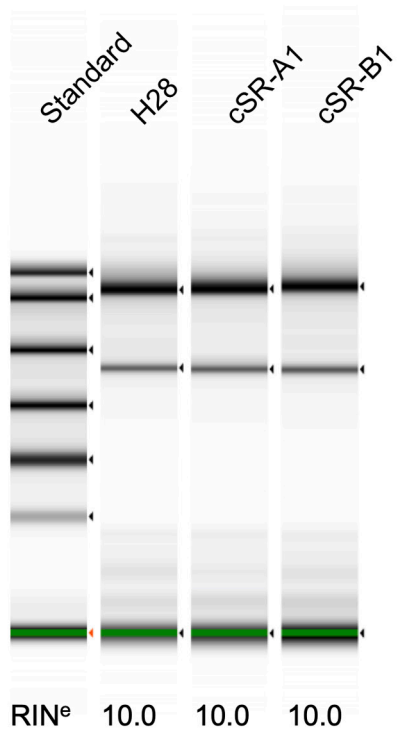


Figure S1. RNA quality determined by RIN^e values. RIN^e values are obtained from Agilent 2200 Tapestation. (A) Electrophoresis and RIN^e values of samples. (B) The electropherograms of samples. Peaks of 28S,18S and Lower Marker are indicated.

A



B

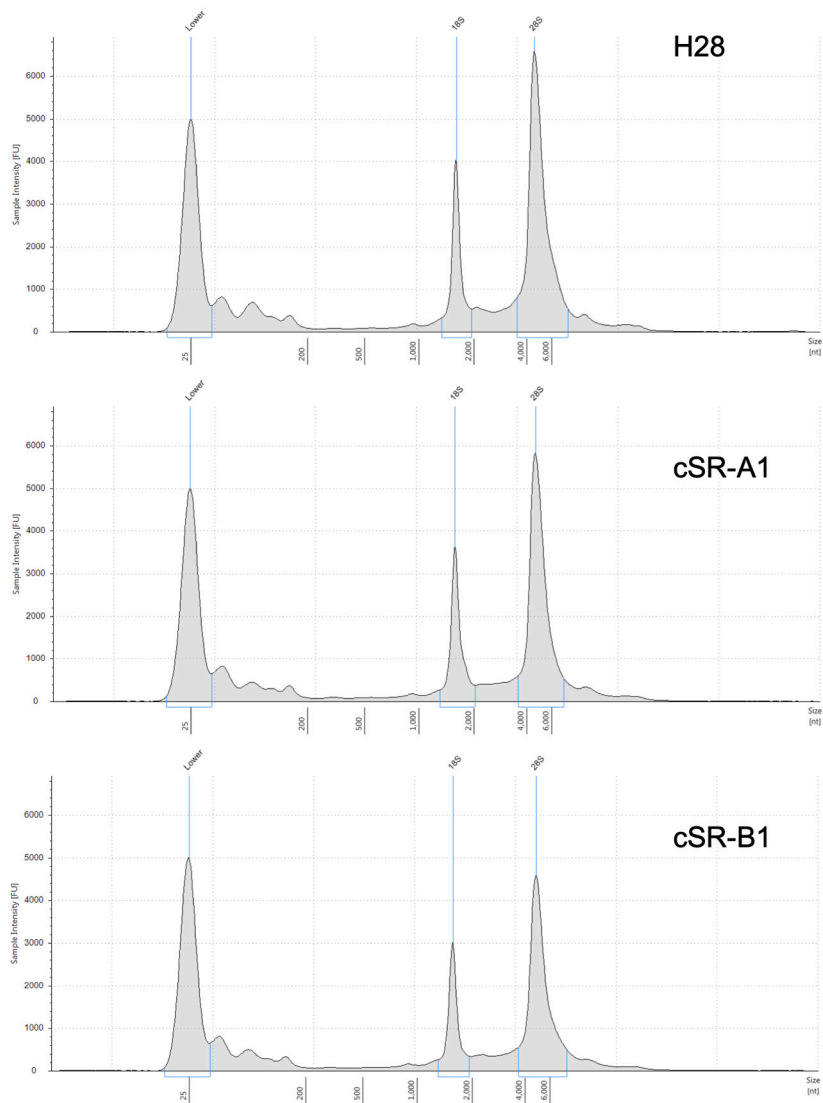


Table SI. Top 20 list of genes up- or down-regulated in cSR cells compared with parent H28 cell line.

Probe ID ^a	Gene symbol	Description	Fold change ^b	Molecular functions ^c
A_23_P88559	<i>LIPC</i>	Lipase, hepatic	934.8	Apolipoprotein binding heparin binding low-density lipoprotein particle binding
A_32_P387648	<i>FLG</i>	Filaggrin	326.6	Calcium ion binding structural molecule activity
A_33_P3331746	<i>ST6GAL2</i>	ST6 beta-galactosamide alpha-2,6-sialyltransferase 2	126.7	Beta-galactoside alpha-2,6-sialyltransferase activity
A_23_P157865	<i>TNC</i>	Tenascin C	112.1	Syndecan binding
A_23_P214821	<i>EDN1</i>	Endothelin 1	100.3	Cytokine activity endothelin A receptor binding endothelin B receptor binding
A_23_P218646	<i>TNFRSF6B</i>	Tumor necrosis factor receptor superfamily, member 6b, decoy	91.9	Receptor activity tumor necrosis factor-activated receptor activity
A_24_P190472	<i>SLPI</i>	Leukocyte peptidase inhibitor	76.8	Endopeptidase inhibitor activity enzyme binding
A_23_P372834	<i>AQP1</i>	Aquaporin 1	76.1	Ammonium transmembrane transporter activity carbon dioxide transmembrane transporter activity glycerol channel activity
A_23_P78782	<i>CA11</i>	Carbonic anhydrase XI	69.4	NOT carbonate dehydratase activity
A_23_P121665	<i>SORCS2</i>	Homo sapiens sortilin-related VPS10 domain containing receptor 2	65.9	Neuropeptide receptor activity
A_23_P258612	<i>ATP8A2</i>	Homo sapiens ATPase, aminophospholipid transporter, class I, type 8A, member 2	61.1	ATP binding magnesium ion binding phospholipid-translocating ATPase activity
A_23_P14892	<i>IGFALS</i>	Homo sapiens insulin-like growth factor binding protein, acid labile subunit	58.5	Insulin-like growth factor binding
A_33_P3397865	<i>TNNT1</i>	Homo sapiens troponin T type 1	54.7	Tropomyosin binding troponin T binding
A_24_P406754	<i>LOXL4</i>	Homo sapiens lysyl oxidase-like 4	51.0	Copper ion binding oxidoreductase activity protein binding
A_23_P150609	<i>IGF2</i>	Homo sapiens insulin-like growth factor 2	48.9	Growth factor activity hormone activity insulin receptor binding
A_33_P3285299	<i>GPRIN2</i>	Homo sapiens G protein regulated inducer of neurite outgrowth	48.8	None
A_33_P3377364	<i>ITGB4</i>	Homo sapiens integrin, beta 4	47.3	G-protein coupled receptor binding contributes_to insulin-like growth factor I binding contributes_to neuregulin binding
A_33_P3314401	<i>CLDN16</i>	Homo sapiens claudin 16	46.1	Identical protein binding magnesium ion transmembrane transporter activity structural molecule activity
A_23_P89431	<i>CCL2</i>	Homo sapiens chemokine (C-C motif) ligand 2	43.5	CCR2 chemokine receptor binding chemokine activity heparin binding
A_23_P250629	<i>PSMB8</i>	Proteasome (prosome, macropain) subunit, beta type, 8	42.0	threonine-type endopeptidase activity
A_33_P3280845	<i>THY1</i>	Thy-1 cell surface antigen	-755.7	GPI anchor binding GTPase activator activity integrin binding
A_33_P3380992	<i>AKR1B15</i>	Aldo-keto reductase family 1, member B15	-562.0	Estradiol 17-beta-dehydrogenase activity oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
A_23_P93641	<i>AKR1B10</i>	Aldo-keto reductase family 1, member B10	-548.5	Aldo-keto reductase (NADP) activity geranylgeranyl reductase activity indanol dehydrogenase activity
A_23_P77908	<i>SLC47A2</i>	Solute carrier family 47 (multidrug and toxin extrusion), member 2	-171.0	Drug:proton antiporter activity drug transmembrane transporter activity

Table SI. Continued.

Probe ID ^a	Gene symbol	Description	Fold change ^b	Molecular functions ^c
A_23_P29046	<i>CBR1</i>	Carbonyl reductase 1	-143.7	15-hydroxyprostaglandin dehydrogenase (NADP+) activity carbonyl reductase (NADPH) activity oxidoreductase activity, acting on NAD(P)H, quinone or similar
A_23_P134237	<i>RARRES2</i>	Retinoic acid receptor responder (tazarotene induced) 2	-130.9	Receptor binding
A_23_P150768	<i>SLCO2B1</i>	Solute carrier organic anion transporter family, member 2B1	-116.6	Bile acid transmembrane transporter activity organic anion transmembrane transporter activity sodium-independent organic anion transmembrane transporter activity
A_24_P166397	<i>KIAA0319</i>	KIAA0319	-105.1	Protein binding
A_24_P190168	<i>TMEM97</i>	Transmembrane protein 97	-80.0	Protein binding
A_23_P13604	<i>PEBP1</i>	Phosphatidylethanolamine binding protein 1	-76.1	ATP binding enzyme binding phosphatidylethanolamine binding
A_23_P15727	<i>FKBP10</i>	FK506 binding protein 10, 65 kDa	-70.9	FK506 binding calcium ion binding peptidyl-prolyl cis-trans isomerase activity
A_23_P251043	<i>SYNDIG1</i>	Synapse differentiation inducing 1	-68.3	Glutamate receptor binding protein binding protein homodimerization activity
A_23_P452	<i>DDR2</i>	Discoidin domain receptor tyrosine kinase 2	-65.0	ATP binding collagen binding protein tyrosine kinase collagen receptor activity
A_23_P409489	<i>DNTT</i>	DNA nucleotidylexotransferase	-60.3	DNA binding DNA nucleotidylexotransferase activity
A_23_P257971	<i>AKR1C1</i>	Aldo-keto reductase family 1, member C1	-54.0	17-alpha,20-alpha-dihydroxypregn-4-en-3-one dehydrogenase activity alditol: NADP+ 1-oxidoreductase activity aldo-keto reductase (NADP) activity
A_23_P114185	<i>TSPAN7</i>	Tetraspanin 7	-52.0	None
A_23_P252817	<i>SST</i>	Somatostatin	-50.2	Hormone activity
A_23_P129101	<i>HEXA</i>	Hexosaminidase A (alpha polypeptide)	-48.1	Acetylglucosaminyltransferase activity beta-N-acetylhexosaminidase activity
A_23_P163227	<i>CKMT1A</i>	Creatine kinase, mitochondrial	-46.6	ATP binding creatine kinase activity
A_24_P262127	<i>RRAD</i>	Creatine kinase, mitochondrial	-43.7	GTP binding GTPase activity

^aData from Agilent Technologies, Inc.; ^baverage expression ratio in cSR-A1 and -B1 cell lines were indicated as fold changes; ^cGO terms registered on each gene in molecular function field. Information was taken from the UniProt database (European Bioinformatics, UK, Swiss Institute of Bioinformatics, Switzerland, Protein Information Resource, USA) (<http://www.uniprot.org>) and the Entrez Gene database (National Center for Biotechnology Information, USA) (<http://www.ncbi.nlm.nih.gov/gene>).

Table SII. The enriched GO terms of DEGs (Top 20 list of each categories).

GO term	Count ^a	P-value
Biological process		
Oxidation-reduction process	47	2.07x10 ⁻⁷
Angiogenesis	26	2.60x10 ⁻⁷
Negative regulation of fibroblast growth factor receptor signaling pathway	6	1.04x10 ⁻⁵
Positive regulation of cell proliferation	36	2.66x10 ⁻⁵
Cell adhesion	34	5.95x10 ⁻⁵
Negative regulation of cell proliferation	31	8.56x10 ⁻⁵
Daunorubicin metabolic process	5	8.72x10 ⁻⁵
Doxorubicin metabolic process	5	8.72x10 ⁻⁵
Response to wounding	11	1.04x10 ⁻⁴
Retinoid metabolic process	10	2.24x10 ⁻⁴
Negative regulation of endopeptidase activity	14	2.73x10 ⁻⁴
Negative regulation of cell adhesion	8	2.76x10 ⁻⁴
Regulation of cell growth	11	4.08x10 ⁻⁴
Negative regulation of cell migration	12	4.57x10 ⁻⁴
Steroid metabolic process	8	5.23x10 ⁻⁴
Positive regulation of ERK1 and ERK2 cascade	17	5.69x10 ⁻⁴
Signal transduction	62	6.42x10 ⁻⁴
Negative regulation of blood coagulation	5	7.76x10 ⁻⁴
Negative regulation of apoptotic process	31	7.95x10 ⁻⁴
Response to drug	25	1.19x10 ⁻³
Molecular function		
Integrin binding	17	6.87x10 ⁻⁷
Receptor binding	32	2.42x10 ⁻⁶
Heparin binding	20	3.82x10 ⁻⁶
Insulin-like growth factor binding	7	2.28x10 ⁻⁵
Aldo-keto reductase (NADP) activity	6	1.14x10 ⁻⁴
Ferric iron binding	5	2.60x10 ⁻⁴
Insulin-like growth factor I binding	5	5.80x10 ⁻⁴
Syndecan binding	4	7.80x10 ⁻⁴
Transmembrane receptor protein tyrosine kinase activity	7	1.87x10 ⁻³
Oxidoreductase activity	17	1.96x10 ⁻³
Oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor	4	2.07x10 ⁻³
Calcium ion binding	41	2.49x10 ⁻³
Indanol dehydrogenase activity	3	3.56x10 ⁻³
Serine-type endopeptidase inhibitor activity	10	6.74x10 ⁻³
Iron ion binding	13	7.03x10 ⁻³
Fibroblast growth factor binding	5	7.65x10 ⁻³
Protease binding	10	8.72x10 ⁻³
Signal transducer activity	15	1.24x10 ⁻²
Electron carrier activity	9	1.32x10 ⁻²
Microtubule binding	15	1.40x10 ⁻²
Cellular component		
Extracellular space	99	1.13x10 ⁻¹²
Extracellular exosome	154	8.62x10 ⁻¹⁰
Extracellular matrix	29	1.64x10 ⁻⁶
Extracellular region	90	3.59x10 ⁻⁶
Cell surface	42	4.23x10 ⁻⁶
Basement membrane	11	5.27x10 ⁻⁴
Plasma membrane	175	7.04x10 ⁻⁴
High-density lipoprotein particle	6	7.50x10 ⁻⁴
Growth cone	13	1.05x10 ⁻³
Proteinaceous extracellular matrix	21	1.10x10 ⁻³
Focal adhesion	27	1.17x10 ⁻³
Apical plasma membrane	22	1.69x10 ⁻³
Organelle membrane	10	2.47x10 ⁻³
Intracellular membrane-bounded organelle	33	2.94x10 ⁻³
Integral component of plasma membrane	67	6.37x10 ⁻³
Microtubule associated complex	6	6.41x10 ⁻³

Table SII. Continued.

GO term	Count ^a	P-value
Extracellular vesicle	7	6.94x10 ⁻³
Endoplasmic reticulum	43	7.58x10 ⁻³
External side of plasma membrane	16	8.26x10 ⁻³
Membrane raft	16	9.33x10 ⁻³

^aNumber of differentially expressed genes that belong to these terms.

Table SIII. KEGG pathway annotation of differentially expressed genes in cSR cells.

KEGG term	Count ^a	P-value
Metabolism of xenobiotics by cytochrome P450	14	1.55x10 ⁻⁶
Chemical carcinogenesis	13	2.13x10 ⁻⁵
Pentose and glucuronate interconversions	8	2.24x10 ⁻⁴
Ascorbate and aldarate metabolism	7	2.95x10 ⁻⁴
Drug metabolism-cytochrome P450	10	6.05x10 ⁻⁴
Transcriptional misregulation in cancer	16	8.66x10 ⁻⁴
Steroid hormone biosynthesis	9	9.20x10 ⁻⁴
Arachidonic acid metabolism	9	1.44x10 ⁻³
Glutathione metabolism	8	1.97x10 ⁻³
Proteoglycans in cancer	16	4.82x10 ⁻³
Drug metabolism-other enzymes	7	5.33x10 ⁻³
Retinol metabolism	8	7.80x10 ⁻³
Rheumatoid arthritis	9	1.24x10 ⁻²
Porphyrin and chlorophyll metabolism	6	1.57x10 ⁻²
Glycerolipid metabolism	7	1.62x10 ⁻²
Metabolic pathways	57	2.34x10 ⁻²
Leukocyte transendothelial migration	10	2.39x10 ⁻²
ECM-receptor interaction	8	3.41x10 ⁻²
Gastric acid secretion	7	4.41x10 ⁻²

^aNumber of differentially expressed genes that belong to these terms.

Table SIV. ABC transporter genes down-regulated in cSR cells compared with parent H28 cell line.

Probe ID ^a	Gene symbol	Description	Fold change ^b	Molecular functions ^c
A_23_P44569	<i>ABCC2</i>	ATP binding cassette subfamily C member 2	-17.3	ATPase-coupled transmembrane transporter activity organic anion transmembrane transporter activity
A_24_P235429	<i>ABCA1</i>	ATP binding cassette subfamily A member 1	-4.7	ATPase-coupled transmembrane transporter activity lipid transporter activity

^aData from Agilent Technologies, Inc.; ^bAverage expression ratio in cSR-A1 and -B1 cell lines were indicated as fold changes; ^cGO terms registered on each gene in molecular function field. Information was taken from the UniProt database (European Bioinformatics, UK, Swiss Institute of Bioinformatics, Switzerland, Protein Information Resource, USA) (<http://www.uniprot.org>) and the Entrez Gene database (National Center for Biotechnology Information, USA) (<http://www.ncbi.nlm.nih.gov/gene>).