Outstanding issues with the current PREDICT Prostate model:

-Revert colours for graphs to previous version

-Switch title for dotted yellow line to ‘survival rate excluding deaths from prostate cancer’ (as per breast cancer model) and info button with equivalent text

-Keep BOTH Gleason scale and 'grade group' tabs (remove other options from settings)

Additions to the current PREDICT Prostate model:

1. Addition of BRCA

-**Proven mutation of the BRCA gene? Yes/No**

Info button: “BRCA is the 'Breast Cancer gene'. In men, abnormalities in this gene are very rare. However, there is some evidence that mutations in the BRCA1/2 genes may worsen the outcomes of prostate cancer. The full research can be read here: <http://ascopubs.org/doi/abs/10.1200/jco.2012.43.1882>

Further information on BRCA is available here:

<https://prostatecanceruk.org/about-us/news-and-views/2013/8/brca-genes-myth-busters>”

Add beta coefficient of +0.956 into piPCSM if ‘Yes’ for BRCA mutation. No change if ‘No’.

1. Number of biopsy cores involved

-**Diagnosed by targeted biopsy? Yes/**No   
(If ‘no’ continue to biopsy section as normal…)  
(If ‘yes’ continue to biopsy section and display a note saying:)  
“Any number of biopsies from ONE target should be considered as ONE biopsy…” (info button: “For example, if 4 cores were taken from a target in addition to 12 ‘systematic’ cores then the total number of biopsy cores taken should be 13 (12+1). If 3 target cores and 6 systematic cores had cancer in them the number of biopsy cores with any prostate cancer should be 7 (6+1)”.)

-**Total number of biopsy cores taken XX**Info button: “This is the total number of biopsies taken from the prostate, counting any number of biopsies from a single target lesion as ONE biopsy core.”

-**Number of biopsy cores with any prostate cancer XX**

Info button: “Biopsy cores with any prostate cancer reported in them should be counted – regardless of grade of cancer. Any number of cores with cancer from a single target lesion should be counted as ONE biopsy core with cancer. ”

Remove ‘biopsy50’ bits from piPCSM code

Generate PPC [percentage positive cores] = (number of cores with cancer/total cores taken)\*100

Add beta coefficient to piPCSM of +(((PPC+0.1811159)/100)^.5-.649019)\*1.890134

No change if Biopsy percentage/info unknown.