Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:43:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524717.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_SRR10524717 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524717.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:43:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524717.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	567,177
Mapped reads	516,008 / 90.98%
Unmapped reads	51,169 / 9.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,579 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	11,100 / 1.96%
Duplication rate	1.53%
Clipped reads	515,479 / 90.89%

2.2. ACGT Content

Number/percentage of A's	7,198,831 / 24.12%
Number/percentage of C's	5,698,007 / 19.09%
Number/percentage of T's	9,984,963 / 33.45%
Number/percentage of G's	6,961,366 / 23.32%
Number/percentage of N's	3,806 / 0.01%
GC Percentage	42.41%

2.3. Coverage

Mean	0.0096

Standard Deviation	0.1265

2.4. Mapping Quality

Mean Mapping Quality	45.48

2.5. Mismatches and indels

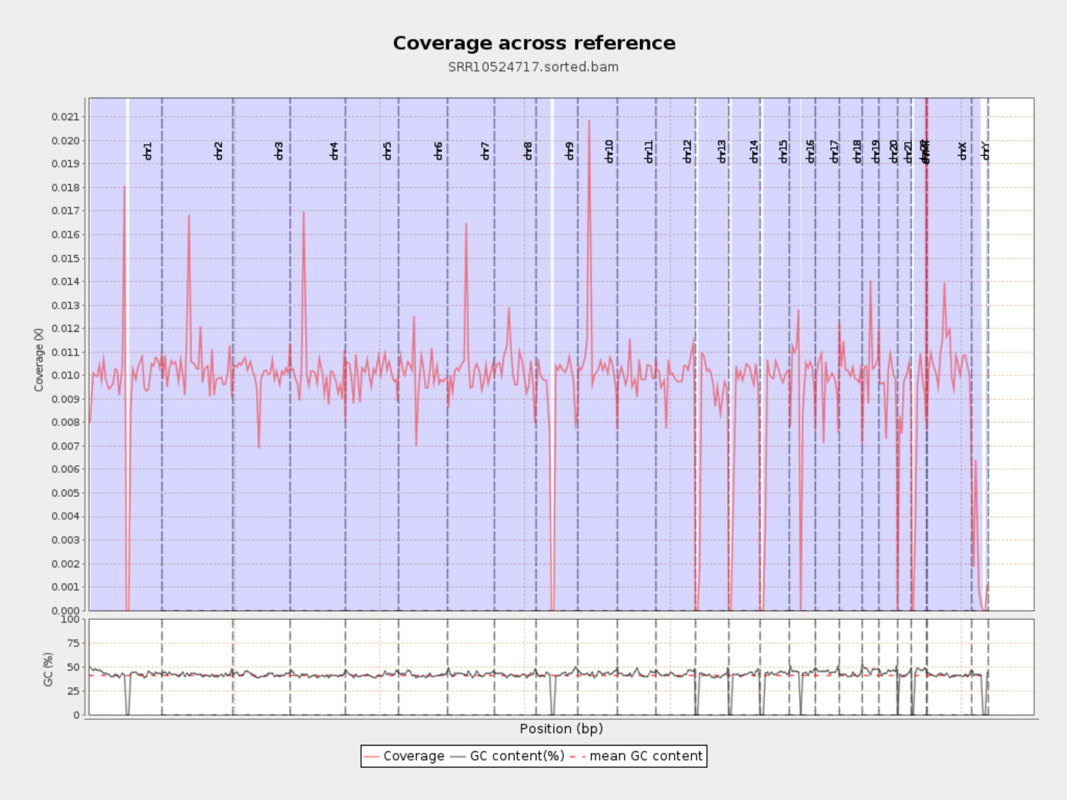
General error rate	0.53%
Mismatches	154,108
Insertions	2,420
Mapped reads with at least one insertion	0.47%
Deletions	5,690
Mapped reads with at least one deletion	1.09%
Homopolymer indels	40.21%

2.6. Chromosome stats

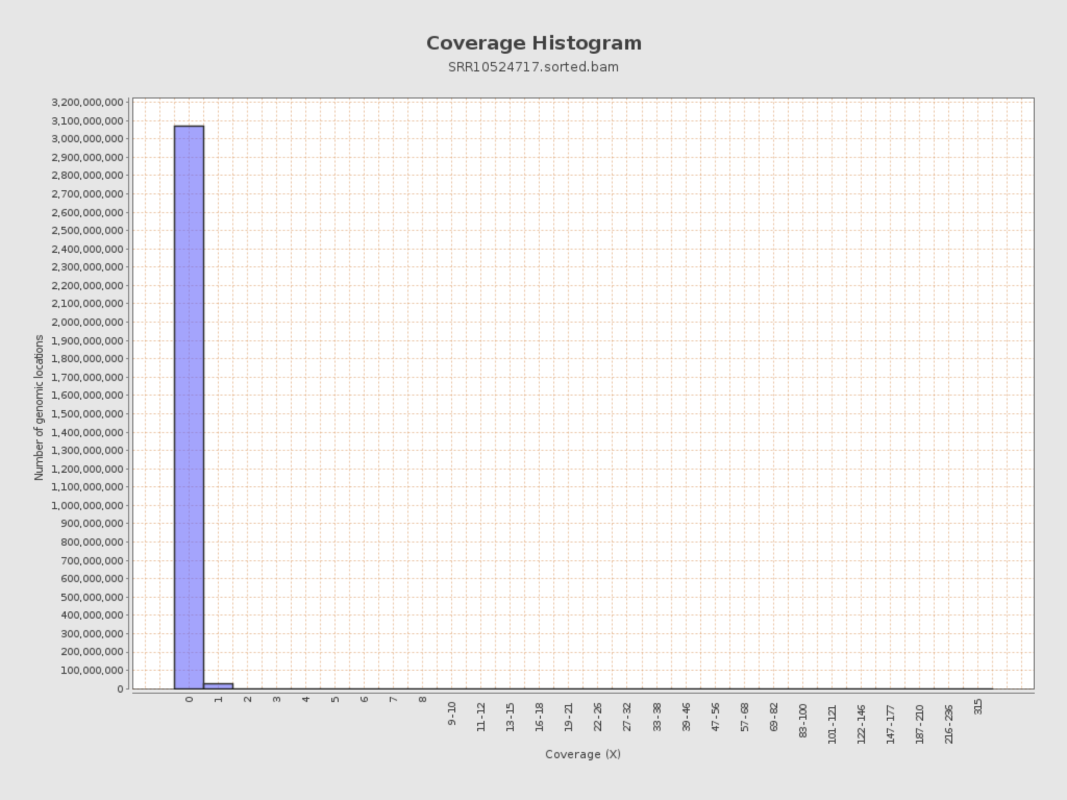
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2392618	0.0096	0.1946
chr2	243199373	2541884	0.0105	0.1676
chr3	198022430	1997385	0.0101	0.1036
chr4	191154276	1940080	0.0101	0.1081
chr5	180915260	1830613	0.0101	0.1037
chr6	171115067	1725428	0.0101	0.1105
chr7	159138663	1647307	0.0104	0.1437

chr8	146364022	1505553	0.0103	0.129
chr9	141213431	1244156	0.0088	0.1098
chr10	135534747	1483315	0.0109	0.1347
chr11	135006516	1349013	0.01	0.1145
chr12	133851895	1340627	0.01	0.1042
chr13	115169878	936331	0.0081	0.0937
chr14	107349540	896798	0.0084	0.0956
chr15	102531392	839710	0.0082	0.0932
chr16	90354753	860947	0.0095	0.1058
chr17	81195210	786820	0.0097	0.1033
chr18	78077248	807398	0.0103	0.1511
chr19	59128983	626281	0.0106	0.1598
chr20	63025520	603443	0.0096	0.1016
chr21	48129895	402673	0.0084	0.1007
chr22	51304566	350061	0.0068	0.0849
chrMT	16571	3317	0.2002	0.4551
chrX	155270560	1645531	0.0106	0.1097
chrY	59373566	98790	0.0017	0.0762

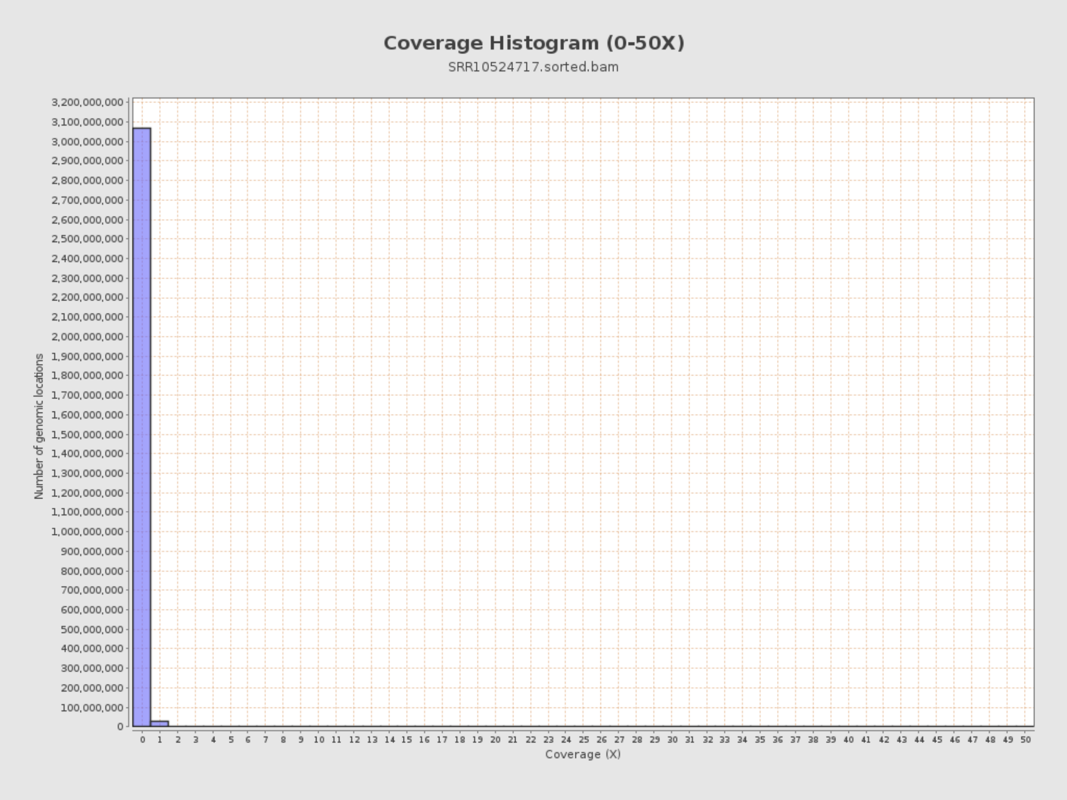
3. Results : Coverage across reference



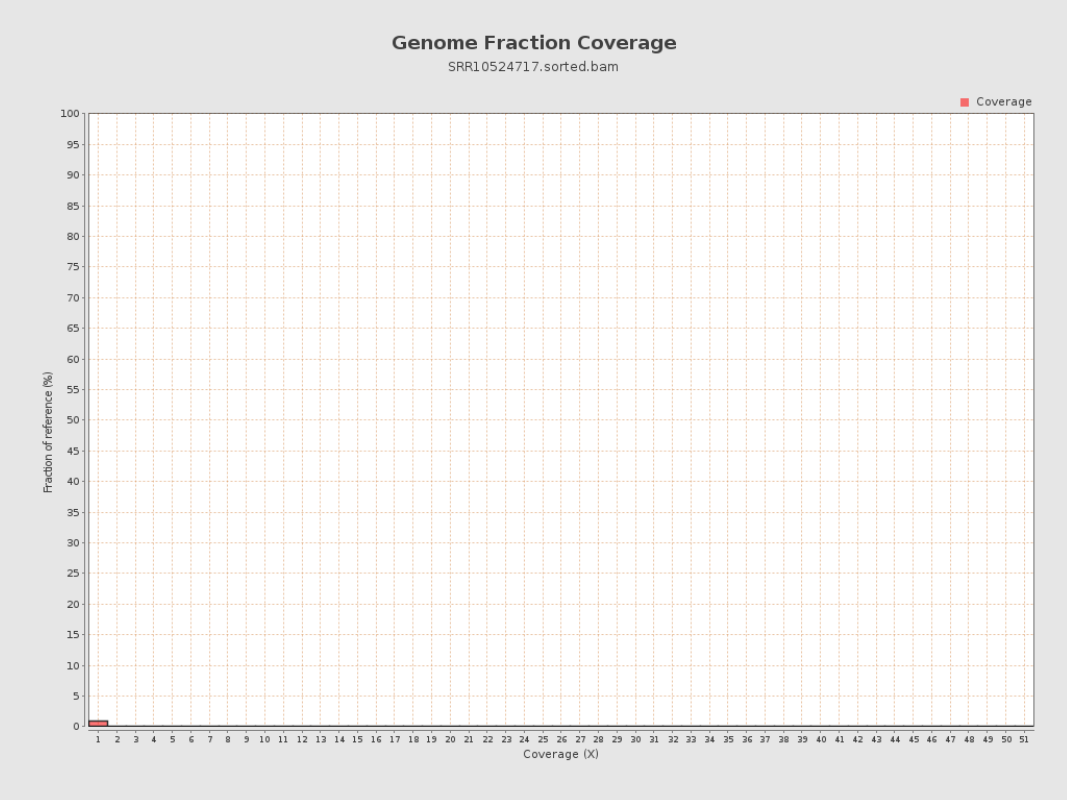
4. Results : Coverage Histogram



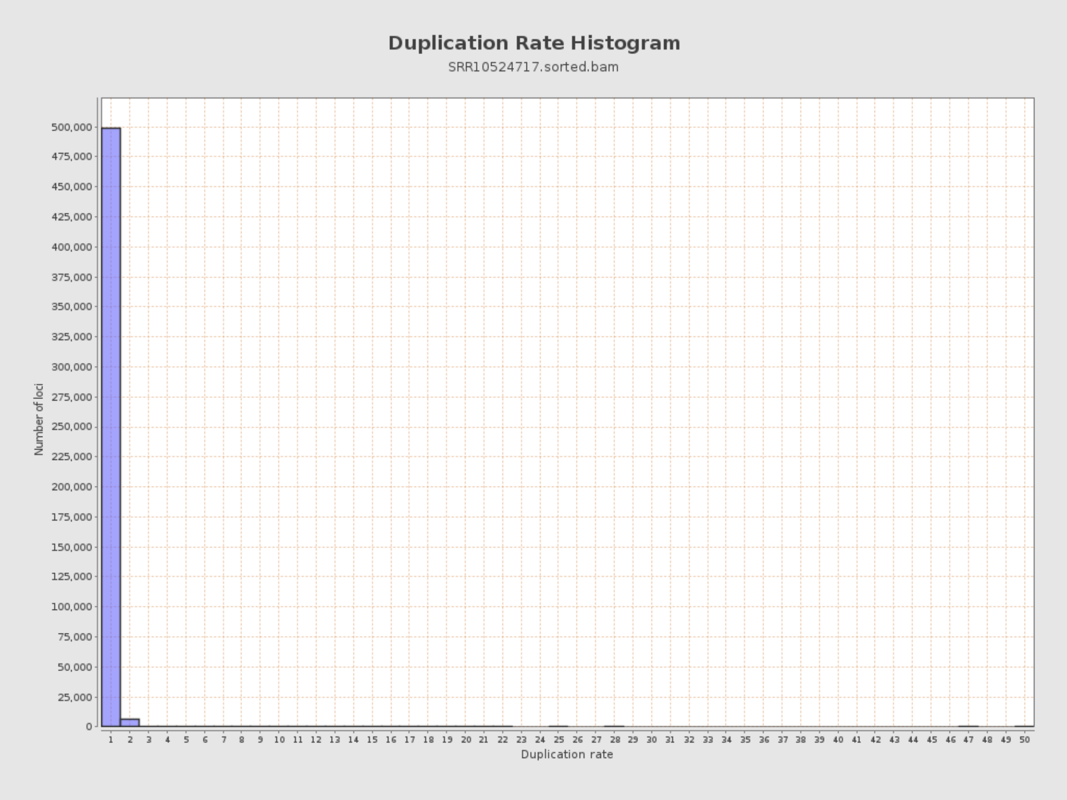
5. Results : Coverage Histogram (0-50X)



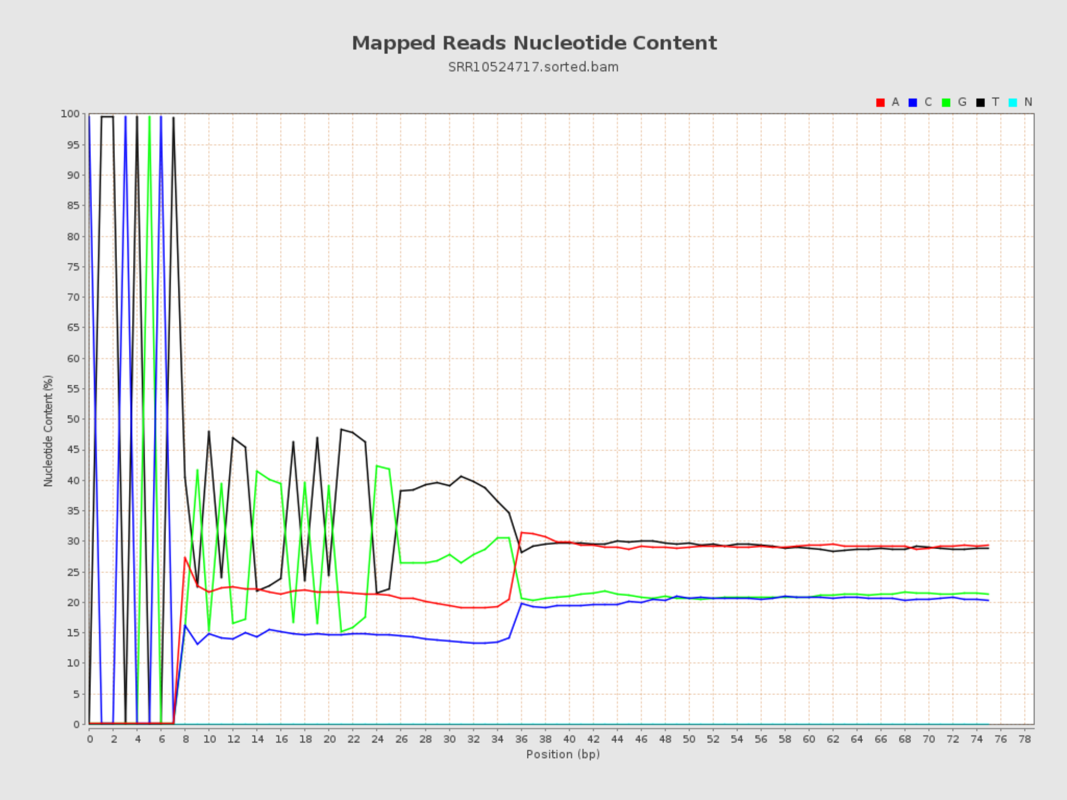
6. Results : Genome Fraction Coverage



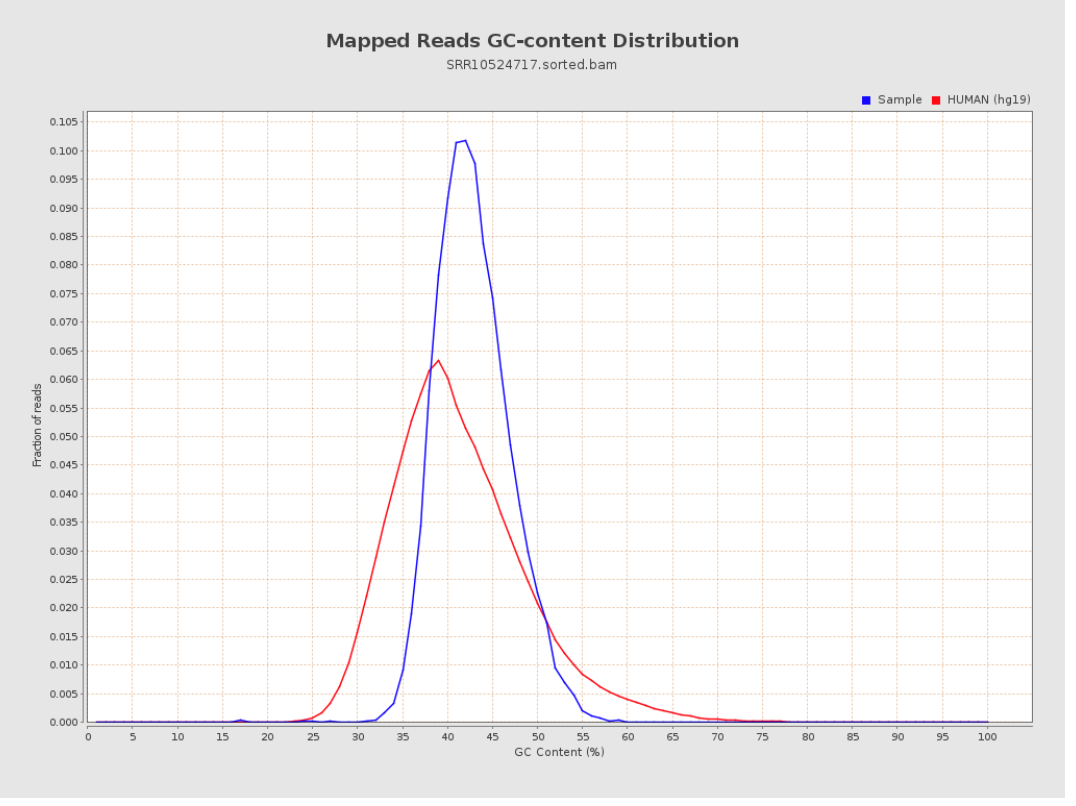
7. Results : Duplication Rate Histogram



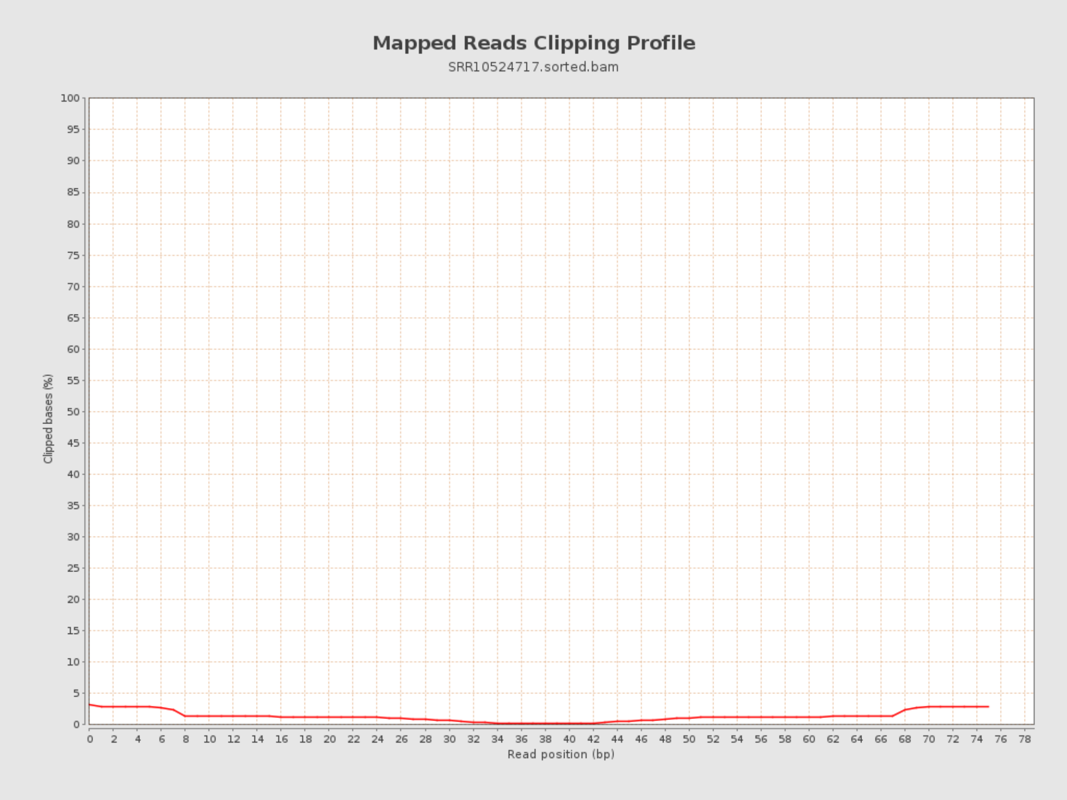
8. Results : Mapped Reads Nucleotide Content



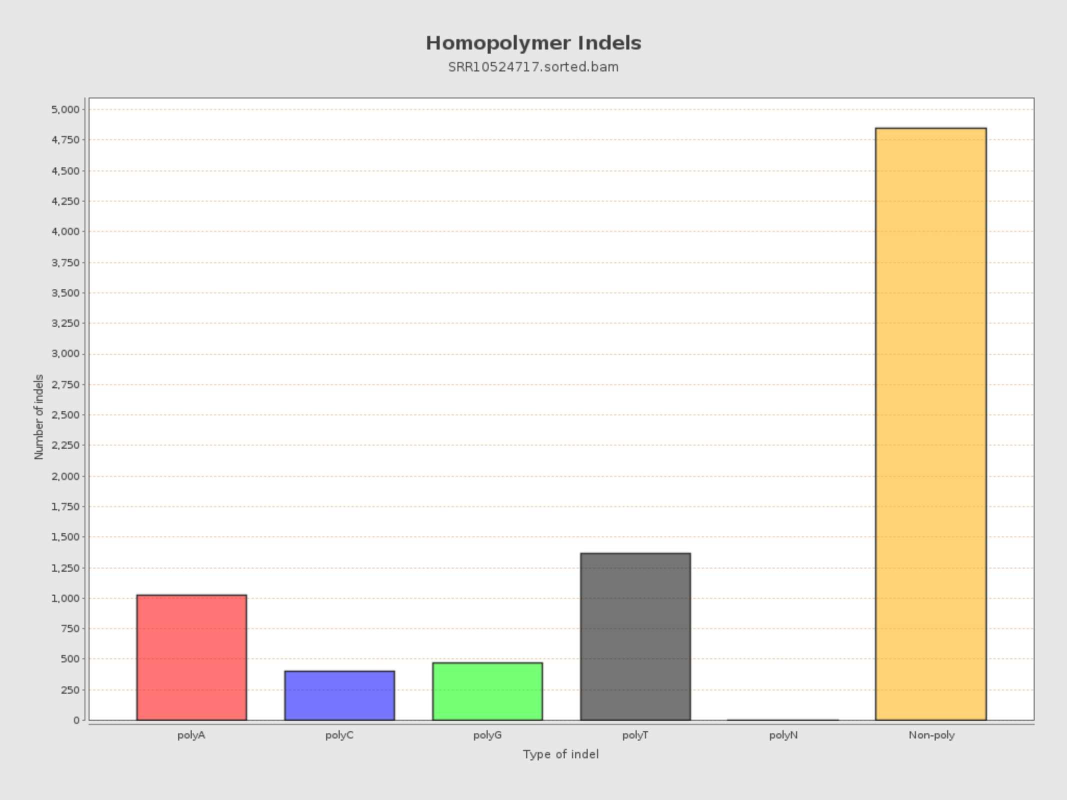
9. Results : Mapped Reads GC-content Distribution



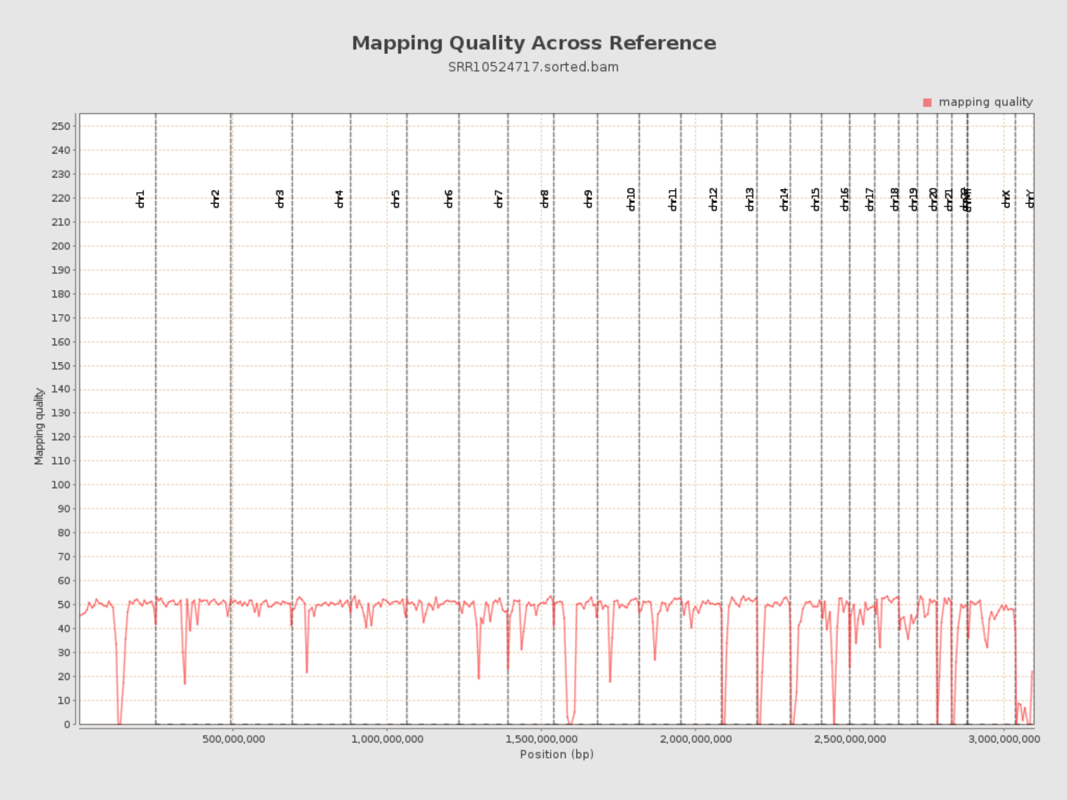
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram