




## Study design

batch_1	batch_2	batch_3	batch_4	batch_5
mTCC	Normal	Normal	Biopsy	sTCC+CIS
	sTCC-CIS			sTCC-CIS
	mTCC			Biopsy

 = Cancer
  = Biopsy
  = Normal

Reference: Dyrskjot, Lars et al. *Gene expression in the urinary bladder: a common carcinoma in situ gene expression signature exists disregarding histopathological classification*

Analysis of sequencing study design for this data suggests that it is not perfectly planned. For example the only samples that were processed in the first batch come from specimens with muscle invasive carcinomas when it would have been better to include some non cancerous samples as well. What is also concerning is the fact that all 12 samples from superficial transitional cell carcinoma with surrounding CIS(sTCC+CIS) were processed together in 5th batch. All in all such a study design makes it impossible to differentiate biological differences from technical bias due to the fact that the samples were sequenced in different batches