

P.S.: p_i is the p -values of the individual significance of each identified gene sets for i^{th} cancer, p represents the p -value of overall significance.

1 Supplementary Tables: Overall profile of primary and metastatic tumors

1.1 Bladder cancer

Table S 1.1.1. Significant common driver gene set between Bladder_P and Bladder_M

k	common gene set	p1	p2	q
4	<i>TERT,MYCN,PTPN11,SMAD3</i>	0.004	0.029	<0.0001
5	<i>TERT,AKT2,COP1,EGFL7,PTPN11</i>	0.002	0.004	<0.0001
6	<i>TERT,AKT2,COP1,EGFL7,PTPN11,BMPR1A</i>	0.002	0.004	<0.0001
7	<i>TERT,AKT2,COP1,EGFL7,PTPN11,BMPR1A,HIST1H3E</i>	<0.0001	0.001	<0.0001
8	<i>TERT,AKT2,COP1,EGFL7,PTPN11,CD276,HIST1H3E,TAF2</i>	<0.0001	0.003	<0.0001
9	<i>TERT,AKT2,COP1,EGFL7,PTPN11,CD276,EIF4E,IGF1,PIBF1</i>	<0.0001	0.002	<0.0001
10	<i>TERT,AKT2,COP1,EGFL7,PTPN11,CD79B,EIF4E,TAF2,TNFRSF14,TNIP2</i>	<0.0001	0.004	<0.0001

Table S 1.1.2. Bladder_P specific mutated driver gene sets relative to Bladder_M

k	specific gene set	p1	p2	q
2	<i>ATRX, TERT</i>	0.003	0.994	0.003
3	<i>ATRX, TERT, NOTCH3</i>	0.001	0.975	0.002
4	<i>TP53, ATM, ERBB2, FGFR3</i>	<0.0001	0.066	<0.0001
5	<i>TP53, ATM, ERBB2, FGFR3, KRAS</i>	<0.0001	0.065	<0.0001
6	<i>TP53, CDKN1A, FGFR3, HRAS, KDM6A, NFE2L2</i>	<0.0001	0.884	<0.0001
7	<i>TP53, CDKN1A, FGFR3, HRAS, KDM6A, NFE2L2, FOXA1</i>	<0.0001	0.895	<0.0001
8	<i>TP53, CDKN1A, FGFR3, HRAS, KDM6A, NFE2L2, FOXA1, KRAS</i>	<0.0001	0.799	<0.0001
9	<i>TP53, CDKN1A, FGFR3, HRAS, KDM6A, NFE2L2, FOXA1, KRAS, FGF19</i>	<0.0001	0.822	<0.0001
10	<i>TP53, CDKN1A, FGFR3, HRAS, KDM6A, NFE2L2, FOXA1, KRAS, FGF19, MALT1</i>	<0.0001	0.784	<0.0001

*Bladder_M has no specific mutated driver gene sets relative to Bladder_P when k=2 ~ 10.

1.2 Breast carcinoma

Table S 1.2.1. Significant common driver gene set between Breast_P and Breast_M

k	common gene set	p1	p2	q
2	<i>TP53,GATA3</i>	<0.0001	<0.0001	<0.0001
3	<i>TP53,GATA3,CDH1</i>	<0.0001	<0.0001	<0.0001
4	<i>TP53,GATA3,CDH1,ESR1</i>	<0.0001	<0.0001	<0.0001
5	<i>TP53,GATA3,CDH1,CDC73,CDKN1B</i>	<0.0001	<0.0001	<0.0001
6	<i>TP53,GATA3,CDH1,CDC73,CDKN1B,ESR1</i>	<0.0001	<0.0001	<0.0001
7	<i>TP53,GATA3,CDH1,CDC73,CDKN1B,ESR1,RHEB</i>	<0.0001	<0.0001	<0.0001
8	<i>TP53,GATA3,CDH1,CDC73,CDKN1B,ESR1,RHEB,PTPN11</i>	<0.0001	<0.0001	<0.0001
9	<i>TP53,GATA3,CDH1,CDC73,CDKN1B,RHEB,CCNE1,PTPN11,SMARCA4</i>	<0.0001	<0.0001	<0.0001
10	<i>TP53,GATA3,CDH1,CDC73,CDKN1B,RHEB,CCNE1,PTPN11,SMARCA4,NFE2L2</i>	<0.0001	<0.0001	<0.0001

*Breast_M has no specific mutated driver gene sets relative to Breast_P when k=2 ~ 10.

*Breast_P has no specific mutated driver gene sets relative to Breast_M when k=2 ~ 10.

1.3 Colorectal cancer

Table S 1.3.1. Significant common driver gene set between Colorectal_P and Colorectal_M

k	common gene set	p1	p2	q
2	<i>APC,RNF43</i>	<0.0001	<0.0001	<0.0001
3	<i>APC,RNF43,H3F3A</i>	<0.0001	<0.0001	<0.0001
4	<i>APC,RNF43,H3F3A,PIM1</i>	<0.0001	<0.0001	<0.0001
5	<i>APC,RNF43,PIM1,HIST1H3H,PPP6C</i>	<0.0001	<0.0001	<0.0001
6	<i>APC,RNF43,ASB17,HIST1H3H,CEBPA,PPP6C</i>	<0.0001	<0.0001	<0.0001
7	<i>APC,RNF43,ASB17,HIST1H3H,PIM1,H3F3A,YTHDC1</i>	<0.0001	<0.0001	<0.0001
8	<i>APC,RNF43,ASB17,HIST1H3H,PIM1,PPP6C,YTHDC1,CUL1</i>	<0.0001	<0.0001	<0.0001
9	<i>APC,RNF43,ASB17,HIST1H3H,PIM1,EIF4A2,YTHDC1,FOXA1,H3F3A</i>	<0.0001	<0.0001	<0.0001
10	<i>APC,RNF43,RAB35,HIST1H3H,PIM1,EIF4A2,SDHAF2,FOXA1,H3F3A,SDHD</i>	<0.0001	<0.0001	<0.0001

Table S 1.3.2. Colorecta_M specific mutated driver gene sets relative to Colorectal_P

k	Specific gene set	p1	p2	q
2	<i>TP53,AXL</i>	0.007	0.604	0.047
4	<i>TP53,AXL,RBM10,RUNX1</i>	<0.0001	0.919	<0.0001
5	<i>TP53,BRAF,RBM10,BRD4,HNF1A</i>	0.012	0.999	<0.0001
6	<i>TP53,BRAF,RBM10,BRD4,HNF1A,NBN</i>	0.005	0.999	<0.0001
7	<i>TP53,BRAF,RBM10,BRD4,HNF1A,NBN,NRAS</i>	0.003	1	<0.0001
8	<i>TP53,BRAF,RBM10,BRD4,HNF1A,NBN,NRAS,RUNX1</i>	0.002	1	<0.0001
9	<i>TP53,BRAF,RBM10,BRD4,HNF1A,NBN,NRAS,RUNX1,STK11</i>	<0.0001	1	<0.0001
10	<i>TP53,BRAF,RBM10,BRD4,HNF1A,NBN,NRAS,RUNX1,BMPR1A,NEGR1</i>	<0.0001	1	<0.0001

*Colorectal_P has no specific mutated driver gene sets relative to Colorectal_M when k=2 ~ 10.

1.4 Endometrial cancer

Table S 1.4.1. Significant common driver gene set between Endometrial_P and Endometrial_M

k	common gene set	p1	p2	q
2	<i>TP53,ARID1A</i>	<0.0001	<0.0001	<0.0001
3	<i>TP53,AKT1,PTEN</i>	<0.0001	<0.0001	<0.0001
4	<i>TP53,AKT1,PTEN,MUTYH</i>	<0.0001	<0.0001	<0.0001
5	<i>TP53,AKT1,PTEN,MUTYH,CD276</i>	<0.0001	<0.0001	<0.0001
6	<i>TP53,AKT1,PTEN,MUTYH,CD276,LRRC20</i>	<0.0001	<0.0001	<0.0001
7	<i>TP53,AKT1,PTEN,MUTYH,CD276,LRRC20,CDKN2A</i>	<0.0001	<0.0001	<0.0001
8	<i>TP53,AKT1,PTEN,MUTYH,CD276,LRRC20,CDKN2A,PAK1</i>	<0.0001	<0.0001	<0.0001
9	<i>TP53,AKT1,PTEN,MUTYH,CD276,LRRC20,CDKN2A,PAK1,SMARCB1</i>	<0.0001	<0.0001	<0.0001
10	<i>TP53,AKT1,PTEN,MUTYH,CD276,LRRC20,CDKN2A,PAK1,SMARCB1,HIST1H1C</i>	<0.0001	<0.0001	<0.0001

Table S 1.4.2. Endometrial_M specific mutated driver gene sets relative to Endometrial_P

k	specific gene set	p1	p2	q
3	<i>CTNNB1,GLI1,KRAS</i>	0.012	0.743	0.018
4	<i>CTNNB1,GLI1,KRAS,PAK5</i>	0.005	0.854	0.006
5	<i>CTNNB1,GLI1,KRAS,XPO1,AR</i>	0.007	0.992	<0.0001
6	<i>CTNNB1,GLI1,KRAS,XPO1,AR,RICTOR</i>	0.012	1	<0.0001

*Endometrial_P has no specific mutated driver gene sets relative to Endometrial_M when k=2 ~ 10.

1.5 Esophagogastric carcinoma

Table S 1.5.1. Significant common driver gene set between Esophagogastric_P and Esophagogastric_M

k	common gene set	p1	p2	q
4	<i>TP53,PLCG2,TGFBR1,TNFAIP3</i>	<0.0001	0.03	<0.0001
5	<i>TP53,PLCG2,TGFBR1,TNFAIP3,IDH1</i>	<0.0001	0.034	<0.0001
6	<i>TP53,PLCG2,TGFBR1,TNFAIP3,IDH1,ERG</i>	<0.0001	0.026	<0.0001
7	<i>TP53,PLCG2,TGFBR1,TNFAIP3,IDH1,ERG,SMAD3</i>	<0.0001	0.01	<0.0001
8	<i>TP53,PLCG2,TGFBR1,TNFAIP3,IDH1,ERG,FGFR2,MAP2K1</i>	<0.0001	0.007	<0.0001
9	<i>TP53,PLCG2,TGFBR1,TNFAIP3,IDH1,ERG,FGFR2,SMAD3,CD276</i>	<0.0001	<0.0001	<0.0001
10	<i>TP53,PLCG2,TGFBR1,TNFAIP3,IDH1,ERG,FGFR2,HGF,MAP2K1,SUFU</i>	<0.0001	<0.0001	<0.0001

Table S 1.5.2. Esophagogastric_P and Esophagogastric_M specific mutated driver gene sets relative to each other
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Type	k	Specific gene set	p1	p2	q
Esophagogastric_P / Esophagogastric_M	2	<i>TP53,ERBB2</i>	0.024	0.787	0.03
	3	<i>TP53,ERBB2,PIK3CA</i>	<0.0001	0.79	<0.0001
	9	<i>ARID1A,BRAF,CDKN2A,CTNNB1,EPHB1,KRAS,NTRK3,RHOA,SMAD4</i>	0.045	0.999	0.005
	10	<i>ARID1A,BRAF,CDKN2A,CTNNB1,EPHB1,KRAS,NTRK3,RHOA,SMAD4,ANKRD11</i>	<0.0001	1	<0.0001
Esophagogastric_M / Esophagogastric_P	10	<i>ARAF,ARID2,DICER1,GNAS,IRS1,MYC,NKX2-1,PGR,PTCH1,TGFBR2</i>	0.034	1	0.001

1.6 Gastrointestinal stromal tumor

Table S 1.6.1. Significant common driver gene set between Gastrointestinal_P and Gastrointestinal_M

k	common gene set	p1	p2	q
4	<i>KIT,NF1,PDGFRA,SDHA</i>	<0.0001	0.026	<0.0001
5	<i>KIT,NF1,PDGFRA,SDHA,EGFR</i>	<0.0001	0.027	<0.0001
6	<i>KIT,NF1,PDGFRA,SDHA,EGFR,B2M</i>	<0.0001	0.036	<0.0001
7	<i>KIT,NF1,PDGFRA,SDHA,EGFR,B2M,TGFBR2</i>	<0.0001	0.004	<0.0001
8	<i>KIT,NF1,PDGFRA,SDHA,EGFR,B2M,CARD11,RASA1</i>	<0.0001	<0.0001	<0.0001
9	<i>KIT,NF1,PDGFRA,SDHA,EGFR,B2M,TGFBR2,RASA1,SDHB</i>	<0.0001	<0.0001	<0.0001
10	<i>KIT,NF1,PDGFRA,SDHA,EGFR,B2M,TGFBR2,RASA1,SDHB,CARD11</i>	<0.0001	<0.0001	<0.0001

Table S 1.6.2. Gastrointestinal_P and Gastrointestinal_M specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Gastrointestinal_P / Gastrointestinal_M	2	<i>KIT,PDGFRA</i>	<0.0001	0.234	0.001
	3	<i>KIT,PDGFRA,NF1</i>	<0.0001	0.103	<0.0001
Gastrointestinal_M / Gastrointestinal_P	8	<i>ANKRD11,FLT4,KRAS,MTOR,PPP2R1A,RB1,SETD2,ALK</i>	0.43	1	0.002
	9	<i>ANKRD11,CLCN5,DOT1L,FLT4,KRAS,MTOR,PPP2R1A,RB1,SETD2</i>	0.027	1	<0.0001
	10	<i>ANKRD11,CLCN5,DOT1L,FLT4,KRAS,MTOR,PPP2R1A,RB1,SETD2,PHOX2B</i>	0.013	1	<0.0001

1.7 Head and Neck carcinoma

Table S 1.7.1. Significant common driver gene set between HeadNeck_P and HeadNeck_M

k	common gene set	p1	p2	q
4	<i>TP53,PIK3CA,PIK3R1,PTEN</i>	0.028	0.026	0.002
5	<i>TP53,PIK3CA,PIK3R1,PTEN,AKT1</i>	0.01	0.008	0.001
6	<i>TP53,PIK3CA,PIK3R1,PTEN,AKT1,CTCF</i>	0.015	0.005	<0.0001
7	<i>TP53,PIK3CA,PIK3R1,PTEN,AKT1,CTCF,EWSR1</i>	0.006	0.001	<0.0001
8	<i>TP53,PIK3CA,PIK3R1,PTEN,AKT1,CTCF,EWSR1,B2M</i>	0.002	0.015	<0.0001
9	<i>TP53,U2AF1,PIK3R1,PTEN,AKT1,CTCF,EWSR1,ARID1A,RAF1</i>	0.002	<0.0001	<0.0001
10	<i>TP53,U2AF1,PIK3R1,PTEN,AKT1,CTCF,EWSR1,ARID1A,RAF1,AXIN1</i>	0.001	<0.0001	<0.0001

Table S 1.7.2. HeadNeck_P and HeadNeck_M specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
HeadNeck_P / HeadNeck_M	2	<i>ARID1A,TERT</i>	0.045	1	0.004
	3	<i>ARID1A,TERT,AXIN2</i>	0.004	1	<0.0001
	4	<i>ARID1A,TERT,AXIN2,MYCN</i>	0.005	1	<0.0001
	6	<i>ARID1A,TERT,AXIN2,MYCN,SYK,RAF1</i>	<0.0001	0.996	<0.0001
	7	<i>AXIN2,TERT,BCL6,MITF,MYCN,SYK,SETD2</i>	0.001	1	<0.0001
	8	<i>AXIN2,TERT,BCL6,MITF,MYCN,SYK,SETD2,PLK2</i>	<0.0001	1	<0.0001
	9	<i>AXIN2,TERT,BCL6,MITF,MYCN,SYK,SETD2,PLK2,CDKN1B</i>	<0.0001	1	<0.0001
	10	<i>AXIN2,TERT,BCL6,MITF,MYCN,SYK,SETD2,PLK2,CDKN1B,ATF1</i>	<0.0001	1	<0.0001
HeadNeck_M / HeadNeck_P	7	<i>ATR,NFKBIA,RB1,MSH2,BMPR1A,ERBB3,KDM6A</i>	0.034	0.999	0.002
	9	<i>ATR,NFKBIA,RB1,BLM,KMT2A,PIK3CA,PIK3CD,SMARCA4,WT1</i>	0.032	1	<0.0001
	10	<i>ATR,NFKBIA,RB1,BLM,BMPR1A,PIK3CA,PIK3CD,SMARCA4,WT1,KMT2A</i>	0.018	1	0.001

1.8 Non-small-cell Lung cancer

Table S 1.8.1. Significant common driver gene set between Lung_P and Lung_M

k	common gene set	p1	p2	q
2	<i>TP53, KRAS</i>	<0.0001	<0.0001	<0.0001
3	<i>TP53, KRAS, EML4</i>	<0.0001	<0.0001	<0.0001
4	<i>TP53, KRAS, EML4, CD74</i>	<0.0001	<0.0001	<0.0001
5	<i>TP53, KRAS, EML4, CD74, CCDC6</i>	<0.0001	<0.0001	<0.0001
6	<i>TP53, KRAS, EML4, CD74, CCDC6, KIF5B</i>	<0.0001	<0.0001	<0.0001
7	<i>TP53, KRAS, EML4, CD74, CCDC6, KIF5B, EIF1AX</i>	<0.0001	<0.0001	<0.0001
8	<i>TP53, KRAS, EML4, CD74, CCDC6, KIF5B, EIF1AX, SLC1A2</i>	<0.0001	<0.0001	<0.0001
9	<i>TP53, KRAS, EML4, CD74, CCDC6, KIF5B, EIF1AX, SLC1A2, DYSF</i>	<0.0001	<0.0001	<0.0001
10	<i>TP53, KRAS, EML4, CD74, CCDC6, KIF5B, EIF1AX, SLC1A2, NCOA4, NDUFAF6</i>	<0.0001	<0.0001	<0.0001

Table S 1.8.2. Lung_P specific mutated driver gene sets relative to Lung_M

k	Specific gene set	p1	p2	q
6	<i>EGFR, KMT2D, PDGFRA, RBM10, STK11, ROS1</i>	<0.0001	0.061	<0.0001
8	<i>EGFR, KMT2D, PDGFRA, RBM10, STK11, RASA1, BRAF, ROS1</i>	<0.0001	0.052	<0.0001
9	<i>EGFR, KMT2D, PDGFRA, RBM10, STK11, RASA1, BRAF, ROS1, NKX2-1</i>	<0.0001	0.096	<0.0001
10	<i>EGFR, KMT2D, PDGFRA, RBM10, STK11, RASA1, BRAF, ROS1, NKX2-1, AR</i>	<0.0001	0.388	<0.0001

*Lung_M has no specific mutated driver gene sets relative to Lung_P when k=2 ~ 10.

1.9 Melanoma

Table S 1.9.1. Significant common driver gene set between Melanoma.P and Melanoma.M

k	common gene set	p1	p2	q
3	<i>GNA11,GNAQ,TERT</i>	<0.0001	0.021	<0.0001
4	<i>GNA11,GNAQ,NRAS,BRAF</i>	<0.0001	0.002	<0.0001
5	<i>GNA11,GNAQ,NRAS,BRAF,KIT</i>	<0.0001	<0.0001	<0.0001
6	<i>GNA11,GNAQ,NRAS,BRAF,KIT,RICTOR</i>	<0.0001	<0.0001	<0.0001
7	<i>GNA11,GNAQ,NRAS,BRAF,KIT,CHEK2,MAP3K1</i>	<0.0001	<0.0001	<0.0001
8	<i>GNA11,GNAQ,NRAS,BRAF,KIT,CHEK2,HNF1A,PIM1</i>	<0.0001	<0.0001	<0.0001
9	<i>GNA11,GNAQ,NRAS,BRAF,KIT,CHEK2,HNF1A,PIM1,RICTOR</i>	<0.0001	<0.0001	<0.0001
10	<i>GNA11,GNAQ,NRAS,BRAF,KIT,CHEK2,HNF1A,PIM1,RICTOR,PAK1</i>	<0.0001	<0.0001	<0.0001

Table S 1.9.2. Melanoma_M specific mutated driver gene sets relative to Melanoma_P

k	Specific gene set	p1	p2	q
2	<i>ATRX, TERT</i>	0.019	0.997	<0.0001
3	<i>BRAF, NF1, NRAS</i>	<0.0001	0.905	<0.0001
4	<i>ATRX, TERT, BAP1, TRAF2</i>	<0.0001	0.993	<0.0001
5	<i>ATRX, TERT, BAP1, TRAF2, PPP6C</i>	<0.0001	0.997	<0.0001
6	<i>ATRX, TERT, BAP1, TRAF2, CASP8, PTEN</i>	<0.0001	0.997	<0.0001
7	<i>ATRX, TERT, BAP1, TRAF2, CASP8, PTEN, DICER1</i>	0.002	0.999	<0.0001
8	<i>ATRX, TERT, BAP1, TRAF2, CASP8, PTEN, DICER1, SETD2</i>	0.012	1	0.001

*Melanoma_P has no specific mutated driver gene sets relative to Melanoma_M when k=2 ~ 10.

1.10 Ovarian cancer

Table S 1.10.1. Significant common driver gene set between Ovarian_P and Ovarian_M

k	common gene set	p1	p2	q
2	<i>TP53,ARID1A</i>	<0.0001	0.005	<0.0001
3	<i>TP53,ARID1A,KRAS</i>	<0.0001	<0.0001	<0.0001
4	<i>TP53,ARID1A,KRAS,NRAS</i>	<0.0001	<0.0001	<0.0001
5	<i>TP53,ARID1A,KRAS,NRAS,PAK5</i>	<0.0001	<0.0001	<0.0001
6	<i>TP53,ARID1A,KRAS,NRAS,PAK5,BRAF</i>	<0.0001	<0.0001	<0.0001
7	<i>TP53,ARID1A,KRAS,NRAS,PAK5,BRAF,BTK</i>	<0.0001	<0.0001	<0.0001
8	<i>TP53,ARID1A,KRAS,NRAS,PAK5,BRAF,BTK,PPM1D</i>	<0.0001	<0.0001	<0.0001
9	<i>TP53,ARID1A,KRAS,NRAS,PAK5,BRAF,BTK,PPM1D,EYA2</i>	<0.0001	<0.0001	<0.0001
10	<i>TP53,ARID1A,KRAS,NRAS,FLCN,BRAF,BTK,PPM1D,EYA2,CDC73</i>	<0.0001	<0.0001	<0.0001

Table S 1.10.2. Ovarian_P and Ovarian_M specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Ovarian_P / Ovarian_M	5	<i>LATS2,MST1R,NF2,PIK3CA,ROS1</i>	0.02	0.748	0.048
	6	<i>LATS1,MST1R,NF2,PIK3CA,ROS1,ERBB3</i>	0.008	0.759	0.028
	7	<i>LATS1,MST1R,NF2,PIK3CA,ROS1,ERBB3,LATS2</i>	0.002	0.666	0.012
	8	<i>LATS1,MST1R,NF2,PIK3CA,ROS1,ERBB3,LATS2,ARID1B</i>	<0.0001	0.945	0.002
	9	<i>LATS1,MST1R,NF2,PIK3CA,ROS1,ERBB3,LATS2,ARID1B,ATRX</i>	<0.0001	0.982	<0.0001
	10	<i>LATS1,MST1R,NF2,PIK3CA,ROS1,ERBB3,LATS2,ARID1B,ATRX,KMT2A</i>	<0.0001	0.999	<0.0001
Ovarian_M / Ovarian_P	9	<i>APC,AXL,IRS2,KDM5A,MAP3K1,NF1,NOTCH1,PTPRS,SPEN</i>	0.027	1	<0.0001
	10	<i>APC,AXL,IRS2,KDM5A,MAP3K1,NF1,NOTCH1,PTPRS,SPEN,BRD4</i>	0.039	1	0.001

1.11 Pancreatic cancer

Table S 1.11.1. Significant common driver gene set between Pancreatic_P and Pancreatic_M

k	common gene set	p1	p2	q
2	<i>KRAS,MEN1</i>	<0.0001	<0.0001	<0.0001
3	<i>KRAS,MEN1,BRAF</i>	<0.0001	<0.0001	<0.0001
4	<i>KRAS,MEN1,BRAF,CTNNB1</i>	<0.0001	<0.0001	<0.0001
5	<i>KRAS,MEN1,BRAF,CTNNB1,AURKB</i>	<0.0001	<0.0001	<0.0001
6	<i>KRAS,MEN1,BRAF,CTNNB1,AURKB,TSC1</i>	<0.0001	<0.0001	<0.0001
7	<i>KRAS,MEN1,BRAF,CTNNB1,AURKB,TSC1,FAT1</i>	<0.0001	<0.0001	<0.0001
8	<i>KRAS,MEN1,BRAF,CTNNB1,AURKB,TSC1,FAT1,NTRK3</i>	<0.0001	<0.0001	<0.0001
9	<i>KRAS,MEN1,BRAF,CTNNB1,AURKB,TSC1,FAT1,NTRK3,VHL</i>	<0.0001	<0.0001	<0.0001
10	<i>KRAS,MEN1,BRAF,CTNNB1,AURKB,TSC1,ARAF,HIST1H1C,VHL,ZNF678</i>	<0.0001	<0.0001	<0.0001

Table S 1.11.2. Pancreatic_P and Pancreatic_M specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Pancreatic_P / Pancreatic_M	2	<i>TP53,GNAS</i>	0.001	0.688	0.001
	3	<i>TP53,GNAS,PTPRT</i>	<0.0001	0.974	<0.0001
	4	<i>TP53,GNAS,PTPRT,ATRX</i>	<0.0001	0.884	<0.0001
	5	<i>TP53,GNAS,PTPRT,ATRX,VHL</i>	<0.0001	0.918	<0.0001
	6	<i>TP53,GNAS,PTPRT,ATRX,VHL,KMT2C</i>	<0.0001	0.976	<0.0001
	7	<i>TP53,GNAS,PTPRT,ATRX,VHL,KMT2C,AXIN1</i>	<0.0001	0.994	<0.0001
	8	<i>TP53,GNAS,PTPRT,ATRX,VHL,KMT2C,AXIN1,RNF43</i>	<0.0001	0.993	<0.0001
	9	<i>TP53,GNAS,PTPRT,ATRX,JAK3,KMT2C,AXIN1,RNF43,PLK2</i>	<0.0001	1	<0.0001
	10	<i>TP53,GNAS,PTPRT,ATRX,JAK3,KMT2C,AXIN1,RNF43,PLK2,NOTCH1</i>	<0.0001	1	<0.0001
Pancreatic_M / Pancreatic_P	4	<i>DAXX,FANCA,KMT2D,PIK3CA</i>	0.047	0.953	0.03

1.12 Prostate cancer

Table S 1.12.1. Significant common driver gene set between Prostate_P and Prostate_M

k	common gene set	p1	p2	q
2	<i>SPOP, TMPRSS2</i>	<0.0001	0.004	<0.0001
3	<i>SPOP, TMPRSS2, FOXA1</i>	<0.0001	<0.0001	<0.0001
4	<i>SPOP, TMPRSS2, FOXA1, AR</i>	<0.0001	0.002	<0.0001
5	<i>SPOP, TMPRSS2, FOXA1, KDM6A, PTEN</i>	<0.0001	<0.0001	<0.0001
6	<i>SPOP, TMPRSS2, FOXA1, KDM6A, AR, MTOR</i>	<0.0001	<0.0001	<0.0001
7	<i>SPOP, TMPRSS2, FOXA1, KDM6A, AR, MTOR, EPHA3</i>	<0.0001	<0.0001	<0.0001
8	<i>SPOP, TMPRSS2, FOXA1, KDM6A, AR, MTOR, EPHA3, PGR</i>	<0.0001	<0.0001	<0.0001
9	<i>SPOP, TMPRSS2, FOXA1, KDM6A, AR, MTOR, EPHA5, PGR, HRAS</i>	<0.0001	<0.0001	<0.0001
10	<i>SPOP, TMPRSS2, FOXA1, KDM6A, AR, MTOR, EPHA5, PGR, HRAS, EPHA3</i>	<0.0001	<0.0001	<0.0001

Table S 1.12.2. Prostate_M specific mutated driver gene sets relative to Prostate_P

k	Specific gene set	p1	p2	q
4	<i>TP53, APC, ERBB4, KMT2D</i>	0.03	0.972	0.004
5	<i>TP53, AR, ARID1A, FLT4, PIK3CA</i>	0.014	0.911	0.005
6	<i>TP53, APC, ARID1A, KMT2D, ERBB4, SOX17</i>	0.022	0.951	0.01
9	<i>TP53, ARID5B, EPHB1, KMT2D, NTRK2, SOX17, PIK3R1, SPEN, TET2</i>	0.038	0.999	0.001
10	<i>TP53, ARID5B, EPHB1, KMT2D, ERBB4, SOX17, PIK3R1, SPEN, TET2, ARID1A</i>	0.014	0.998	<0.0001

*Prostate_P has no specific mutated driver gene sets relative to Prostate_M when k=2 ~ 10.

1.13 Renal cell carcinoma

Table S 1.13.1. Significant common driver gene set between Renal_P and Renal_M

k	common gene set	p1	p2	q
2	<i>NF2, VHL</i>	0.01	<0.0001	<0.0001
3	<i>NF2, VHL, MET</i>	0.002	<0.0001	<0.0001
4	<i>NF2, VHL, MET, TFE3</i>	<0.0001	<0.0001	<0.0001
5	<i>NF2, VHL, MET, TFE3, TSC2</i>	<0.0001	<0.0001	<0.0001
6	<i>NF2, VHL, MET, TFE3, TSC2, KMT2A</i>	<0.0001	<0.0001	<0.0001
7	<i>NF2, VHL, MET, TFE3, TSC2, KMT2A, SMARCB1</i>	<0.0001	<0.0001	<0.0001
8	<i>NF2, VHL, MET, TFE3, TSC2, KMT2A, SMARCB1, ELOC</i>	<0.0001	<0.0001	<0.0001
9	<i>NF2, VHL, MET, TFE3, TSC2, KMT2A, B2M, ELOC, CIC</i>	<0.0001	<0.0001	<0.0001
10	<i>NF2, VHL, MET, TFE3, TSC2, KMT2A, B2M, ELOC, SMARCB1, FYN</i>	<0.0001	<0.0001	<0.0001

Table S 1.13.2. Renal_P and Renal_M specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Renal_P / Renal_M	7	<i>ALK,PBRM1,PIK3C2G,PIK3CB,PIK3CG,MTOR,NCOR1</i>	0.043	1	<0.0001
	8	<i>ALK,PBRM1,PIK3C2G,PIK3CB,PIK3CG,MTOR,NCOR1,PTPRT</i>	0.041	1	<0.0001
	9	<i>ALK,PBRM1,PIK3C2G,PIK3CB,PIK3CG,MTOR,NCOR1,PTPRT,NOTCH3</i>	0.01	1	<0.0001
	10	<i>ALK,PBRM1,PIK3C2G,PIK3CB,PIK3CG,PTPRT,AXL,KMT2C,PAK5,SPEN</i>	0.001	1	<0.0001
Renal_M / Renal_P	2	<i>PTEN,BAP1</i>	0.04	0.965	0.016
	6	<i>HNF1A,MED12,MSH6,PTEN,SF3B1,JAK3</i>	0.04	1	<0.0001
	7	<i>HNF1A,MED12,MSH6,PTEN,SF3B1,ATRX,AKT2</i>	0.015	0.999	<0.0001
	8	<i>HNF1A,MED12,MSH6,PTEN,SF3B1,ATRX,CALR,RECQL4</i>	0.009	0.999	<0.0001
	9	<i>HNF1A,MED12,MSH6,PTEN,SF3B1,ATRX,SH2B3,JAK3,KRAS</i>	0.004	1	<0.0001
	10	<i>HNF1A,MED12,MSH6,PTEN,SF3B1,AKT2,CALR,HLA-A,RECQL4,SH2B3</i>	0.001	1	<0.0001

1.14 Skin cancer, non melanoma

*There is no significant common driver gene set between Skin_P and Skin_M when $k=2 \sim 10$.

Table S 1.14.1. Skin_P and Skin_M specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Skin_P / Skin_M	5	<i>ANKRD11,BCOR,FLT3,MSH2,SPOP</i>	0.044	0.999	0.001
	9	<i>ANKRD11,BCOR,FLT3,MSH2,H3F3A,IKBKE,TBL3,WT1,CSF3R</i>	0.028	1	<0.0001
	10	<i>ANKRD11,BCOR,FLT3,MSH2,H3F3A,IKBKE,TBL3,WT1,CSF3R,CDKN2B</i>	0.011	1	<0.0001
Skin_M / Skin_P	8	<i>FBXW7,FGFR1,ICOSLG,IRF4,MED12,MYD88,STAG2,VTCN1</i>	0.039	1	0.005
	9	<i>FBXW7,FGFR1,ICOSLG,IRF4,MED12,MYD88,STAG2,VTCN1,SDHAF2</i>	0.031	1	0.004
	10	<i>FBXW7,FGFR1,ICOSLG,IRF4,MED12,MYD88,STAG2,VTCN1,SDHAF2,NFKBIA</i>	0.019	1	0.002

1.15 Thyroid cancer

Table S 1.15.1. Significant common driver gene set between Thyroid_P and Thyroid_M

k	common gene set	p1	p2	q
3	<i>KRAS,RET,TERT</i>	0.03	<0.0001	<0.0001
4	<i>KRAS,RET,TERT,ARID1A</i>	0.007	<0.0001	<0.0001
5	<i>KRAS,RET,TERT,ARID1A,MAP2K4</i>	0.004	<0.0001	<0.0001
6	<i>KRAS,RET,BRAF,HRAS,NRAS,NF1</i>	<0.0001	<0.0001	<0.0001
7	<i>KRAS,RET,BRAF,HRAS,NRAS,NF1,PTEN</i>	<0.0001	<0.0001	<0.0001
8	<i>KRAS,RET,BRAF,HRAS,NRAS,NF1,PTEN,TP63</i>	<0.0001	<0.0001	<0.0001
9	<i>KRAS,RET,BRAF,HRAS,NRAS,RB1,PTEN,PTPRT,TBX3</i>	<0.0001	<0.0001	<0.0001
10	<i>KRAS,RET,BRAF,HRAS,NRAS,NF1,DAXX,PTPRT,APC,STK11</i>	<0.0001	<0.0001	<0.0001

Table S 1.15.2. Thyroid_P and Thyroid_M specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Thyroid_P / Thyroid_M	7	<i>CREBBP, EIF1AX, ERCC4, MAX, NF2, NFE2L2, KMT2C</i>	0.031	0.96	0.009
	9	<i>CREBBP, EIF1AX, ERCC4, MAX, NF2, NFE2L2, CDKN1B, DICER1, DIS3</i>	0.014	0.996	<0.0001
	10	<i>CREBBP, EIF1AX, BCOR, PTEN, GRIN2A, NFE2L2, HIST1H3H, DIS3, HLA-A, SOX17</i>	0.049	0.98	0.018
Thyroid_M / Thyroid_P	4	<i>DNMT3A, BRAF, CCDC6, ETV6</i>	0.031	0.99	0.002
	5	<i>DNMT3A, BRAF, CCDC6, ETV6, IRS1</i>	0.021	0.985	0.002
	6	<i>DNMT3A, DAXX, TERT, ARID1B, PTEN, SPEN</i>	<0.0001	0.932	<0.0001
	7	<i>DNMT3A, DAXX, TERT, PIK3CA, PPP2R1A, SYK, TET2</i>	0.005	0.998	<0.0001
	8	<i>DNMT3A, DAXX, TERT, PIK3CA, EP300, SYK, TET2, IRS1</i>	0.003	1	<0.0001
	9	<i>DNMT3A, DAXX, TERT, PIK3CA, EP300, SYK, TET2, IRS1, NCOA4</i>	<0.0001	0.999	<0.0001
10	<i>DNMT3A, ATM, TERT, ETV6, MSH6, PTEN, SPEN, IRS1, KMT2D, TP63</i>	<0.0001	0.983	<0.0001	

2 Supplementary Tables: Abnormal signals may predict the seeding site of metastasis

2.1 Breast carcinoma

Breast_P and other metastatic cancers from Breast

Table S 2.1.1. Breast_P and Breast_Bone specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Breast_P / Breast_Bone	2	<i>PIK3CA,PTEN</i>	0.01	0.503	0.021
	3	<i>PIK3CA,PTEN,BRCA2</i>	<0.0001	0.186	0.007
	4	<i>PIK3CA,PTEN,BRCA2,NF1</i>	0.002	0.444	0.006
	10	<i>PIK3CA,PTEN,ATRX,NF1,ATM,DDR2,KMT2C,MAP3K1,NOTCH1,PIK3CG</i>	0.041	0.996	<0.0001
Breast_Bone / Breast_P	10	<i>BTK,ERBB4,ETV6,GNA11,HIST1H3I,KDR,RICTOR,SDHA,SHQ1,SOX17</i>	0.02	0.999	<0.0001

Table S 2.1.2. Breast_P specific mutated driver gene sets relative to Breast_Chest Wall

k	Specific gene set	p1	p2	q
2	<i>PIK3CA,PTEN</i>	0.014	1	0.006
3	<i>PIK3CA,PTEN,BRCA2</i>	<0.0001	0.86	<0.0001
4	<i>PIK3CA,PTEN,BRCA2,AKT1</i>	<0.0001	0.48	<0.0001
5	<i>PIK3CA,PTEN,BRCA2,AKT1,NF1</i>	<0.0001	0.742	<0.0001
6	<i>PIK3CA,PTEN,BRCA2,AKT1,NF1,MAP3K1</i>	0.028	0.957	0.012
9	<i>PIK3CA,PTEN,BRCA2,AKT1,NF1,MAP3K1,ESR1,GRIN2A,KMT2C</i>	0.041	0.949	0.023
10	<i>PIK3CA,PTEN,BRCA2,AKT1,NF1,MAP3K1,ESR1,GRIN2A,KMT2C,NOTCH1</i>	0.026	0.949	0.008

*Breast_Chest Wall has no specific mutated driver gene sets relative to Breast_P when k=2 ~ 10.

*Breast_Lymph Node has no specific mutated driver gene sets relative to Breast_P when k=2 ~ 10.

Table S 2.1.3. Breast_P and Breast_Liver specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Breast_P / Breast_Liver	2	<i>PIK3CA,PTEN</i>	0.011	0.845	0.008
	3	<i>PIK3CA,PTEN,BRCA2</i>	<0.0001	0.933	<0.0001
	4	<i>PIK3CA,PTEN,BRCA2,NF1</i>	0.002	0.996	<0.0001
	5	<i>PIK3CA,PTEN,BRCA2,NF1,ATRX</i>	<0.0001	0.999	<0.0001
	6	<i>PIK3CA,PTEN,BRCA2,NF1,ATRX,ATM</i>	0.001	1	<0.0001
	7	<i>PIK3CA,PTEN,BRCA2,NF1,ATRX,ATM,AKT1</i>	<0.0001	1	<0.0001
	8	<i>PIK3CA,PTEN,BRCA2,NF1,ATRX,ATM,AKT1,DDR2</i>	<0.0001	1	<0.0001
	9	<i>PIK3CA,PTEN,BRCA2,NF1,ATRX,ATM,AKT1,DDR2,FLT1</i>	<0.0001	0.999	<0.0001
	10	<i>PIK3CA,PTEN,BRCA2,NF1,ATRX,ATM,AKT1,DDR2,FLT1,MED12</i>	<0.0001	1	<0.0001
	Breast_Liver / Breast_P	3	<i>ERBB2,ESR1,FGFR4</i>	0.002	0.591
4		<i>ERBB2,ESR1,FGFR4,BLM</i>	0.002	0.56	0.006
5		<i>ERBB2,ESR1,FGFR4,BLM,SHQ1</i>	<0.0001	0.518	0.002
6		<i>ERBB2,ESR1,FGFR4,BLM,SHQ1,FGFR4</i>	<0.0001	0.813	<0.0001
7		<i>ERBB2,ESR1,FGFR4,BLM,SHQ1,FGFR4,KDR</i>	<0.0001	0.809	<0.0001
8		<i>ERBB2,ESR1,FGFR4,BLM,SHQ1,FGFR4,KDR,CCND2</i>	<0.0001	0.802	0.001
9		<i>ERBB2,ESR1,EP300,BLM,GATA1,ERCC5,MAPK1,MYOD1,ROS1</i>	<0.0001	0.668	<0.0001
10		<i>ERBB2,ESR1,EP300,BLM,SHQ1,CCND2,KDR,MAPK1,ROS1,GATA1</i>	<0.0001	0.696	<0.0001

Table S 2.1.4. Breast_P and Breast_Lung specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Breast_P / Breast_Lung	2	<i>PIK3CA,PTEN</i>	0.006	0.157	0.041
	3	<i>PIK3CA,PTEN,BRCA2</i>	<0.0001	0.614	0.001
	4	<i>PIK3CA,PTEN,BRCA2,AKT1</i>	<0.0001	0.481	<0.0001
	5	<i>PIK3CA,PTEN,BRCA2,AKT1,MAP3K1</i>	0.017	0.944	0.007
	6	<i>PIK3CA,PTEN,BRCA2,AKT1,MAP3K1,NF1</i>	0.024	0.977	0.013
	7	<i>PIK3CA,PTEN,BRCA2,AKT1,MAP3K1,NF1,ATM</i>	0.012	0.966	0.004
	8	<i>PIK3CA,PTEN,BRCA2,AKT1,MAP3K1,NF1,ATM,GRIN2A</i>	0.007	0.97	0.004
	9	<i>PIK3CA,PTEN,BRCA2,AKT1,MAP3K1,NF1,ATM,GRIN2A,MED12</i>	0.003	0.988	0.003
	10	<i>PIK3CA,PTEN,BRCA2,AKT1,MAP3K1,NF1,ATM,GRIN2A,MED12,DDR2</i>	0.002	0.974	<0.0001
Breast_Lung / Breast_P	8	<i>BRIP1,DOT1L,ELOC,EPHA7,FGFR1,INSR,MST1,CSF3R</i>	0.049	0.998	0.003
	9	<i>BRIP1,DOT1L,ELOC,EPHA7,FGFR1,INSR,MST1,IRS1,RAD51B</i>	0.044	1	0.002
	10	<i>BRIP1,DOT1L,ELOC,EPHA7,FGFR1,INSR,MST1,IRS1,RAD51B,CSF3R</i>	0.024	0.996	0.001

Table S 2.1.5. Breast_P specific mutated driver gene sets relative to Breast_Lymph Node

k	Specific gene set	p1	p2	q
3	<i>BRCA2,PIK3CA,PTEN</i>	<0.0001	0.331	0.001
4	<i>BRCA2,PIK3CA,PTEN,AKT1</i>	<0.0001	0.26	<0.0001
5	<i>BRCA2,PIK3CA,PTEN,AKT1,NF1</i>	0.001	0.488	0.003
6	<i>BRCA2,PIK3CA,PTEN,AKT1,NF1,MAP3K1</i>	0.023	0.82	0.012
10	<i>BRCA2,PIK3CA,PTEN,AKT1,NF1,MAP3K1,ARID1A,ARID1B,KMT2C,NOTCH1</i>	0.046	0.999	0.001

Other metastatic cancers from Breast

Table S 2.1.6. Breast_Bone specific mutated driver gene sets relative to Breast_Chest Wall

k	Specific gene set	p1	p2	q
3	<i>AKT1,PIK3CA,RUNX1</i>	0.003	0.377	0.390
5	<i>AKT1,PIK3CA,RUNX1,ESR1,RB1</i>	0.014	0.724	0.013
6	<i>AKT1,PIK3CA,RUNX1,ESR1,RB1,PTEN</i>	0.004	0.735	0.007
7	<i>AKT1,PIK3CA,RUNX1,ESR1,RB1,PTEN,ASXL1</i>	0.006	0.751	0.005
8	<i>DNMT1,PIK3CA,RUNX1,ESR1,RB1,PTEN,ASXL1,NSD1</i>	0.001	0.976	0.001
9	<i>DNMT1,PIK3CA,RUNX1,ESR1,RB1,PTEN,ASXL1,NSD1,BRIP1</i>	0.001	0.976	<0.0001
10	<i>DNMT1,PIK3CA,RUNX1,ESR1,RB1,PTEN,ASXL1,NSD1,BRIP1,GRIN2A</i>	<0.0001	0.979	<0.0001

*Breast_Chest Wall has no specific mutated driver gene sets relative to Breast_Bone when k=2 ~ 10.

Table S 2.1.7. Breast_Bone and Breast_Liver specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Breast_Bone / Breast_Liver	6	<i>ASXL1,BTK,CBFB,GRIN2A,IKBKE,RICTOR</i>	0.019	0.974	0.026
	7	<i>ASXL1,BTK,CBFB,GRIN2A,IKBKE,RICTOR,PAK1</i>	0.011	0.967	0.025
	8	<i>ASXL1,BTK,CBFB,GRIN2A,IKBKE,RICTOR,EPHA7,FGF19</i>	0.023	0.972	0.014
	9	<i>ASXL1,BTK,CBFB,GRIN2A,IKBKE,RICTOR,MSH2,NTRK3,SOX17</i>	0.028	1	<0.0001
	10	<i>ASXL1,BTK,CBFB,GRIN2A,IKBKE,RICTOR,MSH2,NTRK3,SOX17,ERBB4</i>	0.011	0.999	0.001
Breast_Liver / Breast_Bone	10	<i>BLM,ERBB3,ESR1,FAT1,KMT2C,KMT2D,NF1,NOTCH2,SMARCB1,SPEN</i>	0.037	1	<0.0001

*Breast_Lung has no specific mutated driver gene sets relative to Breast_Bone when k=2 ~ 10.

*Breast_Chest Wall has no specific mutated driver gene sets relative to Breast_Liver when k=2 ~ 10.

*Breast_Chest Wall has no specific mutated driver gene sets relative to Breast_Lymph Node when k=2 ~ 10.

*Breast_Lung has no specific mutated driver gene sets relative to Breast_Liver when k=2 ~ 10.

*Breast_Lymph Node has no specific mutated driver gene sets relative to Breast_Liver when k=2 ~ 10.

Table S 2.1.8. Breast_Bone specific mutated driver gene sets relative to Breast_Lung

k	Specific gene set	p1	p2	q
8	<i>ERBB2,ESR1,GRIN2A,IKBKE,NCOR1,NSD1,PIK3CA,DNMT1</i>	0.043	0.941	0.015
9	<i>ERBB2,ESR1,GRIN2A,IKBKE,NCOR1,NSD1,PIK3CA,DNMT1,BTK</i>	0.023	0.919	0.013
10	<i>ERBB2,ESR1,GRIN2A,IKBKE,NCOR1,NSD1,PIK3CA,PIK3CB,TERT,KDR</i>	0.003	0.973	0.002

Table S 2.1.9. Breast_Bone and Breast_Lymph Node specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Breast_Bone / Breast_Lymph Node	4	<i>AKT1,BTK,ESR1,MAP3K1</i>	0.049	0.979	0.013
	7	<i>AKT1,BTK,ESR1,MAP3K1,IKBKE,PARP1,BRCA1</i>	0.027	1	<0.0001
	8	<i>AKT1,BTK,ESR1,MAP3K1,IKBKE,PARP1,PAX5,BRCA1</i>	0.011	1	<0.0001
	9	<i>AKT1,BTK,ESR1,MAP3K1,IKBKE,FUBP1,PAX5,BRCA1,SOX17</i>	<0.0001	1	<0.0001
	10	<i>AKT1,BTK,ESR1,MAP3K1,IKBKE,PARP1,PAX5,BRCA1,KLF4,RPS6KA4</i>	<0.0001	1	<0.0001
Breast_Lymph Node / Breast_Bone	2	<i>TP53,IKZF1</i>	0.043	1	0.013

Table S 2.1.10. Breast_Liver specific mutated driver gene sets relative to Breast_Chest Wall

k	Specific gene set	p1	p2	q
2	<i>ESR1,TP53</i>	<0.0001	0.149	<0.0001

Table S 2.1.11. Breast_Chest Wall and Breast_Lung specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Breast_Chest Wall / Breast_Lung	9	<i>CHEK2,ERG,FLT4,FOXA1,JAK1,KDM6A,KMT2A,TBX3,HIST1H1C</i>	0.035	1	0.037
	10	<i>CHEK2,ERG,FLT4,FOXA1,JAK1,KDM6A,KMT2A,TBX3,NOTCH3,EIF4A2</i>	0.016	1	0.026
Breast_Lung / Breast_Chest Wall	9	<i>AKT2,AMER1,ASXL1,ATR,BRIP1,CIC,DOT1L,INSR,PTEN</i>	0.025	1	0.021
	10	<i>AKT2,AMER1,ASXL1,ATR,BRIP1,CIC,DOT1L,INSR,PTEN,TSC2</i>	0.025	1	0.047

Table S 2.1.12. Breast_Lymph Node specific mutated driver gene sets relative to Breast_Chest Wall

k	Specific gene set	p1	p2	q
5	<i>ERBB2,ESR1,PTEN,PIK3CA,KDM6A</i>	0.036	0.741	0.044
6	<i>ERBB2,ESR1,PTEN,PIK3CA,POLE,BRIP1</i>	0.021	0.731	0.034
7	<i>ERBB2,ESR1,PTEN,PIK3CA,POLE,BRIP1,DNMT3A</i>	0.029	0.732	0.032
8	<i>ERBB2,ESR1,PTEN,PIK3CA,POLE,BRIP1,DNMT3A,EPHA5</i>	0.012	0.857	0.013
9	<i>ERBB2,ESR1,PTEN,PIK3CA,POLE,BRIP1,DNMT3A,EPHA5,GPS2</i>	0.01	0.906	0.005
10	<i>ERBB2,ESR1,PTEN,PIK3CA,POLE,BRIP1,DNMT3A,EPHA5,GPS2,ARID2</i>	0.004	0.86	0.007

Table S 2.1.13. Breast_Liver specific mutated driver gene sets relative to Breast_Lung

k	Specific gene set	p1	p2	q
2	<i>TP53,ESR1</i>	<0.0001	0.266	<0.0001
7	<i>ARID2,EP300,ERBB2,ESR1,KMT2A,NCOR1,PIK3CA</i>	0.03	0.965	0.016
8	<i>ARID2,EP300,ERBB2,ESR1,KMT2A,NCOR1,PIK3CA,CARD11</i>	0.012	0.969	0.007
9	<i>ARID2,EP300,ERBB2,ESR1,KMT2A,NCOR1,PIK3CA,CARD11,DNMT1</i>	0.01	0.969	0.006
10	<i>ARID2,EP300,ERBB2,ESR1,KMT2A,NCOR1,PIK3CA,CARD11,DNMT1,BLM</i>	0.006	0.965	0.003

Table S 2.1.14. Breast_Liver specific mutated driver gene sets relative to Breast_Lymph Node

k	Specific gene set	p1	p2	q
2	<i>TP53,ESR1</i>	<0.0001	0.469	<0.0001
3	<i>ERBB2,ESR1,NF1</i>	0.015	0.956	0.003
4	<i>ERBB2,ESR1,NF1,FOXA1</i>	0.043	0.961	0.01
6	<i>ERBB2,ERBB3,NF1,FOXA1,DNMT1,ESR1</i>	0.036	0.997	0.004
8	<i>ERBB2,ERBB3,NF1,FOXA1,DNMT1,ESR1,DICER1,SHQ1</i>	0.021	0.999	<0.0001
9	<i>ERBB2,ERBB3,NF1,FOXA1,DNMT1,ESR1,ERBB4,ERRFI1,FAT1</i>	0.018	0.99	0.003
10	<i>ERBB2,ERBB3,NF1,FOXA1,DNMT1,ESR1,CDKN1B,SHQ1,FAT1,PALB2</i>	0.002	0.998	<0.0001

Table S 2.1.15. Breast_Chest Wall, Liver specific mutated driver gene sets relative to Breast_Lymph Node

k	Specific gene set	p1	p2	p3	q
10	<i>AKT1,ARAF,BAP1,CDKN1B,ERBB3,ESR1,FOXA1,NOTCH3,PIK3R1,SHQ1</i>	0.033	0.011	0.919	<0.0001

*Breast_Lymph Node has no specific mutated driver gene sets relative to Breast_Chest Wall, Liver when $k=2 \sim 10$.

*Breast_Lung has no specific mutated driver gene sets relative to Breast_Lymph Node when $k=2 \sim 10$.

*Breast_Lymph Node has no specific mutated driver gene sets relative to Breast_Lung when $k=2 \sim 10$.

2.2 Non-small-cell Lung cancer

Lung_P and other metastatic cancers from Lung

Table S 2.2.1. Lung_P specific mutated driver gene sets relative to Lung_Bone

k	Specific gene set	p1	p2	q
2	<i>TP53,KRAS</i>	<0.0001	0.055	<0.0001
3	<i>TP53,KRAS,EML4</i>	<0.0001	0.077	<0.0001
4	<i>TP53,KRAS,EML4,EGFR</i>	<0.0001	0.082	<0.0001
7	<i>TP53,ALK,ATM,CD74,PIK3CA,RBM10,STK11</i>	<0.0001	0.226	<0.0001
8	<i>TP53,ALK,ATM,CD74,PIK3CA,RBM10,STK11,NKX2-1</i>	<0.0001	0.259	<0.0001
9	<i>TP53,ALK,ATM,MED12,PIK3CA,RBM10,STK11,NKX2-1,SETD2</i>	<0.0001	0.398	<0.0001
10	<i>TP53,ALK,ATM,MED12,PIK3CA,RBM10,STK11,NKX2-1,SETD2,CTNNB1</i>	<0.0001	0.443	<0.0001

*Lung_Bone has no specific mutated driver gene sets relative to Lung_P when k=2 ~ 10.

*Lung_Brain has no specific mutated driver gene sets relative to Lung_P when k=2 ~ 10.

*Lung_Liver has no specific mutated driver gene sets relative to Lung_P when k=2 ~ 10.

*Lung_Pleura(Fluid) has no specific mutated driver gene sets relative to Lung_P when k=2 ~ 10.

*Lung_Lymph Node has no specific mutated driver gene sets relative to Lung_P when k=2 ~ 10.

Table S 2.2.2. Lung_P specific mutated driver gene sets relative to Lung_Brain

k	Specific gene set	p1	p2	q
2	<i>TP53,KRAS</i>	<0.0001	0.795	<0.0001
3	<i>TP53,KRAS,EML4</i>	<0.0001	0.613	<0.0001
4	<i>TP53,EGFR,KRAS,MET</i>	<0.0001	0.614	<0.0001
5	<i>TP53,EGFR,KRAS,MET,BRAF</i>	<0.0001	0.675	<0.0001
6	<i>TP53,EGFR,KRAS,MET,BRAF,EML4</i>	<0.0001	0.465	<0.0001
7	<i>TP53,EGFR,KRAS,MET,BRAF,EML4,CD74</i>	<0.0001	0.48	<0.0001
8	<i>TP53,ALK,ATM,NKX2-1,PIK3CA,CD74,RBM10,STK11</i>	<0.0001	0.488	<0.0001
9	<i>TP53,EGFR,KRAS,MET,BRAF,EML4,CD74,ERBB2,STK11</i>	<0.0001	0.541	<0.0001
10	<i>TP53,ALK,ATM,NKX2-1,PIK3CA,RBM10,SETD2,STK11,CTNNB1,MED12</i>	<0.0001	0.832	<0.0001

Table S 2.2.3. Lung_P specific mutated driver gene sets relative to Lung_Liver

k	Specific gene set	p1	p2	q
2	<i>TP53,KRAS</i>	<0.0001	0.346	<0.0001
3	<i>TP53,KRAS,EML4</i>	<0.0001	0.189	<0.0001
4	<i>TP53,KRAS,EGFR,MET,</i>	<0.0001	0.457	<0.0001
5	<i>TP53,KRAS,EGFR,MET,EML4</i>	<0.0001	0.32	<0.0001
6	<i>TP53,KRAS,EGFR,MET,EML4,BRAF</i>	<0.0001	0.222	<0.0001
7	<i>TP53,ALK,ATM,CD74,PIK3CA,RBM10,STK11</i>	<0.0001	0.799	<0.0001
8	<i>TP53,ALK,ATM,CD74,PIK3CA,RBM10,STK11,NKX2-1</i>	<0.0001	0.771	<0.0001
9	<i>TP53,ALK,ATM,CD74,PIK3CA,RBM10,STK11,NKX2-1,MED12</i>	<0.0001	0.847	<0.0001
10	<i>TP53,ALK,ATM,CD74,PIK3CA,RBM10,STK11,NKX2-1,MED12,CTNNB1</i>	<0.0001	0.955	<0.0001

Table S 2.2.4. Lung_P specific mutated driver gene sets relative to Lung_Pleura(Fluid)

k	Specific gene set	p1	p2	q
2	<i>TP53,KRAS</i>	<0.0001	0.426	<0.0001
3	<i>TP53,KRAS,MET</i>	<0.0001	0.45	<0.0001
4	<i>TP53,KRAS,MET,EGFR</i>	<0.0001	0.098	<0.0001
5	<i>TP53,KRAS,MET,EGFR,BRAF</i>	<0.0001	0.072	<0.0001
7	<i>TP53,ALK,NKX2-1,STK11,RBM10,SMAD4,SETD2</i>	<0.0001	0.613	<0.0001
8	<i>TP53,ALK,NKX2-1,STK11,PIK3CA,RBM10,ATM,CD74</i>	<0.0001	0.081	<0.0001
9	<i>TP53,ALK,NKX2-1,STK11,PIK3CA,RBM10,ATM,SETD2,MED12</i>	<0.0001	0.312	<0.0001
10	<i>TP53,ALK,NKX2-1,STK11,PIK3CA,RBM10,ATM,SETD2,MED12,CTNNB1</i>	<0.0001	0.252	<0.0001

Table S 2.2.5. Lung_P specific mutated driver gene sets relative to Lung_Lymph Node

k	Specific gene set	p1	p2	q
3	<i>EGFR,STK11,KMT2D</i>	<0.0001	0.078	<0.0001
4	<i>EGFR,STK11,KMT2D,RBM10</i>	<0.0001	0.341	<0.0001
5	<i>EGFR,STK11,FAT1,RBM10,ROS1</i>	<0.0001	0.89	<0.0001
6	<i>EGFR,STK11,FAT1,RBM10,ROS1,BRAF</i>	<0.0001	0.798	<0.0001
8	<i>EGFR,STK11,FAT1,RBM10,ROS1,BRAF,ALK,KMT2D</i>	<0.0001	0.234	<0.0001
9	<i>TP53,STK11,AMER1,ARAF,ATM,NKX2-1,RBM10,SETD2,SMAD4</i>	<0.0001	0.99	<0.0001
10	<i>TP53,STK11,AMER1,ARAF,ATM,NKX2-1,RBM10,SETD2,SMAD4,ARID1A</i>	0.001	0.998	<0.0001

Other metastatic cancers from Lung

Table S 2.2.6. Lung_Bone and Lung_Brain specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Lung_Bone / Lung_Brain	5	<i>DNMT1,ERBB2,MET,STK11,YAP1</i>	0.019	0.941	0.017
	6	<i>DNMT1,ERBB4,MET,STK11,YAP1,CBL</i>	<0.0001	0.979	<0.0001
	7	<i>DNMT1,KRAS,MET,TOP1,YAP1,CBL,PAK5</i>	<0.0001	1	<0.0001
	8	<i>DNMT1,KRAS,MET,EPHA3,YAP1,CBL,PAK5,SRC</i>	<0.0001	1	<0.0001
	9	<i>DNMT1,KRAS,MET,EPHA3,YAP1,CBL,PAK5,SRC,NOTCH3</i>	<0.0001	1	<0.0001
	10	<i>DNMT1,KRAS,MET,EPHA3,YAP1,CBL,PAK5,SRC,ERCC4,IRS2</i>	<0.0001	1	<0.0001
Lung_Brain / Lung_Bone	3	<i>TP53,FGFR1,WT1</i>	0.001	1	<0.0001
	4	<i>TP53,FGFR1,AR,ERBB2</i>	0.004	1	0.002
	5	<i>NFE2L2,ALK,ATM,PDGFRA,ZFH3</i>	0.013	0.943	0.011
	6	<i>NFE2L2,ALK,ATM,PDGFRA,ZFH3,RAD54L</i>	0.002	0.95	0.002
	7	<i>NFE2L2,ARID5B,CREBBP,IL7R,PIK3CD,ROS1,SETD2</i>	<0.0001	0.905	<0.0001
	8	<i>NFE2L2,ARID5B,CREBBP,IL7R,PIK3CD,ROS1,SETD2,CENPA</i>	<0.0001	0.885	<0.0001
	9	<i>NFE2L2,ARID5B,CREBBP,IL7R,PIK3CD,ROS1,SETD2,CENPA,ARID2</i>	<0.0001	0.843	<0.0001
	10	<i>NFE2L2,ARID5B,CREBBP,IL7R,PIK3CD,ROS1,SETD2,CENPA,ARID2,BTK</i>	<0.0001	0.842	<0.0001

*Lung_Bone has no specific mutated driver gene sets relative to Lung_Lymph Node when k=2 ~ 10.

*Lung_Brain has no specific mutated driver gene sets relative to Lung_Lymph Node when k=2 ~ 10.

*Lung_Liver has no specific mutated driver gene sets relative to Lung_Lymph Node when k=2 ~ 10.

*Lung_Pleura(Fluid) has no specific mutated driver gene sets relative to Lung_Lymph Node when k=2 ~ 10.

Table S 2.2.7. Lung_Bone and Lung_Liver specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Lung_Bone / Lung_Liver	3	<i>EPHA3,KRAS,SRC</i>	0.025	0.994	<0.0001
	4	<i>EPHA3,KRAS,EPHA7,KMT2D</i>	0.002	1	<0.0001
	5	<i>EPHA3,KRAS,EPHA7,KMT2D,ATRX</i>	0.001	1	<0.0001
	6	<i>EPHA3,KRAS,IKZF1,KDM5A,ATRX,SRC</i>	0.002	1	<0.0001
	7	<i>EPHA3,KRAS,IKZF1,KDM5A,ATRX,SRC,MRE11</i>	0.001	1	<0.0001
	8	<i>EPHA3,IKZF1,KRAS,KDM5A,ATRX,SRC,MRE11,STAT5A</i>	0.001	1	<0.0001
	9	<i>EPHA3,IKZF1,KRAS,KDM5A,ATRX,SRC,MRE11,STAT5A,TET1</i>	<0.0001	1	<0.0001
	10	<i>EPHA3,IKZF1,KRAS,KDM5A,ATRX,SRC,MRE11,STAT5A,TET1,XRCC2</i>	<0.0001	1	<0.0001
Lung_Liver / Lung_Bone	3	<i>ATM,EGFR,TERT</i>	0.003	0.784	0.015
	4	<i>ATM,EGFR,TERT,BRCA2</i>	<0.0001	0.896	0.001
	5	<i>ATM,EGFR,TERT,BRCA2,RICTOR</i>	<0.0001	0.972	<0.0001
	6	<i>ATM,EGFR,TERT,BRCA2,RICTOR,TGFBR1</i>	<0.0001	0.989	<0.0001
	7	<i>ATM,EGFR,TERT,BRCA2,RICTOR,TGFBR1,NCOR1</i>	<0.0001	0.996	<0.0001
	8	<i>ATM,EGFR,TERT,BRCA2,RICTOR,TGFBR1,NCOR1,FBXW7</i>	<0.0001	0.999	<0.0001
	9	<i>ATM,EGFR,TERT,BRCA2,RICTOR,TGFBR1,NCOR1,FBXW7,CDKN1B</i>	<0.0001	0.994	<0.0001
	10	<i>ATM,EGFR,TERT,BRCA2,RICTOR,TGFBR1,NCOR1,FBXW7,CDKN1B,HNF1A</i>	<0.0001	0.997	<0.0001

Table S 2.2.8. Lung_Lymph Node specific mutated driver gene sets relative to Lung_Bone

k	Specific gene set	p1	p2	q
2	<i>TP53,KRAS</i>	0.002	0.067	0.033
3	<i>TP53,KRAS,EML4</i>	<0.0001	0.077	<0.0001
4	<i>ALK,ATM,EGFR,KEAP1</i>	<0.0001	0.1	<0.0001
5	<i>ALK,ATM,EGFR,KEAP1,NF1</i>	<0.0001	0.167	<0.0001
6	<i>ALK,ATM,EGFR,KEAP1,NF1,SMARCA4</i>	<0.0001	0.398	<0.0001
7	<i>ALK,ATM,EGFR,KEAP1,NF1,SMARCA4,NOTCH4</i>	<0.0001	0.308	<0.0001
8	<i>ALK,ATM,EGFR,KEAP1,NF1,SMARCA4,NOTCH4,SETD2</i>	<0.0001	0.463	<0.0001
9	<i>ALK,ATM,EGFR,KEAP1,NF1,SMARCA4,NOTCH4,SETD2,RBM10</i>	<0.0001	0.667	<0.0001
10	<i>ALK,ATM,EGFR,KEAP1,NF1,SMARCA4,NOTCH4,SETD2,RBM10,PIK3CA</i>	<0.0001	0.748	<0.0001

Table S 2.2.9. Lung_Bone and Lung_Pleura(Fluid) specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Lung_Bone / Lung_Pleura(Fluid)	3	<i>POLE,AR,STK11</i>	0.043	0.997	0.004
	5	<i>POLE,DIS3,KDM5A,KEAP1,MED12</i>	0.024	1	<0.0001
	6	<i>POLE,DIS3,KDM5A,KEAP1,MED12,PRKN</i>	0.014	1	<0.0001
	7	<i>POLE,DIS3,KDM5A,KEAP1,MED12,PRKN,INHBA</i>	0.007	1	<0.0001
	8	<i>POLE,DIS3,KDM5A,KEAP1,MED12,PRKN,EPHA3,FOXA1</i>	0.003	1	<0.0001
	9	<i>POLE,DIS3,KDM5A,KEAP1,MED12,PRKN,EPHA3,FOXA1,PMS2</i>	0.002	1	<0.0001
	10	<i>POLE,DIS3,KDM5A,KEAP1,MED12,PRKN,EPHA3,FOXA1,TCF7L2,MYC</i>	<0.0001	1	<0.0001
Lung_Pleura(Fluid) / Lung_Bone	2	<i>EGFR,ALK</i>	0.018	1	0.015
	3	<i>EGFR,ALK,KMT2C</i>	0.001	0.507	0.021
	4	<i>EGFR,ALK,KMT2C,SMARCA4</i>	0.002	0.72	0.007
	5	<i>TP53,ALK,KMT2C,POLE,APC</i>	0.005	0.963	0.003
	6	<i>TP53,ALK,KMT2C,PIK3CA,AR,GRIN2A</i>	0.011	0.991	0.001
	7	<i>TP53,ALK,KMT2C,PIK3CA,AR,GRIN2A,ASXL1</i>	0.007	0.999	0.001
	8	<i>TP53,ALK,KMT2A,PIK3CA,AR,GRIN2A,ASXL1,KMT2C</i>	0.006	0.999	0.002
	9	<i>TP53,ALK,KMT2A,PIK3CA,AR,GRIN2A,ASXL1,KMT2C,BRCA1</i>	0.006	1	<0.0001
	10	<i>TP53,ALK,KMT2A,PIK3CA,AR,GRIN2A,ASXL1,KMT2C,KDR,TSC2</i>	0.001	1	<0.0001

Table S 2.2.10. Lung_Brain and Lung_Liver specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Lung_Brain / Lung_Liver	5	<i>ALK,FAT1,INPP4B,PIK3CG,ZFH3</i>	0.001	1	<0.0001
	6	<i>ALK,FAT1,INPP4B,PIK3CG,ZFH3,NOTCH4</i>	<0.0001	1	<0.0001
	7	<i>ALK,FAT1,INPP4B,PIK3CG,ZFH3,NOTCH4,MYCN</i>	<0.0001	1	<0.0001
	8	<i>ALK,CARD11,EPHA7,PIK3CG,ZFH3,JAK1,MAP2K1,NFE2L2</i>	0.006	1	<0.0001
	9	<i>ALK,CARD11,EPHA7,AKT3,ZFH3,JAK1,MAP2K1,NFE2L2,GNA11</i>	0.001	1	<0.0001
	10	<i>ALK,CARD11,EPHA7,AKT3,ZFH3,JAK1,MAP2K1,NFE2L2,GNA11,MDM2</i>	<0.0001	1	<0.0001
Lung_Liver / Lung_Brain	3	<i>ATM,EGFR,MET</i>	0.003	0.515	0.035
	4	<i>ATM,EGFR,MET,IL7R</i>	0.008	0.94	0.006
	5	<i>ATM,EGFR,MET,IL7R,JAK2</i>	0.002	0.879	0.002
	6	<i>ATM,EGFR,MET,IL7R,JAK2,PTCH1</i>	<0.0001	0.899	<0.0001
	7	<i>ATM,EGFR,MET,IL7R,JAK2,PTCH1,RICTOR</i>	<0.0001	0.933	<0.0001
	8	<i>ATM,EGFR,ATR,CDKN1B,PTCH1,RICTOR,MGA,PIK3C3</i>	<0.0001	0.694	<0.0001
	9	<i>ATM,EGFR,ATR,CDKN1B,PTCH1,RICTOR,MGA,PIK3C3,MET</i>	<0.0001	0.611	<0.0001
	10	<i>ATM,EGFR,ATR,CDKN1B,PTCH1,RICTOR,MGA,PIK3C3,MET,SUZ12</i>	<0.0001	0.763	<0.0001

Table S 2.2.11. Lung_Lymph Node specific mutated driver gene sets relative to Lung_Brain

k	Specific gene set	p1	p2	q
2	<i>TP53,KRAS</i>	<0.0001	0.782	<0.0001
3	<i>EGFR,KRAS,PTPRT</i>	<0.0001	0.181	0.004
4	<i>EGFR,KRAS,PTPRT,TERT</i>	<0.0001	0.458	<0.0001
7	<i>EGFR,KRAS,ALK,BRAF,KEAP1,MET,SMARCA4</i>	<0.0001	0.377	<0.0001
8	<i>EGFR,KRAS,ALK,BRAF,KEAP1,RET,SMARCA4,RB1</i>	<0.0001	0.587	<0.0001
9	<i>EGFR,KRAS,ALK,KEAP1,RET,MET,EPHA3,ATM,BRCA2</i>	<0.0001	0.672	<0.0001
10	<i>EGFR,KRAS,ALK,BRAF,KMT2D,RET,SMARCA4,ATRX,PIK3CG,RB1</i>	<0.0001	0.547	<0.0001

Table S 2.2.12. Lung_Brain and Lung_Pleura(Fluid) specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Lung_Brain / Lung_Pleura(Fluid)	3	<i>KEAP1,NFE2L2,PTEN</i>	0.024	0.979	0.006
	7	<i>ARID5B,CREBBP,DDR2,KEAP1,MAP2K1,NFE2L2,PLCG2</i>	0.028	0.998	0.007
	8	<i>ARID5B,CREBBP,DDR2,KEAP1,MAP2K1,NFE2L2,PLCG2,AKT3</i>	0.021	0.995	0.003
	9	<i>ARID5B,ARID1A,AXIN1,KEAP1,MAP2K1,NFE2L2,PLCG2,AKT3,IL7R</i>	0.002	0.974	<0.0001
	10	<i>ARID5B,CDKN2A,MDM2,PAX5,MAP2K1,NFE2L2,PLCG2,AKT3,RAD51B,NOTCH3</i>	0.008	1	<0.0001
Lung_Pleura(Fluid) / Lung_Brain	3	<i>ALK,EGFR,MET</i>	<0.0001	0.512	0.012
	4	<i>ALK,EGFR,MET,ATR</i>	<0.0001	0.493	<0.0001
	5	<i>ALK,EGFR,MET,RASA1,KMT2C</i>	<0.0001	0.814	<0.0001
	6	<i>ALK,EGFR,MET,RASA1,KMT2C,BCOR</i>	<0.0001	0.961	<0.0001
	7	<i>ALK,EGFR,MET,RASA1,KMT2C,BCOR,SMARCA4</i>	<0.0001	0.952	<0.0001
	8	<i>ALK,EGFR,MET,RASA1,KMT2C,KMT2D,SMARCA4,BRAF</i>	<0.0001	0.976	<0.0001
	9	<i>ALK,EGFR,MET,RASA1,KMT2C,KMT2D,SMARCA4,BRAF,ATR</i>	<0.0001	0.986	<0.0001
	10	<i>ALK,EGFR,MET,FOXL2,KMT2C,KMT2D,SMARCA4,BRAF,RASA1,LATS1</i>	<0.0001	0.998	<0.0001

Table S 2.2.13. Lung_Lymph Node specific mutated driver gene sets relative to Lung_Liver

k	Specific gene set	p1	p2	q
2	<i>TP53,KRAS</i>	<0.0001	0.283	0.007
3	<i>TP53,KRAS,EML4</i>	<0.0001	0.189	<0.0001
4	<i>ALK,EGFR,STK11,PTPRD</i>	0.002	0.16	0.042
5	<i>ALK,EGFR,STK11,NOTCH4,PIK3CG</i>	<0.0001	0.537	<0.0001
6	<i>ALK,EGFR,STK11,NOTCH4,PIK3CG,RB1</i>	<0.0001	0.814	<0.0001
7	<i>ALK,EGFR,STK11,NOTCH4,PIK3CG,RB1,RET</i>	<0.0001	0.848	<0.0001
8	<i>ALK,EGFR,STK11,NOTCH4,PIK3CG,RB1,RET,EPHA3</i>	<0.0001	0.79	<0.0001
9	<i>ALK,EGFR,STK11,NOTCH4,PIK3CG,RB1,RET,EPHA3,BRAF</i>	<0.0001	0.8	<0.0001
10	<i>ALK,EGFR,STK11,NOTCH4,PIK3CG,RB1,RET,EPHA3,BRAF,ATRX</i>	<0.0001	0.907	<0.0001

Table S 2.2.14. Lung_Liver and Lung_Pleura(Fluid) specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Lung_Liver / Lung_Pleura(Fluid)	5	<i>FBXW7,FGFR3,KEAP1,TGFBR2,EIF1AX</i>	0.015	1	0.022
	7	<i>FBXW7,FGFR3,KEAP1,TGFBR2,NCOR1,CTNNB1,SPEN</i>	0.03	1	0.005
	8	<i>FBXW7,FGFR3,KEAP1,TGFBR2,NCOR1,CTNNB1,FGFR2,RHOA</i>	0.008	0.995	0.003
	9	<i>FBXW7,FGFR3,KEAP1,TGFBR2,NCOR1,CTNNB1,FGFR2,RHOA,WT1</i>	0.002	0.991	0.002
	10	<i>FBXW7,FGFR3,CDKN2A,TGFBR1,NCOR1,CTNNB1,MGA,MSH6,SPEN,TP63</i>	<0.0001	1	<0.0001
Lung_Pleura(Fluid) / Lung_Liver	3	<i>ALK,EGFR,KRAS</i>	<0.0001	0.73	0.013
	4	<i>ALK,EGFR,KRAS,KMT2D</i>	<0.0001	0.217	0.002
	5	<i>ALK,EGFR,KRAS,KMT2D,DOT1L</i>	<0.0001	0.215	<0.0001
	6	<i>ALK,EGFR,KRAS,KMT2D,DOT1L,ASXL1</i>	<0.0001	0.617	<0.0001
	7	<i>ALK,EGFR,KRAS,KMT2D,DOT1L,ASXL1,ERBB2</i>	<0.0001	0.518	<0.0001
	8	<i>ALK,EGFR,KRAS,KMT2D,DOT1L,ASXL1,ERBB2,NF2</i>	<0.0001	0.611	<0.0001
	9	<i>ALK,EGFR,KRAS,KMT2D,DOT1L,ASXL1,ERBB2,NF2,NOTCH4</i>	<0.0001	0.818	<0.0001
	10	<i>ALK,ATR,BAP1,BRAF,CIC,NCOA3,PTPRT,SMARCD1,SOX17,U2AF1</i>	0.019	1	<0.0001

Table S 2.2.15. Lung_Lymph Node specific mutated driver gene sets relative to Lung_Pleura(Fluid)

k	Specific gene set	p1	p2	q
2	<i>KRAS,PTPRT</i>	0.021	0.987	0.002
3	<i>KRAS,PTPRT,RET</i>	0.008	0.992	0.001
4	<i>KRAS,PTPRT,RET,TERT</i>	0.009	1	<0.0001
5	<i>KRAS,EPHA3,RET,CDKN2A,RB1</i>	0.004	0.971	<0.0001
6	<i>KRAS,EPHA3,RET,CDKN2A,RB1,TERT</i>	0.001	0.997	<0.0001
7	<i>KRAS,EPHA3,RET,CDKN2A,RB1,TERT,MTOR</i>	0.001	0.999	<0.0001
8	<i>KRAS,EPHA3,RET,CDKN2A,RB1,TERT,MTOR,TGFBR2</i>	<0.0001	0.998	<0.0001
9	<i>KRAS,PTPRT,RET,ALK,BRAF,KEAP1,PIK3CA,PIK3CG,SMAD4</i>	0.018	0.997	0.002
10	<i>KRAS,PTPRT,RET,ALK,BRAF,KEAP1,PIK3CA,PIK3CG,SMAD4,RB1</i>	0.019	0.996	<0.0001

2.3 Melanoma

Melanoma_P and other metastatic cancers from Melanoma

Table S 2.3.1. Melanoma_P and Melanoma_Brain specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Melanoma_P / Melanoma_Brain	3	<i>TP53,GNA11,SF3B1</i>	0.006	0.827	0.017
	4	<i>ATRX,GNA11,NF1,SF3B1</i>	0.006	0.9	0.003
	5	<i>ATRX,GNA11,NF1,SF3B1,EGFR</i>	0.001	0.947	<0.0001
	6	<i>ATRX,GNA11,NF1,SF3B1,EGFR,BAP1</i>	<0.0001	0.993	<0.0001
	7	<i>ATRX,GNA11,NF1,SF3B1,EGFR,BAP1,CTNNB1</i>	<0.0001	0.992	<0.0001
	8	<i>ATRX,GNA11,NF1,SF3B1,EGFR,BAP1,CTNNB1,PIK3R1</i>	<0.0001	0.992	<0.0001
	9	<i>ATRX,GNA11,NF1,SF3B1,EGFR,BAP1,CTNNB1,PIK3R1,RAB35</i>	<0.0001	0.994	<0.0001
	10	<i>ATRX,EIF1AX,NF1,SF3B1,EGFR,BAP1,PIK3CA,PIK3R1,PIK3CG,POLE</i>	<0.0001	2	<0.0001
Melanoma_Brain / Melanoma_P	4	<i>AXIN2,MITF,RAD51C,TSC2</i>	0.035	1	0.036
	5	<i>AXIN2,MAP2K2,MDM4,RAD51C,TSC2</i>	0.002	1	0.004
	6	<i>AXIN2,FLCN,HGF,MEN1,PALB2,SETD2</i>	<0.0001	1	<0.0001
	7	<i>AXIN2,FLCN,HGF,MEN1,PALB2,SETD2,RAD51C</i>	0.001	1	<0.0001
	8	<i>AXIN2,FLCN,HGF,MEN1,PALB2,SETD2,RAD51C,STAT5A</i>	<0.0001	1	<0.0001
	9	<i>AXIN2,FLCN,HGF,MEN1,PALB2,SETD2,RAD51C,STAT5A,MAP3K1</i>	<0.0001	2	<0.0001
	10	<i>AXIN2,FLCN,HGF,MEN1,PALB2,SETD2,RAD51C,ANKRD11,BIRC3,MAP3K1</i>	<0.0001	2	<0.0001

Table S 2.3.2. Melanoma_P and Melanoma_Liver specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Melanoma_P / Melanoma_Liver	5	<i>ATRX,EGFR,NF1,PTEN,SF3B1</i>	0.003	0.971	<0.0001
	6	<i>ATRX,EGFR,NF1,PTEN,SF3B1,EIF1AX</i>	0.001	0.94	<0.0001
	7	<i>ATRX,BRAF,EIF1AX,SF3B1,FGFR2,IRS2,PIK3R1</i>	0.001	0.86	0.003
	8	<i>ATRX,BRAF,EIF1AX,SF3B1,IRS2,KMT2D,NOTCH3,PIK3C2G</i>	0.047	0.995	0.004
	9	<i>ATRX,BRAF,EIF1AX,SF3B1,IRS2,KMT2D,NOTCH3,PIK3C2G,PTEN</i>	0.038	0.995	0.001
	10	<i>ATRX,EGFR,EIF1AX,SF3B1,FAT1,MRE11,NF1,PIK3R1,POLE,PTEN</i>	<0.0001	1	<0.0001
Melanoma_Liver / Melanoma_P	5	<i>BAP1,CD79A,GLI1,IGF1R,IGF1</i>	0.009	1	<0.0001
	6	<i>BAP1,CD79A,GLI1,IGF1R,RPS6KB2,TSC2</i>	0.004	1	<0.0001
	7	<i>BAP1,CD79A,GLI1,IGF1R,RPS6KB2,MDM2,TSC2</i>	0.002	1	<0.0001
	8	<i>BAP1,CD79A,GLI1,IGF1R,RPS6KB2,MDM2,TSC2,SMO</i>	0.003	1	<0.0001
	9	<i>BAP1,CD79A,GLI1,IGF1R,RPS6KB2,MDM2,TSC2,CASP8,H3F3A</i>	<0.0001	1	<0.0001
	10	<i>BAP1,CD79A,GLI1,IGF1R,RPS6KB2,MDM2,TSC2,CASP8,RAI14,GALNT11</i>	<0.0001	1	<0.0001

Table S 2.3.3. Melanoma_P and Melanoma_Lung specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Melanoma_P / Melanoma_Lung	3	<i>BAP1,NF1,SF3B1</i>	0.01	1	0.002
	4	<i>BAP1,NF1,SF3B1,EGFR</i>	0.001	1	<0.0001
	5	<i>BAP1,NF1,SF3B1,EGFR,ATRX</i>	<0.0001	1	<0.0001
	6	<i>BAP1,NF1,SF3B1,EGFR,ATRX,CTNNB1</i>	0.001	1	<0.0001
	7	<i>BAP1,NF1,SF3B1,EGFR,ATRX,CTNNB1,EIF1AX</i>	<0.0001	0.999	<0.0001
	8	<i>BAP1,NF1,SF3B1,EGFR,ATRX,CTNNB1,EIF1AX,PIK3R1</i>	<0.0001	1	<0.0001
	9	<i>BAP1,NF1,SF3B1,EGFR,ATRX,CTNNB1,EIF1AX,PIK3R1,PRDM1</i>	<0.0001	1	<0.0001
	10	<i>BAP1,NF1,SF3B1,EGFR,ATRX,CTNNB1,EIF1AX,PIK3R1,PRDM1,RARA</i>	<0.0001	1	<0.0001
Melanoma_Lung / Melanoma_P	7	<i>EP300,GATA3,JAK3,MGA,RPS6KB2,SETD2,SH2D1A</i>	0.034	1	<0.0001
	8	<i>EP300,GATA3,JAK3,MGA,RPS6KB2,SETD2,SH2D1A,SMAD2</i>	0.023	1	<0.0001
	9	<i>EP300,GATA3,JAK3,MGA,RPS6KB2,SETD2,SH2D1A,EIF4E,FBXW7</i>	0.039	1	<0.0001
	10	<i>EP300,GATA3,JAK3,MGA,RPS6KB2,SETD2,SH2D1A,EIF4E,FBXW7,PIM1</i>	0.011	1	<0.0001

Table S 2.3.4. Melanoma_P and Melanoma_Lymph Node specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Melanoma_P / Melanoma_Lymph Node	3	<i>SF3B1,GNA11,NF1</i>	0.008	1	<0.0001
	4	<i>SF3B1,ATRX,EGFR,NF1</i>	0.003	1	<0.0001
	5	<i>SF3B1,ATRX,EGFR,BAP1,RAB35</i>	<0.0001	0.584	0.001
	6	<i>SF3B1,ATRX,EGFR,BAP1,EIF1AX,RAB35</i>	<0.0001	0.499	<0.0001
	7	<i>SF3B1,ATRX,EGFR,BAP1,EIF1AX,RAB35,MET</i>	<0.0001	0.998	<0.0001
	8	<i>SF3B1,ATRX,EGFR,BAP1,EIF1AX,NF1,PIK3R1,POLE</i>	<0.0001	1	<0.0001
	9	<i>SF3B1,ATRX,EGFR,BAP1,EIF1AX,NF1,PIK3R1,MST1R,RAB35</i>	<0.0001	1	<0.0001
	10	<i>SF3B1,ATRX,EGFR,BAP1,EIF1AX,NF1,PIK3R1,MST1R,RAB35,RARA</i>	<0.0001	1	<0.0001
Melanoma_Lymph Node / Melanoma_P	6	<i>FLT3,PIK3CD,PTEN,TERT,TET2,ERBB3</i>	0.024	1	<0.0001
	7	<i>FLT3,PIK3CD,PTEN,TERT,TET2,ERBB3,MUTYH</i>	0.012	1	<0.0001
	8	<i>FLT3,PIK3CD,PTEN,TERT,TET2,ERBB3,MUTYH,AKT3</i>	0.002	1	<0.0001
	9	<i>FLT3,PIK3CD,PTEN,TERT,TET2,MUTYH,AKT3,DNMT3B,FLT1</i>	0.005	1	<0.0001
	10	<i>FLT3,PIK3CD,PTEN,TERT,TET2,MUTYH,AKT3,DNMT3B,FLT1,NF2</i>	0.003	1	<0.0001

Other metastatic cancers from Melanoma

Table S 2.3.5. Melanoma_Brain and Melanoma_Liver specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Melanoma_Brain / Melanoma_Liver	6	<i>ANKRD11, DNMT1, EPHB1, PGR, PTEN, TSC1</i>	0.002	1	<0.0001
	7	<i>ANKRD11, DNMT1, EPHB1, PGR, PTEN, TSC1, DICER1</i>	<0.0001	1	<0.0001
	8	<i>ANKRD11, DNMT1, EPHB1, PGR, PTEN, TSC1, PIK3R2, PRKAR1A</i>	<0.0001	1	<0.0001
	9	<i>ANKRD11, DNMT1, EPHB1, PGR, PTEN, TSC1, PIK3R2, PRKAR1A, DICER1</i>	<0.0001	1	<0.0001
	10	<i>ANKRD11, CSF1R, EPHB1, PGR, PTEN, ERFFI1, PIK3C3, ETV1, IRS2, DICER1</i>	<0.0001	1	<0.0001
Melanoma_Liver / Melanoma_Brain	2	<i>BAP1, SF3B1</i>	0.027	0.933	0.036
	3	<i>BRCA2, GNA11, GNAQ</i>	0.001	1	0.004
	4	<i>BAP1, CTNNB1, GLI1, SF3B1</i>	<0.0001	0.975	<0.0001
	5	<i>BAP1, CTNNB1, GLI1, SF3B1, RARA</i>	<0.0001	0.997	<0.0001
	6	<i>ARID1B, CTNNB1, GNA11, GNAQ, RARA, STAG2</i>	<0.0001	1	<0.0001
	7	<i>ARID1B, CTNNB1, GNA11, GNAQ, RARA, STAG2, RB1</i>	<0.0001	1	<0.0001
	8	<i>BAP1, CTNNB1, EIF1AX, GLI1, RARA, SF3B1, CASP8, PIK3CA</i>	<0.0001	1	<0.0001
	9	<i>BAP1, CTNNB1, EIF1AX, GLI1, RARA, SF3B1, CASP8, PIK3CA, ABL1</i>	<0.0001	1	<0.0001
	10	<i>BAP1, CTNNB1, EIF1AX, GLI1, RARA, SF3B1, CASP8, PIK3CA, MDM2, ST6GALNAC3</i>	<0.0001	0.999	<0.0001

Table S 2.3.6. Melanoma_Brain and Melanoma_Lung specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Melanoma_Brain / Melanoma_Lung	2	<i>KMT2D,PTEN</i>	0.024	0.963	0.02
	3	<i>KMT2D,PTEN,CDK12</i>	0.016	0.995	0.005
	5	<i>KMT2D,PTEN,CDK12,NOTCH2,AXIN2</i>	0.009	1	<0.0001
	6	<i>KMT2D,PTEN,CDK12,NOTCH2,AXIN2,PRKAR1A</i>	0.002	1	<0.0001
	7	<i>KMT2D,PTEN,CDK12,NOTCH2,AXIN2,PRKAR1A,TNFRSF14</i>	<0.0001	1	<0.0001
	8	<i>KMT2D,PTEN,CDK12,NOTCH2,AXIN2,PRKAR1A,TNFRSF14,SOX17</i>	<0.0001	1	<0.0001
	9	<i>BIRC3,EZH2,HGF,MAP3K1,MDM4,AXIN2,RAD51C,TNFRSF14,TSC2</i>	<0.0001	1	<0.0001
	10	<i>KMT2D,ATR,CDK12,NOTCH2,AXIN2,PRKAR1A,TNFRSF14,MAP3K1,PAX5,RAD51C</i>	0.003	1	<0.0001
Melanoma_Lung / Melanoma_Brain	2	<i>TP53,NRAS</i>	0.027	0.814	0.048
	3	<i>TP53,NRAS,ASXL2</i>	0.003	0.862	0.009
	7	<i>ABL1,ARID1B,CIC,GATA1,GNA11,POLE,SH2D1A</i>	0.017	1	<0.0001
	8	<i>ABL1,ARID1B,CIC,GATA1,CHEK1,POLE,SH2D1A,TENT5C</i>	0.007	1	<0.0001
	9	<i>ABL1,ARID1B,CIC,GATA1,GNA11,POLE,SH2D1A,TENT5C,AURKB</i>	<0.0001	1	<0.0001
	10	<i>ABL1,ARID1B,CIC,GATA1,CHEK1,POLE,SH2D1A,TENT5C,TGFBR1,DAXX</i>	0.002	1	<0.0001

Table S 2.3.7. Melanoma_Brain and Melanoma_Lymph Node specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Melanoma_Brain / Melanoma_Lymph Node	4	<i>MRE11,PALB2,JAK1,PAK1</i>	0.026	1	0.047
	5	<i>MRE11,PALB2,HRAS,MPL,XRCC2</i>	0.026	1	0.036
	6	<i>MAP2K2,MDC1,HRAS,PRKAR1A,TNFRSF14,TSC2</i>	0.043	1	0.003
	7	<i>MRE11,PALB2,HRAS,PRKAR1A,TNFRSF14,XRCC2,MPL</i>	0.005	1	0.011
	8	<i>MRE11,PALB2,AURKA,PRKAR1A,TNFRSF14,XRCC2,MPL,HIST1H3H</i>	0.009	1	0.008
	10	<i>MRE11,CBL,HRAS,CHEK2,IRS2,LATS2,TNFRSF14,MPL,RICTOR,MAP2K2</i>	0.002	1	<0.0001
Melanoma_Lymph Node / Melanoma_Brain	2	<i>BRAF,NRAS</i>	<0.0001	0.076	0.001
	4	<i>MSH6,PTEN,TERT,DNMT3B</i>	0.016	1	0.015
	5	<i>MSH6,PTEN,TERT,ERBB3,TET2</i>	0.039	1	0.028
	6	<i>CTNNB1,ERBB4,MAP2K1,PIK3C2G,PTEN,EPHB1</i>	0.001	1	<0.0001
	7	<i>CTNNB1,ERBB4,MAP2K1,PIK3C2G,PTEN,PIK3CG,FLT1</i>	<0.0001	0.999	<0.0001
	8	<i>CTNNB1,IGF1R,MAP2K1,PIK3C2G,PTEN,PIK3CG,ATR,CDKN2A</i>	0.001	0.998	<0.0001
	9	<i>CTNNB1,IGF1R,MAP2K1,PIK3C2G,PTEN,PIK3CG,ATR,CDKN2A,INSR</i>	<0.0001	0.999	<0.0001
	10	<i>CTNNB1,ERBB4,MAP2K1,PIK3C2G,PTEN,PIK3CG,ATR,ATM,ERCC5,TET2</i>	<0.0001	1	<0.0001

Table S 2.3.8. Melanoma_Liver and Melanoma_Lung specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Melanoma_Liver / Melanoma_Lung	3	<i>GNA11,GNAQ,NSD1</i>	0.001	1	0.001
	4	<i>GNA11,GNAQ,NSD1,DNMT3A</i>	<0.0001	1	<0.0001
	5	<i>BAP1,CTNNB1,GLI1,RARA,SF3B1</i>	<0.0001	1	<0.0001
	6	<i>BAP1,CTNNB1,GLI1,RARA,SF3B1,PDGFRA</i>	<0.0001	1	<0.0001
	7	<i>BAP1,CTNNB1,GLI1,RARA,SF3B1,PDGFRA,HRAS</i>	<0.0001	1	<0.0001
	8	<i>BAP1,CTNNB1,GLI1,RARA,SF3B1,PDGFRA,HRAS,ST6GALNAC3</i>	<0.0001	1	<0.0001
	9	<i>BAP1,CTNNB1,GLI1,RARA,SF3B1,PDGFRA,HRAS,ST6GALNAC3,SLC12A6</i>	<0.0001	1	<0.0001
	10	<i>BAP1,CTNNB1,DNMT3A,SF3B1,EIF4A2,HRAS,ST6GALNAC3,SLC12A6,AURKA,NSD1</i>	<0.0001	1	<0.0001
Melanoma_Lung / Melanoma_Liver	4	<i>NRAS,BCOR,CIC,IRS2</i>	0.006	0.994	0.001
	6	<i>NRAS,AR,MED12,PTEN,RAC1,ANKRD11</i>	<0.0001	1	<0.0001
	7	<i>NRAS,AR,MED12,PTEN,RAC1,IKZF1,IRS2</i>	0.001	1	<0.0001
	8	<i>FLT4,AR,MED12,PTEN,MALT1,PGR,IRS2,PMS1</i>	0.01	1	<0.0001
	9	<i>ATM,AR,MED12,PTEN,MALT1,FOXP1,IRS2,PMS1,IKZF1</i>	0.012	1	<0.0001
	10	<i>ATM,AR,MED12,PTEN,MALT1,FOXP1,IRS2,PMS1,IKZF1,PIM1</i>	0.002	1	<0.0001

Table S 2.3.9. Melanoma_Liver and Melanoma_Lymph Node specific mutated driver gene sets relative to each other

N

Type	k	Specific gene set	p1	p2	q
Melanoma_Liver / Melanoma_Lymph Node	2	<i>GNA11,GNAQ</i>	0.043	0.982	0.043
	3	<i>GNA11,GNAQ,EGFR</i>	0.005	0.999	<0.0001
	4	<i>BAP1,CBL,MGA,SF3B1</i>	<0.0001	1	<0.0001
	5	<i>BAP1,DNMT3A,SF3B1,RARA,RNF43</i>	<0.0001	1	<0.0001
	6	<i>BAP1,DNMT3A,SF3B1,RARA,RNF43,LATS2</i>	<0.0001	1	<0.0001
	7	<i>BAP1,DNMT3A,SF3B1,TSC2,RNF43,LATS2,ST6GALNAC3</i>	<0.0001	1	<0.0001
	8	<i>BAP1,DNMT3A,SF3B1,RARA,RNF43,LATS2,ST6GALNAC3,SUB1</i>	<0.0001	1	<0.0001
	9	<i>BAP1,DNMT3A,SF3B1,TSC2,RNF43,LATS2,ST6GALNAC3,SUB1,CD79A</i>	<0.0001	1	<0.0001
	10	<i>BAP1,DNMT3A,SF3B1,RARA,RNF43,LATS2,ST6GALNAC3,SUB1,CD79A,SLC12A6</i>	<0.0001	1	<0.0001
	Melanoma_Lymph Node / Melanoma_Liver	2	<i>BRAF,NRAS</i>	<0.0001	0.661
3		<i>BRAF,NRAS,PDGFRA</i>	<0.0001	0.911	<0.0001
4		<i>MSH6,PTEN,TERT,DNMT3B</i>	0.038	0.994	0.005
5		<i>MSH6,PTEN,TERT,DNMT3B,NF2</i>	0.017	1	0.001
6		<i>MSH6,PTEN,TERT,ATR,TET2,TRAF2</i>	0.018	0.999	<0.0001
7		<i>MSH6,PTEN,TERT,ATR,TET2,AKT3,PIK3CD</i>	0.001	1	<0.0001
8		<i>MSH6,PTEN,TERT,ATR,TET2,AKT3,PIK3CD,TRAF2</i>	<0.0001	1	<0.0001
9		<i>MSH6,PTEN,TERT,NF2,TET2,AKT3,PIK3CD,TRAF2,ERBB3</i>	0.002	1	<0.0001
10		<i>MSH6,PTEN,TERT,NF2,TET2,AKT3,PIK3CD,TRAF2,ATR,ZFH3</i>	<0.0001	1	<0.0001

Table S 2.3.10. Melanoma_Lung and Melanoma_Lymph Node specific mutated driver gene sets relative to each other
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Type	k	Specific gene set	p1	p2	q
Melanoma_Lung / Melanoma_Lymph Node	6	<i>ABL1,GATA1,PMS1,POLE,TCF3,SH2D1A</i>	0.006	0.998	<0.0001
	7	<i>ABL1,GATA1,PMS1,POLE,TCF3,TRAF7,CHEK1</i>	<0.0001	1	<0.0001
	8	<i>ABL1,GATA1,PMS1,POLE,TCF3,TRAF7,CHEK1,AURKB</i>	<0.0001	0.999	<0.0001
	9	<i>ABL1,GATA1,PMS1,POLE,TCF3,TRAF7,CHEK1,MALT1,FH</i>	<0.0001	0.997	<0.0001
	10	<i>ABL1,GATA1,PMS1,POLE,CHEK1,PAK1,CHEK2,MALT1,SH2D1A,IGF2</i>	<0.0001	1	<0.0001
Melanoma_Lymph Node / Melanoma_Lung	2	<i>BRAF,NF1</i>	<0.0001	0.985	<0.0001
	3	<i>ATM,BRAF,NRAS</i>	<0.0001	0.796	<0.0001
	6	<i>CTNNB1,KMT2D,NOTCH2,PIK3C2G,PTEN,TET1</i>	<0.0001	1	<0.0001
	7	<i>CTNNB1,KMT2D,NOTCH2,PIK3C2G,PTEN,TET1,ATR</i>	<0.0001	1	<0.0001
	8	<i>CTNNB1,KMT2D,NOTCH2,PIK3C2G,PTEN,TET1,ERBB4,CDKN2A</i>	0.01	1	<0.0001
	9	<i>CTNNB1,KMT2D,NOTCH2,PIK3C2G,PTEN,TET1,ERBB4,CDKN2A,ATR</i>	0.014	1	<0.0001
	10	<i>CTNNB1,MAP2K1,NF2,INSR,PIK3C2G,PTEN,TET1,PIK3CG,CDKN2A,ATR</i>	<0.0001	1	<0.0001

3 Supplementary Tables: Three main metastatic lesions attract cancer cells to adapt to their tissue microenvironment

3.1 Hepatocellular carcinoma

Table S 3.1.1. Significant common driver gene set between Breast, Lung, Melanoma, Colorectal and Pancreatic Liver

k	common gene set	p1	p2	p3	p4	p5	q
7	<i>TP53,CDH1,EIF1AX,GATA3,GNA11,GNAQ,MEN1</i>	<0.0001	0.026	0.014	0.011	<0.0001	<0.0001
8	<i>TP53,CDH1,EIF1AX,GATA3,GNA11,GNAQ,MEN1,NFE2L2</i>	<0.0001	0.045	0.0132	0.024	<0.0001	<0.0001
9	<i>TP53,CDH1,EIF1AX,GATA3,GNA11,GNAQ,MEN1,EIF4A2,LDLR</i>	<0.0001	0.009	0.003	0.015	<0.0001	<0.0001
10	<i>TP53,CDH1,EIF1AX,GATA3,GNA11,GNAQ,MEN1,EIF4A2,LDLR,CHEK2</i>	<0.0001	0.01	0.004	0.015	<0.0001	<0.0001

Table S 3.1.2. Significant common driver gene set between Colorectal, Pancreatic and Prostate Liver

k	common gene set	p1	p2	p3	q
7	<i>TP53,CD79B,EIF1AX,HIST1H3C,MEN1,SMAD2,STK11</i>	<0.0001	<0.0001	0.042	<0.0001
8	<i>TP53,CD79B,EIF1AX,HIST1H3C,MEN1,SMAD2,STK11,HIST1H3E</i>	<0.0001	<0.0001	0.048	<0.0001

Table S 3.1.3. Significant common driver gene set between Colorectal Liver and Prostate Liver

k	common gene set	p1	p2	q
8	<i>TP53,BRCA1,CD79B,DDR2,EIF1AX,FGFR4,MEN1,SMAD2</i>	<0.0001	0.02	<0.0001
10	<i>TP53,BRCA1,CD79B,DDR2,EIF1AX,FGFR4,MEN1,SMAD2,COX7C,HIST1H3C</i>	<0.0001	0.008	<0.0001

*There is no significant common among driver gene set between Breast, Lung, Melanoma, Colorectal, Pancreatic, Prostate Liver when $k=2 \sim 10$.

Table S 3.1.4. Significant common driver gene set between Breast, Lung and Melanoma_Liver

k	common gene set	p1	p2	p3	q
10	<i>TP53,ASXL1,CDH1,DICER1,ESR1,GNA11,GNAQ,IGF1,MEN1,MSH6</i>	<0.0001	0.016	<0.0001	<0.0001

3.2 Non-small-cell Lung cancer

Table S 3.2.1. Significant common driver gene set between Breast, Colorectal, HeadNeck_Lung

k	common gene set	p1	p2	p3	q
4	<i>TP53,GATA3,PIK3CA,PIK3R1</i>	<0.0001	<0.0001	0.029	<0.0001
5	<i>TP53,GATA3,PIK3CA,PIK3R1,MDC1</i>	<0.0001	0.001	0.007	<0.0001
6	<i>TP53,GATA3,PIK3CA,PIK3R1,MDC1,B2M</i>	<0.0001	<0.0001	0.003	<0.0001
7	<i>TP53,GATA3,PIK3CA,PIK3R1,MDC1,B2M,LATS1</i>	<0.0001	<0.0001	<0.0001	<0.0001
8	<i>TP53,GATA3,PIK3CA,PIK3R1,MDC1,B2M,LATS1,CCND1</i>	<0.0001	<0.0001	<0.0001	<0.0001
9	<i>TP53,GATA3,PIK3CA,PIK3R1,MDC1,B2M,LATS1,CCND1,HIST1H3F</i>	<0.0001	<0.0001	<0.0001	<0.0001
10	<i>TP53,GATA3,PIK3CA,PIK3R1,MDC1,B2M,LATS1,CCND1,HIST1H3F,GREM1</i>	<0.0001	<0.0001	<0.0001	<0.0001

*There is no significant common among driver gene set between Breast, Colorectal, HeadNeck, Melanoma_Lung when k=2 ~ 10.

Table S 3.2.2. Significant common driver gene set between Colorectal, HeadNeck and Melanoma_Lung

k	common gene set	p1	p2	p3	q
7	<i>TP53,AURKB,B2M,NRAS,PIK3CA,PIK3R1,CCND3</i>	<0.0001	0.025	0.04	<0.0001
8	<i>TP53,AURKB,B2M,NRAS,PIK3CA,PIK3R1,BMPR1A,WT1</i>	<0.0001	0.017	0.026	<0.0001
9	<i>TP53,AURKB,B2M,NRAS,PIK3CA,PIK3R1,BMPR1A,RAB35,HIST1H3F</i>	<0.0001	0.008	0.007	<0.0001
10	<i>TP53,AURKB,B2M,NRAS,PIK3CA,PIK3R1,BMPR1A,PIM1,SMAD2,FH</i>	<0.0001	0.016	0.002	<0.0001

Table S 3.2.3. Significant common driver gene set between Breast_Lung and Melanoma_Lung

k	common gene set	p1	p2	q
5	<i>TP53,ASXL2,AURKB,GATA3,NRAS</i>	<0.0001	0.010	<0.0001
6	<i>TP53,ASXL2,AURKB,CCND1,GATA3,NRAS</i>	<0.0001	0.011	<0.0001
7	<i>TP53,ASXL2,AURKB,CCND1,GATA3,NRAS,MAP2K4</i>	<0.0001	0.01	<0.0001
8	<i>TP53,ASXL2,AURKB,CCND1,GATA3,NRAS,MAP2K4,FH</i>	<0.0001	0.006	<0.0001
9	<i>TP53,ASXL2,AURKB,CCND1,GATA3,NRAS,MAP2K4,GNA11,SMAD2</i>	<0.0001	0.004	<0.0001
10	<i>TP53,ASXL2,AURKB,CCND1,GATA3,NRAS,MAP2K4,GNA11,FH,INPP4B</i>	<0.0001	<0.0001	<0.0001

3.3 Brain cancer

Table S 3.3.1. Significant common driver gene set between Breast_Brain and Lung_Brain

k	common gene set	p1	p2	q
4	<i>TP53,FGFR1,HIST1H3E,RAF1</i>	0.022	<0.0001	<0.0001
5	<i>TP53,FGFR1,MAP2K4,RAF1,KIF5B</i>	<0.0001	<0.0001	<0.0001
6	<i>TP53,FGFR1,HIST1H3E,RAF1,KIF5B,MAP2K4</i>	<0.0001	<0.0001	<0.0001
7	<i>TP53,FGFR1,HIST1H3E,RAF1,KIF5B,MAP2K4,EIF1AX</i>	<0.0001	<0.0001	<0.0001
8	<i>TP53,FGFR1,HIST1H3E,RAF1,KIF5B,MAP2K4,EIF1AX,PRDM1</i>	<0.0001	<0.0001	<0.0001
9	<i>TP53,FGFR1,HIST1H3E,RAF1,KIF5B,MAP2K4,EML4,PRDM1,GATA1</i>	<0.0001	<0.0001	<0.0001
10	<i>TP53,FGFR1,HIST1H3E,RAF1,KIF5B,MAP2K4,EML4,PRDM1,GATA1,SDHD</i>	<0.0001	<0.0001	<0.0001

Table S 3.3.2. Significant common driver gene set between Breast_Brain and Melanoma_Brain

k	common gene set	p1	p2	q
6	<i>TP53,BRAF,FLCN,GATA3,HRAS,NRAS</i>	0.033	<0.0001	<0.0001
7	<i>TP53,BRAF,FLCN,GSK3B,HRAS,NRAS,CDK4</i>	<0.0001	<0.0001	<0.0001
8	<i>TP53,BRAF,FLCN,GATA3,HRAS,NRAS,CDK4,AKT3</i>	<0.0001	<0.0001	<0.0001
9	<i>TP53,BRAF,FLCN,GATA3,HRAS,NRAS,CDK4,AKT3,EIF4A2</i>	<0.0001	<0.0001	<0.0001
10	<i>TP53,BRAF,FLCN,GATA3,HRAS,NRAS,KIT,AKT3,EIF4A2,ABRAXAS1</i>	<0.0001	<0.0001	<0.0001

*There is no significant common driver gene set between Lung_Brain and Melanoma_Brain when k=2 ~ 10.

*There is no significant common driver gene set between Breast, Lung and Melanoma_Brain when k=2 ~ 10.

4 Supplementary Tables: Typical patterns with high metastatic tropisms

4.1 colorectal liver metastases

Table S 4.1.1. Significant common driver gene set between Colorectal_Liver and Colorectal_P

k	common gene set	p1	p2	q
9	<i>APC,BMPR1A,EIF4A2,GATA2,H3F3A,PDPK1,RAB35,RHOA,STK40</i>	<0.0001	0.028	<0.0001

Table S 4.1.2. Colorectal_P specific mutated driver gene sets relative to Colorectal_Liver

k	Specific gene set	p1	p2	q
2	<i>BRAF,APC</i>	<0.0001	0.263	<0.0001
9	<i>BRAF,CSF1R,ERBB2,FLT3,FLT4,KRAS,PTEN,RBM10,CDH1</i>	0.022	0.959	0.009
10	<i>BRAF,CSF1R,ERBB2,FLT3,FLT4,KRAS,NSD1,RBM10,PIK3R1,PRKN</i>	0.006	0.851	0.003

*Colorectal_Liver has no specific mutated driver gene sets relative to Colorectal_P when k=2 ~ 10.

Table S 4.1.3. Significant common driver gene set between Colorectal_liver and Hepatocellular_P

k	common gene set	p1	p2	q
10	<i>APC,AXIN1,BCOR,CDH1,CDK4,CTNNB1,EZH2,INPP4B,MAP2K1,NPM1</i>	<0.0001	0.042	<0.0001

Table S 4.1.4. Colorectal_Liver and Hepatocellular_P specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Colorectal_Liver / Hepatocellular_P	3	<i>APC,EGFR,PHOX2B</i>	0.007	1	<0.0001
	4	<i>APC,EGFR,PHOX2B,NOTCH3</i>	<0.0001	1	<0.0001
	5	<i>APC,EGFR,PHOX2B,JUN,NOTCH3</i>	0.002	1	<0.0001
	6	<i>APC,EGFR,PHOX2B,JUN,NOTCH3,ESR1</i>	<0.0001	1	<0.0001
	7	<i>APC,EGFR,PHOX2B,AXL,KRAS,MET,BCOR</i>	0.003	0.943	0.001
	8	<i>APC,EGFR,PHOX2B,AXL,KRAS,MET,LMO1,NPM1</i>	<0.0001	0.941	0.001
	9	<i>APC,EGFR,PHOX2B,AXL,KRAS,MET,LMO1,NPM1,BCOR</i>	<0.0001	0.934	<0.0001
	10	<i>TP53,ATRX,BRAF,ERBB2,FGFR3,KRAS,MST1R,NRAS,RAD51B,STK11</i>	<0.0001	1	<0.0001
Hepatocellular_P / Colorectal_Liver	2	<i>JAK1,TERT</i>	0.034	1	<0.0001
	3	<i>JAK1,TERT,BAP1</i>	0.007	1	<0.0001
	4	<i>JAK1,TERT,BAP1,KLF4</i>	<0.0001	1	<0.0001
	5	<i>JAK1,TERT,BAP1,KLF4,XPO1</i>	<0.0001	1	<0.0001
	6	<i>JAK1,TERT,BAP1,KLF4,XPO1,TGFBR1</i>	<0.0001	1	<0.0001
	7	<i>JAK1,TERT,BAP1,KLF4,XPO1,TGFBR1,PMAIP1</i>	<0.0001	1	<0.0001
	8	<i>JAK1,TERT,BAP1,KLF4,XPO1,TGFBR1,EZH2,NEGR1</i>	<0.0001	1	<0.0001
	9	<i>JAK1,TERT,BAP1,KLF4,XPO1,TGFBR1,PMAIP1,NEGR1,PRKACA</i>	<0.0001	1	<0.0001
	10	<i>JAK1,TERT,BAP1,KLF4,XPO1,TGFBR1,PMAIP1,NEGR1,PRKACA,SDHB</i>	<0.0001	1	<0.0001

4.2 NSCLC cancer with brain metastasis

Table S 4.2.1. Significant common driver gene set between Lung_Brain and Lung_P

k	common gene set	p1	p2	q
8	<i>BRAF,EGFR,EML4,ERBB2,KIF5B,KRAS,MET,ROS1</i>	<0.0001	<0.0001	<0.0001
10	<i>BRAF,EGFR,EML4,ERBB2,KIF5B,KRAS,MET,ROS1,RASA1,GATA1</i>	<0.0001	<0.0001	<0.0001

Lung_P and Lung_Brain specific mutated driver gene sets relative to each other can be seen in S2.2.2.

Table S 4.2.2. Lung_Brain and Brain_P specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Lung_Brain / Brain_P	4	<i>AXIN1,IL7R,KEAP1,NFE2L2</i>	0.43	1	<0.0001
	5	<i>AXIN1,IL7R,KEAP1,KIF5B,NFE2L2</i>	0.012	1	<0.0001
	7	<i>AXIN1,IL7R,KEAP1,KIF5B,NFE2L2,STK11,EPHA7</i>	0.028	1	<0.0001
	8	<i>AXIN1,IL7R,KEAP1,KIF5B,NFE2L2,STK11,EPHA7,AKT3</i>	0.024	1	<0.0001
	9	<i>AXIN1,IL7R,KEAP1,KIF5B,NFE2L2,STK11,EPHA7,AKT3,B2M</i>	0.039	1	<0.0001
	10	<i>AXIN1,IL7R,KEAP1,KIF5B,NFE2L2,STK11,EPHA7,AKT3,B2M,CTNNB1</i>	0.006	1	<0.0001
Brain_P / Lung_Brain	2	<i>ATRX,TERT</i>	<0.0001	0.972	<0.0001
	3	<i>ATRX,TERT,BRAF</i>	<0.0001	1	<0.0001
	4	<i>ATRX,TERT,BRAF,H3F3A</i>	<0.0001	0.999	<0.0001
	5	<i>ATRX,TERT,BRAF,H3F3A,MAX</i>	<0.0001	0.999	<0.0001
	6	<i>ATRX,TERT,BRAF,CDKN2B,H3F3A,MAX</i>	<0.0001	1	<0.0001
	7	<i>ATRX,TERT,BRAF,FANCA,H3F3A,MAX,H3F3C</i>	<0.0001	1	<0.0001
	8	<i>ATRX,TERT,BRAF,FANCA,H3F3A,MAX,CDKN2B,ZNF710</i>	<0.0001	0.999	<0.0001
	9	<i>ATRX,TERT,BRAF,FANCA,H3F3A,MAX,GOPC,H3F3C,RAC1</i>	<0.0001	0.999	<0.0001
	10	<i>ATRX,TERT,BRAF,AHCYL2,H3F3A,CDKN2B,GOPC,HDAC5,IDH1,TRAP1</i>	<0.0001	0.998	<0.0001

4.3 breast and prostate cancer with bone metastasis

Table S 4.3.1. Significant common driver gene set between Breast_P and Breast_Bone

k	common gene set	p1	p2	q
2	<i>TP53,GATA3</i>	<0.0001	0.018	<0.0001
3	<i>TP53,GATA3,CDH1</i>	<0.0001	<0.0001	<0.0001
4	<i>TP53,GATA3,CDH1,SMARCA4</i>	<0.0001	<0.0001	<0.0001
5	<i>TP53,GATA3,CDH1,SMARCA4,AMER1</i>	<0.0001	<0.0001	<0.0001
6	<i>TP53,CDH1,DNMT3B,GATA3,PAK5,SMARCA4</i>	<0.0001	<0.0001	<0.0001
7	<i>TP53,AMER1,CDH1,GATA3,RHEB,SMARCA4,TNFAIP3</i>	<0.0001	<0.0001	<0.0001
8	<i>TP53,CDH1,DNMT3B,GATA3,PAK5,RHEB,SMARCA4,TNFAIP3</i>	<0.0001	<0.0001	<0.0001
9	<i>TP53,CDH1,DNMT3B,GATA3,PAK5,RHEB,SMARCA4,TNFAIP3,SPOP</i>	<0.0001	<0.0001	<0.0001
10	<i>TP53,CDH1,DNMT3B,GATA3,PAK5,RHEB,SMARCA4,TNFAIP3,SPOP,FH</i>	<0.0001	<0.0001	<0.0001

Breast_P and Breast_Bone specific mutated driver gene sets relative to each other can be seen in S2.1.1.

Table S 4.3.2. Significant common driver gene set between Breast_Bone and Prostate_Bone

k	common gene set	p1	p2	q
6	<i>TP53,APC,ARID1A,GATA3,KMT2D,SMARCA4</i>	<0.0001	0.034	<0.0001
7	<i>TP53,APC,ARID1A,GATA3,KMT2D,SMARCA4,MITF</i>	<0.0001	0.011	<0.0001
8	<i>TP53,APC,ARID1A,GATA3,KMT2D,SMARCA4,MITF,TBX3</i>	<0.0001	0.016	<0.0001
9	<i>TP53,APC,ARID1A,GATA3,KMT2D,SMARCA4,MITF,TBX3,NTRK3</i>	<0.0001	0.007	<0.0001
10	<i>TP53,APC,ARID1A,GATA3,KMT2D,SMARCA4,MITF,TBX3,NTRK3,VHL</i>	<0.0001	0.003	<0.0001

*Prostate_P has no specific mutated driver gene sets relative to Prostate_Bone when k=2 ~ 10.

*Prostate_Bone has no specific mutated driver gene sets relative to Prostate_P when k=2 ~ 10.

Table S 4.3.3. Breast_Bone and Prostate_Bone specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Breast_Bone / Prostate_Bone	7	<i>AKT1, BRIP1, CDH1, IKBKE, PIK3CA, SOX17, TBX3</i>	0.033	1	0.047
Prostate_Bone / Breast_Bone	5	<i>CDK12, EGFR, KDM6A, TMPRSS2, AR</i>	0.035	1	0.035
	6	<i>CDK12, EGFR, KDM6A, TMPRSS2, AR, VHL</i>	0.011	1	0.018
	7	<i>CDK12, EGFR, KDM6A, TMPRSS2, AR, NOTCH4, RNF43</i>	0.003	0.999	<0.0001
	8	<i>CDK12, EGFR, KDM6A, TMPRSS2, AR, NOTCH4, RNF43, CTNNB1</i>	<0.0001	0.998	<0.0001
	9	<i>CDK12, EGFR, KDM6A, TMPRSS2, AR, NOTCH4, RNF43, CTNNB1, JAK1</i>	<0.0001	0.999	<0.0001
	10	<i>CDK12, EGFR, KDM6A, TMPRSS2, NOTCH4, RNF43, CTNNB1, JAK1, PBRM1, SPOP</i>	<0.0001	1	<0.0001

Table S 4.3.4. Significant common driver gene set between Prostate_P and Prostate_Bone

k	common gene set	p1	p2	q
3	<i>FOXA1, SPOP, TMPRSS2</i>	0.001	<0.0001	<0.0001
4	<i>FOXA1, SPOP, TMPRSS2, KDM6A</i>	0.002	<0.0001	<0.0001
5	<i>FOXA1, SPOP, TMPRSS2, KMT2A, PTPRD</i>	<0.0001	<0.0001	<0.0001
6	<i>FOXA1, SPOP, TMPRSS2, KMT2A, PTPRD, ASXL2</i>	<0.0001	<0.0001	<0.0001
7	<i>FOXA1, SPOP, TMPRSS2, KDM6A, PTPRD, MTOR, POLE</i>	0.001	<0.0001	<0.0001
8	<i>FOXA1, SPOP, TMPRSS2, KDM6A, PTPRD, MTOR, NOTCH4, ASXL2</i>	0.001	<0.0001	<0.0001
9	<i>FOXA1, SPOP, TMPRSS2, KDM6A, PTPRD, MTOR, NOTCH4, POLE, HRAS</i>	0.024	<0.0001	<0.0001
10	<i>FOXA1, SPOP, TMPRSS2, KMT2A, PTPRD, ARID1B, NOTCH4, ASXL2, FLT1, IKBKE</i>	0.002	<0.0001	<0.0001

5 Supplementary Tables: Metastasis-promoting mechanisms for comparable cancers

5.1 Female-Breast, Endometrium and Ovary

Primary cancers

Table S 5.1.1. Significant common driver gene set between Breast_P and Endometrial_P

k	common gene set	p1	p2	q
4	<i>TP53,CDH1,GATA3,ARID1A</i>	<0.0001	<0.0001	<0.0001
5	<i>TP53,CDH1,GATA3,CD276,PTEN</i>	<0.0001	<0.0001	<0.0001
6	<i>TP53,CDH1,GATA3,CD276,ARID1A,SMARCD1</i>	<0.0001	<0.0001	<0.0001
7	<i>TP53,CDH1,GATA3,CTNNB1,MALT1,NFE2L2,SOX17</i>	<0.0001	<0.0001	<0.0001
8	<i>TP53,CDH1,GATA3,CTNNB1,NFE2L2,SOX17,CD276,YES1</i>	<0.0001	<0.0001	<0.0001
9	<i>TP53,CDH1,GATA3,CTNNB1,NFE2L2,SOX17,CD276,YES1,MALT1</i>	<0.0001	<0.0001	<0.0001
10	<i>TP53,CDH1,GATA3,CTNNB1,NFE2L2,SOX17,CD276,YES1,MALT1,KRAS</i>	<0.0001	<0.0001	<0.0001

Table S 5.1.2. Significant common driver gene set between Breast_P and Ovarian_P

k	common gene set	p1	p2	q
4	<i>TP53,ARID1A,CDH1,GATA3</i>	<0.0001	<0.0001	<0.0001
5	<i>TP53,ARID1A,CDH1,GATA3,CDC73</i>	<0.0001	<0.0001	<0.0001
6	<i>TP53,ARID1A,CDH1,GATA3,CDC73,DAXX</i>	<0.0001	<0.0001	<0.0001
7	<i>TP53,ARID1A,CDH1,GATA3,KRAS,NUP93,TNFAIP3</i>	<0.0001	<0.0001	<0.0001
8	<i>TP53,ARID1A,CDH1,GATA3,KRAS,DAXX,TNFAIP3,CDC73</i>	<0.0001	<0.0001	<0.0001
9	<i>TP53,ARID1A,CDH1,GATA3,KRAS,DAXX,TNFAIP3,CDC73,EED</i>	<0.0001	<0.0001	<0.0001
10	<i>TP53,ARID1A,CDH1,GATA3,KRAS,DAXX,TNFAIP3,CDC73,EED,SMARCD1</i>	<0.0001	<0.0001	<0.0001

Table S 5.1.3. Significant common driver gene set between Endometrial_P and Ovarian_P

k	common gene set	p1	p2	q
2	<i>TP53,ARID1A</i>	<0.0001	<0.0001	<0.0001
3	<i>TP53,ARID1A,CD276</i>	<0.0001	<0.0001	<0.0001
4	<i>TP53,ARID1A,CD276,CTLA4</i>	<0.0001	<0.0001	<0.0001
5	<i>TP53,ARID1A,CD276,CTLA4,NFKBIA</i>	<0.0001	<0.0001	<0.0001
6	<i>TP53,ARID1A,CD276,CTLA4,NFKBIA,GOLGB1</i>	<0.0001	<0.0001	<0.0001
7	<i>TP53,ARID1A,CD276,CTLA4,NFKBIA,GOLGB1,TCEANC2</i>	<0.0001	<0.0001	<0.0001
8	<i>TP53,ARID1A,CD276,CTLA4,NFKBIA,GOLGB1,TCEANC2,EIF1AX</i>	<0.0001	<0.0001	<0.0001
9	<i>TP53,ARID1A,CD276,CTLA4,NFKBIA,GOLGB1,TCEANC2,EIF1AX,NUP93</i>	<0.0001	<0.0001	<0.0001
10	<i>TP53,ARID1A,CD276,CTLA4,NFKBIA,GOLGB1,TCEANC2,EIF1AX,NUP93,CD79B</i>	<0.0001	<0.0001	<0.0001

Table S 5.1.4. Breast_P and Endometrial_P specific mutated driver gene sets relative to each other

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Type	k	Specific gene set	p1	p2	q
Breast_P / Endometrial_P	2	<i>TP53,PIK3CA</i>	0.033	0.962	0.012
	3	<i>TP53,PIK3CA,GATA3</i>	<0.0001	0.976	<0.0001
	4	<i>AKT1,PIK3CA,BRCA2,NF1</i>	<0.0001	1	<0.0001
	7	<i>AKT1,PIK3CA,ARID1A,BRCA2,MAP3K1,NF1,PTEN</i>	0.026	1	<0.0001
	8	<i>AKT1,PIK3CA,ARID1A,BRCA2,MAP3K1,NF1,PTEN,ESR1</i>	0.009	1	<0.0001
	10	<i>AKT1,PIK3CA,ARID1A,BRCA2,MAP3K1,NF1,PTEN,ESR1,BCOR,KMT2C</i>	0.025	1	<0.0001
Endometrial_P / Breast_P	7	<i>ACVR1,FBXW7,NTRK3,PIK3R1,PPP2R1A,NFKBIA,KRAS</i>	0.038	0.981	0.025
	8	<i>ACVR1,FBXW7,NTRK3,PIK3R1,PPP2R1A,NFKBIA,KRAS,EIF3G</i>	0.03	0.978	0.016
	9	<i>ACVR1,FBXW7,NTRK3,PIK3R1,PPP2R1A,NFKBIA,KRAS,HIST1H3G,TACC3</i>	0.015	0.98	0.01
	10	<i>FANCA,FBXW7,NTRK3,PIK3R1,PPP2R1A,NFKBIA,SPOP,HIST1H3G,TMEM64,MITF</i>	0.006	0.984	0.011

Table S 5.1.5. Breast_P and Ovarian_P specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Breast_P / Ovarian_P	2	<i>TP53,GATA3</i>	<0.0001	1	<0.0001
	3	<i>TP53,GATA3,CDH1</i>	<0.0001	1	<0.0001
	4	<i>AKT1,BRCA2,PIK3CA,PTEN</i>	<0.0001	0.989	<0.0001
	5	<i>AKT1,BRCA2,PIK3CA,PTEN,ERBB2</i>	<0.0001	0.997	<0.0001
	6	<i>AKT1,BRCA2,PIK3CA,PTEN,MAP3K1,KDM6A</i>	0.003	0.997	<0.0001
	9	<i>AKT1,BRCA2,PIK3CA,PTEN,MAP3K1,KMT2C,ESR1,NF1,NOTCH1</i>	0.034	0.968	0.018
	10	<i>AKT1,BRCA2,PIK3CA,PTEN,MAP3K1,KMT2C,ESR1,NF1,NOTCH1,GRIN2A</i>	0.024	1	<0.0001
Ovarian_P / Breast_P	10	<i>ASXL1,BRAF,CASC3,CTNNB1,FANCA,LATS1,MST1R,NF2,RAD50,SOCS1</i>	0.046	1	<0.0001

Table S 5.1.6. Endometrial_P and Ovarian_P specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Endometrial_P / Ovarian_P	3	<i>PIK3CA,PIK3R1,SPOP</i>	0.007	0.889	0.01
	4	<i>PIK3CA,PIK3R1,SPOP,EP300</i>	0.002	0.943	0.003
	5	<i>PIK3CA,PIK3R1,SPOP,EP300,CBFB</i>	0.005	0.952	0.002
	10	<i>PIK3CA,PPP2R1A,DPP9,SPOP,FBXW7,HIST1H3G,MED12,PTEN,TGFBR1,ATM</i>	0.021	0.998	0.002
Ovarian_P / Endometrial_P	10	<i>ANKRD11,ATRX,HGF,KIT,KMT2A,MST1R,NF2,PIK3C2G,ROS1,TERT</i>	0.014	1	<0.0001

Table S 5.1.7. Significant common driver gene set among Breast_P, Endometrial_P and Ovarian_P

k	common gene set	p1	p2	p3	q
4	<i>TP53,ARID1A,CDH1,GATA3</i>	<0.0001	<0.0001	<0.0001	<0.0001
5	<i>TP53,ARID1A,CDH1,GATA3,CD276</i>	<0.0001	<0.0001	<0.0001	<0.0001
6	<i>TP53,ARID1A,CDH1,GATA3,CD276,SMARCD1</i>	<0.0001	<0.0001	<0.0001	<0.0001
7	<i>TP53,ARID1A,CDH1,GATA3,CD276,SMARCD1,SRSF2</i>	<0.0001	<0.0001	<0.0001	<0.0001
8	<i>TP53,ARID1A,CDH1,GATA3,CD276,SMARCD1,SRSF2,CTLA4</i>	<0.0001	<0.0001	<0.0001	<0.0001
9	<i>TP53,ARID1A,CDH1,GATA3,CD276,SMARCD1,SRSF2,CTLA4,GOLGB1</i>	<0.0001	<0.0001	<0.0001	<0.0001
10	<i>TP53,ARID1A,CDH1,GATA3,CD276,SMARCD1,SRSF2,CTLA4,GOLGB1,TCEANC2</i>	<0.0001	<0.0001	<0.0001	<0.0001

Metastatic cancers

Table S 5.1.8. Significant common driver gene set between Breast_M and Endometrial_M

k	common gene set	p1	p2	q
2	<i>TP53,ARID1A</i>	<0.0001	<0.0001	<0.0001
3	<i>TP53,ARID1A,CD276</i>	<0.0001	<0.0001	<0.0001
4	<i>TP53,ARID1A,CD276,CTLA4</i>	<0.0001	<0.0001	<0.0001
5	<i>TP53,ARID1A,CD276,CTLA4,NFKBIA</i>	<0.0001	<0.0001	<0.0001
6	<i>TP53,ARID1A,CD276,CTLA4,NFKBIA,GOLGB1</i>	<0.0001	<0.0001	<0.0001
7	<i>TP53,ARID1A,CD276,CTLA4,NFKBIA,GOLGB1,TCEANC2</i>	<0.0001	<0.0001	<0.0001
8	<i>TP53,ARID1A,CD276,CTLA4,NFKBIA,GOLGB1,TCEANC2,EIF1AX</i>	<0.0001	<0.0001	<0.0001
9	<i>TP53,ARID1A,CD276,CTLA4,NFKBIA,GOLGB1,TCEANC2,EIF1AX,NUP93</i>	<0.0001	<0.0001	<0.0001
10	<i>TP53,ARID1A,CD276,CTLA4,NFKBIA,GOLGB1,TCEANC2,EIF1AX,NUP93,CD79B</i>	<0.0001	<0.0001	<0.0001

Table S 5.1.9. Significant common driver gene set between Breast_M and Ovarian_M

k	common gene set	p1	p2	q
7	<i>TP53,CDH1,CDKN1B,GATA3,HGF,KRAS,SMARCA4</i>	<0.0001	<0.0001	<0.0001
8	<i>TP53,CDH1,CDKN1B,GATA3,HGF,KRAS,SMARCA4,CDC73</i>	<0.0001	<0.0001	<0.0001
9	<i>TP53,CDH1,CDKN1B,GATA3,HGF,KRAS,SMARCA4,TSHR,MITF</i>	<0.0001	<0.0001	<0.0001
10	<i>TP53,CDH1,CDKN1B,GATA3,HGF,KRAS,SMARCA4,TSHR,CDC73,POLD1</i>	<0.0001	<0.0001	<0.0001

*Ovarian_M has no specific mutated driver gene sets relative to Breast_M when k=2 ~ 10.

Table S 5.1.10. Significant common driver gene set between Endometrial_M and Ovarian_M

k	common gene set	p1	p2	q
2	<i>TP53,ARID1A</i>	<0.0001	0.003	<0.0001
3	<i>TP53,ARID1A,KRAS</i>	<0.0001	<0.0001	<0.0001
4	<i>TP53,CTNNB1,KRAS,HIST1H3F</i>	<0.0001	<0.0001	<0.0001
5	<i>TP53,CTNNB1,KRAS,HIST1H3F,RPS6KB2</i>	<0.0001	<0.0001	<0.0001
6	<i>TP53,CTNNB1,KRAS,HIST1H3F,RPS6KB2,RYBP</i>	<0.0001	<0.0001	<0.0001
7	<i>TP53,CTNNB1,KRAS,HIST1H3F,RPS6KB2,RYBP,EYA2</i>	<0.0001	<0.0001	<0.0001
8	<i>TP53,CTNNB1,KRAS,HIST1H3F,RPS6KB2,RYBP,EYA2,HNRNPUL1</i>	<0.0001	<0.0001	<0.0001
9	<i>TP53,CTNNB1,KRAS,HIST1H3F,RPS6KB2,RYBP,EYA2,HNRNPUL1,TMPRSS2</i>	<0.0001	<0.0001	<0.0001
10	<i>TP53,CTNNB1,KRAS,HIST1H3F,RPS6KB2,RYBP,EYA2,HNRNPUL1,TMPRSS2,FLCN</i>	<0.0001	<0.0001	<0.0001

Table S 5.1.11. Breast_M and Endometrial_M specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Breast_M / Endometrial_M	2	<i>TP53,GATA3</i>	<0.0001	0.338	<0.0001
	3	<i>TP53,GATA3,PIK3CA</i>	<0.0001	0.257	<0.0001
	4	<i>ERBB2,ESR1,PIK3CA,PTEN</i>	0.043	0.995	0.01
	5	<i>ERBB2,ESR1,PIK3CA,PTEN,AKT1</i>	0.001	0.982	<0.0001
	6	<i>ERBB2,ESR1,PIK3CA,PTEN,AKT1,ARID1A</i>	0.018	1	<0.0001
	7	<i>ERBB2,ESR1,PIK3CA,PTEN,AKT1,ARID1A,KMT2A</i>	0.013	1	<0.0001
Endometrial_M / Breast_M	2	<i>KRAS,CTNNB1</i>	0.021	0.968	0.03
	3	<i>KRAS,CTNNB1,NPM1</i>	0.012	0.965	0.006
	4	<i>KRAS,PIK3R1,ACVR1,CD79A</i>	0.002	0.968	0.003

Table S 5.1.12. Breast_M specific mutated driver gene sets relative to Ovarian_M

k	Specific gene set	p1	p2	q
2	<i>TP53,GATA3</i>	<0.0001	1	<0.0001
3	<i>TP53,GATA3,PIK3CA</i>	<0.0001	0.087	<0.0001
4	<i>TP53,GATA3,PIK3CA,ESR1</i>	<0.0001	0.06	<0.0001
7	<i>AKT1,ARID1A,PIK3CA,ESR1,KMT2A,PTEN,ERBB2</i>	0.013	1	0.001
8	<i>AKT1,ARID1A,PIK3CA,ESR1,KMT2A,PTEN,ERBB2,PIK3R1</i>	0.006	1	0.001

Table S 5.1.13. Endometrial_M and Ovarian_M specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Endometrial_M / Ovarian_M	2	<i>PIK3CA,PIK3R1</i>	<0.0001	0.892	<0.0001
	3	<i>PIK3CA,PIK3R1,AKT1</i>	<0.0001	0.895	<0.0001
	4	<i>PIK3CA,PIK3R1,AKT1,BCL2L11</i>	<0.0001	0.88	<0.0001
	5	<i>PIK3CA,PIK3R1,AKT1,BCL2L11,ERBB3</i>	<0.0001	0.873	<0.0001
	6	<i>PIK3CA,PIK3R1,AKT1,BCL2L11,ERBB3,ARID1B</i>	<0.0001	0.996	<0.0001
	7	<i>PIK3CA,PIK3R1,AKT1,BCL2L11,ERBB3,ARID1B,FOXO1</i>	<0.0001	0.989	<0.0001
	8	<i>PIK3CA,PIK3R1,AKT1,BCL2L11,ERBB3,ARID1B,FOXO1,CD79A</i>	<0.0001	0.991	<0.0001
	9	<i>PIK3CA,PIK3R1,AKT1,BCL2L11,ERBB3,ARID1B,FOXO1,GRB7,GRM4</i>	<0.0001	0.987	<0.0001
10	<i>PIK3CA,PIK3R1,AKT1,BCL2L11,ERBB3,ARID1B,CD79A,GRB7,GRM4,SUFU</i>	<0.0001	0.993	<0.0001	
Ovarian_M / Endometrial_M	10	<i>AXL,BAP1,CDK12,GRIN2A,JAK3,KDM5A,MSH2,NF1,PTPRS,TET2</i>	0.025	1	<0.0001

Table S 5.1.14. Significant common driver gene set between Breast_M, Endometrial_M and Ovarian_M

k	common gene set	p1	p2	p3	q
5	<i>TP53,CDH1,CTNNB1,GATA3,KRAS</i>	<0.0001	<0.0001	<0.0001	<0.0001
6	<i>TP53,CDH1,CTNNB1,GATA3,KRAS,CDKN1B</i>	<0.0001	<0.0001	<0.0001	<0.0001
7	<i>TP53,CDH1,CTNNB1,GATA3,KRAS,CDKN1B,CDC73</i>	<0.0001	<0.0001	<0.0001	<0.0001
8	<i>TP53,CDH1,CTNNB1,GATA3,KRAS,CDKN1B,CDC73,RAD51C</i>	<0.0001	<0.0001	<0.0001	<0.0001
9	<i>TP53,CDH1,CTNNB1,GATA3,KRAS,MYOD1,CDC73,RAD51C,PRKAR1A</i>	<0.0001	<0.0001	<0.0001	<0.0001
10	<i>TP53,CDH1,CTNNB1,GATA3,KRAS,MYOD1,CDC73,RAD51C,PRKAR1A,TMPRSS2</i>	<0.0001	<0.0001	<0.0001	<0.0001

5.2 Male-Bladder, Prostate cancer and Renal cell carcinoma

Primary cancers

*There is no significant common driver gene set between Bladder_P and Prostate_P when $k=2 \sim 10$.

Table S 5.2.1. Significant common driver gene set between Bladder_P and Renal_P

k	common gene set	p1	p2	q
5	<i>AKT3, TERT, TFE3, VHL, PTCH1</i>	0.034	0.015	<0.0001
6	<i>AKT3, TERT, TFE3, VHL, ATRX, NF2</i>	0.024	<0.0001	<0.0001
7	<i>AKT3, TERT, TFE3, VHL, ATRX, NF2, TAFA2</i>	0.007	0.003	<0.0001
8	<i>AKT3, TERT, TFE3, VHL, ATRX, NF2, TNIP2, HCN1</i>	0.005	<0.0001	<0.0001
9	<i>AKT3, TERT, TFE3, VHL, ATRX, NF2, HIST1H3E, RAD52, VPS35</i>	0.002	0.001	<0.0001
10	<i>AKT3, TERT, TFE3, VHL, ATRX, NF2, HIST1H3E, TNFRSF14, VCL, HCN1</i>	0.002	<0.0001	<0.0001

Table S 5.2.2. Significant common driver gene set between Prostate_P and Renal_P

k	common gene set	p1	p2	q
5	<i>FOXA1, NF2, SPOP, TMPRSS2, VHL</i>	<0.0001	0.016	<0.0001
6	<i>FOXA1, NF2, SPOP, TMPRSS2, VHL, PTEN</i>	<0.0001	0.009	<0.0001
7	<i>FOXA1, NF2, SPOP, TMPRSS2, VHL, PTEN, MET</i>	<0.0001	<0.0001	<0.0001
8	<i>FOXA1, NF2, SPOP, TMPRSS2, VHL, PTEN, MET, KMT2A</i>	<0.0001	<0.0001	<0.0001
9	<i>FOXA1, NF2, SPOP, TMPRSS2, VHL, PTEN, MET, KMT2A, BRAF</i>	<0.0001	<0.0001	<0.0001
10	<i>FOXA1, NF2, SPOP, TMPRSS2, VHL, PTEN, MET, NOTCH4, BRAF, TFE3</i>	<0.0001	<0.0001	<0.0001

*There is no significant common driver gene set among Bladder_P, Prostate_P and Renal_P when $k=2 \sim 10$.

Table S 5.2.3. Bladder_P and Prostate_P specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Bladder_P / Prostate_P	3	<i>ATRX, TERT, CTLA4</i>	<0.0001	0.983	0.002
	4	<i>ATRX, TERT, CTLA4, FOXP1</i>	<0.0001	0.96	0.001
	5	<i>ATRX, TERT, BAP1, STAG2, TGFBR1</i>	0.01	0.995	0.002
	6	<i>ATRX, TERT, BAP1, STAG2, TGFBR1, COP1</i>	0.008	0.997	0.004
	7	<i>ATRX, TERT, BAP1, STAG2, TGFBR1, COP1, SMAD3</i>	0.002	0.996	0.001
	9	<i>ATRX, TERT, COP1, ERCC5, FBXW7, KDM6A, NFE2L2, TGFBR1, AKT3</i>	0.041	1	0.003
	10	<i>ATRX, TERT, COP1, ERCC5, FBXW7, KDM6A, NFE2L2, TGFBR1, AKT3, BAP1</i>	0.039	1	0.003
Prostate_P / Bladder_P	2	<i>SPOP, TMPRSS2</i>	<0.0001	0.999	<0.0001
	3	<i>SPOP, TMPRSS2, FOXA1</i>	<0.0001	0.995	<0.0001
	4	<i>SPOP, TMPRSS2, FOXA1, MAP2K4</i>	<0.0001	1	<0.0001
	5	<i>SPOP, TMPRSS2, FOXA1, PTEN, PGR</i>	<0.0001	1	<0.0001
	6	<i>SPOP, TMPRSS2, FOXA1, PTEN, GSK3B, NKX2-1</i>	<0.0001	1	<0.0001
	7	<i>SPOP, TMPRSS2, FOXA1, PTEN, GSK3B, PGR, EIF1AX</i>	<0.0001	1	<0.0001
	8	<i>SPOP, TMPRSS2, FOXA1, PTEN, GSK3B, PGR, EIF1AX, NKX2-1</i>	<0.0001	1	<0.0001
	9	<i>SPOP, TMPRSS2, FOXA1, PTEN, GSK3B, PGR, EIF1AX, NKX2-1, SYF2</i>	<0.0001	1	<0.0001
	10	<i>SPOP, TMPRSS2, FOXA1, PTEN, GSK3B, PGR, EIF1AX, NKX2-1, SPPL3, ANTXR2</i>	<0.0001	1	<0.0001

Table S 5.2.4. Bladder_P and Renal_P specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Bladder_P / Renal_P	2	<i>TERT,PTCH1</i>	0.011	0.755	0.026
	3	<i>TERT,ATRX,CTLA4</i>	0.002	0.734	0.001
	4	<i>TERT,CDKN2A,FOXP1,KRAS</i>	0.003	1	0.001
	5	<i>TP53,ERBB2,FGFR3,HRAS,KRAS</i>	<0.0001	0.951	<0.0001
	6	<i>TP53,ERBB2,FGFR3,HRAS,KRAS,ATR</i>	<0.0001	0.907	<0.0001
	7	<i>TP53,ERBB2,FGFR3,HRAS,KRAS,CDKN1A,CDKN2A</i>	<0.0001	0.952	<0.0001
	8	<i>TP53,ERBB2,FGFR3,HRAS,KRAS,CDKN1A,CDKN2A,BLM</i>	<0.0001	0.939	<0.0001
	9	<i>TP53,MAPK1,FGFR3,HRAS,KRAS,CDKN1A,IFNGR1,KDM6A,NFE2L2</i>	<0.0001	0.869	<0.0001
	10	<i>TP53,MAPK1,FGFR3,HRAS,KRAS,CDKN1A,IFNGR1,KDM6A,NFE2L2,YES1</i>	<0.0001	0.857	<0.0001
	Renal_P / Bladder_P	3	<i>NF2,TFE3,VHL</i>	0.001	0.92
4		<i>NF2,TFE3,VHL,ELOC</i>	<0.0001	0.923	<0.0001
5		<i>KEAP1,NF2,PBRM1,RPS6KA4,SFPQ</i>	0.011	1	<0.0001
6		<i>KEAP1,PAK5,PBRM1,RPS6KA4,SFPQ,CDKN2B</i>	0.046	1	<0.0001
8		<i>KEAP1,PAK5,PBRM1,RPS6KA4,SFPQ,CDKN2B,PIK3CG,TBX3</i>	0.049	1	<0.0001
9		<i>KEAP1,PAK5,PBRM1,RPS6KA4,SFPQ,CDKN2B,PIK3CG,TBX3,TRAF2</i>	0.032	1	<0.0001
10		<i>KEAP1,PAK5,PBRM1,RPS6KA4,SFPQ,CDKN2B,PIK3CG,TBX3,PIM1,FH</i>	0.015	1	<0.0001

Table S 5.2.5. Prostate_P and Renal_P specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Prostate_P / Renal_P	2	<i>SPOP, TMPRSS2</i>	<0.0001	1	<0.0001
	3	<i>SPOP, TMPRSS2, FOXA1</i>	<0.0001	1	<0.0001
	4	<i>SPOP, TMPRSS2, FOXA1, CDK12</i>	<0.0001	1	<0.0001
	5	<i>APC, BRCA2, CDK12, CTNNB1, ERG</i>	0.004	0.97	<0.0001
	8	<i>TP53, APC, BRCA2, CDK12, CTNNB1, ERG, PTPRD, ZFH3</i>	0.048	0.861	0.045
	9	<i>TP53, APC, BRCA2, CDK12, CTNNB1, ERG, PTPRD, ZFH3, CUL3</i>	0.021	0.988	0.012
	10	<i>TP53, APC, BRCA2, CDK12, CTNNB1, ERG, PTPRD, ZFH3, CUL3, IDH1</i>	0.01	0.989	0.003
Renal_P / Prostate_P	2	<i>NF2, VHL</i>	0.008	1	0.007
	3	<i>NF2, VHL, TFE3</i>	0.001	1	<0.0001
	4	<i>NF2, VHL, TERT, TSC2</i>	0.004	0.998	0.002

Metastatic cancers

Table S 5.2.6. Significant common driver gene set between Bladder_M and Prostate_M

k	common gene set	p1	p2	q
4	<i>TP53,CDK12,FGFR3,BRCA2</i>	0.026	<0.0001	<0.0001
5	<i>TP53,CDK12,FGFR3,BRCA2,PIK3R1</i>	0.039	<0.0001	<0.0001
6	<i>TP53,CDK12,FGFR3,BRD4,APC,FLT4</i>	0.018	<0.0001	<0.0001
7	<i>TP53,CDK12,FGFR3,BRD4,APC,DICER1,FLT4</i>	0.025	<0.0001	<0.0001
8	<i>TP53,CDK12,FGFR3,BRD4,APC,DICER1,FLT4,FGFR1</i>	0.01	<0.0001	<0.0001
9	<i>TP53,CDK12,FGFR3,BRD4,APC,DICER1,FLT4,FGFR1,CSF1R</i>	0.01	<0.0001	<0.0001
10	<i>TP53,CDK12,FGFR3,BRD4,APC,DICER1,FLT3,CHEK2,LINC00114,SMO</i>	0.002	<0.0001	<0.0001

Table S 5.2.7. Significant common driver gene set between Bladder_M and Renal_M

k	common gene set	p1	p2	q
5	<i>KRAS,NF2,TERT,TSC2,VHL</i>	0.004	<0.0001	<0.0001
6	<i>KRAS,NF2,TERT,TSC2,VHL,TFE3</i>	0.009	<0.0001	<0.0001
7	<i>KRAS,NF2,TERT,TSC2,VHL,TFE3,SMAD4</i>	<0.0001	<0.0001	<0.0001
8	<i>KRAS,NF2,TERT,TSC2,VHL,TFE3,SMAD4,SMAD3</i>	<0.0001	<0.0001	<0.0001
9	<i>KRAS,NF2,TERT,TSC2,VHL,TFE3,SMAD4,GPS2,ALOX12B</i>	<0.0001	<0.0001	<0.0001
10	<i>KRAS,NF2,TERT,TSC2,VHL,TFE3,SMAD4,GPS2,SMAD3,NRAS</i>	<0.0001	<0.0001	<0.0001

Table S 5.2.8. Significant common driver gene set between Prostate_M and Renal_M

k	common gene set	p1	p2	q
3	<i>TP53,CDK12,VHL</i>	<0.0001	0.004	<0.0001
4	<i>TP53,CDK12,VHL,APC</i>	<0.0001	0.002	<0.0001
5	<i>TP53,CDK12,VHL,APC,NF2</i>	<0.0001	<0.0001	<0.0001
6	<i>TP53,CDK12,VHL,APC,NF2,KDM6A</i>	<0.0001	<0.0001	0.002
7	<i>TP53,CDK12,VHL,APC,NF2,KDM6A,FGFR3</i>	<0.0001	<0.0001	<0.0001
8	<i>TP53,CDK12,VHL,APC,NF2,KDM6A,FGFR3,MEN1</i>	<0.0001	0.001	<0.0001
9	<i>TP53,CDK12,VHL,APC,NF2,KDM6A,FGFR3,MEN1,TFE3</i>	<0.0001	<0.0001	<0.0001
10	<i>TP53,CDK12,VHL,TERT,NF2,KDM6A,ERBB3,SPOP,TFE3,BRCA2</i>	<0.0001	<0.0001	<0.0001

Table S 5.2.9. Bladder_M and Prostate_M specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Bladder_M / Prostate_M	3	<i>TERT,NRAS,AKT2</i>	0.005	0.987	0.001
	5	<i>TERT,NRAS,CDKN1A,KRAS,RBM10</i>	0.011	0.997	0.004
	6	<i>TERT,NRAS,CDKN1A,KRAS,RBM10,H3F3A</i>	0.003	0.993	<0.0001
	7	<i>TERT,NRAS,CDKN1A,KRAS,RBM10,H3F3A,VTCN1</i>	0.003	0.996	0.002
	8	<i>TERT,NRAS,CDKN1A,KRAS,RBM10,H3F3A,VTCN1,ALOX12B</i>	0.001	0.993	<0.0001
	9	<i>TERT,NRAS,CDKN1A,KRAS,RBM10,H3F3A,VTCN1,ALOX12B,SRC</i>	<0.0001	0.998	<0.0001
	10	<i>TERT,NRAS,CDKN1A,KRAS,RBM10,H3F3A,VTCN1,ALOX12B,SRC,SRSF2</i>	<0.0001	0.988	<0.0001
Prostate_M / Bladder_M	2	<i>FOXA1,TMPRSS2</i>	0.01	1	0.014
	3	<i>FOXA1,TMPRSS2,AR</i>	<0.0001	0.91	<0.0001
	4	<i>FOXA1,TMPRSS2,PTEN,SPOP</i>	0.002	0.873	0.001
	5	<i>FOXA1,TMPRSS2,PTEN,SPOP,AR</i>	0.011	0.719	0.008
	6	<i>FOXA1,TMPRSS2,PTEN,SPOP,AR,PIK3R1</i>	0.018	0.705	0.015
	7	<i>FOXA1,TMPRSS2,PTEN,SPOP,AR,PIK3R1,CDKN1B</i>	0.009	0.721	0.012
	8	<i>FOXA1,TMPRSS2,PTEN,SPOP,AR,PIK3R1,CDKN1B,MALT1</i>	0.005	0.698	0.003
	9	<i>FOXA1,TMPRSS2,PTEN,SPOP,AR,PIK3R1,CDKN1B,MALT1,INPP4B</i>	0.003	0.721	0.002
	10	<i>FOXA1,TMPRSS2,PTEN,SPOP,AR,PIK3R1,CDKN1B,MALT1,INPP4B,BRAF</i>	0.007	0.913	0.01

Table S 5.2.10. Bladder_M and Renal_M specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Bladder_M / Renal_M	2	<i>KRAS, TERT</i>	0.006	0.992	0.005
	3	<i>KRAS, TERT, SMAD3</i>	0.003	0.992	<0.0001
	4	<i>KRAS, TERT, KDM6A, NRAS</i>	0.014	0.908	0.006
	6	<i>CDKN1A, ERBB3, KDM6A, RB1, PTPRD, KMT2D</i>	0.013	0.988	0.007
	7	<i>CDKN1A, ERBB3, KDM6A, RB1, RPTOR, CREBBP, INSR</i>	0.004	1	0.001
	8	<i>CDKN1A, ERBB3, KDM6A, RB1, RPTOR, CREBBP, INSR, KDM5A</i>	0.001	1	<0.0001
	9	<i>CDKN1A, ERBB3, KDM6A, RB1, RPTOR, CREBBP, INSR, KDM5A, ERCC2</i>	0.002	1	<0.0001
	10	<i>CDKN1A, ERBB3, KDM6A, RB1, RPTOR, CREBBP, INSR, KDM5A, ERCC2, EWSR1</i>	0.002	1	<0.0001
Renal_M / Bladder_M	2	<i>NF2, VHL</i>	0.001	0.928	0.004
	3	<i>NF2, VHL, MET</i>	<0.0001	0.947	<0.0001
	4	<i>NF2, VHL, MET, TFE3</i>	<0.0001	0.946	<0.0001

Table S 5.2.11. Prostate_M and Renal_M specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Prostate_M / Renal_M	2	<i>FOXA1, TMPRSS2</i>	0.008	1	0.018
	3	<i>FOXA1, TMPRSS2, AR</i>	0.001	1	0.001
	4	<i>FOXA1, TMPRSS2, AR, SPOP</i>	<0.0001	1	<0.0001
	5	<i>FOXA1, TMPRSS2, AR, SPOP, KDM6A</i>	<0.0001	0.983	0.001
	6	<i>FOXA1, TMPRSS2, AR, SPOP, KMT2C, EPHA3</i>	<0.0001	0.992	<0.0001
	7	<i>FOXA1, TMPRSS2, AR, SPOP, KMT2C, EPHA3, EPHA5</i>	<0.0001	0.997	<0.0001
	8	<i>FOXA1, TMPRSS2, AR, SPOP, KMT2C, EPHA3, EPHA5, NCOR1</i>	<0.0001	1	<0.0001
	9	<i>FOXA1, TMPRSS2, AR, SPOP, KMT2C, EPHA3, EPHA5, NCOR1, BRCA2</i>	<0.0001	0.999	<0.0001
	10	<i>FOXA1, TMPRSS2, AR, KMT2D, KMT2C, EPHA3, EPHA5, NCOR1, EPHB1, RPTOR</i>	<0.0001	1	<0.0001
	Renal_M / Prostate_M	2	<i>NF2, VHL</i>	0.007	1
3		<i>BAP1, PBRM1, TERT</i>	0.007	0.987	0.001
4		<i>BAP1, PBRM1, TERT, NF2</i>	0.001	0.992	<0.0001
5		<i>BAP1, PBRM1, TERT, SMARCB1, KDM5C</i>	0.003	0.996	<0.0001
6		<i>BAP1, PBRM1, TERT, SMARCB1, TSC1, SETD2</i>	0.042	0.998	0.016
7		<i>BAP1, PBRM1, TERT, SMARCB1, TSC1, SETD2, IL10</i>	0.011	0.987	0.007
8		<i>BAP1, PBRM1, TERT, SMARCB1, TSC1, SETD2, IL10, TFE3</i>	0.01	0.99	0.003
9		<i>BAP1, PBRM1, TERT, SMARCB1, TSC1, SETD2, IL10, TSC2, DNMT1</i>	0.002	1	<0.0001
10		<i>BAP1, PBRM1, MET, SMARCB1, TSC1, SETD2, IL10, TSC2, DNMT1, INPP4A</i>	0.042	1	0.001

Table S 5.2.12. Significant common driver gene set among Bladder_M, Prostate_M and Renal_M

k	common gene set	p1	p2	p3	q
4	<i>TP53,CDK12,FGFR3,VHL</i>	0.005	<0.0001	0.005	<0.0001
5	<i>TP53,CDK12,FGFR3,VHL,BRCA2</i>	0.005	<0.0001	0.008	<0.0001
6	<i>TP53,CDK12,FGFR3,VHL,BRCA2,NF2</i>	0.031	<0.0001	<0.0001	<0.0001
7	<i>TP53,CDK12,FGFR3,VHL,BRCA2,MET,TFE3</i>	0.006	<0.0001	<0.0001	<0.0001
8	<i>TP53,CDK12,FGFR3,VHL,BRCA2,MET,TFE3,NF2</i>	0.029	<0.0001	<0.0001	<0.0001
9	<i>TP53,CDK12,FGFR3,VHL,BRCA2,MET,TFE3,DIS3,PPM1D</i>	0.004	<0.0001	<0.0001	<0.0001
10	<i>TP53,CDK12,FGFR3,VHL,BRCA2,MET,TFE3,DIS3,PPM1D,LINC00114</i>	0.002	<0.0001	<0.0001	<0.0001

5.3 Esophagogastric & Gastrointestinal Stromal tumor

Primary cancers

Table S 5.3.1. Significant common driver gene set between Esophagogastric_P and GastrointestinalStromal_P

k	common gene set	p1	p2	p3	q
4	<i>TP53,CDK12,FGFR3,VHL</i>	0.005	<0.0001	0.005	<0.0001
5	<i>TP53,CDK12,FGFR3,VHL,BRCA2</i>	0.005	<0.0001	0.008	<0.0001
6	<i>TP53,CDK12,FGFR3,VHL,BRCA2,NF2</i>	0.031	<0.0001	<0.0001	<0.0001
7	<i>TP53,CDK12,FGFR3,VHL,BRCA2,MET,TFE3</i>	0.006	<0.0001	<0.0001	<0.0001
8	<i>TP53,CDK12,FGFR3,VHL,BRCA2,MET,TFE3,NF2</i>	0.029	<0.0001	<0.0001	<0.0001
9	<i>TP53,CDK12,FGFR3,VHL,BRCA2,MET,TFE3,DIS3,PPM1D</i>	0.004	<0.0001	<0.0001	<0.0001
10	<i>TP53,CDK12,FGFR3,VHL,BRCA2,MET,TFE3,DIS3,PPM1D,LINC00114</i>	0.002	<0.0001	<0.0001	<0.0001

*Esophagogastric_P has no specific mutated driver gene sets relative to GastrointestinalStromal_P when k=2 ~ 10.

*GastrointestinalStromal_P has no specific mutated driver gene sets relative to Esophagogastric_P when k=2 ~ 10.

Metastatic cancers

Table S 5.3.2. Significant common driver gene set between Esophagogastric_M and GastrointestinalStromal_M

k	common gene set	p1	p2	q
2	<i>TP53,BCOR</i>	0.018	0.016	0.001
3	<i>TP53,BCOR,TGFBR1</i>	<0.0001	0.001	<0.0001
4	<i>TP53,BCOR,TGFBR1,STK11</i>	<0.0001	<0.0001	<0.0001
5	<i>TP53,BCOR,TGFBR1,FGFR2,TGFBR2</i>	<0.0001	<0.0001	<0.0001
6	<i>TP53,BCOR,TGFBR1,FGFR2,TGFBR2,BRCA1</i>	<0.0001	<0.0001	<0.0001
7	<i>TP53,BCOR,TGFBR1,FGFR2,TGFBR2,NTRK3,PRKAR1A</i>	<0.0001	<0.0001	<0.0001
8	<i>TP53,BCOR,TGFBR1,FGFR2,CCDC6,STK11,PRKAR1A,CMIP</i>	<0.0001	<0.0001	<0.0001
9	<i>TP53,BCOR,TGFBR1,FGFR2,NTRK3,BRCA1,PRKAR1A,CMIP,REL</i>	<0.0001	<0.0001	<0.0001
10	<i>TP53,BCOR,TGFBR1,FGFR2,NTRK3,BRCA1,CCDC6,CMIP,HGF,STK11</i>	<0.0001	<0.0001	<0.0001

*Esophagogastric_M has no specific mutated driver gene sets relative to GastrointestinalStromal_M when k=2 ~ 10.

*GastrointestinalStromal_M has no specific mutated driver gene sets relative to Esophagogastric_M when k=2 ~ 10.

5.4 melamona & skin cancer

Primary cancers *There is no significant common driver gene set between Melamona_P and Skin_P when $k=2 \sim 10$.

Table S 5.4.1. Melamona_P specific mutated driver gene sets relative to Skin_P

k	Specific gene set	p1	p2	q
4	<i>BRAF,GNA11,GNAQ,NRAS</i>	0.001	0.927	0.006
5	<i>BRAF,GNA11,GNAQ,NRAS,RAC1</i>	0.003	1	0.001
6	<i>BRAF,GNA11,GNAQ,NRAS,KIT,GATA1</i>	<0.0001	0.998	<0.0001
7	<i>BRAF,GNA11,GNAQ,NRAS,KIT,GATA1,IRS1</i>	<0.0001	1	<0.0001
8	<i>BRAF,GNA11,GNAQ,NRAS,KIT,GATA1,IRS1,B2M</i>	<0.0001	1	<0.0001
9	<i>BRAF,GNA11,GNAQ,NRAS,KIT,GATA1,ETV6,B2M,PDGFRA</i>	<0.0001	1	<0.0001
10	<i>BRAF,GNA11,GNAQ,NRAS,KIT,GATA1,IRS1,B2M,PDGFRA,PAK1</i>	<0.0001	1	<0.0001

*Skin_P has no specific mutated driver gene sets relative to Melamona_P when $k=2 \sim 10$.

Metastatic cancers *There is no significant common driver gene set between Melamona_M and Skin_M when k=2 ~ 10.

Table S 5.4.2. Melamona_M and Skin_M specific mutated driver gene sets relative to each other

Type	k	Specific gene set	p1	p2	q
Melamona_M / Skin_M	2	<i>BRAF,NRAS</i>	<0.0001	0.885	<0.0001
	3	<i>BRAF,NRAS,GNAQ</i>	<0.0001	0.88	<0.0001
	4	<i>BRAF,NRAS,GNAQ,NF1</i>	<0.0001	0.97	<0.0001
	5	<i>BRAF,NRAS,GNAQ,NF1,GNA11</i>	<0.0001	0.967	<0.0001
	6	<i>BRAF,NRAS,GNAQ,NF1,GNA11,KIT</i>	<0.0001	0.997	<0.0001
	7	<i>BRAF,NRAS,GNAQ,NF1,GNA11,KIT,MAP2K1</i>	<0.0001	1	<0.0001
	8	<i>BRAF,NRAS,GNAQ,NF1,GNA11,KIT,MAP2K1,SDHA</i>	<0.0001	1	<0.0001
	9	<i>BRAF,NRAS,GNAQ,NF1,GNA11,KIT,MAP2K1,SDHA,PIM1</i>	<0.0001	1	<0.0001
	10	<i>BRAF,NRAS,GNAQ,NF1,GNA11,KIT,MAP2K1,SDHA,PIM1,BCL2L14</i>	<0.0001	1	<0.0001
Skin_M / Melamona_M	7	<i>HOXB13,IRS1,MAX,MYOD1,SMARCB1,STK11,TRAF7</i>	0.008	1	<0.0001
	8	<i>HOXB13,IRS1,MAX,MYOD1,SMARCB1,STK11,TRAF7,MYD88</i>	0.005	1	<0.0001
	9	<i>HOXB13,IRS1,MAX,MYOD1,SMARCB1,STK11,TRAF7,MYD88,BBC3</i>	0.004	1	<0.0001
	10	<i>HOXB13,IRS1,MAX,MYOD1,SMARCB1,STK11,TRAF7,MYD88,BBC3,NFKBIA</i>	0.002	1	<0.0001