Table S1. General sequence-based features of input and output pools

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Pool	Detected mutant variants	Depth Sum of aligned reads	Saturation % of annotated genes with at least:		Insertional bias % of inserts within annotated loci**
			Input	78,591	8,206,447
Blood	23,756	7,075,904	95.07	48.85	88.08
PC	38,936	7,671,459	98.08	72.14	88.01
Input	81,096	8,494,073	99.77	98.92	87.84
Blood	31,871	7,049,106	96.20	60.67	88.22
PC	38,842	9,052,580	97.55	70.20	88.42
Input	63,184	8,113,311	99.54	99.00	88.17
Blood	31,927	5,899,109	96.69	62.41	87.78
PC	44,926	7,309,071	97.93	73.21	88.07
	Input Blood PC Input Blood PC Input Blood PC	Input 78,591 Blood 23,756 PC 38,936 Input 81,096 Blood 31,871 PC 38,842 Input 63,184 Blood 31,927	Sum of aligned reads Input 78,591 8,206,447 Blood 23,756 7,075,904 PC 38,936 7,671,459 Input 81,096 8,494,073 Blood 31,871 7,049,106 PC 38,842 9,052,580 Input 63,184 8,113,311 Blood 31,927 5,899,109	Sum of aligned reads % of annotated of 1 insert* Input 78,591 8,206,447 99.90 Blood 23,756 7,075,904 95.07 PC 38,936 7,671,459 98.08 Input 81,096 8,494,073 99.77 Blood 31,871 7,049,106 96.20 PC 38,842 9,052,580 97.55 Input 63,184 8,113,311 99.54 Blood 31,927 5,899,109 96.69	Sum of aligned reads % of annotated genes with at least: 1 insert* 10 insertions* Input 78,591 8,206,447 99.90 98.96 Blood 23,756 7,075,904 95.07 48.85 PC 38,936 7,671,459 98.08 72.14 Input 81,096 8,494,073 99.77 98.92 Blood 31,871 7,049,106 96.20 60.67 PC 38,842 9,052,580 97.55 70.20 Input 63,184 8,113,311 99.54 99.00 Blood 31,927 5,899,109 96.69 62.41

^{*}values reflect proportion of 5,312 annotated regions within the F11 genome.

^{**4,628,529} bp (out of 5,215,961 bp) are contained within annotated F11 loci; therefore, it is expected that the percent of inserts found within annotated regions would be 88.73%.