

In Vitro Derivation and Propagation of Spermatogonial Stem Cell Activity from Mouse Pluripotent Stem Cells

(試験管内における多能性幹細胞から
精原幹細胞活性の誘導と増幅)

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In Vitro Derivation and Propagation of Spermatogonial Stem Cell Activity from Mouse Pluripotent Stem Cells

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SUMMARY

The in vitro derivation and propagation of spermatogonial stem cells (SSCs) from pluripotent stem cells (PSCs) is a key goal in reproductive science. We show here that when aggregated with embryonic testicular somatic cells (reconstituted testes), primordial germ cell-like cells (PGCLCs) induced from mouse embryonic stem cells differentiate into spermatogonia-like cells in vitro and are expandable as cells that resemble germline stem cells (GSCs), a primary cell line with SSC activity. Remarkably, GSC-like cells (GSCLCs), but not PGCLCs, colonize adult testes and, albeit less effectively than GSCs, contribute to spermatogenesis and fertile offspring. Whole-genome analyses reveal that GSCLCs exhibit aberrant methylation at vulnerable regulatory elements, including those critical for spermatogenesis, which may restrain their spermatogenic potential. Our study establishes a strategy for the in vitro derivation of SSC activity from PSCs, which, we propose, relies on faithful epigenomic regulation.

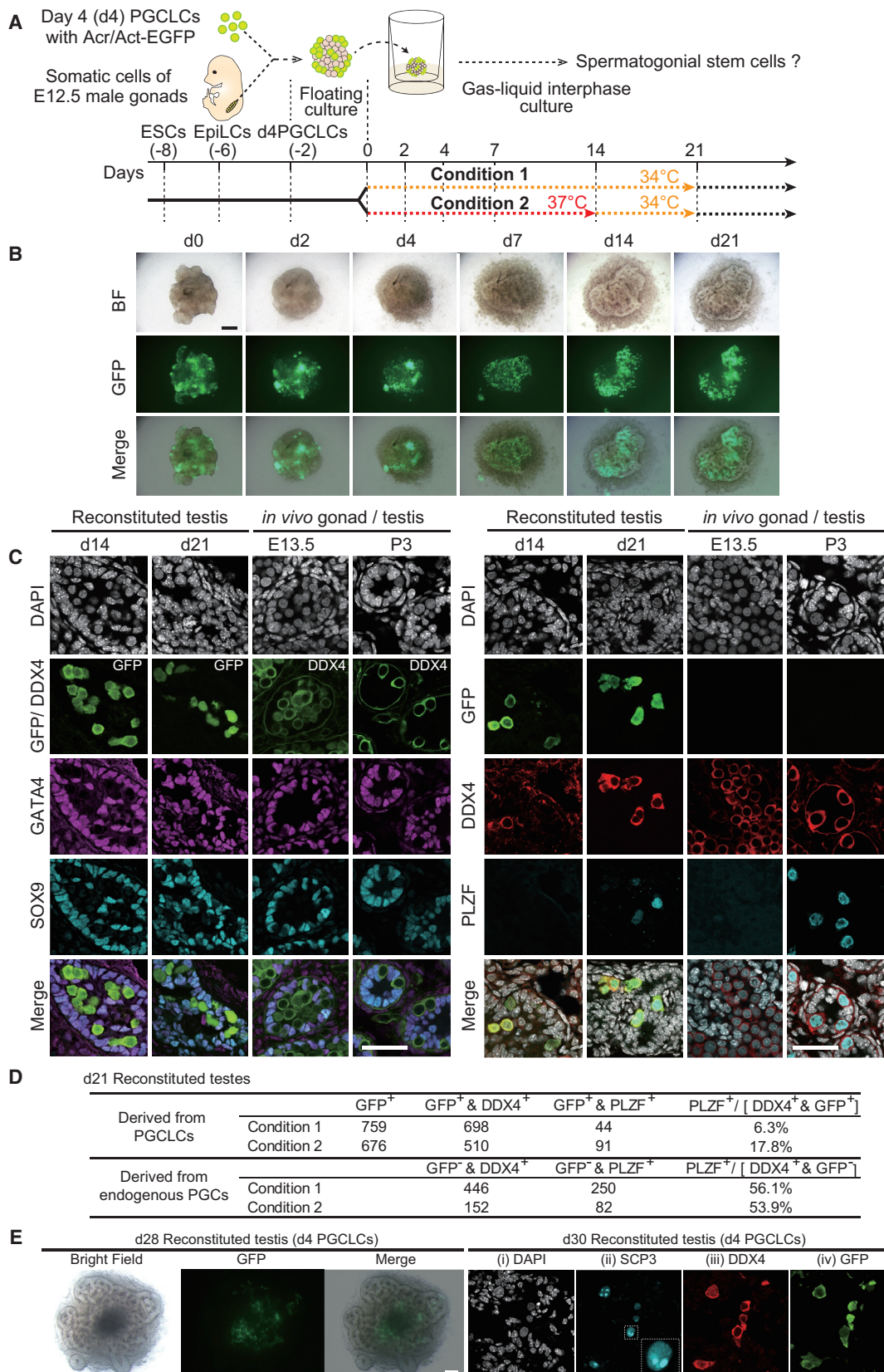
INTRODUCTION

Germ cells are a source of totipotency, underlying reproduction, inheritance, and evolution of a given species. In mice, the germ cell lineage is induced in the epiblast in response to signaling molecules at around embryonic day (E) 6.0 and is established in the extra-embryonic mesoderm as primordial germ cells (PGCs) by around E7.0 (Ginsburg et al., 1990; Lawson et al.,

1999; Saitou et al., 2002). PGCs then initiate migration through the hindgut endoderm and colonize embryonic testes or ovaries at around E10.5, where they continue to proliferate until around E13.5 (Tam and Snow, 1981). A key event that takes place in PGCs is epigenomic reprogramming involving genome-wide DNA demethylation, which leads to erasure of parental imprints and X reactivation in females (Lee et al., 2014; Saitou et al., 2012).

In embryonic testes, PGCs enter mitotic arrest around E13.5 and differentiate into pro-spermatogonia in the luminal compartment of incipient seminiferous tubules (Hilscher et al., 1974) acquiring an androgenetic epigenome, including paternal imprints, by postnatal day (P) 5 (Kobayashi et al., 2013; Kubo et al., 2015; Seisenberger et al., 2012). Thereafter, pro-spermatogonia migrate into the basal compartment of the seminiferous tubules to differentiate as spermatogonia, which undergo first-wave spermatogenesis (Bellvé et al., 1977) or are recruited as spermatogonial stem cells (SSCs) that sustain spermatogenesis throughout the adult period (Kanatsu-Shinohara and Shinohara, 2013; Yang and Oatley, 2014). In contrast, in embryonic ovaries, from around E13.5, PGCs enter directly into the first prophase of the meiosis to differentiate into primary oocytes (Hilscher et al., 1974), which serve as a foundation for oogenesis (McGee and Hsueh, 2000).

Reconstitution of germ cell development in vitro will offer opportunities for understanding the mechanism of germ cell development both under normal and diseased conditions (Saitou and Miyauchi, 2016). It has been demonstrated that mouse pluripotent stem cells (PSCs) are induced into epiblast-like cells (EpiLCs), which are, in turn, induced into primordial germ cell-like cells (PGCLCs) with the capacity for both spermatogenesis and oogenesis: male PGCLCs contribute to spermatogenesis when transplanted into testes of neonatal mice lacking endogenous



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spermatogenesis (*W/W^v* mice) (Hayashi et al., 2011), whereas female PGCLCs, when aggregated with somatic cells of female embryonic gonads and either transplanted under the ovarian bursa (Hayashi et al., 2012) or cultured appropriately (Hikabe et al., 2016), mature into fully grown oocytes. These spermatozoa and oocytes contribute to fertile offspring. A number of key issues associated with germ cell biology have been resolved based on this system (Saitou and Miyauchi, 2016). Moreover, human (h) PGCLCs have been induced from hPSCs (Irie et al., 2015; Sasaki et al., 2015), creating an opportunity for understanding the mechanism of human germ cell development in vitro.

A key next step for male germ cell development in vitro would be to induce PGCLCs into spermatogonia or SSC-like cells, the immediate precursors of spermatogenesis. Here, we set out to achieve such induction by exploiting “reconstituted testes” (Ohinata et al., 2009) in vitro.

RESULTS

PGCLCs Undergo Male Differentiation in Reconstituted Testes

Close interactions between germ cells and testicular somatic cells—particularly Sertoli cells—are essential for male germ cell differentiation (Svingen and Koopman, 2013). We sought to develop a culture system using reconstituted testes to explore whether PGCLCs undergo spermatogenic differentiation in vitro (Figure 1A). We induced embryonic stem cells (ESCs) bearing *Acro/Act-EGFP* (AAG) transgenes (129/SvJcl × C57BL/6 background) (Ohta et al., 2000) into PGCLCs, isolated them at day (d) 4 or d6 PGCLCs based on high levels of SSEA1 and INTEGRIN β 3 using fluorescence-activated cell sorting (FACS), and generated aggregates of PGCLCs with embryonic testicular cells at embryonic day (E) 12.5 depleted of PGCs by magnetic cell sorting (MACS) (Figure 1A). After culturing for 2 days under floating conditions, we placed the reconstituted testes on a permeable membrane for a gas-liquid interphase culture (Steinberger et al., 1964) either at 34°C (condition 1) or at 37°C for 2 weeks followed by 34°C for the remaining period (condition 2) (Figure 1A). Since d6 PGCLCs did not integrate well with reconstituted testes for unknown reasons (data not shown), we used d4 PGCLCs as starting materials. Since we obtained similar results under both conditions 1 and 2, we present representative results from either condition.

At d0 of the gas-liquid interphase culture, the reconstituted testes exhibited a flat and round shape with no obvious substructures (Figures 1B and S1A). AAG-positive (+) cells showed

a random distribution throughout reconstituted testes with the formation of several clumps (Figures 1B and S1A). From around d4, seminiferous tubule-like structures began to be evident, and at d7, they exhibited extensive development and assembled an anastomosed network (Figures 1B and S1A). By d7, AAG (+) cells, including clumps, outside the seminiferous tubule-like structures disappeared, and the vast majority of the AAG (+) cells were inside the seminiferous tubule-like network (Figures 1B and S1A). Thereafter, the reconstituted testes were maintained stably with further development of the seminiferous tubule-like network, and the AAG (+) cells within the network appearing to increase in number (Figures 1B and S1A).

Immunofluorescence (IF) analysis of the reconstituted testes at d14 and d21 revealed robust seminiferous tubule-like structures delineated by cells positive for GATA4 and SOX9, key transcription factors for Sertoli cells (Vidal et al., 2001; Viger et al., 1998), which were underlain by a layer of squamous cells, most likely myoid cells (Figures 1C and S1B). The AAG (+) cells with characteristic nuclear architecture were present almost exclusively within the luminal compartment of seminiferous tubules at d14 and many of them were found in the basal compartment at d21 (Figures 1C and S1B). At d14, many of the AAG (+) cells became (+) for DDX4, a germ cell marker that begins expression in gonadal PGCs (Fujiwara et al., 1994), but were negative for PLZF (ZBTB16), an SSC marker that initiates expression perinatally in pro-spermatogonia (Buaas et al., 2004; Costoya et al., 2004) (Figures 1C and S1B). At d21, some of the AAG (+) cells became both DDX4 and PLZF (+) (Figures 1C and S1B). We examined sections throughout a reconstituted testis at d21 under each condition: a majority of AAG (+) cells became DDX4 (+) (~92% for condition 1 and ~75% for condition 2) and a fraction of DDX4 (+) cells became PLZF (+) (~6.3% for condition 1 and ~18% for condition 2) (Figure 1D). Interestingly, we noted that endogenous PGCs that remained to be depleted by MACS (AAG (–)/DDX4 (+)) acquired PLZF at a higher frequency than d4 PGCLCs (~56% for condition 1 and ~54% for condition 2) (Figures 1D and S1C).

We performed longer cultures of reconstituted testes (until d54): although a few AAG (+) cells or endogenous germ cells were positive for SCP3, a key marker for the onset of meiosis (Figures 1E and S1D) (Yuan et al., 2000), we did not find cells that completed meiosis under our conditions. Collectively, these data indicate that the reconstituted testes in vitro recapitulate testis development, and, within the reconstituted testes, PGCLCs undergo differentiation to form spermatogonia-like cells. The kinetics of differentiation of PGCLCs into such cell types was protracted compared to that of PGCs in vivo.

Figure 1. Development of Reconstituted Testes In Vitro

(A) Scheme for the generation and culture of reconstituted testes under two conditions.

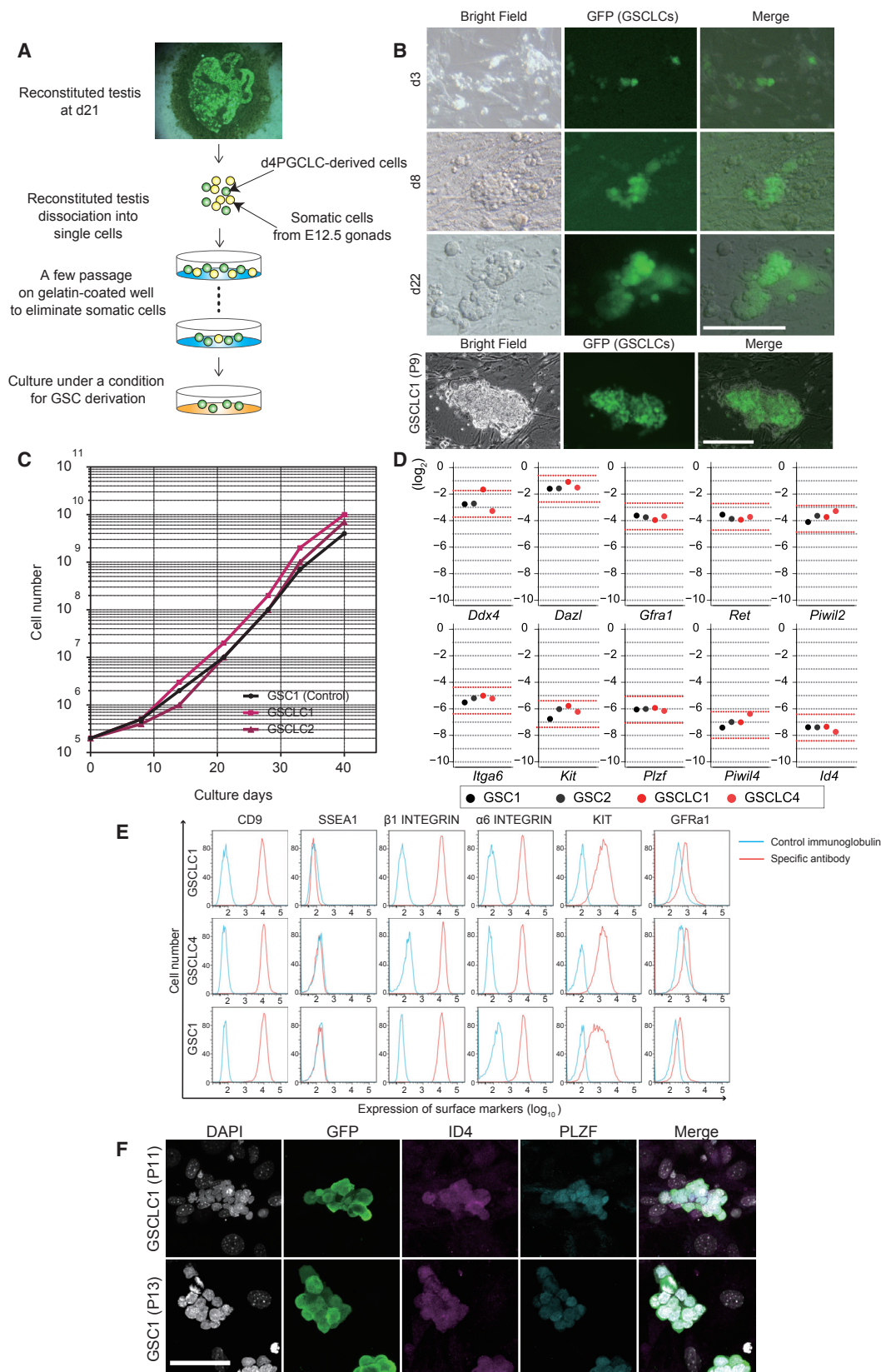
(B) Representative images of the development of reconstituted testes over 3 weeks (condition 2). Bright-field images (BF), AAG fluorescence, and their merges are shown. Bar, 200 μ m.

(C) GATA4 and SOX9 (left) or DDX4 and PLZF (right) expression in reconstituted testes at d14 and d21 (condition 2) or in testes at E13.5 and P3. Bars, 50 μ m. PGCLC-derived cells and endogenous germ cells are identified by GFP and DDX4, respectively (second rows). DAPI staining and merges are also shown.

(D) Rates of differentiation of d4 PGCLCs or E12.5 PGCs into DDX4 (+)/PLZF (–) and DDX4 (+)/PLZF (+) cells in reconstituted testes.

(E) Prolonged cultures of reconstituted testes (condition 1). (left) Morphology of a reconstituted testis cultured for 28 days. Bar, 200 μ m. (right) DDX4 (ii), SCP3 (iii), and GFP (iv) expression of a section of a reconstituted testis cultured for 30 days. (i) DAPI. Bar, 10 μ m.

See also Figure S1.



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Propagation In Vitro of a Spermatogonia-like State from PGCLCs

Perinatal pro-spermatogonia, spermatogonia, or SSCs, but not PGCs, can be propagated in vitro as a primary cell line with the capacity for self-renewal and spermatogenesis, referred to as germline stem cells (GSCs) (Kanatsu-Shinohara et al., 2003; Kubota et al., 2004). Neonatal testes are a robust source for derivation of GSCs (Kanatsu-Shinohara et al., 2003). We therefore examined whether we can derive GSC-like cells (GSCLCs) from d21 reconstituted testes, which bear PGCLC-derived spermatogonia-like cells and may resemble neonatal testes. The d21 reconstituted testes were dissociated into single cells, and the AAG (+) cells were enriched and cultured under GSC derivation conditions (Figure 2A). At d3 of culture, AAG (+) cells were scattered on mouse embryonic feeders (MEFs) as single or pairs of cells (a few thousand cells from a single reconstituted testis), a few of which, at d8, formed small colonies (at most a few dozen colonies) (Figure 2B). Thereafter, such colonies exhibited slow proliferation and, upon several passages, were propagated as stable cell lines bearing a grape cluster-like colony morphology indistinguishable from that of GSCs, with normal karyotype (nine and six lines from conditions 1 and 2, respectively), and with high efficiency for cryopreservation/re-expansion followed by thawing (Figures 2B and S2A). We were able to establish such lines in a consistent fashion when the initial colony numbers were more than ten, and they were propagated similarly to GSCs (129/SvJcl × C57BL/6) (Figure 2C) (Kanatsu-Shinohara et al., 2003).

We compared the expression of key genes (*Ddx4*, *Dazl*, *Gfra1*, *Ret*, *Piwil2*, *Itga6*, *Kit*, *Plzf*, *Piwil4*, and *Id4*), surface markers (CD9, SSEA1, INTEGRIN β 1, INTEGRIN α 6, KIT, and GFR α 1), and transcription factors (PLZF and ID4) (Kanatsu-Shinohara and Shinohara, 2013; Yang and Oatley, 2014) in reconstituted testis-derived cell lines with those in GSCs, which revealed that they exhibit similar gene expression to GSCs (Figures 2D–2F). We thus refer to these cell lines as GSCLCs. To examine whether GSCLCs can be derived from PGCLCs without the formation of reconstituted testes, we cultured d4 or d6 PGCLCs sorted by SSEA1 and INTEGRIN β 3 directly under the GSC-derivation conditions. This, however, resulted in a rapid expansion (within a few days) of strongly alkaline phosphatase-positive, dome-shaped ESC-like colonies with efficiencies similar to those of embryonic germ cell (EGC) derivation from PGCs (~5%) (Figure S2B) (Matsui et al., 1992; Resnick et al., 1992), and we were unable to isolate/detect GSC-like colonies from such cultures.

We conclude that the differentiation of PGCLCs into the male germ cell pathway is essential for the derivation of GSCLCs.

Spermatogenesis in Adult Testes and Fertile Offspring from GSCLCs

Spermatogonia/SSCs can colonize adult testes (approximately >8 weeks) for spermatogenesis (Brinster and Zimmermann, 1994), whereas PGCs colonize and undergo spermatogenesis only in neonatal testes (~5–10 days) (Chuma et al., 2005; Ohta et al., 2004). This would be due to the difference either of homing capacity or of intrinsic/epigenetic capacities for spermatogenesis between these cell types.

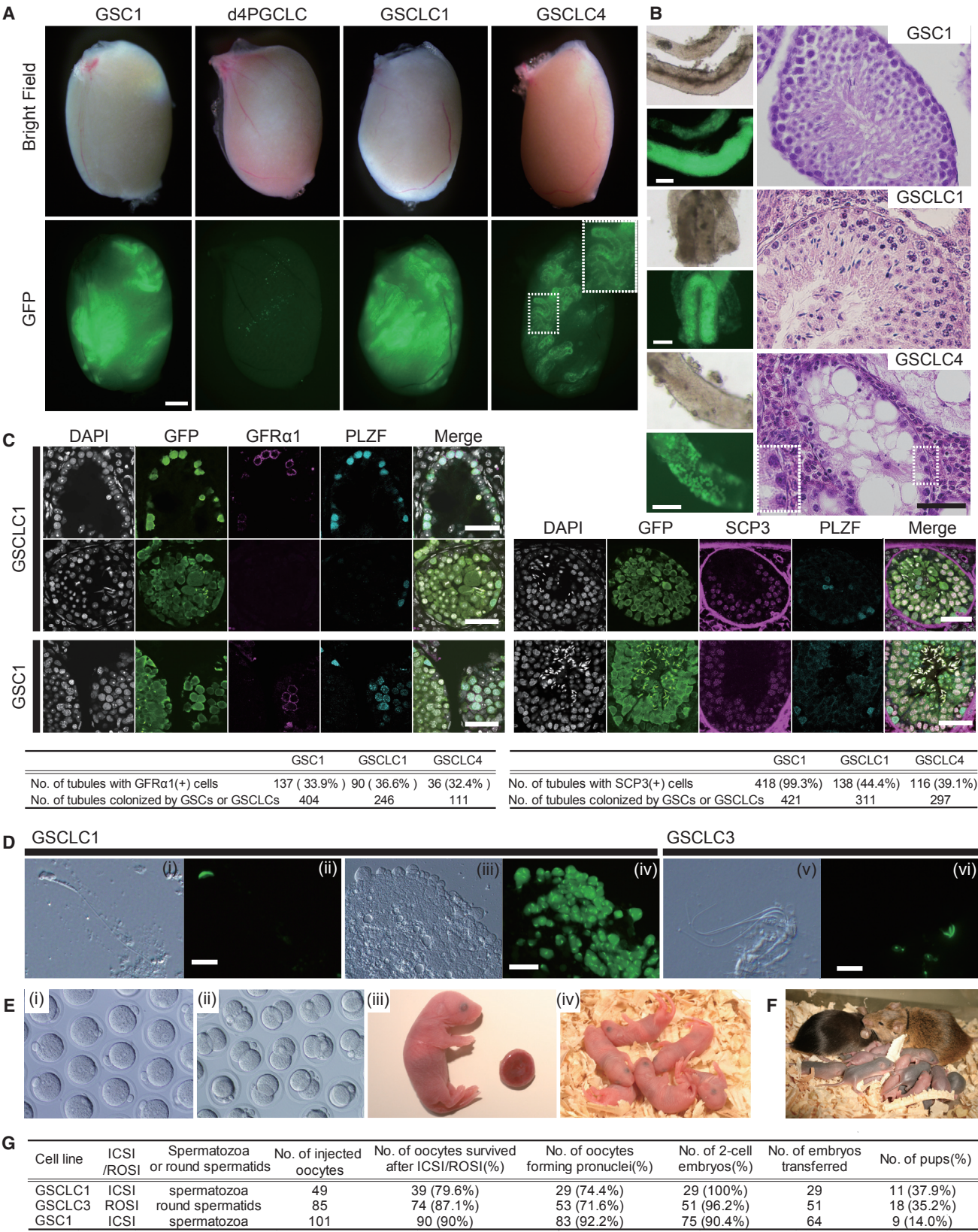
To examine whether GSCLCs acquire a mature stem cell property, we transplanted them into adult testes (8–10 weeks) of *W/W^u* mice. GSCs (AAG (+); 129/SvJcl × C57BL/6) (GSC1) robustly colonized adult testes and underwent spermatogenesis (Figure 3A), whereas PGCLCs failed to show such activity in adults (Figure 3A), although they did so in neonates (Hayashi et al., 2011). Remarkably, unlike PGCLCs, all the GSCLC lines colonized the adult testes (Figures 3A, S3A, and S3B). However, somewhat unexpectedly, a few of them (GSCLC1, 2, 3: 3/15) underwent spermatogenesis in a fraction of colonized tubules (Figures 3A, S3A, and S3B). Histological analyses confirmed that proper spermatogenesis occurred in the tubules fully occupied by GSCLC-derived AAG (+) cells (Figure 3B), whereas only spermatogonia or cells at the first meiotic prophase were present in the tubules bearing aligned chains of AAG (+) cells only around the basal compartment (Figure 3B). No GSCLC lines formed teratomas in transplanted testes, at least until 16 weeks after transplantation.

IF analyses revealed that GFR α 1 (+) spermatogonia/SSC-like cells were present at a similar ratio in tubules colonized by GSCs (~33.9%) and GSCLCs (GSCLC1: ~36.6%; 4: ~32.4%) (Figure 3C). In contrast, while nearly all the tubules colonized by GSCs exhibited SCP3 (+) meocytes (~99.3%), less than half of the tubules colonized by GSCLCs (GSCLC1: ~44.4%; 4: ~39.1%) showed such cells (Figure 3C). Thus, GSCLCs colonize adult seminiferous tubules and exhibit characteristics of spermatogonia/SSCs: however, they have a tendency to halt spermatogenesis at around the entry into or early stages of the first meiotic prophase.

We examined the function of GSCLC-derived spermatozoa or spermatids. We were able to isolate such cells (GSCLC1: spermatozoa; 3: round spermatids) consistently from seminiferous tubules with successful spermatogenesis (Figure 3D) and

Figure 2. Derivation of Germline Stem Cell-like Cells from Reconstituted Testes

- (A) Scheme for GSCLC derivation from reconstituted testes.
 (B) (top) Representative images for colonies of AAG (+) cells during the derivation of GSCLCs. BF images, AAG fluorescence, and their merges are shown. (bottom) Images for a GSCLC line (GSCLC1) at passage 9. Bars, 100 μ m.
 (C) Growth of GSCLCs (GSCLC1, 2) and GSCs (GSC1). 2×10^5 GSCLCs/GSCs were plated, and their proliferation was evaluated every 6 or 7 days.
 (D) Expression levels of the indicated genes as measured by qPCR in GSCLCs (GSCLC1, 4) and GSCs (GSC1, 2). For each gene, the Δ Ct (the threshold-cycle [Ct] value difference) from the average Ct values of the two housekeeping genes *Arbp* and *Ppia* (set as 0) was plotted. The red dotted lines indicate the Ct values ± 1 of the average Cts of GSCs.
 (E) Expression levels (red plots) of the indicated surface markers as measured by FACS analyses in GSCLCs (GSCLC1, 4) and GSCs (GSC1). Blue plots indicate the fluorescence intensities by isotype-matched control antibodies.
 (F) GFP, ID4, and PLZF expression with DAPI and their merges in a colony of GSCLCs (GSCLC1) and GSCs (GSC1). Bar, 50 μ m.
 See also Figure S2.



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performed intra-cytoplasmic sperm injection (ICSI) or round spermatid injection (ROSI), respectively, which resulted in the generation of apparently normal offspring in normal ratios (Figures 3E and 3G). Such offspring bore proper imprints as examined by combined bisulfite restriction analysis (COBRA), exhibited grossly normal development, and were fertile (Figures 3F and S3C–S3E). Thus, through PGCLCs and their differentiation into the male pathway in reconstituted testes, PSCs can be induced into a stable cell line with SSC capacity, an immediate precursor for spermatogenesis in adult testes.

Transcription and DNA Methylation Analysis of GSCLCs

The development of spermatogonia/SSCs from PGCs involves genome-wide DNA demethylation followed by acquisition of an androgenic methylome (Kobayashi et al., 2013; Kubo et al., 2015; Seisenberger et al., 2012). The limited spermatogenic capacity of GSCLCs derived under the present conditions might have resulted from impaired transcription/transcriptional potential associated with epigenetic mis-regulation during their derivation.

Transcriptome

We compared the transcriptomes of GSCLCs (GSCLC1–4) with those of GSCs (GSC1, 2) using RNA sequencing (RNA-seq) (Figures S4A and S4B) (Nakamura et al., 2015). Consistent with the analyses of the expression of key markers (Figures 2D–2F), unsupervised hierarchical clustering (UHC) and principal component analysis (PCA) clustered GSCLCs and GSCs together in comparison to ESCs, EpiLCs, and d4/d6 PGCLCs (Figures 4A and 4B), demonstrating that GSCLCs acquire a transcriptome similar to that of GSCs.

The GSCLCs and GSCs, however, were segregated upon mutual comparison, and each GSCLC line formed a separate cluster (Figure 4C). We identified differentially expressed genes (DEGs) between each GSCLC line and the averages of two GSC lines (Figures 4D, 4E, S4C, and S4D). The DEGs accounted for ~2.5% to ~4.5% of the genes expressed among GSCs/GSCLCs (Figure 4D), and GSCLC1 with better spermatogenic activity (Figures 3 and S3) exhibited the smallest number of DEGs, whereas GSCLC4 with no spermatogenic activity (Figures 3 and S3) showed the largest number of DEGs (Figure 4D). Genes downregulated in GSCLCs (407 in total) were higher in number than those upregulated (355 in total) and DEGs in each GSCLC line partially overlapped (Figures 4D and S4C). The genes commonly downregulated in all four GSCLC lines (55 genes)

included a key pluripotency gene (*Pou5f1*) (Ohbo et al., 2003), genes implicated in the self-renewal of SSCs (*Lhx1*, *T*) (Oatley et al., 2006; Wu et al., 2011), and those critical for meiosis/repression of transposons through DNA methylation (*Tex19.1*, *Tdrd9*) (Ollinger et al., 2008; Shoji et al., 2009). Both the intersection and union of genes downregulated in GSCLCs were enriched with gene ontology (GO) functional terms such as “anterior/posterior pattern formation” (*Hoxb2*, *Hoxb3*, *Hoxb5–9*, *Lhx1*, *T*, *Wnt3*, and *Sfrp2*, etc.) (Figures 4D and 4E; Table S1).

Global DNA Methylation Profiles

We next analyzed the genome-wide DNA methylation profiles of GSCLCs (GSCLC1–4) in comparison to those of GSCs (GSC1, 2) and d4 PGCLCs by whole-genome bisulfite sequencing (WGBS). Although bisulfite sequencing does not discriminate between 5-methylcytosine (5mC) and 5-hydroxymethylcytosine (5hmC) (Hayatsu and Shiragami, 1979), since 5hmC consists only of a fraction of 5mC in germ cells (Shirane et al., 2016), we collectively designate 5mC and 5hmC as 5mC. We also examined the 5mC profiles of other key cell types reported previously (E10.5 PGCs, E13.5 PGCs, E16.5 pro-spermatogonia, P0 pro-spermatogonia, P7 KIT (–) spermatogonia, P7 KIT (+) spermatogonia, sperm, and MEFs [largely C57BL/6 background]) (Kobayashi et al., 2013; Kubo et al., 2015). We analyzed the 5mC levels in all CpG sites, across the genome-wide single-copy loci (2-Kb non-overlapping windows), in promoters (sequences 0.9 Kb upstream and 0.4 Kb downstream of the transcription start sites [TSSs] for 22,837 genes, which were classified into high [11,932], intermediate [3,381], and low [7,524] CpG density promoters [HCPs, ICPs, and LCPs, respectively] [Weber et al., 2007]), and in non-promoter CpG islands (CGIs: exons [2,574], introns [1,399], and intergenic regions [6,815]) (Illingworth et al., 2010) (Figures S5A and S5B).

Genome-wide 5mC levels were similar between GSCLCs (average: ~81.7%) and GSCs (~80.7%) (Figure S5B; Table S2). Figure 5A represents the 5mC-level tracks across chromosome 1 of the cell types analyzed: as reported previously (Kobayashi et al., 2013; Kubo et al., 2015), PGCs at E10.5 and, in particular, at E13.5, are depleted of the vast majority of 5mC and exhibit an extremely low 5mC level. Pro-spermatogonia at E16.5 gain a significant level of 5mC, except around the lamina-associated domains (LADs) (Guelen et al., 2008), and pro-spermatogonia at postnatal day (P) 0 show a nearly fully methylated pattern similar to spermatogonia at P7 that are (–) or (+) for KIT and mature spermatozoa (Figure 5A).

Figure 3. Spermatogenesis and Fertile Offspring from GSCLCs

(A and B) Representative BF and AAG-fluorescence images of testes (A) or isolated seminiferous tubules (B) of *W/W^u* mice 10 weeks after transplantation of GSCs (GSC1), d4 PGCLCs (only in A), and GSCLCs (GSCLC1, 4). The boxed area is magnified, revealing that AAG (+) cells were colonized only at the basal area of seminiferous tubules. The dotted fluorescence seen in the d4 PGCLC transplant (second left, bottom) is autofluorescence. Histological sections stained by H&E are shown in (B). Bar in (A), 1 mm; bars in (B), 100 μ m (left) 50 μ m (right).
(C) (top) GFP, GFR α 1, and PLZF (left) or GFP, SCP, and PLZF (right) expression with DAPI and their merges in sections of seminiferous tubules of *W/W^u* mice 10 weeks after transplantation of GSCLCs (GSCLC1) or GSCs (GSC1). Bar, 50 μ m. (bottom) Representative rates of seminiferous tubules with GFR α 1 (+) (left) or SCP3 (+) (right) cells among tubules colonized by transplanted GSCs (GSC1) or GSCLCs (GSCLC1, 4).
(D) BF (i, iii, v) and AAG-fluorescence (ii, iv, vi) images of spermatozoa (i, ii, v, vi) and spermatids (iii, iv) derived from GSCLC1 (i–iv) or GSCLC3 (v, vi). Bars in (ii, vi), 10 μ m. Bar in (iv), 50 μ m.
(E) Zygotes at pronuclear stages (i), 2-cell embryos (ii), offspring (iii, iv), and placenta (iii) produced by ICSI of GSCLC-derived spermatozoa.
(F) A fertile male offspring (agouti) from a GSCLC1-derived spermatozoon.
(G) Development of oocytes injected with spermatozoa derived from GSCLCs and GSCs.
See also Figure S3.

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d4 PGCLCs showed an average 5mC level of ~50.5%, which is higher than that of E10.5 and E13.5 PGCs (average: ~16.2% and ~3.8%, respectively) (Figures 5A and S5B) (Kobayashi et al., 2013; Shirane et al., 2016). Notably the overall configuration of the methylome of d4 PGCLCs is similar to that of E10.5 PGCs, with relatively flat 5mC levels across the chromosome (Figure 5A), indicating that d4 PGCLCs bear a methylome corresponding to earlier PGCs, and such a configuration would represent the methylome in the middle of genome-wide DNA demethylation (Shirane et al., 2016). In contrast, both GSCLCs and GSCs showed methylation profiles similar to those of postnatal spermatogenic cells with common low methylated regions (LMRs) (Stadler et al., 2011) (Figure 5A). Thus, at a global level, compared to PGCLCs/PGCs, GSCLCs and GSCs bear similar DNA methylomes both to each other and to postnatal spermatogenic cells.

DNA Methylation at Regulatory Elements

On the other hand, GSCLCs showed 5mC levels consistently higher than GSCs in promoters and non-promoter CGIs (Figure S5B). Accordingly, PCA of the 5mC profiles of promoters and non-promoter CGIs clustered GSCLCs apart from GSCs and postnatal spermatogenic cells (Figure S5C). Scatterplot comparisons revealed that, while GSCs and KIT (–) spermatogonia at P7 showed similar 5mC-level distributions across such regions (Figure S5D), GSCLCs bear promoters (particularly LCPs) and non-promoter CGIs with higher 5mC levels than GSCs (Figure S5D). Accordingly, while GSCLCs, GSCs, and KIT (–) spermatogonia at P7 exhibited excellent correlation with regard to the 5mC levels of all promoters, GSCLCs showed divergence from GSCs and KIT (–) spermatogonia at P7 with regard to the 5mC levels of differentially methylated promoters, with GSCLC1 (with better spermatogenic activity) and 4 (with no spermatogenic activity) showing better and worse correlations, respectively (Figure 5B).

We identified the promoters and non-promoter CGIs having differential 5mC levels ($\geq 25\%$) between each GSCLC line and the averages of GSCs, which revealed that differential methylation was mainly attributable to hyper-methylation in GSCLCs and exhibited a modest overlap among the GSCLC lines (Figures 5C and S5D; Table S2). The hyper-methylated promoters in GSCLCs constituted ~3.0%–~5.4% of all promoters (Figure 5C; Table S2) and enriched with genes for “signal transduction” and “immune system process,” whereas the hypo-methylated promoters in GSCLCs were very minor (~0.2%–~0.5%) and were enriched with those for “sensory perception of smell” (Figure S6A; Tables S2 and S3). Importantly, genes bearing hyper-methylated promoters, but not non-promoter CGIs, in GSCLCs (GSCLC – GSC $\geq 25\%$) exhibited a significant tendency to be

repressed in GSCLCs (Figures 5D and S6B), and such genes included *Pou5f1* and genes critical for meiosis/transposon repression through DNA methylation (*Sohlh1*, *Dpep3*, *Tex19.1*, *Tdrd9*) (Ballow et al., 2006; Ollinger et al., 2008; Shoji et al., 2009; Yoshitake et al., 2011) (Figures 5E and S6C). Genes such as *Spo11* (essential for meiosis [Baudat et al., 2000; Romanienko and Camerini-Otero, 2000]) and *Piwi1* (essential for spermiogenesis [Deng and Lin, 2002]), which showed no/low expression in GSCs and GSCLCs, also exhibited higher promoter methylation in GSCLCs (Figures 5E and S6C).

We examined the methylation states of the differentially methylated regions (DMRs) of imprinted genes. While the DMRs of paternally imprinted genes (*H19*, *Rasgrf1*, and *Dlk1-Gtl2*) were properly methylated in all GSCLCs, some of the DMRs of maternally imprinted genes exhibited aberrant methylation profiles: while GSCLC1 and 4 showed apparently normal maternal imprints, GSCLC2 and 3 exhibited aberrant methylation in the DMRs of *Snrpn* and *Impact*, and *Peg1/Mest*, *Lit1/Kcnq1ot1*, *Meg1/Grb10*, and *Impact*, respectively (Figures 5F and S6D; Table S4). We then examined the methylation profiles of the transposons. In contrast to the other regulatory elements, GSCLC2, 4, and to a lesser extent, 1, but not 3, exhibited hypo-methylation in the promoters or long terminal repeats (LTRs) of a number of long interspersed nuclear element 1s (LINE1s) or endogenous retroviruses (ERVs) 1, 2 (including intracisternal A particles [IAPs]), and 3, respectively (Figures 5G and S6E; Table S4). This may be a consequence of the repression of *Tex19.1* and *Tdrd9* (Figures 4 and 5E), which are critical for transposon repression through DNA methylation of their regulatory elements (Ollinger et al., 2008; Shoji et al., 2009). Consistently, IAPs were de-repressed in GSCLC2 and 4 with the second lowest and the lowest LTR methylation levels, and two classes of LINE1s were de-repressed in GSCLC2 with the lowest promoter methylation levels (Figure S6E). Collectively, these findings show that GSCLC induction from PGCLCs entails line-dependent mis-regulation, in particular, hyper-methylation, of a fraction of regulatory elements that exhibit partial overlaps among the GSCLC lines and such hyper-methylation leads to the repression of associated genes.

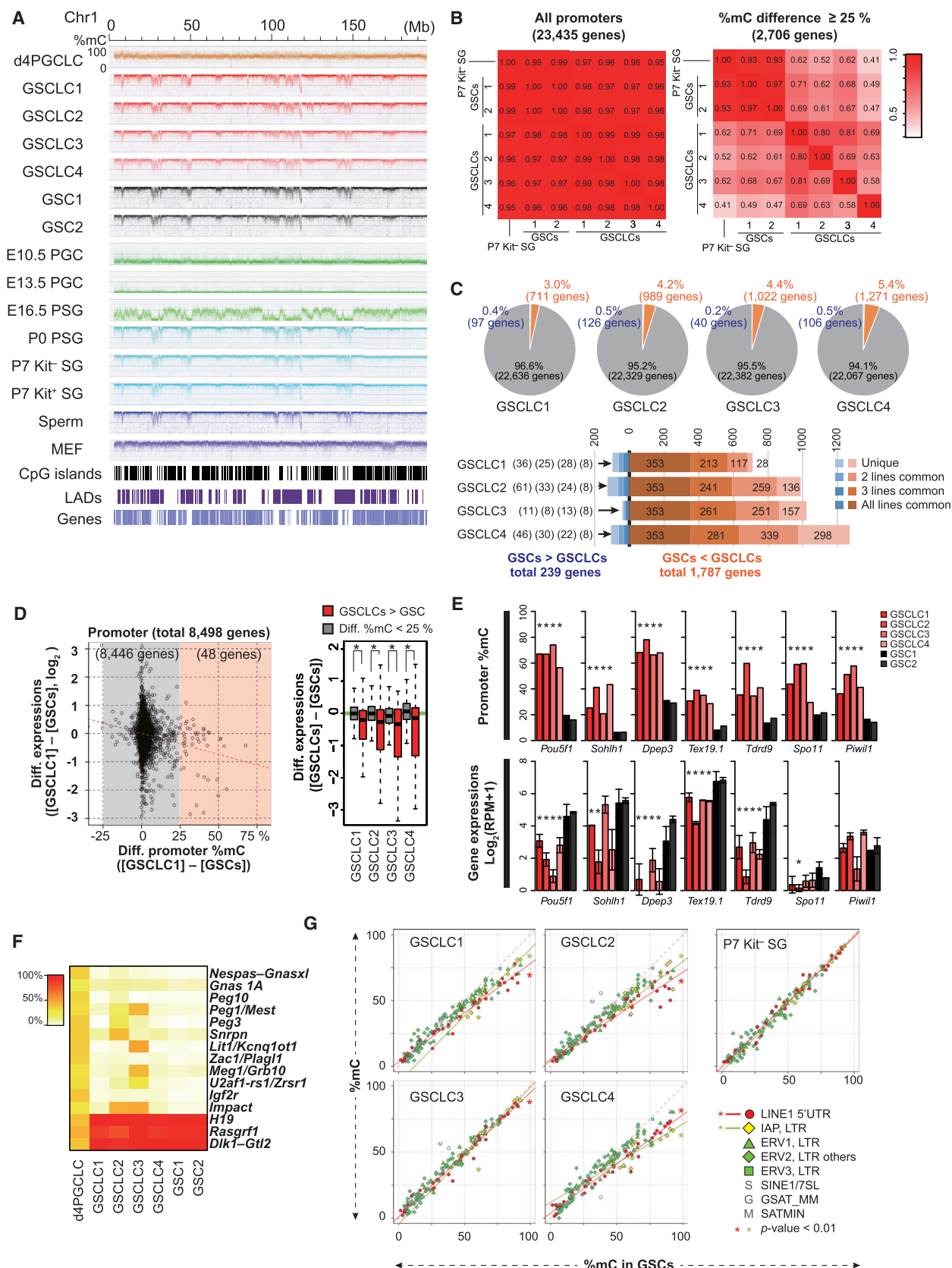
Methylation Dynamics of Regulatory Elements Vulnerable to Mis-regulation

We explored a potential cause of aberrant DNA methylation on key regulatory elements during the derivation of GSCLCs. We identified promoters that exhibited higher 5mC levels in all GSCLCs compared to the averages of GSCs (GSCLCs – GSCs $\geq 25\%$, $p < 0.01$, Welch's t test, 263 promoters) and examined their methylation dynamics during male germ cell

Figure 4. Comparison of the Transcriptomes of GSCLCs and GSCs

(A–C) UHC (A) and PCA (B and C) of transcriptomes of the indicated cell types. (D) (left, top) Pie graphs showing the numbers and percentages of DEGs (down in GSCLCs: blue; up in GSCLCs: orange) between each GSCLC line and the averages of two GSC lines among genes expressed in GSCs/GSCLCs (9,073 genes: $\log_2[\text{RPM}+1] > 4$ in at least one line). (left, bottom) Bar graphs showing the overlap of DEGs between each GSCLC line and the averages of two GSC lines. The color coding is as indicated. (right) The list of genes commonly down (top)/up (bottom)-regulated in all four GSCLCs and their GO enrichments are shown. (E) Heatmap of the expression of the unions of genes up (left)/down (right)-regulated in GSCLCs and their GO enrichments with composite genes. The color coding is as indicated.

See also Figure S4 and Table S1.



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development. The differentially methylated promoters exhibit 5mC-level distributions of from 0% to ~75% in d4 PGCLCs and show nearly complete demethylation in male germ cells at E13.5 (Figure 6). During the differentiation of KIT (–) spermatogonia at P7, their 5mC levels, particularly those with higher 5mC levels in d4 PGCLCs, are elevated but remain relatively low (average: ~30.0%), and their 5mC levels in KIT (–) spermatogonia at P7 are similar to those in GSCs (average: ~35.7%) (Figure 6).

In contrast, such promoters exhibited relatively high 5mC levels in GSCLCs (average: GSCLC1: ~73.4%; 2: ~75.9%; 3: ~81.6%; 4: ~81.7%) (Figure 6). We generated a hypothetical 5mC-level plot in which the 5mC levels of these promoters were shown as the simple sum of their levels in d4 PGCLCs and GSCs, which resulted in a 5mC-level distribution pattern (average: ~82.2%) similar to those in GSCLCs (Figure 6). On the other hand, for some of the promoters with relatively low 5mC levels in d4 PGCLCs, GSCLCs exhibited higher 5mC levels than those determined in the hypothetical model (Figure 6). These findings suggest that GSCLCs acquire higher 5mC levels in a fraction of regulatory elements presumably due to a failure in the DNA demethylation (reprogramming) and the suppression of the elevation of DNA methylation levels (programming).

Heterogeneity among GSCLCs and GSCs

We evaluated the potential heterogeneity/clonality of GSCLCs in comparison to that of GSCs by analyzing their single-cell transcriptomes, which are the culmination of their epigenetic states. We generated single-cell cDNAs from GSCLC1 (with better spermatogenic activity) and 4 (with no spermatogenic activity), and from GSC1 and 2, and analyzed those with sufficient quality by single-cell 3-prime RNA sequencing (SC3-seq) (30, 24, 29, and 24 single cells for GSCLC1, 4, GSC1, and 2, respectively) (Figures S7A–S7C) (Nakamura et al., 2015). The DEGs between GSCLCs and GSCs identified by the population-level analyses were represented appropriately in single-cell cDNAs from GSCLCs and GSCs (Figures 7A and S7D). Accordingly, both

UHC and PCA revealed that single cells from GSC1 and 2 generated intermingled clusters, whereas single cells from GSCLC1 and 4 contributed to separate clusters, with single cells from GSCLC1 generating a cluster closer to those of GSCs (Figures 7B and 7C).

To quantify the extent of heterogeneity among single cells, we calculated the variances of the expression levels of individual genes among single cells from GSCLCs and GSCs. This analysis revealed that the distributions of such variances were similar among GSCLCs and GSCs (Figure 7D). Statistical analyses (Kruskal-Wallis test followed by Bonferroni correction) revealed that due to large numbers of genes analyzed, the distribution of gene-expression variances in GSC1 turned out to be different from that in GSC2 ($p = 8.9 \times 10^{-6}$), but, importantly, not different from that in GSCLC1 ($p > 0.1$) (Figure 7D). Furthermore, the gene-expression variance in GSCLC4 was the smallest among those in GSCs and GSCLCs (Figure 7D), indicating that the heterogeneity of GSCLCs is not larger than that of GSCs.

DISCUSSION

We have shown that PGCLCs induced from ESCs can differentiate into spermatogonia-like cells in reconstituted testes and are then propagated as GSCLCs (Figure 7E). GSCLCs differ from PGCLCs in terms of their transcriptome, DNA methylome, and most critically, capacity for undergoing spermatogenesis in adult testes (Figures 3, 4, and 5). Our system therefore represents a stepwise reconstitution of the male germ cell differentiation pathway in vitro, realizing the induction of a stable cell line with SSC function from PSCs (Figure 7E). Compared to GSCs derived from neonatal testes, GSCLCs exhibited a limited capacity for spermatogenesis (Figure 3). GSCLCs bore hypermethylation in a fraction of promoters and regulatory elements, including at genes critical for meiosis/spermatogenesis and several DMRs of maternally imprinted genes (Figure 5), and such hyper-methylation in promoters is correlated with the repression of associated genes (Figure 5). The observed

Figure 5. Comparison of the DNA Methylomes of GSCLCs and GSCs

- (A) The 5mC-level tracks across chromosome 1 in the indicated cell types (this study and Kobayashi et al., 2013; Kubo et al., 2015; Shirane et al., 2016). The distributions of CGIs, LADs, and genes are shown at the bottom. PSG, pro-spermatogonia; SG, spermatogonia.
- (B) Heatmap of the correlation coefficients among the indicated cells based on the 5mC levels of all promoters (left) or the 5mC levels of differentially methylated promoters (promoters with $\geq 25\%$ 5mC-level differences among GSCLCs/GSCs/ KIT (–) spermatogonia at P7; 2,706 promoters) (right). The color coding is as indicated.
- (C) (top) Pie graphs showing the numbers and percentages of differentially methylated promoters (down in GSCLCs: blue; up: orange) between each GSCLC line and the averages of two GSC lines among all promoters (23,444 promoters). (bottom) Bar graphs showing the overlap of differentially methylated promoters. The color coding is as indicated.
- (D) (left) Scatterplots for the relationship of gene-expression differences ($\log_2[\text{RPM}+1]$) with promoter 5mC-level differences (%5mC levels: gray, $<25\%$; pink, $\geq 25\%$) between GSCLC1 and the averages of two GSC lines. The numbers of the genes ($\log_2[\text{RPM}+1] > 4$ in at least one line) are indicated. (right) Boxplots [the averages (horizontal lines), 25th and 75th percentiles (boxes), and fifth and 95th percentiles (error bars)] of gene-expression differences ($\log_2[\text{RPM}+1]$) between each GSCLC line and the averages of two GSC lines of genes with promoter 5mC-level differences of $<25\%$ (gray) and of $\geq 25\%$ (red). The latter genes exhibited significant repression (*Mann-Whitney-Wilcoxon test, $p < 0.01$).
- (E) Promoter 5mC levels (%5mC) and expression levels ($\log_2[\text{RPM}+1]$) of the indicated genes in the indicated cell types. SDs of the two biological replicates are shown as bars for expression levels. *Statistically significant promoter 5mC-level (Welch's t test [paired], $p < 0.01$) or expression-level differences (Welch's t test [one sided], $p < 0.05$) between GSCLCs and GSCs.
- (F) Heatmap of the 5mC levels in the gametic DMRs of maternally or paternally imprinted genes in the indicated cell types. The color coding is as indicated.
- (G) Scatterplot comparisons of the 5mC levels in the indicated loci between GSCLCs and GSCs. The color coding is as indicated. *Statistically significant LINE1 5' UTR or IAP LTR 5mC-level differences (5' UTR or LTR with $\geq 50\%$ of 5mC levels, Welch's t test [paired], $p < 0.01$) between GSCLCs and GSCs. GSAT_MM, major satellites; SATMIN, minor satellites.

See also Figures S5 and S6 and Tables S2, S3, and S4.

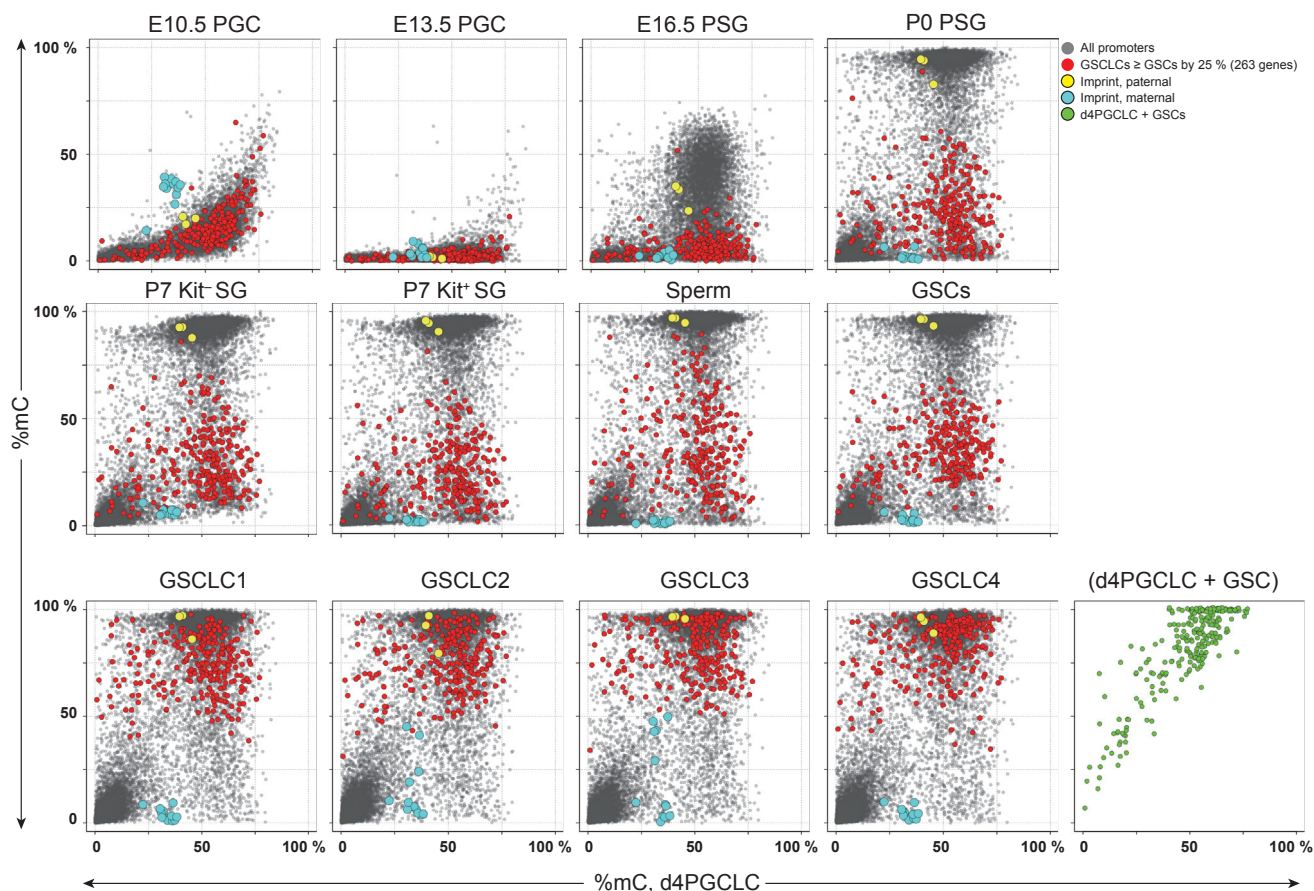


Figure 6. The 5mC-Level Dynamics during Male Germ Cell Development and GSCLC/GSC Derivation

Scatterplot comparisons of promoter 5mC levels between d4PGCLCs and the indicated cell types. Differentially methylated promoters between GSCLCs and GSCs ($\text{GSCLCs} - \text{GSCs} \geq 25\%$, Welch's t test [paired]: $p < 0.01$, 263 promoters) are highlighted by red dots. The simple sum of their levels in d4 PGCLCs and GSCs is shown by green dots (second row, right). The other color coding is as indicated.

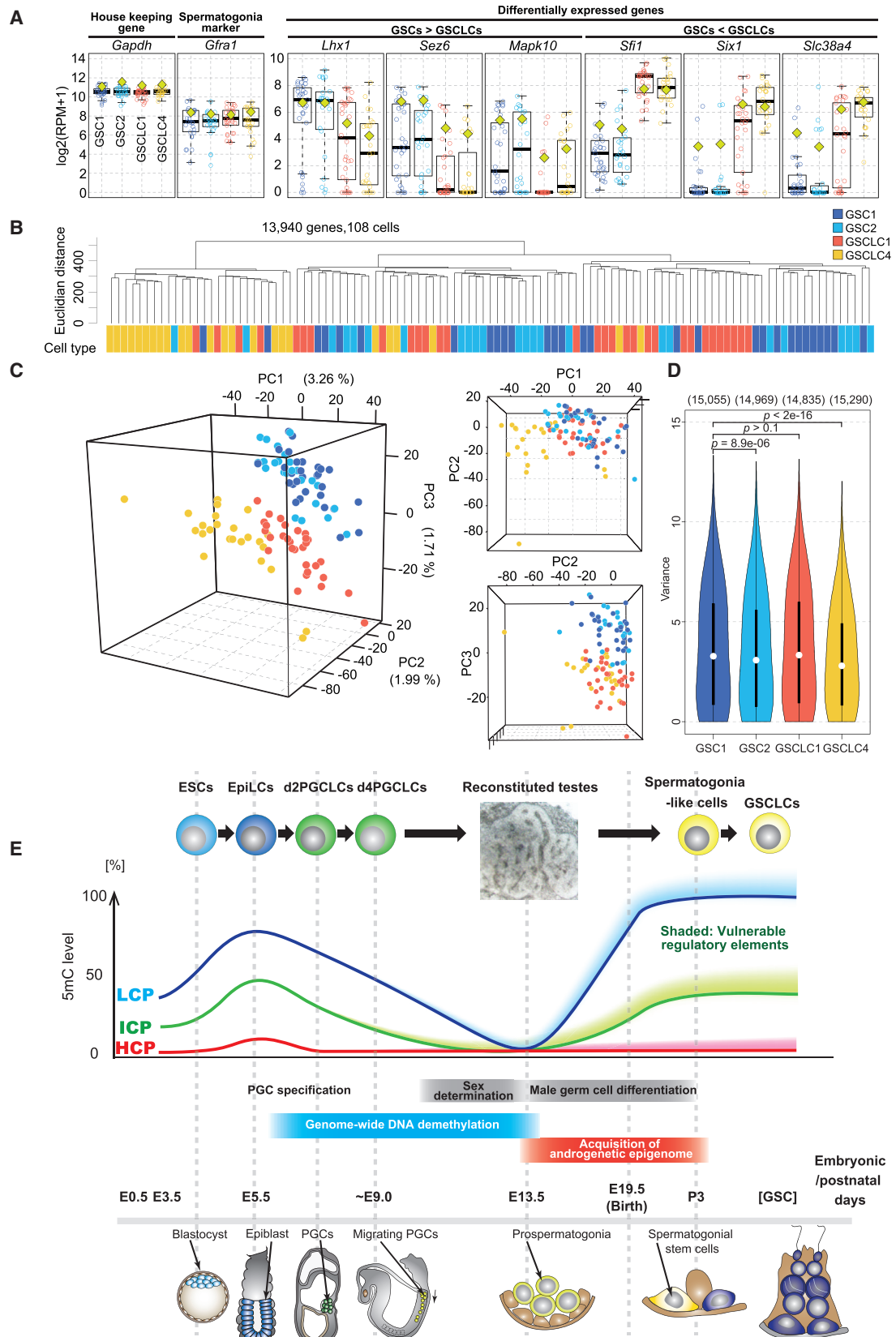
See also Figures S5 and S6.

hyper-methylation may be a combinatorial consequence of an incomplete genome-wide DNA demethylation and aberrant DNA methylation during differentiation of PGCLCs into spermatogonia-like cells in reconstituted testes (Figures 6 and 7E), the clarification of which warrants future investigation.

Despite partially aberrant epigenetic properties of GSCLCs (Figures 5 and 6), the offspring from spermatozoa derived from GSCLCs appeared grossly normal and fertile (Figure 3). Since GSCLCs bear a heterogeneity/clonality similar to GSCs (Figure 7), the spermatogenesis and subsequent embryogenesis following fertilization would be a process that tolerates, to some extent, the epigenetic abnormalities, including those in some imprinted genes, of the founding cell population. The mechanism by which epigenotypes that are compatible with normal development and physiology are segregated during spermatogenesis from GSCLCs requires further investigation, including genome-wide DNA methylation analyses of GSCLC-derived spermatocytes, spermatids, and spermatozoa, ideally at single-cell resolution. Alternatively, aberrant epigenotypes might be nullified by epigenetic reprogramming in pre-implantation development (Lee et al., 2014; Saitou et al., 2012). The

possibility that GSCLC-derived offspring bear certain abnormalities through trans-generational epigenetic inheritance (Heard and Martienssen, 2014) will also require rigorous investigation. Indeed, our system should serve as a unique basis for mechanistic studies on trans-generational epigenetic inheritance through the male germline.

In reconstituted ovaries, a majority of PGCLCs interact with ovarian somatic cells and exhibit robust proliferation, epigenetic reprogramming, and entry into meiosis (Hayashi et al., 2012; Hikabe et al., 2016), whereas in reconstituted testes, PGCLCs initially tended to cluster by themselves and only a fraction of them were successfully incorporated into seminiferous tubule-like structures to go on to form spermatogonia-like cells (Figures 1 and S1). Considering that genome-wide DNA demethylation in PGCLCs appears to be mediated largely through replication-coupled passive demethylation (Kagiwada et al., 2013; Seisenberger et al., 2012; Shirane et al., 2016; Yamaguchi et al., 2012), under the present conditions for reconstituted testes, an initial interaction of PGCLCs with testicular somatic cells for their appropriate proliferation for genome-wide DNA demethylation may not be optimal, and prior to such an event, signals



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reinforcing the androgenetic epigenome may be provided, resulting in the hyper-methylation of a fraction of key regulatory elements. Consistent with this idea, endogenous PGCs at E12.5, which have almost completed genome-wide DNA demethylation (Kobayashi et al., 2013; Seisenberger et al., 2012), underwent differentiation into PLZF (+) spermatogonia-like cells (and most likely into SCP3 (+) spermatocytes) more efficiently than PGCLCs (Figures 1 and S1). Thus, an improvement of culture conditions for reconstituted testes, e.g., by using an appropriate intermediate index for epigenetic reprogramming/proper male germ cell development, or separate culture for PGCLCs for the completion of genome-wide DNA demethylation combined with reconstituted testes, might lead to an induction of spermatogonia-like cells and GSCLCs with better function. Combined with an emerging system for ex vivo maturation of spermatogonia/SSCs into spermatozoa (Komeya et al., 2016; Sato et al., 2011), such improvements would lead to the production of spermatozoa from PSCs entirely in culture.

During the course of this study, it was reported that d6 PGCLCs—when co-cultured with cells dissociated from testes of neonatal *W/W^v* mice and provided with appropriate cytokines and hormones—entered into and then completed meiosis within 2 weeks and resultant spermatid-like cells contributed to apparently normal offspring (Zhou et al., 2016). Moreover, human fibroblasts were directly induced into haploid cells by over-expression of a combination of transcription factors (PRDM1, PRDM14), translational regulators (LIN28A, DAZL, DDX4) and a component of the synaptonemal complex (SCP3) (Medrano et al., 2016). Our study points to the importance of epigenetic regulation—i.e., genome-wide DNA demethylation followed by appropriate installment of the androgenetic epigenome—for the induction of PGCLCs into spermatogonia-like cells and GSCLCs with proper function. Thus, we consider that the epigenetic landscape of the cells reported in these studies (Medrano et al., 2016; Zhou et al., 2016) will require further investigation (Saitou and Miyauchi, 2016).

EXPERIMENTAL PROCEDURES

All animal experiments were performed under the ethical guidelines of Kyoto University. The experimental procedures for animals, fluorescence-activated Cell Sorting (FACS), magnetic-activated cell sorting (MACS), transplantation of PGCLCs and GSCLCs into testes, intra-cytoplasmic sperm injection (ICSI) and round spermatid injection (ROSI), histology and Immunofluorescence (IF) analysis, alkaline phosphatase (AP) staining, karyotype analysis, qPCR, combined bisulfite restriction analysis (COBRA), RNA-seq analysis, mapping reads of RNA-seq, and conversion to gene expression levels, data analysis of the RNA-seq, whole-genome bisulfite analysis (WGBS), processing, mapping and conversion of the data for bisulfite sequencing, annotation of promoters,

non-promoter CGIs, repetitive elements, and imprint DMRs, analysis of DNA methylation in single-copy genomic loci, promoters, and non-promoter CGIs, analysis of published WGBS data, and antibodies/primers/oligonucleotides used in this study are available in [Supplemental Experimental Procedures](#).

Culture of ESCs and Induction of PGCLCs

ESCs bearing the AAG transgenes (C57BL/6 × 129/SvJcl) (Ohta et al., 2000) were cultured in N2B27 medium with 2i (PD0325901: 0.4 μM [Stemgent]; CHIR99021: 3 μM [Stemgent]) and LIF (1,000 U/mL) on wells coated with poly-L-ornithine and laminin (20 ng/mL) (Hayashi et al., 2011; Hayashi and Saitou, 2013; Ying et al., 2008). Epiblast-like cells (EpiLCs) were induced from 1.0×10^5 ESCs on the wells of a 12-well plate coated with human plasma fibronectin (16.7 g/mL) in EpiLC medium (N2B27 containing activin A [20 ng/mL], bFGF [12 ng/mL], and knockout serum replacement [KSR] [1%] [Thermo Fisher Scientific]). The EpiLC medium was changed every day. PGCLCs were induced from 2.0×10^3 EpiLCs under a floating condition in a low-cell-binding U-bottom 96-well Lipidure-Coat Plate in PGCLC medium (GMEM [Invitrogen] with 15% KSR, 0.1 mM NEAA, 1 mM sodium pyruvate, 0.1 mM 2-mercaptoethanol, 100 U/mL penicillin, 0.1 mg/mL streptomycin, and 2 mM L-glutamine with BMP4 [500 ng/mL] [R&D Systems], LIF [1,000 U/mL] [Invitrogen], SCF [100 ng/mL] [R&D Systems], and EGF [50 ng/mL] [R&D Systems] for 4–6 days).

Generation and Culture of Reconstituted Testes

The d4 PGCLCs collected by FACS (10,000 cells/reconstituted testis) (see fluorescence-activated cell sorting) were aggregated with somatic cells of E12.5 gonads (ICR) collected by MACS (40,000 cells/reconstituted testis) (see magnetic-activated cell sorting) under a floating condition in a low-cell-binding U-bottom 96-well Lipidure-Coat Plate in α -Minimum Essential Medium (α -MEM) (Invitrogen) containing 10% KSR (37°C, 5% CO₂). After floating culture for 2 days, the aggregates were transferred to wells of a Falcon Permeable Support for 24-Well Plates with a 0.4 μm transparent PET membrane (Corning) using a glass capillary. Each well was supplemented with 350 μL of α -MEM-10%KSR for a gas-liquid interphase culture (Sato et al., 2011). The medium was changed every week.

Derivation of GSCLCs from Reconstituted Testes and of GSCs from Neonatal Testes

Reconstituted testes were soaked in the dissociation buffer (DMEM containing dispase [1 mg/mL] [Invitrogen] and hyaluronidase [1 mg/mL] [Sigma, H3506]) for 10 min and then incubated with 0.05% Trypsin-0.53 mM EDTA for 15 min with periodic pipetting (every 5 min), which was quenched in DMEM with 10% FBS, followed by dissociation into single cells by rigorous pipetting. The cell suspension was centrifuged at 1,200 rpm for 5 min and the supernatant was removed. The cell pellet was suspended in the GSC/GSCLC culture medium with growth factors (see below), and the cells were plated on a 0.1% (w/v) gelatin-coated culture plate (the cells/reconstituted testis were transferred to one 24-well plate). The somatic cells were removed as much as possible by repeated passages every 12 hr, as somatic cells bind more easily to the culture plate. After two or three passages, the remaining AAG (+) cells were transferred onto plates with MEFs in GSC/GSCLC medium with growth factors (see below). We noted that, when more than approximately 1×10^3 AAG (+) cells/well were plated, GSCLC colonies were expanded during the first 2 weeks. When GSCLC colonies of more than approximately 500 μm in diameter developed, they were passaged into a new well and the GSCLC lines were established after approximately 2 months. The control GSC lines were derived

Figure 7. Single-Cell Transcriptome Analyses of GSCLCs and GSCs

(A) Expression levels of the indicated genes in the indicated cell types analyzed at the single-cell (boxplots) or population (green squares) levels. 30 (GSCLC1), 24 (GSCLC4), 29 (GSC1), and 24 (GSC2) single cells were analyzed. In boxplots, the median (horizontal lines), 25th and 75th percentiles (boxes), and the outlier points (>2 SDs, error bars), and the values for each cell are indicated.

(B and C) UHC (B) and PCA (C) of single-cell transcriptomes of GSCLCs and GSCs. The color coding is as indicated.

(D) The distributions of the variances of the expression levels of individual genes (numbers indicated) among indicated single cells. The differences of the variance distributions compared to those of GSC1 are analyzed by Kruskal-Wallis test followed by Bonferroni correction and the p values are shown.

(E) A model for the relationship between male germ cell development in vivo and in vitro, with reference to DNA methylation reprogramming/programming in promoters.

See also [Figure S7](#) and [Table S5](#).

from neonatal testes at P7 (129/Sv × C57BL/6 with AAG) by using essentially the same procedure.

The medium for GSCs/GSCLCs culture was as described in Kanatsu-Shinohara et al. (2003) with some modifications: StemPro-34 SFM (Invitrogen) was supplemented with StemPro supplement (Invitrogen), 1% FBS, 1 × Gluta-MAX-II (Invitrogen), 1 × minimal essential medium (MEM) Vitamin Solution (Sigma), 5 mg/mL AlbuMAX-II (Invitrogen), 5 × 10⁻⁵ M 2-mercaptoethanol, 1 × MEM nonessential amino acid solution (Invitrogen), 30 µg/mL pyruvic acid, 1 × ITS-G (Invitrogen), 100 U/mL penicillin, 0.1 mg/mL streptomycin, and growth factors (recombinant rat GDNF [10 ng/mL] [R&D Systems], human bFGF [10 ng/mL] [Invitrogen], LIF/ESGRO [10³ U/mL] [Invitrogen], and mouse EGF [20 ng] [Invitrogen]).

ACCESSION NUMBERS

The accession numbers for the RNA-seq data of GSC1, 2 and GSCLC1–4, the SC3-seq data of GSC1, 2, GSCLC1 and 4, the WGBS data of GSC1 and GSCLC1–3, and the WGBS data of GSC2 and GSCLC4 reported in this paper are NCBI GEO: GSE76245, GSE87341, DDBJ: DRA004241, and DRA005141, respectively.

SUPPLEMENTAL INFORMATION

Supplemental Information includes Supplemental Experimental Procedures, seven figures, and five tables and can be found with this article online at <http://dx.doi.org/10.1016/j.celrep.2016.11.026>.

AUTHOR CONTRIBUTIONS

Y.I. conducted all the experiments and analyzed the data. Y.Y. contributed to the analyses of RNA-seq/SC3-seq/WGBS data. H.O. and K.H. assisted in the PGCLC induction, reconstituted testes formation, and GSCLC derivation. T.N. and I.O. contributed to the SC3-seq. K.K., K.S., and H.S. contributed to the WGBS, and T.Y. contributed to the RNA-seq/SC3-seq. M.S. conceived the project, and Y.I. and M.S. designed the experiments and wrote the manuscript.

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Cell Reports, Volume 17

Supplemental Information

In Vitro Derivation and Propagation of Spermatogonial Stem Cell Activity from Mouse Pluripotent Stem Cells

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Inventory of Supplemental Information

SUPPLEMENTAL FIGURES (Figure S1-Figure S7)

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SUPPLEMENTAL EXPERIMENTAL PROCEDURES

SUPPLEMENTAL REFERENCES

Figure S1, related to figure 1, Ishikura et.al.

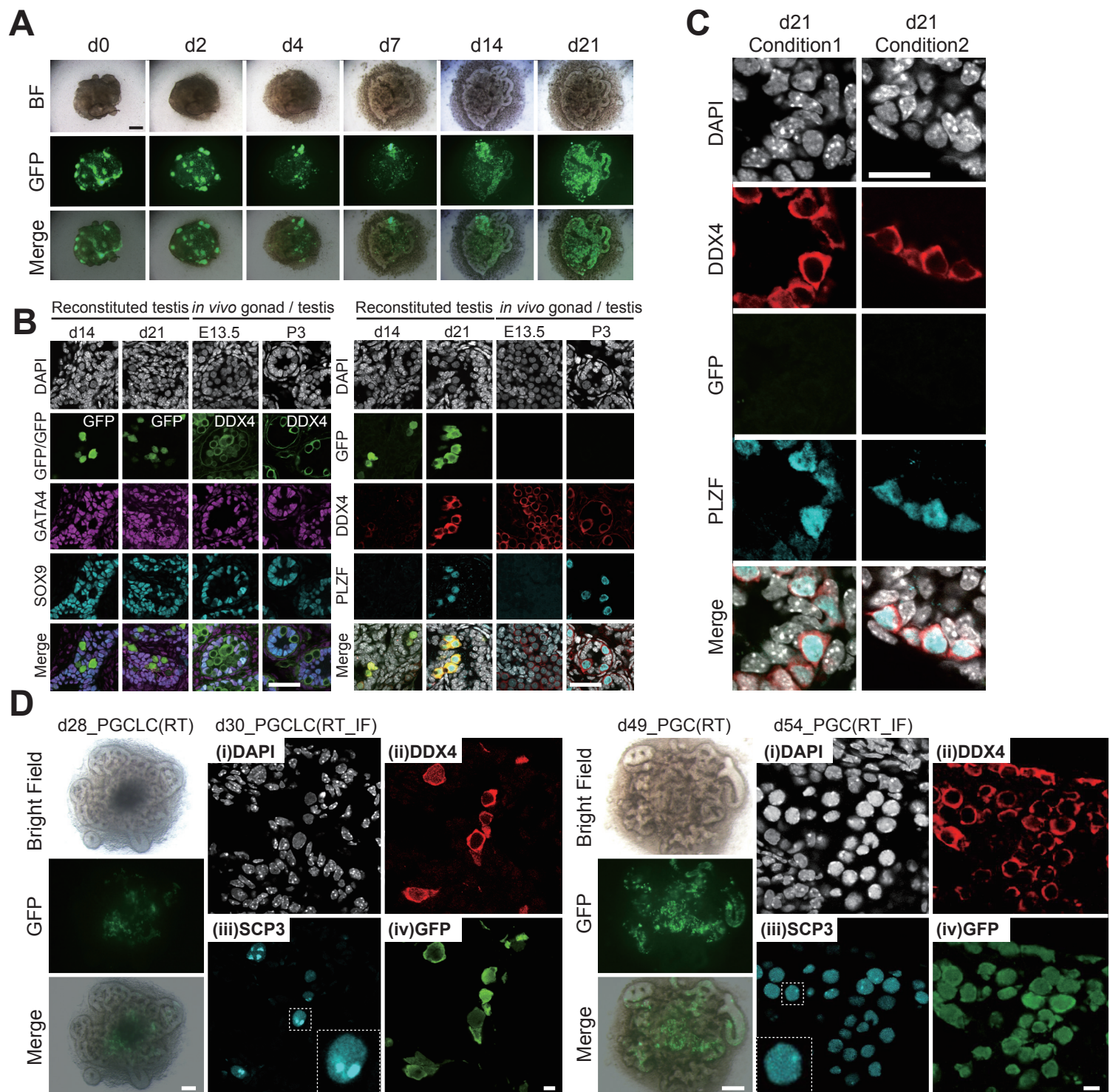


Figure S1. Reconstituted Testes In Vitro, Related to Figure 1

(A) Representative images of the development of reconstituted testes during the three weeks under condition 1. Bright field images (BF, top), GFP fluorescence by AAG (middle), and their merges (bottom) are shown. Bar, 200 μ m.

(B) IF analyses for the expression of GATA4 and SOX9 (left) or DDX4 and PLZF (right) in reconstituted testes at d14 and d21 (condition 1) or in testes at E13.5 and postnatal day (P) 3 as indicated. Bars, 50 μ m. PGCLC-derived cells and endogenous germ cells are identified by GFP and DDX4, respectively (second rows). DAPI staining and merges are shown at the top and bottom rows, respectively.

(C) IF analyses for the expression of DDX4 and PLZF in reconstituted testes at d21 [condition 1 (left) and 2 (right)]. Endogenous germ cells are identified as GFP (-)/DDX4 (+) cells. DAPI staining and merges are shown at the top and bottom rows, respectively. Bars, 50 μ m.

(D) Prolonged cultures of reconstituted testes with AAG (+) PGCs in vivo (condition 1). (left) Morphology of a reconstituted testis cultured for 49 days. Bright field images (BF), GFP fluorescence by AAG, and their merges (bottom) are shown. Bar, 200 μ m. (right) IF analyses for the expression of DDX4 (ii), SCP3 (iii), and GFP (iv) of a section of a reconstituted testis cultured for 54 days are shown with DAPI (i). Bar, 10 μ m.

Figure S2, related to figure 2, Ishikura et.al.

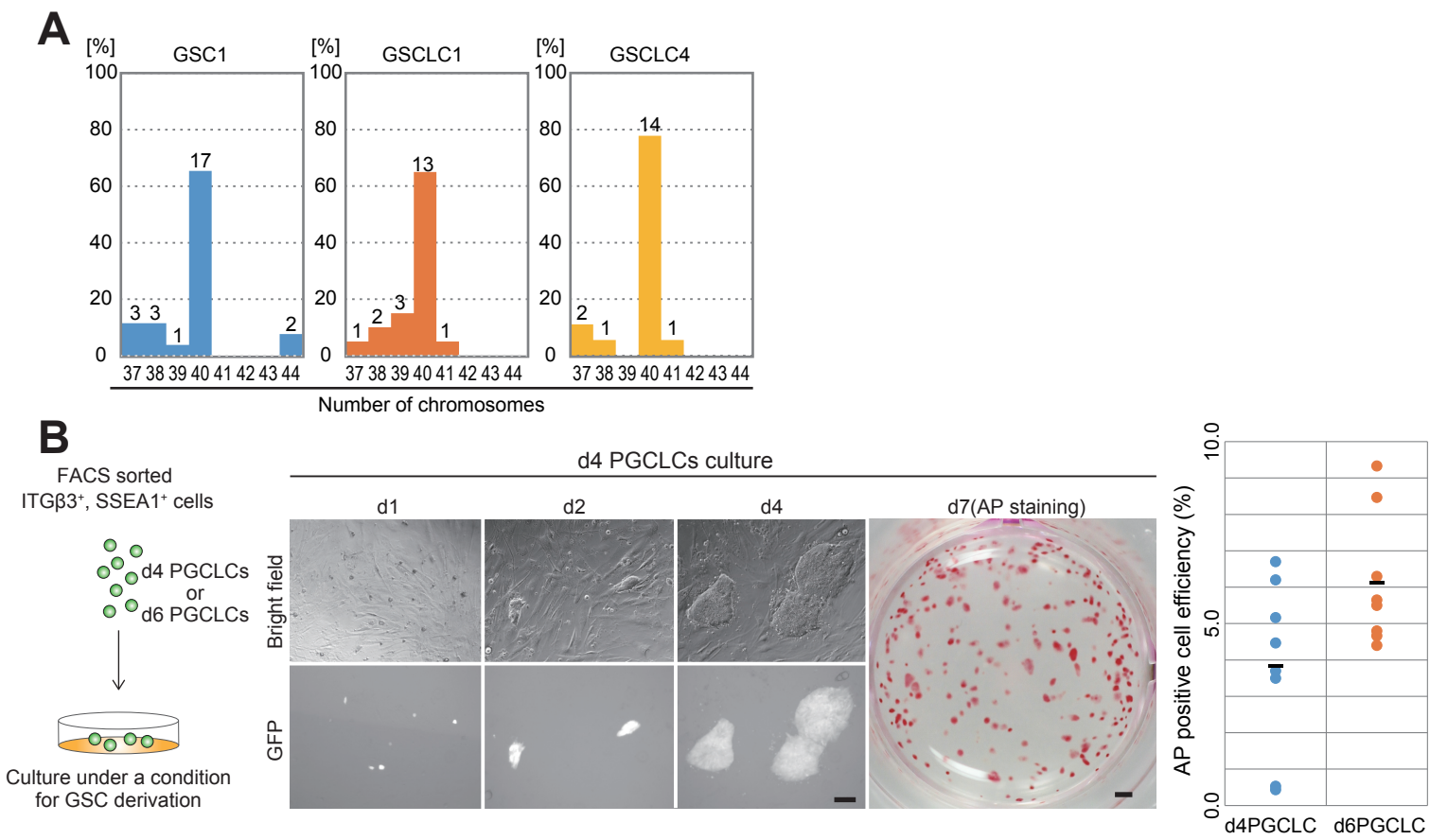


Figure S2. Germline Stem Cell-like Cells (GSCLCs) from Reconstituted Testes, Related to Figure 2

(A) Karyotype analyses of GSC1, GSCLC1, and GSCLC4.

(B) (left) Scheme for culture of d4 PGCLCs directly under the GSC-derivation condition. (middle) Bright field (top) or GFP (AAG) fluorescence (bottom) images of d4 PGCLC cultures under the GSC derivation condition for one, two, and four days. Bar, 100 μ m. An image with alkaline phosphatase (AP) staining of a representative 24-well is shown on the right. Bar, 1 mm. (right) The efficiencies for the derivation of AP-positive colonies from d4 or d6 PGCLCs cultured under GSC derivation conditions. The averages are indicated as bars. 1,000~3,000 PGCLCs were plated in each well and the numbers of AP-positive colonies were counted at d7.

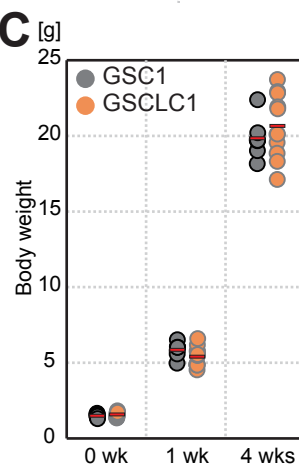
A

GSCLC line	Origin of PSCs	Derivation Condition	No. of transplanted cells / testis	Recipient (weeks)	No. of testes transplanted	No. of testes showing colonies	No. of testes showing spermatogenesis
GSCLC1	AAG ESC	Condition1	2.5x10 ⁵	W/W ^Y (8wks)	6	6	6
GSCLC2	AAG ESC	Condition2	2.5x10 ⁵	W/W ^Y (8wks)	6	6	5
GSCLC3	AAG ESC	Condition2	2.5x10 ⁵	W/W ^Y (8wks)	6	6	5
GSCLC4	AAG ESC	Condition1	2.5x10 ⁵	W/W ^Y (8wks)	4	4	0
GSCLC5	AAG ESC	Condition1	2.5x10 ⁵	W/W ^Y (8wks)	4	4	0
GSCLC6	AAG ESC	Condition1	2.5x10 ⁵	W/W ^Y (8wks)	4	4	0
GSCLC7	AAG ESC	Condition1	2.5x10 ⁵	W/W ^Y (8wks)	4	4	0
GSCLC8	AAG ESC	Condition1	2.5x10 ⁵	W/W ^Y (8wks)	4	4	0
GSCLC9	AAG ESC	Condition1	2.5x10 ⁵	W/W ^Y (8wks)	3	3	0
GSCLC10	AAG ESC	Condition1	2.5x10 ⁵	W/W ^Y (8wks)	14	14	0
GSCLC11	AAG ESC	Condition1	2.5x10 ⁵	W/W ^Y (8wks)	12	12	0
GSCLC12	AAG ESC	Condition2	2.5x10 ⁵	W/W ^Y (8wks)	4	4	0
GSCLC13	AAG ESC	Condition2	2.5x10 ⁵	W/W ^Y (8wks)	3	3	0
GSCLC14	AAG ESC	Condition2	2.5x10 ⁵	W/W ^Y (8wks)	3	3	0
GSCLC15	AAG ESC	Condition2	2.5x10 ⁵	W/W ^Y (8wks)	4	4	0

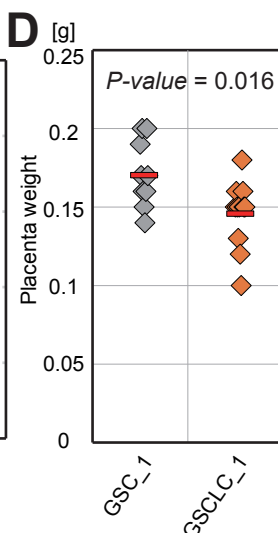
B

GSCLC line	Colony types	No. of transplanted testes				Total	Percentage of colonies with spermatogenesis
		1	2	3	4		
GSCLC1	colonies with spermatogenesis	15	11	5	3	34	
	colonies without spermatogenesis	53	40	32	26	151	18.4%
GSCLC2	colonies with spermatogenesis	2	1	3	—	6	
	colonies without spermatogenesis	5	11	14	—	30	16.7%
GSCLC3	colonies with spermatogenesis	13	6	1	4	24	
	colonies without spermatogenesis	63	12	7	14	96	20.0%

C



D



E

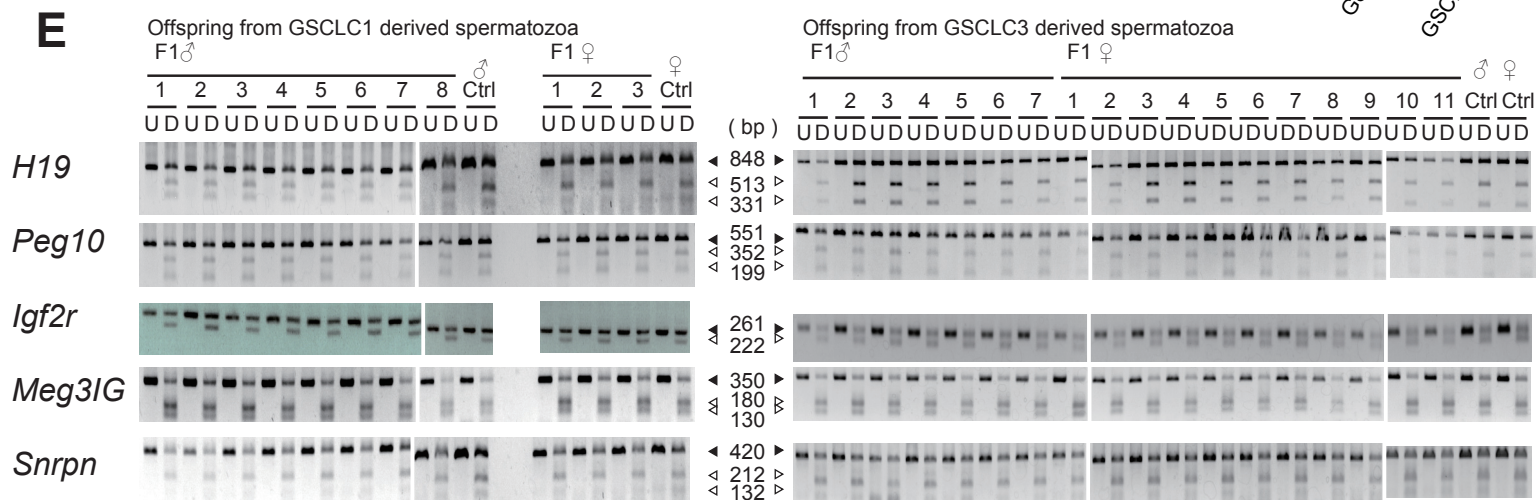


Figure S3. Spermatogenesis and Offspring from GSCLCs, Related to Figure 3

(A) Transplantation into adult testes and spermatogenesis of 15 lines of GSCLCs derived from reconstituted testes under condition 1 or 2.

(B) Numbers of colonies with or without spermatogenesis in testes transplanted with GSCLC1, 2, and 3.

(C, D) Body weights (C) and placenta weights (D) of offspring derived from GSCLC1 and GSC1. *p*-value was obtained by Student *t*-test.

(E) Combined bisulfite restriction analysis (COBRA) of the imprints of the offspring derived from spermatozoa from GSCLC1 and 3.

Methylation states of key CpGs of *H19*, *Peg10*, *Igf2r*, *Meg3/IG*, and *Snrpn* were analyzed as reported previously (Lee et al., 2009)

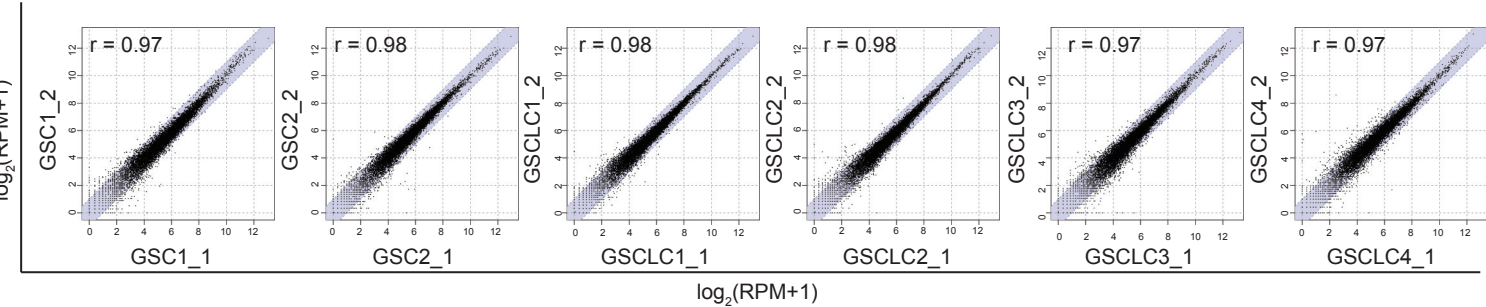
(EXPERIMENTAL PROCEDURES). U: undigested; D: digested with the respective enzyme. Lengths of the undigested (black triangles) and digested (white triangles) fragments are indicated. Note that all the offspring derived from spermatozoa from GSCLC1 and 3 exhibited apparently normal imprinting patterns.

Figure S4, related to figure 4,6, Ishikura et.al.

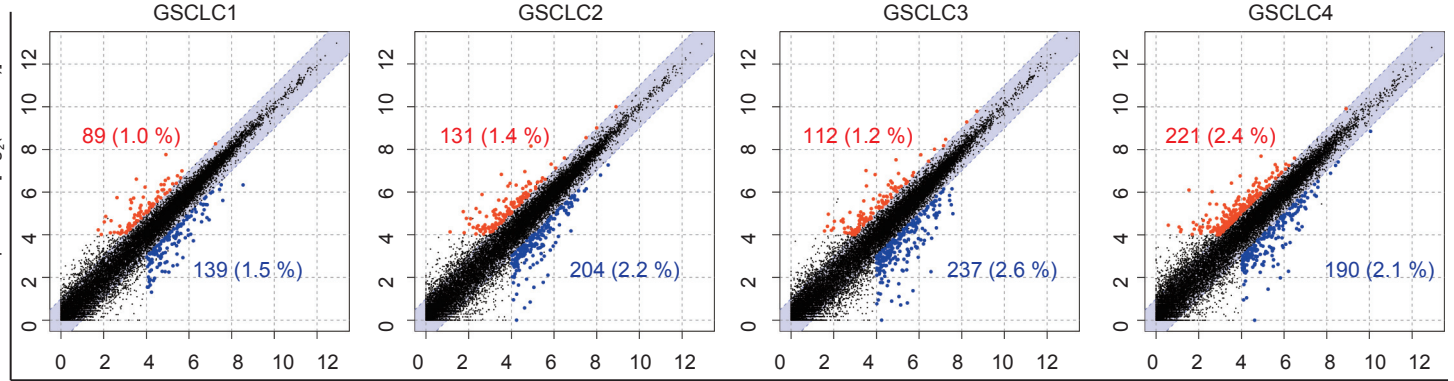
A

GSM_id	Sample name	Passage#	Total read	SC3seq mapped	Others	ERCC	Poly-A	Unmapped
GSM1977552	GSC1_1	8	5,093,243	3,067,893 (60.2%)	800,045 (15.7%)	59,531 (1.2%)	115,576 (2.3%)	1,002,857 (19.7%)
GSM1977553	GSC1_2	9	8,768,887	4,644,183 (53.0%)	1,333,445 (15.2%)	86,014 (1.0%)	476,656 (5.4%)	2,182,536 (24.9%)
GSM1977554	GSC2_1	8	7,200,089	4,062,641 (56.4%)	1,129,122 (15.7%)	81,123 (1.1%)	321,903 (4.5%)	1,574,943 (21.9%)
GSM1977555	GSC2_2	9	6,464,551	3,919,349 (60.6%)	1,070,682 (16.6%)	69,576 (1.1%)	128,804 (2.0%)	1,237,612 (19.1%)
GSM1977556	GSCLC1_1	8	6,369,999	3,504,814 (55.0%)	855,592 (13.4%)	73,602 (1.2%)	299,102 (4.7%)	1,598,123 (25.1%)
GSM1977557	GSCLC1_2	9	7,065,141	4,230,229 (59.9%)	1,025,531 (14.5%)	77,966 (1.1%)	293,314 (4.2%)	1,429,095 (20.2%)
GSM1977558	GSCLC2_1	11	7,874,306	3,988,497 (50.7%)	1,049,438 (13.3%)	82,943 (1.1%)	573,328 (7.3%)	2,151,435 (27.3%)
GSM1977559	GSCLC2_2	12	6,922,939	3,833,269 (55.4%)	1,013,816 (14.6%)	64,165 (0.9%)	302,509 (4.4%)	1,661,290 (24.0%)
GSM1977560	GSCLC3_1	9	6,028,957	3,537,311 (58.7%)	957,608 (15.9%)	82,518 (1.4%)	184,935 (3.1%)	1,238,496 (20.5%)
GSM1977561	GSCLC3_2	9	6,548,875	3,709,926 (56.6%)	941,264 (14.4%)	79,641 (1.2%)	253,522 (3.9%)	1,507,637 (23.0%)
GSM1977562	GSCLC4_1	8	6,817,572	3,992,078 (58.6%)	883,672 (13.0%)	57,408 (0.8%)	231,434 (3.4%)	1,600,148 (23.5%)
GSM1977563	GSCLC4_2	8	4,782,385	3,031,705 (63.4%)	675,155 (14.1%)	47,017 (1.0%)	91,420 (1.9%)	904,356 (18.9%)

B



C



D

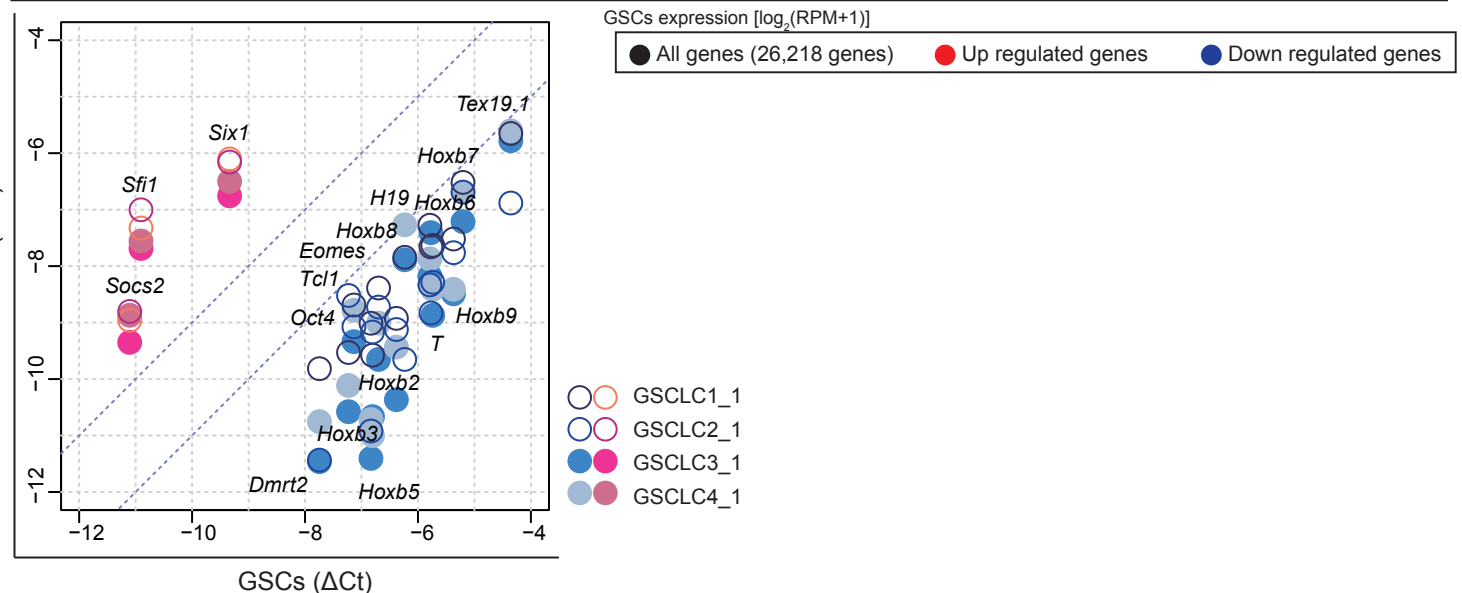


Figure S4. Transcriptome Analyses of GSCLCs and GSCs, Related to Figure 4, 6

(A) Statistics of RNA-seq analyses of GSCLCs and GSCs.

(B) Scatter-plot analyses of the RNA-seq data [$\log_2(\text{RPM}+1)$] of the experimental replicates of the indicated samples. Correlation coefficients (R) are shown in the top-left corner of each plot. The blue-shaded areas indicate expression-level ranges within 2-fold differences between the replicates.

(C) Scatter-plot representations of differentially expressed genes (DEGs) between each GSCLC line (GSCLC1-4) and the averaged values of GSC1 and 2. The blue-shaded areas indicate expression-level ranges within 2-fold differences in each comparison and the genes up/down-regulated in GSCLCs are plotted (numbers indicated) in red and blue, respectively.

(D) Validation by qPCR of the expression levels of representative DEGs identified by the RNA-seq analyses in GSCLCs (GSCLC1-4) and GSCs (the averaged values of GSC1 and 2). For each gene, the ΔCt from the average Ct values of the two independent housekeeping genes *Arbp* and *Ppia* (set as 0) was calculated and plotted. The color coding is as indicated.

Figure S6, related to figure 5,6, Ishikura et.al.

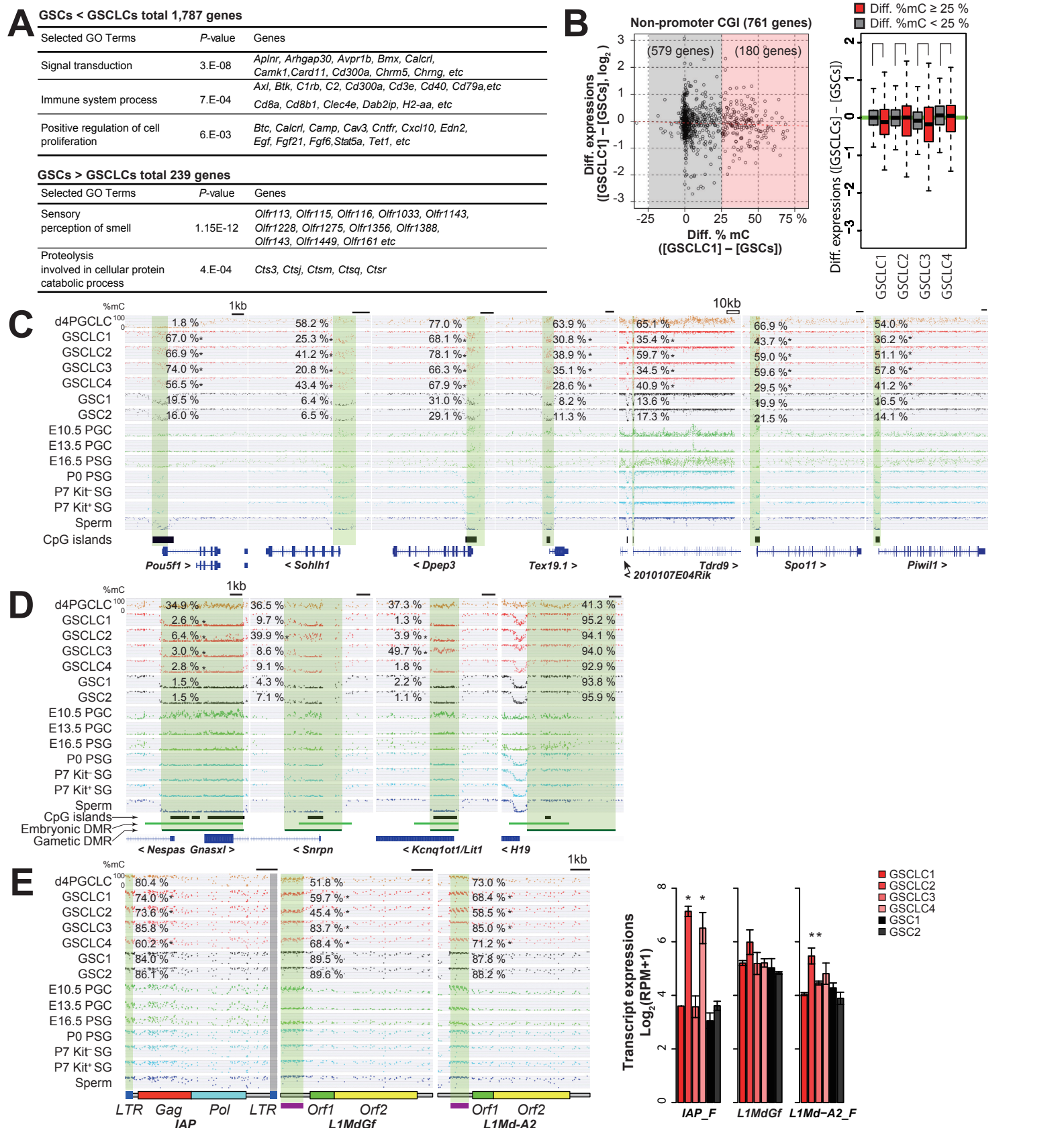


Figure S6. Differentially Methylated Genes between GSCLCs and GSCs, Related to Figure 5, 6

(A) The GO enrichments of genes in which promoters/non-promoter CGIs showed an increase (top) or a decrease (bottom) of 5mC levels by $\geq 25\%$ in GSCLCs as compared to GSCs. Selected genes are listed.

(B) (left) Scatter plots for the relationship of gene-expression differences [$\log_2(\text{RPM}+1)$] with non-promoter CGI 5mC-level differences (%5mC levels: grey, < 25%; pink, $\geq 25\%$) between GSCLC1 and the averages of two GSC lines. The numbers of the genes [$\log_2(\text{RPM}+1) > 4$ in at least one line] are indicated. (right) Box plots [the averages (horizontal lines), 25th and 75th percentiles (boxes), and 5th and 95th percentiles (error bars)] of gene-expression differences [$\log_2(\text{RPM}+1)$] between each GSCLC line and the averages of two GSC lines of genes with non-promoter CGI 5mC-level differences of < 25% (grey) and of $\geq 25\%$ (red). There is no correlation between gene-expression level differences and non-promoter CGI 5mC-level differences (Mann-Whitney-Wilcoxon test, $p < 0.01$).

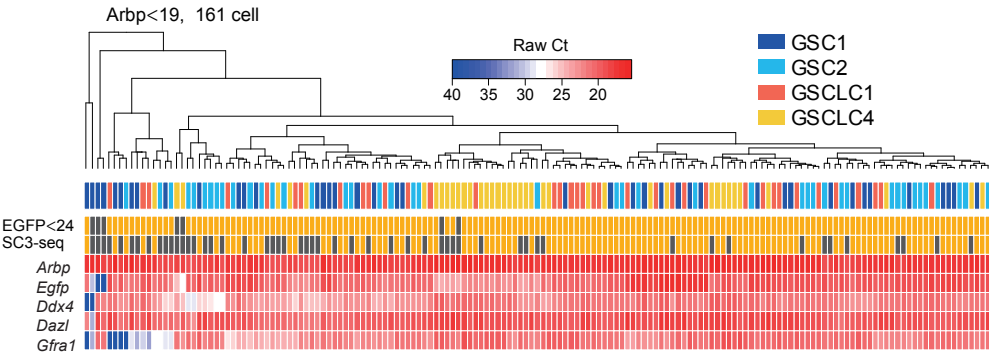
(C-E) The 5mC-level tracks around the indicated key genes (C: genes shown in Figure 5E; D: imprinted genes; E: transposons) in PGCs, male germ cells (Kobayashi et al., 2013; Kubo et al., 2015), d4 PGCLCs (Shirane et al., 2016), GSCLCs and GSCs are shown. (E, right) Expression levels [$\log_2(\text{RPM}+1)$] of the indicated transposable elements in the indicated cell types quantified by the RNA-seq. In (C), (D), (E, left), * denotes statistically significant 5mC-level differences compared to both GSC1 and 2 [Welch's t -test (paired), $p < 0.01$]. In (E, right), * indicates statistically significant gene-expression level differences compared to both GSCs [Welch's t -test (one sided), $p < 0.05$]. SDs of the two biological replicates are shown as bars for expression.

Figure S7, related to figure 7, Ishikura et.al.

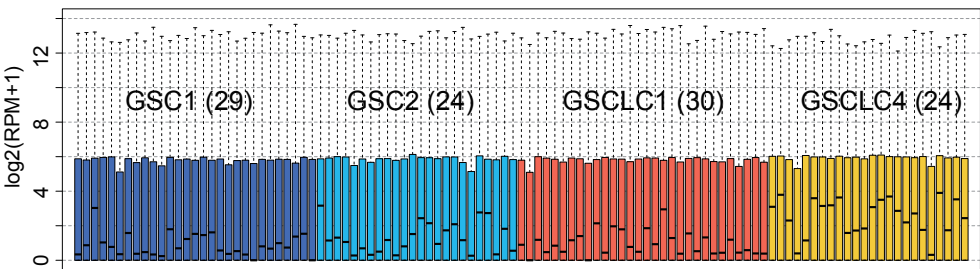
A

Cell line	Passage#	Cell number	All	Arbp<19	Arbp<19 GFP<24	SC3-seq
GSC1	P11		60	41	38	30
GSC2	P11		54	43	43	24
GSCLC1	P10		60	40	37	30
GSCLC4	P9		60	40	36	24
Total			234	161	154	108

B



C



D

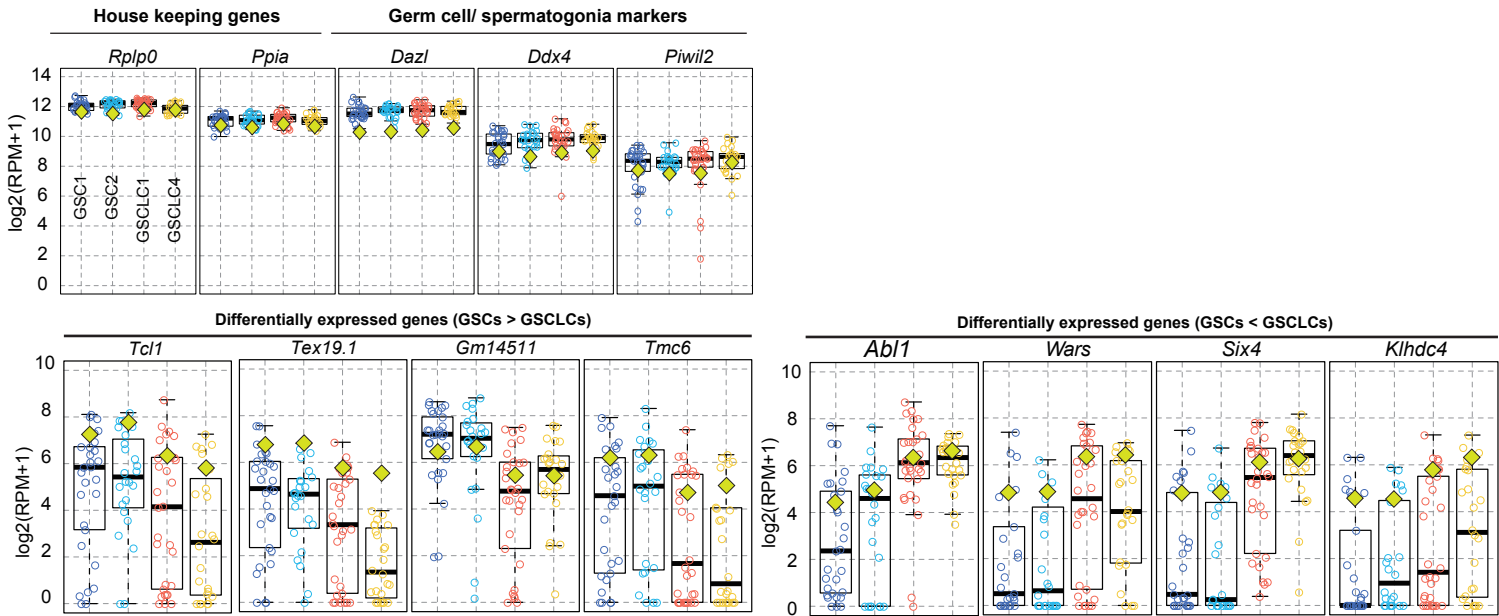


Figure S7. Single-cell Transcriptome Analyses of GSCLCs and GSCs, Related to Figure 7

(A) Statistics of single-cell analyses of GSCLCs (GSCLC1 and 4) and GSCs (GSC1 and 2). The numbers of single-cell cDNAs generated (All), of those with the Ct values by qPCR of *Arbp* <19, of those with the Ct values by qPCR of *EGFP* <24, of those of the SC3-seq libraries prepared, and of those run by SC3-seq analyses for each line are indicated.

(B) UHC by the Ct values by qPCR of *Arbp*, *EGFP*, *Ddx4*, *Dazl*, *Gfra1* of single-cell cDNAs of GSCLC1 and 4, and GSC1 and 2. The color coding is as indicated.

(C) Box plots [the median (horizontal lines), 25th and 75th percentiles (boxes), and the outlier points (> 2SDs, error bars)] of gene-expression levels [$\log_2(\text{RPM}+1)$] in single-cell cDNAs of GSCLC1 and 4, and GSC1 and 2.

(D) Expression levels of the indicated genes in the indicated cell types analyzed at the single-cell (box plots) or population (green squares) levels. 30 (GSCLC1), 24 (GSCLC4), 29 (GSC1), and 24 (GSC2) single cells were analyzed. In box plots, the median (horizontal lines), 25th and 75th percentiles (boxes), and the outlier points (> 2SDs, error bars), and the values for each cell are indicated.

SUPPLEMENTARY TABLES

TABLE S1. Gene Ontology for Genes Differentially Expressed between GSCLCs and GSCs, Related to Figure 4

TABLE S2. Genes Bearing Differentially Methylated Promoters or Non-promoter CGIs between GSCLCs and GSCs, Related to Figure 5, 6

TABLE S3. Gene Ontology for Genes Bearing Differentially Methylated Promoters or Non-promoter CGIs between GSCLCs and GSCs, Related to Figure 5

TABLE S4. Genomic Coordinates and Statistics of the Loci Analyzed in This Study, Related to Figure 5, 6

TABLE S5. Summary of the Samples for SC3-seq, Related to Figure 7.

SUPPLEMENTAL EXPERIMENTAL PROCEDURES

Animals

All animal experiments were performed under the ethical guidelines of Kyoto University. The *Acro/Act-EGFP* (AAG) transgenic mice (a gift of M. Okabe) (Nakanishi et al., 1999; Okabe et al., 1997) were maintained on a largely C57BL/6 background. W/W^v (WB×C57BL/6), BDF1 (C57BL/6×DBA/2), ICR, and 129/SvJcl mice were purchased from SLC (Hamamatsu, Japan). Noon of the day when a copulation plug was identified was designated as embryonic day (E) 0.5.

Fluorescence-activated Cell Sorting (FACS)

The aggregates containing d4 PGCLCs were washed with PBS and were dissociated into single cells by treating with 0.05% Trypsin-0.53 mM EDTA for 7 min, which was quenched by DMEM with 10% FBS, followed by pipetting. The cell suspension was passed through a nylon cell strainer (40 µm in diameter) to remove the cell clumps. The flow-through cells were centrifuged at 1200 rpm for 5 min and the supernatant was removed. The cell pellet was suspended by PBS containing 0.1% bovine serum albumin (BSA) (Thermo Fisher Scientific, San Diego, CA), and the cells were incubated with anti-INTEGRINβ3 antibody (BioLegend) and anti-SSEA1 antibody (eBioscience) conjugated with PE and Alexa Fluor 647, respectively, for 15 min on ice. After washing with PBS-0.1% BSA, the cells were suspended with the same buffer (1×10^6 cells/ml) and were sorted on a flow cytometer (AriaIII: BD Biosciences).

For the analyses of the expression of surface markers for GSCLCs/GSCs, GSCLCs/GSCs were dissociated into single cells by treating with 0.05% Trypsin-0.53 mM EDTA for 4 min, which was quenched by DMEM with 10% FBS, followed by pipetting. The cell suspension was centrifuged at 1,200 rpm for 5 min and the supernatant was removed. The cell pellet was suspended in PBS containing 0.1% BSA (approximately 1×10^6 cells were suspended in 200 µl of PBS-0.1% BSA). A half volume of the suspension was stained with primary antibodies (**Antibodies**) for 15 min on ice. The remaining half was used to establish the unstained controls. After being washed with PBS-0.1%BSA, each suspension was stained with secondary antibodies (**Antibodies**) for 15 min on ice. Then the cells were suspended with PBS-0.1%BSA and analyzed on a flow cytometer (AriaIII; BD Biosciences). The AAG (+) cells were sorted prior to use in all analyses.

Magnetic-activated Cell Sorting (MACS)

Male gonads at E12.5 were isolated in DMEM with 10% FBS, washed with PBS, and dissociated into single cells by 0.05% Trypsin-0.53 mM EDTA. The cell suspension was passed through a nylon cell strainer (70 µm in diameter) (Falcon) to remove the cell clumps. The flow-through cells were centrifuged at 1,200 rpm for 5 min and the supernatant was removed. The cell pellet was suspended in PBS containing 0.5% BSA and 2 mM EDTA, and the cell suspension was incubated with anti-SSEA1 antibody

conjugated with magnetic beads (Miltenyi Biotec, Bergisch, Gladbach, Germany) (**Antibodies**) on ice for 15 min. The cell suspension was washed with PBS-0.5%BSA-0.2 mM EDTA, and then applied to the MS column (Miltenyi Biotec). The flow-through cells, which were eliminated of most of the SSEA-1-positive PGCs, were washed by PBS-0.5%BSA-0.2 mM EDTA and suspended with α MEM-10%KSR for aggregation with PGCLCs for the generation of reconstituted testes.

Transplantation of PGCLCs and GSCLCs into Testes

GSCs and GSCLCs were dissociated into single cells by incubating with 0.05% Trypsin-0.53 mM EDTA for 4 min, which was quenched by DMEM with 10% FBS. The cell suspension was passed through a nylon cell strainer (40 μ m in diameter) (Falcon) to remove the cell clumps, the flow-through cells were centrifuged at 1,200 rpm for 5 min, the supernatant was removed, and the pellet was suspended in the GSC/GSCLC medium without growth factors at a concentration of 2.5×10^7 cells/ml. For transplantation of PGCLCs, 10,000 cells of d4 PGCLCs collected by FACS were suspended in 5 μ l of the GSC/GSCLC medium. Approximately 5 μ l of each donor cell suspension was injected by a pipette equipped with a syringe into the rete testes of adult WBB6F1 W/W^v (8-wks-old) recipients as described previously (Brinster and Avarbock, 1994; Brinster and Zimmermann, 1994). Transplanted testes were analyzed 8-10 weeks after transplantation.

Intra-cytoplasmic Sperm Injection (ICSI) and Round Spermatid Injection (ROSI)

Superovulation was induced in BDF1 females by injecting 5 IU equine chorionic gonadotropin, followed by a second injection of 5 IU human chorionic gonadotropin (hCG) 48 hrs later. At 12 hrs after hCG injection, cumulus-oocyte complexes were collected from the oviducts and oocytes were freed from cumulus cells by treating with 0.1% hyaluronidase. For ICSI, spermatozoa were injected into the cytoplasm of MII oocytes using a Piezo-actuated micromanipulator (Kimura and Yanagimachi, 1995). For ROSI, oocytes that received round spermatids were cultured in KSOM medium containing 5 mM SrCl₂ and 2 mM EGTA for 1 hr (Kishigami and Wakayama, 2007). Two-cell stage embryos after ICSI or ROSI were transferred to the oviducts of 0.5 dpc pseudopregnant ICR females with a standard procedure.

Histology and Immunofluorescence (IF) Analysis

For histological analyses, testes with transplanted cells were fixed with Bouin's fixative for 48 hrs, washed with 70% ethanol three times, dehydrated with a serial concentration of ethanol, and embedded in paraffin. The tissues were sectioned at a thickness of 7 μ m. After de-paraffinization with Xylene (three times) and a graded series of ethanol, the sections were stained with hematoxylin and eosin.

For IF analyses, reconstituted testes were fixed with 4% paraformaldehyde (PFA) on ice

for 2 hrs, washed with PBS three times, replaced with a serial concentration (15%, 30%) of sucrose solution, embedded in OCT compound (Sakura, Tokyo, Japan), frozen and then sectioned at a thickness of 10 μ m at -20°C . After air-drying, the sections were washed in PBS three times, incubated in the blocking buffer (PBS containing 5% BSA and 0.1% Triton X-100) for 30 min and then incubated in the staining buffer (PBS containing 1% BSA and 0.1% Triton X-100) containing primary antibodies (**Antibodies**) for 2 hrs at 4°C . After washing with PBS three times, the samples were incubated in the staining buffer containing secondary antibodies (**Antibodies**) and 1 $\mu\text{g/ml}$ of DAPI for 1 hr. The sections were washed three times in PBS and mounted in Vectashield mounting medium (Vector Laboratories). All samples were analyzed by a confocal microscope (Olympus FV1000).

For IF analyses of GSCs/GSCLCs, GSCs/GSCLCs cultured on coverslips were fixed with 3% PFA for 10 min at room temperature and then washed three times with PBS, followed by permeabilization with methanol at -30°C for 2 min. The samples were then washed twice with PBS, blocked with PBS containing 10% BSA for 30 min at room temperature, and incubated with a solution (PBS containing 0.1% BSA) containing a combination of primary antibodies (**Antibodies**) for 2 hrs at room temperature. The samples were then washed three times with PBS and incubated with a solution (PBS containing 0.1% BSA) containing a combination of primary antibodies (**Antibodies**) and 1 $\mu\text{g/ml}$ of DAPI for 1 hr. The sections were washed three times in PBS and mounted in Vectashield mounting medium (Vector Laboratories). All samples were analyzed by a confocal microscope (Zeiss LSM780).

Alkaline Phosphatase (AP) Staining

d4 PGCLCs cultured directly under the GSC culture condition were washed twice with PBS, and fixed with 4% paraformaldehyde on ice for 1 hr. After washing with PBS containing 0.1% Tween20 (PBST), colonies from d4 PGCLCs were incubated in the AP buffer at room temperature. The AP buffer was prepared by successively dissolving 5 mg of naphthol AS-MX phosphate disodium salt (Sigma) and 10 mg of Fast Red TR salt (Sigma) in 0.5 ml of N,N-dimethylformamide (Sigma) followed by filtration. The reaction was stopped at an appropriate time point by PBST.

Karyotype Analysis

GSCs/GSCLCs were cultured with medium containing 60 ng/ml of demecolcine (Sigma) for 6 hrs, and were dissociated into single cells by incubating in 0.05% Trypsin-0.53 mM EDTA for 4 min, which was quenched by DMEM with 10% FBS. The cells were then swollen with a hypotonic solution (75 mM KCL) and fixed by repeated treatment (three times) with Carnoy's fixative. The fixed cells were then spread on a glass slide (Matsunami) washed with ethanol and stained with DAPI. Karyotype images were obtained by analysis with a confocal microscope (Olympus FV1000), and the number of

chromosomes was counted.

qPCR

RNAs of GSCs/GSCLCs collected by FACS for AAG fluorescence were extracted and purified using an RNeasy Micro Kit (Qiagen, Hilden, Germany) according to the manufacturer's instruction. The purified total RNAs were reverse-transcribed by SuperscriptIII (Invitrogen) to generate the first-strand cDNAs, which were used for qPCR analysis with Power SYBER Green (ABI, Foster City, CA). The primer sequences used are listed in **Primers**.

Combined Bisulfite Restriction Analysis (COBRA)

COBRA was performed as described previously (Lee et al., 2009). GSCs/GSCLCs were collected by FACS for AAG fluorescence, and their genomic DNA as well as the tail genomic DNA of wild-type mice were extracted, and 2 µg of purified DNA from each sample was subjected to bisulfite treatment followed by purification with an Epitect Plus Bisulfite Kit (Qiagen) according to the manufacturer's instructions. The purified DNA was amplified by PCR under a protocol of 40 cycles of 96°C for 30 s, 60°C for 1 min, and 72°C for 1 min, using ExTaq (TakaRa). The PCR primer sequences used are listed in **Primers**. The amplified DNA was digested with the appropriate restriction enzymes (New England BioLabs)—PvuI-HF for *H19*, HhaI for *Peg10*, TaqαI for *Igf2r*, and AciI for *Meg3* IG and *Snrpn*—and the digested samples were resolved through electrophoresis in 2% or 3% agarose gels.

RNA-seq Analysis

For the population-level analyses, total RNAs of ESCs, EpiLCs, d4 and d6 PGCLCs [*Blimp1-mVenus* (+)], GSCs and GSCLCs (purified by FACS for AAG fluorescence) were extracted and purified using an RNeasy Micro Kit (Qiagen) according to the manufacturer's instructions. 1 ng of total RNAs from each sample was reverse-transcribed by SuperscriptIII (Invitrogen) to generate the first-strand cDNAs, which were applied to the RNA sequence analysis using the SOLiD 5500XL system (Thermo Fisher Scientific) as described previously (Nakamura et al., 2015).

For the single-cell analyses, GSCLCs/GSCs were incubated in 0.05% of Trypsin-0.53mM EDTA for around 4 min at 37°C, and dispersed into single cells in 1% (vol/vol) KSR/PBS (Thermo Fisher Scientific). The cDNA synthesis was performed according to the SC3-seq method described previously (Nakamura et al., 2015). The cDNA libraries for Nextseq500 (Illumina) were constructed based on the SC3-seq method with several modifications: Five nanograms of quality-checked cDNAs were added to the pre-amplification buffer [1 × ExTaq buffer [Takara Bio (RR006), Shiga, Japan], 0.2 mM of each dNTP [Takara Bio (RR006)], 0.01 µg/µl of the N-V3 (dT)24 primer (attachment of amine at the 5-prime end), 0.01 µg/µl of the V1(dT)24 primer and 0.025 U/ µl of

ExTaqHS [Takara Bio (RR006)]], and were amplified by four cycles of PCR. The surplus primers and PCR byproducts such as primer dimers were removed by three rounds of purification using a $0.6 \times$ volume of AMPureXP beads for each round [Beckman Coulter (A63881), Tokyo, Japan] according to the manufacturer's instructions. The purified cDNAs were diluted to 50 μ l by DDW and fragmented by shearing with Covaris E220 (duty factor: 20%; peak incident power: 175; cycles per burst: 200; duration: 60 s; an intensifier was installed in the case of E220) [Covaris, Woburn, MA, USA] and then end-polished in the End-polish buffer [$1 \times$ NEBnext EndRepair Reaction buffer [NEB (B6052S), Ipswich, MA, USA], 0.01 U/ μ l of T4 DNA polymerase [NEB (M0203)] and 0.033 U/ μ l of T4 polynucleotide kinase [NEB (M0201)]] for 30 min at 20°C. After incubation, a $0.7 \times$ volume of the AMPureXP was immediately added, the solution was mixed for more than 20 min and then the supernatant was transferred to a $0.9 \times$ volume of the AMPureXP reagent and the cDNAs were purified. Next, to provide the purified cDNAs with an Rd2SP-adaptor sequence, the cDNAs were incubated in 30 μ l of the Rd2SP adaptor extension buffer [$1 \times$ ExTaq Buffer, 0.23 mM of each dNTP, 0.67 μ M of the Rd2SP-V1(dT)20 primer, 0.033 U/ μ l of ExTaqHS] using the following thermal cycler program: 95°C for 3 min, 67°C for 2 min, and 72°C for 2 min. The reactions were terminated by chilling in an ice-block, and after the addition of 20 μ l of the Rd1SP-adaptor ligation buffer [a mixture of 10 μ l of $5 \times$ NEBNext Quick Ligation Reaction Buffer [NEB (B6058S)], 0.6 μ l of 5 μ M of the Pd1SP-T adaptor and 1 μ l of T4 ligase [NEB (M0202M)]]], the solution was incubated for 15 min at 20°C and for 20 min at 72°C. After two rounds of cDNA purification by adding a $0.8 \times$ volume of AMPure XP, the cDNAs were added into the final amplification buffer [$1 \times$ ExTaq buffer, 0.2 mM of each dNTP, 1 μ M of the S5XX index primer, 1 μ M of the N7XX index primer (HPLCpurified), 0.025 U/ μ l of ExTaqHS] and amplified by PCR using the following thermal cycler program: 95°C for 3 min, 55°C for 1 min, and 72°C for 1 min; followed by ten cycles of 95°C for 30 s, 60°C for 1 min and 72°C for 1 min; with a final extension of 72°C for 3 min. Finally, the cDNA libraries were purified two times by using a $0.9 \times$ volume of AMPureXP and dissolved in 30 μ l of TE buffer. The quality and quantity of the resultant library DNAs were evaluated by LabChip GX (Perkin Elmer), a Qubit dsDNA HS assay kit, and Taqman-qPCR assay using Thunderbird Probe qPCR mix (TOYOBO) and a TaqMan probe (Ac04364396; Applied Biosystems). The sequence data were acquired using a NextSeq 500 High output kit v2 75 cycle (Illumina). All the sequences of oligo DNAs used with the SC3-seq method are listed in Table S7.

Mapping Reads of RNA-seq and Conversion to Gene Expression Levels

All the read data were converted into expression levels as described previously (Nakamura et al., 2015). In brief, all reads were treated with cutadapt-1.3 (Martin, 2011) to remove V1 and V3 adaptor sequences and poly-A sequences. The resulting reads of 30-bp and longer were mapped onto the mm10 genome using tophat1.4.1/bowtie1.0.1 with the “-no-coverage-search” option (Kim et al., 2013). The mapped reads were then

converted to the expression level (RPM) using cufflinks-2.2.0 with the “-compatible-hits-norm,” “-no-length-correction,” “-max-mle-iterations 50000” and “library-type fr-secondstrand” options and mm10 reference gene annotations with up to 10-kb extension at the 3'-end.

Data Analysis of the RNA-seq

RNA-seq data analysis was performed using R software version 3.1.1 (2014-07-10) with the gplots, qvalue, amap, MASS, rgl, genefilter, and VennDiagram packages and EXCEL (Microsoft). The raw expression data were converted into $\log_2$ (RPM+1) values, and biological replicate data were averaged. We defined “all expressed genes” as genes whose $\log_2$ (RPM+1) values were > 4 (greater than ~ 10 –20 copies per cell, which is a lower limit for reliable and reproducible detection by our single-cell cDNA amplification method (Nakamura et al., 2015)) in at least one sample. Unsupervised hierarchical clustering (UHC) was calculated using the hclust function with Euclidian distance and the ward method (ward.D2). Principal components analysis (PCA) was calculated using the prcomp function with scaling. Differentially expressed genes (DEGs) were defined as those bearing both $\log_2$ (RPM+1) ≥ 4 and more than 2-fold changes of expression values between the averaged expression levels of GSCs and of every GSCLC. Gene Ontology analysis was performed using the DAVID database (<https://david.ncifcrf.gov/>) and the listed GO terms were the contents of the biological process (Huang da et al., 2009). For the analysis of the heterogeneities among GSCs and GSCLCs, the variances of the expression levels of individual genes among single cells from each line were calculated, and the significance of their differences was evaluated by Kruskal–Wallis test followed by Bonferroni correction using the kruskal.test and pairwise.wilcox.test functions.

Whole-genome Bisulfite Analysis (WGBS)

50 ng of genomic DNA spiked with 0.5 ng of unmethylated lambda phage DNA (Promega) was subjected to bisulfite conversions and library constructions for amplification-free whole-genome bisulfite sequencing analyses, using the post-bisulfite adaptor tagging (PBAT) method as described previously (Miura et al., 2012). Massively parallel sequencing was performed on an Illumina HiSeq 2500 (HCS v2.0.5, RTA v1.17.20) to generate 101-nucleotide single-end sequence reads. Cluster generation and sequencing were performed in single-read mode using the TruSeq SR Cluster Kit v3-cBot-HS and the TruSeq SBS Kit v3-HS (Illumina) according to the manufacturer's protocols.

Processing, Mapping and Conversion of the Data for Bisulfite Sequencing

For quality control of the data, we performed pre-mapping processing of the read sequences; we trimmed 4 bases from the 5' ends, 1 base at the 3' ends, low quality bases from the 3' ends (quality score < 20), and the adaptor sequences of the libraries, by using the TrimGalore program

(http://www.bioinformatics.babraham.ac.uk/projects/trim_galore/). We mapped the processed reads to the mouse reference genome (mm10) using the Bismark program with the “--pbat” option (Krueger and Andrews, 2011), and only uniquely mapped reads were used for the subsequent analyses. The numbers of converted/unconverted CpGs in both strands were combined to calculate methylation rates. Mapping reads on IAP (M17551), L1MdGf (D84391) and L1Md-A2 (M13002) were performed onto the sequences of these three genes separately. The basic mapping stats and conversion rates are listed in Figure S5A.

Annotation of Promoters, Non-promoter CGIs, Repetitive elements, and Imprint DMRs

Promoters are defined as regions between 900-bp upstream and 400-bp downstream of transcription start sites (TSSs). Non-promoter CGIs are defined as CGIs (Illingworth et al., 2010) that overlap with genes and that have no overlap with TSSs as defined above. Lamina-associated domains (LADs) (Peric-Hupkes et al., 2010) were annotated in mm9, and therefore converted to mm10 using the LiftOver tool from the UCSC genome browser. Detailed genomic loci for specific genes, imprint DMRs and repetitive elements are listed in Table S4. Gametic DMRs defined by Tomizawa et al. were used as imprint DMRs (Tomizawa et al., 2011).

Analysis of DNA Methylation in Single-copy Genomic Loci, Promoters, and Non-promoter CGIs

All the percent methylated cytosine (%mC) values were calculated from the average of CpGs, in which the read depth was between 4 and 200, except repetitive elements. For repetitive element analysis (IAP, L1MdGf and L1Md-A2), all CpGs with a read depth ≥ 4 were used for the %mC calculations. Visualization of CpG methylations was performed using R-3.2.2 and IGV-2.3.57 (Robinson et al., 2011). Gene ontology analysis was performed using the DAVID website (Huang et al., 2009).

Analysis of Published WGBS Data

The WGBS data for E10.5 PGCs, E13.5 PGCs and E16.5 PSG were obtained from Kobayashi et al. (Kobayashi et al., 2013) (DDBJ: DRA000607) and those for P0 PSG, P7_Kit⁻, P7_Kit⁺SG and adult sperm were obtained from Kubo et al. (Kubo et al., 2015) (DDBJ: DRA002477). All read data were processed, mapped and converted to %mC as described above. The RNA-seq data of ESCs, EpiLCs, d4 and d6 PGCLCs [BVSC (+)] were obtained from Sasaki et al. (Sasaki et al., 2015) (GEO: GSE67259).

Antibodies

The antibodies used in this study are listed below.

Name	Description	Company	Product #	Concentration	IF/FACS
Primary antibody					
GFP	Chicken polyclonal	Abcam [®]	CM-AB13970	1:500	IF
GFP	Rat monoclonal	Nacalai Tesque	04404-84	1:250	IF
SOX9	Rabbit polyclonal	MILLIPORE	ab5535	1:10000	IF
DDX4	Mouse monoclonal	Abcam [®]	ab27591	1:200	IF
SCP3	Mouse monoclonal	Abcam [®]	ab97672	1:500	IF
GFRa1	Goat polyclonal	R&D System	BAF560	1µg/ml	IF
GATA4	Goat polyclonal	Santa Cruz	sc-1237	1:100	IF
PLZF	Rabbit polyclonal	Santa Cruz	sc-22839	1:40	IF
ID4	Human polyclonal	Abnova	H00003400-B01P	1:200	IF
DAPI	—	WAKO	049-18801	1µg/ml	IF
Conjugated antibody					
CD49f(Itga6)-APC	Mouse/Human	Biolegend	313615	1:50	FACS
CD15(SSEA-1)-Alexa Fluor [®] 647	Mouse/Human	Biolegend	125607	1:20	FACS
CD9-APC	Mouse monoclonal	eBioscience [™]	17-0091	1:50	FACS
CD29(Itgβ1)-Alexa Fluor [®] 647	Hamster monoclonal	BD Pharmingen [™]	562153	1:50	FACS
CD117(KIT:2B8)-PE	Mouse monoclonal	Affymetrix eBioscience	17-1171-81	1:50	FACS
Primary antibody					
GFRa-1	Mouse monoclonal	R&D System	MAB560	25ng/ml	FACS
Isotype control					
PE Rat IgG2b κ	Rat polyclonal	Biolegend	400635	1:50	FACS
APC Rat IgG2a κ	Rat polyclonal	Biolegend	400511	1:50	FACS
Alexa Fluor647 Hamster IgM, λ1	Hamster polyclonal	BD Pharmingen [™]	562110	1:50	FACS
Secondary antibody Fluorescence					
Goat Anti-Chicken IgY	FITC	Abcam [®]	Ab46969	1:250	IF
Goat Anti-Rabbit IgG	Alexa Fluor [®] 568	Invitrogen	A11011	1:250	IF
Goat Anti-Mouse IgG	Alexa Fluor [®] 633	Invitrogen	A21052	1:250	IF/FACS
Donkey Anti-Chicken IgY	Alexa Fluor [®] 488	Abcam [®]	ab63507	1:250	IF
Donkey Anti-Rat IgG	Alexa Fluor [®] 488	ThermoFisher Scientific	A-21208	1:250	IF
Donkey Anti-Goat IgG	Alexa Fluor [®] 568	ThermoFisher Scientific	A-11057	1:250	IF
Donkey Anti-Rabbit IgG	Alexa Fluor [®] 647	ThermoFisher Scientific	A-31573	1:250	IF

Primers

The primers used in this study are listed below.

Forward	Reverse
qPCR	

<i>Arbp</i>	CAAAGCTGAAGCAAAGGAAGAG	AATTAAGCAGGCTGACTTGGTG
<i>Ppia</i>	TTACCCATCAAACCATTCCTTCTG	AACCCAAAGAACTTCAGTGAGAGC
<i>Oct4</i>	GATGCTGTGAGCCAAGGCAAG	GGCTCCTGATCAACAGCATCAC
<i>T</i>	ATCAGAGTCCTTTGCTAGGTAG	GTTACAATCTTCTGGCTATGC
<i>Dmrt2</i>	TAGACAGATGCGCAAAAGACCT	GCCCTTTACTGAGAGACGTGAG
<i>Sohlh1</i>	CCAGAGTTTAGTTTGCTGGGGA	ATACAAACTCCACTCACAGCCC
<i>H19</i>	TAAACCTCTTTGGCAATGCTGC	ATGGAAGTGTCTCCAGACTAGG
<i>Eomes</i>	ACTCACTGCCTTCAATTCCTTG	CCCTTTCTTCTGATCCTCCTG
<i>Ovol2</i>	GTGCCTTGAAATGCTTCCCAT	GAGAAGTTTCACACGAACATTTCATTTA
<i>Tcl1</i>	TGGCCTCACTAGAACAAGAGG	CTCGGTCAAGGATGGAAGC
<i>Tex19.1</i>	CGTGTCAGTGTTTCAGTGTTTG	GTCAACTAGTGCCTCAGAGTCC
<i>Hoxb2</i>	CCATCGACTTGCAGTTTCCCTA	ATGTATCCACGAGTGGAAGG
<i>Hoxb3</i>	GGTTGTTGTGTTTCTGTGTCATGT	AGGAGCTGAGTTCATGCCTTTT
<i>Hoxb5</i>	TATGGGGATAGTCTGGGTCAGG	CAGATTTACACGTAGCACAGC
<i>Hoxb6</i>	ACTTGATGTCTCCTGGAAGCAG	CGAATCTACCAITGAACCGTGC
<i>Hoxb7</i>	TGTAAGCCCTCTTTGAAGCTGT	TGCTACTGGGAAGTATGGGGTA
<i>Hoxb8</i>	TGGTCTGTTTCCTTTGAACGTG	TTACGGCGTGAATAGGCAGTTT
<i>Hoxb9</i>	AGAAGACTCAGAGTGGGGACTT	CGATGTTTGCCTCTTTCCTGTG
<i>Sfi1</i>	ATCCGAGGACCTTCACCTAGAA	GACAAGGCAAGCTGAAAGGAAG
<i>Six1</i>	AGGTCATCGGAAGCTCTTTTGT	GATACATCATTTTGCCCCAGGC
<i>Socs2</i>	GTAGTCTCCATCTCAAGGCAG	TGCACCTGTATAGCGTGACATT
<i>Piwi4</i>	GTCAGTGCTTGAGGTAAATTCTCA	CCTGAAGTTAAACCCCACTATGT
<i>Plzf</i>	CTTCACTTGCCCTCCAGTCCAGA	TACACAGAAGGAAGGCAGGTGT
<i>Ddx4</i>	CAGCTTCAGTAGCAGCACAAAG	CATGACTCGTCATCAACTGGA
<i>Dazl</i>	GATGGACATGAGATCATTTGGAC	ATACCAGGGAGCAATCCTGAC
<i>Piwi2</i>	GCTCGAAGACAACATTGTCCAG	GGCCTTGGTCATAGACTCCAAA
<i>Itga6</i>	CACTGGCTTTAAAGGACACAGC	TTGTTGTTGAACTCCCTCCCAA
<i>Cd9</i>	GGATTGTCTTCGGGTTCTCT	TCCTTGCTCCGTAACCTTTTGGT
<i>Kit</i>	CAGTTACCGCGCTCTGTTTG	GCCCCCTAAGTACCTGACATCC
<i>Gfra1</i>	TTTTACTGACAGTTGCGTCCAC	TGAATGTGCTTCTGCTCAAAGTG
<i>Ret</i>	AGACTGCTGCTTTCACATCCTT	CACAGCACCACAGACTATGTTT
<i>Id4</i>	TCCCTTGAGAGCTTTTGCTAT	ACCAGAGAGCTGTTACCTCTGA
<i>Nanos2</i>	GACCTCATGGGACTGATGACTG	CCAAGCCAACCTCCTAGATAGC
Bisulfite	Ref: (Lee et al., 2009)	
<i>H19</i>	GGAATATTTGTGTTTTTGGAGGG	TTAAACCCCAACCTCTACTTTTATAAC
<i>Meg3</i> <i>IG</i>	GGTTTGGTATATATGGATGTATTGTAATATAGG	ATAAAACACCAAATCTATACCAAAATATACC
<i>Igf2r</i>	TTAGTGGGGTATTTTTATTTGTATGG	AAATATCCTAAAAATACAACTACACAA
<i>Peg10</i>	GTAAAGTGATTGGTTTTGTATTTTAAAGTG	TTAATTACTCTCCTACAACCTTCCAAATT
<i>Snrpn</i>	AATTTGTGTGATGTTTGTAATTATTTGG	ATAAAATACACTTTCCTACTAAAATCCACAA

Oligonucleotides

The oligonucleotides used for SC3-seq are listed below.

Name	Sequence	Grade
V1(dT)24	ATATGGATCCGGCGCGCCGTCGACTTTTTTTTTTTTTTTTTTTTTT	HPLC
V3(dT)24	ATATCTCGAGGGCGCGCCGATCCTTTTTTTTTTTTTTTTTTTTTT	HPLC

N-V3(dT) 24	ATATCTCGAGGGCGCGCCGGATCCTTTTTTTTTTTTTTTTTTTTTT	HPLC
Rd2SPV1 (dT)20	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCATATGGATCCGGCGCGCCGTC GACTTTTTTTTTTTTTTTTTT	HPLC
tRd1SPTs	TCTTCCCTACACGACGCTCTTCCGATCT	HPLC
tRd1SPTas	GATCGGAAGAGCGTCGTGTAGGGAAAGA	HPLC
S502	AATGATACGGCGACCACCGAGATCTACACCTCTCTATACACTCTTCCCTACACG ACGCTCT	HPLC
S503	AATGATACGGCGACCACCGAGATCTACACTATCCTCTACACTCTTCCCTACACG ACGCTCT	HPLC
S505	AATGATACGGCGACCACCGAGATCTACACGTAAGGAGAACTCTTCCCTACAC GACGCTCT	HPLC
S506	AATGATACGGCGACCACCGAGATCTACACACTGCATAAACTCTTCCCTACACG ACGCTCT	HPLC
S507	AATGATACGGCGACCACCGAGATCTACACAAGGAGTAACACTCTTCCCTACAC GACGCTCT	HPLC
S508	AATGATACGGCGACCACCGAGATCTACACCTAAGCCTAACTCTTCCCTACACG ACGCTCT	HPLC
S510	AATGATACGGCGACCACCGAGATCTACACCGTCTAATAAACTCTTCCCTACACG ACGCTCT	HPLC
S511	AATGATACGGCGACCACCGAGATCTAACTCTCTCCGAACTCTTCCCTACACG ACGCTCT	HPLC
S513	AATGATACGGCGACCACCGAGATCTAACTCGACTAGAACTCTTCCCTACAC GACGCTCT	HPLC
S515	AATGATACGGCGACCACCGAGATCTAACTTCTAGCTAACTCTTCCCTACACG ACGCTCT	HPLC
S516	AATGATACGGCGACCACCGAGATCTAACCCCTAGAGTAACTCTTCCCTACAC GACGCTCT	HPLC
S517	AATGATACGGCGACCACCGAGATCTAACGCGTAAGAACTCTTCCCTACAC GACGCTCT	HPLC
S518	AATGATACGGCGACCACCGAGATCTAACCTATTAAGAACTCTTCCCTACACG ACGCTCT	HPLC
S520	AATGATACGGCGACCACCGAGATCTAACAAAGGCTAACTCTTCCCTACACG ACGCTCT	HPLC
S521	AATGATACGGCGACCACCGAGATCTAACGAGCCTAACTCTTCCCTACAC GACGCTCT	HPLC
S522	AATGATACGGCGACCACCGAGATCTAACTTATGCGAACTCTTCCCTACACG ACGCTCT	HPLC
N701	CAAGCAGAAGACGGCATACGAGATTCGCCTTAGTGACTGGAGTTCAGACGTGT	HPLC
N702	CAAGCAGAAGACGGCATACGAGATCTAGTACGGTGACTGGAGTTCAGACGTGT	HPLC
N703	CAAGCAGAAGACGGCATACGAGATTTCTGCCTGTGACTGGAGTTCAGACGTGT	HPLC
N704	CAAGCAGAAGACGGCATACGAGATGCTCAGGAGTGACTGGAGTTCAGACGTGT	HPLC
N705	CAAGCAGAAGACGGCATACGAGATAGGAGTCCGTGACTGGAGTTCAGACGTGT	HPLC
N706	CAAGCAGAAGACGGCATACGAGATCATGCCTAGTGACTGGAGTTCAGACGTGT	HPLC
N707	CAAGCAGAAGACGGCATACGAGATGTAGAGAGGTGACTGGAGTTCAGACGTGT	HPLC
N710	CAAGCAGAAGACGGCATACGAGATCAGCCTCGGTGACTGGAGTTCAGACGTGT	HPLC
N711	CAAGCAGAAGACGGCATACGAGATTGCCTCTTGTGACTGGAGTTCAGACGTGT	HPLC
N712	CAAGCAGAAGACGGCATACGAGATTCCTCTACGTGACTGGAGTTCAGACGTGT	HPLC
N714	CAAGCAGAAGACGGCATACGAGATTCATGAGCGTGACTGGAGTTCAGACGTGT	HPLC
N715	CAAGCAGAAGACGGCATACGAGATCCTGAGATGTGACTGGAGTTCAGACGTGT	HPLC
N716	CAAGCAGAAGACGGCATACGAGATTAGCGAGTGACTGGAGTTCAGACGTGT	HPLC
N718	CAAGCAGAAGACGGCATACGAGATGTAGCTCCGTGACTGGAGTTCAGACGTGT	HPLC
N719	CAAGCAGAAGACGGCATACGAGATTACTACGCGTGACTGGAGTTCAGACGTGT	HPLC
N720	CAAGCAGAAGACGGCATACGAGATAGGCTCCGTGACTGGAGTTCAGACGTGT	HPLC
N721	CAAGCAGAAGACGGCATACGAGATGCAGCGTAGTGACTGGAGTTCAGACGTGT	HPLC

N722	CAAGCAGAAGACGGCATAACGAGATCTGCGCATGTGACTGGAGTTCAGACGTGT	HPLC
N723	CAAGCAGAAGACGGCATAACGAGATGAGCGCTAGTGACTGGAGTTCAGACGTGT	HPLC
N724	CAAGCAGAAGACGGCATAACGAGATCGCTCAGTGTGACTGGAGTTCAGACGTGT	HPLC
N726	CAAGCAGAAGACGGCATAACGAGATGTCTTAGGGTGACTGGAGTTCAGACGTGT	HPLC
N727	CAAGCAGAAGACGGCATAACGAGATACTGATCGGTGACTGGAGTTCAGACGTGT	HPLC
N728	CAAGCAGAAGACGGCATAACGAGATTAGCTGCAGTGACTGGAGTTCAGACGTGT	HPLC
N729	CAAGCAGAAGACGGCATAACGAGATGACGTCGAGTGACTGGAGTTCAGACGTGT	HPLC

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Supplemental Table S1. Gene Ontology for Differentially Expressed Genes between GSCs and GSCs, Related to Figure 4

RNA expression, GSCs > GSCs (407 genes)									
Category	Term	Count	%	PValue	Genes				
GOTERM_BP_DIRECT	GO:0007275-multicellular organismal development	49	12.72727273	2.92E-08	PDGFA, FGF9, PRRX2, TNFSF12, SOHLH1, SPRY4, WNT3, UNC5B, POU5F1, RAPGEF2, ZFP423, ARC, RREB1, BARHL2, EOMES, MCP, SLIT3, PDGFRA, SORT1, TNFRSF25, TDOR9, ADAD1, HOXB13, T, OVOL2, LHX1, CASZ1, WIPF3, NDRG2, TRP53, DDXDC1, FLT1, EPAS1, COL13A1, DLX3, HOXB3, NOTCH1, HOXB2, ARC, HOXB3, T, BARX1, HOXB2, WNT3, HOXB7, LHX1, HOXB8, SFRP2, HOXB5, HOXB6, HOXB9, SCMH1, TCF15				
GOTERM_BP_DIRECT	GO:0009952-anterior/posterior pattern specification	15	3.896103896	6.36E-08	RAMP2, COL4A2, FLT1, CCL2, EPAS1, FGF9, PDGFA, TNFSF12, ECM1, EPHB1, ANXA2, THY1, PRKD2, NOTCH1, UNC5B, OVOL2, HBEGF, RAPGEF3				
GOTERM_BP_DIRECT	GO:0001525-angiogenesis	18	4.675324675	2.78E-06	TRP53, B4GALT1, RXRA, SMAD6, FBXO2, INCA1, TIMP2, SLIT3, SH3BP4, DDR1, NOTCH1, OVOL2, PKP2, SFRP2, NDRG1, RAPGEF2, SMARCA2, HIST1H2AO, TES, AVO74887				
GOTERM_BP_DIRECT	GO:0008285-negative regulation of cell proliferation	20	5.194805195	1.43E-04	TYRO3, DDR1, FLT1, STAT5A, AXL, PDGFRA, AIB3, HK1, EPHB1				
GOTERM_BP_DIRECT	GO:0018108-peptidyl-tyrosine phosphorylation	9	2.237662338	2.20E-04	ZKSCAN6, STAT5A, CBX4, MED24, SOHLH1, BARX1, CRX2, POU5F1, LRRFP1, ZFP423, EGR2, CTBP2, RREB1, RXRA, BARHL2, PKN2, MLXIPL, EOMES, LPIN1, FOXN3, JUNB, CCND1, PARP14, ZZZ3, SMARCA2, ZBTB6, TFE3, WBSR22, HOXB13, T, OVOL2, LHX1, CASZ1, BHLHE40, POU3F1, NFATC2, BAHDI, TRP53, EPAS1, SMAD6, MAPK11, SIRT7, WWTR1, DLX3, HOXB3, NOTCH1, HOXB2, RASL11A, HOXB7, HOXB8, HOXB5, SALL1, SMARCC2, HOXB6, SP6, HOXB9, ZBTB3, SCMH1, TCF15				
GOTERM_BP_DIRECT	GO:0006351-transcription, DNA-templated	59	15.32467532	3.49E-04	PRKD2, RAMP2, FLT1, SFRP2, MMP9, SPHK1, RAPGEF3, THBS1, ECM1, DDAH1				
GOTERM_BP_DIRECT	GO:0045766-positive regulation of angiogenesis	10	2.597402597	6.47E-04	SH3BP4, PACSINI, ARC, LRPI, RABEP2, LIDR, LRPI1, FKBPI15, WIPF3, SORT1, USP33, APLP1				
GOTERM_BP_DIRECT	GO:0006997-endoctrosis	12	3.116883117	8.48E-04	HOXB3, HOXB2, HOXB7, HOXB8, HOXB5, HOXB6, PRRX2				
GOTERM_BP_DIRECT	GO:0004870-embryonic skeletal system morphogenesis	7	1.818181818	8.51E-04	ZKSCAN6, STAT5A, CBX4, MED24, PRRX2, SOHLH1, BARX1, CRX2, POU5F1, CREG1, LRRFP1, ZFP423, EGR2, CTBP2, RREB1, RXRA, BARHL2, PKN2, MLXIPL, EOMES, LPIN1, FOXN3, JUNB, CCND1, PARP14, ZZZ3, SMARCA2, ZBTB6, TFE3, WBSR22, HOXB13, T, OVOL2, LHX1, CASZ1, BHLHE40, POU3F1, NFATC2, BAHDI, TRP53, EPAS1, SMAD6, MAPK11, SIRT7, WWTR1, DLX3, HOXB3, NOTCH1, HOXB2, RASL11A, HOXB7, HOXB8, HOXB5, SALL1, DLX4, SMARCC2, HOXB6, SP6, HOXB9, ZBTB3, SCMH1, TCF15				
GOTERM_BP_DIRECT	GO:0006355-regulation of transcription, DNA-templated	62	16.1038961	1.02E-03	ZFP36, TRP53, RXRA, STAT5A, BARHL2, EOMES, MLXIPL, MED24, ECM1, LPIN1, JUNB, T, NOTCH1, BARX1, SMARCC2, SP6, GNAS, POU3F1				
GOTERM_BP_DIRECT	GO:0006357-regulation of transcription from RNA polymerase II promoter	18	4.675324675	1.33E-03	FGF9, FST, CBX4, T, CRX2, POU5F1, BHLHE40, NFATC2, TRP53, ZFP36, CTBP2, EPAS1, RREB1, RXRA, MLXIPL, EOMES, SIRT7, MAPK10, WWTR1, LPIN1, JUNB, HOXB3, CCND1, NOTCH1, SALL1, DLX4, SMARCC2, BCL6B				
GOTERM_BP_DIRECT	GO:0000122-negative regulation of transcription from RNA polymerase II promoter	28	7.272727273	1.39E-03	B4GALT1, TYRO3, ICAM1, MPZL2, CADM4, COL13A1, TNC, PODXL, PKN2, ITGB5, ITGA3, CDH3, CD24A, COL5A1, APLP1, PRKD2, LAMR2, CD93, COL6A2, THBS1, SPPI				
GOTERM_BP_DIRECT	GO:0007155-cell adhesion	21	5.454545455	1.48E-03	TYRO3, FLT1, ERBB3, PIK3CD, SPHK1, AXL, BRSK2, PKN2, HK1, MAPK11, MAPK10, NACK, DAPK2, MARK4, DGKA, DDR1, PRKD2, MAP3K6, MAP3K5, MAP3K3, RIOK3, PDGFRA, PRKACB, CERK, ITPK1				
GOTERM_BP_DIRECT	GO:0016310-phosphorylation	25	6.493506494	1.53E-03	RAB3A, NOTCH1, EPAS1, FGF9, PDGFRA, MGP, ITGA3, SPARC, LOX				
GOTERM_BP_DIRECT	GO:0030324-lung development	9	2.237662338	1.84E-03	DLX3, MAP3K3, COL3A1, SPHK1, LOX, RAPGEF2, COL5A1				
GOTERM_BP_DIRECT	GO:0001568-blood vessel development	7	1.818181818	2.21E-03	FGF9, PDGFA, TNC, STAT5A, CLU, SPHK1, MLXIPL, NMB, OPTN, WWTR1, RPA1, T, NOTCH1, CCND1, BLOC1S2, CLCF1, SFRP2, PDGFRA, SP6, GNAS				
GOTERM_BP_DIRECT	GO:0008284-positive regulation of cell proliferation	20	5.194805195	2.32E-03	TRP53, MMP9, IFI30, PMAIP1, PARP10				
GOTERM_BP_DIRECT	GO:0048147-negative regulation of fibroblast proliferation	5	1.298701299	2.68E-03	RILP1, APOE, CLU, EPHB1				
GOTERM_BP_DIRECT	GO:1901214-regulation of neuron death	4	1.038961039	3.17E-03	ICAM1, F2RL1, RAPGEF3, RAPGEF2				
GOTERM_BP_DIRECT	GO:0061028-establishment of endothelial barrier	4	1.038961039	3.17E-03	DUSP5, DUSP4, LHX1, EOMES				
GOTERM_BP_DIRECT	GO:0007106-endothelium formation	4	1.038961039	3.84E-03	BCL10, CCL2, PYCARD, THY1				
GOTERM_BP_DIRECT	GO:00050870-positive regulation of T cell activation	4	1.038961039	3.84E-03	ICAM1, CCL2, PLVAP				
GOTERM_BP_DIRECT	GO:0002693-positive regulation of cellular extravasation	3	0.759220779	3.96E-03	TYRO3, FLT1, ERBB3, PIK3CD, PIMI, AXL, BRSK2, PKN2, HK1, MAPK11, MAPK10, DAPK2, MARK4, TRIB1, PRKD2, MAP3K6, DDR1, CCND1, MAP3K5, MAP3K3, RIOK3, PDGFRA, PRKACB				
GOTERM_BP_DIRECT	GO:0006468-protein phosphorylation	23	5.974025974	4.16E-03	SATI, B4GALT1, TRP53, NOTCH1, TNFRSF25, ERBB3, SFRP2, NDRG1, SPARC, RAPGEF2, JUNB, TES				
GOTERM_BP_DIRECT	GO:0042127-negative regulation of cell proliferation	12	3.116883117	4.51E-03	TRP53, ZFP423, CTBP2, RREB1, CBX4, MLXIPL, TRIM11, DUSP5, NOTCH1, CRX2, OVOL2, LHX1, POU5F1, SFRP2, SALL1, SMARCC2, BHLHE40, SCMH1, SMARCA2, BAHDI				
GOTERM_BP_DIRECT	GO:0045892-negative regulation of transcription, DNA-templated	20	5.194805195	4.56E-03	PDGFRA, COL3A1, GNAS, ITGA3, COL5A1, TCF15				
GOTERM_BP_DIRECT	GO:0043588-skin development	6	1.558441558	4.74E-03	TRP53, ZFP423, BCL10, EGR2, FGF9, RXRA, PIMI, TFE3, MLXIPL, MED24, SOHLH1, TRF, NOTCH1, OVOL2, BLOC1S2, LHX1, POU5F1, SALL1, SMARCC2, POU3F1, NFATC2, SMARCA2				
GOTERM_BP_DIRECT	GO:0045893-positive regulation of transcription, DNA-templated	22	5.714285714	5.34E-03	WNT3, LAMB2, UNC5B, CRMP1, EFNA2, USP83, TUBB3, EPHB1, SLIT3				
GOTERM_BP_DIRECT	GO:0007411-axon guidance	9	2.337662338	5.88E-03	ARC, FLT1, PODXL, PDGFRA, HBEGF, NFATC2, THBS1, USP83, CD24A, MYO18A, COL5A1				
GOTERM_BP_DIRECT	GO:0016477-cell migration	11	2.857142857	6.30E-03	PRKD2, RAMP2, NOTCH1, FLT1				
GOTERM_BP_DIRECT	GO:0035924-cellular response to vascular endothelial growth factor stimulus	4	1.038961039	7.37E-03	COL13A1, MMP9, SORT1, MCP, IGF2, ECM1, SPPI				
GOTERM_BP_DIRECT	GO:0001503-ossification	7	1.818181818	7.73E-03	SFRP2, COL3A1, LOX, COL5A1, ANXA2				
GOTERM_BP_DIRECT	GO:0003019-collagen fibril organization	5	1.298701299	7.91E-03	APOE, PDGFA, PDGFRA				
GOTERM_BP_DIRECT	GO:0010544-negative regulation of platelet activation	3	0.759220779	8.10E-03	B4GALT1, MMP9, PODXL, F2RL1				
GOTERM_BP_DIRECT	GO:0050900-leukocyte migration	4	1.038961039	8.46E-03	TYRO3, PRKD2, DDR1, FLT1, MAP3K3, PIMI, PDGFRA, HK1, EPHB1, THY1				
GOTERM_BP_DIRECT	GO:0046777-protein autophosphorylation	10	2.597402597	9.40E-03	DIKDC1, T, CCND1, WNT3, SFRP2, HOXB9, CDH3				
GOTERM_BP_DIRECT	GO:0060070-canonical Wnt signaling pathway	7	1.818181818	1.01E-02	TEX19.1, TEX19.2, FGF9, ADAD1, TDOR9, TNFSF12, SOHLH1, LHX1, WIPF3, NDRG2, RAPGEF2, ZFP423, CTBP2, FLT1, EPAS1, COL13A1, PIK3CD, EOMES, AXL, MCP, SLIT3, NOTCH1, FOXJ3, SEMA6D, SFRP2, SORT1				
GOTERM_BP_DIRECT	GO:0048706-embryonic skeletal system development	5	1.298701299	1.03E-02	STAT5A, PYCARD, IGF2, CD24A				
GOTERM_BP_DIRECT	GO:0030154-cell differentiation	26	6.753246753	1.14E-02	STAT5A, PDGFRA, PTPRN				
GOTERM_BP_DIRECT	GO:0042104-positive regulation of activated T cell proliferation	4	1.038961039	1.23E-02	ICAM1, GBR3, GBP2				
GOTERM_BP_DIRECT	GO:0001553-luteinization	3	0.759220779	1.35E-02	HOXB3, NOTCH1, BCL6B, EOMES				
GOTERM_BP_DIRECT	GO:0044406-adhesion of symbiont to host	3	0.759220779	1.35E-02	ZFP36, ADCY5, SMAD6, PKN2, BRSK2, MAPK11, ARHGAP29, PEA15A, DAPK2, DGKA, LAT, PRKD2, MAP3K3, CNVH4, RASGRP2, RAPGEF3				
GOTERM_BP_DIRECT	GO:0005077-regulation of neurogenesis	4	1.038961039	1.38E-02	PIK3CD, PDGFRA, HBEGF, HOXB9, EPHB1				
GOTERM_BP_DIRECT	GO:0035556-intracellular signal transduction	16	4.155844156	1.48E-02	RAMP2, NOTCH1, FLT1, THBS1				
GOTERM_BP_DIRECT	GO:0003556-intracellular signal transduction	5	1.298701299	1.51E-02	NOTCH1, FLT1, PDGFA, F2RL1, PIK3CD, SPHK1, PDGFRA, HBEGF, THBS1, FURIN				
GOTERM_BP_DIRECT	GO:0060326-cell chemotaxis	5	1.298701299	1.51E-02	TYRO3, AXL, FURIN				
GOTERM_BP_DIRECT	GO:0002040-sprouting angiogenesis	4	1.038961039	1.54E-02					
GOTERM_BP_DIRECT	GO:0003035-positive regulation of cell migration	10	2.597402597	1.66E-02					
GOTERM_BP_DIRECT	GO:0032940-secretion by cell	3	0.759220779	1.67E-02					

GOTERM_BP_DIRECT	GO:0003197-endothelial cushion development	3	0.793220779	2.01-E-02	NOTCH1, ERBB3, THBS1
GOTERM_BP_DIRECT	GO:0006068-vagina development	3	0.793220779	2.01-E-02	TYRO3, LHX1, AXI
GOTERM_BP_DIRECT	GO:0042493-response to drug	8	2.077922078	2.13-E-02	TRP53, SFRP2, MMP9, GNAS, IGF2, NFATC2, AACS, JUNB
GOTERM_BP_DIRECT	GO:0051092-positive regulation of NF-kappaB transcription factor activity	7	1.818181818	2.21-E-02	PRKD2, ICAM1, BCL10, CLU, SPHK1, PYCARD, LRRTP1
GOTERM_BP_DIRECT	GO:0043065-positive regulation of apoptotic process	13	3.376623377	2.34-E-02	TRP53, B4GALT1, BCL10, RXRA, MMP9, CLU, PMAIP1, NOTCH1, MAP3K5, SFRP2, PYCARD, GADD45A, PHILDA1
GOTERM_BP_DIRECT	GO:0006740-prostate gland epithelium morphogenesis	3	0.793220779	2.38-E-02	NOTCH1, TNC, STAT5A
GOTERM_BP_DIRECT	GO:0030178-negative regulation of Wnt signaling pathway	5	1.298701299	2.40-E-02	BARX1, CCND1, LRPI, FGF9, SFRP2
GOTERM_BP_DIRECT	GO:0001897-positive regulation of protein kinase B signaling	6	1.558441538	2.59-E-02	POU5F1, PDGFA, AXL, HBEGF, IGF2, THBS1
GOTERM_BP_DIRECT	GO:0010628-positive regulation of gene expression	14	3.636363636	2.75-E-02	TRP53, RAMP2, FGF9, ERBB3, TNC, PIK3CD, LMNA, MAPK11, ITGA3, CDH3, WNT3, POU5F1, POU3F1, NFATC2
GOTERM_BP_DIRECT	GO:0003214-cardiac left ventricle morphogenesis	3	0.793220779	2.78-E-02	NOTCH1, FGF9, SFRP2
GOTERM_BP_DIRECT	GO:0045576-mast cell activation	3	0.793220779	2.78-E-02	BCL10, CHGA, NDRG1
GOTERM_BP_DIRECT	GO:0035116-embryonic hindlimb morphogenesis	4	1.038961039	2.90-E-02	NOTCH1, WNT3, RSPD2, GNAS
GOTERM_BP_DIRECT	GO:0001934-positive regulation of protein phosphorylation	9	2.337662338	2.97-E-02	MAPK5, CCND1, HSPA2, MMP9, SPHK1, GNAS, IGF2, RAPGEF3, ANXA2
GOTERM_BP_DIRECT	GO:0010875-positive regulation of cholesterol efflux	3	0.793220779	3.20-E-02	LRPI, APOE, ABCA1
GOTERM_BP_DIRECT	GO:0030949-positive regulation of vascular endothelial growth factor receptor signaling pathway	3	0.793220779	3.20-E-02	PRKD2, FLT1, FGF9
GOTERM_BP_DIRECT	GO:0070059-intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	4	1.038961039	3.38-E-02	TRP53, MAP3K5, BRSK2, PMAIP1
GOTERM_BP_DIRECT	GO:1900745-positive regulation of p38MAPK cascade	3	0.793220779	3.64-E-02	MAPK5, MAP3K3, GADD45A
GOTERM_BP_DIRECT	GO:0001881-inactivation of MAPK activity	3	0.793220779	3.64-E-02	DUSP5, DUSP4, DUSP7
GOTERM_BP_DIRECT	GO:0014912-negative regulation of smooth muscle cell migration	3	0.793220779	3.64-E-02	LRPI, SEMA6D, TRIB1
GOTERM_BP_DIRECT	GO:0043277-apoptotic cell clearance	3	0.793220779	3.64-E-02	TYRO3, LRPI, AXI
GOTERM_BP_DIRECT	GO:0007264-small GTPase mediated signal transduction	10	2.597402597	3.76-E-02	RND2, ARHGAP31, RAB3A, RASL11A, RAB4A, RASGRP2, RHOC, RAPGEF3, RAPGEF2, RAB20
GOTERM_BP_DIRECT	GO:0008219-cell death	4	1.038961039	3.90-E-02	PRKD2, BCL10, KILB, CLU
GOTERM_BP_DIRECT	GO:0045944-positive regulation of transcription from RNA polymerase II promoter	29	7.532467532	3.93-E-02	STAT5A, F2RL1, TEER, SOHLH1, T. BLOC1S2, POU5F1, RAPGEF3, POU3F1, NFATC2, TRP53, CTBP2, EGR2, EPAS1, RXRA, BARRHL2, EOMES, MLXIPL, IGF2, WWTR1, LRPI, JUNB, PRKD2, NOTCH1, SFRP2, HOXB5, SALL1, HOXB9, SMARCA2
GOTERM_BP_DIRECT	GO:0043524-negative regulation of neuron apoptotic process	8	2.077922078	3.94-E-02	TYRO3, LRPI, UNC5B, CLCF1, ERBB3, APOE, AXI, OPTN
GOTERM_BP_DIRECT	GO:1900221-regulation of beta-amyloid clearance	2	0.519480519	4.03-E-02	APOE, CLU
GOTERM_BP_DIRECT	GO:0032804-negative regulation of low-density lipoprotein particle receptor catabolic process	2	0.519480519	4.03-E-02	FURIN, ANXA2
GOTERM_BP_DIRECT	GO:0090343-positive regulation of cell aging	2	0.519480519	4.03-E-02	TRP53, LMNA
GOTERM_BP_DIRECT	GO:2001027-negative regulation of endothelial cell chemotaxis	2	0.519480519	4.03-E-02	NOTCH1, THBS1
GOTERM_BP_DIRECT	GO:1902998-positive regulation of neurofibrillary tangle assembly	2	0.519480519	4.03-E-02	APOE, CLU
GOTERM_BP_DIRECT	GO:0001779-natural killer cell differentiation	3	0.793220779	4.11-E-02	TYRO3, STAT5A, AXI
GOTERM_BP_DIRECT	GO:0046330-positive regulation of JNK cascade	5	1.298701299	4.13-E-02	DIADCI1, MAP3K5, F2RL1, PYCARD, GADD45A
GOTERM_BP_DIRECT	GO:0009653-anatomical structure morphogenesis	4	1.038961039	4.17-E-02	T, FOXJ3, LHX1, PDGFRA
GOTERM_BP_DIRECT	GO:0001843-anal tube closure	6	1.558441538	4.29-E-02	BRS4, BCL10, T, SFRP2, SALL1, PRKACB
GOTERM_BP_DIRECT	GO:0007507-heart development	10	2.597402597	4.34-E-02	TRP53, RAMP2, NOTCH1, OVOL2, PKP2, MMP9, SALL1, RXRA, COL3A1, LOX
GOTERM_BP_DIRECT	GO:0001649-osteoblast differentiation	6	1.558441538	4.46-E-02	FGF9, TNC, RSPD2, WWTR1, JUNB, SPPI
GOTERM_BP_DIRECT	GO:0051056-regulation of small GTPase mediated signal transduction	3	0.793220779	4.59-E-02	SIPAL1, RAP1GAP2, ARHGAP26
GOTERM_BP_DIRECT	GO:0007010-cytoskeleton organization	6	1.56	4.63-E-02	PACSIN1, ARC, CCL2, CAP2, VILL, THY1

RNA expression: GSCs < GSCLCs (355 genes)

Category	Term	Count	%	PValue	Genes
GOTERM_BP_DIRECT	GO:0042472-inner ear morphogenesis	8	2.42	1.49-E-04	SPRP2, OTX1, SOX2, SIX1, COL2A1, SIX4, COL11A1, FZD6
GOTERM_BP_DIRECT	GO:0007605-sensory perception of sound	10	3.03	3.55-E-04	SPRP2, CDKN1B, SOX2, SIX1, ALMS1, LRIG1, COL2A1, MYC, COL11A1, CRYM
GOTERM_BP_DIRECT	GO:0048705-skeletal system morphogenesis	6	1.82	1.63-E-03	FMN1, SCHIP1, SIX1, COL2A1, MYC, COL11A1
GOTERM_BP_DIRECT	GO:0001822-kidney development	8	2.42	1.78-E-03	FMN1, CDKN1C, SCHIP1, SULF2, FBN1, SIX1, WTI, DCHS1
GOTERM_BP_DIRECT	GO:0045668-negative regulation of osteoblast differentiation	6	1.82	2.09-E-03	IDI1, SOX2, CDK6, CHRD, HDAC7, IGFBP5
GOTERM_BP_DIRECT	GO:0010468-regulation of gene expression	13	3.94	2.11-E-03	FOXA2, DMD, SIX1, SOX2, HOXA10, PHGDH, COL2A1, CDK6, SIX4, MYC, PHLDA2, WTI, PEG3
GOTERM_BP_DIRECT	GO:0072975-mesangial mesenchyme development	3	0.91	2.53-E-03	SIX1, SIX4, WTI
GOTERM_BP_DIRECT	GO:0061551-trigeminal ganglion development	3	0.91	2.53-E-03	NRP1, SIX1, SIX4
GOTERM_BP_DIRECT	GO:0060606-glucose metabolic process	6	1.82	3.05-E-03	H6PD, PRKAA1, MYC, CACNA1A, FABP5, IGFBP5
GOTERM_BP_DIRECT	GO:0060384-immervation	4	1.21	3.36-E-03	SULF2, SERPINE2, LRIG1, POU4F1
GOTERM_BP_DIRECT	GO:0007275-multicellular organismal development	29	8.79	3.62-E-03	TRD5, NRPI, ZFP41, FOXA2, SOX3, SOX2, RZV2, SPRY2, IFT122, SERPINE2, HEY1, HOXA10, POU4F1, FLRT2, NES, EPAS1, OTX1, BANP, SIX4, CSRP2, TMEM2, FZD6, TET3, IDI1, SIX1, TXNRD3, RBM19, NLRP14, CHRD
GOTERM_BP_DIRECT	GO:0030910-olfactory placode formation	3	0.91	3.76-E-03	SOX2, SIX1, SIX4
GOTERM_BP_DIRECT	GO:0030900-forebrain development	6	1.82	8.22-E-03	HTRA2, SOX3, OTX1, PSEN2, TOP2B, CHRD
GOTERM_BP_DIRECT	GO:0048672-positive regulation of collateral sprouting	3	0.91	8.73-E-03	BCL11A, CRABP2, LPAR3
GOTERM_BP_DIRECT	GO:0048538-thymus development	5	1.52	9.91-E-03	SIX1, PSEN2, FADD, SIX4, ABL1
GOTERM_BP_DIRECT	GO:0043586-tongue development	3	0.91	1.31-E-02	SOX2, SIX1, SIX4
GOTERM_BP_DIRECT	GO:0032060-bleb assembly	3	0.91	1.31-E-02	LPAR3, PMP22, MYLK
GOTERM_BP_DIRECT	GO:0043524-negative regulation of neuron apoptotic process	8	2.42	1.32-E-02	FAM134B, NES, NRPI, SIX1, POU4F1, SIX4, NEFL, CACNA1A
GOTERM_BP_DIRECT	GO:0050885-neuromuscular process controlling balance	5	1.52	1.44-E-02	JPH4, TPPI, ABL1, NEFL, CACNA1A
GOTERM_BP_DIRECT	GO:0006355-regulation of transcription, DNA-templated	46	13.94	1.67-E-02	ZCCHC12, ZFP945, UTF1, KATZB, EPAS1, EGR4, ROR1, OTX1, ZHX1, AFB3, RRP8, BMYC, BANP, SIX4, FOXR1, ZFP574, SALL3, ZFP654, SALL2, IDI1, ETS2, SIX1, KDM4B, OGG1, ZFP189, HDAC7, KLF3
GOTERM_BP_DIRECT	GO:0048008-placenta-derived growth factor receptor signaling pathway	4	1.21	1.74-E-02	PLAT, SCHIP1, NRPI, ABL1
GOTERM_BP_DIRECT	GO:0003007-heart morphogenesis	5	1.52	1.90-E-02	FLRT2, COL2A1, TAB1, COL11A1, DCHS1

GOTERM_BP_DIRECT	GO:0048665~neuron fate specification	3	0.91	2.09.E-02	FOXA2, SIX1, POU4F1
GOTERM_BP_DIRECT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	20	6.06	2.25.E-02	RHOX5, EPAS1, RCOR1, ZHX1, SOX2, WTI, CDKN1C, SALL2, HEY1, ID1, ETS2, IGBP1, SIX1, PSEN2, BCL11A, POU4F1, MYC, CRYM, HDAC7, PEG3
GOTERM_BP_DIRECT	GO:0043281~regulation of cysteine-type endopeptidase activity involved in apoptotic process	3	0.91	2.39.E-02	MGMT, SOX2, PYCARD
GOTERM_BP_DIRECT	GO:0040015~negative regulation of multicellular organism growth	3	0.91	2.70.E-02	ANKRD26, SOCS2, ALMS1
GOTERM_BP_DIRECT	GO:0050678~regulation of epithelial cell proliferation	3	0.91	2.70.E-02	HEY1, SIX1, SIX4
GOTERM_BP_DIRECT	GO:0001736~establishment of planar polarity	3	0.91	3.03.E-02	ALMS1, DCHS1, FZD6
GOTERM_BP_DIRECT	GO:0007628~adult walking behavior	4	1.21	3.03.E-02	HTRA2, MAPT, ATG7, CACNA1A
GOTERM_BP_DIRECT	GO:0035383~sequestering of TGFbeta in extracellular matrix	2	0.61	3.21.E-02	FBN1, FBN2
GOTERM_BP_DIRECT	GO:0060632~regulation of microtubule-based movement	2	0.61	3.21.E-02	MAPT, IGBP1
GOTERM_BP_DIRECT	GO:0061024~membrane organization	3	0.91	3.37.E-02	ATG7, GNPAT, MBP
GOTERM_BP_DIRECT	GO:0050910~detection of mechanical stimulus involved in sensory perception of sound	3	0.91	3.37.E-02	SOX2, MYC, COL11A1
GOTERM_BP_DIRECT	GO:0016558~branching involved in ureteric bud morphogenesis	4	1.21	3.42.E-02	SIX1, MYC, WTI, DCHS1
GOTERM_BP_DIRECT	GO:0042326~negative regulation of phosphorylation	3	0.91	3.73.E-02	CDKN1C, GRB10, CDKN1B
GOTERM_BP_DIRECT	GO:0032956~regulation of actin cytoskeleton organization	4	1.21	4.26.E-02	BST2, BAIAP2, GPM6B, ABL1
GOTERM_BP_DIRECT	GO:0006366~transcription from RNA polymerase II promoter	9	2.73	4.26.E-02	SALL3, SALL2, FOXA2, OTX1, BCL11A, SOX2, SIX1, HOXA10, MYC
GOTERM_BP_DIRECT	GO:0006520~cellular amino acid metabolic process	3	0.91	4.48.E-02	GOT2, ATG7, GOT1L1
GOTERM_BP_DIRECT	GO:0045879~negative regulation of smoothened signalling pathway	3	0.91	4.48.E-02	SALL3, IFT122, SERPINE2
GOTERM_BP_DIRECT	GO:0007050~cell cycle arrest	5	1.52	4.75.E-02	CDKN1C, CDKN1B, SOX2, PMP22, MYC
GOTERM_BP_DIRECT	GO:0061197~fungiform papilla morphogenesis	2	0.61	4.78.E-02	SIX1, SIX4
GOTERM_BP_DIRECT	GO:0006532~aspartate biosynthetic process	2	0.61	4.78.E-02	GOT2, GOT1L1
GOTERM_BP_DIRECT	GO:0048652~encephalon morphogenesis	2	0.61	4.78.E-02	OTX1, SOX2
GOTERM_BP_DIRECT	GO:0061055~myotome development	2	0.61	4.78.E-02	SIX1, SIX4
GOTERM_BP_DIRECT	GO:0072095~regulation of branch elongation involved in ureteric bud branching	2	0.61	4.78.E-02	SIX1, SIX4
GOTERM_BP_DIRECT	GO:0010976~positive regulation of neuron projection development	6	1.82	4.98.E-02	PLK5, KAT2B, SERPINE2, NDRG4, DMD, BCL11A

Supplemental Table S2. Genes Bearing Differentially Methylated Promoters between GSCLCs and GSCs, Related to Figures 5 and 6

Differentially methylated genes at promoters, GSCs ≥ GSCLCs

Name	Entrez_id	chr	st	end	strand	Promoter methylation, vs. GSCs			
						GSCLC1	GSCLC2	GSCLC3	GSCLC4
Neur3	214854	chr1		36273025	36274325 -	ICP			GSCLC_high
C230029F24Rik	442837	chr1		49243716	49245016 +	LCP			GSCLC_low
Gm2666	100040213	chr1		85484742	85486042 -	LCP	GSCLC_low	GSCLC_low	
Heatr7b1	100040766	chr1		88226120	88227420 +	LCP			GSCLC_low
Serpib3c	381286	chr1		107277971	107279271 -	LCP		GSCLC_low	
Gm10191	100042740	chr1		129801369	129802669 -	ICP	GSCLC_low		GSCLC_high
4930590L20Rik	75910	chr1		140656002	140657302 -	ICP	GSCLC_low	GSCLC_low	GSCLC_low
B3gal12	26878	chr1		143639797	143641097 +	ICP		GSCLC_low	
Slc39a12	277468	chr2		14387498	14388798 +	LCP		GSCLC_low	GSCLC_low
Olfr338	258949	chr2		36375878	36377178 +	LCP			GSCLC_low
Olfr342	258950	chr2		36526514	36527814 +	LCP	GSCLC_low		
Olfr360	258615	chr2		37067407	37068707 +	LCP		GSCLC_low	
Olfr365	258656	chr2		37200343	37201643 +	LCP		GSCLC_low	
Neb	17996	chr2		52338398	52339698 -	ICP	GSCLC_low	GSCLC_low	GSCLC_low
4932414N04Rik	75721	chr2		68656984	68658284 +	LCP		GSCLC_low	
D030029J20Rik	100502854	chr2		84588965	84590265 -	LCP			GSCLC_low
4930443O20Rik	74687	chr2		85086061	85087361 -	LCP			GSCLC_low
Olfr1033	258571	chr2		86019740	86021040 +	ICP	GSCLC_low	GSCLC_low	GSCLC_low
Olfr1143	258290	chr2		87801491	87802791 +	LCP		GSCLC_low	
Olfr1228	258973	chr2		89249232	89250592 -	LCP			GSCLC_low
Olfr1275	257980	chr2		111231391	111232691 -	LCP		GSCLC_low	
5330432E05Rik	383820	chr3		8022437	8023737 -	ICP	GSCLC_low	GSCLC_low	GSCLC_low
Gm10745	100038545	chr3		11843959	11845259 -	ICP	GSCLC_low	GSCLC_low	GSCLC_low
Rpr12	19784	chr3		22250470	22251770 +	ICP		GSCLC_low	GSCLC_low
0610031J06Rik	56700	chr3		88324123	88325423 +	LCP	GSCLC_low	GSCLC_low	GSCLC_low
Olfr13	99543	chr3		103737601	103738901 -	LCP		GSCLC_low	
Ptpn22	19260	chr3		103859392	103860692 +	LCP		GSCLC_low	
Gstm7	68312	chr3		107931345	107932645 -	LCP			GSCLC_low
Ank2	109676	chr3		126998052	126999352 -	LCP		GSCLC_low	
Gm6289	622139	chr3		144895611	144896911 -	LCP		GSCLC_low	
Gm12409	100040567	chr4		45763823	45765123 -	ICP		GSCLC_low	
Gm12505	100415914	chr4		55418442	55419742 -	HCP	GSCLC_low	GSCLC_low	
Mup5	17844	chr4		61834780	61836080 -	LCP		GSCLC_low	
Mup21	381531	chr4		62150441	62151741 -	LCP	GSCLC_low		
Ifna13	230396	chr4		88644059	88645359 -	LCP		GSCLC_low	
Gm13089	277667	chr4		143702888	143704188 -	LCP	GSCLC_low		GSCLC_low
Gm13078	277666	chr4		143718555	143719855 +	LCP		GSCLC_low	GSCLC_low
Pramef17	626943	chr4		143993969	143995269 -	LCP	GSCLC_low	GSCLC_low	GSCLC_low
Gm13102	100041077	chr4		144098980	144100280 +	LCP	GSCLC_low	GSCLC_low	GSCLC_low
Oog3	100012	chr4		144162251	144163551 -	LCP	GSCLC_low		GSCLC_low
Nppb	18158	chr4		147984889	147986189 +	LCP		GSCLC_low	
Isg15	100038882	chr4		156200418	156201718 -	LCP			GSCLC_low
LOC670059	670059	chr4		156343379	156344679 +	LCP			GSCLC_low
Lrrc17	74511	chr5		21542627	21543927 +	ICP		GSCLC_low	
Cc2d2a	231214	chr5		43661479	43662779 +	LCP		GSCLC_low	
4930431F12Rik	75783	chr5		44965301	44966601 +	LCP			GSCLC_low
Klhl5	71778	chr5		65130331	65131631 +	LCP		GSCLC_low	GSCLC_high
5830403M04Rik	76003	chr5		100077062	100078362 +	ICP		GSCLC_low	
Vmn2r12	627569	chr5		109097464	109098764 -	LCP	GSCLC_low	GSCLC_low	
Vmn2r16	384220	chr5		109329481	109330781 -	LCP	GSCLC_low		GSCLC_low
Vmn2r17	384221	chr5		109419113	109420413 +	LCP		GSCLC_low	GSCLC_low
1700095B10Rik	67360	chr5		112792392	112793692 +	ICP		GSCLC_low	
C330018A13Rik	320805	chr5		116122714	116124014 +	ICP		GSCLC_low	
Cyp3a11	13112	chr5		145879454	145880754 -	LCP	GSCLC_low	GSCLC_low	
Gm6309	622306	chr5		146170293	146171593 -	LCP	GSCLC_low		
Gm3409	100041566	chr5		146536748	146538048 +	LCP			GSCLC_low
Cald1	109624	chr6		34708544	34709844 +	LCP		GSCLC_low	
Trbv21	100124686	chr6		41201687	41202987 +	LCP			GSCLC_low
Creb5	231991	chr6		53572474	53573774 +	LCP		GSCLC_low	GSCLC_low
Igkv4-71	434586	chr6		69243288	69244588 -	LCP	GSCLC_low	GSCLC_low	GSCLC_low
Rpr11	19783	chr6		69326774	69328074 -	ICP		GSCLC_low	GSCLC_low
Igkv4-60	385277	chr6		69463325	69464625 -	LCP	GSCLC_low		
Igkv3-3	667946	chr6		70686046	70687346 +	LCP			GSCLC_low
Clec4b2	381809	chr6		123172123	123173423 +	LCP	GSCLC_low		
Klrl1	27007	chr6		129623441	129624741 -	LCP		GSCLC_low	
Sox5	20678	chr6		144209168	144210468 -	ICP		GSCLC_low	
1700023A16Rik	69371	chr6		146849210	146850510 +	LCP		GSCLC_low	GSCLC_low
Gm5321	384525	chr7		6018122	6019422 +	ICP			GSCLC_low
Zscan4d	545913	chr7		11165748	11167048 -	LCP			GSCLC_low
Vmn1r77	628946	chr7		12040399	12041699 +	LCP	GSCLC_low		
Vmn1r82	171268	chr7		12303905	12305205 +	LCP			GSCLC_low
Vmn2r55	100042499	chr7		12684591	12685891 -	LCP	GSCLC_low		
Vmn1r85	252909	chr7		13084815	13086115 -	LCP			GSCLC_low
Sult2a4	434121	chr7		13989188	13990488 -	ICP	GSCLC_low		GSCLC_low
Psg18	26438	chr7		18354607	18355907 -	LCP	GSCLC_low	GSCLC_low	GSCLC_low
Psg28	114871	chr7		18431655	18432955 -	LCP	GSCLC_low	GSCLC_low	GSCLC_low
Vmn1r91	667067	chr7		20100258	20101558 +	LCP	GSCLC_low	GSCLC_low	
Vmn1r124	670764	chr7		21260217	21261517 -	ICP	GSCLC_low	GSCLC_low	
Vmn1r178	232959	chr7		23892629	23893929 +	LCP			GSCLC_low
Vmn1r179	404286	chr7		23927486	23928786 +	LCP	GSCLC_low		
Gm10175	100043121	chr7		23946889	23948189 -	LCP	GSCLC_low		
V1rd19	404287	chr7		24002211	24003511 +	LCP		GSCLC_low	
Gm4362	100043326	chr7		31361672	31362972 -	LCP	GSCLC_low	GSCLC_low	GSCLC_low
Gm6003	546954	chr7		33164308	33165608 +	LCP	GSCLC_low		
Gm5895	545948	chr7		33372340	33373640 +	LCP	GSCLC_low		
Abpz	233090	chr7		33738895	33740195 -	LCP		GSCLC_low	
Abpa	11354	chr7		34020667	34021967 +	LCP	GSCLC_low		
Gm12776	100043868	chr7		34094531	34095831 +	LCP			GSCLC_low
Mrgpra4	235854	chr7		47981896	47983196 -	LCP			GSCLC_low
Mrgprb5	404239	chr7		48168585	48169885 -	LCP	GSCLC_low		
Mrgprb8	404240	chr7		48387626	48388926 +	LCP	GSCLC_low		
Ipw	16353	chr7		59678478	59679778 -	LCP	GSCLC_low		
Gm6155	620480	chr7		84841292	84842592 -	LCP	GSCLC_low		GSCLC_low
Pde2a	207728	chr7		101420791	101422091 +	LCP		GSCLC_low	GSCLC_low
Olfr589	259054	chr7		103155345	103156645 -	LCP	GSCLC_low		GSCLC_low
Gm19934	100503865	chr7		104824124	104825424 -	ICP			GSCLC_low
Tpp1	12751	chr7		105751807	105753107 -	LCP	GSCLC_low	GSCLC_low	GSCLC_low
Olfr698	258595	chr7		106752986	106754286 -	LCP	GSCLC_low		
Gm19514	100503026	chr7		134099878	134101178 -	HCP		GSCLC_low	
Ifitm3	66141	chr7		141010344	141011644 -	LCP		GSCLC_low	
Krtap5-3	77215	chr7		142200464	142201764 +	LCP		GSCLC_low	
Cd209a	170786	chr8		3748584	3749884 -	LCP	GSCLC_low	GSCLC_low	
LOC100862276	100862276	chr8		4735071	4736371 +	LCP			GSCLC_low
Fam70b	272465	chr8		13434559	13435859 +	LCP		GSCLC_low	
Delb39	360214	chr8		19064410	19065710 -	LCP	GSCLC_low		GSCLC_low
Delb35	246084	chr8		21937452	21938752 +	LCP	GSCLC_low		
Ces2h	436059	chr8		104999953	105001253 +	LCP		GSCLC_low	GSCLC_low
6030452D12Rik	330837	chr8		106499611	106500911 +	LCP			GSCLC_low
4930568E12Rik	78219	chr9		13105455	13106755 -	ICP	GSCLC_low	GSCLC_low	GSCLC_low

Olfr870	57251	chr9		20171169	20172469	-	LCP	GSCLC_low		GSCLC_low	
Gm9513	671003	chr9		36474738	36476038	+	LCP	GSCLC_low	GSCLC_low		
Gm5615	434396	chr9		36541563	36542863	-	LCP		GSCLC_low		
Olfr893	258333	chr9		38208152	38209452	+	LCP	GSCLC_low			
Olfr143	258802	chr9		38252519	38253819	+	LCP			GSCLC_low	
Olfr944	258500	chr9		39216459	39217759	+	LCP	GSCLC_low	GSCLC_low		GSCLC_low
Htr3a	15561	chr9		48910699	48911999	-	LCP		GSCLC_low		
Cplx3	235415	chr9		57605881	57607181	-	ICP		GSCLC_low		
Alp2c1	235574	chr9		105520857	105522157	-	ICP		GSCLC_low		
Vip	22353	chr10		5638318	5639618	+	LCP			GSCLC_low	
Arg1	11846	chr10		24927070	24928370	-	LCP		GSCLC_low		
Olfr1356	258305	chr10		78847513	78848813	-	LCP		GSCLC_low		
Vmn2r81	216144	chr10		79246877	79248177	+	LCP	GSCLC_low	GSCLC_low	GSCLC_low	
Glt8d2	74782	chr10		82690250	82691550	-	ICP				GSCLC_low
Metap2	56307	chr10		93890802	93892102	-	LCP				GSCLC_low
Gm20110	100504202	chr10		99608271	99609571	+	ICP		GSCLC_low		
Glipr1	73690	chr10		111996864	111998164	-	LCP	GSCLC_low			
Thp2	216343	chr10		115184622	115185922	-	ICP		GSCLC_low	GSCLC_low	
Olfr781	258723	chr10		129331983	129333283	+	LCP				GSCLC_low
Olfr790	258935	chr10		129499986	129501286	+	LCP			GSCLC_low	
Olfr792	258150	chr10		129539639	129540939	+	LCP	GSCLC_low		GSCLC_low	GSCLC_low
Timd2	171284	chr11		46706704	46708004	-	LCP	GSCLC_low			
Olfr1388	258459	chr11		49442953	49444253	+	LCP				GSCLC_low
Cd68	12514	chr11		69665662	69666962	-	LCP				GSCLC_low
Olfr380	259027	chr11		73453810	73455110	-	LCP				GSCLC_low
Zfp735	76390	chr11		73687878	73689178	+	LCP	GSCLC_low			GSCLC_low
Olfr392	259008	chr11		73816477	73817777	-	LCP	GSCLC_low			
Olfr397	258343	chr11		73963710	73965010	+	LCP				GSCLC_low
Zfp616	327963	chr11		74059997	74061297	+	ICP		GSCLC_low		GSCLC_low
Olfr401	258701	chr11		74120391	74121691	+	LCP				GSCLC_low
Olfr403	404316	chr11		74194605	74195905	+	LCP	GSCLC_low	GSCLC_low		
Olfr406-ps	258181	chr11		74268491	74269791	+	LCP		GSCLC_low		GSCLC_low
Olfr412	258153	chr11		74363771	74365071	+	LCP		GSCLC_low		
A130040M12Rik	319269	chr11		86815729	86817029	-	ICP		GSCLC_low		
Gm11596	670464	chr11		99792892	99794192	-	LCP				GSCLC_low
Ghdc	80860	chr11		100770557	100771857	-	LCP		GSCLC_low		GSCLC_low
LOC100862279	100862279	chr11		106299368	106300668	+	ICP				GSCLC_low
LOC100861684	100861684	chr11		117965189	117966489	+	LCP				GSCLC_low
Gm5784	544848	chr12		19430540	19431840	+	LCP	GSCLC_low			
Gm889	380755	chr12		40198915	40200215	-	ICP	GSCLC_low	GSCLC_low	GSCLC_low	
Alu024163	100504027	chr12		57648511	57649811	+	LCP	GSCLC_low	GSCLC_low	GSCLC_low	
Gm2042	100039087	chr12		87953578	87954878	+	LCP	GSCLC_low			
Gm2075	100039162	chr12		88010948	88012248	+	LCP		GSCLC_low		
Gm8587	667350	chr12		88088225	88089525	+	LCP				GSCLC_low
Gm5955	546543	chr12		88123766	88125066	+	LCP	GSCLC_low			GSCLC_low
Gm10436	100039315	chr12		88181494	88182794	-	LCP	GSCLC_low			
Gm8378	666955	chr12		91685713	91687013	-	LCP		GSCLC_low		
Ilfi27l1	52668	chr12		103433289	103434589	+	ICP		GSCLC_low	GSCLC_low	GSCLC_low
Serpina1c	20702	chr12		103904550	103905850	-	LCP	GSCLC_low	GSCLC_low		
Gm19605	100503237	chr12		110485808	110487108	-	ICP		GSCLC_low		
Ighv3-1	780803	chr12		113964283	113965583	-	LCP		GSCLC_low		
Ighv8-8	780938	chr12		115293962	115295262	-	LCP				GSCLC_low
4933404K08Rik	74061	chr13		23277450	23278750	+	ICP	GSCLC_low			GSCLC_low
Serpnb9e	20710	chr13		33248710	33250010	+	LCP		GSCLC_low		GSCLC_low
Serpnb9f	20709	chr13		33323177	33324477	+	LCP	GSCLC_low	GSCLC_low		GSCLC_low
Gm8674	667507	chr13		49904197	49905497	-	ICP		GSCLC_low		
2310081J21Rik	69211	chr13		50260915	50262215	+	LCP		GSCLC_low		
Mir874	100124491	chr13		58022800	58024100	-	ICP	GSCLC_low	GSCLC_low	GSCLC_low	
Gm19852	100503714	chr13		58390999	58392299	+	LCP				GSCLC_low
A530065N20	328263	chr13		60028811	60030111	+	ICP				GSCLC_low
Gm5084	100503759	chr13		60204571	60205871	+	ICP		GSCLC_low		
Ctsj	26898	chr13		61005514	61006814	-	LCP		GSCLC_low		
Ctsq	104002	chr13		61040197	61041497	-	LCP		GSCLC_low		
Ctsr	56835	chr13		61163788	61165088	-	LCP		GSCLC_low		GSCLC_low
Ctsm	64139	chr13		61541439	61542739	-	LCP	GSCLC_low	GSCLC_low		
Cts3	117066	chr13		61569727	61571027	-	LCP	GSCLC_low			
Glrx	93692	chr13		75838986	75840286	+	LCP		GSCLC_low		
D13Mgi7	382823	chr13		77670003	77671303	-	ICP				GSCLC_low
AW495222	105364	chr13		93718775	93720075	-	ICP			GSCLC_low	
Gm3601	100041975	chr14		49989308	49990608	-	LCP	GSCLC_low	GSCLC_low		GSCLC_low
Trav6-1	667449	chr14		52637615	52638915	+	LCP	GSCLC_low		GSCLC_low	
Trav8-1	674098	chr14		53468856	53470156	+	LCP		GSCLC_low		
Trav5-4	21507	chr14		53703107	53704407	+	LCP				GSCLC_low
Trdj2	100118398	chr14		54135879	54137179	+	HCP		GSCLC_low		
Gm10032	791407	chr14		66783580	66784880	+	ICP	GSCLC_low			
Gm10847	100038618	chr14		74921215	74922515	+	LCP				GSCLC_low
BC025446	223631	chr15		75215696	75216996	+	LCP	GSCLC_low			
Cyp2d12	380997	chr15		82554198	82555498	+	LCP	GSCLC_low	GSCLC_low	GSCLC_low	GSCLC_low
Cyp2d34	223706	chr15		82620507	82621807	-	LCP	GSCLC_low			
Aqp6	11831	chr15		99600500	99601800	+	LCP		GSCLC_low		
Olfr161	258859	chr16		3591498	3592798	+	LCP	GSCLC_low			
Gm4262	100043147	chr16		11007998	11009298	+	LCP			GSCLC_high	GSCLC_low
Olfr170	258959	chr16		19606266	19607566	-	LCP	GSCLC_low			
2010005H15Rik	76770	chr16		36220662	36221962	+	LCP		GSCLC_low		GSCLC_low
Cd200r2	271375	chr16		44866197	44867497	+	LCP		GSCLC_low		GSCLC_low
Gm4416	100043404	chr16		50139520	50140820	+	ICP	GSCLC_low			
E330017A01Rik	224247	chr16		58638003	58639303	-	ICP		GSCLC_low		
Speer2	224318	chr16		69863344	69864644	-	LCP	GSCLC_low			
Mx2	17858	chr16		97535181	97536481	+	LCP		GSCLC_low		
Smok2a	27263	chr17		13220288	13221588	+	LCP	GSCLC_low	GSCLC_low		GSCLC_low
Smok2b	236574	chr17		13233971	13235271	+	LCP		GSCLC_low		GSCLC_low
Tcp10c	100041352	chr17		13353672	13354972	+	LCP		GSCLC_low		
2700054A10Rik	72578	chr17		13553694	13554994	-	LCP				GSCLC_low
Vmn2r94	665227	chr17		18277166	18278466	-	LCP	GSCLC_low			GSCLC_low
Zscan10	332221	chr17		23599956	23601256	+	LCP				GSCLC_low
Gm9705	677156	chr17		32620419	32621719	+	LCP				GSCLC_low
AA388235	433100	chr17		33980592	33981892	+	HCP	GSCLC_low	GSCLC_low		GSCLC_low
H2-Eb1	14969	chr17		34304967	34306267	+	LCP	GSCLC_low		GSCLC_low	
H2-T24	15042	chr17		36020160	36021460	-	LCP		GSCLC_low		GSCLC_low
Olfr113	258286	chr17		37575021	37576321	-	LCP	GSCLC_low			
Olfr115	257908	chr17		37610379	37611679	-	LCP	GSCLC_low		GSCLC_low	GSCLC_low
Olfr116	258625	chr17		37624233	37625533	-	LCP	GSCLC_low			
A530064D06Rik	328830	chr17		48166857	48168157	-	LCP		GSCLC_low		GSCLC_low
Gpr151	240239	chr18		42579252	42580552	-	LCP		GSCLC_low		
Npy6r	18169	chr18		44269227	44270527	+	LCP				GSCLC_low
1700044K03Rik	67321	chr18		49522389	49523689	+	ICP	GSCLC_low	GSCLC_low	GSCLC_low	
AA667203	100503467	chr18		64893844	64895144	+	LCP				
D730045A05Rik	77855	chr18		74017007	74018307	+	LCP		GSCLC_low		
Mir5127	100628596	chr18		81991680	81992980	-	LCP		GSCLC_low		
Ptpncap	19265	chr19		4153746	4155046	+	LCP		GSCLC_low		
4930481A15Rik	74931	chr19		5405974	5407274	+	HCP	GSCLC_low	GSCLC_low	GSCLC_low	GSCLC_low
Olfr1449	258300	chr19		12933840	12935140	+	LCP			GSCLC_low	GSCLC_low
Asah2	54447	chr19		32102740	32104040	-	ICP		GSCLC_low		
Entpd1	12495	chr19		40658894	40660194	+	ICP		GSCLC_low		
Gm6747	627352	chr19		41524364	41525664	+	ICP	GSCLC_low			

LOC100503558	100503558	chr19		53459715	53461015	+	ICP		GSCLC_low	GSCLC_high	
Ssxb7	387284	chrX		8636915	8638215	+	ICP	GSCLC_low	GSCLC_low		GSCLC_low
Gm14517	100503053	chrX		15526529	15527829	-	LCP			GSCLC_low	
4930447F04Rik	74862	chrX		66303824	66305124	-	LCP			GSCLC_low	
LOC100503280	100503280	chrX		74968725	74970025	-	LCP		GSCLC_low		
Arr3	170735	chrX		100604597	100605897	+	LCP	GSCLC_low	GSCLC_low	GSCLC_low	GSCLC_low
Satl1	73809	chrX		112406379	112407679	-	LCP	GSCLC_low	GSCLC_low	GSCLC_low	GSCLC_low
Gm5942	546361	chrX		114774248	114775548	-	ICP				GSCLC_low
Pramel3	83565	chrX		135301416	135302716	+	ICP	GSCLC_low	GSCLC_low		GSCLC_low
C330013F16Rik	78526	chrX		139357338	139358638	-	LCP	GSCLC_low	GSCLC_low	GSCLC_high	
Mid2	23947	chrX		140677128	140678428	+	LCP		GSCLC_low		GSCLC_high
Siy	21674	chrY		2663258	2664558	-	LCP				GSCLC_low
LOC100040083	100040083	chrY		8069593	8070893	-	LCP	GSCLC_low		GSCLC_low	GSCLC_low
LOC100861888	100861888	chrY		10066081	10067381	-	LCP	GSCLC_low			
LOC100861837	100861837	chrY		90743797	90745097	+	HCP			GSCLC_low	

Differentially methylated genes at promoters, GSCs $\leq$ GSCLCs

Name	Entrez_id	chr	st	end	strand	Class	Promoter methylation, vs. GSCs			
							GSCLC1	GSCLC2	GSCLC3	GSCLC4
Adhfe1	76187	chr1	9547146	9548446	+	ICP		GSCLC_high		GSCLC_high
3110035E14Rik	76982	chr1	9600367	9601667	+	ICP				GSCLC_high
Snord87	266793	chr1	9942143	9943443	-	ICP		GSCLC_high		
Cpa6	329093	chr1	10719543	10720843	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Kcnb2	98741	chr1	15311552	15312852	+	ICP				GSCLC_high
Pkhd1	241035	chr1	20617657	20618957	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
4933415F23Rik	66755	chr1	23101853	23103153	-	ICP		GSCLC_high		
Gm9898	791350	chr1	30719555	30720855	-	LCP			GSCLC_high	
Gm6489	624262	chr1	31286045	31287345	+	LCP				GSCLC_high
Gm9839	408192	chr1	32520599	32521899	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Prss39	21755	chr1	34497530	34498830	+	ICP			GSCLC_high	GSCLC_high
Prss40	21756	chr1	34560543	34561843	-	ICP		GSCLC_high		GSCLC_high
Neurl3	214854	chr1	36273025	36274325	-	ICP			GSCLC_high	GSCLC_low
Cnga3	12790	chr1	37218361	37219661	+	ICP				GSCLC_high
Il18r1	16182	chr1	40464652	40465952	+	LCP				GSCLC_high
Slc9a4	110895	chr1	40579327	40580627	+	ICP		GSCLC_high		GSCLC_high
Tmem182	381339	chr1	40804701	40806001	+	ICP				GSCLC_high
Gm8210	666642	chr1	43188227	43189527	+	ICP			GSCLC_high	
1500015O10Rik	78896	chr1	43729702	43731002	+	LCP		GSCLC_high		GSCLC_high
Gm3852	100042453	chr1	46011863	46013163	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Sdpr	20324	chr1	51288226	51289526	+	LCP		GSCLC_high		GSCLC_high
1700019A02Rik	69397	chr1	53187217	53188517	-	LCP		GSCLC_high		GSCLC_high
Rftn2	74013	chr1	55226382	55227682	-	ICP				GSCLC_high
Sgol2	68549	chr1	57984440	57985740	+	ICP	GSCLC_high	GSCLC_high		
Aox3	71724	chr1	58112236	58113536	+	ICP				GSCLC_high
Aox4	71872	chr1	58209497	58210797	+	ICP				GSCLC_high
Aox3l1	213043	chr1	58277426	58278726	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Cflar	12633	chr1	58712386	58713686	+	ICP		GSCLC_high		
Als2cr11	73463	chr1	59094500	59095800	-	ICP		GSCLC_high		GSCLC_high
Cdk15	271697	chr1	59256007	59257307	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
9530026F06Rik	77341	chr1	61377532	61378832	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
4930487H11Rik	74992	chr1	62794332	62795632	-	ICP				GSCLC_high
Gm20342	100504668	chr1	63114850	63116150	+	LCP		GSCLC_high		
Gpr1	241070	chr1	63213809	63215109	-	ICP		GSCLC_high		GSCLC_high
Cryge	12968	chr1	65050763	65052063	-	ICP			GSCLC_high	GSCLC_high
Crygd	12967	chr1	65063040	65064340	-	ICP				GSCLC_high
Crygc	12966	chr1	65073121	65074421	-	ICP				GSCLC_high
Crygb	12965	chr1	65081867	65083167	-	ICP				GSCLC_high
Cryga	12964	chr1	65102963	65104263	-	ICP		GSCLC_high		
Myl1	17901	chr1	66944656	66945956	-	ICP				GSCLC_high
Tnp1	21958	chr1	73015499	73016799	-	ICP				GSCLC_high
1700027A15Rik	69449	chr1	73015136	73016436	+	ICP		GSCLC_high		GSCLC_high
Vil1	22349	chr1	74408484	74409784	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Resp18	19711	chr1	75277980	75279280	-	ICP				GSCLC_high
Accn4	241118	chr1	75449610	75450910	+	ICP	GSCLC_high			GSCLC_high
Fam124b	241128	chr1	80213544	80214844	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
9430031J16Rik	241134	chr1	81076417	81077717	+	LCP				GSCLC_high
Krtap28-13	71386	chr1	83060030	83061330	+	LCP		GSCLC_high	GSCLC_high	
Sp140	434484	chr1	85599803	85601103	+	LCP			GSCLC_high	
Spata3	70060	chr1	86021042	86022342	+	ICP		GSCLC_high		
Gm5258	383538	chr1	86322367	86323667	+	ICP	GSCLC_high			
Nmur1	14767	chr1	86387741	86389041	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Prss56	69453	chr1	87182593	87183893	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Chmg	11449	chr1	87204911	87206211	+	LCP			GSCLC_high	
Inpp5d	16331	chr1	87619412	87620712	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
1700067G17Rik	73475	chr1	89015213	89016513	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Iqca	74918	chr1	90153001	90154301	-	ICP			GSCLC_high	
Gm19636	100503326	chr1	91353767	91355067	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
1700020N18Rik	67086	chr1	91405629	91406929	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Pdcd1	18566	chr1	94052153	94053453	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Sco6b1	67854	chr1	96997160	96998460	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Sco6c1	74441	chr1	97127903	97129203	-	ICP		GSCLC_high		GSCLC_high
Gm7133	634331	chr1	97161960	97163260	+	LCP		GSCLC_high		GSCLC_high
Gm7135	634346	chr1	97345529	97346829	+	ICP		GSCLC_high		GSCLC_high
Sco6d1	70866	chr1	98420224	98421524	+	ICP		GSCLC_high		GSCLC_high
Gm20268	100504525	chr1	101154868	101156168	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Gm10193	100042023	chr1	105763544	105764844	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Serpinh5	20724	chr1	106860280	106861580	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Cdh19	227485	chr1	110976972	110978272	-	LCP			GSCLC_high	GSCLC_high
Gm10191	100042740	chr1	129801369	129802669	-	ICP	GSCLC_low		GSCLC_high	GSCLC_low
Avpr1b	26361	chr1	131598214	131599514	+	LCP			GSCLC_high	GSCLC_high
Slc26a9	320718	chr1	131743122	131744422	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Myog	17928	chr1	134289104	134290404	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Elf3	13710	chr1	135258072	135259372	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
Lmod1	93689	chr1	135323913	135325213	+	LCP			GSCLC_high	GSCLC_high
4933409D19Rik	71084	chr1	136605357	136606657	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Mir181a-1	735252	chr1	137965555	137966855	+	ICP	GSCLC_high			GSCLC_high
Mir181b-1	723890	chr1	137965739	137967039	+	ICP	GSCLC_high			GSCLC_high
Gm4845	226472	chr1	141256758	141258058	-	LCP		GSCLC_high		
Fam5c	215378	chr1	146494766	146496066	+	ICP				GSCLC_high

<i>Ncf2</i>	17970	chr1	152806990	152808290	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
<i>E330020D12Rik</i>	626058	chr1	153413833	153415133	-	ICP	GSCLC_high			
<i>Zfp648</i>	207678	chr1	154200287	154201587	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>4930452N14Rik</i>	78112	chr1	154256506	154257806	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Pappa2</i>	23850	chr1	158957038	158958338	-	LCP		GSCLC_high		GSCLC_high
<i>Tnr</i>	21960	chr1	159522869	159524169	+	LCP				GSCLC_high
<i>Tnn</i>	329278	chr1	160153175	160154475	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm6177</i>	620750	chr1	160892220	160893520	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Tnfsf4</i>	22164	chr1	161394538	161395838	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Fasl</i>	14103	chr1	161788095	161789395	-	LCP				GSCLC_high
<i>Dnm3os</i>	474332	chr1	162216723	162218023	+	LCP				GSCLC_high
<i>Mir199a-2</i>	723821	chr1	162216914	162218214	+	LCP				GSCLC_high
<i>Mettl11b</i>	240879	chr1	163724832	163726132	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm16548</i>	100503816	chr1	164151817	164153117	-	LCP			GSCLC_high	
<i>F5</i>	14067	chr1	164150959	164152259	+	LCP			GSCLC_high	
<i>4930568G15Rik</i>	75857	chr1	165091530	165092830	-	ICP			GSCLC_high	
<i>Cd247</i>	12503	chr1	165787781	165789081	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Rgs5</i>	19737	chr1	169654601	169655901	+	LCP			GSCLC_high	
<i>1700084C01Rik</i>	78465	chr1	169928039	169929339	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Fcer1g</i>	14127	chr1	171233949	171235249	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
<i>Arhgap30</i>	226652	chr1	171388060	171389360	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Slamf6</i>	30925	chr1	171916637	171917937	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
<i>4933439K11Rik</i>	71319	chr1	172550406	172551706	-	LCP				GSCLC_high
<i>Olfr414</i>	258756	chr1	174429530	174430830	+	ICP		GSCLC_high		GSCLC_high
<i>Gm7068</i>	631584	chr1	177807575	177808875	+	ICP		GSCLC_high		
<i>Gm16432</i>	545391	chr1	177990535	177991835	+	ICP	GSCLC_high	GSCLC_high		GSCLC_high
<i>1700047M11Rik</i>	67330	chr1	182299934	182301234	+	LCP	GSCLC_high			GSCLC_high
<i>Mosc1</i>	66112	chr1	184810913	184812213	-	HCP				GSCLC_high
<i>Mir1981</i>	100316821	chr1	184822088	184823388	-	LCP			GSCLC_high	GSCLC_high
<i>9330162B11Rik</i>	320272	chr1	188008590	188009890	-	ICP			GSCLC_high	
<i>Mir3473c</i>	100628582	chr1	191998234	191999534	-	LCP		GSCLC_high		
<i>Gm19753</i>	100503531	chr1	193271261	193272561	+	LCP		GSCLC_high		
<i>A330023F24Rik</i>	320977	chr1	195016499	195017799	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
<i>Cellf2</i>	14007	chr2	7395798	7397098	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Gm13262</i>	100126244	chr2	9905251	9906551	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Cubn</i>	65969	chr2	13491476	13492776	-	ICP	GSCLC_high			GSCLC_high
<i>Mrc1</i>	17533	chr2	14228514	14229814	+	LCP				GSCLC_high
<i>H2afb1</i>	68231	chr2	17996546	17997846	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm20093</i>	100504159	chr2	18436409	18437709	-	ICP				GSCLC_high
<i>Psd4</i>	215632	chr2	24384497	24385797	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Pax8</i>	18510	chr2	24475166	24476466	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
<i>Lrrc26</i>	227618	chr2	25289011	25290311	+	HCP				GSCLC_high
<i>Dpp7</i>	83768	chr2	25355932	25357232	-	LCP			GSCLC_high	GSCLC_high
<i>Sohlh1</i>	227631	chr2	25846848	25848148	-	ICP		GSCLC_high		GSCLC_high
<i>Gfi1b</i>	14582	chr2	28621582	28622882	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm14488</i>	100038700	chr2	30716643	30717943	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Ptges</i>	64292	chr2	30902897	30904197	-	ICP	GSCLC_high			
<i>Mir199b</i>	387239	chr2	32317560	32318860	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Eng</i>	13805	chr2	32645695	32646995	+	ICP			GSCLC_high	
<i>Gm13404</i>	100504427	chr2	33977346	33978646	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Traf1</i>	22029	chr2	34961372	34962672	-	ICP	GSCLC_high	GSCLC_high		GSCLC_high
<i>Gm13446</i>	100042194	chr2	35558302	35559602	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Dab2ip</i>	69601	chr2	35557558	35558858	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Olfr352</i>	258942	chr2	36868668	36869968	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Olfr366</i>	236509	chr2	37218591	37219891	+	LCP			GSCLC_high	
<i>Nr5a1</i>	26423	chr2	38714142	38715442	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Kynu</i>	70789	chr2	43554429	43555729	+	LCP			GSCLC_high	GSCLC_high
<i>Tnfrsf6</i>	21930	chr2	52037213	52038513	+	ICP				GSCLC_high
<i>Galnt5</i>	241391	chr2	57997255	57998555	+	LCP		GSCLC_high		GSCLC_high
<i>Cytlp</i>	227929	chr2	58159722	58161022	-	ICP				GSCLC_high
<i>Gm13544</i>	100502932	chr2	58275879	58277179	+	ICP	GSCLC_high	GSCLC_high		GSCLC_high
<i>Gm13570</i>	667103	chr2	60098688	60099988	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Tank</i>	21353	chr2	61577686	61578986	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Tbr1</i>	21375	chr2	61803553	61804853	+	ICP				GSCLC_high
<i>Slc4a10</i>	94229	chr2	62045615	62046915	+	LCP				GSCLC_high
<i>Gcg</i>	14526	chr2	62483253	62484553	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Fap</i>	14089	chr2	62573621	62574921	-	ICP				GSCLC_high
<i>Scn3a</i>	20269	chr2	65567092	65568392	-	ICP				GSCLC_high
<i>Csmp3</i>	77771	chr2	65844867	65846167	+	ICP			GSCLC_high	GSCLC_high
<i>Scn1a</i>	20265	chr2	66440437	66441737	-	LCP			GSCLC_high	GSCLC_high
<i>Gm13629</i>	100038743	chr2	66439980	66441280	+	ICP				GSCLC_high
<i>Scn7a</i>	20272	chr2	66784510	66785810	-	LCP				GSCLC_high
<i>Kbtbd10</i>	228003	chr2	69669220	69670520	+	ICP				GSCLC_high
<i>Myo3b</i>	329421	chr2	70038226	70039526	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Dlx1as</i>	111970	chr2	71537491	71538791	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>8430437L04Rik</i>	74541	chr2	72702610	72703910	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Hoxd12</i>	15432	chr2	74674130	74675430	+	HCP				GSCLC_high
<i>Mir10b</i>	387144	chr2	74725170	74726470	+	ICP			GSCLC_high	GSCLC_high
<i>Gm13653</i>	545423	chr2	75191377	75192677	+	ICP	GSCLC_high	GSCLC_high		GSCLC_high
<i>Ttn</i>	22138	chr2	76982147	76983447	-	ICP				GSCLC_high
<i>Ccdc141</i>	545428	chr2	77170235	77171535	-	ICP				GSCLC_high
<i>Gm9928</i>	100126874	chr2	79409253	79410553	+	ICP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Ppp1r1c</i>	75276	chr2	79706880	79708180	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Pde1a</i>	18573	chr2	80129012	80130312	-	ICP	GSCLC_high			GSCLC_high
<i>Mir684-1</i>	735274	chr2	80628390	80629690	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Fsip2</i>	241516	chr2	82942740	82944040	+	ICP		GSCLC_high		
<i>Zswim2</i>	71861	chr2	83940826	83942126	-	ICP			GSCLC_high	
<i>Calcr1</i>	54598	chr2	84424866	84426166	-	ICP				GSCLC_high
<i>Gm13718</i>	100270744	chr2	84658179	84659479	+	HCP		GSCLC_high	GSCLC_high	
<i>Serping1</i>	12258	chr2	84775029	84776329	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Tnks1bp1</i>	228140	chr2	85049560	85050860	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Aplnr</i>	23796	chr2	85135460	85136760	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>4833423E24Rik</i>	228151	chr2	85518535	85519835	-	LCP				GSCLC_high
<i>Olfr1009</i>	258565	chr2	85720507	85721807	+	ICP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Olfr1045</i>	259019	chr2	86198350	86199650	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Olfr1057</i>	404325	chr2	86375010	86376310	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Olfr152</i>	258640	chr2	87781636	87782936	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	

<i>Olfr48</i>	18347	chr2	89844571	89845871	-	ICP		GSCLC_high		GSCLC_high
<i>Gm13777</i>	279067	chr2	91030722	91032022	-	ICP				GSCLC_high
<i>Slpi1</i>	20375	chr2	91095897	91097197	+	LCP		GSCLC_high		
<i>Nr1h3</i>	22259	chr2	91194716	91196016	-	ICP	GSCLC_high			
<i>F2</i>	14061	chr2	91636014	91637314	-	LCP		GSCLC_high		
<i>Syt13</i>	80976	chr2	92914201	92915501	+	HCP				GSCLC_high
<i>Cd44</i>	12505	chr2	102901265	102902565	-	ICP				GSCLC_high
<i>Gm13939</i>	100038454	chr2	109912919	109914219	-	ICP		GSCLC_high		GSCLC_high
<i>4930430A15Rik</i>	67575	chr2	111229200	111230500	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Chm5</i>	213788	chr2	112480417	112481717	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>LOC100862258</i>	100862258	chr2	113920005	113921305	-	ICP				GSCLC_high
<i>Gm13981</i>	241621	chr2	117054666	117055966	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Plcb2</i>	18796	chr2	118728038	118729338	-	LCP			GSCLC_high	
<i>A430105I19Rik</i>	214239	chr2	118762261	118763561	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Gm12924</i>	100502626	chr2	119292382	119293682	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Ltk</i>	17005	chr2	119760031	119761331	-	LCP		GSCLC_high		
<i>Slc24a5</i>	317750	chr2	125067227	125068527	+	LCP		GSCLC_high		GSCLC_high
<i>Fahd2a</i>	68126	chr2	127444165	127445465	-	HCP			GSCLC_high	
<i>Kcnp3</i>	56461	chr2	127520970	127522270	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Prom2</i>	192212	chr2	127541017	127542317	-	HCP		GSCLC_high		GSCLC_high
<i>Mall</i>	228576	chr2	127729497	127730797	-	ICP	GSCLC_high		GSCLC_high	
<i>AU015228</i>	99169	chr2	130099494	130100794	+	LCP			GSCLC_high	GSCLC_high
<i>Prnd</i>	26434	chr2	131949961	131951261	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Sptlc3</i>	228677	chr2	139493020	139494320	+	LCP				GSCLC_high
<i>1700010M22Rik</i>	66328	chr2	144822766	144824066	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Rin2</i>	74030	chr2	145785216	145786516	+	LCP	GSCLC_high			GSCLC_high
<i>Cd93</i>	17064	chr2	148443135	148444435	-	LCP				GSCLC_high
<i>Cst12</i>	69362	chr2	148788461	148789761	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>9230104L09Rik</i>	77705	chr2	148850534	148851834	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
<i>Vsx1</i>	114889	chr2	150688737	150690037	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>4930442J19Rik</i>	74660	chr2	151301139	151302439	+	ICP	GSCLC_high	GSCLC_high		GSCLC_high
<i>Sdcbp2</i>	228765	chr2	151571732	151573032	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm14164</i>	791417	chr2	152344769	152346069	+	LCP	GSCLC_high		GSCLC_high	
<i>Defb36</i>	266620	chr2	152603427	152604727	+	ICP		GSCLC_high		
<i>Cox4i2</i>	84682	chr2	152753273	152754573	+	ICP		GSCLC_high		
<i>Mylk2</i>	228785	chr2	152910452	152911752	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Foxs1</i>	14239	chr2	152932808	152934108	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>1700007I08Rik</i>	70362	chr2	154550876	154552176	+	LCP		GSCLC_high		GSCLC_high
<i>Fam83c</i>	71405	chr2	155834454	155835754	-	LCP		GSCLC_high		GSCLC_high
<i>Ghrh</i>	14601	chr2	157346255	157347555	-	LCP			GSCLC_high	GSCLC_high
<i>Lbp</i>	16803	chr2	158305593	158306893	+	LCP	GSCLC_high		GSCLC_high	
<i>4933416E03Rik</i>	71081	chr2	159946441	159947741	+	ICP		GSCLC_high		GSCLC_high
<i>Gm11449</i>	383770	chr2	161482638	161483938	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm20267</i>	100504524	chr2	162919284	162920584	-	ICP			GSCLC_high	
<i>Jph2</i>	59091	chr2	163397593	163398893	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Pabpc1l</i>	381404	chr2	164024550	164025850	+	ICP	GSCLC_high			GSCLC_high
<i>Wfdc12</i>	192200	chr2	164190158	164191458	-	LCP	GSCLC_high			GSCLC_high
<i>Wfdc15a</i>	68221	chr2	164199717	164201017	-	ICP	GSCLC_high	GSCLC_high		
<i>Rbpjl</i>	19668	chr2	164402294	164403594	+	ICP	GSCLC_high	GSCLC_high		GSCLC_high
<i>Wfdc9</i>	629754	chr2	164654566	164655866	-	ICP				GSCLC_high
<i>Wfdc10</i>	629756	chr2	164655146	164656446	+	ICP				GSCLC_high
<i>Gm14316</i>	641368	chr2	164714405	164715705	+	LCP		GSCLC_high		
<i>Cd40</i>	21939	chr2	165054736	165056036	+	ICP	GSCLC_high		GSCLC_high	
<i>LOC100862070</i>	100862070	chr2	165180019	165181319	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Slc13a3</i>	114644	chr2	165472797	165474097	-	HCP				GSCLC_high
<i>Kcng1</i>	241794	chr2	168268931	168270231	-	ICP			GSCLC_high	
<i>Cass4</i>	320664	chr2	172392894	172394194	+	ICP	GSCLC_high		GSCLC_high	
<i>Spo11</i>	26972	chr2	172978942	172980242	+	HCP		GSCLC_high	GSCLC_high	
<i>1700021F07Rik</i>	72221	chr2	173521692	173522992	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Zfp831</i>	100043757	chr2	174642634	174643934	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
<i>Gm14439</i>	545487	chr2	175061533	175062833	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm14407</i>	635470	chr2	177085402	177086702	-	ICP	GSCLC_high	GSCLC_high		GSCLC_high
<i>4930591A17Rik</i>	68175	chr2	179414036	179415336	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
<i>Gm6307</i>	622283	chr2	180384704	180386004	+	ICP				GSCLC_high
<i>BC051628</i>	332713	chr2	181219116	181220416	+	ICP			GSCLC_high	
<i>4930526D03Rik</i>	277496	chr2	181698042	181699342	-	LCP		GSCLC_high	GSCLC_high	
<i>Gm17308</i>	100503882	chr3	5089376	5090676	+	ICP	GSCLC_high	GSCLC_high		GSCLC_high
<i>2700069I18Rik</i>	72608	chr3	5220423	5221723	-	ICP		GSCLC_high		GSCLC_high
<i>1700008P02Rik</i>	69347	chr3	6620043	6621343	-	LCP		GSCLC_high		GSCLC_high
<i>Fabp9</i>	21884	chr3	10196822	10198122	-	ICP	GSCLC_high			
<i>Fabp12</i>	75497	chr3	10300783	10302083	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>A930001A20Rik</i>	77127	chr3	14970301	14971601	+	ICP			GSCLC_high	GSCLC_high
<i>2610100L16Rik</i>	70441	chr3	17789021	17790321	+	ICP				GSCLC_high
<i>Cypt12</i>	75439	chr3	17947544	17948844	+	LCP		GSCLC_high		
<i>Naaladl2</i>	635702	chr3	24783137	24784437	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Kcnmb2</i>	72413	chr3	31901803	31903103	+	ICP				GSCLC_high
<i>Sox2ot</i>	320478	chr3	34559481	34560781	+	LCP				GSCLC_high
<i>Mir1897</i>	100316679	chr3	34637564	34638864	+	ICP	GSCLC_high		GSCLC_high	
<i>Ccdc144b</i>	241943	chr3	36053147	36054447	-	ICP		GSCLC_high	GSCLC_high	
<i>1700017G19Rik</i>	100040882	chr3	40522512	40523812	-	ICP				GSCLC_high
<i>1700027H10Rik</i>	72274	chr3	45438909	45440209	-	LCP	GSCLC_high	GSCLC_high		
<i>Mab21l1</i>	17116	chr3	55781610	55782910	+	ICP				GSCLC_high
<i>1700007F19Rik</i>	67850	chr3	58163407	58164707	-	ICP				GSCLC_high
<i>Clrn1</i>	229320	chr3	58884812	58886112	-	ICP				GSCLC_high
<i>LOC100503824</i>	100503824	chr3	62340148	62341448	-	ICP		GSCLC_high		
<i>Gpr149</i>	229357	chr3	62604740	62606040	-	LCP		GSCLC_high		
<i>Iqcj</i>	208426	chr3	67891320	67892620	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Iqcj-schip1</i>	100505386	chr3	67891320	67892620	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Il12a</i>	16159	chr3	68689744	68691044	+	LCP			GSCLC_high	GSCLC_high
<i>Arl14</i>	71619	chr3	69221519	69222819	+	ICP				GSCLC_high
<i>Sis</i>	69983	chr3	72966466	72967766	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>4930509J09Rik</i>	74693	chr3	73481251	73482551	-	LCP		GSCLC_high		GSCLC_high
<i>Gm17359</i>	100233207	chr3	79344476	79345776	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Trim2</i>	80890	chr3	84220477	84221777	-	LCP			GSCLC_high	
<i>Tigd4</i>	403175	chr3	84592674	84593974	+	LCP			GSCLC_high	GSCLC_high
<i>Tmem154</i>	320782	chr3	84665292	84666592	+	ICP				GSCLC_high
<i>4933430H15Rik</i>	74485	chr3	87748223	87749523	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high

Gm19439	100502895	chr3	88029885	88031185	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Gm19451	100502914	chr3	88138998	88140298	-	ICP			GSCLC_high	
Gm3764	100042277	chr3	88205926	88207226	+	LCP		GSCLC_high		GSCLC_high
Mir1905	100316808	chr3	88535982	88537282	-	HCP	GSCLC_high			
Rab25	53868	chr3	88547879	88549179	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Rxlp4	242093	chr3	88652742	88654042	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm15998	100038411	chr3	89314539	89315839	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Dcst1	77772	chr3	89364839	89366139	-	LCP			GSCLC_high	
Dcst2	329702	chr3	89364500	89365800	+	LCP			GSCLC_high	
Mir190b	100124481	chr3	90069120	90070420	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
Nup210l	77595	chr3	90103232	90104532	+	ICP		GSCLC_high	GSCLC_high	
S100a14	66166	chr3	90525949	90527249	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
S100a6	20200	chr3	90611994	90613294	+	ICP				GSCLC_high
Lce3a	545548	chr3	92925830	92927130	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm9782	630994	chr3	92957180	92958480	+	LCP			GSCLC_high	GSCLC_high
Gm19861	100503731	chr3	93017349	93018649	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
C2cd4d	271944	chr3	94361544	94362844	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Rorc	19885	chr3	94371926	94373226	+	LCP		GSCLC_high		GSCLC_high
Lingo4	320747	chr3	94398319	94399619	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Celf3	78784	chr3	94477931	94479231	+	LCP			GSCLC_high	GSCLC_high
Selenbp1	20341	chr3	94932183	94933483	+	LCP			GSCLC_high	GSCLC_high
Anxa9	71790	chr3	95306776	95308076	-	LCP	GSCLC_high		GSCLC_high	
Ecm1	13601	chr3	95739169	95740469	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Car14	23831	chr3	95904239	95905539	-	ICP		GSCLC_high	GSCLC_high	
Mtmr11	194126	chr3	96161070	96162370	+	ICP	GSCLC_high		GSCLC_high	
Rnu1b2	19845	chr3	96373121	96374421	+	HCP			GSCLC_high	
Gja5	14613	chr3	97031516	97032816	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Adam30	71078	chr3	98159912	98161212	+	ICP		GSCLC_high	GSCLC_high	
Reg4	67709	chr3	98221256	98222556	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Hmgcs2	15360	chr3	98279531	98280831	+	LCP				GSCLC_high
4930564D02Rik	75269	chr3	105065944	105067244	+	LCP				GSCLC_high
Al504432	229694	chr3	107038604	107039904	+	ICP			GSCLC_high	GSCLC_high
Fndc7	320181	chr3	108889608	108890908	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
4930443G12Rik	74686	chr3	109079599	109080899	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Vcam1	22329	chr3	116129288	116130588	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
D3Bwg0562e	229791	chr3	117360476	117361776	-	LCP				GSCLC_high
Abca4	11304	chr3	122043560	122044860	+	ICP				GSCLC_high
4930447N08Rik	71647	chr3	122801580	122802880	-	LCP				GSCLC_high
Gm9372	668809	chr3	124291138	124292438	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Ndst4	64580	chr3	125403191	125404491	+	ICP				GSCLC_high
Enpep	13809	chr3	129332349	129333649	-	ICP	GSCLC_high			GSCLC_high
Egf	13645	chr3	129754922	129756222	-	LCP			GSCLC_high	GSCLC_high
6330410L21Rik	319224	chr3	129752858	129754158	+	LCP			GSCLC_high	GSCLC_high
LOC100862291	100862291	chr3	130695025	130696325	+	ICP			GSCLC_high	
Arlhgef38	77669	chr3	133234489	133235789	-	LCP		GSCLC_high		GSCLC_high
Gm9799	791324	chr3	135726444	135727744	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Bank1	242248	chr3	136325646	136326946	-	LCP				GSCLC_high
Emcn	59308	chr3	137340178	137341478	+	LCP			GSCLC_high	GSCLC_high
Dapp1	26377	chr3	137981149	137982449	-	LCP			GSCLC_high	
4930579F01Rik	67741	chr3	138186313	138187613	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Adh6b	100417514	chr3	138333196	138334496	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
4930425O10Rik	74635	chr3	138726584	138727884	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Bmpr1b	12167	chr3	141981851	141983151	-	ICP				GSCLC_high
Gbp5	229898	chr3	142496034	142497334	+	ICP				GSCLC_high
Gm6260	621809	chr3	143711743	143713043	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm16233	100504497	chr3	144946661	144947961	+	LCP		GSCLC_high		GSCLC_high
Gm10287	100038391	chr3	149225345	149226645	-	ICP	GSCLC_high			GSCLC_high
4930555A03Rik	100504653	chr3	151293262	151294562	+	ICP			GSCLC_high	GSCLC_high
Ifi44	99899	chr3	151749559	151750859	-	LCP			GSCLC_high	GSCLC_high
H28	15061	chr3	151762491	151763791	-	ICP			GSCLC_high	
Sdr16c5	242285	chr4	4019263	4020563	-	LCP				GSCLC_high
Mir3471-1	100499521	chr4	10845230	10846530	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm11827	100503518	chr4	11121905	11123205	+	LCP		GSCLC_high	GSCLC_high	
Slc7a13	74087	chr4	19817827	19819127	+	LCP				GSCLC_high
4930480G23Rik	74988	chr4	20005339	20006639	-	LCP		GSCLC_high		GSCLC_high
Gm136	214568	chr4	34755859	34757159	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
4930509K18Rik	75819	chr4	40312332	40313632	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Tmem215	320500	chr4	40471280	40472580	+	ICP				GSCLC_high
Cntfr	12804	chr4	41696691	41697991	-	ICP	GSCLC_high			GSCLC_high
Fam166b	329831	chr4	43428734	43430034	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Cd72	12517	chr4	43454226	43455526	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Slit1	54390	chr4	43483309	43484609	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Gm12454	100503819	chr4	43508347	43509647	-	ICP			GSCLC_high	GSCLC_high
5430416O09Rik	71406	chr4	43729134	43730434	+	LCP			GSCLC_high	
Mir5106	100628618	chr4	44220867	44222167	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Ppp3r2	19059	chr4	49681583	49682883	-	ICP		GSCLC_high		
4930522O17Rik	78180	chr4	53245296	53246596	+	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Al427809	381524	chr4	53269832	53271132	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Actl7b	11471	chr4	56741025	56742325	-	LCP			GSCLC_high	GSCLC_high
Slc46a2	30936	chr4	59914656	59915956	-	ICP				GSCLC_high
Klf12	16552	chr4	63171731	63173031	-	LCP				GSCLC_high
Tnfrsf15	326623	chr4	63744713	63746013	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Tnfrsf8	21949	chr4	63860884	63862184	-	LCP		GSCLC_high		
Tlr4	21898	chr4	66826911	66828211	+	LCP				GSCLC_high
Aldoa1t1	353204	chr4	72852234	72853534	-	LCP		GSCLC_high		
Gm5860	545641	chr4	82064480	82065780	+	LCP		GSCLC_high		GSCLC_high
Cer1	12622	chr4	82884751	82886051	-	LCP			GSCLC_high	GSCLC_high
Fam154a	75811	chr4	86557903	86559203	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Gm13271	435791	chr4	88753968	88755268	+	LCP		GSCLC_high		GSCLC_high
Ifne	230405	chr4	88879801	88881101	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Tek	21687	chr4	94738400	94739700	+	LCP				GSCLC_high
Cyp2j12	242546	chr4	96140752	96142052	-	LCP		GSCLC_high		GSCLC_high
Cyp2j11	100066	chr4	96348280	96349580	-	LCP				GSCLC_high
Cyp2j8	665095	chr4	96506986	96508286	-	LCP		GSCLC_high		
Nfia	18027	chr4	97581043	97582343	+	LCP			GSCLC_high	GSCLC_high
A730085A09Rik	399570	chr4	98792868	98794168	+	LCP			GSCLC_high	
Pde4b	18578	chr4	102253842	102255142	+	LCP			GSCLC_high	GSCLC_high

Tctex1d1	67344	chr4	102985479	102986779	+	LCP	GSCLC_high		GSCLC_high	
Acot11	329910	chr4	106799431	106800731	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Slc1a7	242607	chr4	107967434	107968734	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm12816	433745	chr4	112955886	112957186	-	ICP			GSCLC_high	GSCLC_high
Pdzk1ip1	67182	chr4	115087808	115089108	+	LCP		GSCLC_high	GSCLC_high	
Cyp4b1	13120	chr4	115647305	115648605	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Btbd19	78611	chr4	117125325	117126625	-	LCP		GSCLC_high	GSCLC_high	
Klf17	75753	chr4	117765266	117766566	-	LCP		GSCLC_high		GSCLC_high
4930538K18Rik	75180	chr4	119217817	119219117	-	LCP				GSCLC_high
Edn2	13615	chr4	120160524	120161824	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Tmco2	69469	chr4	1211108826	1211110126	-	LCP			GSCLC_high	GSCLC_high
Gm8359	666914	chr4	121396157	121397457	-	LCP				GSCLC_high
Rhbd12	230726	chr4	123786975	123788275	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
Gm10572	100038647	chr4	123896218	123897518	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Csf3r	12986	chr4	126023759	126025059	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
CK137956	635169	chr4	127970441	127971741	-	ICP				GSCLC_high
E330017L17Rik	319894	chr4	129905326	129906626	+	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Tinag1	94242	chr4	130174722	130176022	-	ICP	GSCLC_high		GSCLC_high	
Snora73b	100306945	chr4	132352126	132353426	-	ICP				GSCLC_high
E130218I03Rik	77490	chr4	134242863	134244163	+	LCP		GSCLC_high		
Trim63	433766	chr4	134314220	134315520	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
1700021N21Rik	69409	chr4	134449771	134451071	-	LCP			GSCLC_high	
1700029M20Rik	73937	chr4	135625755	135627055	+	ICP		GSCLC_high		GSCLC_high
Il22ra1	230828	chr4	135727259	135728559	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Htr1d	15552	chr4	136422624	136423924	+	LCP		GSCLC_high		
Cda	72269	chr4	138367555	138368855	-	ICP	GSCLC_high			
Pla2g5	18784	chr4	138863069	138864369	-	LCP	GSCLC_high		GSCLC_high	
Pad14	18602	chr4	140773803	140775103	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Agmat	75986	chr4	141745775	141747075	+	LCP		GSCLC_high		
4930455G09Rik	78917	chr4	142017113	142018413	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
Gm13141	545718	chr4	147527774	147529074	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Gm13154	433804	chr4	147552377	147553677	+	LCP			GSCLC_high	GSCLC_high
Rbp7	63954	chr4	149454568	149455868	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
4930589P08Rik	67748	chr4	151375543	151376843	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Rnf207	433809	chr4	152318225	152319525	-	ICP		GSCLC_high	GSCLC_high	
Tmem88b	320587	chr4	155785474	155786774	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Plekhn1	231002	chr4	156228142	156229442	-	LCP		GSCLC_high		
Mterf	545725	chr5	3893533	3894833	-	HCP		GSCLC_high	GSCLC_high	GSCLC_high
1700015F17Rik	381716	chr5	5478743	5480043	-	LCP			GSCLC_high	GSCLC_high
Nos3	18127	chr5	24363919	24365219	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Accn3	171209	chr5	24412551	24413851	+	LCP			GSCLC_high	
Mir671	735264	chr5	24591214	24592514	+	ICP	GSCLC_high	GSCLC_high		GSCLC_high
Crygn	214301	chr5	24757443	24758743	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Cct8l1	242891	chr5	25515167	25516467	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
Htr5a	15563	chr5	27841047	27842347	+	ICP				GSCLC_high
Il6	16193	chr5	30012261	30013561	+	ICP		GSCLC_high		GSCLC_high
Trim54	58522	chr5	31115712	31117012	+	LCP			GSCLC_high	GSCLC_high
A1839979	100740	chr5	31570991	31572291	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Plb1	665270	chr5	32231808	32233108	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Bst1	12182	chr5	43817993	43819293	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm5292	384179	chr5	43944083	43945383	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Ldb2	16826	chr5	44799307	44800607	-	LCP		GSCLC_high		GSCLC_high
Gm7931	100503799	chr5	46413444	46414744	+	ICP				GSCLC_high
Mir218-1	723822	chr5	48223042	48224342	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
4930448I18Rik	73965	chr5	50150433	50151733	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm8069	666377	chr5	54651721	54653021	-	ICP		GSCLC_high		GSCLC_high
5830416I19Rik	74757	chr5	64044073	64045373	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm3716	100042198	chr5	64610299	64611599	-	LCP		GSCLC_high		GSCLC_high
Tlr1	21897	chr5	64932299	64933599	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Klhl5	71778	chr5	65130331	65131631	+	ICP		GSCLC_low	GSCLC_high	
Gm3521	100041809	chr5	65857810	65859110	-	ICP		GSCLC_high		
Chma9	231252	chr5	65966224	65967524	+	ICP	GSCLC_high		GSCLC_high	GSCLC_high
9130230L23Rik	231253	chr5	66003885	66005185	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Phox2b	18935	chr5	67098726	67100026	-	ICP			GSCLC_high	GSCLC_high
C330024D21Rik	320479	chr5	67462998	67464298	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
Ociad2	433904	chr5	73338239	73339539	-	HCP				GSCLC_high
Dcun1d4	100737	chr5	73480155	73481455	+	ICP				GSCLC_high
Lrrc66	231296	chr5	73632021	73633321	-	LCP		GSCLC_high		GSCLC_high
Hopx	74318	chr5	77114723	77116023	-	ICP			GSCLC_high	
Tecr1	243078	chr5	83354795	83356095	-	LCP			GSCLC_high	
Stap1	56792	chr5	86070928	86072228	+	ICP			GSCLC_high	
Gnrhr	14715	chr5	86197470	86198770	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Tmprss11g	320454	chr5	86518200	86519500	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Ugt2a3	72094	chr5	87336795	87338095	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gc	14473	chr5	89457498	89458798	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
Pl4	56744	chr5	90771535	90772835	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Cxcl2	20310	chr5	90902999	90904299	+	ICP		GSCLC_high		
Btc	12223	chr5	91402594	91403894	-	LCP		GSCLC_high		GSCLC_high
1700063O14Rik	73452	chr5	91766900	91768200	-	ICP		GSCLC_high	GSCLC_high	
Ppef2	19023	chr5	92252759	92254059	-	ICP	GSCLC_high			GSCLC_high
Art3	109979	chr5	92330941	92332241	+	ICP				GSCLC_high
Cxcl10	15945	chr5	92348489	92349789	-	ICP			GSCLC_high	GSCLC_high
Prdm8	77630	chr5	98179969	98181269	+	ICP				GSCLC_high
Plac8	231507	chr5	100571805	100573105	-	LCP		GSCLC_high	GSCLC_high	
Mapk10	26414	chr5	103210934	103212234	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Spp1	20750	chr5	104434211	104435511	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Abcg3	27405	chr5	104982317	104983617	-	ICP		GSCLC_high	GSCLC_high	
Pde6b	18587	chr5	108387473	108388773	+	LCP		GSCLC_high		GSCLC_high
Plcxd1	403178	chr5	110099069	110100369	+	LCP				GSCLC_high
Gm1679	381667	chr5	110353196	110354496	+	LCP			GSCLC_high	GSCLC_high
C130026L21Rik	330164	chr5	111580661	111581961	+	ICP				GSCLC_high
E130006D01Rik	269683	chr5	111761328	111762628	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
1700028D13Rik	75569	chr5	112205863	112207163	+	ICP	GSCLC_high			
Gm6583	625424	chr5	112355633	112356933	-	LCP		GSCLC_high	GSCLC_high	
Asphd2	72898	chr5	112391813	112393113	-	LCP			GSCLC_high	
2900026A02Rik	243219	chr5	113162913	113164213	-	LCP	GSCLC_high		GSCLC_high	
Cmk1r1	14747	chr5	113649990	113651290	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high

Gm19941	100503883	chr5	113818357	113819657	+	ICP	GSCLC_high		GSCLC_high	
Oasl1	231655	chr5	114922340	114923640	+	ICP			GSCLC_high	
Hnf1a	21405	chr5	114970662	114971962	-	LCP		GSCLC_high		GSCLC_high
Cabp1	29867	chr5	115185721	115187021	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Tmem233	545798	chr5	116082846	116084146	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm7538	665194	chr5	119199618	119200918	-	LCP				GSCLC_high
G630008E18	330183	chr5	119625042	119626342	+	ICP			GSCLC_high	
Gm5563	433945	chr5	119831385	119832685	-	HCP				GSCLC_high
Tbx5	21388	chr5	119833763	119835063	+	LCP				GSCLC_high
Sds	231691	chr5	120475647	120476947	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Oas1g	23960	chr5	120887198	120888498	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Oas1a	246730	chr5	120907125	120908425	-	LCP				GSCLC_high
Cux2	13048	chr5	122047425	122048725	-	ICP	GSCLC_high			
Hvcn1	74096	chr5	122208837	122210137	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
B3gnt4	231727	chr5	123509560	123510860	+	LCP	GSCLC_high			GSCLC_high
Gpr81	243270	chr5	123879620	123880920	-	ICP			GSCLC_high	
Gm19631	100503298	chr5	125350975	125352275	+	LCP	GSCLC_high			
4933438B17Rik	71247	chr5	127029889	127031189	+	LCP				GSCLC_high
Pwif1	57749	chr5	128735346	128736646	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Rimbp2	231760	chr5	128952962	128954262	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Caln1	140904	chr5	130368558	130369858	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Syna	214292	chr5	134559771	134561071	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Eln	13717	chr5	134746854	134748154	-	ICP				GSCLC_high
Cldn4	12740	chr5	134946534	134947834	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Wbscr25	71304	chr5	135000950	135002250	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
2010001M06Rik	69812	chr5	135012757	135014057	-	LCP	GSCLC_high	GSCLC_high		
Trim56	384309	chr5	137115807	137117107	-	ICP	GSCLC_high			
Sap25	751865	chr5	137640573	137641873	+	ICP		GSCLC_high		GSCLC_high
Gjc3	118446	chr5	137962559	137963859	-	LCP	GSCLC_high			GSCLC_high
Gm5294	384244	chr5	138819180	138820480	+	ICP				GSCLC_high
Tmem184a	231832	chr5	139813883	139815183	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Card11	108723	chr5	141000196	141001496	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Papalb	56522	chr5	142529676	142530976	-	HCP		GSCLC_high		
2210019111Rik	70147	chr5	147271121	147272421	-	ICP			GSCLC_high	GSCLC_high
2210417A02Rik	70138	chr5	148740940	148742240	+	ICP		GSCLC_high	GSCLC_high	
8430423G03Rik	71473	chr5	148949350	148950650	+	ICP			GSCLC_high	
Wdr95	381693	chr5	149527779	149529079	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
LOC100861794	100861794	chr5	149811351	149812651	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Rxlp2	140498	chr5	150017775	150019075	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Gm5	194292	chr5	150501819	150503119	-	ICP		GSCLC_high		
Pon1	18979	chr6	5193546	5194846	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Ppp1r3a	140491	chr6	14754874	14756174	-	LCP				GSCLC_high
Gm4876	232599	chr6	17171427	17172727	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Ankrd7	75196	chr6	18865418	18866718	+	ICP				GSCLC_high
Lmod2	93677	chr6	24596871	24598171	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Mir592	735266	chr6	27936350	27937650	-	ICP	GSCLC_high			GSCLC_high
Lep	16846	chr6	29059321	29060621	+	ICP		GSCLC_high		GSCLC_high
Mest	17294	chr6	30732606	30733906	+	ICP		GSCLC_high		
Tmem140	68487	chr6	34862246	34863546	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Fam180a	208164	chr6	35325741	35327041	-	LCP		GSCLC_high		GSCLC_high
1700065J11Rik	73409	chr6	35329946	35331246	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
Mir490	735279	chr6	36420842	36422142	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Tmem213	77522	chr6	38108453	38109753	+	LCP			GSCLC_high	GSCLC_high
8030453O22Rik	77209	chr6	39526622	39527922	+	ICP		GSCLC_high	GSCLC_high	
Wee2	381759	chr6	40441963	40443263	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Olfr460	258381	chr6	40570488	40571788	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
1700074P13Rik	73481	chr6	40940157	40941457	-	ICP	GSCLC_high	GSCLC_high		GSCLC_high
Trbv12-1	100124672	chr6	41112667	41113967	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Trbv12-2	100124674	chr6	41117964	41119264	+	LCP		GSCLC_high		GSCLC_high
Trbv19	100124684	chr6	41177689	41178989	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Trbv23	100124688	chr6	41215173	41216473	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Trbj1-3	100125250	chr6	41533423	41534723	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Trbj1-4	100125251	chr6	41533911	41535211	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Trbj1-5	100125252	chr6	41534184	41535484	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Trbj1-6	100125253	chr6	41534654	41535954	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Trbj1-7	100125254	chr6	41534742	41536042	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Trbd2	100125247	chr6	41541263	41542563	+	LCP				GSCLC_high
Trbj2-1	100125255	chr6	41541854	41543154	+	LCP		GSCLC_high		GSCLC_high
Trbj2-2	100125256	chr6	41542057	41543357	+	LCP		GSCLC_high		GSCLC_high
Trpv6	64177	chr6	41636005	41637305	-	LCP			GSCLC_high	GSCLC_high
Tas2r126	387353	chr6	42433635	42434935	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Olfr448	258270	chr6	42895553	42896853	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Olfr447	258990	chr6	42910625	42911925	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Olfr437	258293	chr6	43166160	43167460	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Nobox	18291	chr6	43309154	43310454	-	ICP				GSCLC_high
9430018G01Rik	319812	chr6	43441529	43442829	+	LCP	GSCLC_high		GSCLC_high	
Gimap5	317757	chr6	48745297	48746597	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
2700086A05Rik	72628	chr6	52200224	52201524	+	HCP		GSCLC_high		GSCLC_high
Hoxa7	15404	chr6	52218173	52219473	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Hoxa9	15405	chr6	52226970	52228270	-	LCP				GSCLC_high
Ppp1r17	19051	chr6	56016615	56017915	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Gm5570	434019	chr6	60077119	60078419	+	LCP			GSCLC_high	
Mmn1	70945	chr6	60943417	60944717	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Hpgds	54486	chr6	65144330	65145630	-	ICP				GSCLC_high
Gm1070	381785	chr6	71292871	71294171	+	ICP			GSCLC_high	
Cd8b1	12526	chr6	71321912	71323212	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Cd8a	12525	chr6	71372527	71373827	+	LCP			GSCLC_high	GSCLC_high
4931417E11Rik	66740	chr6	73469267	73470567	-	LCP		GSCLC_high		GSCLC_high
Gm5576	434050	chr6	78214978	78216278	+	ICP				GSCLC_high
Lrrtm4	243499	chr6	80017977	80019277	+	LCP		GSCLC_high		GSCLC_high
Slc4a5	232156	chr6	83236475	83237775	+	LCP				GSCLC_high
Noto	384452	chr6	85422986	85424286	+	ICP		GSCLC_high	GSCLC_high	
Cml3	93674	chr6	85765344	85766644	-	ICP				GSCLC_high
2310040G24Rik	381792	chr6	86487827	86489127	-	LCP	GSCLC_high			
Asprv1	67855	chr6	86627274	86628574	+	LCP			GSCLC_high	GSCLC_high
Bmp10	12154	chr6	87428102	87429402	+	ICP				GSCLC_high
Gm5879	545864	chr6	87765825	87767125	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high

<i>Grip2</i>	243547	chr6	91806993	91808293	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>1700049E22Rik</i>	73395	chr6	100526500	100527800	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Cntn6</i>	53870	chr6	104492144	104493444	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm4604</i>	100043718	chr6	108140091	108141391	-	HCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Cav3</i>	12391	chr6	112458605	112459905	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Camk1</i>	52163	chr6	113343522	113344822	-	ICP			GSCLC_high	GSCLC_high
<i>Il17rc</i>	171095	chr6	113470555	113471855	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>4931417G12Rik</i>	70979	chr6	113600315	113601615	-	ICP			GSCLC_high	
<i>Timp4</i>	110595	chr6	115251449	115252749	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm8203</i>	666634	chr6	116172734	116174034	+	ICP		GSCLC_high		GSCLC_high
<i>Olfr212</i>	258019	chr6	116505616	116506916	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Olfr214</i>	258754	chr6	116555527	116556827	+	ICP				GSCLC_high
<i>Tmem72</i>	319776	chr6	116716358	116717658	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Klrg1</i>	50928	chr6	122282433	122283733	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>1700063H04Rik</i>	74269	chr6	122390479	122391779	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Aicda</i>	11628	chr6	122552909	122554209	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gdf3</i>	14562	chr6	122609671	122610971	-	ICP			GSCLC_high	GSCLC_high
<i>Dppa3</i>	73708	chr6	122625524	122626824	+	ICP			GSCLC_high	
<i>Gm10224</i>	100043805	chr6	122698628	122699928	-	ICP		GSCLC_high		
<i>Gm10420</i>	639606	chr6	122695101	122696401	+	HCP		GSCLC_high		GSCLC_high
<i>Clec4a3</i>	73149	chr6	122951615	122952915	+	LCP		GSCLC_high		GSCLC_high
<i>Clec4e</i>	56619	chr6	123289471	123290771	-	LCP				GSCLC_high
<i>C1rb</i>	667277	chr6	124569530	124570830	+	LCP		GSCLC_high		
<i>Mir141</i>	387159	chr6	124717585	124718885	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Mir200c</i>	723944	chr6	124717990	124719290	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Ptpn6</i>	15170	chr6	124738309	124739609	-	LCP	GSCLC_high	GSCLC_high		
<i>Gnb3</i>	14695	chr6	124839875	124841175	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Tapbpl</i>	213233	chr6	125231460	125232760	-	LCP	GSCLC_high		GSCLC_high	
<i>E130112N10Rik</i>	78668	chr6	125230376	125231676	+	LCP			GSCLC_high	
<i>Scnn1a</i>	20276	chr6	125320440	125321740	+	LCP			GSCLC_high	
<i>Ano2</i>	243634	chr6	125689519	125690819	+	LCP	GSCLC_high			
<i>Ntf3</i>	18205	chr6	126166344	126167644	-	ICP				GSCLC_high
<i>Fgf6</i>	14177	chr6	127014642	127015942	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Nrip2</i>	60345	chr6	128398866	128400166	+	ICP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Clec2i</i>	93675	chr6	128886714	128888014	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
<i>Cd69</i>	12515	chr6	129274969	129276269	-	LCP			GSCLC_high	GSCLC_high
<i>Clec1a</i>	243653	chr6	129451600	129452900	-	ICP			GSCLC_high	GSCLC_high
<i>Klrc2</i>	16642	chr6	129660196	129661496	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Klrc1</i>	16641	chr6	129678510	129679810	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Mir680-1</i>	735268	chr6	129690635	129691935	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Klra8</i>	16639	chr6	130129498	130130798	-	LCP		GSCLC_high	GSCLC_high	
<i>Gm5886</i>	545886	chr6	133767003	133768303	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Apold1</i>	381823	chr6	134981101	134982401	+	ICP	GSCLC_high		GSCLC_high	
<i>Emp1</i>	13730	chr6	135362031	135363331	+	LCP				GSCLC_high
<i>Mgp</i>	17313	chr6	136875405	136876705	-	ICP			GSCLC_high	GSCLC_high
<i>Rerg</i>	232441	chr6	137170096	137171396	-	ICP			GSCLC_high	
<i>Lmo3</i>	109593	chr6	138581568	138582868	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
<i>4922502N22Rik</i>	70962	chr6	139322176	139323476	-	LCP		GSCLC_high		
<i>D6Erttd474e</i>	52285	chr6	143244988	143246288	+	ICP			GSCLC_high	
<i>Tuba3b</i>	22147	chr6	145615063	145616363	+	ICP			GSCLC_high	
<i>Sspn</i>	16651	chr6	145933247	145934547	-	ICP	GSCLC_high		GSCLC_high	
<i>4930479D17Rik</i>	74925	chr6	146656318	146657618	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>1700049E15Rik</i>	100039727	chr6	147689341	147690641	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Mir290</i>	100049710	chr7	3217726	3219026	+	ICP	GSCLC_high		GSCLC_high	
<i>D7Erttd143e</i>	100303645	chr7	3217884	3219184	+	ICP	GSCLC_high		GSCLC_high	
<i>Mir291a</i>	100049715	chr7	3218019	3219319	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Mir292</i>	100049711	chr7	3218289	3219589	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Mir291b</i>	100124471	chr7	3218582	3219882	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Mir293</i>	100049714	chr7	3219443	3220743	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
<i>Cacng8</i>	81905	chr7	3393217	3394517	+	ICP			GSCLC_high	
<i>Tmc4</i>	353499	chr7	3677153	3678453	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>9430041J12Rik</i>	77323	chr7	4120328	4121628	-	LCP				GSCLC_high
<i>Lilra5</i>	232801	chr7	4236854	4238154	+	ICP		GSCLC_high		GSCLC_high
<i>Eps8l1</i>	67425	chr7	4463842	4465142	+	LCP			GSCLC_high	GSCLC_high
<i>Tnni3</i>	21954	chr7	4522043	4523343	-	LCP		GSCLC_high	GSCLC_high	
<i>Fam71e2</i>	243822	chr7	4770870	4772170	-	LCP			GSCLC_high	GSCLC_high
<i>Il11</i>	16156	chr7	4777741	4779041	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Sbk2</i>	381836	chr7	4963948	4965248	-	LCP		GSCLC_high		
<i>Nlrp2</i>	232827	chr7	5350635	5351935	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Nlrp4c</i>	83564	chr7	6044261	6045561	+	ICP		GSCLC_high		
<i>Olfr1344</i>	257882	chr7	6439002	6440302	+	LCP		GSCLC_high		
<i>Olfr1349</i>	269862	chr7	6515027	6516327	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Peg3</i>	18616	chr7	6730019	6731319	-	HCP		GSCLC_high		
<i>Usp29</i>	57775	chr7	6729841	6731141	+	HCP		GSCLC_high		
<i>Nlrp4b</i>	210045	chr7	10686893	10688193	+	LCP			GSCLC_high	
<i>Gm6909</i>	628737	chr7	11180675	11181975	+	LCP		GSCLC_high		
<i>Slc27a5</i>	26459	chr7	12997792	12999092	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Obox6</i>	252830	chr7	15839279	15840579	-	LCP			GSCLC_high	GSCLC_high
<i>Pglyrp1</i>	21946	chr7	18883790	18885090	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Gipr</i>	381853	chr7	19165727	19167027	-	LCP	GSCLC_high	GSCLC_high		
<i>Apoe</i>	11816	chr7	19698766	19700066	-	LCP			GSCLC_high	
<i>2210010C17Rik</i>	70080	chr7	19950343	19951643	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Nlrp5</i>	23968	chr7	23384997	23386297	+	ICP		GSCLC_high		
<i>Gm19733</i>	100503506	chr7	24267706	24269006	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
<i>Lypd5</i>	76942	chr7	24348324	24349624	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Zfp575</i>	101544	chr7	24587241	24588541	-	ICP				GSCLC_high
<i>Ethe1</i>	66071	chr7	24586643	24587943	+	ICP				GSCLC_high
<i>Lypd3</i>	72434	chr7	24635670	24636970	+	LCP		GSCLC_high		GSCLC_high
<i>Gm1096</i>	381959	chr7	24687840	24689140	+	LCP		GSCLC_high		
<i>BC049730</i>	232972	chr7	24708359	24709659	+	ICP		GSCLC_high		
<i>Cd79a</i>	12518	chr7	24896611	24897911	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm7092</i>	632778	chr7	25615492	25616792	-	LCP			GSCLC_high	GSCLC_high
<i>Axl</i>	26362	chr7	25788333	25789633	-	LCP			GSCLC_high	
<i>Cyp2a4</i>	13086	chr7	26306292	26307592	+	LCP		GSCLC_high	GSCLC_high	
<i>Cyp2a5</i>	13087	chr7	26834439	26835739	+	LCP				GSCLC_high
<i>Mia1</i>	12587	chr7	27180749	27182049	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm10046</i>	100043229	chr7	27764773	27766073	+	ICP		GSCLC_high		

LOC100862275	100862275	chr7	27783477	27784777	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Fcgbp	215384	chr7	28070336	28071636	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Zfp36	22695	chr7	28378828	28380128	-	HCP				GSCLC_high
Gm6537	624918	chr7	28755274	28756574	+	LCP				GSCLC_high
Lgals7	16858	chr7	28863486	28864786	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Capn12	60594	chr7	28880756	28882056	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
4930432E11Rik	243900	chr7	29555413	29556713	+	ICP		GSCLC_high		GSCLC_high
Gm6579	625349	chr7	29799396	29800696	-	LCP			GSCLC_high	
Prodh2	56189	chr7	30492758	30494058	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Ffar1	233081	chr7	30861070	30862370	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Fxyd1	56188	chr7	31055256	31056556	-	LCP			GSCLC_high	
Hpn	15451	chr7	31114890	31116190	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Gm10640	100038516	chr7	31161458	31162758	+	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Abph	57426	chr7	31291416	31292716	-	LCP			GSCLC_high	
Gm12769	100043860	chr7	33742899	33744199	+	LCP			GSCLC_high	
Abpg	110187	chr7	33944585	33945885	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Wdr88	384605	chr7	35274991	35276291	-	ICP				GSCLC_high
4930505M18Rik	67641	chr7	37668899	37670199	+	ICP				GSCLC_high
Gm6871	628359	chr7	41573266	41574566	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Gm5593	434175	chr7	42106785	42108085	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
4933421I07Rik	71162	chr7	42447680	42448980	-	LCP			GSCLC_high	
Kik10	69540	chr7	43780154	43781454	+	LCP		GSCLC_high	GSCLC_high	
Kik9	101533	chr7	43790991	43792291	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Kik5	68668	chr7	43841369	43842669	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Lrrc4b	272381	chr7	44441587	44442887	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Mybpc2	233199	chr7	44524269	44525569	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Tsk5	22116	chr7	44942340	44943640	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Cd37	12493	chr7	45238439	45239739	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
LOC100862214	100862214	chr7	45417459	45418759	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Fg121	56636	chr7	45615090	45616390	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Rasip1	69903	chr7	45626637	45627937	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Sult2b1	54200	chr7	45759155	45760455	-	ICP				GSCLC_high
Ccdc114	211535	chr7	45927498	45928798	+	LCP		GSCLC_high		GSCLC_high
C86187	97402	chr7	46975511	46976811	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Gm9999	629141	chr7	46975732	46977032	+	LCP				GSCLC_high
Mrgpra6	381886	chr7	47188955	47190255	-	ICP		GSCLC_high		
Snurf	84704	chr7	60004756	60006056	-	ICP		GSCLC_high		
Mir344b	100526558	chr7	61790181	61791481	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
Mir344-2	100124439	chr7	61939706	61941006	-	LCP		GSCLC_high	GSCLC_high	
A330076H08Rik	320026	chr7	61981903	61983203	-	LCP	GSCLC_high		GSCLC_high	
Mir344g	100526507	chr7	61981959	61983259	-	LCP	GSCLC_high		GSCLC_high	
Gm7546	665234	chr7	65635454	65636754	-	LCP				GSCLC_high
Gm10295	100038563	chr7	71351085	71352385	-	ICP				GSCLC_high
LOC100505025	100505025	chr7	73309480	73310780	+	ICP			GSCLC_high	GSCLC_high
Hapln3	67666	chr7	79130618	79131918	-	ICP			GSCLC_high	GSCLC_high
Ribp1	19771	chr7	79386627	79387927	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Alpk3	116904	chr7	81056700	81058000	+	ICP		GSCLC_high		
4933430H16Rik	71285	chr7	82970991	82972291	-	LCP		GSCLC_high		
Tmc3	233424	chr7	83584031	83585331	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Olfr303	258612	chr7	86395096	86396396	-	LCP			GSCLC_high	GSCLC_high
E230029C05Rik	319711	chr7	90028259	90029559	+	ICP			GSCLC_high	GSCLC_high
Dlg2	23859	chr7	91089886	91091186	+	ICP				GSCLC_high
Thrsp	21835	chr7	97417110	97418410	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Gm19656	100503364	chr7	98728360	98729660	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Mogat2	233549	chr7	99238211	99239511	-	LCP	GSCLC_high			GSCLC_high
Plekhhb1	27276	chr7	100661994	100663294	-	ICP			GSCLC_high	
Olfr545	258837	chr7	102494373	102495673	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Olfr549	259105	chr7	102553386	102554686	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
Olfr550	259108	chr7	102577569	102578869	+	LCP		GSCLC_high		GSCLC_high
Olfr554	258322	chr7	102639348	102640648	+	LCP				GSCLC_high
Olfr571	259089	chr7	102909437	102910737	-	LCP		GSCLC_high		GSCLC_high
Olfr591	258139	chr7	103173235	103174535	-	LCP		GSCLC_high	GSCLC_high	
Olfr599	258726	chr7	103337156	103338456	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Olfr601	258311	chr7	103358813	103360113	-	LCP		GSCLC_high		
Olfr605	258156	chr7	103442750	103444050	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Olfr606	259098	chr7	103450439	103451739	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Olfr610	259085	chr7	103506544	103507844	-	LCP		GSCLC_high		GSCLC_high
Olfr624	258189	chr7	103670629	103671929	-	LCP		GSCLC_high		
Hbb-b1	15129	chr7	103813523	103814823	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Olfr632	259123	chr7	103936482	103937782	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Olfr633	258351	chr7	103945668	103946968	+	LCP		GSCLC_high		GSCLC_high
4931431F19Rik	70980	chr7	104129423	104130723	-	LCP		GSCLC_high		GSCLC_high
Trim5	667823	chr7	104287732	104289032	-	LCP	GSCLC_high			GSCLC_high
Trim12a	76681	chr7	104315095	104316395	-	LCP	GSCLC_high		GSCLC_high	
LOC622070	622070	chr7	104314131	104315431	+	ICP	GSCLC_high		GSCLC_high	
Olfr656	259078	chr7	104616757	104618057	+	LCP		GSCLC_high	GSCLC_high	
Olfr658	259051	chr7	104646905	104648205	-	ICP		GSCLC_high		
Gm4887	233637	chr7	104820304	104821604	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Olfr676	259099	chr7	105034300	105035600	+	LCP		GSCLC_high	GSCLC_high	
Olfr471	626674	chr7	107862155	107863455	-	ICP			GSCLC_high	
Olfr481	258927	chr7	108079896	108081196	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Trim66	330627	chr7	109507734	109509034	-	LCP				GSCLC_high
Calcb	116903	chr7	114717743	114719043	+	ICP			GSCLC_high	GSCLC_high
Acsn3	20216	chr7	119760023	119761323	+	LCP		GSCLC_high		GSCLC_high
Zp2	22787	chr7	120144890	120146190	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Abca15	320631	chr7	120327784	120329084	+	ICP				GSCLC_high
Gm7226	637957	chr7	120623349	120624649	+	ICP				GSCLC_high
4933432K03Rik	75793	chr7	121589433	121590733	-	LCP				GSCLC_high
Lat	16797	chr7	126369134	126370434	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Cln3	12752	chr7	126583880	126585180	-	LCP		GSCLC_high		
Nupr1	56312	chr7	126625007	126626307	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Aldoa	11674	chr7	126800047	126801347	-	ICP		GSCLC_high		
4930451I11Rik	78118	chr7	126831096	126832396	-	ICP		GSCLC_high		GSCLC_high
Qprt	67375	chr7	127121629	127122929	-	LCP	GSCLC_high	GSCLC_high		
Spn	20737	chr7	127137417	127138717	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
Itgal	16408	chr7	127295360	127296660	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
Prss8	76560	chr7	127929713	127931013	-	LCP			GSCLC_high	

Pycard	66824	chr7	127993467	127994767	-	LCP			GSCLC_high	
Cox6a2	12862	chr7	128205966	128207266	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Mir5102	100628579	chr7	130833537	130834837	+	ICP				GSCLC_high
Caly	68566	chr7	140082148	140083448	-	ICP			GSCLC_high	GSCLC_high
1190003J15Rik	76974	chr7	140834596	140835896	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Deaf1	54006	chr7	141338383	141339683	-	ICP				GSCLC_high
Efcab4a	213573	chr7	141460194	141461494	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
H19	14955	chr7	142577746	142579046	-	ICP			GSCLC_high	
Mir675	735280	chr7	142576747	142578047	-	ICP			GSCLC_high	
Kcnq1ot1	63830	chr7	143296147	143297447	-	HCP			GSCLC_high	
Mrgpre	244238	chr7	143784100	143785400	-	LCP	GSCLC_high			GSCLC_high
Shank2	210274	chr7	144174620	144175920	+	HCP				GSCLC_high
A430078G23Rik	319493	chr8	3352515	3353815	+	ICP				GSCLC_high
Cd209b	69165	chr8	3926414	3927714	-	LCP				GSCLC_high
Cd209g	70192	chr8	4133836	4135136	+	ICP				GSCLC_high
Gm14378	100044509	chr8	4247314	4248614	+	LCP				GSCLC_high
Gm6334	622568	chr8	4777142	4778442	+	ICP		GSCLC_high		GSCLC_high
A630009H07Rik	320406	chr8	8334177	8335477	+	ICP		GSCLC_high		GSCLC_high
Tnfrsf13b	24099	chr8	10005733	10007033	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
AF366264	231201	chr8	13837689	13838989	-	LCP		GSCLC_high	GSCLC_high	
Tpte	234129	chr8	22282541	22283841	+	LCP			GSCLC_high	GSCLC_high
1810011O10Rik	69068	chr8	24438546	24439846	-	ICP				GSCLC_high
Adam18	13524	chr8	24674355	24675655	-	ICP	GSCLC_high	GSCLC_high		GSCLC_high
Adam5	11499	chr8	24823969	24825269	-	ICP				GSCLC_high
5430421F17Rik	74489	chr8	25305870	25307170	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Poteg	70952	chr8	27446770	27448070	+	ICP				GSCLC_high
7420700N18Rik	74517	chr8	31366849	31368149	+	LCP				GSCLC_high
Gm3395	100042715	chr8	32949626	32950926	-	ICP		GSCLC_high		GSCLC_high
Gm16793	100504714	chr8	35588620	35589920	-	ICP		GSCLC_high		
Gm10063	671641	chr8	36024853	36026153	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Dlc1	50768	chr8	36952042	36953342	-	ICP				GSCLC_high
Gm2085	100039179	chr8	40649651	40650951	+	ICP		GSCLC_high		
2810404M03Rik	69966	chr8	41826367	41827667	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Sorbs2	234214	chr8	45506888	45508188	+	ICP				GSCLC_high
Lrp2bp	67620	chr8	46009702	46011002	+	LCP				GSCLC_high
Odz3	23965	chr8	48674290	48675590	-	ICP			GSCLC_high	
Gm9892	100040220	chr8	52196779	52198079	-	ICP		GSCLC_high		GSCLC_high
Asb5	76294	chr8	54549431	54550731	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm2749	100040392	chr8	55115236	55116536	+	LCP			GSCLC_high	GSCLC_high
LOC100862163	100862163	chr8	55345541	55346841	+	LCP			GSCLC_high	GSCLC_high
LOC100862226	100862226	chr8	55368706	55370006	+	ICP			GSCLC_high	
LOC100862253	100862253	chr8	55375284	55376584	+	LCP				GSCLC_high
LOC100862327	100862327	chr8	55494335	55495635	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Gm1153	382364	chr8	55497704	55499004	+	LCP				GSCLC_high
Gm7385	664876	chr8	55539904	55541204	-	LCP		GSCLC_high		GSCLC_high
Gm15881	100271928	chr8	58700396	58701696	-	ICP			GSCLC_high	GSCLC_high
Trim60	234329	chr8	65018288	65019588	-	ICP	GSCLC_high	GSCLC_high		
Trim61	260296	chr8	65018288	65019588	-	ICP	GSCLC_high	GSCLC_high		
Gm10664	100038489	chr8	65036936	65038236	-	ICP				GSCLC_high
BC030870	407795	chr8	65129137	65130437	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Nat3	17962	chr8	67522954	67524254	+	LCP			GSCLC_high	GSCLC_high
Tmem59l	67937	chr8	70486958	70488258	-	HCP		GSCLC_high	GSCLC_high	GSCLC_high
Gdf15	23886	chr8	70631235	70632535	-	ICP	GSCLC_high			GSCLC_high
Gm3336	100502950	chr8	70717643	70718943	+	LCP		GSCLC_high		GSCLC_high
Plvap	84094	chr8	71511369	71512669	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
LOC100861739	100861739	chr8	71595868	71597168	-	HCP	GSCLC_high	GSCLC_high		GSCLC_high
InsI3	16336	chr8	71688352	71689652	+	HCP		GSCLC_high		GSCLC_high
Olfr373	258532	chr8	72098862	72100162	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Nwd1	319555	chr8	72645811	72647111	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
1700092C02Rik	67357	chr8	77623272	77624572	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
4930505O20Rik	74709	chr8	80514073	80515373	-	ICP			GSCLC_high	GSCLC_high
4933434I20Rik	67555	chr8	83347572	83348872	+	ICP		GSCLC_high		
Scoc	56367	chr8	83457991	83459291	-	ICP	GSCLC_high	GSCLC_high		GSCLC_high
Olfr370	258267	chr8	83540193	83541493	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Ptger1	19216	chr8	83665740	83667040	+	LCP			GSCLC_high	GSCLC_high
Palm3	74337	chr8	84020574	84021874	+	ICP			GSCLC_high	
Il27ra	50931	chr8	84042175	84043475	-	HCP	GSCLC_high			
Rln3	212108	chr8	84044579	84045879	-	ICP	GSCLC_high			GSCLC_high
Myk3	213435	chr8	85364924	85366224	-	LCP		GSCLC_high		
Gm6625	625801	chr8	89146667	89147967	-	ICP				GSCLC_high
Mir138-2	723956	chr8	94323411	94324711	+	LCP			GSCLC_high	
Ccl22	20299	chr8	94744784	94746084	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Ccdc135	330830	chr8	95054203	95055503	+	LCP	GSCLC_high	GSCLC_high		
Gm10094	100041953	chr8	95824456	95825756	+	HCP				GSCLC_high
Gm15210	100042069	chr8	100029607	100030907	+	ICP	GSCLC_high	GSCLC_high		GSCLC_high
Cmtm2a	73381	chr8	104292781	104294081	-	ICP		GSCLC_high		GSCLC_high
Cmtm1	100504164	chr8	104309745	104311045	-	ICP		GSCLC_high		
Cmtm2b	75502	chr8	104321337	104322637	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
4932416K20Rik	442809	chr8	104794343	104795643	+	LCP	GSCLC_high			GSCLC_high
Tppp3	67971	chr8	105471022	105472322	-	ICP			GSCLC_high	
Gm8841	667846	chr8	105585800	105587100	-	HCP		GSCLC_high		GSCLC_high
Rltpr	234695	chr8	105690006	105691306	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Dpep3	71854	chr8	105979019	105980319	-	HCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm8842	667847	chr8	107084988	107086288	-	HCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Tat	234724	chr8	109989536	109990836	+	ICP			GSCLC_high	GSCLC_high
LOC100861869	100861869	chr8	110501956	110503256	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Il34	76527	chr8	110805503	110806803	-	ICP			GSCLC_high	
LOC100861890	100861890	chr8	111685617	111686917	+	LCP		GSCLC_high	GSCLC_high	
Syce1l	668110	chr8	113642313	113643613	+	ICP		GSCLC_high		
Fam92b	436062	chr8	120177069	120178369	-	ICP			GSCLC_high	
Foxl1	14241	chr8	121126785	121128085	+	ICP		GSCLC_high		GSCLC_high
C230057M02Rik	319463	chr8	122751925	122753225	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Cdh15	12555	chr8	122847474	122848774	+	LCP			GSCLC_high	GSCLC_high
Sult5a1	57429	chr8	123157880	123159180	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Rn5s23	100861494	chr8	123606331	123607631	-	HCP		GSCLC_high		
Rn5s32	100861503	chr8	123621646	123622946	-	HCP				GSCLC_high
1700008F21Rik	75453	chr8	129066234	129067534	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high

Casp1	12362	chr9	5297617	5298917	+	LCP				GSCLC_high
1700012B09Rik	69325	chr9	14770630	14771930	-	ICP		GSCLC_high		GSCLC_high
AB124611	382062	chr9	21525277	21526577	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
Zfp872	619310	chr9	22187266	22188566	+	HCP		GSCLC_high		
Npsr1	319239	chr9	24097118	24098418	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Glb1l3	70893	chr9	26860423	26861723	-	LCP		GSCLC_high		GSCLC_high
Gm11110	382064	chr9	26922681	26923981	-	LCP			GSCLC_high	GSCLC_high
Gm5614	434394	chr9	35281435	35282735	-	ICP	GSCLC_high	GSCLC_high		GSCLC_high
Gm17252	100312987	chr9	35686971	35688271	-	LCP		GSCLC_high		
Hepacam	72927	chr9	37366706	37368006	+	LCP			GSCLC_high	
Vsig2	57276	chr9	37538355	37539655	+	LCP		GSCLC_high		GSCLC_high
Panx3	208098	chr9	37668822	37670122	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Olfr959	258501	chr9	39572857	39574157	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Olfr975	258825	chr9	39950369	39951669	-	LCP				GSCLC_high
Olfr978	259109	chr9	39992912	39994212	+	LCP				GSCLC_high
Olfr982	258853	chr9	40073397	40074697	+	LCP		GSCLC_high		GSCLC_high
1700110K17Rik	73558	chr9	40332572	40333872	+	ICP		GSCLC_high		
2610203C20Rik	100042464	chr9	41580439	41581739	+	ICP				GSCLC_high
Mir125b-1	387236	chr9	41581026	41582326	+	ICP				GSCLC_high
Trim29	72169	chr9	43309863	43311163	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm3898	100042548	chr9	43820047	43821347	+	LCP				GSCLC_high
C1qtnf5-Mfrp	235312	chr9	44100870	44102170	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Upk2	22269	chr9	44454367	44455667	-	LCP		GSCLC_high		
Cd3e	12501	chr9	45009190	45010490	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Tmprss13	214531	chr9	45318200	45319500	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Tagln	21345	chr9	45935658	45936958	-	ICP			GSCLC_high	GSCLC_high
Gm5616	434401	chr9	48449500	48450800	+	HCP			GSCLC_high	GSCLC_high
Ankk1	244859	chr9	49426621	49427921	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Hspb2	69253	chr9	50751954	50753254	-	LCP			GSCLC_high	
Cryab	12955	chr9	50751858	50753158	+	LCP			GSCLC_high	
Pou2af1	18985	chr9	51212790	51214090	+	ICP				GSCLC_high
9230115E21Rik	408028	chr9	51875485	51876785	-	ICP				GSCLC_high
4933407105Rik	74072	chr9	51913529	51914829	+	ICP			GSCLC_high	GSCLC_high
Sh2d7	244885	chr9	54538084	54539384	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Acsbg1	94180	chr9	54661485	54662785	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Nrg4	83961	chr9	55283225	55284525	-	ICP	GSCLC_high			GSCLC_high
Cspg4	121021	chr9	56864204	56865504	+	ICP			GSCLC_high	
Stra6	20897	chr9	58128188	58129488	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Pml	18854	chr9	58249386	58250686	-	ICP				
1700036A12Rik	100040447	chr9	60742220	60743520	+	ICP	GSCLC_high			GSCLC_high
Calml4	75600	chr9	62857204	62858504	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Slc24a1	214111	chr9	64951207	64952507	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Car12	76459	chr9	66712786	66714086	+	ICP				GSCLC_high
BC065403	100502819	chr9	72409467	72410767	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm5745	436081	chr9	73175341	73176641	-	HCP				GSCLC_high
Unc13c	208898	chr9	73933167	73934467	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Bcl2l10	12049	chr9	75346858	75348158	+	ICP			GSCLC_high	GSCLC_high
Gm7972	666190	chr9	75467722	75469022	+	ICP			GSCLC_high	
Klhl31	244923	chr9	77635832	77637132	+	LCP				GSCLC_high
Gm19606	100503238	chr9	79807622	79808922	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
D430036J16Rik	319405	chr9	81631030	81632330	+	HCP		GSCLC_high		
4930554C24Rik	75253	chr9	84773498	84774798	+	ICP				GSCLC_high
Gm10634	100039674	chr9	88718729	88720029	+	HCP		GSCLC_high		
Bcl2a1d	12047	chr9	88731450	88732750	-	ICP			GSCLC_high	
Bcl2a1b	12045	chr9	89198373	89199673	+	ICP	GSCLC_high	GSCLC_high		GSCLC_high
Mir184	387179	chr9	89801928	89803228	-	ICP	GSCLC_high			GSCLC_high
Gm5620	434428	chr9	91096248	91097548	+	ICP		GSCLC_high		GSCLC_high
Plscr5	100504689	chr9	92192036	92193336	+	ICP				GSCLC_high
E030011O05Rik	319859	chr9	96752431	96753731	-	LCP		GSCLC_high	GSCLC_high	
7420426K07Rik	546157	chr9	98902219	98903519	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Cldn18	56492	chr9	99716867	99718167	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm5161	382099	chr9	101448942	101450242	-	ICP		GSCLC_high		GSCLC_high
Trf	22041	chr9	103229886	103231186	-	ICP			GSCLC_high	GSCLC_high
1300017J02Rik	71775	chr9	103287897	103289197	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
5830418P13Rik	100529079	chr9	103422678	103423978	+	HCP	GSCLC_high			GSCLC_high
Acpp	56318	chr9	104337322	104338622	-	ICP				GSCLC_high
1700080E11Rik	73532	chr9	105144682	105145982	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Col6a6	245026	chr9	105827685	105828985	-	LCP			GSCLC_high	GSCLC_high
Col6a5	665033	chr9	105960243	105961543	-	LCP		GSCLC_high		GSCLC_high
Abhd14b	76491	chr9	106447740	106449040	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Hyal1	15586	chr9	107576052	107577352	+	LCP	GSCLC_high			
Col7a1	12836	chr9	108952845	108954145	+	ICP			GSCLC_high	
Camp	12796	chr9	109849056	109850356	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Prss43	272643	chr9	110825790	110827090	-	LCP	GSCLC_high		GSCLC_high	
Prss45	260408	chr9	110833688	110834988	+	ICP	GSCLC_high		GSCLC_high	
AU023762	102688	chr9	113586752	113588052	-	ICP	GSCLC_high			GSCLC_high
Gadl1	73748	chr9	115908555	115909855	+	ICP			GSCLC_high	
Vill	22351	chr9	119051878	119053178	+	ICP	GSCLC_high		GSCLC_high	
Scn10a	20264	chr9	119718632	119719932	-	ICP			GSCLC_high	GSCLC_high
Gm5922	546166	chr9	120135929	120137229	-	LCP			GSCLC_high	
1700020M21Rik	76402	chr9	120914850	120916150	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
4930593C16Rik	78060	chr9	120930402	120931702	-	ICP	GSCLC_high	GSCLC_high		
Slc6a20b	22599	chr9	123632165	123633465	-	LCP		GSCLC_high	GSCLC_high	
Ppp2r3d	19054	chr9	124476462	124477762	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
9230019H11Rik	215728	chr10	3118941	3120241	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
H60c	670558	chr10	3267371	3268671	-	ICP		GSCLC_high		
Iyd	70337	chr10	3539379	3540679	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Esr1	13982	chr10	4611146	4612446	+	LCP				GSCLC_high
Gm6150	620417	chr10	9683822	9685122	+	ICP				GSCLC_high
Gm1	14816	chr10	11081931	11083231	-	ICP				GSCLC_high
Gm20125	100504235	chr10	17095382	17096682	-	ICP				GSCLC_high
4930444F02Rik	73968	chr10	18831530	18832830	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Olig3	94222	chr10	19355639	19356939	+	ICP		GSCLC_high		
Pde7b	29863	chr10	20724668	20725968	-	ICP		GSCLC_high		GSCLC_high
1700021A07Rik	76924	chr10	21418577	21419877	+	ICP		GSCLC_high	GSCLC_high	
1700020N01Rik	67692	chr10	21592245	21593545	+	ICP		GSCLC_high		
Gm5420	432436	chr10	21689945	21691245	+	ICP		GSCLC_high		

4930444G20Rik	114671	chr10	22067679	22068979	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
C920009B18Rik	606736	chr10	22305820	22307120	+	LCP		GSCLC_high	GSCLC_high	
Gm10825	100038752	chr10	22401913	22403213	+	LCP		GSCLC_high		
Vnn1	22361	chr10	23893788	23895088	+	ICP		GSCLC_high		
Taar3	493809	chr10	23948658	23949958	+	ICP				GSCLC_high
Taar4	209513	chr10	23959594	23960894	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Taar5	215854	chr10	23969806	23971106	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Taar6	215855	chr10	23985246	23986546	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Taar9	503558	chr10	24109134	24110434	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Akap7	432442	chr10	25298763	25300063	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Gm10145	100040961	chr10	27935444	27936744	+	LCP			GSCLC_high	
Themis	210757	chr10	28667495	28668795	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm3258	100041294	chr10	31414035	31415335	-	ICP	GSCLC_high	GSCLC_high		GSCLC_high
Bet3l	692132	chr10	34036697	34037997	+	ICP			GSCLC_high	
Fam26d	270711	chr10	34043913	34045213	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Fam26e	103511	chr10	34096119	34097419	-	ICP		GSCLC_high		GSCLC_high
Wisp3	327743	chr10	39163394	39164694	-	LCP			GSCLC_high	GSCLC_high
Slc22a16	70840	chr10	40569462	40570762	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
D030045P18Rik	320363	chr10	45806804	45808104	+	LCP				GSCLC_high
Gm5423	432460	chr10	53474064	53475364	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Msl3l2	73390	chr10	56106017	56107317	+	ICP			GSCLC_high	
LOC100504180	100504180	chr10	58224793	58226093	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
4933403O03Rik	74399	chr10	58232473	58233773	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Gm4981	245263	chr10	58236260	58237560	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Pla2g12b	69836	chr10	59402785	59404085	+	LCP		GSCLC_high		
Tet1	52463	chr10	62879614	62880914	-	ICP			GSCLC_high	GSCLC_high
Lrrtm3	216028	chr10	64089855	64091155	-	LCP				GSCLC_high
1700023F02Rik	69433	chr10	66123664	66124964	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm10797	100038508	chr10	67571139	67572439	+	ICP			GSCLC_high	GSCLC_high
Gm19746	100503521	chr10	68312108	68313408	+	ICP		GSCLC_high	GSCLC_high	
Rhobtb1	69288	chr10	69207652	69208952	+	LCP		GSCLC_high	GSCLC_high	
Pcdh15	11994	chr10	73820967	73822267	+	ICP				GSCLC_high
Rtdr1	71236	chr10	75032186	75033486	-	LCP				GSCLC_high
Ubp1	103149	chr10	75406134	75407434	+	LCP	GSCLC_high		GSCLC_high	
Susd2	71733	chr10	75643608	75644908	-	LCP				GSCLC_high
Gm10787	100038479	chr10	77011095	77012395	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
Trpm2	28240	chr10	77969472	77970772	-	HCP		GSCLC_high		GSCLC_high
Dnmt3l	54427	chr10	78048942	78050242	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Casp14	12365	chr10	78717893	78719193	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Madcam1	17123	chr10	79663674	79664974	+	LCP	GSCLC_high		GSCLC_high	
Gm19803	100503626	chr10	79794256	79795556	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
LOC100862189	100862189	chr10	80606687	80607987	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Apba3	57267	chr10	81267272	81268572	+	HCP		GSCLC_high		
Gna15	14676	chr10	81523825	81525125	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Eid3	66341	chr10	82865726	82867026	+	ICP		GSCLC_high		
4930486F22Rik	78170	chr10	86094954	86096254	+	LCP	GSCLC_high			GSCLC_high
Gm6653	626115	chr10	88135453	88136753	-	ICP		GSCLC_high		GSCLC_high
Mybpc1	109272	chr10	88604752	88606052	-	ICP			GSCLC_high	GSCLC_high
Ano4	320091	chr10	89257390	89258690	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Nrlh4	20186	chr10	89533222	89534522	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm4792	215472	chr10	94298303	94299603	-	LCP	GSCLC_high	GSCLC_high		
Lum	17022	chr10	97564601	97565901	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Csl	71832	chr10	99759258	99760558	-	ICP		GSCLC_high		GSCLC_high
Nts	67405	chr10	102490018	102491318	-	LCP			GSCLC_high	GSCLC_high
Rassf9	237504	chr10	102511322	102512622	+	LCP		GSCLC_high		GSCLC_high
Myf5	17877	chr10	107485734	107487034	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Myf6	17878	chr10	107494329	107495629	-	ICP				GSCLC_high
Ptprq	237523	chr10	107719627	107720927	-	LCP			GSCLC_high	
Nav3	260315	chr10	109999819	110001119	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
9230102K24Rik	109335	chr10	110599750	110601050	+	ICP	GSCLC_high	GSCLC_high		GSCLC_high
Gm5428	432502	chr10	111124951	111126251	+	ICP		GSCLC_high		GSCLC_high
Glipr1l1	69286	chr10	112059289	112060589	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Glipr1l2	67537	chr10	112082454	112083754	+	ICP	GSCLC_high		GSCLC_high	
Glipr1l3	544736	chr10	112159806	112161106	-	ICP				GSCLC_high
4933416C03Rik	619332	chr10	116113517	116114817	-	HCP		GSCLC_high		
1700058G18Rik	67342	chr10	116417221	116418521	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
1700030O20Rik	72286	chr10	116728777	116730077	-	LCP	GSCLC_high		GSCLC_high	
4933411E08Rik	71067	chr10	117924559	117925859	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
Gm10744	100038589	chr10	118883254	118884554	-	ICP		GSCLC_high	GSCLC_high	
1700025F24Rik	67081	chr10	119412544	119413844	+	ICP			GSCLC_high	
4921513I03Rik	70874	chr10	120764832	120766132	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Arhgap9	216445	chr10	127322827	127324127	+	LCP	GSCLC_high			
Inhbe	16326	chr10	127351372	127352672	-	LCP				GSCLC_high
Inhbc	16325	chr10	127370144	127371444	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
Apon	28194	chr10	128253231	128254531	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
Gm9182	668459	chr10	128614501	128615801	+	ICP	GSCLC_high	GSCLC_high		
Olfir9	18373	chr10	128989014	128990314	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Olfir796	258933	chr10	129608079	129609379	-	LCP				GSCLC_high
Olfir820	258670	chr10	130016463	130017763	+	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Olfir825	258672	chr10	130162924	130164224	-	LCP		GSCLC_high	GSCLC_high	
Neurod4	11923	chr10	130279840	130281140	-	LCP				GSCLC_high
Pik3ip1	216505	chr11	3329831	3331131	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Pla2g3	237625	chr11	3487327	3488627	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Sec14l4	103655	chr11	4030882	4032182	+	LCP	GSCLC_high		GSCLC_high	
Osm	18413	chr11	4235885	4237185	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Ankrd36	76389	chr11	5568784	5570084	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm11964	665181	chr11	5633239	5634539	+	HCP		GSCLC_high	GSCLC_high	GSCLC_high
Pgam2	56012	chr11	5803396	5804696	-	LCP				GSCLC_high
Gm11985	100041347	chr11	7188169	7189469	-	ICP	GSCLC_high	GSCLC_high		GSCLC_high
Igfbp1	16006	chr11	7196887	7198187	+	ICP	GSCLC_high	GSCLC_high		GSCLC_high
Abca13	268379	chr11	9191042	9192342	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm5429	432534	chr11	11463105	11464405	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
1700046C09Rik	73307	chr11	14598825	14600125	-	ICP		GSCLC_high		
Pom121l12	432536	chr11	14598340	14599640	+	ICP		GSCLC_high		
Gm16141	100503713	chr11	19012917	19014217	+	ICP				GSCLC_high
Zrsr1	22183	chr11	22971105	22972405	+	HCP			GSCLC_high	
Nsg2	18197	chr11	31999559	32000859	+	ICP			GSCLC_high	GSCLC_high

LOC100862145	100862145	chr11	32284081	32285381	-	LCP			GSCLC_high	
Kcnp1	70357	chr11	33992793	33994093	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Kcnmb1	16533	chr11	33962113	33963413	+	LCP				GSCLC_high
Foxi1	14233	chr11	34207689	34208989	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Dock2	94176	chr11	34783423	34784723	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Gabrg2	14406	chr11	42000278	42001578	-	ICP				GSCLC_high
F630206G17Rik	100009664	chr11	45807183	45808483	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Olfr1395	258877	chr11	49147359	49148659	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Btnl9	237754	chr11	49186689	49187989	-	LCP		GSCLC_high	GSCLC_high	
4933414I15Rik	74408	chr11	50943365	50944665	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
9230009I02Rik	619293	chr11	51084187	51085487	+	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Gm19835	100503690	chr11	53486975	53488275	-	ICP			GSCLC_high	
Slc36a2	246049	chr11	55184677	55185977	-	LCP			GSCLC_high	
Gria1	14799	chr11	57010718	57012018	+	LCP	GSCLC_high			GSCLC_high
Hand1	15110	chr11	57831747	57833047	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Olfr323	258373	chr11	58625644	58626944	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Olfr179	404346	chr11	58664661	58665961	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Olfr314	257917	chr11	58785239	58786539	+	LCP		GSCLC_high		GSCLC_high
Prss38	216797	chr11	59375253	59376553	-	ICP	GSCLC_high	GSCLC_high		GSCLC_high
Gm12271	626150	chr11	61416415	61417715	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
Rnf112	22671	chr11	61453486	61454786	-	LCP	GSCLC_high			GSCLC_high
Mfap4	76293	chr11	61484544	61485844	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Trim16	94092	chr11	62819353	62820653	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Pirt	193003	chr11	66911091	66912391	+	LCP		GSCLC_high		GSCLC_high
Rcvm	19674	chr11	67694426	67695726	+	ICP		GSCLC_high		GSCLC_high
Glp2r	93896	chr11	67770753	67772053	-	ICP				GSCLC_high
Arhgef15	442801	chr11	68956458	68957758	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Alox12b	11686	chr11	69156172	69157472	+	ICP			GSCLC_high	
Nlgn2	216856	chr11	69834449	69835749	-	LCP			GSCLC_high	
Tnk1	83813	chr11	69858330	69859630	-	ICP	GSCLC_high			
Dlg4	13385	chr11	70017705	70019005	+	LCP			GSCLC_high	
Tm4sf5	75604	chr11	70504374	70505674	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gltpd2	216871	chr11	70518309	70519609	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Olfr398	258705	chr11	73984206	73985506	-	LCP			GSCLC_high	GSCLC_high
Olfr139	259005	chr11	74044872	74046172	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Tusc5	237858	chr11	76678973	76680273	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Efcab5	319634	chr11	77188568	77189868	-	ICP			GSCLC_high	GSCLC_high
Myo18a	360013	chr11	77776365	77777665	+	ICP	GSCLC_high	GSCLC_high		GSCLC_high
Accn1	11418	chr11	81967996	81969296	-	HCP				GSCLC_high
1700071K01Rik	237880	chr11	81573139	81574439	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Sifn9	237886	chr11	82991430	82992730	-	LCP				GSCLC_high
Gm11425	668706	chr11	83027597	83028897	-	ICP			GSCLC_high	GSCLC_high
Sifn10-ps	237887	chr11	83040133	83041433	-	LCP				GSCLC_high
Sifn4	20558	chr11	83174286	83175586	+	ICP				GSCLC_high
Al662270	100043636	chr11	83222676	83223976	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Gas2l2	237891	chr11	83429055	83430355	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
1700125H20Rik	73634	chr11	85170196	85171496	+	ICP	GSCLC_high			
Mir142	387160	chr11	87755964	87757264	+	ICP	GSCLC_high		GSCLC_high	
Bzap1	207777	chr11	87759641	87760941	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Olfr463	258408	chr11	87893522	87894822	-	LCP		GSCLC_high		
Tmem100	67888	chr11	90029448	90030748	+	ICP				GSCLC_high
Wfikkn2	278507	chr11	94242179	94243479	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Epn3	71889	chr11	94499574	94500874	-	ICP			GSCLC_high	GSCLC_high
Chad	12643	chr11	94564174	94565474	+	HCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Abi3	66610	chr11	95842076	95843376	-	LCP			GSCLC_high	
Gngt2	14710	chr11	95841395	95842695	+	LCP	GSCLC_high		GSCLC_high	
Mir196a-1	387191	chr11	96264264	96265564	+	LCP		GSCLC_high		GSCLC_high
Gsdma3	450219	chr11	98625460	98626760	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Krt24	75706	chr11	99284838	99286138	-	LCP			GSCLC_high	
Krt25	70810	chr11	99322541	99323841	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Krt26	320864	chr11	99337565	99338865	-	ICP				GSCLC_high
Krt28	70843	chr11	99374503	99375803	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Krt20	66809	chr11	99437753	99439053	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Krt40	406221	chr11	99542758	99544058	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Krtap4-2	68673	chr11	99634684	99635984	-	LCP			GSCLC_high	
Krtap4-16	435285	chr11	99851205	99852505	-	LCP			GSCLC_high	GSCLC_high
Zfp385c	278304	chr11	100650293	100651593	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Stat5a	20850	chr11	100858451	100859751	+	LCP		GSCLC_high	GSCLC_high	
LOC666331	666331	chr11	101609800	101611100	+	ICP				GSCLC_high
4930417O22Rik	73887	chr11	101951521	101952821	+	ICP			GSCLC_high	
Pyy	217212	chr11	102107376	102108676	-	ICP			GSCLC_high	
2810433D01Rik	77132	chr11	102624016	102625316	-	LCP			GSCLC_high	
Gfap	14580	chr11	102896800	102898100	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
2410004I01Rik	69739	chr11	102963754	102965054	-	ICP			GSCLC_high	
Gm11648	653030	chr11	103343853	103345153	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gh	14599	chr11	106301410	106302710	-	LCP			GSCLC_high	
1700023C21Rik	73257	chr11	109844978	109846278	+	LCP			GSCLC_high	GSCLC_high
Abca8b	27404	chr11	109995416	109996716	-	ICP				GSCLC_high
Abca9	217262	chr11	110167753	110169053	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Abca6	76184	chr11	110251376	110252676	-	ICP			GSCLC_high	
Kcnj16	16517	chr11	110967133	110968433	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Cpsf4l	52670	chr11	113709617	113710917	-	LCP			GSCLC_high	GSCLC_high
Cd300a	217303	chr11	114889141	114890441	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Tmc8	217356	chr11	117781397	117782697	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Gm11725	100503754	chr11	117870350	117871650	+	LCP				GSCLC_high
Ppp1r27	68701	chr11	120550732	120552032	-	HCP	GSCLC_high	GSCLC_high	GSCLC_high	
Tex19.2	70956	chr11	121118277	121119577	-	ICP			GSCLC_high	
Tex19.1	73679	chr11	121145243	121146543	+	ICP			GSCLC_high	
4833432E10Rik	100503871	chr12	3835036	3836336	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
4930417G10Rik	74855	chr12	4737983	4739283	-	ICP	GSCLC_high	GSCLC_high		
Apob	238055	chr12	7976777	7978077	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
1700022H16Rik	69420	chr12	9570185	9571485	-	ICP				GSCLC_high
Msgn1	56184	chr12	11208548	11209848	-	LCP			GSCLC_high	GSCLC_high
1700034J04Rik	73304	chr12	11221804	11223104	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
4921511I17Rik	70858	chr12	12392075	12393375	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
4930448C13Rik	73972	chr12	15049989	15051289	-	LCP			GSCLC_high	GSCLC_high
Gm9178	668455	chr12	20416804	20418104	+	ICP		GSCLC_high		GSCLC_high

<i>Rsad2</i>	58185	chr12	26456052	26457352	-	LCP				GSCLC_high
<i>Gm9866</i>	636791	chr12	27160116	27161416	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Myt1l</i>	17933	chr12	29527484	29528784	+	ICP				GSCLC_high
<i>2310016D03Rik</i>	69566	chr12	30466958	30468258	-	ICP			GSCLC_high	GSCLC_high
<i>Slc26a3</i>	13487	chr12	31437401	31438701	+	ICP		GSCLC_high		GSCLC_high
<i>Pik3cg</i>	30955	chr12	32208249	32209549	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>LOC100861990</i>	100861990	chr12	34248245	34249545	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Prps1l1</i>	75456	chr12	34983861	34985161	+	ICP				GSCLC_high
<i>Agf2</i>	23795	chr12	35992025	35993325	+	ICP				GSCLC_high
<i>1700108M19Rik</i>	71156	chr12	36252998	36254298	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Sostdc1</i>	66042	chr12	36313269	36314569	+	LCP			GSCLC_high	GSCLC_high
<i>Mir5099</i>	100628578	chr12	36815305	36816605	+	ICP		GSCLC_high		GSCLC_high
<i>4930428E07Rik</i>	73867	chr12	38614121	38615421	-	LCP		GSCLC_high		GSCLC_high
<i>Lrm3</i>	16981	chr12	41485351	41486651	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm1818</i>	217536	chr12	48559485	48560785	-	ICP			GSCLC_high	
<i>3110039M20Rik</i>	67293	chr12	49388752	49390052	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>1810007C17Rik</i>	69054	chr12	49480462	49481762	-	ICP		GSCLC_high	GSCLC_high	
<i>Gm6265</i>	621837	chr12	56373423	56374723	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>4921506M07Rik</i>	70846	chr12	57563215	57564515	+	LCP		GSCLC_high		
<i>Mia2</i>	338320	chr12	59094900	59096200	+	ICP		GSCLC_high		GSCLC_high
<i>Spanxn4</i>	73309	chr12	62686904	62688204	+	LCP			GSCLC_high	GSCLC_high
<i>Gm8075</i>	666385	chr12	73792583	73793883	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Slc10a1</i>	20493	chr12	80967679	80968979	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Vrtn</i>	432677	chr12	84640119	84641419	+	LCP		GSCLC_high		GSCLC_high
<i>LOC100861892</i>	100861892	chr12	86077654	86078954	+	ICP		GSCLC_high		GSCLC_high
<i>LOC100862206</i>	100862206	chr12	87765900	87767200	-	LCP		GSCLC_high		
<i>Dio2</i>	13371	chr12	90738038	90739338	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Fam181a</i>	100504156	chr12	103314059	103315359	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Serpina12</i>	68054	chr12	104044043	104045343	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Tcf1</i>	21432	chr12	105222337	105223637	-	ICP			GSCLC_high	GSCLC_high
<i>4933406K04Rik</i>	71033	chr12	106715924	106717224	-	ICP			GSCLC_high	GSCLC_high
<i>Meg3</i>	17263	chr12	109540096	109541396	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>A230087F16Rik</i>	100503323	chr12	111283859	111285159	+	LCP			GSCLC_high	
<i>1200009I06Rik</i>	74190	chr12	111416530	111417830	+	LCP			GSCLC_high	
<i>Tdrd9</i>	74691	chr12	111970659	111971959	+	ICP		GSCLC_high		GSCLC_high
<i>Ighv5-2</i>	777685	chr12	113578590	113579890	-	LCP		GSCLC_high		GSCLC_high
<i>Ighv2-3</i>	238412	chr12	113611076	113612376	-	LCP		GSCLC_high		
<i>Ighv5-6</i>	777780	chr12	113625401	113626701	-	LCP		GSCLC_high		GSCLC_high
<i>Ighv5-12</i>	668395	chr12	113702019	113703319	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Ighv2-6</i>	630486	chr12	113716562	113717862	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Ighv5-9-1</i>	641178	chr12	113736006	113737306	-	LCP		GSCLC_high		GSCLC_high
<i>Ighv2-6-8</i>	791090	chr12	113796030	113797330	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Ighv5-15</i>	780792	chr12	113826541	113827841	-	LCP				GSCLC_high
<i>Ighv5-17</i>	780794	chr12	113859042	113860342	-	LCP		GSCLC_high		GSCLC_high
<i>Ighv4-1</i>	780802	chr12	113948177	113949477	-	LCP		GSCLC_high		GSCLC_high
<i>Ighv11-1</i>	780804	chr12	113981774	113983074	-	LCP		GSCLC_high		GSCLC_high
<i>Ighv11-2</i>	780818	chr12	114048304	114049604	-	LCP				GSCLC_high
<i>Ighv7-4</i>	632654	chr12	114222854	114224154	-	LCP		GSCLC_high		GSCLC_high
<i>Ighv10-1</i>	380808	chr12	114479051	114480351	-	LCP			GSCLC_high	
<i>Ighv1-15</i>	629865	chr12	114657246	114658546	-	LCP		GSCLC_high		
<i>Ighv1-39</i>	780891	chr12	114914492	114915792	-	LCP		GSCLC_high		
<i>Ighv1-56</i>	382695	chr12	115242695	115243995	-	LCP			GSCLC_high	
<i>Calm13</i>	70405	chr13	3803918	3805218	-	LCP		GSCLC_high		
<i>Akr1c14</i>	105387	chr13	4058691	4059991	+	ICP		GSCLC_high		GSCLC_high
<i>Gm5444</i>	432723	chr13	4770757	4772057	+	ICP		GSCLC_high		
<i>1700016G22Rik</i>	71867	chr13	5857692	5858992	-	LCP		GSCLC_high	GSCLC_high	
<i>4933412O06Rik</i>	71071	chr13	15802230	15803530	-	ICP				GSCLC_high
<i>4930448F12Rik</i>	73992	chr13	18099802	18101102	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>A530099J19Rik</i>	319293	chr13	19732551	19733851	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Olfr1370</i>	258528	chr13	21072899	21074199	-	LCP			GSCLC_high	GSCLC_high
<i>Olfr1361</i>	258534	chr13	21658921	21660221	-	LCP			GSCLC_high	GSCLC_high
<i>Olfr1360</i>	258536	chr13	21674580	21675880	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Scgn</i>	214189	chr13	23990814	23992114	-	ICP				GSCLC_high
<i>4932702P03Rik</i>	73326	chr13	24904700	24906000	+	ICP		GSCLC_high	GSCLC_high	
<i>Gpld1</i>	14756	chr13	24942252	24943552	+	ICP			GSCLC_high	
<i>1700092E19Rik</i>	73576	chr13	26312006	26313306	-	LCP				GSCLC_high
<i>1700018A04Rik</i>	71307	chr13	31582113	31583413	-	ICP		GSCLC_high	GSCLC_high	
<i>Serp1nb1a</i>	66222	chr13	32850785	32852085	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Serp1nb6d</i>	238568	chr13	33660505	33661805	+	LCP		GSCLC_high		GSCLC_high
<i>Serp1nb6c</i>	97848	chr13	33905308	33906608	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>LOC100862316</i>	100862316	chr13	34126323	34127623	+	LCP		GSCLC_high		GSCLC_high
<i>Ofcc1</i>	218165	chr13	40287611	40288911	-	ICP			GSCLC_high	GSCLC_high
<i>9530008L14Rik</i>	109254	chr13	41847216	41848516	-	LCP			GSCLC_high	GSCLC_high
<i>Phactr1</i>	218194	chr13	42679723	42681023	+	LCP		GSCLC_high		GSCLC_high
<i>LOC622552</i>	622552	chr13	43715891	43717191	+	ICP		GSCLC_high	GSCLC_high	
<i>Gm1574</i>	380842	chr13	46272821	46274121	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>4931429P17Rik</i>	70971	chr13	48018208	48019508	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>4930518P08Rik</i>	71654	chr13	50764848	50766148	-	LCP		GSCLC_high	GSCLC_high	
<i>Drd1a</i>	13488	chr13	54055258	54056558	-	HCP		GSCLC_high		
<i>Nsd1</i>	18193	chr13	55208882	55210182	+	HCP		GSCLC_high		
<i>Gm10782</i>	100038494	chr13	56362000	56363300	+	ICP				GSCLC_high
<i>Slc28a3</i>	114304	chr13	58610477	58611777	-	ICP		GSCLC_high		GSCLC_high
<i>Gm19866</i>	100503743	chr13	59915422	59916722	-	LCP			GSCLC_high	GSCLC_high
<i>Gm7664</i>	665503	chr13	62528559	62529859	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Fbp2</i>	14120	chr13	62857970	62859270	-	ICP		GSCLC_high		
<i>Prss47</i>	218304	chr13	65052360	65053660	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm3785</i>	100042311	chr13	65124976	65126276	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm5792</i>	544944	chr13	65415699	65416999	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm5451</i>	432768	chr13	66873181	66874481	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Zfp71-rs1</i>	235907	chr13	67728773	67730073	-	ICP		GSCLC_high		GSCLC_high
<i>4930441O14Rik</i>	68271	chr13	67728362	67729662	+	ICP		GSCLC_high		GSCLC_high
<i>A530095I07Rik</i>	210373	chr13	69543617	69544917	-	ICP		GSCLC_high		
<i>4930520P13Rik</i>	75086	chr13	70231922	70233222	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>D730050B12Rik</i>	78446	chr13	72816363	72817663	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Lrrc14b</i>	432779	chr13	74363600	74364900	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Mir682</i>	751556	chr13	75644146	75645446	+	ICP			GSCLC_high	
<i>Mef2c</i>	17260	chr13	83503134	83504434	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high

<i>Atp6ap1l</i>	435376	chr13	90904955	90906255	-	ICP			GSCLC_high	GSCLC_high
<i>Gm4130</i>	100042959	chr13	91262272	91263572	-	ICP			GSCLC_high	GSCLC_high
<i>Gm4814</i>	100502942	chr13	93072404	93073704	+	ICP				GSCLC_high
<i>Bhmt</i>	12116	chr13	93637358	93638658	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Crhbp</i>	12919	chr13	9544431	95445731	-	ICP				GSCLC_high
<i>S100z</i>	268686	chr13	95478255	95479555	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Gm2373</i>	100039691	chr13	97434070	97435370	+	LCP			GSCLC_high	GSCLC_high
<i>5330416C01Rik</i>	403201	chr13	97746973	97748273	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Tmem174</i>	68344	chr13	98637010	98638310	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Gm5453</i>	432798	chr13	98903324	98904624	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
<i>Gm6115</i>	619937	chr13	101038846	101040146	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Al197445</i>	105120	chr13	107468922	107470222	+	LCP			GSCLC_high	GSCLC_high
<i>1700006H21Rik</i>	72257	chr13	107686497	107687797	+	LCP			GSCLC_high	GSCLC_high
<i>Mir582</i>	100124489	chr13	109323844	109325144	+	ICP				GSCLC_high
<i>Actbl2</i>	238880	chr13	111254113	111255413	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm10736</i>	100504654	chr13	111593252	111594552	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
<i>Ankrd55</i>	77318	chr13	112287551	112288851	+	ICP				GSCLC_high
<i>Esm1</i>	71690	chr13	113208759	113210059	+	ICP			GSCLC_high	GSCLC_high
<i>Hspb3</i>	56534	chr13	113663276	113664576	-	ICP			GSCLC_high	GSCLC_high
<i>Gm10734</i>	670198	chr13	115088601	115089901	+	ICP		GSCLC_high		
<i>Gm20349</i>	100504681	chr14	8300153	8301453	+	LCP		GSCLC_high	GSCLC_high	
<i>Olfir31</i>	18330	chr14	14327213	14328513	+	ICP			GSCLC_high	
<i>Dusp13</i>	27389	chr14	21748222	21749522	-	LCP		GSCLC_high		
<i>3425401B19Rik</i>	100504518	chr14	32684872	32686172	-	ICP			GSCLC_high	GSCLC_high
<i>LOC100862308</i>	100862308	chr14	33369743	33371043	-	LCP				GSCLC_high
<i>Ppyr1</i>	19065	chr14	34152019	34153319	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Sncg</i>	20618	chr14	34374269	34375569	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Mmm2</i>	105450	chr14	34374604	34375904	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>9230112D13Rik</i>	78243	chr14	34522401	34523701	-	ICP			GSCLC_high	
<i>Sh2d4b</i>	328381	chr14	40892565	40893865	-	LCP			GSCLC_high	GSCLC_high
<i>Mat1a</i>	11720	chr14	41104481	41105781	+	LCP			GSCLC_high	
<i>Otx2os1</i>	606497	chr14	48668388	48669688	+	HCP				GSCLC_high
<i>4933429O19Rik</i>	66770	chr14	48877973	48879273	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Olfir734</i>	258658	chr14	50320433	50321733	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Kihl33</i>	546611	chr14	50892855	50894155	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Rnase9</i>	328401	chr14	51041467	51042767	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Eddm3b</i>	219026	chr14	51113665	51114965	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm16617</i>	100502764	chr14	51988429	51989729	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Olfir1512</i>	258424	chr14	52372651	52373951	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Trav2</i>	100042372	chr14	52566393	52567693	+	LCP		GSCLC_high		GSCLC_high
<i>Trav5-1</i>	633740	chr14	52621666	52622966	+	LCP		GSCLC_high		GSCLC_high
<i>Trav9d-1</i>	671927	chr14	52791416	52792716	+	ICP		GSCLC_high		GSCLC_high
<i>Trav8d-2</i>	667604	chr14	53041528	53042828	+	LCP		GSCLC_high		
<i>Trav9n-1</i>	279872	chr14	53100901	53102201	+	LCP		GSCLC_high		GSCLC_high
<i>Trav6n-6</i>	620297	chr14	53131800	53133100	+	ICP				GSCLC_high
<i>Trav8n-2</i>	100126458	chr14	53345061	53346361	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
<i>Trav9-1</i>	627324	chr14	53487206	53488506	+	LCP				GSCLC_high
<i>Trav13-1</i>	100126469	chr14	53544114	53545414	+	LCP	GSCLC_high	GSCLC_high		
<i>Trav4-3</i>	100126471	chr14	53598011	53599311	+	LCP		GSCLC_high		
<i>Trav13-2</i>	638566	chr14	53633988	53635288	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Trav3-3</i>	320898	chr14	53665105	53666405	+	LCP				GSCLC_high
<i>Trav4-4-dv10</i>	100113414	chr14	53682777	53684077	+	LCP		GSCLC_high		GSCLC_high
<i>Trav21%2Fdv12</i>	100101940	chr14	53875116	53876416	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
<i>Trdv2-2</i>	320913	chr14	53960093	53961393	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Rem2</i>	140743	chr14	54475200	54476500	+	LCP			GSCLC_high	GSCLC_high
<i>4930579G18Rik</i>	75913	chr14	54649611	54650911	+	ICP			GSCLC_high	
<i>Cebpe</i>	110794	chr14	54711774	54713074	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Fitm1</i>	68680	chr14	55574774	55576074	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Irf9</i>	16391	chr14	55603085	55604385	+	LCP			GSCLC_high	GSCLC_high
<i>Tgm1</i>	21816	chr14	55713092	55714392	-	ICP			GSCLC_high	
<i>Ltb4r2</i>	57260	chr14	55760528	55761828	+	LCP				GSCLC_high
<i>Adcy4</i>	104110	chr14	55783619	55784919	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Nfatc4</i>	73181	chr14	55823895	55825195	+	ICP		GSCLC_high		
<i>Sacs</i>	50720	chr14	61137557	61138857	+	ICP				GSCLC_high
<i>Phoc</i>	18155	chr14	65425072	65426372	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gulo</i>	268756	chr14	66008810	66010110	-	LCP				GSCLC_high
<i>Stmn4</i>	56471	chr14	66343475	66344775	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
<i>1700092C10Rik</i>	73554	chr14	69171443	69172743	-	ICP	GSCLC_high	GSCLC_high		
<i>Nkx2-6</i>	18092	chr14	69170902	69172202	+	ICP		GSCLC_high		
<i>Pdlim2</i>	213019	chr14	70177272	70178572	-	LCP			GSCLC_high	
<i>Phyhip</i>	105653	chr14	70456617	70457917	+	ICP			GSCLC_high	
<i>Cysltr2</i>	70086	chr14	73048714	73050014	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Lpar6</i>	67168	chr14	73236991	73238291	+	ICP			GSCLC_high	
<i>4933402J15Rik</i>	74425	chr14	74354627	74355927	+	ICP				GSCLC_high
<i>Htr2a</i>	15558	chr14	74639940	74641240	+	LCP			GSCLC_high	GSCLC_high
<i>Gm15628</i>	100043176	chr14	75136516	75137816	-	ICP			GSCLC_high	GSCLC_high
<i>Slah3</i>	380918	chr14	75455082	75456382	+	ICP				GSCLC_high
<i>4930564B18Rik</i>	75272	chr14	75641359	75642659	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
<i>Olfm4</i>	380924	chr14	79999402	80000702	+	LCP		GSCLC_high		GSCLC_high
<i>4930529K09Rik</i>	75155	chr14	86245070	86246370	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>1700110M21Rik</i>	76627	chr14	101199669	101200969	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>4933432I03Rik</i>	71264	chr14	103033403	103034703	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Scel</i>	64929	chr14	103512441	103513741	+	ICP			GSCLC_high	GSCLC_high
<i>4921525B02Rik</i>	70898	chr14	103699032	103700332	-	LCP	GSCLC_high		GSCLC_high	
<i>5430440P10Rik</i>	71362	chr14	105426659	105427959	+	ICP				GSCLC_high
<i>4930449E01Rik</i>	74864	chr14	105497888	105499188	-	LCP			GSCLC_high	GSCLC_high
<i>9330188P03Rik</i>	380930	chr14	105587592	105588892	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm6219</i>	621364	chr14	106093433	106094733	-	ICP		GSCLC_high		
<i>Trim52</i>	212085	chr14	106105298	106106598	+	HCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm9325</i>	668738	chr14	106457250	106458550	+	LCP			GSCLC_high	GSCLC_high
<i>Gm9326</i>	668739	chr14	106460595	106461895	+	LCP		GSCLC_high	GSCLC_high	
<i>Gm6232</i>	621487	chr14	106463942	106465242	+	LCP		GSCLC_high	GSCLC_high	
<i>Slitrk6</i>	239250	chr14	110754749	110756049	-	ICP				GSCLC_high
<i>Oxgr1</i>	239283	chr14	120042035	120043335	-	ICP				GSCLC_high
<i>Slc15a1</i>	56643	chr14	121504854	121506154	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Timm8a2</i>	223262	chr14	122033774	122035074	+	ICP			GSCLC_high	
<i>1700108J01Rik</i>	68245	chr14	122233238	122234538	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	

<i>Itgbl1</i>	223272	chr14	123659240	123660540	+	ICP	GSCLC_high	GSCLC_high		
<i>Fgf14</i>	14169	chr14	124676727	124678027	-	ICP				GSCLC_high
<i>1700024B18Rik</i>	69393	chr14	123986735	123988035	+	LCP			GSCLC_high	GSCLC_high
<i>Sepp1</i>	20363	chr15	3269867	3271167	+	ICP				GSCLC_high
<i>Ttc23l</i>	75777	chr15	10558268	10559568	-	LCP		GSCLC_high		GSCLC_high
<i>C1qtnf3</i>	81799	chr15	10951432	10952732	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Slc45a2</i>	22293	chr15	10999821	11001121	+	LCP				GSCLC_high
<i>1700047G03Rik</i>	73339	chr15	11966162	11967462	+	ICP		GSCLC_high		GSCLC_high
<i>Acot10</i>	64833	chr15	20666350	20667650	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Cdh12</i>	215654	chr15	21110552	21111852	+	ICP				GSCLC_high
<i>Gm5803</i>	545091	chr15	22714584	22715884	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm2824</i>	100040529	chr15	25026940	25028240	-	ICP			GSCLC_high	GSCLC_high
<i>2310043O21Rik</i>	69679	chr15	38594534	38595834	-	LCP	GSCLC_high			GSCLC_high
<i>Abra</i>	223513	chr15	41869320	41870620	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Trhr</i>	22045	chr15	44195235	44196535	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm5471</i>	432950	chr15	44971735	44973035	-	ICP		GSCLC_high		GSCLC_high
<i>1700022A22Rik</i>	71120	chr15	46323685	46324985	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>4930523O13Rik</i>	74726	chr15	46495779	46497079	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
<i>4930548G14Rik</i>	75281	chr15	46622405	46623705	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm5215</i>	383032	chr15	54311965	54313265	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Enpp2</i>	18606	chr15	54919746	54921046	-	ICP				GSCLC_high
<i>Fam83a</i>	239463	chr15	57985003	57986303	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>4933412E24Rik</i>	71088	chr15	60016218	60017518	-	LCP		GSCLC_high		GSCLC_high
<i>1700065I16Rik</i>	78462	chr15	63816288	63817588	+	LCP		GSCLC_high		
<i>Gsdmcl1</i>	74236	chr15	63846409	63847709	+	LCP		GSCLC_high		GSCLC_high
<i>Gsdmcl2</i>	665769	chr15	63879826	63881126	+	LCP		GSCLC_high	GSCLC_high	
<i>Wisp1</i>	22402	chr15	66890493	66891793	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Ly6k</i>	76486	chr15	74799568	74800868	-	HCP		GSCLC_high		
<i>Gml</i>	625599	chr15	74818415	74819715	-	ICP		GSCLC_high		GSCLC_high
<i>Hemt1</i>	15202	chr15	74818176	74819476	+	ICP		GSCLC_high		
<i>LOC223645</i>	223645	chr15	75888323	75889623	-	LCP		GSCLC_high		GSCLC_high
<i>Nrbp2</i>	223649	chr15	76089613	76090913	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Gm19945</i>	100503893	chr15	76149468	76150768	+	ICP		GSCLC_high		GSCLC_high
<i>Oplah</i>	75475	chr15	76306845	76308145	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
<i>Scx</i>	20289	chr15	76456538	76457838	+	HCP				GSCLC_high
<i>Slc39a4</i>	72027	chr15	76616452	76617752	-	LCP	GSCLC_high			
<i>Foxh1</i>	14106	chr15	76669473	76670773	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
<i>Gm3787</i>	100042318	chr15	77369882	77371182	-	ICP		GSCLC_high	GSCLC_high	
<i>C1qtnf6</i>	72709	chr15	78529251	78530551	-	LCP	GSCLC_high		GSCLC_high	
<i>Sstr3</i>	20607	chr15	78543945	78545245	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Mfnq</i>	17305	chr15	78773045	78774345	-	LCP	GSCLC_high		GSCLC_high	
<i>Gm20044</i>	100504071	chr15	78926887	78928187	-	LCP		GSCLC_high		
<i>Lgals1</i>	16852	chr15	78925825	78927125	+	LCP	GSCLC_high			
<i>Gm17753</i>	654469	chr15	79025554	79026854	-	ICP			GSCLC_high	
<i>Gm10864</i>	100038573	chr15	79192612	79193912	+	LCP		GSCLC_high	GSCLC_high	
<i>Mchr1</i>	207911	chr15	81234599	81235899	+	ICP				GSCLC_high
<i>Dnajb7</i>	57755	chr15	81407873	81409173	-	ICP			GSCLC_high	
<i>Gm17597</i>	100504312	chr15	81802213	81803513	-	LCP			GSCLC_high	
<i>Tef</i>	21685	chr15	81801773	81803073	+	LCP			GSCLC_high	
<i>1700029P11Rik</i>	66346	chr15	81979640	81980940	+	HCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm5806</i>	545124	chr15	82515512	82516812	+	HCP		GSCLC_high	GSCLC_high	
<i>Tcf20</i>	21411	chr15	82911734	82913034	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>1810041L15Rik</i>	72301	chr15	84446697	84447997	-	LCP			GSCLC_high	
<i>Gramd4</i>	223752	chr15	86056795	86058095	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Zdhhc25</i>	70073	chr15	88599402	88600702	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Adm2</i>	223780	chr15	89322072	89323372	+	ICP		GSCLC_high		
<i>Tymp</i>	72962	chr15	89376636	89377936	-	ICP			GSCLC_high	GSCLC_high
<i>Gm17546</i>	100502979	chr15	95829672	95830972	-	ICP	GSCLC_high		GSCLC_high	
<i>Gm16256</i>	100503050	chr15	97765649	97766949	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>H1fnt</i>	70069	chr15	98256907	98258207	-	ICP		GSCLC_high		GSCLC_high
<i>Olfr284</i>	258278	chr15	98340539	98341839	-	ICP			GSCLC_high	GSCLC_high
<i>Olfr283</i>	259038	chr15	98378708	98380008	-	ICP	GSCLC_high	GSCLC_high		GSCLC_high
<i>Olfr282</i>	258449	chr15	98436570	98437870	+	ICP				GSCLC_high
<i>Olfr281</i>	258277	chr15	98455412	98456712	+	ICP		GSCLC_high		GSCLC_high
<i>Olfr279</i>	258502	chr15	98496574	98497874	+	ICP		GSCLC_high		GSCLC_high
<i>Faim2</i>	72393	chr15	99527617	99528917	-	ICP	GSCLC_high			
<i>Aqp2</i>	11827	chr15	99578156	99579456	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Tmprss12</i>	75002	chr15	100279937	100281237	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
<i>Mettl7a3</i>	668178	chr15	100334029	100335329	+	ICP			GSCLC_high	GSCLC_high
<i>Scn9a</i>	20273	chr15	100935371	100936671	+	HCP	GSCLC_high		GSCLC_high	
<i>Krt7</i>	110310	chr15	101411503	101412803	+	HCP				GSCLC_high
<i>Krt81</i>	64818	chr15	101463365	101464665	-	ICP			GSCLC_high	GSCLC_high
<i>Krt84</i>	16680	chr15	101532420	101533720	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Krt82</i>	114566	chr15	101550259	101551559	-	ICP		GSCLC_high	GSCLC_high	
<i>Krt75</i>	109052	chr15	101573504	101574804	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Krt6b</i>	16688	chr15	101679889	101681189	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Krt71</i>	56735	chr15	101742697	101743997	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Krt72-ps</i>	105866	chr15	101786058	101787358	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Krt73</i>	223915	chr15	101801932	101803232	-	LCP				GSCLC_high
<i>Krt2</i>	16681	chr15	101817769	101819069	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Krt4</i>	16682	chr15	101924335	101925635	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Krt79</i>	223917	chr15	101939924	101941224	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Igf1bp6</i>	16012	chr15	102143286	102144586	+	ICP			GSCLC_high	
<i>Soat2</i>	223920	chr15	102149675	102150975	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Mir196a-2</i>	723958	chr15	102972450	102973750	+	ICP		GSCLC_high		GSCLC_high
<i>Nfe2</i>	18022	chr15	103255016	103256316	-	ICP	GSCLC_high	GSCLC_high		
<i>LOC100862049</i>	100862049	chr15	103299463	103300763	-	ICP			GSCLC_high	
<i>Nckap1l</i>	105855	chr15	103452925	103454225	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
<i>Olfr15</i>	18312	chr16	3838075	3839375	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
<i>Gm5480</i>	432995	chr16	5006388	5007688	+	LCP	GSCLC_high		GSCLC_high	
<i>Gm4262</i>	100043147	chr16	11007998	11009298	+	LCP			GSCLC_high	GSCLC_low
<i>Mir193b</i>	100124432	chr16	13448623	13449923	+	ICP		GSCLC_high		
<i>Gm7689</i>	665562	chr16	16819723	16821023	-	ICP		GSCLC_high	GSCLC_high	
<i>Dgcr6</i>	13353	chr16	18051960	18053260	+	LCP		GSCLC_high		
<i>Gp1bb</i>	14724	chr16	18622003	18623303	-	ICP			GSCLC_high	GSCLC_high
<i>Kihl6</i>	239743	chr16	19982649	19983949	-	ICP	GSCLC_high			GSCLC_high
<i>Fam131a</i>	78408	chr16	20694157	20695457	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	

Thpo	21832	chr16	20734111	20735411	-	HCP		GSCLC_high		GSCLC_high
Gm6557	625123	chr16	21062694	21063994	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm20191	100504359	chr16	21644275	21645575	-	LCP		GSCLC_high		
Liph	239759	chr16	21995142	21996442	-	ICP	GSCLC_high		GSCLC_high	
Gm4943	239760	chr16	22052604	22053904	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Fetub	59083	chr16	22917482	22918782	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Rtp4	67775	chr16	23609019	23610319	+	ICP				GSCLC_high
Rtp2	224055	chr16	23930394	23931694	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Cldn16	114141	chr16	26462235	26463535	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm606	239789	chr16	26989574	26990874	-	ICP		GSCLC_high		GSCLC_high
Uts2d	224065	chr16	27369839	27371139	-	ICP	GSCLC_high			GSCLC_high
Lrrc15	74488	chr16	30282854	30284154	-	HCP		GSCLC_high	GSCLC_high	
Gm536	224098	chr16	31617233	31618533	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Mfi2	30060	chr16	31877910	31879210	+	LCP				GSCLC_high
2310010M20Rik	69576	chr16	32270709	32272009	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Tm4sf19	277203	chr16	32399606	32400906	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm10913	100503125	chr16	36208378	36209678	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm5416	408196	chr16	36209503	36210803	+	LCP		GSCLC_high	GSCLC_high	
Popdc2	64082	chr16	38361273	38362573	+	ICP			GSCLC_high	
Upk1b	22268	chr16	38799803	38801103	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Cd200r1	57781	chr16	44764836	44766136	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Slc9a10	208169	chr16	45534366	45535666	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Cd96	84544	chr16	46119848	46121148	-	ICP				GSCLC_high
1700026J12Rik	73255	chr16	49255366	49256666	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm6936	628951	chr16	49979560	49980860	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
4930404A05Rik	73820	chr16	52815344	52816644	-	LCP				GSCLC_high
Abi3bp	320712	chr16	56476946	56478246	+	LCP				GSCLC_high
Gpr15	71223	chr16	58718324	58719624	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Olfr187	258319	chr16	59039349	59040649	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Olfr198	258036	chr16	59202024	59203324	-	LCP			GSCLC_high	GSCLC_high
Olfr201	258996	chr16	59269265	59270565	-	LCP			GSCLC_high	
Csnka2ip	224291	chr16	64478734	64480034	+	ICP				GSCLC_high
Pou1f1	18736	chr16	65519729	65521029	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
1700010K23Rik	75501	chr16	66656218	66657518	+	ICP				GSCLC_high
D16Etd519e	52645	chr16	70615525	70616825	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
4930567J20Rik	78221	chr16	71249004	71250304	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
1700063K16Rik	76610	chr16	76821341	76822641	-	LCP				GSCLC_high
2810055G20Rik	77994	chr16	77328428	77329728	+	ICP				GSCLC_high
4930478L05Rik	75818	chr16	78559416	78560716	+	ICP	GSCLC_high		GSCLC_high	
4930553E22Rik	75247	chr16	84370243	84371543	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
ORF63	224419	chr16	87552430	87553730	+	ICP				GSCLC_high
4930420G21Rik	78924	chr16	88375711	88377011	+	LCP		GSCLC_high		GSCLC_high
Cldn17	239931	chr16	88506578	88507878	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Cldn8	54420	chr16	88562783	88564083	-	LCP				GSCLC_high
Krtap24-1	239932	chr16	88611879	88613179	-	ICP			GSCLC_high	GSCLC_high
2310079G19Rik	69699	chr16	88627266	88628566	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Krtap26-1	69533	chr16	88647396	88648696	-	LCP		GSCLC_high		GSCLC_high
2310061N02Rik	69661	chr16	88707562	88708862	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Krtap13-1	268905	chr16	88727962	88729262	+	LCP			GSCLC_high	GSCLC_high
Krtap13	16699	chr16	88751228	88752528	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
2310057N15Rik	69696	chr16	88773806	88775106	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm5965	546672	chr16	88776935	88778235	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Krtap14	23927	chr16	88825745	88827045	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Krtap15	26560	chr16	88828109	88829409	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Krtap22-2	68740	chr16	89010359	89011659	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Krtap11-1	16693	chr16	89570783	89572083	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
4932438H23Rik	74387	chr16	91068745	91070045	-	ICP			GSCLC_high	
Kcne1	16509	chr16	92359068	92360368	-	LCP	GSCLC_high			GSCLC_high
2410124H12Rik	76785	chr16	92477842	92479142	+	ICP				GSCLC_high
1700029J03Rik	72264	chr16	93458472	93459772	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Gm15340	100040997	chr16	95899498	95900798	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
B3galt5	93961	chr16	96234901	96236201	+	ICP				GSCLC_high
Igsf5	72058	chr16	96360857	96362157	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Pcp4	18546	chr16	96466706	96468006	+	LCP		GSCLC_high		GSCLC_high
C530047H08Rik	319358	chr17	3230371	3231671	+	LCP	GSCLC_high	GSCLC_high		
4930579D07Rik	75934	chr17	4854082	4855382	-	ICP			GSCLC_high	
Gm2808	100040500	chr17	6582303	6583603	+	ICP	GSCLC_high			GSCLC_high
T2	21331	chr17	8371496	8372796	+	ICP				GSCLC_high
Slc22a2	20518	chr17	12583289	12584589	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Slc22a1	20517	chr17	12675438	12676738	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Thbs2	21826	chr17	14693862	14695162	-	LCP		GSCLC_high		GSCLC_high
4933401D09Rik	71008	chr17	15630888	15632188	+	ICP				GSCLC_high
Mir99b	387230	chr17	17829288	17830588	+	ICP	GSCLC_high	GSCLC_high		
Mirlet7e	387248	chr17	17829452	17830752	+	ICP	GSCLC_high	GSCLC_high		
Mir125a	387235	chr17	17829912	17831212	+	ICP	GSCLC_high	GSCLC_high		
Ncma00085	75202	chr17	17830075	17831375	+	ICP	GSCLC_high	GSCLC_high		
Gm19747	100503522	chr17	17912748	17914048	-	LCP		GSCLC_high		GSCLC_high
Cldn9	56863	chr17	23683626	23684926	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Prss41	71003	chr17	23843756	23845056	-	ICP		GSCLC_high		
Prss21	57256	chr17	23867172	23868472	+	ICP		GSCLC_high		GSCLC_high
Prss27	213171	chr17	24037343	24038643	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Rpl3l	66211	chr17	24726929	24728229	+	LCP		GSCLC_high	GSCLC_high	
Tekt4	71840	chr17	25470690	25471990	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Jmjd8	72106	chr17	25828143	25829443	+	ICP		GSCLC_high		GSCLC_high
Gm8225	666668	chr17	26541860	26543160	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Syngap1	240057	chr17	26940552	26941852	+	LCP		GSCLC_high		
Gm4	268934	chr17	27502904	27504204	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Def6	23853	chr17	28206878	28208178	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm749	328788	chr17	28548587	28549887	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
1700030A11Rik	74179	chr17	28904365	28905665	+	LCP	GSCLC_high	GSCLC_high		
Gm16197	100504267	chr17	29078561	29079861	-	ICP	GSCLC_high		GSCLC_high	
Rasa13	320484	chr17	32403181	32404481	-	LCP			GSCLC_high	
Zfp563	240068	chr17	33088467	33089767	+	HCP	GSCLC_high			
Morc2b	240069	chr17	33139283	33140583	-	ICP		GSCLC_high		GSCLC_high
Actf9	69481	chr17	33431999	33433299	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
BC033916	474160	chr17	33904235	33905535	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
BC051537	414076	chr17	34094909	34096209	-	ICP	GSCLC_high		GSCLC_high	

H2-Aa	14960	chr17	34287371	34288671	-	LCP		GSCLC_high		
H2-Eb2	381091	chr17	34324775	34326075	+	LCP				GSCLC_high
Prrt1	260297	chr17	34628786	34630086	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Tnxb	81877	chr17	34669635	34670935	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
C2	12263	chr17	34881700	34883000	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
G6b	114763	chr17	35063537	35064837	+	LCP			GSCLC_high	
Ly6g6d	114654	chr17	35074064	35075364	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
Ltb	16994	chr17	35193607	35194907	+	ICP			GSCLC_high	
Lta	16992	chr17	35204951	35206251	-	ICP				GSCLC_high
H2-Q10	15007	chr17	35469189	35470489	+	HCP		GSCLC_high		GSCLC_high
Pou5f1	18999	chr17	35505132	35506432	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
2300002M23Rik	69542	chr17	35566585	35567885	+	LCP				GSCLC_high
Gm11127	100529082	chr17	36057971	36059271	-	ICP			GSCLC_high	
H2-T10	15024	chr17	36121044	36122344	-	ICP				GSCLC_high
Gm7030	630294	chr17	36129025	36130325	-	ICP				GSCLC_high
H2-T3	15043	chr17	36189751	36191051	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
H2-M10.1	14985	chr17	36325750	36327050	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
H2-M10.4	224753	chr17	36461929	36463229	-	LCP				GSCLC_high
Trim15	69097	chr17	36866810	36868110	-	ICP			GSCLC_high	GSCLC_high
2410137M14Rik	76797	chr17	36980837	36982137	-	ICP				GSCLC_high
H2-M2	14990	chr17	37483129	37484429	-	LCP				GSCLC_high
Olfr118	404308	chr17	37671125	37672425	+	LCP			GSCLC_high	
Olfr130	258480	chr17	38066273	38067573	+	LCP				GSCLC_high
Gm5494	433107	chr17	40560607	40561907	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Gm5978	546797	chr17	42726273	42727573	+	LCP			GSCLC_high	GSCLC_high
E130008D07Rik	545207	chr17	43157891	43159191	-	LCP	GSCLC_high			GSCLC_high
Gpr116	224792	chr17	43388566	43389866	+	ICP				GSCLC_high
Gm7325	653016	chr17	45601702	45603002	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gnmt	14711	chr17	46728765	46730065	-	ICP			GSCLC_high	
Prph2	19133	chr17	46909585	46910885	+	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Gm4945	240110	chr17	47042639	47043939	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
Guca1b	107477	chr17	47384493	47385793	+	ICP		GSCLC_high		
Gm14873	100126242	chr17	47701596	47702896	-	LCP	GSCLC_high		GSCLC_high	
Apobec2	11811	chr17	48432328	48433628	-	ICP			GSCLC_high	
Unc5cl	76589	chr17	48454001	48455301	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
1700008K24Rik	69311	chr17	49113133	49114433	-	LCP		GSCLC_high		GSCLC_high
Gm5094	328839	chr17	52461365	52462665	-	ICP				GSCLC_high
Tubb4a	22153	chr17	57087382	57088682	-	HCP				GSCLC_high
Vav1	22324	chr17	57278200	57279500	+	LCP		GSCLC_high		
4930583I09Rik	78057	chr17	64835665	64836965	-	ICP			GSCLC_high	
Gm4701	100043871	chr17	64875301	64876601	+	ICP				GSCLC_high
Gm9386	668830	chr17	80938314	80939614	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Slc8a1	20541	chr17	81737977	81739277	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm6594	625514	chr17	82538358	82539658	+	ICP				GSCLC_high
Gm19689	100503434	chr17	83077825	83079125	-	ICP			GSCLC_high	
Slc3a1	20532	chr17	85027447	85028747	+	ICP		GSCLC_high		GSCLC_high
Atp6v1e2	74915	chr17	86947487	86948787	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
1700011E24Rik	75467	chr17	87427341	87428641	-	HCP				GSCLC_high
Lhcgr	16867	chr17	88791576	88792876	-	ICP	GSCLC_high	GSCLC_high		GSCLC_high
Fshr	14309	chr17	89200275	89201575	-	ICP				GSCLC_high
Impact	16210	chr18	12971352	12972652	+	ICP		GSCLC_high	GSCLC_high	
4933424G05Rik	74456	chr18	14988095	14989395	+	LCP				GSCLC_high
E430002N23Rik	319440	chr18	15312299	15313599	-	ICP				GSCLC_high
4921528I01Rik	70950	chr18	22170996	22172296	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Mir187	387182	chr18	24428770	24430070	-	LCP				GSCLC_high
4930578E11Rik	78058	chr18	29496016	29497316	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Rit2	19762	chr18	31316728	31318028	-	ICP				GSCLC_high
Wnt8a	20890	chr18	34541428	34542728	+	LCP	GSCLC_high		GSCLC_high	
Slc23a1	20522	chr18	35626827	35628127	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
2010001M09Rik	69816	chr18	35648967	35650267	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Ecscr	68545	chr18	35721091	35722391	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Eif4ebp3	108112	chr18	36663160	36664460	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
E230025N22Rik	240216	chr18	36695525	36696825	-	LCP	GSCLC_high			GSCLC_high
Pcdha7	12939	chr18	36973024	36974324	+	HCP		GSCLC_high		
Pcdha8	353235	chr18	36991567	36992867	+	ICP	GSCLC_high	GSCLC_high		
Pcdhb10	93881	chr18	37410774	37412074	+	ICP		GSCLC_high		
Pcdhb11	93882	chr18	37420518	37421818	+	ICP				GSCLC_high
Pcdhb14	93885	chr18	37446757	37448057	+	ICP		GSCLC_high		
Pcdhb15	93886	chr18	37472646	37473946	+	LCP				GSCLC_high
Pcdhb22	93893	chr18	37517453	37518753	+	ICP				GSCLC_high
Pcdhga1	93709	chr18	37661045	37662345	+	ICP				GSCLC_high
Pcdhga11	93723	chr18	37754873	37756173	+	ICP				GSCLC_high
Pcdhgb8	93705	chr18	37760901	37762201	+	ICP		GSCLC_high		GSCLC_high
Pcdhga12	93724	chr18	37764680	37765980	+	ICP		GSCLC_high		GSCLC_high
Nr3c1	14815	chr18	39486845	39488145	-	ICP		GSCLC_high		
Kctd16	383348	chr18	40257461	40258761	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Mir5097	100628617	chr18	41195549	41196849	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Grxcr2	332309	chr18	41998649	41999949	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm5095	328953	chr18	47536835	47538135	+	ICP	GSCLC_high		GSCLC_high	GSCLC_high
Hdhd1a	67365	chr18	50568299	50569599	-	ICP		GSCLC_high		
Ftmt	67634	chr18	52330636	52331936	+	ICP		GSCLC_high		
Zfp474	66758	chr18	52615015	52616315	+	LCP		GSCLC_high		GSCLC_high
9330117O12	328957	chr18	54610844	54612144	+	LCP			GSCLC_high	GSCLC_high
A730017C20Rik	225583	chr18	59061481	59062781	+	ICP				GSCLC_high
Pdgfrb	18596	chr18	61044250	61045550	+	ICP	GSCLC_high			
E330013P06	328968	chr18	61665138	61666438	-	LCP		GSCLC_high		
Mir143	387161	chr18	61648858	61650158	-	ICP	GSCLC_high	GSCLC_high		
Sh3tc2	225608	chr18	61952175	61953475	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Cplx4	225644	chr18	65969778	65971078	-	ICP			GSCLC_high	GSCLC_high
Gm17669	100504629	chr18	67561231	67562531	+	ICP			GSCLC_high	GSCLC_high
4930546C10Rik	78931	chr18	68951128	68952428	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Rab27b	80718	chr18	70141190	70142490	-	ICP				GSCLC_high
Loxhd1	240411	chr18	77281058	77282358	+	HCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Slc14a1	108052	chr18	78141719	78143019	-	ICP	GSCLC_high	GSCLC_high		GSCLC_high
LOC100861811	100861811	chr18	80011735	80013035	+	ICP			GSCLC_high	
LOC100861827	100861827	chr18	80018654	80019954	+	ICP			GSCLC_high	GSCLC_high
Kcng2	240444	chr18	80363854	80365154	-	LCP			GSCLC_high	GSCLC_high

Cd226	225825	chr18	89196527	89197827	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
Aldh3b1	67689	chr19	3929316	3930616	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gstp2	14869	chr19	4041821	4043121	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm6293	622178	chr19	5415359	5416659	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Naalad1	381204	chr19	6104898	6106198	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
LOC100862017	100862017	chr19	6234114	6235414	+	LCP		GSCLC_high		
Tmem223	66836	chr19	8770096	8771396	+	HCP	GSCLC_high			
Lrrn4cl	68852	chr19	8849885	8851185	+	LCP			GSCLC_high	
Slc15a3	65221	chr19	10841644	10842944	+	LCP			GSCLC_high	
Ms4a15	545279	chr19	10992850	10994150	-	LCP			GSCLC_high	GSCLC_high
1700017D01Rik	69369	chr19	11130478	11131778	-	LCP				GSCLC_high
1700025F22Rik	69416	chr19	11164920	11166220	-	LCP		GSCLC_high		GSCLC_high
Ms4a4d	66607	chr19	11535949	11537249	+	LCP			GSCLC_high	GSCLC_high
Olfr1423	258675	chr19	12036340	12037640	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Olfr1491	258342	chr19	13703929	13705229	+	LCP		GSCLC_high		GSCLC_high
Olfr1495	258341	chr19	13767444	13768744	+	ICP	GSCLC_high	GSCLC_high		GSCLC_high
Olfr1500	258097	chr19	13827994	13829294	-	LCP			GSCLC_high	
Aldh1a1	11668	chr19	20601082	20602382	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
1700021P04Rik	75521	chr19	24063893	24065193	+	ICP	GSCLC_high			
E030010A14Rik	226040	chr19	24673108	24674408	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Kcnv2	240595	chr19	27321719	27323019	+	LCP		GSCLC_high		
Trpd52i3	66745	chr19	30002890	30004190	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
Gm19602	100503233	chr19	30295540	30296840	+	LCP		GSCLC_high		GSCLC_high
Acta2	11475	chr19	34254936	34256236	-	ICP				GSCLC_high
Ankrd1	107765	chr19	36119444	36120744	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
4931408D14Rik	77059	chr19	37263695	37264995	-	ICP			GSCLC_high	
Pde6c	110855	chr19	38131881	38133181	+	LCP		GSCLC_high		GSCLC_high
Lgi1	56839	chr19	38263882	38265182	+	ICP				GSCLC_high
Plce1	74055	chr19	38523297	38524597	+	ICP		GSCLC_high	GSCLC_high	
Cpn1	93721	chr19	43986120	43987420	-	ICP	GSCLC_high		GSCLC_high	
Elov13	12686	chr19	46130999	46132299	+	HCP				GSCLC_high
Calhm2	72691	chr19	47137894	47139194	-	ICP	GSCLC_high		GSCLC_high	GSCLC_high
1700054A03Rik	78457	chr19	53075352	53076652	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
LOC100503558	100503558	chr19	53459715	53461015	+	ICP		GSCLC_low	GSCLC_high	GSCLC_high
4930449E18Rik	78120	chr19	57273060	57274360	+	LCP	GSCLC_high		GSCLC_high	
Pnlp	69060	chr19	58669465	58670765	+	ICP		GSCLC_high		GSCLC_high
Pnliprp2	18947	chr19	58758823	58760123	+	LCP		GSCLC_high		GSCLC_high
1700019N19Rik	67507	chr19	58794014	58795314	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm3763	100042275	chrX	4951235	4952535	+	LCP			GSCLC_high	GSCLC_high
AU022751	102991	chrX	6083020	6084320	-	ICP			GSCLC_high	
Bmp15	12155	chrX	6320323	6321623	-			GSCLC_high		
Magix	54634	chrX	7680851	7682151	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
Kcnd1	16506	chrX	7822943	7824243	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Was	22376	chrX	8090091	8091391	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Slc38a5	209837	chrX	8270492	8271792	+	ICP				GSCLC_high
Gm5634	434726	chrX	8962575	8963875	-	ICP		GSCLC_high	GSCLC_high	
4930402K13Rik	75775	chrX	9103662	9104962	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
4933416E14Rik	71180	chrX	10419719	10421019	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm14535	100043002	chrX	13218255	13219555	-	ICP			GSCLC_high	
Gm5382	385328	chrX	14210248	14211548	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
Cypt1	66742	chrX	16521972	16523272	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Ndp	17986	chrX	16911364	16912664	-	ICP				GSCLC_high
Dusp21	73547	chrX	18144970	18146270	+	ICP		GSCLC_high		GSCLC_high
4930578C19Rik	75905	chrX	18460874	18462174	-	LCP		GSCLC_high		GSCLC_high
LOC100503338	100503338	chrX	19166841	19168141	-	LCP		GSCLC_high		GSCLC_high
BC049702	278255	chrX	19480919	19482219	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Gm6938	629024	chrX	21334327	21335627	-	ICP		GSCLC_high		
Gm5934	546272	chrX	24500360	24501660	-	LCP		GSCLC_high	GSCLC_high	
Gm4297	100043216	chrX	24574495	24575795	-	LCP			GSCLC_high	
LOC100862274	100862274	chrX	31716756	31718056	-	LCP		GSCLC_high	GSCLC_high	
Gm9	194854	chrX	37210641	37211941	-	ICP		GSCLC_high		
Rhox4b	57737	chrX	37431594	37432894	+	ICP				GSCLC_high
Rhox3c	100135654	chrX	37468968	37470268	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Rhox4c	434759	chrX	37479437	37480737	+	ICP	GSCLC_high			GSCLC_high
Rhox2f	434764	chrX	37570521	37571821	+		GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Rhox3f	621852	chrX	37580452	37581752	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
Rhox4f	636177	chrX	37607286	37608586	-	ICP				GSCLC_high
Rhox3g-ps	546294	chrX	37627869	37629169	-	LCP			GSCLC_high	GSCLC_high
Rhox2g	434766	chrX	37643070	37644370	-	LCP	GSCLC_high			
Rhox2h	622301	chrX	37672877	37674177	-	LCP	GSCLC_high	GSCLC_high		
Rhox7	547168	chrX	37830786	37832086	+	LCP			GSCLC_high	GSCLC_high
Mir3110	100526512	chrX	38209541	38210841	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Aip1b4	67821	chrX	38315367	38316667	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
6030498E09Rik	77883	chrX	38771880	38773180	+	ICP		GSCLC_high		
Gm362	236774	chrX	43590089	43591389	+	LCP		GSCLC_high		GSCLC_high
Fmd7	385354	chrX	50942310	50943610	-	ICP	GSCLC_high	GSCLC_high		GSCLC_high
1700080O16Rik	74279	chrX	51972372	51973672	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
LOC100861693	100861693	chrX	52271529	52272829	-	LCP			GSCLC_high	
Mir351	723910	chrX	53052953	53054253	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Mir503	723879	chrX	53053654	53054954	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Mir322	723907	chrX	53053949	53055249	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	
Plac1	56096	chrX	53114005	53115305	-	LCP				GSCLC_high
4933416I08Rik	71159	chrX	53579603	53580903	-	LCP				GSCLC_high
Gm14598	100040317	chrX	54235255	54236555	+	LCP		GSCLC_high	GSCLC_high	
Gm14625	625210	chrX	55429335	55430635	+	LCP		GSCLC_high	GSCLC_high	
1600025M17Rik	72030	chrX	56316708	56318008	+	LCP			GSCLC_high	
Arhgef6	73341	chrX	57338329	57339629	-	ICP				GSCLC_high
Gm364	245423	chrX	57408254	57409554	+	ICP			GSCLC_high	
F9	14071	chrX	59998564	59999864	+	ICP	GSCLC_high	GSCLC_high		GSCLC_high
Gm5637	434782	chrX	60045829	60047129	-	ICP		GSCLC_high		
Mcl2	109904	chrX	60147243	60148543	-	ICP				GSCLC_high
C230004F18Rik	331424	chrX	61115478	61116778	+	ICP				GSCLC_high
Cdr1	631990	chrX	61185158	61186458	-	ICP			GSCLC_high	
4933402E13Rik	74437	chrX	62282599	62283899	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
Gm14680	671878	chrX	62776342	62777642	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
3830417A13Rik	70696	chrX	64172648	64173948	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	
Gm6812	627927	chrX	68892653	68893953	-	ICP				GSCLC_high

<i>Magea10</i>	236852	chrX	72386458	72387758	-	LCP		GSCLC_high		
<i>4930408F14Rik</i>	100504429	chrX	73176589	73177889	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm5639</i>	434795	chrX	73296729	73298029	+	LCP			GSCLC_high	GSCLC_high
<i>Bgn</i>	12111	chrX	73482735	73484035	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>4930428D18Rik</i>	619294	chrX	76392450	76393750	+	LCP			GSCLC_high	
<i>Fam47a-ps</i>	70864	chrX	78736863	78738163	+	LCP		GSCLC_high		
<i>4930415L06Rik</i>	245511	chrX	89932452	89933752	-	ICP		GSCLC_high	GSCLC_high	
<i>Mageb17-ps</i>	236891	chrX	91624495	91625795	+	ICP		GSCLC_high		
<i>Gm5941</i>	546347	chrX	92489049	92490349	+	LCP		GSCLC_high		
<i>Gm6987</i>	629591	chrX	94022960	94024260	+	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm7061</i>	631331	chrX	94775281	94776581	-	ICP		GSCLC_high		GSCLC_high
<i>Heph</i>	15203	chrX	96454536	96455836	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Zmym3</i>	56364	chrX	101420285	101421585	-	LCP		GSCLC_high		
<i>Dmrtc1b</i>	632708	chrX	102706981	102708281	+	LCP		GSCLC_high	GSCLC_high	
<i>Dmrtc1c1</i>	71083	chrX	102802063	102803363	+	LCP		GSCLC_high		
<i>Dmrtc1a</i>	70887	chrX	102908287	102909587	-	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>1700011M02Rik</i>	75443	chrX	102908005	102909305	+	LCP		GSCLC_high	GSCLC_high	
<i>Cdx4</i>	12592	chrX	103320498	103321798	+	ICP				GSCLC_high
<i>Gm6222</i>	621381	chrX	103763145	103764445	-	LCP				GSCLC_high
<i>1700121L16Rik</i>	76643	chrX	104815876	104817176	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>5330434G04Rik</i>	100043213	chrX	105391354	105392654	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
<i>Cypt2-ps</i>	245566	chrX	105498872	105500172	+	ICP		GSCLC_high		
<i>Cysltr1</i>	58861	chrX	106603062	106604362	-	LCP				GSCLC_high
<i>Zcchc5</i>	213436	chrX	106840243	106841543	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm378</i>	213454	chrX	108404955	108406255	+	ICP				GSCLC_high
<i>Pof1b</i>	69693	chrX	112698251	112699551	-	LCP				GSCLC_high
<i>4930524E20Rik</i>	75097	chrX	114906682	114907982	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm14920</i>	100039319	chrX	117013857	117015157	+	LCP	GSCLC_high	GSCLC_high		GSCLC_high
<i>H2afb3-ps</i>	624957	chrX	120312695	120313995	-	ICP			GSCLC_high	
<i>Gm17267</i>	100502716	chrX	126016003	126017303	+	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Gm4916</i>	237030	chrX	128374515	128375815	+	ICP				GSCLC_high
<i>Blk</i>	12229	chrX	134582740	134584040	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Kir3dl1</i>	245616	chrX	136517099	136518399	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Morf4l2</i>	56397	chrX	136743286	136744586	-	ICP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Tex13a</i>	67944	chrX	138209180	138210480	-	LCP	GSCLC_high		GSCLC_high	GSCLC_high
<i>4933428M09Rik</i>	71248	chrX	139178328	139179628	+	ICP			GSCLC_high	
<i>C330013F16Rik</i>	78526	chrX	139357338	139358638	-	LCP	GSCLC_low	GSCLC_low	GSCLC_high	
<i>Mid2</i>	23947	chrX	140677128	140678428	+	LCP		GSCLC_low		GSCLC_high
<i>Eif2c5</i>	286951	chrX	140775335	140776635	+	LCP		GSCLC_high		
<i>A730046J19Rik</i>	319764	chrX	144152795	144154095	+	ICP				GSCLC_high
<i>Amot</i>	27494	chrX	145486646	145487946	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Snora35</i>	100303736	chrX	146993490	146994790	+	LCP	GSCLC_high		GSCLC_high	GSCLC_high
<i>Gm15128</i>	434863	chrX	147796418	147797718	+	LCP		GSCLC_high		GSCLC_high
<i>Gm5946</i>	546387	chrX	150228104	150229404	-	LCP				GSCLC_high
<i>Alas2</i>	11656	chrX	150546517	150547817	+	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Foxr2</i>	436240	chrX	153117888	153119188	+	LCP		GSCLC_high	GSCLC_high	GSCLC_high
<i>Kctd12b</i>	207474	chrX	153695880	153697180	-	LCP				GSCLC_high
<i>Magea2</i>	17138	chrX	155032892	155034192	-	ICP		GSCLC_high		
<i>Gm4997</i>	245676	chrX	155150911	155152211	-	ICP				GSCLC_high
<i>Scml2</i>	107815	chrX	161161872	161163172	+	ICP				GSCLC_high
<i>Grpr</i>	14829	chrX	163549247	163550547	-	LCP	GSCLC_high	GSCLC_high		GSCLC_high
<i>Bmx</i>	12169	chrX	164257793	164259093	-	LCP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high
<i>Kdm5d</i>	20592	chrY	896888	898188	+	ICP		GSCLC_high		GSCLC_high
<i>Ddx3y</i>	26900	chrY	1286213	1287513	-	ICP		GSCLC_high		
<i>Usp9y</i>	107868	chrY	1459382	1460682	-	ICP		GSCLC_high		GSCLC_high
<i>Zfy2</i>	22768	chrY	2170009	2171309	-	LCP		GSCLC_high	GSCLC_high	
<i>LOC100861598</i>	100861598	chrY	4340227	4341527	+	LCP		GSCLC_high	GSCLC_high	
<i>LOC100862250</i>	100862250	chrY	32713437	32714737	-	ICP	GSCLC_high	GSCLC_high	GSCLC_high	GSCLC_high

Supplemental Table S3. Gene Ontology for Genes Bearing Differentially Methylated Promoters or Non-promoter CGIs between GSCLCs and GSCs, Related to Figure 5

Methylation GSCs ≥ GSCLCs (239 genes)					Genes				
Category	Term	Count	%	PValue					
GOTERM_BP_DIRECT	GO:0007608~sensory perception of smell	31	15.05	1.15E-12	OLFRL412, OLFRL781, OLFRL338, OLFRL1275, OLFRL115, OLFRL170, OLFRL116, OLFRL1356, OLFRL360, OLFRL1449, OLFRL380, OLFRL944, OLFRL698, OLFRL033, OLFRL365, OLFRL388, OLFRL870, OLFRL403, OLFRL342, OLFRL401, OLFRL893, OLFRL143, OLFRL790, OLFRL161, OLFRL589, OLFRL143, OLFRL397, OLFRL1228, OLFRL392				
GOTERM_BP_DIRECT	GO:0007186~G-protein coupled receptor signaling pathway	37	17.96	1.70E-12	OLFRL412, MRCGP844, OLFRL781, OLFRL338, OLFRL1275, OLFRL115, OLFRL116, NP68R, OLFRL113, OLFRL1356, OLFRL360, OLFRL944, OLFRL380, OLFRL944, OLFRL698, OLFRL033, OLFRL365, ENTPD1, OLFRL1388, OLFRL670, MRCGR85, OLFRL403, OLFRL342, OLFRL401, OLFRL893, OLFRL143, OLFRL792, GPR151, MRCGR88, OLFRL161, OLFRL790, OLFRL589, OLFRL1143, OLFRL397, OLFRL1228, OLFRL392				
GOTERM_BP_DIRECT	GO:0051603~proteolysis involved in cellular protein catabolic process	5	2.43	3.54E-04	CTSM, CTSL, CTSS, CTSS				
GOTERM_BP_DIRECT	GO:0050907~detection of chemical stimulus involved in sensory perception	7	3.40	1.38E-03	OLFRL412, OLFRL380, OLFRL397, OLFRL1275, OLFRL115, OLFRL170, OLFRL113, OLFRL1356, OLFRL360, OLFRL944, OLFRL380, OLFRL944, OLFRL698, OLFRL033, OLFRL365, ENTPD1, OLFRL1388, OLFRL670, MRCGR85, OLFRL403, OLFRL342, OLFRL401, OLFRL893, OLFRL143, OLFRL792, GPR151, MRCGR88, OLFRL161, OLFRL790, OLFRL589, OLFRL1143, OLFRL397, OLFRL1228, OLFRL392				
GOTERM_BP_DIRECT	GO:0045071~negative regulation of viral genome replication	3	1.46	1.35E-02	ISG15, IFITM3, MX2				
GOTERM_BP_DIRECT	GO:0060952~defense response	4	1.94	2.08E-02	DEFB39, IFNA13, DEFB35, PTPRCAP				
GOTERM_BP_DIRECT	GO:0050911~detection of chemical stimulus involved in sensory perception of smell	3	1.46	2.55E-02	OLFRL412, OLFRL870, OLFRL1356				
GOTERM_BP_DIRECT	GO:0051607~defense response to virus	4	1.94	3.93E-02	ISG15, IFITM3, IFNA13, MX2				
GOTERM_BP_DIRECT	GO:0034340~response to type I interferon	2	0.97	4.06E-02	ISG15, MX2				
Methylation GSCs ≤ GSCLCs (1,787 genes)					Genes				
Category	Term	Count	%	PValue					
GOTERM_BP_DIRECT	GO:0007165~signal transduction	111	6.87	2.67E-08	DLC1, GDF3, GNA15, STAT5A, LHCGR, TLR1, CSFG4, TLR4, OLFRL610, MRCGP846, OLFRL554, PPP1R1C, ZFP831, GLP2R, NP5R1, HTR1D, OLFRL550, DAB2IP, UNC5CL, MRCGP86, OLFRL624, PLCE1, SSTR3, LPAR6, REM2, CAMK1, PDGFRB, TRAF1, CYSLTR1, CYSLTR2, GPR149, TRHR, PDE6B, PDE6C, RASA13, GPRR, FCER1G, OLFRL481, OLFRL571, OLFRL676, LGALS1, BMY, ECM1, OLFRL187, OLFRL601, RERG, LAT, PDE7B, OLFRL606, GNGT2, OLFRL605, CD300A, LTBR42, AVPR1B, RGSS5, RIT2, SYNGAP1, CHRNA, MCHRI, RASSF9, GNRHR, OLFRL658, TAA8, TAA86, WISP3, NMURI, NOS3, CALCR1, TAA84, PLCE2, TAA85, HTR5A, TAA83, RXFP4, PTGER1, OLFRL591, SITI, CMKLRI, RYFP2, RASIP1, OLFRL599, OXGR1, FSHR, GRM1, OLFRL1009, OLFRL463, GRM4, CHRM5, OLFRL734, OLFRL398, GIPR, GPR15, GNB3, OLFRL5, CXCL2, OLFRL460, CMKLR1, RXFP2, OLFRL599, OXGR1, FSHR, GRM1, OLFRL1009, OLFRL463, GRM4, CHRM5, OLFRL734, OLFRL398, GIPR, GPR15, GNB3, OLFRL5, CXCL2, OLFRL460, CMKLR1, RXFP2, OLFRL599, GPR1, OLFRL437, APLNR, CCL22, OLFRL633, OLFRL632, TAS2R126, OLFRL796, OLFRL549, OLFRL, OLFRL447, OLFRL545, HTR2A				
GOTERM_BP_DIRECT	GO:0071222~cellular response to lipopolysaccharide	24	1.49	1.87E-05	MEF2C, MRC1, IL6, DAB2IP, TNFSF4, STAP1, MIR200C, AXL, TLR4, ANKRD1, CXCL10, MIR181A-1, MIR142, MIR125A, MIR199A-2, PYCARD, IL12A, AUCDA, LBP, MIR293, NR1H4, NR1H3				
GOTERM_BP_DIRECT	GO:0007186~G-protein coupled receptor signaling pathway	126	7.80	5.43E-05	GNA15, OLFRL414, OLFRL982, LHCGR, OLFRL610, OLFRL152, CXCL10, MRCGP846, OLFRL554, APOE, GLP2R, NP5R1, HTR1D, OLFRL1057, OLFRL365, OLFRL550, PIK3CG, OLFRL975, MRCGP86, OLFRL1344, OLFRL624, OLFRL352, PLCE1, SSTR3, OLFRL1349, LPAR6, OLFRL214, OLFRL978, OLFRL045, OLFRL212, OLFRL1370, CYSLTR1, CYSLTR2, GPR149, TRHR, OLFRL1500, OLFRL279, OLFRL825, OLFRL48, OLFRL820, GRPR, OLFRL201, OLFRL481, OLFRL571, OLFRL676, OLFRL284, OLFRL361, OLFRL283, OLFRL360, OLFRL282, OLFRL281, OLFRL303, OLFRL1512, VAV1, OLFRL601, OLFRL187, OLFRL606, GNGT2, OLFRL495, OLFRL605, OLFRL73, LTBR42, AVPR1B, RGSS5, OLFRL471, OLFRL81, OLFRL99, OLFRL491, MCHRI, OLFRL314, OLFRL118, GNRHR, OLFRL1423, OLFRL658, OLFRL1395, TAA8, TAA86, OLFRL198, OLFRL656, NMURI, CALCR1, TAA84, TAA85, HTR5A, TAA83, RXFP4, PTGER1, OLFRL591, OLFRL460, CMKLR1, RXFP2, OLFRL599, OXGR1, FSHR, GRM1, OLFRL1009, OLFRL463, GRM4, CHRM5, OLFRL734, OLFRL398, GIPR, GPR15, GNB3, OLFRL5, CXCL2, OLFRL460, CMKLR1, RXFP2, OLFRL599, GPR1, OLFRL437, APLNR, CCL22, OLFRL633, OLFRL632, TAS2R126, OLFRL796, OLFRL549, OLFRL, OLFRL447, OLFRL545, HTR2A				
GOTERM_BP_DIRECT	GO:0032729~positive regulation of interferon-gamma production	12	0.74	5.93E-05	IL18R1, TNFSF4, IL27RA, CD3E, PDE4B, RLTPR, SLAMF6, PYCARD, IL12A, TLR4, CD226, LTA				
GOTERM_BP_DIRECT	GO:0007601~visual perception	18	1.11	2.18E-04	GUCA1B, SLC45A2, CLRN1, LUM, MYO3B, PCDH15, RCVNR, CNGA3, ABCA4, VSNR, PRPH2, PDE6B, CRYGC, PDE6C, CRYGD, PPEF2, SLITRK6, RLBP1				
GOTERM_BP_DIRECT	GO:0007200~phospholipase C-activating G-protein coupled receptor signaling pathway	10	0.62	7.04E-04	RXP4, PLCE1, GNA15, CYSLTR1, CYSLTR2, NMURI, LHCGR, LTBR42, ESRI, FSHR				
GOTERM_BP_DIRECT	GO:0002376~immune system process	36	2.23	7.40E-04	CD8A, TLR1, PML, PGLYRP1, RSAD2, TLR4, IL34, PDCD1, BTK, CIRB, CLEC4E, OASL1, PYCARD, LBP, C2, INP5D, PIK3CG, H2-Q10, DAB2IP, CD8B1, SITI, GBB5, CD3E, THEMIS, SLAMF6, AXL, SERPING1, PAD14, CD40, TRIM56, LAT, KLRC1, CD300A, H2-AA, CD79A, TAPBP1				
GOTERM_BP_DIRECT	GO:0042102~positive regulation of T cell proliferation	11	0.68	9.86E-04	LEP, VCAM1, ITGAL, CARD11, IL6, TNFSF13B, CD3E, RLTPR, IL12A, NCKAP1L, SPN				
GOTERM_BP_DIRECT	GO:006955~immune response	26	1.61	9.98E-04	ENP22, TLR1, SUSD2, CXCL2, TNFSF15, PH4, CXCL10, CCL22, CLEC4E, OASL1, FASL, LTB, LTA, IL6, H2-Q10, TNFSF4, CD40, TINAGL1, VAV1, WAS, TNFSF8, OSM, LAT, TNFSF13B, IL12A, H2-AA				
GOTERM_BP_DIRECT	GO:006935~chemotaxis	16	0.99	1.10E-03	PIK3CG, CYSLTR1, ENP22, CMKLR1, CXCL2, NCKAP1L, PH4, CXCL10, CMTM2A, CCL22, DOCK2, TMIP, CMTM2B, EGSCR, PDGFRB, AMOT				
GOTERM_BP_DIRECT	GO:0006811~ion transport	49	3.03	1.22E-03	FXYD1, CLDN16, KCN16, CALHM2, SLC22A16, SLC9A4, PANK3, HVCN1, KCNIP3, KCNMB2, SLC23A1, KCNE1, ANO2, TRPV6, SLC39A4, SCNN1A, KCNG1, SLC22A2, SLC4A5, SLC22A1, SCN10A, FAM26D, FAM26E, GABRG2, SLC8A1, TMCB, KCND1, TMCG, CACNG8, KCNR2, MFD2, TMCG4, SLC24A5, CNGA3, KCNV2, LBR2C6, TRPM2, SLC10A1, SLC4A10, GRAL, SLC26A9, ATP9V1E2, SLC13A3, HEPH, SCN8A, CHRNA				
GOTERM_BP_DIRECT	GO:0007218~neuropeptide signaling pathway	13	0.80	1.38E-03	RXP4, MCHRI, CYSLTR1, CYSLTR2, GPR149, GPR1, SSTR3, PNOX, NMURI, LTBR42, GIPR, PYY, NP5R1				
GOTERM_BP_DIRECT	GO:0007268~synaptic transmission	16	0.99	1.70E-03	SNCG, GABRG2, FGF14, GPR149, GPR1, KCNMB1, KCNMB2, GRM4, SSTR3, PNOX, GRAL, APMR3, DLG4, UNC13C, HTR1D, DLG2				
GOTERM_BP_DIRECT	GO:0045109~intermediate filament organization	6	0.37	2.59E-03	KRT25, GFAP, KRT6B, KRT2, KRT20, KRT71				
GOTERM_BP_DIRECT	GO:0042535~positive regulation of tumor necrosis factor biosynthetic process	5	0.31	2.76E-03	TLR1, TLR4, LBP, CD209B, SPN				
GOTERM_BP_DIRECT	GO:0050896~response to stimulus	22	1.36	3.35E-03	GUCA1B, SLC45A2, CLRN1, MYO3B, SLC24A5, OLFRL9, RCVNR, OLFRL139, CNGA3, ABCA4, VSNR, OLFRL1009, OLFRL187, PDE6B, PDE6C, PPEF2, OLFRL481, TASR126, OLFRL15, SLITRK6, SCNN1A, RLBP1				
GOTERM_BP_DIRECT	GO:006941~contracted muscle contraction	5	0.31	3.82E-03	ALDOA, PGAM2, MYLK2, TTN, TNNT3				
GOTERM_BP_DIRECT	GO:0071241~cellular response to inorganic substance	9	0.56	3.95E-03	MIR108, MIR125B-1, MIR222, MIR351, GIPD1, MIR199A-2, MIR181B-1, MIR196A-2, MIR196A-1				
GOTERM_BP_DIRECT	GO:0030593~neutrophil chemotaxis	10	0.62	4.62E-03	PIK3CG, CCL22, EDN2, PDE4B, CXCL2, NCKAP1L, CSFR3, FCER1G, VAV1, SPPI				
GOTERM_BP_DIRECT	GO:006936~muscle contraction	8	0.50	5.34E-03	MYBP2, MYBP21, ACTA2, MYL1, LMOTD1, LMOTD2, ITIN, TRIM63				
GOTERM_BP_DIRECT	GO:0045087~innate immune response	31	1.92	5.72E-03	TLR1, PGLYRP1, PML, RSAD2, TLR4, TRIM15, IL34, BTK, CIRB, CLEC4E, 4933415F23RIK, OASL1, PYCARD, VNN1, FCER1G, LBP, C2, PIK3CG, DAB2IP, TNFSF4, CAMP, DEFB36, SLAMF6, AXL, BMY, SERPING1, PAD14, MID2, TRIM56, KLRC1, TNK1				
GOTERM_BP_DIRECT	GO:008284~positive regulation of cell proliferation	38	2.35	5.73E-03	FCG6, CAV3, FMT2, INSL3, PKHD1, ENP22, STAT5A, EDN2, BTK, CNTR, ESM1, POU1F1, IL34, IL11, CXCL10, FASL, RAB25, CALCR1, EGF, SCX, LTA, PTPN6, IL6, NTF3, NKX2-6, CAMP, RASIP1, NLGN2, FGF21, TET1, PLAC8, LEP, OSM, GHRH, F2, PDGFRB, MAB21L1, HTR2A				
GOTERM_BP_DIRECT	GO:0035725~sodium ion transmembrane transport	9	0.56	6.45E-03	SCN23A1, SLC8A1, SCN1A, SCN3A, SLC24A1, SLC24A5, SCN8A, SCN10A				
GOTERM_BP_DIRECT	GO:0019228~neuronal action potential	7	0.43	7.09E-03	SCN1A, SCN3A, GRAL1, SCN7A, SCN8A, KCNMB2, SCN10A				
GOTERM_BP_DIRECT	GO:0035914~skeletal muscle cell differentiation	9	0.56	7.23E-03	MEF2C, MYF6, PHOX2B, NUPR1, MYF5, MYLK2, MYOG, ANKRD1, SCX				
GOTERM_BP_DIRECT	GO:006954~inflammatory response	27	1.67	7.86E-03	ELF3, CYSLTR1, CRHRP, TLR1, CXCL2, CSFG4, TLR4, PH4, IL34, CXCL10, CCL22, NLRP4C, PYCARD, VNN1, NLRP4B, LTA, PIK3CG, HYAL1, DAB2IP, IL6, TNFSF4, GBB5, AXL, CD40, ECM1, LAT, LTBR42				
GOTERM_BP_DIRECT	GO:0007188~adenylate cyclase-modulating G-protein coupled receptor signaling pathway	7	0.43	8.23E-03	CCG, ADCY4, GHRH, LHCGR, GLP2R, OXGR1, FSHR				
GOTERM_BP_DIRECT	GO:0043408~regulation of MAPK cascade	10	0.62	8.60E-03	GDF3, BMP10, INHBE, INHBC, MYLK2, SYNGAP1, GDF15, BMP15, GRM1, FSHR				

GOTERM_BP_DIRECT	GO:0007204~positive regulation of cytosolic calcium ion concentration	15	0.93	9.09E-03	CAV3, PIK3CG, MCHRI, SLC8A1, GNAI5, JPH2, EDN2, TRHR, CXCL2, ESR1, CHRNA9, GHRH, GIPR, DLG4, HTR2A
GOTERM_BP_DIRECT	GO:0071391~cellular response to estrogen stimulus	7	0.43	9.49E-03	MIR142, MIR143, MIR125A, MIR125B-1, CRHRP, ESR1
GOTERM_BP_DIRECT	GO:0001654~eye development	7	0.43	9.49E-03	CRYGA, GDF3, CRYGB, CRYGC, CRYGD, CRYGE, CRYCE, BMP1B
GOTERM_BP_DIRECT	GO:0007155~cell adhesion	38	2.35	9.93E-03	BMP10, ITGA1, OLFML4, MYBPC2, PCDHB14, YCAM1, CD96, WISP1, CD44, COL16A6, CD93, COL7A1, COL6A5, KLRA8, GP1BB, WISP3, SORBS2, TNF, FAP, CSF3R, THBS2, SPPI, HAPLN3, CNTN6, BMX, NLGN2, PCDH15, TNAGLI1, PRPH2, CDH12, TNFAIP6, CDH15, CASS4, HEPACAM, MADCAM1, MFAP4, CD226, ENG
GOTERM_BP_DIRECT	GO:0034220~ion transmembrane transport	9	0.56	1.11E-02	FAM26D, CALHM2, FAM26E, S100A6, SLC24A5, CNGA3, TRPM2, AQP2, CHRNA9
GOTERM_BP_DIRECT	GO:0016525~negative regulation of angiogenesis	10	0.62	1.14E-02	DAB2IP, WISP3, ECSCR, TEK, PML, AMOT, FASL, PF4, THBS2, CXCL10
GOTERM_BP_DIRECT	GO:0019221~cytokine-mediated signaling pathway	16	0.99	1.21E-02	PTPN6, IL6, IL22RA1, EDN2, STAT5A, LRRCA8, PIF4, GM13271, IL17RC, LRRCL15, CHAD, BGN, LRRITM4, IFNE, LRRITM3, LRRRC66
GOTERM_BP_DIRECT	GO:0032689~negative regulation of interferon-gamma production	6	0.37	1.27E-02	CD96, TNFSF4, PGLYBP1, AXI, TLR4, NR1H4
GOTERM_BP_DIRECT	GO:0070374~positive regulation of ERK1 and ERK2 cascade	17	1.05	1.37E-02	IL6, CSISLR2, ESR1, TLR4, FGFR2, FSHR, GCG, CCL22, C1QTNF3, CD44, TEK, PTCARD, PDGFRB, NPSR1, PLA2G5, HTR2A, THPO
GOTERM_BP_DIRECT	GO:0031295~T cell costimulation	5	0.31	1.61E-02	CARD11, TNFSF13B, CD3E, LGALS1, SPN
GOTERM_BP_DIRECT	GO:0007519~skeletal muscle tissue development	8	0.50	1.92E-02	MEF2C, MYF6, CFLAR, MYF5, ELN, MEG3, KLHL31, MYOG
GOTERM_BP_DIRECT	GO:0046426~negative regulation of JAK-STAT cascade	7	0.43	2.01E-02	BGN, LRRITM4, LRRITM3, LRRCA8, LRRRC66, LRRCL15, CHAD
GOTERM_BP_DIRECT	GO:0030890~positive regulation of B cell proliferation	7	0.43	2.01E-02	MEF2C, CARD11, TNFSF13B, BST1, NCKAP1L, TLR4, CD40
GOTERM_BP_DIRECT	GO:0032700~negative regulation of interleukin-17 production	4	0.25	2.28E-02	TNFSF4, IL12A, NCKAP1L, TLR4
GOTERM_BP_DIRECT	GO:0049544~negative regulation of natural killer cell mediated cytotoxicity	5	0.31	2.29E-02	STAT5A, SIAMF6, IL12A, VAV1, CD226
GOTERM_BP_DIRECT	GO:0051965~positive regulation of synapse assembly	9	0.56	2.49E-02	LINGO4, LRRITM4, LRRITM3, LRRN3, LRRCA8, NLGN2, CUX2, SLITRK6, THBS2
GOTERM_BP_DIRECT	GO:0045621~positive regulation of lymphocyte differentiation	3	0.19	2.52E-02	STAT5A, NCKAP1L, INPP5D
GOTERM_BP_DIRECT	GO:0070633~transphenetic transport	3	0.19	2.52E-02	PRSS8, CLDN16, GHLDI
GOTERM_BP_DIRECT	GO:0097113~AMPA glutamate receptor clustering	3	0.19	2.52E-02	LRRITM4, APOE, DLG4
GOTERM_BP_DIRECT	GO:0043523~regulation of neuron apoptotic process	6	0.37	2.54E-02	MEF2C, TRIM2, NTF3, ESR1, FAIM2, KCNIP3
GOTERM_BP_DIRECT	GO:0006814~sodium ion transport	13	0.80	2.70E-02	SLC23A1, SLC8A1, SLC4A10, SCN1A, SLC9A4, ATP1B4, SLC24A5, SLC13A3, SCN8A, SCN1A, TRPM2, SLC10A1, SCN10A
GOTERM_BP_DIRECT	GO:0006469~negative regulation of protein kinase activity	7	0.43	2.71E-02	CAV3, IL6, BGN, LRRITM4, PPP1R1C, LRRITM3, PCP4, LRRCA8, LRRRC66, LRRCL15, CHAD
GOTERM_BP_DIRECT	GO:0007189~adenylate cyclase-activating G-protein coupled receptor signaling pathway	7	0.43	3.36E-02	ADCY4, GHRH, LHCGR, RXFP2, ADNM2, CALCR1, FSHR
GOTERM_BP_DIRECT	GO:0050852~T cell receptor signaling pathway	7	0.43	3.36E-02	BCL2A1D, THEMIS, CD3E, PDE4B, CD247, TLRP, CLEC2I
GOTERM_BP_DIRECT	GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	11	0.68	3.49E-02	OSM, IL6, CD44, NTF3, CD3E, ENPP2, CSPG4, TLR4, EGF, IL11, HTR2A
GOTERM_BP_DIRECT	GO:0007187~G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	4	0.25	3.49E-02	SSTR3, GPR149, GPR1, HTR5A
GOTERM_BP_DIRECT	GO:0046888~negative regulation of hormone secretion	4	0.25	3.49E-02	OSM, IL6, EDN2, IL11
GOTERM_BP_DIRECT	GO:0035641~locomotory exploration behavior	4	0.25	3.49E-02	SLC4A10, TNF, DLG4, NLGN2
GOTERM_BP_DIRECT	GO:0006813~potassium ion transport	13	0.80	3.54E-02	KCNJ16, KCND1, KCNB2, ATP1B4, SLC24A5, KCNV2, KCNIP1, GJA5, KCAMB1, KCNIP3, KCNMB2, KCNE1, KCNE1
GOTERM_BP_DIRECT	GO:0015872~dopamine transport	3	0.19	3.66E-02	CHRM5, SLC22A2, SLC22A1
GOTERM_BP_DIRECT	GO:0043567~regulation of insulin-like growth factor receptor signaling pathway	3	0.19	3.66E-02	IGFBP6, IGFBP1, POU1F1
GOTERM_BP_DIRECT	GO:0071347~cellular response to interleukin-1	7	0.43	3.68E-02	HYAL1, IL6, CCL22, DAB2IP, MYLK3, PYCARD, ANKRD1
GOTERM_BP_DIRECT	GO:006508~proteolysis	42	2.60	3.79E-02	PRSS40, PRSS41, ENPEP, NAALADL1, CPN1, PRSS8, PRSS39, C1RB, ADAMS, FAP, DPEF3, KLK10, C2, TMPRSS12, CASP1, DPP7, TMPRSS13, PRSS3B, AF366264, PRSS56, CFAR, 4930444G20R1, HPN, KIK9, CPA6, UNC5CL, F9, TINAGLI1, NRIP2, USP29, TMPRSS11G, F5, CAPN12, CASP14, F2, PRSS27, PRSS45, ADAM18, PAPPA2, RHBDL2, PRSS21, ASPRV1
GOTERM_BP_DIRECT	GO:0042632~cholesterol homeostasis	8	0.50	3.87E-02	CRYGA, CRYGB, CRYGD, CRYAB, SLITRK6, CRYGE
GOTERM_BP_DIRECT	GO:002088~lens development in camera-type eye	6	0.37	4.00E-02	CAV3, MIA2, SOAT2, HPN, APOB, APOE, PLA2G12B, NRIH3
GOTERM_BP_DIRECT	GO:0010862~positive regulation of pathway-restricted SMAD protein phosphorylation	7	0.43	4.03E-02	GDF3, BMP10, INHBE, INHBC, GDF15, BMP15, ENG
GOTERM_BP_DIRECT	GO:0007166~cell surface receptor signaling pathway	19	1.18	4.05E-02	ITGAL, MCHRI, OLFRA460, CD8A, CSISLR1, CD3E, CD247, PRPH2, CD37, KLRG1, GIPR, UPK1B, F2, FCER1G, CD79A, CD79A, GLP2R, CALCR1, TAAR5, SPN
GOTERM_BP_DIRECT	GO:0048044~urey morphogenesis	5	0.31	4.09E-02	APOB, APOE, STRA6, ENG, GJA5
GOTERM_BP_DIRECT	GO:006885~regulation of pH	5	0.31	4.09E-02	SLC4A10, CAR14, SLC9A4, CAR12, SLC26A9
GOTERM_BP_DIRECT	GO:1902187~negative regulation of vital release from host cell	4	0.25	4.20E-02	TRIM56, PML, TRIM15, MID2
GOTERM_BP_DIRECT	GO:0055117~regulation of cardiac muscle contraction	4	0.25	4.20E-02	CAV3, BMP10, GJA5, SCN10A
GOTERM_BP_DIRECT	GO:0030819~positive regulation of cAMP biosynthetic process	7	0.43	4.39E-02	GCG, INS13, GHRH, RLN3, GIPR, RXFP2, CALCR1
GOTERM_BP_DIRECT	GO:0060395~SMAD protein signal transduction	9	0.56	4.47E-02	GDF3, BMP10, HNF1A, INHBE, INHBC, MEG3, GDF15, BMP15, TRF
GOTERM_BP_DIRECT	GO:0001525~regogenesis	19	1.18	4.53E-02	FGF6, PIK3CG, DAB2IP, CSPC4, RASIP1, ENPEP, ESM1, ESM1, IGFBP1
GOTERM_BP_DIRECT	GO:0001558~regulation of cell growth	7	0.43	4.78E-02	TM3B, WISP1, CD44, WISP3, IGFBP6, ESM1, IGFBP1
GOTERM_BP_DIRECT	GO:0071467~cellular response to pH	3	0.19	4.94E-02	HYAL1, GGLI1, HVCN1
GOTERM_BP_DIRECT	GO:2000653~regulation of genetic imprinting	3	0.19	4.94E-02	DPPA3, TET1, H19
GOTERM_BP_DIRECT	GO:0048743~positive regulation of skeletal muscle fiber development	3	0.19	4.94E-02	MYF6, MYF5, MYOG

Supplemental Table S4. Genomic Coordinates and Statistics of the Loci Analyzed in This Study, Related to Figures 5 and 6

Genomic loci of specific genes				
Names	Genomic loci shown in figures	Length (Kb)		
<i>Pou5f1</i>	chr17:35,503,000-35,513,000	10		
<i>Sohlh1</i>	chr2:25,842,000-25,849,000	7		
<i>Dpep3</i>	chr8:105,972,000-105,981,000	9		
<i>Tex19.1</i>	chr11:121,140,000-121,154,000	14		
<i>Tdrd9</i>	chr12:111,960,000-112,060,000	100		
<i>Spo11</i>	chr2:172,978,000-172,994,000	16		
<i>Piwi1</i>	chr5:128,734,000-128,756,000	22		
Imprint loci				
Names	Genomic loci shown in figures	Length (Kb)	Genomic loci of Gametic DMR	COBRA_enzyme_site
<i>Nespas-Gnasxl</i>	chr2:174291500-174301500	10	chr2:174294362-174301063	
<i>Gnas 1A</i>		9	chr2:174325376-174329137	
<i>peg10</i>		9	chr6:4746743-4749483	chr6:478244
<i>peg1/Mest</i>		9	chr6:30734932-30739966	
<i>peg3</i>		9	chr7:6727076-6731546	
<i>Snrpn</i>	chr7:60000000-60009000	9	chr7:60002495-60006697	chr7:60005198
<i>Lit1/Kcnq1ot1</i>	chr7:143290790-143299790	9	chr7:143294831-143296905	
<i>Zac1/Plagl1</i>		9	chr10:13089891-13092325	
<i>Meg1/Grb10</i>		9	chr11:12025124-12027097	
<i>U2af1-rs1/Zrsr1</i>		9	chr11:22971610-22974212	
<i>Igf2r</i>		9	chr17:12741303-12742950	chr17:12742527
<i>Impact</i>		9	chr18:12971926-12975001	
<i>H19</i>	chr7:142576644-142586644	10	chr7:142578768-142586025	chr7:142580375(PvuI)
<i>Rasgrf1</i>		15	chr9:89872252-89880290	
<i>Dlk1-Gtl2</i>		12	chr12:109524493-109534883	chr12:109527608
Repeat loci				
Names	Gene_id	Length(bp)	LTR or 5'-UTR loci	
L1MdGf	D84391	7104	1-1072 (5'-UTR, CpG enriched)	
L1Md-A2	M13002	7713	1-1560 (5'-UTR, CpG enriched)	
IAP	M17551	7096	1-338 (LTR)	

Supplemental Table S5. Summary of the Samples for SC3-Seq, Related to Figure 7

Sample name	GSC/GSCLC lines	SpikeRNA	Species	Genome version	Total reads	Cutadapt qualified reads	SC3seq mapped reads	mapped others	ERCC F	ERCC R	Unmapped
GSC1_MS094.065	GSC1	ERCC	Mus musculus	mm10	6,529,318	5,901,297	3,772,961	1,595,482	158,723	14,285	359,846
GSC1_MS094.067	GSC1	ERCC	Mus musculus	mm10	7,839,291	7,615,903	6,040,021	880,965	278,850	26,481	389,586
GSC1_MS094.068	GSC1	ERCC	Mus musculus	mm10	5,898,079	5,550,639	4,048,249	1,087,024	91,654	6,603	317,109
GSC1_MS094.069	GSC1	ERCC	Mus musculus	mm10	7,379,679	6,830,042	4,783,194	1,470,833	186,999	15,349	373,667
GSC1_MS094.070	GSC1	ERCC	Mus musculus	mm10	4,112,575	3,883,683	2,819,277	693,499	146,835	13,875	210,197
GSC1_MS094.071	GSC1	ERCC	Mus musculus	mm10	5,240,333	5,078,990	3,627,379	951,983	218,835	20,748	260,045
GSC1_MS094.072	GSC1	ERCC	Mus musculus	mm10	4,001,268	3,540,290	2,516,240	733,303	80,215	7,369	203,163
GSC1_MS094.073	GSC1	ERCC	Mus musculus	mm10	7,409,060	6,632,240	4,716,099	1,365,223	200,394	16,833	333,691
GSC1_MS094.075	GSC1	ERCC	Mus musculus	mm10	8,076,840	7,660,838	5,167,027	1,771,383	307,673	24,890	389,865
GSC1_MS094.076	GSC1	ERCC	Mus musculus	mm10	6,576,272	5,659,253	3,832,871	1,089,208	235,496	23,382	478,296
GSC1_MS094.077	GSC1	ERCC	Mus musculus	mm10	6,955,419	6,900,878	5,507,004	965,891	124,612	14,148	289,223
GSC1_MS094.079	GSC1	ERCC	Mus musculus	mm10	6,565,252	5,847,170	4,046,071	1,212,414	245,960	18,403	324,322
GSC1_MS094.080	GSC1	ERCC	Mus musculus	mm10	5,097,393	4,577,902	3,244,452	949,157	132,014	10,596	241,683
GSC1_MS094.129	GSC1	ERCC	Mus musculus	mm10	5,469,912	5,216,387	3,709,084	1,064,469	161,251	15,069	266,514
GSC1_MS094.131	GSC1	ERCC	Mus musculus	mm10	5,875,059	5,465,239	3,720,173	1,297,052	157,761	15,120	275,133
GSC1_MS094.132	GSC1	ERCC	Mus musculus	mm10	6,791,949	6,364,407	4,572,221	1,249,963	197,607	15,879	328,737
GSC1_MS094.133	GSC1	ERCC	Mus musculus	mm10	5,379,816	5,161,563	3,874,584	866,656	166,767	11,557	241,999
GSC1_MS094.136	GSC1	ERCC	Mus musculus	mm10	3,265,299	2,885,765	2,079,319	553,559	86,074	6,713	160,100
GSC1_MS094.137	GSC1	ERCC	Mus musculus	mm10	4,677,177	4,511,104	3,426,858	731,802	117,795	10,633	224,016
GSC1_MS094.138	GSC1	ERCC	Mus musculus	mm10	6,084,298	5,979,180	4,505,578	1,034,180	137,931	14,123	287,368
GSC1_MS094.140	GSC1	ERCC	Mus musculus	mm10	5,353,812	5,185,918	3,873,799	875,094	165,163	17,120	254,742
GSC1_MS094.141	GSC1	ERCC	Mus musculus	mm10	4,794,331	4,557,243	3,235,278	905,857	157,814	13,993	244,301
GSC1_MS094.142	GSC1	ERCC	Mus musculus	mm10	3,962,442	3,626,494	2,676,086	675,876	70,786	5,896	197,850
GSC1_MS094.143	GSC1	ERCC	Mus musculus	mm10	4,423,077	3,953,904	2,745,359	808,450	156,703	12,606	230,786
GSC1_MS094.144	GSC1	ERCC	Mus musculus	mm10	3,277,353	2,886,890	2,024,211	561,250	118,006	9,020	174,403
GSC1_MS094.145	GSC1	ERCC	Mus musculus	mm10	4,775,133	4,153,734	3,007,835	794,736	117,492	11,440	222,231
GSC1_MS094.146	GSC1	ERCC	Mus musculus	mm10	5,273,599	4,886,169	3,033,056	1,286,053	277,485	23,579	265,996
GSC1_MS094.147	GSC1	ERCC	Mus musculus	mm10	5,212,975	5,016,678	3,780,292	865,586	119,695	12,768	238,337
GSC1_MS094.149	GSC1	ERCC	Mus musculus	mm10	5,478,178	4,468,078	3,161,578	963,135	91,442	7,215	244,708
GSC1_MS094.150	GSC1	ERCC	Mus musculus	mm10	4,187,918	3,548,598	2,400,365	789,786	146,668	12,493	199,286
GSC2_MS094.021	GSC2	ERCC	Mus musculus	mm10	8,280,008	8,057,815	5,589,173	1,986,774	71,701	5,522	404,645
GSC2_MS094.022	GSC2	ERCC	Mus musculus	mm10	6,209,277	5,980,541	4,128,118	1,387,737	135,919	13,181	315,586
GSC2_MS094.023	GSC2	ERCC	Mus musculus	mm10	5,032,368	4,736,190	3,377,398	973,092	100,532	8,370	276,798
GSC2_MS094.024	GSC2	ERCC	Mus musculus	mm10	4,486,786	3,946,131	2,766,692	763,221	144,646	11,233	260,339
GSC2_MS094.027	GSC2	ERCC	Mus musculus	mm10	8,158,580	7,415,021	4,740,424	1,991,830	268,820	23,769	390,178
GSC2_MS094.029	GSC2	ERCC	Mus musculus	mm10	8,419,041	7,247,789	4,887,513	1,731,171	209,338	16,614	403,153
GSC2_MS094.031	GSC2	ERCC	Mus musculus	mm10	6,314,384	5,882,981	4,077,912	1,338,201	131,767	13,506	321,595
GSC2_MS094.032	GSC2	ERCC	Mus musculus	mm10	3,605,538	3,432,614	2,416,943	738,083	84,429	7,380	185,779
GSC2_MS094.033	GSC2	ERCC	Mus musculus	mm10	6,456,475	5,580,927	3,984,849	1,098,011	155,017	16,315	326,735
GSC2_MS094.036	GSC2	ERCC	Mus musculus	mm10	7,740,629	7,294,157	4,556,817	2,214,429	169,479	16,651	336,781
GSC2_MS094.037	GSC2	ERCC	Mus musculus	mm10	7,906,955	7,240,817	5,348,795	1,333,453	183,277	17,832	357,460
GSC2_MS094.039	GSC2	ERCC	Mus musculus	mm10	5,061,063	4,760,776	3,218,698	1,179,221	95,909	9,742	257,206
GSC2_MS094.041	GSC2	ERCC	Mus musculus	mm10	7,640,883	7,105,142	4,987,774	1,562,068	107,498	8,484	439,318
GSC2_MS094.042	GSC2	ERCC	Mus musculus	mm10	7,072,206	6,390,406	4,375,739	1,463,558	146,061	11,972	393,076
GSC2_MS094.043	GSC2	ERCC	Mus musculus	mm10	6,263,656	5,870,468	4,310,192	1,091,249	126,464	9,874	332,689
GSC2_MS094.044	GSC2	ERCC	Mus musculus	mm10	9,376,684	8,348,691	5,653,176	1,984,833	188,224	16,746	505,712
GSC2_MS094.045	GSC2	ERCC	Mus musculus	mm10	8,845,055	8,044,092	5,850,369	1,522,500	184,188	14,666	472,369
GSC2_MS094.048	GSC2	ERCC	Mus musculus	mm10	4,622,061	4,520,758	3,228,526	931,433	113,621	11,394	235,784
GSC2_MS094.052	GSC2	ERCC	Mus musculus	mm10	6,793,921	6,726,034	4,992,774	1,285,756	140,343	15,332	291,829
GSC2_MS094.055	GSC2	ERCC	Mus musculus	mm10	5,471,684	4,882,234	3,607,838	898,236	82,074	9,404	284,682
GSC2_MS094.059	GSC2	ERCC	Mus musculus	mm10	7,520,632	7,175,626	5,138,663	1,457,877	188,406	19,579	371,101
GSC2_MS094.060	GSC2	ERCC	Mus musculus	mm10	5,950,956	5,426,854	3,734,745	1,249,157	136,688	11,323	294,941
GSC2_MS094.061	GSC2	ERCC	Mus musculus	mm10	5,255,604	5,039,036	3,548,905	1,105,149	110,230	11,850	262,902
GSC2_MS094.062	GSC2	ERCC	Mus musculus	mm10	6,545,367	6,111,550	4,291,847	1,317,196	167,777	14,856	319,874
GSCLC1_MS094.151	GSCLC1	ERCC	Mus musculus	mm10	4,667,220	4,562,115	3,479,989	722,007	123,834	8,490	227,795
GSCLC1_MS094.153	GSCLC1	ERCC	Mus musculus	mm10	4,624,904	4,286,889	3,256,389	530,756	251,338	25,126	223,280
GSCLC1_MS094.155	GSCLC1	ERCC	Mus musculus	mm10	5,016,954	4,275,888	3,146,173	720,899	152,701	16,268	239,847
GSCLC1_MS094.156	GSCLC1	ERCC	Mus musculus	mm10	4,071,249	3,526,501	2,593,621	607,231	110,959	18,517	196,173
GSCLC1_MS094.157	GSCLC1	ERCC	Mus musculus	mm10	5,379,104	5,005,625	3,772,366	851,186	134,902	13,000	234,171
GSCLC1_MS094.158	GSCLC1	ERCC	Mus musculus	mm10	3,470,367	3,272,087	2,463,853	537,737	103,151	9,438	157,908
GSCLC1_MS094.159	GSCLC1	ERCC	Mus musculus	mm10	4,880,977	4,497,145	3,243,363	867,255	142,269	8,419	235,839
GSCLC1_MS094.161	GSCLC1	ERCC	Mus musculus	mm10	4,972,103	4,871,082	3,735,715	766,927	109,470	11,360	247,610
GSCLC1_MS094.162	GSCLC1	ERCC	Mus musculus	mm10	4,322,834	4,200,503	3,159,575	694,082	127,204	13,503	206,139
GSCLC1_MS094.163	GSCLC1	ERCC	Mus musculus	mm10	4,200,011	3,990,499	2,955,822	748,683	82,681	8,274	215,039
GSCLC1_MS094.164	GSCLC1	ERCC	Mus musculus	mm10	4,516,118	4,113,798	2,804,804	895,999	170,675	17,014	225,306
GSCLC1_MS094.165	GSCLC1	ERCC	Mus musculus	mm10	4,766,624	4,111,620	2,980,337	767,880	109,396	10,023	243,984
GSCLC1_MS094.166	GSCLC1	ERCC	Mus musculus	mm10	3,566,942	3,189,103	2,438,363	470,652	95,943	8,373	175,772
GSCLC1_MS094.167	GSCLC1	ERCC	Mus musculus	mm10	5,464,236	5,238,097	4,232,441	549,497	174,093	17,268	264,798
GSCLC1_MS094.168	GSCLC1	ERCC	Mus musculus	mm10	3,570,671	3,402,711	2,464,240	601,179	148,158	13,165	175,969
GSCLC1_MS094.169	GSCLC1	ERCC	Mus musculus	mm10	5,083,658	4,758,485	3,431,421	965,281	109,842	6,927	245,014
GSCLC1_MS094.170	GSCLC1	ERCC	Mus musculus	mm10	4,862,939	4,478,007	3,308,056	789,997	143,282	10,350	226,322
GSCLC1_MS094.171	GSCLC1	ERCC	Mus musculus	mm10	5,598,307	5,329,664	4,164,722	792,831	96,875	7,993	267,243
GSCLC1_MS094.172	GSCLC1	ERCC	Mus musculus	mm10	5,179,947	4,684,829	3,470,470	802,171	161,107	13,555	237,526
GSCLC1_MS094.173	GSCLC1	ERCC	Mus musculus	mm10	7,250,845	6,782,534	4,970,856	1,137,445	311,683	30,284	332,266
GSCLC1_MS094.175	GSCLC1	ERCC	Mus musculus	mm10	5,126,660	4,773,481	3,617,670	763,259	135,627	10,294	246,631
GSCLC1_MS094.176	GSCLC1	ERCC	Mus musculus	mm10	3,110,715	3,003,848	2,280,692	454,434	113,927	7,249	147,546
GSCLC1_MS094.177	GSCLC1	ERCC	Mus musculus	mm10	4,732,047	4,510,355	3,332,401	777,912	142,311	13,238	244,493
GSCLC1_MS094.180	GSCLC1	ERCC	Mus musculus	mm10	4,530,083	4,393,630	3,200,769	808,242	157,595	16,872	210,152
GSCLC1_MS094.181	GSCLC1	ERCC	Mus musculus	mm10	4,346,877	3,854,308	2,844,507	666,291	130,971	11,195	201,344
GSCLC1_MS094.182	GSCLC1	ERCC	Mus musculus	mm10	3,338,974	3,172,254	2,337,064	580,854	83,713	7,734	162,889
GSCLC1_MS094.183	GSCLC1	ERCC	Mus musculus	mm10	4,252,773	3,949,612	2,781,906	778,384	177,604	15,180	196,538
GSCLC1_MS094.184	GSCLC1	ERCC	Mus musculus	mm10	2,661,234	2,597,987	1,998,592	373,728	85,699	7,467	132,501
GSCLC1_MS094.185	GSCLC1	ERCC	Mus musculus	mm10	4,887,028	4,473,056	3,173,543	818,003	164,794	10,173	306,543
GSCLC1_MS094.186	GSCLC1	ERCC	Mus musculus	mm10	4,562,919	4,424,358	3,261,974	773,160	164,370	16,191	208,663
GSCLC4_MS094.091	GSCLC4	ERCC	Mus musculus	mm10	5,730,524	5,517,090	4,104,438	991,028	126,955	12,969	281,700
GSCLC4_MS094.092	GSCLC4	ERCC	Mus musculus	mm10	6,155,530	5,891,013	4,513,042	933,129	130,203	12,358	302,281
GSCLC4_MS094.093	GSCLC4	ERCC	Mus musculus	mm10	6,764,911	6,702,987	5,339,026	857,736	183,586	22,052	300,587
GSCLC4_MS094.095	GSCLC4	ERCC	Mus musculus								