Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 12:28:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089542.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_SRR089542 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089542.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 12:28:07 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089542.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,232,694
Mapped reads	10,160,992 / 83.06%
Unmapped reads	2,071,702 / 16.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	357 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,116,866 / 25.48%
Duplication rate	20.55%
Clipped reads	1,086,850 / 8.88%

2.2. ACGT Content

Number/percentage of A's	154,649,714 / 32.37%
Number/percentage of C's	89,419,248 / 18.72%
Number/percentage of T's	130,854,431 / 27.39%
Number/percentage of G's	102,786,206 / 21.52%
Number/percentage of N's	23,081 / 0%
GC Percentage	40.23%

2.3. Coverage

Mean	0.1544

Standard Deviation	1.297

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

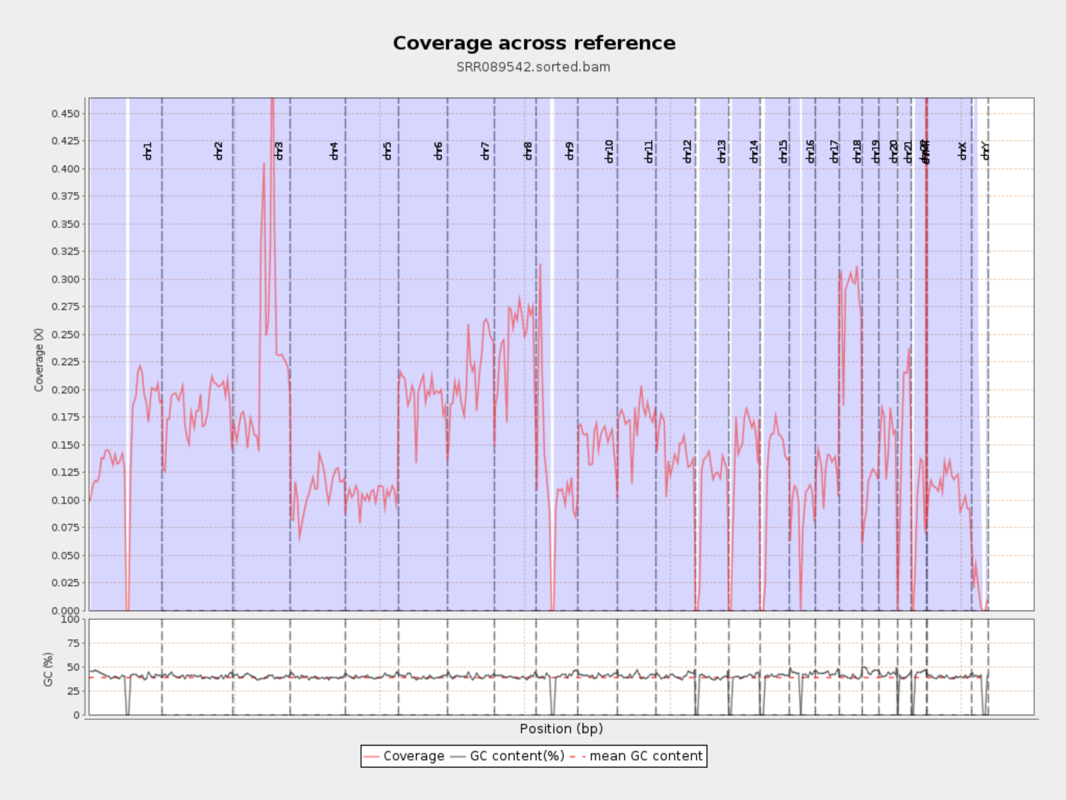
General error rate	0.5%
Mismatches	2,355,471
Insertions	19,152
Mapped reads with at least one insertion	0.19%
Deletions	60,936
Mapped reads with at least one deletion	0.6%
Homopolymer indels	45.84%

2.6. Chromosome stats

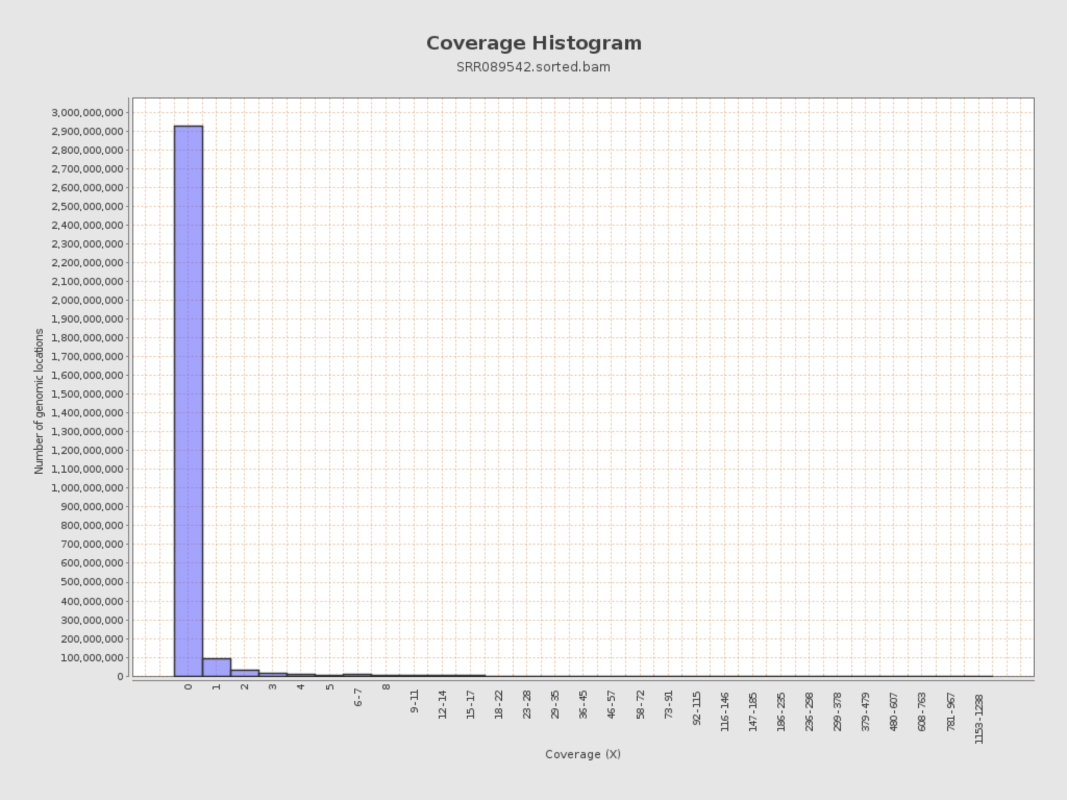
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	37390403	0.15	1.2568
chr2	243199373	44622814	0.1835	1.5226
chr3	198022430	45747099	0.231	1.6664
chr4	191154276	20835314	0.109	0.9786
chr5	180915260	18910345	0.1045	0.9464
chr6	171115067	33376345	0.1951	1.4609
chr7	159138663	34477152	0.2166	1.6339

chr8	146364022	35869464	0.2451	1.8283
chr9	141213431	16607100	0.1176	1.0955
chr10	135534747	21043912	0.1553	1.2442
chr11	135006516	23332833	0.1728	1.3564
chr12	133851895	18972181	0.1417	1.139
chr13	115169878	12476368	0.1083	0.9906
chr14	107349540	14484040	0.1349	1.1745
chr15	102531392	12390735	0.1208	1.0395
chr16	90354753	8229254	0.0911	0.8595
chr17	81195210	10471010	0.129	1.051
chr18	78077248	22258260	0.2851	1.8983
chr19	59128983	6539920	0.1106	1.0961
chr20	63025520	9866143	0.1565	1.2742
chr21	48129895	7698130	0.1599	1.3368
chr22	51304566	3993244	0.0778	0.7905
chrMT	16571	122462	7.3901	14.9298
chrX	155270560	17168831	0.1106	0.9906
chrY	59373566	939859	0.0158	0.3613

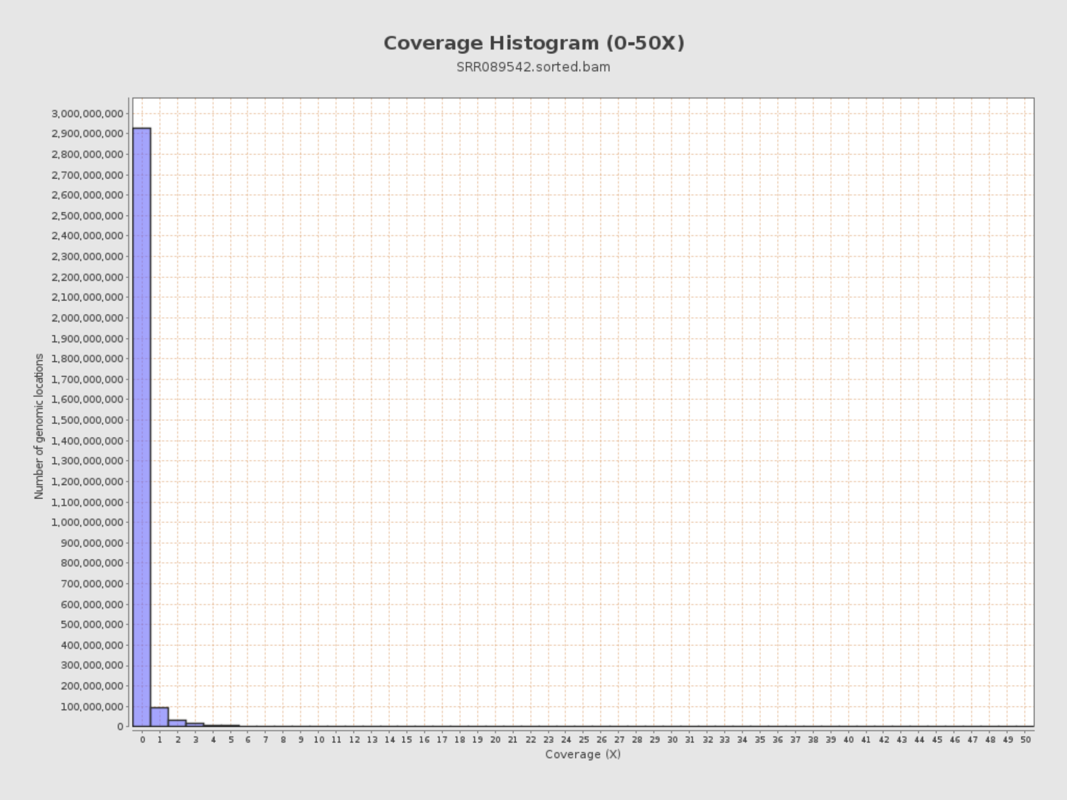
3. Results : Coverage across reference



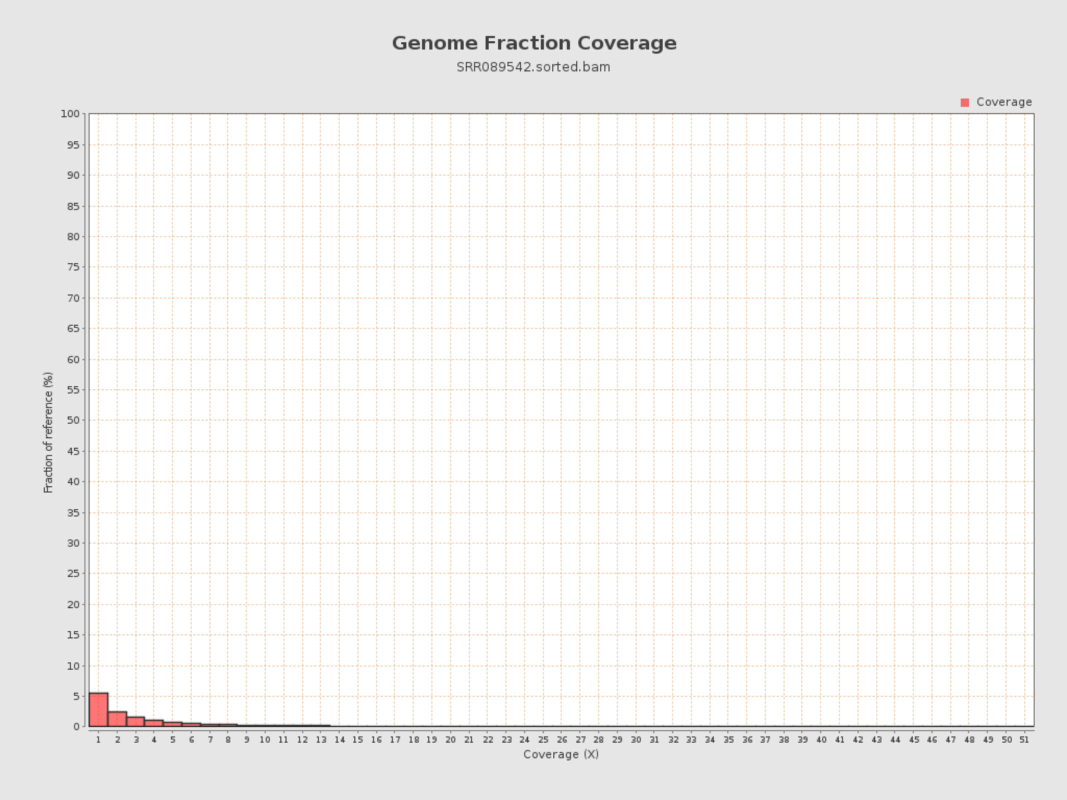
4. Results : Coverage Histogram



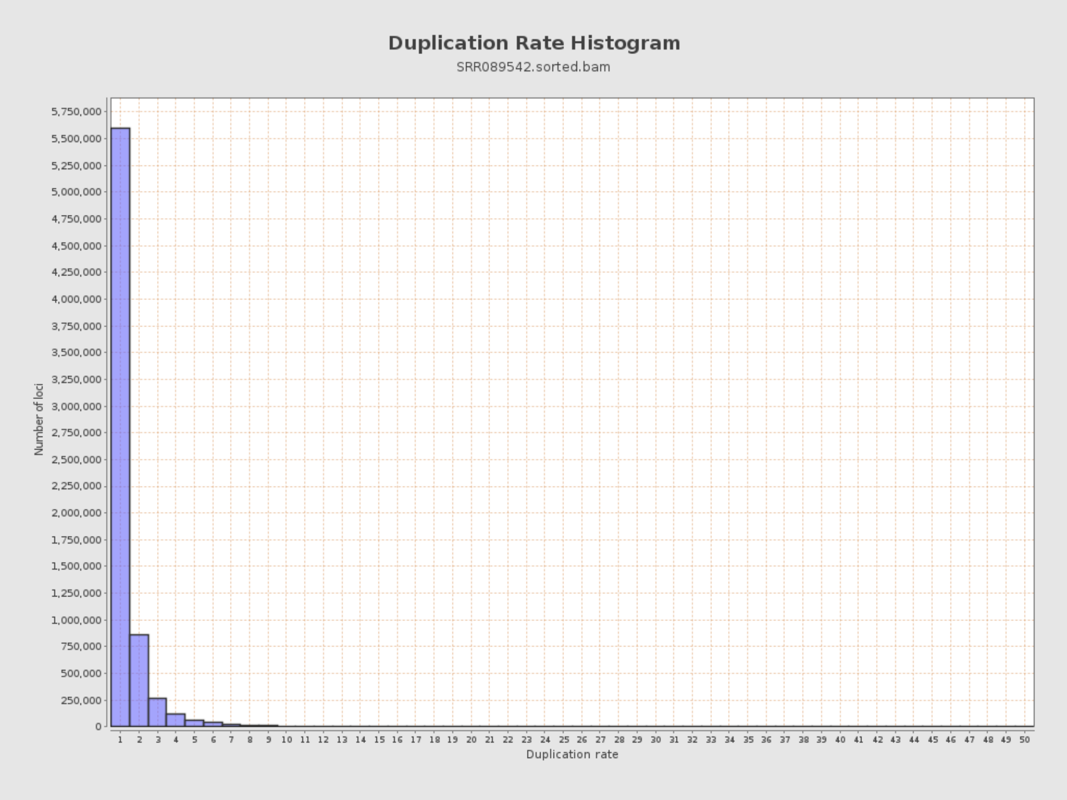
5. Results : Coverage Histogram (0-50X)



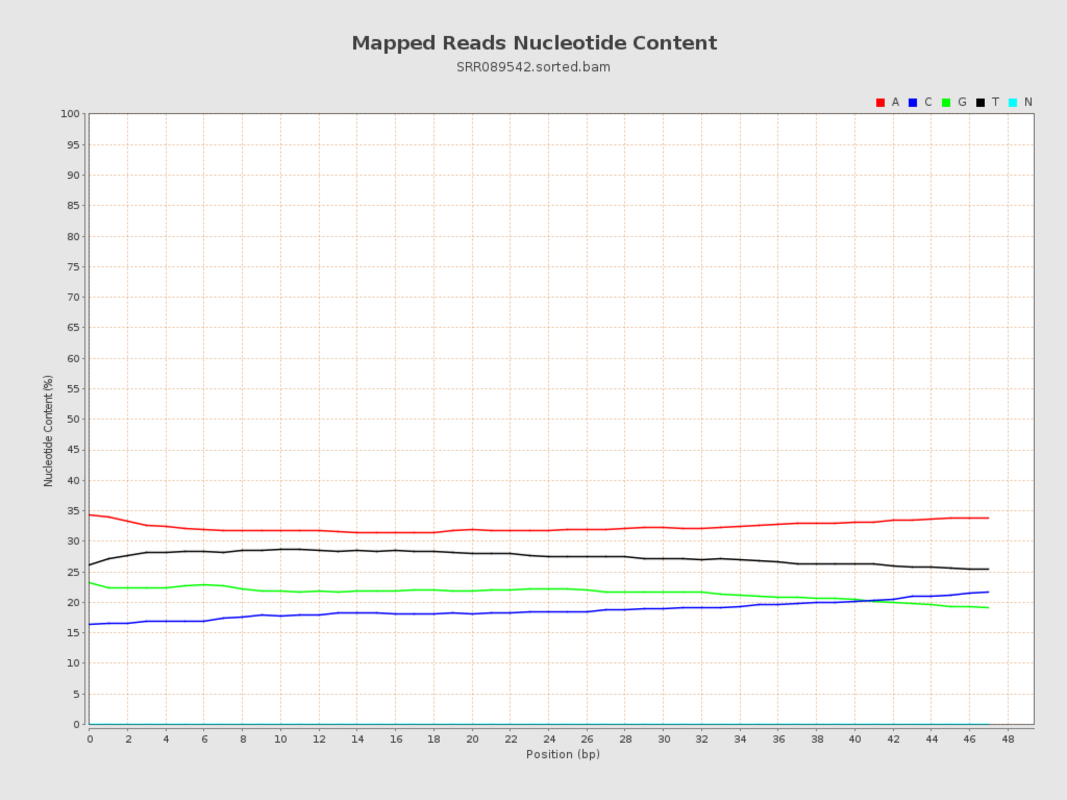
6. Results : Genome Fraction Coverage



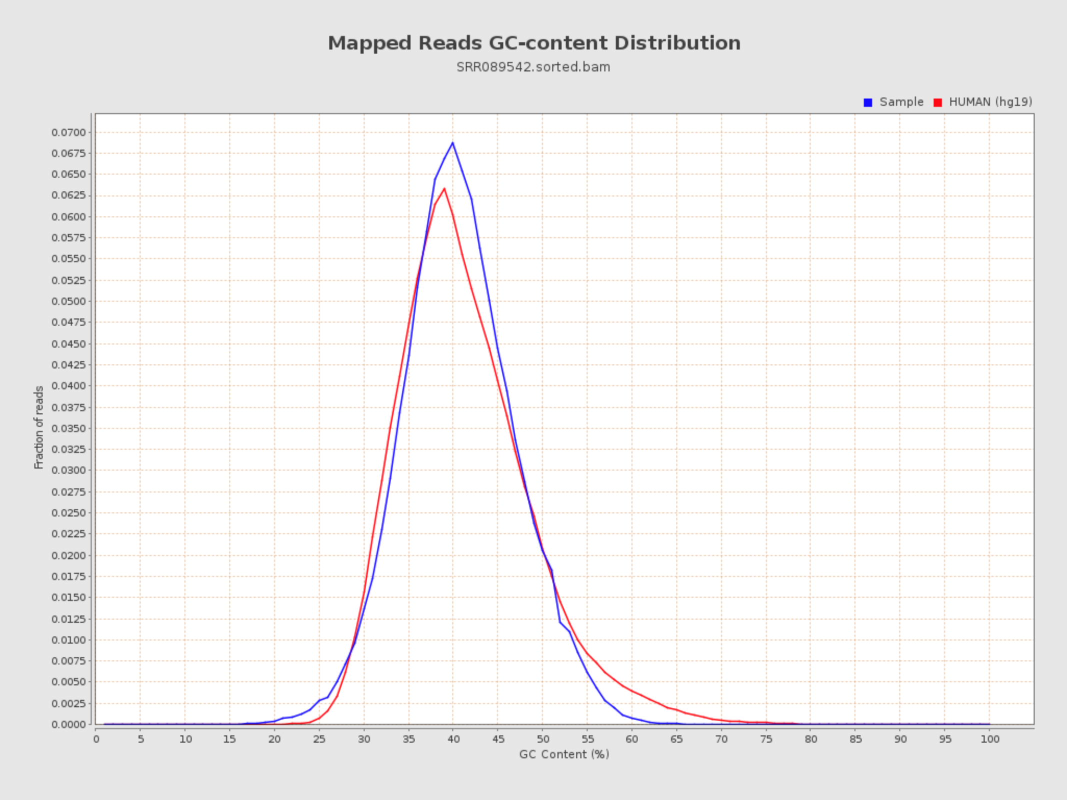
7. Results : Duplication Rate Histogram



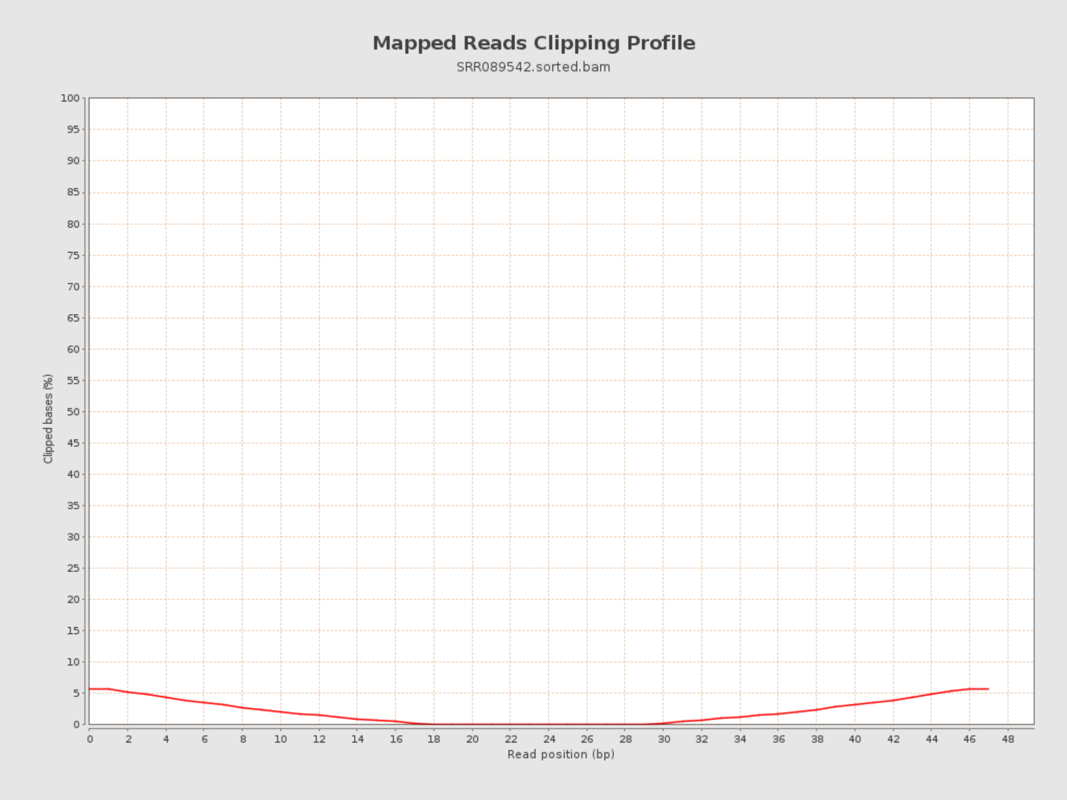
8. Results : Mapped Reads Nucleotide Content



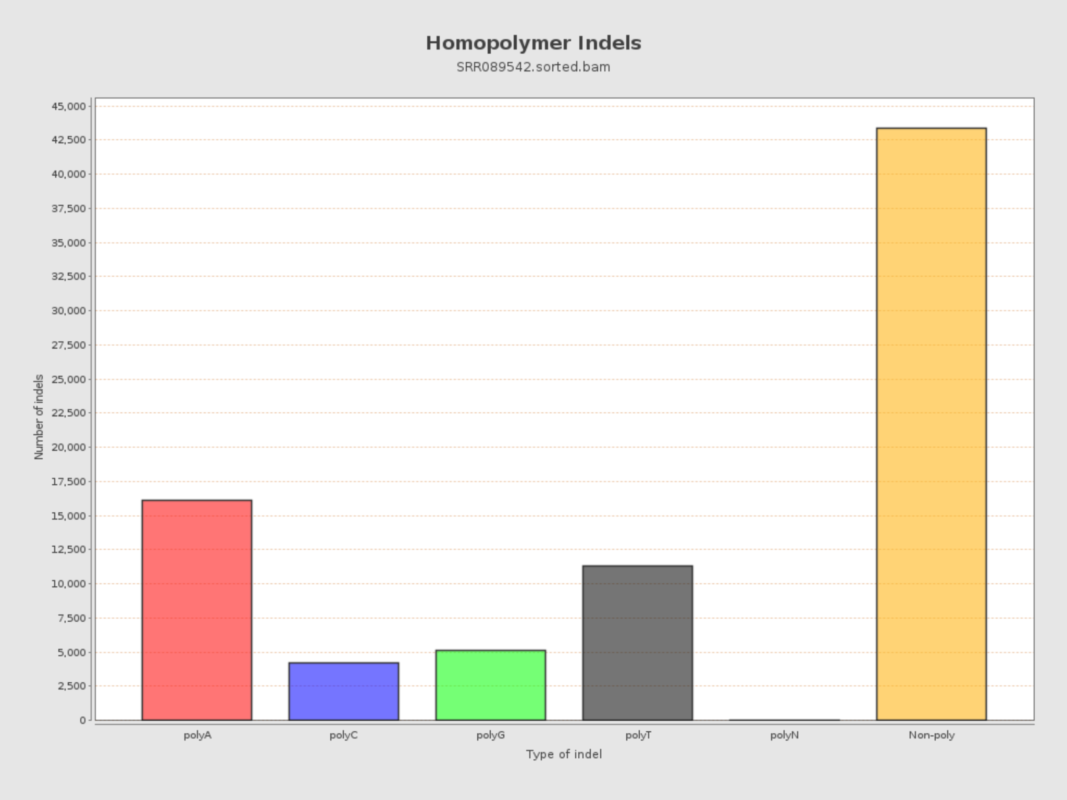
9. Results : Mapped Reads GC-content Distribution



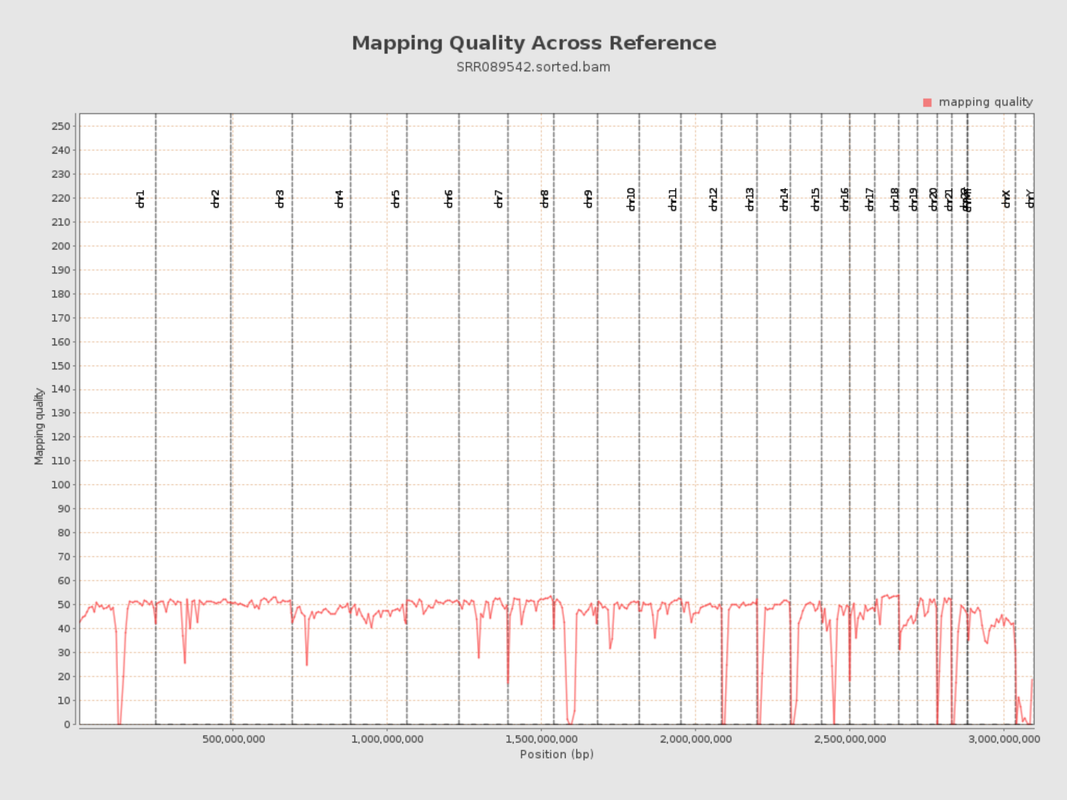
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram