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| **FOR DACC USE ONLY** | |
| **Concept No:** |  |
| **Approval Code:** |  |

**Breast Cancer Association Consortium (BCAC)**

**Analysis Concept Form**

Please provide the following information on the analyses you wish to perform and then either upload through the BCAC website or send it to Manjeet Bolla (mkh39@medschl.cam.ac.uk). This will be reviewed by the Data Access Coordination Committee (DACC) and then placed on the website for review by PIs. ***PIs will then be given a month to opt out of any particular proposals.*** *Data for approved concepts will be sent only to the Investigators listed below****A****, all of whose Institutions need to sign the DTA.*

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| **Date:** |  |

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| **Title of Proposed Project:** |  |

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| **Is this an amendment?** | Yes  No | If yes, provide Concept Number of the original form: |

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| **Contact Investigator(s):** |  |
| **Institution:** |  |
| **Contact E-mail:** |  |
| **Member of BCAC:** | Yes  No  **Note:** Non-members of BCAC will be required to pay a fee for data access. |
| **BCAC Study Acronym(s) for the Contact Investigator:** |  |

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| **OTHER Investigators and their institutions:** |  |
| **Please list individually all InvestigatorsA (and their institutions) who will require access to the data requested:** | **Note:** The dataset cannot be exchanged between institutions (see DTA).  All non- members of BCAC be required to pay a fee for data access. |
| **Please confirm that all the named investigators have read AND agreed to be named on this proposal?** | Yes |

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| **Concept Description:** *Please provide a concise description of Background/Aims* |

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| **Primary Endpoint** *(please check box)***:** | | |
| Breast cancer risk |  |  |
| Subtype of breast cancer |  | Specify: |
| Survival |  |  |
| Other |  | Specify: |

1. **GENETIC DATA REQUESTED**

|  |  |  |
| --- | --- | --- |
| **i. Subset of data being requested** *(please check all boxes that apply)***:** | | |
| Case data |  |  |
| Control data |  |  |
| European data |  |  |
| Asian data |  |  |
| African data |  |  |
| Hispanic data |  |  |
| Data from other subset of studies |  | Specify: |

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| **ii. Genotyping Project** *(please check all boxes that apply)***:** | | |
| iCOGS |  |  |
| OncoArray |  |  |
| Other |  | Specify: |
| ***Data Type*** |  |  |
| Summary data |  |  |
| Individual-level genotyped data |  |  |
|  | File format: Plink  Text | |
| Individual-level imputed data |  |  |
|  | File format: Text file with imputed dosages  Text file with probabilities (Impute2/Gen)  BGEN file with probabilities | |
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| **iii. Whole Exome Sequencing** *(please check all boxes that apply)***:** | | | | | |
| PERSPECTIVE |  | | |  | |
| BRIDGES |  | |  | | |
| ***Data Type***  Summary data |  | |  | | |
| VCF files |  | |  | | |
| Raw (BAM) files *[N.B. only specify if essential to your analysis]* |  |  | | | |
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| **iv. BRIDGES Panel Sequencing Project** *(please check all boxes that apply)***:** | | |
| BRIDGES Panel 1 |  |  |
| ***Data Type***  Summary data |  |  |
| Genotype files |  |  |
| VCF files |  |  |
| Raw (BAM) files *[N.B. only specify if essential to your analysis]* |  |  |

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| **v. B-CAST Panel Sequencing Project** *(please check all boxes that apply)***:** | | |
| B-CAST Panel – tumour |  |  |
| B-CAST Panel – germline [*restrictions apply to reporting individual study data*!] |  |  |
| ***Data Type***  Summary data |  |  |
| Genotype files |  |  |
| VCF files |  |  |
| Raw (BAM) files *[N.B. only select if essential to your analysis and justify this clearly in the analysis plan]* |  |  |

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| **v. Genetic Data** |
| *Provide information below for:*   1. ***Genotype data requested.***   *Attach separate file(s) (.csv) with a list of either:*   1. *SNPs (e.g. with their iCOGS/Onco SNP\_name, see BCAC website)* ***or*** 2. *Gene region(s) (with chromosome number, and, start and end positions. Specify whether using Build 37 or Build 38.* 3. ***Sequence data requested.***   *Provide details of genes/variants for which you are requesting sequence data.* |

1. **PHENOTYPE DATA REQUESTED**

Data on the following core variables will be sent as standard:

*Status* (case/control)*, Studytype, StudytypeOt, Study, SubStudy, Sex, AgeInt, AgeDiagIndex, EthnicityClass, EthnicitySubClass, FamHist, Fhnumber, Fhscore, Bilateral, Index\_corr, ER\_statusIndex, and ER\_statusIndex\_source*. Principal components (if applicable) will also be sent as standard as part of the phenotype file.

*Note: Due to data protection legislation, no dates (e.g. intDate, DateDiagnosis etc.) can be sent.*

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| **i. Variables from Extended Risk Factor Data Dictionary\***: |

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| **ii. Variables from Pathology Data Dictionary\*:** |

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| **iii. Variables from TMA project:**  Data  Images  Please specify markers: |

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| **iv. Variables from Survival Data Dictionary\*:** |

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| **v. Variables from Treatment Data Dictionary\*:** |

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| **vi. Variables from Mammographic Density Data Dictionary\*:** |

*\*Further information on these additional datasets is available on the BCAC website*

**3. ADDITIONAL INFORMATION**

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| **i. Analysis Plan:** |

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| **ii. Timeline:** |

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| **iii. Please confirm that you agree to comply with BCAC default authorship requirements\*?** | Yes  \*Default authorship:   * **Predefined “main” papers from large grants**: up to 4 authors per BCAC study contributing data * **Other papers based on Concepts submitted in 2023 or later and requesting only Genotyping Project data [Section 1 (ii)] and standard phenotype data:** no BCAC authors * **All other papers:** up to 4 authors per BCAC study contributing data for more than 3,000 cases and up to 2 authors from other BCAC studies contributing data   Any deviation from the above must be approved by the BCAC DACC. The onus is on the corresponding author to confirm prior to submission that a journal can accommodate these requirements. |

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| **iv. Any other considerations you would like the DACC to be aware of:** |

\* Information about variables in the BCAC database and data dictionary can be found on the website (<https://bcac.ccge.medschl.cam.ac.uk/>).