Salmonella (with plasmids)

Salmonella Distance and Pangenome Size (With Plasmids)
Adj R2 = 0.39416 Intercept = 6083.9 Slope = 1252.6 P = 1.6496e−12
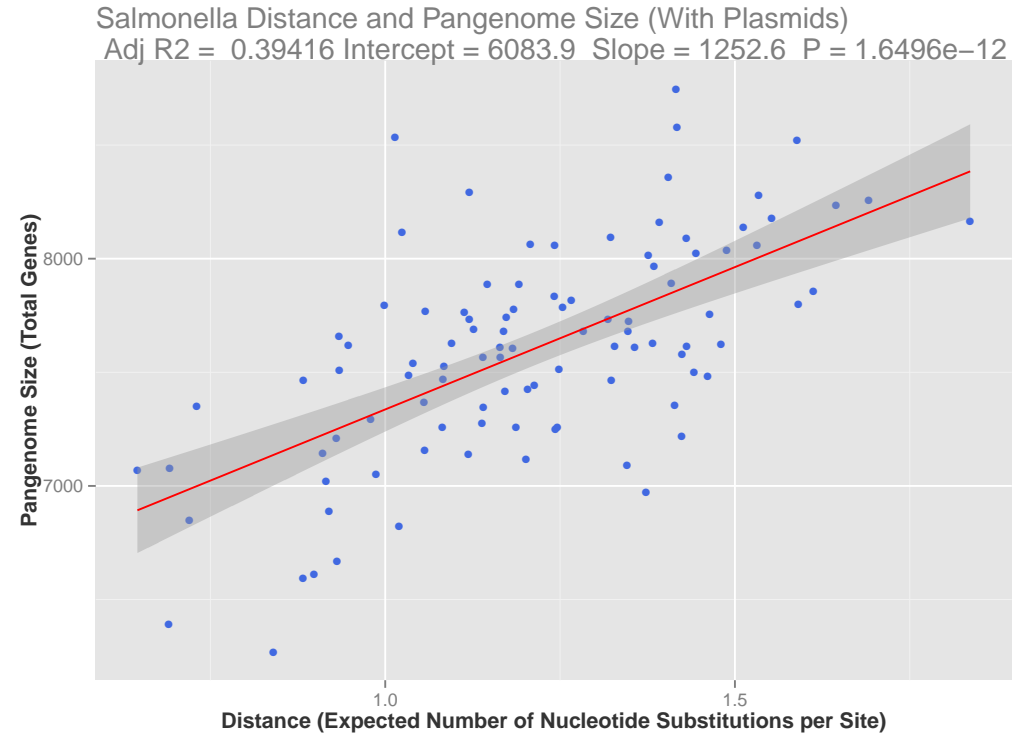


```
Residuals:
    Min       1Q  Median       3Q      Max
 −867.44  −248.82    34.71   208.10  1180.96


Coefficients:
           Estimate  Std. Error  t value  Pr(>|t|)
Intercept)   6083.9       190.8   31.887   < 2e−16 ***
distance     1252.6       154.9    8.088  1.65e−12 ***
___
Signif. codes:  0  ***  0.001  **  0.01  *  0.05  .  0.1
1

Residual standard error: 369.3 on 98 degrees of freedom
Multiple R−squared:  0.4003,     Adjusted R−squared:  0.3942
F−statistic: 65.41 on 1 and 98 DF,  p−value: 1.65e−12
```
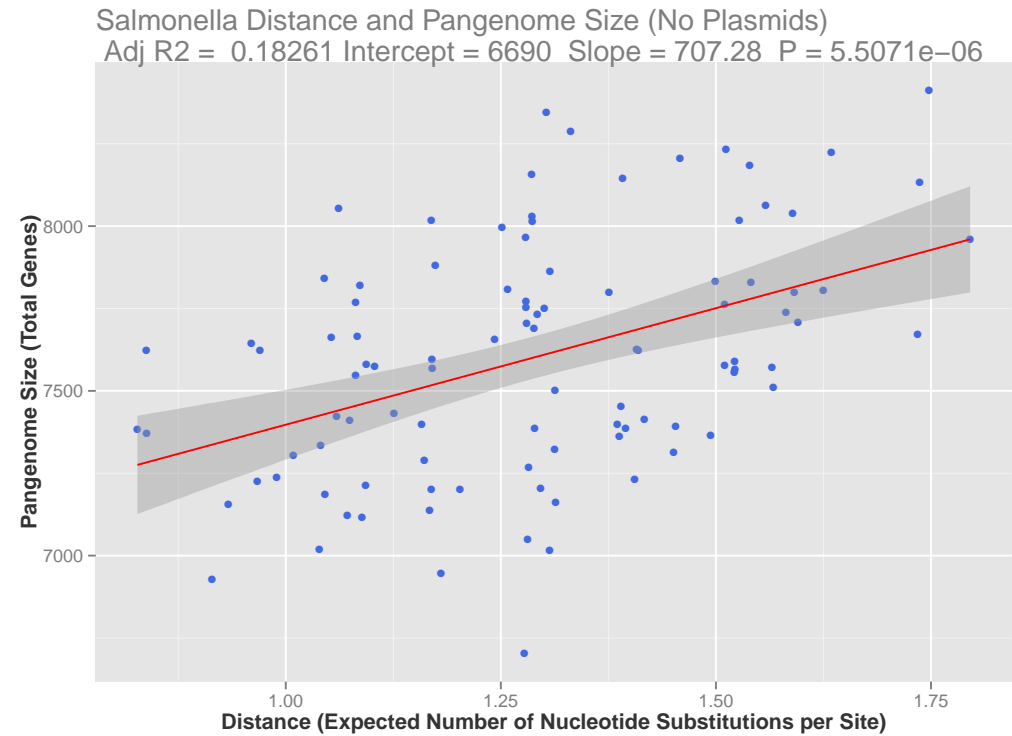
1

Salmonella

Salmonella Distance and Pangenome Size (No Plasmids)
Adj R2 = 0.18261 Intercept = 6690 Slope = 707.28 P = 5.5071e−06

Residuals:
Min	1Q	Median	3Q	Max
-890.36	-247.15	-16.13	232.67	733.39

Coefficients:

	Estimate	Std. Error	t value	$\Pr(>|t|)$	
(Intercept)	6690.0	192.3	34.789	$< 2e-16$	***
distance	707.3	147.1	4.808	$5.51e-06$	***

———

Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

Residual standard error: 323.1 on 98 degrees of freedom
Multiple R−squared: 0.1909,   Adjusted R−squared: 0.1826
F−statistic: 23.12 on 1 and 98 DF, p−value: 5.507e−06

2

E. coli

E. Coli Distance and Pangenome Size
Adj R2 = 0.40525 Intercept = 7015.5 Slope = 2759.8 P = 6.5818e−13
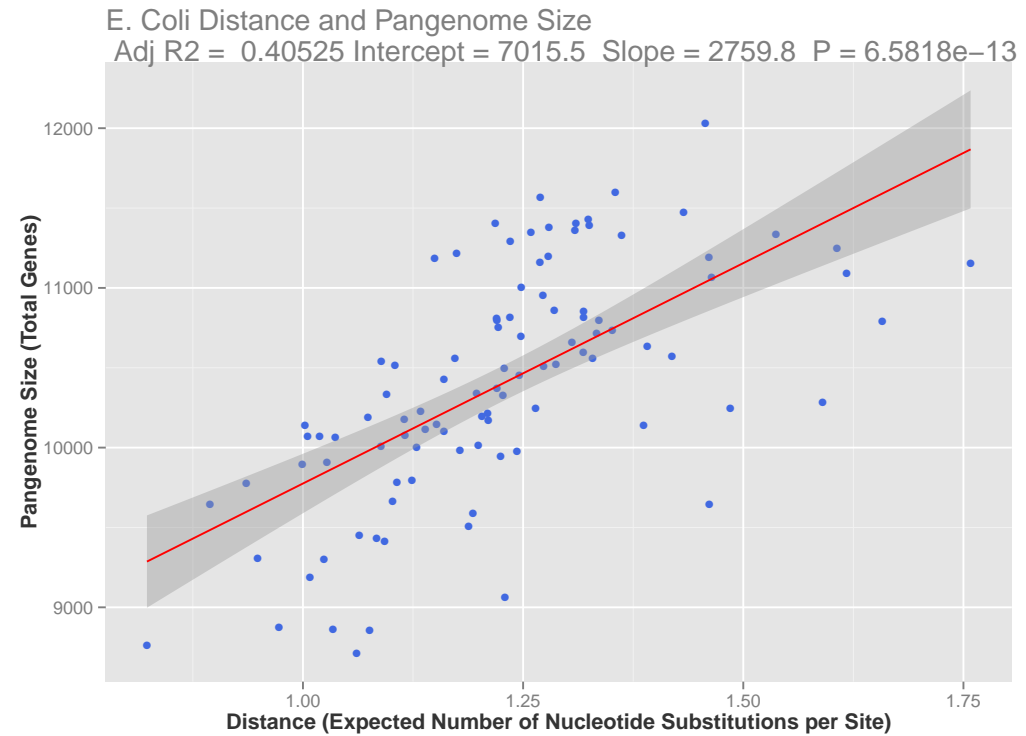
```
Residuals :
      Min          1Q     Median          3Q         Max
−1402.98    −320.12      16.56     360.71    1050.86


Coefficients :
              Estimate  Std. Error  t value  Pr(>|t|)
(Intercept)     7015.5       412.7   16.997   < 2e−16 ***
distance        2759.8       333.6    8.274  6.58e−13 ***
−−−
Signif . codes :  0  ***   0.001   **   0.01   *   0.05   .   0.1
1

Residual standard error : 559.6 on 98 degrees of freedom
Multiple R−squared :   0.4113 ,      Adjusted R−squared :   0.4053
F−statistic : 68.46 on 1 and 98 DF,   p−value : 6.582e−13
```
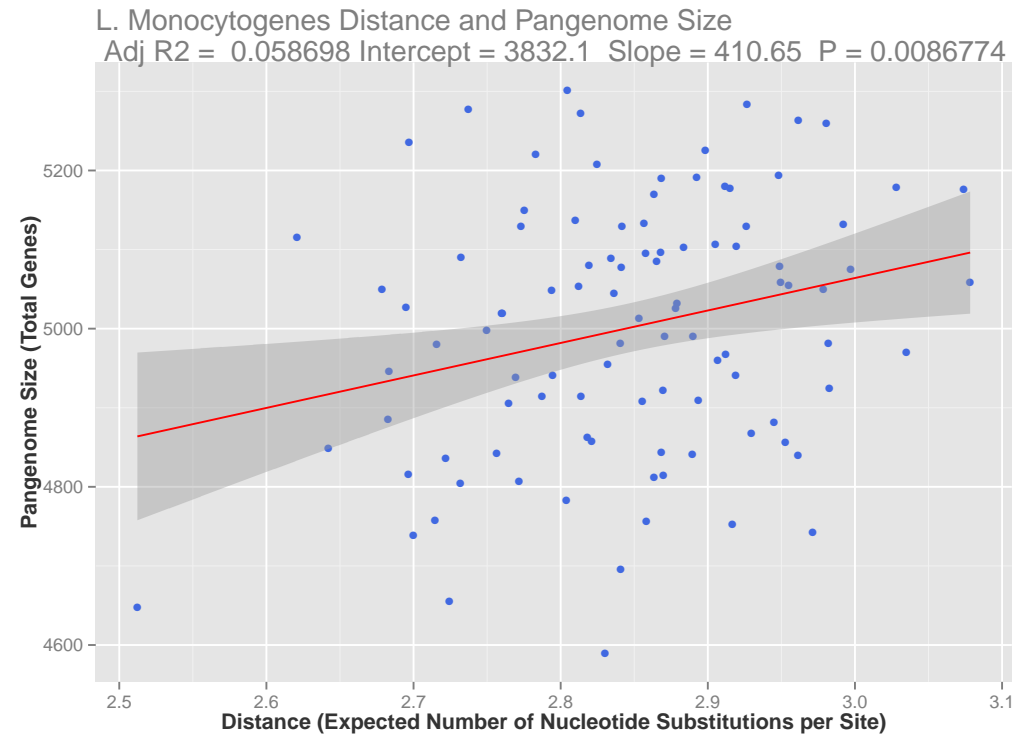
L. monocytogenes

L. Monocytogenes Distance and Pangenome Size
Adj R2 = 0.058698 Intercept = 3832.1 Slope = 410.65 P = 0.0086774

```
Residuals:
    Min        1Q    Median        3Q       Max
-405.30   -115.82     12.03     98.10    320.87

Coefficients:
               Estimate  Std. Error  t value  Pr(>|t|)
(Intercept)      3832.1       436.6    8.777  5.42e-14 ***
distance          410.7       153.3    2.678   0.00868 **
---
Signif. codes:  0  ***  0.001  **  0.01  *  0.05  .  0.1
1

Residual standard error: 156 on 98 degrees of freedom
Multiple R-squared:  0.06821,    Adjusted R-squared:  0.0587
F-statistic: 7.173 on 1 and 98 DF,  p-value: 0.008677
```
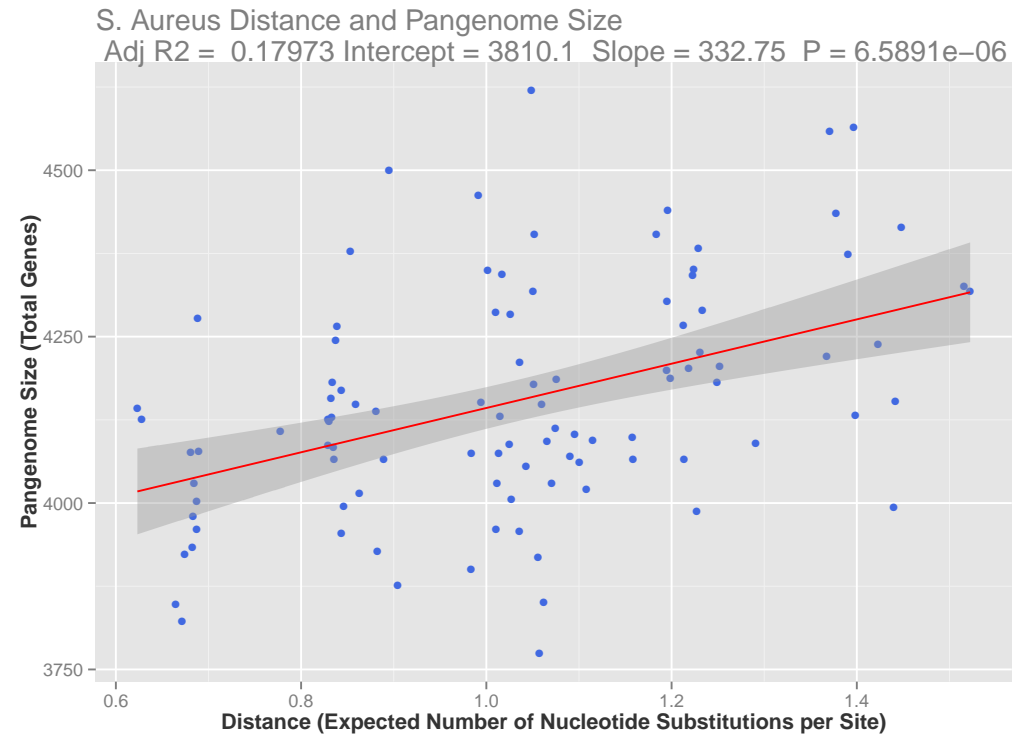
S.aureus

Residuals:

Min	1Q	Median	3Q	Max
-387.80	-102.91	-10.11	96.52	461.03

Coefficients:

	Estimate	Std. Error	t value	Pr($>$|t|)	
(Intercept)	3810.05	73.66	51.723	$< 2e-16$	$***$
distance	332.75	69.85	4.764	$6.59e-06$	$***$

———

Signif. codes: 0 $***$ 0.001 $**$ 0.01 $*$ 0.05 . 0.1
1

Residual standard error: 156.5 on 98 degrees of freedom
Multiple R−squared: 0.188,   Adjusted R−squared: 0.1797
F−statistic: 22.69 on 1 and 98 DF, p−value: 6.589e−06

S.pyogenes

S. Pyogenes Distance and Pangenome Size
Adj R2 = 0.41397 Intercept = 2553.2 Slope = 447.59 P = 3.1602e−13
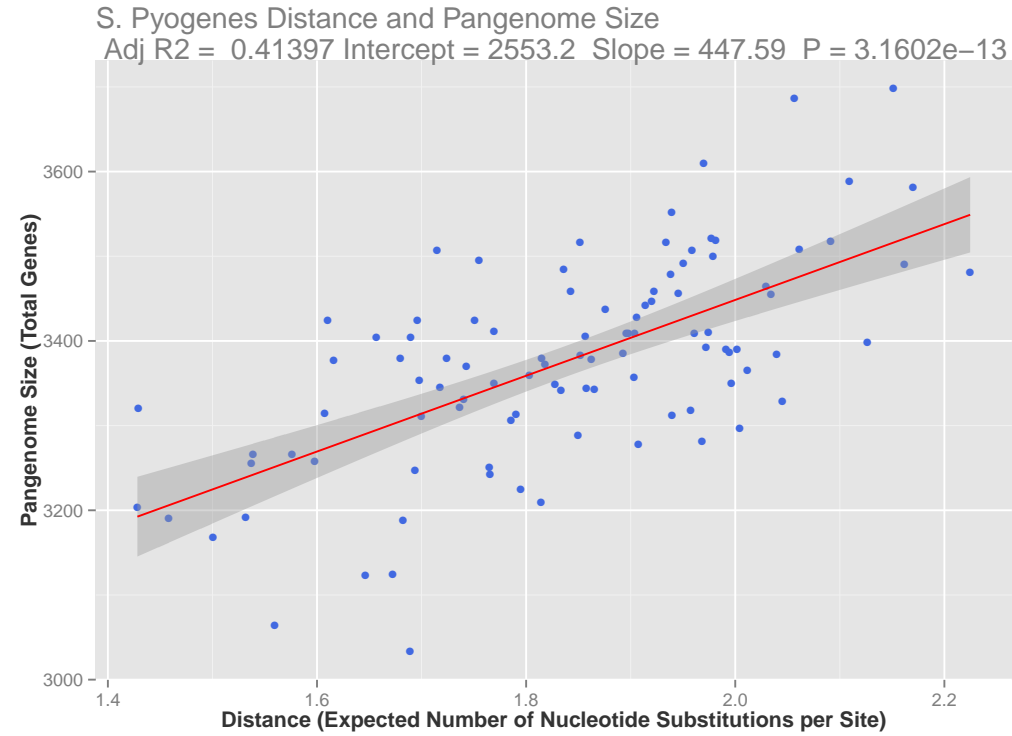

```
Residuals:
      Min         1Q     Median        3Q        Max
  −276.200    −55.087      4.264    58.879    213.287

Coefficients:
               Estimate  Std. Error  t value  Pr(>|t|)
(Intercept)    2553.23        98.21   25.998   < 2e−16 ***
distance        447.59        53.14    8.422  3.16e−13 ***
−−−
Signif. codes:  0  ***  0.001  **  0.01  *  0.05  .  0.1
1

Residual standard error: 92.02 on 98 degrees of freedom
Multiple R−squared:  0.4199,    Adjusted R−squared:  0.414
F−statistic: 70.93 on 1 and 98 DF,  p−value: 3.16e−13
```
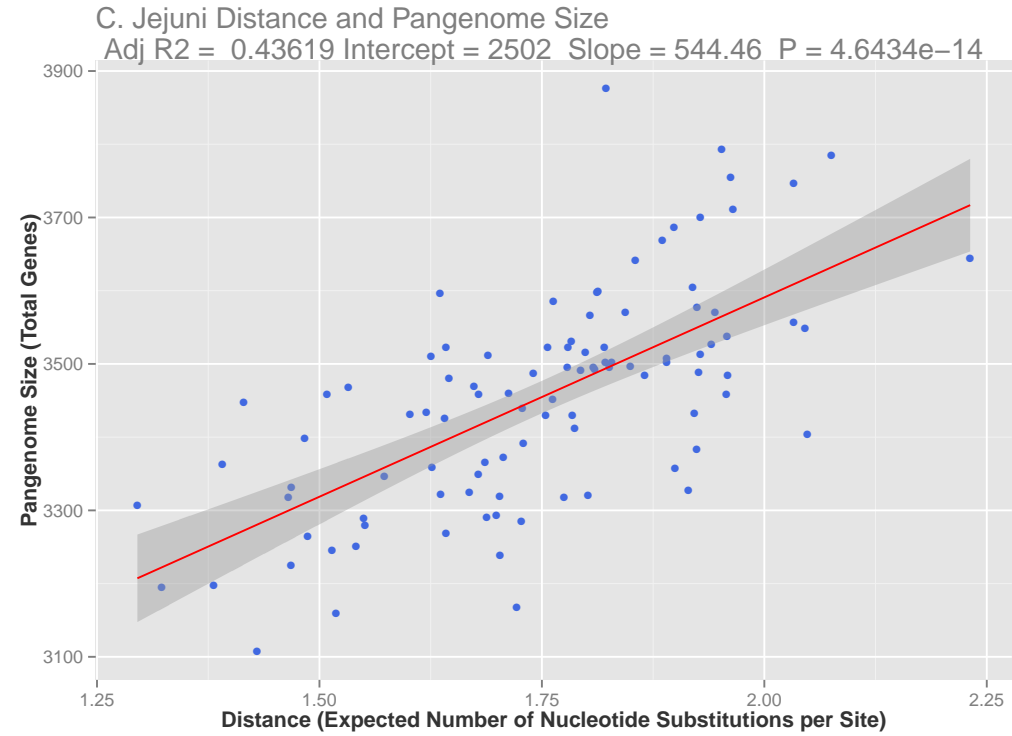
C. jejuni

C. Jejuni Distance and Pangenome Size
Adj R2 = 0.43619 Intercept = 2502 Slope = 544.46 P = 4.6434e−14

```
Residuals:
    Min       1Q    Median       3Q      Max
−271.35   −66.78    −2.52    68.55   382.06

Coefficients:
             Estimate  Std. Error  t value  Pr(>|t|)
(Intercept)   2501.96      108.62   23.035   < 2e−16 ***
distance       544.46       61.81    8.809  4.64e−14 ***
−−−
Signif. codes:  0  ***  0.001  **  0.01  *  0.05  .  0.1
1

Residual standard error: 111.6 on 98 degrees of freedom
Multiple R−squared:  0.4419,     Adjusted R−squared:  0.4362
F−statistic: 77.59 on 1 and 98 DF,  p−value: 4.643e−14
```
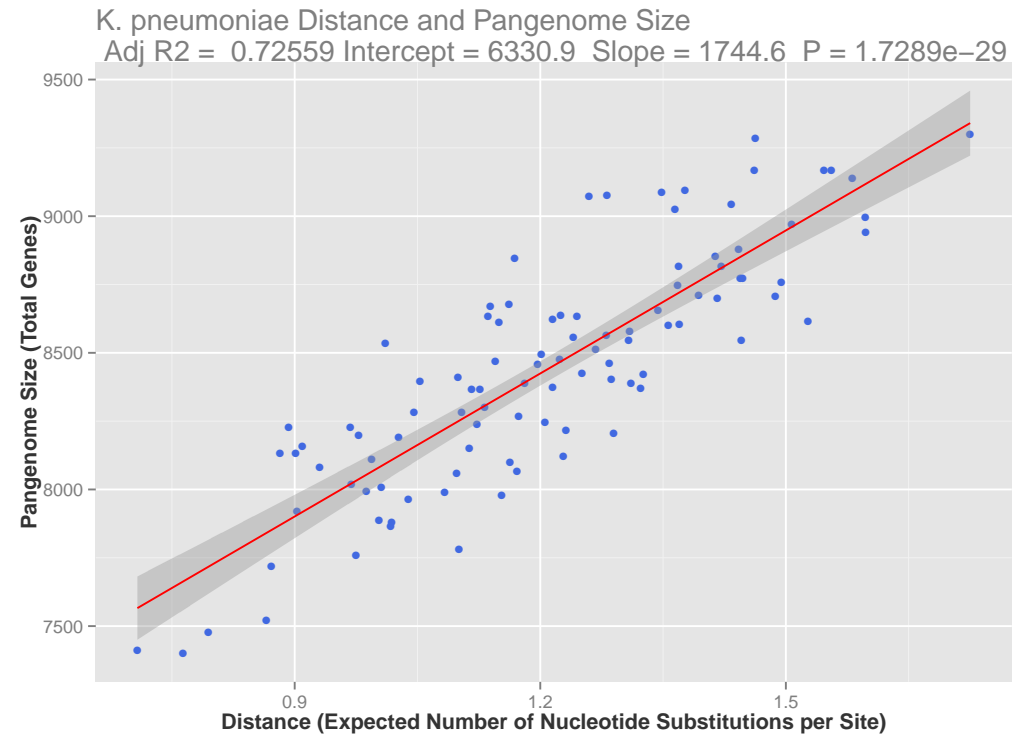
K. pneumoniae

K. pneumoniae Distance and Pangenome Size
Adj R2 = 0.72559 Intercept = 6330.9 Slope = 1744.6 P = 1.7289e−29

```
Residuals:
    Min       1Q   Median       3Q      Max
−470.28  −176.73    −3.73   138.30   543.38

Coefficients:
             Estimate  Std. Error  t value  Pr(>|t|)
(Intercept)   6330.9       132.0     47.97   <2e−16 ***
distance      1744.6       107.6     16.21   <2e−16 ***
−−−
Signif. codes:  0  ***  0.001  **  0.01  *  0.05  .  0.1
1

Residual standard error: 223.6 on 98 degrees of freedom
Multiple R−squared:  0.7284,     Adjusted R−squared:  0.7256
F−statistic: 262.8 on 1 and 98 DF,   p−value: < 2.2e−16
```
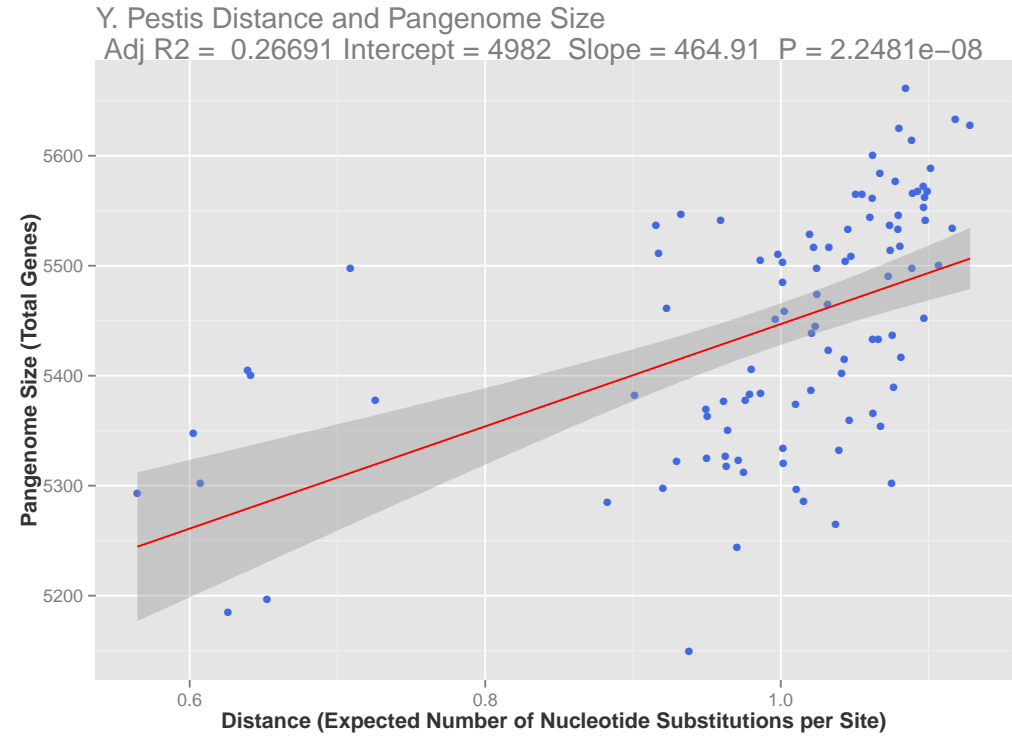
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Y. pestis (Roary with plasmids)

Y. Pestis Distance and Pangenome Size
Adj R2 = 0.26691 Intercept = 4982 Slope = 464.91 P = 2.2481e−08

Residuals:

Min	1Q	Median	3Q	Max
−269.14	−71.55	13.31	70.56	186.45

Coefficients:

	Estimate	Std. Error	t value	Pr($>$|t|)	
(Intercept)	4982.04	76.43	65.181	$< 2e-16$	***
distance	464.91	76.38	6.087	$2.25e-08$	***

___

Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1
1

Residual standard error: 95.16 on 98 degrees of freedom
Multiple R−squared: 0.2743,   Adjusted R−squared: 0.2669
F−statistic: 37.05 on 1 and 98 DF, p−value: 2.248e−08

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Y. Pestis (no plasmids)

Y. Pestis Pangenome Size and Distance (No Plasmid)
Adj R2 = 0.42301 Intercept = 4736 Slope = 424.89 P = 1.4614e−13


```
Residuals :
     Min        1Q    Median        3Q       Max
−168.458   −45.574     8.002    50.453   178.932

Coefficients :
              Estimate  Std.  Error  t  value  Pr(>|t|)
(Intercept)   4735.96          49.17    96.326   < 2e−16  ***
distance       424.89          49.53     8.578  1.46e−13  ***
___

Signif. codes:  0  ***  0.001  **  0.01  *  0.05  .  0.1
1

Residual standard error: 72.68 on 98 degrees of freedom
Multiple R−squared:  0.4288,      Adjusted R−squared:  0.423
F−statistic: 73.58 on 1 and 98 DF,  p−value: 1.461e−13
```
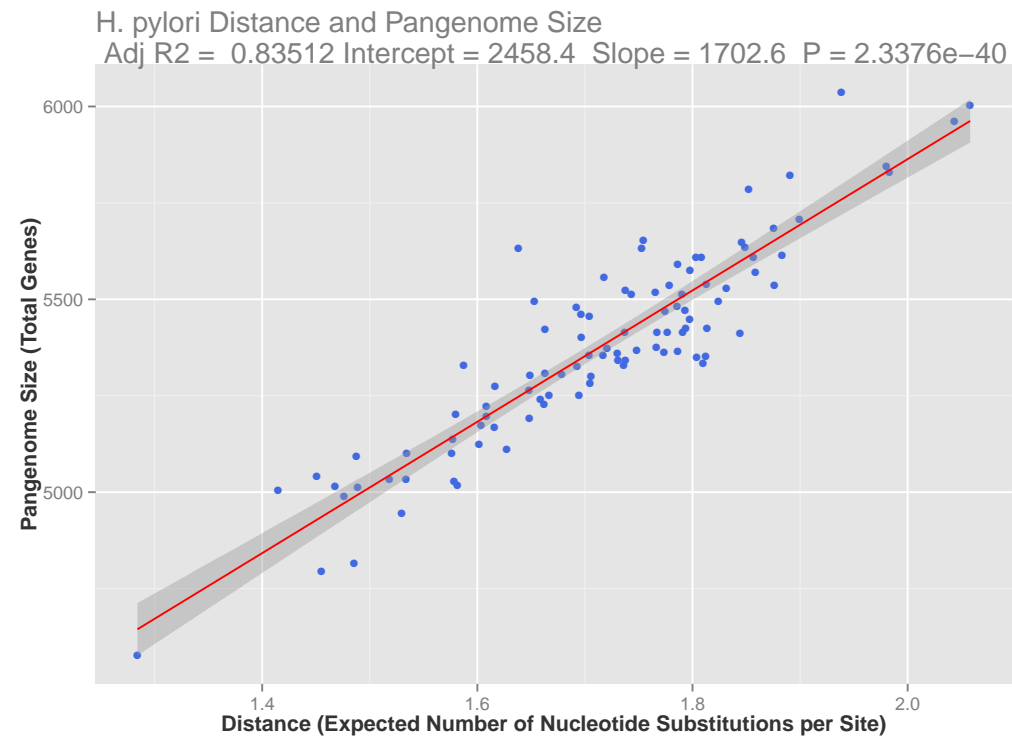
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H. pylori


```
Residuals:
    Min       1Q    Median       3Q       Max
-204.67   -68.46    -9.40    54.63    385.49

Coefficients:
             Estimate  Std. Error  t value  Pr(>|t|)
(Intercept)   2458.40      130.57    18.83   <2e-16 ***
distance      1702.57       75.96    22.41   <2e-16 ***
---
Signif. codes:  0  ***  0.001  **  0.01  *  0.05  .  0.1
1

Residual standard error: 104.6 on 98 degrees of freedom
Multiple R-squared:  0.8368,    Adjusted R-squared:  0.8351
F-statistic: 502.4 on 1 and 98 DF,  p-value: < 2.2e-16
```
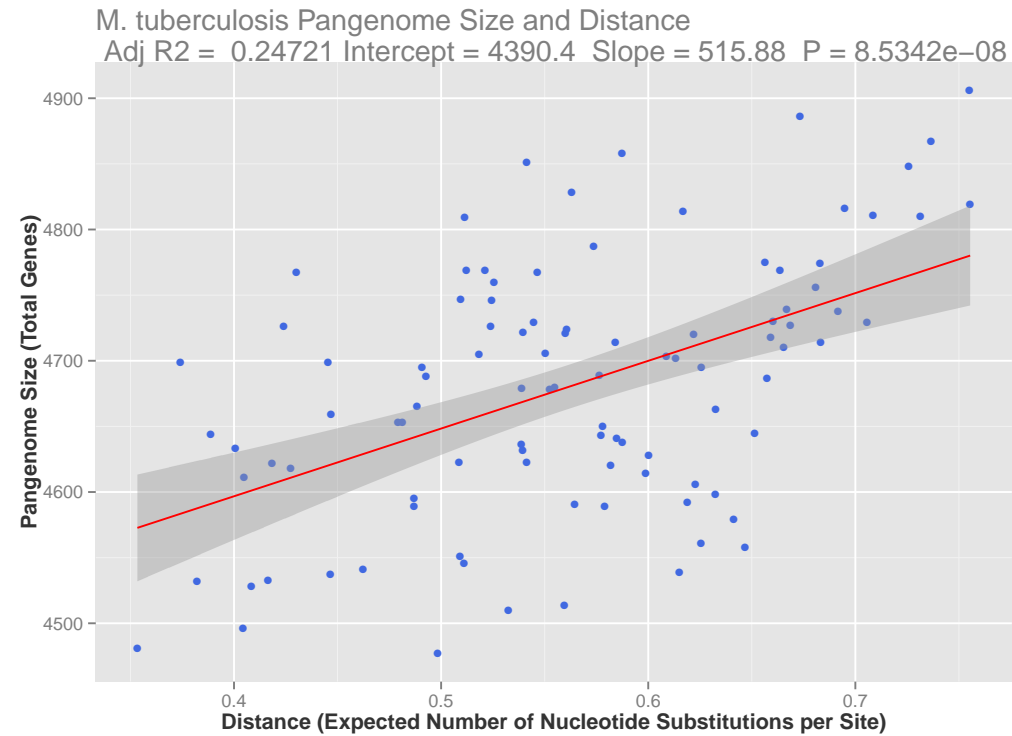
11

M. tuberculosis

M. tuberculosis Pangenome Size and Distance
Adj R2 = 0.24721 Intercept = 4390.4 Slope = 515.88 P = 8.5342e−08

```
Residuals :
    Min        1Q    Median        3Q       Max
−269.14    −71.55     13.31     70.56    186.45

Coefficients :
              Estimate  Std. Error  t value  Pr(>|t|)
(Intercept)    4982.04       76.43   65.181   < 2e−16  ***
distance        464.91       76.38    6.087  2.25e−08  ***
−−−
Signif. codes:  0  ***  0.001  **  0.01  *  0.05  .  0.1
1

Residual standard error: 95.16 on 98 degrees of freedom
Multiple R−squared:  0.2743,     Adjusted R−squared:  0.2669
F−statistic: 37.05 on 1 and 98 DF,   p−value: 2.248e−08
```

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