Table Everett A.
Total number of unique integration sites and uniquely mapped sequence reads.

Patient	Number of ISs	Sequence Reads
b0/bE	102,818	4,886,180
bS/bS	7,392	3,848,397
WAS2	20,847	13,615,549
WAS4	32,614	14,847,313
WAS5	5,237	9,933,325
WAS7	8,799	7,736,253

Table Everett B.
Cumulative number of unique integration sites retrieved from different sample types.

Samples	WAS2	WAS4	WAS5	WAS7	b0/bE	bS/bS
TCELLS	11,273	23,690	1,856	5,785	8,380	1,541
MONOCYTES	2,866	1,965	881	368	28,324	1,471
GRANULOCYTES	3,949	4,794	939	1,535	42,451	3,560
BCELLS	2,571	7,417	1,629	1,264	27,593	4,613
NKCELLS	1,558	3,662	1,285	265	2,437	1,611

Table Everett C.
Enrichment of intSites near oncogenes in lineage tracing intSites compared to d0 intSites (WAS2, WAS4, WAS5, WAS7).

There is an 5.02% increase in the number of intSites within 50KB of oncogenes in the lineage tracing data set compared to the d0 intSite data set (454 data, Fisher's exact test p-value: 2.63e-15)

	Not near oncogenes 50K	Near oncogenes 50K
d0 intSites	3,788	1,094
Lineage intSites	128,256	48,480

Table Everett D.

subject	Fishers_Pval	EarlyPercentNearOnco	LatePerentNearOnco
WAS4	2.642e-10	25.89%	22.57%
WAS7	1.097e-06	22.23%	27.31%
All	0.0004309	27.79%	27.01%
WAS5	0.03465	27.51%	25.04%
b0/bE	0.21	28.70%	28.29%
WAS2	0.4233	26.48%	26.95%
bS/bS	0.8433	29.36%	29.17%

```
knitr::knit_exit()
```