

Supplementary Materials to Robust biomarker screening from gene expression data by stable machine learning-recursive feature elimination methods (Table 5)

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1. Existing literature checking

Table 1: The literature supports for the 15 screened biomarker genes of HGSOC.

Gene symbol	ENTREZID	Gene name	Literature verification
TSPAN8	7103	Tetraspanin 8	TSPAN8 is identified as the hub factor associated with the progression of HGSOC by a series of bioinformatics analyses [1].
CRABP2	1382	Cellular retinoic acid binding protein 2	CRABP2 is a novel biomarker and potential therapeutic target for HGSOC [2].
WDR17	116966	WD repeat domain 17	Missense and synonymous mutations in WDR17 have been occasionally reported in ovary carcinoma [3].
ALDH1A1	216	Aldehyde dehydrogenase 1 family member A1	ALDH1A1 is a possible stemness marker in HGSOC [4].
ALDH1A2	8854	Aldehyde dehydrogenase 1 family member A2	Stem cells express proteins including ALDH1A2 have been observed in the ovarian surface epithelium [5].
CENPF	1063	Centromere protein F	CENPF expression has been associated with cell cycle progression, and malignancy through FOXM1 [6].
KRT7	3855	Keratin 7	KRT7 is one of the known epithelial HGSOC markers [7].
LAMA2	3908	Laminin subunit alpha 2	The interactions with the highest increase in stress-high tumors were related to epithelial-mesenchymal transition (EMT)-high subtype of HGSOC with poor prognosis. It has been observed significantly higher scores for interactions related to laminins LAMA2 that bind to integrin receptors. [8].
HBB	3043	Hemoglobin subunit beta	—
RUNX1T1	862	RUNX1 Partner transcriptional co-repressor 1	—
SESN1	27244	Sestrin 1	—
VGLL1	51442	Vestigial like family member 1	—
VWA3B	200403	Von Willebrand factor A domain containing 3B	—
LOC101928635	—	—	—

—: No literature support so far.

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