Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 07:08:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083784.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_SRR3083784 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083784.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 07:07:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083784.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,821,499
Mapped reads	2,830,842 / 74.08%
Unmapped reads	990,657 / 25.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,731 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	115,895 / 3.03%
Duplication rate	3.1%
Clipped reads	1,559,007 / 40.8%

2.2. ACGT Content

Number/percentage of A's	50,927,888 / 28.16%
Number/percentage of C's	34,753,595 / 19.22%
Number/percentage of T's	54,575,438 / 30.18%
Number/percentage of G's	40,562,414 / 22.43%
Number/percentage of N's	2,028 / 0%
GC Percentage	41.65%

2.3. Coverage

Mean	0.0584

Standard Deviation	0.4548

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Mismatches and indels

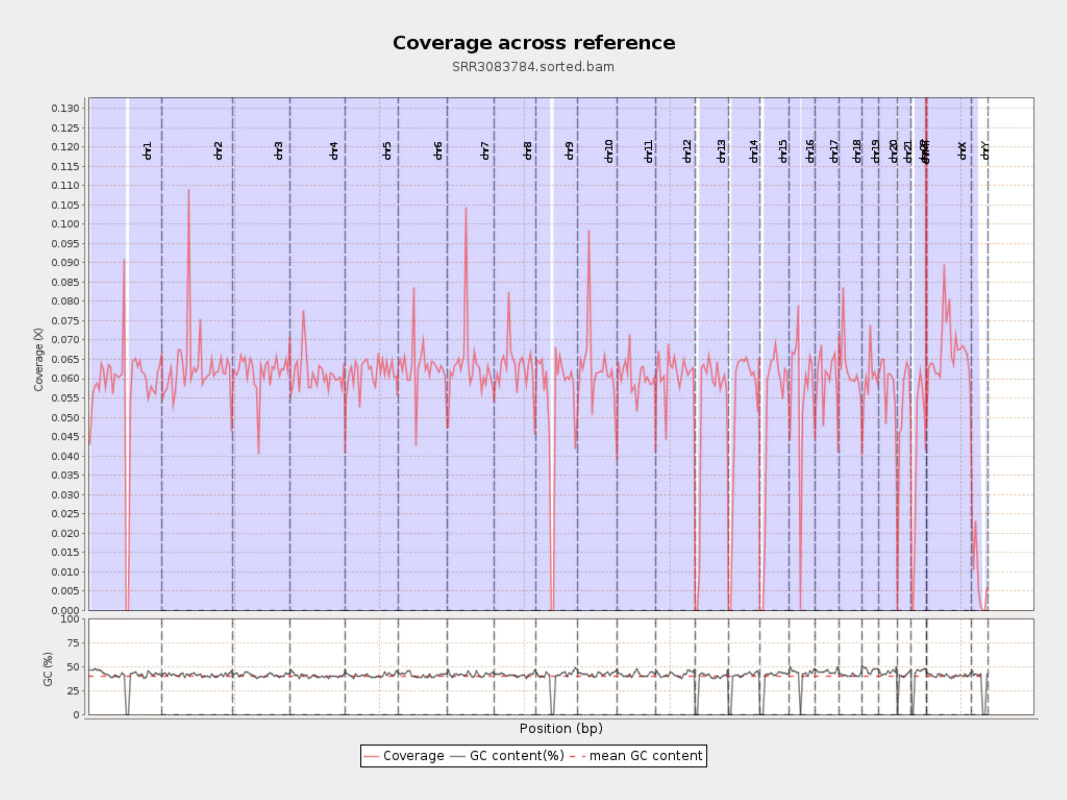
General error rate	0.89%
Mismatches	1,575,432
Insertions	14,119
Mapped reads with at least one insertion	0.49%
Deletions	41,130
Mapped reads with at least one deletion	1.44%
Homopolymer indels	45.29%

2.6. Chromosome stats

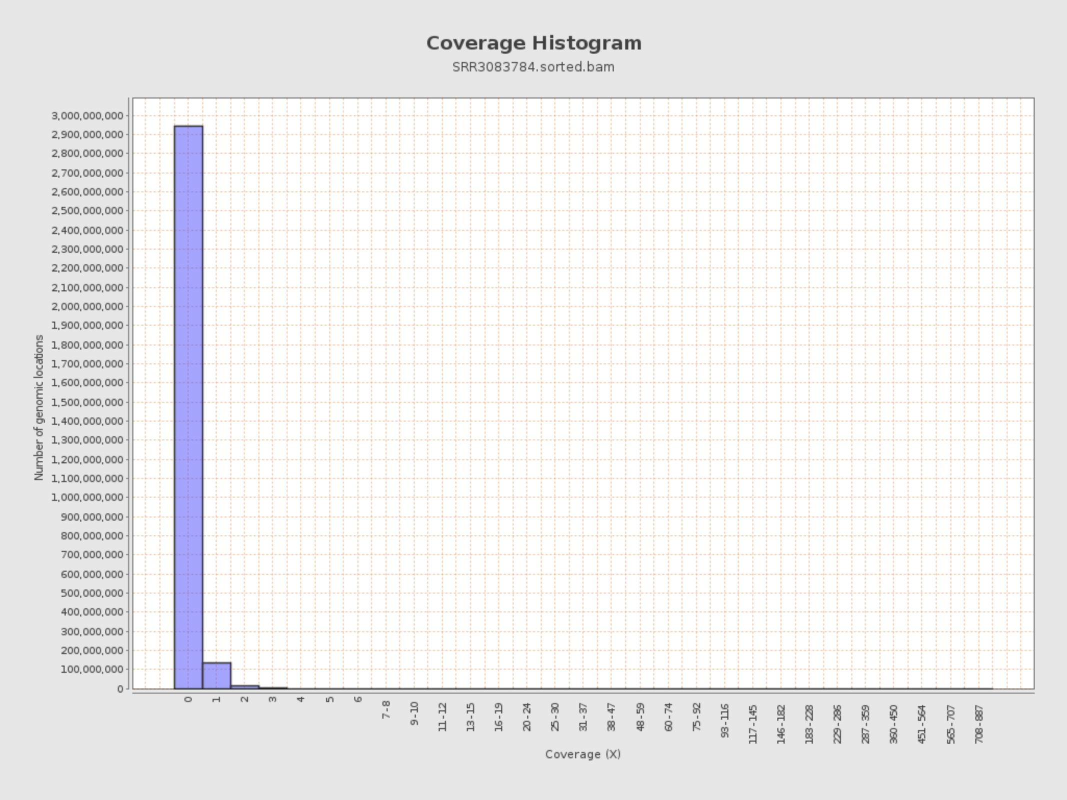
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14199775	0.057	0.7527
chr2	243199373	15316803	0.063	0.5923
chr3	198022430	12212033	0.0617	0.282
chr4	191154276	11697972	0.0612	0.2981
chr5	180915260	11140043	0.0616	0.2818
chr6	171115067	10760072	0.0629	0.3719
chr7	159138663	10137122	0.0637	0.6454

chr8	146364022	9217847	0.063	0.429
chr9	141213431	7532751	0.0533	0.4127
chr10	135534747	8510513	0.0628	0.463
chr11	135006516	8131237	0.0602	0.3945
chr12	133851895	8200547	0.0613	0.2864
chr13	115169878	5834916	0.0507	0.2549
chr14	107349540	5545314	0.0517	0.2885
chr15	102531392	5091204	0.0497	0.2625
chr16	90354753	5115270	0.0566	0.3261
chr17	81195210	4820300	0.0594	0.3306
chr18	78077248	4935108	0.0632	0.9569
chr19	59128983	3543794	0.0599	0.5464
chr20	63025520	3660546	0.0581	0.2888
chr21	48129895	2404027	0.0499	0.2779
chr22	51304566	1984296	0.0387	0.2216
chrMT	16571	37437	2.2592	1.9739
chrX	155270560	10396261	0.067	0.3594
chrY	59373566	462153	0.0078	0.1611

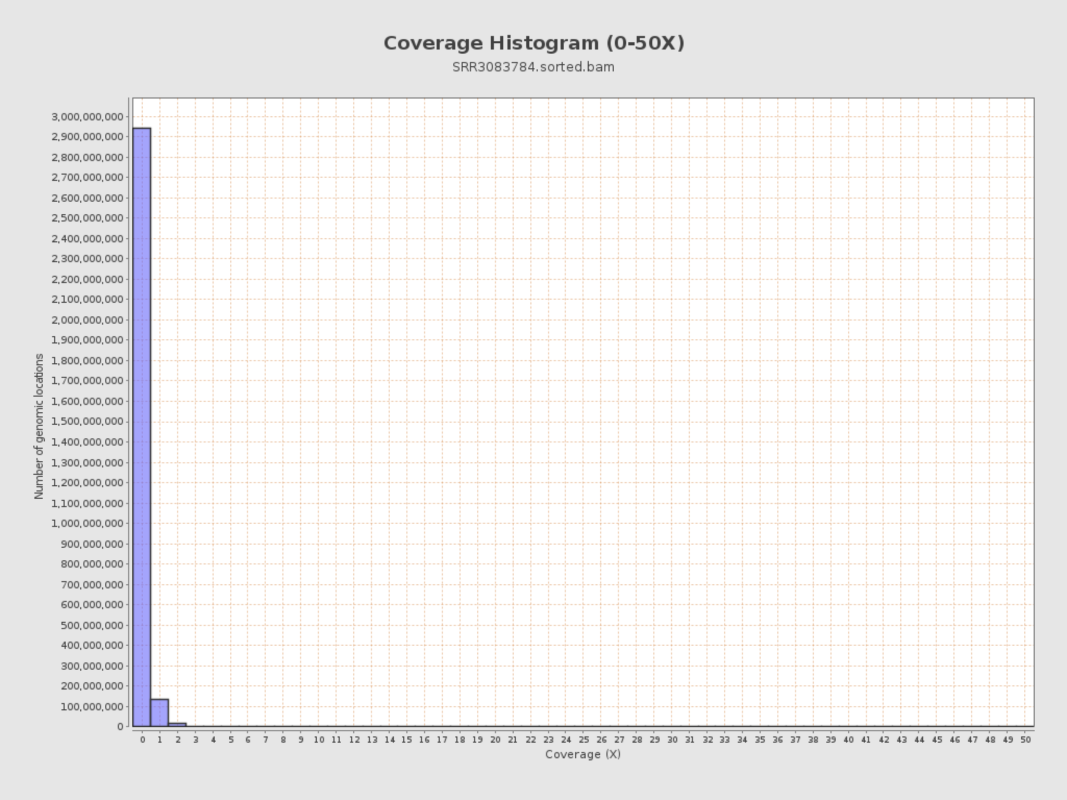
3. Results : Coverage across reference



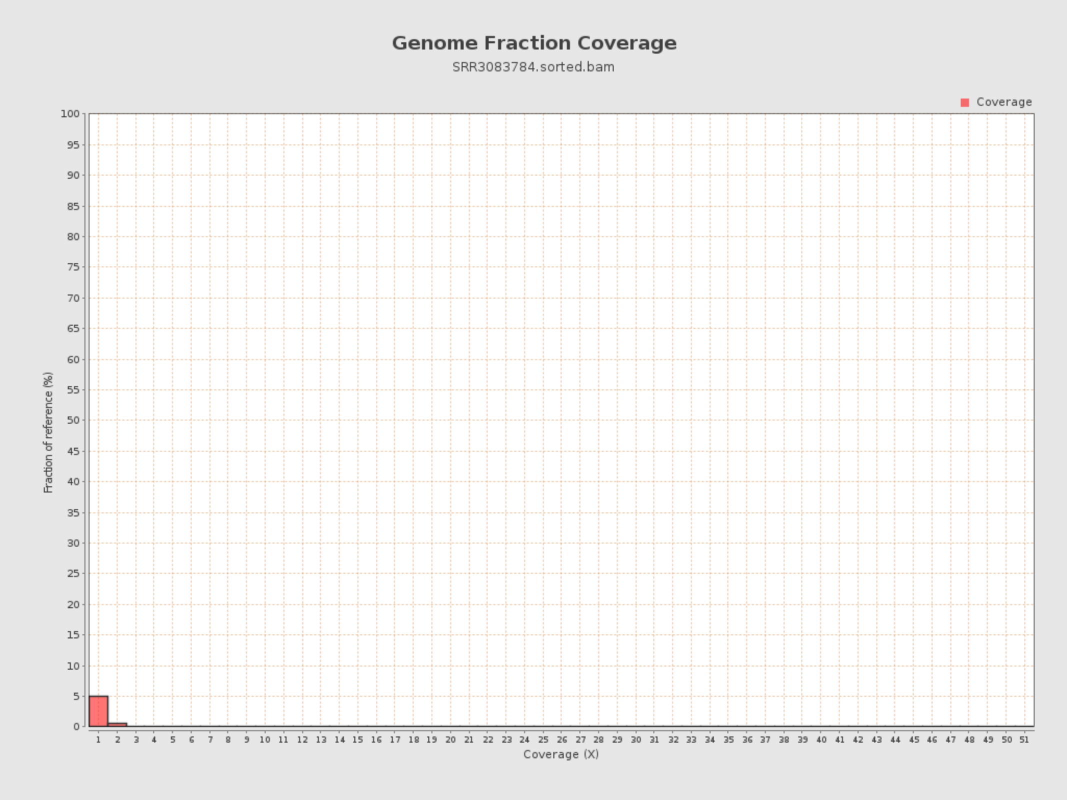
4. Results : Coverage Histogram



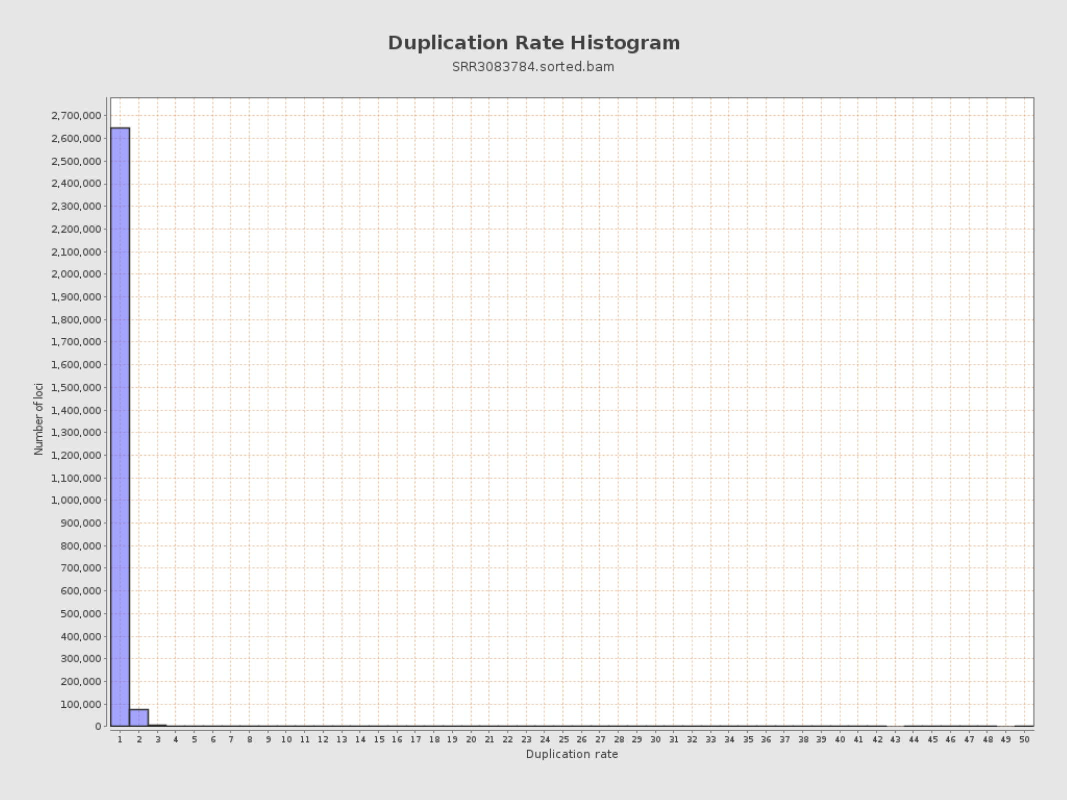
5. Results : Coverage Histogram (0-50X)



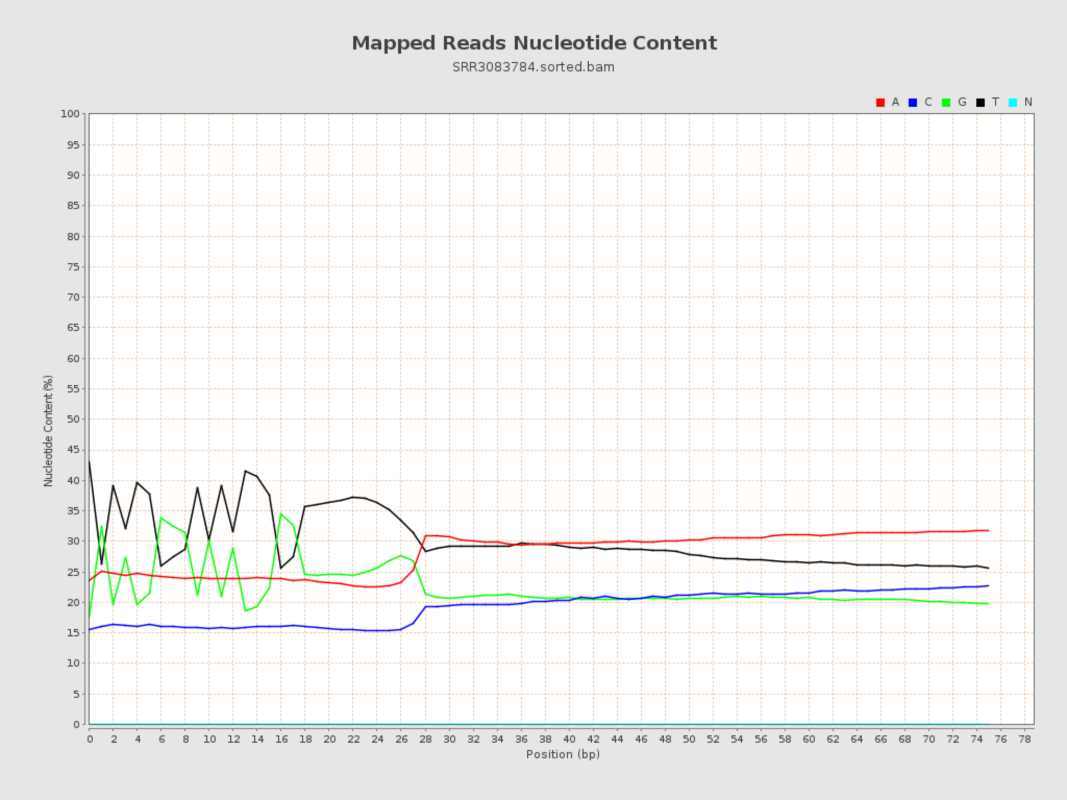
6. Results : Genome Fraction Coverage



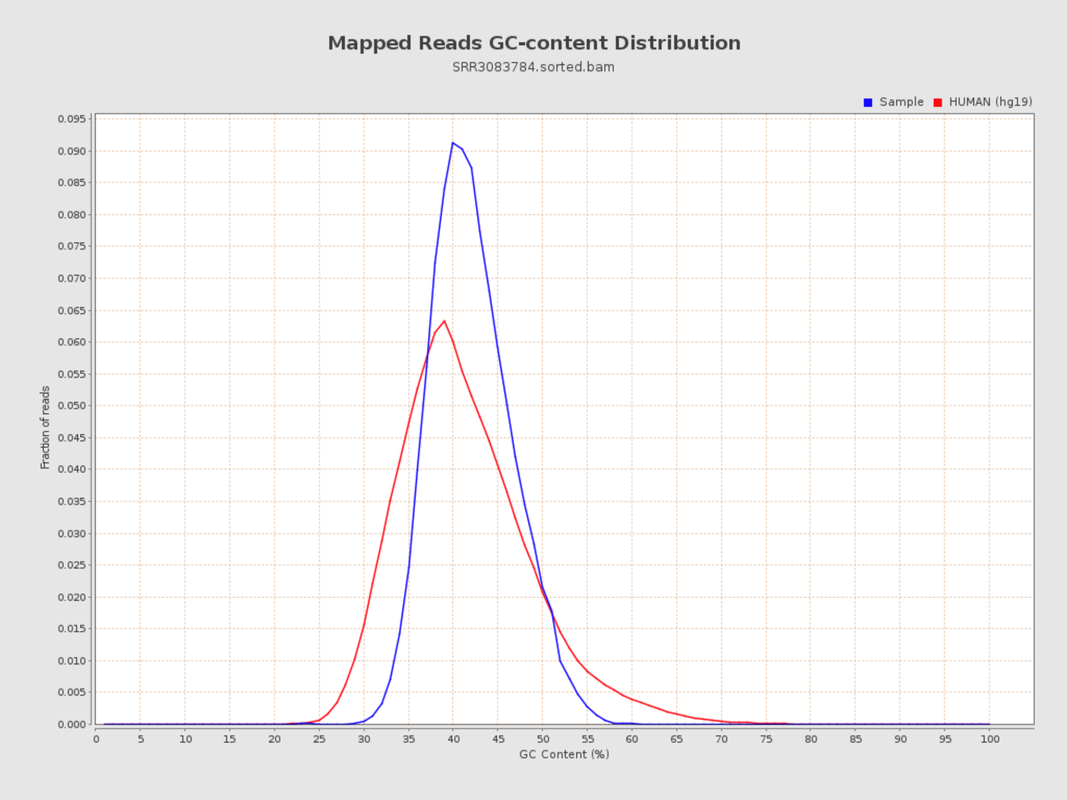
7. Results : Duplication Rate Histogram



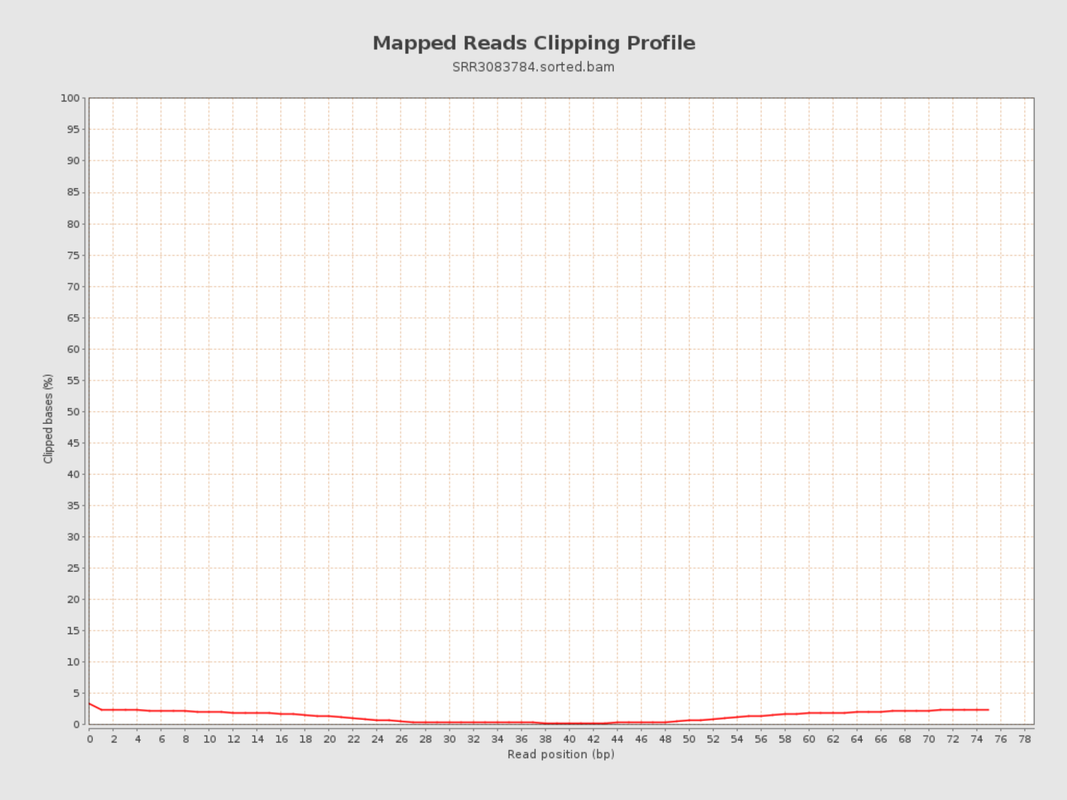
8. Results : Mapped Reads Nucleotide Content



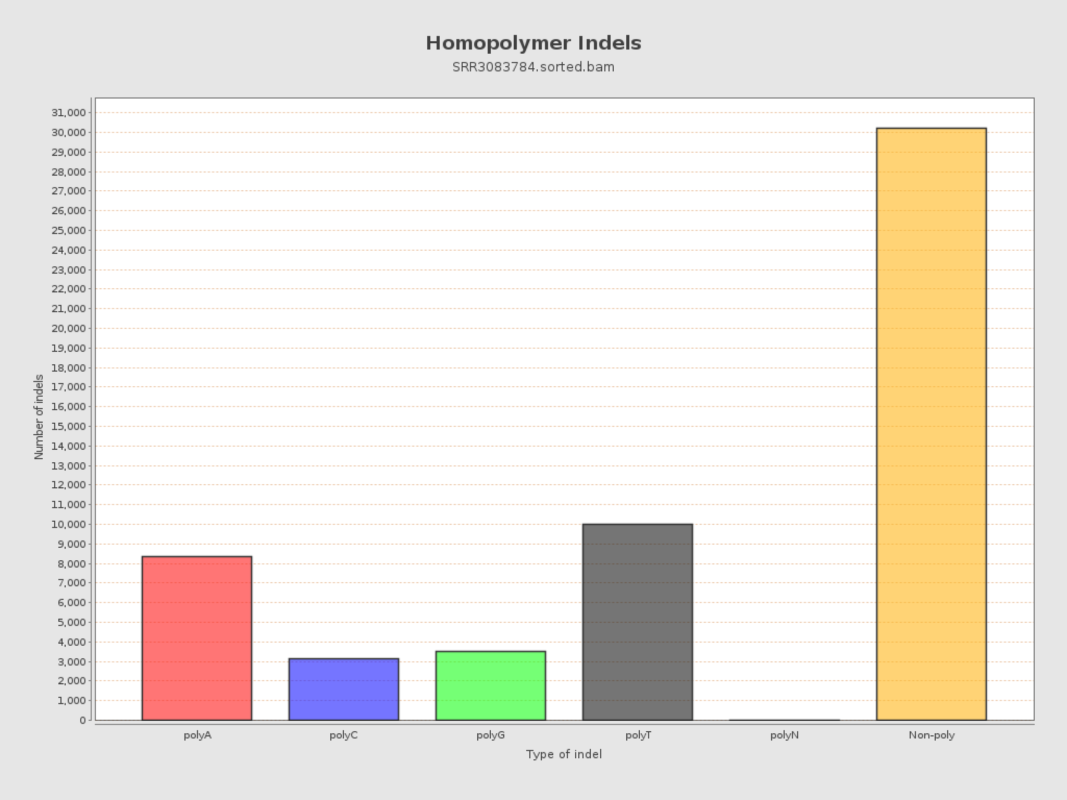
9. Results : Mapped Reads GC-content Distribution



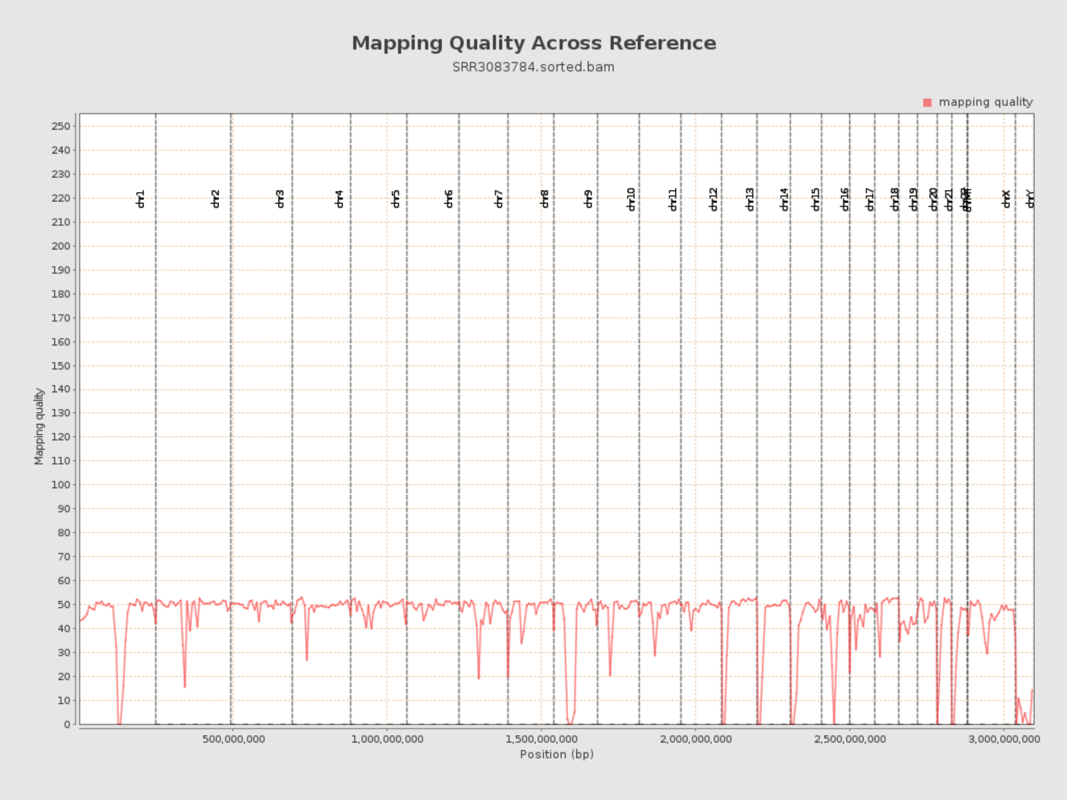
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram