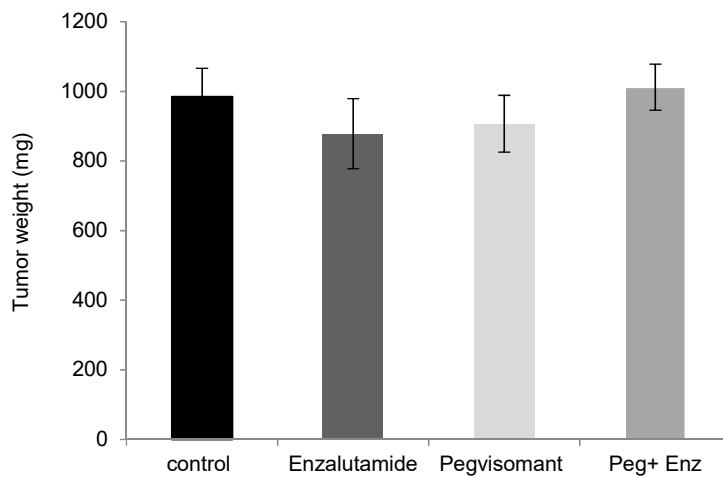
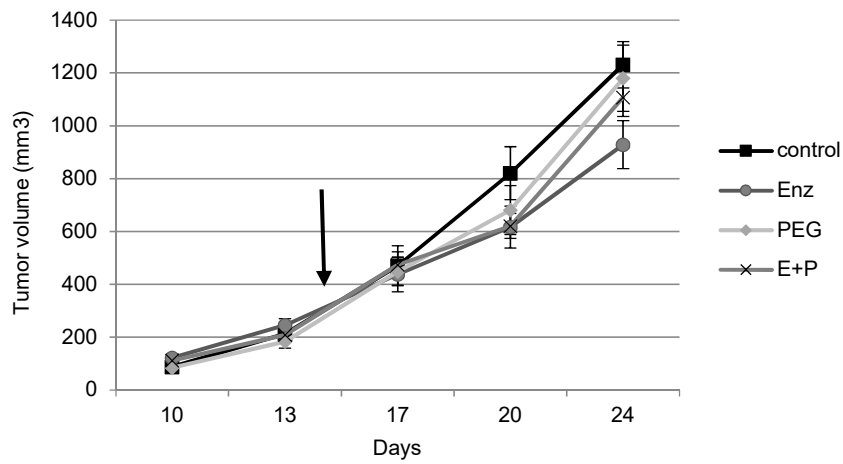


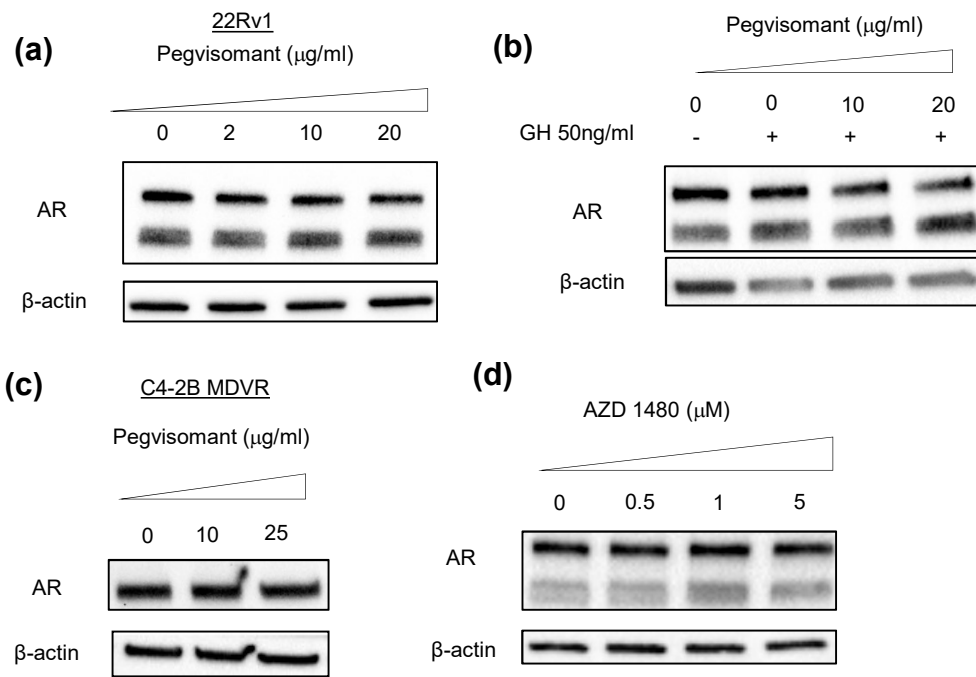
**Supplemental Fig 1. Correlation between GH expression and ARv7 target genes in human PCa datasets.**

Correlation between GH and ARv7 target genes: UBE2C (upper panel) and CCNA2 (lower panel) gene expression in human prostate cancer datasets downloaded from Oncomine. Three different datasets were analyzed by Pearson's correlation test. A larger set of AR and AR-v7 regulated genes correlating with GH can be found in supplementary tables 1 and 2.



**Supplemental Fig 2. 22Rv1 xenograft tumor growth.**

a) Tumor volume was measured with a caliper twice a week starting from day 10 after 22Rv1 cell injection and up to day 24 when the experiment finished. The arrow indicates starting point of treatments. b) Tumor weight was measured after resection in a precision scale.



### Supplemental figure 3. Full length AR is not modulated by hGH

Western blot analysis of AR expression levels in 22Rv1 cells treated with the indicated concentrations of Pegvisomant alone (A) or in combination with 50ng/ml GH treatment for 24h (B). C) C4-2B MDVR cells treated with indicated concentrations of pegvisomant for 24h and D) 22Rv1 cells treated with Jack2/Stat5 inhibitor AZD 1480 for 24h. Experiments in panels A-D were repeated 3 times. No significant differences were found on AR intensity levels.

Gene	Grasso (n=93)		Taylor 3 (n=150)		Glinsky (n=79)		Yu (n=89)	
	r	p	r	p	r	p	r	p
ABHD2	0.0890	0.3960	-0.3898	<0.0001	0.0653	0.5675	0.0305	0.7764
ACSL3	-0.3726	0.0002	-0.5295	<0.0001	-0.5534	<0.0001	-0.1905	0.0738
BRP44	-0.4865	<0.0001	-0.3851	<0.0001	-0.3402	0.0022	-0.1874	0.0787
DBI	-0.3680	0.0003	-0.4178	<0.0001	-0.1310	0.2500	-0.2641	0.0124
FKBP5	0.4534	<0.0001	-0.5298	<0.0001	-0.2780	0.0131	-0.2306	0.0297
KLK2	-0.3571	0.0004	-0.2283	0.0050	-0.3337	0.0027	-0.1893	0.0756
KLK3	-0.5280	<0.0001	-0.2228	0.0061	-0.3251	0.0035	-0.2467	0.0198
KRT8	0.3263	0.0014	-0.4961	<0.0001	-0.2170	0.0548	-0.2224	0.0362
MAOA	-0.2284	0.0276	-0.2346	0.0039	-0.2386	0.0342	-0.0833	0.4379
NDRG1	-0.0384	0.7146	-0.5314	<0.0001	-0.4276	<0.0001	-0.2564	0.0153
NKX3-1	-0.3871	0.0001	-0.3918	<0.0001	-0.0214	0.8515	0.0973	0.3646
SORD	-0.2967	0.0039	-0.3204	<0.0001	-0.1492	0.1893	-0.1976	0.0635

**Supplemental Table 1. A summary of co-expression correlations between GH1 and a AR target gene set from 4 independent clinical PCa data sets deposited at Oncomine.**

Pearson's r and p value of each correlation are shown. Each correlation shadowed in green indicates a significant negative co-expression correlation between GH1 and individual AR target gene as indicated in each data set. The AR target gene set was constructed based on a published study (Miyamoto et al, Cancer Discov, 2012, 2:995-1003).  $p < 0.05$  was considered statistically significant.

Gene	Grasso (n=93)		Taylor 3 (n=150)		Glinsky (n=79)		Yu (n=89)		Singh (n=52)	
	r	p	r	p	r	p	r	p	r	p
AKT1	0.0400	0.7036	-0.5563	<0.0001	-0.0757	0.5074	-0.2686	0.0109	-0.5786	<0.0001
BIRC5	0.4615	<0.0001	0.7630	<0.0001	0.5933	<0.0001	0.2281	0.0316	0.3729	0.0065
BUB1	0.3038	0.0034	0.1797	0.0278	0.2868	0.0104	-0.1835	0.0852	0.3537	0.0101
BUB1B	0.1650	0.1159	0.2416	0.0029	0.0980	0.3901	-0.0081	0.9400	0.4658	0.0005
CCNA2	0.1496	0.1717	0.0639	0.4369	0.5151	<0.0001	0.3172	0.0025	0.6838	<0.0001
CDC20	0.3237	0.0016	0.6443	<0.0001	0.2329	0.0388	0.3598	0.0005	-0.2469	0.0776
CDC25C	0.2312	0.0355	0.7008	<0.0001	0.2952	0.0083	0.2720	0.0099	0.7237	<0.0001
CDCA5	0.4688	<0.0001	0.5943	<0.0001	NA	NA	NA	NA	NA	NA
CENPE	-0.0398	0.7131	-0.1285	0.1170	0.4637	<0.0001	0.1182	0.2701	-0.0398	0.7792
CIT	0.5588	<0.0001	0.3102	0.0001	0.3732	0.0007	0.1552	0.1464	-0.4556	0.0007
ESPL1	0.3625	0.0004	0.8442	<0.0001	0.4842	<0.0001	0.3504	0.0008	0.6271	<0.0001
KIF15	0.1023	0.3290	0.2326	0.0042	0.4505	<0.0001	NA	NA	NA	NA
KIF2C	0.4533	<0.0001	0.4170	<0.0001	0.2715	0.0155	0.1743	0.1022	0.3864	0.0047
KNTC1	0.3528	0.0006	-0.3179	<0.0001	0.1061	0.3519	0.0007	0.9947	-0.0200	0.8883
KPNA2	0.2057	0.0479	-0.3543	<0.0001	-0.1924	0.0894	-0.2557	0.0156	-0.5381	<0.0001
MAD2L2	0.2270	0.0287	-0.2912	0.0003	NA	NA	NA	NA	NA	NA
MYC	0.4725	<0.0001	-0.4758	<0.0001	-0.0260	0.8202	0.5676	<0.0001	0.7993	<0.0001
NEK2	0.1772	0.0892	0.1658	0.0426	0.0067	0.9534	0.2238	0.0350	0.1430	0.3118
NUSAP1	0.2683	0.0097	-0.0844	0.3043	0.1429	0.2089	NA	NA	NA	NA
PKMYT1	0.4946	<0.0001	0.8139	<0.0001	0.5215	<0.0001	0.1444	0.1771	-0.2274	0.1050
PLK1	0.4967	<0.0001	0.4031	<0.0001	0.4695	<0.0001	0.2494	0.0184	0.5430	<0.0001
TPX2	0.2633	0.0108	0.1069	0.1928	0.4733	<0.0001	0.2001	0.0601	0.5615	<0.0001
UBE2C	0.4896	<0.0001	0.2516	0.0019	0.4290	<0.0001	0.2370	0.0254	-0.5577	<0.0001
UGT2B1	0.3090	0.0026	0.2855	0.0004	0.2835	0.0114	0.1226	0.2230	0.4586	0.0006
ZWINT	NA	NA	0.3766	<0.0001	0.0738	0.5182	-0.1295	0.2265	0.2875	0.0388

**Supplemental Table 2. A summary of co-expression correlations between GH1 and a AR-V7 target gene set from 5 independent clinical PCa data sets deposited at Oncomine.**

Pearson's r and p value of each correlation are shown. Each correlation shadowed in green indicates a significant positive co-expression correlation between GH1 and individual AR-V7 target gene as indicated in each data set. The AR-V7 target gene set was constructed based on two published studies (Hu et al, Cancer Res, 2012, 72:3457-62; Zhang et al, PLoS One, 2011, 6:e27970).  $p < 0.05$  was considered statistically significant.