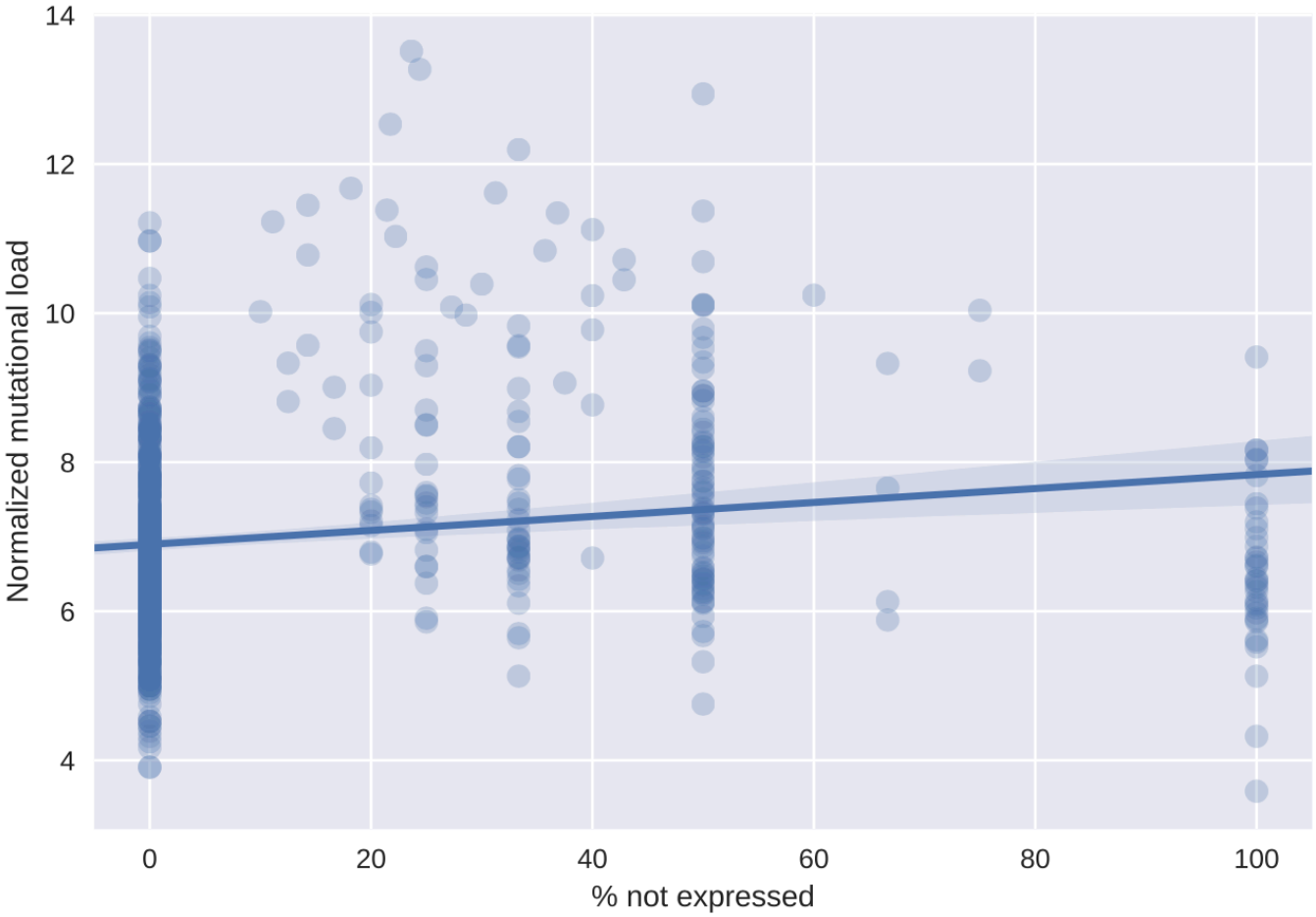
Supplemental Table 1. Demographics overview for cohort (N=1879)

Cancer Type	No. of Patients*	No. of Women	Minimum Age (years)	Maximum Age (years)	Median Age (years)
Breast	336	334	20	86	56
Colon	180	94	17	87	58
Lung	149	82	9	90	65
Bone and Soft Tissue Cancers (including Sarcoma)	139	65	0	82	49
Pancreatic	123	52	3	87	63
Ovarian	103	103	25	86	58
Brain	93	37	0	79	49
Cancer Type Unknown	75	31	6	91	59
Other Cancer	71	31	1	83	62
Cancers With N < 10*	52	20	0	87	65.5
Prostate	51	0	40	83	65
Gastric (Stomach)	45	19	15	85	61
Head and Neck	41	9	19	86	64
Kidney	38	12	0	72	62
Liver	37	11	9	77	63
Melanoma	37	13	29	87	64
Oral/Throat/Thyroid Cancers	35	11	42	83	63
Esophageal	35	13	46	86	64
Rectal	31	10	28	80	57
Bladder	30	13	49	92	72
Unknown Primary	29	18	29	83	57
Uterine (Endometrial)	29	29	34	89	66
Soft Tissue	22	7	2	80	18
Gall Bladder	20	13	39	87	65.5
Thymic	17	8	24	73	59
Cervical	16	16	27	75	49
Adrenal	13	5	1	74	48
Lymphoma	12	3	18	81	66
Renal Pelvis and Ureter Cancers	10	5	8	71	42
Biliary Tract (intrahepatic)	10	4	46	78	61

***** Diagnosis with ≥10 cases are included in Table.

Supplemental Figure 1: Mutational load and non-expression rate are related. Percentage of tumor-specific SNVs detectably expressed in RNA (x-axis) vs. normalized mutational load (i.e. log(TMB+1), y-axis) per patient. There is a very weak correlation between mutational load and percent of variants that are not expressed (Pearson R=0.17, p=2.5e-7).



Supplemental Figure 2: Relative frequency of rare germline variants across hotspot genes. Counts of all potential variants in each hotspot gene, broken into annotation categories. Rare (magenta) and unannotated (black) germline variants are at high risk of being falsely reported as tumor-associated SNVs.

