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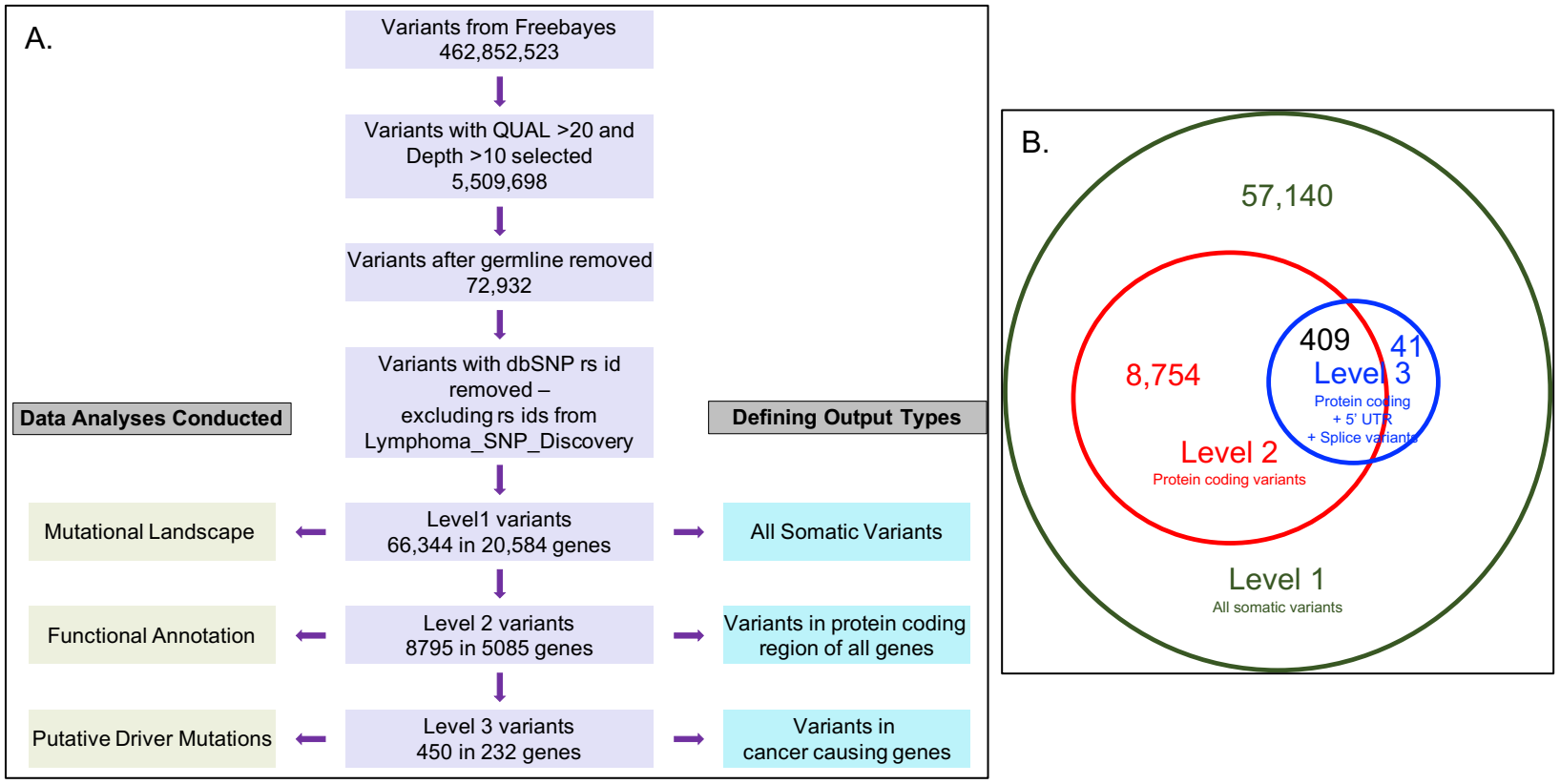
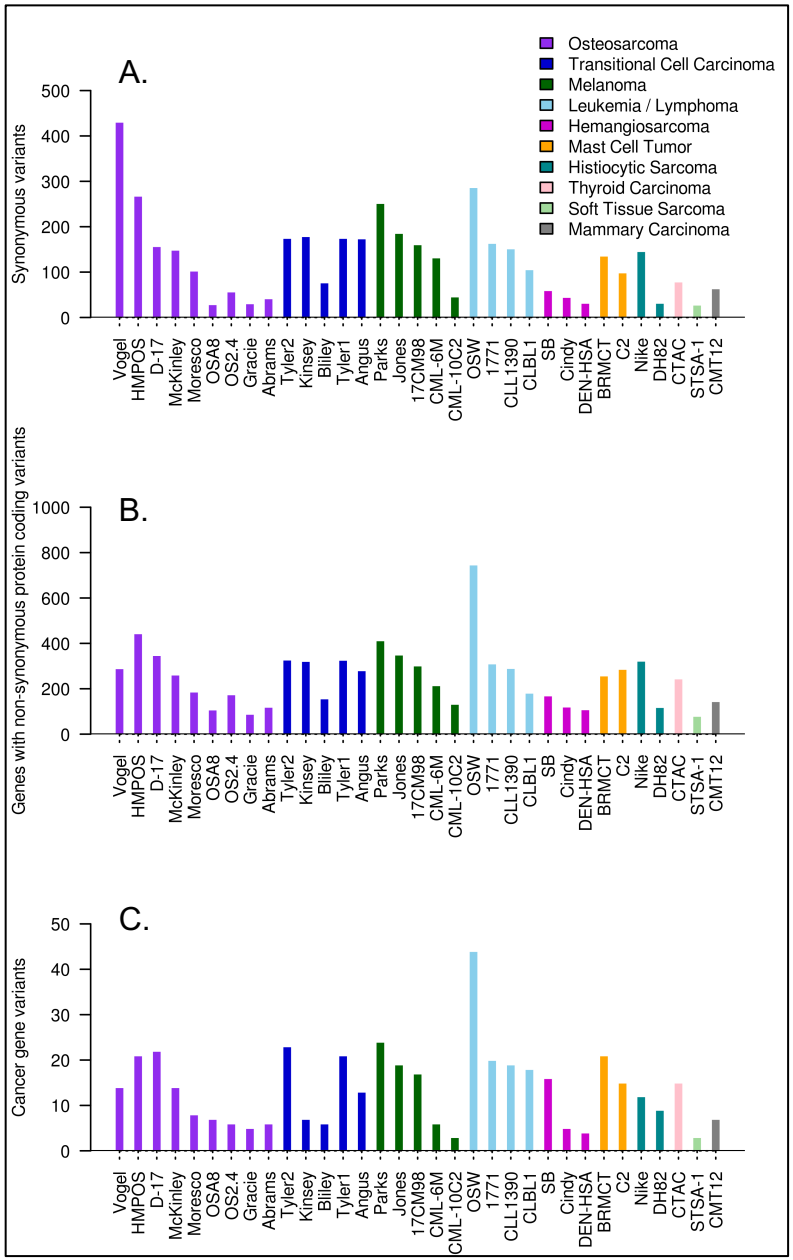
Supplementary Fig. S1. Pipeline for post-processing of somatic variants.



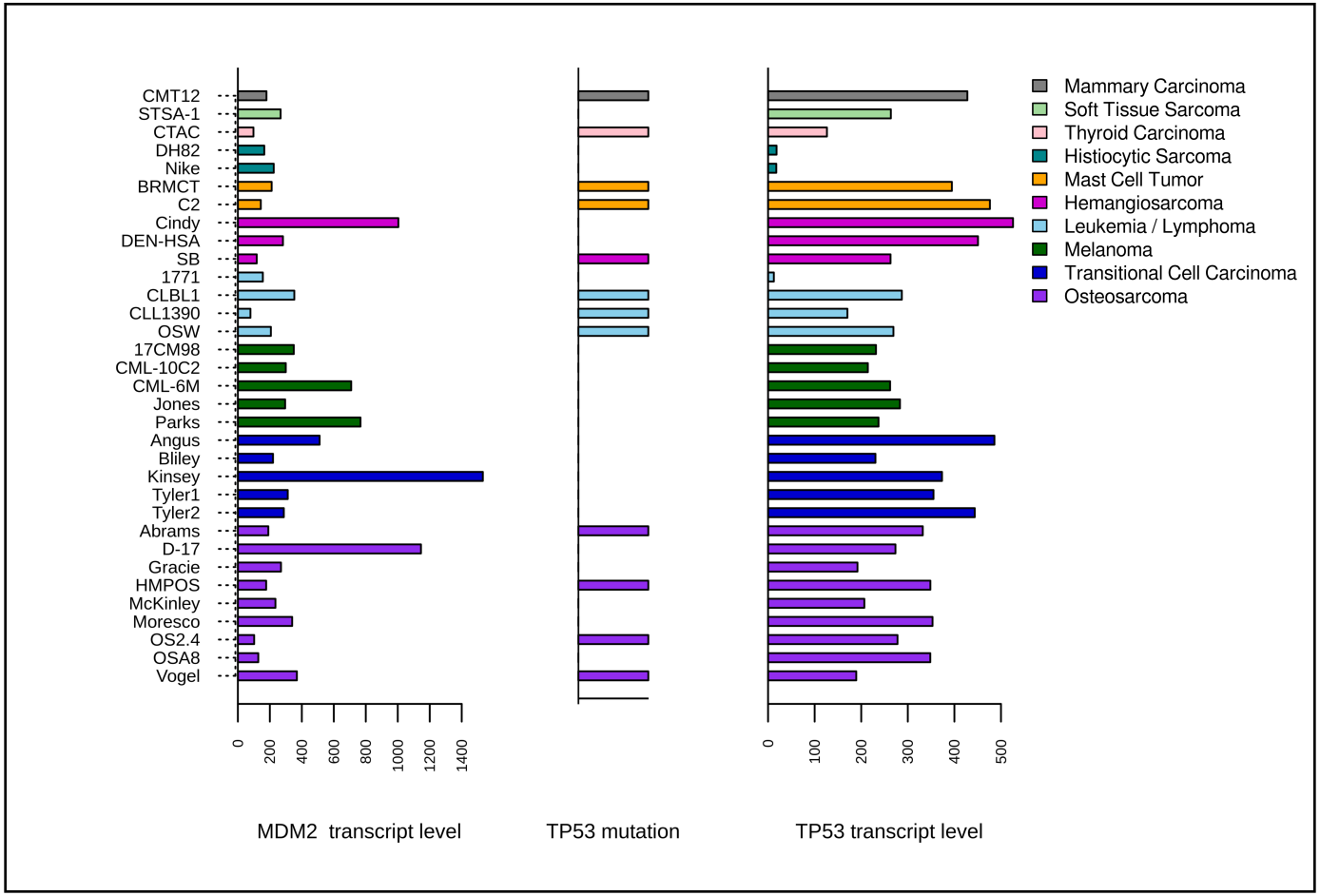
Supplementary Fig. S1. **A**. **Pipeline for post-processing of somatic variants.** The selection criteria, analyses tools, and results from post-procession of raw variants are outlined here. The variants listed in Lymphoma_SNP_Discovery were downloaded from Broad institute database (×https://data.broadinstitute.org/vgb/dog/dog/canFam3/variation/elvers.lymphoma.somatic.snps.vcf.gz. These somatic variants were identified in Elvers et al. 2016, and are cataloged in NCBI dbSNP database with unique accession number (https://www.ncbi.nlm.nih.gov/projects/SNP/snp_batchSearch.cgi?org=9615&type=SNP). In this study we have eliminated all the SNPs with dbSNP accession number with the exception of the variants that are listed as somatic variants from dog lymphoma study. **B.** A Venn diagram showing the number of variants and their overlap at each of the three levels used in this study.

Supplementary Fig. S2. Distribution of genes and variants.



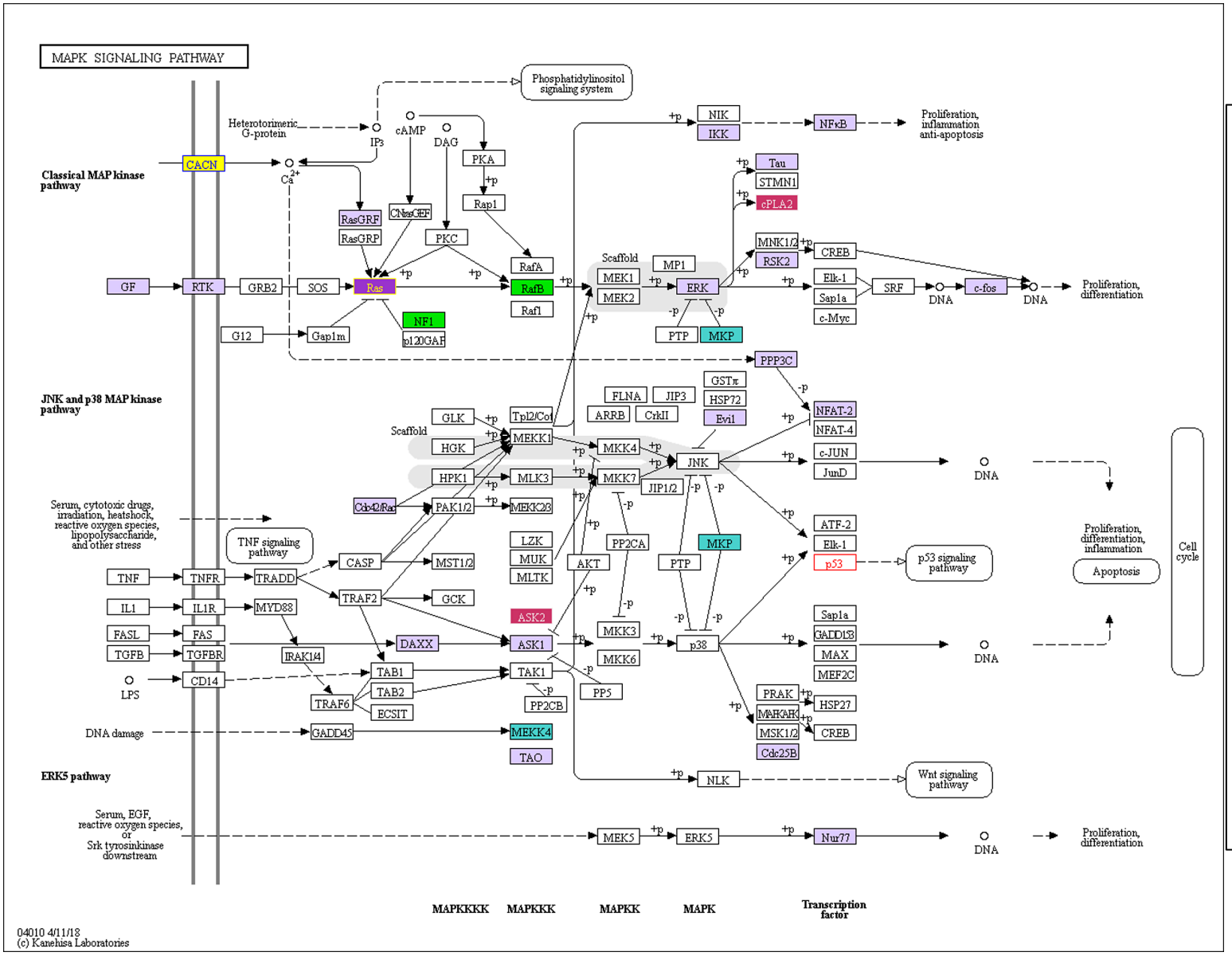
Supplementary Fig. S2. Distribution of genes and variants. Number of synonymous variants (A), level 2 genes (B), and COSMIC cancer gene variants (C) across FACC cancer cell line panel are plotted here.

Supplementary Fig. S3. MDM2 and TP53 transcript levels.



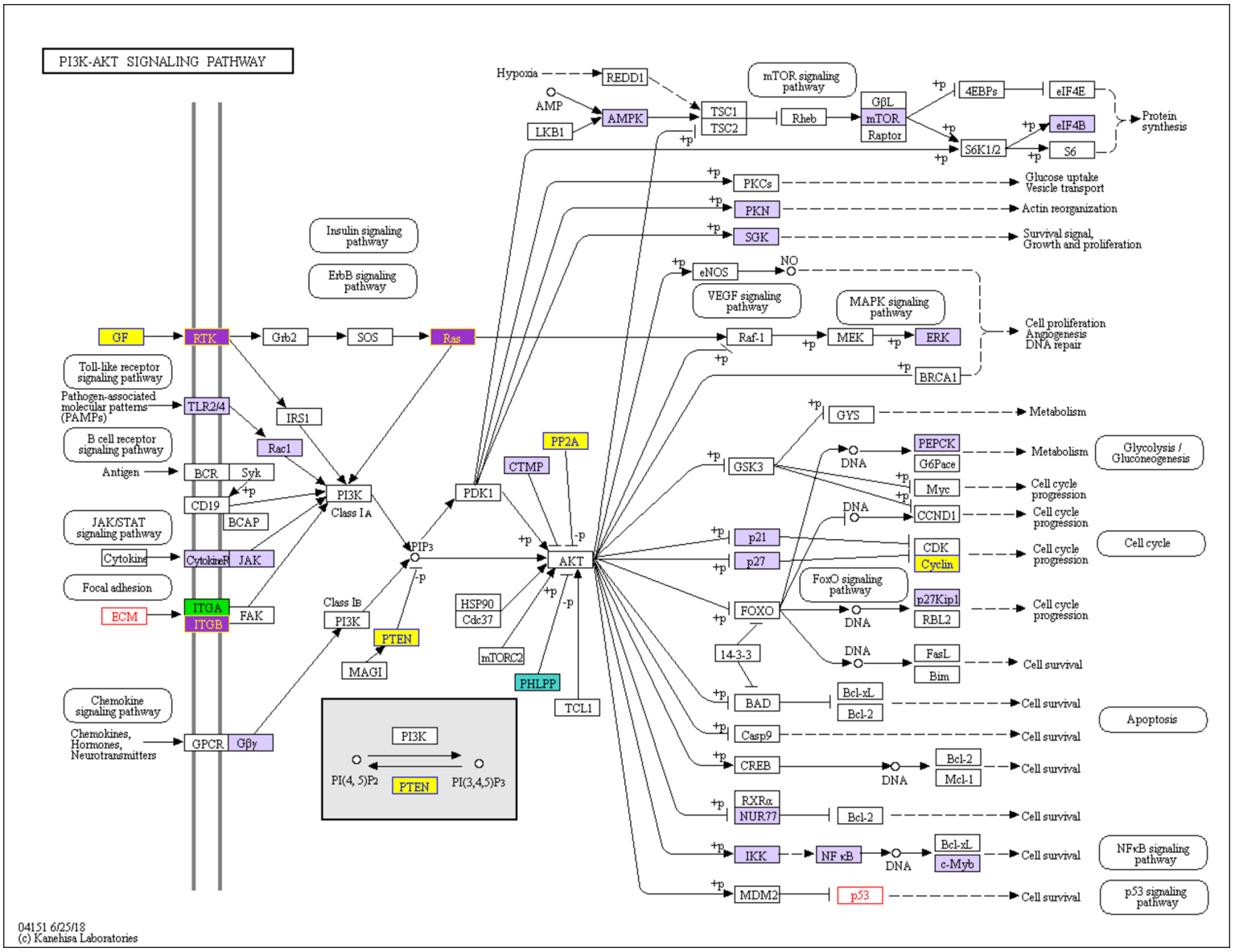
Supplementary Fig. S3. MDM2 and TP53 transcript levels. The expression profile of MDM2 and TP53, along with TP53 mutations status across 33 cell lines are plotted here. The cell lines are colored based on their cancer type.

Supplementary Fig. S4. KEGG MAPK pathway.



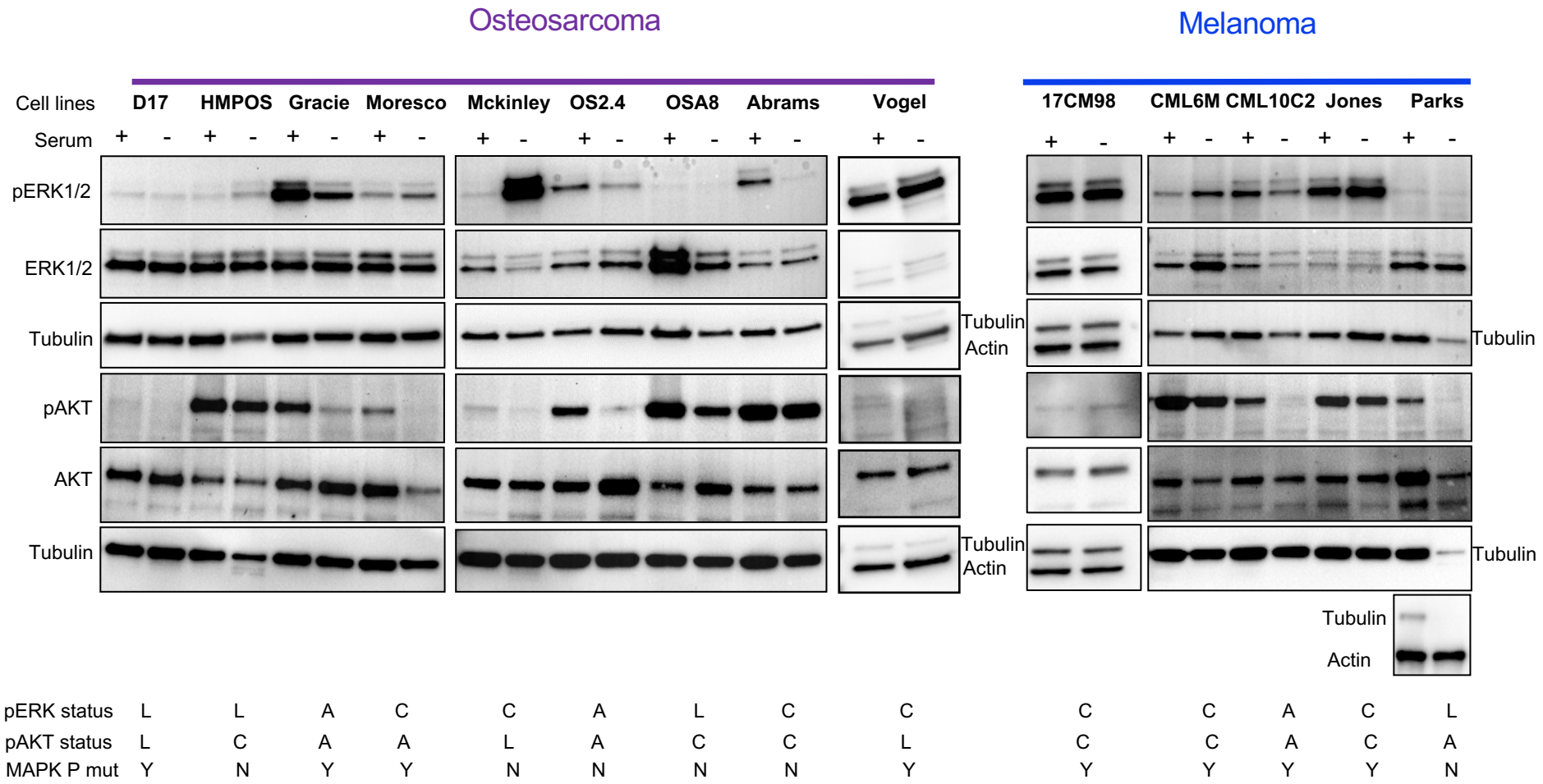
Supplementary Fig. S4. KEGG MAPK pathway (cfa:04010). Genes mutated across the entire FACC panel are mapped to KEGG pathway. The differential color designates number of variants:
Lavender – 1;
Yellow with blue letters – 2;
Turquoise – 3;
Green – 4;
Purple with yellow letters – 5;
White with red letter – Greater than or equal to 10.
The supporting data incorporating the gene variants and corresponding cell lines are listed in supplementary table S8.

Supplementary Fig. S5. KEGG PI3K-AKT pathway.



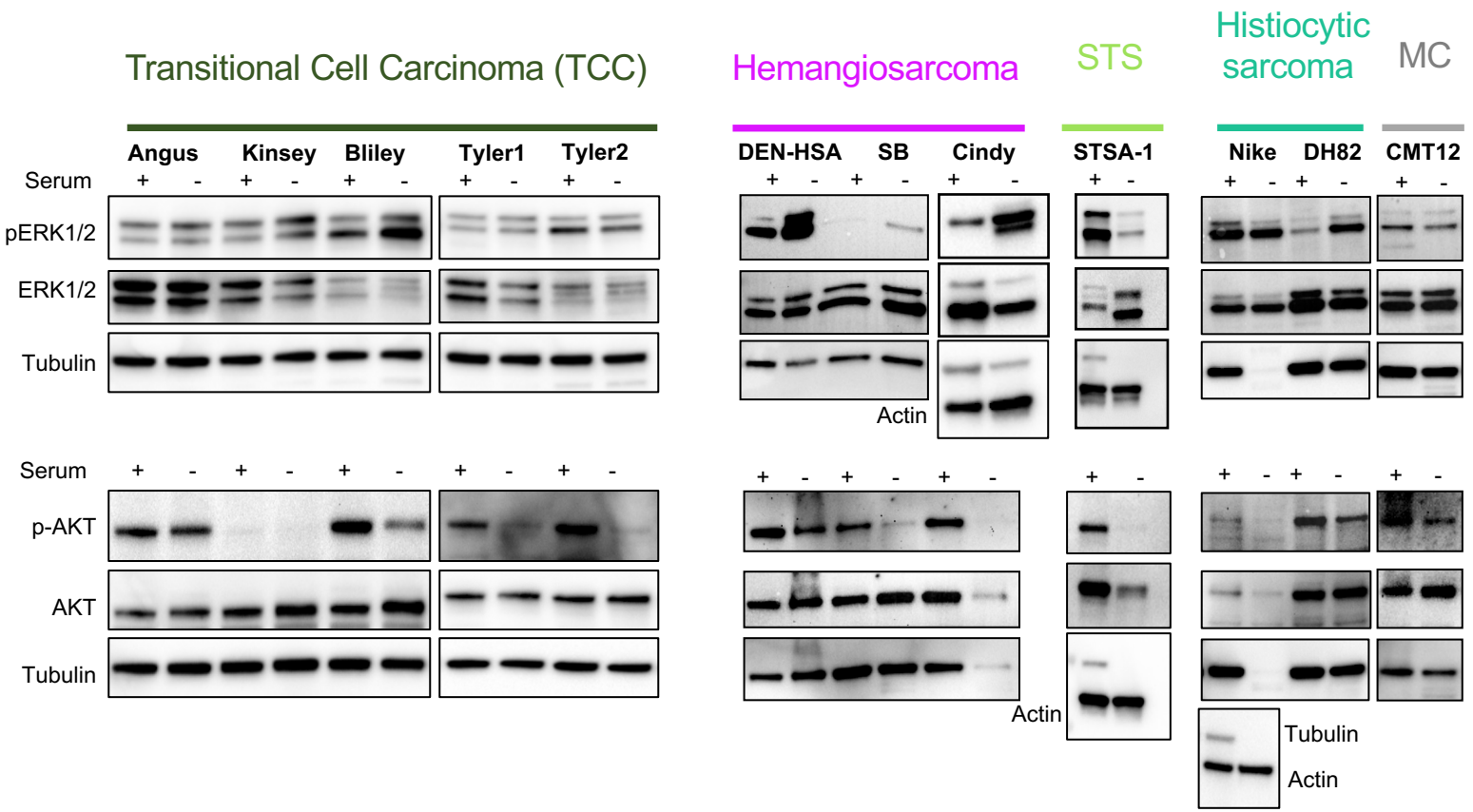
Supplementary Fig. S5. KEGG PI3K-Akt pathway (cfa:04151). Genes mutated across the entire FACC panel are mapped to KEGG pathway. The color designates number of variants:
Lavender – 1;
Yellow with blue letters – 2;
Turquoise – 3;
Green – 4;
Purple with yellow letters – 5 to 8;
White with red letter – Greater than and equal to 10.
The supporting data incorporating the gene variants and corresponding cell lines are listed in supplementary table S9.

Supplementary Fig. S6. Western blot analyses for ERK/pERK and AKT/pAKT.



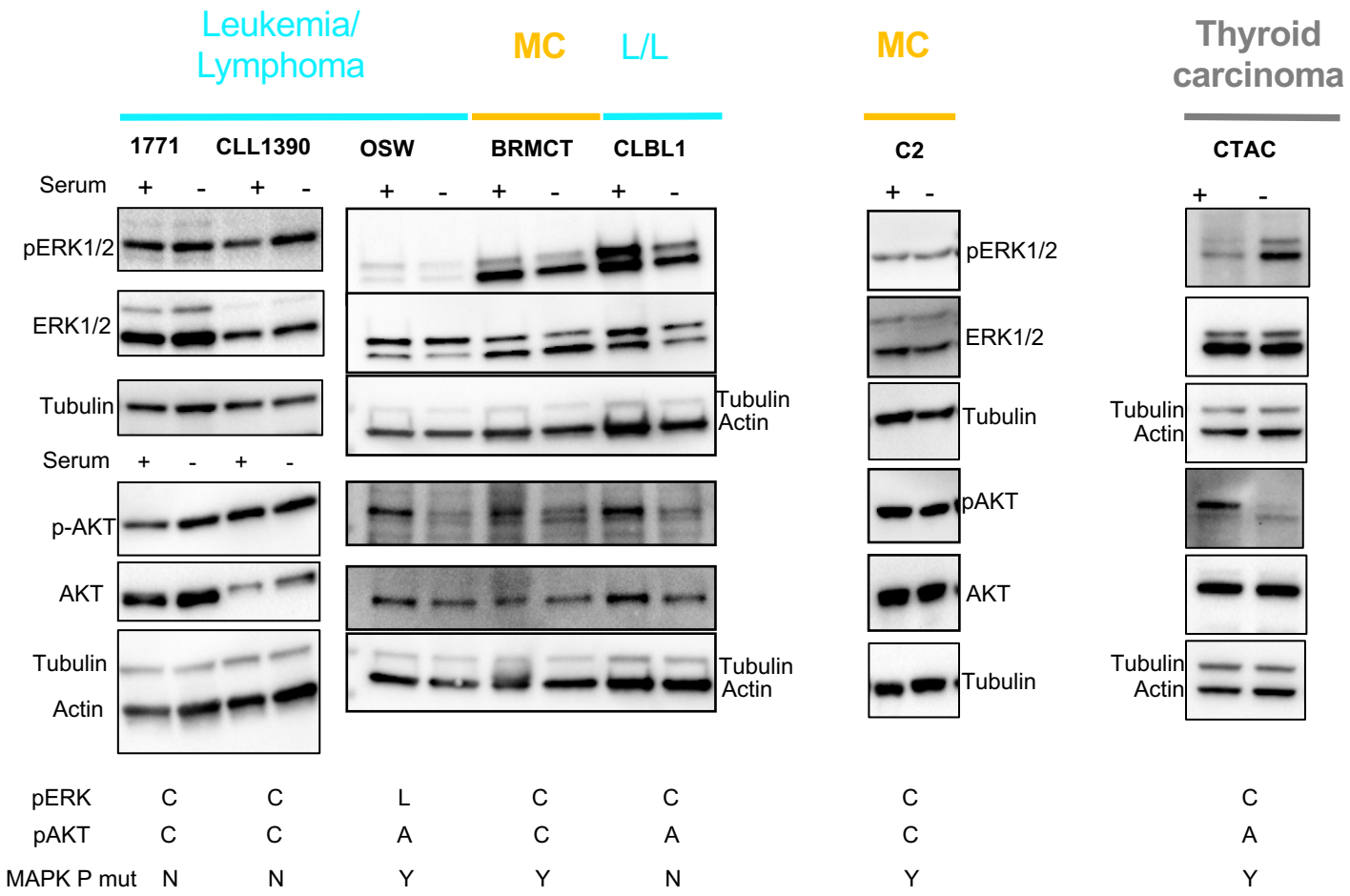
Supplementary Fig. S6. Western blot analyses for ERK/pERK and AKT/pAKT. Western blot analysis was used to determine the levels of ERK/pERK and AKT/pAKT following 24 hours with (+) and without (-) serum.
The panels are divided based on cancer type of cell lines. Actin was added as an additional loading control for samples that exhibited decreased tubulin in response to serum starvation. Actin was added as an additional loading control for samples that exhibited decreased tubulin in response to serum starvation. The pERK and pAKT status as reported in Table 1 is added in the bottom panel. The panel "MAPK P mut" is designated as Y (yes) if there is any MAPK pathway driver gene mutation identified in the corresponding cell line. N – No.

Supplementary Fig. S6. Western blot analyses for ERK/pERK and AKT/pAKT (contd.).



Supplementary Fig. S6. Western blot analyses for ERK/pERK and AKT/pAKT (contd.). Western blot analysis was used to determine the levels of ERK/pERK and AKT/pAKT following 24 hours with (+) and without (-) serum. Actin was added as an additional loading control for samples that exhibited decreased tubulin in response to serum starvation. The pERK and pAKT status as reported in Table 1 is added in the bottom panel. The panel "MAPK P mut" is designated as Y (yes) if there is any MAPK pathway driver gene mutation identified in the corresponding cell line.
N – No; STS - Soft tissue sarcoma; MC – mammary carcinoma.

Supplementary Fig. S6. Western blot analyses for ERK/pERK and AKT/pAKT (contd.).



Supplementary Fig. S6. Western blot analyses for ERK/pERK and AKT/pAKT (contd.). Western blot analysis was used to determine the levels of ERK/pERK and AKT/pAKT following 24 hours with (+) and without (-) serum.
The panels are divided based on cancer type of cell lines. Actin was added as an additional loading control for samples that exhibited decreased tubulin in response to serum starvation. The pERK and pAKT status as reported in Table 1 is added in the bottom panel. The panel "MAPK P mut" is designated as Y (yes) if there is any MAPK pathway driver gene mutation identified in the corresponding cell line.
N – No; MC – Mast cell tumor. L/L – Lymphoma/Leukemia.