

## Supplementary Figure 1

Sample ID	Bases Sequenced	PF Bases Aligned to hg19 genome	% Bases that PF and Aligned to hg19 genome	% PF Bases aligned to mRNA	% PF Bases aligned to rRNA/tRNA/mtRNA	% PF Bases aligned to intronic regions	% PF Bases aligned to intergenic regions
ALS1	21,525,372,600	13,482,235,967	62.6	30.3	24.1	30.8	14.8
ALS2	17,620,068,900	11,688,557,657	66.3	25.4	39.7	22.8	12.2
ALS3	23,518,969,200	15,062,468,598	64.0	35.8	24.1	24.8	15.3
ALS4	19,429,933,500	12,750,324,647	65.6	37.1	25.8	22.4	14.7
ALS9	25,847,743,800	15,956,695,398	61.7	36.7	21.4	27.4	14.4
ALS10	18,557,838,300	12,691,363,772	68.4	31.8	25.7	27.8	14.7
ALS14	18,327,581,100	12,410,814,921	67.7	43.7	19.7	25.6	11.0
CTL6	25,560,552,300	15,739,588,406	61.6	37.3	19.7	26.5	16.5
CTL8	24,262,752,600	15,323,900,550	63.2	33.1	22.7	27.9	16.3
CTL16	22,605,558,600	14,017,986,644	62.0	28.7	30.1	26.9	14.3
CTL22	16,823,823,300	11,171,823,684	66.4	30.2	32.4	25.0	12.4
CTL23	18,963,078,300	13,009,938,471	68.6	30.1	43.4	16.3	10.2
CTL24	18,073,171,500	12,555,674,242	69.5	30.4	38.4	17.8	13.5
CTL25	19,274,686,800	13,257,578,863	68.8	35.5	34.3	17.8	12.4
CTL27	18,371,600,100	12,471,242,885	67.9	32.5	33.7	21.3	12.5

Supplementary Figure 1: Sample metrics collected using Picard's CollectRNASeqMetrics command. PF = Passed Filter