C

Correlation Coefficient
Tier 1: 0.70
Tier 1-3: 0.69

D

Correlation Coefficient
Tier 1: 0.26
Tier 1-3: 0.32
G

WHIM12

Correlation Coefficient
Tier 1: 0.73
Tier 1-3: 0.66

H

WHIM13

Correlation Coefficient
Tier 1: 0.71
Tier 1-3: 0.70
Tumor (VAF) vs Xenograft (VAF)

**WHIM14**
- Gene expression:
  - TET3, TET2, MLL3, PIWIL1, NEK5, MLL4, TP53, MAP2K6, DOCK6, MLL4
- Correlation Coefficients:
  - Tier 1: 0.73
  - Tier 1-3: 0.71

**WHIM16**
- Gene expression:
  - PIK3CA, TET2, PTPRD, MAP4K2, ZNF841, MYH9, PIK3CA
- Correlation Coefficients:
  - Tier 1: 0.45
  - Tier 1-3: 0.49
Figure S7. The Circos plots and variant allele frequency plots for all 13 WHIM PDX models subjected to whole genome sequencing (A) WHIM2, (B) WHIM5, (C) WHIM6, (D) WHIM8, (E) WHIM9, (F) WHIM11, (G) WHIM12, (H) WHIM13, (I) WHIM14, (J) WHIM16, (K) WHIM18, (L) WHIM20, (M) WHIM21. Overall the Circos plots show closely matched SV and CNV in the tumor of origin and the paired WHIM line. To compare differences in mutant allele frequency between the originating tumor and the PDX counterpart, the read counts for each mutant and wild-type allele were expressed as a percentage of all reads at that position and analyzed by scatter plot and simple correlation coefficient. These show considerably more variation in the human to PDX comparisons.