

Figure 1. Comparison of LNCaP-C and LNCaP-T SAGE tag libraries. SAGE tags corresponding to 15,593 and 15,920 transcripts in C and T libraries respectively were analyzed. 136 transcripts (red diamond) were upregulated and 215 transcripts (blue diamond) were down regulated ($p < 0.05$). The X-axis shows the frequency of occurrence each unique transcript in LNCaP-C. The Y-axis shows the frequency of occurrence each unique transcript in LNCaP-T.

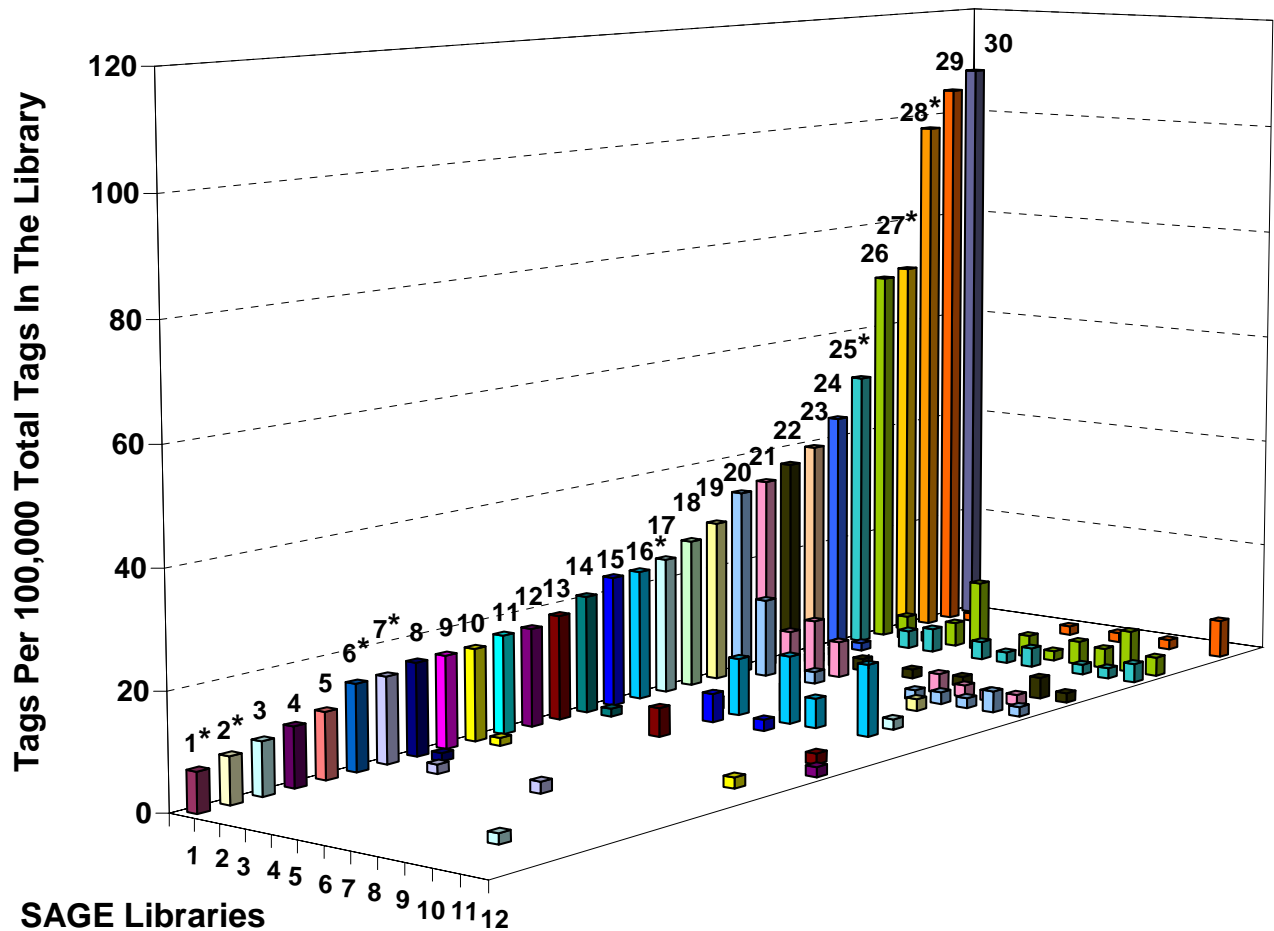


Figure 2. Identification of Prostate Specific Transcripts by Comparison of SAGE libraries. Inter-library comparisons were performed between our combined LNCaP-C and -T SAGE libraries (CPDR LNCaP SAGE library) and 35 SAGE tag libraries from NIH-SAGE website. Shown here are comparison between 12 SAGE libraries that had high total tag numbers. Thirty representative genes shown here are based on the fold difference (≥ 8 fold) in the frequency of occurrence of specific tag between CPDR-LNCaP-SAGE library and other SAGE libraries. The X-axis shows the 12 libraries, which are 1. CPDR-LNCaP-SAGE; 2. SAGE Duke GBM H111; 3. SAGE Normal pool (6th); 4. SAGE Mammary Epithelium; 5. SAGE DCIS; 6. SAGE HCT116; 7. SAGE NC1; 8. SAGE Tu102; 9. SAGE HOSE4; 10. SAGE OVT7; 11. SAGE Duke HMVEC; 12. SAGE Duke HMVEC VEGF. These libraries were derived from prostate (1), brain (2, 3), breast (4, 5), colon (6, 7, 8), ovary (9, 10) and vascular (11, 12) tissues or cells. The Y-axis shows tag frequency of specific tags / 100,000 total tags. The genes in column 1 to 30 are 1. *NKX3.1* (U80669), 2. *TMPRSS2* (U75329), 3. Arginase II (U75667), 4. *CALLA/NEP* (M26624), 5. EST (N46609), 6. *PAP* (M34840), 7. *HOXB13* (U81599), 8. EST (AA974479), 9. EST (AA890637), 10. *KIAA0787* (AB018330), 11. prepro-relaxin H2 (X00948), 12. *GATA2* (M68891), 13. *BTF2p44* (U21910), 14. Enkephalinase (X07166), 15. *HNF-3 alpha* (U39840), 16. *PDEF* (AF071538), 17. *MAGE6* (U10691), 18. EST (AA640928), 19. EST (AF078749), 20. *rab3-GAP regulatory domain* (AF004828), 21. *PMEPA1* (AF224278), 22. *AMD1* (NM_001634), 23. EST (AA151796), 24. *NCAM2* (NM_004540), 25. *STEAP1* (AF186249), 26. gene from PAC 295C6 (AL035304), 27. *PSMA* (M99487), 28. *PSA* (X05332), 29. *SPON2* (AB027466), and 30. *DDC* (M88700). The character in the brackets following each gene symbol is the accession number for the gene. "*" indicates the genes are publicly known as prostate specific and/or abundant.

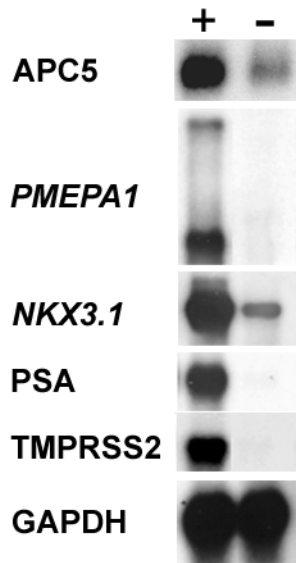


Figure 3. Northern blot hybridization of representative ARGs. Northern blot analysis were performed on five representative ARGs show concordance with the differential expression noted in LNCaP-C and LNCaP-T SAGE libraries. Northern blots were prepared as described in “Materials and Methods”. “+”, LNCaP cells stimulated with R1881 at 10^{-8} M for 24 hours and “-” indicates control LNCaP cells processed in parallel without R1881 treatment.

Table 1. Functional Categories of ARGs

Tag	T/C	Acces #	Name, Description
Transcription Regulators			
GCCAGCCCAG	11/1	H41030	KAP1/TIF1beta, KRAB-associated protein 1
GTGCAGGGAG	18/2	AF071538	PDEF, ets transcription factor
GACAAACATT	8/1	NM_003201	mtTF1, mitochondrial transcription factor 1
ATGACTCAAG	8/1	X12794	ear-2, v-erbA related
GAAAAGAAGG	8/1	U80669	Nkx3.1, homeobox
CCTGTACCCC	5/1	AF072836	Sox-like transcriptional factor
CCTGAACTGG	1/8	NM_001273	CHD4/Mi2-beta, histone acetylase/deacetylase, chromodomain helicase
TGACAGCCCA	1/7	U81599	Hox B13, homeobox
RNA Processing and Translational Regulators			
TACAAAACCA	12/1	NM_005381	NCL, Nucleolin
AATTTCTCCTA	8/1	U41387	GURDB, nucleolar RNA helicase
TGCATATCAT	8/1	D89729	XPO1, exportin 1
CTTGACACAC	14/2	AL080102	EIF5, translation initiation factor 5
TGTCTAACTA	5/1	AF078865	CGI-79, RNA-binding protein
GTGGACCCCA	10/2	AF190744	SiahBP1/PUF60, poly-U binding splicing factor
ATAAAGTAAC	1/11	NM_007178	UNRIP, unr-interacting protein.
TACATTTTCA	1/7	X85373	SNRPG, small nuclear RNP polypeptide G
TCAGAACAGT	1/7	NM_002092	GRSF-1, G-rich RNA binding factor 1
CAACTTCAAC	0/5	NM_006451	PAIP1, poly A BP-interacting protein 1
GATAGGTCGG	0/5	Z11559	IREBP1, Iron-responsive element BP 1
CTAAAAGGAG	2/10	M15919	SNRPE, small nuclear RNP polypeptide E
Genomic Maintenance and Cell Cycle Regulation			
GTGGTGCGTG	10/1	AF035587	XRCC2, X-ray repair protein 2
TCCCCGTGGC	7/1	D13643	KIAA0018, Dimunuto-like
ATTGATCTTG	6/1	NM_002947	RPA3, Replication protein A 14kDa subunit
AGTGTGTTTC	16/3	NM_004879	PIG8, p53 induced protein
CCTCCCCCGT	10/2	AF044773	BAF, barrier-to-autointegration factor
ATGTACTCTG	1/7	NM_000884	IMPDH2, IMP dehydrogenase 2
GATGAAATAC	0/5	NM_006325	ARA24, androgen receptor assoc protein 24
GTGCATCCCG	0/5	X16312	Phosvitin/casein kinase II beta subunit
Protein Trafficking and Chaperoning			
GAAATTAGGG	12/1	AB020637	KIAA0830, similar to golgi antigen
TTTCTAGGGG	10/1	AF15189	CGI-140, lysosomal alpha B mannosidase
CCCAGGGAGA	7/1	AF026291	CCT, chaperonin t-complex polypeptide 1
GTGGCGCACA	13/2	S79862	26 S protease subunit 5b
TTGCTTTTGT	15/3	NM_001660	ARF4, ADP-ribosylation factor 4
ATGTCCTTTC	10/2	NM_005570	LMAN1, mannose BP involved in EPR/Golgi traffic
Energy Metabolism, Apoptosis and Redox Regulators			
TGTTTATCCT	13/2	M14200	DBI, diazepam binding inhibitor
GCTTTGTATC	6/1	D16373	dihydrolipoamide succinyltransferase
GTTCAGTGA	6/1	AA653318	FKBP5, FK506-binding protein 5
TAGCAGAGGC	6/1	AA425929	NDUFB10, NADH dehydrogenase 1 beta subcomplex 10
ACAAATTATG	5/1	NM_003375	VDAC, voltage-dependent anion channel
CAGTTTGTAC	5/1	NM_000284	PDHA1, Pyruvate dehydrogenase E1-alpha subunit
GATTACTTGC	5/1	NM_004813	PEX16, peroxisomal membrane biogenesis factor
GGCCAGCCCT	5/1	X15573	PFKL, 1-phosphofructokinase
CAATTGTAAA	1/10	NM_004786	TXNL, thioredoxin-like protein
AAAGCCAAGA	2/15	NM_001985	ETFB, electron transfer flavoprotein beta subunit
CAACTAATTC	1/7	NM_001831	CLU, Clustrin
AAGAGCTAAT	0/5	NM_004446	EPRS, glutamyl-prolyl-tRNA synthetase
Signal Transduction			
CTTTTCAAGA	9/1	X59408	CD46, complement system membrane cofactor
GTGTGTAAAA	9/1	NM_005745	BAP31/BAP29 IgD accessory proteins
ACAAAATGTA	8/1	NM_000856	GUCY1A3, Guanylate cyclase 1, alpha 3
AAGGTAGCAG	7/1	NM_006367	CAP, Adenylyl cyclase-associated protein
GGCGGGGCCA	7/1	AB002301	microtubule assoc. serine/threonine kinase
GGCCAGTAAC	6/1	AL096857	similar to BAT2, integrin receptor
AACTTAAGAG	12/2	AB018330	calmodulin-dependent protein kinase beta
AGGGATGGCC	5/1	NM_006858	IL1RL1LG, Putative T1/ST2 receptor
CTTAAGGATT	2/10	AF151813	CGI-55 protein

(Table 1 legend)

The “tag to gene” identification is based on the analysis performed by SAGE software and/or “tag to gene” application of the NIH SAGE Website. T/C represent the number of tags for each transcript in androgen treated (T) and control (C) LNCaP libraries. The differences in expression levels of genes identified by tags shown here were statistically significant ($p < 0.05$) as determined by the SAGE software.