Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 04:14:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506337.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_SRR1506337 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506337.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 04:14:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506337.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,233,429
Mapped reads	8,649,026 / 84.52%
Unmapped reads	1,584,403 / 15.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	172,942 / 1.69%
Read min/max/mean length	30 / 94 / 94.61
Duplicated reads (estimated)	1,186,327 / 11.59%
Duplication rate	10.02%
Clipped reads	5,361,779 / 52.39%

2.2. ACGT Content

Number/percentage of A's	196,611,551 / 28.89%
Number/percentage of C's	124,547,703 / 18.3%
Number/percentage of T's	197,564,966 / 29.03%
Number/percentage of G's	161,775,894 / 23.77%
Number/percentage of N's	162,458 / 0.02%
GC Percentage	42.07%

2.3. Coverage

Mean	0.22

Standard Deviation	1.5323

2.4. Mapping Quality

Mean Mapping Quality	48

2.5. Mismatches and indels

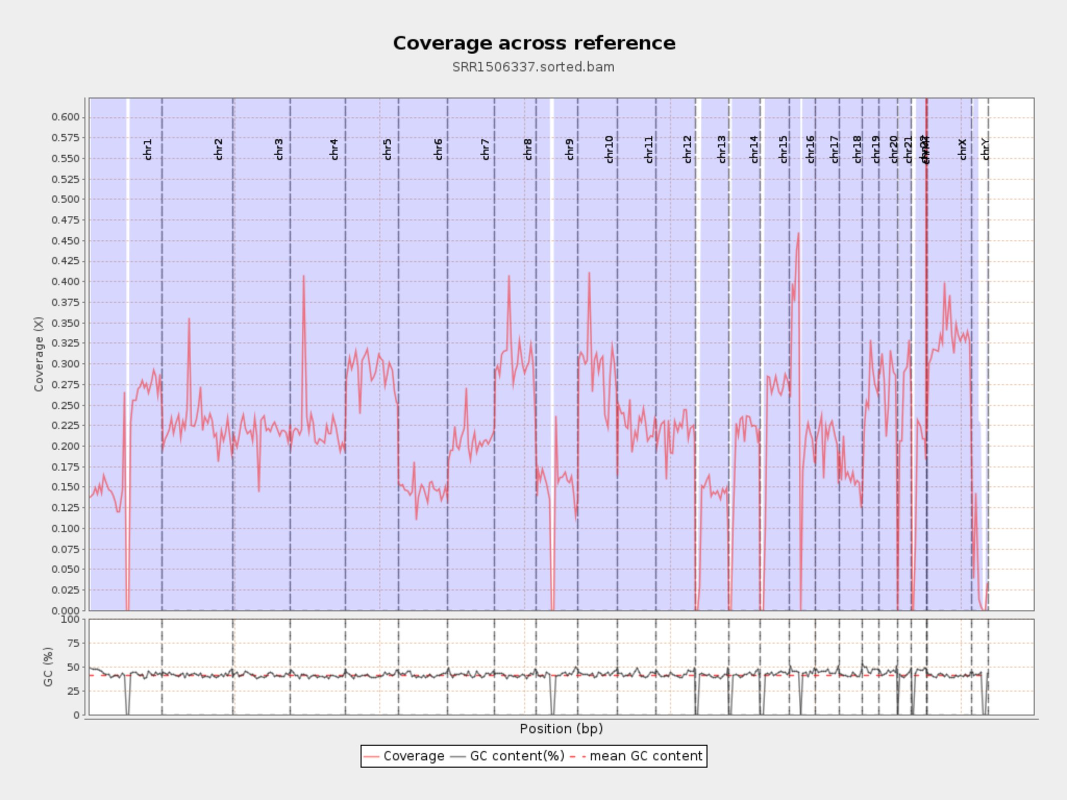
General error rate	0.72%
Mismatches	4,789,112
Insertions	55,587
Mapped reads with at least one insertion	0.63%
Deletions	150,406
Mapped reads with at least one deletion	1.71%
Homopolymer indels	45.41%

2.6. Chromosome stats

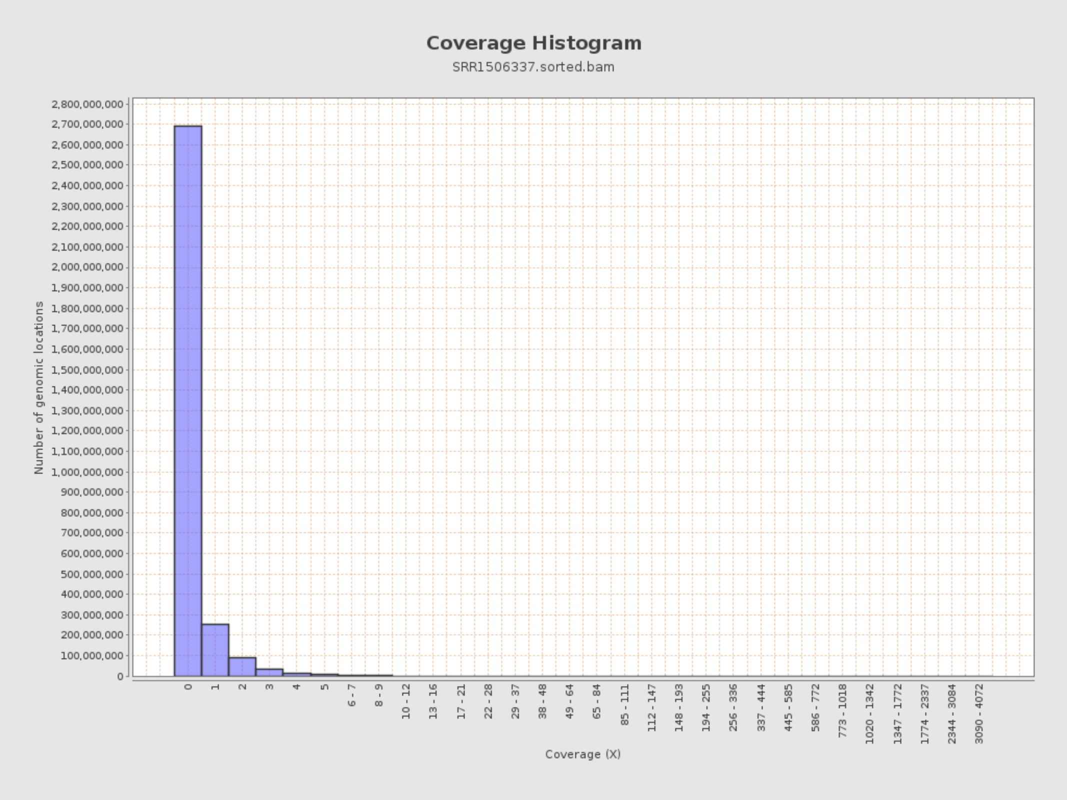
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	48280450	0.1937	2.9001
chr2	243199373	55328146	0.2275	1.5102
chr3	198022430	42901657	0.2167	0.6936
chr4	191154276	42629231	0.223	1.0674
chr5	180915260	52741458	0.2915	0.8356
chr6	171115067	24962789	0.1459	0.6788
chr7	159138663	32953258	0.2071	1.6744

chr8	146364022	44704055	0.3054	2.9144
chr9	141213431	20193124	0.143	1.442
chr10	135534747	40523924	0.299	1.5719
chr11	135006516	30460944	0.2256	1.3524
chr12	133851895	29038476	0.2169	0.7327
chr13	115169878	14115397	0.1226	0.5109
chr14	107349540	20105358	0.1873	0.856
chr15	102531392	22939004	0.2237	0.7348
chr16	90354753	23684040	0.2621	0.9675
chr17	81195210	17015754	0.2096	0.8709
chr18	78077248	12849281	0.1646	2.4983
chr19	59128983	15639089	0.2645	2.1635
chr20	63025520	17285781	0.2743	0.8605
chr21	48129895	11578425	0.2406	0.9997
chr22	51304566	7751266	0.1511	0.6003
chrMT	16571	37694	2.2747	2.8449
chrX	155270560	50918510	0.3279	1.0841
chrY	59373566	2317824	0.039	1.1724

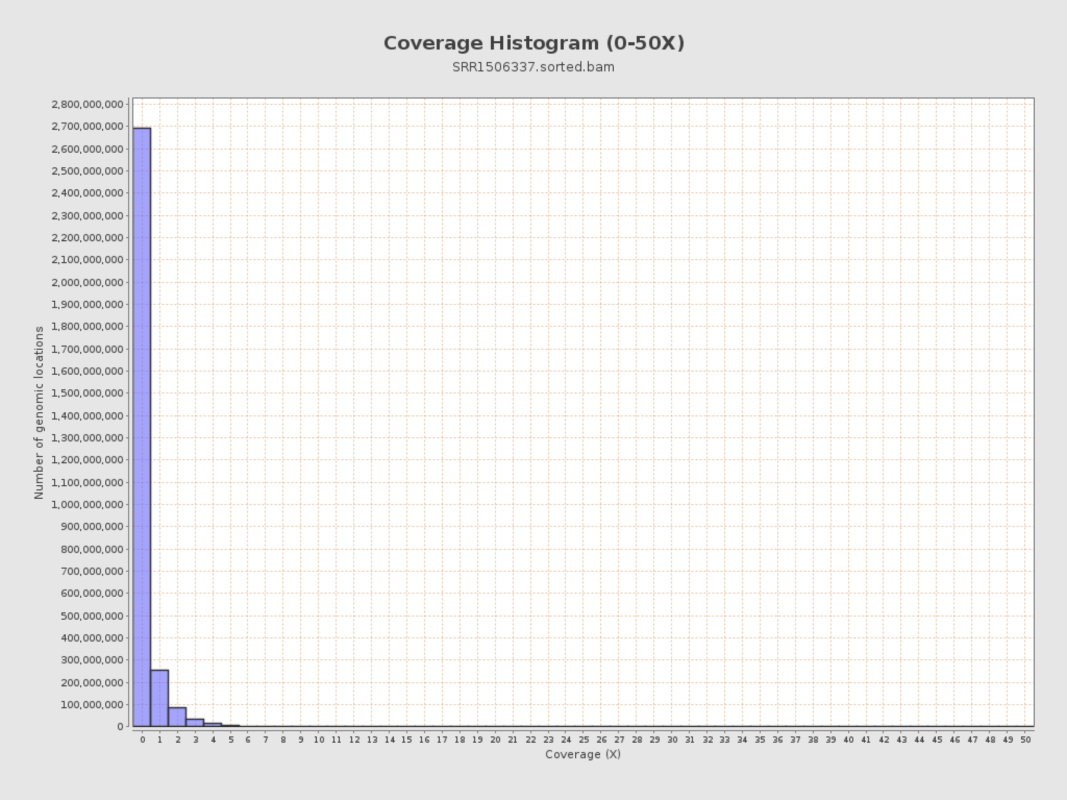
3. Results : Coverage across reference



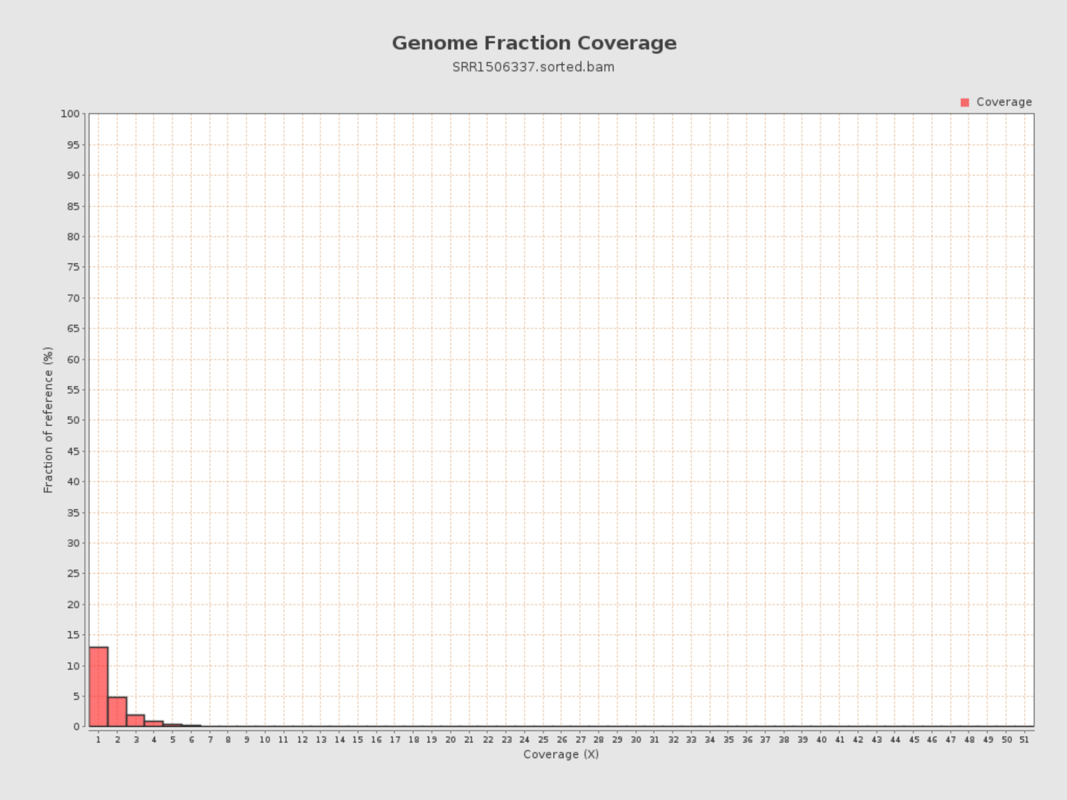
4. Results : Coverage Histogram



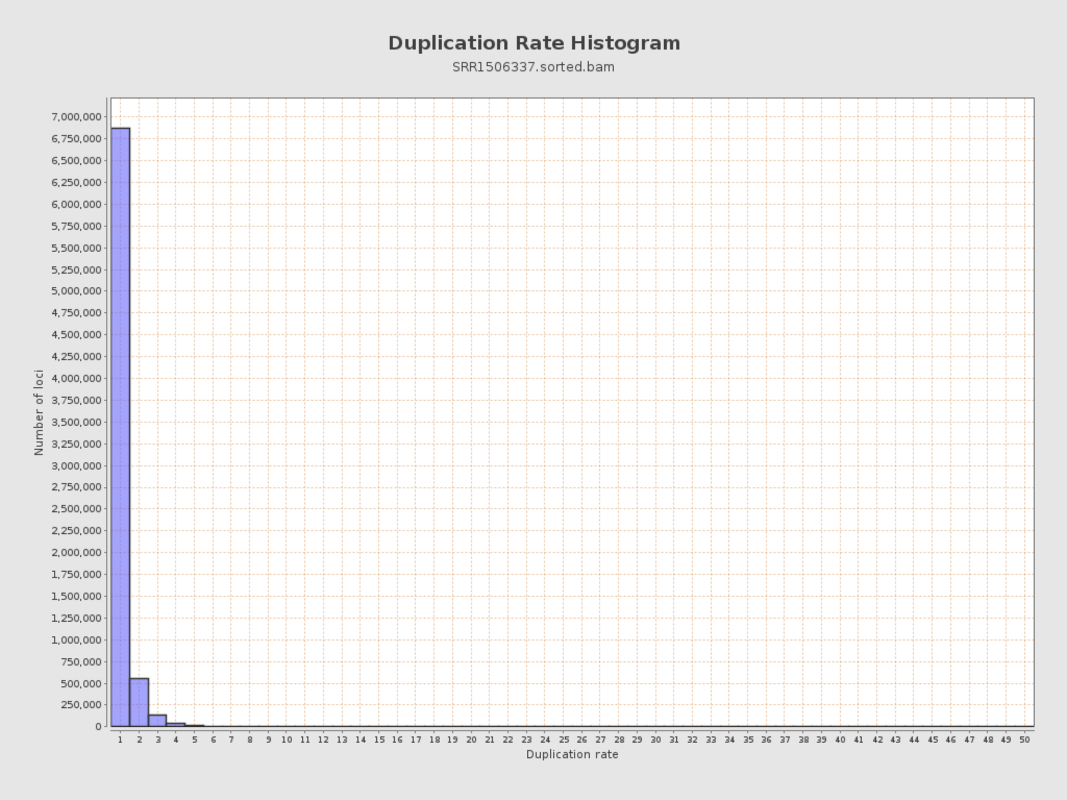
5. Results : Coverage Histogram (0-50X)



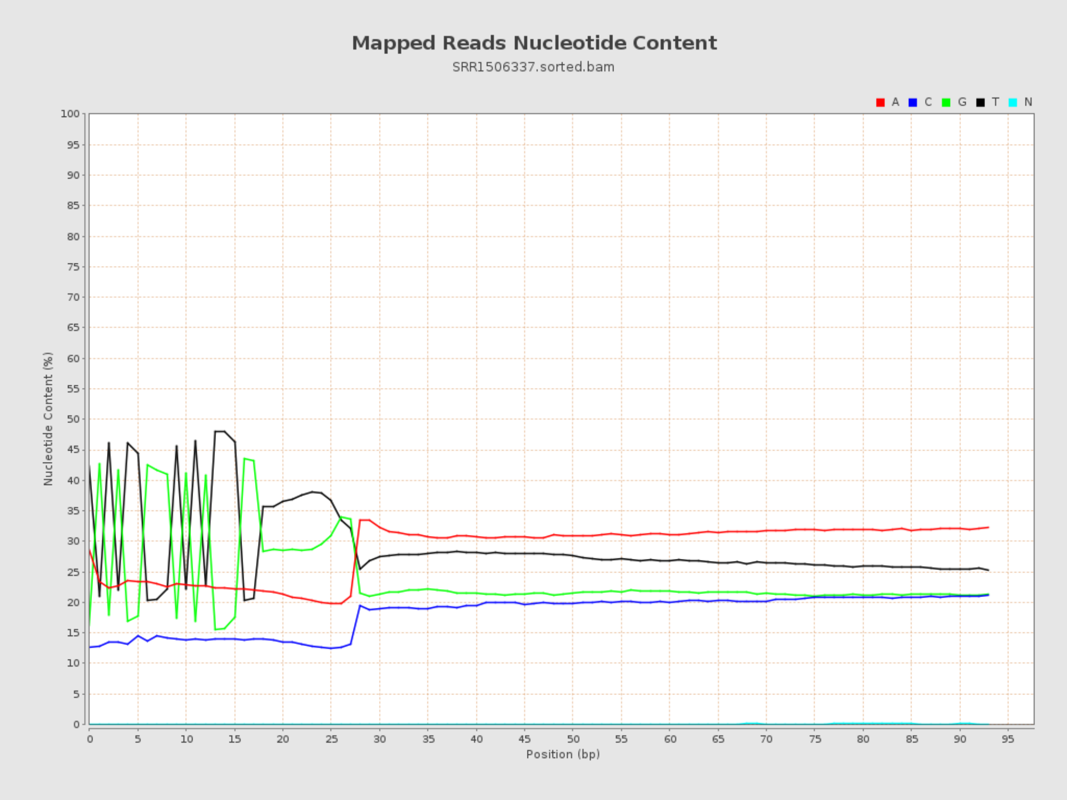
6. Results : Genome Fraction Coverage



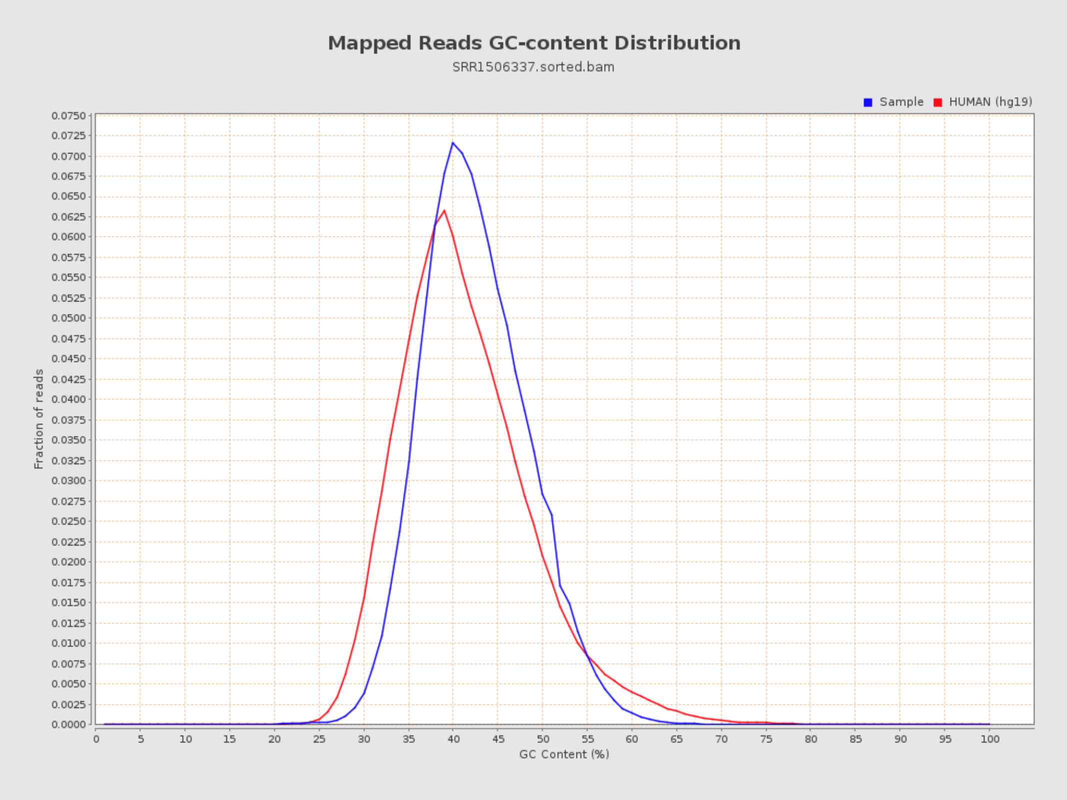
7. Results : Duplication Rate Histogram



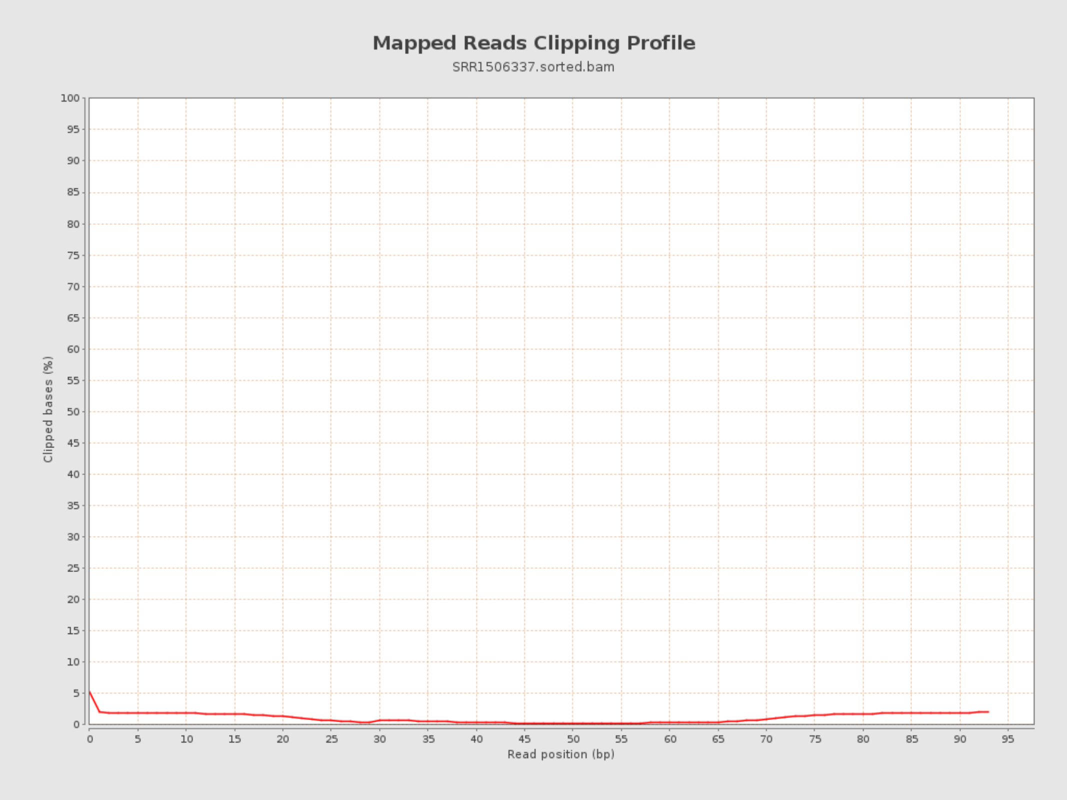
8. Results : Mapped Reads Nucleotide Content



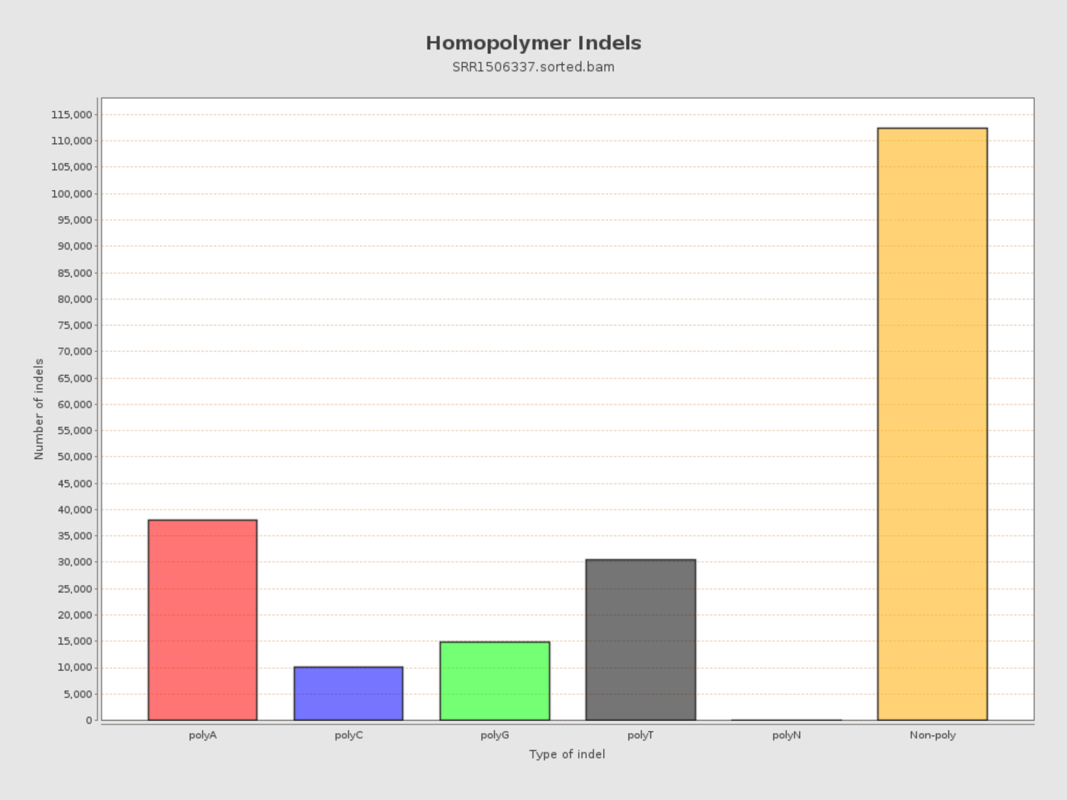
9. Results : Mapped Reads GC-content Distribution



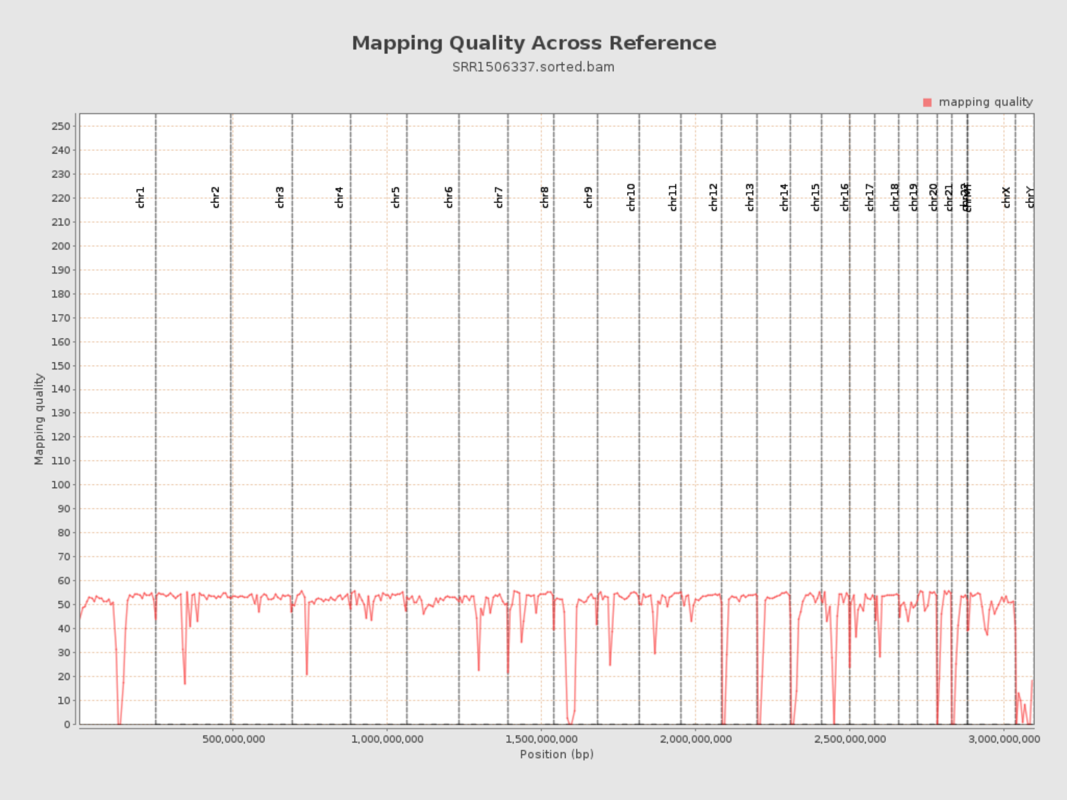
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram