Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 04:10:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083750.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_SRR3083750 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083750.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 04:10:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083750.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,324,165
Mapped reads	2,157,870 / 92.84%
Unmapped reads	166,295 / 7.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,841 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	97,365 / 4.19%
Duplication rate	3.76%
Clipped reads	885,202 / 38.09%

2.2. ACGT Content

Number/percentage of A's	41,154,670 / 28.36%
Number/percentage of C's	26,004,437 / 17.92%
Number/percentage of T's	46,802,624 / 32.25%
Number/percentage of G's	31,143,991 / 21.46%
Number/percentage of N's	22,735 / 0.02%
GC Percentage	39.38%

2.3. Coverage

Mean	0.0469

Standard Deviation	0.3932

2.4. Mapping Quality

Mean Mapping Quality	47.55

2.5. Mismatches and indels

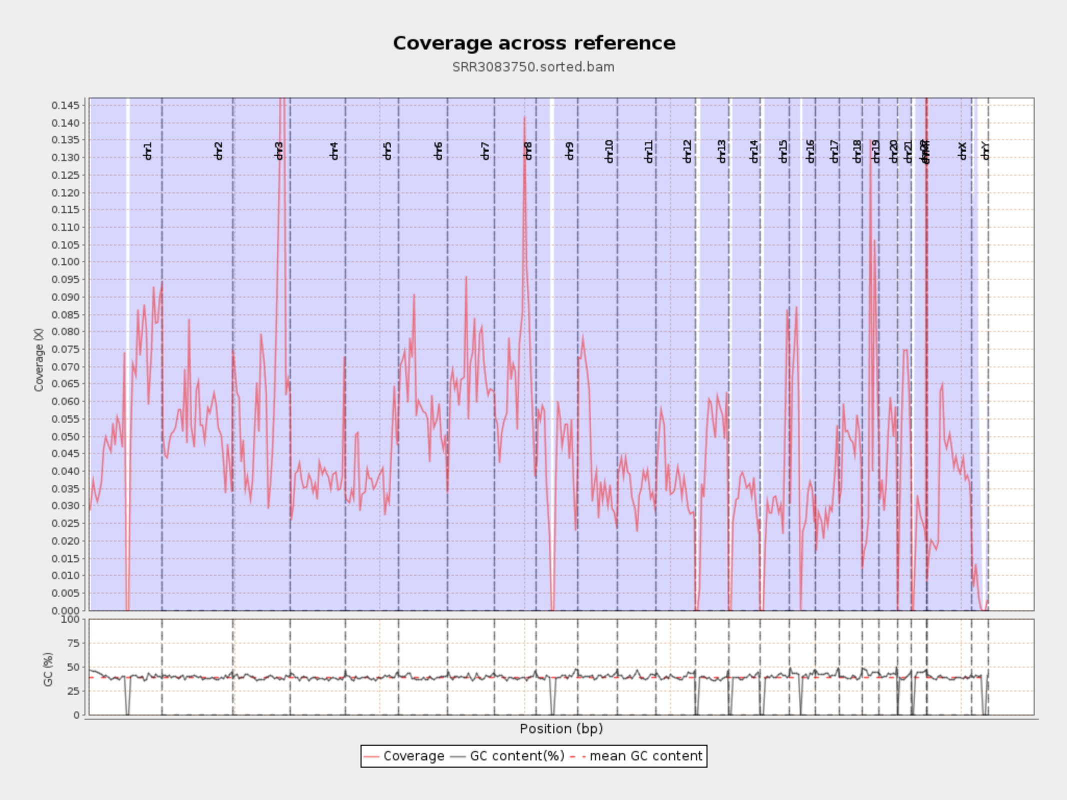
General error rate	0.77%
Mismatches	1,096,240
Insertions	10,826
Mapped reads with at least one insertion	0.5%
Deletions	33,337
Mapped reads with at least one deletion	1.53%
Homopolymer indels	48.75%

2.6. Chromosome stats

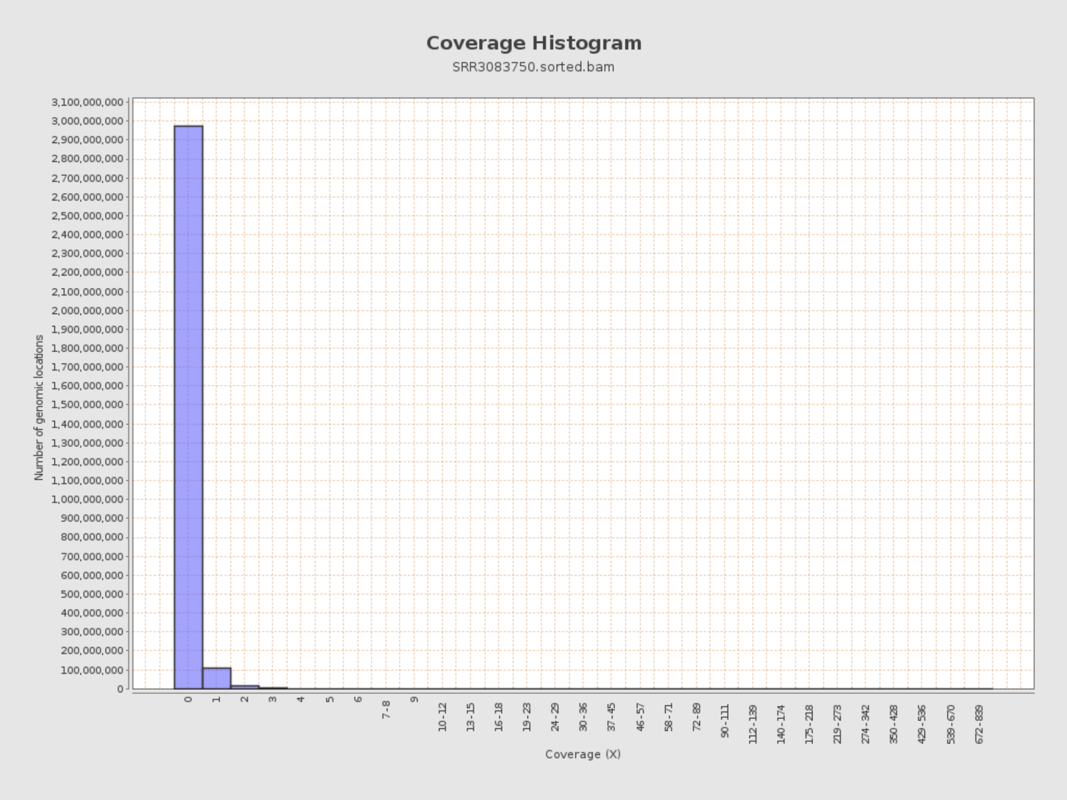
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14084707	0.0565	0.8008
chr2	243199373	12921820	0.0531	0.3452
chr3	198022430	13428823	0.0678	0.2965
chr4	191154276	7341699	0.0384	0.2228
chr5	180915260	7029690	0.0389	0.2221
chr6	171115067	10325028	0.0603	0.3176
chr7	159138663	10865868	0.0683	0.6704

chr8	146364022	10047795	0.0686	0.5818
chr9	141213431	5901605	0.0418	0.2846
chr10	135534747	6179850	0.0456	0.3212
chr11	135006516	4830001	0.0358	0.2502
chr12	133851895	5082827	0.038	0.2204
chr13	115169878	5016223	0.0436	0.2345
chr14	107349540	3137888	0.0292	0.1971
chr15	102531392	3254298	0.0317	0.2011
chr16	90354753	3807041	0.0421	0.242
chr17	81195210	2457158	0.0303	0.2002
chr18	78077248	3780303	0.0484	0.4877
chr19	59128983	3265802	0.0552	0.5182
chr20	63025520	2820481	0.0448	0.2425
chr21	48129895	2502043	0.052	0.2613
chr22	51304566	1010489	0.0197	0.1551
chrMT	16571	9166	0.5531	0.8147
chrX	155270560	5821819	0.0375	0.2297
chrY	59373566	260856	0.0044	0.101

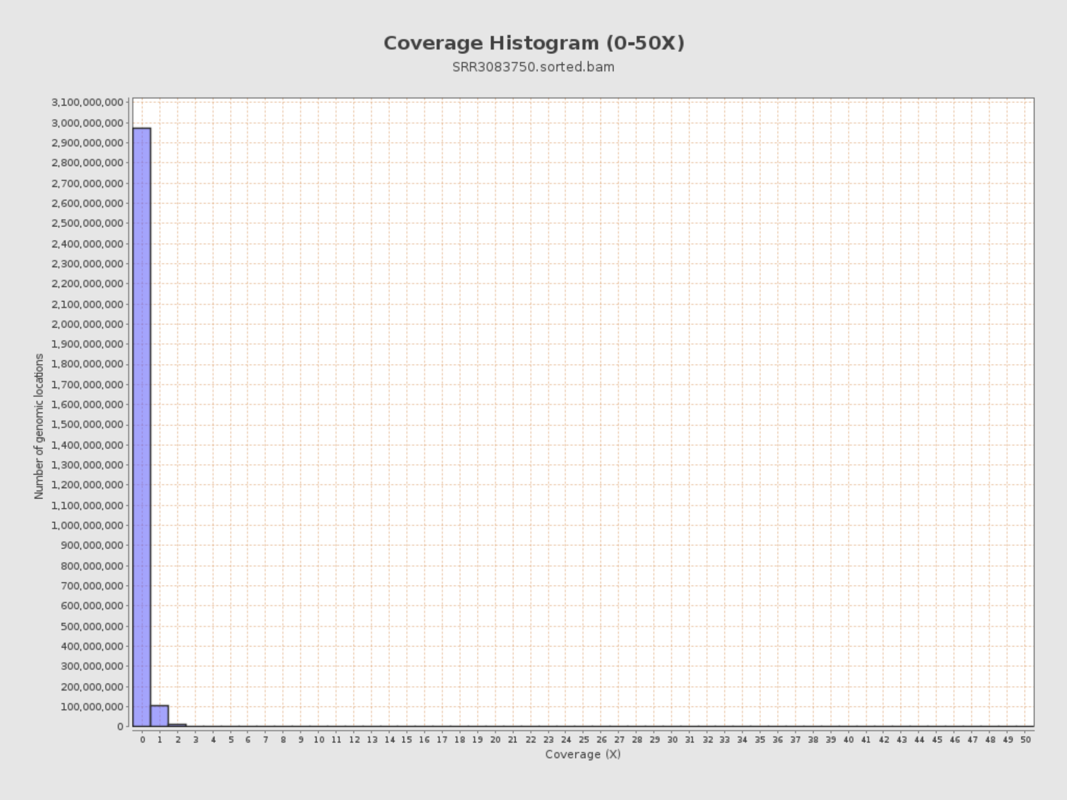
3. Results : Coverage across reference



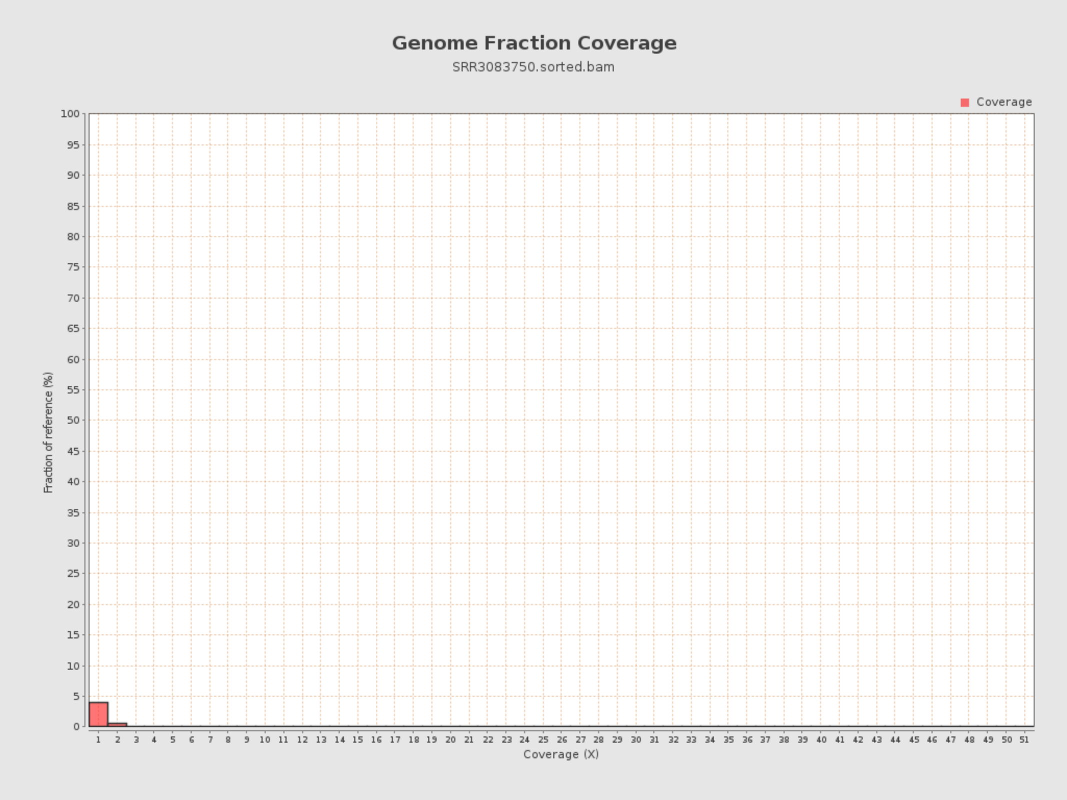
4. Results : Coverage Histogram



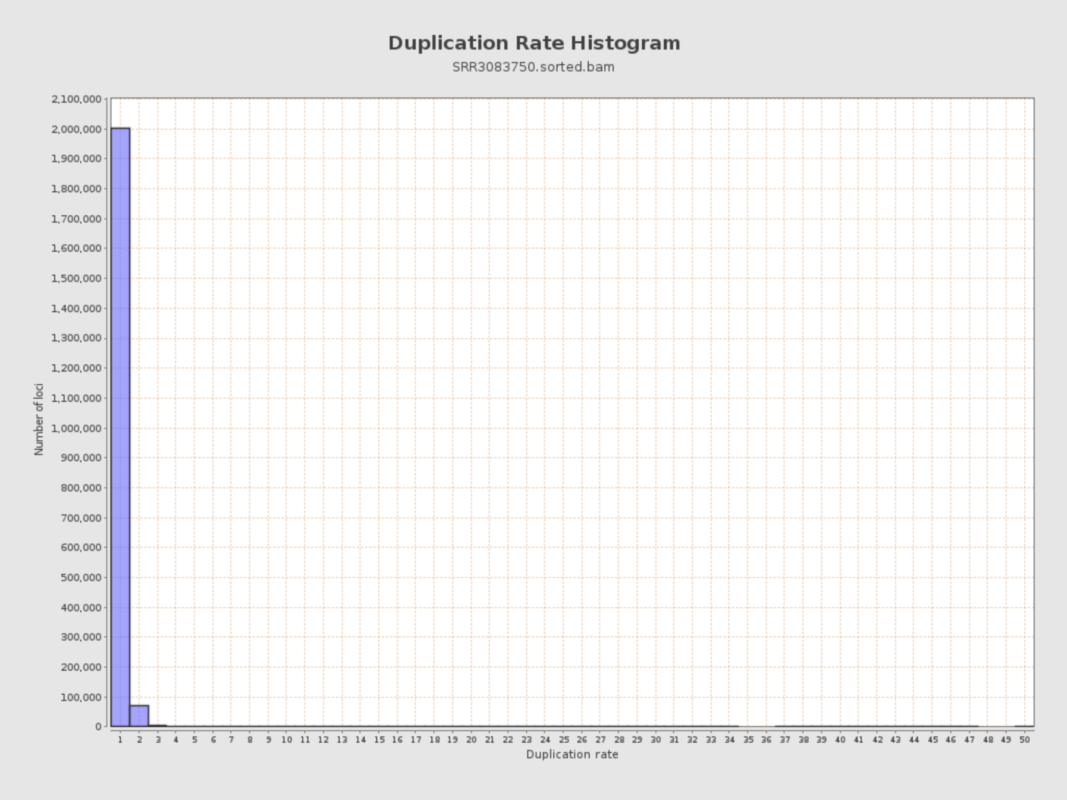
5. Results : Coverage Histogram (0-50X)



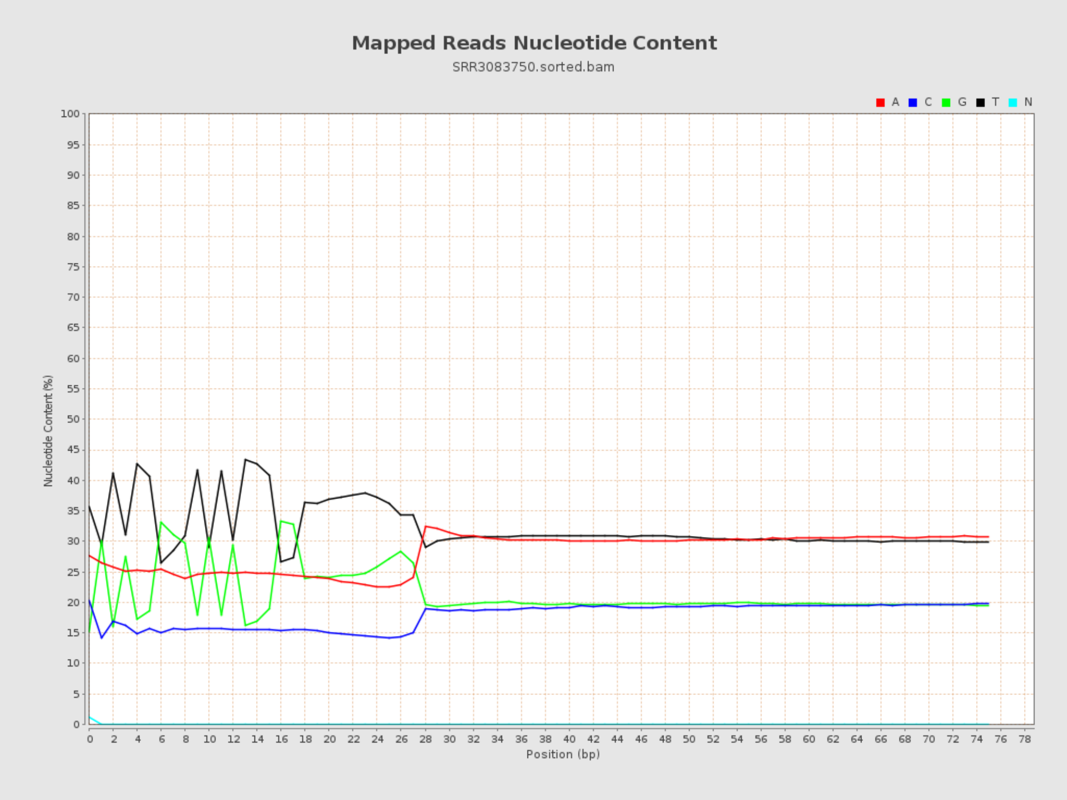
6. Results : Genome Fraction Coverage



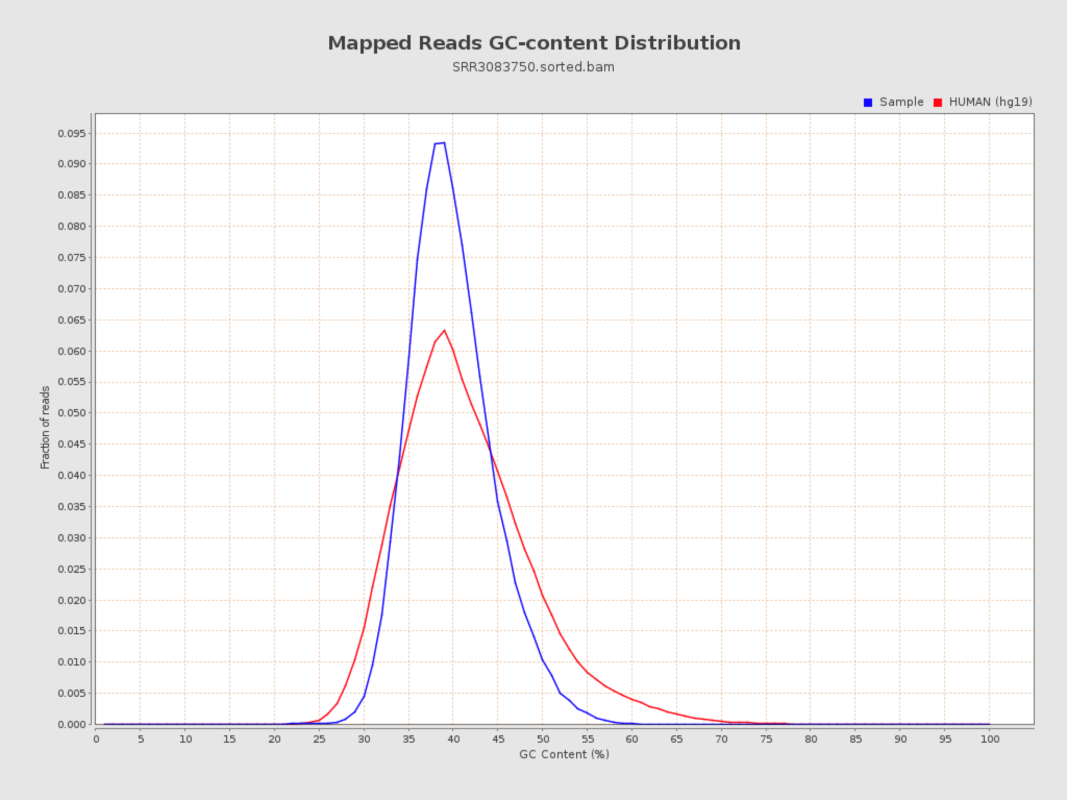
7. Results : Duplication Rate Histogram



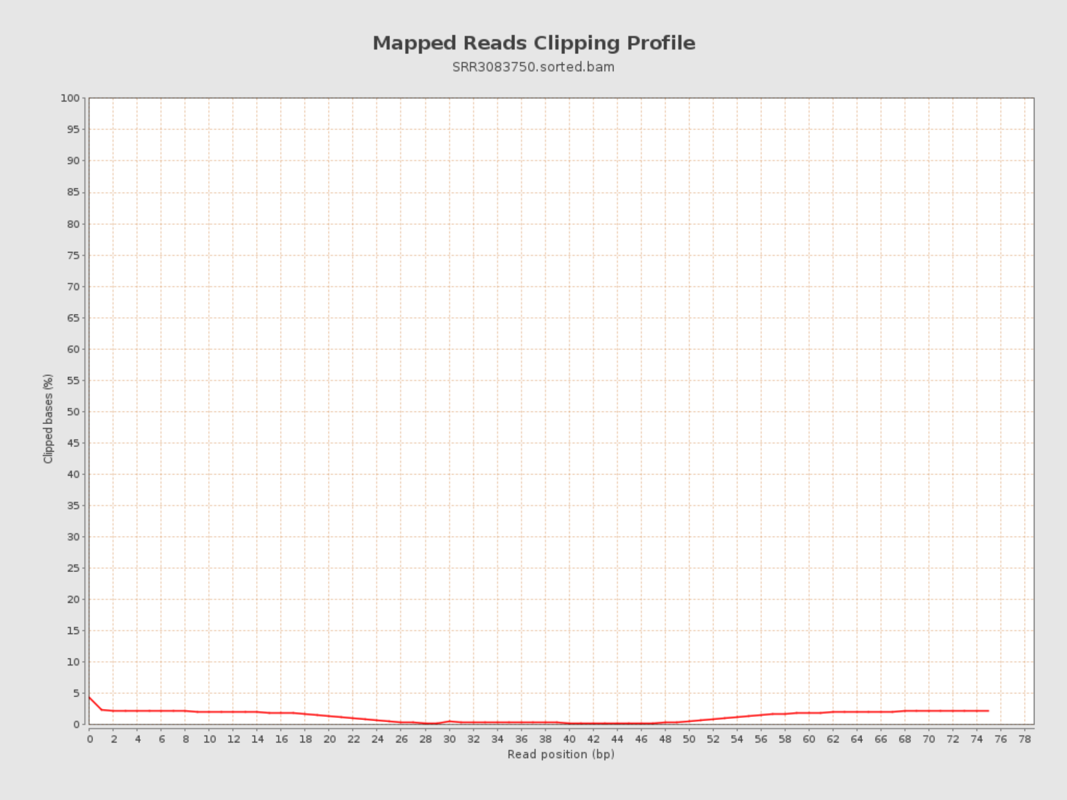
8. Results : Mapped Reads Nucleotide Content



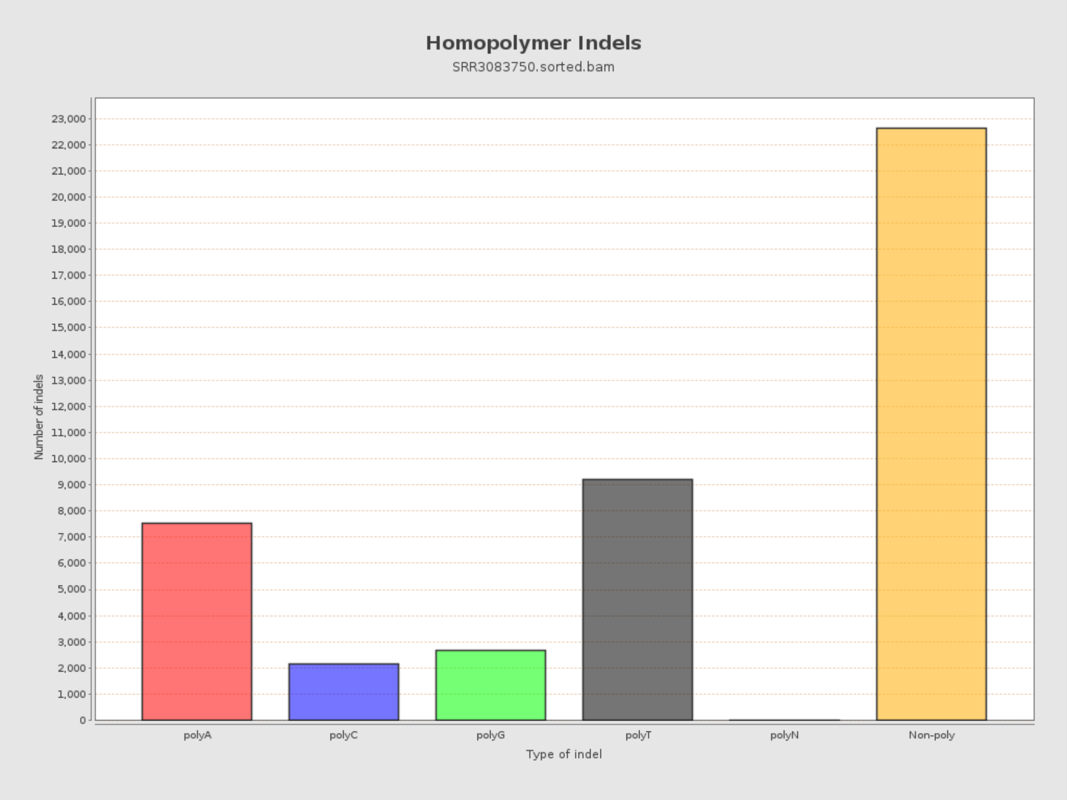
9. Results : Mapped Reads GC-content Distribution



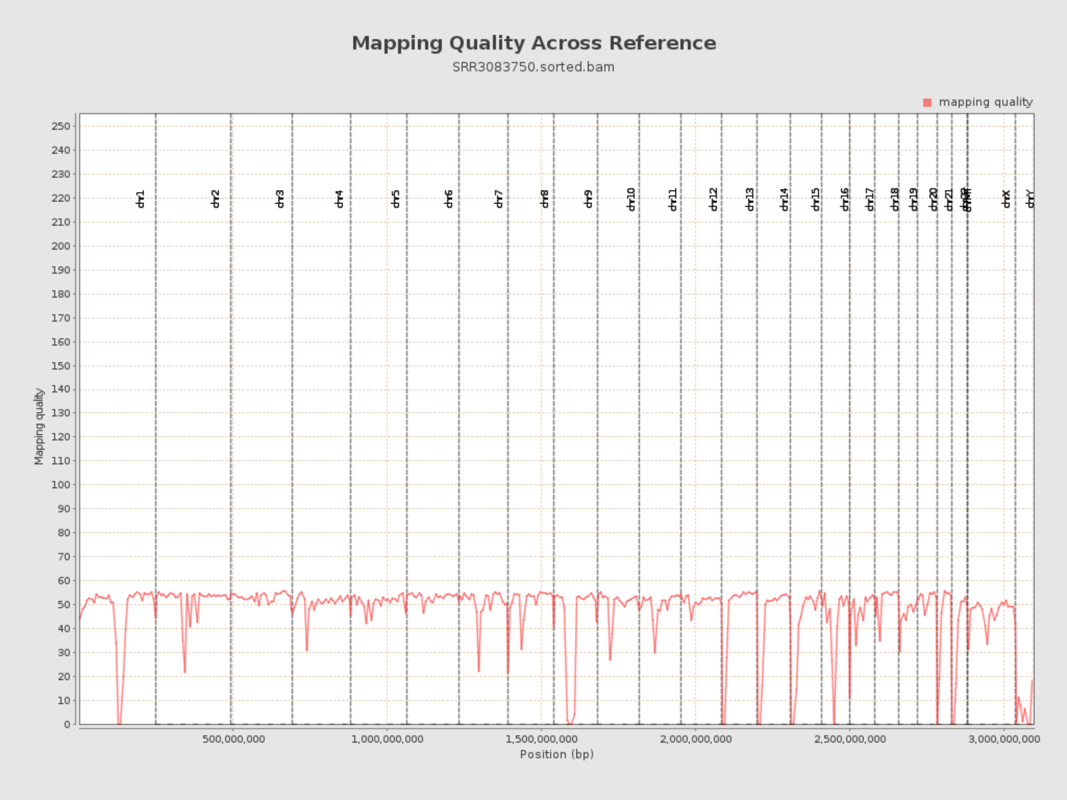
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram