RESPOND – suggestions for coding registry vars for cohort B

Items in red not available from Texas

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|  | 2015 | 2016-2017 | 2018 |
| Gleason (biopsy) | csSiteSpecificFactor8\*  categorize as  <=6: “002”-“006”  7: “007”  8-10: “008 – “010”  Unknown/not done “000”, “988”, “998”, “999” | csSiteSpecificFactor8\*  categorize as  <=6: “002”-“006”  7: “007”  8-10: “008 – “010”  Unknown/not done “000”, “988”, “998”, “999” | gleasonScoreClinical  categorize as  <=6: “02”-“06”  7: “07”  8-10: “08 – “10”  Unknown/not done “”X7”, “X8”, “X9” |
| Gleason (RP) | csSiteSpecificFactor10\*  categorize as  <=6: “002”-“006”  7: “007”  8-10: “008 – “010”  Unknown/not done “000”, “988”, “998”, “999” | csSiteSpecificFactor10\*  categorize as  <=6: “002”-“006”  7: “007”  8-10: “008 – “010”  Unknown/not done “000”, “988”, “998”, “999” | gleasonScorePathological  categorize as  <=6: “02”-“06”  7: “07”  8-10: “08 – “10”  Unknown/not done “”X7”, “X8”, “X9” |
| PSA | csSiteSpecificFactor1  categorize as  <10ng/ml: “001”-“099”  10-20 ng/ml: “100”- “200”  >20 ng/ml: “201”-“980”  Unknown/not done/result not available: “000”, “981”-“990”, “997”-“999” | csSiteSpecificFactor1  categorize as  <10ng/ml:  10-20 ng/ml: “100”- “200”  >20 ng/ml: “201”-“980”  Unknown/not done/result not available: “000”, “981”-“990”, “997”-“999” | psaLabValue  <10ng/ml: 0.1-9.9  10-20 ng/ml: 10.0-20.0  >20 ng/ml: 20.1-999.9, “XXX.1”  Unknown/not done/result not available: “XXX.7”, “XXX.9” |
| T stage (clinical) | csExtension  categorize as  <=T2a: “100”- “150”, “210”  T2b-T2c, T2NOS: “200”, “220”-“240”, “300”  T3-T4: “410”- “750”  Unknown/no evidence of primary tumor: “000”, “950”, “999” | tnmClinT  categorize as  <=T2a: “c1”, “c1A”, “c1B”, “c1C”, “c2A”, “p2A”  T2b-T2c, T2NOS: “c2”, “c2B”, “c2C”, “p2”, “p2B”, “p2C”  T3-T4 (based on 1st 2 chars): “c3”, “c4”, “p3”, “p4”  Unknown/no evidence of primary tumor: “cX”, “c0”, “88”, “ “ | eodPrimaryTumor  categorize as  <=T2a: “100”- “200”  T2b-T2c, T2NOS: “210”, “220”, “250”, “300”  T3-T4: “350”- “700”  Unknown/no evidence of primary tumor: “000”, “800”, “999” |
| LN involvement (combined clinical and pathologic) | csLymphNodes  *categorize as*  N0: “000”  N1: “100”, “800”  NX: “999” | derivedSeerCombinedN  *categorize based on 1st 2 characters as*  N0: “c0”, “p0”  N1: “c1”, “p1”  NX: “cX”, “pX”, “ “, “88”  or use combination of tnmClinN + tnmPathN variables to obtain equivalent of above | eodRegionalNodes  categorize as  N0: “000”  N1: “300”, “800”  NX: “999” |
| Distant metastases (combined clinical and pathologic) | csMetsAtDx  *categorize as*  M0/MX: “00” ,“99”  M1: “11”-“60” | derivedSeerCombinedM  *categorize based on 1st 2 characters as*  M0/MX: “c0”, “p0”, “ “, “88”  M1: “c1”, “p1”  or use combination of tnmClinM + tnmPathM to obtain equivalent of above | eodMets  *categorize as*  M0/MX: “00”, “99”  M1: “10”-“70” |
| SEER Summary stage | seerSummaryStage2000  categorize as  Localized: “1”  Regional: “2”-“5”  Distant: “7”  Unknown: “9” | seerSummaryStage2000  categorize as  Localized: “1”  Regional: “2”-“5”  Distant: “7”  Unknown: “9” | summaryStage2018  categorize as  Localized: “1”  Regional: “2”-“4”  Distant: “7”  Unknown: “9” |

**\*Note: TX does not list CS Site Specific Factors 8 and 10 in data dictionary but did collect them 2011-2017 and they should be available if requested**

Possible modifications to include 2018 TX data

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| TX does not have available | Affects | Possible Workaround |
| eodPrimaryTumor | Clinical T (2018) | Use summary stage 2018 (may be able to delineate T2 or less vs T3/T4) |
| eodRegionalNodes | LN involvement (2018) | Use summary stage2018 to identify LN involvement |
| eodMets | Distant mets (2018) | Use summary stage 2018 to identify distant mets |
| derivedSEERCombinedN |  | Use combination of tnmClinN + tnmPathN to derive equivalent |
| derivedSEERCombinedM |  | Use combination of tnmClinM + tnmPathM to derive equivalent |
| GleasonScoreClinical | Gleason biopsy (2018) | Use gradeClinical |
| gleasonScorePathological | Gleason RP (2018) | Use gradePathological |

Risk groups

Would prefer to create risk groups based on clinical T, lymph node status, distant metastases, PSA value, and biopsy Gleason score

TX does not collect the necessary variables in 2018 to be able to do this. If want to use TX data for risk groups can use SEER summary stage to infer the T, N, and M. Still would use PSA value. For Gleason score could use grade clinical. Would not be able to define low risk because SEER summary stage Localized encompasses both low and intermediate categories for T stage. Would therefore end up with 2 categories: low/intermediate and high/N1/M1

Approximations:

SS2018 to TNM

1: <=T2, N0, M0

2: T3-T4, N0, M0

3: <=T2, N1, M0

4: T3-T4,N1, M0

7: Any T, Any N, M1

GradeClinical/Pathological to Gleason score:

Gleason <=6: “1” (probably could also include “A”)

Gleason 7: “2”, “3”, “E” (probably could include “B”)

Gleason 8-10: “4”, “5”, (probably could also include “C”, “D”)

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| --- | --- | --- | --- | --- | --- |
| Risk group | SS2018 |  | Grade Clinical (2018) |  | PSA value (2018) |
| Low/intermediate | 1 | AND | 1,2,3,E (A,B) | AND | 0.1-20.0 |
| High risk localized/N1/M1 | 2,3,4,7 | OR | 4,5, (C,D) | OR | 20.1-999.9, XXX.1 |