Supplementary spreadsheet legends:

Supplementary Mutation-correlated expression. Spreadsheet describing the relationship for gene mutation and drastic over- and under-expression for all genes presented in this study. The spreadsheet contains 41 *sheets*, one for each gene whose mutation status is correlated with the drastic over- and under-expression of other genes—each sheet is named for said mutated gene. Column one of each sheet is the hugo symbol for the mutated gene; column two describes the correlation type (up-regulated (*UpReg*) or down-regulated (*DownReg*) and co-occurring (*Co-occ*) or mutually exclusive (*MutExc*)); column three is the hugo symbol for each corresponding over- and under-expressied gene; column four is the Fishers exact p-value for the correlation. This spreadsheet is meant to accompany *Supplementary Heatmaps*.

Supplementary Mutation-mutation correlation. Spreadsheet describing the relationship for each mutation-mutation correlation. Columns one and three are the hugo symbols of each gene involved in the pairwise mutation-mutation correlation; column two describes the correlation type (co-occurring (*Co-occ*) or mutually exclusive (*MutExc*)); column four is the Fishers exact p-value for the correlation.

Supplementary Mutation type, zygosity, and score. Site-specific information for each of the 41 genes whose mutation status was correlated with the drastic over- and under-expression of other genes. Column one is the TCGA sample barcode; column two is the hugo gene symbol; column three is the mutation type (nonsense, splice site, frame shift, etc., (missense mutations are notated by amino acid substitution))*;* column four describes the zygosity of the gene (homozygous (*homo*) or heterozygous (*hetero*)), column five is the CHASM[1] score for each missense mutation, column six is the corresponding p-value, and column seven is the corresponding Benjamini and Hochberg false discovery rate*;* column eight indicates if that substitution was in the CHASM training set. CHASM scores range from 0 (most *driver* like) to 1 (most *passenger* like)—a missense mutation with a CHASM score of less than 0.3 predicted to be very driver like.

1. Carter, H., Chen, S. Isik, L., Tyekucheva, S., Velculescu, V. E., Kinzler, K. W., Volgelstein, B., and Karchin, R. *Cancer-Specific High-Throughput Annotation of Somatic Mutations: Computational Prediction of Driver Missense Mutations*. Cancer Research **2009** 69; 6660