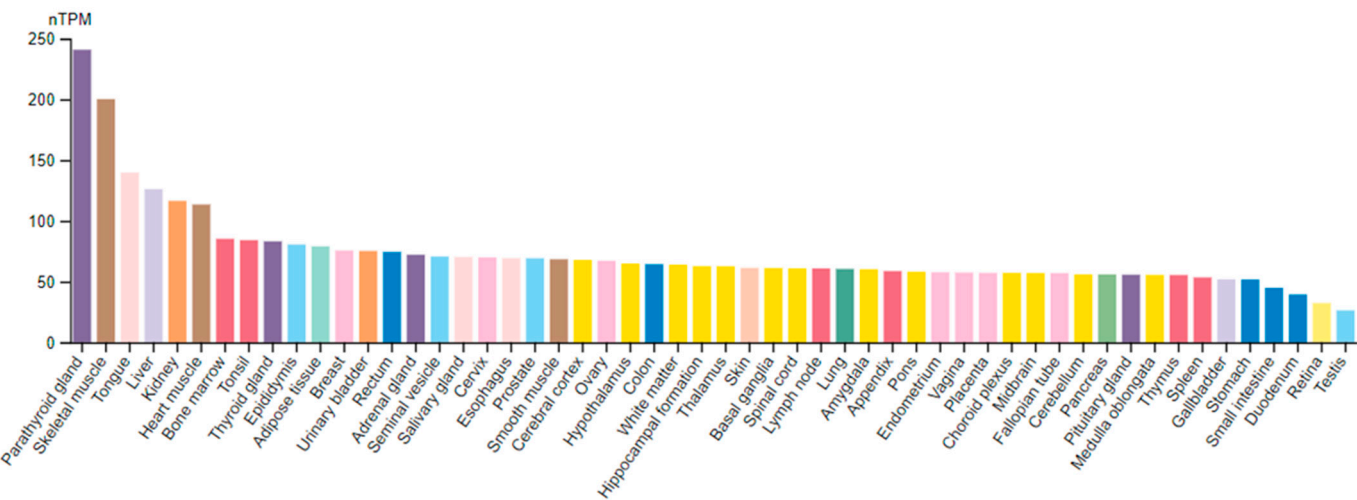


## Supplementary Data

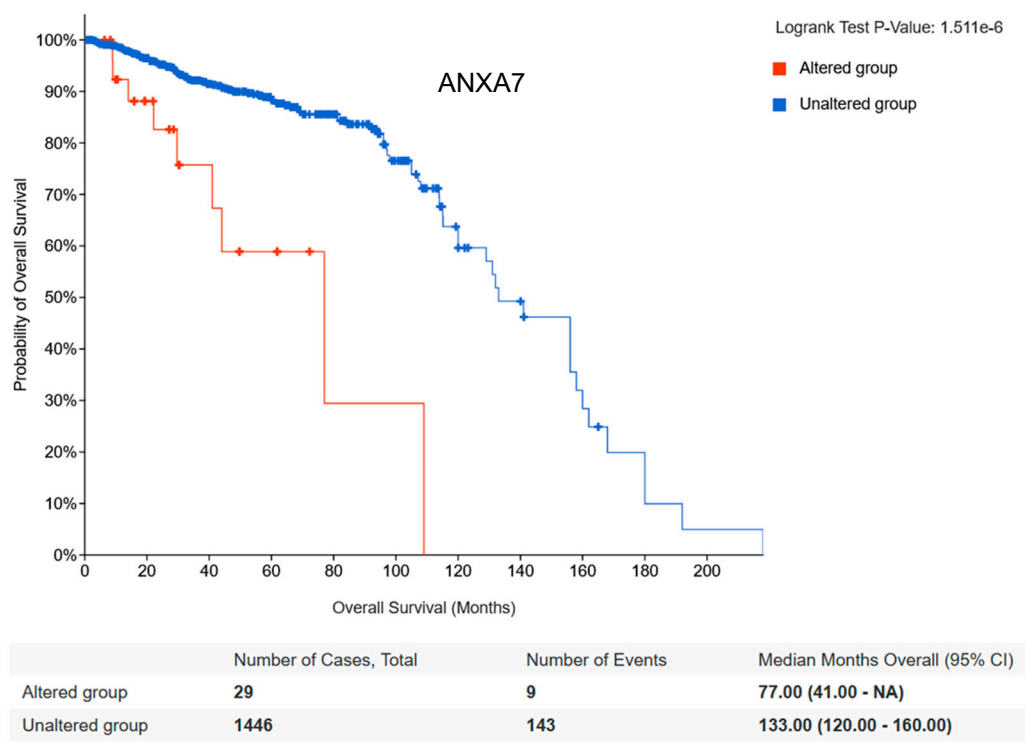
**Table S1:** *ANXA7 cellular clustering with neighboring genes:* The RNA data was used to cluster genes according to their expression across samples. The resulting clusters have been manually annotated to describe common features in terms of function and specificity. The annotation of the cluster is displayed together with a confidence score of the gene's assignment to the cluster. The confidence is calculated as the fraction of times the gene was assigned to this cluster in repeated calculations and is reported between 0 to 1, where 1 is the highest possible confidence. Table shows the 15 most similar genes in terms of expression profile. Data analyzed from the publicly available data from Human Protein Atlas and Genotype-Tissue Expression (GTEx) project.

| Neighbour | Description  | Correlation | Cluster |
|-----------|--|-------------|---------|
| MRPL39    | Mitochondrial ribosomal protein L39                            | 0.8982      | 8       |
| RABL3     | RAB, member of RAS oncogene family like 3                      | 0.8982      | 8       |
| DENR      | Density regulated re-initiation and release factor             | 0.8842      | 8       |
| RRM2B     | Ribonucleotide reductase regulatory TP53 inducible subunit M2B | 0.8737      | 8       |
| HNRNPH2   | Heterogeneous nuclear ribonucleoprotein H2                     | 0.8702      | 48      |
| TSNAX     | Translin associated factor X                                   | 0.8667      | 8       |
| IARS2     | Isoleucyl-tRNA synthetase 2, mitochondrial                     | 0.8596      | 8       |
| APOOL     | Apolipoprotein O like  | 0.8579      | 8       |
| ATPAF2    | ATP synthase mitochondrial F1 complex assembly factor 2        | 0.8544      | 8       |
| RNF14     | Ring finger protein 14   | 0.8491      | 8       |
| CISD1     | CDGSH iron sulfur domain 1                                     | 0.8474      | 8       |
| PRDX3     | Peroxiredoxin 3  | 0.8456      | 8       |
| OPA3      | Outer mitochondrial membrane lipid metabolism regulator OPA3   | 0.8439      | 8       |
| TRAPPC13  | Trafficking protein particle complex 13                        | 0.8368      | 8       |
| EI24      | EI24 autophagy associated transmembrane protein                | 0.8368      | 48      |

Supplementary Figures



**Figure S1:** Organ/tissue-based RNA expression of ANXA7. The consensus dataset consists of normalized expression (nTPM) levels for 55 tissue types, created by combining the HPA and GTEx transcriptomics datasets using the internal normalization pipeline. Color-coding is based on tissue groups, each consisting of tissues with functional features in common. Data obtained from The human protein atlas (<https://www.proteinatlas.org>).



**Figure S2:** Prostate cancer survival data in terms of ANXA7 Copy number alteration (CNA) Vs un-altered in tumor samples from patients' samples. The data was generated from a combined Study (n=10999; samples) Querying 10999 samples / 10580 patients in 26 studies using cBioportal platform. Gene name: ANXA7.