SUPPLEMENTAL INFORMATION FOR:

Cross-species genomics matches driver mutations and cell compartments to model ependymoma

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CONTENTS

Supplemental Methods

Tumor Samples.

204 snap frozen ependymomas were collected centrally from collaborating -80°C tumor banks with the approval of the St. Jude Children's Research Hospital Institution Review Board. RNA and DNA were extracted using standard techniques including the Trizol reagent and phenol/chloroform as described (main reference section, 7). Tissue microarrays (TMA) were prepared from formalin fixed paraffin embedded samples of an additional 74 ependymomas (15 cerebral, 55 posterior fossa and 4 spinal tumors) that were distinct from the fresh frozen tumor cohort. All tumors (frozen and formalin fixed) had an institutional histopathological diagnosis of ependymoma and D.W.E., performed an additional central pathology review of all tumors incorporated into the TMAs. Tumors isolated from mice were processed in the same way to acquire RNA, DNA and tissue sections for histology.

DNA based analyses

Construction of Single Nucleotide Polymorphism (SNP) microarray profiles of human tumors. SNP microarray profiles were generated in collaboration with the Hartwell Center for Bioinformatics and Biotechnology at St Jude Children's Research Hospital using the Affymetrix GeneChip Human Mapping 500K assay which interrogates ~500,000 total SNPs with median inter-marker distance of 2.5kb. Purity and integrity of DNA samples was confirmed by UV spectrophotometry and by agarose gel electrophoresis. Processing of DNA samples was performed according to the Affymetrix 500K SNP protocol. Briefly, total genomic DNA (250 ng) was digested to completion using NspI or StyI restriction enzyme and ligated to oligonucleotide adapters. Ninety micrograms of amplified DNA were fragmented using DNase I and end-labeled with biotinylated-nucleotide using terminal deoxynucleotidyl transferase. Labeled DNA targets were added to a hybridization cocktail containing array controls, blocking agents (human Cot-1 and herring sperm DNA), and incubated overnight at 48°C on a GeneChip array. Arrays were washed and stained with Streptavidin Phycoerythrin (SAPE, Molecular Probes) using the GeneChip Fluidics Station 400, then scanned using an Affymetrix GeneChip Scanner 3000.

SNP microarray data were analyzed using the general strategy of Mullighan et al.,[31]. Initial signal values were obtained using the Affymetrix PLIER algorithm. Genotype calls were generated using the BRLMM algorithm[32]. Subsequent signal processing and copy number analysis was performed separately for each tumor sample as described below.

For each tumor sample and each array (Nsp and Sty), the reference selection algorithm (RSA)[33] was used to select a chromosome to use as a reference to normalize the signal data with the reference alignment procedure[33]. Comparative normalized signals from gender-matched controls were obtained by using the same reference chromosome to normalize the PLIER signals with RAP. For each marker, an estimate of the log-ratio of the copy number in tumor to the copy number in controls was obtained by subtracting the mean of the RAP signals of the gender matched controls from the mean of the RAP signals of the tumor. For each tumor, an empirical quantile-based transformation was used to adjust log-ratios for distributional differences due to platform (Nsp vs. Sty). For each chromosome, the empirical quantile function, also known as a quantile plot, of log-ratios was determined for each array[34]. The quantiles of the adjusted log-ratios for the sty platform were defined as the average of the observed quantiles of the log-ratios from the Sty platform and approximations of the corresponding quantiles of the log-ratios of the Nsp platform obtained by linear interpolation. The quantiles of the adjusted log-ratios for the Nsp platform were obtained in an analogous manner by reversing the roles of the Nsp and Sty platforms in the calculation described above. This adjustment of log-ratios for platform differences preserved the information about copy number status from each array while enhancing the performance of the segmentation analysis described below. By using a permutation testing procedure, the segmentation analysis implicitly assumes that log-ratios are exchangeable under the null hypothesis that the entire series of log-ratio values represent the same copy number status[35]. The platform-adjusted log-ratios are more accurately modelled under this assumption than are the unadjusted log-ratios.

Change-points in the series of platform-adjusted log-ratios (ordered by chromosome and position) were identified by circular binary segmentation[36,37] as implemented in the Bioconductor package version 1.16.0 (www.bioconductor.org). The p-value threshold was set to 0.01 and default settings were used for all other algorithm parameters. Several summary statistics of the platform-adjusted log-ratios were computed for each segment: number of markers, mean, standard deviation, median, inter-quartile range, and proportion of adjusted log-ratios that are positive. Adjacent segments with a similar proportion of positive adjusted log-ratios were combined. For each pair of adjacent segments, a 2x2 table was generated that categorized each adjusted log-ratio as being positive or negative (rows) and as being in segment A or B (columns). Fisher's exact test was applied to the 2x2 table. The adjacent segments were combined if the p-value was greater than 0.2. A large p-value threshold was used here to avoid the error of combining segments that represent different copy number states. Each segment was then categorized as a region of putative amplification, putative deletion, or not having strong statistical evidence of a copy number change. Approximately 50% of the log-ratios should be positive for a segment with no copy number change. Pounds et al.,[33] noted that the actual proportion of positive log-ratios for two-copy segments varies between 0.4 and 0.6. Thus, for each segment, a two-sided statistical test based on the binomial distribution was used to test whether the observed proportion of log-ratios greater than zero was significantly less than 0.4 (indicating evidence for deletion) or greater than 0.6 (indicating evidence for amplification). To further characterize the statistical evidence for amplification or deletion, a one-sample t-test was applied to the log-ratios of each segment to determine if there is significant evidence that the mean is less than -0.1 (indicating deletion) or greater than 0.1 (indicating amplification). Segments with p-value less than 0.01 from both statistical tests were declared as regions of amplification or deletion. The list of significant segments is provided in Supplementary Table 2 and the Supplemental Gene Cards.

Finally, scores were assigned to the segments for purposes of visualization. A score of zero was assigned to all segments which were not declared a region of amplification or deletion. Scores of -4, -3, -2, and -1 were assigned to segments declared a region of deletion with fewer than 10%, 20%, 30%, or 40% log-ratios greater than zero, respectively. Scores of +1, +2, +3, and +4 were assigned to segments declared a region of amplification with greater than 60%, 70%, 80%, and 90% log-ratios greater than zero. These scores were then represented in a matrix format (tumor samples as columns and markers as rows).

Inference of focal copy number alterations (CNAs). We defined focal CNAs (amplifications and deletions) as described previously as alterations of 10kb to 10 Mb involving 3 or more contiguously and consistently altered SNPs[38]. Since our experiments were designed to identify the most likely candidate ependymoma genes, we also specified that CNAs had to effect at least 5% of samples (n=10/203) detected by SNP array and/or iFISH (see below). All focal CNAs are described in Supplemental Tables 2-4 and the Supplemental Gene Cards.

Criteria for selection of CNAs for further study.

The following criteria were used to select CNAs inferred by SNP microarray analysis for further validation and study:

(a) Inferred high-level amplification or homozygous deletion. Chromosomal regions that are deleted homozygously from tumors or amplified to very high levels (>15 copies) are very likely to contain TSG and oncogenes, respectively. Therefore, we prioritized for further study any candidates that mapped within inferred regions of homozygous deletion or high-level amplification.

(b) Known oncogene or TSG function. We searched a variety of resources including: the literature; the Catalogue of Somatic Mutations in Cancer (COSMIC) (http://www.sanger.ac.uk/genetics/CGP/cosmic/), to determine whether any of the genes within areas of chromosome alteration have established roles in oncogenesis. We also identified genes that play major regulatory roles in cell cycle progression, apoptosis, differentiation, or angiogenesis.

(c) Genes within the same family or with related function. Tumors of the same histologic type often accumulate mutations in genes that have related functions. These mutations can identify cell signal pathways that play a pivotal role in tumor development. In light of this, we prioritized chromosomal alterations that target genes that encode members of the same family or cell signal pathway. These analyses were assisted by the use of a number of online resources including ‘KEGG: Kyoto Encyclopedia of Genes and Genomes’ (http://www.genome.jp/kegg/).

(d) Frequency of inferred involvement. Genes that are the target of amplification or deletion events in <5% of tumors were given a low priority for further study, unless these mutations represented one component of a series of alterations that target genes with related function (see (c), above).

Validation of focal CNAs by Real-Time Reverse Transcriptase Polymerase Chain Reaction. CNAs inferred by SNP analysis were validated in human tumor samples using Real-Time polymerase chain reaction, Taq Man probes and the BioRad iCycler single color real-time PCR detection system (BioRad, Hercules, CA) as described previously (main reference section, 7). All primer and probe sequences are listed in Supplementary Table 4. A minimum of seven inferred diploid samples and a mean of five (range 3 to 8) inferred CNA samples were employed in each analysis. For each CNA, DNA copy levels were measured relative to a standard curve generated from a dilution series of concurrently analyzed human genomic DNA (Roche Diagnostics, Indianapolis, IN) and normalized to the internal reference gene (*CPO*; chromosome 2q33.3).

Validation of focal CNAs by interphase fluorescence *in situ* hybridisation (iFISH). Dual-color interphase FISH was performed on 6-8μm formalin fixed paraffin embedded tissue sections from archived samples of 79 human ependymomas encorporated into a TMA (see above). Probes were derived from BAC clones (Invitrogen, Carlsbad, CA) and labelled with either FITC or rhodamine fluorochromes. BAC clones were chosen for probe construction as follows: *EPHB2* RP11-431G10, with 1q22 control RP11-54H19 + RP11-336K24; *EXO1* RP11-610O24 RP11-

384I6, with 1p13 control CTD-3241G19; *CRIPAK* CTD-2553A8 + CTD-2547M24, with 4q12 control RP11-1005B7; *CDC2L6* RP11-109D10, with 6p12 control RP11-945O22 + RP11-186N7; *CDKN2A* RP11-149I2 + RP11-145E5, with 9q31 control RP11-235C23; *NOTCH1* RP11-370H5 + RP11-1008C19, with 9p21 control RP11-149I2 + RP11-145E5; *PTEN* CTD-2553L21, with 10p11.2 control RP11-254A5 + RP11-322I; *ARID3A* CTD-2582H10 + CTD-2378A10, with 19q13.4 control CTD-3079O7; *NF2* RP11-155B12 + RP11-551L12, with 22q13 control RP11-350L11 + RP11-46J14; *SOX10* RP11-1080C13, with 22q11.2 control RP11-1150L22 + RP11-91O6.

All probe mixtures were diluted 1:50 in DenHyb buffer (Insitus Biotechnologies, Albuquerque, NM) and co-denatured with the target cells on a slide moat at 90°C for 12 minutes. Slides were incubated overnight at 37°C on a slide moat and then washed in 4M urea / 2xSSC at 25°C for 2 minutes. Nuclei were counterstained with DAPI (200ng/ml; Vector Labs) for viewing on a Nikon Eclipse E800 fluorescence microscope equipped with a 100 watt mercury lamp; FITC, Rhodamine, and DAPI filters; 100X PlanApo (1.40) oil objective; and a COHU CCD camera. Images were captured and processed with an exposure time ranging from 0.5-1.5 seconds for each fluorochrome using Cytovision v3.6 software. The results of all iFISH analyses are reported on the corresponding Supplemental Gene Card.

RNA based analyses.

Constructrion of mRNA expression profiles. mRNA expression profiles were generated using total RNA isolated from human and mouse tissues and the U133 Plus 2.0 and 430 v 2 microarrays, respectively (Affymetrix, Santa Clara, CA). Gene expression data were normalized using the MAS 5.0 algorithm. The data were then transformed and variance stabilized by addition of small factor of 20 that shrinks the effects of small numbers and then taking the natural logarithm. The median absolute difference (MAD) of these transformed signals was calculated for each probe set across all samples on each array separately within species. The data was then imported into Spotfire Decision Site (Palo Alto CA, USA) and for each probe set and subject z-scores were calculated by computing the mean and standard deviation across subjects within each probeset. Expression data is available through http://www.ncbi.nlm.nih.gov/geo acc=GSE21687

Hierarchical cluster analyses was perfomed through as series of discrete tests aimed at identifying the largest number of informative probes that segregate biologically distinct samples. First, the z scores of the top 5% MAD score (most variable) probe sets and not located on chromosome X or Y (to avoid the influence of patient sex in clustering) were used to hierarchically cluster samples in an unsupervised manner using average linked Euclidean distance metrics. The structure of the dendrogram, including the major and minor branches and the tumor samples that comprised each subgroup was recorded. The next 1% most varying probes (based on MAD score) were then added to the dataset and heirarchical clustering and dendrogram review repeated as described. This process was repeated through serial additions of 1% varying probes until two or more samples 'jumped' subgroups from two or more subgroups. We validated the resulting clusters from this analysis by performing a separate analysis of mRNA expression profiles. Briefly, for each probe set, the dip statistic[39] was used to measure the evidence for multiple modes in the distribution of log-transformed expression values. The log-transformed expression values of 644 probe sets with dip statistic ≥ 0.06 and not located on chromosome X or Y were used for subsequent hierarchical cluster analysis. Hierarchical cluster analysis was performed using complete linkage and Euclidean distance computed on log-transformed expression values. To assess the level of agreement of the resulting dendrograms we partitioned these into distinct clusters by cutting the tree at a variety of distance measurements. The Rand index[40] was used to measure the agreement of group assignments by the two different clustering methods. The statistical significance of the Rand index was determined by permutation of one set of group assignment labels.

Following this process clusters were defined and these codes used to perform a series of Welch t-tests. In each t-test those arrays in the cluster were tested against all other arrays from the same species. The resultant lists of p-values were used to define probesets that passed the Bonferroni threshold at 0.05 percent

Constructrion of miRNA expression profiles. A human miRNA microarray consisting of probes for 723 human and 76 human viral miRNAs from the Sanger database v10.1, was employed to generated miRNA profiles of human tumors (Agilent technologies). Array hybridization was performed according to the manufacturer's recommended protocols. In brief, total RNA was labeled using the Agilent miRNA Labeling kit. Hybridization was carried out in an Agilent oven at 55°C for 20 hours at 20 rpm, followed by standard wash procedures. The microarray was then scanned in an Agilent scanner at 5µm resolution, and the array data was extracted using the default miRNA settings of Agilent Feature Extraction Software (v10.5.1.1). Signal intensity was normalized, scaled and log transformed. The minimum detecting miRNA expression signal was set at a threshold such that fewer than 1% of the detected probe sets were negative controls. Samples were clustered according to miRNA profiles as described for mRNA.

Pathway analysis. One-sided Fisher's exact test P values were calculated to determine whether a particular pathway was statistically significantly enriched in mRNA sets. The q-values were then estimated for a given set of p-values[41].

mRNA, miRNA cluster comparison. The Rand Index[40] was used to assess the agreement of two distinct group assignments (such as cluster analysis and tumor type). The Rand Index is the proportion of pairs of individuals that either have the same group designation in both assignments or have different group designations in both assignments. The statistical significant of the Rand Index was determined by permuting the designation labels for one of the assignments 10,000 times.

DNA-RNA integration to assess copy number driven changes in gene expression

Large chromosomal changes: Tumor samples were first classified as having extensive ($\geq$50% SNPs per arm) chromosome arm gain (or loss) or diploid copy number as described above. We then conducted a Welch t-test to compare expression of each transcript in the region of interest across the two groups. A transcript was considered to have overexpression (underexpression) among samples with the gain (loss) if the t-statistic was positive (negative) and the p-value was less than 0.01. This gave the number of transcripts along the chromosome arm that are overexpressed (underexpressed) among samples with the gain (loss). The statistical significance of the observed number of overexpressed (underexpressed) transcripts was determined by repeating the entire process for 10,000 random permutations of the label of having a gain (loss). The p-value for the number of overexpressed (underexpressed) transcripts was given by the proportion of permutations yielding a larger number of overexpressed (underexpressed) than the assignments in the observed data. The heatmaps and statistics reporting the results of these tests are shown in Supplemental Figure 4a to d.

Focal CNAs: Pathological changes in the expression of oncogenes and tumor suppressor genes can result from both large and focal chromosomal alterations. Therefore, to test if genes located within validated focal CNAs in ependymoma might be the target of copy number driven expression we first classified tumors as having focal CNA gain (or loss) defined above, large (>10 Mb) CNAs gain (or loss) that included the region of CNA, or diploid copy number. We then conducted an ANOVA test with appropriate Bonferroni correction to compare the expression of each transcript in the region of interest across the three groups. Heatmaps and the ANOVA statistic for each validated CNA are reported on the second Supplemental Gene Card for each CNA.

Comparative analysis of gene expression between tumors that do or do not contain CNAs but otherwise share similar global patterns of gene expression can be especially informative for detecting copy number driven expression changes. Therefore, we also constructed heatmaps that report the impact of CNAs on the expression of transcripts by tumors within a particular subgroup (A to I). When subgroups contained three or more tumors each containing the CNA or diploid copy number we conducted a Welch t-test with appropriate Bonferroni correction to compare expression of the appropriate transcript(s) within the CNA across the two groups (subgroup members with focal gain [or loss] or subgroup members with diploid copy number). Heatmaps and the statistic for each validated CNA are reported on the third Supplemental Gene Card for each CNA

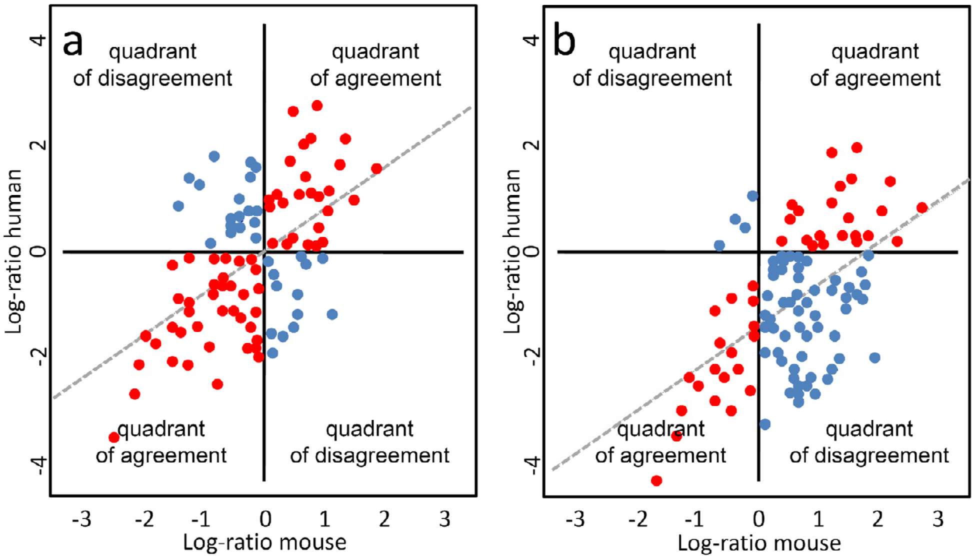
Human-mouse expression integration

Human expression datasets. The expression profiles analyzed included the 83 ependymoma mRNA expression profiles generated in the current study (Affymetrix U133 Plus v 2.0), as well as previously published profiles of 46 medulloblastomas (main reference section, 30) and 115 glioblastomas (main reference section, 29) (Affymetrix U133 A/B).

Ortholog selection. Matching of mouse 430v2.0 probesets with human Affymetrix probesets was made possible through an ortholog mapping file provided by Affymetrix. Nearly all of the probesets that had orthologs represented on microarrays of both species were reference sequences. Redundant probes were removed (based on MAD) so that no mouse probeset or human probeset appeared more than once. 14,261, and 8,628 orthologs were identified for the human U133 Plus 2.0 and Affymetrix U133 A/B datasets, respectively.

Agreement of differential expression (AGDEX). The agreement between transcriptomes in human and mouse tissues was evaluated using a novel statistical procedure developed for the current study that we have called agreement of differential expression (AGDEX).

Overview of AGDEX: AGDEX measures the statistical metric of agreement rather than correlation between transcriptomes. In the context of our analysis, the correlation statistic merely tests the degree to which a comparison of the Log-ratios of ortholog expression between two tissues distributes in a linear fashion. Importantly, the correlation statistic does not require that compared tissues display similar relative expression levels of each ortholog (i.e., relatively under- or overexpressed) to be both positive and significant. In contrast, the agreement statistic accounts not only for the linear relationship of the Log-ratios, but also the degree to which the orthologs display similar relative levels of expression in the two tissues (i.e., orthologs must display common relative levels of expression).



Spearman=0.45
AGDEX=0.53

Spearman=0.45
AGDEX=0.00

Supplemental Methods Figure 1. Graphs illustrating the difference between statistical correlation and agreement

For example, Supplemental Methods Figure 1a illustrates a comparison of ortholog expression Log-ratios between a human and mouse tissue that display both strong correlation (Spearman Rank=0.45) and agreement (AGDEX=0.53). Points that show agreement (i.e., common + or – Log ratio in both species) are colored red. Points not showing agreement (i.e., discordant Log-ratio between the species) are colored blue. In contrast, while the transcriptomes of two tissues shown in Supplemental Methods Figure 1b display an equal level of correlation to those in Figure 1a, there is no agreement in comparative ortholog expression between these tissues (AGDEX=0). The failure of the agreement of transcriptome matching in

Figure 1b results from the fact that the majority of orthologs that are relatively overexpressed in mouse tissue are under-expressed in the human tissue even though they organize in a linear fashion. Thus, AGDEX represents a rigorous and relevant test of transcriptome matching above that provided by standard correlation approaches.

The AGDEX algorithm: Let $i = 1, \dots, m$ index ortholog-matched probe set pairs for $j = 1, 2$ species. Thus, for each species j, i indexes the probe set belonging to ortholog-matched probe set pair i. Also, let $k = 1, 2$ index two experimental subgroups within each species and $l = 1, \dots, n_{jk}$ index individuals of experimental subgroup k within species j. Let y_{ijkl} represent the log-transformed expression value of probe set i of individual l in experimental group k of species j.

Define $\bar{y}_{ijk}$ as the average log-expression of probe set i for experimental group k of species j. Let $d_{ij} = \bar{y}_{ij2} - \bar{y}_{ij1}$ represent the difference of average expression of probe set i between the two experimental groups of species j.

Now, define

$$A = \frac{\sum_{i=1}^{m} d_{i1} d_{i2}}{\sqrt{\sum_{i=1}^{m} d_{i1}^2 \sum_{i=1}^{m} d_{i2}^2}}$$

as the agreement of differential expression (AGDEX) statistic. Note that A is the cosine of the angle between the vectors $\boldsymbol{d_1} = \{d_{11}, d_{21}, \dots, d_{m1}\}$ and $\boldsymbol{d_2} = \{d_{12}, d_{22}, \dots, d_{m2}\}$ in m-dimensional Euclidean space. Therefore, $A = 1$ indicates excellent agreement of differential expression in the sense that the angle between $\boldsymbol{d_1}$and $\boldsymbol{d_2}$ is zero. Also, $A = 0$ indicates $\boldsymbol{d_1} = \mathbf{0}$, $\boldsymbol{d_2} = \mathbf{0}$, or that $\boldsymbol{d_1}$ and $\boldsymbol{d_2}$ are orthogonal. Finally, $A = -1$ indicates that the vectors point in exactly opposite directions.

The statistical significance of an observed value A_{obs} of A can be determined using permutation. To determine the significance of A against the null hypothesis that the group assignments of species 2 are exchangeable, one may generate vectors $\boldsymbol{d_{jb}^*}$ for a series of $b = 1, \ldots, B$ permutations of the group assignments (k=1 or k =2) within species 2. By substituting $\boldsymbol{d_{jb}^*}$ into the definition of A, a series of values A_b^* is generated. Finally, a p-value is defined as

$$p = \frac{1}{B}\sum_{b=1}^{B} I(|A_b^*| \geq |A_{obs}|)$$

where $I(\cdot)$ is the indicator function that equals 1 if the enclosed statement is true and equals 0 if the enclosed statement is false. Thus, the p-value is the proportion of permutations of the group assignments for species 2 that give a value of A with greater magnitude than the observed data.

In this study, AGDEX was used to study the agreement of differential expression between two human groups (species j = 2) with the differential expression between two mouse groups (species j = 1). Figure 4C reports the value of the AGDEX statistic (defined as A in the notation above) and the p-value (defined as p in the notation above) obtained by permuting the group labels of the human data (species j=2). Each row of Figure 4C uses a heatmap format to report the results (A-statistic and p-value) of one analysis assessing the agreement of differential expression of a human disease subgroup (species $j = 2$, subgroup k=2) to other human tumors of the same disease (species $j = 2$, subgroup k=1) with the differential expression of the *EphB2*-driven mouse tumor (species j=1, subgroup k=2) to the non-cancerous mouse neural stem cells(species j=1, subgroup k=1). The 17 rows of AGDEX results evaluate the agreement of the comparison of the EphB2-driven mouse tumor to the set of all mouse NSCs with comparisons of each of 9 human ependymoma subgroups to other human ependymoms, comparisons of each of 5 human medulloblastomas to other human medulloblastomas, and comparisons of each of three human gliomas (Philips study). For example, the biologically most interesting result ($A = 0.41$, $p = 0.0009$) in Figure 4C reports the result of the agreement of the comparison of human ependymoma subgroup D (species $j = 2$, subgroup k=2) to other human ependymomas (species $j = 2$, subgroup $k = 1$) with the comparison of the *EphB2*-driven mouse tumor (species j=1, subgroup k=2) to the set of all non-cancerous mouse neural stem cells (species j=1, subgroup k=1).

Isolation and *in vitro* analysis and transduction of multipotent NSCs

Isolation of NSCs. eGFP^{+} NSCs were isolated from *Blbp-eGFP Ink4a/Arf* $^{-/-}$ and *Ink4a/Arf* $^{+/+}$ transgenic mice. Briefly, the forebrain, hindbrain and spine were macrodisected from embryonic day (E) 14.5 and adult mice. Tissues were minced and digested with collagenase type IV and hyaluronidase for 30 minutes at 37°C and single cells prepared as described (main reference section, 7). Isolated cells were grown in Neurobasal medium containing 2mM L-glutamine, 100U/ml penicillin, 100 µg/ml streptomycin, N2 supplement, B27 supplement, 20ng/ml EGF, 20 ng/ml bFGF and 50 µg/ml BSA in 5% CO_2. Suspensions of single cells were sorted at second passage for GFP expression using the Becton Dickinson Aria II Cell Sorter. GFP positive cells were used for all subsequent experiments.

Retroviral production and transduction of NSCs. Replication incompetent retroviruses were generated by co-transfecting packaging cells with the pCX4-IRES-Red Fluorescence (cRFP) construct and the appropriate packaging constructs. The pCX4-*EphB2*-IRES-RFP (*Ephb2*$^{\mathrm{RFP}}$) was similarly made following cloning of the full length mouse *EphB2* cDNA (a gift from Tony Pawson) into the NotI and BamHI sites within the multicloning region of the pCX4 backbone. Retrovirus was produced by the St Jude Vector Core Laboratory. NSCs were transduced with 1ml of cRFP ($6.5X10^5$ iu/ml) or 500ul of *EphB2*$^{\mathrm{RFP}}$ ($2.5X10^5$ iu/ml) in neural basal medium with retrovirus at a density of $1X10^6$ cells/10cm^2 dish for 2 days. Cells were then washed and cultured for an additional 48 hrs and eGFP$^+$/RFP$^+$ cells isolated by FACS sorting prior to study as indicated below.

FACS assessment of multipotency. NSCs were isolated and cultures as clonal neurospheres as described above. NSCs were then dissociated and re-plated in either differentiation media (Neurobasal medium containing 2mM L-glutamine, 100 U/mL penicillin, 100 μg/mL streptomycin, N2 supplement, B27 supplement, 10% fetal calf serum) or neural stem cell medium as described above (control cells). Cells were cultured for seven days at 37°C, 5% CO_2 incubator and then dissociated into single cells and pelleted. Cells (control and differentiated) were resuspended in PBS and live cells counted. One million cells were then washed, fixed, and permeabilized. Aliquots of control and differentiated cells were incubated withanti-β-tubulin III-PE-Cy5 (1:20 dilution, Millipore), anti-GFAP-Alexa647 (1:20 dilution, BD Pharmingen) and anti-CNPase-biotinylted (1:50 dilution, Abcam) antibodies or a mixture of the appropriately fluor- or biotin-labeled non-specific isotype control antibodies. Subsequently, streptavidin-PE-Cy7 was added to all samples. Cells were then rinsed, filtered and subject to FACS analysis using the Becton Dickinson LSR II Cell Analyzer. Data analysis was performed using FlowJo Flow Cytometry Analysis Software (Tree Star, Inc., Ashland, OR).

Morphologic and immunofluorescence assessment of NSCs and multipotency. Serial dilutions of single cell suspensions of eGFP$^+$/RFP$^+$ NSCs were made in 96 well plates (1000 to 1 cell/well). The number of spheres/well was quantified after 7 days as described (main reference section, 7). Spheres were then broken apart and suspensions of single cells re-plated. Secondary neurospheres were then counted seven days later and transferred to poly-L-lysine and laminin-coated coverslips and differentiation medium containing 2mM L-glutamine and 10% FBS for 14 days. Cells were fixed with 4% PFA and stained with antibodies to glial cell markers (GFAP, 1:1000 dilution, Dako and S100, 1:500 dilution, Sigma) and neural cell markers (MAP2, 1:200 dilution, Chemicon and β-III tubulin, 1:200 dilution, Chemicon). The percentage of multipotent neurospheres relative to input cells was then recorded. This process was repeated over 4 to five cycles in all NSC cultures analyzed and shown to be stable. Results reported in the paper are for 2'/primary input multipotent spheres. The immunophenotype of neurospheres prepared at clonal densities was determined by fixation in 4% PFA and immunofluorescence analysis with antibodies directed to Blbp (Chemicon), RC2 (Iowa Hybridoma Bank) and Nestin (Abcam), Prom1 (Millipore).

Western Blot. Total cell protein was isolated by placing cells in lysis buffer (50mM Hepes, pH7.5, 150 mM NaCl, 1mM EDTA, 2.5mM EGTA, 0.1% Tween 20, 20mM NaF, 0.3mM NaVO4, 1:10 protease inhibitor cocktail [Sigma]). Protein concentrations were determined using

BCA protein assay kit (Pierce). 40µg of protein was run on a 4-15% Criterion precast gel (Bio-Rad) and blotted with EphB2 antibody (1:500, Sigma).

NSC implants and ependymoma generation in the mouse

eGFP$^+$/RFP$^+$ NSCs were resuspended in Matrigel (BD BioScience) at a density of 400 x 10^6 cells/ml. Cells (2 x 10^6/5µl) were implanted into the cerebral cortex of CD-1 nu/nu immunocompromised mice exactly as described (main reference section, 7). Mice were subject to daily clinical assessment for neurological signs of brain tumor.

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Supplemental Data Legends.

Supplemental Figures.

Supplemental Figure 1. Overview of the integrated strategy to catalog and validate genome-wide expression and copy number alterations among 278 human ependymomas. Green boxes denote assays employing RNA. Blue boxes denote assays employing DNA. Boxes also include references to Figures and Tables that report the specific analyses described.

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Supplemental Figure 4. Impact of large chromosomal changes on gene expression in ependymomas. (**a**) Large chromosomal alterations that drive gene expression change in supratentorial tumors. (**b**) Large chromosomal alterations that drive gene expression change in posterior fossa tumors. (**c**) Large chromosomal alterations driving gene expression changes that affect subgroup C and subgroup E and F. **(d)** Large chromosomal alterations driving gene expression changes that affect subgroup C and subgroup F and H.

Supplemental Figure 5. Blbp-eGFP$^+$ cells are multipotent NSCs. (a) FACS analysis of markers of neuronal (Beta III tubulin), astrocytic (glial fibrillary acidic protein, Gfap) and oligodenodrocytic (CNPase) differentiation in Blbp-eGFP$^+$ cells that were disaggregated from neurospheres and then grown in the presence of differentiation (differentiated, 'dif') or control (control, 'ctl') medium (see Supplemental Methods section for more details). Two exemplary Blbp-eGFP$^+$ cell isolates for each of the three anatomic regions are shown. Similar results were obtained with Blbp-eGFP$^+$ cells isolated from the four other distinct NSC isolates. Horizontal bar marks the range of expression of the corresponding differentiation marker **(b)** Blbp-eGFP$^+$ cells of the indicated developmental, regional and genetic type were treated as detailed in **(a).** Cells were then immunostained with antibodies and scored as *neurons* if they extended long dendritic processes and were Beta III tubulin positive, *astrocytes* if they displayed a characteristic stellate appearance and were Gfap positive. Together, the assays described in both (a) and (b) show that each of the Blbp-eGFP$^+$ NSC isolates are multipotent. E=embryonic, A=adult, C=cerebral, PF=posterior fossa, SP=spinal, WT=Ink4a/Arf wild-type, null=Ink4a/Arf null.

Supplemental Figure 6. EphB2-driven tumors derived from regionally, developmentally and genetically distinct NSCs display different morphologies and growth patterns. Top two panels show low (left, scale bar=200μm) and high (right, scale bar=50μm) power micrographs of tumors derived from *EphB2* transformed embryonic hindbrain *Ink4a/Arf* null NSCs. These tumors are highly invasive with an indistinct border between normal brain (NB) and tumor (T) and high-grade glioma morphology. **NB.** Tumors derived from other hindbrain and spinal NSCs as well as adult cerebral NSCs were also glioma like. Bottom two panels show low (left, scale bar=400µm) and high (right, scale bar=50µm) power micrographs of tumors derived from *EphB2* transformed embryonic cerebral *Ink4a/Arf* null NSCs. Note these tumors display an ependymoma morphology and are relatively non-invasive. Arrows indicate the distinct, relatively intact junction between normal brain and tumor in mouse ependymomas.

Supplemental Tables.

Supplemental Table 1. Summary of the tumor site, patient age and sex and genomic analyses completed of the 204 snap frozen ependymomas employed in the current study.

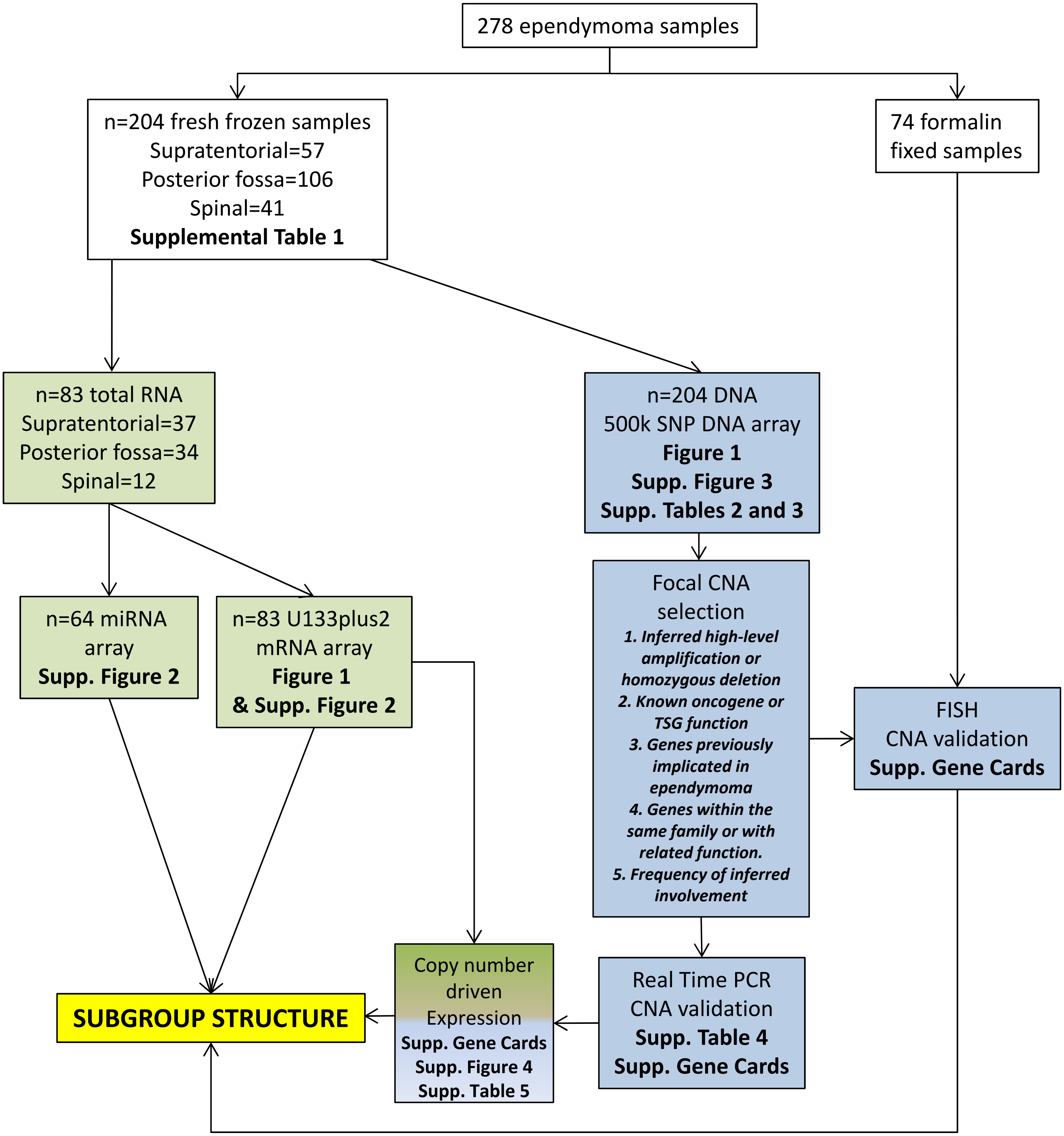
Supplemental Table 2. Summary of the incidence of large chromosomal alterations and CNAs among 203 ependymomas. (a) Columns report the percentage of supratentorial (n=57), posterior fossa (n=106) and spinal (n=41) ependymomas showing gain or loss of the indicated chromosome arm. **(b)** Reports the incidence of focal amplifications and deletions among supratentorial, posterior fossa and spinal tumors. Columns report for amplifications and deletions, the total number and percentage of tumors affected within each 'site', and the average and median number per sample of the corresponding CNA.

Supplemental Table 3. Summary of focal copy number alterations (CNAs) detected by 500K SNP DNA microarray analysis among 204 snap frozen ependymomas. Columns in the two tables report for each CNA: (1) the chromosome; (2) start and (3) end point base pair, (4) the minimal size of the CNA; (5, 7, 9) the number (n) and (6, 8, 10) percentage of supratentorial (ST), posterior fossa (PF) and spinal (SP) tumors affected by the CNA; (11) the sample reference numbers from Supplemental Table 1 of affected samples; (12) the number of RegSeq genes contained with the CNA and (13) their gene symbols. **(a)** Focal amplifications. **(b)** Focal deletions. **NB.** All validated CNAs are reported separately within the Supplemental Gene Cards.

Supplemental Table 4. Real-Time Polymerase Chain Reaction (RT-PCR) validation of focal CNAs among 203 ependymomas. Columns report: (1) the chromosome; (2) cytoband; (3) target gene within the CNA assayed by RT-PCR; (4) whether (+) or not (-) the CNA is a known copy normal variation (CNV); (5) the Gene Card number; (6) the average copy number (normalized to Chromosome 2 control [*CPO*, chromosome 2q33.3, see Supplemental Methods]) of the target gene in samples inferred to have the CNA; (7) the average copy number (normalized to Chromosome 2 control [see Supplemental Methods]) of the target gene in samples inferred to be diploid and the CNA locus (Control); (8) the ratio of columns (6) and (7); (9 to 11) the primers and probe used in RT-PCR. **NB. The table includes 50 of the 51 validated regions since *AMP#6 1q43, EXO1* was validated by FISH alone and not subject to RT-PCR.**

Supplemental Table 5. Summary of genes within validated CNAs demonstrating evidence of copy number driven expression. Columns in the two tables report for each CNA: (1) the Gene Card number; (2) the genes in the region (3) genes demonstrating evidence of copy number driven expression regardless of tumor subgroup; (4) genes demonstrating evidence of copy number driven expression within a specific subgroup.

Supplemental Table 6. Summary of the most significant differentially expressed orthologs observed in both EphB2-driven mouse and human subgroup D ependymomas. Orthologs showing agreement of expression (i.e., common over- or underexpression in ependymomas in the two species) with a relative differential expression at P<0.00005 level are shown. Columns report for each ortholog: (1) the human chromosome; (2) human cytoband (3) start point base pair, (4) end point base pair (5) human gene symbol, (6) human Affymetrix probe ID, (7) mouse Affymetrix probe ID, (8) role in neural tissues, (9) validated target gene in subgroup D [Y=Yes, N=No, SNP=inferred alteration in ependymoma not yet validated, (10) human subgroup D expression Log Ratio, (11) p value of t-test differential expression in human subgroup D, (12) mouse ependymoma expression Log Ratio, (13) p value of t-test differential expression in mouse ependymoma.



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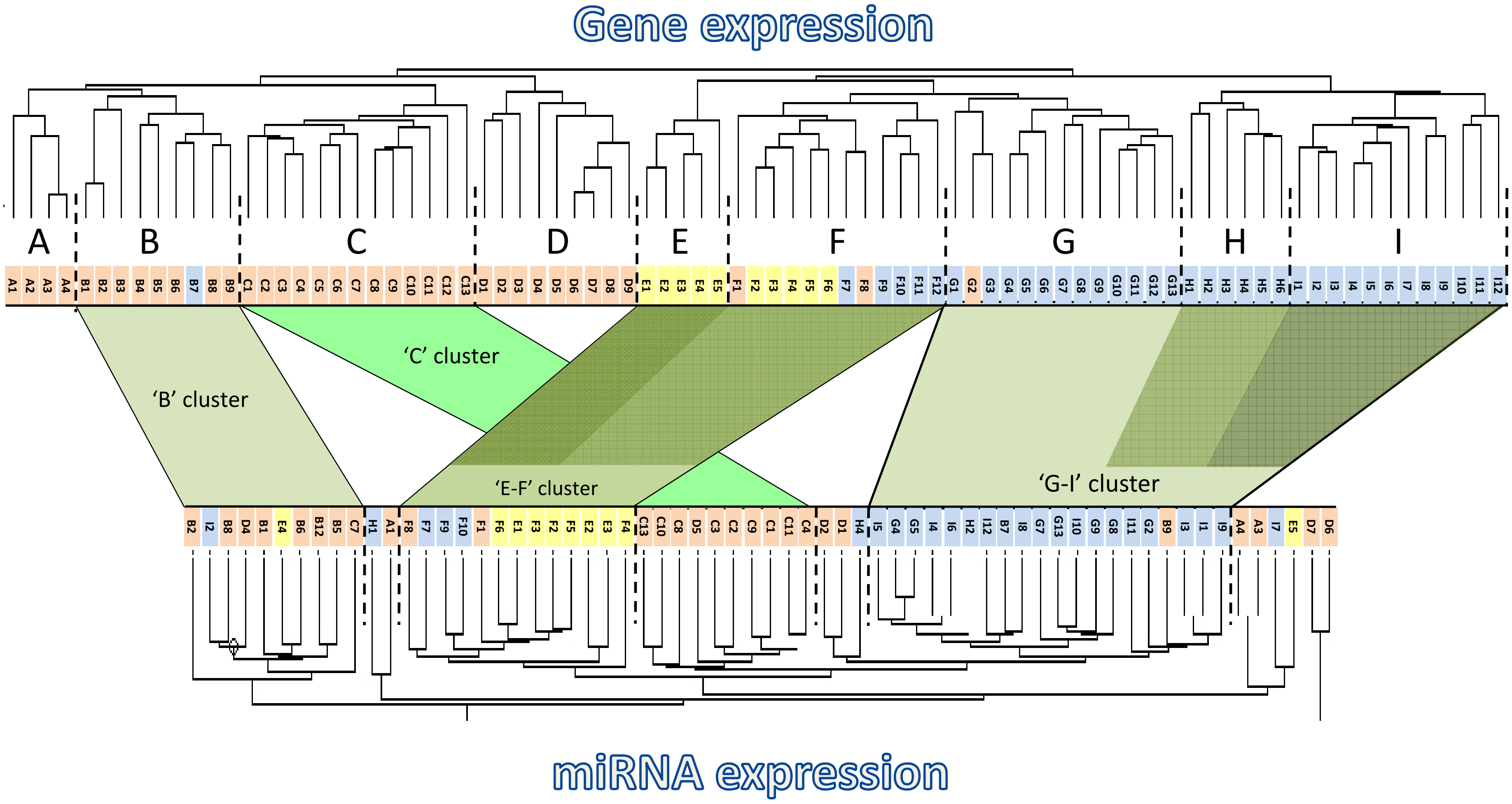

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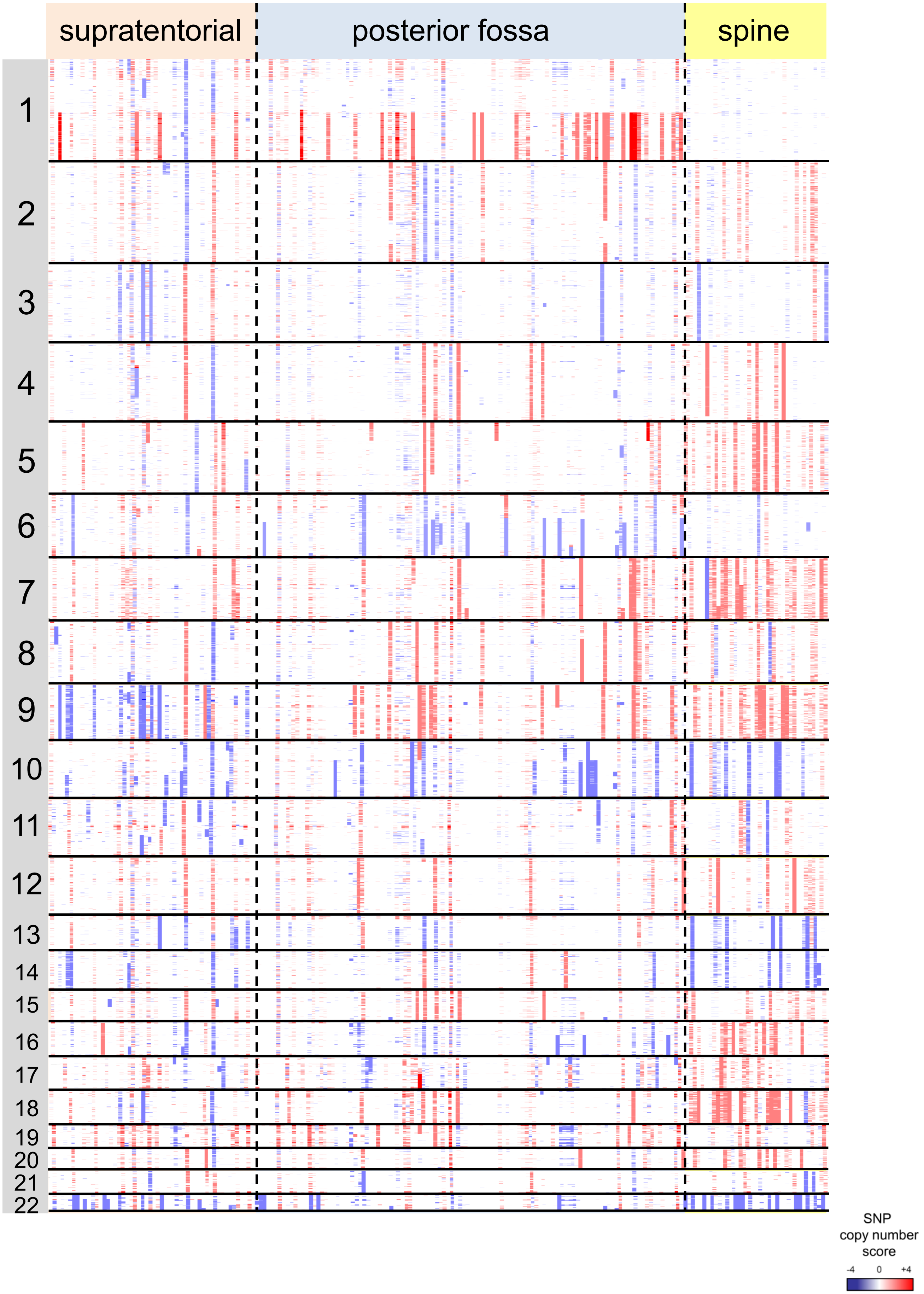
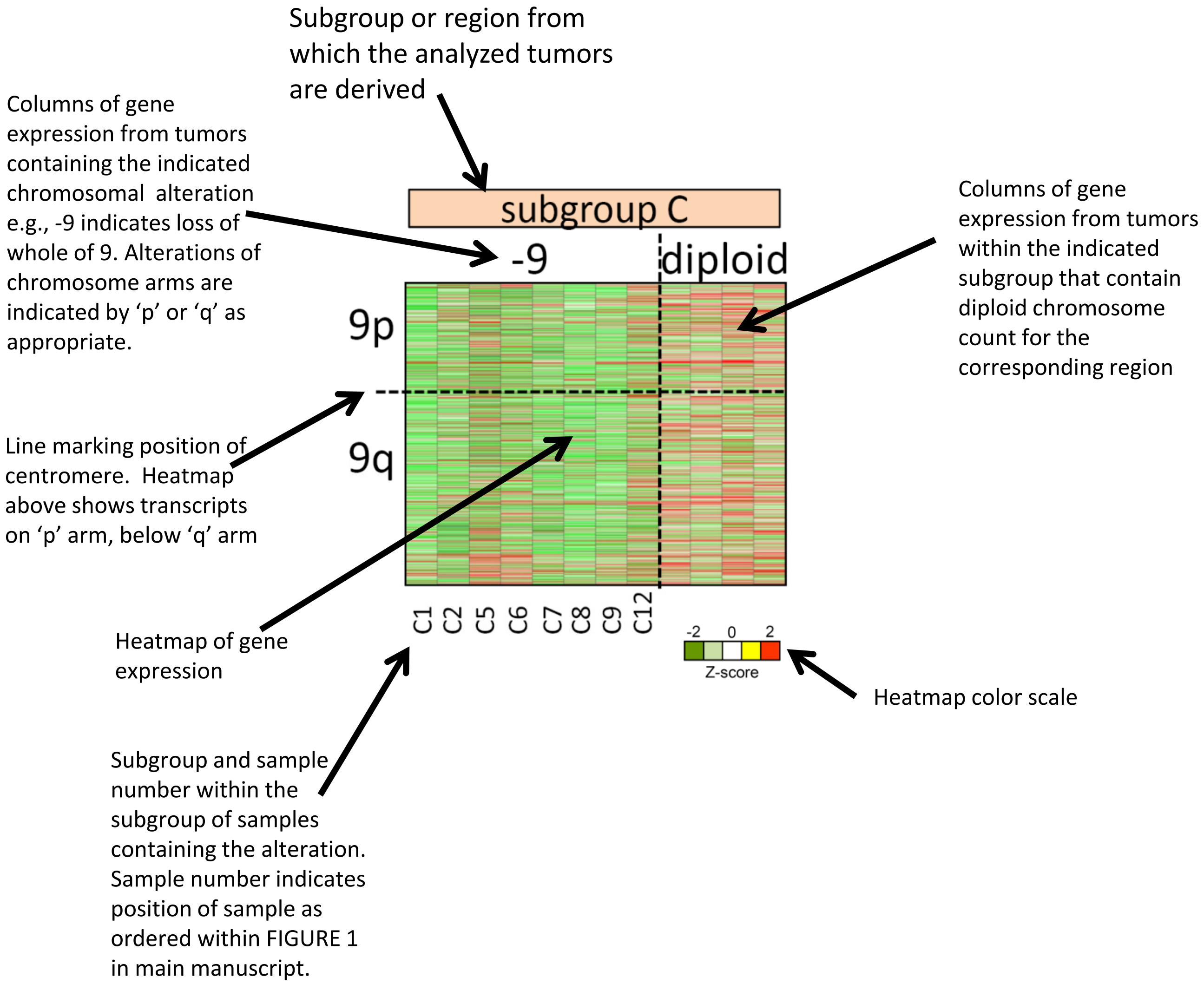

supratentorial
posterior fossa
spine
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
SNP
copy number
score
-4
0
+4

Supplemental Figure 4. Impact of large chromosomal changes on gene expression in ependymomas. Figures report the impact of large chromosomal alterations on gene expression within tumors from the same region or disease subgroup.

Chromosome expression card key



Subgroup or region from which the analyzed tumors are derived

Columns of gene expression from tumors containing the indicated chromosomal alteration e.g., -9 indicates loss of whole of 9. Alterations of chromosome arms are indicated by ‘p’ or ‘q’ as appropriate.

Columns of gene expression from tumors within the indicated subgroup that contain diploid chromosome count for the corresponding region

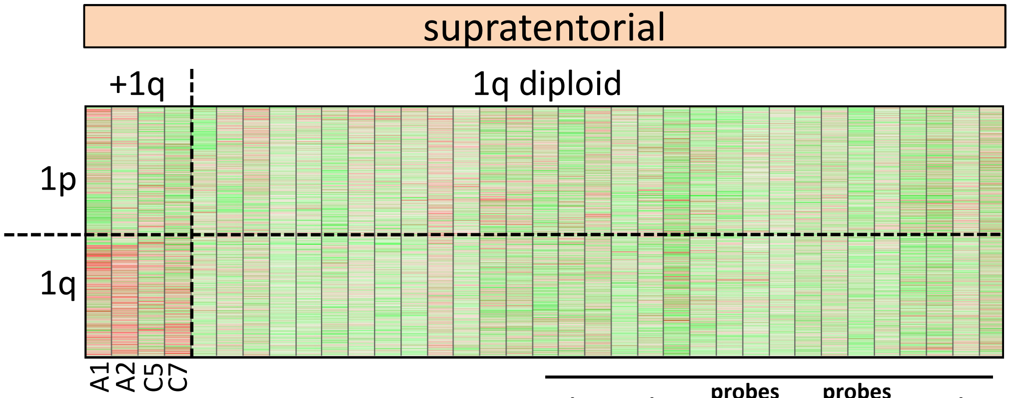
Line marking position of centromere. Heatmap above shows transcripts on ‘p’ arm, below ‘q’ arm

Heatmap of gene expression

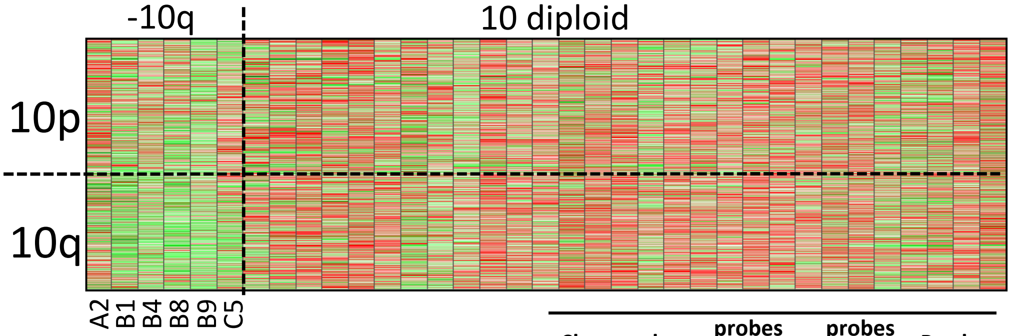
Heatmap color scale

Subgroup and sample number within the subgroup of samples containing the alteration. Sample number indicates position of sample as ordered within FIGURE 1 in main manuscript.

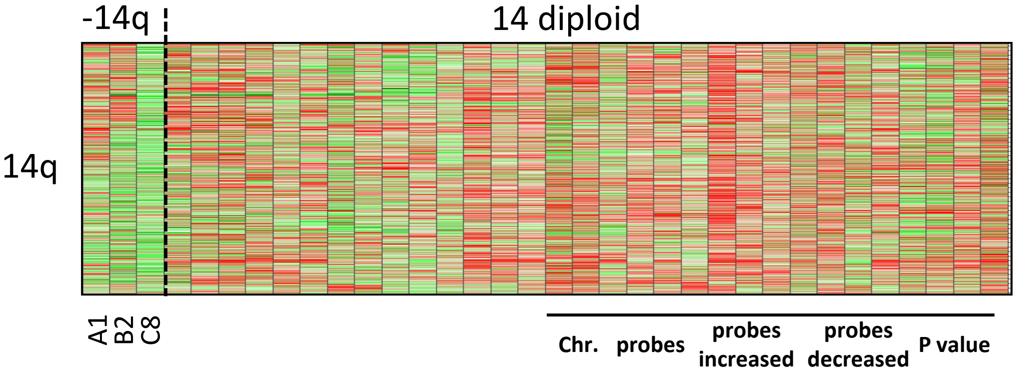
Supplemental Figure 4a. Large chromosomal alterations that drive gene expression change in supratentorial tumors.



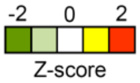
Chr.	probes	probes increased	probes decreased	P value
1q	1893	198	33	<0.0001



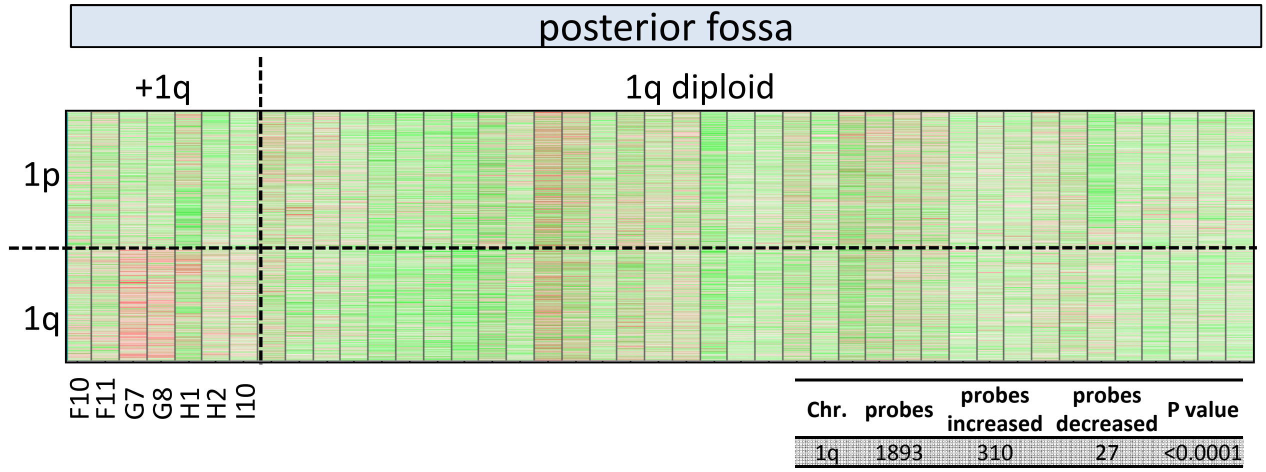
Chr.	probes	probes increased	probes decreased	P value
10q	1224	5	74	0.0005



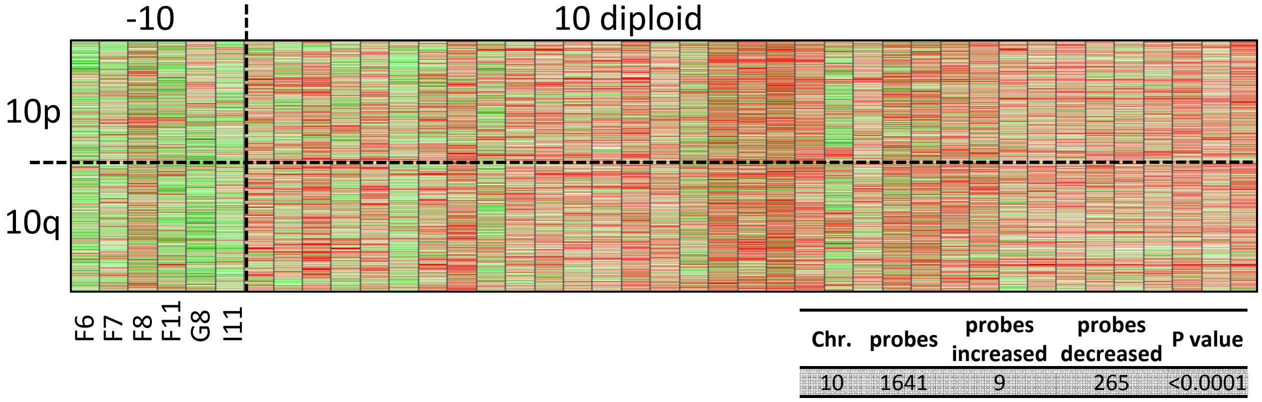
Chr.	probes	probes increased	probes decreased	P value
14q	1350	1	88	0.005



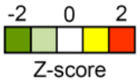
Supplemental Figure 4b. Large chromosomal alterations that drive gene expression change in posterior fossa tumors.



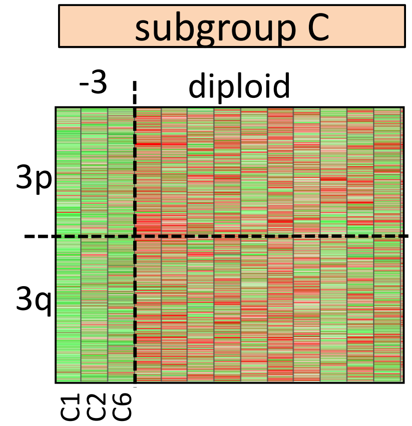
Chr.	probes	probes increased	probes decreased	P value
1q	1893	310	27	<0.0001



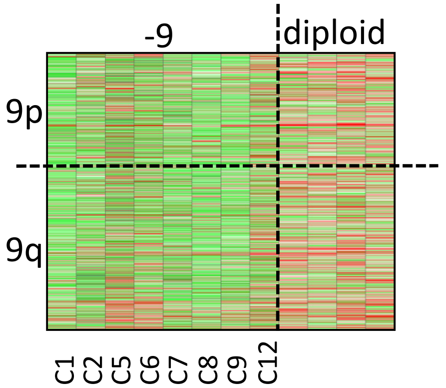
Chr.	probes	probes increased	probes decreased	P value
10	1641	9	265	<0.0001



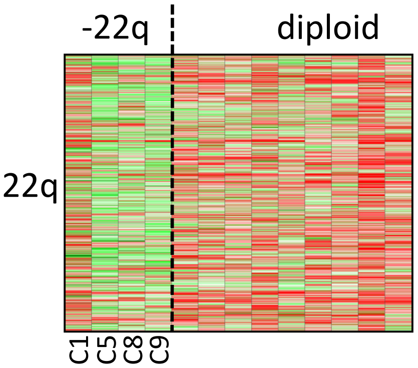
Supplemental Figure 4c. Large chromosomal alterations driving gene expression changes that affect subgroup C and subgroup E and F



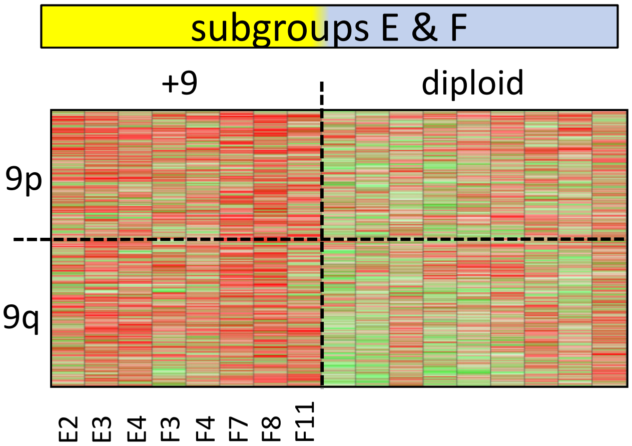
Chr.	probes	probes increased	probes decreased	P value
3	2353	3	247	0.004



Chr.	probes	probes increased	probes decreased	P value
9	1653	4	308	0.0007



Chr.	Probes	probes increased	probes decreased	P value
22	1008	2	76	0.002



Chr.	probes	probes increased	probes decreased	P value
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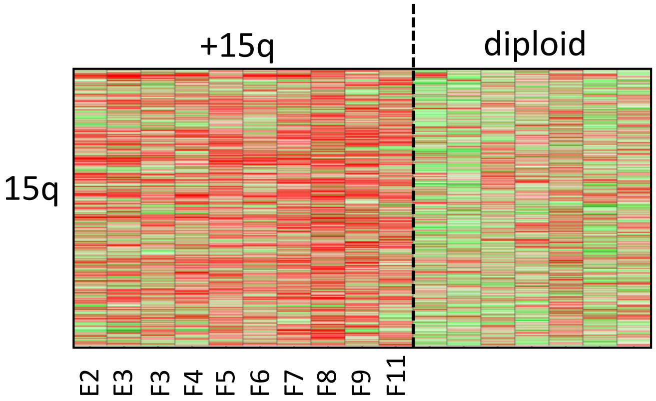
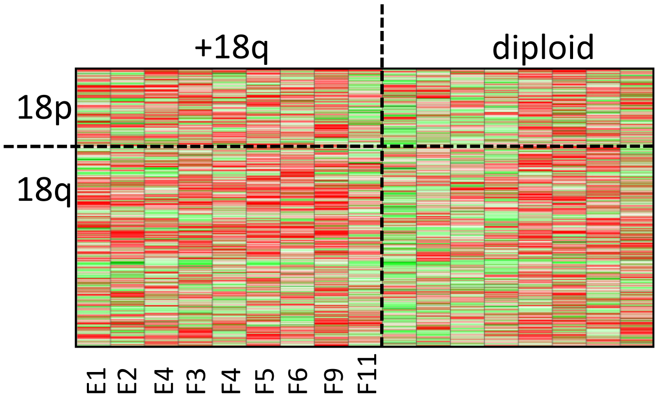
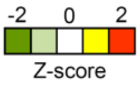


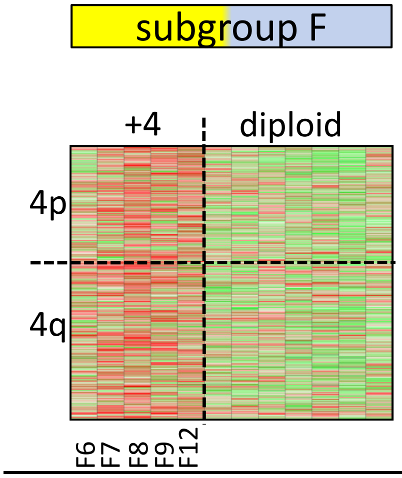
Chr.	probes	probes increased	probes decreased	P value
15	1307	87	3	<0.0001



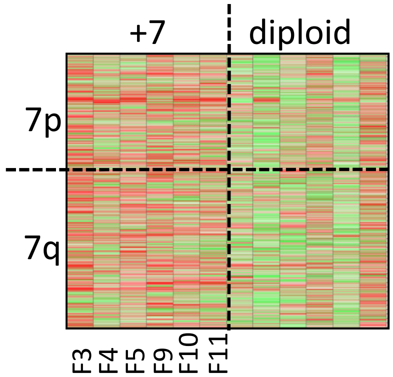
Chr.	probes	probes increased	probes decreased	P value
18	675	33	3	<0.0001



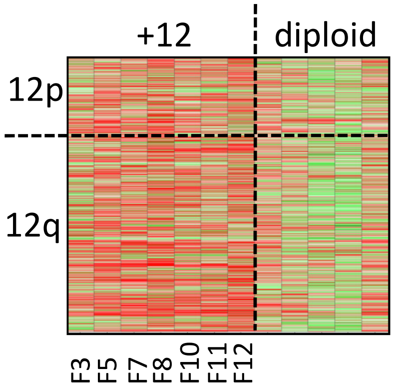
Supplemental Figure 4d. Large chromosomal alterations driving gene expression changes that affect subgroup C and subgroup F and H



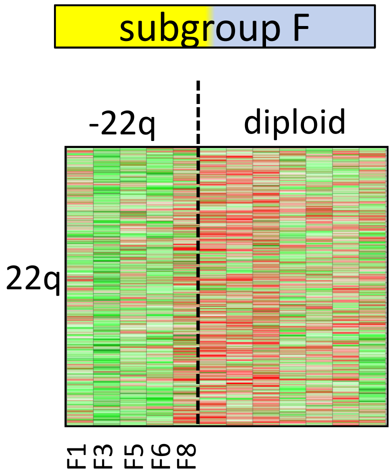
Chr.	probes	probes increased	probes decreased	P value
4	1630	60	2	0.002



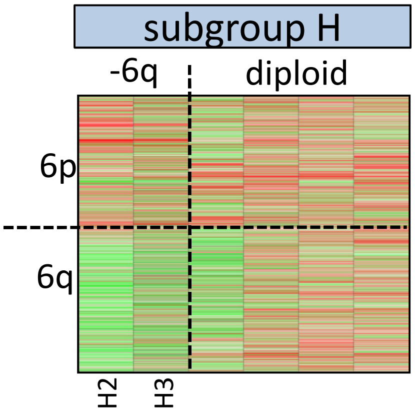
Chr.	probes	probes increased	probes decreased	P value
7	2007	77	4	0.004

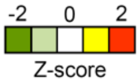


Chr.	probes	probes increased	probes decreased	P value
12	2143	50	0	0.009



Chr.	probes	probes increased	probes decreased	P value
22	1008	3	50	0.003





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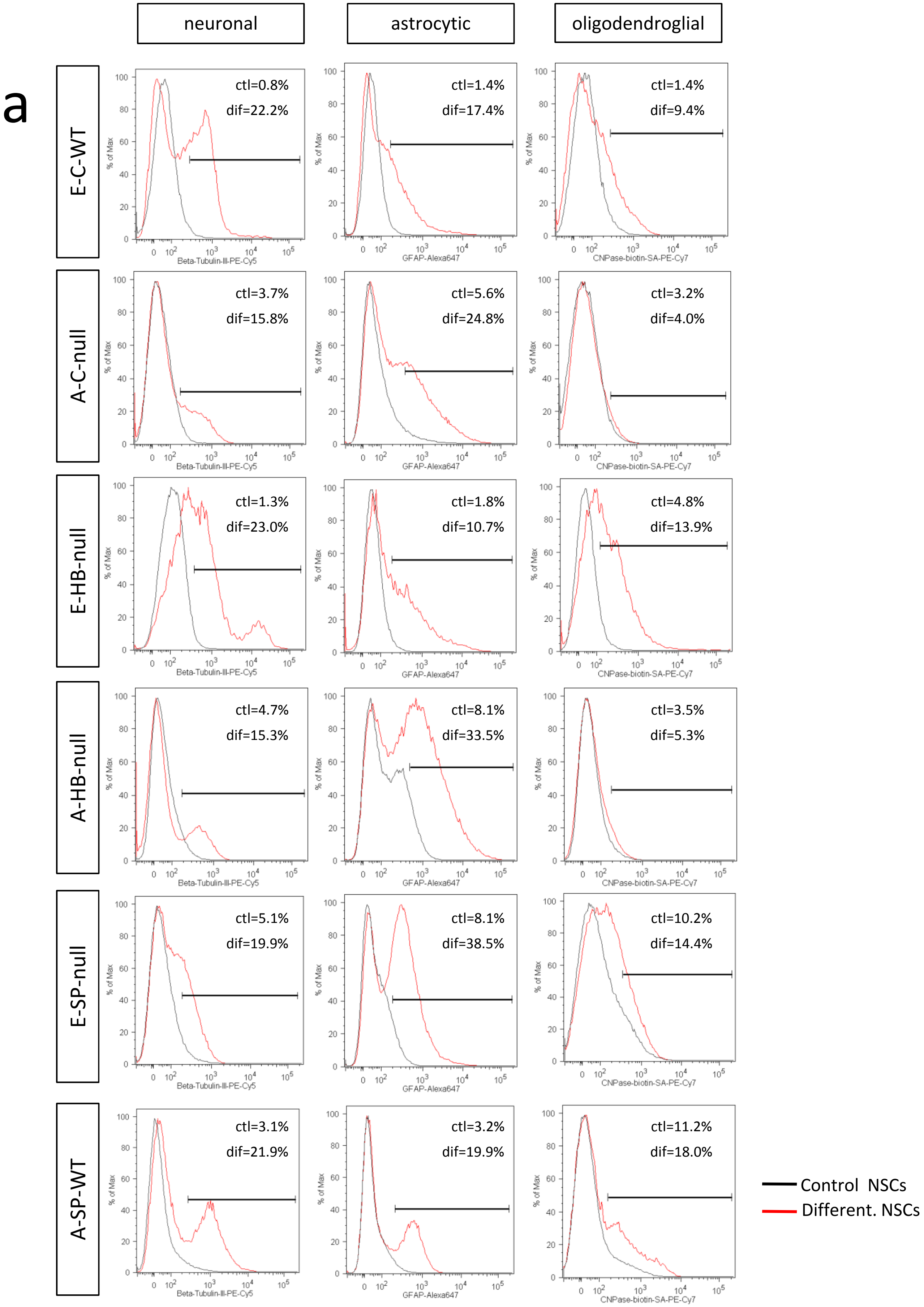
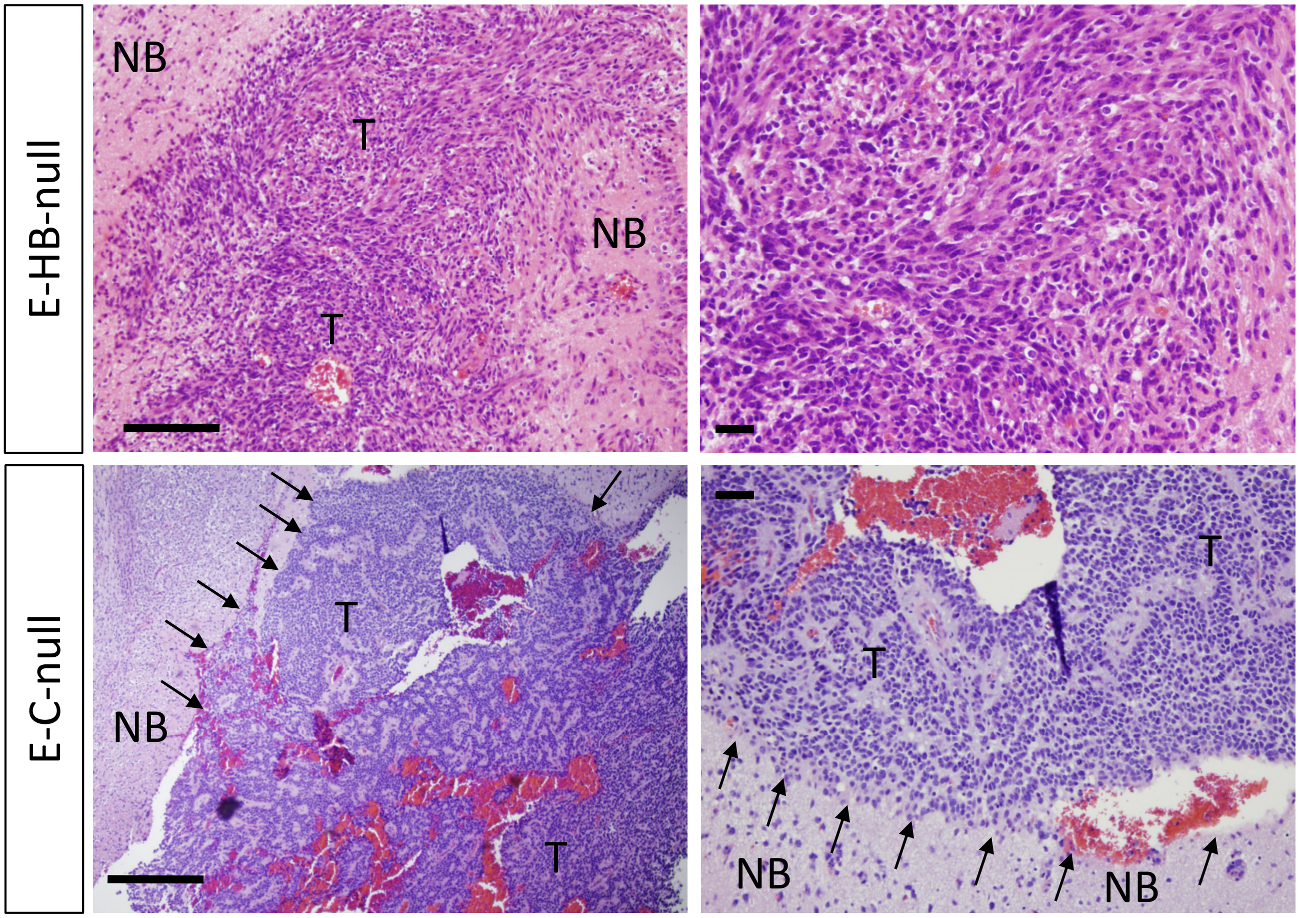

a
neuronal
astrocytic
oligodendroglial
E-C-WT
ctl=0.8%
dif=22.2%
ctl=1.4%
dif=17.4%
ctl=1.4%
dif=9.4%
A-C-null
ctl=3.7%
dif=15.8%
ctl=5.6%
dif=24.8%
ctl=3.2%
dif=4.0%
E-HB-null
ctl=1.3%
dif=23.0%
ctl=1.8%
dif=10.7%
ctl=4.8%
dif=13.9%
A-HB-null
ctl=4.7%
dif=15.3%
ctl=8.1%
dif=33.5%
ctl=3.5%
dif=5.3%
E-SP-null
ctl=5.1%
dif=19.9%
ctl=8.1%
dif=38.5%
ctl=10.2%
dif=14.4%
A-SP-WT
ctl=3.1%
dif=21.9%
ctl=3.2%
dif=19.9%
ctl=11.2%
dif=18.0%
% of Max
0
20
40
60
80
100
0
10^2
10^3
10^4
10^5
Beta-Tubulin-III-PE-Cy5
GFAP-Alexa647
CNPase-biotin-SA-PE-Cy7
Control NSCs
Different. NSCs

b

	morphology + immunophenotype	
RG	Beta III Tub (%)	Gfap (%)
E-C-WT	25.2	17.2
E-C-NULL	7.8	17.1
A-C-WT	7.4	14.1
A-C-NULL	2.2	9.7
E-HB-WT	18.4	26.8
E-HB-NULL	50.7	13.6
A-HB-WT	26.5	23.0
A-HB-NULL	19.9	25.1
E-SP-WT	23.1	21.2
E-SP-NULL	NA	NA
A-SP-WT	18.1	13.0
A-SP-NULL	23.7	23.6
E-C-WT	25.2	17.2



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Johnson, Wright et al., Supplemental Table 1

EPT Number	Site	Patient Age (years)	Patient Sex (M/F)	SNP (Y/N)	U133EXP (Y/N)	miRNA (Y/N)
EPT041	ST	11	F	Y	N	N
EPT088	ST	8	F	Y	N	N
EPT104	ST	20	F	Y	Y	Y
EPT110	ST	1.4	F	Y	N	N
EPT112	ST	6.1	F	Y	N	N
EPT114	ST	1.8	F	Y	N	N
EPT130	ST	16.3	F	Y	N	N
EPT152	ST	14.8	F	Y	Y	N
EPT230	ST	1	F	Y	N	N
EPT275	ST	1	F	Y	Y	Y
EPT294	ST	7	F	Y	Y	Y
EPT296	ST	18	F	Y	Y	Y
EPT305	ST	6	F	Y	Y	N
EPT309	ST	14	F	Y	Y	Y
EPT053	ST	9.8	F	Y	Y	N
EPT079	ST	9	F	Y	Y	Y
EPT087	ST	5	F	Y	Y	Y
EPT093	ST	3	F	Y	Y	Y
EPT099	ST	7	F	Y	Y	Y
EPT101	ST	16	F	Y	Y	Y
EPT109	ST	6.7	F	Y	N	N
EPT113	ST	6.9	F	Y	N	N
EPT125	ST	7.1	F	Y	N	N
EPT151	ST	3.8	F	Y	N	N
EPT276	ST	21	F	Y	Y	Y
EPT289	ST	17	F	Y	Y	Y
EPT304	ST	7	F	Y	Y	Y
EPT159	ST	31.6	F	Y	N	N
EPT051	ST	4.2	M	Y	Y	N
EPT068	ST	10.3	M	Y	Y	Y
EPT078	ST	6	M	Y	Y	Y
EPT084	ST	1	M	Y	Y	Y
EPT116	ST	6.3	M	Y	N	N
EPT134	ST	12.7	M	Y	N	N
EPT200	ST	39.7	M	Y	N	N
EPT205	ST	48	M	Y	N	N
EPT254	ST	21.4	M	Y	Y	Y
EPT273	ST	6	M	Y	Y	Y
EPT284	ST	10	M	Y	Y	Y
EPT303	ST	2	M	Y	Y	Y
EPT307	ST	13	M	Y	Y	Y
EPT015	ST	6	M	Y	Y	N
EPT057	ST	5.6	M	Y	Y	N

Johnson, Wright et al., Supplemental Table 1

EPT Number	Site	Patient Age (years)	Patient Sex (M/F)	SNP (Y/N)	U133EXP (Y/N)	miRNA (Y/N)
EPT061	ST	15.5	M	Y	Y	N
EPT089	ST	10	M	Y	Y	Y
EPT105	ST	8	M	Y	Y	Y
EPT116	ST	6.9	M	Y	N	N
EPT127	ST	15.7	M	Y	N	N
EPT135	ST	13	M	Y	N	N
EPT247	ST	59.2	M	Y	N	N
EPT255	ST	22.7	M	Y	Y	Y
EPT257	ST	35	M	Y	Y	Y
EPT293	ST	55	M	Y	Y	Y
EPT302	ST	4	M	Y	Y	Y
EPT306	ST	16	M	Y	Y	Y
EPT308	ST	9	M	Y	Y	N
EPT310	ST	11	M	Y	Y	Y
EPT012	PF	2.9	F	Y	N	N
EPT020	PF	2.5	F	Y	N	N
EPT043	PF	2.3	F	Y	N	N
EPT045	PF	2	F	Y	N	N
EPT054	PF	7.7	F	Y	N	N
EPT056	PF	2	F	Y	Y	N
EPT058	PF	1.8	F	Y	N	N
EPT064	PF	9.2	F	Y	Y	Y
EPT070	PF	0.4	F	Y	Y	Y
EPT076	PF	5.5	F	Y	N	N
EPT092	PF	35	F	Y	Y	N
EPT094	PF	1	F	Y	Y	Y
EPT138	PF	1.3	F	Y	N	N
EPT140	PF	7.7	F	Y	N	N
EPT142	PF	4.8	F	Y	N	N
EPT144	PF	13	F	Y	N	N
EPT192	PF	34	F	Y	N	N
EPT220	PF	44.2	F	Y	N	N
EPT250	PF	8	F	Y	N	N
EPT281	PF	1	F	Y	Y	Y
EPT005	PF	3.7	F	Y	N	N
EPT011	PF	1.8	F	Y	Y	Y
EPT021	PF	6	F	Y	N	N
EPT046	PF	12.2	F	Y	N	N
EPT069	PF	3.5	F	Y	N	N
EPT075	PF	4.5	F	Y	N	N
EPT083	PF	2	F	Y	N	N
EPT103	PF	9	F	Y	Y	Y
EPT117	PF	2.5	F	Y	N	N

Johnson, Wright et al., Supplemental Table 1

EPT Number	Site	Patient Age (years)	Patient Sex (M/F)	SNP (Y/N)	U133EXP (Y/N)	miRNA (Y/N)
EPT129	PF	2.6	F	Y	N	N
EPT139	PF	3.8	F	Y	N	N
EPT141	PF	8.6	F	Y	N	N
EPT143	PF	7.2	F	Y	N	N
EPT206	PF	48	F	Y	N	N
EPT219	PF	25.5	F	Y	N	N
EPT222	PF	13.1	F	Y	N	N
EPT226	PF	6.4	F	Y	N	N
EPT272	PF	1	F	Y	Y	Y
EPT283	PF	1	F	Y	Y	Y
EPT297	PF	2	F	Y	Y	Y
EPT002	PF	3.6	M	Y	Y	Y
EPT001	PF	2.6	M	Y	N	N
EPT008	PF	8.6	M	Y	N	N
EPT010	PF	2.4	M	Y	Y	N
EPT018	PF	2.8	M	Y	Y	N
EPT024	PF	2	M	Y	N	N
EPT026	PF	5.7	M	Y	Y	Y
EPT028	PF	2.6	M	Y	N	N
EPT032	PF	3.3	M	Y	Y	Y
EPT038	PF	2.8	M	Y	N	N
EPT047	PF	14.8	M	Y	N	N
EPT049	PF	0.66	M	Y	N	N
EPT060	PF	2.4	M	Y	N	N
EPT062	PF	2.6	M	Y	N	N
EPT066	PF	2.6	M	Y	Y	Y
EPT080	PF	1	M	Y	N	N
EPT082	PF	6	M	Y	Y	N
EPT090	PF	15	M	Y	N	N
ET106	PF	61	M	Y	Y	N
EPT124	PF	2.6	M	Y	N	N
EPT128	PF	5.4	M	Y	N	N
EPT132	PF	2.8	M	Y	N	N
EPT136	PF	12.8	M	Y	N	N
EPT150	PF	2.5	M	Y	N	N
EPT197	PF	6.9	M	Y	N	N
EPT228	PF	0.7	M	Y	N	N
EPT256	PF	45	M	Y	Y	Y
EPT279	PF	6	M	Y	N	N
EPT286	PF	1	M	Y	Y	Y
EPT288	PF	10	M	Y	N	N
EPT290	PF	1	M	Y	Y	Y
EPT292	PF	8	M	Y	Y	Y

Johnson, Wright et al., Supplemental Table 1

EPT Number	Site	Patient Age (years)	Patient Sex (M/F)	SNP (Y/N)	U133EXP (Y/N)	miRNA (Y/N)
EPT298	PF	8	M	Y	Y	Y
EPT311	PF	8	M	Y	N	N
EPT009	PF	7.3	M	Y	Y	N
EPT017	PF	11.7	M	Y	N	N
EPT019	PF	1.8	M	Y	N	N
EPT023	PF	2.5	M	Y	Y	N
EPT025	PF	1.6	M	Y	Y	N
EPT027	PF	2.3	M	Y	N	N
EPT029	PF	3.6	M	Y	N	N
EPT034	PF	2.2	M	Y	N	N
EPT039	PF	2.8	M	Y	N	N
EPT042	PF	2.8	M	Y	N	N
EPT044	PF	44	M	Y	N	N
EPT048	PF	1.3	M	Y	N	N
EPT050	PF	13	M	Y	Y	N
EPT055	PF	3.3	M	Y	N	N
EPT063	PF	1	M	Y	N	N
EPT067	PF	6	M	Y	Y	N
EPT071	PF	8	M	Y	Y	Y
EPT077	PF	8.8	M	Y	N	N
EPT081	PF	9	M	Y	N	N
EPT095	PF	7	M	Y	Y	Y
EPT107	PF	2	M	Y	Y	Y
EPT111	PF	7	M	Y	N	N
EPT131	PF	2.9	M	Y	N	N
EPT133	PF	4.9	M	Y	N	N
EPT137	PF	13.3	M	Y	N	N
EPT145	PF	6.9	M	Y	N	N
EPT147	PF	7.7	M	Y	N	N
EPT188	PF	9.8	M	Y	N	N
EPT253	PF	8.8	M	Y	N	N
EPT274	PF	37	M	Y	Y	Y
EPT278	PF	6	M	Y	Y	Y
EPT287	PF	74	M	Y	N	N
EPT312	SP	1	F	Y	N	N
EPT108	SP	18	F	Y	N	N
EPT126	SP	7.3	F	Y	N	N
EPT171	SP	35.4	F	Y	N	N
EPT217	SP	44.3	F	Y	N	N
EPT235	SP	53.7	F	Y	N	N
EPT239	SP	29.3	F	Y	N	N
EPT277	SP	31	F	Y	Y	Y
EPT315	SP	1	F	Y	Y	Y

Johnson, Wright et al., Supplemental Table 1

EPT Number	Site	Patient Age (years)	Patient Sex (M/F)	SNP (Y/N)	U133EXP (Y/N)	miRNA (Y/N)
EPT013	SP	10	F	Y	N	N
EPT059	SP	11.4	F	Y	N	N
EPT175	SP	36	F	Y	N	N
EPT209	SP	49	F	Y	N	N
EPT237	SP	61.5	F	Y	N	N
EPT295	SP	41	F	Y	Y	Y
EPT314	SP	5	M	Y	Y	Y
EPT313	SP	5	M	Y	Y	Y
EPT014	SP	9.2	M	Y	N	N
EPT022	SP	17.4	M	Y	N	N
EPT100	SP	51	M	Y	Y	Y
EPT102	SP	7	M	Y	Y	Y
EPT155	SP	39.9	M	Y	N	N
EPT157	SP	31.9	M	Y	N	N
EPT181	SP	45.8	M	Y	N	N
EPT185	SP	49.8	M	Y	N	N
EPT208	SP	18.2	M	Y	N	N
EPT245	SP	56.8	M	Y	N	N
EPT260	SP	42	M	Y	Y	Y
EPT065	SP	11.7	M	Y	Y	Y
EPT091	SP	36	M	Y	Y	Y
EPT153	SP	16	M	Y	N	N
EPT156	SP	40.7	M	Y	N	N
EPT158	SP	23.1	M	Y	N	N
EPT177	SP	46.9	M	Y	N	N
EPT193	SP	15.9	M	Y	N	N
EPT198	SP	50.2	M	Y	N	N
EPT203	SP	58	M	Y	N	N
EPT244	SP	31.8	M	Y	N	N
EPT280	SP	27	M	Y	N	N
EPT285	SP	17	M	Y	Y	Y
EPT291	SP	59	M	Y	Y	Y
	ST (n=57) PF (n=106) SP (n=41)	Average ST (13.2) Average PF (8.8) Average SP (30.3)	F (83) M (121)	204	83	64

Supplemental Table 2a: Summary of the incidence of large chromosomal alterations among 203 ependymomas: supratentorial (n=57) , posterior fossa (n=106) and spinal (n=41) ependymomas

Chromosome	ST (%)		PF (%)		SP (%)		Chi-square P-value
	gain	loss	gain	loss	gain	loss	
1p	0	3.5	0	0	0	0	0.1183
1q	8.8	1.7	20.7	0	4.8	0	**0.0154**
2p	1.7	1.7	2.8	0.9	2.4	0	1.0000
2q	1.7	1.7	0.9	0.9	2.4	0	1.0000
3p	3.5	7.0	0	0	0	4.8	**0.0086**
3q	3.5	7.0	0	0	0	4.8	**0.0082**
4p	1.7	1.7	4.7	0	7.3	0	0.3791
4q	1.7	3.5	4.7	0	7.3	0	0.1168
5p	3.5	1.7	5.7	0	17.1	0	**0.0195**
5q	1.7	1.7	1.8	0	17.1	0	**0.0006**
6p	1.7	3.5	1.8	2.8	2.4	2.4	1.0000
6q	0	3.5	0	11.3	0	2.4	0.0878
7p	3.5	0	8.5	0	19.5	2.4	**0.0090**
7q	5.3	0	4.7	0	19.5	2.4	**0.0029**
8p	1.7	3.5	5.7	0	4.8	2.4	0.3008
8q	1.7	1.7	7.5	0	2.4	2.4	0.2195
9p	1.7	21.0	9.4	0	26.8	0	**0.0001**
9q	3.5	17.5	6.6	0	26.8	0	**0.0001**
10p	0	5.3	0	4.7	0	12.1	0.2411
10q	0	8.8	0	9.4	0	12.1	0.9074
11p	1.7	8.8	0.9	0	4.8	4.8	**0.0190**
11q	3.5	3.5	0.9	0	4.8	4.8	0.0996
12p	1.7	0	2.8	0	9.8	0	0.1072
12q	3.5	0	2.8	0	9.8	0	0.2081
13	0	7.0	0.9	0.9	0	14.6	**0.0053**
14	0	7.0	1.8	0.9	0	14.6	**0.0088**
15	3.5	0	5.7	0	7.3	0	0.7874
16p	1.7	3.5	0	3.8	21.9	0	**0.0001**
16q	1.7	3.5	0	4.7	21.9	0	**0.0001**
17p	1.7	3.5	2.8	3.8	12.2	2.4	0.1068
17q	1.7	1.7	0.9	1.8	9.8	0	0.0524
18p	0	3.5	7.5	0	39.0	2.4	**0.0001**
18q	1.7	3.5	7.5	0	36.6	2.4	**0.0001**
19p	3.5	3.5	8.5	4.7	12.2	0	0.3524
19q	5.3	1.7	6.6	1.8	7.3	0	0.9510
20p	3.5	1.7	1.8	0	22.0	0	**0.0001**
20q	1.7	1.7	1.8	0	22.0	0	**0.0002**
21q	3.5	1.7	0.9	0.9	0	4.8	0.2998
22q	1.7	19.3	1.8	7.5	2.4	36.6	**0.0014**

Percentage of samples affected

deletions--gains

>30%	**>20-<30%**	**>10-<20%**	**0**	**>10-<20%**	**>20-<30%**	**>30%**

Supplemental Table 2b: Summary of the distribution of focal amplifications and deletions among 203 ependymomas: supratentorial (n=57), posterior fossa (n=106) and spinal (n=41) ependymomas

Tumor site	**Focal Amplifications**			**Focal Deletions**		
	Total samples (%)	Average per sample	Median per sample	Total samples (%)	Average per sample	Median per sample
Supratentorial	32 (56)	5.8	2	39 (68)	6.2	2
Posterior Fossa	64 (60)	10.6	1	70 (66)	6.3	1
Spine	22 (54)	9.1	1	24 (56)	5.4	1

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
1	2869431	2902617	0.03	2	3.5	7	6.6	1	2.4	STept015, PFept027, PFept028, PFept034, PFept055, PFept056, PFept128, PFept281, SPept295, STept308	1	TLR5
1	116080654	116108285	0.03	2	3.5	8	7.5	2	4.9	STept015, PFept032, PFept046, PFept047, PFept049, PFept050, PFept056, SPept277, PFept281, PFept283, SPept295, STept308	1	NHLH2
1	198898833	198920273	0.02	3	5.3	7	6.6	0	0.0	STept015, PFept021, PFept032, PFept047, PFept055, PFept056, PFept064, PFept141, STept307, STept308	1	LGR6
2	236893003	236912344	0.02	1	1.8	7	6.6	2	4.9	PFept027, PFept028, PFept029, PFept032, PFept046, PFept055, PFept060, SPept260, SPept277, STept296	1	ASB18

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
2	238857935	239130995	0.27	2	3.5	7	6.6	2	4.9	STept015, PFept027, PFept028, PFept032, PFept046, PFept055, PFept128, SPept260, PFept283, SPept295, STept308	5	ASB1, HES6, ILKAP, PER2, TRAF3IP1
3	41866	127592	0.09	4	7.0	7	6.6	0	0.0	PFept026, PFept064, PFept081, PFept082, STept084, PFept092, STept093, PFept095, STept099, STept105, PFept107	2	HGD, NDUFB4
3	8777046	8791344	0.01	3	5.3	7	6.6	2	4.9	STept015, PFept032, PFept046, PFept047, PFept049, PFept056, PFept058, SPept277, PFept283, SPept295, STept296, STept308	1	OXTR
3	60502519	60518523	0.02	4	7.0	8	7.5	2	4.9	PFept025, PFept026, PFept029, PFept032, PFept046, PFept250, STept257, STept276, SPept277, PFept279, SPept280, PFept283, STept296, STept307	1	FHIT

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
3	71850103	71911932	0.06	3	5.3	7	6.6	1	2.4	PFept032, PFept046, PFept049, PFept050, PFept056, PFept058, STept257, SPept277, PFept283, STept296, STept308	3	EIF4E3, GPR27, PROK2
3	178385363	178407416	0.02	4	7.0	7	6.6	1	2.4	PFept005, STept015, PFept032, PFept043, PFept044, PFept049, PFept055, PFept058, STept257, SPept285, STept305, STept308	1	TBL1XR1
3	196965669	196968445	0.00	2	3.5	9	8.5	2	4.9	STept015, PFept027, PFept043, PFept044, PFept056, PFept058, PFept076, PFept128, PFept219, PFept222, SPept239, SPept277, STept308	1	MUC4
4	2203430	2439033	0.24	3	5.3	6	5.7	2	4.9	SPept014, STept015, PFept027, PFept034, PFept050, PFept055, PFept056, STept255, PFept256, SPept277, STept308	4	C4orf15, MXD4, RNF4, ZFYVE28

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
4	2780639	2852637	0.07	2	3.5	6	5.7	2	4.9	SPept014, PFept027, PFept034, PFept046, PFept050, PFept055, STept255, PFept256, SPept277, STept308	1	TNIP2
4	3406614	3619620	0.21	3	5.3	7	6.6	1	2.4	SPept014, STept015, PFept027, PFept034, PFept050, PFept055, PFept056, PFept128, STept255, PFept256, STept308	5	DOK7, FLJ35424, HGFAC, LRPAP1, RGS12
4	3766621	4093125	0.33	2	3.5	6	5.7	2	4.9	SPept014, STept015, PFept027, PFept034, PFept050, PFept055, PFept128, SPept235, PFept256, STept308	1	ADRA2C
4	6321628	6441537	0.12	2	3.5	7	6.6	2	4.9	SPept014, STept015, PFept027, PFept032, PFept034, PFept050, PFept055, PFept056, SPept059, PFept256, STept308	2	PPP2R2C, WFS1

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
4	6565679	6764292	0.20	3	5.3	5	4.7	2	4.9	SPept014, STept015, PFept027, PFept034, PFept050, PFept055, SPept059, PFept256, STept257, STept308	3	MAN2B2, MRFAP1, PPP2R2C
4	8691988	8781701	0.09	2	3.5	7	6.6	3	7.3	SPept014, STept015, PFept027, PFept032, PFept034, PFept050, PFept055, PFept056, SPept059, PFept256, SPept277, STept308	2	CPZ, GPR78
4	9783360	9802214	0.02	1	1.8	9	8.5	2	4.9	SPept014, PFept027, PFept028, PFept032, PFept046, PFept050, PFept058, PFept060, PFept063, PFept256, SPept277, STept308	1	WDR1
4	124056726	124114142	0.06	1	1.8	7	6.6	3	7.3	SPept014, PFept027, PFept032, PFept046, PFept047, PFept049, PFept256, SPept277, PFept283, SPept295, STept308	1	FGF2

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
4	183423845	183466352	0.04	2	3.5	5	4.7	3	7.3	SPept014, PFept032, PFept045, PFept046, PFept049, PFept056, SPept059, STept257, SPept277, STept308	1	MGC45800
4	187432961	187497209	0.06	2	3.5	5	4.7	4	9.8	SPept014, PFept032, PFept049, PFept050, PFept056, SPept059, PFept063, SPept235, STept257, SPept277, STept308	2	CYP4V2, DKFZP564J1
5	1322006	1404538	0.08	4	7.0	16	15.1	3	7.3	PFept008, STept015, PFept021, PFept027, PFept028, PFept032, PFept034, PFept047, PFept050, PFept055, PFept056, PFept058, SPept059, PFept075, PFept128, PFept226, STept254, STept255, SPept277, PFept279, PFept281, SPept295, STept308	2	CLPTM1L, TERT

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
5	1871630	1961980	0.09	2	3.5	12	11.3	4	9.8	STept015, PFept021, PFept027, PFept028, PFept032, PFept047, PFept055, PFept056, PFept058, SPept059, PFept128, PFept226, SPept277, PFept279, SPept280, PFept281, SPept295, STept308	2	IRX4, NDUFS6
5	6763506	6774067	0.01	4	7.0	6	5.7	1	2.4	STept015, PFept028, PFept046, PFept047, PFept050, PFept226, STept257, PFept283, SPept285, STept296, STept308	1	POLS
5	7896211	7929611	0.03	2	3.5	8	7.5	0	0.0	STept015, PFept032, PFept046, PFept049, PFept050, PFept055, PFept056, PFept058, PFept226, STept308	2	FASTKD3, MTRR
5	175880104	175996155	0.12	2	3.5	7	6.6	2	4.9	STept015, PFept027, PFept028, PFept032, PFept034, PFept047, PFept055, PFept056, SPept059, SPept277, STept308	4	KIAA1893, PCLKC, RNF44, SNCB

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
5	176658608	177422743	0.76	2	3.5	5	4.7	3	7.3	STept015, PFept027, PFept028, PFept034, PFept047, PFept055, SPept059, SPept277, SPept295, STept308	18	B4GALT7, DBN1, DDX41, DOK3, F12, FLJ10404, GRK6, LMAN2, MXD3, PDLIM7, PROP1, PRR7, PX19, RAB24, RGS14, SLC34A1, THOC3, TMED9
5	177844702	177893478	0.05	2	3.5	7	6.6	3	7.3	STept015, PFept027, PFept028, PFept032, PFept034, PFept047, PFept055, PFept058, SPept059, SPept277, SPept295, STept308	1	COL23A1
5	177903023	177934931	0.03	2	3.5	7	6.6	3	7.3	STept015, PFept027, PFept028, PFept032, PFept047, PFept049, PFept055, PFept058, SPept059, SPept277, SPept295, STept308	1	COL23A1
6	10479637	10526556	0.05	1	1.8	7	6.6	2	4.9	STept015, PFept027, PFept032, PFept047, PFept049, PFept055, PFept056, SPept277, PFept281, SPept295	1	TFAP2A

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
7	639710	810040	0.17	3	5.3	14	13.2	5	12.2	SPept014, STept015, PFept027, PFept028, PFept032, PFept034, PFept043, PFept047, PFept049, PFept050, PFept055, PFept056, PFept058, PFept128, STept254, PFept256, SPept260, SPept277, PFept281, SPept291, SPept295, STept308	6	C7orf20, CENTA1, CYP2W1, MGC11257, PRKAR1B, UNC84A
7	1941180	2526908	0.59	3	5.3	11	10.4	4	9.8	SPept014, STept015, PFept027, PFept028, PFept032, PFept034, PFept047, PFept050, PFept055, PFept056, PFept058, STept254, PFept256, SPept260, PFept281, SPept291, SPept295, STept308	11	AMZ1, C7orf27, CHST12, EIF3S9, FTSJ2, IQCE, LFNG, MAD1L1, NUDT1, SNX8, TTYH3
7	2667675	2752274	0.08	2	3.5	7	6.6	4	9.8	SPept014, PFept027, PFept034, PFept047, PFept050, PFept055, STept254, PFept256, SPept260, PFept281, SPept291, SPept295, STept308	1	CARD11

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
7	3922078	3946854	0.02	1	1.8	7	6.6	3	7.3	SPept014, STept015, PFept028, PFept032, PFept034, PFept047, PFept055, PFept128, SPept260, PFept281, SPept291	1	SDK1
7	6401482	6453914	0.05	2	3.5	9	8.5	3	7.3	SPept014, PFept032, PFept046, PFept047, PFept049, PFept050, PFept056, PFept128, STept257, SPept260, SPept277, PFept281, PFept283, STept307	2	C7orf26, ZDHHC4
7	142563019	142644608	0.08	2	3.5	6	5.7	3	7.3	SPept014, STept015, PFept032, PFept046, PFept049, PFept055, PFept056, PFept147, SPept260, SPept277, STept308	4	CLCN1, EPHA1, KIAA0773, ZYX
7	150170460	150268937	0.10	2	3.5	7	6.6	3	7.3	SPept014, PFept027, PFept028, PFept034, PFept046, PFept047, PFept055, PFept056, STept257, SPept277, SPept295, STept308	7	ABCB8, ACCN3, CDK5, CENTG3, FASTK, SLC4A2, TMUB1

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
7	156222318	156248512	0.03	2	3.5	7	6.6	3	7.3	SPept014, STept015, PFept028, PFept046, PFept055, PFept056, PFept128, SPept277, PFept283, PFept292, SPept295, STept308	1	NOM1
7	158271648	158347407	0.08	2	3.5	6	5.7	3	7.3	SPept014, PFept027, PFept028, PFept032, PFept047, SPept091, STept273, PFept292, SPept295, STept308, PFept311	1	VIPR2
8	1368018	1964808	0.60	2	3.5	7	6.6	2	4.9	SPept014, STept015, PFept027, PFept055, PFept058, SPept059, PFept128, PFept136, PFept256, PFept281, STept308	4	ARHGEF10, CLN8, DLGAP2, KBTBD11
8	4010104	4032278	0.02	3	5.3	6	5.7	1	2.4	PFept025, PFept026, PFept032, PFept046, Stept151, PFept219, STept257, SPept277, PFept283, STept296	1	CSMD1

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
8	8584520	8624542	0.04	1	1.8	7	6.6	2	4.9	SPept014, STept015, PFept032, PFept049, PFept055, PFept056, PFept058, SPept059, PFept136, PFept256	1	CLDN23
8	11575198	11610054	0.03	0	0.0	7	6.6	4	9.8	SPept014, PFept032, PFept044, PFept046, PFept049, PFept056, SPept059, PFept136, PFept256, SPept277, SPept295	1	GATA4
8	12814377	12857802	0.04	0	0.0	7	6.6	3	7.3	SPept014, PFept032, PFept046, PFept049, SPept059, PFept063, PFept136, PFept256, SPept277, PFept283	1	C8orf79
8	61743230	61789086	0.05	2	3.5	6	5.7	2	4.9	PFept032, PFept044, PFept050, PFept058, PFept063, STept257, SPept277, SPept280, PFept283, STept296	1	CHD7

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
8	140774059	140796877	0.02	1	1.8	9	8.5	3	7.3	SPept014, PFept027, PFept028, PFept032, PFept034, PFept046, SPept059, PFept128, PFept136, PFept256, SPept277, PFept283, STept308	1	KCNK9
8	142248984	142338396	0.09	2	3.5	8	7.5	3	7.3	SPept014, STept015, PFept027, PFept034, PFept055, PFept056, SPept059, PFept075, PFept136, PFept256, SPept277, PFept281, STept308	1	DENND3
8	143309560	143736649	0.43	3	5.3	10	9.4	2	4.9	SPept014, STept015, PFept027, PFept032, PFept034, PFept055, PFept056, PFept058, SPept059, STept113, PFept128, PFept136, PFept256, PFept281, STept308	3	ARC, BAI1, TSNARE1

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
8	144405211	146039965	1.63	2	3.5	10	9.4	3	7.3	SPept014, STept015, PFept027, PFept032, PFept034, PFept055, PFept056, PFept058, SPept059, PFept128, PFept136, PFept256, PFept281, SPept295, STept308	61	ADCK5, BOP1, C8orf30A, C8orf51, COMMD5, CPSF1, CYC1, CYHR1, DGAT1, EEF1D, EPPK1, EXOSC4, FAM83H, FBXL6, FOXH1, GLI4, GPAA1, GPR172A, GPT, GRINA, GSDMDC1, HSF1, KIAA1688, KIAA1875, KIFC2, LOC286076, LRRC14, LRRC24, MAF1, MAFA, MAPK15, MFSD3, MGC70857, NAPRT1, NFKBIL2, NRBP2, OPLAH, PARP10, PLEC1, PPP1R16A, PYCRL, RECQL4, RHPN1, RPL8, SCRIB, SHARPIN, SIAHBP1, SLC39A4, SPATC1, TIGD5, TOP1MT, TSTA3, VPS28, ZC3H3, ZFP41, ZNF34, ZNF517, ZNF623, ZNF696, ZNF7, ZNF707
9	487479	508675	0.02	1	1.8	6	5.7	4	9.8	PFept032, PFept046, SPept059, PFept128, PFept136, PFept137, PFept256, SPept260, SPept277, SPept295, STept308	1	ANKRD15
9	792053	862364	0.07	1	1.8	6	5.7	3	7.3	STept015, PFept027, PFept056, SPept059, PFept128, PFept136, PFept137, PFept256, SPept260, SPept295	1	DMRT1

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
9	1026552	1053193	0.03	2	3.5	6	5.7	3	7.3	STept015, PFept027, PFept032, PFept049, SPept059, PFept136, PFept137, PFept219, SPept260, SPept295, STept308	1	DMRT2
9	6608004	6646619	0.04	2	3.5	11	10.4	3	7.3	PFept032, PFept047, PFept049, PFept055, PFept056, PFept058, SPept059, PFept075, STept114, PFept128, PFept136, PFept137, STept254, PFept256, SPept260, SPept295	1	GLDC
9	133162427	134617798	1.46	1	1.8	8	7.5	2	4.9	STept015, PFept032, PFept034, PFept047, PFept055, PFept056, PFept128, PFept256, SPept277, PFept281, SPept295	18	ABO, ADAMTS13, ADAMTSL2, BRD3, C9orf7, C9orf96, DBH, REXO4, RPL7A, RXRA, SARDH, SLC2A6, SURF1, SURF2, SURF4, SURF5, SURF6, VAV2

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
9	136198806	137940702	1.74	2	3.5	10	9.4	2	4.9	STept015, PFept032, PFept034, PFept047, PFept050, PFept055, PFept056, PFept058, PFept128, PFept256, SPept277, PFept281, SPept295, STept308	66	ABCA2, AGPAT2, ANAPC2, ARRDC1, BTBD14A, C8G, C9orf139, C9orf140, C9orf142, C9orf163, C9orf37, C9orf75, C9orf86, CARD9, CLIC3, COBRA1, DPP7, EDF1, EGFL7, EHMT1, ENTPD2, ENTPD8, FAM69B, FBXW5, FLJ20245, FLJ20433, FLJ45224, FUT7, GPSM1, GRIN1, INPP5E, KIAA1984, LCN10, LCN12, LCN6, LCN8, LHX3, LOC401565, LOC441476, MAMDC4, MAN1B1, MGC14327, MGC61598, MRPL41, NDOR1, NELF, NOTCH1, NOXA1, NPDC1, PHPT1, PMPCA, PNPLA7, PTGDS, QSCN6L1, RP11-350O1, SDCCAG3, SLC34A3, SNAPC4, SSNA1, TMEM141, TRAF2, TUBB2C, UAP1L1, UNQ2541, WDR85, ZMYND19
10	133827559	133847021	0.02	2	3.5	10	9.4	2	4.9	STept015, PFept027, PFept028, PFept032, PFept034, PFept046, PFept050, PFept055, PFept056, PFept058, PFept128, SPept280, SPept295, STept308	1	C10orf39

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
10	135073302	135095235	0.02	3	5.3	19	17.9	4	9.8	PFept002, STept015, PFept024, PFept027, PFept028, PFept029, PFept032, PFept034, PFept044, PFept046, PFept049, PFept050, PFept055, PFept056, PFept058, SPept059, PFept060, PFept063, PFept076, PFept128, SPept277, SPept280, PFept283, SPept295, STept307, STept308	2	ECHS1, PAOX
11	2126350	2197791	0.07	3	5.3	7	6.6	3	7.3	SPept014, STept015, PFept027, PFept028, PFept034, PFept047, PFept055, PFept056, SPept059, PFept281, SPept295, STept304, STept308	3	IGF2AS, INS, TH
11	2667398	2692602	0.03	2	3.5	5	4.7	3	7.3	SPept014, STept015, PFept027, PFept028, PFept047, PFept055, SPept059, SPept277, PFept283, STept308	1	KCNQ1

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
11	2814194	2879069	0.06	2	3.5	5	4.7	3	7.3	SPept014, STept015, PFept027, PFept028, PFept047, PFept055, PFept056, SPept059, SPept277, STept308	4	CDKN1C, KCNQ1, KCNQ1DN, SLC22A18AS
11	6580757	6595175	0.01	3	5.3	7	6.6	1	2.4	PFept028, PFept046, PFept047, PFept055, PFept075, PFept128, STept257, PFept283, SPept295, STept307, STept308	4	ILK, KIAA0409, TAF10, TPP1
11	7993714	8066385	0.07	2	3.5	7	6.6	1	2.4	SPept014, STept015, PFept028, PFept032, PFept055, PFept056, PFept058, PFept281, PFept283, STept308	1	TUB
11	18907033	18918255	0.01	2	3.5	11	10.4	5	12.2	PFept005, SPept014, PFept018, PFept019, PFept028, PFept029, PFept039, PFept067, PFept070, STept087, STept088, PFept128, PFept188, PFept197, SPept198, SPept235, SPept245, SPept291	1	MRGPRX1

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
11	32409501	32419218	0.01	1	1.8	8	7.5	3	7.3	SPept014, PFept032, PFept044, PFept046, PFept049, PFept055, PFept056, PFept058, PFept128, SPept277, SPept295, STept308	2	WIT1, WT1
11	60449795	60484274	0.03	3	5.3	4	3.8	3	7.3	SPept014, PFept027, PFept046, PFept047, SPept277, PFept283, SPept295, STept296, STept307, STept308	2	SLC15A3, TMEM132A
11	133698952	133730902	0.03	3	5.3	5	4.7	3	7.3	SPept014, STept015, PFept027, PFept032, PFept046, PFept047, PFept056, SPept059, STept257, SPept277, STept308	1	LOC89944
12	2975009	3093017	0.12	2	3.5	8	7.5	2	4.9	PFept002, SPept014, STept015, PFept027, PFept028, PFept032, PFept049, PFept055, PFept256, SPept277, PFept281, STept308	2	TEAD4, TSPAN9

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
12	6453648	6492607	0.04	2	3.5	6	5.7	2	4.9	SPept014, STept015, PFept027, PFept032, PFept047, PFept050, PFept055, STept114, SPept157, PFept256	2	CNAP1, MRPL51
12	7908762	7963275	0.05	1	1.8	9	8.5	3	7.3	PFept002, SPept014, PFept032, PFept046, PFept047, PFept050, PFept055, PFept056, PFept075, PFept256, SPept277, SPept295, STept308	2	SLC2A14, SLC2A3
12	43236324	43310884	0.07	6	10.5	4	3.8	1	2.4	SPept014, PFept082, PFept083, STept087, STept088, STept093, STept099, PFept103, STept104, STept105, PFept107	1	NELL2
12	50488291	50598555	0.11	1	1.8	10	9.4	2	4.9	SPept014, STept015, PFept027, PFept028, PFept032, PFept044, PFept047, PFept050, PFept055, PFept056, PFept058, PFept256, SPept295	4	ACVRL1, ANKRD33, LOC401720, SCN8A

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
12	50965167	51002143	0.04	2	3.5	8	7.5	2	4.9	SPept014, STept015, PFept027, PFept028, PFept032, PFept047, PFept050, PFept055, PFept056, PFept256, SPept295, STept308	3	KRT81, KRT83, KRT86
12	51081854	51093628	0.01	2	3.5	10	9.4	1	2.4	SPept014, STept015, PFept025, PFept026, PFept027, PFept028, PFept032, PFept046, PFept047, PFept050, PFept256, PFept279, STept308	1	KRT82
12	51198620	51344781	0.15	1	1.8	8	7.5	2	4.9	SPept014, STept015, PFept027, PFept028, PFept032, PFept046, PFept047, PFept049, PFept050, PFept256, SPept277	6	KRT2, KRT5, KRT71, KRT72, KRT73, KRT74
12	66320777	66335342	0.01	3	5.3	6	5.7	3	7.3	SPept014, PFept032, PFept046, PFept047, PFept049, PFept058, STept257, SPept277, PFept283, SPept295, STept296, STept308	1	DYRK2

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
12	112767476	112782936	0.02	1	1.8	7	6.6	2	4.9	SPept014, PFept027, PFept032, PFept047, PFept049, PFept050, PFept063, PFept256, SPept280, STept296	1	RBM19
12	123281172	123584807	0.30	2	3.5	7	6.6	2	4.9	SPept014, STept015, PFept028, PFept034, PFept047, PFept050, PFept055, PFept056, PFept256, SPept277, STept308	2	FAM101A, NCOR2
12	129026825	129184406	0.16	2	3.5	8	7.5	1	2.4	SPept014, STept015, PFept027, PFept028, PFept032, PFept047, PFept050, PFept055, PFept256, PFept281, STept308	1	FZD10
12	129425575	129465840	0.04	2	3.5	7	6.6	1	2.4	SPept014, STept015, PFept027, PFept028, PFept034, PFept047, PFept050, PFept128, PFept256, STept308	1	RIMBP2

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
12	130915718	132074850	1.16	2	3.5	10	9.4	2	4.9	SPept014, STept015, PFept027, PFept028, PFept034, PFept047, PFept050, PFept055, PFept056, PFept058, PFept128, PFept256, SPept277, STept308	15	CHFR, DDX51, EP400, EP400NL, GALNT9, GOLGA3, MMP17, NOC4L, P2RX2, PGAM5, POLE, PUS1, PXMP2, SFRS8, ULK1
13	19627842	19690082	0.06	2	3.5	8	7.5	1	2.4	STept015, PFept032, PFept046, PFept047, PFept049, PFept050, PFept055, PFept056, PFept058, SPept295, STept308	1	GJB2
13	79810102	79834010	0.02	4	7.0	6	5.7	1	2.4	STept015, PFept032, PFept046, PFept049, PFept056, PFept075, STept257, SPept277, PFept283, STept296, STept308	1	SPRY2

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
14	19272965	19424016	0.15	3	5.3	15	14.2	2	4.9	PFept029, PFept044, PFept050, STept053, PFept083, PFept103, PFept107, PFept129, PFept132, PFept141, PFept147, SPept153, PFept219, PFept250, PFept256, STept276, PFept281, SPept285, PFept290, STept304	4	OR4K2, OR4M1, OR4N2, OR4Q3
14	20236123	20258525	0.02	2	3.5	5	4.7	3	7.3	PFept025, PFept046, PFept050, Stept151, SPept277, PFept279, SPept280, PFept283, SPept295, STept308	1	RNASE4
14	92247404	92293743	0.05	6	10.5	8	7.5	1	2.4	PFept025, PFept026, PFept027, PFept032, PFept050, Stept151, PFept250, STept257, STept273, PFept279, PFept283, SPept285, STept296, STept305, STept307	1	LGMN

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
14	95057986	95085817	0.03	3	5.3	8	7.5	1	2.4	PFept032, PFept044, PFept046, PFept049, PFept056, PFept058, PFept063, STept257, SPept277, PFept283, STept296, STept308	1	GLRX5
15	18824589	19178339	0.35	5	8.8	4	3.8	5	12.2	PFept011, SPept014, PFept019, SPept100, STept101, STept110, PFept132, SPept193, STept230, SPept235, PFept292, SPept295, STept296, STept309	1	LOC283755
15	19882296	19989036	0.11	6	10.5	4	3.8	3	7.3	SPept014, PFept019, PFept070, STept101, STept110, STept112, PFept132, PFept147, SPept193, STept230, SPept295, STept296, STept309	1	OR4N4
15	24562625	24579934	0.02	3	5.3	4	3.8	3	7.3	SPept014, STept015, PFept047, PFept075, PFept256, SPept277, PFept283, SPept295, STept296, STept308	1	GABRB3

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
15	38384136	38450393	0.07	2	3.5	5	4.7	4	9.8	SPept014, STept015, PFept027, PFept046, PFept076, PFept256, SPept260, SPept277, PFept283, SPept295, STept308	3	DISP2, FLJ43339, PLCB2
15	49809647	49844296	0.03	4	7.0	7	6.6	4	9.8	SPept014, STept015, SPept022, PFept032, PFept046, PFept047, PFept049, PFept056, PFept075, STept257, SPept260, SPept277, PFept283, STept296, STept308	2	LYSMD2, TMOD2
15	91404612	91435937	0.03	3	5.3	5	4.7	2	4.9	SPept014, STept015, PFept028, PFept032, PFept056, PFept128, PFept256, SPept277, STept307, STept308	1	RGMA
16	26671	81659	0.05	2	3.5	11	10.4	3	7.3	STept015, PFept027, PFept028, PFept032, PFept034, PFept044, PFept046, PFept055, SPept059, PFept064, PFept128, SPept260, PFept281, PFept283, SPept295, STept308	7	C16orf33, C16orf35, C16orf54, MPG, POLR3K, RHBDF1, ZG16

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
16	447905	487298	0.04	2	3.5	13	12.3	4	9.8	PFept002, STept015, PFept027, PFept028, PFept032, PFept034, PFept044, PFept046, PFept055, PFept056, PFept058, SPept059, PFept128, SPept260, SPept277, PFept281, PFept283, SPept295, STept308	1	RAB11FIP3
16	56783625	56796999	0.01	3	5.3	4	3.8	3	7.3	PFept025, PFept029, PFept046, STept257, SPept260, STept276, SPept277, PFept283, SPept285, STept296	1	CSNK2A2
16	83226394	83295586	0.07	1	1.8	6	5.7	3	7.3	PFept027, PFept028, PFept032, PFept049, PFept055, PFept076, SPept235, SPept260, SPept295, STept308	2	C16orf44, USP10

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
16	83586351	83640211	0.05	2	3.5	5	4.7	3	7.3	STept015, PFept027, PFept028, PFept032, PFept049, PFept055, SPept235, SPept260, SPept295, STept308	2	KIAA0513, ZDHHC7
16	83763410	84264134	0.50	2	3.5	6	5.7	4	9.8	STept015, PFept027, PFept028, PFept034, PFept055, PFept056, SPept059, PFept128, SPept235, SPept260, SPept295, STept308	2	KIAA0182, TMEM148
16	85897888	86098581	0.20	2	3.5	4	3.8	4	9.8	STept015, PFept027, PFept028, PFept055, SPept059, SPept235, SPept260, PFept281, SPept295, STept308	3	FBXO31, MAP1LC3B, ZCCHC14
16	87453490	87801384	0.35	2	3.5	9	8.5	4	9.8	STept015, PFept027, PFept028, PFept032, PFept034, PFept055, PFept056, SPept059, PFept128, SPept235, SPept260, PFept279, PFept281, SPept295, STept308	5	C16orf81, CBFA2T3, CDH15, LOC197322, TRAPPC2L

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
17	41587072	41597441	0.01	3	5.3	3	2.8	4	9.8	PFept001, SPept022, STept079, STept125, PFept129, PFept137, SPept181, SPept209, SPept260, STept305	1	KIAA1267
17	72850005	72878858	0.03	2	3.5	7	6.6	3	7.3	PFept027, PFept032, PFept034, PFept044, PFept046, PFept055, SPept059, SPept277, PFept283, SPept295, STept296, STept308	1	MARCH9
17	74979374	75322859	0.34	2	3.5	6	5.7	4	9.8	STept015, PFept025, PFept027, PFept028, PFept034, PFept055, SPept059, SPept277, SPept280, PFept281, SPept295, STept308	1	ENPP7
17	78457146	78605474	0.15	2	3.5	7	6.6	3	7.3	STept015, PFept027, PFept028, PFept034, PFept055, PFept056, SPept059, SPept091, PFept128, PFept281, SPept295, STept308	2	B3GNTL1, TBCD

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
18	5251246	5311715	0.06	2	3.5	9	8.5	3	7.3	PFept028, PFept029, PFept032, PFept044, PFept046, PFept049, PFept050, PFept058, STept257, SPept277, SPept280, PFept283, SPept285, STept308	1	ZFP161
18	44634180	44765784	0.13	2	3.5	7	6.6	1	2.4	STept015, PFept027, PFept028, PFept032, PFept034, PFept047, PFept128, PFept256, SPept260, STept308	2	KIAA0427, SMAD7
18	71039209	71062175	0.02	2	3.5	7	6.6	2	4.9	PFept027, PFept028, PFept032, PFept047, PFept049, PFept058, PFept256, SPept260, SPept277, STept296, STept308	1	ZADH2
18	72597889	72974341	0.38	2	3.5	8	7.5	1	2.4	STept015, PFept027, PFept028, PFept047, PFept055, PFept058, PFept128, PFept256, SPept260, PFept281, STept308	2	MBP, ZNF236

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
18	74748072	74914475	0.17	0	0.0	8	7.5	2	4.9	PFept027, PFept028, PFept034, PFept047, PFept058, PFept062, PFept128, PFept256, SPept260, SPept280	1	SALL3
18	75551903	75740573	0.19	2	3.5	12	11.3	3	7.3	STept015, PFept024, PFept027, PFept028, PFept034, PFept047, PFept049, PFept050, PFept055, PFept056, PFept058, PFept128, PFept256, SPept260, SPept277, SPept295, STept308	2	CTDP1, KCNG2
18	76056369	76115554	0.06	0	0.0	10	9.4	3	7.3	PFept024, PFept027, PFept028, PFept034, PFept047, PFept049, PFept050, PFept058, PFept128, SPept156, PFept256, SPept260, SPept295	1	PARD6G

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
19	513530	1325641	0.81	2	3.5	15	14.2	4	9.8	SPept014, STept015, PFept018, PFept024, PFept027, PFept028, PFept032, PFept034, PFept043, PFept047, PFept049, PFept055, PFept056, PFept058, SPept059, PFept128, PFept256, SPept277, PFept281, SPept295, STept308	37	ABCA7, ARID3A, ATP5D, AZU1, BSG, C19orf21, C19orf22, C19orf23, C19orf24, C19orf26, C19orf6, CFD, CIRBP, CNN2, EFNA2, ELA2, FGF22, FLJ45684, FSTL3, GPX4, GRIN3B, HCN2, HMHA1, KIAA0963, KISS1R, MIDN, MUM1, PALM, POLR2E, POLRMT, PRSSL1, PRTN3, PTBP1, RNF126, STK11, THRAP5, WDR18
19	1788061	1999598	0.21	3	5.3	15	14.2	4	9.8	SPept014, STept015, PFept018, PFept024, PFept027, PFept028, PFept032, PFept034, PFept043, PFept047, PFept049, PFept055, PFept056, SPept059, PFept128, PFept256, SPept277, PFept281, PFept283, SPept295, STept305, STept308	9	BTBD2, C19orf34, CSNK1G2, FAM108A1, KLF16, LOC113179, MKNK2, REXO1, SCAMP4
19	4859389	5029415	0.17	2	3.5	9	8.5	2	4.9	STept015, PFept027, PFept028, PFept034, PFept047, PFept055, PFept056, SPept059, PFept128, PFept256, PFept281, SPept295, STept308	3	C19orf31, JMJD2B, UHRF1

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
19	5446197	5986621	0.54	2	3.5	7	6.6	1	2.4	STept015, PFept027, PFept034, PFept047, PFept055, PFept128, PFept256, PFept281, SPept295, STept308	19	CAPS, DUS3L, FUT3, FUT5, FUT6, HSD11B1L, MGC24975, NDUFA11, NRTN, P117, PLAC2, PRSS15, RANBP3, RFX2, RPL36, SAFB, SAFB2, TMEM146, VMAC
19	8459322	8677581	0.22	3	5.3	6	5.7	1	2.4	STept015, PFept027, PFept034, PFept047, PFept055, PFept128, PFept256, SPept295, STept305, STept308	6	ADAMTS10, HNRPM, MGC33407, MYO1F, PRAM1, ZNF414
19	15596238	15642246	0.05	2	3.5	5	4.7	3	7.3	STept015, PFept026, PFept027, PFept047, SPept059, PFept128, STept293, SPept295, PFept298, SPept314	2	CYP4F3, CYP4F8
19	18961490	19385105	0.42	4	7.0	5	4.7	2	4.9	STept015, PFept027, PFept034, PFept047, PFept055, SPept059, STept114, PFept128, STept254, SPept295, STept308	12	ARMC6, CSPG3, HAPLN4, KIAA0892, MEF2B, MGC26694, RFXANK, SF4, SFRS14, TM6SF2, TMEM161A, TRA16

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
19	43364676	43599425	0.23	3	5.3	7	6.6	1	2.4	STept015, PFept024, PFept047, PFept055, PFept056, STept114, PFept128, PFept256, PFept281, SPept295, STept308	12	C19orf15, C19orf33, DPF1, FAM98C, GGN, KCNK6, LOC541469, PPP1R14A, PSMD8, RASGRP4, SPINT2, YIF1B
19	48722838	48888066	0.17	2	3.5	6	5.7	3	7.3	PFept032, PFept047, PFept055, PFept058, SPept059, STept114, PFept128, PFept256, SPept277, SPept295, STept308	8	ETHE1, IGSF4C, IRGQ, PLAUR, XRCC1, ZNF428, ZNF575, ZNF576
19	60245950	60831491	0.59	4	7.0	7	6.6	2	4.9	STept015, PFept032, PFept047, PFept055, PFept056, PFept058, SPept059, PFept128, STept254, STept255, PFept256, SPept295, STept308	27	BRSK1, C19orf51, COX6B2, EPS8L1, FIZ1, FLJ35258, HSPBP1, IL11, ISOC2, LOC284296, MDAC1, NAT14, PPP1R12C, PTPRH, RDH13, RPL28, SAPS1, SUV420H2, SYT5, TMEM86B, TNNI3, TNNT1, UBE2S, ZNF524, ZNF579, ZNF628, ZNF784
19	63590994	63785051	0.19	4	7.0	8	7.5	2	4.9	STept015, PFept024, PFept028, PFept032, PFept047, PFept055, PFept058, SPept059, PFept128, PFept256, SPept280, STept305, STept307, STept308	13	CHMP2A, MGC2752, MZF1, RPS5, SLC27A5, TRIM28, UBE2M, ZNF132, ZNF324, ZNF324B, ZNF446, ZNF499, ZNF584

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
20	192092	231877	0.04	2	3.5	4	3.8	5	12.2	SPept014, STept015, PFept025, PFept049, PFept055, PFept056, SPept059, SPept260, SPept280, SPept295, STept308	2	C20orf96, ZCCHC3
20	567392	613551	0.05	3	5.3	4	3.8	4	9.8	SPept014, STept015, PFept032, PFept046, PFept049, SPept059, SPept260, SPept277, PFept283, STept307, STept308	2	SCRT2, SRXN1
20	3628280	3748517	0.12	2	3.5	5	4.7	3	7.3	SPept014, STept015, PFept032, PFept046, PFept055, PFept056, SPept059, PFept128, SPept260, STept308	6	C20orf27, C20orf28, CDC25B, CENPB, HSPA12B, SIGLEC1
20	4759846	4781623	0.02	0	0.0	7	6.6	5	12.2	SPept014, PFept025, PFept029, PFept032, PFept046, SPept059, PFept250, PFept256, SPept260, SPept277, PFept279, SPept285	1	SLC23A2

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
20	22494275	22515942	0.02	3	5.3	6	5.7	3	7.3	SPept014, STept015, PFept032, PFept046, PFept049, PFept050, PFept055, PFept056, SPept059, STept257, SPept277, STept308	1	FOXA2
20	22954327	22988948	0.03	2	3.5	9	8.5	1	2.4	SPept014, PFept027, PFept032, PFept034, PFept047, PFept049, PFept050, PFept056, PFept058, SPept059, PFept283, STept308	2	SSTR4, THBD
20	23267225	23295553	0.03	2	3.5	8	7.5	3	7.3	SPept014, STept015, PFept027, PFept032, PFept034, PFept047, PFept049, PFept050, PFept055, PFept056, SPept059, SPept277, STept308	2	NXT1, ZNF336
20	42184075	42232494	0.05	1	1.8	7	6.6	4	9.8	SPept014, PFept027, PFept032, PFept046, PFept047, PFept055, PFept058, SPept059, PFept063, SPept277, SPept295, STept296	1	JPH2

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
20	59241454	59334918	0.09	2	3.5	12	11.3	4	9.8	SPept014, STept015, PFept027, PFept028, PFept032, PFept034, PFept047, PFept049, PFept050, PFept055, SPept059, PFept075, STept114, PFept128, SPept260, SPept277, PFept281, STept308	1	CDH4
20	59944585	60058583	0.11	3	5.3	10	9.4	4	9.8	SPept014, STept015, PFept027, PFept028, PFept032, PFept034, PFept047, PFept050, PFept055, PFept056, SPept059, STept114, PFept128, SPept260, SPept277, PFept281, STept308	2	CDH4, TAF4
20	60113673	60176588	0.06	3	5.3	12	11.3	4	9.8	SPept014, STept015, PFept027, PFept028, PFept032, PFept034, PFept046, PFept047, PFept050, PFept055, PFept056, PFept058, SPept059, STept114, PFept128, SPept260, PFept281, SPept295, STept308	3	LSM14B, PSMA7, SS18L1

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
20	62298377	62376958	0.08	4	7.0	11	10.4	4	9.8	SPept014, STept015, PFept027, PFept028, PFept032, PFept034, PFept047, PFept050, PFept055, PFept056, PFept058, SPept059, STept114, PFept128, STept130, SPept260, PFept281, SPept295, STept308	2	MYT1, PCMTD2
21	42481725	42560211	0.08	0	0.0	8	7.5	2	4.9	PFept027, PFept028, PFept032, PFept034, PFept047, PFept050, PFept055, PFept128, SPept260, SPept295	1	ABCG1
21	45493645	45862760	0.37	2	3.5	9	8.5	3	7.3	PFept027, PFept028, PFept032, PFept034, PFept047, PFept050, PFept055, PFept056, PFept128, STept254, SPept260, SPept277, SPept295, STept308	6	C21orf123, C21orf86, C21orf93, COL18A1, POFUT2, SLC19A1

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
21	46375182	46402997	0.03	2	3.5	9	8.5	3	7.3	PFept027, PFept028, PFept034, PFept047, PFept050, PFept055, PFept056, PFept250, STept254, SPept260, SPept277, PFept279, SPept295, STept308	1	FTCD
21	46788563	46902240	0.11	1	1.8	7	6.6	2	4.9	PFept027, PFept028, PFept034, PFept047, PFept050, PFept055, PFept064, STept254, SPept260, SPept295	3	DIP2A, PRMT2, S100B
22	15961025	15984379	0.02	5	8.8	8	7.5	6	14.6	STept015, PFept027, PFept032, PFept044, PFept046, PFept056, PFept058, PFept060, PFept076, SPept235, STept257, SPept277, SPept280, PFept283, SPept285, SPept295, STept296, STept305, STept308	2	CECR6, IL17RA

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
22	18683947	19129051	0.45	3	5.3	7	6.6	1	2.4	STept015, PFept027, PFept034, PFept044, PFept046, PFept049, PFept056, SPept235, STept257, PFept283, STept308	3	KLHL22, SCARF2, ZNF74
22	42576090	42593477	0.02	4	7.0	12	11.3	2	4.9	STept015, PFept027, PFept029, PFept032, PFept044, PFept046, PFept049, PFept055, PFept058, PFept063, PFept076, PFept128, STept257, SPept277, PFept283, SPept295, STept296, STept308	1	SULT4A1
22	44767616	44803467	0.04	1	1.8	7	6.6	2	4.9	PFept027, PFept032, PFept046, PFept049, PFept055, PFept056, PFept128, SPept277, SPept295, STept308	2	C22orf26, FLJ27365
22	44972672	44986189	0.01	4	7.0	10	9.4	3	7.3	PFept002, STept015, SPept022, PFept027, PFept032, PFept046, PFept047, PFept049, PFept055, PFept056, PFept058, PFept128, SPept277, SPept295, STept296, STept305, STept308	2	FLJ20699, PKDREJ

Johnson, Wright et al., Supplemental Table 3a

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
22	48528880	48837366	0.31	2	3.5	9	8.5	1	2.4	STept015, PFept027, PFept032, PFept044, PFept055, PFept056, PFept060, PFept128, PFept281, PFept283, SPept295, STept308	8	ALG12, BRD1, CRELD2, FLJ41993, MLC1, MOV10L1, PIM3, ZBED4
22	49211838	49519949	0.31	3	5.3	8	7.5	1	2.4	STept015, PFept027, PFept034, PFept044, PFept055, PFept056, PFept058, PFept128, PFept281, SPept295, STept296, STept308	15	ACR, ADM2, ARSA, CHKB, CPT1B, ECGF1, hCAP-H2, KLHDC7B, LOC440836, MAPK8IP2, MGC70863, MIOX, RABL2B, SCO2, TMEM153

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
1	117745152	117779348	0.03	4	7.0	8	7.5	0	0.0	PFept027, PFept034, PFept043, PFept055, STept114, STept116, STept125, PFept151, PFept136, PFept139, PFept140, STept255	1	MAN1A2
2	10401763	10430896	0.03	3	5.3	6	5.7	1	2.4	PFept032, PFept054, STept079, STept087, STept105, PFept139, SPept175, PFept192, PFept206, PFept220	1	HPCAL1
2	55551684	55761984	0.21	2	3.5	8	7.5	1	2.4	PFept081, PFept082, PFept083, STept084, PFept094, PFept095, PFept103, STept104, SPept171, PFept192, PFept219	3	CCDC104, KIAA1212, SMEK2
2	66122954	66143730	0.02	3	5.3	7	6.6	0	0.0	PFept027, PFept034, PFept047, PFept050, STept105, PFept192, PFept219, STept254, STept255, PFept256	1	FLJ16124

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
2	140789404	140939061	0.15	3	5.3	7	6.6	0	0.0	PFept027, PFept034, PFept047, STept125, PFept140, PFept147, STept254, STept255, PFept281, PFept286	1	LRP1B
2	186468070	186518155	0.05	4	7.0	7	6.6	0	0.0	PFept027, PFept034, PFept043, STept116, STept130, PFept136, PFept147, STept254, STept255, PFept281, PFept286	1	FLJ44048
2	202893100	204103114	1.21	8	14.0	9	8.5	1	2.4	STept079, PFept081, PFept082, PFept083, STept084, STept087, STept089, PFept090, SPept091, PFept092, STept093, PFept095, STept099, PFept103, STept104, STept105, PFept106, PFept107	11	ABI2, ALS2CR13, ALS2CR16, ALS2CR8, BMPR2, CYP20A1, ICA1L, NBEAL1, NOP5/NOP58, SUMO1, WDR12
2	213006821	213012709	0.01	2	3.5	14	13.2	1	2.4	PFept005, SPept014, PFept027, PFept034, PFept043, PFept047, PFept058, STept116, STept125, PFept151, PFept136, PFept139, PFept140, PFept147, PFept256, PFept281, PFept286	1	ERBB4

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
2	214851603	214882001	0.03	3	5.3	7	6.6	0	0.0	PFept034, PFept047, PFept055, STept116, PFept151, STept134, PFept136, PFept140, STept254, PFept256	1	SPAG16
2	242445742	242642787	0.20	4	7.0	8	7.5	0	0.0	PFept010, PFept054, PFept069, PFept077, STept110, STept114, STept135, PFept192, PFept206, PFept219, STept230, PFept286	2	GAL3ST2, NEU4
2	242659035	242730382	0.07	5	8.8	7	6.6	0	0.0	PFept010, PFept054, PFept077, STept110, STept114, STept135, STStept151, PFept192, PFept206, PFept219, STept230, PFept286	1	FLJ41327
3	50101219	50404286	0.30	4	7.0	4	3.8	3	7.3	SPept022, PFept054, PFept083, SPept091, STept104, STept130, PFept139, PFept206, SPept237, STept289, STept296	19	C3orf45, CACNA2D2, CYB561D2, GNAI2, GNAT1, HYAL1, HYAL2, HYAL3, IFRD2, NAT6, RASSF1, RBM5, SEMA3B, SEMA3F, SLC38A3, TMEM115, TUSC2, TUSC4, ZMYND10

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
3	139692042	140078942	0.39	4	7.0	5	4.7	1	2.4	PFept050, STept079, PFept081, PFept082, STept084, STept089, SPept091, PFept095, STept104, PFept107	3	CEP70, FAIM, PIK3CB
3	184532480	184611940	0.08	3	5.3	5	4.7	2	4.9	STept015, PFept080, PFept081, STept087, SPept091, PFept103, STept104, SPept155, PFept192, PFept281	1	MCF2L2
3	197315515	197854075	0.54	6	10.5	6	5.7	1	2.4	STept079, PFept081, PFept082, PFept083, STept087, SPept091, PFept092, STept093, STept099, PFept103, STept104, PFept192, STept309	8	FLJ25996, MGC33212, OSTalpha, PCYT1A, RNF168, TM4SF19, WDR53, ZDHHC19
4	57547766	57618873	0.07	5	8.8	5	4.7	0	0.0	PFept081, PFept083, PFept103, STept104, PFept250, STept294, STept306, STept307, STept309, PFept311	1	REST

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
4	72705277	72812456	0.11	4	7.0	10	9.4	0	0.0	PFept027, PFept034, PFept047, PFept055, STept125, PFept151, PFept139, PFept140, PFept147, STept254, STept255, PFept256, PFept286, STept305	1	SLC4A4
4	96758195	96782101	0.02	5	8.8	8	7.5	0	0.0	PFept005, PFept027, PFept034, PFept047, STept116, STept125, PFept151, PFept136, PFept139, PFept140, STept254, STept255, STept305	1	UNC5C
4	113809641	114030931	0.22	5	8.8	6	5.7	0	0.0	PFept081, PFept082, PFept083, STept084, PFept092, STept093, PFept094, STept099, PFept103, STept104, STept305	3	C4orf21, LARP7, LOC91431
5	32065395	32356401	0.29	5	8.8	6	5.7	0	0.0	STept079, PFept081, PFept082, PFept083, STept089, STept093, PFept095, STept104, STept105, PFept106, PFept107	3	GOLPH3, MTMR12, PDZD2

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
5	115517964	115521512	0.00	3	5.3	10	9.4	0	0.0	PFept005, PFept027, PFept034, PFept043, PFept058, STept116, STept125, PFept151, PFept139, PFept140, PFept147, STept254, PFept286	1	COMMD10
6	42677064	42746542	0.07	3	5.3	6	5.7	2	4.9	PFept081, PFept083, PFept092, PFept095, PFept103, STept104, STept105, PFept219, SPept237, SPept277, STept307	1	UBR2
6	42767957	43634442	0.87	2	3.5	7	6.6	1	2.4	PFept054, PFept081, PFept083, PFept092, PFept095, PFept103, STept104, STept105, PFept219, SPept237	31	ABCC10, C6orf108, C6orf153, C6orf154, CRIP3, CUL7, EGFL9, GNMT, KIAA0240, KLC4, KLHDC3, LOC441150, MEA1, MRPL2, PARC, PEX6, POLR1C, PPP2R5D, PTCRA, PTK7, RDS, RPL7L1, SLC22A7, SRF, TBCC, TJAP1, TNRC5, TTBK1, XPO5, YIPF3, ZNF318
6	46213456	46224408	0.01	5	8.8	4	3.8	1	2.4	STept114, STept116, STept125, STept130, PFept136, PFept140, PFept141, STept254, PFept256, SPept260	1	ENPP4

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
6	55476461	55503779	0.03	4	7.0	13	12.3	1	2.4	PFept005, PFept034, PFept043, PFept044, PFept050, PFept055, PFept056, STept116, STept125, PFept151, PFept136, PFept140, STept254, STept255, PFept256, SPept260, PFept281, PFept286	1	HMGCLL1
6	74395913	74507950	0.11	5	8.8	5	4.7	2	4.9	PFept081, PFept082, STept084, STept089, SPept091, PFept092, STept099, PFept103, STept104, PFept107, SPept277, STept293	2	CD109, SLC17A5
6	151736311	151737683	0.00	2	3.5	7	6.6	1	2.4	PFept054, PFept081, PFept092, PFept095, PFept103, STept104, STept105, PFept147, PFept250, SPept277	1	AKAP12
6	157068763	157748361	0.68	3	5.3	7	6.6	1	2.4	PFept081, PFept092, PFept095, STept104, STept105, PFept147, PFept220, SPept237, PFept250, STept296	1	ARID1B

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
6	166559979	167200028	0.64	1	1.8	7	6.6	2	4.9	PFept047, PFept092, STept104, PFept147, PFept192, PFept206, PFept219, PFept220, SPept235, SPept237	4	BRP44L, MGC35308, RPS6KA2, SFT2D1
6	167380182	167425550	0.05	2	3.5	6	5.7	2	4.9	STept015, PFept092, STept104, PFept147, PFept192, PFept206, PFept219, PFept220, SPept235, SPept237	1	FGFR1OP
6	167922453	168038385	0.12	1	1.8	7	6.6	2	4.9	PFept054, PFept092, STept104, PFept147, PFept192, PFept206, PFept219, PFept220, SPept235, SPept237	1	LOC441179
6	168425764	168681130	0.26	1	1.8	9	8.5	2	4.9	PFept008, PFept054, PFept092, STept104, PFept139, PFept147, PFept192, PFept206, PFept219, PFept220, SPept235, SPept237	2	DACT2, SMOC2

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
6	170732323	170823609	0.09	2	3.5	8	7.5	2	4.9	PFept008, PFept029, PFept092, STept104, PFept147, PFept192, PFept206, PFept219, PFept220, SPept235, SPept237, STept307	3	PDCD2, PSMB1, TBP
7	77668167	77765386	0.10	4	7.0	6	5.7	1	2.4	PFept024, PFept034, PFept049, STept114, STept125, PFept136, PFept140, STept254, STept255, SPept277, PFept281	1	MAGI2
7	134532088	134576672	0.04	2	3.5	7	6.6	1	2.4	PFept027, PFept082, PFept083, PFept094, PFept095, STept101, PFept103, STept104, SPept155, PFept281	1	CNOT4
9	134785501	134834219	0.05	3	5.3	2	1.9	5	12.2	SPept022, PFept054, STept088, STept104, STept130, PFept139, SPept158, SPept177, SPept239, SPept244	1	COL5A1

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
10	3169189	3180797	0.01	4	7.0	3	2.8	4	9.8	PFept092, STept101, SPept158, STept159, PFept192, SPept217, PFept219, STept230, SPept235, SPept277, STept289	1	PITRM1
10	5175582	5187881	0.01	4	7.0	4	3.8	2	4.9	PFept092, STept101, PFept140, SPept158, STept159, PFept192, PFept219, SPept277, STept289, STept293	1	AKR1CL1
10	6170011	6268419	0.10	3	5.3	6	5.7	2	4.9	PFept054, PFept083, PFept092, PFept103, SPept158, STept159, PFept192, PFept219, SPept277, STept289, STept293	1	RBM17
10	8130007	8150030	0.02	7	12.3	5	4.7	2	4.9	PFept054, PFept092, STept093, STept099, STept101, STept104, SPept158, STept159, PFept192, PFept219, SPept277, STept289, STept293, PFept297	2	FLJ45983, GATA3

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
10	11151805	11236375	0.08	3	5.3	5	4.7	2	4.9	PFept024, PFept027, PFept075, SPept158, STept159, PFept192, PFept219, SPept277, STept289, STept293	1	CUGBP2
10	13344307	13497936	0.15	5	8.8	9	8.5	2	4.9	PFept023, PFept067, PFept081, PFept083, STept089, PFept092, PFept103, STept105, SPept158, STept159, PFept192, PFept219, SPept277, STept289, STept293, PFept311	2	PHYH, SEPHS1
10	25665327	25756077	0.09	4	7.0	6	5.7	1	2.4	PFept047, PFept092, STept114, STept125, PFept151, PFept136, PFept140, STept254, STept255, PFept256, SPept277	1	GPR158
10	53651276	53712562	0.06	3	5.3	6	5.7	2	4.9	PFept034, PFept055, STept114, PFept151, PFept140, PFept147, SPept158, STept254, STept255, SPept277, PFept281	1	PRKG1

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
10	68970214	69114993	0.14	3	5.3	6	5.7	1	2.4	PFept047, PFept055, PFept064, PFept083, PFept092, STept104, STept105, PFept151, SPept277, STept294	1	CTNNA3
10	69645873	69701073	0.06	4	7.0	8	7.5	1	2.4	PFept055, PFept064, PFept081, PFept082, PFept083, PFept092, STept104, STept105, PFept151, PFept192, SPept277, STept293, STept294	1	ATOH7
10	70846341	70896472	0.05	4	7.0	7	6.6	1	2.4	PFept064, PFept082, PFept083, PFept092, STept101, STept104, STept105, PFept151, PFept192, PFept219, SPept277, STept294	1	TSPAN15
10	71234506	71351772	0.12	2	3.5	7	6.6	3	7.3	PFept054, PFept064, PFept083, STept105, PFept151, PFept139, PFept192, SPept208, PFept219, SPept237, SPept277, STept294	1	COL13A1

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
10	71990162	72295747	0.31	3	5.3	7	6.6	3	7.3	PFept054, PFept064, PFept083, PFept092, STept101, STept105, PFept151, PFept192, SPept208, PFept219, SPept237, SPept277, STept294	5	ADAMTS14, C10orf27, KIAA1274, PRF1, SGPL1
10	72636128	72774965	0.14	4	7.0	7	6.6	3	7.3	PFept054, PFept083, PFept092, STept101, STept105, STept130, PFept151, PFept139, PFept192, SPept208, PFept219, SPept237, SPept277, STept294	2	SLC29A3, UNC5B
10	73121579	73231404	0.11	4	7.0	8	7.5	4	9.8	PFept054, PFept064, PFept083, PFept092, STept101, STept105, STept130, PFept151, PFept139, SPept157, PFept192, SPept208, PFept219, SPept237, SPept277, STept294	1	C10orf54
10	73528460	73528555	0.00	4	7.0	10	9.4	2	4.9	PFept054, PFept064, PFept081, PFept082, PFept083, PFept092, PFept095, STept101, STept104, STept105, PFept151, PFept192, PFept219, SPept237, SPept277, STept294	1	ASCC1

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
10	74961876	75140051	0.18	4	7.0	10	9.4	1	2.4	PFept054, PFept064, PFept081, PFept082, PFept083, PFept092, PFept095, STept101, STept104, STept105, PFept151, PFept192, PFept219, SPept277, STept294	3	MYOZ1, SYNPO2L, USP54
10	76252033	76386287	0.13	4	7.0	9	8.5	1	2.4	PFept055, PFept064, PFept081, PFept082, PFept083, PFept092, STept101, STept104, STept105, PFept151, PFept192, PFept219, SPept277, STept294	1	MYST4
10	79199813	79512927	0.31	1	1.8	7	6.6	2	4.9	SPept022, PFept064, PFept083, PFept092, STept104, PFept151, PFept192, PFept219, SPept277, PFept297	3	DLG5, POLR3A, RPS24
10	80472952	80774861	0.30	2	3.5	8	7.5	1	2.4	SPept022, PFept054, PFept064, PFept083, PFept092, STept130, PFept151, PFept139, PFept192, PFept219, STept230	1	RAI17

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
10	83766071	83789535	0.02	1	1.8	8	7.5	1	2.4	PFept027, PFept034, PFept055, PFept075, PFept151, PFept140, PFept143, STept255, PFept256, SPept277	1	NRG3
10	87964009	88041083	0.08	4	7.0	6	5.7	2	4.9	SPept022, PFept054, PFept064, PFept083, PFept092, STept101, STept104, STept130, PFept151, PFept139, SPept277, STept305	1	GRID1
10	90081520	90201144	0.12	3	5.3	7	6.6	1	2.4	PFept027, PFept055, STept101, PFept151, PFept136, PFept140, PFept256, SPept277, STept294, STept305	1	C10orf59
10	90324159	90357870	0.03	4	7.0	7	6.6	1	2.4	PFept027, PFept055, STept101, STept130, PFept151, PFept136, PFept140, PFept256, SPept277, PFept281, STept294, STept305	2	C10orf59, LIPL1

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
10	90578581	90656013	0.08	4	7.0	6	5.7	1	2.4	STept015, PFept027, PFept034, PFept055, STept101, PFept151, PFept256, SPept277, PFept281, STept294, STept305	2	ANKRD22, STAMBPL1
10	98857284	99268440	0.41	6	10.5	4	3.8	1	2.4	PFept064, PFept081, PFept083, PFept092, STept093, STept101, STept104, SPept277, STept289, STept294, STept305	10	ARHGAP19, EXOSC1, FRAT1, FRAT2, KIAA0690, MMS19L, PGAM1, SLIT1, UBTD1, ZDHHC16
10	101279725	101300855	0.02	6	10.5	4	3.8	0	0.0	PFept064, PFept083, STept087, PFept092, STept101, STept104, PFept139, STept289, STept294, STept305	1	NKX2-3
10	102724768	102752246	0.03	7	12.3	5	4.7	1	2.4	PFept054, PFept064, PFept083, STept087, PFept092, STept101, STept104, STept130, PFept139, SPept277, STept289, STept294, STept305	4	LZTS2, MRPL43, PEO1, SEMA4G

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
10	105634726	105742493	0.11	5	8.8	4	3.8	1	2.4	PFept055, PFept064, PFept083, PFept092, STept101, STept105, SPept277, STept289, STept294, STept305	2	OBFC1, SLK
10	106855945	106907237	0.05	2	3.5	7	6.6	1	2.4	PFept034, PFept047, PFept055, PFept063, STept101, PFept151, STept255, PFept256, SPept277, PFept281	1	SORCS3
10	133852261	133910912	0.06	2	3.5	6	5.7	2	4.9	PFept054, PFept083, PFept092, STept104, PFept107, STept130, PFept139, SPept181, PFept220, SPept237	2	DPYSL4, STK32C
10	134410586	134892955	0.48	2	3.5	7	6.6	3	7.3	SPept022, PFept054, PFept080, PFept083, PFept092, STept104, STept130, PFept139, SPept181, PFept206, PFept220, SPept237	6	C10orf92, C10orf93, GPR123, INPP5A, KNDC1, NKX6-2

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
10	135176625	135276748	0.10	1	1.8	6	5.7	3	7.3	PFept042, PFept080, PFept083, PFept092, STept104, SPept181, PFept206, PFept220, SPept237, SPept277	3	CYP2E1, FLJ44653, SYCE1
11	373554	2917788	2.54	5	8.8	4	3.8	3	7.3	PFept054, STept068, STept087, SPept091, STept125, STept130, PFept139, PFept192, PFept219, SPept235, SPept237, STept296	62	AP2A2, ASCL2, BRSK2, C11orf35, CD151, CD81, CDKN1C, CEND1, CHID1, CTSD, DEAF1, DRD4, DUSP8, EFCAB4A, EPS8L2, FAM99A, HCCA2, HRAS, IGF2, IGF2AS, INS, IRF7, KCNQ1, KCNQ1DN, KIAA1542, KRTAP5-1, KRTAP5-2, KRTAP5-3, KRTAP5-4, KRTAP5-6, LRDD, LRRC56, LSP1, MRPL23, MUC2, MUCDHL, PDDC1, PHLDA2, PKP3, PNPLA2, POLR2L, PTDSS2, RASSF7, RNH1, RPLP2, SCT, SIGIRR, SLC22A18, SLC22A18AS, SLC25A22, SYT8, TALDO1, TH, TMEM16J, TMEM80, TNNI2, TNNT3, TOLLIP, TRPM5, TSPAN32, TSPAN4, TSSC4
11	5822800	5858528	0.04	4	7.0	5	4.7	1	2.4	PFept027, PFept034, PFept055, STept087, STept114, STept125, PFept151, PFept140, STept255, SPept277	1	OR52E8

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
11	8951543	9571659	0.62	6	10.5	2	1.9	2	4.9	PFept081, PFept082, STept087, STept088, SPept091, STept093, STept099, STept104, STept125, SPept277	7	IPO7, NRIP3, RAB6IP1, SCUBE2, TMEM41B, WEE1, ZNF143
11	16222459	16222993	0.00	6	10.5	6	5.7	2	4.9	PFept027, PFept034, PFept043, PFept055, STept068, STept087, SPept091, STept114, STept116, STept125, PFept147, STept254, SPept277, PFept286	1	SOX6
11	16281025	16382534	0.10	5	8.8	7	6.6	2	4.9	PFept024, PFept027, PFept034, PFept043, PFept055, STept068, STept087, SPept091, STept114, STept125, PFept147, STept254, SPept277, PFept286	1	SOX6
11	26631293	26780450	0.15	4	7.0	5	4.7	1	2.4	PFept005, STept068, STept125, PFept136, PFept140, STept254, STept255, SPept277, PFept281, PFept286	2	SLC5A12, TMEM16C

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
11	32816714	33041493	0.22	7	12.3	4	3.8	2	4.9	STept079, PFept080, PFept081, STept087, STept089, SPept091, STept093, STept099, STept104, STept125, PFept192, PFept219, SPept277	4	DEPDC7, PRRG4, QSER1, TCP11L1
11	47130638	47376239	0.25	4	7.0	7	6.6	1	2.4	PFept069, PFept081, PFept082, PFept083, STept087, SPept091, STept093, PFept103, STept104, STept125, PFept192, PFept219	9	ACP2, C11orf49, DDB2, MADD, MYBPC3, NR1H3, PACSIN3, SPI1, ZNF289
11	48011370	48072413	0.06	3	5.3	7	6.6	1	2.4	PFept050, PFept080, PFept081, PFept082, STept087, SPept091, STept093, PFept103, STept104, PFept192, PFept219	1	PTPRJ
11	83842973	83876998	0.03	3	5.3	7	6.6	2	4.9	PFept005, STept116, STept135, PFept136, PFept139, PFept141, PFept147, STept254, SPept260, SPept277, PFept281, PFept286	1	DLG2

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
11	88074716	88119830	0.05	6	10.5	6	5.7	1	2.4	PFept027, PFept034, STept114, STept125, STept134, STept135, PFept140, PFept147, STept254, STept255, PFept256, SPept277, PFept281	1	GRM5
11	123670101	123747614	0.08	3	5.3	8	7.5	1	2.4	PFept027, PFept034, PFept050, STept114, STept125, PFept128, PFept140, PFept147, PFept192, STept254, SPept277, PFept281	2	OR8D1, OR8D2
12	7809727	7908762	0.10	5	8.8	8	7.5	2	4.9	PFept026, PFept029, PFept054, PFept064, PFept069, SPept091, STStept151, PFept250, STept273, STept276, STept294, PFept297, PFept298, STept304, SPept313	2	NANOG, SLC2A14
12	28526130	28543542	0.02	3	5.3	11	10.4	0	0.0	PFept012, PFept027, PFept034, PFept043, PFept055, STept116, STept125, PFept151, PFept136, PFept139, PFept140, STept254, PFept256, PFept281	1	CCDC91

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
12	54665694	54890101	0.22	3	5.3	9	8.5	0	0.0	PFept054, PFept070, PFept080, PFept081, PFept082, PFept083, STept087, PFept092, STept093, PFept094, STept099, PFept103	13	ERBB3, FAM62A, IKZF4, MYL6, MYL6B, PA2G4, RAB5B, RNF41, RPL41, RPS26, SMARCC2, SUOX, ZC3H10
12	89942675	89960920	0.02	5	8.8	9	8.5	0	0.0	PFept043, STept112, STept116, STept125, PFept151, PFept136, PFept139, PFept140, PFept141, PFept147, STept254, STept255, PFept256, PFept281	1	KERA
13	93301393	93318026	0.02	4	7.0	7	6.6	0	0.0	PFept005, PFept034, PFept047, STept125, PFept151, PFept136, PFept140, STept254, STept255, PFept286, STept308	1	GPC6
13	110052342	110089193	0.04	1	1.8	4	3.8	5	12.2	PFept054, PFept081, PFept095, STept105, SPept153, SPept158, PFept206, SPept209, SPept235, SPept237	1	FLJ10769

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
13	112461756	112843262	0.38	1	1.8	5	4.7	5	12.2	PFept054, PFept069, PFept103, STept105, PFept139, SPept153, SPept158, PFept206, SPept209, SPept235, SPept237	4	ATP11A, F10, F7, MCF2L
13	113530653	113944993	0.41	3	5.3	3	2.8	5	12.2	PFept054, STept105, STept130, PFept139, SPept153, SPept158, PFept206, SPept209, SPept235, SPept237, STept247	3	FAM70B, GAS6, RASA3
14	19581513	19696043	0.11	3	5.3	5	4.7	4	9.8	PFept009, PFept034, PFept047, PFept080, STept088, SPept091, STept104, PFept140, SPept208, SPept235, SPept237, STept255	3	OR4K17, OR4L1, OR4N5
14	20686715	20699738	0.01	3	5.3	3	2.8	6	14.6	PFept047, PFept081, STept088, SPept091, STept104, STept114, SPept158, SPept208, SPept235, SPept237, SPept277	1	OR5AU1

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
14	20786733	21088750	0.30	2	3.5	4	3.8	5	12.2	PFept026, PFept081, STept088, SPept091, PFept095, PFept103, STept104, SPept158, SPept235, SPept237, SPept277	8	C14orf92, CHD8, HNRPC, METTL3, RAB2B, RPGRIP1, SALL2, SUPT16H
14	32932320	32962713	0.03	3	5.3	6	5.7	2	4.9	PFept027, PFept034, STept114, PFept139, PFept147, SPept158, STept254, STept255, PFept256, SPept277, PFept281	1	NPAS3
14	33046738	33072996	0.03	3	5.3	6	5.7	3	7.3	SPept014, PFept027, PFept034, PFept080, STept125, PFept147, SPept158, STept254, STept255, PFept256, SPept277, PFept281	1	NPAS3
14	54241556	54282039	0.04	3	5.3	5	4.7	2	4.9	PFept027, PFept034, PFept055, SPept091, STept104, PFept140, STept255, SPept277, PFept281, STept296	1	SAMD4A

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
14	74039781	74073889	0.03	3	5.3	5	4.7	2	4.9	PFept054, PFept081, PFept082, SPept091, PFept092, PFept103, STept104, STept130, SPept285, STept296	1	LTBP2
14	104674460	105071276	0.40	3	5.3	5	4.7	2	4.9	PFept054, PFept080, STept088, SPept091, PFept092, PFept103, STept104, PFept139, STept159, SPept235	10	BRF1, BTBD6, C14orf80, CRIP1, CRIP2, JAG2, MTA1, NUDT14, PACS2, TMEM121
15	20414442	20422689	0.01	5	8.8	6	5.7	0	0.0	PFept021, PFept080, PFept081, PFept082, STept084, PFept095, PFept106, STept159, STept205, STept293, STept305	1	TUBGCP5
15	48407932	48896243	0.49	4	7.0	6	5.7	0	0.0	PFept081, PFept082, PFept083, PFept095, STept099, PFept103, STept104, PFept107, STept254, STept255	5	GABPB2, SPPL2A, TRPM7, USP50, USP8

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
15	98161303	98216230	0.05	5	8.8	9	8.5	0	0.0	STept015, PFept027, PFept034, PFept049, PFept055, PFept056, STept114, STept125, PFept136, PFept137, PFept140, STept254, STept255, PFept281	2	C15orf51, LOC400464
16	5062785	5101775	0.04	2	3.5	9	8.5	1	2.4	PFept024, PFept054, PFept069, PFept082, PFept083, PFept103, STept104, STept105, PFept192, PFept219, PFept220, SPept237	2	ALG1, FAM86A
16	60270894	60322602	0.05	5	8.8	5	4.7	0	0.0	STept114, STept116, STept130, PFept136, PFept139, PFept140, PFept147, STept254, STept255, PFept256	1	CDH8
16	70223486	70480682	0.26	3	5.3	6	5.7	1	2.4	PFept081, PFept082, PFept083, STept089, SPept091, PFept092, PFept095, PFept103, STept104, STept105	4	AP1G1, LOC55565, MARVELD3, PHLPPL

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
16	80663800	80686278	0.02	3	5.3	7	6.6	0	0.0	PFept027, PFept034, PFept047, STept104, PFept192, PFept219, STept255, PFept256, PFept281, STept296	1	HSD17B2
16	81397804	81413514	0.02	3	5.3	7	6.6	0	0.0	PFept027, PFept034, PFept050, PFept140, PFept192, PFept219, STept254, STept255, PFept256, STept296	1	CDH13
16	82507007	82581425	0.07	3	5.3	6	5.7	1	2.4	PFept054, PFept117, STept130, PFept139, PFept192, PFept219, PFept220, SPept237, STept247, STept296	3	EFCBP2, MLYCD, OKL38
16	82584041	82639297	0.06	2	3.5	7	6.6	1	2.4	PFept050, PFept054, PFept117, PFept139, PFept192, PFept219, PFept220, SPept237, STept247, STept296	1	EFCBP2

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
16	83747731	84274333	0.53	3	5.3	7	6.6	1	2.4	PFept054, PFept117, STept130, PFept139, PFept192, PFept219, PFept220, SPept237, STept247, PFept274, STept296	3	GINS2, KIAA0182, TMEM148
16	86126636	86308811	0.18	3	5.3	7	6.6	1	2.4	PFept054, PFept070, PFept117, STept130, PFept192, PFept219, PFept220, SPept237, STept247, PFept274, STept296	2	JPH3, KLHDC4
16	86674516	88690776	2.02	2	3.5	7	6.6	1	2.4	PFept054, PFept070, PFept117, PFept192, PFept219, PFept220, SPept237, STept247, PFept274, STept296	43	AFG3L1, ANKRD11, APRT, C16orf3, C16orf55, C16orf7, C16orf76, C16orf81, CBFA2T3, CDH15, CDK10, CDT1, CPNE7, CYBA, DBNDD1, DPEP1, FAM38A, FANCA, FLJ20186, FLJ40448, FLJ45121, FLJ45530, GALNS, GAS8, IL17C, LOC197322, LOC348180, MC1R, MGC16385, MVD, NHN1, PCOLN3, PRDM7, RNF166, RPL13, SPG7, SPIRE2, TCF25, TRAPPC2L, TUBB3, ZFPM1, ZNF276, ZNF778

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
17	41602774	41610190	0.01	8	14.0	22	20.8	1	2.4	PFept011, PFept018, PFept039, PFept050, PFept058, PFept064, PFept067, STept068, PFept069, PFept071, PFept082, PFept090, PFept103, PFept107, STept109, STept110, STept116, PFept132, PFept138, PFept188, STept200, PFept206, PFept219, PFept226, STept230, STept247, SPept285, PFept287, PFept290, PFept297, STept309	1	KIAA1267
21	43016879	43326441	0.31	1	1.8	8	7.5	3	7.3	PFept054, PFept081, PFept082, SPept091, PFept092, PFept095, STept104, PFept107, PFept206, PFept219, SPept235, SPept237	4	NDUFV3, PDE9A, PKNOX1, WDR4
22	14433758	15475051	1.04	2	3.5	7	6.6	2	4.9	PFept001, PFept008, SPept014, PFept047, PFept054, PFept077, PFept080, SPept091, STept104, PFept219, STept307	2	CESK1, OR11H1
22	15898744	15960362	0.06	3	5.3	7	6.6	5	12.2	PFept001, PFept008, SPept014, PFept047, PFept054, PFept080, SPept091, PFept103, STept104, STept105, PFept219, SPept237, SPept239, SPept280, STept307	1	IL17RA

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
22	17462469	17535453	0.07	4	7.0	5	4.7	6	14.6	PFept001, SPept014, PFept047, PFept054, SPept091, PFept103, STept104, STept105, STept130, PFept139, PFept219, SPept237, SPept239, SPept280, STept307	5	DGCR13, DGCR14, DGCR2, GSCL, TSSK2
22	17545510	18351388	0.81	4	7.0	5	4.7	5	12.2	PFept001, SPept014, PFept054, SPept091, PFept103, STept104, STept105, STept130, PFept139, PFept219, SPept237, SPept239, SPept280, STept307	15	5-Sep, ARVCF, C22orf29, CDC45L, CLDN5, CLTCL1, COMT, GNB1L, GP1BB, HIRA, LOC128977, MRPL40, TBX1, TXNRD2, UFD1L
22	19113144	19129051	0.02	4	7.0	4	3.8	5	12.2	PFept001, SPept014, PFept054, SPept091, PFept103, STept104, STept105, STept130, PFept219, SPept237, SPept239, SPept280, STept307	2	KLHL22, SCARF2
22	20438590	20844621	0.41	3	5.3	6	5.7	5	12.2	PFept001, PFept002, SPept014, PFept047, PFept054, SPept091, PFept103, STept104, STept105, PFept219, SPept237, SPept239, SPept280, STept307	3	MAPK1, PPM1F, TOP3B

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
22	23169502	23429901	0.26	3	5.3	5	4.7	6	14.6	PFept001, PFept002, SPept014, PFept047, PFept054, SPept091, STept104, STept105, PFept219, SPept237, SPept239, SPept277, SPept280, STept307	5	C22orf13, GGT1, LOC388886, SNRPD3, UPB1
22	23983115	24117253	0.13	7	12.3	4	3.8	5	12.2	PFept002, PFept047, PFept054, SPept091, SPept102, STept104, STept105, PFept219, SPept237, PFept274, STept276, SPept277, SPept280, STept289, STept293, STept307	2	CTA-246H3., LRP5L
22	24511164	24519984	0.01	3	5.3	6	5.7	5	12.2	PFept002, SPept014, PFept047, PFept050, PFept054, SPept091, STept104, STept105, PFept219, SPept237, PFept256, SPept277, SPept280, STept307	1	MYO18B
22	26391943	26766025	0.37	4	7.0	3	2.8	7	17.1	PFept002, SPept014, PFept047, PFept054, SPept091, STept104, STept105, STept114, PFept219, STept230, SPept277, SPept280, SPept285, SPept291	2	MN1, PITPNB

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
22	28829206	28902143	0.07	5	8.8	8	7.5	5	12.2	SPept014, STept015, PFept047, PFept054, PFept081, PFept082, PFept083, SPept091, PFept092, PFept103, STept104, STept105, STept114, PFept219, STept230, SPept280, SPept285, SPept291	1	HORMAD2
22	42272004	42444899	0.17	2	3.5	5	4.7	4	9.8	STept015, PFept050, PFept054, SPept091, PFept103, PFept136, PFept137, SPept277, SPept285, STept289, SPept291	1	FLJ23588
22	44777122	44854565	0.08	2	3.5	5	4.7	3	7.3	PFept054, SPept091, PFept103, STept125, PFept136, PFept137, PFept139, SPept285, STept289, SPept291	1	FLJ27365
22	44875287	44957773	0.08	2	3.5	4	3.8	4	9.8	PFept054, SPept091, PFept103, STept125, PFept136, PFept137, SPept277, SPept285, STept289, SPept291	1	PPARA

Johnson, Wright et al., Supplemental Table 3b

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
22	45490194	45517043	0.03	4	7.0	7	6.6	3	7.3	PFept002, PFept054, SPept091, PFept103, STept104, STept125, PFept136, PFept137, PFept139, PFept143, SPept277, STept289, SPept291, STept307	1	TBC1D22A
22	48406592	48528880	0.12	4	7.0	6	5.7	3	7.3	PFept002, PFept054, PFept069, SPept091, STept104, STept125, PFept136, PFept137, PFept143, SPept239, STept289, SPept291, STept307	1	BRD1
22	48900002	48920735	0.02	4	7.0	6	5.7	4	9.8	PFept047, PFept054, PFept069, SPept091, STept104, STept125, STept130, PFept136, PFept137, PFept143, SPept239, SPept277, STept289, SPept291	2	MOV10L1, PANX2
23	40815297	41099173	0.28	4	7.0	6	5.7	0	0.0	PFept054, PFept081, PFept082, PFept083, STept087, PFept092, PFept095, STept101, STept289, STept296	3	DDX3X, NYX, USP9X

Chr	Start	End	Size (Mb)	ST (n)	ST (%)	PF (n)	PF (%)	SP (n)	SP (%)	Samples	Number of RefSeq genes	Genes
23	117348664	117384262	0.04	4	7.0	7	6.6	0	0.0	PFept080, PFept081, PFept082, PFept083, STept087, PFept092, PFept095, STept101, PFept140, STStept151, STept296	1	WDR44
23	118358071	118791118	0.43	7	12.3	7	6.6	0	0.0	PFept081, PFept082, PFept083, STept087, PFept092, STept093, PFept095, STept101, PFept103, STept104, PFept140, STStept151, STept296, STept304	10	SEPT6, CXorf56, LOC203427, NDUFA1, NKRF, RNF113A, RPL39, SLC25A5, UBE2A, UPF3B
23	152351895	152796737	0.44	1	1.8	7	6.6	2	4.9	PFept054, PFept083, PFept092, PFept103, STept130, PFept139, PFept140, PFept206, SPept208, SPept235	19	ABCD1, ARD1A, ARHGAP4, ATP2B3, AVPR2, BCAP31, CXorf12, DUSP9, FAM58A, HCFC1, IDH3G, L1CAM, PDZD4, PLXNB3, PNCK, RENBP, SLC6A8, SRPK3, SSR4

Johnson, Wright et al., Supplemental Table 4

Chr	Cyto	RT-PCR Target gene	CNV	Gene Card #	average RT-PCR CNA samples	average RT-PCR CNTRL samples	RATIO	Forward Primer	Reverse Primer	Fam Probe
1	1p36.33	UBE2J2	+	AMP#1	27.40	1.10	24.91	TGAGCAGCACCAGCAGTAAGA	TGCGAAGGTAGTCCTGCTTCA	CTCCGACCACGGCAACCCAGA
1	1p36.3	TP73	+	AMP#2	15.00	1.02	14.65	GGCCGGGAGAACTTTGAGAT	TGCGGCACCAACTCCAT	CTGATGAAGCTGAAAGAGAGCCTGGAGC
1	1p36.1-p35	EPHB2	+	AMP#3	39.588	1	39.588	TGAACACGATCCGCACGTA	TTGGTCCGTAGCCAGTTGTTCT	CAGGTGTGCAACGTGTTTGAGTCAAGC
1	1p35.3	GMEB1	-	DEL#1	0.35	3.14	0.11	TGATGGACTCCGGACAGATTG	TTTGGTGCTTCTGCAGGTATTG	TTTTTACCAACATGACAAAGTTTGCT
1	1q21	CGN	-	AMP#4	1.36	0.70	1.95	ACTCTCAGGTCAAGGGATTTCCT	GGCCCCAGGCTCCTCAT	CCCCTCGCAGAGCAGCACATC
1	1q42	WNT3A	+	AMP#5	2.15	0.91	2.35	GCCTTTGTCCACGCCATT	TCTGCACATGAGCGTGTCACT	CCTCAGCCGGTGTGGCCTT
3	3p25.3	IL17RC	-	DEL#2	0.57	1.40	0.41	GCATCTGGTTCTGAATGTCTCTGA	GGCCCTGGACCTGATTCC	AGCAGCACTTCGGCCTCTCCCTG
3	3p21.3-p21.2	PRKAR2A	-	DEL#3	0.68	2.53	0.27	CCGTGGCAGTTTTGGAGAAC	CTGAGGTAGCAACAATGGTAGCA	AGCTCTGATGTACAACACCCCGAGA
3	3q22.3	STAG1	-	DEL#4	0.352	2.338	0.15056	GATTCGACAGTGTCAGTATAGCATAATTT	TGACCTGGGAGTCTGACAAACC	ATATGATGGACACAGTAATCTCCCTTTT
4	4p16	GAK	+	AMP#7	8.41448	1.211215	6.94714	GCGACACGGTTCTGAAGATCT	CTTCTGCCGGTGCATGTG	CTACCAGACGTGCCGCGCCG
4	4p16.3	CRIPAK	-	AMP#8	3.85	0.88	4.35	TGGCATGGTGGTTCTGTAGGT	AGAATGTACGGTAACAGCGTCTGA	TCCTGTCCTGCCGGCCG
5	5p15.33	SEC6L1	+	AMP#9	5.66	0.81	6.96	CCGCCATCCAGTCACAGTT	AGCGACTGCTGGATGTCTTTG	CCAGCTCCACAACGCCCTGAA
5	5q31	PCDHB8	+	AMP#10	4.12	0.85	4.86	CGTTCTGATTCAAGTGATAGATGTGA	GGTATTGGGCTGGTAAATGCA	CGACCATGCCCCAGAAGTTACCATGT
6	6p25.2	RIPK1	-	AMP#11	8.88	0.45	19.93	AATGGCGGCACCCTCTACTA	CTGTGGGCTTTGCGTTGAC	ATGGCGCCCGAGCACCTG
6	6p21.1	USP49	-	DEL#5	1.75	7.25	0.24	CACGCCCTGAAACACTTTGA	GAACACGTAGAGATCCCGGACTT	AGACGGGACACCCGCTAGCCATG
6	6q12	PTP4A1	-	DEL#6	0.4625	2.304	0.20074	CAGCAAGCAACTTCTGTATTTGGA	TGTTTCTATGACCGTTGGAATCTTT	TCGTCCTAAAATGCGGCTGCGTTT
6	6q16	EPHA7	-	DEL#7	0.5679	1.151	0.4934	AATGAGATATTTGGCTGATATGGGATA	AACGAGATTGCTGTTGACAAGAAT	TTCACAGGGACCTTGCAGCTCGC
6	6q21	CDC2L6	-	DEL#8	0.206	0.4038	0.51015	GCAGTTGCCAAGATCTATGGTTAA	CAATTTGCATGGAGGTAATGGA	TCCTTACTTTACCAGATTCTTGATGG
6	6q24-q25.1	LATS1	+	DEL#9	0.36	0.57	0.63	GGTCACTGGAGAAGTCAATTGTTTT	GGACCCGAAGATCGCTTAGG	TGGATGAGCTTTTATTTCATCAGCACCATTCT

Johnson, Wright et al., Supplemental Table 4

Chr	Cyto	RT-PCR Target gene	CNV	Gene Card #	average RT-PCR CNA samples	average RT-PCR CNTRL samples	RATIO	Forward Primer	Reverse Primer	Fam Probe
6	6q25.2	RBM16	-	DEL#10	0.281	0.931	0.30183	GGCTCTAGAAAGCGTAAACACAGAA	GAATACGACCGTGATGATTTCCT	CGATCACGCTCCCGCTCAAGA
7	7p12	GBAS	-	AMP#12	2.83	1.70	1.66	CGTAAGGCAAGAAGTGACATGCT	AGGCTCATTCCAGAAACTGAACTC	CTCTCCAGGAAGAATCAGCTCCTGT
7	7q36.3	PTPRN2	+	AMP#13	6.42724	1.345524	4.77676	GCAGCCTGGAGCCACAGT	GCAAAGGCCTGGGCATT	CCTTCTGCGTGCACCCTCAA
8	8p23.3	ERICH1	+	AMP#14	6.2755	3.329696	1.88471	GCCTTGCGTCACACAGCAT	AGGAGCAGCAGCGTTTTCAT	CTGCCCTCAGACGTGTCCATCC
9	9p21	MTAP	-	DEL#11	0.34	0.94	0.37	AGGAAGTCACGAAATGAGGAGTTC	GGGACACCGCCAAACCTTA	TGCCACATTTGCAGAGTCCCTCCTTG
9	9q31.3	LTB4DH	-	AMP#15	2.70	0.52	5.16	TTGTTGGAGCAGTAGGGTCTGA	GCTTTCTTCAAGGTTTCTTCCAAA	AAAAGGTTGCCTACCTTCAAAAGCTTGGATTT
9	9q34.1	CDK9	-	DEL#12	0.4114	1.367	0.30095	TCCCCTCTTTCTCACCCAGTT	TCTCGTGTTTTAGAAGCTGAAGGA	CCCATTACAGCCTTGCGGGAGATCA
9	9q34.3	NOTCH1	+	AMP#16	1.65	0.75	2.19	CGTGGGCTCCCGTGTTT	GGCGTTGCACAGCTCAATG	TAGGAGACTTGCCAGAGCCGGG
10	10q21	CXXC6	-	DEL#13	0.61	0.99	0.62	AATGGAAGCCAAGATCAAATCTG	GAGTGAAACACGTTCTTTTTTTGC	CCATCGAGGTCCTGGCACCCC
10	10q23.3	PTEN	-	DEL#14	0.6129	0.993	0.61722	GATCTTGACCAATGGCTAAGTGAA	TCGTCCCTTTCCAGCTTTACA	ATGACAATCATGTTGCAGCAATTCA
10	10q23.32	CPEB3	-	DEL#15	1.083	7.533	0.14377	CGGCCCGGACAAGATG	AGGAGGCTGATGGAAACTCAAG	AGATGGAATCACCGCTCCTGCC
10	10q24.32	PPRC1	-	DEL#16	0.42	4.40	0.09	TGAGGAGGCGGGTGATTCT	CAGGTCCTTGTCCCTCAGAGAT	CTTTGTCAGTCTCTCTCGGCTGGGCC
11	11p15.5	HRAS	+	AMP#17	1.20	0.74	1.63	CCTGTTGGACATCCTGGATACC	TGTTGATGGCAAACACACACA	TACAGCGCCATGCGGGACCA
11	11q13.3	CCND1	+	AMP#18	33.12	1.14	29.13	CGTGGCCTCTAAGATGAAGGA	TGTCGGTGTAGATGCACAGCTT	ACCATCCCCCTGACGGCCGA
12	12q14	CDK4	-	AMP#19	30.6608	2.308333	13.2827	TTCTAAGAGGCCTAGATTTCCTTCAT	CACCACTTGTCACCAGAATGTTC	CCAATTGCATCGTTCACCGAGATCTG
13	13q11-q12	GJA3	-	AMP#20	12.35	2.16	5.73	CTGTTCGAGGTGGGCTTCA	GCGGTAGAGCGGCTTCAG	CGCCGGCCAGTACTTTCTGTACGG
14	14q13.1	SNX6	-	DEL#17	0.6065	1.254	0.48365	ACCAGCGAAGGTTACGTGAAG	CCAGTGCTGTTTGAACTGTTGAG	AAAACGCACTCAGCCAGCAACGG
14	14q21.3	FANCM	-	DEL#18	0.2521	1.014	0.24862	GGAAGGAAATATGGTGCAGTAAGAGA	CGGGACAAGCTCCTCTAGAAAG	TGCTTTTTCTTACACCTCAGGTCATGGTAAATGA
16	16p13.3	CLDN6	-	AMP#21	3.15	0.77	4.06	GGCCCCAGCCATTACATG	GACGTAATTCTTGGTAGGGTACTCAGA	CTGCCCCTGCCATCTCTCGGG

Johnson, Wright et al., Supplemental Table 4

Chr	Cyto	RT-PCR Target gene	CNV	Gene Card #	average RT-PCR CNA samples	average RT-PCR CNTRL samples	RATIO	Forward Primer	Reverse Primer	Fam Probe
16	16p11.2	STX4A	+	AMP#22	11.6663	0.699543	16.677	GGGTCCTGTCCCAGCAATT	CGTTCTTCTCCCGGTATTCG	TGGAGCTCATCAACAAGTGCAATTCAATG
16	16q22.1	FBXL9	-	AMP#23	8.32	3.67	2.26	TGCCTTCTTTTGGGATTGTTG	TCCCGATGCCATCACAGTT	CCCCCGGGTCTTTACCGAGTTGG
17	17p13	SRR	-	DEL#19	0.35	1.37	0.25	GCTCAGTATTGCATCTCCTTTGC	AGCACTGGTGTGAGGTGGATAGA	TGTTGAAAAAGCTCATATCAACATTCG
17	17p11.2	NCOR1	-	DEL#20	0.3293	1.186	0.27766	TGATTATCGTTCCTCTCATCTTGAAGT	AAGGAAGGTCGCCTTCGAA	AGTCAGGCATCACAGCTTTTGCAGCA
18	18q11.2	RBBP8	-	AMP#24	37.10	1.43	25.89	GAGGCTTTGAAGACCATTCCAA	TTGGGCAACGTGCAGTTG	TTTTCCTCAAGCCGTAAGGCCTCAGATG
19	19p13.3	TJP3	-	AMP#25	6.10	1.33	4.59	GGTGTCTAGCCAGAACCTGTCACT	CAGGCTTAGCTTCCCTTCTGACT	ACGACACCCGGCGACTGATTGAG
19	19p13.2	JUNB	+	AMP#26	1.68	0.53	3.19	ACTCATACACAGCTACGGGATACG	GGCTCGGTTTCAGGAGTTTG	CCCCTGGTGGCCTCTCTCTACACGA
19	19p13.11	JUND	-	AMP#27	4.37	1.36	3.21	AGAAAGTGAAGACCCTCAAGAGTCA	GACGTGGCTGAGGACTTTCTG	AACACGGAGCTGGCGTCCACG
19	19q13.2	SPTBN4	-	AMP#28	2.73	1.83	1.49	AAACCTTCACCAAGTGGGTGAA	CACATAGAGGTCCCCGATGTG	TCGCACCTCGCCCGCGT
22	22q11.23	BCR	-	DEL#21	1.005	3.202	0.31387	CCCATGAAGCCTTTGAAAGC	AAGATGGTCTCGATCTGCTGACT	CTGCCACCACCTCTCAGCCGG
22	22q12.2	SF3A1	-	DEL#22	0.35	0.64	0.54	CAATGACCCTTACCATGCCTACT	TCCTGAGCCTTCCCTTCCTT	CCGCCACAAGGTCAGCGAGTT
22	22q13.1	TNRC6B	-	DEL#23	0.36	0.74	0.48	GCCGCCGCGATTCC	GGGCTGCCCACGTTTTAGT	TTGCCAGCAGGACCACAAAGTGT

Johnson, Wright et al., Supplemental Table 5a

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Amplification #1	C1orf159	CENTTB5	
Amplification #1	TTLL10	MRPL20	
Amplification #1	MIR200B	ATAD3B	
Amplification #1	MIR200A	ATAD3A	
Amplification #1	MIR429	MIB2	
Amplification #1	TNFRSF18		
Amplification #1	TNFRSF4		
Amplification #1	FAM132A		
Amplification #1	UBE2J2		
Amplification #1	SDF4		
Amplification #1	B3GALT6		
Amplification #1	SCNN1D		
Amplification #1	ACAP3		
Amplification #1	PUSL1		
Amplification #1	CPSF3L		
Amplification #1	TAS1R3		
Amplification #1	DVL1		
Amplification #1	GLTPD1		
Amplification #1	MXRAS		
Amplification #1	AURKAIP1		
Amplification #1	LOC148413		
Amplification #1	MRPL20		
Amplification #1	LOC441869		
Amplification #1	TMEM88B		
Amplification #1	VWA1		
Amplification #1	ATAD3C		
Amplification #1	ATAD3B		
Amplification #1	ATAD3A		
Amplification #1	C1orf70(MIB2)		
Amplification #1	SSU72		
Amplification #2	PRDM16		
Amplification #2	ARHGEF16		
Amplification #3	MEGF6		
Amplification #4	MIR551A		
Amplification #5	TPRG1L		
Amplification #6	WDR8		
Amplification #7	TP73		
Amplification #8	KIAA0495		
Amplification #9	CCDC27		
Amplification #3	C1QB		
Amplification #3	EPHB2		
Amplification #4	LASS2	CDC42SE1	
Amplification #4	ANXA9	MLLT11	
Amplification #4	FAM63A	LYSMD1	
Amplification #4	PRUNE	SCNM1	

Johnson, Wright et al., Supplemental Table 5a

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Amplification #4	BNIPL	VPS72	
Amplification #4	C1orf56	PIP5K1A	
Amplification #4	CDC42SE1	PSMD4	
Amplification #4	MLLT11	ZNF687	
Amplification #4	GABPB2	PI4KB	
Amplification #4	SEMA6C	HIST2H3D	
Amplification #4	TNFAIP8L2	RFX5	
Amplification #4	LYSMD1	PSMB4	
Amplification #4	SCNM1	POGZ	
Amplification #4	TMOD4	TUFT1	
Amplification #4	VPS72	SNX27	
Amplification #4	PIP5K1A	MRPL9	
Amplification #4	PSMD4	OAZ3	
Amplification #4	ZNF687	TDRKH	
Amplification #4	PI4KB		
Amplification #4	RFX5		
Amplification #4	SELENBP1		
Amplification #4	PSMB4		
Amplification #4	POGZ		
Amplification #4	CGN		
Amplification #4	TUFT1		
Amplification #4	MIR554		
Amplification #4	SNX27		
Amplification #4	TNRC4		
Amplification #4	C1orf230		
Amplification #4	MRPL9		
Amplification #4	OAZ3		
Amplification #4	TDRKH		
Amplification #4	LINGO4		
Amplification #4	RORC		
Amplification #4	THEM5		
Amplification #4	C2CD4D		
Amplification #4	LOC100132111		
Amplification #5	WNT9A	ARF1	
Amplification #5	WNT3A	C1ORF35	
Amplification #5	ARF1	MRPL55	
Amplification #5	MRPL55	GUK1	
Amplification #5	C1ORF35	C1ORF69	
Amplification #5	GUK1		
Amplification #5	GJC2		
Amplification #5	C1ORF69		
Amplification #5	OBSCN		
Amplification #6	EXO1	EXO1	
Amplification #7	PIGG	PIGG	ATP5I
Amplification #7	PDE6B	ATP5I	GAK

Johnson, Wright et al., Supplemental Table 5a

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Amplification #7	ATP5I	GAK	
Amplification #7	MYL5		
Amplification #7	MFSD7		
Amplification #7	PCGF3		
Amplification #7	CPLX1		
Amplification #7	GAK		
Amplification #7	TMEM175		
Amplification #7	DGKQ		
Amplification #7	SLC26A1		
Amplification #7	IDUA		
Amplification #7	FGFRL1		
Amplification #8	SPON2	CTBP1	RNF212
Amplification #8	LOC100130872	KIAA1530	CTBP1
Amplification #8	CTBP1	CRIPAK	LOC730744
Amplification #8	C4orf42	FAM53A	CRIPAK
Amplification #8	MAEA	SLBP	SLBP
Amplification #8	KIAA1530	WHSC1	TMEM129
Amplification #8	CRIPAK	WHSC2	LETM1
Amplification #8	FAM53A		WHSC1
Amplification #8	SLBP		WHSC2
Amplification #8	TMEM129		
Amplification #8	TACC3		
Amplification #8	FGFR3		
Amplification #8	LETM1		
Amplification #8	WHSC2		
Amplification #8	WHSC1		
Amplification #8	SCARNA22		
Amplification #8	C4orf48		
Amplification #8	MIR943		
Amplification #9	SDHA	SDHA	
Amplification #9	PDCD6	LOC728613	
Amplification #9	AHRR	PDCD6	
Amplification #9	LOC100310782	LOC116349	
Amplification #9	C5orf55	EXOC3	
Amplification #9	EXOC3		
Amplification #9	LOC25845		
Amplification #9	SLC9A3		
Amplification #10	S1L1	LRRTM2	
Amplification #10	SNHG4	LOC727839	
Amplification #10	SNORA74A	PURA	
Amplification #10	MATR3	LOC492311	
Amplification #10	PA1P2	ANKHD1	
Amplification #10	SLC23A1	APBB3	
Amplification #10	MCC29506	ZMAT2	
Amplification #10	LOC389333	PCDHA5	

Johnson, Wright et al., Supplemental Table 5a

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Amplification #10	SPATA24	PCDHA1	
Amplification #10	DNAJC18	PCDHB2	
Amplification #10	ECSCR	PCDHB6	
Amplification #10	THEM173	PCDHB13	
Amplification #10	UBE2D2	PCDHB15	
Amplification #10	CXXC5	PCDHGA3	
Amplification #10	PSD2	PCDHGA11	
Amplification #10	NRG2	PCDHGA1	
Amplification #10	PURA	DIAPHA1	
Amplification #10	C5orf53	RELL2	
Amplification #10	C5orf32	KIAA0141	
Amplification #10	PPDN1	PCDH12	
Amplification #10	HBECF		
Amplification #10	SLC4A9		
Amplification #10	ANKHD1		
Amplification #10	SRA1		
Amplification #10	EIF4EBF3		
Amplification #10	APBB3		
Amplification #10	SLC35A4		
Amplification #10	CD14		
Amplification #10	DND1		
Amplification #10	TMCO5		
Amplification #10	NDUFAA2		
Amplification #10	IK		
Amplification #10	WDR55		
Amplification #10	HARS		
Amplification #10	HARS2		
Amplification #10	ZMAT2		
Amplification #10	VTRNA1-1		
Amplification #10	VTRNA1-2		
Amplification #10	VTRNA1-3		
Amplification #10	PCDHA1		
Amplification #10	PCDHA2		
Amplification #10	PCDHA3		
Amplification #10	PCDHA4		
Amplification #10	PCDHA5		
Amplification #10	PCDHA6		
Amplification #10	PCDHA7		
Amplification #10	PCDHA8		
Amplification #10	PCDHA9		
Amplification #10	PCDHA10		
Amplification #10	PCDHA11		
Amplification #10	PCDHA12		
Amplification #10	PCDHA13		
Amplification #10	PCDHAC1		

Johnson, Wright et al., Supplemental Table 5a

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Amplification #10	PCDHAC2		
Amplification #10	PCDHB1		
Amplification #10	PCDHB2		
Amplification #10	PCDHB3		
Amplification #10	PCDHB4		
Amplification #10	PCDHB5		
Amplification #10	PCDHB6		
Amplification #10	PCDHB7		
Amplification #10	PCDHB8		
Amplification #10	PCDHB9		
Amplification #10	PCDHB10		
Amplification #10	PCDHB11		
Amplification #10	PCDHB12		
Amplification #10	PCDHB13		
Amplification #10	PCDHB16		
Amplification #10	PCDHB17		
Amplification #10	PCDHB18		
Amplification #10	PCDHB19		
Amplification #10	PCDHB15		
Amplification #10	PCDHB14		
Amplification #10	SLC23A2		
Amplification #10	TAF7		
Amplification #10	PCDHGA8		
Amplification #10	PCDHGB5		
Amplification #10	PCDHGA1		
Amplification #10	PCDHGB7		
Amplification #10	PCDHGA2		
Amplification #10	PCDHGC3		
Amplification #10	PCDHGA3		
Amplification #10	PCDHGB1		
Amplification #10	PCDHGC4		
Amplification #10	PCDHGC5		
Amplification #10	DIAPHA1		
Amplification #10	PCDHGA4		
Amplification #10	PCDHGB2		
Amplification #10	PCDHGA5		
Amplification #10	PCDHGB3		
Amplification #10	PCDHGA6		
Amplification #10	PCDHGA7		
Amplification #10	PCDHGB4		
Amplification #10	PCDHGA8		
Amplification #10	PCDHGB5		
Amplification #10	PCDHGA9		
Amplification #10	PCDHGB6		
Amplification #10	PCDHGA10		

Johnson, Wright et al., Supplemental Table 5a

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Amplification #10	PCDHGB7		
Amplification #10	PCDHGA11		
Amplification #10	PCDHGB8P		
Amplification #10	PCDHGA12		
Amplification #10	HDAC3		
Amplification #10	RELL2		
Amplification #10	ARAP3		
Amplification #10	FCHSD1		
Amplification #11	SERPINB6	TUBB2B	
Amplification #11	DKFZP686I151217		
Amplification #11	NQO2		
Amplification #11	FAM136B		
Amplification #11	RIPK1		
Amplification #11	BPHL		
Amplification #11	TUBB2A		
Amplification #11	TUBB2B		
Amplification #12	ZNF713	MRPS17	PSPH
Amplification #12	MRPS17	GBAS	SUMF2
Amplification #12	GBAS	PSPH	CHCHD2
Amplification #12	PSPH	SUMF2	MRPS17
Amplification #12	CCT6A	CHCHD2	GBAS
Amplification #12	SNORA15		CCT6A
Amplification #12	SUMF2		PHKG1
Amplification #12	PHKG1		
Amplification #12	CHCHD2		
Amplification #12	LOC389493		
Amplification #13	PTPRN2	PTPRN2	
Amplification #14	ERICH1	ERICH1	ERICH1
Amplification #15	LTBH4		
Amplification #15	AK091948		
Amplification #15	BC040897		
Amplification #15	BC048318		
Amplification #15	BA16L21.2.1		
Amplification #15	LOC552891		
Amplification #16	SOHLH1	FAM69B	CAMSAP1
Amplification #16	KCNT1	C9ORF86	
Amplification #16	CAMSAP1	PHPT1	
Amplification #16	UBAC1	WDR85	
Amplification #16	NACC2	ZMYND19	
Amplification #16	C9ORF69	EHMT1	
Amplification #16	LHX3		
Amplification #16	QSOX2		
Amplification #16	GPSM1		
Amplification #16	LOC26102		
Amplification #16	DNLZ		

Johnson, Wright et al., Supplemental Table 5a

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Amplification #16	CARD9		
Amplification #16	SNAPC4		
Amplification #16	SDCCAG3		
Amplification #16	PMPCA		
Amplification #16	INPP5E		
Amplification #16	SEC16A		
Amplification #16	C9ORF163		
Amplification #16	NOTCH1		
Amplification #16	EGFL7		
Amplification #16	MIR126		
Amplification #16	AGPAT2		
Amplification #16	FAM69B		
Amplification #16	SNHG7		
Amplification #16	SNORA43		
Amplification #16	SNORA17		
Amplification #16	LCN10		
Amplification #16	LCN6		
Amplification #16	LCN8		
Amplification #16	LCN15		
Amplification #16	PHPT1		
Amplification #16	EDF1		
Amplification #16	THEM141		
Amplification #16	KIAA1984		
Amplification #16	LOC100131193		
Amplification #16	C9ORF86		
Amplification #16	C9ORF172		
Amplification #16	MAMDC4		
Amplification #16	TRAF2		
Amplification #16	FBXW5		
Amplification #16	C8G		
Amplification #16	LCN12		
Amplification #16	PTGDS		
Amplification #16	LCNL1		
Amplification #16	C9ORF142		
Amplification #16	CLIC3		
Amplification #16	FUT7		
Amplification #16	NPDC1		
Amplification #16	ABCA2		
Amplification #16	C9ORF139		
Amplification #16	ENTPD2		
Amplification #16	C9ORF140		
Amplification #16	UAP1LA		
Amplification #16	MAN1N1		
Amplification #16	DPP7		
Amplification #16	GRIN1		

Johnson, Wright et al., Supplemental Table 5a

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Amplification #16	LOC100289341		
Amplification #16	NDOR1		
Amplification #16	TUBB2C		
Amplification #16	SSNA1		
Amplification #16	TMEM203		
Amplification #16	COBRA1		
Amplification #16	LRRC26		
Amplification #16	ANAPC2		
Amplification #16	C9ORF75		
Amplification #16	RNF208		
Amplification #16	C9ORF169		
Amplification #16	SLC34A3		
Amplification #16	FAM166A		
Amplification #16	C9ORF173		
Amplification #16	C9ORF167		
Amplification #16	NRARP		
Amplification #16	EXD3		
Amplification #16	NELF		
Amplification #16	ENTPD8		
Amplification #16	PNPLA7		
Amplification #16	NOXA1		
Amplification #16	EHMT1		
Amplification #16	MRPL41		
Amplification #16	WDR85		
Amplification #16	ZMYND19		
Amplification #16	ARRDC1		
Amplification #16	C9ORF37		
Amplification #17	B4GALNT4	PKP3	PKP3
Amplification #17	PKP3		
Amplification #17	SIGIRR		
Amplification #17	ANO9		
Amplification #17	PTDSS2		
Amplification #17	RNH1		
Amplification #17	HRAS		
Amplification #17	LRRC56		
Amplification #17	C11ORF35		
Amplification #17	RASSF7		
Amplification #17	MIR210		
Amplification #17	PHRF1		
Amplification #17	LOC143666		
Amplification #17	IRF7		
Amplification #17	MUPCDH		
Amplification #17	SCT		
Amplification #17	DRD4		
Amplification #18	CCND1		

Johnson, Wright et al., Supplemental Table 5a

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Amplification #18	ORAOV1		
Amplification #18	FGF19		
Amplification #18	FGF4		
Amplification #18	FGF3		
Amplification #19	MYO1A	MBD6	
Amplification #19	TMEM194A	TSPAN31	
Amplification #19	NAB2		
Amplification #19	STAT6		
Amplification #19	LRP1		
Amplification #19	NXPH4		
Amplification #19	SHMT2		
Amplification #19	NDUFA4L2		
Amplification #19	STAC3		
Amplification #19	R3HDM2		
Amplification #19	INHBC		
Amplification #19	INHBE		
Amplification #19	GLI1		
Amplification #19	ARHGAP9		
Amplification #19	MBD6		
Amplification #19	MARS		
Amplification #19	DDTN2		
Amplification #19	DDIT3		
Amplification #19	KIF5A		
Amplification #19	DTX3		
Amplification #19	PIP4K2C		
Amplification #19	GEFT		
Amplification #19	SLC26A10		
Amplification #19	B4GALNT1		
Amplification #19	OS9		
Amplification #19	AGAP2		
Amplification #19	TSPAN31		
Amplification #19	CDK4		
Amplification #19	LOC100130776		
Amplification #19	MARCH9		
Amplification #19	CYP27B1		
Amplification #19	METTL1		
Amplification #19	FAM119B		
Amplification #19	TSFM		
Amplification #19	MIR26A2		
Amplification #19	AVIL		
Amplification #19	CTDSP2		
Amplification #19	XRCC6BP1		
Amplification #20	ZYYM2	ZYYM2	
Amplification #20	GJA3		
Amplification #20	GJB2		

Johnson, Wright et al., Supplemental Table 5a

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Amplification #20	GJB6		
Amplification #21	PKMYT1	MMP25	HCFC1R1
Amplification #21	CLDN9	ZNF200	
Amplification #21	CLDN6		
Amplification #21	TNFRSF12A		
Amplification #21	HCFC1R1		
Amplification #21	THOC6		
Amplification #21	CCDC64B		
Amplification #21	MMP25		
Amplification #21	IL32		
Amplification #21	ZSCAN10		
Amplification #21	MGC3771		
Amplification #21	ZNF205		
Amplification #21	ZNF213		
Amplification #21	OR1F1		
Amplification #21	OR1F2P		
Amplification #21	ZNF200		
Amplification #21	MEFV		
Amplification #21	ZNF263		
Amplification #22	FBRS	FBRS	FBRS
Amplification #22	SRCAP	PHKG2	SRCAP
Amplification #22	SNORA30	LOC90835	PHKG2
Amplification #22	PHKG2	STX1B	LOC90835
Amplification #22	RNF40	VKORC1	RNF40
Amplification #22	C16ORF93	BCKDK	ZNF629
Amplification #22	ZNF629		BCL7C
Amplification #22	BCL7C		CTF1
Amplification #22	CTF1		LOC283932
Amplification #22	NCRNA00095		FBXL19
Amplification #22	FBXL19		ORAI3
Amplification #22	ORAI3		SETD1A
Amplification #22	SETD1A		HSD3N7
Amplification #22	HSD3N7		STX1B
Amplification #22	STX1B		STX4
Amplification #22	STX4		ZNF668
Amplification #22	ZNF668		ZNF646
Amplification #22	ZNF646		POL3S
Amplification #22	POL3S		VKORC1
Amplification #22	VKORC1		BCKDK
Amplification #22	BCKDK		MYST1
Amplification #22	PRSS8		PRSS8
Amplification #22	PRSS36		PRSS36
Amplification #22	MYST1		FUS
Amplification #22	FUS		
Amplification #23	FBXL8	PLEKHG4	SLC9A5

Johnson, Wright et al., Supplemental Table 5a

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Amplification #23	HSF4	LRRC36	THAP11
Amplification #23	NOL3	ACD	
Amplification #23	KIAA0895L	SLC12A4	
Amplification #23	EXOC3L	DDX28	
Amplification #23	E2F4	RBM35B	
Amplification #23	ELMO3		
Amplification #23	MIR326		
Amplification #23	LRRC29		
Amplification #23	TMEM208		
Amplification #23	FHOD1		
Amplification #23	SLC9A5		
Amplification #23	PLEKHG4		
Amplification #23	KCTD19		
Amplification #23	LRRC36		
Amplification #23	TPPP3		
Amplification #23	ZDHHC1		
Amplification #23	HSD11B2		
Amplification #23	ATP56V0D1		
Amplification #23	AGRP		
Amplification #23	FAM65A		
Amplification #23	RLTPR		
Amplification #23	ACD		
Amplification #23	CTCF		
Amplification #23	PARD6A		
Amplification #23	C16ORF48		
Amplification #23	C16ORF86		
Amplification #23	GFOD2		
Amplification #23	RANBP10		
Amplification #23	TSNAXIP1		
Amplification #23	CENPT		
Amplification #23	THAP11		
Amplification #23	NUTF2		
Amplification #23	EDC4		
Amplification #23	NRN1L		
Amplification #23	PSKH1		
Amplification #23	PSMB10		
Amplification #23	SLC12A4		
Amplification #23	CTRL		
Amplification #23	LCAT		
Amplification #23	DPEP3		
Amplification #23	DPEP2		
Amplification #23	DDX28		
Amplification #23	DUS2L		
Amplification #23	NFATC3		
Amplification #23	ESRP2		

Johnson, Wright et al., Supplemental Table 5a

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Amplification #23	PLA2G15		
Amplification #23	SLC7A6		
Amplification #24	RBBP8	CABLES1	
Amplification #24	CABLES1	RIOK3	
Amplification #24	C18ORF45	C18ORF8	
Amplification #24	RIOK3		
Amplification #24	NPC1		
Amplification #24	C18ORF8		
Amplification #24	ANKRD29		
Amplification #24	LAMA3		
Amplification #25	TLE2	BRUNOL5	
Amplification #25	AES	DOHH	
Amplification #25	GNA11	CHAF1A	
Amplification #25	S1PR4		
Amplification #25	NCLN		
Amplification #25	BRUNOL5		
Amplification #25	GNA15		
Amplification #25	NFIC		
Amplification #25	DOHH		
Amplification #25	C19ORF77		
Amplification #25	FZR1		
Amplification #25	C19ORF28		
Amplification #25	C19ORF71		
Amplification #25	C19ORF26		
Amplification #25	HMG20B		
Amplification #25	GIPC3		
Amplification #25	TBXA2R		
Amplification #25	C19ORF29		
Amplification #25	PIP5K1C		
Amplification #25	TJP3		
Amplification #25	APBA3		
Amplification #25	MRPL54		
Amplification #25	RAX2		
Amplification #25	MATK		
Amplification #25	ZFR2		
Amplification #25	ATCAY		
Amplification #25	ITGB1BP3		
Amplification #25	DAPK3		
Amplification #25	MIR637		
Amplification #25	EEF2		
Amplification #25	SNORA37		
Amplification #25	PIAS4		
Amplification #25	ZBTB7A		
Amplification #25	MAP2K2		
Amplification #25	CREB3L3		

Johnson, Wright et al., Supplemental Table 5a

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Amplification #25	SIRT6		
Amplification #25	ANKRD24		
Amplification #25	EBI3		
Amplification #25	CCDC94		
Amplification #25	TMIGD2		
Amplification #25	SHD		
Amplification #25	FSD1		
Amplification #25	MPND		
Amplification #25	CHAF1A		
Amplification #25	STAP2		
Amplification #25	SH3GL1		
Amplification #25	UBXN6		
Amplification #25	HDGF2		
Amplification #25	PLIN4		
Amplification #25	PLIN5		
Amplification #25	LRG1		
Amplification #25	SEMA6B		
Amplification #26	TNP02	MAST1	TNP02
Amplification #26	SNORD41	NFIX	C19ORF43
Amplification #26	C19ORF43		BEST2
Amplification #26	BEST2		ASNA1
Amplification #26	ASNA1		HOOK2
Amplification #26	HOOK2		JUNB
Amplification #26	JUNB		PRDX2
Amplification #26	PRDX2		RTBDN
Amplification #26	RTBDN		RNASEH2A
Amplification #26	RNASEH2A		MAST1
Amplification #26	MAST1		DNASE2
Amplification #26	DNASE2		KLF1
Amplification #26	KLF1		GCDH
Amplification #26	GCDH		SYCE2
Amplification #26	SYCE2		FARSA
Amplification #26	FARSA		CALR
Amplification #26	CALR		RAD23A
Amplification #26	RAD23A		DAND5
Amplification #26	DAND5		GADD45GIP1
Amplification #26	GADD45GIP1		NFIX
Amplification #26	NFIX		LYL1
Amplification #26	LYL1		TRMT1
Amplification #26	TRMT1		BTBD14B
Amplification #26	NACC1		STX10
Amplification #26	STX10		IER2
Amplification #26	IER2		CACANA1A
Amplification #26	CACANA1A		
Amplification #27	KCNN1	PDE4C	KCNN1

Johnson, Wright et al., Supplemental Table 5a

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Amplification #27	ARRDC2		ARRDC2
Amplification #27	MAST3		MAST3
Amplification #27	IL12RB1		RAB3A
Amplification #27	PIK3R2		PDE4C
Amplification #27	IFI30		JUND
Amplification #27	RAB3A		LSM4
Amplification #27	PDE4C		
Amplification #27	MPV17L2		
Amplification #27	KIAA1683		
Amplification #27	JUND		
Amplification #27	GDF15		
Amplification #27	LSM4		
Amplification #27	PGPEP1		
Amplification #27	LRRC25		
Amplification #27	SSBP4		
Amplification #27	ISYNA1		
Amplification #27	ELL		
Amplification #27	FKBP8		
Amplification #27	C19ORF50		
Amplification #27	UBA52		
Amplification #27	C19ORF60		
Amplification #27	CRLF1		
Amplification #27	TMEM59L		
Amplification #27	KLHL26		
Amplification #27	CRTC1		
Amplification #27	COMP		
Amplification #27	GDF1		
Amplification #27	LASS1		
Amplification #27	UPF1		
Amplification #27	COPE		
Amplification #27	DDX49		
Amplification #27	HOMER3		
Amplification #28	MAP3K10	MAP3K10	AKT2
Amplification #28	TTC9B	BLVRB	MAP3K10
Amplification #28	CNTD2		TTC9B
Amplification #28	AKT2		SERTAD3
Amplification #28	MIR641		
Amplification #28	PLD3		
Amplification #28	C19ORF47		
Amplification #28	PRX		
Amplification #28	HIPK4		
Amplification #28	SERTAD1		
Amplification #28	SERTAD3		
Amplification #28	BLVRB		
Amplification #28	SPTBN4		

Johnson, Wright et al., Supplemental Table 5a

GENE CARD #	**Genes in region**	**copy number driven expression**	**Subgroup specific expression**
Amplification #28	SHKBP1		
Amplification #28	LTBP4		
TOTAL	**632**	**107**	**85**

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#1	TRIM63	TRSPAP1	
Deletion#1	PDIK1L		
Deletion#1	GRRP1		
Deletion#1	ZNF593		
Deletion#1	CNKSR1		
Deletion#1	CATSPER4		
Deletion#1	CCDC21		
Deletion#1	SH3BGRL3		
Deletion#1	UBXN11		
Deletion#1	CD52		
Deletion#1	AIM1L		
Deletion#1	ZNF683		
Deletion#1	LIN28		
Deletion#1	DHDDS		
Deletion#1	HMGN2		
Deletion#1	RPS6KA1		
Deletion#1	ARID1A		
Deletion#1	PIGV		
Deletion#1	ZDHHC18		
Deletion#1	SFN		
Deletion#1	GPN2		
Deletion#1	NR0B2		
Deletion#1	NUDC		
Deletion#1	GPATCH3		
Deletion#1	C1orf172		
Deletion#1	TRNP1		
Deletion#1	FAM46B		
Deletion#1	SLC9A1		
Deletion#1	WDTC1		
Deletion#1	TMEM222		
Deletion#1	SYTL1		
Deletion#1	MAP3K6		
Deletion#1	FCN3		
Deletion#1	CD164L2		
Deletion#1	GPR3		
Deletion#1	WASF2		
Deletion#1	AHDC1		
Deletion#1	FGR		
Deletion#1	TFI6		
Deletion#1	FAM76A		
Deletion#1	STX12		
Deletion#1	PPP1R8		
Deletion#1	SCARNA1		
Deletion#1	C1orf38		
Deletion#1	SMPDL3B		

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#1	RPA2		
Deletion#1	XKR8		
Deletion#1	EYA3		
Deletion#1	PTAFR		
Deletion#1	DNAJC8		
Deletion#1	ATP1F1		
Deletion#1	SESN2		
Deletion#1	MED18		
Deletion#1	PHACTR4		
Deletion#1	SNHG3		
Deletion#1	RCC1		
Deletion#1	SNHG3-RCC1		
Deletion#1	TRNAU1AP		
Deletion#1	SNHG12		
Deletion#1	SNORD99		
Deletion#1	SNORD61		
Deletion#1	SNORD44		
Deletion#1	SNORA16A		
Deletion#1	RAB42		
Deletion#1	TAF12		
Deletion#1	RNU11		
Deletion#1	GMEB1		
Deletion#1	YTHDF2		
Deletion#1	OPRD1		
Deletion#1	EPB41		
Deletion#2	MTMR14	OGG1	
Deletion#2	CPNE9	CAMK1	
Deletion#2	BRPF1	TADA3L	
Deletion#2	OGG1	ARPC4	
Deletion#2	CAMK1	RPUSD3	
Deletion#2	TADA3L	CIDEC	
Deletion#2	ARPC4	JAGN1	
Deletion#2	TTLL3	IL17RC	
Deletion#2	RPUSD3	CRELD1	
Deletion#2	CIDEC	PRRT3	
Deletion#2	JAGN1	THEM111	
Deletion#2	IL17RE	C3orf10	
Deletion#2	IL17RC	VHL	
Deletion#2	CRELD1		
Deletion#2	PRRT3		
Deletion#2	THEM111		
Deletion#2	LOC401052		
Deletion#2	CIDECP		
Deletion#2	FANCD2		
Deletion#2	C3orf24		

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#2	C3orf10		
Deletion#2	VHL		
Deletion#2	IRAK2		
Deletion#3	SCAP	CCDC72	PRKAR2A
Deletion#3	C3orf75	SLC25A20	USP4
Deletion#3	CSPG5	ARIH2	
Deletion#3	SMARCC1	WDR6	
Deletion#3	DHX30	USP19	
Deletion#3	MAP4	USP4	
Deletion#3	CDC25A		
Deletion#3	CAMP		
Deletion#3	ZNF589		
Deletion#3	NME6		
Deletion#3	SPINK8		
Deletion#3	FBXW12		
Deletion#3	PLXNB1		
Deletion#3	CCDC51		
Deletion#3	ATR1P		
Deletion#3	CCDC72		
Deletion#3	TREX1		
Deletion#3	SH1SA5		
Deletion#3	PFKFB4		
Deletion#3	UCN2		
Deletion#3	COL7A1		
Deletion#3	UQCRC1		
Deletion#3	TMEM89		
Deletion#3	SLC26A6		
Deletion#3	CELSR3		
Deletion#3	NCKIPSD		
Deletion#3	IP6K2		
Deletion#3	PRKAR2A		
Deletion#3	SLC25A20		
Deletion#3	C3orf71		
Deletion#3	ARIH2		
Deletion#3	P4HTM		
Deletion#3	WDR6		
Deletion#3	DALRD3		
Deletion#3	MIR425		
Deletion#3	NDUFAF3		
Deletion#3	IMPDH2		
Deletion#3	QRICH1		
Deletion#3	QARS		
Deletion#3	LAMB2		
Deletion#3	CCDC71		
Deletion#3	KLHDC8B		

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#3	LOC646498		
Deletion#3	CCDC36		
Deletion#3	USP4		
Deletion#3	USP19		
Deletion#3	GPX1		
Deletion#3	RHOA		
Deletion#3	TCTA		
Deletion#4	PCCB	TMEM22	STAG1
Deletion#4	STAG1	NCK1	
Deletion#4	TMEM22		
Deletion#4	NCK1		
Deletion#4	IL20RB		
Deletion#5	USP49	CCND3	
Deletion#5	MED20	TAF8	
Deletion#5	BYSL	GUCA1B	
Deletion#5	CCND3	UBR2	
Deletion#5	TAF8	TNRC5	
Deletion#5	GUCA1A	MEA1	
Deletion#5	GUCA1B	KLC4	
Deletion#5	MRPS10	MRPS18A	
Deletion#5	TRERF1		
Deletion#5	UBR2		
Deletion#5	PRPH2		
Deletion#5	TBCC		
Deletion#5	KIAA0240		
Deletion#5	RPL741		
Deletion#5	C6ORF226		
Deletion#5	PTCRA		
Deletion#5	CNPY3		
Deletion#5	GNMT		
Deletion#5	PEX6		
Deletion#5	MEA1		
Deletion#5	PPP2R5D		
Deletion#5	KLHDC3		
Deletion#5	C6ORF153		
Deletion#5	CUL7		
Deletion#5	PTK7		
Deletion#5	MRPL2		
Deletion#5	KLC4		
Deletion#5	SRF		
Deletion#5	CUL9		
Deletion#5	TTBK1		
Deletion#5	SLC22A7		
Deletion#5	C6ORF108		
Deletion#5	CRIP3		

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#5	ZNF318		
Deletion#5	ABCC10		
Deletion#5	DLK2		
Deletion#5	TJAP1		
Deletion#5	XPO5		
Deletion#5	C6ORF154		
Deletion#5	YIPF3		
Deletion#5	POLR1C		
Deletion#5	FOLH		
Deletion#5	GTPBP2		
Deletion#5	MAD2L1BP		
Deletion#5	RSPH9		
Deletion#5	MRPS18A		
Deletion#5	VEGFA		
Deletion#6	LGSN	PHF3	
Deletion#6	PTP4A1		
Deletion#6	PHF3		
Deletion#6	EYS		
Deletion#7	EPHA7		
Deletion#7	TSG1		
Deletion#8	CDC2L6	CDC2L6	CDC2L6
Deletion#8	AMD1	GTF3C6	
Deletion#8	GTF3C6		
Deletion#8	RFF2		
Deletion#9	PPIL4	C6ORF72	PCMT1
Deletion#9	C6ORF72	NUP43	
Deletion#9	KATNA1	PCMT1	
Deletion#9	LATS1		
Deletion#9	NUP43		
Deletion#9	PCMT1		
Deletion#10	OPRM1	CNKSA3	
Deletion#10	IPCEF1		
Deletion#10	CNKSA3		
Deletion#10	RBM16		
Deletion#10	TIAM2		
Deletion#11	MTAF	CDKN2A	CDKN2B
Deletion#11	C9ORF53	CDKN2B	
Deletion#11	CDKN2A		
Deletion#11	CDKN2BAS		
Deletion#11	CDKN2B		
Deletion#12	GARNL3	RPL12	RPL12
Deletion#12	SLC2A8	C9ORF117	SET
Deletion#12	ZNF79	ST6GALNAC6	hCG_1644608
Deletion#12	RPL12	C9ORF16	C9ORF32
Deletion#12	SNORA65	CIZ1	TOR1A

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#12	LRSAM1	SLC27A4	EXOSC2
Deletion#12	FAM129B	SPTAN1	
Deletion#12	STXBP1	SET	
Deletion#12	PTRH1	hCG_1644608	
Deletion#12	TTC16	ZER1	
Deletion#12	TOR2A	ENDOG	
Deletion#12	C9ORF117	LRRC8A	
Deletion#12	SH2D3C	SH3GLB2	
Deletion#12	CDK9	PPP2R4	
Deletion#12	FPGS	C9ORF32	
Deletion#12	ENG	CDK9	
Deletion#12	AK1	GPR107	
Deletion#12	DPM2	EXOSC2	
Deletion#12	ST6GALNAC6		
Deletion#12	ST6GALNAC4		
Deletion#12	PIP5KL1		
Deletion#12	FAM102A		
Deletion#12	COQ4		
Deletion#12	NAIF1		
Deletion#12	PTGES2		
Deletion#12	LCN2		
Deletion#12	CIZ1		
Deletion#12	DNM1		
Deletion#12	LOC389791		
Deletion#12	SLC25A25		
Deletion#12	C9ORF16		
Deletion#12	MIR199B		
Deletion#12	GOLGA2		
Deletion#12	C9ORF119		
Deletion#12	TRUB2		
Deletion#12	SLC27A4		
Deletion#12	URM1		
Deletion#12	MIR219-2		
Deletion#12	CERCAM		
Deletion#12	ODF2		
Deletion#12	GLE1		
Deletion#12	SPTAN1		
Deletion#12	WDR34		
Deletion#12	SET		
Deletion#12	PKN3		
Deletion#12	ZDHHC12		
Deletion#12	ZER1		
Deletion#12	ENDOG		
Deletion#12	CCBL1		
Deletion#12	TBC1D13		

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#12	C9ORF114		
Deletion#12	LRRC8A		
Deletion#12	PHYHD1		
Deletion#12	DOLK		
Deletion#12	NUP188		
Deletion#12	CRAT		
Deletion#12	IER5L		
Deletion#12	C9ORF106		
Deletion#12	SH3GLB2		
Deletion#12	FAM73B		
Deletion#12	DOLPP1		
Deletion#12	PPP2R4		
Deletion#12	C9ORG50		
Deletion#12	METTL11A		
Deletion#12	ASB6		
Deletion#12	PRRX2		
Deletion#12	PTGES		
Deletion#12	TOR1B		
Deletion#12	TOR1A		
Deletion#12	C9ORF78		
Deletion#12	USP20		
Deletion#12	FNBP1		
Deletion#12	GPR107		
Deletion#12	FREQ		
Deletion#12	ASS1		
Deletion#12	FUBP3		
Deletion#12	PRDM12		
Deletion#12	EXOSC2		
Deletion#12	LOC100272217		
Deletion#12	ABL		
Deletion#13	PDLD	HNRNPH3	HNRNPH3
Deletion#13	HNRNPH3	RUFY2	RUFY2
Deletion#13	RUFY2	SLC25A16	DNA2L
Deletion#13	DNA2L	CXXC6	SLC25A16
Deletion#13	SLC25A16	CCAR1	CXXC6
Deletion#13	TET1	DDX50	CCAR1
Deletion#13	CCAR1	DDX21	STOX1
Deletion#13	SNORD98	KIAA1279	DDX50
Deletion#13	STOX1		DDX21
Deletion#13	DDX50		KIAA1279
Deletion#13	DDX21		
Deletion#13	KIAA1279		
Deletion#14	PAPSS2	ATAD1	PTEN
Deletion#14	ATAD1	PTEN	
Deletion#14	CFLP1		

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#14	KILLIN		
Deletion#14	PTEN		
Deletion#15	CPEB3	39512	CPEB3
Deletion#15	MARCH5	IDE	39512
Deletion#15	IDE	EXOC6	
Deletion#15	KIF11		
Deletion#15	HHEX		
Deletion#15	EXOC6		
Deletion#15	CYP26C1		
Deletion#15	CYP26A1		
Deletion#16	BTRC	FBXW4	NFKB2
Deletion#16	POLL	C10orf76	C10ORF26
Deletion#16	RP11-529I10.4	HPS6	GBF1
Deletion#16	FBXW4	PPRC1	FBXL15
Deletion#16	FGF8	NOLC1	CUEDC2
Deletion#16	NPM3	GBF1	ACTR1A
Deletion#16	MGEA5	CUEDC2	TRIM8
Deletion#16	KCNIP2	ACTR1A	ARL3
Deletion#16	C10orf76	SUFU	C10ORF32
Deletion#16	HPS6	TRIM8	SUFU
Deletion#16	LDB1	ARL3	
Deletion#16	PPRC1	C10ORF26	
Deletion#16	NOLC1	C10ORF32	
Deletion#16	ELOVL3	AS3MT	
Deletion#16	GBF1	CNNM2	
Deletion#16	PITX3		
Deletion#16	NFKB2		
Deletion#16	PSD		
Deletion#16	FBXL15		
Deletion#16	CUEDC2		
Deletion#16	MIR146B		
Deletion#16	C10orf95		
Deletion#16	TMEM180		
Deletion#16	ACTR1A		
Deletion#16	TRIM8		
Deletion#16	SUFU		
Deletion#16	ARL3		
Deletion#16	SFXN2		
Deletion#16	C10ORF26		
Deletion#16	CYP17A1		
Deletion#16	C10ORF32		
Deletion#16	AS3MT		
Deletion#16	CNNM2		
Deletion#17	EAPP	SNX6	SNX6
Deletion#17	SNX6		

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#18	C14ORF28		
Deletion#18	KLHL28		
Deletion#18	FAM179B		
Deletion#18	PRPF39		
Deletion#18	SNORD127		
Deletion#18	FKBP3		
Deletion#18	FANCM		
Deletion#18	C14ORF106		
Deletion#19	RPH3AL	TIMM22	TSR1
Deletion#19	C17orf97	CRK	
Deletion#19	FAM101B	DPH1	
Deletion#19	FAM57A	TSR1	
Deletion#19	ELP2P	LOC284009	
Deletion#19	NXN	KIAA0664	
Deletion#19	VPS53	ZZEF1	
Deletion#19	GEMIN4		
Deletion#19	GLOD4		
Deletion#19	RNMTL1		
Deletion#19	TIMM22		
Deletion#19	ABR		
Deletion#19	BHLHA9		
Deletion#19	TUSC5		
Deletion#19	YWHAE		
Deletion#19	CRK		
Deletion#19	SCARF1		
Deletion#19	RILP		
Deletion#19	PRFF8		
Deletion#19	MYO1C		
Deletion#19	INPP5K		
Deletion#19	LOC100306951		
Deletion#19	PITPNA		
Deletion#19	SLC43A2		
Deletion#19	TLCD2		
Deletion#19	C17orf91		
Deletion#19	MIR22		
Deletion#19	WDR81		
Deletion#19	SERP INF2		
Deletion#19	SERP INF1		
Deletion#19	RPA1		
Deletion#19	SMYD4		
Deletion#19	RTN4RL1		
Deletion#19	DPH1		
Deletion#19	OVCA2		
Deletion#19	MIR132		
Deletion#19	MIR212		

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#19	HIC1		
Deletion#19	SMG6		
Deletion#19	SRR		
Deletion#19	TSR1		
Deletion#19	SNORD91B		
Deletion#19	MNT		
Deletion#19	SGSM2		
Deletion#19	LOC284009		
Deletion#19	METT10D		
Deletion#19	SNORD911		
Deletion#19	PRFAH1B1		
Deletion#19	KIAA0664		
Deletion#19	RAP1GAP2		
Deletion#19	OR1D5		
Deletion#19	OR1D4		
Deletion#19	OR1D2		
Deletion#19	OR1G1		
Deletion#19	OR1A2		
Deletion#19	OR1A1		
Deletion#19	OR3A2		
Deletion#19	OR3A1		
Deletion#19	OR3A4		
Deletion#19	OR1E1		
Deletion#19	OR3A3		
Deletion#19	OR1E2		
Deletion#19	ASPA		
Deletion#19	TRPV1		
Deletion#19	TRPV3		
Deletion#19	SHPK		
Deletion#19	CTNS		
Deletion#19	SPATA22		
Deletion#19	TAX1BP3		
Deletion#19	TMEM93		
Deletion#19	P2RX5		
Deletion#19	ITGAE		
Deletion#19	C17ORF85		
Deletion#19	ATP2A3		
Deletion#19	GSG2		
Deletion#19	CAMKK1		
Deletion#19	P2RX1		
Deletion#19	ZZEF1		
Deletion#20	CDRT4	CDRT4	EPPB9
Deletion#20	FAM18B2	ZNF286A	MAPK7
Deletion#20	CDRT1	C20ORF191	ZNF179
Deletion#20	TRIM16	PRR6	ALDH3A2

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#20	ZNF286A	MPRIP	ULK2
Deletion#20	TBC1D26	RAI1	SPECC1
Deletion#20	MEIS3P1		USP22
Deletion#20	ADDRA2B		
Deletion#20	NCOR1		
Deletion#20	PICL		
Deletion#20	CENPV		
Deletion#20	UBB		
Deletion#20	TRPV2		
Deletion#20	SNORd65		
Deletion#20	ZNF287		
Deletion#20	ZNF624		
Deletion#20	CCDC144A		
Deletion#20	TNFRSF13B		
Deletion#20	ZSWIM7		
Deletion#20	TTC19		
Deletion#20	NORNA00188		
Deletion#20	SNORD49B		
Deletion#20	SNORD49A		
Deletion#20	C17orf76		
Deletion#20	LOC162632		
Deletion#20	LOC100129396		
Deletion#20	LOC400578		
Deletion#20	MPRIP		
Deletion#20	PLD6		
Deletion#20	FLCN		
Deletion#20	COPS3		
Deletion#20	NT5M		
Deletion#20	MED9		
Deletion#20	RASD1		
Deletion#20	PEMT		
Deletion#20	RAI1		
Deletion#20	SMCR5		
Deletion#20	LRRC48		
Deletion#20	ATPAF2		
Deletion#20	DRG2		
Deletion#20	ALKBH5		
Deletion#20	LLGL1		
Deletion#20	FLII		
Deletion#20	SMCR7		
Deletion#20	EVPLL		
Deletion#20	FAM106A		
Deletion#20	SREBF1		
Deletion#20	MIR33B		
Deletion#20	TOM1L2		

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#20	C17ORF39		
Deletion#20	MYO15A		
Deletion#20	TOP3A		
Deletion#20	SMCR8		
Deletion#20	SHMT1		
Deletion#20	LOC339240		
Deletion#20	LGALS9C		
Deletion#20	LOC2205094		
Deletion#20	CCDC144B		
Deletion#20	FOXO3B		
Deletion#20	FBXW10		
Deletion#20	FAM18B		
Deletion#20	TBC1D28		
Deletion#20	ZNF286B		
Deletion#20	TRIM16L		
Deletion#20	GRAP		
Deletion#20	GRAPL		
Deletion#20	PRPSAP2		
Deletion#20	SLC5A10		
Deletion#20	FAM83G		
Deletion#20	EPN2		
Deletion#20	B9D1		
Deletion#20	MAPK7		
Deletion#20	MFAP4		
Deletion#20	RNF112		
Deletion#20	SLC47A1		
Deletion#20	SNORA59A		
Deletion#20	SNORA59B		
Deletion#20	ALDH3A2		
Deletion#20	SLC47A2		
Deletion#20	ALDH3A1		
Deletion#20	ULK2		
Deletion#20	CYTSB		
Deletion#20	LGALS9B		
Deletion#20	CCDC144C		
Deletion#20	AKAP10		
Deletion#20	MGC102966		
Deletion#20	CCDC144NL		
Deletion#20	USP22		
Deletion#20	DHRS7B		
Deletion#20	TMEM11		
Deletion#20	MAP2K3		
Deletion#20	C17ORF103		
Deletion#20	KCNJ12		
Deletion#20	C17ORF51		

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#20	FAM27L		
Deletion#20	FLJ36000		
Deletion#21	RTDR1	BCR	SLC2A11
Deletion#21	GNAZ	FLJ31588	MIF
Deletion#21	RAB36	C22ORF16	DDT
Deletion#21	BCR	MMP11	
Deletion#21	ZDHHC8P	DDT	
Deletion#21	IGLL1		
Deletion#21	C22ORF43		
Deletion#21	LOC91316		
Deletion#21	RGL4		
Deletion#21	ZNF70		
Deletion#21	MMP11		
Deletion#21	VPREB3		
Deletion#21	C22ORF15		
Deletion#21	CHCHD10		
Deletion#21	SMARCB1		
Deletion#21	DERL3		
Deletion#21	SLC2A11		
Deletion#21	GSTT1		
Deletion#21	MIF		
Deletion#21	GSTT2B		
Deletion#21	DDTL		
Deletion#21	DDT		
Deletion#21	GSTT2		
Deletion#21	GSTTP1		
Deletion#21	LOC391322		
Deletion#21	GSTTP2		
Deletion#21	CABIN1		
Deletion#21	SUSD2		
Deletion#21	GGT5		
Deletion#21	POM121L9P		
Deletion#22	TTC28	RHBDD3	RFPL1S
Deletion#22	CHEK2	THOC5	NEFH
Deletion#22	HSCB	ASCC2	
Deletion#22	CCDC117	LOC652968	
Deletion#22	XBP1	SEC14L2	
Deletion#22	ZNRF3	SEC14L3	
Deletion#22	C22ORF31	PES1	
Deletion#22	KREMEN1	TI-227H	
Deletion#22	EMID1	LIMK2	
Deletion#22	RHBDD3	YWHAH	
Deletion#22	EWSR1	C22ORF30	
Deletion#22	GAS2L1		
Deletion#22	RASL10A		

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#22	AP1B1		
Deletion#22	SNORD125		
Deletion#22	RFPL1S		
Deletion#22	RFPL1		
Deletion#22	NEFH		
Deletion#22	THOC5		
Deletion#22	NIPSNAP1		
Deletion#22	NF2		
Deletion#22	UCRC		
Deletion#22	MTMR3		
Deletion#22	CABP7		
Deletion#22	ZAMT5		
Deletion#22	ASCC2		
Deletion#22	HORMAD2		
Deletion#22	LIF		
Deletion#22	OSM		
Deletion#22	GATSL3		
Deletion#22	TSC1D1OA		
Deletion#22	SF3A1		
Deletion#22	CCDC157		
Deletion#22	RNF215		
Deletion#22	SEC14L2		
Deletion#22	MTP16		
Deletion#22	SEC14L3		
Deletion#22	MTP18		
Deletion#22	SEC14L4		
Deletion#22	GAL3ST1		
Deletion#22	SLC35E4		
Deletion#22	PES1		
Deletion#22	TCN2		
Deletion#22	DUSF18		
Deletion#22	OSBF2		
Deletion#22	C22ORF27		
Deletion#22	MORC2		
Deletion#22	TUG1		
Deletion#22	PATZ1		
Deletion#22	DRG1		
Deletion#22	SMTN		
Deletion#22	LIMK2		
Deletion#22	SELM		
Deletion#22	INPP5J		
Deletion#22	PLA2G3		
Deletion#22	RNF185		
Deletion#22	PIK3IP1		
Deletion#22	EIF4ENIF1		

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#22	PISD		
Deletion#22	DEPDC5		
Deletion#22	SFI1		
Deletion#22	C22ORF30		
Deletion#22	YWHAH		
Deletion#22	C22ORF24		
Deletion#22	SLC5A1		
Deletion#23	APOBEC3A	RPL3	ADSL
Deletion#23	APOBEC3B	LOC642741	
Deletion#23	APOBEC3C	TNRC6B	
Deletion#23	APOBEC3D	ST13	
Deletion#23	APOBEC3E	EP300	
Deletion#23	APOBEC3F	PMM1	
Deletion#23	APOBEC3G	NHP2L1	
Deletion#23	APOBEC3H	RP5-821D11.2	
Deletion#23	CBX7	C22ORF32	
Deletion#23	PDGFB	NDUFA6	
Deletion#23	SNORD83B	SERHL	
Deletion#23	SNORD83A	SERHL2	
Deletion#23	SNORD43	ARFGAP3	
Deletion#23	MAP3K71P1	PACSIN2	
Deletion#23	RPL3	TSPO	
Deletion#23	MGAT3		
Deletion#23	SMCR7L		
Deletion#23	ENTHD1		
Deletion#23	ATF4		
Deletion#23	RNU86		
Deletion#23	SYNGR1		
Deletion#23	RPS19BP1		
Deletion#23	CACNA1 I		
Deletion#23	GRAP2		
Deletion#23	FAM83F		
Deletion#23	TNRC6B		
Deletion#23	ADSL		
Deletion#23	MKL1		
Deletion#23	SGSM3		
Deletion#23	MCHR1		
Deletion#23	SLC25A17		
Deletion#23	ST13		
Deletion#23	XPNPEP3		
Deletion#23	DNAJB7		
Deletion#23	RBX1		
Deletion#23	EP300		
Deletion#23	L3MBTL2		
Deletion#23	CHADL		

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#23	RANGAP1		
Deletion#23	ZC3H7B		
Deletion#23	TEF		
Deletion#23	TOB2		
Deletion#23	PHF5A		
Deletion#23	ACO2		
Deletion#23	POLR3H		
Deletion#23	CSDC2		
Deletion#23	PPPDE2		
Deletion#23	NHP2L1		
Deletion#23	C22ORF46		
Deletion#23	ME11		
Deletion#23	PMM1		
Deletion#23	XRCC6		
Deletion#23	CCDC134		
Deletion#23	SEPT3		
Deletion#23	SREBF2		
Deletion#23	MIR33A		
Deletion#23	CERNPM		
Deletion#23	NAGA		
Deletion#23	TNFRSF13C		
Deletion#23	WBP2NL		
Deletion#23	FAM109B		
Deletion#23	NDUFA6		
Deletion#23	CYP2D6		
Deletion#23	TCF20		
Deletion#23	LOC339674		
Deletion#23	C22ORF32		
Deletion#23	CYP2D7P		
Deletion#23	NFAM1		
Deletion#23	SERHL		
Deletion#23	RRP7A		
Deletion#23	SERHL2		
Deletion#23	RRP7B		
Deletion#23	POLDIP3		
Deletion#23	RNU12		
Deletion#23	CYB5R3		
Deletion#23	ATP5L2		
Deletion#23	A4GALT		
Deletion#23	ARFGAP3		
Deletion#23	PACSIN2		
Deletion#23	TTLL1		
Deletion#23	BIK		
Deletion#23	MCAT		
Deletion#23	TSPO		

Johnson, Wright et al., Supplemental Table 5b

GENE CARD #	Genes in region	copy number driven expression	Subgroup specific expression
Deletion#23	TTLL12		
Deletion#23	SCUBE1		
Deletion#23	MPPED1		
TOTAL	**728**	**130**	**85**

Johnson, Wright et al., Supplemental Table 6

Hu chr	Hu cytoband	Hu start	Hu end	Human gene	human_probe	mouse_probe	NEURAL FUNCTION	valdtd CNA hu D	Human subgroup D Log Ratio	T test Human subgroup D expression	mouse subgroup D Log Ratio	ependymoma subgroup D expression
9	q33.3	128045216	128097081	DNM1	215116_s_at	1460365_a_at	Synapse	Y	4.275439829	1.25E-06	14.68832096	5.27474E-58
19	p13.11	18168610	18175839	RAB3A	204974_at	1459980_x_at	Synapse	Y	3.802935753	2.69E-08	4.777522019	7.15463E-38
9	q33.3	127454121	127534549	STXBP1	202260_s_at	1420505_a_at	Synapse	Y	3.481047565	2.25E-08	6.674716947	1.81627E-48
13	q12.11	19694101	19703067	GJB6	231771_at	1448397_at	Neurogenesis/maintenance	Y	6.690424694	8.21E-08	13.24980982	1.16742E-81
9	q34.3	137308678	137339043	GRIN1	211125_x_at	1437968_at	Neurogenesis/maintenance	Y	2.337353287	7.33E-06	6.623906922	3.25362E-32
12	q13.3	56230113	56264821	KIF5A	223933_at	1434670_at	Axon guidance	Y	2.453628134	5.95E-07	18.13013867	1.4929E-84
19	p13.3	3175700	3248071	BRUNOL5	230497_at	1434969_at	-	Y	4.666406682	3.14E-07	8.469078851	1.03174E-36
1	q42.13	225763495	225785470	LOC126731	225904_at	1451483_s_at	-	Y	2.509554787	6.65E-07	3.883767734	1.81774E-27
19	p13.13	12810347	12846765	MAST1	217231_s_at	1432255_at	-	Y	2.637502834	2.01E-07	3.02288659	5.22268E-18
19	p13.11	18069604	18123499	MAST3	213045_at	1435666_at	-	Y	3.021227607	5.93E-07	4.075461939	7.31558E-33
19	q13.2	45413804	45416138	MGC33962	235375_x_at	1429416_at	-	Y	4.37232497	3.62E-12	7.886520786	8.06458E-23
11	q12.3	62432727	62445588	CHRM1	231783_at	1439611_at	Synapse	N	4.714758121	1.01E-10	5.059802933	7.70795E-36
16	q23.1	74901249	75086596	CNTNAP4	232388_at	1419044_at	Synapse	N	3.883820882	4.53E-08	5.953755156	1.42638E-35
5	q35.2	175156215	175243629	CPLX2	225815_at	1455672_s_at	Synapse	N	4.910094413	1.53E-09	4.468382024	3.58406E-21
5	q34	161206982	161258990	GABRA1	206678_at	1421280_at	Synapse	N	5.726609612	3.26E-08	8.856412341	1.44249E-60
4	p12	46092633	46232873	GABRA2	207014_at	1455444_at	Synapse	N	6.104972959	3.25E-06	6.604919385	7.10338E-20
4	p12	46761846	46836508	GABRA4	233437_at	1433707_at	Synapse	N	5.259588434	1.68E-08	6.339661202	2.09446E-07
4	p12	46874506	47269373	GABRB1	207010_at	1419719_at	Synapse	N	7.206941715	1.94E-06	10.10624475	1.7534E-13
5	q34	161427294	161515106	GABRG2	1568612_at	1418177_at	Synapse	N	6.660968161	1.72E-10	9.878956124	1.43135E-53
1	p35.1	33021190	33029339	HPCA	205454_at	1450930_at	Synapse	N	3.901019722	1.26E-08	12.30234066	8.07251E-59
19	q13.33	54309429	54313529	LIN7B	241957_x_at	1449172_a_at	Synapse	N	1.629621324	1.43E-06	9.038518606	8.16733E-54
17	q21.32	42023397	42189993	NSF	202395_at	1422455_s_at	Synapse	N	2.401531388	4.32E-08	6.119078574	4.9582E-47
20	p12.2	10147476	10236065	SNAP25	202508_s_at	1416828_at	Synapse	N	7.707606164	3.00E-08	13.75877887	1.04129E-69
6	q14.2	84319331	84475495	SNAP91	204953_at	1416688_at	Synapse	N	5.9824943	7.18E-07	7.735188608	1.49313E-22
10	q25.1	106390848	107014983	SORCS3	215522_at	1425111_at	Synapse	SNP	4.960812837	2.45E-06	5.835805049	1.9258E-16
1	q21.1	146688307	146702503	SV2A	203069_at	1423406_at	Synapse	N	3.490150257	3.47E-07	8.604671692	4.8183E-53
15	q26.1	89444548	89639514	SV2B	205551_at	1435687_at	Synapse	N	7.500804734	8.25E-13	9.858824079	1.2146E-47
16	p13.3	1979968	1984276	SYNGR3	205691_at	1416098_at	Synapse	N	6.405739609	1.06E-07	7.921497344	2.72354E-47
3	p14.2	63404063	63577636	SYNPR	230303_at	1423640_at	Synapse	N	6.230814516	8.21E-08	9.267501618	1.82317E-39
15	q21.3	52314519	52708095	UNC13C	1556095_at	1455304_at	Synapse	N	4.252789374	1.23E-07	12.69899799	6.52168E-60
7	q22.1	99885378	99898701	ACTL6B	206013_s_at	1422564_at	Neurogenesis/maintenance	N	3.547422567	8.34E-08	6.169326159	9.68867E-31
1	q32.1	199791438	199868189	ADORA1	205481_at	1427331_at	Neurogenesis/maintenance	N	3.669210209	8.64E-08	2.82266348	7.43179E-16
9	q21.32	85391008	85586443	AGTPBP1	237141_x_at	1418332_a_at	Neurogenesis/maintenance	N	1.900865002	1.09E-06	4.125210948	1.82153E-47
2	q35	219649902	219652381	CDK5R2	205852_at	1450466_at	Neurogenesis/maintenance	N	4.29528763	4.84E-08	6.664496113	2.1216E-28
14	q32.12	92459244	92471389	CHGA	204697_s_at	1418149_at	Neurogenesis/maintenance	N	4.684325827	1.20E-07	5.877696447	4.14086E-29
14	q32.2	99220507	99263390	CYP46A1	220331_at	1417709_at	Neurogenesis/maintenance	N	4.387016197	2.50E-07	5.290138209	8.18926E-26
1	p33	50440975	50441468	ELAVL4	238073_at	1452894_at	Neurogenesis/maintenance	N	5.117267068	5.15E-07	3.632367098	2.24537E-11
2	p13.2	73056258	73073131	EMX1	215264_at	1441777_at	Neurogenesis/maintenance	N	2.003331092	7.35E-07	3.894225452	5.20722E-11
19	q13.12	40325993	40337045	FXYD7	220131_at	1419200_at	Neurogenesis/maintenance	N	4.552100022	3.88E-10	6.746475203	3.62027E-65
2	q24.1	154626518	155135996	GALNT13	234472_at	1439899_at	Neurogenesis/maintenance	N	5.970969757	5.64E-08	9.167958453	3.7727E-21
10	q26.13	125415860	125444113	GPR26	244617_at	1440623_at	Neurogenesis/maintenance	N	4.316955515	8.90E-10	2.51148951	9.78979E-10

Johnson, Wright et al., Supplemental Table 6

Hu chr	Hu cytoband	Hu start	Hu end	Human gene	human_probe	mouse_probe	NEURAL FUNCTION	valdtd CNA hu D	Human subgroup D Log Ratio	T test Human subgroup D expression	mouse subgroup D Log Ratio	ependymoma subgroup D expression
10	q24.33	105026909	105040091	INA	204465_s_at	1448991_a_at	Neurogenesis/maintenance	N	7.002498025	5.80E-13	6.625285186	5.41013E-13
1	p21.2	99441920	99487157	LPPR4	213496_at	1427247_at	Neurogenesis/maintenance	N	5.718430637	9.59E-07	13.13504318	3.90725E-84
19	q13.12	40474877	40496547	MAG	216617_s_at	1460219_at	Neurogenesis/maintenance	N	3.244709544	6.01E-07	11.36446182	1.38516E-62
4	p16.1	6173557	6320354	MARLIN1	238600_at	1441317_x_at	Neurogenesis/maintenance	N	6.294895339	3.72E-07	15.62266769	4.9627E-89
3	p22.1	39484174	39542859	MOBP	210193_at	1450088_a_at	Neurogenesis/maintenance	N	4.02452015	1.15E-06	6.97269056	4.6892E-58
20	p11.21	23303165	23350081	NAPB	225111_s_at	1423172_at	Neurogenesis/maintenance	N	2.832677902	2.19E-08	11.64919107	1.82588E-91
2	q31.3	182366700	182370760	NEUROD1	206282_at	1426413_at	Neurogenesis/maintenance	N	3.296299254	2.69E-07	8.884531652	1.67002E-28
11	p12	40092328	40272240	NGL-1	232226_at	1437201_at	Neurogenesis/maintenance	N	4.551023718	4.82E-07	5.415956075	1.3692E-07
11	q24.2	124114951	124122309	NRGN	204081_at	1423231_at	Neurogenesis/maintenance	N	5.521837216	7.07E-07	4.16210807	3.03497E-17
6	p25.1	5943233	5952632	NRN1	218625_at	1428393_at	Neurogenesis/maintenance	N	7.023728356	2.85E-07	8.633745938	9.70433E-18
17	q11.2	26645794	26648481	OMG	207093_s_at	1418212_at	Neurogenesis/maintenance	N	5.617702026	9.85E-07	7.55152908	1.13175E-16
6	p21.31	34541882	34610976	PACSIN1	227053_at	1449381_a_at	Neurogenesis/maintenance	N	5.84503048	2.73E-10	10.60485599	3.56171E-62
1	p36.12	20705253	20723309	PINK1	209018_s_at	1451148_at	Neurogenesis/maintenance	N	2.211801624	2.12E-08	4.869446727	1.34433E-24
22	q13.33	49055540	49061131	PLXNB2	208890_s_at	1416683_at	Neurogenesis/maintenance	N	-1.77515981	0.007629645	-4.02482573	3.60615E-41
11	p15.1	18706052	18769874	PTPN5	236456_at	1423544_at	Neurogenesis/maintenance	N	5.806546995	2.05E-10	5.81745265	1.36446E-15
11	q24.1	123007132	123030522	SCN3B	204723_at	1435767_at	Neurogenesis/maintenance	N	5.38489433	2.59E-08	7.679818532	7.80929E-27
5	q35.2	175979816	175990163	SNCB	207853_s_at	1418053_at	Neurogenesis/maintenance	N	4.532985261	3.82E-09	6.630801931	1.46897E-38
14	q22.1	50096513	50169532	SPG3A	223340_at	1428260_at	Neurogenesis/maintenance	N	2.424743527	9.21E-10	8.753753464	2.79999E-32
3	q27.3	188869406	188870808	SST	213921_at	1417954_at	Neurogenesis/maintenance	N	4.990329829	9.34E-07	9.943212399	2.2857E-53
8	q21.13	80685934	80739779	STMN2	203001_s_at	1423280_at	Neurogenesis/maintenance	N	8.445163173	3.19E-09	15.46567275	4.88289E-85
22	q13.2	42545289	42583257	SULT4A1	219425_at	1433714_at	Neurogenesis/maintenance	SNP	4.108545774	3.09E-06	11.76568499	2.02589E-49
8	q24.22	131861728	132123854	ADCY8	206811_at	1418754_at	Channel	N	4.690758353	0.001165511	5.488561901	9.83324E-15
19	q13.2	47162575	47190222	ATP1A3	214432_at	1427481_a_at	Channel	N	4.681585568	6.58E-07	7.691354435	1.98934E-32
16	p12.1	24174376	24281238	CACNG3	206384_at	1450520_at	Channel	N	4.117357853	5.27E-08	5.967398009	1.00595E-37
5	q33.1	149579247	149649529	CAMK2A	213108_at	1457311_at	Channel	N	5.966215192	3.60E-11	6.544154688	4.3271E-21
10	q22.2	75242264	75304344	CAMK2G	214322_at	1423941_at	Channel	N	4.094860427	1.63E-06	3.236173398	1.12085E-33
5	q22.1	110587980	110848645	CAMK4	241871_at	1439843_at	Channel	N	3.755341327	3.26E-06	10.49713055	4.69389E-52
16	q13	54783648	54935363	GNAO1	204762_s_at	1421152_a_at	Channel	N	4.198297406	2.14E-07	9.551765866	4.08458E-44
3	q25.31	157321049	157739095	KCNAB1	210078_s_at	1454043_a_at	Channel	N	2.873528261	4.76E-07	5.832010556	2.37548E-39
1	p36.31	6020645	6094789	KCNAB2	203402_at	1416956_at	Channel	N	3.054466099	3.56E-08	4.50936333	2.07037E-17
2	p16.3	47659567	47709121	KCNK12	220448_at	1441280_at	Channel	N	3.690374324	1.68E-06	5.50660243	5.81566E-40
11	q23.3	117538728	117552546	SCN2B	210364_at	1436134_at	Channel	N	2.4614118	1.69E-06	13.02203211	5.06451E-83
19	p13.12	14921990	14944730	SLC1A6	1554593_s_at	1418933_at	Channel	N	4.732349668	1.03E-09	2.729641685	2.68737E-06
6	q15	88906301	88911775	CNR1	213436_at	1419425_at	Axon guidance	N	6.225494669	2.48E-06	1.963096968	8.28291E-09
2	q21.1	131241723	131242177	---	244709_at	1436407_at	-	N	2.098579408	2.67E-06	8.157604287	1.95536E-45
2	q35	216948094	217062256	---	230112_at	1441223_at	-	N	3.704050148	2.23E-08	4.71717472	7.74862E-20
2	q24.1	158095841	158096595	---	1563182_at	1443225_at	-	N	4.019171403	1.55E-06	6.748960281	1.40114E-50
2	q24.3	165976098	166072046	---	229057_at	1435933_at	-	N	5.857933402	1.05E-08	14.13979576	3.33176E-87
5	q34	160648089	160648586	---	242344_at	1450319_at	-	N	5.774642533	2.47E-07	1.464098015	9.44593E-07
5	q35.2	173405329	173468787	---	218623_at	1456685_at	-	N	4.980324956	3.84E-07	3.495973105	5.78125E-17
12	p12.1	21570522	21575477	---	229778_at	1441161_at	-	N	7.245800468	1.91E-07	2.82003223	1.70231E-13

Johnson, Wright et al., Supplemental Table 6

Hu chr	Hu cytoband	Hu start	Hu end	Human gene	human_probe	mouse_probe	NEURAL FUNCTION	valdtd CNA hu D	Human subgroup D Log Ratio	T test Human subgroup D expression	mouse subgroup D Log Ratio	ependymoma subgroup D expression
14	q23.3	64023309	64040307	---	230846_at	1431717_at	-	N	3.117794617	1.49E-06	2.593026836	1.08161E-08
11	p15.1	17371008	17455025	ABCC8	210246_s_at	1457066_at	-	N	5.223912033	2.07E-06	3.076132073	7.64549E-18
4	q25	110020807	110041813	AGXT2L1	221008_s_at	1431406_at	-	N	8.775735491	3.85E-10	2.300048377	4.67265E-13
1	q21.1	144185493	144187004	ANKRD34	232735_at	1435809_at	-	N	3.890033608	1.62E-07	5.859390947	9.43415E-33
3	p22.3	35697432	35702381	ARPP-21	220359_s_at	1424248_at	-	N	4.871410063	5.24E-08	12.2229855	2.61299E-34
11	q13.4	74654129	74740521	ARRB1	222912_at	1460444_at	-	N	3.42604319	1.44E-07	5.937382996	9.65021E-36
6	p21.33	31620217	31622606	ATP6V1G2	214762_at	1417799_at	-	N	4.178949058	4.66E-09	9.665087407	7.44659E-74
13	q12.13	24941114	25492996	ATP8A2	219659_at	1460294_at	-	N	4.394266139	2.63E-07	3.683418407	1.85874E-16
14	q11.2	22845875	22850798	BCL2L2	209311_at	1451029_at	-	N	2.571958867	2.35E-09	2.311328969	4.65173E-13
8	q12.3	65655367	65658739	BHLHB5	228636_at	1418271_at	-	N	6.560008012	5.99E-08	7.833183942	1.76117E-18
18	q12.2	33077827	33399941	BRUNOL4	223654_s_at	1452240_at	-	N	4.698877311	4.07E-07	12.83872031	1.46642E-64
17	p13.2	4812016	4831655	CAMTA2	212948_at	1426901_s_at	-	N	1.537266297	2.97E-06	5.132696502	4.59755E-43
3	p22.1	42274321	42281399	CCK	205827_at	1419473_a_at	-	N	6.480015706	1.25E-07	13.67507959	8.63455E-85
5	p14.1	26916465	27074431	CDH9	207729_at	1427618_at	-	N	2.543422065	4.45E-07	7.306621066	2.28801E-40
2	q11.2	101423742	101462575	CREG2	1552714_at	1436850_at	-	N	4.94423946	1.35E-08	7.138203634	3.82272E-31
9	q33.1	119008461	119211255	DBC1	205818_at	1417318_at	-	N	6.687906507	2.41E-11	8.974236233	5.1997E-20
12	q24.11	107807127	107835197	DKFZp761H03	229818_at	1452663_at	-	N	4.928391926	3.05E-12	5.780259246	2.23731E-15
7	q22.1	98088762	98112288	DKFZp761L14	238426_at	1455148_at	-	N	5.362172674	3.44E-08	14.01117566	3.35711E-83
1	q32.1	202269821	202302994	DKFZp761N11	242372_s_at	1436021_at	-	N	3.477444602	1.80E-06	5.061107522	7.12283E-33
1	p31.3	65442450	65593573	DNAJC6	204720_s_at	1431215_at	-	N	5.693965523	2.07E-10	1.609538189	3.42764E-07
12	q15	66329020	66340410	DYRK2	202968_s_at	1456502_at	-	SNP	-3.150200579	8.60E-11	-2.780410989	1.35322E-12
17	q12	35109779	35138441	ERBB2	216836_s_at	1424919_at	-	N	-2.526946243	2.43E-06	-2.801156683	1.05576E-12
3	p14.1	68136143	68677459	FAM19A1	230923_at	1457092_at	-	N	5.268907937	5.38E-09	10.54842533	7.60368E-53
16	p13.3	682506	695809	FBXL16	227641_at	1440286_at	-	N	5.446188996	1.92E-07	4.657047325	1.25767E-18
2	p13.2	73335340	73335790	FBXO41	44040_at	1456444_at	-	N	3.21913175	3.98E-07	8.608530372	4.44684E-32
3	q27.1	185016371	185026067	FLJ12748	221713_s_at	1433630_at	-	N	3.119616473	8.64E-09	3.817337373	1.499E-26
1	p31.3	68303061	68410274	FLJ23091	221958_s_at	1423824_at	-	N	-3.518752501	7.39E-07	-3.91219734	3.39908E-26
13	q31.3	90848887	92317486	GPC5	207174_at	1457536_at	-	N	7.108798561	3.46E-12	11.47769355	2.30022E-80
9	q22.32	96292041	96332342	HABP4	232341_x_at	1418927_a_at	-	N	2.28709772	1.59E-08	4.011916956	2.72297E-35
12	q21.31	84874991	85735113	HGNT-IV-H	207447_s_at	1421178_at	-	N	5.727669805	1.15E-07	2.923667391	3.04952E-15
1	p34.2	39813738	39826182	HPCAL4	219671_at	1433987_at	-	N	5.821439918	2.27E-07	17.02983831	3.63495E-94
16	p12.1	25610847	26056510	HS3ST4	228206_at	1455620_at	-	N	5.852306388	8.40E-12	7.700276757	8.36343E-43
10	q25.3	118420693	118492075	HSPA12A	214434_at	1434051_s_at	-	N	3.78907905	1.48E-07	8.103495151	2.1224E-47
10	q26.11	121475598	121541710	INPP5F	203607_at	1433542_at	-	N	2.961835353	1.30E-08	2.795352174	5.89318E-13
16	q24.2	86193999	86289263	JPH3	229294_at	1418161_at	-	N	7.044074889	7.58E-08	8.762333057	6.21218E-28
2	p23.3	27221770	27235252	KHK	205175_s_at	1449062_at	-	N	1.889477211	2.79E-11	2.77698551	1.36918E-14
16	q24.1	83618910	83685327	KIAA0513	204546_at	1426446_at	-	N	3.113608987	2.03E-08	4.966615053	7.09299E-37
7	q34	142567331	142575729	KIAA0773	205368_at	1455421_x_at	-	N	3.766785867	2.33E-06	5.755158824	1.02006E-31
13	q12.3	28900776	28975872	KIAA0774	214961_at	1432205_a_at	-	N	3.186977147	2.62E-06	8.182554304	6.4697E-63
9	p13.3	34948320	34972541	KIAA1045	37566_at	1445465_at	-	N	5.530626651	1.02E-13	5.384898951	1.30589E-28
2	q24.1	158000633	158007924	KIAA1189	231911_at	1436578_at	-	N	6.24093488	2.27E-06	10.64069445	3.40055E-76

Johnson, Wright et al., Supplemental Table 6

Hu chr	Hu cytoband	Hu start	Hu end	Human gene	human_probe	mouse_probe	NEURAL FUNCTION	valdtd CNA hu D	Human subgroup D Log Ratio	T test Human subgroup D expression	mouse subgroup D Log Ratio	ependymoma subgroup D expression
4	p14	37122482	37127476	KIAA1239	230765_at	1441025_at	-	N	5.004481242	2.26E-10	1.898264085	4.28244E-14
2	p23.3	26061118	26117054	KIF3C	203389_at	1448946_at	-	N	2.690210815	1.85E-09	2.115003171	7.15847E-08
2	q23.1	149349288	149591519	KIF5C	203130_s_at	1455266_at	-	N	4.101633839	4.02E-07	10.45602631	1.51318E-56
8	p21.3	22060289	22070289	LGI3	238061_at	1433667_at	-	N	3.219511778	4.00E-08	8.537175853	5.28885E-27
4	q32.1	159793529	159793969	LGR7	238206_at	1440785_at	-	N	3.505907601	9.30E-08	1.17711621	3.60897E-12
17	q25.3	74743322	74931566	LOC339162	229406_at	1436450_at	-	N	4.246524328	3.67E-10	13.67203442	7.16793E-47
17	q21.32	42410520	42411613	LOC388394	1554655_a_at	1436408_at	-	N	3.454696426	8.33E-07	3.98781876	1.5181E-11
8	p12	33568397	33576981	MGC1136	219144_at	1425848_a_at	-	N	3.027291067	5.83E-08	11.94386489	2.08315E-57
17	q21.2	36066044	36074890	MGC45562	244111_at	1434535_at	-	N	3.130293482	2.03E-06	6.435939331	5.53438E-40
17	p13.2	4683350	4742134	MINK1	214246_x_at	1449362_a_at	-	N	2.160850279	1.23E-06	1.516707275	5.60841E-07
2	p25.3	1763183	2305342	MYT1L	210016_at	1421175_at	-	N	8.522122392	7.91E-13	12.75333484	1.7198E-82
3	p24.2	23908575	23933541	NKIRAS1	225930_at	1428503_a_at	-	N	1.824801264	8.80E-08	5.246381525	7.1868E-51
3	q26.33	181000751	181237219	PEX5L	222910_s_at	1438399_at	-	N	3.376958602	1.26E-07	8.07652953	1.78006E-37
5	q33.1	149090056	149207460	PPARGC1B	1555282_a_at	1449945_at	-	N	1.893673083	1.09E-07	4.256665327	2.69983E-33
16	p11.2	29994884	30004196	PPP4C	208932_at	1460288_a_at	-	N	-1.891740718	9.03E-07	-2.26728274	7.26271E-14
12	q15	69318128	69434632	PTPRR	206084_at	1426047_a_at	-	N	3.55214574	2.17E-06	8.01880299	8.43965E-39
17	q11.2	26742767	26889352	RAB11FIP4	224482_s_at	1434156_at	-	N	4.001278225	4.56E-08	6.112482714	3.55947E-32
1	q24.3	170860311	171684885	RABGAP1L	203020_at	1429196_at	-	N	1.912146104	2.68E-06	4.408977891	7.1573E-35
2	q31.1	173426113	173743122	RAPGEF4	205651_x_at	1425518_at	-	N	4.058943519	1.51E-07	9.380438159	2.34086E-33
10	q11.21	42892532	42944955	RET	211421_s_at	1436359_at	-	N	4.242233061	1.83E-07	7.790454709	6.9006E-55
20	q13.12	44091244	44122196	SLC12A5	210040_at	1451674_at	-	N	6.246037971	3.91E-11	14.92567191	8.4241E-109
12	p12.1	21313093	21439638	SLCO1A2	207308_at	1420405_at	-	N	3.358729965	1.51E-08	11.72673953	1.10128E-75
11	q13.1	66209298	66245446	SPTBN2	205155_s_at	1452269_at	-	N	3.285744824	2.98E-06	7.851298442	2.03503E-32
18	p11.31	3402071	3448404	TGIF	203313_s_at	1422286_a_at	-	N	-2.577016558	2.40E-06	-3.061273264	4.67336E-07
15	q22.2	60841760	60923883	TLN2	212701_at	1435700_at	-	N	3.202971123	3.79E-08	2.315744005	1.51305E-16
12	q21.1	70952729	71345688	TRHDE	219937_at	1457156_at	-	N	4.006478316	3.63E-07	7.801846459	9.9457E-54
14	q32.11	90076685	90352514	TTC7B	226152_at	1433460_at	-	N	1.942076731	1.32E-07	3.610039639	1.15892E-18
19	p13.3	6445329	6453330	TUBB4	212664_at	1423221_at	-	N	4.420734376	9.58E-08	8.555478905	7.30037E-33
17	q21.31	38064836	38072549	TUBG2	203894_at	1449318_at	-	N	2.380386098	8.39E-09	5.198242114	4.43681E-41
6	q25.3	158704100	158903263	TULP4	218184_at	1448548_at	-	N	1.666159875	3.79E-07	3.071199872	2.89541E-29
6	p22.2	24234328	24255609	VMP	239293_at	1418588_at	-	N	6.050343685	8.71E-12	15.13620269	3.48783E-58
1	p13.3	109224877	109296777	WDR47	203855_at	1434558_at	-	N	1.846946676	1.12E-06	5.664197424	1.34545E-61
11	p15.4	9550915	9567874	WEE1	212533_at	1416773_at	-	N	-3.402742024	2.87E-07	-2.527642987	1.38923E-14
17	q22	53403908	53420614	ZNF161	202171_at	1429084_at	-	N	-1.907339163	1.07E-07	-2.184866313	1.01183E-08
20	q13.2	51617018	51633043	ZNF217	203739_at	1437414_at	-	N	-3.627427717	5.20E-08	-2.397402608	2.79853E-07
3	p14.2	62330398	62334061	ZNF312	221086_s_at	1418790_at	-	N	5.617977746	4.12E-08	6.636699148	3.03994E-29
10	q21.2	63950212	64101777	ZNF365	206448_at	1433583_at	-	N	3.445978966	1.60E-08	5.315669186	5.47926E-22