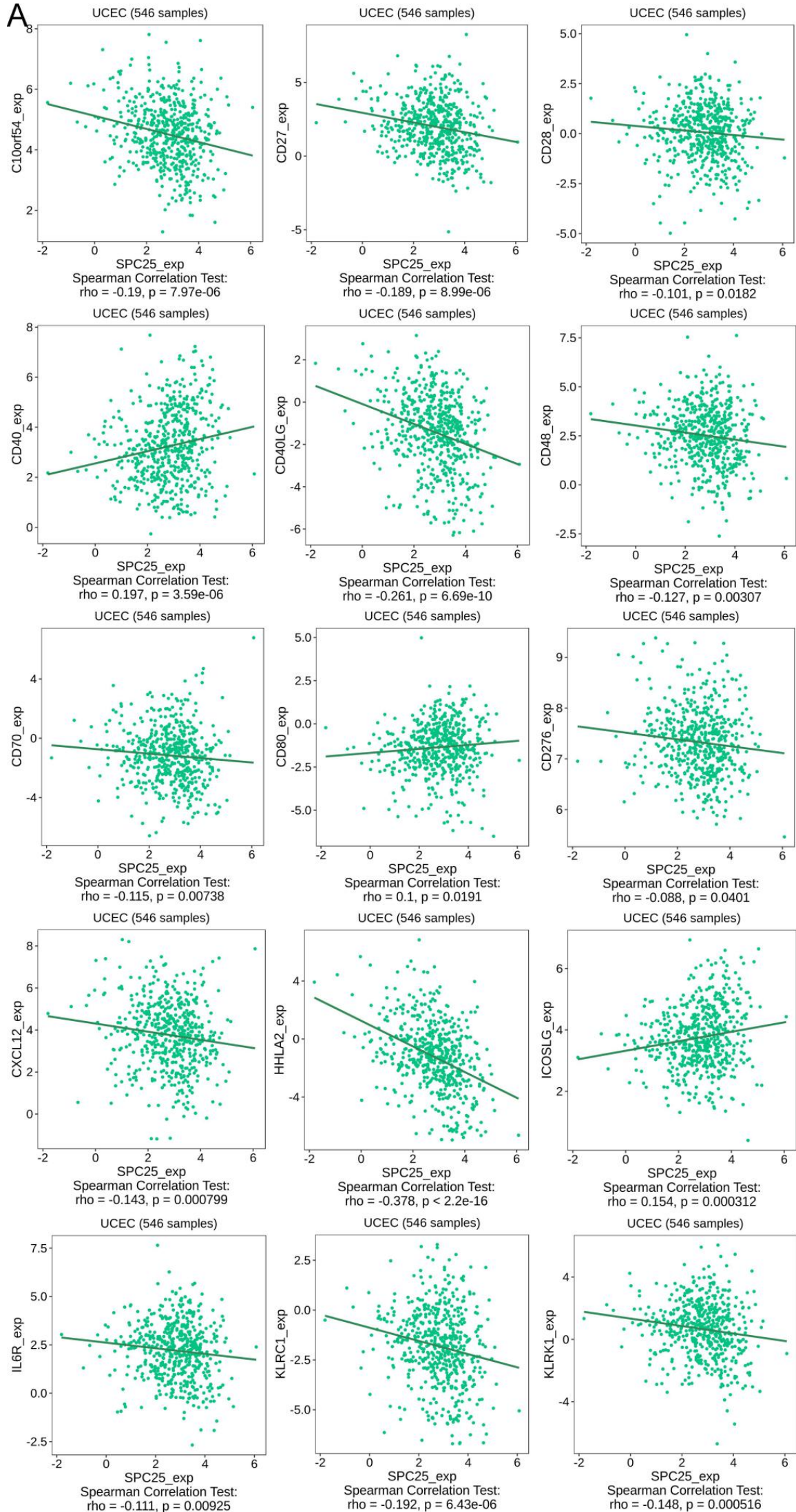
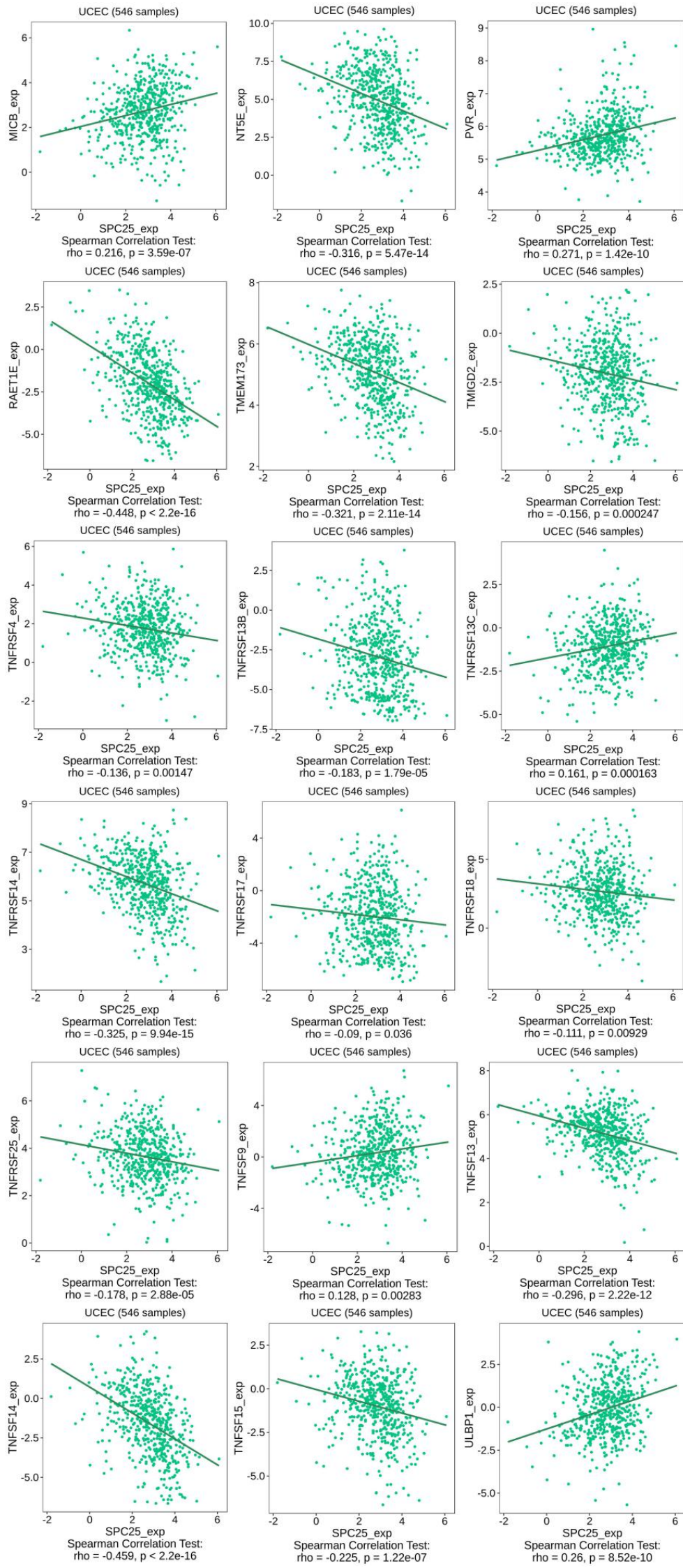
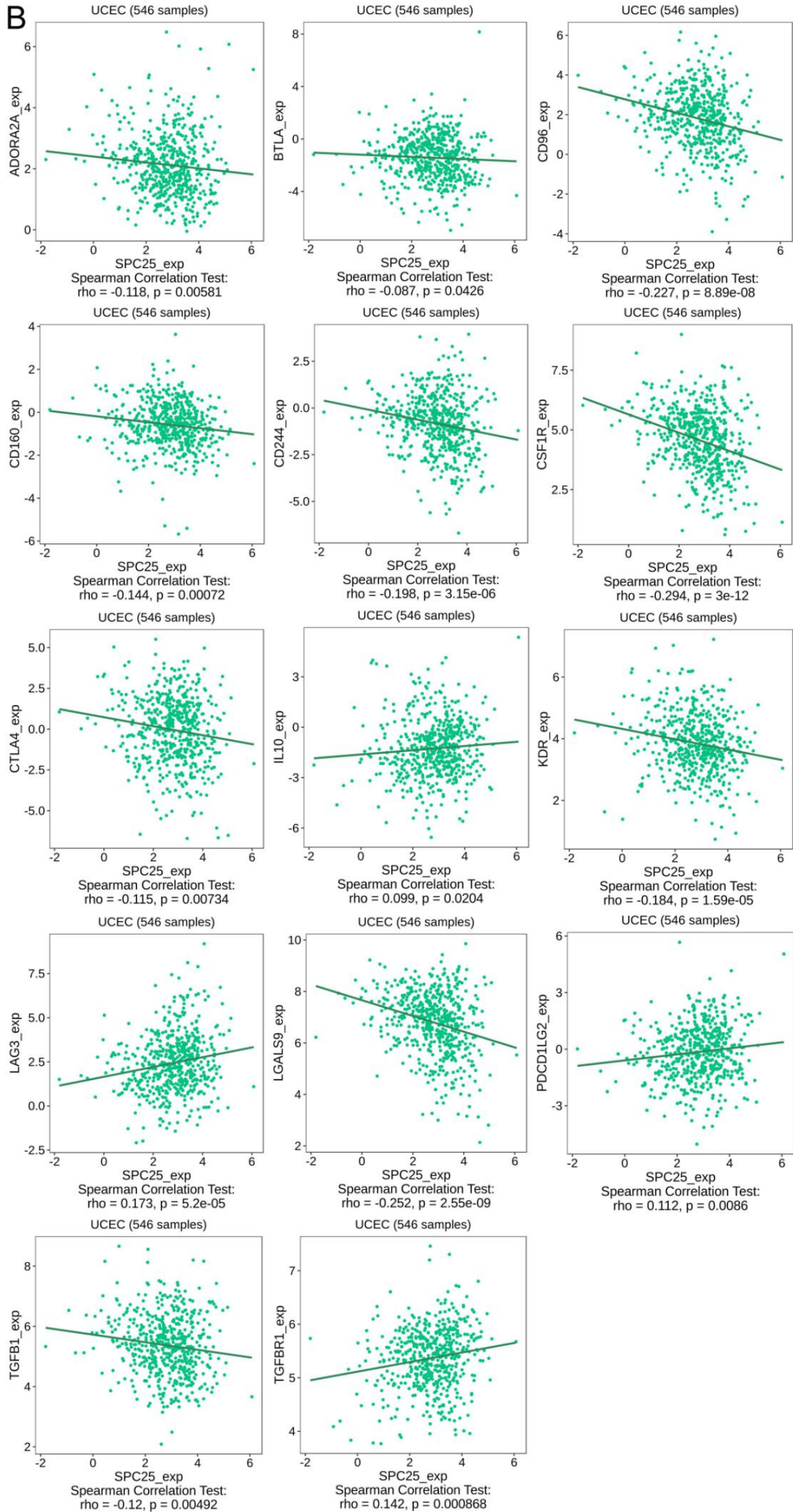


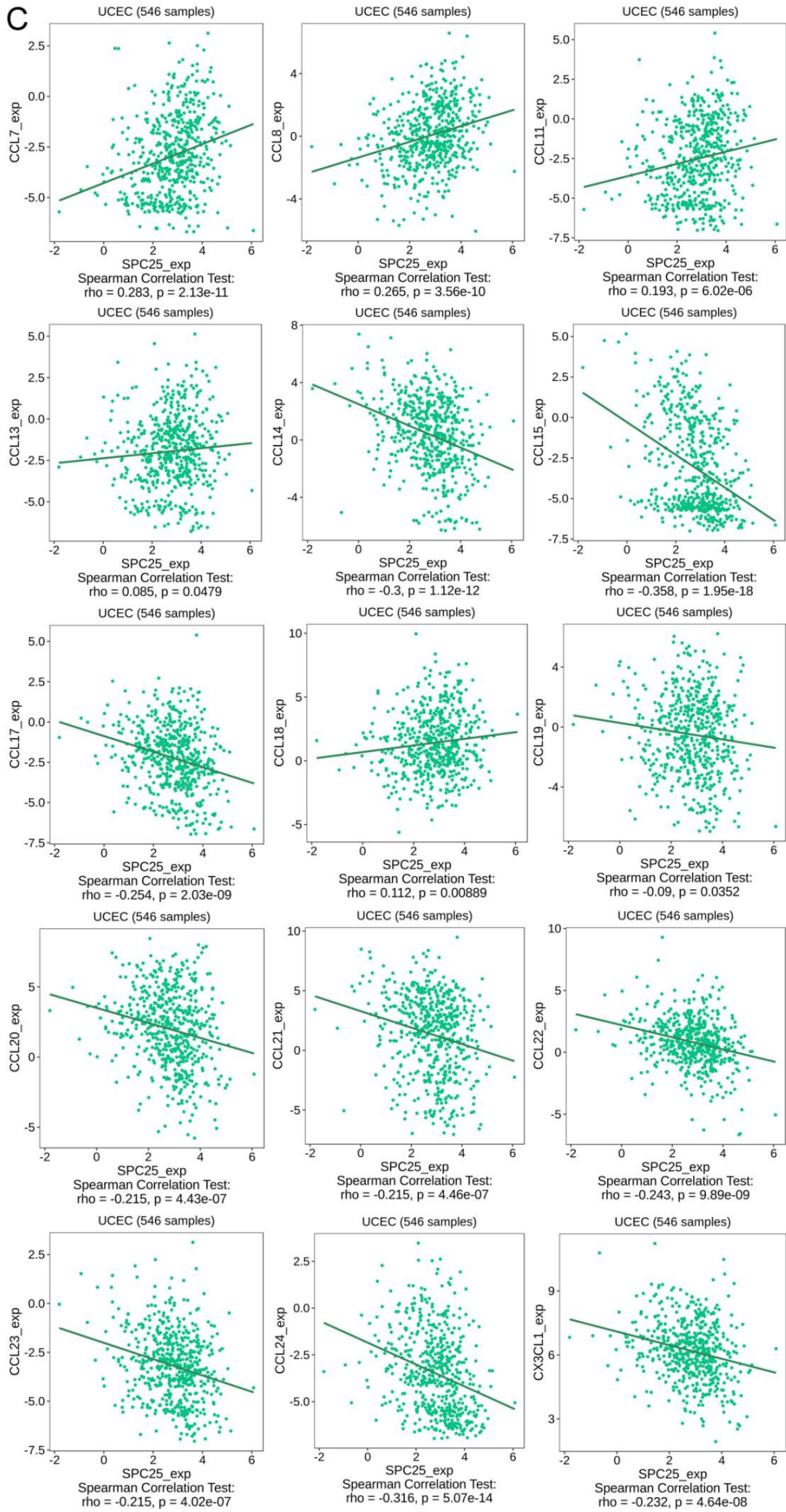
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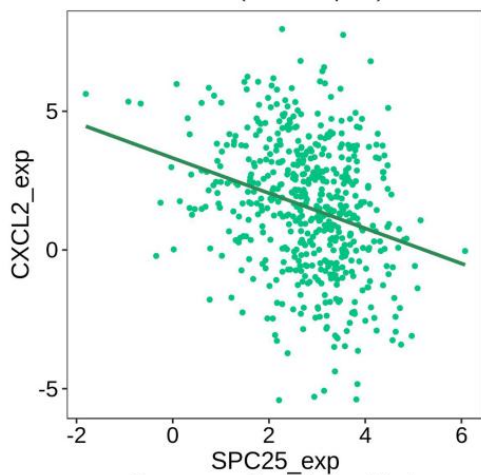




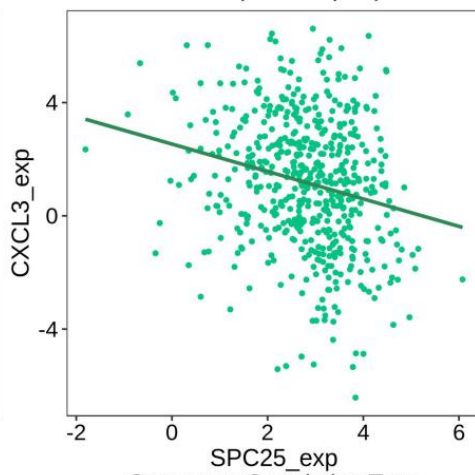




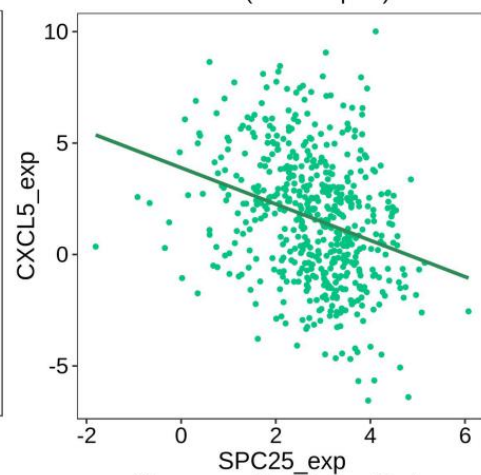
UCEC (546 samples)



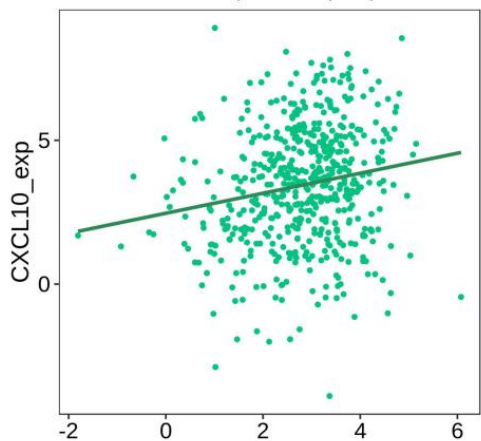
UCEC (546 samples)



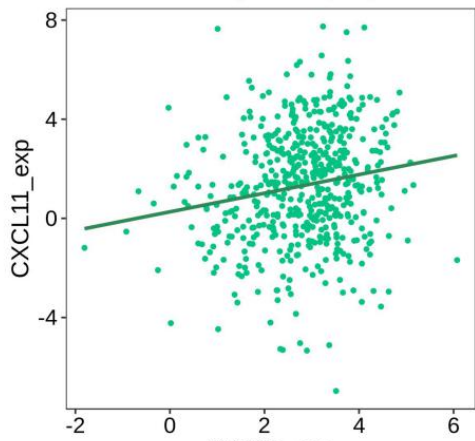
UCEC (546 samples)



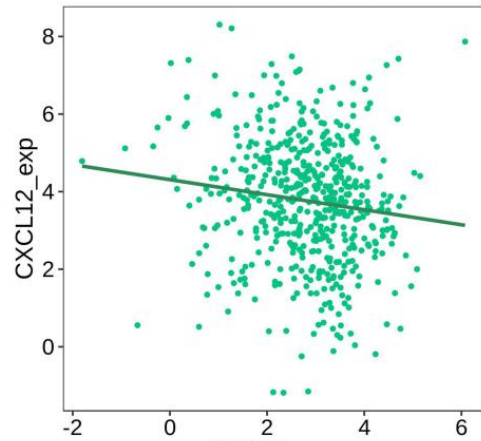
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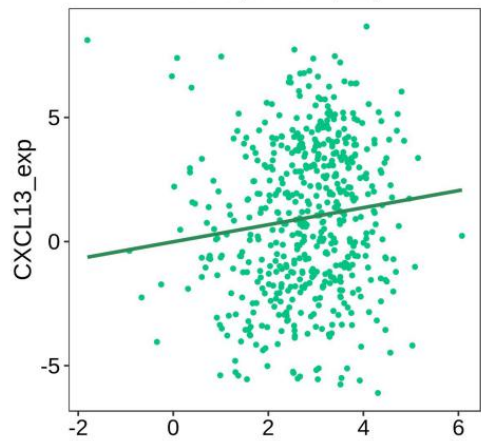
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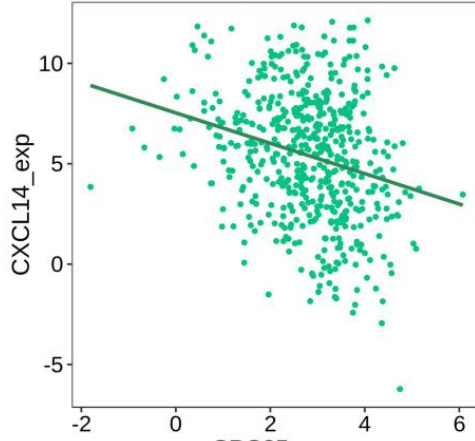
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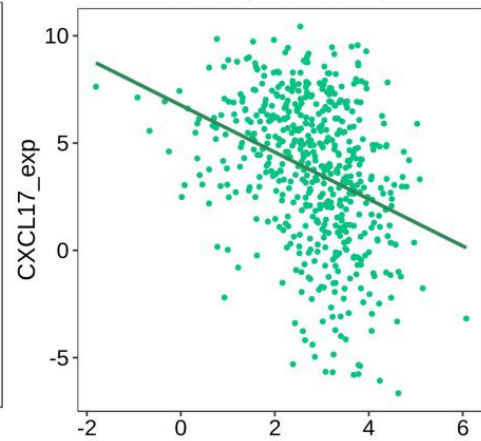
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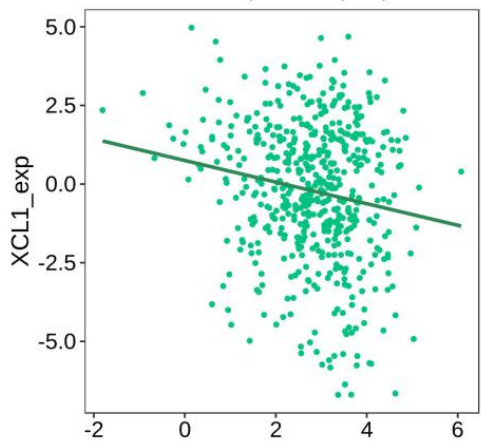
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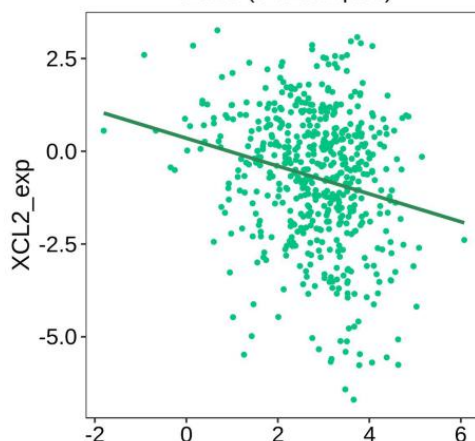
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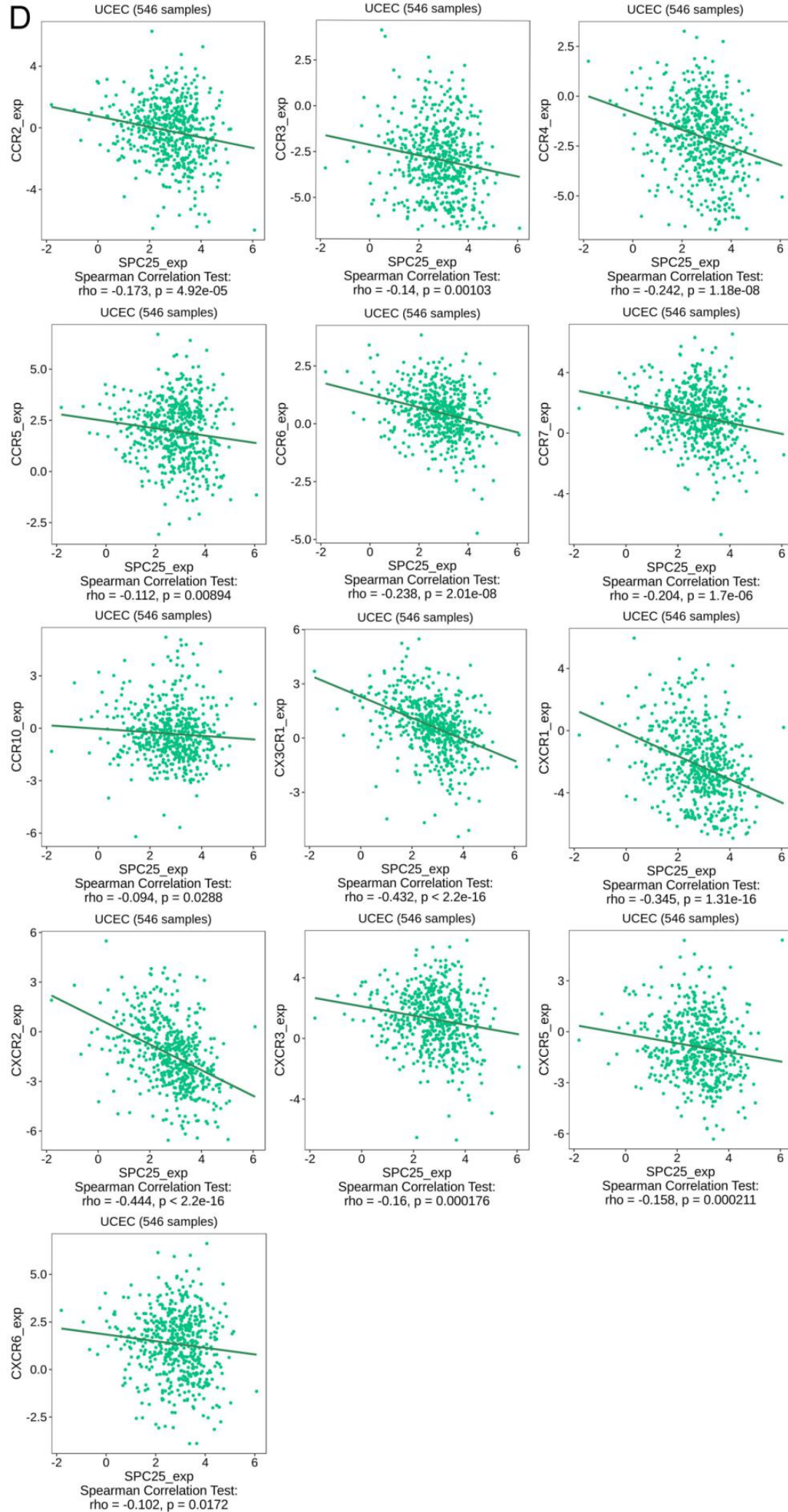


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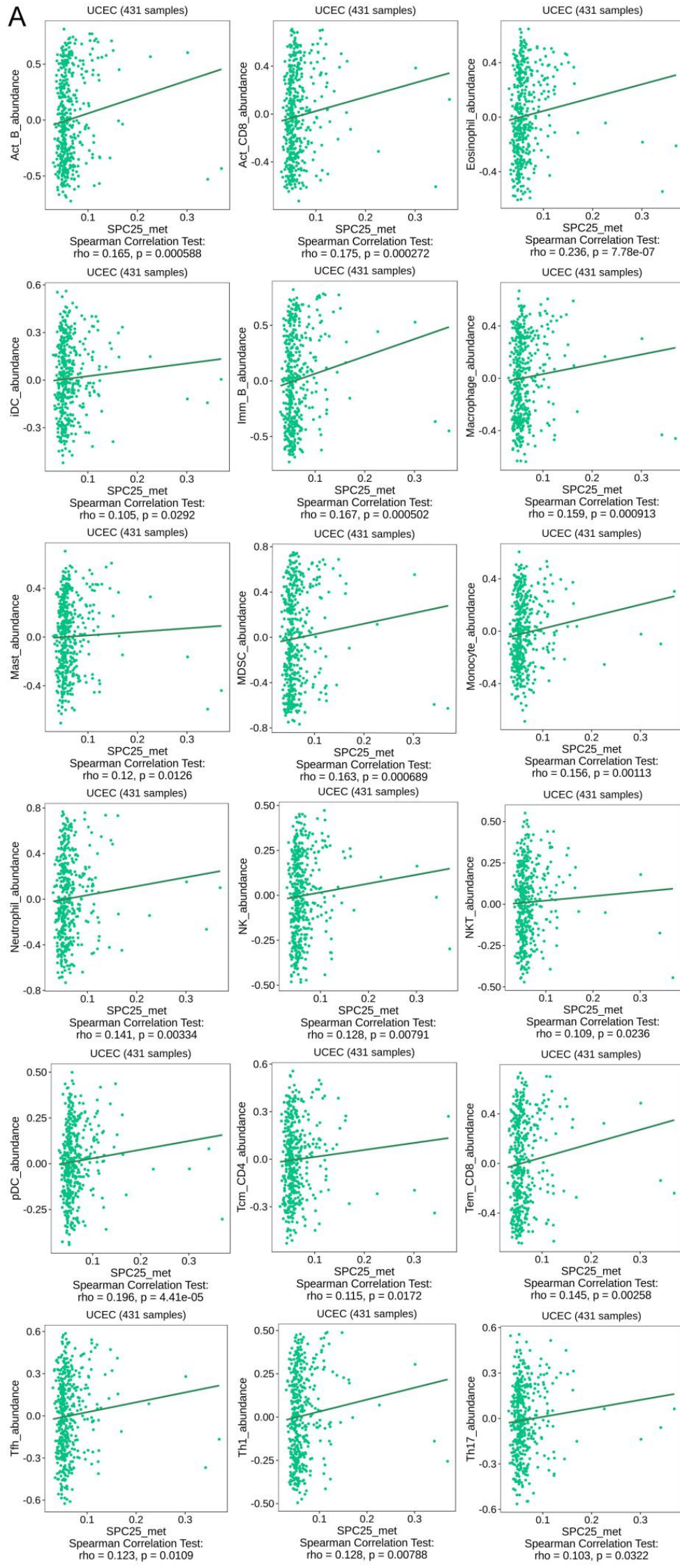
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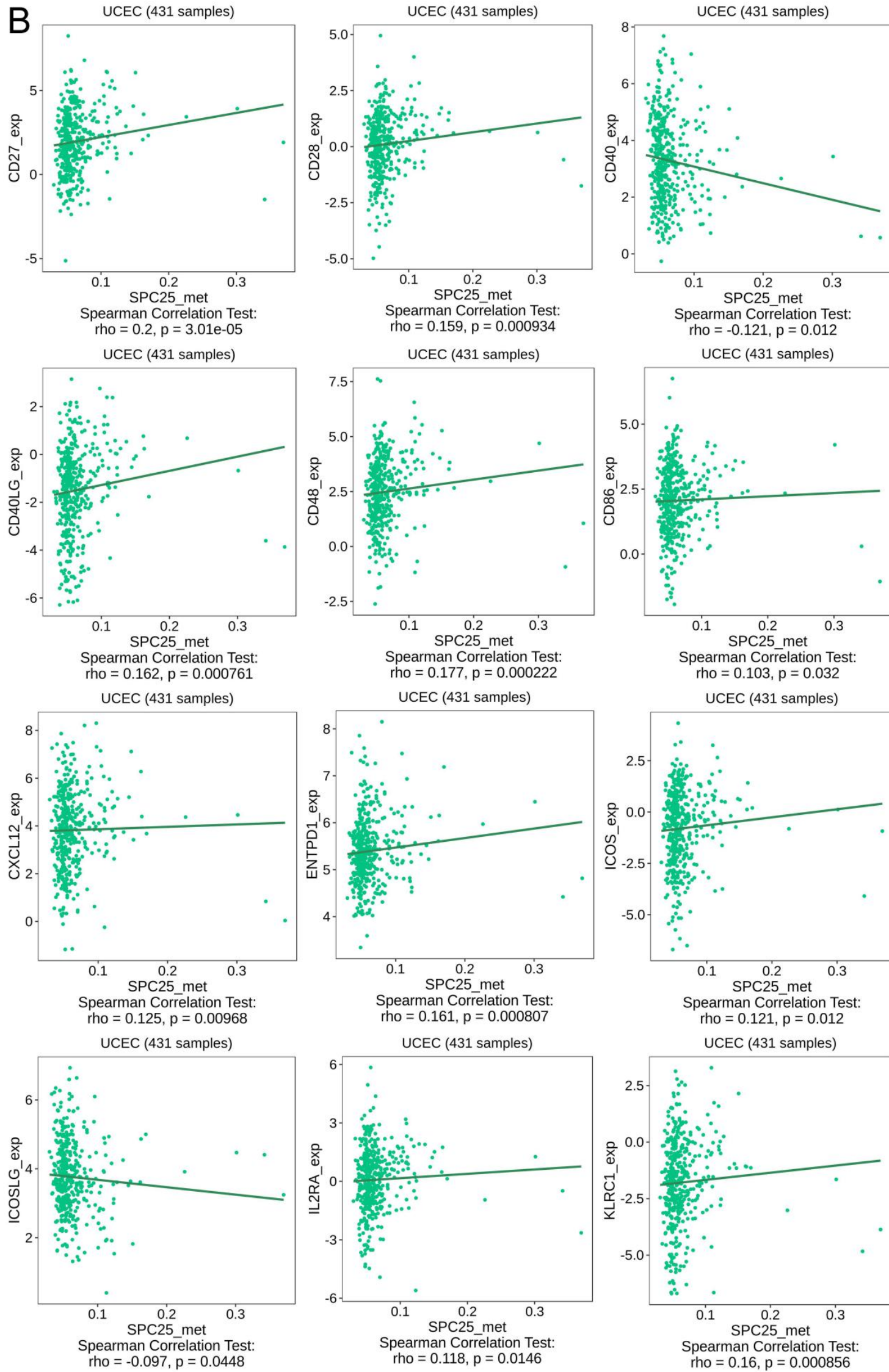




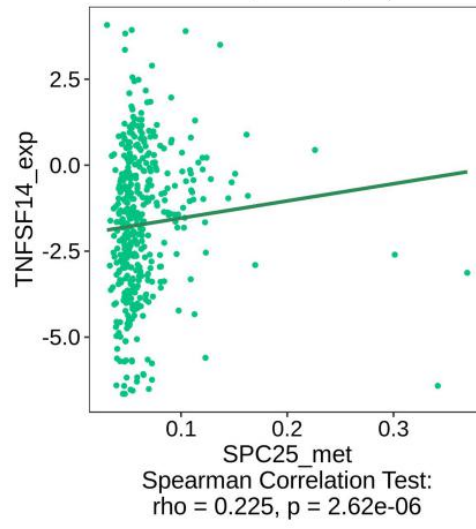
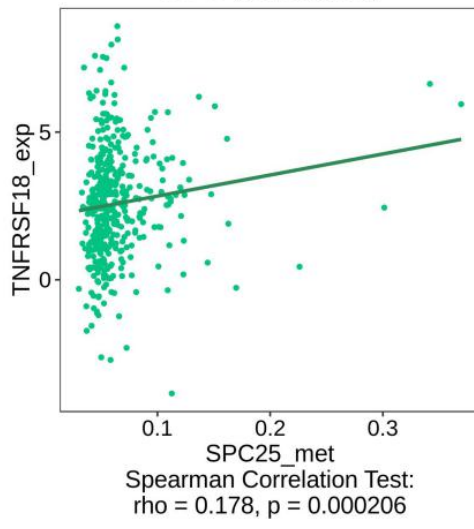
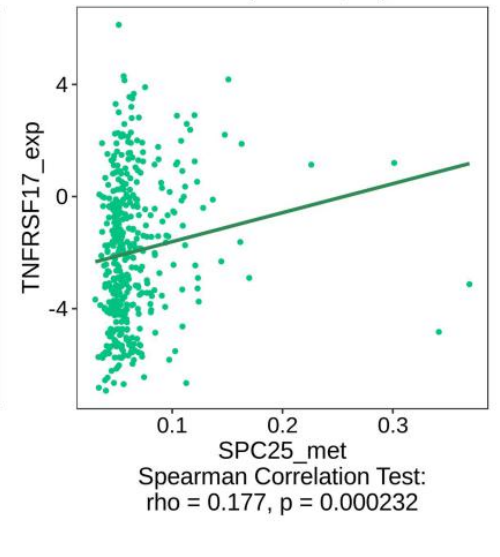
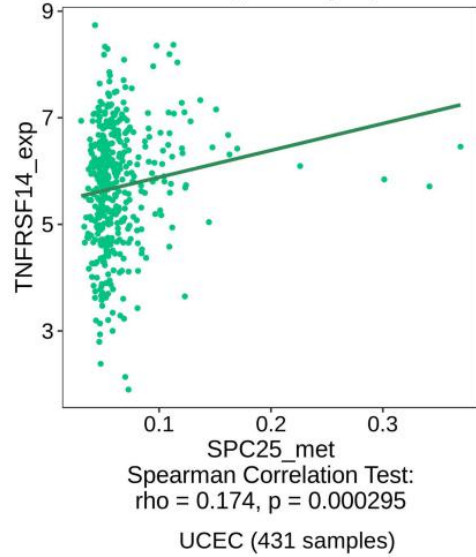
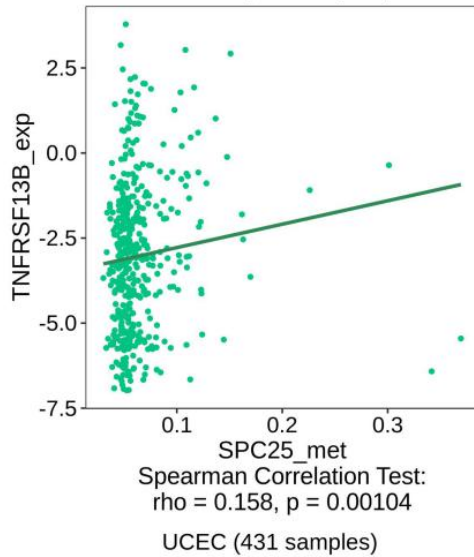
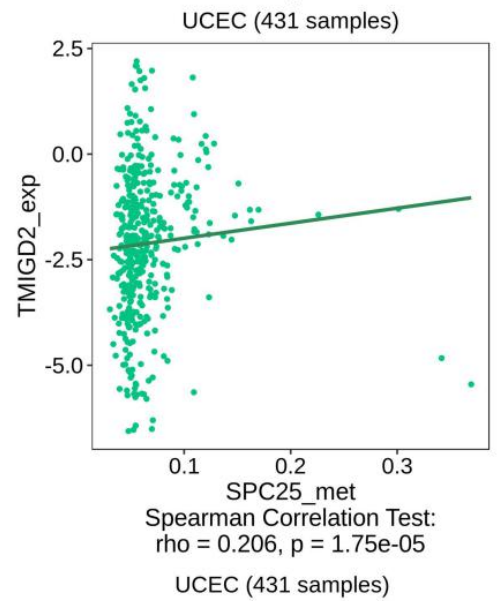
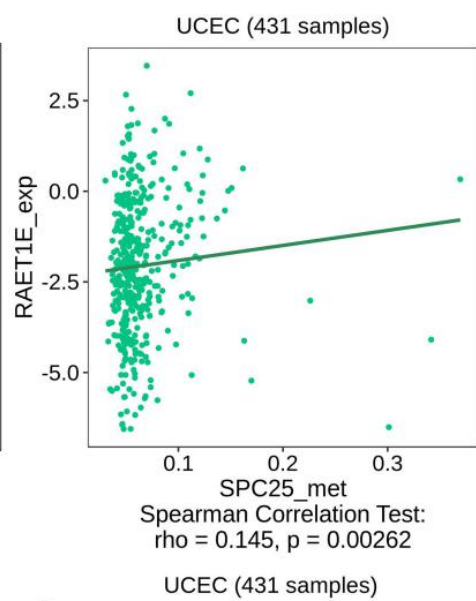
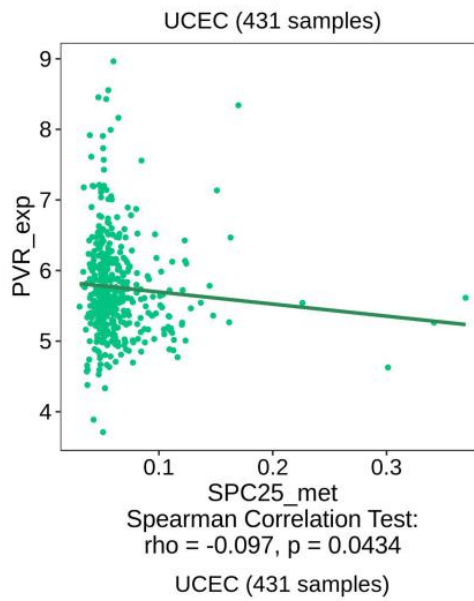
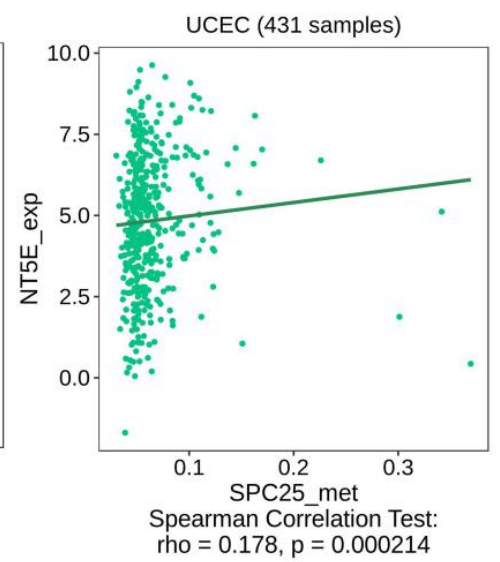
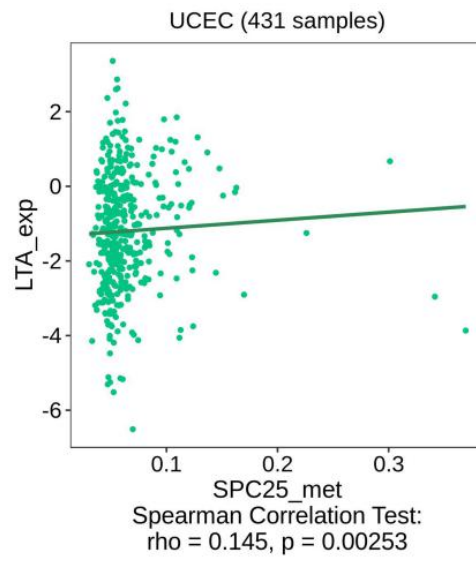
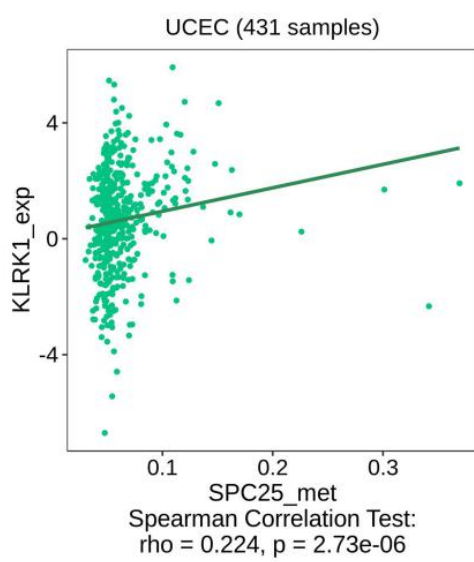
**Supplementary Fig. 1** Correlation between SPC25 with immunomodulators and chemokines in UCEC analyzed in the TISIDB database. **A–D** Expression correlation between SPC25 and immunostimulators **A**, immunoinhibitors **B**, chemokines **C**, and chemokine receptors **D** in UCEC available from the TISIDB database. A Spearman P value of less than 0.05 was considered statistically significant

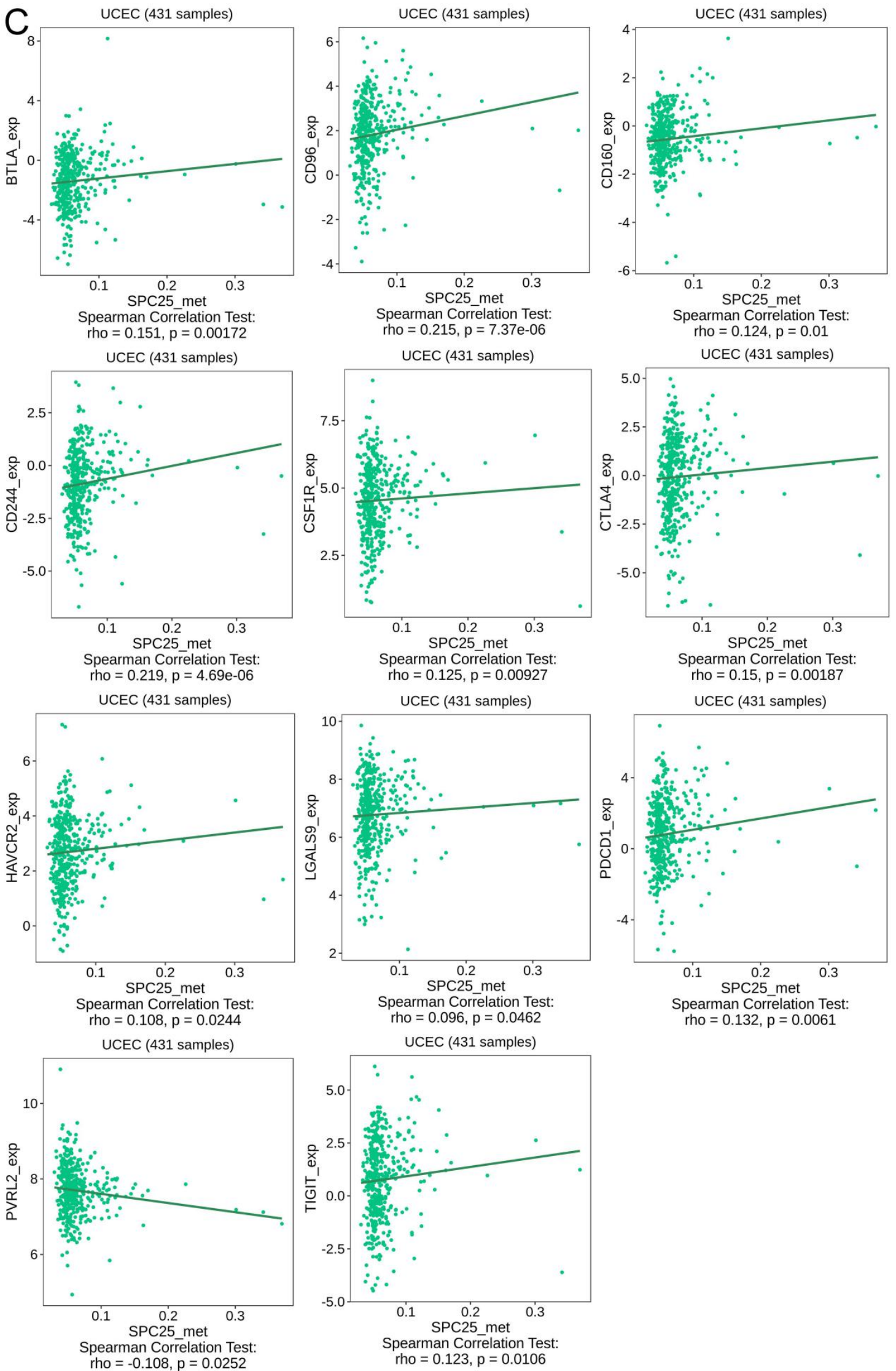




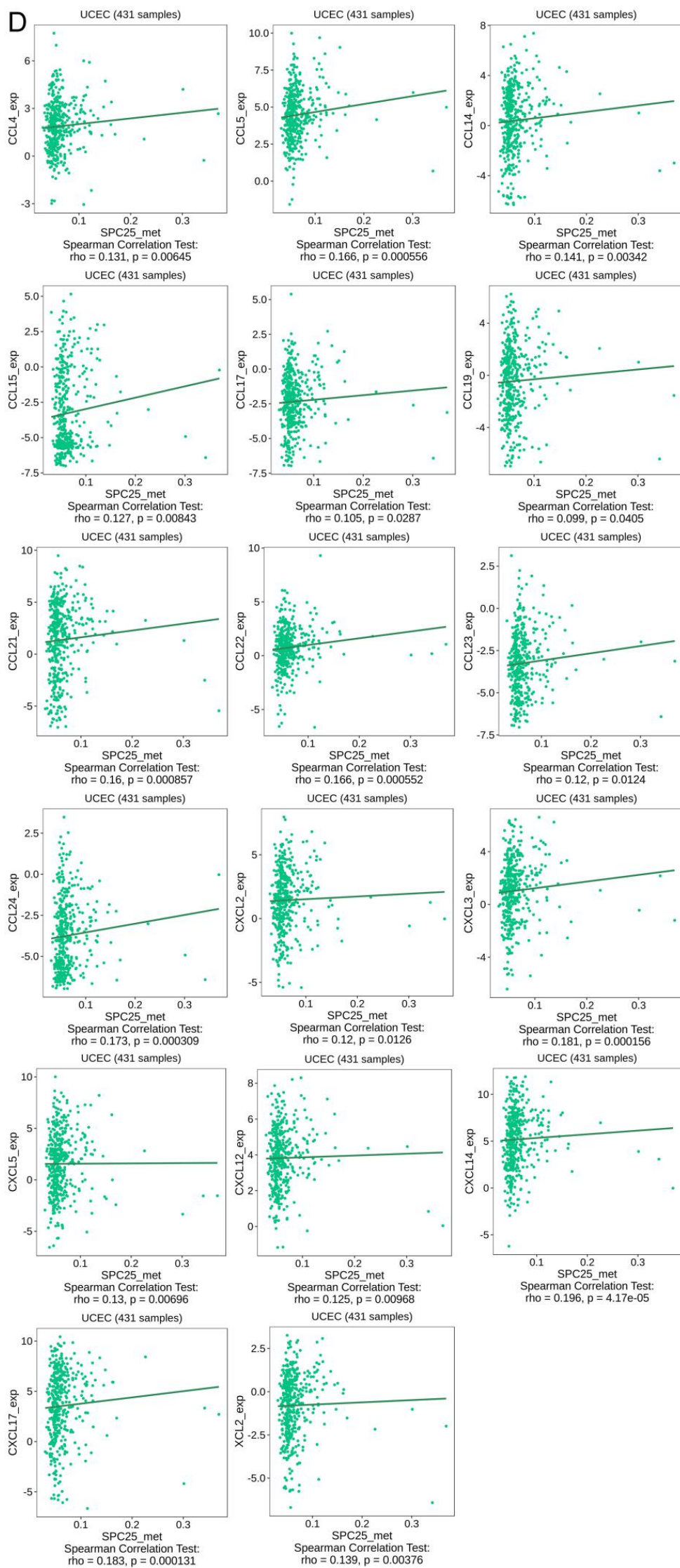
**B**

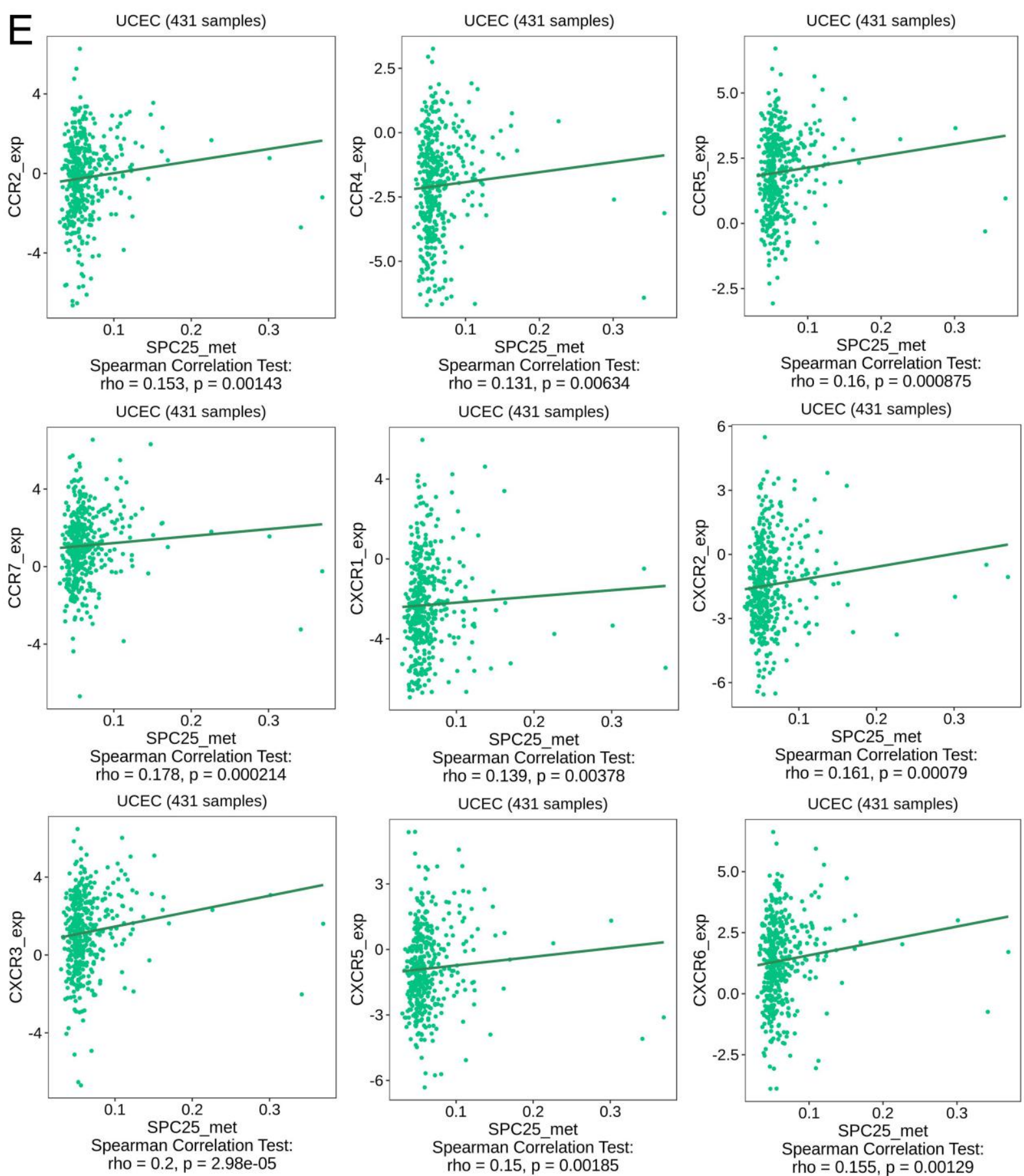












**Supplementary Fig. 2** Association between the methylation status of SPC25 with immune infiltration, immunomodulators, and chemokines in UCEC conducted in the TISIDB database. **A** Correlation of the methylation status of SPC25 with degree of immune cell infiltration in UCEC available from the TISIDB database. **B–E** Correlation of the methylation status of SPC25 with immunostimulators **B**, immunoinhibitors **C**, chemokines **D**, and chemokine receptors **E** in UCEC available from the TISIDB database. A Spearman P value of less than 0.05 was considered statistically significant



## Supplementary Tables

Since Supplementary Table 1 was too long to be displayed in this Word file, we considered uploading it in Excel format.

**Supplementary Table 1** SPC25 co-expressed genes tested by Pearson test in UCEC cohort analyzed by the LinkedOmics database. P < 0.05 or FDR  $\leq$  0.05 was considered statistically significant

Gene Set	Description	Size	Leading Edge Number	ES	NES	P Value	FDR
GO:0007059	chromosome segregation	262	97	0.86345	2.6851	<2.2e-16	<2.2e-16
GO:0006260	DNA replication	233	96	0.83949	2.5565	<2.2e-16	<2.2e-16
GO:0000075	cell cycle checkpoint	196	64	0.81667	2.485	<2.2e-16	<2.2e-16
GO:0007051	spindle organization	152	47	0.83142	2.4561	<2.2e-16	<2.2e-16
GO:0010948	negative regulation of cell cycle process	257	65	0.77523	2.4227	<2.2e-16	<2.2e-16
GO:0006302	double-strand break repair	180	71	0.80682	2.4052	<2.2e-16	<2.2e-16
GO:0006310	DNA recombination	233	87	0.75244	2.3207	<2.2e-16	<2.2e-16
GO:0000910	cytokinesis	150	31	0.76089	2.213	<2.2e-16	<2.2e-16
GO:0006403	RNA localization	208	97	0.72696	2.2071	<2.2e-16	<2.2e-16
GO:0006333	chromatin assembly or disassembly	137	45	0.76767	2.2024	<2.2e-16	<2.2e-16
GO:0006338	chromatin remodeling	141	47	0.73767	2.1613	<2.2e-16	<2.2e-16
GO:0016072	rRNA metabolic process	210	105	0.71008	2.1446	<2.2e-16	<2.2e-16
GO:0022613	ribonucleoprotein complex biogenesis	386	177	0.67149	2.1238	<2.2e-16	<2.2e-16
GO:0008380	RNA splicing	360	148	0.66583	2.0777	<2.2e-16	<2.2e-16
GO:0010639	negative regulation of organelle organization	339	63	0.65779	2.0661	<2.2e-16	<2.2e-16
GO:0006397	mRNA processing	420	173	0.65869	2.0618	<2.2e-16	<2.2e-16
GO:0015931	nucleobase-containing compound transport	213	84	0.65635	2.0146	<2.2e-16	<2.2e-16
GO:0006289	nucleotide-excision repair	106	48	0.70432	2.0119	<2.2e-16	<2.2e-16
GO:0006399	tRNA metabolic process	162	76	0.68064	2.0097	<2.2e-16	<2.2e-16
GO:0006997	nucleus organization	117	35	0.6919	1.9988	<2.2e-16	<2.2e-16
GO:0001539	cilium or flagellum-dependent cell motility	25	16	-0.8347	-2.1636	<2.2e-16	<2.2e-16
GO:0009112	nucleobase metabolic process	34	14	0.8198	1.9891	<2.2e-16	<2.2e-16
GO:0061512	protein localization to cilium	43	22	-0.66008	-1.9826	<2.2e-16	0.0011165
GO:0002251	organ or tissue specific immune response	25	13	-0.76132	-2.0152	<2.2e-16	0.0014887
GO:0002526	acute inflammatory response	151	48	-0.57028	-2.0247	<2.2e-16	0.002233
GO:1990868	response to chemokine	86	39	-0.5826	-1.9266	<2.2e-16	0.0044661
GO:0097722	sperm motility	70	20	-0.58978	-1.851	<2.2e-16	0.010049
GO:0072376	protein activation cascade	87	37	-0.55878	-1.8578	<2.2e-16	0.010421
GO:0042092	type 2 immune response	35	13	-0.66198	-1.855	<2.2e-16	0.010846
GO:0042537	benzene-containing compound metabolic process	22	6	-0.70746	-1.8147	<2.2e-16	0.016376
GO:0006968	cellular defense response	53	25	-0.5745	-1.7906	<2.2e-16	0.020991
GO:0032620	interleukin-17 production	28	7	-0.65453	-1.7409	<2.2e-16	0.040195
GO:0042445	hormone metabolic process	209	52	-0.45754	-1.7285	<2.2e-16	0.041569
GO:0007224	smoothened signaling pathway	125	33	-0.48571	-1.7308	<2.2e-16	0.043916
GO:0006959	humoral immune response	218	105	-0.43997	-1.6928	<2.2e-16	0.044214
GO:0007586	digestion	126	37	-0.48224	-1.7095	<2.2e-16	0.044382
GO:0032103	positive regulation of response to external stimulus	286	114	-0.4371	-1.7114	<2.2e-16	0.044661
GO:0048771	tissue remodeling	151	46	-0.47687	-1.7176	<2.2e-16	0.044661
GO:0042044	fluid transport	30	16	-0.64658	-1.7017	0.011173	0.044661
GO:0060191	regulation of lipase activity	92	32	-0.51302	-1.6936	<2.2e-16	0.046071
GO:0032637	interleukin-8 production	67	29	-0.5287	-1.6811	0.013986	0.047213
GO:0050900	leukocyte migration	395	129	-0.43294	-1.7018	<2.2e-16	0.047288
GO:0015850	organic hydroxy compound transport	227	87	-0.43605	-1.6224	<2.2e-16	0.078475
hsa04110	Cell cycle	118	50	0.84866	2.4352	<2.2e-16	<2.2e-16
hsa03040	Spliceosome	115	68	0.79212	2.2423	<2.2e-16	<2.2e-16
hsa03030	DNA replication	36	27	0.90104	2.1732	<2.2e-16	<2.2e-16
hsa03013	RNA transport	158	70	0.72402	2.1511	<2.2e-16	<2.2e-16
hsa03008	Ribosome biogenesis in eukaryotes	70	40	0.77862	2.0794	<2.2e-16	<2.2e-16
hsa04114	Oocyte meiosis	118	26	0.72398	2.067	<2.2e-16	<2.2e-16
hsa04914	Progesterone-mediated oocyte maturation	94	19	0.74096	2.0605	<2.2e-16	<2.2e-16



hsa03460	Fanconi anemia pathway	44	17	0.82372	2.0575	<2.2e-16	<2.2e-16
hsa03440	Homologous recombination	34	21	0.85325	2.0551	<2.2e-16	<2.2e-16
hsa04218	Cellular senescence	155	27	0.68675	2.0318	<2.2e-16	<2.2e-16
hsa03050	Proteasome	44	30	0.80285	1.9993	<2.2e-16	<2.2e-16
hsa04115	p53 signaling pathway	69	12	0.72363	1.9817	<2.2e-16	<2.2e-16
hsa03420	Nucleotide excision repair	45	19	0.78043	1.9686	<2.2e-16	<2.2e-16
hsa03430	Mismatch repair	23	14	0.88389	1.966	<2.2e-16	<2.2e-16
hsa04610	Complement and coagulation cascades	78	33	-0.69909	-2.2252	<2.2e-16	<2.2e-16
hsa00240	Pyrimidine metabolism	96	38	0.66663	1.8876	<2.2e-16	0.0005119
hsa03410	Base excision repair	33	18	0.79454	1.876	<2.2e-16	0.00071986
hsa00062	Fatty acid elongation	23	9	0.82092	1.8684	<2.2e-16	0.00082808
hsa00982	Drug metabolism	66	21	-0.64727	-2.0399	<2.2e-16	0.00092625
hsa05150	Staphylococcus aureus infection	52	23	-0.69239	-2.0777	<2.2e-16	0.001235
hsa05206	MicroRNAs in cancer	149	32	0.62047	1.826	<2.2e-16	0.0017063
hsa04640	Hematopoietic cell lineage	93	47	-0.62739	-2.1047	<2.2e-16	0.0018525
hsa00970	Aminoacyl-tRNA biosynthesis	43	23	0.72525	1.8104	<2.2e-16	0.0020207
hsa00350	Tyrosine metabolism	36	14	-0.70187	-1.9468	<2.2e-16	0.002223
hsa05166	Human T-cell leukemia virus 1 infection	253	43	0.58229	1.7844	<2.2e-16	0.0030714
hsa05321	Inflammatory bowel disease (IBD)	63	25	-0.61346	-1.9083	<2.2e-16	0.003705
hsa00670	One carbon pool by folate	18	9	0.82114	1.7685	<2.2e-16	0.004144
hsa03015	mRNA surveillance pathway	87	28	0.62573	1.7566	<2.2e-16	0.0043957
hsa02010	ABC transporters	44	25	-0.62027	-1.8448	<2.2e-16	0.006175
hsa04060	Cytokine-cytokine receptor interaction	276	111	-0.49068	-1.8778	<2.2e-16	0.0063514
hsa05204	Chemical carcinogenesis	75	25	-0.5711	-1.8535	<2.2e-16	0.0069469
hsa05323	Rheumatoid arthritis	85	32	-0.55323	-1.7949	<2.2e-16	0.0087573
hsa00980	Metabolism of xenobiotics by cytochrome P450	70	19	-0.56005	-1.8065	<2.2e-16	0.0092625
hsa04913	Ovarian steroidogenesis	48	19	-0.5795	-1.7816	<2.2e-16	0.010189
hsa04927	Cortisol synthesis and secretion	64	30	-0.55271	-1.7729	<2.2e-16	0.010545
hsa05330	Allograft rejection	35	21	-0.60933	-1.7608	<2.2e-16	0.011115
hsa05222	Small cell lung cancer	92	14	0.61194	1.6956	<2.2e-16	0.011944
hsa05310	Asthma	27	12	-0.6529	-1.7251	0.011173	0.014357
hsa00591	Linoleic acid metabolism	28	10	-0.64684	-1.7299	0.0049505	0.01482
hsa05144	Malaria	46	17	-0.57636	-1.6974	<2.2e-16	0.020377
hsa05332	Graft-versus-host disease	37	21	-0.6083	-1.6993	<2.2e-16	0.020704
hsa04659	Th17 cell differentiation	105	53	-0.49565	-1.6756	<2.2e-16	0.025009
hsa05320	Autoimmune thyroid disease	46	22	-0.56487	-1.6687	0.0061728	0.025093
hsa05143	African trypanosomiasis	34	20	-0.59052	-1.6581	0.0053191	0.027385
hsa04710	Circadian rhythm	30	12	-0.59049	-1.6059	0.014423	0.045794

FDR: false discovery rate

**Supplementary Table 2** The three-line table of SPC25’s GO\_BP (biological process) and KEGG pathway analysis based on the SPC25’s co-expressed genes via the LinkedOmics website. P < 0.05 or FDR ≤ 0.05 was considered statistically significant

Cell cycle regulatory genes	Pearson		Spearman	
	Cor	P	Cor	P
CDK2	0.74	<0.001	0.726	<0.001
WEE1	0.47	<0.001	0.457	<0.001
TP53	0.171	<0.001	0.251	<0.001
CDK6	0.269	<0.001	0.252	<0.001
CCNB1	0.832	<0.001	0.827	<0.001
CDK4	0.586	<0.001	0.613	<0.001
CDKN1A	-0.192	<0.001	-0.183	<0.001
ATM	0.286	<0.001	0.296	<0.001
CDK1	0.809	<0.001	0.794	<0.001
CDK7	0.287	<0.001	0.24	<0.001
MDM2	0.059	0.166	0.026	0.538
MYC	0.422	<0.001	0.421	<0.001
CDKN1B	0.55	<0.001	0.575	<0.001
E2F3	0.624	<0.001	0.611	<0.001
ORC4	0.562	<0.001	0.565	<0.001
ORC5	0.571	<0.001	0.55	<0.001
CDC45	0.796	<0.001	0.775	<0.001
CCNE2	0.53	<0.001	0.586	<0.001
RB1	0.307	<0.001	0.289	<0.001
PCNA	0.753	<0.001	0.747	<0.001
GADD45A	0.109	0.01	0.088	0.038
CCND1	0.058	0.17	0.102	0.017
MCM3	0.708	<0.001	0.715	<0.001
CCNE1	0.582	<0.001	0.574	<0.001
CCND2	-0.005	0.907	-0.058	0.171
CCND3	0.28	<0.001	0.278	<0.001
CDC25A	0.81	<0.001	0.79	<0.001
MCM4	0.761	<0.001	0.744	<0.001
MCM5	0.482	<0.001	0.483	<0.001
MCM7	0.644	<0.001	0.654	<0.001
CDKN2A	0.19	<0.001	0.157	<0.001
CDKN2B	0.171	<0.001	0.186	<0.001
CDKN2C	0.417	<0.001	0.426	<0.001
CDKN1C	0.04	0.353	0.044	0.303
MCM2	0.666	<0.001	0.666	<0.001
CCNH	0.412	<0.001	0.382	<0.001
CDKN2D	0.353	<0.001	0.344	<0.001
CCNA1	-0.011	0.804	-0.026	0.534
E2F1	0.721	<0.001	0.722	<0.001
E2F2	0.763	<0.001	0.741	<0.001
MCM6	0.831	<0.001	0.814	<0.001
ORC1	0.782	<0.001	0.77	<0.001
ORC2	0.642	<0.001	0.615	<0.001
TFDP1	0.577	<0.001	0.569	<0.001
TFDP2	0.466	<0.001	0.469	<0.001
ORC3	0.603	<0.001	0.617	<0.001
ORC6	0.734	<0.001	0.708	<0.001
SMAD2	0.445	<0.001	0.457	<0.001
SMAD3	0.194	<0.001	0.198	<0.001



CDC25B	0.626	<0.001	0.633	<0.001
CCNA2	0.857	<0.001	0.845	<0.001
CHEK2	0.766	<0.001	0.755	<0.001
TGFB1	0.022	0.612	0.014	0.751
CHEK1	0.838	<0.001	0.83	<0.001
GSK3B	0.518	<0.001	0.514	<0.001
ATR	0.279	<0.001	0.29	<0.001
CDC7	0.806	<0.001	0.796	<0.001
EP300	0.217	<0.001	0.236	<0.001
HDAC2	0.685	<0.001	0.674	<0.001
CUL1	0.542	<0.001	0.512	<0.001
CDC25C	0.839	<0.001	0.817	<0.001
ABL1	0.196	<0.001	0.209	<0.001
HDAC1	0.535	<0.001	0.543	<0.001
PLK1	0.699	<0.001	0.685	<0.001
BUB1	0.857	<0.001	0.848	<0.001
TTK	0.841	<0.001	0.822	<0.001
YWHAB	0.668	<0.001	0.683	<0.001
MAD1L1	0.097	0.022	0.124	0.004
PKMYT1	0.641	<0.001	0.623	<0.001
PRKDC	0.567	<0.001	0.57	<0.001
YWHAG	0.56	<0.001	0.557	<0.001
RBX1	0.363	<0.001	0.336	<0.001
BUB3	0.61	<0.001	0.576	<0.001
RAD21	0.7	<0.001	0.719	<0.001
CDC14B	0.307	<0.001	0.303	<0.001
GADD45B	-0.21	<0.001	-0.193	<0.001
GADD45G	-0.352	<0.001	-0.37	<0.001
CCNB2	0.818	<0.001	0.804	<0.001
PTTG1	0.77	<0.001	0.746	<0.001
WEE2	0.041	0.337	0.059	0.167
TGFB3	0.125	0.003	0.122	0.004
YWHAQ	0.614	<0.001	0.613	<0.001
RBL1	0.717	<0.001	0.719	<0.001
CDC27	0.586	<0.001	0.584	<0.001
SFN	-0.112	0.009	-0.087	0.04
TGFB2	0.147	<0.001	0.121	0.004
YWHAE	0.395	<0.001	0.39	<0.001
SKP1	0.537	<0.001	0.528	<0.001
YWHAZ	0.618	<0.001	0.607	<0.001
YWHAH	0.37	<0.001	0.346	<0.001
RBL2	0.218	<0.001	0.225	<0.001
ZBTB17	0.103	0.015	0.128	0.003
CDC16	0.23	<0.001	0.206	<0.001
CDC20	0.706	<0.001	0.7	<0.001
SMAD4	0.384	<0.001	0.384	<0.001
SKP2	0.703	<0.001	0.68	<0.001
ESPL1	0.754	<0.001	0.733	<0.001
E2F4	0.384	<0.001	0.389	<0.001
E2F5	0.492	<0.001	0.507	<0.001
STAG2	0.499	<0.001	0.49	<0.001

SMC1B	0.325	<0.001	0.331	<0.001
STAG1	0.49	<0.001	0.504	<0.001
CCNB3	0.216	<0.001	0.172	<0.001
CDC6	0.769	<0.001	0.731	<0.001
ANAPC1	0.614	<0.001	0.647	<0.001
ANAPC11	0.076	0.073	0.106	<b>0.013</b>
DBF4	0.756	<0.001	0.745	<0.001
ANAPC2	0.014	0.742	0.01	0.806
ANAPC4	-0.264	<0.001	-0.254	<0.001
FZR1	0.135	<b>0.001</b>	0.146	<0.001
ANAPC5	0.351	<0.001	0.346	<0.001
ANAPC7	0.364	<0.001	0.329	<0.001
CDC14A	0.151	<0.001	0.149	<0.001
CDC23	0.633	<0.001	0.624	<0.001
SMC3	0.63	<0.001	0.636	<0.001
PTTG2	-0.068	0.111	-0.063	0.139
ANAPC13	0.393	<0.001	0.352	<0.001
CREB3	0.24	<0.001	0.244	<0.001
RPA2	0.622	<0.001	0.613	<0.001
RPA1	0.541	<0.001	0.525	<0.001
RPA3	0.642	<0.001	0.637	<0.001
PRIM1	0.781	<0.001	0.762	<0.001
PRIM2	0.718	<0.001	0.727	<0.001
MNAT1	0.503	<0.001	0.481	<0.001
POLE2	0.735	<0.001	0.714	<0.001
MYT1	0.247	<0.001	0.242	<0.001
POLE	0.615	<0.001	0.603	<0.001
POLA2	0.607	<0.001	0.614	<0.001
CREB3L3	-0.034	0.429	-0.075	0.077
CREB3L4	-0.187	<0.001	-0.246	<0.001
CREB3L1	-0.398	<0.001	-0.405	<0.001
ATF6B	0.34	<0.001	0.31	<0.001

**Supplementary Table 3** The correlation between SPC25 and the genes in the cell cycle pathway network in UCEC analyzed from the Xiantao Academic web. Pearson or Spearman  $p < 0.05$  was considered statistically significant



Since Supplementary Table 4 was too long to be displayed in this Word file, we considered uploading it in Excel format.

**Supplementary Table 4** The association between SPC25 gene and immune cell markers in UCEC obtained from Xiantao academic web. Pearson p value or Spearman p value less than 0.05 was considered statistically significant