S2 Table. Slippage in repeat tracts during single colony analyses

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| **Gene** | **Area of the Major Peak Relative to Flanking Peaks1** |
| **G8** | **G9** | **G10** | **G11** | **G12** |
| *cj0275* | **90%**n=90, s.d.=0.8 |  |  |  |  |
| *cj0685* | **84%**n=79, s.d.=4.5 | **82%**n=13, s.d.=0.8 |  |  |  |
| *cj1139* | **83%**n=77, s.d.=2.8 | **80%**n=13, s.d.=7.1 |  |  |  |
| *cj1144* |  | **77%**n=87, s.d.=2.8 |  |  |  |
| *cj1295* |  | **82%**n=36, s.d.=5.8 | **68%**n=52, s.d.=2.1 |  |  |
| *cj1310* |  | **80%**n=35, s.d.=6.0 | **68%**n=55, s.d.=1.1 |  |  |
| *cj1422* |  | **80%**n=30, s.d.=1.1 | **67%**n=51, s.d.=3.6 | **54%**n=4, s.d.=0.5 |  |
| *cj1321* |  |  | **75%**n=79, s.d.=2.6 | **64%**n=10, s.d.=1.0 |  |
| *cj1426* |  |  | **72%**n=84, s.d.=1.0 | **63%**n=6, s.d.=2.0 |  |
| *cj1429* |  |  | **77%**n=86, s.d.=1.2 |  |  |
| *cj0628* (*capA*) |  |  | **74%**n=24, s.d.=11.2 | **62%**n=57, s.d.=4.8 | **63%**n=9, s.d.=0.7 |
| **Average** | **86%**n=246, s.d.=4.3 | **79%**n=214, s.d.=4.7 | **72%**n=431, s.d.=4.9 | **62%**n=77, s.d.=4.6 | **63%**n=9, s.d.= 0.7 |

1The percentage area under the major peak is determined by dividing the area under the major peak by the combined areas under all the peaks and multiplying by 100; n, number of colonies; sd, standard deviation of all measurements.