Supplementary Material: Utility of Circulating Tumor DNA for Detection and Monitoring of Endometrial Cancer Recurrence and Progression

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Table S1. Genomic coordinates for personalised ctDNA panel and target mutations derived from whole exome sequencing of the primary tumor.

Chromosome	Start	End	Target
chr1	37984113	37984293	SF3A3 p.C92S_1,SF3A3 p.C92S_2
chr2	47414258	47414558	BAT-26_1,BAT-26_2,BAT-26_3,BAT-26_4
chr2	95183472	95183653	NR-24_1,NR-24_2,NR-24_3,NR-24_4
chr3	195783832	195784012	MUC4 p.P2562S_MUC4 p.S2544P_1,MUC4 p.P2562S_MUC4 p.S2544P_2
chr3	195784551	195784731	MUC4 p.A2313V_1,MUC4 p.A2313V_2
chr4	54731896	54732196	BAT-25_1,BAT-25_2,BAT-25_3,BAT-25_4
chr6	32221013	32221193	NOTCH4 p.G225R_1,NOTCH4 p.G225R_2
chr7	100952460	100952640	MUC3A p.P258S_1,MUC3A p.P258S_2
chr7	100953384	100953564	MUC3A p.H563Q_MUC3Ap.S568Y_1,MUC3A p.H563Q_MUC3Ap.S568Y_2
chr9	8375930	8376110	PTPRD p.E1119K_1,PTPRD p.E1119K_2
chr10	87933057	87933237	PTEN p.R130Q_PTEN p.R130L_1,PTEN p.R130Q_PTEN p.R130L_2
chr10	121520072	121520252	FGFR2 p.S252W_1,FGFR2 p.S252W_2
chr11	1017234	1017414	MUC6 p.Y1826D_1,MUC6 p.Y1826D_2
chr11	1017562	1017764	MUC6 p.P1716S_1,MUC6 p.P1716S_2,MUC6 p.P1716S_3
chr11	14358713	14358893	RRAS p.G23C_1,RRAS p.G23C_2
chr11	46898858	46899038	LRP4 p.D211H_1,LRP4 p.D211H_2
chr11	102322679	102322919	NR-27_1,NR-27_2,NR-27_3
chr13	48459617	48459797	RB1 p.R661W_1,RB1 p.R661W_2
chr14	23182997	23183297	NR-21_1,NR-21_2,NR-21_3,NR-21_4
chr17	43091512	43091692	BRCA1 p.T1263S_1,BRCA1 p.T1263S_2
chr19	8888681	8888861	MUC16 p.S13577G_MUC16 p.H13576N_1,MUC16 p.S13577G_MUC16 p.H13576N_2
chr19	52212627	52212807	PPP2R1A p.P179R_1,PPP2R1A p.P179R_2

Table S2. The somatic mutations identified in the matched tumour-normal patient samples analysed (n = 13).

Patient ID	ctDNA Detected?	Mutations Detected in Tumor	%VAF in Tumour	Mutation(s) detected in ctDNA (Any Timepoint)	Timepoint Detected (%VAF)	Total Timepoints
1 ᐞ	Y *	*PTEN* p.R130Q	14.3	*MUC4* p.H2306P	3 (9.57%), 5 (7.34%)	6
		MUC16 p.H13577G	14.6	MSI markers	3 (1/5 markers), 4 (1/5 markers), 6 (3/5 MSI markers)	
		MUC4 p.S2544P	26.2			
		MSI markers	5/5 detected			
2 ᐞ	Y	*MUC4* p.A2313V	16	*MUC4* p.A2313V	2 (42.3%), 3 (54.35%)	3
		PTEN p.R130L	19.3	MSI markers	3 (2/5 MSI markers)	
		MSI markers	None			
3 ᐞ	Y *	*PTPRD* p.E1119K	20.3	*MUC4* p.H2290L	1 (9.48%%)	1
		MUC6 p.P1716S	20.7	*MUC4* p.A2313V	1 (19.48%)	
		SF3A3 p.C92S	21.2			
		MUC4 p.P2562S	24.8			
		PPP2R1A p.P179R	27.3			
		MUC6 p.Y1826D	37.5			
		LRP4 p.D211H	55.2			
		RRAS p.G23C	58.3			
4	Y±	*PIK3CA* p.H1047L	18.53	*PIK3CA* p.E545A	1 (0.16%)	1
		KRAS p.G12A	20.67	*PIK3CA* p.H1047L	1 (2.19%)	
				KRAS p.G12A	1 (2.12%)	
				CTNNB1 p.T41A	1 (2.29%)	
5	Y	*TP53* p.Y220C (primary tumor and 2 metastatic sites)	91.59 (primary tumour), 80.91 (ovary), 69.63 (omentum)	*TP53* p.Y220C	1 (19.05%), 4 (2.72%), 5 (4.3%), 6 (6.76%), 7 (14.3%)	7
				AKT p.E17K	4 (3.05%)	
6	Y ±	*PIK3CA* p.H1047R	59.65	*PIK3CA* p.H1047R	1 (1.18%)	1
		PTEN p.Y155C	33.58	*ESR1* p.D538G	1 (2.75%)	
7	Y	*TP53* p.R273C	85.39	*TP53* p.R273C	1 (1.53%)	1
8 ᐞ	Y ±	*BRCA1* p.T1263S	14.9	*MUC4* p.A2313V	1 (10.56%)	1
		MUC16 p.H13576N	15.7	*NOTCH4* p.G225R	1 (50.59%)	
		MUC3A p.H563Q	20.2			
		RB1 p.R661W	21.4			
		NOTCH4 p.G225R	21.5			

9	Y ±	*PIK3CA* p.H1047R (primary and relapse)	27.94 (primary tumour), 35.33 (relapse biopsy)	*PIK3CA* p.H1047R	1 (3.03%)	3
				MET p.T1010I	1 (16.71%)	
				FGFR2 p.S252W	1 (2.15%)	
				KRAS p.G12A	1 (1.89%)	
10	Y *	*KRAS* p.G12A	22.78	*PIK3CA* p.E545A	1 (0.43%)	1
		PIK3CA p.G1049R	12.6			
11	N	*PIK3CA* p.G106V	35.14	None detected	-	3
12	N	*PIK3CA* p.R88Q	18.32	None detected (*KRAS* p.G12D)	-	1
		KRAS p.G12D	23.99			
13	Y *	*PIK3CA* p.E545A	38.09	TP53 p.S241F	1 (0.28%)	1
		TP53 p.C242F	40			

Δ Patient's whose tumor underwent whole exome sequencing. * ctDNA positive patient where mutation in ctDNA did not correlate with tumor. ± Additional mutations detected in ctDNA. Note that mutations in bold were validated by ddPCR. For patient 1, mutation was also detected at timepoint 2 but not called due to poor sequencing over the locus.