

Fig 1a. SV Impact Score Analysis

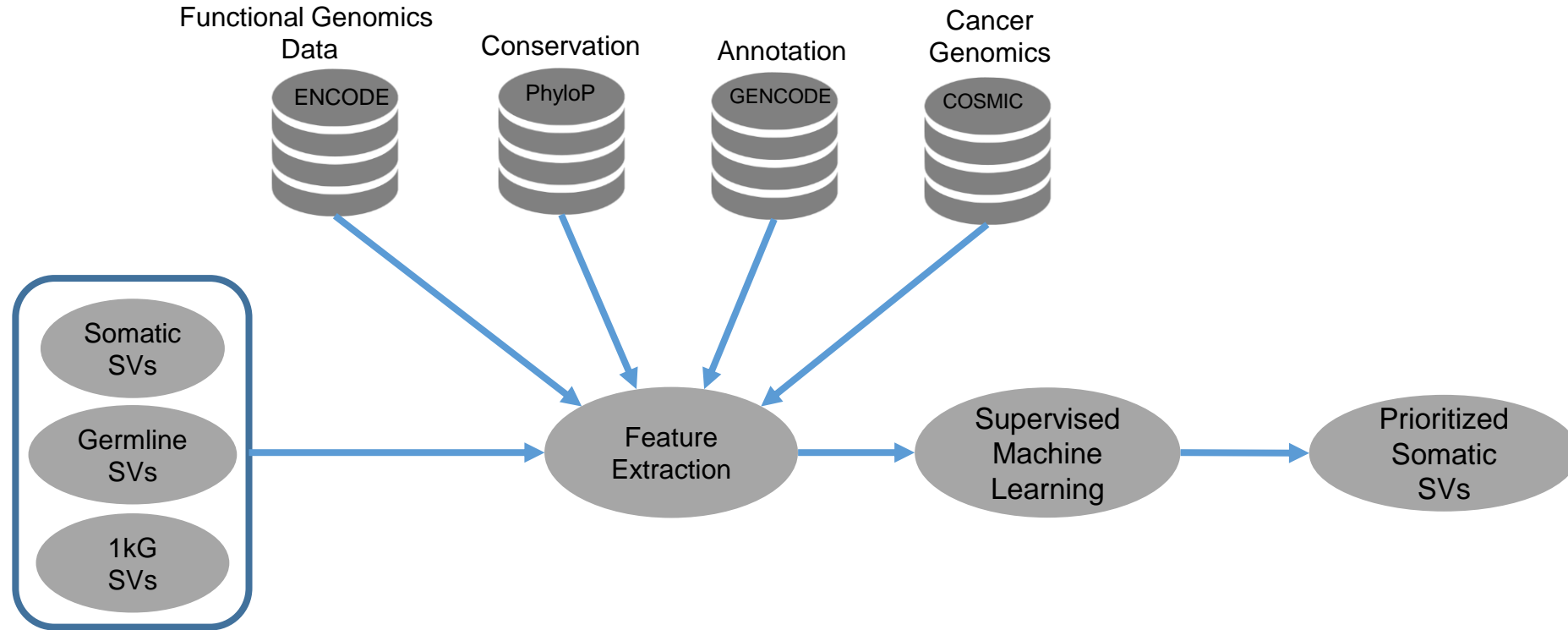


Fig 1b. Confusion Matrix of the Random Forest (Full Model)

Deletions

Duplications

SV classified as

SV classified as

	Somatic	Germline	1kG
Somatic	566	321	113
Germline	318	508	174
1kG	243	299	458

	Somatic	1kG
Somatic	644	356
1kG	650	350

SV belongs to

Fig 2. Distribution of SVIS versus SV length for different classes (Full Model)

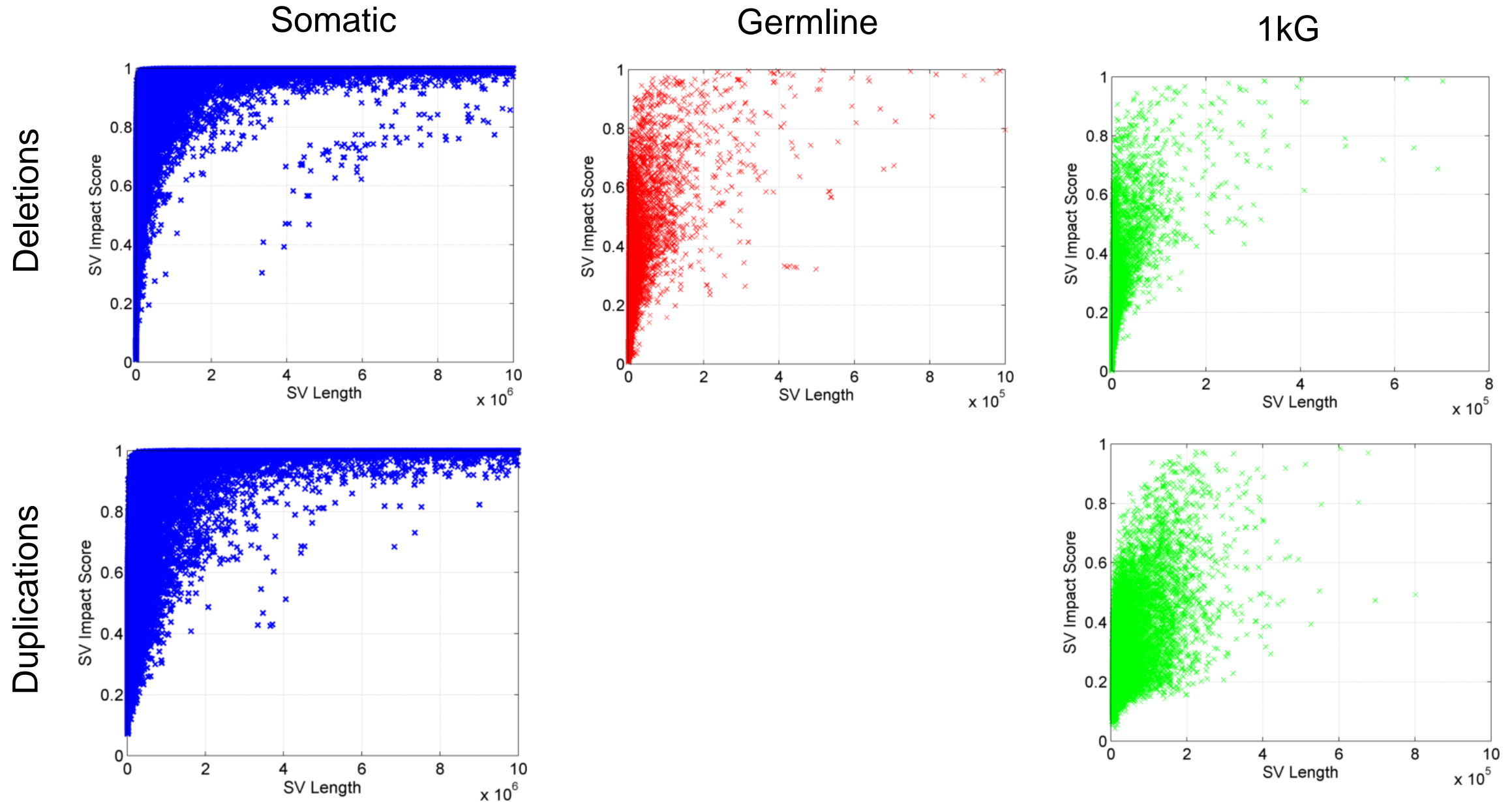


Fig 3. Cancer census gene-set enrichment (<100kb SVs) (Restricted Model)

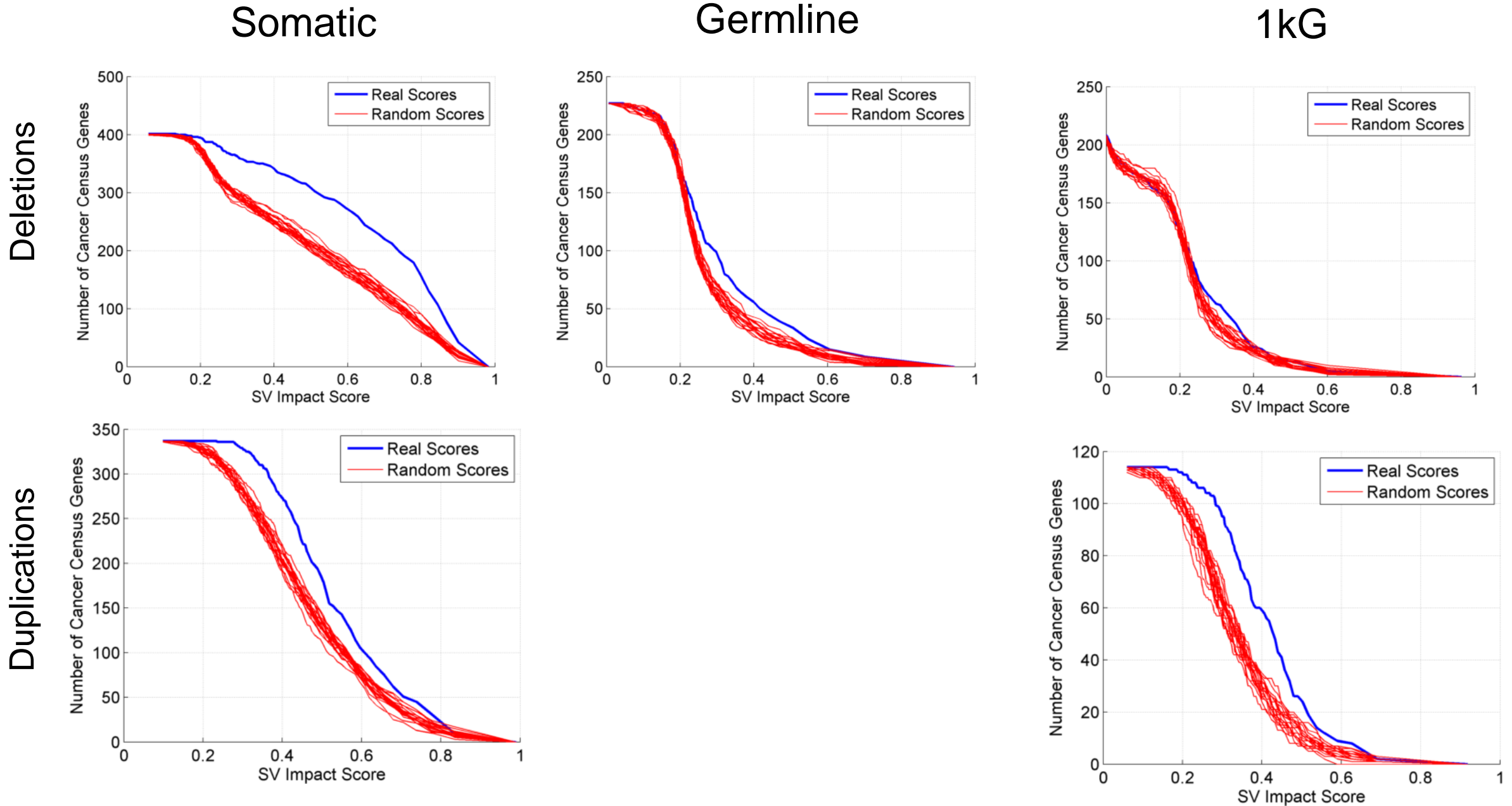
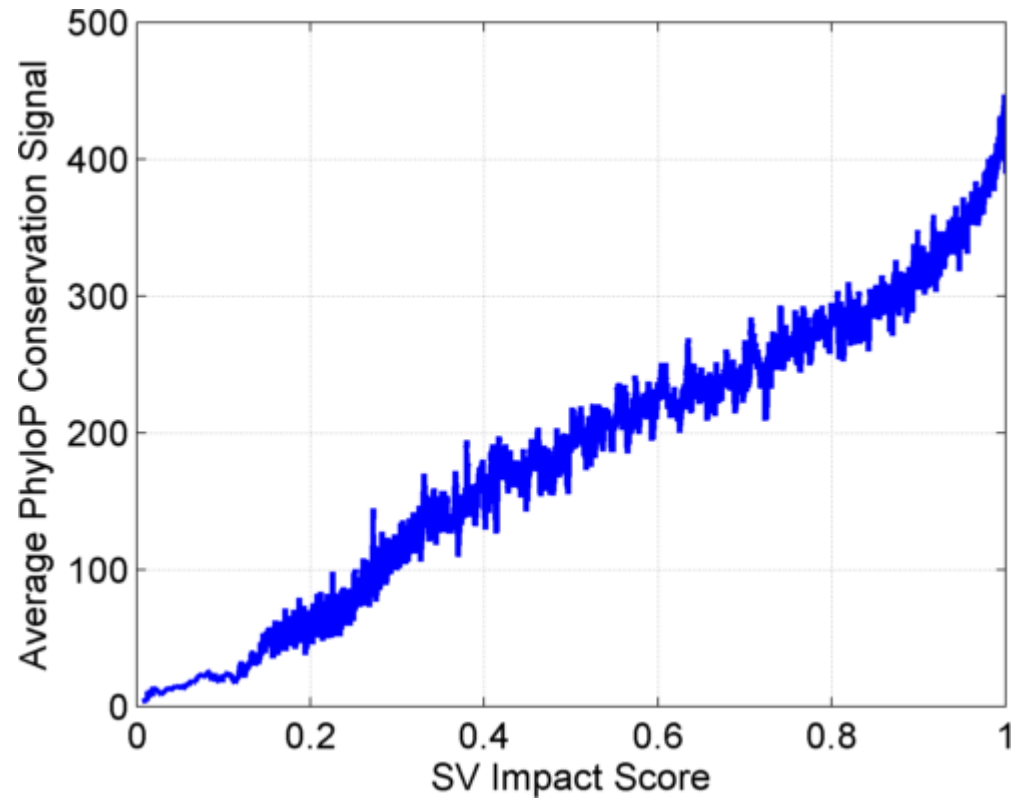


Fig 4. Conservation (Restricted Model)

Deletions



Duplications

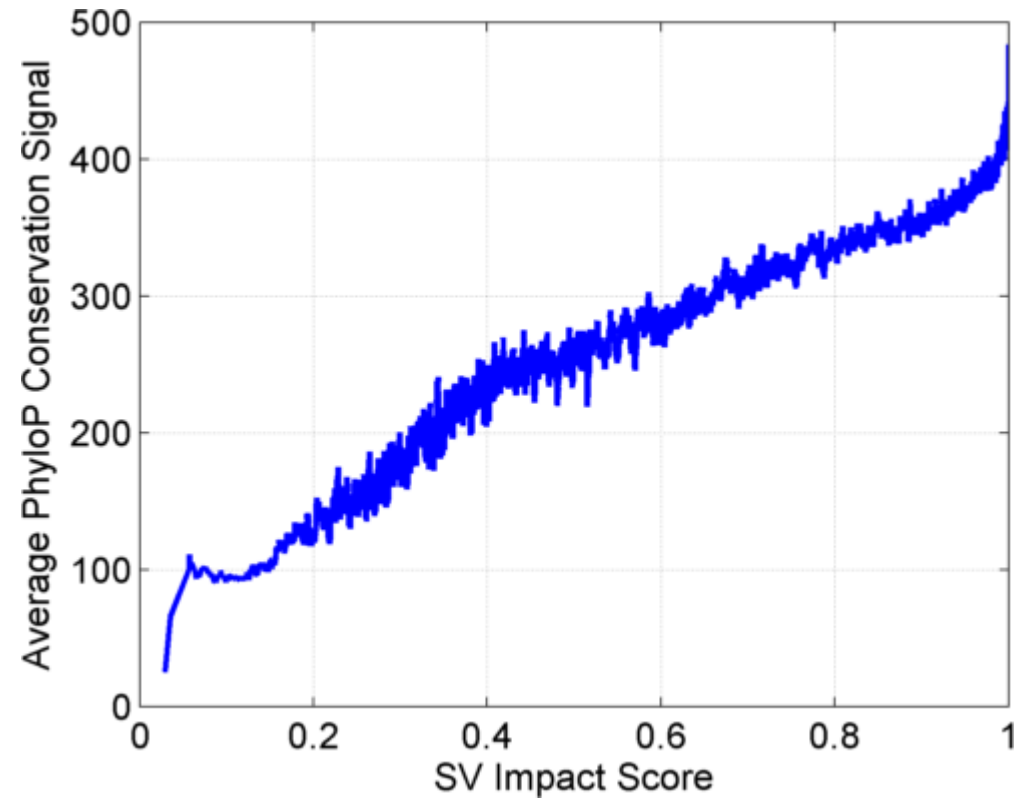


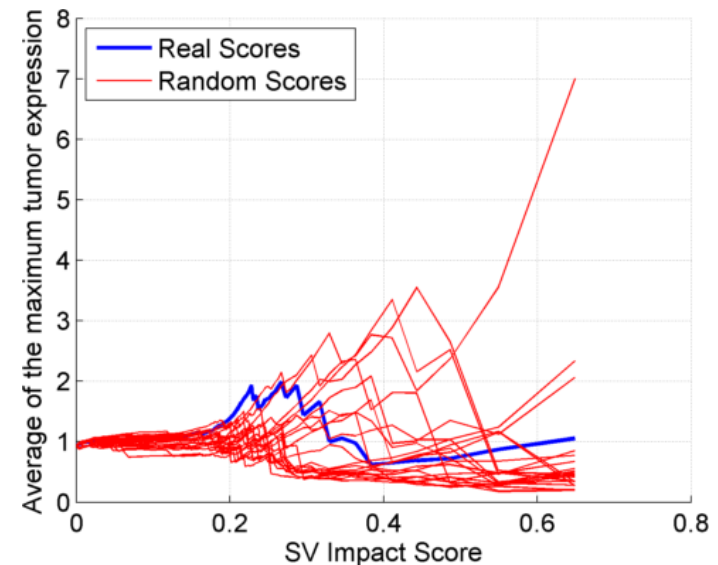
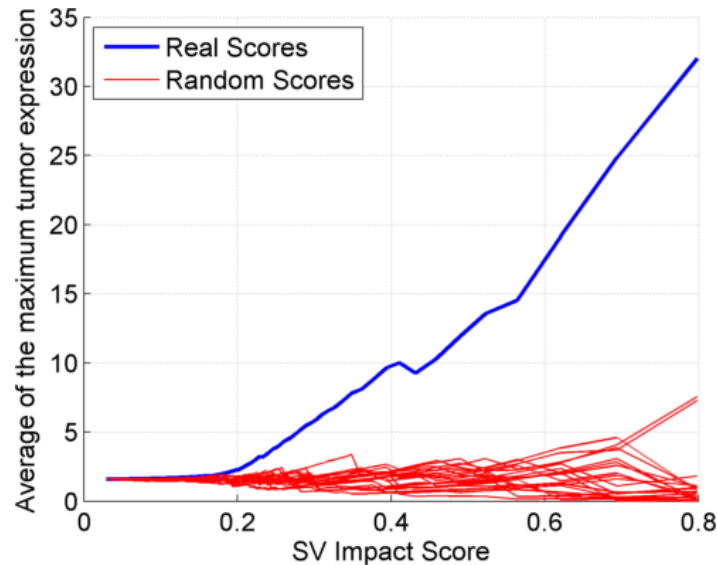
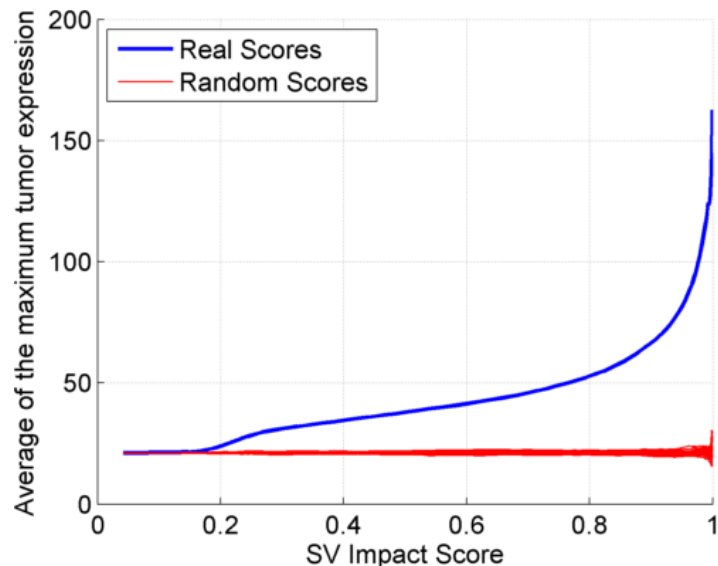
Fig 5. Gene expression data (Cancer Census Only) (Restricted Model)

Somatic

Germline

1kG

Deletions



Duplications

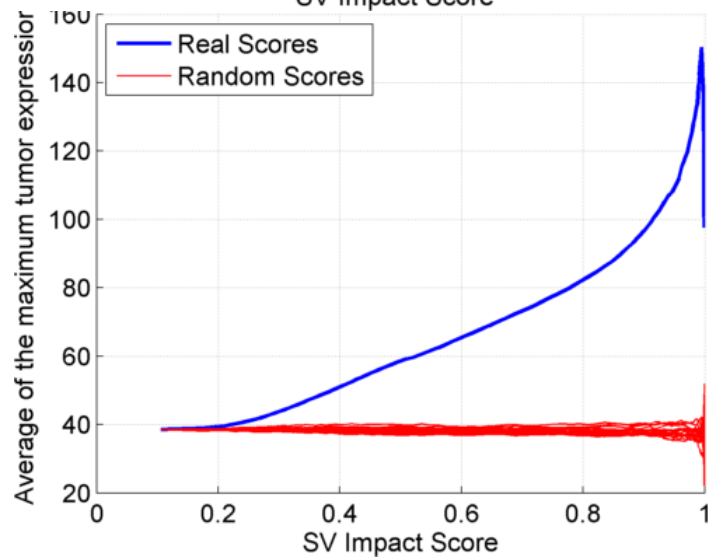
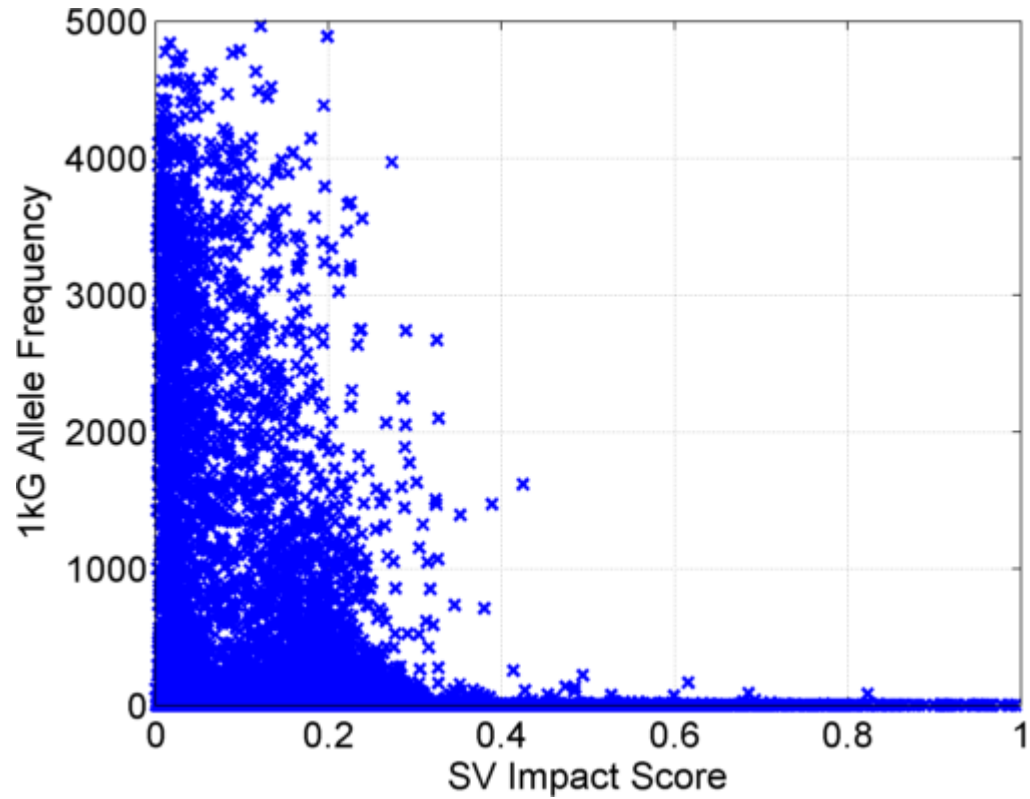


Fig 6. 1000 Genomes Allele Frequencies (Full Model)

Deletions



Duplications

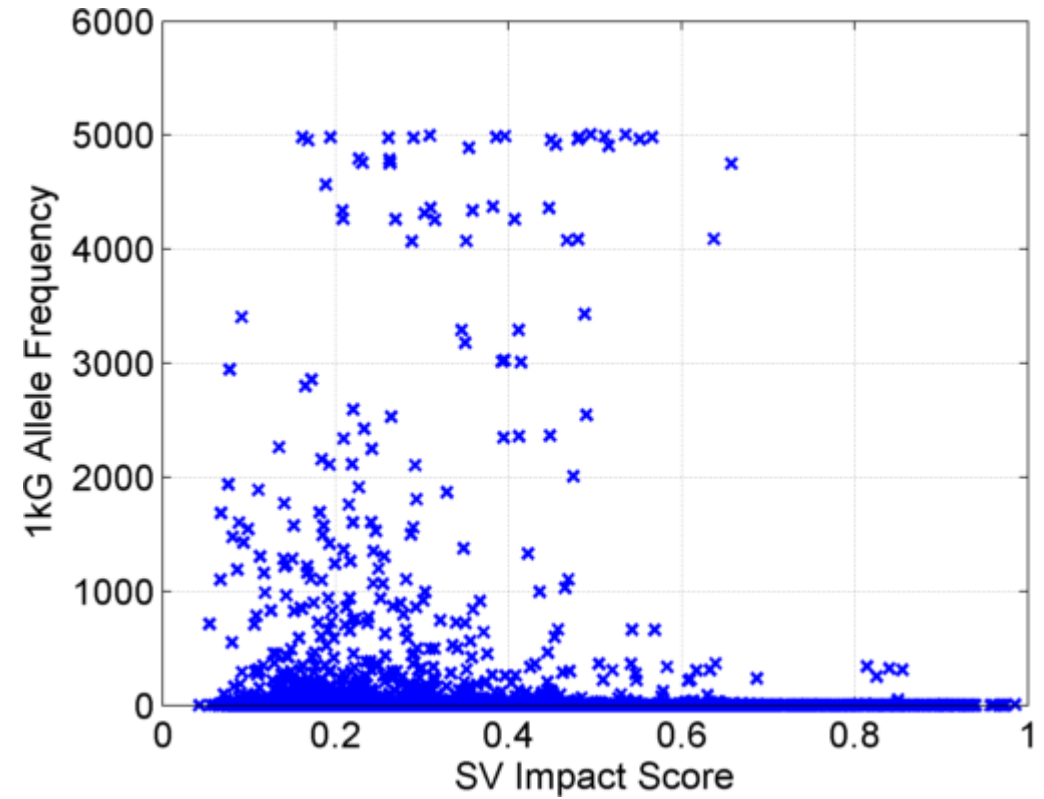
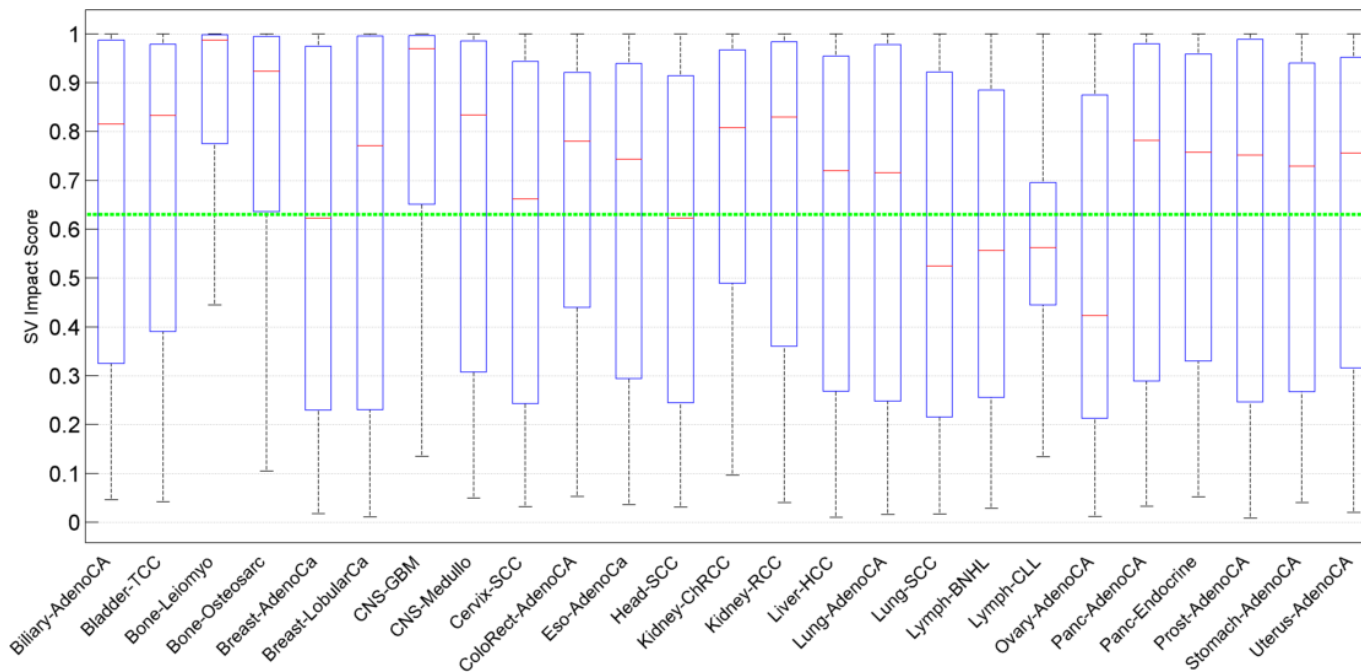


Fig 7. Distribution of SVIS among different cancers (Deletions)

All SVs



SVs < 100kb

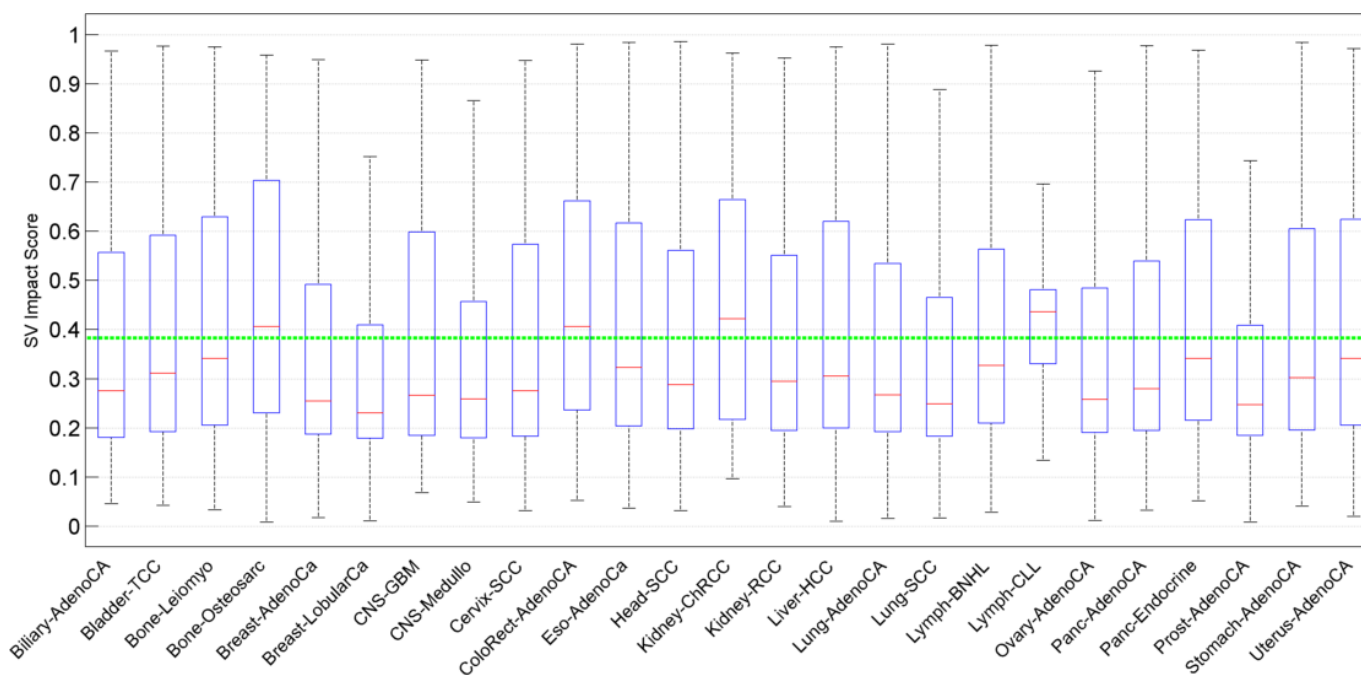
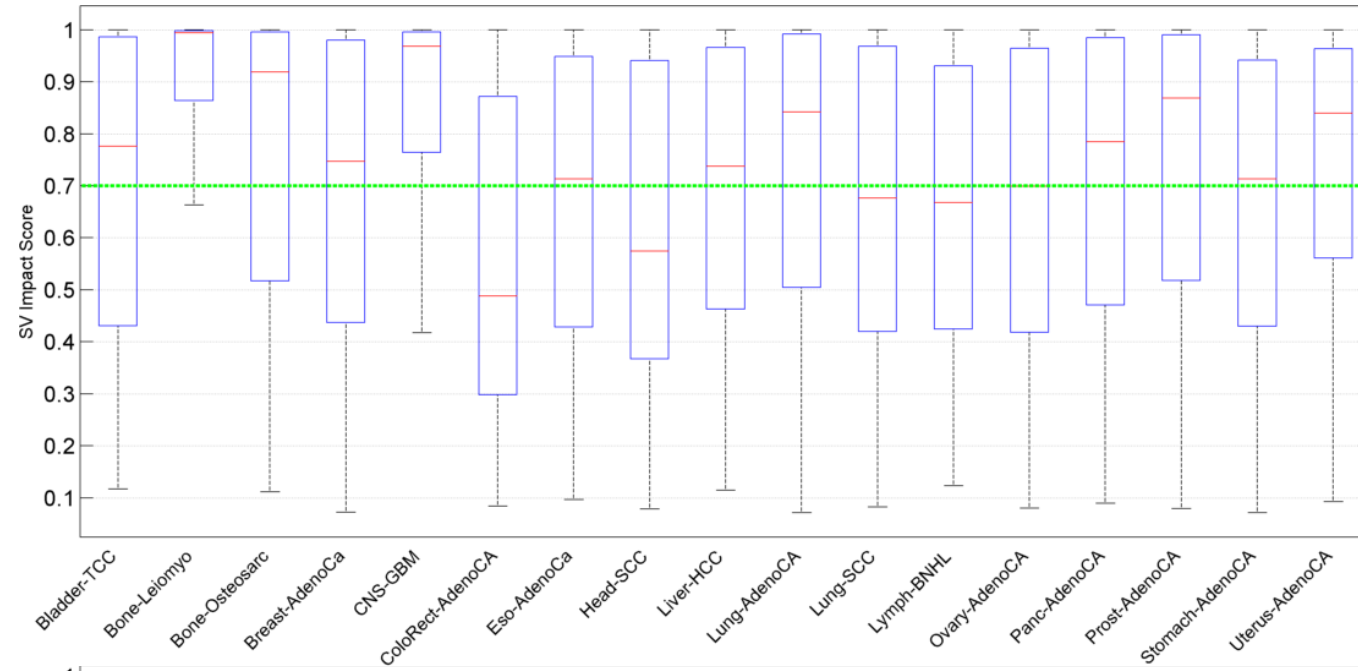


Fig 8. Distribution of SVIS among different cancers (Duplications)

All SVs



SVs<100kb

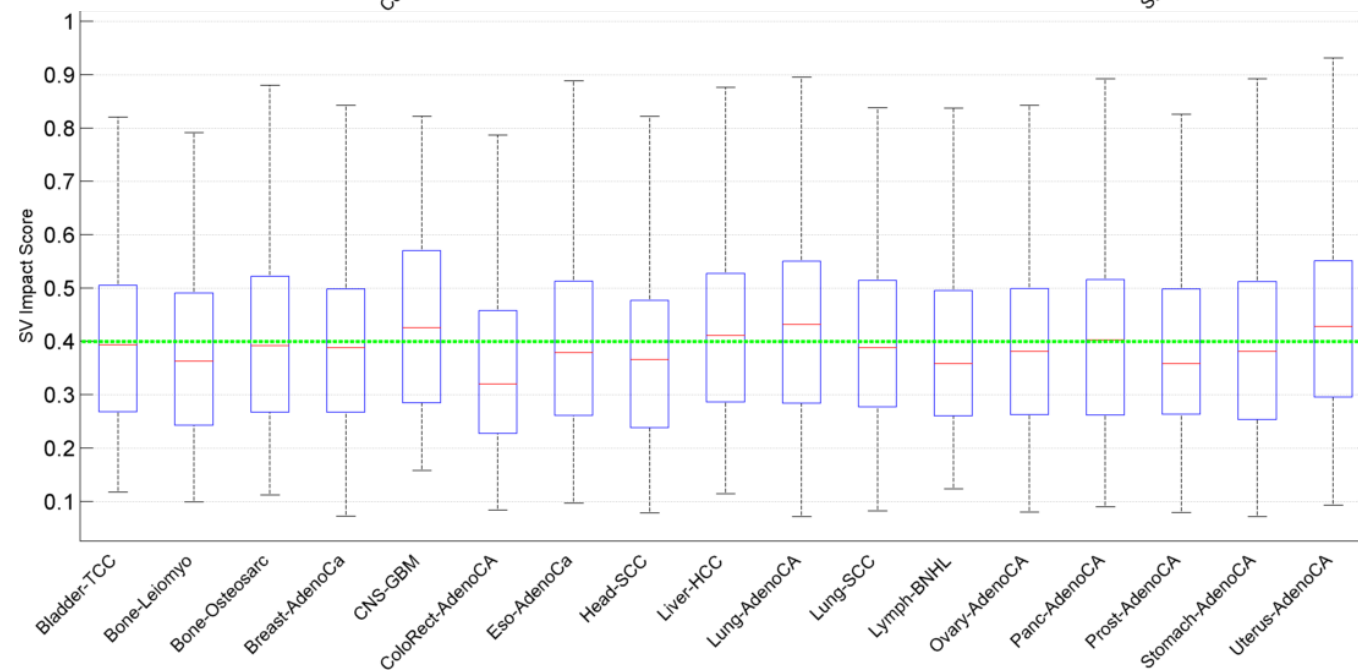
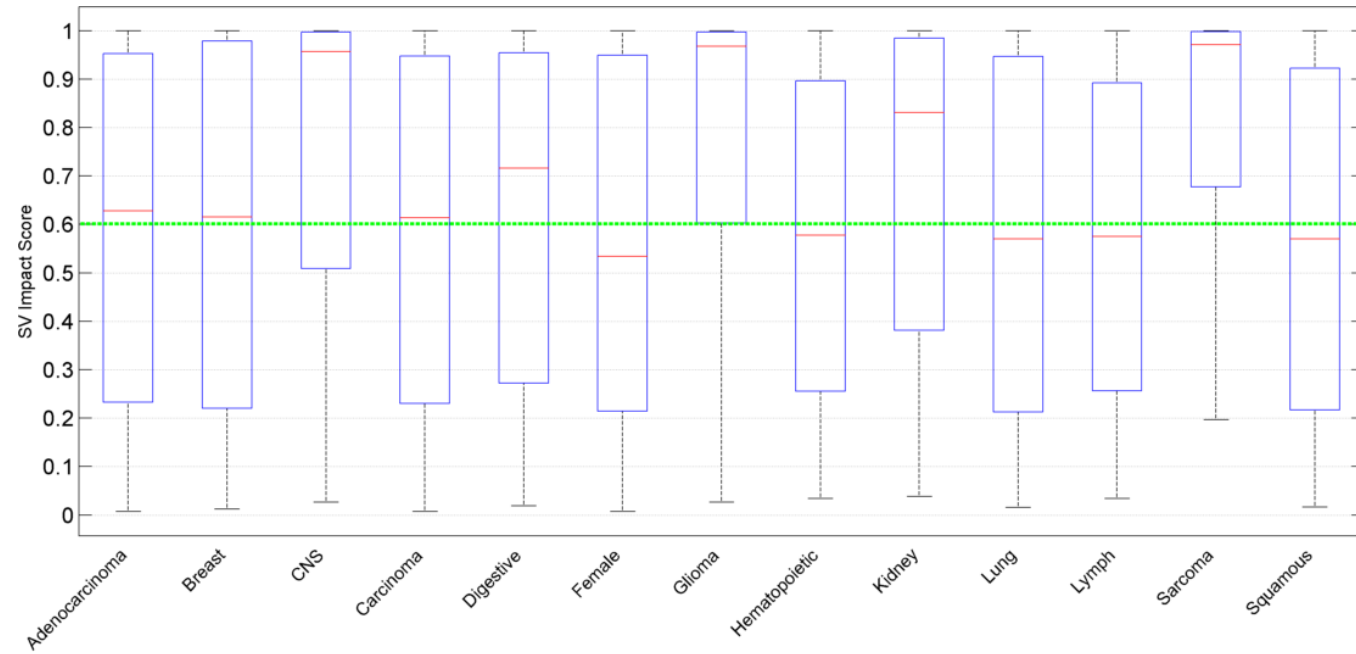


Fig 9. Distribution of SVIS among meta-cohorts cancers (Deletions)

All SVs



SVs < 100kb

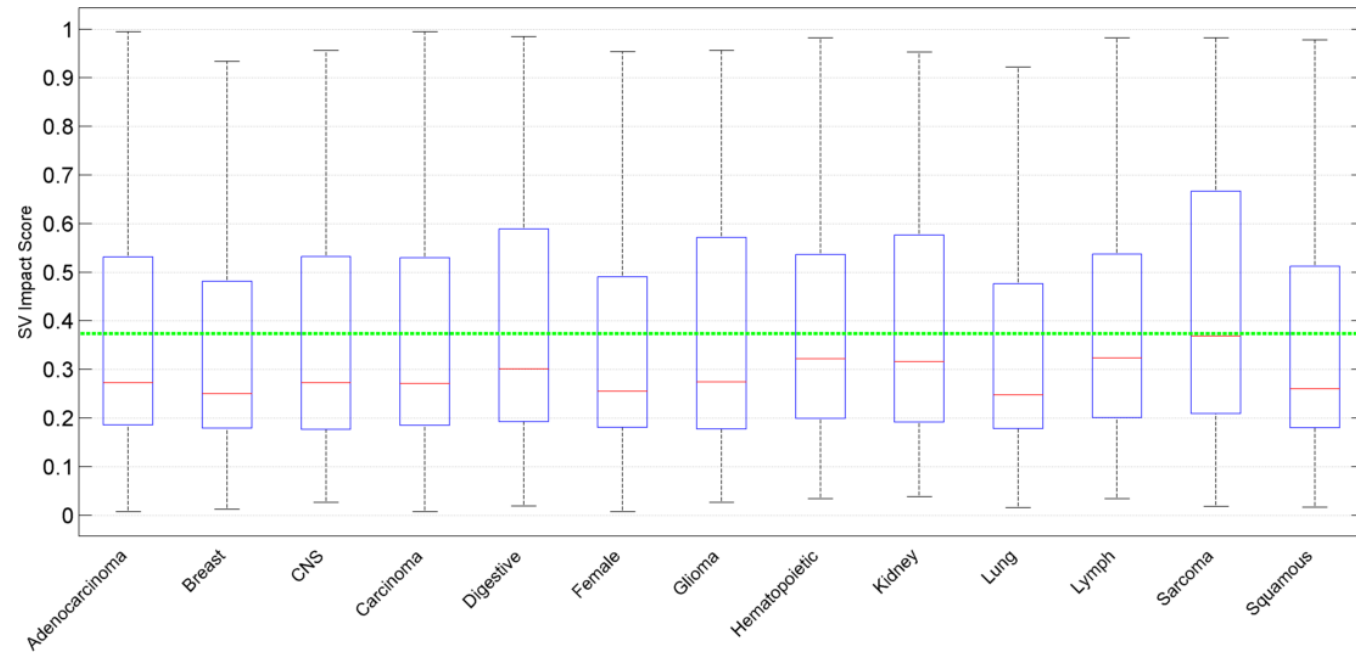
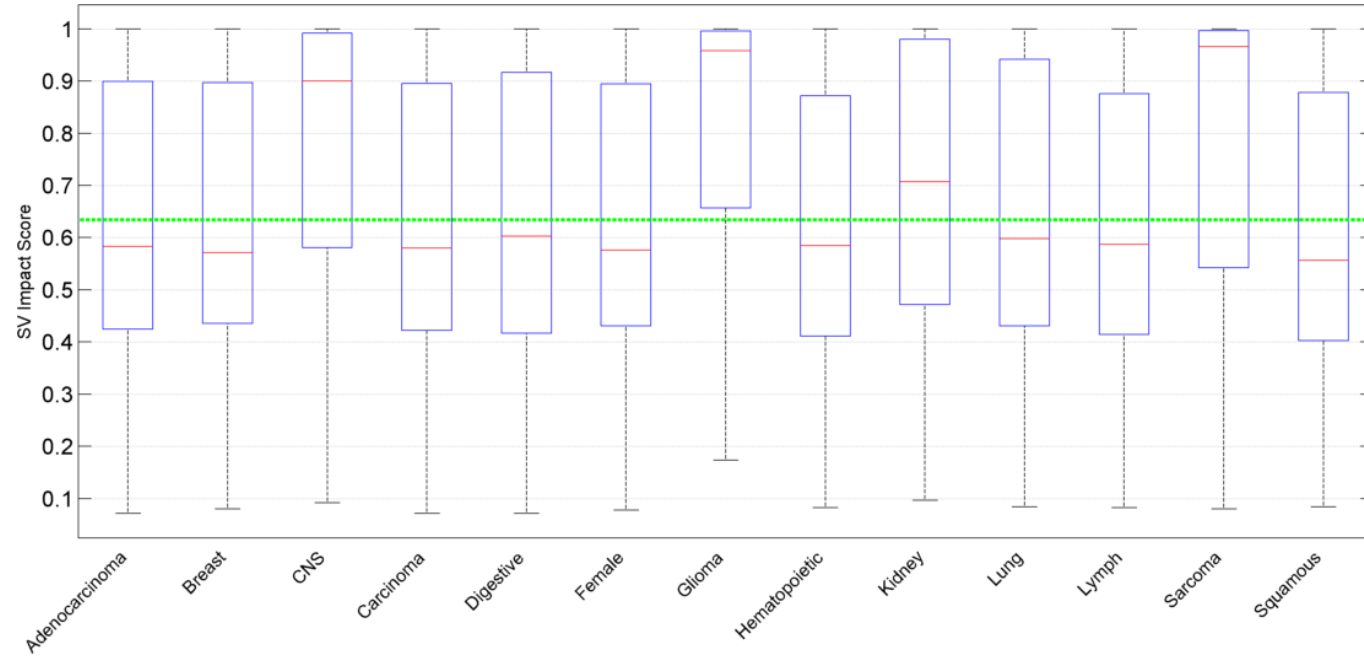


Fig 10. Distribution of SVIS among meta-cohorts cancers (Duplications)

All SVs



SVs < 100kb

