**Supplementary Figure Legends**

### Figure S1. Workflow diagram of TCGA / 1000 Genome exome data analysis. (A) Raw whole exome sequencing alignment BAM files were downloaded from TCGA for 300 tumor specimens obtained from 300 individuals diagnosed with GBM. (B) Exome sequencing reads were aligned to the human reference genome (hg19/GRCh37). Duplicate reads were marked using MarkDuplicates function of Picard. Reads were realigned around indels and quality scores recalibrated using methods described in best practices for the Genome Analysis Toolkit (GATK 3.5). (C) The variant calling on each sample were performed by HaplotypeCaller in -ERC GVCF mode before applying (D) joint genotyping using GenotypeGVCFs. The false positive and highly sensitive variants were removed by VariantRecalibrator and VariantFilteration. (E) KIR2DS4 variants were extracted and tabulated as validation set for both TCGA and 1000 Genomes Project data. (F) TCGA clinical and 1000 Genome population data were downloaded and used for further analysis.

### Figure S2. Base Quality Score Recalibration (BQSR) recalibration plots. (A, B, and C) showing reported quality score *vs*. empirical quality score and (D, E, and F) showing residual error by machine cycle before (pink) and after (blue) GATK BQSR which correct for variation in quality for substitution, insertion and deletion respectively.

### Figure S3. KIR2DS4 variant analysis of the variant call sets. Integrative Genomics Viewer (IGV) screen shot of exome sequencing results of the KIR2DS4 22 bp deleted variants of GBM patients obtained from The Cancer Genome Atlas (TCGA) project. A) Alignment of a raw sample bam file with the reference sequence showing an insertion of 22bp sequence, in chromosome 19q13.4, exon 5 of KIR2DS4 (nucleotide position 55350963)). B) In the Final processed VCF file, column indicated by the solid arrow showing the 22 bp deleted variants of KIR2DS4 (box = homozygous reference (DEL/DEL), box = homozygous alternate (FUNC/FUNC) and box = heterozygous (FUNC/DEL) in chromosome 19q13.4, exon 5 of KIR2DS4 (nucleotide position 55350963)). Left panel showing the TCGA sample ID and the lower panel showing the sequence is the RefSeq gene for KIR2DS4 (partial sequence).