Supplementary Materials 2 – Modelling of changes

Method

Contingency tables described in box 1 of the main paper were compiled with starting values based on 1000 cancers as follows:

- True Positive, sensitivity*1000;
- False Negatives, (1-sensitivty)*1000
- False positives ,2 * True Positives;
- True Negative, reciprocal of assumed cancer prevalence rate in symptomatic patients multiplying factor *1000 – (sum of other three cells).

Initial specificity was calculated as true negative / (false positive + true negative) and was compared with the observed specificity from the data (reported to a precision of 4 decimal places). The algorithm then successively incremented the False Positive cell and decremented the False Negative cell by one and recalculated the specificity until this equalled or was below the observed specificity from the original data. At this point the algorithm stopped and the value of the False Positive cell was noted.

The algorithm was run separately for each quintile of age-standardised fast-track referral rate and the difference between quintiles calculated for number of additional cancers diagnosed via the urgent pathway (difference in True Positives), and number of additional referrals (difference in True Positives + False Positives)