

S1 Table. The Pan-genome and core genome development projections for investigated nineteen *T. pyogenes* strains.

Pan-genome development extrapolations		Core genome development extrapolations	
Contigs	Mean number of genes	Contigs	Mean number of genes
2	2258.020	2	1866.175
3	2379.335	3	1794.530
4	2480.355	4	1751.895
5	2556.745	5	1727.975
6	2626.260	6	1696.270
7	2691.545	7	1688.715
8	2755.005	8	1652.275
9	2810.825	9	1647.690
10	2866.105	10	1634.280
11	2903.440	11	1611.755
12	2951.120	12	1601.465
13	2996.825	13	1590.550
14	3035.105	14	1575.790
15	3074.840	15	1567.640
16	3109.275	16	1558.030
17	3141.885	17	1545.250
18	3180.080	18	1533.075
19	3215.565	19	1520.560
Heap's Law extrapolation		Heap's Law extrapolation	
Growth exponent y: 0.162 (alpha 0.838)		Converges to: 1488.954	
Confidence interval (95%) for y: 0.157 to 0.167		Confidence interval (95%): from 1457.440 to 1520.468	
Fitted model: $1980.179 * x^{0.162}$		Fitted model: $451.953 * \exp(-x/8.271) + 1488.954$	
Lower confidence interval formula: $1956.250 * x^{0.157}$		Lower confidence interval formula: $427.939 * \exp(-x/6.530) + 1457.440$	
Upper confidence interval formula: $2004.109 * x^{0.167}$		Upper confidence interval formula: $475.966 * \exp(-x/10.013) + 1520.468$	