

Supplementary Table S1: Kaplan-Meier curve p-values obtained from cBioPortal and Benjamini-Hochberg adjusted p-values.

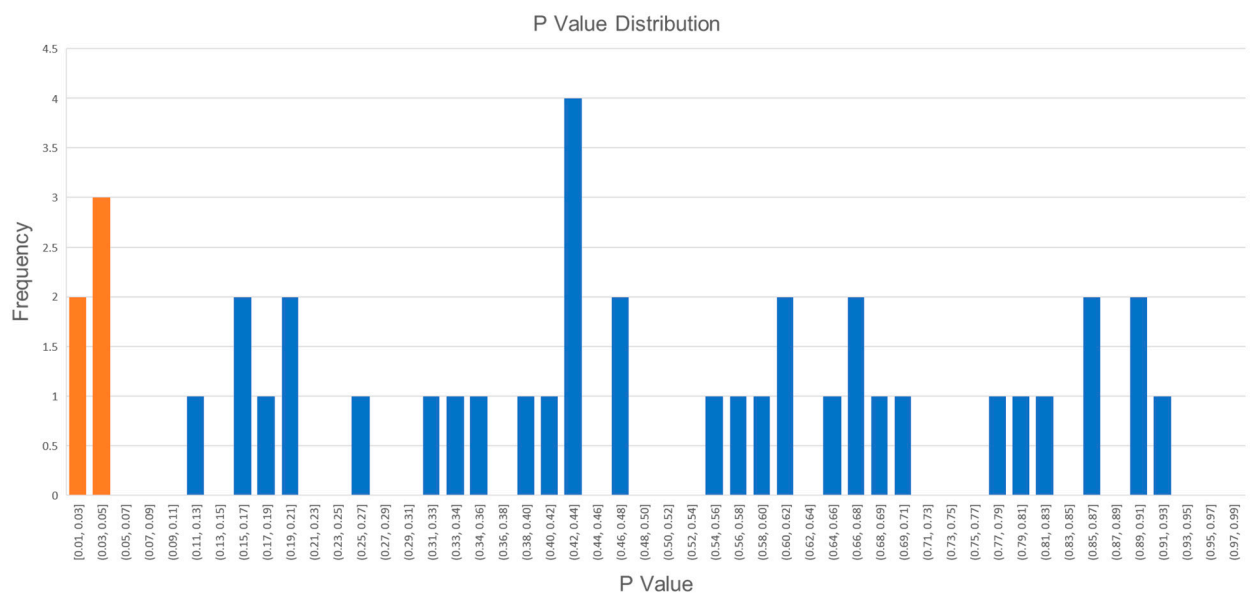
Gene	Survival LogRank Test P-Value	BH-Adjusted P-Values
ACAP1	0.342	0.845478
ARHGAP9	0.546	0.894727
CCR5	0.0471	0.41244
CD274	0.349	0.845478
CD80	0.803	0.9471
CD96	0.194	0.771273
COX19	0.114	0.771273
CST7	0.828	0.9471
CXCR6	0.0136	0.41244
DNASE1	0.694	0.894727
DUS1L	0.674	0.894727
GATD3A	0.0354	0.41244
GBP1	0.902	0.9471
GBP5	0.608	0.894727
GIMAP5	0.462	0.845478
GPR171	0.407	0.845478
GZMA	0.0326	0.41244
GZMH	0.855	0.9471
GZMK	0.789	0.9471
GZMM	0.26	0.845478
HCST	0.202	0.771273
IKZF1	0.463	0.845478
IL21R	0.596	0.894727
JAK2	0.18	0.771273
JAKMIP1	0.987	0.987
LCP2	0.439	0.845478
LTA	0.16	0.771273
MAP4K1	0.567	0.894727
NKG7	0.424	0.845478
P2RY10	0.432	0.845478
PDCD1	0.617	0.894727
PDCD1LG2	0.432	0.845478
PSTPIP1	0.87	0.9471
PTPRCAP	0.393	0.845478
PYHIN1	0.644	0.894727
RASAL3	0.925	0.947561
SAMD9L	0.159	0.771273
SEPTIN1	0.67	0.894727
SH2D1A	0.901	0.9471

TBC1D10C	0.0491	0.41244
TRAF3IP3	0.307	0.845478
ZNF831	0.703	0.894727

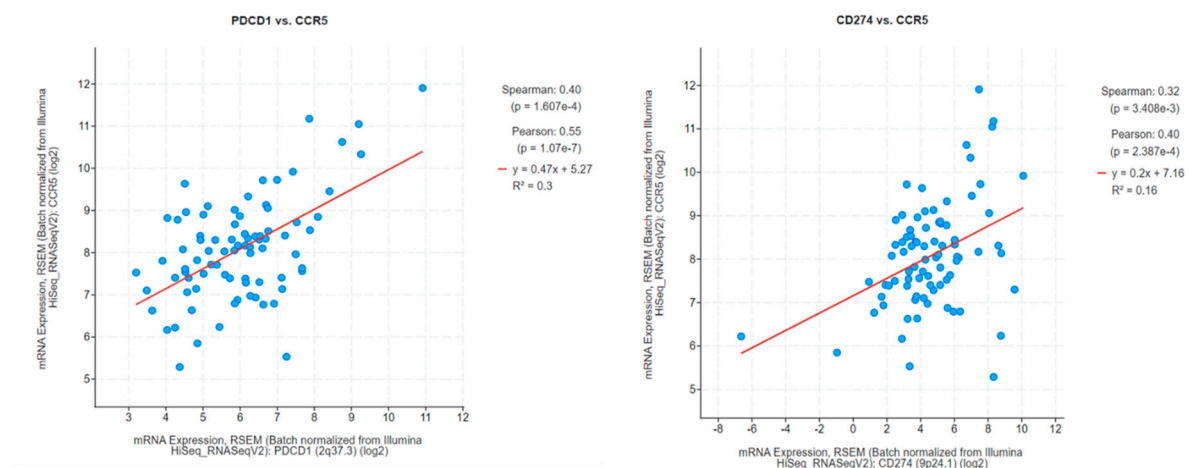
Supplementary Table S2: Node degree distribution for the PDCD1/CD274 network as identified by STRING analysis.

#node	node_degree
ACAP1	2
ARHGAP9	5
C21orf33	0
CCR5	12
CD274	9
CD80	10
CD96	2
COX19	0
CST7	9
CXCR6	5
DNASE1	0
DUS1L	0
GBP1	3
GBP5	5
GIMAP5	4
GPR171	0
GZMA	14
GZMH	8
GZMK	8
GZMM	1
HCST	5
IKZF1	9
IL21R	7
JAK2	9
JAKMIP1	0
LCP2	12
LTA	4
MAP4K1	3
NKG7	9
P2RY10	3
PDCD1	10
PDCD1LG2	5
PSTPIP1	3
PTPRCAP	3
PYHIN1	0

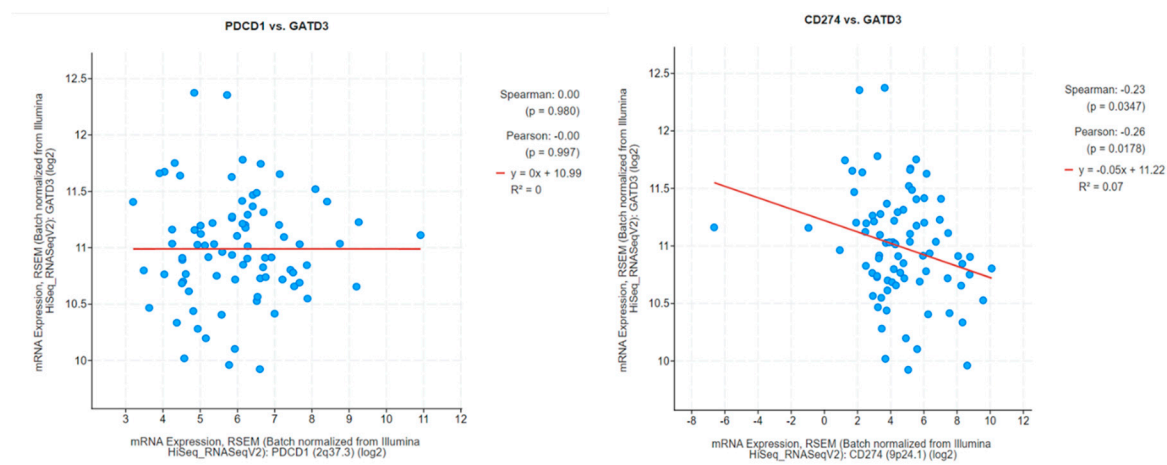
RASAL3	4
SAMD9L	2
SEPTIN1	0
SH2D1A	2
TBC1D10C	7
TRAF3IP3	8
ZNF831	0



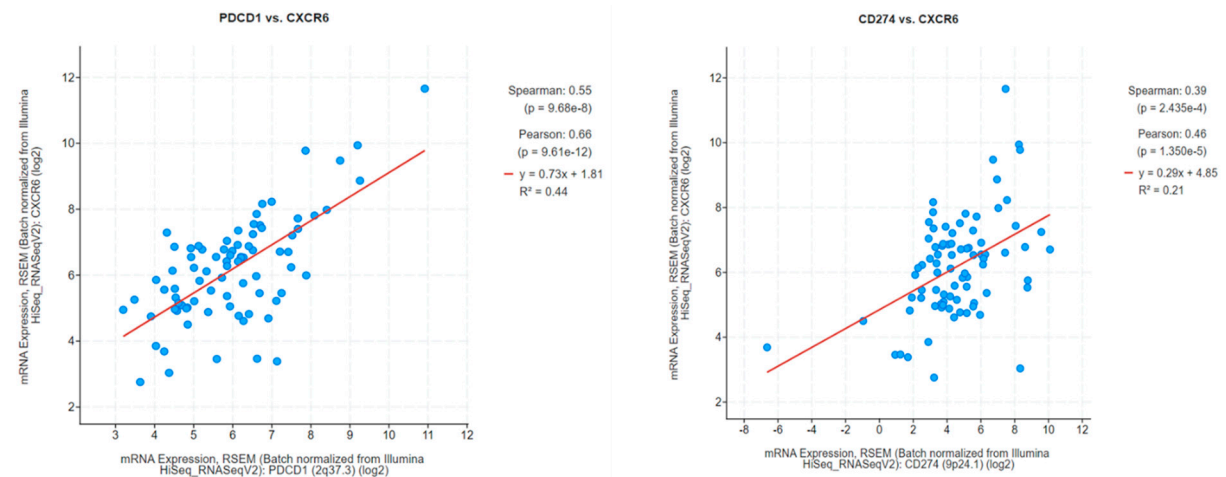
Supplementary Figure S1: Distribution of p-values from Kaplan–Meier plots for CD274, PDCD1, and 40 PDCD1/CD274-related genes. Data were generated using the mRNA expression z-scores relative to diploid samples (RNA Seq V2 RSEM) for the Mesothelioma (TCGA, PanCancer Atlas) study available on cBioPortal.



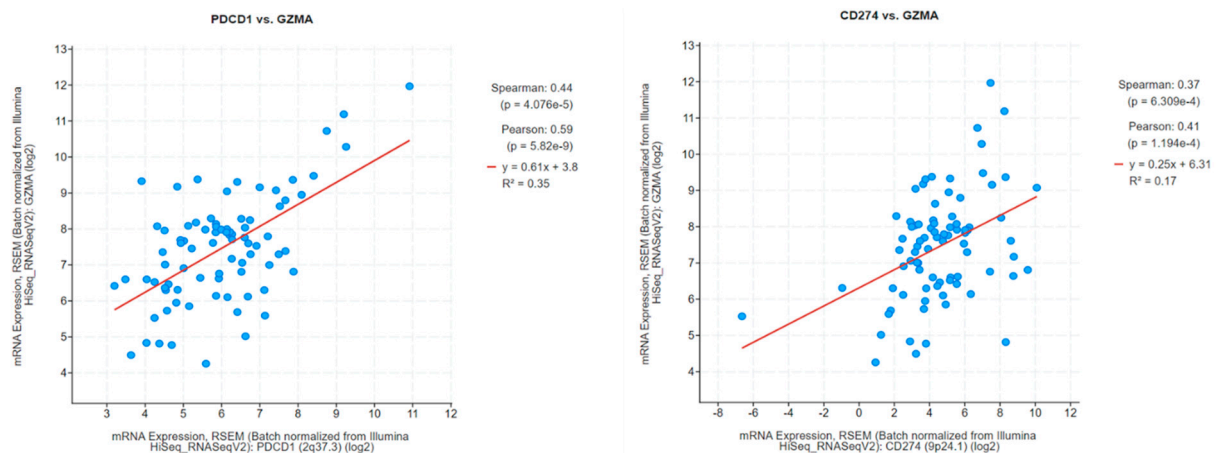
Supplementary Figure S2: Co-expression analysis of PDCD1 and CD274 with CCR5. Data was generated on cBioPortal using the “Mesothelioma (TCGA, PanCancer Atlas)” study on the cBioPortal homepage. This study was selected and “Query by Gene” was chosen. “mRNA expression z-scores relative to diploid samples (RNA Seq V2 RSEM)” was selected as the ‘type’ of mRNA expression and the default Patient/Case set was used. PDCD1 and CD274 were then inputted separately in turn and the Co-Expression tab under the “mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2) (82 Samples)” setting was used.



Supplementary Figure S3: Co-expression analysis of PDCD1 and CD274 with GATD3. Data was generated on cBioPortal using the “Mesothelioma (TCGA, PanCancer Atlas)” study on the cBioPortal homepage. This study was selected and “Query by Gene” was chosen. “mRNA expression z-scores relative to diploid samples (RNA Seq V2 RSEM)” was selected as the ‘type’ of mRNA expression and the default Patient/Case set was used. PDCD1 and CD274 were then inputted separately in turn and the Co-Expression tab under the “mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2) (82 Samples)” setting was used.

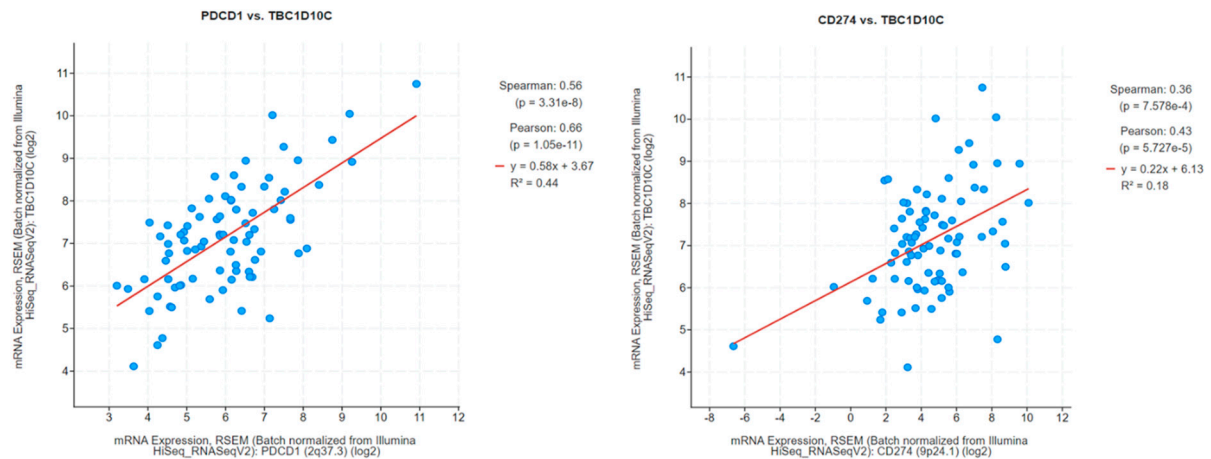


Supplementary Figure S4: Co-expression analysis of PDCD1 and CD274 with CXCR6. Data was generated on cBioPortal using the “Mesothelioma (TCGA, PanCancer Atlas)” study on the cBioPortal homepage. This study was selected and “Query by Gene” was chosen. “mRNA expression z-scores relative to diploid samples (RNA Seq V2 RSEM)” was selected as the ‘type’ of mRNA expression and the default Patient/Case set was used. PDCD1 and CD274 were then inputted separately in turn and the Co-Expression tab under the “mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2) (82 Samples)” setting was used.



Supplementary Figure S5: Co-expression analysis of PDCD1 and CD274 with GZMA. Data was generated on cBioPortal using the “Mesothelioma (TCGA, PanCancer Atlas)” study on the cBioPortal

homepage. This study was selected and “Query by Gene” was chosen. “mRNA expression z-scores relative to diploid samples (RNA Seq V2 RSEM)” was selected as the ‘type’ of mRNA expression and the default Patient/Case set was used. PDCD1 and CD274 were then inputted separately in turn and the Co-Expression tab under the “mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2) (82 Samples)” setting was used.



Supplementary Figure S6: Co-expression analysis of PDCD1 and CD274 with TBC1D10C. Data was generated on cBioPortal using the “Mesothelioma (TCGA, PanCancer Atlas)” study on the cBioPortal homepage. This study was selected and “Query by Gene” was chosen. “mRNA expression z-scores relative to diploid samples (RNA Seq V2 RSEM)” was selected as the ‘type’ of mRNA expression and the default Patient/Case set was used. PDCD1 and CD274 were then inputted separately in turn and the Co-Expression tab under the “mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2) (82 Samples)” setting was used.