

SUPPLEMENTAL MATERIAL

Table S1: Summary of sequencing results from WGS.

Sample	Sequencing Type	Read Length (bp)	Fold Coverage	Mean Q-score	Total Variants	Unique Variants	%Unique Variants
<i>adf1-2</i>	HiSeq	126	27.9	35.84	232411	5952	2.6
<i>adf1-3</i>	HiSeq	126	73.9	35.82	255376	21892	8.6
<i>adf1-3R</i>	HiSeq	101	39.1	34.89	264015	49431	18.7
<i>adf1-3R</i>	HiSeq	126	56.1	35.20	314922	85617	27.2
<i>adf1-4</i>	HiSeq	126	89.7	34.72	237680	14070	5.9
<i>adf1-5</i>	HiSeq	126	71.2	34.97	234785	11447	4.9
<i>adf1-6</i>	HiSeq	126	51.8	35.60	257873	32072	12.4
<i>adf1-7</i>	HiSeq	126	57.0	34.94	10562	2382	22.6
<i>adf1-12</i>	HiSeq	126	76.4	35.00	4541	965	21.3
<i>adf1-13</i>	HiSeq	126	48.8	35.55	9726	2221	22.8
<i>adf1-14</i>	HiSeq	101	45.9	33.23	8072	1287	15.9
<i>adf1-15</i>	HiSeq	126	70.2	35.60	10762	1836	17.1
<i>adf1-16</i>	HiSeq	101	34.4	34.01	8537	1887	22.1
<i>adf1-17</i>	HiSeq	126	76.2	34.00	4703	876	18.6
<i>adf2-1</i>	MiSeq	151	21.7	33.99	7190	1891	26.3
<i>adf3-1</i>	MiSeq	151	15.9	34.15	7340	2758	37.6
<i>adf3-2</i>	HiSeq	101	33.3	33.89	8554	1577	18.4
<i>adf4-1</i>	HiSeq	101	31.0	34.15	8449	2035	24.1
E4.1 P1 H3	HiSeq	101	32.5	34.23	8414	1799	21.4
E5.1 P8 A12	HiSeq	101	35.0	34.08	8725	1833	21.0
<i>fa1-6</i>	HiSeq	126	73.3	34.76	4366	840	19.2
<i>fa1-7</i>	HiSeq	101	34.9	34.07	12607	2460	19.5
<i>fa2-5</i>	HiSeq	126	67.6	34.76	4730	938	19.8
<i>fa2-6</i>	HiSeq	126	69.7	34.58	4586	831	18.1
<i>fa2-7</i>	HiSeq	126	72.5	34.66	4406	764	17.3