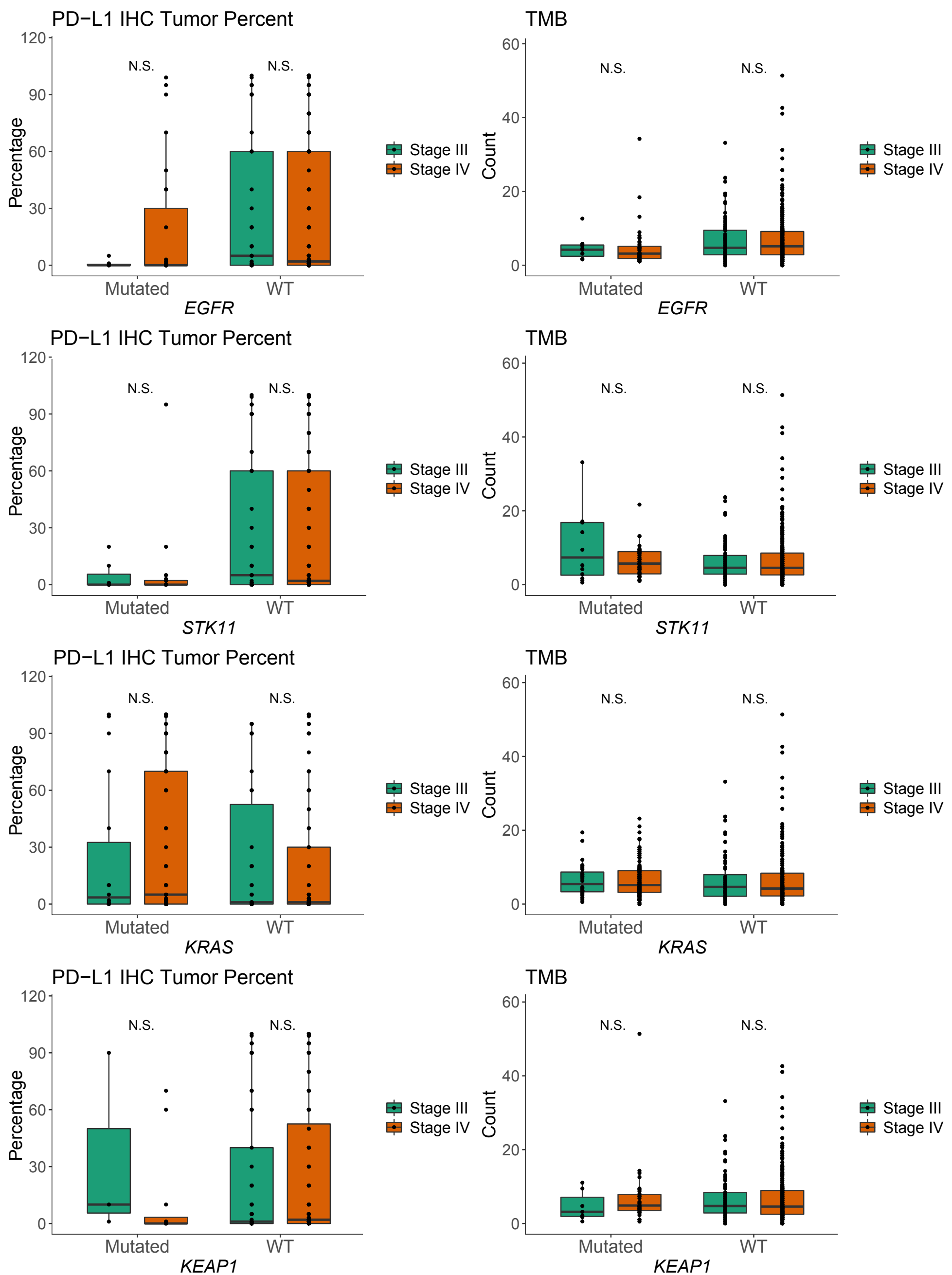
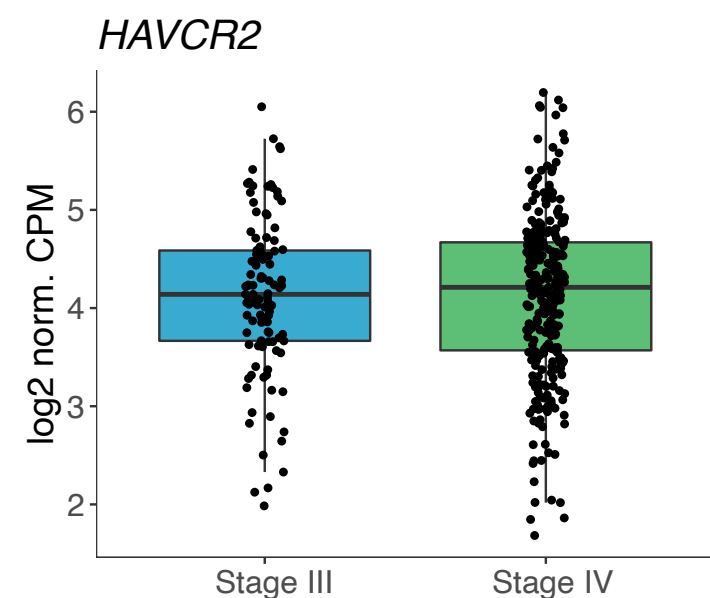
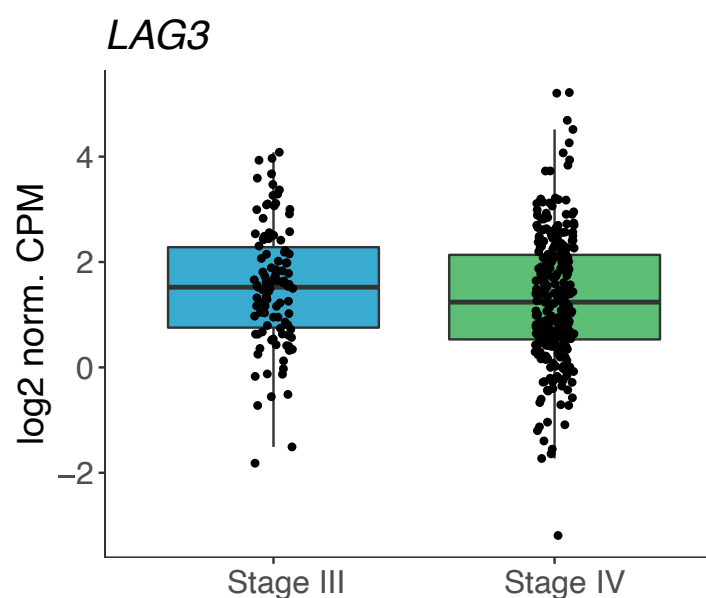
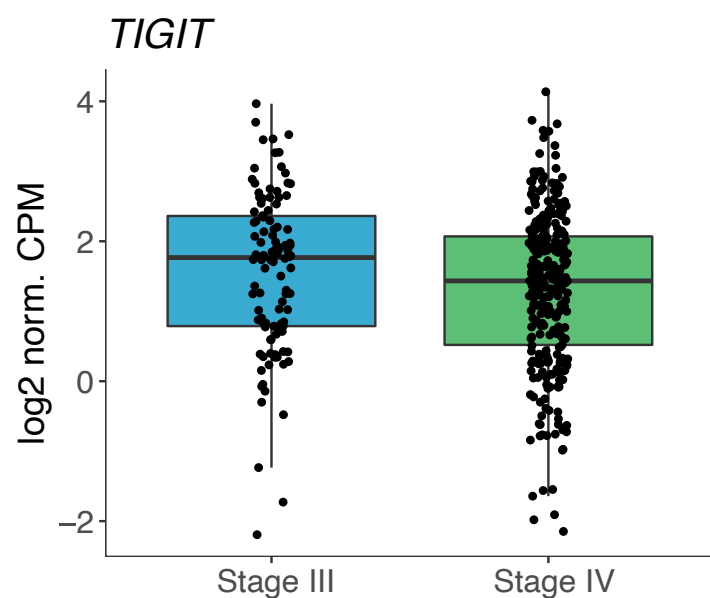
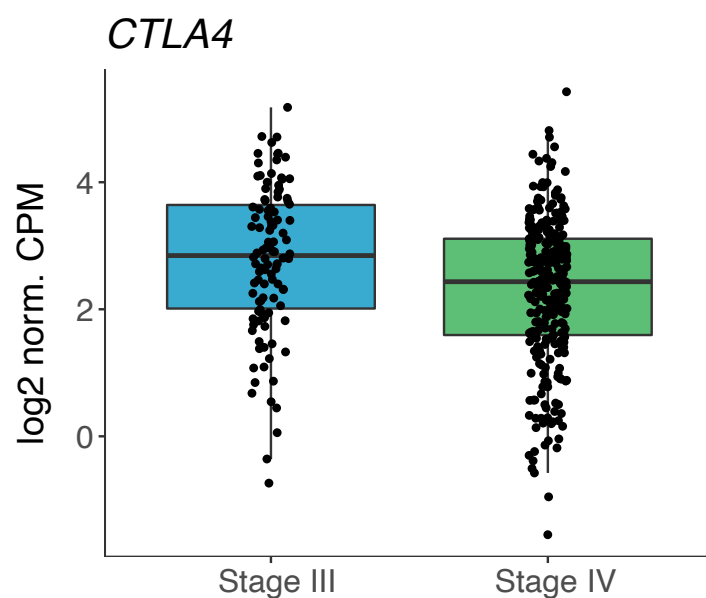
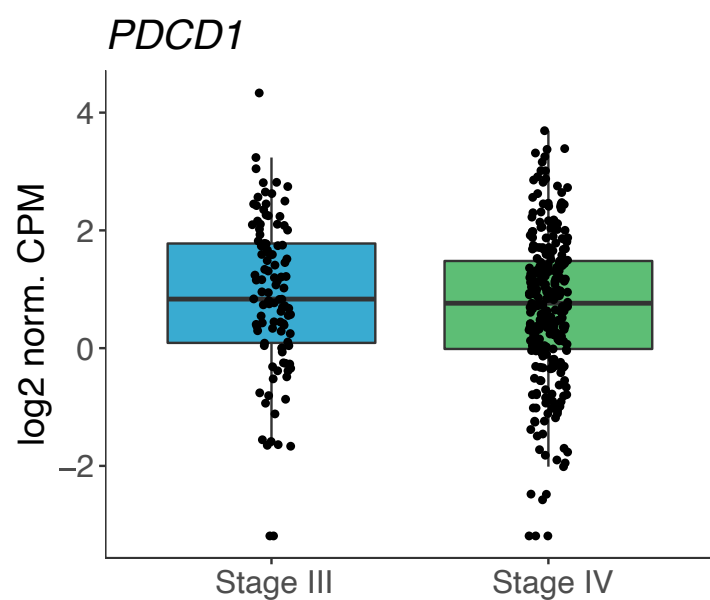
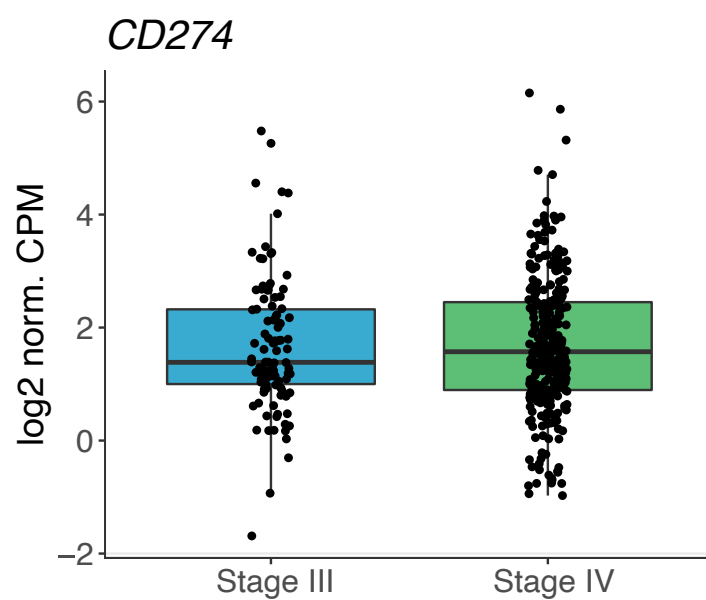
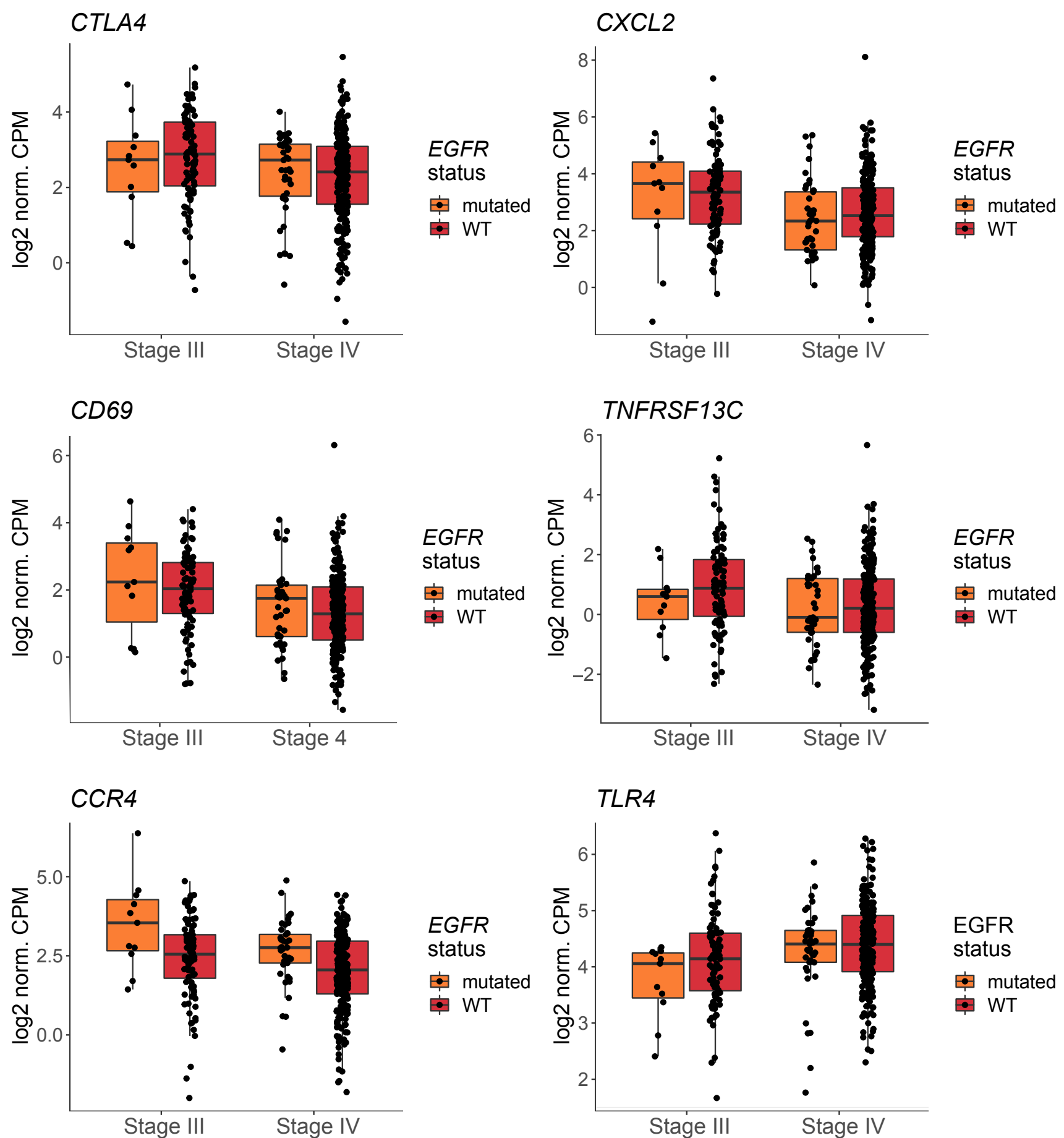




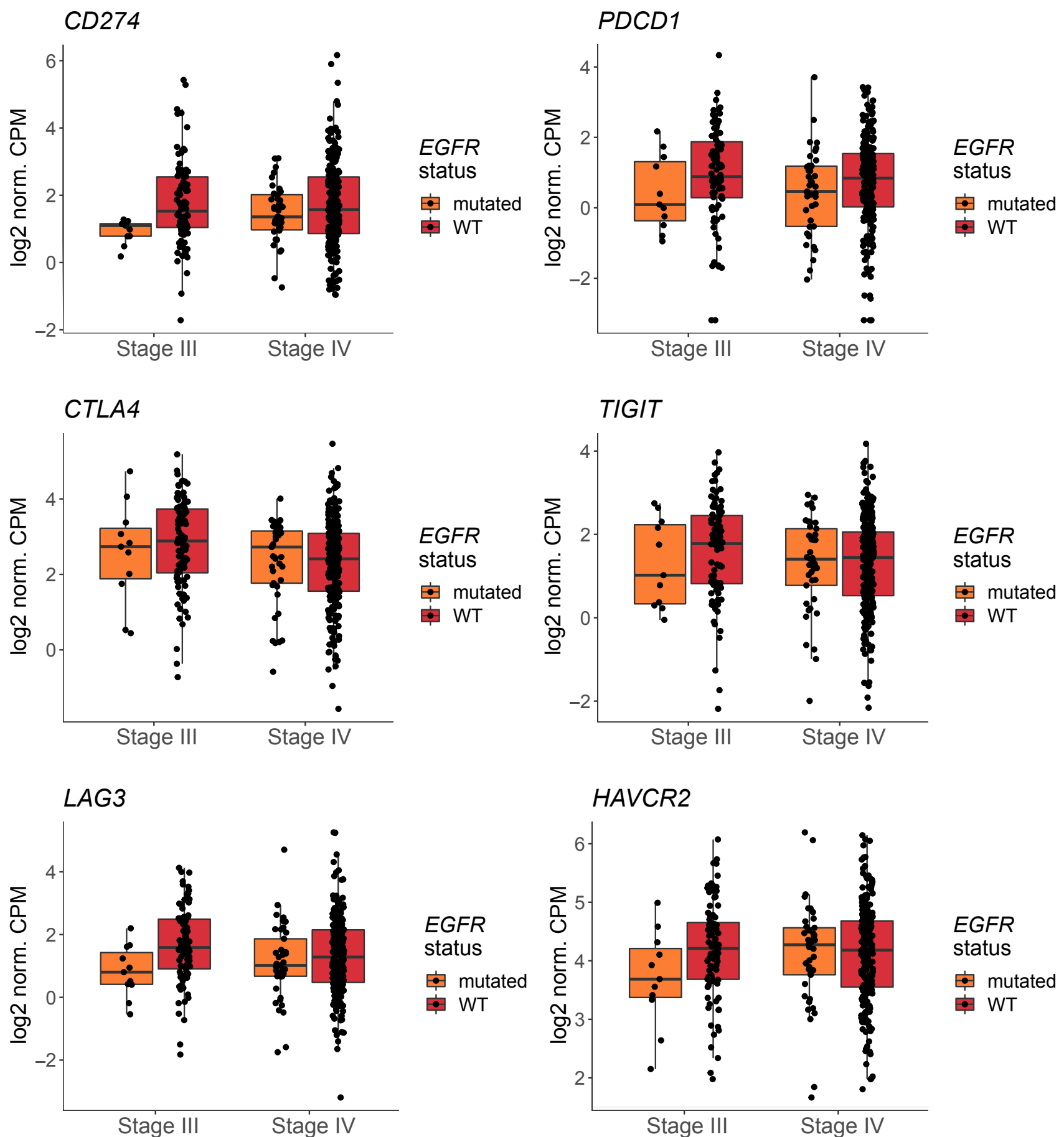
Supplementary Figure 1. Differences in oncogenic driver-mutant patients. Boxplots on the left show differences in PD-L1 tumor percent between EGFR-mutated (stage III n=7, stage IV n=27) vs. EGFR-wild-type (WT; stage III n=56, stage IV n=128), STK11-mutated (stage III n=7, stage IV n=19) vs. STK11-WT (stage III n=54, stage n=133), KRAS-mutated (stage III n=17, stage IV n=61) vs. KRAS-WT (stage III n=44, stage IV n=91), and KEAP1-mutated (stage III n=3, stage IV n=10) vs. KEAP1-WT (stage III n=58, stage IV n=142) tumors, colored by stage (stage III: green, stage IV: orange). Boxplots on the right show differences in TMB between EGFR-mutated (stage III n=11, stage IV n=42) vs. EGFR-wild-type (WT; stage III n=93, stage IV n=232), STK11-mutated (stage III n=13, stage IV n=44) vs. STK11-WT (stage III n=88, stage n=228), KRAS-mutated (stage III n=36, stage IV n=118) vs. KRAS-WT (stage III n=65, stage IV n=154), and KEAP1-mutated (stage III n=8, stage IV n=24) vs. KEAP1-WT (stage III n=93, stage IV n=248) tumors. No significant difference in either PD-L1 or TMB were identified between stage III and stage IV tumors after stratifying by the mutation status of those oncogenic drivers.



Supplementary Figure 2. Immune checkpoint gene expression boxplots by tumor stage (stage III n=106, stage IV n=285). Boxes represent the interquartile ranges, whiskers indicate the 95% confidence intervals. CD274, Programmed Cell Death 1 Ligand; PDCD1, Programmed Cell Death 1; CTLA4, Cytotoxic T-Lymphocyte Associated Protein 4; TIGIT, T Cell Immunoreceptor with Ig and ITIM Domain; LAG3, Lymphocyte Activating 3; HAVCR2, T-Cell Immunoglobulin And Mucin Domain-Containing Protein 3. Of the genes above, only the expression of CTLA4 significantly differed by stage ($P=1.32e-04$).

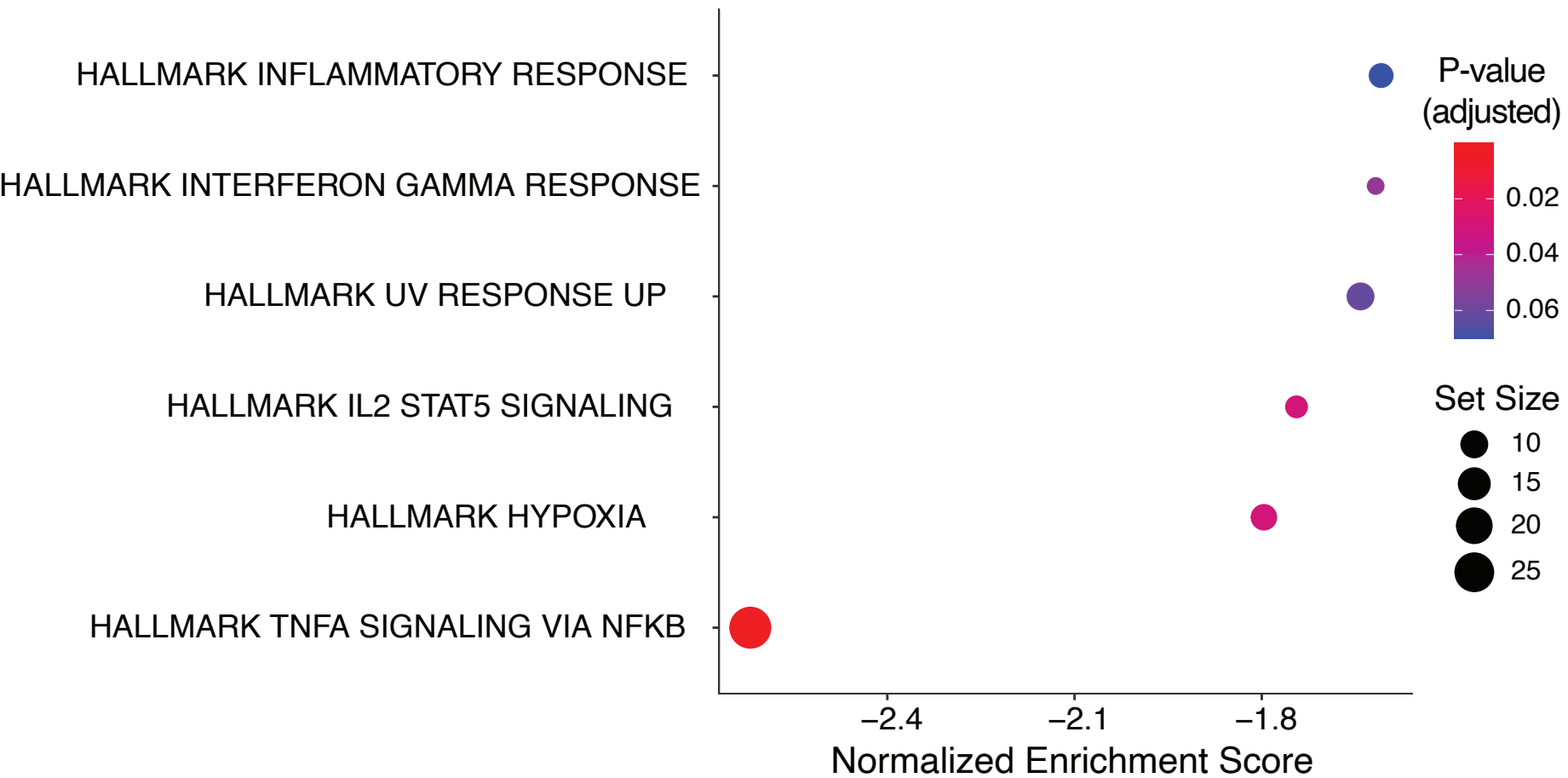


Supplementary Figure 3. Expression of genes differentially expressed by tumor stage by EGFR mutation status (mutated=pathogenic mutation in EGFR, stage III n=11 and stage IV n=42; WT= wild-type EGFR, n=338). Boxes represent the interquartile ranges, whiskers indicate the 95% confidence intervals. CTLA4, Cytotoxic T-Lymphocyte Associated Protein 4; CXCL2, C-X-C Motif Chemokine Ligand 2; CD69, Cluster of Differentiation 69; TNFRSF13C, Tumor Necrosis Factor Receptor Superfamily Member 13C; CCR4, C-C Motif Chemokine Receptor 4; TLR4, Toll Like Receptor 4. CCR4 was differentially expressed (FDR 5% significance threshold) by stage ($P=6.50e-05$) and EGFR status ($P=2.11e-05$). For all other genes, expression difference by EGFR status was not significant.

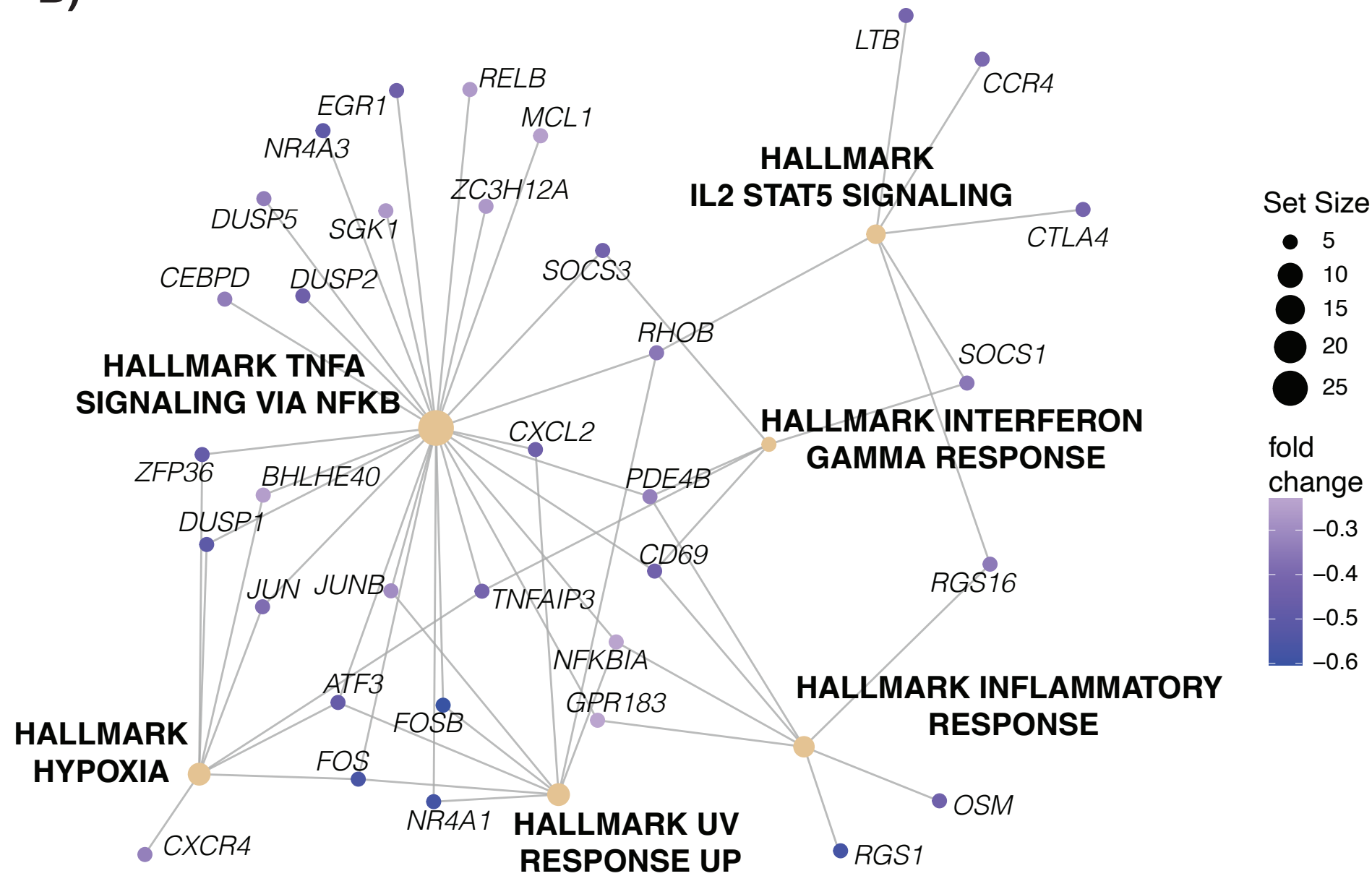


Supplementary Figure 4. Immune checkpoint gene expression boxplots by stage and EGFR mutation status (mutated=pathogenic mutation in EGFR, stage III n=11 and stage IV n=42; WT= wild-type EGFR, n=338). Boxes represent the interquartile ranges, whiskers indicate the 95% confidence intervals. CD274, Programmed Cell Death 1 Ligand; PDCD1, Programmed Cell Death 1; CTLA4, Cytotoxic T-Lymphocyte Associated Protein 4; TIGIT, T Cell Immunoreceptor with Ig And ITIM Domain; LAG3, Lymphocyte Activating 3; HAVCR2, T-Cell Immunoglobulin And Mucin Domain-Containing Protein 3. Expression of CTLA4 significantly differed by stage ($P=1.32e-04$) but none of the genes shown had significantly different expression levels by EGFR mutation status.

A)

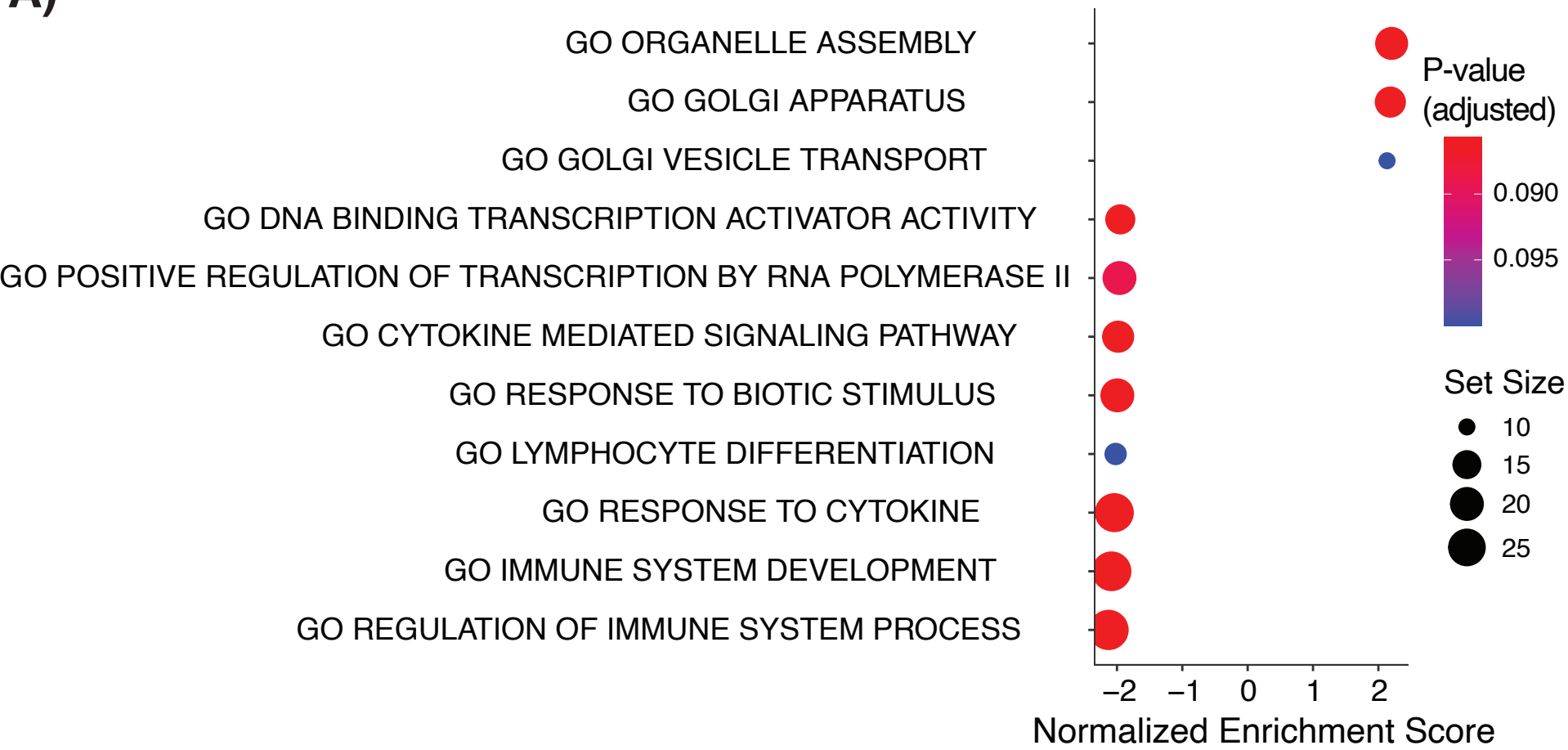


B)

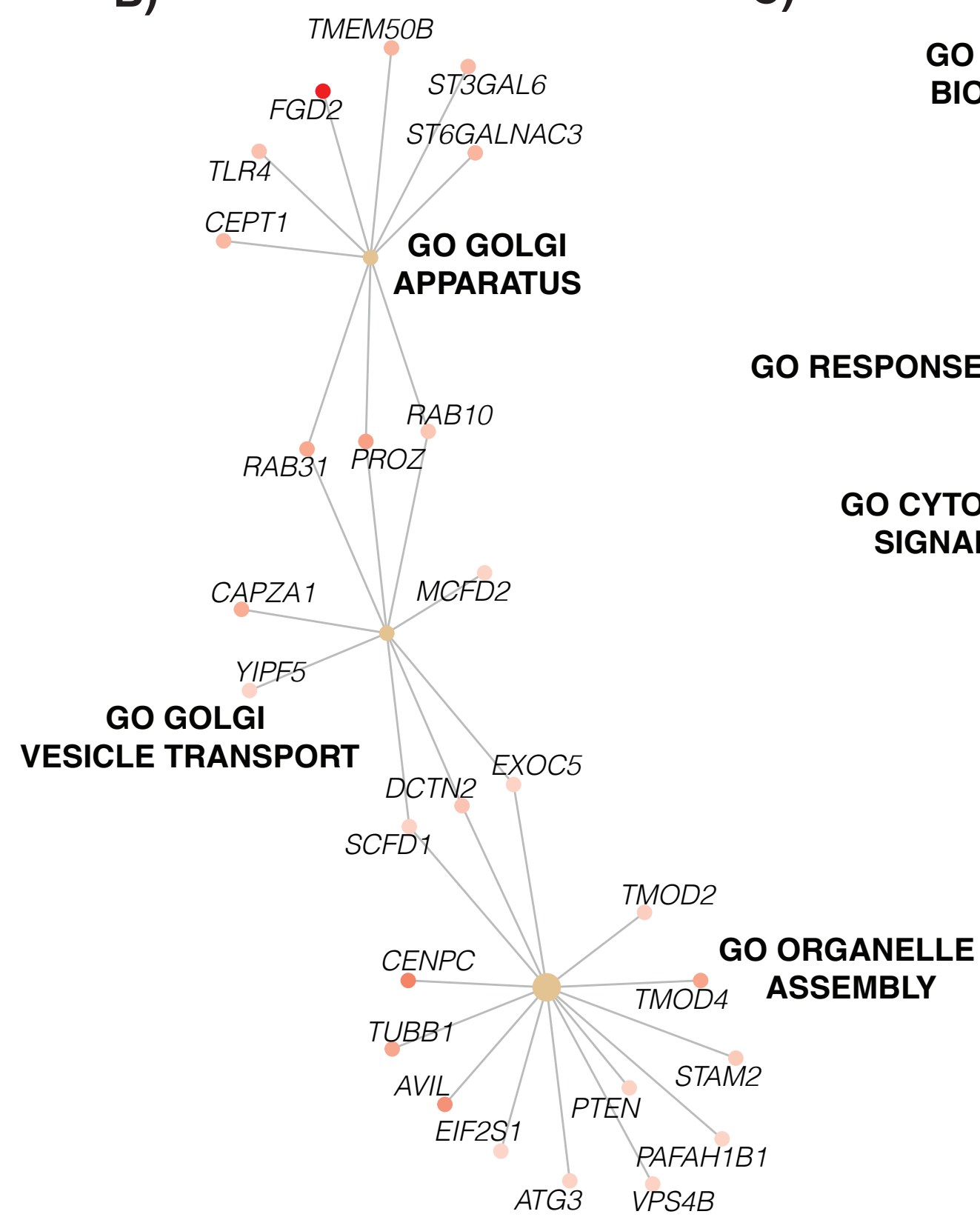


Supplementary Figure 5. Hallmark gene set enrichment analysis (GSEA) of differentially expressed genes by tumor stage (stage III n=106, stage IV n=285). (A) Dotplot of Hallmark pathway enrichment of pathways with adjusted P-value <0.1, x-axis indicates normalized enrichment score (NES). Color of dot represents the adjusted P-value of the GSEA score. (B) Network visualization of genes in the listed pathways upregulated in stage III tumors. Color of gene represents the fold change between stage III and stage IV tumors, where a positive fold change (red) indicates genes with increased expression in stage IV tumors, and negative fold change (blue) represents increased expression in stage III tumors.

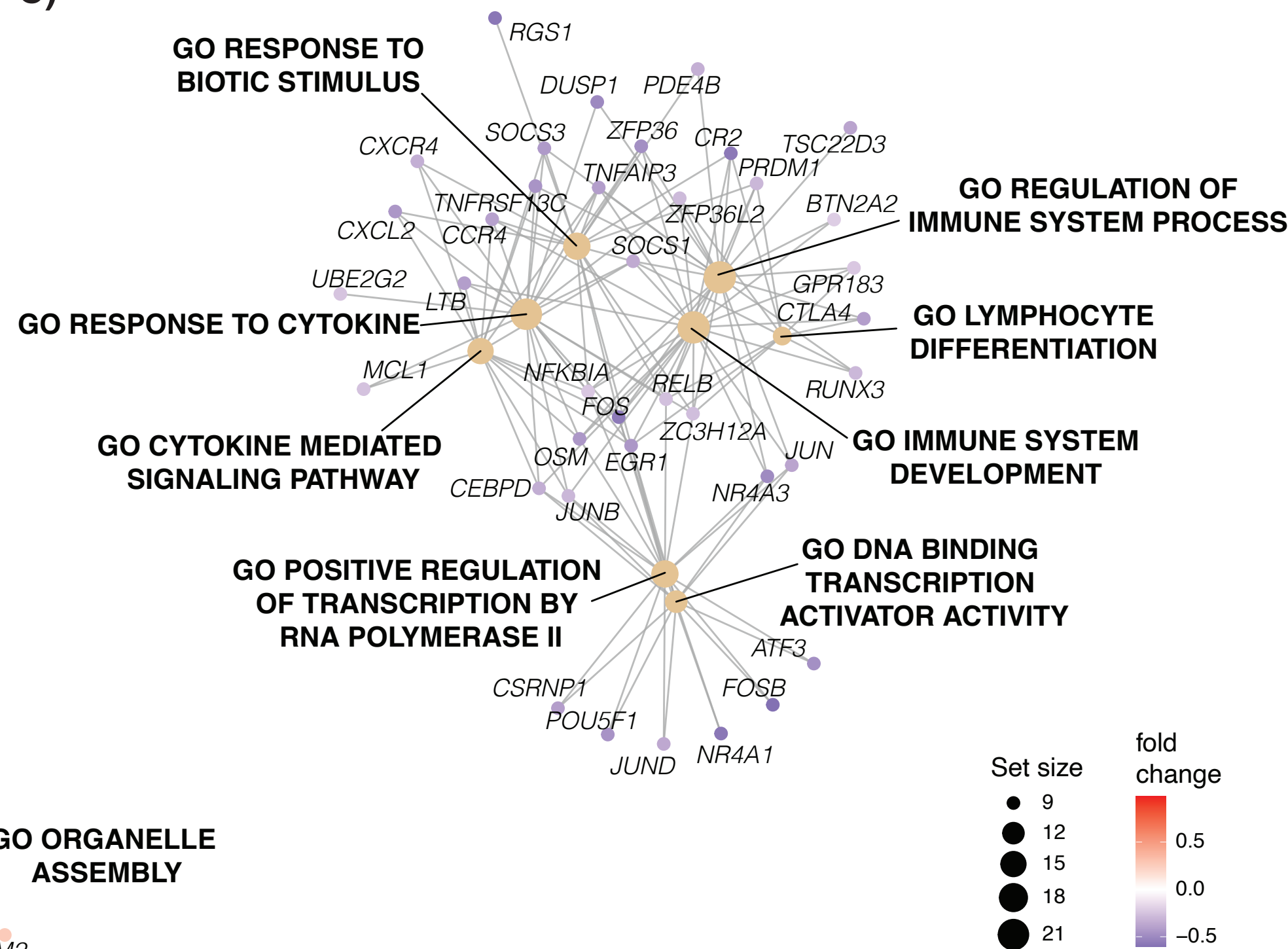
A)



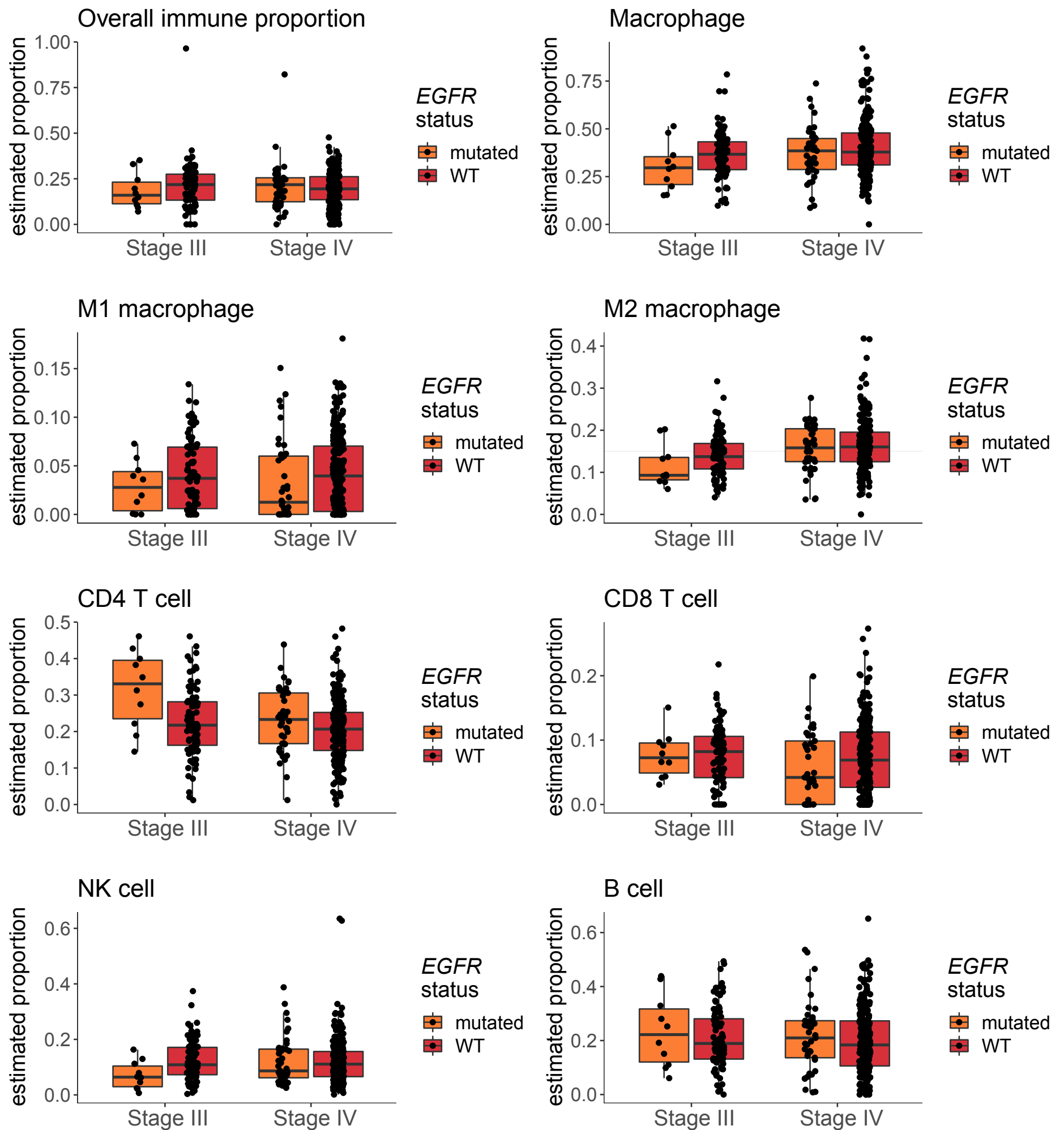
B)



C)



Supplementary Figure 6. Gene ontology (GO) Gene set enrichment analysis (GSEA) of differentially expressed genes by tumor stage (stage III n=106, stage IV n=285). (A) Dotplot of GO pathway enrichment of pathways with adjusted P-value <0.1 , x-axis indicates normalized enrichment score (NES). Dot color represents the adjusted P-value of the gene set enrichment score. Network visualization of genes in the listed pathways upregulated in stage IV tumors (B) or stage III tumors (C). Color of gene represents the fold change between stage III and stage IV tumors, where a positive fold change (red) indicates genes with increased expression in stage IV tumors, and negative fold change (blue) represents increased expression in stage III tumors.



Supplementary Figure 7. RNA-estimated immune compartment boxplots by stage and EGFR mutation status (mutated=pathogenic mutation in EGFR, stage III n=11 and stage IV n=42; WT= wild-type EGFR, n=338). Boxes represent the interquartile ranges, whiskers indicate the 95% confidence intervals. Macrophage and CD4+ T cell proportions significantly differed by stage. CD4+ T cell proportions also significantly differed by EGFR status.

Supplementary Table 1.

List of differentially expressed genes by tumor stage (FDR 5%) with regression P-value and direction of effect (stage III n=106, stage IV n=285).

Gene Symbol	P-value	Direction of Effect (increased expression)
<i>ZFP36</i>	6.09E-08	stage III
<i>H1FX</i>	1.08E-07	stage III
<i>RGS1</i>	1.62E-07	stage III
<i>NR4A3</i>	3.60E-07	stage III
<i>NR4A1</i>	4.38E-07	stage III
<i>SMIM7</i>	6.89E-07	stage III
<i>ATF3</i>	8.91E-07	stage III
<i>JUND</i>	1.31E-06	stage III
<i>CSRNP1</i>	1.56E-06	stage III
<i>TNFAIP3</i>	1.65E-06	stage III
<i>DUSP1</i>	1.67E-06	stage III
<i>ITPKC</i>	2.33E-06	stage III
<i>DCUN1D3</i>	2.46E-06	stage III
<i>FOSB</i>	5.09E-06	stage III
<i>C11orf96</i>	5.49E-06	stage III
<i>MCL1</i>	5.73E-06	stage III
<i>JUN</i>	7.40E-06	stage III
<i>EXOC3L4</i>	1.32E-05	stage III
<i>DUSP2</i>	1.49E-05	stage III
<i>FAM120AOS</i>	1.53E-05	stage III
<i>CD69</i>	1.99E-05	stage III
<i>RELB</i>	2.63E-05	stage III
<i>ITPRIP</i>	3.12E-05	stage III
<i>PDE4B</i>	3.93E-05	stage III
<i>FOS</i>	4.37E-05	stage III
<i>GRASP</i>	4.40E-05	stage III

Gene Symbol	P-value	Direction of Effect (increased expression)
<i>GNAT2</i>	1.19E-07	stage IV
<i>SLC10A1</i>	1.36E-07	stage IV
<i>C15orf60</i>	1.46E-07	stage IV
<i>ZNF317</i>	8.14E-07	stage IV
<i>UBE2E1</i>	8.38E-07	stage IV
<i>LDHAL6A</i>	9.17E-07	stage IV
<i>NFYB</i>	1.71E-06	stage IV
<i>DDX19A</i>	3.54E-06	stage IV
<i>CAPZA1</i>	5.83E-06	stage IV
<i>CSNK1G1</i>	7.17E-06	stage IV
<i>LIN37</i>	8.13E-06	stage IV
<i>PROZ</i>	8.71E-06	stage IV
<i>TPRKB</i>	1.14E-05	stage IV
<i>EIF5</i>	1.32E-05	stage IV
<i>DIS3L</i>	1.95E-05	stage IV
<i>CRYBA1</i>	2.43E-05	stage IV
<i>STAM2</i>	2.69E-05	stage IV
<i>UFSP2</i>	3.31E-05	stage IV
<i>ELOVL1</i>	3.58E-05	stage IV
<i>EXOC5</i>	3.75E-05	stage IV
<i>ZNF561</i>	3.89E-05	stage IV
<i>C18orf21</i>	3.90E-05	stage IV
<i>CRYBG3</i>	4.11E-05	stage IV
<i>TMOD4</i>	4.19E-05	stage IV
<i>ZNF701</i>	4.40E-05	stage IV
<i>AVIL</i>	5.33E-05	stage IV

<i>PSPC1</i>	4.95E-05	stage III
<i>SOCS3</i>	5.00E-05	stage III
<i>HIST1H1E</i>	5.56E-05	stage III
<i>XIRP1</i>	6.09E-05	stage III
<i>STRADA</i>	6.24E-05	stage III
<i>RGPD5</i>	6.50E-05	stage III
<i>C1orf111</i>	7.05E-05	stage III
<i>MED26</i>	8.13E-05	stage III
<i>HIST1H2BD</i>	8.68E-05	stage III
<i>DHDDS</i>	8.81E-05	stage III
<i>CYR61</i>	1.04E-04	stage III
<i>MRPL20</i>	1.11E-04	stage III
<i>SOCS1</i>	1.13E-04	stage III
<i>APOLD1</i>	1.16E-04	stage III
<i>TNFRSF13C</i>	1.20E-04	stage III
<i>TMEM160</i>	1.28E-04	stage III
<i>CTLA4</i>	1.32E-04	stage III
<i>RHOB</i>	1.32E-04	stage III
<i>SGK1</i>	1.40E-04	stage III
<i>GNB2L1</i>	1.46E-04	stage III
<i>ZC3H12A</i>	1.53E-04	stage III
<i>OSM</i>	1.67E-04	stage III
<i>ADAMTS1</i>	1.67E-04	stage III
<i>DDX5</i>	1.72E-04	stage III
<i>CDK11B</i>	1.80E-04	stage III
<i>CXCL2</i>	1.94E-04	stage III
<i>ZFP36L2</i>	1.97E-04	stage III
<i>RGS16</i>	2.12E-04	stage III
<i>CNNM3</i>	2.29E-04	stage III
<i>POU5F1</i>	2.36E-04	stage III
<i>PIM3</i>	2.49E-04	stage III

<i>ZNF555</i>	5.60E-05	stage IV
<i>TRIQQ</i>	6.23E-05	stage IV
<i>RAB31</i>	6.35E-05	stage IV
<i>MCFD2</i>	7.19E-05	stage IV
<i>ADORA3</i>	7.30E-05	stage IV
<i>RAB10</i>	7.82E-05	stage IV
<i>CEPT1</i>	9.39E-05	stage IV
<i>C14orf183</i>	9.83E-05	stage IV
<i>ZNF845</i>	1.00E-04	stage IV
<i>TXNL4B</i>	1.03E-04	stage IV
<i>AGPAT6</i>	1.05E-04	stage IV
<i>LMBRD1</i>	1.12E-04	stage IV
<i>ZNF836</i>	1.15E-04	stage IV
<i>ZHX1</i>	1.27E-04	stage IV
<i>UBE2B</i>	1.27E-04	stage IV
<i>THAP1</i>	1.29E-04	stage IV
<i>AIDA</i>	1.29E-04	stage IV
<i>ATG3</i>	1.31E-04	stage IV
<i>FSD2</i>	1.32E-04	stage IV
<i>FAM63B</i>	1.39E-04	stage IV
<i>CCNL1</i>	1.45E-04	stage IV
<i>ZNF611</i>	1.54E-04	stage IV
<i>C14orf28</i>	1.66E-04	stage IV
<i>MRPL13</i>	1.67E-04	stage IV
<i>C8orf59</i>	1.69E-04	stage IV
<i>GTPBP10</i>	1.74E-04	stage IV
<i>DENND4C</i>	1.77E-04	stage IV
<i>CLPX</i>	1.86E-04	stage IV
<i>PP2D1</i>	1.98E-04	stage IV
<i>PTEN</i>	2.01E-04	stage IV
<i>DCTN2</i>	2.06E-04	stage IV

<i>CR2</i>	2.56E-04	stage III
<i>EGR1</i>	2.63E-04	stage III
<i>PRDM1</i>	2.85E-04	stage III
<i>LTB</i>	2.89E-04	stage III
<i>PGS1</i>	2.93E-04	stage III
<i>GPR183</i>	3.09E-04	stage III
<i>RUNX3</i>	3.16E-04	stage III
<i>RNF122</i>	3.18E-04	stage III
<i>RNF19B</i>	3.44E-04	stage III
<i>HIST1H4K</i>	3.56E-04	stage III
<i>ZFAND5</i>	3.63E-04	stage III
<i>EXOSC7</i>	3.77E-04	stage III
<i>CEBPD</i>	4.02E-04	stage III
<i>SNRNP70</i>	4.06E-04	stage III
<i>CCR4</i>	4.24E-04	stage III
<i>HIST1H2AK</i>	4.27E-04	stage III
<i>SIRT3</i>	4.75E-04	stage III
<i>TUT1</i>	4.99E-04	stage III
<i>CDHR1</i>	5.09E-04	stage III
<i>UBE2G2</i>	5.16E-04	stage III
<i>NFKBIA</i>	5.24E-04	stage III
<i>BHLHE40</i>	5.34E-04	stage III
<i>JUNB</i>	5.48E-04	stage III
<i>HUS1B</i>	5.57E-04	stage III
<i>GPR89C</i>	5.60E-04	stage III
<i>CXCR4</i>	5.80E-04	stage III
<i>MAB21L2</i>	5.84E-04	stage III
<i>CATSPER2</i>	6.30E-04	stage III
<i>MOGS</i>	6.34E-04	stage III
<i>OSGEP</i>	6.42E-04	stage III
<i>TSC22D3</i>	6.68E-04	stage III

<i>RYK</i>	2.27E-04	stage IV
<i>GNPDA2</i>	2.34E-04	stage IV
<i>UBA3</i>	2.41E-04	stage IV
<i>WDR1</i>	2.42E-04	stage IV
<i>HCFC2</i>	2.47E-04	stage IV
<i>YIPF5</i>	2.63E-04	stage IV
<i>ITFG1</i>	2.74E-04	stage IV
<i>ST3GAL6</i>	2.80E-04	stage IV
<i>ZNF436</i>	2.85E-04	stage IV
<i>TMEM50B</i>	2.91E-04	stage IV
<i>VPS4B</i>	2.94E-04	stage IV
<i>DNAJA2</i>	2.97E-04	stage IV
<i>ST6GALNAC3</i>	3.04E-04	stage IV
<i>GLUL</i>	3.07E-04	stage IV
<i>TLR4</i>	3.07E-04	stage IV
<i>ZNF654</i>	3.11E-04	stage IV
<i>AP1G1</i>	3.17E-04	stage IV
<i>FEM1B</i>	3.18E-04	stage IV
<i>SRSF1</i>	3.43E-04	stage IV
<i>NCOA5</i>	3.44E-04	stage IV
<i>CD164</i>	3.50E-04	stage IV
<i>OPN1SW</i>	3.58E-04	stage IV
<i>CNOT1</i>	3.60E-04	stage IV
<i>EYS</i>	3.65E-04	stage IV
<i>CHURC1</i>	3.88E-04	stage IV
<i>RBMS2</i>	3.98E-04	stage IV
<i>TUBB1</i>	4.19E-04	stage IV
<i>EMC2</i>	4.27E-04	stage IV
<i>PSEN1</i>	4.35E-04	stage IV
<i>CNEP1R1</i>	4.38E-04	stage IV
<i>BMI1</i>	4.38E-04	stage IV

<i>DUSP5</i>	6.83E-04	stage III
<i>C12orf71</i>	6.97E-04	stage III
<i>BTN2A2</i>	7.08E-04	stage III

<i>EFR3A</i>	4.39E-04	stage IV
<i>ADM5</i>	4.43E-04	stage IV
<i>TMEM86A</i>	4.65E-04	stage IV
<i>RNF130</i>	4.71E-04	stage IV
<i>WWP1</i>	4.82E-04	stage IV
<i>SCFD1</i>	4.85E-04	stage IV
<i>TMOD2</i>	4.87E-04	stage IV
<i>MTRF1L</i>	4.99E-04	stage IV
<i>ZNF280D</i>	5.07E-04	stage IV
<i>STXBP5</i>	5.20E-04	stage IV
<i>C12orf4</i>	5.23E-04	stage IV
<i>FGD2</i>	5.26E-04	stage IV
<i>SLC30A9</i>	5.29E-04	stage IV
<i>CENPC</i>	5.69E-04	stage IV
<i>IL6ST</i>	5.72E-04	stage IV
<i>NCKAP1</i>	5.80E-04	stage IV
<i>PAFAH1B1</i>	5.82E-04	stage IV
<i>C5orf22</i>	6.04E-04	stage IV
<i>CMTR2</i>	6.14E-04	stage IV
<i>UGP2</i>	6.18E-04	stage IV
<i>KPNA4</i>	6.55E-04	stage IV
<i>USP53</i>	6.78E-04	stage IV
<i>CUL4B</i>	6.80E-04	stage IV
<i>EIF2S1</i>	6.88E-04	stage IV
<i>LATS1</i>	6.93E-04	stage IV
<i>ZNF765</i>	7.06E-04	stage IV

Supplementary Table 2.

Genes with differences in mutation frequency ($P < 0.1$) between stage III and stage IV patients (stage III $n=106$, stage IV $n=285$).

	Stage III (n=106)	Stage IV (n=284)	P-Value	Adjusted P- Value (Bonferroni)
<i>RNF139</i>	5 (4.7%)	0 (0%)	0.00	0.04
<i>ERG</i>	5 (4.7%)	1 (0.4%)	0.01	0.21
<i>MUTYH</i>	5 (4.7%)	1 (0.4%)	0.01	0.21
<i>FOXO3</i>	6 (5.7%)	3 (1.1%)	0.01	0.46
<i>FANCD2</i>	7 (6.6%)	5 (1.8%)	0.02	0.67
<i>PHF6</i>	4 (3.8%)	1 (0.4%)	0.02	0.66
<i>RBM10</i>	21 (19.8%)	30 (10.6%)	0.03	0.80
<i>KDM6A</i>	6 (5.7%)	4 (1.4%)	0.03	0.89
<i>ERRFI1</i>	4 (3.8%)	2 (0.7%)	0.05	1.00
<i>FOXP1</i>	4 (3.8%)	2 (0.7%)	0.05	1.00
<i>PRCC</i>	4 (3.8%)	2 (0.7%)	0.05	1.00
<i>ABCB1</i>	4 (3.8%)	30 (10.6%)	0.06	1.00
<i>CTCF</i>	3 (2.8%)	1 (0.4%)	0.06	1.00
<i>HLA-F</i>	3 (2.8%)	1 (0.4%)	0.06	1.00
<i>TCL1A</i>	3 (2.8%)	1 (0.4%)	0.06	1.00
<i>SETD2</i>	14 (13.2%)	19 (6.7%)	0.06	1.00
<i>STAT5A</i>	5 (4.7%)	4 (1.4%)	0.07	1.00
<i>FBXW7</i>	0 (0%)	10 (3.5%)	0.07	1.00
<i>HLA-DRB1</i>	0 (0%)	10 (3.5%)	0.07	1.00
<i>TNFAIP3</i>	0 (0%)	10 (3.5%)	0.07	1.00
<i>MAFB</i>	2 (1.9%)	0 (0%)	0.07	1.00
<i>RIT1</i>	2 (1.9%)	0 (0%)	0.07	1.00

<i>ASXL1</i>	9 (8.5%)	10 (3.5%)	0.08	1.00
<i>CTNNB1</i>	9 (8.5%)	10 (3.5%)	0.08	1.00
<i>BCR</i>	1 (0.9%)	14 (4.9%)	0.08	1.00
<i>DICER1</i>	1 (0.9%)	14 (4.9%)	0.08	1.00
<i>FANCB</i>	1 (0.9%)	14 (4.9%)	0.08	1.00
<i>SMARCA1</i>	1 (0.9%)	15 (5.3%)	0.08	1.00
<i>RUNX1T1</i>	11 (10.4%)	14 (4.9%)	0.09	1.00
<i>MTOR</i>	2 (1.9%)	20 (7.0%)	0.09	1.00
<i>CYP1B1</i>	4 (3.8%)	3 (1.1%)	0.09	1.00
<i>SRSF2</i>	4 (3.8%)	3 (1.1%)	0.09	1.00

Supplementary Table 3. Differential expression results of immune checkpoint genes by tumor stage, unadjusted P-value shown (stage III n=106, stage IV n=285). Asterisk (*) indicates the gene was significantly differentially expressed (FDR 5%) in a transcriptome-wide analysis, with direction of effect noted in “If DE”.

ICB Gene	P-value	If DE, increased in:
<i>BTLA</i>	2.85E-01	
<i>CD200</i>	2.97E-01	
<i>CD200R1</i>	4.32E-01	
<i>CD27</i>	1.74E-01	
<i>CD274</i>	8.58E-01	
<i>CD276</i>	2.51E-01	
<i>CD28</i>	4.11E-02	
<i>CD40</i>	4.13E-01	
<i>CD80</i>	7.69E-02	
<i>CD86</i>	5.38E-01	
<i>CEACAM1</i>	6.82E-01	
<i>CTLA4</i>	1.32E-04*	stage III
<i>HAVCR1</i>	1.88E-01	
<i>HAVCR2</i>	8.09E-01	
<i>ICOS</i>	7.83E-02	
<i>IDO1</i>	2.09E-01	
<i>IL2RB</i>	1.96E-01	
<i>LAG3</i>	6.13E-02	
<i>LAIR1</i>	1.71E-02	
<i>PDCD1</i>	6.28E-02	
<i>PDCD1LG2</i>	9.11E-01	
<i>PVR</i>	3.62E-01	
<i>PVRL2</i>	1.22E-01	

<i>TIGIT</i>	1.65E-02	
<i>TNFRSF14</i>	5.99E-01	
<i>TNFRSF18</i>	6.45E-03	
<i>TNFRSF4</i>	3.16E-01	
<i>TNFRSF9</i>	1.00E-02	
<i>TNFSF14</i>	8.19E-02	
<i>TNFSF4</i>	4.20E-01	
<i>TNFSF9</i>	9.04E-03	
<i>VTCN1</i>	4.64E-01	

Supplementary Table 4. Differential expression results of immune checkpoint genes by mutation status (mutated vs. wild-type). Unadjusted P-value shown for each gene and mutation. Asterisk (*) indicates the gene was significantly differentially expressed (FDR <5%) in a transcriptome-wide analysis, with direction of effect noted in “If DE”.

ICB Gene	<i>EGFR</i> mutation (n=53)		<i>STK11</i> mutation (n=59)		<i>KRAS</i> mutation (n=160)		<i>KEAP1</i> mutation (n=39)	
	P-value	If DE, increased in:	P-value	If DE, increased in:	P-value	If DE, increased in:	P-value	If DE, increased in:
<i>BTLA</i>	6.41E-02		4.72E-02		2.04E-01		2.31E-01	
<i>CD200</i>	8.73E-01		1.76E-01		5.48E-01		5.53E-01	
<i>CD200R1</i>	1.72E-01		6.60E-01		4.79E-02		2.67E-01	
<i>CD27</i>	7.20E-01		5.79E-01		6.37E-01		1.33E-01	
<i>CD274</i>	3.94E-01		2.59E-04*	WT	2.64E-02		3.33E-02	
<i>CD276</i>	1.65E-03*	WT	3.30E-01		1.89E-04*	KRAS mut	8.62E-01	
<i>CD28</i>	4.08E-01		1.04E-02		7.38E-01		8.21E-02	
<i>CD40</i>	5.87E-01		4.26E-04*	WT	8.35E-01		3.66E-02	
<i>CD80</i>	4.90E-02		2.04E-04*	WT	2.81E-01		1.03E-02	
<i>CD86</i>	2.40E-01		7.82E-03		6.99E-01		3.08E-02	
<i>CEACAM1</i>	8.57E-03		7.66E-02		2.35E-01		3.65E-02	
<i>CTLA4</i>	2.01E-01		3.01E-01		2.72E-01		1.41E-01	

<i>HAVCR1</i>	4.43E-01		4.75E-03*	STK11 mut	4.06E-02		5.17E-10*	KEAP1 mut
<i>HAVCR2</i>	5.76E-01		8.32E-03		3.38E-01		8.94E-02	
<i>ICOS</i>	8.38E-02		5.46E-02		8.09E-01		1.48E-01	
<i>IDO1</i>	1.57E-01		5.99E-01		9.53E-01		6.76E-01	
<i>IL2RB</i>	8.84E-01		6.35E-01		4.41E-01		6.17E-01	
<i>LAG3</i>	2.42E-01		9.89E-01		7.99E-01		5.42E-01	
<i>LAIR1</i>	4.69E-01		1.59E-02		7.50E-01		5.23E-01	
<i>PDCD1</i>	5.90E-01		6.87E-01		4.51E-01		5.90E-01	
<i>PDCD1LG2</i>	6.70E-01		1.65E-01		6.91E-01		5.19E-02	
<i>PVR</i>	1.06E-02		1.13E-01		1.73E-04*	KRAS mut	2.47E-01	
<i>PVRL2</i>	1.52E-02		2.81E-01		2.02E-05*	KRAS mut	5.38E-01	
<i>TIGIT</i>	4.08E-01		1.53E-01		8.82E-01		2.77E-01	
<i>TNFRSF14</i>	8.68E-01		8.02E-02		1.05E-01		2.29E-01	
<i>TNFRSF18</i>	9.60E-01		1.59E-01		3.70E-01		9.11E-02	
<i>TNFRSF4</i>	1.02E-01		3.50E-01		1.26E-01		6.91E-01	
<i>TNFRSF9</i>	1.53E-01		1.38E-02		9.11E-01		3.74E-02	
<i>TNFSF14</i>	3.95E-01		1.27E-02		5.77E-02		5.86E-04*	KEAP1 mut

<i>TNFSF4</i>	9.62E-01		6.15E-01		7.44E-01		4.57E-02	
<i>TNFSF9</i>	3.40E-01		2.84E-01		2.64E-01		3.27E-02	
<i>VTCN1</i>	1.04E-01		4.59E-01		1.71E-04*	WT	1.67E-01	