Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:23:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524755.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_SRR10524755 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524755.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:23:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524755.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,787,844
Mapped reads	2,535,460 / 90.95%
Unmapped reads	252,384 / 9.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,530 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	131,944 / 4.73%
Duplication rate	3.86%
Clipped reads	2,538,420 / 91.05%

2.2. ACGT Content

Number/percentage of A's	36,376,741 / 24.82%
Number/percentage of C's	28,948,750 / 19.75%
Number/percentage of T's	48,222,038 / 32.9%
Number/percentage of G's	33,008,490 / 22.52%
Number/percentage of N's	2,836 / 0%
GC Percentage	42.27%

2.3. Coverage

Mean	0.0474

Standard Deviation	0.443

2.4. Mapping Quality

Mean Mapping Quality	45.16

2.5. Mismatches and indels

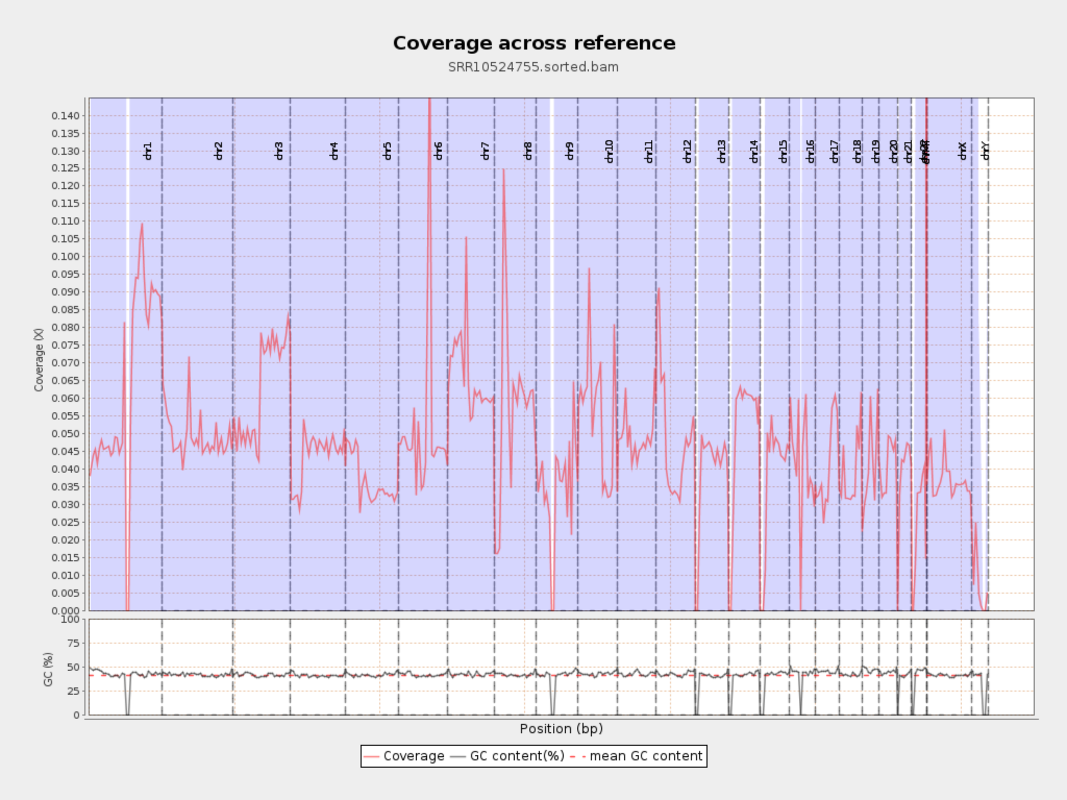
General error rate	0.53%
Mismatches	757,805
Insertions	9,595
Mapped reads with at least one insertion	0.38%
Deletions	32,060
Mapped reads with at least one deletion	1.26%
Homopolymer indels	43.64%

2.6. Chromosome stats

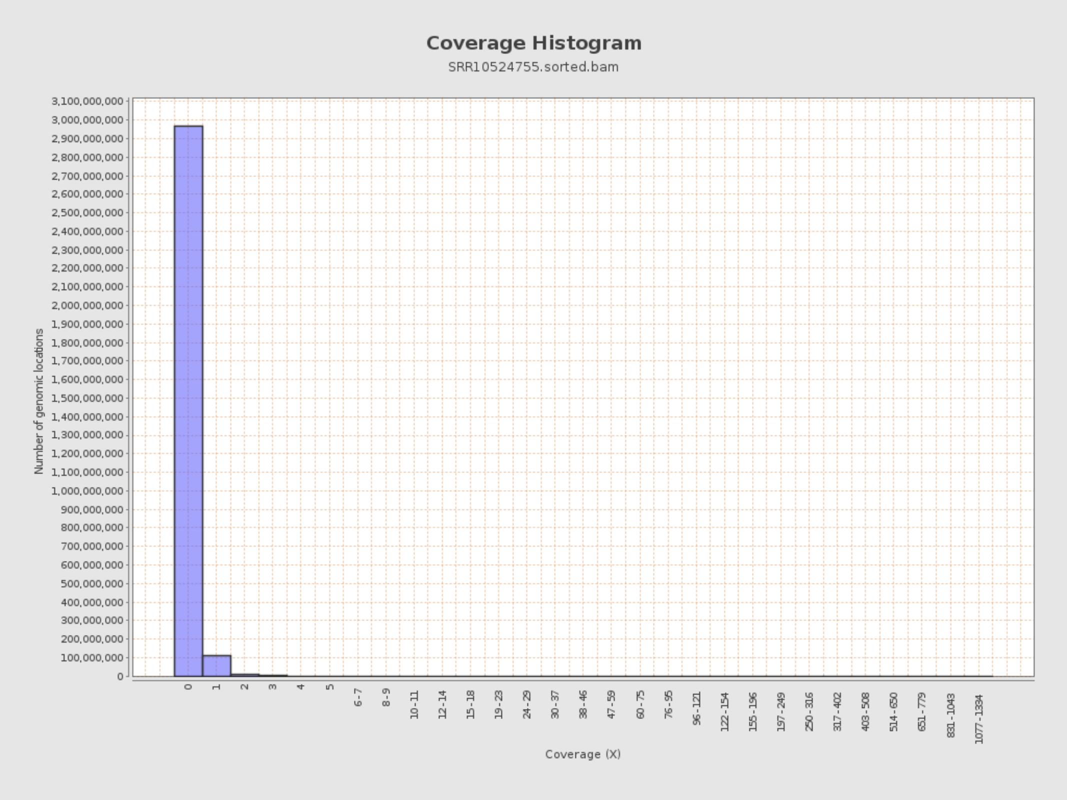
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15717276	0.0631	0.8647
chr2	243199373	11999629	0.0493	0.6004
chr3	198022430	12433416	0.0628	0.2827
chr4	191154276	8318970	0.0435	0.26
chr5	180915260	6594018	0.0364	0.2158
chr6	171115067	9018495	0.0527	0.303
chr7	159138663	10625784	0.0668	0.7696

chr8	146364022	8257419	0.0564	0.4404
chr9	141213431	4815906	0.0341	0.308
chr10	135534747	7618092	0.0562	0.4232
chr11	135006516	6630297	0.0491	0.3412
chr12	133851895	6508721	0.0486	0.2546
chr13	115169878	4499306	0.0391	0.2261
chr14	107349540	5367207	0.05	0.2623
chr15	102531392	3843597	0.0375	0.2237
chr16	90354753	3637395	0.0403	0.2576
chr17	81195210	3327610	0.041	0.2362
chr18	78077248	3032751	0.0388	0.5912
chr19	59128983	2475450	0.0419	0.568
chr20	63025520	2578099	0.0409	0.2342
chr21	48129895	1846014	0.0384	0.2513
chr22	51304566	1259017	0.0245	0.1759
chrMT	16571	8274	0.4993	0.7846
chrX	155270560	5781063	0.0372	0.2448
chrY	59373566	415961	0.007	0.2173

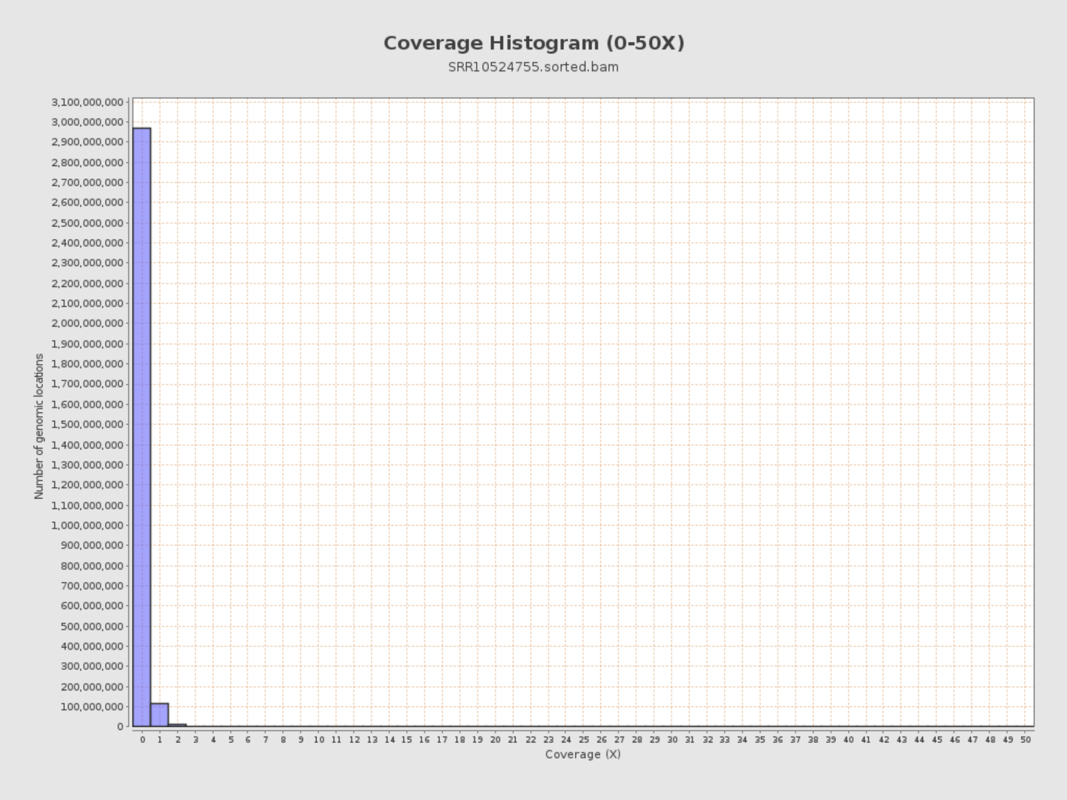
3. Results : Coverage across reference



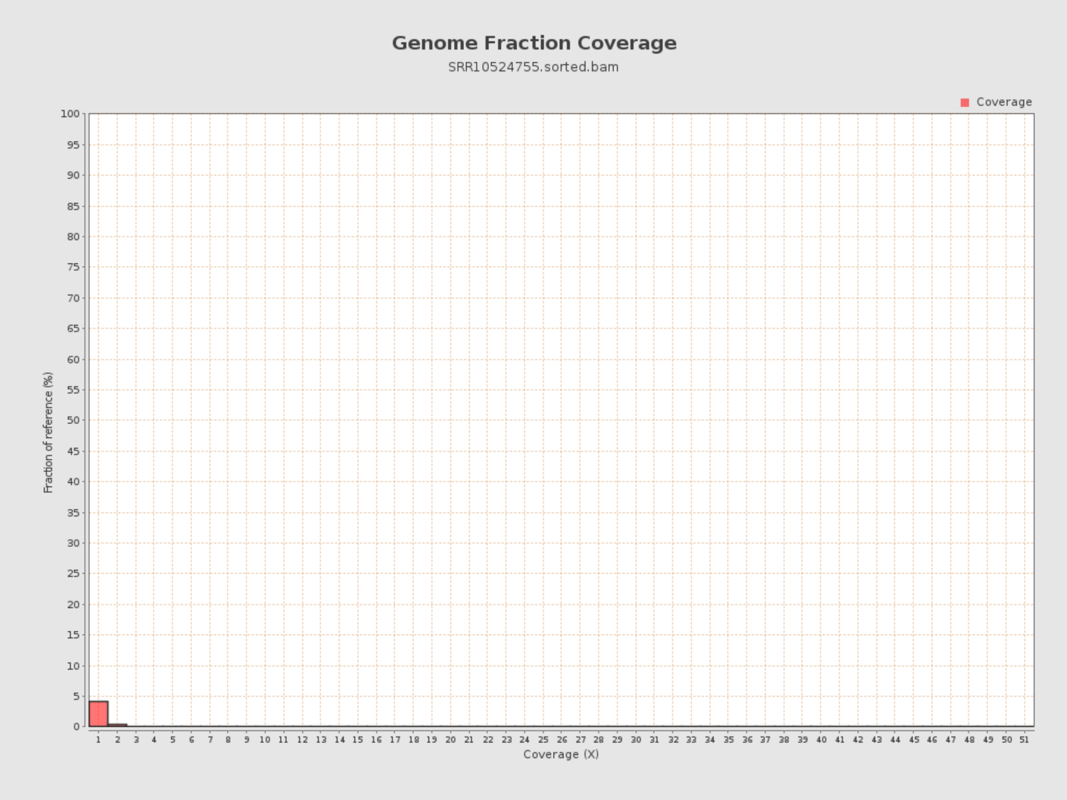
4. Results : Coverage Histogram



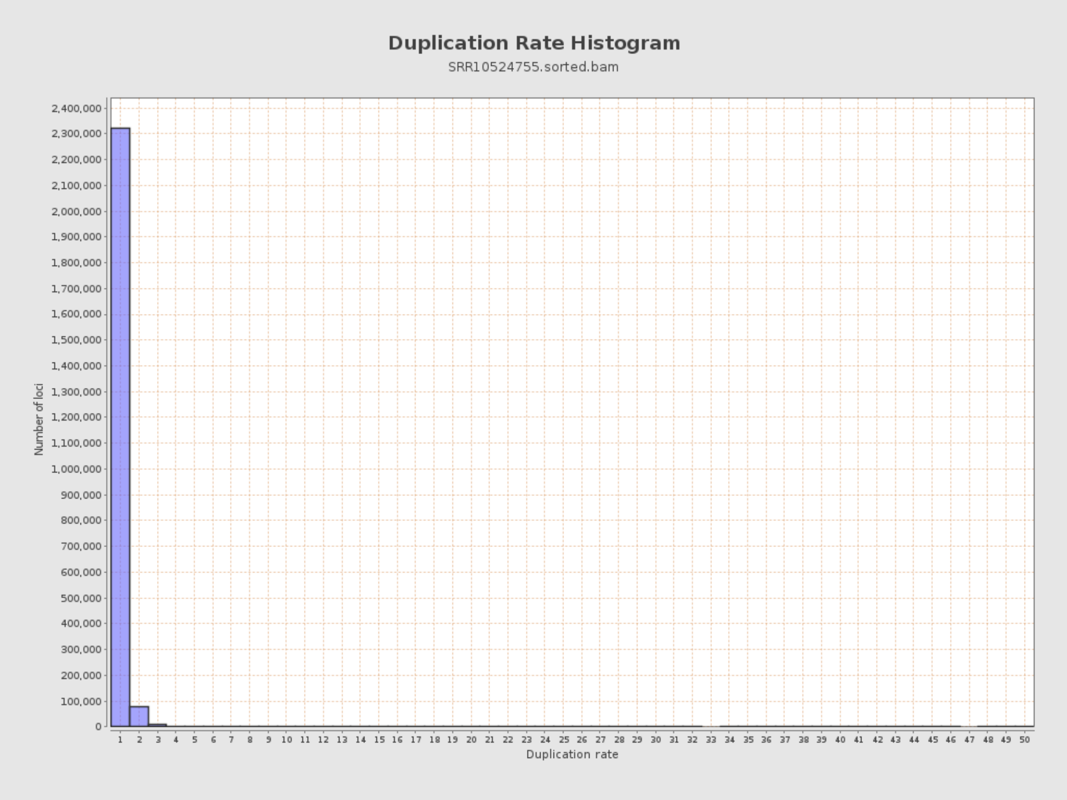
5. Results : Coverage Histogram (0-50X)



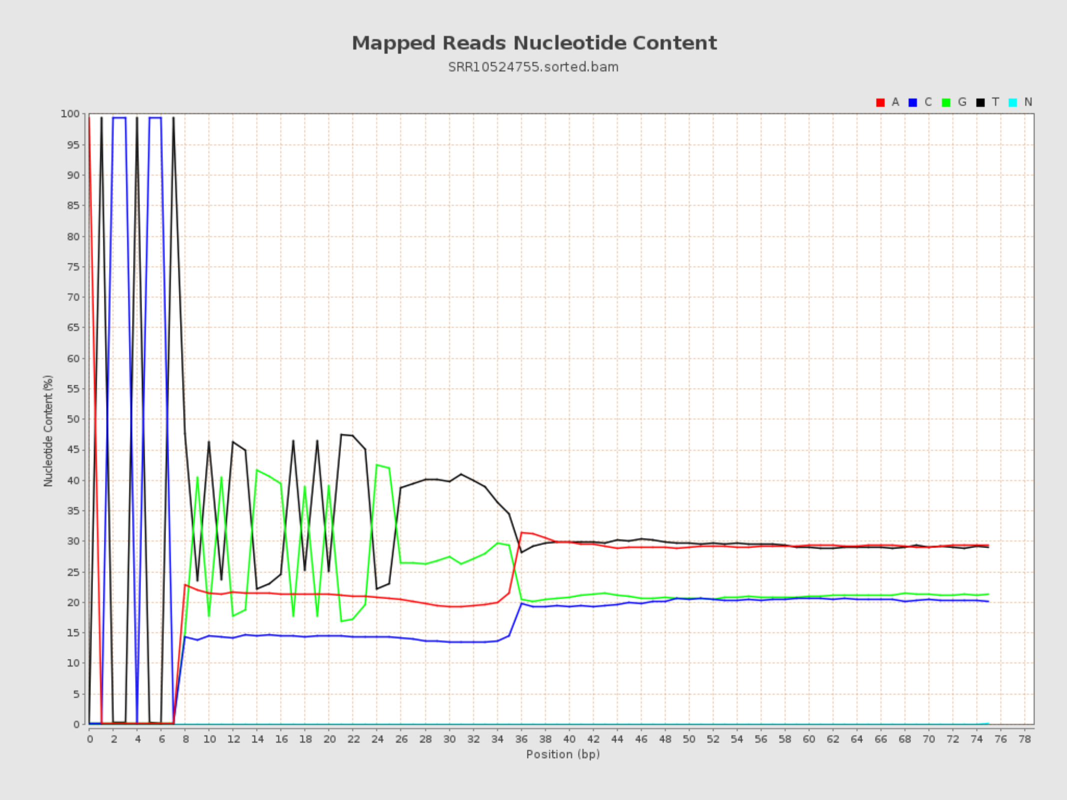
6. Results : Genome Fraction Coverage



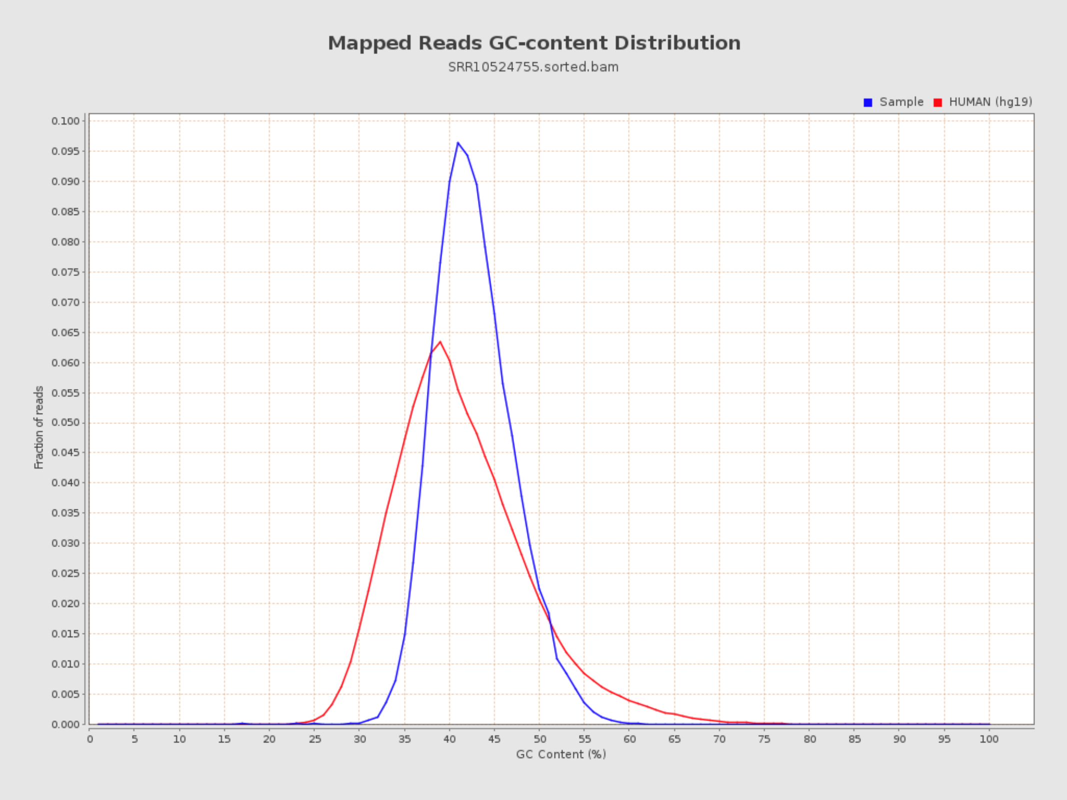
7. Results : Duplication Rate Histogram



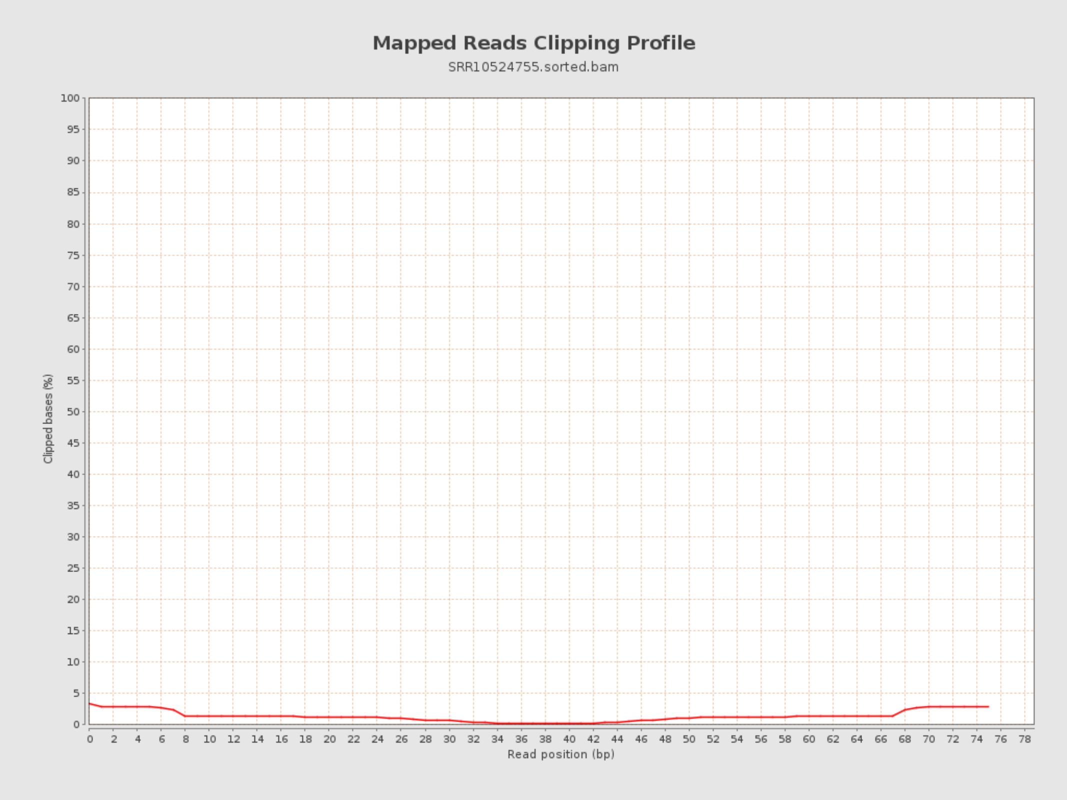
8. Results : Mapped Reads Nucleotide Content



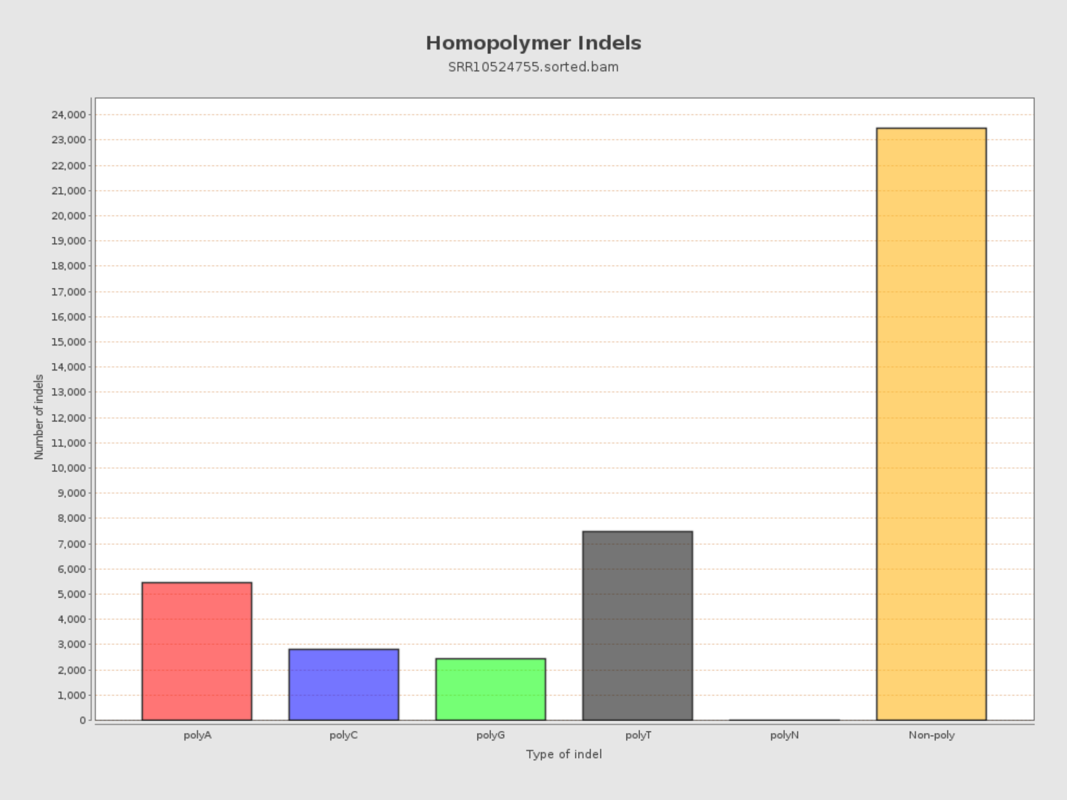
9. Results : Mapped Reads GC-content Distribution



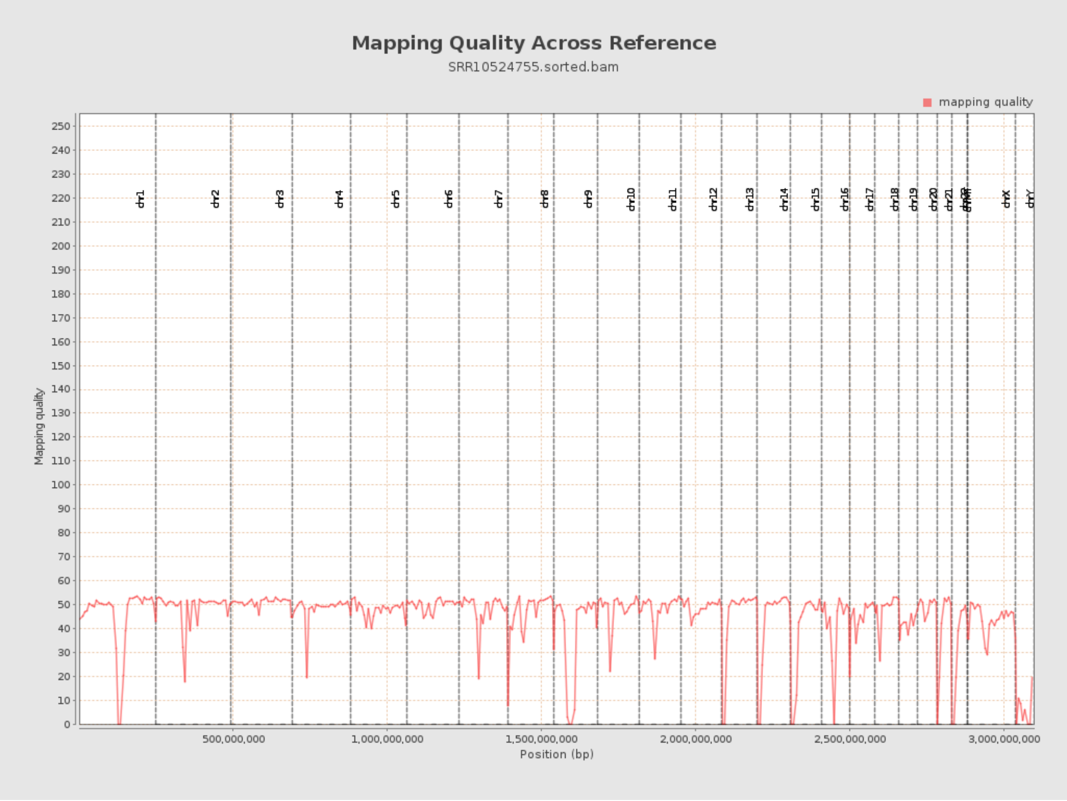
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram