S4 Table. Run time analysis.

# of cores Family	1	2	4	8	12	24	48
16S	59289	30113	14916	11563	5598	4267	2976
23S	3638	2533	1088	465	389	192	211
5S	0	0	0	0	0	0	1
g1	3323	1837	880	549	327	232	194
g2	3265	1728	884	509	300	219	196
rnasep	190229	97012	45339	32373	18631	14114	10434
tRNA	1165	540	269	175	101	75	52
tmRNA	3627	1822	967	662	331	221	204

This table shows the average runtime (unit: seconds, rounded to the nearest integer) versus different number of cores for the subgraph sampling algorithm to calculate the fingerprints in each functional RNA family. The runtime reduces as the number of cores increases.