

Local path /data/genome/human/illumina/ERR317482WGS/tmp/9827_2#49.sam
File format SAM
Organism Homo sapiens
Misc The first 100,000 alignments have been used

Summary

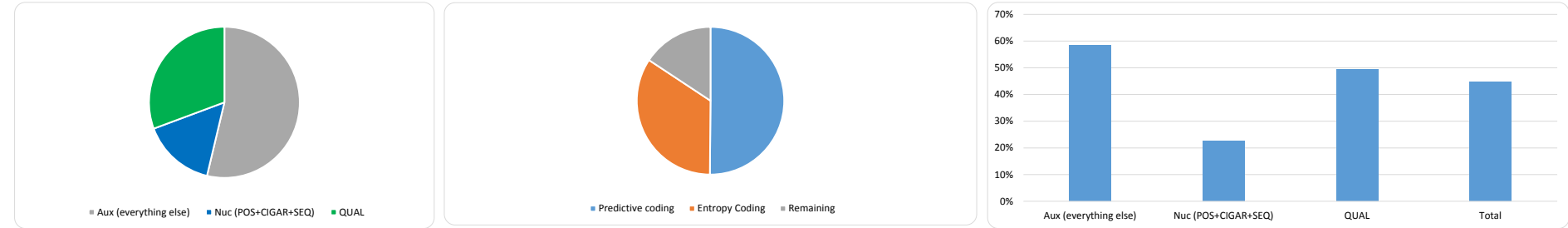
	File size (B)	File size (GiB)	Ratio	Factor	Time (us)	Time (h)	Parameters	Misc	Platform specification
Original File	360427371	0,34	100,00%	1,00					
Tsc	161678231	0,15	44,86%	2,23	741570270	0,21	FILECODEC_BLK_LC 10000 NUCCODEC_WINDOW_SZ 10		Intel® Xeon® CPU E5405 @ 2.00 GHz, 39GiB RAM, openSUSE 12.3 (Dartmouth) (x86_64)

Data distribution

	SAM size (B)	SAM size (GiB)	Ratio	Tsc size (B)	Tsc size (GiB)	Ratio	Compression ratio	Compression factor	Method
File format	0	0,00	0,00%	5628	0,00	0,00%			
SAM header	29279	0,00	0,01%	29279	0,00	0,02%	100,00%	1,00	
Aux (everything else)	148387525	0,14	41,17%	86824841	0,08	53,70%	58,51%	1,71	Predictive coding: nothing, entropy coding: 0-order arithmetic coder
Nuc (POS+CIGAR+SEQ)	112021467	0,10	31,08%	25260964	0,02	15,62%	22,55%	4,43	Predictive coding: local sequence alignment with short-time memory reference, entropy coding: 0-order arithmetic coder
QUAL	99989100	0,09	27,74%	49557519	0,05	30,65%	49,56%	2,02	Predictive coding: nothing, entropy coding: 0-order arithmetic coder
Total	360427371	0,34	100,00%	161678231	0,15	100,00%	44,86%	2,23	

Tsc timing statistics

	Time (us)	Time (h)	Ratio
Total	741570270	0,21	100,00%
Predictive coding	371774640	0,10	50,13%
Entropy Coding	253233893	0,07	34,15%
Remaining	116561737	0,03	15,72%
Misc	0	0,00	0,00%



Local path /data/genome/bacteria/DH10B/tmp/MiSeq_Ecoli_DH10B_110721_PF.sam
File format SAM
Organism Bacteria
Misc The first 100,000 alignments have been used

Summary

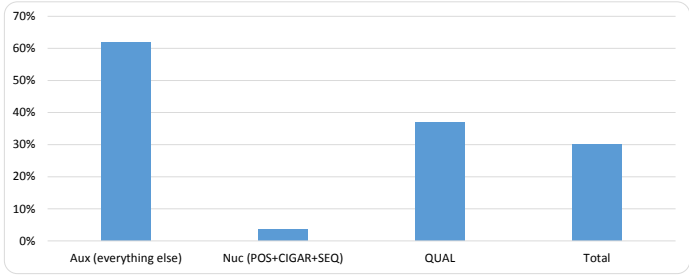
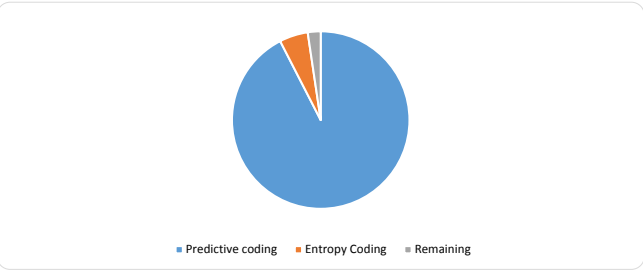
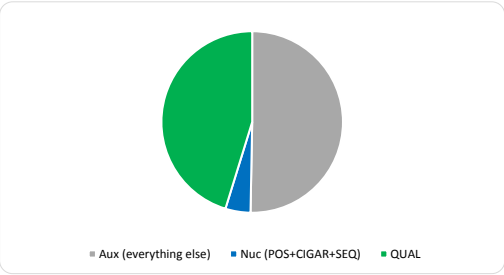
	File size (B)	File size (GiB)	Ratio	Factor	Time (us)	Time (h)	Parameters	Misc	Platform specification
Original File	409375634	0,38	100,00%	1,00					
Tsc	122698208	0,11	29,97%	3,34	1056081405	0,29	FILECODEC_BLK_LC 20000 NUCCODEC_WINDOW_SZ 10		Intel® Xeon® CPU E5405 @ 2.00 GHz, 39GiB RAM, openSUSE 12.3 (Dartmouth) (x86_64)

Data distribution

	SAM size (B)	SAM size (GiB)	Ratio	Tsc size (B)	Tsc size (GiB)	Ratio	Compression ratio	Compression factor	Method
File format	0	0,00	0,00%	5628	0,00	0,00%			
SAM header	197	0,00	0,00%	197	0,00	0,00%	100,00%	1,00	
Aux (everything else)	99699744	0,09	24,35%	61711510	0,06	50,30%	61,90%	1,62	Predictive coding: nothing, entropy coding: 0-order arithmetic coder
Nuc (POS+CIGAR+SEQ)	159676293	0,15	39,00%	5485868	0,01	4,47%	3,44%	29,11	Predictive coding: local sequence alignment with short-time memory reference, entropy coding: 0-order arithmetic coder
QUAL	149999400	0,14	36,64%	55495005	0,05	45,23%	37,00%	2,70	Predictive coding: nothing, entropy coding: 0-order arithmetic coder
Total	409375634	0,38	100,00%	122698208	0,11	100,00%	29,97%	3,34	

Tsc timing statistics

	Time (us)	Time (h)	Ratio
Total	1056081405	0,29	100,00%
Predictive coding	976340483	0,27	92,45%
Entropy Coding	54922435	0,02	5,20%
Remaining	24818487	0,01	2,35%
Misc	0	0,00	0,00%



Local path /data/genome/human/illumina/ERP001960/tmp/NA12878_S1.sam
File format SAM
Organism Homo sapiens
Misc The first 100,000 alignments have been used

Summary

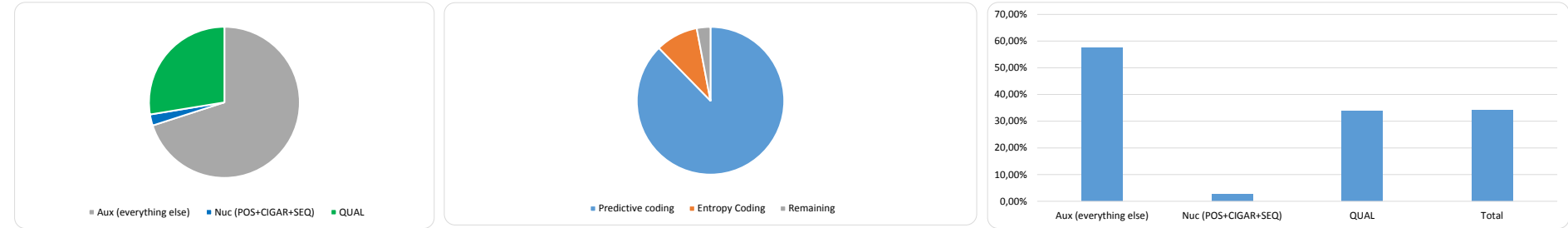
	File size (B)	File size (GiB)	Ratio	Factor	Time (us)	Time (h)	Parameters	Misc	Platform specification
Original File	360371641	0,34	100,00%	1,00					
Tsc	123395952	0,11	34,24%	2,92	66820930381	18,56	FILECODEC_BLK_LC 20000 NUCCODEC_WINDOW_SZ 10		Intel® Xeon® CPU E5620 @ 2.40 GHz, 94GiB RAM, openSUSE 13.1 (Bottle) (x86_64)

Data distribution

	SAM size (B)	SAM size (GiB)	Ratio	Tsc size (B)	Tsc size (GiB)	Ratio	Compression ratio	Compression factor	Method
File format	0	0,00	0,00%	5628	0,00	0,00%			
SAM header	696	0,00	0,00%	696	0,00	0,00%	100,00%	1,00	
Aux (everything else)	150486207	0,14	41,76%	86417617	0,08	70,03%	57,43%	1,74	Predictive coding: nothing, entropy coding: 0-order arithmetic coder
Nuc (POS+CIGAR+SEQ)	108887465	0,10	30,22%	2948748	0,00	2,39%	2,71%	36,93	Predictive coding: local sequence alignment with short-time memory reference, entropy coding: 0-order arithmetic coder
QUAL	100997273	0,09	28,03%	34023263	0,03	27,57%	33,69%	2,97	Predictive coding: nothing, entropy coding: 0-order arithmetic coder
Total	360371641	0,34	100,00%	123395952	0,11	100,00%	34,24%	2,92	

Tsc timing statistics

	Time (us)	Time (h)	Ratio
Total	66820930381	18,56	100,00%
Predictive coding	58572428778	16,27	87,66%
Entropy Coding	6243013640	1,73	9,34%
Remaining	2005487963	0,56	3,00%
Misc	0	0,00	0,00%



Local path /data/genome/human/RNAseq/tmp/K562_cytosol_LID8465_TopHat_v2.sam.short.sam
File format SAM
Organism Homo sapiens
Misc The first 100,000 alignments have been used

Summary

	File size (B)	File size (GiB)	Ratio	Factor	Time (us)	Time (h)	Parameters	Misc	Platform specification
Original File	31167813	0,03	100,00%	1,00					
Tsc	13593736	0,01	43,61%	2,29	30943206	0,01	FILECODEC_BLK_LC 20000 NUCCODEC_WINDOW_SZ 10		Intel® Xeon® CPU E5-2690 v2 @ 3.00 GHz, 126GiB RAM, openSUSE 13.1 (Bottle) (x86_64)

Data distribution

	SAM size (B)	SAM size (GiB)	Ratio	Tsc size (B)	Tsc size (GiB)	Ratio	Compression ratio	Compression factor	Method
File format	0	0,00	0,00%	588	0,00	0,00%			
SAM header	3576	0,00	0,01%	3576	0,00	0,03%	100,00%	1,00	
Aux (everything else)	15057730	0,01	48,31%	9124121	0,01	67,12%	60,59%	1,65	Predictive coding: nothing, entropy coding: 0-order arithmetic coder
Nuc (POS+CIGAR+SEQ)	8513043	0,01	27,31%	1712317	0,00	12,60%	20,11%	4,97	Predictive coding: local sequence alignment with short-time memory reference, entropy coding: 0-order arithmetic coder
QUAL	7593464	0,01	24,36%	2753134	0,00	20,25%	36,26%	2,76	Predictive coding: nothing, entropy coding: 0-order arithmetic coder
Total	31167813	0,03	100,00%	13593736	0,01	100,00%	43,61%	2,29	

Timing statistics

	Time (us)	Time (h)	Ratio
Total	30943206	0,01	100,00%
Predictive coding	26625257	0,01	86,05%
Entropy Coding	2793129	0,00	9,03%
Remaining	1524820	0,00	4,93%
Misc	0	0,00	0,00%

