Workshop Programme

Start (BST)	Finish (BST)	Presenter details
Wednesday 12 July 2023		
14:00	14:20	**Registration and networking**
14:20	14:30	**Welcome** *Clare Turnbull, The Institute of Cancer Research, UK*
14:30	15:00	**Session 1: Introductory Talks** *Chair: Clare Turnbull*
14:30	14:45	Developing clinical-grade multiplex assays of variant effect *Greg Findlay, The Francis Crick Institute, UK*
14:45	15:00	Overview of ACMG variant classification and evidence weighting *Leslie Biesecker, NIH, USA*
15:00	15:20	BRCA1, TP53, PTEN and CDH1: what have we learnt so far from corelating MAVE data with clinical observations? *Shawn Fayer, University of Washington, USA*
15:20	15:40	Q&A and room-wide discussion
15:40	17:00	**Session 2: Correlating clinical pathogenicity with assay readouts** *Chair: Lea Starita*
15:40	15:50	"Hot Takes" question
15:50	16:10	Open-ended discussion questions
16:10	16:30	Refreshment break and networking
16:30	17:00	Room-wide discussion and summary
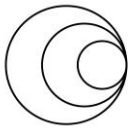
17:00	18:00	**Session 3: Disseminating outputs of MAVEs**
		Chair: Fritz Roth
17:00	17:10	MaveDB plans, integration between MaveDB and other resources and "Hot Takes" question *Alan Rubin, Walter and Eliza Hall Institute of Medical Research, Australia*
17:10	17:30	Open-ended discussion questions
17:30	18:00	Room-wide discussion and summary
18:00	18:15	**Workshop reflection**
18:30	20:30	Dinner
18:30		Bar open (card payments only)