

Supplementary Figure 2

Sample ID	Paired End Reads uniquely aligned to hg19 genes	Paired End Reads Multiply aligned to hg19 genes
ALS1	17,079,872	13,923,290
ALS2	12,142,430	14,946,592
ALS3	22,456,944	20,252,817
ALS4	20,074,506	29,925,873
ALS9	25,147,130	18,710,778
ALS10	16,567,040	22,428,047
ALS14	22,785,166	15,660,804
CTL6	24,978,566	32,026,378
CTL8	21,336,355	31,498,430
CTL16	17,091,970	21,962,757
CTL22	14,265,193	21,672,506
CTL23	16,029,151	16,133,502
CTL24	15,524,378	25,106,385
CTL25	18,959,037	21,189,291
CTL27	16,821,773	20,867,799

Supplementary Figure 2 details the number of paired end reads that aligned either uniquely or multiply to hg19 genes. Uniquely aligned reads were used for DeSeq2 and EdgeR analyses.