

**Supplementary Table 1. TCGA tumours used in this study.**

<i>Endometrial</i>			<i>Breast</i>		
<i>bcr_patient_barcode</i>	<i>Log<sub>2</sub></i> <i>RPPA</i>	<i>Percentile</i>	<i>bcr_patient_barcode</i>	<i>Log<sub>2</sub></i> <i>RPPA</i>	<i>Percentile</i>
TCGA-A5-A0GQ	-1.93	0-25	TCGA-A8-A07W	-3.93	0-25
TCGA-A5-A0GG	-1.90	0-25	TCGA-AR-A0U3	-3.91	0-25
TCGA-D1-A0ZR	-1.89	0-25	TCGA-A8-A07P	-3.48	0-25
TCGA-BG-A0VV	-1.84	0-25	TCGA-A2-A0CT	-3.41	0-25
TCGA-BG-A0W1	-1.75	0-25	TCGA-AN-A0FD	-3.40	0-25
TCGA-BG-A0M7	-1.69	0-25	TCGA-A8-A09C	-3.39	0-25
TCGA-D1-A17L	-1.45	0-25	TCGA-AN-A0XT	-3.35	0-25
TCGA-AP-A0LN	-1.44	0-25	TCGA-A2-A0CU	-3.21	0-25
TCGA-BG-A0MG	-1.41	0-25	TCGA-E2-A15T	-3.19	0-25
TCGA-BS-A0TD	-1.36	0-25	TCGA-C8-A12M	-3.08	0-25
TCGA-B5-A0K1	-1.32	0-25	TCGA-A8-A06N	-2.97	0-25
TCGA-D1-A16D	-1.28	0-25	TCGA-BH-A0HX	-2.93	0-25
TCGA-D1-A161	-1.10	0-25	TCGA-AR-A0TV	-2.87	0-25
TCGA-AP-A0LP	-1.08	0-25	TCGA-B6-A0RL	-2.78	0-25
TCGA-A5-A0GX	-1.08	0-25	TCGA-BH-A18N	-2.73	0-25
TCGA-AP-A1E1	-1.06	0-25	TCGA-A8-A07S	-2.73	0-25
TCGA-A5-A0GE	-1.02	0-25	TCGA-AO-A0JC	-2.69	0-25
TCGA-BG-A187	-0.98	0-25	TCGA-E2-A1B4	-2.68	0-25
TCGA-A5-A0GU	-0.95	0-25	TCGA-E2-A15R	-2.65	0-25
TCGA-D1-A16X	-0.95	0-25	TCGA-AR-A0TR	-2.57	0-25
TCGA-BG-A0M3	-0.94	0-25	TCGA-A2-A0SU	-2.53	0-25
TCGA-D1-A167	-0.93	0-25	TCGA-E2-A15S	-2.50	0-25
TCGA-D1-A103	-0.89	0-25	TCGA-BH-A0B1	-2.48	0-25
TCGA-AX-A05T	-0.86	0-25	TCGA-AO-A0JI	-2.45	0-25
TCGA-B5-A11L	-0.85	0-25	TCGA-A2-A0CV	-2.44	0-25
TCGA-D1-A16B	-0.81	0-25	TCGA-AN-A0XP	-2.43	0-25
TCGA-D1-A17T	-0.77	0-25	TCGA-AO-A12G	-2.43	0-25
TCGA-BG-A0M9	-0.67	0-25	TCGA-BH-A0EB	-2.42	0-25
TCGA-BG-A0M0	-0.65	0-25	TCGA-E2-A14S	-2.35	0-25
TCGA-BS-A0TC	-0.64	0-25	TCGA-E2-A15O	-2.32	0-25
TCGA-D1-A17M	-0.63	0-25	TCGA-A8-A09M	-2.31	0-25
TCGA-D1-A176	-0.59	0-25	TCGA-E2-A14O	-2.29	0-25
TCGA-AX-A05U	-0.52	0-25	TCGA-A7-A0DB	-2.29	26-50
TCGA-EY-A1GF	-0.52	0-25	TCGA-AO-A03P	-2.27	26-50
TCGA-AX-A05W	-0.49	0-25	TCGA-A8-A07Z	-2.25	26-50
TCGA-B5-A121	-0.49	26-50	TCGA-AO-A0JG	-2.23	26-50
TCGA-D1-A17U	-0.47	26-50	TCGA-AN-A0FW	-2.21	26-50
TCGA-D1-A101	-0.44	26-50	TCGA-AO-A0J7	-2.20	26-50
TCGA-BG-A0LX	-0.44	26-50	TCGA-B6-A0RM	-2.15	26-50
TCGA-D1-A16J	-0.43	26-50	TCGA-A8-A08A	-2.13	26-50
TCGA-D1-A17H	-0.39	26-50	TCGA-E2-A10E	-2.12	26-50
TCGA-D1-A17C	-0.39	26-50	TCGA-A7-A0CD	-2.10	26-50
TCGA-AP-A0LV	-0.38	26-50	TCGA-E2-A14T	-2.08	26-50
TCGA-BS-A0TG	-0.38	26-50	TCGA-A8-A06Y	-2.02	26-50
TCGA-BG-A18A	-0.36	26-50	TCGA-B6-A0IB	-2.01	26-50
TCGA-AX-A06L	-0.36	26-50	TCGA-A2-A0CQ	-1.99	26-50
TCGA-D1-A16Q	-0.33	26-50	TCGA-D8-A140	-1.99	26-50
TCGA-BG-A186	-0.33	26-50	TCGA-BH-A18H	-1.95	26-50
TCGA-B5-A11Y	-0.32	26-50	TCGA-BH-A0HW	-1.94	26-50
TCGA-BK-A0C9	-0.32	26-50	TCGA-A8-A079	-1.93	26-50

TCGA-BK-A13C	-0.31	26-50	TCGA-AO-A12B	-1.93	26-50
TCGA-B5-A1MZ	-0.30	26-50	TCGA-A8-A06X	-1.89	26-50
TCGA-AP-A0LJ	-0.29	26-50	TCGA-E2-A154	-1.87	26-50
TCGA-AX-A0J1	-0.29	26-50	TCGA-A8-A091	-1.85	26-50
TCGA-B5-A11S	-0.28	26-50	TCGA-BH-A0C7	-1.85	26-50
TCGA-D1-A165	-0.27	26-50	TCGA-BH-A0HK	-1.83	26-50
TCGA-A5-A0RA	-0.24	26-50	TCGA-AO-A0JJ	-1.82	26-50
TCGA-BG-A0MU	-0.23	26-50	TCGA-A8-A06U	-1.80	26-50
TCGA-AP-A1DR	-0.18	26-50	TCGA-A8-A099	-1.79	26-50
TCGA-B5-A1MV	-0.18	26-50	TCGA-E2-A107	-1.79	26-50
TCGA-EY-A1GD	-0.18	26-50	TCGA-AN-A0AJ	-1.78	26-50
TCGA-BS-A0UJ	-0.16	26-50	TCGA-E2-A15G	-1.73	26-50
TCGA-BG-A0M2	-0.14	26-50	TCGA-E2-A109	-1.73	26-50
TCGA-B5-A11V	-0.12	26-50	TCGA-E2-A14Q	-1.70	26-50
TCGA-D1-A17S	-0.12	26-50	TCGA-AO-A03O	-1.68	51-75
TCGA-EC-A1NJ	-0.11	26-50	TCGA-AO-A0J3	-1.67	51-75
TCGA-A5-A0R9	-0.08	26-50	TCGA-AN-A0XO	-1.62	51-75
TCGA-D1-A15W	-0.07	26-50	TCGA-BH-A0BS	-1.53	51-75
TCGA-A5-A0R8	-0.07	26-50	TCGA-E2-A10B	-1.53	51-75
TCGA-AX-A0IS	-0.05	51-75	TCGA-E2-A14Z	-1.53	51-75
TCGA-DI-A1BY	-0.04	51-75	TCGA-A8-A08G	-1.52	51-75
TCGA-D1-A16O	-0.04	51-75	TCGA-BH-A0BV	-1.47	51-75
TCGA-D1-A17F	0.01	51-75	TCGA-A8-A08T	-1.45	51-75
TCGA-B5-A11H	0.01	51-75	TCGA-BH-A0H9	-1.44	51-75
TCGA-D1-A0ZU	0.06	51-75	TCGA-B6-A0RP	-1.41	51-75
TCGA-B5-A0K2	0.07	51-75	TCGA-AR-A0TT	-1.38	51-75
TCGA-B5-A11Q	0.07	51-75	TCGA-A8-A09A	-1.38	51-75
TCGA-D1-A16Y	0.07	51-75	TCGA-AO-A12H	-1.24	51-75
TCGA-EY-A1GX	0.09	51-75	TCGA-BH-A0E7	-1.23	51-75
TCGA-AX-A063	0.09	51-75	TCGA-AN-A0FK	-1.21	51-75
TCGA-BG-A0MT	0.11	51-75	TCGA-AR-A1AP	-1.21	51-75
TCGA-BS-A0V4	0.11	51-75	TCGA-A2-A04V	-1.20	51-75
TCGA-EY-A1H0	0.11	51-75	TCGA-A2-A0CW	-1.19	51-75
TCGA-AP-A05P	0.12	51-75	TCGA-C8-A12X	-1.19	51-75
TCGA-B5-A0JU	0.14	51-75	TCGA-E2-A156	-1.17	51-75
TCGA-B5-A0K4	0.15	51-75	TCGA-E2-A155	-1.17	51-75
TCGA-AP-A0LS	0.15	51-75	TCGA-A8-A083	-1.15	51-75
TCGA-B5-A0K7	0.15	51-75	TCGA-AN-A0AM	-1.15	51-75
TCGA-D1-A17B	0.16	51-75	TCGA-BH-A18S	-1.13	51-75
TCGA-AP-A1DM	0.16	51-75	TCGA-BH-A0W5	-1.11	51-75
TCGA-EY-A1GE	0.17	51-75	TCGA-A8-A086	-1.08	51-75
TCGA-BG-A0LW	0.22	51-75	TCGA-AR-A0TY	-1.08	51-75
TCGA-EY-A1GU	0.24	51-75	TCGA-E2-A15K	-1.01	51-75
TCGA-AP-A1E0	0.24	51-75	TCGA-A8-A08Z	-1.00	51-75
TCGA-D1-A1NS	0.25	51-75	TCGA-B6-A0X0	-0.99	51-75
TCGA-D1-A177	0.27	51-75	TCGA-A7-A0CJ	-0.94	51-75
TCGA-B5-A0K9	0.28	51-75	TCGA-BH-A0DS	-0.94	76-100
TCGA-B5-A0JT	0.32	51-75	TCGA-A2-A0D4	-0.92	76-100
TCGA-BG-A18B	0.33	51-75	TCGA-A2-A0D3	-0.91	76-100
TCGA-D1-A163	0.35	51-75	TCGA-A8-A09B	-0.90	76-100
TCGA-D1-A160	0.38	51-75	TCGA-A2-A0YH	-0.90	76-100
TCGA-B5-A11G	0.39	51-75	TCGA-C8-A133	-0.89	76-100
TCGA-D1-A15Z	0.39	51-75	TCGA-A8-A082	-0.86	76-100
TCGA-B5-A11F	0.41	76-100	TCGA-AN-A04A	-0.80	76-100

TCGA-AP-A1DO	0.44	76-100	TCGA-AN-A0FY	-0.77	76-100
TCGA-D1-A1O5	0.45	76-100	TCGA-AO-A12E	-0.72	76-100
TCGA-BK-A0CB	0.45	76-100	TCGA-AN-A0FZ	-0.64	76-100
TCGA-B5-A11W	0.46	76-100	TCGA-E2-A10A	-0.53	76-100
TCGA-D1-A17Q	0.49	76-100	TCGA-BH-A0EI	-0.51	76-100
TCGA-AP-A0LL	0.50	76-100	TCGA-AN-A041	-0.50	76-100
TCGA-BS-A0U8	0.51	76-100	TCGA-E2-A1BD	-0.43	76-100
TCGA-B5-A11Z	0.51	76-100	TCGA-A2-A0T5	-0.33	76-100
TCGA-A5-A1OJ	0.53	76-100	TCGA-E2-A15D	-0.33	76-100
TCGA-BS-A0V7	0.54	76-100	TCGA-BH-A0DT	-0.29	76-100
TCGA-BG-A0MC	0.54	76-100	TCGA-A2-A0CS	-0.28	76-100
TCGA-BS-A0U7	0.54	76-100	TCGA-A2-A04Y	-0.22	76-100
TCGA-BG-A0RY	0.57	76-100	TCGA-AR-A1AS	-0.21	76-100
TCGA-D1-A17R	0.58	76-100	TCGA-A2-A0YD	-0.19	76-100
TCGA-AX-A064	0.58	76-100	TCGA-A2-A0EO	-0.11	76-100
TCGA-AP-A05N	0.59	76-100	TCGA-BH-A0DK	-0.11	76-100
TCGA-BG-A0VT	0.60	76-100	TCGA-AN-A0FF	-0.06	76-100
TCGA-B5-A0K0	0.67	76-100	TCGA-A2-A04N	-0.03	76-100
TCGA-AP-A0LT	0.67	76-100	TCGA-BH-A0W4	0.00	76-100
TCGA-D1-A16E	0.71	76-100	TCGA-E2-A153	0.02	76-100
TCGA-AP-A1DP	0.73	76-100	TCGA-E2-A15J	0.15	76-100
TCGA-EY-A1GL	0.77	76-100	TCGA-BH-A0E2	0.20	76-100
TCGA-B5-A11N	0.91	76-100	TCGA-AO-A12A	0.21	76-100
TCGA-EY-A1GO	0.95	76-100	TCGA-A7-A13F	0.39	76-100
TCGA-EY-A1GH	0.95	76-100			
TCGA-A5-A0GV	1.04	76-100			
TCGA-BG-A0YU	1.08	76-100			
TCGA-AX-A05Z	1.10	76-100			
TCGA-EY-A1GI	1.28	76-100			
TCGA-AX-A062	1.45	76-100			
TCGA-EY-A1GT	1.57	76-100			
TCGA-D1-A1NZ	1.61	76-100			
TCGA-AP-A1E4	1.65	76-100			
TCGA-D1-A17N	2.16	76-100			