

10k sub-FLs generated from DNA-protein binding affinities (Rowe et al.)

	$K=4, L=5$		$K=2, L=10$	
	Experimental	Randomized	Experimental	Randomized
accessibility A	0.86	0.51	0.67	0.13
\langle coverage of FL \rangle^*	28%	8%	26%	3%
\langle pathway length \rangle	16.8	10.0	15.4	11.1
\langle forward mutations \rangle	43%	57%	82%	95%
\langle distance – neutral mutations \rangle	44%	37%	0%	0%
\langle backward mutations \rangle	13%	7%	18%	5%
\langle pathway number \rangle	1.2×10^{10}	1.9×10^3	2.3×10^6	19
$\langle \log_{10}(\text{pathway number}) \rangle$	5.4	2.1	3.9	0.8

1k sub-FLs generated from RNA-protein binding affinities (Guenther et al.)

	$K=4, L=3$		$K=2, L=6$	
	Experimental	Randomized	Experimental	Randomized
accessibility A	0.95	0.59	0.78	0.20
\langle coverage of FL \rangle	42%	24%	44%	19%
\langle pathway length \rangle	6.7	5.3	7.1	6.4
\langle forward mutations \rangle	52%	61%	92%	97%
\langle distance – neutral mutations \rangle	41%	35%	0%	0%
\langle backward mutations \rangle	7%	4%	8%	3%
\langle pathway number \rangle	1.8×10^3	58	131	6.1
$\langle \log_{10}(\text{pathway number}) \rangle$	2.2	1.2	1.6	0.6

*) The average $\langle \dots \rangle$ was restricted to accessible FLs: for each such FL we first calculated the corresponding quantity, and then averaged it over all accessible FLs. Statistical errors (s.e.m.) are at most +/-1 of the last digit.