

**Supplementary Table 1: Characteristics of the BioVU replication cohort overall and by immune checkpoint inhibitor-mediated colitis (IMC)**

<b>Characteristics</b>	<b>Overall</b>	<b>All-grade IMC</b>	<b>Severe IMC</b>
	(n=1147)	(n=104)	(n=83)
<b>Mean age at diagnosis (SD)</b>	62.1 (13.1)	61.6 (12.7)	61.4 (12.9)
<b>Sex, n (%)</b>			
<i>Male</i>	727 (63.4)	62 (59.6)	48 (57.8)
<i>Female</i>	420 (36.6)	42 (40.4)	35 (42.2)
<b>Type of therapy, n (%)</b>			
<i>Anti PD-1/PD-L1 monotherapy</i>	828 (72.7)	34 (32.7)	23 (27.7)
<i>Anti PD-1/PD-L1 + Anti CTLA4 therapy</i>	45 (3.9)	25 (24.0)	22 (26.5)
<i>Anti CTLA4 monotherapy</i>	274 (23.9)	45 (43.3)	38 (45.8)

IMC: Immune checkpoint inhibitor-mediated colitis, SD: Standard deviation

**Supplementary Table 2: Previously published polygenic risk score (PRS) of ulcerative colitis as a predictor of time to development of all-grade immune checkpoint inhibitor-mediated colitis (IMC) in the entire GeRI cohort, using Cox proportional hazards models**

<i>All-grade IMC</i>					
<i>PRS<sup>a</sup></i>	<i>PRS method</i>	<i>HR per SD</i>	<i>95% CI</i>	<i>P</i>	<i>Ref.</i>
179-SNP PRS	SNPnet	1.24	0.94 - 1.64	0.13	1
809-SNP PRS	SNPnet	<b>1.33</b>	<b>1.01 – 1.74</b>	<b>0.04</b>	1
1,505-SNP PRS	Penalized Regression	<b>1.37</b>	<b>1.02 – 1.85</b>	<b>0.04</b>	2
566,637-SNP PRS	LDPred2	<b>1.41</b>	<b>1.04 – 1.91</b>	<b>0.03</b>	2

<sup>a</sup>Models are adjusted for age at diagnosis, sex, histology, type of therapy, recruiting site, and 5 principal components. IMC: Immune checkpoint inhibitor-mediated colitis, PRS: Polygenic risk score, HR: Hazard ratio, SD: Standard deviation, CI: Confidence interval, SNP: Single nucleotide polymorphism

1. Tanigawa Y, Qian J, Venkataraman G, et al. Significant sparse polygenic risk scores across 813 traits in UK Biobank. *PLoS Genetics*. 2022;18(3):e1010105. doi:10.1371/journal.pgen.1010105
2. Privé F, Aschard H, Carmi S, et al. Portability of 245 polygenic scores when derived from the UK Biobank and applied to 9 ancestry groups from the same cohort. *The American Journal of Human Genetics*. 2022;109(1):12-23. doi:10.1016/j.ajhg.2021.11.008