

ICOGS Polygenic Risk Score Variables		
Name	Description	CIMBA Publication
prs_bcacpub_bc	Standardised PRS based on 77 variants associated with BC risk in BCAC (Mavaddat et al, J Natl Cancer Inst., 2015)	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_bcacpub_erpos	Standardised PRS based on 77 variants associated with risk of ER-positive BC in BCAC (Mavaddat et al, J Natl Cancer Inst., 2015)	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_bcacpub_erneg	Standardised PRS based on 77 variants associated with risk of ER-negative BC in BCAC (Mavaddat et al, J Natl Cancer Inst., 2015)	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_bcacpub_bc_raw	Unstandardised PRS based on 77 variants associated with BC risk in BCAC (Mavaddat et al, J Natl Cancer Inst., 2015)	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_bcacpub_erpos_raw	Unstandardised PRS based on 77 variants associated with risk of ER-positive BC in BCAC (Mavaddat et al, J Natl Cancer Inst., 2015)	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_bcacpub_erneg_raw	Unstandardised PRS based on 77 variants associated with risk of ER-negative BC in BCAC (Mavaddat et al, J Natl Cancer Inst., 2015)	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_bcac_bc_raw	Unstandardised PRS based on variants associated with BC risk in BCAC	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_bcac_bc	Standardised PRS based on variants associated with BC risk in BCAC	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_bcac_erpos_raw	Unstandardised PRS based on variants associated with risk of ER-positive BC in BCAC	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_bcac_erpos	Standardised PRS based on variants associated with risk of ER-positive BC in BCAC	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_bcac_erneg_raw	Unstandardised PRS based on variants associated with risk of ER-negative BC in BCAC	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_bcac_erneg	Standardised PRS based on variants associated with risk of ER-negative BC in BCAC	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_brca2_bc_d_raw	* Unstandardised PRS based on variants that are associated at genome-wide significance in BRCA2 carriers in CIMBA or are associated at genome-wide significance in BCAC and at p<5% in BRCA2 carriers (alternative SNP selection method used - see below)	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_brca2_bc_d	* Standardised PRS based on variants that are associated at genome-wide significance in BRCA2 carriers in CIMBA or are associated at genome-wide significance in BCAC and at p<5% in BRCA2 carriers (alternative SNP selection method used - see below)	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_brca2_bc_raw	Unstandardised PRS based on variants that are associated at genome-wide significance in BRCA2 carriers in CIMBA or are associated at genome-wide significance in BCAC and at p<5% in BRCA2 carriers	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_brca2_bc	Standardised PRS based on variants that are associated at genome-wide significance in BRCA2 carriers in CIMBA or are associated at genome-wide significance in BCAC and at p<5% in BRCA2 carriers	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_brca1_bc_d_raw	* Unstandardised PRS based on variants that are associated at genome-wide significance in BRCA1 carriers in CIMBA or are associated at genome-wide significance in BCAC and at p<5% in BRCA1 carriers (alternative SNP selection method used - see below)	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_brca1_bc_d	* Standardised PRS based on variants that are associated at genome-wide significance in BRCA1 carriers in CIMBA or are associated at genome-wide significance in BCAC and at p<5% in BRCA1 carriers (alternative SNP selection method used - see below)	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_brca1_bc_raw	Unstandardised PRS based on variants that are associated at genome-wide significance in BRCA1 carriers in CIMBA or are associated at genome-wide significance in BCAC and at p<5% in BRCA1 carriers	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_brca1_bc	Standardised PRS based on variants that are associated at genome-wide significance in BRCA1 carriers in CIMBA or are associated at genome-wide significance in BCAC and at p<5% in BRCA1 carriers	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_ocac_raw	Unstandardised PRS based on variants associated with OC risk in OCAC	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_ocac	Standardised PRS based on variants associated with OC risk in OCAC	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_brca2_oc_d_raw	* Unstandardised PRS based on variants that are associated with ovarian cancer risk at genome-wide significance in BRCA2 carriers in CIMBA or are associated at genome-wide significance in OCAC and at p<5% in BRCA2 carriers (alternative SNP selection method used - see below)	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_brca2_oc_d	* Standardised PRS based on variants that are associated with ovarian cancer risk at genome-wide significance in BRCA2 carriers in CIMBA or are associated at genome-wide significance in OCAC and at p<5% in BRCA2 carriers (alternative SNP selection method used - see below)	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_brca2_oc_raw	Unstandardised PRS based on variants that are associated with ovarian cancer risk at genome-wide significance in BRCA2 carriers in CIMBA or are associated at genome-wide significance in OCAC and at p<5% in BRCA2 carriers	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_brca2_oc	Standardised PRS based on variants that are associated with ovarian cancer risk at genome-wide significance in BRCA2 carriers in CIMBA or are associated at genome-wide significance in OCAC and at p<5% in BRCA2 carriers	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_brca1_oc_d_raw	* Unstandardised PRS based on variants that are associated with ovarian cancer risk at genome-wide significance in BRCA1 carriers in CIMBA or are associated at genome-wide significance in OCAC and at p<5% in BRCA1 carriers (alternative SNP selection method used - see below)	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_brca1_oc_d	* Standardised PRS based on variants that are associated with ovarian cancer risk at genome-wide significance in BRCA1 carriers in CIMBA or are associated at genome-wide significance in OCAC and at p<5% in BRCA1 carriers (alternative SNP selection method used - see below)	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_brca1_oc_raw	Unstandardised PRS based on variants that are associated with ovarian cancer risk at genome-wide significance in BRCA1 carriers in CIMBA or are associated at genome-wide significance in OCAC and at p<5% in BRCA1 carriers	Kuchenbaecker et al, J Natl Cancer Inst., 2017
prs_brca1_oc	Standardised PRS based on variants that are associated with ovarian cancer risk at genome-wide significance in BRCA1 carriers in CIMBA or are associated at genome-wide significance in OCAC and at p<5% in BRCA1 carriers	Kuchenbaecker et al, J Natl Cancer Inst., 2017
	* The SNP selection process for the CIMBA-specific PRSs was the one described in the CIMBA PRS paper (Kuchenbaecker et al, J Natl Cancer Inst., 2017) except for those indicated with "_d" in the table above. For those with "_d", the process was different - instead of using only SNPs with p of at least 5% in CIMBA, known BCAC or OCAC hits were included as long as the direction of effect was the same in BCAC/OCAC and CIMBA.	
	N.B. The standardisation of the PRS was based on the distribution in the entire CIMBA sample. For subset analyses, a different standardisation may be more appropriate	