

**Additional data file 6:**

**Replicate-to-replicate comparisons of transcript microarray signal intensities from wild-type polysome gradients\***

|                               | fraction 1 | fraction 2 | fraction 3 | fraction 4 |
|-------------------------------|------------|------------|------------|------------|
| replicate 1 v.<br>replicate 2 | 0.51       | 0.69       | 0.69       | 0.83       |
| replicate 1 v.<br>replicate 3 | 0.57       | 0.86       | 0.87       | 0.95       |
| replicate 2 v.<br>replicate 3 | 0.86       | 0.68       | 0.77       | 0.87       |

**Replicate-to-replicate comparisons of transcript microarray signal intensities from *smaug* mutant polysome gradients\***

|                               | fraction 1 | fraction 2 | fraction 3 | fraction 4 |
|-------------------------------|------------|------------|------------|------------|
| replicate 1 v.<br>replicate 2 | 0.67       | 0.77       | 0.79       | 0.70       |
| replicate 1 v.<br>replicate 3 | 0.63       | 0.69       | 0.84       | 0.82       |
| replicate 2 v.<br>replicate 3 | 0.60       | 0.70       | 0.84       | 0.82       |

**Replicate-to-replicate comparisons of transcript microarray signal intensities from *smaug* mutant polysome gradients +/- puromycin\***

|                                                | fraction 1 | fraction 2 | fraction 3 | fraction 4 |
|------------------------------------------------|------------|------------|------------|------------|
| replicate 1 v.<br>replicate 2<br>(- puromycin) | 0.68       | 0.95       | 0.95       | 0.96       |
| replicate 1 v.<br>replicate 2<br>(+ puromycin) | 0.90       | 0.96       | 0.96       | 0.74       |

\*The Pearson correlation coefficient was calculated for each pair of replicates and was used to determine the degree of similarity between them. All replicates are biological replicates.