**Table 2.** *Boruta-derived features positively selected for each model. Features are selected for each model by being confirmed as important for predicting biopsy outcome, categorised as a modified ordinal variable (see Methods) by Boruta in ≥ 90% of bootstrap resamples. Variables selected for the fully integrated model (ExoMeth) are in the highlighted column; for example; Age is selected within the SoC model, but not in ExoMeth.*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Models:** | | | |
| **SoC** | **Methylation** | **ExoRNA** | **ExoMeth** |
| Clinical Parameters: | Serum PSA | *-* | ***-*** | Serum PSA |
| Age | *-* | ***-*** | ***-*** |
| Methylation  Targets: | ***-*** | *GSTP1* | ***-*** | *GSTP1* |
| ***-*** | *APC* | ***-*** | *APC* |
| ***-*** | *SFRP2* | ***-*** | *SFRP2* |
| ***-*** | *IGFBP3* | ***-*** | *IGFBP3* |
| ***-*** | *IGFBP7* | ***-*** | *IGFBP7* |
| ***-*** | *PTGS2* | ***-*** | *PTGS2* |
| Transcript  Targets | ***-*** | ***-*** | *AMACR* | ***-*** |
| ***-*** | ***-*** | *ERG exons 4-5* | *ERG exons 4-5* |
| ***-*** | ***-*** | *ERG exons 6-7* | *ERG exons 6-7* |
| ***-*** | ***-*** | *GJB1* | *GJB1* |
| ***-*** | ***-*** | *HOXC6* | *HOXC6* |
| ***-*** | ***-*** | *HPN* | *HPN* |
| ***-*** | ***-*** | *PCA3* | *PCA3* |
| ***-*** | ***-*** | *PPFIA2* | ***-*** |
| ***-*** | ***-*** | *RPS10* | ***-*** |
| ***-*** | ***-*** | *SNORA20* | *SNORA20* |
| ***-*** | ***-*** | *TIMP4* | *TIMP4* |
| ***-*** | ***-*** | *TMPRSS2/ERG fusion* | *TMPRSS2/ERG fusion* |