Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 02:40:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089733.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_SRR089733 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089733.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 02:40:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089733.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,414,726
Mapped reads	21,868,887 / 86.05%
Unmapped reads	3,545,839 / 13.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,237 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	4,006,582 / 15.76%
Duplication rate	11.9%
Clipped reads	1,656,658 / 6.52%

2.2. ACGT Content

Number/percentage of A's	313,881,150 / 30.36%
Number/percentage of C's	205,353,610 / 19.86%
Number/percentage of T's	298,180,584 / 28.84%
Number/percentage of G's	216,532,092 / 20.94%
Number/percentage of N's	22,549 / 0%
GC Percentage	40.8%

2.3. Coverage

Mean	0.3341

Standard Deviation	2.249

2.4. Mapping Quality

Mean Mapping Quality	45.13

2.5. Mismatches and indels

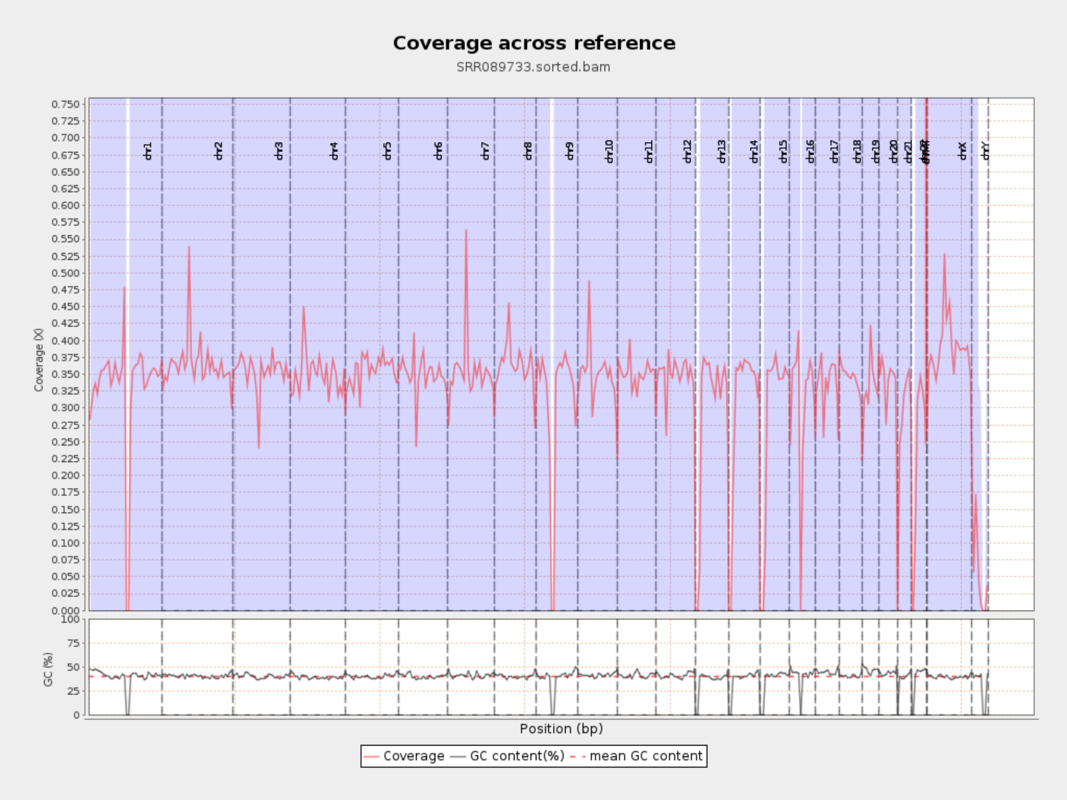
General error rate	0.39%
Mismatches	4,001,132
Insertions	43,821
Mapped reads with at least one insertion	0.2%
Deletions	140,114
Mapped reads with at least one deletion	0.64%
Homopolymer indels	49.15%

2.6. Chromosome stats

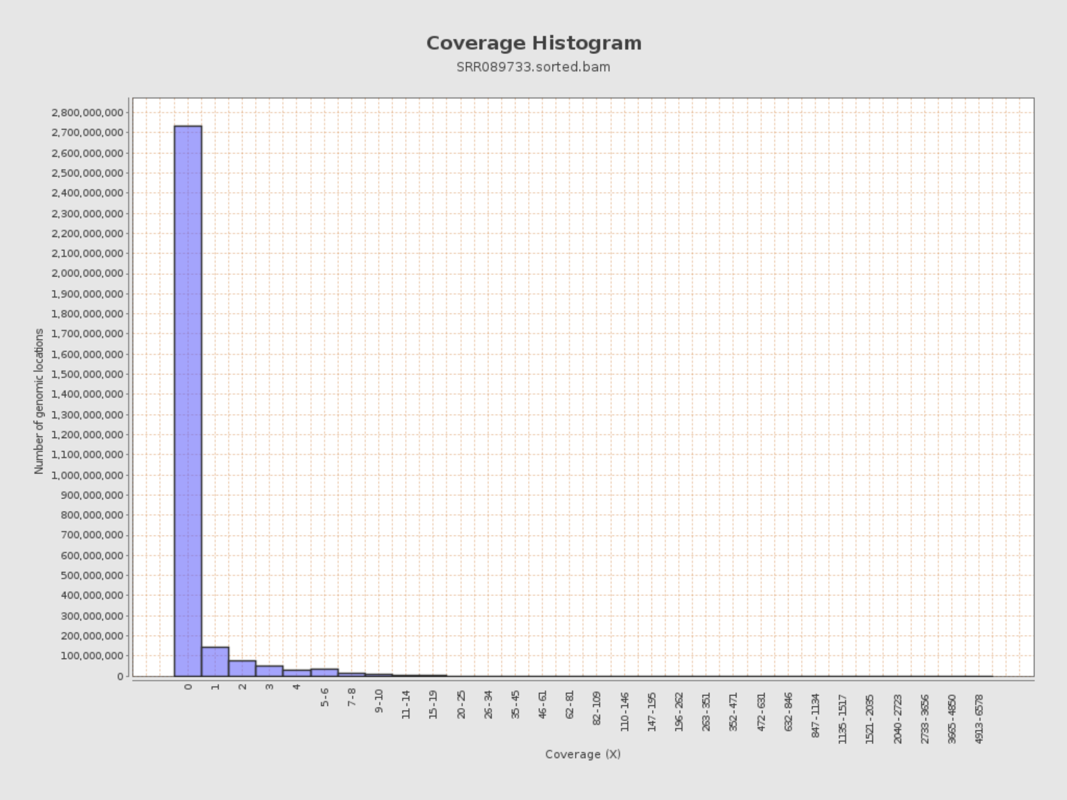
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	82220998	0.3299	3.8197
chr2	243199373	88904706	0.3656	2.2467
chr3	198022430	70086076	0.3539	1.3179
chr4	191154276	66770180	0.3493	1.4469
chr5	180915260	64360436	0.3557	1.3429
chr6	171115067	59870810	0.3499	1.5538
chr7	159138663	56817059	0.357	3.3214

chr8	146364022	53199923	0.3635	3.8357
chr9	141213431	43431136	0.3076	1.9781
chr10	135534747	47710868	0.352	1.9587
chr11	135006516	47121851	0.349	2.0555
chr12	133851895	46742633	0.3492	1.4469
chr13	115169878	33213542	0.2884	1.1881
chr14	107349540	31992745	0.298	1.4409
chr15	102531392	29212948	0.2849	1.1899
chr16	90354753	28063269	0.3106	1.348
chr17	81195210	27130469	0.3341	1.5726
chr18	78077248	27048556	0.3464	3.7779
chr19	59128983	19861127	0.3359	3.1612
chr20	63025520	21324079	0.3383	1.3931
chr21	48129895	13380363	0.278	1.4304
chr22	51304566	11329608	0.2208	0.9996
chrMT	16571	980649	59.1786	33.9814
chrX	155270560	60229188	0.3879	1.6826
chrY	59373566	3177859	0.0535	1.1724

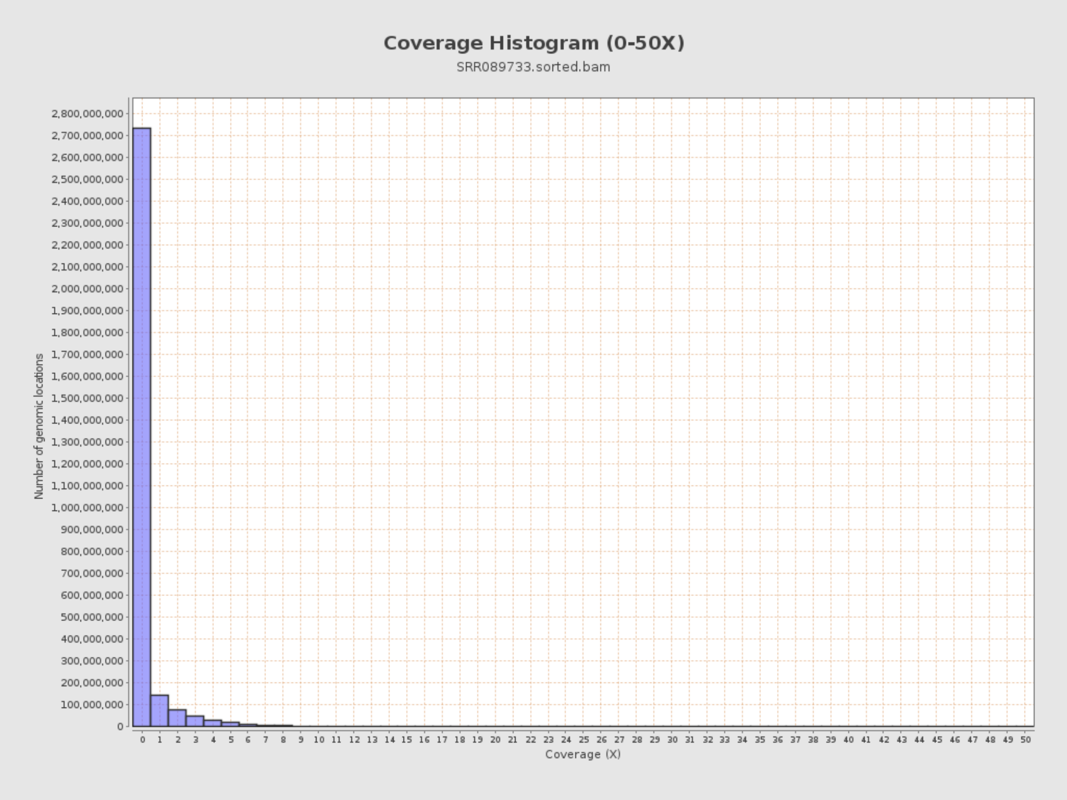
3. Results : Coverage across reference



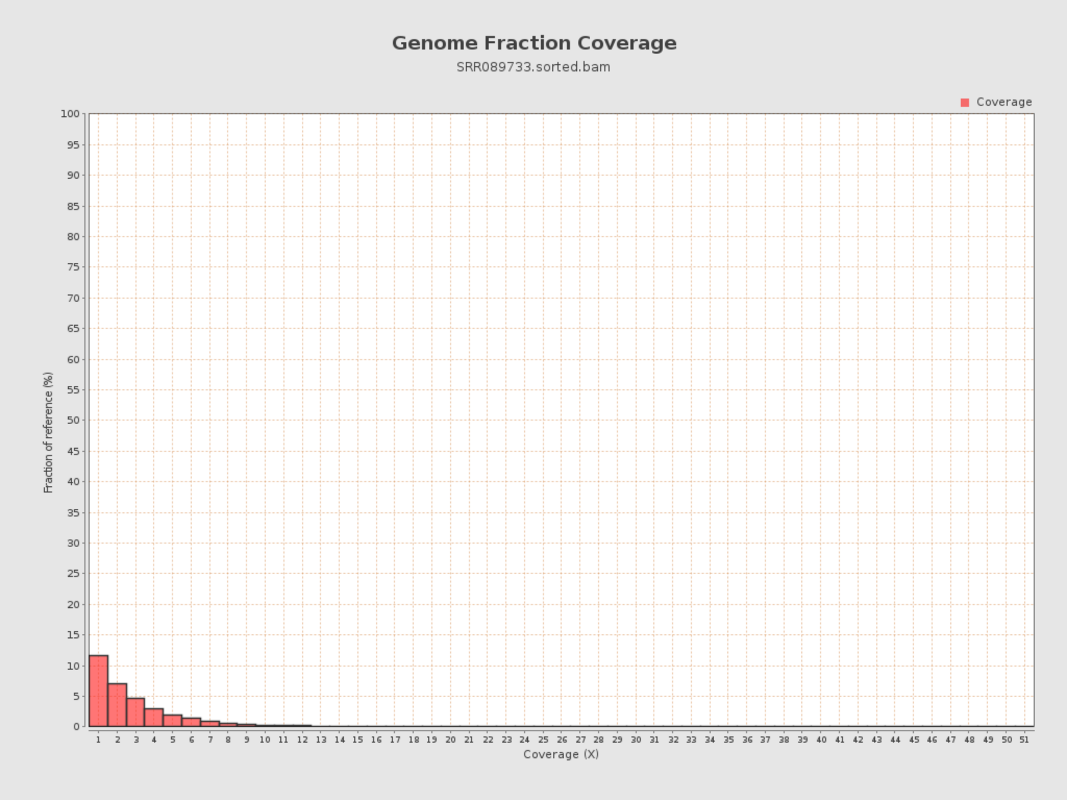
4. Results : Coverage Histogram



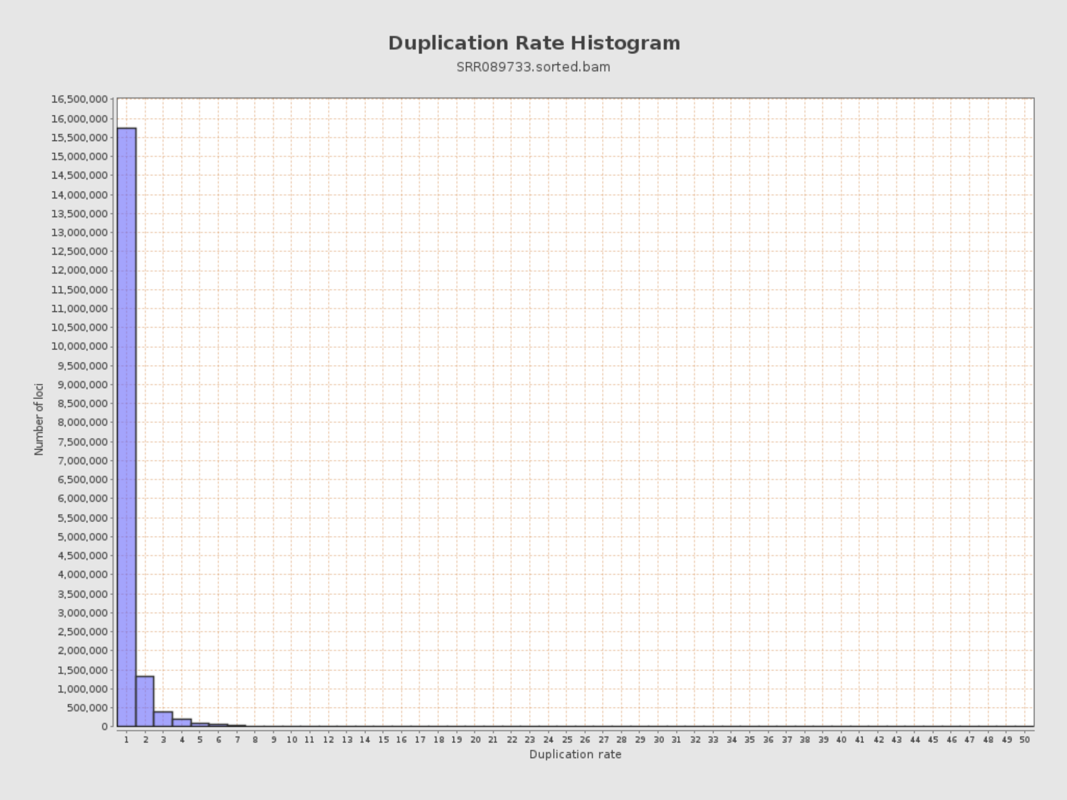
5. Results : Coverage Histogram (0-50X)



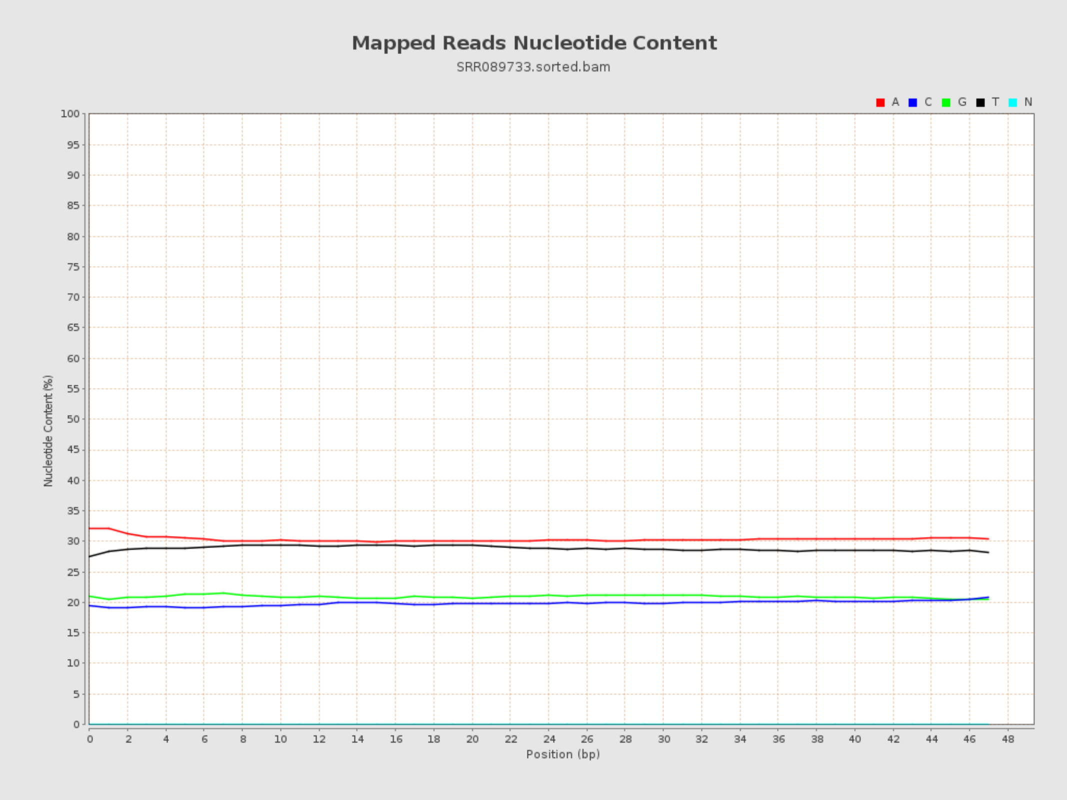
6. Results : Genome Fraction Coverage



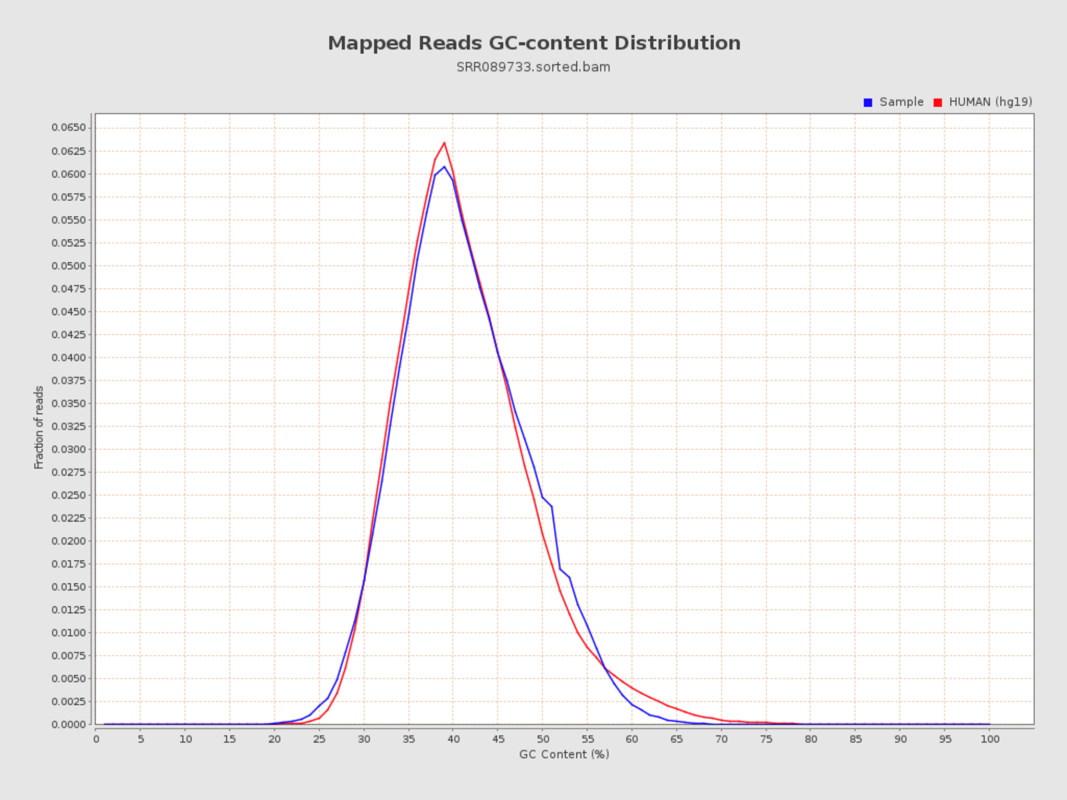
7. Results : Duplication Rate Histogram



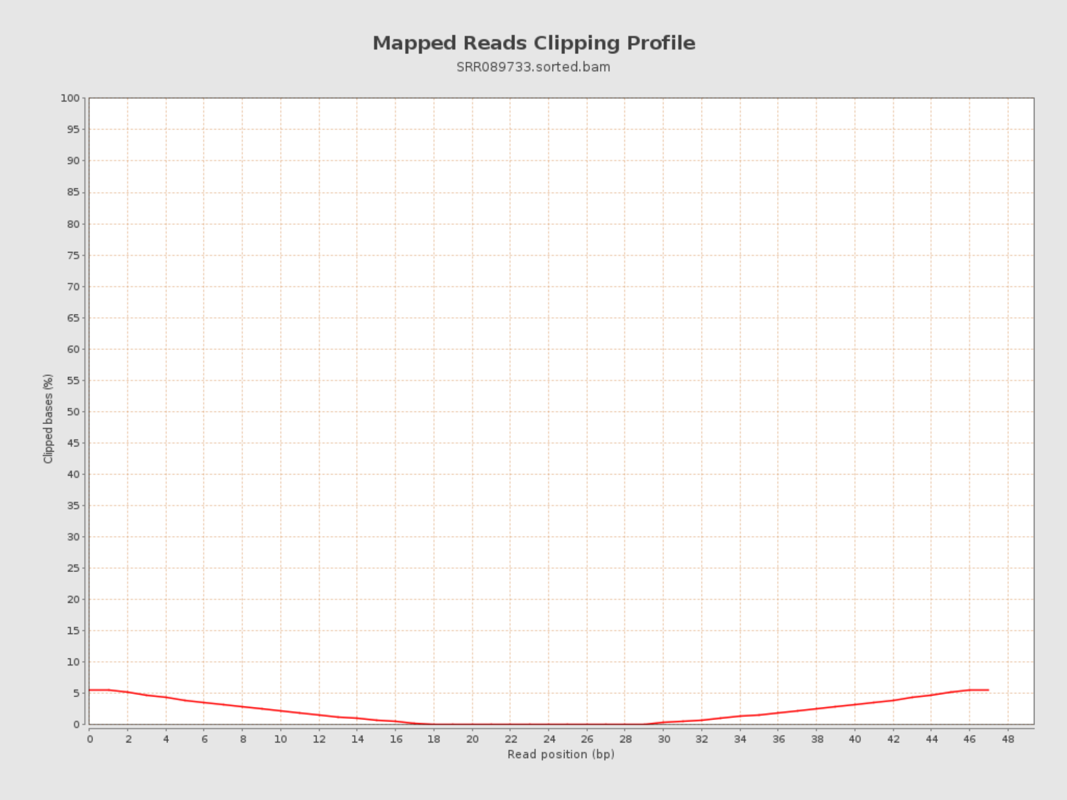
8. Results : Mapped Reads Nucleotide Content



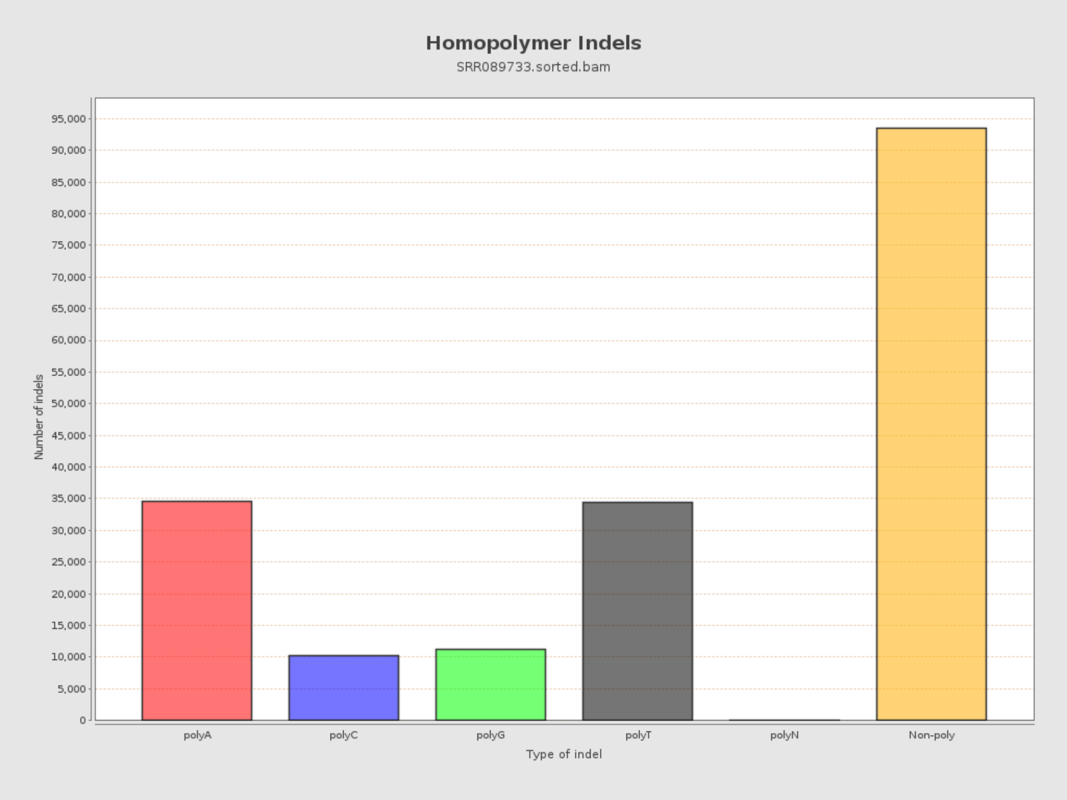
9. Results : Mapped Reads GC-content Distribution



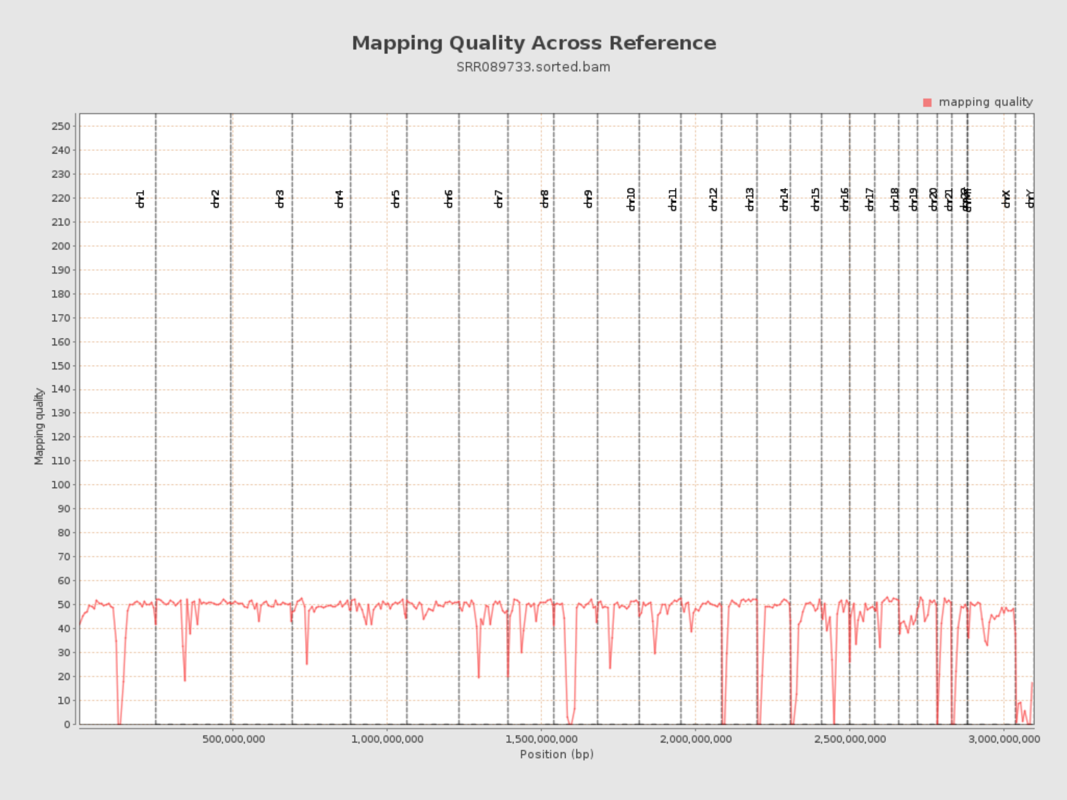
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram