Figure S1. Examples of the full range of weak, moderate and strong staining. (A) weak staining, (B) moderate staining and (C) strong staining. MLH1, MutL protein homolog 1; MDM2, mouse double minute 2 homolog; P21, cyclin-dependent kinase inhibitor 1A.
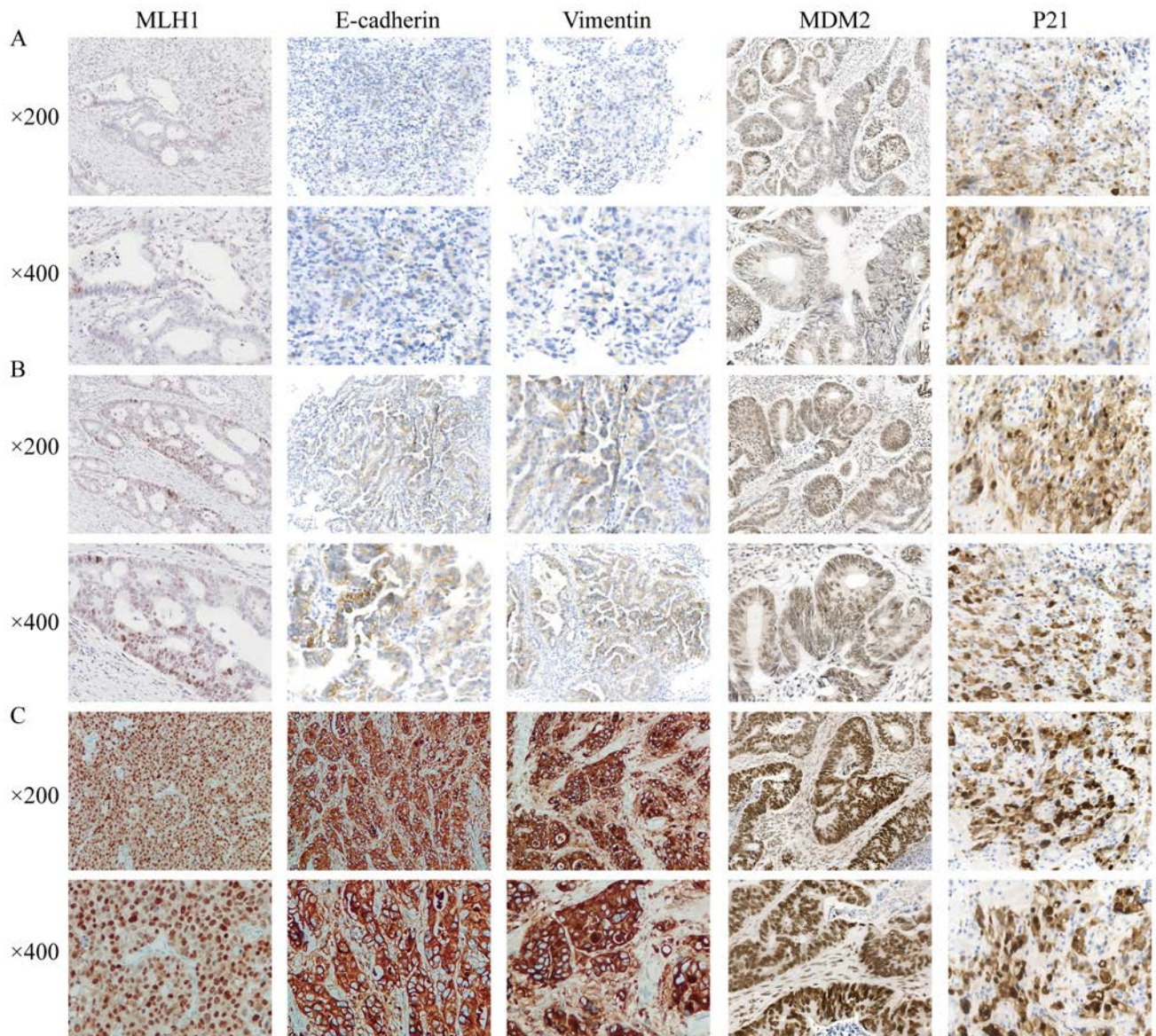
Table SI. The Cancer Genome Atlas molecular subtypes and mutated and amplified genes.

Abnormal genes	n	EBV[+], n (%)	MSI, n (%)	GS, n (%)	CIN, n (%)
Mutation					
TP53	52	0 (0)	11 (21.2)	11 (21.2)	30 (57.7)
APC	18	2 (11.1)	2 (11.1)	2 (11.1)	12 (66.7)
ARID1A	14	1 (7.1)	1 (7.1)	9 (64.3)	3 (21.4)
PLK3CA	11	5 (45.5)	2 (18.2)	2 (18.2)	2 (18.2)
ERBB3	9	0 (0)	3 (33.3)	2 (22.2)	4 (44.4)
Amplification					
CCNE1	13	1 (7.7)	0 (0)	2 (15.4)	10 (76.9)
MYC	7	0 (0)	0 (0)	6 (85.7)	1 (14.3)
CDK6	4	0 (0)	0 (0)	1 (25)	3 (75)
EGFR	4	0 (0)	0 (0)	0 (0)	4 (100.0)
KRAS	2	0 (0)	0 (0)	1 (50.0)	1 (50.0)

EBV, Epstein-Barr virus; MSI, microsatellite instability; GS, gene stable; CIN, chromosome instability.