Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 08:38:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090156.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_SRR090156 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090156.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 08:38:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090156.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,061,838
Mapped reads	16,918,088 / 93.67%
Unmapped reads	1,143,750 / 6.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	115,594 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	3,380,214 / 18.71%
Duplication rate	13.62%
Clipped reads	8,486,925 / 46.99%

2.2. ACGT Content

Number/percentage of A's	287,359,857 / 26.05%
Number/percentage of C's	198,974,352 / 18.03%
Number/percentage of T's	352,171,206 / 31.92%
Number/percentage of G's	264,426,793 / 23.97%
Number/percentage of N's	373,132 / 0.03%
GC Percentage	42%

2.3. Coverage

Mean	0.3565

Standard Deviation	2.5292

2.4. Mapping Quality

Mean Mapping Quality	46.54

2.5. Mismatches and indels

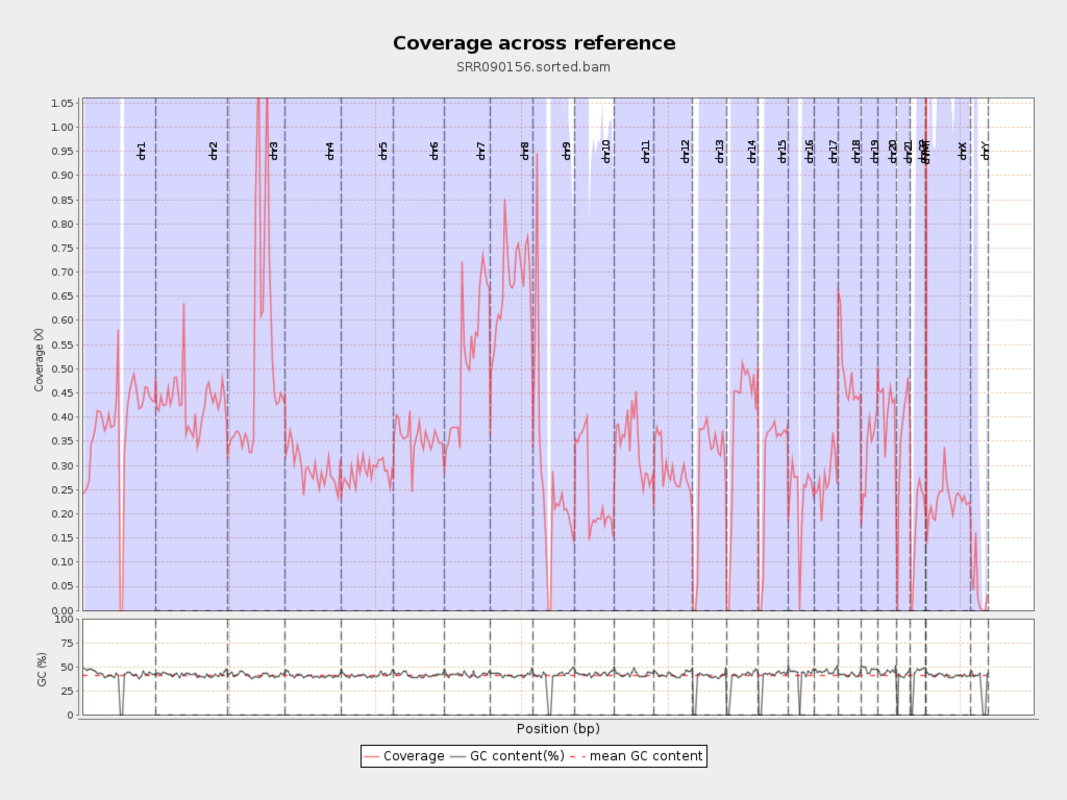
General error rate	0.59%
Mismatches	6,347,445
Insertions	70,681
Mapped reads with at least one insertion	0.41%
Deletions	234,707
Mapped reads with at least one deletion	1.37%
Homopolymer indels	48.38%

2.6. Chromosome stats

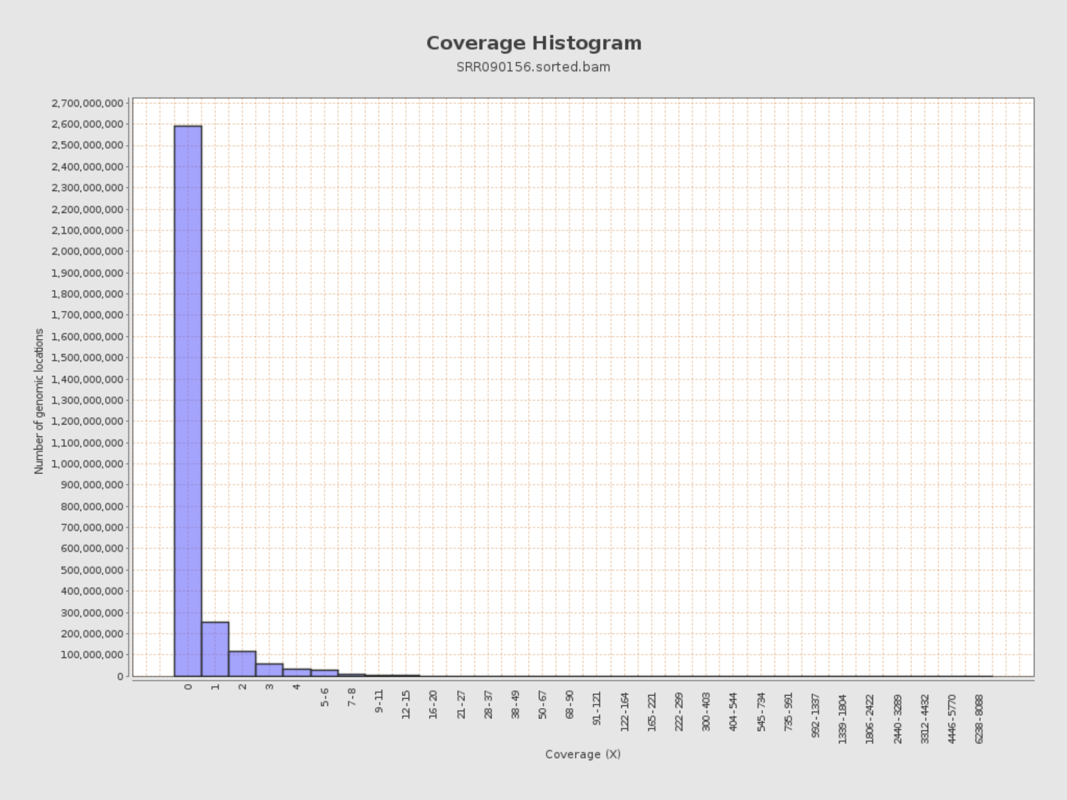
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	94750689	0.3801	4.7563
chr2	243199373	104442811	0.4295	2.7488
chr3	198022430	101453761	0.5123	1.3888
chr4	191154276	56394974	0.295	1.1317
chr5	180915260	51934312	0.2871	1.0078
chr6	171115067	61084142	0.357	1.4089
chr7	159138663	82421879	0.5179	4.3505

chr8	146364022	98280692	0.6715	5.076
chr9	141213431	36932842	0.2615	1.9621
chr10	135534747	33333580	0.2459	1.9304
chr11	135006516	45750355	0.3389	1.8262
chr12	133851895	39297596	0.2936	1.1114
chr13	115169878	33975371	0.295	0.9939
chr14	107349540	42024036	0.3915	1.203
chr15	102531392	30214766	0.2947	1.0544
chr16	90354753	21112668	0.2337	1.0033
chr17	81195210	22300952	0.2747	1.2226
chr18	78077248	38025536	0.487	3.7387
chr19	59128983	19841620	0.3356	2.6252
chr20	63025520	26332732	0.4178	1.3686
chr21	48129895	16766681	0.3484	1.2593
chr22	51304566	9025013	0.1759	0.758
chrMT	16571	268784	16.2201	10.2522
chrX	155270560	35318212	0.2275	1.1008
chrY	59373566	2432405	0.041	1.7031

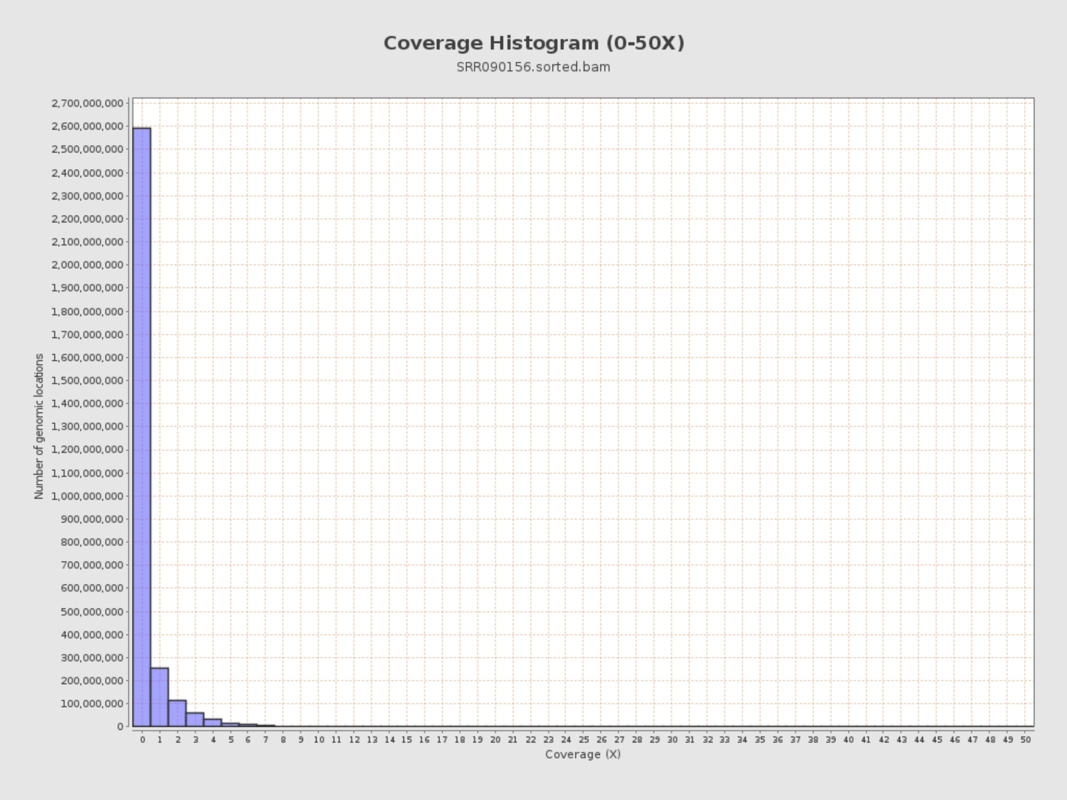
3. Results : Coverage across reference



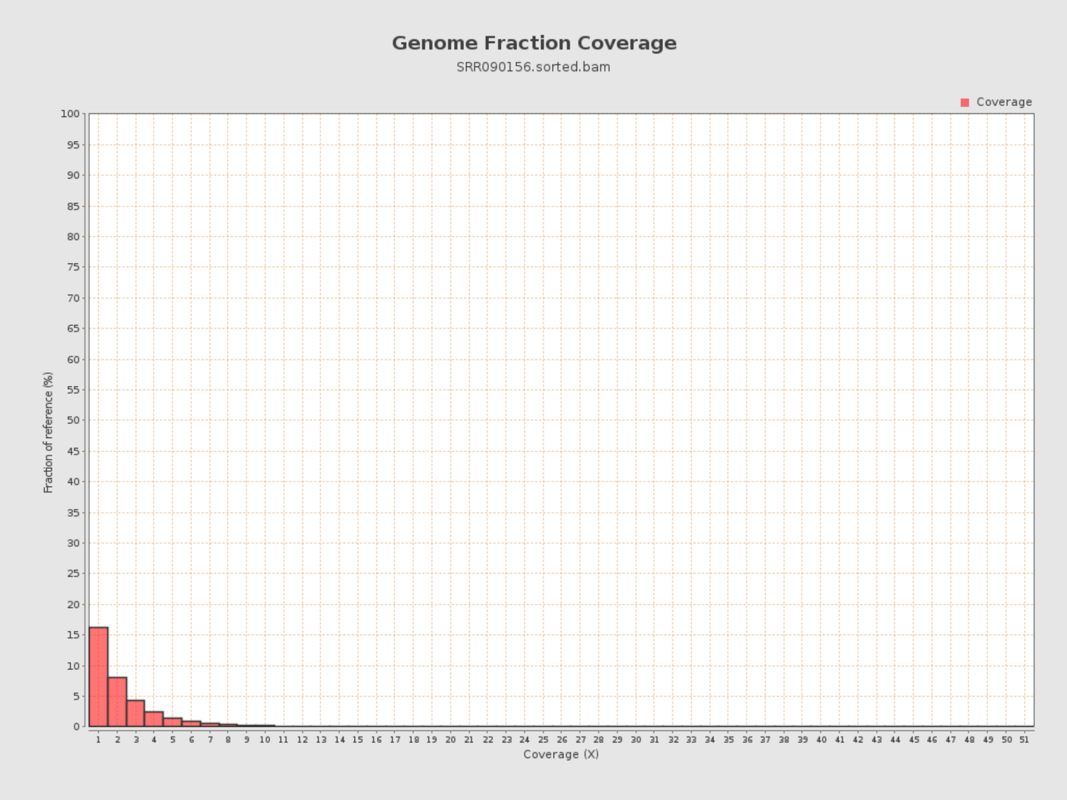
4. Results : Coverage Histogram



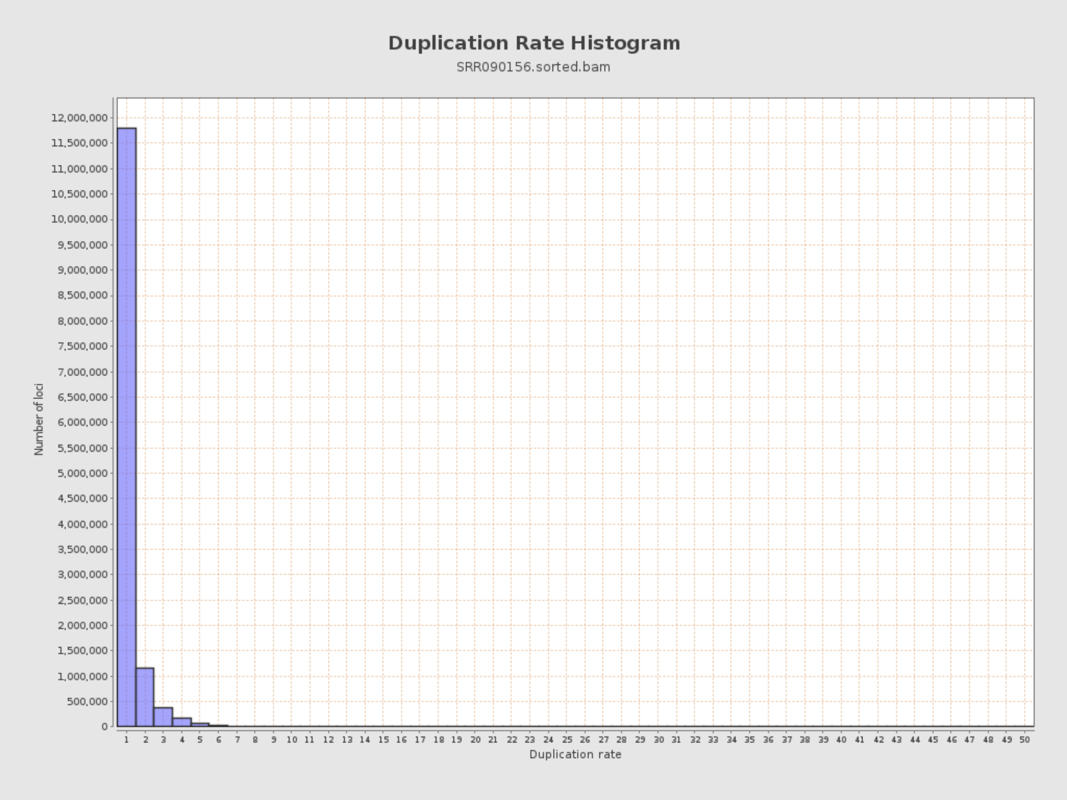
5. Results : Coverage Histogram (0-50X)



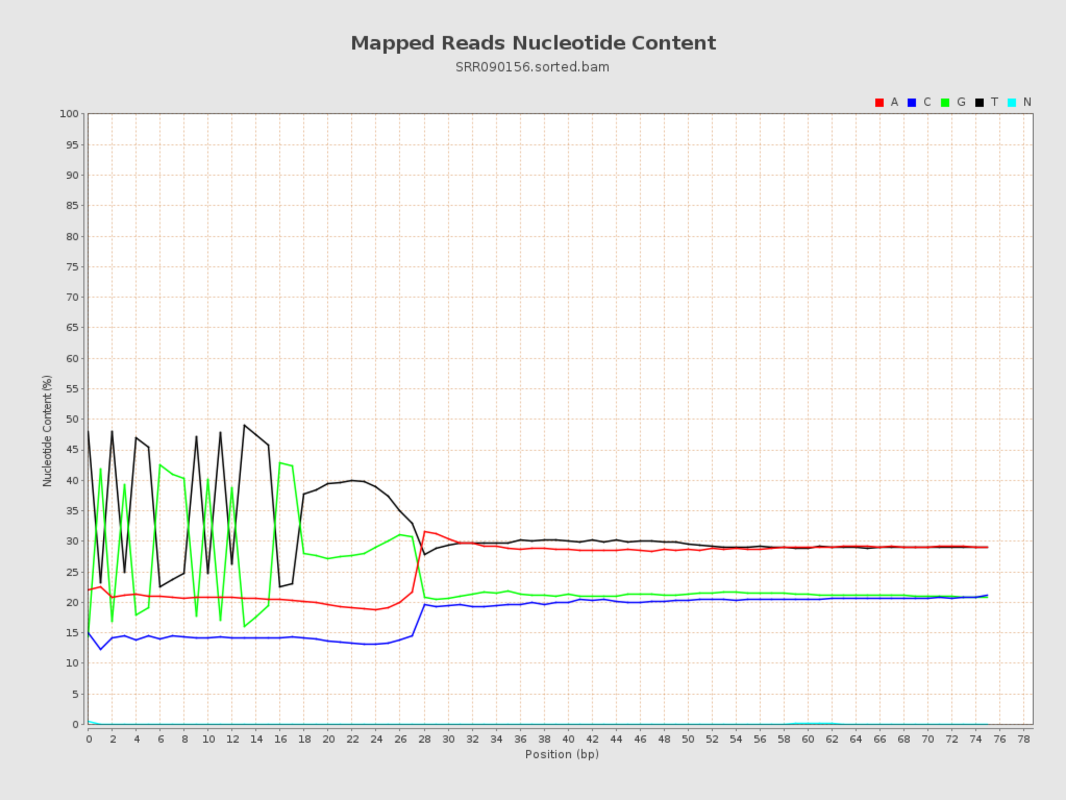
6. Results : Genome Fraction Coverage



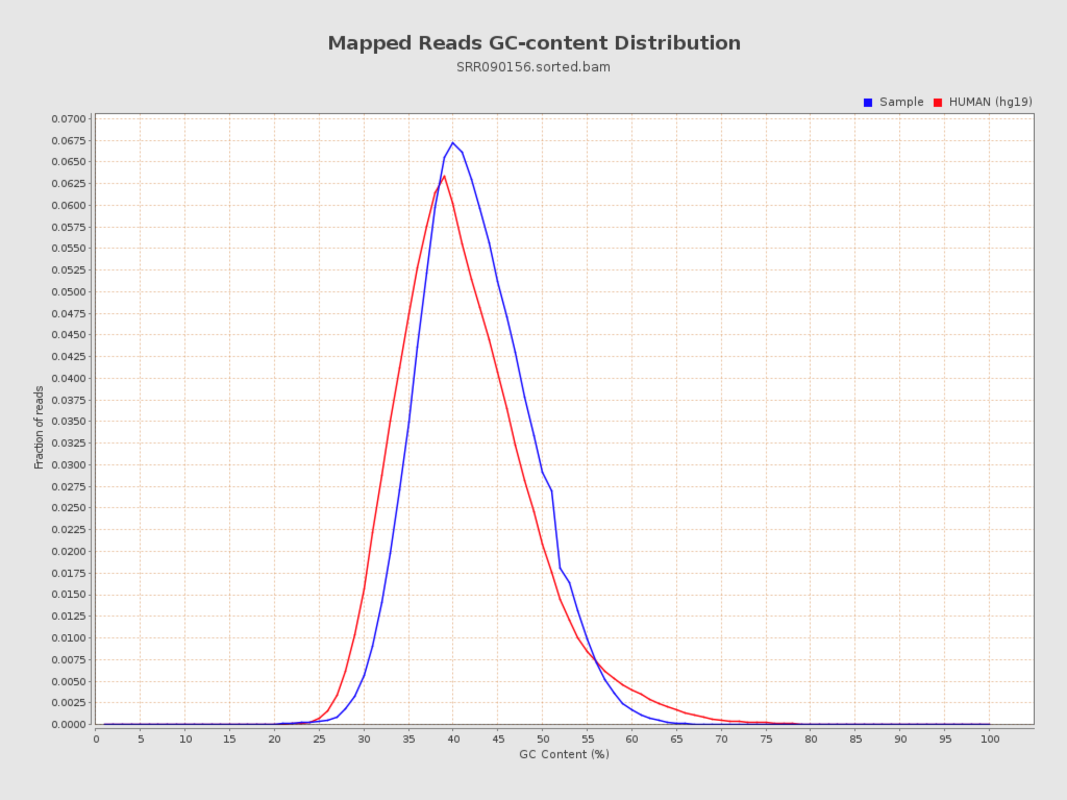
7. Results : Duplication Rate Histogram



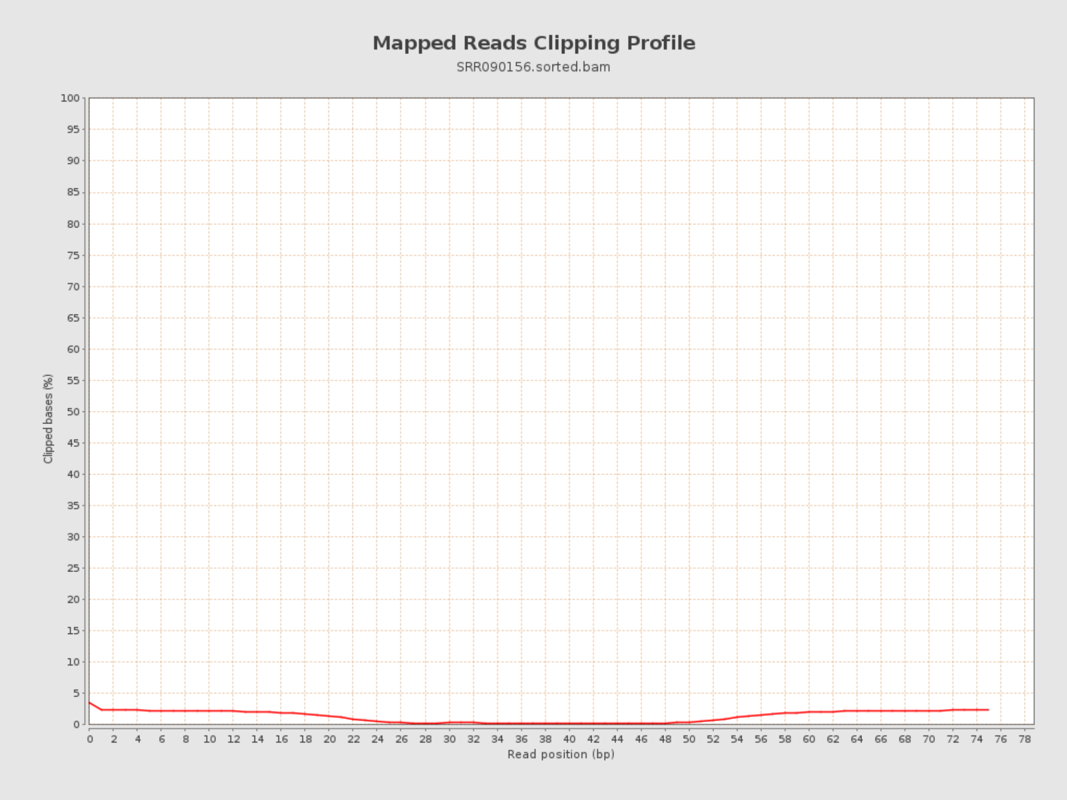
8. Results : Mapped Reads Nucleotide Content



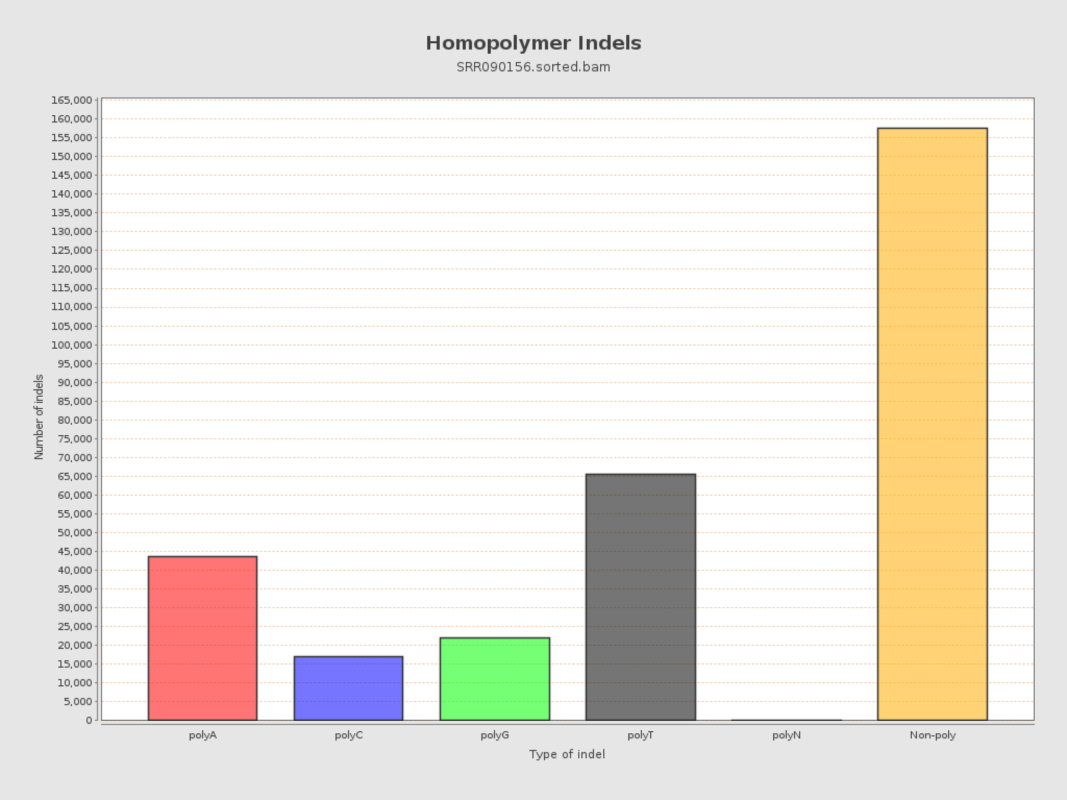
9. Results : Mapped Reads GC-content Distribution



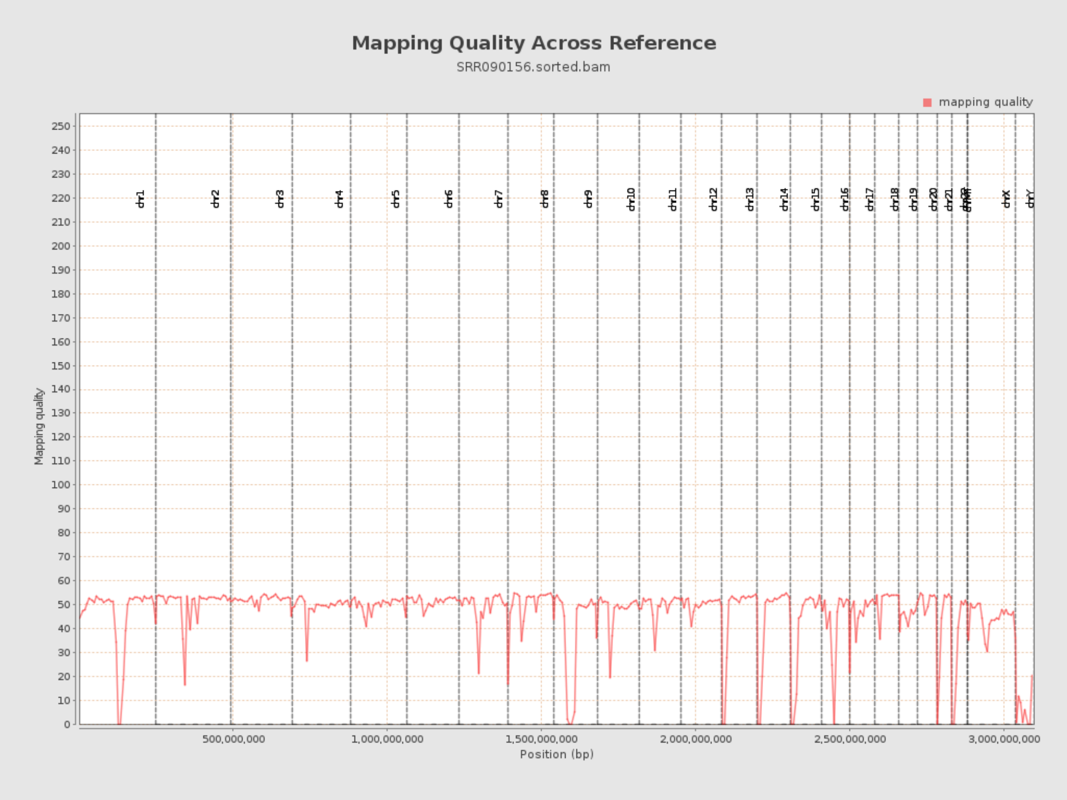
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram