

Table S1: Performance evaluation of computing a 2D layout of all chromosomal HPRC pangenome graphs. From GFA to the actual layout. **comps**: Number of weakly connected components. **pg-sgd**: *odgi layout* 2D PG-SGD implementation. **bng**: *BandageNG layout* implementation. **32T**: Number of threads: 32. **64T**: Number of threads: 64. \**BandageNG* did not finish within the job wall clock time limit of 7 days. Therefore, no layout was produced.

							time in minutes		memory in gigabytes					
							32T		64T		32T		64T	
name	len	nodes	edges	paths	steps	comps	pg – sgd	bng	pg – sgd	bng	pg – sgd	bng	pg – sgd	bng
chr1	1.12e+09	1.11e+07	1.54e+07	2.26e+03	6.01e+08	63	110	1439	<b>68</b>	1427	<b>55.73</b>	149.91	56.00	195.33
chr2	3.47e+08	6.68e+06	9.27e+06	1.65e+03	3.89e+08	15	67	576	<b>47</b>	521	37.31	81.97	<b>37.29</b>	81.97
chr3	4.06e+08	6.20e+06	8.62e+06	1.56e+03	4.55e+08	106	81	473	<b>52</b>	481	<b>41.34</b>	81.41	41.71	93.83
chr4	2.73e+08	5.91e+06	8.23e+06	1.35e+03	4.97e+08	36	88	422	<b>56</b>	423	<b>44.90</b>	79.40	45.02	79.48
chr5	3.35e+08	5.39e+06	7.51e+06	1.20e+03	4.04e+08	19	73	349	<b>46</b>	375	<b>35.83</b>	75.13	36.48	75.10
chr6	2.29e+08	4.70e+06	6.56e+06	1.41e+03	4.03e+08	40	70	270	<b>46</b>	271	<b>36.74</b>	71.25	37.22	71.26
chr7	2.71e+08	5.17e+06	7.25e+06	1.22e+03	4.10e+08	24	70	328	<b>46</b>	346	<b>37.39</b>	73.70	37.88	73.81
chr8	1.93e+08	4.26e+06	5.95e+06	8.55e+02	4.29e+08	16	71	224	<b>47</b>	233	<b>37.73</b>	54.72	38.07	54.70
chr9	1.01e+09	8.80e+06	1.23e+07	8.67e+02	3.31e+08	11	44	931	<b>38</b>	957	<b>31.76</b>	131.93	31.79	131.96
chr10	2.56e+08	4.50e+06	6.26e+06	8.79e+02	2.72e+08	14	36	256	<b>32</b>	260	25.32	67.85	<b>25.25</b>	67.87
chr11	2.83e+08	4.73e+06	6.54e+06	6.53e+02	2.38e+08	8	31	277	<b>28</b>	286	21.81	68.49	<b>21.77</b>	68.54
chr12	2.44e+08	4.10e+06	5.71e+06	7.68e+02	2.54e+08	9	44	210	<b>27</b>	206	<b>23.55</b>	51.19	23.99	51.22
chr13	3.47e+08	4.34e+06	6.08e+06	2.58e+03	3.12e+08	153	52	242	<b>34</b>	237	<b>27.98</b>	54.02	28.64	85.85
chr14	2.73e+08	4.15e+06	5.79e+06	1.82e+03	2.62e+08	133	45	222	<b>28</b>	222	<b>23.56</b>	51.67	24.17	78.13
chr15	5.64e+08	5.20e+06	7.26e+06	2.06e+03	4.02e+08	131	64	347	<b>35</b>	334	<b>35.20</b>	74.27	35.69	102.97
chr16	3.39e+08	3.91e+06	5.53e+06	1.52e+03	6.91e+08	25	<b>152</b>	216	512	244	58.88	<b>53.00</b>	61.02	<b>53.00</b>
chr17	1.73e+08	2.76e+06	3.93e+06	1.42e+03	3.25e+08	77	50	102	<b>33</b>	102	<b>27.83</b>	40.68	28.69	49.50
chr18	2.44e+08	2.83e+06	3.98e+06	1.27e+03	3.00e+08	111	44	108	<b>31</b>	106	<b>26.61</b>	40.80	26.78	45.01
chr19	2.91e+08	3.02e+06	4.21e+06	1.07e+03	2.03e+08	19	31	123	<b>21</b>	117	<b>18.12</b>	40.14	18.43	40.18
chr20	1.87e+08	2.82e+06	3.97e+06	8.24e+02	2.35e+08	17	35	114	<b>25</b>	108	<b>20.79</b>	39.02	21.04	39.05
chr21	2.74e+08	2.76e+06	3.88e+06	3.03e+03	2.21e+08	218	33	110	<b>23</b>	103	<b>18.79</b>	38.07	19.12	46.47
chr22	4.64e+08	3.76e+06	5.22e+06	1.76e+03	2.05e+08	82	32	181	<b>22</b>	183	<b>18.30</b>	44.73	18.65	45.13
chrX	2.07e+08	3.46e+06	4.89e+06	2.42e+03	2.70e+08	11	41	156	<b>28</b>	155	<b>24.66</b>	43.05	24.84	43.05
chrY	8.80e+07	3.18e+05	4.41e+05	3.07e+02	1.34e+07	7	2	5	<b>1</b>	5	<b>1.47</b>	4.65	1.57	4.65
chrM	1.76e+04	1.40e+03	1.89e+03	4.40e+01	4.06e+04	1	<b>1</b>	<b>1</b>	<b>1</b>	<b>1</b>	0.21	<b>0.04</b>	0.49	<b>0.04</b>
all chrs	8.42e+09	1.11e+08	1.55e+08	3.48e+04	8.12e+09	1346	1630	-*	<b>1020</b>	-*	<b>737.15</b>	-*	738.76	-*

6 Supplement

6.1 Supplementary data

6.1.1 Performance evaluation

The results of the performance evaluation are given in Table S1.

6.1.2 1D visualizations

The 1D PG-SGD algorithm creates a 1D layout of the nodes of the graph. Theoretically, it is possible that 2 nodes have the same 1D coordinate or

overlap. But, in our 1D visualizations, we arrange the nodes from left to right. Therefore, we project the 1D coordinates into a 1D node order: We sort the final layout by graph component, graph position, and node rank.

