

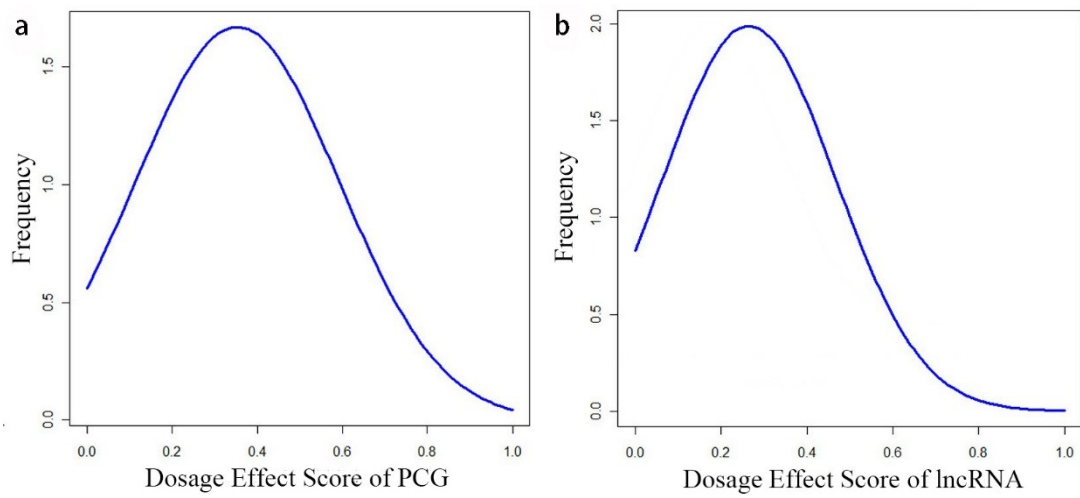
## Comparative analysis revealed dosage sensitivity and regulatory patterns of lncRNA in prostate cancer

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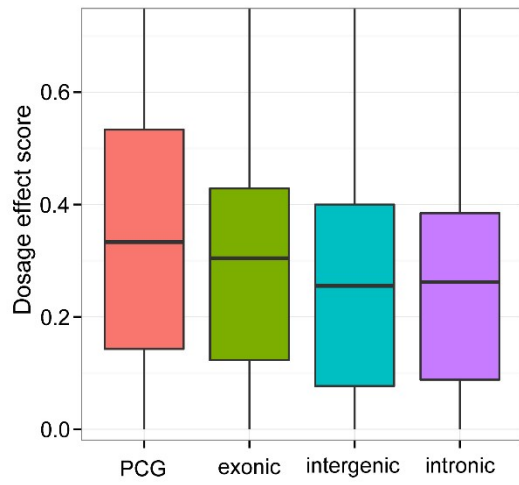
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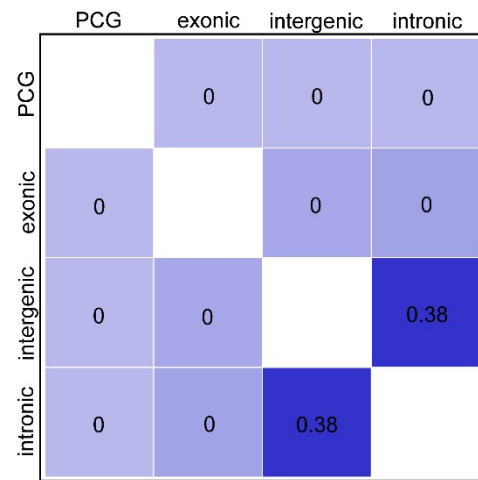
**Supplementary Figure 1 The dosage effect score distributions.**

The two panels are the DES score distributions of PCGs and lncRNAs in prostate cancer. The distribution plot is consistent with Samur et al.'s study.

a



b



**Supplementary Figure 2 The difference of DES between PCGs and lncRNAs at different genomic locations.**

**Supplementary Table S1 GO terms enriched by PCGs with high dosage sensitivity**

Category	Term	Count	P-Value
BP	GO:0030163~protein catabolic process	43	1.52E-03
BP	GO:0009057~macromolecule catabolic process	51	1.75E-03
	GO:0051603~proteolysis involved in cellular protein catabolic		
BP	process	41	2.43E-03
BP	GO:0044257~cellular protein catabolic process	41	2.69E-03
BP	GO:0044265~cellular macromolecule catabolic process	47	3.21E-03
BP	GO:0007156~homophilic cell adhesion	14	3.33E-03
BP	GO:0008286~insulin receptor signaling pathway	7	4.02E-03
	GO:0007167~enzyme linked receptor protein signaling		
BP	pathway	26	4.88E-03
	GO:0019941~modification-dependent protein catabolic		
BP	process	38	5.98E-03
	GO:0043632~modification-dependent macromolecule		
BP	catabolic process	38	5.98E-03
BP	GO:0034329~cell junction assembly	7	6.75E-03
BP	GO:0008104~protein localization	53	7.54E-03
BP	GO:0033554~cellular response to stress	37	8.17E-03
BP	GO:0034330~cell junction organization	8	9.33E-03
BP	GO:0034644~cellular response to UV	3	9.91E-03
BP	GO:0048598~embryonic morphogenesis	23	1.00E-02
BP	GO:0001702~gastrulation with mouth forming second	5	1.03E-02
BP	GO:0007049~cell cycle	47	1.04E-02
BP	GO:0006939~smooth muscle contraction	6	1.13E-02
	GO:0007179~transforming growth factor beta receptor		
BP	signaling pathway	8	1.22E-02
BP	GO:0016265~death	44	1.25E-02
BP	GO:0006511~ubiquitin-dependent protein catabolic process	19	1.32E-02
BP	GO:0034613~cellular protein localization	28	1.42E-02
BP	GO:0010876~lipid localization	14	1.46E-02
BP	GO:0070727~cellular macromolecule localization	28	1.51E-02
BP	GO:0006607~NLS-bearing substrate import into nucleus	4	1.52E-02
BP	GO:0046907~intracellular transport	40	1.76E-02
BP	GO:0008219~cell death	43	1.78E-02
BP	GO:0016044~membrane organization	26	1.78E-02
BP	GO:0006869~lipid transport	13	1.86E-02
BP	GO:0048729~tissue morphogenesis	15	1.90E-02
BP	GO:0060562~epithelial tube morphogenesis	8	2.15E-02
BP	GO:0043966~histone H3 acetylation	5	2.18E-02
BP	GO:0035295~tube development	17	2.26E-02
BP	GO:0021955~central nervous system neuron axonogenesis	4	2.28E-02
BP	GO:0032869~cellular response to insulin stimulus	8	2.31E-02
BP	GO:0021915~neural tube development	8	2.31E-02

BP	GO:0043982~histone H4-K8 acetylation	3	2.34E-02
BP	GO:0043981~histone H4-K5 acetylation	3	2.34E-02
BP	GO:0043984~histone H4-K16 acetylation	3	2.34E-02
BP	GO:0070198~protein localization to telomere	3	2.34E-02
BP	GO:0043983~histone H4-K12 acetylation	3	2.34E-02
BP	GO:0001841~neural tube formation	6	2.48E-02
BP	GO:0021953~central nervous system neuron differentiation	6	2.48E-02
BP	GO:0002009~morphogenesis of an epithelium	10	2.55E-02
BP	GO:0007369~gastrulation	8	2.67E-02
BP	GO:0007178~transmembrane receptor protein serine/threonine kinase signaling pathway	10	2.85E-02
BP	GO:0006644~phospholipid metabolic process	15	2.87E-02
BP	GO:0034502~protein localization to chromosome	3	3.19E-02
BP	GO:0034109~homotypic cell-cell adhesion	3	3.19E-02
BP	GO:0001838~embryonic epithelial tube formation	6	3.27E-02
BP	GO:0016331~morphogenesis of embryonic epithelium	7	3.36E-02
BP	GO:0001843~neural tube closure	5	3.51E-02
BP	GO:0060606~tube closure	5	3.51E-02
BP	GO:0035148~tube lumen formation	6	3.57E-02
BP	GO:0060541~respiratory system development	10	3.70E-02
BP	GO:0043543~protein amino acid acylation	7	3.88E-02
BP	GO:0008637~apoptotic mitochondrial changes	5	3.90E-02
BP	GO:0015031~protein transport	43	4.02E-02
BP	GO:0019637~organophosphate metabolic process	15	4.16E-02
BP	GO:0016337~cell-cell adhesion	19	4.19E-02
BP	GO:0000226~microtubule cytoskeleton organization	12	4.45E-02
BP	GO:0045184~establishment of protein localization	43	4.67E-02
BP	GO:0006468~protein amino acid phosphorylation	38	4.72E-02
BP	GO:0014020~primary neural tube formation	5	4.75E-02
BP	GO:0060284~regulation of cell development	15	4.93E-02
BP	GO:0034976~response to endoplasmic reticulum stress	5	5.22E-02
BP	GO:0046328~regulation of JNK cascade	7	5.39E-02
BP	GO:0030900~forebrain development	12	5.43E-02
BP	GO:0030324~lung development	9	5.54E-02
BP	GO:0016202~regulation of striated muscle tissue development	6	5.70E-02
BP	GO:0045216~cell-cell junction organization	5	5.70E-02
BP	GO:0042060~wound healing	14	5.80E-02
BP	GO:0032868~response to insulin stimulus	9	5.81E-02
BP	GO:0034660~ncRNA metabolic process	16	6.06E-02
BP	GO:0007281~germ cell development	9	6.09E-02
BP	GO:0048634~regulation of muscle development	6	6.11E-02
BP	GO:0030071~regulation of mitotic metaphase/anaphase transition	4	6.22E-02
BP	GO:0016192~vesicle-mediated transport	33	6.23E-02

BP	GO:0051149~positive regulation of muscle cell differentiation	3	6.29E-02
BP	GO:0032925~regulation of activin receptor signaling pathway	3	6.29E-02
BP	GO:0008654~phospholipid biosynthetic process	9	6.38E-02
BP	GO:0030323~respiratory tube development	9	6.38E-02
BP	GO:0006473~protein amino acid acetylation	6	6.54E-02
	GO:0070302~regulation of stress-activated protein kinase signaling pathway	7	6.82E-02
BP	GO:0006606~protein import into nucleus	8	6.83E-02
BP	GO:0007286~spermatid development	6	7.44E-02
BP	GO:0007004~telomere maintenance via telomerase	3	7.49E-02
BP	GO:0031623~receptor internalization	3	7.49E-02
BP	GO:0022402~cell cycle process	32	7.52E-02
BP	GO:0051170~nuclear import	8	7.52E-02
BP	GO:0016310~phosphorylation	43	7.55E-02
BP	GO:0006796~phosphate metabolic process	51	7.55E-02
BP	GO:0006793~phosphorus metabolic process	51	7.55E-02
BP	GO:0009260~ribonucleotide biosynthetic process	10	7.58E-02
BP	GO:0048610~reproductive cellular process	12	7.79E-02
BP	GO:0006461~protein complex assembly	29	7.88E-02
BP	GO:0070271~protein complex biogenesis	29	7.88E-02
BP	GO:0018209~peptidyl-serine modification	5	7.88E-02
BP	GO:0010033~response to organic substance	39	8.18E-02
BP	GO:0030397~membrane disassembly	2	8.19E-02
	GO:0031146~SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	2	8.19E-02
BP	GO:0051081~nuclear envelope disassembly	2	8.19E-02
BP	GO:0035239~tube morphogenesis	10	8.51E-02
BP	GO:0033365~protein localization in organelle	11	8.60E-02
BP	GO:0010833~telomere maintenance via telomere lengthening	3	8.74E-02
BP	GO:0032204~regulation of telomere maintenance	3	8.74E-02
	GO:0021952~central nervous system projection neuron axonogenesis	3	8.74E-02
	GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	15	8.78E-02
BP	GO:0009259~ribonucleotide metabolic process	11	8.90E-02
BP	GO:0048515~spermatid differentiation	6	8.92E-02
BP	GO:0045926~negative regulation of growth	9	8.99E-02
BP	GO:0045766~positive regulation of angiogenesis	4	9.30E-02

**Supplementary Table S2 GO terms enriched by PCGs with low dosage sensitivity**

Category	Term	Count	P-Value
BP	GO:0031424~keratinization	6	2.69E-03
BP	GO:0030216~keratinocyte differentiation	7	3.65E-03
BP	GO:0009913~epidermal cell differentiation	7	5.62E-03
BP	GO:0045761~regulation of adenylate cyclase activity	8	5.96E-03
BP	GO:0031279~regulation of cyclase activity	8	7.03E-03
BP	GO:0030817~regulation of cAMP biosynthetic process	8	7.82E-03
BP	GO:0051339~regulation of lyase activity	8	7.82E-03
BP	GO:0030814~regulation of cAMP metabolic process	8	8.67E-03
BP	GO:0030802~regulation of cyclic nucleotide biosynthetic process	8	1.22E-02
BP	GO:0030808~regulation of nucleotide biosynthetic process	8	1.22E-02
BP	GO:0030799~regulation of cyclic nucleotide metabolic process	8	1.40E-02
BP	GO:0006140~regulation of nucleotide metabolic process	8	1.60E-02
BP	GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	5	2.11E-02
BP	GO:0006913~nucleocytoplasmic transport	9	2.51E-02
BP	GO:0051169~nuclear transport	9	2.68E-02
BP	GO:0007616~long-term memory	3	2.88E-02
BP	GO:0055085~transmembrane transport	21	3.31E-02
BP	GO:0051350~negative regulation of lyase activity	5	3.52E-02
BP	GO:0031280~negative regulation of cyclase activity	5	3.52E-02
BP	GO:0007190~activation of adenylate cyclase activity	5	3.52E-02
BP	GO:0007194~negative regulation of adenylate cyclase activity	5	3.52E-02
BP	GO:0045762~positive regulation of adenylate cyclase activity	5	3.72E-02
BP	GO:0031281~positive regulation of cyclase activity	5	3.94E-02
BP	GO:0007611~learning or memory	7	3.96E-02
BP	GO:0007188~G-protein signaling, coupled to cAMP nucleotide second messenger	6	4.29E-02
BP	GO:0051349~positive regulation of lyase activity	5	4.38E-02
BP	GO:0008272~sulfate transport	3	4.38E-02
BP	GO:0009953~dorsal/ventral pattern formation	5	4.61E-02
BP	GO:0051091~positive regulation of transcription factor activity	5	4.61E-02
BP	GO:0030282~bone mineralization	3	4.94E-02
BP	GO:0001934~positive regulation of protein amino acid phosphorylation	6	5.06E-02
BP	GO:0010817~regulation of hormone levels	8	5.50E-02
BP	GO:0050890~cognition	29	5.72E-02
BP	GO:0048754~branching morphogenesis of a tube	5	5.88E-02

BP	GO:0060348~bone development	7	5.98E-02
BP	GO:0010578~regulation of adenylyate cyclase activity involved in G-protein signaling	4	6.08E-02
BP	GO:0007193~inhibition of adenylyate cyclase activity by G-protein signaling	4	6.08E-02
BP	GO:0010579~positive regulation of adenylyate cyclase activity by G-protein signaling pathway	4	6.08E-02
BP	GO:0007189~activation of adenylyate cyclase activity by G-protein signaling pathway	4	6.08E-02
BP	GO:0009595~detection of biotic stimulus	3	6.11E-02
BP	GO:0019933~cAMP-mediated signaling	6	6.35E-02
BP	GO:0032497~detection of lipopolysaccharide	2	6.61E-02
BP	GO:0050730~regulation of peptidyl-tyrosine phosphorylation	5	6.72E-02
BP	GO:0032755~positive regulation of interleukin-6 production	3	6.73E-02
BP	GO:0042327~positive regulation of phosphorylation	6	6.82E-02
BP	GO:0035270~endocrine system development	5	7.01E-02
BP	GO:0060429~epithelium development	10	7.21E-02
BP	GO:0043388~positive regulation of DNA binding	5	7.31E-02
BP	GO:0019935~cyclic-nucleotide-mediated signaling	7	7.39E-02
BP	GO:0045597~positive regulation of cell differentiation	10	7.50E-02
BP	GO:0010562~positive regulation of phosphorus metabolic process	6	7.55E-02
BP	GO:0045937~positive regulation of phosphate metabolic process	6	7.55E-02
BP	GO:0046903~secretion	12	7.80E-02
BP	GO:0003002~regionalization	9	7.81E-02
BP	GO:0051090~regulation of transcription factor activity	6	8.33E-02
BP	GO:0001763~morphogenesis of a branching structure	5	8.58E-02
BP	GO:0060441~branching involved in lung morphogenesis	2	8.72E-02
BP	GO:0060438~trachea development	2	8.72E-02
BP	GO:0021569~rhombomere 3 development	2	8.72E-02
BP	GO:0030855~epithelial cell differentiation	7	8.98E-02
BP	GO:0043410~positive regulation of MAPKKK cascade	4	9.36E-02
BP	GO:0048706~embryonic skeletal system development	5	9.59E-02
BP	GO:0009952~anterior/posterior pattern formation	7	9.71E-02
BP	GO:0009914~hormone transport	4	9.81E-02
BP	GO:0051099~positive regulation of binding	5	9.94E-02
BP	GO:0051094~positive regulation of developmental process	11	9.97E-02



**Supplementary table S3 GO terms enriched by lncRNA ENSG00000250303**

Category	Term	Count	P-Value
BP	GO:0006631~fatty acid metabolic process	10	6.49E-12
BP	GO:0009062~fatty acid catabolic process	5	2.45E-07
BP	GO:0019395~fatty acid oxidation	5	3.41E-07
BP	GO:0034440~lipid oxidation	5	3.41E-07
BP	GO:0030258~lipid modification	5	3.47E-06
BP	GO:0044242~cellular lipid catabolic process	5	5.12E-06
BP	GO:0016054~organic acid catabolic process	5	2.31E-05
BP	GO:0046395~carboxylic acid catabolic process	5	2.31E-05
BP	GO:0016042~lipid catabolic process	5	1.30E-04
BP	GO:0006633~fatty acid biosynthetic process	4	2.36E-04
BP	GO:0055114~oxidation reduction	7	3.20E-04
BP	GO:0006635~fatty acid beta-oxidation	3	8.47E-04
BP	GO:0016053~organic acid biosynthetic process	4	1.69E-03
BP	GO:0046394~carboxylic acid biosynthetic process	4	1.69E-03
BP	GO:0001561~fatty acid alpha-oxidation	2	6.20E-03
BP	GO:0008610~lipid biosynthetic process	4	1.30E-02
BP	GO:0006637~acyl-CoA metabolic process	2	2.46E-02
BP	GO:0000038~very-long-chain fatty acid metabolic process	2	2.91E-02
BP	GO:0008543~fibroblast growth factor receptor signaling pathway	2	4.41E-02
BP	GO:0051781~positive regulation of cell division	2	5.89E-02
BP	GO:0051302~regulation of cell division	2	7.05E-02