Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 19:26:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514737.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_SRR5514737 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514737.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 19:26:03 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514737.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	50,558,673
Mapped reads	47,757,138 / 94.46%
Unmapped reads	2,801,535 / 5.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,915,629 / 3.79%
Read min/max/mean length	30 / 100 / 99.43
Duplicated reads (estimated)	34,185,096 / 67.61%
Duplication rate	39.93%
Clipped reads	11,661,946 / 23.07%

2.2. ACGT Content

Number/percentage of A's	1,142,726,839 / 25.85%
Number/percentage of C's	1,041,489,635 / 23.56%
Number/percentage of T's	1,155,514,845 / 26.14%
Number/percentage of G's	1,046,475,068 / 23.67%
Number/percentage of N's	34,303,669 / 0.78%
GC Percentage	47.23%

2.3. Coverage

Mean	1.4292

Standard Deviation	75.2075

2.4. Mapping Quality

Mean Mapping Quality	43.62

2.5. Mismatches and indels

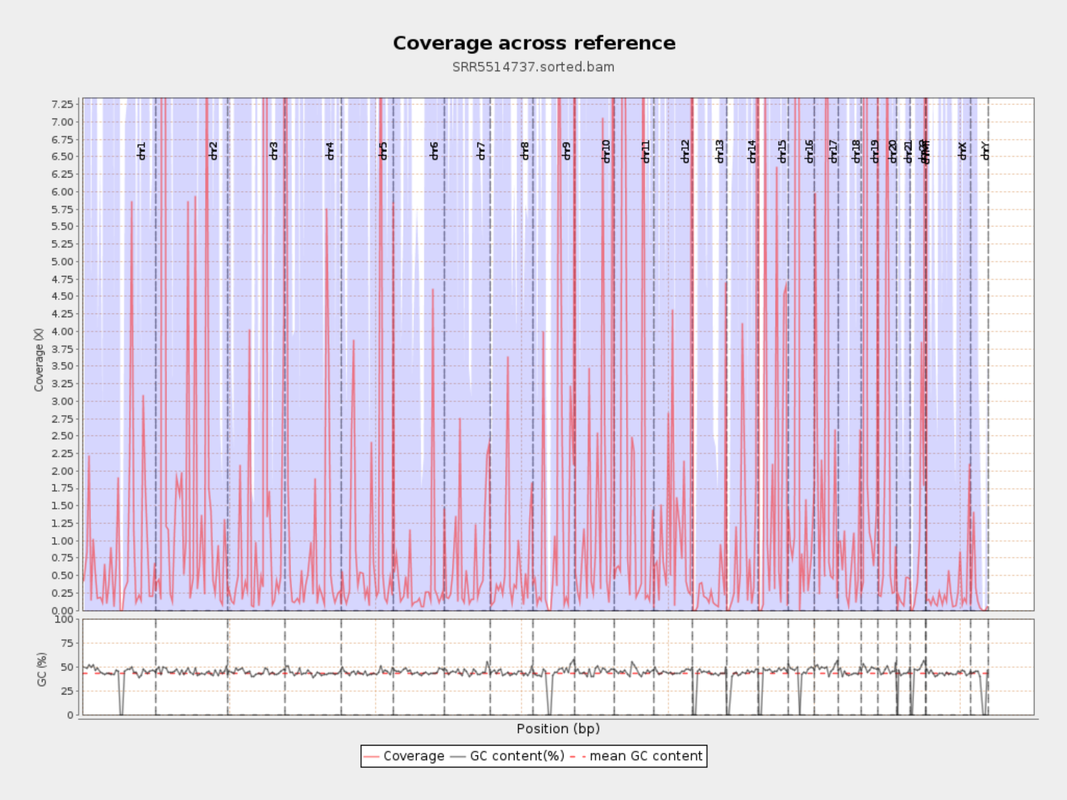
General error rate	1.12%
Mismatches	44,882,278
Insertions	2,356,250
Mapped reads with at least one insertion	4.61%
Deletions	1,565,707
Mapped reads with at least one deletion	3.12%
Homopolymer indels	37.38%

2.6. Chromosome stats

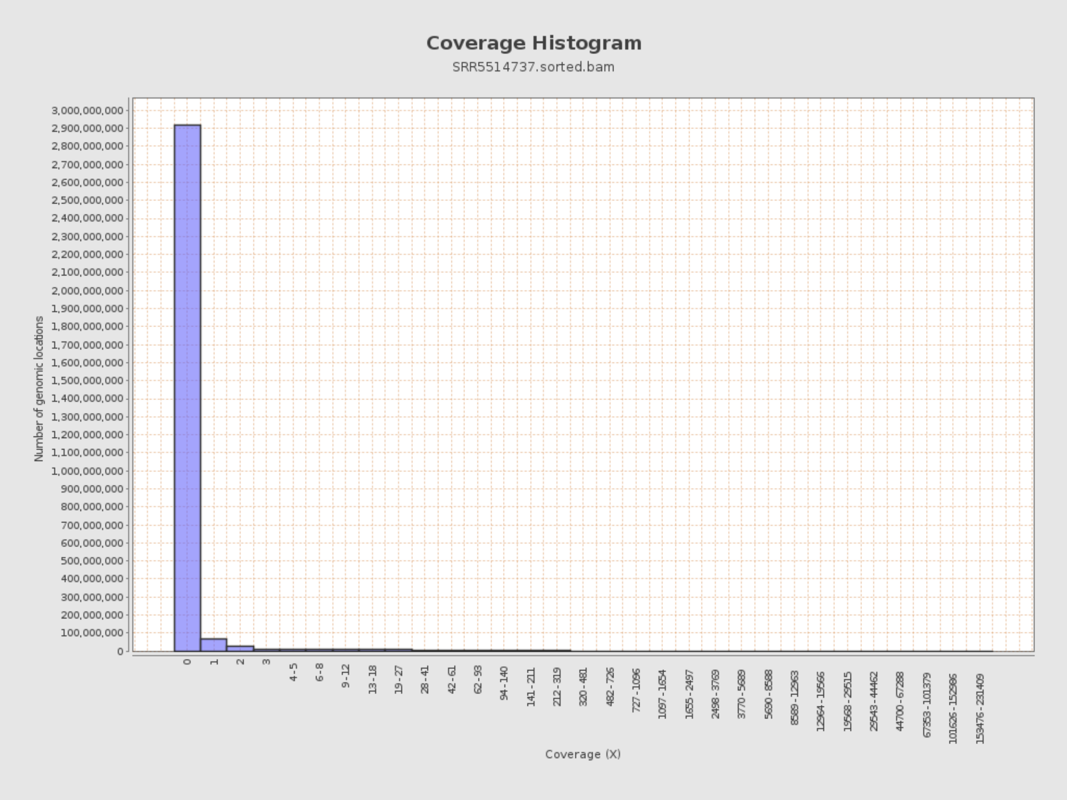
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	214097485	0.859	137.2372
chr2	243199373	553716076	2.2768	75.7454
chr3	198022430	521029017	2.6312	81.8528
chr4	191154276	210334693	1.1003	36.5571
chr5	180915260	210309249	1.1625	41.1518
chr6	171115067	82432143	0.4817	14.7693
chr7	159138663	121733675	0.765	43.2625

chr8	146364022	92009576	0.6286	18.0136
chr9	141213431	207638714	1.4704	181.9339
chr10	135534747	223130398	1.6463	56.5363
chr11	135006516	312671177	2.316	32.5827
chr12	133851895	184064708	1.3751	28.4989
chr13	115169878	37240206	0.3234	41.2931
chr14	107349540	101151168	0.9423	34.3161
chr15	102531392	214230840	2.0894	52.4022
chr16	90354753	290596447	3.2162	131.1949
chr17	81195210	225681411	2.7795	44.9906
chr18	78077248	57411939	0.7353	22.757
chr19	59128983	291503457	4.93	128.162
chr20	63025520	101895123	1.6167	25.3673
chr21	48129895	12685746	0.2636	13.2815
chr22	51304566	88375313	1.7226	67.6769
chrMT	16571	7165169	432.3921	355.8834
chrX	155270560	46265160	0.298	16.3056
chrY	59373566	17068388	0.2875	45.0675

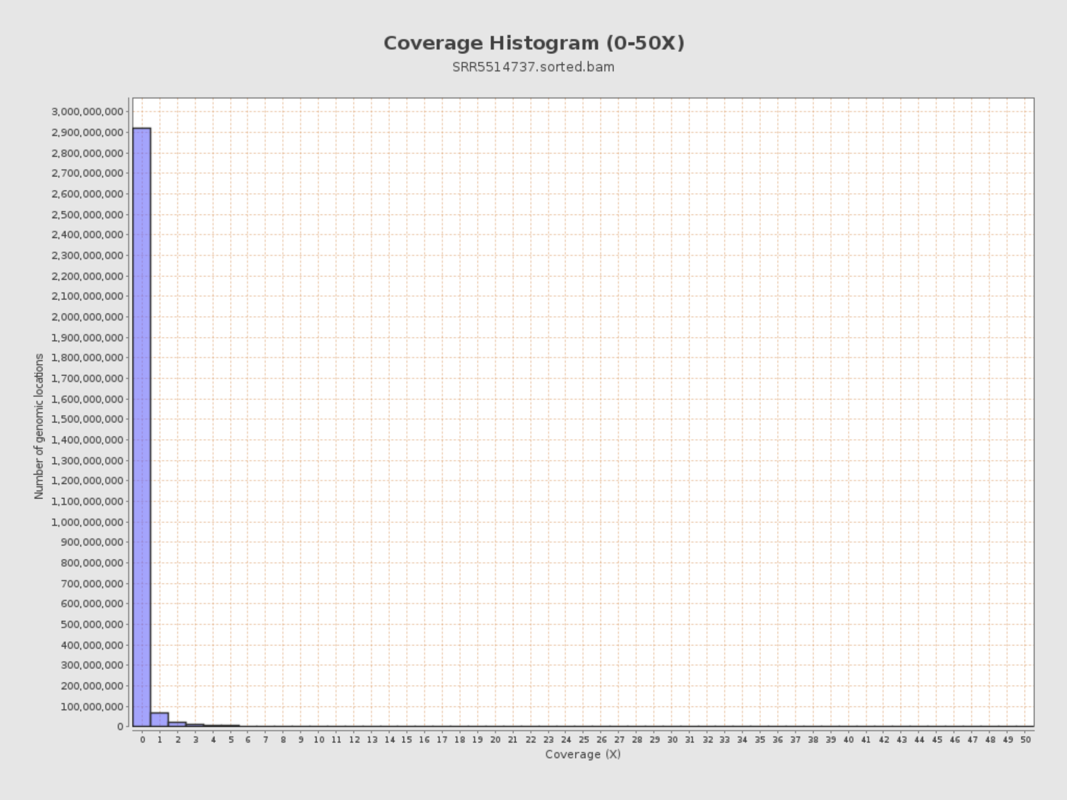
3. Results : Coverage across reference



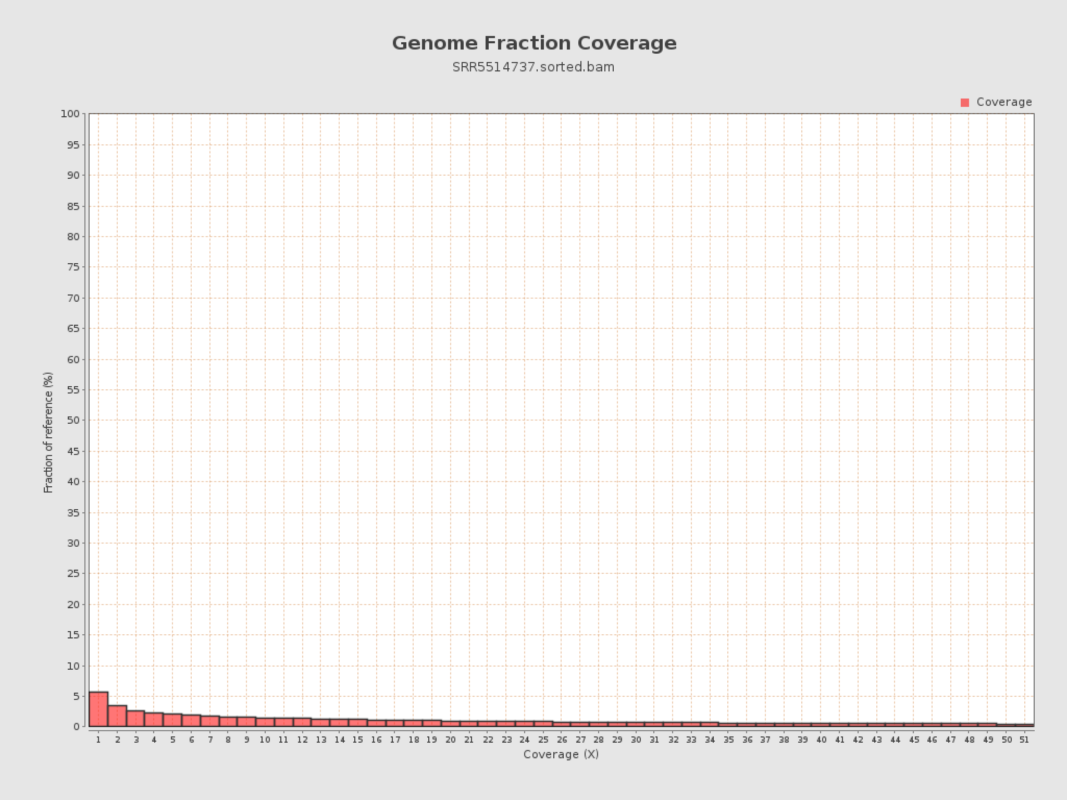
4. Results : Coverage Histogram



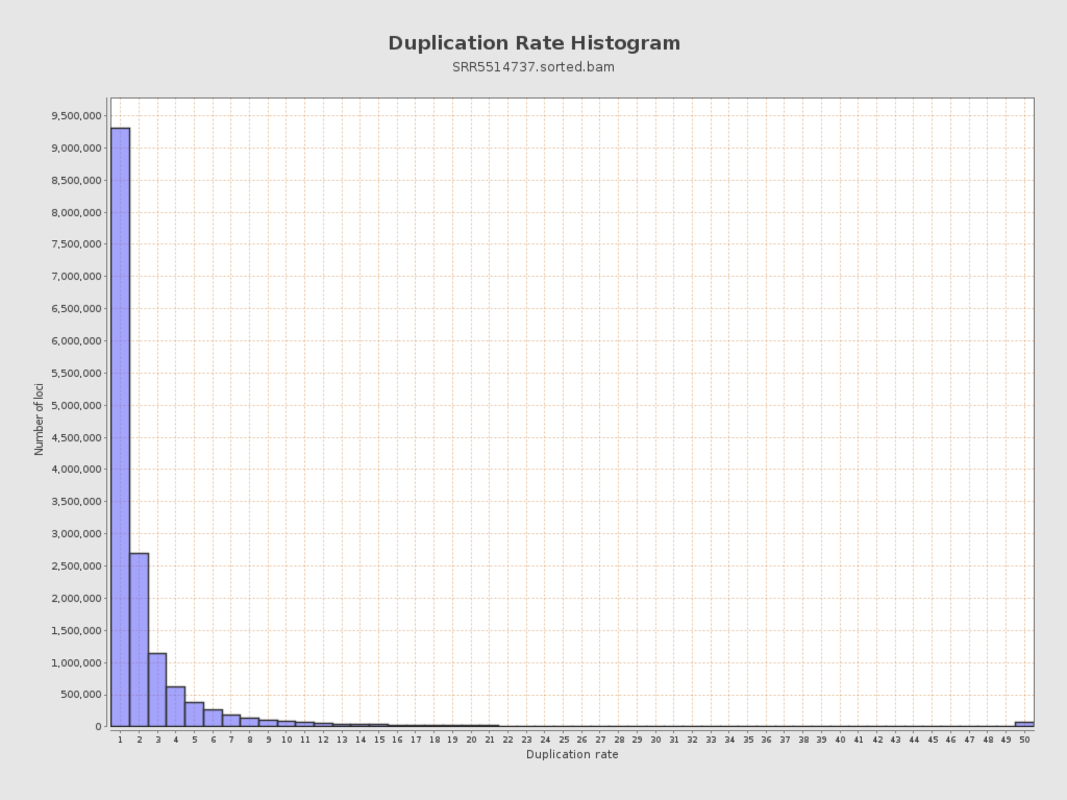
5. Results : Coverage Histogram (0-50X)



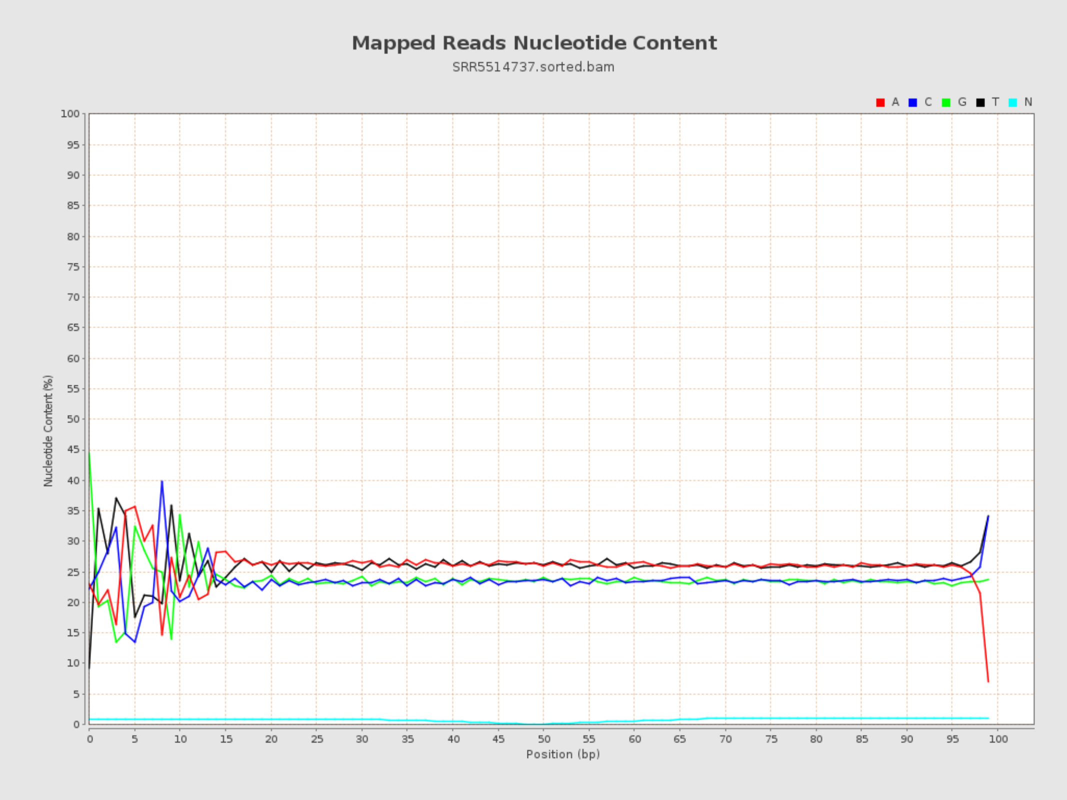
6. Results : Genome Fraction Coverage



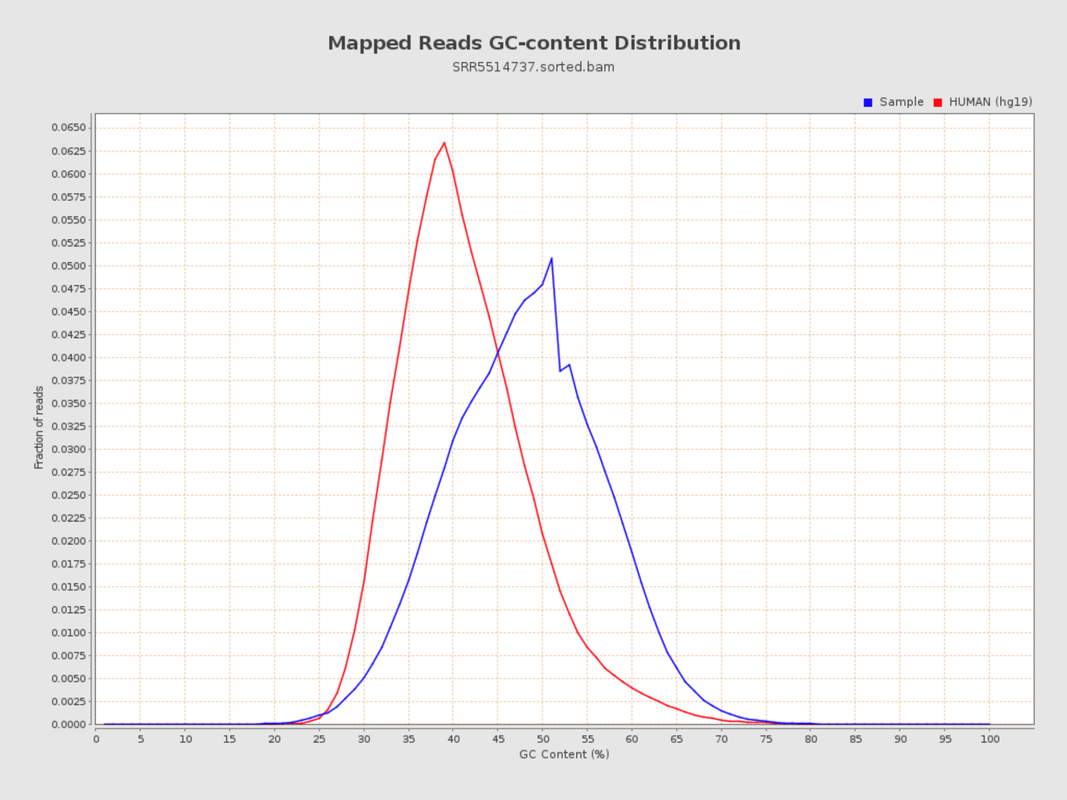
7. Results : Duplication Rate Histogram



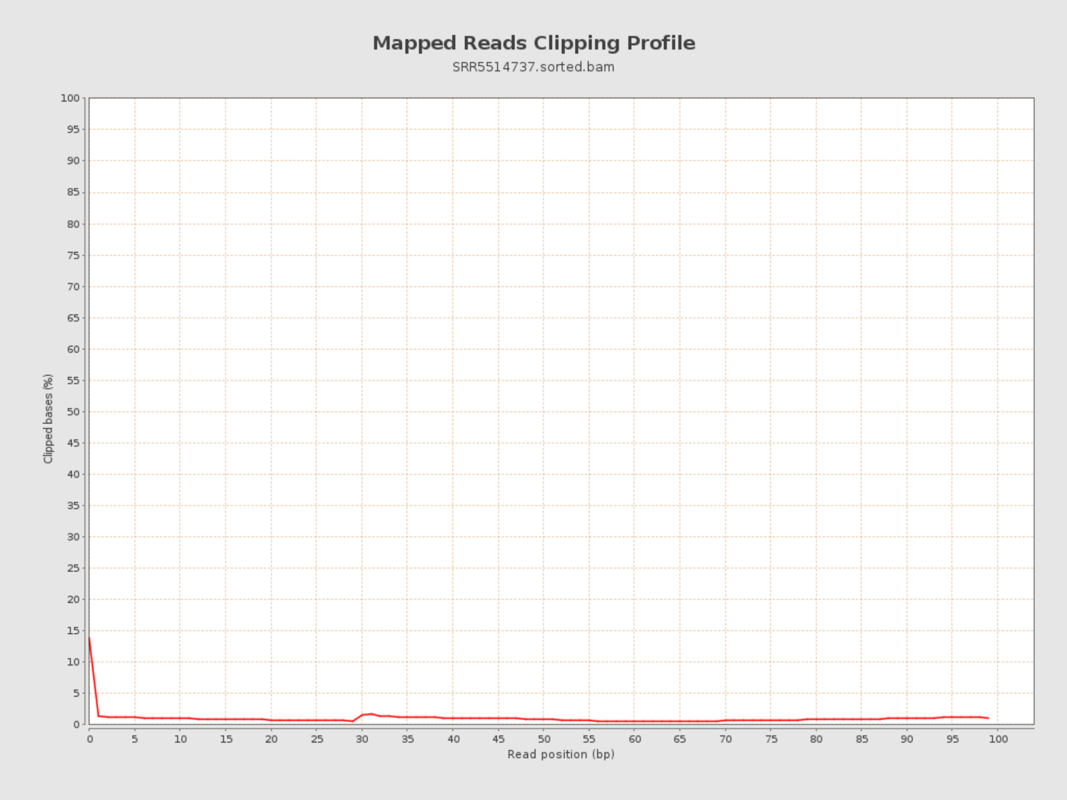
8. Results : Mapped Reads Nucleotide Content



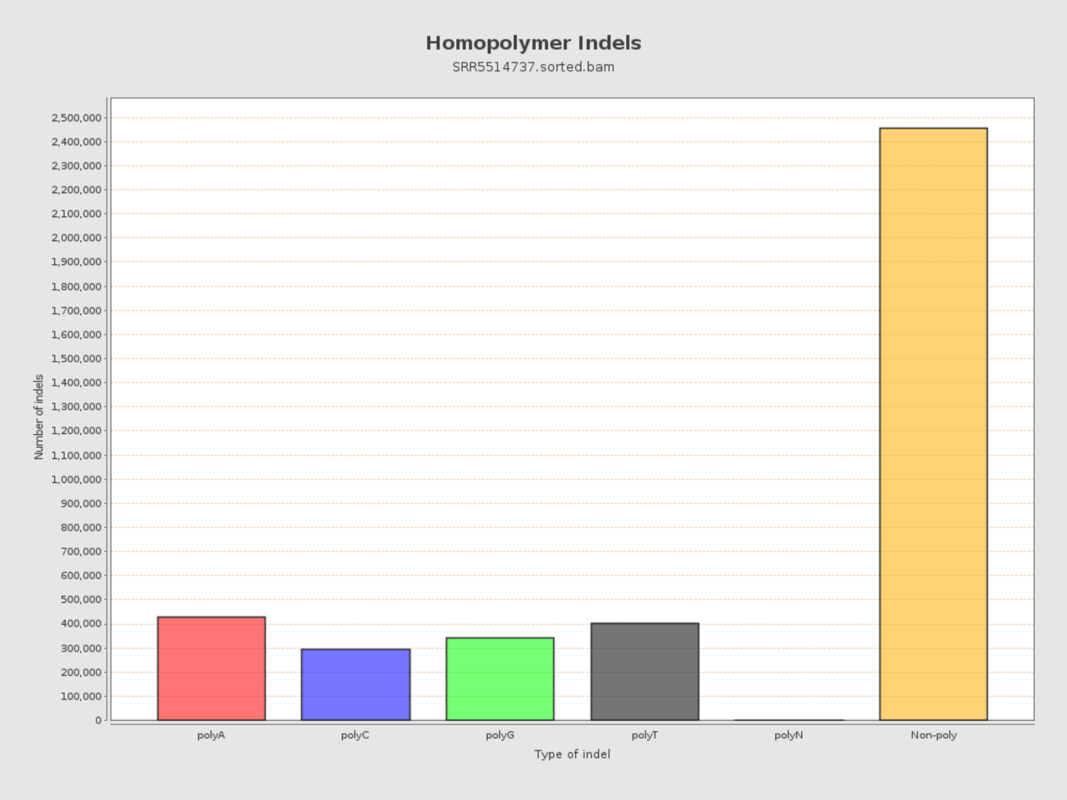
9. Results : Mapped Reads GC-content Distribution



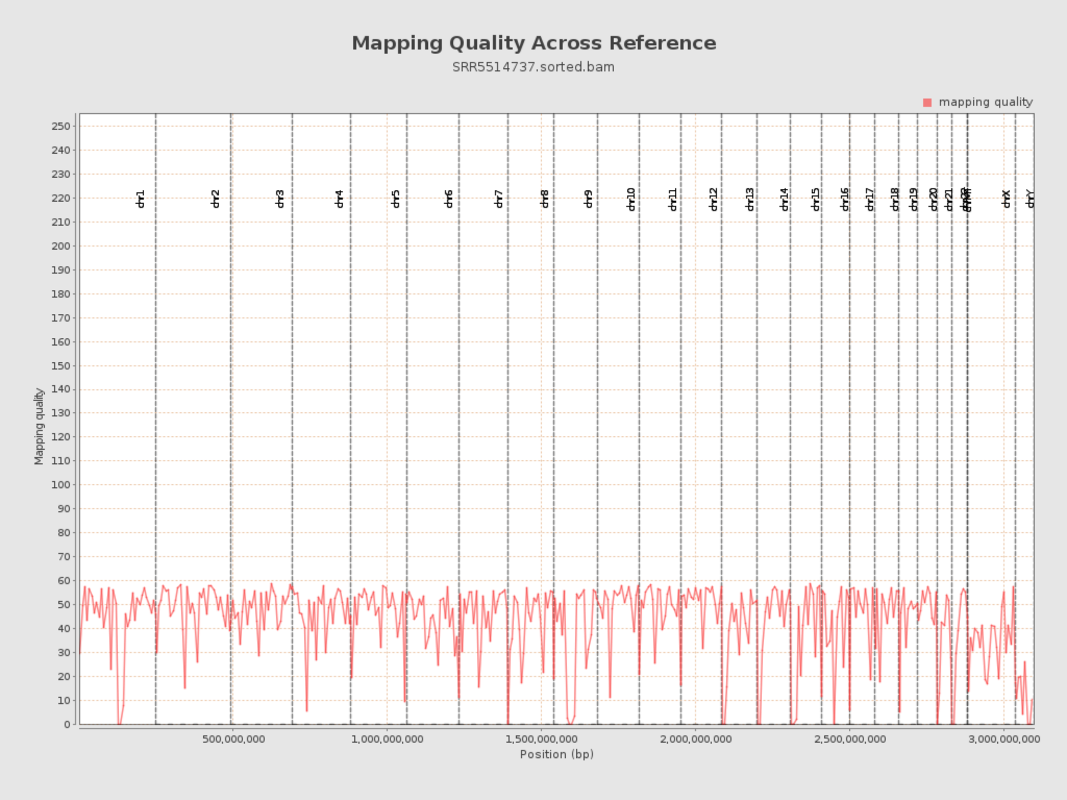
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram