

Report

	22-320_filtered	22-312_filtered	22-324_filtered	22-336_filtered	22-310_filtered	22-309_filtered	22-301_filtered	22-315_filtered	22-329B_filtered	22-333_filtered	22-318_filtered	22-302_filtered	22-330_filtered	22-304_filtered	22-299_filtered	22-329A_filtered	22-311_filtered	22-317_filtered	22-337_filtered	22-332_filtered	22-331_filtered	22-316_filtered	22-303_filtered	22-334_filtered	22-335_filtered	22-300_filtered	22-314_filtered	22-322_filtered	22-319_filtered	
# contigs (>= 0 bp)	222	218	173	178	181	200	183	191	174	173	244	198	181	195	187	180	187	192	179	210	175	193	191	170	236	183	208	171	214	
# contigs (>= 1000 bp)	99	102	93	78	80	82	89	89	78	77	142	89	84	88	85	85	94	88	79	95	77	92	83	78	136	80	97	90	93	
# contigs (>= 5000 bp)	78	83	78	59	63	64	71	66	59	58	117	71	63	68	66	64	75	70	60	73	59	73	66	59	110	62	76	75	73	
# contigs (>= 10000 bp)	71	74	68	54	56	57	63	59	54	53	104	63	57	61	58	58	66	63	54	65	53	65	58	53	93	56	67	64	67	
# contigs (>= 25000 bp)	56	54	54	46	46	47	50	48	45	44	76	52	48	50	48	48	52	50	45	52	44	51	48	45	69	46	52	53	53	
# contigs (>= 50000 bp)	37	40	41	36	36	36	37	34	34	33	42	39	34	37	37	37	41	39	33	41	33	38	35	34	39	36	39	42	41	
Total length (>= 0 bp)	5251576	5249524	5369584	5251456	5250760	5252332	5248367	5249315	5250045	5248998	5246520	5252074	5249716	5251313	5251304	5249320	5249236	5250469	5250820	5251939	5250220	5250912	5249950	5249249	5246559	5249540	5251082	5180419	5252664	
Total length (>= 1000 bp)	5217344	5216942	5345685	5220903	5221408	5220124	5222034	5219048	5220785	5219682	5214974	5221638	5220727	5221198	5221904	5221268	5223647	5220595	5221262	5218735	5221705	5221074	5219465	5220769	5216929	5219188	5218571	5157254	5218144	
Total length (>= 5000 bp)	5167301	5170358	5307127	5176927	5182995	5179261	5182088	5161216	5176812	5173768	5147440	5180830	5172682	5172099	5177482	5173729	5178354	5177264	5176849	5166250	5179833	5175599	5178808	5176755	5148445	5179076	5168218	5117540	5170323	
Total length (>= 10000 bp)	5121500	5103741	5233546	5143565	5134560	5103741	5130833	5126377	5143450	5140406	5058808	5124356	5129753	5123264	5122584	5133706	5114002	5123640	5136730	5108057	5139300	5175809	5123611	5134331	5025163	5136352	5099510	5035793	5127627	
Total length (>= 25000 bp)	4849983	4759128	5012794	5005931	4954243	4950516	4904218	4911177	4984377	4980791	4577900	4930665	4970797	4926914	4945226	4960802	4875697	4885524	4977541	4878003	4977386	4875043	4943294	4996733	4632360	4956034	4828910	4839189	4882556	
Total length (>= 50000 bp)	4155120	4252626	4548592	4629788	4591512	4541049	4429767	4383255	4561900	4570112	3357254	4439778	4422680	4444554	4556999	4548825	4466230	4476058	4522733	4484227	4554797	4405103	4451306	4580723	3573547	4591292	4366036	4448349	4443709	
# contigs	114	116	106	92	94	96	101	102	92	93	156	104	98	102	99	98	106	103	90	110	89	108	97	93	149	96	113	102	110	
Largest contig	367715	249065	281783	301450	617275	533180	367634	553767	315914	617203	135209	313931	315827	367669	533206	244575	283837	367622	617224	249172	617210	367664	617132	368444	248843	617117	367616	249200	248899	
Total length	5227783	5227039	5354904	5231039	5231743	5230030	5230240	5228645	5231095	5231400	5225331	5232291	5230433	5231157	5231968	5230768	5231964	5231248	5229604	5229230	5230549	5232575	5229478	5231676	5226578	5230562	5229901	5164927	5230158	
Reference length	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	5230549	
GC (%)	63.78	63.78	63.62	63.77	63.78	63.78	63.78	63.78	63.77	63.77	63.78	63.78	63.78	63.78	63.77	63.77	63.77	63.77	63.77	63.77	63.78	63.77	63.77	63.77	63.78	63.78	63.78	63.79	63.78	
Reference GC (%)	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	63.78	
N50	110047	110047	120024	134378	127800	130617	116250	130617	127800	134378	135039	64876	124829	130310	127800	127800	130617	110047	127800	135285	116465	134378	117293	130617	135285	70884	127800	111400	110150	127800
NG50	110047	110047	120773	134378	127800	130617	116250	130617	134378	135039	64876	124829	130310	127800	127800	130617	110047	127800	135285	116465	134378	117293	130617	135285	70884	127800	111400	102849	127800	
N90	31781	27745	38010	46904	40137	40137	37349	37349	45731	40132	22988	38010	40137	37349	38010	40137	37349	37349	39887	37349	45731	33787	38388	45731	23778	40137	32743	37328	37349	
NG90	31084	26954	39415	46904	40137	40137	37349	37349	45731	40132	22988	38010	40137	37349	38010	40137	37349	37349	39887	37349	45731	33787	38388	45731	22979	40137	32743	33787	37349	
auN	120099.8	106256.2	119960.1	138192.0	174825.9	157604.6	133072.3	159060.1	145718.3	182355.5	66026.7	121785.2	138316.6	132757.2	155090.0	122711.0	115900.5	131690.7	179446.0	116372.2	181296.7	130248.1	172883.9	148369.4	85031.4	174559.9	127465.0	113054.8	114670.6	
auNG	120036.3	106184.9	122812.1	138204.9	174865.8	157589.0	133064.5	159002.2	145733.5	182385.2	65960.8	121825.7	138313.6	132772.7	155132.1	122716.1	115931.8	131708.3	179413.6	116342.8	181296.7	130298.5	172848.5	148401.4	84966.9	174560.3	127449.2	111636.4	114662.0	
L50	17	18	17	15	14	14	15	14	14	13	30	16	15	16	15	17	17	15	13	17	13	16	14	14	24	14	16	17	17	
LG50	17	18	16	15	14	14	15	14	14	13	30	16	15	16	15	17	17	15	13	17	13	16	14	14	24	14	16	18	17	
L90	51	52	48	38	39	40	44	42	38	37	82	46	41	44	41	41	47	45	38	47	37	46	41	37	72	39	48	47	48	
LG90	52	53	45	38	39	40	44	42	38	37	82	46	41	44	41	41	47	45	38	47	37	46	41	37	73	39	48	49	48	
# misassemblies	3	6	22	3	6	7	9	3	4	5	6	7	4	5	8	7	9	8	2	4	0	8	6	4	10	4	8	22	4	
# misassembled contigs	3	5	15	3	4	5	7	3	4	5	6	4	4	4	6	6	5	5	2	4	0	4	5	4	8	3	7	14	3	
Misassembled contigs length	314591	489079	1282358	377219	357650	357235	533908	225395	310511	300007	376767	356895	197808	353860	678138	392621	410633	477839	228928	344746	0	344508	502062	297870	573334	355012	405085	708709	310939	
# local misassemblies	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	2	0	
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# unaligned mis. contigs	0	1	2	0	0	0	0	0	0	0	1	1	0	0	1	0	1	1	0	0	0	1	1	1	0	1	0	1	1	
# unaligned contigs	0 + 0 part	0 + 0 part	1 + 7 part	2 + 0 part	0 + 1 part	0 + 0 part	1 + 0 part	0 + 0 part	0 + 0 part	1 + 0 part	0 + 1 part	1 + 0 part	0 + 0 part	0 + 1 part	0 + 1 part	0 + 0 part	1 + 0 part	1 + 0 part	0 + 0 part	1 + 0 part	0 + 0 part	1 + 0 part	0 + 1 part	0 + 0 part	0 + 0 part	1 + 0 part	0 + 1 part	1 + 2 part	1 + 0 part	
Unaligned length	0	0	207876	1180	850	0	589	0	0	733	1068	589	0	1268	1306	0	589	589	0	589	0	945	641	0	0	790	951	43842	790	
Genome fraction (%)	99.897	99.882	98.335	99.965	99.948	99.940	99.925	99.922	99.967	99.959	99.797	99.951	99.966	99.931	99.928	99.898	99.937	99.938	99.955	99.902	100.000	99.941	99.908	99.975	99.790	99.940	99.906	97.789	99.930	
Duplication ratio	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.001	1.000	1.000	1.000	1.001	1.001	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.001	1.000	1.001	1.000	1.000	1.000	
# N's per 100 kbp	4.90	4.04	6.24	5.70	6.96	4.40	3.00	7.61	7.61	5.52	7.83	6.71	7.42	2.33	6.98	5.49	4.40	2.45	7.42	6.27	5.77	4.22	4.95	6.93	4.61	6.29	2.90	3.88		
# mismatches per 100 kbp	1.49	1.59	8.48	0.31	1.17	1.68	1.26	0.57	0.31	0.31	2.43	1.19	0.55	1.38	1.78	3.92	1.59	1.78	0.17	1.09	0.04	1.01	2.18	0.15	4.19	1.22	1.43	5.90	0.99	
# indels per 100 kbp	0.48	0.36	1.01	0.11	0.38	0.48	0.46	0.21	0.11	0.17	0.82	0.52	0.15	0.44	0.61	0.19	0.40	0.40	0.08	0.52	0.00	0.27	0.55	0.11	1.36	0.40	0.48	1.00	0.17	
Largest alignment	367715	249065	217645	301416	617275	533180	367634	553767	315817	617203	135175	313931																		

Misassemblies report

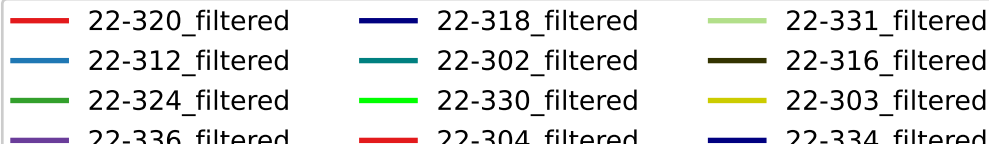
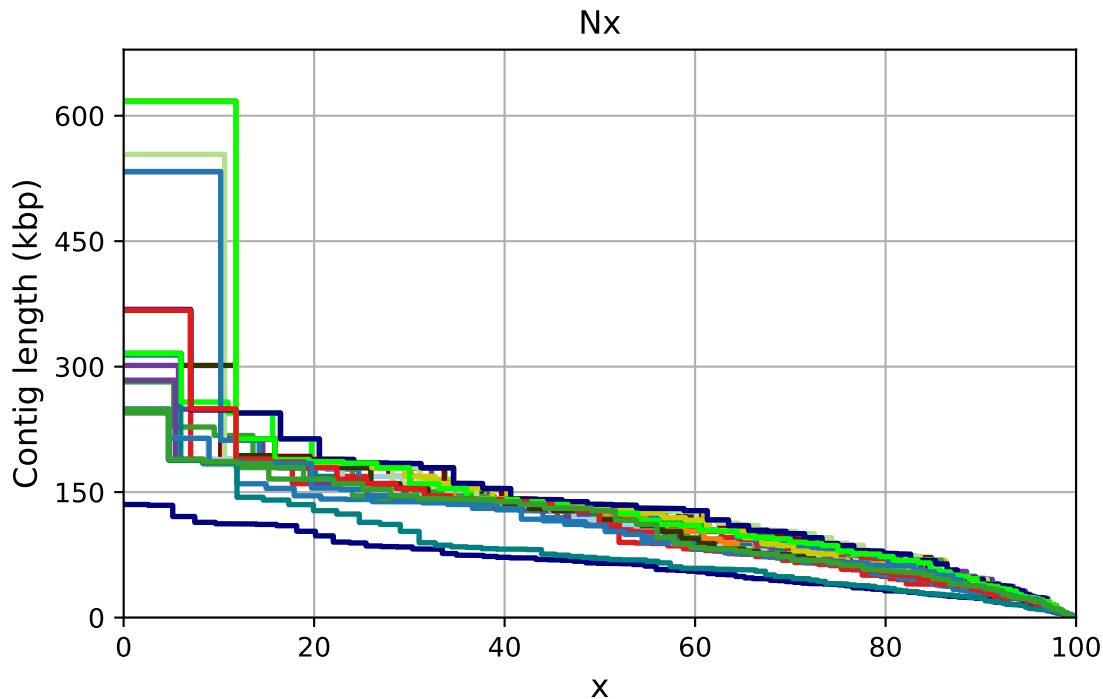
	22-320_filtered	22-312_filtered	22-324_filtered	22-336_filtered	22-310_filtered	22-309_filtered	22-301_filtered	22-315_filtered	22-329B_filtered	22-333_filtered	22-318_filtered	22-302_filtered	22-330_filtered	22-304_filtered	22-299_filtered	22-329A_filtered	22-311_filtered	22-317_filtered	22-337_filtered	22-332_filtered	22-331_filtered	22-316_filtered	22-303_filtered	22-334_filtered	22-335_filtered	22-300_filtered	22-314_filtered	22-322_filtered	22-319_filtered
# misassemblies	3	6	22	3	6	7	9	3	4	5	6	7	4	5	8	7	9	8	2	4	0	8	6	4	10	4	8	22	4
# contig misassemblies	3	6	22	3	6	7	9	3	4	5	6	7	4	5	8	7	9	8	2	4	0	8	6	4	10	4	8	22	4
# c. relocations	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	3	6	21	3	6	7	9	3	4	5	6	7	4	5	8	7	9	8	2	4	0	8	6	4	10	4	8	22	4
# c. inversions	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# misassembled contigs	3	5	15	3	4	5	7	3	4	5	6	4	4	4	6	6	5	5	2	4	0	4	5	4	8	3	7	14	3
Misassembled contigs length	314591	489079	1282358	377219	357650	357235	533908	225395	310511	300007	376767	356895	197808	353860	678138	392621	410633	477839	228928	344746	0	344508	502062	297870	573334	355012	405085	708709	310939
# local misassemblies	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	2	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	1	2	0	0	0	0	0	0	1	0	1	0	0	1	0	1	1	0	0	0	1	1	1	0	1	0	1	1
# mismatches	78	83	436	16	61	88	66	30	16	16	127	62	29	72	93	205	83	93	9	57	2	53	114	8	219	64	75	302	52
# indels	25	19	52	6	20	25	24	11	6	9	43	27	8	23	32	10	21	21	4	27	0	14	29	6	71	21	25	51	9
# indels (<= 5 bp)	12	10	19	0	10	14	4	5	0	1	22	13	1	12	17	1	10	11	0	17	0	4	15	0	46	9	17	12	3
# indels (> 5 bp)	13	9	33	6	10	11	20	6	6	8	21	14	7	11	15	9	11	10	4	10	0	10	14	6	25	12	8	39	6
Indels length	1043	838	1476	358	947	1028	1920	461	439	593	1600	959	523	1090	1487	622	988	1078	333	793	0	1311	1086	335	1403	885	738	1720	769

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

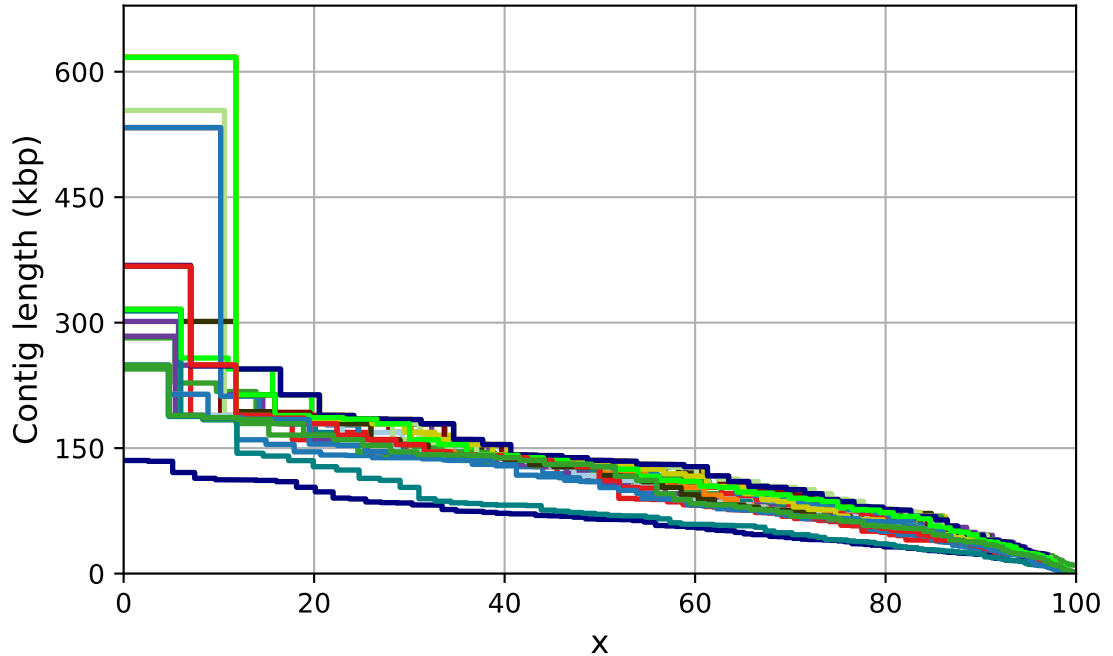
Unaligned report

	22-320_filtered	22-312_filtered	22-324_filtered	22-336_filtered	22-310_filtered	22-309_filtered	22-301_filtered	22-315_filtered	22-329B_filtered	22-333_filtered	22-318_filtered	22-302_filtered	22-330_filtered	22-304_filtered	22-299_filtered	22-329A_filtered	22-311_filtered	22-317_filtered	22-337_filtered	22-332_filtered	22-331_filtered	22-316_filtered	22-303_filtered	22-334_filtered	22-335_filtered	22-300_filtered	22-314_filtered	22-322_filtered	22-319_filtered
# fully unaligned contigs	0	0	1	2	0	0	1	0	0	1	0	1	0	0	0	0	1	1	0	1	0	1	0	0	0	1	0	1	1
Fully unaligned length	0	0	859	1180	0	0	589	0	0	733	0	589	0	0	0	0	589	589	0	589	0	945	0	0	0	790	0	34577	790
# partially unaligned contigs	0	0	7	0	1	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	1	0	0	0	1	2	0
Partially unaligned length	0	0	207017	0	850	0	0	0	0	0	1068	0	0	1268	1306	0	0	0	0	0	0	0	641	0	0	0	951	9265	0
# N's	256	211	334	298	364	230	157	398	398	289	409	351	388	122	365	287	230	128	388	328	302	221	259	403	362	241	329	150	203

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted
(e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

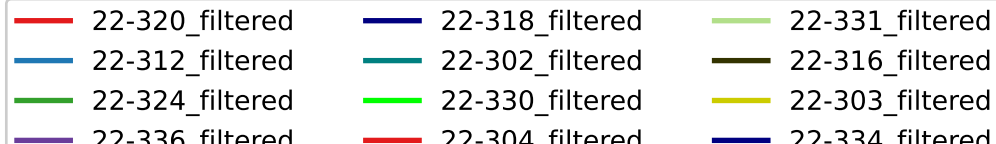
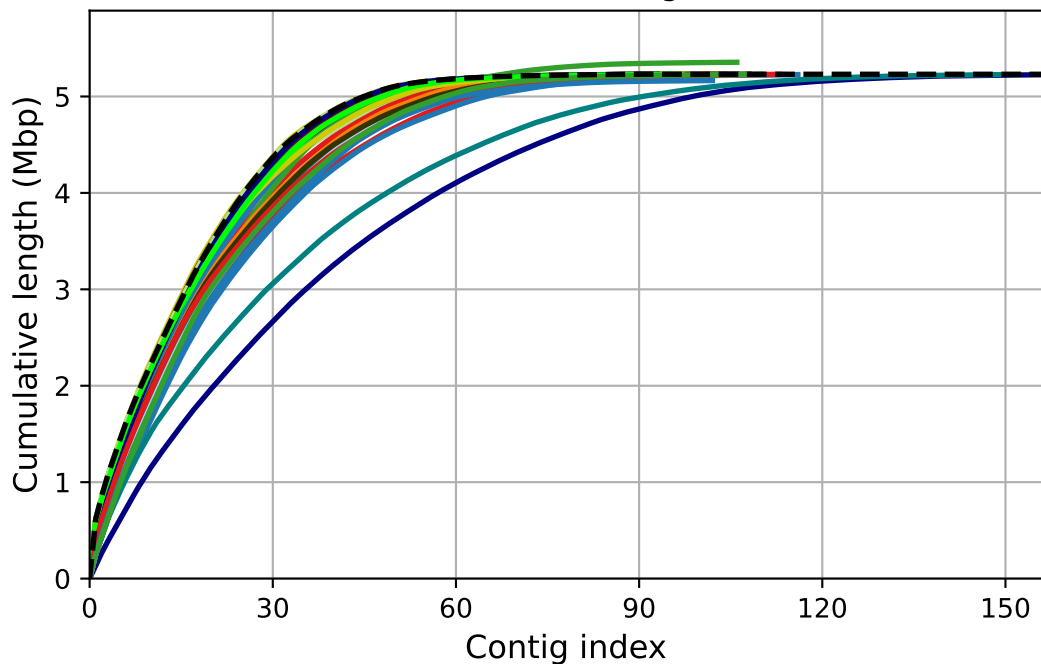


NGx

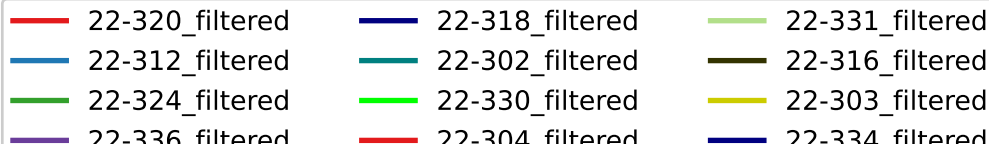
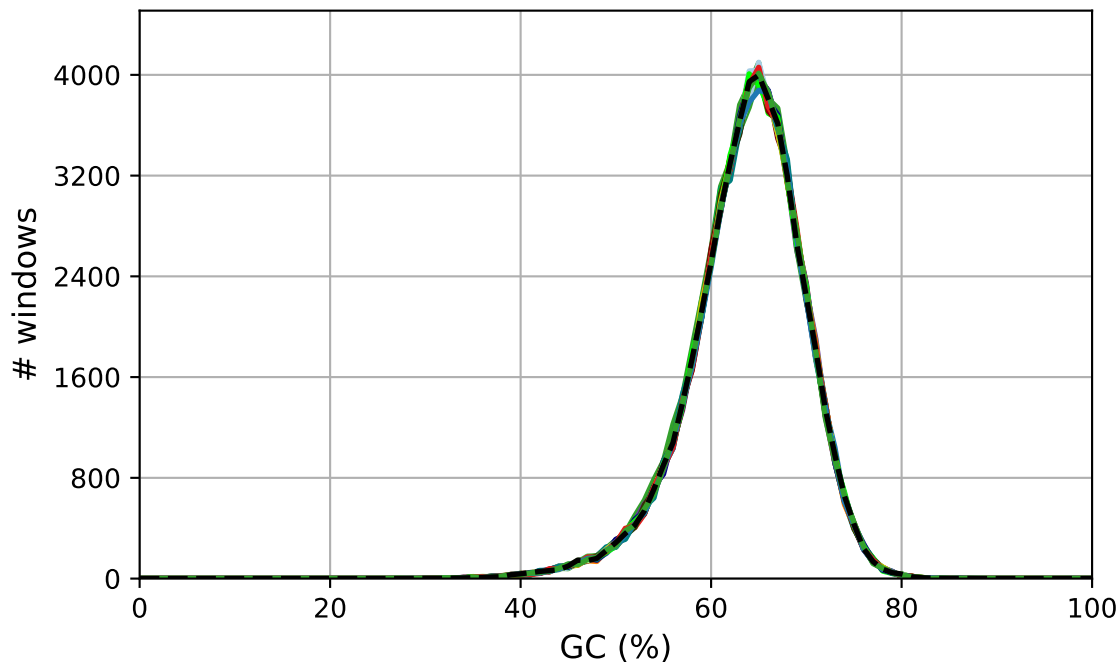


- | | | |
|-----------------|-----------------|-----------------|
| 22-320_filtered | 22-318_filtered | 22-331_filtered |
| 22-312_filtered | 22-302_filtered | 22-316_filtered |
| 22-324_filtered | 22-330_filtered | 22-303_filtered |
| 22-336_filtered | 22-304_filtered | 22-334_filtered |

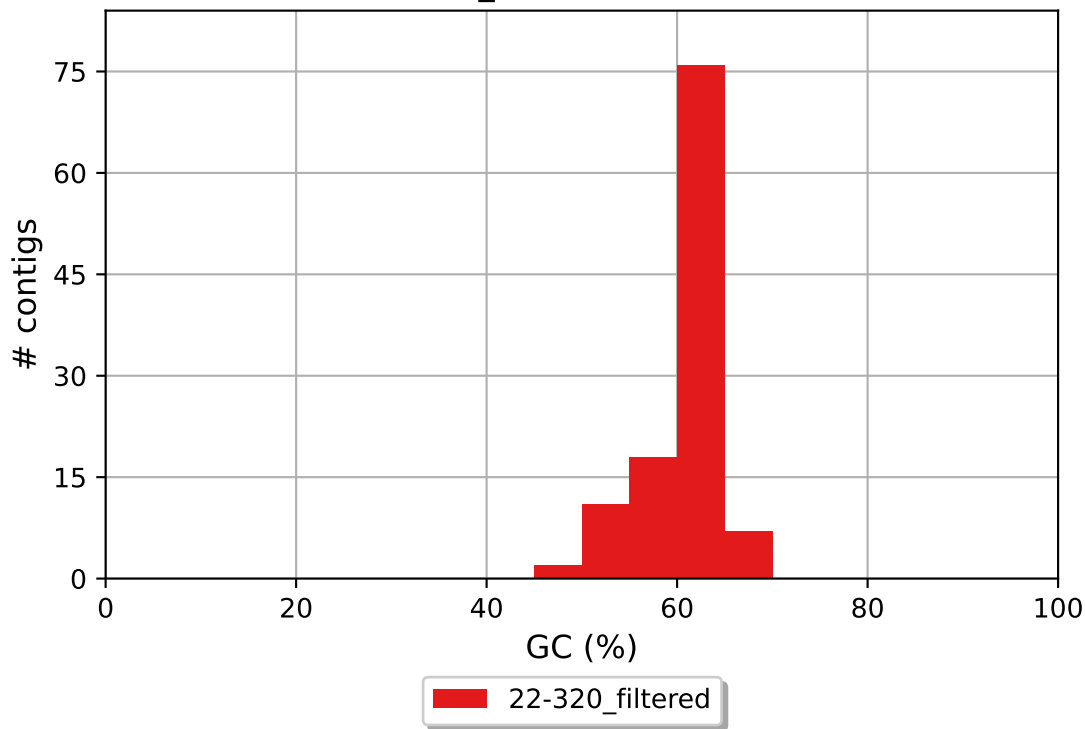
Cumulative length



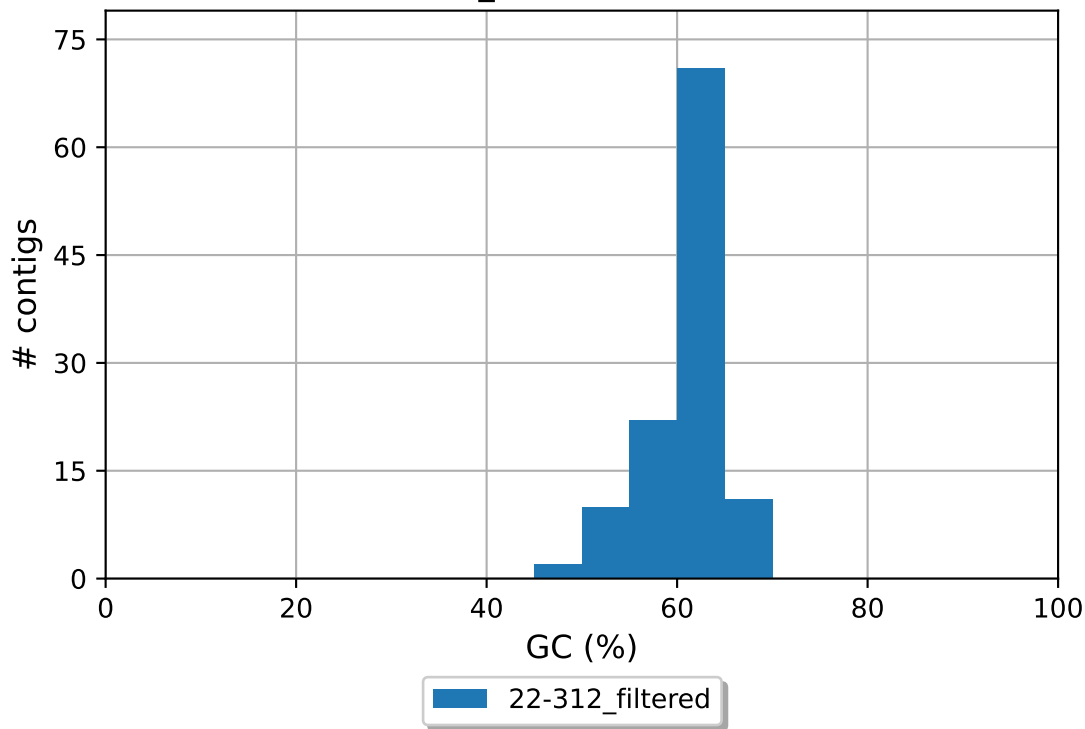
GC content



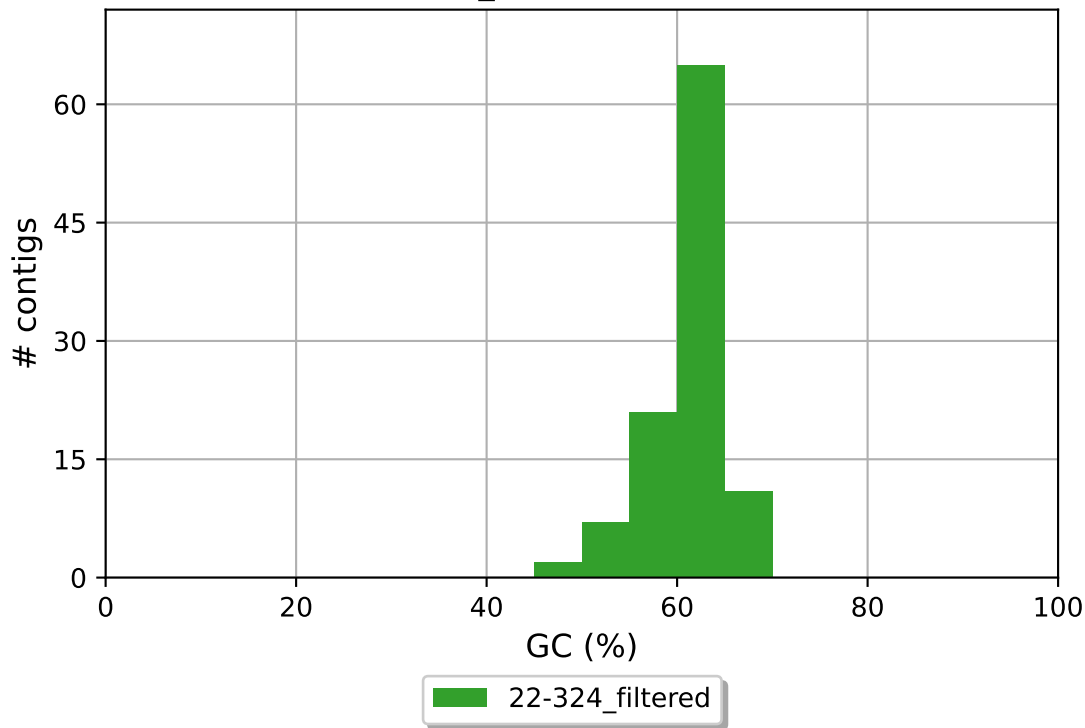
22-320_filtered GC content



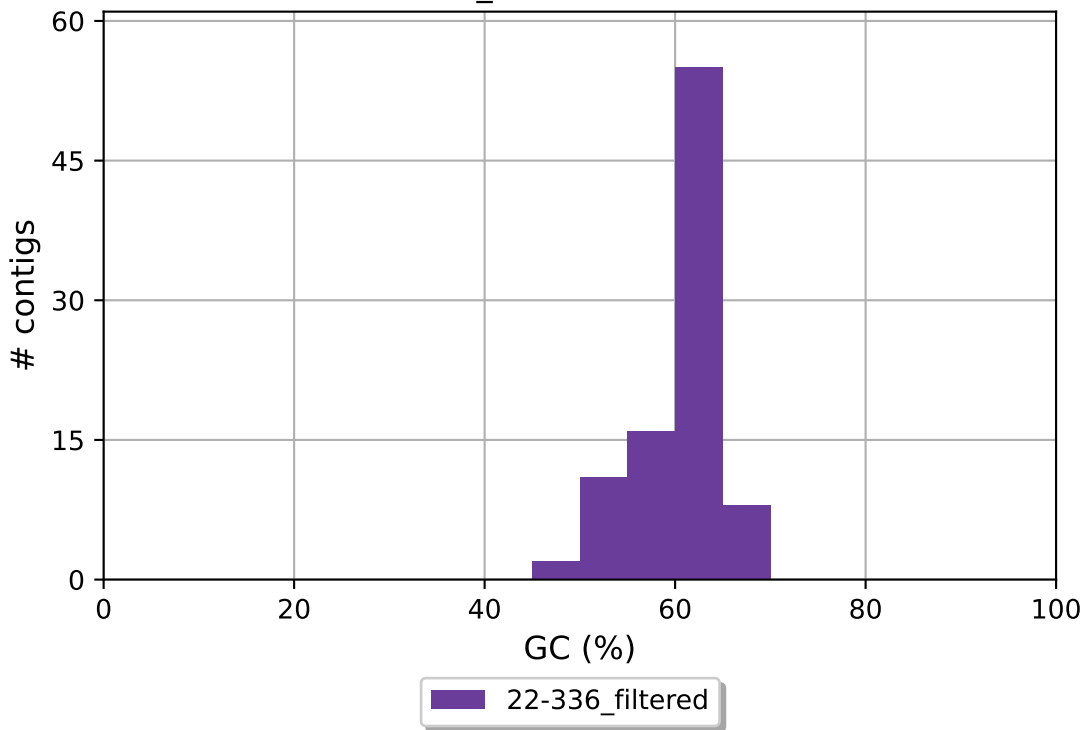
22-312_filtered GC content



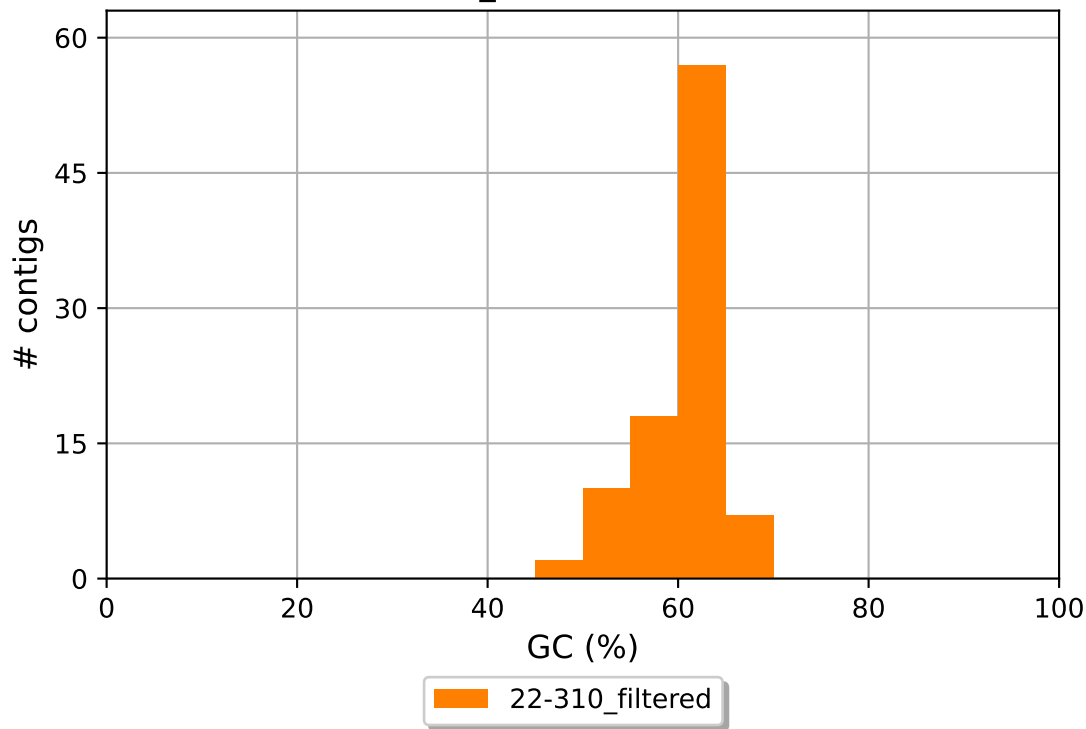
22-324_filtered GC content



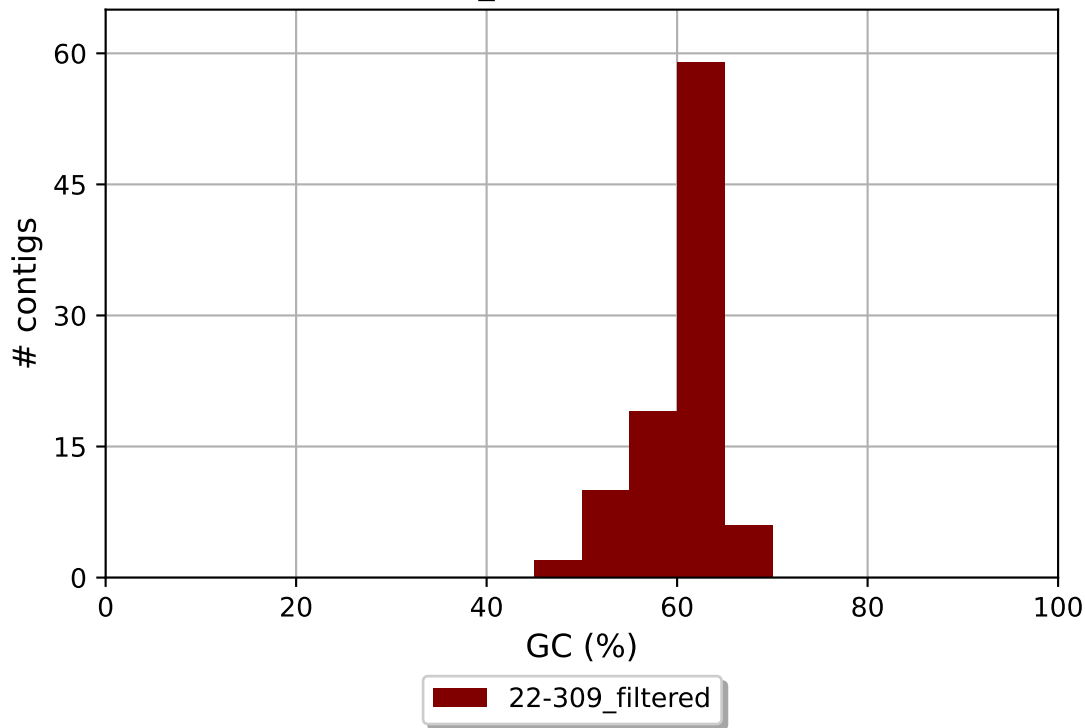
22-336_filtered GC content



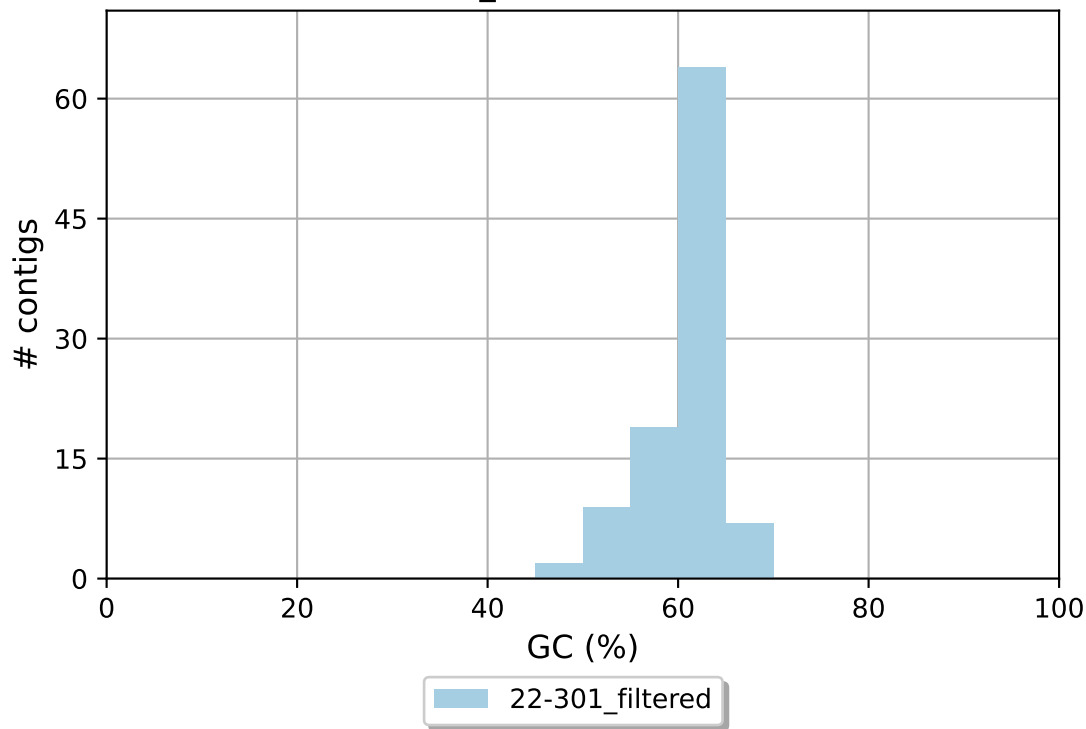
22-310_filtered GC content



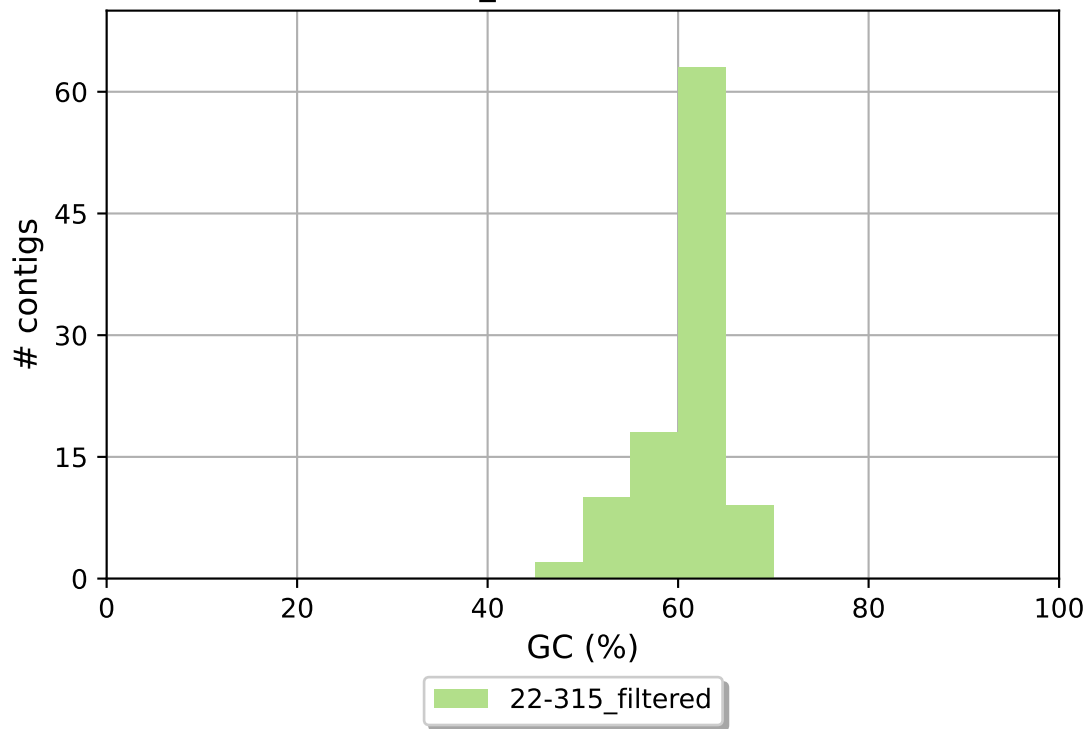
22-309_filtered GC content



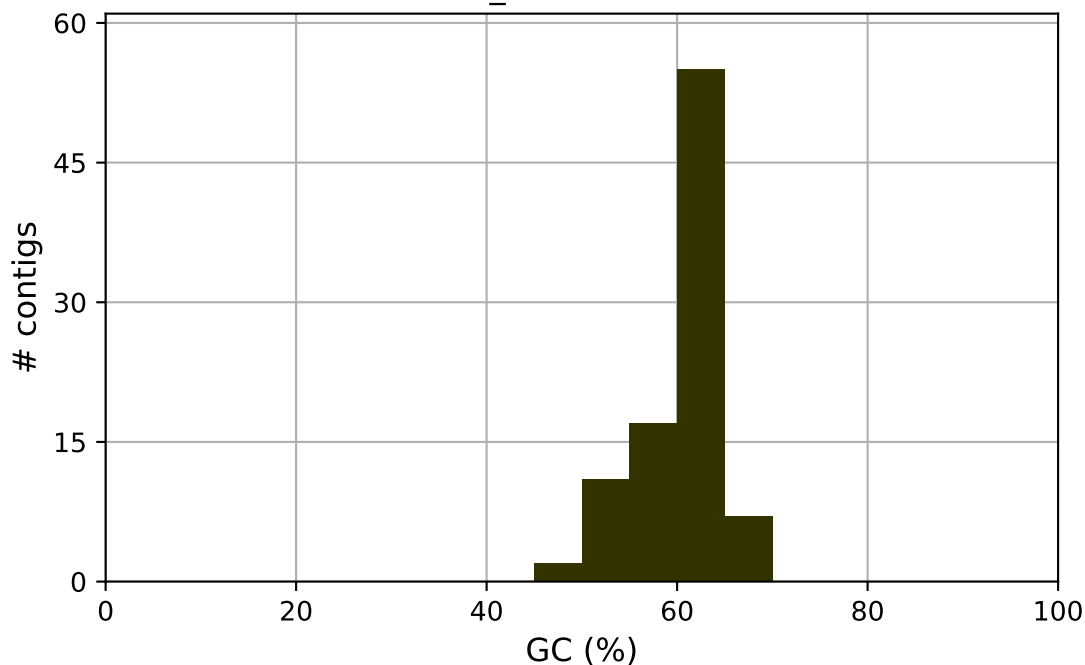
22-301_filtered GC content



22-315_filtered GC content

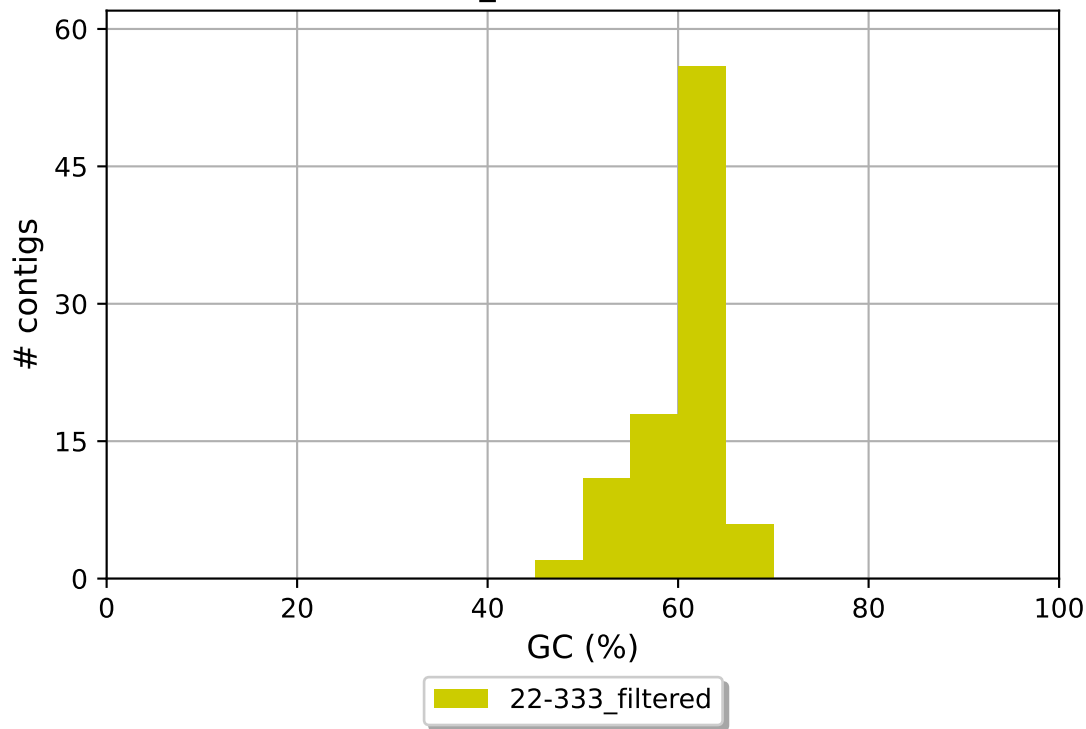


22-329B_filtered GC content

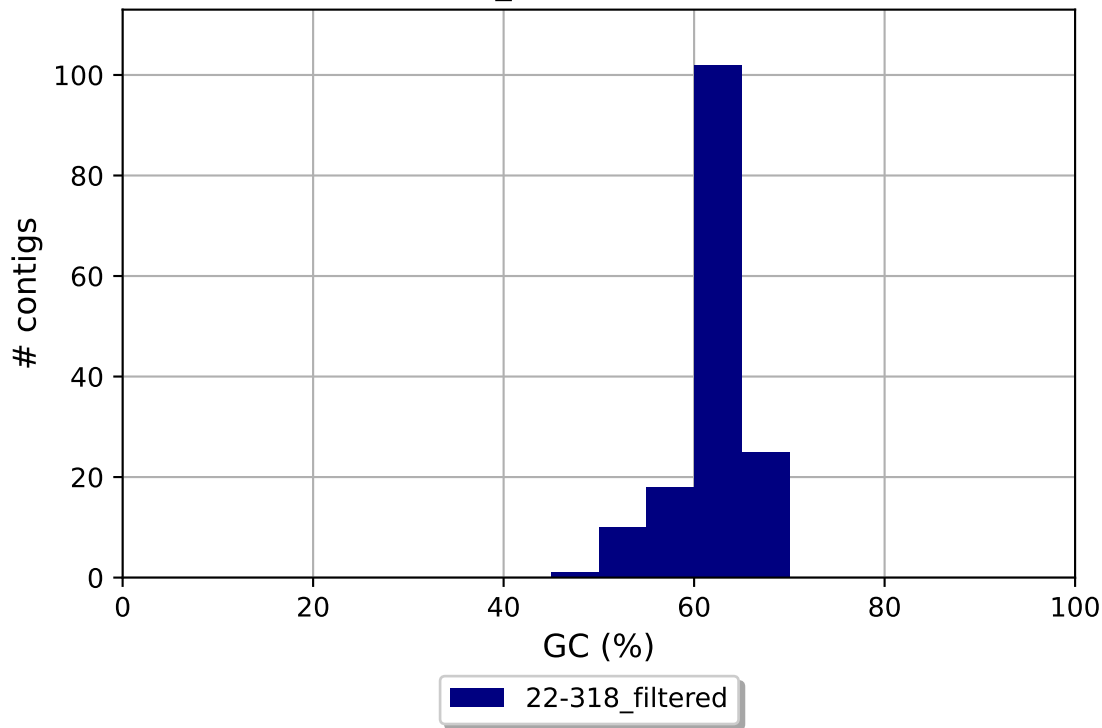


22-329B_filtered

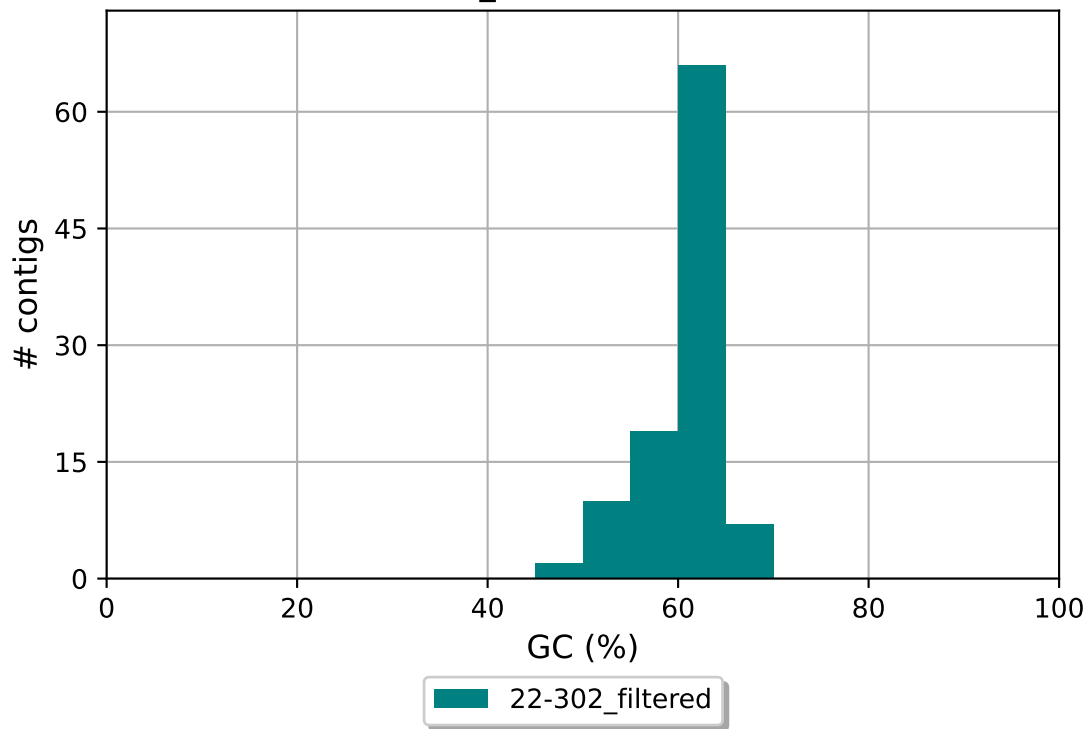
22-333_filtered GC content



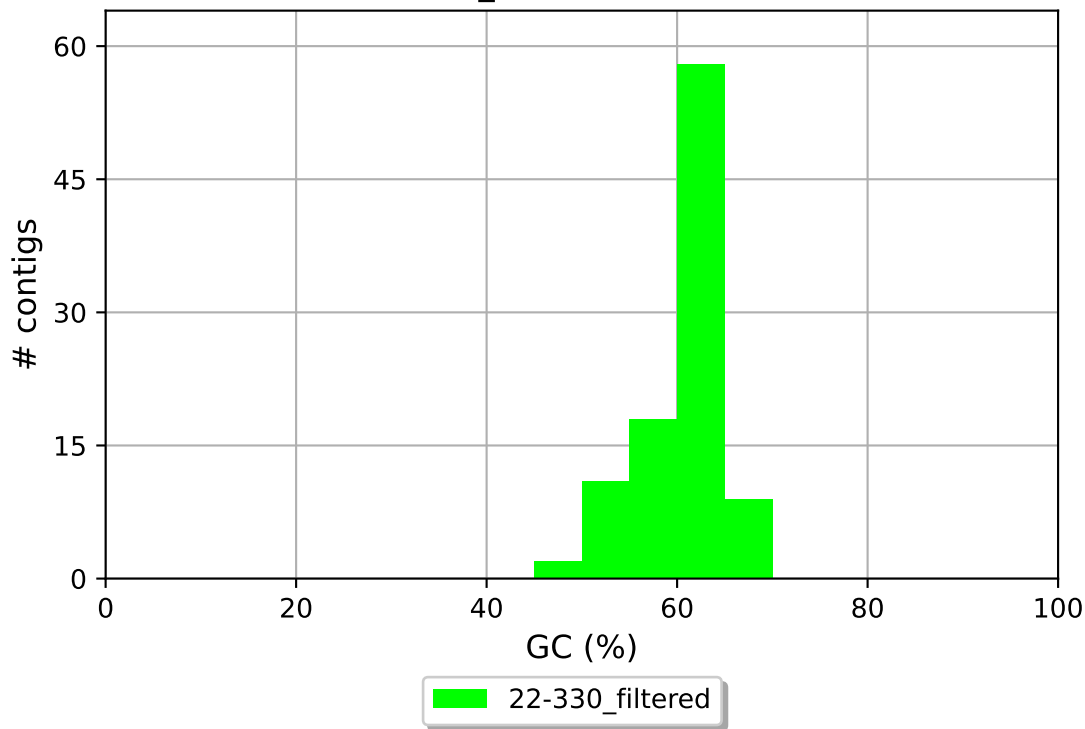
22-318_filtered GC content



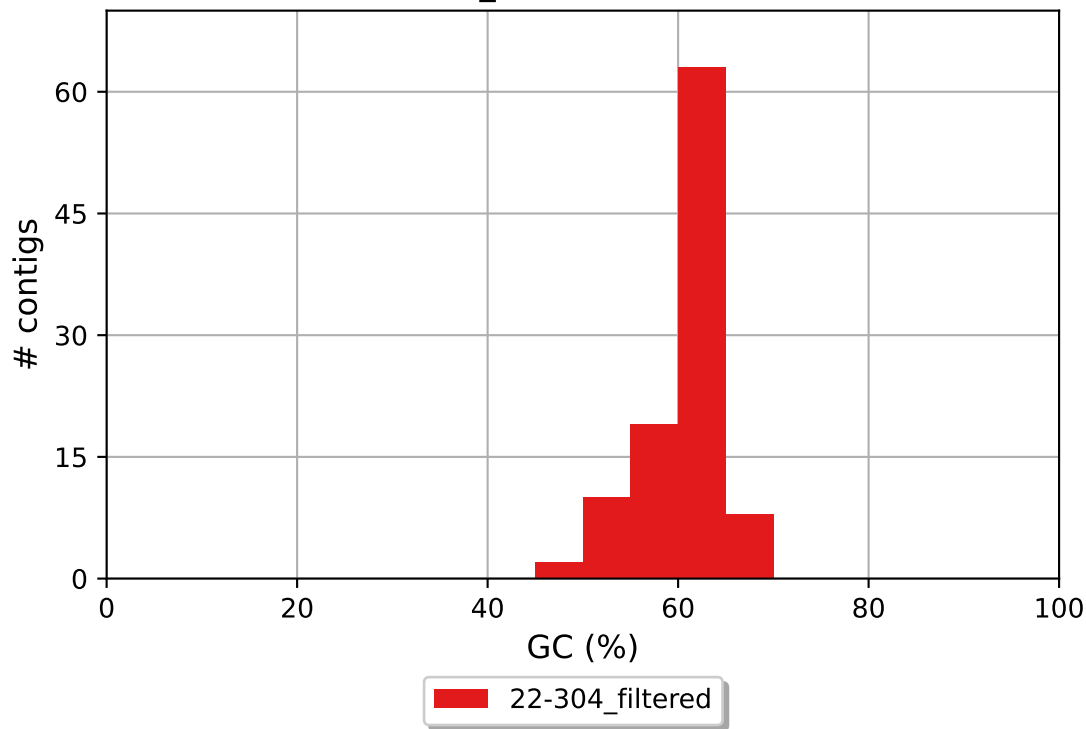
22-302_filtered GC content



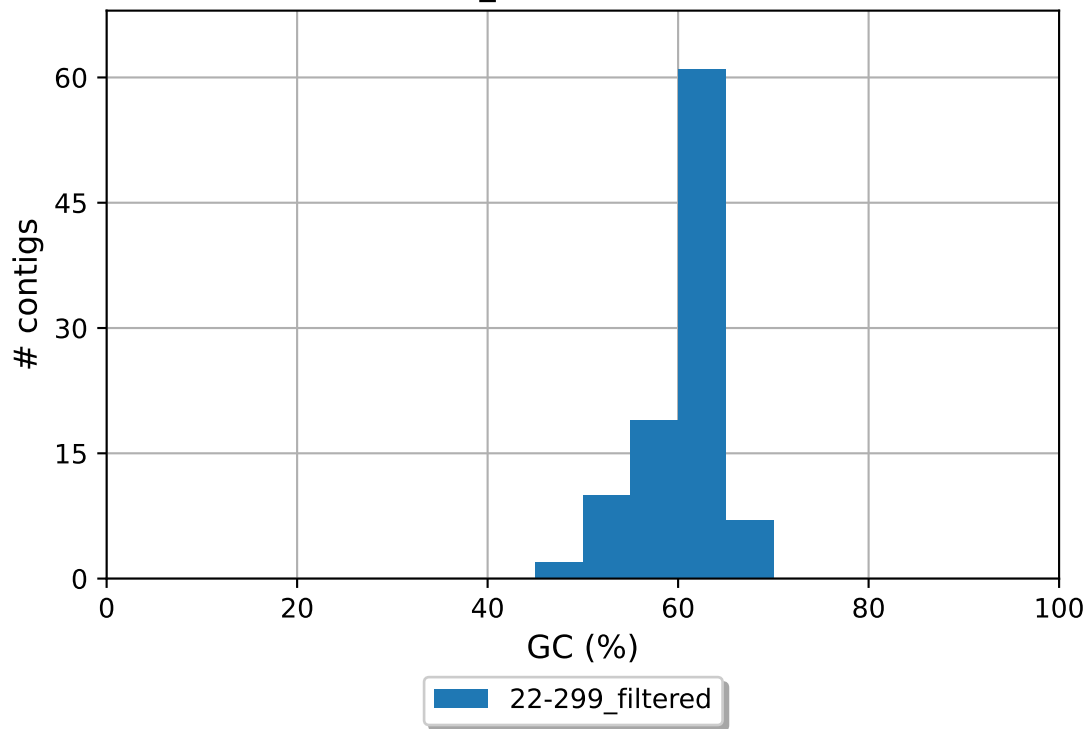
22-330_filtered GC content



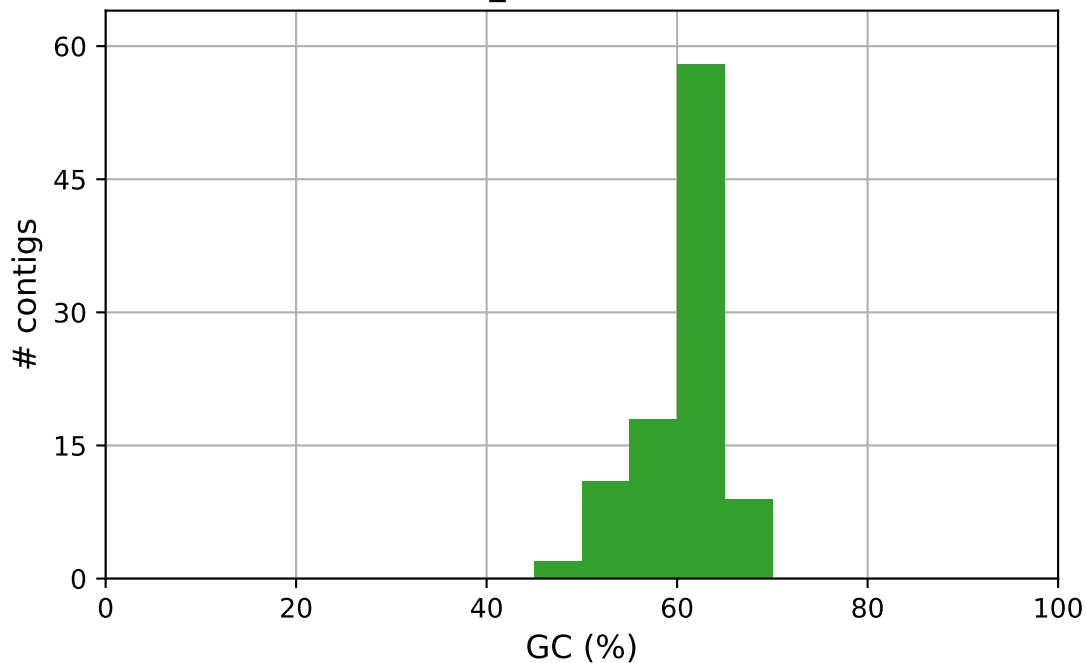
22-304_filtered GC content



22-299_filtered GC content

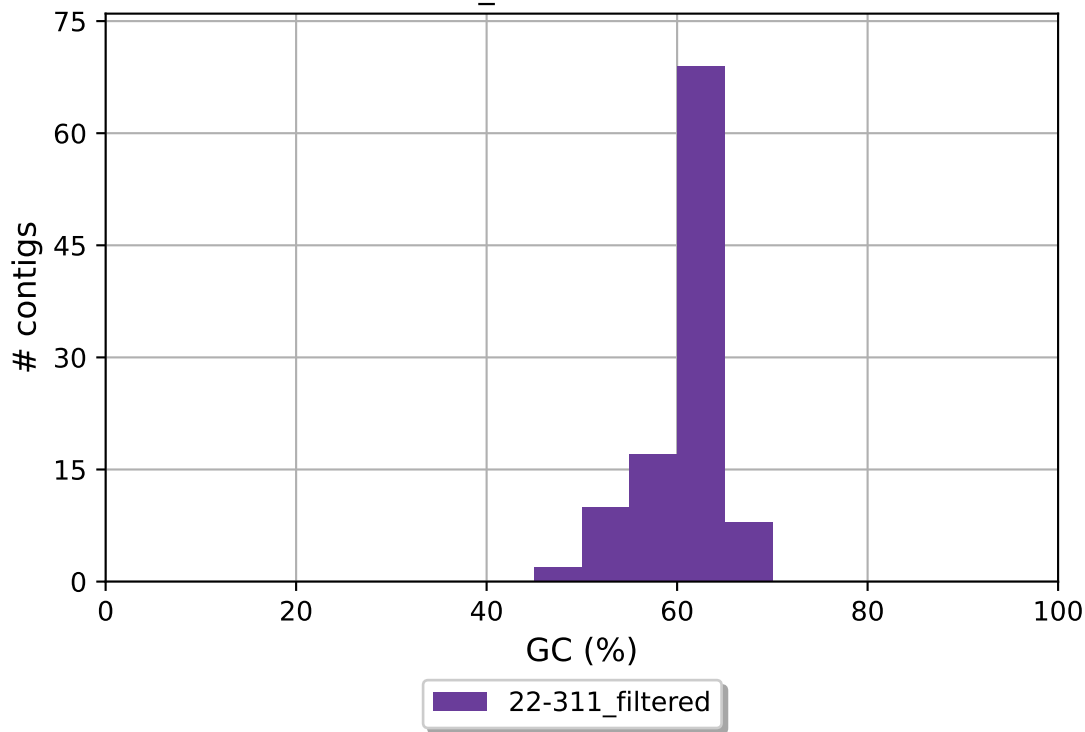


22-329A_filtered GC content

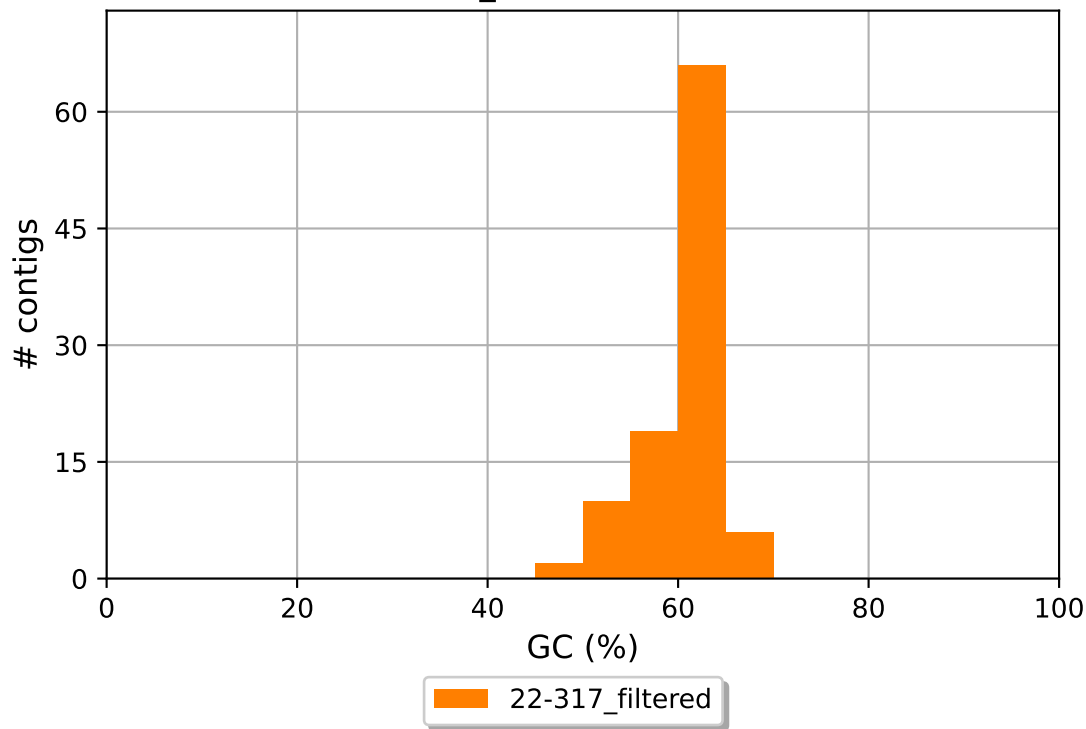


22-329A_filtered

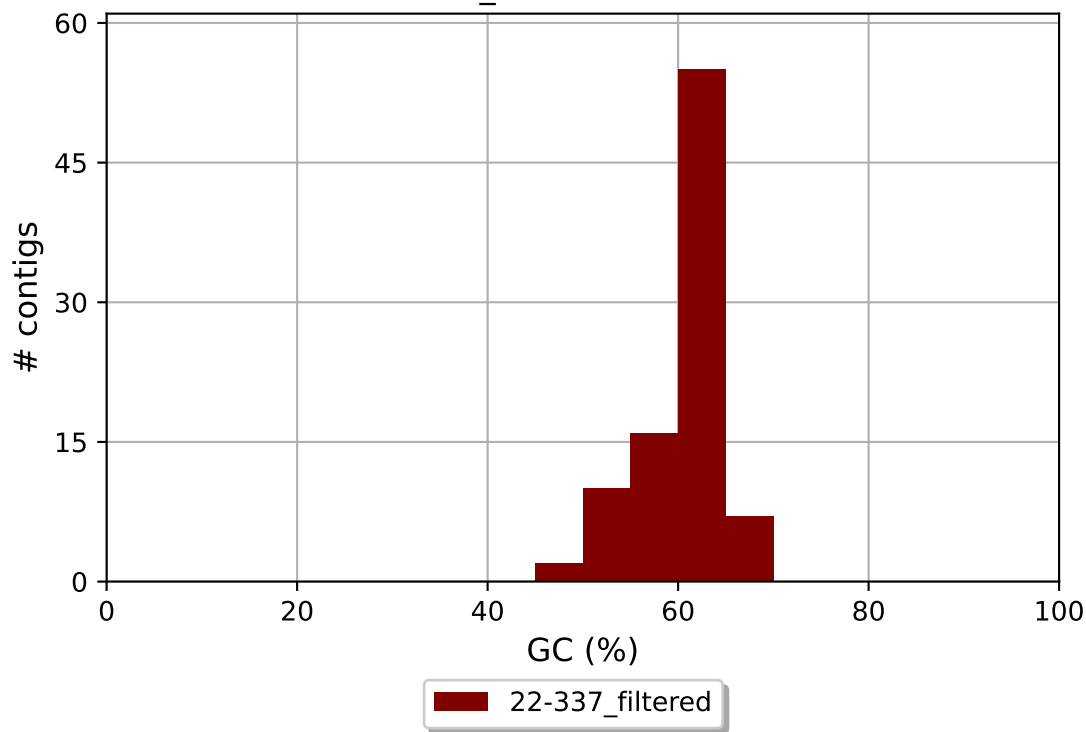
22-311_filtered GC content



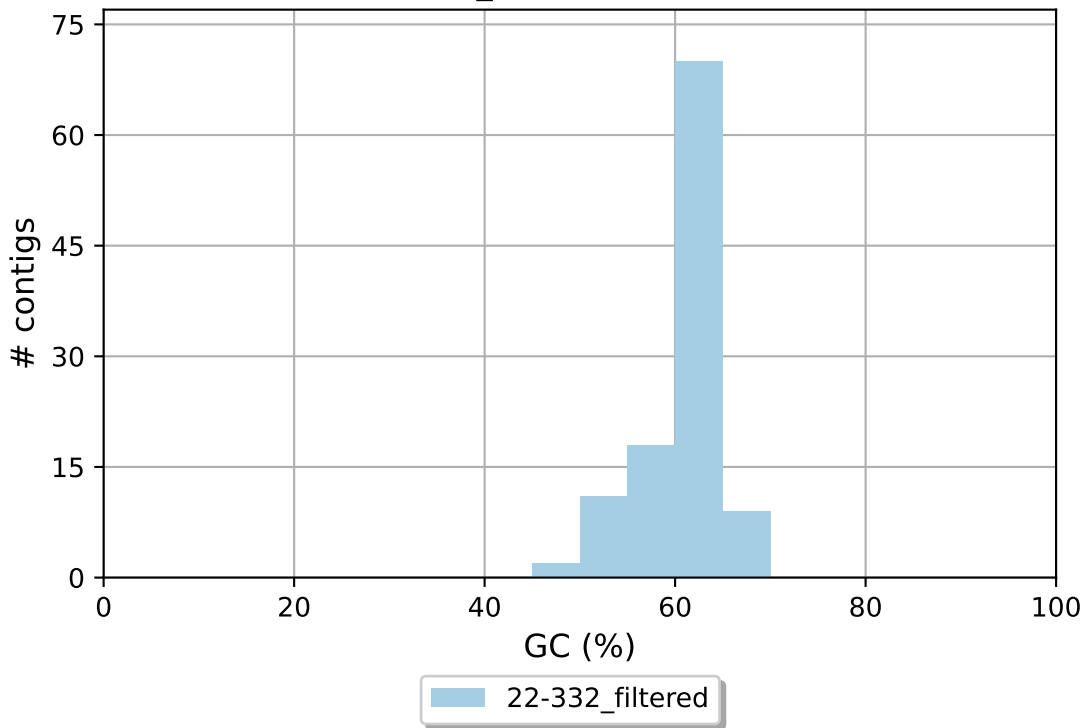
22-317_filtered GC content



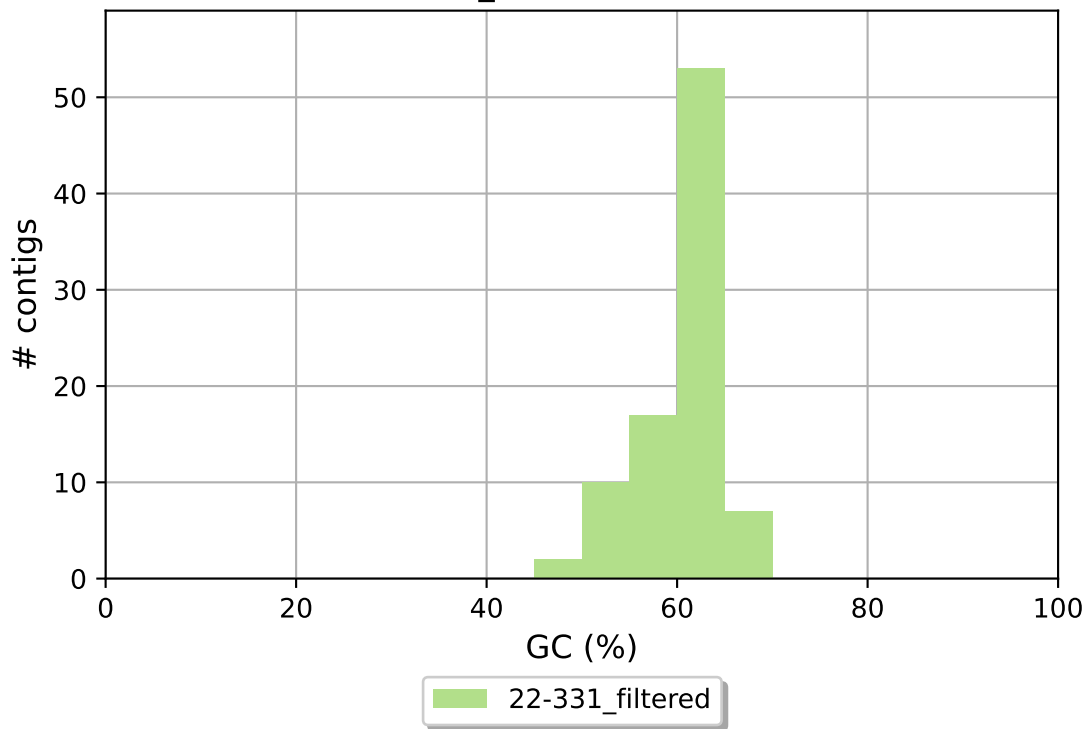
22-337_filtered GC content



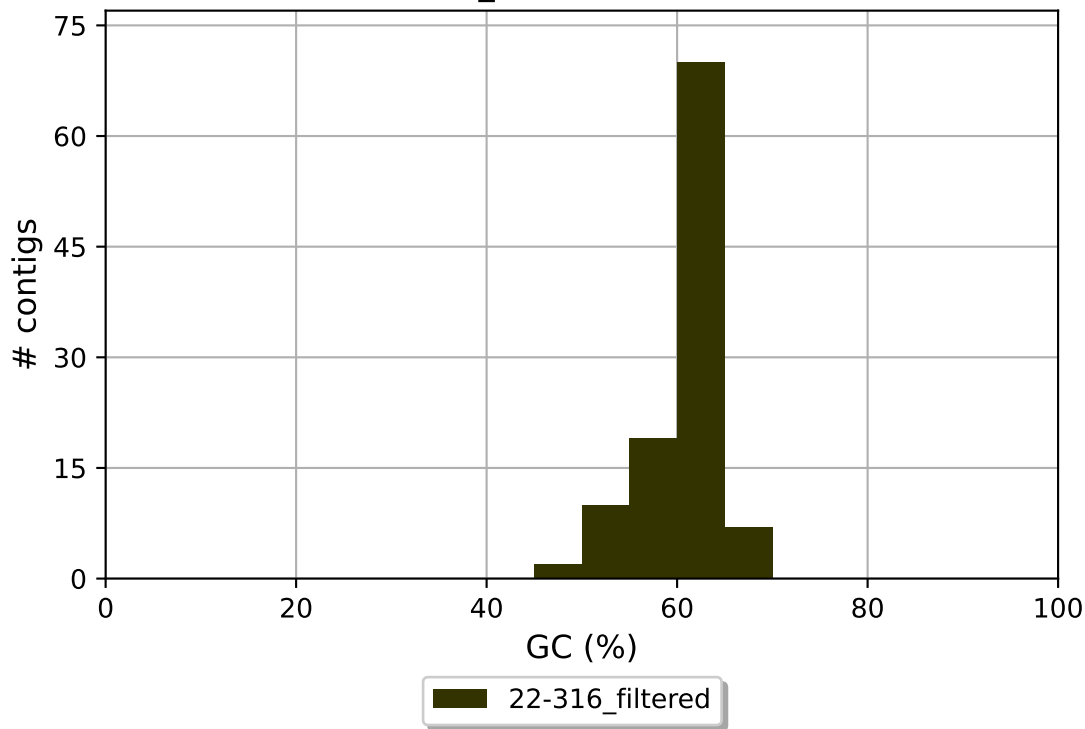
22-332_filtered GC content



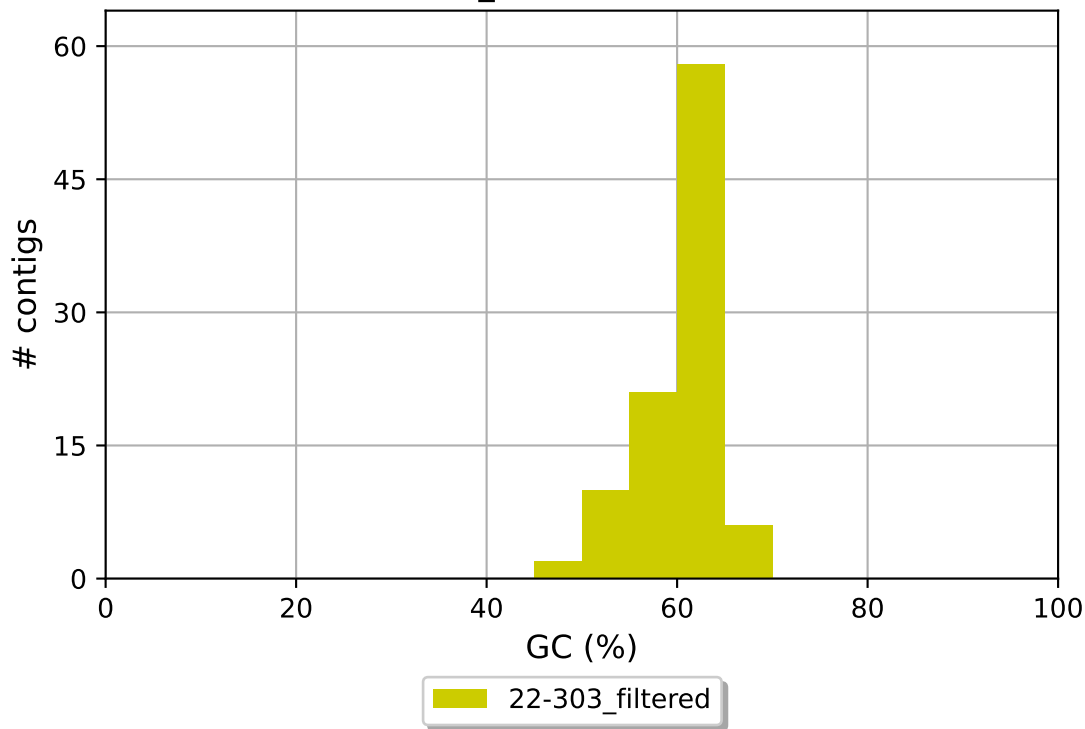
22-331_filtered GC content



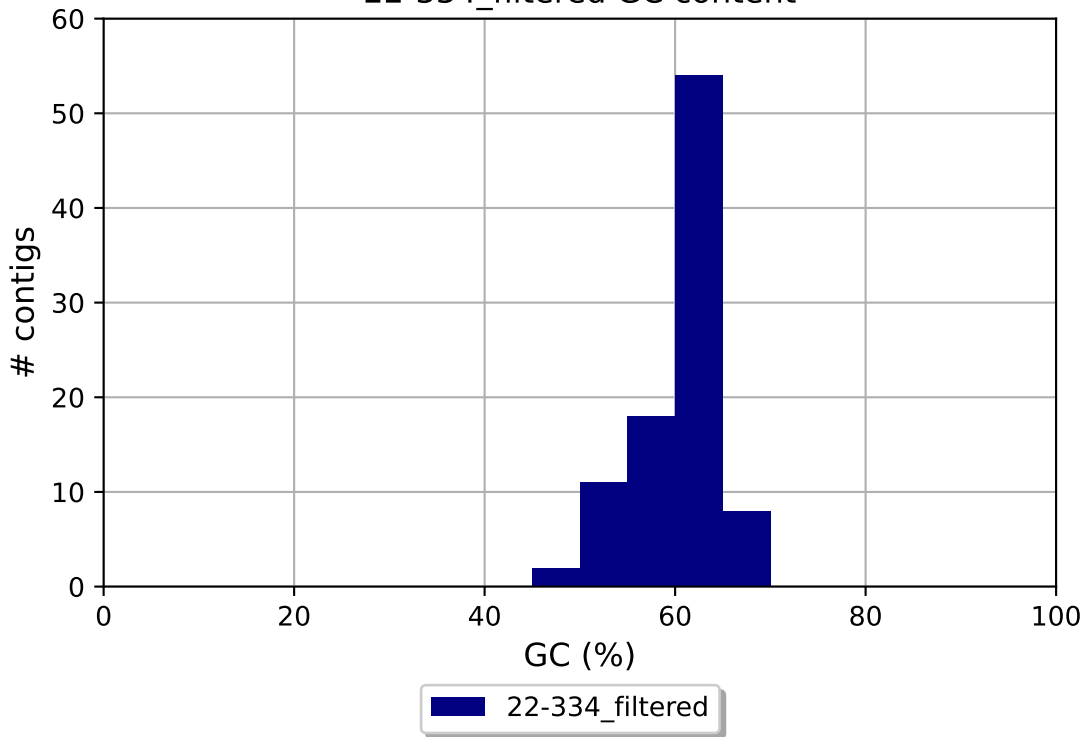
22-316_filtered GC content



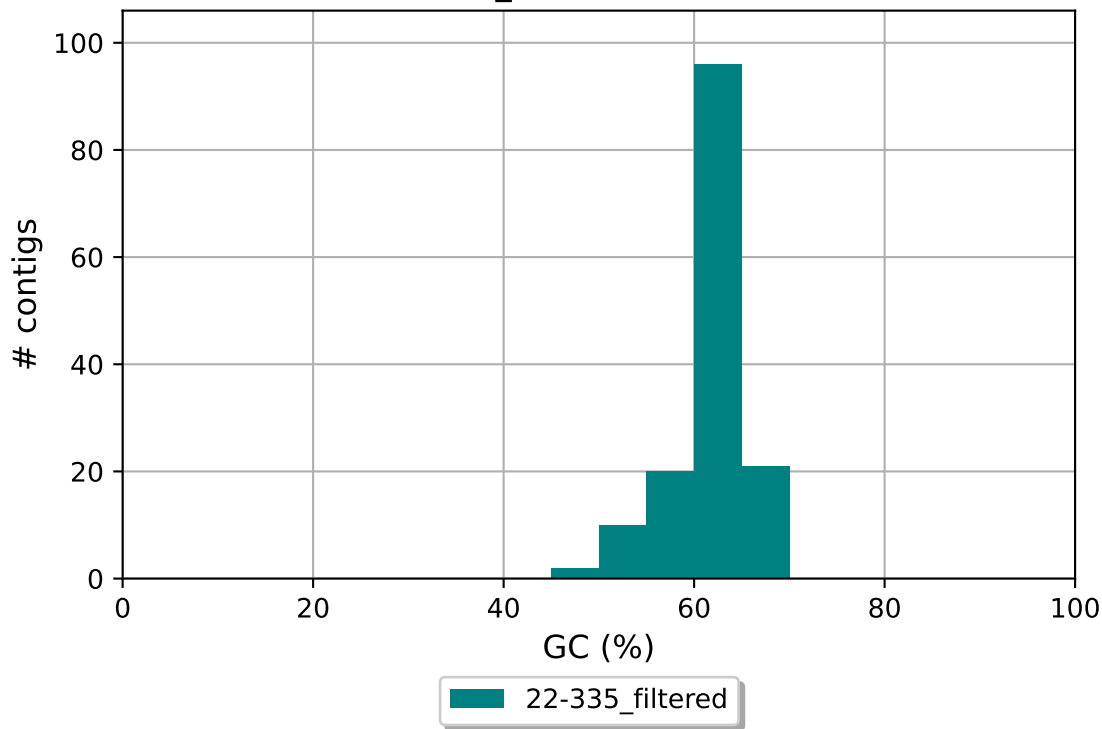
22-303_filtered GC content



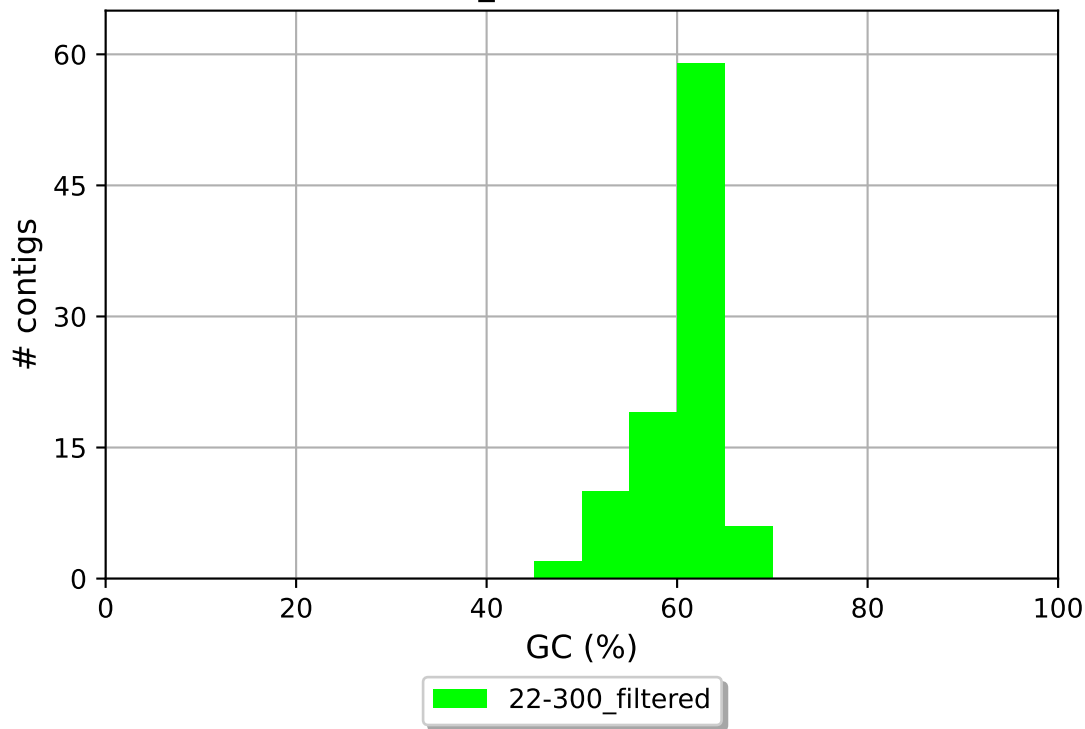
22-334_filtered GC content



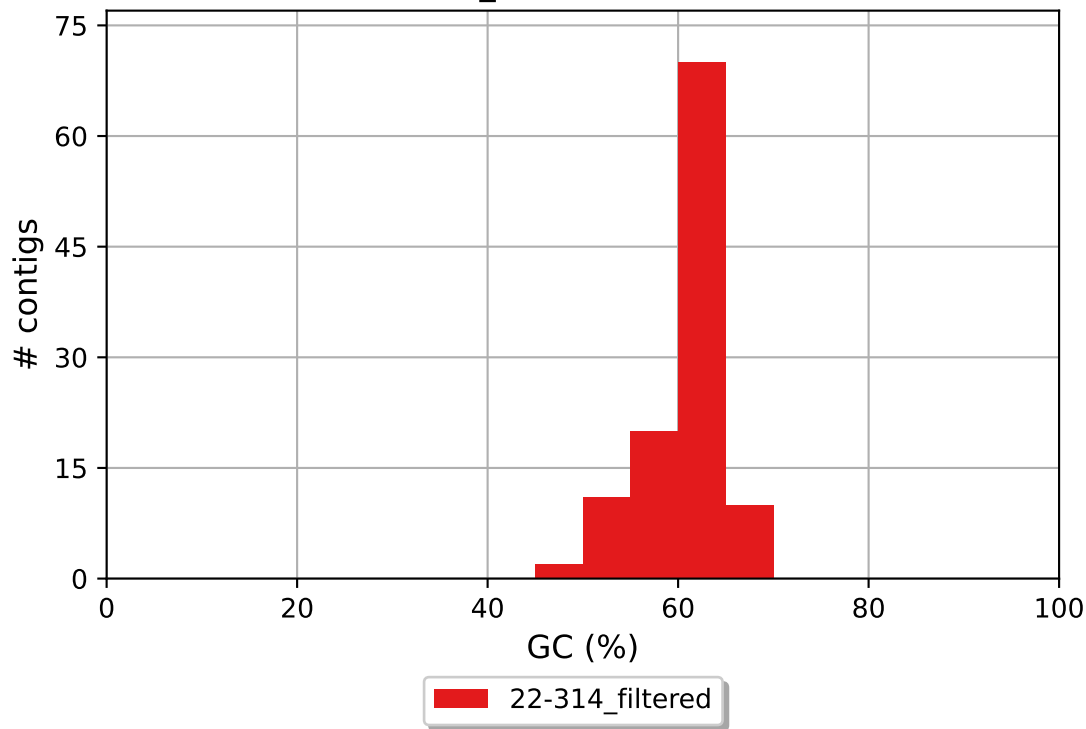
22-335_filtered GC content



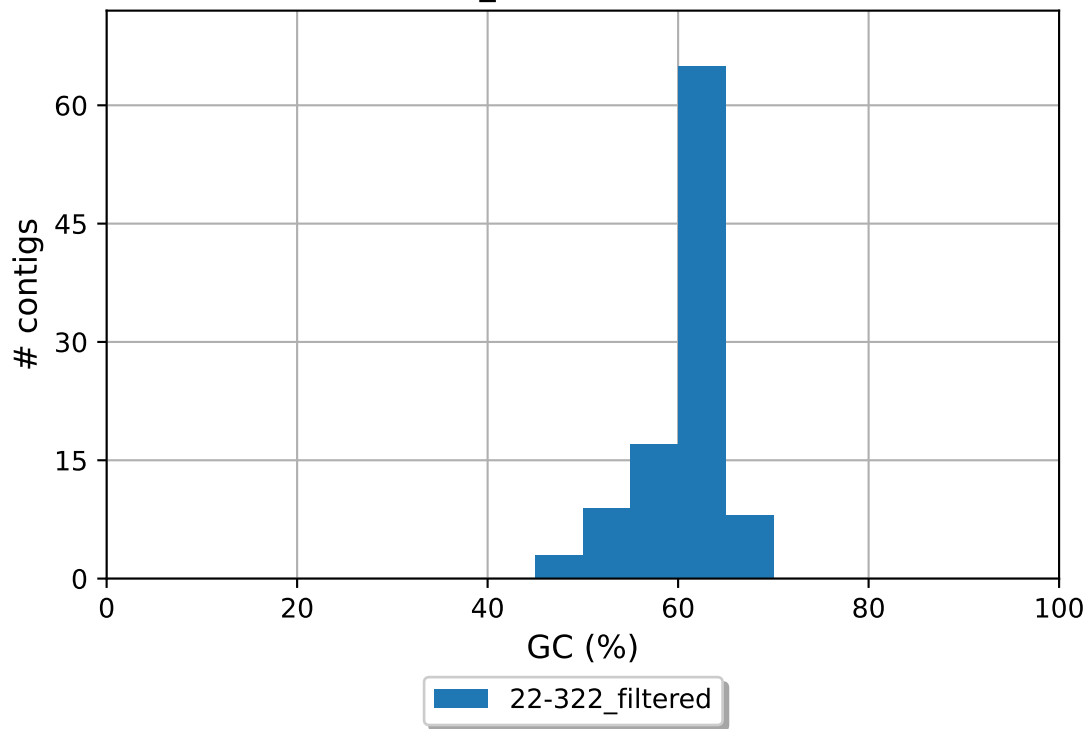
22-300_filtered GC content



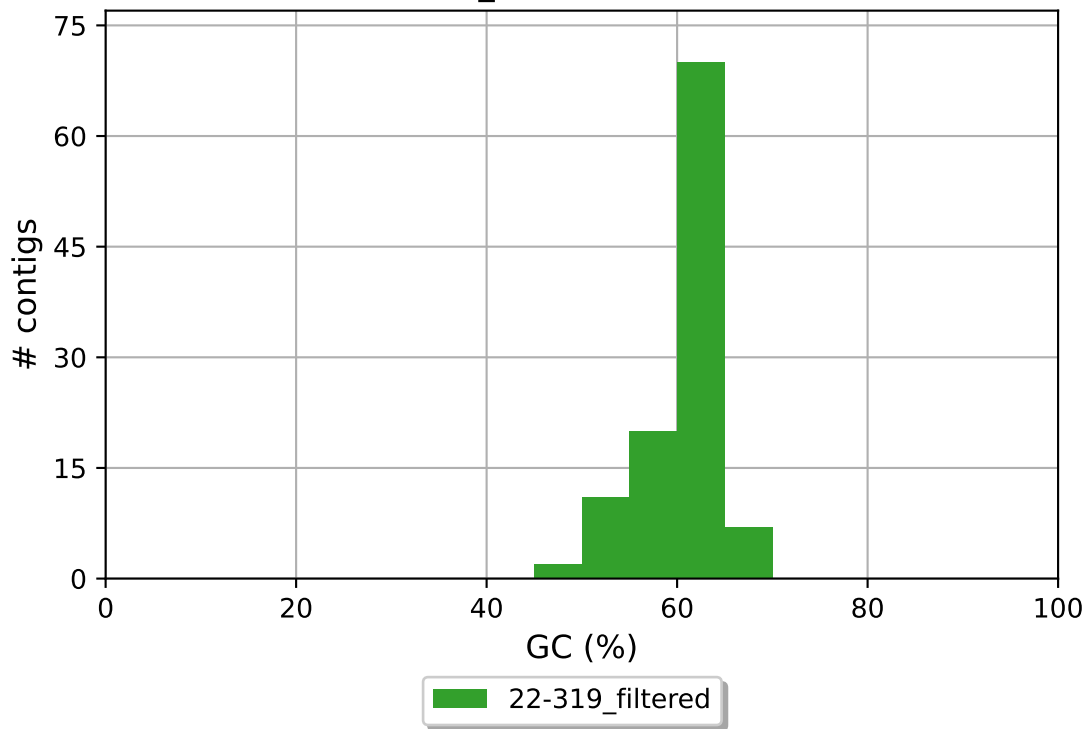
22-314_filtered GC content



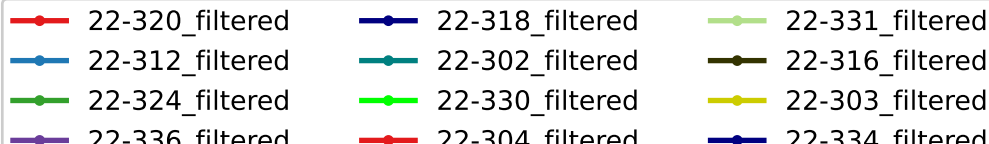
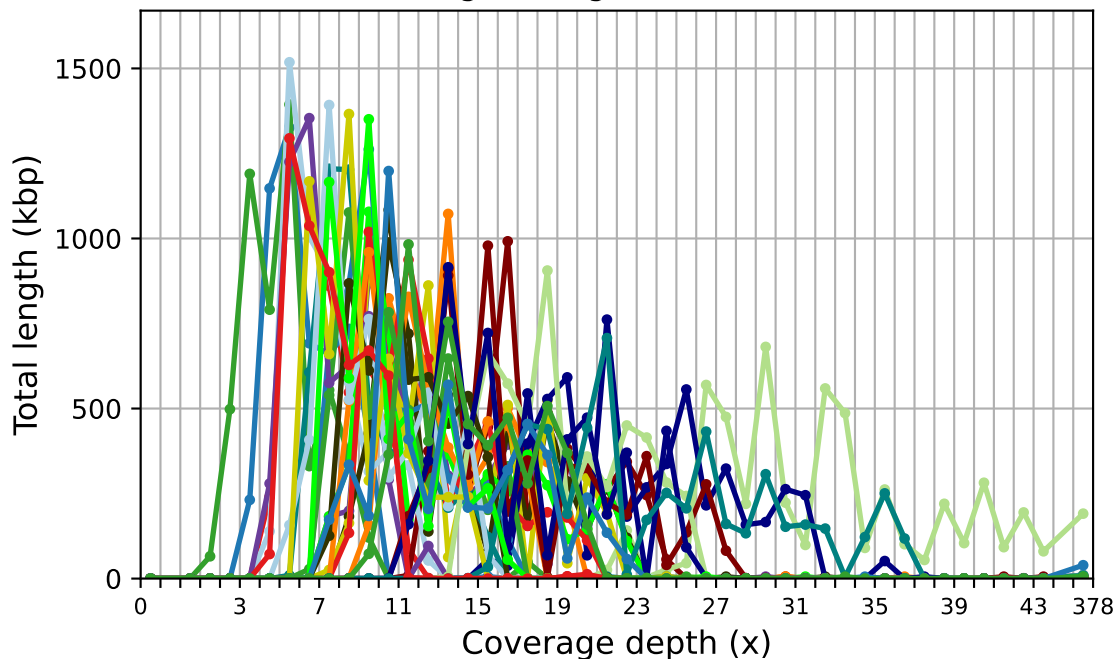
22-322_filtered GC content



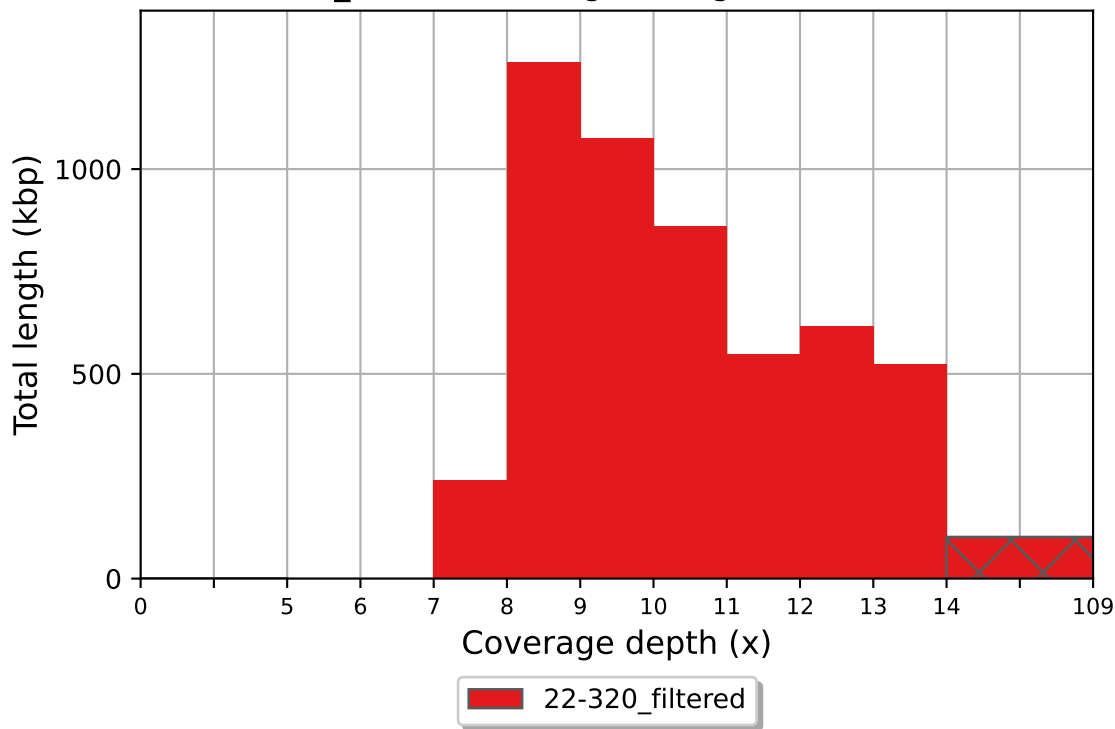
22-319_filtered GC content



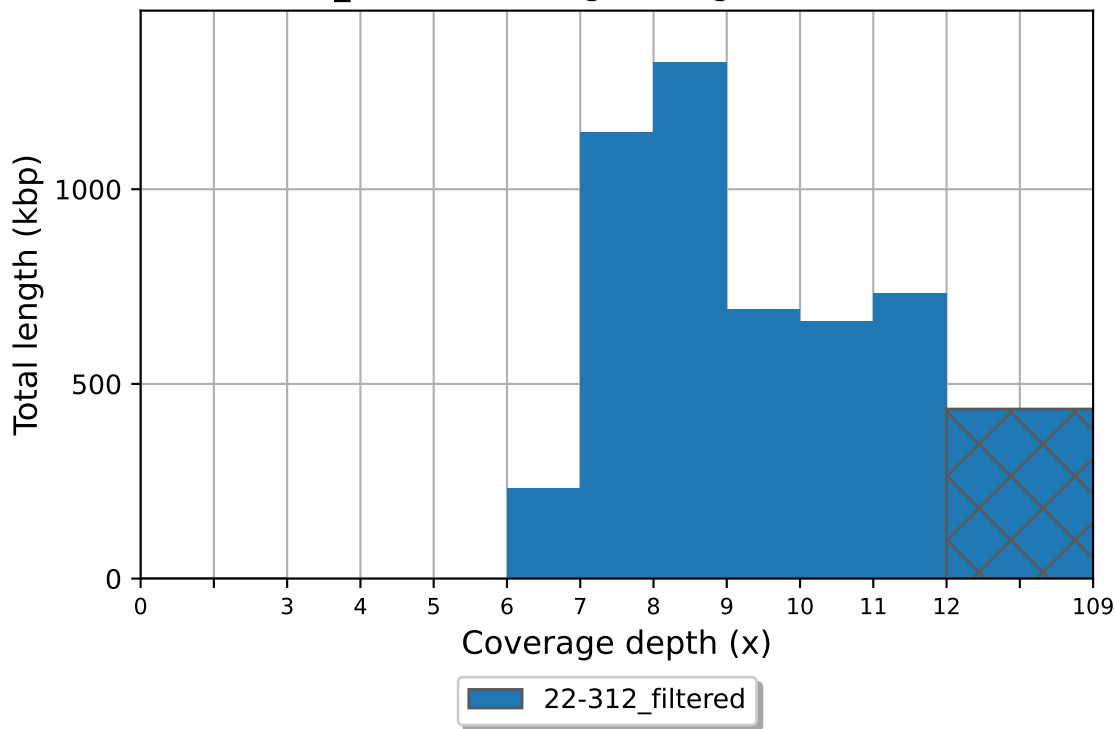
Coverage histogram (bin size: 1x)



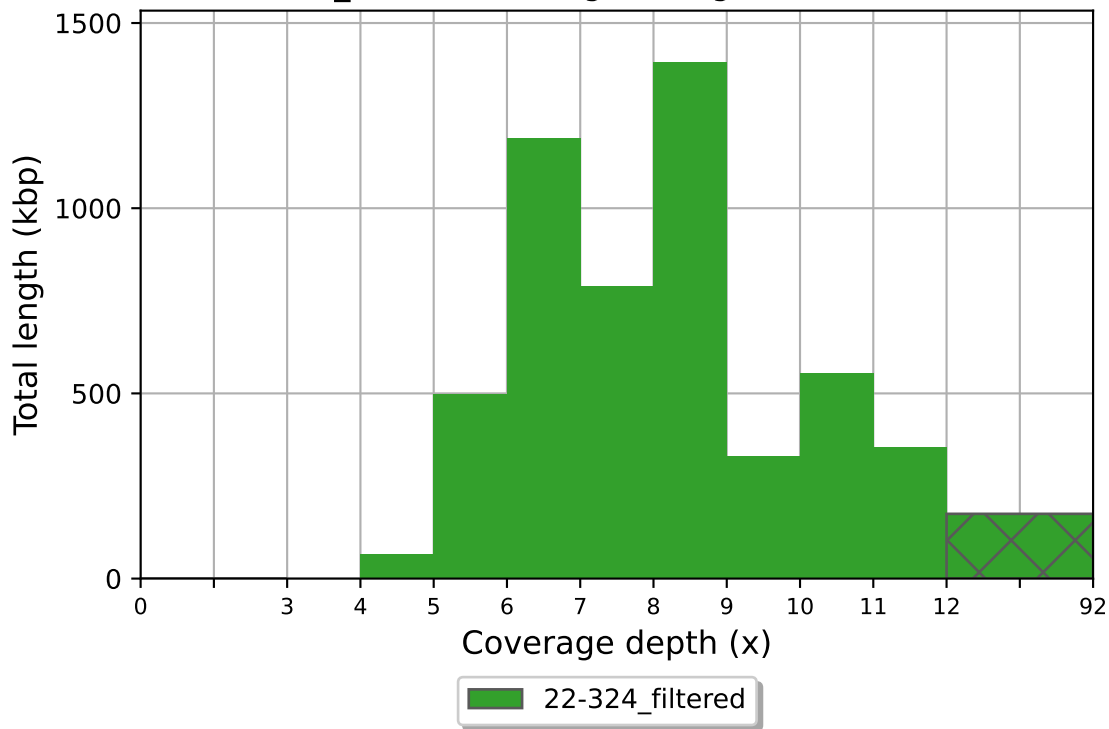
22-320_filtered coverage histogram (bin size: 1x)



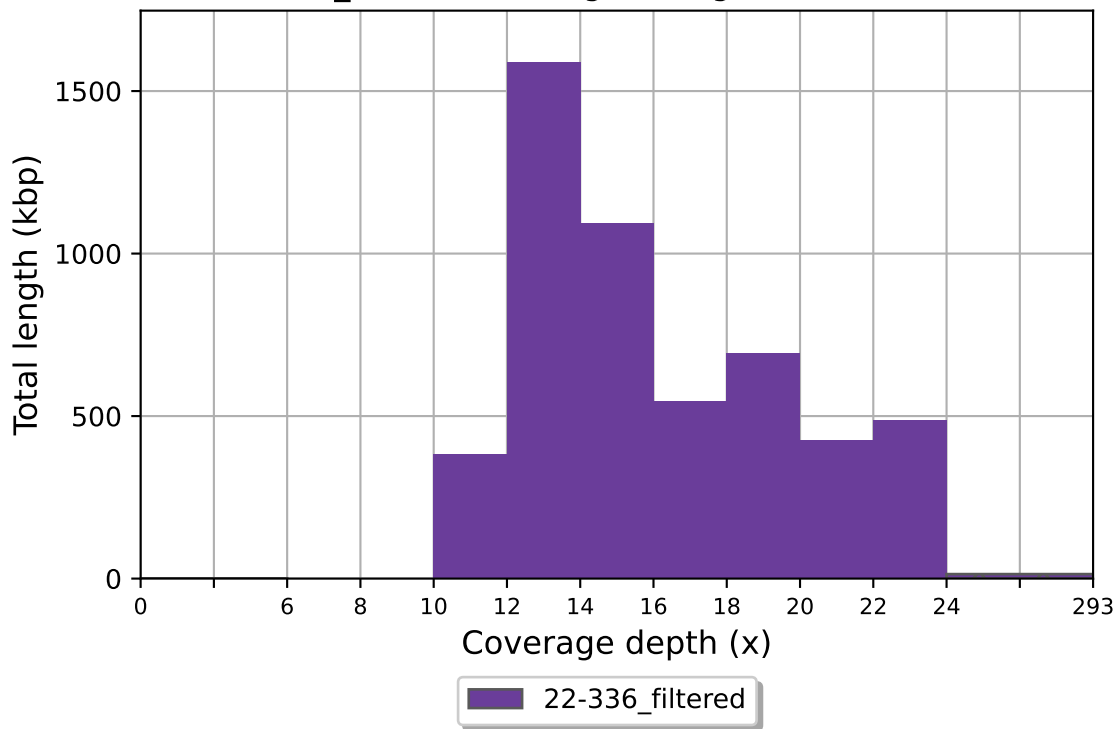
22-312_filtered coverage histogram (bin size: 1x)



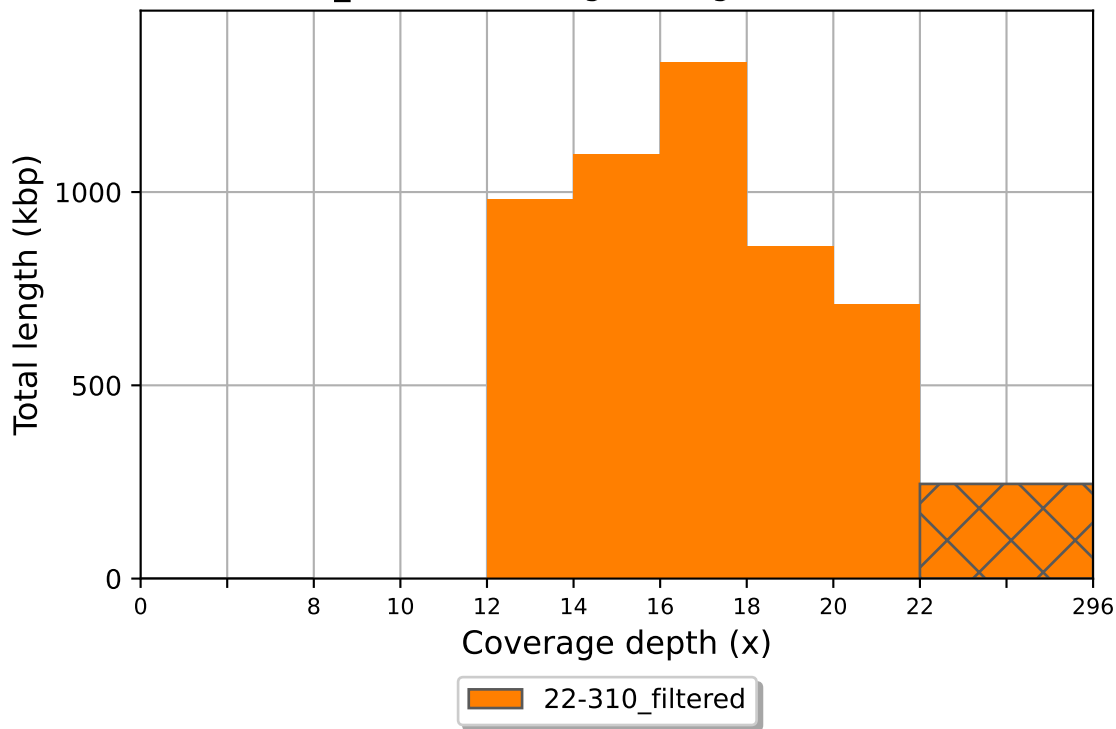
22-324_filtered coverage histogram (bin size: 1x)



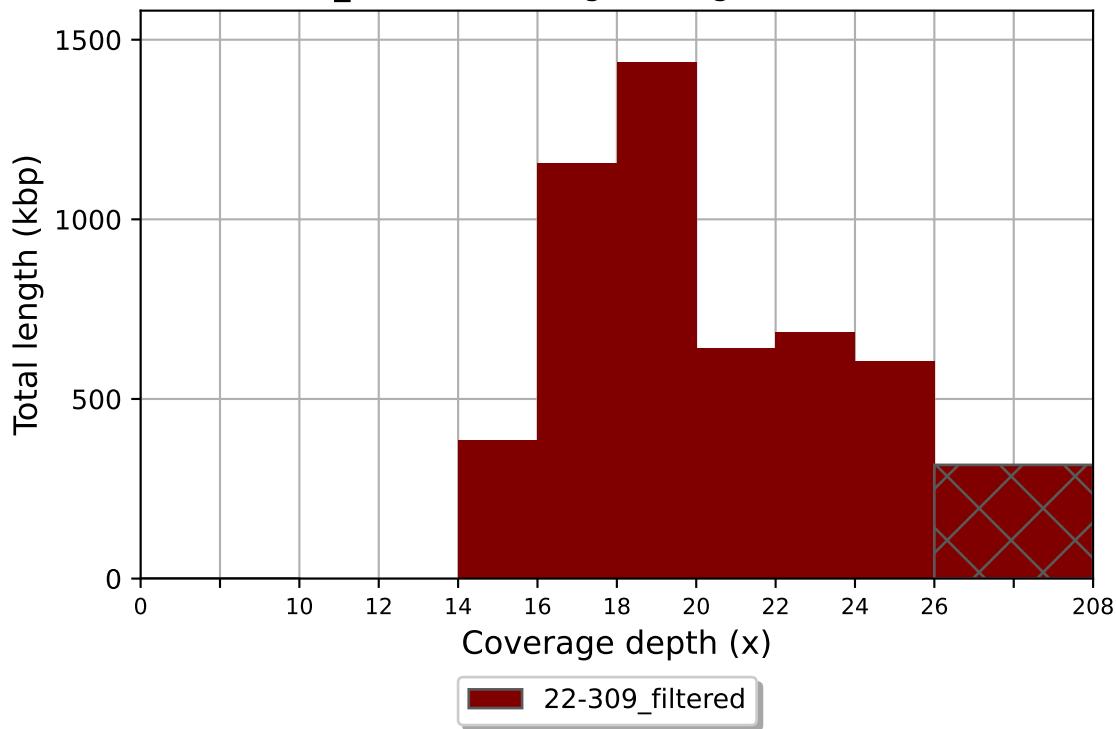
22-336_filtered coverage histogram (bin size: 2x)



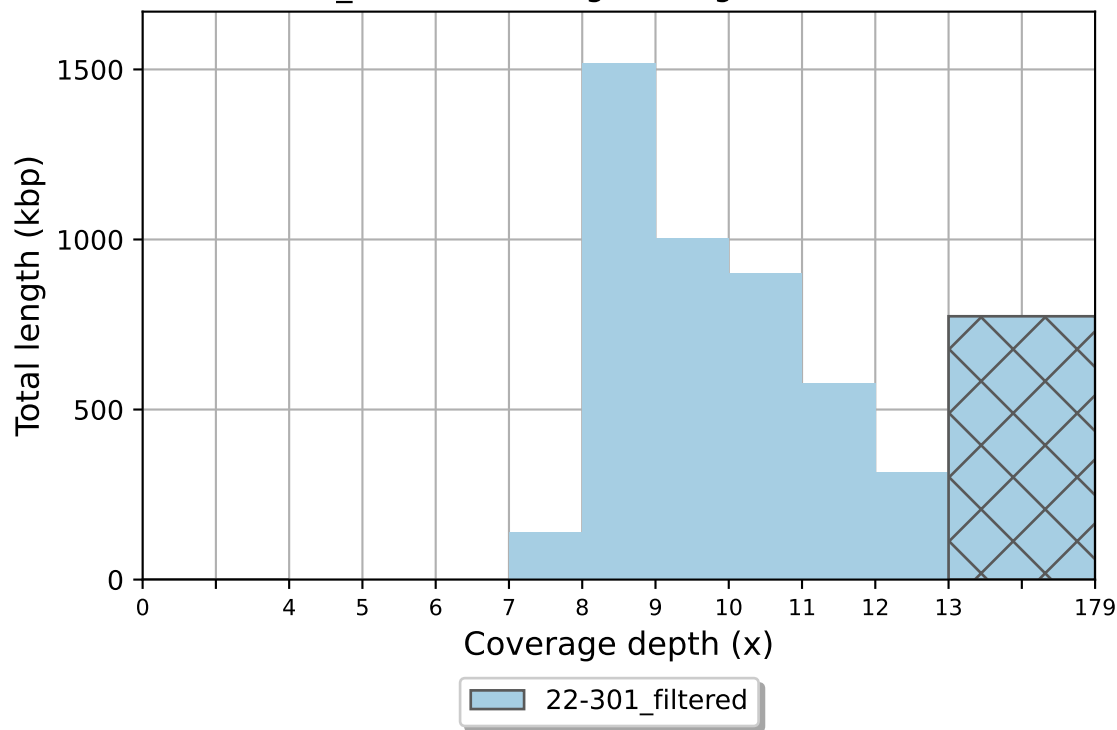
22-310_filtered coverage histogram (bin size: 2x)



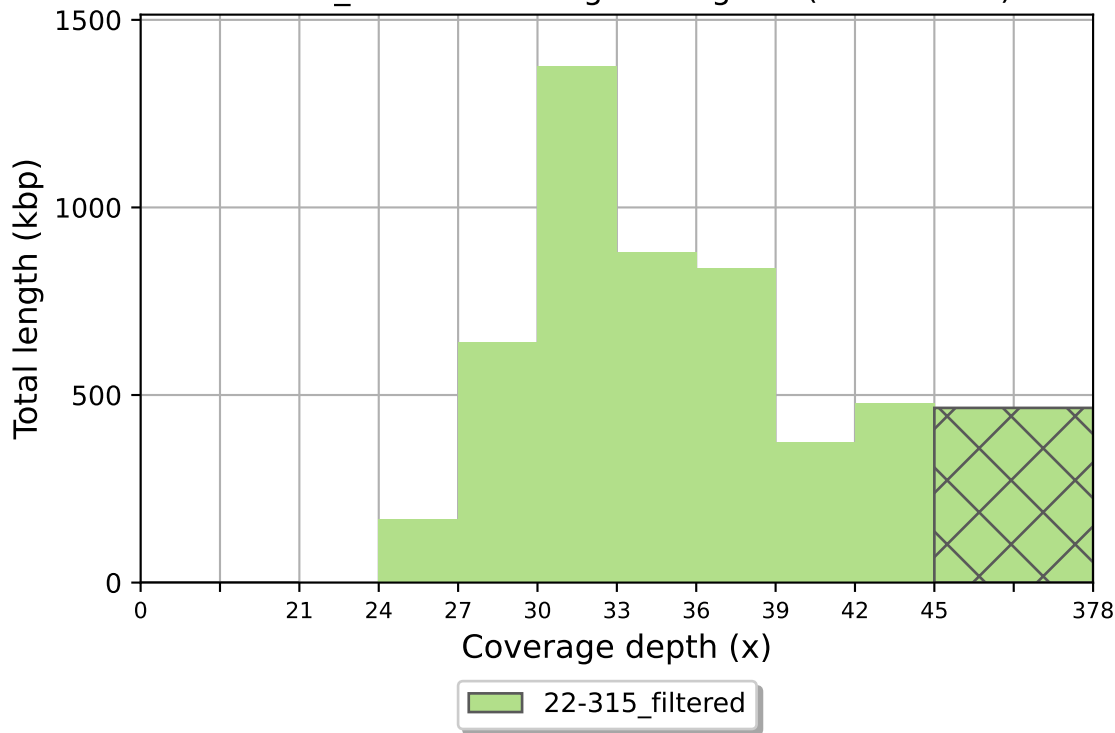
22-309_filtered coverage histogram (bin size: 2x)



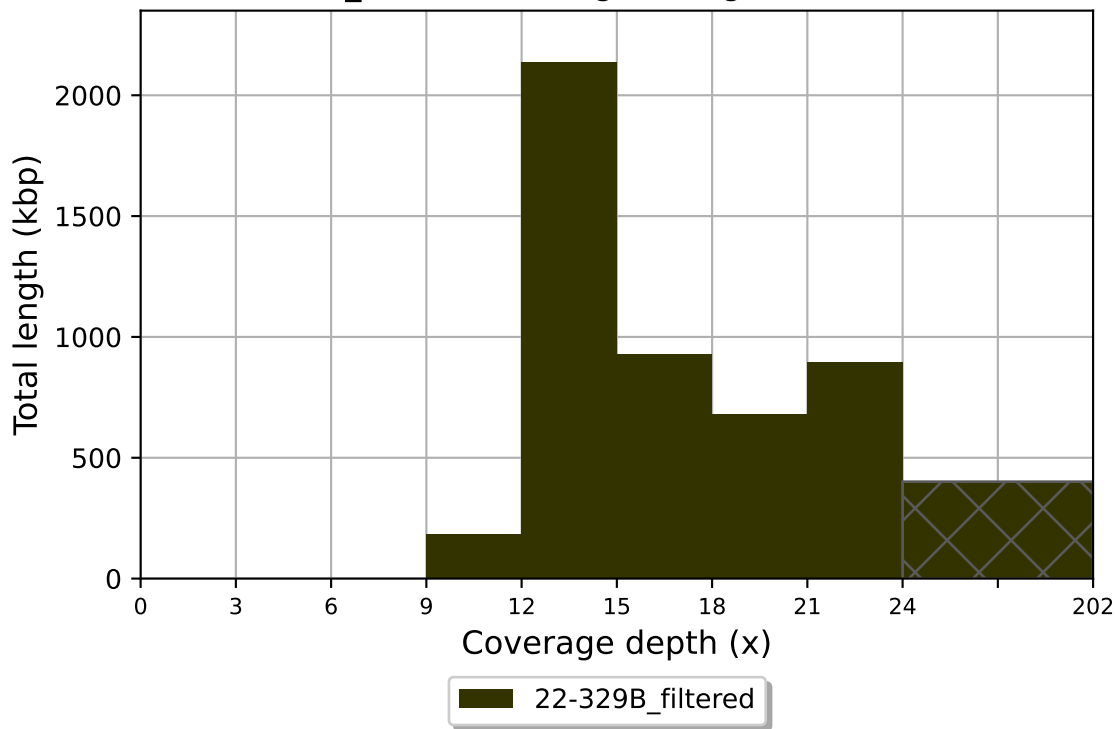
22-301_filtered coverage histogram (bin size: 1x)



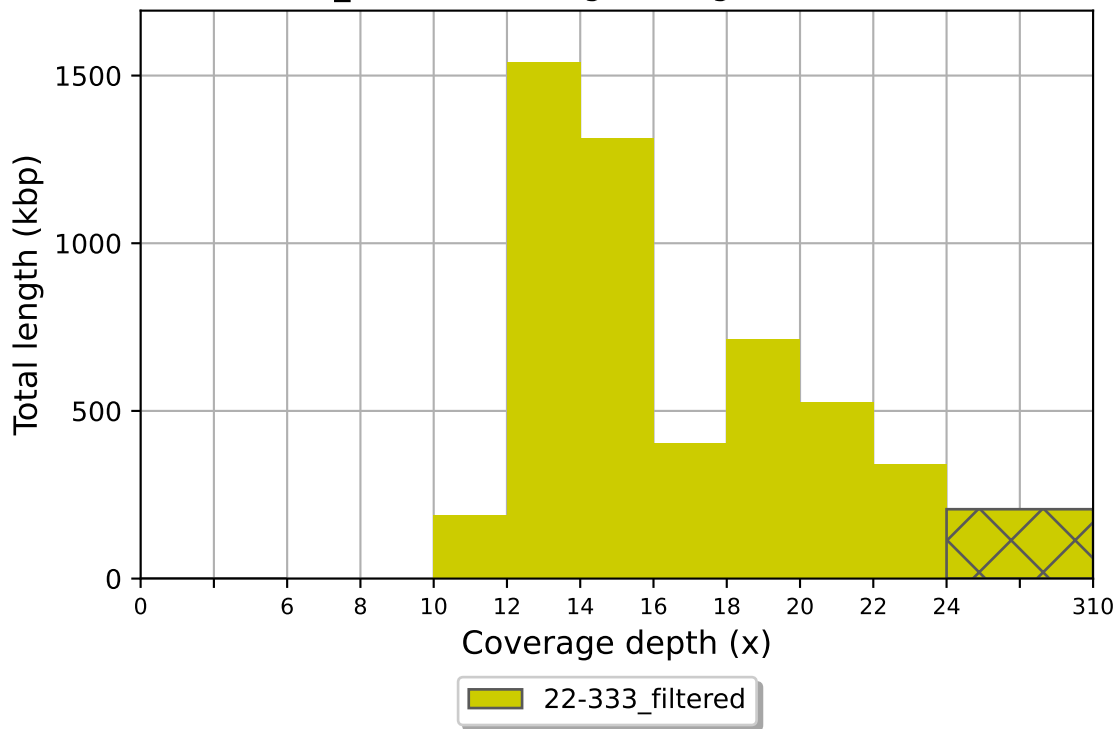
22-315_filtered coverage histogram (bin size: 3x)



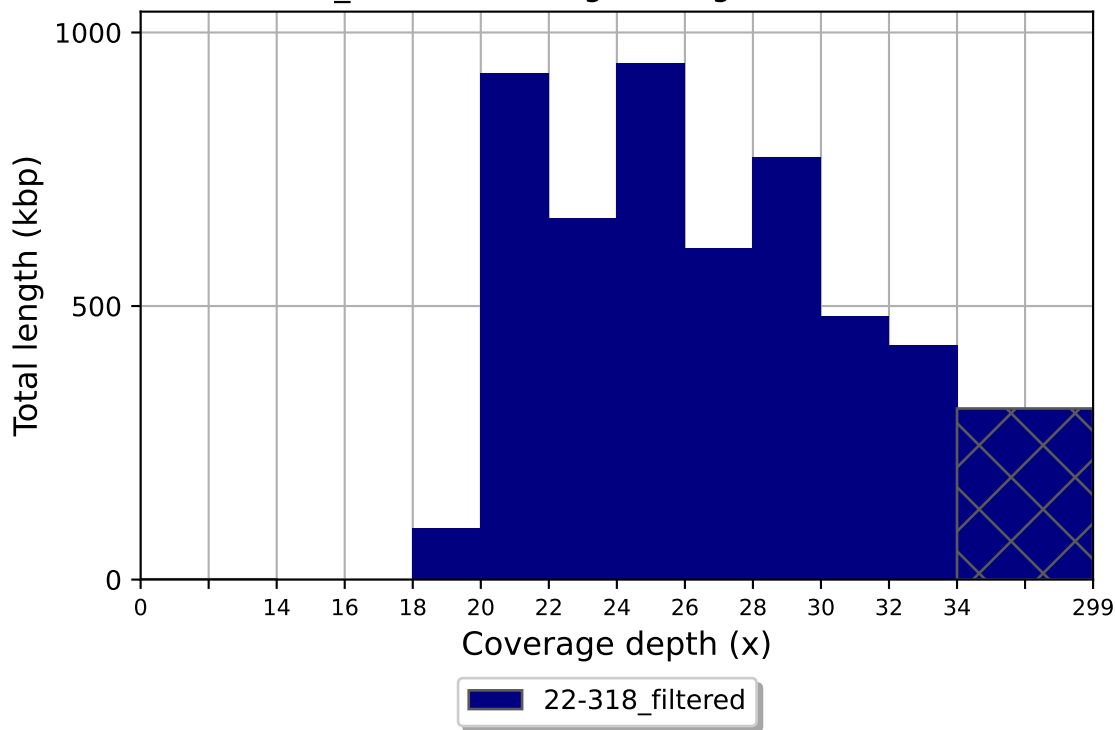
22-329B_filtered coverage histogram (bin size: 3x)



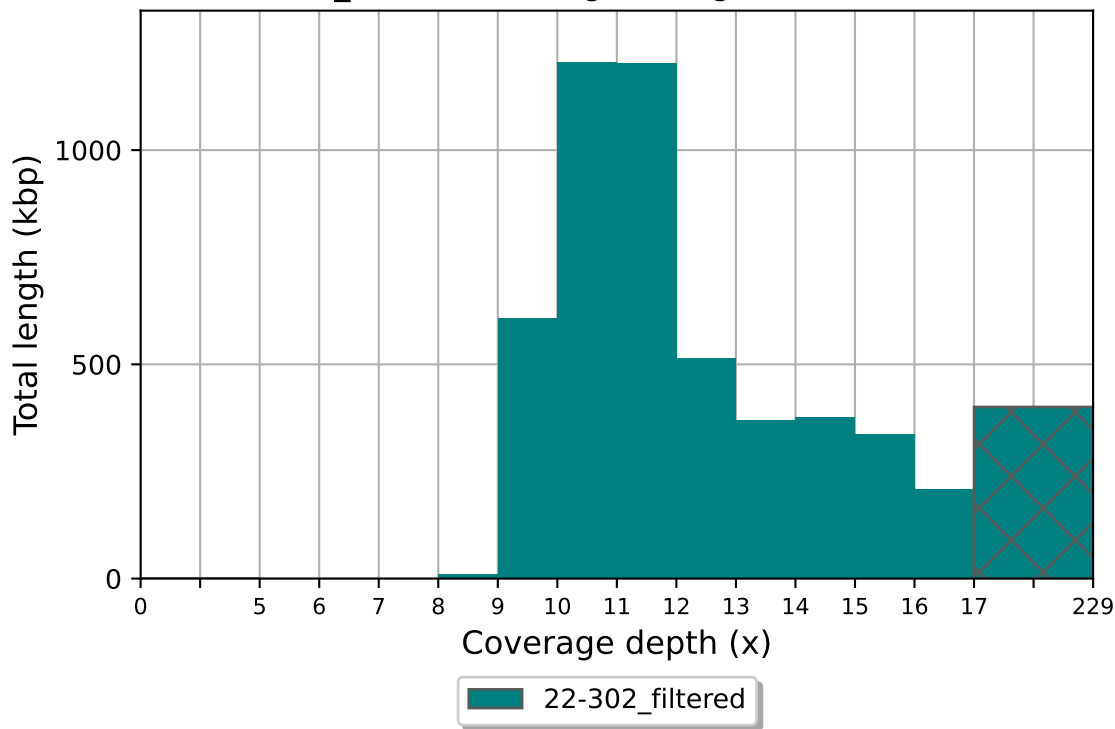
22-333_filtered coverage histogram (bin size: 2x)



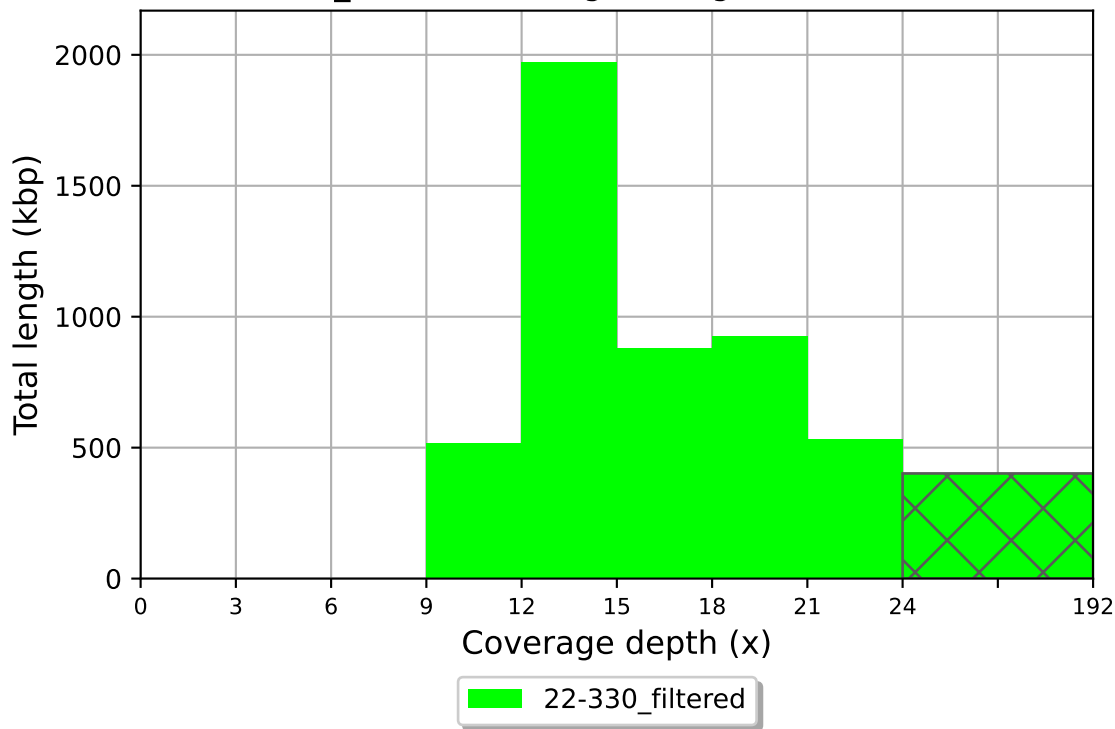
22-318_filtered coverage histogram (bin size: 2x)



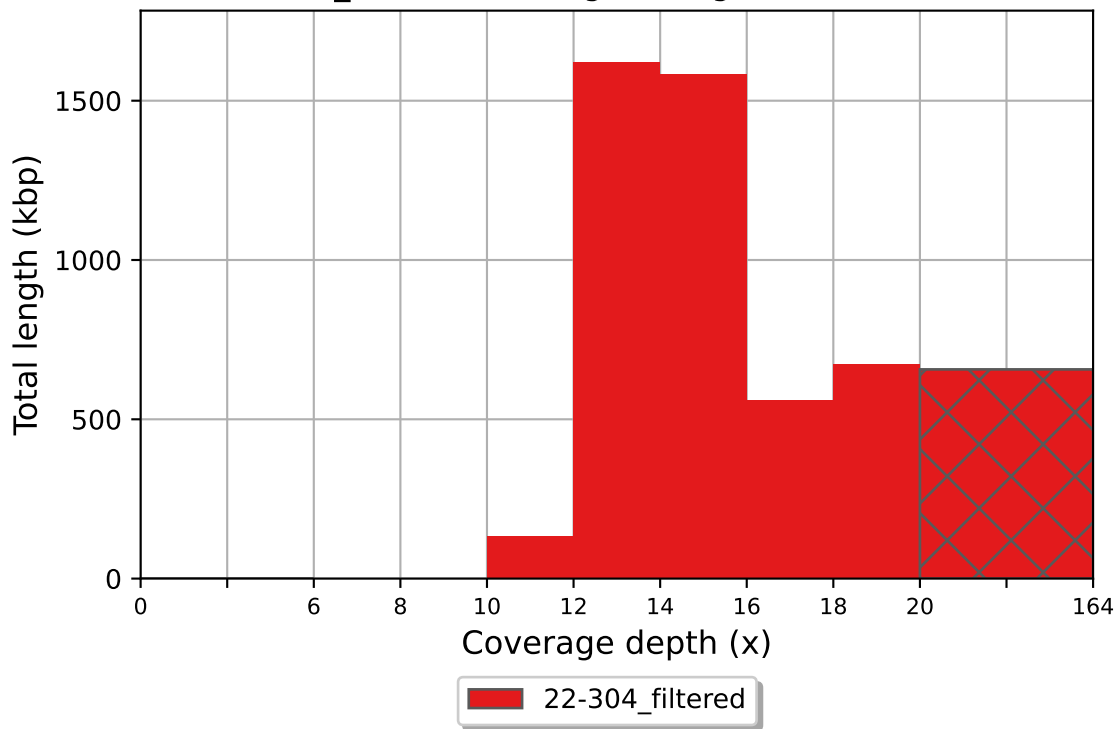
22-302_filtered coverage histogram (bin size: 1x)



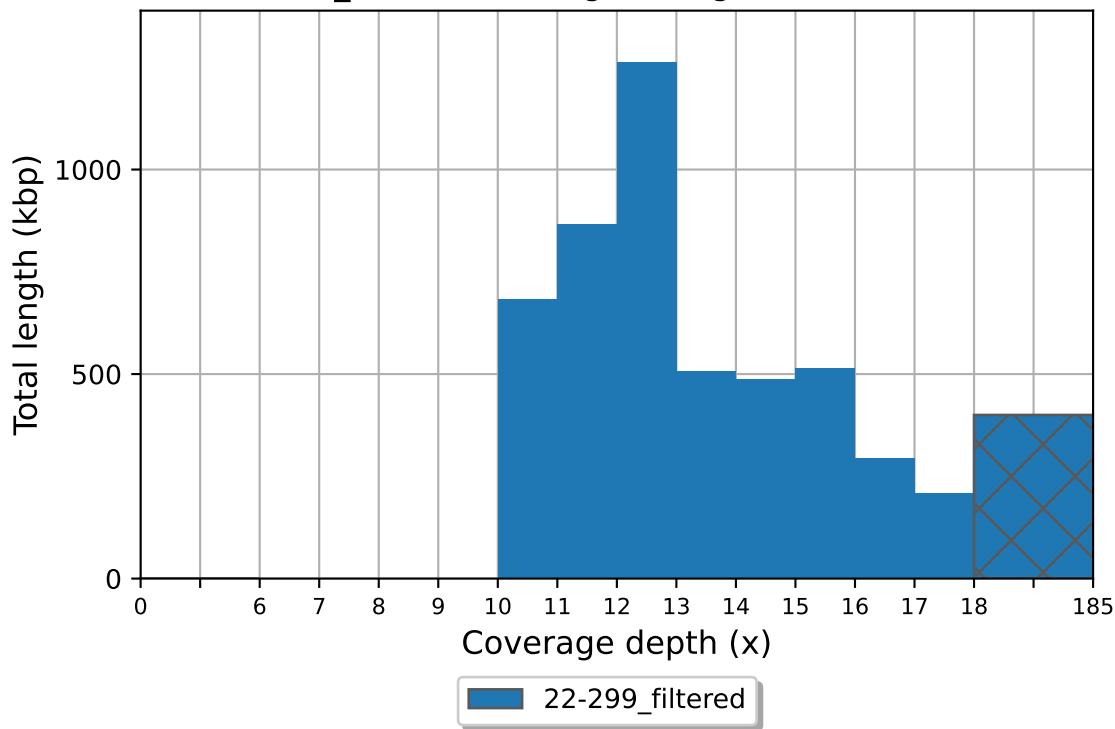
22-330_filtered coverage histogram (bin size: 3x)



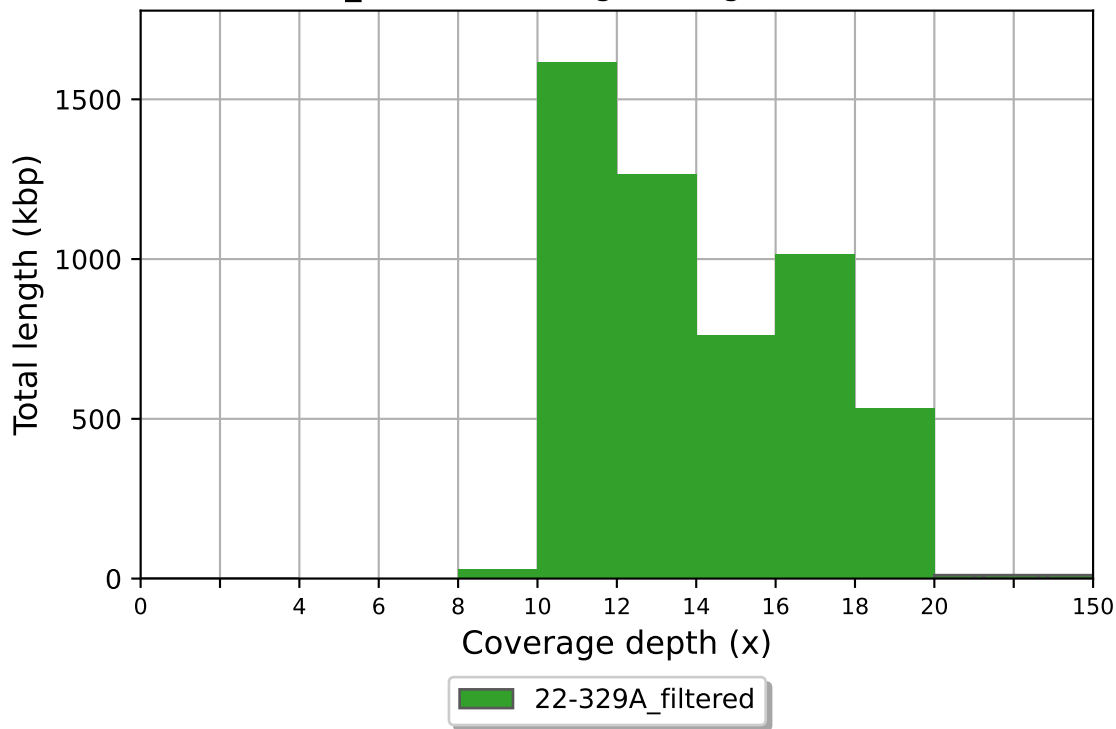
22-304_filtered coverage histogram (bin size: 2x)



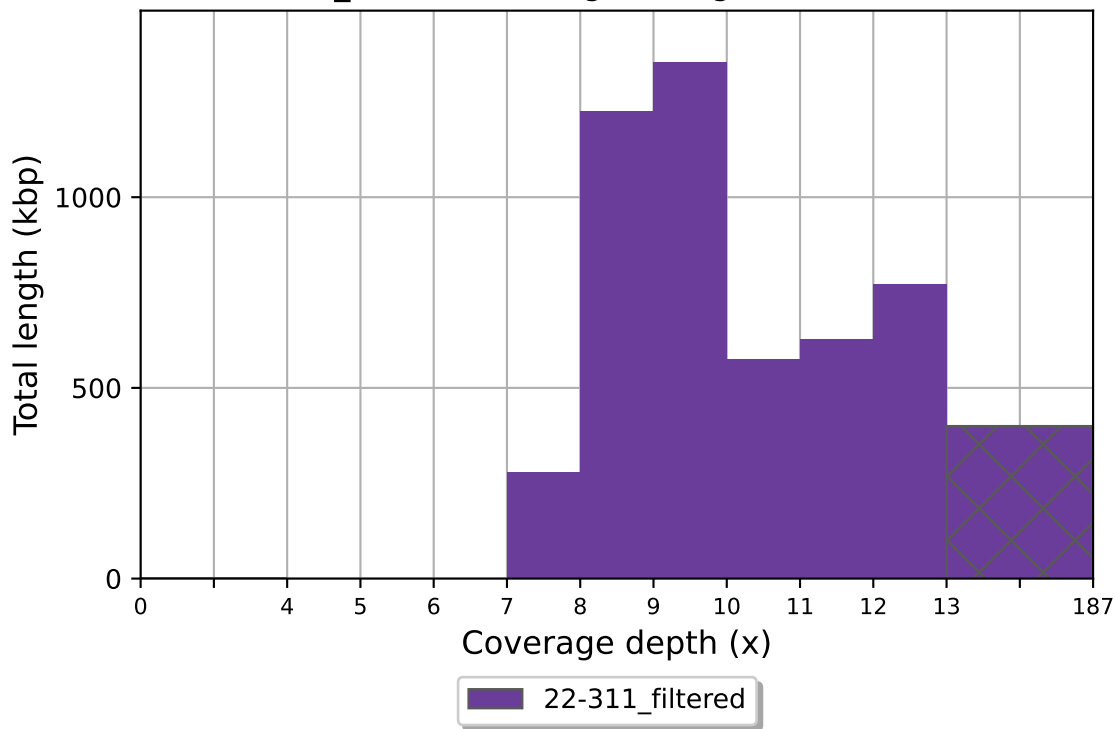
22-299_filtered coverage histogram (bin size: 1x)



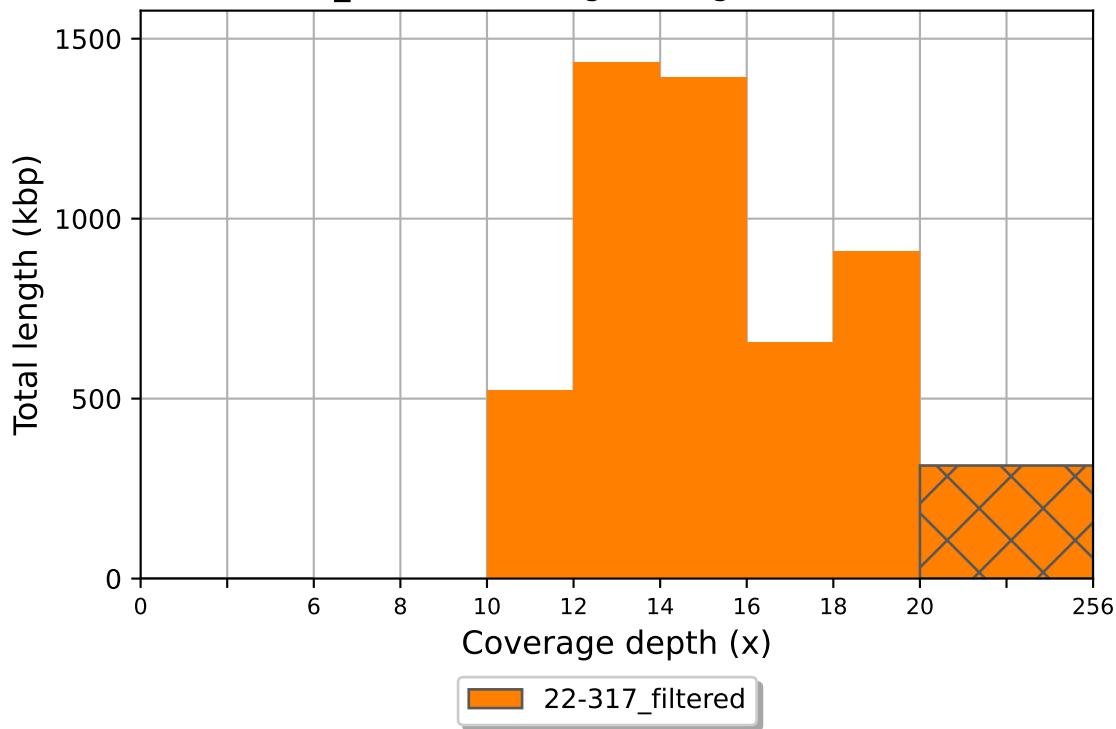
22-329A_filtered coverage histogram (bin size: 2x)



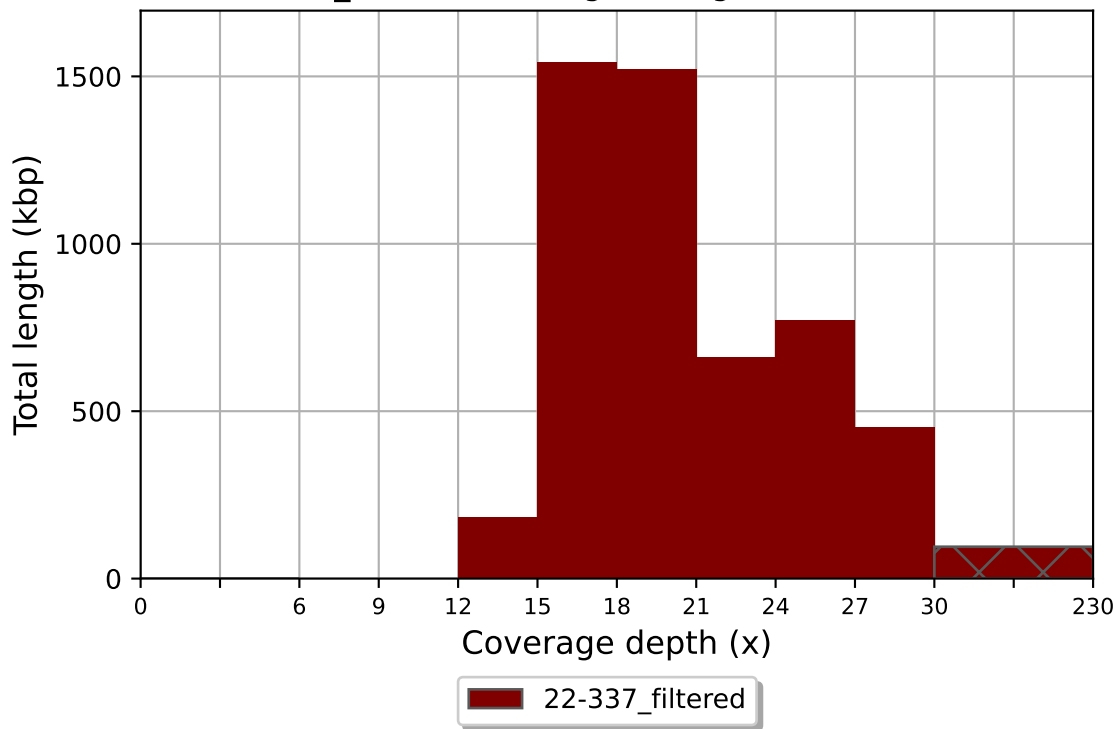
22-311_filtered coverage histogram (bin size: 1x)



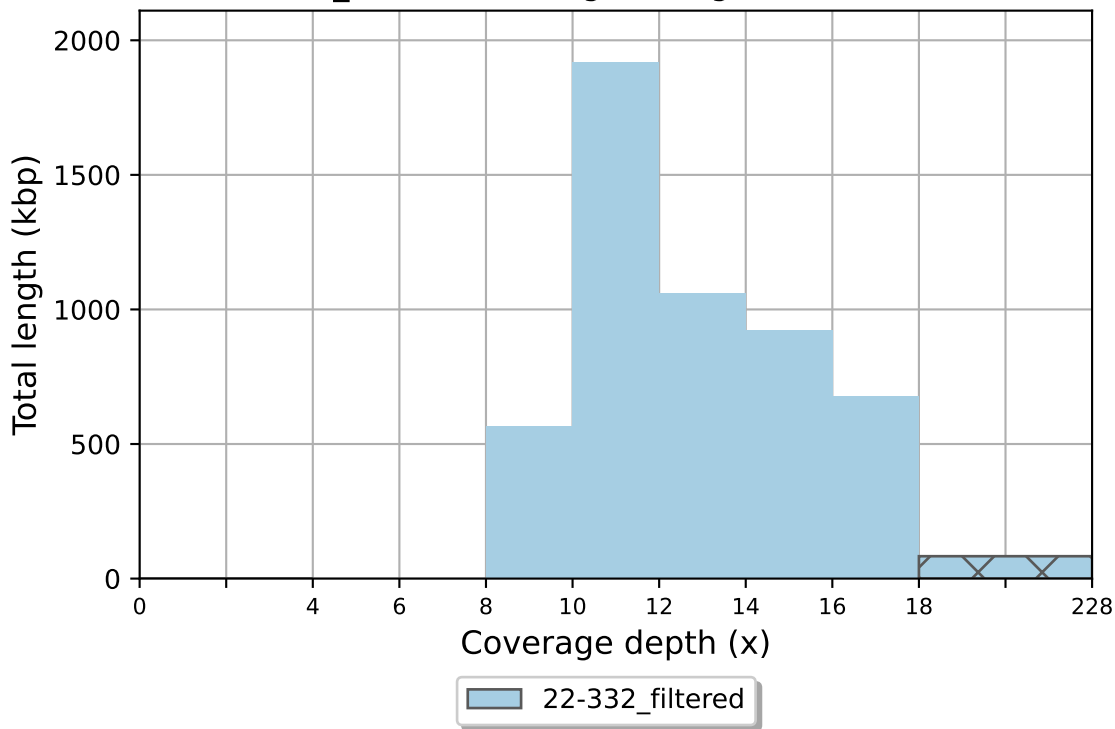
22-317_filtered coverage histogram (bin size: 2x)



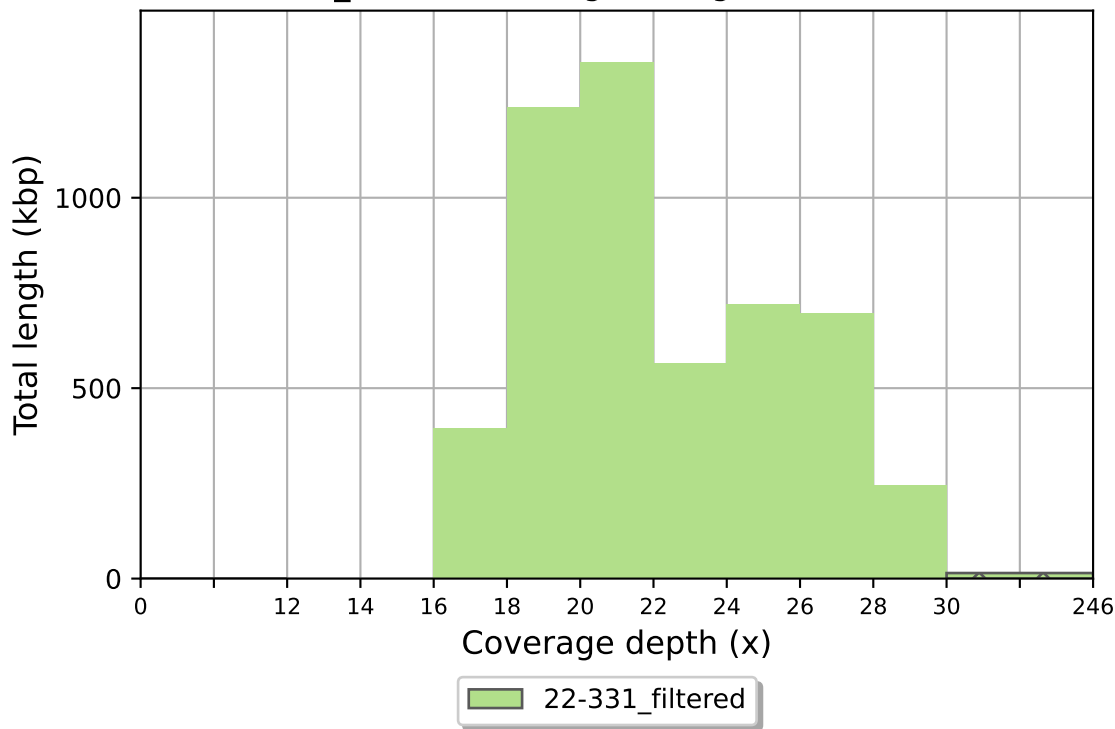
22-337_filtered coverage histogram (bin size: 3x)



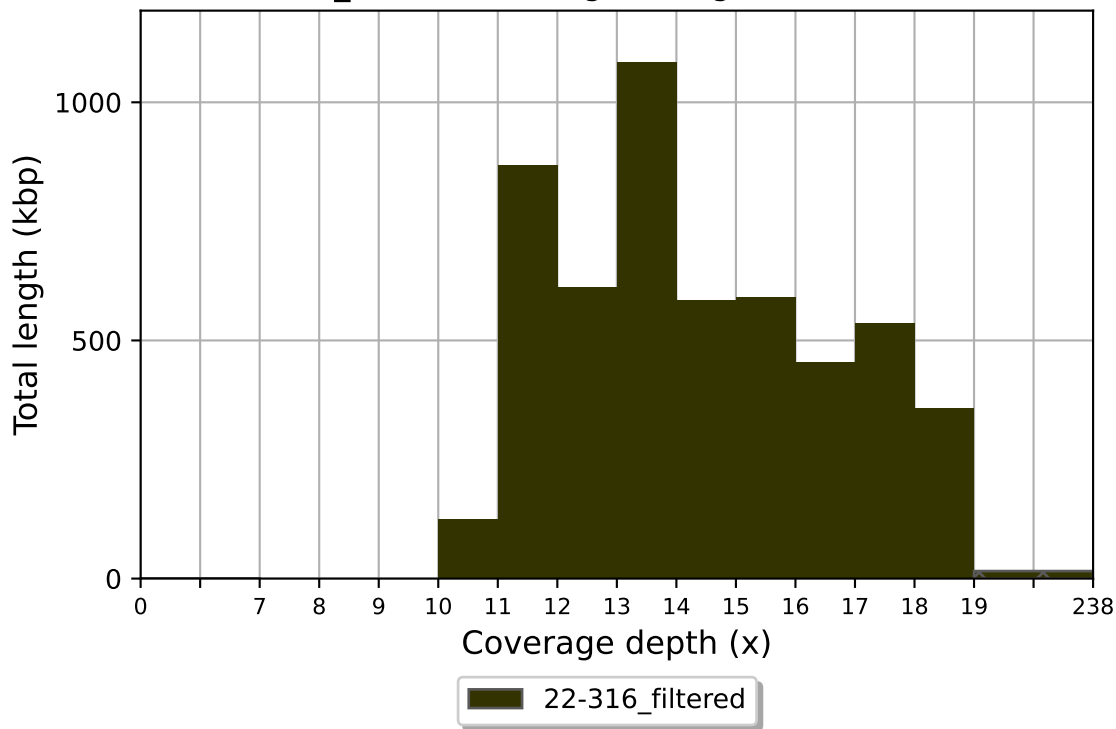
22-332_filtered coverage histogram (bin size: 2x)



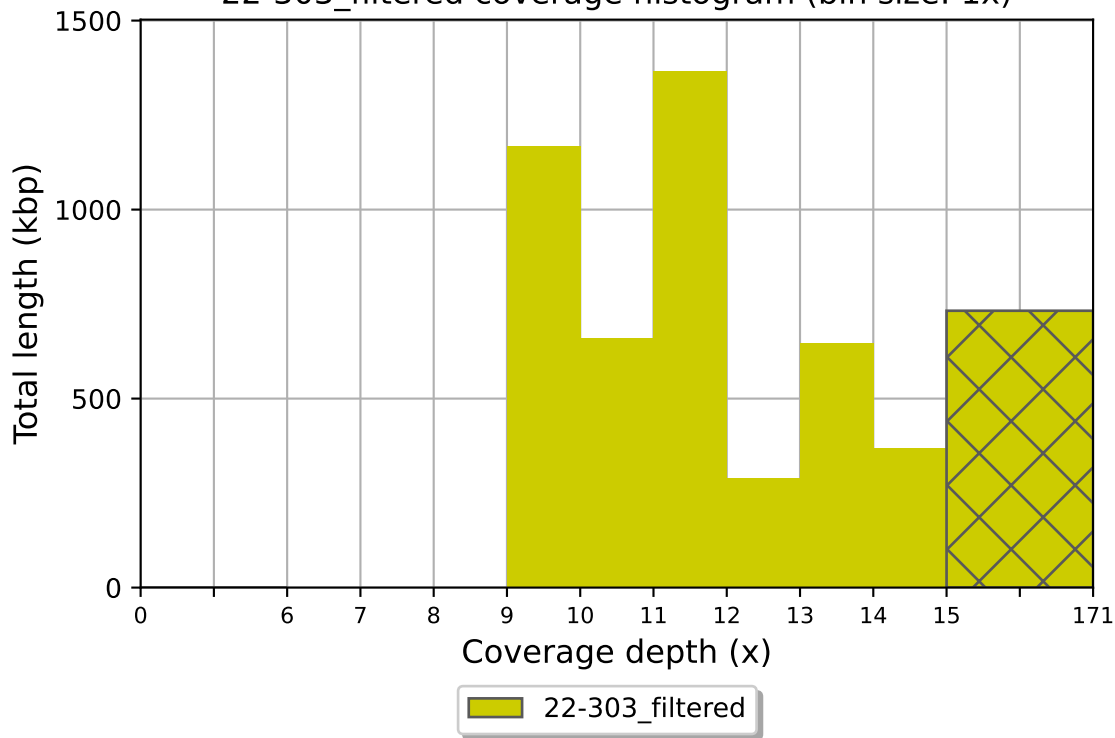
22-331_filtered coverage histogram (bin size: 2x)



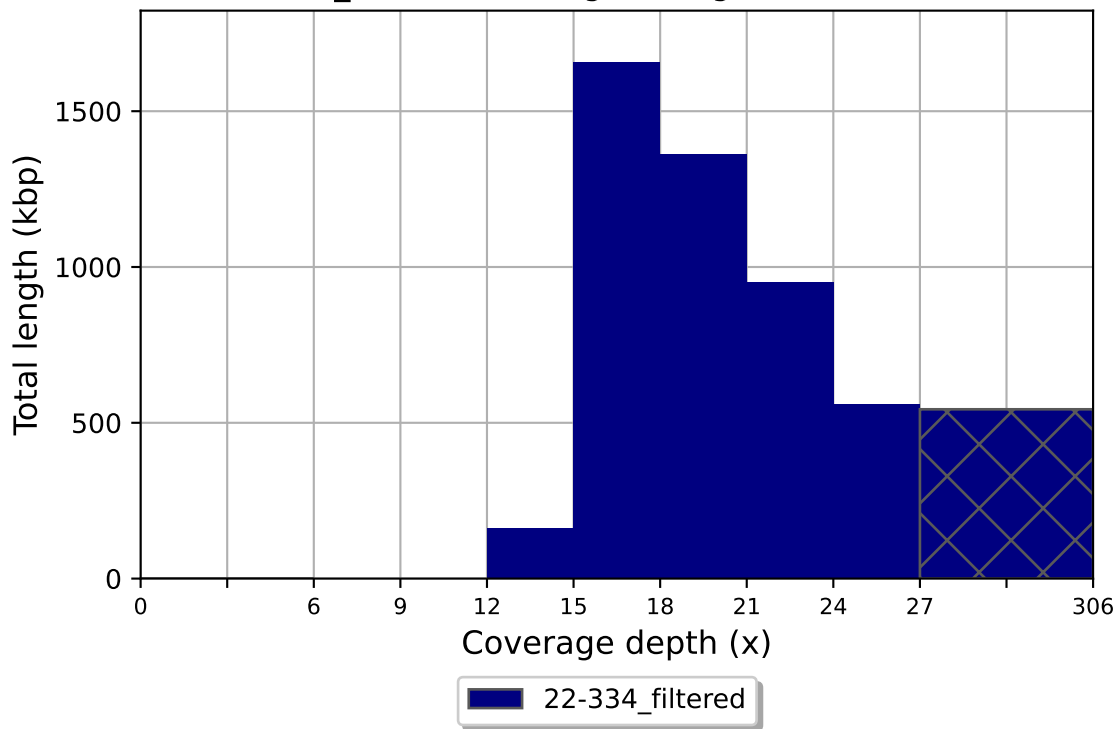
22-316_filtered coverage histogram (bin size: 1x)



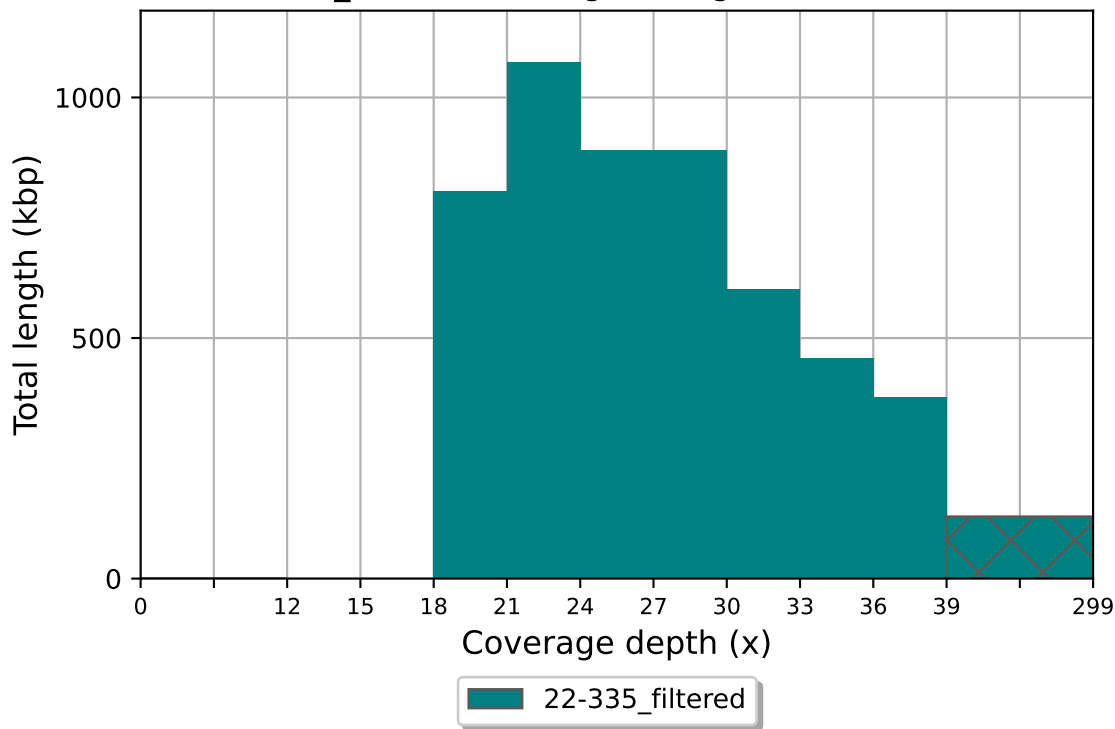
22-303_filtered coverage histogram (bin size: 1x)



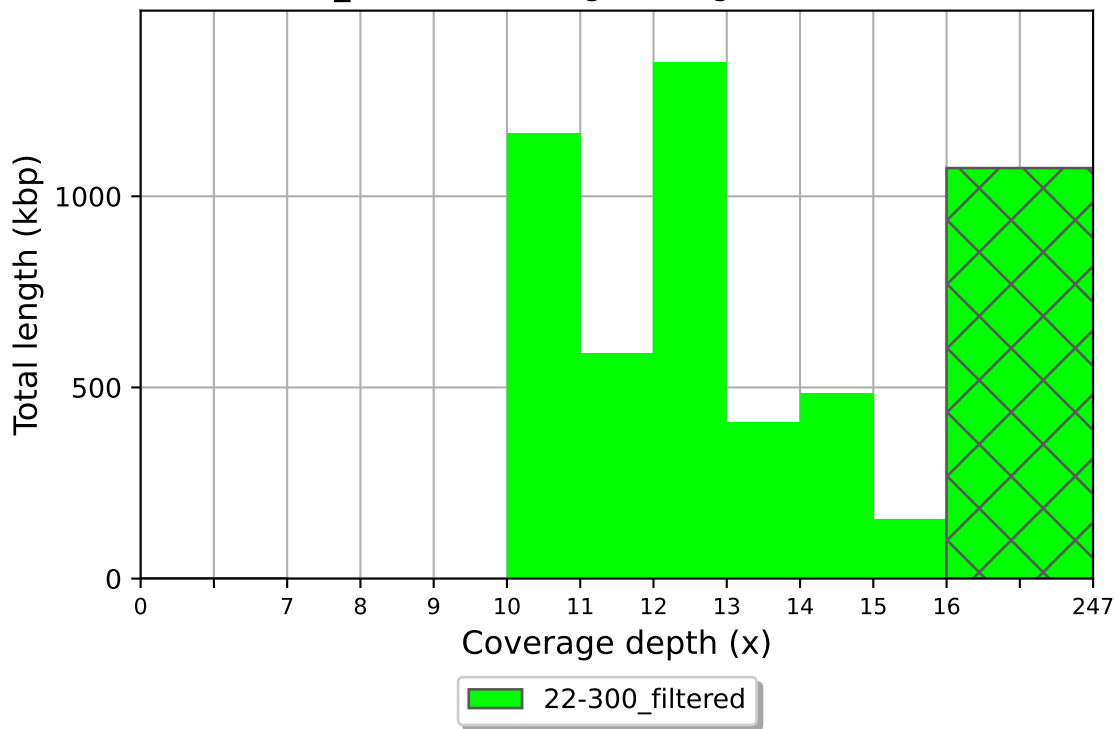
22-334_filtered coverage histogram (bin size: 3x)



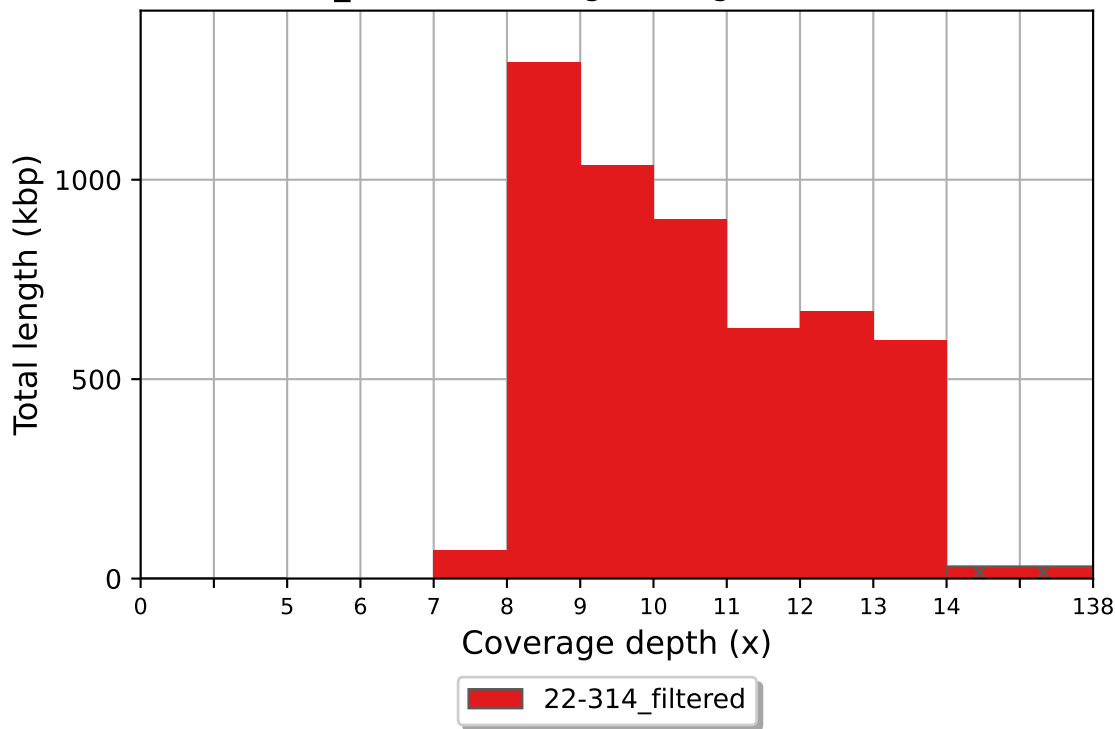
22-335_filtered coverage histogram (bin size: 3x)



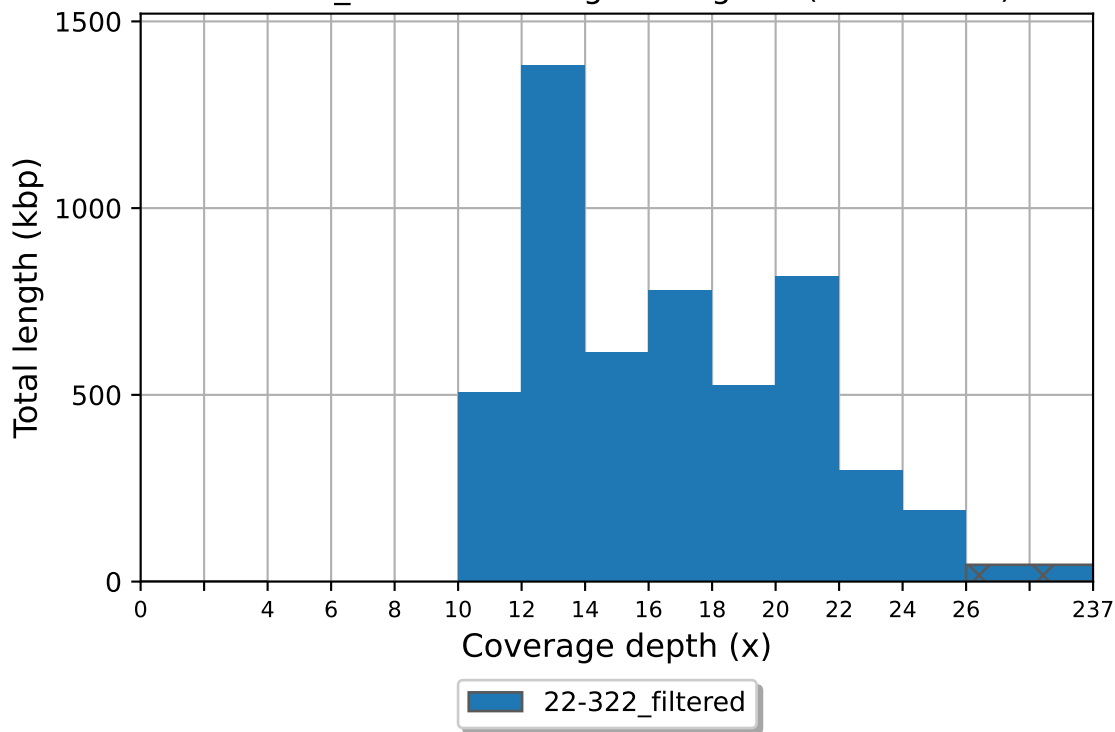
22-300_filtered coverage histogram (bin size: 1x)



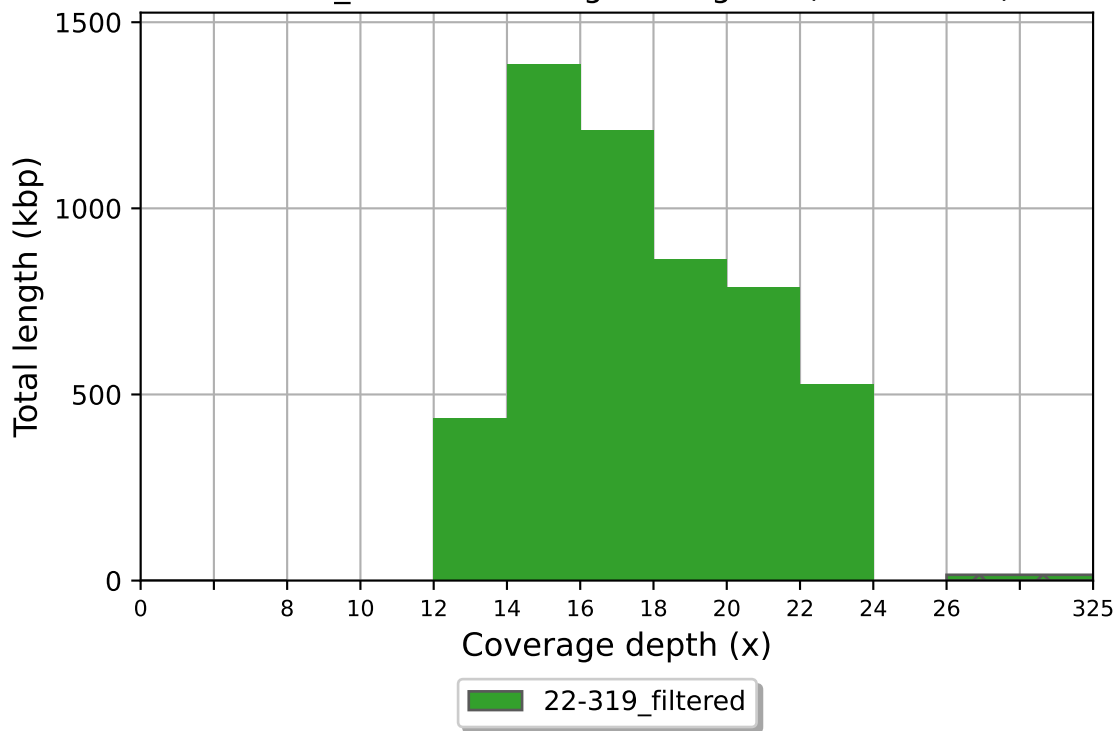
22-314_filtered coverage histogram (bin size: 1x)



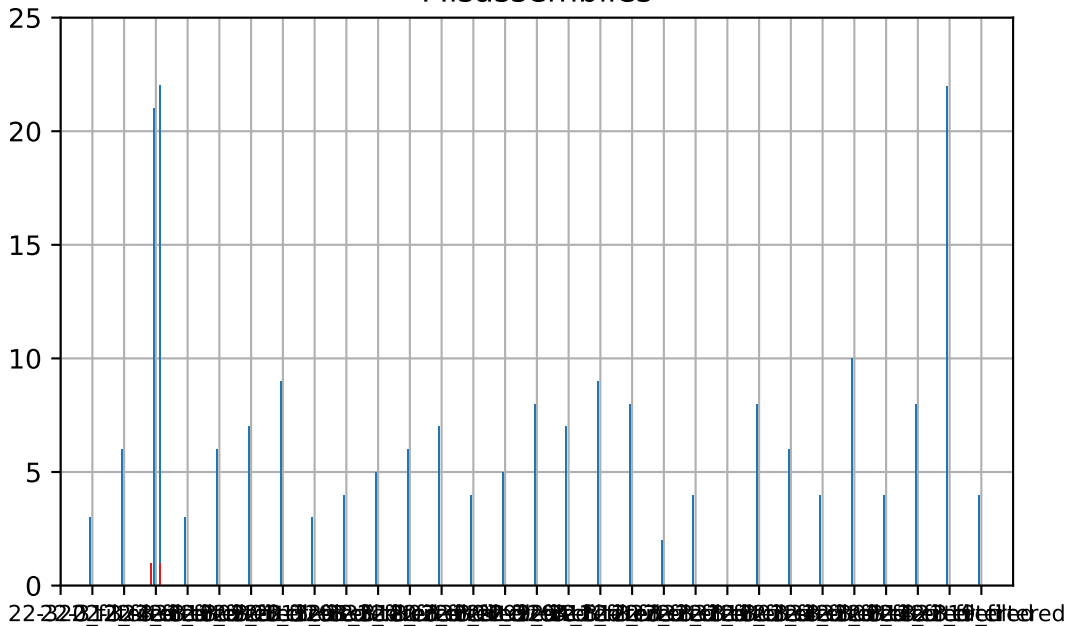
22-322_filtered coverage histogram (bin size: 2x)



22-319_filtered coverage histogram (bin size: 2x)



Misassemblies

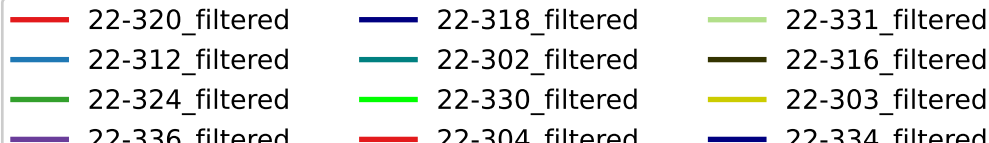
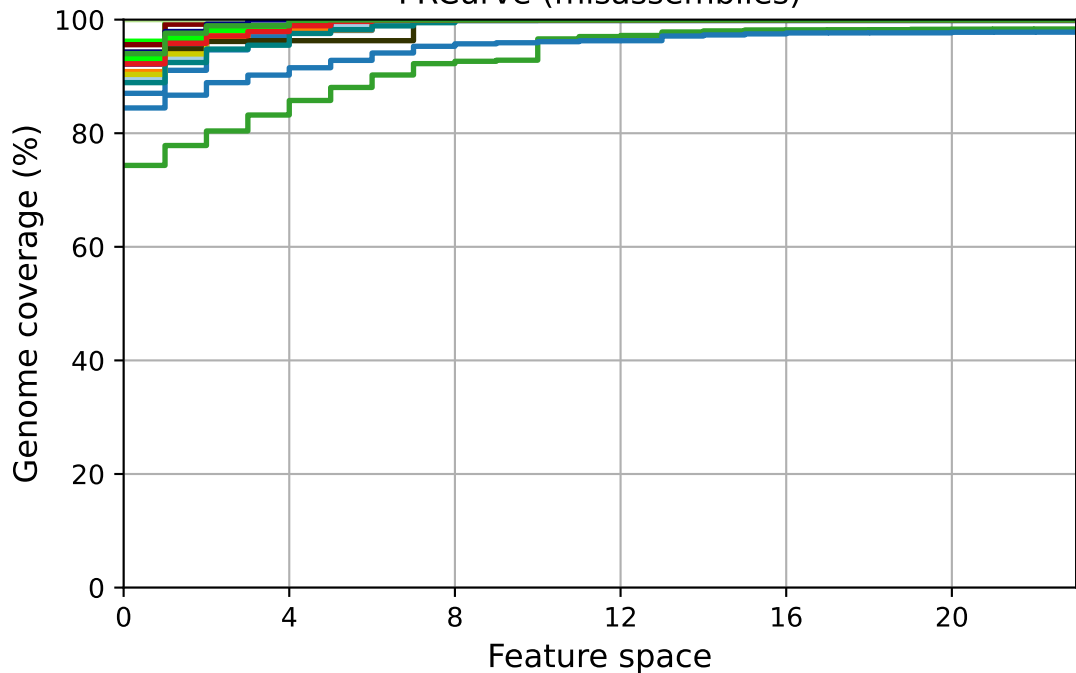


relocations

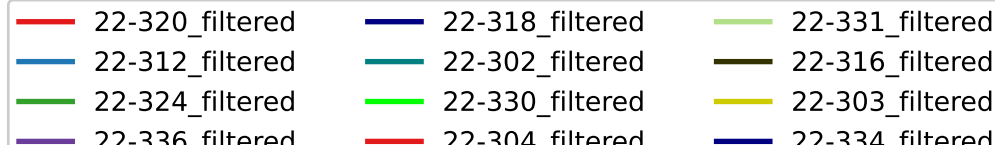
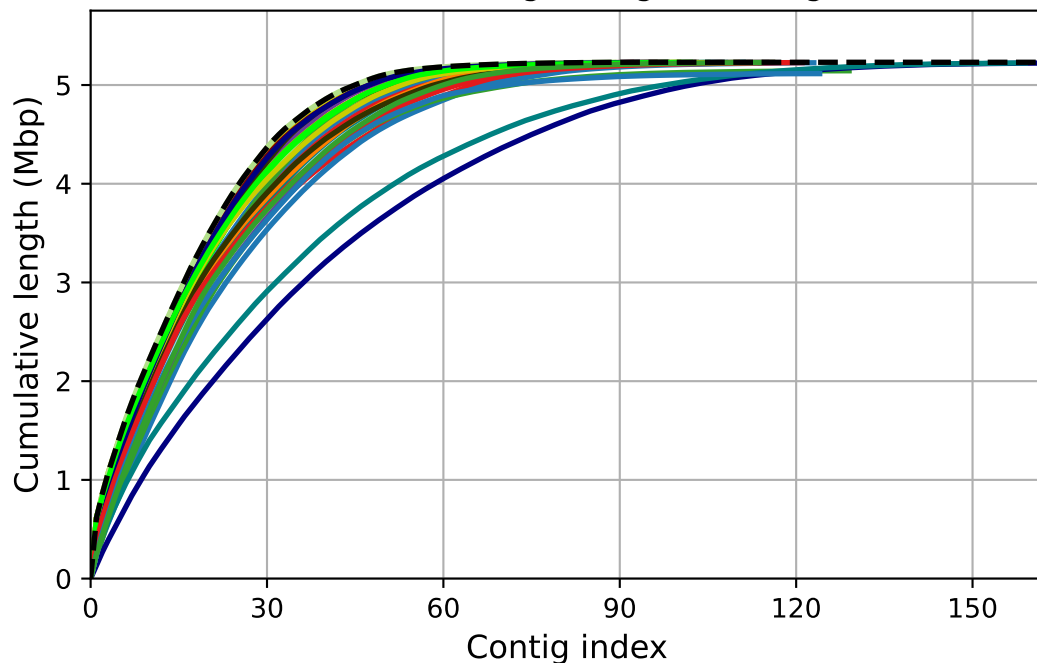


translocations

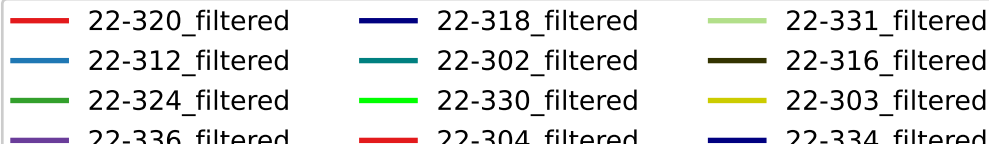
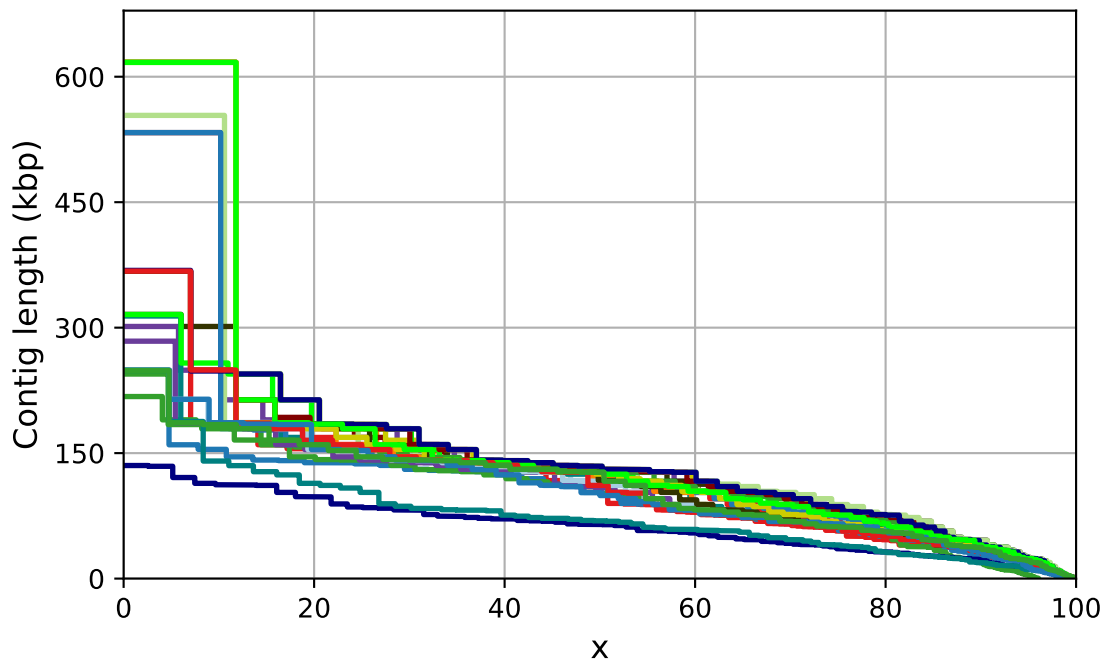
FRCurve (misassemblies)



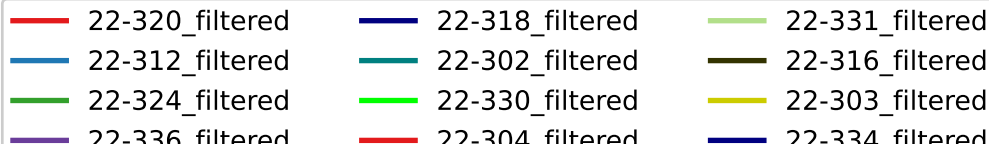
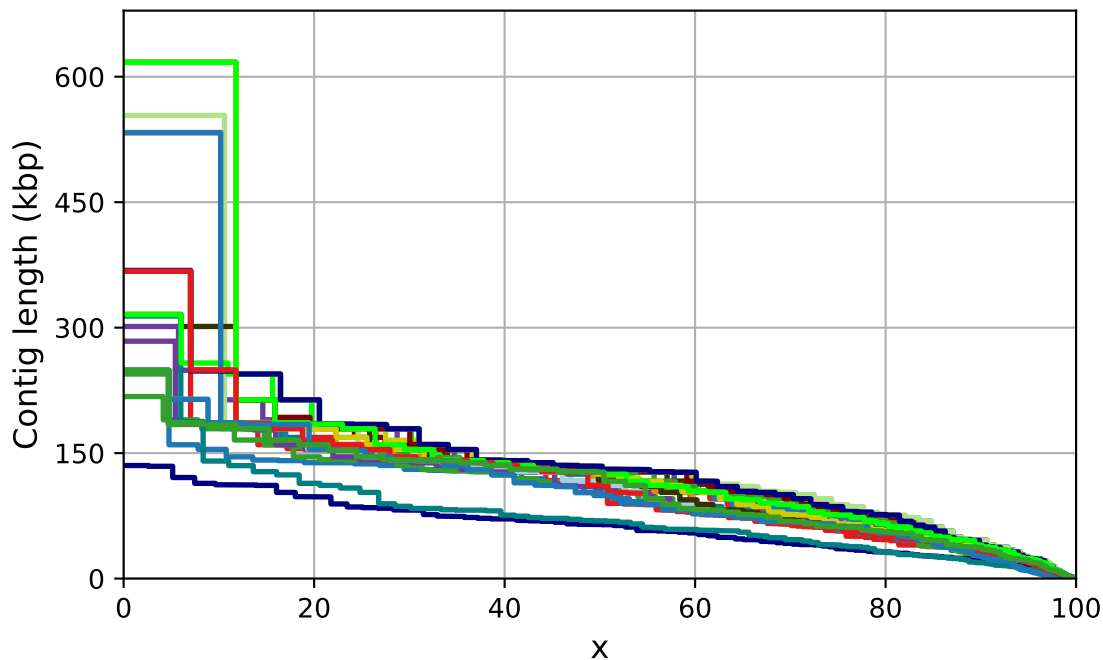
Cumulative length (aligned contigs)

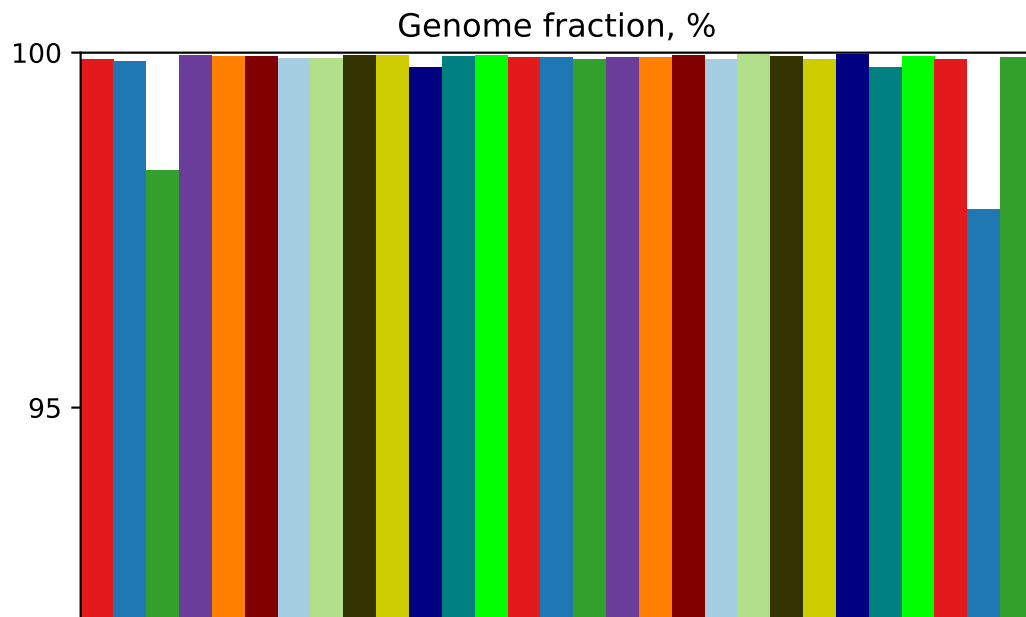


NAx



NGAx





22-320_filtered

22-312_filtered

22-324_filtered

22-336_filtered

22-318_filtered

22-302_filtered

22-330_filtered

22-304_filtered

22-331_filtered

22-316_filtered

22-303_filtered

22-334_filtered