```
==== Set Summary: set1 | Target: ompW ====
Total Genomes: 562
Genomes with ALL oligos: 514 (91.46%)
Genomes with SOME oligos: 48
Genomes with NONE: 0


Per-oligo coverage:
   F3 : 546 (97.15%)
   B3 : 523 (93.06%)
   LF : 522 (92.88%)
   LB : 527 (93.77%)
   FIP_1 : 562 (100.00%)
   FIP_2 : 520 (92.53%)
   BIP_1 : 540 (96.09%)
   BIP_2 : 527 (93.77%)


Mismatch Summary (per oligo):
   F3 : mean 0.04 | median 0 | sd 0.19 | min 0 | max 1 | n 546
   B3 : mean 0.02 | median 0 | sd 0.16 | min 0 | max 2 | n 523
   LF : mean 0.26 | median 0 | sd 0.48 | min 0 | max 2 | n 522
   LB : mean 0 | median 0 | sd 0.06 | min 0 | max 1 | n 527
   FIP_1 : mean 1.8 | median 2 | sd 0.59 | min 0 | max 2 | n 562
   FIP_2 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 520
   BIP_1 : mean 0.14 | median 0 | sd 0.41 | min 0 | max 2 | n 540
   BIP_2 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 527



==== Set Summary: set2 | Target: tcpA ====
Total Genomes: 26
Genomes with ALL oligos: 24 (92.31%)
Genomes with SOME oligos: 0
Genomes with NONE: 2


Per-oligo coverage:
   F3 : 24 (92.31%)
   B3 : 24 (92.31%)
   LF : 24 (92.31%)
   LB : 24 (92.31%)
   FIP_1 : 24 (92.31%)
   FIP_2 : 24 (92.31%)
   BIP_1 : 24 (92.31%)
```

```
    BIP_2 : 24 (92.31%)


Mismatch Summary (per oligo):
    F3 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 24
    B3 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 24
    LF : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 24
    LB : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 24
    FIP_1 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 24
    FIP_2 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 24
    BIP_1 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 24
    BIP_2 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 24



==== Set Summary: set3 | Target: O1rfb ====
Total Genomes: 26
Genomes with ALL oligos: 26 (100.00%)
Genomes with SOME oligos: 0
Genomes with NONE: 0


Per-oligo coverage:
    F3 : 26 (100.00%)
    B3 : 26 (100.00%)
    LF : 26 (100.00%)
    LB : 26 (100.00%)
    FIP_1 : 26 (100.00%)
    FIP_2 : 26 (100.00%)
    BIP_1 : 26 (100.00%)
    BIP_2 : 26 (100.00%)


Mismatch Summary (per oligo):
    F3 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 26
    B3 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 26
    LF : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 26
    LB : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 26
    FIP_1 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 26
    FIP_2 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 26
    BIP_1 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 26
    BIP_2 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 26



==== Set Summary: set4 | Target: O139rfb ====
Total Genomes: 3700
```

```
Genomes with ALL oligos: 26 (0.70%)
Genomes with SOME oligos: 28
Genomes with NONE: 3646


Per-oligo coverage:
   F3 : 28 (0.76%)
   B3 : 52 (1.41%)
   LF : 26 (0.70%)
   LB : 26 (0.70%)
   FIP_1 : 26 (0.70%)
   FIP_2 : 26 (0.70%)
   BIP_1 : 26 (0.70%)
   BIP_2 : 26 (0.70%)


Mismatch Summary (per oligo):
   F3 : mean 0.14 | median 0 | sd 0.52 | min 0 | max 2 | n 28
   B3 : mean 1 | median 1 | sd 1.01 | min 0 | max 2 | n 52
   LF : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 26
   LB : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 26
   FIP_1 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 26
   FIP_2 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 26
   BIP_1 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 26
   BIP_2 : mean 0 | median 0 | sd 0 | min 0 | max 0 | n 26
```