

SUPPLEMENTAL DATA

Glioblastoma recruits and activates CAF-like astrocytes via the AKT/m-TOR-SERPINH1/COL5A1 axis

Full article is available at the following link : <https://www.bjbms.org/ojs/index.php/bjbms/article/view/11898>.

Table S1 : Sequences of primers used in this research

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Targets	Forward5'-3'	Reverse5'-3'
SERPINH1	TGCTAGTCAACGCCATGTTCT	ATAGGACCGAGTCACCATGAA
COL5A1	TACCCTGCGTCTGCATTTCC	GCTCGTTGTAGATGGAGACCA
β -actin	AAGATCATTGCTCCTCCTG	CATACTCCTGCTTGCTGAT

Table S2: TCGA CAFscoring

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ID	CAF_EPIC	CAF_MCPcounter	CAF_xCell	StromalScore
TCGA-76-4927	0.015705825	7.050923348	0.0332	430.2030344
TCGA-28-5215	0.017913877	7.408992369	0.0476	571.6330431
TCGA-06-2559	0.011012553	5.702827479	0	-221.6008929
TCGA-06-0644	0.020413563	8.142818246	0.0324	882.6147167
TCGA-06-2567	0.012068218	5.166675337	0.026	131.2257621
TCGA-06-0158	0.010241083	5.99571934	0.0082	-117.0664065
TCGA-06-5416	0.012171164	5.132755742	0	-932.6127001
TCGA-06-5408	0.011813797	5.561597263	0	-328.1519004
TCGA-12-5295	0.010290633	4.762030745	0	-138.9690995
TCGA-06-2569	0.019489447	7.827380864	0.2973	61.09389614
TCGA-06-0238	0.010728141	4.426566115	0	9.814916407
TCGA-28-5213	0.016803298	6.981835344	0.1073	887.6673001
TCGA-28-2509	0.012331877	5.232664658	0	-471.8916864
TCGA-26-5136	0.011947815	5.28472943	0.0501	242.9595615
TCGA-06-5414	0.012373182	5.954626321	0	-95.31717172
TCGA-06-0138	0.012080474	5.454856373	0.065	449.30644
TCGA-28-1747	0.006352844	4.059813309	0	-287.0257643
TCGA-06-0156	0.01317163	5.693000613	0.0294	100.9287228
TCGA-32-5222	0.010565581	5.453650633	0	32.89452016
TCGA-28-5208	0.012248882	6.092050075	0	108.6812858
TCGA-26-5133	0.01246022	4.940317875	0.0301	-622.4623859
TCGA-06-2563	0.013229919	5.532519982	0	-219.180252
TCGA-19-0957	0.010910637	5.291456239	0.014	38.1494751
TCGA-06-2557	0.010455448	4.651254097	0.0092	213.9101604
TCGA-76-4932	0.009935776	5.0799366	0.01	-580.4944087
TCGA-06-5858	0.013171619	5.841430382	0	115.6424163
TCGA-28-2513	0.01551472	6.881745898	0.0734	710.977697
TCGA-19-1787	0.012197119	4.997137613	0.0128	-118.3875823
TCGA-16-1045	0.014758366	6.285076424	0.0156	797.3603109
TCGA-27-2519	0.011251084	4.694352296	0	263.4574345
TCGA-32-2615	0.015215795	6.852285378	0.0417	183.5364536
TCGA-41-4097	0.016796561	7.443887899	0.0219	575.4713413
TCGA-19-1389	0.020751834	7.535115223	0.1388	1071.295952
TCGA-28-5218	0.02401071	8.846558995	0.187	1283.33327
TCGA-27-1837	0.011188928	5.197821136	0	-231.3099538
TCGA-06-5413	0.016801755	7.172563641	0.0703	559.7060707
TCGA-76-4928	0.014018538	5.8699068	0	56.29200384
TCGA-27-1835	0.010664199	4.259119561	0	-720.9868527
TCGA-15-1444	0.009958763	4.499295026	0	28.07277912
TCGA-06-0747	0.008205635	4.856815983	0	-919.5496836
TCGA-28-1753	0.01905662	7.50514772	0.0528	708.3457935
TCGA-06-0219	0.009406109	4.429254284	0.0104	-129.2639798
TCGA-06-0749	0.006884421	3.780749993	0	-194.9871756
TCGA-06-0750	0.017548459	6.673556865	0.1077	467.0594563
TCGA-19-5960	0.007871325	3.841714979	0	-1029.721816
TCGA-06-0125	0.012990598	6.791387307	0.0268	-55.6440006
TCGA-06-5415	0.01227391	5.604122454	0.0295	-430.3427275
TCGA-06-0745	0.013179615	5.549524591	0.0654	65.40008009
TCGA-27-2528	0.017568067	6.908549201	0.0849	-50.52318393
TCGA-06-2558	0.012086218	5.551952566	4.00E-04	101.1790217
TCGA-06-2561	0.01100919	4.732245659	0.0031	-47.05316537
TCGA-27-1830	0.014209199	5.946581346	0.0314	398.18738

TCGA-41-5651	0.00936886	4.721018441	0	-757.4775551
TCGA-06-0211	0.014417854	6.509243944	0.0115	132.2757869
TCGA-16-0846	0.007173135	3.840989058	0	-59.69046413
TCGA-28-5204	0.01179288	5.461422054	0	-340.9631249
TCGA-32-2616	0.010781541	4.516399707	0	-340.1000794
TCGA-27-2523	0.011011456	5.232981616	0	-753.3540593
TCGA-28-5207	0.011241155	5.287973606	0	222.612346
TCGA-14-0787	0.012225159	5.581673359	0	-422.8803553
TCGA-12-3653	0.009015456	4.405741541	0	-506.0987099
TCGA-02-2483	0.01275223	5.523225171	0.0276	-166.7982393
TCGA-06-0171	0.018283043	7.257260584	0.0826	1397.219098
TCGA-06-0184	0.013325536	5.249764449	0.0022	402.2581127
TCGA-06-0178	0.010705493	4.119848408	0.0789	-122.7511971
TCGA-41-3915	0.017108199	7.448965489	0.0838	552.7556918
TCGA-19-4065	0.019329832	7.473981143	0	628.3692153
TCGA-06-1804	0.009462302	4.296280163	0.0183	-282.4522744
TCGA-12-0619	0.014875857	5.840230931	0.0395	132.8033775
TCGA-02-2485	0.009510468	4.47669636	0	-470.4040093
TCGA-02-0047	0.012718065	5.765277268	0.0247	298.2018146
TCGA-14-0781	0.014653282	6.521319418	0.0648	579.6047079
TCGA-27-2521	0.011052924	5.208244233	0.0584	-695.0635858
TCGA-06-0132	0.015641489	5.835422331	0.0363	694.4248623
TCGA-32-1970	0.008676026	4.750822313	0	-420.732632
TCGA-06-0882	0.011460831	5.316204981	0	218.5547815
TCGA-14-1402	0.011842269	5.491787855	0.0521	-119.1534447
TCGA-32-1982	0.011743937	5.748989011	0.0329	451.4924318
TCGA-27-2524	0.013187123	6.073983515	0.0192	123.4357693
TCGA-32-1980	0.013379532	5.687771251	0	517.2926323
TCGA-06-0646	0.011551364	5.642730353	0	181.1837178
TCGA-27-1831	0.013741375	5.176030138	0.0782	358.1561112
TCGA-32-2632	0.010701205	4.414839658	0.0526	292.2309794
TCGA-06-0210	0.013090865	5.690403951	0.0561	359.0974251
TCGA-06-0139	0.021171457	7.289257508	0.079	1332.37779
TCGA-06-5411	0.011723664	5.488516824	0	-79.86451221
TCGA-12-3652	0.007907447	4.872497613	0.0113	-853.7777887
TCGA-28-2514	0.010155003	5.459748343	0	-497.9098161
TCGA-32-4213	0.016516195	6.612315205	0.051	689.7935471
TCGA-19-2619	0.012692524	5.657356962	0.0439	-357.824521
TCGA-12-1597	0.009153535	4.619729427	0	-414.3794882
TCGA-14-0790	0.007436982	3.8457736	0.0013	-687.9742733
TCGA-14-1034	0.011696563	5.129067576	0	-480.3152441
TCGA-06-0129	0.006701377	3.894136792	0	-584.8882079
TCGA-76-4931	0.0098075	5.271361318	0	-818.6943412
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TCGA-06-5859	0.007682964	3.875887231	0	-116.2020089

TCGA-06-0190	0.021667764	8.51328881	0.1603	1303.66645
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TCGA-27-1834	0.009680416	4.75016851	0.0084	20.72650249
TCGA-28-5209	0.012940364	6.107935307	0.0457	-391.9459048
TCGA-06-0168	0.014857385	5.792587294	1.00E-04	479.3855511
TCGA-19-2624	0.010174343	4.884402118	0	-1202.092386
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TCGA-15-0742	0.011199933	5.342610013	0	-814.7508602
TCGA-28-5216	0.01511174	6.515451795	0.0818	61.09779726
TCGA-12-5299	0.013728518	6.298218207	0.0016	-115.269129
TCGA-19-2629	0.009699753	4.192323964	0.0066	-111.5804938
TCGA-14-1825	0.010529671	4.837664705	0	-678.3535246
TCGA-06-0130	0.022274198	8.091603035	0.1054	1365.399112
TCGA-76-4929	0.009484678	5.413099065	0	-265.2774772
TCGA-06-5412	0.014685594	6.121639171	0.0161	876.119198
TCGA-76-4926	0.008352641	5.02297688	0	-544.0489446
TCGA-12-0618	0.00850874	4.46109117	0	-838.3961043
TCGA-14-0789	0.013955715	6.157142766	0.0275	341.2603315
TCGA-06-5417	0.009401941	4.309627615	0	-712.3497975
TCGA-14-0817	0.011856287	5.171083693	0.0017	351.649132
TCGA-76-4925	0.012299577	5.172585762	0	-703.0889524
TCGA-06-0187	0.012218342	5.685206544	0.0266	-77.64868779
TCGA-26-5135	0.014280781	6.441352174	0.065	115.3410223
TCGA-06-2564	0.011159161	5.966699035	0.0078	-39.15002382
TCGA-06-5418	0.01231	5.503101116	0.0263	-108.9430221
TCGA-06-0649	0.014937944	5.854759416	0.0485	526.274285
TCGA-28-2510	0.014797345	6.210675595	0	-32.86367595
TCGA-14-0736	0.012449138	5.516364559	0.0144	554.0330553
TCGA-06-0743	0.012171389	4.826805786	0.06	-234.2894026
TCGA-06-2570	0.010912856	4.970940181	0.0079	-122.3547341
TCGA-06-0157	0.011708602	5.041600232	0.0124	53.80740398
TCGA-12-0821	0.010797855	4.988090124	0.0217	-337.4529035
TCGA-06-0174	0.011231393	5.3013992	0	-524.3738688
TCGA-28-5220	0.008073598	3.757121894	0.0399	-301.620181
TCGA-27-2526	0.008205208	3.825370492	0	-460.3943812
TCGA-06-0221	0.014656466	5.699302156	0	-679.4618384
TCGA-06-0878	0.013615714	6.145802655	0.0179	194.1014638
TCGA-12-3650	0.009915145	4.8551384	0	-529.0398973
TCGA-08-0386	0.011842854	5.407066105	0	-437.2910325
TCGA-32-2634	0.011035096	5.487527249	0	-497.8753219
TCGA-02-0055	0.022932533	8.412383124	0.2225	1341.53274
TCGA-32-2638	0.014981043	6.628590866	0.0386	391.9581699
TCGA-19-1390	0.009883294	4.673057142	0	-1051.443913
TCGA-28-2499	0.010178989	5.094421093	0	-355.5811754
TCGA-14-1823	0.01141377	4.40782057	0.0052	190.0436903
TCGA-12-0616	0.01096992	4.721962598	0	-335.6702185
TCGA-06-0152	0.01413099	6.340918522	0.0059	174.9475955
TCGA-02-2486	0.011760839	6.386550668	0.0241	342.56225
TCGA-19-2620	0.011016846	5.855892508	0.042	-210.9358114
TCGA-14-1829	0.012681185	5.101727876	0.101	394.0995012
TCGA-26-5134	0.011231431	4.7767009	0.0242	-460.0685506
TCGA-41-2571	0.011145091	5.072217797	0	-709.8186263
TCGA-41-2572	0.010742239	5.302410116	0	-152.4743135
TCGA-26-5139	0.013237402	6.33850395	0.047	-55.59932107

TCGA-06-0141	0.017656898	6.076283292	0.0753	637.0657116
TCGA-06-5856	0.012637587	5.743724156	0	61.62093709

Table S3: GEO CAFscoring

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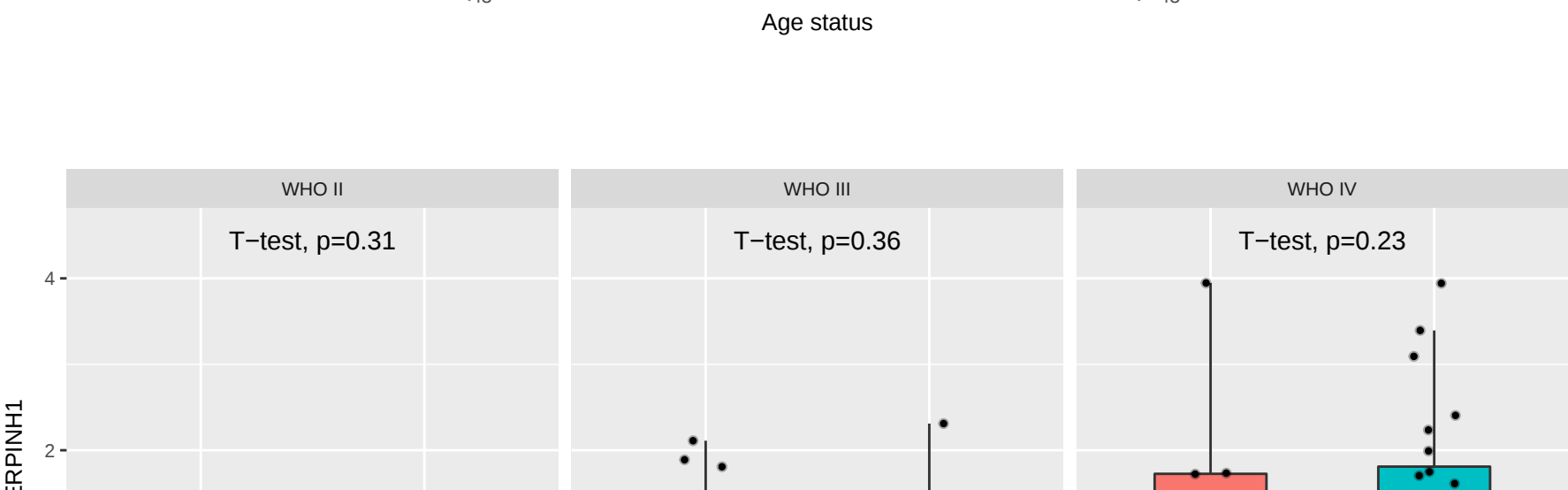
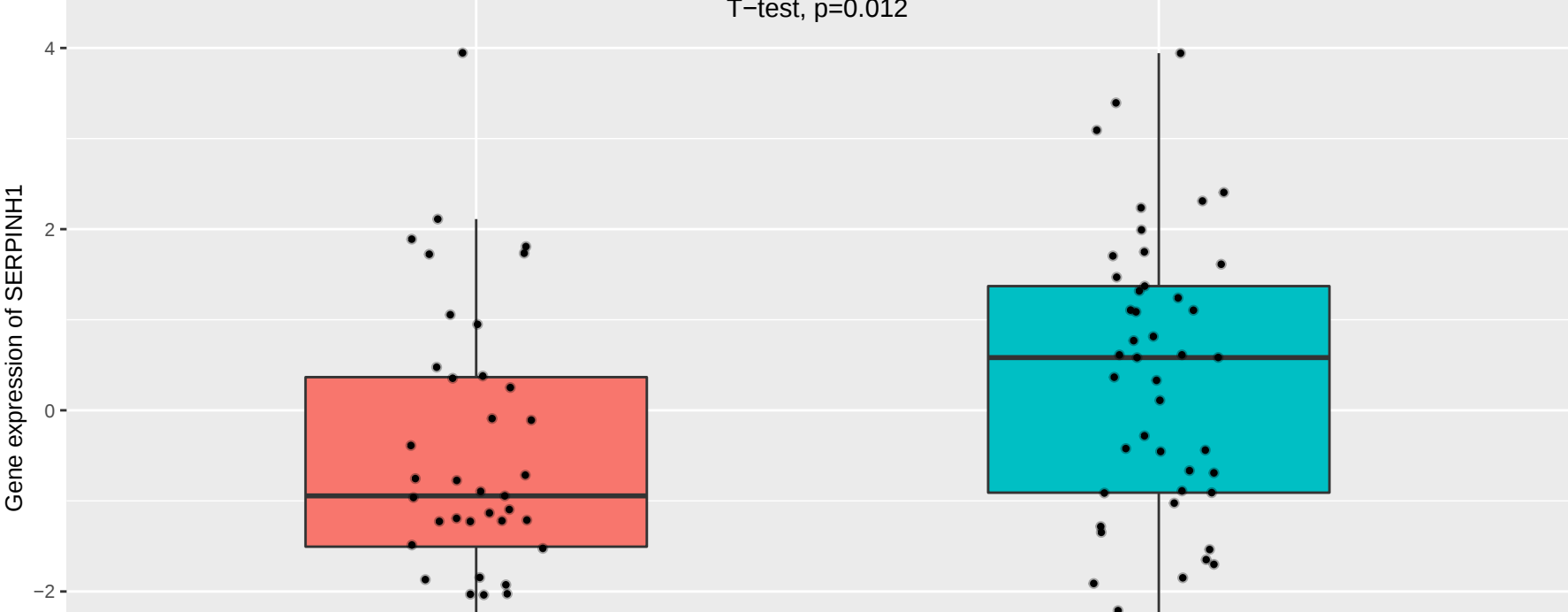
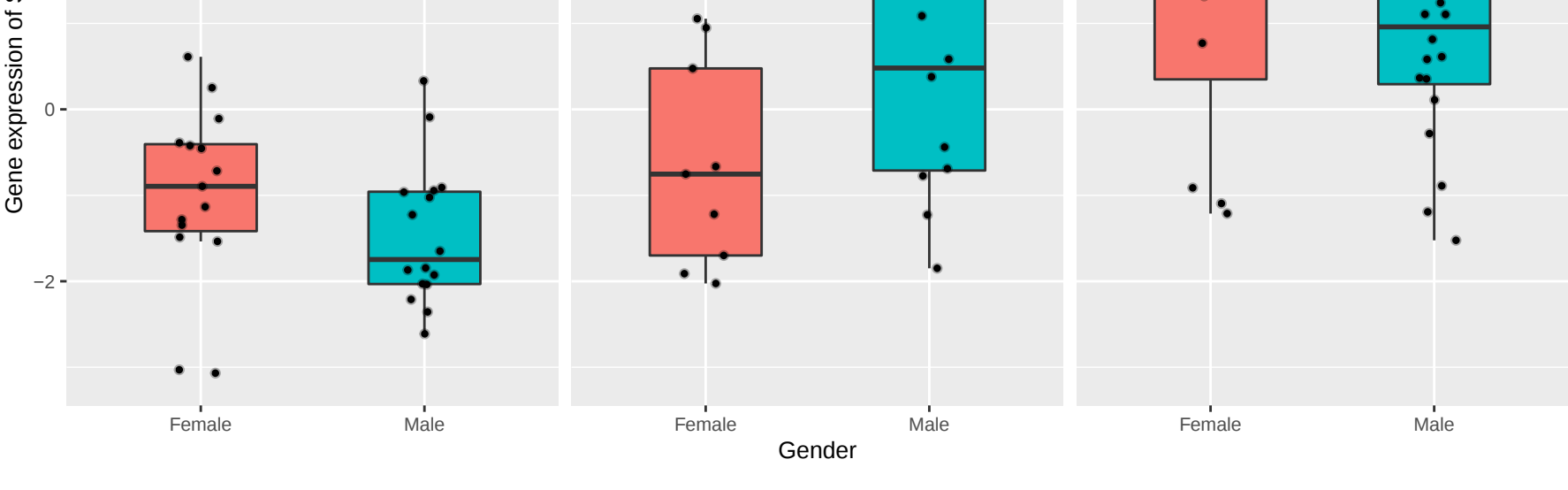
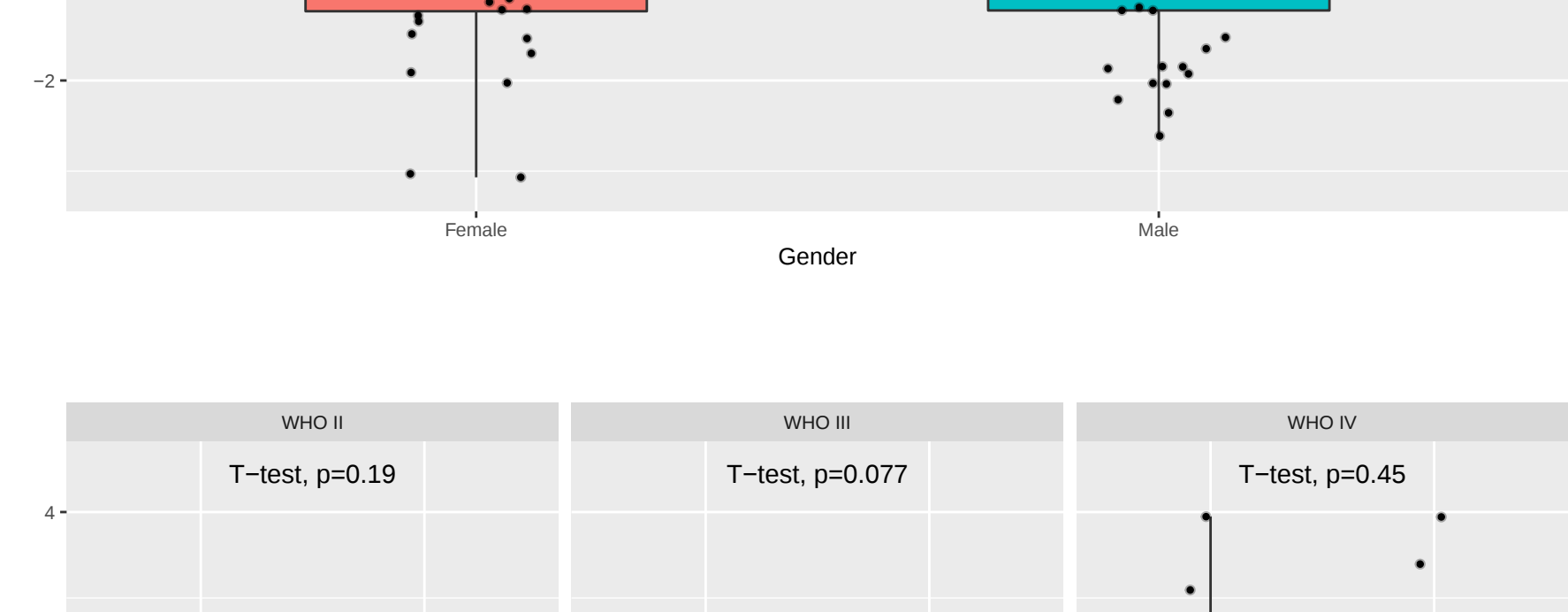
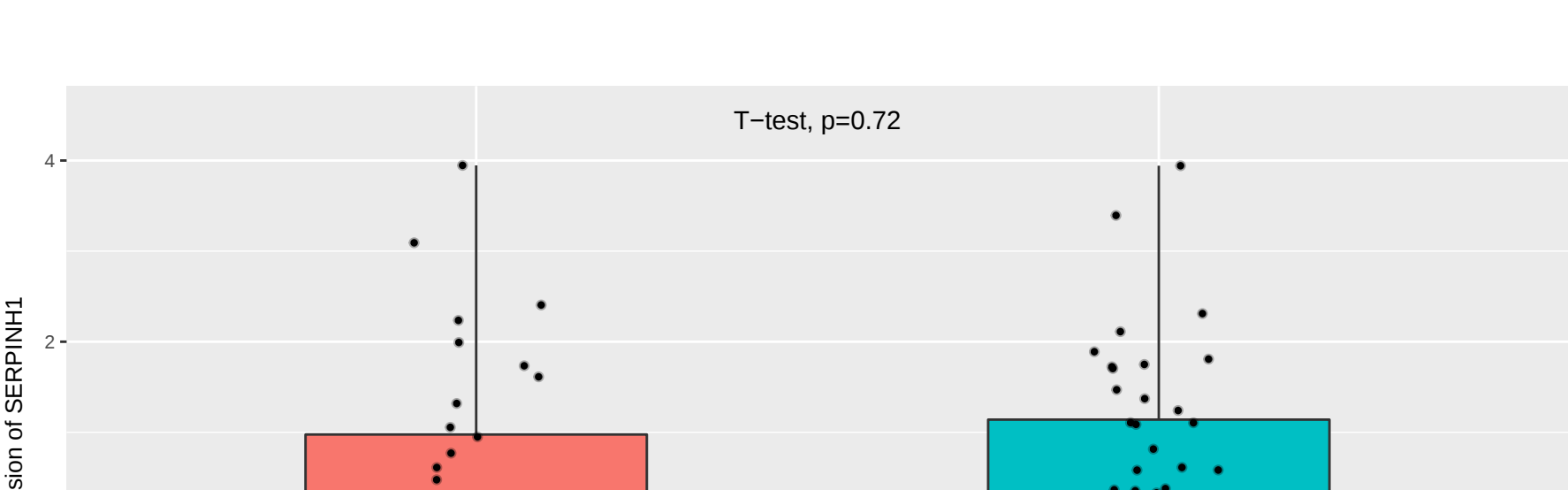
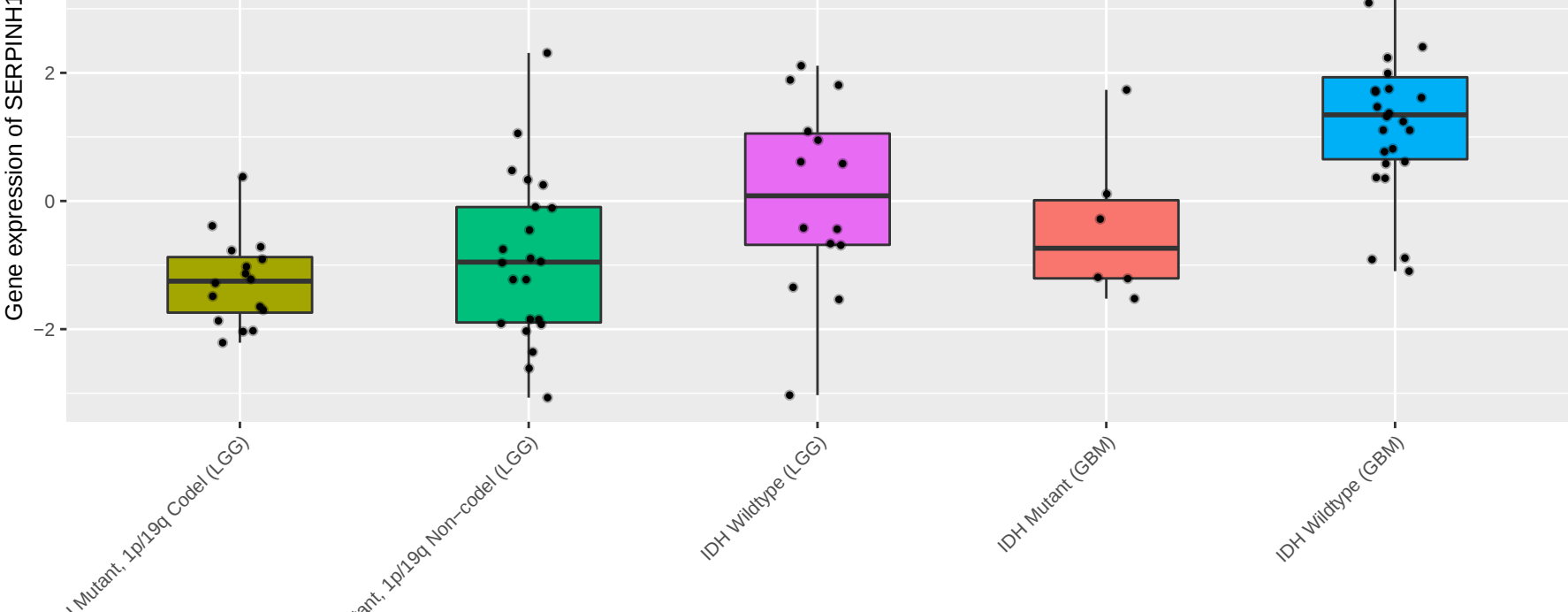
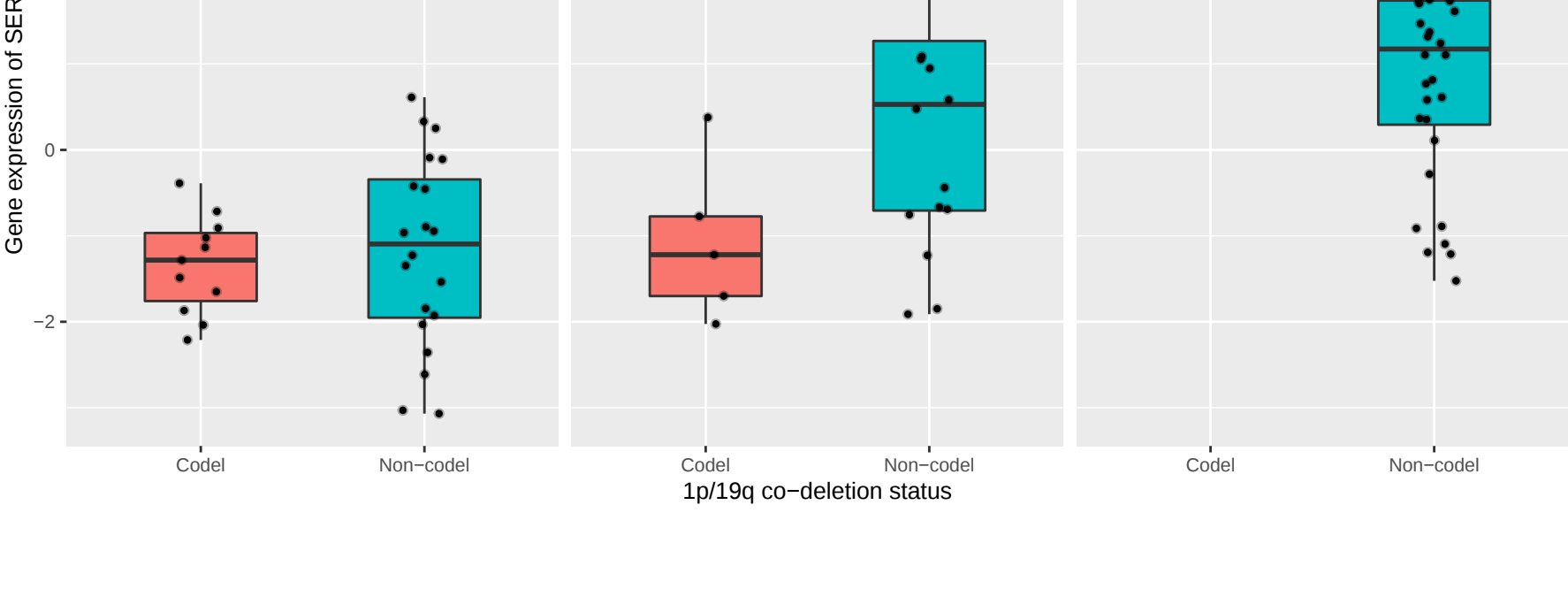
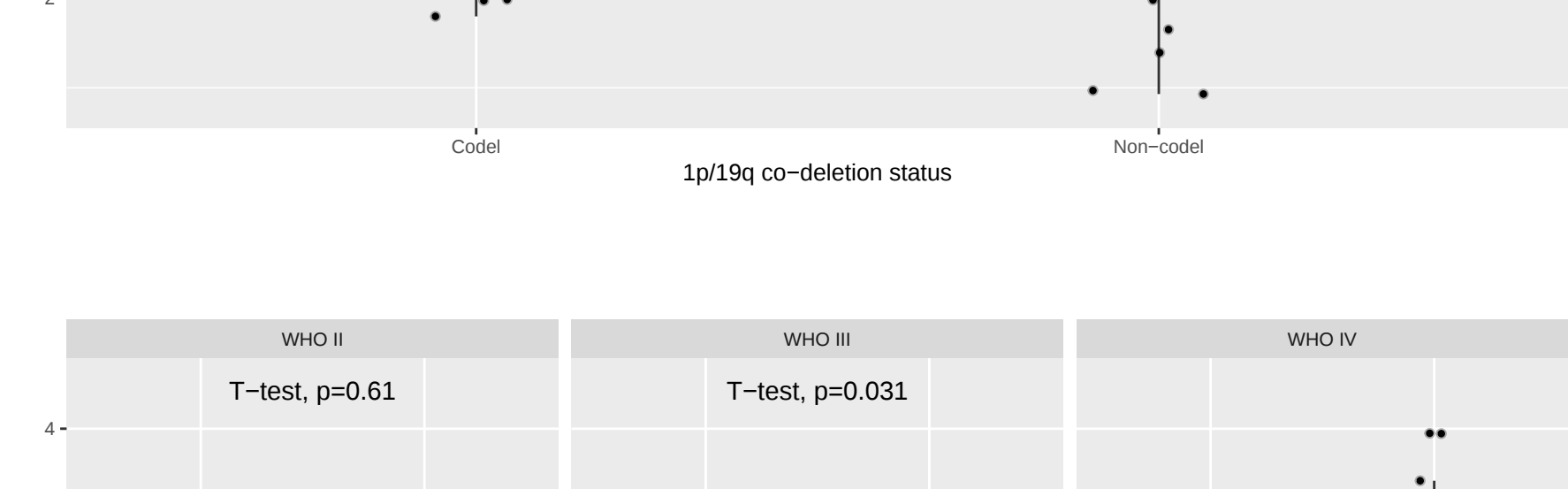
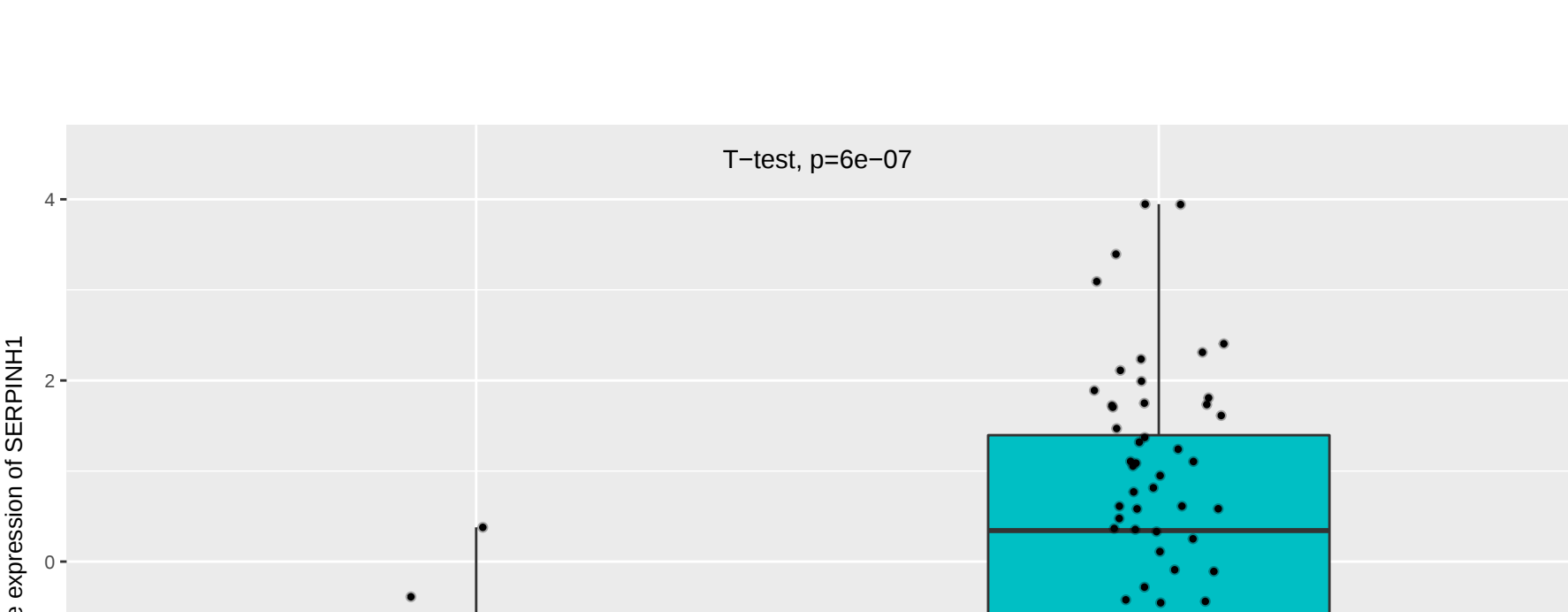
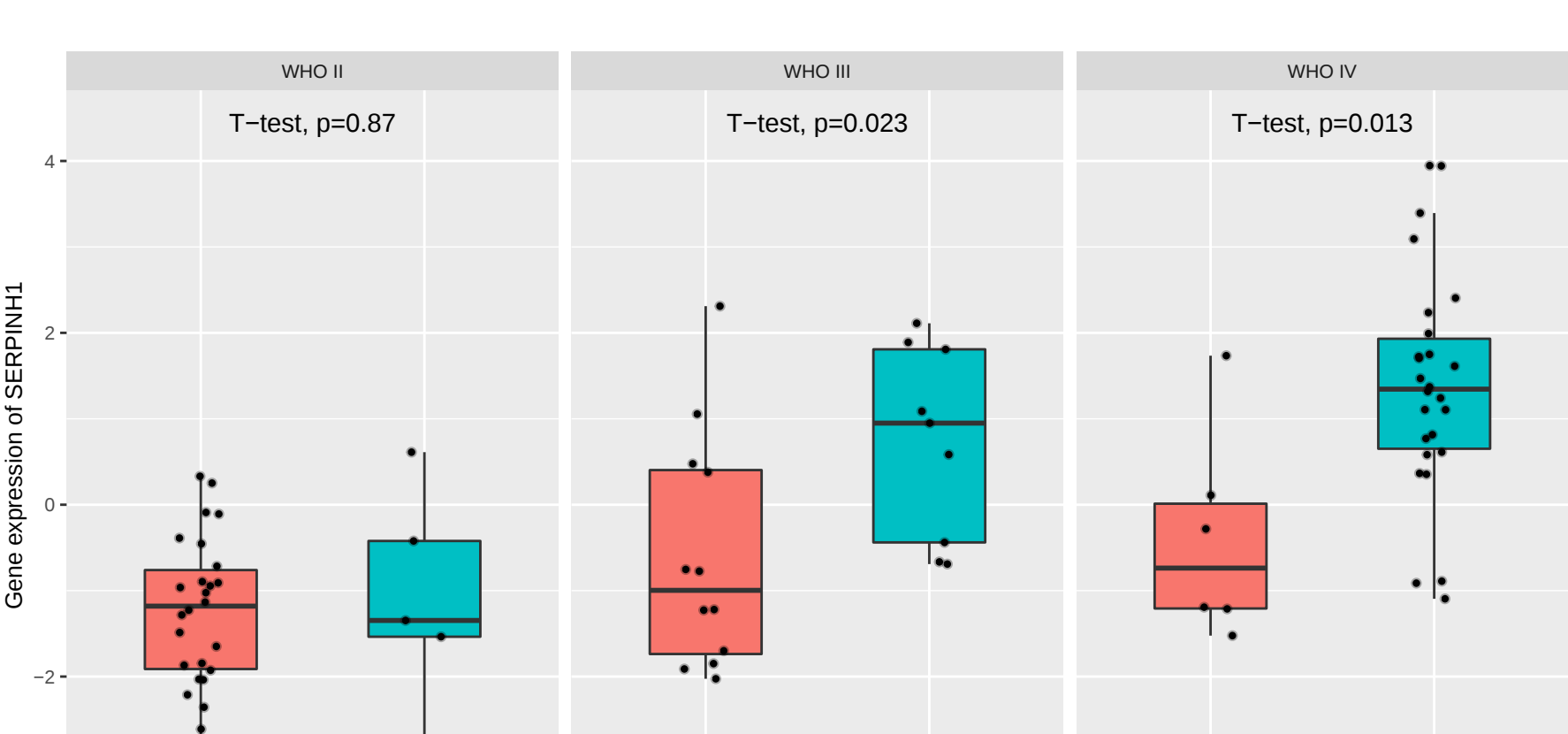
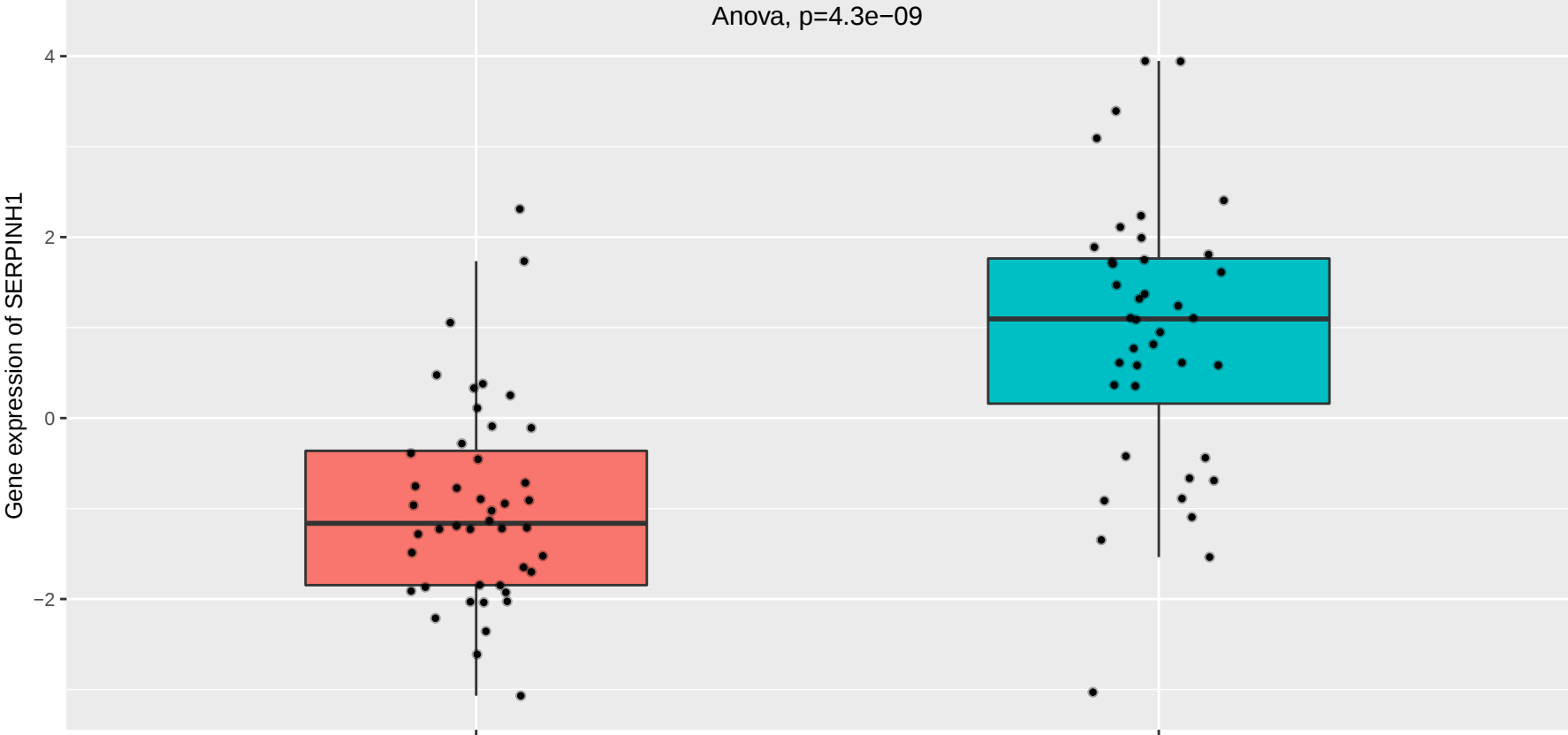
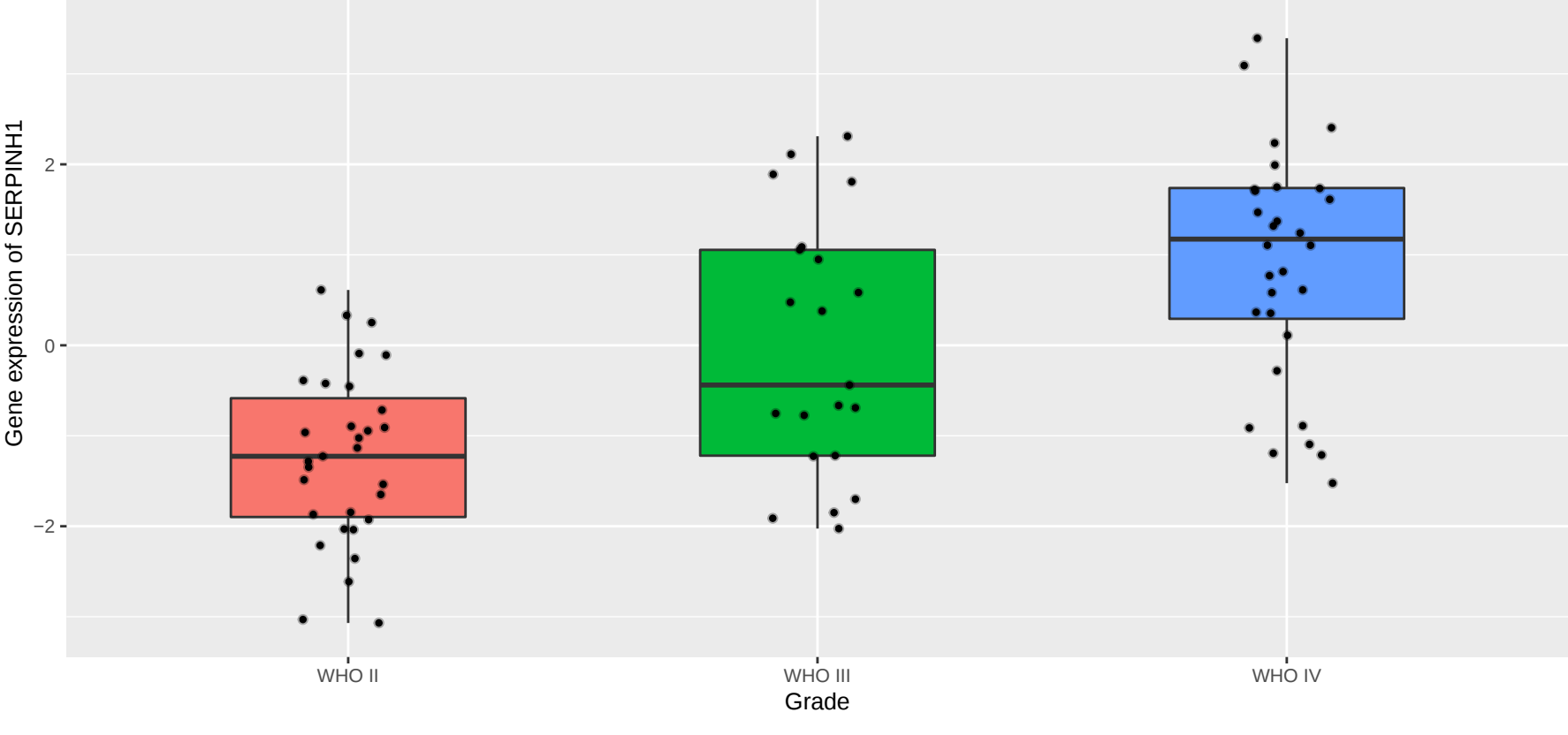
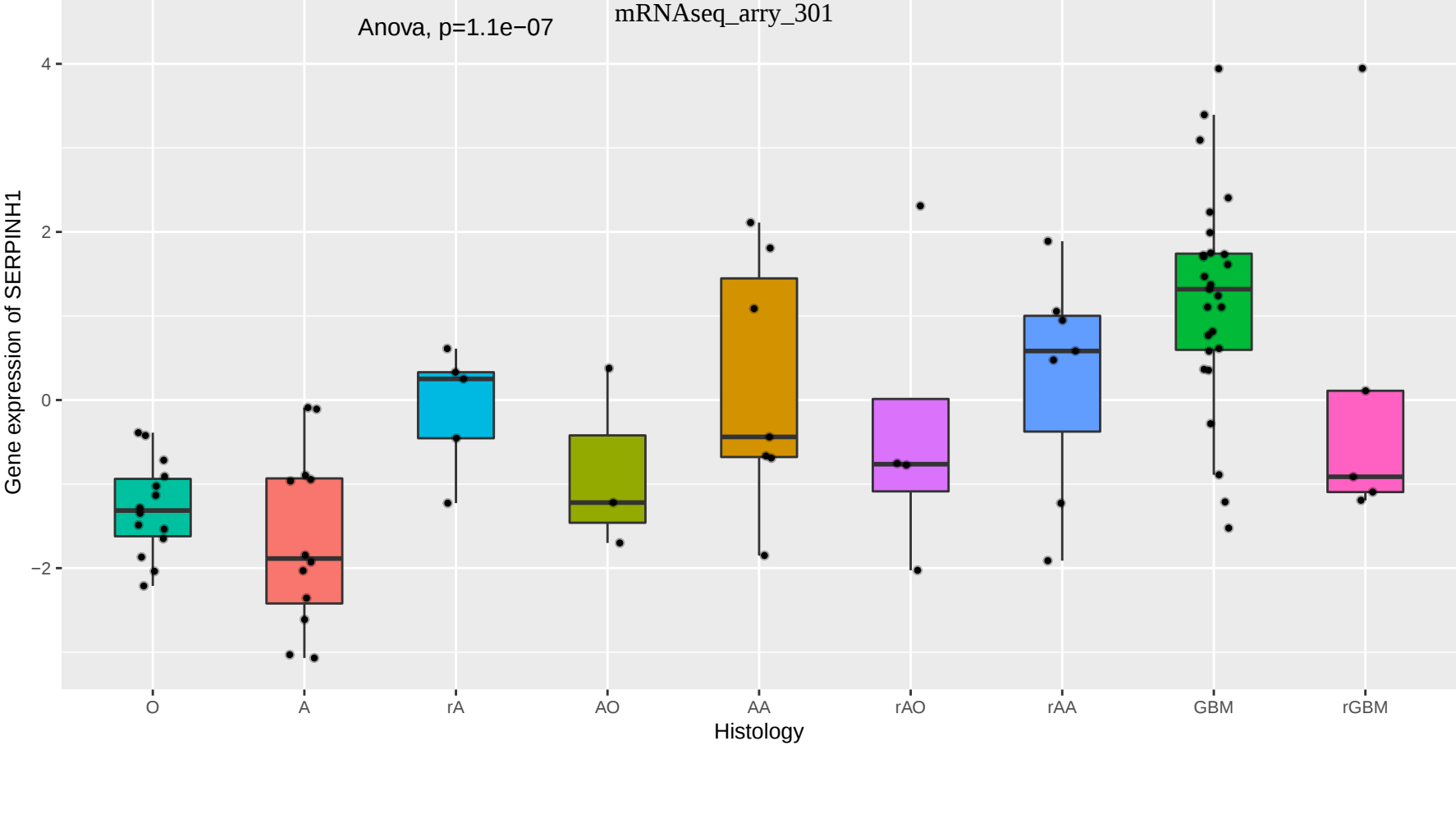
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GSM1061661	0.005338579	4.482801097	0	-471.1746522
GSM1061662	0.006764345	5.449493233	0	193.3251905
GSM1061663	0.005300006	4.333283722	0	-511.6276256
GSM1061664	0.006795163	5.597117787	0	-234.3622509
GSM1061665	0.006174663	5.432845794	0	-336.7924362
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GSM1061667	0.005001302	4.532348898	0	-793.5037043
GSM1061668	0.005217978	4.570022741	0	-617.5192502
GSM1061669	0.006793528	4.553219382	0	-569.3595644
GSM1061670	0.005121915	4.270468683	0	-430.6496893
GSM1061671	0.007274186	5.134582362	0	145.7211153
GSM1061672	0.007198133	6.142524659	0.0258	-303.3981658
GSM1061673	0.005715992	4.652438624	0	-647.8387956
GSM1061674	0.008733069	6.650852006	0	507.9060462
GSM1061675	0.006392541	4.821434566	0	-730.2427507
GSM1061676	0.008706532	6.584561278	0	398.9309317
GSM1061677	0.004286728	4.569275795	0	-537.5083501
GSM1061678	0.006733144	5.407312495	0	417.1056206
GSM1061679	0.00654421	5.328214777	0	-387.973911
GSM1061680	0.007777194	5.65733087	0	172.3569502
GSM1061681	0.007099213	5.692631086	0	-141.0135855
GSM1061682	0.00698947	5.841620703	0	233.066526
GSM1061683	0.009183617	6.850912245	0.0069	385.4698248
GSM1061684	0.007559099	5.829155616	0	125.6752228
GSM1061685	0.005664802	4.181954449	0	-578.165831
GSM1061686	0.004239422	4.375303244	0	-464.431252
GSM1061687	0.005033748	4.547511899	0	-468.984921
GSM1061688	0.007914717	6.045539089	0.0241	400.3004969
GSM1061689	0.009219523	5.942652764	0.1103	-340.3705328
GSM1061690	0.006157571	4.92638314	0	88.66565288
GSM1061691	0.008476058	6.581785946	0	413.3501615
GSM1061692	0.00688979	4.942205415	0.0477	-499.7796479
GSM1061693	0.004173865	3.80229291	0	-497.9554386
GSM1061694	0.007730447	5.650101389	0	-198.5617481
GSM1061695	0.006558065	4.746062086	0	-549.7211407
GSM1061696	0.007259666	5.56383691	0	-12.59365646
GSM1061697	0.005291621	4.254797953	0	-405.2563661
GSM1061698	0.006618112	4.699984681	0	-152.4608469
GSM1061699	0.006927504	5.739217558	0	284.5660677
GSM1061700	0.009270265	6.00297468	0.0842	-190.4295089
GSM1061701	0.007234124	4.850469813	0	-892.1323269
GSM1061702	0.006939654	5.90326515	0.0219	292.0389568
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GSM1061704	0.005938164	3.932754156	0.0174	-571.0067181
GSM1061705	0.006893694	5.497670308	0	-145.594704
GSM1061706	0.005419472	4.481786431	0	-445.3679158
GSM1061707	0.004715967	4.714255761	0	-631.8335896
GSM1061708	0.008975985	6.937207267	0	851.6887256
GSM1061709	0.011339097	7.803523566	0	1706.436838
GSM1061710	0.008850576	6.893869958	0.00E+00	828.4811354
TCGA-06-2561	0.01100919	4.732245659	0.0031	-47.05316537
TCGA-27-1830	0.014209199	5.946581346	0.0314	398.18738

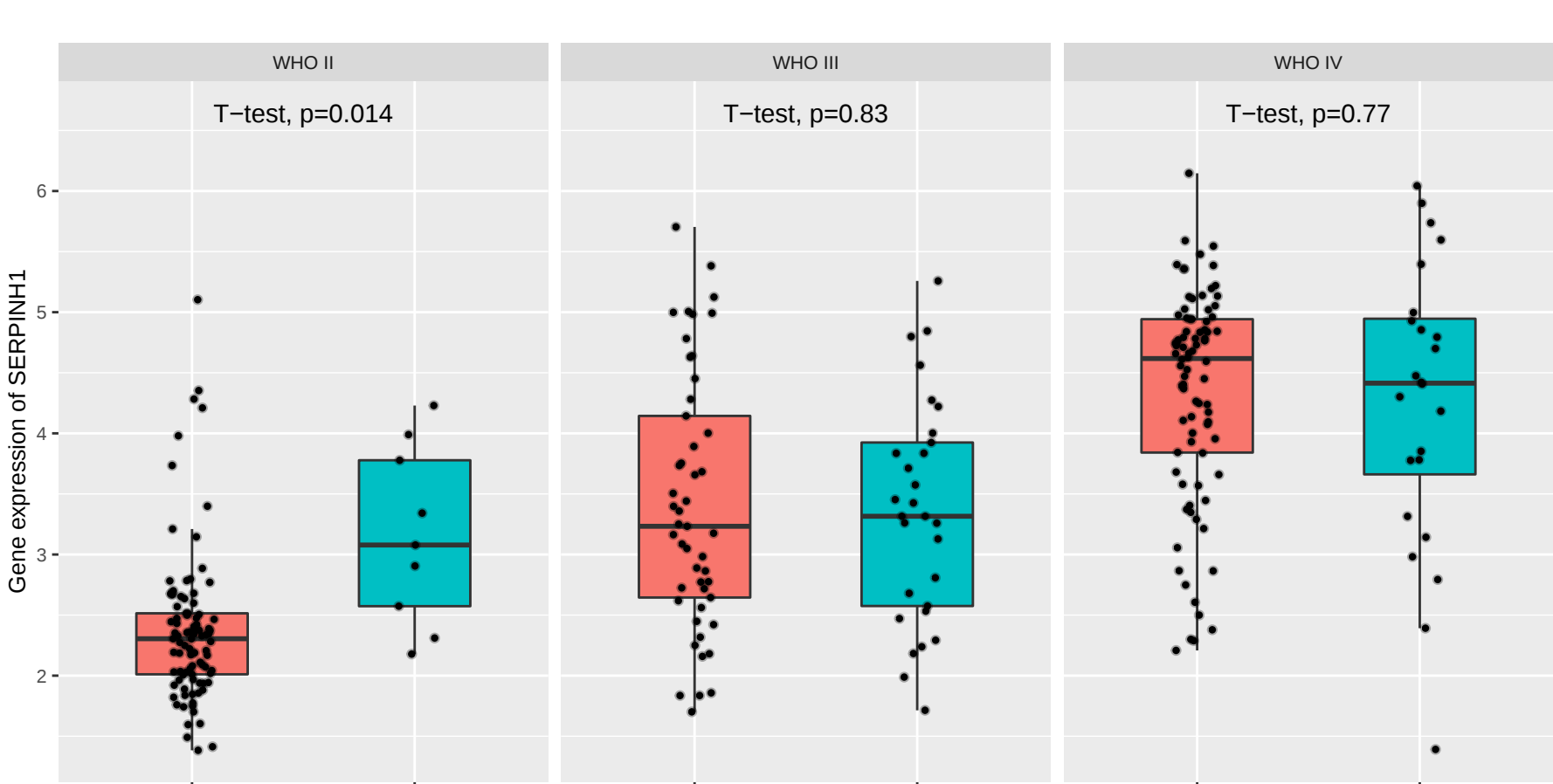
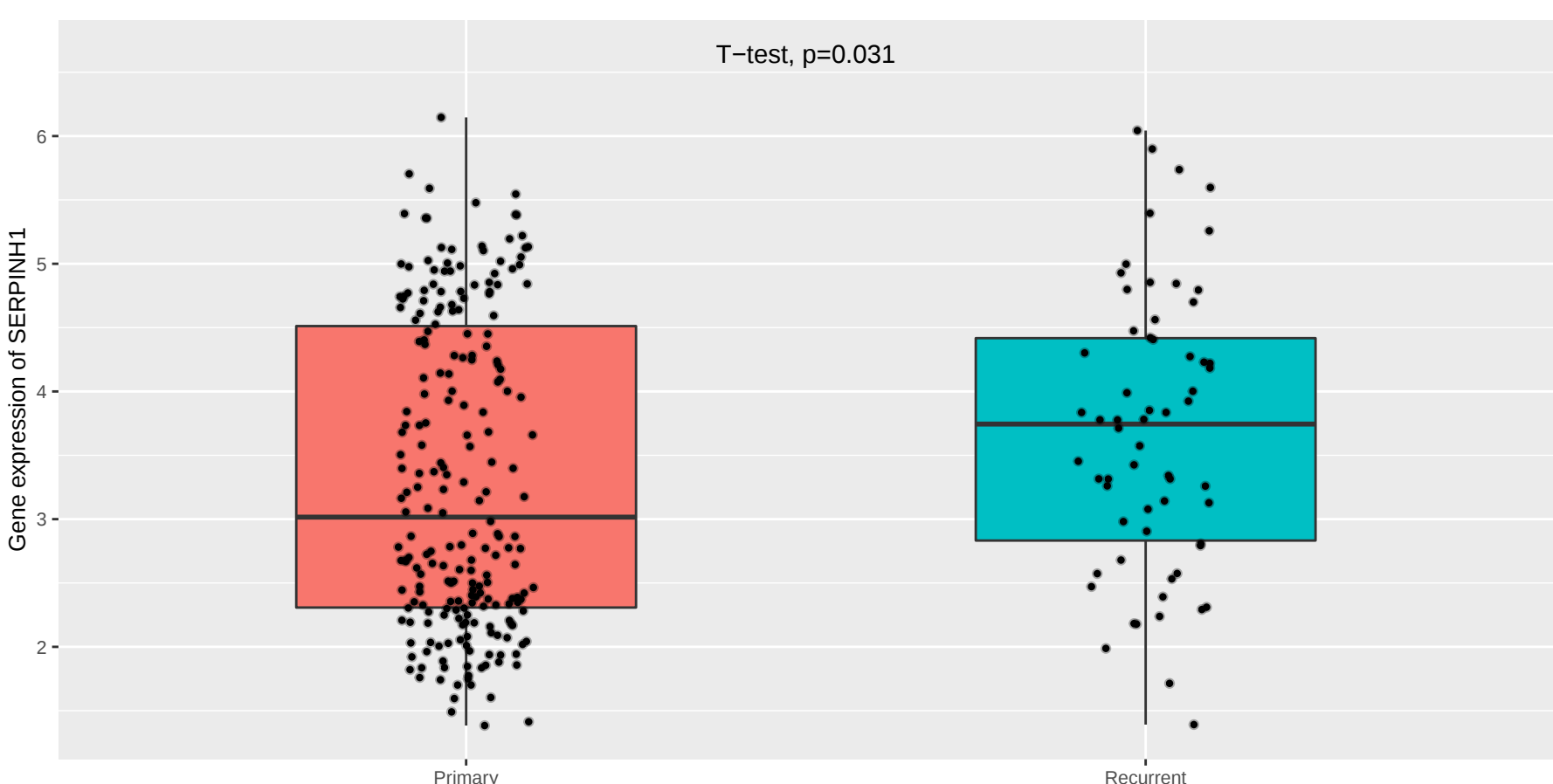
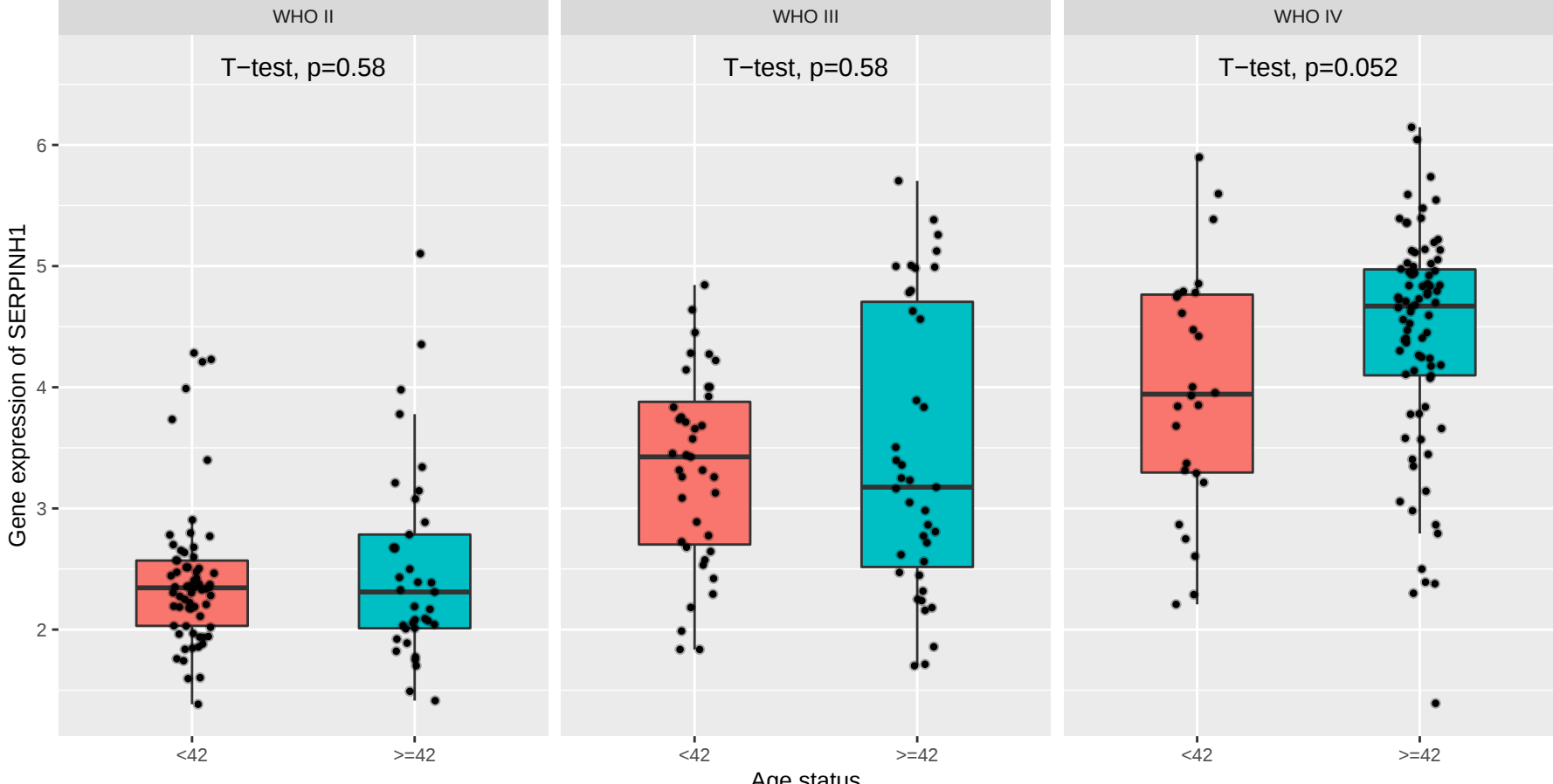
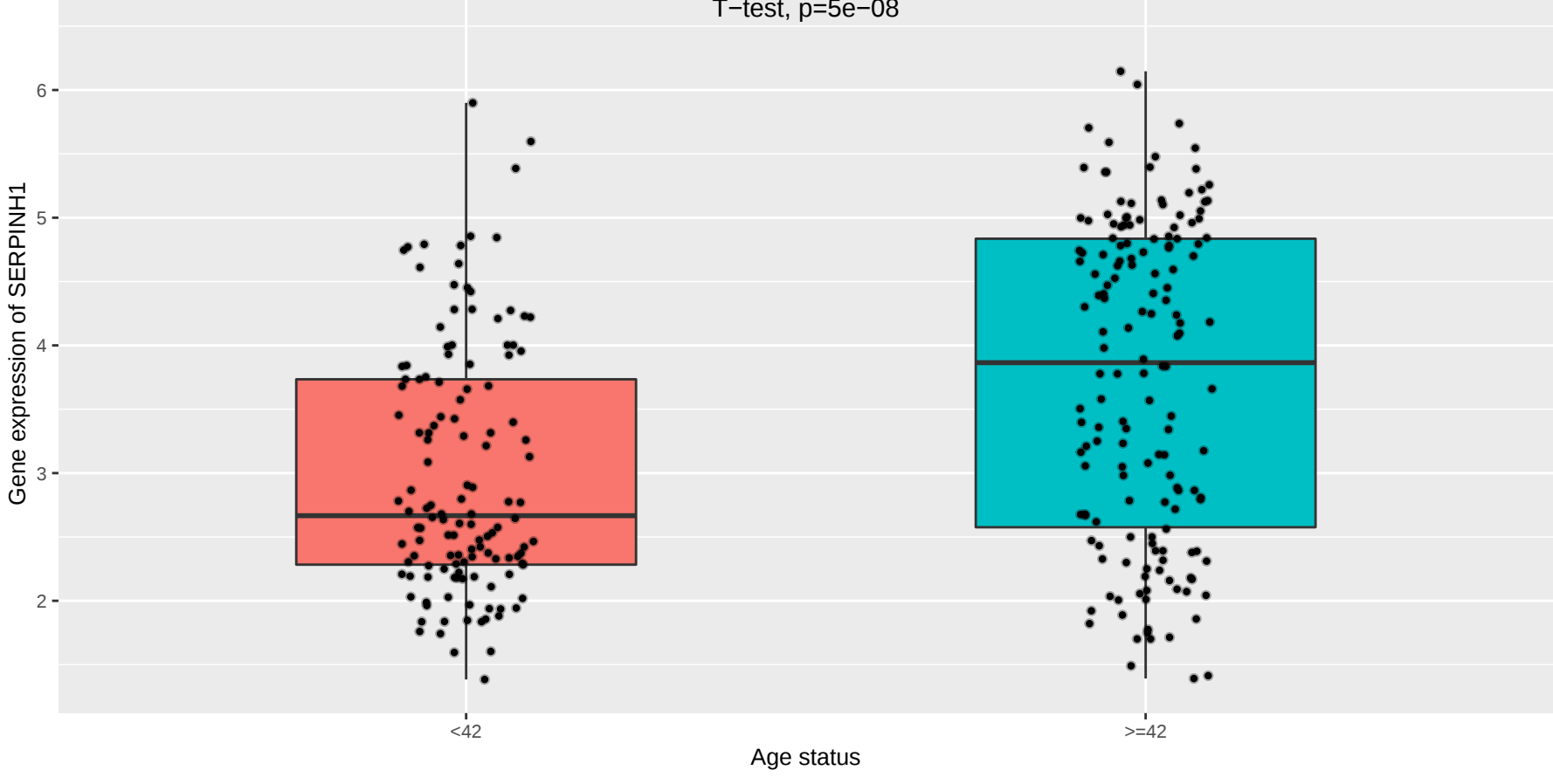
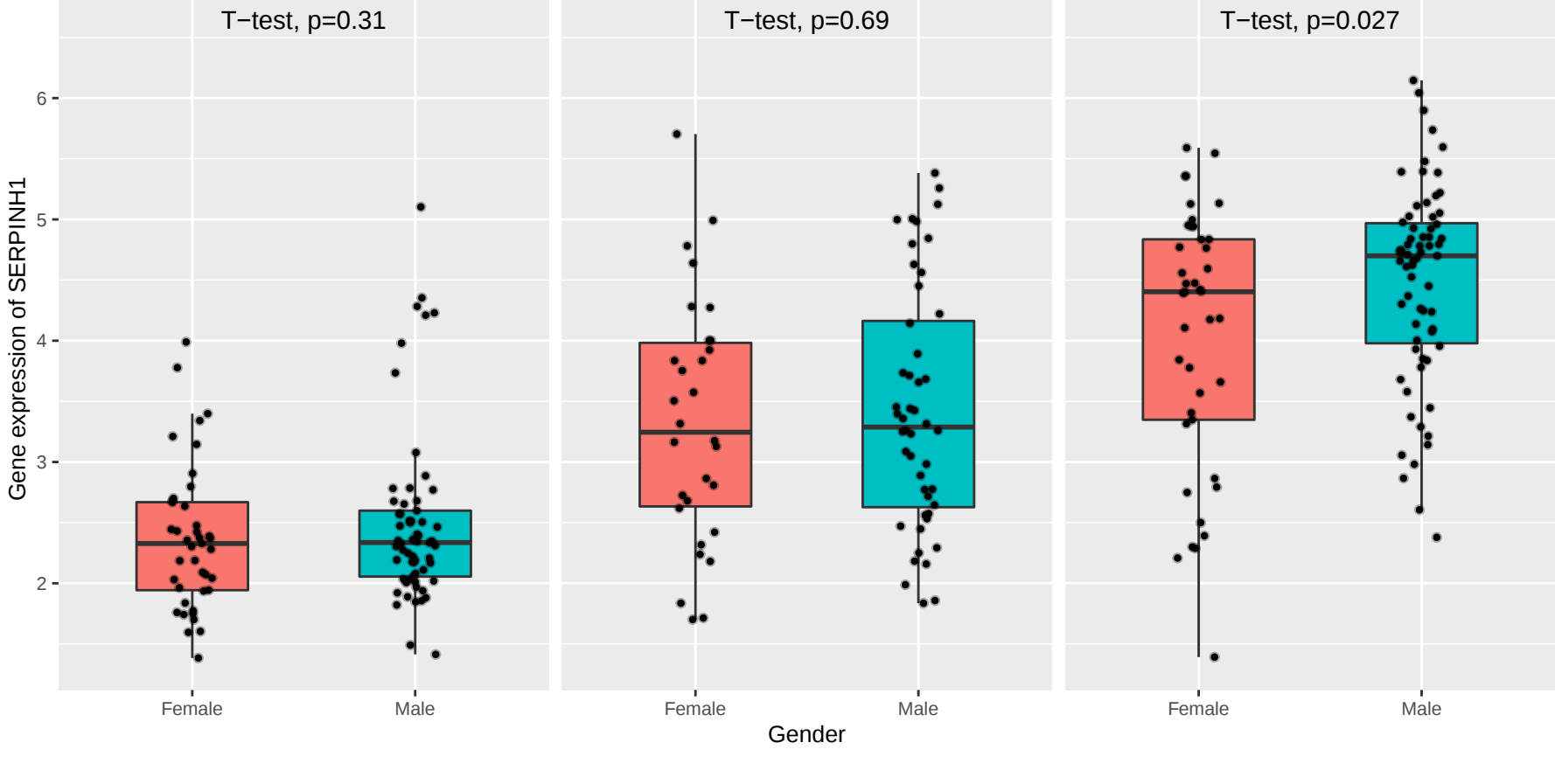
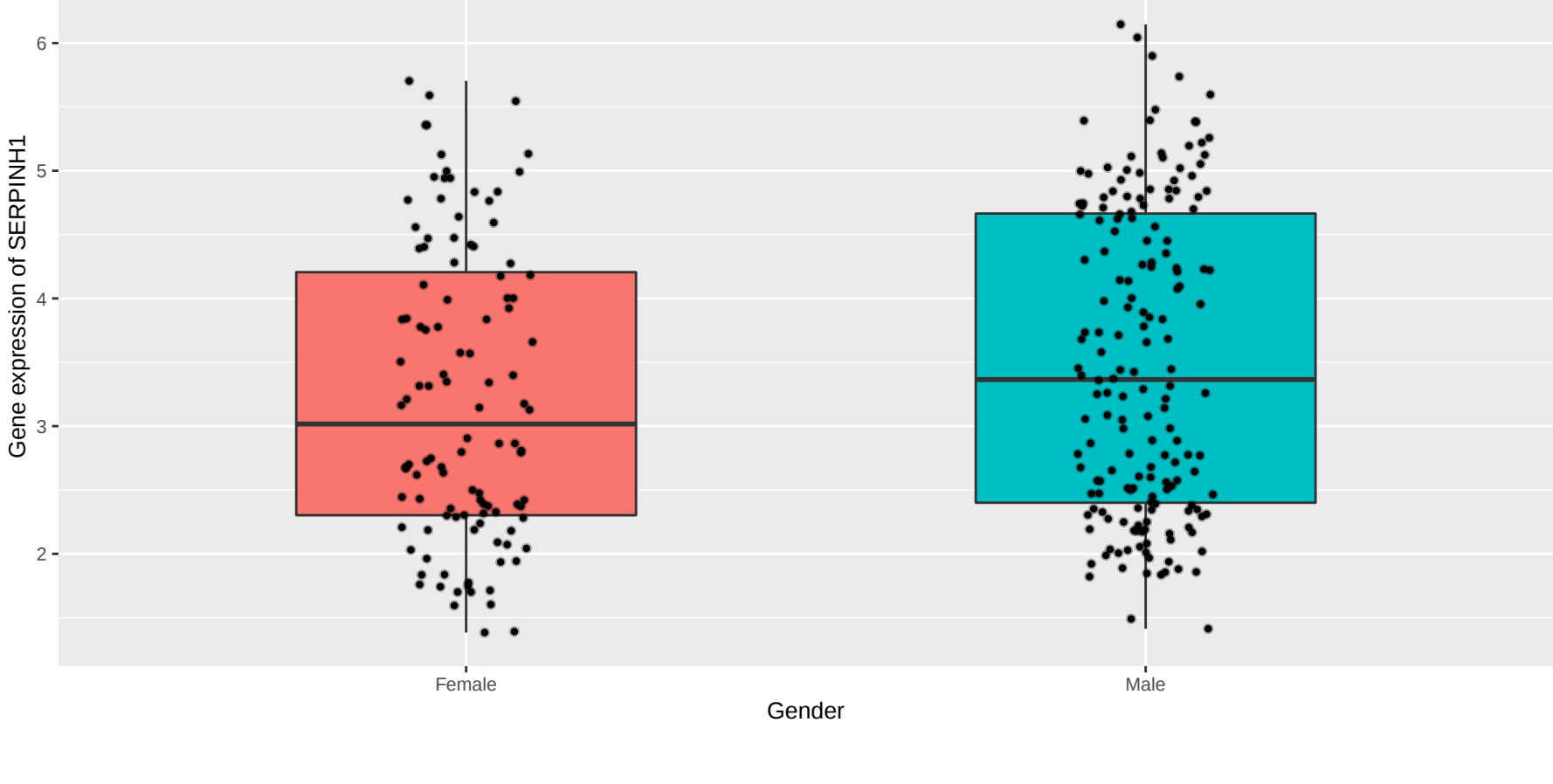
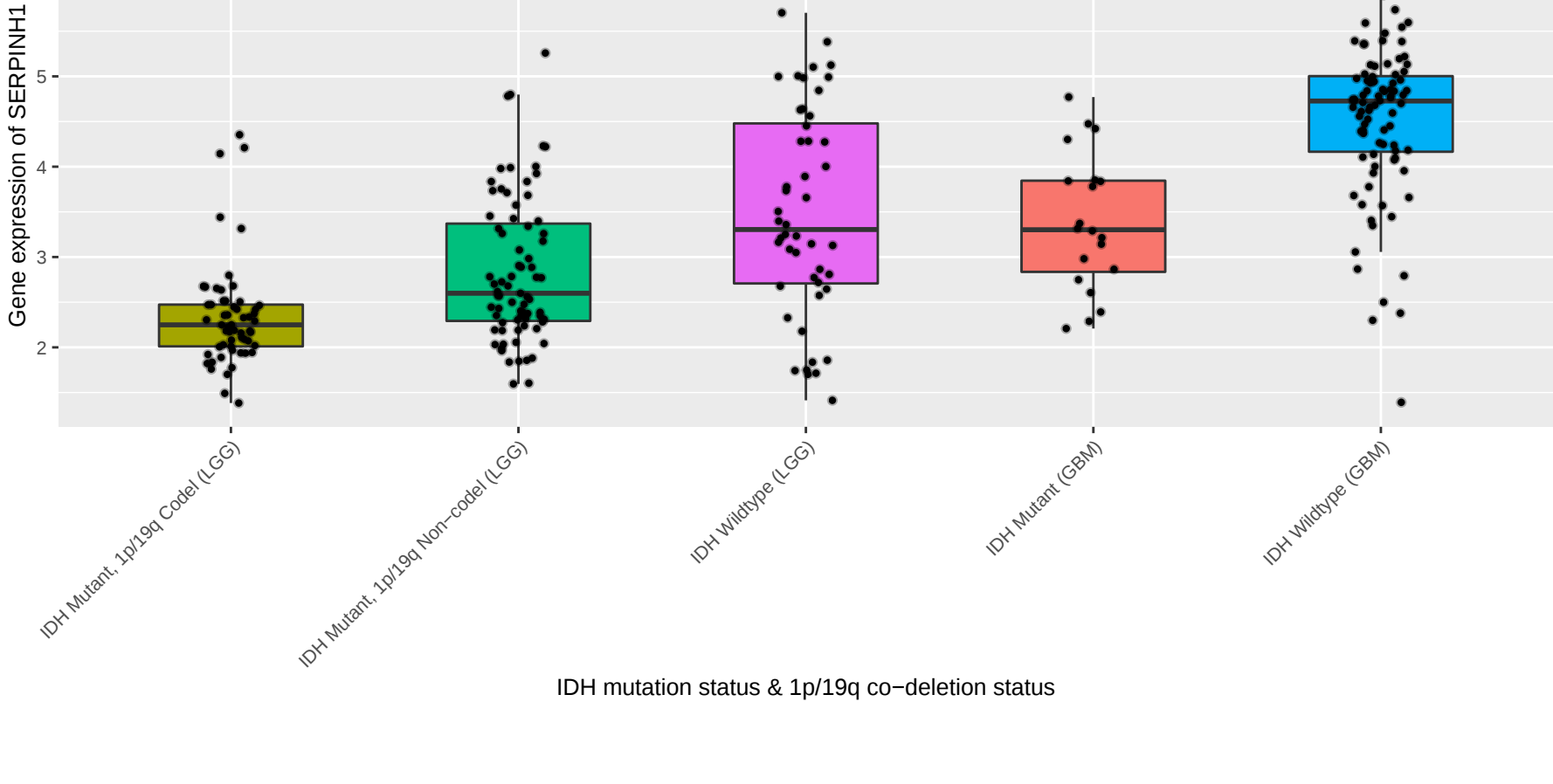
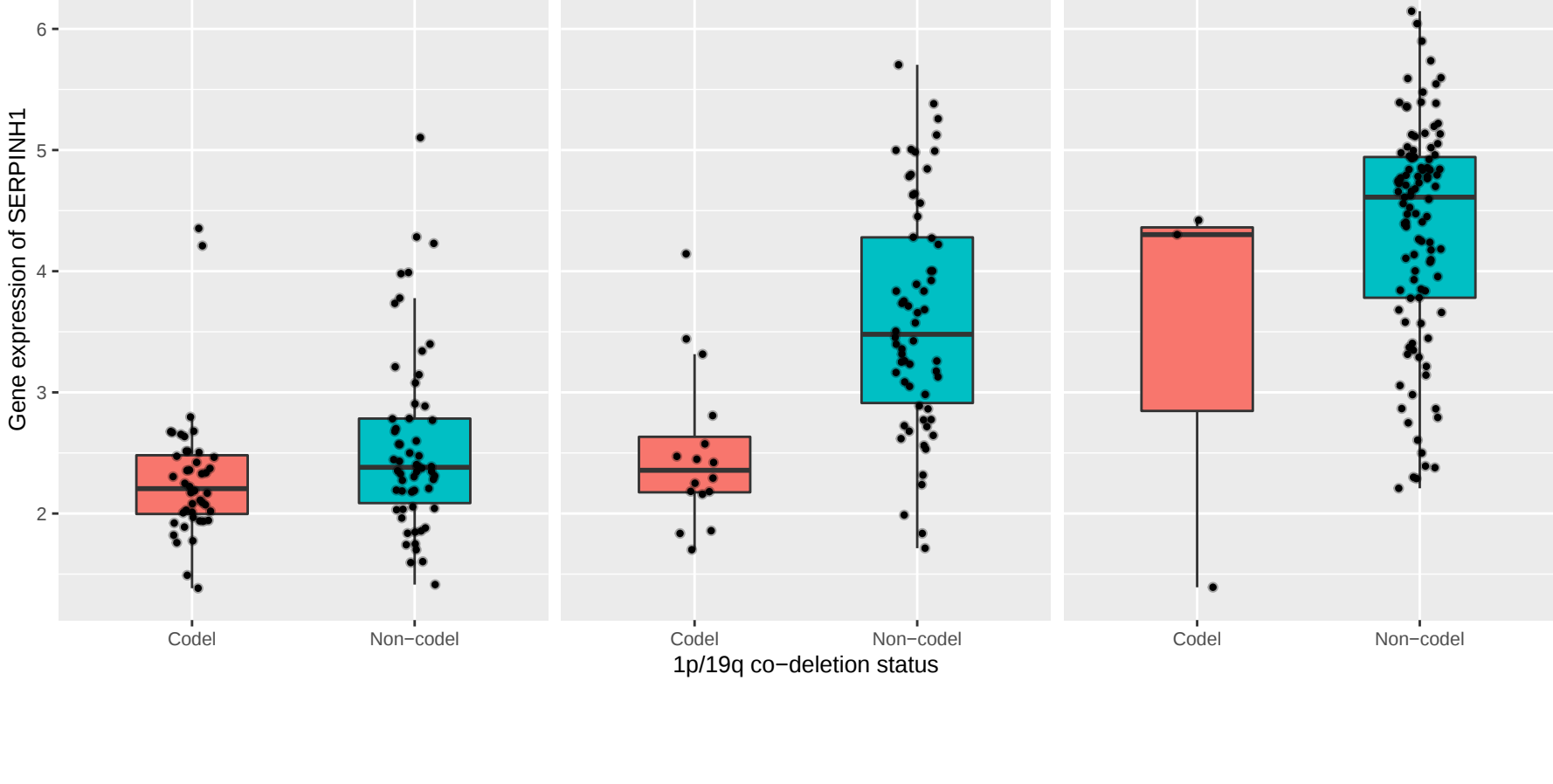
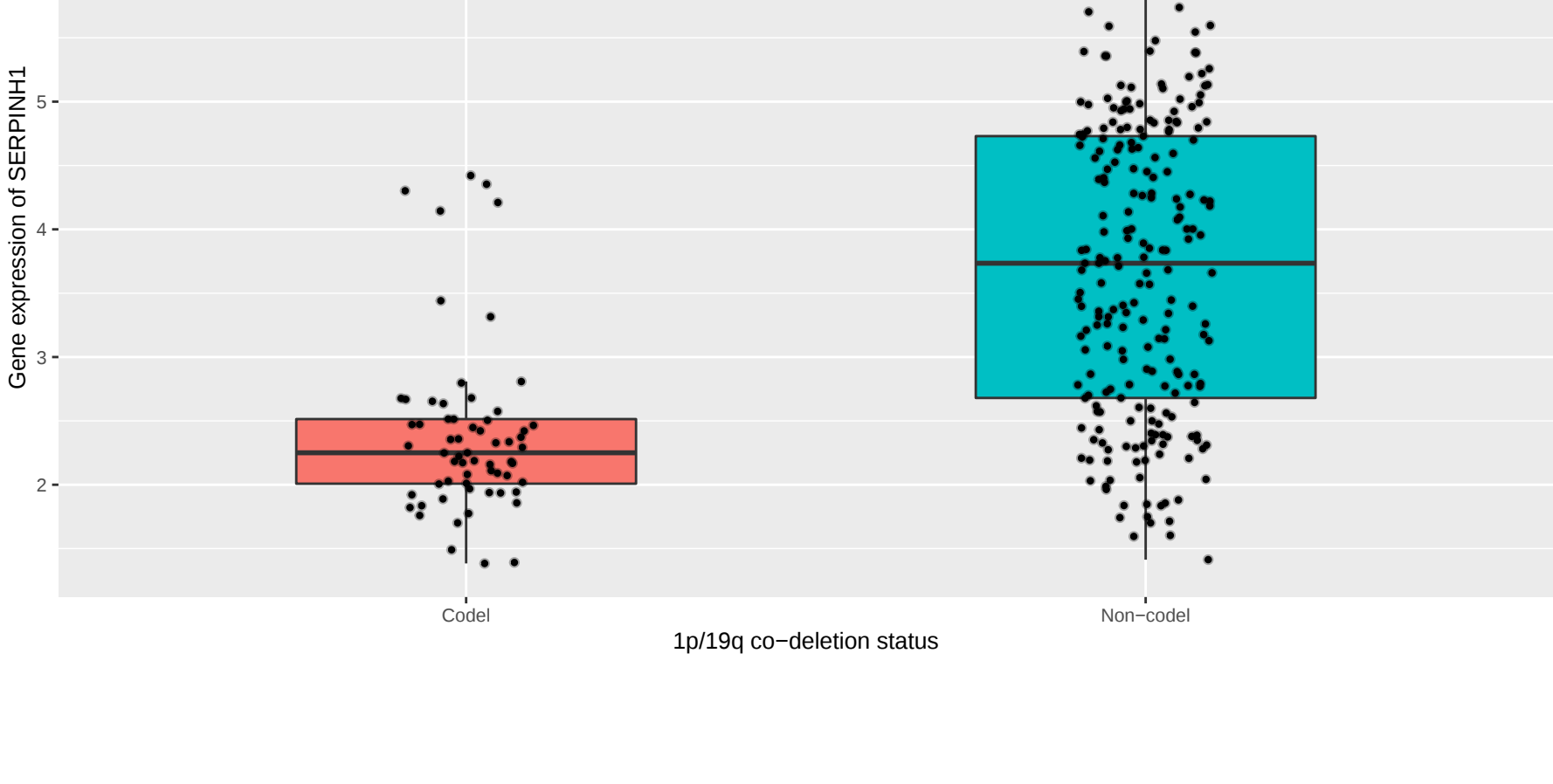
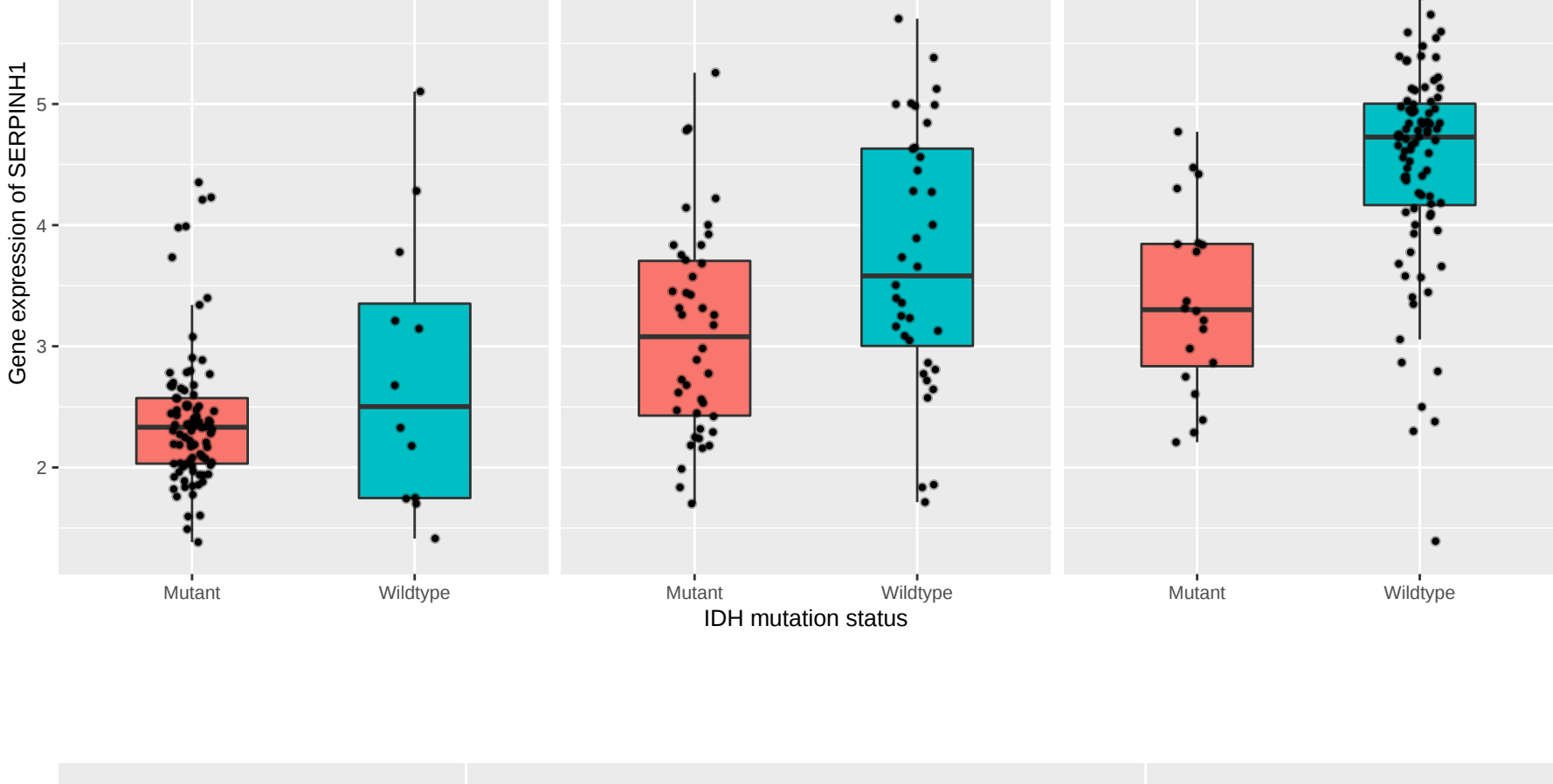
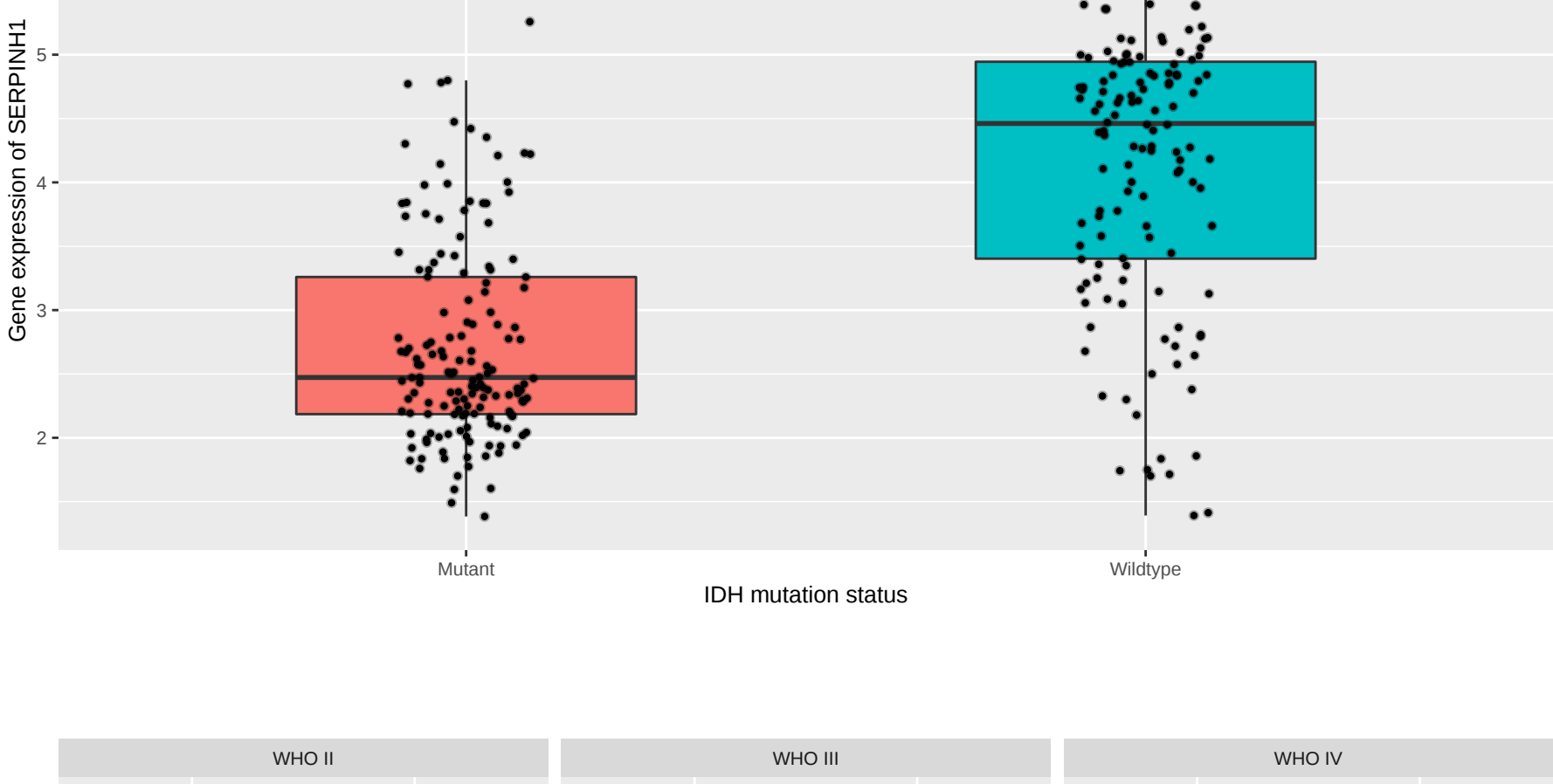
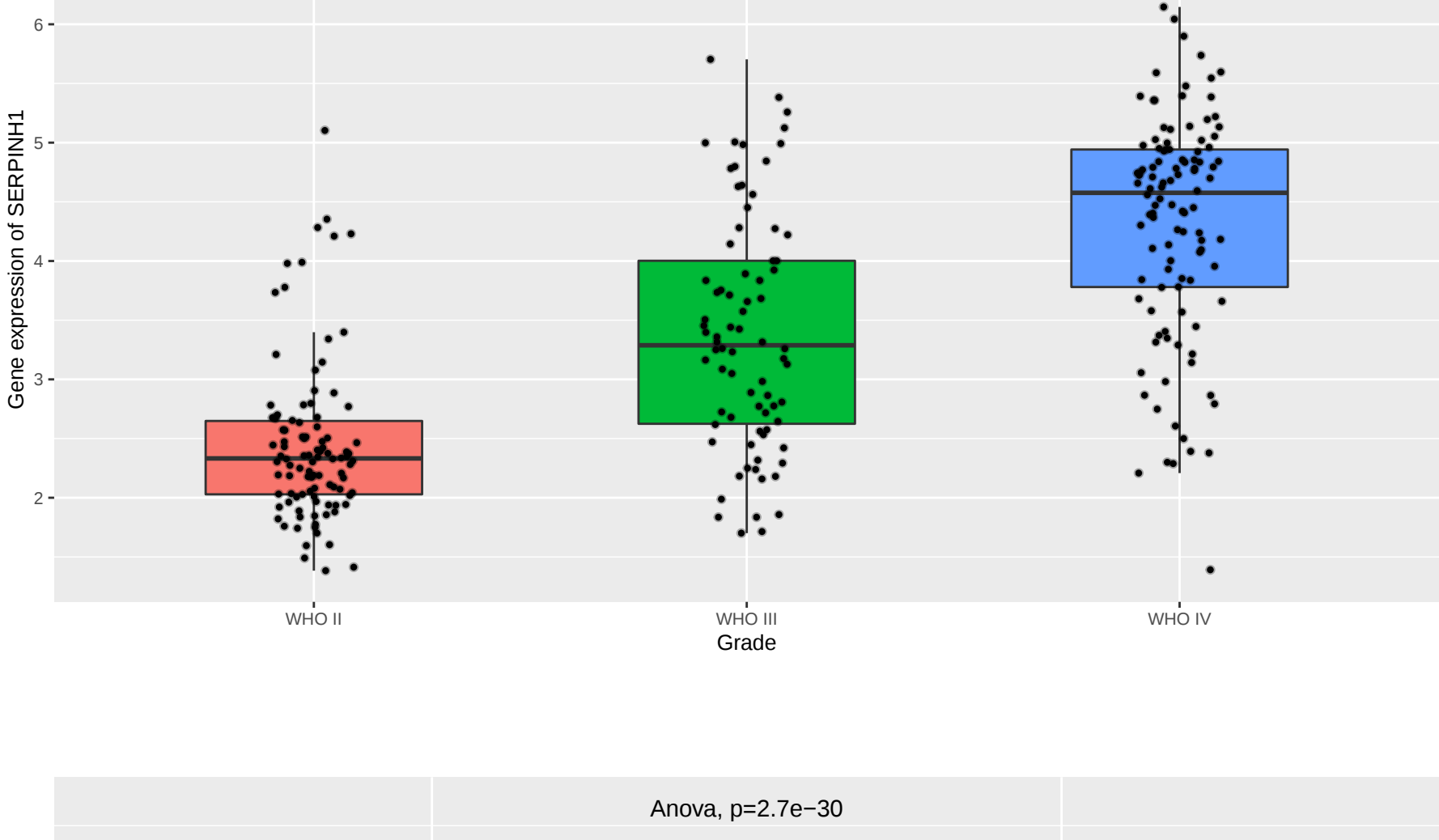
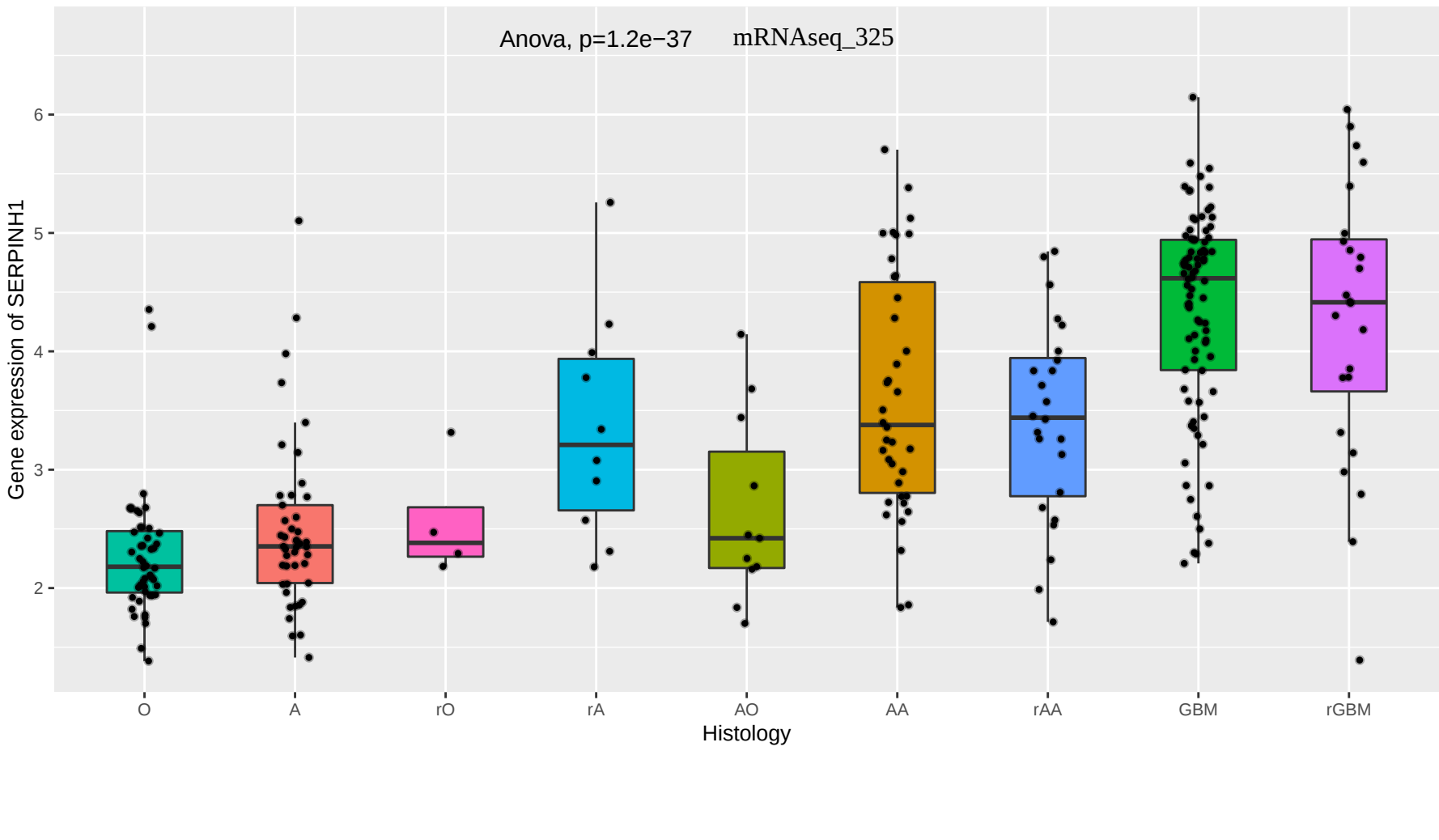
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TCGA-16-0846	0.007173135	3.840989058	0	-59.69046413
TCGA-28-5204	0.01179288	5.461422054	0	-340.9631249
TCGA-32-2616	0.010781541	4.516399707	0	-340.1000794
TCGA-27-2523	0.011011456	5.232981616	0	-753.3540593
TCGA-28-5207	0.011241155	5.287973606	0	222.612346
TCGA-14-0787	0.012225159	5.581673359	0	-422.8803553
TCGA-12-3653	0.009015456	4.405741541	0	-506.0987099
TCGA-02-2483	0.01275223	5.523225171	0.0276	-166.7982393
TCGA-06-0171	0.018283043	7.257260584	0.0826	1397.219098
TCGA-06-0184	0.013325536	5.249764449	0.0022	402.2581127
TCGA-06-0178	0.010705493	4.119848408	0.0789	-122.7511971
TCGA-41-3915	0.017108199	7.448965489	0.0838	552.7556918
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TCGA-06-1804	0.009462302	4.296280163	0.0183	-282.4522744
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TCGA-02-2485	0.009510468	4.47669636	0	-470.4040093
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TCGA-32-1982	0.011743937	5.748989011	0.0329	451.4924318
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TCGA-27-1831	0.013741375	5.176030138	0.0782	358.1561112
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TCGA-12-3652	0.007907447	4.872497613	0.0113	-853.7777887
TCGA-28-2514	0.010155003	5.459748343	0	-497.9098161
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TCGA-14-0871	0.017885441	6.497971229	0.0789	-327.2865445
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TCGA-12-0618	0.00850874	4.46109117	0	-838.3961043
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TCGA-06-5417	0.009401941	4.309627615	0	-712.3497975
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TCGA-06-0187	0.012218342	5.685206544	0.0266	-77.64868779
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TCGA-06-5418	0.01231	5.503101116	0.0263	-108.9430221
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TCGA-26-5134	0.011231431	4.7767009	0.0242	-460.0685506
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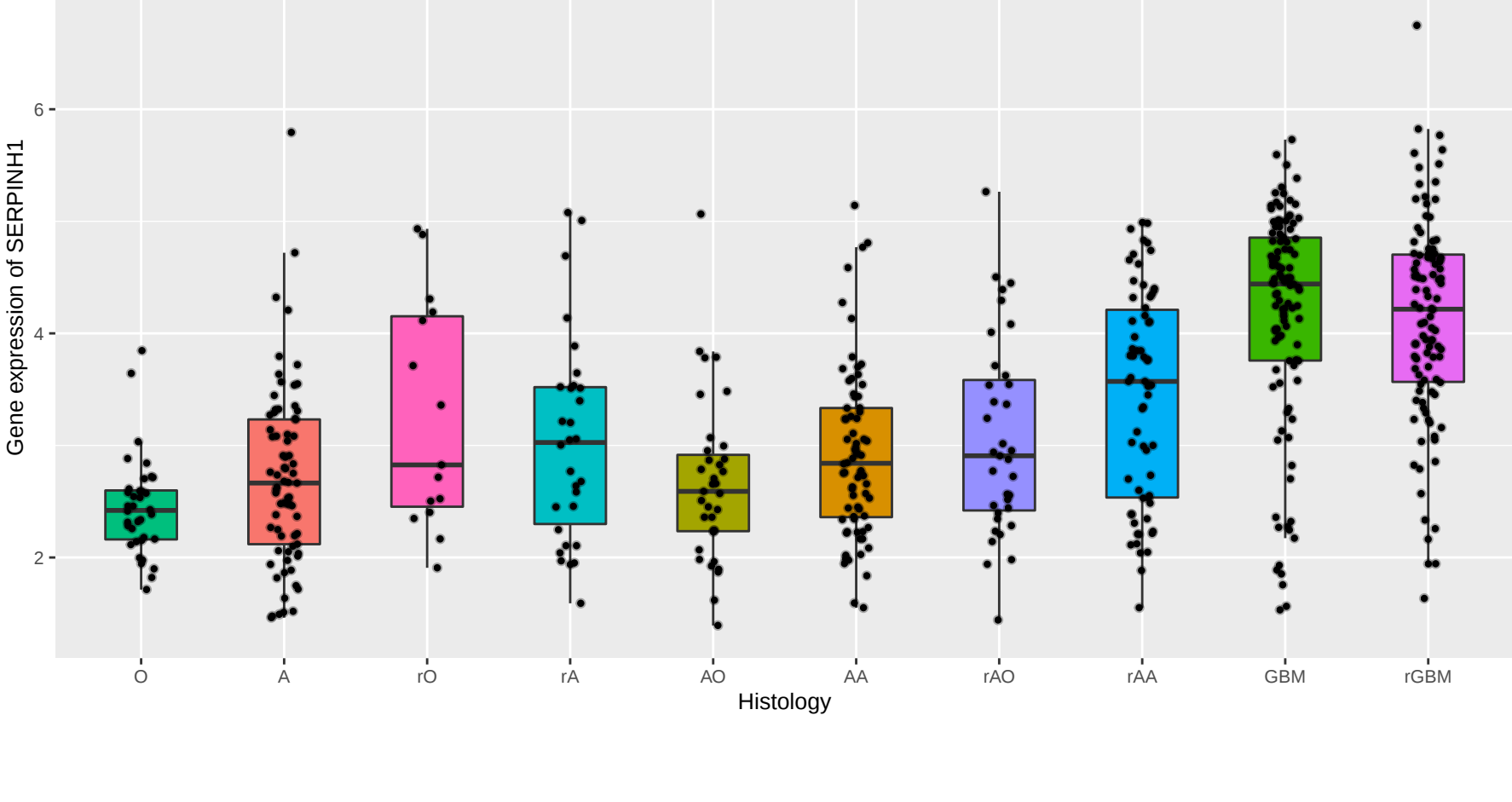
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Figure S1:
SERPINH1 expression analysis in CGGA

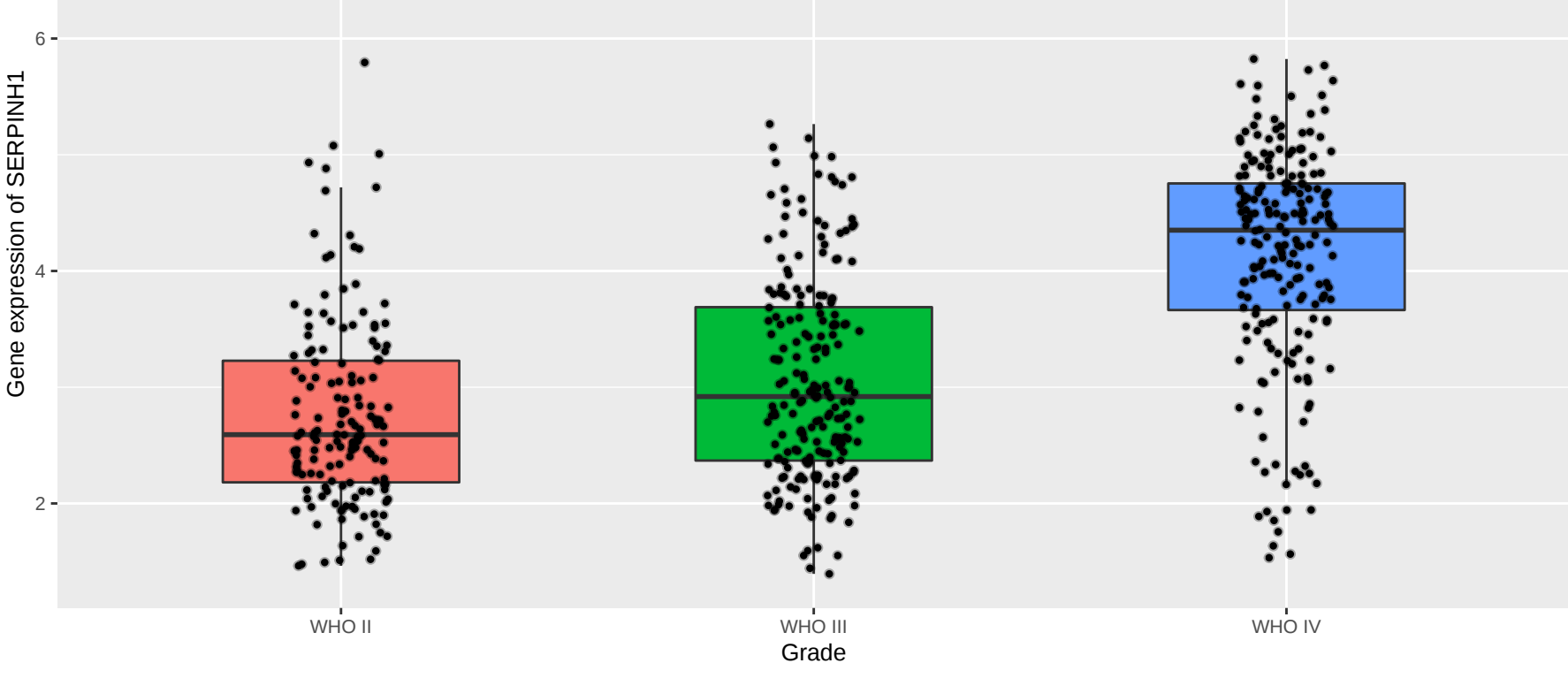




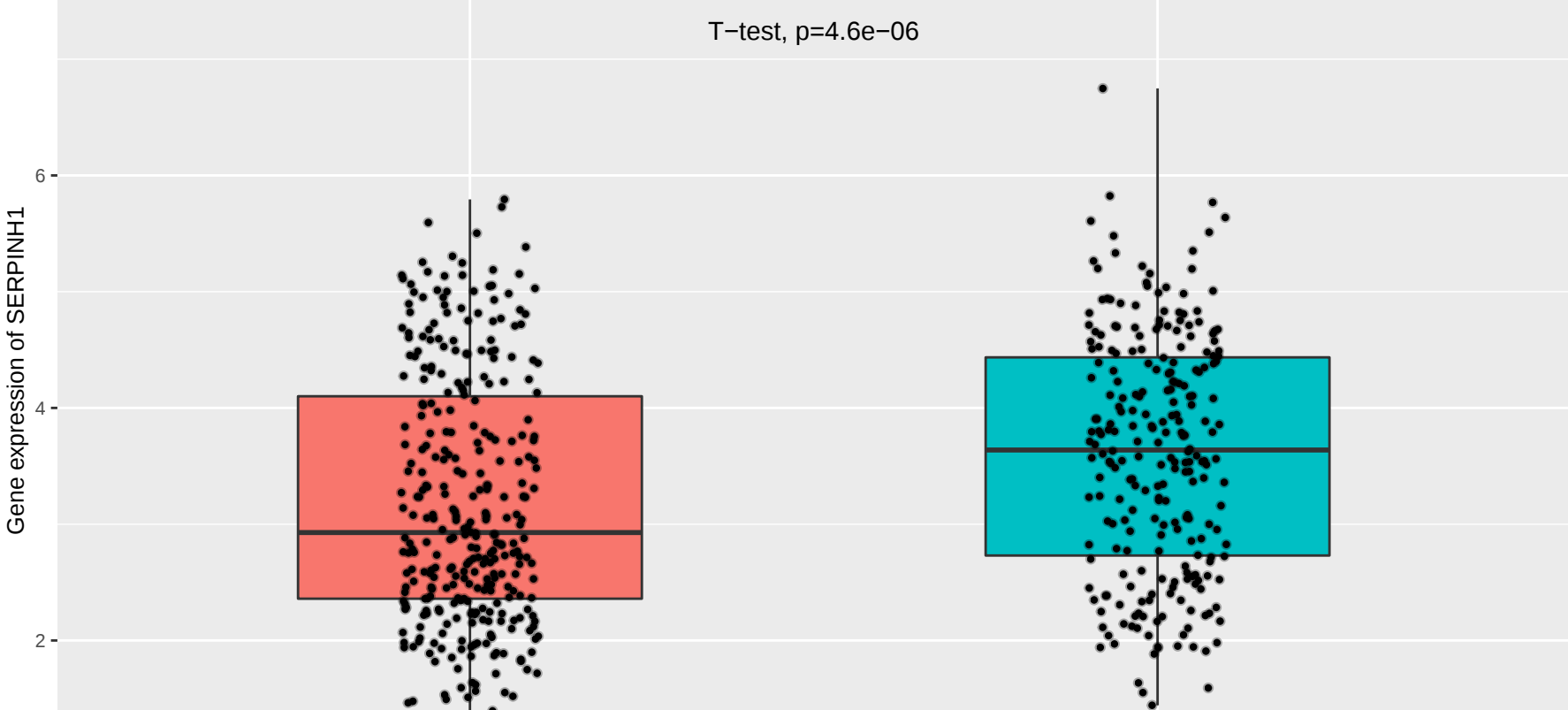
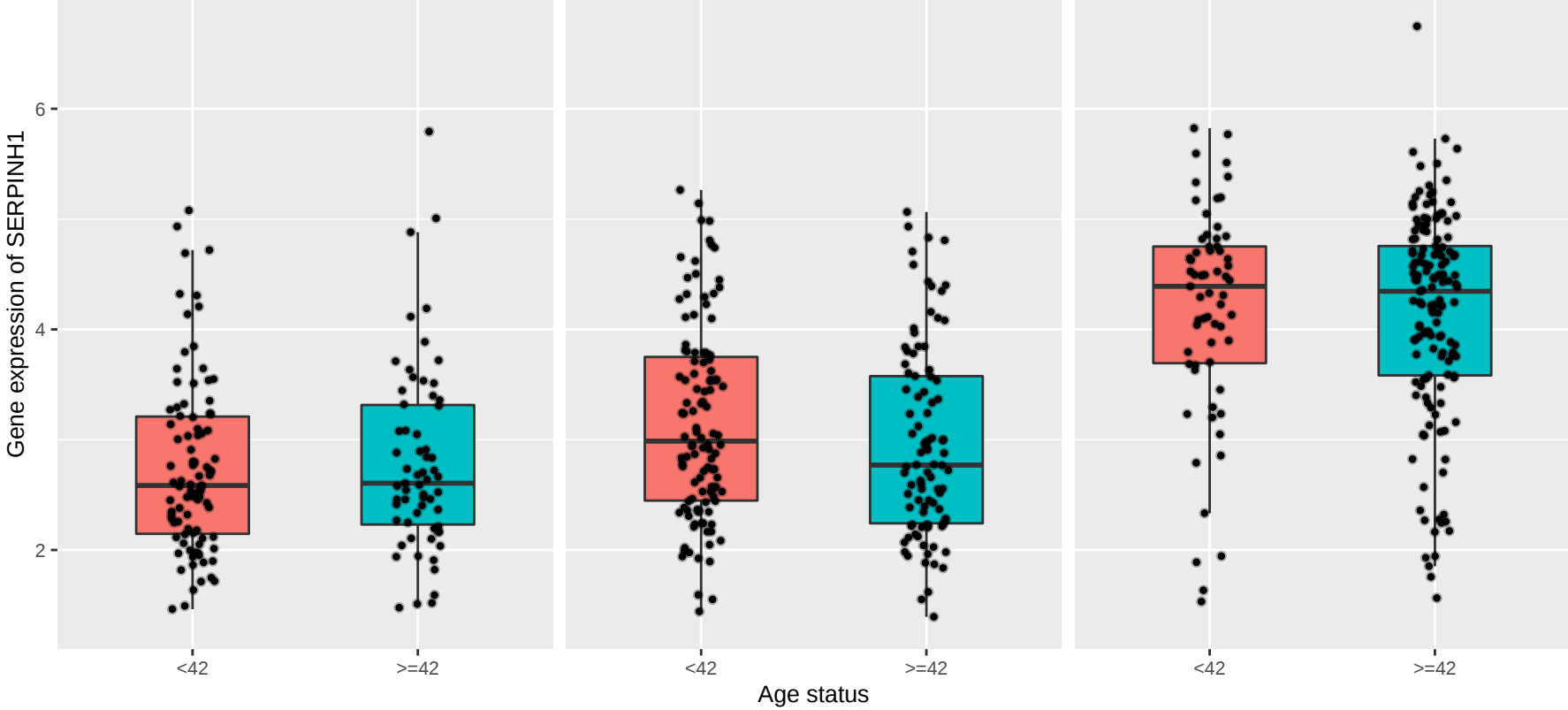
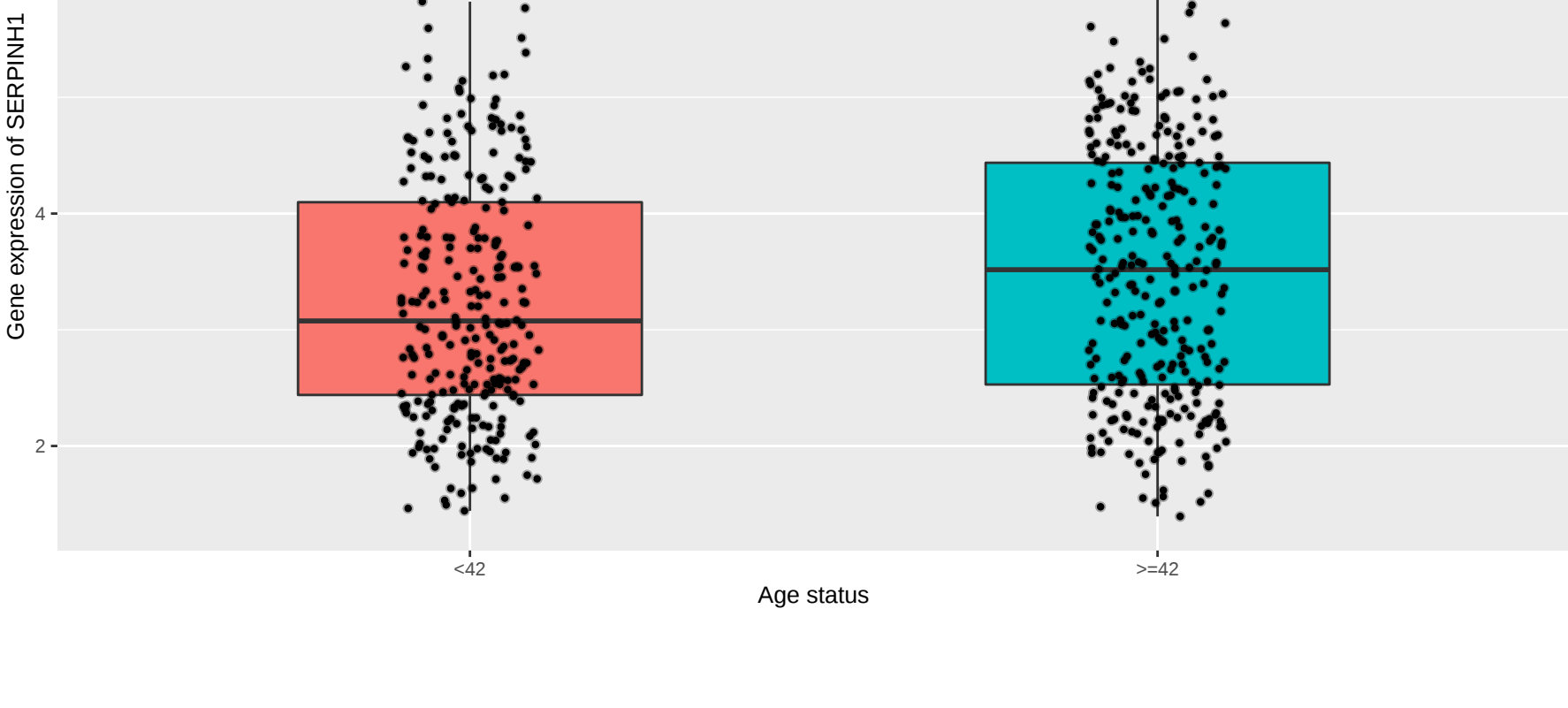
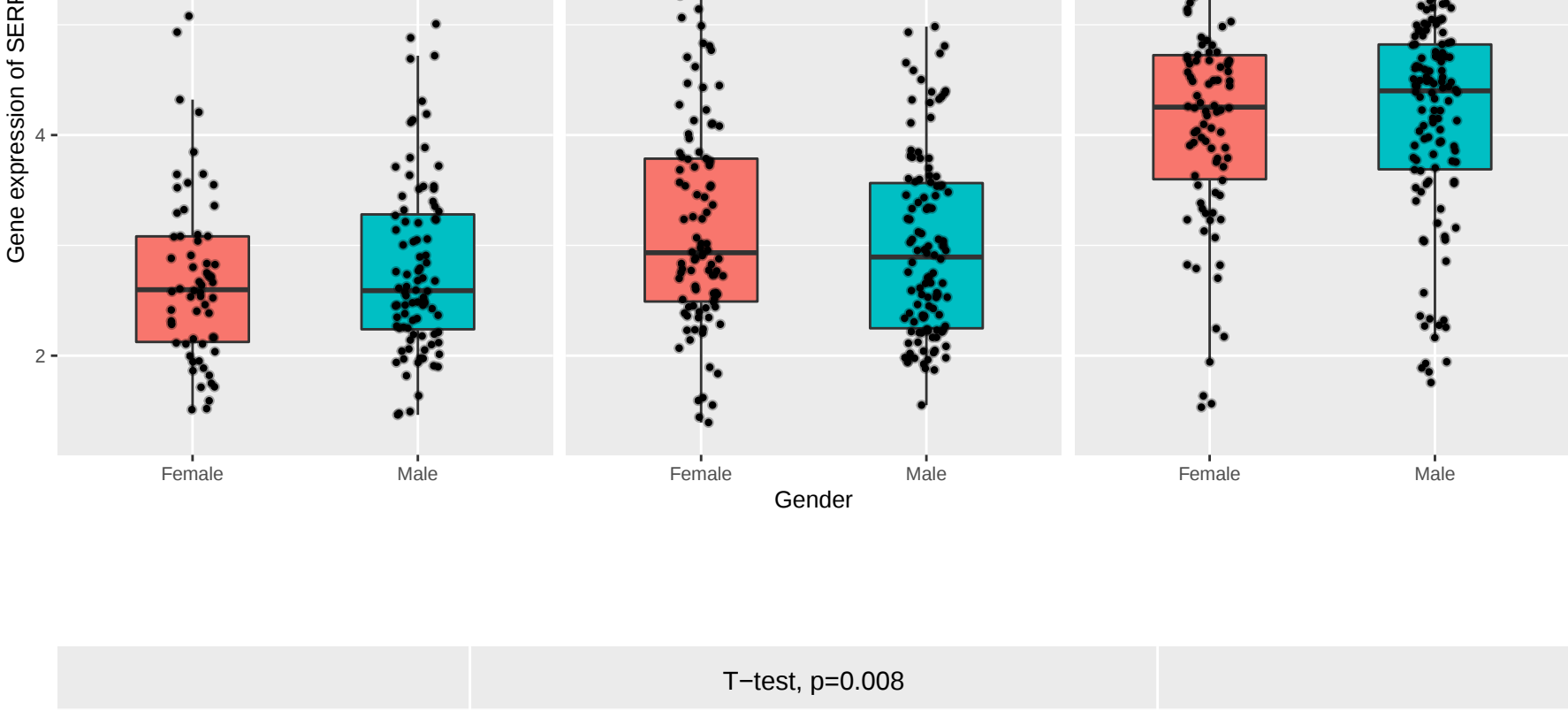
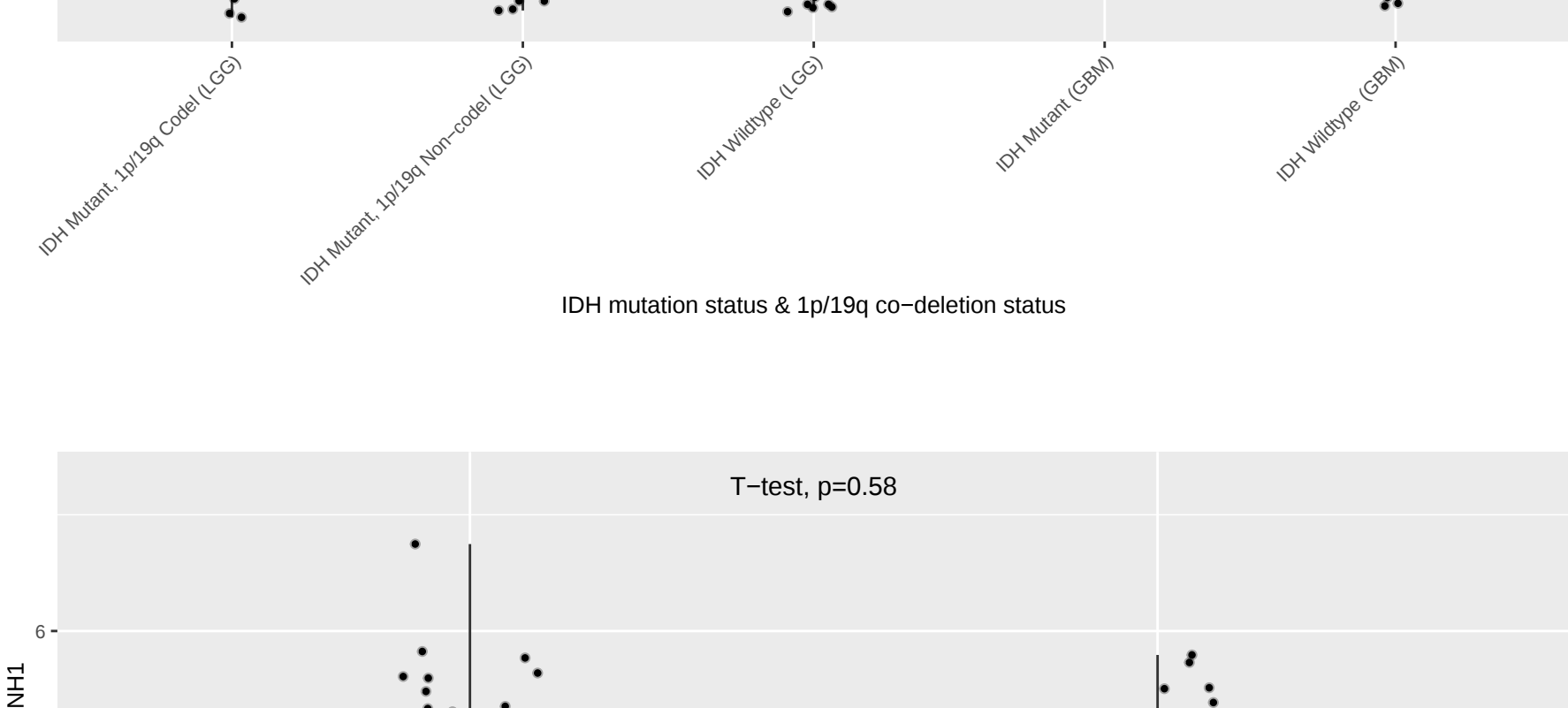
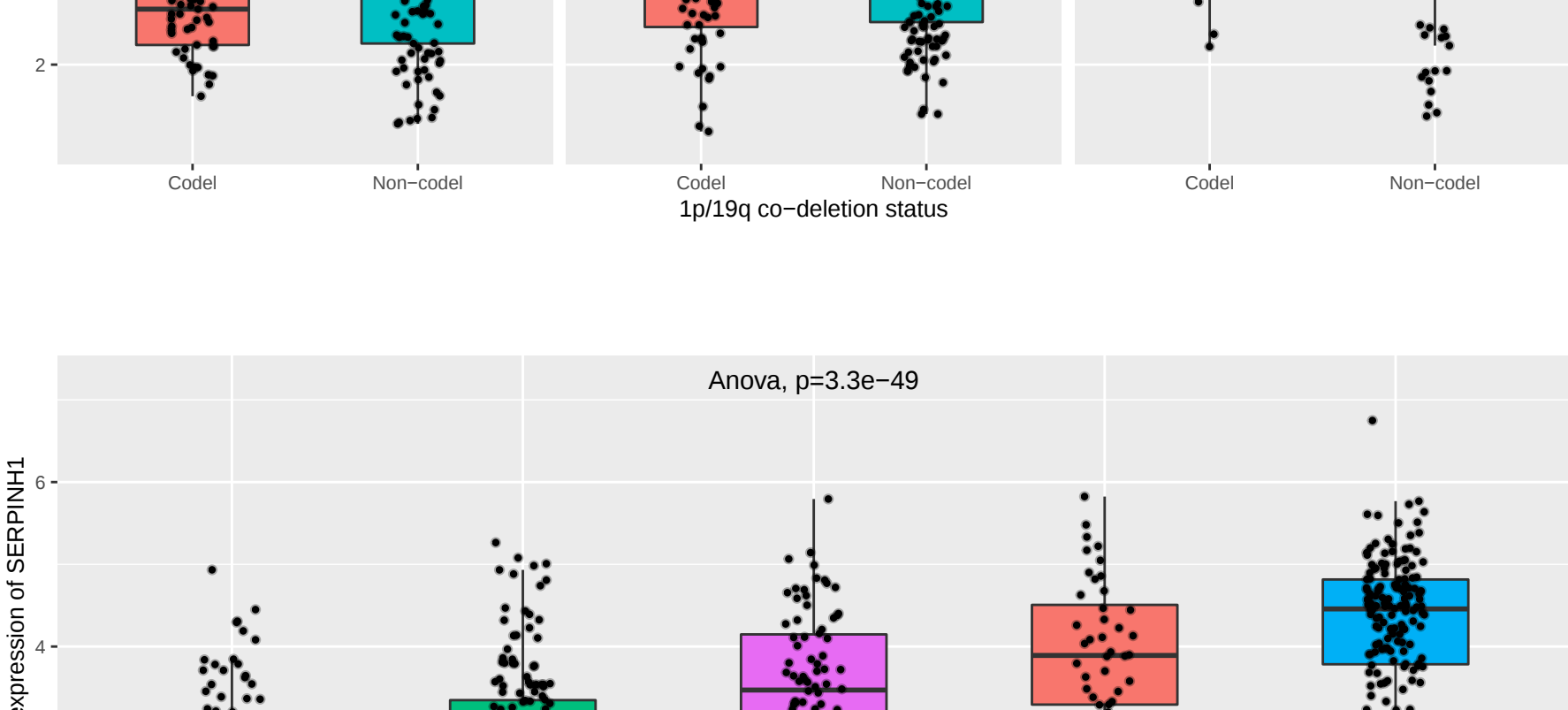
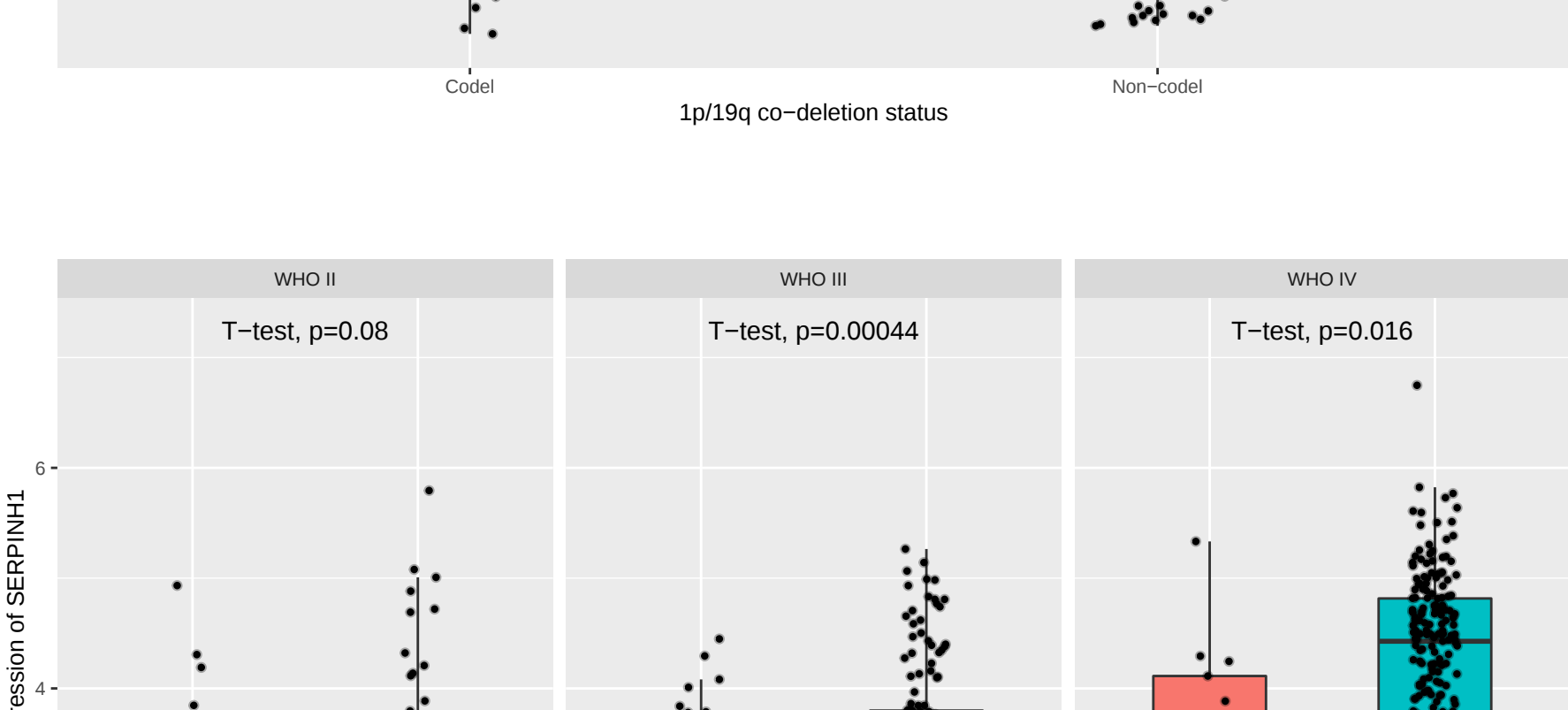
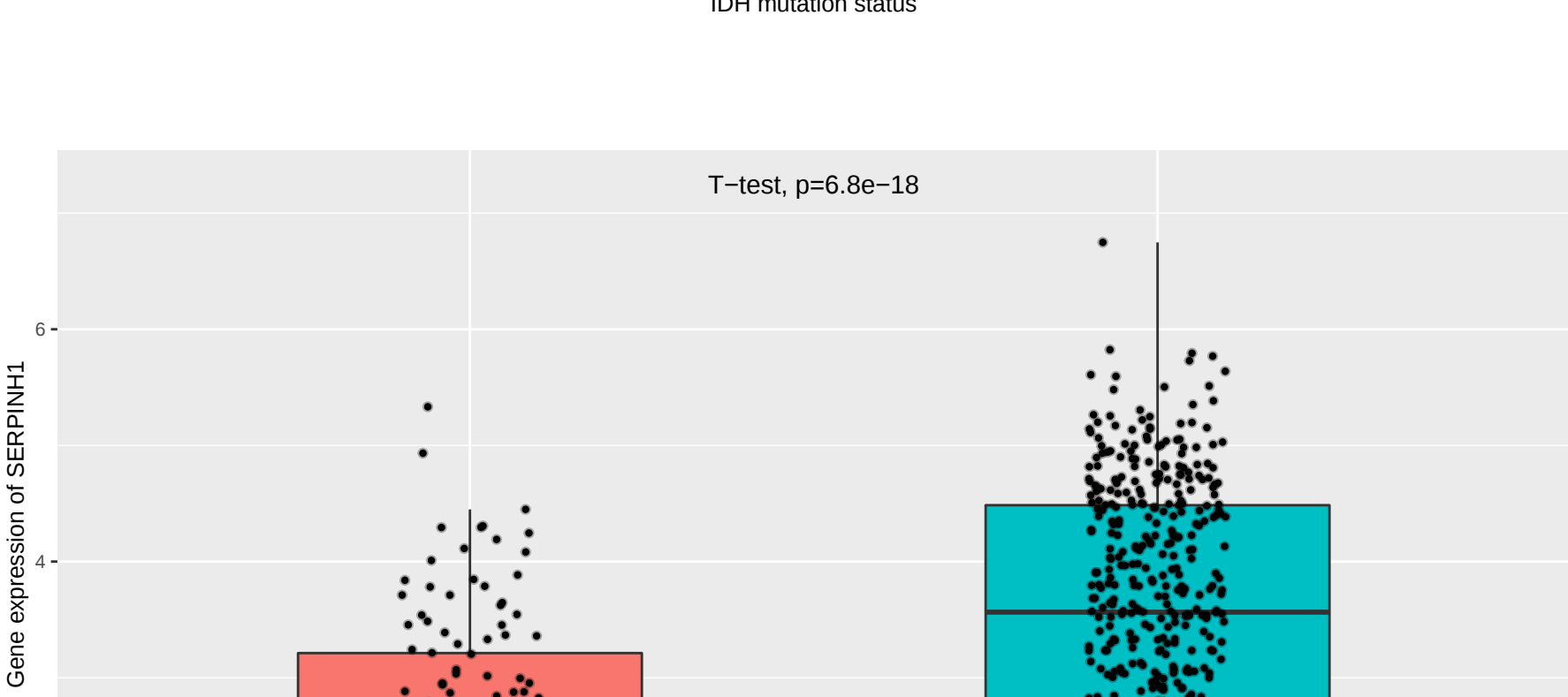
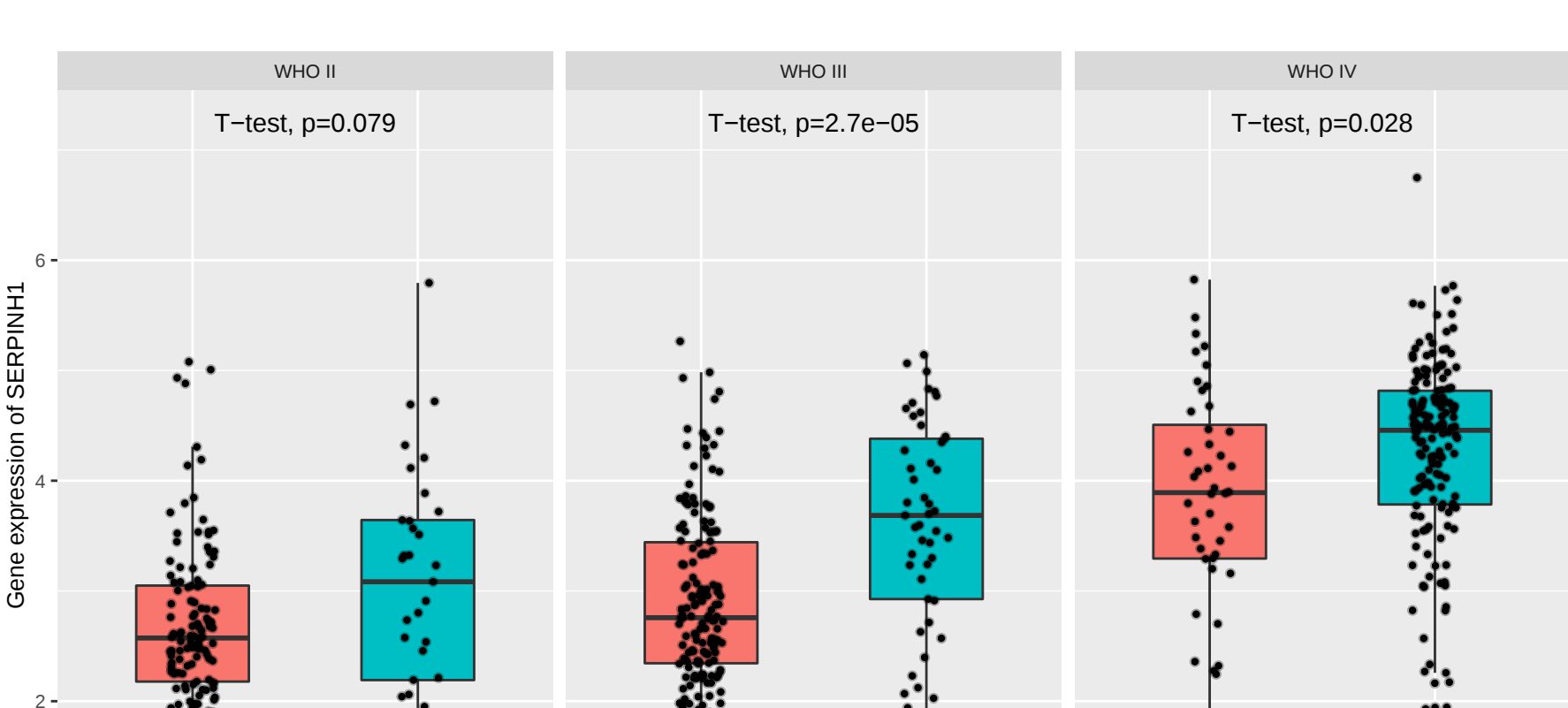
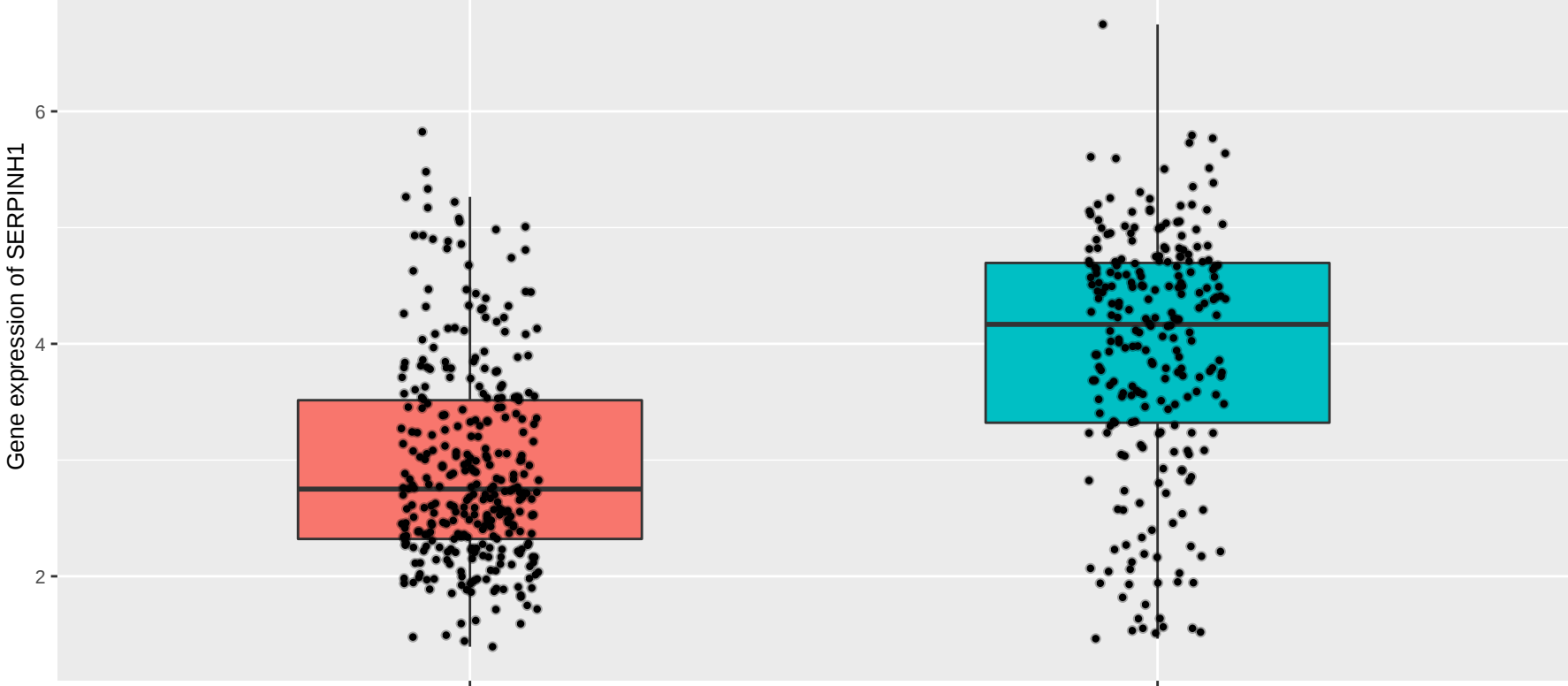
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Anova, $p=4.5e-46$



Anova, $p=7.7e-31$



FigureS2: COL5A1 expression analysis in CGGA

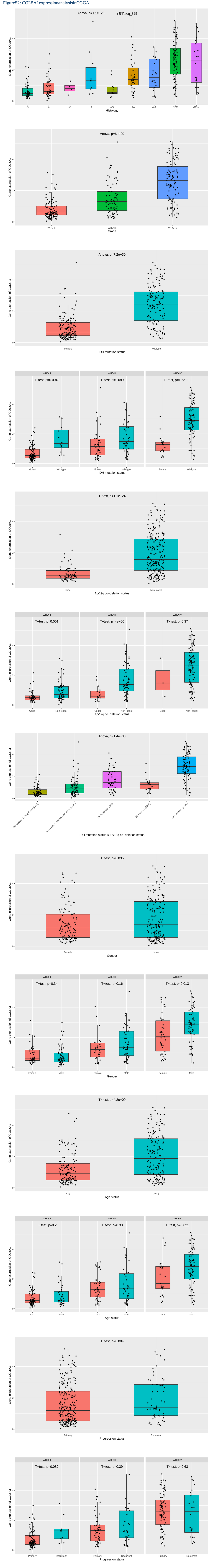
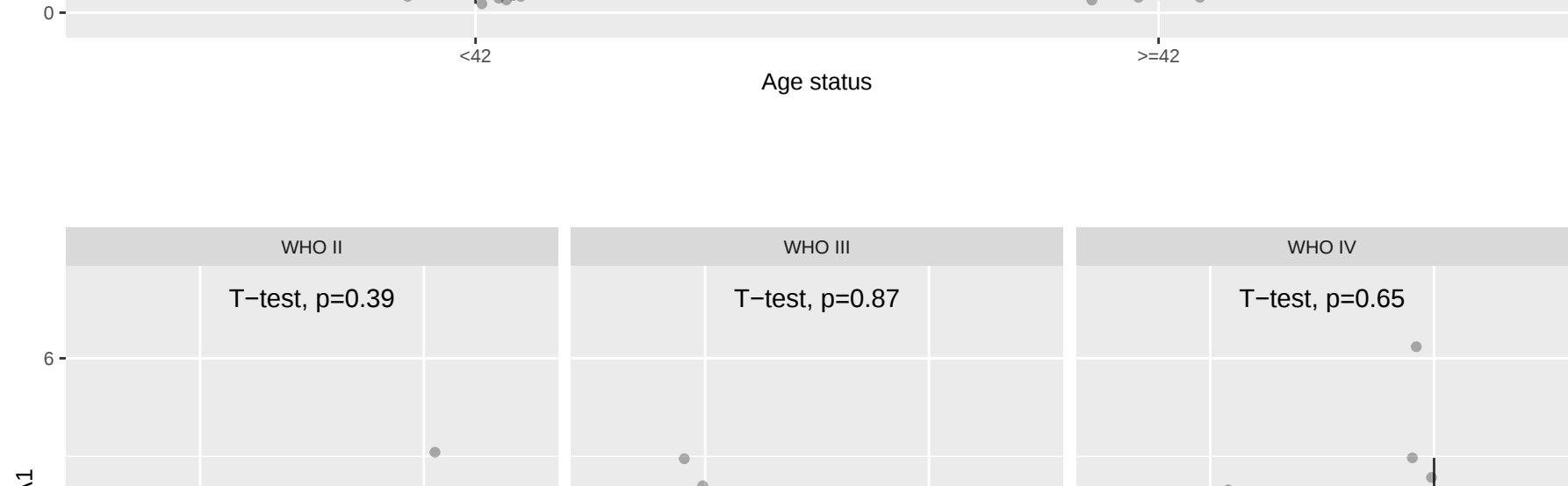
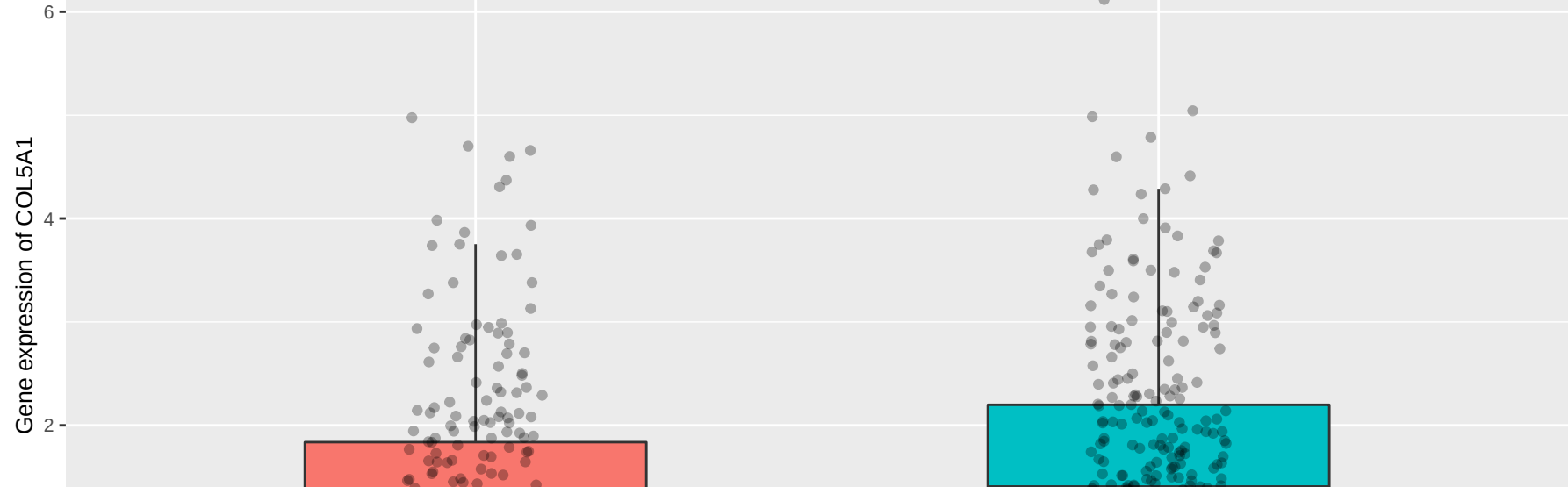
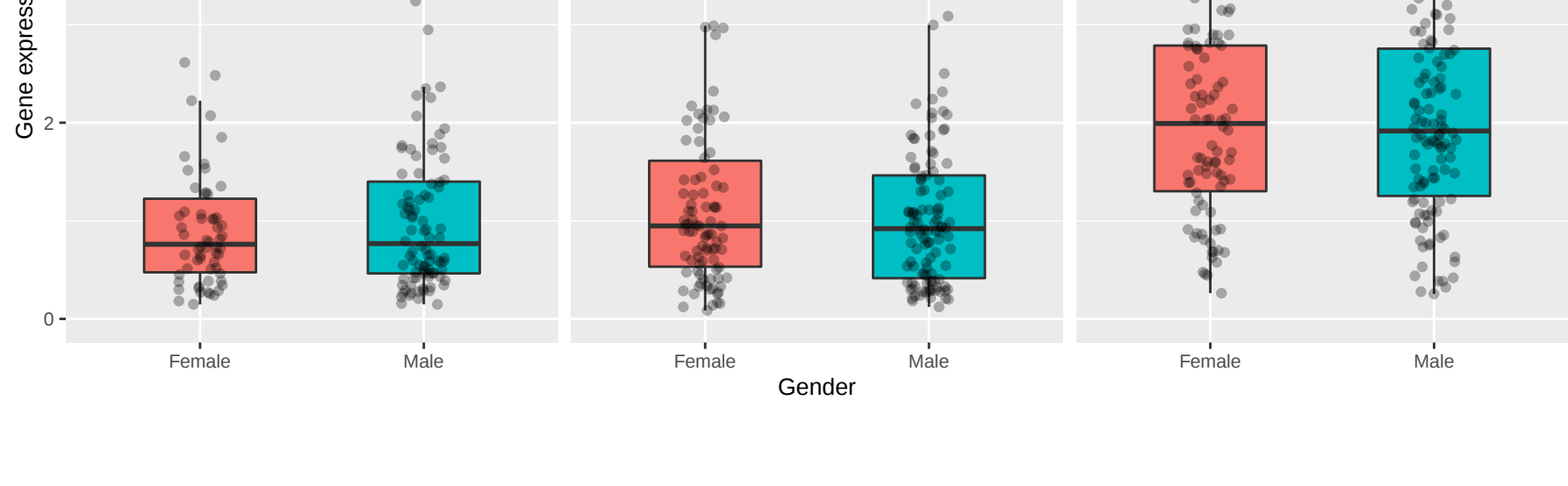
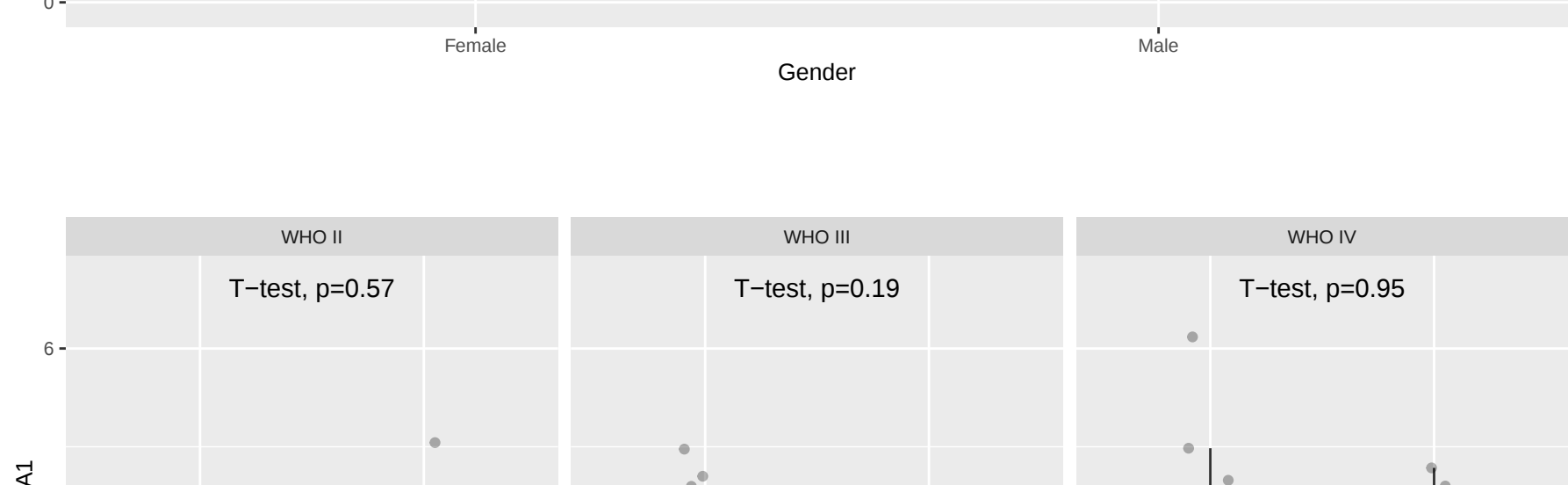
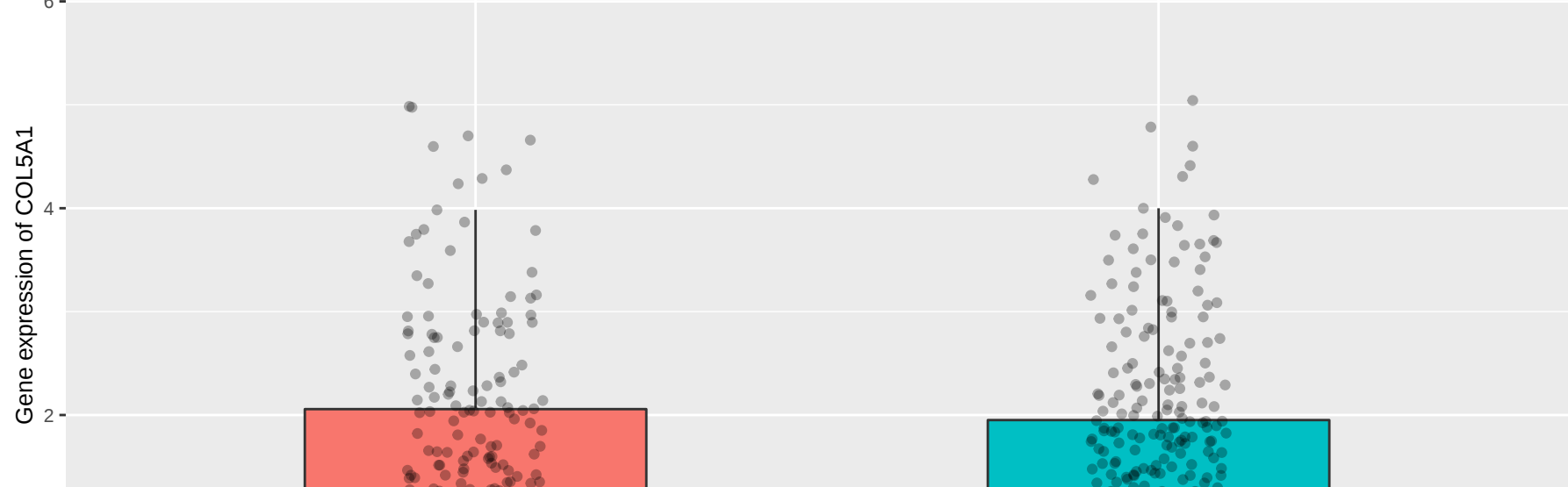
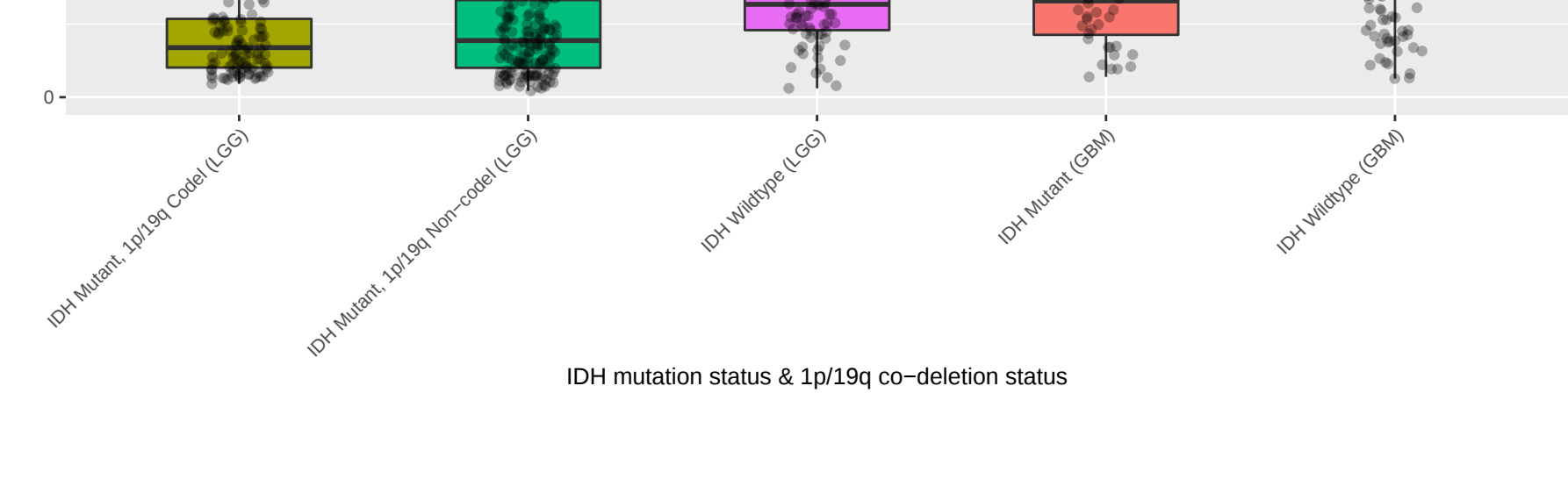
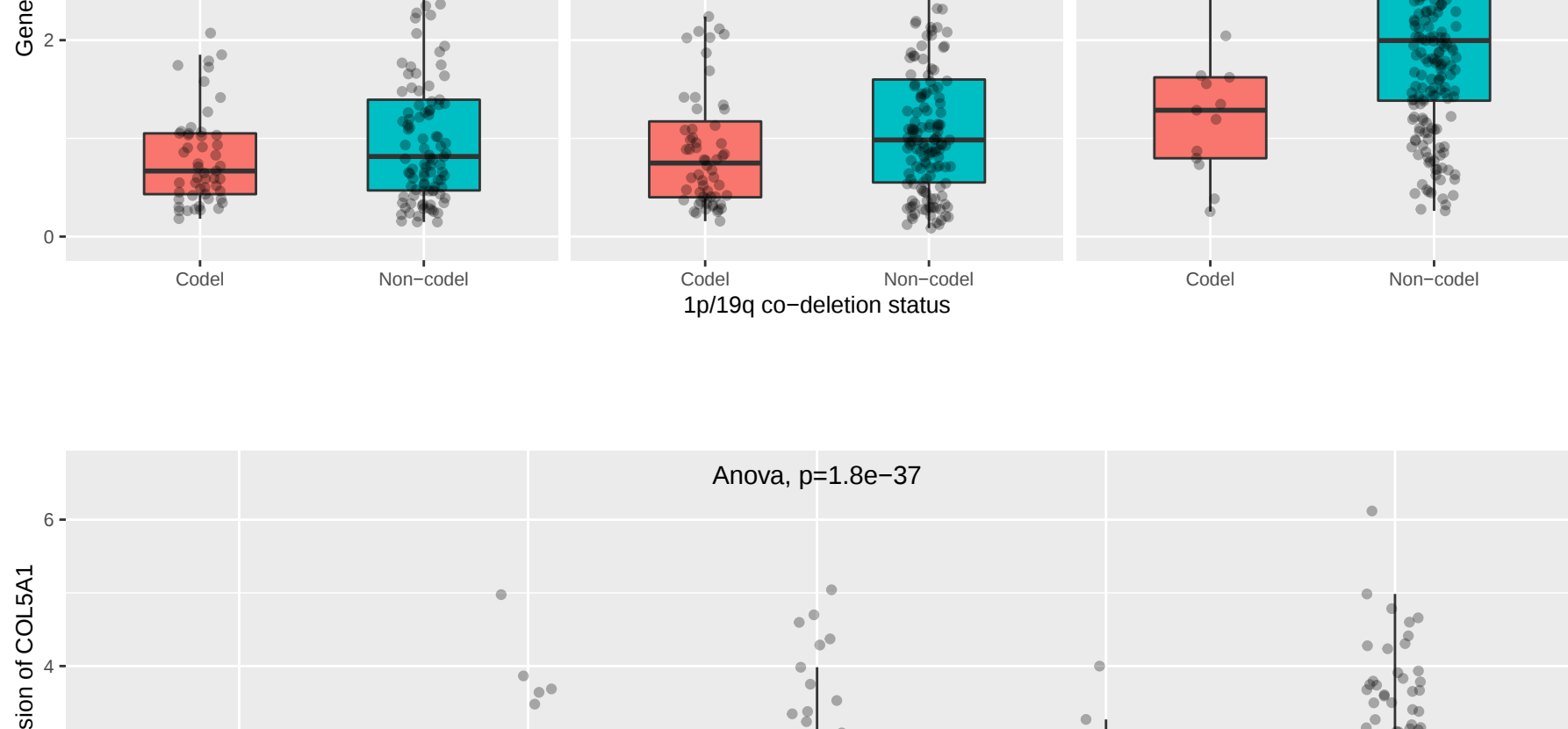
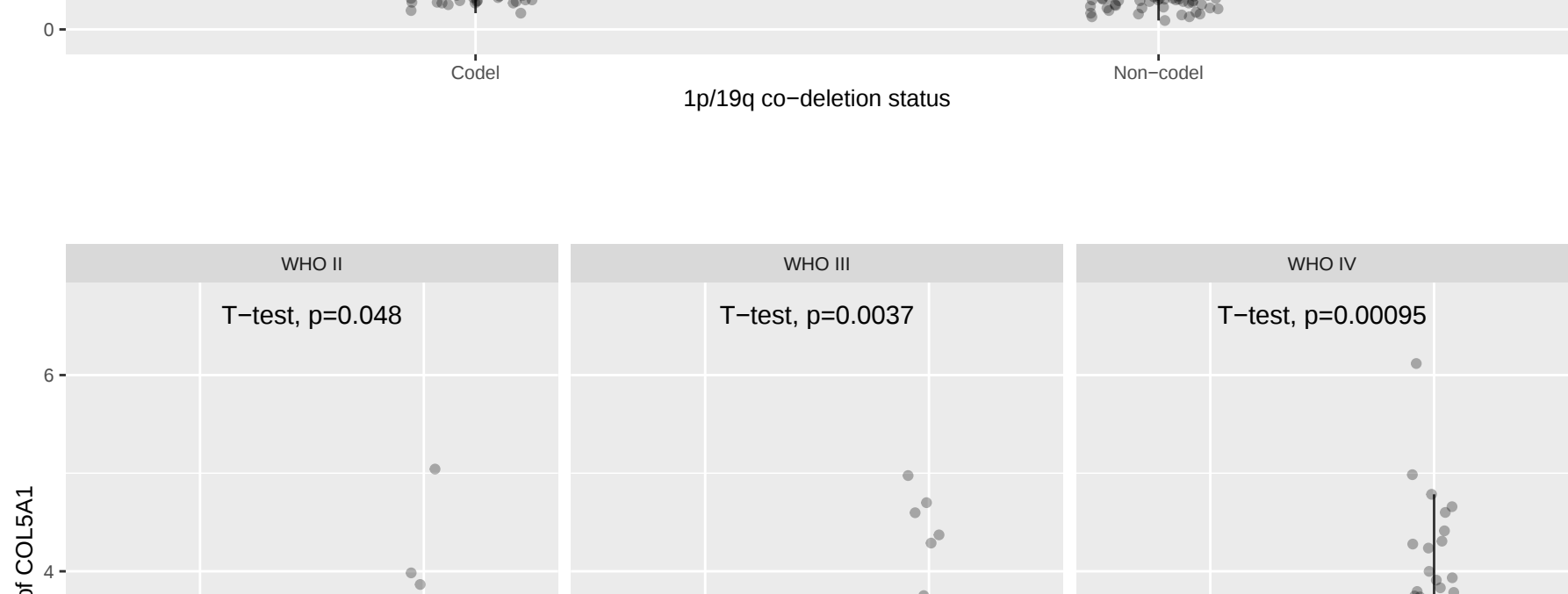
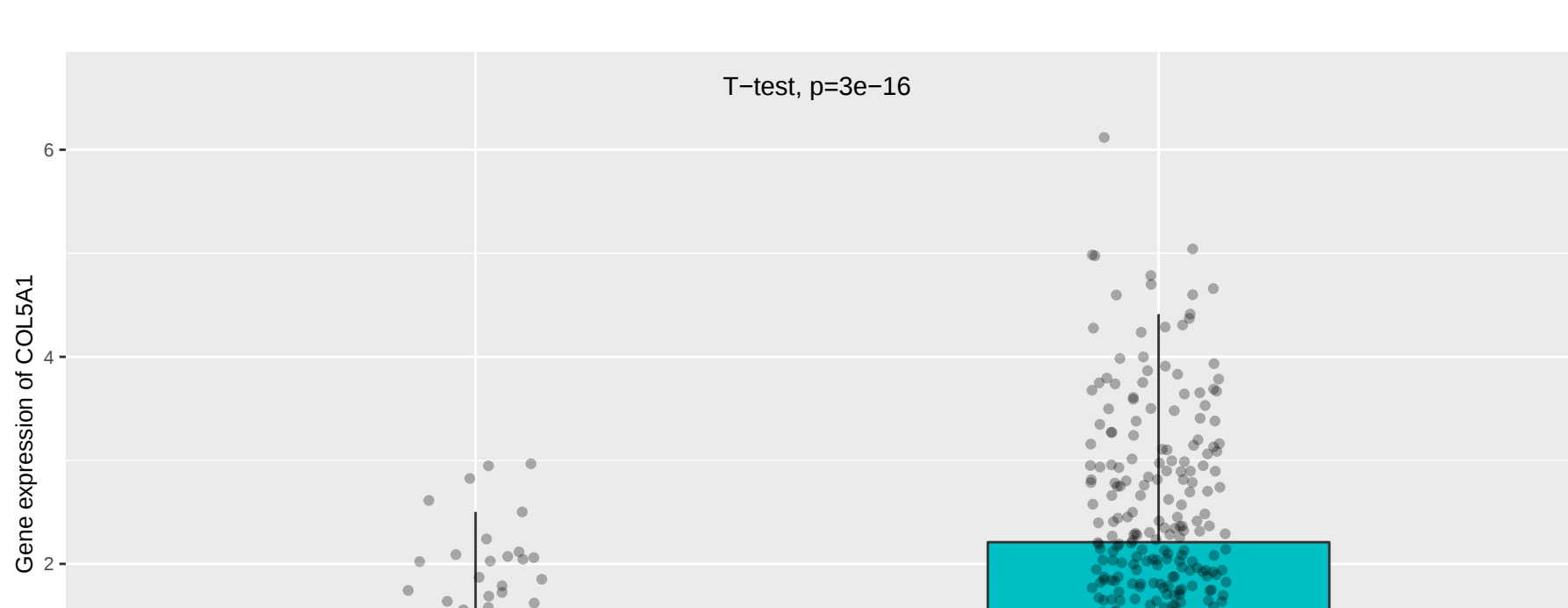
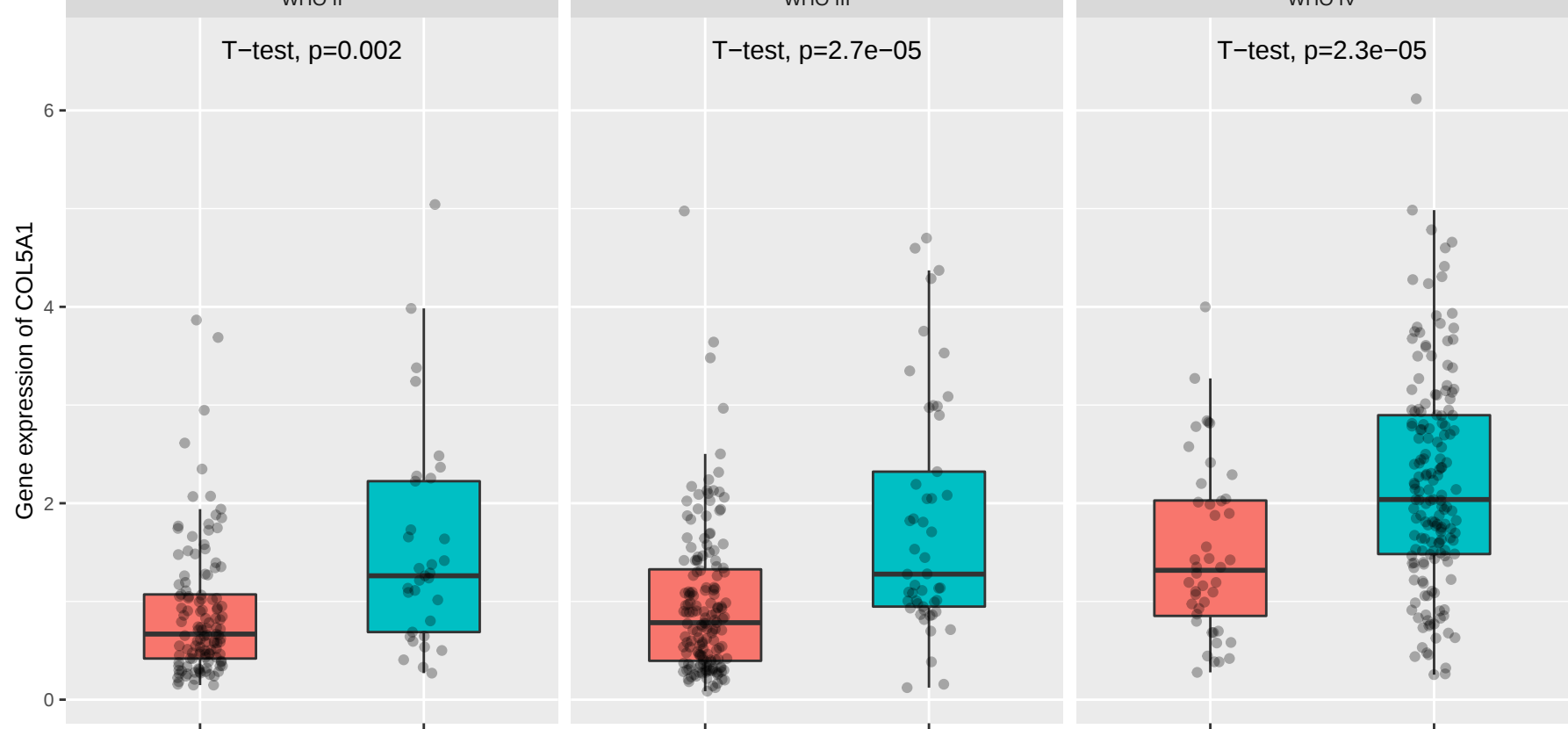
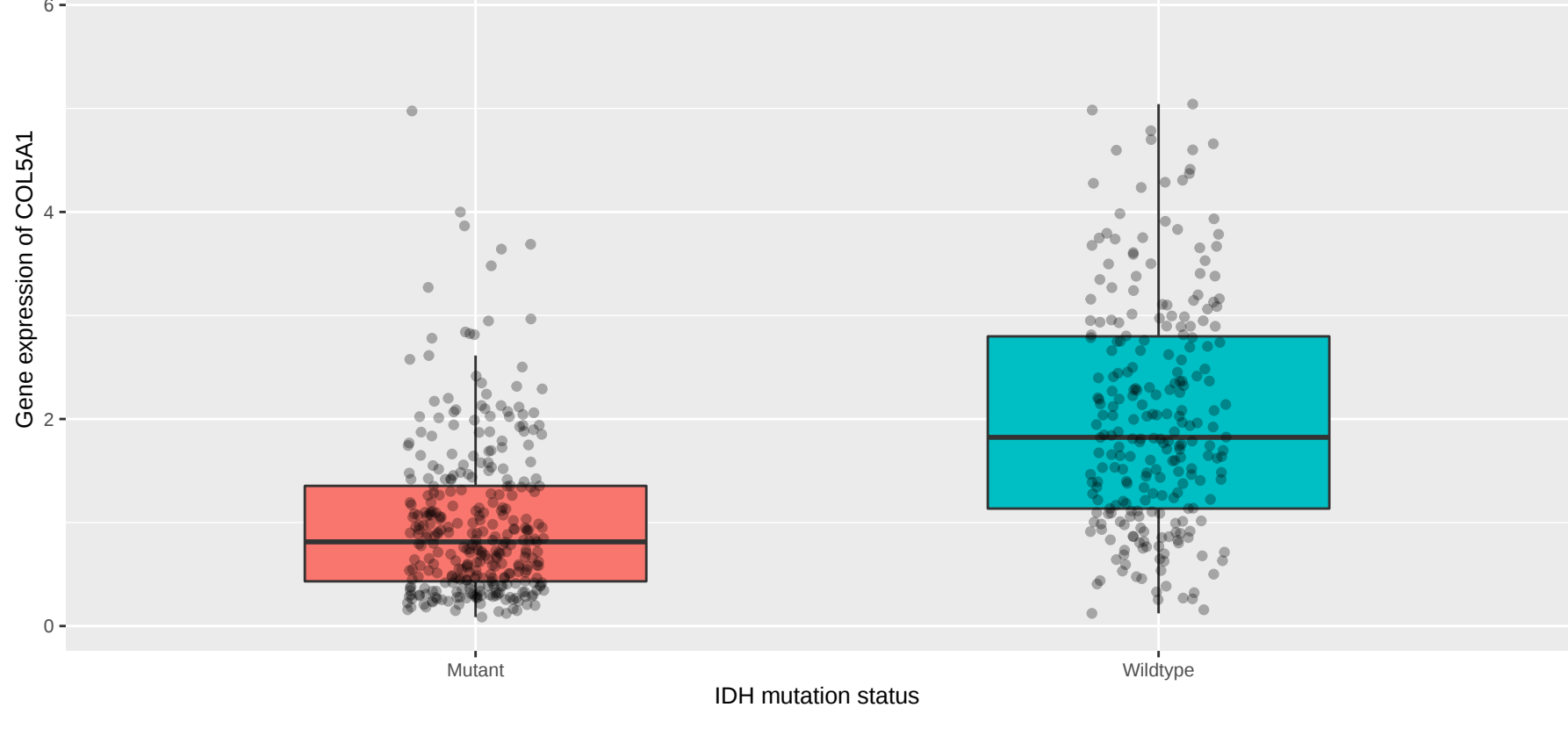
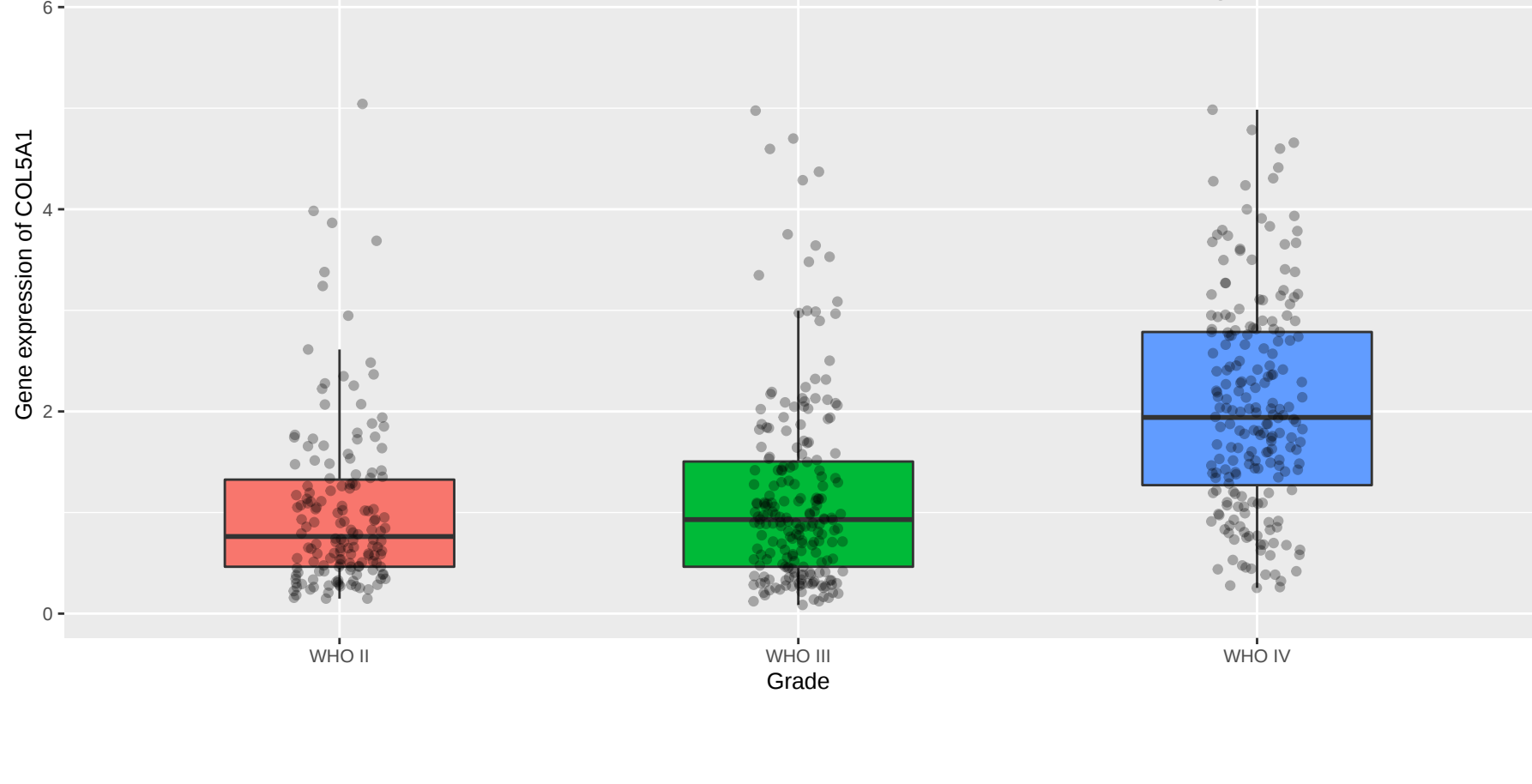
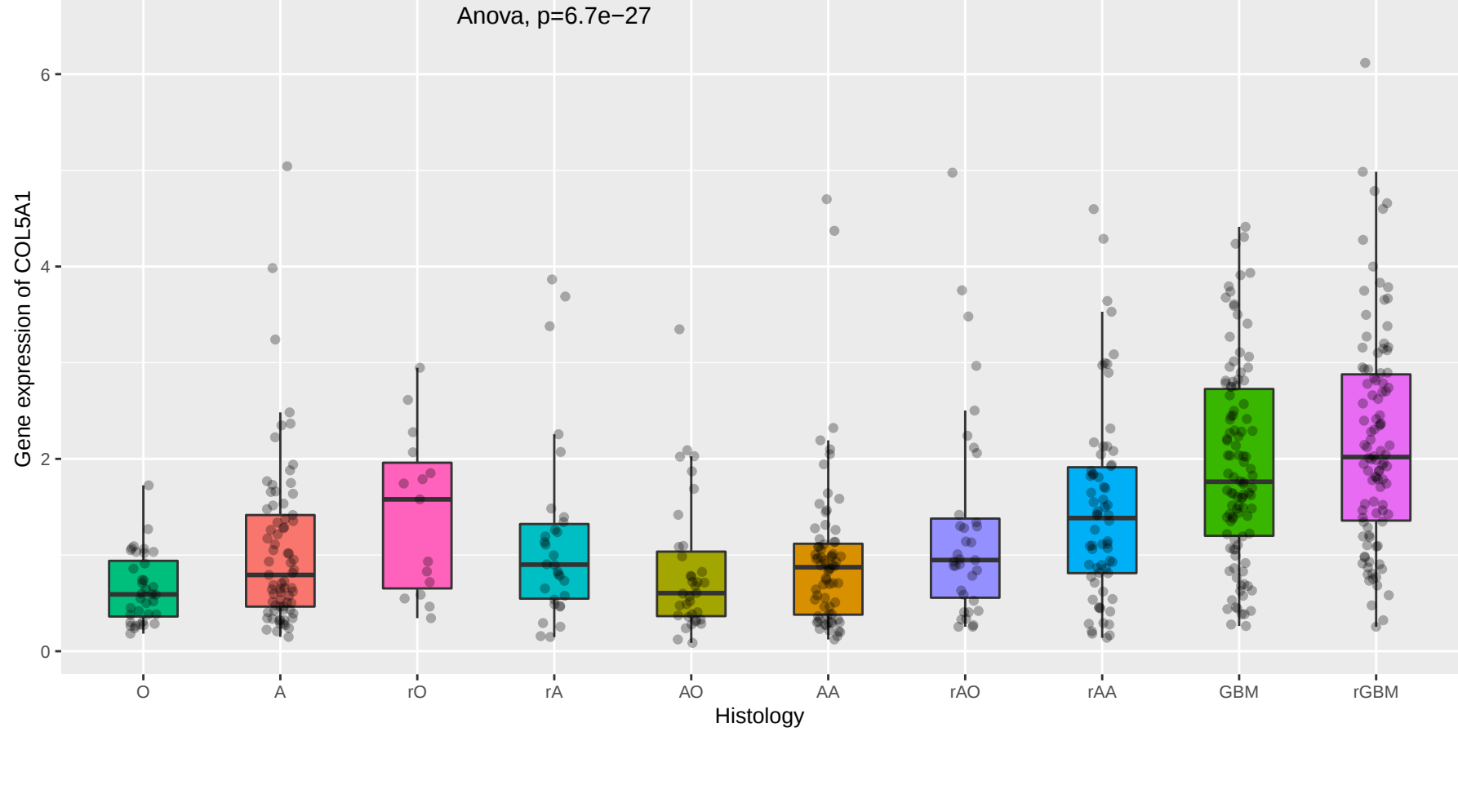


Figure S2:
COL5A1 expression analysis in CGGA



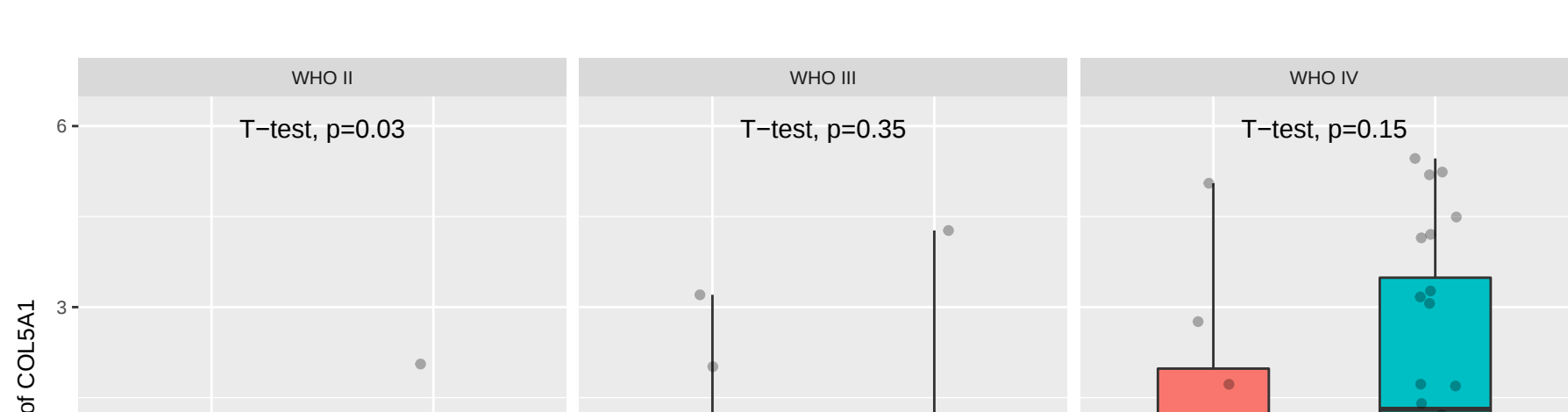
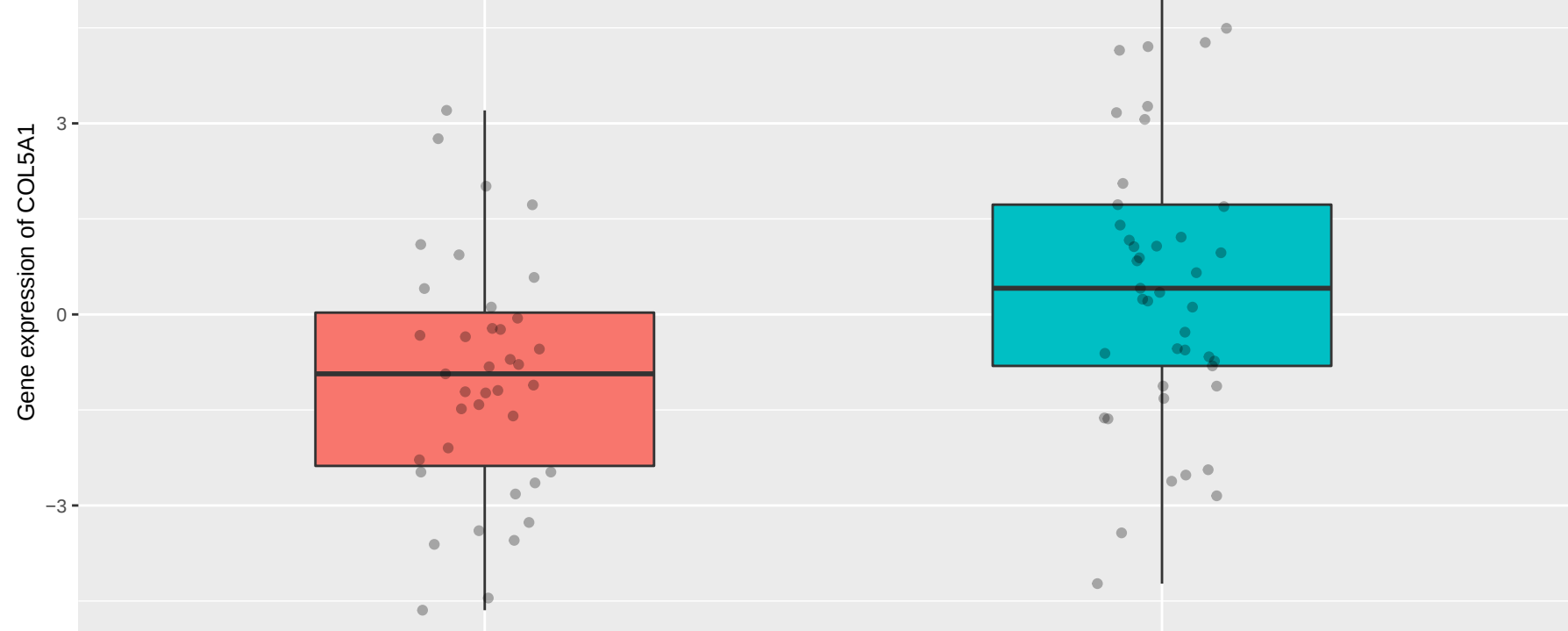
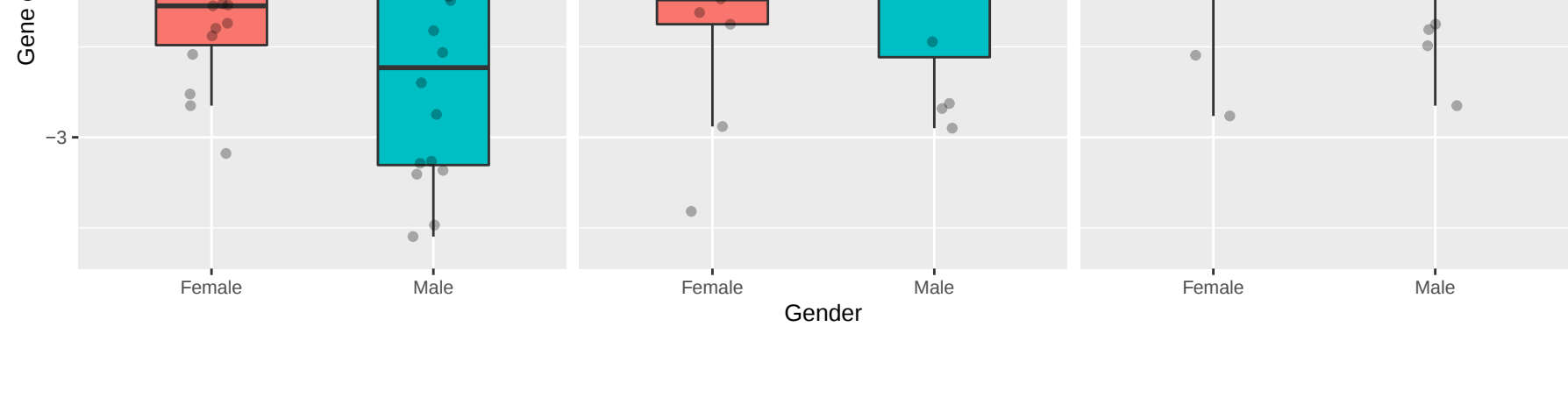
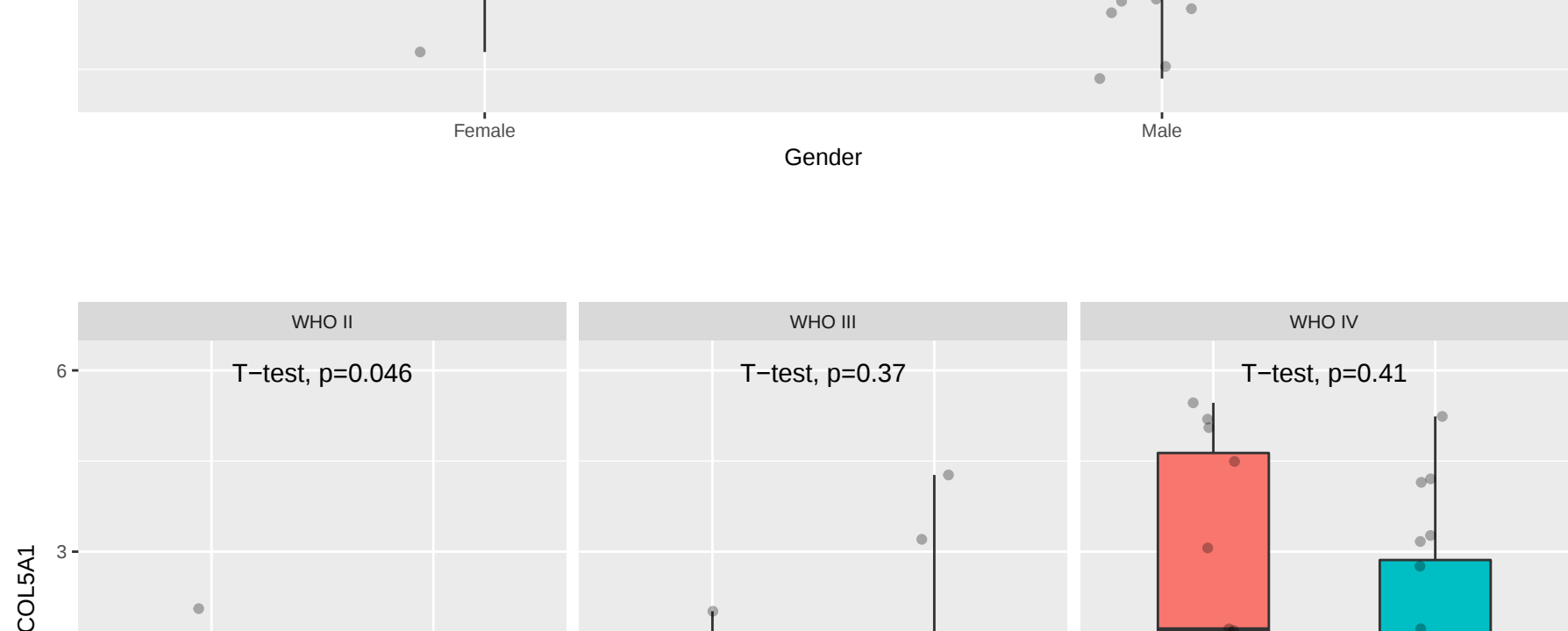
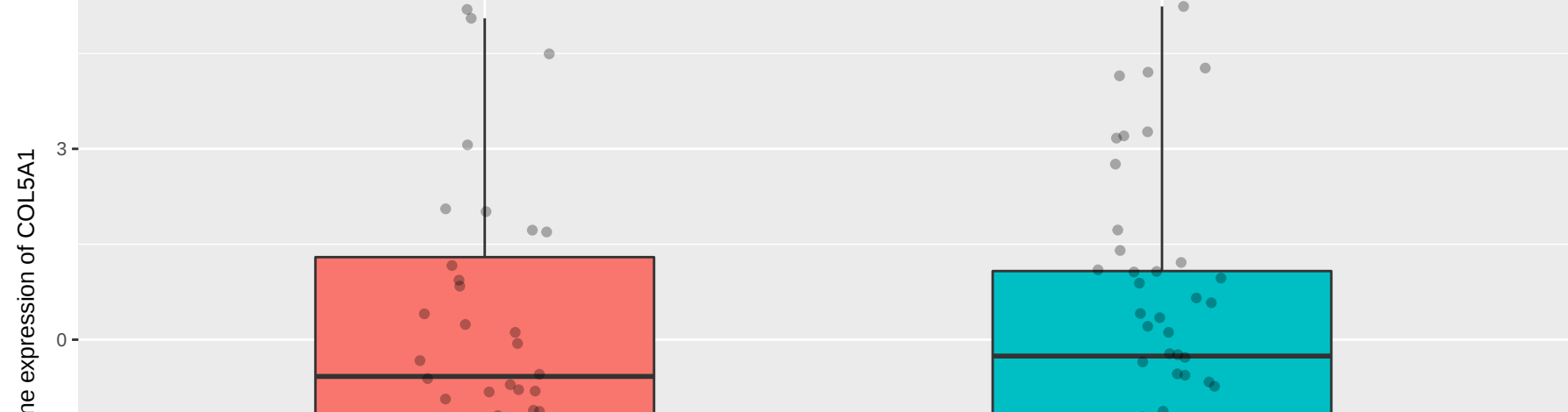
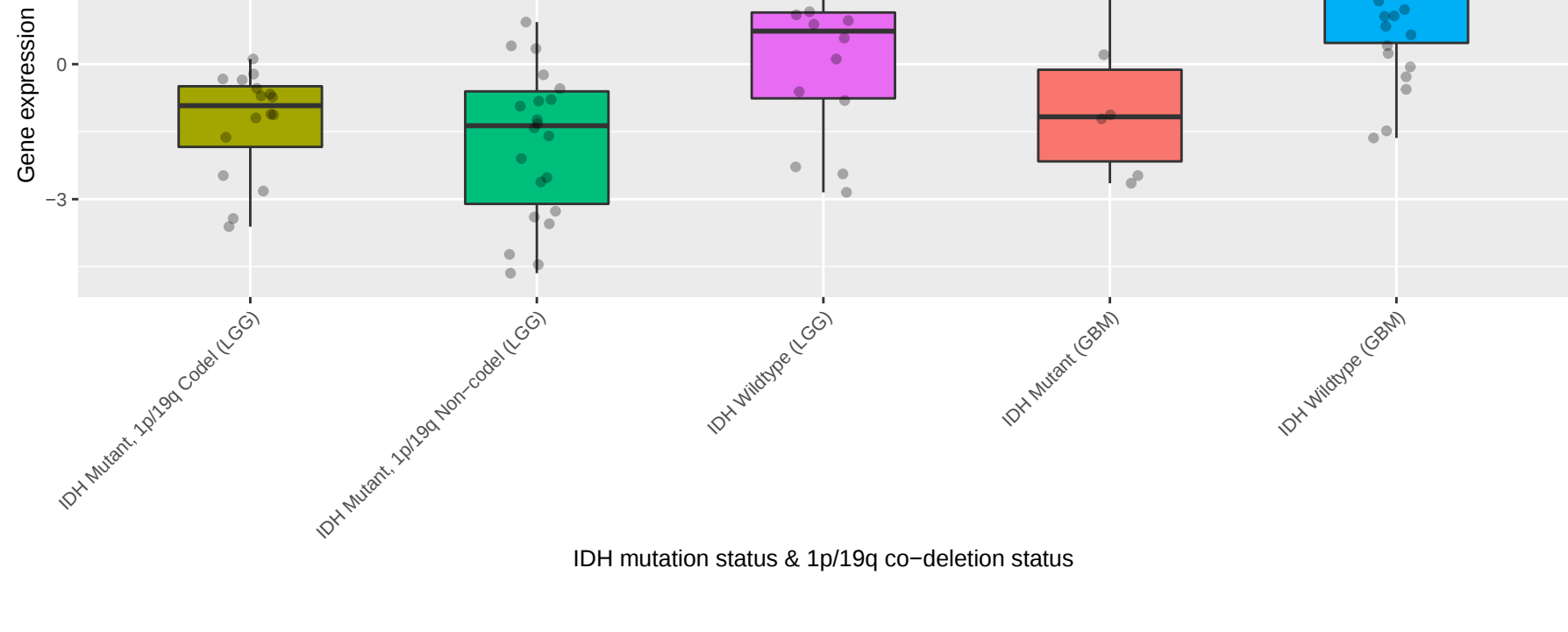
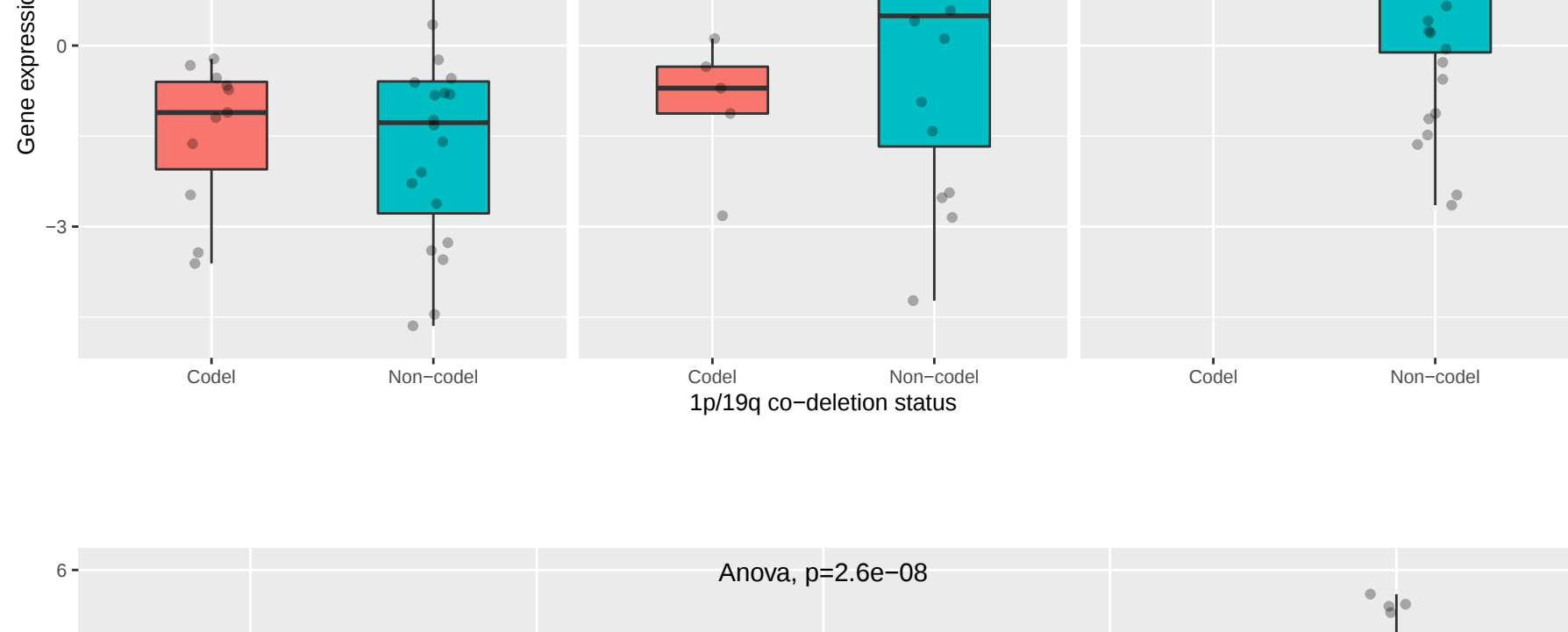
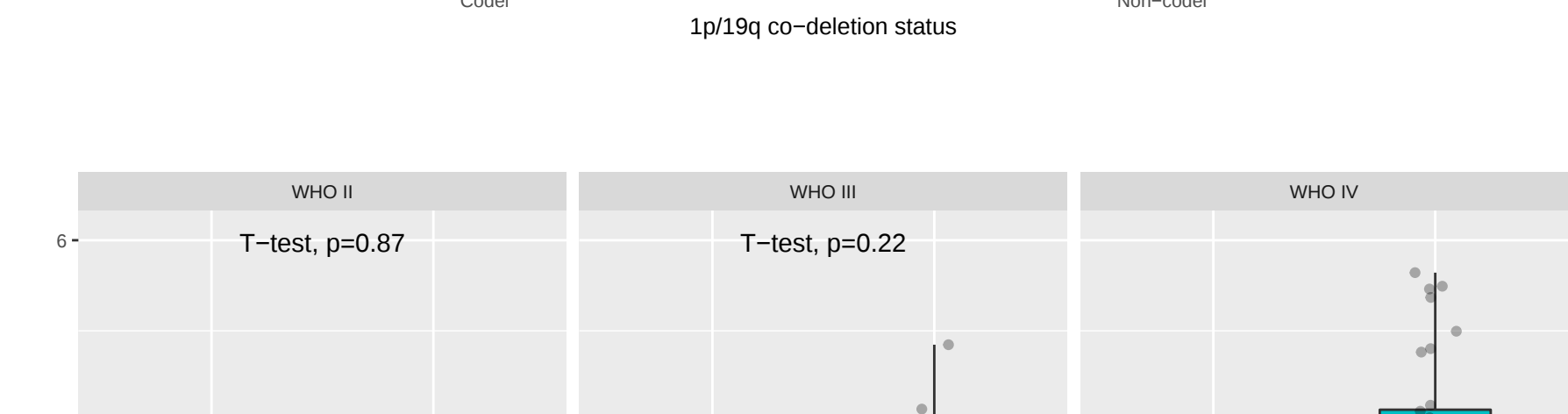
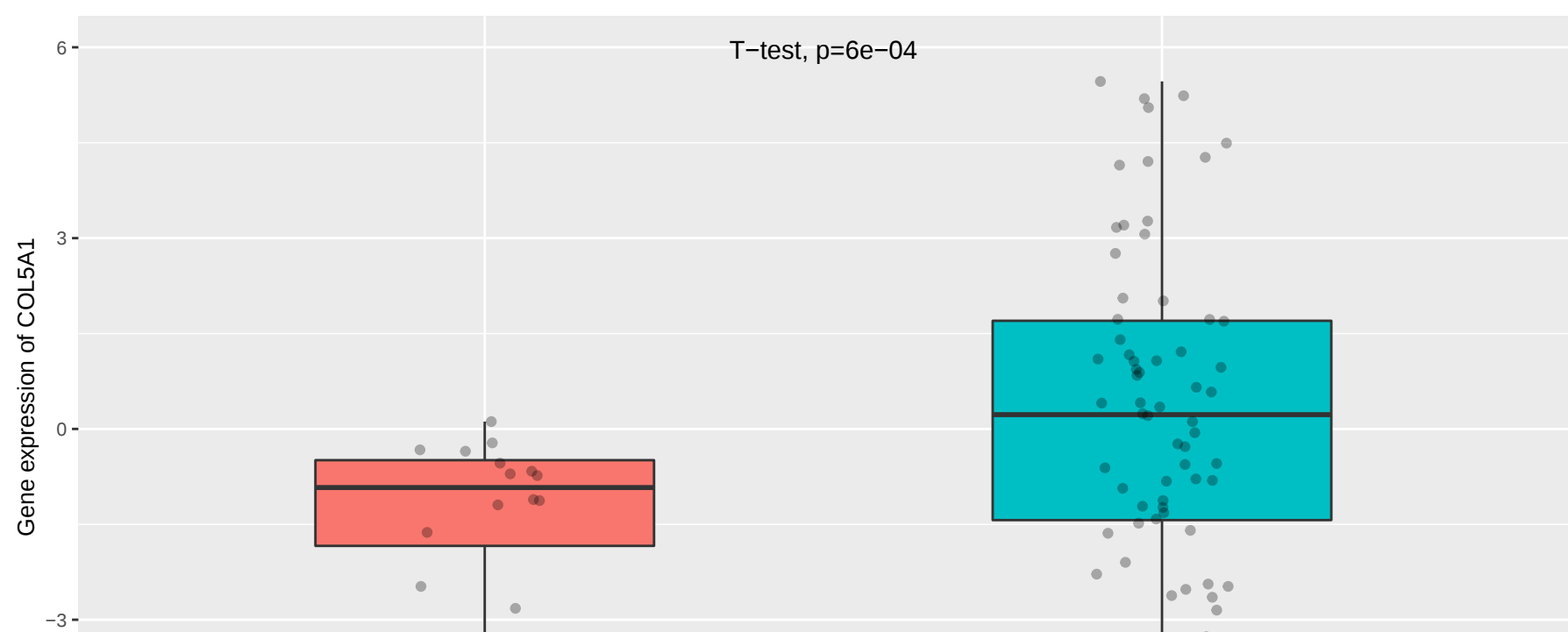
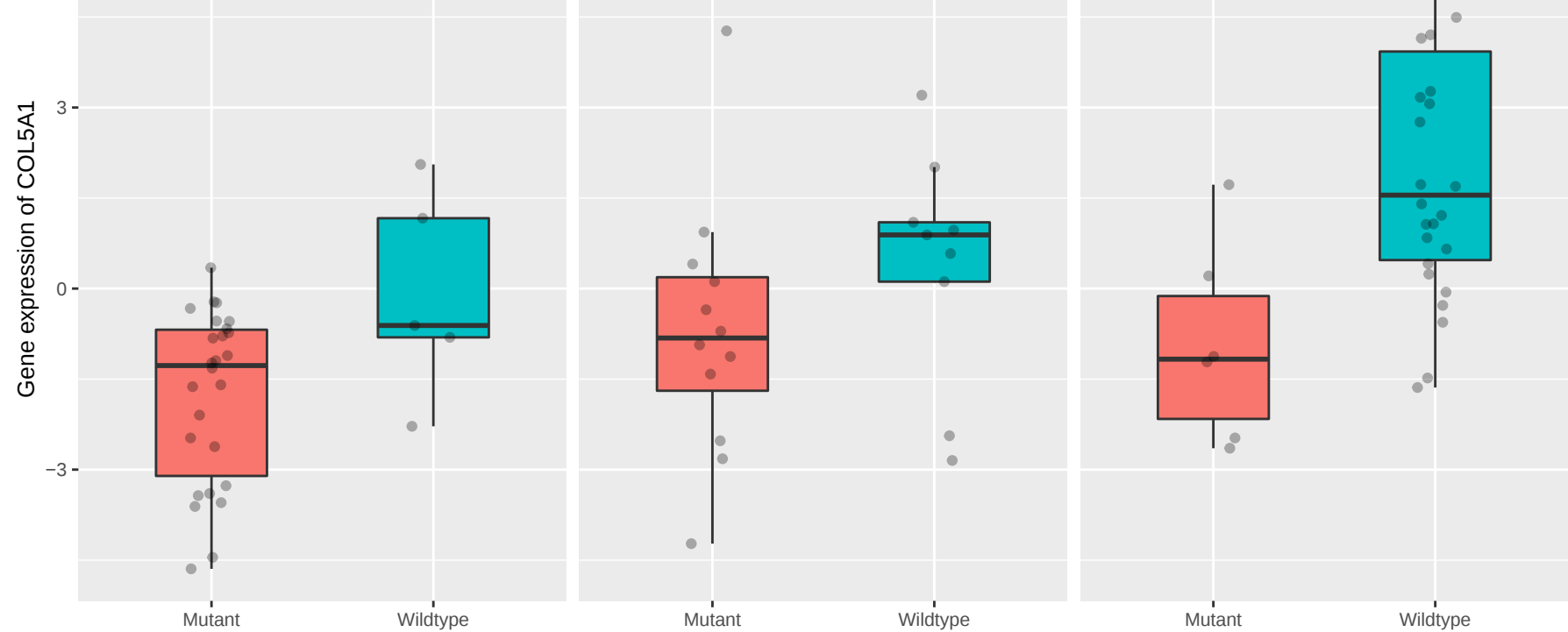
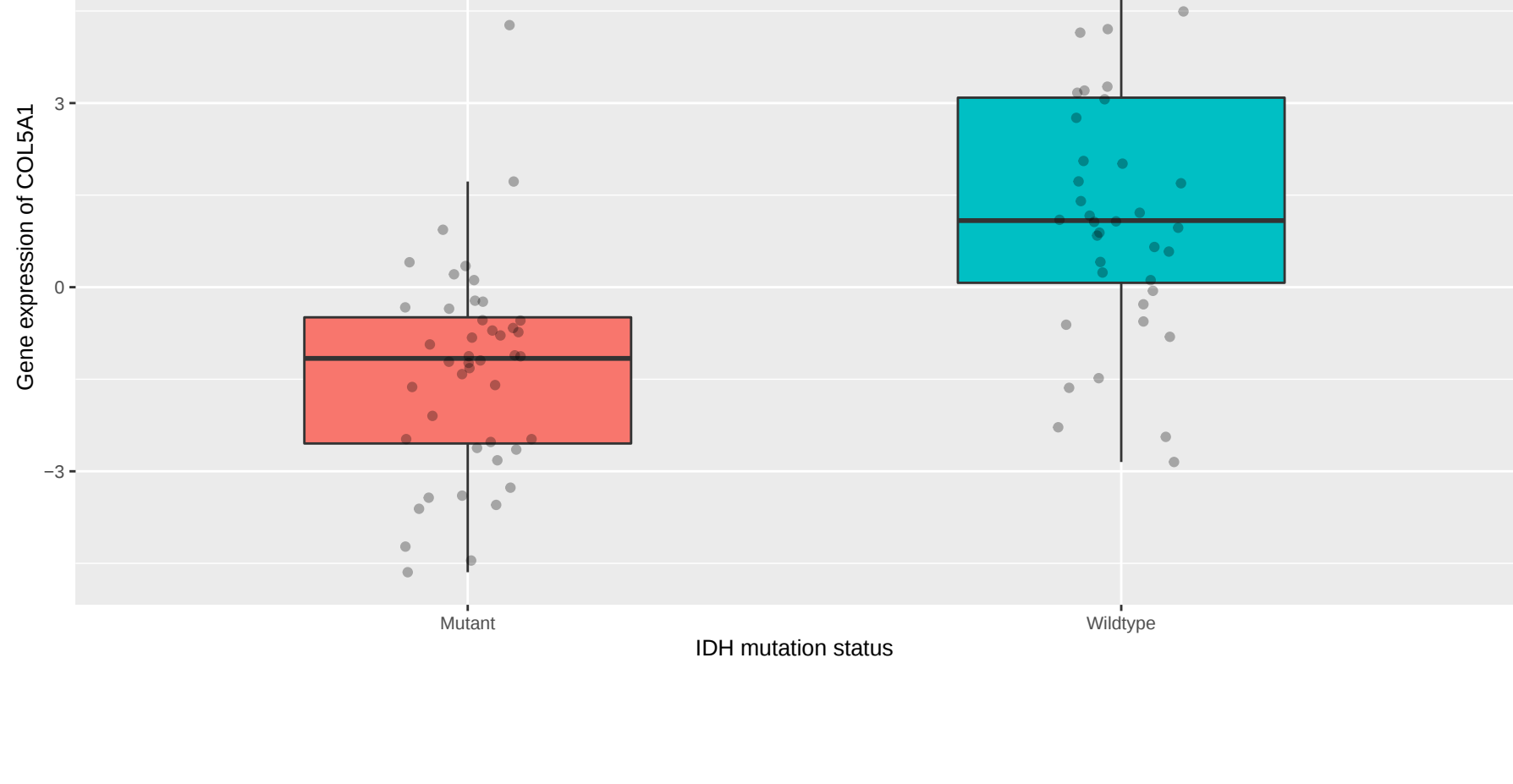
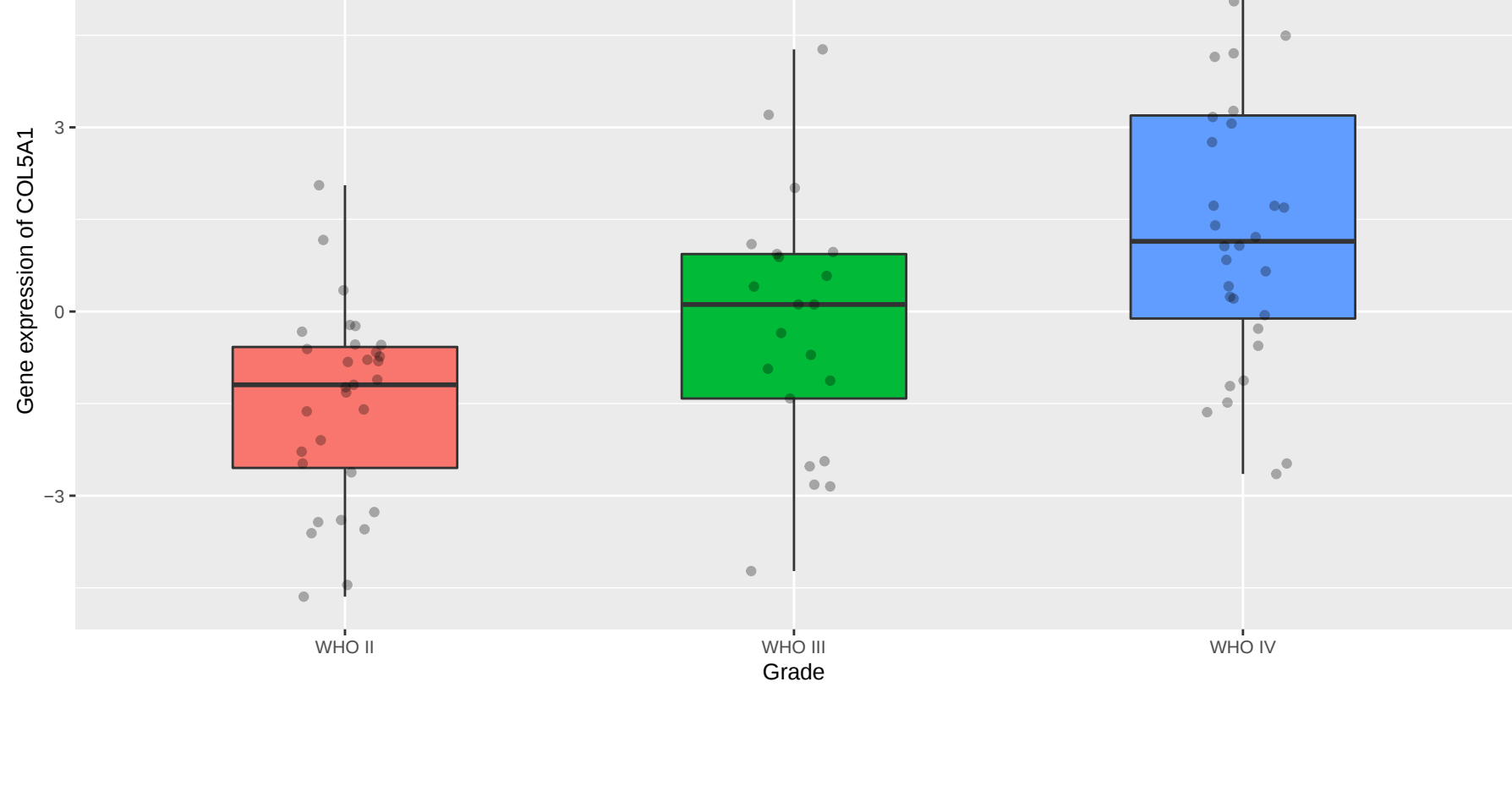
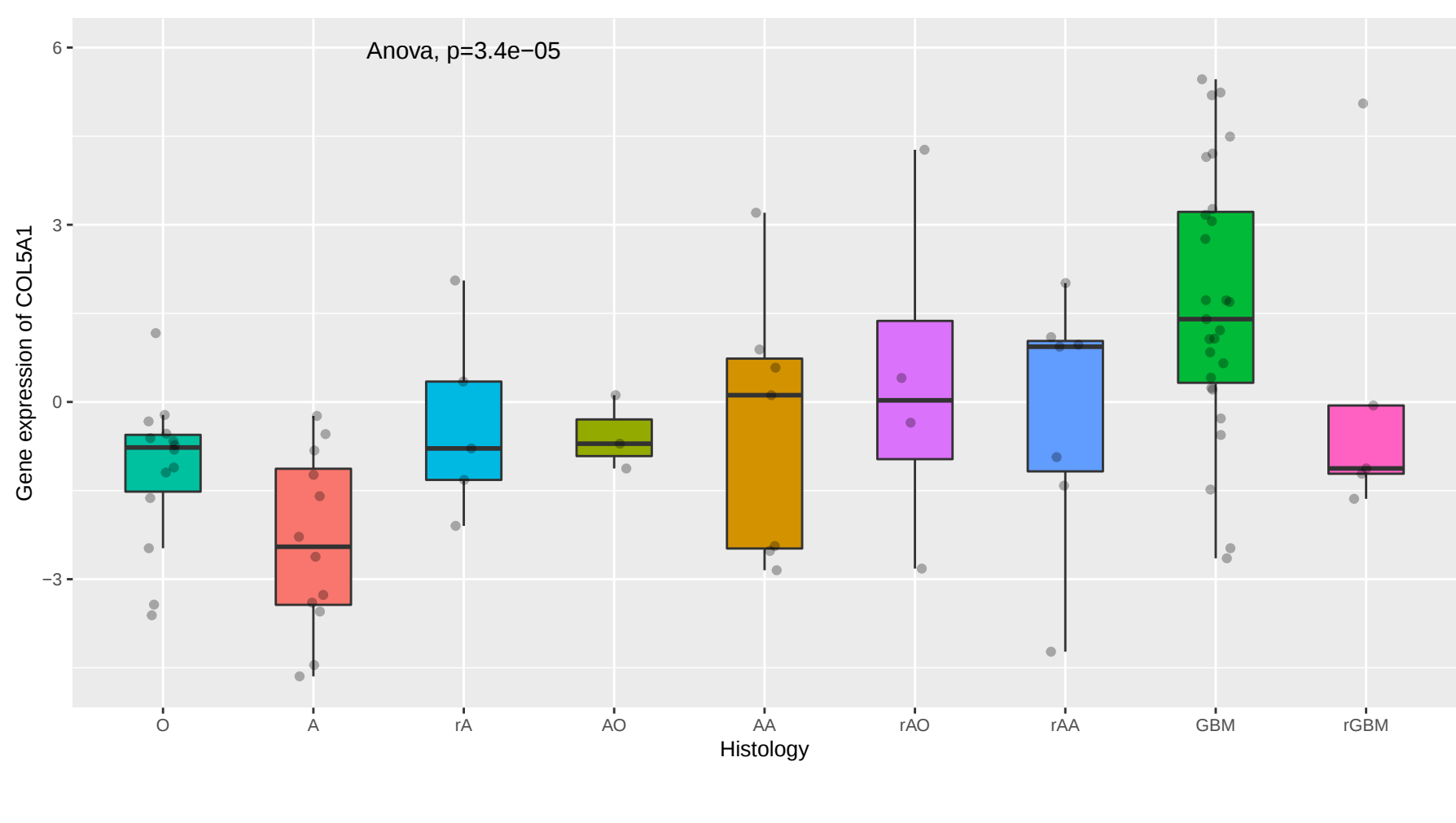
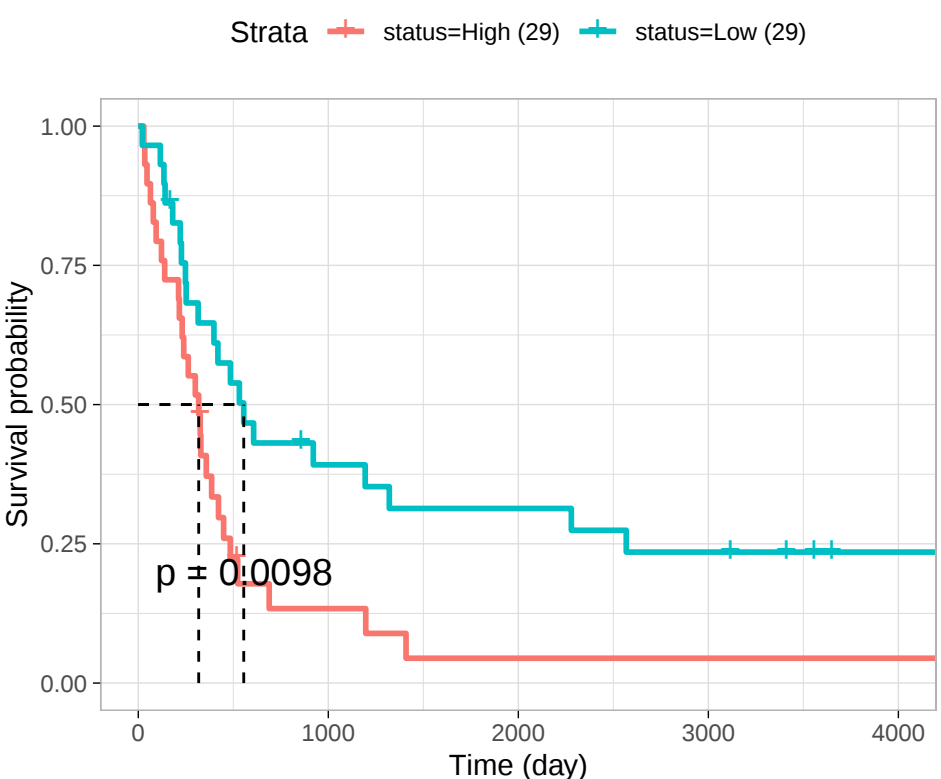
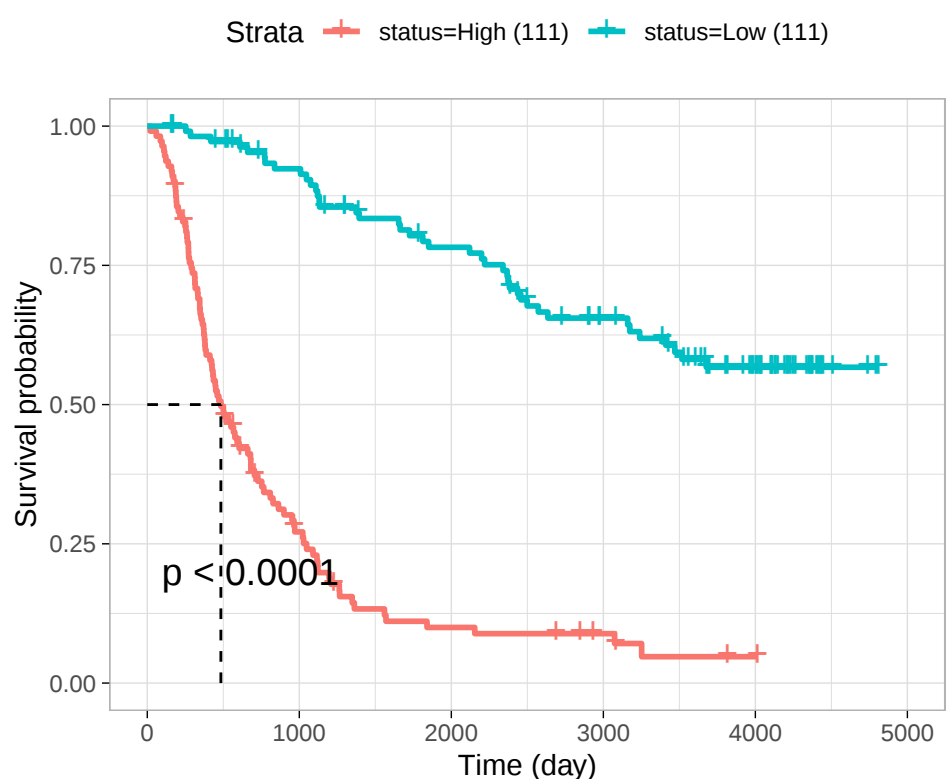


Figure S3:
SERPINH1 survival analysis in CGGA

All WHO grade survival (primary glioma)

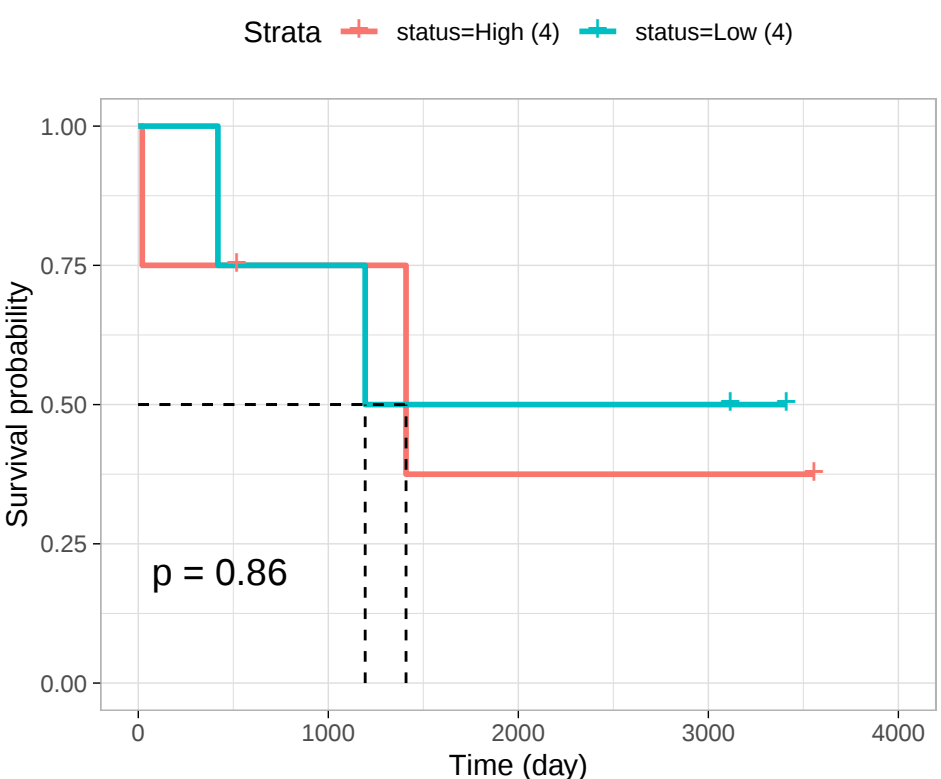
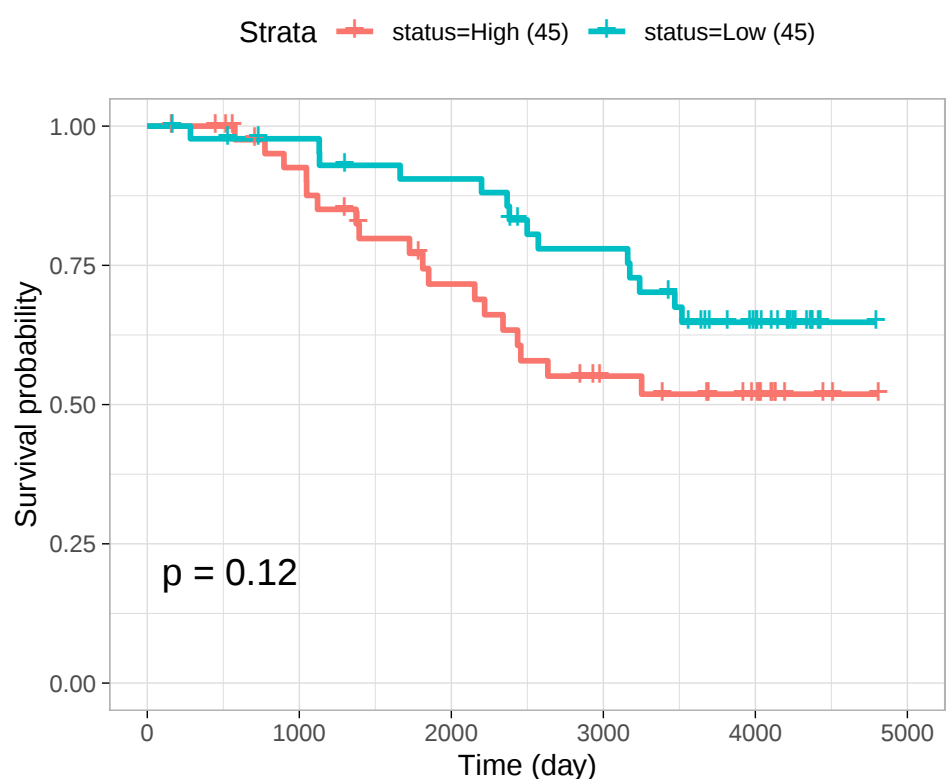
mRNAseq_325

All WHO grade survival (recurrent glioma)



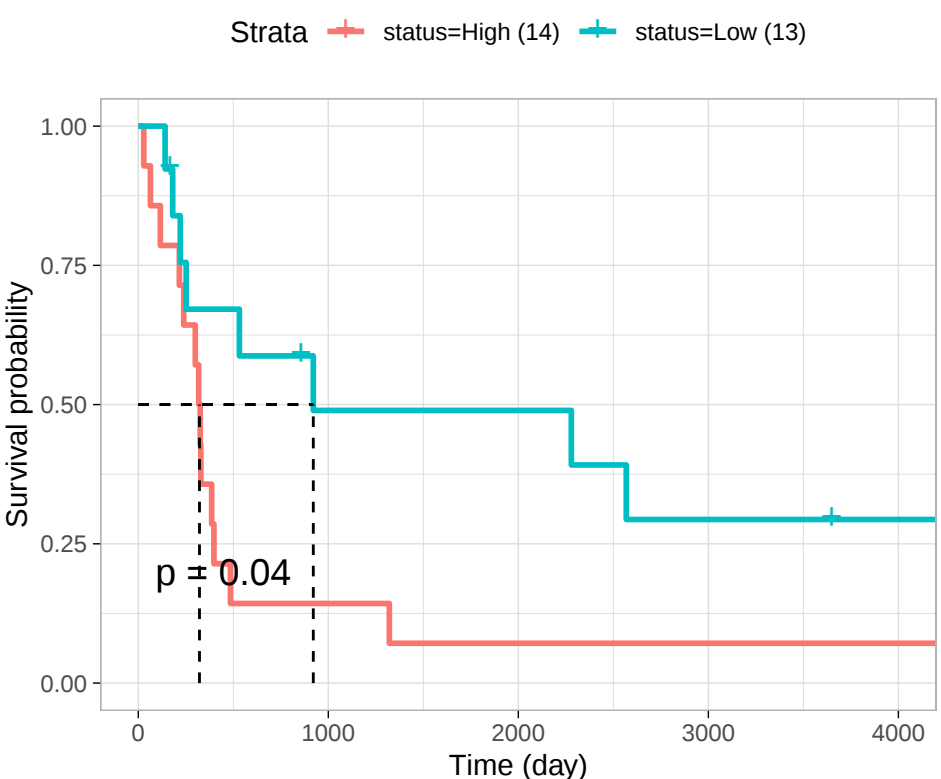
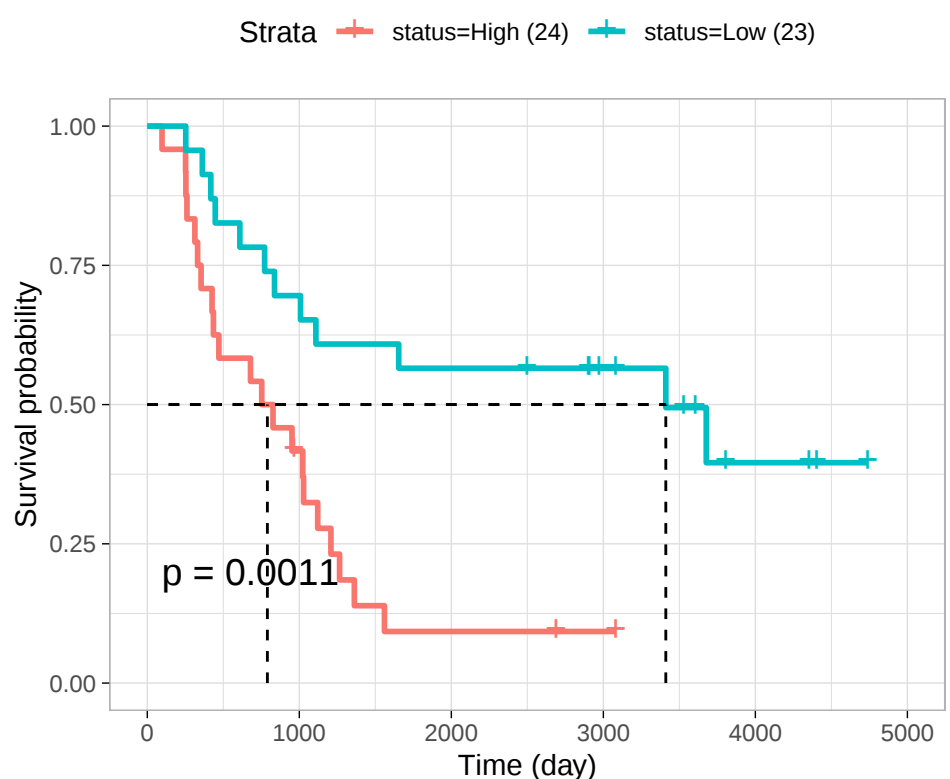
WHO grade II survival (primary glioma)

WHO grade II survival (recurrent glioma)



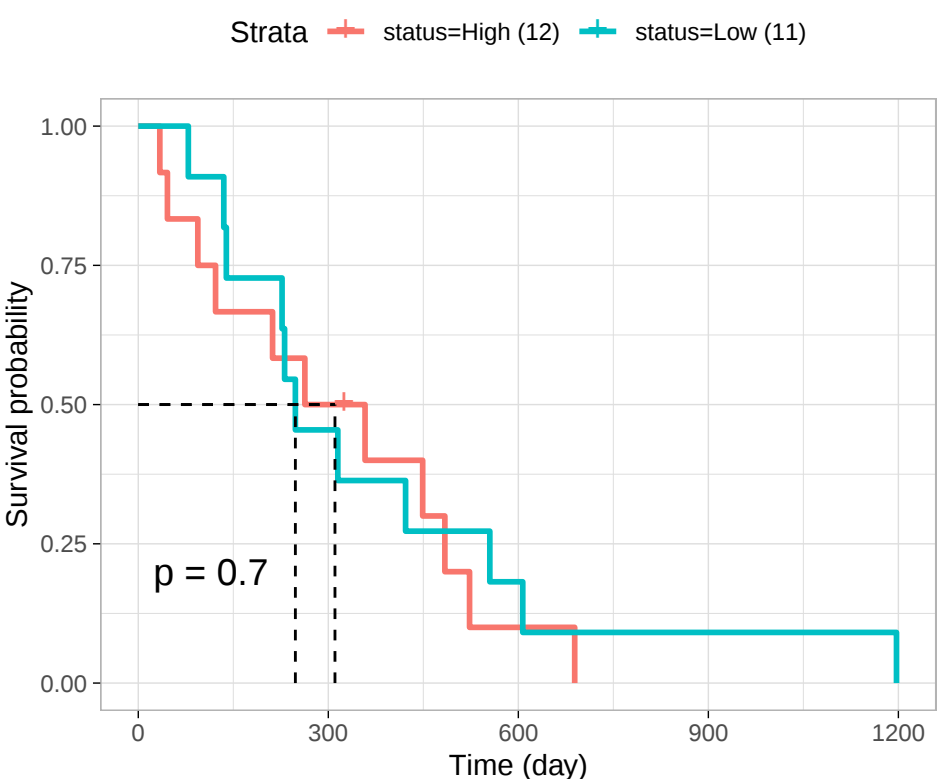
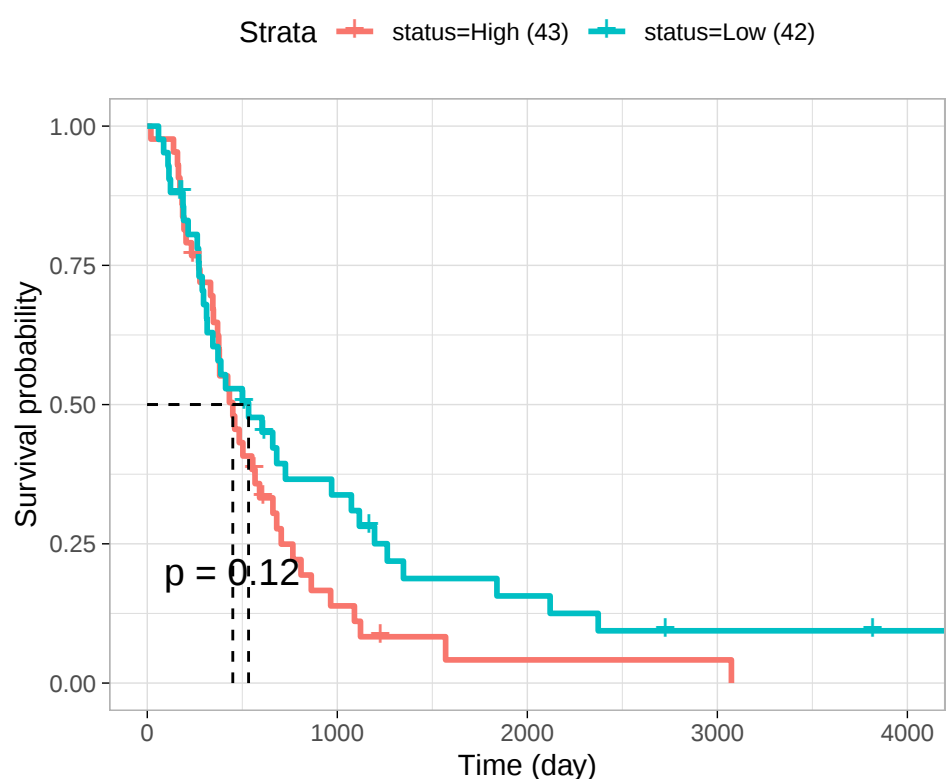
WHO grade III survival (primary glioma)

WHO grade III survival (recurrent glioma)



WHO grade IV survival (primary glioma)

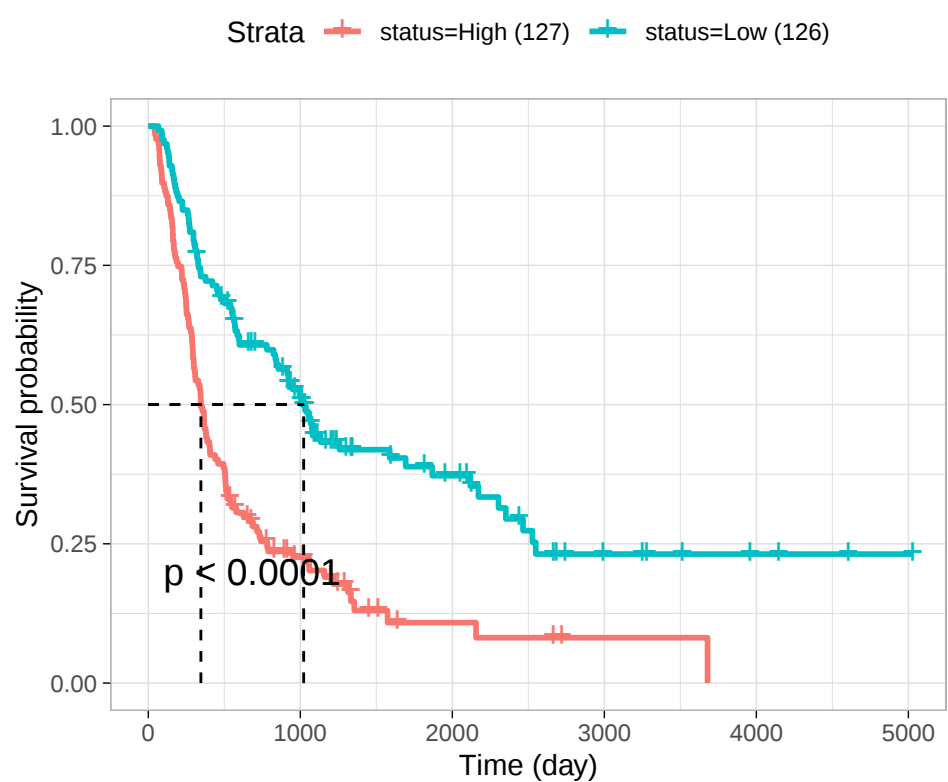
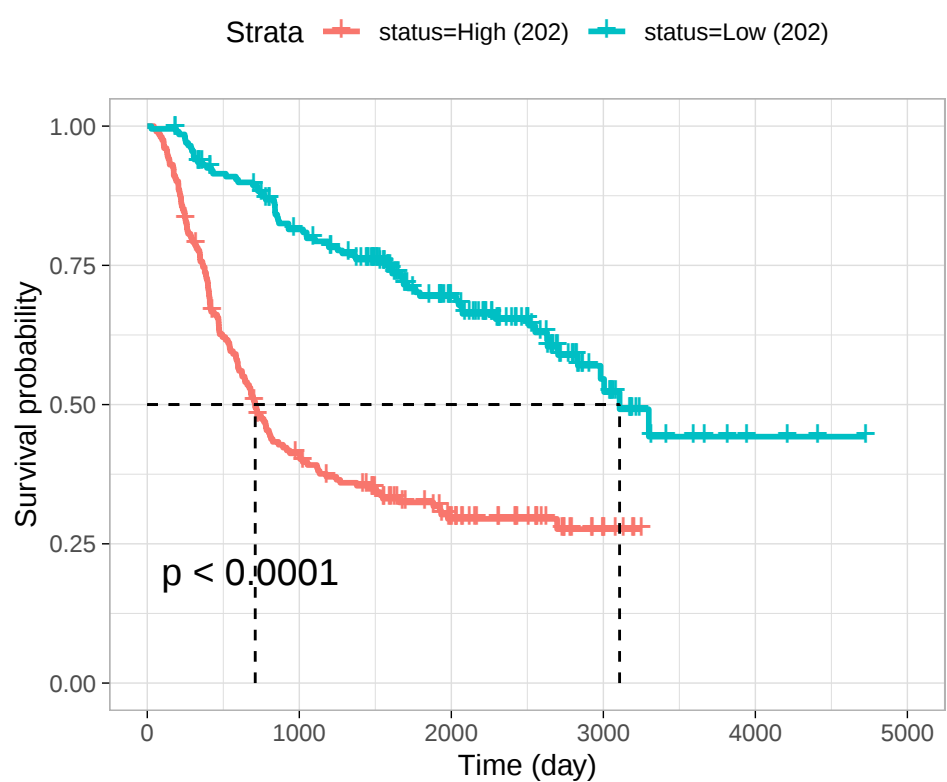
WHO grade IV survival (recurrent glioma)



All WHO grade survival (primary glioma)

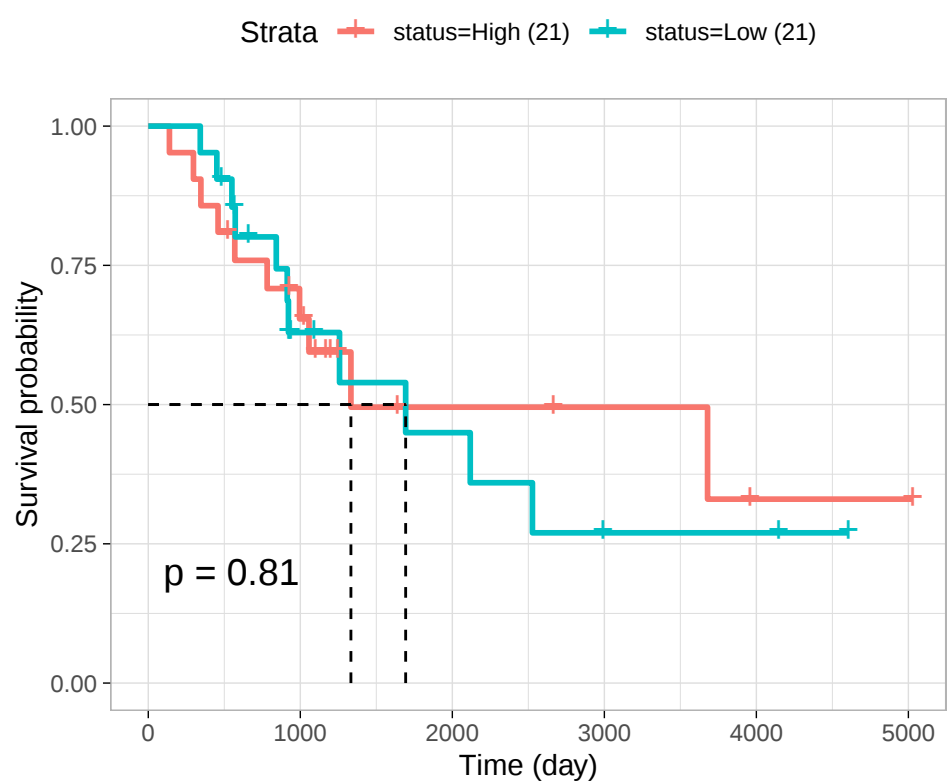
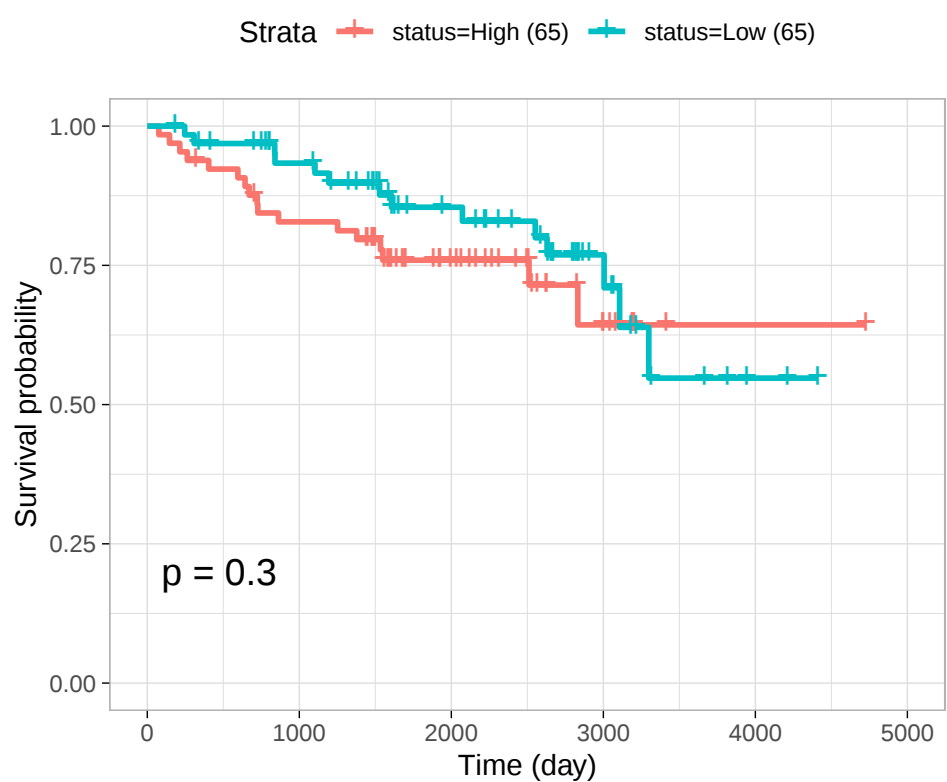
mRNAseq_693

All WHO grade survival (recurrent glioma)



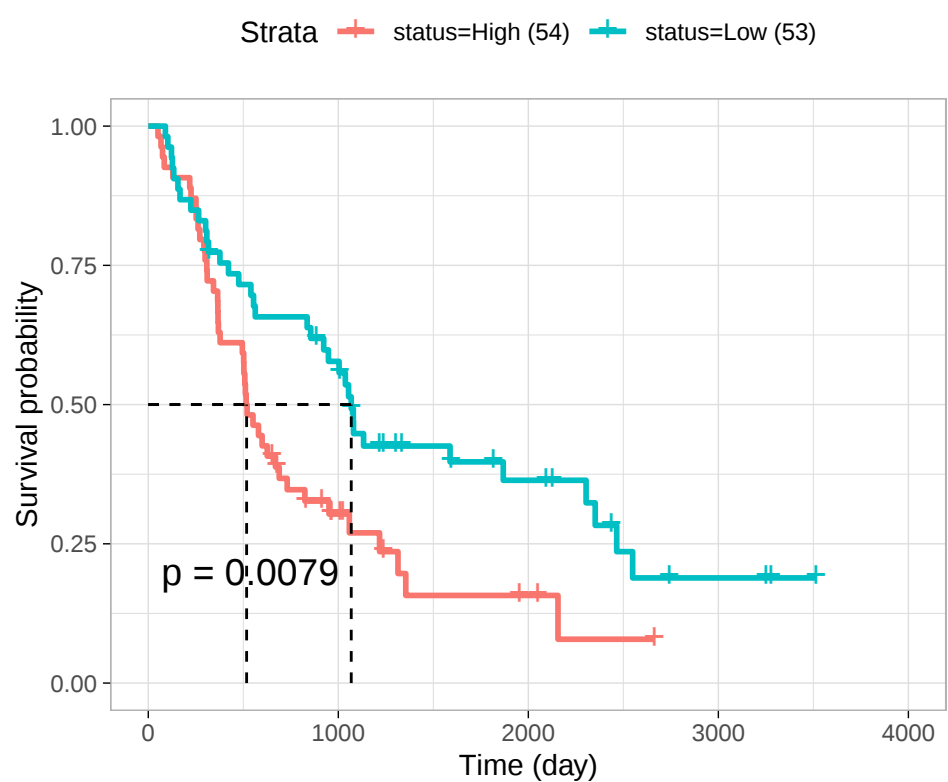
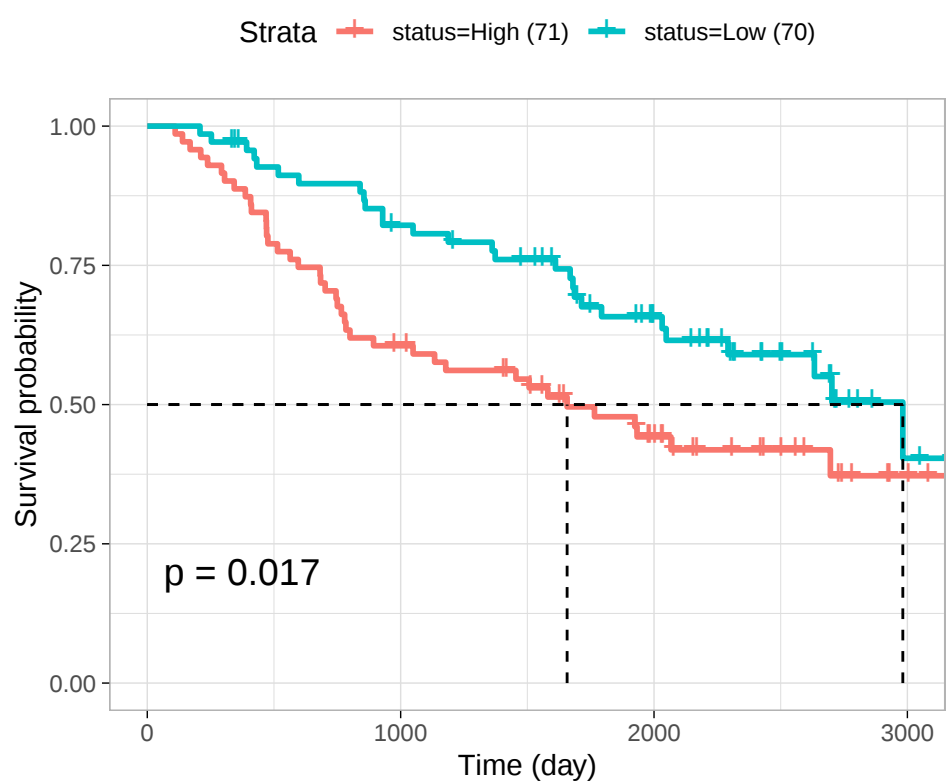
WHO grade II survival (primary glioma)

WHO grade II survival (recurrent glioma)



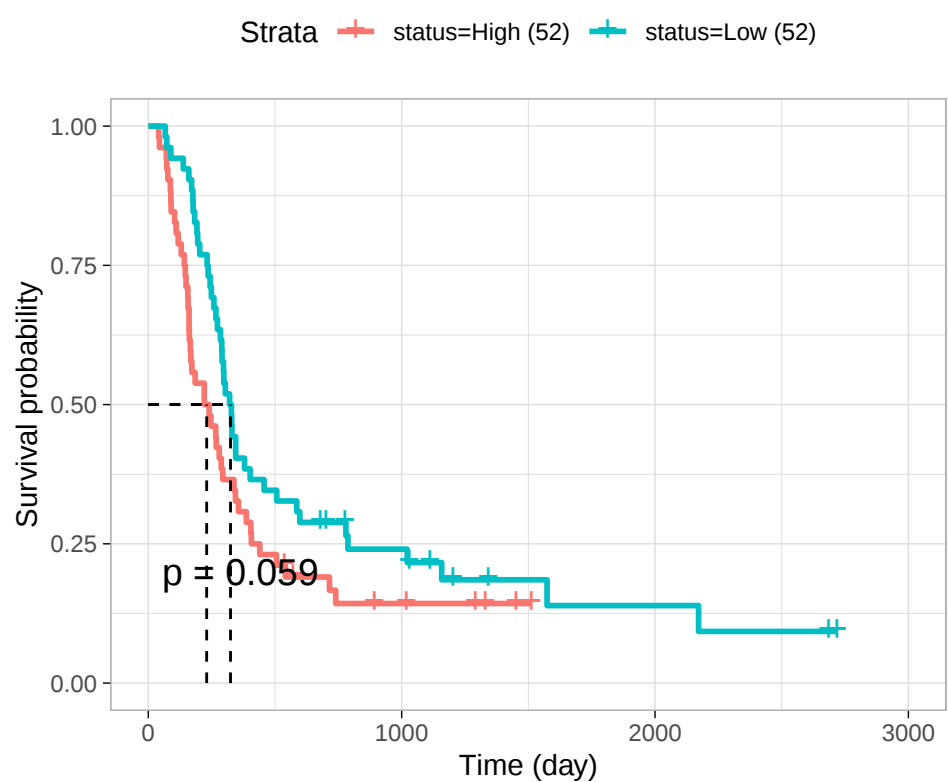
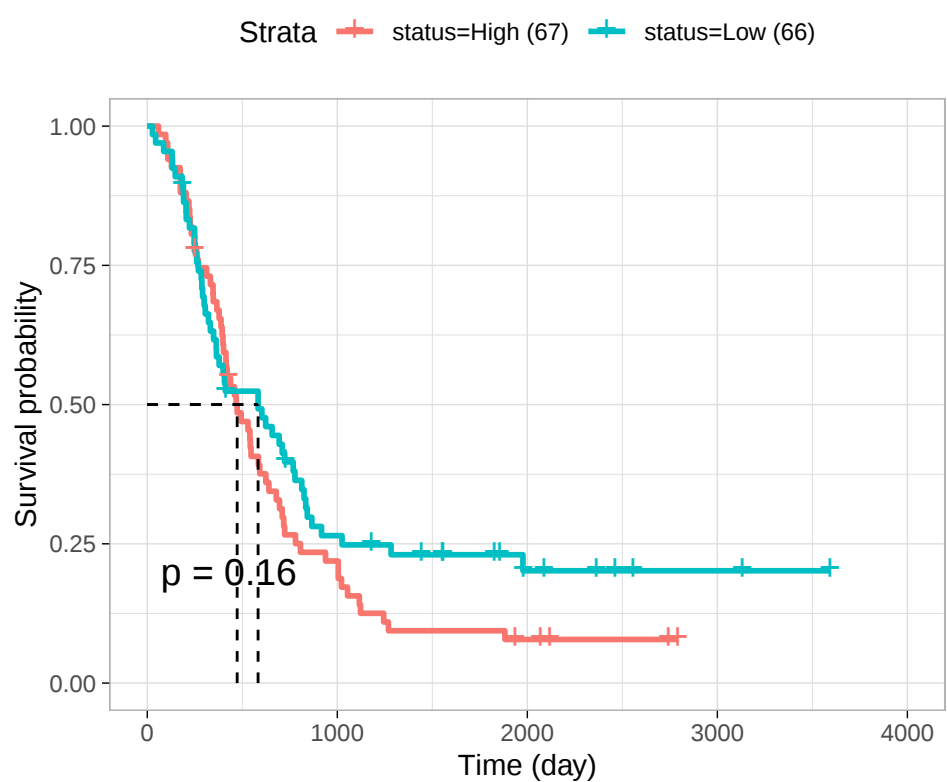
WHO grade III survival (primary glioma)

WHO grade III survival (recurrent glioma)

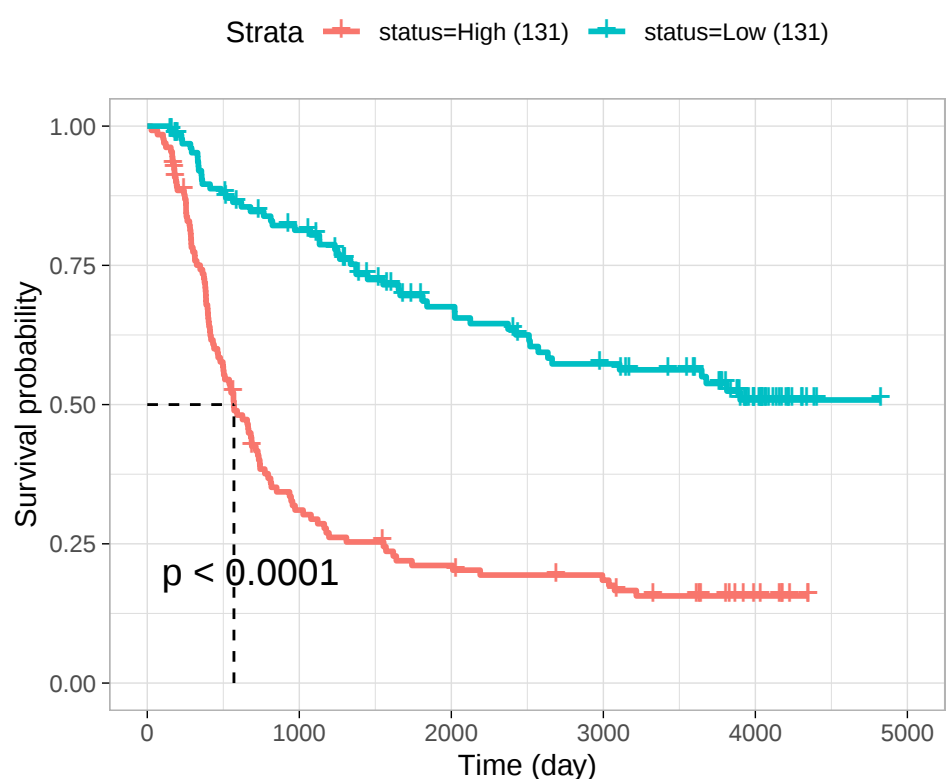


WHO grade IV survival (primary glioma)

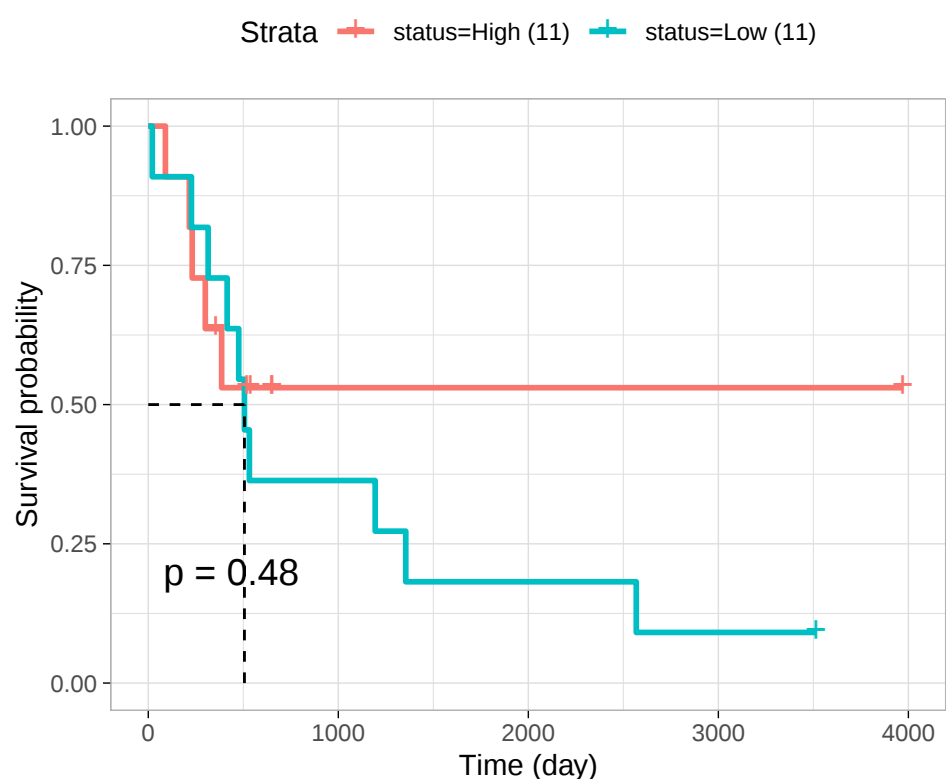
WHO grade IV survival (recurrent glioma)



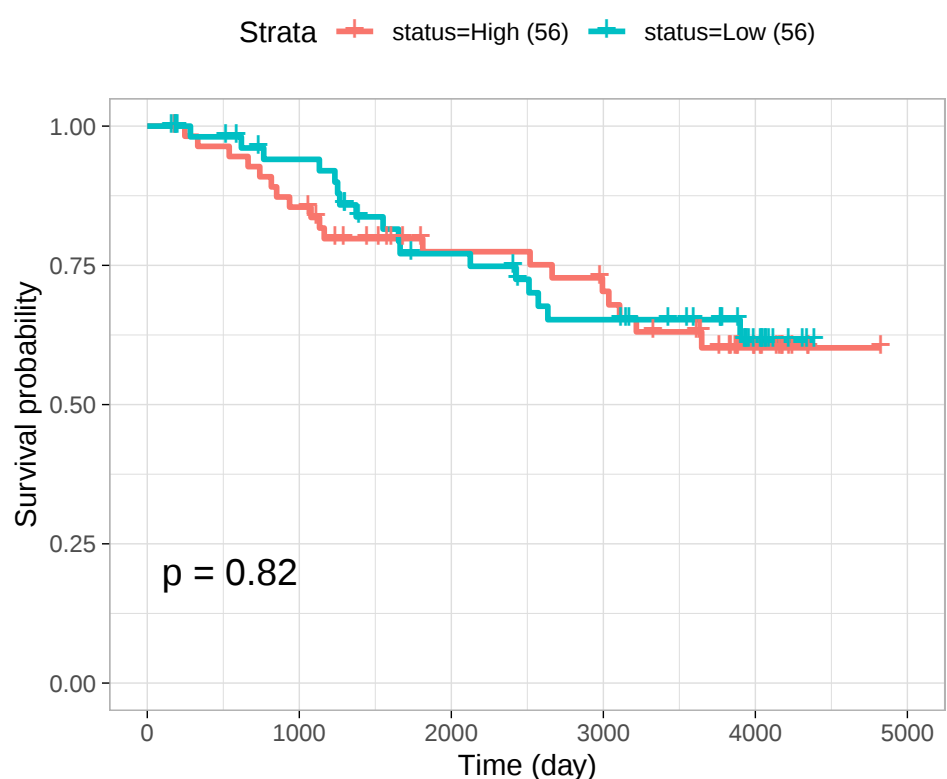
All WHO grade survival (primary glioma) mRNAseq_ary_301



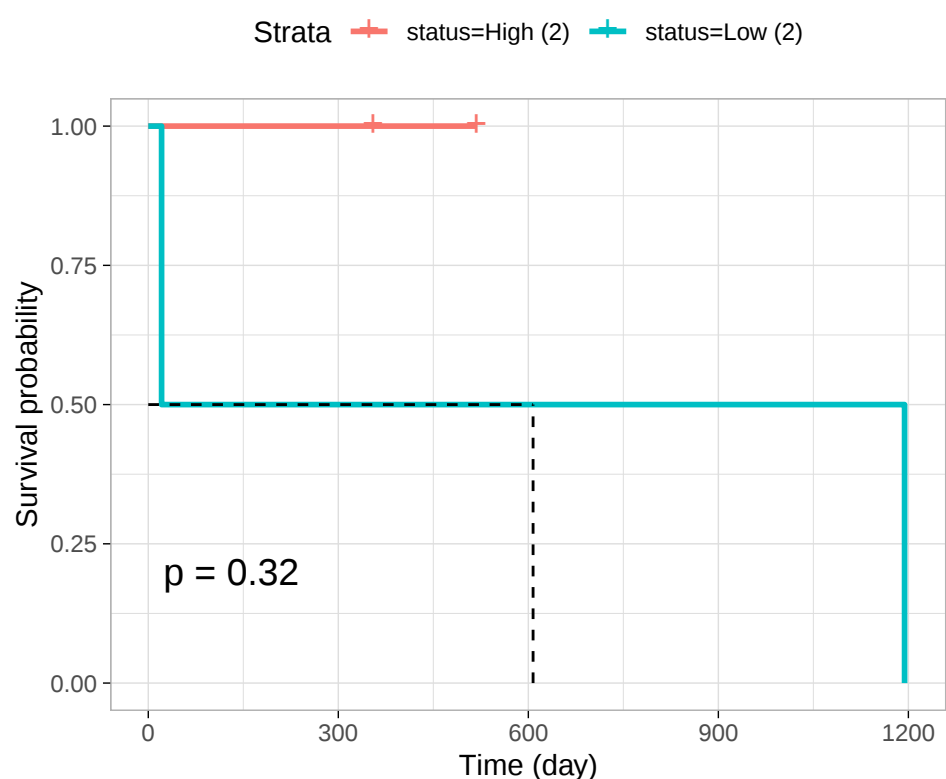
All WHO grade survival (recurrent glioma)



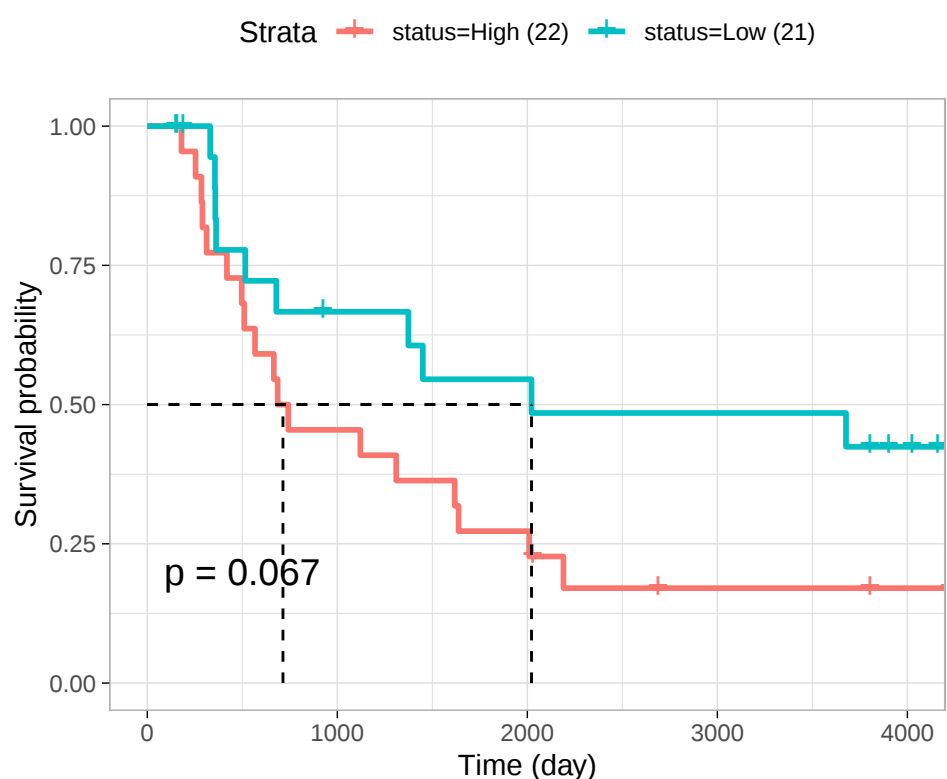
WHO grade II survival (primary glioma)



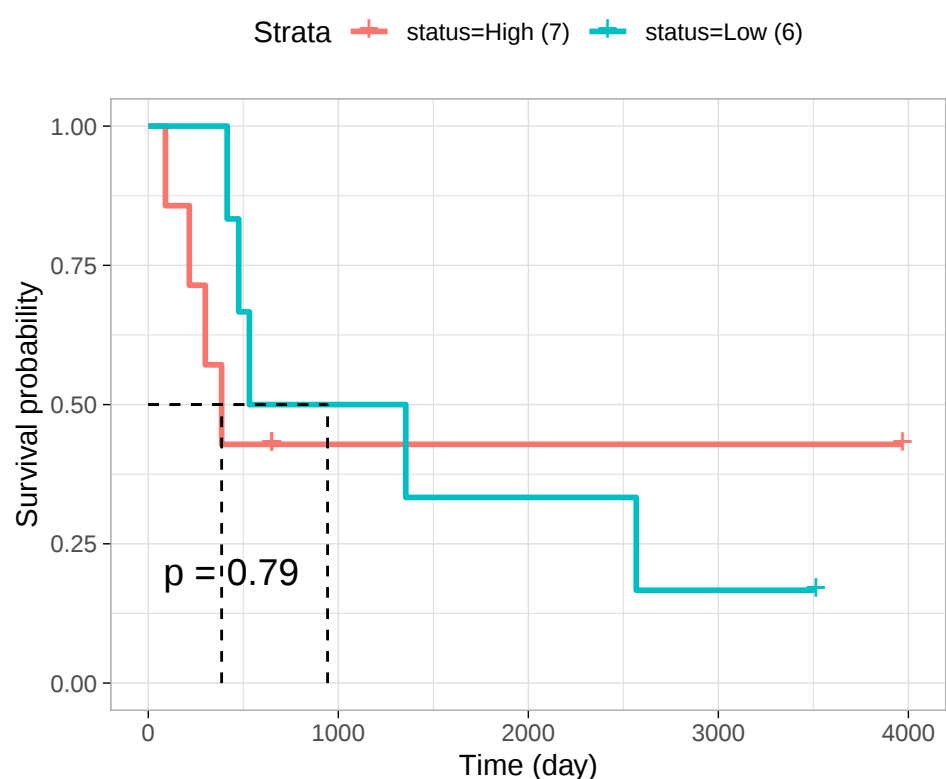
WHO grade II survival (recurrent glioma)



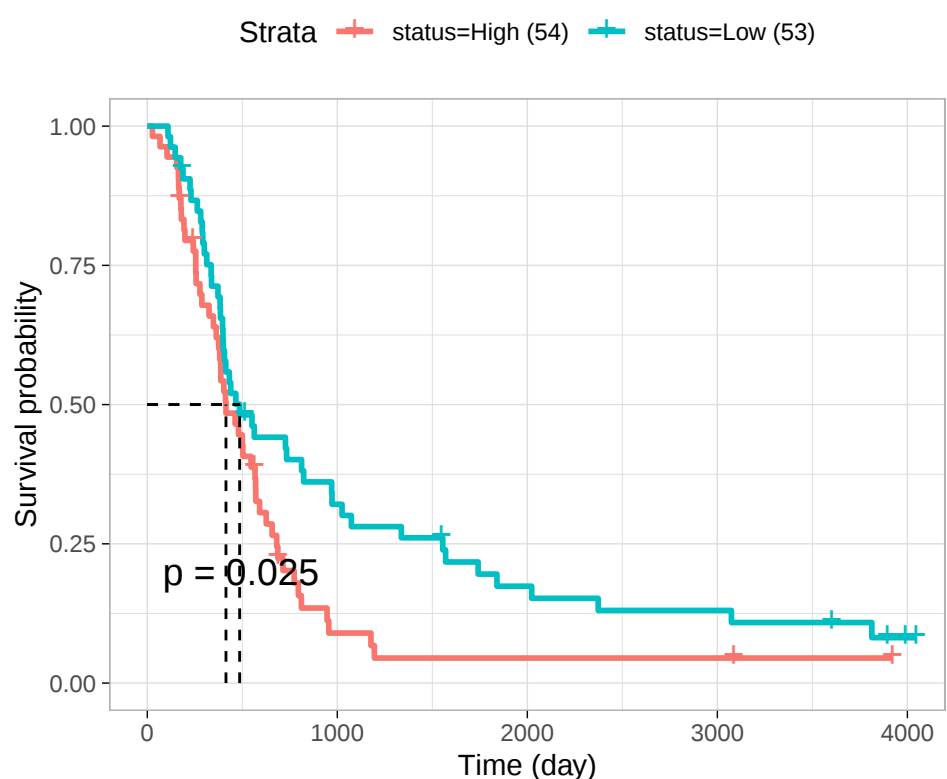
WHO grade III survival (primary glioma)



WHO grade III survival (recurrent glioma)



WHO grade IV survival (primary glioma)



WHO grade IV survival (recurrent glioma)

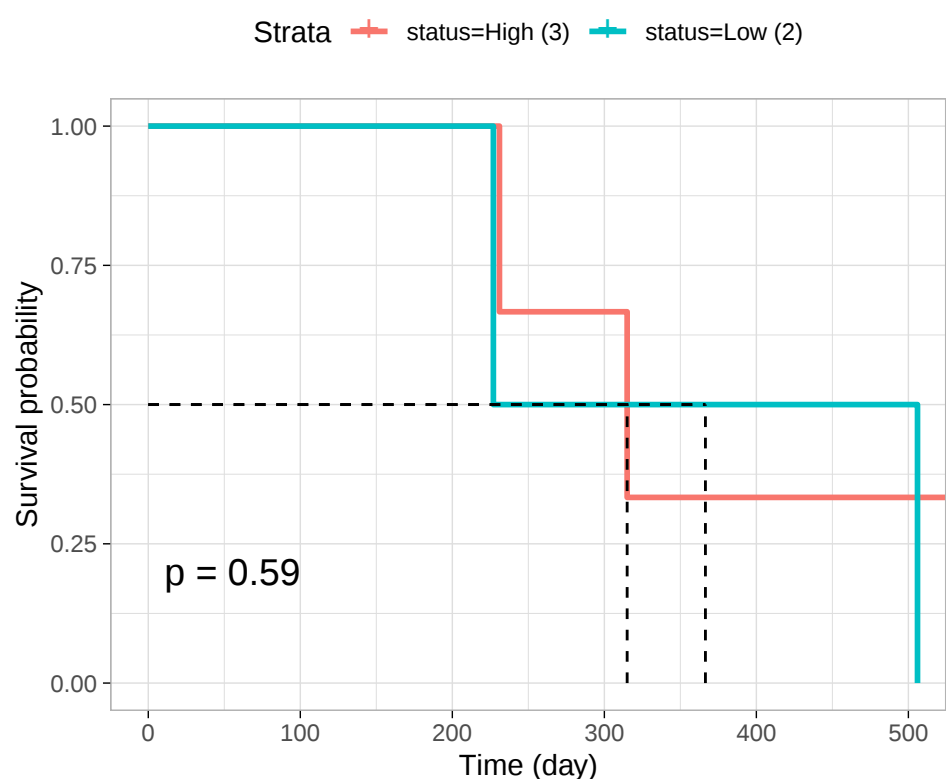
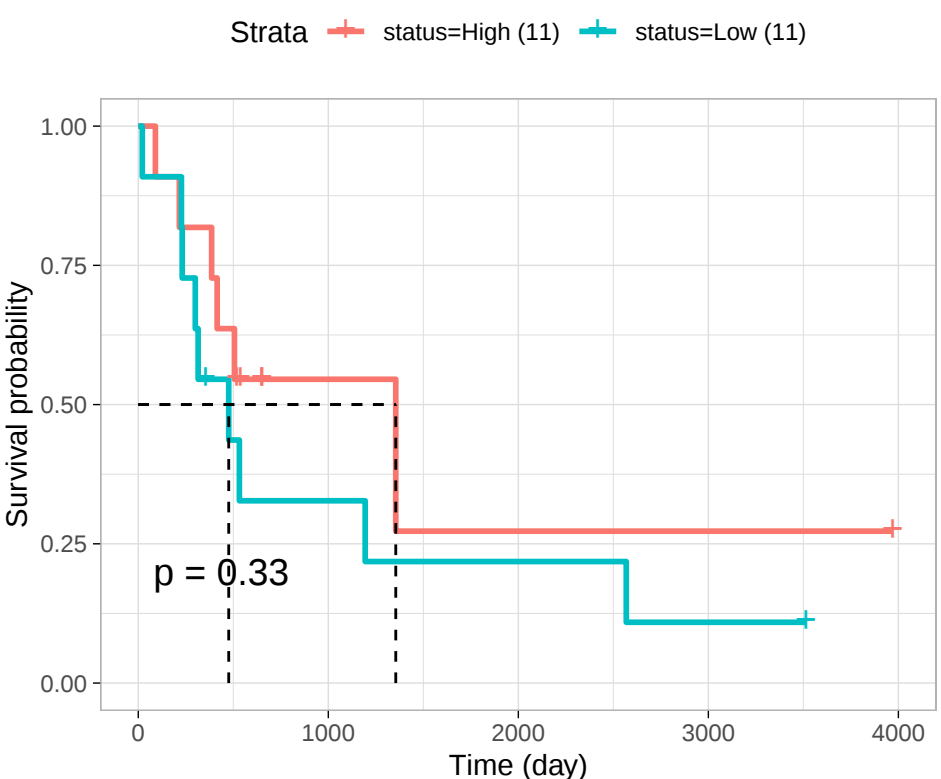
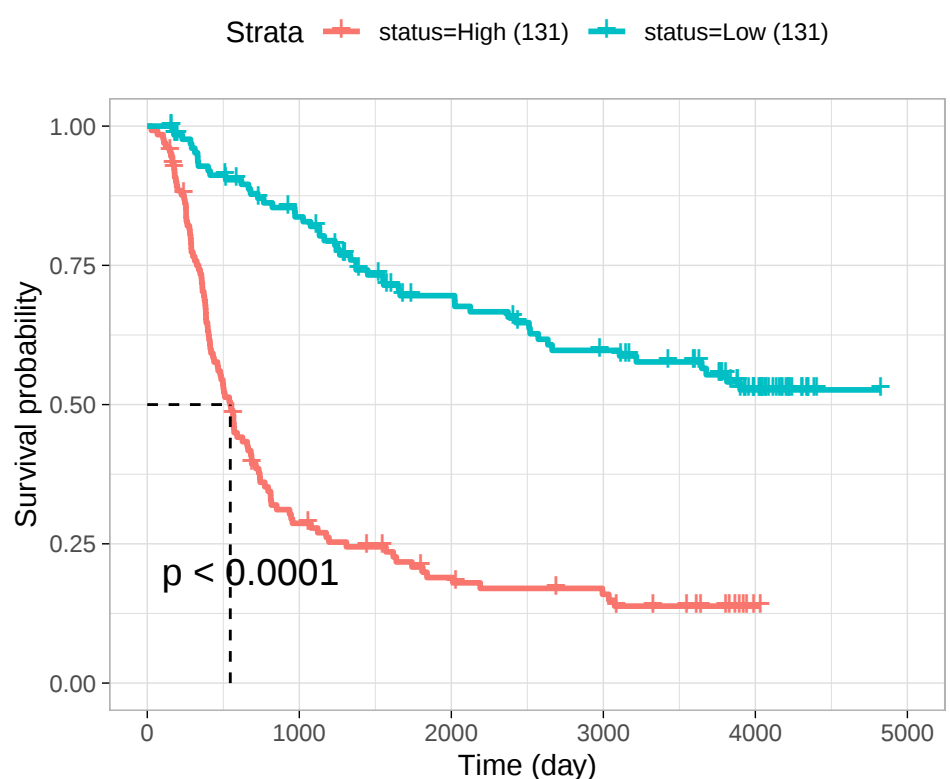


Figure S4:
COL5A1 survival analysis in CGGA

All WHO grade survival (primary glioma)

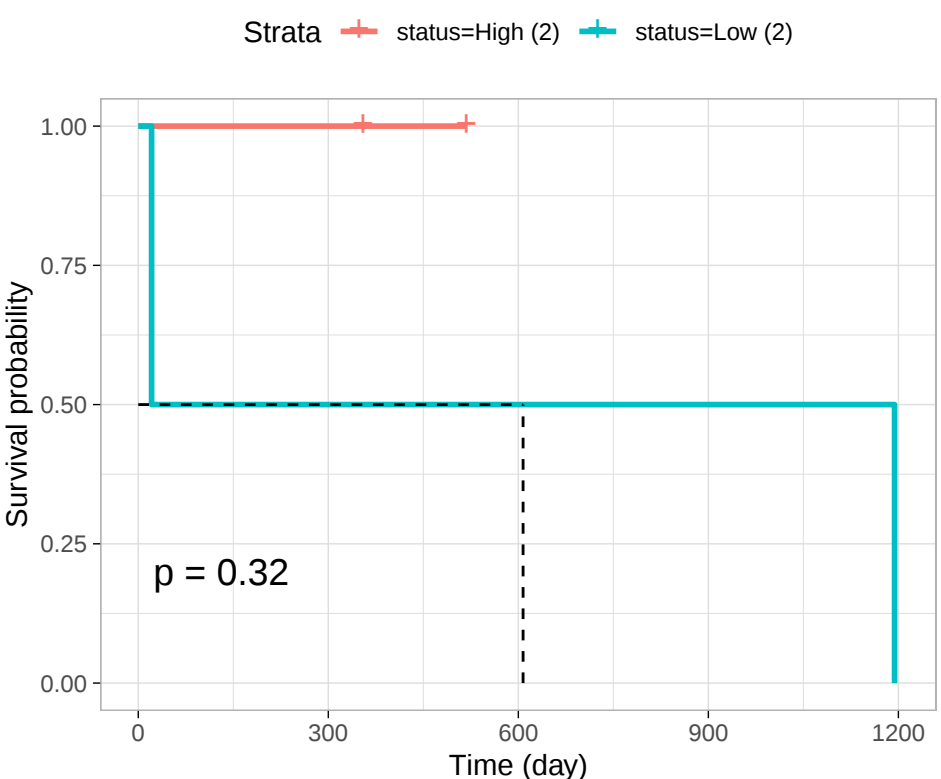
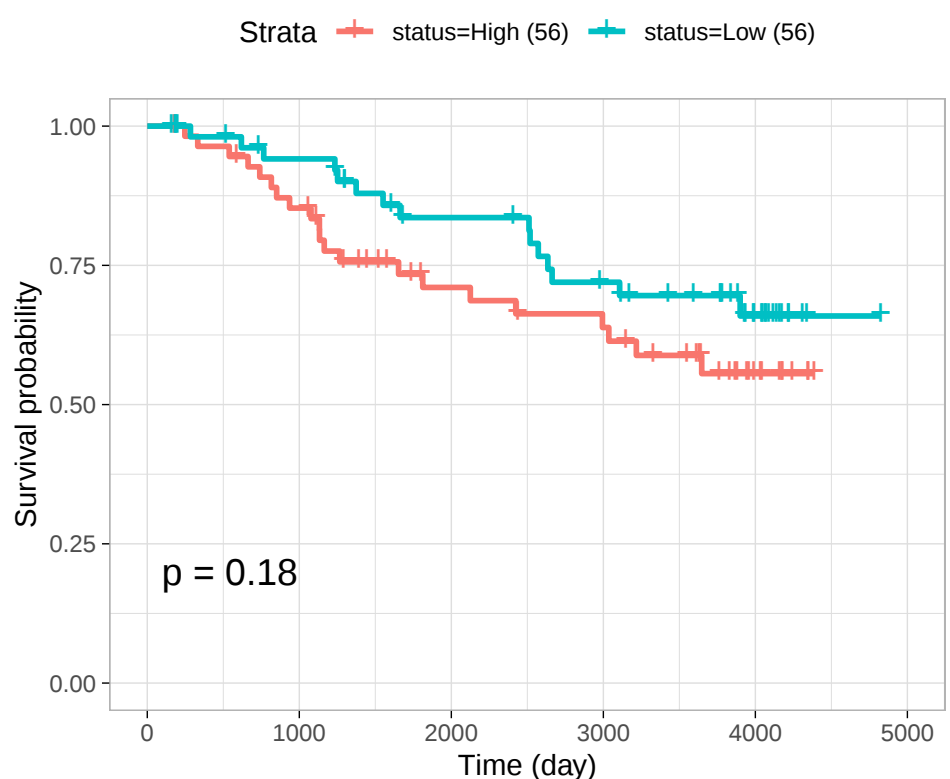
mRNAseq_arry_301

All WHO grade survival (recurrent glioma)



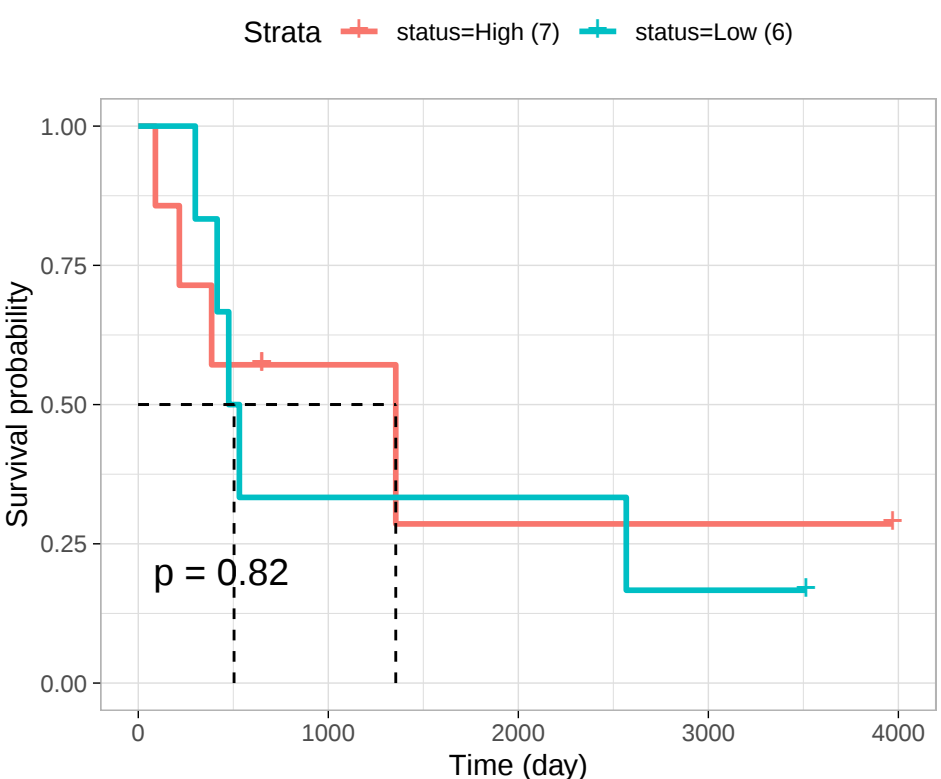
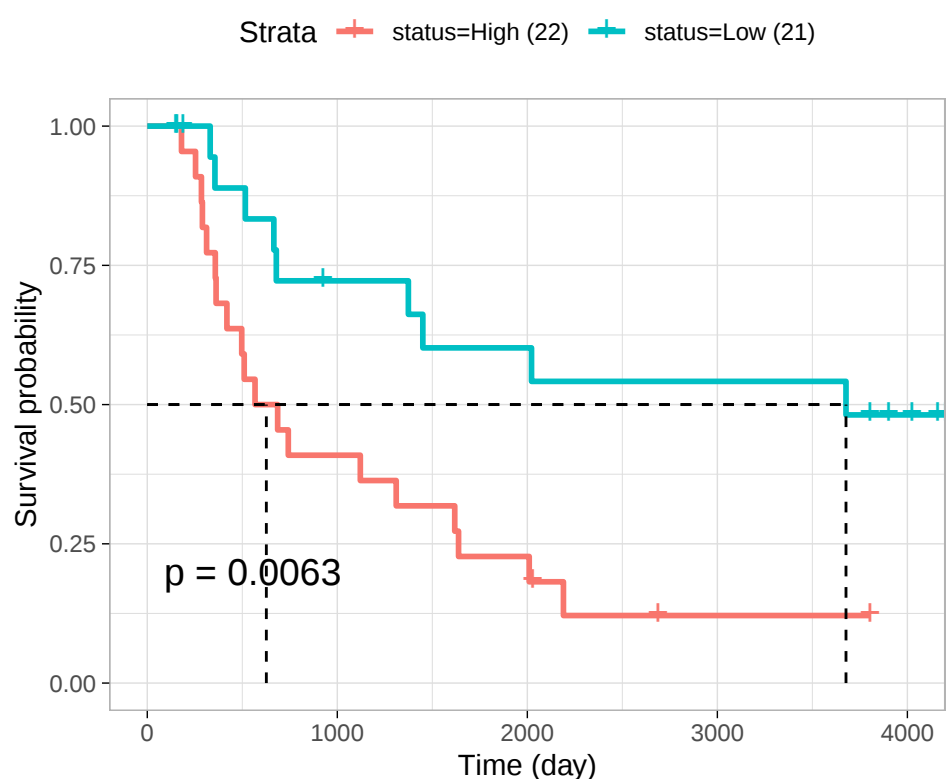
WHO grade II survival (primary glioma)

WHO grade II survival (recurrent glioma)



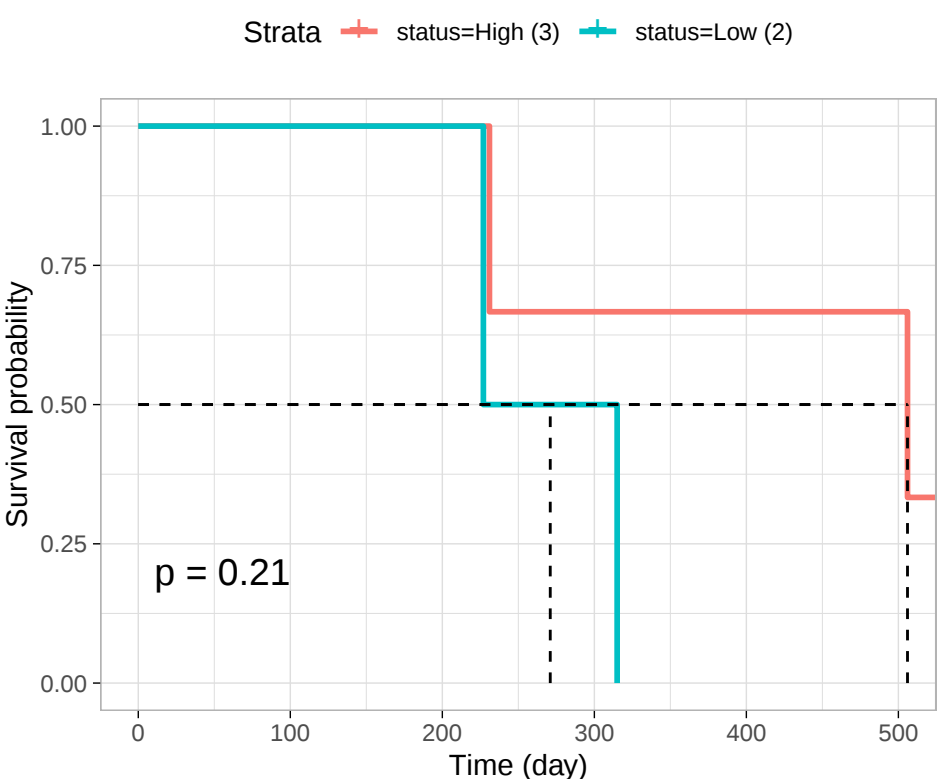
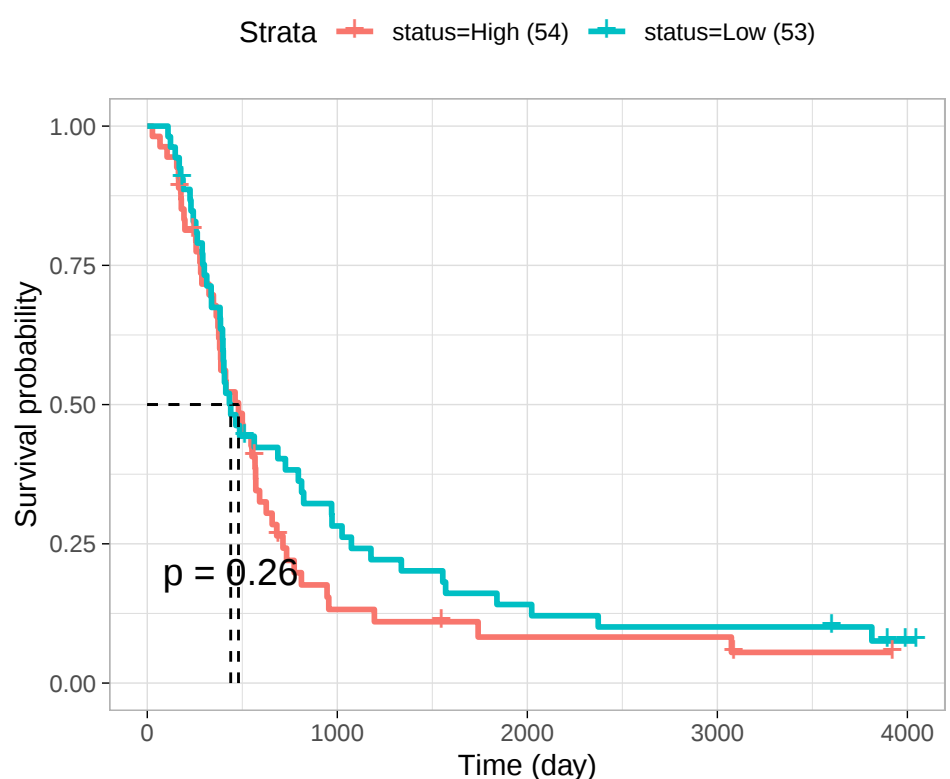
WHO grade III survival (primary glioma)

WHO grade III survival (recurrent glioma)

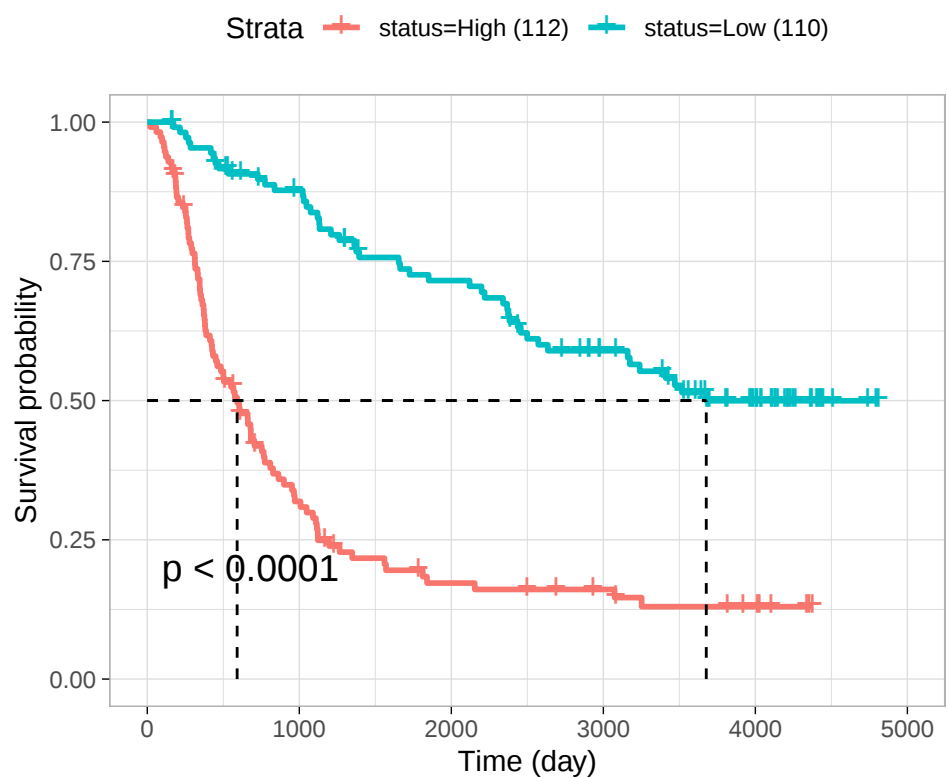


WHO grade IV survival (primary glioma)

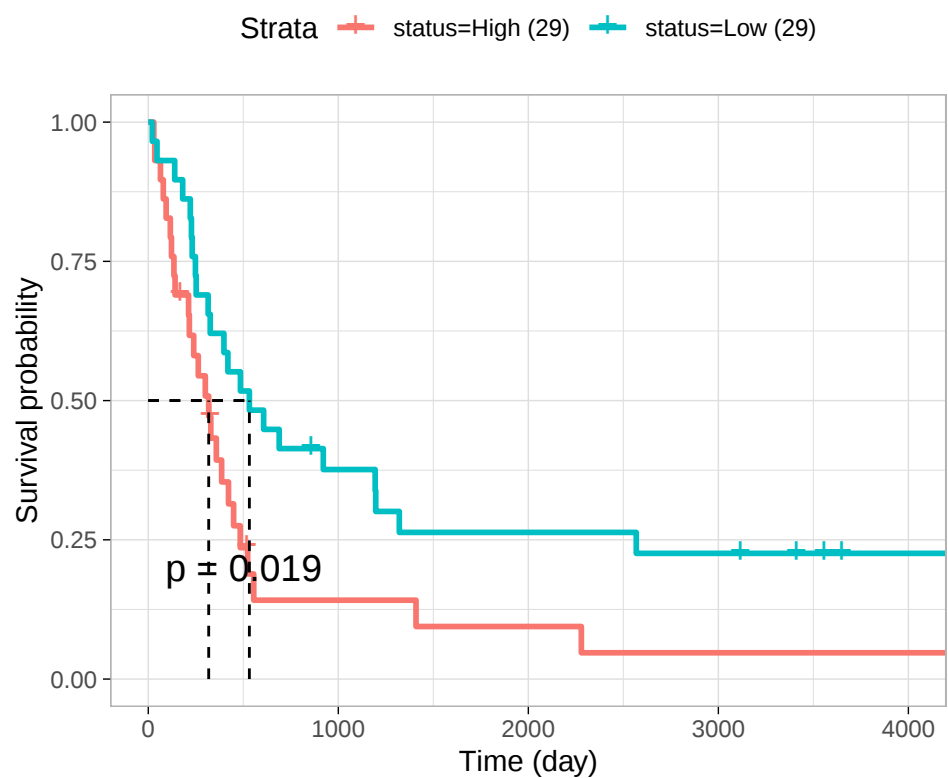
WHO grade IV survival (recurrent glioma)



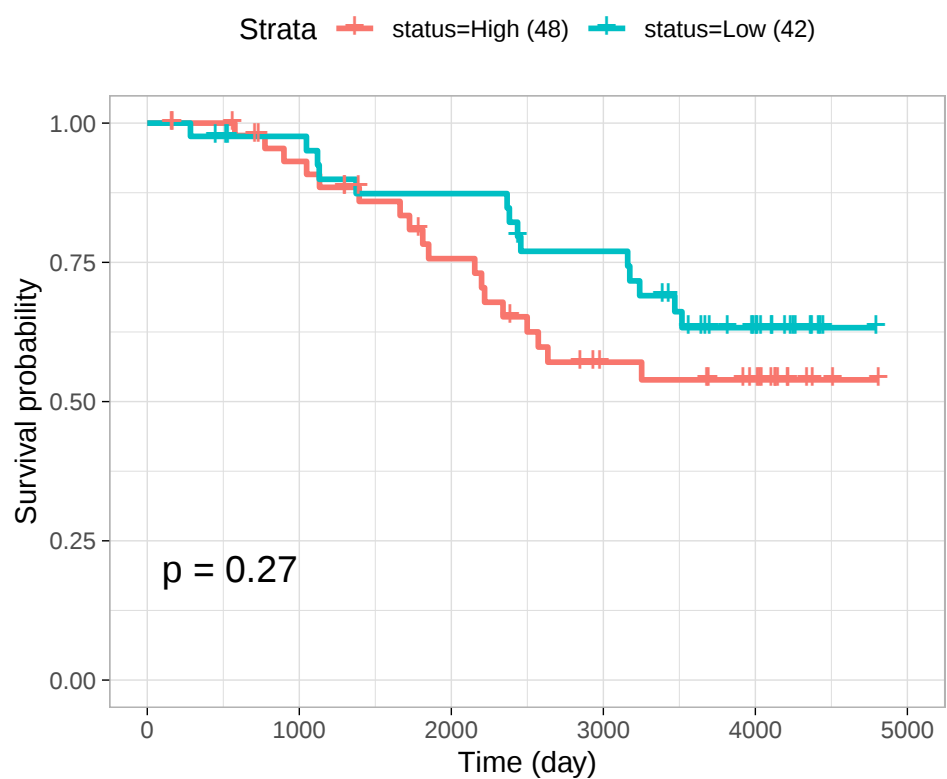
All WHO grade survival (primary glioma) mRNAseq_325



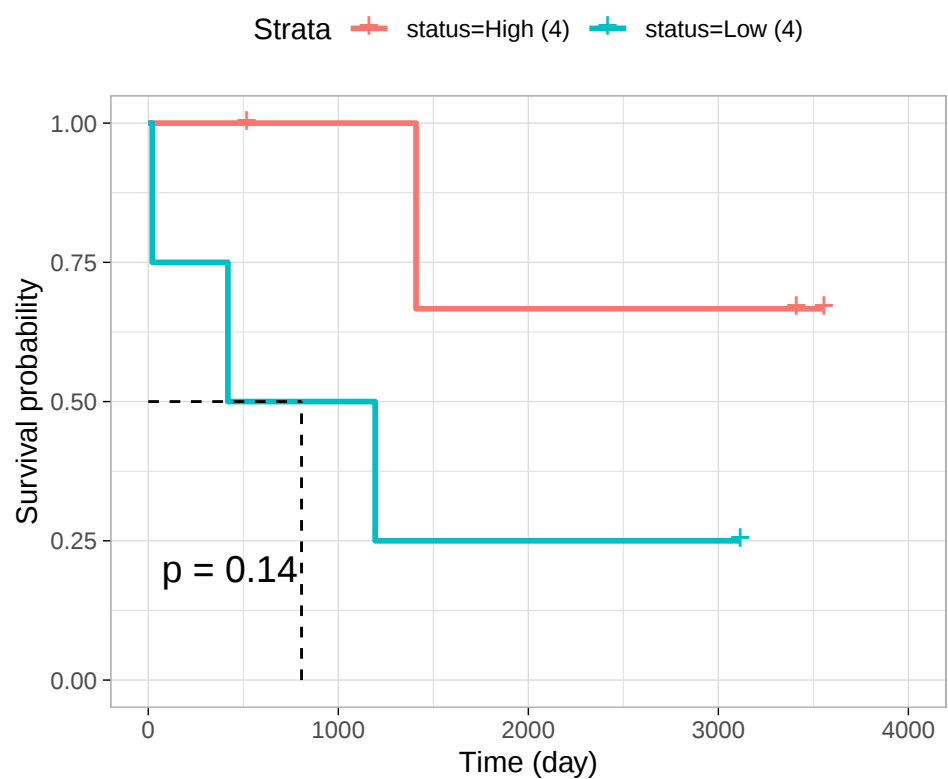
All WHO grade survival (recurrent glioma)



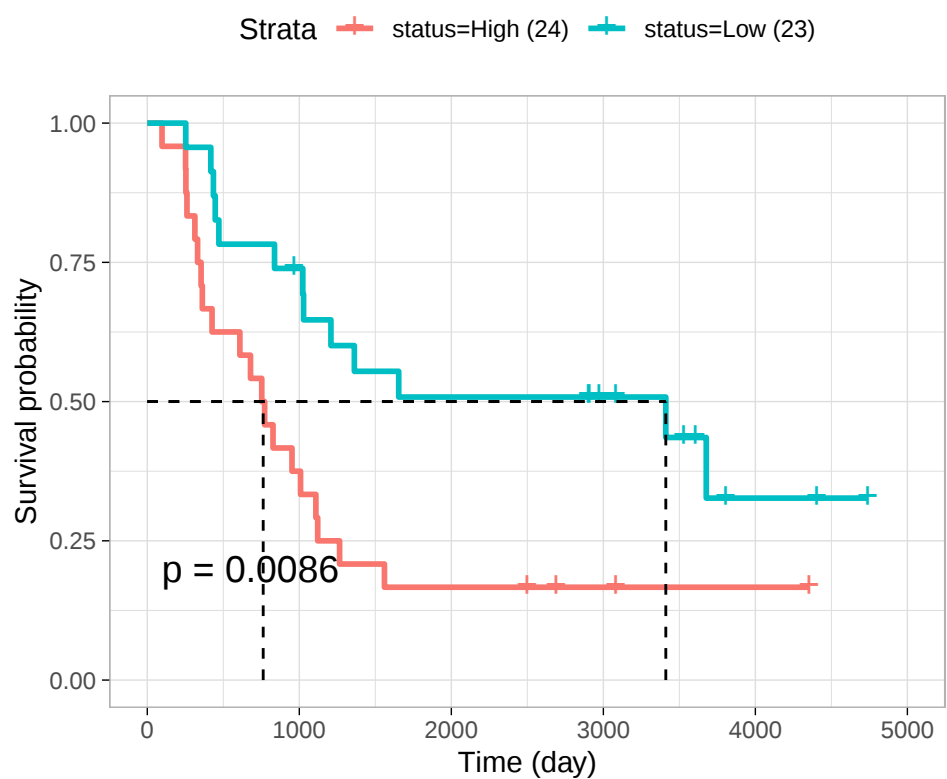
WHO grade II survival (primary glioma)



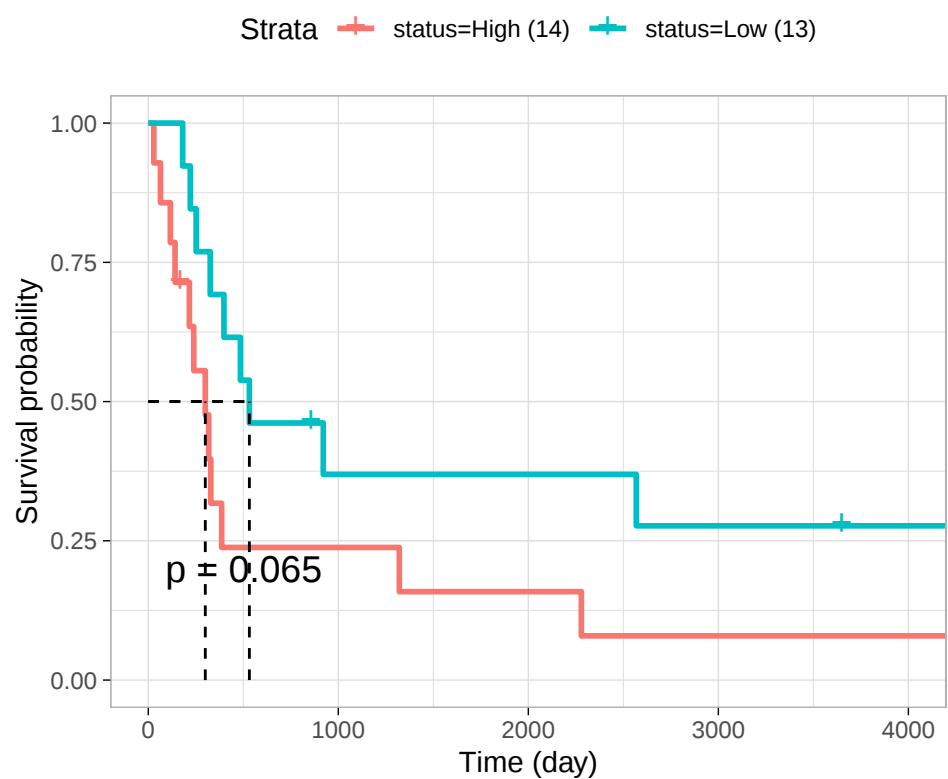
WHO grade II survival (recurrent glioma)



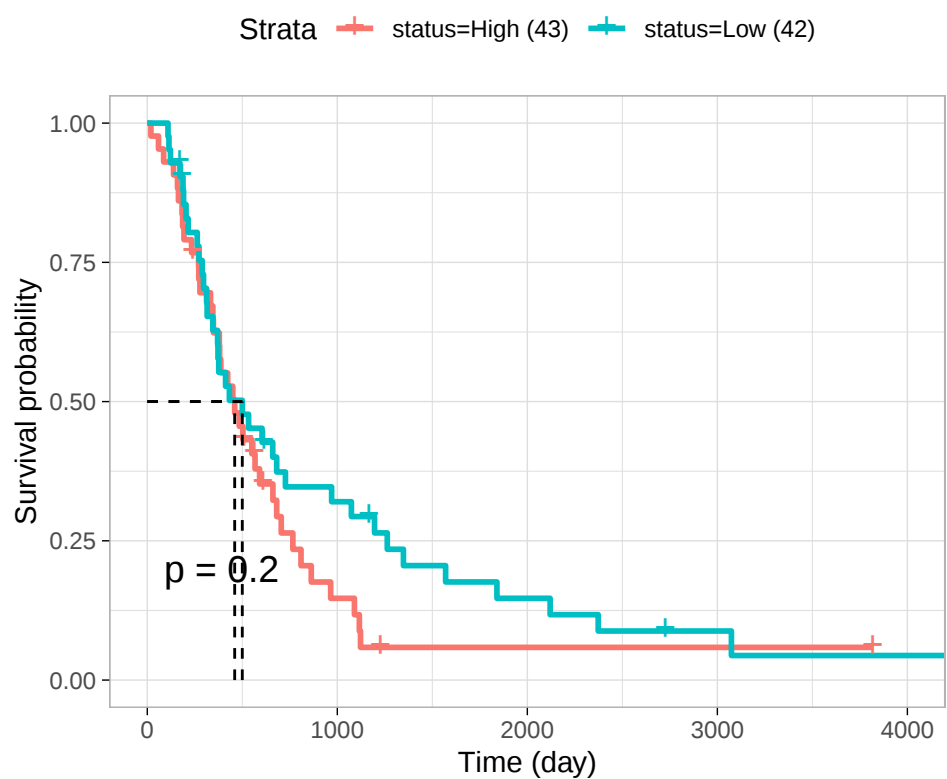
WHO grade III survival (primary glioma)



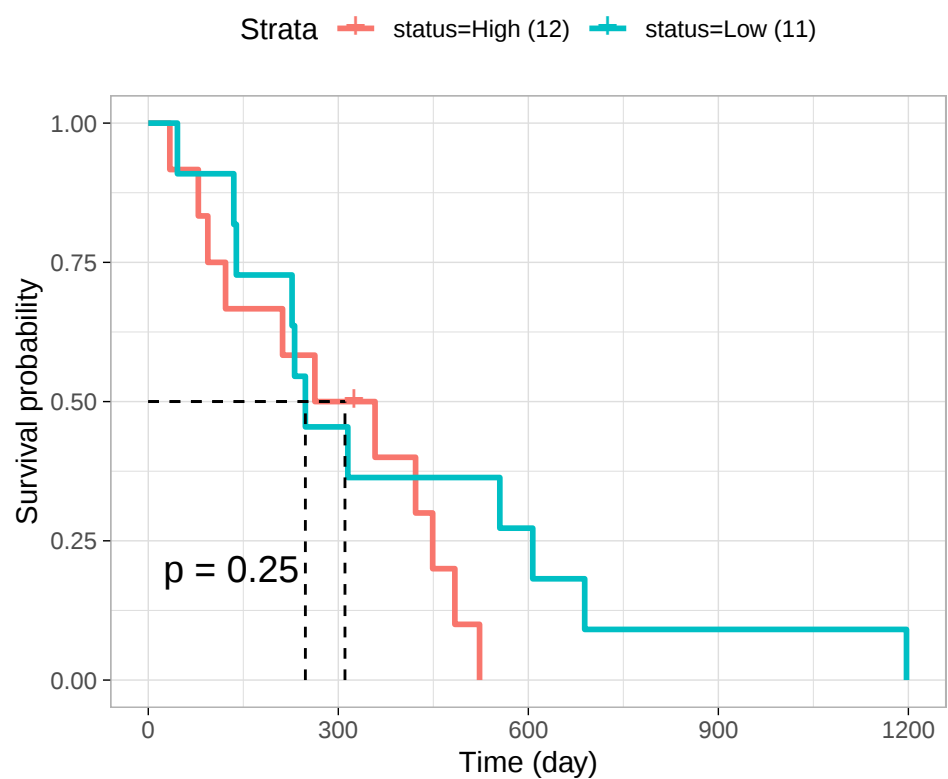
WHO grade III survival (recurrent glioma)



WHO grade IV survival (primary glioma)



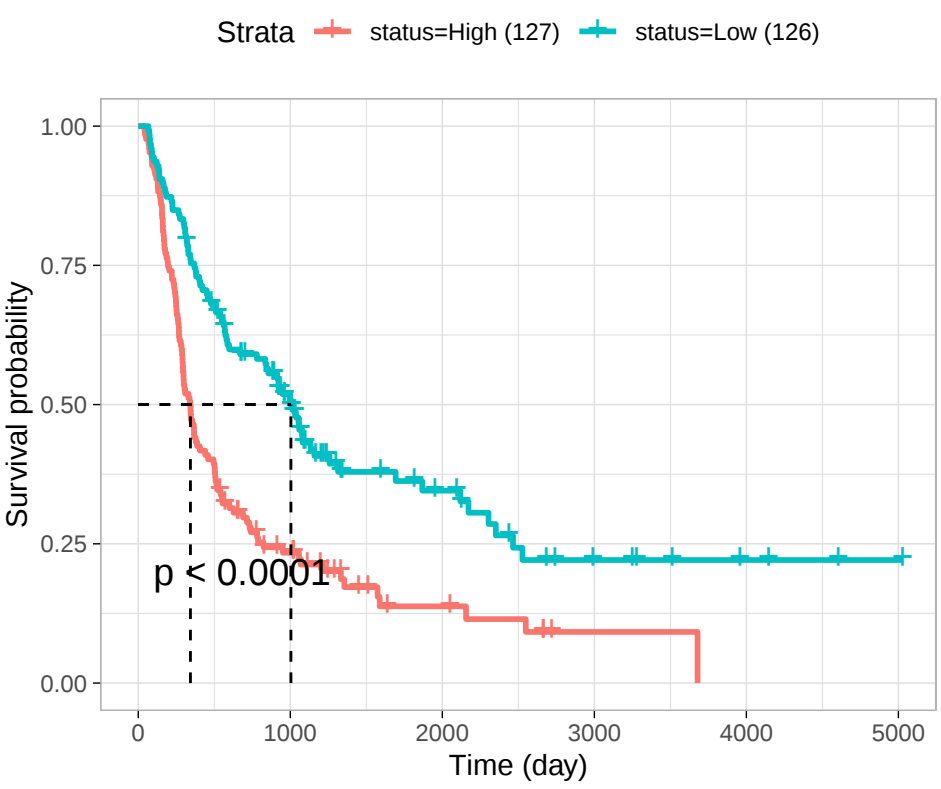
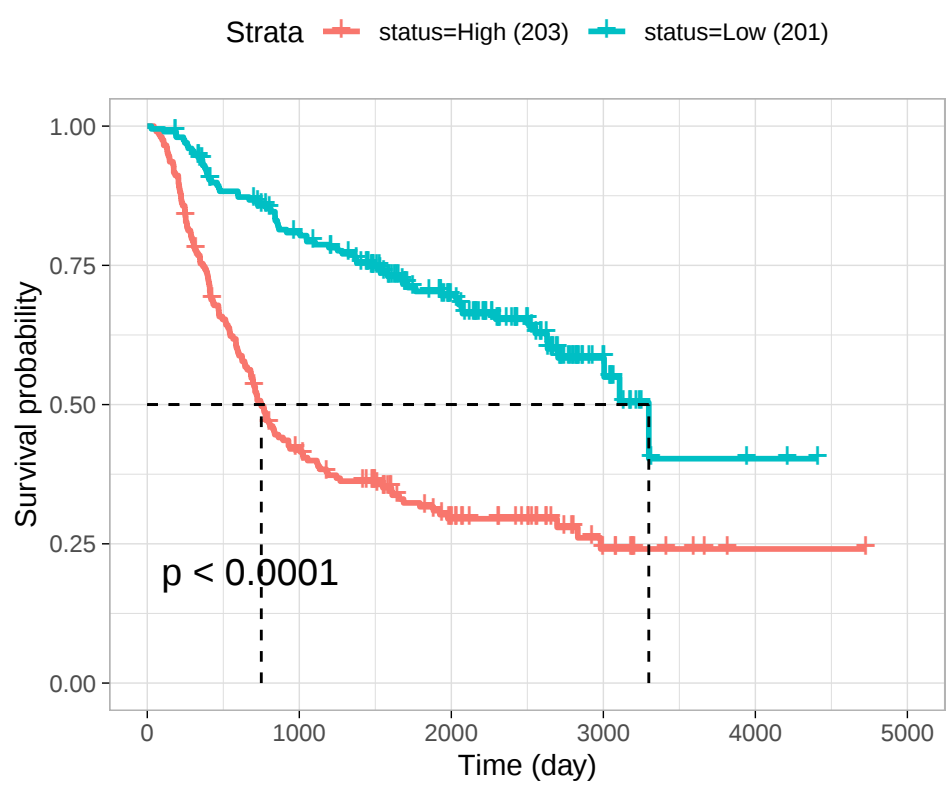
WHO grade IV survival (recurrent glioma)



All WHO grade survival (primary glioma)

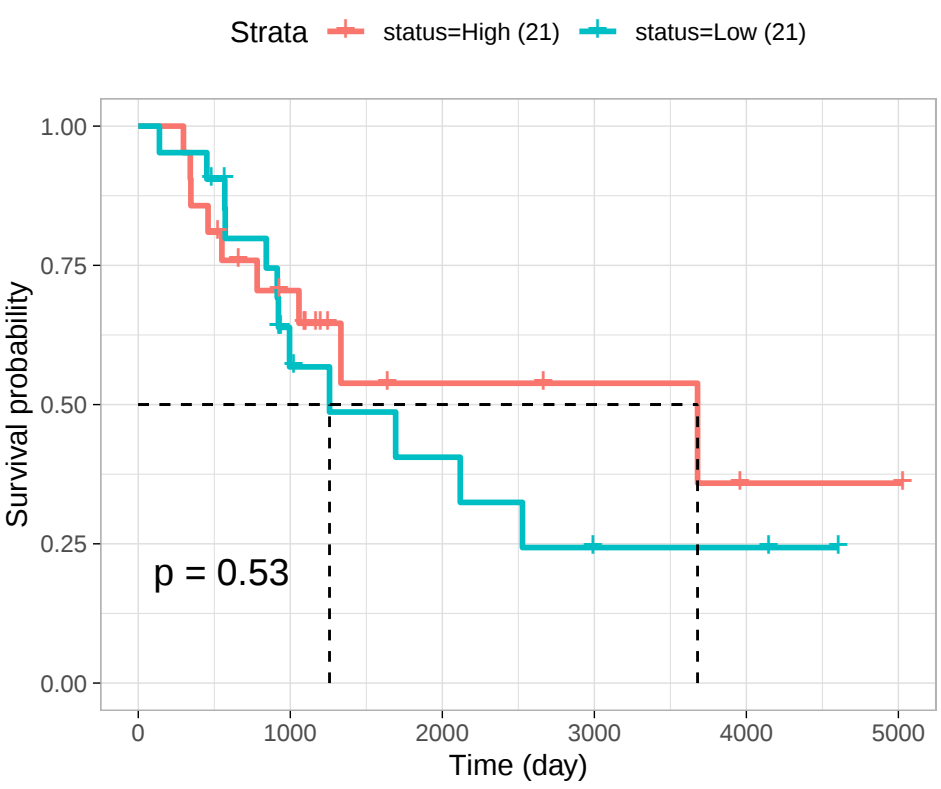
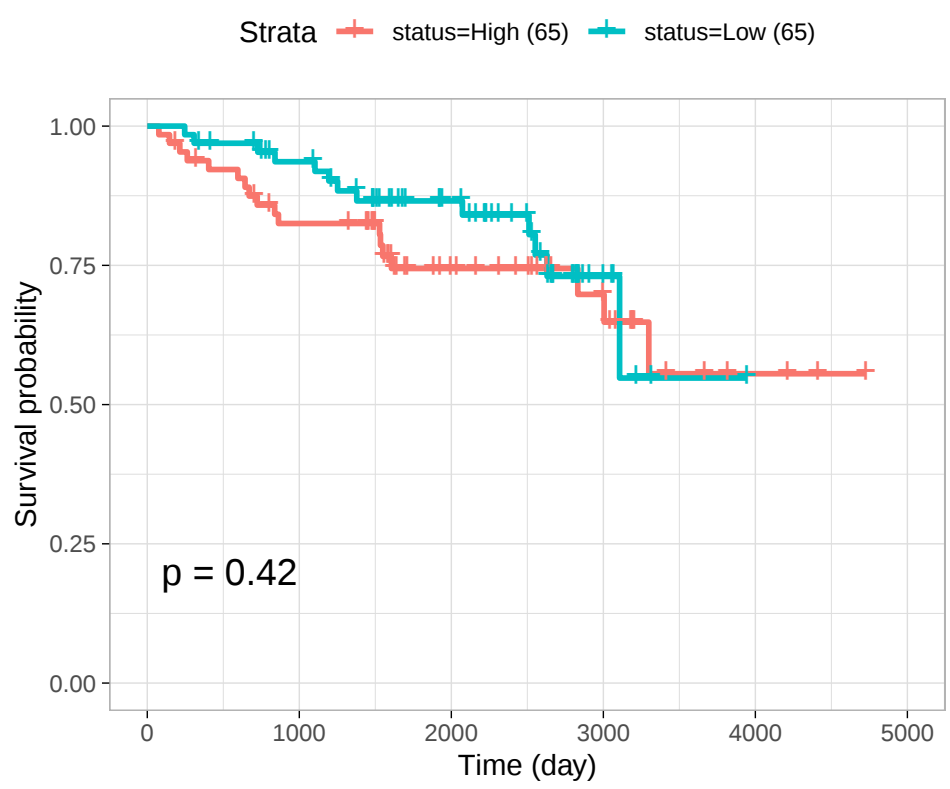
mRNAseq_693

All WHO grade survival (recurrent glioma)



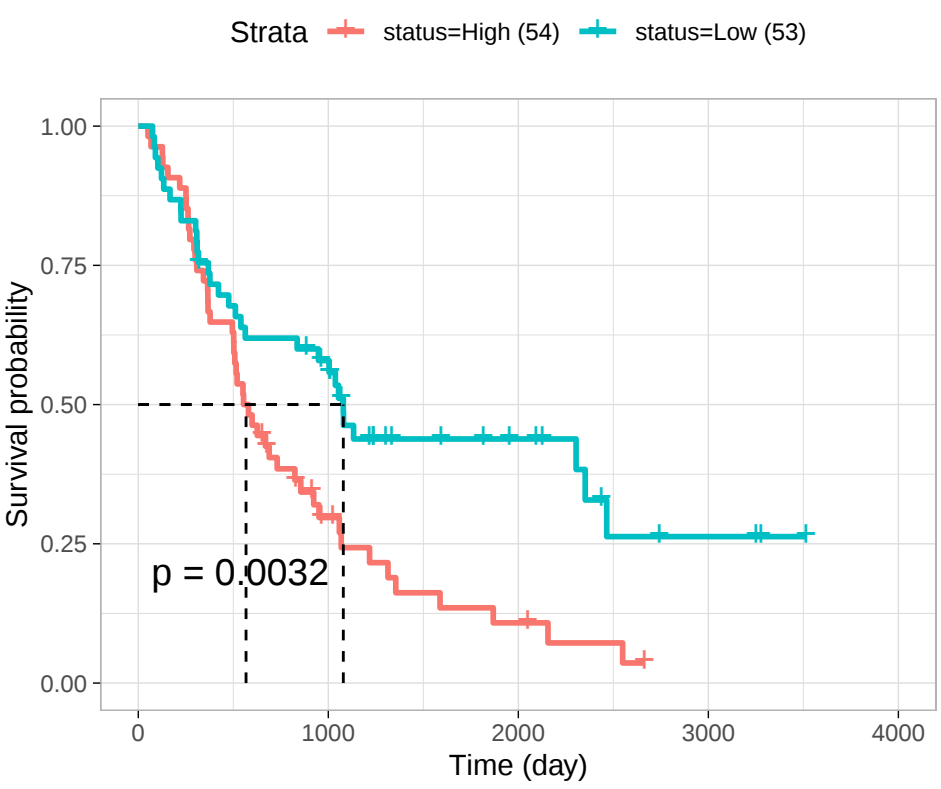
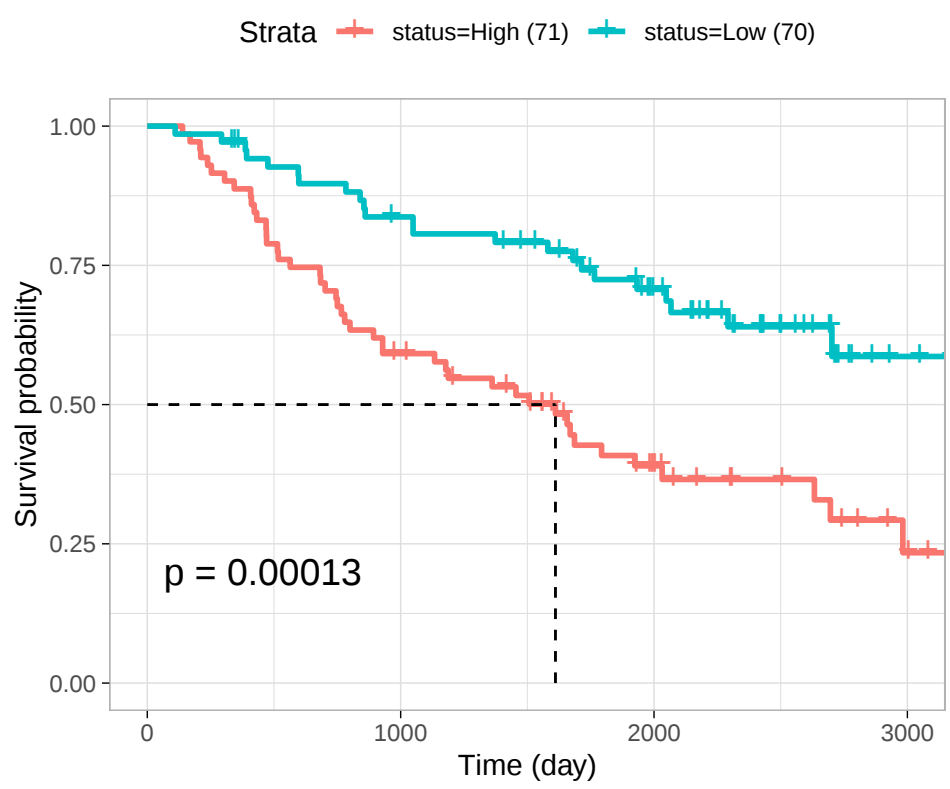
WHO grade II survival (primary glioma)

WHO grade II survival (recurrent glioma)



WHO grade III survival (primary glioma)

WHO grade III survival (recurrent glioma)



WHO grade IV survival (primary glioma)

WHO grade IV survival (recurrent glioma)

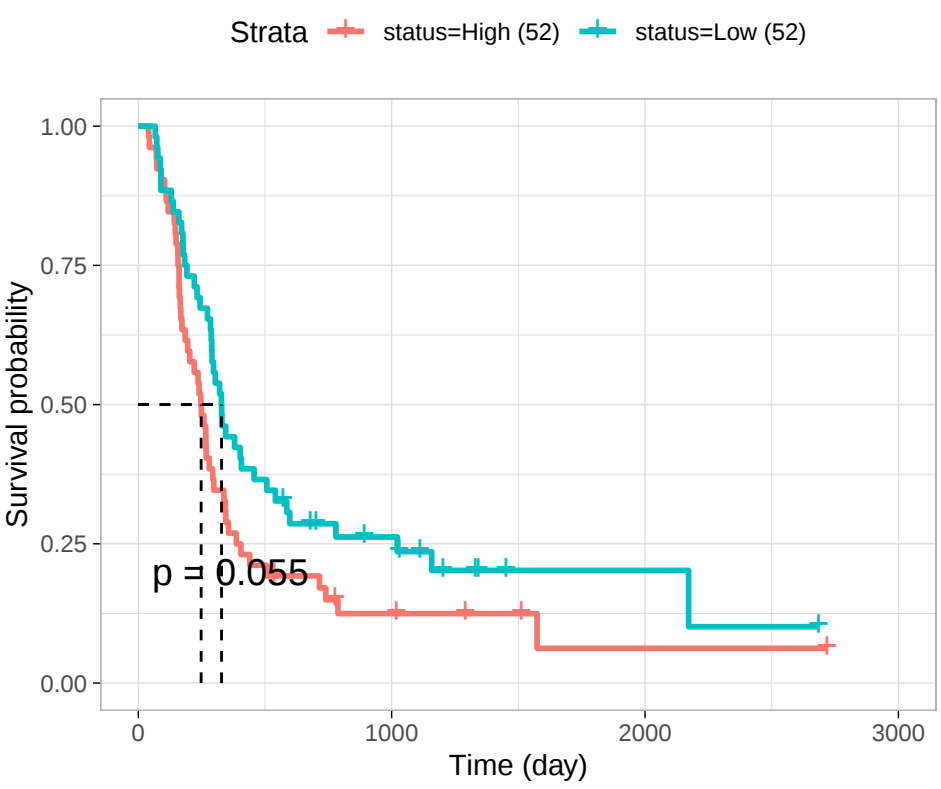
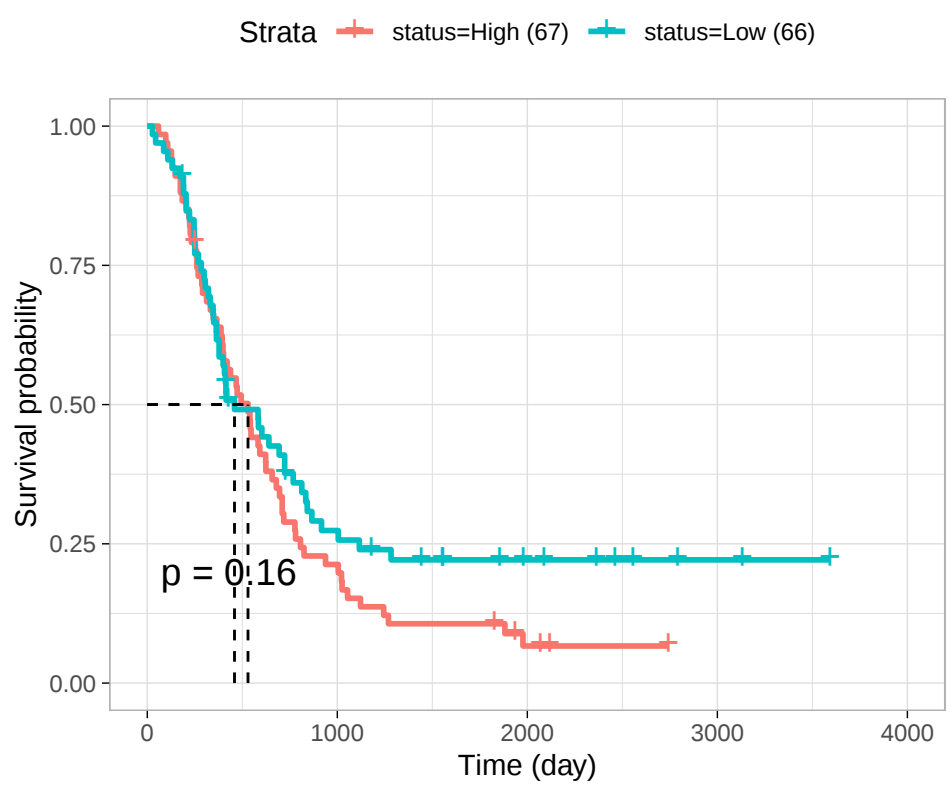
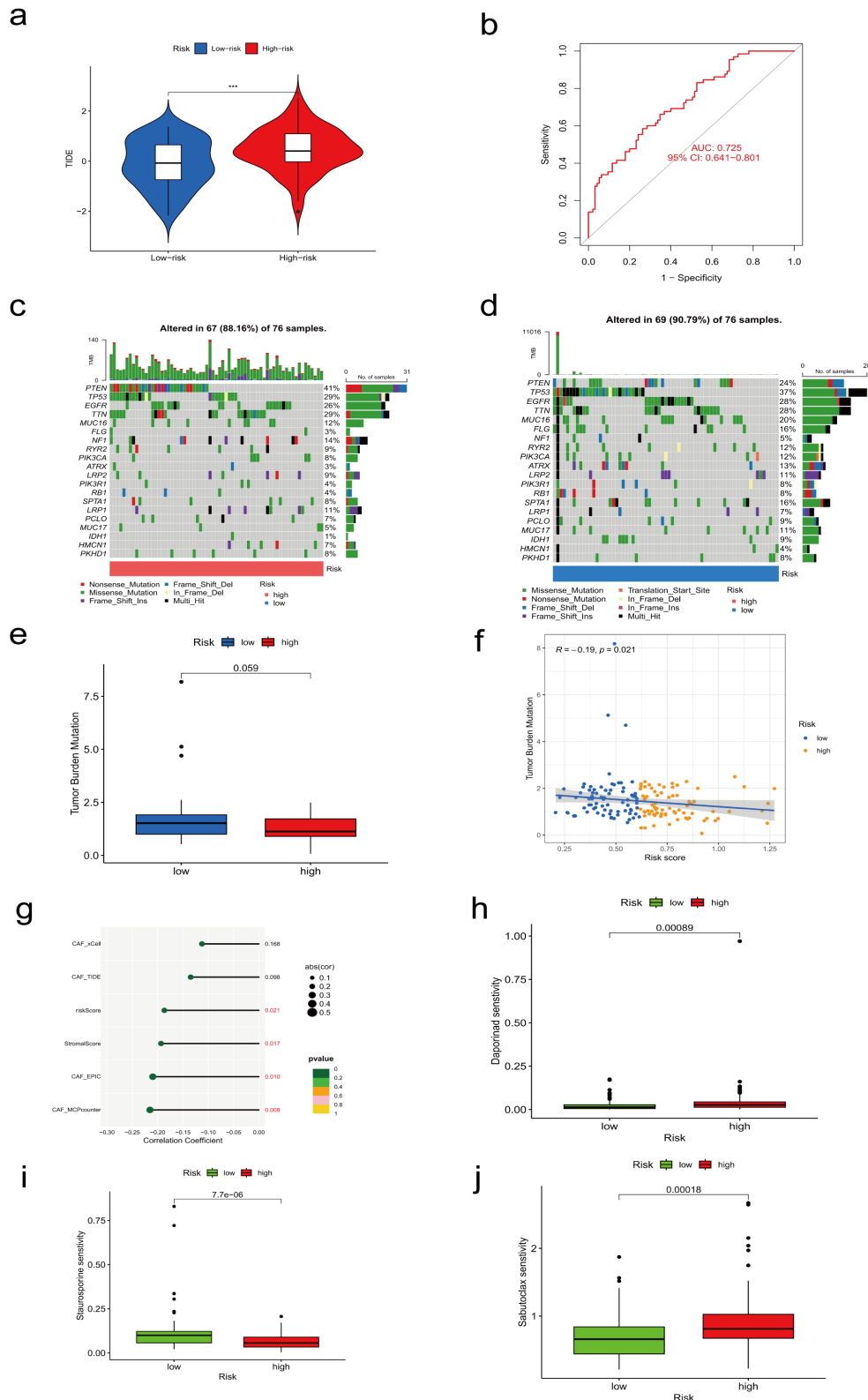


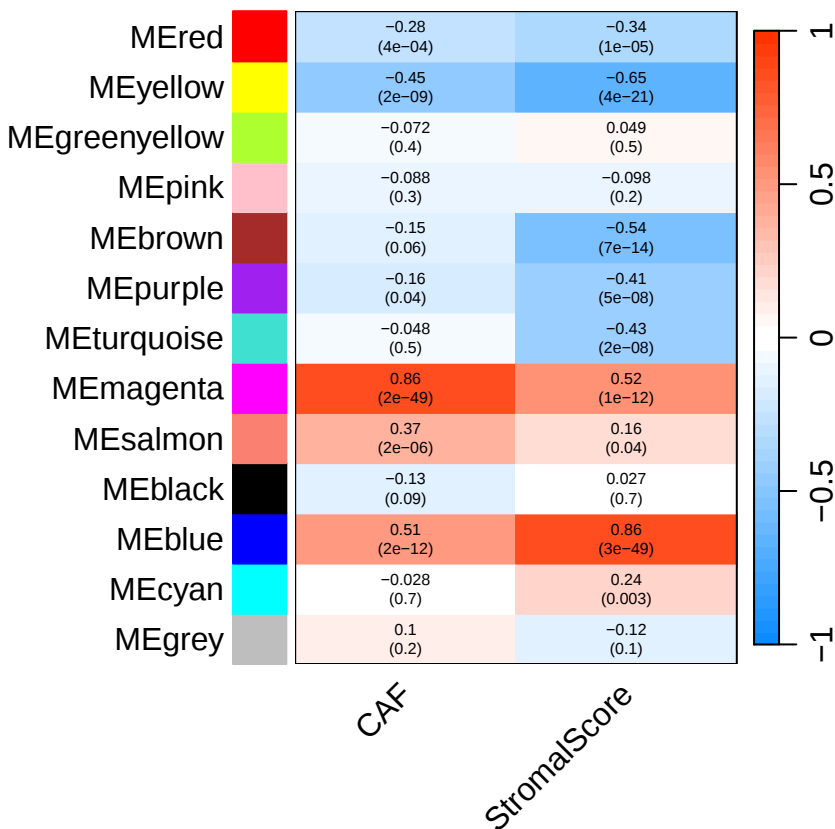
Figure S5 :

**Analysis of immunotherapy, tumor mutations and
drug sensitivities in high- and low-risk group**



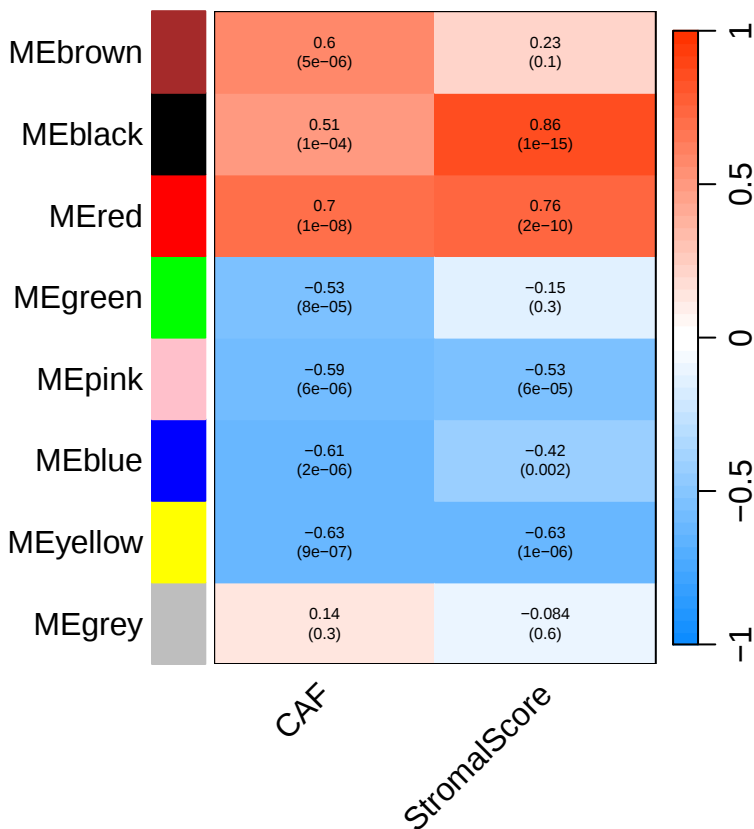
Supplementary Figure S5 Analysis of immunotherapy, tumor mutations and drug sensitivities. (a) Differences between high and low risk groups receiving immunotherapy according to TIDE. Blue represents the low-risk group, and red represents the high-risk group. *** represents $p < 0.001$. (b) ROC curve. AUC = 0.725. (c) The waterfall plot of tumor mutations in the high-risk group. The left vertical axis represents the common mutation types, and the right vertical axis represents the mutation rate. Different colors represent the different in-coming mutation patterns. (d) The waterfall plot of tumor mutations in the low-risk group. (e) Total mutation differences between high and low risk groups. $p > 0.05$, no significant difference. (f) Correlation between TBM and patient risk score. Vertical coordinate is TBM, and horizontal coordinate is risk score. Both are negatively correlated. $p = 0.021 < 0.05$. (g) CAF score and tumor mutation correlation. Larger dots indicates stronger correlation and greener color indicates smaller p-values. (h) Daporinad sensitivity in high- and low-risk group. (i) Staurosporine sensitivity in high- and low-risk group. (j) Sabutoclax sensitivity in high- and low-risk group. Green represents low risk group, and red represents high risk group. Vertical coordinate represents drug sensitivity score. Smaller score means more sensitive to drugs.

Figure S6:
MCPcounter analysis

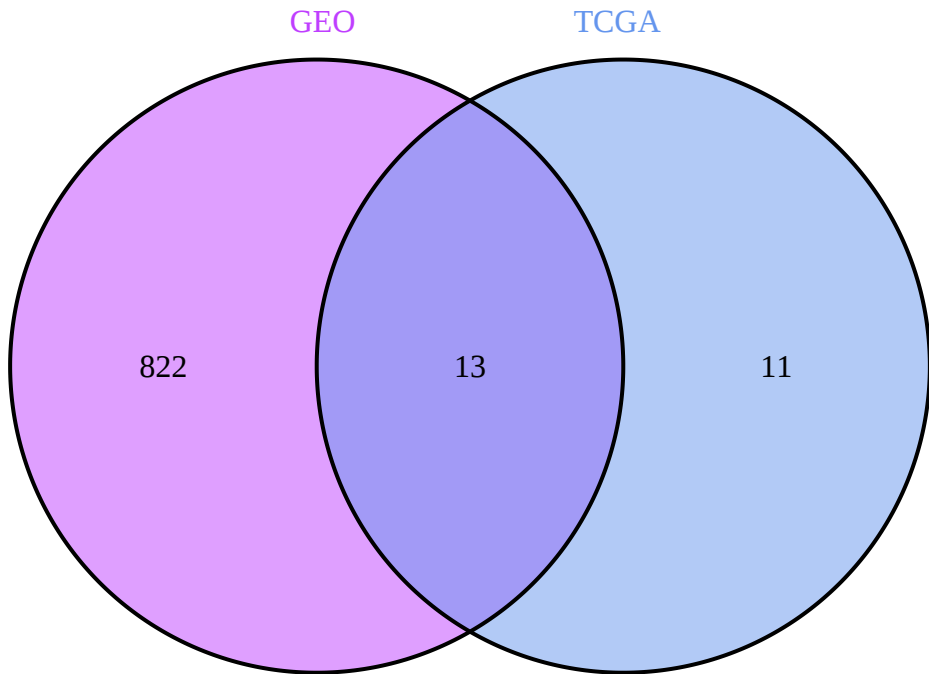


GEO WGCNA

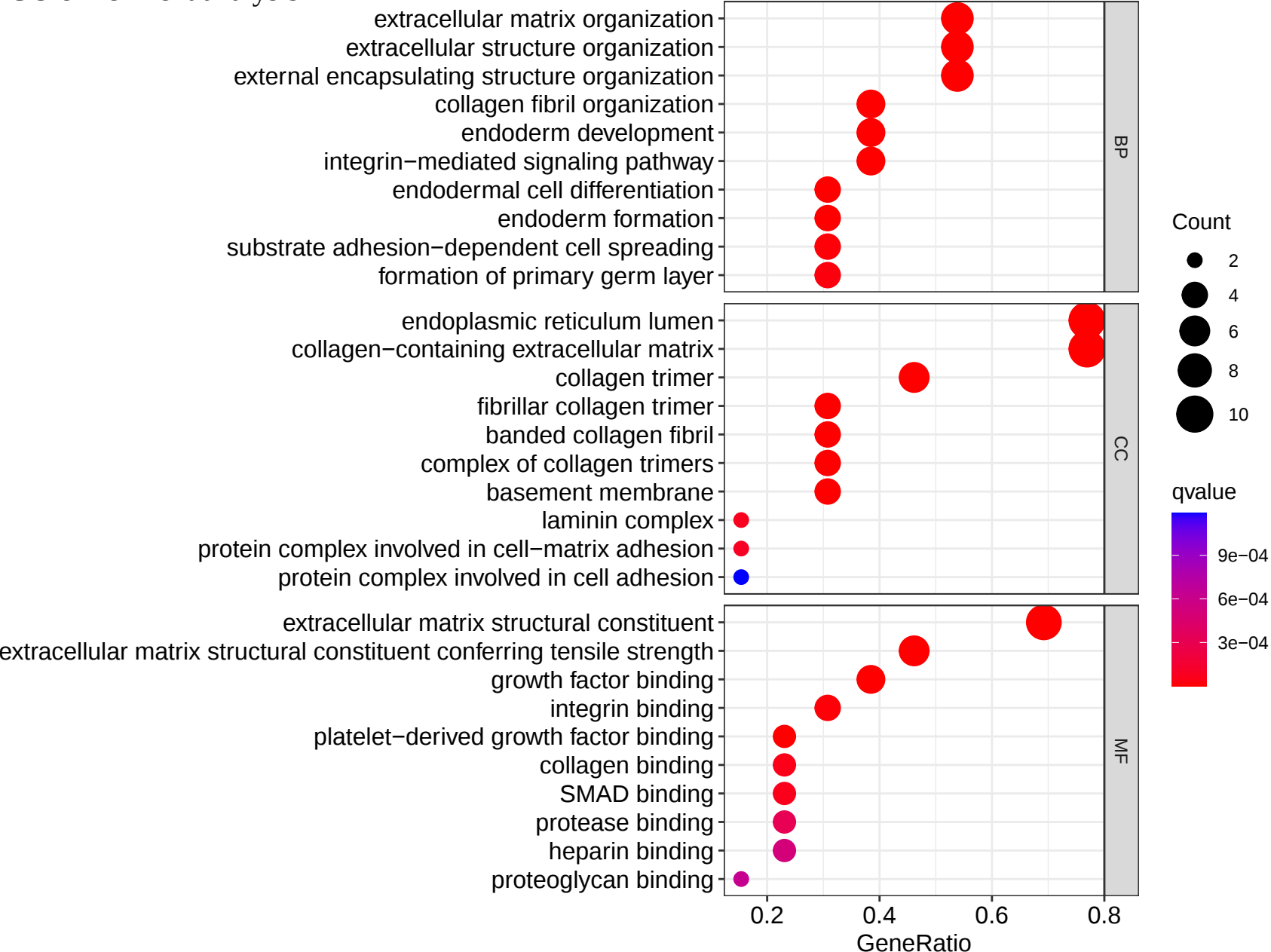
Module-trait relationships



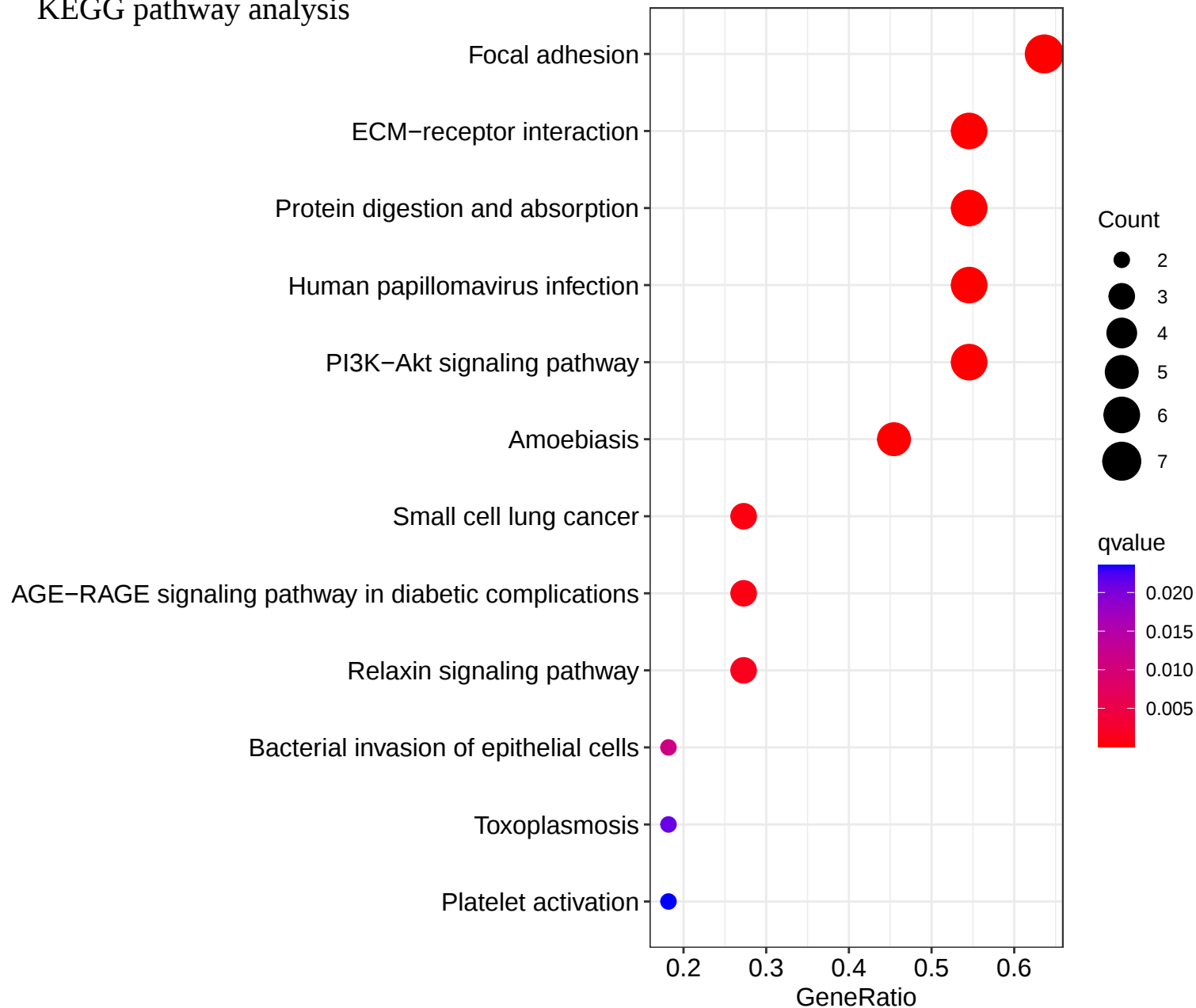
Intersection genes



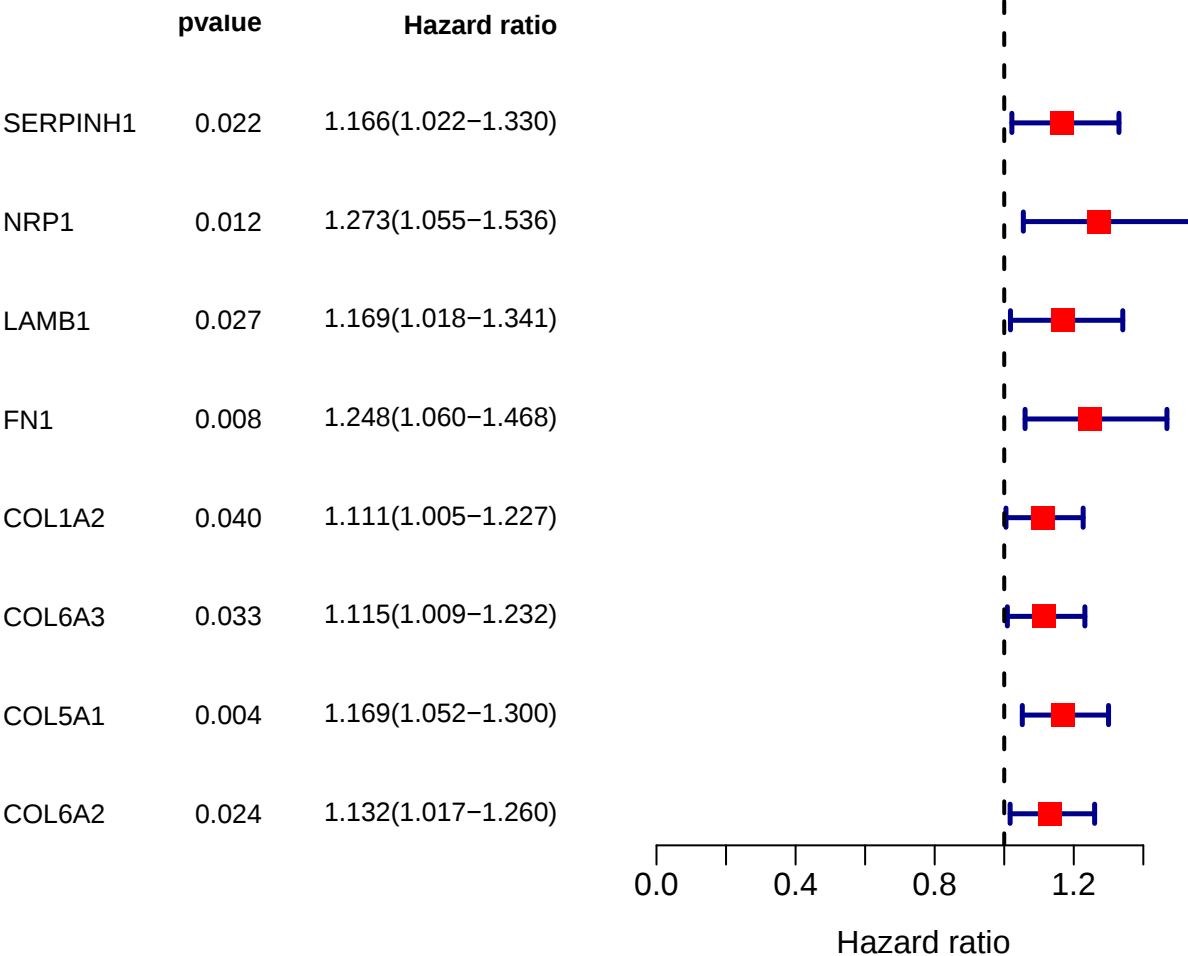
GO enrichment analysis



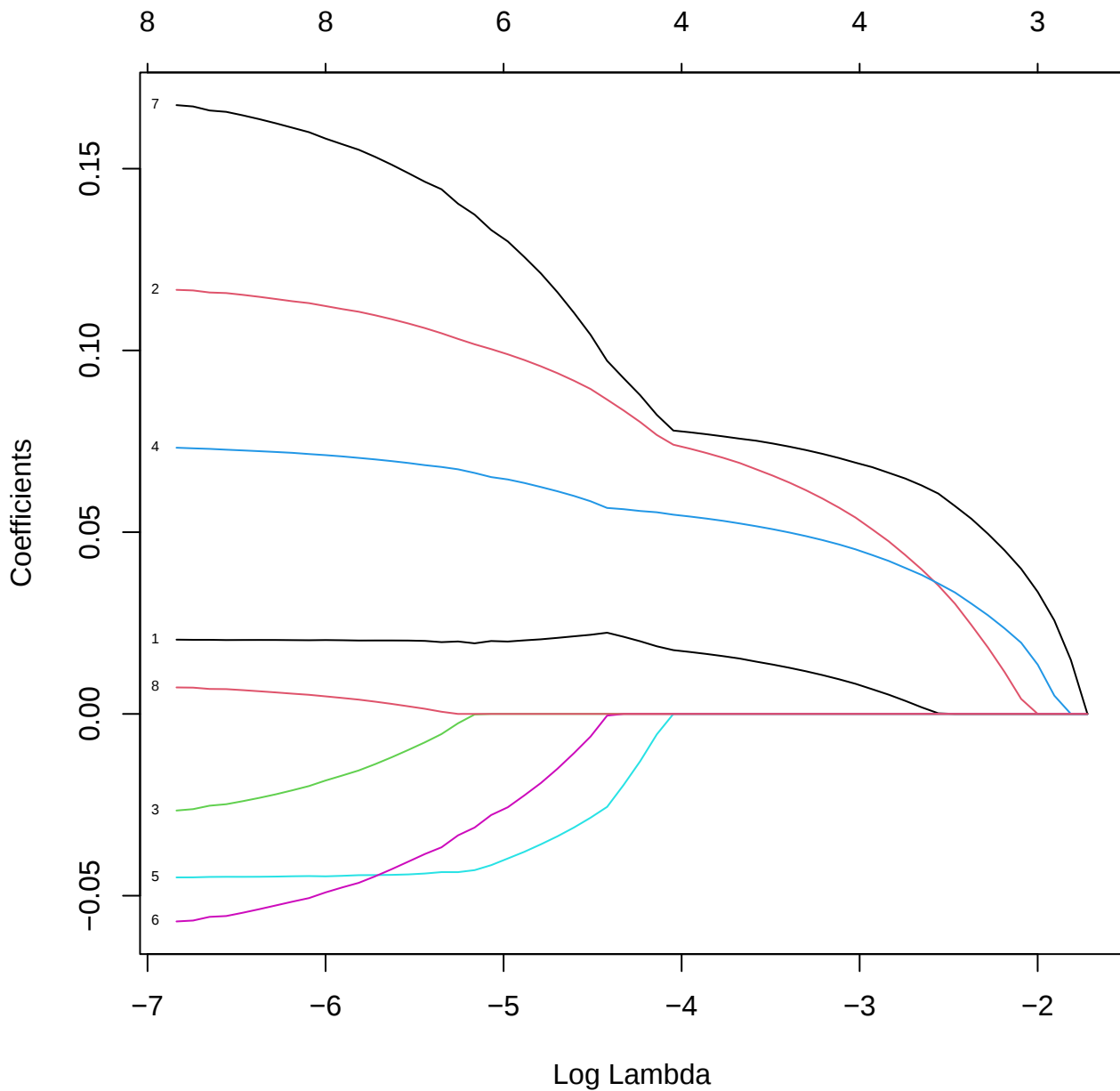
KEGG pathway analysis



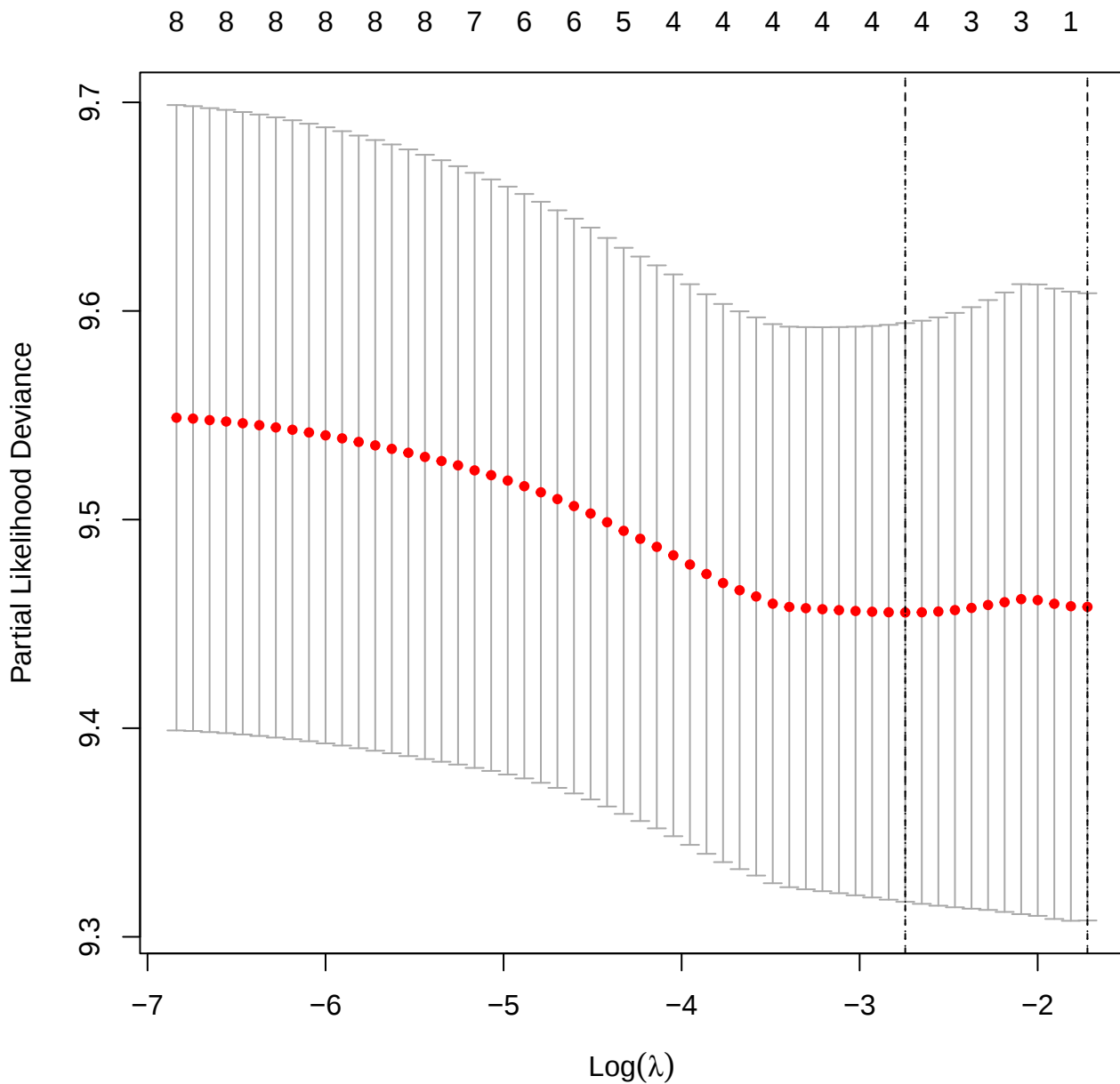
Forest plot



Lasso regression model

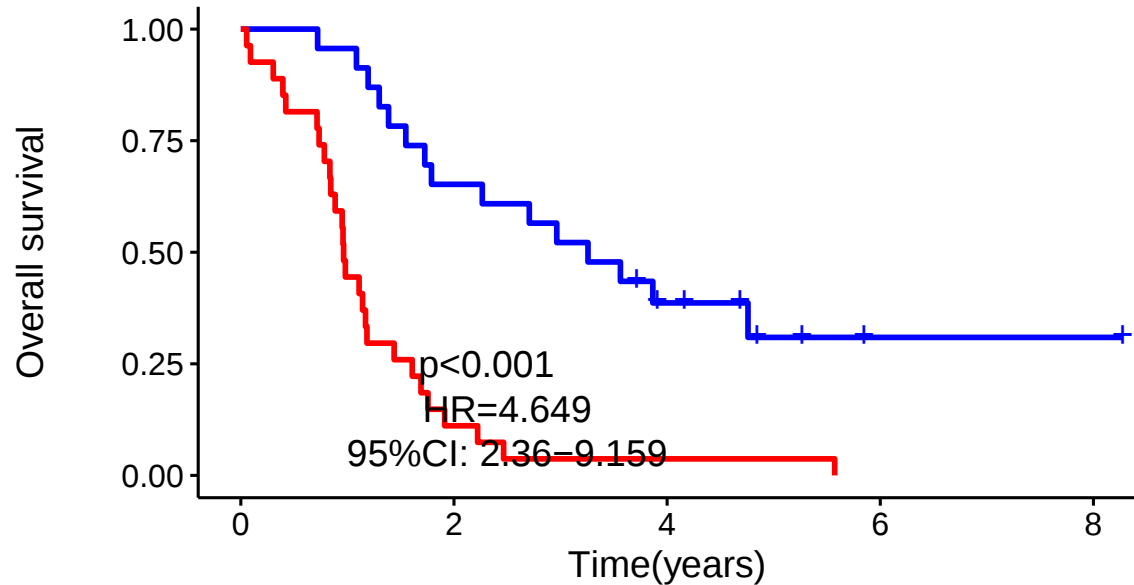


Lasso regression model cross-validat



GEO survival

Risk Low risk High risk



TCGA survival

Risk Low risk High risk

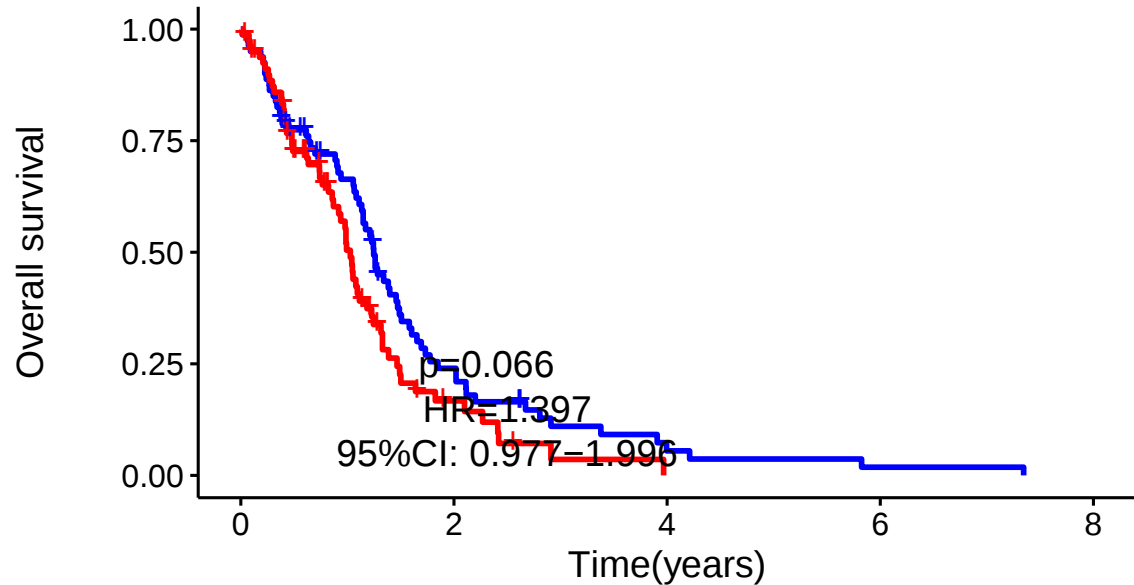


Figure S7:
Statistical analysis of result images presented
in the manuscript

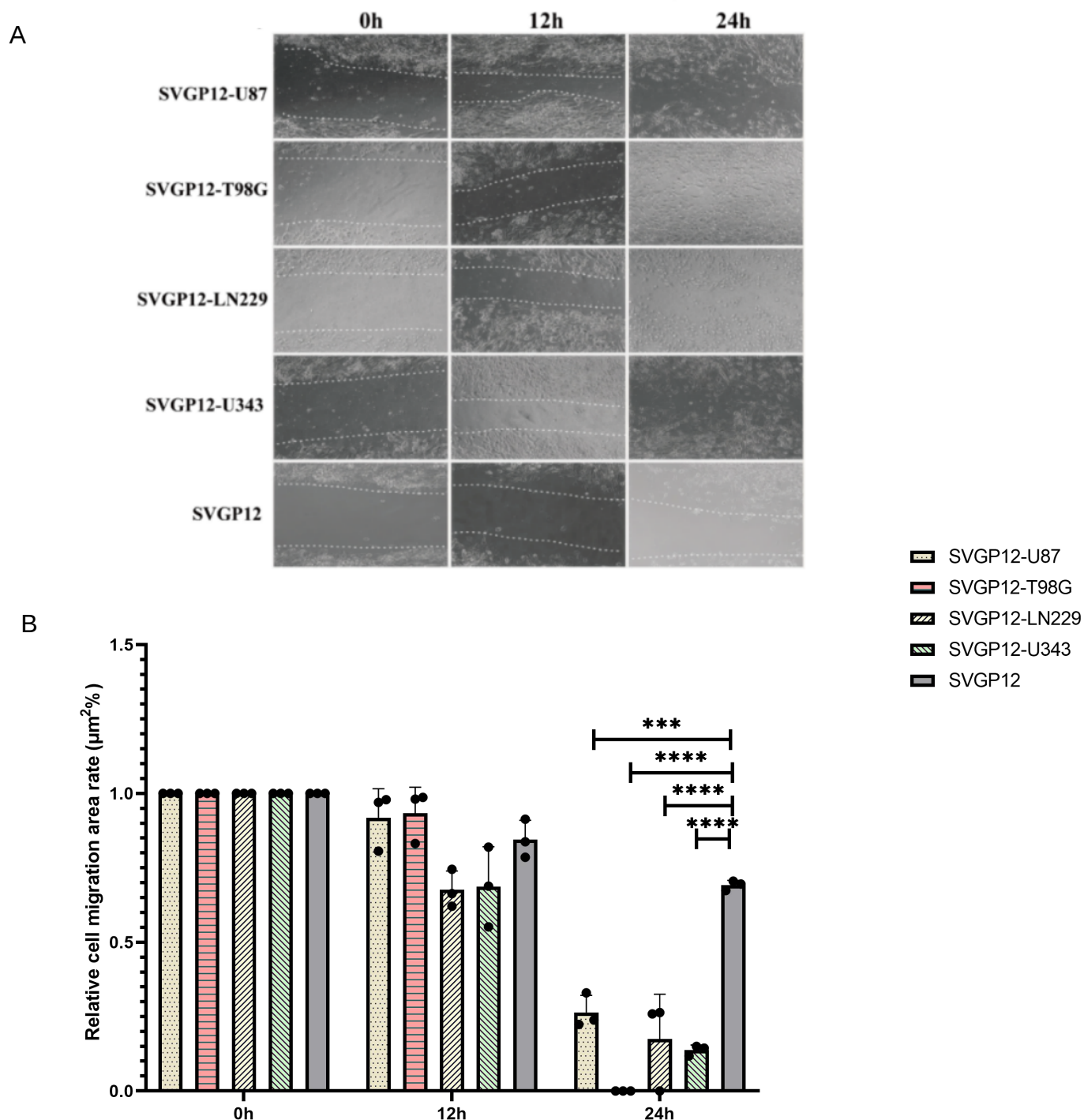
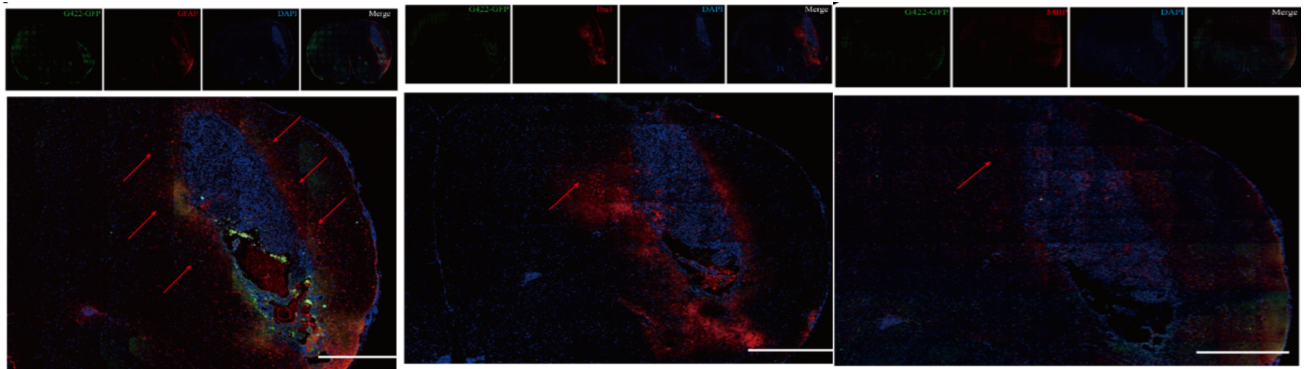


Figure 1. Statistical Analysis of Wound Healing Assay.

(A) Wound healing assay image corresponding to Figure 4F in the manuscript. (B) Quantitative analysis of wound healing assay results. The experiment was repeated three times, and the results are representative of three independent experiments. All experimental data were statistically analyzed using one-way ANOVA. A p-value less than 0.05 was considered statistically significant. In the statistical figures, p-values are indicated with asterisks, where * represents $p < 0.05$, ** represents $p < 0.01$, *** represents $p < 0.001$, and **** represents $p < 0.0001$.

A



B

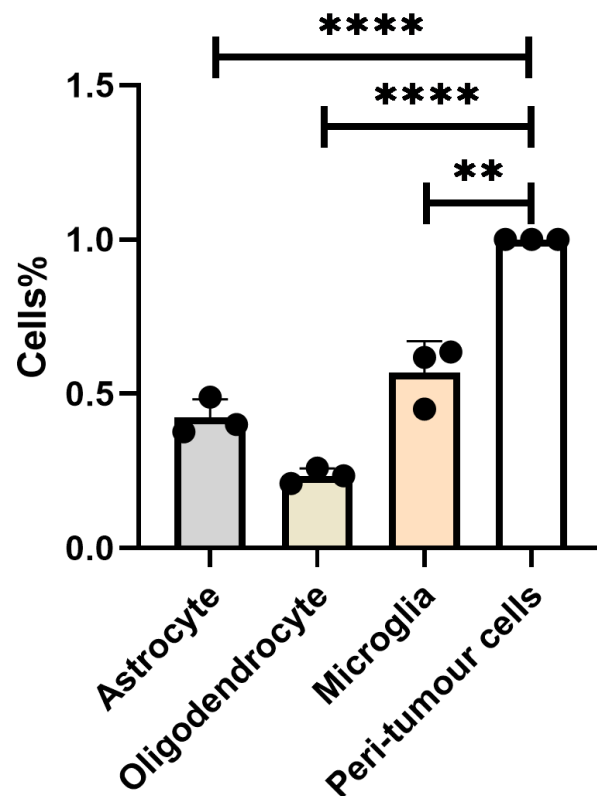


Figure 2. Statistical analysis of cell composition in the peritumoral region. (A) Image corresponding to Figure 3A-C in the manuscript. (B) Quantitative analysis of cell composition in the peritumoral region. The experiment was repeated three times, and the results are representative of three independent experiments. All experimental data were statistically analyzed using one-way ANOVA. A p-value less than 0.05 was considered statistically significant. In the statistical figures, p-values are indicated with asterisks, where * represents $p < 0.05$, ** represents $p < 0.01$, *** represents $p < 0.001$, and **** represents $p < 0.0001$.

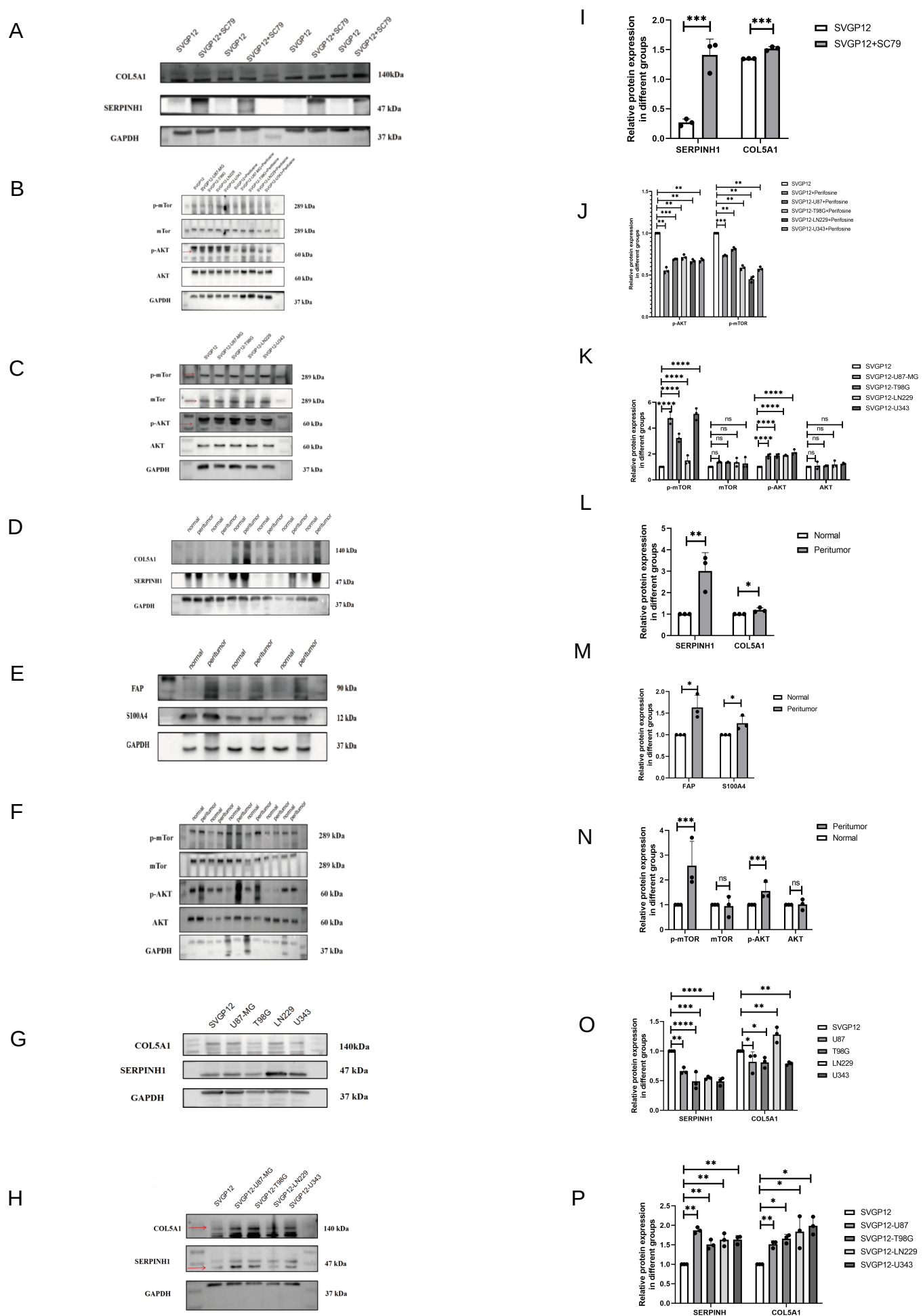
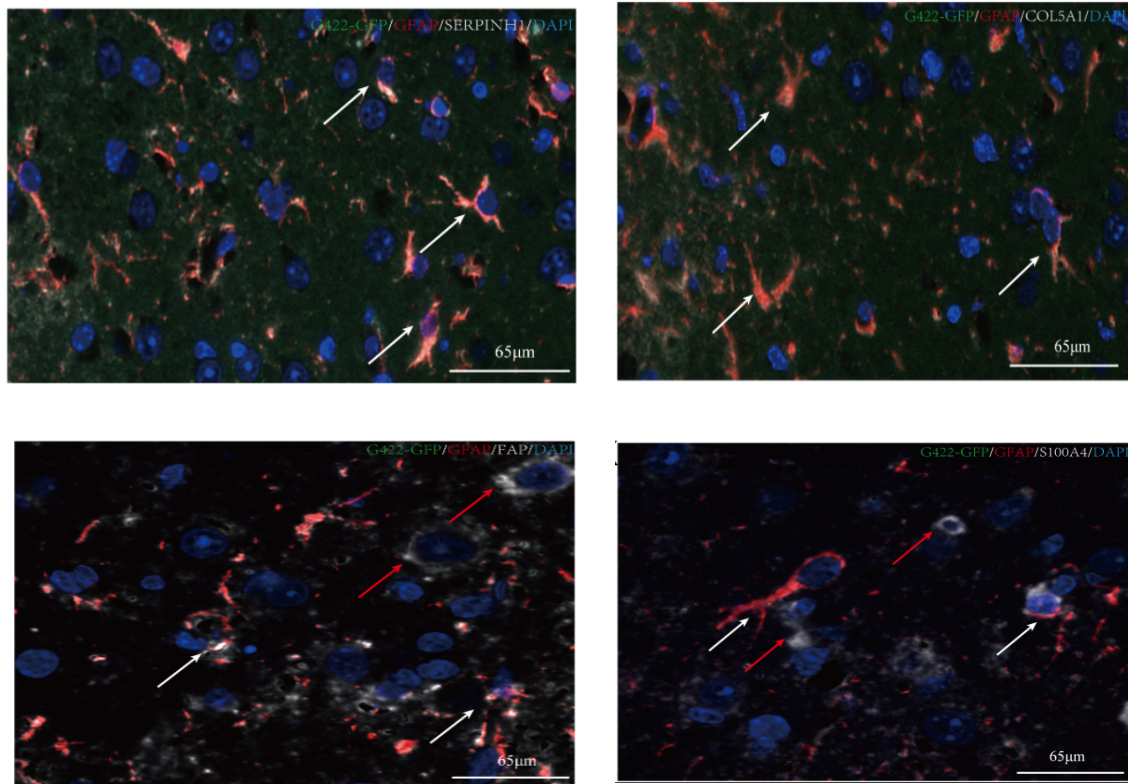


Figure 3. Statistical Analysis of western blot.

(A-H) Western blot result in the manuscript.(I-P) Quantitative analysis of Western blot result.

The experiment was repeated three times, and the results are representative of three independent experiments. The Student's t-test was used for comparisons between two groups, while one-way ANOVA (analysis of variance) was employed for comparisons among multiple groups.. A p-value less than 0.05 was considered statistically significant. In the statistical figures, p-values are indicated with asterisks, where * represents $p < 0.05$, ** represents $p < 0.01$, *** represents $p < 0.001$, and **** represents $p < 0.0001$.

A



B

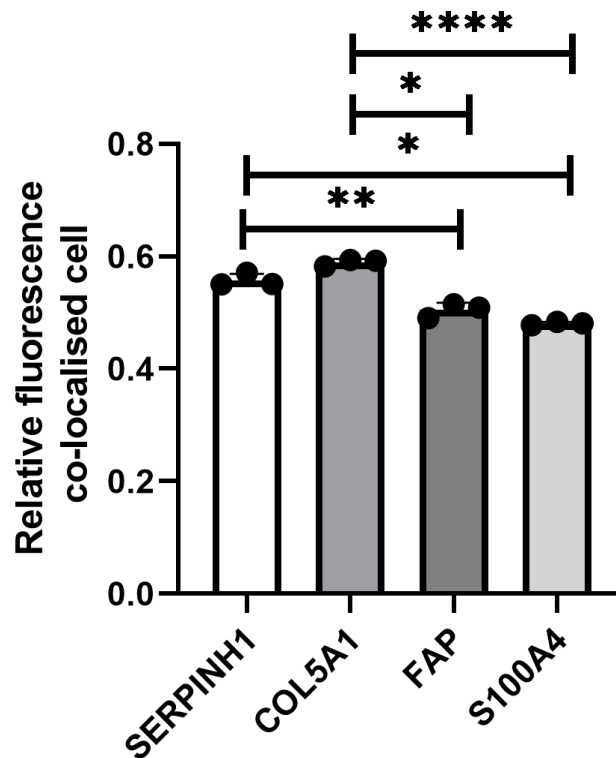
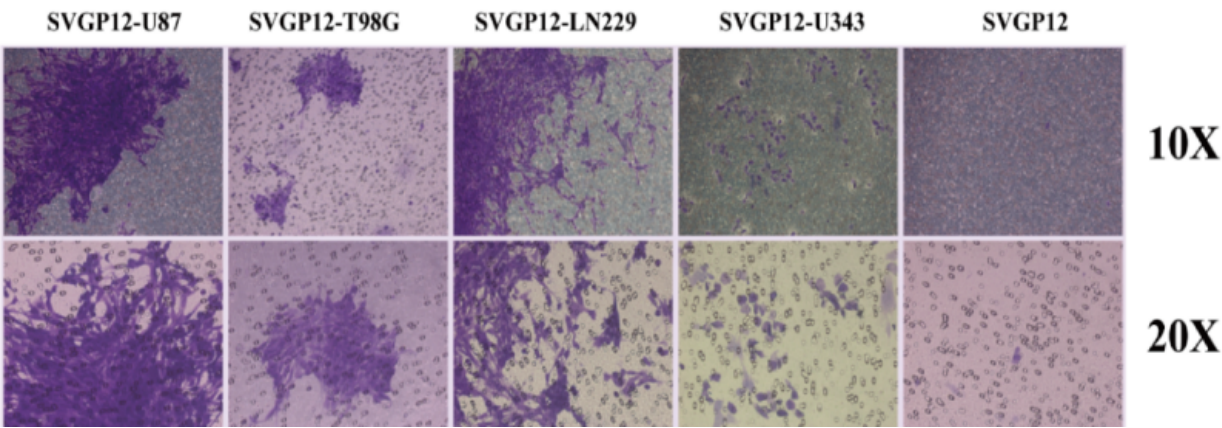


Figure 4. Statistical Analysis of co-localization expression of SERPINH1 and COL5A1 in GBM mouse model.

(A) Co-localization of SERPINH1 and COL5A1 in GBM mouse model corresponding to Figure 3E-K in the manuscript. (B) Quantitative analysis of expression of SERPINH1 and COL5A1 results. The experiment was repeated three times, and the results are representative of three independent experiments. All experimental data were statistically analyzed using one-way ANOVA. A p-value less than 0.05 was considered statistically significant. In the statistical figures, p-values are indicated with asterisks, where * represents $p < 0.05$, ** represents $p < 0.01$, *** represents $p < 0.001$, and **** represents $p < 0.0001$.

A



B

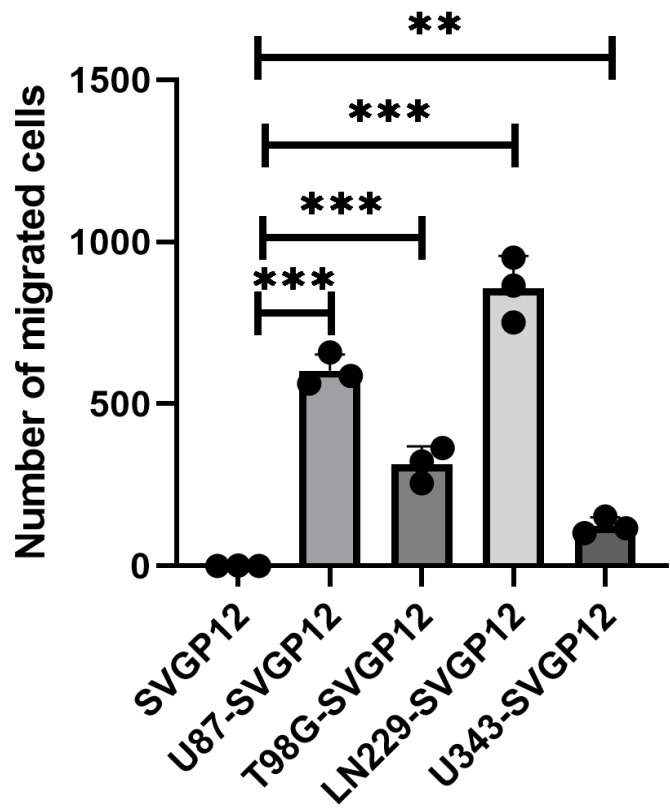


Figure 5. Statistical Analysis of Migration assay.
(A) Migration assay image corresponding to Figure 4G in the manuscript.(B) Quantitative analysis of Migration assay results. The experiment was repeated three times, and the results are representative of three independent experiments. All experimental data were statistically analyzed using one-way ANOVA. A p-value less than 0.05 was considered statistically significant. In the statistical figures, p-values are indicated with asterisks, where * represents $p < 0.05$, ** represents $p < 0.01$, *** represents $p < 0.001$, and **** represents $p < 0.0001$.

Material S1

Declaration of animal experiment and Animal Ethics Review Certificate

The animal experiments in this study(*Glioblastoma recruits and activates CAF-like astrocytes via the AKT/m-TOR-SERPINH1/COL5A1 axis*) carried out in accordance with Guidance on the operation of the Animals (Scientific Procedures) Act 1986 and associated guidelines, EU Directive 2010/63 for the protection of animals used for scientific purposes or the NIH (National Research Council) Guide for the Care and Use of Laboratory Animals. All animal treatments and experiments were approved by the Laboratory Animal Ethics Committee of Shantou University Medical College (The ethical review number: SUMCSY2024-002). The experimental Animal Ethics Review Certificate is as follow.

Shantou University Medical College

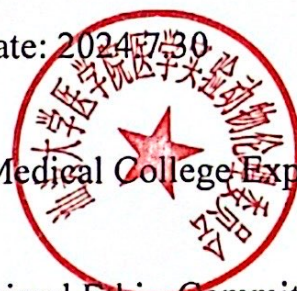
Experimental Animal Ethics Review Certificate

This certifies that the animal experiment Exploring the role of astrocytes in the microenvironment of mouse glioblastoma conducted by the project leader Zhang Jingxian, has been carried out in our Experimental Animal Center at Shantou University Medical College. The entire project process has been supervised by the Shantou University Medical College Experimental Animal Ethics Committee and has passed ethical review. The ethical review number is SUMCSY2024-002.

Date: 2024.7.30

Shantou University Medical College Experimental

Animal Ethics Committee (Seal)



Material S2

CERTIFICATE

OF ENGLISH LANGUAGE EDITING



Glioblastoma recruits and activates CAF-like astrocytes via the AKT/m-TOR-SERPINH1/COL5A1 axis

Background: Glioblastoma multiforme (GBM), the highest-grade glioma, remains the most malignant tumor of the central nervous system, and is one of the most poorly understood malignancies worldwide. Despite treatment options such as surgery and chemotherapy, the prognosis for patients with GBM remains poor, highlighting an urgent need for new therapeutics to inhibit GBM development. The tumor microenvironment is a crucial factor in tumor development. Cancer-associated fibroblasts (CAFs) play multiple roles as important components of the tumor microenvironment. The roles of CAFs in tumorigenesis and drug resistance have been investigated using subgroup analysis and functional studies to discover CAF-specific markers and secretagogues. However, the origin, composition, and localization of CAFs within the GBM microenvironment have not been clarified. Exploring CAFs will provide ...

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Material S3

We have uploaded the code and data from the manuscript to a database. The link and schematic representation are as follows.
https://osf.io/ztyg7/?view_only=69d98a240c954d9fbb105f6877e59dd0

Glioblastoma recruits and activates CAF...

MetadataFiles

Glioblastoma recruits and activates CAF-like astrocytes via the AKT/m-TOR-SERPINH1/COL5A1 axis

Contributors: Anonymous Contributors

Date created: 2024-12-20 09:42 AM | Last Updated: 2024-12-20 09:55 AM

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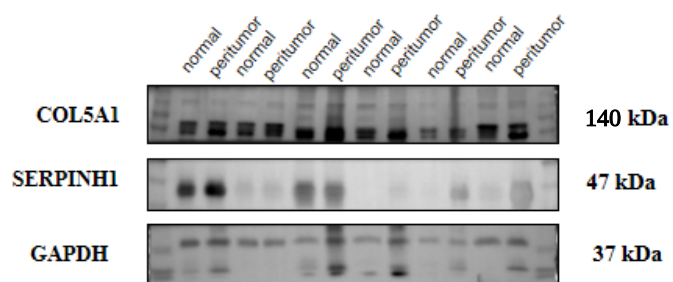
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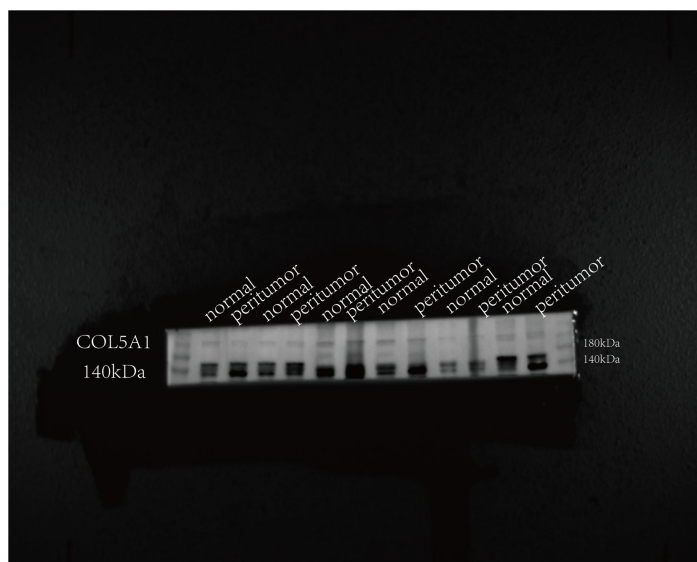
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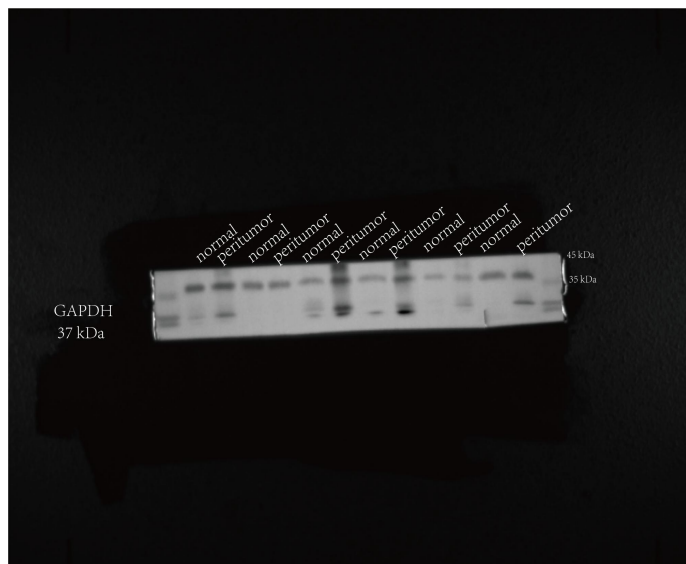
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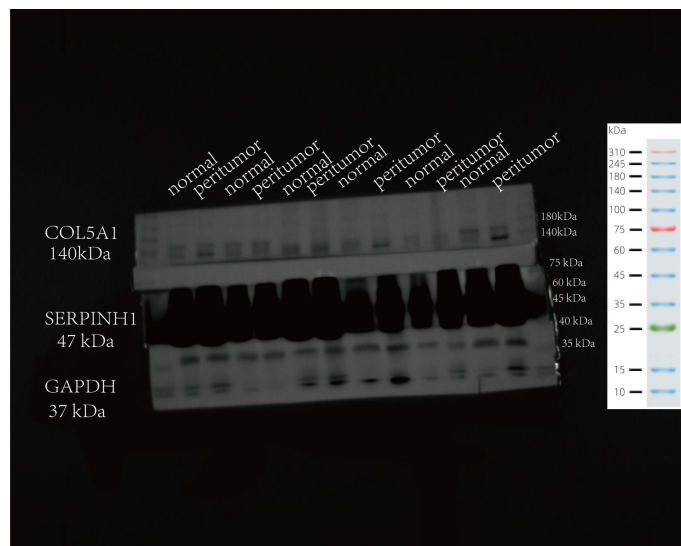
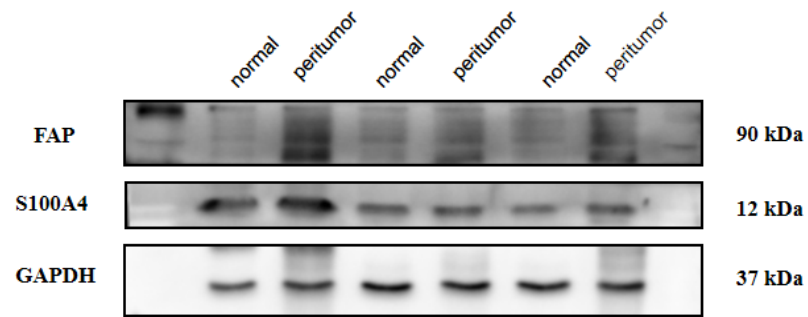


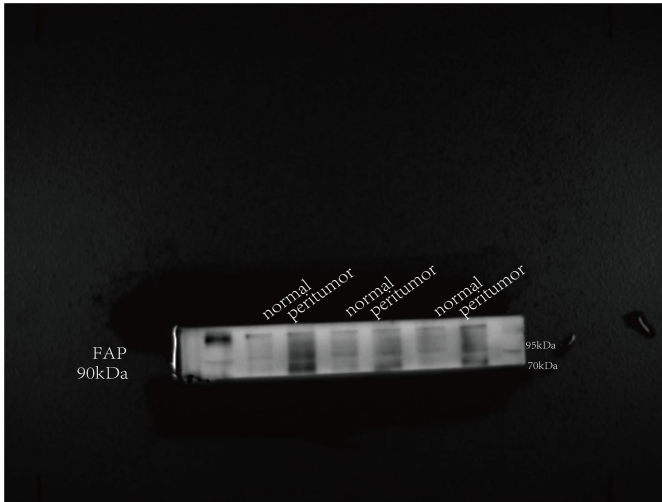
Figure1. The full uncropped westernblot figure of Figure 2I .

(A)Westernblot figure in the artical. (B)Single COL5A1 image. (C) Single SERPINH1 images. (D) Single GAPDH images. (E)The whole exposure film membrane image.

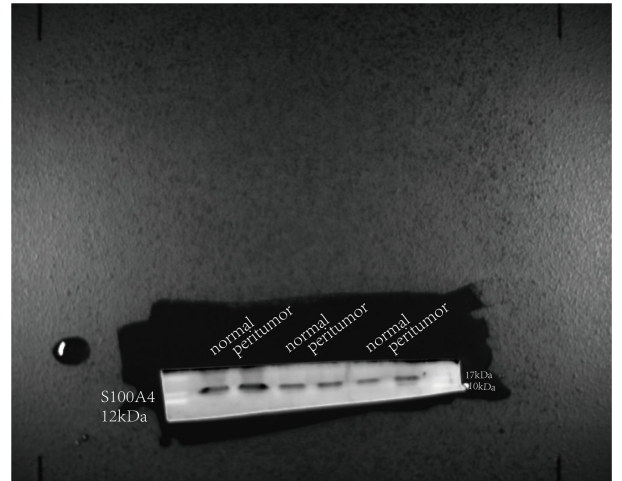
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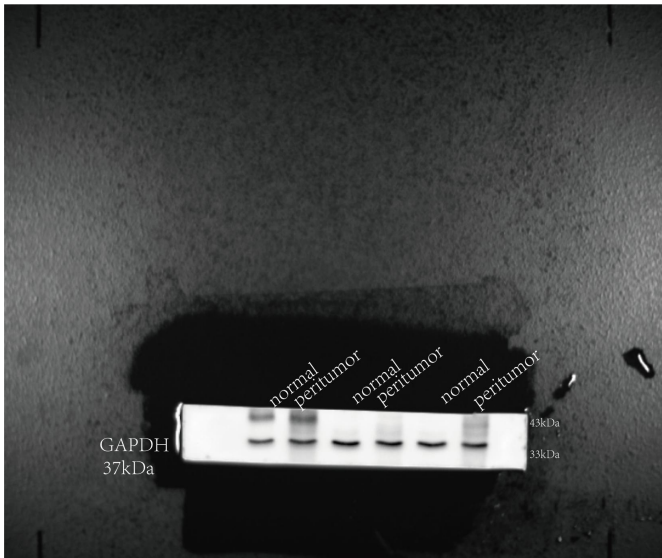


Figure2. The full uncropped westernblot figure of Figure 2J.

(A)Westernblot figure in the artical. (B)Single FAP image. (C) Single S100A4 images. (D) Single GAPDHimages.

Due to the large difference in protein size, each protein needs to be separated for Westernblot experiments. Therefore, there is no whole exposure film membrane image.

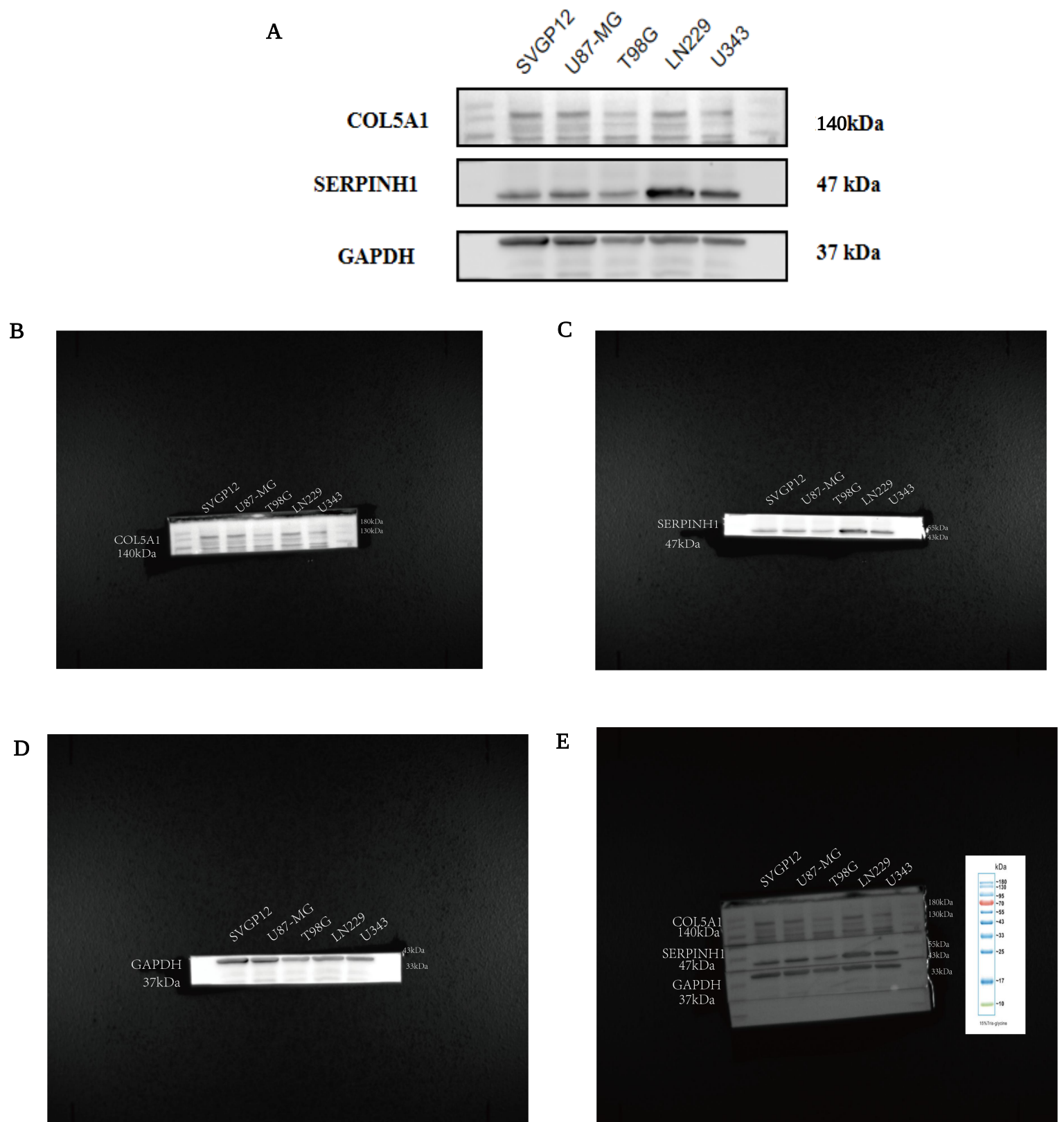


Figure3. The full uncropped westernblot figure of Figure 4A.

(A)Westernblot figure in the artical. (B)Single COL5A1 image. (C) Single SERPINH1 images. (D) Single GAPDH images. (E)The whole exposure film membrane image.

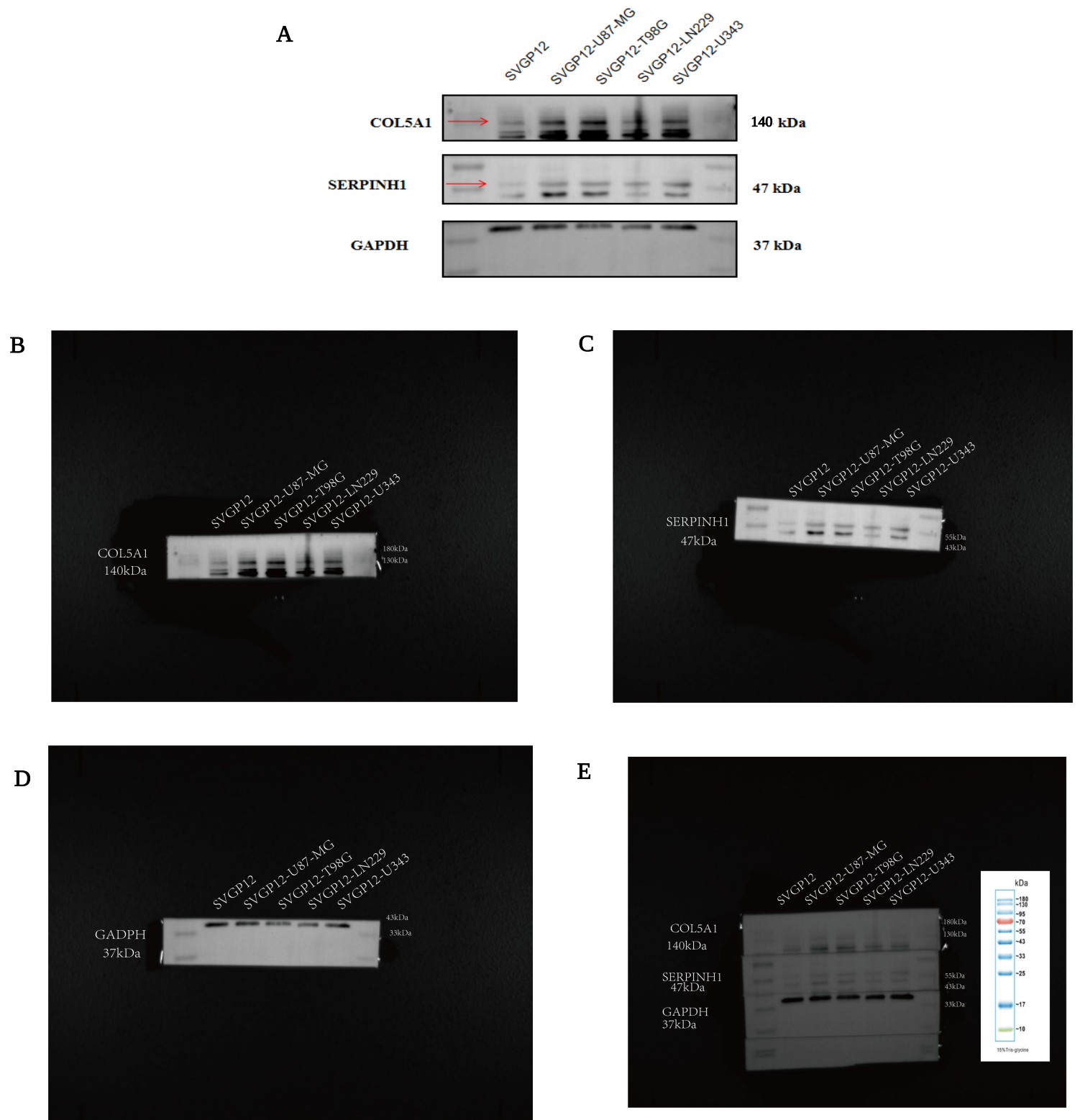


Figure4. The full uncropped westernblot figure of Figure 4C .

(A)Westernblot figure in the artical. (B)Single COL5A1 image. (C) Single SERPINH1 images. (D) Single GAPDH images. (E)The whole exposure film membrane image.

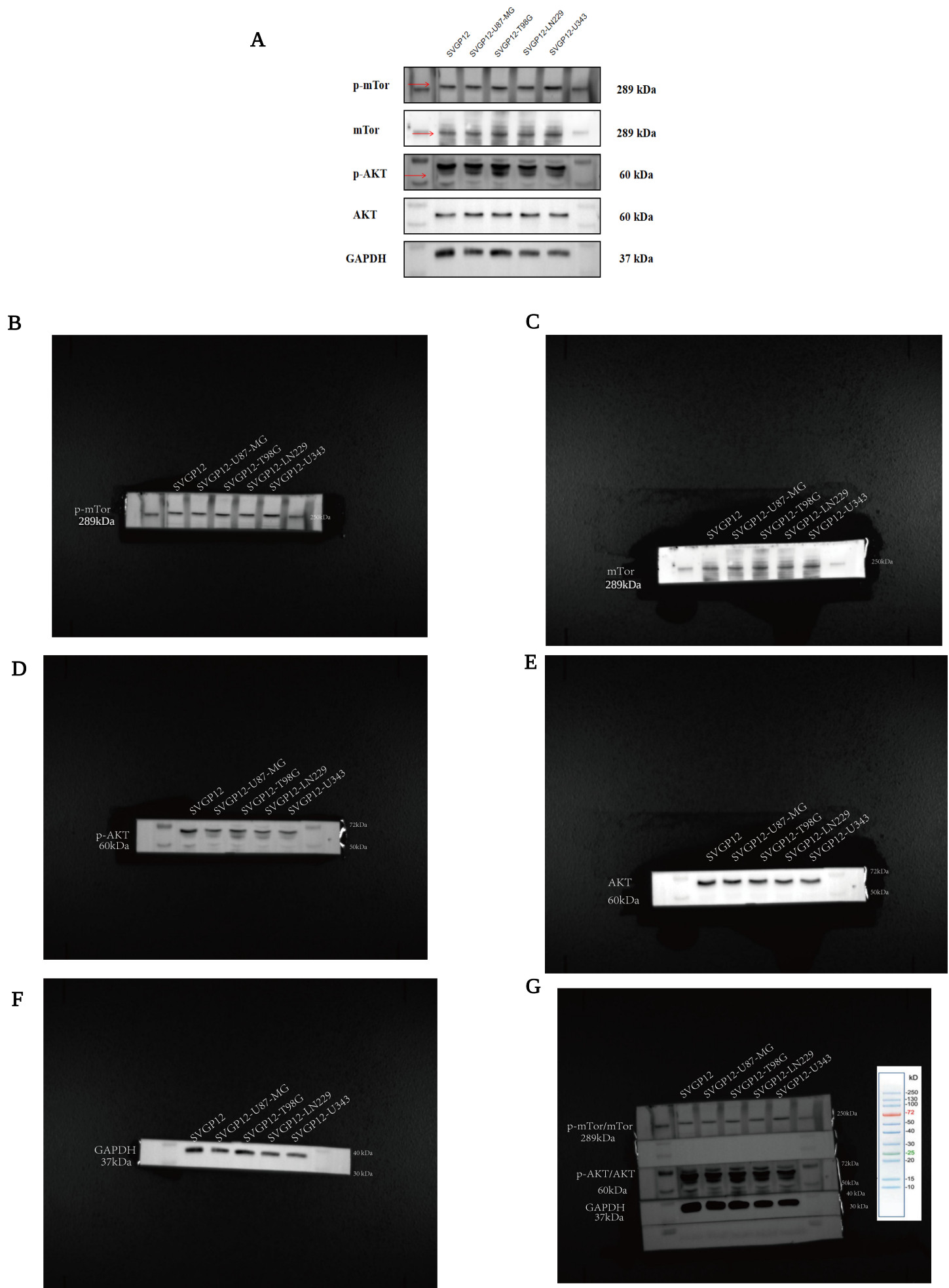


Figure5. The full uncropped westernblot figure of Figure 5B .

(A)Westernblot figure in the artical. (B)Single p-mTOR image. (C) Single mTOR images. (D) Single p-AKT images. (E) Single AKT images. (F)Single GAPDH images.(G)The whole exposure film membrane image. After exposure of the phosphorylated protein strips, the strips were eluted before incubating the non-phosphorylated proteins. So, the same housekeeping gene protein strips were used.

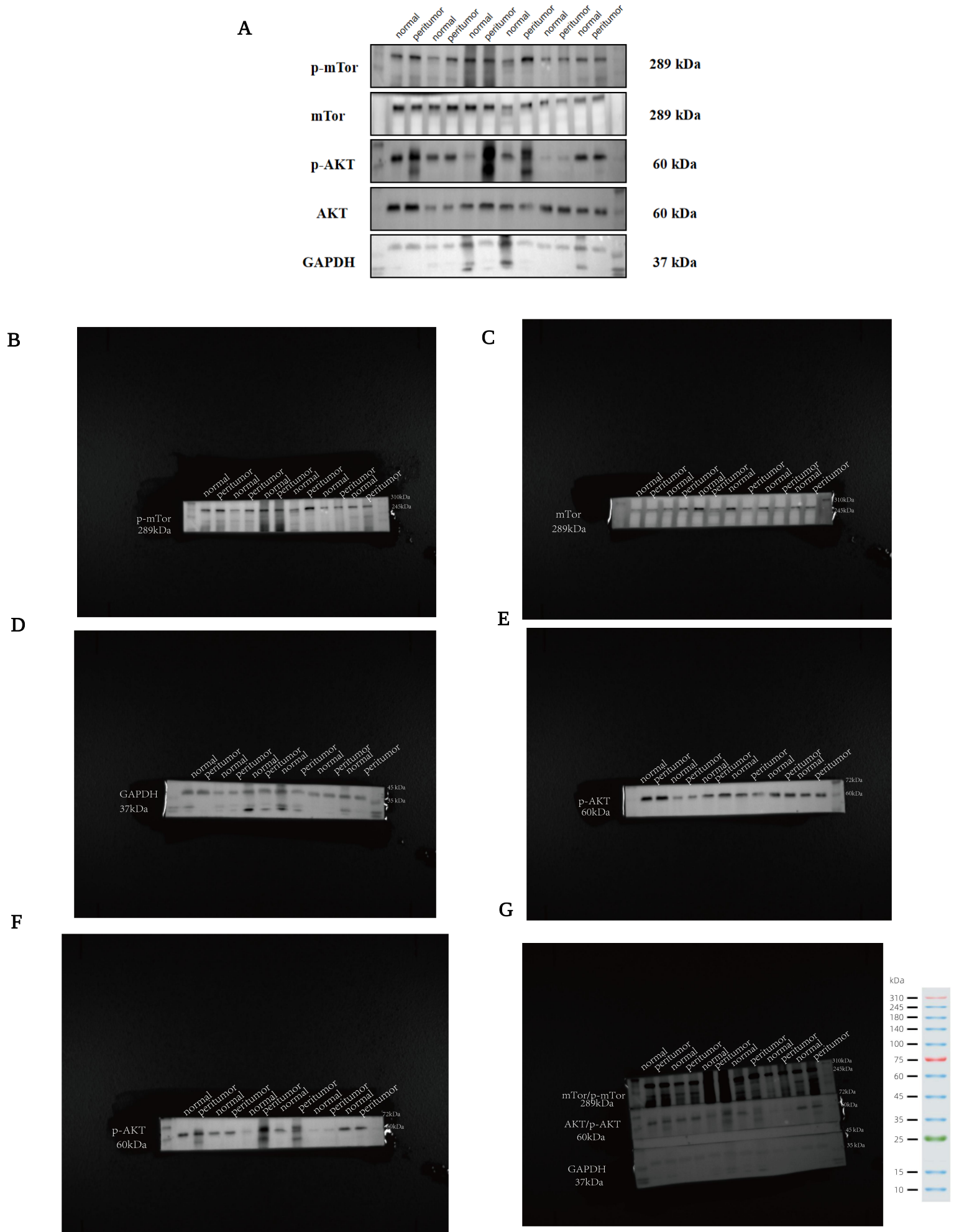
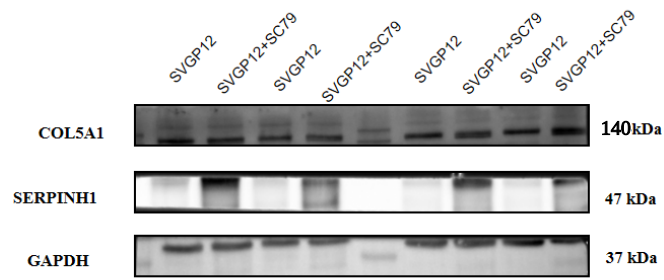


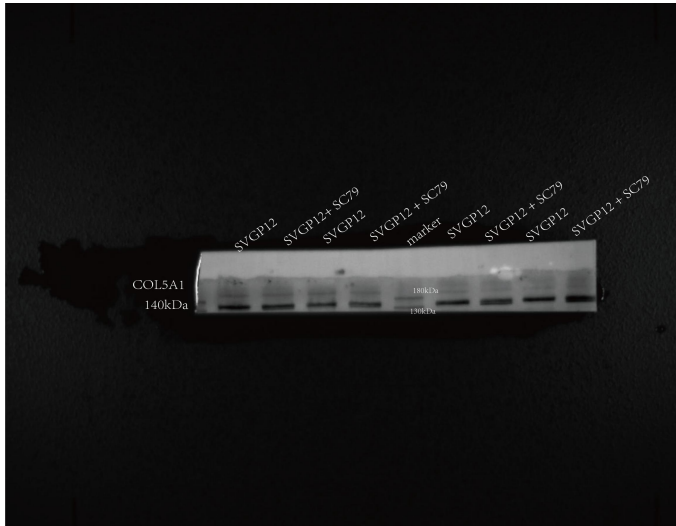
Figure6. The full uncropped westernblot figure of Figure 5C.

(A)Westernblot figure in the artical. (B)Single p-mTOR image. (C) Single mTOR images. (D) Single p-AKT images. (E) Single AKT images. (F)Single GAPDH images.(G)The whole exposure film membrane image. After exposure of the phosphorylated protein strips, the strips were eluted before incubating the non-phosphorylated proteins. So, the same housekeeping gene protein strips were used.

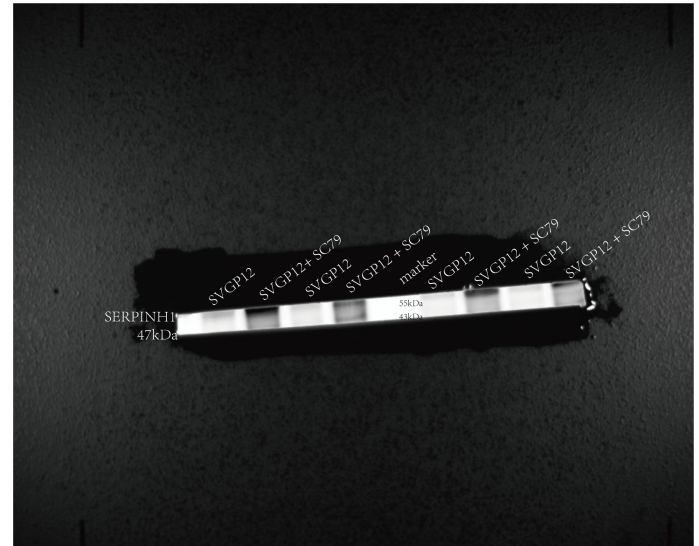
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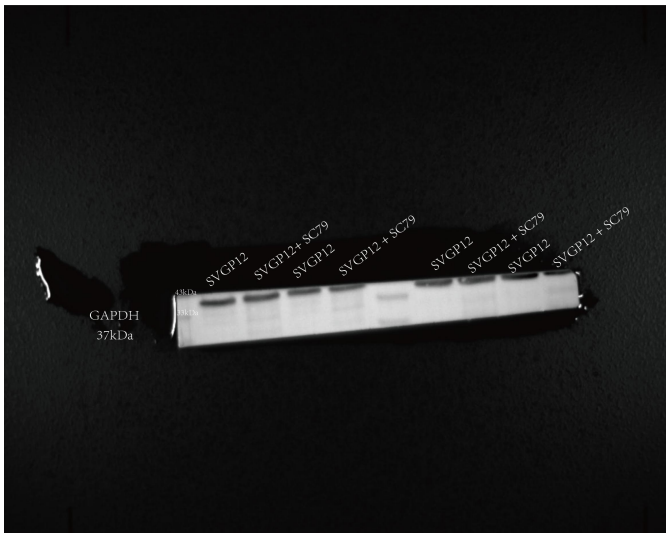
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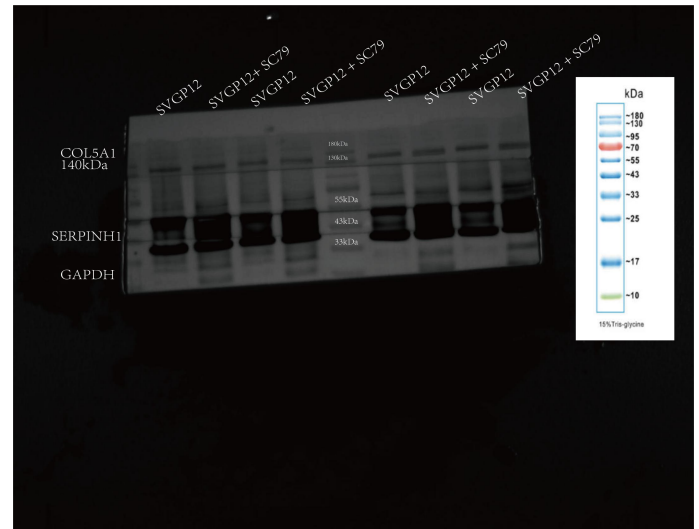


Figure7. The full uncropped westernblot figure of Figure 5D.

(A)Westernblot figure in the artical. (B)Single COL5A1 image. (C) Single SERPINH1 images. (D) Single GAPDH images. (E)The whole exposure film membrane image.

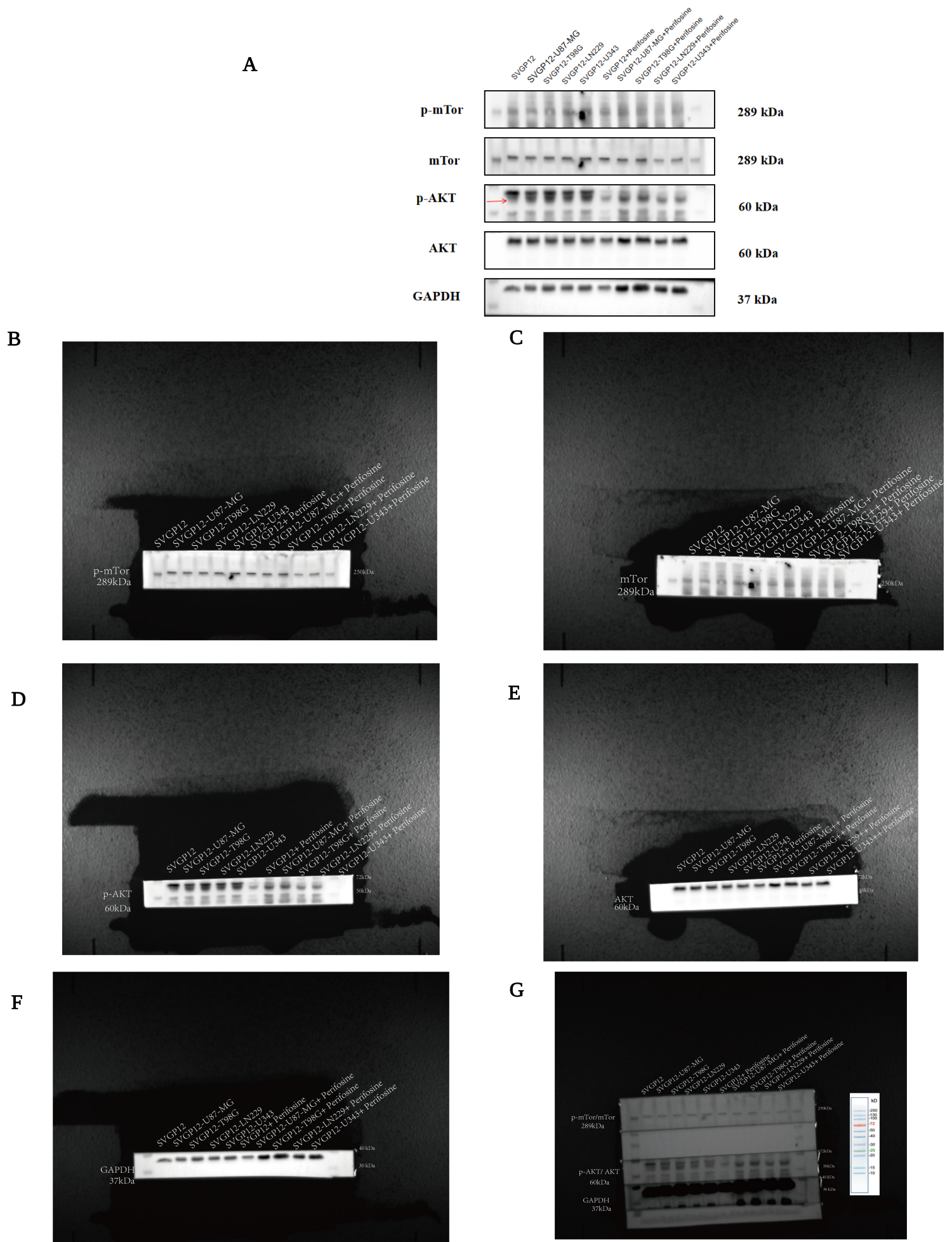


Figure8. The full uncropped westernblot figure of Figure 5F. (A)Westernblot figure in the artical. (B)Single p-mTOR image. (C) Single mTOR images. (D) Single p-AKT images. (E) Single AKT images. (F)Single GAPDH images.(G)The whole exposure film membrane image. After exposure of the phosphorylated protein strips, the strips were eluted before incubating the non-phosphorylated proteins. So, the same housekeeping gene protein strips were used.

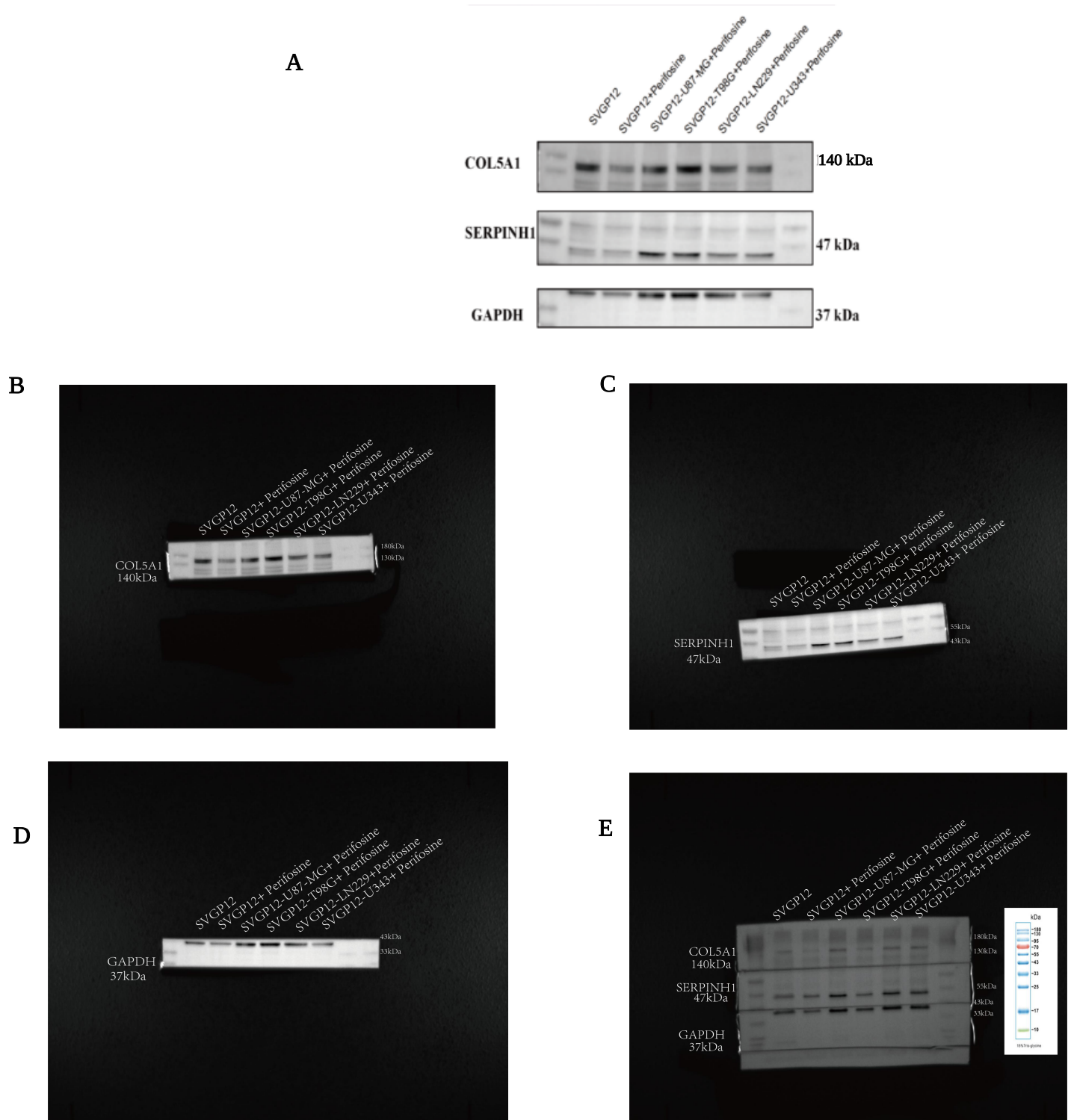


Figure9. The full uncropped westernblot figure of Figure 5G.

(A)Westernblot figure in the artical. (B)Single COL5A1 image. (C) Single SERPINH1 images. (D) Single GAPDH images. (E)The whole exposure film membrane image.