Table 1. Contributing consortia and characteristics of data sets.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **GAME-ON/GECCO Analysis** | | | | | | |  | **Replication Stage**  **(European ancestry)** | | | | |  | **Generalizability  (Other ancestry)** | | |
| **Cancer Site (Consortium)** | | **No.**  **studies** | **Cases** | **Controls**\* | **Variants†** | **Genotyping Platform** | **Imputation threshold‡** |  | **Study** | **Cases** | **Controls\*** |  | **Study** | | | **Cases** | **Controls\*** |
| Lung (TRICL)10 | | 6 | 12160 | 16838 | 8492272 | Illumina | R2>0.3 |  | deCODE10,13 | 3865 | 196658 |  | Nanjing18 | | | 2331 | 3077 |
|  | Harvard14,15 | 984 | 970 |  |
| Adenocarcinoma | |  | 3718 | 15871 | 8472145 |  | deCODE | 1434 | 198663 |  | Nanjing | | | 1304 | 3077 |
|  |  | Harvard | 597 | 970 |  | Japan17 | | | 1575 | 3363 |
| Squamous cell  carcinoma | |  | 3422 | 16015 | 8478230 |  | deCODE | 784 | 171059 |  | Nanjing | | | 822 | 3077 |
|  |  | Harvard | 216 | 970 |  |
|  | |  |  |  |  |  |  |  |  |  |  |  |  | | |  |  |
| Colorectal (CORECT)11 | | 6 | 5100 | 4831 | 7229595 | Affymetrix Axiom | None |  | deCODE | 3546 | 236404 |  |  | | |  |  |
|  | |  |  |  |  |  |  |  |  |  | | |  |  |
| Colorectal (GECCO)5 | | 13 | 10314 | 12857 | 9193926 | Illumina, Affymetrix | R2>0.3 |  |  |  | | |  |  |
|  | |  |  |  |  |  |  |  |  |  |  |  |  | | |  |  |
| Prostate (ELLIPSE) | |  | 14160 | 12724 | 9084781 | Illumina, Affymetrix | R2>0.3 |  | deCODE | 4858 | 83103 |  | LAPC/MEC20 | | | 1034 | 1046 |
| 6 |  | iCOGS16 | 20219 | 20440 |  | AAPC23 | | | 4853 | 4678 |
|  |  |  |  |  |  | JAPC/MEC20 | | | 980 | 1005 |
| Prostate  Aggressive | | 6 | 4450 | 12724 | 9003304 |  |  |  |  |  |  | | |  |  |
|  | |  |  |  |  |  |  |  |  |  |  |  |  | | |  |  |
| Breast (DRIVE)7,9 | |  | 15748 | 18084 | 9331393 | Illumina, Affymetrix | R2>0.3 |  |  |  |  |  | Shanghai19 | | | 2867 | 2285 |
| 11 | deCODE  iCOGS7 | 5318  46785 | 280808  42892 | LABC/MEC,  SF21 | | | 1497 | 3213 |
|  |  |  |  |  |  | AABC22 | | | 3015 | 2743 |
| Breast ER6 | | 8 | 4939 | 13128 | 9250406 |  |  |  |  |  |  | | |  |  |
|  | |  |  |  |  |  |  |  |  |  |  |  |  | | |  |  |
| Ovary (FOCI)8 | | 3 | 4369 | 9123 | 9911464 | Illumina | R2>0.3 |  | deCODE | 716 | 111373 |  |  | | |  |  |
|  | iCOGS8 | 16283 | 23491 |  |
| Ovary - Serous | | 3 | 2556 | 9123 | 9911279 |  | iCOGS | 10316 | 23491 |  |  | | |  |  |
| Ovary - Endometrial | | 3 | 715 | 9123 | 9910229 |  | iCOGS | 2338 | 23491 |  |  | | |  |  |
| **Total\*** | | 45 | 61851 | 61820 | 9916564 |  |  |  |  | 55789 | 330490 |  |  | | | 18152 | 21410 |

**\*** The number of unique individuals after accounting for cancer subtypes and overlapping controls. Breast iCOGS included only 1q22 variants, so total for replicates without breast iCOGS is shown. **†**Subset meta-analyses were performed for a specific variant if at least 3 sites (i.e., three of lung, colorectal, prostate, breast or ovary) contributed data. ‡Imputation performed using the 1000 genome reference panel. Exclusion threshold shown.