

Table S1 Raw PEA data for all patients at response

Proteins	Patient ID																									
	1	2	3	4	5	6	7	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	
TXLNA	8.45	3.10	3.48	6.20	5.54	4.22	4.27	7.87	4.19	4.26	4.67	4.65	3.85	4.25	3.68	4.74	4.78	4.45	3.69	3.96	3.20	4.35	5.21	4.38	5.02	
VEGFA	11.56	10.27	10.61	10.86	11.31	10.40	10.73	11.10	9.85	10.06	10.98	10.36	10.54	10.21	10.54	10.35	12.02	9.94	10.53	10.39	10.57	10.34	10.28	10.20	10.77	
CPE	4.23	4.15	4.33	3.64	3.93	4.11	4.20	4.88	4.37	4.22	3.82	3.89	4.10	4.42	4.70	4.52	4.59	4.29	4.54	4.60	4.15	4.79	4.56	4.05	4.11	
KLK13	3.21	4.26	2.62	2.89	4.30	3.80	2.80	3.18	2.60	3.51	3.36	3.85	3.59	3.62	4.38	2.55	4.25	3.32	4.04	3.89	2.09	2.91	3.41	3.06	2.92	
CEACAM1	8.84	8.55	8.51	8.88	8.84	8.56	8.64	8.82	8.52	8.50	8.88	8.64	8.57	8.66	8.80	8.86	9.01	8.75	8.73	9.01	8.74	8.73	8.55	8.70	8.87	
MSLN	4.62	4.92	4.78	6.34	5.25	3.69	3.70	4.80	6.41	4.33	4.71	4.47	3.80	4.35	5.10	5.96	5.38	3.55	4.41	4.03	5.73	4.02	5.02	3.60	5.98	
TNFSF13	9.17	8.67	9.78	9.62	10.09	9.42	9.68	9.50	8.95	9.39	9.89	9.50	9.75	9.25	9.88	9.54	9.60	9.00	9.40	9.66	9.41	8.79	9.53	8.59	9.84	
EGF	10.74	4.43	4.88	6.26	6.44	4.97	6.80	9.63	6.23	5.63	6.18	4.27	7.28	6.15	4.16	6.84	9.13	6.33	5.73	5.43	5.38	7.98	5.78	6.47	6.03	
TNFRSF6B	5.40	5.53	5.26	4.97	7.70	5.67	5.12	6.52	5.10	6.54	7.26	6.21	5.87	5.27	6.79	4.96	6.24	5.66	5.68	5.28	4.36	4.82	6.26	4.94	5.88	
SDC1	6.36	6.63	8.25	8.11	7.58	9.21	7.84	8.49	9.37	6.75	7.00	6.95	8.91	7.11	7.41	8.56	7.75	7.52	8.31	7.70	7.22	6.45	6.64	6.41	9.11	
TGFBR2	7.22	7.64	8.33	8.01	8.68	7.46	8.02	7.32	7.16	7.77	8.43	7.67	7.45	7.55	8.15	7.53	8.07	7.32	8.17	7.94	7.35	7.57	8.02	7.12	6.56	
IL6	2.30	3.16	3.53	2.77	5.35	4.06	3.59	4.02	3.37	3.08	3.36	4.03	4.04	2.71	4.57	2.87	4.18	3.25	3.71	5.29	2.62	2.13	3.31	3.23	3.65	
CD48	7.20	7.68	6.98	6.18	7.88	6.78	7.26	7.57	6.67	7.31	7.87	7.43	7.00	7.46	7.87	7.53	7.95	7.35	7.62	8.26	6.82	7.12	7.16	7.18	7.11	
SCAMP3	10.22	5.00	4.68	6.55	7.19	5.32	5.60	9.13	5.15	6.04	6.30	4.44	5.22	6.03	4.87	6.18	5.39	6.08	5.14	5.25	4.71	5.90	5.51	5.74	5.55	
LY9	6.38	7.59	5.91	5.44	6.46	6.02	5.96	6.45	6.24	6.43	6.63	6.61	6.70	6.87	7.32	6.78	6.93	6.38	6.61	6.51	6.03	6.32	6.46	5.82	6.48	
IFNGR1	7.37	7.01	7.40	7.42	7.49	7.26	7.22	7.13	6.95	7.05	7.46	7.12	6.97	6.95	7.31	7.23	7.16	6.87	7.20	7.39	7.00	7.09	7.25	6.69	6.87	
ITGAV	4.61	4.91	4.36	4.84	4.90	4.40	4.60	4.93	4.54	4.74	4.97	4.68	4.50	4.84	4.92	5.03	5.10	4.98	4.94	5.27	4.72	4.99	4.98	4.41	4.80	
TNFSF10	9.07	8.79	8.94	8.39	8.39	8.49	8.33	8.71	8.32	8.65	9.31	8.46	8.67	8.17	8.39	9.06	8.79	8.39	8.86	8.87	8.62	8.28	8.70	8.42	9.12	
KLK11	5.01	5.35	5.71	5.06	5.54	5.82	5.38	5.19	4.66	5.23	5.78	5.04	5.93	4.97	5.50	5.45	6.17	5.24	5.24	5.35	5.18	5.00	5.15	5.34	5.31	
GPC1	4.97	5.29	5.40	5.41	5.34	5.32	5.01	4.96	5.03	5.45	5.25	5.35	4.64	5.40	5.32	5.39	5.37	5.39	5.58	5.35	4.95	5.88	5.55	4.98	4.94	
TFPI2	9.51	7.96	8.76	9.06	8.82	11.34	7.92	9.57	11.28	8.89	8.99	8.68	12.24	8.74	9.05	8.36	8.29	8.43	9.76	8.74	8.40	7.39	8.46	8.24	9.69	
KLK8	5.91	6.27	6.41	6.01	6.83	4.42	6.31	5.74	5.54	6.41	6.31	5.90	5.78	5.75	5.86	6.15	6.77	6.46	6.25	6.16	5.53	6.38	5.73	6.25	5.37	
KDR	7.96	7.81	7.96	8.55	7.73	8.02	8.06	7.88	7.76	7.77	8.34	7.69	7.87	8.04	7.84	8.28	8.20	8.07	8.16	8.29	8.11	7.86	8.02	8.38	7.97	
LYPD3	6.38	6.80	6.13	5.63	6.66	6.28	6.26	6.90	6.32	6.44	6.48	6.66	6.41	6.51	6.82	6.76	6.65	6.38	5.99	6.95	6.20	6.35	6.86	6.60	5.60	
PODXL	4.85	4.56	4.57	4.80	4.52	4.57	4.80	4.68	4.55	4.52	4.81	4.59	5.05	4.75	4.77	4.85	4.79	4.66	4.75	4.99	4.54	4.84	4.80	4.65	4.33	
S100A4	6.55	5.77	6.29	4.82	5.95	4.47	6.55	6.78	5.01	5.43	6.54	6.19	5.93	6.76	6.00	6.19	6.27	6.45	6.28	6.52	6.07	6.64	6.85	5.86	6.06	
IGF1R	5.43	4.58	5.13	5.29	5.09	4.75	4.92	4.91	4.24	4.86	4.92	4.65	5.00	4.70	5.21	5.12	5.50	4.75	4.89	5.00	4.93	4.76	4.95	4.65	4.85	
ERBB2	5.32	5.44	5.10	5.41	5.44	5.97	5.35	5.34	5.45	5.25	5.64	5.13	5.50	5.22	5.47	5.49	5.96	5.61	5.45	5.56	5.37	5.45	5.49	4.92	5.37	
ERBB3	9.01	8.76	8.67	9.07	8.95	8.76	8.76	9.10	8.54	8.65	9.32	8.77	8.82	8.91	8.69	9.04	9.44	8.83	8.73	9.21	8.98	8.85	8.81	8.70	9.33	
KITLG	8.69	9.01	9.48	8.66	9.16	8.92	8.61	9.01	8.39	8.49	8.79	8.86	8.11	8.82	8.46	8.82	9.15	9.30	9.46	9.14	8.46	9.62	8.89	8.01	8.67	
SPARC	9.70	9.45	9.52	9.61	9.70	9.50	9.79	9.77	9.38	9.66	9.95	9.40	9.80	9.56	9.47	9.56	10.01	9.42	10.06	9.82	9.69	9.75	9.58	9.63	9.45	
GZMH	12.35	4.78	4.36	4.19	4.17	4.44	3.64	12.27	5.89	3.91	5.61	4.83	6.55	5.91	6.16	5.59	4.93	5.00	5.54	5.82	3.78	4.93	5.68	4.30	8.05	
TGFA	3.25	2.91	2.81	3.08	3.85	3.30	3.26	3.18	2.90	2.93	3.55	3.23	3.54	2.78	3.55	3.05	3.31	2.66	3.11	3.18	3.34	2.93	3.05	2.88	3.58	
FURIN	7.87	6.88	7.02	7.39	8.21	6.91	7.13	8.19	7.03	7.03	7.87	7.73	7.71	7.53	7.06	7.16	8.16	7.18	7.86	7.09	7.44	6.45	7.03	6.91	7.95	
CCN1	6.55	5.12	5.19	7.13	4.99	6.39	5.43	6.84	6.40	5.99	6.36	5.86	8.03	5.55	5.65	6.95	6.73	6.20	6.64	6.03	6.81	5.81	6.51	5.60	7.56	

Table S1 (Continued)

Table S1 (Continued)

Proteins	Patient ID																								
	1	2	3	4	5	6	7	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
KLK14	5.69	5.10	5.32	5.45	5.97	5.51	5.04	6.31	6.01	5.92	5.81	5.51	5.78	6.38	5.66	5.88	5.57	5.47	5.77	6.11	6.26	5.92	6.10	6.19	6.36
FADD	4.52	0.24	0.24	1.16	1.31	0.36	0.20	3.77	0.32	0.46	0.87	0.07	0.44	0.38	-0.03	1.04	0.75	0.61	0.31	0.36	0.06	0.48	0.51	0.02	0.55
METAP2	7.61	4.76	4.67	6.26	5.85	5.12	5.33	7.54	4.78	5.57	5.24	4.41	5.08	4.93	4.53	5.65	5.56	5.36	4.69	4.67	4.01	5.37	5.40	4.47	5.45
NECTIN4	4.84	5.19	5.30	6.27	6.11	6.37	5.35	4.90	5.31	5.09	5.40	4.75	5.90	4.84	5.04	5.03	7.40	5.24	5.15	5.00	4.62	5.20	5.21	4.56	5.41
FASLG	11.00	9.95	9.81	9.75	9.86	9.39	9.97	10.25	9.09	10.23	11.07	9.62	10.33	9.80	10.08	9.89	9.40	9.76	10.46	10.65	9.38	9.09	10.63	10.41	9.93
EPHA2	3.76	4.29	4.07	3.84	4.71	4.29	3.88	3.81	3.63	4.32	4.21	4.06	3.90	3.57	4.64	3.75	4.43	3.44	4.25	4.32	3.28	3.22	4.31	3.31	3.66
ITGB5	9.55	8.17	7.81	8.29	8.22	7.67	7.96	8.78	7.57	8.14	8.23	8.01	7.74	8.05	8.20	8.29	8.33	7.99	8.10	8.14	7.99	8.16	8.21	7.15	8.16
LGALS1	8.18	7.40	7.67	7.67	7.88	7.21	7.52	8.02	6.92	7.54	7.90	7.35	7.69	7.54	7.68	7.41	7.71	7.45	7.48	7.69	7.42	7.33	7.83	7.28	7.42
SEZ6L	6.13	5.52	5.74	5.86	5.31	5.60	5.47	6.08	5.37	5.48	6.04	5.77	5.71	5.76	5.87	6.10	6.05	5.20	5.80	5.94	5.72	6.07	6.09	5.48	5.84
GPNMB	6.24	6.04	6.06	6.02	6.32	5.98	5.96	6.03	5.23	6.23	6.29	6.21	5.99	5.83	6.24	6.22	6.42	6.00	6.13	6.31	6.02	6.12	6.35	5.77	5.99
CA9	4.85	5.65	5.10	4.90	5.94	5.42	5.35	5.66	5.29	5.23	5.89	5.22	5.12	5.85	6.28	4.85	6.61	5.57	5.24	5.63	5.65	5.23	5.63	4.41	5.05
MIA	10.83	10.54	10.52	10.45	10.16	10.34	10.45	10.79	9.79	10.22	10.64	10.02	10.17	10.38	10.34	10.24	11.00	10.49	10.56	10.52	10.75	10.64	10.50	10.39	10.18
CTSV	1.74	1.85	2.05	1.72	1.06	1.23	1.80	2.60	1.71	1.86	1.96	1.84	2.10	1.89	2.28	1.56	2.32	2.45	3.51	3.21	1.32	2.35	2.32	3.06	2.09
CD27	7.89	7.64	8.05	7.78	9.27	8.32	8.12	8.47	8.06	8.24	8.76	8.11	8.23	8.02	8.92	8.45	8.95	8.06	8.38	8.21	8.01	8.15	7.99	7.87	7.59
XPNPEP2	8.91	9.33	6.81	8.82	7.49	9.74	7.07	10.06	9.73	7.44	9.48	7.66	9.62	9.20	8.17	9.73	10.05	9.29	9.72	9.94	9.69	9.34	9.68	9.50	9.81
ERBB4	10.83	10.70	10.63	10.85	10.83	10.38	11.11	11.41	10.69	10.51	10.86	10.83	10.05	10.91	10.67	11.02	11.22	10.97	10.63	11.44	11.06	10.75	11.09	10.53	11.26
HGF	9.45	8.91	8.82	8.91	9.80	12.15	9.09	9.72	11.48	8.48	9.13	9.30	12.76	8.44	9.43	8.65	8.96	8.51	8.62	8.51	8.86	8.32	8.79	8.22	8.85
ADAM8	5.93	6.23	5.30	5.86	6.36	6.43	5.83	6.31	4.50	5.95	6.76	5.72	6.25	6.02	6.88	6.04	6.69	5.95	6.14	6.26	5.64	5.37	6.41	5.76	5.77
NT5E	12.37	10.35	10.38	11.16	10.31	11.48	10.07	11.84	9.98	11.46	12.15	10.32	10.03	10.17	12.05	11.08	10.04	9.70	11.45	10.66	9.86	9.92	10.61	10.50	10.25
CDKN1A	8.80	4.17	3.94	6.34	6.65	5.20	4.66	8.81	4.82	4.97	5.84	3.29	4.03	5.13	3.77	5.81	5.17	6.18	5.31	5.32	3.90	5.01	5.04	4.96	5.48
DLL1	12.05	12.11	12.00	12.08	12.59	11.98	12.11	12.27	11.42	12.02	12.56	11.86	11.89	11.91	12.33	12.01	12.53	11.91	12.31	12.41	11.83	12.07	12.11	11.75	11.47
MDK	9.05	7.55	8.26	7.95	8.43	9.96	8.21	8.86	10.35	8.46	8.06	8.04	9.78	8.05	8.66	8.47	9.27	7.92	8.31	8.56	7.91	7.76	8.47	7.85	8.32
ABL1	8.57	3.77	3.89	5.23	5.39	4.26	4.13	7.96	3.78	4.38	4.91	3.68	4.36	4.08	4.13	4.59	4.35	4.26	4.04	4.15	3.66	4.09	4.16	3.92	4.57
FGFBP1	5.75	5.38	4.85	6.05	5.81	9.97	5.90	5.58	10.35	5.06	5.08	5.54	9.73	5.36	5.70	5.61	5.94	5.68	5.09	5.23	5.49	5.63	5.46	5.53	5.83
TLR3	4.77	3.24	4.24	5.10	5.59	4.94	4.90	5.32	4.32	5.21	5.35	4.25	3.43	4.38	4.83	4.59	5.19	3.30	4.51	4.63	3.20	3.45	5.18	4.07	5.09
LYN	5.55	3.99	3.45	4.94	4.73	4.10	4.20	5.66	3.63	4.28	4.50	3.32	3.64	3.72	3.45	4.59	4.19	4.04	4.00	3.60	3.29	4.41	3.65	3.75	3.87
RET	3.20	4.22	3.09	3.92	5.21	4.53	4.35	4.70	3.94	4.49	5.73	4.79	3.83	4.92	4.64	4.95	4.80	5.98	6.11	5.28	4.20	5.12	5.23	5.56	2.75
VIM	9.67	2.16	2.70	3.66	3.57	2.97	3.76	9.26	2.87	3.42	3.53	2.64	1.85	2.96	3.56	3.85	3.05	2.81	2.99	2.47	3.19	2.54	3.20	3.45	3.81
TNFRSF19	5.75	6.35	6.54	6.51	6.90	6.41	6.17	5.93	5.46	6.22	6.87	5.75	6.04	5.88	6.83	5.68	6.53	5.96	6.30	6.42	5.79	6.20	6.65	5.89	5.25
CRNN	6.41	5.52	6.54	6.58	6.14	4.56	5.63	5.30	4.43	5.01	5.92	6.27	5.34	6.72	4.98	5.60	6.75	6.56	6.32	6.11	7.20	4.73	5.42	6.87	7.17
TCL1A	8.44	3.51	4.06	2.67	4.17	4.35	6.44	10.57	4.81	4.32	4.10	2.22	4.22	3.99	6.50	2.96	2.48	5.12	4.72	3.62	5.29	5.39	5.28	4.76	5.39
CD160	5.63	5.98	4.98	4.55	5.98	5.80	4.83	5.31	4.06	5.17	6.70	5.37	5.16	4.97	6.09	5.38	5.14	5.05	5.30	5.67	4.53	4.48	5.16	5.17	4.55
TNFRSF4	6.09	6.43	6.92	6.24	8.18	6.87	6.91	7.29	5.85	7.42	8.38	6.84	6.75	6.51	7.49	7.11	7.20	6.76	8.26	7.41	5.92	6.11	7.16	6.48	5.50
MICB	6.43	5.35	5.55	1.42	5.39	4.89	5.76	5.62	1.29	5.65	5.61	6.28	6.31	5.35	6.28	5.80	5.47	5.90	5.10	5.61	1.48	5.57	5.84	1.32	5.60
CCN4	6.06	6.40	6.95	7.09	7.70	6.85	6.59	6.62	6.47	6.95	7.23	6.46	7.22	5.95	7.27	6.49	7.43	6.01	6.89	6.88	5.94	5.75	7.12	6.06	6.03

Table S1 (Continued)

Table S1 (Continued)

Proteins	Patient ID																									
	1	2	3	4	5	6	7	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	
CXCL17	5.17	6.02	5.51	6.41	8.29	6.29	6.24	7.06	7.08	6.20	6.55	6.77	7.15	7.08	7.36	7.05	8.40	5.92	6.93	5.74	6.50	5.92	6.45	4.83	7.44	
PPY	8.38	12.09	11.26	9.35	13.05	9.38	11.90	11.01	10.37	9.61	11.57	10.19	10.99	11.18	7.58	11.48	11.38	10.65	9.51	12.01	12.44	11.50	11.85	9.35	12.16	
S100A11	4.98	2.97	3.14	3.84	3.75	3.37	3.59	4.72	3.13	3.10	3.62	3.25	3.67	3.63	3.32	3.63	4.02	3.12	3.33	3.54	3.23	3.16	3.32	3.10	3.66	
AREG	4.10	3.56	3.45	4.85	4.02	2.75	3.37	2.92	3.61	2.83	3.71	3.42	3.70	2.47	3.93	3.42	4.02	2.66	3.06	3.34	3.32	3.09	2.76	3.47	4.67	
ESM1	10.62	10.69	11.43	11.34	10.47	12.25	11.12	11.68	12.30	11.24	10.76	10.77	11.71	10.68	11.58	10.68	10.78	10.68	11.31	11.52	10.91	10.16	11.64	11.04	10.86	
CD207	3.75	4.04	3.08	2.08	3.82	3.75	3.78	3.83	3.18	3.57	3.92	3.98	3.40	3.84	3.43	3.51	3.70	3.32	3.78	3.84	2.97	4.08	4.43	4.30	3.79	
ICOSLG	5.39	5.39	5.22	5.31	5.60	5.32	5.16	5.12	5.00	5.31	5.72	5.19	5.06	5.11	5.62	5.56	5.67	5.20	5.35	5.70	5.09	5.40	5.57	5.19	5.01	
WFDC2	7.67	7.51	7.85	8.43	8.52	8.12	7.78	7.59	8.23	7.42	8.03	7.10	8.46	7.36	7.82	8.12	8.98	7.60	7.68	7.31	7.61	7.26	7.80	7.26	8.11	
CXCL13	10.65	7.75	7.86	12.34	8.69	8.33	7.53	9.57	9.02	8.79	8.41	7.75	8.09	7.24	9.40	8.35	8.08	7.45	8.62	8.69	9.15	6.75	8.44	7.86	11.92	
SMAD5	5.59	4.88	4.84	4.82	4.88	4.69	4.79	5.16	4.80	4.78	4.91	4.92	4.58	4.77	4.73	5.01	4.94	4.85	4.83	5.01	4.86	4.81	4.89	4.71	4.84	
ADAMTS15	4.72	4.65	4.86	4.95	6.05	5.71	5.01	5.01	4.81	4.81	6.36	4.87	4.93	4.90	5.63	4.86	5.37	4.92	5.61	5.71	5.12	4.88	5.24	5.40	4.92	
CD70	4.28	4.63	4.54	4.35	5.17	4.49	4.61	5.15	4.21	4.42	5.22	4.64	4.82	4.85	5.14	4.78	4.91	3.61	4.58	4.94	4.42	4.05	4.74	4.25	4.65	
RSPO3	6.29	6.27	6.65	6.51	6.90	9.30	6.64	6.26	7.50	6.48	7.06	6.73	9.52	6.41	7.22	6.80	7.12	5.89	6.27	6.70	6.57	6.31	6.80	6.06	7.30	
FOLR3	7.03	12.03	6.47	6.33	7.39	6.94	7.07	7.05	6.33	6.90	12.25	6.78	6.73	6.65	7.28	6.91	7.00	6.73	7.01	12.37	6.47	6.61	7.11	6.76	6.14	
CEACAM5	5.41	6.77	3.17	4.47	4.17	7.80	8.59	2.92	4.70	4.14	2.69	6.31	7.70	2.78	5.99	3.25	8.02	5.99	8.35	7.95	2.36	2.83	3.41	4.41	5.41	
FLT4	7.51	7.23	6.99	7.34	7.16	7.43	7.42	6.99	7.02	7.06	7.55	7.08	7.51	7.24	7.35	7.38	7.44	7.41	7.48	7.72	7.31	7.24	7.57	7.52	6.39	
MUC16	2.10	3.64	3.13	3.10	2.26	5.67	4.62	3.65	2.93	1.49	2.67	2.84	2.00	2.43	2.87	3.61	6.02	2.78	4.22	3.94	2.40	0.82	1.87	2.61	5.36	
WIF1	5.40	5.93	6.17	6.29	5.80	5.46	5.41	7.24	5.46	6.41	5.91	5.76	5.43	5.58	5.78	5.67	6.89	5.72	6.73	7.78	5.66	5.90	6.09	5.82	5.41	
GZMB	11.68	3.53	5.56	4.64	5.35	4.45	4.95	11.48	4.11	4.40	5.37	4.12	4.78	4.71	5.85	4.41	4.32	4.47	4.13	4.76	4.30	4.12	4.90	4.31	6.98	
FCRLB	2.56	3.81	1.41	2.53	3.06	3.16	2.16	2.41	2.88	3.00	2.97	3.82	2.67	3.01	2.90	3.10	3.31	1.67	2.75	2.23	1.38	2.15	1.73	2.70	1.94	
ANXA1	6.76	2.80	3.40	4.16	3.88	3.09	3.56	5.76	3.23	3.01	3.65	3.15	3.40	3.70	3.51	3.10	3.37	3.12	3.12	2.67	3.80	3.35	3.32	2.38	4.36	
FOLR1	9.66	9.04	9.41	10.00	9.87	11.44	9.22	9.54	10.07	9.37	9.49	9.03	9.76	9.28	9.65	10.00	10.95	9.02	9.22	9.68	9.36	9.24	9.45	8.71	10.07	

PEA, proximity extension assay.

Table S2 Raw PEA data for all patients at progression

Proteins	Patient ID																									
	1	2	3	4	5	6	7	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	
TXLNA	3.89	4.02	4.48	5.27	4.68	4.23	3.39	5.95	4.06	5.34	3.92	4.86	6.37	5.24	5.73	4.73	5.76	3.51	4.07	5.90	3.87	1.73	7.00	3.16	6.34	
VEGFA	10.16	10.58	11.22	11.70	11.10	10.61	10.46	10.37	10.07	10.81	10.97	10.61	11.14	10.30	10.25	10.03	11.86	9.98	10.28	11.04	9.89	9.55	10.81	10.18	10.92	
CPE	3.91	3.60	4.80	3.63	4.13	3.87	3.99	4.47	4.58	3.76	3.58	4.15	4.05	4.05	4.04	4.48	4.85	4.08	4.31	3.79	4.00	4.00	4.68	4.13	4.01	
KLK13	3.57	4.10	3.72	3.61	3.47	3.30	3.02	2.56	2.93	3.12	3.34	4.35	2.85	3.66	3.49	2.79	3.73	3.26	4.14	4.29	2.20	2.79	3.02	3.05	2.82	
CEACAM1	8.61	8.52	8.86	8.91	8.73	8.67	8.04	8.68	8.75	8.61	8.87	7.95	8.78	8.58	8.87	8.80	8.95	8.55	8.93	8.55	8.79	8.19	8.73	8.62	8.93	
MSLN	4.43	5.22	4.32	7.56	5.36	3.73	3.47	4.49	6.86	4.96	4.76	4.36	3.83	4.54	5.02	4.16	5.50	3.65	4.07	4.20	4.54	4.03	5.35	3.65	4.38	
TNFSF13	8.67	9.25	10.11	10.16	9.75	9.15	9.65	9.45	9.03	9.77	9.68	9.83	9.83	9.37	9.88	9.31	9.65	8.78	9.45	9.72	9.01	7.87	9.67	8.78	9.83	
EGF	5.82	5.52	6.15	4.90	4.67	5.07	4.90	8.22	5.11	6.87	5.59	5.50	9.97	7.91	7.00	7.02	8.86	4.74	5.82	6.75	4.92	4.55	8.82	5.78	9.00	

Table S2 (Continued)

Table S2 (Continued)

Proteins	Patient ID																								
	1	2	3	4	5	6	7	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
TNFRSF6B	5.08	5.74	5.99	6.14	6.75	5.73	5.14	5.61	5.18	6.01	6.86	6.64	5.84	5.25	5.36	4.46	6.95	5.40	5.06	6.24	3.90	4.31	5.87	4.22	4.73
SDC1	6.03	7.38	7.77	9.86	7.45	9.75	8.13	8.23	8.92	8.03	8.34	8.96	9.29	6.94	6.55	6.86	8.51	7.37	9.37	9.41	6.47	6.06	6.64	6.32	8.20
TGFBR2	7.12	7.55	8.64	8.27	8.57	7.49	7.79	7.15	7.41	7.60	8.00	7.69	7.58	7.38	7.83	7.42	8.29	7.14	7.54	7.93	7.26	7.15	7.94	6.82	6.83
IL6	1.82	4.54	4.65	5.63	4.50	4.52	3.41	3.46	3.24	4.52	4.57	4.08	3.98	2.60	3.29	2.70	4.58	3.37	3.52	6.26	2.62	1.55	3.69	2.49	2.23
CD48	6.99	7.59	7.35	6.41	7.65	6.74	7.00	7.28	6.73	6.81	7.17	7.29	7.18	7.45	7.46	7.12	8.07	7.10	7.26	8.01	6.97	6.49	7.17	7.12	6.91
SCAMP3	5.53	5.53	6.32	6.66	6.32	5.53	4.81	7.87	4.94	7.15	5.94	5.85	6.87	6.96	6.73	6.20	6.52	5.08	5.54	7.93	6.03	3.07	8.26	4.20	7.71
LY9	6.29	7.13	6.08	5.70	6.55	5.73	5.69	6.26	6.11	5.72	5.60	6.48	6.63	6.81	6.83	6.35	6.89	6.15	6.33	6.33	6.17	5.68	6.51	5.69	6.16
IFNGR1	7.10	6.97	7.58	7.56	7.38	7.20	7.20	6.95	7.18	7.18	7.27	7.09	7.01	6.92	7.37	7.06	7.44	6.70	7.38	7.31	6.90	6.48	7.26	6.72	7.10
ITGAV	4.37	4.32	4.75	4.35	4.86	4.43	4.71	4.96	4.71	4.75	4.80	4.74	4.50	4.77	4.46	4.97	5.09	4.79	4.64	5.01	4.82	4.68	4.98	4.73	4.76
TNFSF10	8.61	8.73	8.85	8.62	8.76	8.19	8.37	8.66	8.11	8.88	9.03	8.73	8.58	8.30	8.69	8.92	8.66	8.25	8.59	8.88	8.32	7.90	8.68	8.09	9.02
KLK11	5.14	5.30	6.26	5.51	5.57	5.59	5.27	5.39	5.02	4.93	5.38	5.25	6.48	4.97	5.14	5.61	6.63	5.12	4.93	5.48	5.01	4.61	5.16	5.16	5.64
GPC1	4.99	4.85	5.91	5.29	5.53	5.13	5.09	5.09	5.19	5.48	5.07	6.13	4.57	5.23	5.01	5.54	5.49	5.21	5.38	5.40	5.10	5.28	5.56	5.09	4.88
TFPI2	8.17	9.06	9.06	10.71	8.89	8.68	7.68	8.82	10.31	10.20	9.60	9.28	9.41	8.89	8.21	8.43	8.37	9.31	8.94	10.03	8.08	6.70	8.51	8.00	9.47
KLK8	6.04	6.01	7.04	5.56	6.32	4.23	6.15	5.56	5.58	6.17	6.03	6.14	6.00	5.72	4.93	6.50	7.06	6.08	5.63	6.67	5.74	6.17	5.54	6.25	5.59
KDR	7.82	7.67	8.10	8.51	7.77	7.97	7.92	7.77	8.10	7.90	8.10	7.62	8.02	7.86	7.94	8.09	8.11	7.92	8.19	7.93	8.01	7.33	8.10	8.26	8.03
LYPD3	6.45	6.61	6.62	5.30	6.48	6.43	6.46	6.72	6.58	6.52	6.08	6.86	6.59	6.45	6.61	6.52	6.71	6.16	6.06	7.06	6.50	5.92	6.78	6.61	5.56
PODXL	4.85	4.41	4.90	4.88	4.53	4.85	4.86	4.86	4.66	4.80	4.39	5.55	5.30	4.64	4.80	4.73	5.08	4.42	4.61	4.94	4.56	4.28	4.78	4.65	4.44
S100A4	5.92	5.81	7.07	6.42	6.38	4.34	6.63	6.67	5.22	5.30	5.73	6.97	6.44	6.52	5.57	6.69	5.78	6.15	5.55	6.54	6.49	5.56	6.86	6.51	6.07
IGF1R	5.09	4.71	5.49	6.07	5.19	4.65	5.05	4.90	4.55	4.93	4.78	5.05	4.92	4.87	5.24	5.02	5.67	4.64	5.01	5.33	4.82	4.36	5.21	4.58	4.81
ERBB2	5.94	5.00	5.28	5.29	5.36	5.74	5.53	5.68	5.99	5.82	5.40	5.62	5.77	5.12	5.27	5.35	6.14	5.48	5.40	5.67	5.40	5.11	5.57	5.18	5.49
ERBB3	8.93	8.62	8.99	9.46	8.97	8.79	8.60	9.04	8.90	9.00	9.23	8.70	8.95	8.85	8.86	8.88	9.45	8.71	8.78	9.11	8.75	8.49	9.03	8.75	9.20
KITLG	9.07	9.17	9.63	8.30	9.08	8.98	9.13	8.65	9.12	9.12	9.15	9.03	7.89	8.82	8.48	8.94	9.00	9.19	8.74	8.87	8.93	9.24	8.94	7.90	9.04
SPARC	8.94	9.19	9.79	9.14	9.46	9.46	9.80	9.72	9.37	9.82	9.69	10.08	9.93	9.73	9.72	9.57	10.00	9.19	9.90	9.71	9.23	9.30	9.64	9.78	9.79
GZMH	5.46	6.01	4.81	6.25	3.97	3.60	3.25	7.93	4.85	3.70	4.51	5.19	7.07	6.57	6.55	5.40	4.98	4.28	5.44	5.02	3.32	4.47	11.34	6.12	6.62
TGFA	2.85	3.18	3.47	3.92	3.55	3.45	3.07	2.86	2.84	3.69	3.53	3.85	4.07	2.91	3.61	2.87	3.47	2.79	3.29	3.84	2.76	4.15	3.16	2.70	3.41
FURIN	7.24	6.98	7.30	7.04	7.77	7.17	7.40	7.77	7.48	7.82	7.63	7.81	8.20	7.42	7.06	6.87	7.72	7.24	7.68	7.42	6.85	5.86	7.58	6.76	7.22
CCN1	6.07	5.13	6.29	7.60	5.98	4.72	5.39	6.63	6.50	6.48	5.83	6.06	6.70	5.75	6.47	6.71	6.93	6.64	6.47	6.42	6.17	4.21	6.54	5.69	6.75
KLK14	5.54	5.12	6.20	5.08	5.88	6.27	4.66	5.62	5.79	5.80	5.40	5.49	5.56	6.43	4.79	6.01	5.63	5.44	5.58	5.81	6.12	5.10	5.96	6.34	6.24
FADD	0.42	0.47	0.78	1.21	0.73	0.53	-0.11	2.24	0.09	1.07	0.33	0.23	1.77	1.28	1.33	0.93	1.51	0.14	0.58	1.24	0.25	-0.53	2.11	-0.03	1.66
METAP2	4.62	5.02	5.06	5.52	4.90	4.86	4.38	6.67	4.22	6.68	4.32	4.90	7.00	5.90	6.31	5.74	6.40	4.92	4.93	6.10	4.81	2.83	7.16	3.84	6.60
NECTIN4	5.15	5.17	6.18	7.54	6.15	6.66	5.55	6.04	5.60	6.81	5.60	6.90	6.68	5.05	4.84	5.01	7.94	5.31	5.81	6.83	4.49	4.83	5.07	4.50	5.84
FASLG	10.44	9.68	10.05	9.84	9.85	9.59	9.76	9.73	9.17	9.36	10.17	9.59	10.75	9.80	9.83	9.59	9.27	9.45	9.71	10.14	9.29	8.84	10.61	10.29	9.64
EPHA2	3.47	3.94	4.49	4.57	4.51	3.87	3.81	3.45	3.68	4.76	4.10	6.53	4.21	3.54	4.00	3.58	4.88	3.39	3.90	5.55	3.21	2.84	4.16	3.33	3.52
ITGB5	7.87	7.84	8.07	7.74	8.01	7.63	8.01	8.36	7.95	8.20	8.11	8.24	7.87	7.95	7.81	8.31	8.46	7.63	7.94	8.11	8.08	7.63	8.52	7.57	8.03
LGALS1	7.37	7.22	7.94	7.90	7.80	7.06	7.41	7.66	7.26	7.56	7.67	7.60	7.88	7.47	7.95	7.45	7.61	7.28	7.06	7.74	7.35	6.15	8.12	6.99	7.60
SEZ6L	6.06	5.23	6.86	5.77	5.60	5.56	5.36	6.21	5.57	5.62	5.78	5.71	5.63	5.63	5.79	6.07	6.56	5.03	6.68	5.53	5.65	5.52	6.07	5.50	5.95

Table S2 (Continued)

Table S2 (Continued)

Proteins	Patient ID																									
	1	2	3	4	5	6	7	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	
GNPMB	6.03	6.03	5.86	5.85	6.34	5.93	5.97	6.07	5.37	6.26	5.88	6.26	6.02	5.78	6.15	6.17	6.41	5.88	6.14	6.28	6.10	5.76	6.40	5.89	6.09	
CA9	5.99	5.13	7.68	5.15	6.32	5.20	5.47	6.66	5.64	7.38	5.43	5.59	5.09	5.93	5.37	4.91	7.17	5.48	5.73	6.08	5.19	4.76	5.82	5.03	5.38	
MIA	10.80	10.42	10.79	10.56	10.33	10.37	10.45	10.61	10.09	10.30	10.39	10.24	10.10	10.37	10.06	10.43	11.05	10.31	10.21	10.33	10.75	10.20	10.66	10.25	10.39	
CTSV	1.33	1.10	3.25	1.77	1.50	1.07	1.87	2.53	2.27	2.08	1.56	1.71	2.09	1.65	2.18	1.87	2.40	2.41	2.77	2.60	1.03	1.12	2.34	3.33	2.33	
CD27	7.73	7.59	8.24	8.44	9.08	8.26	7.91	7.76	7.91	7.73	7.99	8.09	8.22	7.94	8.29	7.93	9.04	7.78	7.96	8.11	7.92	7.59	7.84	7.35	7.16	
XPNPEP2	8.86	8.92	7.10	8.69	7.63	9.66	7.05	9.98	9.77	7.49	8.75	7.75	9.45	9.01	7.91	9.56	9.89	9.04	9.74	9.40	9.78	9.00	9.91	9.34	9.91	
ERBB4	10.58	10.54	10.99	10.87	10.92	10.35	11.07	11.36	11.41	10.49	10.41	10.75	10.11	10.90	10.72	10.89	11.26	10.87	10.82	11.18	11.03	10.40	11.37	10.62	10.98	
HGF	8.45	8.59	9.19	9.62	9.66	8.82	9.40	9.28	11.09	9.24	8.97	9.38	9.87	8.48	8.99	8.51	9.19	8.57	8.37	8.73	8.42	7.37	8.98	8.28	9.17	
ADAM8	5.38	6.03	6.06	6.54	6.07	6.37	5.90	6.15	4.73	5.96	5.84	6.06	6.66	6.04	6.27	5.83	7.13	5.79	5.56	6.81	5.57	4.98	6.27	5.51	5.49	
NT5E	12.09	9.86	11.09	11.30	10.37	10.62	10.23	11.98	10.19	10.90	11.54	10.45	9.69	10.79	11.13	10.18	10.48	9.87	10.88	11.14	10.65	9.76	10.57	10.15	11.00	
CDKN1A	4.08	5.16	4.86	5.40	5.72	5.20	3.68	7.90	4.91	5.34	4.70	4.30	6.31	6.20	6.84	5.95	6.35	4.53	4.98	7.08	5.53	2.22	7.25	2.96	7.15	
DLL1	11.84	12.15	12.29	12.28	12.63	11.89	12.01	12.01	11.80	12.01	12.20	11.93	11.98	11.95	12.02	11.75	12.81	11.83	12.09	12.53	11.61	11.64	12.17	11.49	11.09	
MDK	8.04	7.66	9.02	8.60	8.51	9.25	7.83	8.86	10.38	7.58	7.29	8.51	9.07	8.32	8.54	8.56	9.16	8.15	8.29	8.89	7.95	6.37	8.72	7.93	9.97	
ABL1	4.05	3.79	4.64	5.36	4.75	3.98	3.40	6.11	3.90	5.31	4.24	4.05	5.75	4.80	5.39	4.58	5.22	3.82	3.84	5.42	3.92	2.79	6.56	3.35	6.09	
FGFBP1	5.64	5.53	5.61	5.81	5.67	8.39	5.89	5.02	10.20	5.12	5.54	5.87	7.68	5.40	5.08	5.58	6.55	5.47	5.21	5.54	5.52	5.40	5.55	5.41	9.85	
TLR3	2.79	2.60	4.29	5.22	5.66	4.82	4.76	4.67	4.78	5.36	4.56	4.09	3.19	4.42	4.68	4.22	5.26	2.98	3.99	4.33	3.38	3.08	5.21	4.07	5.01	
LYN	3.88	4.08	3.86	4.59	4.26	3.78	3.32	5.32	3.49	4.66	3.95	3.82	5.09	4.70	5.25	4.48	4.81	3.24	3.73	5.27	3.95	2.11	4.87	2.79	5.16	
RET	2.73	3.34	4.16	4.04	5.07	4.31	4.80	4.72	4.79	3.47	4.15	4.26	3.84	4.94	3.77	4.81	4.73	5.63	4.60	4.92	4.73	4.67	4.87	4.88	3.23	
VIM	2.30	2.48	2.17	4.28	3.01	2.70	2.28	4.89	2.75	3.26	2.96	2.40	4.70	3.43	5.22	3.94	2.69	2.66	3.34	4.44	3.21	2.16	8.95	3.49	4.32	
TNFRSF19	5.54	6.21	7.13	7.58	6.91	5.99	5.92	5.56	5.65	6.21	6.10	6.70	6.40	5.92	6.49	5.79	7.13	5.78	5.23	6.56	5.67	5.99	6.54	5.46	5.65	
CRNN	6.13	5.92	7.24	5.79	6.37	4.42	5.68	4.66	4.75	4.21	5.29	6.11	5.15	6.42	5.75	5.97	6.80	6.37	5.81	5.87	6.88	4.06	5.86	7.09	6.98	
TCL1A	1.44	2.80	4.44	4.45	4.41	4.57	5.84	7.39	4.39	5.45	4.51	2.09	5.16	4.67	6.67	2.73	2.33	4.34	4.03	2.71	5.16	4.53	9.33	5.83	4.90	
CD160	5.34	5.99	5.49	5.03	5.85	5.69	4.69	5.04	3.99	4.36	5.60	5.21	5.01	5.19	5.45	5.04	5.38	4.84	4.34	5.52	4.47	4.08	5.10	4.78	4.60	
TNFRSF4	5.79	6.15	7.30	7.38	7.64	6.79	6.77	6.61	5.93	6.57	6.43	6.78	6.98	6.36	5.97	6.57	7.74	6.55	5.99	7.44	6.29	5.30	6.78	6.02	5.10	
MICB	6.01	5.44	5.84	1.97	5.33	4.89	5.64	5.49	1.34	6.47	5.13	6.42	6.51	5.31	5.73	5.50	6.21	5.88	4.74	6.15	1.49	4.78	5.92	1.08	5.50	
CCN4	5.77	6.31	7.06	7.36	7.45	6.46	6.62	6.14	6.52	6.90	6.44	7.32	7.63	5.84	6.43	6.47	7.78	6.00	6.51	7.04	5.82	5.34	6.80	5.86	5.99	
CXCL17	5.57	6.04	6.41	8.06	8.15	6.42	6.41	6.95	7.48	6.84	6.00	7.85	6.95	7.04	6.68	6.33	8.49	6.01	6.28	6.83	6.21	4.71	6.72	4.65	7.36	
PPY	8.84	12.58	11.44	10.76	12.77	8.99	12.30	10.67	11.06	9.33	10.76	11.22	12.77	10.60	8.16	10.66	12.51	11.48	8.52	9.78	12.99	11.75	12.70	9.76	10.96	
S100A11	2.74	2.94	3.71	4.91	4.01	3.17	3.58	3.81	3.18	4.30	3.23	4.74	4.64	3.67	3.12	3.19	4.66	3.60	3.21	4.60	3.07	2.66	4.38	3.23	3.49	
AREG	3.71	4.04	3.64	5.28	4.01	2.74	3.23	2.51	3.33	4.10	4.67	3.74	3.73	2.74	4.33	2.97	4.70	2.98	4.13	5.62	2.37	2.71	3.12	2.45	3.84	
ESM1	9.95	11.20	11.44	11.49	10.49	11.79	10.83	11.57	12.15	11.79	10.81	11.45	11.19	10.70	11.04	10.55	11.08	10.78	10.91	11.07	10.70	9.71	11.84	11.24	11.90	
CD207	3.63	3.30	3.82	3.89	3.79	3.68	3.72	4.05	3.40	3.63	3.20	3.99	3.11	4.12	2.95	3.62	3.58	3.33	2.94	3.86	3.62	3.69	4.40	4.15	3.19	
ICOSLG	5.29	5.09	5.17	5.46	5.39	5.22	5.15	5.12	5.10	5.26	5.19	5.18	4.96	5.05	5.31	5.33	5.64	4.90	5.08	5.40	4.99	4.77	5.46	5.14	5.20	
WFDC2	7.87	7.92	8.65	8.94	8.49	8.66	7.91	8.08	8.24	8.57	7.84	8.11	8.65	7.63	7.87	7.76	8.88	7.90	7.73	7.68	7.21	6.91	7.86	6.59	7.98	
CXCL13	10.23	10.60	7.82	10.43	7.87	8.25	7.03	8.00	8.82	7.73	8.46	7.33	7.88	6.80	9.40	6.90	7.54	7.37	10.37	8.46	7.03	5.45	8.34	7.45	11.90	

Table S2 (Continued)

Table S2 (Continued)

Proteins	Patient ID																								
	1	2	3	4	5	6	7	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
SMAD5	4.70	4.83	4.87	4.56	4.81	4.89	4.84	4.86	4.82	4.79	4.80	4.79	5.00	4.75	4.96	4.86	4.79	4.65	4.92	4.91	4.75	4.22	5.08	4.74	5.03
ADAMTS15	5.06	4.46	5.25	5.07	6.01	4.89	5.03	4.85	5.07	4.25	5.68	4.54	4.96	4.74	5.49	4.56	5.79	4.83	4.68	5.23	4.66	3.20	5.20	5.19	5.06
CD70	4.44	4.49	4.23	4.53	5.05	3.80	4.62	4.61	3.55	3.75	4.22	4.57	4.73	4.59	4.13	4.57	5.04	3.62	4.18	4.30	4.10	3.63	4.79	3.93	4.26
RSPO3	6.21	6.05	7.19	8.03	7.04	5.96	6.35	6.41	7.17	6.12	6.53	7.09	6.24	6.31	7.42	6.84	6.97	5.82	5.73	6.63	6.17	5.96	7.05	6.01	6.87
FOLR3	6.65	12.05	6.81	6.20	7.25	6.80	6.80	6.80	6.50	6.57	12.35	6.90	6.82	6.76	6.90	6.98	7.19	6.70	6.68	12.33	6.88	6.10	7.21	6.74	6.41
CEACAM5	7.05	6.25	6.69	5.03	5.84	7.72	8.39	6.69	5.67	7.18	2.94	8.26	7.86	2.35	5.74	2.69	8.23	6.38	8.68	8.05	2.60	2.44	5.40	5.08	6.12
FLT4	7.29	7.29	6.96	7.45	7.26	7.55	7.34	6.88	7.41	7.14	7.26	7.13	7.59	7.04	7.05	7.04	7.63	7.24	7.37	7.61	7.18	6.36	7.71	7.34	6.74
MUC16	2.25	4.04	3.84	3.67	3.78	4.05	6.13	6.17	2.43	1.69	3.28	6.00	3.54	2.74	2.68	3.28	7.00	3.24	5.22	6.76	1.82	0.28	4.08	2.78	6.14
WIF1	5.04	5.86	6.42	6.65	5.84	5.39	5.60	6.96	5.63	6.48	5.80	6.55	5.75	5.56	5.66	5.86	7.19	5.70	6.86	7.41	5.79	5.32	6.73	6.22	5.40
GZMB	3.38	3.50	5.33	6.09	4.72	3.86	4.41	7.36	3.44	4.51	4.41	4.29	5.46	5.11	6.25	4.51	4.09	3.80	3.64	4.29	3.94	3.31	10.24	5.31	5.60
FCRLB	1.95	2.69	1.78	2.88	2.96	3.24	2.39	2.26	2.67	2.91	2.26	3.80	2.86	2.73	2.10	2.74	3.39	1.62	2.09	2.65	1.58	1.48	2.14	2.56	1.85
ANXA1	2.57	2.63	3.37	5.02	3.65	2.98	3.36	4.06	3.29	4.16	3.48	3.88	5.49	4.03	4.41	3.01	3.87	2.89	3.38	3.86	2.86	1.78	5.34	2.77	4.07
FOLR1	9.24	9.18	10.27	10.23	10.04	11.52	9.08	9.98	10.59	9.89	9.32	9.46	10.70	9.20	9.59	9.53	11.60	8.97	9.08	9.66	8.98	8.89	9.67	8.81	9.14

PEA, proximity extension assay.

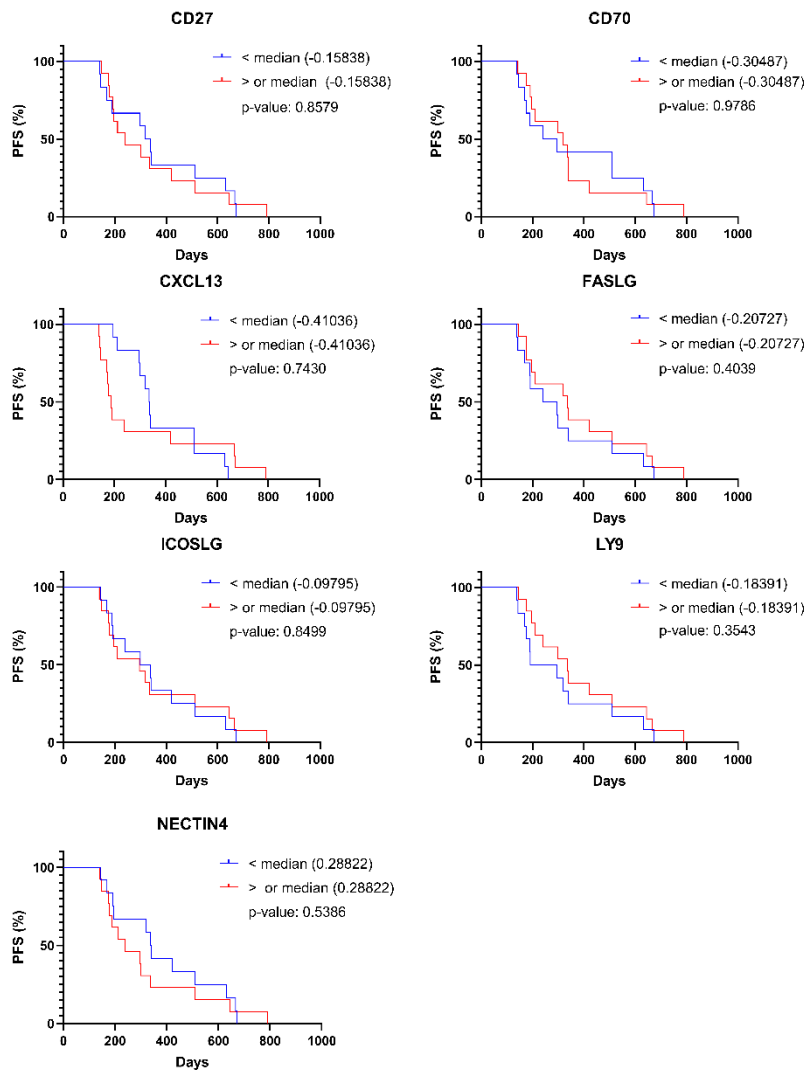


Figure S1 The relation between differences between response and PD for differentially regulated proteins and PFS. PD, progressive disease; PFS, progression free survival.

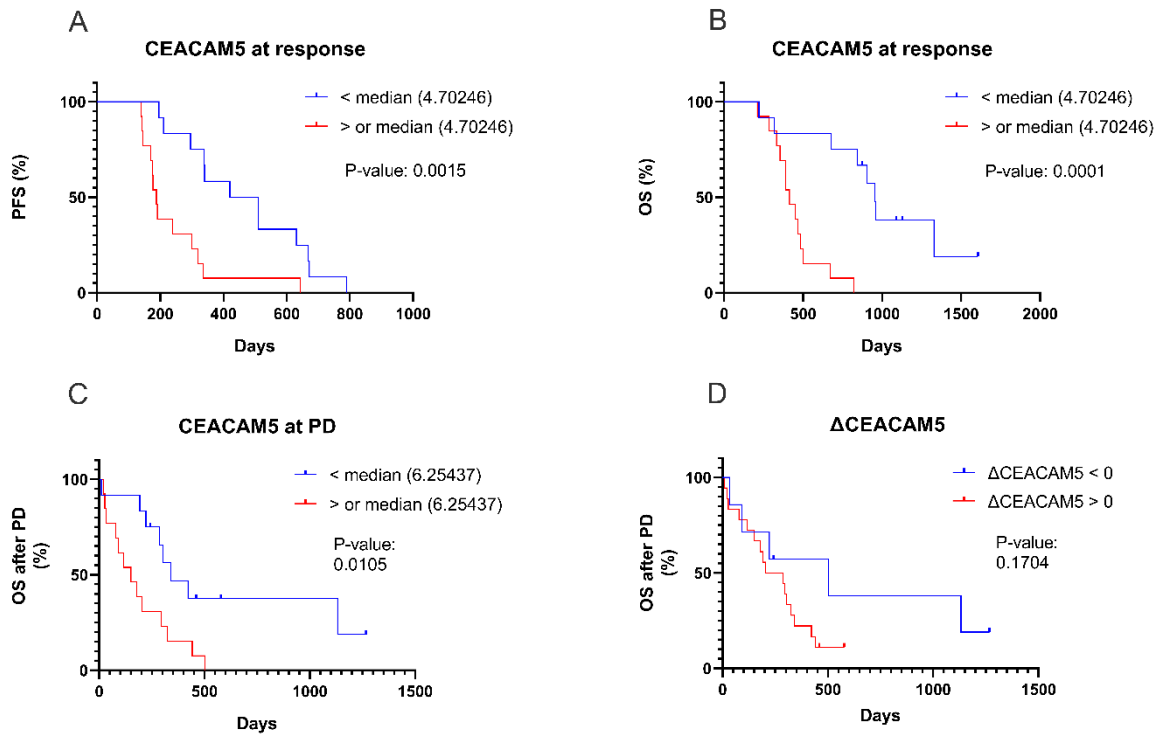


Figure S2 Effect of CEACAM5 at response and PD on PFS and OS. Patients are divided based on the CEACAM5 level below or above the median at response (A,B), at PD (C), or based on the difference between response and PD (D). Δ CEACAM5 <0 indicates a decrease in CEACAM5 from response to PD, whereas Δ CEACAM5 >0 indicates an increase. PFS, progression free survival; OS, overall survival; PD, progressive disease.

Table S3 Significant GO terms and associated genes

GO.ID	Term	Annotated	Significant	Expected	P value	Genes
GO:0002250	adaptive immune response	14	5	1.08	0.00075	<i>CD27, CD70, CXCL13, ICOSLG, LY9</i>
GO:0002460	adaptive immune response based on somatic recombination...	9	4	0.69	0.00143	<i>CD27, CD70, CXCL13, LY9</i>
GO:0022409	positive regulation of cell-cell adhesion	14	4	1.08	0.0098	<i>CD27, CD70, CXCL13, ICOSLG</i>
GO:0006955	immune response	34	6	2.62	0.01014	<i>CD27, CD70, CXCL13, FASLG, ICOSLG, LY9</i>
GO:0019724	B cell mediated immunity	3	2	0.23	0.01481	<i>CD27, CD70</i>
GO:0007155	cell adhesion	40	6	3.08	0.02649	<i>CD27, CD70, CXCL13, ICOSLG, LY9, NECTIN4</i>
GO:0022610	biological adhesion	40	6	3.08	0.02649	<i>CD27, CD70, CXCL13, ICOSLG, LY9, NECTIN4</i>
GO:0098609	cell-cell adhesion	28	5	2.15	0.02679	<i>CD27, CD70, CXCL13, ICOSLG, NECTIN4</i>
GO:0070231	T cell apoptotic process	4	2	0,31	0.0285	<i>CD27, FASLG</i>
GO:0019221	cytokine-mediated signaling pathway	19	4	1.46	0.03248	<i>CD27, CD70, CXCL13, FASLG</i>
GO:0022407	regulation of cell-cell adhesion	19	4	1.46	0.03248	<i>CD27, CD70, CXCL13, ICOSLG</i>
GO:0042110	T cell activation	19	4	1.46	0.03248	<i>CD27, CD70, ICOSLG, LY9</i>
GO:0097191	extrinsic apoptotic signaling pathway	11	3	0.85	0.03578	<i>CD27, CD70, FASLG</i>
GO:0006873	cellular ion homeostasis	5	2	0.38	0.04571	<i>CXCL13, FASLG</i>
GO:0006874	cellular calcium ion homeostasis	5	2	0.38	0.04571	<i>CXCL13, FASLG</i>
GO:0006875	cellular metal ion homeostasis	5	2	0.38	0.04571	<i>CXCL13, FASLG</i>
GO:0007204	positive regulation of cytosolic calcium ion...	5	2	0.38	0.04571	<i>CXCL13, FASLG</i>
GO:0030003	cellular cation homeostasis	5	2	0.38	0.04571	<i>CXCL13, FASLG</i>
GO:0051480	regulation of cytosolic calcium ion concentration	5	2	0.38	0.04571	<i>CXCL13, FASLG</i>
GO:0055065	metal ion homeostasis	5	2	0.38	0.04571	<i>CXCL13, FASLG</i>
GO:0055074	calcium ion homeostasis	5	2	0.38	0.04571	<i>CXCL13, FASLG</i>
GO:0055080	cation homeostasis	5	2	0.38	0.04571	<i>CXCL13, FASLG</i>
GO:0070227	lymphocyte apoptotic process	5	2	0.38	0.04571	<i>CD27, FASLG</i>
GO:0072503	cellular divalent inorganic cation homeostasis	5	2	0.38	0.04571	<i>CXCL13, FASLG</i>
GO:0072507	divalent inorganic cation homeostasis	5	2	0.38	0.04571	<i>CXCL13, FASLG</i>
GO:0098771	inorganic ion homeostasis	5	2	0.38	0.04571	<i>CXCL13, FASLG</i>
GO:0042113	B cell activation	12	3	0.92	0.04599	<i>CD27, CD70, ICOSLG</i>
GO:0050870	positive regulation of T cell activation	12	3	0.92	0.04599	<i>CD27, CD70, ICOSLG</i>
GO:1903039	positive regulation of leukocyte cell-cell adhesion...	12	3	0.92	0.04599	<i>CD27, CD70, ICOSLG</i>
GO:0045785	positive regulation of cell adhesion	21	4	1.62	0.04703	<i>CD27, CD70, CXCL13, ICOSLG</i>

GO, Gene Ontology.

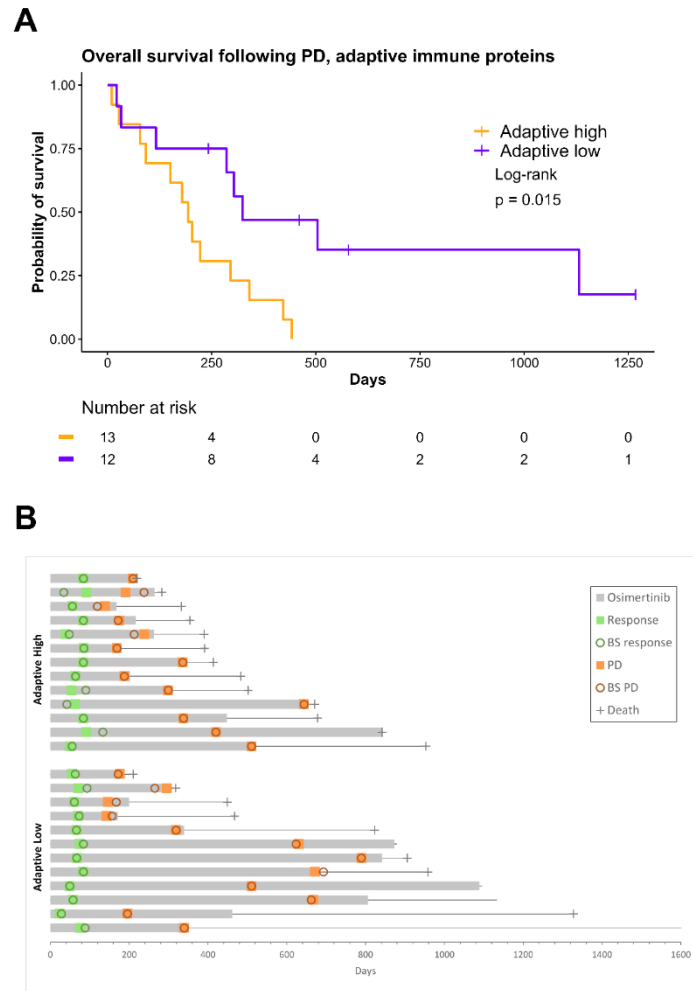


Figure S3 Proteins related to “Adaptive immune response” predict OS after PD. (A) OS after PD for patients with high or low levels of “Adaptive immune response” proteins. Statistical analysis was performed using a log-rank test. (B) The 25 patients are divided into “Adaptive-high” and “Adaptive-low” groups based on their sNPX values for adaptive proteins. The course of their disease, treatment, and blood samples are shown. PD, progressive disease; BS, blood sample; OS, overall survival; sNPX, summarized Normalized Protein eXpression.

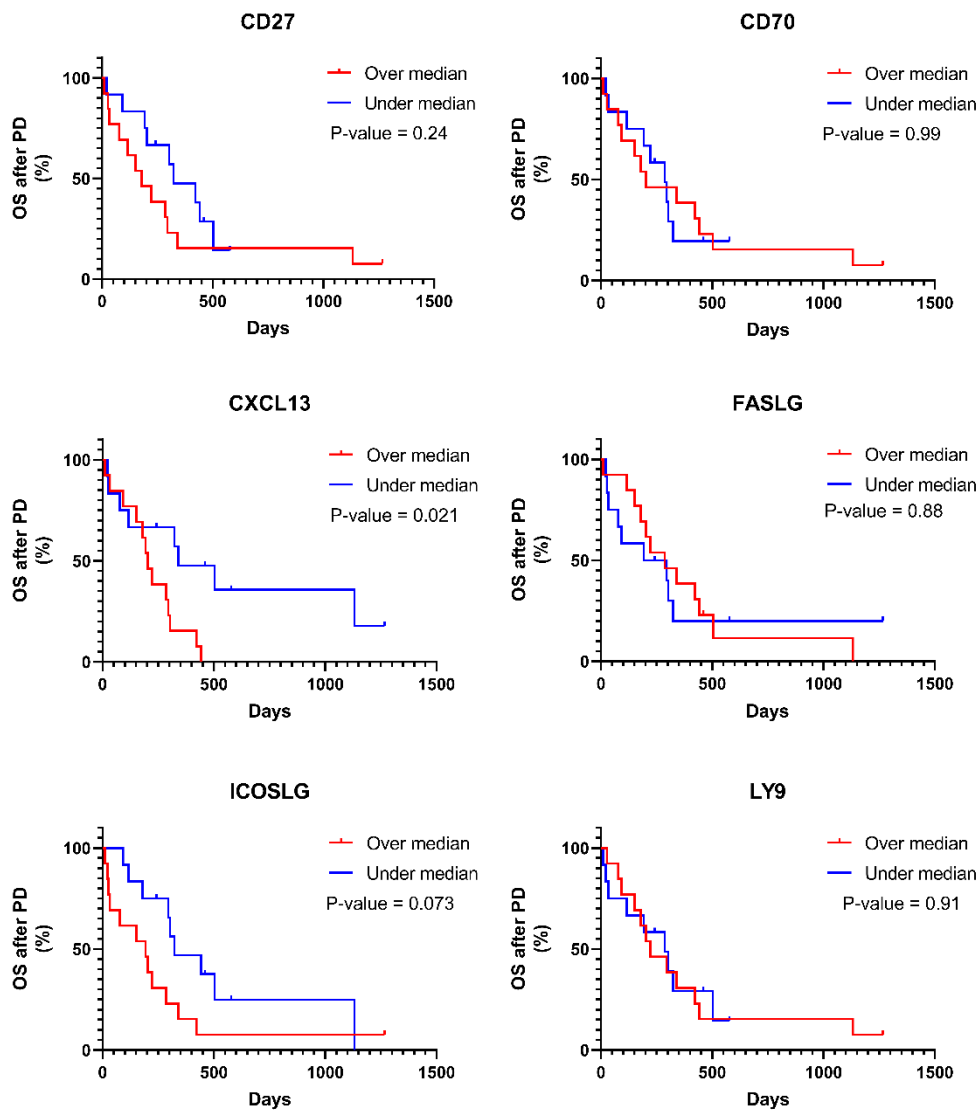


Figure S4 The relation between protein levels related to the immune response at PD and OS after PD. OS, overall survival; PD, progressive disease.