Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 12:19:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089533.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_SRR089533 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089533.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 12:19:33 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089533.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,407,991
Mapped reads	9,648,132 / 84.57%
Unmapped reads	1,759,859 / 15.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	338 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,950,845 / 25.87%
Duplication rate	21.91%
Clipped reads	941,480 / 8.25%

2.2. ACGT Content

Number/percentage of A's	143,651,580 / 31.59%
Number/percentage of C's	85,955,335 / 18.9%
Number/percentage of T's	127,123,414 / 27.96%
Number/percentage of G's	97,971,336 / 21.55%
Number/percentage of N's	12,578 / 0%
GC Percentage	40.45%

2.3. Coverage

Mean	0.1469

Standard Deviation	1.1792

2.4. Mapping Quality

Mean Mapping Quality	45.16

2.5. Mismatches and indels

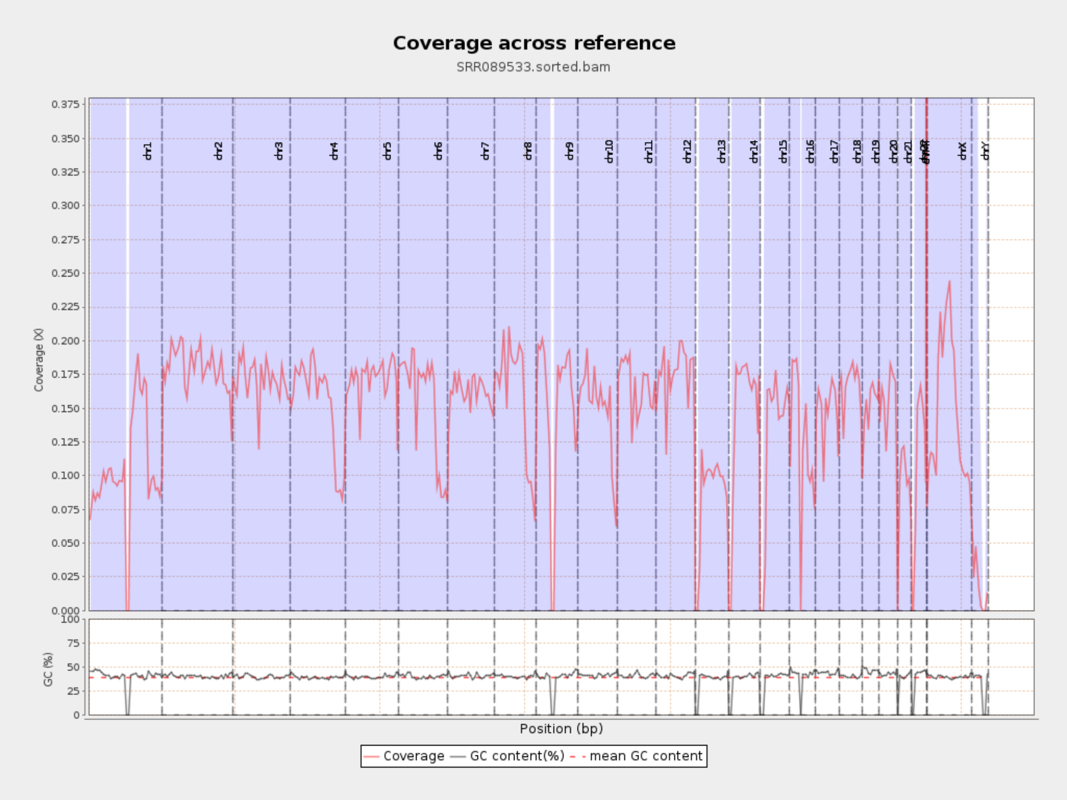
General error rate	0.5%
Mismatches	2,250,356
Insertions	18,942
Mapped reads with at least one insertion	0.2%
Deletions	60,512
Mapped reads with at least one deletion	0.63%
Homopolymer indels	47.03%

2.6. Chromosome stats

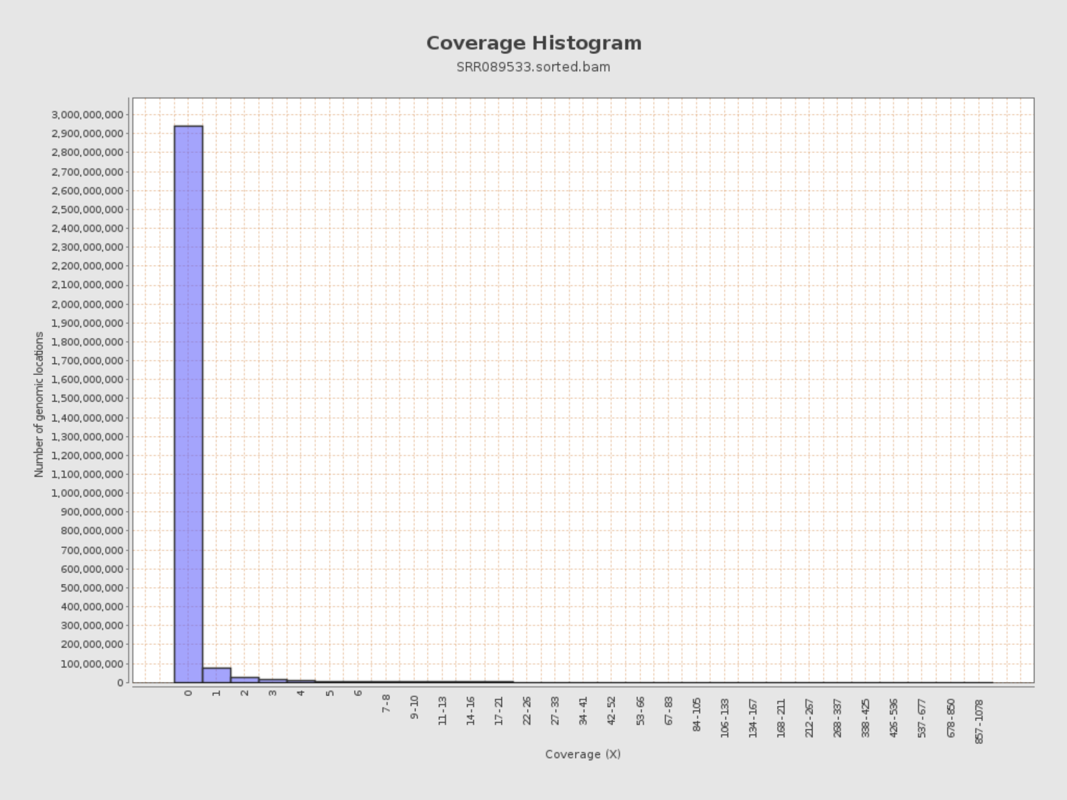
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26149427	0.1049	1.156
chr2	243199373	43888330	0.1805	1.4433
chr3	198022430	33938339	0.1714	1.1914
chr4	191154276	29428551	0.154	1.1601
chr5	180915260	31168642	0.1723	1.1982
chr6	171115067	26421843	0.1544	1.1914
chr7	159138663	25832912	0.1623	1.2607

chr8	146364022	23085794	0.1577	1.3405
chr9	141213431	21405657	0.1516	1.1646
chr10	135534747	20401429	0.1505	1.1858
chr11	135006516	22384670	0.1658	1.2541
chr12	133851895	23515310	0.1757	1.2119
chr13	115169878	9761805	0.0848	0.7913
chr14	107349540	15378866	0.1433	1.2089
chr15	102531392	12881409	0.1256	0.9803
chr16	90354753	11195125	0.1239	0.9846
chr17	81195210	12012583	0.1479	1.0632
chr18	78077248	13109549	0.1679	1.329
chr19	59128983	9002046	0.1522	1.238
chr20	63025520	9780288	0.1552	1.1428
chr21	48129895	4420897	0.0919	0.903
chr22	51304566	5334679	0.104	0.8888
chrMT	16571	22699	1.3698	3.8488
chrX	155270560	23201451	0.1494	1.1553
chrY	59373566	1082732	0.0182	0.3918

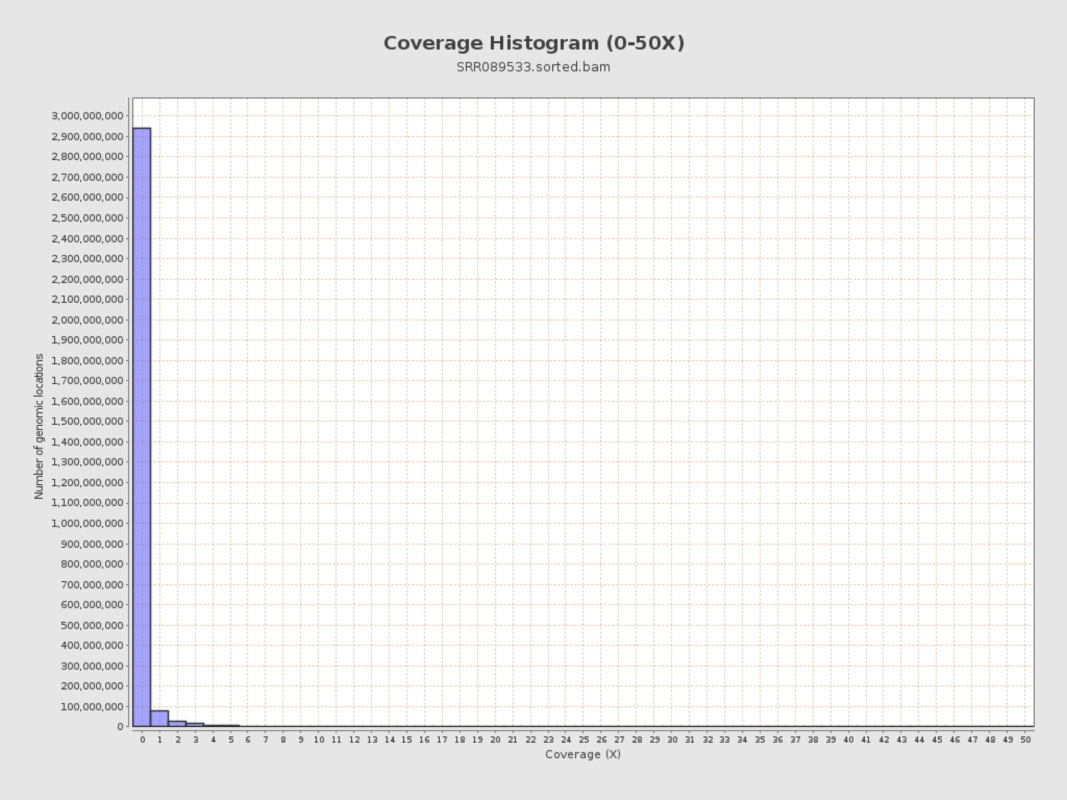
3. Results : Coverage across reference



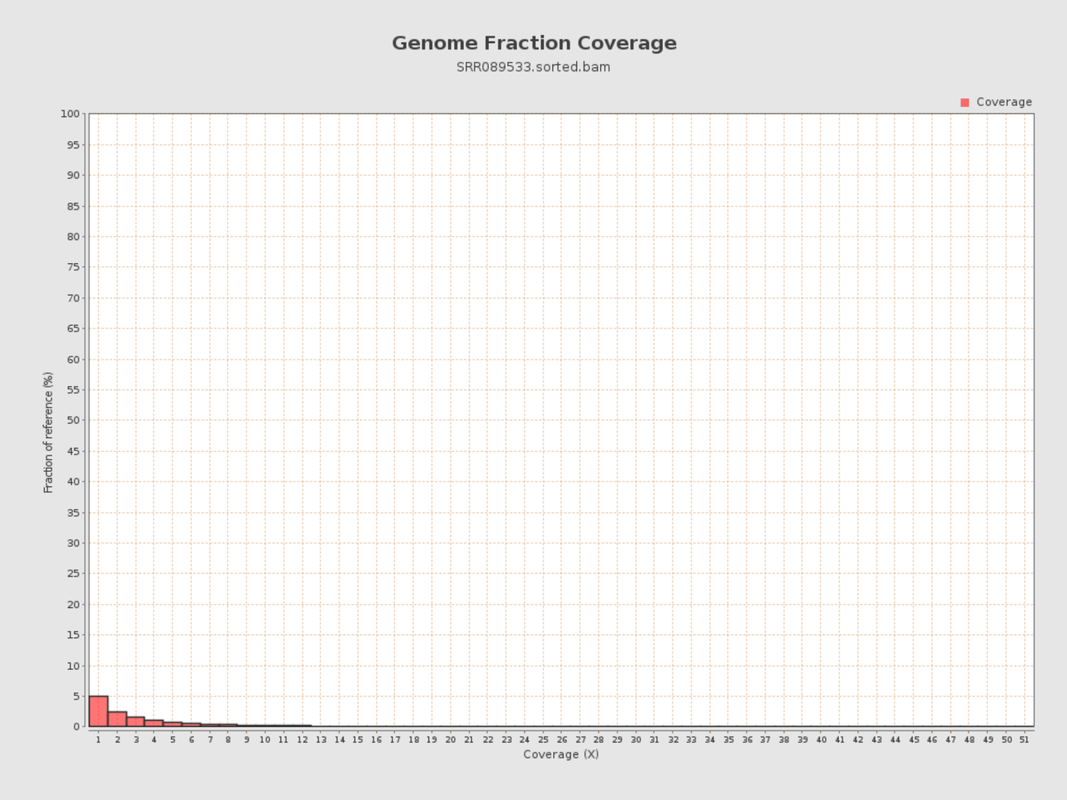
4. Results : Coverage Histogram



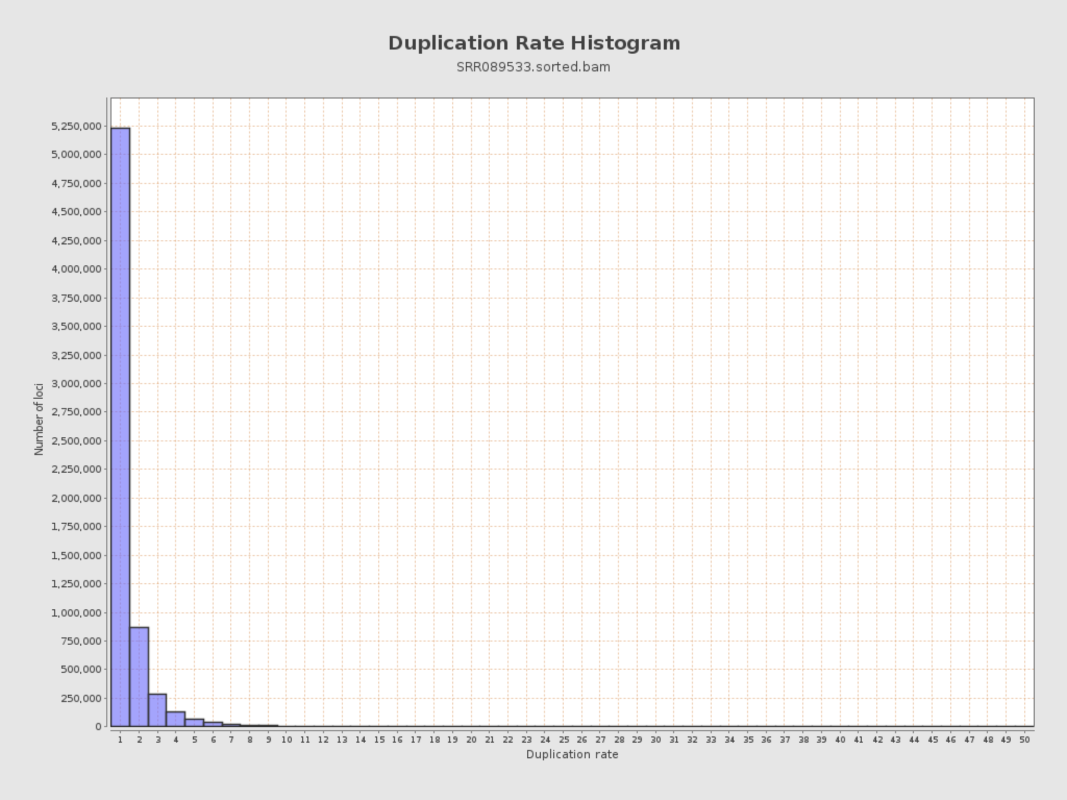
5. Results : Coverage Histogram (0-50X)



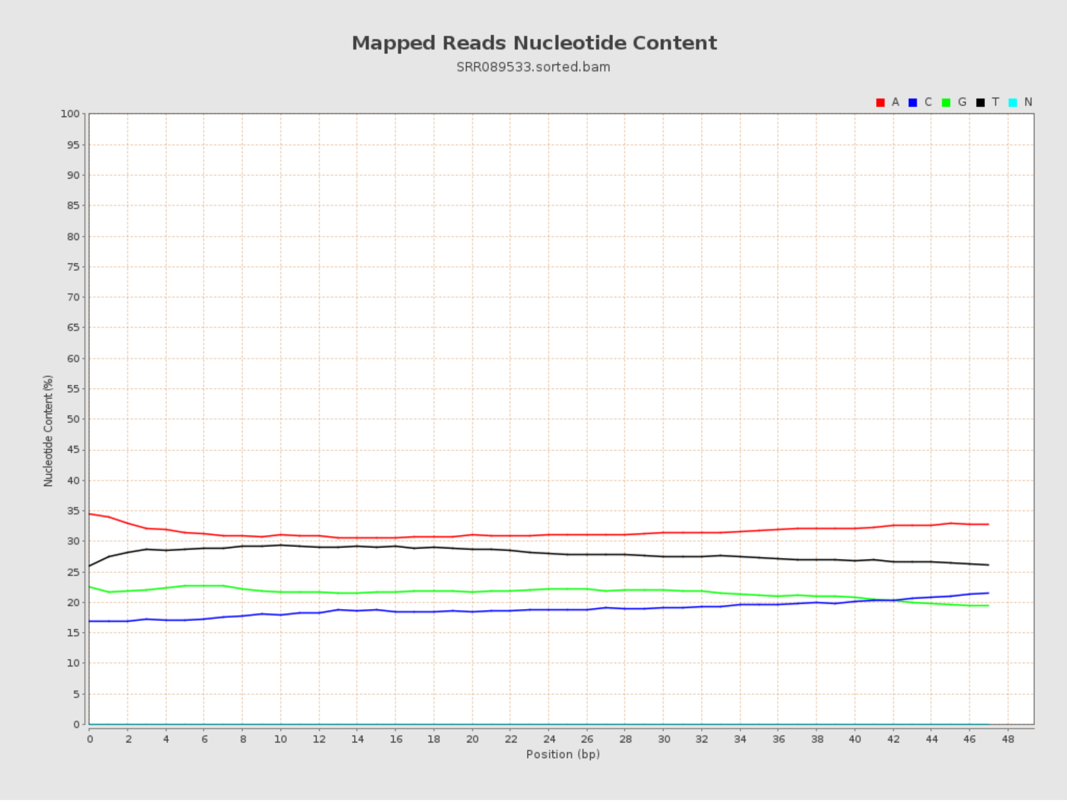
6. Results : Genome Fraction Coverage



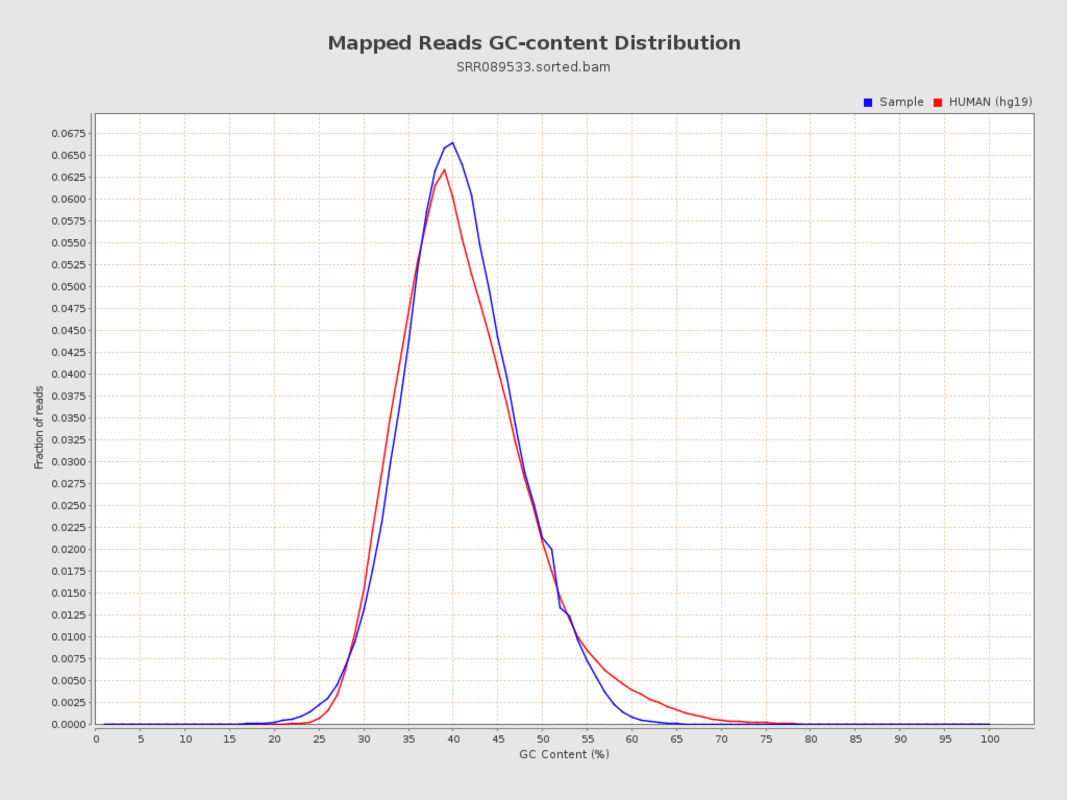
7. Results : Duplication Rate Histogram



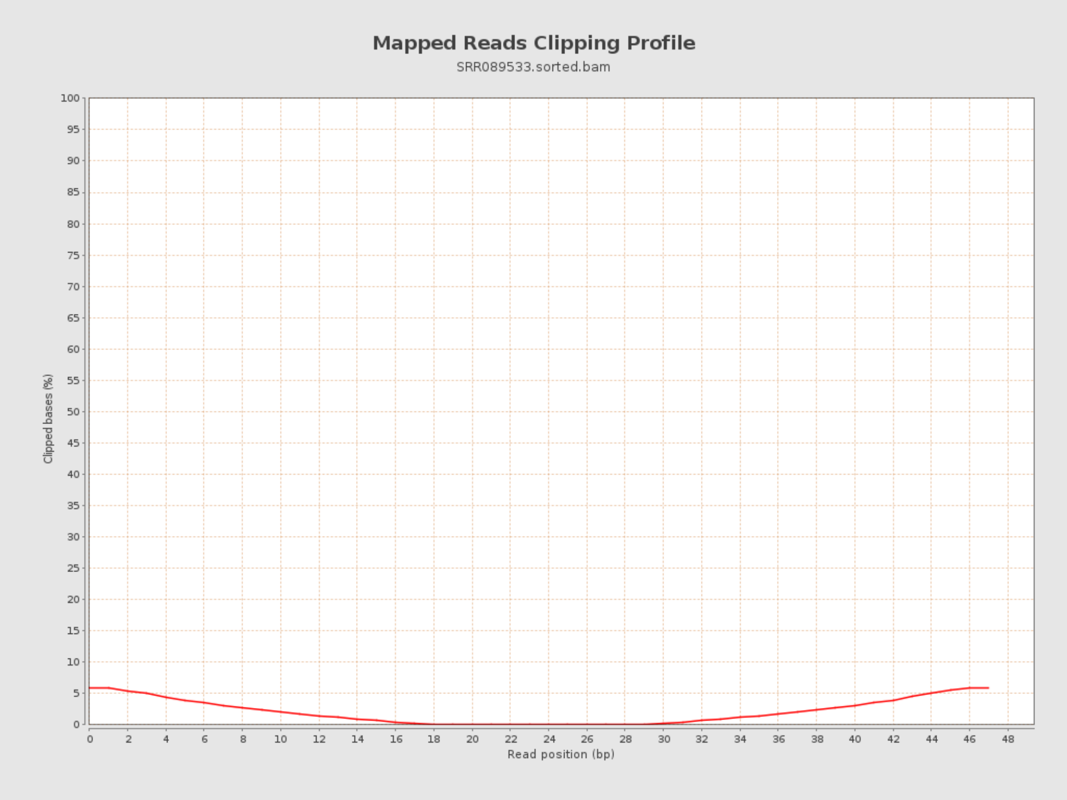
8. Results : Mapped Reads Nucleotide Content



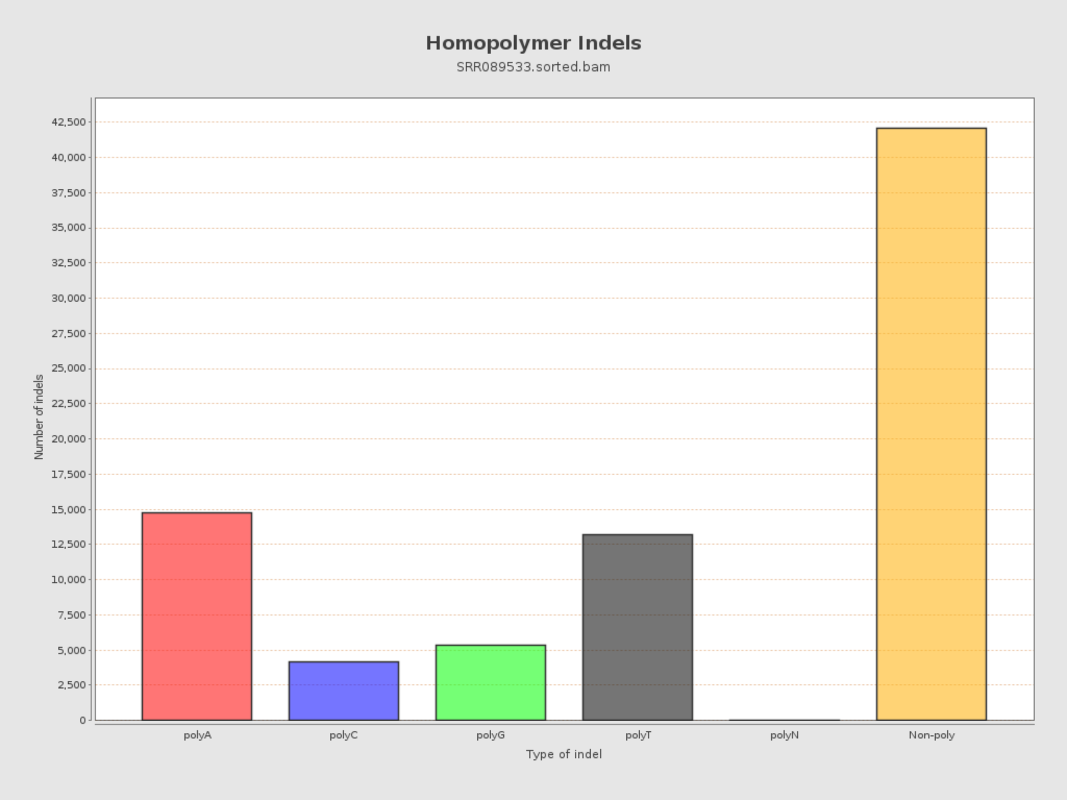
9. Results : Mapped Reads GC-content Distribution



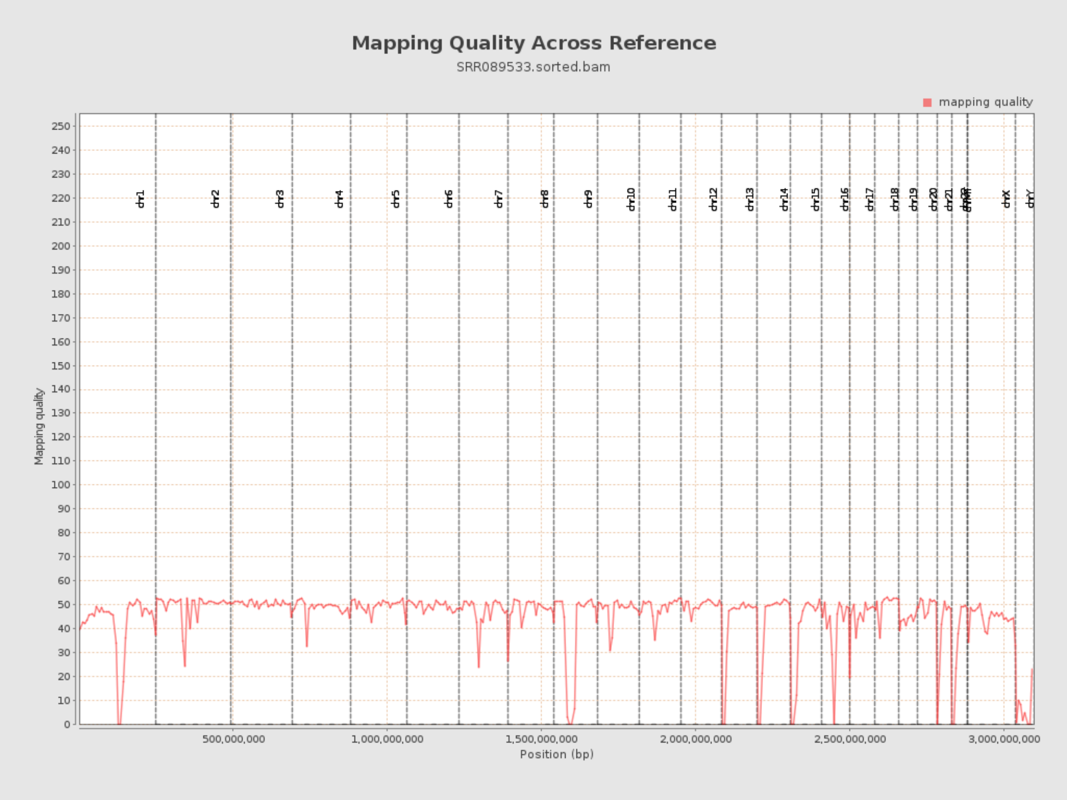
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram