	FM- HF - BV		FM-HI	$FM-HF-R^3-15$		FM-RLMN		$FM-HF-R^3-63$	
	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	
ENGLISH.200MB	0.596	61	1.228	38	1.631	69	2.228	27	
DBLP.XML.200MB	0.643	70	1.159	32	1.621	34	1.770	17	
DNA.200MB	0.226	29	0.594	28	1.082	79	1.362	24	
PROTEINS. 200MB	0.531	56	1.326	53	1.563	89	2.758	48	
SOURCES.200MB	0.728	73	1.408	39	1.712	53	2.410	26	

Table 1: Time in μ sec per pattern symbol in a count query. Index space as fraction of original file size. Compile options: -DUSE_HP -msse4.2 -09 -funroll-loops -fomit-frame-pointer -ffast-math -DNDEBUG.

	FM- HF - BV		$FM-HF-R^3-15$		FM-RLMN		$FM-HF-R^3-63$	
	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)
ENGLISH.200MB	0.753	61	1.254	38	1.918	69	2.212	27
DBLP.XML.200MB	0.849	70	1.145	32	2.635	34	1.749	17
DNA.200MB	0.311	29	0.605	28	1.233	79	1.328	24
PROTEINS.200MB SOURCES.200MB	$0.671 \\ 0.936$	56 73	1.306 1.406	53 39	1.811 2.129	89 53	2.746 2.418	48 26

Table 2: Time in μ sec per pattern symbol in a count query. Index space as fraction of original file size. Compile options: -DPOPCOUNT_TL -09 -funroll-loops -fomit-frame-pointer -ffast-math -DNDEBUG.

	FM-HF-BV		$FM-HF-R^3-15$		FM-RLMN		$FM-HF-R^3-63$	
	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)
ENGLISH.200MB	0.656	61	1.234	38	1.830	69	2.261	27
DBLP.XML.200MB	0.734	70	1.145	32	2.015	34	1.742	17
DNA.200MB	0.270	29	0.602	28	1.175	79	1.330	24
PROTEINS.200MB SOURCES.200MB	$0.583 \\ 0.804$	56 73	1.305 1.434	53 39	1.728 1.921	89 53	2.739 2.412	$\frac{48}{26}$

Table 3: Time in μsec per pattern symbol in a count query. Index space as fraction of original file size. Compile options: -09 -funroll-loops -fomit-frame-pointer -ffast-math -DNDEBUG.

	FM-HF-BV		FM - HF - R^3 - 15		FM-RLMN		$FM-HF-R^3-63$	
	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)
ENGLISH.200MB	1.198	61	2.268	38	3.056	69	5.342	27
DBLP.XML.200MB	1.365	70	2.130	32	5.524	34	4.364	17
DNA.200MB	0.562	29	1.190	28	2.096	79	2.962	24
PROTEINS.200MB SOURCES.200MB	1.075 1.441	56 73	2.438 2.574	53 39	2.831 3.386	89 53	5.950 5.894	$\frac{48}{26}$

Table 4: Time in μsec per pattern symbol in a count query. Index space as fraction of original file size. Compile options: -00 -DNDEBUG.

	FM- HF - BV		$FM-HF-R^3-15$		FM-RLMN		$FM-HF-R^3-63$	
	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)
ENGLISH.200MB	0.668	61	1.251	38	1.840	69	2.300	27
DBLP.XML.200MB	0.742	70	1.156	32	2.071	34	1.778	17
DNA.200MB	0.278	29	0.609	28	1.214	79	1.353	24
PROTEINS.200MB SOURCES.200MB	$0.591 \\ 0.821$	56 73	1.299 1.439	53 39	1.757 1.975	89 53	2.685 2.439	$\frac{48}{26}$

Table 5: Time in μsec per pattern symbol in a count query. Index space as fraction of original file size. Compile options: -01 -DNDEBUG.

	FM-HF-BV		$FM-HF-R^3-15$		FM-RLMN		$FM-HF-R^3-63$	
	Time (μs)	Space (%)						
ENGLISH.200MB	0.599	61	1.243	38	1.644	69	2.228	27
DBLP.XML. $200MB$	0.631	70	1.141	32	1.593	34	1.754	17
DNA.200MB	0.230	29	0.593	28	1.073	79	1.352	24
PROTEINS. 200MB	0.532	56	1.298	53	1.538	89	2.760	48
SOURCES.200MB	0.720	73	1.457	39	1.699	53	2.428	26

Table 6: Time in μ sec per pattern symbol in a count query. Index space as fraction of original file size. Compile options: -msse4.2 -09 -funroll-loops -fomit-frame-pointer -ffast-math -DNDEBUG.

Identifier	sdsl type
FM-HF-BV	csa_wt <wt_huff<bit_vector, rank_support_v5<="">, select_support_scan<>>, select_support_scan<0>>, 1<<20, 1<<20></wt_huff<bit_vector,>
$FM\text{-}HF\text{-}R^3\text{-}15$	csa_wt <wt_huff<rrr_vector<15>>, 1<<20, 1<<20></wt_huff<rrr_vector<15>
FM-RLMN	csa_wt <wt_rlmn<>, 1<<20, 1<<20></wt_rlmn<>
$FM-HF-R^3-63$	${\tt csa_wt>,\ 1<<20,\ 1<<20>}$

Table 7: Index identifier and corresponding sdsl-type.