	TCGA Tumor	
Gene	Type(s)	Gene Details
AP2B1	ESCA	Involved in FGFR signaling. Knockdown promotes the formation of matrix degrading invadopodia, adhesion structures linked to invasive migration in cancer cells (Pignatelli 2012).
CAND1	BLCA*	Component of many protein complexes involved in proteasome-dependent protein degration via ubiquitination and neddylation. CAND1 binding to the complexes inactivates ubiquitin ligase activity and may block adaptor and NEDD8 conjugation sites. (Bosu 2008). May play a role in PLK4-mediated centriole overduplication and Disrupted in prostate cancer (Korzeniewski 2012).
CHEK2	ESCA, LGG, BLCA, HNSC, PRAD,	Checkpoint kinase involved in DNA damage response signaling. Significantly mutated gene and candidate <b>OG</b> in papillary thyroid carcinoma (PTC) cohort of 296 patients (TCGA 2014 #85). <b>Breast cancer susceptibility gene</b> (inherited germline variants) (Vogelstein 2013)
CUL1	BLCA	Candidate <b>TSG</b> . SCF complex E3 ubiquitin ligase scaffold protein. Suppressor of centriole multiplication through regulation of PLK4 level (Korzeniewski 2009)
ERCC2	BLCA, LGG*	DNA-repair (Nucleotide excision repair) protein. Significantly mutated in cisplatin-responders vs. non-responders in cohort of 50 patients with muscle-invasive urothelial carcinoma (MIUC). ERCC2 mutation status may inform cisplatin-containing regimen usage in MIUC (Van Allen 2014). Recurrently mutated in cohort of 17 patients with urothelial bladder cancer (UBC) (Balbas-Martinez 2013). Xeroderma pigmentosum susceptibility gene (inherited germline variants) (Vogelstein 2013)
FSIP2	ESCA*	Candidate <b>OG</b> . Recurrently amplified in testicular germ cell tumors (TGCTs)(Litchfield 2015).
GNA13	BLCA	Significantly mutated in cohort of 55 patients with diffuse large B-cell lymphoma (DLBCL) (Lohr 2012)
GTF2I	UCEC	Highly recurrent missense mutation in Thymic epithelial tumors and associated with increased patient survival (Petrini 2014).
HDAC4	ESCA	Histone de-aceytlation enzyme. <b>Drug target</b> . Overexpression shown to promote growth of colon cancer cells via p21 repression. Regulator of colon cell profliferation. (Wilson 2008). May regulate cancer cell response to hypoxia via its regulates HIF1a acetylation and stability (Geng 2011)
HLA-A	BLCA, HNSC, LGG, PRAD	Immune system. Encodes MHC-Class 1A protein, which presents antigens for T cell recognition. Somatic mutations previously suggested to contribute to tumor immune escape (Shukla 2015).
KEAP1	LUAD*	Candidate <b>TSG</b> . Inhibits NRF2 (aka NFE2L2). In cohort of 76 non-small cell lung cancer (NSCLC) patients, KEAP1 found mutated in 2 patients with advanced adenocarcinoma and smoking history. KEAP1 mutation was mutually exclusive of EGFR, Kas, ERBB2 and NFE2L2 mutation in the cohort and KEAP1 mutation status proposed as marker for personalized therapy selection. (Sasaki 2013) Proposed TSG in lung squamous cell carcinomas (Hast 2014) Proposed as therapeutic target for thyroid-transcription-factor-1 (TTF1)-negative lung adenocarcinoma (LUAD) (Cardnell 2015).
KLF5	BLCA*	Transcription factor that promotes breast cancer cell proliferation, survival, migration and tumour growth. Upregulates TNFAIP2, which interacts with the two small GTPases Rac1 and Cdc42, thereby increasing their activities to change actin cytoskeleton and cell morphology (Jia 2015). Proposed as playing dual role as both <b>TSG</b> when acetylated and <b>OG</b> when de-acetylated in prostate cancer (Atala 2015). Recurrently mutated in mucinous ovarian carcinoma (Ryland 2015)
MAPK1	CESC*, HNSC	Kinase involved in cell proliferation, differentiation, transcription regulation, and development; key signaling component of the toll-like receptor pathway. Candidate <b>OG</b> in pancreatic cancer (Furukawa 2006), laryngeal squamous cell carcinoma cell lines (Kostrzewska-Poczekaj 2010). Significantly mutated in cohort of 91 chronic lymphocytic leukemia CLL patients.(Wang 2011).
MSN	ESCA*	Protein homolog of TSG NF2 (Merlin) (Golovnina 2005). Member of the Ezrin-Radixin-Moesin (ERM) protein family. Links membrane and cytoskeleton involved in contact-dependent regulation of EGFR (Chiasson-MacKenzie 2015). Regulates the motility of oral cancer cells via MT1-MMP and E-cadherin/p120-catenin adhesion complex. Cytoplasmic expression of MSN correlates with nodal metastasis and poor prognosis of oral squamous cell carcinomas (OSCCs), may be potential candidate for targeted gene therapy for OSCCs (Li 2015).
MTOR	KIRC	Candidate <b>OG</b> . Serine/threonine protein kinase regulates cell growth, proliferatin and survival. Frequently activated in human cancer and a major therapeutic target. Randomly selected mutants in HEAT repeats and kinase domain induced transformation in NIH3T3 cells and rapid tumor growth in nude mice (Mueugan 2013)
NBPF10	BLCA*	Somatic missense mutation reported in prostate cancer cohort of 141 patients (Manson-Bahr 2015). In gene family with numerous tandem repeats and pseudogenes, possible read alignment and mutation calling errors.
PARG	GBM, LGG, BLCA, HNSC, PRAD, LUAD, PCPG, KIRC*	Involved in DNA damage repair (with PARP1). Cells deficient in these proteins are sensitive to lethal effects of ionizing radiation and alkylating agents (17). Potential <b>Drug target</b> for BRCA2-deficient cancers (Fathers 2012).
RANBP2	ESCA	Candidate <b>OG</b> (Gylfe 2013). A large multimodular and pleiotropic protein with SUMO E3 ligase function. (Zhu 2015) Interacts with mTOR (to regulate cell growth and proliferation via cellular anabolic processes) (Kazyken 2014). Hot spot mutation previously found in MSI colorectal cancer (CRC). Hot spot suggested as useful for personalized tumor profling and therapy in CRC. (Gylfe 2013)
RASA1	HNSC*	Identified as <b>TSG</b> in another squamous cell cancer, cutaneous squamous cell skin cancer (cSCC) (Pickering 2014)
RGPD3	BLCA*, UCEC, PAAD	Component of ubiqutin E3 ligase complex. Named for similarity to RANBP2.
SIRPB1	HNSC, PRAD	Ig-like cell-surface receptor. Negatively regulates RTK processes. Related to FGFR signaling.  Actin-dependent regulator of chromatin. Its ATPase domain named as <b>Drug target</b> in SWI/SNF mutant cancers (e.g., lung, synovial sarcoma, leukemia, and rhabdoid tumors) (Vangamudi 2015). Proposed <b>TSG</b> , and synthetic lethal target in SMARCA4 (aka BRG1) -deficient
SMARCA2	BLCA*	cancers.(Hoffman 2014) TSG in HNSC (Bothonberg 2012) MSL CBC (Bigwas 2008), epitholial transformation and invasive squameus cell careinama in the mouse
TGFBR2	HNSC	TSG in HNSC (Rothenberg, 2012) MSI CRC (Biswas 2008), epithelial transformation and invasive squamous cell carcinoma in the mouse forestomach (Yang 2014).