Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:38:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524413.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_SRR10524413 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524413.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:38:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524413.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	548,571
Mapped reads	503,870 / 91.85%
Unmapped reads	44,701 / 8.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,798 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	10,266 / 1.87%
Duplication rate	1.52%
Clipped reads	503,588 / 91.8%

2.2. ACGT Content

Number/percentage of A's	6,950,375 / 23.82%
Number/percentage of C's	5,628,039 / 19.29%
Number/percentage of T's	9,678,054 / 33.17%
Number/percentage of G's	6,920,334 / 23.72%
Number/percentage of N's	3,393 / 0.01%
GC Percentage	43%

2.3. Coverage

Mean	0.0094

Standard Deviation	0.1247

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

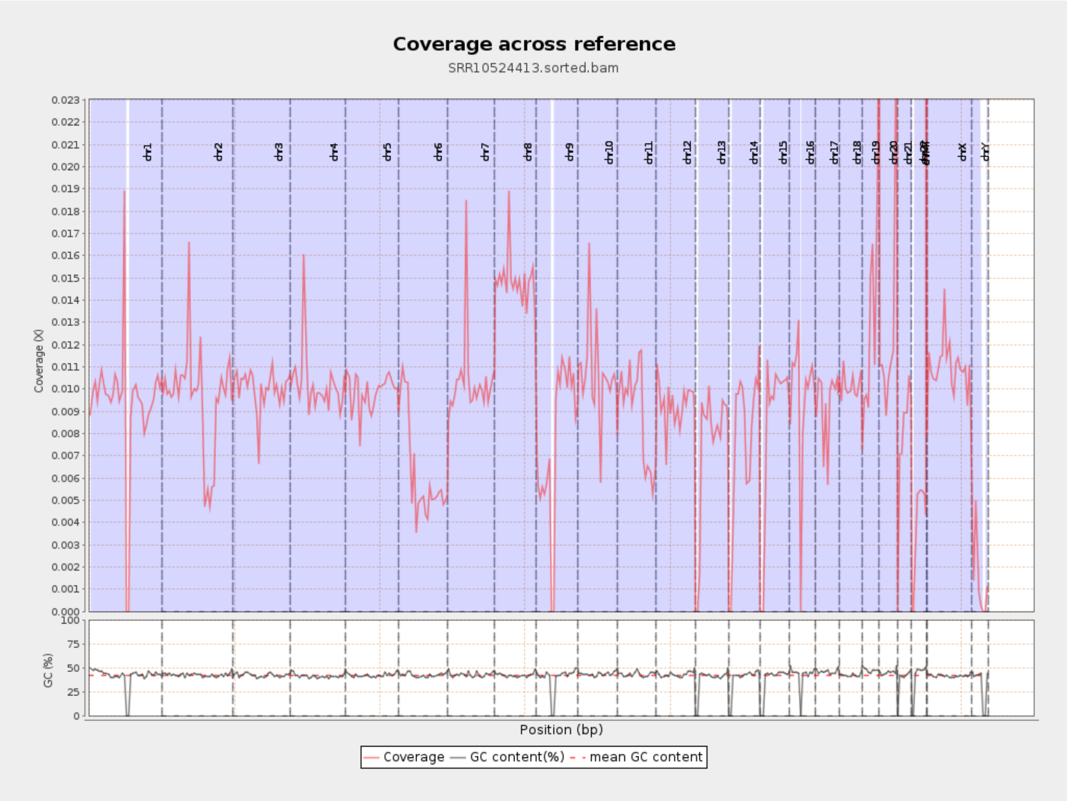
General error rate	0.51%
Mismatches	144,073
Insertions	2,290
Mapped reads with at least one insertion	0.45%
Deletions	5,370
Mapped reads with at least one deletion	1.05%
Homopolymer indels	41.42%

2.6. Chromosome stats

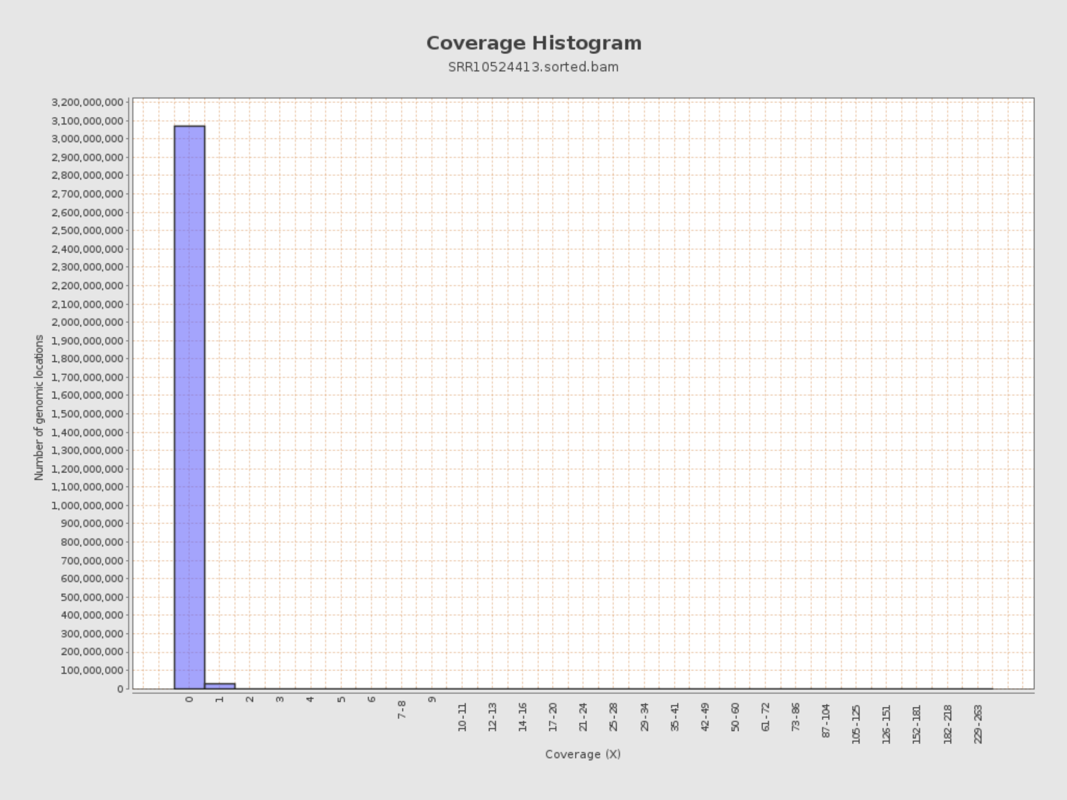
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2340097	0.0094	0.2156
chr2	243199373	2341064	0.0096	0.1337
chr3	198022430	1981325	0.01	0.103
chr4	191154276	1951637	0.0102	0.1101
chr5	180915260	1784887	0.0099	0.1025
chr6	171115067	1069698	0.0063	0.0843
chr7	159138663	1649489	0.0104	0.1598

chr8	146364022	2179725	0.0149	0.1428
chr9	141213431	1084139	0.0077	0.0998
chr10	135534747	1448472	0.0107	0.121
chr11	135006516	1196061	0.0089	0.1081
chr12	133851895	1250035	0.0093	0.1009
chr13	115169878	845717	0.0073	0.0886
chr14	107349540	809379	0.0075	0.0903
chr15	102531392	857436	0.0084	0.0943
chr16	90354753	874215	0.0097	0.1036
chr17	81195210	748200	0.0092	0.1011
chr18	78077248	793890	0.0102	0.1436
chr19	59128983	803818	0.0136	0.1595
chr20	63025520	812895	0.0129	0.1184
chr21	48129895	377275	0.0078	0.0948
chr22	51304566	195367	0.0038	0.0635
chrMT	16571	9908	0.5979	0.8284
chrX	155270560	1698959	0.0109	0.1126
chrY	59373566	85012	0.0014	0.0511

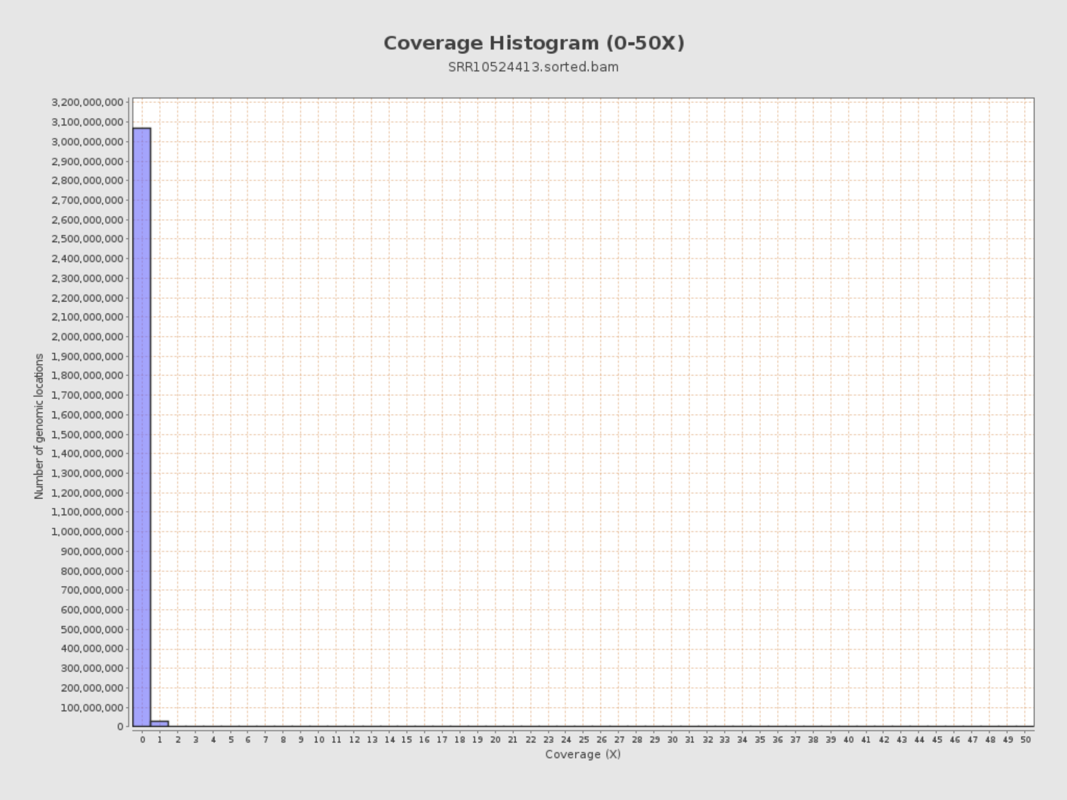
3. Results : Coverage across reference



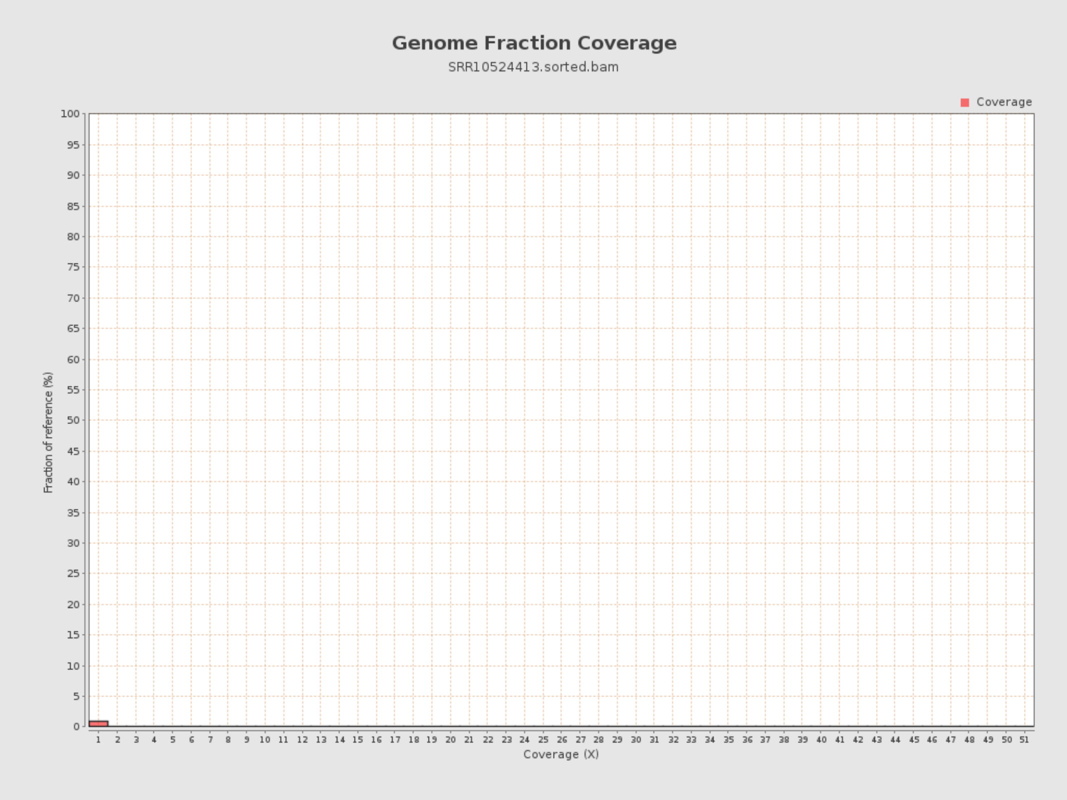
4. Results : Coverage Histogram



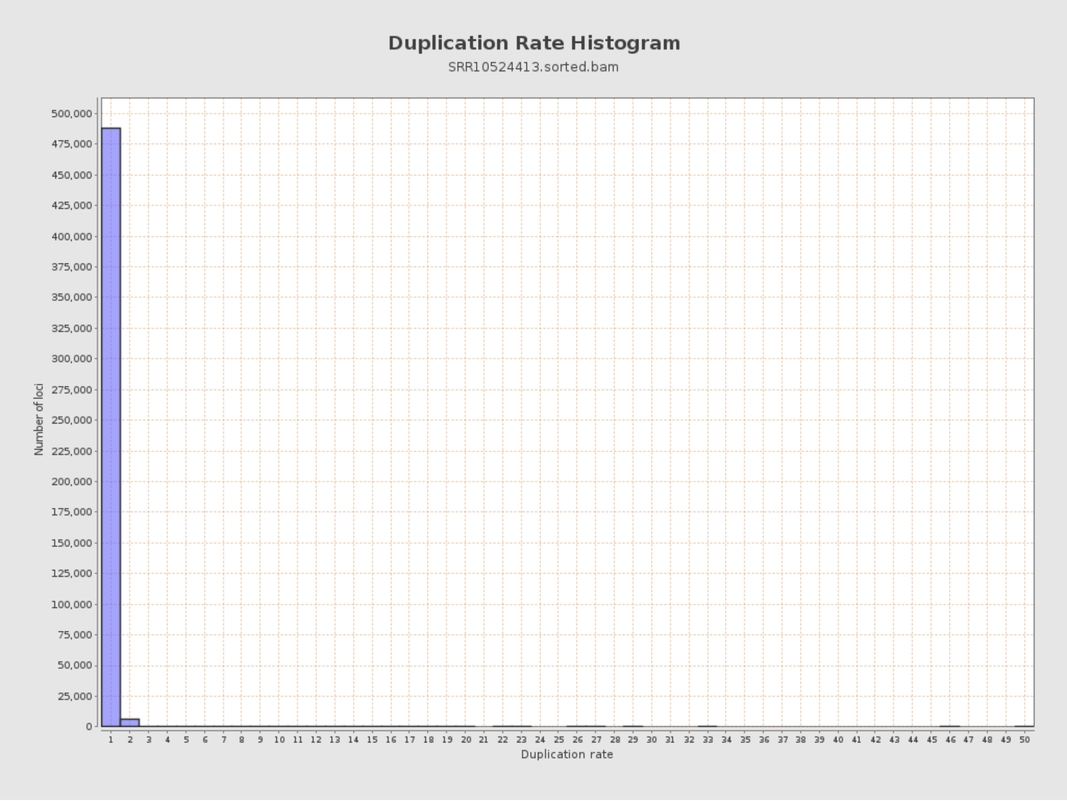
5. Results : Coverage Histogram (0-50X)



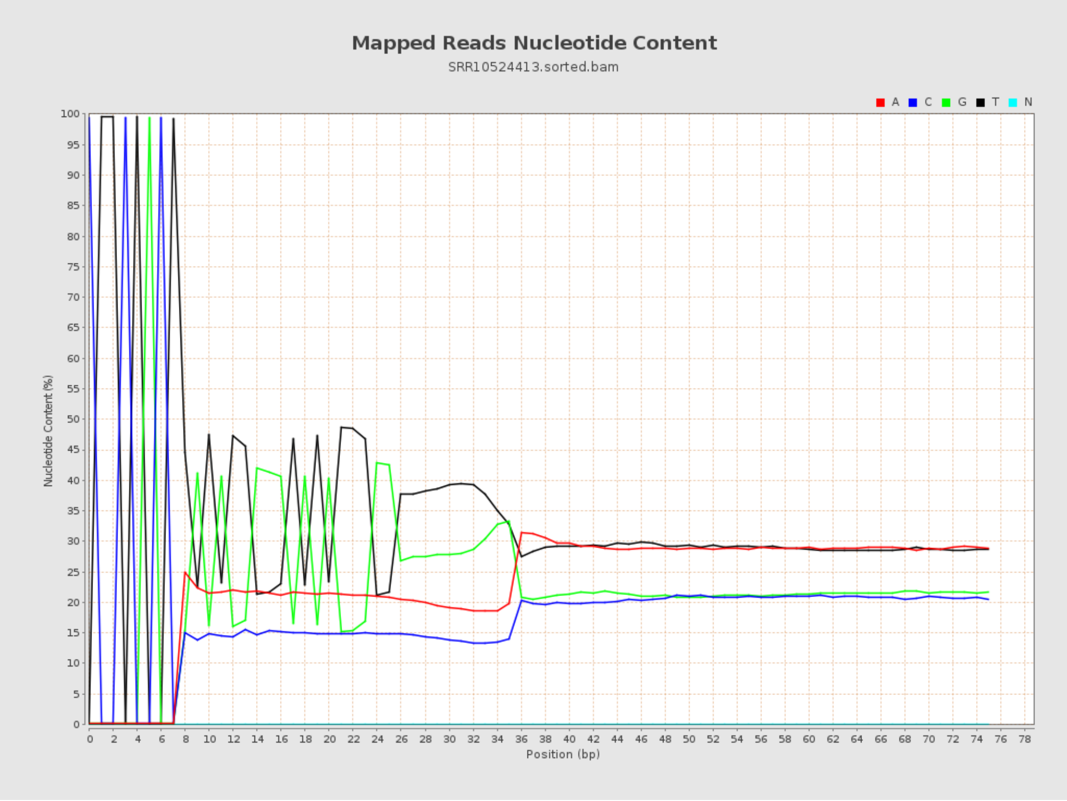
6. Results : Genome Fraction Coverage



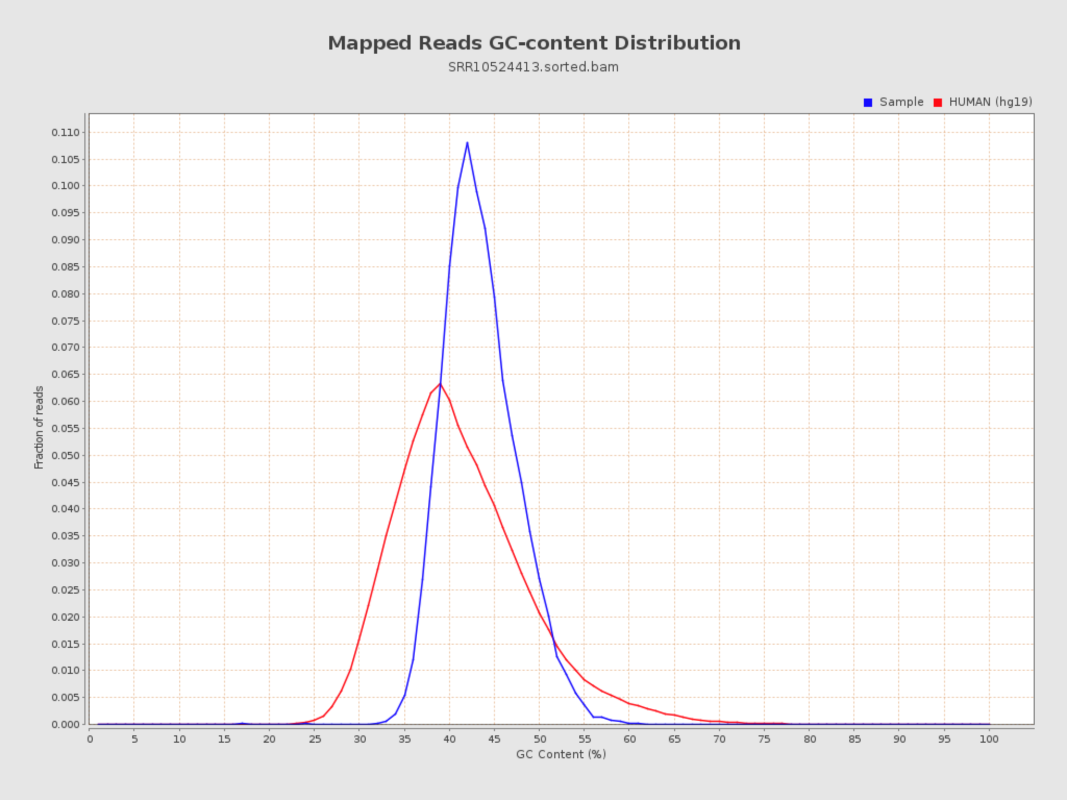
7. Results : Duplication Rate Histogram



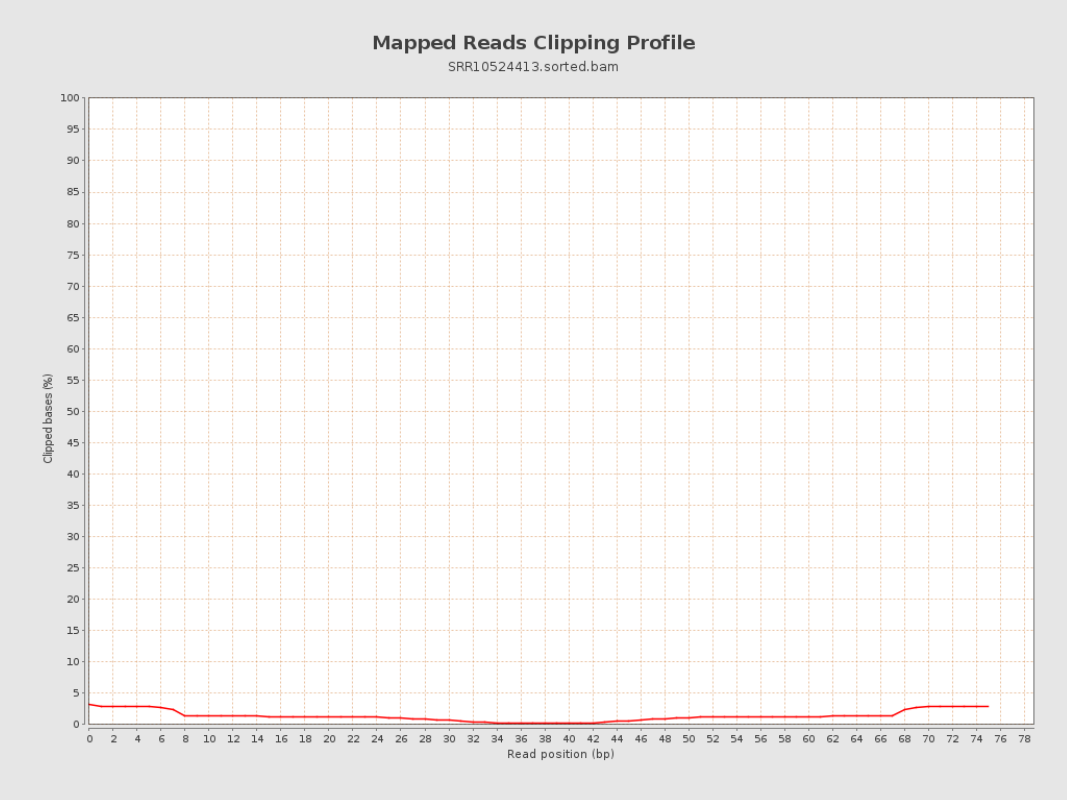
8. Results : Mapped Reads Nucleotide Content



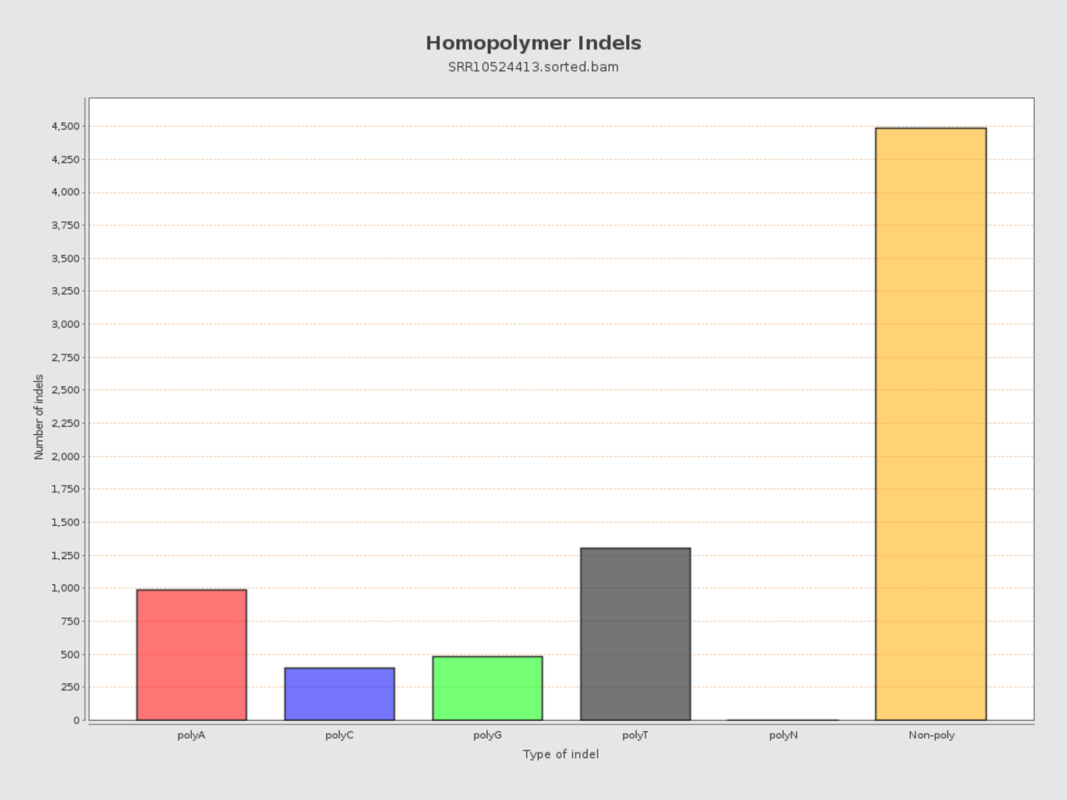
9. Results : Mapped Reads GC-content Distribution



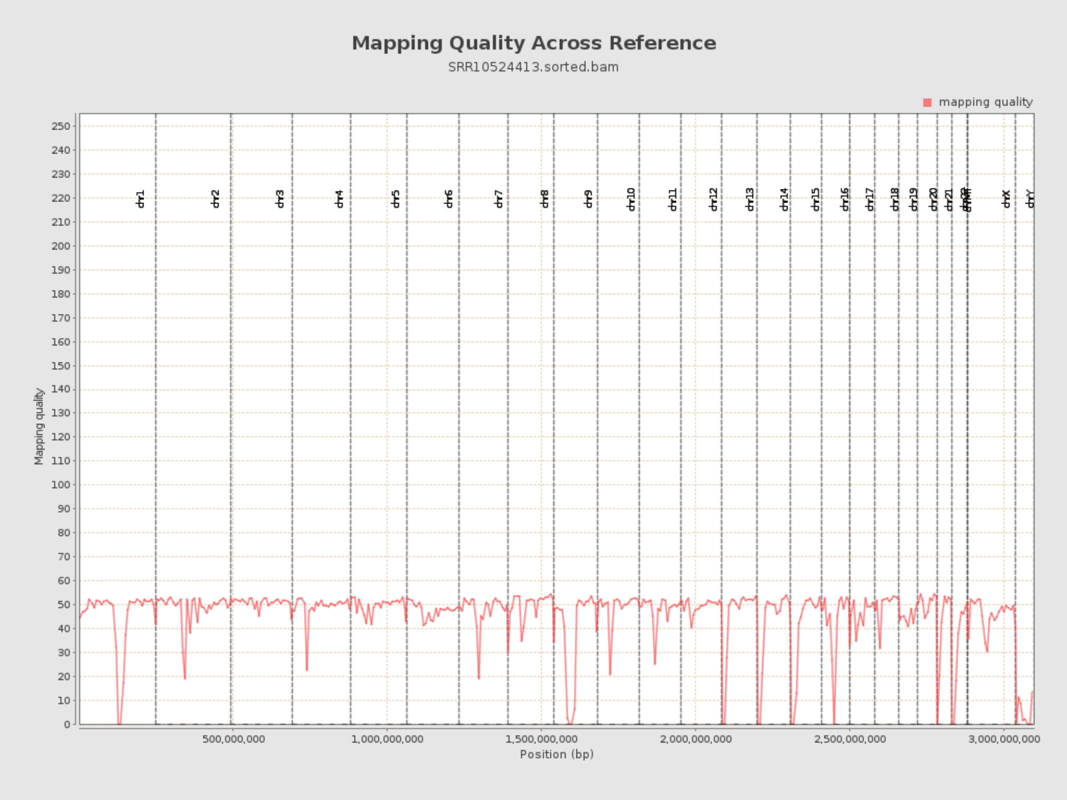
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram