

Molecular Subtypes as a Basis for Stratified Use of Neoadjuvant Chemotherapy for Muscle-Invasive Bladder Cancer—A Narrative Review

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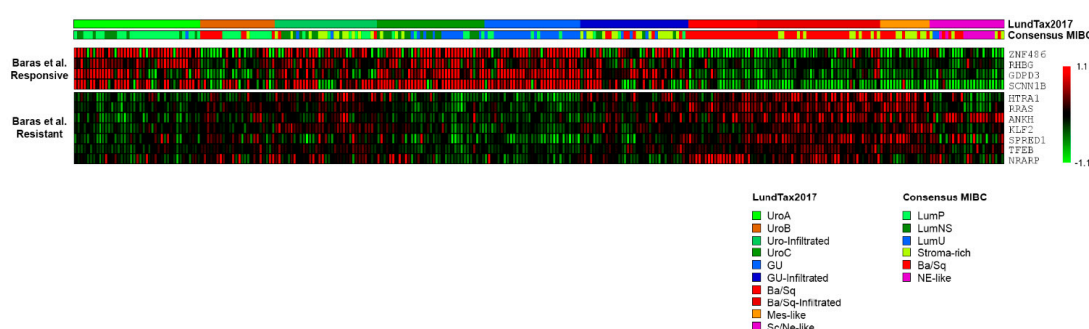


Figure S1. Genes associated with NAC response/resistance in Baras et al. [48] are expressed in luminal and Basal/squamous MIBC subtypes, respectively. The 21 genes shown in Figure1 of Baras et al. [38] identified as associated with NAC response were investigated in the Lund2017 consecutive RC cohort gene expression data set ($n = 307$). All mapped genes in the responsive cluster were highly expressed in luminal-like subtypes, whereas all mapped genes in the Baras et al. Resistant cluster were highly expressed in the Ba/Sq subtype.

Table S1. Fraction of chemotherapy response in Taber et al. [20] ($n = 121$), stratified by consensus subtypes, treatment setting, and DDR-mutations. Number of cases with a potentially predictive mutation (ERCC2, BRCA2, or any DDR-mutation) or wild-type for all three mutation types, is shown separately for responders treated with NAC (left) or first-line only (right). Based on manual review of source data from Taber et al [20]. The last columns show the fraction of responders with presence of at least one of the three potentially predictive mutation types.

Chemotherapy response by consensus subtype, treatment setting, and DDR-mutation status in Taber et al. 2020											
Consensus Subtype	NAC-Response	ERCC2	BRCA2	DDR	3xWT	1L only-Response	ERCC2	BRCA2	DDR	3xWT	% of responses explained by DDR-status
LumP	9/15 (60%)	1	2	1	7	21/29 (72%)	3	3	8	12	37% (NAC: 22%, 1L only: 43%)
LumU	8/10 (80%)	2	2	2	5	10/15 (66%)	1	2	5	4	50% (NAC: 37%, 1L only: 60%)
Stroma-rich	6/7 (86%)	2	2	5	1	7/11 (64%)	0	1	0	6	46% (NAC: 83%, 1L only: 14%)
BASQ	6/12 (50%)	3	2	3	2	9/20 (45%)	1	1	3	5	53% (NAC: 67%, 1L only: 44%)
NE-like	-	-	-	-	-	1/1 (100%)	0	0	0	1	0% (1L only: 0%)