Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 18:44:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089659.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_SRR089659 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089659.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 18:44:30 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089659.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,292,377
Mapped reads	19,599,384 / 84.15%
Unmapped reads	3,692,993 / 15.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	830 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,621,635 / 6.96%
Duplication rate	6.01%
Clipped reads	2,611,847 / 11.21%

2.2. ACGT Content

Number/percentage of A's	270,712,400 / 29.54%
Number/percentage of C's	193,558,835 / 21.12%
Number/percentage of T's	257,303,967 / 28.08%
Number/percentage of G's	194,671,508 / 21.25%
Number/percentage of N's	37,940 / 0%
GC Percentage	42.37%

2.3. Coverage

Mean	0.296

Standard Deviation	1.7041

2.4. Mapping Quality

Mean Mapping Quality	41.94

2.5. Mismatches and indels

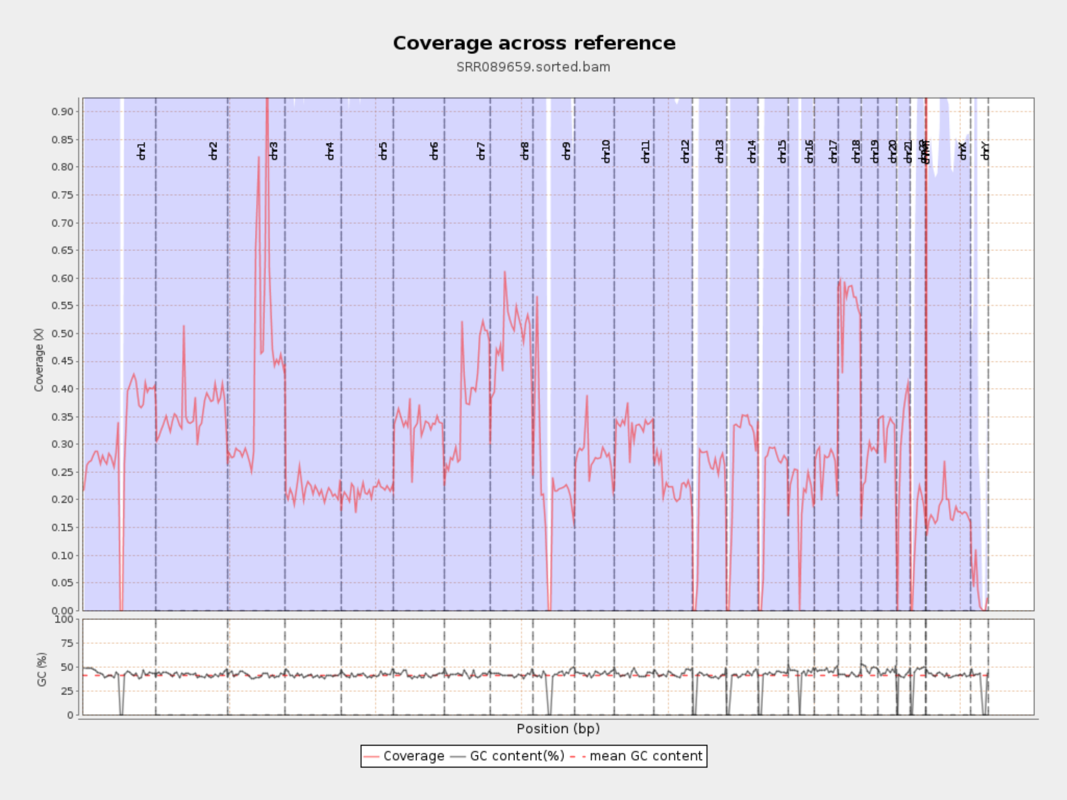
General error rate	0.5%
Mismatches	4,550,675
Insertions	39,521
Mapped reads with at least one insertion	0.2%
Deletions	126,405
Mapped reads with at least one deletion	0.64%
Homopolymer indels	44.19%

2.6. Chromosome stats

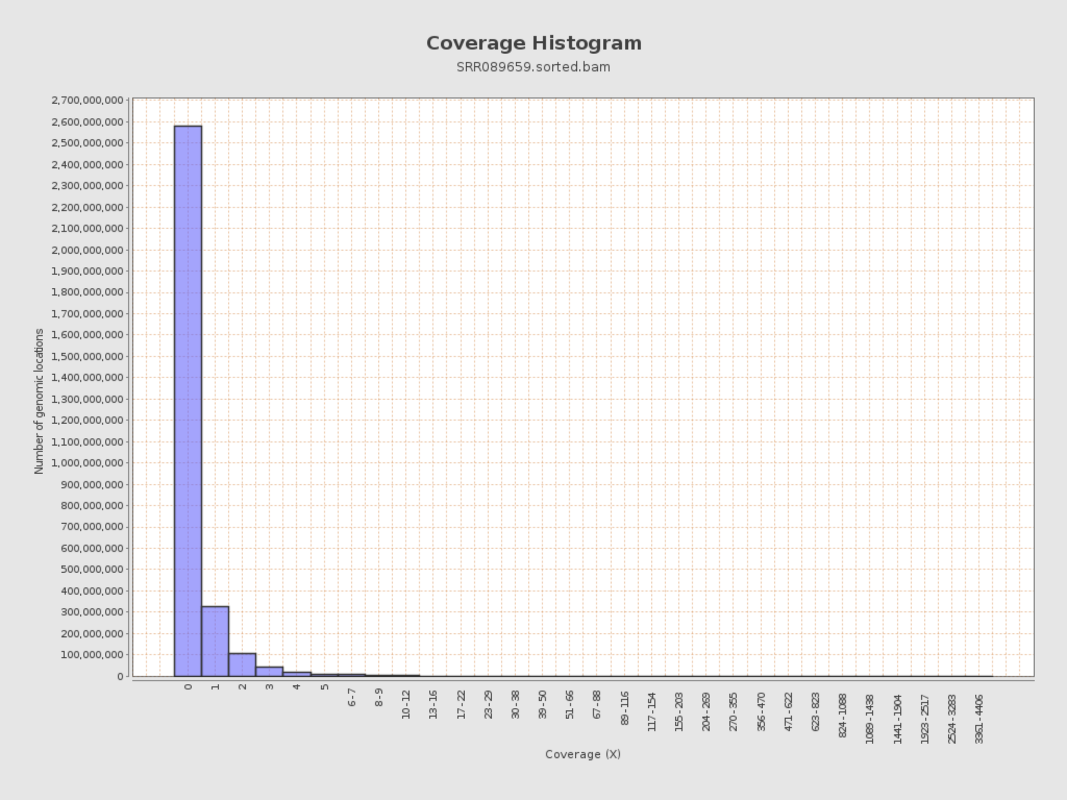
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	76861430	0.3084	2.1587
chr2	243199373	87087102	0.3581	2.8445
chr3	198022430	84778891	0.4281	1.1927
chr4	191154276	41398224	0.2166	0.8108
chr5	180915260	38983994	0.2155	0.7738
chr6	171115067	57514174	0.3361	1.3037
chr7	159138663	60800888	0.3821	2.9782

chr8	146364022	72119203	0.4927	2.5351
chr9	141213431	31944469	0.2262	1.561
chr10	135534747	38051118	0.2807	1.5971
chr11	135006516	44669105	0.3309	1.5683
chr12	133851895	30920633	0.231	0.8639
chr13	115169878	26079160	0.2264	0.7794
chr14	107349540	29924596	0.2788	1.0486
chr15	102531392	22978413	0.2241	0.7774
chr16	90354753	18300340	0.2025	0.9126
chr17	81195210	21927074	0.2701	1.0319
chr18	78077248	43592000	0.5583	2.3907
chr19	59128983	15849415	0.268	2.1256
chr20	63025520	20571447	0.3264	1.0356
chr21	48129895	14213879	0.2953	1.0876
chr22	51304566	7424508	0.1447	0.6087
chrMT	16571	426260	25.7233	21.0603
chrX	155270560	27894998	0.1797	1.248
chrY	59373566	2160229	0.0364	0.5992

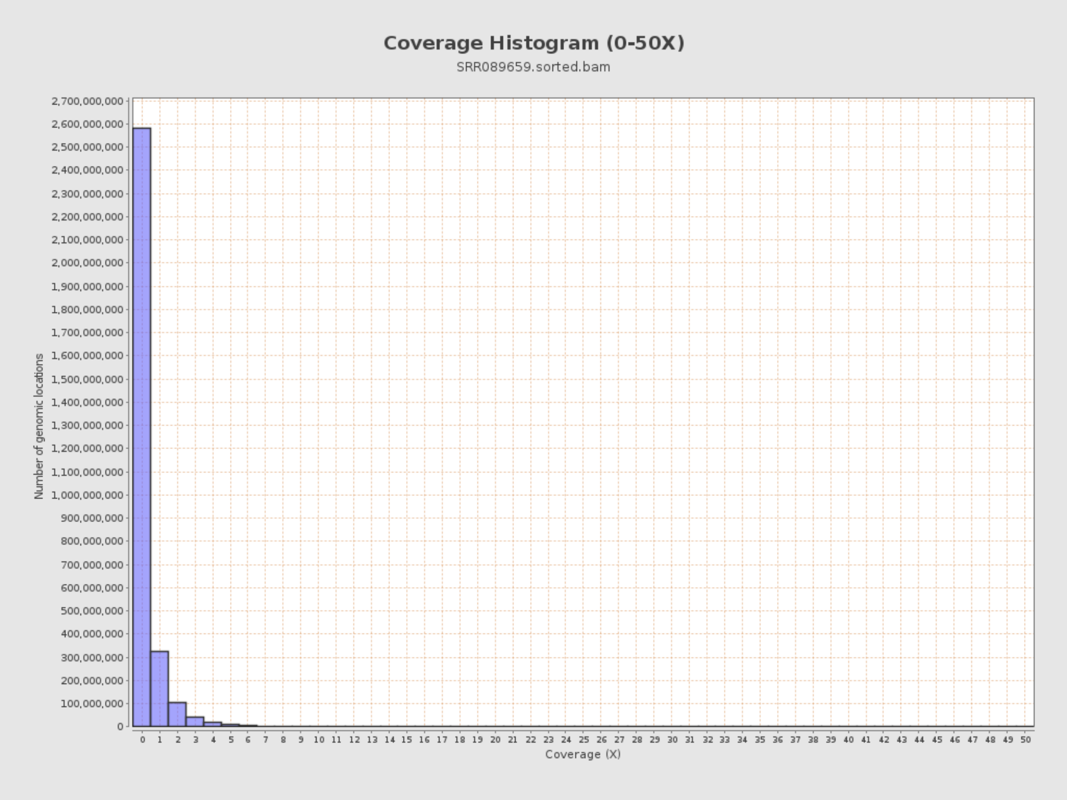
3. Results : Coverage across reference



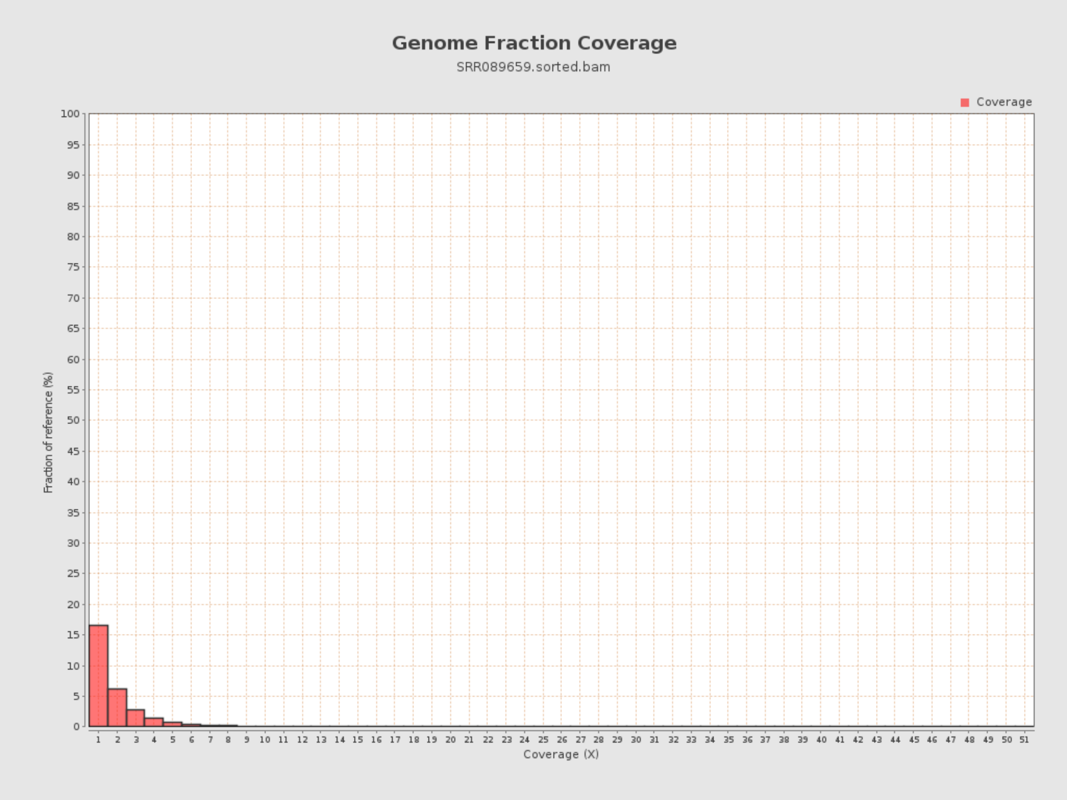
4. Results : Coverage Histogram



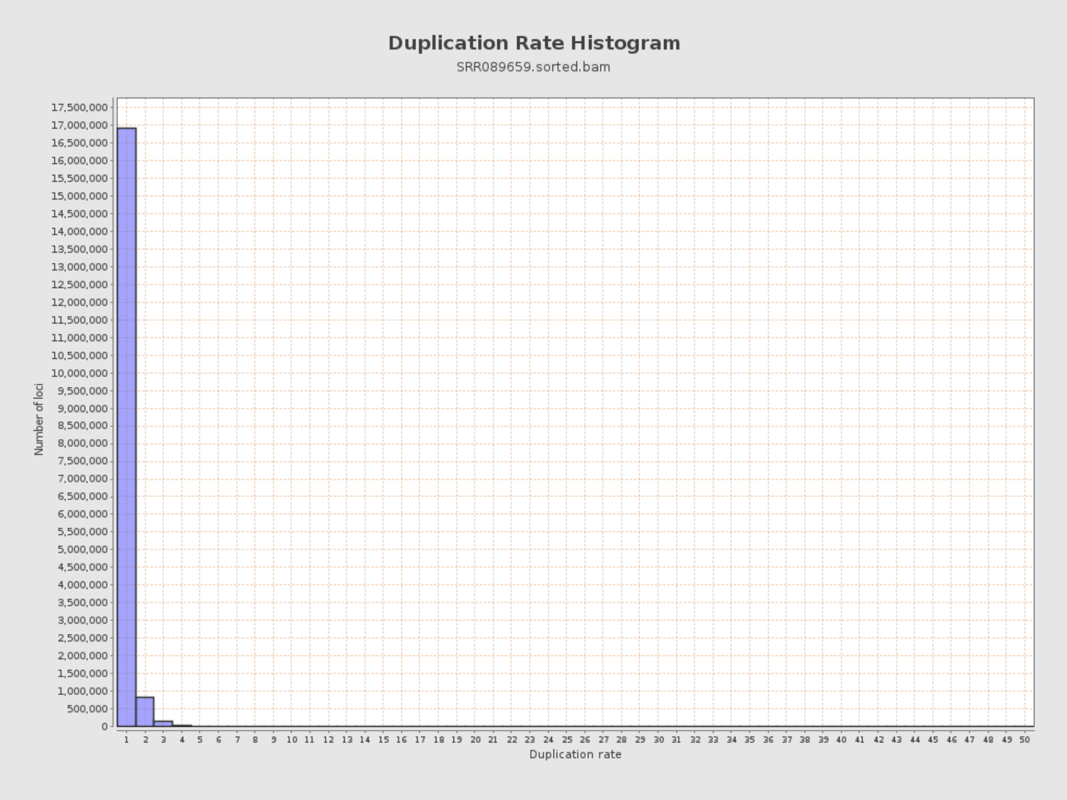
5. Results : Coverage Histogram (0-50X)



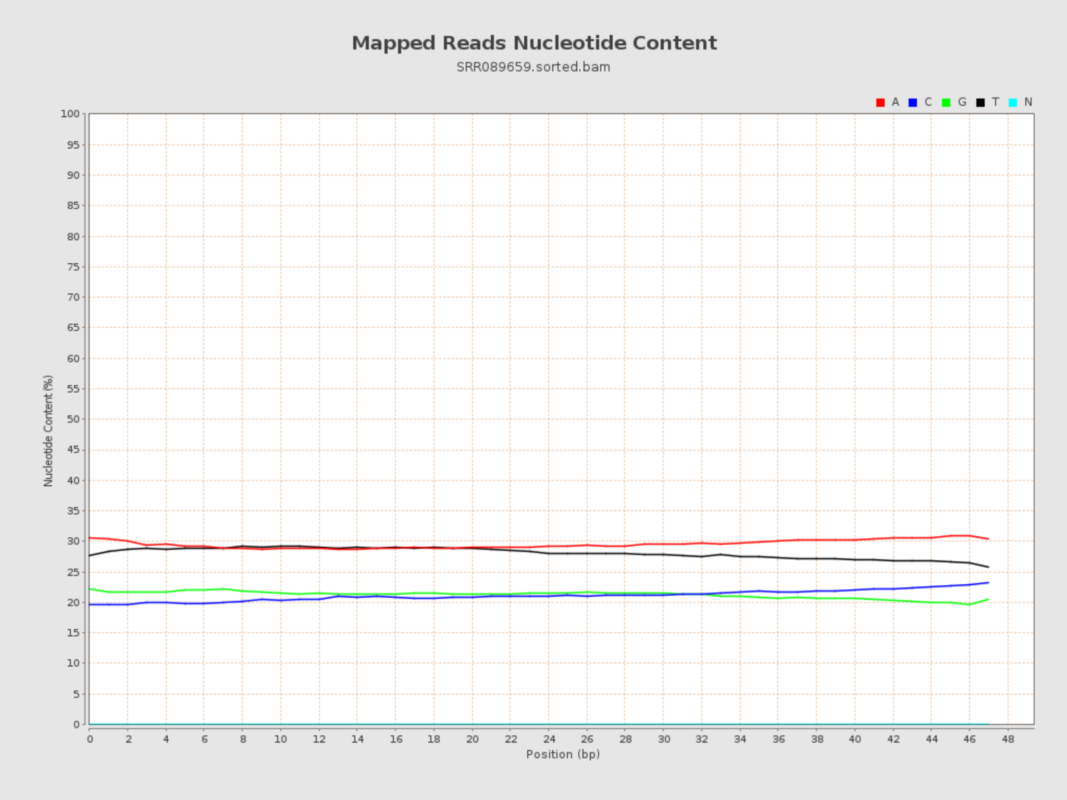
6. Results : Genome Fraction Coverage



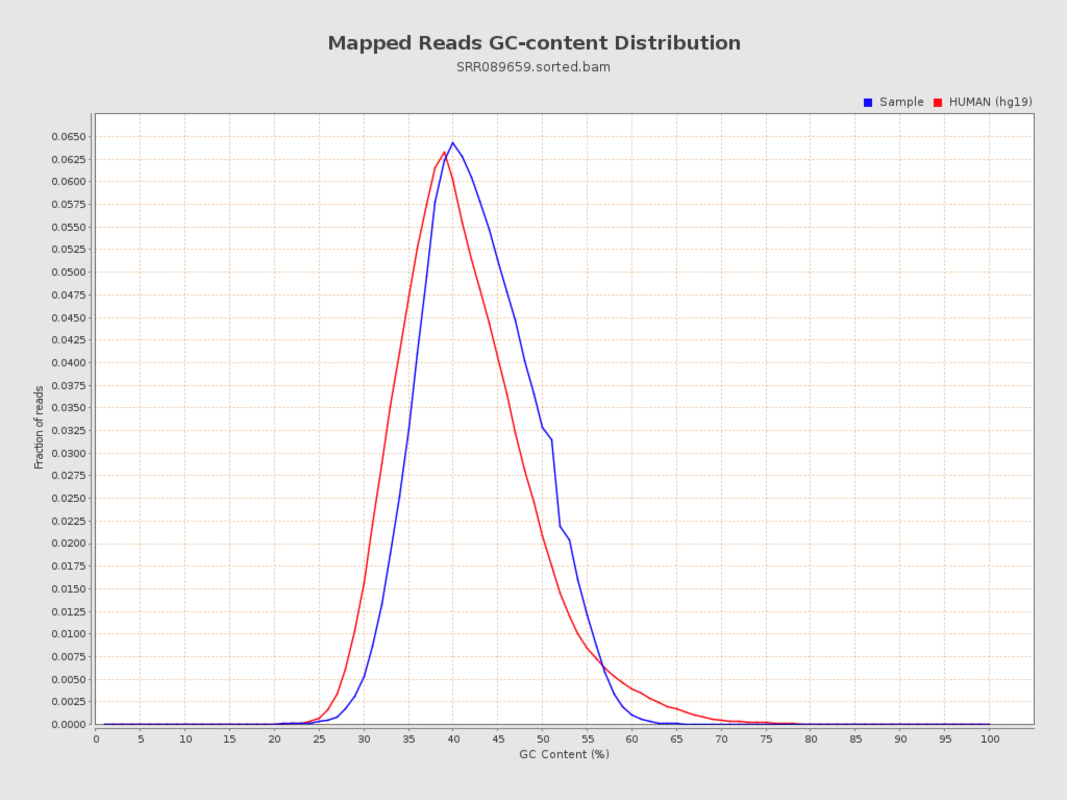
7. Results : Duplication Rate Histogram



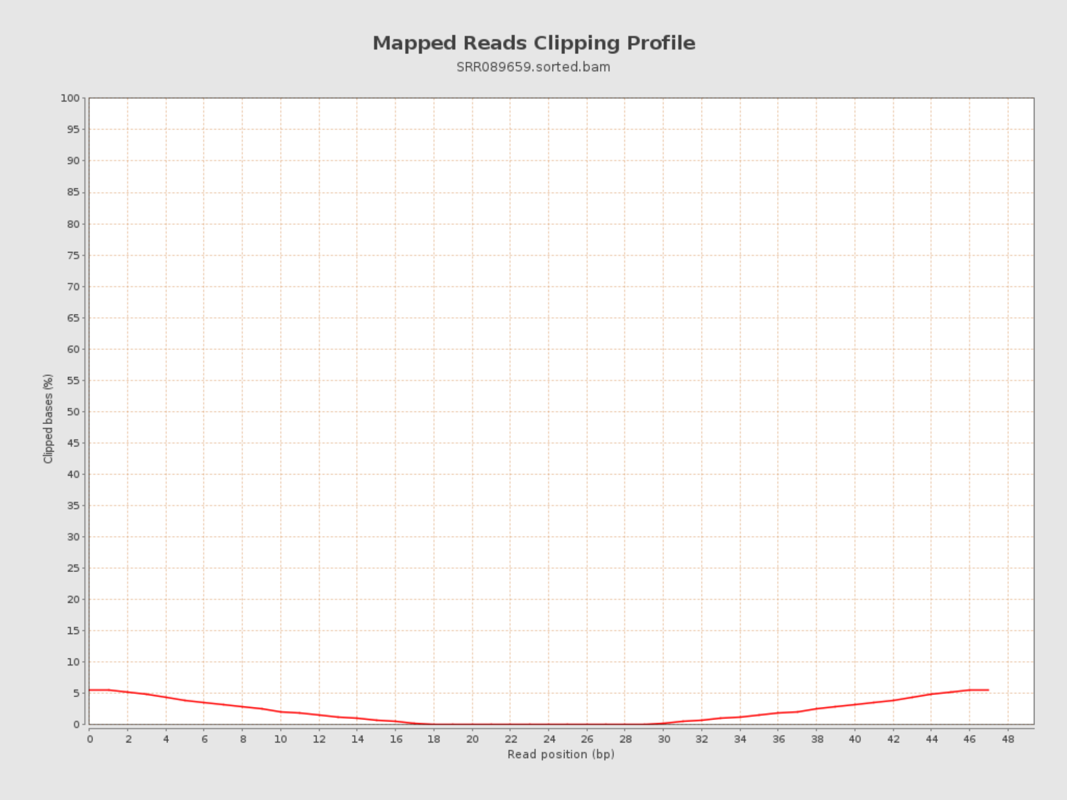
8. Results : Mapped Reads Nucleotide Content



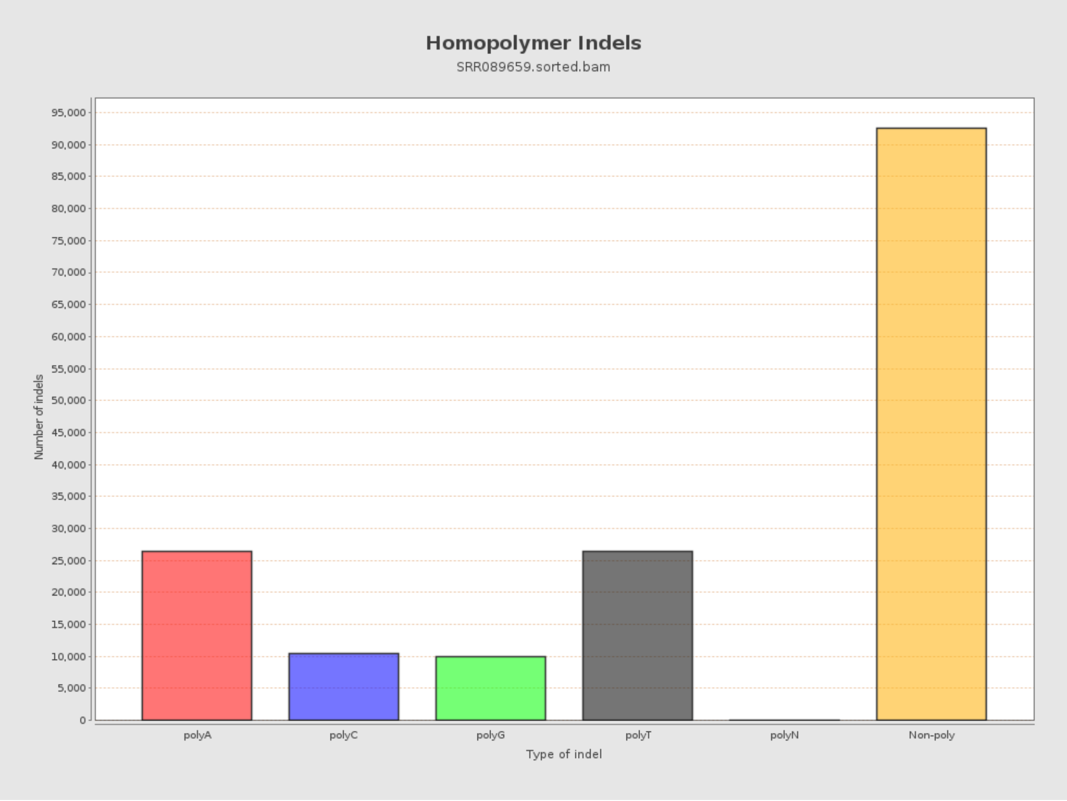
9. Results : Mapped Reads GC-content Distribution



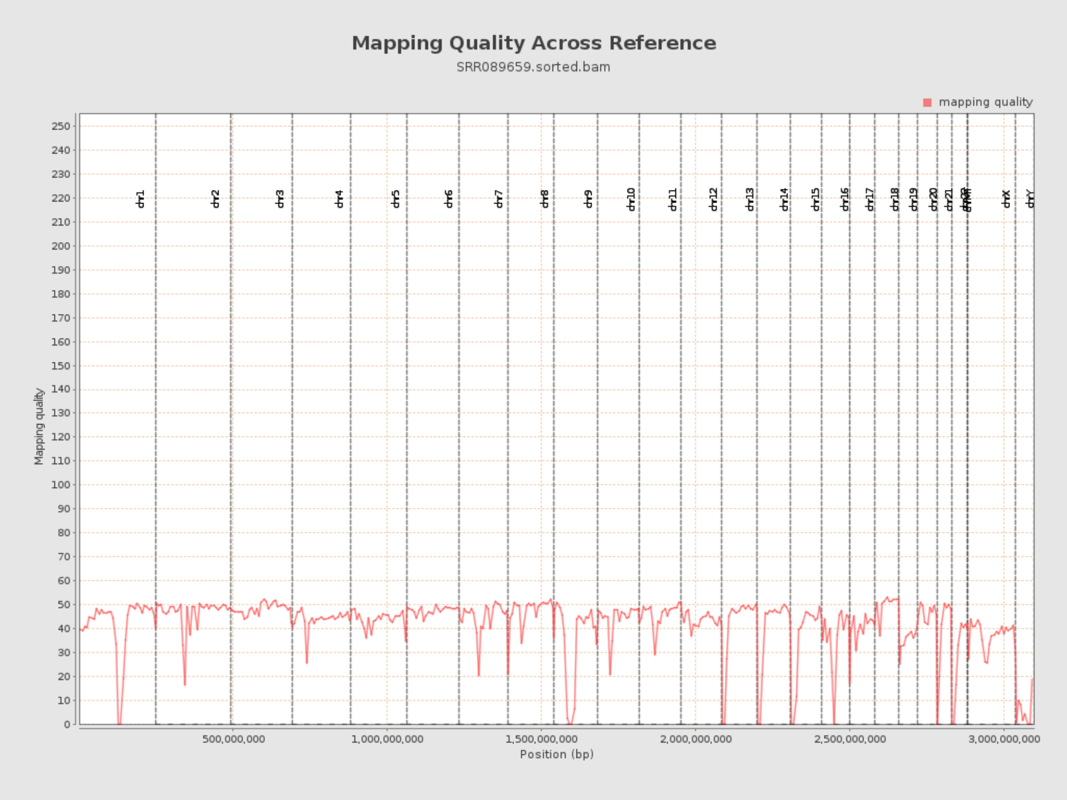
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram