

Table S1. One-way ANOVA for candidate protein markers in ALDH fractions.

A, Descriptive statistics									
	BMI-1 (n=2)	NANOG (n=2)	LGR5 (n=2)	SOX2 (n=2)	CD44 (n=2)	C-Myc (n=2)	FOXO3 (n=2)	FOXCl (n=2)	
ALDH ^{low-untreated}									
Mean ROD	1.1715	0.695	0.680	0.771	0.761	0.761	0.761	0.761	0.761
SEM	0.034	0.021	0.005	0.023	0.026	0.026	0.026	0.026	0.026
ALDH ^{high-untreated}									
Mean ROD	0.9883	1.398	1.413	1.351	1.320	1.320	1.320	1.320	1.320
SEM	0.039	0.087	0.005	0.026	0.029	0.029	0.029	0.029	0.029
ALDH ^{low-PRP}									
Mean ROD	0.9974	1.398	1.413	1.351	1.320	1.320	1.320	1.320	1.320
SEM	0.0415	0.087	0.005	0.026	0.029	0.029	0.029	0.029	0.029
B, One-Way ANOVA									
	BMI-1 (n=2)	NANOG (n=2)	LGR5 (n=2)	SOX2 (n=2)	CD44 (n=2)	C-Myc (n=2)	FOXO3 (n=2)	FOXCl (n=2)	
F-value	11.00	62.05	45.43	675.9	15.64	169.6	4.408	77.80	
P-value	0.0416	0.0036	0.0057	0.0001	0.0259	0.0008	0.1279	0.0026	
C, Tukey's HSD									
	BMI-1 (n=2)	NANOG (n=2)	LGR5 (n=2)	SOX2 (n=2)	CD44 (n=2)	C-Myc (n=2)	FOXO3 (n=2)	FOXCl (n=2)	
ALDH ^{low-untreated} vs. ALDH ^{high-untreated}									
Mean difference	-0.1449	0.5366	0.7189	-0.9669	0.5000	1.737	-0.03227	0.5369	
95% CI	-0.4624, 0.1727	-0.1548, 1.228	0.3958, 1.042	-1.175, -0.7583	-0.008754, 1.009	1.126, 2.348	-0.3287, 0.2641	0.2951, 0.7787	
P-value	0.5000	0.0940	0.0054	0.0007	0.0523	0.0027	0.8959	0.0054	
ALDH ^{low-untreated} vs. ALDH ^{low-PRP}									
Mean difference	0.6425	1.795	0.4996	-1.834	0.6504	2.651	-0.1964	0.6863	
95% CI	0.3250, 0.9600	1.104, 2.487	0.1765, 0.8226	-2.043, -1.626	0.1416, 1.159	2.040, 3.262	-0.4928, 0.1000	0.4445, 0.9281	
P-value	0.0001	0.0035	0.0153	<0.0001	0.0260	0.0008	0.1351	0.0027	
ALDH ^{high-untreated} vs. ALDH ^{low-PRP}									
Mean difference	0.7874	1.259	-0.2193	-0.8674	0.1504	0.9138	-0.1641	0.1493	
95% CI	0.4699, 1.105	0.5674, 1.950	-0.5424, 0.1037	-1.076, -0.6589	-0.3584, 0.6591	0.3028, 1.525	-0.4605, 0.1323	-0.09246, 0.3911	
P-value	<0.0001	0.0096	0.1279	0.0009	0.5138	0.0168	0.1968	0.1573	

ALDH, aldehyde dehydrogenase; ROD, relative optical density; PRP-1, proline-rich polypeptide-1; BMI-1, B lymphoma Mo-MLV insertion region 1 homolog; NANOG, nanog homeobox; LGR5, leucine-rich repeat-containing G protein-coupled receptor 5; FOXO3, forkhead box O3; FOXCl, forkhead box Cl.

Table SII. Flow cytometry statistical analysis of PRP-treated and untreated ALDH fractions.

Group	ALDH ^{Low} (n=10)	ALDH ^{High} (n=10)
Untreated		
Mean ROD	45.03%	46.72%
SEM	11.54%	11.11%
PRP-1-treated		
Mean ROD	87.53%	8.27%
SEM	2.22%	1.74%
T-test summary, treated vs. untreated		
t-value	3.617	3.419
Degrees of freedom	18	18
P-value	<0.002	<0.003

ALDH, aldehyde dehydrogenase; ROD, relative optical density; PRP-1, proline-rich polypeptide-1.

Table SIII. Cell viability in the control and experimental populations.

Group	Mean % viable	SEM
JJ012 Control	76.37	8.305
PRP-1 treated JJ012	49.40	2.902
ALDH ^{high} -untreated	62.17	0.6692
ALDH ^{high} -PRP-1	35.57	7.370
ALDH ^{low} -untreated	49.37	5.206
ALDH ^{low} -PRP-1	46.00	3.579

ALDH, aldehyde dehydrogenase; PRP-1, proline-rich polypeptide-1.

Table SIV. Dunnett's multiple comparisons analysis of cell viability between control and experimental populations.

Comparison	Mean diff.	95% CI of diff.	P-value
JJ012 Control vs. PRP-1 treated JJ012	26.97	4.994 to 48.94	0.0156
JJ012 Control vs. ALDH ^{high} -untreated	14.20	-7.773 to 36.17	0.2728
JJ012 Control vs. ALDH ^{high} -PRP-1	40.80	18.83 to 62.77	0.0007
JJ012 Control vs. ALDH ^{low} -untreated	27.00	5.027 to 48.97	0.0154
JJ012 Control vs. ALDH ^{low} -PRP-1	30.37	8.394 to 52.34	0.0071

ALDH, aldehyde dehydrogenase; PRP-1, proline-rich polypeptide-1.

Table SV. Student's t-test analysis of relative optical densities of ALDH fractions.

Group	Statistic
ALDH ^{High}	
Mean ROD	3.58994262
SEM	0.05714874
PRP-treated	
Mean ROD	1.22391134
SEM	0.01235984
T-test summary	
t-score (n=2)	-3.4269
P-value	0.0003

ALDH, aldehyde dehydrogenase; ROD, relative optical density.

Table SVI. Statistical analysis of Switch/sucrose non-fermenting complex western blot data.

Statistics	Markers									
	ALDH ^{High}	BAF 170 (n=2)	BAF 155 (n=2)	BRG1 (n=2)	BRM (n=2)	BMI-1 (n=2)	STRO-1 (n=2)	p14ARF (n=2)	p15/p16 (n=2)	
Mean		1.234707801	1.01511283	1.61260785	1.63870867	1.0757403	0.95625332	1.14780385	1.01403212	
SEM		0.12929143	0.11809404	0.05485906	0.16883639	0.03148291	0.00471526	0.21242473	0.10882179	
PRP-1-treated										
Mean		0.747923993	0.9991434	0.36004628	0.52149193	0.93623372	1.07054	0.85668253	1.0086374	
SEM		0.02178659	0.18541296	0.00701836	0.02910204	0.0618979	0.20510656	0.30012807	0.0640748	
T-test summary										
t-score (2)		18.481	0.1143	654.03	55.089	6.0207	0.9589	1.4751	0.0671	
P-value		0.034	0.928	0.000973	0.0115	0.1048	0.5133	0.3792	0.9573	

ALDH, aldehyde dehydrogenase; PRP-1, proline-rich polypeptide-1; BRG1, protein Brahma homolog 1; BAF170, BRG1-associated factor 170; BRM, Brahma protein; BAF 155, BRG1-associated factor 155; BMI-1, polycomb complex protein oncogene BMI-1; STRO-1, anti CD34 + mesenchymal stem cell monoclonal antibody; p14ARF, ARF tumor suppressor; p15/p16, cyclin-dependent kinase inhibitor 2A.