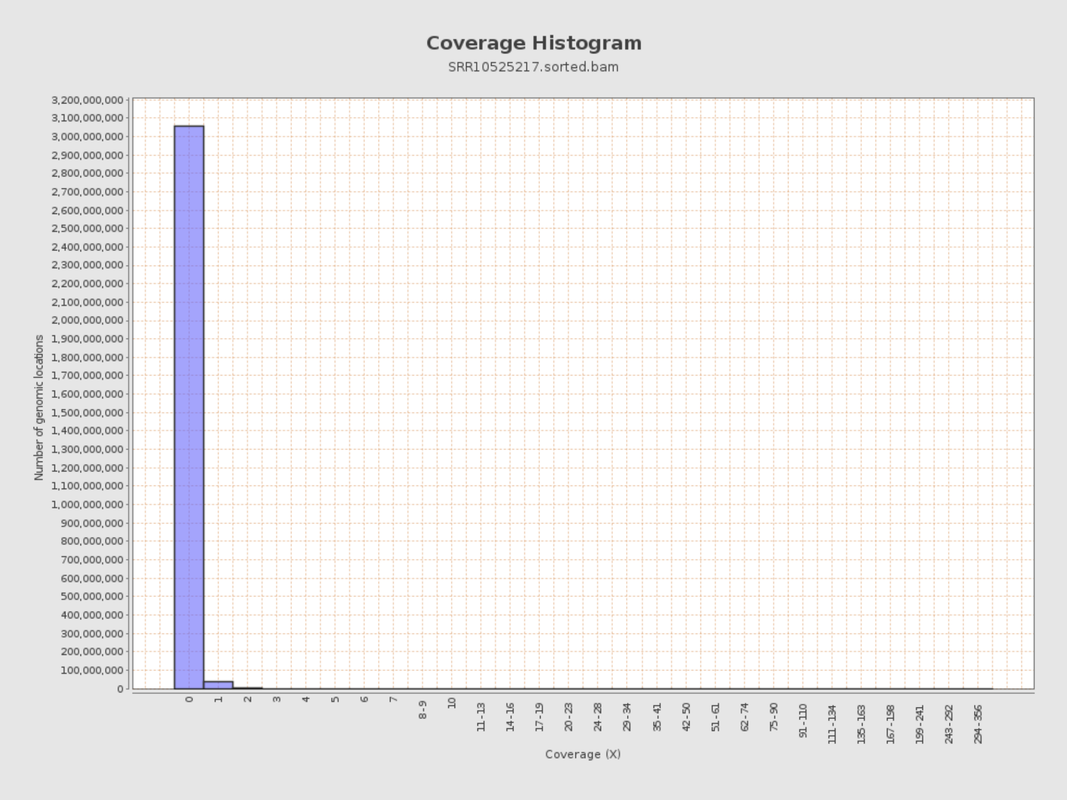
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5071954	0.0203	0.3075
chr2	243199373	3613014	0.0149	0.1864
chr3	198022430	2681092	0.0135	0.122
chr4	191154276	2415642	0.0126	0.1221
chr5	180915260	1911223	0.0106	0.107
chr6	171115067	2439195	0.0143	0.1303
chr7	159138663	3184885	0.02	0.2592

chr8	146364022	2899295	0.0198	0.1682
chr9	141213431	1441596	0.0102	0.1195
chr10	135534747	2985384	0.022	0.1854
chr11	135006516	1978525	0.0147	0.1403
chr12	133851895	1930677	0.0144	0.1256
chr13	115169878	1351463	0.0117	0.1124
chr14	107349540	980466	0.0091	0.1017
chr15	102531392	1212216	0.0118	0.1127
chr16	90354753	1188672	0.0132	0.1261
chr17	81195210	772994	0.0095	0.1042
chr18	78077248	933383	0.012	0.2163
chr19	59128983	867109	0.0147	0.2058
chr20	63025520	824172	0.0131	0.1208
chr21	48129895	631494	0.0131	0.1234
chr22	51304566	516742	0.0101	0.1042
chrMT	16571	113179	6.8299	4.3664
chrX	155270560	2414468	0.0156	0.1339
chrY	59373566	142434	0.0024	0.0827

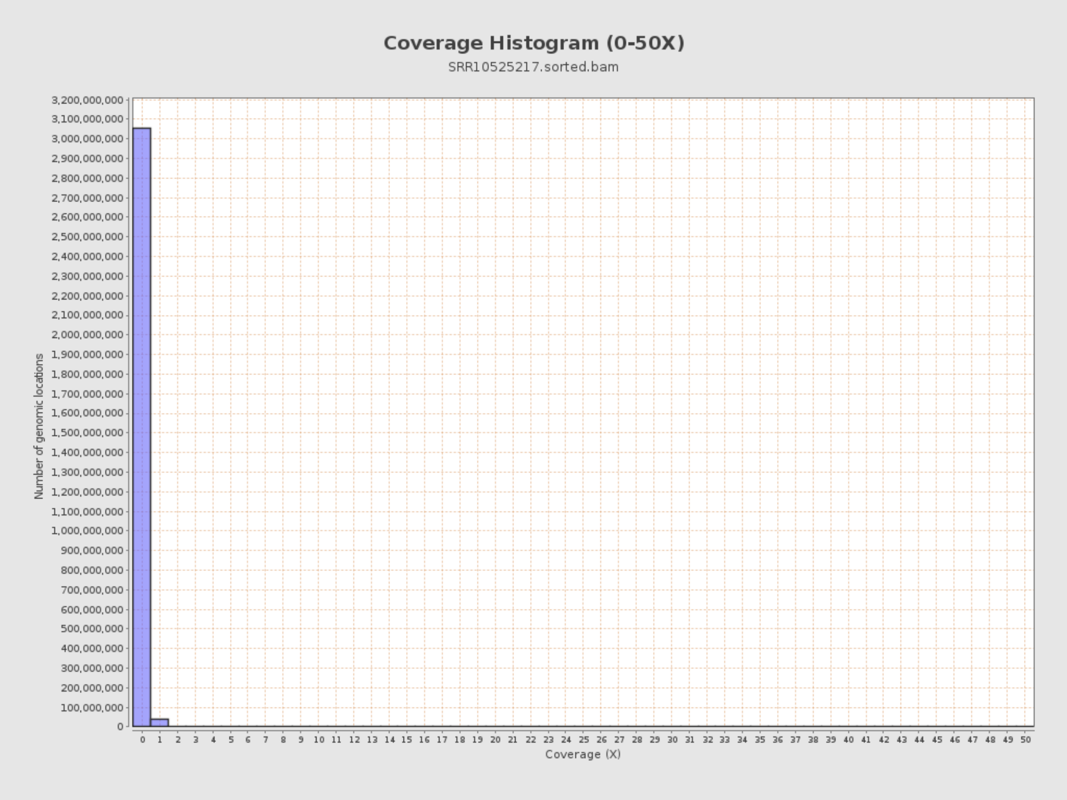
3. Results : Coverage across reference



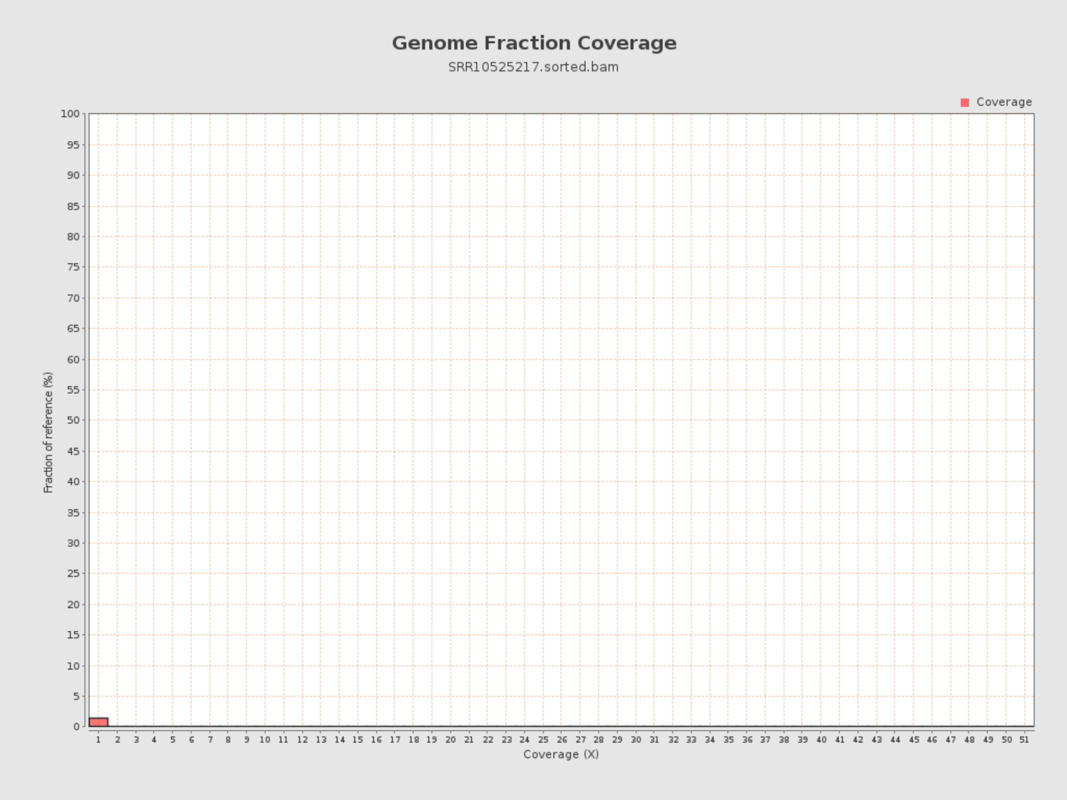
4. Results : Coverage Histogram



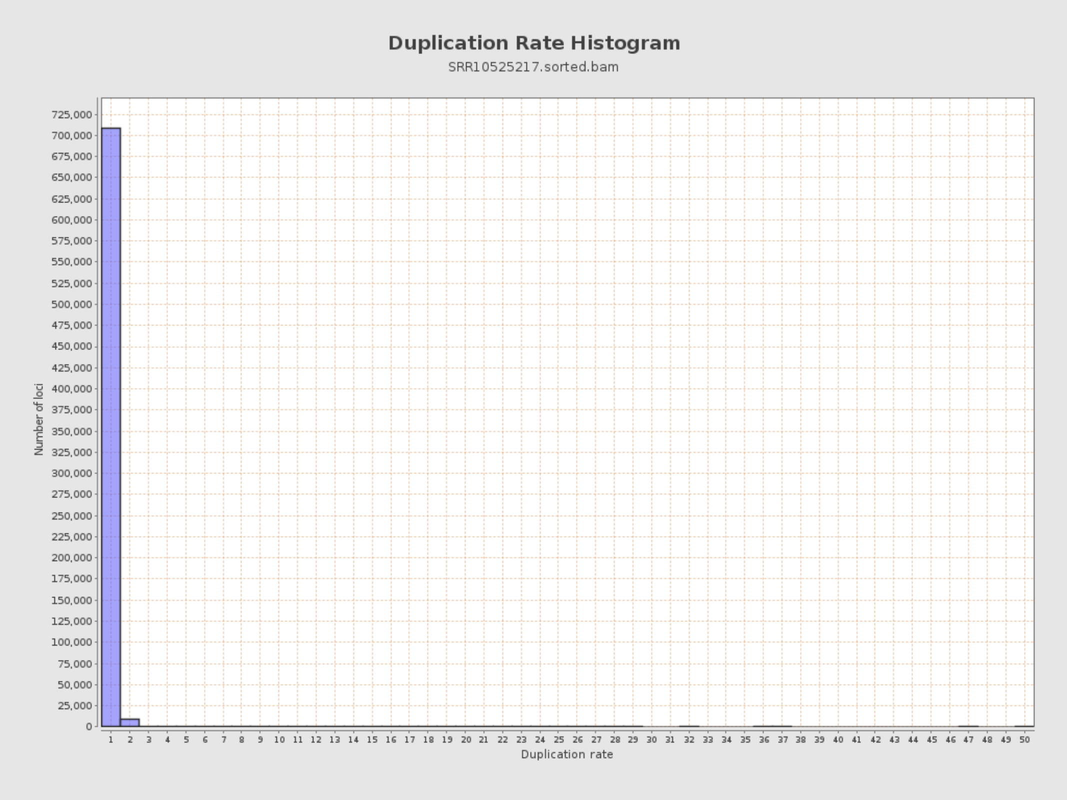
5. Results : Coverage Histogram (0-50X)



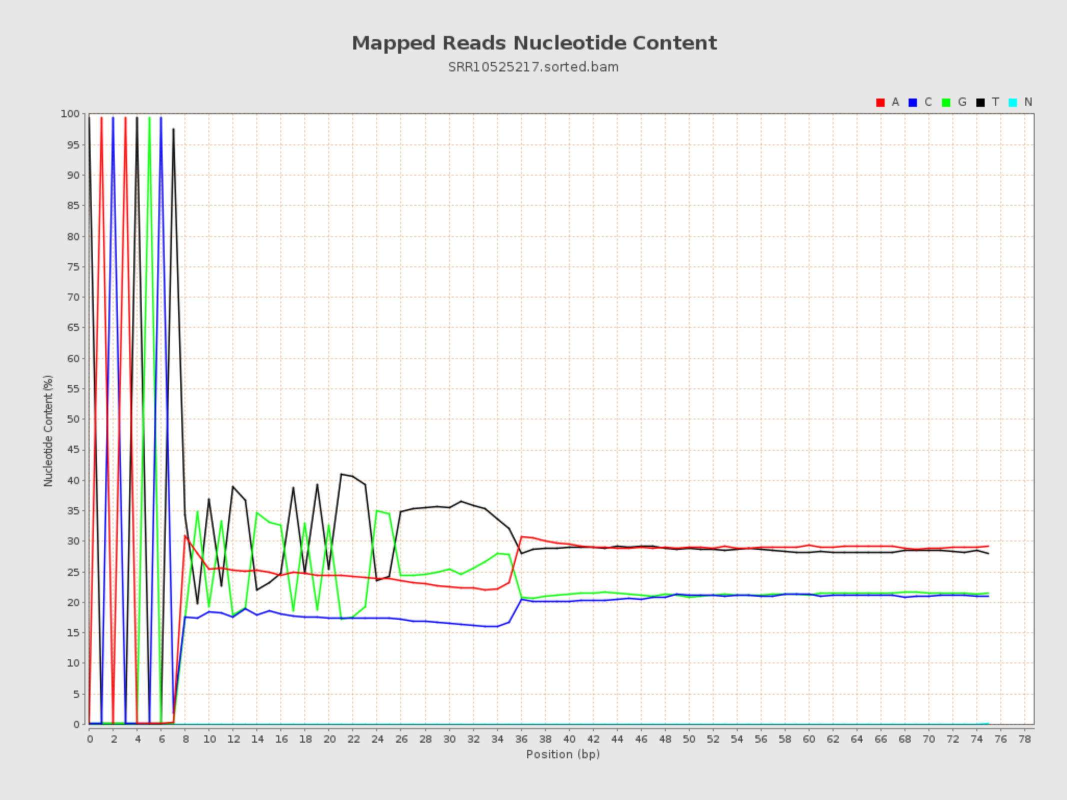
6. Results : Genome Fraction Coverage



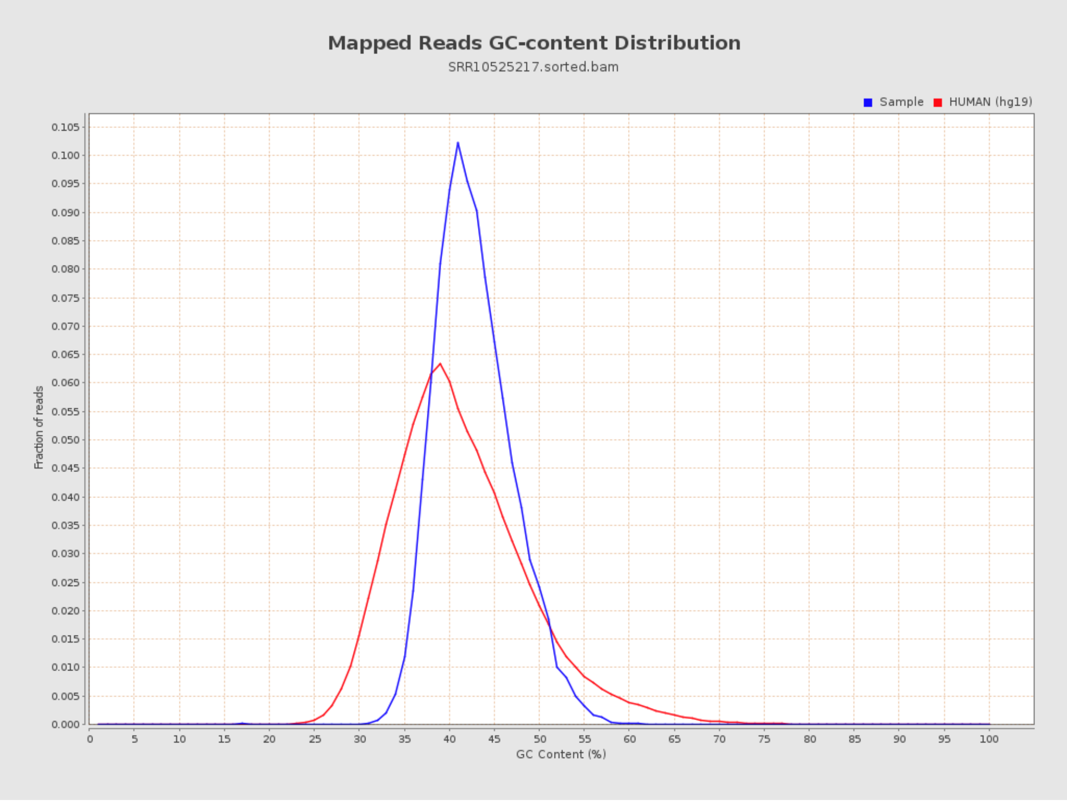
7. Results : Duplication Rate Histogram



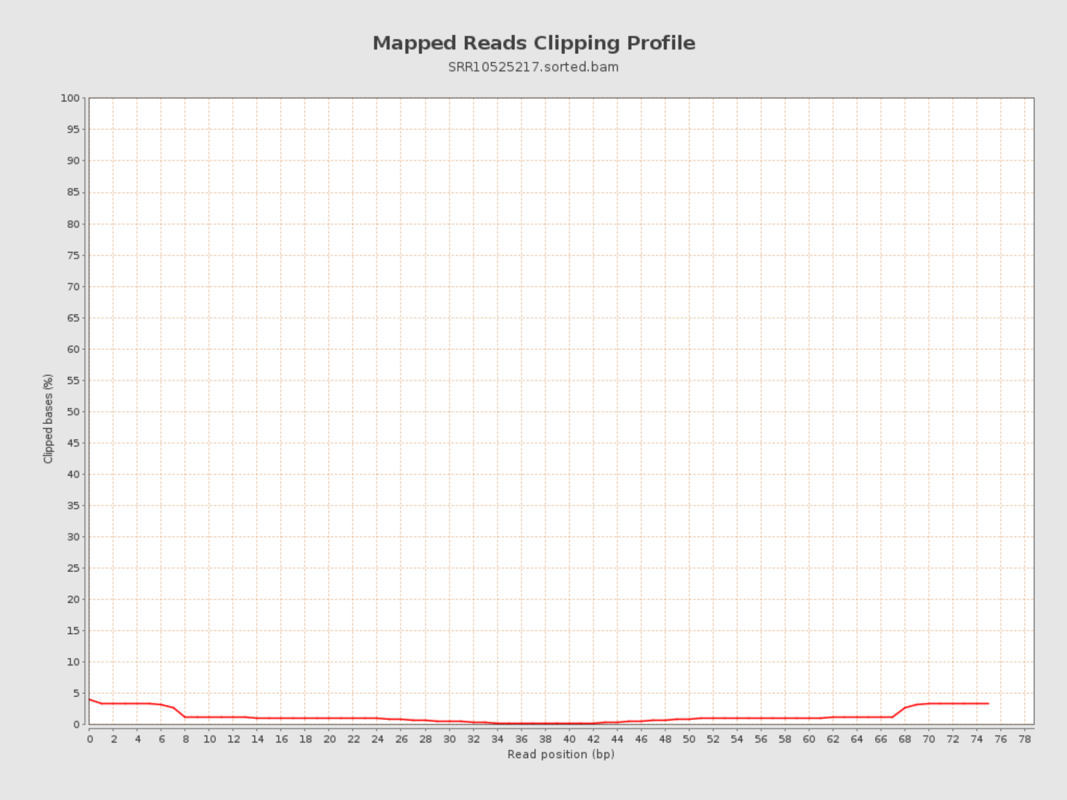
8. Results : Mapped Reads Nucleotide Content



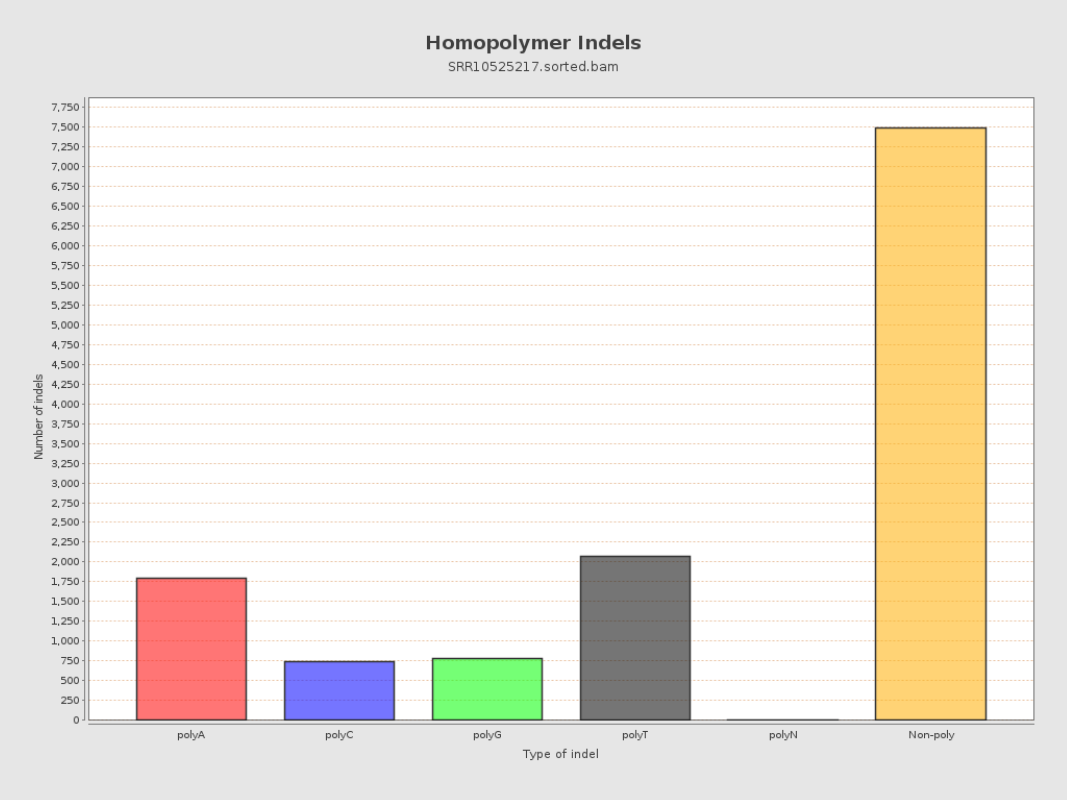
9. Results : Mapped Reads GC-content Distribution



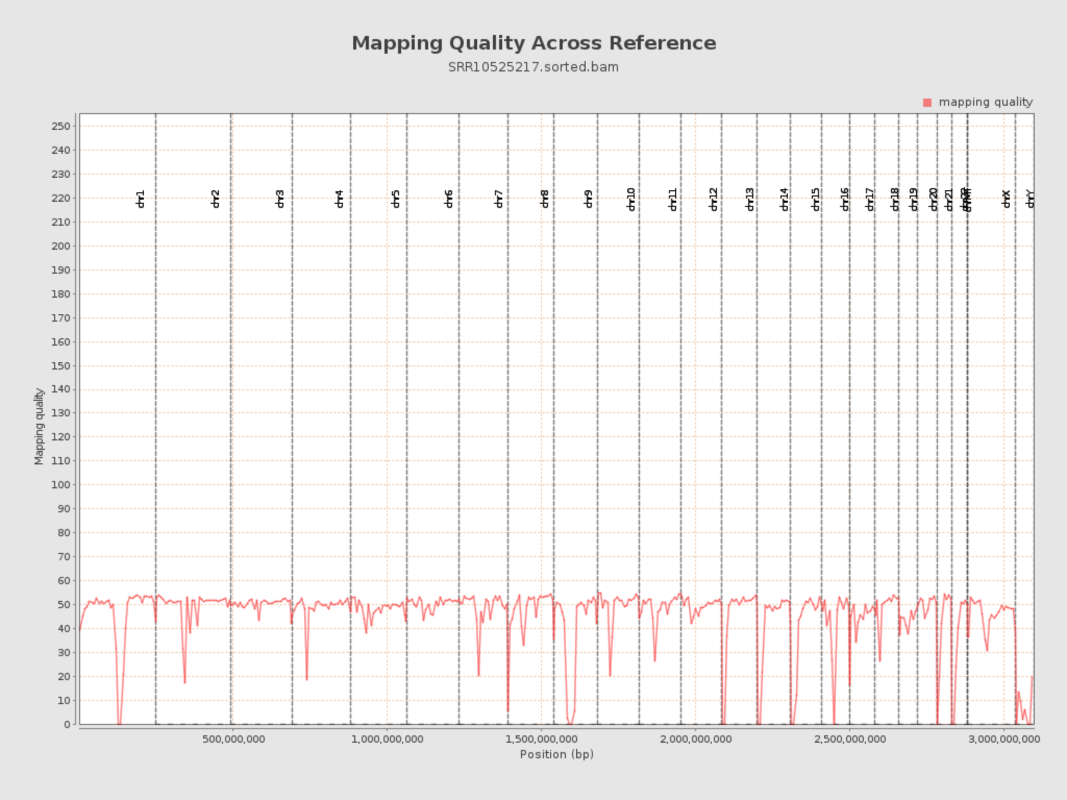
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram