

Translation of TCGA data

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TCGA GBM program: summary

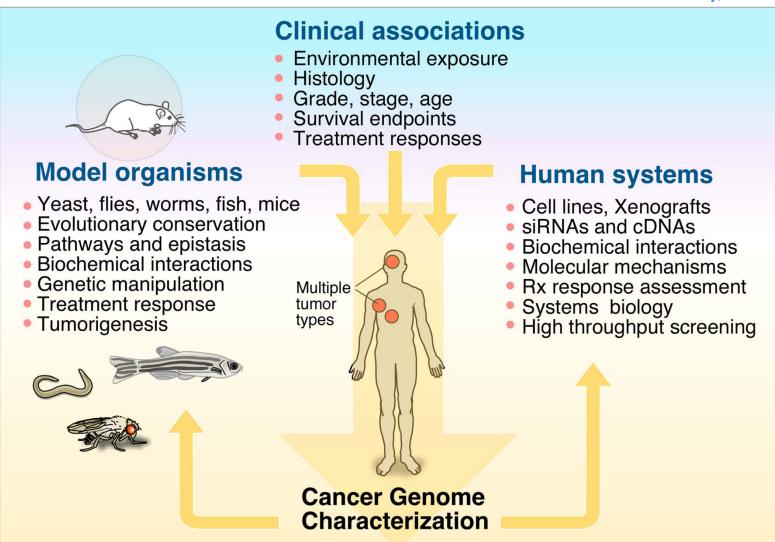


- Defining the atlas of changes in human GBM
 - Deeper insights into known mutations
 - Many novel gene candidates identified
 - Cross-platform validation & interpretation of alterations
- Distinct molecular subtypes of primary GBM defined
 - Potential implication for patient stratification
- New technology for sequencing
 - More data, better data, lower cost...
 - New ways of looking at cancer genomes

Integration and Synergy



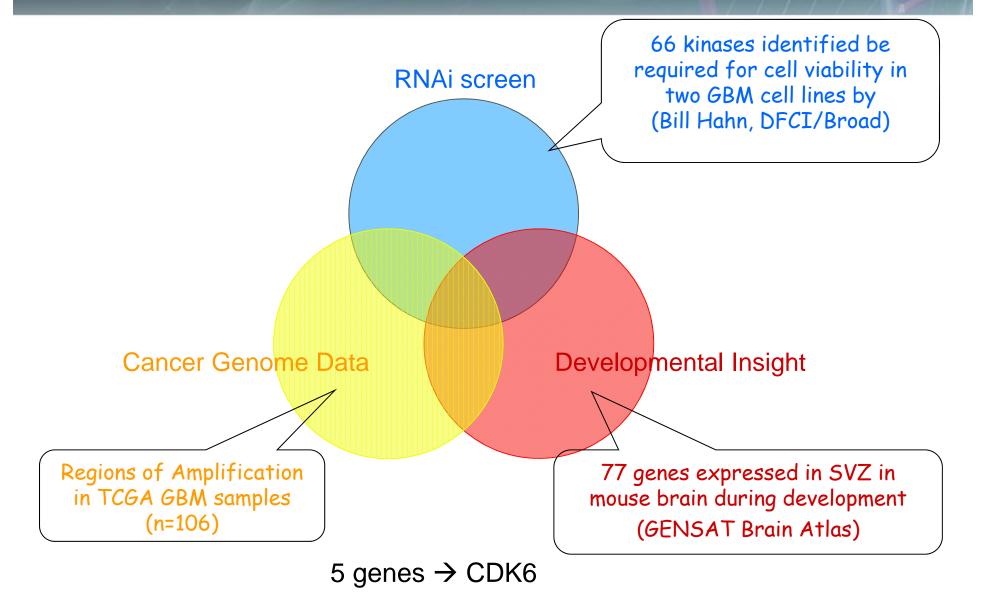
Chin and Gray, Nature, in press



An example...

THE CANCER GENOME ATLAS

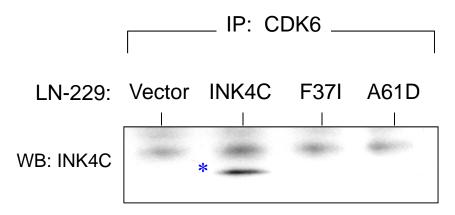




CDK6 and p18^{INK4C} in GBM



- CDK6, not CDK4, is the major CDK that complexes with p16^{INK4A} or p18^{INK4C} on co-IP
- p18^{INK4C} loss-of-function mutants do not bind to CDK6



- p18^{INK4C} is a backup tumor suppressor engaged in the relatively common setting of p16^{INK4A} inactivation
 - Loss of p16^{INK4A} → enhanced proliferation → increased E2F1
 - E2F1 binding to p18^{INK4C} promoter → induction of backup

Integration and Triangulation



Chin and Gray, Nature, in press

