Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:29:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524360.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_SRR10524360 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524360.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:29:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524360.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	836,428
Mapped reads	761,838 / 91.08%
Unmapped reads	74,590 / 8.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,609 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	20,452 / 2.45%
Duplication rate	1.99%
Clipped reads	762,688 / 91.18%

2.2. ACGT Content

Number/percentage of A's	11,686,561 / 26.31%
Number/percentage of C's	8,002,736 / 18.02%
Number/percentage of T's	13,864,120 / 31.21%
Number/percentage of G's	10,860,833 / 24.45%
Number/percentage of N's	6,171 / 0.01%
GC Percentage	42.47%

2.3. Coverage

Mean	0.0144

Standard Deviation	0.1645

2.4. Mapping Quality

Mean Mapping Quality	44.93

2.5. Mismatches and indels

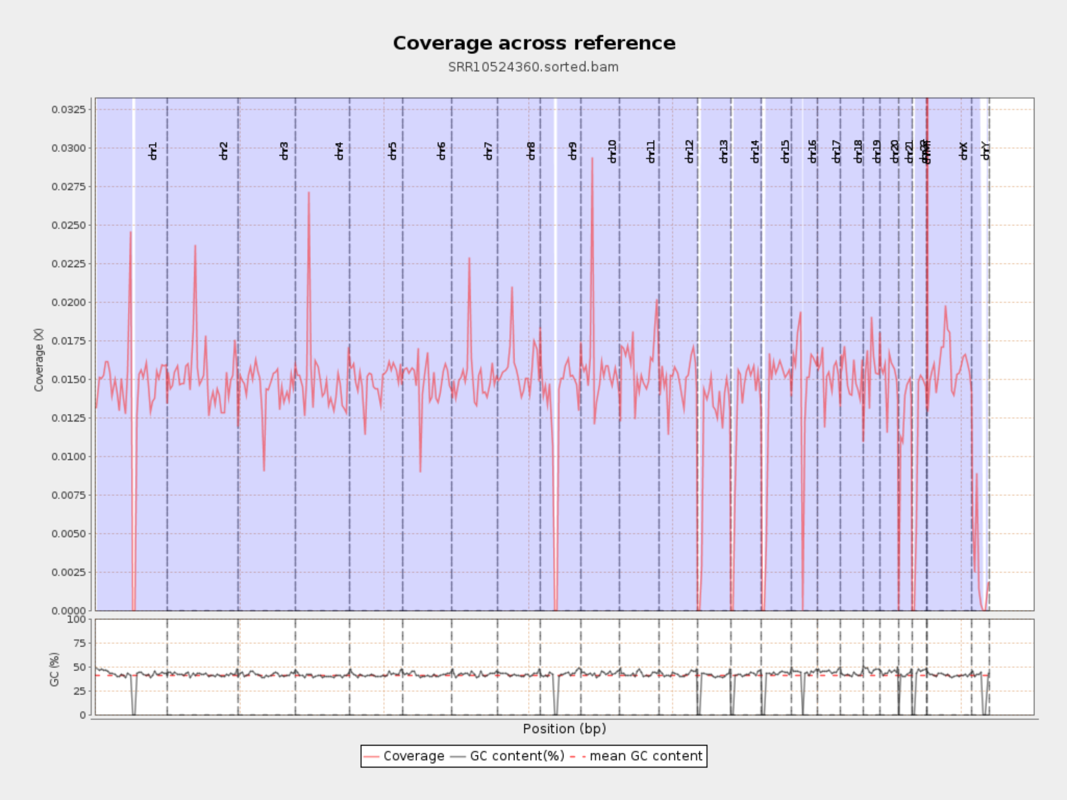
General error rate	0.54%
Mismatches	230,824
Insertions	3,563
Mapped reads with at least one insertion	0.46%
Deletions	7,995
Mapped reads with at least one deletion	1.04%
Homopolymer indels	41.11%

2.6. Chromosome stats

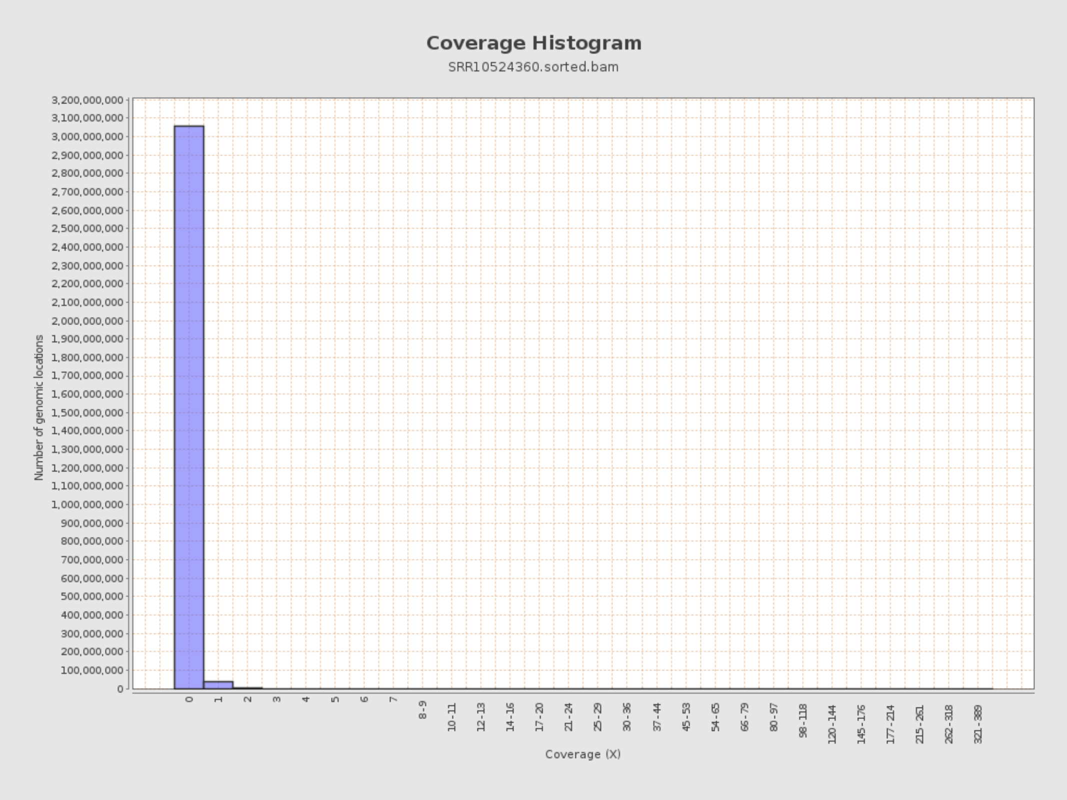
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3520613	0.0141	0.2777
chr2	243199373	3699434	0.0152	0.2096
chr3	198022430	2867549	0.0145	0.1269
chr4	191154276	2865625	0.015	0.1428
chr5	180915260	2717813	0.015	0.1287
chr6	171115067	2535090	0.0148	0.1339
chr7	159138663	2417668	0.0152	0.1862

chr8	146364022	2304283	0.0157	0.1543
chr9	141213431	1837929	0.013	0.1425
chr10	135534747	2156788	0.0159	0.1675
chr11	135006516	2167317	0.0161	0.153
chr12	133851895	2004295	0.015	0.1307
chr13	115169878	1328625	0.0115	0.1129
chr14	107349540	1353212	0.0126	0.1214
chr15	102531392	1293843	0.0126	0.118
chr16	90354753	1323228	0.0146	0.1331
chr17	81195210	1233326	0.0152	0.1336
chr18	78077248	1181973	0.0151	0.226
chr19	59128983	933108	0.0158	0.1942
chr20	63025520	956606	0.0152	0.1315
chr21	48129895	578187	0.012	0.1262
chr22	51304566	530756	0.0103	0.1064
chrMT	16571	6097	0.3679	0.6291
chrX	155270560	2472937	0.0159	0.14
chrY	59373566	146791	0.0025	0.0764

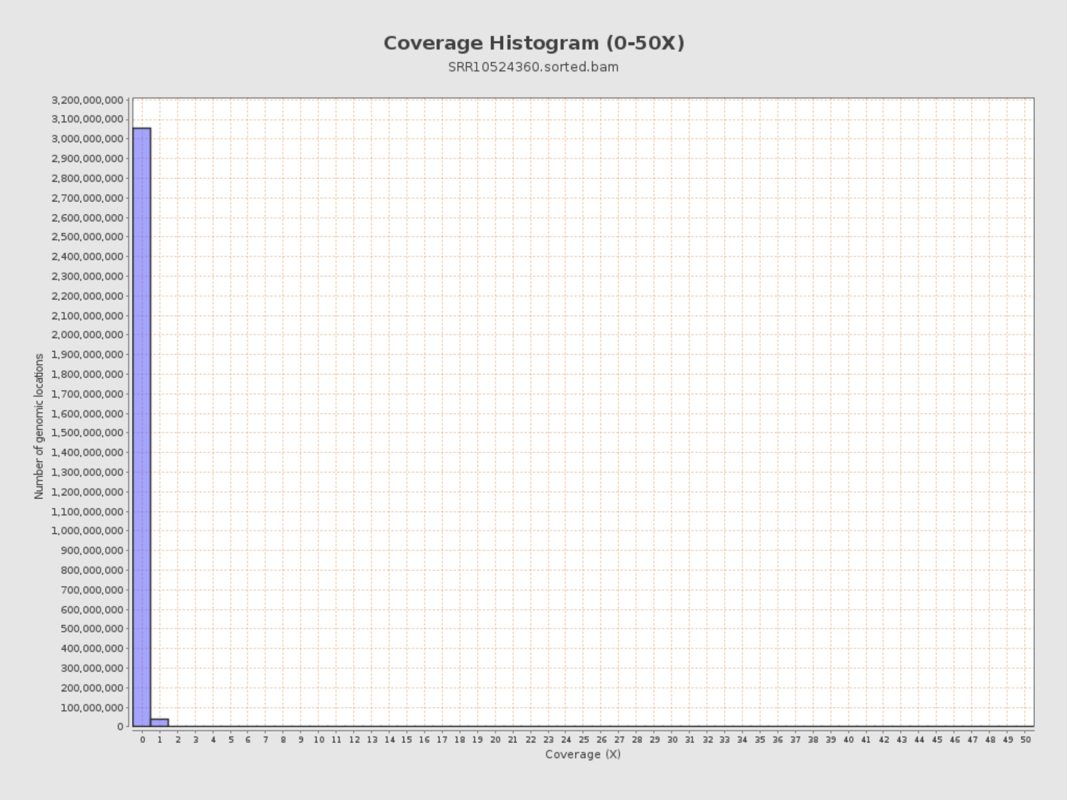
3. Results : Coverage across reference



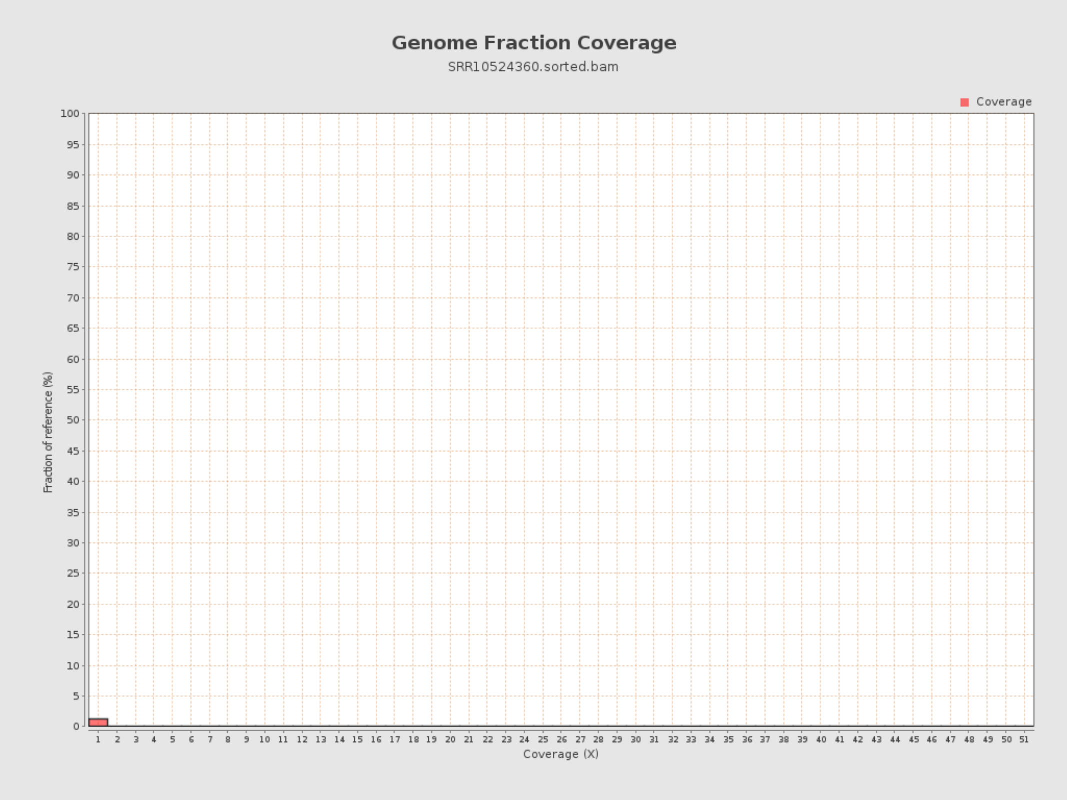
4. Results : Coverage Histogram



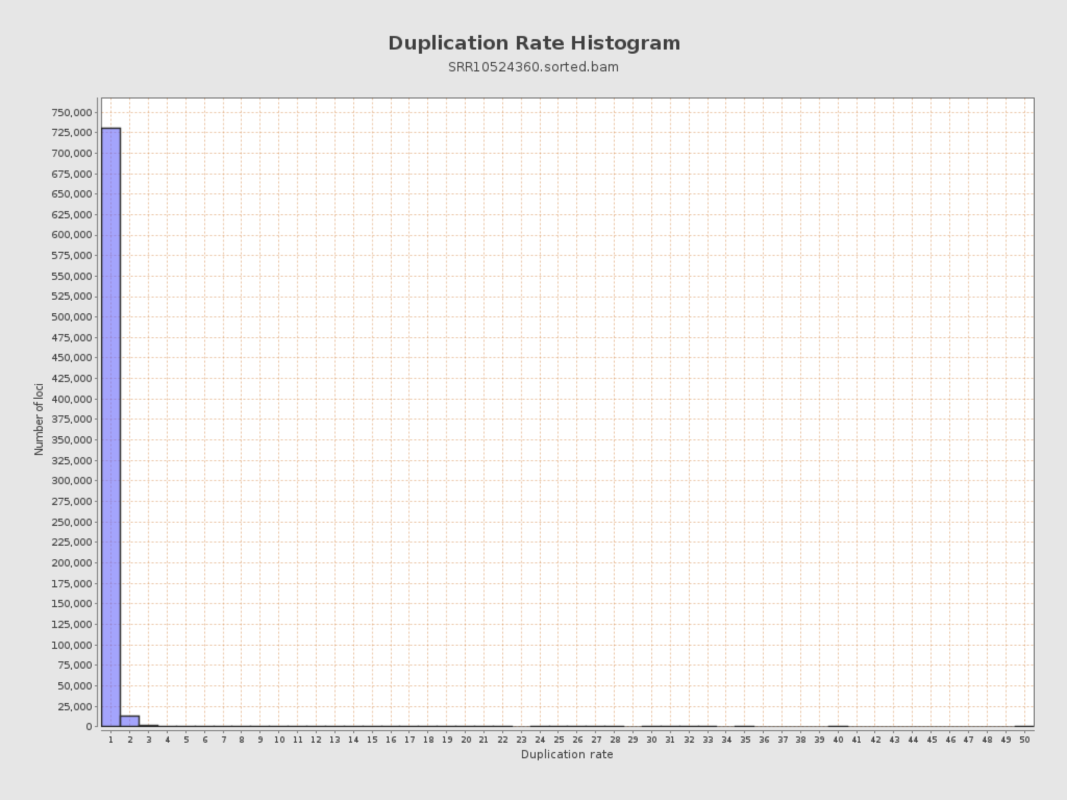
5. Results : Coverage Histogram (0-50X)



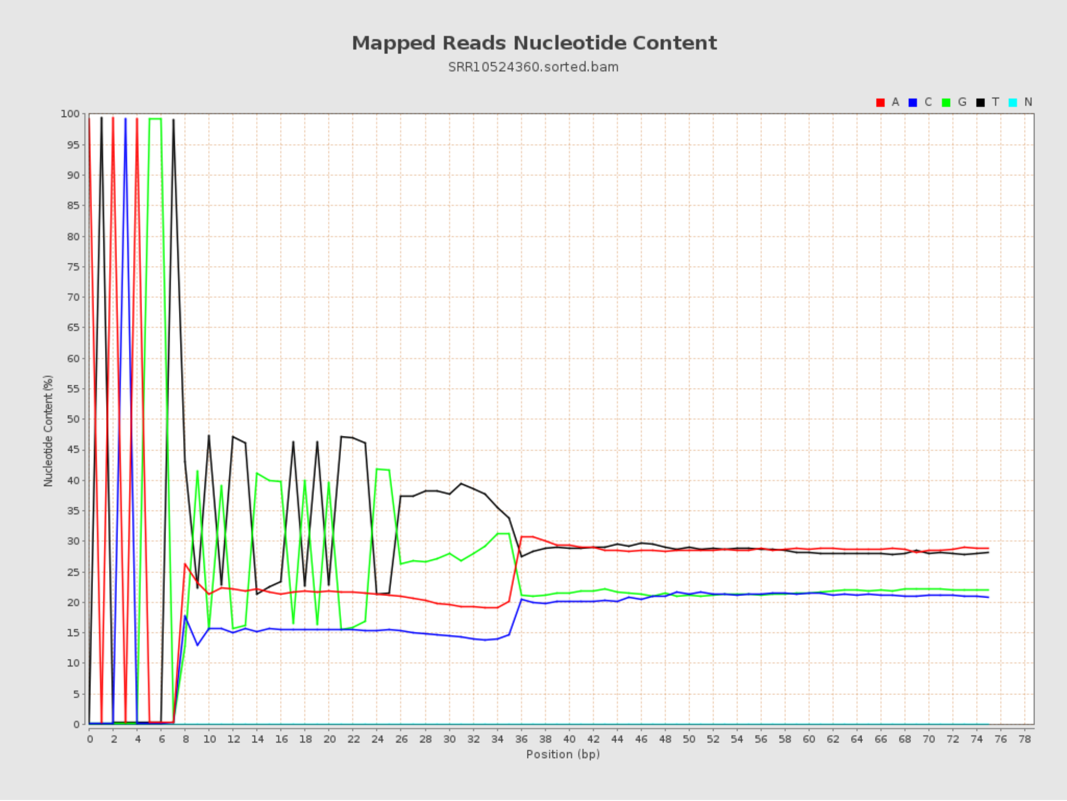
6. Results : Genome Fraction Coverage



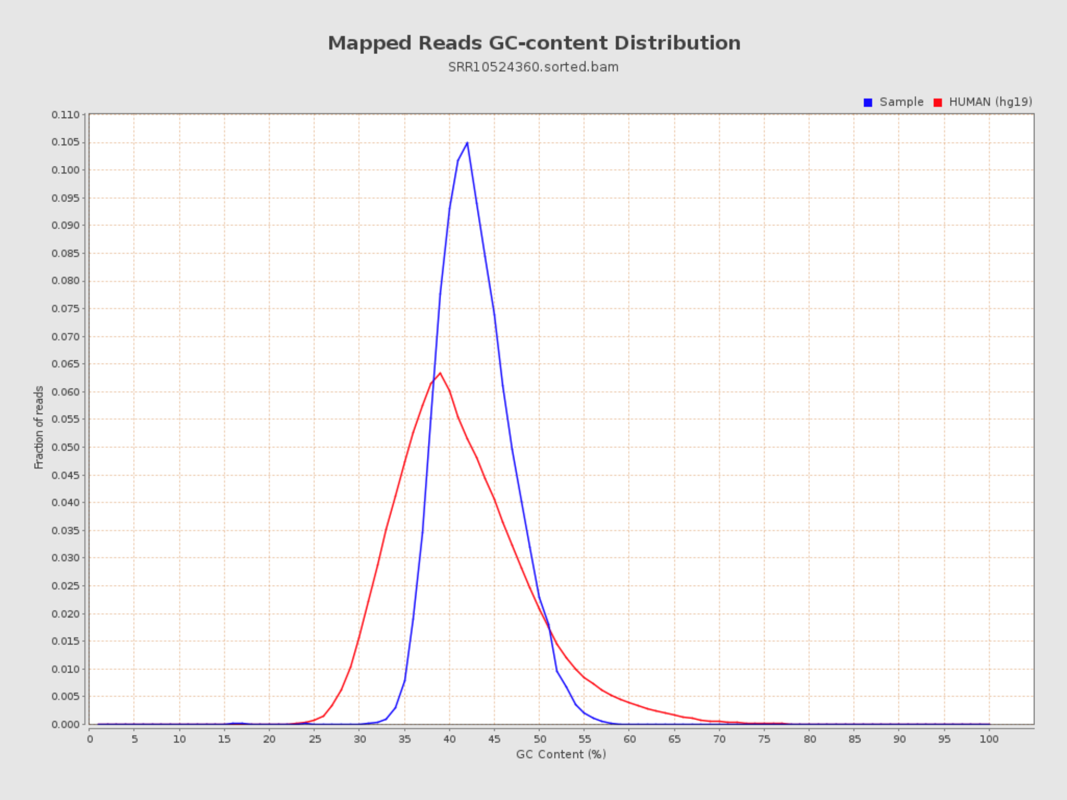
7. Results : Duplication Rate Histogram



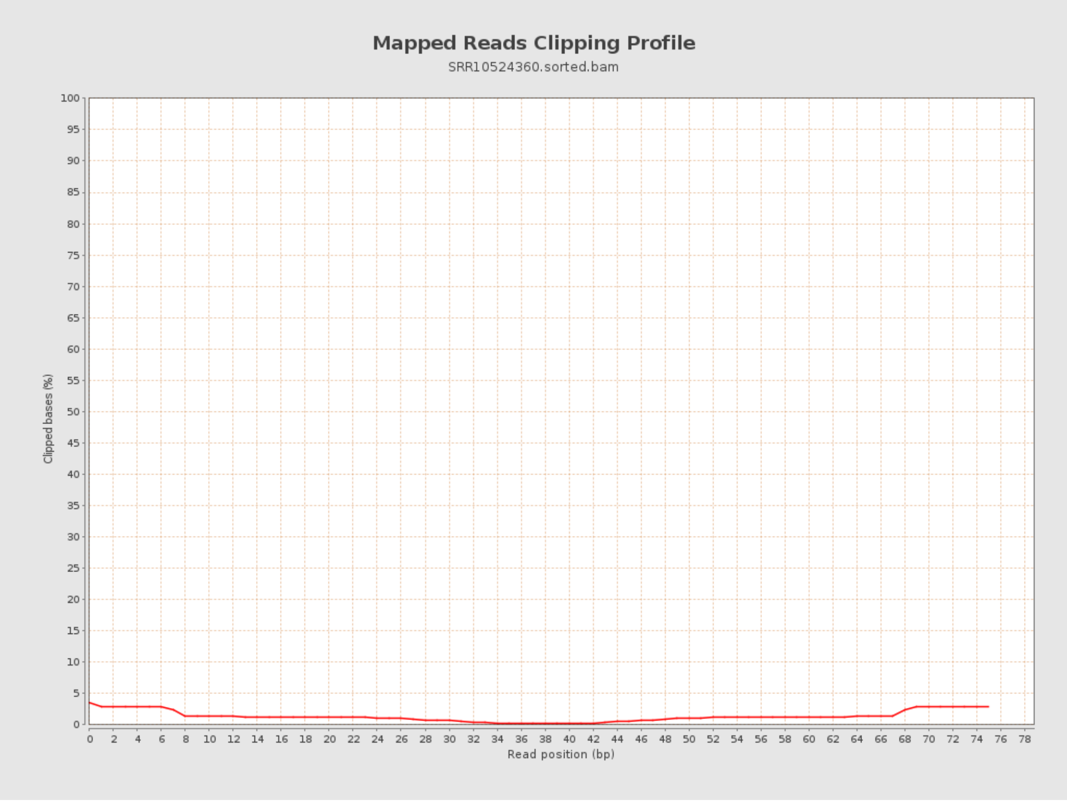
8. Results : Mapped Reads Nucleotide Content



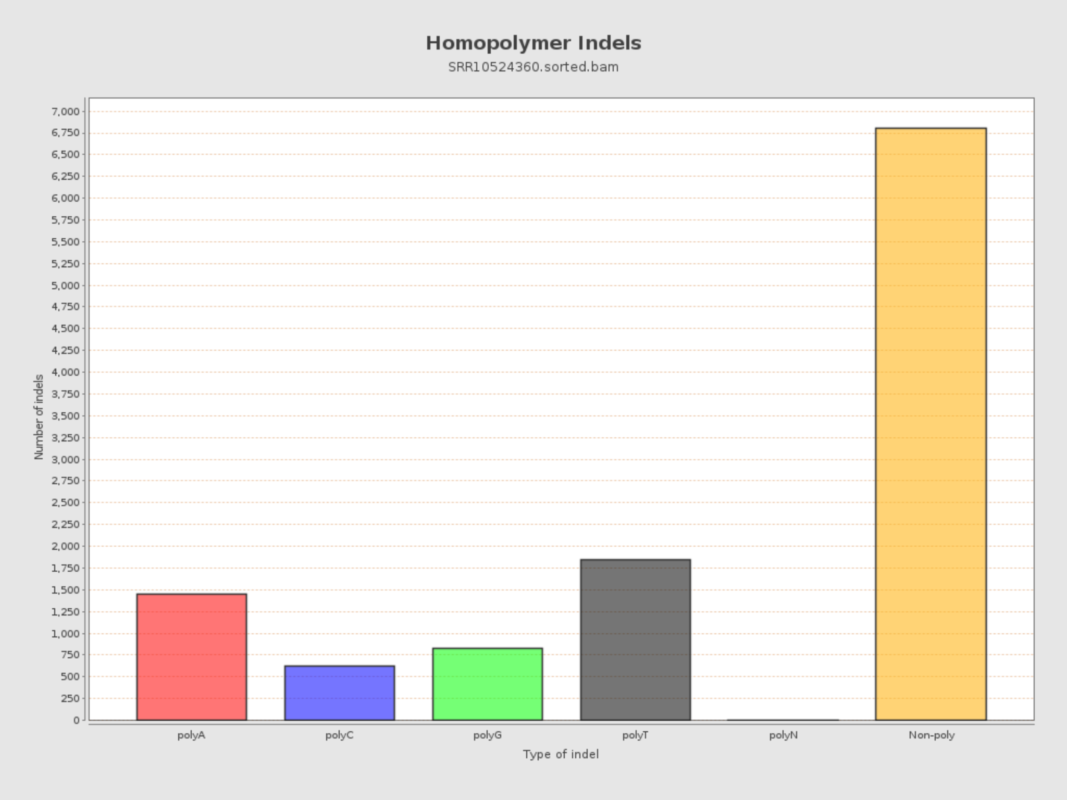
9. Results : Mapped Reads GC-content Distribution



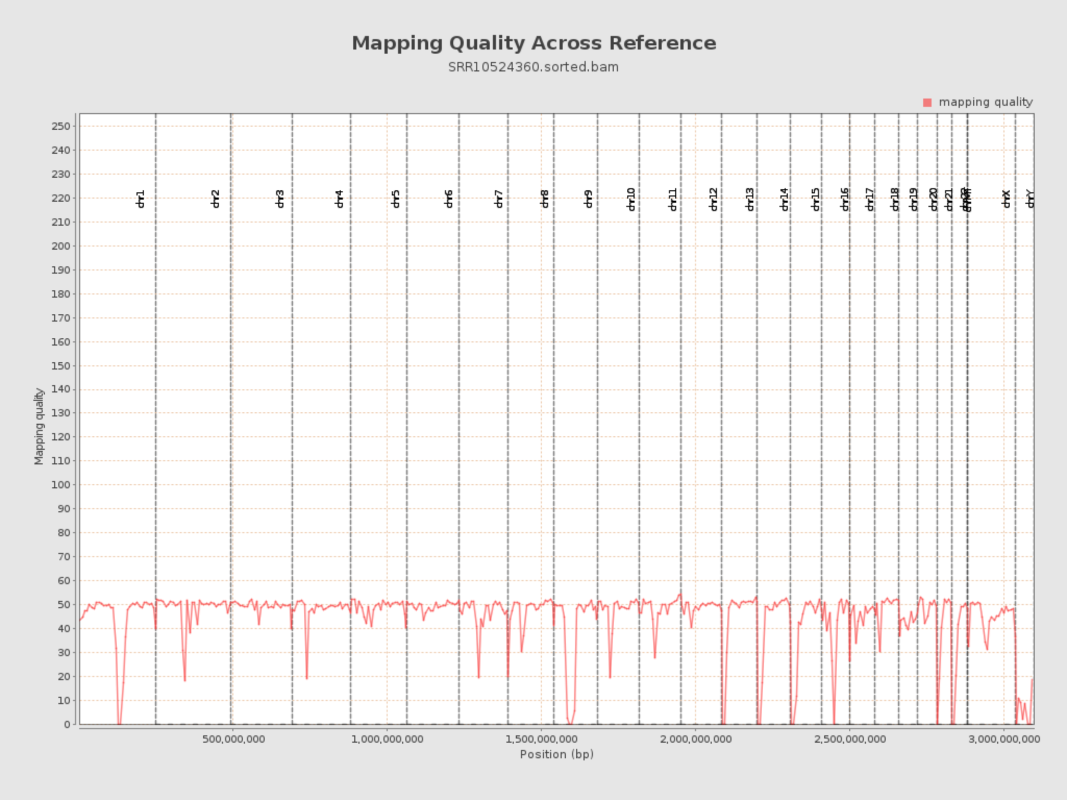
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram