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The following report contains a description of the request, request specifications, and results from the modular program run(s).

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Overview for Request cder_mpl1r_wp022_nsdp_v02

Request ID: cder_mpl1r_wp022_nsdp_v02

Query Description: This report contains estimated distribution of baseline covariates among members receiving various genetic tests: KRAS, BRAF, EGFR, BCR-ABL, and BRCA.

Sentinel Modular Program Tool Used: Cohort Identification and Descriptive Analysis (CIDA) tool, version 2.2.1

<u>Data Source:</u> The query was run against the Sentinel Distributed Database (SDD) for the time period of January 1, 2013 to December 31, 2015. The request was distributed to 14 Data Partners on June 17, 2016. See Appendix A for a list of the latest dates of available data for each Data Partner.

Study Design: This request was designed to assess baseline covariates for each cohort of interest.

Exposure of Interest: The exposures of interest were five different genetic tests of the respective genes V-Ki-ras2 Kirsten rat sarcoma viral oncogene (KRAS), v-raf murine sarcoma viral oncogene homolog B1 (BRAF), epidermal growth factor receptor (EGFR), breakpoint cluster region-abelson (BCR-ABL), and the breast cancer susceptibility gene (BRCA). These tests were defined using Healthcare Common Procedure Coding System (HCPCS) Level II procedure codes and Current Procedural Terminology (CPT), 4th Edition procedure codes. Please refer to Appendix B for specific codes.

<u>Cohort Eligibility Criteria:</u> Those included in the cohort were required to be continuously enrolled in plans with both medical and drug coverage for at least 6 months (183 days) prior to their genetic test date, during which gaps in coverage of up to 45 days were allowed. The first valid incident genetic test in the query period to occur was examined.

<u>Baseline Covariates</u>: The following covariates were assessed during the baseline period: age, sex, comorbidity score, and health service utilization. Occurrence of these covariates was evaluated in the 6 months (183 days) prior to the date of genetic test.

Limitations: Algorithms to define exposures are imperfect and, therefore, may be misclassified.

Please see the Appendix C for the specifications of parameters used in the analyses for this request.

Notes: Please contact the Sentinel Operations Center Query Fulfillment Team (production@mini-sentinel.org) for questions and to provide comments/suggestions for future enhancements to this document.



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Glossary of Terms for Analyses Using Cohort Identification and Descriptive Analysis (CIDA) Tool*

Amount Supplied - number of units (pills, tablets, vials) dispensed. Net amount per NDC per dispensing. This is equivalent to the "RxAmt" value in the MSCDM.

Blackout Period - number of days at the beginning of a treatment episode that events are to be ignored. If an event occurs during the blackout period, the episode is excluded.

Care Setting - type of medical encounter or facility where the exposure, event, or condition code was recorded. Possible care settings include: Inpatient Hospital Stay (IP), Non-Acute Institutional Stay (IS), Emergency Department (ED), Ambulatory Visit (AV), and Other Ambulatory Visit (OA). For laboratory results, possible care settings include: Emergency department (E), Home (H), Inpatient (I), Outpatient (O), or Unknown or Missing (U). Along with the Principal Diagnosis Indicator, forms the Care Setting/PDX parameter.

Cohort Definition (drug/exposure) - indicates how the cohort will be defined: 1: Cohort includes only the first valid incident treatment episode during the query period; 2: Cohort includes all valid incident treatment episodes during the query period; 3: Cohort includes all valid incident treatment episodes during the query period until an event occurs.

Days Supplied - number of days supplied for all dispensings in qualifying treatment episodes.

Episodes - treatment episodes; length of episode is determined by days supplied in one dispensing or consecutive dispensings bridged by **Eligible Members** - number of members eligible for an incident treatment episode (defined by the drug/exposure and event washout periods) with drug and medical coverage during the query period.

Years at Risk - number of days supplied plus any episode gaps and exposure extension periods all divided by 365.25.

Enrollment Gap - number of days allowed between two consecutive enrollment periods without breaking a "continuously enrolled" **Episode Gap** - number of days allowed between two (or more) consecutive exposures (dispensings/procedures) to be considered the same treatment enisode

Event Deduplication - specifies how events are counted by the MP algorithm: 0: Counts all occurrences of an HOI during an exposure episode; 1: de-duplicates occurrences of the same HOI code and code type on the same day; 2: de-duplicates occurrences of the same HOI group on the same day (e.g., de-duplicates at the group level).

Exposure Extension Period - number of days post treatment period in which the outcomes/events are counted for a treatment episode.

Exposure Episode Length - number of days after exposure initiation that is considered "exposed time."

Lookback Period (pre-existing condition) - number of days wherein a member is required to have evidence of pre-existing condition (diagnosis/procedure/drug dispensing).

Member-Years - sum of all days of enrollment with medical and drug coverage** in the query period preceded by an exposure washout **Minimum Days Supplied** - specifies a minimum number of days in length of the days supplied for the episode to be considered.

Minimum Episode Duration - specifies a minimum number of days in length of the episode for it to be considered.

Principal Diagnosis (PDX) - diagnosis or condition established to be chiefly responsible for admission of the patient to the hospital. 'P' = principal diagnosis, 'S' = secondary diagnosis, 'X' = unspecified diagnosis, '.' = blank. Along with the Care Setting values, forms the **Treatment Episode Truncation Indicator** - indicates whether observation of the incident query code during follow-up requires truncation of valid treatment episodes. A value of Y indicates that the treatment episodes should be truncated at the first occurrence of an incident query code. A value of N indicates that the treatment episodes should not be truncated at the occurrence of the incident query code. **Users** - number of members with exposure during the query period. Member must have no evidence of exposure(s) of interest (defined by incidence criteria) in the prior washout period. A user may only be counted once in a query period.

Washout Period (drug/exposure)** - number of days a user is required to have no evidence of prior exposure (drug dispensing/procedure) and continuous drug and medical coverage prior to an incident treatment episode.

Washout Period (event/outcome)** - number of days a user is required to have no evidence of a prior event (procedure/diagnosis) and continuous drug and medical coverage prior to an incident treatment episode.

^{*}all terms may not be used in this report

^{**}incident treatment episodes must be incident to both the exposure and the event



Table 1. Baseline Characteristics of Cohort of Patients Receiving the KRAS Genetic Test¹ from January 1, 2013 to December 31, 2015

| naracteristic | KRAS | | |
|--|------|------------------------|--|
| | N | %/Std Dev ² | |
| Patients | 5210 | 100.0% | |
| atient Characteristics | | | |
| Mean age (std dev) | 57.5 | 13.8 | |
| Age: 0-21 years | 90 | 1.7% | |
| Age: 22-44 years | 674 | 12.9% | |
| Age: 45-64 years | 3161 | 60.7% | |
| Age: 65+ years | 1285 | 24.7% | |
| Gender (Female) | 2926 | 56.2% | |
| Gender (Male) | 2284 | 43.8% | |
| ecorded History of: | | | |
| Combined Comorbidity Score | 4.3 | 3.3 | |
| lealth Service Utilization Intensity: | | | |
| Mean number of generic drugs | 20.6 | 16.2 | |
| Mean number of unique drug classes | 0.7 | 1.5 | |
| Mean number of filled prescriptions | 14.9 | 14 | |
| Mean number of inpatient hospital encounters (IP) | 7 | 5.5 | |
| Mean number of non-acute institutional encounters (IS) | 0.5 | 0.9 | |
| Mean number of emergency room encounters (ED) | 0 | 0.2 | |
| Mean number of ambulatory encounters (AV) | 2.7 | 7.1 | |
| Mean number of other ambulatory encounters (OA) | 6.6 | 5 | |

²Value represents standard deviation where no % follows the value



Table 2. Baseline Characteristics of Cohort of Patients Receiving the BRAF Genetic Test¹ from January 1, 2013 to December 31, 2015

| racteristic | E | BRAF | |
|--|--------------|------------------------|--|
| | N | %/Std Dev ² | |
| Patients | 4907 | 100.0% | |
| ient Characteristics | | | |
| Mean age (std dev) | 55.6 | 14.5 | |
| Age: 0-21 years | 121 | 2.5% | |
| Age: 22-44 years | 821 | 16.7% | |
| Age: 45-64 years | 2919 | 59.5% 21.3% | |
| Age: 65+ years | 1046 2789 | | |
| Gender (Female) | | 56.8% | |
| Gender (Male) | 2118 | 43.2% | |
| orded History of: | | | |
| Combined Comorbidity Score | 3.9 | 3.3 | |
| alth Service Utilization Intensity: | | | |
| Mean number of generic drugs | 20 | 15.8 | |
| Mean number of unique drug classes | 0.7 | 1.3 | |
| Mean number of filled prescriptions | 14.6 | 13.7 | |
| Mean number of inpatient hospital encounters (IP) | 6.8 | 5.4 | |
| Mean number of non-acute institutional encounters (IS) | 0.5 | 0.9 | |
| Mean number of emergency room encounters (ED) | 0 | 0.2 | |
| Mean number of ambulatory encounters (AV) | 2.4 | 7 | |
| Mean number of other ambulatory encounters (OA) | 6.4 | 4.9 | |

¹See Appendix B for the list of codes used to define exposures

²Value represents standard deviation where no % follows the value



Table 3. Baseline Characteristics of Cohort of Patients Receiving the EGFR Genetic Test¹ from January 1, 2013 to December 31, 2015

| aracteristic | EGFR | | |
|--|------|------------------------|--|
| | N | %/Std Dev ² | |
| Patients | 4730 | 100.0% | |
| atient Characteristics | | | |
| Mean age (std dev) | 60.4 | 12.9 | |
| Age: 0-21 years | 40 | 0.8% | |
| Age: 22-44 years | 408 | 8.6% | |
| Age: 45-64 years | 2803 | 59.3% | |
| Age: 65+ years | 1479 | 31.3% | |
| Gender (Female) | 2641 | 55.8% | |
| Gender (Male) | 2089 | 44.2% | |
| ecorded History of: | | | |
| Combined Comorbidity Score | 4.4 | 3.3 | |
| ealth Service Utilization Intensity: | | | |
| Mean number of generic drugs | 20.5 | 15.6 | |
| Mean number of unique drug classes | 0.8 | 1.4 | |
| Mean number of filled prescriptions | 16 | 14.1 | |
| Mean number of inpatient hospital encounters (IP) | 7.6 | 5.6 | |
| Mean number of non-acute institutional encounters (IS) | 0.5 | 0.9 | |
| Mean number of emergency room encounters (ED) | 0 | 0.2 | |
| Mean number of ambulatory encounters (AV) | 2.5 | 7.1 | |
| Mean number of other ambulatory encounters (OA) | 7.2 | 5.1 | |

¹See Appendix B for the list of codes used to define exposures

²Value represents standard deviation where no % follows the value



Table 4. Baseline Characteristics of Cohort of Patients Receiving the BCR-ABL Genetic Test¹ from January 1, 2013 to December 31, 2015

| aracteristic | BCR-ABL | | |
|--|---------|------------------------|--|
| | N | %/Std Dev ² | |
| Patients | 5,360 | 100.0% | |
| tient Characteristics | | | |
| Mean age (std dev) | 53.5 | 14.8 | |
| Age: 0-21 years | 98 | 1.8% | |
| Age: 22-44 years | 1314 | 24.5% | |
| Age: 45-64 years | 2952 | 55.1% 18.6% | |
| Age: 65+ years | 996 | | |
| Gender (Female) | 2868 | 53.5% | |
| Gender (Male) | 2492 | 46.5% | |
| corded History of: | | | |
| Combined Comorbidity Score | 2.2 | 2.9 | |
| alth Service Utilization Intensity: | | | |
| Mean number of generic drugs | 15.3 | 15.1 | |
| Mean number of unique drug classes | 0.6 | 1.5 | |
| Mean number of filled prescriptions | 15.5 | 14.7 | |
| Mean number of inpatient hospital encounters (IP) | 6.5 | 5.4 | |
| Mean number of non-acute institutional encounters (IS) | 0.3 | 0.8 | |
| Mean number of emergency room encounters (ED) | 0 | 0.1 | |
| Mean number of ambulatory encounters (AV) | 1.7 | 6.1 | |
| Mean number of other ambulatory encounters (OA) | 6.2 | 5 | |

¹See Appendix B for the list of codes used to define exposures

²Value represents standard deviation where no % follows the value



Table 5. Baseline Characteristics of Cohort of Patients Receiving the BRCA Genetic Test¹ from January 1, 2013 to December 31, 2015

| aracteristic | В | BRCA | | |
|--|--------|------------------------|--|--|
| | N | %/Std Dev ² | | |
| Patients | 23,111 | 100.0% | | |
| tient Characteristics | | | | |
| Mean age (std dev) | 48.4 | 11.8 | | |
| Age: 0-21 years | 247 | 1.1% | | |
| Age: 22-44 years | 8527 | 36.9% | | |
| Age: 45-64 years | 12992 | 56.2% | | |
| Age: 65+ years | 1345 | 5.8% | | |
| Gender (Female) | 21776 | 94.2% | | |
| Gender (Male) | 1335 | 5.8% | | |
| corded History of: | | | | |
| Combined Comorbidity Score | 1.2 | 2.3 | | |
| alth Service Utilization Intensity: | | | | |
| Mean number of generic drugs | 11.8 | 12 | | |
| Mean number of unique drug classes | 0.3 | 0.8 | | |
| Mean number of filled prescriptions | 9.7 | 11 | | |
| Mean number of inpatient hospital encounters (IP) | 4.5 | 4.3 | | |
| Mean number of non-acute institutional encounters (IS) | 0.1 | 0.5 | | |
| Mean number of emergency room encounters (ED) | 0 | 0.1 | | |
| Mean number of ambulatory encounters (AV) | 0.7 | 3.5 | | |
| Mean number of other ambulatory encounters (OA) | 4.3 | 4.1 | | |

¹See Appendix B for the list of codes used to define exposures

²Value represents standard deviation where no % follows the value



Appendix A: Latest Date of Available Data for Each Data Partner up to Request End Date (12/31/2015)

| DP ID | End Date |
|--------|------------|
| DP0001 | 6/30/2015 |
| DP0002 | 4/30/2015 |
| DP0003 | 12/31/2014 |
| DP0004 | 10/31/2014 |
| DP0005 | 11/30/2015 |
| DP0006 | 2/28/2015 |
| DP0007 | 12/31/2015 |
| DP0008 | 9/30/2015 |
| DP0009 | 11/30/2015 |
| DP0010 | 7/31/2015 |
| DP0011 | 7/31/2014 |
| DP0012 | 9/30/2015 |
| DP0013 | 6/30/2015 |
| DP0014 | 10/31/2015 |



Appendix B: List of Procedure Codes used to Define Exposures in this Request

| Code | Description | Code Type |
|---------------|--|---------------------|
| KRAS | | |
| 81275 | KRAS (v-Ki-ras2 Kirsten rat sarcoma viral oncogene) (eg, carcinoma) gene analysis, variants in codons 12 and 13 | CPT-4 Procedure |
| S3713 | Kras mutation analysis testing | HCPCS Procedure |
| BRAF | | |
| 81210 | BRAF (v-raf murine sarcoma viral oncogene homolog B1) (eg, colon cancer), gene | CPT-4 Procedure |
| | analysis, V600E variant | |
| EGFR | | |
| 81235 | EGFR (epidermal growth factor receptor) (eg, non-small cell lung cancer) gene | CPT-4 Procedure |
| | analysis, common variants (eg, exon 19 LREA deletion, L858R, T790M, G719A, G719S, | |
| - | L861O) | |
| BCR-ABL | | |
| 81207 | BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis; minor | CPT-4 Procedure |
| | breakpoint, qualitative or quantitative | |
| 81206 | BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis; major | CPT-4 Procedure |
| | breakpoint, qualitative or quantitative | |
| 81208 | BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis; other | CPT-4 Procedure |
| DDC4 | breakpoint, qualitative or quantitative | |
| BRCA 81211 | DDCA4 DDCA2 (based assessed and 2) (as beneditional and assessed assessed assessed | CDT 4 Due es de une |
| 01211 | BRCA1, BRCA2 (breast cancer 1 and 2) (eg, hereditary breast and ovarian cancer) gene | CPT-4 Procedure |
| | analysis; full sequence analysis and common duplication/deletion variants in BRCA1 | |
| | (ie, exon 13 del 3.835kb, exon 13 dup 6kb, exon 14-20 del 26kb, exon 22 del 510bp, | |
| 81212 | exon 8-9 del 7.1kb) BRCA1, BRCA2 (breast cancer 1 and 2) (eg, hereditary breast and ovarian cancer) gene | CPT-4 Procedure |
| 04040 | analysis; 185delAG, 5385insC, 6174delT variants | |
| 81213 | BRCA1, BRCA2 (breast cancer 1 and 2) (eg, hereditary breast and ovarian cancer) gene | CPT-4 Procedure |
| 01214 | analysis; uncommon duplication/deletion variants | CDT 4 Due ee down |
| 81214 | BRCA1 (breast cancer 1) (eg, hereditary breast and ovarian cancer) gene analysis; full | CPT-4 Procedure |
| | sequence analysis and common duplication/deletion variants (ie, exon 13 del | |
| | 3.835kb, exon 13 dup 6kb, exon 14-20 del 26kb, exon 22 del 510bp, exon 8-9 del | |
| 81215 | 7.1kb) BRCA1 (breast cancer 1) (eg, hereditary breast and ovarian cancer) gene analysis; | CPT-4 Procedure |
| 81216 | known familial variant BRCA2 (breast cancer 2) (eg, hereditary breast and ovarian cancer) gene analysis; full | CPT-4 Procedure |
| 81217 | sequence analysis BRCA2 (breast cancer 2) (eg, hereditary breast and ovarian cancer) gene analysis; | CPT-4 Procedure |
| | known familial variant | |
| S3818 | Complete gene sequence analysis; BRCA1 gene | HCPCS Procedure |
| S3819 | Complete gene sequence analysis; BRCA2 gene | HCPCS Procedure |
| S3820 | Complete BRCA1 and BRCA2 gene sequence analysis for susceptibility to breast and | HCPCS Procedure |
| 62022 | ovarian cancer | |
| S3822 | Single mutation analysis (in individual with a known BRCA1 or BRCA2 mutation in the | HCPCS Procedure |
| S3823 | family) for susceptibility to breast and ovarian cancer Three-mutation BRCA1 and BRCA2 analysis for susceptibility to breast and ovarian cancer in Ashkenazi individuals | HCPCS Procedure |

Appendix C: Modular Program Specifications for cder_mpl1r_wp022_nsdp_v02

Sentinel's Cohort Identification and Descriptive Analysis (CIDA) tool, version 2.2.1, will be used to investigate the characteristics of individuals receiving the tests of interest. Covariates will be calculated based on a 183 Day Look-Back Period. The query period was from January 1, 2013 - December 31, 2015, and the enrollment gap was set at 45 days. Age groups were split as follows: 0-21, 22-44, 45-64, 65+. In total, 5 scenarios were examined in this request.

Enrollment Gap: 45 Days

Age Groups: 0-21, 22-44, 45-64, 65+

Query Period: January 1, 2013 - December 31, 2015

Coverage Requirement: Medical and Drug

Covariate Evaluation Window: 183 Days

| Drug/Exposure Covariates to Consider: | |
|---------------------------------------|--|
|---------------------------------------|--|

| Scenario | Enrollment Requirement (days) | Incident exposure | Incident w/ respecto: | t Washout (days) | Cohort Definition | Covariates |
|----------|-------------------------------------|-------------------|-----------------------|---------------------|-------------------|---|
| 1 | 183 | KRAS | KRAS | 183 | 01 | Age, Gender, Combined Comorbidity Index |
| 2 | 183 | BRAF | BRAF | 183 | 01 | Age, Gender, Combined Comorbidity Index |
| 3 | 183 | EGFR | EGFR | 183 | 01 | Age, Gender, Combined Comorbidity Index |
| 4 | 183 | BCR-ABL | BCR-ABL | 183 | 01 | Age, Gender, Combined Comorbidity Index |
| 5 | 183 | BRCA | BRCA | 183 | 01 | Age, Gender, Combined Comorbidity Index |

ICD-9, ICD-10, HCPCS, and CPT codes are provided by Optum360. NDC codes are checked against First Data Bank's "National Drug Data File (NDDF®) Plus"

Cohort Definition of 01 will only consider the first incident episode for each user during the query period that satisfies the washout period.