

**Supplemental Table S14****Similarity in classification between Ki67 and prognostic gene signatures, Stockholm material**

| <b>GGI</b>               | <b>Ki67 (%)</b> |   |    |    |    |    |    |     | <b>AUC</b> | <b>Similarity</b> |
|--------------------------|-----------------|---|----|----|----|----|----|-----|------------|-------------------|
|                          | <8              | 8 | 10 | 11 | 12 | 17 | 20 | >20 |            |                   |
| Grade1                   | 33              | 4 | 0  | 2  | 14 | 1  | 2  | 7   | 0.71       | 64 %              |
| Grade3                   | 6               | 3 | 1  | 0  | 5  | 2  | 0  | 14  |            |                   |
| <b>70-gene signature</b> |                 |   |    |    |    |    |    |     |            |                   |
| Good                     | 32              | 2 | 0  | 1  | 9  | 2  | 2  | 6   | 0.73       | 69 %              |
| Poor                     | 7               | 5 | 1  | 1  | 10 | 1  | 0  | 15  |            |                   |
| <b>Recurrence score</b>  |                 |   |    |    |    |    |    |     |            |                   |
| Low                      | 18              | 1 | 0  | 1  | 7  | 2  | 2  | 6   | 0.66       | 64 %              |
| Intermediate             | 11              | 1 | 0  | 0  | 3  | 0  | 0  | 1   |            |                   |
| High                     | 10              | 5 | 1  | 1  | 9  | 1  | 0  | 14  |            |                   |

Best signature-reproducing Ki67 cutoffs were identified with receiver operating characteristics (ROC). For recurrence score levels were grouped to most accurately reflect outcome similarities/ dissimilarities: high vs. intermediate/low. The area under the curve (AUC; from ROC-analysis) and similarity with best performing cut-off (indicated with dashed red line) for each gene classifier on the right.