Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 03:42:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506333.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_SRR1506333 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506333.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 03:42:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506333.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,128,136
Mapped reads	4,641,328 / 75.74%
Unmapped reads	1,486,808 / 24.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	77,817 / 1.27%
Read min/max/mean length	30 / 94 / 94.46
Duplicated reads (estimated)	537,505 / 8.77%
Duplication rate	8.87%
Clipped reads	2,865,845 / 46.77%

2.2. ACGT Content

Number/percentage of A's	102,957,576 / 28.19%
Number/percentage of C's	68,041,265 / 18.63%
Number/percentage of T's	106,582,273 / 29.19%
Number/percentage of G's	87,510,278 / 23.96%
Number/percentage of N's	94,640 / 0.03%
GC Percentage	42.6%

2.3. Coverage

Mean	0.118

Standard Deviation	0.8307

2.4. Mapping Quality

Mean Mapping Quality	47.99

2.5. Mismatches and indels

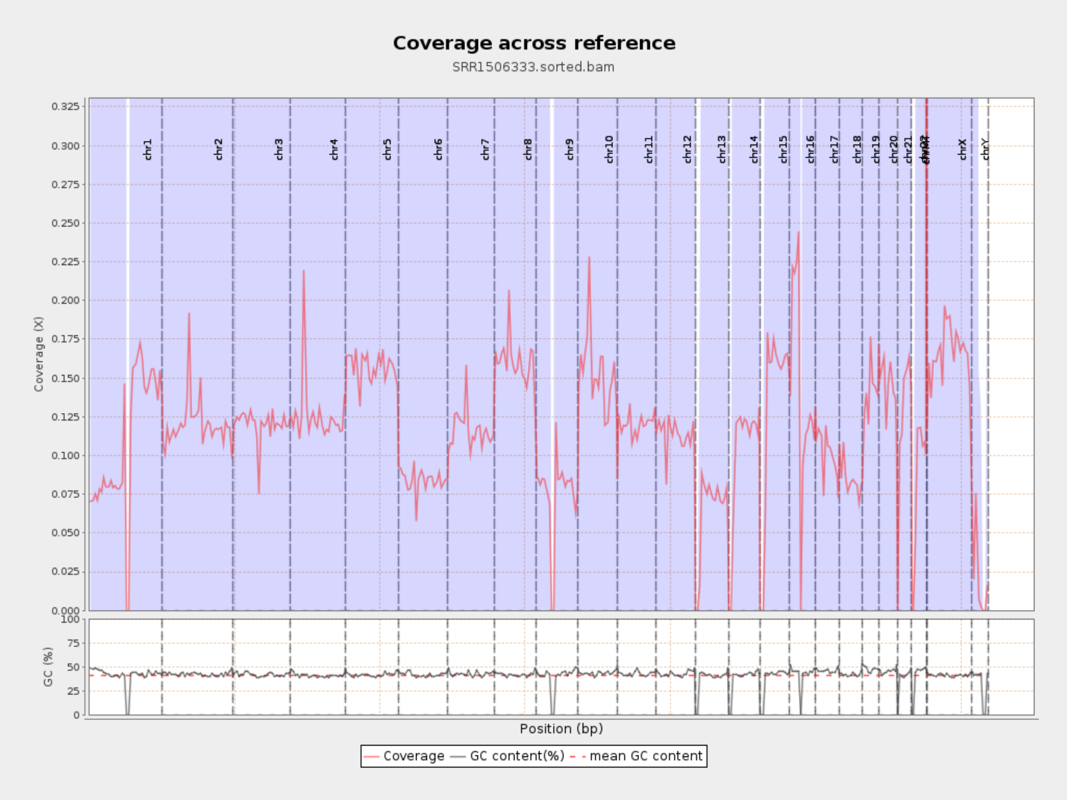
General error rate	0.74%
Mismatches	2,631,399
Insertions	29,903
Mapped reads with at least one insertion	0.63%
Deletions	78,584
Mapped reads with at least one deletion	1.66%
Homopolymer indels	44.85%

2.6. Chromosome stats

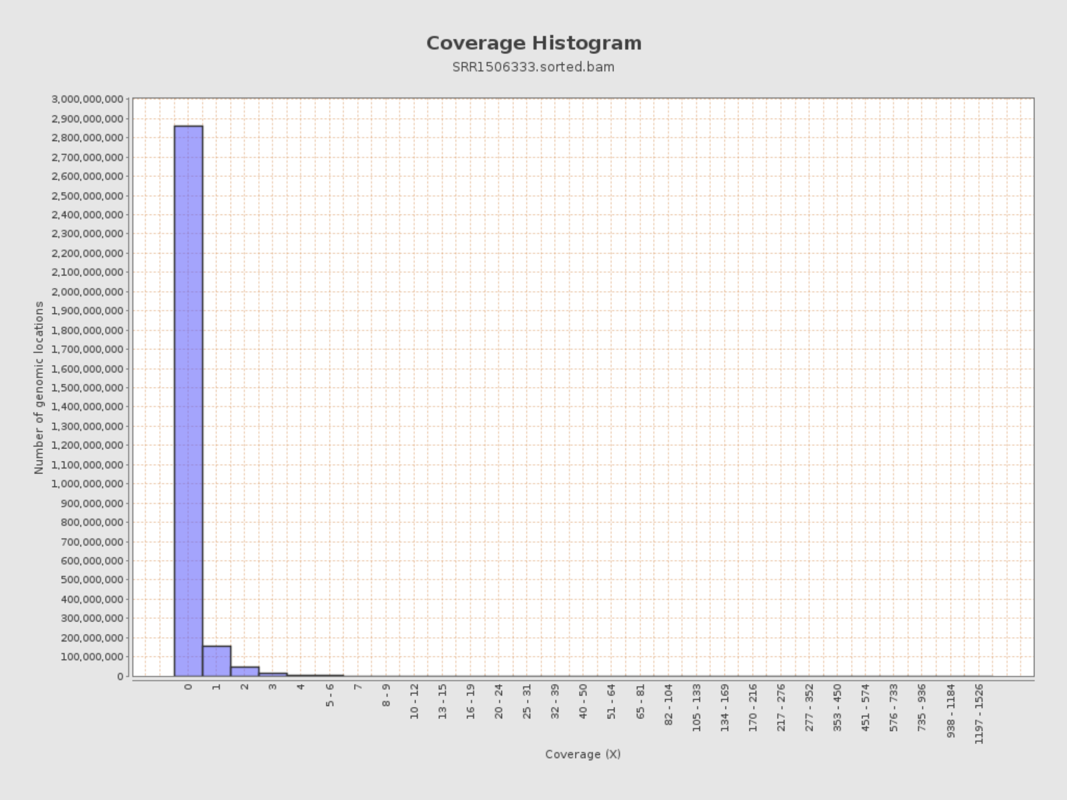
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26830006	0.1076	1.4401
chr2	243199373	29325028	0.1206	0.8781
chr3	198022430	23716398	0.1198	0.4934
chr4	191154276	24002157	0.1256	0.6756
chr5	180915260	28373345	0.1568	0.5773
chr6	171115067	14373116	0.084	0.4632
chr7	159138663	18560302	0.1166	1.0045

chr8	146364022	23488364	0.1605	1.2313
chr9	141213431	10468712	0.0741	0.8177
chr10	135534747	20898089	0.1542	0.9337
chr11	135006516	16180025	0.1198	0.796
chr12	133851895	15168109	0.1133	0.4973
chr13	115169878	7324526	0.0636	0.3549
chr14	107349540	10769001	0.1003	0.5338
chr15	102531392	13662395	0.1333	0.5349
chr16	90354753	13054113	0.1445	0.6548
chr17	81195210	8190390	0.1009	0.5369
chr18	78077248	6633908	0.085	1.2873
chr19	59128983	8284155	0.1401	1.0771
chr20	63025520	9091440	0.1443	0.5871
chr21	48129895	6058010	0.1259	0.6429
chr22	51304566	4028117	0.0785	0.4181
chrMT	16571	36547	2.2055	2.2949
chrX	155270560	25620137	0.165	0.6793
chrY	59373566	1202972	0.0203	0.6607

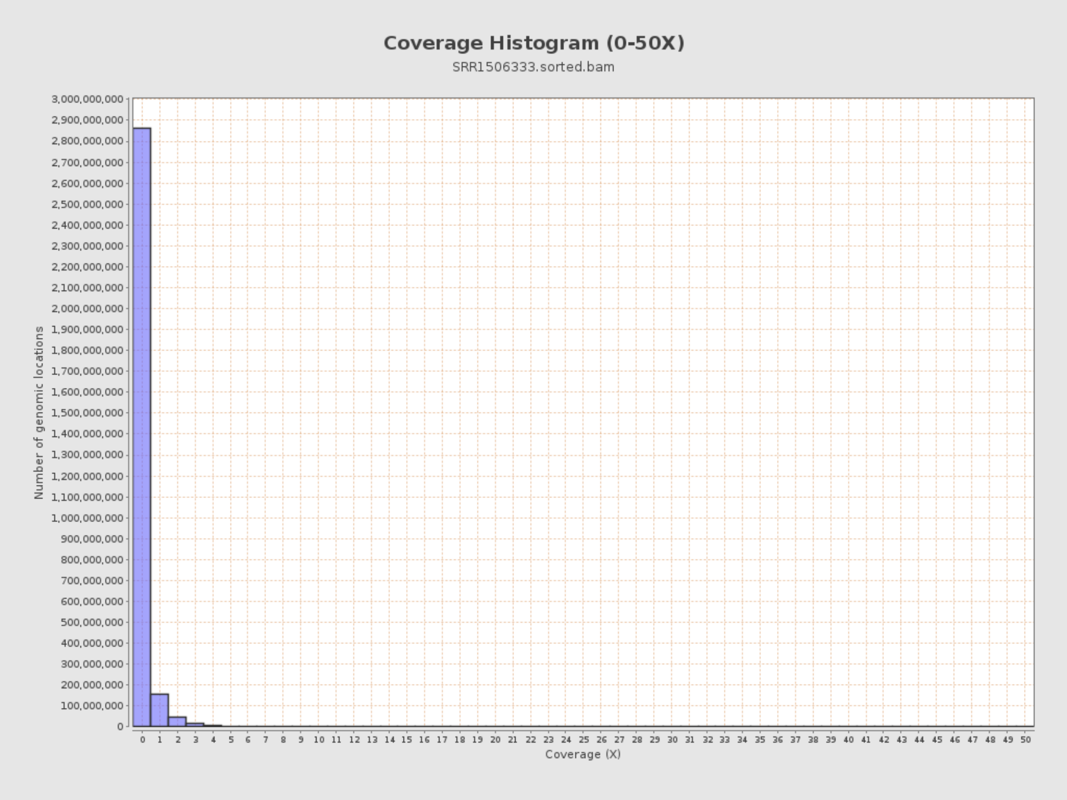
3. Results : Coverage across reference



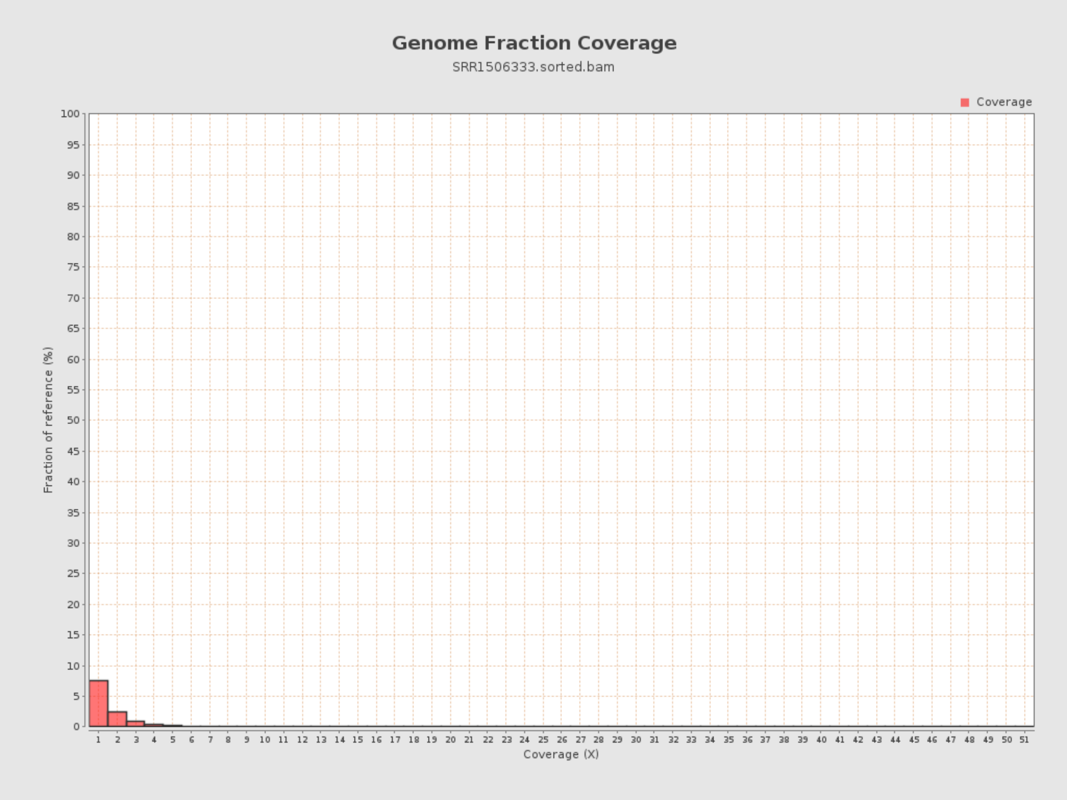
4. Results : Coverage Histogram



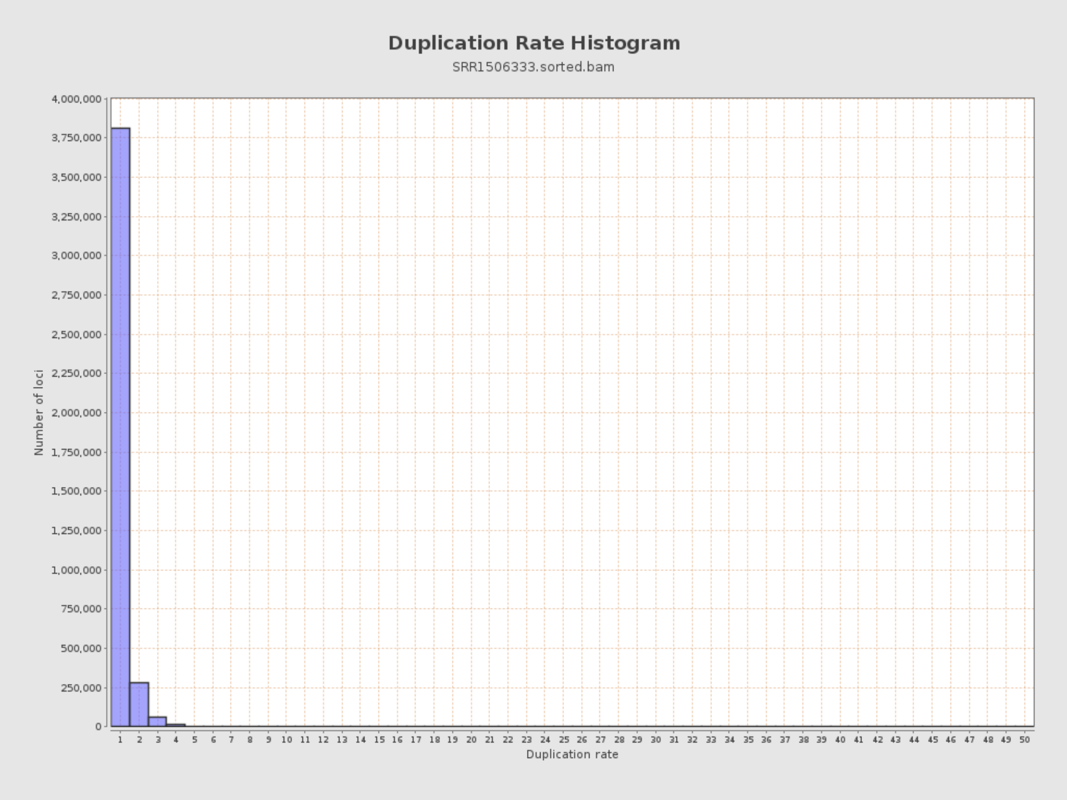
5. Results : Coverage Histogram (0-50X)



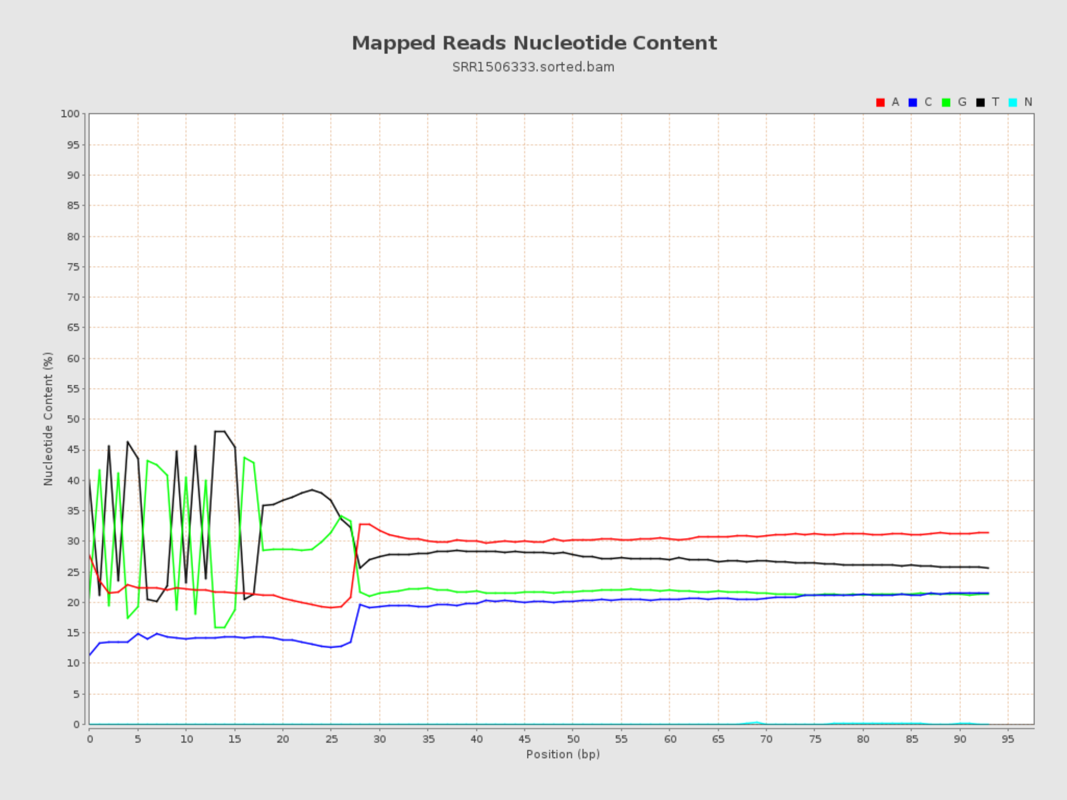
6. Results : Genome Fraction Coverage



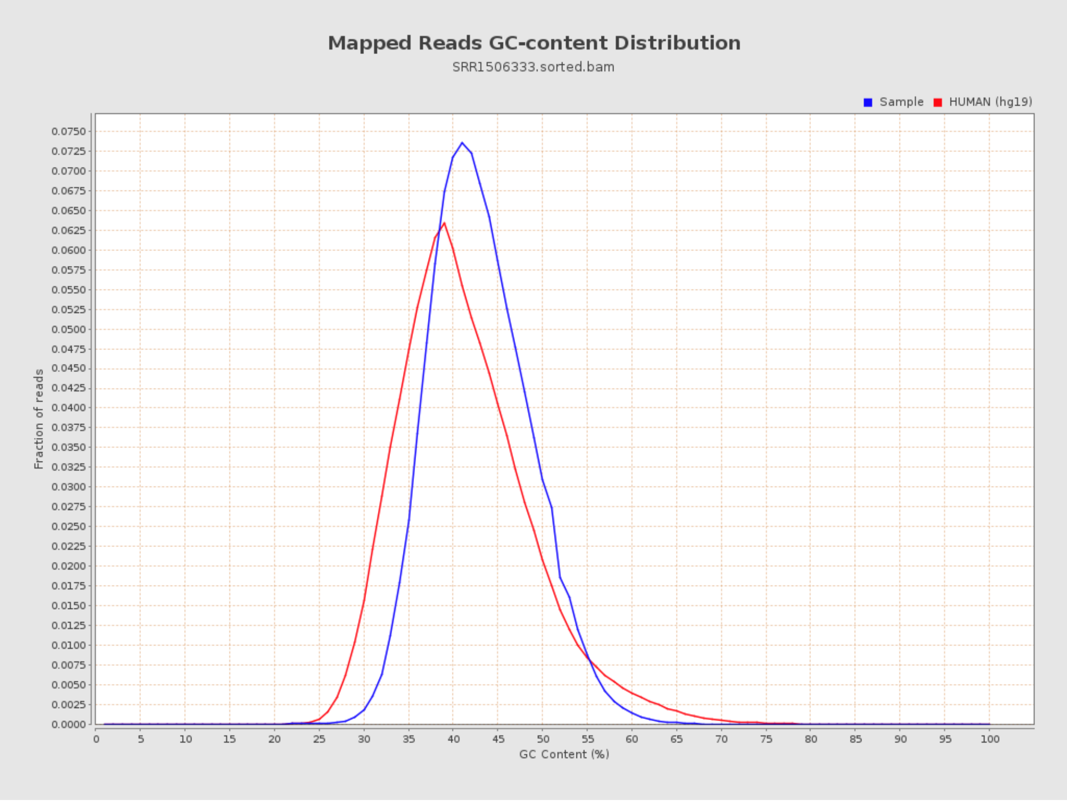
7. Results : Duplication Rate Histogram



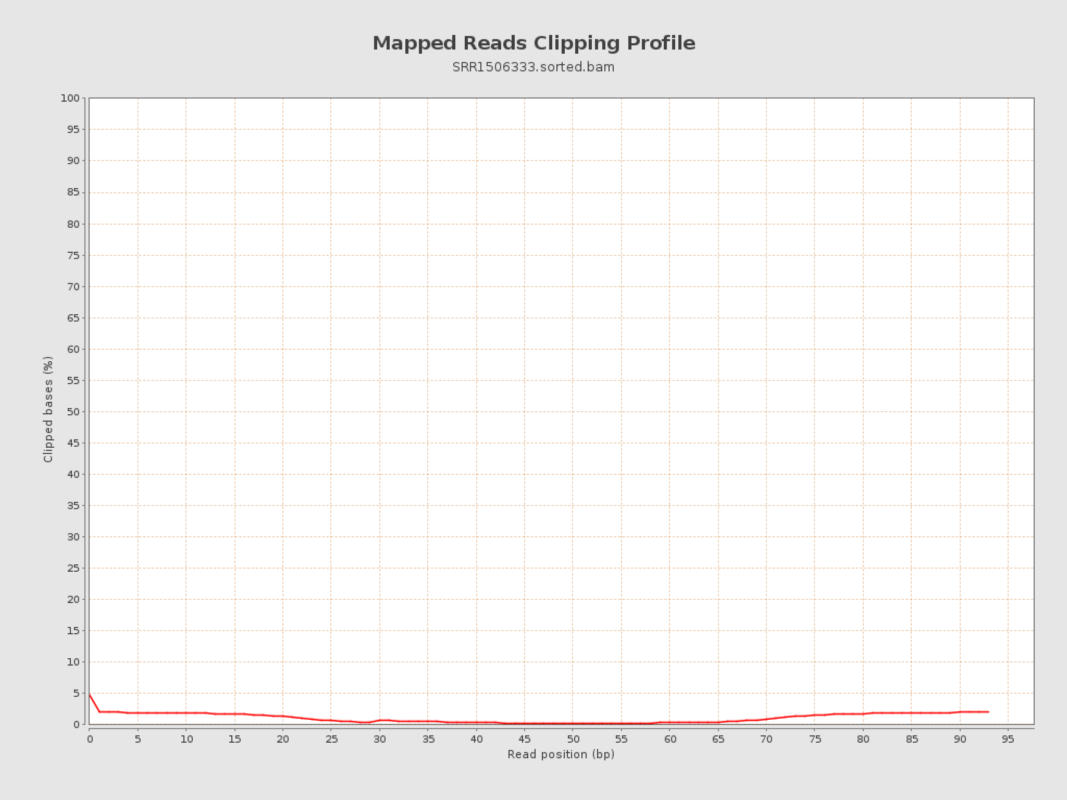
8. Results : Mapped Reads Nucleotide Content



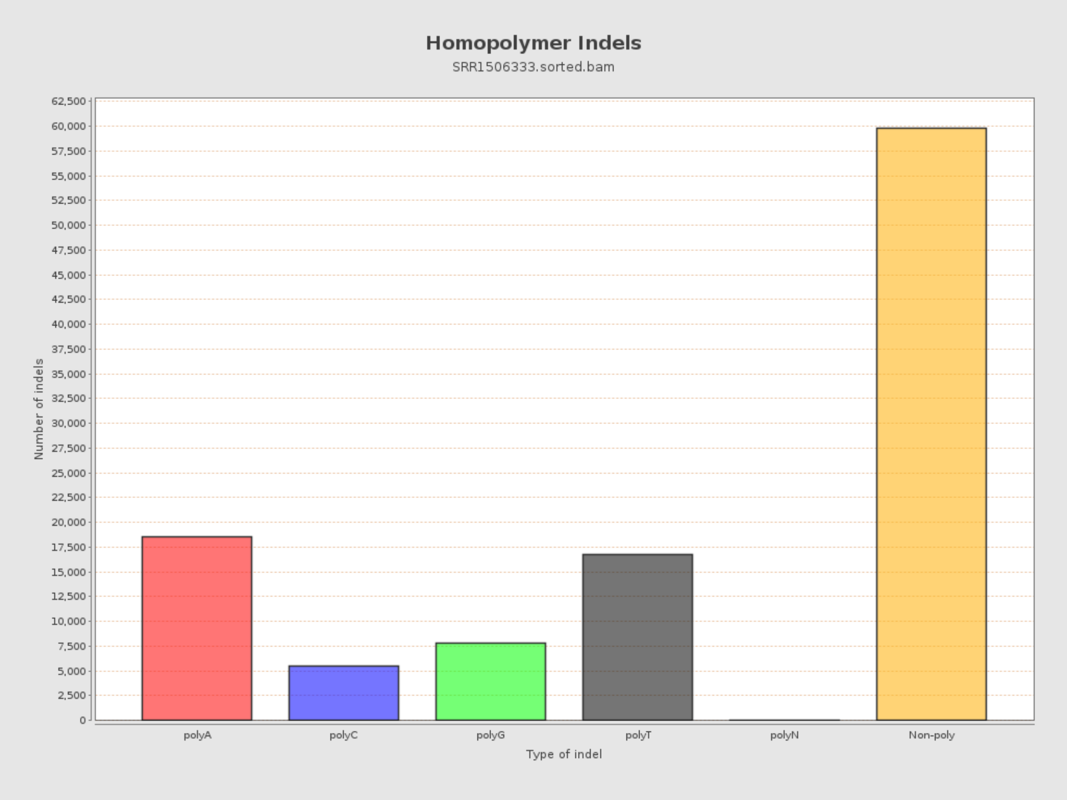
9. Results : Mapped Reads GC-content Distribution



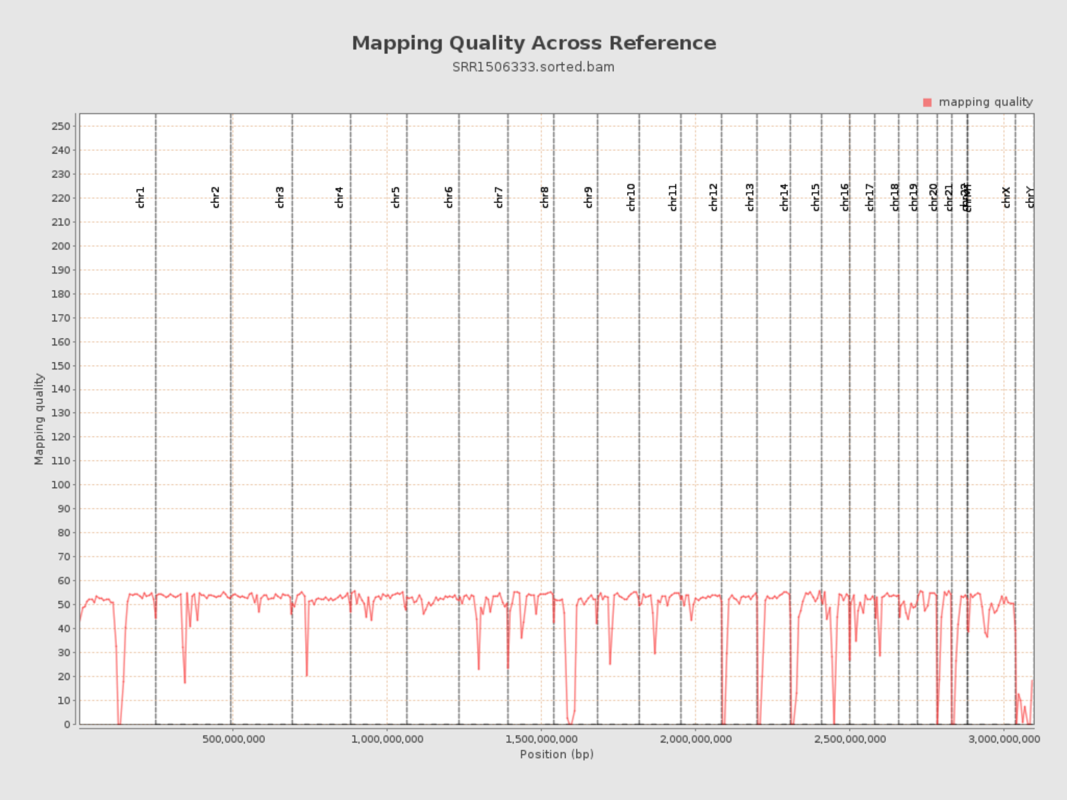
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram