**Last modified: 8/26/2021**

This document contains updated versions of Table 1 and Table 2 for BC-BET, v2.0. The original tables can be found in:

Dancik, G.M. An online tool for evaluating diagnostic and prognostic gene expression biomarkers in bladder cancer. *BMC Urol* 2015, **15**:59 ([link](http://biomedcentral.com/1471-2490/15/59)),

Modifications to the table are colored red.

**Table 1.** The 15 patient cohorts (N = 1559) included in *BC-BET.* The numbers in the table correspond to the number of patients with each clinical characteristic or available endpoint that are included in the database and analyzed. A '-' denotes insufficient sample size for analysis.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | # of samples | | | | | | |
| Cohort (availability)\* | Platform | Normal,  Tumor | LG, HG | NMI, MI | DSS | OS | RFS | **Total**  **(N)** |
| AUH-1 [1] ([GSE3167](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3167)) | Affymetrix Human Genome U133A | 9,41 | 8, 32 | 28, 13 | - | - | - | **50** |
| AUH-2 [2] ([GSE5479](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5479)) | MDL Human 3k | - | 98, 271 | 351, 51 | - | - | - | **404** |
| Blaveri [3] (S) | UCSF Human Array 2.0 | - | 10, 68 | 27, 53 | - | 74 | - | **74** |
| CNUH [4] ([GSE13507](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE13507)) | Illumina human-6 v2.0 | 10, 165 | 105, 60 | 104, 61 | 165 | 165 | - | **175** |
| DFCI [5] ([GSE31684](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE31864)) | Affymetrix Human Genome U133 Plus 2.0 | - | 6, 84 | 15, 78 | - | - | 90 | **93** |
| Lindgren [6]([GSE19915](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19915)) | Swegene | 12,144 | 72, 72 | 97, 45 | - | 142 | - | **156** |
| Lindgren-2 [7]  ([GSE32548](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32548)) | Illumina HumanHT-12  V3.0 | - | 56, 75 | 92, 38 | - | 89 | - | **131** |
| MDA-1 [8]([GSE48276](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE48276)) | Illumina HumanHT-12 WG-DASL V4.0 R2 | - | - | - | - | 22† | - | **22** |
| MDA-2 [8]([GSE48075](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE48075)) | Illumina HumanHT-12 V3.0 | - | - | 67, 73 | - | 73† | - | **140** |
| MSKCC [9] (S) | Affymetrix Human Genome U133A | 38,91 | 18, 73 | 25, 66 | 87 | - | - | **129** |
| UVA[10]  ([GSE37317](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE37317)) | Affymetrix Human  Genome U133A | - | - | 8, 10 | - | - | - | **18** |
| Stransky-1[11] ([E-TABM-147](https://www.ebi.ac.uk/arrayexpress/experiments/E-TABM-147/)) | Affymetrix Human Genome U95A | 5,26 | 11, 15 | 9, 17 | - | - | - | **31** |
| Stransky-2[11] ([E-TABM-147](https://www.ebi.ac.uk/arrayexpress/experiments/E-TABM-147/)) | Affymetrix Human Genome U95Av2 | - | 13, 16 | 16, 15 | - | - | - | **31** |
| Chen ([GSE77952](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE77952)) | Agilent Whole Genome Microarray | - | - | 14, 16 | - | - | - | **30** |
| Elamin\_blood ([GSE138118](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE138118)) | Affymetrix Human Gene 2.1 ST Array | 29, 46 | - | - | - | - | - | **75** |
| Total |  | 103, 513 | 397, 769 | 853, 539 | 252 | 565 | 90 | **1559** |

\*Gene expression data for all cohorts are publicly available from the Gene Expression Omnibus (GEO)

[12] with the given Accession # (GSE ID), from Array Express [13] (Accession # E-TABM-147) or as Supplementary material to publication (S). †patients have MI, HG tumors (MDA-1) or MI tumors with unspecified grade (MDA-2). Abbreviations: LG, low grade; HG, high grade; NMI, non-muscle invasive; MI, muscle-invasive; DSS, disease-specific survival; OS, overall survival; RFS, recurrence-free survival.

**Supporting Table 1.** Summary of patient cohorts, sample exclusion and processing for *BC- BET*. The ***Complete cohort*** columns correspond to all samples available at the given accession number or publication, while the ***BC-BET*** columns corresponds to the samples included in the database.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Complete Cohort** | | | **BC-BET, v2.0** | |
| Cohort (availability)\* | N | Description | N | Sample Exclusion, Processing, and Additional Notes |
| AUH-1 [1] (GSE3167) | 60 | Forty-one tumor biopsies, 9 biopsies of normal bladder mucosa from patients without bladder cancer, and 5 paired samples consisting of a normal biopsy and a biopsy with CIS were profiled. | 50 | The paired biopsy samples are excluded. |
| AUH-2 [2] (GSE5479) | 808 | Tumors from 404 patients were obtained from bladder cancer patients from hospitals in Denmark, Sweden, England, Spain, and France and were profiled in duplicate. | 404 | Replicate profiles were averaged to produce a single gene expression profile for each patient. Eighteen samples are also profiled in AUH-1 and are removed if  AUH-1 is analyzed. |
| Blaveri [3] (S) | 80 | Eighty tumor samples were obtained from the tissue bank of the University of California at San Francisco Comprehensive Cancer Center. Six of these samples had squamous histology. All patients receive either transurethral resection of the bladder (TURBT) or cystectomy. Specifically, of those from transitional cell carcinomas, 25/27 patients with NMI tumors underwent TURBT while 44/47 patients with MI  tumors receive cystectomies. | 74 | The 6 samples with squamous histology are excluded. For prognostic biomarker evaluation, only the NMI samples obtained from TURBT and MI samples obtained from cystectomy are analyzed. |
| CNUH [4] (GSE13507) | 256 | Samples were collected at Chungbuk National University Hospital (CNUH), and consisted of 165 primary bladder cancer samples, 23 recurrent tumor samples, 58 normal samples surrounding tumors, and 10 normal bladder samples from patients with benign disease. Profiles from NMI tumors were obtained by transurethral resection of the bladder while those from MI tumors were obtained by cystectomy. Fifty-six patients with intermediate- or high-risk NMI tumors received intravesical Bacillus Calmette-Guerin therapy while 26 patients with MI tumors and 1 patient with an MI tumor received  cisplatin-based adjuvant chemotherapy. | 175 | Samples from recurrent tumors and samples of bladder mucosae surrounding cancer are excluded. The user has the option of excluding patients treated with intravesical therapy or chemotherapy in the prognostic biomarker evaluation. |
| DFCI [5] (GSE31684) | 93 | Tumors were profiled from 93 patients undergoing radical cystectomy at Memorial Sloan Kettering Cancer Center between 1993 and 2004. Three patients received neoadjuvant chemotherapy, 16 received adjuvant chemotherapy, and 19 patients received salvage chemotherapy for recurrent disease. | 93 | Patients receiving neoadjuvant chemotherapy are excluded from the prognostic biomarker evaluation.  Optionally, the user can exclude chemotherapy-treated patients from the prognostic biomarker evaluation. |
| Lindgren [6]  (GSE19915) | 156 | Tumor profiles were obtained from 144 patients undergoing transurethral resection of the bladder from the University Hospital of Lund, Sweden, as well as normal profiles from 12 patients with non-bladder cancer related disorders. Forty-six patients are later cystectomized, the majority (N = 32) who had HG, MI tumors. | 156 | ~~In the prognostic biomarker evaluation in patients with HG, MI tumors, 11 patients not cystectomized are excluded~~. Prognostic biomarker evaluation is not carried out for LG,NMI and HG, MI subsets, due to low sample size and inconsistent cystectomy status among samples. Ninety patients are profiled in Lindgren-2 and are excluded if Lindgren-2 is analyzed. This cohort is now labeled lindgren1a, which compares tumor vs normal samples; lindgren1b, which includes only genes in lindgren1 not profiled in lindgren2; and lindgren1c, which contains genes profiled in both lindgren1 and lindgren2. |
| Lindgren-2 [7] (GSE32548) | 131 | Tumor profiles were obtained from 131 patients undergoing transurethral resection of the bladder from University Hospital of Lund, Sweden. Thirty-two patients are later cystectomized, the majority (N = 21)  who had HG, MI tumors. | 131 | In the prognostic biomarker evaluation in patients with HG, MI tumors, 14 patients not cystectomized are excluded. |
| MDA-1 [8] (GSE48276) | 128 | Profiles were obtained from 128 bladder tumors from patients at MD Anderson (MDA) or Fox-Chase Cancer Center and Thomas Jefferson University (Philadelphia samples). Of the MDA tumor samples, only 24 had urothelial histology at cystectomy and were not treated by neoadjuvant chemotherapy | 22 | The Philadelphia samples were all MI and did not have survival information, and were therefore not analyzed. Of the MDA samples, tumors not having urothelial histology at cystectomy and those treated with neoadjuvant chemotherapy were excluded. Two additional NMI tumors  were also excluded. |
| MDA-2 [8] (GSE48075) | 142 | Gene expression profiles from 142 primary bladder tumors were obtained. | 142 | No samples were excluded. |
| MSKCC [9]  (S) | 157 | Gene expression profiles from 105 patients with bladder cancer were obtained along with normal samples, with some samples in duplicate or triplicate. | 91 | Previously processed data is included [14], which averaged replicate profiles to produce a single gene expression profile for each patient and removed several low quality samples. |
| UVA [10]  (GSE37317) | 19 | Gene expression profiles of 19 bladder cancer  patients were obtained at the University of Virginia. | 18 | One sample with squamous cell histology was excluded. |
| Stransky-1 and Stransky- 2 [11]  (E-TABM-147) | 103 | Gene expression profiles from 52 bladder cancer patients from Henri Mondor Hosptial are available, with many samples profiled in duplicate. Ten normal samples were also obtained. | 82 | Replicate profiles were averaged to produce a single gene expression profile for each patient |
| Chen (GSE77952) | 30 | Newly diagnosed bladder cancer patients with the greatest tumor diameter >2.5 cm and without tumor peduncle preoperatively observed by cystoscopy were selected. | 30 | All samples are included |
| Elamin\_blood (GSE138118) | 75 | Blood samples for healthy volunteers and bladder cancer patients | 75 | All samples are included; note that gene expression profiles are obtained from blood and not tumor cells |

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