

Supplementary Table S6. Longitudinal statistical analyses performed on LCN2 and SLC22A17 protein abundance in the LTL331 patient-derived xenograft from Zhang et. al. Model profiled at baseline (0 weeks), during residual disease (8–12 weeks post-castration), and at tumor relapse (32 weeks). **A)** Group-level descriptive statistics including sample size (n), mean, and standard deviation (SD) for each time point. **B)** One-way ANOVA results assessing overall differences across time points. **C)** Tukey’s post-hoc multiple comparison tests with adjusted p-values and 95% confidence intervals. **D)** Linear regression analysis modeling time as a continuous variable (coded as 0, 10, and 32 weeks), including regression coefficient (β), standard error (SE), p-value, and coefficient of determination (R^2).

LCN2					SLC22A17				
A									
Time	n	mean	sd		Time	n	mean	sd	
0 W	3	-0.798	0.302		0 W	3	1.386	0.252	
8-12W	4	0.512	0.329		8-12W	4	0.104	0.283	
32 W	3	-0.024	0.490		32 W	3	-0.555	0.143	
B									
ANOVA_Df	ANOVA_F	ANOVA_p			ANOVA_Df	ANOVA_F	ANOVA_p		
2	10.437	0.008			2	50.503	6.93E-05		
C									
Comparison	Diff	Lower_CI	Upper_CI	Adj_p	Comparison	Diff	Lower_CI	Upper_CI	Adj_p
0 W	1.31	0.465	2.155	0.006	0 W	-1.282	-1.825	-0.739	0.001
8-12W	0.773	-0.130	1.676	0.089	8-12W	-1.941	-2.521	-1.361	6.03E-05
32 W	-0.537	-1.381	0.308	0.216	32 W	-0.659	-1.202	-0.116	0.022
D									
Beta_time	SE_time	t_value	p_value	R_squared	Beta_time	SE_time	t_value	p_value	R_squared
0.014	0.017	0.884	0.402	0.089	-0.055	0.011	-5.182	0.001	0.770