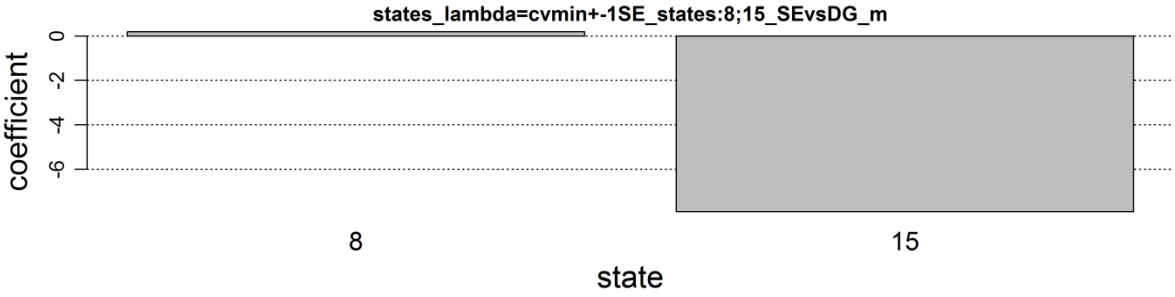
groupwise comparison
merging of gct subtypes - motivation

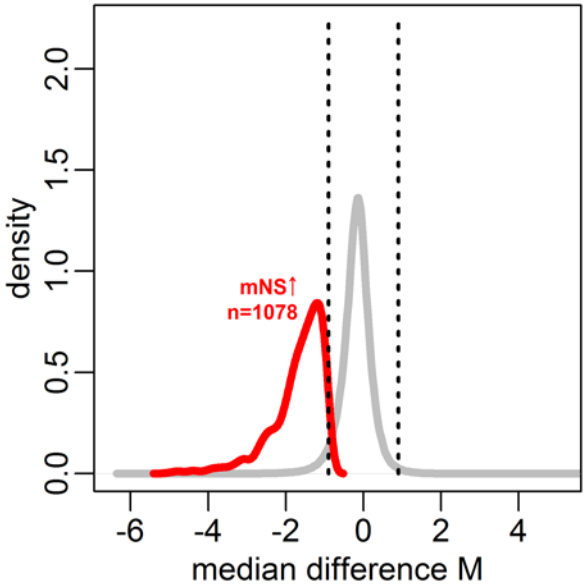
- Within the Type II GCTs, the seminomatous (SE and DG) tumors showed highly comparable profiles and clustered together in the PCA as was the case for the non-seminomatous (EC and mNS) samples (Figure 2A-F, Figure S2A, B). Indeed, upon pairwise comparison SE vs DG showed no statistically significant results other than the obvious case of the X chromosome in the LASSO analysis on the HMM states (Figure S4A). In EC vs mNS the mNS samples showed a small number of DMPs hypermethylated in mNS (n=1078). This small difference is expected as EC is the progenitor of mNS and mNS generally still contain an EC fraction. To focus on the main differences between the GCT subtypes, subsequent analyses were therefore performed on the combined seminomatous (SE/DG) and non-seminomatous (EC/mNS) tumor samples. Despite the similarity between DC and TE (Figure 2A-F, Figure S2A,B, Figure S4A), these classes were not merged because they are clinically and biologically separate entities (Figure 1A). The small DC class and individual cell lines could not be included in the group wise comparisons but will be included in some of the final visualizations.

SE versus DG

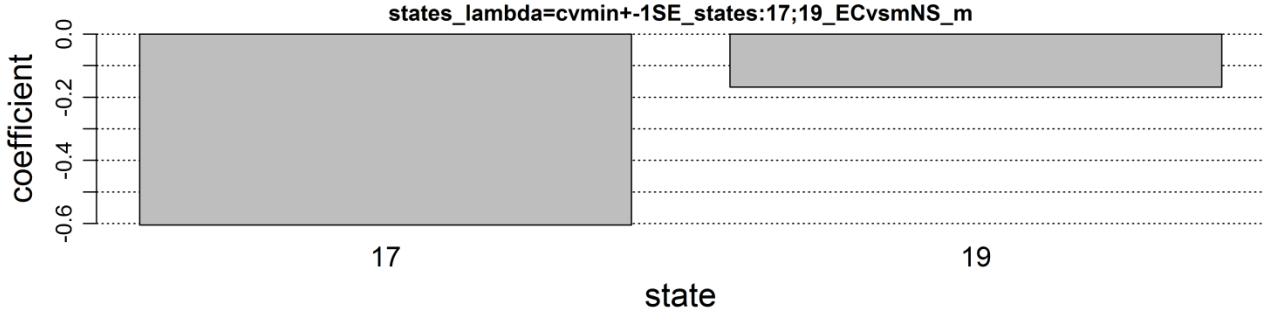
- 0 discriminating probes
- 0 discriminating segments
- state 15 was discriminating between SE and DG but contains almost exclusively probes on the X chromosome. Hence this difference indicates the male/female origin of SE/DG rather than tumor specific differences.



EC versus mNS



- n probes [**EC**-MNS] = 211
- n probes [EC-**mNS**] = 5488
- n segments [**EC**-MNS] = 53
- n segments [EC-**mNS**] = 1256
- discriminating states:



- n DMP[**EC**-MNS] = 0
- n DMP[EC-**mNS**] = 1078

DC vs type I TE

- 0 discriminating probes
- 0 discriminating segments
- no discriminating states