

Figure S1 Landscape of somatic mutations in each group. The most frequently mutated genes in this cohort were shown. The top panel represents the TMB in each sample. The middle panel represents the matrix of alterations in a selection of frequently mutated genes. Columns represent samples. Clinicopathological characteristics of the LN stage are presented below. TMB, tumor mutational burden; LN, lymph node.

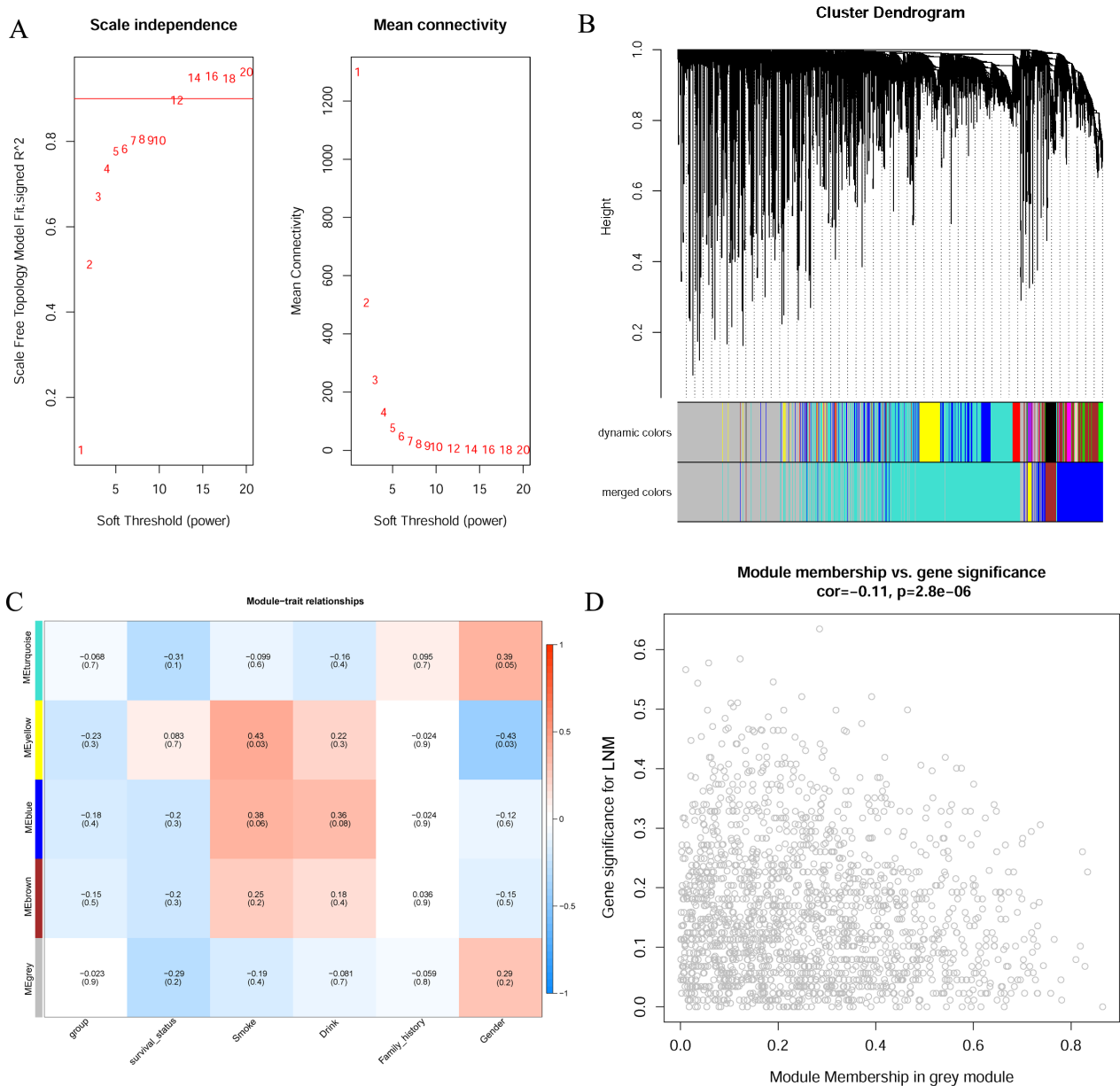


Figure S2 Construction of co-expression network through WGCNA. (A) Network topology for different soft-thresholding powers. (B) A cluster diagram of gene cluster of SCLC. (C) Heatmap of the correlation between module eigengenes and the clinical features. (D) The correlation of LNM-related module membership and gene significance. WGCNA, weighted gene co-expression network analysis. LNM, lymph node metastasis.

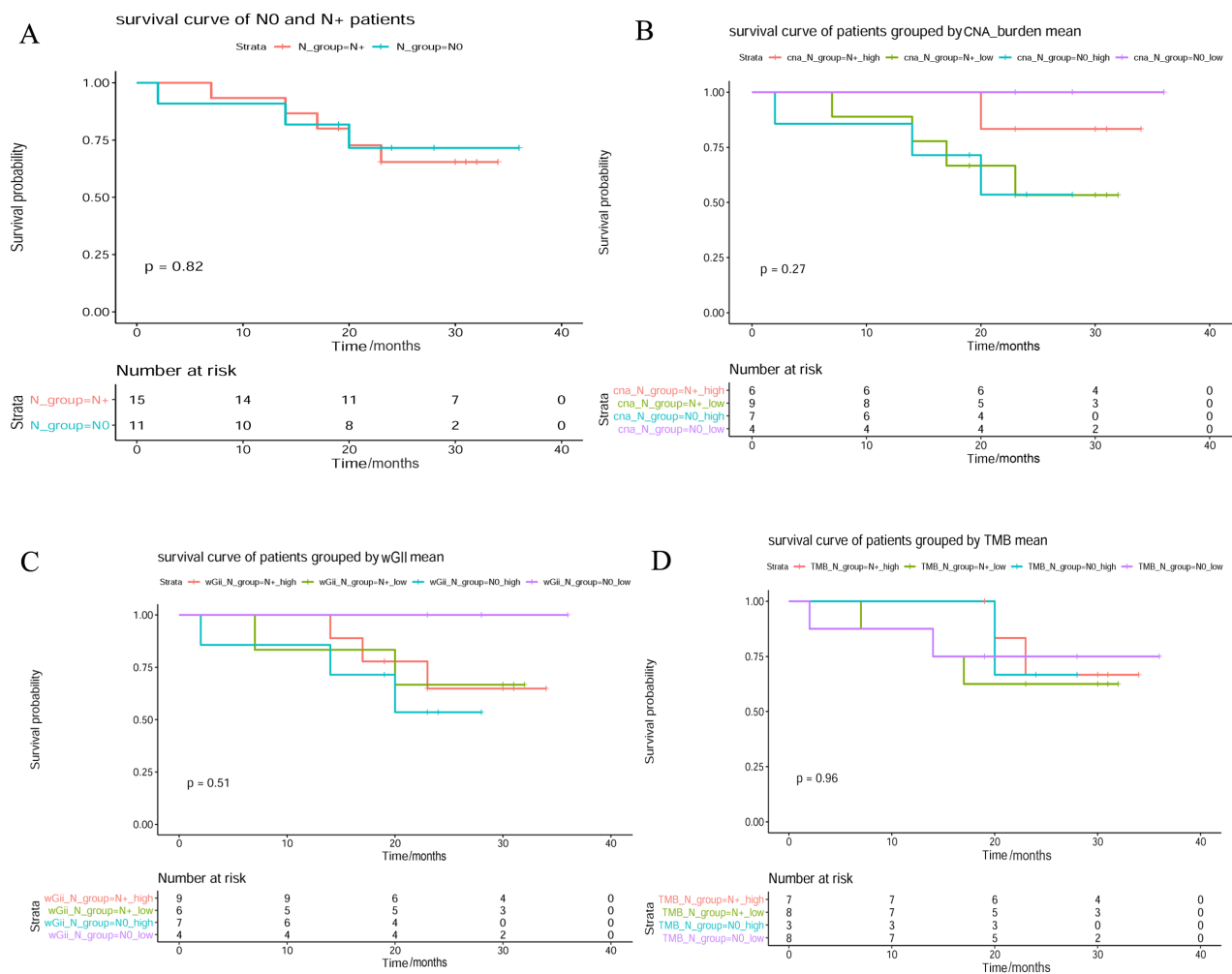


Figure S3 Overall survival analysis. (A) Survival analysis of N0 and N+; (B) survival analysis of CNA burden in N0 and N+ patients; (C) survival analysis of wGII in N0 and N+ patients; (D) survival analysis of TMB in N0 and N+ patients. CNA, copy number alteration; wGII, weighted Genome Instability Index; TMB, tumor mutational burden.

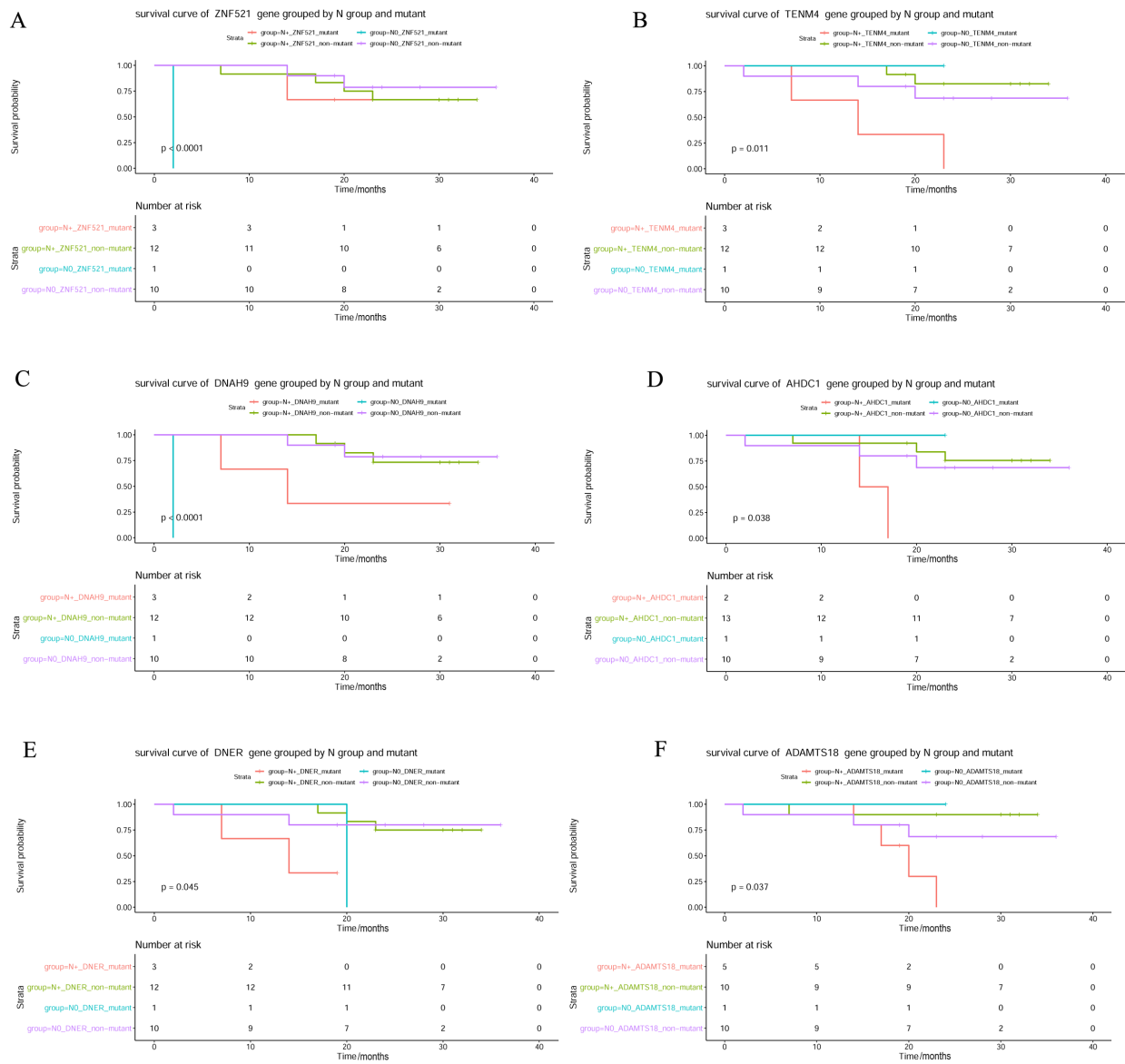


Figure S4 Overall survival analysis. (A) Survival analysis of ZNF521 mutation in N0 and N+ patients; Survival analysis of TENM4, DNAH9, AHDC1, DNER, and ADAMTS18 mutation (B-F) in N0 and N+ patients.

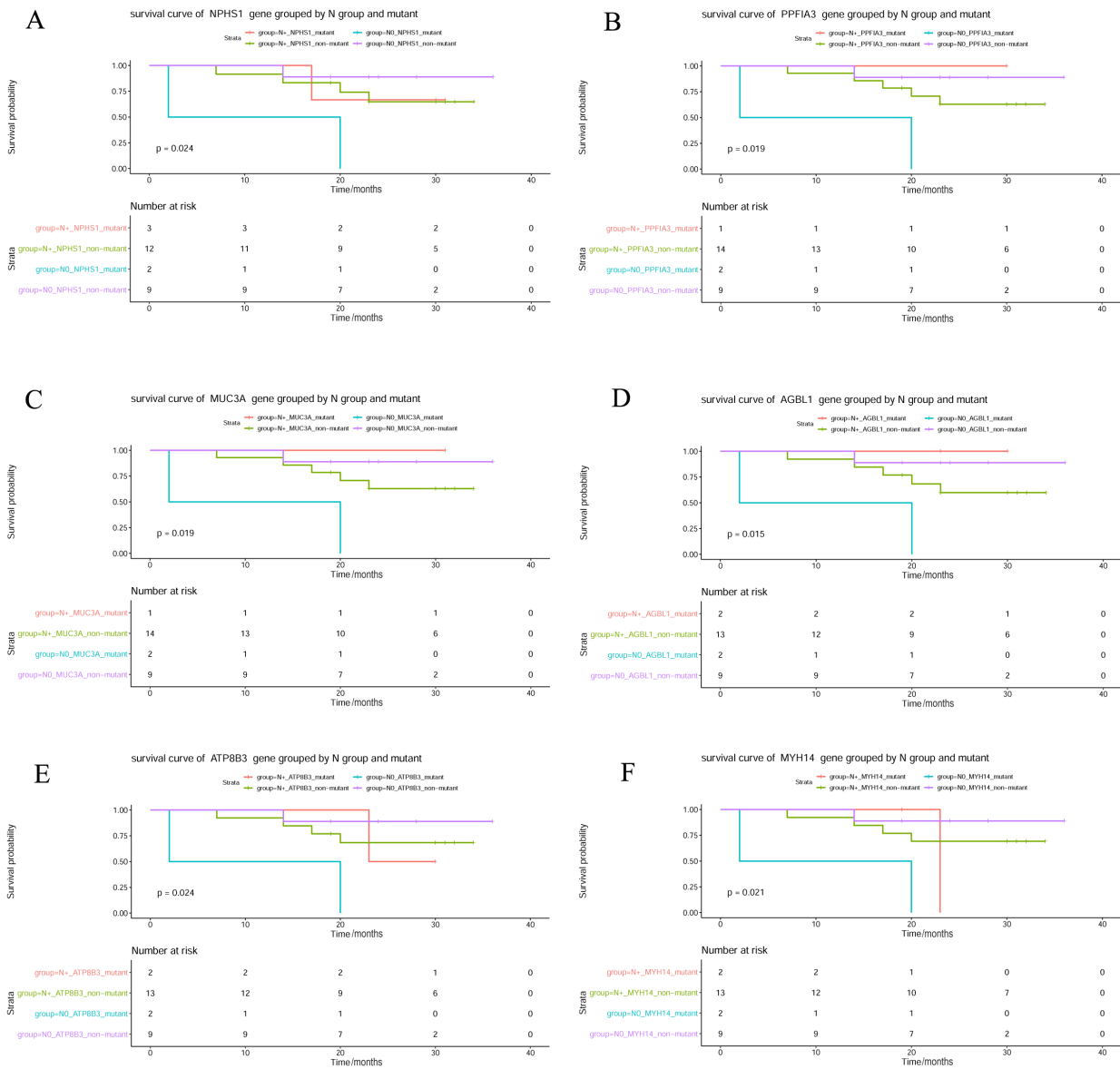


Figure S5 Overall survival analysis. Survival analysis of *NPHS1*, *PPFIA3*, *MUC3A*, *AGBL1*, *ATP8B3*, and *MYH14* mutation (A-F) in N0 and N+ patients.

Table S1 Comparison of CNV in N0 and N+ SCLC

	N0			N+				
	Cytoband	q value	Residual q value	Wide peak boundaries	Cytoband	q value	Residual q value	Wide peak boundaries
	9p24.3	1.15E-18	1.15E-18	chr9:107381-179012	16p11.2	3.19E-25	3.19E-25	chr16:31917855-46467006
	22q11.1	1.15E-18	1.15E-18	chr22:1-17048481	22q11.1	3.19E-25	3.19E-25	chr22:1-17048418
	9q13	1.15E-18	3.71E-11	chr9:47307204-70928318	9q13	4.35E-25	5.98E-18	chr9:47307203-70928318
	7p13	1.19E-18	1.19E-18	chr7:43982540-44095178	2q12.2	4.68E-25	4.68E-25	chr2:106800892-107094587
	16p11.2	1.19E-18	1.19E-18	chr16:31927566-46467006	12q24.31	7.71E-25	7.71E-25	chr12:125296404-125408863
	12q24.31	1.64E-18	2.35E-15	chr12:125297491-125407110	17q21.2	1.95E-24	1.95E-24	chr17:39183147-39427187
	2q11.2	1.79E-18	1.79E-18	chr2:97771742-98215296	1q21.2	3.69E-24	2.56E-16	chr1:147456277-149709685
	1q21.2	7.00E-18	9.37E-14	chr1:147994869-149859509	14q11.2	1.40E-23	1.40E-23	chr14:1-20181853
	17q12	1.67E-17	1.67E-17	chr17:36275041-36463073	7q22.1	1.89E-22	1.89E-22	chr7:100635464-100656953
	14q11.2	3.41E-17	3.41E-17	chr14:1-20181853	7p13	4.71E-22	4.71E-22	chr7:43982540-44095178
	11q14.3	3.49E-16	3.49E-16	chr11:89522931-89712272	11q14.3	1.33E-21	1.33E-21	chr11:89443434-89711422
	7q22.1	5.62E-16	5.62E-16	chr7:101952394-101996816	1p21.1	1.41E-21	1.78E-21	chr1:104083769-104761379
	2p11.2	7.46E-16	7.46E-16	chr2:88043238-88337138	13q21.1	1.52E-21	1.52E-21	chr13:57704909-57903580
	13q21.1	9.39E-16	9.39E-16	chr13:57705133-57903414	18q21.1	1.52E-21	1.52E-21	chr18:44517288-44569285
	13q21.1	9.39E-16	1	chr13:1-115169878	9p24.3	2.58E-21	2.58E-21	chr9:107381-179012
	10q23.2	1.47E-14	3.46E-07	chr10:88760075-88782161	16q23.1	4.57E-19	4.57E-19	chr16:74419231-74455225
	6p25.2	1.91E-14	1.91E-14	chr6:3152707-3236338	2p11.2	8.97E-18	8.97E-18	chr2:88043238-88337271
	8p23.1	4.06E-14	4.06E-14	chr8:6784636-7282345	6p25.2	1.12E-17	1.12E-17	chr6:3152707-3236275
	19p12	7.07E-14	7.07E-14	chr19:22145150-22166723	18p11.21	2.48E-17	2.48E-17	chr18:14132216-14758294
Gain	10q22.2	7.07E-14	0.000222	chr10:75405781-75515680	15q11.2	4.58E-17	4.58E-17	chr15:1-22378561
	18q21.1	1.18E-13	1.18E-13	chr18:44534810-44569285	10q23.2	1.60E-15	1.60E-15	chr10:88760075-88791677
	12p13.2	1.46E-13	1.46E-13	chr12:11420126-11557260	12p13.2	1.60E-15	1.60E-15	chr12:11496049-11685746
	16q23.1	3.64E-13	3.64E-13	chr16:74415497-74455225	10q23.2	1.60E-15	1	chr10:1-135534747
	18p11.21	5.40E-13	5.40E-13	chr18:14502027-14758294	1q21.1	6.29E-15	0.011336	chr1:121474967-144611963
	1q21.1	1.74E-11	0.11796	chr1:121474974-144614416	19p12	4.82E-14	4.82E-14	chr19:22145150-22166061
	15q11.2	2.53E-11	2.53E-11	chr15:20737152-22378437	8p23.1	7.24E-14	7.24E-14	chr8:6784636-7282306
	3q29	8.27E-11	8.27E-11	chr3:195296404-195456623	21q22.3	1.43E-13	1.43E-13	chr21:45944022-46140892
	1p21.1	2.27E-10	0.0001026	chr1:104083752-104162410	9q21.32	2.95E-13	2.45E-09	chr9:84413337-84608030
	10p11.21	6.24E-10	6.24E-10	chr10:37426483-37500112	5q35.2	4.84E-12	4.84E-12	chr5:175394899-175540875
	5p15.33	7.66E-10	7.66E-10	chr5:741667-850724	5p15.33	1.11E-11	1.11E-11	chr5:741667-850724
	21q22.3	1.62E-09	1.62E-09	chr21:45943807-46076172	10p11.21	8.34E-10	1.19E-08	chr10:37426483-37486430
	9q21.32	1.73E-09	4.70E-05	chr9:84413337-84571467	10p11.21	8.34E-10	1	chr10:1-135534747
	19q13.31	1.18E-08	1.18E-08	chr19:43218317-43717356	3q29	7.24E-08	7.24E-08	chr3:195296864-195456623
	1p36.13	6.64E-08	0.0013874	chr1:16775662-17215903	19q13.31	0.00061854	0.00061854	chr19:43218317-43702466
5q35.2	4.93E-07	4.93E-07	chr5:175394899-175541064	11p11.12	0.01835	0.01835	chr11:48501609-49178190	
5q35.2	4.93E-07	1	chr5:1-180915260	4p16.1	0.051361	0.051361	chr4:9153195-9793628	
12q12	2.78E-05	0.057356	chr12:33550349-39074501	8q24.21	0.14024	0.14024	chr8:127846011-130761793	
11p11.12	0.0012849	0.0012849	chr11:48501415-49168521					
8q12.3	0.057356	0.057356	chr8:62550476-63171905					
4p16.1	0.21674	0.21674	chr4:9154130-9410691					

Table S1 (continued)

Table S1 (continued)

	N0				N+			
	Cytoband	q value	Residual q value	Wide peak boundaries	Cytoband	q value	Residual q value	Wide peak boundaries
	16q12.2	1.07E-13	1.07E-13	chr16:56226267-56294594	16q22.2	1.05E-20	1.05E-20	chr16:56196234-88872136
	9q21.33	3.42E-13	3.42E-13	chr9:89772196-90341960	6p21.33	2.11E-20	2.11E-20	chr6:28851652-33382945
	16p13.3	1.51E-12	1.51E-12	chr16:2153702-2169209	16p13.3	2.11E-20	2.11E-20	chr16:2142906-2168486
	6p21.32	1.03E-11	1.03E-11	chr6:32066515-33382945	7p21.3	4.10E-17	4.10E-17	chr7:7308189-7681446
	7p21.3	1.10E-11	1.06E-11	chr7:7313638-7592328	9q21.33	1.00E-16	1.09E-16	chr9:89771576-90341960
	15q21.2	1.40E-11	1.40E-11	chr15:51519055-51535657	10p14	6.01E-16	6.01E-16	chr10:6883574-7601373
	5q23.3	4.04E-11	4.04E-11	chr5:129090788-130496432	19p13.11	2.00E-13	1.98E-13	chr19:18122653-18228056
	10q26.3	1.87E-10	1.81E-10	chr10:135028776-135053367	22q13.33	3.05E-13	1.13E-12	chr22:50687350-50750508
	10p14	7.17E-09	7.17E-09	chr10:6883574-7601895	3q13.31	1.38E-12	1.38E-12	chr3:113528789-113677406
	11q13.4	1.46E-08	1.46E-08	chr11:72315314-72342211	10q24.32	1.64E-12	1.64E-12	chr10:103922569-104011301
	19p13.11	3.29E-08	3.16E-08	chr19:18121090-18228345	21q22.3	7.11E-10	7.11E-10	chr21:46646003-47610594
	12q23.1	1.91E-07	1.91E-07	chr12:96340707-96404735	17p13.2	4.46E-09	4.46E-09	chr17:3553132-3714472
	3q13.31	2.43E-07	2.43E-07	chr3:113597195-113677359	12q23.1	2.76E-08	2.76E-08	chr12:96311085-96394765
	22q13.33	1.09E-06	1.07E-06	chr22:50687350-50719421	8p21.3	1.16E-07	1.16E-07	chr8:21166235-21766771
	3p21.31	1.75E-06	1.75E-06	chr3:50248198-50316035	1p36.32	4.62E-07	4.62E-07	chr1:2341792-2461229
	21q22.3	9.66E-06	9.67E-06	chr21:46646003-47610504	5q32	2.70E-14	6.57E-07	chr5:149465024-149676755
	7q22.1	3.32E-05	3.32E-05	chr7:100808810-100883075	13q14.11	1.16E-06	1.16E-06	chr13:40174636-40765798
	12p12.3	0.0001999	0.0002052	chr12:14719948-14923682	2p23.3	1.26E-06	1.26E-06	chr2:26357529-26531400
	17q11.2	5.99E-06	0.0002516	chr17:27879812-27920755	11q13.4	1.67E-06	1.68E-06	chr11:72145557-72396776
	17p11.2	2.33E-07	0.0002977	chr17:18061962-18164521	12p12.3	2.11E-05	2.08E-05	chr12:14706357-14923682
	1p36.32	0.0004121	0.0004356	chr1:2341911-2461229	15q14	2.11E-05	2.08E-05	chr15:34490977-34651296
Loss	19q13.12	0.0004401	0.0004356	chr19:35422473-35725649	9p13.2	2.57E-05	2.56E-05	chr9:37592485-37771784
	2p23.3	0.0005916	0.0005916	chr2:26404841-26539970	20q13.33	5.68E-05	5.68E-05	chr20:60892413-60908102
	1q42.13	0.0015564	0.0014458	chr1:228375245-228581878	5q23.3	5.20E-16	0.00014408	chr5:129090958-130502899
	8q23.3	0.0015398	0.0014458	chr8:113645048-113674856	3p21.1	0.00022158	0.00021336	chr3:52414398-52530528
	5p13.3	0.0018373	0.0018151	chr5:31918938-31948832	5p13.3	0.00029203	0.00027496	chr5:31926019-31955247
	9p13.2	1.02E-07	0.0024337	chr9:37745977-37790444	14q32.33	0.00039547	0.00038518	chr14:105753235-105895234
	20p13	0.0033853	0.0032572	chr20:3215366-3458645	7q22.1	0.00044295	0.00044295	chr7:100808810-101014359
	20q13.33	0.0038791	0.0039992	chr20:62180738-62279698	1q42.2	0.00063422	0.00063511	chr1:231357049-231471514
	13q21.32	0.0043252	0.0042037	chr13:67370724-67517500	2q11.2	0.00073236	0.00071167	chr2:101767032-102603229
	2q21.3	0.017652	0.017391	chr2:136631169-136872405	6q16.3	0.0049843	0.0049064	chr6:101328965-105389199
	6q16.3	0.022785	0.022552	chr6:101327299-105388592	19q13.42	0.0050347	0.0049064	chr19:55284532-55587667
	9p13.2	1.02E-07	0.022552	chr9:37582748-37790444	20p13	0.027174	0.027174	chr20:3213061-3451889
	8p12	0.027744	0.028298	chr8:30231258-30601690	17q11.2	1.48E-05	0.034344	chr17:27869849-27953970
	14q32.33	0.030971	0.030971	chr14:105842533-105895202	17q12	0.0021862	0.034344	chr17:38030908-38105010
	4p16.3	0.044324	0.044095	chr4:476415-686055	18q12.2	0.060671	0.060734	chr18:34388917-36793563
	11p15.5	0.055869	0.055869	chr11:1-3242809	8q12.3	0.00045153	0.088859	chr8:62623338-63973276
	17p13.1	9.67E-06	0.11086	chr17:9684951-10204333	4p14	0.14042	0.1356	chr4:39780579-40046173
	4q35.1	0.18979	0.1905	chr4:184236428-190949996	4q13.2	0.14859	0.14777	chr4:69207411-69513266
	18p11.21	0.22781	0.22359	chr18:11649717-11983108	22q11.21	0.002507	0.1654	chr22:19707589-19868126
	17q11.2	5.99E-06	0.71063	chr17:1-81195210	8q12.3	0.00045153	0.18993	chr8:62623338-63973276
	2q21.3	0.017652	1	chr2:1-243199373				
	16q12.2	1.07E-13	1	chr16:1-90354753				

"Red" represents private chromosomes with CNVs in N0 or N+ group. "Bold" indicates shared chromosomes with different CNV in N0 and N+ group. CNV, copy number variation; SCLC, small cell lung cancer.